The natural history of clonal haematopoiesis

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Declaration

This thesis is the result of my own work and includes nothing which is the outcome of work done in collaboration except as declared in the Acknowledgements and specified in the text. I further state that no substantial part of my thesis has already been submitted, or, is being concurrently submitted for any such degree, diploma or other qualification at the University of Cambridge or any other University or similar institution except as declared in the Preface and specified in the text. It does not exceed the prescribed word limit (60,000 words).

Summary

The natural history of clonal haematopoiesis

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Introduction. Human cells acquire somatic mutations throughout life, some of which can drive clonal expansion. Such expansions are frequent in the haematopoietic system of healthy individuals and have been termed clonal haematopoiesis (CH). While CH predisposes to myeloid neoplasia and other diseases, we have limited understanding of its natural history and how this relates to clinical phenotype.

Objectives
1. To characterise the behaviour of CH across the human lifespan;
2. To identify and quantify determinants of clonal behaviour;
3. To understand how CH clonal dynamics relate to malignant progression.

Results. By tracking 697 CH clones from 385 individuals aged 55 or older over a median of 13 years, we found that 92.4% of clones expanded at a stable exponential rate in old age, with different mutations driving substantially different growth rates, ranging from 5% (*DNMT3A*, *TP53*) to over 50%/yr (*SRSF2*-P95H). Growth rates of clones with the same mutation differed by +/-5%/yr, proportionately impacting "slow" drivers more substantially.

Combining these time-series data with phylogenetic analysis of 1,731 whole genome-sequenced haematopoietic colonies from 7 older individuals revealed distinct patterns of lifelong clonal behaviour. *DNMT3A*-mutant clones preferentially expanded early in life and displayed slower growth in old age, in the context of an increasingly competitive oligoclonal landscape. By contrast, splicing gene mutations only drove expansion later in life, while *TET2*-mutant clones emerged across all ages.

Using a separate cohort of 158 twins, we found that concordance for CH was no higher within monozygotic vs dizygotic pairs, suggesting that the inherited genome does not exert a dominant influence on CH behaviour. The identification of two monozygotic pairs in which both twins harboured identical rare somatic mutations confirmed that the origins of adult CH can be traced back to early life, even *in utero*.

Finally, by comparing CH growth dynamics with (i) driver mutation selection patterns in large myeloid cancer data sets and (ii) driver-specific AML risk scores, we show that mutations driving faster clonal growth also carry a higher risk of malignant progression.

Conclusions. These findings characterise the origins and lifelong natural history of CH and give fundamental insights into the interactions between somatic mutation, ageing and clonal selection.

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Abbreviations

ALL	Acute lymphoblastic leukaemia
AML	Acute myeloid leukaemia
ARCH	Age-related clonal haematopoiesis
ASXL1	ASXL transcriptional regulator 1
bp	Base pair
CCUS	Clonal cytopenia of undetermined significance
CH	Clonal haematopoiesis
CHIP	Clonal haematopoiesis of indeterminate significance
CLL	Chronic lymphocytic leukaemia
CML	Chronic myeloid leukaemia
CNA	Copy number aberration
COPD	Chronic obstructive pulmonary disease
DDR	DNA damage response
DNA	Deoxyribonucleic acid
DNMT3A	DNA methyltransferase 3 alpha
DS-AMKL	Down Syndrome-Acute Megakaryoblastic Leukaemia
DZ	Dizygotic
HB	Haemoglobin
HCC	Hepatocellular carcinoma
HDAC	Histone deacetylase
HMC	Hamiltonian Monte Carlo
HSC	Haematopoietic stem cell
HSPC	Haematopoietic stem and progenitor cell
ICUS	Idiopathic cytopenia of undetermined significance
IFNγ	Interferon gamma
IL	Interleukin
JAK	Janus kinase 2
LOH	Loss of heterozygosity
LOY	Loss of Y-chromosome
LYMPH	Lymphocytes
MAE	Mean absolute error
MBL	Monoclonal B-cell lymphocytosis
mCA	Mosaic chromosomal alteration
MCMC	Markov Chain Monte Carlo

MCV	Mean cell volume
MDS	Myelodysplastic syndrome
MGUS	Monoclonal gammopathy of undetermined significance
MM	Multiple myeloma
MONO	Monocytes
MPN	Myeloproliferative neoplasm
MRCA	Most recent common ancestor
MZ	Monozygotic
Neff	Effective population size
NEUT	Neutrophils
NGS	Next-generation sequencing
PCR	Polymerase chain reaction
PGF	Placental Growth Factor
PLT	Platelets
PPM1D	Protein phosphatase Mg2+/Mn2+ dependent 1D
PRC	Polycomb repressive complex
RDW	Red cell distribution width
REC	Research ethics committee
RNA	Ribonucleic acid
SF3B1	Splicing factor 3b subunit 1
SNP	Single nucleotide polymorphism
SNV	Single nucleotide variant
SRSF2	Serine and arginine rich splicing factor 2
TET2	Tet methylcytosine dioxygenase 2
TNFα	Tumour necrosis factor alpha
TP53	Tumour protein P53
U2AF1	U2 small nuclear RNA auxillary factor 1
VAF	Variant allele fraction
WBC	White blood cells

Chapter 1

Introduction

"*…if variations useful to any organic being do occur, assuredly individuals thus characterised will have the best chance of being preserved in the struggle for life; and from the strong principle of inheritance they will tend to produce offspring similarly characterised. This principle of preservation, I have called, for the sake of brevity, Natural Selection*."[1]

While Charles Darwin set out this theory of evolution in relation to the adaptation of biological organisms over generations, the same fundamental principles apply to the microcosm in which haematopoietic stem cells (HSCs) operate over the lifetime of a single individual.

From the moment a human zygote undergoes its first cell division, its genetic material is susceptible to alteration, such that the DNA sequences of its two daughter cells might not be identical. This process of somatic mutation acquisition continues inexorably through life in all tissues, including in the haematopoietic system[2–8]. In young individuals, the absolute number of mutations in HSCs is small; diversity in the pool is therefore low and these relatively homogeneous stem cells exist in a rich bone marrow environment. In this setting, the forces of Darwinian selection are weak and many or all of the 50-200,000 HSCs will be equally adept at self-renewal and production of mature blood cell progeny. In contrast, by old age, the passage of time has allowed substantial accumulation of somatic mutations - it is estimated that a typical 70-year-old human harbours up to 70 mutations per protein-coding gene across the HSC population - giving rise to considerable diversity in the stem cell pool[3–6]. These conditions are ideal for strong natural selection, with functionally variable HSCs now existing in a bone marrow niche altered by ageing[9]. In line with Darwin's theory of evolution, the particular HSCs best suited to the ageing niche "will have the best chance of being preserved in the struggle for life", and their cognate clones will expand relative to those less fit. This relative fitness advantage and subsequent expansion is the defining feature of clonal haematopoiesis (CH).

1.1 A historical perspective on clonal haematopoiesis

Blood cancers are the prototypical example of CH, and their clonal nature was first demonstrated by karyotypic analyses in the 1970s[10]. However, it would be a further two decades until CH was discovered in individuals without cancer. An elegant study in the 1990s utilised the fact that one X-chromosome is randomly inactivated in each cell during female embryonic development and that this epigenetic state is stably maintained across cell divisions. The observation that some women possessed skewed allelic ratios of X inactivation in blood cells, and that the likelihood of this increased with advancing age, was suggestive of a clonal process[11]. The fact that mutant clones might be pre-malignant was first suggested in 2000, with the detection of a leukaemia driver mutation, an AML1/ETO translocation, in a fraction of phenotypically normal HSCs and mature blood cells in AML remission samples[12].

The first demonstration that mutation-driven CH can occur in healthy individuals came in 2012, when mutations in *TET2* (a gene coding for an enzyme that oxidises methylated DNA) were found in some elderly women with non-random X inactivation[13]. The existence of this phenomenon was crystallised two years later, with the examination of whole exome sequencing data from the peripheral blood DNA of more than 30,000 individuals unselected for haematological phenotypes[14–16]. Here, given the tens of thousands of HSCs contributing to the mature blood cell pool and the limited sensitivity of mutation-calling, it can be assumed that any mutation that has reached detectable levels in blood DNA must be present in an expanded clone. Given the huge number of possible mutations across the genome, it follows that if the same mutations are recurrently identified across different individuals, these are likely to have been under selective pressure and to have actually caused the clonal expansion. These so-called 'driver mutations' contrast with 'passenger mutations', which are neutral to HSC fitness and, if detectable in blood DNA, are present by chance, having been carried along on an expanding clone rather than having caused its expansion[2,17,18].

These whole exome studies were illuminating for two main reasons. *Firstly*, driver mutations were rare in young people and became progressively more prevalent with advancing age. *Secondly*, over 95% of mutations occurred in just 8 driver genes, coding for enzymes involved in DNA methylation (*DNMT3A* and *TET2*) and chromatin regulation (*ASXL1*), proteins involved in cellular growth signalling (*JAK2*) and the DNA damage response (*TP53*, *PPM1D*), and splicing factors (*SF3B1*, *SRSF2*) (Fig 1.1). Most of these genes were already known to be frequently mutated in adult myeloid malignancies.

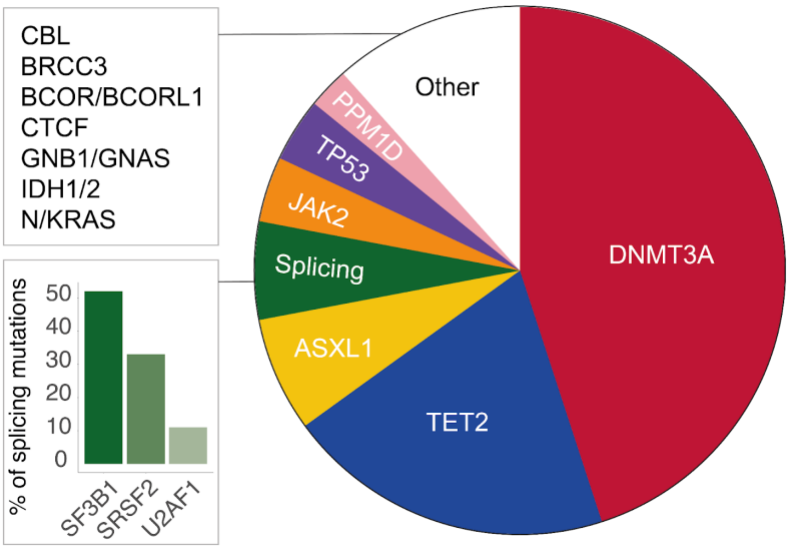


Figure 1.1: Relative prevalence of mutations in different CH driver genes. Proportions vary between studies, due mainly to differences in age distribution, but also to sequencing technology / depth of coverage. For this reason, specific percentages are not given and the depicted fractions reflect the general consensus from the majority of studies that analysed individuals with an average age of ~60 years. Driver genes in the "Other" segment are much less commonly found in CH than the individually labelled genes on the pie chart. The list of "Other" driver genes given in the adjacent box is not exhaustive, but includes the more recurrent members of this group.

1.2 Defining clonal haematopoiesis

While there is consensus that CH constitutes the over-representation of blood cells derived from a single clone, the precise definition remains a matter of some debate and a series of related descriptors have been used[19]. CH of indeterminate potential (CHIP) and age-related CH (ARCH) can be regarded as technical terms rather than clinical states, characterised by the presence of a somatic driver mutation without cytopenia. Idiopathic cytopenia of undetermined significance (ICUS) and clonal cytopenia of undetermined significance (CCUS) are clinical conditions, both defined by the presence of at least one cytopenia in the context of a normal bone marrow examination, and only the latter by the detection of a somatic driver mutation[20–22].

Importantly, all of these descriptors require that a minimum clone size (or variant allele fraction, VAF) is stipulated to define whether or not an individual possesses a bona fide somatic mutation that is driving a biologically and/or clinically meaningful clonal expansion[20]. Whether or not an expanded clone is detectable depends on the sequencing technology used, and crucially on depth of coverage achieved, as illustrated in Figure 1.2. A minimum VAF of 2% (corresponding to 4% of cells for heterozygous mutations) has been suggested as a useful

cut-off, since clinical sequelae have been demonstrated for some individuals with clones larger than this threshold[16,20,23]. However, the VAF measured at a single point in time has limited value in determining the clinical significance of the associated clone, since it gives little indication of the clonal dynamics. Therefore, instead of arbitrarily stipulating minimum clone size, one can consider any somatic driver mutation detected by standard next-generation sequencing technologies as representing a clonal expansion and, as such, CH; decisions about clinical relevance require more nuanced consideration.

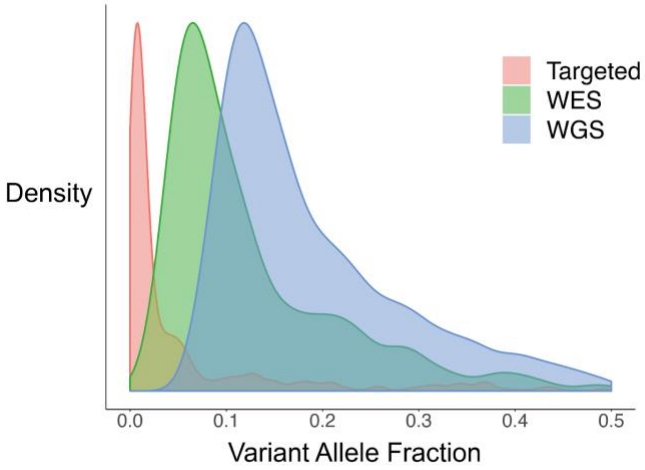


Figure 1.2: Scaled density plots for Variant Allele Fraction (VAF) of driver mutations. Distribution of VAFs of identified driver mutations using different sequencing methods, in descending order of depth of coverage: Targeted sequencing[24], Whole exome sequencing (WES)[16] and Whole Genome Sequencing (WGS)[25]. This demonstrates that smaller clones (with lower VAFs) are able to be detected when the depth of sequencing is higher.

One further point of classification concerns cell type. While monoclonal B-cell lymphocytosis (MBL) describes benign clonal lymphoid expansions[26], and monoclonal gammopathy of unknown significance (MGUS) reflects clonal plasma cell expansions[27], CH refers to clonal expansions with multilineage and predominantly myeloid cell output.

1.3 Mechanisms underlying clonal expansion

At the heart of any persistent clonal expansion is the increased self-renewal capacity of the HSC lying at the apex of its differentiation hierarchy[28]. A bias towards self-renewal generates

an imbalance such that the net effect, over time, is generation of more clonal HSCs. Stronger bias gives greater advantage and more marked clonal expansion (Fig. 1.3).

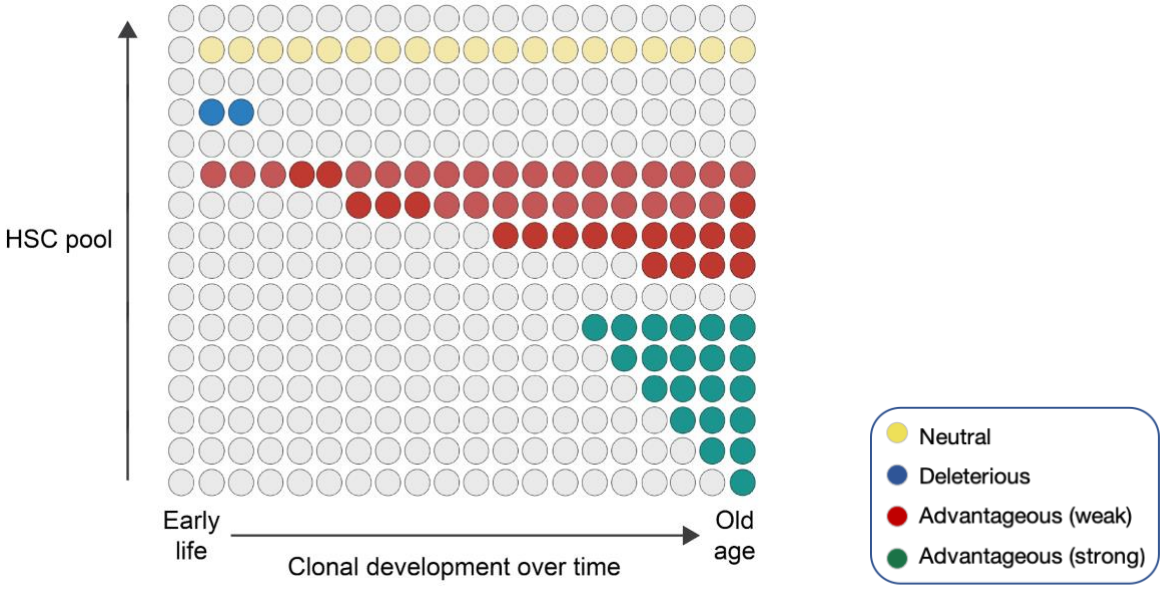


Figure 1.3: Clonal selection and its influence on HSC composition over life. In this schematic, an HSC is represented by a circle, the colour of which reflects the mutational status: non-grey depicts carriage of a potential somatic CH driver mutation, while grey depicts no such mutation. On the left side of the schematic, depicting early life, few somatic mutations have been acquired - in this example, none that drive clonal expansion - and the polyclonal HSC pool is relatively uniform. Over time, HSCs accumulate somatic mutations, which can impact fitness in a number of different ways: (1) Neutral (yellow) - these mutations do not alter fitness and there is no clonal expansion; (2) Deleterious (blue) - these mutations diminish fitness and affected HSCs are removed from the pool; (3) Advantageous - these mutations can confer a subtle advantage (red), in which case clonal expansion is slow and might only become evident many decades after mutation acquisition, or stronger advantage (green), when expansion is more rapid. It is important to note that, even among mutations that confer a fitness advantage, fixation of the mutant HSC clone in the pool and subsequent expansion is not inevitable, and many clones die out; a clone's chance of persistence is proportional to its fitness or growth rate. The lifelong process of selection and clonal expansion or extinction is universal, and haematopoiesis inevitably becomes oligoclonal by advanced old age.

While this shift in stem cell biology - a stronger tendency for self-renewal - is a prerequisite for persistent clonal expansion, the precise factors underlying it are complex and varied, with different mechanisms converging on this same fundamental tendency in different scenarios. It is believed that factors both *intrinsic* and *extrinsic* to HSCs contribute, with intricate interplay between the two in operation.

Ageing is one factor that impacts both HSCs themselves and the environment in which they reside, and remains the most clear clinical correlate with the development of CH[14–16,29,30]. The mere passage of time allows for somatic mutations to be acquired, and for mutant clones to expand to detectable levels. Indeed, the number and type of mutations found in CH and myeloid malignancies are identical to those found in normal aged HSCs, consistent with the premise that no additional mutagen operates in the aetiology of these clonal disorders[31,32].

This is unlike most other adult cancers, where specific mutagens cause larger numbers of particular types of mutation, as illustrated in Figure 1.4.

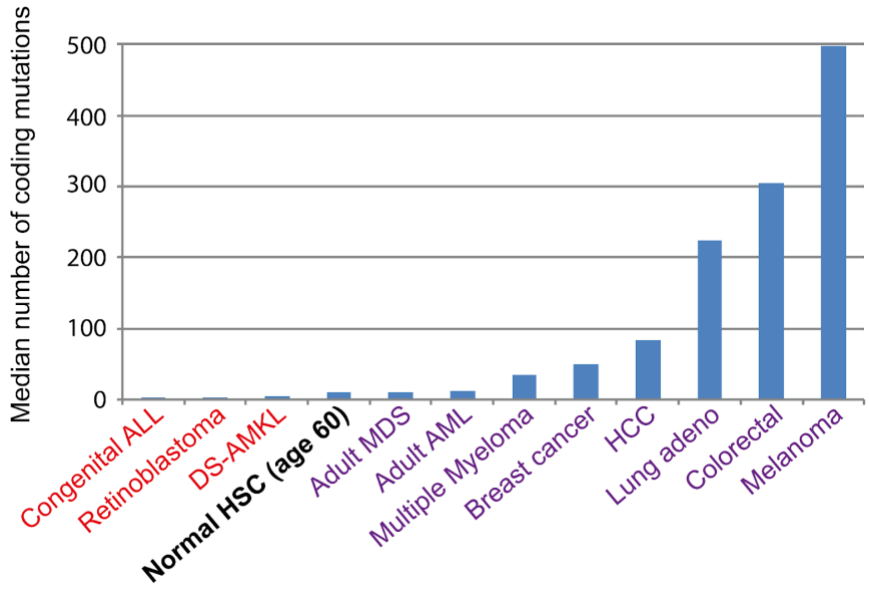


Figure 1.4: Median number of coding mutations in different cancer types and in normal HSCs. In the x-axis labelling, paediatric cancers are coloured red, adult cancers are coloured purple, and normal HSCs from individuals aged ~60 are in black (bold) font. Notably, the average number of coding mutations in normal aged HSCs (10) is roughly the same as the number in adult AML (10) and adult MDS (13), and considerably lower than the number in the depicted common adult cancer types.
ALL, Acute lymphoblastic leukaemia; DS-AMKL, Down Syndrome-Acute Megakaryoblastic Leukaemia; HSC, haematopoietic stem cell; MDS, Myelodysplastic Syndrome; AML, Acute Myeloid Leukaemia; HCC, Hepatocellular carcinoma.

However, the influence of ageing on the development of CH is substantially more far-reaching than simply its association with time. Most significantly, aged HSCs possess reduced engraftment potential, suggestive of impaired self-renewal capacity[33]. They display cell-intrinsic defects, with altered transcriptional and epigenetic landscapes suggestive of a molecular hardwiring of the ageing process, as well as defects in DNA repair and polarity[33]. These cell-autonomous processes can also be influenced by extrinsic signals and, importantly, the bone marrow stroma changes significantly with age[9]; for example, adipogenesis is favoured over osteogenesis, there is a decline in specialised vascular niches, and the chemical milieu is increasingly inflammatory. In this setting of progressive degeneration of HSCs and their environment, the ‘winners’ - the HSCs that self-renew more effectively than their peers and thereby seed clonal expansions - might be best thought of as those retaining some functionality in the face of general decline, where “in the land of the blind the one-eyed man is king”.

While ageing influences haematopoiesis very broadly, other factors operate more specifically on either cell-intrinsic or cell-extrinsic processes, and these will be considered separately below.

1.3.1 Clonal haematopoiesis driver genes

The genes recurrently mutated in CH broadly fall into three main classes: epigenetic regulators (*DNMT3A*, *TET2*, *ASXL1*), splicing factors (*SF3B1*, *SRSF2*, *U2AF1*) and DNA damage response (DDR) genes (*TP53*, *PPM1D*), with rarer contributions from the genes coding for signalling molecules, cohesins and haematopoietic transcription factors (Fig. 1.1)[14–16,29]. An understanding of the biology of these genes is crucial for understanding their role in CH, but mechanistic investigation is challenging. Even if mutations cause only minor changes to HSC molecular and cellular function, leading to subtle advantages, when these changes operate over decades they can result in significant clonal expansions. In addition, any such advantage might only be evident when a mutant HSC resides in a particular environment, which might be difficult to recapitulate experimentally. Nevertheless, some progress has been made in dissecting the mechanistic role these genes play in driving clonal expansion.

Epigenetic regulators: DNMT3A and TET2

DNA cytosine methylation plays a key role in gene regulation and cellular identity / behaviour, with methylation, particularly at promoters, generally considered a repressive mark[34]. Central to this regulatory process are the enzymes responsible for establishing methylation marks, DNA methyltransferases (DNMTs), and the ten-eleven translocation (TET) family, which are capable of removing these marks[34]. While a number of TET and DNMT family members are able to catalyse these reactions, *TET2* and *DNMT3A* are the genes most commonly mutated in CH and haematological malignancies. Loss of *TET2* function is associated with DNA hypermethylation, while loss of *DNMT3A* function is associated with hypomethylation[35,36]. Mechanistic studies in the mouse have shed some light on the consequences of mutations in these genes, detailed below, but the question of why they lead to clonal expansion remains incompletely answered.

DNMT3A mutations in CH are spread across the length of the gene, with missense mutations clustering in the known structural and functional domains. Importantly, the variant spectrum in CH is distinct from that observed in myeloid neoplasms, being notably less enriched for mutations at the R882 hotspot residue[37]. The distribution of mutations in *TET2* is similar, with

missense changes concentrated in the two conserved regions, and truncating mutations spread uniformly across the entire gene. However, unlike in *DNMT3A*, there are no major mutation hotspots in *TET2*. Mutations in *DNMT3A* and *TET2* are usually heterozygous and probably lead to loss of protein function by divergent mechanisms, with some evidence that *DNMT3A*-R882 mutations have a dominant negative effect[38]. Mouse models carrying loss-of-function mutations in either of these genes clearly show an HSC competitive advantage *in vivo* as well as a propensity for leukaemia when cooperating mutations are present[39–42]. Stem cells from these mice are able to serially re-plate in colony-forming assays over many generations, whereas wild-type stem cells quickly lose this capacity, suggestive of enhanced self-renewal capacity in the mutant HSCs[43,44].

Why loss of function of either *TET2* or *DNMT3A* has such a profound impact on HSC biology remains elusive. Mechanisms have been suggested - substantial hypomethylation at "canyons" in the presence of *DNMT3A* mutation, leading to up-regulation of genes involved in HSC self-renewal[39,45–47], for example - but, in truth, much more remains to be elucidated and our understanding of the precise molecular mechanisms is in its infancy. For example, In both human and mouse haematopoietic stem and progenitor cell (HSPCs) with *DNMT3A* or *TET2* mutations, there is relatively poor overall correlation between alterations in DNA methylation and concomitant changes in expression levels of downstream genes[39,46]. In addition, these enzymes have complex interactions with other epigenetic regulators, their associated methylation changes might influence 3D genome interactions, and they might play roles entirely independent of methylation[41,45,48]. Especially perplexing is the fact that *TET2* and *DNMT3A* have ostensibly opposite biochemical functions, yet mutations in either gene results in the same clonal expansion phenotype, and this remains a major conundrum in the field.

Splicing factors: SF3B1, SRSF2 and U2AF1

Precursor messenger RNA splicing is a critical step in the post-transcriptional regulation of gene expression, providing substantial expansion of the functional proteome of eukaryotic organisms with limited gene numbers[49]. The process is executed by repeated assembly of a large and highly dynamic ribonucleoprotein complex, the spliceosome. Alternative splicing patterns are tightly regulated but are fluid, changing, for example, over each 24-hour cycle with the mammalian circadian rhythm, and over a lifetime with advancing age[50,51].

Disruption of alternative splicing is observed in many tumours, in many cases mediated by mutation of components of the spliceosome[52]. Spliceosomal gene mutations are prevalent in myeloid cancers and in CH, and are most commonly found in three genes involved in 3'

splicing: *SF3B1*, *SRSF2* and *U2AF1*[29,53,54]. Mutations in each of these occur primarily as heterozygous substitutions at specific residues, suggesting gain-of-function alterations. Indeed, mutant SF3B1 promotes usage of alternative branch points, leading to cryptic 3' splice site selection, and SRSF2 / U2AF1 mutations are characterised by alternative exon usage[53,55–57]. In addition, mutations in spliceosome genes are mutually exclusive with one another, presumably due to redundant effects and/or a limit on cellular tolerance of disrupted spliceosome function[29,53,54,58–60]. While these biochemical abnormalities lead to aberrant splicing of hundreds of genes, the exact mechanisms by which these mutations lead to clonal expansion remain unknown. Extensive analysis has revealed little overlap between the aberrantly spliced genes associated with each of the different splicing mutations, and no evidence for enrichment of cancer driver genes. This suggests that the clonal advantage imparted by these mutations might not be explained by a single mis-splicing event, and instead that multiple splicing alterations, perhaps with a range of different potential constituents, cooperatively drive clonal expansion. Alternatively, other molecular effects of spliceosome mutations might operate, such as altered R-loop formation[61], although these are generally disadvantageous to cell growth.

The observation that HSCs from mice mutant for *Sf3b1*, *Srsf2* or *U2af1* have a competitive disadvantage *in vivo*, unlike the clonal expansion observed in humans with these mutations, adds further intrigue to the biology of these mutations[56,62–64]. It is not known whether the disparity of phenotypes between humans and mice is simply due to the lack of recapitulation in the mouse model of the disrupted human transcriptome/proteome, or whether it tells us something more fundamental about the requirement for splicing gene mutations to exist in a very particular context in order that they confer clonal advantage. This 'context' could relate to conditions within the HSC bearing the mutation, or to the environment in which the cell resides. The idea of context-dependency is supported by the observation that CH driven by splicing gene mutations is almost exclusively detected in the elderly[29], but which features of ageing confer the pressure for this apparent late selection are entirely unknown.

Additional classes of driver mutation

For some other mutant genes, mechanisms underlying clonal expansion have been more clearly characterised. *Firstly*, there is evidence that activating mutations in *JAK2*, the driver in ~4% of CH[14–16], allow constitutive signalling through growth factor receptors, thus leading to clonal expansion by enhanced proliferation of mutant cells[65,66]. *Secondly*, a number of genes involved in the DDR are recurrently mutated in CH, notably *TP53* and *PPM1D*. TP53 is a key

tumour suppressor in humans and driver mutations lead to loss of protein function[67,68]. PPM1D is a negative regulator of the DDR; driver mutations occur almost exclusively in the terminal exon of the gene, truncating the protein to generate a highly stabilised form that attenuates the entire DDR[69,70]. HSCs bearing mutations in these genes are able to enter the cell cycle despite the presence of DNA damage, leading to a relative fitness advantage when exposed to DNA-damaging agents[69–71]. The archetypal mutagen, and the context in which *TP53*- and *PPM1D*- mutant HSCs expand most notably, is cytotoxic chemotherapy. However, these mutations drive CH quite commonly, including in individuals without prior exposure to any known cytotoxic agent, suggesting that they might confer advantage through multiple mechanisms unrelated to tolerance of DNA damage, or that endogenous levels of DNA damage can also exert a selective pressure.

Other drivers of CH remain less extensively studied, and their biology poorly understood. *ASXL1*, for example, the third most common driver gene in CH after *DNMT3A* and *TET2* in most age groups, is a member of the polycomb repressive complex 2 (PRC2), which plays a key role in stem cell biology and Hox gene regulation[72,73]. Driver mutations in this gene are always truncating and occur exclusively in the terminal two exons (11 and 12), but whether truncation leads to a stable protein product and how it alters PRC2 function, remain areas of active study[74,75]. Recent advances propose that *ASXL1* mutations are associated with increased activity of the deubiquitinase BAP1, leading to decreased levels of histone H2 ubiquitination[76].

In addition to the more recurrently mutated genes driving CH, there is a long tail of less common drivers, including, for example, other DDR regulators such as *BRCC3* and *ATM*, and cohesin-associated genes such as *RAD21*, *SMC3* and *STAG2*[15,16]. In fact, it is almost certain that this 'tail' of drivers extends well beyond what has been characterised; that mutations in many different genes can confer growth advantage but that this advantage is slight and selective pressure weak enough that mutations in particular genes are not sufficiently recurrent to be identified in cohorts of the sizes studied to date. In addition, multiple weak drivers might cooperate in a single HSC to cumulatively confer more substantial advantage; such drivers would be unlikely to be identified in exploratory cohort studies.

Finally, somatic acquisition of larger chromosomal alterations has also been found to drive clonal expansion in some individuals[77–79]. In fact, the commonest genetic lesion seen in CH is mosaic loss of the Y chromosome (mLOY) in men; 1.7-20% of men harbour some amount of mLOY, with the prevalence increasing to >40% by the age of 70[80,81]. Other less common mosaic chromosomal alterations (mCAs) are also observed and are broadly the same as those found in haematological cancers, affecting, for example 5q, 20q and 17p.

1.3.2 Non-driver-mutation factors

Simple calculations based on the number of HSCs, the size of the genome and the rate of acquisition of somatic mutations, as well as studies using exquisitely sensitive error-corrected sequencing, demonstrate that essentially all individuals harbour HSCs with coding mutations in CH driver genes by middle age[28,82]. However, only in a fraction of individuals do mutant clones expand to levels detectable by standard sequencing techniques. Consistent with this, small studies comparing clonal size over two time-points suggest that clones in different individuals with similar or even identical mutations might behave differently[24,82,83]. Furthermore, variable growth rates are inferred by the fact that clinically silent CH is ubiquitous by middle-age, yet its potential sequelae, namely haematological cancers, are rare. It is known that acquisition of additional mutations is not always necessary for progression, but which factors allow mutant clones to expand and cause disease in some individuals, and which factors restrain this in others, is poorly understood. The identity of the mutation and the timing of its acquisition are likely to be important determinants of clonal behaviour, but do additional factors influence whether, or to what degree, a mutation with driver potential stimulates growth?

Inherited factors

There is some evidence that the inherited genome might play a role in shaping CH. A heritable component was initially implied by epidemiological observations: for example, CH has been reported to be more common in men and less common in individuals identifying as Hispanic or East Asian[15,16]. More recent studies have reported (i) heritable genetic variants associated with increased risk of developing MPNs[84,85], (ii) familial clustering of CH driven by *TET2* mutations[86], and (iii) increased prevalence of CH among relatives of individuals with myeloid, but not lymphoid, malignancies[87]. Moreover, a number of germline variants have emerged as important determinants of haematological phenotypes in the general population and it is plausible that these exert epistatic effects on CH emergence[88]. However, at the outset of this project, there was no specific data on whether the inherited genome influences the development of CH.

Environmental factors

A clear indication that the environment can determine whether a mutation drives clonal growth or not, comes from the observation that the identities of 'driver' genes vary depending on the context, as illustrated in Figure 1.5. For example, in aplastic anaemia, where autoreactive T cells target HSCs, clones with mutations that enhance immune evasion are selected for[89]. In the very different scenario of genotoxic stress induced by cytotoxic chemotherapy, as discussed above, clones with mutations in DDR genes expand[69–71]. As these new environments arise, previously neutral mutations now confer a growth advantage, implying that the mutations themselves are not inherently advantageous in isolation, but only in the presence of particular extrinsic signals.

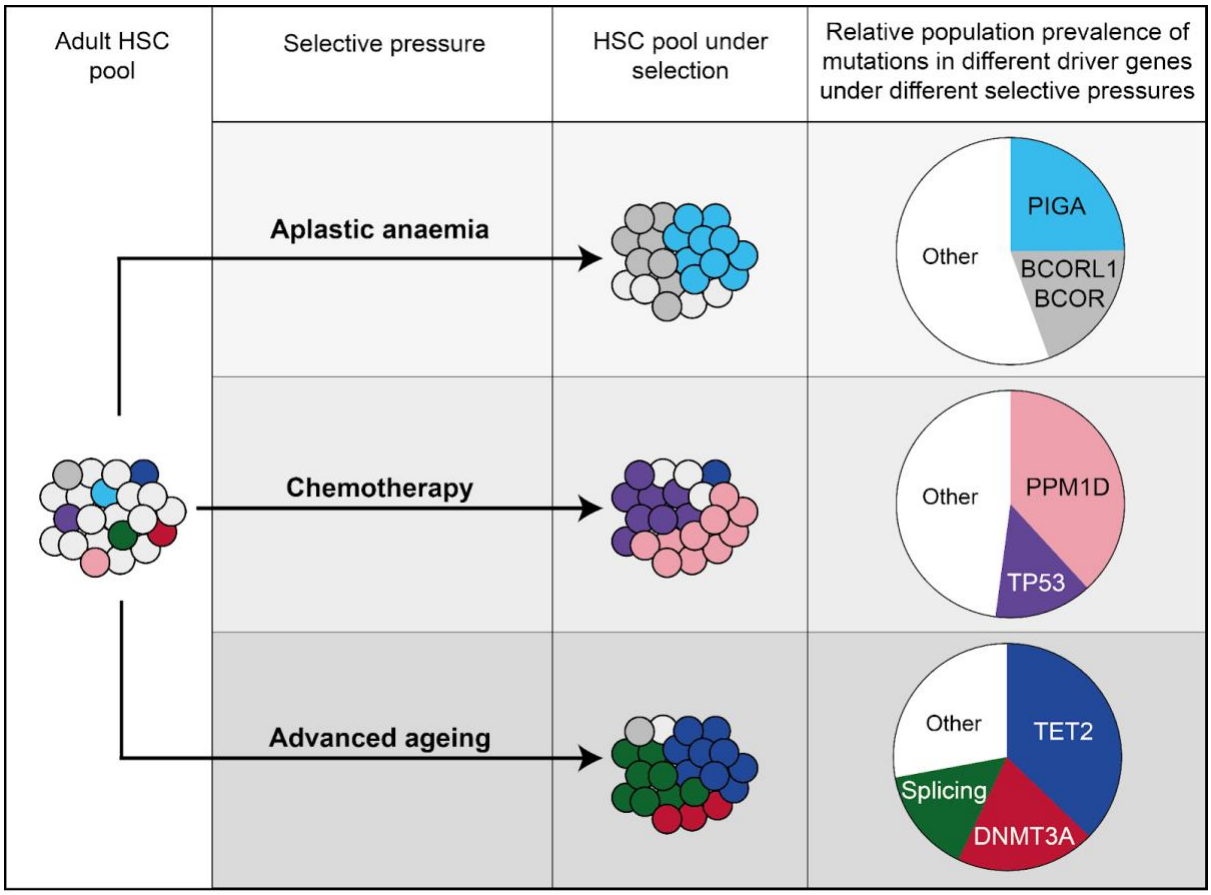


Figure 1.5: Driver gene spectra in different contexts. HSCs acquire somatic mutations inexorably over time; heterogeneity in the HSC pool is represented by variably coloured cells in the left-most column. Particular mutations confer a fitness advantage in specific contexts, leading to clonal selection and expansion. In aplastic anaemia (an autoimmune condition), mutations in genes that allow an HSC to evade immune attack (eg. *PIGA*) are advantageous, as are mutations in the related *BCOR* and *BCORL1* genes (for uncertain but potentially related reasons). With exposure to chemotherapy, mutations in DNA-damage-response pathway genes (eg. *TP53*, *PPM1D*) are selected. In advanced ageing, there is increasing selection for HSCs with mutations in splicing genes. Pie charts on the right of the figure illustrate the relative prevalence of mutations in different driver genes in different contexts; segments representing genes under particular selective pressure are coloured.

Further evidence for the importance of cell-extrinsic factors is suggested by observations in allogeneic sibling transplantation[87,90,91]. In one study, CH passed from donor to recipient, where the mutant HSC was identical (in all respects, not just the identity of the driver mutation) but now housed in two independent individuals, was found to expand more rapidly in the recipient compared to the donor in most cases. This suggested that some aspect of the transplantation process or the milieu of the recipient bone marrow was particularly conducive to clonal expansion[91].

In the search for which cell-extrinsic factors influence clonal growth, much interest has focussed on a potential role for inflammation, a pervasive feature of human ageing, particularly in relation to *TET2*-mutant CH. One hypothesis proposes that, while the long-term function of normal HSCs is perturbed by consistent exposure to proinflammatory cytokines such as tumour necrosis factor alpha (TNFα) and interleukin-6 (IL-6), *TET2*-mutant HSCs are refractory to these signals and maintain functional integrity, providing them with a competitive advantage in a chronic inflammatory environment[92]. Furthermore, TET2 normally functions as a negative regulator of the inflammatory response in myeloid cells, in part by recruiting HDAC2 to suppress IL-6 production[93]. *TET2* loss-of-function mutations therefore potentially set up a positive feedback loop whereby the mutant myeloid cells secrete more IL-6, further augmenting their relative advantage over wild-type HSCs. Recent evidence suggests that the dependence of *TET2*-mutant clonal expansion on IL-6 inflammatory signals might be microbially-mediated; it only occurred in mice in the context of small intestinal dysfunction and bacterial translocation, was reversed by antibiotic treatment and was absent in germ-free mice[94]. Concurrent evidence is emerging that different proinflammatory cytokines might induce expansion of CH with particular driver mutations, such as positive selection of *DNMT3A*-mutant clones by interferon gamma (IFNγ) signalling during chronic infection[95,96].

Finally, some studies have reported a weak association between smoking and CH, predominantly that driven by *ASXL1* mutations[15]. Recently, large genetic studies using Mendelian randomisation (an unbiased genetic approach for removing confounders) have suggested that smoking is a causative risk factor[97]. As it is improbable that smoking induces mutations in HSCs, the reason for the link between smoking and CH remains unclear, although the chronic inflammatory state induced by smoking has been postulated as a factor.

1.4 The consequences of clonal haematopoiesis

A key driver of the intensity of research into CH, beyond its high prevalence and biological parallels with somatic clonal phenomena in other tissues, is the clinical importance of its associations with both haematological cancers and non-haematological disease.

1.4.1 Clonal haematopoiesis and haematological malignancy

Based on an elevated risk of haematological malignancy and the demonstration of clonal progression, it is now clear that CH is a premalignant state[16]. And while this is unequivocal, the nomenclature and the way in which 'premalignancy' is framed might require re-thinking in light of the inevitability of CH and the universality of the phenomenon of clonal expansions driven by cancer-associated mutations in all tissues studied to date[2–8]. According to current definitions, at least by old age, all humans live in a perpetual state of premalignancy across tissues. While this might be true, a descriptor more consistent with its existence as a feature of normal ageing might be more appropriate.

An association between CH and myeloid malignancy - encompassing Acute Myeloid Leukaemia (AML), myelodysplastic syndromes (MDS) and myeloproliferative neoplasms (MPNs) - is perhaps unsurprising given the fact that many recurrently mutated genes are drivers of expansion in both clinical states[98–100]. The simplest logic would be that individuals with CH have already acquired the 'first hit' on the path to malignant transformation. Indeed, sequential acquisition of cooperating mutations and clonal evolution to cancer is well-described[101]. For example, in the case of *DNMT3A*, large AML cohorts have identified co-mutations in the receptor tyrosine kinase *FLT3*, in RAS pathway members (*NRAS*, *KRAS* and *PTPN11*), and in the multifunctional nuclear protein *NPM1*[99,102]. Studies identifying *DNMT3A* mutations in both AML blasts and sorted T lymphocytes, with the cooperating mutation found only in AML blasts, confirmed that the *DNMT3A* mutation must have been acquired in a pre-leukaemic HSC capable of multilineage differentiation[103]. However, acquisition of collaborating mutations by no means explains all malignant progression; *SF3B1*, for example, is the sole driver in one-third of *SF3B1*-mutant MDS cases[54,100], and half of patients with *JAK2*-V617F-mutant MPN in chronic phase lack additional drivers[98].

Quantifying and dissecting the risk of malignant progression associated with CH has been the focus of recent research, particularly in relation to AML. It has been consistently demonstrated that an individual's risk of progression is higher if their CH clone is larger[24,104]. This is intuitive but means that quantification of the absolute risk of developing AML among individuals with

antecedent CH varies between studies with different sequencing depths and sensitivities of variant-calling, with the increase in relative risk ranging from ~3-10-fold[15,16,24,104]. Importantly, as well as clone size, the identity of the CH driver mutation is a key determinant of progression risk; mutations in *SRSF2*, for example, impart a substantially higher risk than either *TET2* or *DNMT3A* mutations[24,104]. By combining mutation type and clonal size, Abelson et al developed a regression model that can identify up to 40% of those at highest risk of AML with a false positive rate of approximately 2%[24]. More precise prognostication / risk stratification is an area of intense interest, since the period of pre-malignancy provides a potential therapeutic window for preventing malignant disease[105].

1.4.2 Clonal haematopoiesis and non-haematological disease

CH, unlike other pre-malignant states, has the potential to lead to dysfunction in other organ systems since *(i)* clonal selection and function are uncoupled, such that HSCs gain advantage through enhanced self-renewal and survival, while the quality of their differentiated progeny has no impact on selection; *(ii)* HSCs are not spatially constrained, so clones can expand to constitute a very large fraction of haematopoiesis; *(iii)* HSCs give rise to many differentiated immune effector cells, which traffic to every organ. Indeed, CH is associated with increased mortality, explained not predominantly by an excess of blood cancer deaths but instead by increased cardiovascular mortality[16]. Several studies have quantified the excess mortality risk in individuals with mutant clones constituting at least 4% of haematopoiesis (VAF ≥ 2%, ie. CHIP), and found it to be 30-40% higher than in individuals with smaller/no clonal expansions[15,16,106]. In one study of primarily middle-aged individuals, the risk of coronary heart disease and ischaemic stroke was more than two times higher in those with CHIP, and was even higher in individuals with larger mutant clones[16]. This level of risk was comparable to that conferred by well-known cardiovascular risk factors, such as high LDL-cholesterol levels, smoking and hypertension. A causal relationship between CH and ischaemic cardiovascular disease was demonstrated in mice, with the finding that abnormal pro-inflammatory *TET2*-mutant macrophages, derived from mutant clones in the bone marrow, mediate accelerated atherosclerosis in susceptible animals[107]. Recent epidemiological evidence suggests that CH is also associated with congestive heart failure[108], and *TET2* or *DNMT3A* loss-of-function mutations led to worsening heart function in a mouse model of this disease, consistent with causality[109,110]. In models of either atherosclerosis or heart failure, pathology in the presence of CH was diminished/reversed by blockade of the pro-inflammatory cytokine IL-1beta[107,110]. A role for IL-6 has also been suggested by the observation that genetic IL-6 deficiency (defined by carriage of a polymorphism in the IL-6 receptor associated with diminished signalling)

attenuates cardiovascular risk, but only in individuals with large CH clones[111], although this was not recapitulated in a subsequent larger cohort[112].

A preprint of a recent study unexpectedly reported that CH is protective against Alzheimer's dementia, and that the degree of protection scales with clone size[113]. Mendelian randomisation analyses and microglial profiling suggested a causal link and it was proposed that mutant, marrow-derived cells might replace/supplement a failing microglial system during ageing. It will be fascinating to understand how CH interacts with other neurodegenerative disorders as this area of research broadens.

Apart from the examples discussed above, there is no robust evidence for causal associations between CH and other diseases of ageing. Links have been postulated with type 2 diabetes[16] and chronic obstructive pulmonary disease (COPD)[86,106], for example, but causality has not been established. It is possible that these associations are driven simply by CH representing a biomarker for advanced biological ageing, or by confounders that are difficult to fully account for in regression models (such as smoking in the context of COPD). Specific experimental models will be required for more informative exploration of these relationships.

A key question is how CH mutations change the molecular biology of immune cells to effect influences on diverse disease types. The importance of *TET2* and *DNMT3A* in restraining inflammatory gene expression in innate immune cells is emerging, with a pro-inflammatory phenotype developing when function is perturbed[23,25,93,107,114,115]. While the progressive low-level inflammation associated with ageing might be permissive for mutant clonal growth (as discussed in Section 1.3.2, 'Environmental factors'), it is also possible that age-related CH itself contributes to this 'inflammaging', or, indeed, that both processes operate contemporaneously in a cycle of positive feedback. A role for CH genes in the adaptive immune response is also suggested, for example, by *DNMT3A* loss-of-function preventing CD8 T-cell exhaustion in the setting of persistent viral infection[116], and by *TET2* mutations in CAR-T cell persistence[117]. It is also notable that bone marrow transplant recipients with haematological cancers who receive donor marrow from carriers of CH have higher rates of graft-versus-host disease and reduced relapse rates, potentially due to stronger adaptive immune responses against both normal host tissues and tumour[87].

1.5 Thesis aims

The discovery that cancer-associated mutations drive benign clonal expansions in all individuals with advancing age brought about a paradigm shift in our perception of the distinction between normality and cancer. The fact that larger clonal expansions are associated with elevated risks of both malignant and non-malignant disease augmented the significance of this discovery. However, we have limited understanding of how and when CH develops, what factors govern its behaviour, how it interacts with ageing and how these variables relate to malignant progression. A deeper understanding of these features of CH is essential if there is to be a realistic prospect of using therapeutic interventions to prevent its sequelae.

In this thesis, by tracking blood cell clones over long periods in a large cohort, by reconstructing haematopoietic phylogenies, and by studying concordance patterns in twins, I set out to tackle these questions and uncover the lifelong dynamics and natural history of CH.

The key objectives of this thesis are:

1. To characterise the behaviour of CH across the human lifespan;
2. To identify and quantify determinants of clonal behaviour;
3. To understand how CH clonal dynamics relate to risk of malignant progression.

Chapter 2

Materials and Methods

2.1 Study participants

2.1.1 SardiNIA cohort

The SardiNIA longitudinal study recruited individuals from four towns in the Lanusei Valley in Sardinia, capturing 5 phases of sample and data collection over more than 20 years[118]. Informed consent was obtained from all participants. We analysed serial samples from 385 individuals in the SardiNIA project, none of whom had a history of haematological malignancy. Ethical permission for this study was granted by The East of England (Essex) Research Ethics Committee (REC reference 15/EE/0327). Samples from this cohort were used for all analyses of CH dynamics.

2.1.2 TwinsUK cohort

We studied blood DNA from 158 individuals from the TwinsUK cohort, comprising 52 monozygotic (MZ) and 27 dizygotic (DZ) twin pairs with no history of haematological malignancy, aged 70 to 99 years (150 women, 8 men)[119]. Samples were obtained with informed consent and appropriate ethics committee approval (REC reference EC04/015). Samples from this cohort were used solely for examination of concordance for CH in twin pairs (results in Chapter 4)

2.2 Targeted sequencing and variant-calling

2.2.1 Method

Target enrichment of whole blood DNA was performed using custom RNA bait sets (Agilent SureSelect ELID 3156971 for SardiNIA samples; ELID 0735431 for TwinsUK samples), designed complementary to genes implicated in CH and haematological malignancies (Table 1). Libraries were sequenced on Illumina HiSeq 2000 and variant-calling was performed as described previously[24]. Briefly, somatic single-nucleotide variants and small indels were called using Shearwater (v.1.21.5), an algorithm designed to detect subclonal mutations in deep sequencing experiments[120]. Two additional variant-calling algorithms were applied to complement this approach: CaVEMan (v.1.11.2) for single-nucleotide variants, and Pindel (v.2.2) for small indels[121,122]. VAF correction was performed using an in-house script (https://github.com/cancerit/vafCorrect). Finally, allele counts at recurrent mutation hotspots were verified using an in-house script (github.com/cancerit/allelecount). Variants were filtered as we described previously[24].

For the SardiNIA longitudinal samples, variants were not curated with regard to existing notions of oncogenicity, i.e. all somatic variants passing quality filters were retained for analysis. If a variant was identified in an individual at any time-point in the study, this site was re-queried in the same individual at all other time-points, using an in-house script (cgpVAF) to provide pileup (SNV) and Exonerate (indel) output (https://github.com/cancerit/vafCorrect). No additional filters were applied to these back-called variants.

For the TwinsUK samples, driver mutations were curated according to evidence for functional relevance in CH and haematological malignancy (Table 2).

2.2.2 Validation

Validation of the use of whole blood DNA. Since CH mutations are primarily harboured by myeloid cells, we tested whether whole blood DNA was a suitable surrogate for the myeloid fraction. We obtained fresh peripheral blood samples from 11 individuals in the SardiNIA cohort and purified granulocytes by lymphoprep (STEMCELL Technologies 07861) separation, followed by red cell lysis of the red cell/granulocyte layer. We sequenced granulocyte DNA in parallel with whole blood DNA (from the same blood sample), using the targeted protocol described above. Comparison of VAFs in granulocytes versus whole blood

showed an excellent correlation (Fig. 2.1; simple linear regression: R^2 = 0.94, p = $2.3x10^{-9}$). This confirmed that VAF measured in whole blood was a faithful reflection of VAF in the myeloid compartment, and supported the use of whole blood VAF measurements to infer the behaviour of CH.

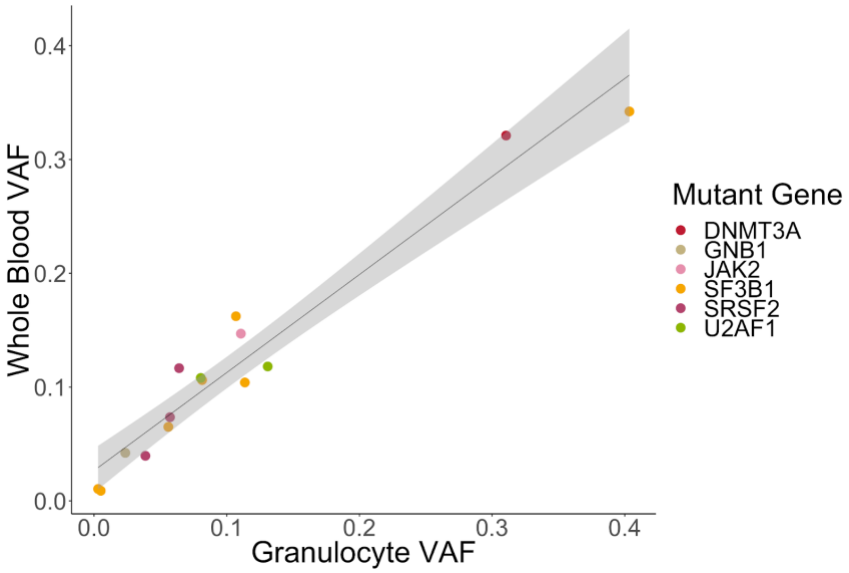


Figure 2.1: Comparison of VAFs measured in DNA extracted from granulocytes versus whole blood

Validation of variant calls using alternative methodology (multiplex PCR). DNA samples from 16 individuals were analysed in an independent validation experiment using alternative methodology, namely multiplex polymerase chain reaction (PCR) amplification followed by sequencing on Illumina MiSeq, as described previously[123]. All mutations called using Agilent SureSelect bait capture methodology were also detected using multiplex PCR, and VAF correlation was strong (simple linear regression R^2 =0.998, p < $2.2x10^{-16}$; Fig. 2.2, Table 3).

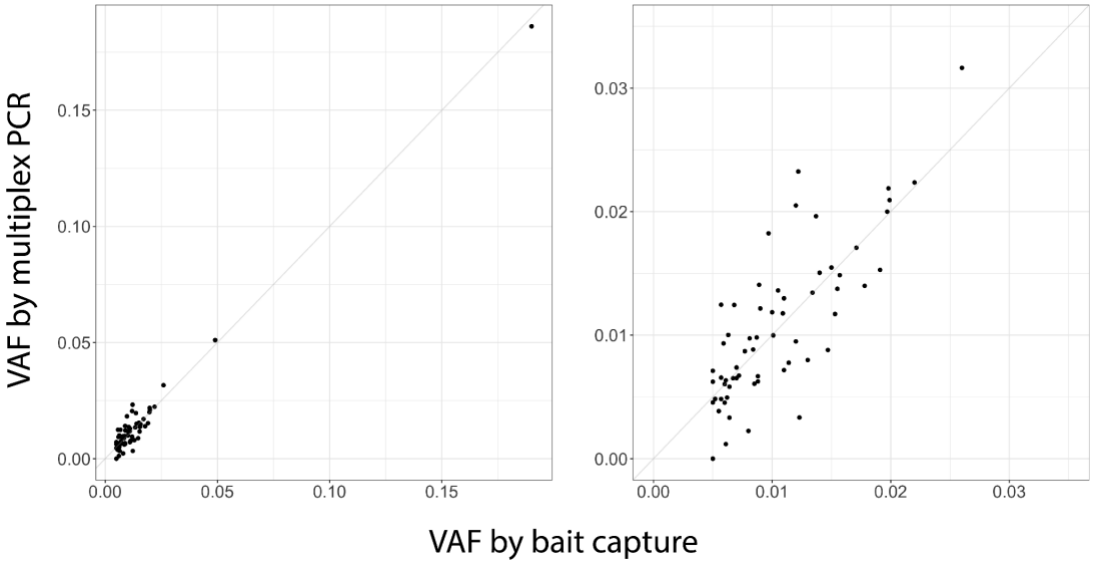


Figure 2.2: PCR validation of variant calls. VAF correlation between DNA samples sequenced using bait capture vs multiplex PCR. Left panel represents the full range of VAFs; right panel focuses on low VAF variants. The grey diagonal follows the theoretical line of perfect VAF correlation.

Negative controls. The Horizon Tru-Q wildtype reference standard DNA (Horizon Tru-Q-0) is commercially verified as 100% wildtype for 5 variant positions covered by our bait sets. When sequenced in triplicate alongside our cohort samples using identical bait capture methodology, only a single read was erroneously reported as non-reference, corresponding to a VAF of 0.001, well below our lower limit for variant-calling (Table 4). Thus, in these negative control samples, no false positives were called using our bait-capture-sequencing and variant-calling pipeline.

Positive controls. Firstly, Horizon Tru-Q-1 DNA, with verified mutations at defined cancer hotspots, was serially diluted to VAFs of 0.05, 0.02, 0.01, 0.005 and 0 using Horizon Tru-Q-0 (verified wild-type at these variant sites), then sequenced in duplicate or triplicate. Secondly, SardiNIA samples with mutations across 15 genes at a range of VAFs, were sequenced in triplicate. These replicates were used to estimate technical overdispersion (as described in Section 2.3). Variant calls for these replicate samples are in Table 5.

All replicate samples were picked from the same stock of DNA, then library preparation and sequencing steps were performed in parallel.

2.3 Modelling of clonal trajectories through time

2.3.1 The model

We use Bayesian hierarchical modelling to model clonal trajectories in the SardiNIA cohort. Since we are unable to reliably phase different mutations into specific clones (Supplementary Note 1) and given that individual CH clones typically harbour a single driver mutation[124], we assume that each mutation is heterozygous and its VAF is representative of the prevalence of a single clone. Accordingly, for a given individual j and mutation i, we have a mutant clone c_{ij}. We model the counts $counts_{c_{ij}}$for c_{ij} at age t as a binomial distribution, such that $counts_{c_{ij}}(t) \sim Bin(cov_{ij}(t), p_{ij}(t))$, with cov_{ij} as the coverage of this mutation at age t and $p_{ij}(t) \sim Beta(\alpha(t), \beta)$ as the expected proportion of mutant allele copies. As such, $counts_{c_{ij}}(t) \sim BB(cov_{ij}(t), \alpha(t), \beta)$. Here, $\beta \sim N(\mu_{od}, \sigma_{od})$ is the technical overdispersion whose parameters are estimated using replicate data (details below) and $\alpha(t) = \frac{\beta q(t)}{1-q(t)}$, where $q(t) = ilogit((b_{gene_i} + b_{site_i} + b_{c_{ij}}) * t + u_{ij})$. We use this parameterization to guarantee that $E[counts_{c_{ij}}] = p_{ij} cov_{ij}$. $b_{gene_i} \sim N(0,0.1)$ and $b_{site_i} \sim N(0,0.1)$ are the gene and site growth effects for mutation i, respectively. $b_{c_{ij}} \sim N(0,0.05)$ is the growth effect associated exclusively with mutation i in individual j - i.e. of mutant clone c_{ij} - and $u_{ij}$is the offset accounting for the onset of different clones at different points in time. We also define the growth effect of c_{ij}as $b_{total_{ij}} = (b_{gene_i} + b_{site_i} + b_{uc_{ij}})$. Along this work we will refer to $b_{gene_i} + b_{site_i}$ as the *driver (growth) effect*. We refer to $b_{c_{ij}}$ as the *unknown-cause (growth) effect* - the fraction of growth that is quantifiable but not explained by the driver mutation, and is attributable to other factors that may affect clonal growth, but differ between individuals, such as age, sex, interclonal competition and others.

2.3.2 Preventing identifiability issues and reducing uninformed estimates

To address possible identifiability issues in our model, when a *gene* has a single mutant site (*JAK2*-V617F and *IDH2*-R140Q), the growth effect is considered to occur only at the *site* level. To avoid estimating the dynamics of a site from a single individual, we only model b_{site_i} when two or more individuals have a missense mutation on site i - we refer to these sites as “recurrent sites”. Overall, we consider a total of 17 genes and 39 recurrent sites (Table 6).

Estimating growth parameters. Using the model described above, we use Markov Chain Monte Carlo (MCMC) with a Hamiltonian Monte Carlo (HMC) sampler with 150-300 leapfrog steps as implemented in greta[125]. We sample for 5,000 iterations and discard the initial 2,500 to get estimates for the distribution of our parameters. As such, our estimates for each parameter are obtained considering their mean, median and 95% highest density posterior interval (HDPI) for 2,500 samples.

We assess the goodness-of-fit using the number of outliers detected in any trajectory and consider only trajectories with no outliers as being explained by our model and, as such, growing at constant rate. Outliers are assessed by calculating the tail probabilities of the counts under our model with a hard cut-off at 2.5%. As such, $P_{outlier} = 1$ if $P(counts \mid b_{gene_i}, b_{site_i}, b_{c_{ij}}, u_{ij}, t) < 0.025 \mid P(counts \mid b_{gene_i}, b_{site_i}, b_{c_{ij}}, u_{ij}, t) > 0.975$ and $P_{outlier} = 0$ otherwise.

2.3.3 Estimating the technical overdispersion parameter

Technical VAF overdispersion used two distinct sets of data (Table 5) as described above in Section 2.2.2, specifically:

(1) Horizon Tru-Q-1 was serially diluted to VAFs of 0.05, 0.02, 0.01, 0.005 and 0 using Horizon Tru-Q-0 (verified wild-type at these variant sites), then sequenced in duplicate or triplicate;

(2) 19 SardiNIA samples with mutations across 15 genes at a range of VAFs, were sequenced in triplicate.

For (1), we model the distribution over the expected VAF as a beta distribution such that $VAF \sim Beta(\alpha, \beta)$. For (2) we adopt a model identical to the one described earlier in this section but use only gene growth effects ($counts_{c_{ij}}(t) \sim BB(cov_{ij}(t), \alpha(t), \beta)$, $\alpha(t) = \frac{\beta q(t)}{1-q(t)}$, $q(t) = ilogit(b_{gene_i} * t + u_{ij})$). Here, we model $\beta \sim exp(r)$ with r as a variable with no prior. We use MCMC with HMC sampling with 400-500 leapfrog-steps as implemented in greta[125] to estimate the mean and standard deviation of β. For this estimate we use 1,000 samples from the posterior distribution.

2.3.4 Validating growth parameters

We use Wright-Fisher simulations[126] with a fixed population of 200,000 cells and 50 possible drivers, a range of fitness advantages (0.001-0.030) and a range of mutation rates ($1.0*10^{-10}$-$4.0*10^{-9}$)[5]. These ranges were based on the expectation of approximately 13 generations of HSC per year and a population size of 200,000 HSCs[5], and were anticipated to include the values inferred.

To simulate the conditions under which the experimental data was obtained, we fit Gamma distributions to the observed coverage and observed age at first time-point, truncated at the minimum and maximum values for each. For each simulation we sample from these distributions the first time-point and a random number of subsequent timepoints (between 2 and 4) from a uniform distribution, and the coverage for each driver at each timepoint. We simulate the sequencing process as drawing samples from a beta-binomial distribution: counts~BB(pβ/(1-p),β,cov), where p is the allele frequency of a mutation, β is the technical overdispersion parameter and cov is the coverage (sampled from the coverage distribution as inferred from our data). We assess the fit between inferred and observed coefficients considering these values.

To better understand the impact that population size and generation times have on these simulations, we conduct the same analysis considering two additional scenarios: a population size of 100,000 HSC and 5 generations per year, and a population size of 50,000 HSC and 1 generation per year.

2.4 Predicting future clonal growth

To test predictive performance, we use an additional time-point (phase 6) not used in the inference of parameters in our model. This was available for 11 individuals with mutations in *CBL* (c.2434+1G>A), *DNMT3A* (P385fs, R882H, W330X), *GNB1* (K57E), *JAK2* (V617F), *PPM1D* (Q524X), *SF3B1* (K666N, K700E, R625L), *SRSF2* (P95H, P95L), *TET2* (Q1542X) and *U2AF1* (Q157P, Q157R). Using the model described in Section 2.3.1 and conditioning on the previous timepoints, we predict the VAF at the additional time-point and assess the performance through the mean absolute error (MAE) to the true VAF value.

2.5 Non-mutation factors and clonal growth rate

Inherited polymorphisms and JAK2-mutant clonal growth. The SardiNIA cohort had previously been characterised using two Illumina custom arrays: the Cardio-MetaboChip and the ImmunoChip[118]. Inherited genotypes at 12 loci previously associated with MPN risk were extracted for the 12 individuals with *JAK2*-V617F mutation[25,84]. The relationship between each individual's total number of inherited risk alleles and *JAK2*-mutant clonal growth rate was assessed by Pearson's correlation. The 46/1 haplotype, which harbours 4 SNPs in complete linkage disequilibrium, was considered as a single risk allele.

Age, sex and smoking experience. We assess the association between unknown-cause growth and age through the calculation of a Pearson correlation considering (i) all CH together, and (ii) individual driver genes separately, while controlling for multiple testing. We also assess the association between unknown-cause growth and (i) sex and (ii) smoking history, using a multivariate regression where unknown-cause growth is the dependent variable and sex and previous smoking experience are the covariates, while also controlling for age.

Serum cytokines and TET2- / DNMT3A- mutant clonal growth. 737 serum samples were analysed from the 230 study participants with somatic mutations in *TET2* and/or *DNMT3A*, collected contemporaneously with DNA samples at multiple time-points per individual (4 collections, n=100; 3 collections, n=80; 2 collections, n=47; 1 collection, n=3). Quantification of 54 biomarkers was performed on each serum sample using the V-Plex Human Biomarker 54-plex kit (Meso Scale Diagnostics) (Table 7a). We used mean analyte level during the study period to assess each for its association with unknown-cause clonal growth of *TET2*- and *DNMT3A*-mutant clones separately, using Spearman rank correlation. The Benjamini-Hochberg procedure was used to account for multiple comparisons.

2.6 Determining the age at clone onset

We consider that HSC clones grow according to a Wright-Fisher model. According to this, for an initial population of HSC $n/2$, we can consider two scenarios - that of a single growth process where the time at which the cell first starts growing $t_0$is described as $t_0 = \frac{log\left(\frac{1}{n}\right)-u}{b_{total}}$, or that of a two step growth process, where $t_0 adjusted = t_0 + \frac{log(g/b_{total})}{b_{total}} - \frac{1}{b_{total}}$, where g is the number of generations per year. The latter scenario is the one chosen, due to its strong theoretical foundation and previous application to mathematical modelling of cancer evolution[127]. Its two phases are an initial stochastic growth period and, once the clone reaches a sufficient population size, a deterministic growth phase. The adjustment made to t_0 in $t_0 adjusted$ can be interpreted as first estimating the age at which the clone reached the deterministic growth phase ($t_0 + \frac{log(g/b_{total})}{b_{total}}$) followed by subtracting the expected time for a clone to overcome its stochastic growth phase ($\frac{1}{b_{total}}$). For both n and g we use the estimates based on[5] ($n = 50{,}000$ and $g = 2$). We validate this approach using simulations and test the approach (by calculating the coefficient of correlation) against our serial VAF data and verify that changes in n and g do not have a dramatic impact on age at onset estimates by considering a range of values ($n = \{10{,}000; 50{,}000; 100{,}000; 200{,}000; 600{,}000\}$ and $g = \{1; 2; 5; 10; 13; 20\}$).

2.7 Haematopoietic phylogenetic trees

2.7.1 Sample preparation and sequencing

We selected 3 individuals with splicing gene mutations from the SardiNIA cohort for detailed blood phylogenetic analysis. Peripheral blood samples were drawn into Lithium-heparin tubes (vacutest, kima, 9ml) and buccal samples were taken (Orangene DNA OG-250). Peripheral blood mononuclear cells were isolated from blood and plated at 50,000 cells per ml in MethoCult 4034 (Stemcell Technologies). After 14 days in culture, 96 single haematopoietic colonies were plucked per individual (total 288 colonies, each made up of hundreds to thousands of cells) and lysed in 50µl of RLT lysis buffer (Qiagen).

Library preparation for whole genome sequencing (WGS) was performed using our low-input pipeline as previously described[128,129]. 150bp paired-end sequencing reads were generated using the NovaSeq® 6000 platform to a mean sequencing depth of 15x per sample. Reads were aligned to the human reference genome (NCBI build37) using BWA-MEM.

Variant-calling and filtering. Single-nucleotide variants (SNVs) and small indels were called against an unmatched reference genome using the in-house pipelines CaVEMan and Pindel, respectively[121,122]. 'Normal contamination of tumour' was set to 0.05; otherwise standard settings and filters were applied. For all mutations passing quality filters in at least one sample, in-house software (cgpVAF, https://github.com/cancerit/vafCorrect) was used to produce matrices of variant and normal reads at each mutant site for all colonies from that individual. Copy-number aberrations and structural variants were identified using matched-normal ASCAT[130] and BRASS (https://github.com/cancerit/BRASS). Low-coverage samples (mean <4x) were excluded from downstream analysis (n=1, PD41305). Samples in which the peak density of somatic mutation VAFs was lower than expected for heterozygous changes (in practice VAF<0.4) were suspected to be contaminated or mixed colonies, and were also excluded from further analysis (n=3, PD41305; n=9, PD41276; n=3, PD34493).

Multiple post-hoc filtering steps were then applied to remove germline mutations, recurrent library prep / sequencing artefacts, and in vitro mutations, as described previously[131] and detailed in custom R scripts (https://github.com/margaretefabre/Clonal_dynamics). Buccal samples were used as an additional filter; mutations were removed if the variant:normal count in the buccal sample was consistent with that expected for a germline mutation (0.5 for autosomes and 0.95 for XY chromosomes, binomial probability >0.01), and were retained if (i) the variant:normal count in the buccal sample was *not* consistent with germline (binomial

probability $<1x10^{-4}$) and (ii) the mutation was not present in either of 2 large SNP databases (1000 Genomes Project and Kaviar) with MAF > 0.001.

2.7.2 Phylogenetic tree construction and assignment of mutations back to the tree

These steps were also performed as described previously[131] and are detailed here: https://github.com/margaretefabre/Clonal_dynamics. Briefly, samples were assigned a genotype for each mutation site passing filtering steps ('present' = ≥2 variant reads and probability > 0.05 that counts came from a somatic distribution; 'absent' = 0 variant reads and depth ≥6; 'unknown' = neither 'absent' nor 'present' criteria met). The proportion of "unknown" genotypes going into tree-building was low: 1.5% (PD34493), 1.4% (PD41276) and 1.3% (PD41305; Fig. 2.3a-c). A genotype matrix of shared mutations was fed into the MPBoot program[132], which constructs a maximum parsimony phylogenetic tree with bootstrap approximation. The in-house-developed R package treemut (https://github.com/NickWilliamsSanger/treemut), which uses original count data and a maximum likelihood approach, was then utilised to assign mutations back to individual branches on the tree. Since individual edge length is influenced by the sensitivity of variant-calling, lengths were scaled by 1/sensitivity, where sensitivity was calculated as the proportion of germline variants called (mean sensitivity: 85.4%, 87.0% and 83.5% for PD41305, PD41276 and PD34493, respectively).

2.7.3 Validating the phylogenies

We used two established approaches to assess the internal consistency, stability and robustness of the shared mutation data and inferred phylogenetic trees, as used previously[3,131]:

(1) *Assessment of the internal consistency of shared mutation data using the disagreement score.*

A perfect phylogeny contains pairs of mutations that are either in discrete clades or nested one within the other. To test the consistency of our data with this assumption, we calculated a 'disagreement score'. For every pair of loci, we calculated the number of samples in

disagreement with this assumption, and then calculated the mean score across all pairs[133]. Samples with unknown genotypes were assumed to be in agreement. Scores from observed phylogenies were then compared to scores generated from random shuffles of the corresponding genotype matrix, internal to each locus. In this way, the number of mutations for each locus is preserved, and the disagreement score in the observed genotype matrix can be compared to the score in the randomly generated matrix. For each of our three phylogenies, the disagreement scores were extremely low at <0.02 in all cases, which was ~100,000-fold lower compared to random shuffles of the genotypes at each locus (Fig. 2.3d). This demonstrates that our data have high internal consistency and that the phylogenies are close to what would be expected in a perfect phylogeny, where the disagreement score is 0.

(2) *Comparison of the MPBoot phylogeny with an alternative phylogeny-inference algorithm (SCITE).*

To assess the reliability and stability of the phylogeny inferred by MPBoot, we fed the same genotype data into an alternative algorithm, SCITE[134]. SCITE is a tree-inference algorithm designed for somatic single-cell data that uses Markov chain Monte Carlo sampling with an error model that takes potential false positives and false negatives into account for tree-scoring. We used false positive and false negative rates of 0.001. SCITE produced phylogenies with high agreement to the original MPBoot phylogenies, with Robinson-Foulds similarities of 0.989 (PD34493), 0.996 (PD41305) and 1.000 (PD41276) (Fig. 2.3e).

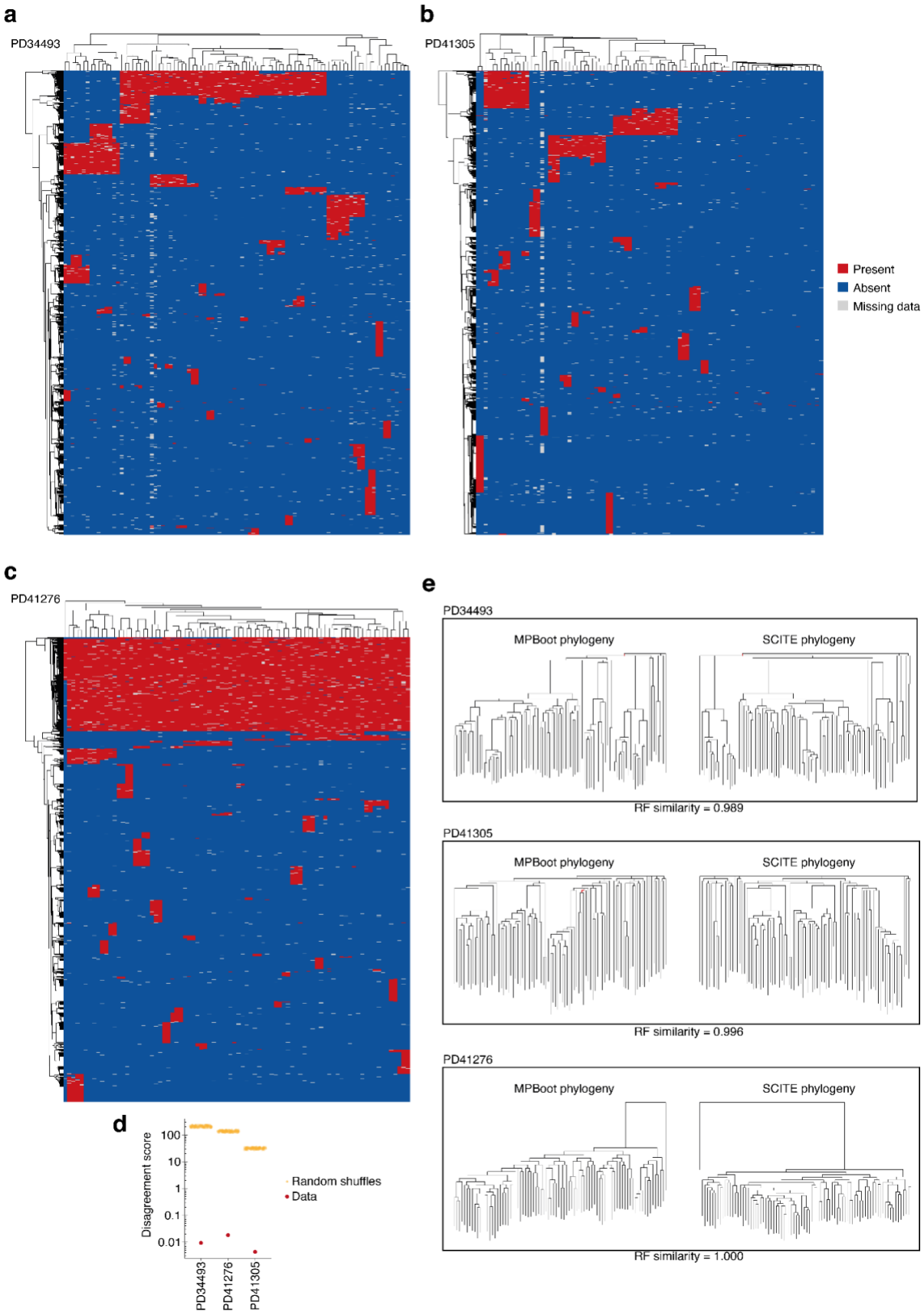


Figure 2.3: Data quality and validation of phylogenetic trees. a-c, Heatmaps of the genotype data used for tree inference for the three individuals for which trees were derived in our study (PD34493, PD41305 and PD41276, respectively), with colours corresponding to the presence (red), absence (blue) and uncertainty (grey) of each

genotype (rows) across all colonies (columns). For both colonies and genotypes, dendrograms derived from the hierarchical clustering of each are shown and are not representative of the derived phylogenetic trees. **d**, Internal consistency of the shared mutation data for each individual as determined by the disagreement score. A perfect phylogeny has a score of zero. We compare scores for the data with scores for random shuffles of the genotype data at each locus. **e**, Comparison of phylogenetic trees built by alternative phylogeny-inference algorithms, MPBoot and SCITE, for each of the 3 individuals. For all three we present the Robinson-Fould (RF) similarity between trees built by the two methods, with 0 representing completely different trees and 1 representing identical trees. Branching events that are different between trees constructed using the two methods are highlighted in red.

2.7.4 Reconstructing population trajectories

Phylogenies were made ultrametric (branch lengths normalised) using a bespoke R function (make.tree.ultrametric, https://github.com/margaretefabre/Clonal_dynamics/my_functions). With the root of the tree representing conception and the tips representing age at sampling, we scaled the age axis in two phases by: (1) assigning the first 55 mutations to the period between conception and birth (in light of evidence for this higher rate of mutation acquisition during this period[3,131]), and (2) scaling the axis linearly throughout life after birth (in light of evidence for a constant rate of mutation acquisition in HSCs during postnatal life[3–7]). We then analysed population size trajectories by fitting Bayesian nonparametric phylodynamic reconstructions (BNPR) as implemented in the phylodyn R package[135,136] to clades - sets of samples in a phylogenetic tree sharing a most recent common ancestor (MRCA) - defined by either having a driver mutation on the MRCA or a MRCA branch length that spans more than 10% of the tree depth and with 5 tips or more. We also estimated the lower and upper bounds for age at onset of clonal expansion to be the limits of the branch containing the most recent common ancestor.

2.7.5 Validating growth rates inferred from phylogenies (Figs 2.4 and 2.5)

We use Wright-Fisher simulations[126] with 50 possible drivers and test a range of different fitness advantages ([0.005,0.010,0.015,0.020,0.025,0.030]) over 800 generations at a fixed population size of 200,000 HSC. For each fitness effect we define a driver mutation rate ([$200*10^{-9}$,$50*10^{-9}$,$20*10^{-9}$,$15*10^{-9}$,$8*10^{-9}$,$5*10^{-9}$], respectively) that guarantees that some simulations lead to clones that expand to sufficient sizes, while avoiding many competing expansions and keeping the passenger mutation rate constant ($2*10^{-5}$). For each simulation we infer phylogenetic trees by sampling 100 representative clones from our population and using a neighbour-joining algorithm based on mutation presence. The representative sampling is done by defining for each clone a probability of being sampled that is equivalent to its

proportion in the population. We then detect the clades that contain drivers, isolate them and infer their effective population size (Neff) trajectory using BNPR[134,135].

We fit different models to the inferred Neff trajectories, namely:

1. A log-linear fit (assumes exponential growth);
2. A scaled and shifted sigmoidal fit (assumes that growth saturates based on the Neff trajectory);
3. A shifted sigmoidal fit (assumes that growth saturates at 1 and that the most recent Neff estimate corresponds to the proportion of tips in the clade);
4. A biphasic log-linear fit (assumes that growth is exponential and has two distinct coefficients corresponding to early and late growth; the boundary between early and late growth - otherwise referred to as the changepoint between both - is also fitted with the other parameters and is constrained to lie in the central part of the trajectory: for the time t over which the clone expands, the changepoint cannot be inferior to min(t)+0.25*range(t) nor superior to max(t)-0.25*range(t), where range(t)=max(t)-min(t). This constraint prevents fits that are too close to the clonal inception or to the clone at later stages).

We compare these models by assessing how closely they are able to recapitulate the original fitness in the simulations. To do so, we calculate their coefficient of determination and root mean squared error. We also visually assess how similar these trajectories are to the true driver trajectories as reconstructed from simulations - to match clones from a Wright-Fisher simulation to an expansion in a phylogenetic tree we assign each clone from the Wright-Fisher simulation to its nearest clone in a phylogenetic tree using the Hamming distance between the mutations in each clone.

We additionally estimate the effective population size using two other methods for validation - mcmc.popsize and skyline from the ape package[137] in R .

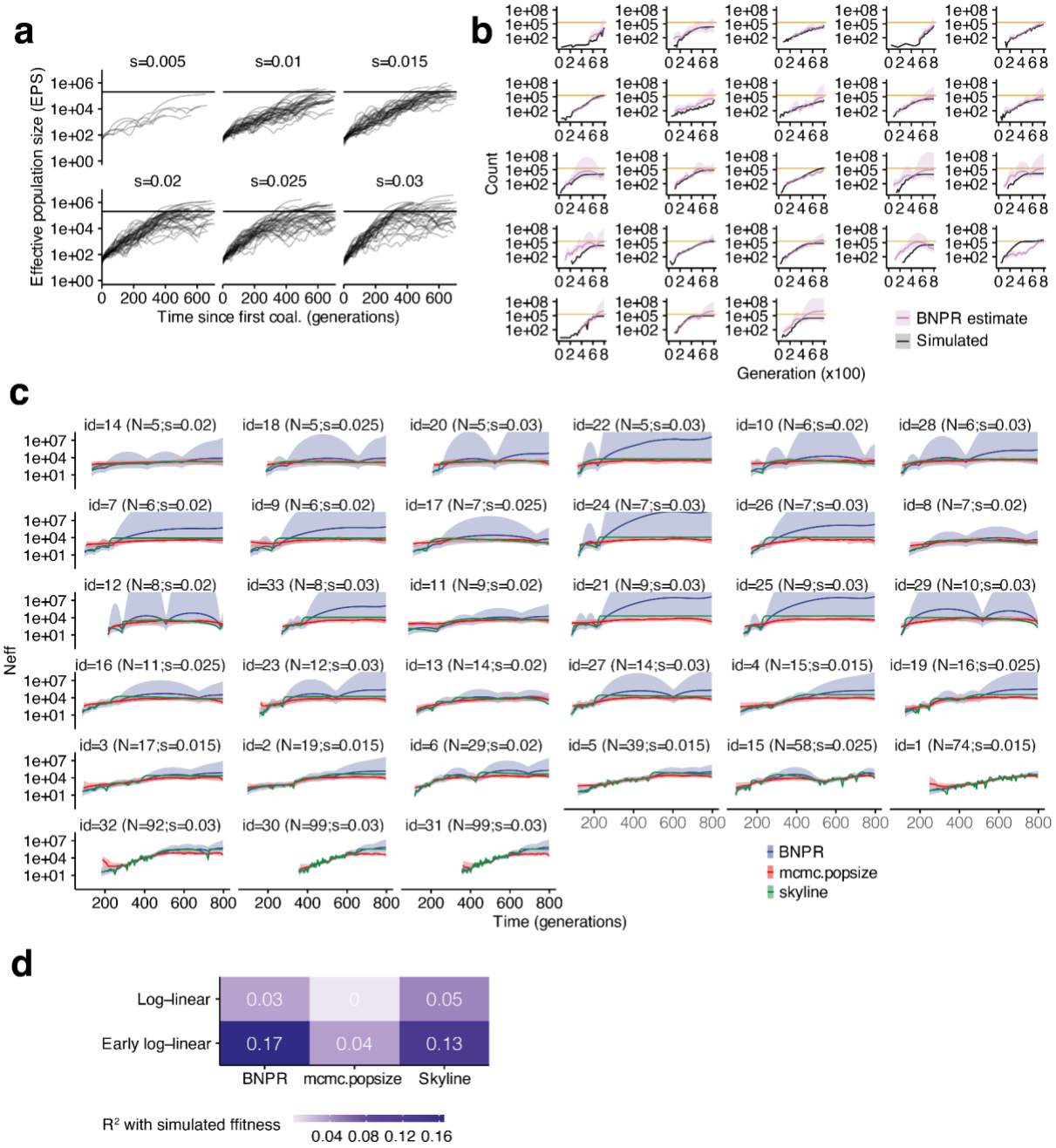


Figure 2.4: Validating growth rate inferences. a, Simulated BNPR trajectories from Wright-Fisher simulations with a fixed population size across 800 generations for a range of fitness effects (0.005, 0.010, 0.015, 0.020, 0.025, 0.030). **b**, Comparison between Wright-Fisher simulations (grey) and BNPR estimates from phylogenies obtained from these simulations (pink). The horizontal golden line in each plot represents the HSC population carrying capacity (200,000). **c**, Representation of effective population size (Neff) trajectories using three distinct methods (BNPR, mcmc.popsize and skyline) for their estimation across a range of clade sizes and fitness effects. **d**, Quantification of the association between true and inferred fitness values for three distinct methods of Neff estimation.

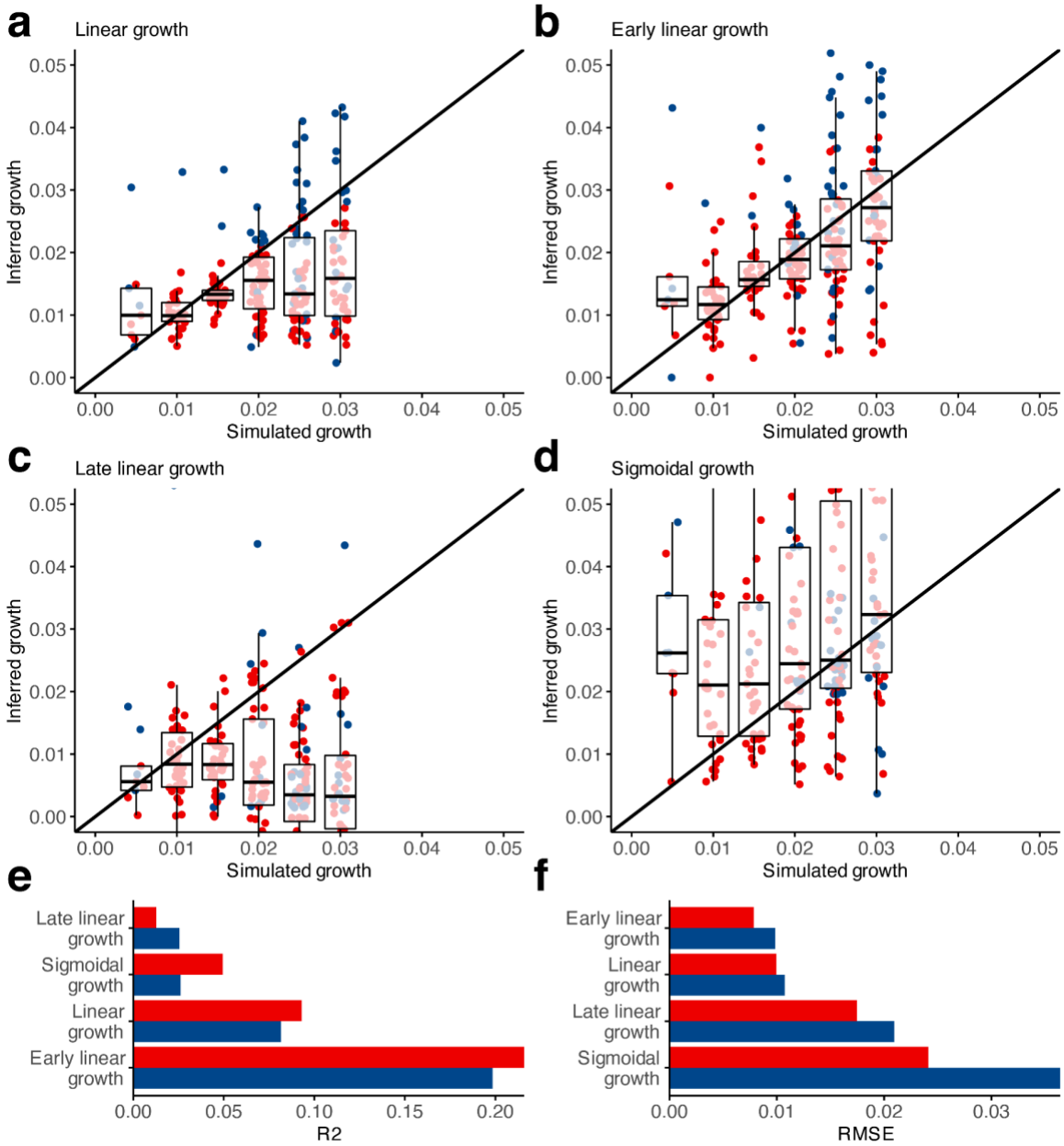


Figure 2.5: Estimation of the true clone fitness from phylodynamic estimation. Three fits were tested to estimate the true clone fitness from phylodynamic estimation of the population size and these estimates were plotted as a function of the true fitness size (0.005, 0.010, 0.015, 0.020, 0.025 or 0.030). **a**, A log-linear fit; **b-c**, A biphasic fit that estimates an early and a late growth rate and a change-point between both and **d**, a sigmoidal fit (n=241 simulated trajectories). **e**, Coefficient of correlation (R2) for all four inferred coefficients. **f**, Root mean squared error (RMSE) for all four inferred coefficients. In this figure red represents “low variance trajectories” (the average estimated variance for the logarithm of the trajectory is under 5) and blue represents “all trajectories”. The boxes in **a-d** represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile.

2.8 Detecting clonal deceleration

We detect deceleration using two different approaches - the ratio between expected and observed clone size using phylodynamic estimates and the ratios between observed and historical (from longitudinal data) and between late and expected (from phylogenetic data), respectively. To obtain early and late growth rates from phylogenetic data, we fit a biphasic log-linear model to our phylodynamic estimation of Neff.

Expected and observed clone size in phylogenetic data. The expected clone size is calculated by extrapolating the early growth rate until the age of sampling, assuming constant growth. The observed clone size is the fraction of mutant tips in the phylogenetic tree. We then calculate the ratio between expected and observed growth as a measure of change in growth rate.

Growth ratio in phylogenetic data. We use sigmoidal regression and the changepoint log-linear fit, described in Section 2.7.3, to calculate late growth and expected growth (the latter assuming growth is constant through life and carrying capacity is fixed at 200,000 HSCs). We use the ratio between late and expected growth to infer change in growth rate through life.

Growth ratio in longitudinal data. The observed growth rate is defined as the growth rate inferred directly from the serial VAF measurements in old age. The minimal historical growth is the growth rate estimate obtained by restricting clone initiation solutions to a time after conception, i.e. excluding all posterior samples that lead to implausible age at onset estimates. Finally, we calculate the ratio between observed and historical growth.

For each of these analyses, the ratio is a measure of change in rate of growth (1 implies no change; <1 implies deceleration, >1 implies acceleration).

2.9 Selection analyses (dN/dS)

To quantify selection, we used the dNdScv algorithm, a maximum-likelihood implementation of dN/dS, which measures the ratio of non-synonymous (N) to synonymous (S) mutations, while controlling for gene sequence composition and variable substitution rates[2]. We first applied this method to the mutation calls from the longitudinal SardiNIA cohort in order to identify which genes are under positive selection in the context of CH. For this analysis, any mutation that was present in a single individual at multiple time-points was counted only once. We also compared dN/dS ratios at the beginning and end of study, and found the latter to be higher, consistent with stronger cumulative effects of selection at older ages (Supplementary Note 2).

To characterise patterns of selection in AML and MDS, we applied dNdScv to two published data sets. The AML set was derived from 1540 patients enrolled in three prospective trials of intensive therapy[99]. The MDS set included 738 patients with MDS or closely related neoplasms such as chronic myelomonocytic leukaemia[100]. Both used deep targeted sequencing of 111 cancer genes, which overlapped with 13 of the 17 genes of interest in our longitudinal CH study (*PPM1D, CTCF, GNB1* and *BRCC3* were not sequenced in the AML/MDS studies). We called and filtered variants in the 13 overlapping genes using the strategy described above (Section 2.2.1, 'Targeted sequencing and variant-calling'). We calculated dN/dS values both at the level of individual genes, and at single-site level for hotspots, the latter using the sitednds function in the dNdScv R package.

Finally, we compared dN/dS ratios in shared and private branches of the three phylogenies, and found selection to be stronger in the former, consistent with the fact that mutations along shared branches were the ones driving subsequent clonal expansions (and therefore were more strongly selected) (Supplementary Note 2).

2.10 CH dynamics and malignant progression

To assess the relationship between CH dynamics and progression to AML, we used previously-derived AML risk coefficients[24], which were derived by fitting a Cox-proportional hazards model to quantify the AML risk associated with individual CH driver genes (agnostic of clone size). We calculated the coefficient of correlation between driver-gene-specific growth rates observed in our longitudinal CH data and the corresponding AML risk coefficients.

To test the association between driver-related CH dynamics and selection strength in MDS and AML, we used dN/dS ratios derived from two large disease data sets (see Section 2.9)[99,100]. We calculated disease-specific dN/dS values for all hotspots, and assessed their coefficient of correlation with the hotspot-specific growth rates observed in our longitudinal CH data.

2.11 CH and blood counts

Using serial blood count measurements from individuals in the SardiNIA cohort, we studied correlates of blood parameters, while accounting for potential confounders. To do this, we used the lme4 package in R to fit mixed effects regression models with age, sex and CH features as fixed effects and a random effect for the intercept across individuals.

First, we tested CH as a binary variable (presence vs absence, with presence defined as VAF>2% at the end-of-study), with CH considered firstly as presence of any driver mutation and, secondly, by presence of driver mutations in particular genes. In R code:

lmer(BloodParameter ~ Age + Sex + CH + (1|individual), REML=F)

To assess the impact of individual fixed effects on blood parameters, we used a likelihood ratio test to compare the 'full' model with the 'null' model. For example, to assess whether haemoglobin is associated with CH, while controlling for age and sex, in R code:

model_full = lmer(HB ~ Age + Sex + CH + (1| individual), REML=F)

model_null = lmer(HB ~ Age + Sex + (1| individual), REML=F)

anova(model_full, model_null)

We performed such comparisons for each blood parameter of interest (Hb, MCV, RDW, PLT, WBC, NEUT, MONO, LYMPH) and each fixed effect. We corrected for multiple tests using the Benjamini-Hochberg method.

Finally, we tested the association of blood parameters with the unknown-cause component of clonal growth (UCgrowth), while controlling for clone size (VAF), age and sex. In R code:

lmer(BloodParameter ~ Age + Sex + UCgrowth + VAF + (1| individual), REML=F)

Significance testing was again performed using likelihood ratio tests as above.

2.12 Testing concordance for CH in twin pairs

In the TwinsUK cohort, Fisher's Exact Test was used to assess twin concordance for CH. Null distributions of CH within the MZ and DZ groups were generated using random sample permutation (1000 iterations). The openMX R package was used for maximum likelihood modelling of genetic and environmental contributions to CH[138].

Chapter 3

Selection patterns and longitudinal behaviour of CH in the elderly

3.1 Introduction

The observation that CH-associated mutations affect a restricted set of genes that are also frequently mutated in leukaemia - most commonly those involved in epigenetic regulation (*DNMT3A*, *TET2* and *ASXL1*), splicing (*SF3B1* and *SRSF2*) and apoptosis (*TP53* and *PPM1D*)[14–16,29] - implies that these mutations inherently confer fitness to HSCs. In fact, recent evolutionary models assume that each specific mutation carries a fixed fitness advantage, and find that this largely explains the relative proportions and clonal sizes of CH driven by different mutations[139]. However, several observations suggest that non-mutation factors are also influential. For example, a handful of CH cases studied at two time-points propose that clones driven by the same or similar mutations can behave differently between individuals[82,83]. Also, the relative prevalence of different CH-driver gene mutations changes significantly depending on context; for example, in aplastic anaemia CH is commonly driven by mutations that enhance immune evasion[89,140–142], whereas genotoxic stress favours clones with mutations in DNA damage genes[143–145]. Furthermore, factors like inflammation[94] and heritable genetic variation[25,84,106] can affect CH emergence.

A major limitation to our understanding of the determinants of CH behaviour/fate to date has been its reliance on cross-sectional studies capturing CH at single time-points. Here, by tracking blood cell clones over long periods in a large cohort of elderly individuals, we uncover the longitudinal dynamics of CH and the factors determining behaviour.

3.2 Results

3.2.1 Cohort overview and study design

We analysed 1,593 blood DNA samples from 385 adults aged 55-93 years at the time of entry into the SardiNIA longitudinal study[118]. The participants, who had no history of haematological malignancy, were sampled up to 5 times (median 4) over 3.2-16 years (median 12.9 years) (Figs. 3.1 and 3.2).

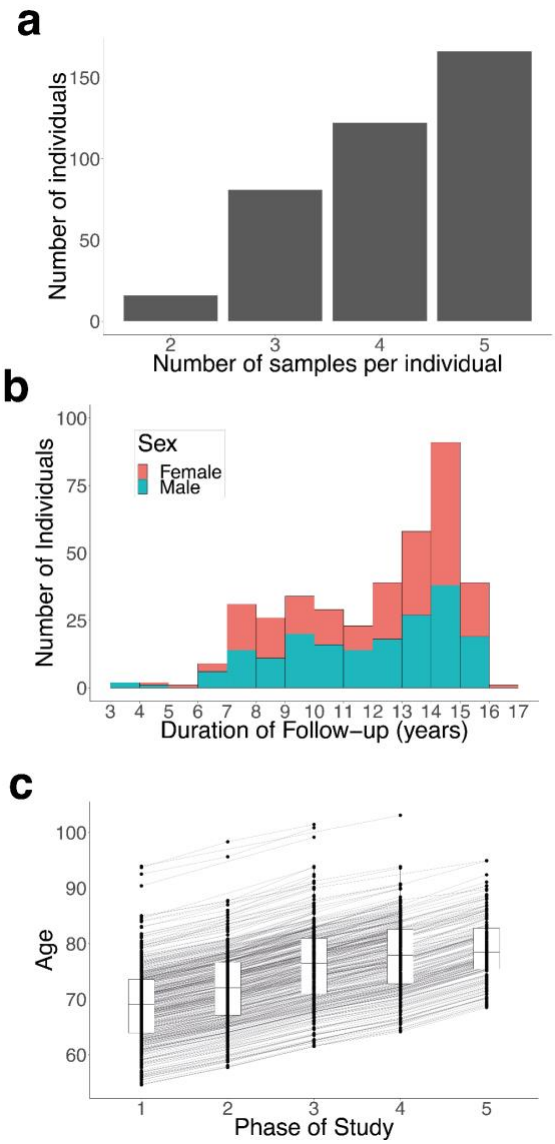


Figure 3.1: Longitudinal cohort characteristics. **a**, Distribution of the number of serial samples obtained per individual. **b**, Duration of follow-up per individual. **c**, Distribution of participants' ages at each of the five sampling phases of the SardiNIA study. The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile.

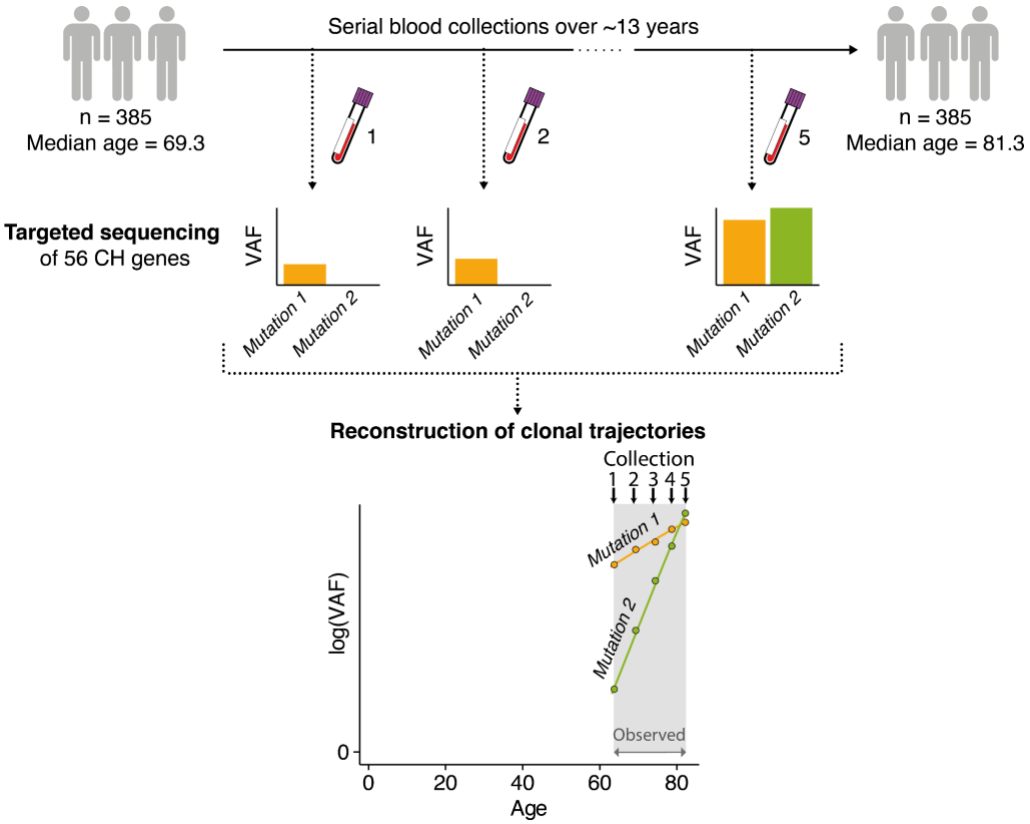


Figure 3.2: Experimental workflow. 1,593 blood DNA samples were obtained from 385 elderly individuals sampled 2-5 times (median 4) over 3.2-16 years (median 12.9) and sequenced for mutations in 56 CH genes. Measured variant allele fractions (VAFs) were used to fit observed clonal trajectories.

3.2.2 The mutational landscape of CH

We performed deep sequencing (mean 1,065x) of 56 genes associated with CH and haematological malignancy (Table 1a) and identified somatic mutations in 52 (Table 8). Using the dNdScv algorithm, an implementation of dN/dS that corrects for trinucleotide mutation rates, sequence composition, and variable mutation rates across genes, we identified positive selection of missense and/or truncating variants in 17 of these genes (dN/dS ratio>1 with q<0.1) (Fig. 3.3; Table 9)[2]. We defined these as driver genes and focussed downstream analyses on this set. The type and distribution of somatic mutations within driver genes are depicted in Figure 3.4; the distribution of mutations within the cohort is shown in Figure 3.5.



Figure 3.3: Genes under positive selection. Observed-to-expected (dN/dS) ratios for the 17 genes with missense and/or truncating mutations under positive selection (with q<0.1). The dashed line indicates a dN/dS value of 1, which represents neutrality (no selection). Error bars depict 95% CIs.

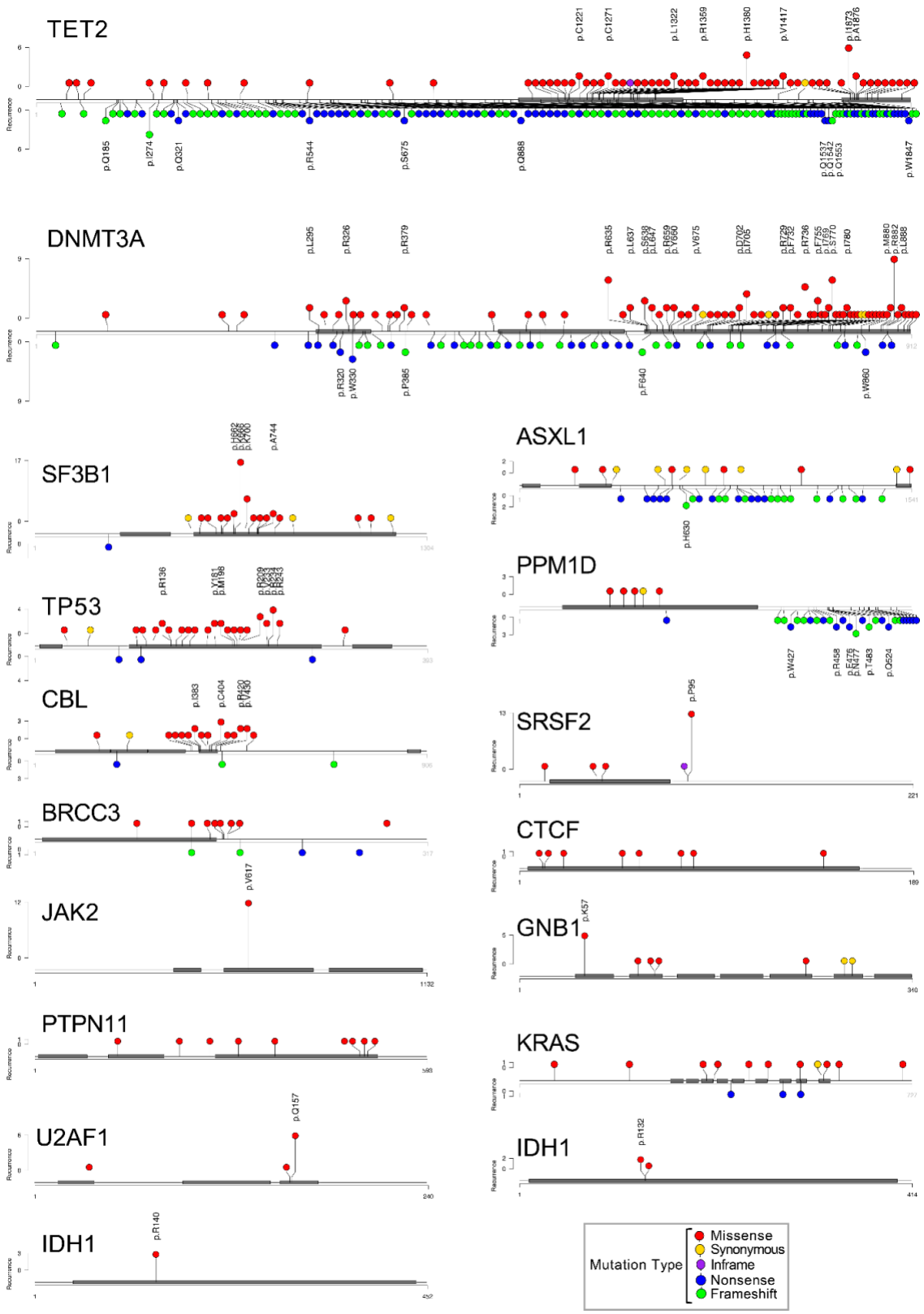


Figure 3.4: Distribution of somatic mutations within driver genes. The longest protein isoforms are shown, with protein domains depicted by grey rectangles. Each circle represents a somatic mutation. The vertical distance of the circle from the protein indicates the mutation's recurrence in the cohort. Recurrent mutations are explicitly labelled. Circle colours indicate mutation (key). Non-truncating (missense, inframe, synonymous) and truncating mutations (nonsense, frameshift) are depicted above and below the protein cartoon, respectively.

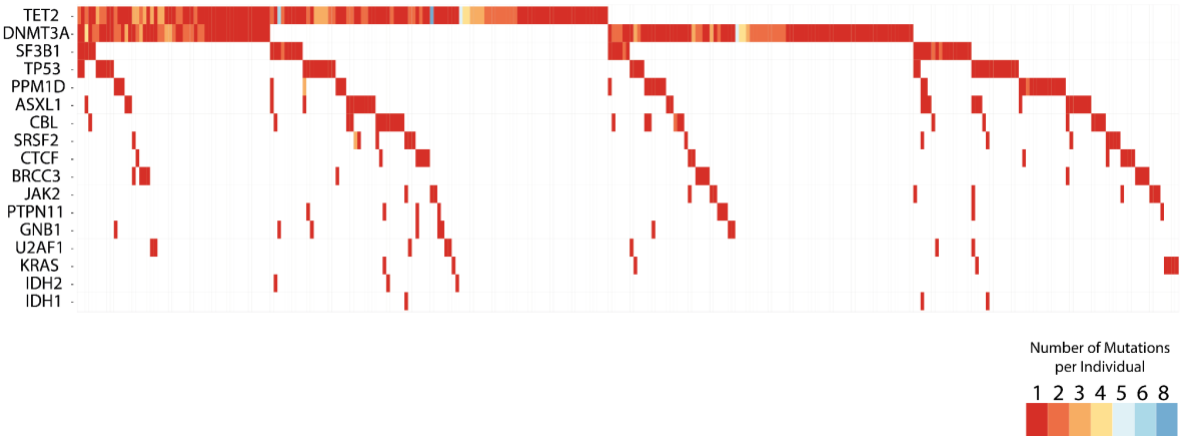


Figure 3.5: Distribution of somatic mutations within the cohort. Waterfall plot showing the number and distribution of mutations among participants. Each column represents 1 individual, and each row 1 gene. Coloured squares indicate the presence of a mutation with the specific colour indicating the number of distinct mutations in that gene identified in that individual. For individuals with the same mutation identified at multiple serial time-points, the serially-observed mutation is counted only once.

At least one somatic non-synonymous mutation was identified in 305 of 385 individuals (79.2%), with CH prevalence, average clone size and number of mutations per individual increasing with advancing age, and CH identified in >90% of those aged 85 years or older (Fig. 3.6a,b). Mutations were most common in epigenetic regulator genes *TET2* and *DNMT3A*, and also frequent in *ASXL1*, *TP53*, *PPM1D* and spliceosome genes (Fig. 3.6d, upper panel). Interestingly, in this elderly cohort, advancing age impacted the prevalence of different driver mutations in a gene-dependent manner (Fig. 3.6d, lower panel). In particular, the prevalence of *DNMT3A* mutations showed no significant relationship with age overall (p=0.12 for a binomial regression of gene prevalence vs age, controlling for sex). By contrast, *TET2* mutations showed a consistent rise with age, averaging at 6.8%/yr (p=0.00037), as did mutations in splicing genes (*U2AF1*, *SRSF2* and *SF3B1*), whose prevalence increased by 5.4%/yr (p=0.025). These changes in driver prevalence with age could not have resulted from exclusion of individuals with haematological malignancies, as the incidence of these in the complete SardiNIA cohort was only 0.28% (22/7816), the majority of which were lymphoid.

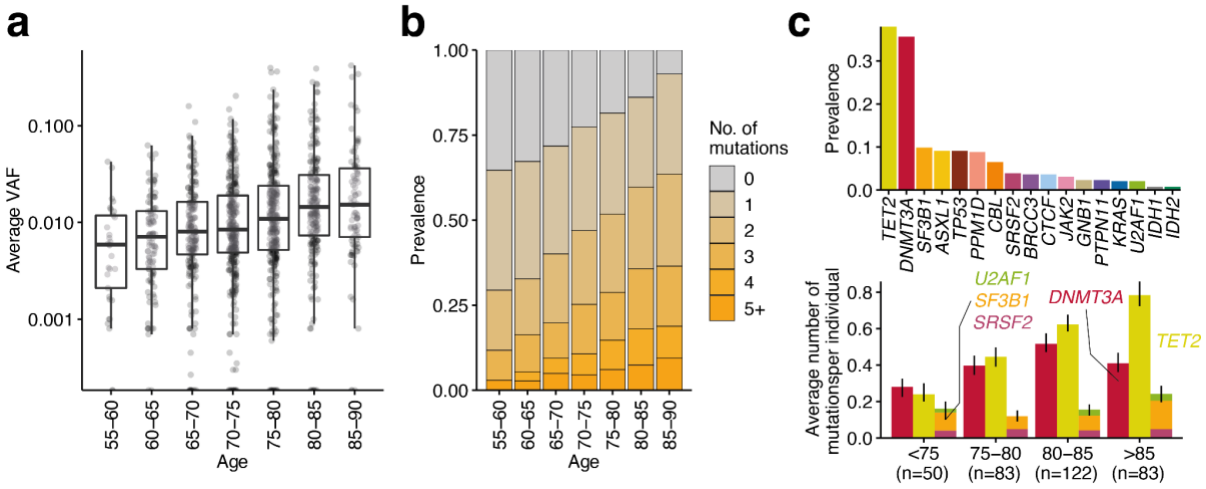


Figure 3.6: Changing mutation landscape with age. a, Age distribution of average VAF per individual (n=1,258 VAF measurements). The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile. **b,** Age-stratified prevalence of the number of mutations per individual. **c,** Prevalence of mutations in driver genes: upper panel shows absolute prevalence in the cohort; lower panel shows average number of mutations per individual in *DNMT3A*, *TET2* and splicing genes (*SF3B1, SRSF2, U2AF1*) at different ages, with error bars representing bootstrap 90% confidence intervals.

3.2.3 Most clones expand steadily during older age

To investigate clonal behaviour over time, we used serial Variant Allele Fraction (VAF; the fraction of sequencing reads reporting a mutation) measurements as a surrogate for clone size, and fitted a saturating (logistic) exponential curve with a constant growth rate over time to each clonal trajectory. Such logistic growth behaviour is supported by simulations of evolutionary dynamics using Wright-Fisher models with constant fitness (Fig. 3.7a,b).

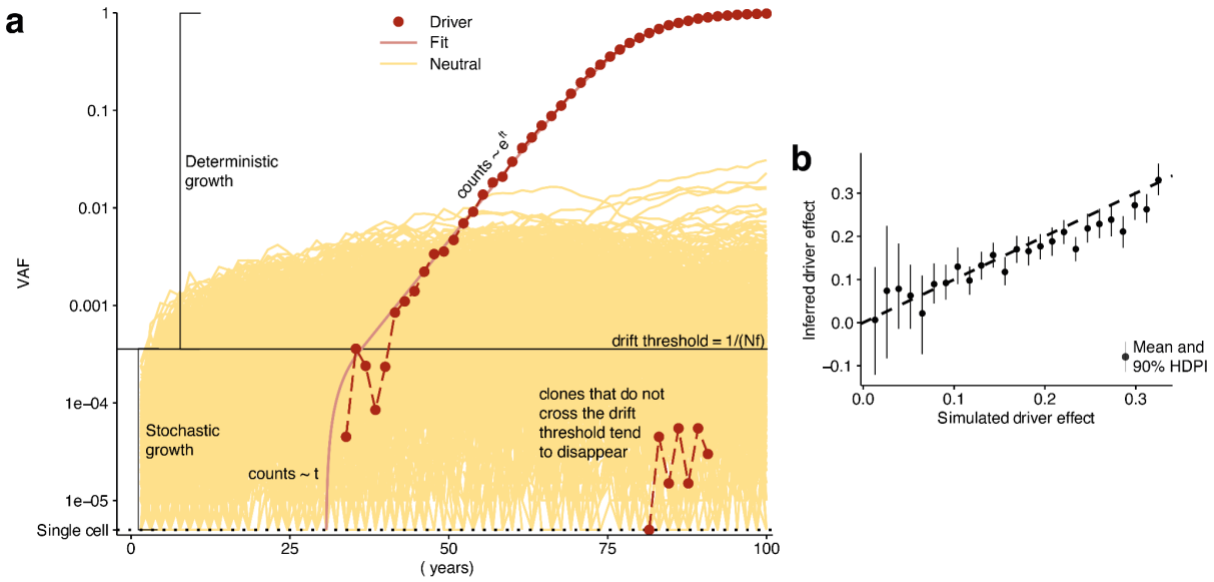


Figure 3.7: Simulating clonal dynamics using Wright-Fisher models. a, Representation of a Wright-Fisher simulation, showing two phases of clonal growth. The likelihood of a clone transitioning from stochastic to deterministic growth is inversely proportional to the product of its fitness (f) and the total number of stem cells (N). Clones with no fitness advantage (depicted in yellow) are unlikely to exceed their drift thresholds and tend to disappear or remain undetectable. Fitter clones (depicted in red) are more likely to reach deterministic growth. **b**, Association between the driver mutation effect used in the Wright-Fisher simulations and the driver effect inferred using our model (R^2 = 0.92; n=270 simulated clones). Error bars represent 90% highest posterior density interval (HDPI).

Remarkably, by assessing the fit between serial VAF measurements and the trajectories inferred by our model, we find that the great majority of clones (92.4%) expanded at a constant exponential rate over the study period (Fig. 3.8a,b). The predominance of fixed-rate growth was particularly striking for genes like *DNMT3A* and *TET2*, for which 99% and 94.3% of clones, respectively, grew steadily over time. Nevertheless, some clones behaved unpredictably, with proportions varying by mutant gene. Most notable were *JAK2*-V617F-mutant clones, for which growth trajectories were particularly erratic, with only 58% displaying stable growth. The likelihood of mutant clones displaying non-constant growth at older age was not affected by the number of mutations in the same individual (Fig. 3.8c).

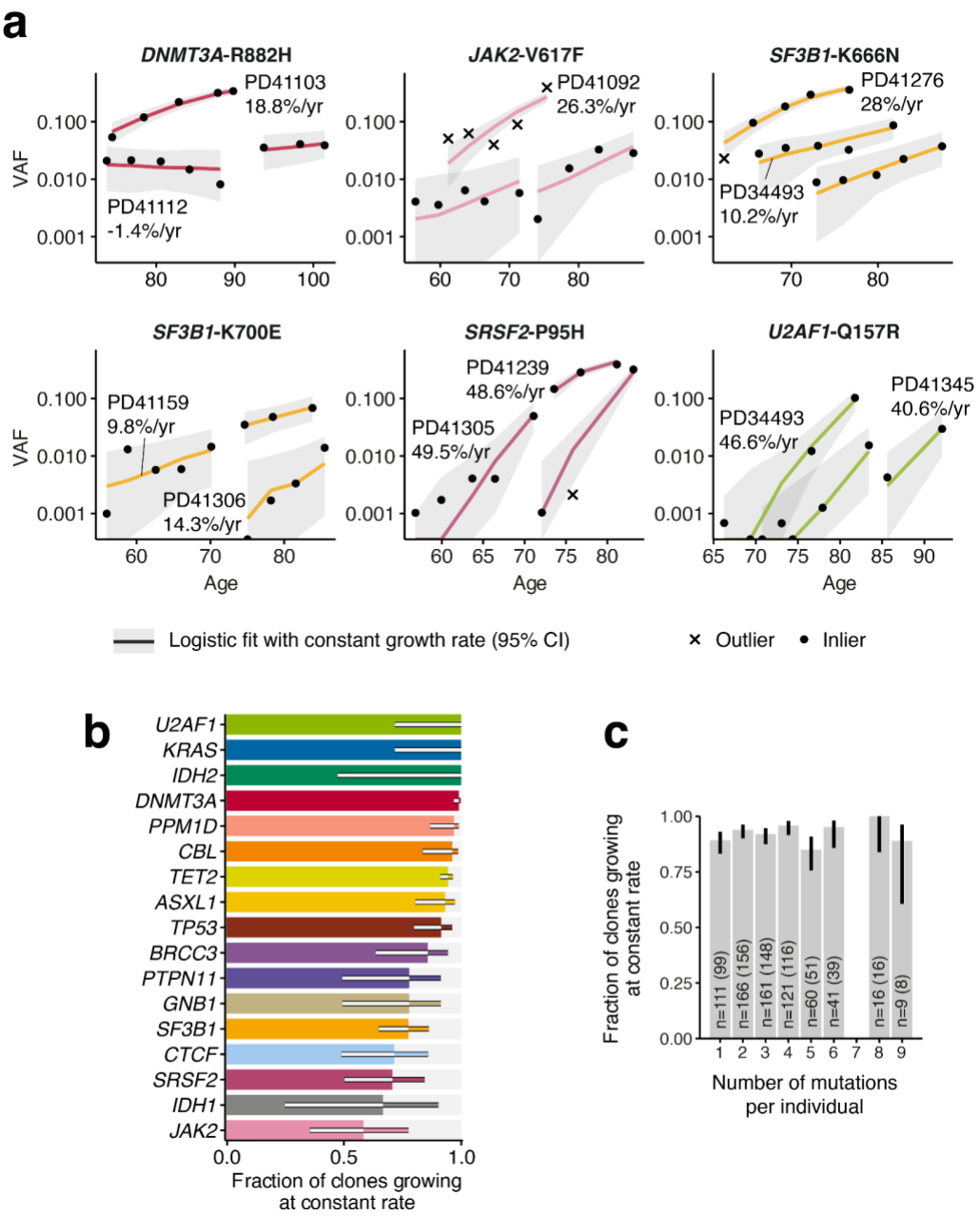


Figure 3.8: The longitudinal dynamics of CH in older age. a, Examples of fitted exponential growth of clones with mutations at 6 common hotspots. Points represent observed data, coloured lines represent estimated VAF trajectories and grey bands represent the 90% highest posterior density interval (HPDI). Each data point is represented by a dot if it conforms to our model of fixed-rate exponential growth and by a cross otherwise (outlier, defined as tail probability<2.5%). **b**, Proportion of clonal trajectories showing fixed-rate growth, ie. those with no outlying data-points as defined in (a). Bars represent this proportion and error bars represent the 90% beta-distributed confidence interval (CI). **c**, Relationship between the number of mutations co-occurring within an individual and the proportion of clones growing at a fixed rate over time (n=685 clones; the number of clones used to calculate each ratio estimate is shown on each bar and the number growing at fixed rate is shown in brackets).

We further assessed the consistency of clonal trajectories by testing our ability to predict future clonal growth. Using additional prospectively-obtained blood samples from 11 individuals, we compared observed versus predicted VAFs (Fig. 3.9a-c, Table 10) and found good concordance (mean absolute error: 3.5%), corroborating our model and providing further evidence that fixed-rate growth is the norm in old age.

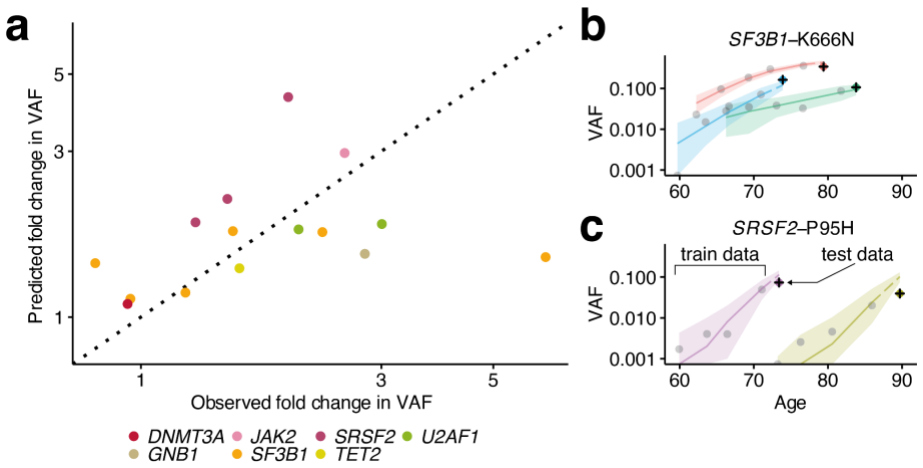


Figure 3.9: Prediction of future clonal growth. a, Association between predicted and observed VAF in additional prospectively-collected samples from 11 individuals with 15 CH driver mutations, not used for growth rate inference. The dotted line depicts theoretical perfect agreement between predicted and observed VAF. **b**,**c**, Example trajectories of clones with *SF3B1*-K666N (f) and *SRSF2*-P95H (g) mutations. Points represent VAFs used in our model to fit the growth curve (train), and crosses represent prospectively tested VAFs used (test), showing good agreement between predicted and observed VAFs. Bands represent the 95% HPDI.

3.2.4 Determinants of clonal growth rate

To delineate the factors that determine each clone's growth rate, our logistic regression model fits the following contributions of the driver mutation: i) mutated gene; ii) specific amino acid change (for recurrently mutated sites) and iii) mutation type (truncating versus non-truncating) (Table 6). An additional component in our model, measuring variation not captured by (i-iii), was also used and termed "unknown-cause growth" (Fig. 3.10).

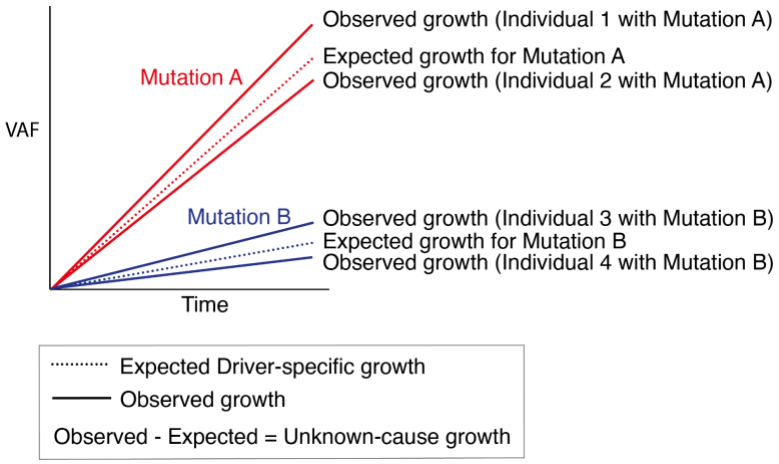


Figure 3.10: Schematic to illustrate the determinants of growth delineated by our model. Each mutant gene and/or site drives an expected rate of clonal growth. In this example, Mutation A is expected to drive faster growth than Mutation B. The growth rates of different clones bearing the same mutation, either in different individuals or in distinct clones within the same individual, can differ. Some grow faster than expected from the identity of the driver mutation (eg. Individual 1 with Mutation A), and some grow slower (eg. Individual 2 with Mutation A). The residual term in our model, the difference between observed and expected growth rate, is referred to as "unknown-cause growth".

We found that clones bearing mutations in different genes expanded at different rates, with mutations affecting *DNMT3A* and *TP53* displaying the slowest average annual growth rates of ~5% (Fig. 3.11a, Table 11). Clones with mutations in the other most common driver genes (*TET2*, *ASXL1*, *PPM1D* and *SF3B1*), expanded at roughly twice this rate, i.e. ~10%/yr. The most rapidly expanding clones were those carrying mutations in *SRSF2*, *PTPN11* and *U2AF1*, growing at over 15-20%/yr on average. The only specific mutation displaying distinctive behaviour was *SRSF2*-P95H, which was associated with significantly faster expansion compared to other *SRSF2* mutations. By contrast, all other hotspot mutations drove growth at

rates similar to mutations elsewhere in the same gene, including commonly mutated sites such as *DNMT3A*-R882, *SF3B1*-K666N and *SF3B1*-K700E.

For most genes, truncating and missense mutations drove comparable rates of growth, including *TET2* and *DNMT3A*, in keeping with the similar functional consequences of these two types of mutation in these genes[146,147]. Exceptions were (i) TP53, where missense grew 10%/yr (90% CI=[3-18%]) faster than truncating mutations (which usually did not expand or even contracted), consistent with the reported strong dominant negative effect of missense mutations in this gene[67], and (ii) CBL, where missense grew 11%/yr (90% CI=[3-19%]) slower than truncating mutations (Fig. 3.11a,b, Table 11).

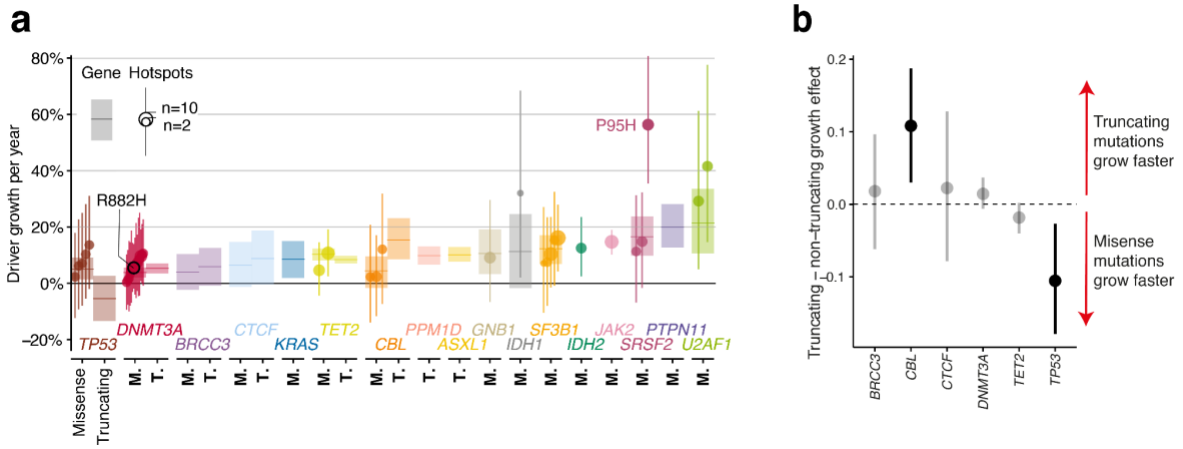


Figure 3.11: Clonal growth determined by driver mutation identity. a, Annual clonal growth associated with different driver mutations, for both genes and specific sites. For gene-wise growth, truncating and missense mutations are modelled separately for genes where both are enriched. Sites are modelled separately to genes if mutated recurrently within our cohort. Point estimates for growth and 90% HPDI are represented for each site (dot and line, respectively, with dot size proportional to recurrence) and each gene (horizontal line and rectangle, respectively). **b**, Comparison of growth rate associated with truncating vs non-truncating mutations in genes with both driver types. Points above the dashed line show faster growth for truncating mutations, and points below show faster growth for non-truncating mutations (n=514 clones). Intervals represent the 90% HPDI for the difference between truncating and non-truncating mutations.

To quantify the impact of factors other than driver mutations, we compared the observed growth rate of each clone with that predicted by the mutation (Fig. 3.12a). In Figure 3.12a, horizontal spread thereby represents variability in growth rate between clones with the same driver mutation. On average, this unknown-cause growth contributed approximately +/- 5%/yr to clonal expansion (Fig. 3.12b). Consequently, for fast-growing clones, including those associated with *SRSF2*-P95H or mutant *U2AF1*, this effect was proportionately small and

there was relatively little inter-individual variability in growth rate. By contrast, the impact on "slow" drivers, such as *DNMT3A*, was more substantial, with some clones growing twice as fast as predicted by the mutation, and others showing negligible expansion. Clones harbouring *JAK2*-V617F mutations were an exception as they displayed an unusually high degree of inter-individual variability in relation to average growth rate (Fig. 3.12a-c). In view of the well-described heritable contribution to myeloproliferative neoplasm (MPN) susceptibility[25,84], we tested if *JAK2*-V617F-mutant clones grew faster in individuals carrying more MPN risk alleles, but found no such relationship (Pearson R^2=0.03; p=0.27, two-sided), Table 12).

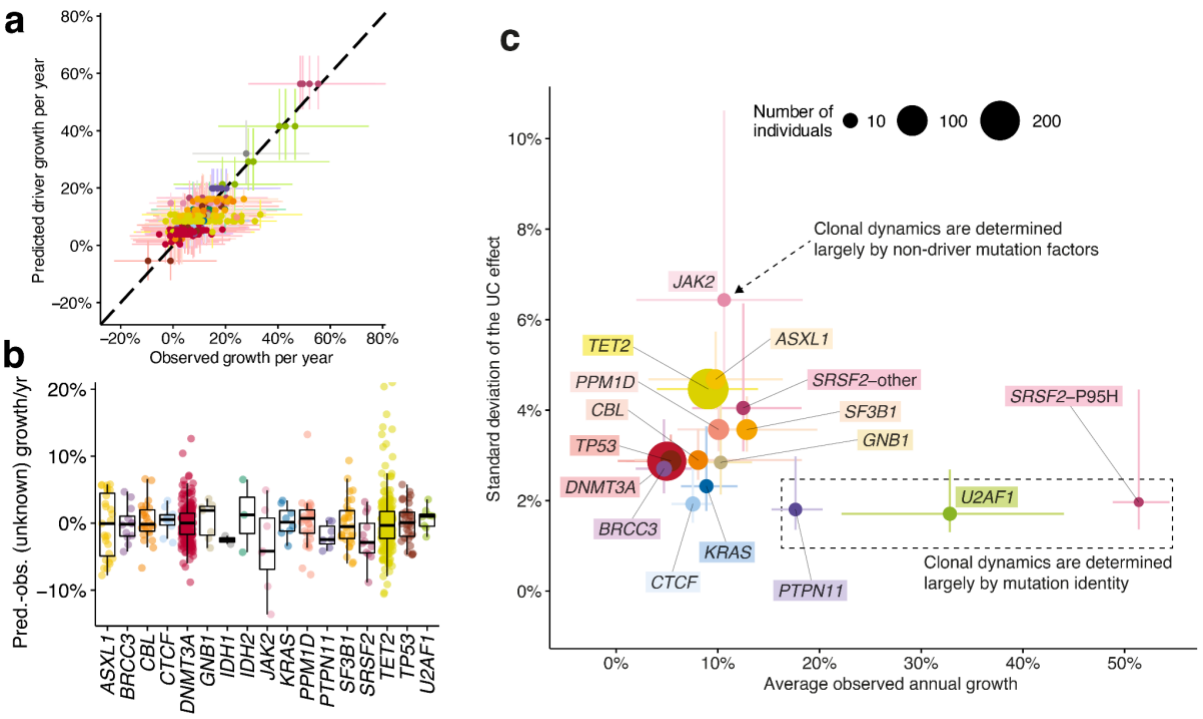


Figure 3.12: Differences in growth rate between clones with the same driver. a, Relationship between clonal growth predicted by the identity of the driver mutation and actual observed growth (points), with 90% HPDI represented by vertical and horizontal lines, respectively. **b**, Distribution of the unknown-cause effect for different genes. Each point represents a single clone and boxplots represent the distribution of these effects for each gene. The value of unknown-cause growth is *positive* for clones growing faster than expected by the identity of the driver mutation, and *negative* for clones growing slower than expected. The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile. **c**, For each gene, we contrast the mean annual growth rate among individuals/clones bearing a mutation in that gene, with the spread in this rate (defined here as the standard deviation of the unknown-cause (UC) growth). Circles represent point estimates, with circle size indicating the number of clones bearing a mutation in that gene, and lines representing the 90% confidence interval (CI). For the standard deviation, the 90% CI was calculated assuming that $((n-1)s^2 / \sigma^2) \sim Chisq(n-1)$, with n being the sample size, s the standard deviation estimate and σ^2 the true population variance. *SRSF2*-P95H mutations are plotted separately to other SRSF2 mutations, as they are associated with significantly different growth dynamics.

The more general observation that certain individuals harboured more mutations in the same gene than would be expected by chance (Fig. 3.13a) suggests that non-mutation factors influencing clonal growth are both individual- and gene-specific. We found no evidence that these non-mutation factors include either sex or smoking history, whilst age was a significant factor specifically for *TET2*-mutant clones, which grew faster in older individuals (Spearman's rho=0.31; $S=1.15*10^{6}$; adj. $p=2*10^{-6}$) (Fig. 3.13b,c).

In view of experimental data in mice suggesting that specific inflammatory signals might influence particular subtypes of CH[94,96], we tested whether these non-mutation influences on growth might include certain serum analytes. Specifically, we investigated the relationship between growth rates of clones in our longitudinal study and levels of 54 cytokines and chemokines involved in key biological processes, including inflammation, chemotaxis, angiogenesis and broader immune function (Table 7b). For this analysis, we focussed on the 230 individuals with mutations in the commonest driver genes, *TET2* and *DNMT3A*, and tested 737 serum samples collected contemporaneously with DNA samples at multiple time-points per individual (4 collections, n=100; 3 collections, n=80; 2 collections, n=47; 1 collection, n=3). While *DNMT3A*-mutant clone growth showed no significant associations, *TET2*-mutant clones grew faster in the context of elevated levels of two analytes, Placental Growth Factor (PGF) and Interleukin-7 (IL-7) (Spearman rho = 0.29 (PGF), 0.27 (IL-7); FDR = 0.025 (PGF), 0.027 (IL-7); Table 7b, Fig. 3.13d). Levels of these two analytes were not associated with each other (Spearman rho=0.05, p=0.45; Fig. 3.13e) or with absolute *TET2*-mutant clone size (Spearman rho=0.007, p=0.9 (PGF); Spearman rho=0.008, p=0.14 (IL-7)), the latter observation meaning it unlikely that these cytokines are produced by the mutant clone.

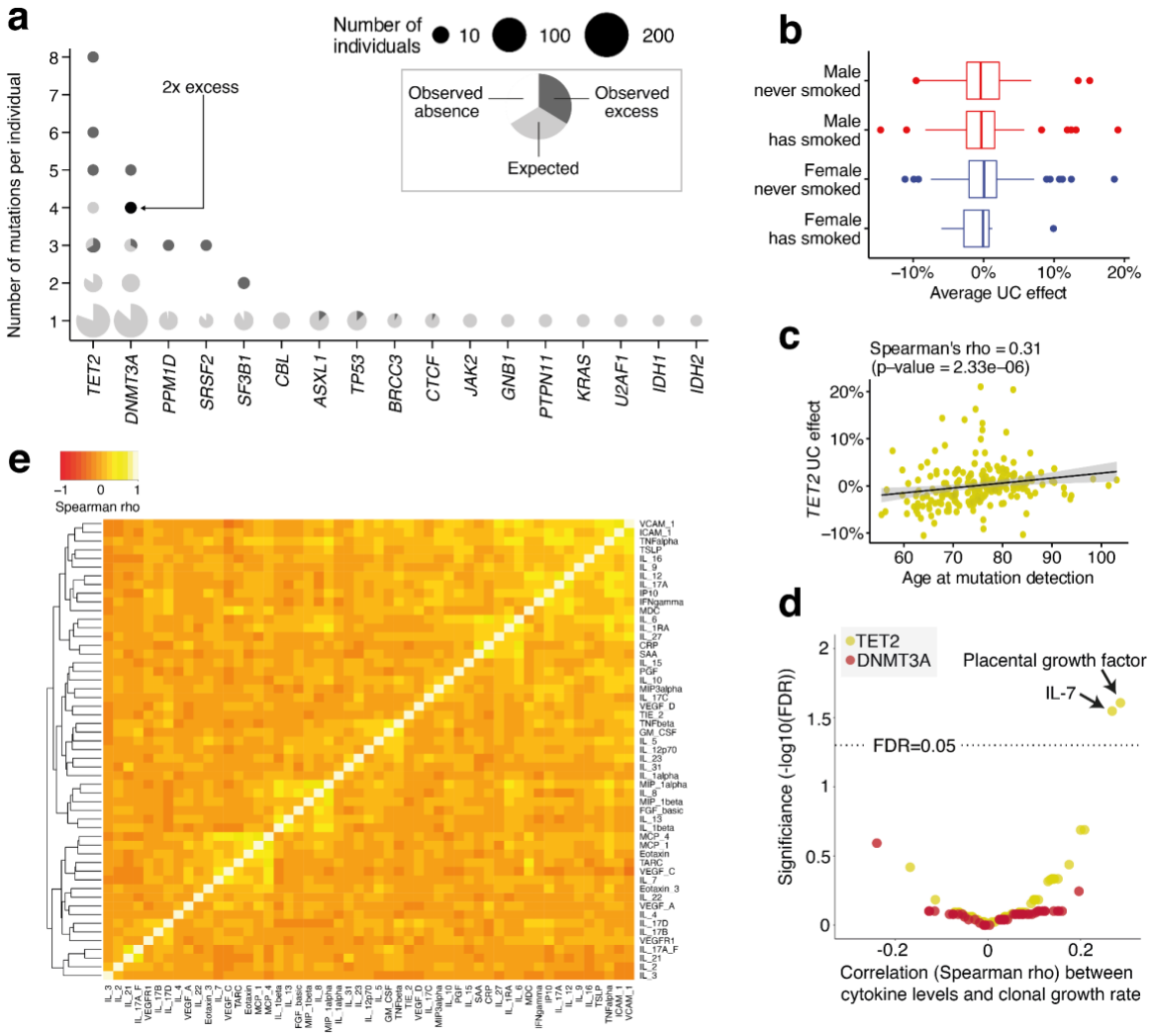


Figure 3.13: Non-driver determinants of clonal growth rate. a, This plot illustrates the recurrence of mutations in given driver genes within single individuals. Each data-point is a pie-chart. The overall **size** of the pie-chart represents how many individuals in the cohort harboured the specified number of distinct mutations (as indicated on the y-axis) in the specified gene (as indicated on the x-axis). For example, 1 individual harboured 8 distinct mutations in *TET2*, whereas 96 individuals harboured just 1 mutation in *TET2*. The relationship between number of individuals and pie-chart size is indicated in the key. The **colour** of the pie-chart represents how these observations (i.e. the degree of mutation recurrence in particular genes within single individuals) compare to what we would expect by chance. To model what would be expected by chance ("Expected"), for each gene, we take the total number of observed mutations in a gene within the cohort and distribute these randomly among the individuals in the cohort. We repeat this process iteratively 1,000 times to generate a null distribution of mutations for each gene. We then compare this "expected" distribution to that which we actually observed. In the plot, if the pie-chart is fully light-grey, the number of individuals we observed with the specified number of mutations (y-axis) in the specified gene (x-axis) was the same as that expected by chance. The presence of a white segment indicates that we found fewer individuals with that number of mutations than expected. The presence of a dark-grey segment indicates that we found an excess of individuals with that number of mutations. For both white and dark-grey, the size of the segment reflects the degree of deviation from the expected. **b,** Association between sex and smoking history and the average unknown-cause (UC; the component of clonal growth not explained by the driver gene) effect for each individual. Positive UC effect would have indicated faster growth than expected by the driver gene; negative UC effect would have indicated slower growth, but all comparisons here were non-significant (n=628 clones). The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile. **c,** Association between age at mutation detection and UC effect for each *TET2*-mutant clone (Spearman's rho = 0.31; $p=2.33*10^{-6}$ (two-sided)). The grey band represents the 95% confidence interval for the linear regression. **d**, Volcano plot showing Spearman rank associations between UC growth of *TET2* and *DNMT3A*-mutant clones and levels of 54 serum

cytokines and chemokines. FDRs are Benjamini-Hochberg-corrected for multiple testing. Horizontal dashed line indicates FDR significance level of 0.05. **e**, Heatmap showing co-correlation between the 54 cytokines/chemokines analysed. The order of analytes on the map is dictated by hierarchical clustering, reflected in the dendrogram, with analytes connected by the shortest branches sharing the strongest correlation. Colour indicates correlation strength and direction (see key).

3.3 Discussion

Here, we characterised the longitudinal behaviour of CH over long periods of time in elderly individuals. Remarkably, we found that most clones (92.4%) displayed stable exponential growth rates. This allowed for accurate prediction of future clonal trajectories, a finding with potentially important implications for clinical practice.

Different mutations drove substantially different growth rates, ranging from 5% (*DNMT3A*, *TP53*) to over 50%/yr (*SRSF2*-P95H). It was surprising that mutations in *DNMT3A*, reportedly the most common CH driver gene[14–16], were associated with slower clonal expansion than most other CH genes. Also, *DNMT3A* hotspot mutations (e.g. at codon R882) were not associated with faster growth than other *DNMT3A* mutations. By contrast, *TET2*-mutant clones expanded significantly faster over the study period. This resulted in *TET2* becoming the most prevalent CH driver after the age of 75 years. These findings suggested that, while clonal growth is remarkably stable in old age, dynamics in earlier life may deviate from this behaviour, challenging the premise that mutation fitness is constant lifelong[139]. We address this directly in Chapter 5.

Comparing the growth dynamics associated with truncating vs non-truncating driver mutations was interesting. We saw no significant difference for the two most common driver genes, *TET2* and *DNMT3A*. It is notable that recent evidence suggests that the functional consequences of these two types of mutation can be similar in *DNMT3A*, with many missense mutations leading to protein instability and degradation[146], as truncating mutations do. Also, for *TET2*, whilst truncating mutations were spread fairly evenly across the gene, missense mutations were clustered in its conserved domains, in keeping with both types of mutation resulting in reduced *TET2* function.

In comparison, for *TP53* and *CBL* we found that truncating and missense mutations had distinct impacts on clonal growth (missense faster in *TP53*, truncating faster in *CBL*). It is interesting to note the previously reported functional differences in *TP53* mutations, with missense variants exerting a strong dominant negative effect[67], which would be predicted to be more detrimental than heterozygous truncating mutations, and compatible with a stronger

phenotype (in our study, faster expansion). It is also notable that prognosis in some haematological malignancies is worse in individuals with missense vs truncating *TP53* mutations and it is plausible that this relates to a stronger anti-apoptotic phenotype associated with the former[148,149].

Growth rates of clones with the same mutation differed by approximately +/-5%/yr, proportionately impacting "slow" drivers more substantially. Our observation that mutations in particular genes tended to cluster within individuals – for example, 3 individuals harboured 5 or more distinct *TET2* mutations, one with 8 – is in line with findings in other non-malignant tissues[1]. Along with previous studies suggesting that some driver mutations confer little or no competitive advantage without particular external pressures[62,92,94,140–142,145], this points to the importance of additional individual- and driver-specific factors in influencing mutation fitness.

Indeed, we found that *TET2*-mutant clonal growth was faster in older individuals and also in those with elevated levels of particular cytokines, and PGF is of particular interest for future investigation here. PGF is a member of the vascular endothelial growth factor (VEGF) family, its receptor (VEGFR1) is expressed on HSCs where PGF binding promotes exit from quiescence and, while it has many pleiotropic roles in pathologic conditions (including autoimmunity and cancer), it is largely redundant in healthy physiology[150–157]. This last feature makes it an attractive potential therapeutic target[158], and a promising focus for future confirmatory studies.

Two features of *JAK2*^{V617F} clonal dynamics were notable. First, only 58% (7/12) of clones grew at a constant rate over time, compared to a cohort average across drivers of 92.4%. Second, when comparing the 7 individuals with clones showing constant growth, the differences in growth rate were higher than we observed for any other mutant gene or site. These observations suggest that JAK2-mutant clonal growth is especially sensitive to additional influences. We did not find that inheritance of MPN risk alleles plays a major role here, but it will be interesting to investigate this and other potential factors, such as loss-of-heterozygosity at the V617F locus[159] and variable IL-18 levels[25], in future studies.

In summary, we observed largely constant clonal growth in elderly individuals, at a rate determined in large part by the identity of the driver mutation. Whilst we uncovered several additional factors influencing the component of growth *not* explained by driver identity, the determinants of this non-driver component remained incompletely defined. We questioned whether the inherited genome might play a role here and, since our longitudinal cohort was not suitable to address this question, we instead used an orthogonal approach, as detailed in the next chapter (Chapter 4).

Chapter 4

The influence of the inherited genome on CH

4.1 Introduction

Our investigation of the potential influence of the inherited genome on CH was prompted by a number of observations. From our own work, we noted that *(i)* there is variability in growth rate between clones with the same driver mutation (Fig. 3.12), and *(ii)* the non-mutation factors driving this variability are, at least in part, individual-specific, with clones bearing mutations in particular driver genes tending to cluster within certain individuals (Fig. 3.13a), a phenomenon also observed in other tissues[160]. In addition, a number of studies suggest that these observations might be contributed to by heritable genetic factors, reporting: *(i)* heritable genetic variants associated with increased risk of developing MPNs[84,85], *(ii)* familial clustering of CH driven by *TET2* mutations[86], and *(iii)* increased prevalence of CH among relatives of individuals with myeloid, but not lymphoid, malignancies[87].

Moreover, a number of germline variants have emerged as important determinants of haematological phenotypes in the general population and it is plausible that these exert epistatic effects on CH evolution[88]. To investigate whether the inherited genome influences CH development, we performed deep targeted sequencing on blood DNA from 52 monozygotic (MZ) and 27 dizygotic (DZ) twin pairs, and analysed patterns of twin-to-twin concordance for CH.

4.2 Results

4.2.1 Cohort overview

We studied blood DNA from 158 individuals from the TwinsUK cohort, comprising 52 MZ and 27 DZ twin pairs with no history of haematological malignancy, aged 70-99 years (150 females, 8 males)[119].

4.2.2 Mutational landscape in elderly twins

Using deep targeted sequencing (mean 1650X) of 41 genes implicated in CH and myeloid malignancies (Table 1b) and sensitive variant-calling, we identified CH (VAF ≥0.5%) in 62% of individuals (95/154; Fig. 4.1a). The distribution of clone size was skewed towards low VAFs; larger clones (VAF ≥2%) were present in 41 individuals (Fig. 4.1b). Somatic driver mutations were identified in 16 of the 41 genes sequenced, with mutations in the epigenetic regulators *DNMT3A* and *TET2* predominant (Fig. 4.1c; Table 13). Almost one third of individuals (48/154) harboured multiple distinct mutations (range 0-5) (Fig. 4.1d).

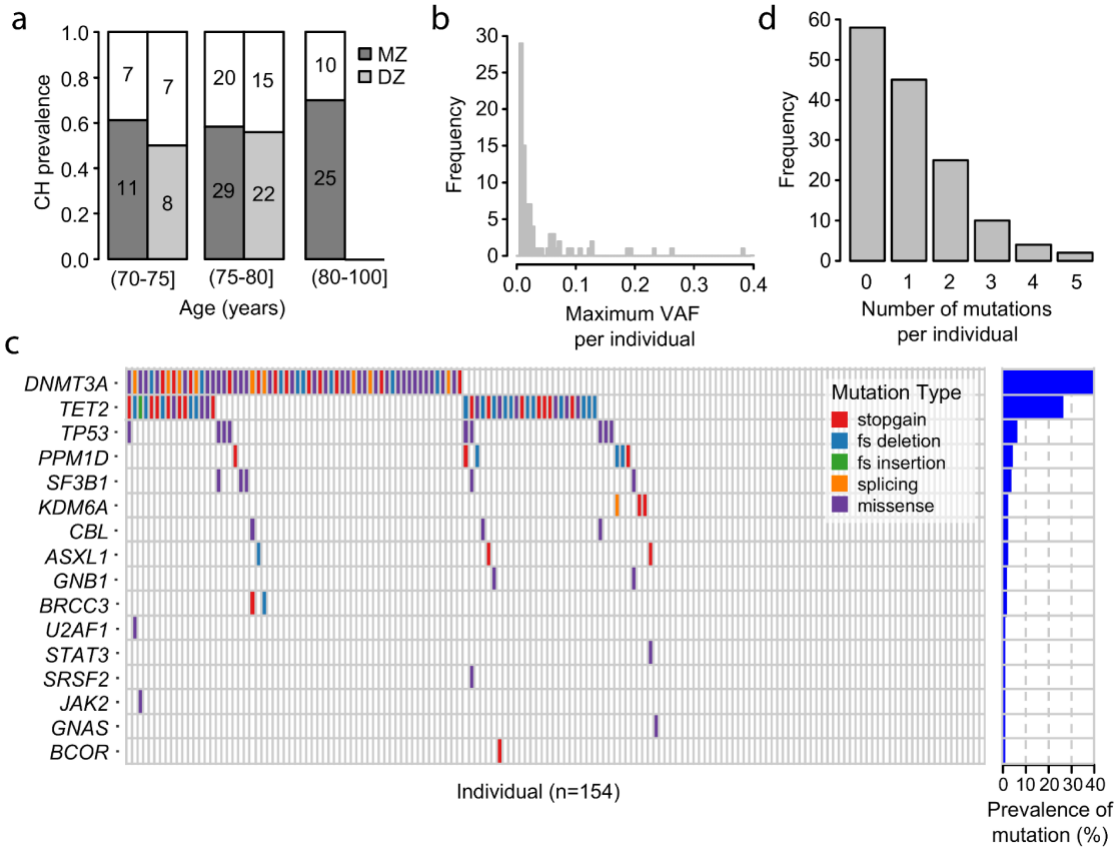


Figure 4.1: Mutational landscape in twins cohort. a, Prevalence of CH. Dark grey bars (and white bars directly above) represent individuals in MZ twin pairs; light grey bars (and white bars directly above) represent those in DZ pairs. Lower stacks depict the proportions *with* CH; upper stacks depict those *without* CH. Absolute numbers of individuals in each proportion are shown within each bar. There were no DZ individuals above the age of 80 years. **b**, Distribution of the maximum VAF per individual among those with CH. VAFs are divided into 0.5% bins. **c**, In the main grid, each column represents 1 individual, and each row 1 gene. If a grid square is colored, a mutation was detected, and the specific colour indicates the mutation type (see key). The plot on the right shows the proportion of the cohort harbouring a mutation in each gene. **d**, Distribution of the total number of mutations per individual. fs, frameshift.

4.2.3 Limited CH concordance in twin pairs

Comparing age-matched samples from MZ and DZ groups (age range, 70-80 years; n = 33 MZ pairs and 24 DZ pairs), the overall prevalence of CH was very similar (59% and 54%, respectively; *P* = .70). We did not observe significantly higher concordance for CH within MZ twin pairs as compared with DZ pairs (*P* = .59; Fig. 4.2a). Furthermore, using random permutation to model the null distribution, we found no difference in the observed distributions of CH among either MZ or DZ twins as compared with those expected by chance (*P* = 1 for MZ; *P* = .86 for DZ; Fig. 4.2a). Excess twin concordance was also not observed when CH

positivity was defined by (i) mutation in *DNMT3A*, (ii) mutation in *TET2*, and (iii) mutation in any gene with VAF >2%.

In 8 individuals (4 MZ twin pairs), serial blood samples were taken 4 to 5 years apart. CH clones were identified in both twins in 3 of 4 of these pairs, and inter-twin variability in clonal size and trajectory was seen in all 3 (Fig. 4.2b). This was the case even for clones harbouring mutations in the same gene.

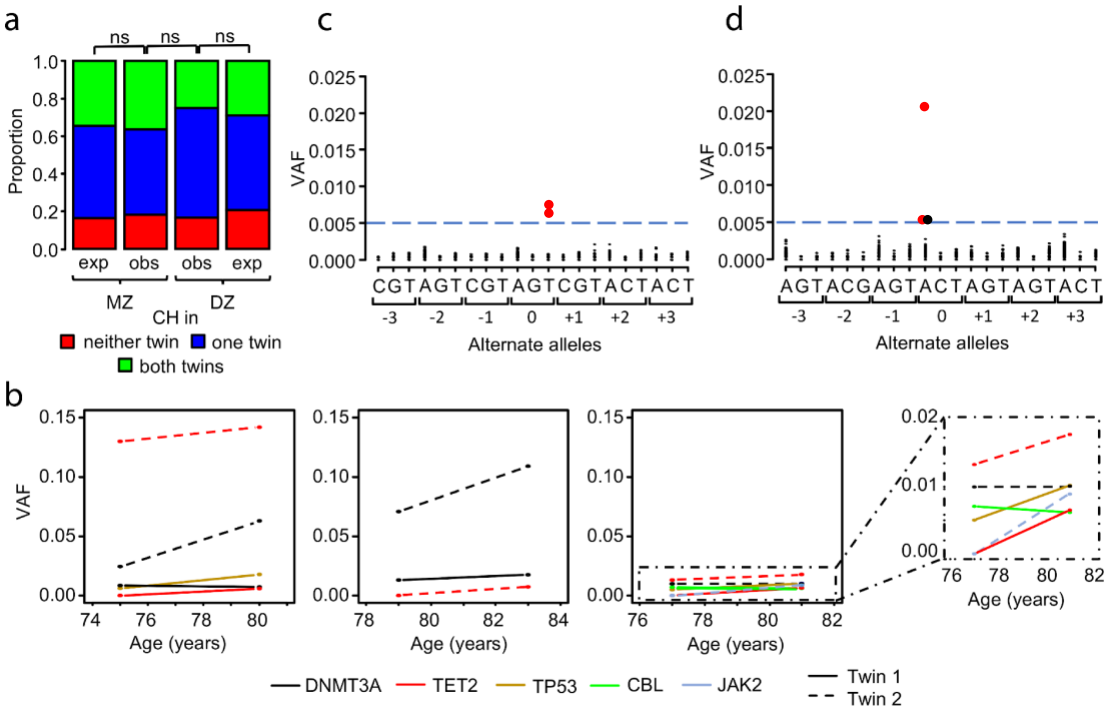


Figure 4.2: CH in twin pairs. a, Concordance for CH status in age-matched MZ (n = 33) and DZ (n = 24) twin pairs. Observed (obs) proportions are those identified in the cohort, and expected (exp) are those generated by random sample permutation. There was no significant difference when comparing (i) the observed distributions between MZ and DZ twins (*P* = .59) and (ii) the observed vs expected distributions within the MZ (*P* = 1) or DZ (*P* = .86) twin groups (Fisher exact test). **b**, Change in VAF over time in the 3 twin pairs in which both individuals had CH and serial samples were available. Each box surrounded by a solid line represents a twin pair. The fourth box surrounded by a dashed line is data from the third twin pair with the y-scale magnified to the lower VAFs. In each box, change in VAF over time is represented by a solid line for 1 twin, and a dotted line for the other, with line colour indicating which gene was mutated. **c,d** The variants identified in 2 MZ twin pairs in which both twins harboured identical nonsense mutations: *KDM6A* (NM_021140:c.C2074T:p.Q692X) (**c**) and *DNMT3A* (NM_175629:c.C1792T:p.R598X) (**d**). Each "triplet" represents the 3 non-reference bases at each genomic position, centred on the identified variant position (denoted as 0). For each alternate allele, the VAF of each of the 154 individuals in the cohort is plotted. The horizontal dashed line represents the lower limit of sensitivity of variant calling, with calls below this VAF considered error. MZ twins with identical mutations are plotted in red; unrelated individuals are in black. ns, not significant.

4.2.3 Early origins of CH

Despite the overall lack of concordance for CH, we did identify 2 MZ pairs in which both twins harboured identical nonsense mutations, namely *KDM6A* Q692X in 1 pair and *DNMT3A* R598X in the other (Fig. 4.2c,d; Table 13). KDM6A (= UTX) is a histone H3 lysine 27 demethylase that acts as a tumour suppressor in a number of different cancers, including 2% to 3% of myeloid malignancies[161]. There are no somatic mutation hotspots in *KDM6A* and the substitution identified here is not reported in either the Catalogue Of Somatic Mutations In Cancer (COSMIC) database (cancer.sanger.ac.uk/cosmic) or in several large, albeit less sensitive, CH studies (total number of participants >30 000)[14–16]. Although mutations in *DNMT3A* are generally more prevalent, the particular mutation detected here is not common. In this light, the likelihood that each member of these 2 twin pairs acquired the same mutation independently and by chance is extremely small. A more plausible explanation is that the somatic mutation occurred just once during embryogenesis, either prior to twinning or in an HSC whose progeny reached both twins through shared circulation in utero. Although monozygotic twin sharing of somatic mutations has been demonstrated in other settings, including paediatric leukaemia, this was the first description of possible acquisition of adult-type CH driver mutations in utero[162,163].

4.3 Discussion

In summary, we found no evidence of high concordance for CH in elderly MZ twins. This finding was corroborated by a separate larger study of 594 elderly twins[164]. In addition, we observed disparity in clonal size and trajectory over time, even between MZ twins harbouring mutations in the same driver genes. Although our cohort size was too small to precisely quantify genetic vs environmental contributions, maximum likelihood modelling provided support for a substantial influence of non-inherited factors upon CH emergence and behaviour (Table 14).

Overwhelming evidence shows that mutation acquisition is widespread and inevitable in the ageing hematopoietic system[82], as is the case in all other healthy tissues studied to date[160,165,166], indicating that this is not the rate-limiting step in CH development. By suggesting that the inherited genome does not play a dominant role, these findings frame non-genetic events as important factors in CH emergence. Altered interactions of the HSC with its environment, associated with processes such as ageing, senescence, inflammation, and infection, are plausible operators, some of which are supported by evidence from experimental models[94,96].

In conclusion, the lack of strong concordance for CH and the variable clonal trajectories between MZ twins indicate that the inherited genome does not exert a profound influence on the emergence and behaviour of CH in older adults. In addition, sharing of rare somatic mutations by MZ twins raises the possibility that mutations driving adult CH can be acquired *in utero*. This last observation has profound implications for our understanding of clonal behaviour, suggesting that many decades may pass between driver mutation acquisition and the development of detectable CH. In conjunction with our findings detailed in Chapter 3, this compelled the next phase of study: investigation of CH dynamics across the entire human lifespan (Chapter 5).

Chapter 5

Clonal dynamics across the human lifespan

5.1 Introduction

A number of questions were raised by our longitudinal study of clonal behaviour in elderly individuals (Chapter 3) and by our study of CH concordance in twins (Chapter 4):

1. How could *DNMT3A*, the gene driving one of the slowest rates of clonal growth in old age, also be the commonest CH driver gene, by a considerable margin, in younger individuals[14–16]?
2. Why is *TET2* a substantially less common driver of CH in younger individuals compared to *DNMT3A*[14–16], despite our observation that it drives growth twice as fast as *DNMT3A* in old age?
3. How could *DNMT3A*-R882 mutations drive the same rate of clonal growth as all other *DNMT3A* mutations, yet be such a marked hotspot, especially in younger individuals[146]?
4. Why are the genes driving the fastest rates of growth in old age (*U2AF1* and *SRSF2*) almost never found to drive CH in younger individuals[29]? Do these mutant clones emerge early but remain undetectable until they 'take-off' in old age, or do they arise only late in life?
5. With the demonstration that mutations driving CH in elderly adults can be acquired in utero, what is the nature of clonal behaviour across so many decades?

The apparent discrepancies between the clonal dynamics we observed in old age and driver prevalence patterns found at different stages of life suggested that, while clonal growth is remarkably stable in old age, dynamics in earlier life might deviate from this behaviour. Our objective in this next phase of study was to characterise the driver-specific behaviours of CH across the entire human lifespan.

5.2 Results

5.2.1 Study design

We utilised two orthogonal approaches to investigate lifelong clonal behaviour. First, we used our longitudinal cohort, described in Chapter 3, extrapolating the observed (fitted) trajectory of each clone backwards in time to infer the age at clonal onset. Second, we whole-genome-sequenced 96 single-cell-derived haematopoietic colonies from each of 3 elderly individuals in the longitudinal cohort, and constructed phylogenetic trees to infer lifelong clonal structure and dynamics.

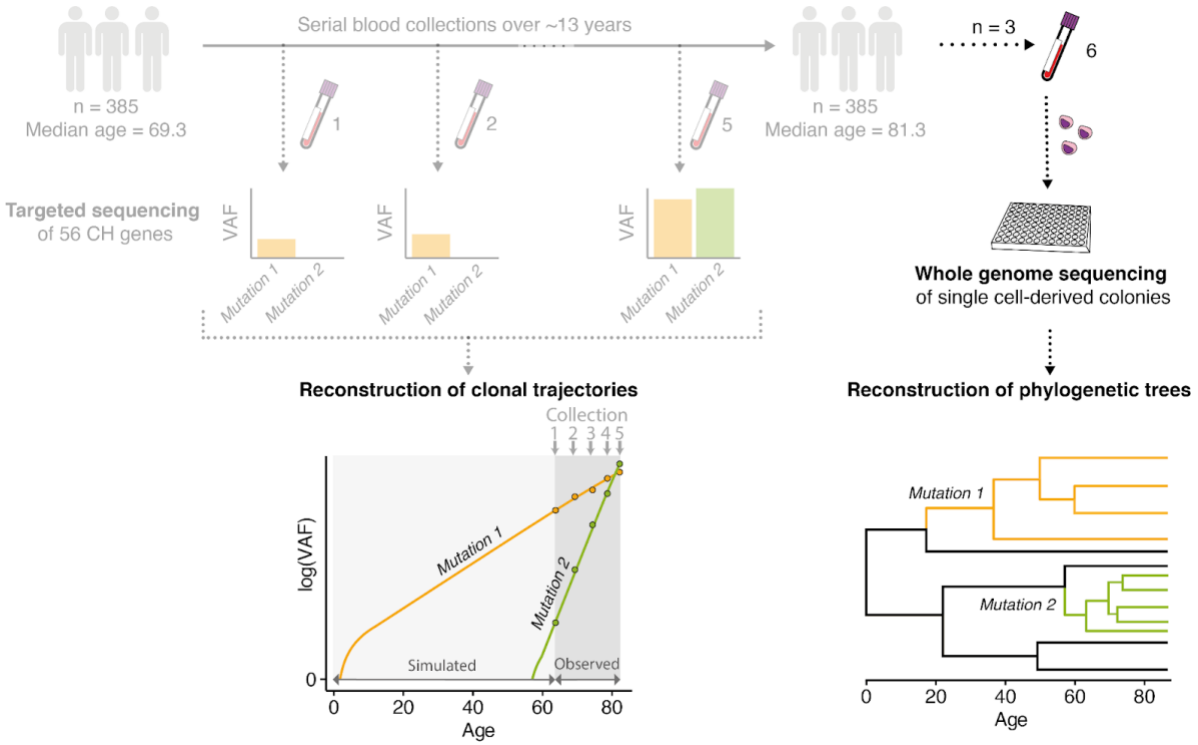


Figure 5.1: Experimental workflow phase 2. Fitted clonal trajectories derived from the longitudinal data were extrapolated back in time to estimate the age at clonal emergence. Additional blood samples from 3 selected individuals were used to generate 288 (3x96) whole-genome sequenced single cell-derived colonies for phylogeny reconstructions.

5.2.2 Phylogenies reveal clonal architecture and lifelong dynamics

We derived and whole-genome-sequenced (WGS) 96 haematopoietic colonies, each originating from a single stem/progenitor cell and expanded *in vitro* to a clone of hundreds to thousands of cells, from each of three individuals with splicing gene mutations (Fig. 5.2a-c), particularly as previous reports suggested a sharp increase in prevalence of these driver mutations late in life[29]. We constructed phylogenetic trees using somatic mutations as lineage-tracing barcodes and, since HSCs accumulate mutations at a near constant rate, we used phylogenetic branch lengths to time the onset of clonal expansions ("clades")[3–8]. In PD41276, the phylogeny was dominated by an *SF3B1*-K666N-mutant clone, beginning between 23-47 years of age, with only a single *SF3B1*-wild type colony, consistent with a near-complete clonal sweep (Fig. 5.2a). In PD34493, *SF3B1*-K666N was acquired prior to the age of 35 years, whilst *U2AF1*-Q157R initiated clonal growth later (age 41-61) in a previously expanded clade lacking recognisable drivers (Fig. 3b). Interestingly, an additional apparently driverless expansion - a phenomenon recognised in old age[3,15] - was observed in this individual (Fig. 5.2b), and a further 3 such expansions in PD41305 (Fig. 5.2c). In PD41305, since the *SRSF2*-P95H mutation was present in only one colony, we could only time its acquisition to the broad interval between 13 years and the age of sampling (73 years).

We next used the timing and density of clonal branchings (or "coalescences") to reconstruct the entire growth trajectories of expanded clades using phylodynamic principles (Fig. 5.2d-h)[5,135,136]. This revealed that the three clades with identified drivers (*SF3B1*-K666N and *U2AF1*-Q157R in PD34493, and *SF3B1*-K666N in PD41276), expanded (Fig. 5.2d-f) at calculated rates similar to those observed in our time-series VAF measurements during older age (Fig. 5.2i, left panel). Of note, *SF3B1*-K666N was associated with a substantially different growth rate in PD41276, where it expanded at 28%/yr by serial VAFs (29%/yr by phylodynamic estimate), versus 10%/yr in PD34493 (17%/yr by phylodynamics) (Fig. 5.2i). Reasons for this difference are unclear, but it is notable that the faster-growing clone had antecedent Y loss (Fig. 5.2a), an aberration seen in clades from all three individuals and associated with only modest clonal expansion when isolated (Fig. 5.2a-c). Interestingly, clones without known drivers began to expand within the first two decades of life and grew over their lifetimes at rates comparable to clones with known drivers (14-32%/yr) (Fig. 5.2g,h; Fig. 5.3).

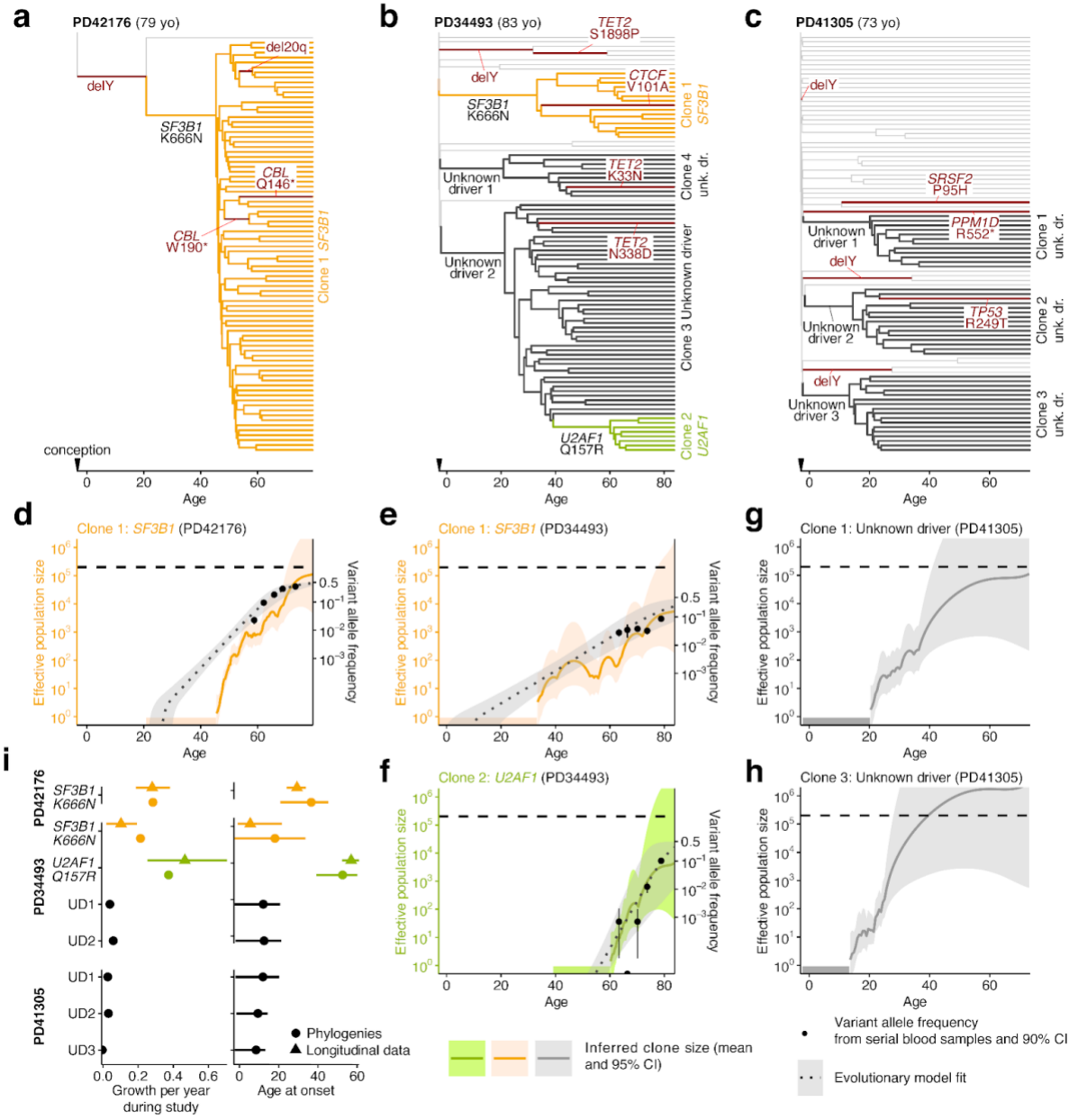


Figure 5.2: Haematopoietic phylogenetic trees. a-c, Haematopoietic phylogenies of participants PD41276 (a), PD34493 (b) and PD41305 (c). Each tree tip is a single cell-derived colony and tips with shared mutations coalesce to an ancestral branch, from which all colonies in such a "clade" arose. Branch lengths are proportional to the number of somatic mutations, which accumulate linearly with age except before birth, at which point ~55 mutations have been acquired[167]. Branches containing known driver mutations or chromosomal aberrations are annotated. Clonal expansions are coloured: *SF3B1*-K666N-mutant expansions in orange, *U2AF1*-Q157R-mutant expansions in green, and expansions without identified drivers ('Unknown driver' or 'UD') in black. **d-h**, Growth trajectories of each clonal expansion, as determined by (i) phylogenies (effective population size (Neff) estimated using phylodynamic methods), and (ii) time-series data (using serial VAF measurements and modelled historical growth, as illustrated in Fig. 2, if available). Phylogeny-derived age at clone onset range is represented as a horizontal coloured bar on the x-axis, with the limits of the bar corresponding to the age range of the phylogeny branch along which the corresponding driver mutation was acquired. **i**, Comparison of the ages at onset (right) and growth rate during study period (left) derived from phylogenetic trees and longitudinal data. For the age at onset and growth rates derived from longitudinal data, the intervals represent the 90% HPDI; age at onset intervals derived from phylogenies represent the age limits defined by phylogenetic branching patterns. For annual growth estimates using phylogenies, intervals represent +/- the standard error.

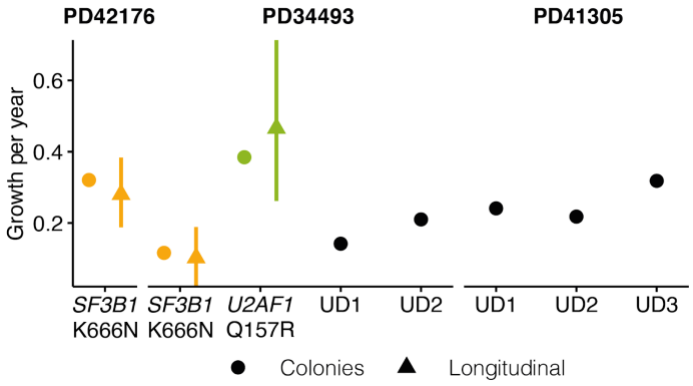


Figure 5.3: Lifelong growth in phylogenetic trees. Comparison between annual growth derived from phylogenies and growth observed in longitudinal data. For the phylogenies, this was obtained by fitting an exponential growth curve to the entire phylodynamic trajectory. For growth rates derived from longitudinal data, error bars represent the 90% HPDI; for growth rates derived from phylogenies (colonies), error bars represent +/- the standard error.

5.2.3 Many clones decelerate before old age

As the phylodynamic reconstruction of a clone goes back to its inception, we investigated whether clonal growth dynamics during earlier life deviate from the stable growth observed during older age. To corroborate observations from the three individuals depicted in Figure 5.2, we conducted additional phylodynamic analyses of trees derived from 1,461 whole-genome sequenced single cell-derived colonies from another four individuals aged 75-81yrs from the study by Mitchell *et al*[3]. This revealed that, in many instances, the reconstructed effective population size (Neff) of any individual clone grew more slowly towards the sampling date and before it saturated the HSC compartment (Fig. 5.4a-b; Fig. 2.3 in Methods, Chapter 2). This characteristic deceleration was quantified by fitting a biphasic exponential growth model to early and late parts of the trajectories (Fig. 5.4c). In most cases, extrapolating early growth (a consistent estimator of the fitness advantage of a clone in Wright-Fisher simulations, Fig. 2.3d and Fig. 2.4 in Methods, Chapter 2) led to dramatic overestimations of clade size (median 35x; Fig. 5.4d).

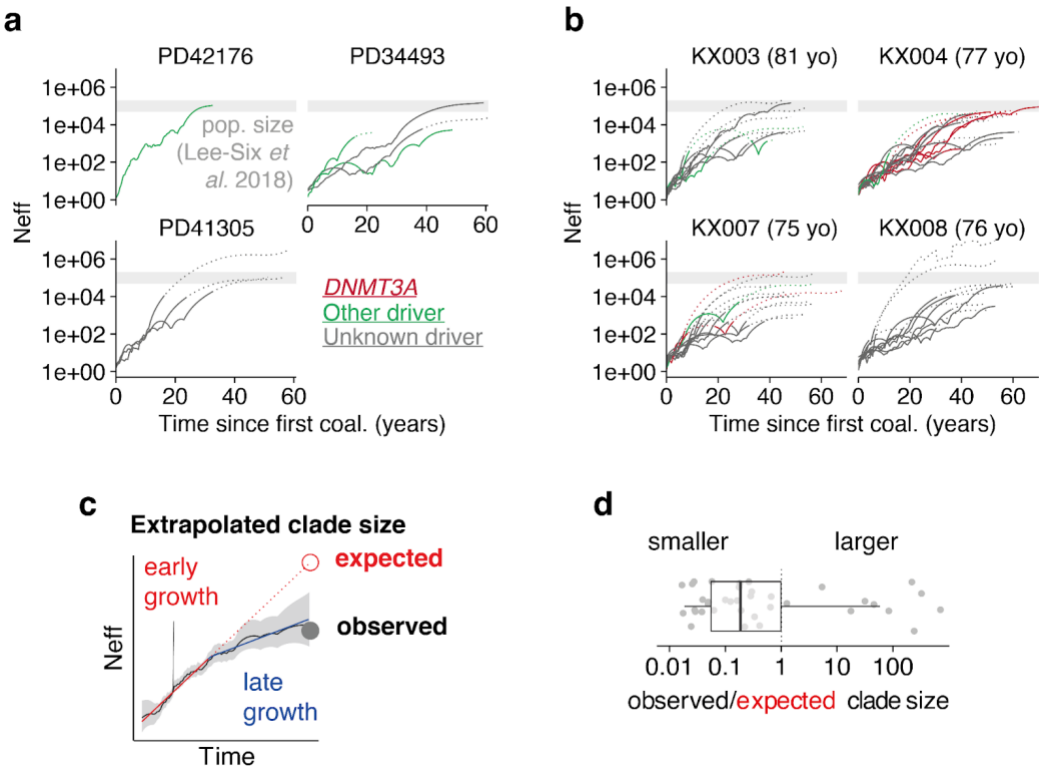


Figure 5.4: Evidence for clonal deceleration from phylogenies. a,b. Effective population size (Neff) trajectories inferred from single cell phylogenies in this paper (a) and in Mitchell et al[3] (b). Dotted lines represent parts of the trajectory with high variance (log(var(Neff)) > 5). **c.** Representation of biphasic fit to Neff estimates and extrapolation from early growth (observed clone size is calculated as the clonal fraction in the phylogeny scaled by a Neff of 200,000 HSC x yr). **d.** Ratio between observed and expected (extrapolated from early growth) clone size from phylogenies (n=37 expanded clones detected in haematopoietic phylogenies).

We used our longitudinal cohort to orthogonally test the lifelong stability of clonal growth by extrapolating the observed (fitted) trajectory of each clone backwards in time to infer the age at clonal onset. To account for stochastic drift, which can lead to faster growth of small clones, and the finite carrying capacity of the HSC population, which naturally limits/slows large clones, we derived and used an approximation to a Wright-Fisher process (Fig. 3.7 in Chapter 3). While estimates of age at clonal onset agreed with phylogenetic estimates for the fast-growing splice factor mutations (Fig. 5.2i), for many other clones, constant lifelong growth at the rate we observed during old age would be too slow to explain the observed VAFs (Fig. 5.5), proposing that clonal expansion was faster in earlier life. These observations reveal that, at least for some clones/genes, the dynamics observed in later life are not representative of those that prevail earlier.

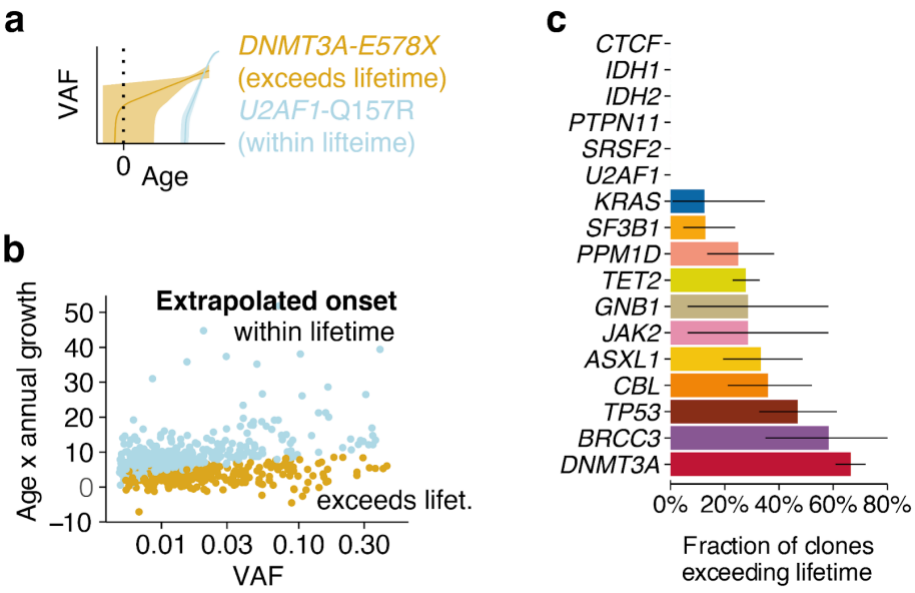


Figure 5.5: Retrograde extrapolation of trajectories observed in old age. a, Representation of extrapolated trajectories derived from longitudinal data, assuming stable lifelong growth at the same fixed rate we observed during older age; some projections are not feasible (ie. exceeding lifetime, with onset pre-conception). **b**, Relationship between age and observed growth rate of clones and VAF (longitudinal data; light blue represents clones with projected onset within lifetime and golden represents those exceeding lifetime). **c,** Quantification of unfeasible clones (exceeding lifetime) per gene (longitudinal data, n=633). Intervals represent the beta-distributed 90% confidence interval.

We then assessed the minimum lifetime rate at which clones must have grown in order to reach the observed VAFs in our longitudinal data, henceforth termed 'historical growth', by restricting fits/solutions to growth rates that would place the age of clonal onset within individuals' lifetimes (Fig. 5.6a, Table 15). Expectedly, this minimal historical growth rate was typically higher than the growth rate observed during the study period (i.e. in older age; Fig. 5.2b). Moreover, the fold-changes between historical and observed growth rates derived from longitudinal data were qualitatively in good agreement with the fold-changes between late growth and expected growth (the latter assuming growth is constant through life and carrying capacity is fixed) derived from phylodynamic data (Fig. 5.4c, Fig. 5.6b). Taken together it thus emerges that many clones grew more rapidly early in life compared with the rate in old age.

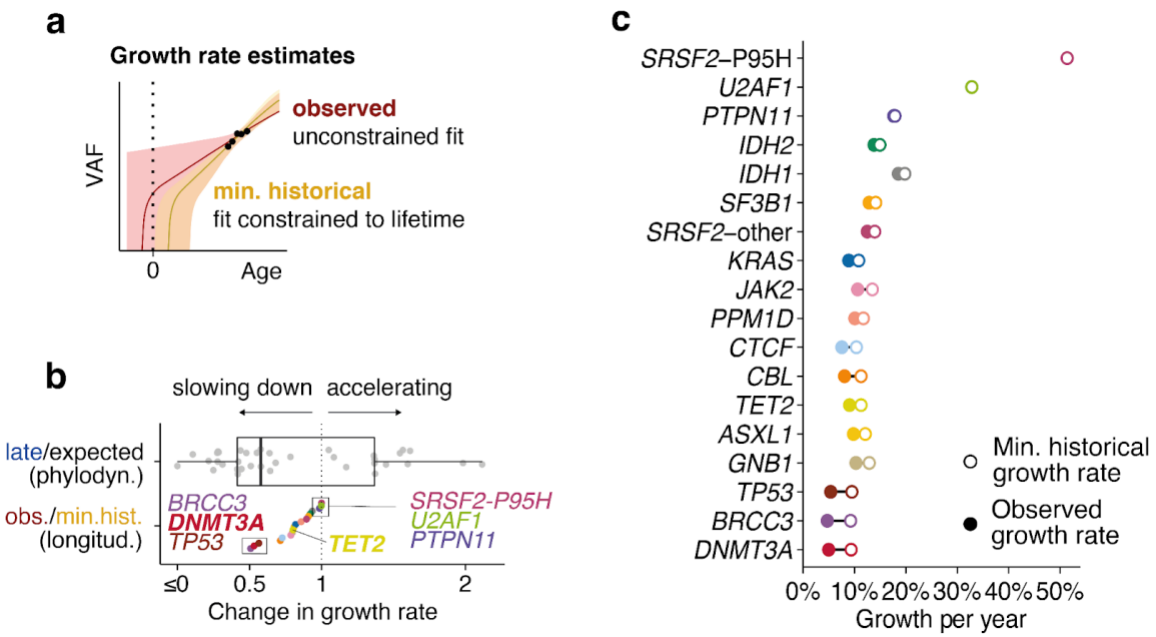


Figure 5.6: Minimum lifetime (historical) clonal growth rate. a, Representation of the calculation of minimum historical growth. **b.** Quantification of the ratios between observed and historical (longitudinal data) and between late and expected (phylogenetic data) growth (n=37 clones detected in phylogenies (top); n=633 in longitudinal data (bottom)). **c,** Differences between the median observed and historical growth per year for each gene.

5.2.4 Driver genes and lifelong clonal growth

The effect of deceleration was most marked for clones bearing mutations in *DNMT3A*, *BRCC3* and *TP53*, whose early growth was at least twice as fast as that measured during old age (Fig. 5.6b,c). Conversely, we observed almost no deceleration of fast-growing clones harbouring *U2AF1*, *SRSF2*-P95H, *PTPN11* or *IDH1* mutations (Fig. 5.6b,c). It is particularly notable that the *TET2*-mutant clones were much less susceptible to deceleration than *DNMT3A*-mutant clones (Fig. 5.6b,c). This is consistent with the observation that the prevalence of *TET2*-mutant CH rises at older ages and eventually exceeds that of *DNMT3A*-mutant CH, which is more prevalent at younger ages (Fig. 3.6c). A declining relative advantage of *DNMT3A* mutations in older age was also suggested by the much lower proportion of *DNMT3A* mutant-clones reaching detectable limits during our study period compared to clones bearing mutations in other genes (“incipient clones”, Fig. 5.7).

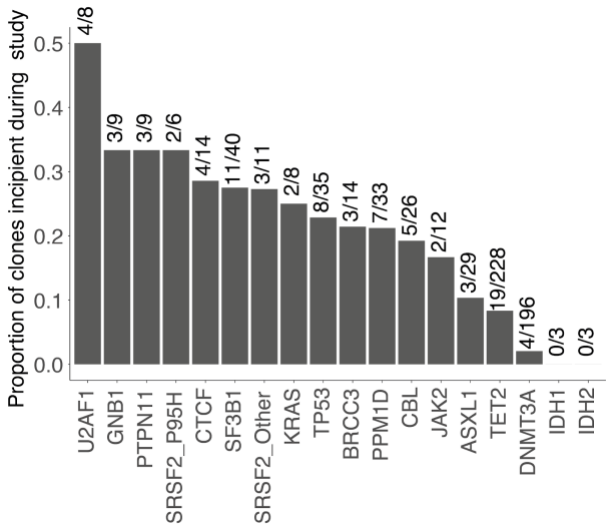


Figure 5.7: Incipient clones. a, Proportion of clones driven by different driver mutations that were incipient on-study, i.e. undetectable at time-point 1 and detectable by the end-of-study. Absolute numbers are given above each bar.

To derive representative ranges for age at clone onset for each driver gene, we capped individual estimates at conception, thus avoiding estimates that projected beyond individuals' lifetimes (Fig. 5.8, Table 11b).

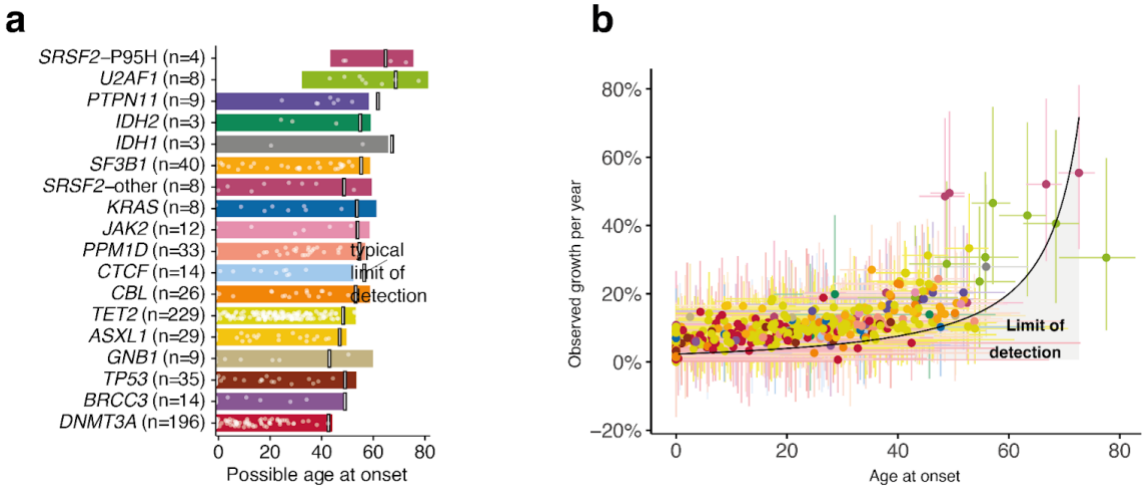


Figure 5.8: Projected age at clone foundation. a, Projected ages at onset for all clones, assuming stable lifelong growth at the same fixed rate we observed during older age. **b**, Relationship between age at onset and observed annual growth rate, with points representing the mean annual growth/median age at onset and intervals representing, respectively, the 90%/95% highest posterior density intervals (HPDI). The black line and grey shaded area represent the theoretical limit of detection at 80 years of age.

We also validated this method using simulations and confirm that these ranges are not affected by changes in Neff or generation time (Fig. 5.9).

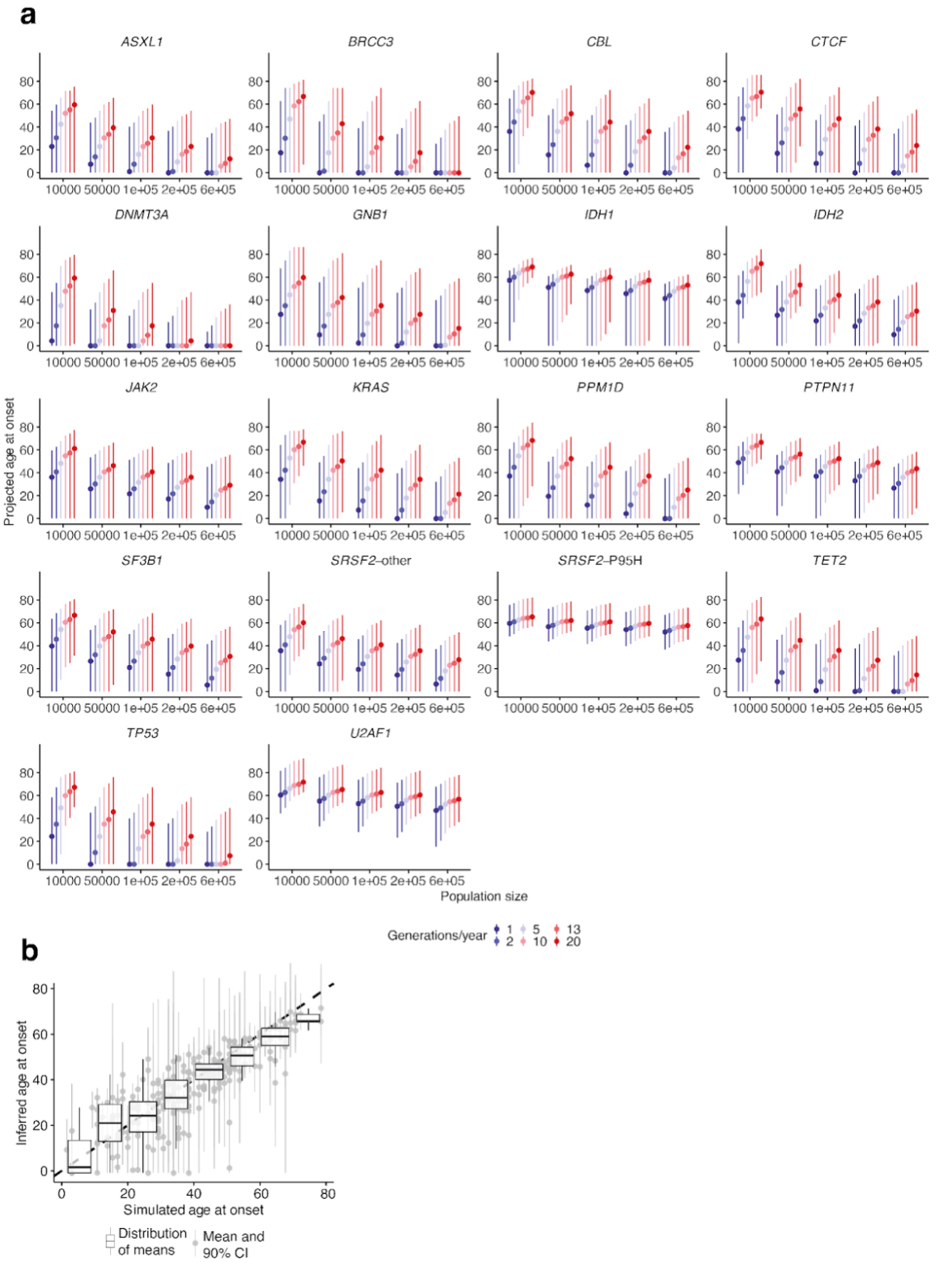


Figure 5.9: Validation of estimates for age at clone foundation. a, Sensitivity analysis depicting the median (dot) and the 95% confidence interval of the ages at onset for each gene when considering different population sizes (10e3, 50e3, 100e3, 200e3 and 600e3) and numbers of generations per year (1, 2, 5, 10, 13, 20; n=615 clones). **b**, Association between the age at which clones appeared in the simulations and the age at clone foundation inferred using our time-series data (R^2 = 0.75). Boxplots show that, while these estimates may have high variance, the distribution of expected values is close to the true value (n=250 simulated clones). The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile.

We estimated that the average latency between clone foundation and detection in peripheral blood at VAF≥0.2% (Supplementary Note 3) was 30 years across all clones, with considerable variability between mutant genes, ranging from 38 years for *DNMT3A*-mutant clones to 12 years for *U2AF1*-mutant clones. Most drivers were projected to initiate expansions of clones throughout life, compatible with the notion that somatic mutations occur at a constant rate[4–6]. However, solutions for *DNMT3A*-mutant clones concentrated earlier in life, consistent with early initiation and rapid expansion followed by marked deceleration then slow growth, as discussed earlier. Of note, capping onset at conception is arbitrary and it remains possible that some clones start later and exhibit faster initial growth followed by even stronger deceleration, a scenario that would be more consistent with published fitness estimates of 11-19%/yr based on cross-sectional VAF measurements[139]. In contrast, *SRSF2*-P95H and *U2AF1* mutations initiated clonal expansion always after 30 years of age and with a median age at onset of 58 and 57 years, respectively (Fig. 5.8a). This indicates that the reported rarity of these mutant clones in people aged <60 years[15,16,29] is not due to slow growth over decades, but rather due to their late onset followed by rapid expansion and provides a plausible explanation for the high risk of leukaemic progression associated with these mutations[24,104].

Further evidence for deceleration of *DNMT3A*-mutant clones over life can be derived from comparison of our findings with those of Watson et al[139], who used mathematical modelling and evolutionary theory to derive growth rates/coefficients from single time point data in younger individuals. Specifically, they applied population genetic theory to analyse cross-sectional VAF spectra from ~50,000 individuals and infer the fitness of individual CH driver mutations[139]. Two important assumptions in this study were that (i) mutation fitness was constant from the time of clone foundation to the time of sampling, and (ii) that the propensity for a mutation to found a clone was constant throughout life. Therefore, their fitness estimates reflect each mutation's *average* growth rate from mutation acquisition to blood sampling. As the mean age of the 50,000 individuals studied was 55 years (SD 11.4 years), their fitness estimates reflect average clonal growth prior to this age. In comparison, the growth rates we measured in our longitudinal study relate solely to old age, covering, on average, the period between the ages of 69-81 years (median ages at the start and end of study). Thus, the findings of Watson *et al* reflect average clonal growth in earlier life, and those of our longitudinal study reflect clonal growth in later life. To compare our data to Watson *et al*, we focussed on the mutant sites in *DNMT3A* for which both of our studies had derived site-specific fitness effects, namely R882C, R882H, R736C and R736H. This confirmed that the expansion of clones associated with each of these mutations was substantially faster in younger (Watson et al[139]) vs older (our study) individuals (Box 1).

Gene_Mutation	Annual growth in older age (our study) (%/y)		Annual growth in younger age (Watson *et al*) (%/y)[139]	
	Rate	95% CI	Rate	95% CI
DNMT3A_R882C	1.8	(-6.8 - 11.5)	18.7	(18.2 - 19.4)
DNMT3A_R882H	5.5	(0.7 - 10.9)	14.8	(14.1 - 15.7)
DNMT3A_R736H	10.3	(3.2 - 17.6)	14.1	(13.2 - 15.4)
DNMT3A_R736C	7.3	(0.7 - 14.1)	12.3	(11.6 - 13.4)

Box 1: Annual growth rates associated with *DNMT3A* hotspots in younger (Watson *et al.*)[139] vs older (our study) individuals.

5.3 Discussion

In this Chapter, we characterise the emergence and dynamics of CH across the entire human lifespan. Simple retrograde extrapolation of the trajectories we observed in old age (Chapter 3) led to projected ages at clonal foundation that preceded conception for a large number of clones (Fig. 5.5b,c), implying that their early growth must have been faster than that we observed during old age. This was most striking for *DNMT3A*, for which more than two thirds of projections were implausible (ie. onset pre-conception), but less common for *TET2* and very uncommon for splicing factor genes (Fig. 5.5c).

To further investigate lifelong clonal behaviour, we analysed haematopoietic phylogenies from healthy old individuals and found that aged haematopoiesis was dominated by a small number of expanded HSC clones, some of which lacked recognisable drivers[167]. Using phylodynamic approaches to track clonal growth rates through life, in conjunction with findings from our longitudinal cohort, we reveal widespread clonal deceleration prior to the period of stable growth during old age, in the context of an increasingly competitive oligoclonal HSC compartment (Fig. 5.6b). *DNMT3A*-mutant clones, as well as those bearing mutations in *TP53* and *BRCC3* and also apparently driverless clones, were among those displaying the most marked degree of deceleration (Fig. 5.6b). The faster growth of *DNMT3A*-mutant clones in early life is supported by comparison with the findings of Watson *et al.*, who analysed cross-sectional VAF spectra from 50,000 individuals and estimated average clonal growth rates across the first ~55years of life[139]; expansion of clones was substantially faster in younger (Watson *et al.*[139]) vs older (our study) individuals, on average 15.0%/yr vs 6.2%/yr, respectively (Box 1). In contrast, *TET2* mutations appeared to drive more stable lifelong growth (Fig. 5.6b,c), which may underlie their apparent ability to initiate clonal expansion fairly uniformly through life (Fig. 5.8a) and the fact that *TET2* "overtakes" *DNMT3A* as the most common CH driver after the age of 75 years (Fig. 3.6c and[168]).

In diametric contrast to *DNMT3A* and unlike other genes, CH driven by mutant *U2AF1* and *SRSF2*-P95H only initiated late in life (Fig. 5.8a) and exhibited some of the fastest expansion dynamics (Fig. 3.11a). These data were corroborated by phylogenetic analyses (Fig. 5.2b,f) and tally with the sharp increase in prevalence of splice factor-mutant CH[29], MDS[54,100,169] and AML[99,170] in old age and the high risk of progression to myeloid cancers associated with these mutations[24]. The particular behaviour of these clones proposes a specific interaction with ageing, which could relate to cell-intrinsic factors or to cell-extrinsic changes in the ageing haematopoietic niche that favour splice factor mutations[9,171].

Chapter 6

Clonal dynamics and clinical phenotype

6.1 Introduction

Understanding the biology and behaviour of CH has implications far beyond basic science; in fact, this phenomenon has broad links with human disease. There remains some debate about whether associations with non-haematological disease, such as cardiovascular disorders, are causal, or whether they reflect shared but independent links with biological ageing[97]. There is no such debate about the relationship between CH, which has been characterised as a pre-malignant state, and progression to haematological cancer. In exome-sequenced population-based cohorts, the presence of CH at VAF>2% was associated with ~10-fold increased relative risk of progression over several years of follow-up[15,16].

Risk estimates for AML development were refined by two groups, who used nested case-control studies within large population-based cohorts[24,104]. Both groups found that individuals with antecedent CH were at ~3-5-fold increased risk for developing AML in the subsequent years, lower than earlier estimates due to the more sensitive sequencing technologies used. Intriguingly, certain drivers, such as *U2AF1*, and large clones, carried a particularly high risk of progression.

However, many questions remain about the underlying mechanics of the relationship between CH and malignant progression. For example, why are different driver genes associated with different levels of risk? Does absolute clone size *cause* higher risk, or is it actually the clonal dynamics that are influential?

With the realisation that clones expanded by cancer-associated mutations exist throughout the human body by old age[2,129,160,165], the distinction between normality and cancer has become blurred. From the haematological perspective, this is particularly pertinent for cancers

in which there is often no genetic ‘transformation’; in the Myelodysplastic Syndromes (MDS), for example, two-thirds of *SF3B1*-mutant cases have no additional somatic driver[54]. It follows that, at some point in the transition between *SF3B1*-mutant CH and *SF3B1*-mutant MDS, malignancy has developed without further mutation acquisition. Whether this transition occurs simply due to clonal expansion exceeding a certain threshold, or whether non-driver-mutation factors dictate malignancy development, is not known. These questions have critical implications for understanding the mechanisms of cancer development and for potential therapeutic interventions.

In this Chapter, we explore the relationships between (i) CH clonal dynamics and malignant progression, and (ii) blood counts.

6.2 Results

6.2.1 CH and malignant progression

To explore the relationship between mutation fitness and malignant progression, we built on our previous study of AML risk prediction[24] and revealed that, among CH driver genes, a faster growth rate was associated with a higher AML risk (adjusted R^2=0.55, p=0.0037, Fig. 6.1). For example, genes driving fast CH growth like *SRSF2* and *U2AF1* were associated with the highest risks of leukaemogenesis, while slow-growing clones such as those bearing *DNMT3A* mutations, conferred a lower risk.

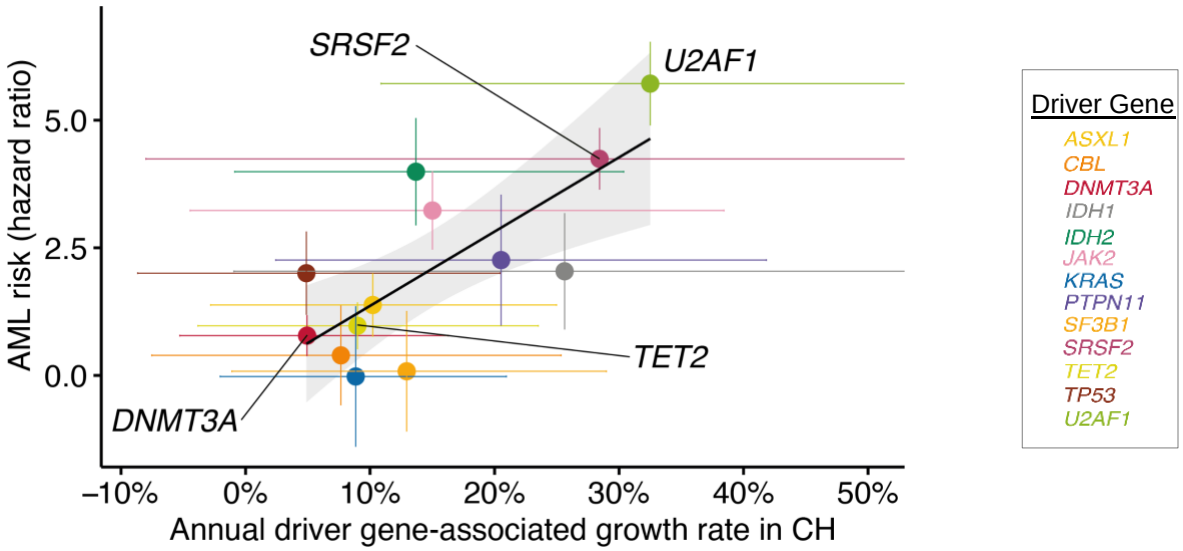


Fig. 6.1: CH dynamics and AML risk. Relationship between the growth rate associated with each driver gene in CH, and the risk of AML progression associated with that driver gene. AML risk intervals are +/- standard error for the estimate as calculated in[24] and annual growth error bars are the 90% HPDI. The confidence band represents the 95% confidence interval for the association between annual growth rate and AML risk. Data-points are coloured by driver gene, as indicated in the key to the right of the figure.

Importantly, this analysis was agnostic of clone size. To appreciate the significance of this, it is important to note that clone size at a single time-point is simply a derivative of clonal growth rate and time since emergence, i.e. if sampled later, most clones would be bigger. We demonstrate the arbitrariness of clone size in assessing the relationship between clonal dynamics and AML risk by examining the relationship between average driver-related growth rate and median VAF at study entry vs study exit. This changes with time (Fig. 6.2), unlike

growth rate, which remained stable over long periods. This illustrates why any single time-point VAF measure in a cohort of individuals is not a universal quantity as it depends on time, and is therefore not a useful cohort-level indicator of AML risk. However, unlike in a cohort[24,104], *for any given individual*, having a larger clone might be a risk factor for future AML development, as larger clones must have been captured further along their trajectories.

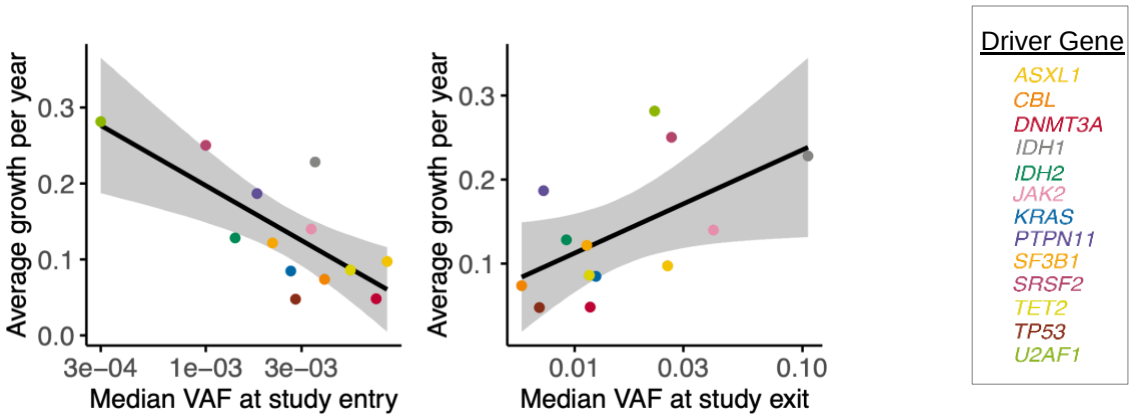


Figure 6.2: Associations between CH driver gene growth per year and (**i**) median VAF at study entry (left panel); (**ii**) median VAF at study exit (right panel). Data-points are coloured by driver gene, as indicated in the key to the right of the figure.

To confirm our findings in larger studies and include myeloid malignancies in addition to AML, we analysed large published datasets of AML (n=1540)[99] and myelodysplastic syndromes (MDS, n=738)[100]. We re-called all somatic variants, including synonymous, using the identical pipeline used for our longitudinal CH data set (Table 16). We then applied a site-specific extension of the dNdScv algorithm to formally quantify the extent to which individual hotspots are under the influence of positive selection in these cancers (Table 17)[2]. This analysis revealed a positive correlation between each hotspot's growth coefficient in CH and its selection strength in myeloid cancer (Figure 6.3; adjusted R^2=0.19, p=0.0016), corroborating the AML risk analysis.

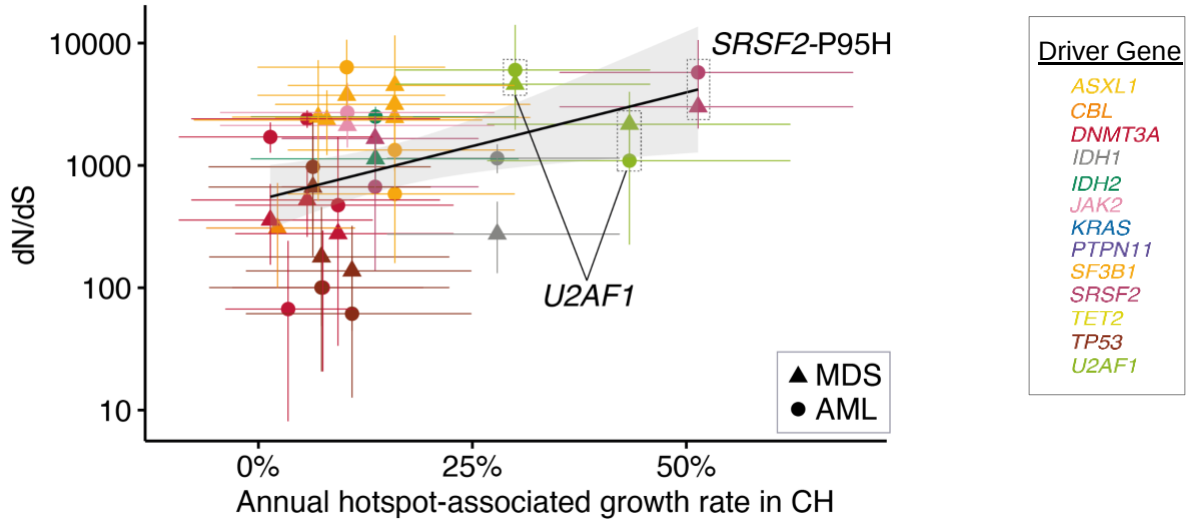


Fig. 6.3: CH dynamics and selective advantage in AML and MDS. Relationship between the growth rate associated with each recurrent mutation (hotspot) in CH, and the dN/dS ratio (a measure of selection strength[2]) associated with that same mutation in AML (circles) and MDS (triangles). Error bars for dN/dS show 95% confidence intervals; error bars for annual growth show 90% HPDI. The confidence band (shaded region) represents the 95% confidence interval for the association between annual growth rate and dN/dS. Genes and hotspots with the highest growth rates in CH are highlighted with labels. Data-points are coloured by driver gene, as indicated in the key to the right of the figure.

Nevertheless, the observation that the same CH driver gene can progress to either AML or MDS, with variable predilections as quantified by gene-level dN/dS comparison (Fig. 6.4, Table 17), supports the premise that factors other than growth rate can also influence a mutation's malignant potential.

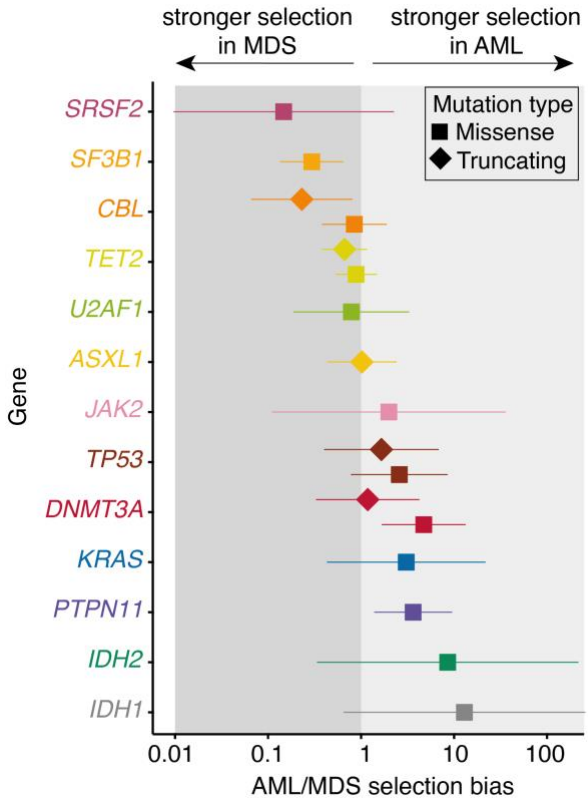


Figure 6.4: Selection in myeloid malignancies. Ratio between AML dN/dS and MDS dN/dS for different genes and mutation types (missense, truncating). If this ratio is >1 there is a bias towards AML, if it is <1 there is a bias towards MDS. Error bars depict 95% CIs.

Indeed, more detailed within-gene analysis of the relationship between each hotspot's growth coefficient in CH and its selection strength in myeloid cancer, reveals that the overall positive correlation conceals some gene-specific detail. A notable example is *DNMT3A*; while all hotspot mutations in *DNMT3A* drive similarly slow growth rates in CH, their degree of enrichment in myeloid disease and by implication their propensity to malignant progression, vary considerably (Fig. 6.5a). Mutations affecting the R882 codon are particularly enriched in cancer, especially AML, yet drive similarly modest growth to all other *DNMT3A* mutations in CH. This suggests that, at least for some genes, a mutation's propensity for malignant transformation is not related to the rate of clonal growth it drives in CH, and is instead influenced by other factors, likely genetic and/or environmental. On this note, one intriguing observation is the tendency for *DNMT3A*-R882 mutations to specifically co-occur with *NPM1* mutations in AML; in the AML cohort[99], 147/211 (69.7%) individuals with R882 mutations also bore *NPM1* mutations, compared to only 59/125 (47.2%) individuals with non-R882 *DNMT3A* mutations (Chi-square p=0.00004) (Fig. 6.5b). This suggests that the particular enrichment of the R882 mutation in AML is not due to its inherent growth-promoting properties, but instead

either because it confers risk for *NPM1* mutation acquisition, or because it synergises with *NPM1* to promote growth.

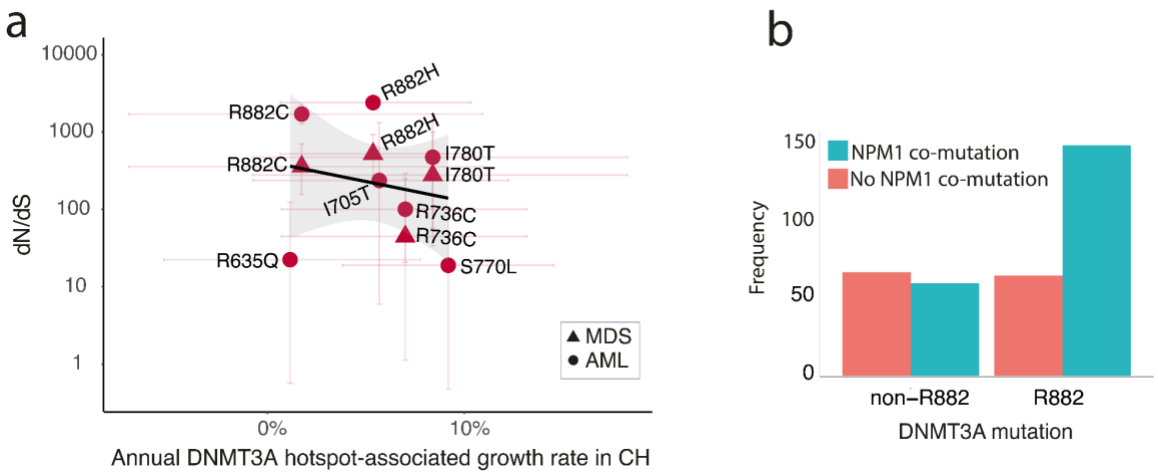


Fig. 6.5: *DNMT3A*-mutant CH and myeloid cancer. a, Relationship between the growth rate associated with each recurrent *DNMT3A* mutation in CH, and the strength of selection of that mutation in AML (circles) and MDS (triangles). dN/dS error bars are 95% confidence intervals and annual growth error bars are the 90% HPDI. The confidence band represents the 95% confidence interval for the association between annual growth rates and dN/dS. **b**, Co-mutation of *NPM1* with *DNMT3A* (either R882 or non-R882) in AML[99].

6.2.2 CH and peripheral blood counts

Next, using serial complete blood count data collected contemporaneously with genomic DNA for CH sequencing, we built mixed effect regression models to investigate the relationship between CH and blood count trajectories (Fig. 6.6, Table 18a). While many blood parameters were, as expected, strongly associated with age and sex (for example, haemoglobin was lower in females and with advancing age), associations with CH (here defined as VAF>2% by the end of study) were comparatively limited (Fig. 6.6, Table 18a). Similarly, rate of clonal growth driven by mutations in particular genes was not associated with blood parameters when controlling for age, sex and clone size (Table 18b).

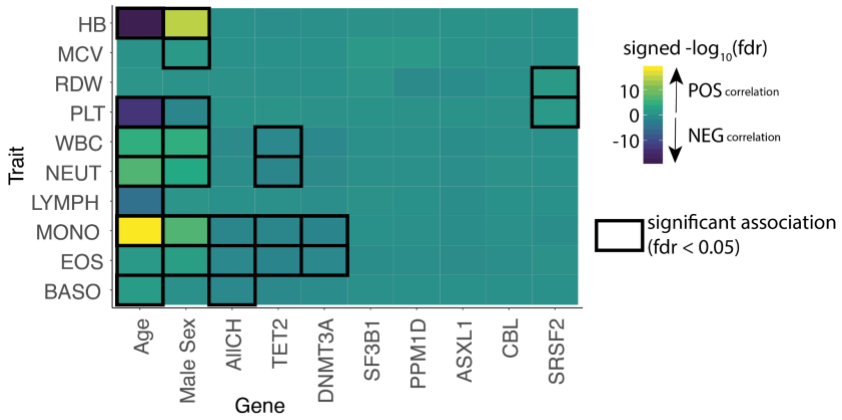


Fig. 6.6: Predictors of blood count parameters. Relationship between blood counts and age, sex and CH (VAF>2%). Serial blood counts were used in mixed effects regression models with age, sex and CH (both as a single entity, and analysing each mutant gene separately) as fixed effects, and a random effect for the intercept across individuals. The significance of association between each blood parameter and each fixed effect, and whether the association was positive or negative, is indicated by grid square colour, and those with FDR<0.05 are highlighted with a black outline. FDRs are Benjamini-Hochberg-corrected for multiple testing.

Indeed, some individuals with very large mutant clones, even those in whom essentially the entire peripheral blood cell pool was derived from stem/progenitor cells bearing the mutation, were able to maintain normal peripheral blood counts over many years (examples in Fig. 6.7a-e). Since cytopenia is a ‘sine qua non’ for the diagnosis of MDS, this demonstrates that MDS is not simply the result of extreme expansion of clones with particular driver mutations. Instead, the MDS phenotype must require additional factors to perturb haematopoiesis in the presence of a mutant clone.

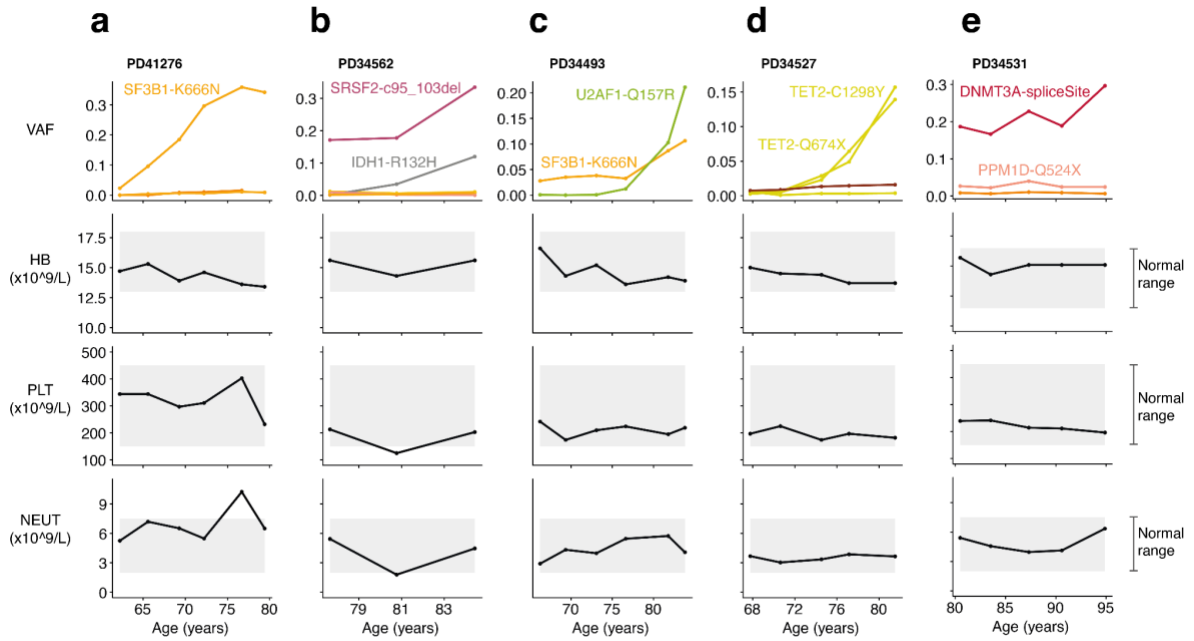


Figure 6.7: Examples of contemporaneous trajectories of CH clones and peripheral blood counts. Five individuals with high-VAF clones bearing mutations in *SF3B1*^{K666N} (**a**), *SRSF2*$^{c95\text{-}103del}$ and *IDH1*^{R132H} (**b**), *U2AF1*^{Q157R} and *SF3B1*^{K666N} (**c**), *TET2* (**d**) and *DNMT3A* (**e**), who maintained normal levels of haemoglobin, platelets and neutrophils over many years.

6.3 Discussion

In this Chapter, we explore the relationship between CH and clinical phenotype, starting with myeloid cancers. We find that mutations associated with faster CH growth are also those associated with higher risk of progression to AML (Fig. 6.1) and are under the strongest selective pressure in AML and MDS (Fig. 6.3). Indeed, we show that the average annual growth per gene explains over 50% of the variance in AML risk progression. This shows that an improved understanding of growth dynamics in CH can help identify those at risk of myeloid malignancies.

However, it is clear that mutation fitness is not the sole determinant of malignant progression. Differing patterns of cooperating mutations might provide some explanation; the particular malignant potential of *DNMT3A*-R882, for example, might be partly explained by its synergy with aberrant NPM1. However, co-mutation does not explain all malignant progression; *SF3B1*, for example, is the only identifiable driver in one-third of *SF3B1*-mutant MDS cases[54], and *JAK2* is the sole driver in many cases of MPNs[98].

Consistent with the notion that factors beyond clonal behaviour determine haematological phenotype is the observation that, in some cases, peripheral blood counts can be largely unaffected by CH. Even among individuals with very large and/or rapidly expanding mutant clones, some can maintain normal blood production over many years. Individual PD41276, for example, with an overwhelming *SF3B1*-K666N-mutant clone (Fig. 5.2a and 6.6a), maintained normal levels of trilineage haematopoiesis (Hb 13.4g/L, neutrophils $6.5x10^9$/L, platelets $232x10^9$/L at the final time-point), precluding a diagnosis of MDS. This asserts that, while CH is the precursor of myeloid cancer, the two are distinct entities. Especially in light of our finding of expansions *without* identifiable drivers, which appear to be common[3,15,106,172] and show remarkably similar dynamics to expansions *with* drivers (Fig. 5.2c,g,h and Fig. 5.3), it is likely that oligoclonality is a feature of normal ageing. Expansion of functioning clones might even be *required* for maintenance of adequate haematopoiesis in an ageing environment. In contrast, it appears that the dysfunction defining myeloid cancer is precipitated by interaction of the mutant clone with genetic/environmental factors *additional* to those promoting expansion in CH.

Chapter 7

Discussion

Human cells acquire somatic mutations throughout life, but how these mutations interplay with ageing, clonal selection and oncogenesis remains poorly understood. While CH can serve as an exemplar in the study of these phenomena, they change over time and their consequences develop only slowly, limiting the utility of insights derived from single time-point data. In this thesis, I present the first characterisation of the longitudinal behaviour of CH across the human lifespan, elucidating these fundamental biological processes and how they change with age.
In the following discussion, I will emphasise common themes emerging from the preceding results chapters, highlight new or unanswered questions and areas for further investigation, and emphasise aspects with therapeutic implications.

Why do different driver genes show different patterns of lifelong clonal growth?

One intriguing aspect of longitudinal CH clonal dynamics is our demonstration that different driver genes are associated with different lifelong patterns. *DNMT3A*-mutant clones preferentially expand early in life and grow very slowly in old age, *TET2*-mutant clones show more uniform patterns of emergence and growth across ages, and splicing gene mutations only drive expansion later in life and do so with some of the fastest dynamics. Why do mutations in different genes drive such disparate patterns of growth? While some tentative progress has been made in elucidating the mechanisms by which driver genes confer competitive advantage to HSCs[28], our understanding is still in its infancy. The more nuanced question of why such advantages might change over life in driver-specific patterns is completely unexplored.
There are two plausible explanations for drivers, such as *DNMT3A*, showing decelerating growth trajectories over life. *First*, it is possible that the inherent fitness conferred by the

mutation remains constant, but that deceleration results from increasing competition of the mutant clone with other expanded clones. Indeed, we demonstrate marked oligoclonality in the haematopoiesis of all elderly individuals studied, often due to expansion of clones without identifiable driver mutations, suggesting that the repressive effect of competing clones is pervasive by old age. In this environment, it is logical to assume that any given expanding clone grows more slowly than it would in a different landscape in which it was the only clone with a competitive advantage. *Second*, it is possible that the inherent fitness conferred by the mutation also wanes with time, due to changes in the interaction of the mutation with the ageing intracellular or extracellular milieu. We can only speculate at a mechanism here, but perhaps transient early-life events, such as hormonal changes during puberty, are permissive for early expansion of these mutant clones. The observation that germline *DNMT3A* mutations cause Tatton-Brown-Rahman syndrome, of which overgrowth is a cardinal feature[173], hints at some relationship between *DNMT3A* and the action of hormones or processes involved in tissue/organismal growth, and this conjecture might be an interesting avenue to pursue in future.

We also have no clear explanation for the relative agnosia of TET2 to age in terms of its ability to found clones and drive growth. However, in the context of early life advantage for *DNMT3A* mutations, but no such age-dependence for *TET2*, it is interesting to note that *DNMT3A* mutations are almost always initiating, whereas *TET2* mutations can serve either as initiating or as later-acquired mutations during clonal progression of cancer[124].

It has been noted previously that clonal expansions driven by splicing gene mutations only become detectable in old age[15,16,29]. Here, for the first time, we demonstrate that this late detectability is not due to early emergence and maintenance at low levels followed by accelerated growth at older ages, but rather due to late emergence and immediate, rapid expansion. One potential explanation for the absence of earlier-emerging clones in our longitudinal study is selection bias, with such clones causing haematological cancer and thus precluding inclusion in the cohort. However, the prevalence of these mutations in our cohort is far too high for this to be true. 3.4% of individuals (13/385) harboured a mutation either at *SRSF2*-P95H or in *U2AF1*. Assuming that mutations at these sites are acquired at the same rate earlier in life as we detect here[5,139], if it were also true that they drove similarly rapid clonal expansion at that stage, we would observe dramatically higher rates of *U2AF1*- and *SRSF2*-mutant CH and blood cancer in younger individuals. In reality, these mutations are almost never observed in large cohort studies of CH in younger individuals[15,16,29], and the myeloid cancers they drive are rare diseases almost entirely confined to the elderly. Therefore, the only plausible explanation is that *SRSF2*- and *U2AF1*-driven clonal expansions are genuinely age-restricted, and that this restriction is attributable to their ability to endow HSCs with increased fitness specifically in older age.

Which feature(s) of ageing allow splicing gene mutations to switch from neutral/disadvantageous to advantageous, whether it be cell-intrinsic HSC ageing or environmental attrition, or whether the change is instead relative and simply reflects persistence of these mutant clones in the face of failing driverless HSCs – will be a crucial focus for future studies.

It is interesting that there is marked bone marrow hypercellularity in the majority of cases of MDS, most of which involve splicing gene mutations, in stark contrast to the declining cellularity of normal aged bone marrow (from >90% in childhood to ~30% by the age of 70 years). This might suggest that splicing-mutant HSCs can migrate to, and thrive, in regions of the aged marrow that are inaccessible and/or inhospitable to wild-type cells. This is just one of many avenues of investigation to be considered in the pursuit of an improved understanding of why splicing gene mutations confer clonal advantage late in life.

Why do clones with the same driver mutation grow at different rates in different individuals?

In Chapter 3, we model the growth rate of clones with the same driver mutation in different individuals, and find that this rate differs by approximately +/-5%/yr (Figure 3.12). This degree of variability has, proportionally, minimal impact on fast-growing clones. For example, for *SRSF2*-P95H-mutant clones, which expand on average by over 50% annually, the difference between annual growth rates of 45% vs 55% among individuals is modest as a fraction of the total growth. In contrast, inter-individual variability is proportionately more significant for “slow” drivers; for *DNMT3A*-mutant clones, for example, which grow at average rates of 5% annually, the actual rate might be 10% in one individual and 0% in another. In fact, we even observed slight negative clonal growth rates in a small number of individuals.

Whilst we explain a small component of this variability for *TET2*-mutant clones (Fig. 3.13), implicating certain cytokines and age, the reasons for inter-individual differences in growth rate remain entirely unexplained for most drivers. As discussed in some detail in Supplementary Note 1, we can be confident that the vast majority of clones harbour only a single driver mutation, and that varying patterns of co-mutation cannot therefore be the cause of differing growth rates between individuals. In contrast, a factor that might play a causative role is the influence of competing clones, which is likely to differ between individuals with distinct clonal landscapes. In addition, it is likely that a number of cell-intrinsic and -extrinsic factors interact with a driver mutation to modify its inherent level of fitness. We show in Chapter 4 that the inherited genome is unlikely to play a dominant role here, but emerging evidence suggests that it does exert a degree of influence[25,97]. Interestingly, a recent genome-wide

association study of over 200,000 UK Biobank participants identified multiple genetic loci associated with an increased risk of CH, including two loci (*TCL1A* and *CD164*) with opposite influences on *DNMT3A*- versus *TET2*-mutant CH, mirroring our finding of the disparate lifelong behaviours of these two most common types of CH[97]. An important future study will be to combine germline with longitudinal somatic data, to determine the extent to which inherited factors determine inter-individual variation in clonal growth rate.

Our understanding of the mechanisms behind the differing growth rates of clones with the same driver in different individuals is in its infancy, but will be critical for more accurate prediction of future clonal growth and malignancy risk. Crucially, elucidating these mechanisms might reveal factors/pathways that can be modified therapeutically in the clinical setting.

The remarkable stability of clonal growth over many years in old age

Despite all of these unknowns, and despite varying patterns of lifelong behaviour, the remarkable fact remains that the vast majority of CH clones in older individuals grow at a constant rate over decades (Fig. 3.8). This must mean that whatever the identity of the factors influencing growth rate (beyond the driver mutation), they must remain relatively stable over this period. From a practical perspective, it means that, once we know an individual's clonal growth trajectory, we can accurately predict future growth. As malignancy risk stratification improves, and preventive therapeutic interventions are trialled, this high degree of predictability will likely be invaluable in decision-making around the timing and intensity of any intervention.

While we observe stable growth over long periods, more frequent monitoring over a shorter time-scale would be required to identify transient fluctuations in clonal size. For example, it would be interesting to investigate, in light of evidence in mice that inflammatory stimuli promote *TET2*-mutant clonal growth[94], whether viral/bacterial infections or vaccinations are associated with transient expansion of *TET2*-mutant clones in humans. Such analyses could give valuable insight into the mechanisms contributing to clonal growth.

What constitutes normality?

Our perception of normality has changed dramatically over the past decade. The idea that a normal cell is set on an inevitable path towards malignancy if it happens to acquire a cancer-associated mutation, is outdated. In fact, with age, all tissues become mosaics of expanded

clones, some of which are driven by cancer mutations. While faster-growing clones are more likely to progress towards malignancy (Fig. 6.1 and 6.3), the distinction between normality and cancer has become blurred, and our understanding of the transition between the two is poor. Haematological malignancy is not inevitable even when a clone expanded by an unequivocal cancer driver completely overwhelms haematopoiesis (Fig. 6.7). Incredibly, there is direct evidence in normal epithelial tissue that expanded mutant clones can even exert an anti-tumorigenic role by purging early tumours through cell competition[174]. With our demonstration of oligoclonality and competition in elderly haematopoiesis, it is plausible that an analogous process operates in bone marrow. These observations illustrate the huge challenges we face in distinguishing normality from cancer, and in accurately predicting an individual's risk of malignancy. Better risk stratification is critical if we are to identify and potentially intervene for those at highest risk.

Will we ever prevent myeloid malignancies?

We tend to believe that, although there might be obvious gaps in our knowledge, we in fact understand things quite well. 2,500 years ago, there was certainly this sense of accomplishment among Hippocratic doctors:

> PLACES IN MAN: Ch. 46: "*Medicine in its present state is, it seems to me, by now completely discovered, insofar as it teaches in each instance the particular details and the correct measures. For anyone who has an understanding of medicine in this way depends very little upon good luck, but is able to do good with or without luck. For the whole of medicine has been established, and the excellent principles discovered in it clearly have very little need of good luck*" (Loeb, Vol. VIII, p93).

However, we can be sure that monumental discoveries are waiting to be made in the coming years, and that future generations will marvel at today's rudimentary understanding of haematopoiesis and cancer. But, for now, we inch closer to the goal of preventing haematological cancers. I hope that the new insights in this thesis - into lifelong clonal dynamics, the impact of ageing on haematopoiesis, and the processes linking somatic mutation, clonal expansion and malignant progression - will contribute to achieving this goal.

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Appendices

Appendix 1

Work published /submitted during PhD fellowship

- **Fabre MA**, …, Vassiliou GS. The longitudinal dynamics and natural history of clonal haematopoiesis. ***Nature*** (*in press*).
- Mitchell E, …, **Fabre MA**, …, Campbell PJ. Clonal dynamics of haematopoiesis across the human lifespan. ***Nature*** (*in press*).
- Kar SP, …, **Fabre MA**, …, Vassiliou GS. Genome-wide analyses of 200,453 individuals yields new insights into the causes and consequences of clonal haematopoiesis. ***Nature Genetics*** (*in press*).
- Janssen M, …, **Fabre MA**, …, Dietrich S. Venetoclax synergizes with Gilteritinib in FLT3 wildtype high-risk Acute Myeloid Leukemia by suppressing MCL-1*.* ***Blood*** *(in press).*
- Zhou Y, …, **Fabre MA**, …, Dunbar CE. Macaque clonal hematopoiesis model demonstrates expansion of TET2-disrupted clones and utility for testing interventions. ***Blood*** (in press).
- **Fabre MA** and Vassiliou GS**.** Clonal haematopoiesis. ***Postgraduate Haematology 8th Edition*** book chapter (*in press*).
- Dunn WG, …, **Fabre MA**, …, Vassiliou GS. The PML-RARA fusion is not detectable in historical blood samples of acute promyelocytic leukaemia patients. ***Ann Haematol*** 101:443-445 (2022).
- Dobson R, …, **Fabre MA**, … Du MQ. Early detection of T-cell lymphoma with T follicular helper phenotype by RHOA mutation analysis. ***Haematologica*** 107(2): 489-499 (2022)
- **Fabre MA** and Vassiliou GS. Home and away: clonal hematopoiesis in sibling transplants*.* ***Blood*** 135:1511-1512 (2020).
- **Fabre MA**, …, Vassiliou GS. Concordance for clonal hematopoiesis is limited in elderly twins. ***Blood*** 135, 269-273 (2020).

Under review:

- **Fabre MA**, …, Vassiliou GS. Parkinson's disease is not associated with clonal haematopoiesis. (under review in ***Haematologica***).
- Chapman MS, … **Fabre MA**, … Kent DG. Clonal dynamics after gene therapy in sickle cell disease. (*under review in* ***NEJM****)*.
- Zhou Y, …**Fabre MA**, …, Vassiliou GS. Age-related clonal haematopoiesis is not significantly associated with Covid-19 disease severity. (*under review in* ***Blood***).

Appendix 2

Supplementary Notes

Supplementary Note 1 - Investigating clonality and its possible impact on inference

In this Supplementary Note, we tentatively infer co-clonality (whether two or more mutations are in the same clone) and investigate the potential impact this may have on our inference of clonal growth.

Clonality inference from targeted sequencing data

Our initial assumption, backed up by single-cell studies[1], was that CH clones commonly harbour a single driver mutation. Nonetheless, we try here to investigate the possibility that two or more driver mutations occur in the same clone. Typically, clonality can be successfully inferred when information on large parts of the genome is available (e.g. with whole genome or exome sequencing). The longitudinal part of our study required deep sequencing of 56 genes in 1593 samples, such that we needed to focus our sequencing on the relevant genes in order to robustly track small and large clones over time. Unfortunately, such highly targeted sequencing does not normally provide sufficient information to facilitate clonality inferences. Nevertheless, here we attempt a number of heuristic tests to investigate this specifically using the following tools/approaches:

- **PyClone** - PyClone is a software tool that relies on copy number data and deep sequencing to infer the clonal architecture of a sample [2];
- **Fisher test consistency** - if mutation counts are consistently identical (i.e. non-significant in a Fisher's test) through time, it becomes more likely that they are present in the same clone;
- **Pigeonhole principle** - if the sum of VAF for a set of heterozygous mutations is greater than 50%, it is biologically impossible for them to be all in separate clones;
- **Dynamic similarity** - if two mutations are dynamically similar (i.e. their annual growth rates are similar) this suggests that they may reside in the same clone.

On clonal structure

Here, it should be noted that, in the absence of genome-scale data, it is possible that clustering mutations by relative frequencies can be indicative of the following:

1. Two separate but similarly sized clones (false positive);
2. A clone carrying one mutation acquires a second mutation (true positive);
3. A parental clone with one or more unknown drivers acquires one or more known drivers in the same subclone (true positive);
4. A parental clone with one or more unknown drivers acquires two known drivers in distinct subclones: here, while both new drivers are acquired in cells of the ancestral clone (marked by the unknown driver), each are actually in distinct subclones (false positive).

For cases 3 and 4 (represented in Fig. S5), we should be clear in our nomenclature as both imply that "two mutations are in the same clone" but only one of them is of relevance (3). As such and for clarity, we are interested in detecting 3 and this is what we mean by "two mutations in the same clone"; 4 should be further specified and defined as "two mutations in separate subclones in the same parental clone".

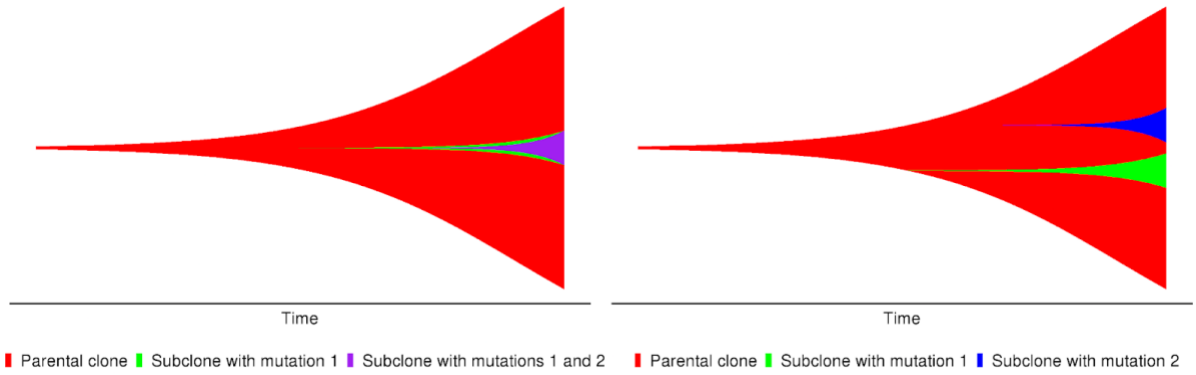


Fig. S1 - Representation of two different scenarios of possible confusion when referring to “two mutations being in the same clone”. On the left, two consecutive mutations are acquired in the same parental clone and subclone, while on the right two mutations are acquired in separate subclones, having nonetheless similar sizes.

PyClone analysis

PyClone[2] typically relies on deeply sequenced somatic mutations and copy number information to phase mutations into specific clones. However, our data is limited for this purpose, given the very small number of somatic mutations identified in each individual's blood DNA (median 2). Indeed, if we analyse our longitudinal data using PyClone (the PyClone input for each individual were their respective mutation calls for all timepoints), the limited input data leads the software to propose co-clonality in *all* individuals with more than one mutation. Furthermore, for the 76 individuals with 3 mutations, Pyclone proposed that all 3 belonged to just one clone in 67% of cases (51/76). These inferences are implausible and almost certainly a consequence of the limited input mutation data. In fact, evidence suggests that CH mutations are not commonly co-clonal, including the following. *First*, a recent study used single-cell DNA sequencing to specifically determine whether CH driver mutations existed in separate cells or coexisted in the same cell [1]. In this study, individuals with CH never harboured more than one mutation in epigenetic regulator genes in the same cell/clone (including in the two most common CH driver genes, *DNMT3A*, *TET2*, and also *ASXL1* and *IDH1/2*). Also, only 2/21 (9.5%) individuals were found to harbour more than one CH mutation in the same cell/clone. *Second*, upon close inspection, several instances of co-clonality proposed by PyClone in our data are functionally implausible. For example, there were instances of putative co-clonal mutations that are known to not co-occur in the same cell (e.g. *SF3B1* and *U2AF1* mutations, proposed by PyClone to exist in the same clone in one individual, but previously shown to be mutually exclusive[3]). For these reasons, we did not use Pyclone for clonality inference as it is not a suitable tool for our data.

Longitudinal consistency of Fisher's test

We used a Fisher's test to compare the VAFs of any two mutations within an individual. If this comparison was consistently non-significant over time (i.e. the VAFs of the two mutations did not differ), we considered these two mutations to be putatively in the same clone. For each time-point and for each mutation pair within an individual, we tested for significance according to a Fisher's test using a contingency table with the number of mutant and reference reads for each mutation. We define potential co-clonality (i.e. two mutations in the same clone) in cases where the Fisher's test is not significant at all time-points. Using this definition, out of 752 mutation pairs, 102 are putatively co-clonal.

Importantly, while this analysis detects clones which are consistently similar in size over a median period of 13 years (consistent with co-clonality), it does not exclude the alternative

(and realistic) scenario that two independent clones show similar growth trajectories within an individual.

Pigeonhole principle

The pigeonhole principle states that if the combined VAFs of a group of mutations within an individual is greater than the carrying capacity of the population then the mutations cannot be in distinct clones. Applying this principle, we found only six pairs of mutations that are proposed to exist in the same clone.

Dynamic similarity

If two mutations have similar annual growth rates, they may be in the same clone. To assess this, we subtract the posterior samples for growth rate of every mutation in a mutation pair *within* an individual. If the difference in coefficients is close to 0, this makes co-clonality of the two mutations more likely. To obtain a background distribution, we compare random mutation pairs *between* individuals (i.e. the growth rates from two distinct mutations in different individuals). As shown in Fig. S6, the distribution of differences in growth coefficients between any two randomly selected mutations is practically identical to that of the difference in growth coefficients between two mutations within the same individual. Therefore, this approach is not adequate for determining clonality.

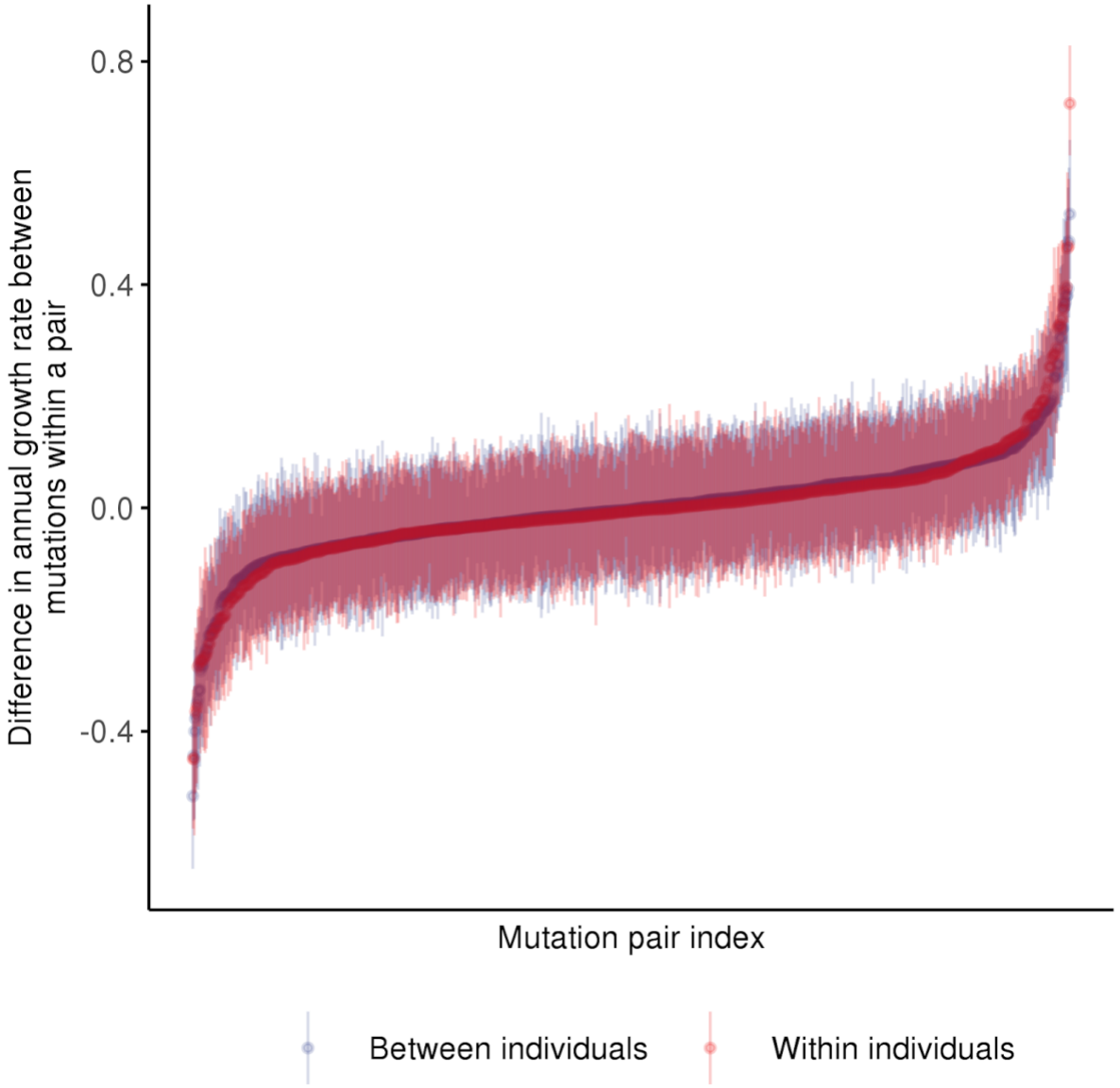


Fig. S2 - Distribution of differences in growth rates between mutations within pairs, where the two mutations are either (i) present in the same individual (*within* individuals) or (ii) randomly selected from our cohort (*between* individuals). The point estimates represent the average value of the difference, whereas the intervals represent the 90% confidence interval for the difference.

The impact of clonality on the inference of clonal growth rates

As discussed above, our data do not allow us to determine co-clonal events with any confidence. Importantly, this lack of certainty would be of no tangible consequence for our modelling of clonal growth rates, if potential co-clonality had no impact on our inferences of CH growth dynamics. To assess this, we checked whether there was any association between the number of clones within an individual (where multiple mutations could be consistent with co-clonal events) and: **(i)** the unknown-cause growth (i.e. the component of overall clonal growth not accounted for by the identity of the driver mutation) and **(ii)** the fraction of clonal

trajectories growing at a constant rate over time (referred to here as 'explained trajectories'). As observable in Fig. S7, no such associations were detectable.

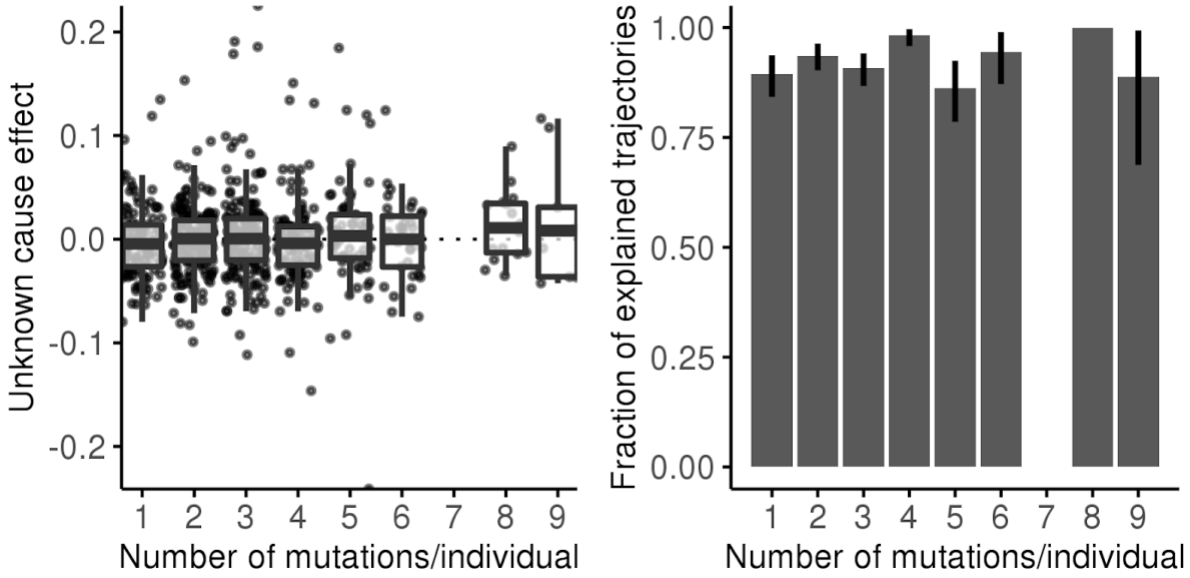


Fig. S3 - Association between number of mutations per individual and unknown cause effect (left) and fraction of explained trajectories (right; n=685). The boxes represent the 25th, 50th (median) and 75th percentiles of the data; the whiskers represent the lowest (or highest) datum within 1 interquartile range from the 25th (or 75th) percentile. Intervals in the right panel are beta-distributed 90% confidence intervals.

We confirmed this lack of relationship between the number of mutations and growth rate in *DNMT3A* or *TET2* (the two genes for which sufficient numbers are available for this comparison), where we find no association between the number of mutations in a given individual and the average *DNMT3A* or *TET2* growth rate (R=-0.12, p=0.15 and R=0.03, p=0.68, respectively).

In conclusion, while there may be a small number of clones that harbour more than one mutation, these do not affect our inferences relating to CH clonal dynamics [1,4].

Summary and conclusions

While there are several methodologies for phasing clonal/subclonal mutations, these rely on the identification of a sufficient number of somatic mutations to allow for this to be performed in a statistically robust manner. In the longitudinal part of our study, we performed targeted sequencing of 56 CH-associated genes in 1593 samples with emphasis on the robust

identification of CH driver mutations, even when these were present in small clones. Since we focused on a small part of the genome, we only identified a small number of somatic mutations in each individual, limiting the ability to phase drivers into different clones. Also, importantly, we find that the number of mutations within an individual has no impact on inferred clonal growth rates; i.e. driver-specific growth rates observed in individuals with single mutations (where co-clonality cannot exist), did not differ from those observed in individuals with multiple mutations (where co-clonality could theoretically exist) (Fig. S3).

Despite the unsuitability of our data for use in this context, we attempt to infer the clonality of driver mutations using four different approaches. Two of these approaches give results that are not informative for phasing mutations. *First*, PyClone proposed co-clonality in *all* individuals with more than one mutation, which is implausible because it **(i)** conflicts with the available literature on clonal architecture in CH, where a single driver per CH clone is the norm[1], and **(ii)** is functionally implausible for certain mutation pairs. *Second*, we tried to use clonal growth rates to inform clonal structure, assuming that mutations in a single individual could exist in the same clone if their VAFs were changing at a similar rate over time. For this, we calculate a background distribution of differences in growth rates between any two randomly picked mutations from our cohort (across individuals) and find that these differences in mutation-specific growth rates *between* individuals were indistinguishable from differences in growth rates *within* individuals (Fig. S2), rendering this approach also uninformative.

The other two approaches for inferring clonal structure give some tentative information, albeit inconclusive. *First*, we assumed that mutations in a single individual could exist in the same clone if their VAFs were of a similar size at all time-points; this was the case in 13.6% of mutation pairs. However, this does not prove co-clonality, as it is also possible that the mutations exist in distinct clones with similar size trajectories. *Second*, using the pigeonhole principle, which stipulates that heterozygous mutations can only exist in entirely separate clones if their VAFs sum to ≤0.5, we identify only 6 pairs of mutations which could be co-clonal.

In summary:

1. While demonstrating the clonal architecture could be informative, we have no way to reliably resolve this given the very targeted nature of our sequencing data.
2. The actual number of co-clonal mutations is likely to be very low given the reported rarity in CH[1].
3. Most importantly, the number of mutations within an individual had no significant impact on our clonal growth rate inferences (Fig. S3), suggesting that even if some co-clonal events did exist, the main findings of our study would not change.

Supplementary Note 2 - Patterns of selection in longitudinal and phylogenetic data

In this Supplementary Note we examine changes in selection, as quantified by the dN/dS ratio, in two settings: (i) in our longitudinal cohort, we ask whether dN/dS ratios change with age, and (ii) in our phylogenies, we compare dN/dS ratios in shared and private branches.

We use the dNdScv algorithm, an implementation of dN/dS that corrects for trinucleotide mutation rates, sequence composition, and variable mutation rates across genes[5].

dN/dS ratios in longitudinal data

First, using the 385 individuals included in our longitudinal data set, we compared the dN/dS ratio at the time of study entry (median age 69.3 years) with the ratio at the end-of-study (median age 81.3 years). We derived both global dN/dS ratios across all targeted genes (**Fig. S1**), and gene-specific dN/dS ratios (**Fig. S2**).

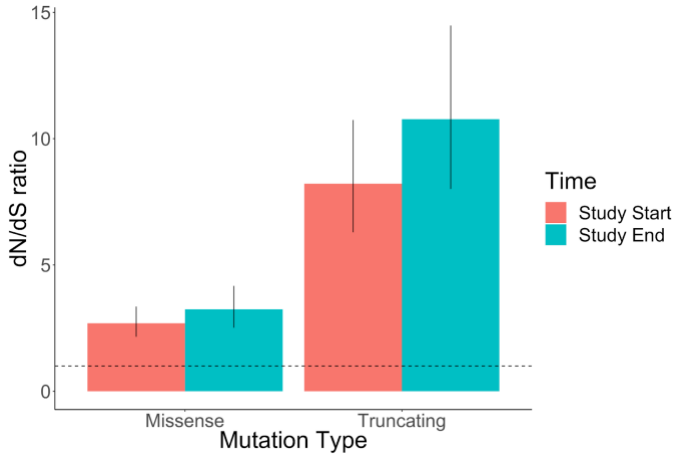


Fig. S4 - Global dN/dS ratios at the start vs end of study. Error bars depict 95% CIs.

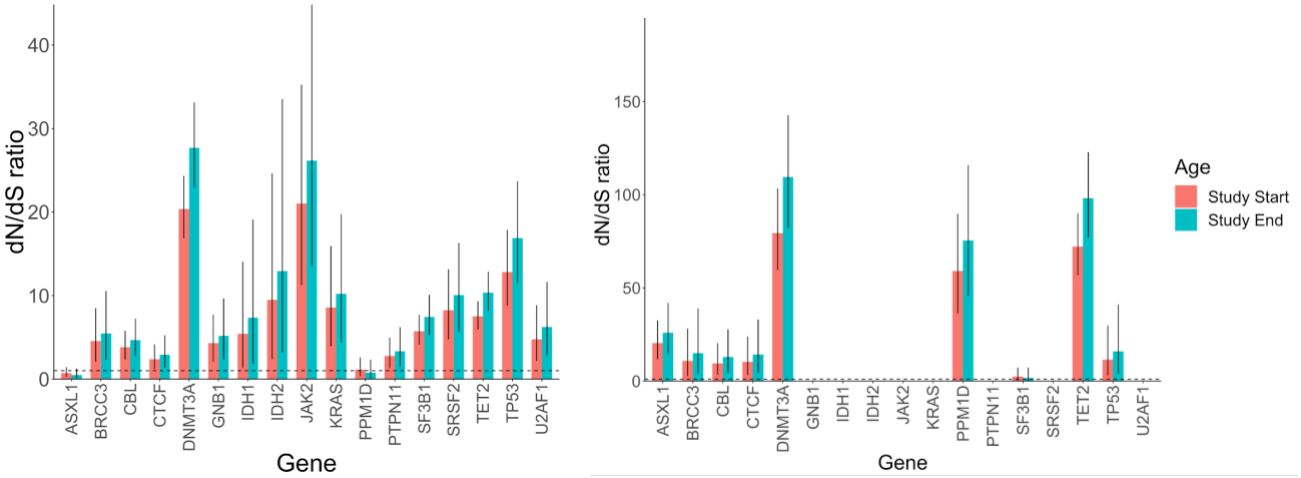


Fig. S5 - Gene-specific dN/dS ratios at the start vs end of study, for missense (left) and truncating (right) mutations. Error bars depict 95% CIs.

We noted a consistent trend for higher dN/dS ratios at older ages. One interpretation of this is that selection tends to strengthen with age. However, we now know from our longitudinal and phylogenetic data that this is not universally true, and that the relationship between age and mutation 'fitness' is gene-specific. For example, we found that *DNMT3A*-mutant clones preferentially expanded early in life and displayed slower growth in old age (suggesting falling selective pressure with advancing age), while splicing gene mutations only drove expansion later in life (suggesting increasing selective pressure with advancing age). Despite this, all driver genes display higher dN/dS ratios at older ages (**Fig. S2**), including, for example, *DNMT3A*. This highlights the inability of dN/dS to quantify selection strength at a particular point in time. Instead, dN/dS reflects the cumulative effects of selection up to the time of sampling. As such, while selection might strengthen with advancing age for many mutations, higher dN/dS ratios at later time-points also reflect the fact that additional mutant clones are identified at older ages, having had longer to reach detectable levels. In this case, drivers are not necessarily 'fitter' in older people, they have simply had longer to expand their cognate clones to a detectable level (by conventional sequencing). This illustrates that dN/dS ratios cannot disentangle the effects of driver fitness and duration of clonal expansion. In contrast, our longitudinal modelling of clonal trajectories, using serial and phylogenetic data, allows for quantitation of driver mutation fitness specifically.

dN/dS ratios in phylogenetic data

Next we explored how dN/dS ratios vary within haematopoietic phylogenies. Specifically, we asked whether selection strength differs between phylogenetic branches that precede clonal expansions (shared branches, coloured red in **Fig. S3**), as compared to selection along branches that do not (private branches, coloured grey in **Fig. S3**).

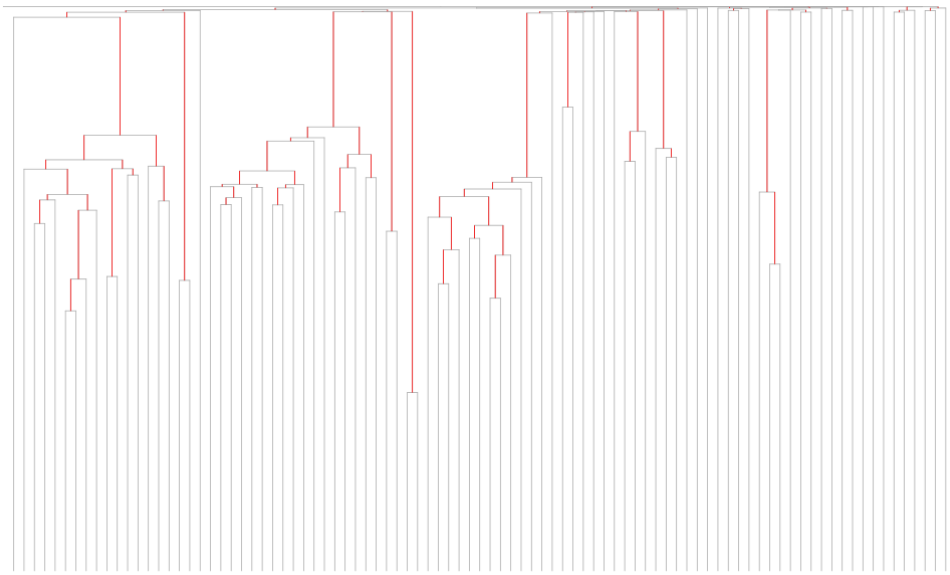


Figure S6. Example phylogeny (PD41305), illustrating the distinction between shared (red) and private (grey) branches.

We combined our three phylogenies (as depicted in **Fig. 5.2** in Chapter 5) into a single analysis to maximise our power to detect signal from the limited number of coding mutations across the genomes of just 3 individuals (total of 245 shared and 1885 private somatic mutations). Applying the dNdScv algorithm, we observe a trend towards higher global dN/dS ratios along shared vs private branches (**Fig. S4**).

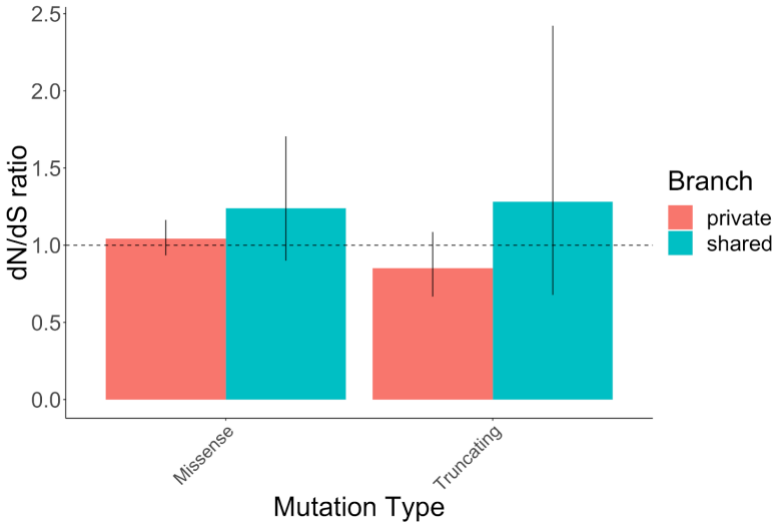


Fig. S7. Global dN/dS ratios among shared vs private mutations. Error bars depict 95% CIs.

Since mutations acquired along shared phylogeny branches are, by definition, those preceding clonal expansion, it is expected that selection would be strongest here, as compared to along private branches, where mutations do not, by definition, lead to clonal expansion. Excluding known CH driver mutations (defined as those in the 17 genes included in our longitudinal model), or excluding any mutation in a cancer gene (defined as those in Tier 1 of the Cancer Gene Census; https://cancer.sanger.ac.uk/census), made almost no impact on the dN/dS ratios derived as above. This is consistent with the existence of clones without known drivers in elderly individuals, and our observation that such clones grow over their lifetimes at rates comparable to clones with known drivers.

Supplementary Note 3 - Determining the effect of repeated sampling on the theoretical limit of detection

In the longitudinal component of this study, we sequence individuals a median of 4 times across their lifetimes. We define a detection threshold of 0.5% VAF as the minimum clone size for detection on individual timepoints, but the repeated sampling leads to 0.5% VAF being an overestimation of the actual limit of detection (LOD) - the size at which clones become detectable.

To show this, we simulate the repeated sampling of variants existing at a true clone proportion between 0 and 2%. We use this proportion p as the probability parameter in a beta binomial distribution, the overdispersion β calculated using technical replicates as the overdispersion in the same beta binomial distribution and a coverage of 1000. Having fully parameterized this distribution ($counts \sim BB(\frac{p\beta}{1-p}, \beta, 1000)$) we sample counts from it between 1 to 5 times. For each combination of clone size and number of samples we perform 1,000 realisations and calculate the number of detected clones at a threshold of 0.5%. This allows us to assess the fraction of clones with a specific size which are detected if we sample them multiple times - in other words, are able to assess the detection rate for different clone sizes and different numbers of samples.

With this, we show that, at a threshold of 0.5% and sampling only once, we detect 14.8% of all clones existing at 0.5% (**Fig. S8**). However, repeating this sampling 3 and 5 times leads to the detection of approximately 37.7% and 54.3% of all clones existing at 0.5%, respectively. As such, under regular conditions - a single sample - we would detect 13.5% of all clones present at 0.5% with a detection threshold of 0.5%. The question we should now ask is: what is the smallest possible clone size we detect at the same rate of detection - 13.5% - if we increase the number of samples? Using the same set of simulations, we can calculate the likely minimal size of the detected clones with clones as small as 0.21% and 0.14% being detected with 3 and 5 samples, respectively, using the same detection rate (with 2 and 4 samples, the theoretical LOD is 0.30% and 0.16%, respectively). As such, when considering the theoretical LOD used in **Fig. 5.8**, we avoided using 0.5% which, as we show, would be at least twice as high as the theoretical LOD obtained from simulations.

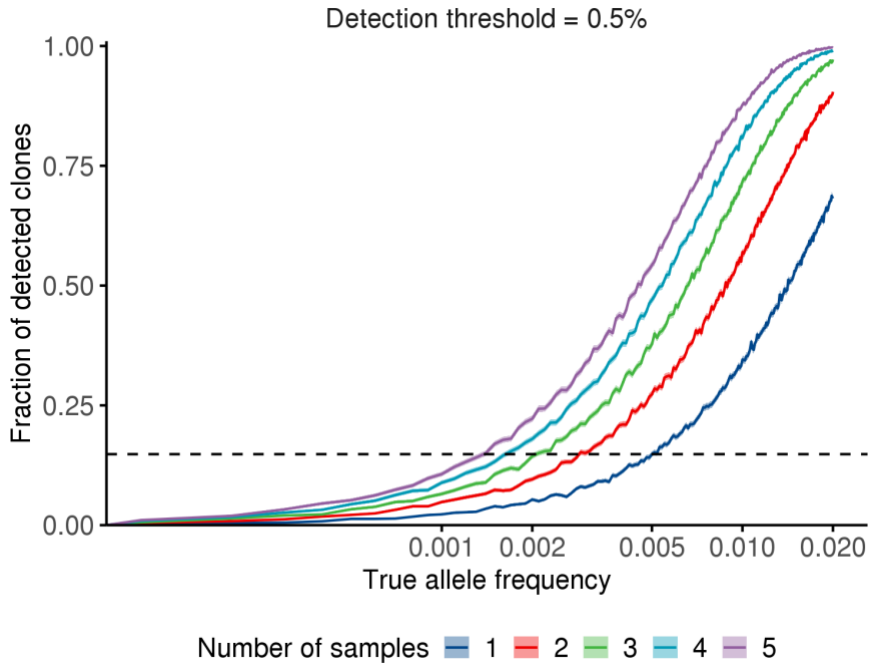


Fig. S8 - Fraction of detected clones upon repeated samples/timepoints at a detection threshold of 0.5%.

Supplementary References

1. Miles, L. A. *et al.* Single-cell mutation analysis of clonal evolution in myeloid malignancies. *Nature* **587**, 477–482 (2020).
2. Roth, A. *et al.* PyClone: statistical inference of clonal population structure in cancer. *Nat. Methods* **11**, 396–398 (2014).
3. Thol, F. *et al.* Frequency and prognostic impact of mutations in SRSF2, U2AF1, and ZRSR2 in patients with myelodysplastic syndromes. *Blood* **119**, 3578–3584 (2012).
4. Mitchell, E. *et al.* Clonal dynamics of haematopoiesis across the human lifespan. *bioRxiv* (2021).
5. Martincorena, I. *et al.* Universal Patterns of Selection in Cancer and Somatic Tissues. *Cell* **173**, 1823 (2018).

Appendix 3

Tables

Table 1a | 56 genes sequenced in SardiNIA samples (Agilent SureSelect ELID 3156971)

ASXL1	*ETV6*	*MPL*	*SF1*
BCOR	*EZH2*	*MYD88*	*SF3A1*
BCORL1	*FLT3*	*NOTCH1*	*SF3B1*
BRAF	*GATA2*	*NPM1*	*SMC1A*
BRCC3	*GNAS*	*NRAS*	*SMC3*
CALR	*GNB1*	*PHF6*	*SRSF2*
CBL	*IDH1*	*PIGA*	*STAG2*
CEBPA	*IDH2*	*PPM1D*	*STAT3*
CREBBP	*JAK2*	*PRPF40B*	*TET2*
CSF1R	*JAK3*	*PTEN*	*TP53*
CSF3R	*KDM6A*	*PTPN11*	*U2AF1*
CTCF	*KIT*	*RAD21*	*U2AF2*
CUX1	*KMT2A*	*RUNX1*	*WT1*
DNMT3A	*KRAS*	*SETBP1*	*ZRSR2*

Table 1b | 41 genes sequenced in TwinsUK samples (Agilent SureSelect ELID 0735431)

ASXL1	*GNAS*	*PHF6*	*SMC3*
BCOR	*GNB1*	*PPM1D*	*SRSF2*
BCORL1	*IDH1*	*PRPF40B*	*STAG2*
BRAF	*IDH2*	*PTEN*	*STAT3*
BRCC3	*JAK2*	*PTPN11*	*TET2*
CALR	*KDM6A*	*RAD21*	*TP53*
CBL	*KRAS*	*SF1*	*U2AF1*
CREBBP	*NPM1*	*SF3A1*	*U2AF2*
CSF1R	*NRAS*	*SF3B1*	*ZAN*
DNMT3A	*NUP98*	*SMC1A*	*ZRSR2*
EZH2			

Table 2 | Driver classification for TwinsUK analysis

Gene name	Criteria for classification of somatic mutations as drivers	Transcript
ASXL1	Frameshift/nonsense/splice-site in exon 11-12	NM_015338
BCOR	Frameshift/nonsense/splice-site	NM_001123385
BCORL1	Frameshift/nonsense/splice-site	NM_021946
BRAF	Missense in aa range p.590-615; Missense at G469	NM_004333
BRCC3	Frameshift/nonsense/splice-site	NM_024332
CALR	Frameshift in exon 9	NM_004343
CBL	Missense in Linker/RING finger domains (p.345-434)	NM_005188
CREBBP	Frameshift/nonsense/splice-site	NM_004380
CSF1R	Missense at L301 / Y969	NM_005211
DNMT3A	Frameshift/nonsense/splice-site; Missense in PWWP (p.292-350) / ADD (p.482-614) / MTase (p.634-912) domains	NM_022552
EZH2	Frameshift/nonsense/splice-site; Missense in SET domain (p.617-732)	NM_001203247
GNAS	Missense at R201 (844)	NM_016592
GNB1	Missense at K57 / I80	NM_002074
IDH1	Missense at R132	NM_005896
IDH2	Missense at R140 / R172	NM_002168
JAK2	V617F; Missense/indel in aa range p.536-547	NM_004972
KDM6A	Frameshift/nonsense/splice-site	NM_021140
KRAS	Missense at G12 / G13 / Q61 / A146	NM_033360
NPM1	Frameshift in exon 12	NM_002520
NRAS	Missense at G12 / G13 / Q61	NM_002524
NUP98	No definitive CH driver mutations identified in the literature	NM_139132
PHF6	Frameshift/nonsense/splice-site	NM_001015877
PPM1D	Frameshift/nonsense in exon 5/6	NM_003620
PRPF40B	Frameshift/nonsense/splice-site	NM_001031698
PTEN	Frameshift/nonsense/splice-site	NM_000314
PTPN11	Missense in aa range p.58-76 and p.491-510	NM_002834
RAD21	Frameshift/nonsense/splice-site	NM_006265
SF1	Frameshift/nonsense/splice-site	NM_004630
SF3A1	Frameshift/nonsense/splice-site	NM_005877
SF3B1	Missense in terminal HEAT domains (p.529-1201)	NM_012433
SMC1A	Missense at R96 / R586	NM_006306
SMC3	Frameshift/nonsense/splice-site	NM_005445
SRSF2	Missense/deletion involving p.P95	NM_003016
STAG2	Frameshift/nonsense/splice-site	NM_006603
STAT3	Missense in SH2 domain (p.580-670)	NM_139276
TET2	Frameshift/nonsense/splice-site; Missense in conserved domains (p.1104-1481 and p.1843-2002)	NM_001127208
TP53	Frameshift/nonsense/splice-site; Missense in DNA-binding domain (p.95-288); Missense at P72 / R337	NM_001126112
U2AF1	Missense at S34 / R156 / Q157	NM_006758
U2AF2	Missense in RNA recognition motifs domains (p.149-231, p.259-337, p.381-462)	NM_007279
ZAN	No definitive CH driver mutations identified in the literature	NM_003386
ZRSR2	Frameshift/nonsense/splice-site	NM_005089

Table 3 | Validation of mutation calls using multiplex PCR

Sample ID	Gene	Chrom	Position	WT	MT	Protein	"A" count by PCR	"C" count by PCR	"G" count by PCR	"T" count by PCR	Depth by PCR	VAF by PCR	VAF by bait capture
PD42410b	DNMT3A	2	25457192	G	A	p.R899C	126	0	3857	0	3983	0.032	0.026
PD42358b	DNMT3A	2	25457192	G	C	p.R899G	1	37	3861	0	3899	0.009	0.012
PD42346b	DNMT3A	2	25457243	G	A	p.R882C	23	0	2857	0	2880	0.008	0.013
PD42350b	SF3B1	2	198266834	T	C	p.K700E	0	124	0	2304	2428	0.051	0.049
PD42355b	SF3B1	2	198266834	T	C	p.K700E	0	13	0	1980	1993	0.007	0.007
PD42399b	SF3B1	2	198267361	T	C	p.K666E	0	422	2	1843	2267	0.186	0.19
PD42370b	TP53	17	7577120	C	T	p.R273H	0	3229	0	24	3253	0.007	0.007
PD42448b	TP53	17	7577141	C	T	p.G266E	2	2661	0	6	2669	0.002	0.008
PD42308b	TP53	17	7577538	C	A	p.R248L	177	14752	0	1	14930	0.012	0.01
PD42354b	TP53	17	7577539	G	A	p.R248W	244	0	17193	0	17437	0.014	0.018
PD42317b	TP53	17	7578372	A	T	p.D186E	6516	0	0	149	6665	0.022	0.022
PD42357c	TP53	17	7578522	T	A	p.Q136H	32	0	0	5102	5134	0.006	0.005
PD42460b	PPM1D	17	58740546	T	A	p.L484X	149	0	15	12086	12250	0.012	0.009
PD42428b	PPM1D	17	58740665	C	T	p.Q524X	1	10213	0	62	10276	0.006	0.006
PD42331b	SRSF2	17	74732959	G	C	p.P95R	0	14	3072	0	3086	0.005	0.006
PD42467b	U2AF1	21	44524456	G	A	p.S34F	46	0	3497	0	3543	0.013	0.011

Table 4 | Negative controls (Horizon TruQ wild-type)

Sample ID	Replicate	Gene	Chrom	Position	WT	MT	Protein	VAF
PD41771a	1	IDH1	2	209113113	G	A	R132C	0
PD41771a	2	IDH1	2	209113113	G	A	R132C	0
PD41771a	3	IDH1	2	209113113	G	A	R132C	0.001
PD41771a	1	JAK2	9	5073770	G	T	V617F	0
PD41771a	2	JAK2	9	5073770	G	T	V617F	0
PD41771a	3	JAK2	9	5073770	G	T	V617F	0
PD41771a	1	KRAS	12	25398284	C	G	G12A	0
PD41771a	2	KRAS	12	25398284	C	G	G12A	0
PD41771a	3	KRAS	12	25398284	C	G	G12A	0
PD41771a	1	KRAS	12	25398285	C	G	G12R	0
PD41771a	2	KRAS	12	25398285	C	G	G12R	0
PD41771a	3	KRAS	12	25398285	C	G	G12R	0
PD41771a	1	NRAS	1	115256530	G	T	Q61K	0
PD41771a	2	NRAS	1	115256530	G	T	Q61K	0
PD41771a	3	NRAS	1	115256530	G	T	Q61K	0

Table 5a | Positive controls: SardiNIA samples sequenced in replicate

Sample ID	Study Phase	Replicate	Chr	Position	WT	MT	VAF	Gene	Protein	Effect
PD34543	4	1	2	209113112	C	T	0.106	IDH1	p.R132H	Missense
PD34543	4	2	2	209113112	C	T	0.114	IDH1	p.R132H	Missense
PD34543	4	3	2	209113112	C	T	0.127	IDH1	p.R132H	Missense
PD34543	4	1	9	5073770	G	T	0.053	JAK2	p.V617F	Missense
PD34543	4	2	9	5073770	G	T	0.043	JAK2	p.V617F	Missense
PD34543	4	3	9	5073770	G	T	0.048	JAK2	p.V617F	Missense
PD34543	4	1	17	74732959	G	T	0.072	SRSF2	p.P95H	Missense
PD34543	4	2	17	74732959	G	T	0.093	SRSF2	p.P95H	Missense
PD34543	4	3	17	74732959	G	T	0.074	SRSF2	p.P95H	Missense
PD34543	4	1	20	57428431	T	C	0.021	GNAS	p.A37A	Synonymous
PD34543	4	2	20	57428431	T	C	0.016	GNAS	p.A37A	Synonymous
PD34543	4	3	20	57428431	T	C	0.022	GNAS	p.A37A	Synonymous
PD34543	4	1	X	133551331	A	G	0.023	PHF6	p.?	SpliceSite
PD34543	4	2	X	133551331	A	G	0.017	PHF6	p.?	SpliceSite
PD34543	4	3	X	133551331	A	G	0.027	PHF6	p.?	SpliceSite
PD41087	2	1	17	74732959	G	A	0.001	SRSF2	p.P95L	Missense
PD41087	2	2	17	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41087	2	3	17	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41087	3	1	17	74732959	G	A	0.006	SRSF2	p.P95L	Missense
PD41087	3	2	17	74732959	G	A	0.002	SRSF2	p.P95L	Missense
PD41087	3	3	17	74732959	G	A	0.005	SRSF2	p.P95L	Missense
PD41087	4	1	17	74732959	G	A	0.116	SRSF2	p.P95L	Missense
PD41087	4	2	17	74732959	G	A	0.135	SRSF2	p.P95L	Missense
PD41087	4	3	17	74732959	G	A	0.110	SRSF2	p.P95L	Missense
PD41087	5	1	17	74732959	G	A	0.016	SRSF2	p.P95L	Missense
PD41087	5	2	17	74732959	G	A	0.011	SRSF2	p.P95L	Missense
PD41087	5	3	17	74732959	G	A	0.007	SRSF2	p.P95L	Missense
PD41087	2	1	17	74732959	G	T	0.001	SRSF2	p.P95H	Missense
PD41087	2	2	17	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41087	2	3	17	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41087	3	1	17	74732959	G	T	0.002	SRSF2	p.P95H	Missense
PD41087	3	2	17	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41087	3	3	17	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41087	4	1	17	74732959	G	T	0.013	SRSF2	p.P95H	Missense
PD41087	4	2	17	74732959	G	T	0.028	SRSF2	p.P95H	Missense
PD41087	4	3	17	74732959	G	T	0.028	SRSF2	p.P95H	Missense
PD41087	5	1	17	74732959	G	T	0.292	SRSF2	p.P95H	Missense
PD41087	5	2	17	74732959	G	T	0.300	SRSF2	p.P95H	Missense
PD41087	5	3	17	74732959	G	T	0.295	SRSF2	p.P95H	Missense
PD41087	2	1	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	2	2	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	2	3	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	3	1	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	3	2	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	3	3	17	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	4	1	17	74733113	A	G	0.020	SRSF2	p.Y44H	Missense
PD41087	4	2	17	74733113	A	G	0.021	SRSF2	p.Y44H	Missense
PD41087	4	3	17	74733113	A	G	0.015	SRSF2	p.Y44H	Missense
PD41087	5	1	17	74733113	A	G	0.017	SRSF2	p.Y44H	Missense
PD41087	5	2	17	74733113	A	G	0.016	SRSF2	p.Y44H	Missense
PD41087	5	3	17	74733113	A	G	0.030	SRSF2	p.Y44H	Missense
PD41087	2	1	20	31023231	G	T	0.001	ASXL1	p.E906X	Nonsense
PD41087	2	2	20	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	2	3	20	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	3	1	20	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	3	2	20	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	3	3	20	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	4	1	20	31023231	G	T	0.001	ASXL1	p.E906X	Nonsense

Sample ID	Study Phase	Replicate	Chr	Position	WT	MT	VAF	Gene	Protein	Effect
PD41087	4	2	20	31023231	G	T	0.003	ASXL1	p.E906X	Nonsense
PD41087	4	3	20	31023231	G	T	0.003	ASXL1	p.E906X	Nonsense
PD41087	5	1	20	31023231	G	T	0.014	ASXL1	p.E906X	Nonsense
PD41087	5	2	20	31023231	G	T	0.025	ASXL1	p.E906X	Nonsense
PD41087	5	3	20	31023231	G	T	0.028	ASXL1	p.E906X	Nonsense
PD41087	2	1	X	53436412	C	T	0.322	SMC1A	p.R404Q	Missense
PD41087	2	2	X	53436412	C	T	0.304	SMC1A	p.R404Q	Missense
PD41087	2	3	X	53436412	C	T	0.308	SMC1A	p.R404Q	Missense
PD41087	3	1	X	53436412	C	T	0.357	SMC1A	p.R404Q	Missense
PD41087	3	2	X	53436412	C	T	0.373	SMC1A	p.R404Q	Missense
PD41087	3	3	X	53436412	C	T	0.365	SMC1A	p.R404Q	Missense
PD41087	4	1	X	53436412	C	T	0.378	SMC1A	p.R404Q	Missense
PD41087	4	2	X	53436412	C	T	0.394	SMC1A	p.R404Q	Missense
PD41087	4	3	X	53436412	C	T	0.389	SMC1A	p.R404Q	Missense
PD41087	5	1	X	53436412	C	T	0.390	SMC1A	p.R404Q	Missense
PD41087	5	2	X	53436412	C	T	0.380	SMC1A	p.R404Q	Missense
PD41087	5	3	X	53436412	C	T	0.388	SMC1A	p.R404Q	Missense
PD41087	2	1	X	133527665	G	A	0.000	PHF6	p.?	SpliceSite
PD41087	2	2	X	133527665	G	A	0.000	PHF6	p.?	SpliceSite
PD41087	2	3	X	133527665	G	A	0.000	PHF6	p.?	SpliceSite
PD41087	3	1	X	133527665	G	A	0.002	PHF6	p.?	SpliceSite
PD41087	3	2	X	133527665	G	A	0.003	PHF6	p.?	SpliceSite
PD41087	3	3	X	133527665	G	A	0.003	PHF6	p.?	SpliceSite
PD41087	4	1	X	133527665	G	A	0.029	PHF6	p.?	SpliceSite
PD41087	4	2	X	133527665	G	A	0.027	PHF6	p.?	SpliceSite
PD41087	4	3	X	133527665	G	A	0.020	PHF6	p.?	SpliceSite
PD41087	5	1	X	133527665	G	A	0.056	PHF6	p.?	SpliceSite
PD41087	5	2	X	133527665	G	A	0.064	PHF6	p.?	SpliceSite
PD41087	5	3	X	133527665	G	A	0.060	PHF6	p.?	SpliceSite
PD41160	1	2	2	25466800	G	A	0.017	DNMT3A	p.R635W	Missense
PD41160	1	3	2	25466800	G	A	0.006	DNMT3A	p.R635W	Missense
PD41160	2	1	2	25466800	G	A	0.007	DNMT3A	p.R635W	Missense
PD41160	2	2	2	25466800	G	A	0.011	DNMT3A	p.R635W	Missense
PD41160	2	3	2	25466800	G	A	0.016	DNMT3A	p.R635W	Missense
PD41160	3	1	2	25466800	G	A	0.017	DNMT3A	p.R635W	Missense
PD41160	3	2	2	25466800	G	A	0.033	DNMT3A	p.R635W	Missense
PD41160	3	3	2	25466800	G	A	0.015	DNMT3A	p.R635W	Missense
PD41160	4	1	2	25466800	G	A	0.032	DNMT3A	p.R635W	Missense
PD41160	4	2	2	25466800	G	A	0.023	DNMT3A	p.R635W	Missense
PD41160	4	3	2	25466800	G	A	0.035	DNMT3A	p.R635W	Missense
PD41160	5	1	2	25466800	G	A	0.049	DNMT3A	p.R635W	Missense
PD41160	5	2	2	25466800	G	A	0.044	DNMT3A	p.R635W	Missense
PD41160	5	3	2	25466800	G	A	0.071	DNMT3A	p.R635W	Missense
PD41160	1	1	2	25466800	G	A	0.005	DNMT3A	p.R635W	Missense
PD41246	1	1	4	106164929	A	G	0.012	TET2	p.N1266S	Missense
PD41246	1	2	4	106164929	A	G	0.036	TET2	p.N1266S	Missense
PD41246	1	3	4	106164929	A	G	0.015	TET2	p.N1266S	Missense
PD41246	2	1	4	106164929	A	G	0.019	TET2	p.N1266S	Missense
PD41246	2	2	4	106164929	A	G	0.008	TET2	p.N1266S	Missense
PD41246	2	3	4	106164929	A	G	0.017	TET2	p.N1266S	Missense
PD41246	3	1	4	106164929	A	G	0.017	TET2	p.N1266S	Missense
PD41246	3	2	4	106164929	A	G	0.019	TET2	p.N1266S	Missense
PD41246	3	3	4	106164929	A	G	0.021	TET2	p.N1266S	Missense
PD41246	4	1	4	106164929	A	G	0.021	TET2	p.N1266S	Missense
PD41246	4	2	4	106164929	A	G	0.033	TET2	p.N1266S	Missense
PD41246	4	3	4	106164929	A	G	0.050	TET2	p.N1266S	Missense
PD41246	1	1	7	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	1	2	7	148511184	G	A	0.005	EZH2	p.T573I	Missense
PD41246	1	3	7	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	2	1	7	148511184	G	A	0.001	EZH2	p.T573I	Missense

Sample ID	Study Phase	Replicate	Chr	Position	WT	MT	VAF	Gene	Protein	Effect
PD41246	2	2	7	148511184	G	A	0.002	EZH2	p.T573I	Missense
PD41246	2	3	7	148511184	G	A	0.004	EZH2	p.T573I	Missense
PD41246	3	1	7	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	3	2	7	148511184	G	A	0.000	EZH2	p.T573I	Missense
PD41246	3	3	7	148511184	G	A	0.009	EZH2	p.T573I	Missense
PD41246	4	1	7	148511184	G	A	0.005	EZH2	p.T573I	Missense
PD41246	4	2	7	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	4	3	7	148511184	G	A	0.000	EZH2	p.T573I	Missense
PD41246	1	1	9	5073770	G	T	0.005	JAK2	p.V617F	Missense
PD41246	1	2	9	5073770	G	T	0.014	JAK2	p.V617F	Missense
PD41246	1	3	9	5073770	G	T	0.019	JAK2	p.V617F	Missense
PD41246	2	1	9	5073770	G	T	0.014	JAK2	p.V617F	Missense
PD41246	2	2	9	5073770	G	T	0.010	JAK2	p.V617F	Missense
PD41246	2	3	9	5073770	G	T	0.021	JAK2	p.V617F	Missense
PD41246	3	1	9	5073770	G	T	0.026	JAK2	p.V617F	Missense
PD41246	3	2	9	5073770	G	T	0.021	JAK2	p.V617F	Missense
PD41246	3	3	9	5073770	G	T	0.022	JAK2	p.V617F	Missense
PD41246	4	1	9	5073770	G	T	0.058	JAK2	p.V617F	Missense
PD41246	4	2	9	5073770	G	T	0.064	JAK2	p.V617F	Missense
PD41246	4	3	9	5073770	G	T	0.054	JAK2	p.V617F	Missense
PD41276	1	1	2	198266834	T	C	0.000	SF3B1	p.K700E	Missense
PD41276	1	2	2	198266834	T	C	0.000	SF3B1	p.K700E	Missense
PD41276	1	3	2	198266834	T	C	0.004	SF3B1	p.K700E	Missense
PD41276	2	1	2	198266834	T	C	0.004	SF3B1	p.K700E	Missense
PD41276	2	2	2	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41276	2	3	2	198266834	T	C	0.002	SF3B1	p.K700E	Missense
PD41276	3	1	2	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41276	3	2	2	198266834	T	C	0.007	SF3B1	p.K700E	Missense
PD41276	3	3	2	198266834	T	C	0.005	SF3B1	p.K700E	Missense
PD41276	4	1	2	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41276	4	2	2	198266834	T	C	0.005	SF3B1	p.K700E	Missense
PD41276	4	3	2	198266834	T	C	0.002	SF3B1	p.K700E	Missense
PD41276	5	1	2	198266834	T	C	0.011	SF3B1	p.K700E	Missense
PD41276	5	2	2	198266834	T	C	0.003	SF3B1	p.K700E	Missense
PD41276	5	3	2	198266834	T	C	0.012	SF3B1	p.K700E	Missense
PD41276	1	1	2	198267359	C	G	0.023	SF3B1	p.K666N	Missense
PD41276	1	2	2	198267359	C	G	0.042	SF3B1	p.K666N	Missense
PD41276	1	3	2	198267359	C	G	0.029	SF3B1	p.K666N	Missense
PD41276	2	1	2	198267359	C	G	0.096	SF3B1	p.K666N	Missense
PD41276	2	2	2	198267359	C	G	0.111	SF3B1	p.K666N	Missense
PD41276	2	3	2	198267359	C	G	0.108	SF3B1	p.K666N	Missense
PD41276	3	1	2	198267359	C	G	0.185	SF3B1	p.K666N	Missense
PD41276	3	2	2	198267359	C	G	0.197	SF3B1	p.K666N	Missense
PD41276	3	3	2	198267359	C	G	0.188	SF3B1	p.K666N	Missense
PD41276	4	1	2	198267359	C	G	0.297	SF3B1	p.K666N	Missense
PD41276	4	2	2	198267359	C	G	0.261	SF3B1	p.K666N	Missense
PD41276	4	3	2	198267359	C	G	0.315	SF3B1	p.K666N	Missense
PD41276	5	1	2	198267359	C	G	0.359	SF3B1	p.K666N	Missense
PD41276	5	2	2	198267359	C	G	0.346	SF3B1	p.K666N	Missense
PD41276	5	3	2	198267359	C	G	0.365	SF3B1	p.K666N	Missense
PD41276	1	1	9	139438556	T	C	0.006	NOTCH1	p.?	SpliceSite
PD41276	1	2	9	139438556	T	C	0.010	NOTCH1	p.?	SpliceSite
PD41276	1	3	9	139438556	T	C	0.012	NOTCH1	p.?	SpliceSite
PD41276	2	1	9	139438556	T	C	0.002	NOTCH1	p.?	SpliceSite
PD41276	2	2	9	139438556	T	C	0.003	NOTCH1	p.?	SpliceSite
PD41276	2	3	9	139438556	T	C	0.002	NOTCH1	p.?	SpliceSite
PD41276	3	1	9	139438556	T	C	0.001	NOTCH1	p.?	SpliceSite
PD41276	3	2	9	139438556	T	C	0.002	NOTCH1	p.?	SpliceSite
PD41276	3	3	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite
PD41276	4	1	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite

Sample ID	Study Phase	Replicate	Chr	Position	WT	MT	VAF	Gene	Protein	Effect
PD41276	4	2	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite
PD41276	4	3	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite
PD41276	5	1	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite
PD41276	5	2	9	139438556	T	C	0.000	NOTCH1	p.?	SpliceSite
PD41276	5	3	9	139438556	T	C	0.002	NOTCH1	p.?	SpliceSite
PD41276	1	1	11	119142571	G	A	0.000	CBL	p.W190X	Nonsense
PD41276	1	2	11	119142571	G	A	0.000	CBL	p.W190X	Nonsense
PD41276	1	3	11	119142571	G	A	0.001	CBL	p.W190X	Nonsense
PD41276	2	1	11	119142571	G	A	0.000	CBL	p.W190X	Nonsense
PD41276	2	2	11	119142571	G	A	0.001	CBL	p.W190X	Nonsense
PD41276	2	3	11	119142571	G	A	0.002	CBL	p.W190X	Nonsense
PD41276	3	1	11	119142571	G	A	0.008	CBL	p.W190X	Nonsense
PD41276	3	2	11	119142571	G	A	0.006	CBL	p.W190X	Nonsense
PD41276	3	3	11	119142571	G	A	0.006	CBL	p.W190X	Nonsense
PD41276	4	1	11	119142571	G	A	0.010	CBL	p.W190X	Nonsense
PD41276	4	2	11	119142571	G	A	0.004	CBL	p.W190X	Nonsense
PD41276	4	3	11	119142571	G	A	0.010	CBL	p.W190X	Nonsense
PD41276	5	1	11	119142571	G	A	0.015	CBL	p.W190X	Nonsense
PD41276	5	2	11	119142571	G	A	0.010	CBL	p.W190X	Nonsense
PD41276	5	3	11	119142571	G	A	0.015	CBL	p.W190X	Nonsense
PD41276	1	1	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	1	2	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	1	3	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	2	1	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	2	2	X	15809085	A	G	0.001	ZRSR2	p.K24E	Missense
PD41276	2	3	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	3	1	X	15809085	A	G	0.001	ZRSR2	p.K24E	Missense
PD41276	3	2	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	3	3	X	15809085	A	G	0.001	ZRSR2	p.K24E	Missense
PD41276	4	1	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	4	2	X	15809085	A	G	0.003	ZRSR2	p.K24E	Missense
PD41276	4	3	X	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	5	1	X	15809085	A	G	0.004	ZRSR2	p.K24E	Missense
PD41276	5	2	X	15809085	A	G	0.004	ZRSR2	p.K24E	Missense
PD41276	5	3	X	15809085	A	G	0.001	ZRSR2	p.K24E	Missense
PD41276	1	1	X	39922886	A	T	0.035	BCOR	p.S1240S	Synonymous
PD41276	1	2	X	39922886	A	T	0.022	BCOR	p.S1240S	Synonymous
PD41276	1	3	X	39922886	A	T	0.026	BCOR	p.S1240S	Synonymous
PD41276	2	1	X	39922886	A	T	0.097	BCOR	p.S1240S	Synonymous
PD41276	2	2	X	39922886	A	T	0.106	BCOR	p.S1240S	Synonymous
PD41276	2	3	X	39922886	A	T	0.108	BCOR	p.S1240S	Synonymous
PD41276	3	1	X	39922886	A	T	0.203	BCOR	p.S1240S	Synonymous
PD41276	3	2	X	39922886	A	T	0.203	BCOR	p.S1240S	Synonymous
PD41276	3	3	X	39922886	A	T	0.190	BCOR	p.S1240S	Synonymous
PD41276	4	1	X	39922886	A	T	0.269	BCOR	p.S1240S	Synonymous
PD41276	4	2	X	39922886	A	T	0.267	BCOR	p.S1240S	Synonymous
PD41276	4	3	X	39922886	A	T	0.273	BCOR	p.S1240S	Synonymous
PD41276	5	1	X	39922886	A	T	0.352	BCOR	p.S1240S	Synonymous
PD41276	5	2	X	39922886	A	T	0.312	BCOR	p.S1240S	Synonymous
PD41276	5	3	X	39922886	A	T	0.334	BCOR	p.S1240S	Synonymous

Table 5b | Positive controls: Horizon Tru-Q DNA reference samples sequenced in replicate

Sample ID	Replicate	Chr	Position	WT	MT	VAF expected	VAF observed	Gene	Protein	Effect
PD41772a	1	1	1E+08	G	T	0.050	0.069	NRAS	Q61K	Missense
PD41772a	2	1	1E+08	G	T	0.050	0.054	NRAS	Q61K	Missense
PD41772a	3	1	1E+08	G	T	0.050	0.041	NRAS	Q61K	Missense
PD41772a	1	2	2E+08	G	A	0.050	0.030	IDH1	R132C	Missense
PD41772a	2	2	2E+08	G	A	0.050	0.050	IDH1	R132C	Missense
PD41772a	3	2	2E+08	G	A	0.050	0.046	IDH1	R132C	Missense
PD41772a	1	9	5E+06	G	T	0.050	0.070	JAK2	V617F	Missense
PD41772a	2	9	5E+06	G	T	0.050	0.049	JAK2	V617F	Missense
PD41772a	3	9	5E+06	G	T	0.050	0.059	JAK2	V617F	Missense
PD41772a	1	12	3E+07	C	G	0.050	0.039	KRAS	G12A	Missense
PD41772a	2	12	3E+07	C	G	0.050	0.043	KRAS	G12A	Missense
PD41772a	3	12	3E+07	C	G	0.050	0.062	KRAS	G12A	Missense
PD41772a	1	12	3E+07	C	G	0.050	0.046	KRAS	G12R	Missense
PD41772a	2	12	3E+07	C	G	0.050	0.043	KRAS	G12R	Missense
PD41772a	3	12	3E+07	C	G	0.050	0.040	KRAS	G12R	Missense
PD41773a	1	1	1E+08	G	T	0.020	0.019	NRAS	Q61K	Missense
PD41773a	2	1	1E+08	G	T	0.020	0.025	NRAS	Q61K	Missense
PD41773a	1	2	2E+08	G	A	0.020	0.006	IDH1	R132C	Missense
PD41773a	2	2	2E+08	G	A	0.020	0.013	IDH1	R132C	Missense
PD41773a	1	9	5E+06	G	T	0.020	0.020	JAK2	V617F	Missense
PD41773a	2	9	5E+06	G	T	0.020	0.017	JAK2	V617F	Missense
PD41773a	1	12	3E+07	C	G	0.020	0.021	KRAS	G12A	Missense
PD41773a	2	12	3E+07	C	G	0.020	0.013	KRAS	G12A	Missense
PD41773a	1	12	3E+07	C	G	0.020	0.021	KRAS	G12R	Missense
PD41773a	2	12	3E+07	C	G	0.020	0.008	KRAS	G12R	Missense
PD41774a	1	1	1E+08	G	T	0.010	0.004	NRAS	Q61K	Missense
PD41774a	2	1	1E+08	G	T	0.010	0.008	NRAS	Q61K	Missense
PD41774a	1	2	2E+08	G	A	0.010	0.006	IDH1	R132C	Missense
PD41774a	2	2	2E+08	G	A	0.010	0.013	IDH1	R132C	Missense
PD41774a	1	9	5E+06	G	T	0.010	0.010	JAK2	V617F	Missense
PD41774a	2	9	5E+06	G	T	0.010	0.015	JAK2	V617F	Missense
PD41774a	1	12	3E+07	C	G	0.010	0.005	KRAS	G12A	Missense
PD41774a	2	12	3E+07	C	G	0.010	0.009	KRAS	G12A	Missense
PD41774a	1	12	3E+07	C	G	0.010	0.005	KRAS	G12R	Missense
PD41774a	2	12	3E+07	C	G	0.010	0.009	KRAS	G12R	Missense
PD41775a	1	1	1E+08	G	T	0.005	0.000	NRAS	Q61K	Missense
PD41775a	2	1	1E+08	G	T	0.005	0.006	NRAS	Q61K	Missense
PD41775a	1	2	2E+08	G	A	0.005	0.000	IDH1	R132C	Missense
PD41775a	2	2	2E+08	G	A	0.005	0.006	IDH1	R132C	Missense
PD41775a	1	9	5E+06	G	T	0.005	0.010	JAK2	V617F	Missense
PD41775a	2	9	5E+06	G	T	0.005	0.013	JAK2	V617F	Missense
PD41775a	1	12	3E+07	C	G	0.005	0.009	KRAS	G12A	Missense
PD41775a	2	12	3E+07	C	G	0.005	0.011	KRAS	G12A	Missense
PD41775a	1	12	3E+07	C	G	0.005	0.007	KRAS	G12R	Missense
PD41775a	2	12	3E+07	C	G	0.005	0.002	KRAS	G12R	Missense
PD41771a	1	1	1E+08	G	T	0.000	0.000	NRAS	Q61K	Missense
PD41771a	2	1	1E+08	G	T	0.000	0.000	NRAS	Q61K	Missense
PD41771a	1	2	2E+08	G	A	0.000	0.000	IDH1	R132C	Missense
PD41771a	2	2	2E+08	G	A	0.000	0.000	IDH1	R132C	Missense
PD41771a	1	9	5E+06	G	T	0.000	0.000	JAK2	V617F	Missense
PD41771a	2	9	5E+06	G	T	0.000	0.000	JAK2	V617F	Missense
PD41771a	1	12	3E+07	C	G	0.000	0.000	KRAS	G12A	Missense
PD41771a	2	12	3E+07	C	G	0.000	0.000	KRAS	G12A	Missense
PD41771a	1	12	3E+07	C	G	0.000	0.000	KRAS	G12R	Missense
PD41771a	2	12	3E+07	C	G	0.000	0.000	KRAS	G12R	Missense

Table 6 | Genes, mutation types and sites modelled

Gene	Truncating effect	Non-truncating effect	Explicitly modelled sites (number of occurrences in the cohort)
ASXL1	x		
BRCC3	x	x	
CBL	x	x	I383M (2), C404Y (3), V430M (2)
CTCF	x	x	
DNMT3A	x	x	L295P (2), R635Q (2), R635W (4), S638F (2), L647R (2), R659H (2), I705T (4), R736C (3), R736H (2), F755S (3), S770L (5), I780T (2), M880V (2), R882C (2), R882H (6)
GNB1		x	K57E (4)
IDH1		x	R132H (2)
IDH2			R140Q (3)
JAK2			V617F (12)
KRAS		x	
PPM1D	x		
PTPN11		x	
SF3B1		x	H662Q (2), K666N (13), K666R (2), K700E (7), A744P (2)
SRSF2		x	P95A (2), P95H (6), P95L (4)
TET2	x	x	H1380Y (4), I1873T (6)
TP53	x	x	Y220C (2), M237V (2), R248W (2), R273H (2), R282W (2)
U2AF1		x	Q157P (3), Q157R (3)

Table 7a | Cohort summary measures of serum analytes tested

Cytokine	Units	Mean	Median	Max	Min
CRP	mg/L	5.11	3	170.1	0.1
Eotaxin	pg/ml	544.91	497.705	1501.76	158.36
Eotaxin_3	pg/ml	54.4	22.76	10646.99	22.76
FGF_basic	pg/ml	9.82	7.22	99.12	0.52
GM_CSF	pg/ml	0.75	0.74	3.57	0.74
ICAM_1	mg/L	0.55	0.5	2.8	0.2
IFNgamma	pg/ml	9.18	5.83	433.37	3.58
IL_10	pg/ml	0.56	0.36	33.87	0.27
IL_12	pg/ml	191.39	166	1489.31	12.87
IL_12p70	pg/ml	0.82	0.79	4.75	0.79
IL_13	pg/ml	3.17	3.14	8.92	3.14
IL_15	pg/ml	2.83	2.72	8.19	1.28
IL_16	pg/ml	196.77	190.7	636.78	12.58
IL_17A	pg/ml	4.73	3.82	39.44	2.05
IL_17A_F	pg/ml	14.38	14.34	40.48	14.34
IL_17B	pg/ml	4.32	4.22	20.48	4.22
IL_17C	pg/ml	7.95	7.72	35.24	7.72
IL_17D	pg/ml	49.49	40.17	493.86	36.71
IL_1alpha	pg/ml	2.75	2.4	21.04	2.4
IL_1beta	pg/ml	0.36	0.33	3.72	0.33
IL_1RA	pg/ml	319.07	277.48	2188.04	61.26
IL_2	pg/ml	0.75	0.59	39.75	0.59
IL_21	pg/ml	5.04	5	29.32	5
IL_22	pg/ml	3.19	1.445	380.72	1.32
IL_23	pg/ml	8.29	8.25	17.64	8.25
IL_27	pg/ml	2185.3	2035.435	10670.78	167.9
IL_3	pg/ml	25.25	24.63	136.24	24.63
IL_31	pg/ml	1.02	1.01	4.92	1.01
IL_4	pg/ml	0.2	0.2	0.84	0.2
IL_5	pg/ml	0.7	0.56	4.87	0.56
IL_6	pg/ml	1.61	1.18	16.61	0.82
IL_7	pg/ml	15.41	14.59	57.66	1.55
IL_8	pg/ml	62.93	19.49	1242	3.76
IL_9	pg/ml	1.19	1.13	4.12	1.13
IP10	pg/ml	574.39	453.915	4487.03	101
MCP_1	pg/ml	355.72	335.07	1227.54	62.96
MCP_4	pg/ml	300.46	265.13	1710.76	39.77
MDC	pg/ml	1326.24	1286.035	4149.55	379.54
MIP_1alpha	pg/ml	34.58	27.83	373.13	24.9
MIP_1beta	pg/ml	152.21	136.55	1814.94	30.6
MIP3alpha	pg/ml	20.48	8.715	1759.14	3.36
PIGF	pg/ml	10	9.78	23.66	2.79
SAA	mg/L	6.69	3.2	240	0.2
TARC	pg/ml	369.63	299.315	6074.8	40.48
TIE_2	pg/ml	5066.15	4954.33	18771.91	833.1
TNFalpha	pg/ml	3.02	2.75	38.21	0.79
TNFbeta	pg/ml	0.52	0.5	3.63	0.5
TSLP	pg/ml	1.5	1.27	7.75	1.01
VCAM_1	mg/L	0.64	0.6	2.6	0.3
VEGF_A	pg/ml	567.67	470.38	4300	55.83
VEGF_C	pg/ml	550.97	530.99	1681.57	43.28
VEGF_D	pg/ml	1346.51	1143.01	6818.2	254.84
VEGFR1	Flt_1	141.29	139.19	379.24	37.17

Table 7b | Spearman correlation between unknown-cause clonal growth rate and serum analytes

Gene	Cytokine	Spearman rho	p	fdr	n
TET2	PGF	0.286	0.00047	0.025	146
TET2	IL_7	0.268	0.00107	0.028	146
TET2	IL_9	0.208	0.01157	0.204	146
TET2	IL_27	0.2	0.01547	0.205	146
TET2	IL_16	0.175	0.03442	0.365	146
TET2	IL_21	-0.168	0.04314	0.381	146
TET2	IL_17A	0.151	0.06867	0.463	146
TET2	IL_17C	0.143	0.08418	0.463	146
TET2	TSLP	0.142	0.08843	0.463	146
TET2	CRP	0.138	0.09561	0.463	146
TET2	IL_6	0.138	0.096	0.463	146
TET2	FGF_basic	0.134	0.10649	0.47	146
TET2	TIE_2	0.13	0.11842	0.483	146
TET2	IL_17A_F	-0.113	0.17331	0.655	146
TET2	VEGFR1	0.109	0.19053	0.655	146
TET2	IL_12	0.102	0.21833	0.655	146
TET2	MIP_1beta	0.102	0.2226	0.655	146
TET2	IL_1RA	0.101	0.22654	0.655	146
TET2	MCP_4	0.099	0.23476	0.655	146
TET2	VCAM_1	0.093	0.26306	0.697	146
TET2	MDC	0.082	0.32667	0.807	146
TET2	IL_12p70	0.075	0.368	0.807	146
TET2	IL_5	0.075	0.36845	0.807	146
TET2	IL_2	-0.072	0.38828	0.807	146
TET2	IL_17B	-0.07	0.40111	0.807	146
TET2	TNFalpha	0.068	0.41429	0.807	146
TET2	IL_15	0.068	0.41646	0.807	146
TET2	TARC	-0.064	0.44526	0.807	146
TET2	Eotaxin	-0.063	0.45125	0.807	146
TET2	IL_4	-0.062	0.45672	0.807	146
TET2	IL_3	-0.056	0.50117	0.83	146
TET2	IL_8	-0.055	0.51317	0.83	146
TET2	IL_17D	0.054	0.51833	0.83	146
TET2	SAA	0.052	0.53225	0.83	146
TET2	TNFbeta	-0.048	0.56855	0.861	146
TET2	IL_1alpha	0.043	0.60968	0.869	146
TET2	IL_13	-0.039	0.6412	0.869	146
TET2	IL_23	0.038	0.64927	0.869	146
TET2	MIP3alpha	0.036	0.66347	0.869	146
TET2	IFNgamma	0.036	0.66494	0.869	146
TET2	MCP_1	-0.035	0.67692	0.869	146
TET2	IL_10	-0.033	0.68877	0.869	146
TET2	ICAM_1	0.025	0.76147	0.911	146
TET2	GM_CSF	-0.025	0.76738	0.911	146
TET2	VEGF_C	0.024	0.77389	0.911	146
TET2	IL_1beta	-0.022	0.79263	0.913	146
TET2	Eotaxin_3	-0.015	0.85959	0.948	146
TET2	IL_31	0.015	0.86021	0.948	146
TET2	MIP_1alpha	-0.012	0.8817	0.948	146
TET2	IP10	-0.011	0.89758	0.948	146
TET2	VEGF_D	0.009	0.91841	0.948	146
TET2	VEGF_A	-0.007	0.93023	0.948	146
TET2	IL_22	0.003	0.97278	0.973	146
DNMT3A	VEGF_C	-0.24	0.00482	0.255	137
DNMT3A	FGF_basic	0.196	0.02145	0.568	137
DNMT3A	Eotaxin_3	0.16	0.06168	0.791	137
DNMT3A	IL_10	0.153	0.07402	0.791	137
DNMT3A	IL_12	0.151	0.07903	0.791	137

Gene	Cytokine	Spearman rho	p	fdr	n
DNMT3A	IL_12p70	0.142	0.09773	0.791	137
DNMT3A	PGF	-0.127	0.13869	0.791	137
DNMT3A	VEGFR1	-0.126	0.14237	0.791	137
DNMT3A	IL_1beta	0.123	0.15108	0.791	137
DNMT3A	IL_3	0.122	0.15515	0.791	137
DNMT3A	TSLP	0.118	0.17075	0.791	137
DNMT3A	IL_4	-0.115	0.18266	0.791	137
DNMT3A	TNFbeta	0.111	0.19837	0.791	137
DNMT3A	TIE_2	0.108	0.20902	0.791	137
DNMT3A	IL_6	0.103	0.22967	0.811	137
DNMT3A	IL_17A	0.095	0.26845	0.834	137
DNMT3A	IFNgamma	0.089	0.3025	0.834	137
DNMT3A	IL_15	0.085	0.32276	0.834	137
DNMT3A	CRP	-0.083	0.33689	0.834	137
DNMT3A	IL_9	0.076	0.37898	0.834	137
DNMT3A	MCP_1	0.076	0.38052	0.834	137
DNMT3A	IL_27	-0.075	0.38359	0.834	137
DNMT3A	IL_1RA	-0.075	0.38371	0.834	137
DNMT3A	IL_7	0.075	0.38539	0.834	137
DNMT3A	SAA	0.073	0.39927	0.834	137
DNMT3A	IL_1alpha	0.068	0.42944	0.834	137
DNMT3A	Eotaxin	0.067	0.43512	0.834	137
DNMT3A	IL_17B	0.066	0.44463	0.834	137
DNMT3A	MIP3alpha	-0.064	0.45749	0.834	137
DNMT3A	TNFalpha	0.06	0.48764	0.834	137
DNMT3A	IL_2	0.06	0.48819	0.834	137
DNMT3A	IL_5	0.056	0.51823	0.834	137
DNMT3A	VEGF_D	-0.056	0.51915	0.834	137
DNMT3A	IL_17D	-0.05	0.55863	0.871	137
DNMT3A	IL_13	0.042	0.62598	0.911	137
DNMT3A	IL_31	-0.042	0.62701	0.911	137
DNMT3A	IL_8	0.036	0.67603	0.911	137
DNMT3A	GM_CSF	0.035	0.68547	0.911	137
DNMT3A	IL_23	0.035	0.68748	0.911	137
DNMT3A	IP10	0.035	0.68764	0.911	137
DNMT3A	MIP_1alpha	0.03	0.72985	0.911	137
DNMT3A	IL_17C	0.029	0.73223	0.911	137
DNMT3A	MDC	-0.028	0.74454	0.911	137
DNMT3A	ICAM_1	0.025	0.76805	0.911	137
DNMT3A	VEGF_A	0.025	0.77356	0.911	137
DNMT3A	MCP_4	-0.018	0.83576	0.963	137
DNMT3A	IL_22	-0.009	0.91886	1	137
DNMT3A	MIP_1beta	-0.007	0.93878	1	137
DNMT3A	TARC	-0.006	0.94433	1	137
DNMT3A	IL_16	-0.005	0.95205	1	137
DNMT3A	VCAM_1	0.004	0.96637	1	137

Table 8 | Somatic mutations identified in individuals at different phases of the longitudinal study

[Note that, for each individual, if a mutation was identified at any time-point in the study, all time-points are shown, even if the mutation was not identified at one or more of the other time-points (ie. VAF==0)]

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34428	2	74.2	2	25466800	25466800	G	A	0.009	DNMT3A	p.R635W	Missense
PD34428	3	80.3	2	25466800	25466800	G	A	0.010	DNMT3A	p.R635W	Missense
PD34428	5	85.3	2	25466800	25466800	G	A	0.003	DNMT3A	p.R635W	Missense
PD34428	2	74.2	11	119149280	119149280	G	A	0.014	CBL	p.V430M	Missense
PD34428	3	80.3	11	119149280	119149280	G	A	0.017	CBL	p.V430M	Missense
PD34428	5	85.3	11	119149280	119149280	G	A	0.023	CBL	p.V430M	Missense
PD34428	2	74.2	17	58734162	58734163	GT	G	0.000	PPM1D	p.C407fs	Frameshift
PD34428	3	80.3	17	58734162	58734163	GT	G	0.000	PPM1D	p.C407fs	Frameshift
PD34428	5	85.3	17	58734162	58734163	GT	G	0.006	PPM1D	p.C407fs	Frameshift
PD34428	2	74.2	19	13054715	13054715	G	A	0.000	CALR	p.K414K	Synonymous
PD34428	3	80.3	19	13054715	13054715	G	A	0.011	CALR	p.K414K	Synonymous
PD34428	5	85.3	19	13054715	13054715	G	A	0.000	CALR	p.K414K	Synonymous
PD34469	1	70.6	2	198267360	198267360	T	G	0.000	SF3B1	p.K666T	Missense
PD34469	2	73.6	2	198267360	198267360	T	G	0.011	SF3B1	p.K666T	Missense
PD34469	3	78.1	2	198267360	198267360	T	G	0.042	SF3B1	p.K666T	Missense
PD34469	1	70.6	2	25464490	25464490	C	T	0.005	DNMT3A	p.V675M	Missense
PD34469	2	73.6	2	25464490	25464490	C	T	0.007	DNMT3A	p.V675M	Missense
PD34469	3	78.1	2	25464490	25464490	C	T	0.009	DNMT3A	p.V675M	Missense
PD34469	1	70.6	2	25470020	25470021	CC	C	0.010	DNMT3A	p.V341fs	Frameshift
PD34469	2	73.6	2	25470020	25470021	CC	C	0.007	DNMT3A	p.V341fs	Frameshift
PD34469	3	78.1	2	25470020	25470021	CC	C	0.011	DNMT3A	p.V341fs	Frameshift
PD34469	1	70.6	9	139412340	139412340	G	C	0.000	NOTCH1	p.S435S	Synonymous
PD34469	2	73.6	9	139412340	139412340	G	C	0.010	NOTCH1	p.S435S	Synonymous
PD34469	3	78.1	9	139412340	139412340	G	C	0.000	NOTCH1	p.S435S	Synonymous
PD34469	1	70.6	17	58700982	58700982	T	C	0.000	PPM1D	p.G191G	Synonymous
PD34469	2	73.6	17	58700982	58700982	T	C	0.006	PPM1D	p.G191G	Synonymous
PD34469	3	78.1	17	58700982	58700982	T	C	0.000	PPM1D	p.G191G	Synonymous
PD34473	1	66.2	10	112343675	112343675	C	T	0.000	SMC3	p.P349L	Missense
PD34473	2	69.2	10	112343675	112343675	C	T	0.000	SMC3	p.P349L	Missense
PD34473	3	74.3	10	112343675	112343675	C	T	0.000	SMC3	p.P349L	Missense
PD34473	4	78.8	10	112343675	112343675	C	T	0.008	SMC3	p.P349L	Missense
PD34475	1	65.8	4	106193748	106193748	C	T	0.020	TET2	p.R1404X	Nonsense
PD34475	2	68.8	4	106193748	106193748	C	T	0.019	TET2	p.R1404X	Nonsense
PD34475	3	73.5	4	106193748	106193748	C	T	0.063	TET2	p.R1404X	Nonsense
PD34475	4	76.2	4	106193748	106193748	C	T	0.118	TET2	p.R1404X	Nonsense
PD34475	5	81.0	4	106193748	106193748	C	T	0.125	TET2	p.R1404X	Nonsense
PD34475	1	65.8	X	15343148	15343148	A	G	0.008	PIGA	p.G325G	Synonymous
PD34475	2	68.8	X	15343148	15343148	A	G	0.002	PIGA	p.G325G	Synonymous
PD34475	3	73.5	X	15343148	15343148	A	G	0.000	PIGA	p.G325G	Synonymous
PD34475	4	76.2	X	15343148	15343148	A	G	0.000	PIGA	p.G325G	Synonymous
PD34475	5	81.0	X	15343148	15343148	A	G	0.000	PIGA	p.G325G	Synonymous
PD34475	1	65.8	X	44913189	44913189	T	C	0.003	KDM6A	p.Y288Y	Synonymous
PD34475	2	68.8	X	44913189	44913189	T	C	0.002	KDM6A	p.Y288Y	Synonymous
PD34475	3	73.5	X	44913189	44913189	T	C	0.001	KDM6A	p.Y288Y	Synonymous
PD34475	4	76.2	X	44913189	44913189	T	C	0.005	KDM6A	p.Y288Y	Synonymous
PD34475	5	81.0	X	44913189	44913189	T	C	0.005	KDM6A	p.Y288Y	Synonymous
PD34477	1	65.6	2	25462030	25462030	A	T	0.003	DNMT3A	p.Y793N	Missense
PD34477	2	68.3	2	25462030	25462030	A	T	0.002	DNMT3A	p.Y793N	Missense
PD34477	3	72.0	2	25462030	25462030	A	T	0.003	DNMT3A	p.Y793N	Missense
PD34477	4	75.3	2	25462030	25462030	A	T	0.006	DNMT3A	p.Y793N	Missense
PD34477	5	79.6	2	25462030	25462030	A	T	0.002	DNMT3A	p.Y793N	Missense
PD34477	1	65.6	4	106156960	106156961	AC	A	0.001	TET2	p.T621fs	Frameshift
PD34477	2	68.3	4	106156960	106156961	AC	A	0.002	TET2	p.T621fs	Frameshift
PD34477	3	72.0	4	106156960	106156961	AC	A	0.000	TET2	p.T621fs	Frameshift
PD34477	4	75.3	4	106156960	106156961	AC	A	0.003	TET2	p.T621fs	Frameshift
PD34477	5	79.6	4	106156960	106156961	AC	A	0.009	TET2	p.T621fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34477	1	65.6	4	106157983	106157983	C	T	0.010	TET2	p.Q962X	Nonsense
PD34477	2	68.3	4	106157983	106157983	C	T	0.014	TET2	p.Q962X	Nonsense
PD34477	3	72.0	4	106157983	106157983	C	T	0.009	TET2	p.Q962X	Nonsense
PD34477	4	75.3	4	106157983	106157983	C	T	0.008	TET2	p.Q962X	Nonsense
PD34477	5	79.6	4	106157983	106157983	C	T	0.005	TET2	p.Q962X	Nonsense
PD34477	1	65.6	9	139396487	139396487	C	G	0.001	NOTCH1	p.W1813S	Missense
PD34477	2	68.3	9	139396487	139396487	C	G	0.007	NOTCH1	p.W1813S	Missense
PD34477	3	72.0	9	139396487	139396487	C	G	0.011	NOTCH1	p.W1813S	Missense
PD34477	4	75.3	9	139396487	139396487	C	G	0.009	NOTCH1	p.W1813S	Missense
PD34477	5	79.6	9	139396487	139396487	C	G	0.016	NOTCH1	p.W1813S	Missense
PD34477	1	65.6	17	7578478	7578478	G	C	0.008	TP53	p.P112R	Missense
PD34477	2	68.3	17	7578478	7578478	G	C	0.005	TP53	p.P112R	Missense
PD34477	3	72.0	17	7578478	7578478	G	C	0.007	TP53	p.P112R	Missense
PD34477	4	75.3	17	7578478	7578478	G	C	0.007	TP53	p.P112R	Missense
PD34477	5	79.6	17	7578478	7578478	G	C	0.007	TP53	p.P112R	Missense
PD34479	1	66.5	2	25463568	25463568	A	G	0.006	DNMT3A	p.I705T	Missense
PD34479	2	70.0	2	25463568	25463568	A	G	0.009	DNMT3A	p.I705T	Missense
PD34479	3	74.4	2	25463568	25463568	A	G	0.002	DNMT3A	p.I705T	Missense
PD34481	1	76.5	2	198267359	198267359	C	A	0.005	SF3B1	p.K666N	Missense
PD34481	2	79.6	2	198267359	198267359	C	A	0.006	SF3B1	p.K666N	Missense
PD34481	3	83.1	2	198267359	198267359	C	A	0.022	SF3B1	p.K666N	Missense
PD34481	4	85.7	2	198267359	198267359	C	A	0.054	SF3B1	p.K666N	Missense
PD34482	1	71.5	2	198266796	198266796	C	A	0.006	SF3B1	p.L712F	Missense
PD34482	2	74.5	2	198266796	198266796	C	A	0.000	SF3B1	p.L712F	Missense
PD34482	3	78.3	2	198266796	198266796	C	A	0.001	SF3B1	p.L712F	Missense
PD34482	4	81.1	2	198266796	198266796	C	A	0.000	SF3B1	p.L712F	Missense
PD34482	5	86.0	2	198266796	198266796	C	A	0.000	SF3B1	p.L712F	Missense
PD34483	1	69.7	2	25469607	25469607	G	C	0.000	DNMT3A	p.C387W	Missense
PD34483	2	73.2	2	25469607	25469607	G	C	0.004	DNMT3A	p.C387W	Missense
PD34483	3	77.2	2	25469607	25469607	G	C	0.004	DNMT3A	p.C387W	Missense
PD34483	4	80.0	2	25469607	25469607	G	C	0.006	DNMT3A	p.C387W	Missense
PD34483	1	69.7	4	106155920	106155921	TC	T	0.014	TET2	p.I274fs	Frameshift
PD34483	2	73.2	4	106155920	106155921	TC	T	0.014	TET2	p.I274fs	Frameshift
PD34483	3	77.2	4	106155920	106155921	TC	T	0.013	TET2	p.I274fs	Frameshift
PD34483	4	80.0	4	106155920	106155921	TC	T	0.020	TET2	p.I274fs	Frameshift
PD34483	1	69.7	X	15343152	15343152	C	T	0.000	PIGA	p.C324Y	Missense
PD34483	2	73.2	X	15343152	15343152	C	T	0.000	PIGA	p.C324Y	Missense
PD34483	3	77.2	X	15343152	15343152	C	T	0.006	PIGA	p.C324Y	Missense
PD34483	4	80.0	X	15343152	15343152	C	T	0.000	PIGA	p.C324Y	Missense
PD34484	1	68.5	2	25466782	25466784	AAA	A	0.016	DNMT3A	p.F640fs	Frameshift
PD34484	2	71.5	2	25466782	25466784	AAA	A	0.009	DNMT3A	p.F640fs	Frameshift
PD34484	3	75.3	2	25466782	25466784	AAA	A	0.011	DNMT3A	p.F640fs	Frameshift
PD34484	4	79.8	2	25466782	25466784	AAA	A	0.004	DNMT3A	p.F640fs	Frameshift
PD34484	1	68.5	16	3900873	3900873	G	A	0.002	CREBBP	p.R75X	Nonsense
PD34484	2	71.5	16	3900873	3900873	G	A	0.007	CREBBP	p.R75X	Nonsense
PD34484	3	75.3	16	3900873	3900873	G	A	0.007	CREBBP	p.R75X	Nonsense
PD34484	4	79.8	16	3900873	3900873	G	A	0.004	CREBBP	p.R75X	Nonsense
PD34485	1	71.3	5	149433680	149433680	C	T	0.002	CSF1R	p.G957G	Synonymous
PD34485	2	74.3	5	149433680	149433680	C	T	0.002	CSF1R	p.G957G	Synonymous
PD34485	4	80.0	5	149433680	149433680	C	T	0.010	CSF1R	p.G957G	Synonymous
PD34485	1	71.3	17	7577539	7577539	G	A	0.010	TP53	p.R209W	Missense
PD34485	2	74.3	17	7577539	7577539	G	A	0.007	TP53	p.R209W	Missense
PD34485	4	80.0	17	7577539	7577539	G	A	0.006	TP53	p.R209W	Missense
PD34485	1	71.3	20	31023125	31023125	C	A	0.001	ASXL1	p.G870G	Synonymous
PD34485	2	74.3	20	31023125	31023125	C	A	0.007	ASXL1	p.G870G	Synonymous
PD34485	4	80.0	20	31023125	31023125	C	A	0.000	ASXL1	p.G870G	Synonymous
PD34486	1	72.7	12	25380285	25380285	G	A	0.007	KRAS	p.T58I	Missense
PD34486	2	75.7	12	25380285	25380285	G	A	0.013	KRAS	p.T58I	Missense
PD34486	3	79.6	12	25380285	25380285	G	A	0.010	KRAS	p.T58I	Missense
PD34486	4	84.7	12	25380285	25380285	G	A	0.020	KRAS	p.T58I	Missense
PD34487	1	68.1	4	106190860	106190860	C	T	0.006	TET2	p.H1380Y	Missense
PD34487	2	71.5	4	106190860	106190860	C	T	0.007	TET2	p.H1380Y	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34487	3	74.7	4	106190860	106190860	C	T	0.012	TET2	p.H1380Y	Missense
PD34487	4	78.2	4	106190860	106190860	C	T	0.012	TET2	p.H1380Y	Missense
PD34487	1	68.1	7	101882800	101882800	G	T	0.008	CUX1	p.E1275X	Nonsense
PD34487	2	71.5	7	101882800	101882800	G	T	0.010	CUX1	p.E1275X	Nonsense
PD34487	3	74.7	7	101882800	101882800	G	T	0.009	CUX1	p.E1275X	Nonsense
PD34487	4	78.2	7	101882800	101882800	G	T	0.007	CUX1	p.E1275X	Nonsense
PD34487	1	68.1	20	31024266	31024266	C	T	0.001	ASXL1	p.Q1251X	Nonsense
PD34487	2	71.5	20	31024266	31024266	C	T	0.003	ASXL1	p.Q1251X	Nonsense
PD34487	3	74.7	20	31024266	31024266	C	T	0.008	ASXL1	p.Q1251X	Nonsense
PD34487	4	78.2	20	31024266	31024266	C	T	0.026	ASXL1	p.Q1251X	Nonsense
PD34488	1	73.8	4	106156304	106156304	C	G	0.002	TET2	p.S402X	Nonsense
PD34488	2	76.9	4	106156304	106156304	C	G	0.002	TET2	p.S402X	Nonsense
PD34488	3	80.7	4	106156304	106156304	C	G	0.002	TET2	p.S402X	Nonsense
PD34488	4	84.1	4	106156304	106156304	C	G	0.002	TET2	p.S402X	Nonsense
PD34488	5	88.1	4	106156304	106156304	C	G	0.008	TET2	p.S402X	Nonsense
PD34488	1	73.8	11	119148991	119148991	G	A	0.002	CBL	p.C404Y	Missense
PD34488	2	76.9	11	119148991	119148991	G	A	0.005	CBL	p.C404Y	Missense
PD34488	3	80.7	11	119148991	119148991	G	A	0.004	CBL	p.C404Y	Missense
PD34488	4	84.1	11	119148991	119148991	G	A	0.008	CBL	p.C404Y	Missense
PD34488	5	88.1	11	119148991	119148991	G	A	0.002	CBL	p.C404Y	Missense
PD34488	1	73.8	17	74733103	74733103	C	G	0.008	SRSF2	p.R47P	Missense
PD34488	2	76.9	17	74733103	74733103	C	G	0.010	SRSF2	p.R47P	Missense
PD34488	3	80.7	17	74733103	74733103	C	G	0.010	SRSF2	p.R47P	Missense
PD34488	4	84.1	17	74733103	74733103	C	G	0.006	SRSF2	p.R47P	Missense
PD34488	5	88.1	17	74733103	74733103	C	G	0.004	SRSF2	p.R47P	Missense
PD34489	1	93.9	4	106156481	106156482	AG	A	0.001	TET2	p.Q461fs	Frameshift
PD34489	4	103.1	4	106156481	106156482	AG	A	0.006	TET2	p.Q461fs	Frameshift
PD34489	1	93.9	4	106196973	106196974	CT	C	0.012	TET2	p.A1769fs	Frameshift
PD34489	4	103.1	4	106196973	106196974	CT	C	0.013	TET2	p.A1769fs	Frameshift
PD34489	1	93.9	11	118342472	118342472	A	G	0.013	KMT2A	p.N200D	Missense
PD34489	4	103.1	11	118342472	118342472	A	G	0.020	KMT2A	p.N200D	Missense
PD34489	1	93.9	11	119149250	119149250	C	G	0.004	CBL	p.R420G	Missense
PD34489	4	103.1	11	119149250	119149250	C	G	0.020	CBL	p.R420G	Missense
PD34489	1	93.9	12	50029182	50029183	TG	T	0.000	PRPF40B	p.W401fs	Frameshift
PD34489	4	103.1	12	50029182	50029183	TG	T	0.008	PRPF40B	p.W401fs	Frameshift
PD34489	1	93.9	17	7576626	7576626	T	C	0.009	TP53	p.X303X	Synonymous
PD34489	4	103.1	17	7576626	7576626	T	C	0.022	TP53	p.X303X	Synonymous
PD34489	1	93.9	20	31023070	31023070	C	A	0.152	ASXL1	p.S852X	Nonsense
PD34489	4	103.1	20	31023070	31023070	C	A	0.152	ASXL1	p.S852X	Nonsense
PD34489	1	93.9	X	39933883	39933883	G	C	0.005	BCOR	p.T239S	Missense
PD34489	4	103.1	X	39933883	39933883	G	C	0.004	BCOR	p.T239S	Missense
PD34490	1	67.4	16	3779378	3779378	G	T	0.002	CREBBP	p.P1890P	Synonymous
PD34490	3	75.6	16	3779378	3779378	G	T	0.011	CREBBP	p.P1890P	Synonymous
PD34490	1	67.4	X	129148434	129148434	A	T	0.006	BCORL1	p.P562P	Synonymous
PD34490	3	75.6	X	129148434	129148434	A	T	0.002	BCORL1	p.P562P	Synonymous
PD34491	1	84.0	17	58740710	58740710	G	T	0.010	PPM1D	p.E539X	Nonsense
PD34491	2	87.0	17	58740710	58740710	G	T	0.011	PPM1D	p.E539X	Nonsense
PD34491	3	92.4	17	58740710	58740710	G	T	0.009	PPM1D	p.E539X	Nonsense
PD34492	1	81.1	2	198267496	198267496	C	T	0.002	SF3B1	p.D621N	Missense
PD34492	2	84.1	2	198267496	198267496	C	T	0.000	SF3B1	p.D621N	Missense
PD34492	3	88.0	2	198267496	198267496	C	T	0.007	SF3B1	p.D621N	Missense
PD34492	4	90.5	2	198267496	198267496	C	T	0.008	SF3B1	p.D621N	Missense
PD34492	1	81.1	4	106164778	106164778	C	T	0.004	TET2	p.R1216X	Nonsense
PD34492	2	84.1	4	106164778	106164778	C	T	0.008	TET2	p.R1216X	Nonsense
PD34492	3	88.0	4	106164778	106164778	C	T	0.006	TET2	p.R1216X	Nonsense
PD34492	4	90.5	4	106164778	106164778	C	T	0.009	TET2	p.R1216X	Nonsense
PD34492	1	81.1	X	129189983	129189983	G	T	0.005	BCORL1	p.E1744X	Nonsense
PD34492	2	84.1	X	129189983	129189983	G	T	0.000	BCORL1	p.E1744X	Nonsense
PD34492	3	88.0	X	129189983	129189983	G	T	0.000	BCORL1	p.E1744X	Nonsense
PD34492	4	90.5	X	129189983	129189983	G	T	0.000	BCORL1	p.E1744X	Nonsense
PD34493	1	66.3	2	198267359	198267359	C	A	0.028	SF3B1	p.K666N	Missense
PD34493	2	69.3	2	198267359	198267359	C	A	0.035	SF3B1	p.K666N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34493	3	73.1	2	198267359	198267359	C	A	0.038	SF3B1	p.K666N	Missense
PD34493	4	76.6	2	198267359	198267359	C	A	0.033	SF3B1	p.K666N	Missense
PD34493	5	81.8	2	198267359	198267359	C	A	0.087	SF3B1	p.K666N	Missense
PD34493	1	66.3	9	139412322	139412322	C	T	0.000	NOTCH1	p.L441L	Synonymous
PD34493	2	69.3	9	139412322	139412322	C	T	0.000	NOTCH1	p.L441L	Synonymous
PD34493	3	73.1	9	139412322	139412322	C	T	0.006	NOTCH1	p.L441L	Synonymous
PD34493	4	76.6	9	139412322	139412322	C	T	0.000	NOTCH1	p.L441L	Synonymous
PD34493	5	81.8	9	139412322	139412322	C	T	0.003	NOTCH1	p.L441L	Synonymous
PD34493	1	66.3	21	44514777	44514777	T	C	0.001	U2AF1	p.Q84R	Missense
PD34493	2	69.3	21	44514777	44514777	T	C	0.000	U2AF1	p.Q84R	Missense
PD34493	3	73.1	21	44514777	44514777	T	C	0.001	U2AF1	p.Q84R	Missense
PD34493	4	76.6	21	44514777	44514777	T	C	0.012	U2AF1	p.Q84R	Missense
PD34493	5	81.8	21	44514777	44514777	T	C	0.103	U2AF1	p.Q84R	Missense
PD34494	1	84.8	2	25470619	25470619	C	T	0.001	DNMT3A	c.856-1G>A	Splice site
PD34494	2	87.8	2	25470619	25470619	C	T	0.006	DNMT3A	c.856-1G>A	Splice site
PD34494	3	91.3	2	25470619	25470619	C	T	0.000	DNMT3A	c.856-1G>A	Splice site
PD34494	4	93.9	2	25470619	25470619	C	T	0.001	DNMT3A	c.856-1G>A	Splice site
PD34494	1	84.8	4	106164023	106164023	A	G	0.033	TET2	p.E1178G	Missense
PD34494	2	87.8	4	106164023	106164023	A	G	0.026	TET2	p.E1178G	Missense
PD34494	3	91.3	4	106164023	106164023	A	G	0.025	TET2	p.E1178G	Missense
PD34494	4	93.9	4	106164023	106164023	A	G	0.024	TET2	p.E1178G	Missense
PD34494	1	84.8	17	58740626	58740626	A	T	0.033	PPM1D	p.K511X	Nonsense
PD34494	2	87.8	17	58740626	58740626	A	T	0.040	PPM1D	p.K511X	Nonsense
PD34494	3	91.3	17	58740626	58740626	A	T	0.044	PPM1D	p.K511X	Nonsense
PD34494	4	93.9	17	58740626	58740626	A	T	0.083	PPM1D	p.K511X	Nonsense
PD34494	1	84.8	X	53436031	53436031	T	C	0.026	SMC1A	p.I481V	Missense
PD34494	2	87.8	X	53436031	53436031	T	C	0.044	SMC1A	p.I481V	Missense
PD34494	3	91.3	X	53436031	53436031	T	C	0.063	SMC1A	p.I481V	Missense
PD34494	4	93.9	X	53436031	53436031	T	C	0.068	SMC1A	p.I481V	Missense
PD34495	1	82.9	4	106158413	106158415	TAG	T	0.009	TET2	p.I1105fs	Frameshift
PD34495	3	90.9	4	106158413	106158415	TAG	T	0.005	TET2	p.I1105fs	Frameshift
PD34495	1	82.9	17	58740685	58740686	TC	T	0.007	PPM1D	p.P531fs	Frameshift
PD34495	3	90.9	17	58740685	58740686	TC	T	0.010	PPM1D	p.P531fs	Frameshift
PD34495	1	82.9	X	133551229	133551229	A	G	0.002	PHF6	p.T289A	Missense
PD34495	3	90.9	X	133551229	133551229	A	G	0.010	PHF6	p.T289A	Missense
PD34495	1	82.9	X	44929085	44929085	G	A	0.000	KDM6A	p.E781K	Missense
PD34495	3	90.9	X	44929085	44929085	G	A	0.006	KDM6A	p.E781K	Missense
PD34495	1	82.9	X	44945109	44945109	G	T	0.000	KDM6A	c.3434-1G>T	Splice site
PD34495	3	90.9	X	44945109	44945109	G	T	0.009	KDM6A	c.3434-1G>T	Splice site
PD34495	1	82.9	X	154305493	154305493	C	T	0.120	BRCC3	p.R82C	Missense
PD34495	3	90.9	X	154305493	154305493	C	T	0.150	BRCC3	p.R82C	Missense
PD34496	1	69.1	2	25467204	25467204	G	T	0.013	DNMT3A	p.C557X	Nonsense
PD34496	2	71.8	2	25467204	25467204	G	T	0.006	DNMT3A	p.C557X	Nonsense
PD34496	3	75.6	2	25467204	25467204	G	T	0.008	DNMT3A	p.C557X	Nonsense
PD34496	4	80.0	2	25467204	25467204	G	T	0.006	DNMT3A	p.C557X	Nonsense
PD34497	1	68.3	4	106156729	106156729	C	T	0.009	TET2	p.R544X	Nonsense
PD34497	2	70.9	4	106156729	106156729	C	T	0.008	TET2	p.R544X	Nonsense
PD34497	3	74.3	4	106156729	106156729	C	T	0.016	TET2	p.R544X	Nonsense
PD34497	4	77.5	4	106156729	106156729	C	T	0.010	TET2	p.R544X	Nonsense
PD34497	1	68.3	4	106162548	106162549	TC	T	0.004	TET2	p.P1155fs	Frameshift
PD34497	2	70.9	4	106162548	106162549	TC	T	0.005	TET2	p.P1155fs	Frameshift
PD34497	3	74.3	4	106162548	106162549	TC	T	0.006	TET2	p.P1155fs	Frameshift
PD34497	4	77.5	4	106162548	106162549	TC	T	0.004	TET2	p.P1155fs	Frameshift
PD34497	1	68.3	4	106190905	106190906	G	GT	0.078	TET2	c.4182+2->T	Splice site
PD34497	2	70.9	4	106190905	106190906	G	GT	0.098	TET2	c.4182+2->T	Splice site
PD34497	3	74.3	4	106190905	106190906	G	GT	0.181	TET2	c.4182+2->T	Splice site
PD34497	4	77.5	4	106190905	106190906	G	GT	0.239	TET2	c.4182+2->T	Splice site
PD34498	1	78.0	21	36171717	36171717	T	A	0.003	RUNX1	p.Q283L	Missense
PD34498	2	80.6	21	36171717	36171717	T	A	0.006	RUNX1	p.Q283L	Missense
PD34498	3	85.8	21	36171717	36171717	T	A	0.003	RUNX1	p.Q283L	Missense
PD34499	1	70.7	4	106155904	106155904	C	A	0.001	TET2	p.H269N	Missense
PD34499	2	73.8	4	106155904	106155904	C	A	0.005	TET2	p.H269N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34499	3	77.6	4	106155904	106155904	C	A	0.000	TET2	p.H269N	Missense
PD34499	4	80.7	4	106155904	106155904	C	A	0.001	TET2	p.H269N	Missense
PD34499	5	85.2	4	106155904	106155904	C	A	0.000	TET2	p.H269N	Missense
PD34499	1	70.7	4	106156348	106156348	C	T	0.002	TET2	p.Q417X	Nonsense
PD34499	2	73.8	4	106156348	106156348	C	T	0.000	TET2	p.Q417X	Nonsense
PD34499	3	77.6	4	106156348	106156348	C	T	0.002	TET2	p.Q417X	Nonsense
PD34499	4	80.7	4	106156348	106156348	C	T	0.008	TET2	p.Q417X	Nonsense
PD34499	5	85.2	4	106156348	106156348	C	T	0.005	TET2	p.Q417X	Nonsense
PD34499	1	70.7	4	106157123	106157123	C	G	0.005	TET2	p.S675X	Nonsense
PD34499	2	73.8	4	106157123	106157123	C	G	0.008	TET2	p.S675X	Nonsense
PD34499	3	77.6	4	106157123	106157123	C	G	0.006	TET2	p.S675X	Nonsense
PD34499	4	80.7	4	106157123	106157123	C	G	0.005	TET2	p.S675X	Nonsense
PD34499	5	85.2	4	106157123	106157123	C	G	0.006	TET2	p.S675X	Nonsense
PD34499	1	70.7	4	106158503	106158503	G	A	0.002	TET2	p.C1135Y	Missense
PD34499	2	73.8	4	106158503	106158503	G	A	0.002	TET2	p.C1135Y	Missense
PD34499	3	77.6	4	106158503	106158503	G	A	0.008	TET2	p.C1135Y	Missense
PD34499	4	80.7	4	106158503	106158503	G	A	0.007	TET2	p.C1135Y	Missense
PD34499	5	85.2	4	106158503	106158503	G	A	0.007	TET2	p.C1135Y	Missense
PD34499	1	70.7	4	106164761	106164761	T	C	0.001	TET2	p.L1210P	Missense
PD34499	2	73.8	4	106164761	106164761	T	C	0.003	TET2	p.L1210P	Missense
PD34499	3	77.6	4	106164761	106164761	T	C	0.007	TET2	p.L1210P	Missense
PD34499	4	80.7	4	106164761	106164761	T	C	0.013	TET2	p.L1210P	Missense
PD34499	5	85.2	4	106164761	106164761	T	C	0.090	TET2	p.L1210P	Missense
PD34499	1	70.7	4	106180851	106180852	GT	G	0.001	TET2	p.Y1294fs	Frameshift
PD34499	2	73.8	4	106180851	106180852	GT	G	0.001	TET2	p.Y1294fs	Frameshift
PD34499	3	77.6	4	106180851	106180852	GT	G	0.004	TET2	p.Y1294fs	Frameshift
PD34499	4	80.7	4	106180851	106180852	GT	G	0.029	TET2	p.Y1294fs	Frameshift
PD34499	5	85.2	4	106180851	106180852	GT	G	0.047	TET2	p.Y1294fs	Frameshift
PD34499	1	70.7	4	106193877	106193878	CT	C	0.003	TET2	p.L1447fs	Frameshift
PD34499	2	73.8	4	106193877	106193878	CT	C	0.001	TET2	p.L1447fs	Frameshift
PD34499	3	77.6	4	106193877	106193878	CT	C	0.005	TET2	p.L1447fs	Frameshift
PD34499	4	80.7	4	106193877	106193878	CT	C	0.017	TET2	p.L1447fs	Frameshift
PD34499	5	85.2	4	106193877	106193878	CT	C	0.008	TET2	p.L1447fs	Frameshift
PD34499	1	70.7	4	106197285	106197285	T	C	0.128	TET2	p.I1873T	Missense
PD34499	2	73.8	4	106197285	106197285	T	C	0.125	TET2	p.I1873T	Missense
PD34499	3	77.6	4	106197285	106197285	T	C	0.199	TET2	p.I1873T	Missense
PD34499	4	80.7	4	106197285	106197285	T	C	0.291	TET2	p.I1873T	Missense
PD34499	5	85.2	4	106197285	106197285	T	C	0.323	TET2	p.I1873T	Missense
PD34499	1	70.7	8	117878910	117878910	G	A	0.004	RAD21	p.A20V	Missense
PD34499	2	73.8	8	117878910	117878910	G	A	0.006	RAD21	p.A20V	Missense
PD34499	3	77.6	8	117878910	117878910	G	A	0.004	RAD21	p.A20V	Missense
PD34499	4	80.7	8	117878910	117878910	G	A	0.008	RAD21	p.A20V	Missense
PD34499	5	85.2	8	117878910	117878910	G	A	0.001	RAD21	p.A20V	Missense
PD34499	1	70.7	9	5073770	5073770	G	T	0.001	JAK2	p.V617F	Missense
PD34499	2	73.8	9	5073770	5073770	G	T	0.002	JAK2	p.V617F	Missense
PD34499	3	77.6	9	5073770	5073770	G	T	0.012	JAK2	p.V617F	Missense
PD34499	4	80.7	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD34499	5	85.2	9	5073770	5073770	G	T	0.002	JAK2	p.V617F	Missense
PD34499	1	70.7	10	112337231	112337231	A	G	0.000	SMC3	p.N84S	Missense
PD34499	2	73.8	10	112337231	112337231	A	G	0.004	SMC3	p.N84S	Missense
PD34499	3	77.6	10	112337231	112337231	A	G	0.012	SMC3	p.N84S	Missense
PD34499	4	80.7	10	112337231	112337231	A	G	0.031	SMC3	p.N84S	Missense
PD34499	5	85.2	10	112337231	112337231	A	G	0.060	SMC3	p.N84S	Missense
PD34499	1	70.7	X	39932479	39932479	G	A	0.002	BCOR	p.P707L	Missense
PD34499	2	73.8	X	39932479	39932479	G	A	0.004	BCOR	p.P707L	Missense
PD34499	3	77.6	X	39932479	39932479	G	A	0.005	BCOR	p.P707L	Missense
PD34499	4	80.7	X	39932479	39932479	G	A	0.010	BCOR	p.P707L	Missense
PD34499	5	85.2	X	39932479	39932479	G	A	0.021	BCOR	p.P707L	Missense
PD34500	1	83.1	17	58740375	58740375	G	A	0.003	PPM1D	p.W427X	Nonsense
PD34500	2	86.0	17	58740375	58740375	G	A	0.016	PPM1D	p.W427X	Nonsense
PD34500	3	91.0	17	58740375	58740375	G	A	0.016	PPM1D	p.W427X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34501	1	79.5	4	106157531	106157541	ATAT AAAT CGT	A	0.009	TET2	p.N811fs	Frameshift
PD34501	2	84.2	4	106157531	106157541	ATAT AAAT CGT	A	0.018	TET2	p.N811fs	Frameshift
PD34502	1	71.1	2	25458684	25458684	A	G	0.020	DNMT3A	p.V830A	Missense
PD34502	2	74.1	2	25458684	25458684	A	G	0.031	DNMT3A	p.V830A	Missense
PD34502	3	78.5	2	25458684	25458684	A	G	0.041	DNMT3A	p.V830A	Missense
PD34502	4	82.7	2	25458684	25458684	A	G	0.035	DNMT3A	p.V830A	Missense
PD34502	2	74.1	4	106158243	106158244	CA	C	0.008	TET2	p.K1049fs	Frameshift
PD34502	3	78.5	4	106158243	106158244	CA	C	0.004	TET2	p.K1049fs	Frameshift
PD34502	4	82.7	4	106158243	106158244	CA	C	0.000	TET2	p.K1049fs	Frameshift
PD34502	1	71.1	4	106197300	106197300	G	C	0.003	TET2	p.R1878P	Missense
PD34502	2	74.1	4	106197300	106197300	G	C	0.003	TET2	p.R1878P	Missense
PD34502	3	78.5	4	106197300	106197300	G	C	0.008	TET2	p.R1878P	Missense
PD34502	4	82.7	4	106197300	106197300	G	C	0.006	TET2	p.R1878P	Missense
PD34502	1	71.1	7	148544311	148544311	C	A	0.000	EZH2	p.R27I	Missense
PD34502	2	74.1	7	148544311	148544311	C	A	0.006	EZH2	p.R27I	Missense
PD34502	3	78.5	7	148544311	148544311	C	A	0.000	EZH2	p.R27I	Missense
PD34502	4	82.7	7	148544311	148544311	C	A	0.000	EZH2	p.R27I	Missense
PD34502	1	71.1	17	7578190	7578190	T	C	0.001	TP53	p.Y181C	Missense
PD34502	2	74.1	17	7578190	7578190	T	C	0.006	TP53	p.Y181C	Missense
PD34502	3	78.5	17	7578190	7578190	T	C	0.001	TP53	p.Y181C	Missense
PD34502	4	82.7	17	7578190	7578190	T	C	0.003	TP53	p.Y181C	Missense
PD34503	1	70.8	2	25470590	25470590	A	G	0.001	DNMT3A	p.L295P	Missense
PD34503	2	74.2	2	25470590	25470590	A	G	0.001	DNMT3A	p.L295P	Missense
PD34503	3	77.7	2	25470590	25470590	A	G	0.004	DNMT3A	p.L295P	Missense
PD34503	4	80.9	2	25470590	25470590	A	G	0.005	DNMT3A	p.L295P	Missense
PD34503	5	86.0	2	25470590	25470590	A	G	0.012	DNMT3A	p.L295P	Missense
PD34503	1	70.8	4	106197149	106197149	C	T	0.002	TET2	p.Q1828X	Nonsense
PD34503	2	74.2	4	106197149	106197149	C	T	0.003	TET2	p.Q1828X	Nonsense
PD34503	3	77.7	4	106197149	106197149	C	T	0.004	TET2	p.Q1828X	Nonsense
PD34503	4	80.9	4	106197149	106197149	C	T	0.009	TET2	p.Q1828X	Nonsense
PD34503	5	86.0	4	106197149	106197149	C	T	0.013	TET2	p.Q1828X	Nonsense
PD34503	1	70.8	20	31022437	31022442	TCGG AG	T	0.083	ASXL1	p.I641fs	Frameshift
PD34503	2	74.2	20	31022437	31022442	TCGG AG	T	0.095	ASXL1	p.I641fs	Frameshift
PD34503	3	77.7	20	31022437	31022442	TCGG AG	T	0.101	ASXL1	p.I641fs	Frameshift
PD34503	4	80.9	20	31022437	31022442	TCGG AG	T	0.127	ASXL1	p.I641fs	Frameshift
PD34503	5	86.0	20	31022437	31022442	TCGG AG	T	0.117	ASXL1	p.I641fs	Frameshift
PD34503	1	70.8	X	129147427	129147427	G	T	0.009	BCORL1	p.V227F	Missense
PD34503	2	74.2	X	129147427	129147427	G	T	0.005	BCORL1	p.V227F	Missense
PD34503	3	77.7	X	129147427	129147427	G	T	0.001	BCORL1	p.V227F	Missense
PD34503	4	80.9	X	129147427	129147427	G	T	0.004	BCORL1	p.V227F	Missense
PD34503	5	86.0	X	129147427	129147427	G	T	0.004	BCORL1	p.V227F	Missense
PD34504	1	67.4	2	25466852	25466852	C	T	0.001	DNMT3A	c.1852-1G>A	Splice site
PD34504	2	70.6	2	25466852	25466852	C	T	0.001	DNMT3A	c.1852-1G>A	Splice site
PD34504	3	74.2	2	25466852	25466852	C	T	0.003	DNMT3A	c.1852-1G>A	Splice site
PD34504	4	77.2	2	25466852	25466852	C	T	0.005	DNMT3A	c.1852-1G>A	Splice site
PD34504	5	81.6	2	25466852	25466852	C	T	0.009	DNMT3A	c.1852-1G>A	Splice site
PD34505	1	66.6	4	106197208	106197208	G	A	0.009	TET2	p.W1847X	Nonsense
PD34505	2	69.5	4	106197208	106197208	G	A	0.018	TET2	p.W1847X	Nonsense
PD34505	3	75.1	4	106197208	106197208	G	A	0.040	TET2	p.W1847X	Nonsense
PD34505	1	66.6	20	57485816	57485816	C	T	0.022	GNAS	p.R1016C	Missense
PD34505	2	69.5	20	57485816	57485816	C	T	0.025	GNAS	p.R1016C	Missense
PD34505	3	75.1	20	57485816	57485816	C	T	0.023	GNAS	p.R1016C	Missense
PD34506	1	66.5	13	28601331	28601331	T	C	0.000	FLT3	p.N701D	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34506	2	69.9	13	28601331	28601331	T	C	0.006	FLT3	p.N701D	Missense
PD34506	3	73.2	13	28601331	28601331	T	C	0.000	FLT3	p.N701D	Missense
PD34506	4	76.3	13	28601331	28601331	T	C	0.000	FLT3	p.N701D	Missense
PD34506	1	66.5	17	7577120	7577120	C	A	0.014	TP53	p.R234L	Missense
PD34506	2	69.9	17	7577120	7577120	C	A	0.011	TP53	p.R234L	Missense
PD34506	3	73.2	17	7577120	7577120	C	A	0.007	TP53	p.R234L	Missense
PD34506	4	76.3	17	7577120	7577120	C	A	0.004	TP53	p.R234L	Missense
PD34509	1	70.4	4	106164821	106164822	TC	T	0.026	TET2	p.I1230fs	Frameshift
PD34509	2	73.6	4	106164821	106164822	TC	T	0.034	TET2	p.I1230fs	Frameshift
PD34509	3	79.2	4	106164821	106164822	TC	T	0.032	TET2	p.I1230fs	Frameshift
PD34510	2	70.0	4	106193832	106193833	GT	G	0.006	TET2	p.V1432fs	Frameshift
PD34510	3	75.1	4	106193832	106193833	GT	G	0.018	TET2	p.V1432fs	Frameshift
PD34510	4	79.8	4	106193832	106193833	GT	G	0.007	TET2	p.V1432fs	Frameshift
PD34510	1	66.9	X	129189907	129189907	G	A	0.000	BCORL1	p.P1718P	Synonymous
PD34510	2	70.0	X	129189907	129189907	G	A	0.001	BCORL1	p.P1718P	Synonymous
PD34510	3	75.1	X	129189907	129189907	G	A	0.000	BCORL1	p.P1718P	Synonymous
PD34510	4	79.8	X	129189907	129189907	G	A	0.011	BCORL1	p.P1718P	Synonymous
PD34511	1	74.6	2	198266834	198266834	T	C	0.035	SF3B1	p.K700E	Missense
PD34511	2	78.5	2	198266834	198266834	T	C	0.048	SF3B1	p.K700E	Missense
PD34511	3	83.8	2	198266834	198266834	T	C	0.068	SF3B1	p.K700E	Missense
PD34511	1	74.6	2	198267483	198267483	C	A	0.020	SF3B1	p.R625L	Missense
PD34511	2	78.5	2	198267483	198267483	C	A	0.040	SF3B1	p.R625L	Missense
PD34511	3	83.8	2	198267483	198267483	C	A	0.046	SF3B1	p.R625L	Missense
PD34511	1	74.6	2	25469613	25469614	CG	C	0.051	DNMT3A	p.P385fs	Frameshift
PD34511	2	78.5	2	25469613	25469614	CG	C	0.069	DNMT3A	p.P385fs	Frameshift
PD34511	3	83.8	2	25469613	25469614	CG	C	0.091	DNMT3A	p.P385fs	Frameshift
PD34512	1	79.8	2	25469961	25469961	T	C	0.012	DNMT3A	p.K361E	Missense
PD34512	2	82.8	2	25469961	25469961	T	C	0.007	DNMT3A	p.K361E	Missense
PD34512	3	86.8	2	25469961	25469961	T	C	0.002	DNMT3A	p.K361E	Missense
PD34512	1	79.8	4	106197282	106197282	T	C	0.016	TET2	p.L1872P	Missense
PD34512	2	82.8	4	106197282	106197282	T	C	0.010	TET2	p.L1872P	Missense
PD34512	3	86.8	4	106197282	106197282	T	C	0.004	TET2	p.L1872P	Missense
PD34512	1	79.8	20	57478808	57478808	C	T	0.010	GNAS	p.L775L	Synonymous
PD34512	2	82.8	20	57478808	57478808	C	T	0.018	GNAS	p.L775L	Synonymous
PD34512	3	86.8	20	57478808	57478808	C	T	0.008	GNAS	p.L775L	Synonymous
PD34512	1	79.8	21	44514777	44514777	T	G	0.008	U2AF1	p.Q84P	Missense
PD34512	2	82.8	21	44514777	44514777	T	G	0.014	U2AF1	p.Q84P	Missense
PD34512	3	86.8	21	44514777	44514777	T	G	0.054	U2AF1	p.Q84P	Missense
PD34512	1	79.8	X	39931977	39931978	TG	T	0.010	BCOR	p.P874fs	Frameshift
PD34512	2	82.8	X	39931977	39931978	TG	T	0.017	BCOR	p.P874fs	Frameshift
PD34512	3	86.8	X	39931977	39931978	TG	T	0.044	BCOR	p.P874fs	Frameshift
PD34513	1	67.7	1	36937199	36937199	A	G	0.007	CSF3R	p.S374P	Missense
PD34513	2	71.0	1	36937199	36937199	A	G	0.002	CSF3R	p.S374P	Missense
PD34513	3	75.6	1	36937199	36937199	A	G	0.002	CSF3R	p.S374P	Missense
PD34513	4	78.5	1	36937199	36937199	A	G	0.001	CSF3R	p.S374P	Missense
PD34513	1	67.7	2	25457228	25457228	T	A	0.005	DNMT3A	p.R887X	Nonsense
PD34513	2	71.0	2	25457228	25457228	T	A	0.007	DNMT3A	p.R887X	Nonsense
PD34513	3	75.6	2	25457228	25457228	T	A	0.008	DNMT3A	p.R887X	Nonsense
PD34513	4	78.5	2	25457228	25457228	T	A	0.001	DNMT3A	p.R887X	Nonsense
PD34514	1	70.2	2	25463308	25463308	G	A	0.092	DNMT3A	p.R729W	Missense
PD34514	2	73.8	2	25463308	25463308	G	A	0.083	DNMT3A	p.R729W	Missense
PD34514	3	77.8	2	25463308	25463308	G	A	0.085	DNMT3A	p.R729W	Missense
PD34514	5	84.7	2	25463308	25463308	G	A	0.075	DNMT3A	p.R729W	Missense
PD34514	1	70.2	2	25466800	25466800	G	A	0.022	DNMT3A	p.R635W	Missense
PD34514	2	73.8	2	25466800	25466800	G	A	0.036	DNMT3A	p.R635W	Missense
PD34514	3	77.8	2	25466800	25466800	G	A	0.036	DNMT3A	p.R635W	Missense
PD34514	5	84.7	2	25466800	25466800	G	A	0.025	DNMT3A	p.R635W	Missense
PD34514	1	70.2	2	25468144	25468144	C	T	0.007	DNMT3A	p.G511E	Missense
PD34514	2	73.8	2	25468144	25468144	C	T	0.012	DNMT3A	p.G511E	Missense
PD34514	3	77.8	2	25468144	25468144	C	T	0.012	DNMT3A	p.G511E	Missense
PD34514	5	84.7	2	25468144	25468144	C	T	0.013	DNMT3A	p.G511E	Missense
PD34514	1	70.2	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34514	2	73.8	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense
PD34514	3	77.8	9	5073770	5073770	G	T	0.001	JAK2	p.V617F	Missense
PD34514	5	84.7	9	5073770	5073770	G	T	0.006	JAK2	p.V617F	Missense
PD34514	1	70.2	X	123164924	123164924	G	T	0.005	STAG2	p.V79V	Synonymous
PD34514	2	73.8	X	123164924	123164924	G	T	0.000	STAG2	p.V79V	Synonymous
PD34514	3	77.8	X	123164924	123164924	G	T	0.000	STAG2	p.V79V	Synonymous
PD34514	5	84.7	X	123164924	123164924	G	T	0.000	STAG2	p.V79V	Synonymous
PD34515	1	74.8	2	25459805	25459805	C	T	0.095	DNMT3A	p.K826K	Synonymous
PD34515	2	77.8	2	25459805	25459805	C	T	0.101	DNMT3A	p.K826K	Synonymous
PD34515	3	82.7	2	25459805	25459805	C	T	0.129	DNMT3A	p.K826K	Synonymous
PD34515	1	74.8	2	25463601	25463601	T	C	0.009	DNMT3A	c.2083-2A>G	Splice site
PD34515	2	77.8	2	25463601	25463601	T	C	0.011	DNMT3A	c.2083-2A>G	Splice site
PD34515	3	82.7	2	25463601	25463601	T	C	0.014	DNMT3A	c.2083-2A>G	Splice site
PD34515	1	74.8	12	50037035	50037035	C	A	0.000	PRPF40B	p.P745P	Synonymous
PD34515	2	77.8	12	50037035	50037035	C	A	0.000	PRPF40B	p.P745P	Synonymous
PD34515	3	82.7	12	50037035	50037035	C	A	0.012	PRPF40B	p.P745P	Synonymous
PD34515	1	74.8	20	31024961	31024961	G	A	0.006	ASXL1	p.A1482A	Synonymous
PD34515	2	77.8	20	31024961	31024961	G	A	0.013	ASXL1	p.A1482A	Synonymous
PD34515	3	82.7	20	31024961	31024961	G	A	0.015	ASXL1	p.A1482A	Synonymous
PD34515	1	74.8	21	36206802	36206802	C	T	0.006	RUNX1	p.R237K	Missense
PD34515	2	77.8	21	36206802	36206802	C	T	0.000	RUNX1	p.R237K	Missense
PD34515	3	82.7	21	36206802	36206802	C	T	0.000	RUNX1	p.R237K	Missense
PD34517	1	67.4	2	25463184	25463184	G	A	0.012	DNMT3A	p.S770L	Missense
PD34517	2	69.9	2	25463184	25463184	G	A	0.012	DNMT3A	p.S770L	Missense
PD34517	3	73.8	2	25463184	25463184	G	A	0.012	DNMT3A	p.S770L	Missense
PD34517	4	76.7	2	25463184	25463184	G	A	0.020	DNMT3A	p.S770L	Missense
PD34517	1	67.4	2	25469176	25469177	TT	T	0.010	DNMT3A	p.E427fs	Frameshift
PD34517	2	69.9	2	25469176	25469177	TT	T	0.009	DNMT3A	p.E427fs	Frameshift
PD34517	3	73.8	2	25469176	25469177	TT	T	0.011	DNMT3A	p.E427fs	Frameshift
PD34517	4	76.7	2	25469176	25469177	TT	T	0.006	DNMT3A	p.E427fs	Frameshift
PD34517	1	67.4	2	25469931	25469932	GG	G	0.028	DNMT3A	p.Y370X	Nonsense
PD34517	2	69.9	2	25469931	25469932	GG	G	0.032	DNMT3A	p.Y370X	Nonsense
PD34517	3	73.8	2	25469931	25469932	GG	G	0.044	DNMT3A	p.Y370X	Nonsense
PD34517	4	76.7	2	25469931	25469932	GG	G	0.033	DNMT3A	p.Y370X	Nonsense
PD34517	1	67.4	12	25398285	25398285	C	A	0.000	KRAS	p.G12C	Missense
PD34517	2	69.9	12	25398285	25398285	C	A	0.000	KRAS	p.G12C	Missense
PD34517	3	73.8	12	25398285	25398285	C	A	0.000	KRAS	p.G12C	Missense
PD34517	4	76.7	12	25398285	25398285	C	A	0.005	KRAS	p.G12C	Missense
PD34517	1	67.4	17	7576572	7576572	A	C	0.007	TP53	p.L297V	Missense
PD34517	2	69.9	17	7576572	7576572	A	C	0.002	TP53	p.L297V	Missense
PD34517	3	73.8	17	7576572	7576572	A	C	0.001	TP53	p.L297V	Missense
PD34517	4	76.7	17	7576572	7576572	A	C	0.002	TP53	p.L297V	Missense
PD34519	1	67.2	7	101847817	101847817	G	T	0.006	CUX1	p.Q1018H	Missense
PD34519	2	70.5	7	101847817	101847817	G	T	0.000	CUX1	p.Q1018H	Missense
PD34519	3	74.0	7	101847817	101847817	G	T	0.000	CUX1	p.Q1018H	Missense
PD34519	4	77.5	7	101847817	101847817	G	T	0.001	CUX1	p.Q1018H	Missense
PD34519	5	82.8	7	101847817	101847817	G	T	0.000	CUX1	p.Q1018H	Missense
PD34519	1	67.2	17	58740432	58740433	CA	C	0.001	PPM1D	p.S446fs	Frameshift
PD34519	2	70.5	17	58740432	58740433	CA	C	0.000	PPM1D	p.S446fs	Frameshift
PD34519	3	74.0	17	58740432	58740433	CA	C	0.000	PPM1D	p.S446fs	Frameshift
PD34519	4	77.5	17	58740432	58740433	CA	C	0.006	PPM1D	p.S446fs	Frameshift
PD34519	5	82.8	17	58740432	58740433	CA	C	0.006	PPM1D	p.S446fs	Frameshift
PD34520	1	73.1	1	1720544	1720544	C	A	0.000	GNB1	p.G288G	Synonymous
PD34520	2	76.0	1	1720544	1720544	C	A	0.000	GNB1	p.G288G	Synonymous
PD34520	3	79.3	1	1720544	1720544	C	A	0.000	GNB1	p.G288G	Synonymous
PD34520	4	82.7	1	1720544	1720544	C	A	0.005	GNB1	p.G288G	Synonymous
PD34520	1	73.1	4	106163989	106163989	A	C	0.081	TET2	c.3501-2A>C	Splice site
PD34520	2	76.0	4	106163989	106163989	A	C	0.124	TET2	c.3501-2A>C	Splice site
PD34520	3	79.3	4	106163989	106163989	A	C	0.180	TET2	c.3501-2A>C	Splice site
PD34520	4	82.7	4	106163989	106163989	A	C	0.174	TET2	c.3501-2A>C	Splice site
PD34520	1	73.1	4	106180783	106180783	T	G	0.009	TET2	p.C1271G	Missense
PD34520	2	76.0	4	106180783	106180783	T	G	0.007	TET2	p.C1271G	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34520	3	79.3	4	106180783	106180783	T	G	0.004	TET2	p.C1271G	Missense
PD34520	4	82.7	4	106180783	106180783	T	G	0.005	TET2	p.C1271G	Missense
PD34521	1	71.7	9	5073770	5073770	G	T	0.098	JAK2	p.V617F	Missense
PD34521	2	74.8	9	5073770	5073770	G	T	0.099	JAK2	p.V617F	Missense
PD34521	3	79.8	9	5073770	5073770	G	T	0.084	JAK2	p.V617F	Missense
PD34521	1	71.7	16	67662442	67662442	C	T	0.003	CTCF	p.T563I	Missense
PD34521	2	74.8	16	67662442	67662442	C	T	0.004	CTCF	p.T563I	Missense
PD34521	3	79.8	16	67662442	67662442	C	T	0.009	CTCF	p.T563I	Missense
PD34521	1	71.7	19	17945679	17945679	A	T	0.007	JAK3	p.S727R	Missense
PD34521	2	74.8	19	17945679	17945679	A	T	0.000	JAK3	p.S727R	Missense
PD34521	3	79.8	19	17945679	17945679	A	T	0.000	JAK3	p.S727R	Missense
PD34521	1	71.7	X	15350004	15350004	G	A	0.003	PIGA	p.L17F	Missense
PD34521	2	74.8	X	15350004	15350004	G	A	0.007	PIGA	p.L17F	Missense
PD34521	3	79.8	X	15350004	15350004	G	A	0.010	PIGA	p.L17F	Missense
PD34523	1	75.8	4	106157824	106157824	C	A	0.006	TET2	p.Q909K	Missense
PD34523	2	78.3	4	106157824	106157824	C	A	0.001	TET2	p.Q909K	Missense
PD34523	3	84.3	4	106157824	106157824	C	A	0.000	TET2	p.Q909K	Missense
PD34523	1	75.8	4	106196276	106196276	C	T	0.008	TET2	p.Q1537X	Nonsense
PD34523	2	78.3	4	106196276	106196276	C	T	0.010	TET2	p.Q1537X	Nonsense
PD34523	3	84.3	4	106196276	106196276	C	T	0.030	TET2	p.Q1537X	Nonsense
PD34523	1	75.8	16	67645852	67645852	A	G	0.007	CTCF	c.782-2A>G	Splice site
PD34523	2	78.3	16	67645852	67645852	A	G	0.013	CTCF	c.782-2A>G	Splice site
PD34523	3	84.3	16	67645852	67645852	A	G	0.037	CTCF	c.782-2A>G	Splice site
PD34523	1	75.8	17	58700941	58700941	G	T	0.000	PPM1D	p.V178F	Missense
PD34523	2	78.3	17	58700941	58700941	G	T	0.000	PPM1D	p.V178F	Missense
PD34523	3	84.3	17	58700941	58700941	G	T	0.006	PPM1D	p.V178F	Missense
PD34524	1	74.2	19	13050337	13050337	G	T	0.018	CALR	p.V97L	Missense
PD34524	2	77.1	19	13050337	13050337	G	T	0.011	CALR	p.V97L	Missense
PD34524	3	80.9	19	13050337	13050337	G	T	0.014	CALR	p.V97L	Missense
PD34524	4	83.6	19	13050337	13050337	G	T	0.013	CALR	p.V97L	Missense
PD34524	1	74.2	22	30738794	30738794	C	A	0.000	SF3A1	p.Q242H	Missense
PD34524	2	77.1	22	30738794	30738794	C	A	0.000	SF3A1	p.Q242H	Missense
PD34524	3	80.9	22	30738794	30738794	C	A	0.007	SF3A1	p.Q242H	Missense
PD34524	4	83.6	22	30738794	30738794	C	A	0.000	SF3A1	p.Q242H	Missense
PD34525	1	71.6	2	25469136	25469137	CC	C	0.006	DNMT3A	p.V441fs	Frameshift
PD34525	2	74.7	2	25469136	25469137	CC	C	0.007	DNMT3A	p.V441fs	Frameshift
PD34525	3	78.1	2	25469136	25469137	CC	C	0.012	DNMT3A	p.V441fs	Frameshift
PD34525	4	81.6	2	25469136	25469137	CC	C	0.009	DNMT3A	p.V441fs	Frameshift
PD34526	1	80.2	2	25457243	25457243	G	A	0.014	DNMT3A	p.R882C	Missense
PD34526	2	83.1	2	25457243	25457243	G	A	0.016	DNMT3A	p.R882C	Missense
PD34526	3	88.7	2	25457243	25457243	G	A	0.012	DNMT3A	p.R882C	Missense
PD34526	1	80.2	16	3778037	3778037	C	T	0.019	CREBBP	p.T2337T	Synonymous
PD34526	2	83.1	16	3778037	3778037	C	T	0.018	CREBBP	p.T2337T	Synonymous
PD34526	3	88.7	16	3778037	3778037	C	T	0.037	CREBBP	p.T2337T	Synonymous
PD34526	1	80.2	22	30733780	30733780	A	G	0.000	SF3A1	p.M617T	Missense
PD34526	2	83.1	22	30733780	30733780	A	G	0.000	SF3A1	p.M617T	Missense
PD34526	3	88.7	22	30733780	30733780	A	G	0.006	SF3A1	p.M617T	Missense
PD34527	1	67.8	4	106157119	106157119	C	T	0.003	TET2	p.Q674X	Nonsense
PD34527	2	70.6	4	106157119	106157119	C	T	0.005	TET2	p.Q674X	Nonsense
PD34527	3	74.5	4	106157119	106157119	C	T	0.023	TET2	p.Q674X	Nonsense
PD34527	4	77.1	4	106157119	106157119	C	T	0.064	TET2	p.Q674X	Nonsense
PD34527	5	81.5	4	106157119	106157119	C	T	0.139	TET2	p.Q674X	Nonsense
PD34527	1	67.8	4	106180865	106180865	G	A	0.005	TET2	p.C1298Y	Missense
PD34527	2	70.6	4	106180865	106180865	G	A	0.006	TET2	p.C1298Y	Missense
PD34527	3	74.5	4	106180865	106180865	G	A	0.029	TET2	p.C1298Y	Missense
PD34527	4	77.1	4	106180865	106180865	G	A	0.049	TET2	p.C1298Y	Missense
PD34527	5	81.5	4	106180865	106180865	G	A	0.157	TET2	p.C1298Y	Missense
PD34527	1	67.8	4	106193787	106193787	G	T	0.006	TET2	p.V1417F	Missense
PD34527	2	70.6	4	106193787	106193787	G	T	0.001	TET2	p.V1417F	Missense
PD34527	3	74.5	4	106193787	106193787	G	T	0.003	TET2	p.V1417F	Missense
PD34527	4	77.1	4	106193787	106193787	G	T	0.003	TET2	p.V1417F	Missense
PD34527	5	81.5	4	106193787	106193787	G	T	0.004	TET2	p.V1417F	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34527	1	67.8	12	12022603	12022603	G	T	0.001	ETV6	p.V237L	Missense
PD34527	2	70.6	12	12022603	12022603	G	T	0.001	ETV6	p.V237L	Missense
PD34527	3	74.5	12	12022603	12022603	G	T	0.002	ETV6	p.V237L	Missense
PD34527	4	77.1	12	12022603	12022603	G	T	0.003	ETV6	p.V237L	Missense
PD34527	5	81.5	12	12022603	12022603	G	T	0.006	ETV6	p.V237L	Missense
PD34527	1	67.8	17	7578407	7578407	G	C	0.007	TP53	p.R136G	Missense
PD34527	2	70.6	17	7578407	7578407	G	C	0.009	TP53	p.R136G	Missense
PD34527	3	74.5	17	7578407	7578407	G	C	0.013	TP53	p.R136G	Missense
PD34527	4	77.1	17	7578407	7578407	G	C	0.014	TP53	p.R136G	Missense
PD34527	5	81.5	17	7578407	7578407	G	C	0.016	TP53	p.R136G	Missense
PD34528	1	77.9	19	56174996	56174996	C	A	0.006	U2AF2	p.Q210K	Missense
PD34528	2	80.8	19	56174996	56174996	C	A	0.000	U2AF2	p.Q210K	Missense
PD34528	3	85.7	19	56174996	56174996	C	A	0.001	U2AF2	p.Q210K	Missense
PD34528	1	77.9	20	57429113	57429113	C	T	0.010	GNAS	p.R265C	Missense
PD34528	2	80.8	20	57429113	57429113	C	T	0.020	GNAS	p.R265C	Missense
PD34528	3	85.7	20	57429113	57429113	C	T	0.018	GNAS	p.R265C	Missense
PD34529	1	75.1	2	198260970	198260970	C	A	0.000	SF3B1	p.A1117S	Missense
PD34529	2	78.3	2	198260970	198260970	C	A	0.001	SF3B1	p.A1117S	Missense
PD34529	3	81.9	2	198260970	198260970	C	A	0.007	SF3B1	p.A1117S	Missense
PD34529	4	85.3	2	198260970	198260970	C	A	0.001	SF3B1	p.A1117S	Missense
PD34529	1	75.1	7	148523568	148523568	G	T	0.001	EZH2	p.F295L	Missense
PD34529	2	78.3	7	148523568	148523568	G	T	0.002	EZH2	p.F295L	Missense
PD34529	3	81.9	7	148523568	148523568	G	T	0.005	EZH2	p.F295L	Missense
PD34529	4	85.3	7	148523568	148523568	G	T	0.000	EZH2	p.F295L	Missense
PD34529	1	75.1	X	39923090	39923090	T	C	0.001	BCOR	p.K1172K	Synonymous
PD34529	2	78.3	X	39923090	39923090	T	C	0.001	BCOR	p.K1172K	Synonymous
PD34529	3	81.9	X	39923090	39923090	T	C	0.004	BCOR	p.K1172K	Synonymous
PD34529	4	85.3	X	39923090	39923090	T	C	0.001	BCOR	p.K1172K	Synonymous
PD34530	1	84.5	7	148512059	148512059	G	T	0.000	EZH2	p.P540H	Missense
PD34530	3	93.7	7	148512059	148512059	G	T	0.000	EZH2	p.P540H	Missense
PD34530	1	84.5	X	44928854	44928854	G	T	0.006	KDM6A	p.A704S	Missense
PD34530	3	93.7	X	44928854	44928854	G	T	0.000	KDM6A	p.A704S	Missense
PD34531	1	80.5	2	25463508	25463508	C	T	0.187	DNMT3A	c.2173+1G>A	Splice site
PD34531	2	83.5	2	25463508	25463508	C	T	0.167	DNMT3A	c.2173+1G>A	Splice site
PD34531	3	87.3	2	25463508	25463508	C	T	0.228	DNMT3A	c.2173+1G>A	Splice site
PD34531	4	90.6	2	25463508	25463508	C	T	0.189	DNMT3A	c.2173+1G>A	Splice site
PD34531	5	94.9	2	25463508	25463508	C	T	0.297	DNMT3A	c.2173+1G>A	Splice site
PD34531	1	80.5	7	148514353	148514353	A	G	0.000	EZH2	p.C457C	Synonymous
PD34531	2	83.5	7	148514353	148514353	A	G	0.002	EZH2	p.C457C	Synonymous
PD34531	3	87.3	7	148514353	148514353	A	G	0.006	EZH2	p.C457C	Synonymous
PD34531	4	90.6	7	148514353	148514353	A	G	0.001	EZH2	p.C457C	Synonymous
PD34531	5	94.9	7	148514353	148514353	A	G	0.000	EZH2	p.C457C	Synonymous
PD34531	1	80.5	11	119169251	119169251	G	A	0.008	CBL	c.2434+1G>A	Splice site
PD34531	2	83.5	11	119169251	119169251	G	A	0.006	CBL	c.2434+1G>A	Splice site
PD34531	3	87.3	11	119169251	119169251	G	A	0.010	CBL	c.2434+1G>A	Splice site
PD34531	4	90.6	11	119169251	119169251	G	A	0.009	CBL	c.2434+1G>A	Splice site
PD34531	5	94.9	11	119169251	119169251	G	A	0.006	CBL	c.2434+1G>A	Splice site
PD34531	1	80.5	16	3781818	3781818	G	C	0.011	CREBBP	p.L1617V	Missense
PD34531	2	83.5	16	3781818	3781818	G	C	0.016	CREBBP	p.L1617V	Missense
PD34531	3	87.3	16	3781818	3781818	G	C	0.013	CREBBP	p.L1617V	Missense
PD34531	4	90.6	16	3781818	3781818	G	C	0.012	CREBBP	p.L1617V	Missense
PD34531	5	94.9	16	3781818	3781818	G	C	0.011	CREBBP	p.L1617V	Missense
PD34531	1	80.5	17	58740665	58740665	C	T	0.027	PPM1D	p.Q524X	Nonsense
PD34531	2	83.5	17	58740665	58740665	C	T	0.022	PPM1D	p.Q524X	Nonsense
PD34531	3	87.3	17	58740665	58740665	C	T	0.040	PPM1D	p.Q524X	Nonsense
PD34531	4	90.6	17	58740665	58740665	C	T	0.024	PPM1D	p.Q524X	Nonsense
PD34531	5	94.9	17	58740665	58740665	C	T	0.024	PPM1D	p.Q524X	Nonsense
PD34532	1	73.8	12	50030583	50030583	C	A	0.000	PRPF40B	p.A504D	Missense
PD34532	2	76.9	12	50030583	50030583	C	A	0.000	PRPF40B	p.A504D	Missense
PD34532	3	81.8	12	50030583	50030583	C	A	0.009	PRPF40B	p.A504D	Missense
PD34533	1	74.9	17	7578215	7578215	A	C	0.002	TP53	p.F173V	Missense
PD34533	2	77.9	17	7578215	7578215	A	C	0.004	TP53	p.F173V	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34533	3	83.0	17	7578215	7578215	A	C	0.008	TP53	p.F173V	Missense
PD34533	1	74.9	X	129148289	129148289	C	T	0.000	BCORL1	p.S514L	Missense
PD34533	2	77.9	X	129148289	129148289	C	T	0.000	BCORL1	p.S514L	Missense
PD34533	3	83.0	X	129148289	129148289	C	T	0.007	BCORL1	p.S514L	Missense
PD34534	1	68.1	7	101916641	101916641	C	A	0.007	CUX1	p.R418R	Synonymous
PD34534	2	71.4	7	101916641	101916641	C	A	0.002	CUX1	p.R418R	Synonymous
PD34534	3	77.0	7	101916641	101916641	C	A	0.000	CUX1	p.R418R	Synonymous
PD34534	4	81.0	7	101916641	101916641	C	A	0.002	CUX1	p.R418R	Synonymous
PD34535	1	69.0	1	36937088	36937088	A	G	0.005	CSF3R	p.Y411H	Missense
PD34535	2	72.6	1	36937088	36937088	A	G	0.000	CSF3R	p.Y411H	Missense
PD34535	3	76.3	1	36937088	36937088	A	G	0.000	CSF3R	p.Y411H	Missense
PD34535	1	69.0	11	118342446	118342446	C	A	0.000	KMT2A	p.S191X	Nonsense
PD34535	2	72.6	11	118342446	118342446	C	A	0.001	KMT2A	p.S191X	Nonsense
PD34535	3	76.3	11	118342446	118342446	C	A	0.008	KMT2A	p.S191X	Nonsense
PD34536	1	68.6	2	25470012	25470013	CC	C	0.005	DNMT3A	p.K343fs	Frameshift
PD34536	2	71.7	2	25470012	25470013	CC	C	0.003	DNMT3A	p.K343fs	Frameshift
PD34536	3	77.7	2	25470012	25470013	CC	C	0.003	DNMT3A	p.K343fs	Frameshift
PD34536	4	81.6	2	25470012	25470013	CC	C	0.014	DNMT3A	p.K343fs	Frameshift
PD34536	1	68.6	4	106164794	106164794	G	A	0.001	TET2	p.C1221Y	Missense
PD34536	2	71.7	4	106164794	106164794	G	A	0.003	TET2	p.C1221Y	Missense
PD34536	3	77.7	4	106164794	106164794	G	A	0.010	TET2	p.C1221Y	Missense
PD34536	4	81.6	4	106164794	106164794	G	A	0.002	TET2	p.C1221Y	Missense
PD34537	1	73.7	11	119148546	119148546	G	A	0.005	CBL	p.V363M	Missense
PD34537	3	81.7	11	119148546	119148546	G	A	0.000	CBL	p.V363M	Missense
PD34538	1	74.6	1	115258744	115258744	C	G	0.001	NRAS	p.G13A	Missense
PD34538	2	77.5	1	115258744	115258744	C	G	0.006	NRAS	p.G13A	Missense
PD34538	3	81.3	1	115258744	115258744	C	G	0.001	NRAS	p.G13A	Missense
PD34538	4	84.0	1	115258744	115258744	C	G	0.000	NRAS	p.G13A	Missense
PD34538	5	88.6	1	115258744	115258744	C	G	0.000	NRAS	p.G13A	Missense
PD34538	1	74.6	2	198267371	198267371	G	C	0.004	SF3B1	p.H662Q	Missense
PD34538	2	77.5	2	198267371	198267371	G	C	0.004	SF3B1	p.H662Q	Missense
PD34538	3	81.3	2	198267371	198267371	G	C	0.009	SF3B1	p.H662Q	Missense
PD34538	4	84.0	2	198267371	198267371	G	C	0.009	SF3B1	p.H662Q	Missense
PD34538	5	88.6	2	198267371	198267371	G	C	0.009	SF3B1	p.H662Q	Missense
PD34538	1	74.6	4	55589795	55589795	T	C	0.001	KIT	p.L426P	Missense
PD34538	2	77.5	4	55589795	55589795	T	C	0.009	KIT	p.L426P	Missense
PD34538	3	81.3	4	55589795	55589795	T	C	0.009	KIT	p.L426P	Missense
PD34538	4	84.0	4	55589795	55589795	T	C	0.001	KIT	p.L426P	Missense
PD34538	5	88.6	4	55589795	55589795	T	C	0.001	KIT	p.L426P	Missense
PD34538	1	74.6	7	101758505	101758505	C	A	0.001	CUX1	p.T209K	Missense
PD34538	2	77.5	7	101758505	101758505	C	A	0.006	CUX1	p.T209K	Missense
PD34538	3	81.3	7	101758505	101758505	C	A	0.000	CUX1	p.T209K	Missense
PD34538	4	84.0	7	101758505	101758505	C	A	0.000	CUX1	p.T209K	Missense
PD34538	5	88.6	7	101758505	101758505	C	A	0.000	CUX1	p.T209K	Missense
PD34538	1	74.6	17	58740809	58740809	C	T	0.005	PPM1D	p.R572X	Nonsense
PD34538	2	77.5	17	58740809	58740809	C	T	0.003	PPM1D	p.R572X	Nonsense
PD34538	3	81.3	17	58740809	58740809	C	T	0.013	PPM1D	p.R572X	Nonsense
PD34538	4	84.0	17	58740809	58740809	C	T	0.005	PPM1D	p.R572X	Nonsense
PD34538	5	88.6	17	58740809	58740809	C	T	0.011	PPM1D	p.R572X	Nonsense
PD34538	1	74.6	20	57429297	57429297	A	G	0.000	GNAS	p.D326G	Missense
PD34538	2	77.5	20	57429297	57429297	A	G	0.001	GNAS	p.D326G	Missense
PD34538	3	81.3	20	57429297	57429297	A	G	0.001	GNAS	p.D326G	Missense
PD34538	4	84.0	20	57429297	57429297	A	G	0.000	GNAS	p.D326G	Missense
PD34538	5	88.6	20	57429297	57429297	A	G	0.005	GNAS	p.D326G	Missense
PD34538	1	74.6	20	31024026	31024027	AG	A	0.003	ASXL1	p.R1171fs	Frameshift
PD34538	2	77.5	20	31024026	31024027	AG	A	0.006	ASXL1	p.R1171fs	Frameshift
PD34538	3	81.3	20	31024026	31024027	AG	A	0.001	ASXL1	p.R1171fs	Frameshift
PD34538	4	84.0	20	31024026	31024027	AG	A	0.007	ASXL1	p.R1171fs	Frameshift
PD34538	5	88.6	20	31024026	31024027	AG	A	0.005	ASXL1	p.R1171fs	Frameshift
PD34539	1	69.5	4	106196323	106196327	TCAG A	T	0.001	TET2	p.Q1553fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34539	2	72.5	4	106196323	106196327	TCAGA	T	0.004	TET2	p.Q1553fs	Frameshift
PD34539	3	76.0	4	106196323	106196327	TCAGA	T	0.003	TET2	p.Q1553fs	Frameshift
PD34539	4	78.9	4	106196323	106196327	TCAGA	T	0.012	TET2	p.Q1553fs	Frameshift
PD34539	5	83.3	4	106196323	106196327	TCAGA	T	0.020	TET2	p.Q1553fs	Frameshift
PD34539	1	69.5	9	139405695	139405695	C	T	0.013	NOTCH1	p.P832P	Synonymous
PD34539	2	72.5	9	139405695	139405695	C	T	0.008	NOTCH1	p.P832P	Synonymous
PD34539	3	76.0	9	139405695	139405695	C	T	0.020	NOTCH1	p.P832P	Synonymous
PD34539	4	78.9	9	139405695	139405695	C	T	0.022	NOTCH1	p.P832P	Synonymous
PD34539	5	83.3	9	139405695	139405695	C	T	0.018	NOTCH1	p.P832P	Synonymous
PD34540	1	65.8	2	198266611	198266611	C	T	0.000	SF3B1	p.G742D	Missense
PD34540	2	70.2	2	198266611	198266611	C	T	0.000	SF3B1	p.G742D	Missense
PD34540	3	73.9	2	198266611	198266611	C	T	0.004	SF3B1	p.G742D	Missense
PD34540	4	76.3	2	198266611	198266611	C	T	0.009	SF3B1	p.G742D	Missense
PD34540	1	65.8	4	106182944	106182945	AC	A	0.016	TET2	p.N1328fs	Frameshift
PD34540	2	70.2	4	106182944	106182945	AC	A	0.010	TET2	p.N1328fs	Frameshift
PD34540	3	73.9	4	106182944	106182945	AC	A	0.018	TET2	p.N1328fs	Frameshift
PD34540	4	76.3	4	106182944	106182945	AC	A	0.027	TET2	p.N1328fs	Frameshift
PD34540	1	65.8	10	89692883	89692883	C	T	0.000	PTEN	p.H296Y	Missense
PD34540	2	70.2	10	89692883	89692883	C	T	0.006	PTEN	p.H296Y	Missense
PD34540	3	73.9	10	89692883	89692883	C	T	0.001	PTEN	p.H296Y	Missense
PD34540	4	76.3	10	89692883	89692883	C	T	0.001	PTEN	p.H296Y	Missense
PD34540	1	65.8	20	57415671	57415671	C	A	0.001	GNAS	p.S170R	Missense
PD34540	2	70.2	20	57415671	57415671	C	A	0.009	GNAS	p.S170R	Missense
PD34540	3	73.9	20	57415671	57415671	C	A	0.000	GNAS	p.S170R	Missense
PD34540	4	76.3	20	57415671	57415671	C	A	0.001	GNAS	p.S170R	Missense
PD34541	1	67.0	2	25470484	25470484	C	T	0.004	DNMT3A	p.W330X	Nonsense
PD34541	2	70.2	2	25470484	25470484	C	T	0.002	DNMT3A	p.W330X	Nonsense
PD34541	3	74.0	2	25470484	25470484	C	T	0.007	DNMT3A	p.W330X	Nonsense
PD34541	4	77.1	2	25470484	25470484	C	T	0.008	DNMT3A	p.W330X	Nonsense
PD34541	5	81.5	2	25470484	25470484	C	T	0.007	DNMT3A	p.W330X	Nonsense
PD34541	1	67.0	4	106190822	106190822	C	T	0.003	TET2	p.P1367L	Missense
PD34541	2	70.2	4	106190822	106190822	C	T	0.006	TET2	p.P1367L	Missense
PD34541	3	74.0	4	106190822	106190822	C	T	0.003	TET2	p.P1367L	Missense
PD34541	4	77.1	4	106190822	106190822	C	T	0.006	TET2	p.P1367L	Missense
PD34541	5	81.5	4	106190822	106190822	C	T	0.007	TET2	p.P1367L	Missense
PD34541	1	67.0	4	106196886	106196886	T	A	0.005	TET2	p.L1740X	Nonsense
PD34541	2	70.2	4	106196886	106196886	T	A	0.005	TET2	p.L1740X	Nonsense
PD34541	3	74.0	4	106196886	106196886	T	A	0.002	TET2	p.L1740X	Nonsense
PD34541	4	77.1	4	106196886	106196886	T	A	0.003	TET2	p.L1740X	Nonsense
PD34541	5	81.5	4	106196886	106196886	T	A	0.000	TET2	p.L1740X	Nonsense
PD34541	1	67.0	4	106197608	106197608	G	A	0.004	TET2	p.D1981N	Missense
PD34541	2	70.2	4	106197608	106197608	G	A	0.002	TET2	p.D1981N	Missense
PD34541	3	74.0	4	106197608	106197608	G	A	0.005	TET2	p.D1981N	Missense
PD34541	4	77.1	4	106197608	106197608	G	A	0.001	TET2	p.D1981N	Missense
PD34541	5	81.5	4	106197608	106197608	G	A	0.000	TET2	p.D1981N	Missense
PD34541	1	67.0	20	57429868	57429868	A	G	0.000	GNAS	p.Q454R	Missense
PD34541	2	70.2	20	57429868	57429868	A	G	0.000	GNAS	p.Q454R	Missense
PD34541	3	74.0	20	57429868	57429868	A	G	0.000	GNAS	p.Q454R	Missense
PD34541	4	77.1	20	57429868	57429868	A	G	0.000	GNAS	p.Q454R	Missense
PD34541	5	81.5	20	57429868	57429868	A	G	0.009	GNAS	p.Q454R	Missense
PD34541	1	67.0	20	57484420	57484420	C	T	0.010	GNAS	p.R844C	Missense
PD34541	2	70.2	20	57484420	57484420	C	T	0.015	GNAS	p.R844C	Missense
PD34541	3	74.0	20	57484420	57484420	C	T	0.010	GNAS	p.R844C	Missense
PD34541	4	77.1	20	57484420	57484420	C	T	0.015	GNAS	p.R844C	Missense
PD34541	5	81.5	20	57484420	57484420	C	T	0.010	GNAS	p.R844C	Missense
PD34541	1	67.0	X	154317600	154317600	T	C	0.000	BRCC3	p.C156R	Missense
PD34541	2	70.2	X	154317600	154317600	T	C	0.000	BRCC3	p.C156R	Missense
PD34541	3	74.0	X	154317600	154317600	T	C	0.006	BRCC3	p.C156R	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34541	4	77.1	X	154317600	154317600	T	C	0.000	BRCC3	p.C156R	Missense
PD34541	5	81.5	X	154317600	154317600	T	C	0.000	BRCC3	p.C156R	Missense
PD34542	1	66.2	4	106197249	106197249	G	T	0.032	TET2	p.G1861V	Missense
PD34542	2	69.5	4	106197249	106197249	G	T	0.032	TET2	p.G1861V	Missense
PD34542	3	73.2	4	106197249	106197249	G	T	0.030	TET2	p.G1861V	Missense
PD34542	4	76.1	4	106197249	106197249	G	T	0.026	TET2	p.G1861V	Missense
PD34542	5	81.5	4	106197249	106197249	G	T	0.029	TET2	p.G1861V	Missense
PD34542	1	66.2	21	44524456	44524456	G	A	0.000	U2AF1	p.S34F	Missense
PD34542	2	69.5	21	44524456	44524456	G	A	0.000	U2AF1	p.S34F	Missense
PD34542	3	73.2	21	44524456	44524456	G	A	0.000	U2AF1	p.S34F	Missense
PD34542	4	76.1	21	44524456	44524456	G	A	0.002	U2AF1	p.S34F	Missense
PD34542	5	81.5	21	44524456	44524456	G	A	0.006	U2AF1	p.S34F	Missense
PD34543	1	84.1	2	209113112	209113112	C	T	0.020	IDH1	p.R132H	Missense
PD34543	4	93.6	2	209113112	209113112	C	T	0.106	IDH1	p.R132H	Missense
PD34543	1	84.1	4	106196868	106196869	TG	T	0.107	TET2	p.M1734fs	Frameshift
PD34543	4	93.6	4	106196868	106196869	TG	T	0.047	TET2	p.M1734fs	Frameshift
PD34543	1	84.1	9	5073770	5073770	G	T	0.113	JAK2	p.V617F	Missense
PD34543	4	93.6	9	5073770	5073770	G	T	0.053	JAK2	p.V617F	Missense
PD34543	1	84.1	17	74732959	74732959	G	T	0.001	SRSF2	p.P95H	Missense
PD34543	4	93.6	17	74732959	74732959	G	T	0.072	SRSF2	p.P95H	Missense
PD34543	1	84.1	20	57428431	57428431	T	C	0.007	GNAS	p.A37A	Synonymous
PD34543	4	93.6	20	57428431	57428431	T	C	0.021	GNAS	p.A37A	Synonymous
PD34543	1	84.1	X	133551331	133551331	A	G	0.000	PHF6	p.K323E	Missense
PD34543	4	93.6	X	133551331	133551331	A	G	0.023	PHF6	p.K323E	Missense
PD34545	1	79.3	2	25467023	25467023	C	T	0.041	DNMT3A	c.1851+1G>A	Splice site
PD34545	2	82.2	2	25467023	25467023	C	T	0.058	DNMT3A	c.1851+1G>A	Splice site
PD34545	3	87.2	2	25467023	25467023	C	T	0.073	DNMT3A	c.1851+1G>A	Splice site
PD34545	1	79.3	2	25470594	25470594	C	A	0.012	DNMT3A	p.E294X	Nonsense
PD34545	2	82.2	2	25470594	25470594	C	A	0.009	DNMT3A	p.E294X	Nonsense
PD34545	3	87.2	2	25470594	25470594	C	A	0.014	DNMT3A	p.E294X	Nonsense
PD34545	1	79.3	4	106193733	106193733	A	C	0.007	TET2	p.T1399P	Missense
PD34545	2	82.2	4	106193733	106193733	A	C	0.008	TET2	p.T1399P	Missense
PD34545	3	87.2	4	106193733	106193733	A	C	0.007	TET2	p.T1399P	Missense
PD34545	1	79.3	4	106196234	106196234	C	T	0.012	TET2	p.Q1523X	Nonsense
PD34545	2	82.2	4	106196234	106196234	C	T	0.030	TET2	p.Q1523X	Nonsense
PD34545	3	87.2	4	106196234	106196234	C	T	0.021	TET2	p.Q1523X	Nonsense
PD34545	1	79.3	4	106197360	106197360	C	T	0.007	TET2	p.S1898F	Missense
PD34545	2	82.2	4	106197360	106197360	C	T	0.003	TET2	p.S1898F	Missense
PD34545	3	87.2	4	106197360	106197360	C	T	0.015	TET2	p.S1898F	Missense
PD34546	1	70.2	12	112891043	112891043	T	C	0.000	PTPN11	p.L126S	Missense
PD34546	2	74.4	12	112891043	112891043	T	C	0.006	PTPN11	p.L126S	Missense
PD34546	3	77.5	12	112891043	112891043	T	C	0.000	PTPN11	p.L126S	Missense
PD34546	1	70.2	X	129148193	129148193	C	T	0.007	BCORL1	p.P482L	Missense
PD34546	2	74.4	X	129148193	129148193	C	T	0.008	BCORL1	p.P482L	Missense
PD34546	3	77.5	X	129148193	129148193	C	T	0.006	BCORL1	p.P482L	Missense
PD34547	1	75.6	2	25458696	25458696	T	G	0.005	DNMT3A	c.2479-2A>C	Splice site
PD34547	2	78.6	2	25458696	25458696	T	G	0.006	DNMT3A	c.2479-2A>C	Splice site
PD34547	3	82.3	2	25458696	25458696	T	G	0.002	DNMT3A	c.2479-2A>C	Splice site
PD34547	4	85.6	2	25458696	25458696	T	G	0.008	DNMT3A	c.2479-2A>C	Splice site
PD34547	1	75.6	2	25463316	25463316	C	T	0.007	DNMT3A	p.G726D	Missense
PD34547	2	78.6	2	25463316	25463316	C	T	0.003	DNMT3A	p.G726D	Missense
PD34547	3	82.3	2	25463316	25463316	C	T	0.005	DNMT3A	p.G726D	Missense
PD34547	4	85.6	2	25463316	25463316	C	T	0.002	DNMT3A	p.G726D	Missense
PD34547	1	75.6	2	25466790	25466790	G	A	0.005	DNMT3A	p.S638F	Missense
PD34547	2	78.6	2	25466790	25466790	G	A	0.006	DNMT3A	p.S638F	Missense
PD34547	3	82.3	2	25466790	25466790	G	A	0.009	DNMT3A	p.S638F	Missense
PD34547	4	85.6	2	25466790	25466790	G	A	0.012	DNMT3A	p.S638F	Missense
PD34547	1	75.6	16	67655411	67655411	A	G	0.000	CTCF	p.H425R	Missense
PD34547	2	78.6	16	67655411	67655411	A	G	0.000	CTCF	p.H425R	Missense
PD34547	3	82.3	16	67655411	67655411	A	G	0.000	CTCF	p.H425R	Missense
PD34547	4	85.6	16	67655411	67655411	A	G	0.006	CTCF	p.H425R	Missense
PD34548	1	75.6	2	25470483	25470483	A	C	0.004	DNMT3A	p.F331V	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34548	2	78.6	2	25470483	25470483	A	C	0.004	DNMT3A	p.F331V	Missense
PD34548	3	82.2	2	25470483	25470483	A	C	0.013	DNMT3A	p.F331V	Missense
PD34548	4	85.1	2	25470483	25470483	A	C	0.013	DNMT3A	p.F331V	Missense
PD34548	1	75.6	4	106164891	106164892	GA	G	0.004	TET2	p.K1254fs	Frameshift
PD34548	2	78.6	4	106164891	106164892	GA	G	0.002	TET2	p.K1254fs	Frameshift
PD34548	3	82.2	4	106164891	106164892	GA	G	0.012	TET2	p.K1254fs	Frameshift
PD34548	4	85.1	4	106164891	106164892	GA	G	0.005	TET2	p.K1254fs	Frameshift
PD34549	1	69.1	2	25464523	25464523	C	A	0.001	DNMT3A	p.E664X	Nonsense
PD34549	2	72.5	2	25464523	25464523	C	A	0.007	DNMT3A	p.E664X	Nonsense
PD34549	3	75.7	2	25464523	25464523	C	A	0.003	DNMT3A	p.E664X	Nonsense
PD34549	1	69.1	9	139409805	139409805	C	T	0.012	NOTCH1	p.D651N	Missense
PD34549	2	72.5	9	139409805	139409805	C	T	0.030	NOTCH1	p.D651N	Missense
PD34549	3	75.7	9	139409805	139409805	C	T	0.011	NOTCH1	p.D651N	Missense
PD34549	1	69.1	17	58740543	58740544	CT	C	0.000	PPM1D	p.T483fs	Frameshift
PD34549	2	72.5	17	58740543	58740544	CT	C	0.003	PPM1D	p.T483fs	Frameshift
PD34549	3	75.7	17	58740543	58740544	CT	C	0.008	PPM1D	p.T483fs	Frameshift
PD34550	1	67.2	4	106196821	106196822	AG	A	0.001	TET2	p.G1719fs	Frameshift
PD34550	2	71.2	4	106196821	106196822	AG	A	0.011	TET2	p.G1719fs	Frameshift
PD34550	3	75.0	4	106196821	106196822	AG	A	0.007	TET2	p.G1719fs	Frameshift
PD34550	4	77.6	4	106196821	106196822	AG	A	0.009	TET2	p.G1719fs	Frameshift
PD34550	1	67.2	7	101821928	101821928	C	A	0.000	CUX1	p.S336R	Missense
PD34550	2	71.2	7	101821928	101821928	C	A	0.014	CUX1	p.S336R	Missense
PD34550	3	75.0	7	101821928	101821928	C	A	0.003	CUX1	p.S336R	Missense
PD34550	4	77.6	7	101821928	101821928	C	A	0.000	CUX1	p.S336R	Missense
PD34550	1	67.2	16	67650776	67650776	G	A	0.006	CTCF	p.V361I	Missense
PD34550	2	71.2	16	67650776	67650776	G	A	0.003	CTCF	p.V361I	Missense
PD34550	3	75.0	16	67650776	67650776	G	A	0.002	CTCF	p.V361I	Missense
PD34550	4	77.6	16	67650776	67650776	G	A	0.002	CTCF	p.V361I	Missense
PD34551	1	65.7	12	11905425	11905425	G	A	0.000	ETV6	p.P25P	Synonymous
PD34551	2	69.1	12	11905425	11905425	G	A	0.006	ETV6	p.P25P	Synonymous
PD34551	3	74.0	12	11905425	11905425	G	A	0.000	ETV6	p.P25P	Synonymous
PD34551	1	65.7	17	58740836	58740836	C	T	0.012	PPM1D	p.R581X	Nonsense
PD34551	2	69.1	17	58740836	58740836	C	T	0.012	PPM1D	p.R581X	Nonsense
PD34551	3	74.0	17	58740836	58740836	C	T	0.006	PPM1D	p.R581X	Nonsense
PD34552	1	71.5	17	58700891	58700891	C	A	0.000	PPM1D	p.P161Q	Missense
PD34552	2	74.5	17	58700891	58700891	C	A	0.007	PPM1D	p.P161Q	Missense
PD34552	3	78.2	17	58700891	58700891	C	A	0.000	PPM1D	p.P161Q	Missense
PD34552	4	81.7	17	58700891	58700891	C	A	0.000	PPM1D	p.P161Q	Missense
PD34552	5	86.3	17	58700891	58700891	C	A	0.000	PPM1D	p.P161Q	Missense
PD34553	1	65.5	2	198267359	198267359	C	G	0.141	SF3B1	p.K666N	Missense
PD34553	2	68.9	2	198267359	198267359	C	G	0.215	SF3B1	p.K666N	Missense
PD34553	3	72.2	2	198267359	198267359	C	G	0.294	SF3B1	p.K666N	Missense
PD34553	4	75.7	2	198267359	198267359	C	G	0.319	SF3B1	p.K666N	Missense
PD34553	5	79.9	2	198267359	198267359	C	G	0.304	SF3B1	p.K666N	Missense
PD34553	1	65.5	4	106156694	106156694	T	A	0.008	TET2	p.L532X	Nonsense
PD34553	2	68.9	4	106156694	106156694	T	A	0.003	TET2	p.L532X	Nonsense
PD34553	3	72.2	4	106156694	106156694	T	A	0.001	TET2	p.L532X	Nonsense
PD34553	4	75.7	4	106156694	106156694	T	A	0.002	TET2	p.L532X	Nonsense
PD34553	5	79.9	4	106156694	106156694	T	A	0.005	TET2	p.L532X	Nonsense
PD34554	1	76.1	2	25458593	25458593	C	T	0.003	DNMT3A	p.W860X	Nonsense
PD34554	2	79.5	2	25458593	25458593	C	T	0.005	DNMT3A	p.W860X	Nonsense
PD34554	3	85.4	2	25458593	25458593	C	T	0.002	DNMT3A	p.W860X	Nonsense
PD34554	1	76.1	2	25463290	25463291	GG	G	0.006	DNMT3A	p.F734fs	Frameshift
PD34554	2	79.5	2	25463290	25463291	GG	G	0.001	DNMT3A	p.F734fs	Frameshift
PD34554	3	85.4	2	25463290	25463291	GG	G	0.007	DNMT3A	p.F734fs	Frameshift
PD34554	1	76.1	4	106157048	106157049	AT	A	0.060	TET2	p.H650fs	Frameshift
PD34554	2	79.5	4	106157048	106157049	AT	A	0.065	TET2	p.H650fs	Frameshift
PD34554	3	85.4	4	106157048	106157049	AT	A	0.047	TET2	p.H650fs	Frameshift
PD34554	1	76.1	4	106180823	106180826	CCTT	C	0.021	TET2	p.1284_1285 del	Inframe
PD34554	2	79.5	4	106180823	106180826	CCTT	C	0.028	TET2	p.1284_1285 del	Inframe

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34554	3	85.4	4	106180823	106180826	CCTT	C	0.055	TET2	p.1284_1285 del	Inframe
PD34554	1	76.1	4	106180908	106180909	TG	T	0.011	TET2	p.G1313fs	Frameshift
PD34554	2	79.5	4	106180908	106180909	TG	T	0.019	TET2	p.G1313fs	Frameshift
PD34554	3	85.4	4	106180908	106180909	TG	T	0.043	TET2	p.G1313fs	Frameshift
PD34554	1	76.1	16	67660481	67660481	T	C	0.000	CTCF	p.S461P	Missense
PD34554	2	79.5	16	67660481	67660481	T	C	0.003	CTCF	p.S461P	Missense
PD34554	3	85.4	16	67660481	67660481	T	C	0.010	CTCF	p.S461P	Missense
PD34556	1	76.0	1	1735939	1735939	G	T	0.000	GNB1	p.L117M	Missense
PD34556	2	79.2	1	1735939	1735939	G	T	0.000	GNB1	p.L117M	Missense
PD34556	3	82.8	1	1735939	1735939	G	T	0.001	GNB1	p.L117M	Missense
PD34556	4	86.2	1	1735939	1735939	G	T	0.007	GNB1	p.L117M	Missense
PD34556	5	90.5	1	1735939	1735939	G	T	0.000	GNB1	p.L117M	Missense
PD34556	1	76.0	2	25457283	25457283	A	C	0.011	DNMT3A	p.F868L	Missense
PD34556	2	79.2	2	25457283	25457283	A	C	0.009	DNMT3A	p.F868L	Missense
PD34556	3	82.8	2	25457283	25457283	A	C	0.008	DNMT3A	p.F868L	Missense
PD34556	4	86.2	2	25457283	25457283	A	C	0.011	DNMT3A	p.F868L	Missense
PD34556	5	90.5	2	25457283	25457283	A	C	0.004	DNMT3A	p.F868L	Missense
PD34556	1	76.0	2	25458594	25458594	C	T	0.000	DNMT3A	p.W860X	Nonsense
PD34556	2	79.2	2	25458594	25458594	C	T	0.000	DNMT3A	p.W860X	Nonsense
PD34556	3	82.8	2	25458594	25458594	C	T	0.003	DNMT3A	p.W860X	Nonsense
PD34556	4	86.2	2	25458594	25458594	C	T	0.007	DNMT3A	p.W860X	Nonsense
PD34556	5	90.5	2	25458594	25458594	C	T	0.007	DNMT3A	p.W860X	Nonsense
PD34556	1	76.0	4	106157607	106157608	CA	C	0.002	TET2	p.N837fs	Frameshift
PD34556	2	79.2	4	106157607	106157608	CA	C	0.000	TET2	p.N837fs	Frameshift
PD34556	3	82.8	4	106157607	106157608	CA	C	0.002	TET2	p.N837fs	Frameshift
PD34556	4	86.2	4	106157607	106157608	CA	C	0.001	TET2	p.N837fs	Frameshift
PD34556	5	90.5	4	106157607	106157608	CA	C	0.005	TET2	p.N837fs	Frameshift
PD34556	1	76.0	4	106158356	106158357	CT	C	0.000	TET2	p.T1086fs	Frameshift
PD34556	2	79.2	4	106158356	106158357	CT	C	0.002	TET2	p.T1086fs	Frameshift
PD34556	3	82.8	4	106158356	106158357	CT	C	0.004	TET2	p.T1086fs	Frameshift
PD34556	4	86.2	4	106158356	106158357	CT	C	0.002	TET2	p.T1086fs	Frameshift
PD34556	5	90.5	4	106158356	106158357	CT	C	0.013	TET2	p.T1086fs	Frameshift
PD34556	1	76.0	7	101747736	101747736	A	G	0.000	CUX1	p.E176G	Missense
PD34556	2	79.2	7	101747736	101747736	A	G	0.000	CUX1	p.E176G	Missense
PD34556	3	82.8	7	101747736	101747736	A	G	0.000	CUX1	p.E176G	Missense
PD34556	4	86.2	7	101747736	101747736	A	G	0.000	CUX1	p.E176G	Missense
PD34556	5	90.5	7	101747736	101747736	A	G	0.007	CUX1	p.E176G	Missense
PD34556	1	76.0	7	101892209	101892209	C	A	0.010	CUX1	p.R1469R	Synonymous
PD34556	2	79.2	7	101892209	101892209	C	A	0.000	CUX1	p.R1469R	Synonymous
PD34556	3	82.8	7	101892209	101892209	C	A	0.001	CUX1	p.R1469R	Synonymous
PD34556	4	86.2	7	101892209	101892209	C	A	0.003	CUX1	p.R1469R	Synonymous
PD34556	5	90.5	7	101892209	101892209	C	A	0.000	CUX1	p.R1469R	Synonymous
PD34556	1	76.0	17	58740446	58740446	G	T	0.000	PPM1D	p.E451X	Nonsense
PD34556	2	79.2	17	58740446	58740446	G	T	0.000	PPM1D	p.E451X	Nonsense
PD34556	3	82.8	17	58740446	58740446	G	T	0.004	PPM1D	p.E451X	Nonsense
PD34556	4	86.2	17	58740446	58740446	G	T	0.009	PPM1D	p.E451X	Nonsense
PD34556	5	90.5	17	58740446	58740446	G	T	0.006	PPM1D	p.E451X	Nonsense
PD34556	1	76.0	19	33793087	33793087	C	A	0.008	CEBPA	p.L78L	Synonymous
PD34556	2	79.2	19	33793087	33793087	C	A	0.000	CEBPA	p.L78L	Synonymous
PD34556	3	82.8	19	33793087	33793087	C	A	0.003	CEBPA	p.L78L	Synonymous
PD34556	4	86.2	19	33793087	33793087	C	A	0.000	CEBPA	p.L78L	Synonymous
PD34556	5	90.5	19	33793087	33793087	C	A	0.000	CEBPA	p.L78L	Synonymous
PD34558	1	72.9	2	198267359	198267359	C	A	0.001	SF3B1	p.K666N	Missense
PD34558	2	75.9	2	198267359	198267359	C	A	0.003	SF3B1	p.K666N	Missense
PD34558	3	79.8	2	198267359	198267359	C	A	0.000	SF3B1	p.K666N	Missense
PD34558	4	82.4	2	198267359	198267359	C	A	0.001	SF3B1	p.K666N	Missense
PD34558	5	86.8	2	198267359	198267359	C	A	0.005	SF3B1	p.K666N	Missense
PD34558	1	72.9	20	31023702	31023704	CAG	C	0.015	ASXL1	p.Q1063fs	Frameshift
PD34558	2	75.9	20	31023702	31023704	CAG	C	0.009	ASXL1	p.Q1063fs	Frameshift
PD34558	3	79.8	20	31023702	31023704	CAG	C	0.018	ASXL1	p.Q1063fs	Frameshift
PD34558	4	82.4	20	31023702	31023704	CAG	C	0.017	ASXL1	p.Q1063fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34558	5	86.8	20	31023702	31023704	CAG	C	0.012	ASXL1	p.Q1063fs	Frameshift
PD34559	1	85.0	2	198266605	198266605	G	T	0.069	SF3B1	p.A744D	Missense
PD34559	2	87.6	2	198266605	198266605	G	T	0.067	SF3B1	p.A744D	Missense
PD34559	3	93.9	2	198266605	198266605	G	T	0.102	SF3B1	p.A744D	Missense
PD34559	1	85.0	2	198266714	198266714	C	T	0.028	SF3B1	p.G740R	Missense
PD34559	2	87.6	2	198266714	198266714	C	T	0.036	SF3B1	p.G740R	Missense
PD34559	3	93.9	2	198266714	198266714	C	T	0.050	SF3B1	p.G740R	Missense
PD34559	1	85.0	4	106164762	106164766	GTGT	G	0.011	TET2	p.C1211fs	Frameshift
PD34559	2	87.6	4	106164762	106164766	GTGT	G	0.009	TET2	p.C1211fs	Frameshift
PD34559	3	93.9	4	106164762	106164766	GTGT	G	0.015	TET2	p.C1211fs	Frameshift
PD34559	1	85.0	4	106190899	106190899	A	G	0.006	TET2	p.T1393A	Missense
PD34559	2	87.6	4	106190899	106190899	A	G	0.009	TET2	p.T1393A	Missense
PD34559	3	93.9	4	106190899	106190899	A	G	0.021	TET2	p.T1393A	Missense
PD34559	1	85.0	16	3820766	3820766	G	A	0.005	CREBBP	p.S895S	Synonymous
PD34559	2	87.6	16	3820766	3820766	G	A	0.008	CREBBP	p.S895S	Synonymous
PD34559	3	93.9	16	3820766	3820766	G	A	0.002	CREBBP	p.S895S	Synonymous
PD34561	1	72.0	4	106157791	106157791	G	T	0.003	TET2	p.G898X	Nonsense
PD34561	2	75.1	4	106157791	106157791	G	T	0.004	TET2	p.G898X	Nonsense
PD34561	3	79.2	4	106157791	106157791	G	T	0.005	TET2	p.G898X	Nonsense
PD34561	4	82.3	4	106157791	106157791	G	T	0.018	TET2	p.G898X	Nonsense
PD34561	5	86.3	4	106157791	106157791	G	T	0.022	TET2	p.G898X	Nonsense
PD34561	1	72.0	4	106180838	106180838	G	T	0.006	TET2	p.C1289F	Missense
PD34561	2	75.1	4	106180838	106180838	G	T	0.006	TET2	p.C1289F	Missense
PD34561	3	79.2	4	106180838	106180838	G	T	0.024	TET2	p.C1289F	Missense
PD34561	4	82.3	4	106180838	106180838	G	T	0.034	TET2	p.C1289F	Missense
PD34561	5	86.3	4	106180838	106180838	G	T	0.041	TET2	p.C1289F	Missense
PD34561	1	72.0	7	101877362	101877362	G	T	0.000	CUX1	p.G1155V	Missense
PD34561	2	75.1	7	101877362	101877362	G	T	0.000	CUX1	p.G1155V	Missense
PD34561	3	79.2	7	101877362	101877362	G	T	0.000	CUX1	p.G1155V	Missense
PD34561	4	82.3	7	101877362	101877362	G	T	0.006	CUX1	p.G1155V	Missense
PD34561	5	86.3	7	101877362	101877362	G	T	0.000	CUX1	p.G1155V	Missense
PD34562	1	77.7	2	198267360	198267360	T	C	0.002	SF3B1	p.K666R	Missense
PD34562	2	80.8	2	198267360	198267360	T	C	0.003	SF3B1	p.K666R	Missense
PD34562	3	84.4	2	198267360	198267360	T	C	0.008	SF3B1	p.K666R	Missense
PD34562	1	77.7	2	209113112	209113112	C	T	0.001	IDH1	p.R132H	Missense
PD34562	2	80.8	2	209113112	209113112	C	T	0.035	IDH1	p.R132H	Missense
PD34562	3	84.4	2	209113112	209113112	C	T	0.120	IDH1	p.R132H	Missense
PD34562	1	77.7	7	148515099	148515099	G	C	0.005	EZH2	p.P370P	Synonymous
PD34562	2	80.8	7	148515099	148515099	G	C	0.001	EZH2	p.P370P	Synonymous
PD34562	3	84.4	7	148515099	148515099	G	C	0.000	EZH2	p.P370P	Synonymous
PD34562	1	77.7	17	74732935	74732959	CGGCGGCTGTGGTGTGAGTCCGGGG	C	0.171	SRSF2	p.95_103del	Inframe
PD34562	2	80.8	17	74732935	74732959	CGGCGGCTGTGGTGTGAGTCCGGGG	C	0.177	SRSF2	p.95_103del	Inframe
PD34562	3	84.4	17	74732935	74732959	CGGCGGCTGTGGTGTGAGTC	C	0.334	SRSF2	p.95_103del	Inframe

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
						CGGGG					
PD34562	1	77.7	17	58740432	58740432	C	A	0.010	PPM1D	p.S446X	Nonsense
PD34562	2	80.8	17	58740432	58740432	C	A	0.002	PPM1D	p.S446X	Nonsense
PD34562	3	84.4	17	58740432	58740432	C	A	0.001	PPM1D	p.S446X	Nonsense
PD34562	1	77.7	20	57484420	57484420	C	T	0.000	GNAS	p.R844C	Missense
PD34562	2	80.8	20	57484420	57484420	C	T	0.003	GNAS	p.R844C	Missense
PD34562	3	84.4	20	57484420	57484420	C	T	0.039	GNAS	p.R844C	Missense
PD34562	1	77.7	20	57484421	57484421	G	A	0.002	GNAS	p.R844H	Missense
PD34562	2	80.8	20	57484421	57484421	G	A	0.021	GNAS	p.R844H	Missense
PD34562	3	84.4	20	57484421	57484421	G	A	0.073	GNAS	p.R844H	Missense
PD34562	1	77.7	20	31023082	31023083	GC	G	0.012	ASXL1	p.C856fs	Frameshift
PD34562	2	80.8	20	31023082	31023083	GC	G	0.006	ASXL1	p.C856fs	Frameshift
PD34562	3	84.4	20	31023082	31023083	GC	G	0.011	ASXL1	p.C856fs	Frameshift
PD34562	1	77.7	X	15827408	15827408	A	G	0.012	ZRSR2	p.Y175C	Missense
PD34562	2	80.8	X	15827408	15827408	A	G	0.002	ZRSR2	p.Y175C	Missense
PD34562	3	84.4	X	15827408	15827408	A	G	0.000	ZRSR2	p.Y175C	Missense
PD34563	1	71.4	2	25463212	25463212	T	C	0.004	DNMT3A	p.M761V	Missense
PD34563	2	74.6	2	25463212	25463212	T	C	0.004	DNMT3A	p.M761V	Missense
PD34563	3	78.2	2	25463212	25463212	T	C	0.002	DNMT3A	p.M761V	Missense
PD34563	4	81.6	2	25463212	25463212	T	C	0.005	DNMT3A	p.M761V	Missense
PD34563	5	86.8	2	25463212	25463212	T	C	0.008	DNMT3A	p.M761V	Missense
PD34563	1	71.4	3	128200062	128200062	C	A	0.000	GATA2	p.E415X	Nonsense
PD34563	2	74.6	3	128200062	128200062	C	A	0.000	GATA2	p.E415X	Nonsense
PD34563	3	78.2	3	128200062	128200062	C	A	0.001	GATA2	p.E415X	Nonsense
PD34563	4	81.6	3	128200062	128200062	C	A	0.008	GATA2	p.E415X	Nonsense
PD34563	5	86.8	3	128200062	128200062	C	A	0.001	GATA2	p.E415X	Nonsense
PD34563	1	71.4	9	139402503	139402503	T	A	0.000	NOTCH1	p.T1138T	Synonymous
PD34563	2	74.6	9	139402503	139402503	T	A	0.000	NOTCH1	p.T1138T	Synonymous
PD34563	3	78.2	9	139402503	139402503	T	A	0.000	NOTCH1	p.T1138T	Synonymous
PD34563	4	81.6	9	139402503	139402503	T	A	0.000	NOTCH1	p.T1138T	Synonymous
PD34563	5	86.8	9	139402503	139402503	T	A	0.006	NOTCH1	p.T1138T	Synonymous
PD34563	1	71.4	17	7578493	7578493	C	T	0.000	TP53	p.W107X	Nonsense
PD34563	2	74.6	17	7578493	7578493	C	T	0.002	TP53	p.W107X	Nonsense
PD34563	3	78.2	17	7578493	7578493	C	T	0.001	TP53	p.W107X	Nonsense
PD34563	4	81.6	17	7578493	7578493	C	T	0.001	TP53	p.W107X	Nonsense
PD34563	5	86.8	17	7578493	7578493	C	T	0.006	TP53	p.W107X	Nonsense
PD34565	1	67.0	4	106157549	106157549	C	T	0.002	TET2	p.S817F	Missense
PD34565	2	70.4	4	106157549	106157549	C	T	0.002	TET2	p.S817F	Missense
PD34565	3	74.1	4	106157549	106157549	C	T	0.006	TET2	p.S817F	Missense
PD34565	4	77.0	4	106157549	106157549	C	T	0.008	TET2	p.S817F	Missense
PD34565	5	81.7	4	106157549	106157549	C	T	0.013	TET2	p.S817F	Missense
PD34565	1	67.0	4	106180904	106180904	T	A	0.006	TET2	p.L1311Q	Missense
PD34565	2	70.4	4	106180904	106180904	T	A	0.013	TET2	p.L1311Q	Missense
PD34565	3	74.1	4	106180904	106180904	T	A	0.013	TET2	p.L1311Q	Missense
PD34565	4	77.0	4	106180904	106180904	T	A	0.008	TET2	p.L1311Q	Missense
PD34565	5	81.7	4	106180904	106180904	T	A	0.014	TET2	p.L1311Q	Missense
PD34565	1	67.0	10	112343996	112343996	A	G	0.000	SMC3	p.S383G	Missense
PD34565	2	70.4	10	112343996	112343996	A	G	0.005	SMC3	p.S383G	Missense
PD34565	3	74.1	10	112343996	112343996	A	G	0.000	SMC3	p.S383G	Missense
PD34565	4	77.0	10	112343996	112343996	A	G	0.000	SMC3	p.S383G	Missense
PD34565	5	81.7	10	112343996	112343996	A	G	0.000	SMC3	p.S383G	Missense
PD34565	1	67.0	11	119144629	119144629	C	A	0.007	CBL	p.P214P	Synonymous
PD34565	2	70.4	11	119144629	119144629	C	A	0.000	CBL	p.P214P	Synonymous
PD34565	3	74.1	11	119144629	119144629	C	A	0.000	CBL	p.P214P	Synonymous
PD34565	4	77.0	11	119144629	119144629	C	A	0.002	CBL	p.P214P	Synonymous
PD34565	5	81.7	11	119144629	119144629	C	A	0.001	CBL	p.P214P	Synonymous
PD34565	1	67.0	X	129148310	129148311	TG	T	0.001	BCORL1	p.L521fs	Frameshift
PD34565	2	70.4	X	129148310	129148311	TG	T	0.004	BCORL1	p.L521fs	Frameshift
PD34565	3	74.1	X	129148310	129148311	TG	T	0.002	BCORL1	p.L521fs	Frameshift
PD34565	4	77.0	X	129148310	129148311	TG	T	0.005	BCORL1	p.L521fs	Frameshift
PD34565	5	81.7	X	129148310	129148311	TG	T	0.004	BCORL1	p.L521fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34566	1	67.6	4	106180835	106180835	G	T	0.000	TET2	p.G1288V	Missense
PD34566	2	70.5	4	106180835	106180835	G	T	0.002	TET2	p.G1288V	Missense
PD34566	3	74.0	4	106180835	106180835	G	T	0.003	TET2	p.G1288V	Missense
PD34566	4	77.0	4	106180835	106180835	G	T	0.007	TET2	p.G1288V	Missense
PD34566	5	81.3	4	106180835	106180835	G	T	0.004	TET2	p.G1288V	Missense
PD34566	1	67.6	4	106193785	106193785	A	G	0.012	TET2	p.H1416R	Missense
PD34566	2	70.5	4	106193785	106193785	A	G	0.005	TET2	p.H1416R	Missense
PD34566	3	74.0	4	106193785	106193785	A	G	0.011	TET2	p.H1416R	Missense
PD34566	4	77.0	4	106193785	106193785	A	G	0.007	TET2	p.H1416R	Missense
PD34566	5	81.3	4	106193785	106193785	A	G	0.011	TET2	p.H1416R	Missense
PD34566	1	67.6	12	112926852	112926852	C	T	0.002	PTPN11	p.P491L	Missense
PD34566	2	70.5	12	112926852	112926852	C	T	0.000	PTPN11	p.P491L	Missense
PD34566	3	74.0	12	112926852	112926852	C	T	0.005	PTPN11	p.P491L	Missense
PD34566	4	77.0	12	112926852	112926852	C	T	0.003	PTPN11	p.P491L	Missense
PD34566	5	81.3	12	112926852	112926852	C	T	0.010	PTPN11	p.P491L	Missense
PD34566	1	67.6	17	7578406	7578406	C	T	0.008	TP53	p.R136H	Missense
PD34566	2	70.5	17	7578406	7578406	C	T	0.003	TP53	p.R136H	Missense
PD34566	3	74.0	17	7578406	7578406	C	T	0.003	TP53	p.R136H	Missense
PD34566	4	77.0	17	7578406	7578406	C	T	0.000	TP53	p.R136H	Missense
PD34566	5	81.3	17	7578406	7578406	C	T	0.001	TP53	p.R136H	Missense
PD34567	1	69.0	17	58740467	58740467	C	T	0.021	PPM1D	p.R458X	Nonsense
PD34567	2	72.6	17	58740467	58740467	C	T	0.025	PPM1D	p.R458X	Nonsense
PD34567	3	76.3	17	58740467	58740467	C	T	0.020	PPM1D	p.R458X	Nonsense
PD34567	4	79.3	17	58740467	58740467	C	T	0.025	PPM1D	p.R458X	Nonsense
PD34567	5	84.5	17	58740467	58740467	C	T	0.015	PPM1D	p.R458X	Nonsense
PD34567	1	69.0	X	53407952	53407952	G	A	0.007	SMC1A	p.T1143I	Missense
PD34567	2	72.6	X	53407952	53407952	G	A	0.006	SMC1A	p.T1143I	Missense
PD34567	3	76.3	X	53407952	53407952	G	A	0.012	SMC1A	p.T1143I	Missense
PD34567	4	79.3	X	53407952	53407952	G	A	0.001	SMC1A	p.T1143I	Missense
PD34567	5	84.5	X	53407952	53407952	G	A	0.003	SMC1A	p.T1143I	Missense
PD34568	1	67.2	16	67645346	67645346	C	T	0.001	CTCF	p.T204I	Missense
PD34568	2	70.4	16	67645346	67645346	C	T	0.001	CTCF	p.T204I	Missense
PD34568	3	76.0	16	67645346	67645346	C	T	0.004	CTCF	p.T204I	Missense
PD34568	4	79.5	16	67645346	67645346	C	T	0.005	CTCF	p.T204I	Missense
PD34568	1	67.2	20	31025116	31025116	G	A	0.000	ASXL1	p.C1534Y	Missense
PD34568	2	70.4	20	31025116	31025116	G	A	0.000	ASXL1	p.C1534Y	Missense
PD34568	3	76.0	20	31025116	31025116	G	A	0.008	ASXL1	p.C1534Y	Missense
PD34568	4	79.5	20	31025116	31025116	G	A	0.000	ASXL1	p.C1534Y	Missense
PD34569	1	74.7	2	198267359	198267359	C	A	0.045	SF3B1	p.K666N	Missense
PD34569	2	77.7	2	198267359	198267359	C	A	0.068	SF3B1	p.K666N	Missense
PD34569	3	82.3	2	198267359	198267359	C	A	0.061	SF3B1	p.K666N	Missense
PD34569	1	74.7	2	25457194	25457194	A	G	0.016	DNMT3A	p.I898T	Missense
PD34569	2	77.7	2	25457194	25457194	A	G	0.009	DNMT3A	p.I898T	Missense
PD34569	3	82.3	2	25457194	25457194	A	G	0.008	DNMT3A	p.I898T	Missense
PD34569	1	74.7	2	25463588	25463588	C	T	0.031	DNMT3A	p.W698X	Nonsense
PD34569	2	77.7	2	25463588	25463588	C	T	0.061	DNMT3A	p.W698X	Nonsense
PD34569	3	82.3	2	25463588	25463588	C	T	0.098	DNMT3A	p.W698X	Nonsense
PD34569	1	74.7	11	119167662	119167663	AA	A	0.004	CBL	p.Q691fs	Frameshift
PD34569	2	77.7	11	119167662	119167663	AA	A	0.010	CBL	p.Q691fs	Frameshift
PD34569	3	82.3	11	119167662	119167663	AA	A	0.004	CBL	p.Q691fs	Frameshift
PD34570	1	70.7	2	25468912	25468913	GG	G	0.004	DNMT3A	p.R484fs	Frameshift
PD34570	2	74.5	2	25468912	25468913	GG	G	0.002	DNMT3A	p.R484fs	Frameshift
PD34570	3	78.3	2	25468912	25468913	GG	G	0.000	DNMT3A	p.R484fs	Frameshift
PD34570	4	81.0	2	25468912	25468913	GG	G	0.005	DNMT3A	p.R484fs	Frameshift
PD34570	1	70.7	4	106158181	106158182	AT	A	0.030	TET2	p.M1028fs	Frameshift
PD34570	2	74.5	4	106158181	106158182	AT	A	0.029	TET2	p.M1028fs	Frameshift
PD34570	3	78.3	4	106158181	106158182	AT	A	0.024	TET2	p.M1028fs	Frameshift
PD34570	4	81.0	4	106158181	106158182	AT	A	0.027	TET2	p.M1028fs	Frameshift
PD34570	1	70.7	7	101892232	101892232	G	T	0.000	CUX1	p.L1476L	Synonymous
PD34570	2	74.5	7	101892232	101892232	G	T	0.002	CUX1	p.L1476L	Synonymous
PD34570	3	78.3	7	101892232	101892232	G	T	0.006	CUX1	p.L1476L	Synonymous
PD34570	4	81.0	7	101892232	101892232	G	T	0.000	CUX1	p.L1476L	Synonymous

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34571	1	79.7	17	58740380	58740381	AG	A	0.004	PPM1D	p.R429fs	Frameshift
PD34571	2	82.7	17	58740380	58740381	AG	A	0.012	PPM1D	p.R429fs	Frameshift
PD34571	3	86.5	17	58740380	58740381	AG	A	0.016	PPM1D	p.R429fs	Frameshift
PD34573	1	74.7	2	25497819	25497819	C	A	0.003	DNMT3A	p.W210C	Missense
PD34573	2	77.7	2	25497819	25497819	C	A	0.001	DNMT3A	p.W210C	Missense
PD34573	3	83.2	2	25497819	25497819	C	A	0.002	DNMT3A	p.W210C	Missense
PD34573	4	87.3	2	25497819	25497819	C	A	0.011	DNMT3A	p.W210C	Missense
PD34574	1	72.2	12	50031354	50031354	G	T	0.000	PRPF40B	p.M554I	Missense
PD34574	2	75.2	12	50031354	50031354	G	T	0.001	PRPF40B	p.M554I	Missense
PD34574	3	78.7	12	50031354	50031354	G	T	0.006	PRPF40B	p.M554I	Missense
PD34574	4	82.1	12	50031354	50031354	G	T	0.001	PRPF40B	p.M554I	Missense
PD34574	1	72.2	20	57415425	57415425	C	G	0.021	GNAS	p.H88Q	Missense
PD34574	2	75.2	20	57415425	57415425	C	G	0.024	GNAS	p.H88Q	Missense
PD34574	3	78.7	20	57415425	57415425	C	G	0.015	GNAS	p.H88Q	Missense
PD34574	4	82.1	20	57415425	57415425	C	G	0.013	GNAS	p.H88Q	Missense
PD34575	1	81.8	2	198267359	198267359	C	G	0.003	SF3B1	p.K666N	Missense
PD34575	2	85.2	2	198267359	198267359	C	G	0.006	SF3B1	p.K666N	Missense
PD34575	3	90.9	2	198267359	198267359	C	G	0.012	SF3B1	p.K666N	Missense
PD34575	1	81.8	2	25463186	25463186	G	C	0.006	DNMT3A	p.I769M	Missense
PD34575	2	85.2	2	25463186	25463186	G	C	0.004	DNMT3A	p.I769M	Missense
PD34575	3	90.9	2	25463186	25463186	G	C	0.000	DNMT3A	p.I769M	Missense
PD34575	1	81.8	3	128202777	128202777	G	A	0.009	GATA2	p.L315L	Synonymous
PD34575	2	85.2	3	128202777	128202777	G	A	0.009	GATA2	p.L315L	Synonymous
PD34575	3	90.9	3	128202777	128202777	G	A	0.006	GATA2	p.L315L	Synonymous
PD34575	1	81.8	17	58740525	58740526	AT	A	0.002	PPM1D	p.N477fs	Frameshift
PD34575	2	85.2	17	58740525	58740526	AT	A	0.004	PPM1D	p.N477fs	Frameshift
PD34575	3	90.9	17	58740525	58740526	AT	A	0.016	PPM1D	p.N477fs	Frameshift
PD34575	1	81.8	X	133511741	133511741	C	G	0.009	PHF6	p.L32V	Missense
PD34575	2	85.2	X	133511741	133511741	C	G	0.007	PHF6	p.L32V	Missense
PD34575	3	90.9	X	133511741	133511741	C	G	0.004	PHF6	p.L32V	Missense
PD34576	1	70.1	2	198267359	198267359	C	G	0.008	SF3B1	p.K666N	Missense
PD34576	2	72.9	2	198267359	198267359	C	G	0.014	SF3B1	p.K666N	Missense
PD34576	3	76.7	2	198267359	198267359	C	G	0.025	SF3B1	p.K666N	Missense
PD34576	4	79.5	2	198267359	198267359	C	G	0.019	SF3B1	p.K666N	Missense
PD34576	1	70.1	4	106196726	106196726	C	T	0.003	TET2	p.Q1687X	Nonsense
PD34576	2	72.9	4	106196726	106196726	C	T	0.005	TET2	p.Q1687X	Nonsense
PD34576	3	76.7	4	106196726	106196726	C	T	0.007	TET2	p.Q1687X	Nonsense
PD34576	4	79.5	4	106196726	106196726	C	T	0.006	TET2	p.Q1687X	Nonsense
PD34576	1	70.1	7	101839919	101839919	G	A	0.010	CUX1	p.A410T	Missense
PD34576	2	72.9	7	101839919	101839919	G	A	0.000	CUX1	p.A410T	Missense
PD34576	3	76.7	7	101839919	101839919	G	A	0.000	CUX1	p.A410T	Missense
PD34576	4	79.5	7	101839919	101839919	G	A	0.000	CUX1	p.A410T	Missense
PD34577	1	80.1	2	25457230	25457230	T	C	0.015	DNMT3A	p.Q886R	Missense
PD34577	2	84.7	2	25457230	25457230	T	C	0.007	DNMT3A	p.Q886R	Missense
PD34577	3	89.8	2	25457230	25457230	T	C	0.004	DNMT3A	p.Q886R	Missense
PD34577	1	80.1	2	25470516	25470516	G	A	0.267	DNMT3A	p.R320X	Nonsense
PD34577	2	84.7	2	25470516	25470516	G	A	0.327	DNMT3A	p.R320X	Nonsense
PD34577	3	89.8	2	25470516	25470516	G	A	0.324	DNMT3A	p.R320X	Nonsense
PD34578	1	67.6	2	25536792	25536793	CC	C	0.000	DNMT3A	p.E21fs	Frameshift
PD34578	2	70.1	2	25536792	25536793	CC	C	0.005	DNMT3A	p.E21fs	Frameshift
PD34578	3	74.0	2	25536792	25536793	CC	C	0.026	DNMT3A	p.E21fs	Frameshift
PD34578	4	77.0	2	25536792	25536793	CC	C	0.009	DNMT3A	p.E21fs	Frameshift
PD34578	1	67.6	17	58734148	58734149	TA	T	0.011	PPM1D	p.S403fs	Frameshift
PD34578	2	70.1	17	58734148	58734149	TA	T	0.009	PPM1D	p.S403fs	Frameshift
PD34578	3	74.0	17	58734148	58734149	TA	T	0.011	PPM1D	p.S403fs	Frameshift
PD34578	4	77.0	17	58734148	58734149	TA	T	0.009	PPM1D	p.S403fs	Frameshift
PD34579	1	76.6	2	25458676	25458676	T	C	0.018	DNMT3A	p.I833V	Missense
PD34579	2	80.1	2	25458676	25458676	T	C	0.014	DNMT3A	p.I833V	Missense
PD34579	3	84.1	2	25458676	25458676	T	C	0.018	DNMT3A	p.I833V	Missense
PD34579	4	86.7	2	25458676	25458676	T	C	0.019	DNMT3A	p.I833V	Missense
PD34579	1	76.6	11	119149006	119149006	A	G	0.006	CBL	p.Q409R	Missense
PD34579	2	80.1	11	119149006	119149006	A	G	0.000	CBL	p.Q409R	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD34579	3	84.1	11	119149006	119149006	A	G	0.000	CBL	p.Q409R	Missense
PD34579	4	86.7	11	119149006	119149006	A	G	0.000	CBL	p.Q409R	Missense
PD34580	1	72.4	2	25464537	25464537	C	T	0.030	DNMT3A	p.R659H	Missense
PD34580	2	75.4	2	25464537	25464537	C	T	0.042	DNMT3A	p.R659H	Missense
PD34580	3	79.5	2	25464537	25464537	C	T	0.052	DNMT3A	p.R659H	Missense
PD34580	4	82.1	2	25464537	25464537	C	T	0.043	DNMT3A	p.R659H	Missense
PD34580	1	72.4	X	129149211	129149211	G	T	0.002	BCORL1	p.G821G	Synonymous
PD34580	2	75.4	X	129149211	129149211	G	T	0.001	BCORL1	p.G821G	Synonymous
PD34580	3	79.5	X	129149211	129149211	G	T	0.005	BCORL1	p.G821G	Synonymous
PD34580	4	82.1	X	129149211	129149211	G	T	0.004	BCORL1	p.G821G	Synonymous
PD41067	1	61.6	1	1720565	1720565	G	A	0.000	GNB1	p.S281S	Synonymous
PD41067	2	65.0	1	1720565	1720565	G	A	0.001	GNB1	p.S281S	Synonymous
PD41067	3	68.1	1	1720565	1720565	G	A	0.000	GNB1	p.S281S	Synonymous
PD41067	4	71.6	1	1720565	1720565	G	A	0.001	GNB1	p.S281S	Synonymous
PD41067	5	76.1	1	1720565	1720565	G	A	0.008	GNB1	p.S281S	Synonymous
PD41067	1	61.6	2	25470909	25470909	G	C	0.026	DNMT3A	p.Y284X	Nonsense
PD41067	2	65.0	2	25470909	25470909	G	C	0.037	DNMT3A	p.Y284X	Nonsense
PD41067	3	68.1	2	25470909	25470909	G	C	0.060	DNMT3A	p.Y284X	Nonsense
PD41067	4	71.6	2	25470909	25470909	G	C	0.053	DNMT3A	p.Y284X	Nonsense
PD41067	5	76.1	2	25470909	25470909	G	C	0.070	DNMT3A	p.Y284X	Nonsense
PD41067	1	61.6	17	58701055	58701055	G	T	0.000	PPM1D	p.D216Y	Missense
PD41067	2	65.0	17	58701055	58701055	G	T	0.000	PPM1D	p.D216Y	Missense
PD41067	3	68.1	17	58701055	58701055	G	T	0.005	PPM1D	p.D216Y	Missense
PD41067	4	71.6	17	58701055	58701055	G	T	0.001	PPM1D	p.D216Y	Missense
PD41067	5	76.1	17	58701055	58701055	G	T	0.000	PPM1D	p.D216Y	Missense
PD41067	1	61.6	X	39933465	39933465	T	C	0.000	BCOR	p.T378T	Synonymous
PD41067	2	65.0	X	39933465	39933465	T	C	0.000	BCOR	p.T378T	Synonymous
PD41067	3	68.1	X	39933465	39933465	T	C	0.003	BCOR	p.T378T	Synonymous
PD41067	4	71.6	X	39933465	39933465	T	C	0.001	BCOR	p.T378T	Synonymous
PD41067	5	76.1	X	39933465	39933465	T	C	0.000	BCOR	p.T378T	Synonymous
PD41068	1	65.1	1	43814986	43814986	C	T	0.022	MPL	p.V507V	Synonymous
PD41068	2	68.3	1	43814986	43814986	C	T	0.022	MPL	p.V507V	Synonymous
PD41068	3	72.0	1	43814986	43814986	C	T	0.014	MPL	p.V507V	Synonymous
PD41068	4	75.2	1	43814986	43814986	C	T	0.015	MPL	p.V507V	Synonymous
PD41068	1	65.1	20	31022708	31022708	A	G	0.000	ASXL1	p.L731L	Synonymous
PD41068	2	68.3	20	31022708	31022708	A	G	0.002	ASXL1	p.L731L	Synonymous
PD41068	3	72.0	20	31022708	31022708	A	G	0.003	ASXL1	p.L731L	Synonymous
PD41068	4	75.2	20	31022708	31022708	A	G	0.006	ASXL1	p.L731L	Synonymous
PD41070	1	64.7	2	25469633	25469633	G	A	0.007	DNMT3A	p.R379C	Missense
PD41070	2	67.8	2	25469633	25469633	G	A	0.005	DNMT3A	p.R379C	Missense
PD41070	3	74.1	2	25469633	25469633	G	A	0.017	DNMT3A	p.R379C	Missense
PD41070	4	77.8	2	25469633	25469633	G	A	0.010	DNMT3A	p.R379C	Missense
PD41070	1	64.7	4	106182926	106182926	T	C	0.008	TET2	p.L1322P	Missense
PD41070	2	67.8	4	106182926	106182926	T	C	0.007	TET2	p.L1322P	Missense
PD41070	3	74.1	4	106182926	106182926	T	C	0.016	TET2	p.L1322P	Missense
PD41070	4	77.8	4	106182926	106182926	T	C	0.012	TET2	p.L1322P	Missense
PD41070	1	64.7	7	101845151	101845151	A	T	0.015	CUX1	p.G858G	Synonymous
PD41070	2	67.8	7	101845151	101845151	A	T	0.016	CUX1	p.G858G	Synonymous
PD41070	3	74.1	7	101845151	101845151	A	T	0.026	CUX1	p.G858G	Synonymous
PD41070	4	77.8	7	101845151	101845151	A	T	0.025	CUX1	p.G858G	Synonymous
PD41071	1	65.7	4	106157088	106157089	CA	C	0.003	TET2	p.K664fs	Frameshift
PD41071	2	68.9	4	106157088	106157089	CA	C	0.001	TET2	p.K664fs	Frameshift
PD41071	3	72.5	4	106157088	106157089	CA	C	0.001	TET2	p.K664fs	Frameshift
PD41071	4	76.0	4	106157088	106157089	CA	C	0.001	TET2	p.K664fs	Frameshift
PD41071	5	80.8	4	106157088	106157089	CA	C	0.007	TET2	p.K664fs	Frameshift
PD41071	1	65.7	4	106164079	106164079	A	T	0.003	TET2	p.K1197X	Nonsense
PD41071	2	68.9	4	106164079	106164079	A	T	0.000	TET2	p.K1197X	Nonsense
PD41071	3	72.5	4	106164079	106164079	A	T	0.004	TET2	p.K1197X	Nonsense
PD41071	4	76.0	4	106164079	106164079	A	T	0.008	TET2	p.K1197X	Nonsense
PD41071	5	80.8	4	106164079	106164079	A	T	0.006	TET2	p.K1197X	Nonsense
PD41071	1	65.7	4	55594180	55594180	G	A	0.000	KIT	p.S624N	Missense
PD41071	2	68.9	4	55594180	55594180	G	A	0.000	KIT	p.S624N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41071	3	72.5	4	55594180	55594180	G	A	0.000	KIT	p.S624N	Missense
PD41071	4	76.0	4	55594180	55594180	G	A	0.001	KIT	p.S624N	Missense
PD41071	5	80.8	4	55594180	55594180	G	A	0.005	KIT	p.S624N	Missense
PD41071	1	65.7	17	7579473	7579473	G	A	0.011	TP53	p.P33S	Missense
PD41071	2	68.9	17	7579473	7579473	G	A	0.008	TP53	p.P33S	Missense
PD41071	3	72.5	17	7579473	7579473	G	A	0.009	TP53	p.P33S	Missense
PD41071	4	76.0	17	7579473	7579473	G	A	0.008	TP53	p.P33S	Missense
PD41071	5	80.8	17	7579473	7579473	G	A	0.017	TP53	p.P33S	Missense
PD41072	1	54.7	9	139438551	139438551	G	A	0.000	NOTCH1	p.P22L	Missense
PD41072	2	57.9	9	139438551	139438551	G	A	0.000	NOTCH1	p.P22L	Missense
PD41072	3	61.5	9	139438551	139438551	G	A	0.006	NOTCH1	p.P22L	Missense
PD41072	4	64.8	9	139438551	139438551	G	A	0.001	NOTCH1	p.P22L	Missense
PD41072	5	69.4	9	139438551	139438551	G	A	0.001	NOTCH1	p.P22L	Missense
PD41072	1	54.7	11	32410624	32410624	T	C	0.000	WT1	p.K512E	Missense
PD41072	2	57.9	11	32410624	32410624	T	C	0.000	WT1	p.K512E	Missense
PD41072	3	61.5	11	32410624	32410624	T	C	0.000	WT1	p.K512E	Missense
PD41072	4	64.8	11	32410624	32410624	T	C	0.006	WT1	p.K512E	Missense
PD41072	5	69.4	11	32410624	32410624	T	C	0.000	WT1	p.K512E	Missense
PD41073	1	77.5	2	25466782	25466784	AAA	A	0.001	DNMT3A	p.F640fs	Frameshift
PD41073	2	80.7	2	25466782	25466784	AAA	A	0.004	DNMT3A	p.F640fs	Frameshift
PD41073	3	84.5	2	25466782	25466784	AAA	A	0.006	DNMT3A	p.F640fs	Frameshift
PD41073	1	77.5	2	25466794	25466794	G	C	0.069	DNMT3A	p.L637V	Missense
PD41073	2	80.7	2	25466794	25466794	G	C	0.079	DNMT3A	p.L637V	Missense
PD41073	3	84.5	2	25466794	25466794	G	C	0.086	DNMT3A	p.L637V	Missense
PD41073	1	77.5	4	106196323	106196327	TCAG A	T	0.003	TET2	p.Q1553fs	Frameshift
PD41073	2	80.7	4	106196323	106196327	TCAG A	T	0.004	TET2	p.Q1553fs	Frameshift
PD41073	3	84.5	4	106196323	106196327	TCAG A	T	0.005	TET2	p.Q1553fs	Frameshift
PD41073	1	77.5	16	3824635	3824635	C	A	0.000	CREBBP	p.G740X	Nonsense
PD41073	2	80.7	16	3824635	3824635	C	A	0.000	CREBBP	p.G740X	Nonsense
PD41073	3	84.5	16	3824635	3824635	C	A	0.005	CREBBP	p.G740X	Nonsense
PD41073	1	77.5	17	58740521	58740521	G	T	0.004	PPM1D	p.E476X	Nonsense
PD41073	2	80.7	17	58740521	58740521	G	T	0.006	PPM1D	p.E476X	Nonsense
PD41073	3	84.5	17	58740521	58740521	G	T	0.014	PPM1D	p.E476X	Nonsense
PD41074	1	67.0	2	25466766	25466766	C	T	0.021	DNMT3A	c.1936+1G>A	Splice site
PD41074	2	70.1	2	25466766	25466766	C	T	0.009	DNMT3A	c.1936+1G>A	Splice site
PD41074	3	73.9	2	25466766	25466766	C	T	0.015	DNMT3A	c.1936+1G>A	Splice site
PD41074	4	77.3	2	25466766	25466766	C	T	0.017	DNMT3A	c.1936+1G>A	Splice site
PD41074	5	82.7	2	25466766	25466766	C	T	0.017	DNMT3A	c.1936+1G>A	Splice site
PD41074	1	67.0	9	139395289	139395289	G	A	0.052	NOTCH1	p.T1883T	Synonymous
PD41074	2	70.1	9	139395289	139395289	G	A	0.042	NOTCH1	p.T1883T	Synonymous
PD41074	3	73.9	9	139395289	139395289	G	A	0.032	NOTCH1	p.T1883T	Synonymous
PD41074	4	77.3	9	139395289	139395289	G	A	0.046	NOTCH1	p.T1883T	Synonymous
PD41074	5	82.7	9	139395289	139395289	G	A	0.025	NOTCH1	p.T1883T	Synonymous
PD41075	1	70.7	17	74732959	74732959	G	A	0.045	SRSF2	p.P95L	Missense
PD41075	2	73.8	17	74732959	74732959	G	A	0.078	SRSF2	p.P95L	Missense
PD41075	3	79.8	17	74732959	74732959	G	A	0.091	SRSF2	p.P95L	Missense
PD41077	1	69.3	2	25469029	25469029	C	T	0.146	DNMT3A	p.E477K	Missense
PD41077	2	72.4	2	25469029	25469029	C	T	0.130	DNMT3A	p.E477K	Missense
PD41077	3	76.1	2	25469029	25469029	C	T	0.134	DNMT3A	p.E477K	Missense
PD41077	4	79.5	2	25469029	25469029	C	T	0.158	DNMT3A	p.E477K	Missense
PD41077	1	69.3	2	25469071	25469073	CCG	C	0.001	DNMT3A	p.A462fs	Frameshift
PD41077	2	72.4	2	25469071	25469073	CCG	C	0.001	DNMT3A	p.A462fs	Frameshift
PD41077	3	76.1	2	25469071	25469073	CCG	C	0.008	DNMT3A	p.A462fs	Frameshift
PD41077	4	79.5	2	25469071	25469073	CCG	C	0.010	DNMT3A	p.A462fs	Frameshift
PD41077	1	69.3	X	154306952	154306952	A	C	0.001	BRCC3	p.H126P	Missense
PD41077	2	72.4	X	154306952	154306952	A	C	0.001	BRCC3	p.H126P	Missense
PD41077	3	76.1	X	154306952	154306952	A	C	0.007	BRCC3	p.H126P	Missense
PD41077	4	79.5	X	154306952	154306952	A	C	0.009	BRCC3	p.H126P	Missense
PD41078	1	62.8	2	25466799	25466799	C	T	0.126	DNMT3A	p.R635Q	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41078	2	65.9	2	25466799	25466799	C	T	0.142	DNMT3A	p.R635Q	Missense
PD41078	3	69.9	2	25466799	25466799	C	T	0.141	DNMT3A	p.R635Q	Missense
PD41078	4	73.1	2	25466799	25466799	C	T	0.157	DNMT3A	p.R635Q	Missense
PD41078	5	77.3	2	25466799	25466799	C	T	0.163	DNMT3A	p.R635Q	Missense
PD41078	1	62.8	4	106180796	106180796	G	A	0.010	TET2	p.G1275E	Missense
PD41078	2	65.9	4	106180796	106180796	G	A	0.015	TET2	p.G1275E	Missense
PD41078	3	69.9	4	106180796	106180796	G	A	0.010	TET2	p.G1275E	Missense
PD41078	4	73.1	4	106180796	106180796	G	A	0.007	TET2	p.G1275E	Missense
PD41078	5	77.3	4	106180796	106180796	G	A	0.010	TET2	p.G1275E	Missense
PD41078	1	62.8	17	7577556	7577556	C	A	0.001	TP53	p.C203F	Missense
PD41078	2	65.9	17	7577556	7577556	C	A	0.006	TP53	p.C203F	Missense
PD41078	3	69.9	17	7577556	7577556	C	A	0.007	TP53	p.C203F	Missense
PD41078	4	73.1	17	7577556	7577556	C	A	0.010	TP53	p.C203F	Missense
PD41078	5	77.3	17	7577556	7577556	C	A	0.009	TP53	p.C203F	Missense
PD41079	1	78.7	2	25463229	25463229	A	G	0.006	DNMT3A	p.F755S	Missense
PD41079	2	84.1	2	25463229	25463229	A	G	0.003	DNMT3A	p.F755S	Missense
PD41079	3	88.5	2	25463229	25463229	A	G	0.003	DNMT3A	p.F755S	Missense
PD41079	1	78.7	2	25467408	25467408	C	T	0.001	DNMT3A	c.1667+1G>A	Splice site
PD41079	2	84.1	2	25467408	25467408	C	T	0.007	DNMT3A	c.1667+1G>A	Splice site
PD41079	3	88.5	2	25467408	25467408	C	T	0.006	DNMT3A	c.1667+1G>A	Splice site
PD41079	1	78.7	16	3820620	3820620	G	C	0.001	CREBBP	p.S944X	Nonsense
PD41079	2	84.1	16	3820620	3820620	G	C	0.002	CREBBP	p.S944X	Nonsense
PD41079	3	88.5	16	3820620	3820620	G	C	0.037	CREBBP	p.S944X	Nonsense
PD41079	1	78.7	19	17945703	17945703	A	G	0.001	JAK3	p.F719F	Synonymous
PD41079	2	84.1	19	17945703	17945703	A	G	0.002	JAK3	p.F719F	Synonymous
PD41079	3	88.5	19	17945703	17945703	A	G	0.036	JAK3	p.F719F	Synonymous
PD41079	1	78.7	X	154348332	154348332	G	A	0.040	BRCC3	p.W286X	Nonsense
PD41079	2	84.1	X	154348332	154348332	G	A	0.041	BRCC3	p.W286X	Nonsense
PD41079	3	88.5	X	154348332	154348332	G	A	0.026	BRCC3	p.W286X	Nonsense
PD41080	1	60.6	4	106155793	106155793	C	T	0.003	TET2	p.Q232X	Nonsense
PD41080	2	63.8	4	106155793	106155793	C	T	0.006	TET2	p.Q232X	Nonsense
PD41080	3	67.6	4	106155793	106155793	C	T	0.002	TET2	p.Q232X	Nonsense
PD41080	4	70.8	4	106155793	106155793	C	T	0.006	TET2	p.Q232X	Nonsense
PD41080	5	75.1	4	106155793	106155793	C	T	0.004	TET2	p.Q232X	Nonsense
PD41080	1	60.6	4	106156362	106156363	AG	A	0.008	TET2	p.G422fs	Frameshift
PD41080	2	63.8	4	106156362	106156363	AG	A	0.014	TET2	p.G422fs	Frameshift
PD41080	3	67.6	4	106156362	106156363	AG	A	0.014	TET2	p.G422fs	Frameshift
PD41080	4	70.8	4	106156362	106156363	AG	A	0.012	TET2	p.G422fs	Frameshift
PD41080	5	75.1	4	106156362	106156363	AG	A	0.015	TET2	p.G422fs	Frameshift
PD41080	1	60.6	4	106197269	106197269	C	T	0.020	TET2	p.H1868Y	Missense
PD41080	2	63.8	4	106197269	106197269	C	T	0.025	TET2	p.H1868Y	Missense
PD41080	3	67.6	4	106197269	106197269	C	T	0.032	TET2	p.H1868Y	Missense
PD41080	4	70.8	4	106197269	106197269	C	T	0.033	TET2	p.H1868Y	Missense
PD41080	5	75.1	4	106197269	106197269	C	T	0.024	TET2	p.H1868Y	Missense
PD41080	1	60.6	17	7578403	7578403	C	A	0.008	TP53	p.C137F	Missense
PD41080	2	63.8	17	7578403	7578403	C	A	0.010	TP53	p.C137F	Missense
PD41080	3	67.6	17	7578403	7578403	C	A	0.012	TP53	p.C137F	Missense
PD41080	4	70.8	17	7578403	7578403	C	A	0.011	TP53	p.C137F	Missense
PD41080	5	75.1	17	7578403	7578403	C	A	0.005	TP53	p.C137F	Missense
PD41081	1	67.0	2	25463595	25463596	GG	G	0.002	DNMT3A	p.Q696fs	Frameshift
PD41081	2	70.1	2	25463595	25463596	GG	G	0.004	DNMT3A	p.Q696fs	Frameshift
PD41081	3	73.9	2	25463595	25463596	GG	G	0.004	DNMT3A	p.Q696fs	Frameshift
PD41081	4	77.2	2	25463595	25463596	GG	G	0.005	DNMT3A	p.Q696fs	Frameshift
PD41081	5	81.5	2	25463595	25463596	GG	G	0.008	DNMT3A	p.Q696fs	Frameshift
PD41081	1	67.0	17	7577120	7577120	C	T	0.006	TP53	p.R234H	Missense
PD41081	2	70.1	17	7577120	7577120	C	T	0.005	TP53	p.R234H	Missense
PD41081	3	73.9	17	7577120	7577120	C	T	0.007	TP53	p.R234H	Missense
PD41081	4	77.2	17	7577120	7577120	C	T	0.023	TP53	p.R234H	Missense
PD41081	5	81.5	17	7577120	7577120	C	T	0.018	TP53	p.R234H	Missense
PD41081	1	67.0	21	44514777	44514777	T	G	0.000	U2AF1	p.Q84P	Missense
PD41081	2	70.1	21	44514777	44514777	T	G	0.002	U2AF1	p.Q84P	Missense
PD41081	3	73.9	21	44514777	44514777	T	G	0.008	U2AF1	p.Q84P	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41081	4	77.2	21	44514777	44514777	T	G	0.030	U2AF1	p.Q84P	Missense
PD41081	5	81.5	21	44514777	44514777	T	G	0.039	U2AF1	p.Q84P	Missense
PD41082	1	56.5	1	1747229	1747229	T	C	0.002	GNB1	p.K57E	Missense
PD41082	2	59.7	1	1747229	1747229	T	C	0.000	GNB1	p.K57E	Missense
PD41082	3	63.5	1	1747229	1747229	T	C	0.006	GNB1	p.K57E	Missense
PD41082	4	66.6	1	1747229	1747229	T	C	0.013	GNB1	p.K57E	Missense
PD41082	5	71.0	1	1747229	1747229	T	C	0.015	GNB1	p.K57E	Missense
PD41082	1	56.5	2	198267359	198267359	C	A	0.000	SF3B1	p.K666N	Missense
PD41082	2	59.7	2	198267359	198267359	C	A	0.000	SF3B1	p.K666N	Missense
PD41082	3	63.5	2	198267359	198267359	C	A	0.015	SF3B1	p.K666N	Missense
PD41082	4	66.6	2	198267359	198267359	C	A	0.037	SF3B1	p.K666N	Missense
PD41082	5	71.0	2	198267359	198267359	C	A	0.071	SF3B1	p.K666N	Missense
PD41082	1	56.5	4	106156042	106156043	TC	T	0.002	TET2	p.S315fs	Frameshift
PD41082	2	59.7	4	106156042	106156043	TC	T	0.011	TET2	p.S315fs	Frameshift
PD41082	3	63.5	4	106156042	106156043	TC	T	0.020	TET2	p.S315fs	Frameshift
PD41082	4	66.6	4	106156042	106156043	TC	T	0.027	TET2	p.S315fs	Frameshift
PD41082	5	71.0	4	106156042	106156043	TC	T	0.032	TET2	p.S315fs	Frameshift
PD41082	1	56.5	4	106156403	106156404	AC	A	0.000	TET2	p.H435fs	Frameshift
PD41082	2	59.7	4	106156403	106156404	AC	A	0.004	TET2	p.H435fs	Frameshift
PD41082	3	63.5	4	106156403	106156404	AC	A	0.007	TET2	p.H435fs	Frameshift
PD41082	4	66.6	4	106156403	106156404	AC	A	0.012	TET2	p.H435fs	Frameshift
PD41082	5	71.0	4	106156403	106156404	AC	A	0.012	TET2	p.H435fs	Frameshift
PD41082	1	56.5	4	106180793	106180793	A	G	0.003	TET2	p.Q1274R	Missense
PD41082	2	59.7	4	106180793	106180793	A	G	0.008	TET2	p.Q1274R	Missense
PD41082	3	63.5	4	106180793	106180793	A	G	0.025	TET2	p.Q1274R	Missense
PD41082	4	66.6	4	106180793	106180793	A	G	0.023	TET2	p.Q1274R	Missense
PD41082	5	71.0	4	106180793	106180793	A	G	0.011	TET2	p.Q1274R	Missense
PD41082	1	56.5	4	106182926	106182926	T	A	0.000	TET2	p.L1322Q	Missense
PD41082	2	59.7	4	106182926	106182926	T	A	0.001	TET2	p.L1322Q	Missense
PD41082	3	63.5	4	106182926	106182926	T	A	0.000	TET2	p.L1322Q	Missense
PD41082	4	66.6	4	106182926	106182926	T	A	0.002	TET2	p.L1322Q	Missense
PD41082	5	71.0	4	106182926	106182926	T	A	0.013	TET2	p.L1322Q	Missense
PD41082	1	56.5	4	106196291	106196291	C	T	0.000	TET2	p.Q1542X	Nonsense
PD41082	2	59.7	4	106196291	106196291	C	T	0.002	TET2	p.Q1542X	Nonsense
PD41082	3	63.5	4	106196291	106196291	C	T	0.005	TET2	p.Q1542X	Nonsense
PD41082	4	66.6	4	106196291	106196291	C	T	0.011	TET2	p.Q1542X	Nonsense
PD41082	5	71.0	4	106196291	106196291	C	T	0.008	TET2	p.Q1542X	Nonsense
PD41082	1	56.5	4	106197140	106197140	C	T	0.288	TET2	p.Q1825X	Nonsense
PD41082	2	59.7	4	106197140	106197140	C	T	0.314	TET2	p.Q1825X	Nonsense
PD41082	3	63.5	4	106197140	106197140	C	T	0.320	TET2	p.Q1825X	Nonsense
PD41082	4	66.6	4	106197140	106197140	C	T	0.361	TET2	p.Q1825X	Nonsense
PD41082	5	71.0	4	106197140	106197140	C	T	0.338	TET2	p.Q1825X	Nonsense
PD41083	1	74.3	2	25470485	25470485	C	T	0.001	DNMT3A	p.W330X	Nonsense
PD41083	2	77.5	2	25470485	25470485	C	T	0.002	DNMT3A	p.W330X	Nonsense
PD41083	3	81.1	2	25470485	25470485	C	T	0.002	DNMT3A	p.W330X	Nonsense
PD41083	4	85.5	2	25470485	25470485	C	T	0.003	DNMT3A	p.W330X	Nonsense
PD41083	5	89.6	2	25470485	25470485	C	T	0.015	DNMT3A	p.W330X	Nonsense
PD41083	1	74.3	4	106156951	106156951	C	T	0.003	TET2	p.Q618X	Nonsense
PD41083	2	77.5	4	106156951	106156951	C	T	0.007	TET2	p.Q618X	Nonsense
PD41083	3	81.1	4	106156951	106156951	C	T	0.002	TET2	p.Q618X	Nonsense
PD41083	4	85.5	4	106156951	106156951	C	T	0.001	TET2	p.Q618X	Nonsense
PD41083	5	89.6	4	106156951	106156951	C	T	0.003	TET2	p.Q618X	Nonsense
PD41084	1	74.1	9	5073770	5073770	G	T	0.002	JAK2	p.V617F	Missense
PD41084	2	78.7	9	5073770	5073770	G	T	0.016	JAK2	p.V617F	Missense
PD41084	3	82.9	9	5073770	5073770	G	T	0.033	JAK2	p.V617F	Missense
PD41084	4	87.9	9	5073770	5073770	G	T	0.029	JAK2	p.V617F	Missense
PD41085	1	61.5	2	25463298	25463298	A	G	0.002	DNMT3A	p.F732S	Missense
PD41085	2	64.9	2	25463298	25463298	A	G	0.002	DNMT3A	p.F732S	Missense
PD41085	3	70.3	2	25463298	25463298	A	G	0.005	DNMT3A	p.F732S	Missense
PD41085	4	74.1	2	25463298	25463298	A	G	0.009	DNMT3A	p.F732S	Missense
PD41085	5	77.3	2	25463298	25463298	A	G	0.005	DNMT3A	p.F732S	Missense
PD41085	1	61.5	16	3828039	3828039	G	T	0.001	CREBBP	p.P696T	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41085	2	64.9	16	3828039	3828039	G	T	0.000	CREBBP	p.P696T	Missense
PD41085	3	70.3	16	3828039	3828039	G	T	0.005	CREBBP	p.P696T	Missense
PD41085	4	74.1	16	3828039	3828039	G	T	0.000	CREBBP	p.P696T	Missense
PD41085	5	77.3	16	3828039	3828039	G	T	0.001	CREBBP	p.P696T	Missense
PD41086	1	73.4	2	198266606	198266606	C	G	0.008	SF3B1	p.A744P	Missense
PD41086	2	76.7	2	198266606	198266606	C	G	0.004	SF3B1	p.A744P	Missense
PD41086	3	82.9	2	198266606	198266606	C	G	0.016	SF3B1	p.A744P	Missense
PD41086	4	86.5	2	198266606	198266606	C	G	0.018	SF3B1	p.A744P	Missense
PD41086	1	73.4	4	106196763	106196763	A	G	0.010	TET2	p.Q1699R	Missense
PD41086	2	76.7	4	106196763	106196763	A	G	0.005	TET2	p.Q1699R	Missense
PD41086	3	82.9	4	106196763	106196763	A	G	0.002	TET2	p.Q1699R	Missense
PD41086	4	86.5	4	106196763	106196763	A	G	0.007	TET2	p.Q1699R	Missense
PD41086	1	73.4	7	101821885	101821886	GC	G	0.001	CUX1	p.S322fs	Frameshift
PD41086	2	76.7	7	101821885	101821886	GC	G	0.000	CUX1	p.S322fs	Frameshift
PD41086	3	82.9	7	101821885	101821886	GC	G	0.007	CUX1	p.S322fs	Frameshift
PD41086	4	86.5	7	101821885	101821886	GC	G	0.000	CUX1	p.S322fs	Frameshift
PD41086	1	73.4	13	28597517	28597517	G	A	0.018	FLT3	p.A796A	Synonymous
PD41086	2	76.7	13	28597517	28597517	G	A	0.023	FLT3	p.A796A	Synonymous
PD41086	3	82.9	13	28597517	28597517	G	A	0.026	FLT3	p.A796A	Synonymous
PD41086	4	86.5	13	28597517	28597517	G	A	0.008	FLT3	p.A796A	Synonymous
PD41087	1	61.0	4	106158142	106158143	AG	A	0.061	TET2	p.S1015fs	Frameshift
PD41087	2	64.0	4	106158142	106158143	AG	A	0.046	TET2	p.S1015fs	Frameshift
PD41087	3	67.8	4	106158142	106158143	AG	A	0.026	TET2	p.S1015fs	Frameshift
PD41087	4	71.1	4	106158142	106158143	AG	A	0.004	TET2	p.S1015fs	Frameshift
PD41087	5	75.4	4	106158142	106158143	AG	A	0.000	TET2	p.S1015fs	Frameshift
PD41087	1	61.0	17	74732959	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41087	2	64.0	17	74732959	74732959	G	A	0.001	SRSF2	p.P95L	Missense
PD41087	3	67.8	17	74732959	74732959	G	A	0.006	SRSF2	p.P95L	Missense
PD41087	4	71.1	17	74732959	74732959	G	A	0.116	SRSF2	p.P95L	Missense
PD41087	5	75.4	17	74732959	74732959	G	A	0.016	SRSF2	p.P95L	Missense
PD41087	1	61.0	17	74732959	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41087	2	64.0	17	74732959	74732959	G	T	0.001	SRSF2	p.P95H	Missense
PD41087	3	67.8	17	74732959	74732959	G	T	0.002	SRSF2	p.P95H	Missense
PD41087	4	71.1	17	74732959	74732959	G	T	0.013	SRSF2	p.P95H	Missense
PD41087	5	75.4	17	74732959	74732959	G	T	0.292	SRSF2	p.P95H	Missense
PD41087	1	61.0	17	74733113	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	2	64.0	17	74733113	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	3	67.8	17	74733113	74733113	A	G	0.000	SRSF2	p.Y44H	Missense
PD41087	4	71.1	17	74733113	74733113	A	G	0.020	SRSF2	p.Y44H	Missense
PD41087	5	75.4	17	74733113	74733113	A	G	0.017	SRSF2	p.Y44H	Missense
PD41087	1	61.0	20	31023231	31023231	G	T	0.001	ASXL1	p.E906X	Nonsense
PD41087	2	64.0	20	31023231	31023231	G	T	0.001	ASXL1	p.E906X	Nonsense
PD41087	3	67.8	20	31023231	31023231	G	T	0.000	ASXL1	p.E906X	Nonsense
PD41087	4	71.1	20	31023231	31023231	G	T	0.001	ASXL1	p.E906X	Nonsense
PD41087	5	75.4	20	31023231	31023231	G	T	0.014	ASXL1	p.E906X	Nonsense
PD41087	1	61.0	X	53436412	53436412	C	T	0.300	SMC1A	p.R404Q	Missense
PD41087	2	64.0	X	53436412	53436412	C	T	0.322	SMC1A	p.R404Q	Missense
PD41087	3	67.8	X	53436412	53436412	C	T	0.357	SMC1A	p.R404Q	Missense
PD41087	4	71.1	X	53436412	53436412	C	T	0.378	SMC1A	p.R404Q	Missense
PD41087	5	75.4	X	53436412	53436412	C	T	0.390	SMC1A	p.R404Q	Missense
PD41087	1	61.0	X	133527665	133527665	G	A	0.000	PHF6	c.374+1G>A	Splice site
PD41087	2	64.0	X	133527665	133527665	G	A	0.000	PHF6	c.374+1G>A	Splice site
PD41087	3	67.8	X	133527665	133527665	G	A	0.002	PHF6	c.374+1G>A	Splice site
PD41087	4	71.1	X	133527665	133527665	G	A	0.029	PHF6	c.374+1G>A	Splice site
PD41087	5	75.4	X	133527665	133527665	G	A	0.056	PHF6	c.374+1G>A	Splice site
PD41088	1	90.4	11	119142447	119142447	G	A	0.004	CBL	p.R149Q	Missense
PD41088	3	99.2	11	119142447	119142447	G	A	0.014	CBL	p.R149Q	Missense
PD41088	1	90.4	17	7577124	7577124	C	T	0.012	TP53	p.V233M	Missense
PD41088	3	99.2	17	7577124	7577124	C	T	0.005	TP53	p.V233M	Missense
PD41089	1	70.5	2	25470498	25470498	G	T	0.008	DNMT3A	p.R326S	Missense
PD41089	2	73.8	2	25470498	25470498	G	T	0.012	DNMT3A	p.R326S	Missense
PD41089	3	77.8	2	25470498	25470498	G	T	0.008	DNMT3A	p.R326S	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41089	4	80.8	2	25470498	25470498	G	T	0.011	DNMT3A	p.R326S	Missense
PD41089	5	86.0	2	25470498	25470498	G	T	0.006	DNMT3A	p.R326S	Missense
PD41089	1	70.5	X	15833977	15833977	C	T	0.012	ZRSR2	p.P245P	Synonymous
PD41089	2	73.8	X	15833977	15833977	C	T	0.006	ZRSR2	p.P245P	Synonymous
PD41089	3	77.8	X	15833977	15833977	C	T	0.005	ZRSR2	p.P245P	Synonymous
PD41089	4	80.8	X	15833977	15833977	C	T	0.000	ZRSR2	p.P245P	Synonymous
PD41089	5	86.0	X	15833977	15833977	C	T	0.001	ZRSR2	p.P245P	Synonymous
PD41089	1	70.5	X	44942732	44942733	TA	T	0.016	KDM6A	p.K1157fs	Frameshift
PD41089	2	73.8	X	44942732	44942733	TA	T	0.042	KDM6A	p.K1157fs	Frameshift
PD41089	3	77.8	X	44942732	44942733	TA	T	0.048	KDM6A	p.K1157fs	Frameshift
PD41089	4	80.8	X	44942732	44942733	TA	T	0.067	KDM6A	p.K1157fs	Frameshift
PD41089	5	86.0	X	44942732	44942733	TA	T	0.053	KDM6A	p.K1157fs	Frameshift
PD41089	1	70.5	X	129149730	129149730	G	A	0.007	BCORL1	p.E994E	Synonymous
PD41089	2	73.8	X	129149730	129149730	G	A	0.009	BCORL1	p.E994E	Synonymous
PD41089	3	77.8	X	129149730	129149730	G	A	0.010	BCORL1	p.E994E	Synonymous
PD41089	4	80.8	X	129149730	129149730	G	A	0.007	BCORL1	p.E994E	Synonymous
PD41089	5	86.0	X	129149730	129149730	G	A	0.001	BCORL1	p.E994E	Synonymous
PD41090	1	64.6	1	36932318	36932318	G	T	0.005	CSF3R	p.T717T	Synonymous
PD41090	2	68.2	1	36932318	36932318	G	T	0.004	CSF3R	p.T717T	Synonymous
PD41090	3	71.9	1	36932318	36932318	G	T	0.008	CSF3R	p.T717T	Synonymous
PD41090	4	78.3	1	36932318	36932318	G	T	0.017	CSF3R	p.T717T	Synonymous
PD41090	1	64.6	7	101838829	101838829	C	A	0.013	CUX1	p.R390S	Missense
PD41090	2	68.2	7	101838829	101838829	C	A	0.008	CUX1	p.R390S	Missense
PD41090	3	71.9	7	101838829	101838829	C	A	0.006	CUX1	p.R390S	Missense
PD41090	4	78.3	7	101838829	101838829	C	A	0.018	CUX1	p.R390S	Missense
PD41090	1	64.6	X	44936071	44936071	C	T	0.001	KDM6A	p.Y996Y	Synonymous
PD41090	2	68.2	X	44936071	44936071	C	T	0.009	KDM6A	p.Y996Y	Synonymous
PD41090	3	71.9	X	44936071	44936071	C	T	0.001	KDM6A	p.Y996Y	Synonymous
PD41090	4	78.3	X	44936071	44936071	C	T	0.000	KDM6A	p.Y996Y	Synonymous
PD41091	1	67.9	10	112363018	112363018	C	T	0.004	SMC3	p.D1184D	Synonymous
PD41091	2	71.2	10	112363018	112363018	C	T	0.005	SMC3	p.D1184D	Synonymous
PD41091	3	74.7	10	112363018	112363018	C	T	0.012	SMC3	p.D1184D	Synonymous
PD41091	4	77.9	10	112363018	112363018	C	T	0.012	SMC3	p.D1184D	Synonymous
PD41091	5	83.4	10	112363018	112363018	C	T	0.019	SMC3	p.D1184D	Synonymous
PD41092	1	61.1	9	5073770	5073770	G	T	0.051	JAK2	p.V617F	Missense
PD41092	2	64.1	9	5073770	5073770	G	T	0.063	JAK2	p.V617F	Missense
PD41092	3	67.7	9	5073770	5073770	G	T	0.040	JAK2	p.V617F	Missense
PD41092	4	71.2	9	5073770	5073770	G	T	0.089	JAK2	p.V617F	Missense
PD41092	5	75.4	9	5073770	5073770	G	T	0.395	JAK2	p.V617F	Missense
PD41092	1	61.1	X	53432002	53432002	T	C	0.004	SMC1A	p.K691R	Missense
PD41092	2	64.1	X	53432002	53432002	T	C	0.004	SMC1A	p.K691R	Missense
PD41092	3	67.7	X	53432002	53432002	T	C	0.007	SMC1A	p.K691R	Missense
PD41092	4	71.2	X	53432002	53432002	T	C	0.009	SMC1A	p.K691R	Missense
PD41092	5	75.4	X	53432002	53432002	T	C	0.003	SMC1A	p.K691R	Missense
PD41092	1	61.1	X	44919918	44919918	A	G	0.000	KDM6A	p.Q465R	Missense
PD41092	2	64.1	X	44919918	44919918	A	G	0.000	KDM6A	p.Q465R	Missense
PD41092	3	67.7	X	44919918	44919918	A	G	0.001	KDM6A	p.Q465R	Missense
PD41092	4	71.2	X	44919918	44919918	A	G	0.006	KDM6A	p.Q465R	Missense
PD41092	5	75.4	X	44919918	44919918	A	G	0.000	KDM6A	p.Q465R	Missense
PD41093	1	78.2	9	139399891	139399891	G	A	0.007	NOTCH1	p.P1486L	Missense
PD41093	2	81.6	9	139399891	139399891	G	A	0.004	NOTCH1	p.P1486L	Missense
PD41093	3	87.0	9	139399891	139399891	G	A	0.005	NOTCH1	p.P1486L	Missense
PD41093	1	78.2	X	154317589	154317589	T	C	0.002	BRCC3	p.L152P	Missense
PD41093	2	81.6	X	154317589	154317589	T	C	0.000	BRCC3	p.L152P	Missense
PD41093	3	87.0	X	154317589	154317589	T	C	0.005	BRCC3	p.L152P	Missense
PD41095	1	61.7	2	25470590	25470590	A	G	0.003	DNMT3A	p.L295P	Missense
PD41095	2	64.9	2	25470590	25470590	A	G	0.003	DNMT3A	p.L295P	Missense
PD41095	3	68.4	2	25470590	25470590	A	G	0.005	DNMT3A	p.L295P	Missense
PD41095	4	71.7	2	25470590	25470590	A	G	0.010	DNMT3A	p.L295P	Missense
PD41095	5	76.4	2	25470590	25470590	A	G	0.015	DNMT3A	p.L295P	Missense
PD41096	1	76.2	X	129159151	129159151	G	A	0.006	BCORL1	p.R1292Q	Missense
PD41096	2	79.7	X	129159151	129159151	G	A	0.007	BCORL1	p.R1292Q	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41096	3	85.5	X	129159151	129159151	G	A	0.018	BCORL1	p.R1292Q	Missense
PD41097	1	63.8	10	89717739	89717739	T	G	0.006	PTEN	p.V428G	Missense
PD41097	2	66.7	10	89717739	89717739	T	G	0.008	PTEN	p.V428G	Missense
PD41097	3	71.0	10	89717739	89717739	T	G	0.006	PTEN	p.V428G	Missense
PD41097	4	73.9	10	89717739	89717739	T	G	0.005	PTEN	p.V428G	Missense
PD41097	5	79.4	10	89717739	89717739	T	G	0.004	PTEN	p.V428G	Missense
PD41097	1	63.8	12	12022745	12022749	CCGTG	C	0.000	ETV6	p.S284fs	Frameshift
PD41097	2	66.7	12	12022745	12022749	CCGTG	C	0.004	ETV6	p.S284fs	Frameshift
PD41097	3	71.0	12	12022745	12022749	CCGTG	C	0.015	ETV6	p.S284fs	Frameshift
PD41097	4	73.9	12	12022745	12022749	CCGTG	C	0.010	ETV6	p.S284fs	Frameshift
PD41097	5	79.4	12	12022745	12022749	CCGTG	C	0.023	ETV6	p.S284fs	Frameshift
PD41097	1	63.8	X	39932158	39932158	T	A	0.000	BCOR	p.D814V	Missense
PD41097	2	66.7	X	39932158	39932158	T	A	0.000	BCOR	p.D814V	Missense
PD41097	3	71.0	X	39932158	39932158	T	A	0.000	BCOR	p.D814V	Missense
PD41097	4	73.9	X	39932158	39932158	T	A	0.004	BCOR	p.D814V	Missense
PD41097	5	79.4	X	39932158	39932158	T	A	0.000	BCOR	p.D814V	Missense
PD41098	1	70.3	4	106155787	106155789	CTG	C	0.000	TET2	p.L230fs	Frameshift
PD41098	2	74.4	4	106155787	106155789	CTG	C	0.000	TET2	p.L230fs	Frameshift
PD41098	3	78.9	4	106155787	106155789	CTG	C	0.000	TET2	p.L230fs	Frameshift
PD41098	4	83.5	4	106155787	106155789	CTG	C	0.006	TET2	p.L230fs	Frameshift
PD41098	1	70.3	4	106156961	106156961	C	A	0.002	TET2	p.T621N	Missense
PD41098	2	74.4	4	106156961	106156961	C	A	0.003	TET2	p.T621N	Missense
PD41098	3	78.9	4	106156961	106156961	C	A	0.001	TET2	p.T621N	Missense
PD41098	4	83.5	4	106156961	106156961	C	A	0.011	TET2	p.T621N	Missense
PD41099	1	61.0	2	209113109	209113109	T	C	0.004	IDH1	p.H133R	Missense
PD41099	2	64.4	2	209113109	209113109	T	C	0.002	IDH1	p.H133R	Missense
PD41099	3	68.2	2	209113109	209113109	T	C	0.004	IDH1	p.H133R	Missense
PD41099	4	71.2	2	209113109	209113109	T	C	0.000	IDH1	p.H133R	Missense
PD41099	5	76.5	2	209113109	209113109	T	C	0.009	IDH1	p.H133R	Missense
PD41099	1	61.0	9	139399771	139399771	C	T	0.000	NOTCH1	p.G1526D	Missense
PD41099	2	64.4	9	139399771	139399771	C	T	0.000	NOTCH1	p.G1526D	Missense
PD41099	3	68.2	9	139399771	139399771	C	T	0.007	NOTCH1	p.G1526D	Missense
PD41099	4	71.2	9	139399771	139399771	C	T	0.000	NOTCH1	p.G1526D	Missense
PD41099	5	76.5	9	139399771	139399771	C	T	0.000	NOTCH1	p.G1526D	Missense
PD41099	1	61.0	17	7577121	7577121	G	C	0.000	TP53	p.R234G	Missense
PD41099	2	64.4	17	7577121	7577121	G	C	0.000	TP53	p.R234G	Missense
PD41099	3	68.2	17	7577121	7577121	G	C	0.001	TP53	p.R234G	Missense
PD41099	4	71.2	17	7577121	7577121	G	C	0.000	TP53	p.R234G	Missense
PD41099	5	76.5	17	7577121	7577121	G	C	0.008	TP53	p.R234G	Missense
PD41099	1	61.0	17	74732959	74732959	G	C	0.001	SRSF2	p.P95R	Missense
PD41099	2	64.4	17	74732959	74732959	G	C	0.002	SRSF2	p.P95R	Missense
PD41099	3	68.2	17	74732959	74732959	G	C	0.007	SRSF2	p.P95R	Missense
PD41099	4	71.2	17	74732959	74732959	G	C	0.002	SRSF2	p.P95R	Missense
PD41099	5	76.5	17	74732959	74732959	G	C	0.002	SRSF2	p.P95R	Missense
PD41101	1	63.2	4	106158301	106158301	C	T	0.002	TET2	p.Q1068X	Nonsense
PD41101	2	66.6	4	106158301	106158301	C	T	0.004	TET2	p.Q1068X	Nonsense
PD41101	3	70.3	4	106158301	106158301	C	T	0.008	TET2	p.Q1068X	Nonsense
PD41101	4	73.5	4	106158301	106158301	C	T	0.019	TET2	p.Q1068X	Nonsense
PD41101	5	79.2	4	106158301	106158301	C	T	0.020	TET2	p.Q1068X	Nonsense
PD41101	1	63.2	X	39914756	39914756	C	T	0.017	BCOR	p.D1502N	Missense
PD41101	2	66.6	X	39914756	39914756	C	T	0.011	BCOR	p.D1502N	Missense
PD41101	3	70.3	X	39914756	39914756	C	T	0.010	BCOR	p.D1502N	Missense
PD41101	4	73.5	X	39914756	39914756	C	T	0.011	BCOR	p.D1502N	Missense
PD41101	5	79.2	X	39914756	39914756	C	T	0.003	BCOR	p.D1502N	Missense
PD41102	1	74.5	17	74733199	74733200	GA	TC	0.013	SRSF2	c.43_44GA	Missense
PD41102	2	78.2	17	74733199	74733200	GA	TC	0.026	SRSF2	c.43_44GA	Missense
PD41102	3	81.5	17	74733199	74733200	GA	TC	0.064	SRSF2	c.43_44GA	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41102	1	74.5	19	33792251	33792251	C	A	0.006	CEBPA	p.C357F	Missense
PD41102	2	78.2	19	33792251	33792251	C	A	0.000	CEBPA	p.C357F	Missense
PD41102	3	81.5	19	33792251	33792251	C	A	0.002	CEBPA	p.C357F	Missense
PD41103	1	74.4	2	25457242	25457242	C	T	0.054	DNMT3A	p.R882H	Missense
PD41103	2	78.4	2	25457242	25457242	C	T	0.119	DNMT3A	p.R882H	Missense
PD41103	3	82.9	2	25457242	25457242	C	T	0.221	DNMT3A	p.R882H	Missense
PD41103	4	87.8	2	25457242	25457242	C	T	0.319	DNMT3A	p.R882H	Missense
PD41103	5	89.8	2	25457242	25457242	C	T	0.341	DNMT3A	p.R882H	Missense
PD41104	1	76.2	1	43815009	43815009	G	T	0.004	MPL	p.W515L	Missense
PD41104	2	79.2	1	43815009	43815009	G	T	0.005	MPL	p.W515L	Missense
PD41104	3	82.8	1	43815009	43815009	G	T	0.009	MPL	p.W515L	Missense
PD41104	4	86.4	1	43815009	43815009	G	T	0.029	MPL	p.W515L	Missense
PD41104	5	91.1	1	43815009	43815009	G	T	0.058	MPL	p.W515L	Missense
PD41104	1	76.2	1	1747229	1747229	T	C	0.367	GNB1	p.K57E	Missense
PD41104	2	79.2	1	1747229	1747229	T	C	0.362	GNB1	p.K57E	Missense
PD41104	3	82.8	1	1747229	1747229	T	C	0.365	GNB1	p.K57E	Missense
PD41104	4	86.4	1	1747229	1747229	T	C	0.439	GNB1	p.K57E	Missense
PD41104	5	91.1	1	1747229	1747229	T	C	0.393	GNB1	p.K57E	Missense
PD41104	1	76.2	2	25458661	25458661	T	C	0.344	DNMT3A	p.N838D	Missense
PD41104	2	79.2	2	25458661	25458661	T	C	0.364	DNMT3A	p.N838D	Missense
PD41104	3	82.8	2	25458661	25458661	T	C	0.412	DNMT3A	p.N838D	Missense
PD41104	4	86.4	2	25458661	25458661	T	C	0.399	DNMT3A	p.N838D	Missense
PD41104	5	91.1	2	25458661	25458661	T	C	0.381	DNMT3A	p.N838D	Missense
PD41105	1	77.2	4	106155308	106155308	A	G	0.039	TET2	p.Q70R	Missense
PD41105	2	80.6	4	106155308	106155308	A	G	0.046	TET2	p.Q70R	Missense
PD41105	3	84.3	4	106155308	106155308	A	G	0.080	TET2	p.Q70R	Missense
PD41105	4	87.5	4	106155308	106155308	A	G	0.079	TET2	p.Q70R	Missense
PD41105	1	77.2	4	106155399	106155416	ACCTTCTCTCTCTGGGCT	A	0.029	TET2	p.P101fs	Frameshift
PD41105	2	80.6	4	106155399	106155416	ACCTTCTCTCTCTGGGCT	A	0.039	TET2	p.P101fs	Frameshift
PD41105	3	84.3	4	106155399	106155416	ACCTTCTCTCTCTGGGCT	A	0.066	TET2	p.P101fs	Frameshift
PD41105	4	87.5	4	106155399	106155416	ACCTTCTCTCTCTGGGCT	A	0.054	TET2	p.P101fs	Frameshift
PD41105	1	77.2	20	31021102	31021102	A	G	0.006	ASXL1	p.K367K	Synonymous
PD41105	2	80.6	20	31021102	31021102	A	G	0.000	ASXL1	p.K367K	Synonymous
PD41105	3	84.3	20	31021102	31021102	A	G	0.000	ASXL1	p.K367K	Synonymous
PD41105	4	87.5	20	31021102	31021102	A	G	0.000	ASXL1	p.K367K	Synonymous
PD41106	1	66.5	2	25457164	25457164	T	C	0.003	DNMT3A	p.Y908C	Missense
PD41106	2	70.4	2	25457164	25457164	T	C	0.002	DNMT3A	p.Y908C	Missense
PD41106	3	74.3	2	25457164	25457164	T	C	0.009	DNMT3A	p.Y908C	Missense
PD41106	4	76.9	2	25457164	25457164	T	C	0.011	DNMT3A	p.Y908C	Missense
PD41106	5	81.9	2	25457164	25457164	T	C	0.020	DNMT3A	p.Y908C	Missense
PD41106	1	66.5	2	25458645	25458645	C	T	0.039	DNMT3A	p.G843D	Missense
PD41106	2	70.4	2	25458645	25458645	C	T	0.063	DNMT3A	p.G843D	Missense
PD41106	3	74.3	2	25458645	25458645	C	T	0.067	DNMT3A	p.G843D	Missense
PD41106	4	76.9	2	25458645	25458645	C	T	0.075	DNMT3A	p.G843D	Missense
PD41106	5	81.9	2	25458645	25458645	C	T	0.077	DNMT3A	p.G843D	Missense
PD41106	1	66.5	2	25466793	25466793	A	T	0.001	DNMT3A	p.L637Q	Missense
PD41106	2	70.4	2	25466793	25466793	A	T	0.003	DNMT3A	p.L637Q	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41106	3	74.3	2	25466793	25466793	A	T	0.005	DNMT3A	p.L637Q	Missense
PD41106	4	76.9	2	25466793	25466793	A	T	0.001	DNMT3A	p.L637Q	Missense
PD41106	5	81.9	2	25466793	25466793	A	T	0.006	DNMT3A	p.L637Q	Missense
PD41106	1	66.5	4	106193778	106193778	C	G	0.001	TET2	p.Q1414E	Missense
PD41106	2	70.4	4	106193778	106193778	C	G	0.003	TET2	p.Q1414E	Missense
PD41106	3	74.3	4	106193778	106193778	C	G	0.004	TET2	p.Q1414E	Missense
PD41106	4	76.9	4	106193778	106193778	C	G	0.007	TET2	p.Q1414E	Missense
PD41106	5	81.9	4	106193778	106193778	C	G	0.028	TET2	p.Q1414E	Missense
PD41106	1	66.5	7	148523603	148523603	G	T	0.004	EZH2	p.L284I	Missense
PD41106	2	70.4	7	148523603	148523603	G	T	0.006	EZH2	p.L284I	Missense
PD41106	3	74.3	7	148523603	148523603	G	T	0.005	EZH2	p.L284I	Missense
PD41106	4	76.9	7	148523603	148523603	G	T	0.008	EZH2	p.L284I	Missense
PD41106	5	81.9	7	148523603	148523603	G	T	0.013	EZH2	p.L284I	Missense
PD41106	1	66.5	20	31024394	31024395	TC	T	0.000	ASXL1	p.Q1294fs	Frameshift
PD41106	2	70.4	20	31024394	31024395	TC	T	0.002	ASXL1	p.Q1294fs	Frameshift
PD41106	3	74.3	20	31024394	31024395	TC	T	0.001	ASXL1	p.Q1294fs	Frameshift
PD41106	4	76.9	20	31024394	31024395	TC	T	0.005	ASXL1	p.Q1294fs	Frameshift
PD41106	5	81.9	20	31024394	31024395	TC	T	0.007	ASXL1	p.Q1294fs	Frameshift
PD41107	1	73.6	2	25463184	25463184	G	A	0.004	DNMT3A	p.S770L	Missense
PD41107	2	77.6	2	25463184	25463184	G	A	0.002	DNMT3A	p.S770L	Missense
PD41107	3	82.7	2	25463184	25463184	G	A	0.010	DNMT3A	p.S770L	Missense
PD41107	1	73.6	4	106164787	106164787	C	T	0.037	TET2	p.H1219Y	Missense
PD41107	2	77.6	4	106164787	106164787	C	T	0.060	TET2	p.H1219Y	Missense
PD41107	3	82.7	4	106164787	106164787	C	T	0.081	TET2	p.H1219Y	Missense
PD41107	1	73.6	20	31023834	31023834	C	A	0.000	ASXL1	p.L1107I	Missense
PD41107	2	77.6	20	31023834	31023834	C	A	0.000	ASXL1	p.L1107I	Missense
PD41107	3	82.7	20	31023834	31023834	C	A	0.008	ASXL1	p.L1107I	Missense
PD41107	1	73.6	X	39931642	39931642	G	T	0.006	BCOR	p.A986E	Missense
PD41107	2	77.6	X	39931642	39931642	G	T	0.000	BCOR	p.A986E	Missense
PD41107	3	82.7	X	39931642	39931642	G	T	0.000	BCOR	p.A986E	Missense
PD41108	1	60.9	2	25464507	25464507	G	A	0.004	DNMT3A	p.S669F	Missense
PD41108	2	64.1	2	25464507	25464507	G	A	0.006	DNMT3A	p.S669F	Missense
PD41108	3	67.8	2	25464507	25464507	G	A	0.009	DNMT3A	p.S669F	Missense
PD41108	4	70.8	2	25464507	25464507	G	A	0.023	DNMT3A	p.S669F	Missense
PD41108	5	76.0	2	25464507	25464507	G	A	0.016	DNMT3A	p.S669F	Missense
PD41108	1	60.9	2	25468887	25468888	CC	C	0.002	DNMT3A	c.1474+1G>-	Splice site
PD41108	2	64.1	2	25468887	25468888	CC	C	0.001	DNMT3A	c.1474+1G>-	Splice site
PD41108	3	67.8	2	25468887	25468888	CC	C	0.001	DNMT3A	c.1474+1G>-	Splice site
PD41108	4	70.8	2	25468887	25468888	CC	C	0.007	DNMT3A	c.1474+1G>-	Splice site
PD41108	5	76.0	2	25468887	25468888	CC	C	0.017	DNMT3A	c.1474+1G>-	Splice site
PD41108	1	60.9	2	25470497	25470497	C	G	0.010	DNMT3A	p.R326P	Missense
PD41108	2	64.1	2	25470497	25470497	C	G	0.011	DNMT3A	p.R326P	Missense
PD41108	3	67.8	2	25470497	25470497	C	G	0.013	DNMT3A	p.R326P	Missense
PD41108	4	70.8	2	25470497	25470497	C	G	0.023	DNMT3A	p.R326P	Missense
PD41108	5	76.0	2	25470497	25470497	C	G	0.024	DNMT3A	p.R326P	Missense
PD41108	1	60.9	4	106157123	106157123	C	A	0.001	TET2	p.S675X	Nonsense
PD41108	2	64.1	4	106157123	106157123	C	A	0.003	TET2	p.S675X	Nonsense
PD41108	3	67.8	4	106157123	106157123	C	A	0.003	TET2	p.S675X	Nonsense
PD41108	4	70.8	4	106157123	106157123	C	A	0.005	TET2	p.S675X	Nonsense
PD41108	5	76.0	4	106157123	106157123	C	A	0.008	TET2	p.S675X	Nonsense
PD41109	1	63.6	X	129149730	129149730	G	A	0.008	BCORL1	p.E994E	Synonymous
PD41109	2	67.1	X	129149730	129149730	G	A	0.003	BCORL1	p.E994E	Synonymous
PD41109	3	73.1	X	129149730	129149730	G	A	0.000	BCORL1	p.E994E	Synonymous
PD41109	4	76.3	X	129149730	129149730	G	A	0.000	BCORL1	p.E994E	Synonymous
PD41110	1	62.9	17	58740740	58740740	A	T	0.010	PPM1D	p.K549X	Nonsense
PD41110	2	66.0	17	58740740	58740740	A	T	0.007	PPM1D	p.K549X	Nonsense
PD41110	3	69.8	17	58740740	58740740	A	T	0.016	PPM1D	p.K549X	Nonsense
PD41110	4	72.8	17	58740740	58740740	A	T	0.021	PPM1D	p.K549X	Nonsense
PD41110	5	77.1	17	58740740	58740740	A	T	0.021	PPM1D	p.K549X	Nonsense
PD41110	1	62.9	20	57429526	57429526	T	C	0.006	GNAS	p.L340P	Missense
PD41110	2	66.0	20	57429526	57429526	T	C	0.001	GNAS	p.L340P	Missense
PD41110	3	69.8	20	57429526	57429526	T	C	0.001	GNAS	p.L340P	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41110	4	72.8	20	57429526	57429526	T	C	0.000	GNAS	p.L340P	Missense
PD41110	5	77.1	20	57429526	57429526	T	C	0.002	GNAS	p.L340P	Missense
PD41112	1	73.7	2	25457242	25457242	C	T	0.021	DNMT3A	p.R882H	Missense
PD41112	2	76.8	2	25457242	25457242	C	T	0.021	DNMT3A	p.R882H	Missense
PD41112	3	80.6	2	25457242	25457242	C	T	0.020	DNMT3A	p.R882H	Missense
PD41112	4	84.2	2	25457242	25457242	C	T	0.015	DNMT3A	p.R882H	Missense
PD41112	5	88.2	2	25457242	25457242	C	T	0.008	DNMT3A	p.R882H	Missense
PD41112	1	73.7	11	119148968	119148968	T	G	0.002	CBL	p.C396W	Missense
PD41112	2	76.8	11	119148968	119148968	T	G	0.003	CBL	p.C396W	Missense
PD41112	3	80.6	11	119148968	119148968	T	G	0.008	CBL	p.C396W	Missense
PD41112	4	84.2	11	119148968	119148968	T	G	0.011	CBL	p.C396W	Missense
PD41112	5	88.2	11	119148968	119148968	T	G	0.004	CBL	p.C396W	Missense
PD41112	1	73.7	11	119169251	119169251	G	A	0.002	CBL	c.2434+1G>A	Splice site
PD41112	2	76.8	11	119169251	119169251	G	A	0.004	CBL	c.2434+1G>A	Splice site
PD41112	3	80.6	11	119169251	119169251	G	A	0.004	CBL	c.2434+1G>A	Splice site
PD41112	4	84.2	11	119169251	119169251	G	A	0.009	CBL	c.2434+1G>A	Splice site
PD41112	5	88.2	11	119169251	119169251	G	A	0.004	CBL	c.2434+1G>A	Splice site
PD41113	1	74.0	2	25457242	25457242	C	T	0.006	DNMT3A	p.R882H	Missense
PD41113	2	78.1	2	25457242	25457242	C	T	0.005	DNMT3A	p.R882H	Missense
PD41113	3	83.0	2	25457242	25457242	C	T	0.013	DNMT3A	p.R882H	Missense
PD41113	4	87.4	2	25457242	25457242	C	T	0.006	DNMT3A	p.R882H	Missense
PD41114	1	56.4	2	25463286	25463286	C	T	0.003	DNMT3A	p.R736H	Missense
PD41114	2	59.7	2	25463286	25463286	C	T	0.008	DNMT3A	p.R736H	Missense
PD41114	3	63.6	2	25463286	25463286	C	T	0.009	DNMT3A	p.R736H	Missense
PD41114	4	66.4	2	25463286	25463286	C	T	0.012	DNMT3A	p.R736H	Missense
PD41114	5	71.4	2	25463286	25463286	C	T	0.012	DNMT3A	p.R736H	Missense
PD41114	1	56.4	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD41114	2	59.7	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD41114	3	63.6	9	5073770	5073770	G	T	0.006	JAK2	p.V617F	Missense
PD41114	4	66.4	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD41114	5	71.4	9	5073770	5073770	G	T	0.006	JAK2	p.V617F	Missense
PD41115	1	72.6	16	67660563	67660563	C	G	0.003	CTCF	p.S488X	Nonsense
PD41115	2	75.8	16	67660563	67660563	C	G	0.002	CTCF	p.S488X	Nonsense
PD41115	3	79.2	16	67660563	67660563	C	G	0.001	CTCF	p.S488X	Nonsense
PD41115	4	82.6	16	67660563	67660563	C	G	0.005	CTCF	p.S488X	Nonsense
PD41115	5	88.0	16	67660563	67660563	C	G	0.007	CTCF	p.S488X	Nonsense
PD41115	1	72.6	17	74732959	74732959	G	A	0.005	SRSF2	p.P95L	Missense
PD41115	2	75.8	17	74732959	74732959	G	A	0.011	SRSF2	p.P95L	Missense
PD41115	3	79.2	17	74732959	74732959	G	A	0.005	SRSF2	p.P95L	Missense
PD41115	4	82.6	17	74732959	74732959	G	A	0.005	SRSF2	p.P95L	Missense
PD41115	5	88.0	17	74732959	74732959	G	A	0.027	SRSF2	p.P95L	Missense
PD41115	1	72.6	19	56170666	56170666	G	A	0.005	U2AF2	p.R47H	Missense
PD41115	2	75.8	19	56170666	56170666	G	A	0.005	U2AF2	p.R47H	Missense
PD41115	3	79.2	19	56170666	56170666	G	A	0.004	U2AF2	p.R47H	Missense
PD41115	4	82.6	19	56170666	56170666	G	A	0.009	U2AF2	p.R47H	Missense
PD41115	5	88.0	19	56170666	56170666	G	A	0.005	U2AF2	p.R47H	Missense
PD41117	1	72.8	4	106156279	106156279	G	A	0.000	TET2	p.A394T	Missense
PD41117	2	76.7	4	106156279	106156279	G	A	0.002	TET2	p.A394T	Missense
PD41117	3	82.1	4	106156279	106156279	G	A	0.000	TET2	p.A394T	Missense
PD41117	4	85.9	4	106156279	106156279	G	A	0.007	TET2	p.A394T	Missense
PD41117	1	72.8	4	106190819	106190819	G	A	0.023	TET2	p.R1366H	Missense
PD41117	2	76.7	4	106190819	106190819	G	A	0.042	TET2	p.R1366H	Missense
PD41117	3	82.1	4	106190819	106190819	G	A	0.084	TET2	p.R1366H	Missense
PD41117	4	85.9	4	106190819	106190819	G	A	0.039	TET2	p.R1366H	Missense
PD41117	1	72.8	4	106197285	106197285	T	C	0.000	TET2	p.I1873T	Missense
PD41117	2	76.7	4	106197285	106197285	T	C	0.004	TET2	p.I1873T	Missense
PD41117	3	82.1	4	106197285	106197285	T	C	0.043	TET2	p.I1873T	Missense
PD41117	4	85.9	4	106197285	106197285	T	C	0.163	TET2	p.I1873T	Missense
PD41117	1	72.8	7	140453193	140453193	T	A	0.000	BRAF	p.N581I	Missense
PD41117	2	76.7	7	140453193	140453193	T	A	0.000	BRAF	p.N581I	Missense
PD41117	3	82.1	7	140453193	140453193	T	A	0.008	BRAF	p.N581I	Missense
PD41117	4	85.9	7	140453193	140453193	T	A	0.016	BRAF	p.N581I	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41117	1	72.8	9	139412251	139412251	G	T	0.000	NOTCH1	p.A465D	Missense
PD41117	2	76.7	9	139412251	139412251	G	T	0.001	NOTCH1	p.A465D	Missense
PD41117	3	82.1	9	139412251	139412251	G	T	0.000	NOTCH1	p.A465D	Missense
PD41117	4	85.9	9	139412251	139412251	G	T	0.008	NOTCH1	p.A465D	Missense
PD41117	1	72.8	20	57429247	57429247	C	T	0.000	GNAS	p.S247L	Missense
PD41117	2	76.7	20	57429247	57429247	C	T	0.001	GNAS	p.S247L	Missense
PD41117	3	82.1	20	57429247	57429247	C	T	0.009	GNAS	p.S247L	Missense
PD41117	4	85.9	20	57429247	57429247	C	T	0.009	GNAS	p.S247L	Missense
PD41118	1	69.1	2	25468933	25468934	CC	C	0.001	DNMT3A	c.1430-1G>-	Splice site
PD41118	2	73.0	2	25468933	25468934	CC	C	0.002	DNMT3A	c.1430-1G>-	Splice site
PD41118	3	78.5	2	25468933	25468934	CC	C	0.008	DNMT3A	c.1430-1G>-	Splice site
PD41118	4	82.3	2	25468933	25468934	CC	C	0.004	DNMT3A	c.1430-1G>-	Splice site
PD41118	1	69.1	2	25469613	25469614	CG	C	0.097	DNMT3A	p.P385fs	Frameshift
PD41118	2	73.0	2	25469613	25469614	CG	C	0.117	DNMT3A	p.P385fs	Frameshift
PD41118	3	78.5	2	25469613	25469614	CG	C	0.114	DNMT3A	p.P385fs	Frameshift
PD41118	4	82.3	2	25469613	25469614	CG	C	0.113	DNMT3A	p.P385fs	Frameshift
PD41118	1	69.1	2	25469941	25469941	T	G	0.020	DNMT3A	p.K367N	Missense
PD41118	2	73.0	2	25469941	25469941	T	G	0.014	DNMT3A	p.K367N	Missense
PD41118	3	78.5	2	25469941	25469941	T	G	0.016	DNMT3A	p.K367N	Missense
PD41118	4	82.3	2	25469941	25469941	T	G	0.008	DNMT3A	p.K367N	Missense
PD41118	1	69.1	4	106155653	106155654	AG	A	0.019	TET2	p.Q185fs	Frameshift
PD41118	2	73.0	4	106155653	106155654	AG	A	0.009	TET2	p.Q185fs	Frameshift
PD41118	3	78.5	4	106155653	106155654	AG	A	0.015	TET2	p.Q185fs	Frameshift
PD41118	4	82.3	4	106155653	106155654	AG	A	0.014	TET2	p.Q185fs	Frameshift
PD41118	1	69.1	4	106155660	106155661	GA	G	0.024	TET2	p.K188fs	Frameshift
PD41118	2	73.0	4	106155660	106155661	GA	G	0.012	TET2	p.K188fs	Frameshift
PD41118	3	78.5	4	106155660	106155661	GA	G	0.015	TET2	p.K188fs	Frameshift
PD41118	4	82.3	4	106155660	106155661	GA	G	0.018	TET2	p.K188fs	Frameshift
PD41118	1	69.1	16	3779344	3779344	T	C	0.003	CREBBP	p.T1902A	Missense
PD41118	2	73.0	16	3779344	3779344	T	C	0.010	CREBBP	p.T1902A	Missense
PD41118	3	78.5	16	3779344	3779344	T	C	0.020	CREBBP	p.T1902A	Missense
PD41118	4	82.3	16	3779344	3779344	T	C	0.006	CREBBP	p.T1902A	Missense
PD41118	1	69.1	X	154300619	154300619	G	A	0.000	BRCC3	c.140+1G>A	Splice site
PD41118	2	73.0	X	154300619	154300619	G	A	0.000	BRCC3	c.140+1G>A	Splice site
PD41118	3	78.5	X	154300619	154300619	G	A	0.020	BRCC3	c.140+1G>A	Splice site
PD41118	4	82.3	X	154300619	154300619	G	A	0.012	BRCC3	c.140+1G>A	Splice site
PD41119	1	66.5	2	25463190	25463190	T	C	0.005	DNMT3A	p.D768G	Missense
PD41119	2	69.8	2	25463190	25463190	T	C	0.009	DNMT3A	p.D768G	Missense
PD41119	3	73.5	2	25463190	25463190	T	C	0.007	DNMT3A	p.D768G	Missense
PD41119	4	77.5	2	25463190	25463190	T	C	0.005	DNMT3A	p.D768G	Missense
PD41119	5	81.5	2	25463190	25463190	T	C	0.005	DNMT3A	p.D768G	Missense
PD41119	1	66.5	12	50037492	50037492	C	A	0.000	PRPF40B	p.A800D	Missense
PD41119	2	69.8	12	50037492	50037492	C	A	0.008	PRPF40B	p.A800D	Missense
PD41119	3	73.5	12	50037492	50037492	C	A	0.001	PRPF40B	p.A800D	Missense
PD41119	4	77.5	12	50037492	50037492	C	A	0.001	PRPF40B	p.A800D	Missense
PD41119	5	81.5	12	50037492	50037492	C	A	0.000	PRPF40B	p.A800D	Missense
PD41120	1	58.3	4	106157329	106157329	C	T	0.002	TET2	p.Q744X	Nonsense
PD41120	2	61.0	4	106157329	106157329	C	T	0.002	TET2	p.Q744X	Nonsense
PD41120	3	64.6	4	106157329	106157329	C	T	0.004	TET2	p.Q744X	Nonsense
PD41120	4	68.6	4	106157329	106157329	C	T	0.017	TET2	p.Q744X	Nonsense
PD41120	5	73.0	4	106157329	106157329	C	T	0.000	TET2	p.Q744X	Nonsense
PD41120	1	58.3	4	106196267	106196267	C	T	0.003	TET2	p.Q1534X	Nonsense
PD41120	2	61.0	4	106196267	106196267	C	T	0.000	TET2	p.Q1534X	Nonsense
PD41120	3	64.6	4	106196267	106196267	C	T	0.004	TET2	p.Q1534X	Nonsense
PD41120	4	68.6	4	106196267	106196267	C	T	0.006	TET2	p.Q1534X	Nonsense
PD41120	5	73.0	4	106196267	106196267	C	T	0.006	TET2	p.Q1534X	Nonsense
PD41120	1	58.3	7	148544373	148544373	C	A	0.000	EZH2	p.K6N	Missense
PD41120	2	61.0	7	148544373	148544373	C	A	0.000	EZH2	p.K6N	Missense
PD41120	3	64.6	7	148544373	148544373	C	A	0.006	EZH2	p.K6N	Missense
PD41120	4	68.6	7	148544373	148544373	C	A	0.000	EZH2	p.K6N	Missense
PD41120	5	73.0	7	148544373	148544373	C	A	0.000	EZH2	p.K6N	Missense
PD41120	1	58.3	20	31023555	31023556	AG	A	0.000	ASXL1	p.S1014fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41120	2	61.0	20	31023555	31023556	AG	A	0.004	ASXL1	p.S1014fs	Frameshift
PD41120	3	64.6	20	31023555	31023556	AG	A	0.003	ASXL1	p.S1014fs	Frameshift
PD41120	4	68.6	20	31023555	31023556	AG	A	0.006	ASXL1	p.S1014fs	Frameshift
PD41120	5	73.0	20	31023555	31023556	AG	A	0.003	ASXL1	p.S1014fs	Frameshift
PD41120	1	58.3	X	15827434	15827434	G	A	0.000	ZRSR2	p.G184R	Missense
PD41120	2	61.0	X	15827434	15827434	G	A	0.001	ZRSR2	p.G184R	Missense
PD41120	3	64.6	X	15827434	15827434	G	A	0.003	ZRSR2	p.G184R	Missense
PD41120	4	68.6	X	15827434	15827434	G	A	0.000	ZRSR2	p.G184R	Missense
PD41120	5	73.0	X	15827434	15827434	G	A	0.000	ZRSR2	p.G184R	Missense
PD41121	1	81.3	4	106157474	106157474	C	G	0.001	TET2	p.S792X	Nonsense
PD41121	2	85.2	4	106157474	106157474	C	G	0.006	TET2	p.S792X	Nonsense
PD41121	3	90.1	4	106157474	106157474	C	G	0.012	TET2	p.S792X	Nonsense
PD41121	1	81.3	4	106196902	106196902	C	T	0.000	TET2	p.S1745S	Synonymous
PD41121	2	85.2	4	106196902	106196902	C	T	0.000	TET2	p.S1745S	Synonymous
PD41121	3	90.1	4	106196902	106196902	C	T	0.007	TET2	p.S1745S	Synonymous
PD41121	1	81.3	X	44920577	44920577	T	C	0.000	KDM6A	p.S498S	Synonymous
PD41121	2	85.2	X	44920577	44920577	T	C	0.006	KDM6A	p.S498S	Synonymous
PD41121	3	90.1	X	44920577	44920577	T	C	0.000	KDM6A	p.S498S	Synonymous
PD41122	1	65.5	2	25469083	25469084	CC	C	0.005	DNMT3A	p.R458fs	Frameshift
PD41122	2	68.7	2	25469083	25469084	CC	C	0.007	DNMT3A	p.R458fs	Frameshift
PD41122	3	72.6	2	25469083	25469084	CC	C	0.013	DNMT3A	p.R458fs	Frameshift
PD41122	4	75.4	2	25469083	25469084	CC	C	0.022	DNMT3A	p.R458fs	Frameshift
PD41122	5	79.6	2	25469083	25469084	CC	C	0.039	DNMT3A	p.R458fs	Frameshift
PD41122	1	65.5	16	3779157	3779157	C	T	0.005	CREBBP	p.R1964H	Missense
PD41122	2	68.7	16	3779157	3779157	C	T	0.006	CREBBP	p.R1964H	Missense
PD41122	3	72.6	16	3779157	3779157	C	T	0.013	CREBBP	p.R1964H	Missense
PD41122	4	75.4	16	3779157	3779157	C	T	0.022	CREBBP	p.R1964H	Missense
PD41122	5	79.6	16	3779157	3779157	C	T	0.038	CREBBP	p.R1964H	Missense
PD41122	1	65.5	20	57484427	57484427	T	C	0.002	GNAS	p.L846P	Missense
PD41122	2	68.7	20	57484427	57484427	T	C	0.005	GNAS	p.L846P	Missense
PD41122	3	72.6	20	57484427	57484427	T	C	0.022	GNAS	p.L846P	Missense
PD41122	4	75.4	20	57484427	57484427	T	C	0.019	GNAS	p.L846P	Missense
PD41122	5	79.6	20	57484427	57484427	T	C	0.019	GNAS	p.L846P	Missense
PD41123	1	64.6	2	25470533	25470533	C	T	0.012	DNMT3A	p.W314X	Nonsense
PD41123	2	67.6	2	25470533	25470533	C	T	0.001	DNMT3A	p.W314X	Nonsense
PD41123	3	71.6	2	25470533	25470533	C	T	0.015	DNMT3A	p.W314X	Nonsense
PD41123	4	74.5	2	25470533	25470533	C	T	0.012	DNMT3A	p.W314X	Nonsense
PD41123	5	80.4	2	25470533	25470533	C	T	0.047	DNMT3A	p.W314X	Nonsense
PD41123	1	64.6	20	31024563	31024563	C	T	0.044	ASXL1	p.Q1350X	Nonsense
PD41123	2	67.6	20	31024563	31024563	C	T	0.051	ASXL1	p.Q1350X	Nonsense
PD41123	3	71.6	20	31024563	31024563	C	T	0.042	ASXL1	p.Q1350X	Nonsense
PD41123	4	74.5	20	31024563	31024563	C	T	0.032	ASXL1	p.Q1350X	Nonsense
PD41123	5	80.4	20	31024563	31024563	C	T	0.051	ASXL1	p.Q1350X	Nonsense
PD41124	1	74.1	4	106156048	106156048	C	T	0.010	TET2	p.Q317X	Nonsense
PD41124	2	76.8	4	106156048	106156048	C	T	0.007	TET2	p.Q317X	Nonsense
PD41124	3	80.5	4	106156048	106156048	C	T	0.004	TET2	p.Q317X	Nonsense
PD41124	4	84.0	4	106156048	106156048	C	T	0.006	TET2	p.Q317X	Nonsense
PD41124	5	88.5	4	106156048	106156048	C	T	0.010	TET2	p.Q317X	Nonsense
PD41124	1	74.1	4	106157929	106157929	A	T	0.001	TET2	p.K944X	Nonsense
PD41124	2	76.8	4	106157929	106157929	A	T	0.003	TET2	p.K944X	Nonsense
PD41124	3	80.5	4	106157929	106157929	A	T	0.007	TET2	p.K944X	Nonsense
PD41124	4	84.0	4	106157929	106157929	A	T	0.003	TET2	p.K944X	Nonsense
PD41124	5	88.5	4	106157929	106157929	A	T	0.008	TET2	p.K944X	Nonsense
PD41124	1	74.1	4	106180785	106180785	C	A	0.001	TET2	p.C1271X	Nonsense
PD41124	2	76.8	4	106180785	106180785	C	A	0.000	TET2	p.C1271X	Nonsense
PD41124	3	80.5	4	106180785	106180785	C	A	0.001	TET2	p.C1271X	Nonsense
PD41124	4	84.0	4	106180785	106180785	C	A	0.006	TET2	p.C1271X	Nonsense
PD41124	5	88.5	4	106180785	106180785	C	A	0.001	TET2	p.C1271X	Nonsense
PD41124	1	74.1	7	101917530	101917530	C	A	0.002	CUX1	p.R465S	Missense
PD41124	2	76.8	7	101917530	101917530	C	A	0.002	CUX1	p.R465S	Missense
PD41124	3	80.5	7	101917530	101917530	C	A	0.000	CUX1	p.R465S	Missense
PD41124	4	84.0	7	101917530	101917530	C	A	0.007	CUX1	p.R465S	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41124	5	88.5	7	101917530	101917530	C	A	0.001	CUX1	p.R465S	Missense
PD41124	1	74.1	17	7578388	7578388	C	G	0.006	TP53	p.R142P	Missense
PD41124	2	76.8	17	7578388	7578388	C	G	0.003	TP53	p.R142P	Missense
PD41124	3	80.5	17	7578388	7578388	C	G	0.005	TP53	p.R142P	Missense
PD41124	4	84.0	17	7578388	7578388	C	G	0.009	TP53	p.R142P	Missense
PD41124	5	88.5	17	7578388	7578388	C	G	0.005	TP53	p.R142P	Missense
PD41125	1	64.5	1	36937220	36937220	G	A	0.011	CSF3R	p.R367W	Missense
PD41125	2	67.6	1	36937220	36937220	G	A	0.011	CSF3R	p.R367W	Missense
PD41125	3	70.9	1	36937220	36937220	G	A	0.014	CSF3R	p.R367W	Missense
PD41125	4	74.2	1	36937220	36937220	G	A	0.010	CSF3R	p.R367W	Missense
PD41125	5	78.5	1	36937220	36937220	G	A	0.012	CSF3R	p.R367W	Missense
PD41125	1	64.5	16	67644930	67644930	G	T	0.008	CTCF	p.Q65H	Missense
PD41125	2	67.6	16	67644930	67644930	G	T	0.000	CTCF	p.Q65H	Missense
PD41125	3	70.9	16	67644930	67644930	G	T	0.001	CTCF	p.Q65H	Missense
PD41125	4	74.2	16	67644930	67644930	G	T	0.000	CTCF	p.Q65H	Missense
PD41125	5	78.5	16	67644930	67644930	G	T	0.001	CTCF	p.Q65H	Missense
PD41126	1	59.1	11	32456703	32456703	C	T	0.001	WT1	p.G63G	Synonymous
PD41126	2	61.9	11	32456703	32456703	C	T	0.000	WT1	p.G63G	Synonymous
PD41126	3	65.7	11	32456703	32456703	C	T	0.000	WT1	p.G63G	Synonymous
PD41126	4	68.8	11	32456703	32456703	C	T	0.000	WT1	p.G63G	Synonymous
PD41126	5	73.0	11	32456703	32456703	C	T	0.010	WT1	p.G63G	Synonymous
PD41127	1	75.4	4	106197285	106197285	T	C	0.004	TET2	p.I1873T	Missense
PD41127	2	78.4	4	106197285	106197285	T	C	0.008	TET2	p.I1873T	Missense
PD41127	3	81.6	4	106197285	106197285	T	C	0.015	TET2	p.I1873T	Missense
PD41127	4	85.1	4	106197285	106197285	T	C	0.013	TET2	p.I1873T	Missense
PD41127	1	75.4	4	106197294	106197294	C	T	0.008	TET2	p.A1876V	Missense
PD41127	2	78.4	4	106197294	106197294	C	T	0.004	TET2	p.A1876V	Missense
PD41127	3	81.6	4	106197294	106197294	C	T	0.005	TET2	p.A1876V	Missense
PD41127	4	85.1	4	106197294	106197294	C	T	0.009	TET2	p.A1876V	Missense
PD41127	1	75.4	7	148511201	148511202	CC	C	0.001	EZH2	p.C567fs	Frameshift
PD41127	2	78.4	7	148511201	148511202	CC	C	0.002	EZH2	p.C567fs	Frameshift
PD41127	3	81.6	7	148511201	148511202	CC	C	0.003	EZH2	p.C567fs	Frameshift
PD41127	4	85.1	7	148511201	148511202	CC	C	0.005	EZH2	p.C567fs	Frameshift
PD41128	1	81.7	2	25458692	25458692	G	A	0.001	DNMT3A	p.F827F	Synonymous
PD41128	2	85.1	2	25458692	25458692	G	A	0.001	DNMT3A	p.F827F	Synonymous
PD41128	3	90.0	2	25458692	25458692	G	A	0.008	DNMT3A	p.F827F	Synonymous
PD41128	1	81.7	2	25464573	25464573	A	C	0.034	DNMT3A	p.L647R	Missense
PD41128	2	85.1	2	25464573	25464573	A	C	0.051	DNMT3A	p.L647R	Missense
PD41128	3	90.0	2	25464573	25464573	A	C	0.079	DNMT3A	p.L647R	Missense
PD41128	1	81.7	4	106164913	106164913	C	T	0.009	TET2	p.R1261C	Missense
PD41128	2	85.1	4	106164913	106164913	C	T	0.013	TET2	p.R1261C	Missense
PD41128	3	90.0	4	106164913	106164913	C	T	0.008	TET2	p.R1261C	Missense
PD41129	1	63.1	2	25464528	25464528	G	C	0.005	DNMT3A	p.A662G	Missense
PD41129	2	67.9	2	25464528	25464528	G	C	0.005	DNMT3A	p.A662G	Missense
PD41129	3	71.0	2	25464528	25464528	G	C	0.015	DNMT3A	p.A662G	Missense
PD41129	4	73.6	2	25464528	25464528	G	C	0.006	DNMT3A	p.A662G	Missense
PD41129	5	77.8	2	25464528	25464528	G	C	0.019	DNMT3A	p.A662G	Missense
PD41129	1	63.1	11	118343886	118343886	G	T	0.001	KMT2A	p.G671V	Missense
PD41129	2	67.9	11	118343886	118343886	G	T	0.002	KMT2A	p.G671V	Missense
PD41129	3	71.0	11	118343886	118343886	G	T	0.006	KMT2A	p.G671V	Missense
PD41129	4	73.6	11	118343886	118343886	G	T	0.006	KMT2A	p.G671V	Missense
PD41129	5	77.8	11	118343886	118343886	G	T	0.006	KMT2A	p.G671V	Missense
PD41130	1	76.2	16	67650735	67650735	A	G	0.007	CTCF	p.H347R	Missense
PD41130	2	79.4	16	67650735	67650735	A	G	0.016	CTCF	p.H347R	Missense
PD41130	3	82.6	16	67650735	67650735	A	G	0.014	CTCF	p.H347R	Missense
PD41130	4	86.0	16	67650735	67650735	A	G	0.016	CTCF	p.H347R	Missense
PD41130	1	76.2	17	58740438	58740439	AT	A	0.187	PPM1D	p.N448fs	Frameshift
PD41130	2	79.4	17	58740438	58740439	AT	A	0.231	PPM1D	p.N448fs	Frameshift
PD41130	3	82.6	17	58740438	58740439	AT	A	0.275	PPM1D	p.N448fs	Frameshift
PD41130	4	86.0	17	58740438	58740439	AT	A	0.294	PPM1D	p.N448fs	Frameshift
PD41130	1	76.2	X	123190021	123190021	T	A	0.000	STAG2	p.Y414N	Missense
PD41130	2	79.4	X	123190021	123190021	T	A	0.000	STAG2	p.Y414N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41130	3	82.6	X	123190021	123190021	T	A	0.000	STAG2	p.Y414N	Missense
PD41130	4	86.0	X	123190021	123190021	T	A	0.006	STAG2	p.Y414N	Missense
PD41131	1	72.7	4	55561793	55561793	G	A	0.011	KIT	p.P61P	Synonymous
PD41131	2	75.8	4	55561793	55561793	G	A	0.010	KIT	p.P61P	Synonymous
PD41131	3	78.8	4	55561793	55561793	G	A	0.002	KIT	p.P61P	Synonymous
PD41131	4	82.8	4	55561793	55561793	G	A	0.002	KIT	p.P61P	Synonymous
PD41131	5	86.9	4	55561793	55561793	G	A	0.000	KIT	p.P61P	Synonymous
PD41131	1	72.7	16	3819335	3819335	C	A	0.000	CREBBP	p.S967I	Missense
PD41131	2	75.8	16	3819335	3819335	C	A	0.007	CREBBP	p.S967I	Missense
PD41131	3	78.8	16	3819335	3819335	C	A	0.000	CREBBP	p.S967I	Missense
PD41131	4	82.8	16	3819335	3819335	C	A	0.000	CREBBP	p.S967I	Missense
PD41131	5	86.9	16	3819335	3819335	C	A	0.000	CREBBP	p.S967I	Missense
PD41131	1	72.7	17	7578371	7578371	C	T	0.006	TP53	p.G148S	Missense
PD41131	2	75.8	17	7578371	7578371	C	T	0.005	TP53	p.G148S	Missense
PD41131	3	78.8	17	7578371	7578371	C	T	0.003	TP53	p.G148S	Missense
PD41131	4	82.8	17	7578371	7578371	C	T	0.006	TP53	p.G148S	Missense
PD41131	5	86.9	17	7578371	7578371	C	T	0.000	TP53	p.G148S	Missense
PD41132	1	62.7	1	1747229	1747229	T	C	0.002	GNB1	p.K57E	Missense
PD41132	2	65.8	1	1747229	1747229	T	C	0.005	GNB1	p.K57E	Missense
PD41132	3	69.5	1	1747229	1747229	T	C	0.007	GNB1	p.K57E	Missense
PD41132	4	72.4	1	1747229	1747229	T	C	0.006	GNB1	p.K57E	Missense
PD41132	5	78.2	1	1747229	1747229	T	C	0.002	GNB1	p.K57E	Missense
PD41132	1	62.7	4	106196264	106196264	A	T	0.003	TET2	p.K1533X	Nonsense
PD41132	2	65.8	4	106196264	106196264	A	T	0.002	TET2	p.K1533X	Nonsense
PD41132	3	69.5	4	106196264	106196264	A	T	0.007	TET2	p.K1533X	Nonsense
PD41132	4	72.4	4	106196264	106196264	A	T	0.002	TET2	p.K1533X	Nonsense
PD41132	5	78.2	4	106196264	106196264	A	T	0.004	TET2	p.K1533X	Nonsense
PD41132	1	62.7	7	101758534	101758534	G	T	0.006	CUX1	p.D219Y	Missense
PD41132	2	65.8	7	101758534	101758534	G	T	0.000	CUX1	p.D219Y	Missense
PD41132	3	69.5	7	101758534	101758534	G	T	0.000	CUX1	p.D219Y	Missense
PD41132	4	72.4	7	101758534	101758534	G	T	0.001	CUX1	p.D219Y	Missense
PD41132	5	78.2	7	101758534	101758534	G	T	0.002	CUX1	p.D219Y	Missense
PD41133	1	61.3	17	7579408	7579408	C	T	0.000	TP53	p.L54L	Synonymous
PD41133	2	64.4	17	7579408	7579408	C	T	0.007	TP53	p.L54L	Synonymous
PD41133	3	68.1	17	7579408	7579408	C	T	0.001	TP53	p.L54L	Synonymous
PD41133	4	71.0	17	7579408	7579408	C	T	0.002	TP53	p.L54L	Synonymous
PD41133	5	75.1	17	7579408	7579408	C	T	0.000	TP53	p.L54L	Synonymous
PD41133	1	61.3	X	44949125	44949125	A	G	0.004	KDM6A	p.Q1281R	Missense
PD41133	2	64.4	X	44949125	44949125	A	G	0.000	KDM6A	p.Q1281R	Missense
PD41133	3	68.1	X	44949125	44949125	A	G	0.001	KDM6A	p.Q1281R	Missense
PD41133	4	71.0	X	44949125	44949125	A	G	0.000	KDM6A	p.Q1281R	Missense
PD41133	5	75.1	X	44949125	44949125	A	G	0.000	KDM6A	p.Q1281R	Missense
PD41134	1	76.9	4	106157355	106157356	TA	T	0.005	TET2	p.K753fs	Frameshift
PD41134	2	80.2	4	106157355	106157356	TA	T	0.007	TET2	p.K753fs	Frameshift
PD41134	3	85.5	4	106157355	106157356	TA	T	0.005	TET2	p.K753fs	Frameshift
PD41134	4	89.9	4	106157355	106157356	TA	T	0.004	TET2	p.K753fs	Frameshift
PD41134	1	76.9	12	11905504	11905504	G	A	0.000	ETV6	p.A52T	Missense
PD41134	2	80.2	12	11905504	11905504	G	A	0.000	ETV6	p.A52T	Missense
PD41134	3	85.5	12	11905504	11905504	G	A	0.010	ETV6	p.A52T	Missense
PD41134	4	89.9	12	11905504	11905504	G	A	0.000	ETV6	p.A52T	Missense
PD41135	1	59.9	2	25464551	25464552	CC	C	0.004	DNMT3A	p.G654fs	Frameshift
PD41135	2	63.0	2	25464551	25464552	CC	C	0.005	DNMT3A	p.G654fs	Frameshift
PD41135	3	66.7	2	25464551	25464552	CC	C	0.011	DNMT3A	p.G654fs	Frameshift
PD41135	4	69.6	2	25464551	25464552	CC	C	0.008	DNMT3A	p.G654fs	Frameshift
PD41135	5	74.0	2	25464551	25464552	CC	C	0.011	DNMT3A	p.G654fs	Frameshift
PD41135	1	59.9	2	25466790	25466790	G	A	0.001	DNMT3A	p.S638F	Missense
PD41135	2	63.0	2	25466790	25466790	G	A	0.004	DNMT3A	p.S638F	Missense
PD41135	3	66.7	2	25466790	25466790	G	A	0.008	DNMT3A	p.S638F	Missense
PD41135	4	69.6	2	25466790	25466790	G	A	0.007	DNMT3A	p.S638F	Missense
PD41135	5	74.0	2	25466790	25466790	G	A	0.010	DNMT3A	p.S638F	Missense
PD41135	1	59.9	4	106157344	106157344	C	T	0.004	TET2	p.Q749X	Nonsense
PD41135	2	63.0	4	106157344	106157344	C	T	0.006	TET2	p.Q749X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41135	3	66.7	4	106157344	106157344	C	T	0.004	TET2	p.Q749X	Nonsense
PD41135	4	69.6	4	106157344	106157344	C	T	0.007	TET2	p.Q749X	Nonsense
PD41135	5	74.0	4	106157344	106157344	C	T	0.010	TET2	p.Q749X	Nonsense
PD41135	1	59.9	4	55561887	55561887	G	T	0.000	KIT	p.G93C	Missense
PD41135	2	63.0	4	55561887	55561887	G	T	0.003	KIT	p.G93C	Missense
PD41135	3	66.7	4	55561887	55561887	G	T	0.007	KIT	p.G93C	Missense
PD41135	4	69.6	4	55561887	55561887	G	T	0.000	KIT	p.G93C	Missense
PD41135	5	74.0	4	55561887	55561887	G	T	0.000	KIT	p.G93C	Missense
PD41135	1	59.9	X	44942757	44942757	G	T	0.004	KDM6A	p.V1165L	Missense
PD41135	2	63.0	X	44942757	44942757	G	T	0.004	KDM6A	p.V1165L	Missense
PD41135	3	66.7	X	44942757	44942757	G	T	0.002	KDM6A	p.V1165L	Missense
PD41135	4	69.6	X	44942757	44942757	G	T	0.004	KDM6A	p.V1165L	Missense
PD41135	5	74.0	X	44942757	44942757	G	T	0.012	KDM6A	p.V1165L	Missense
PD41136	1	63.5	4	106156690	106156691	CA	C	0.039	TET2	p.Q531fs	Frameshift
PD41136	2	66.8	4	106156690	106156691	CA	C	0.037	TET2	p.Q531fs	Frameshift
PD41136	3	70.6	4	106156690	106156691	CA	C	0.054	TET2	p.Q531fs	Frameshift
PD41136	4	76.5	4	106156690	106156691	CA	C	0.031	TET2	p.Q531fs	Frameshift
PD41136	1	63.5	4	106156741	106156741	C	T	0.036	TET2	p.Q548X	Nonsense
PD41136	2	66.8	4	106156741	106156741	C	T	0.041	TET2	p.Q548X	Nonsense
PD41136	3	70.6	4	106156741	106156741	C	T	0.075	TET2	p.Q548X	Nonsense
PD41136	4	76.5	4	106156741	106156741	C	T	0.033	TET2	p.Q548X	Nonsense
PD41136	1	63.5	20	31017790	31017790	C	A	0.007	ASXL1	p.R218S	Missense
PD41136	2	66.8	20	31017790	31017790	C	A	0.002	ASXL1	p.R218S	Missense
PD41136	3	70.6	20	31017790	31017790	C	A	0.000	ASXL1	p.R218S	Missense
PD41136	4	76.5	20	31017790	31017790	C	A	0.000	ASXL1	p.R218S	Missense
PD41139	1	56.3	2	25459828	25459828	G	C	0.029	DNMT3A	p.L819V	Missense
PD41139	2	59.5	2	25459828	25459828	G	C	0.022	DNMT3A	p.L819V	Missense
PD41139	3	62.7	2	25459828	25459828	G	C	0.061	DNMT3A	p.L819V	Missense
PD41139	4	65.7	2	25459828	25459828	G	C	0.054	DNMT3A	p.L819V	Missense
PD41139	5	70.1	2	25459828	25459828	G	C	0.042	DNMT3A	p.L819V	Missense
PD41139	1	56.3	4	106180784	106180784	G	C	0.007	TET2	p.C1271S	Missense
PD41139	2	59.5	4	106180784	106180784	G	C	0.006	TET2	p.C1271S	Missense
PD41139	3	62.7	4	106180784	106180784	G	C	0.004	TET2	p.C1271S	Missense
PD41139	4	65.7	4	106180784	106180784	G	C	0.000	TET2	p.C1271S	Missense
PD41139	5	70.1	4	106180784	106180784	G	C	0.002	TET2	p.C1271S	Missense
PD41140	1	58.1	2	25469488	25469488	C	T	0.033	DNMT3A	c.1279+1G>A	Splice site
PD41140	2	61.2	2	25469488	25469488	C	T	0.032	DNMT3A	c.1279+1G>A	Splice site
PD41140	3	64.9	2	25469488	25469488	C	T	0.053	DNMT3A	c.1279+1G>A	Splice site
PD41140	4	67.7	2	25469488	25469488	C	T	0.043	DNMT3A	c.1279+1G>A	Splice site
PD41140	5	72.1	2	25469488	25469488	C	T	0.029	DNMT3A	c.1279+1G>A	Splice site
PD41140	1	58.1	12	112893767	112893767	C	A	0.000	PTPN11	p.T219N	Missense
PD41140	2	61.2	12	112893767	112893767	C	A	0.000	PTPN11	p.T219N	Missense
PD41140	3	64.9	12	112893767	112893767	C	A	0.000	PTPN11	p.T219N	Missense
PD41140	4	67.7	12	112893767	112893767	C	A	0.005	PTPN11	p.T219N	Missense
PD41140	5	72.1	12	112893767	112893767	C	A	0.001	PTPN11	p.T219N	Missense
PD41142	1	79.2	2	198267359	198267359	C	G	0.001	SF3B1	p.K666N	Missense
PD41142	2	83.6	2	198267359	198267359	C	G	0.002	SF3B1	p.K666N	Missense
PD41142	3	86.6	2	198267359	198267359	C	G	0.009	SF3B1	p.K666N	Missense
PD41142	4	89.8	2	198267359	198267359	C	G	0.012	SF3B1	p.K666N	Missense
PD41142	1	79.2	2	25463182	25463182	G	A	0.013	DNMT3A	p.R771X	Nonsense
PD41142	2	83.6	2	25463182	25463182	G	A	0.009	DNMT3A	p.R771X	Nonsense
PD41142	3	86.6	2	25463182	25463182	G	A	0.012	DNMT3A	p.R771X	Nonsense
PD41142	4	89.8	2	25463182	25463182	G	A	0.006	DNMT3A	p.R771X	Nonsense
PD41142	1	79.2	4	106156729	106156729	C	T	0.002	TET2	p.R544X	Nonsense
PD41142	2	83.6	4	106156729	106156729	C	T	0.002	TET2	p.R544X	Nonsense
PD41142	3	86.6	4	106156729	106156729	C	T	0.005	TET2	p.R544X	Nonsense
PD41142	4	89.8	4	106156729	106156729	C	T	0.001	TET2	p.R544X	Nonsense
PD41142	1	79.2	11	119148919	119148919	T	C	0.012	CBL	p.L380P	Missense
PD41142	2	83.6	11	119148919	119148919	T	C	0.011	CBL	p.L380P	Missense
PD41142	3	86.6	11	119148919	119148919	T	C	0.004	CBL	p.L380P	Missense
PD41142	4	89.8	11	119148919	119148919	T	C	0.010	CBL	p.L380P	Missense
PD41142	1	79.2	X	129149879	129149880	TG	T	0.003	BCORL1	p.V1044fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41142	2	83.6	X	129149879	129149880	TG	T	0.000	BCORL1	p.V1044fs	Frameshift
PD41142	3	86.6	X	129149879	129149880	TG	T	0.000	BCORL1	p.V1044fs	Frameshift
PD41142	4	89.8	X	129149879	129149880	TG	T	0.001	BCORL1	p.V1044fs	Frameshift
PD41143	1	71.2	2	25463568	25463568	A	G	0.002	DNMT3A	p.I705T	Missense
PD41143	2	74.6	2	25463568	25463568	A	G	0.008	DNMT3A	p.I705T	Missense
PD41143	3	78.3	2	25463568	25463568	A	G	0.007	DNMT3A	p.I705T	Missense
PD41143	4	81.4	2	25463568	25463568	A	G	0.014	DNMT3A	p.I705T	Missense
PD41143	1	71.2	2	25469488	25469488	C	T	0.012	DNMT3A	c.1279+1G>A	Splice site
PD41143	2	74.6	2	25469488	25469488	C	T	0.021	DNMT3A	c.1279+1G>A	Splice site
PD41143	3	78.3	2	25469488	25469488	C	T	0.029	DNMT3A	c.1279+1G>A	Splice site
PD41143	4	81.4	2	25469488	25469488	C	T	0.037	DNMT3A	c.1279+1G>A	Splice site
PD41143	1	71.2	4	106180784	106180785	GC	G	0.015	TET2	p.C1271fs	Frameshift
PD41143	2	74.6	4	106180784	106180785	GC	G	0.014	TET2	p.C1271fs	Frameshift
PD41143	3	78.3	4	106180784	106180785	GC	G	0.011	TET2	p.C1271fs	Frameshift
PD41143	4	81.4	4	106180784	106180785	GC	G	0.012	TET2	p.C1271fs	Frameshift
PD41143	1	71.2	X	39934190	39934190	C	T	0.002	BCOR	p.V137I	Missense
PD41143	2	74.6	X	39934190	39934190	C	T	0.002	BCOR	p.V137I	Missense
PD41143	3	78.3	X	39934190	39934190	C	T	0.005	BCOR	p.V137I	Missense
PD41143	4	81.4	X	39934190	39934190	C	T	0.003	BCOR	p.V137I	Missense
PD41144	1	74.3	2	198267359	198267359	C	G	0.000	SF3B1	p.K666N	Missense
PD41144	2	77.4	2	198267359	198267359	C	G	0.001	SF3B1	p.K666N	Missense
PD41144	3	80.8	2	198267359	198267359	C	G	0.002	SF3B1	p.K666N	Missense
PD41144	4	83.8	2	198267359	198267359	C	G	0.004	SF3B1	p.K666N	Missense
PD41144	5	88.2	2	198267359	198267359	C	G	0.011	SF3B1	p.K666N	Missense
PD41144	1	74.3	2	25463287	25463287	G	A	0.004	DNMT3A	p.R736C	Missense
PD41144	2	77.4	2	25463287	25463287	G	A	0.002	DNMT3A	p.R736C	Missense
PD41144	3	80.8	2	25463287	25463287	G	A	0.003	DNMT3A	p.R736C	Missense
PD41144	4	83.8	2	25463287	25463287	G	A	0.009	DNMT3A	p.R736C	Missense
PD41144	5	88.2	2	25463287	25463287	G	A	0.015	DNMT3A	p.R736C	Missense
PD41144	1	74.3	12	50029014	50029014	G	T	0.000	PRPF40B	p.Q378H	Missense
PD41144	2	77.4	12	50029014	50029014	G	T	0.005	PRPF40B	p.Q378H	Missense
PD41144	3	80.8	12	50029014	50029014	G	T	0.003	PRPF40B	p.Q378H	Missense
PD41144	4	83.8	12	50029014	50029014	G	T	0.000	PRPF40B	p.Q378H	Missense
PD41144	5	88.2	12	50029014	50029014	G	T	0.000	PRPF40B	p.Q378H	Missense
PD41145	1	65.2	4	106156747	106156747	C	T	0.005	TET2	p.R550X	Nonsense
PD41145	2	68.3	4	106156747	106156747	C	T	0.001	TET2	p.R550X	Nonsense
PD41145	3	71.6	4	106156747	106156747	C	T	0.002	TET2	p.R550X	Nonsense
PD41145	4	74.6	4	106156747	106156747	C	T	0.001	TET2	p.R550X	Nonsense
PD41145	5	79.6	4	106156747	106156747	C	T	0.000	TET2	p.R550X	Nonsense
PD41145	1	65.2	11	118342857	118342863	AGAAAGT	A	0.055	KMT2A	p.328_330del	Inframe
PD41145	2	68.3	11	118342857	118342863	AGAAAGT	A	0.044	KMT2A	p.328_330del	Inframe
PD41145	3	71.6	11	118342857	118342863	AGAAAGT	A	0.051	KMT2A	p.328_330del	Inframe
PD41145	4	74.6	11	118342857	118342863	AGAAAGT	A	0.063	KMT2A	p.328_330del	Inframe
PD41145	5	79.6	11	118342857	118342863	AGAAAGT	A	0.035	KMT2A	p.328_330del	Inframe
PD41145	1	65.2	16	3794900	3794900	G	T	0.000	CREBBP	p.A1326D	Missense
PD41145	2	68.3	16	3794900	3794900	G	T	0.000	CREBBP	p.A1326D	Missense
PD41145	3	71.6	16	3794900	3794900	G	T	0.000	CREBBP	p.A1326D	Missense
PD41145	4	74.6	16	3794900	3794900	G	T	0.006	CREBBP	p.A1326D	Missense
PD41145	5	79.6	16	3794900	3794900	G	T	0.000	CREBBP	p.A1326D	Missense
PD41146	1	72.9	4	106156220	106156221	AT	A	0.009	TET2	p.N374fs	Frameshift
PD41146	2	76.3	4	106156220	106156221	AT	A	0.022	TET2	p.N374fs	Frameshift
PD41146	3	80.6	4	106156220	106156221	AT	A	0.036	TET2	p.N374fs	Frameshift
PD41146	4	85.7	4	106156220	106156221	AT	A	0.036	TET2	p.N374fs	Frameshift
PD41146	1	72.9	4	106157695	106157695	C	T	0.003	TET2	p.Q866X	Nonsense
PD41146	2	76.3	4	106157695	106157695	C	T	0.007	TET2	p.Q866X	Nonsense
PD41146	3	80.6	4	106157695	106157695	C	T	0.003	TET2	p.Q866X	Nonsense
PD41146	4	85.7	4	106157695	106157695	C	T	0.005	TET2	p.Q866X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41146	1	72.9	4	106164021	106164022	TG	T	0.034	TET2	p.E1178fs	Frameshift
PD41146	2	76.3	4	106164021	106164022	TG	T	0.073	TET2	p.E1178fs	Frameshift
PD41146	3	80.6	4	106164021	106164022	TG	T	0.072	TET2	p.E1178fs	Frameshift
PD41146	4	85.7	4	106164021	106164022	TG	T	0.086	TET2	p.E1178fs	Frameshift
PD41148	1	73.6	4	106156135	106156136	CT	C	0.011	TET2	p.L346fs	Frameshift
PD41148	2	76.6	4	106156135	106156136	CT	C	0.014	TET2	p.L346fs	Frameshift
PD41148	3	80.4	4	106156135	106156136	CT	C	0.021	TET2	p.L346fs	Frameshift
PD41148	4	83.4	4	106156135	106156136	CT	C	0.036	TET2	p.L346fs	Frameshift
PD41148	1	73.6	11	119149251	119149251	G	A	0.002	CBL	p.R420Q	Missense
PD41148	2	76.6	11	119149251	119149251	G	A	0.009	CBL	p.R420Q	Missense
PD41148	3	80.4	11	119149251	119149251	G	A	0.005	CBL	p.R420Q	Missense
PD41148	4	83.4	11	119149251	119149251	G	A	0.003	CBL	p.R420Q	Missense
PD41148	1	73.6	20	57484586	57484586	G	A	0.007	GNAS	p.V867M	Missense
PD41148	2	76.6	20	57484586	57484586	G	A	0.008	GNAS	p.V867M	Missense
PD41148	3	80.4	20	57484586	57484586	G	A	0.006	GNAS	p.V867M	Missense
PD41148	4	83.4	20	57484586	57484586	G	A	0.006	GNAS	p.V867M	Missense
PD41148	1	73.6	X	123229241	123229241	G	A	0.007	STAG2	p.R1242Q	Missense
PD41148	2	76.6	X	123229241	123229241	G	A	0.008	STAG2	p.R1242Q	Missense
PD41148	3	80.4	X	123229241	123229241	G	A	0.004	STAG2	p.R1242Q	Missense
PD41148	4	83.4	X	123229241	123229241	G	A	0.004	STAG2	p.R1242Q	Missense
PD41148	1	73.6	X	129190004	129190004	G	A	0.011	BCORL1	p.D1751N	Missense
PD41148	2	76.6	X	129190004	129190004	G	A	0.016	BCORL1	p.D1751N	Missense
PD41148	3	80.4	X	129190004	129190004	G	A	0.028	BCORL1	p.D1751N	Missense
PD41148	4	83.4	X	129190004	129190004	G	A	0.018	BCORL1	p.D1751N	Missense
PD41149	1	62.8	2	25469028	25469028	C	T	0.001	DNMT3A	c.1429+1G>A	Splice site
PD41149	2	66.0	2	25469028	25469028	C	T	0.001	DNMT3A	c.1429+1G>A	Splice site
PD41149	3	69.9	2	25469028	25469028	C	T	0.001	DNMT3A	c.1429+1G>A	Splice site
PD41149	4	72.5	2	25469028	25469028	C	T	0.004	DNMT3A	c.1429+1G>A	Splice site
PD41149	5	76.9	2	25469028	25469028	C	T	0.018	DNMT3A	c.1429+1G>A	Splice site
PD41149	1	62.8	2	25470029	25470029	T	C	0.001	DNMT3A	c.1015-2A>G	Splice site
PD41149	2	66.0	2	25470029	25470029	T	C	0.005	DNMT3A	c.1015-2A>G	Splice site
PD41149	3	69.9	2	25470029	25470029	T	C	0.006	DNMT3A	c.1015-2A>G	Splice site
PD41149	4	72.5	2	25470029	25470029	T	C	0.009	DNMT3A	c.1015-2A>G	Splice site
PD41149	5	76.9	2	25470029	25470029	T	C	0.004	DNMT3A	c.1015-2A>G	Splice site
PD41150	1	74.7	2	25462068	25462068	A	G	0.004	DNMT3A	p.I780T	Missense
PD41150	2	78.1	2	25462068	25462068	A	G	0.007	DNMT3A	p.I780T	Missense
PD41150	3	83.1	2	25462068	25462068	A	G	0.008	DNMT3A	p.I780T	Missense
PD41150	1	74.7	2	25463232	25463232	A	T	0.006	DNMT3A	p.L754H	Missense
PD41150	2	78.1	2	25463232	25463232	A	T	0.009	DNMT3A	p.L754H	Missense
PD41150	3	83.1	2	25463232	25463232	A	T	0.009	DNMT3A	p.L754H	Missense
PD41150	1	74.7	4	106155941	106155943	ACT	A	0.003	TET2	p.N281fs	Frameshift
PD41150	2	78.1	4	106155941	106155943	ACT	A	0.004	TET2	p.N281fs	Frameshift
PD41150	3	83.1	4	106155941	106155943	ACT	A	0.005	TET2	p.N281fs	Frameshift
PD41151	1	74.9	2	25463299	25463299	A	G	0.071	DNMT3A	p.F732L	Missense
PD41151	2	78.4	2	25463299	25463299	A	G	0.103	DNMT3A	p.F732L	Missense
PD41151	3	83.4	2	25463299	25463299	A	G	0.146	DNMT3A	p.F732L	Missense
PD41151	1	74.9	2	25469646	25469646	C	T	0.012	DNMT3A	c.1123-1G>A	Splice site
PD41151	2	78.4	2	25469646	25469646	C	T	0.004	DNMT3A	c.1123-1G>A	Splice site
PD41151	3	83.4	2	25469646	25469646	C	T	0.006	DNMT3A	c.1123-1G>A	Splice site
PD41151	1	74.9	4	106155676	106155677	CA	C	0.007	TET2	p.H193fs	Frameshift
PD41151	2	78.4	4	106155676	106155677	CA	C	0.007	TET2	p.H193fs	Frameshift
PD41151	3	83.4	4	106155676	106155677	CA	C	0.006	TET2	p.H193fs	Frameshift
PD41151	1	74.9	4	106157589	106157590	AC	A	0.013	TET2	p.Q831fs	Frameshift
PD41151	2	78.4	4	106157589	106157590	AC	A	0.008	TET2	p.Q831fs	Frameshift
PD41151	3	83.4	4	106157589	106157590	AC	A	0.020	TET2	p.Q831fs	Frameshift
PD41151	1	74.9	4	106193999	106194000	TA	T	0.004	TET2	p.K1488fs	Frameshift
PD41151	2	78.4	4	106193999	106194000	TA	T	0.005	TET2	p.K1488fs	Frameshift
PD41151	3	83.4	4	106193999	106194000	TA	T	0.006	TET2	p.K1488fs	Frameshift
PD41151	1	74.9	16	3781267	3781267	G	T	0.001	CREBBP	p.Q1700K	Missense
PD41151	2	78.4	16	3781267	3781267	G	T	0.002	CREBBP	p.Q1700K	Missense
PD41151	3	83.4	16	3781267	3781267	G	T	0.011	CREBBP	p.Q1700K	Missense
PD41152	1	62.9	20	31021722	31021722	T	C	0.000	ASXL1	c.1719+2T>C	Splice site

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41152	2	65.6	20	31021722	31021722	T	C	0.007	ASXL1	c.1719+2T>C	Splice site
PD41152	3	69.7	20	31021722	31021722	T	C	0.000	ASXL1	c.1719+2T>C	Splice site
PD41152	4	72.4	20	31021722	31021722	T	C	0.000	ASXL1	c.1719+2T>C	Splice site
PD41152	5	76.8	20	31021722	31021722	T	C	0.000	ASXL1	c.1719+2T>C	Splice site
PD41152	1	62.9	X	53432807	53432807	C	A	0.000	SMC1A	p.D521Y	Missense
PD41152	2	65.6	X	53432807	53432807	C	A	0.001	SMC1A	p.D521Y	Missense
PD41152	3	69.7	X	53432807	53432807	C	A	0.005	SMC1A	p.D521Y	Missense
PD41152	4	72.4	X	53432807	53432807	C	A	0.000	SMC1A	p.D521Y	Missense
PD41152	5	76.8	X	53432807	53432807	C	A	0.000	SMC1A	p.D521Y	Missense
PD41153	1	73.3	10	89690833	89690834	AT	A	0.000	PTEN	p.F254fs	Frameshift
PD41153	2	76.8	10	89690833	89690834	AT	A	0.000	PTEN	p.F254fs	Frameshift
PD41153	3	81.7	10	89690833	89690834	AT	A	0.009	PTEN	p.F254fs	Frameshift
PD41153	1	73.3	X	133527601	133527601	A	G	0.043	PHF6	p.H104R	Missense
PD41153	2	76.8	X	133527601	133527601	A	G	0.065	PHF6	p.H104R	Missense
PD41153	3	81.7	X	133527601	133527601	A	G	0.098	PHF6	p.H104R	Missense
PD41154	1	59.1	2	25463513	25463514	GA	G	0.007	DNMT3A	p.L723fs	Frameshift
PD41154	3	66.2	2	25463513	25463514	GA	G	0.009	DNMT3A	p.L723fs	Frameshift
PD41154	4	68.8	2	25463513	25463514	GA	G	0.001	DNMT3A	p.L723fs	Frameshift
PD41154	5	73.1	2	25463513	25463514	GA	G	0.001	DNMT3A	p.L723fs	Frameshift
PD41154	1	59.1	9	139396278	139396278	G	A	0.000	NOTCH1	p.R1854C	Missense
PD41154	3	66.2	9	139396278	139396278	G	A	0.001	NOTCH1	p.R1854C	Missense
PD41154	4	68.8	9	139396278	139396278	G	A	0.007	NOTCH1	p.R1854C	Missense
PD41154	5	73.1	9	139396278	139396278	G	A	0.003	NOTCH1	p.R1854C	Missense
PD41154	1	59.1	11	118343002	118343002	A	G	0.000	KMT2A	p.L376L	Synonymous
PD41154	3	66.2	11	118343002	118343002	A	G	0.000	KMT2A	p.L376L	Synonymous
PD41154	4	68.8	11	118343002	118343002	A	G	0.000	KMT2A	p.L376L	Synonymous
PD41154	5	73.1	11	118343002	118343002	A	G	0.005	KMT2A	p.L376L	Synonymous
PD41154	1	59.1	17	74732960	74732960	G	C	0.002	SRSF2	p.P95A	Missense
PD41154	3	66.2	17	74732960	74732960	G	C	0.015	SRSF2	p.P95A	Missense
PD41154	4	68.8	17	74732960	74732960	G	C	0.014	SRSF2	p.P95A	Missense
PD41154	5	73.1	17	74732960	74732960	G	C	0.026	SRSF2	p.P95A	Missense
PD41155	1	71.5	2	25463185	25463185	A	G	0.006	DNMT3A	p.S770P	Missense
PD41155	2	75.0	2	25463185	25463185	A	G	0.010	DNMT3A	p.S770P	Missense
PD41155	3	79.5	2	25463185	25463185	A	G	0.011	DNMT3A	p.S770P	Missense
PD41155	1	71.5	12	112926888	112926888	G	C	0.006	PTPN11	p.G503A	Missense
PD41155	2	75.0	12	112926888	112926888	G	C	0.003	PTPN11	p.G503A	Missense
PD41155	3	79.5	12	112926888	112926888	G	C	0.003	PTPN11	p.G503A	Missense
PD41156	1	73.6	2	198267360	198267360	T	A	0.000	SF3B1	p.K666M	Missense
PD41156	2	76.8	2	198267360	198267360	T	A	0.002	SF3B1	p.K666M	Missense
PD41156	3	80.8	2	198267360	198267360	T	A	0.010	SF3B1	p.K666M	Missense
PD41156	4	84.0	2	198267360	198267360	T	A	0.090	SF3B1	p.K666M	Missense
PD41156	1	73.6	19	33792852	33792852	G	A	0.000	CEBPA	p.P157S	Missense
PD41156	2	76.8	19	33792852	33792852	G	A	0.003	CEBPA	p.P157S	Missense
PD41156	3	80.8	19	33792852	33792852	G	A	0.000	CEBPA	p.P157S	Missense
PD41156	4	84.0	19	33792852	33792852	G	A	0.025	CEBPA	p.P157S	Missense
PD41156	1	73.6	20	57428948	57428948	G	C	0.000	GNAS	p.A210P	Missense
PD41156	2	76.8	20	57428948	57428948	G	C	0.000	GNAS	p.A210P	Missense
PD41156	3	80.8	20	57428948	57428948	G	C	0.000	GNAS	p.A210P	Missense
PD41156	4	84.0	20	57428948	57428948	G	C	0.009	GNAS	p.A210P	Missense
PD41157	1	60.9	4	106157044	106157044	C	T	0.010	TET2	p.Q649X	Nonsense
PD41157	2	64.0	4	106157044	106157044	C	T	0.011	TET2	p.Q649X	Nonsense
PD41157	3	68.0	4	106157044	106157044	C	T	0.025	TET2	p.Q649X	Nonsense
PD41157	4	70.6	4	106157044	106157044	C	T	0.020	TET2	p.Q649X	Nonsense
PD41157	5	75.1	4	106157044	106157044	C	T	0.035	TET2	p.Q649X	Nonsense
PD41158	1	71.9	X	129148531	129148532	TC	T	0.004	BCORL1	p.S595fs	Frameshift
PD41158	2	75.0	X	129148531	129148532	TC	T	0.001	BCORL1	p.S595fs	Frameshift
PD41158	3	80.1	X	129148531	129148532	TC	T	0.006	BCORL1	p.S595fs	Frameshift
PD41159	1	56.0	2	198266834	198266834	T	C	0.001	SF3B1	p.K700E	Missense
PD41159	2	58.8	2	198266834	198266834	T	C	0.013	SF3B1	p.K700E	Missense
PD41159	3	62.6	2	198266834	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41159	4	66.1	2	198266834	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41159	5	70.1	2	198266834	198266834	T	C	0.015	SF3B1	p.K700E	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41159	1	56.0	7	101747740	101747740	G	A	0.005	CUX1	c.530+1G>A	Splice site
PD41159	2	58.8	7	101747740	101747740	G	A	0.000	CUX1	c.530+1G>A	Splice site
PD41159	3	62.6	7	101747740	101747740	G	A	0.000	CUX1	c.530+1G>A	Splice site
PD41159	4	66.1	7	101747740	101747740	G	A	0.000	CUX1	c.530+1G>A	Splice site
PD41159	5	70.1	7	101747740	101747740	G	A	0.000	CUX1	c.530+1G>A	Splice site
PD41160	1	54.7	2	25466800	25466800	G	A	0.005	DNMT3A	p.R635W	Missense
PD41160	2	57.7	2	25466800	25466800	G	A	0.007	DNMT3A	p.R635W	Missense
PD41160	3	61.5	2	25466800	25466800	G	A	0.017	DNMT3A	p.R635W	Missense
PD41160	4	64.1	2	25466800	25466800	G	A	0.032	DNMT3A	p.R635W	Missense
PD41160	5	68.5	2	25466800	25466800	G	A	0.049	DNMT3A	p.R635W	Missense
PD41160	1	54.7	4	106193900	106193907	CAGGATGT	C	0.003	TET2	p.R1455fs	Frameshift
PD41160	2	57.7	4	106193900	106193907	CAGGATGT	C	0.006	TET2	p.R1455fs	Frameshift
PD41160	3	61.5	4	106193900	106193907	CAGGATGT	C	0.012	TET2	p.R1455fs	Frameshift
PD41160	4	64.1	4	106193900	106193907	CAGGATGT	C	0.023	TET2	p.R1455fs	Frameshift
PD41160	5	68.5	4	106193900	106193907	CAGGATGT	C	0.048	TET2	p.R1455fs	Frameshift
PD41161	1	73.2	2	25470485	25470485	C	T	0.031	DNMT3A	p.W330X	Nonsense
PD41161	2	76.3	2	25470485	25470485	C	T	0.023	DNMT3A	p.W330X	Nonsense
PD41161	3	80.6	2	25470485	25470485	C	T	0.030	DNMT3A	p.W330X	Nonsense
PD41161	4	85.9	2	25470485	25470485	C	T	0.063	DNMT3A	p.W330X	Nonsense
PD41161	1	73.2	4	106158215	106158215	C	A	0.001	TET2	p.S1039X	Nonsense
PD41161	2	76.3	4	106158215	106158215	C	A	0.004	TET2	p.S1039X	Nonsense
PD41161	3	80.6	4	106158215	106158215	C	A	0.004	TET2	p.S1039X	Nonsense
PD41161	4	85.9	4	106158215	106158215	C	A	0.012	TET2	p.S1039X	Nonsense
PD41161	1	73.2	4	106193765	106193766	AC	A	0.001	TET2	p.P1410fs	Frameshift
PD41161	2	76.3	4	106193765	106193766	AC	A	0.003	TET2	p.P1410fs	Frameshift
PD41161	3	80.6	4	106193765	106193766	AC	A	0.004	TET2	p.P1410fs	Frameshift
PD41161	4	85.9	4	106193765	106193766	AC	A	0.010	TET2	p.P1410fs	Frameshift
PD41161	1	73.2	4	106196597	106196602	CCATAT	C	0.003	TET2	p.P1644fs	Frameshift
PD41161	2	76.3	4	106196597	106196602	CCATAT	C	0.013	TET2	p.P1644fs	Frameshift
PD41161	3	80.6	4	106196597	106196602	CCATAT	C	0.005	TET2	p.P1644fs	Frameshift
PD41161	4	85.9	4	106196597	106196602	CCATAT	C	0.016	TET2	p.P1644fs	Frameshift
PD41161	1	73.2	11	64540941	64540941	C	T	0.016	SF1	p.R66H	Missense
PD41161	2	76.3	11	64540941	64540941	C	T	0.010	SF1	p.R66H	Missense
PD41161	3	80.6	11	64540941	64540941	C	T	0.004	SF1	p.R66H	Missense
PD41161	4	85.9	11	64540941	64540941	C	T	0.007	SF1	p.R66H	Missense
PD41161	1	73.2	17	74732959	74732959	G	T	0.000	SRSF2	p.P95H	Missense
PD41161	2	76.3	17	74732959	74732959	G	T	0.003	SRSF2	p.P95H	Missense
PD41161	3	80.6	17	74732959	74732959	G	T	0.005	SRSF2	p.P95H	Missense
PD41161	4	85.9	17	74732959	74732959	G	T	0.020	SRSF2	p.P95H	Missense
PD41161	1	73.2	X	154306951	154306953	CAT	C	0.001	BRCC3	p.H126fs	Frameshift
PD41161	2	76.3	X	154306951	154306953	CAT	C	0.006	BRCC3	p.H126fs	Frameshift
PD41161	3	80.6	X	154306951	154306953	CAT	C	0.002	BRCC3	p.H126fs	Frameshift
PD41161	4	85.9	X	154306951	154306953	CAT	C	0.003	BRCC3	p.H126fs	Frameshift
PD41162	1	65.4	4	106155389	106155389	C	A	0.001	TET2	p.T97K	Missense
PD41162	2	68.4	4	106155389	106155389	C	A	0.008	TET2	p.T97K	Missense
PD41162	3	72.3	4	106155389	106155389	C	A	0.000	TET2	p.T97K	Missense
PD41162	4	77.1	4	106155389	106155389	C	A	0.000	TET2	p.T97K	Missense
PD41163	1	78.4	2	25457243	25457243	G	A	0.058	DNMT3A	p.R882C	Missense
PD41163	2	81.6	2	25457243	25457243	G	A	0.061	DNMT3A	p.R882C	Missense
PD41163	1	78.4	4	106197402	106197402	A	G	0.006	TET2	p.H1912R	Missense
PD41163	2	81.6	4	106197402	106197402	A	G	0.002	TET2	p.H1912R	Missense
PD41164	1	68.0	2	25467500	25467501	GC	G	0.004	DNMT3A	p.A525fs	Frameshift
PD41164	2	71.1	2	25467500	25467501	GC	G	0.006	DNMT3A	p.A525fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41164	3	76.1	2	25467500	25467501	GC	G	0.005	DNMT3A	p.A525fs	Frameshift
PD41164	4	80.1	2	25467500	25467501	GC	G	0.014	DNMT3A	p.A525fs	Frameshift
PD41164	1	68.0	2	25469540	25469540	C	T	0.009	DNMT3A	p.A410T	Missense
PD41164	2	71.1	2	25469540	25469540	C	T	0.009	DNMT3A	p.A410T	Missense
PD41164	3	76.1	2	25469540	25469540	C	T	0.005	DNMT3A	p.A410T	Missense
PD41164	4	80.1	2	25469540	25469540	C	T	0.011	DNMT3A	p.A410T	Missense
PD41164	1	68.0	3	128200149	128200149	G	A	0.007	GATA2	p.L386L	Synonymous
PD41164	2	71.1	3	128200149	128200149	G	A	0.000	GATA2	p.L386L	Synonymous
PD41164	3	76.1	3	128200149	128200149	G	A	0.000	GATA2	p.L386L	Synonymous
PD41164	4	80.1	3	128200149	128200149	G	A	0.000	GATA2	p.L386L	Synonymous
PD41165	1	75.3	2	25463568	25463568	A	G	0.002	DNMT3A	p.I705T	Missense
PD41165	2	78.3	2	25463568	25463568	A	G	0.004	DNMT3A	p.I705T	Missense
PD41165	3	82.2	2	25463568	25463568	A	G	0.003	DNMT3A	p.I705T	Missense
PD41165	4	85.0	2	25463568	25463568	A	G	0.002	DNMT3A	p.I705T	Missense
PD41165	5	88.8	2	25463568	25463568	A	G	0.007	DNMT3A	p.I705T	Missense
PD41165	1	75.3	2	25471016	25471016	G	A	0.004	DNMT3A	p.Q249X	Nonsense
PD41165	2	78.3	2	25471016	25471016	G	A	0.009	DNMT3A	p.Q249X	Nonsense
PD41165	3	82.2	2	25471016	25471016	G	A	0.008	DNMT3A	p.Q249X	Nonsense
PD41165	4	85.0	2	25471016	25471016	G	A	0.006	DNMT3A	p.Q249X	Nonsense
PD41165	5	88.8	2	25471016	25471016	G	A	0.004	DNMT3A	p.Q249X	Nonsense
PD41165	1	75.3	4	106157139	106157140	AT	A	0.007	TET2	p.F681fs	Frameshift
PD41165	2	78.3	4	106157139	106157140	AT	A	0.010	TET2	p.F681fs	Frameshift
PD41165	3	82.2	4	106157139	106157140	AT	A	0.011	TET2	p.F681fs	Frameshift
PD41165	4	85.0	4	106157139	106157140	AT	A	0.006	TET2	p.F681fs	Frameshift
PD41165	5	88.8	4	106157139	106157140	AT	A	0.011	TET2	p.F681fs	Frameshift
PD41165	1	75.3	4	106158260	106158261	TA	T	0.001	TET2	p.V1054fs	Frameshift
PD41165	2	78.3	4	106158260	106158261	TA	T	0.000	TET2	p.V1054fs	Frameshift
PD41165	3	82.2	4	106158260	106158261	TA	T	0.007	TET2	p.V1054fs	Frameshift
PD41165	4	85.0	4	106158260	106158261	TA	T	0.002	TET2	p.V1054fs	Frameshift
PD41165	5	88.8	4	106158260	106158261	TA	T	0.002	TET2	p.V1054fs	Frameshift
PD41165	1	75.3	4	106190797	106190797	C	A	0.000	TET2	p.R1359S	Missense
PD41165	2	78.3	4	106190797	106190797	C	A	0.003	TET2	p.R1359S	Missense
PD41165	3	82.2	4	106190797	106190797	C	A	0.006	TET2	p.R1359S	Missense
PD41165	4	85.0	4	106190797	106190797	C	A	0.011	TET2	p.R1359S	Missense
PD41165	5	88.8	4	106190797	106190797	C	A	0.021	TET2	p.R1359S	Missense
PD41165	1	75.3	17	7577572	7577572	T	C	0.003	TP53	p.M198V	Missense
PD41165	2	78.3	17	7577572	7577572	T	C	0.003	TP53	p.M198V	Missense
PD41165	3	82.2	17	7577572	7577572	T	C	0.005	TP53	p.M198V	Missense
PD41165	4	85.0	17	7577572	7577572	T	C	0.003	TP53	p.M198V	Missense
PD41165	5	88.8	17	7577572	7577572	T	C	0.008	TP53	p.M198V	Missense
PD41165	1	75.3	21	36164659	36164659	A	G	0.002	RUNX1	p.Y406H	Missense
PD41165	2	78.3	21	36164659	36164659	A	G	0.003	RUNX1	p.Y406H	Missense
PD41165	3	82.2	21	36164659	36164659	A	G	0.004	RUNX1	p.Y406H	Missense
PD41165	4	85.0	21	36164659	36164659	A	G	0.005	RUNX1	p.Y406H	Missense
PD41165	5	88.8	21	36164659	36164659	A	G	0.015	RUNX1	p.Y406H	Missense
PD41166	1	72.7	2	25464534	25464534	T	C	0.009	DNMT3A	p.Y660C	Missense
PD41166	2	77.4	2	25464534	25464534	T	C	0.009	DNMT3A	p.Y660C	Missense
PD41166	3	81.1	2	25464534	25464534	T	C	0.015	DNMT3A	p.Y660C	Missense
PD41166	4	84.9	2	25464534	25464534	T	C	0.016	DNMT3A	p.Y660C	Missense
PD41166	1	72.7	4	106182959	106182959	T	G	0.001	TET2	p.M1333R	Missense
PD41166	2	77.4	4	106182959	106182959	T	G	0.007	TET2	p.M1333R	Missense
PD41166	3	81.1	4	106182959	106182959	T	G	0.009	TET2	p.M1333R	Missense
PD41166	4	84.9	4	106182959	106182959	T	G	0.013	TET2	p.M1333R	Missense
PD41167	1	65.4	2	25463184	25463184	G	T	0.014	DNMT3A	p.S770X	Nonsense
PD41167	2	68.0	2	25463184	25463184	G	T	0.022	DNMT3A	p.S770X	Nonsense
PD41167	3	71.8	2	25463184	25463184	G	T	0.038	DNMT3A	p.S770X	Nonsense
PD41167	4	74.7	2	25463184	25463184	G	T	0.033	DNMT3A	p.S770X	Nonsense
PD41167	5	79.1	2	25463184	25463184	G	T	0.038	DNMT3A	p.S770X	Nonsense
PD41167	1	65.4	X	39932767	39932767	C	T	0.000	BCOR	p.S611N	Missense
PD41167	2	68.0	X	39932767	39932767	C	T	0.001	BCOR	p.S611N	Missense
PD41167	3	71.8	X	39932767	39932767	C	T	0.006	BCOR	p.S611N	Missense
PD41167	4	74.7	X	39932767	39932767	C	T	0.001	BCOR	p.S611N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41167	5	79.1	X	39932767	39932767	C	T	0.000	BCOR	p.S611N	Missense
PD41168	1	56.9	20	57430104	57430104	G	A	0.000	GNAS	p.R595Q	Missense
PD41168	2	59.9	20	57430104	57430104	G	A	0.006	GNAS	p.R595Q	Missense
PD41168	3	63.6	20	57430104	57430104	G	A	0.006	GNAS	p.R595Q	Missense
PD41168	4	66.3	20	57430104	57430104	G	A	0.000	GNAS	p.R595Q	Missense
PD41168	5	71.0	20	57430104	57430104	G	A	0.000	GNAS	p.R595Q	Missense
PD41169	1	70.8	4	106196291	106196291	C	T	0.004	TET2	p.Q1542X	Nonsense
PD41169	2	74.4	4	106196291	106196291	C	T	0.000	TET2	p.Q1542X	Nonsense
PD41169	3	77.9	4	106196291	106196291	C	T	0.009	TET2	p.Q1542X	Nonsense
PD41169	4	83.4	4	106196291	106196291	C	T	0.009	TET2	p.Q1542X	Nonsense
PD41169	1	70.8	21	44514777	44514777	T	C	0.000	U2AF1	p.Q84R	Missense
PD41169	2	74.4	21	44514777	44514777	T	C	0.000	U2AF1	p.Q84R	Missense
PD41169	3	77.9	21	44514777	44514777	T	C	0.001	U2AF1	p.Q84R	Missense
PD41169	4	83.4	21	44514777	44514777	T	C	0.015	U2AF1	p.Q84R	Missense
PD41169	1	70.8	X	129155113	129155113	A	G	0.000	BCORL1	p.S1199G	Missense
PD41169	2	74.4	X	129155113	129155113	A	G	0.000	BCORL1	p.S1199G	Missense
PD41169	3	77.9	X	129155113	129155113	A	G	0.005	BCORL1	p.S1199G	Missense
PD41169	4	83.4	X	129155113	129155113	A	G	0.000	BCORL1	p.S1199G	Missense
PD41171	1	69.3	12	50025301	50025301	A	G	0.001	PRPF40B	p.M68V	Missense
PD41171	2	72.6	12	50025301	50025301	A	G	0.006	PRPF40B	p.M68V	Missense
PD41171	3	77.4	12	50025301	50025301	A	G	0.000	PRPF40B	p.M68V	Missense
PD41171	4	81.8	12	50025301	50025301	A	G	0.000	PRPF40B	p.M68V	Missense
PD41171	1	69.3	20	31022936	31022937	TC	T	0.000	ASXL1	p.P808fs	Frameshift
PD41171	2	72.6	20	31022936	31022937	TC	T	0.003	ASXL1	p.P808fs	Frameshift
PD41171	3	77.4	20	31022936	31022937	TC	T	0.001	ASXL1	p.P808fs	Frameshift
PD41171	4	81.8	20	31022936	31022937	TC	T	0.018	ASXL1	p.P808fs	Frameshift
PD41171	1	69.3	X	129156934	129156934	C	A	0.004	BCORL1	p.R1224S	Missense
PD41171	2	72.6	X	129156934	129156934	C	A	0.000	BCORL1	p.R1224S	Missense
PD41171	3	77.4	X	129156934	129156934	C	A	0.002	BCORL1	p.R1224S	Missense
PD41171	4	81.8	X	129156934	129156934	C	A	0.001	BCORL1	p.R1224S	Missense
PD41172	1	61.0	11	118343396	118343396	G	A	0.002	KMT2A	p.E508K	Missense
PD41172	2	64.0	11	118343396	118343396	G	A	0.009	KMT2A	p.E508K	Missense
PD41172	3	67.9	11	118343396	118343396	G	A	0.008	KMT2A	p.E508K	Missense
PD41172	4	70.5	11	118343396	118343396	G	A	0.004	KMT2A	p.E508K	Missense
PD41172	5	75.5	11	118343396	118343396	G	A	0.005	KMT2A	p.E508K	Missense
PD41174	1	64.3	16	3823896	3823896	C	A	0.001	CREBBP	p.P773P	Synonymous
PD41174	2	67.2	16	3823896	3823896	C	A	0.000	CREBBP	p.P773P	Synonymous
PD41174	3	71.0	16	3823896	3823896	C	A	0.001	CREBBP	p.P773P	Synonymous
PD41174	4	73.6	16	3823896	3823896	C	A	0.002	CREBBP	p.P773P	Synonymous
PD41174	5	77.7	16	3823896	3823896	C	A	0.010	CREBBP	p.P773P	Synonymous
PD41174	1	64.3	17	7577539	7577539	G	A	0.000	TP53	p.R209W	Missense
PD41174	2	67.2	17	7577539	7577539	G	A	0.003	TP53	p.R209W	Missense
PD41174	3	71.0	17	7577539	7577539	G	A	0.006	TP53	p.R209W	Missense
PD41174	4	73.6	17	7577539	7577539	G	A	0.005	TP53	p.R209W	Missense
PD41174	5	77.7	17	7577539	7577539	G	A	0.010	TP53	p.R209W	Missense
PD41174	1	64.3	X	129150090	129150090	G	A	0.001	BCORL1	p.L1114L	Synonymous
PD41174	2	67.2	X	129150090	129150090	G	A	0.006	BCORL1	p.L1114L	Synonymous
PD41174	3	71.0	X	129150090	129150090	G	A	0.000	BCORL1	p.L1114L	Synonymous
PD41174	4	73.6	X	129150090	129150090	G	A	0.000	BCORL1	p.L1114L	Synonymous
PD41174	5	77.7	X	129150090	129150090	G	A	0.000	BCORL1	p.L1114L	Synonymous
PD41175	1	69.5	1	1720666	1720666	C	T	0.000	GNB1	p.A248T	Missense
PD41175	2	72.5	1	1720666	1720666	C	T	0.000	GNB1	p.A248T	Missense
PD41175	3	77.4	1	1720666	1720666	C	T	0.000	GNB1	p.A248T	Missense
PD41175	5	83.2	1	1720666	1720666	C	T	0.007	GNB1	p.A248T	Missense
PD41175	1	69.5	2	25464455	25464455	G	T	0.006	DNMT3A	p.D686E	Missense
PD41175	2	72.5	2	25464455	25464455	G	T	0.012	DNMT3A	p.D686E	Missense
PD41175	3	77.4	2	25464455	25464455	G	T	0.016	DNMT3A	p.D686E	Missense
PD41175	5	83.2	2	25464455	25464455	G	T	0.013	DNMT3A	p.D686E	Missense
PD41175	1	69.5	17	58740376	58740376	G	A	0.004	PPM1D	p.W427X	Nonsense
PD41175	2	72.5	17	58740376	58740376	G	A	0.001	PPM1D	p.W427X	Nonsense
PD41175	3	77.4	17	58740376	58740376	G	A	0.008	PPM1D	p.W427X	Nonsense
PD41175	5	83.2	17	58740376	58740376	G	A	0.009	PPM1D	p.W427X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41176	1	71.4	4	106197294	106197294	C	G	0.002	TET2	p.A1876G	Missense
PD41176	3	79.5	4	106197294	106197294	C	G	0.007	TET2	p.A1876G	Missense
PD41176	5	86.1	4	106197294	106197294	C	G	0.009	TET2	p.A1876G	Missense
PD41176	1	71.4	17	58701085	58701085	G	T	0.006	PPM1D	p.E226X	Nonsense
PD41176	3	79.5	17	58701085	58701085	G	T	0.000	PPM1D	p.E226X	Nonsense
PD41176	5	86.1	17	58701085	58701085	G	T	0.000	PPM1D	p.E226X	Nonsense
PD41176	1	71.4	X	123191784	123191784	C	T	0.000	STAG2	p.A458V	Missense
PD41176	3	79.5	X	123191784	123191784	C	T	0.000	STAG2	p.A458V	Missense
PD41176	5	86.1	X	123191784	123191784	C	T	0.001	STAG2	p.A458V	Missense
PD41177	1	67.9	2	25463184	25463184	G	A	0.018	DNMT3A	p.S770L	Missense
PD41177	2	71.4	2	25463184	25463184	G	A	0.027	DNMT3A	p.S770L	Missense
PD41177	3	75.3	2	25463184	25463184	G	A	0.060	DNMT3A	p.S770L	Missense
PD41177	4	80.1	2	25463184	25463184	G	A	0.047	DNMT3A	p.S770L	Missense
PD41177	1	67.9	2	25468133	25468133	G	A	0.005	DNMT3A	p.Q515X	Nonsense
PD41177	2	71.4	2	25468133	25468133	G	A	0.003	DNMT3A	p.Q515X	Nonsense
PD41177	3	75.3	2	25468133	25468133	G	A	0.005	DNMT3A	p.Q515X	Nonsense
PD41177	4	80.1	2	25468133	25468133	G	A	0.019	DNMT3A	p.Q515X	Nonsense
PD41178	1	70.3	8	117862856	117862856	C	A	0.007	RAD21	c.1620+1G>T	Splice site
PD41178	2	73.3	8	117862856	117862856	C	A	0.001	RAD21	c.1620+1G>T	Splice site
PD41178	3	78.2	8	117862856	117862856	C	A	0.000	RAD21	c.1620+1G>T	Splice site
PD41178	4	82.8	8	117862856	117862856	C	A	0.000	RAD21	c.1620+1G>T	Splice site
PD41178	1	70.3	11	32456840	32456840	G	A	0.000	WT1	p.L18F	Missense
PD41178	2	73.3	11	32456840	32456840	G	A	0.008	WT1	p.L18F	Missense
PD41178	3	78.2	11	32456840	32456840	G	A	0.000	WT1	p.L18F	Missense
PD41178	4	82.8	11	32456840	32456840	G	A	0.000	WT1	p.L18F	Missense
PD41178	1	70.3	17	58740546	58740554	TAAGGATAC	T	0.054	PPM1D	p.L484fs	Frameshift
PD41178	2	73.3	17	58740546	58740554	TAAGGATAC	T	0.098	PPM1D	p.L484fs	Frameshift
PD41178	3	78.2	17	58740546	58740554	TAAGGATAC	T	0.086	PPM1D	p.L484fs	Frameshift
PD41178	4	82.8	17	58740546	58740554	TAAGGATAC	T	0.140	PPM1D	p.L484fs	Frameshift
PD41178	1	70.3	20	31022592	31022592	C	T	0.006	ASXL1	p.R693X	Nonsense
PD41178	2	73.3	20	31022592	31022592	C	T	0.006	ASXL1	p.R693X	Nonsense
PD41178	3	78.2	20	31022592	31022592	C	T	0.014	ASXL1	p.R693X	Nonsense
PD41178	4	82.8	20	31022592	31022592	C	T	0.026	ASXL1	p.R693X	Nonsense
PD41179	1	69.8	X	44942787	44942787	G	A	0.008	KDM6A	p.G1175S	Missense
PD41179	2	72.9	X	44942787	44942787	G	A	0.024	KDM6A	p.G1175S	Missense
PD41179	3	77.8	X	44942787	44942787	G	A	0.078	KDM6A	p.G1175S	Missense
PD41179	4	81.7	X	44942787	44942787	G	A	0.134	KDM6A	p.G1175S	Missense
PD41180	1	67.7	8	117878916	117878916	C	A	0.001	RAD21	p.W18L	Missense
PD41180	2	70.7	8	117878916	117878916	C	A	0.002	RAD21	p.W18L	Missense
PD41180	3	74.6	8	117878916	117878916	C	A	0.006	RAD21	p.W18L	Missense
PD41180	4	77.2	8	117878916	117878916	C	A	0.008	RAD21	p.W18L	Missense
PD41180	5	81.2	8	117878916	117878916	C	A	0.007	RAD21	p.W18L	Missense
PD41180	1	67.7	19	56171946	56171946	T	C	0.006	U2AF2	p.F99L	Missense
PD41180	2	70.7	19	56171946	56171946	T	C	0.004	U2AF2	p.F99L	Missense
PD41180	3	74.6	19	56171946	56171946	T	C	0.006	U2AF2	p.F99L	Missense
PD41180	4	77.2	19	56171946	56171946	T	C	0.010	U2AF2	p.F99L	Missense
PD41180	5	81.2	19	56171946	56171946	T	C	0.007	U2AF2	p.F99L	Missense
PD41181	1	70.1	2	25459804	25459804	C	T	0.005	DNMT3A	c.2478+1G>A	Splice site
PD41181	2	73.1	2	25459804	25459804	C	T	0.011	DNMT3A	c.2478+1G>A	Splice site
PD41181	3	78.0	2	25459804	25459804	C	T	0.011	DNMT3A	c.2478+1G>A	Splice site
PD41181	4	83.0	2	25459804	25459804	C	T	0.023	DNMT3A	c.2478+1G>A	Splice site
PD41181	1	70.1	2	25463287	25463287	G	A	0.001	DNMT3A	p.R736C	Missense
PD41181	2	73.1	2	25463287	25463287	G	A	0.003	DNMT3A	p.R736C	Missense
PD41181	3	78.0	2	25463287	25463287	G	A	0.008	DNMT3A	p.R736C	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41181	4	83.0	2	25463287	25463287	G	A	0.013	DNMT3A	p.R736C	Missense
PD41182	1	92.5	2	198272720	198272720	A	G	0.005	SF3B1	c.1239+2T>C	Splice site
PD41182	2	95.6	2	198272720	198272720	A	G	0.000	SF3B1	c.1239+2T>C	Splice site
PD41182	3	100.8	2	198272720	198272720	A	G	0.000	SF3B1	c.1239+2T>C	Splice site
PD41182	1	92.5	4	106156786	106156786	G	T	0.006	TET2	p.G563X	Nonsense
PD41182	2	95.6	4	106156786	106156786	G	T	0.003	TET2	p.G563X	Nonsense
PD41182	3	100.8	4	106156786	106156786	G	T	0.002	TET2	p.G563X	Nonsense
PD41182	1	92.5	20	31023589	31023590	AG	A	0.020	ASXL1	p.K1025fs	Frameshift
PD41182	2	95.6	20	31023589	31023590	AG	A	0.032	ASXL1	p.K1025fs	Frameshift
PD41182	3	100.8	20	31023589	31023590	AG	A	0.075	ASXL1	p.K1025fs	Frameshift
PD41183	1	62.4	1	115258748	115258748	C	T	0.003	NRAS	p.G12S	Missense
PD41183	2	65.4	1	115258748	115258748	C	T	0.004	NRAS	p.G12S	Missense
PD41183	3	69.0	1	115258748	115258748	C	T	0.010	NRAS	p.G12S	Missense
PD41183	4	71.6	1	115258748	115258748	C	T	0.005	NRAS	p.G12S	Missense
PD41183	5	75.7	1	115258748	115258748	C	T	0.011	NRAS	p.G12S	Missense
PD41183	1	62.4	4	106157332	106157332	C	T	0.001	TET2	p.Q745X	Nonsense
PD41183	2	65.4	4	106157332	106157332	C	T	0.005	TET2	p.Q745X	Nonsense
PD41183	3	69.0	4	106157332	106157332	C	T	0.009	TET2	p.Q745X	Nonsense
PD41183	4	71.6	4	106157332	106157332	C	T	0.012	TET2	p.Q745X	Nonsense
PD41183	5	75.7	4	106157332	106157332	C	T	0.013	TET2	p.Q745X	Nonsense
PD41183	1	62.4	7	101892220	101892220	C	T	0.002	CUX1	p.R1472R	Synonymous
PD41183	2	65.4	7	101892220	101892220	C	T	0.007	CUX1	p.R1472R	Synonymous
PD41183	3	69.0	7	101892220	101892220	C	T	0.001	CUX1	p.R1472R	Synonymous
PD41183	4	71.6	7	101892220	101892220	C	T	0.001	CUX1	p.R1472R	Synonymous
PD41183	5	75.7	7	101892220	101892220	C	T	0.000	CUX1	p.R1472R	Synonymous
PD41183	1	62.4	X	53430554	53430554	G	A	0.000	SMC1A	p.N766N	Synonymous
PD41183	2	65.4	X	53430554	53430554	G	A	0.000	SMC1A	p.N766N	Synonymous
PD41183	3	69.0	X	53430554	53430554	G	A	0.004	SMC1A	p.N766N	Synonymous
PD41183	4	71.6	X	53430554	53430554	G	A	0.000	SMC1A	p.N766N	Synonymous
PD41183	5	75.7	X	53430554	53430554	G	A	0.000	SMC1A	p.N766N	Synonymous
PD41184	1	73.0	2	25457158	25457158	G	A	0.015	DNMT3A	p.A910V	Missense
PD41184	2	76.1	2	25457158	25457158	G	A	0.017	DNMT3A	p.A910V	Missense
PD41184	3	80.5	2	25457158	25457158	G	A	0.018	DNMT3A	p.A910V	Missense
PD41184	1	73.0	2	25459872	25459872	G	A	0.007	DNMT3A	p.P804L	Missense
PD41184	2	76.1	2	25459872	25459872	G	A	0.006	DNMT3A	p.P804L	Missense
PD41184	3	80.5	2	25459872	25459872	G	A	0.019	DNMT3A	p.P804L	Missense
PD41184	1	73.0	2	25464537	25464537	C	T	0.054	DNMT3A	p.R659H	Missense
PD41184	2	76.1	2	25464537	25464537	C	T	0.040	DNMT3A	p.R659H	Missense
PD41184	3	80.5	2	25464537	25464537	C	T	0.032	DNMT3A	p.R659H	Missense
PD41184	1	73.0	2	25470459	25470459	C	T	0.025	DNMT3A	c.1014+1G>A	Splice site
PD41184	2	76.1	2	25470459	25470459	C	T	0.036	DNMT3A	c.1014+1G>A	Splice site
PD41184	3	80.5	2	25470459	25470459	C	T	0.041	DNMT3A	c.1014+1G>A	Splice site
PD41184	1	73.0	7	101926032	101926032	G	A	0.007	CUX1	p.S642N	Missense
PD41184	2	76.1	7	101926032	101926032	G	A	0.000	CUX1	p.S642N	Missense
PD41184	3	80.5	7	101926032	101926032	G	A	0.000	CUX1	p.S642N	Missense
PD41185	1	69.6	2	25463568	25463568	A	G	0.059	DNMT3A	p.I705T	Missense
PD41185	2	72.5	2	25463568	25463568	A	G	0.075	DNMT3A	p.I705T	Missense
PD41185	3	75.6	2	25463568	25463568	A	G	0.081	DNMT3A	p.I705T	Missense
PD41185	4	78.5	2	25463568	25463568	A	G	0.110	DNMT3A	p.I705T	Missense
PD41185	5	82.8	2	25463568	25463568	A	G	0.116	DNMT3A	p.I705T	Missense
PD41186	1	72.6	17	7573983	7573983	C	A	0.000	TP53	p.L309F	Missense
PD41186	2	76.1	17	7573983	7573983	C	A	0.005	TP53	p.L309F	Missense
PD41186	3	80.9	17	7573983	7573983	C	A	0.000	TP53	p.L309F	Missense
PD41186	4	84.2	17	7573983	7573983	C	A	0.000	TP53	p.L309F	Missense
PD41188	1	73.2	1	1747228	1747228	T	A	0.015	GNB1	p.K57M	Missense
PD41188	2	76.3	1	1747228	1747228	T	A	0.018	GNB1	p.K57M	Missense
PD41188	3	81.5	1	1747228	1747228	T	A	0.025	GNB1	p.K57M	Missense
PD41188	1	73.2	4	106197443	106197443	C	G	0.002	TET2	p.R1926G	Missense
PD41188	2	76.3	4	106197443	106197443	C	G	0.006	TET2	p.R1926G	Missense
PD41188	3	81.5	4	106197443	106197443	C	G	0.012	TET2	p.R1926G	Missense
PD41188	1	73.2	12	112915814	112915814	G	A	0.001	PTPN11	p.G363R	Missense
PD41188	2	76.3	12	112915814	112915814	G	A	0.000	PTPN11	p.G363R	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41188	3	81.5	12	112915814	112915814	G	A	0.007	PTPN11	p.G363R	Missense
PD41190	1	66.3	4	106190837	106190837	C	T	0.081	TET2	p.T1372I	Missense
PD41190	2	69.4	4	106190837	106190837	C	T	0.109	TET2	p.T1372I	Missense
PD41190	3	72.9	4	106190837	106190837	C	T	0.155	TET2	p.T1372I	Missense
PD41190	4	75.7	4	106190837	106190837	C	T	0.220	TET2	p.T1372I	Missense
PD41190	5	79.7	4	106190837	106190837	C	T	0.346	TET2	p.T1372I	Missense
PD41190	1	66.3	4	106197309	106197309	A	G	0.005	TET2	p.H1881R	Missense
PD41190	2	69.4	4	106197309	106197309	A	G	0.007	TET2	p.H1881R	Missense
PD41190	3	72.9	4	106197309	106197309	A	G	0.008	TET2	p.H1881R	Missense
PD41190	4	75.7	4	106197309	106197309	A	G	0.009	TET2	p.H1881R	Missense
PD41190	5	79.7	4	106197309	106197309	A	G	0.007	TET2	p.H1881R	Missense
PD41190	1	66.3	7	148504766	148504766	C	T	0.013	EZH2	p.G743D	Missense
PD41190	2	69.4	7	148504766	148504766	C	T	0.018	EZH2	p.G743D	Missense
PD41190	3	72.9	7	148504766	148504766	C	T	0.028	EZH2	p.G743D	Missense
PD41190	4	75.7	7	148504766	148504766	C	T	0.035	EZH2	p.G743D	Missense
PD41190	5	79.7	7	148504766	148504766	C	T	0.047	EZH2	p.G743D	Missense
PD41190	1	66.3	11	119149290	119149291	TG	T	0.000	CBL	p.P433fs	Frameshift
PD41190	2	69.4	11	119149290	119149291	TG	T	0.000	CBL	p.P433fs	Frameshift
PD41190	3	72.9	11	119149290	119149291	TG	T	0.002	CBL	p.P433fs	Frameshift
PD41190	4	75.7	11	119149290	119149291	TG	T	0.004	CBL	p.P433fs	Frameshift
PD41190	5	79.7	11	119149290	119149291	TG	T	0.007	CBL	p.P433fs	Frameshift
PD41190	1	66.3	19	56173940	56173940	T	G	0.000	U2AF2	p.L187V	Missense
PD41190	2	69.4	19	56173940	56173940	T	G	0.002	U2AF2	p.L187V	Missense
PD41190	3	72.9	19	56173940	56173940	T	G	0.000	U2AF2	p.L187V	Missense
PD41190	4	75.7	19	56173940	56173940	T	G	0.000	U2AF2	p.L187V	Missense
PD41190	5	79.7	19	56173940	56173940	T	G	0.017	U2AF2	p.L187V	Missense
PD41190	1	66.3	20	31022233	31022233	A	C	0.060	ASXL1	c.1720-2A>C	Splice site
PD41190	2	69.4	20	31022233	31022233	A	C	0.120	ASXL1	c.1720-2A>C	Splice site
PD41190	3	72.9	20	31022233	31022233	A	C	0.174	ASXL1	c.1720-2A>C	Splice site
PD41190	4	75.7	20	31022233	31022233	A	C	0.198	ASXL1	c.1720-2A>C	Splice site
PD41190	5	79.7	20	31022233	31022233	A	C	0.295	ASXL1	c.1720-2A>C	Splice site
PD41191	1	70.5	4	106156516	106156517	TC	T	0.005	TET2	p.S473fs	Frameshift
PD41191	3	76.5	4	106156516	106156517	TC	T	0.002	TET2	p.S473fs	Frameshift
PD41191	1	70.5	4	106157856	106157857	CT	C	0.010	TET2	p.L920X	Nonsense
PD41191	3	76.5	4	106157856	106157857	CT	C	0.007	TET2	p.L920X	Nonsense
PD41191	1	70.5	4	106197207	106197207	G	A	0.131	TET2	p.W1847X	Nonsense
PD41191	3	76.5	4	106197207	106197207	G	A	0.162	TET2	p.W1847X	Nonsense
PD41191	1	70.5	X	129159339	129159339	C	T	0.004	BCORL1	p.R1355W	Missense
PD41191	3	76.5	X	129159339	129159339	C	T	0.006	BCORL1	p.R1355W	Missense
PD41192	1	70.7	2	198266227	198266227	G	A	0.001	SF3B1	p.T798I	Missense
PD41192	2	73.7	2	198266227	198266227	G	A	0.007	SF3B1	p.T798I	Missense
PD41192	3	78.4	2	198266227	198266227	G	A	0.000	SF3B1	p.T798I	Missense
PD41192	4	82.6	2	198266227	198266227	G	A	0.000	SF3B1	p.T798I	Missense
PD41192	1	70.7	2	25464454	25464454	C	G	0.007	DNMT3A	p.V687L	Missense
PD41192	2	73.7	2	25464454	25464454	C	G	0.005	DNMT3A	p.V687L	Missense
PD41192	3	78.4	2	25464454	25464454	C	G	0.002	DNMT3A	p.V687L	Missense
PD41192	4	82.6	2	25464454	25464454	C	G	0.000	DNMT3A	p.V687L	Missense
PD41192	1	70.7	2	25470498	25470498	G	A	0.135	DNMT3A	p.R326C	Missense
PD41192	2	73.7	2	25470498	25470498	G	A	0.222	DNMT3A	p.R326C	Missense
PD41192	3	78.4	2	25470498	25470498	G	A	0.317	DNMT3A	p.R326C	Missense
PD41192	4	82.6	2	25470498	25470498	G	A	0.347	DNMT3A	p.R326C	Missense
PD41192	1	70.7	9	139407571	139407571	G	A	0.000	NOTCH1	p.T790I	Missense
PD41192	2	73.7	9	139407571	139407571	G	A	0.010	NOTCH1	p.T790I	Missense
PD41192	3	78.4	9	139407571	139407571	G	A	0.002	NOTCH1	p.T790I	Missense
PD41192	4	82.6	9	139407571	139407571	G	A	0.000	NOTCH1	p.T790I	Missense
PD41193	1	64.0	4	106197285	106197285	T	C	0.087	TET2	p.I1873T	Missense
PD41193	2	67.0	4	106197285	106197285	T	C	0.093	TET2	p.I1873T	Missense
PD41193	3	72.3	4	106197285	106197285	T	C	0.074	TET2	p.I1873T	Missense
PD41193	4	75.6	4	106197285	106197285	T	C	0.060	TET2	p.I1873T	Missense
PD41193	1	64.0	11	119149219	119149219	G	A	0.000	CBL	c.1228-1G>A	Splice site
PD41193	2	67.0	11	119149219	119149219	G	A	0.000	CBL	c.1228-1G>A	Splice site
PD41193	3	72.3	11	119149219	119149219	G	A	0.017	CBL	c.1228-1G>A	Splice site

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41193	4	75.6	11	119149219	119149219	G	A	0.038	CBL	c.1228-1G>A	Splice site
PD41193	1	64.0	15	90631934	90631934	C	T	0.005	IDH2	p.R140Q	Missense
PD41193	2	67.0	15	90631934	90631934	C	T	0.019	IDH2	p.R140Q	Missense
PD41193	3	72.3	15	90631934	90631934	C	T	0.062	IDH2	p.R140Q	Missense
PD41193	4	75.6	15	90631934	90631934	C	T	0.081	IDH2	p.R140Q	Missense
PD41193	1	64.0	X	129148387	129148387	C	T	0.014	BCORL1	p.P547S	Missense
PD41193	2	67.0	X	129148387	129148387	C	T	0.005	BCORL1	p.P547S	Missense
PD41193	3	72.3	X	129148387	129148387	C	T	0.002	BCORL1	p.P547S	Missense
PD41193	4	75.6	X	129148387	129148387	C	T	0.001	BCORL1	p.P547S	Missense
PD41194	1	72.3	2	198268382	198268382	C	T	0.000	SF3B1	p.R549H	Missense
PD41194	2	75.5	2	198268382	198268382	C	T	0.000	SF3B1	p.R549H	Missense
PD41194	3	79.4	2	198268382	198268382	C	T	0.003	SF3B1	p.R549H	Missense
PD41194	4	84.7	2	198268382	198268382	C	T	0.012	SF3B1	p.R549H	Missense
PD41194	1	72.3	2	25463188	25463188	T	C	0.008	DNMT3A	p.I769V	Missense
PD41194	2	75.5	2	25463188	25463188	T	C	0.005	DNMT3A	p.I769V	Missense
PD41194	3	79.4	2	25463188	25463188	T	C	0.012	DNMT3A	p.I769V	Missense
PD41194	4	84.7	2	25463188	25463188	T	C	0.003	DNMT3A	p.I769V	Missense
PD41194	1	72.3	4	106156950	106156960	GCAA GCTT ACA	G	0.012	TET2	p.Q618fs	Frameshift
PD41194	2	75.5	4	106156950	106156960	GCAA GCTT ACA	G	0.018	TET2	p.Q618fs	Frameshift
PD41194	3	79.4	4	106156950	106156960	GCAA GCTT ACA	G	0.059	TET2	p.Q618fs	Frameshift
PD41194	4	84.7	4	106156950	106156960	GCAA GCTT ACA	G	0.165	TET2	p.Q618fs	Frameshift
PD41194	1	72.3	9	139405693	139405693	C	T	0.000	NOTCH1	p.C833Y	Missense
PD41194	2	75.5	9	139405693	139405693	C	T	0.000	NOTCH1	p.C833Y	Missense
PD41194	3	79.4	9	139405693	139405693	C	T	0.000	NOTCH1	p.C833Y	Missense
PD41194	4	84.7	9	139405693	139405693	C	T	0.009	NOTCH1	p.C833Y	Missense
PD41194	1	72.3	10	112361484	112361484	A	G	0.005	SMC3	p.M912V	Missense
PD41194	2	75.5	10	112361484	112361484	A	G	0.004	SMC3	p.M912V	Missense
PD41194	3	79.4	10	112361484	112361484	A	G	0.003	SMC3	p.M912V	Missense
PD41194	4	84.7	10	112361484	112361484	A	G	0.004	SMC3	p.M912V	Missense
PD41194	1	72.3	17	7577094	7577094	G	A	0.002	TP53	p.R243W	Missense
PD41194	2	75.5	17	7577094	7577094	G	A	0.009	TP53	p.R243W	Missense
PD41194	3	79.4	17	7577094	7577094	G	A	0.007	TP53	p.R243W	Missense
PD41194	4	84.7	17	7577094	7577094	G	A	0.004	TP53	p.R243W	Missense
PD41195	1	73.3	7	101838851	101838851	C	T	0.007	CUX1	p.A397V	Missense
PD41195	2	76.3	7	101838851	101838851	C	T	0.000	CUX1	p.A397V	Missense
PD41195	3	81.0	7	101838851	101838851	C	T	0.002	CUX1	p.A397V	Missense
PD41195	1	73.3	X	123211887	123211887	C	T	0.013	STAG2	p.T918T	Synonymous
PD41195	2	76.3	X	123211887	123211887	C	T	0.004	STAG2	p.T918T	Synonymous
PD41195	3	81.0	X	123211887	123211887	C	T	0.004	STAG2	p.T918T	Synonymous
PD41196	1	64.0	2	25463184	25463184	G	A	0.008	DNMT3A	p.S770L	Missense
PD41196	2	67.0	2	25463184	25463184	G	A	0.009	DNMT3A	p.S770L	Missense
PD41196	3	70.3	2	25463184	25463184	G	A	0.017	DNMT3A	p.S770L	Missense
PD41196	4	73.1	2	25463184	25463184	G	A	0.025	DNMT3A	p.S770L	Missense
PD41196	5	76.7	2	25463184	25463184	G	A	0.033	DNMT3A	p.S770L	Missense
PD41196	1	64.0	19	17945696	17945696	C	A	0.006	JAK3	p.V722F	Missense
PD41196	2	67.0	19	17945696	17945696	C	A	0.000	JAK3	p.V722F	Missense
PD41196	3	70.3	19	17945696	17945696	C	A	0.001	JAK3	p.V722F	Missense
PD41196	4	73.1	19	17945696	17945696	C	A	0.000	JAK3	p.V722F	Missense
PD41196	5	76.7	19	17945696	17945696	C	A	0.000	JAK3	p.V722F	Missense
PD41197	1	73.2	2	25463181	25463181	C	T	0.006	DNMT3A	p.R771Q	Missense
PD41197	3	80.9	2	25463181	25463181	C	T	0.002	DNMT3A	p.R771Q	Missense
PD41197	5	86.8	2	25463181	25463181	C	T	0.008	DNMT3A	p.R771Q	Missense
PD41197	1	73.2	2	25463289	25463289	T	C	0.016	DNMT3A	p.Y735C	Missense
PD41197	3	80.9	2	25463289	25463289	T	C	0.011	DNMT3A	p.Y735C	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41197	5	86.8	2	25463289	25463289	T	C	0.020	DNMT3A	p.Y735C	Missense
PD41197	1	73.2	2	25469053	25469053	C	A	0.009	DNMT3A	p.E469X	Nonsense
PD41197	3	80.9	2	25469053	25469053	C	A	0.024	DNMT3A	p.E469X	Nonsense
PD41197	5	86.8	2	25469053	25469053	C	A	0.051	DNMT3A	p.E469X	Nonsense
PD41197	1	73.2	X	53432009	53432009	G	C	0.002	SMC1A	p.R689G	Missense
PD41197	3	80.9	X	53432009	53432009	G	C	0.006	SMC1A	p.R689G	Missense
PD41197	5	86.8	X	53432009	53432009	G	C	0.002	SMC1A	p.R689G	Missense
PD41198	1	67.9	20	57415326	57415326	C	T	0.000	GNAS	p.R55R	Synonymous
PD41198	2	70.8	20	57415326	57415326	C	T	0.009	GNAS	p.R55R	Synonymous
PD41198	3	75.3	20	57415326	57415326	C	T	0.001	GNAS	p.R55R	Synonymous
PD41198	4	79.0	20	57415326	57415326	C	T	0.000	GNAS	p.R55R	Synonymous
PD41198	5	82.1	20	57415326	57415326	C	T	0.000	GNAS	p.R55R	Synonymous
PD41199	1	73.4	2	25464573	25464573	A	C	0.007	DNMT3A	p.L647R	Missense
PD41199	2	76.6	2	25464573	25464573	A	C	0.008	DNMT3A	p.L647R	Missense
PD41199	3	81.3	2	25464573	25464573	A	C	0.005	DNMT3A	p.L647R	Missense
PD41199	4	85.4	2	25464573	25464573	A	C	0.000	DNMT3A	p.L647R	Missense
PD41199	1	73.4	X	44928857	44928857	G	C	0.005	KDM6A	p.G705R	Missense
PD41199	2	76.6	X	44928857	44928857	G	C	0.006	KDM6A	p.G705R	Missense
PD41199	3	81.3	X	44928857	44928857	G	C	0.020	KDM6A	p.G705R	Missense
PD41199	4	85.4	X	44928857	44928857	G	C	0.012	KDM6A	p.G705R	Missense
PD41199	1	73.4	X	44942757	44942757	G	C	0.008	KDM6A	p.V1165L	Missense
PD41199	2	76.6	X	44942757	44942757	G	C	0.004	KDM6A	p.V1165L	Missense
PD41199	3	81.3	X	44942757	44942757	G	C	0.004	KDM6A	p.V1165L	Missense
PD41199	4	85.4	X	44942757	44942757	G	C	0.002	KDM6A	p.V1165L	Missense
PD41199	1	73.4	X	154348397	154348397	T	C	0.015	BRCC3	p.L308P	Missense
PD41199	2	76.6	X	154348397	154348397	T	C	0.020	BRCC3	p.L308P	Missense
PD41199	3	81.3	X	154348397	154348397	T	C	0.019	BRCC3	p.L308P	Missense
PD41199	4	85.4	X	154348397	154348397	T	C	0.017	BRCC3	p.L308P	Missense
PD41201	1	65.4	11	64533429	64533429	C	T	0.009	SF1	p.G594D	Missense
PD41201	2	68.5	11	64533429	64533429	C	T	0.003	SF1	p.G594D	Missense
PD41201	4	76.7	11	64533429	64533429	C	T	0.002	SF1	p.G594D	Missense
PD41202	1	68.9	2	198267359	198267359	C	A	0.009	SF3B1	p.K666N	Missense
PD41202	2	71.9	2	198267359	198267359	C	A	0.000	SF3B1	p.K666N	Missense
PD41202	3	76.3	2	198267359	198267359	C	A	0.002	SF3B1	p.K666N	Missense
PD41202	4	80.5	2	198267359	198267359	C	A	0.000	SF3B1	p.K666N	Missense
PD41202	1	68.9	2	198267547	198267547	C	T	0.000	SF3B1	p.A604T	Missense
PD41202	2	71.9	2	198267547	198267547	C	T	0.008	SF3B1	p.A604T	Missense
PD41202	3	76.3	2	198267547	198267547	C	T	0.000	SF3B1	p.A604T	Missense
PD41202	4	80.5	2	198267547	198267547	C	T	0.000	SF3B1	p.A604T	Missense
PD41202	1	68.9	4	55593586	55593586	C	T	0.000	KIT	p.P547L	Missense
PD41202	2	71.9	4	55593586	55593586	C	T	0.005	KIT	p.P547L	Missense
PD41202	3	76.3	4	55593586	55593586	C	T	0.000	KIT	p.P547L	Missense
PD41202	4	80.5	4	55593586	55593586	C	T	0.000	KIT	p.P547L	Missense
PD41203	1	76.4	4	106156335	106156336	TC	T	0.020	TET2	p.P413fs	Frameshift
PD41203	2	79.3	4	106156335	106156336	TC	T	0.048	TET2	p.P413fs	Frameshift
PD41203	3	83.7	4	106156335	106156336	TC	T	0.090	TET2	p.P413fs	Frameshift
PD41203	1	76.4	4	106190798	106190798	G	A	0.007	TET2	p.R1359H	Missense
PD41203	2	79.3	4	106190798	106190798	G	A	0.007	TET2	p.R1359H	Missense
PD41203	3	83.7	4	106190798	106190798	G	A	0.017	TET2	p.R1359H	Missense
PD41203	1	76.4	4	106196424	106196426	CAG	C	0.002	TET2	p.S1586fs	Frameshift
PD41203	2	79.3	4	106196424	106196426	CAG	C	0.005	TET2	p.S1586fs	Frameshift
PD41203	3	83.7	4	106196424	106196426	CAG	C	0.005	TET2	p.S1586fs	Frameshift
PD41203	1	76.4	17	7577094	7577094	G	A	0.015	TP53	p.R243W	Missense
PD41203	2	79.3	17	7577094	7577094	G	A	0.014	TP53	p.R243W	Missense
PD41203	3	83.7	17	7577094	7577094	G	A	0.016	TP53	p.R243W	Missense
PD41207	1	56.2	11	64537026	64537026	C	A	0.001	SF1	p.G179W	Missense
PD41207	2	59.1	11	64537026	64537026	C	A	0.005	SF1	p.G179W	Missense
PD41207	3	62.2	11	64537026	64537026	C	A	0.001	SF1	p.G179W	Missense
PD41207	4	64.8	11	64537026	64537026	C	A	0.000	SF1	p.G179W	Missense
PD41207	5	68.9	11	64537026	64537026	C	A	0.000	SF1	p.G179W	Missense
PD41208	1	64.7	12	25378562	25378562	C	T	0.011	KRAS	p.A146T	Missense
PD41208	2	67.7	12	25378562	25378562	C	T	0.016	KRAS	p.A146T	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41208	3	70.9	12	25378562	25378562	C	T	0.009	KRAS	p.A146T	Missense
PD41208	4	73.8	12	25378562	25378562	C	T	0.010	KRAS	p.A146T	Missense
PD41208	5	77.9	12	25378562	25378562	C	T	0.025	KRAS	p.A146T	Missense
PD41209	1	63.0	2	25458657	25458658	TA	T	0.028	DNMT3A	p.S839fs	Frameshift
PD41209	2	65.8	2	25458657	25458658	TA	T	0.025	DNMT3A	p.S839fs	Frameshift
PD41209	3	69.2	2	25458657	25458658	TA	T	0.028	DNMT3A	p.S839fs	Frameshift
PD41209	4	71.9	2	25458657	25458658	TA	T	0.039	DNMT3A	p.S839fs	Frameshift
PD41209	5	76.2	2	25458657	25458658	TA	T	0.025	DNMT3A	p.S839fs	Frameshift
PD41209	1	63.0	2	25468910	25468910	G	A	0.009	DNMT3A	p.Q485X	Nonsense
PD41209	2	65.8	2	25468910	25468910	G	A	0.005	DNMT3A	p.Q485X	Nonsense
PD41209	3	69.2	2	25468910	25468910	G	A	0.009	DNMT3A	p.Q485X	Nonsense
PD41209	4	71.9	2	25468910	25468910	G	A	0.012	DNMT3A	p.Q485X	Nonsense
PD41209	5	76.2	2	25468910	25468910	G	A	0.010	DNMT3A	p.Q485X	Nonsense
PD41211	1	75.6	4	106190860	106190860	C	T	0.007	TET2	p.H1380Y	Missense
PD41211	2	78.7	4	106190860	106190860	C	T	0.009	TET2	p.H1380Y	Missense
PD41211	3	82.8	4	106190860	106190860	C	T	0.031	TET2	p.H1380Y	Missense
PD41211	4	85.9	4	106190860	106190860	C	T	0.064	TET2	p.H1380Y	Missense
PD41211	5	90.4	4	106190860	106190860	C	T	0.076	TET2	p.H1380Y	Missense
PD41211	1	75.6	10	112360810	112360810	G	T	0.003	SMC3	p.G856C	Missense
PD41211	2	78.7	10	112360810	112360810	G	T	0.004	SMC3	p.G856C	Missense
PD41211	3	82.8	10	112360810	112360810	G	T	0.006	SMC3	p.G856C	Missense
PD41211	4	85.9	10	112360810	112360810	G	T	0.012	SMC3	p.G856C	Missense
PD41211	5	90.4	10	112360810	112360810	G	T	0.006	SMC3	p.G856C	Missense
PD41211	1	75.6	11	119148929	119148929	A	G	0.002	CBL	p.I383M	Missense
PD41211	2	78.7	11	119148929	119148929	A	G	0.000	CBL	p.I383M	Missense
PD41211	3	82.8	11	119148929	119148929	A	G	0.000	CBL	p.I383M	Missense
PD41211	4	85.9	11	119148929	119148929	A	G	0.003	CBL	p.I383M	Missense
PD41211	5	90.4	11	119148929	119148929	A	G	0.012	CBL	p.I383M	Missense
PD41211	1	75.6	12	50037970	50037970	C	A	0.001	PRPF40B	p.Q892K	Missense
PD41211	2	78.7	12	50037970	50037970	C	A	0.000	PRPF40B	p.Q892K	Missense
PD41211	3	82.8	12	50037970	50037970	C	A	0.005	PRPF40B	p.Q892K	Missense
PD41211	4	85.9	12	50037970	50037970	C	A	0.000	PRPF40B	p.Q892K	Missense
PD41211	5	90.4	12	50037970	50037970	C	A	0.000	PRPF40B	p.Q892K	Missense
PD41211	1	75.6	22	30742364	30742364	G	A	0.006	SF3A1	p.S110S	Synonymous
PD41211	2	78.7	22	30742364	30742364	G	A	0.005	SF3A1	p.S110S	Synonymous
PD41211	3	82.8	22	30742364	30742364	G	A	0.013	SF3A1	p.S110S	Synonymous
PD41211	4	85.9	22	30742364	30742364	G	A	0.007	SF3A1	p.S110S	Synonymous
PD41211	5	90.4	22	30742364	30742364	G	A	0.031	SF3A1	p.S110S	Synonymous
PD41213	1	66.0	3	128205057	128205057	G	A	0.007	GATA2	p.P128P	Synonymous
PD41213	2	69.2	3	128205057	128205057	G	A	0.006	GATA2	p.P128P	Synonymous
PD41213	3	72.6	3	128205057	128205057	G	A	0.003	GATA2	p.P128P	Synonymous
PD41213	4	76.2	3	128205057	128205057	G	A	0.006	GATA2	p.P128P	Synonymous
PD41213	5	80.8	3	128205057	128205057	G	A	0.021	GATA2	p.P128P	Synonymous
PD41213	1	66.0	X	44922883	44922884	TC	T	0.000	KDM6A	p.S634X	Nonsense
PD41213	2	69.2	X	44922883	44922884	TC	T	0.002	KDM6A	p.S634X	Nonsense
PD41213	3	72.6	X	44922883	44922884	TC	T	0.005	KDM6A	p.S634X	Nonsense
PD41213	4	76.2	X	44922883	44922884	TC	T	0.002	KDM6A	p.S634X	Nonsense
PD41213	5	80.8	X	44922883	44922884	TC	T	0.006	KDM6A	p.S634X	Nonsense
PD41214	1	67.3	4	106197167	106197167	C	T	0.009	TET2	p.Q1834X	Nonsense
PD41214	2	70.7	4	106197167	106197167	C	T	0.005	TET2	p.Q1834X	Nonsense
PD41214	3	75.1	4	106197167	106197167	C	T	0.003	TET2	p.Q1834X	Nonsense
PD41214	4	78.2	4	106197167	106197167	C	T	0.006	TET2	p.Q1834X	Nonsense
PD41214	5	82.1	4	106197167	106197167	C	T	0.053	TET2	p.Q1834X	Nonsense
PD41214	1	67.3	10	89692995	89692995	C	G	0.004	PTEN	p.T333S	Missense
PD41214	2	70.7	10	89692995	89692995	C	G	0.009	PTEN	p.T333S	Missense
PD41214	3	75.1	10	89692995	89692995	C	G	0.014	PTEN	p.T333S	Missense
PD41214	4	78.2	10	89692995	89692995	C	G	0.013	PTEN	p.T333S	Missense
PD41214	5	82.1	10	89692995	89692995	C	G	0.016	PTEN	p.T333S	Missense
PD41214	1	67.3	15	90631934	90631934	C	T	0.001	IDH2	p.R140Q	Missense
PD41214	2	70.7	15	90631934	90631934	C	T	0.002	IDH2	p.R140Q	Missense
PD41214	3	75.1	15	90631934	90631934	C	T	0.009	IDH2	p.R140Q	Missense
PD41214	4	78.2	15	90631934	90631934	C	T	0.002	IDH2	p.R140Q	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41214	5	82.1	15	90631934	90631934	C	T	0.000	IDH2	p.R140Q	Missense
PD41214	1	67.3	X	133547597	133547597	A	G	0.000	PHF6	p.G165G	Synonymous
PD41214	2	70.7	X	133547597	133547597	A	G	0.006	PHF6	p.G165G	Synonymous
PD41214	3	75.1	X	133547597	133547597	A	G	0.000	PHF6	p.G165G	Synonymous
PD41214	4	78.2	X	133547597	133547597	A	G	0.000	PHF6	p.G165G	Synonymous
PD41214	5	82.1	X	133547597	133547597	A	G	0.000	PHF6	p.G165G	Synonymous
PD41215	1	71.6	2	198257879	198257879	C	A	0.000	SF3B1	p.V1191V	Synonymous
PD41215	2	75.0	2	198257879	198257879	C	A	0.006	SF3B1	p.V1191V	Synonymous
PD41215	3	81.5	2	198257879	198257879	C	A	0.000	SF3B1	p.V1191V	Synonymous
PD41216	1	74.9	2	25463583	25463583	G	A	0.008	DNMT3A	p.P700L	Missense
PD41216	2	79.0	2	25463583	25463583	G	A	0.012	DNMT3A	p.P700L	Missense
PD41216	3	83.7	2	25463583	25463583	G	A	0.010	DNMT3A	p.P700L	Missense
PD41216	4	87.6	2	25463583	25463583	G	A	0.004	DNMT3A	p.P700L	Missense
PD41216	1	74.9	4	106156625	106156625	C	G	0.054	TET2	p.S509X	Nonsense
PD41216	2	79.0	4	106156625	106156625	C	G	0.067	TET2	p.S509X	Nonsense
PD41216	3	83.7	4	106156625	106156625	C	G	0.068	TET2	p.S509X	Nonsense
PD41216	4	87.6	4	106156625	106156625	C	G	0.092	TET2	p.S509X	Nonsense
PD41216	1	74.9	4	106182914	106182914	A	G	0.002	TET2	c.3955-2A>G	Splice site
PD41216	2	79.0	4	106182914	106182914	A	G	0.002	TET2	c.3955-2A>G	Splice site
PD41216	3	83.7	4	106182914	106182914	A	G	0.006	TET2	c.3955-2A>G	Splice site
PD41216	4	87.6	4	106182914	106182914	A	G	0.012	TET2	c.3955-2A>G	Splice site
PD41216	1	74.9	16	3781311	3781311	T	C	0.001	CREBBP	p.K1685R	Missense
PD41216	2	79.0	16	3781311	3781311	T	C	0.000	CREBBP	p.K1685R	Missense
PD41216	3	83.7	16	3781311	3781311	T	C	0.009	CREBBP	p.K1685R	Missense
PD41216	4	87.6	16	3781311	3781311	T	C	0.000	CREBBP	p.K1685R	Missense
PD41216	1	74.9	X	53410058	53410058	C	A	0.004	SMC1A	p.K1008N	Missense
PD41216	2	79.0	X	53410058	53410058	C	A	0.001	SMC1A	p.K1008N	Missense
PD41216	3	83.7	X	53410058	53410058	C	A	0.000	SMC1A	p.K1008N	Missense
PD41216	4	87.6	X	53410058	53410058	C	A	0.000	SMC1A	p.K1008N	Missense
PD41217	1	69.0	2	25464429	25464429	A	C	0.015	DNMT3A	c.2082+2T>G	Splice site
PD41217	2	73.2	2	25464429	25464429	A	C	0.016	DNMT3A	c.2082+2T>G	Splice site
PD41217	3	77.8	2	25464429	25464429	A	C	0.026	DNMT3A	c.2082+2T>G	Splice site
PD41217	4	81.7	2	25464429	25464429	A	C	0.019	DNMT3A	c.2082+2T>G	Splice site
PD41217	1	69.0	2	25470516	25470516	G	A	0.031	DNMT3A	p.R320X	Nonsense
PD41217	2	73.2	2	25470516	25470516	G	A	0.030	DNMT3A	p.R320X	Nonsense
PD41217	3	77.8	2	25470516	25470516	G	A	0.035	DNMT3A	p.R320X	Nonsense
PD41217	4	81.7	2	25470516	25470516	G	A	0.025	DNMT3A	p.R320X	Nonsense
PD41218	1	79.3	2	25463308	25463308	G	C	0.008	DNMT3A	p.R729G	Missense
PD41218	2	82.4	2	25463308	25463308	G	C	0.007	DNMT3A	p.R729G	Missense
PD41218	3	86.1	2	25463308	25463308	G	C	0.007	DNMT3A	p.R729G	Missense
PD41218	4	90.0	2	25463308	25463308	G	C	0.005	DNMT3A	p.R729G	Missense
PD41218	1	79.3	2	25466766	25466766	C	T	0.007	DNMT3A	c.1936+1G>A	Splice site
PD41218	2	82.4	2	25466766	25466766	C	T	0.004	DNMT3A	c.1936+1G>A	Splice site
PD41218	3	86.1	2	25466766	25466766	C	T	0.008	DNMT3A	c.1936+1G>A	Splice site
PD41218	4	90.0	2	25466766	25466766	C	T	0.014	DNMT3A	c.1936+1G>A	Splice site
PD41218	1	79.3	2	25470480	25470480	C	T	0.140	DNMT3A	p.G332R	Missense
PD41218	2	82.4	2	25470480	25470480	C	T	0.136	DNMT3A	p.G332R	Missense
PD41218	3	86.1	2	25470480	25470480	C	T	0.138	DNMT3A	p.G332R	Missense
PD41218	4	90.0	2	25470480	25470480	C	T	0.122	DNMT3A	p.G332R	Missense
PD41218	1	79.3	4	106196614	106196614	T	A	0.001	TET2	p.Y1649X	Nonsense
PD41218	2	82.4	4	106196614	106196614	T	A	0.003	TET2	p.Y1649X	Nonsense
PD41218	3	86.1	4	106196614	106196614	T	A	0.001	TET2	p.Y1649X	Nonsense
PD41218	4	90.0	4	106196614	106196614	T	A	0.008	TET2	p.Y1649X	Nonsense
PD41218	1	79.3	11	32413610	32413610	C	A	0.007	WT1	p.G447V	Missense
PD41218	2	82.4	11	32413610	32413610	C	A	0.000	WT1	p.G447V	Missense
PD41218	3	86.1	11	32413610	32413610	C	A	0.001	WT1	p.G447V	Missense
PD41218	4	90.0	11	32413610	32413610	C	A	0.000	WT1	p.G447V	Missense
PD41218	1	79.3	12	50026847	50026847	C	T	0.000	PRPF40B	p.Y133Y	Synonymous
PD41218	2	82.4	12	50026847	50026847	C	T	0.000	PRPF40B	p.Y133Y	Synonymous
PD41218	3	86.1	12	50026847	50026847	C	T	0.007	PRPF40B	p.Y133Y	Synonymous
PD41218	4	90.0	12	50026847	50026847	C	T	0.000	PRPF40B	p.Y133Y	Synonymous
PD41219	1	73.9	17	58740521	58740521	G	T	0.001	PPM1D	p.E476X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41219	2	77.0	17	58740521	58740521	G	T	0.002	PPM1D	p.E476X	Nonsense
PD41219	3	80.8	17	58740521	58740521	G	T	0.003	PPM1D	p.E476X	Nonsense
PD41219	4	84.1	17	58740521	58740521	G	T	0.006	PPM1D	p.E476X	Nonsense
PD41219	1	73.9	X	39911392	39911392	G	T	0.000	BCOR	p.P1712P	Synonymous
PD41219	2	77.0	X	39911392	39911392	G	T	0.006	BCOR	p.P1712P	Synonymous
PD41219	3	80.8	X	39911392	39911392	G	T	0.000	BCOR	p.P1712P	Synonymous
PD41219	4	84.1	X	39911392	39911392	G	T	0.000	BCOR	p.P1712P	Synonymous
PD41220	1	72.9	7	148514467	148514467	A	T	0.003	EZH2	p.C419X	Nonsense
PD41220	2	76.0	7	148514467	148514467	A	T	0.002	EZH2	p.C419X	Nonsense
PD41220	3	79.9	7	148514467	148514467	A	T	0.005	EZH2	p.C419X	Nonsense
PD41220	4	83.1	7	148514467	148514467	A	T	0.006	EZH2	p.C419X	Nonsense
PD41221	1	93.7	2	25457242	25457242	C	T	0.036	DNMT3A	p.R882H	Missense
PD41221	2	98.3	2	25457242	25457242	C	T	0.041	DNMT3A	p.R882H	Missense
PD41221	3	101.5	2	25457242	25457242	C	T	0.039	DNMT3A	p.R882H	Missense
PD41221	1	93.7	4	106157761	106157761	C	T	0.004	TET2	p.Q888X	Nonsense
PD41221	2	98.3	4	106157761	106157761	C	T	0.009	TET2	p.Q888X	Nonsense
PD41221	3	101.5	4	106157761	106157761	C	T	0.017	TET2	p.Q888X	Nonsense
PD41221	1	93.7	4	106157845	106157845	C	T	0.029	TET2	p.Q916X	Nonsense
PD41221	2	98.3	4	106157845	106157845	C	T	0.023	TET2	p.Q916X	Nonsense
PD41221	3	101.5	4	106157845	106157845	C	T	0.030	TET2	p.Q916X	Nonsense
PD41221	1	93.7	4	106197371	106197371	T	C	0.003	TET2	p.Y1902H	Missense
PD41221	2	98.3	4	106197371	106197371	T	C	0.001	TET2	p.Y1902H	Missense
PD41221	3	101.5	4	106197371	106197371	T	C	0.006	TET2	p.Y1902H	Missense
PD41221	1	93.7	21	44514777	44514777	T	G	0.000	U2AF1	p.Q84P	Missense
PD41221	2	98.3	21	44514777	44514777	T	G	0.005	U2AF1	p.Q84P	Missense
PD41221	3	101.5	21	44514777	44514777	T	G	0.009	U2AF1	p.Q84P	Missense
PD41222	1	55.5	4	106190860	106190860	C	T	0.006	TET2	p.H1380Y	Missense
PD41222	2	58.7	4	106190860	106190860	C	T	0.009	TET2	p.H1380Y	Missense
PD41222	3	62.5	4	106190860	106190860	C	T	0.001	TET2	p.H1380Y	Missense
PD41222	4	65.6	4	106190860	106190860	C	T	0.000	TET2	p.H1380Y	Missense
PD41222	5	70.4	4	106190860	106190860	C	T	0.000	TET2	p.H1380Y	Missense
PD41222	1	55.5	10	112361414	112361414	T	C	0.000	SMC3	p.D888D	Synonymous
PD41222	2	58.7	10	112361414	112361414	T	C	0.001	SMC3	p.D888D	Synonymous
PD41222	3	62.5	10	112361414	112361414	T	C	0.006	SMC3	p.D888D	Synonymous
PD41222	4	65.6	10	112361414	112361414	T	C	0.001	SMC3	p.D888D	Synonymous
PD41222	5	70.4	10	112361414	112361414	T	C	0.000	SMC3	p.D888D	Synonymous
PD41222	1	55.5	X	123159701	123159701	C	T	0.009	STAG2	p.T19I	Missense
PD41222	2	58.7	X	123159701	123159701	C	T	0.010	STAG2	p.T19I	Missense
PD41222	3	62.5	X	123159701	123159701	C	T	0.013	STAG2	p.T19I	Missense
PD41222	4	65.6	X	123159701	123159701	C	T	0.015	STAG2	p.T19I	Missense
PD41222	5	70.4	X	123159701	123159701	C	T	0.013	STAG2	p.T19I	Missense
PD41222	1	55.5	X	39931744	39931744	C	A	0.000	BCOR	p.G952V	Missense
PD41222	2	58.7	X	39931744	39931744	C	A	0.000	BCOR	p.G952V	Missense
PD41222	3	62.5	X	39931744	39931744	C	A	0.004	BCOR	p.G952V	Missense
PD41222	4	65.6	X	39931744	39931744	C	A	0.000	BCOR	p.G952V	Missense
PD41222	5	70.4	X	39931744	39931744	C	A	0.000	BCOR	p.G952V	Missense
PD41223	1	57.8	4	106158025	106158025	C	T	0.003	TET2	p.Q976X	Nonsense
PD41223	2	61.0	4	106158025	106158025	C	T	0.003	TET2	p.Q976X	Nonsense
PD41223	3	64.7	4	106158025	106158025	C	T	0.006	TET2	p.Q976X	Nonsense
PD41223	4	67.9	4	106158025	106158025	C	T	0.004	TET2	p.Q976X	Nonsense
PD41223	5	72.2	4	106158025	106158025	C	T	0.005	TET2	p.Q976X	Nonsense
PD41224	1	76.7	4	106190803	106190803	G	C	0.001	TET2	p.G1361R	Missense
PD41224	2	80.4	4	106190803	106190803	G	C	0.002	TET2	p.G1361R	Missense
PD41224	3	83.9	4	106190803	106190803	G	C	0.002	TET2	p.G1361R	Missense
PD41224	4	86.9	4	106190803	106190803	G	C	0.002	TET2	p.G1361R	Missense
PD41224	5	92.4	4	106190803	106190803	G	C	0.006	TET2	p.G1361R	Missense
PD41224	1	76.7	X	129149032	129149032	A	T	0.003	BCORL1	p.T762S	Missense
PD41224	2	80.4	X	129149032	129149032	A	T	0.000	BCORL1	p.T762S	Missense
PD41224	3	83.9	X	129149032	129149032	A	T	0.000	BCORL1	p.T762S	Missense
PD41224	4	86.9	X	129149032	129149032	A	T	0.000	BCORL1	p.T762S	Missense
PD41224	5	92.4	X	129149032	129149032	A	T	0.000	BCORL1	p.T762S	Missense
PD41224	1	76.7	X	39932255	39932255	C	T	0.013	BCOR	p.D782N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41224	2	80.4	X	39932255	39932255	C	T	0.012	BCOR	p.D782N	Missense
PD41224	3	83.9	X	39932255	39932255	C	T	0.017	BCOR	p.D782N	Missense
PD41224	4	86.9	X	39932255	39932255	C	T	0.013	BCOR	p.D782N	Missense
PD41224	5	92.4	X	39932255	39932255	C	T	0.016	BCOR	p.D782N	Missense
PD41225	1	69.8	2	25457243	25457243	G	T	0.014	DNMT3A	p.R882S	Missense
PD41225	2	73.5	2	25457243	25457243	G	T	0.024	DNMT3A	p.R882S	Missense
PD41225	3	77.0	2	25457243	25457243	G	T	0.031	DNMT3A	p.R882S	Missense
PD41225	5	85.5	2	25457243	25457243	G	T	0.070	DNMT3A	p.R882S	Missense
PD41225	1	69.8	11	64544009	64544009	G	T	0.000	SF1	p.P41T	Missense
PD41225	2	73.5	11	64544009	64544009	G	T	0.000	SF1	p.P41T	Missense
PD41225	3	77.0	11	64544009	64544009	G	T	0.007	SF1	p.P41T	Missense
PD41225	5	85.5	11	64544009	64544009	G	T	0.000	SF1	p.P41T	Missense
PD41226	1	60.1	2	25466797	25466797	C	T	0.007	DNMT3A	p.V636M	Missense
PD41226	2	63.4	2	25466797	25466797	C	T	0.011	DNMT3A	p.V636M	Missense
PD41226	3	67.2	2	25466797	25466797	C	T	0.010	DNMT3A	p.V636M	Missense
PD41226	4	70.1	2	25466797	25466797	C	T	0.007	DNMT3A	p.V636M	Missense
PD41226	5	74.4	2	25466797	25466797	C	T	0.008	DNMT3A	p.V636M	Missense
PD41226	1	60.1	2	25497848	25497848	G	A	0.002	DNMT3A	p.R201C	Missense
PD41226	2	63.4	2	25497848	25497848	G	A	0.002	DNMT3A	p.R201C	Missense
PD41226	3	67.2	2	25497848	25497848	G	A	0.004	DNMT3A	p.R201C	Missense
PD41226	4	70.1	2	25497848	25497848	G	A	0.007	DNMT3A	p.R201C	Missense
PD41226	5	74.4	2	25497848	25497848	G	A	0.007	DNMT3A	p.R201C	Missense
PD41226	1	60.1	7	101891755	101891755	C	G	0.000	CUX1	p.G1317G	Synonymous
PD41226	2	63.4	7	101891755	101891755	C	G	0.000	CUX1	p.G1317G	Synonymous
PD41226	3	67.2	7	101891755	101891755	C	G	0.000	CUX1	p.G1317G	Synonymous
PD41226	4	70.1	7	101891755	101891755	C	G	0.008	CUX1	p.G1317G	Synonymous
PD41226	5	74.4	7	101891755	101891755	C	G	0.000	CUX1	p.G1317G	Synonymous
PD41226	1	60.1	8	117861253	117861254	CT	C	0.007	RAD21	p.S545fs	Frameshift
PD41226	2	63.4	8	117861253	117861254	CT	C	0.012	RAD21	p.S545fs	Frameshift
PD41226	3	67.2	8	117861253	117861254	CT	C	0.012	RAD21	p.S545fs	Frameshift
PD41226	4	70.1	8	117861253	117861254	CT	C	0.030	RAD21	p.S545fs	Frameshift
PD41226	5	74.4	8	117861253	117861254	CT	C	0.048	RAD21	p.S545fs	Frameshift
PD41226	1	60.1	9	139400019	139400019	C	T	0.003	NOTCH1	p.P1443P	Synonymous
PD41226	2	63.4	9	139400019	139400019	C	T	0.006	NOTCH1	p.P1443P	Synonymous
PD41226	3	67.2	9	139400019	139400019	C	T	0.002	NOTCH1	p.P1443P	Synonymous
PD41226	4	70.1	9	139400019	139400019	C	T	0.009	NOTCH1	p.P1443P	Synonymous
PD41226	5	74.4	9	139400019	139400019	C	T	0.004	NOTCH1	p.P1443P	Synonymous
PD41227	1	62.2	2	25470570	25470570	C	T	0.010	DNMT3A	p.G302S	Missense
PD41227	2	65.5	2	25470570	25470570	C	T	0.017	DNMT3A	p.G302S	Missense
PD41227	3	69.2	2	25470570	25470570	C	T	0.007	DNMT3A	p.G302S	Missense
PD41227	4	72.2	2	25470570	25470570	C	T	0.009	DNMT3A	p.G302S	Missense
PD41227	5	77.4	2	25470570	25470570	C	T	0.005	DNMT3A	p.G302S	Missense
PD41227	1	62.2	11	119148541	119148541	T	G	0.005	CBL	p.I361S	Missense
PD41227	2	65.5	11	119148541	119148541	T	G	0.001	CBL	p.I361S	Missense
PD41227	3	69.2	11	119148541	119148541	T	G	0.009	CBL	p.I361S	Missense
PD41227	4	72.2	11	119148541	119148541	T	G	0.003	CBL	p.I361S	Missense
PD41227	5	77.4	11	119148541	119148541	T	G	0.004	CBL	p.I361S	Missense
PD41227	1	62.2	X	129146975	129146975	C	T	0.000	BCORL1	p.P76L	Missense
PD41227	2	65.5	X	129146975	129146975	C	T	0.000	BCORL1	p.P76L	Missense
PD41227	3	69.2	X	129146975	129146975	C	T	0.000	BCORL1	p.P76L	Missense
PD41227	4	72.2	X	129146975	129146975	C	T	0.006	BCORL1	p.P76L	Missense
PD41227	5	77.4	X	129146975	129146975	C	T	0.000	BCORL1	p.P76L	Missense
PD41229	1	62.5	4	106156681	106156695	AACTGCCAGCAGTTG	A	0.022	TET2	p.N528fs	Frameshift
PD41229	2	65.7	4	106156681	106156695	AACTGCCAGCAGTTG	A	0.019	TET2	p.N528fs	Frameshift
PD41229	3	68.8	4	106156681	106156695	AACTGCCA	A	0.032	TET2	p.N528fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
						GCAG TTG					
PD41229	4	72.2	4	106156681	106156695	AACT GCCA GCAG TTG	A	0.024	TET2	p.N528fs	Frameshift
PD41229	5	77.7	4	106156681	106156695	AACT GCCA GCAG TTG	A	0.023	TET2	p.N528fs	Frameshift
PD41229	1	62.5	X	123176462	123176462	G	C	0.003	STAG2	p.E143D	Missense
PD41229	2	65.7	X	123176462	123176462	G	C	0.003	STAG2	p.E143D	Missense
PD41229	3	68.8	X	123176462	123176462	G	C	0.004	STAG2	p.E143D	Missense
PD41229	4	72.2	X	123176462	123176462	G	C	0.003	STAG2	p.E143D	Missense
PD41229	5	77.7	X	123176462	123176462	G	C	0.007	STAG2	p.E143D	Missense
PD41230	1	66.9	11	119148991	119148991	G	A	0.012	CBL	p.C404Y	Missense
PD41230	2	70.8	11	119148991	119148991	G	A	0.019	CBL	p.C404Y	Missense
PD41230	3	74.7	11	119148991	119148991	G	A	0.021	CBL	p.C404Y	Missense
PD41230	5	81.3	11	119148991	119148991	G	A	0.023	CBL	p.C404Y	Missense
PD41230	1	66.9	20	31023492	31023503	AGTC CTCA CGGT	A	0.001	ASXL1	p.S993fs	Frameshift
PD41230	2	70.8	20	31023492	31023503	AGTC CTCA CGGT	A	0.000	ASXL1	p.S993fs	Frameshift
PD41230	3	74.7	20	31023492	31023503	AGTC CTCA CGGT	A	0.001	ASXL1	p.S993fs	Frameshift
PD41230	5	81.3	20	31023492	31023503	AGTC CTCA CGGT	A	0.006	ASXL1	p.S993fs	Frameshift
PD41230	1	66.9	X	123176443	123176443	G	C	0.006	STAG2	p.R137T	Missense
PD41230	2	70.8	X	123176443	123176443	G	C	0.005	STAG2	p.R137T	Missense
PD41230	3	74.7	X	123176443	123176443	G	C	0.003	STAG2	p.R137T	Missense
PD41230	5	81.3	X	123176443	123176443	G	C	0.008	STAG2	p.R137T	Missense
PD41230	1	66.9	X	44928839	44928839	C	G	0.003	KDM6A	p.Q699E	Missense
PD41230	2	70.8	X	44928839	44928839	C	G	0.001	KDM6A	p.Q699E	Missense
PD41230	3	74.7	X	44928839	44928839	C	G	0.007	KDM6A	p.Q699E	Missense
PD41230	5	81.3	X	44928839	44928839	C	G	0.000	KDM6A	p.Q699E	Missense
PD41230	1	66.9	X	154344428	154344428	C	A	0.000	BRCC3	p.C240X	Nonsense
PD41230	2	70.8	X	154344428	154344428	C	A	0.000	BRCC3	p.C240X	Nonsense
PD41230	3	74.7	X	154344428	154344428	C	A	0.004	BRCC3	p.C240X	Nonsense
PD41230	5	81.3	X	154344428	154344428	C	A	0.011	BRCC3	p.C240X	Nonsense
PD41231	1	76.6	2	25469646	25469646	C	T	0.020	DNMT3A	c.1123-1G>A	Splice site
PD41231	2	79.7	2	25469646	25469646	C	T	0.012	DNMT3A	c.1123-1G>A	Splice site
PD41231	3	82.8	2	25469646	25469646	C	T	0.013	DNMT3A	c.1123-1G>A	Splice site
PD41231	4	86.7	2	25469646	25469646	C	T	0.011	DNMT3A	c.1123-1G>A	Splice site
PD41231	1	76.6	16	67662431	67662431	G	A	0.014	CTCF	p.K559K	Synonymous
PD41231	2	79.7	16	67662431	67662431	G	A	0.005	CTCF	p.K559K	Synonymous
PD41231	3	82.8	16	67662431	67662431	G	A	0.010	CTCF	p.K559K	Synonymous
PD41231	4	86.7	16	67662431	67662431	G	A	0.004	CTCF	p.K559K	Synonymous
PD41231	1	76.6	19	17945741	17945741	C	A	0.003	JAK3	p.D707Y	Missense
PD41231	2	79.7	19	17945741	17945741	C	A	0.000	JAK3	p.D707Y	Missense
PD41231	3	82.8	19	17945741	17945741	C	A	0.007	JAK3	p.D707Y	Missense
PD41231	4	86.7	19	17945741	17945741	C	A	0.000	JAK3	p.D707Y	Missense
PD41232	1	68.1	X	129148620	129148620	G	C	0.005	BCORL1	p.L624L	Synonymous
PD41232	2	71.7	X	129148620	129148620	G	C	0.011	BCORL1	p.L624L	Synonymous
PD41232	3	76.5	X	129148620	129148620	G	C	0.007	BCORL1	p.L624L	Synonymous
PD41232	4	80.4	X	129148620	129148620	G	C	0.005	BCORL1	p.L624L	Synonymous
PD41233	1	60.1	9	5073770	5073770	G	T	0.003	JAK2	p.V617F	Missense
PD41233	2	63.6	9	5073770	5073770	G	T	0.009	JAK2	p.V617F	Missense
PD41233	3	67.4	9	5073770	5073770	G	T	0.037	JAK2	p.V617F	Missense
PD41233	4	70.1	9	5073770	5073770	G	T	0.056	JAK2	p.V617F	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41233	5	74.4	9	5073770	5073770	G	T	0.010	JAK2	p.V617F	Missense
PD41233	1	60.1	12	112915523	112915523	A	G	0.000	PTPN11	p.N308D	Missense
PD41233	2	63.6	12	112915523	112915523	A	G	0.004	PTPN11	p.N308D	Missense
PD41233	3	67.4	12	112915523	112915523	A	G	0.012	PTPN11	p.N308D	Missense
PD41233	4	70.1	12	112915523	112915523	A	G	0.032	PTPN11	p.N308D	Missense
PD41233	5	74.4	12	112915523	112915523	A	G	0.229	PTPN11	p.N308D	Missense
PD41233	1	60.1	17	7576897	7576897	G	A	0.007	TP53	p.Q278X	Nonsense
PD41233	2	63.6	17	7576897	7576897	G	A	0.007	TP53	p.Q278X	Nonsense
PD41233	3	67.4	17	7576897	7576897	G	A	0.000	TP53	p.Q278X	Nonsense
PD41233	4	70.1	17	7576897	7576897	G	A	0.000	TP53	p.Q278X	Nonsense
PD41233	5	74.4	17	7576897	7576897	G	A	0.000	TP53	p.Q278X	Nonsense
PD41233	1	60.1	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.051	ASXL1	p.H630fs	Frameshift
PD41233	2	63.6	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.074	ASXL1	p.H630fs	Frameshift
PD41233	3	67.4	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.142	ASXL1	p.H630fs	Frameshift
PD41233	4	70.1	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.144	ASXL1	p.H630fs	Frameshift
PD41233	5	74.4	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.272	ASXL1	p.H630fs	Frameshift
PD41233	1	60.1	21	44514780	44514780	C	T	0.001	U2AF1	p.R83H	Missense
PD41233	2	63.6	21	44514780	44514780	C	T	0.001	U2AF1	p.R83H	Missense
PD41233	3	67.4	21	44514780	44514780	C	T	0.001	U2AF1	p.R83H	Missense
PD41233	4	70.1	21	44514780	44514780	C	T	0.000	U2AF1	p.R83H	Missense
PD41233	5	74.4	21	44514780	44514780	C	T	0.005	U2AF1	p.R83H	Missense
PD41233	1	60.1	X	15840874	15840874	T	C	0.000	ZRSR2	p.C320R	Missense
PD41233	2	63.6	X	15840874	15840874	T	C	0.002	ZRSR2	p.C320R	Missense
PD41233	3	67.4	X	15840874	15840874	T	C	0.006	ZRSR2	p.C320R	Missense
PD41233	4	70.1	X	15840874	15840874	T	C	0.032	ZRSR2	p.C320R	Missense
PD41233	5	74.4	X	15840874	15840874	T	C	0.234	ZRSR2	p.C320R	Missense
PD41234	1	69.9	4	106197255	106197255	C	T	0.003	TET2	p.A1863V	Missense
PD41234	2	73.6	4	106197255	106197255	C	T	0.008	TET2	p.A1863V	Missense
PD41234	3	78.9	4	106197255	106197255	C	T	0.014	TET2	p.A1863V	Missense
PD41234	4	82.6	4	106197255	106197255	C	T	0.028	TET2	p.A1863V	Missense
PD41234	1	69.9	12	25398254	25398254	T	A	0.001	KRAS	p.Q22L	Missense
PD41234	2	73.6	12	25398254	25398254	T	A	0.000	KRAS	p.Q22L	Missense
PD41234	3	78.9	12	25398254	25398254	T	A	0.008	KRAS	p.Q22L	Missense
PD41234	4	82.6	12	25398254	25398254	T	A	0.003	KRAS	p.Q22L	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41235	1	68.7	4	106157173	106157173	G	T	0.012	TET2	p.E692X	Nonsense
PD41235	2	71.9	4	106157173	106157173	G	T	0.013	TET2	p.E692X	Nonsense
PD41235	3	77.4	4	106157173	106157173	G	T	0.010	TET2	p.E692X	Nonsense
PD41235	4	81.5	4	106157173	106157173	G	T	0.007	TET2	p.E692X	Nonsense
PD41235	1	68.7	4	106158017	106158018	GC	G	0.002	TET2	p.C973fs	Frameshift
PD41235	2	71.9	4	106158017	106158018	GC	G	0.001	TET2	p.C973fs	Frameshift
PD41235	3	77.4	4	106158017	106158018	GC	G	0.011	TET2	p.C973fs	Frameshift
PD41235	4	81.5	4	106158017	106158018	GC	G	0.015	TET2	p.C973fs	Frameshift
PD41235	1	68.7	17	74732959	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41235	2	71.9	17	74732959	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41235	3	77.4	17	74732959	74732959	G	A	0.000	SRSF2	p.P95L	Missense
PD41235	4	81.5	17	74732959	74732959	G	A	0.010	SRSF2	p.P95L	Missense
PD41235	1	68.7	20	31022923	31022923	A	G	0.025	ASXL1	p.Q803R	Missense
PD41235	2	71.9	20	31022923	31022923	A	G	0.020	ASXL1	p.Q803R	Missense
PD41235	3	77.4	20	31022923	31022923	A	G	0.033	ASXL1	p.Q803R	Missense
PD41235	4	81.5	20	31022923	31022923	A	G	0.035	ASXL1	p.Q803R	Missense
PD41235	1	68.7	X	53410092	53410092	C	T	0.001	SMC1A	p.R997H	Missense
PD41235	2	71.9	X	53410092	53410092	C	T	0.002	SMC1A	p.R997H	Missense
PD41235	3	77.4	X	53410092	53410092	C	T	0.012	SMC1A	p.R997H	Missense
PD41235	4	81.5	X	53410092	53410092	C	T	0.002	SMC1A	p.R997H	Missense
PD41236	1	72.5	4	106197413	106197414	CT	C	0.003	TET2	p.L1916fs	Frameshift
PD41236	2	75.5	4	106197413	106197414	CT	C	0.007	TET2	p.L1916fs	Frameshift
PD41236	3	79.4	4	106197413	106197414	CT	C	0.006	TET2	p.L1916fs	Frameshift
PD41236	4	82.2	4	106197413	106197414	CT	C	0.006	TET2	p.L1916fs	Frameshift
PD41236	5	86.0	4	106197413	106197414	CT	C	0.004	TET2	p.L1916fs	Frameshift
PD41237	1	72.0	2	25472586	25472586	C	T	0.007	DNMT3A	p.L4L	Synonymous
PD41237	2	74.5	2	25472586	25472586	C	T	0.000	DNMT3A	p.L4L	Synonymous
PD41237	3	78.2	2	25472586	25472586	C	T	0.000	DNMT3A	p.L4L	Synonymous
PD41237	4	82.1	2	25472586	25472586	C	T	0.000	DNMT3A	p.L4L	Synonymous
PD41237	1	72.0	4	106157848	106157848	C	T	0.003	TET2	p.Q917X	Nonsense
PD41237	2	74.5	4	106157848	106157848	C	T	0.007	TET2	p.Q917X	Nonsense
PD41237	3	78.2	4	106157848	106157848	C	T	0.022	TET2	p.Q917X	Nonsense
PD41237	4	82.1	4	106157848	106157848	C	T	0.044	TET2	p.Q917X	Nonsense
PD41237	1	72.0	11	118378314	118378314	C	T	0.000	KMT2A	p.Q3606X	Nonsense
PD41237	2	74.5	11	118378314	118378314	C	T	0.000	KMT2A	p.Q3606X	Nonsense
PD41237	3	78.2	11	118378314	118378314	C	T	0.008	KMT2A	p.Q3606X	Nonsense
PD41237	4	82.1	11	118378314	118378314	C	T	0.000	KMT2A	p.Q3606X	Nonsense
PD41237	1	72.0	11	119148976	119148976	T	A	0.000	CBL	p.L399H	Missense
PD41237	2	74.5	11	119148976	119148976	T	A	0.000	CBL	p.L399H	Missense
PD41237	3	78.2	11	119148976	119148976	T	A	0.002	CBL	p.L399H	Missense
PD41237	4	82.1	11	119148976	119148976	T	A	0.005	CBL	p.L399H	Missense
PD41237	1	72.0	16	67654689	67654689	C	G	0.005	CTCF	p.Y392X	Nonsense
PD41237	2	74.5	16	67654689	67654689	C	G	0.002	CTCF	p.Y392X	Nonsense
PD41237	3	78.2	16	67654689	67654689	C	G	0.006	CTCF	p.Y392X	Nonsense
PD41237	4	82.1	16	67654689	67654689	C	G	0.001	CTCF	p.Y392X	Nonsense
PD41237	1	72.0	20	57429319	57429319	C	T	0.000	GNAS	p.T271M	Missense
PD41237	2	74.5	20	57429319	57429319	C	T	0.001	GNAS	p.T271M	Missense
PD41237	3	78.2	20	57429319	57429319	C	T	0.008	GNAS	p.T271M	Missense
PD41237	4	82.1	20	57429319	57429319	C	T	0.002	GNAS	p.T271M	Missense
PD41237	1	72.0	X	129150058	129150058	A	T	0.001	BCORL1	p.K1104X	Nonsense
PD41237	2	74.5	X	129150058	129150058	A	T	0.002	BCORL1	p.K1104X	Nonsense
PD41237	3	78.2	X	129150058	129150058	A	T	0.003	BCORL1	p.K1104X	Nonsense
PD41237	4	82.1	X	129150058	129150058	A	T	0.014	BCORL1	p.K1104X	Nonsense
PD41238	1	73.6	2	198266834	198266834	T	C	0.003	SF3B1	p.K700E	Missense
PD41238	2	77.5	2	198266834	198266834	T	C	0.004	SF3B1	p.K700E	Missense
PD41238	3	81.3	2	198266834	198266834	T	C	0.010	SF3B1	p.K700E	Missense
PD41238	1	73.6	9	139401026	139401026	C	A	0.000	NOTCH1	p.A1323S	Missense
PD41238	2	77.5	9	139401026	139401026	C	A	0.002	NOTCH1	p.A1323S	Missense
PD41238	3	81.3	9	139401026	139401026	C	A	0.013	NOTCH1	p.A1323S	Missense
PD41238	1	73.6	17	7577123	7577123	A	C	0.004	TP53	p.V233G	Missense
PD41238	2	77.5	17	7577123	7577123	A	C	0.006	TP53	p.V233G	Missense
PD41238	3	81.3	17	7577123	7577123	A	C	0.008	TP53	p.V233G	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41239	1	73.6	4	106197315	106197315	C	A	0.001	TET2	p.T1883K	Missense
PD41239	2	76.8	4	106197315	106197315	C	A	0.000	TET2	p.T1883K	Missense
PD41239	3	81.2	4	106197315	106197315	C	A	0.062	TET2	p.T1883K	Missense
PD41239	1	73.6	17	74732959	74732959	G	T	0.146	SRSF2	p.P95H	Missense
PD41239	2	76.8	17	74732959	74732959	G	T	0.285	SRSF2	p.P95H	Missense
PD41239	3	81.2	17	74732959	74732959	G	T	0.391	SRSF2	p.P95H	Missense
PD41239	1	73.6	20	31022998	31022999	GC	G	0.205	ASXL1	p.G828fs	Frameshift
PD41239	2	76.8	20	31022998	31022999	GC	G	0.311	ASXL1	p.G828fs	Frameshift
PD41239	3	81.2	20	31022998	31022999	GC	G	0.362	ASXL1	p.G828fs	Frameshift
PD41240	1	74.9	4	106155920	106155921	TC	T	0.009	TET2	p.I274fs	Frameshift
PD41240	2	77.9	4	106155920	106155921	TC	T	0.002	TET2	p.I274fs	Frameshift
PD41240	3	83.0	4	106155920	106155921	TC	T	0.001	TET2	p.I274fs	Frameshift
PD41240	1	74.9	4	106156795	106156795	G	T	0.010	TET2	p.E566X	Nonsense
PD41240	2	77.9	4	106156795	106156795	G	T	0.015	TET2	p.E566X	Nonsense
PD41240	3	83.0	4	106156795	106156795	G	T	0.010	TET2	p.E566X	Nonsense
PD41241	1	70.9	2	25457176	25457176	G	A	0.005	DNMT3A	p.P904L	Missense
PD41241	2	74.0	2	25457176	25457176	G	A	0.007	DNMT3A	p.P904L	Missense
PD41241	3	77.8	2	25457176	25457176	G	A	0.008	DNMT3A	p.P904L	Missense
PD41241	4	82.0	2	25457176	25457176	G	A	0.007	DNMT3A	p.P904L	Missense
PD41241	1	70.9	13	28601321	28601321	C	A	0.007	FLT3	p.R704I	Missense
PD41241	2	74.0	13	28601321	28601321	C	A	0.000	FLT3	p.R704I	Missense
PD41241	3	77.8	13	28601321	28601321	C	A	0.000	FLT3	p.R704I	Missense
PD41241	4	82.0	13	28601321	28601321	C	A	0.000	FLT3	p.R704I	Missense
PD41241	2	74.0	X	53432009	53432009	G	A	0.018	SMC1A	p.R689W	Missense
PD41241	3	77.8	X	53432009	53432009	G	A	0.037	SMC1A	p.R689W	Missense
PD41241	4	82.0	X	53432009	53432009	G	A	0.011	SMC1A	p.R689W	Missense
PD41242	1	69.0	2	198274662	198274662	C	A	0.001	SF3B1	p.G246X	Nonsense
PD41242	2	71.9	2	198274662	198274662	C	A	0.006	SF3B1	p.G246X	Nonsense
PD41242	3	75.9	2	198274662	198274662	C	A	0.000	SF3B1	p.G246X	Nonsense
PD41242	5	82.1	2	198274662	198274662	C	A	0.000	SF3B1	p.G246X	Nonsense
PD41242	1	69.0	4	106155920	106155921	TC	T	0.000	TET2	p.I274fs	Frameshift
PD41242	2	71.9	4	106155920	106155921	TC	T	0.001	TET2	p.I274fs	Frameshift
PD41242	3	75.9	4	106155920	106155921	TC	T	0.007	TET2	p.I274fs	Frameshift
PD41242	5	82.1	4	106155920	106155921	TC	T	0.047	TET2	p.I274fs	Frameshift
PD41242	1	69.0	4	106156906	106156906	A	T	0.000	TET2	p.K603X	Nonsense
PD41242	2	71.9	4	106156906	106156906	A	T	0.001	TET2	p.K603X	Nonsense
PD41242	3	75.9	4	106156906	106156906	A	T	0.000	TET2	p.K603X	Nonsense
PD41242	5	82.1	4	106156906	106156906	A	T	0.006	TET2	p.K603X	Nonsense
PD41242	1	69.0	4	106182956	106182956	T	C	0.000	TET2	p.L1332P	Missense
PD41242	2	71.9	4	106182956	106182956	T	C	0.002	TET2	p.L1332P	Missense
PD41242	3	75.9	4	106182956	106182956	T	C	0.009	TET2	p.L1332P	Missense
PD41242	5	82.1	4	106182956	106182956	T	C	0.066	TET2	p.L1332P	Missense
PD41242	1	69.0	4	106193978	106193985	CTCC CTGG	C	0.198	TET2	p.S1481fs	Frameshift
PD41242	2	71.9	4	106193978	106193985	CTCC CTGG	C	0.255	TET2	p.S1481fs	Frameshift
PD41242	3	75.9	4	106193978	106193985	CTCC CTGG	C	0.245	TET2	p.S1481fs	Frameshift
PD41242	5	82.1	4	106193978	106193985	CTCC CTGG	C	0.265	TET2	p.S1481fs	Frameshift
PD41242	1	69.0	4	106197060	106197060	C	G	0.001	TET2	p.S1798X	Nonsense
PD41242	2	71.9	4	106197060	106197060	C	G	0.001	TET2	p.S1798X	Nonsense
PD41242	3	75.9	4	106197060	106197060	C	G	0.003	TET2	p.S1798X	Nonsense
PD41242	5	82.1	4	106197060	106197060	C	G	0.011	TET2	p.S1798X	Nonsense
PD41242	1	69.0	16	3900813	3900813	C	T	0.012	CREBBP	p.V95M	Missense
PD41242	2	71.9	16	3900813	3900813	C	T	0.006	CREBBP	p.V95M	Missense
PD41242	3	75.9	16	3900813	3900813	C	T	0.014	CREBBP	p.V95M	Missense
PD41242	5	82.1	16	3900813	3900813	C	T	0.016	CREBBP	p.V95M	Missense
PD41243	1	77.4	2	25457249	25457249	T	C	0.003	DNMT3A	p.M880V	Missense
PD41243	2	80.2	2	25457249	25457249	T	C	0.006	DNMT3A	p.M880V	Missense
PD41243	3	84.6	2	25457249	25457249	T	C	0.012	DNMT3A	p.M880V	Missense
PD41243	4	88.4	2	25457249	25457249	T	C	0.006	DNMT3A	p.M880V	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41243	1	77.4	2	25462068	25462068	A	G	0.007	DNMT3A	p.I780T	Missense
PD41243	2	80.2	2	25462068	25462068	A	G	0.013	DNMT3A	p.I780T	Missense
PD41243	3	84.6	2	25462068	25462068	A	G	0.024	DNMT3A	p.I780T	Missense
PD41243	4	88.4	2	25462068	25462068	A	G	0.026	DNMT3A	p.I780T	Missense
PD41243	1	77.4	2	25467032	25467032	G	A	0.016	DNMT3A	p.Q615X	Nonsense
PD41243	2	80.2	2	25467032	25467032	G	A	0.016	DNMT3A	p.Q615X	Nonsense
PD41243	3	84.6	2	25467032	25467032	G	A	0.014	DNMT3A	p.Q615X	Nonsense
PD41243	4	88.4	2	25467032	25467032	G	A	0.018	DNMT3A	p.Q615X	Nonsense
PD41243	1	77.4	2	25469150	25469150	G	T	0.006	DNMT3A	p.Y436X	Nonsense
PD41243	2	80.2	2	25469150	25469150	G	T	0.007	DNMT3A	p.Y436X	Nonsense
PD41243	3	84.6	2	25469150	25469150	G	T	0.008	DNMT3A	p.Y436X	Nonsense
PD41243	4	88.4	2	25469150	25469150	G	T	0.011	DNMT3A	p.Y436X	Nonsense
PD41244	1	70.6	2	25457242	25457242	C	T	0.009	DNMT3A	p.R882H	Missense
PD41244	2	75.9	2	25457242	25457242	C	T	0.010	DNMT3A	p.R882H	Missense
PD41244	3	80.2	2	25457242	25457242	C	T	0.008	DNMT3A	p.R882H	Missense
PD41244	1	70.6	2	25462076	25462077	GG	G	0.019	DNMT3A	p.P777fs	Frameshift
PD41244	2	75.9	2	25462076	25462077	GG	G	0.021	DNMT3A	p.P777fs	Frameshift
PD41244	3	80.2	2	25462076	25462077	GG	G	0.035	DNMT3A	p.P777fs	Frameshift
PD41244	1	70.6	2	25463577	25463577	T	C	0.005	DNMT3A	p.D702G	Missense
PD41244	2	75.9	2	25463577	25463577	T	C	0.011	DNMT3A	p.D702G	Missense
PD41244	3	80.2	2	25463577	25463577	T	C	0.016	DNMT3A	p.D702G	Missense
PD41244	1	70.6	2	25464535	25464535	A	G	0.014	DNMT3A	p.Y660H	Missense
PD41244	2	75.9	2	25464535	25464535	A	G	0.011	DNMT3A	p.Y660H	Missense
PD41244	3	80.2	2	25464535	25464535	A	G	0.016	DNMT3A	p.Y660H	Missense
PD41244	1	70.6	2	25467110	25467110	T	A	0.009	DNMT3A	p.K589X	Nonsense
PD41244	2	75.9	2	25467110	25467110	T	A	0.011	DNMT3A	p.K589X	Nonsense
PD41244	3	80.2	2	25467110	25467110	T	A	0.010	DNMT3A	p.K589X	Nonsense
PD41245	1	74.4	19	56181006	56181006	C	T	0.008	U2AF2	p.S414F	Missense
PD41245	2	78.3	19	56181006	56181006	C	T	0.001	U2AF2	p.S414F	Missense
PD41245	3	82.0	19	56181006	56181006	C	T	0.000	U2AF2	p.S414F	Missense
PD41245	1	74.4	X	154317585	154317585	G	A	0.007	BRCC3	p.G151R	Missense
PD41245	2	78.3	X	154317585	154317585	G	A	0.007	BRCC3	p.G151R	Missense
PD41245	3	82.0	X	154317585	154317585	G	A	0.002	BRCC3	p.G151R	Missense
PD41246	1	76.5	4	106164929	106164929	A	G	0.012	TET2	p.N1266S	Missense
PD41246	2	79.6	4	106164929	106164929	A	G	0.020	TET2	p.N1266S	Missense
PD41246	3	82.6	4	106164929	106164929	A	G	0.018	TET2	p.N1266S	Missense
PD41246	4	85.6	4	106164929	106164929	A	G	0.021	TET2	p.N1266S	Missense
PD41246	1	76.5	7	148511184	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	2	79.6	7	148511184	148511184	G	A	0.001	EZH2	p.T573I	Missense
PD41246	3	82.6	7	148511184	148511184	G	A	0.006	EZH2	p.T573I	Missense
PD41246	4	85.6	7	148511184	148511184	G	A	0.005	EZH2	p.T573I	Missense
PD41246	1	76.5	9	5073770	5073770	G	T	0.005	JAK2	p.V617F	Missense
PD41246	2	79.6	9	5073770	5073770	G	T	0.014	JAK2	p.V617F	Missense
PD41246	3	82.6	9	5073770	5073770	G	T	0.027	JAK2	p.V617F	Missense
PD41246	4	85.6	9	5073770	5073770	G	T	0.058	JAK2	p.V617F	Missense
PD41247	1	77.0	2	198262730	198262730	C	A	0.000	SF3B1	p.G1082V	Missense
PD41247	2	79.9	2	198262730	198262730	C	A	0.006	SF3B1	p.G1082V	Missense
PD41247	3	84.3	2	198262730	198262730	C	A	0.000	SF3B1	p.G1082V	Missense
PD41247	1	77.0	4	106182951	106182952	CA	C	0.001	TET2	p.T1331fs	Frameshift
PD41247	2	79.9	4	106182951	106182952	CA	C	0.010	TET2	p.T1331fs	Frameshift
PD41247	3	84.3	4	106182951	106182952	CA	C	0.012	TET2	p.T1331fs	Frameshift
PD41247	1	77.0	11	119148916	119148916	A	G	0.003	CBL	p.Q379R	Missense
PD41247	2	79.9	11	119148916	119148916	A	G	0.007	CBL	p.Q379R	Missense
PD41247	3	84.3	11	119148916	119148916	A	G	0.005	CBL	p.Q379R	Missense
PD41247	1	77.0	15	90631934	90631934	C	T	0.001	IDH2	p.R140Q	Missense
PD41247	2	79.9	15	90631934	90631934	C	T	0.001	IDH2	p.R140Q	Missense
PD41247	3	84.3	15	90631934	90631934	C	T	0.009	IDH2	p.R140Q	Missense
PD41247	1	77.0	X	123196759	123196759	C	A	0.008	STAG2	p.T549K	Missense
PD41247	2	79.9	X	123196759	123196759	C	A	0.000	STAG2	p.T549K	Missense
PD41247	3	84.3	X	123196759	123196759	C	A	0.000	STAG2	p.T549K	Missense
PD41248	1	73.5	4	106157375	106157377	CTT	C	0.000	TET2	p.T759fs	Frameshift
PD41248	2	76.6	4	106157375	106157377	CTT	C	0.001	TET2	p.T759fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41248	3	81.0	4	106157375	106157377	CTT	C	0.007	TET2	p.T759fs	Frameshift
PD41248	1	73.5	9	139417558	139417558	G	A	0.006	NOTCH1	p.Y162Y	Synonymous
PD41248	2	76.6	9	139417558	139417558	G	A	0.001	NOTCH1	p.Y162Y	Synonymous
PD41248	3	81.0	9	139417558	139417558	G	A	0.000	NOTCH1	p.Y162Y	Synonymous
PD41248	1	73.5	11	119148929	119148929	A	G	0.006	CBL	p.I383M	Missense
PD41248	2	76.6	11	119148929	119148929	A	G	0.013	CBL	p.I383M	Missense
PD41248	3	81.0	11	119148929	119148929	A	G	0.015	CBL	p.I383M	Missense
PD41248	1	73.5	12	112910785	112910785	G	A	0.028	PTPN11	p.R265Q	Missense
PD41248	2	76.6	12	112910785	112910785	G	A	0.037	PTPN11	p.R265Q	Missense
PD41248	3	81.0	12	112910785	112910785	G	A	0.048	PTPN11	p.R265Q	Missense
PD41248	1	73.5	12	25380309	25380309	G	A	0.004	KRAS	p.T50I	Missense
PD41248	2	76.6	12	25380309	25380309	G	A	0.006	KRAS	p.T50I	Missense
PD41248	3	81.0	12	25380309	25380309	G	A	0.025	KRAS	p.T50I	Missense
PD41248	1	73.5	X	129146640	129146640	C	A	0.001	BCORL1	p.S58Y	Missense
PD41248	2	76.6	X	129146640	129146640	C	A	0.005	BCORL1	p.S58Y	Missense
PD41248	3	81.0	X	129146640	129146640	C	A	0.000	BCORL1	p.S58Y	Missense
PD41249	1	67.7	2	25468165	25468166	GG	G	0.002	DNMT3A	p.L504fs	Frameshift
PD41249	2	70.9	2	25468165	25468166	GG	G	0.003	DNMT3A	p.L504fs	Frameshift
PD41249	3	74.4	2	25468165	25468166	GG	G	0.007	DNMT3A	p.L504fs	Frameshift
PD41249	4	78.0	2	25468165	25468166	GG	G	0.005	DNMT3A	p.L504fs	Frameshift
PD41249	1	67.7	4	106164794	106164794	G	C	0.005	TET2	p.C1221S	Missense
PD41249	2	70.9	4	106164794	106164794	G	C	0.005	TET2	p.C1221S	Missense
PD41249	3	74.4	4	106164794	106164794	G	C	0.003	TET2	p.C1221S	Missense
PD41249	4	78.0	4	106164794	106164794	G	C	0.006	TET2	p.C1221S	Missense
PD41250	1	62.0	9	139413235	139413235	G	A	0.030	NOTCH1	p.P303S	Missense
PD41250	2	65.1	9	139413235	139413235	G	A	0.035	NOTCH1	p.P303S	Missense
PD41250	3	68.7	9	139413235	139413235	G	A	0.061	NOTCH1	p.P303S	Missense
PD41250	4	72.2	9	139413235	139413235	G	A	0.086	NOTCH1	p.P303S	Missense
PD41250	5	76.4	9	139413235	139413235	G	A	0.098	NOTCH1	p.P303S	Missense
PD41251	1	55.5	9	139399374	139399374	A	G	0.005	NOTCH1	p.F1590S	Missense
PD41251	2	58.8	9	139399374	139399374	A	G	0.009	NOTCH1	p.F1590S	Missense
PD41251	3	62.6	9	139399374	139399374	A	G	0.008	NOTCH1	p.F1590S	Missense
PD41251	4	65.8	9	139399374	139399374	A	G	0.005	NOTCH1	p.F1590S	Missense
PD41251	5	70.3	9	139399374	139399374	A	G	0.004	NOTCH1	p.F1590S	Missense
PD41251	1	55.5	20	31020724	31020724	A	T	0.001	ASXL1	p.M341L	Missense
PD41251	2	58.8	20	31020724	31020724	A	T	0.007	ASXL1	p.M341L	Missense
PD41251	3	62.6	20	31020724	31020724	A	T	0.019	ASXL1	p.M341L	Missense
PD41251	4	65.8	20	31020724	31020724	A	T	0.037	ASXL1	p.M341L	Missense
PD41251	5	70.3	20	31020724	31020724	A	T	0.057	ASXL1	p.M341L	Missense
PD41253	1	68.6	4	106156111	106156113	AAT	A	0.007	TET2	p.N338fs	Frameshift
PD41253	2	71.9	4	106156111	106156113	AAT	A	0.009	TET2	p.N338fs	Frameshift
PD41253	3	75.5	4	106156111	106156113	AAT	A	0.017	TET2	p.N338fs	Frameshift
PD41253	4	78.9	4	106156111	106156113	AAT	A	0.029	TET2	p.N338fs	Frameshift
PD41253	5	84.4	4	106156111	106156113	AAT	A	0.045	TET2	p.N338fs	Frameshift
PD41253	1	68.6	17	58740525	58740526	AT	A	0.000	PPM1D	p.N477fs	Frameshift
PD41253	2	71.9	17	58740525	58740526	AT	A	0.002	PPM1D	p.N477fs	Frameshift
PD41253	3	75.5	17	58740525	58740526	AT	A	0.001	PPM1D	p.N477fs	Frameshift
PD41253	4	78.9	17	58740525	58740526	AT	A	0.007	PPM1D	p.N477fs	Frameshift
PD41253	5	84.4	17	58740525	58740526	AT	A	0.013	PPM1D	p.N477fs	Frameshift
PD41253	1	68.6	X	53407608	53407608	G	A	0.000	SMC1A	p.A1162V	Missense
PD41253	2	71.9	X	53407608	53407608	G	A	0.000	SMC1A	p.A1162V	Missense
PD41253	3	75.5	X	53407608	53407608	G	A	0.000	SMC1A	p.A1162V	Missense
PD41253	4	78.9	X	53407608	53407608	G	A	0.003	SMC1A	p.A1162V	Missense
PD41253	5	84.4	X	53407608	53407608	G	A	0.001	SMC1A	p.A1162V	Missense
PD41254	1	66.1	10	112337249	112337249	C	T	0.009	SMC3	p.P90L	Missense
PD41254	2	69.5	10	112337249	112337249	C	T	0.018	SMC3	p.P90L	Missense
PD41254	3	73.0	10	112337249	112337249	C	T	0.008	SMC3	p.P90L	Missense
PD41254	4	76.4	10	112337249	112337249	C	T	0.011	SMC3	p.P90L	Missense
PD41254	5	82.0	10	112337249	112337249	C	T	0.009	SMC3	p.P90L	Missense
PD41254	1	66.1	12	25380226	25380226	A	G	0.000	KRAS	p.F78L	Missense
PD41254	2	69.5	12	25380226	25380226	A	G	0.001	KRAS	p.F78L	Missense
PD41254	3	73.0	12	25380226	25380226	A	G	0.005	KRAS	p.F78L	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41254	4	76.4	12	25380226	25380226	A	G	0.000	KRAS	p.F78L	Missense
PD41254	5	82.0	12	25380226	25380226	A	G	0.001	KRAS	p.F78L	Missense
PD41255	1	63.0	20	31021187	31021187	C	T	0.027	ASXL1	p.Q396X	Nonsense
PD41255	2	66.2	20	31021187	31021187	C	T	0.044	ASXL1	p.Q396X	Nonsense
PD41255	3	72.2	20	31021187	31021187	C	T	0.069	ASXL1	p.Q396X	Nonsense
PD41255	4	75.9	20	31021187	31021187	C	T	0.087	ASXL1	p.Q396X	Nonsense
PD41256	1	77.6	4	106196328	106196330	CAG	C	0.000	TET2	p.T1554fs	Frameshift
PD41256	2	80.8	4	106196328	106196330	CAG	C	0.000	TET2	p.T1554fs	Frameshift
PD41256	3	84.4	4	106196328	106196330	CAG	C	0.002	TET2	p.T1554fs	Frameshift
PD41256	4	87.8	4	106196328	106196330	CAG	C	0.007	TET2	p.T1554fs	Frameshift
PD41256	1	77.6	4	106196537	106196537	C	T	0.004	TET2	p.Q1624X	Nonsense
PD41256	2	80.8	4	106196537	106196537	C	T	0.017	TET2	p.Q1624X	Nonsense
PD41256	3	84.4	4	106196537	106196537	C	T	0.024	TET2	p.Q1624X	Nonsense
PD41256	4	87.8	4	106196537	106196537	C	T	0.032	TET2	p.Q1624X	Nonsense
PD41256	1	77.6	16	3819299	3819302	GCCA	G	0.031	CREBBP	p.978_979del	Inframe
PD41256	2	80.8	16	3819299	3819302	GCCA	G	0.063	CREBBP	p.978_979del	Inframe
PD41256	3	84.4	16	3819299	3819302	GCCA	G	0.087	CREBBP	p.978_979del	Inframe
PD41256	4	87.8	16	3819299	3819302	GCCA	G	0.072	CREBBP	p.978_979del	Inframe
PD41256	1	77.6	20	57429312	57429312	C	T	0.004	GNAS	p.A331V	Missense
PD41256	2	80.8	20	57429312	57429312	C	T	0.008	GNAS	p.A331V	Missense
PD41256	3	84.4	20	57429312	57429312	C	T	0.012	GNAS	p.A331V	Missense
PD41256	4	87.8	20	57429312	57429312	C	T	0.006	GNAS	p.A331V	Missense
PD41257	1	64.0	12	25380207	25380207	A	G	0.002	KRAS	p.I84T	Missense
PD41257	2	67.2	12	25380207	25380207	A	G	0.002	KRAS	p.I84T	Missense
PD41257	3	70.8	12	25380207	25380207	A	G	0.015	KRAS	p.I84T	Missense
PD41257	4	74.2	12	25380207	25380207	A	G	0.023	KRAS	p.I84T	Missense
PD41257	5	78.8	12	25380207	25380207	A	G	0.021	KRAS	p.I84T	Missense
PD41257	1	64.0	X	39933742	39933742	C	G	0.000	BCOR	p.S286T	Missense
PD41257	2	67.2	X	39933742	39933742	C	G	0.000	BCOR	p.S286T	Missense
PD41257	3	70.8	X	39933742	39933742	C	G	0.004	BCOR	p.S286T	Missense
PD41257	4	74.2	X	39933742	39933742	C	G	0.000	BCOR	p.S286T	Missense
PD41257	5	78.8	X	39933742	39933742	C	G	0.000	BCOR	p.S286T	Missense
PD41260	1	66.3	2	25463287	25463287	G	A	0.010	DNMT3A	p.R736C	Missense
PD41260	2	69.4	2	25463287	25463287	G	A	0.013	DNMT3A	p.R736C	Missense
PD41260	3	75.6	2	25463287	25463287	G	A	0.019	DNMT3A	p.R736C	Missense
PD41260	4	80.6	2	25463287	25463287	G	A	0.009	DNMT3A	p.R736C	Missense
PD41260	1	66.3	17	58678193	58678193	G	A	0.000	PPM1D	p.A140T	Missense
PD41260	2	69.4	17	58678193	58678193	G	A	0.001	PPM1D	p.A140T	Missense
PD41260	3	75.6	17	58678193	58678193	G	A	0.000	PPM1D	p.A140T	Missense
PD41260	4	80.6	17	58678193	58678193	G	A	0.008	PPM1D	p.A140T	Missense
PD41260	1	66.3	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.020	ASXL1	p.H630fs	Frameshift
PD41260	2	69.4	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.019	ASXL1	p.H630fs	Frameshift
PD41260	3	75.6	20	31022402	31022425	TCACCACTGCCATAGAGAG	T	0.045	ASXL1	p.H630fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
						GCGGC					
PD41260	4	80.6	20	31022402	31022425	TCACCACTGCCATAGAGAGGCGGC	T	0.088	ASXL1	p.H630fs	Frameshift
PD41261	1	65.3	9	139390799	139390799	C	T	0.002	NOTCH1	p.L2464L	Synonymous
PD41261	2	68.4	9	139390799	139390799	C	T	0.000	NOTCH1	p.L2464L	Synonymous
PD41261	3	74.6	9	139390799	139390799	C	T	0.012	NOTCH1	p.L2464L	Synonymous
PD41261	4	79.6	9	139390799	139390799	C	T	0.000	NOTCH1	p.L2464L	Synonymous
PD41261	1	65.3	X	129162655	129162655	A	G	0.002	BCORL1	p.E1375G	Missense
PD41261	2	68.4	X	129162655	129162655	A	G	0.002	BCORL1	p.E1375G	Missense
PD41261	3	74.6	X	129162655	129162655	A	G	0.002	BCORL1	p.E1375G	Missense
PD41261	4	79.6	X	129162655	129162655	A	G	0.007	BCORL1	p.E1375G	Missense
PD41262	1	70.8	2	25458649	25458649	G	A	0.001	DNMT3A	p.Q842X	Nonsense
PD41262	2	74.0	2	25458649	25458649	G	A	0.008	DNMT3A	p.Q842X	Nonsense
PD41262	3	77.8	2	25458649	25458649	G	A	0.001	DNMT3A	p.Q842X	Nonsense
PD41262	4	82.0	2	25458649	25458649	G	A	0.001	DNMT3A	p.Q842X	Nonsense
PD41262	1	70.8	2	25463286	25463286	C	T	0.072	DNMT3A	p.R736H	Missense
PD41262	2	74.0	2	25463286	25463286	C	T	0.101	DNMT3A	p.R736H	Missense
PD41262	3	77.8	2	25463286	25463286	C	T	0.172	DNMT3A	p.R736H	Missense
PD41262	4	82.0	2	25463286	25463286	C	T	0.209	DNMT3A	p.R736H	Missense
PD41262	1	70.8	4	106158371	106158375	CACCA	C	0.049	TET2	p.T1091fs	Frameshift
PD41262	2	74.0	4	106158371	106158375	CACCA	C	0.058	TET2	p.T1091fs	Frameshift
PD41262	3	77.8	4	106158371	106158375	CACCA	C	0.114	TET2	p.T1091fs	Frameshift
PD41262	4	82.0	4	106158371	106158375	CACCA	C	0.140	TET2	p.T1091fs	Frameshift
PD41263	1	69.0	9	139412379	139412379	G	T	0.000	NOTCH1	p.P422P	Synonymous
PD41263	2	72.0	9	139412379	139412379	G	T	0.005	NOTCH1	p.P422P	Synonymous
PD41263	3	75.7	9	139412379	139412379	G	T	0.000	NOTCH1	p.P422P	Synonymous
PD41263	4	80.2	9	139412379	139412379	G	T	0.000	NOTCH1	p.P422P	Synonymous
PD41263	5	83.8	9	139412379	139412379	G	T	0.000	NOTCH1	p.P422P	Synonymous
PD41263	1	69.0	11	32421555	32421555	G	A	0.003	WT1	p.T346M	Missense
PD41263	2	72.0	11	32421555	32421555	G	A	0.010	WT1	p.T346M	Missense
PD41263	3	75.7	11	32421555	32421555	G	A	0.008	WT1	p.T346M	Missense
PD41263	4	80.2	11	32421555	32421555	G	A	0.023	WT1	p.T346M	Missense
PD41263	5	83.8	11	32421555	32421555	G	A	0.021	WT1	p.T346M	Missense
PD41264	1	70.8	2	25467118	25467119	AA	A	0.001	DNMT3A	p.C586fs	Frameshift
PD41264	2	74.2	2	25467118	25467119	AA	A	0.002	DNMT3A	p.C586fs	Frameshift
PD41264	3	78.7	2	25467118	25467119	AA	A	0.001	DNMT3A	p.C586fs	Frameshift
PD41264	4	81.4	2	25467118	25467119	AA	A	0.006	DNMT3A	p.C586fs	Frameshift
PD41264	1	70.8	4	106180774	106180774	A	G	0.018	TET2	c.3804-2A>G	Splice site
PD41264	2	74.2	4	106180774	106180774	A	G	0.032	TET2	c.3804-2A>G	Splice site
PD41264	3	78.7	4	106180774	106180774	A	G	0.039	TET2	c.3804-2A>G	Splice site
PD41264	4	81.4	4	106180774	106180774	A	G	0.044	TET2	c.3804-2A>G	Splice site
PD41264	1	70.8	X	154319115	154319115	G	A	0.006	BRCC3	c.548+1G>A	Splice site
PD41264	2	74.2	X	154319115	154319115	G	A	0.005	BRCC3	c.548+1G>A	Splice site
PD41264	3	78.7	X	154319115	154319115	G	A	0.009	BRCC3	c.548+1G>A	Splice site
PD41264	4	81.4	X	154319115	154319115	G	A	0.009	BRCC3	c.548+1G>A	Splice site
PD41265	1	63.9	2	25462086	25462086	T	C	0.015	DNMT3A	c.2323-2A>G	Splice site
PD41265	2	67.1	2	25462086	25462086	T	C	0.019	DNMT3A	c.2323-2A>G	Splice site
PD41265	3	72.1	2	25462086	25462086	T	C	0.041	DNMT3A	c.2323-2A>G	Splice site
PD41265	4	74.8	2	25462086	25462086	T	C	0.029	DNMT3A	c.2323-2A>G	Splice site
PD41265	5	79.1	2	25462086	25462086	T	C	0.058	DNMT3A	c.2323-2A>G	Splice site
PD41265	1	63.9	2	25464464	25464464	G	A	0.019	DNMT3A	p.Y683Y	Synonymous
PD41265	2	67.1	2	25464464	25464464	G	A	0.023	DNMT3A	p.Y683Y	Synonymous

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41265	3	72.1	2	25464464	25464464	G	A	0.042	DNMT3A	p.Y683Y	Synonymous
PD41265	4	74.8	2	25464464	25464464	G	A	0.044	DNMT3A	p.Y683Y	Synonymous
PD41265	5	79.1	2	25464464	25464464	G	A	0.053	DNMT3A	p.Y683Y	Synonymous
PD41265	1	63.9	2	25470029	25470029	T	A	0.020	DNMT3A	c.1015-2A>T	Splice site
PD41265	2	67.1	2	25470029	25470029	T	A	0.028	DNMT3A	c.1015-2A>T	Splice site
PD41265	3	72.1	2	25470029	25470029	T	A	0.025	DNMT3A	c.1015-2A>T	Splice site
PD41265	4	74.8	2	25470029	25470029	T	A	0.013	DNMT3A	c.1015-2A>T	Splice site
PD41265	5	79.1	2	25470029	25470029	T	A	0.013	DNMT3A	c.1015-2A>T	Splice site
PD41265	1	63.9	12	112926873	112926873	G	T	0.002	PTPN11	p.R498L	Missense
PD41265	2	67.1	12	112926873	112926873	G	T	0.002	PTPN11	p.R498L	Missense
PD41265	3	72.1	12	112926873	112926873	G	T	0.003	PTPN11	p.R498L	Missense
PD41265	4	74.8	12	112926873	112926873	G	T	0.004	PTPN11	p.R498L	Missense
PD41265	5	79.1	12	112926873	112926873	G	T	0.006	PTPN11	p.R498L	Missense
PD41265	1	63.9	12	12022364	12022364	G	A	0.000	ETV6	p.C157Y	Missense
PD41265	2	67.1	12	12022364	12022364	G	A	0.001	ETV6	p.C157Y	Missense
PD41265	3	72.1	12	12022364	12022364	G	A	0.000	ETV6	p.C157Y	Missense
PD41265	4	74.8	12	12022364	12022364	G	A	0.000	ETV6	p.C157Y	Missense
PD41265	5	79.1	12	12022364	12022364	G	A	0.006	ETV6	p.C157Y	Missense
PD41266	1	65.1	4	106157521	106157521	G	T	0.001	TET2	p.E808X	Nonsense
PD41266	2	68.3	4	106157521	106157521	G	T	0.003	TET2	p.E808X	Nonsense
PD41266	3	72.1	4	106157521	106157521	G	T	0.005	TET2	p.E808X	Nonsense
PD41266	4	75.2	4	106157521	106157521	G	T	0.001	TET2	p.E808X	Nonsense
PD41266	5	80.2	4	106157521	106157521	G	T	0.007	TET2	p.E808X	Nonsense
PD41266	1	65.1	4	106180841	106180841	C	T	0.000	TET2	p.S1290L	Missense
PD41266	2	68.3	4	106180841	106180841	C	T	0.001	TET2	p.S1290L	Missense
PD41266	3	72.1	4	106180841	106180841	C	T	0.002	TET2	p.S1290L	Missense
PD41266	4	75.2	4	106180841	106180841	C	T	0.003	TET2	p.S1290L	Missense
PD41266	5	80.2	4	106180841	106180841	C	T	0.023	TET2	p.S1290L	Missense
PD41266	1	65.1	4	106196964	106196965	AC	A	0.000	TET2	p.Y1766X	Nonsense
PD41266	2	68.3	4	106196964	106196965	AC	A	0.001	TET2	p.Y1766X	Nonsense
PD41266	3	72.1	4	106196964	106196965	AC	A	0.000	TET2	p.Y1766X	Nonsense
PD41266	4	75.2	4	106196964	106196965	AC	A	0.003	TET2	p.Y1766X	Nonsense
PD41266	5	80.2	4	106196964	106196965	AC	A	0.009	TET2	p.Y1766X	Nonsense
PD41266	1	65.1	4	106197123	106197123	T	G	0.013	TET2	p.L1819X	Nonsense
PD41266	2	68.3	4	106197123	106197123	T	G	0.022	TET2	p.L1819X	Nonsense
PD41266	3	72.1	4	106197123	106197123	T	G	0.012	TET2	p.L1819X	Nonsense
PD41266	4	75.2	4	106197123	106197123	T	G	0.010	TET2	p.L1819X	Nonsense
PD41266	5	80.2	4	106197123	106197123	T	G	0.022	TET2	p.L1819X	Nonsense
PD41266	1	65.1	20	31021717	31021717	C	T	0.003	ASXL1	p.I572I	Synonymous
PD41266	2	68.3	20	31021717	31021717	C	T	0.009	ASXL1	p.I572I	Synonymous
PD41266	3	72.1	20	31021717	31021717	C	T	0.005	ASXL1	p.I572I	Synonymous
PD41266	4	75.2	20	31021717	31021717	C	T	0.010	ASXL1	p.I572I	Synonymous
PD41266	5	80.2	20	31021717	31021717	C	T	0.018	ASXL1	p.I572I	Synonymous
PD41267	1	75.0	2	25467426	25467427	CC	C	0.008	DNMT3A	p.G550fs	Frameshift
PD41267	2	78.4	2	25467426	25467427	CC	C	0.007	DNMT3A	p.G550fs	Frameshift
PD41267	3	83.8	2	25467426	25467427	CC	C	0.003	DNMT3A	p.G550fs	Frameshift
PD41267	1	75.0	2	25505534	25505534	G	A	0.000	DNMT3A	p.S75F	Missense
PD41267	2	78.4	2	25505534	25505534	G	A	0.000	DNMT3A	p.S75F	Missense
PD41267	3	83.8	2	25505534	25505534	G	A	0.005	DNMT3A	p.S75F	Missense
PD41268	1	57.1	9	139401046	139401046	C	A	0.007	NOTCH1	p.C1316F	Missense
PD41268	2	60.5	9	139401046	139401046	C	A	0.000	NOTCH1	p.C1316F	Missense
PD41268	3	63.8	9	139401046	139401046	C	A	0.000	NOTCH1	p.C1316F	Missense
PD41268	4	67.2	9	139401046	139401046	C	A	0.000	NOTCH1	p.C1316F	Missense
PD41268	5	71.5	9	139401046	139401046	C	A	0.000	NOTCH1	p.C1316F	Missense
PD41268	1	57.1	9	5073770	5073770	G	T	0.001	JAK2	p.V617F	Missense
PD41268	2	60.5	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD41268	3	63.8	9	5073770	5073770	G	T	0.006	JAK2	p.V617F	Missense
PD41268	4	67.2	9	5073770	5073770	G	T	0.079	JAK2	p.V617F	Missense
PD41268	5	71.5	9	5073770	5073770	G	T	0.005	JAK2	p.V617F	Missense
PD41269	1	61.9	2	25466790	25466790	G	C	0.001	DNMT3A	p.S638C	Missense
PD41269	2	65.2	2	25466790	25466790	G	C	0.002	DNMT3A	p.S638C	Missense
PD41269	3	68.9	2	25466790	25466790	G	C	0.005	DNMT3A	p.S638C	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41269	4	72.9	2	25466790	25466790	G	C	0.007	DNMT3A	p.S638C	Missense
PD41269	5	77.0	2	25466790	25466790	G	C	0.011	DNMT3A	p.S638C	Missense
PD41270	1	57.7	2	25467083	25467083	G	A	0.018	DNMT3A	p.R598X	Nonsense
PD41270	2	60.9	2	25467083	25467083	G	A	0.031	DNMT3A	p.R598X	Nonsense
PD41270	3	64.6	2	25467083	25467083	G	A	0.046	DNMT3A	p.R598X	Nonsense
PD41270	4	67.8	2	25467083	25467083	G	A	0.050	DNMT3A	p.R598X	Nonsense
PD41270	5	72.2	2	25467083	25467083	G	A	0.049	DNMT3A	p.R598X	Nonsense
PD41270	1	57.7	2	25467143	25467143	C	A	0.005	DNMT3A	p.E578X	Nonsense
PD41270	2	60.9	2	25467143	25467143	C	A	0.007	DNMT3A	p.E578X	Nonsense
PD41270	3	64.6	2	25467143	25467143	C	A	0.012	DNMT3A	p.E578X	Nonsense
PD41270	4	67.8	2	25467143	25467143	C	A	0.012	DNMT3A	p.E578X	Nonsense
PD41270	5	72.2	2	25467143	25467143	C	A	0.015	DNMT3A	p.E578X	Nonsense
PD41270	1	57.7	8	117868478	117868478	T	C	0.006	RAD21	p.P288P	Synonymous
PD41270	2	60.9	8	117868478	117868478	T	C	0.000	RAD21	p.P288P	Synonymous
PD41270	3	64.6	8	117868478	117868478	T	C	0.000	RAD21	p.P288P	Synonymous
PD41270	4	67.8	8	117868478	117868478	T	C	0.000	RAD21	p.P288P	Synonymous
PD41270	5	72.2	8	117868478	117868478	T	C	0.000	RAD21	p.P288P	Synonymous
PD41270	1	57.7	17	7577538	7577538	C	T	0.000	TP53	p.R209Q	Missense
PD41270	2	60.9	17	7577538	7577538	C	T	0.002	TP53	p.R209Q	Missense
PD41270	3	64.6	17	7577538	7577538	C	T	0.003	TP53	p.R209Q	Missense
PD41270	4	67.8	17	7577538	7577538	C	T	0.007	TP53	p.R209Q	Missense
PD41270	5	72.2	17	7577538	7577538	C	T	0.014	TP53	p.R209Q	Missense
PD41271	1	71.2	17	58740518	58740518	G	T	0.001	PPM1D	p.E475X	Nonsense
PD41271	2	74.6	17	58740518	58740518	G	T	0.002	PPM1D	p.E475X	Nonsense
PD41271	3	78.4	17	58740518	58740518	G	T	0.001	PPM1D	p.E475X	Nonsense
PD41271	4	81.4	17	58740518	58740518	G	T	0.002	PPM1D	p.E475X	Nonsense
PD41271	5	86.9	17	58740518	58740518	G	T	0.008	PPM1D	p.E475X	Nonsense
PD41271	1	71.2	17	58740525	58740526	AT	A	0.000	PPM1D	p.N477fs	Frameshift
PD41271	2	74.6	17	58740525	58740526	AT	A	0.002	PPM1D	p.N477fs	Frameshift
PD41271	3	78.4	17	58740525	58740526	AT	A	0.001	PPM1D	p.N477fs	Frameshift
PD41271	4	81.4	17	58740525	58740526	AT	A	0.000	PPM1D	p.N477fs	Frameshift
PD41271	5	86.9	17	58740525	58740526	AT	A	0.007	PPM1D	p.N477fs	Frameshift
PD41272	1	72.9	2	198267359	198267359	C	A	0.009	SF3B1	p.K666N	Missense
PD41272	2	76.0	2	198267359	198267359	C	A	0.010	SF3B1	p.K666N	Missense
PD41272	3	79.8	2	198267359	198267359	C	A	0.012	SF3B1	p.K666N	Missense
PD41272	4	82.9	2	198267359	198267359	C	A	0.023	SF3B1	p.K666N	Missense
PD41272	5	87.4	2	198267359	198267359	C	A	0.037	SF3B1	p.K666N	Missense
PD41273	1	59.2	16	67663375	67663375	G	T	0.000	CTCF	p.K592N	Missense
PD41273	2	62.1	16	67663375	67663375	G	T	0.001	CTCF	p.K592N	Missense
PD41273	3	66.8	16	67663375	67663375	G	T	0.005	CTCF	p.K592N	Missense
PD41273	4	69.9	16	67663375	67663375	G	T	0.000	CTCF	p.K592N	Missense
PD41273	5	74.4	16	67663375	67663375	G	T	0.000	CTCF	p.K592N	Missense
PD41273	1	59.2	19	56180105	56180105	C	A	0.001	U2AF2	p.L298I	Missense
PD41273	2	62.1	19	56180105	56180105	C	A	0.002	U2AF2	p.L298I	Missense
PD41273	3	66.8	19	56180105	56180105	C	A	0.002	U2AF2	p.L298I	Missense
PD41273	4	69.9	19	56180105	56180105	C	A	0.007	U2AF2	p.L298I	Missense
PD41273	5	74.4	19	56180105	56180105	C	A	0.000	U2AF2	p.L298I	Missense
PD41273	1	59.2	X	53438722	53438722	C	A	0.004	SMC1A	p.V393L	Missense
PD41273	2	62.1	X	53438722	53438722	C	A	0.000	SMC1A	p.V393L	Missense
PD41273	3	66.8	X	53438722	53438722	C	A	0.000	SMC1A	p.V393L	Missense
PD41273	4	69.9	X	53438722	53438722	C	A	0.000	SMC1A	p.V393L	Missense
PD41273	5	74.4	X	53438722	53438722	C	A	0.000	SMC1A	p.V393L	Missense
PD41274	1	61.6	20	31024311	31024312	CT	C	0.007	ASXL1	p.L1266fs	Frameshift
PD41274	2	64.6	20	31024311	31024312	CT	C	0.003	ASXL1	p.L1266fs	Frameshift
PD41274	3	68.4	20	31024311	31024312	CT	C	0.004	ASXL1	p.L1266fs	Frameshift
PD41274	4	71.5	20	31024311	31024312	CT	C	0.003	ASXL1	p.L1266fs	Frameshift
PD41274	5	75.8	20	31024311	31024312	CT	C	0.001	ASXL1	p.L1266fs	Frameshift
PD41275	1	62.2	2	25467522	25467522	C	A	0.004	DNMT3A	c.1555-1G>T	Splice site
PD41275	2	65.5	2	25467522	25467522	C	A	0.004	DNMT3A	c.1555-1G>T	Splice site
PD41275	3	69.1	2	25467522	25467522	C	A	0.005	DNMT3A	c.1555-1G>T	Splice site
PD41275	4	72.1	2	25467522	25467522	C	A	0.003	DNMT3A	c.1555-1G>T	Splice site
PD41275	5	77.4	2	25467522	25467522	C	A	0.011	DNMT3A	c.1555-1G>T	Splice site

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41275	1	62.2	4	106197285	106197285	T	C	0.001	TET2	p.I1873T	Missense
PD41275	2	65.5	4	106197285	106197285	T	C	0.003	TET2	p.I1873T	Missense
PD41275	3	69.1	4	106197285	106197285	T	C	0.008	TET2	p.I1873T	Missense
PD41275	4	72.1	4	106197285	106197285	T	C	0.007	TET2	p.I1873T	Missense
PD41275	5	77.4	4	106197285	106197285	T	C	0.010	TET2	p.I1873T	Missense
PD41276	1	62.2	2	198266834	198266834	T	C	0.000	SF3B1	p.K700E	Missense
PD41276	2	65.6	2	198266834	198266834	T	C	0.004	SF3B1	p.K700E	Missense
PD41276	3	69.3	2	198266834	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41276	4	72.2	2	198266834	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41276	5	76.7	2	198266834	198266834	T	C	0.011	SF3B1	p.K700E	Missense
PD41276	1	62.2	2	198267359	198267359	C	G	0.023	SF3B1	p.K666N	Missense
PD41276	2	65.6	2	198267359	198267359	C	G	0.096	SF3B1	p.K666N	Missense
PD41276	3	69.3	2	198267359	198267359	C	G	0.185	SF3B1	p.K666N	Missense
PD41276	4	72.2	2	198267359	198267359	C	G	0.297	SF3B1	p.K666N	Missense
PD41276	5	76.7	2	198267359	198267359	C	G	0.359	SF3B1	p.K666N	Missense
PD41276	1	62.2	9	139438556	139438556	T	C	0.006	NOTCH1	c.62-2A>G	Splice site
PD41276	2	65.6	9	139438556	139438556	T	C	0.002	NOTCH1	c.62-2A>G	Splice site
PD41276	3	69.3	9	139438556	139438556	T	C	0.001	NOTCH1	c.62-2A>G	Splice site
PD41276	4	72.2	9	139438556	139438556	T	C	0.000	NOTCH1	c.62-2A>G	Splice site
PD41276	5	76.7	9	139438556	139438556	T	C	0.000	NOTCH1	c.62-2A>G	Splice site
PD41276	1	62.2	11	119142571	119142571	G	A	0.000	CBL	p.W190X	Nonsense
PD41276	2	65.6	11	119142571	119142571	G	A	0.000	CBL	p.W190X	Nonsense
PD41276	3	69.3	11	119142571	119142571	G	A	0.008	CBL	p.W190X	Nonsense
PD41276	4	72.2	11	119142571	119142571	G	A	0.010	CBL	p.W190X	Nonsense
PD41276	5	76.7	11	119142571	119142571	G	A	0.015	CBL	p.W190X	Nonsense
PD41276	1	62.2	X	15809085	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	2	65.6	X	15809085	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	3	69.3	X	15809085	15809085	A	G	0.001	ZRSR2	p.K24E	Missense
PD41276	4	72.2	X	15809085	15809085	A	G	0.000	ZRSR2	p.K24E	Missense
PD41276	5	76.7	X	15809085	15809085	A	G	0.004	ZRSR2	p.K24E	Missense
PD41276	1	62.2	X	39922886	39922886	A	T	0.035	BCOR	p.S1240S	Synonymous
PD41276	2	65.6	X	39922886	39922886	A	T	0.097	BCOR	p.S1240S	Synonymous
PD41276	3	69.3	X	39922886	39922886	A	T	0.203	BCOR	p.S1240S	Synonymous
PD41276	4	72.2	X	39922886	39922886	A	T	0.269	BCOR	p.S1240S	Synonymous
PD41276	5	76.7	X	39922886	39922886	A	T	0.352	BCOR	p.S1240S	Synonymous
PD41277	1	59.0	12	50027272	50027272	T	C	0.008	PRPF40B	p.Y174Y	Synonymous
PD41277	2	62.3	12	50027272	50027272	T	C	0.013	PRPF40B	p.Y174Y	Synonymous
PD41277	3	66.0	12	50027272	50027272	T	C	0.009	PRPF40B	p.Y174Y	Synonymous
PD41277	4	69.0	12	50027272	50027272	T	C	0.006	PRPF40B	p.Y174Y	Synonymous
PD41277	5	73.4	12	50027272	50027272	T	C	0.004	PRPF40B	p.Y174Y	Synonymous
PD41278	1	61.7	2	25458595	25458595	A	G	0.005	DNMT3A	p.W860R	Missense
PD41278	2	64.9	2	25458595	25458595	A	G	0.005	DNMT3A	p.W860R	Missense
PD41278	3	68.6	2	25458595	25458595	A	G	0.004	DNMT3A	p.W860R	Missense
PD41278	4	71.6	2	25458595	25458595	A	G	0.008	DNMT3A	p.W860R	Missense
PD41278	5	76.9	2	25458595	25458595	A	G	0.004	DNMT3A	p.W860R	Missense
PD41278	1	61.7	17	58740529	58740529	C	A	0.001	PPM1D	p.C478X	Nonsense
PD41278	2	64.9	17	58740529	58740529	C	A	0.000	PPM1D	p.C478X	Nonsense
PD41278	3	68.6	17	58740529	58740529	C	A	0.001	PPM1D	p.C478X	Nonsense
PD41278	4	71.6	17	58740529	58740529	C	A	0.005	PPM1D	p.C478X	Nonsense
PD41278	5	76.9	17	58740529	58740529	C	A	0.012	PPM1D	p.C478X	Nonsense
PD41278	1	61.7	X	129148036	129148036	A	G	0.000	BCORL1	p.M430V	Missense
PD41278	2	64.9	X	129148036	129148036	A	G	0.000	BCORL1	p.M430V	Missense
PD41278	3	68.6	X	129148036	129148036	A	G	0.000	BCORL1	p.M430V	Missense
PD41278	4	71.6	X	129148036	129148036	A	G	0.001	BCORL1	p.M430V	Missense
PD41278	5	76.9	X	129148036	129148036	A	G	0.010	BCORL1	p.M430V	Missense
PD41279	1	56.9	X	129189834	129189834	G	T	0.000	BCORL1	p.C1694F	Missense
PD41279	2	60.1	X	129189834	129189834	G	T	0.005	BCORL1	p.C1694F	Missense
PD41279	3	63.6	X	129189834	129189834	G	T	0.000	BCORL1	p.C1694F	Missense
PD41279	4	66.6	X	129189834	129189834	G	T	0.000	BCORL1	p.C1694F	Missense
PD41279	5	70.9	X	129189834	129189834	G	T	0.000	BCORL1	p.C1694F	Missense
PD41280	1	60.5	4	106197121	106197123	ATT	A	0.004	TET2	p.L1819fs	Frameshift
PD41280	2	63.5	4	106197121	106197123	ATT	A	0.001	TET2	p.L1819fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41280	3	67.2	4	106197121	106197123	ATT	A	0.004	TET2	p.L1819fs	Frameshift
PD41280	4	70.3	4	106197121	106197123	ATT	A	0.005	TET2	p.L1819fs	Frameshift
PD41280	5	75.4	4	106197121	106197123	ATT	A	0.007	TET2	p.L1819fs	Frameshift
PD41280	1	60.5	11	119148991	119148991	G	A	0.004	CBL	p.C404Y	Missense
PD41280	2	63.5	11	119148991	119148991	G	A	0.004	CBL	p.C404Y	Missense
PD41280	3	67.2	11	119148991	119148991	G	A	0.001	CBL	p.C404Y	Missense
PD41280	4	70.3	11	119148991	119148991	G	A	0.006	CBL	p.C404Y	Missense
PD41280	5	75.4	11	119148991	119148991	G	A	0.004	CBL	p.C404Y	Missense
PD41280	1	60.5	22	30734818	30734818	C	T	0.000	SF3A1	p.S568N	Missense
PD41280	2	63.5	22	30734818	30734818	C	T	0.000	SF3A1	p.S568N	Missense
PD41280	3	67.2	22	30734818	30734818	C	T	0.001	SF3A1	p.S568N	Missense
PD41280	4	70.3	22	30734818	30734818	C	T	0.002	SF3A1	p.S568N	Missense
PD41280	5	75.4	22	30734818	30734818	C	T	0.006	SF3A1	p.S568N	Missense
PD41280	1	60.5	X	53409450	53409450	G	T	0.000	SMC1A	p.L1066M	Missense
PD41280	2	63.5	X	53409450	53409450	G	T	0.004	SMC1A	p.L1066M	Missense
PD41280	3	67.2	X	53409450	53409450	G	T	0.000	SMC1A	p.L1066M	Missense
PD41280	4	70.3	X	53409450	53409450	G	T	0.000	SMC1A	p.L1066M	Missense
PD41280	5	75.4	X	53409450	53409450	G	T	0.000	SMC1A	p.L1066M	Missense
PD41283	1	64.8	11	118343151	118343151	G	A	0.000	KMT2A	p.R426Q	Missense
PD41283	2	68.2	11	118343151	118343151	G	A	0.005	KMT2A	p.R426Q	Missense
PD41283	3	71.9	11	118343151	118343151	G	A	0.000	KMT2A	p.R426Q	Missense
PD41283	4	74.8	11	118343151	118343151	G	A	0.002	KMT2A	p.R426Q	Missense
PD41283	5	79.5	11	118343151	118343151	G	A	0.000	KMT2A	p.R426Q	Missense
PD41284	1	60.8	8	117878878	117878878	G	A	0.004	RAD21	p.H31Y	Missense
PD41284	2	64.1	8	117878878	117878878	G	A	0.004	RAD21	p.H31Y	Missense
PD41284	3	67.8	8	117878878	117878878	G	A	0.004	RAD21	p.H31Y	Missense
PD41284	4	70.7	8	117878878	117878878	G	A	0.002	RAD21	p.H31Y	Missense
PD41284	5	75.8	8	117878878	117878878	G	A	0.009	RAD21	p.H31Y	Missense
PD41284	1	60.8	19	33792923	33792923	C	T	0.000	CEBPA	p.C133Y	Missense
PD41284	2	64.1	19	33792923	33792923	C	T	0.000	CEBPA	p.C133Y	Missense
PD41284	3	67.8	19	33792923	33792923	C	T	0.000	CEBPA	p.C133Y	Missense
PD41284	4	70.7	19	33792923	33792923	C	T	0.018	CEBPA	p.C133Y	Missense
PD41284	5	75.8	19	33792923	33792923	C	T	0.000	CEBPA	p.C133Y	Missense
PD41284	1	60.8	X	44942752	44942752	G	C	0.001	KDM6A	p.R1163P	Missense
PD41284	2	64.1	X	44942752	44942752	G	C	0.001	KDM6A	p.R1163P	Missense
PD41284	3	67.8	X	44942752	44942752	G	C	0.004	KDM6A	p.R1163P	Missense
PD41284	4	70.7	X	44942752	44942752	G	C	0.008	KDM6A	p.R1163P	Missense
PD41284	5	75.8	X	44942752	44942752	G	C	0.006	KDM6A	p.R1163P	Missense
PD41285	1	62.5	2	198266834	198266834	T	C	0.001	SF3B1	p.K700E	Missense
PD41285	2	65.2	2	198266834	198266834	T	C	0.001	SF3B1	p.K700E	Missense
PD41285	3	68.9	2	198266834	198266834	T	C	0.003	SF3B1	p.K700E	Missense
PD41285	4	72.1	2	198266834	198266834	T	C	0.006	SF3B1	p.K700E	Missense
PD41285	5	76.5	2	198266834	198266834	T	C	0.002	SF3B1	p.K700E	Missense
PD41285	1	62.5	2	25458605	25458606	CT	C	0.005	DNMT3A	p.E856fs	Frameshift
PD41285	2	65.2	2	25458605	25458606	CT	C	0.016	DNMT3A	p.E856fs	Frameshift
PD41285	3	68.9	2	25458605	25458606	CT	C	0.012	DNMT3A	p.E856fs	Frameshift
PD41285	4	72.1	2	25458605	25458606	CT	C	0.025	DNMT3A	p.E856fs	Frameshift
PD41285	5	76.5	2	25458605	25458606	CT	C	0.054	DNMT3A	p.E856fs	Frameshift
PD41285	1	62.5	2	25469918	25469919	CC	C	0.002	DNMT3A	c.1122+1G>-	Splice site
PD41285	2	65.2	2	25469918	25469919	CC	C	0.001	DNMT3A	c.1122+1G>-	Splice site
PD41285	3	68.9	2	25469918	25469919	CC	C	0.002	DNMT3A	c.1122+1G>-	Splice site
PD41285	4	72.1	2	25469918	25469919	CC	C	0.008	DNMT3A	c.1122+1G>-	Splice site
PD41285	5	76.5	2	25469918	25469919	CC	C	0.001	DNMT3A	c.1122+1G>-	Splice site
PD41285	1	62.5	4	106155962	106155962	C	G	0.008	TET2	p.P288R	Missense
PD41285	2	65.2	4	106155962	106155962	C	G	0.005	TET2	p.P288R	Missense
PD41285	3	68.9	4	106155962	106155962	C	G	0.005	TET2	p.P288R	Missense
PD41285	4	72.1	4	106155962	106155962	C	G	0.008	TET2	p.P288R	Missense
PD41285	5	76.5	4	106155962	106155962	C	G	0.013	TET2	p.P288R	Missense
PD41285	1	62.5	X	39931877	39931877	C	A	0.001	BCOR	p.D908Y	Missense
PD41285	2	65.2	X	39931877	39931877	C	A	0.000	BCOR	p.D908Y	Missense
PD41285	3	68.9	X	39931877	39931877	C	A	0.001	BCOR	p.D908Y	Missense
PD41285	4	72.1	X	39931877	39931877	C	A	0.000	BCOR	p.D908Y	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41285	5	76.5	X	39931877	39931877	C	A	0.004	BCOR	p.D908Y	Missense
PD41286	1	61.3	2	25464554	25464554	C	A	0.023	DNMT3A	p.L653F	Missense
PD41286	2	64.0	2	25464554	25464554	C	A	0.028	DNMT3A	p.L653F	Missense
PD41286	3	67.7	2	25464554	25464554	C	A	0.050	DNMT3A	p.L653F	Missense
PD41286	4	71.0	2	25464554	25464554	C	A	0.077	DNMT3A	p.L653F	Missense
PD41286	5	75.3	2	25464554	25464554	C	A	0.069	DNMT3A	p.L653F	Missense
PD41286	1	61.3	2	25469525	25469525	G	A	0.014	DNMT3A	p.Q415X	Nonsense
PD41286	2	64.0	2	25469525	25469525	G	A	0.022	DNMT3A	p.Q415X	Nonsense
PD41286	3	67.7	2	25469525	25469525	G	A	0.037	DNMT3A	p.Q415X	Nonsense
PD41286	4	71.0	2	25469525	25469525	G	A	0.035	DNMT3A	p.Q415X	Nonsense
PD41286	5	75.3	2	25469525	25469525	G	A	0.029	DNMT3A	p.Q415X	Nonsense
PD41286	1	61.3	7	101926019	101926019	G	A	0.001	CUX1	p.A638T	Missense
PD41286	2	64.0	7	101926019	101926019	G	A	0.000	CUX1	p.A638T	Missense
PD41286	3	67.7	7	101926019	101926019	G	A	0.000	CUX1	p.A638T	Missense
PD41286	4	71.0	7	101926019	101926019	G	A	0.000	CUX1	p.A638T	Missense
PD41286	5	75.3	7	101926019	101926019	G	A	0.008	CUX1	p.A638T	Missense
PD41287	1	60.8	X	154319060	154319061	CT	C	0.003	BRCC3	p.T165fs	Frameshift
PD41287	2	64.1	X	154319060	154319061	CT	C	0.004	BRCC3	p.T165fs	Frameshift
PD41287	3	67.8	X	154319060	154319061	CT	C	0.005	BRCC3	p.T165fs	Frameshift
PD41287	4	70.7	X	154319060	154319061	CT	C	0.006	BRCC3	p.T165fs	Frameshift
PD41287	5	75.4	X	154319060	154319061	CT	C	0.001	BRCC3	p.T165fs	Frameshift
PD41288	1	54.6	10	112349439	112349439	A	T	0.000	SMC3	p.K461M	Missense
PD41288	2	57.8	10	112349439	112349439	A	T	0.003	SMC3	p.K461M	Missense
PD41288	3	61.5	10	112349439	112349439	A	T	0.001	SMC3	p.K461M	Missense
PD41288	4	64.4	10	112349439	112349439	A	T	0.003	SMC3	p.K461M	Missense
PD41288	5	69.1	10	112349439	112349439	A	T	0.008	SMC3	p.K461M	Missense
PD41288	1	54.6	17	7578190	7578190	T	C	0.005	TP53	p.Y181C	Missense
PD41288	2	57.8	17	7578190	7578190	T	C	0.002	TP53	p.Y181C	Missense
PD41288	3	61.5	17	7578190	7578190	T	C	0.001	TP53	p.Y181C	Missense
PD41288	4	64.4	17	7578190	7578190	T	C	0.006	TP53	p.Y181C	Missense
PD41288	5	69.1	17	7578190	7578190	T	C	0.011	TP53	p.Y181C	Missense
PD41289	1	65.0	2	25464489	25464489	A	G	0.004	DNMT3A	p.V675A	Missense
PD41289	2	68.0	2	25464489	25464489	A	G	0.014	DNMT3A	p.V675A	Missense
PD41289	3	72.1	2	25464489	25464489	A	G	0.014	DNMT3A	p.V675A	Missense
PD41289	4	75.6	2	25464489	25464489	A	G	0.029	DNMT3A	p.V675A	Missense
PD41289	5	79.7	2	25464489	25464489	A	G	0.035	DNMT3A	p.V675A	Missense
PD41291	1	74.3	2	198267360	198267360	T	C	0.002	SF3B1	p.K666R	Missense
PD41291	2	77.7	2	198267360	198267360	T	C	0.004	SF3B1	p.K666R	Missense
PD41291	3	82.9	2	198267360	198267360	T	C	0.031	SF3B1	p.K666R	Missense
PD41291	4	87.4	2	198267360	198267360	T	C	0.000	SF3B1	p.K666R	Missense
PD41291	1	74.3	9	5073770	5073770	G	T	0.004	JAK2	p.V617F	Missense
PD41291	2	77.7	9	5073770	5073770	G	T	0.007	JAK2	p.V617F	Missense
PD41291	3	82.9	9	5073770	5073770	G	T	0.085	JAK2	p.V617F	Missense
PD41291	4	87.4	9	5073770	5073770	G	T	0.280	JAK2	p.V617F	Missense
PD41291	1	74.3	16	3820647	3820647	T	G	0.042	CREBBP	p.Q935P	Missense
PD41291	2	77.7	16	3820647	3820647	T	G	0.093	CREBBP	p.Q935P	Missense
PD41291	3	82.9	16	3820647	3820647	T	G	0.047	CREBBP	p.Q935P	Missense
PD41291	4	87.4	16	3820647	3820647	T	G	0.002	CREBBP	p.Q935P	Missense
PD41291	1	74.3	16	3843456	3843456	G	A	0.000	CREBBP	p.P383S	Missense
PD41291	2	77.7	16	3843456	3843456	G	A	0.000	CREBBP	p.P383S	Missense
PD41291	3	82.9	16	3843456	3843456	G	A	0.000	CREBBP	p.P383S	Missense
PD41291	4	87.4	16	3843456	3843456	G	A	0.008	CREBBP	p.P383S	Missense
PD41291	1	74.3	17	7579315	7579315	G	T	0.030	TP53	p.C85X	Nonsense
PD41291	2	77.7	17	7579315	7579315	G	T	0.092	TP53	p.C85X	Nonsense
PD41291	3	82.9	17	7579315	7579315	G	T	0.025	TP53	p.C85X	Nonsense
PD41291	4	87.4	17	7579315	7579315	G	T	0.000	TP53	p.C85X	Nonsense
PD41291	1	74.3	20	31022311	31022311	C	A	0.000	ASXL1	p.P599H	Missense
PD41291	2	77.7	20	31022311	31022311	C	A	0.000	ASXL1	p.P599H	Missense
PD41291	3	82.9	20	31022311	31022311	C	A	0.000	ASXL1	p.P599H	Missense
PD41291	4	87.4	20	31022311	31022311	C	A	0.013	ASXL1	p.P599H	Missense
PD41293	1	59.6	2	25463511	25463511	T	C	0.003	DNMT3A	p.Y724C	Missense
PD41293	2	62.9	2	25463511	25463511	T	C	0.005	DNMT3A	p.Y724C	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41293	3	66.6	2	25463511	25463511	T	C	0.022	DNMT3A	p.Y724C	Missense
PD41293	4	69.3	2	25463511	25463511	T	C	0.015	DNMT3A	p.Y724C	Missense
PD41293	5	73.6	2	25463511	25463511	T	C	0.012	DNMT3A	p.Y724C	Missense
PD41293	1	59.6	4	106155653	106155654	AG	A	0.004	TET2	p.Q185fs	Frameshift
PD41293	2	62.9	4	106155653	106155654	AG	A	0.006	TET2	p.Q185fs	Frameshift
PD41293	3	66.6	4	106155653	106155654	AG	A	0.009	TET2	p.Q185fs	Frameshift
PD41293	4	69.3	4	106155653	106155654	AG	A	0.012	TET2	p.Q185fs	Frameshift
PD41293	5	73.6	4	106155653	106155654	AG	A	0.020	TET2	p.Q185fs	Frameshift
PD41293	1	59.6	7	101821766	101821766	G	T	0.000	CUX1	p.V282V	Synonymous
PD41293	2	62.9	7	101821766	101821766	G	T	0.002	CUX1	p.V282V	Synonymous
PD41293	3	66.6	7	101821766	101821766	G	T	0.000	CUX1	p.V282V	Synonymous
PD41293	4	69.3	7	101821766	101821766	G	T	0.000	CUX1	p.V282V	Synonymous
PD41293	5	73.6	7	101821766	101821766	G	T	0.012	CUX1	p.V282V	Synonymous
PD41294	1	66.5	2	25469632	25469632	C	T	0.008	DNMT3A	p.R379H	Missense
PD41294	2	69.8	2	25469632	25469632	C	T	0.009	DNMT3A	p.R379H	Missense
PD41294	3	73.6	2	25469632	25469632	C	T	0.010	DNMT3A	p.R379H	Missense
PD41294	4	76.3	2	25469632	25469632	C	T	0.008	DNMT3A	p.R379H	Missense
PD41294	5	81.3	2	25469632	25469632	C	T	0.013	DNMT3A	p.R379H	Missense
PD41294	1	66.5	4	106156060	106156060	C	T	0.008	TET2	p.Q321X	Nonsense
PD41294	2	69.8	4	106156060	106156060	C	T	0.011	TET2	p.Q321X	Nonsense
PD41294	3	73.6	4	106156060	106156060	C	T	0.016	TET2	p.Q321X	Nonsense
PD41294	4	76.3	4	106156060	106156060	C	T	0.016	TET2	p.Q321X	Nonsense
PD41294	5	81.3	4	106156060	106156060	C	T	0.021	TET2	p.Q321X	Nonsense
PD41294	1	66.5	19	56179924	56179924	G	T	0.000	U2AF2	p.G265V	Missense
PD41294	2	69.8	19	56179924	56179924	G	T	0.001	U2AF2	p.G265V	Missense
PD41294	3	73.6	19	56179924	56179924	G	T	0.007	U2AF2	p.G265V	Missense
PD41294	4	76.3	19	56179924	56179924	G	T	0.000	U2AF2	p.G265V	Missense
PD41294	5	81.3	19	56179924	56179924	G	T	0.000	U2AF2	p.G265V	Missense
PD41294	1	66.5	X	53436098	53436098	C	T	0.000	SMC1A	p.V458V	Synonymous
PD41294	2	69.8	X	53436098	53436098	C	T	0.001	SMC1A	p.V458V	Synonymous
PD41294	3	73.6	X	53436098	53436098	C	T	0.001	SMC1A	p.V458V	Synonymous
PD41294	4	76.3	X	53436098	53436098	C	T	0.002	SMC1A	p.V458V	Synonymous
PD41294	5	81.3	X	53436098	53436098	C	T	0.005	SMC1A	p.V458V	Synonymous
PD41295	1	64.3	2	25458575	25458575	C	T	0.016	DNMT3A	c.2597+1G>A	Splice site
PD41295	2	67.6	2	25458575	25458575	C	T	0.016	DNMT3A	c.2597+1G>A	Splice site
PD41295	3	73.1	2	25458575	25458575	C	T	0.029	DNMT3A	c.2597+1G>A	Splice site
PD41295	4	76.8	2	25458575	25458575	C	T	0.019	DNMT3A	c.2597+1G>A	Splice site
PD41296	1	66.6	2	198267373	198267373	G	A	0.006	SF3B1	p.H662Y	Missense
PD41296	2	69.9	2	198267373	198267373	G	A	0.009	SF3B1	p.H662Y	Missense
PD41296	3	73.0	2	198267373	198267373	G	A	0.005	SF3B1	p.H662Y	Missense
PD41296	4	76.2	2	198267373	198267373	G	A	0.002	SF3B1	p.H662Y	Missense
PD41296	5	81.0	2	198267373	198267373	G	A	0.004	SF3B1	p.H662Y	Missense
PD41297	1	70.5	4	106193791	106193791	T	C	0.003	TET2	p.L1418P	Missense
PD41297	2	74.1	4	106193791	106193791	T	C	0.003	TET2	p.L1418P	Missense
PD41297	3	78.6	4	106193791	106193791	T	C	0.008	TET2	p.L1418P	Missense
PD41297	4	82.4	4	106193791	106193791	T	C	0.006	TET2	p.L1418P	Missense
PD41297	1	70.5	16	67671719	67671719	G	T	0.001	CTCF	p.D710Y	Missense
PD41297	2	74.1	16	67671719	67671719	G	T	0.001	CTCF	p.D710Y	Missense
PD41297	3	78.6	16	67671719	67671719	G	T	0.000	CTCF	p.D710Y	Missense
PD41297	4	82.4	16	67671719	67671719	G	T	0.007	CTCF	p.D710Y	Missense
PD41297	1	70.5	19	17945751	17945751	G	T	0.000	JAK3	p.S703R	Missense
PD41297	2	74.1	19	17945751	17945751	G	T	0.005	JAK3	p.S703R	Missense
PD41297	3	78.6	19	17945751	17945751	G	T	0.000	JAK3	p.S703R	Missense
PD41297	4	82.4	19	17945751	17945751	G	T	0.000	JAK3	p.S703R	Missense
PD41297	1	70.5	X	129149430	129149431	CT	C	0.000	BCORL1	p.F895fs	Frameshift
PD41297	2	74.1	X	129149430	129149431	CT	C	0.000	BCORL1	p.F895fs	Frameshift
PD41297	3	78.6	X	129149430	129149431	CT	C	0.003	BCORL1	p.F895fs	Frameshift
PD41297	4	82.4	X	129149430	129149431	CT	C	0.000	BCORL1	p.F895fs	Frameshift
PD41297	1	70.5	X	39932400	39932400	C	A	0.000	BCOR	p.T733T	Synonymous
PD41297	2	74.1	X	39932400	39932400	C	A	0.001	BCOR	p.T733T	Synonymous
PD41297	3	78.6	X	39932400	39932400	C	A	0.007	BCOR	p.T733T	Synonymous
PD41297	4	82.4	X	39932400	39932400	C	A	0.001	BCOR	p.T733T	Synonymous

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41298	1	62.8	4	106155920	106155921	TC	T	0.010	TET2	p.I274fs	Frameshift
PD41298	2	66.1	4	106155920	106155921	TC	T	0.004	TET2	p.I274fs	Frameshift
PD41298	3	69.9	4	106155920	106155921	TC	T	0.014	TET2	p.I274fs	Frameshift
PD41298	4	72.6	4	106155920	106155921	TC	T	0.013	TET2	p.I274fs	Frameshift
PD41298	5	77.8	4	106155920	106155921	TC	T	0.009	TET2	p.I274fs	Frameshift
PD41298	1	62.8	7	101877338	101877338	G	A	0.011	CUX1	p.R1147H	Missense
PD41298	2	66.1	7	101877338	101877338	G	A	0.000	CUX1	p.R1147H	Missense
PD41298	3	69.9	7	101877338	101877338	G	A	0.003	CUX1	p.R1147H	Missense
PD41298	4	72.6	7	101877338	101877338	G	A	0.000	CUX1	p.R1147H	Missense
PD41298	5	77.8	7	101877338	101877338	G	A	0.000	CUX1	p.R1147H	Missense
PD41300	1	67.4	20	31021472	31021472	C	T	0.159	ASXL1	p.Q491X	Nonsense
PD41300	2	70.9	20	31021472	31021472	C	T	0.203	ASXL1	p.Q491X	Nonsense
PD41300	3	75.8	20	31021472	31021472	C	T	0.236	ASXL1	p.Q491X	Nonsense
PD41300	4	79.5	20	31021472	31021472	C	T	0.209	ASXL1	p.Q491X	Nonsense
PD41300	5	82.9	20	31021472	31021472	C	T	0.266	ASXL1	p.Q491X	Nonsense
PD41301	1	59.2	11	119169066	119169066	A	G	0.000	CBL	c.2252-2A>G	Splice site
PD41301	2	62.7	11	119169066	119169066	A	G	0.001	CBL	c.2252-2A>G	Splice site
PD41301	3	66.7	11	119169066	119169066	A	G	0.000	CBL	c.2252-2A>G	Splice site
PD41301	4	69.2	11	119169066	119169066	A	G	0.006	CBL	c.2252-2A>G	Splice site
PD41301	5	73.3	11	119169066	119169066	A	G	0.030	CBL	c.2252-2A>G	Splice site
PD41301	1	59.2	20	31022402	31022402	T	C	0.002	ASXL1	p.G629G	Synonymous
PD41301	2	62.7	20	31022402	31022402	T	C	0.002	ASXL1	p.G629G	Synonymous
PD41301	3	66.7	20	31022402	31022402	T	C	0.003	ASXL1	p.G629G	Synonymous
PD41301	4	69.2	20	31022402	31022402	T	C	0.006	ASXL1	p.G629G	Synonymous
PD41301	5	73.3	20	31022402	31022402	T	C	0.010	ASXL1	p.G629G	Synonymous
PD41302	1	64.8	2	25457231	25457231	G	A	0.002	DNMT3A	p.Q886X	Nonsense
PD41302	2	68.0	2	25457231	25457231	G	A	0.003	DNMT3A	p.Q886X	Nonsense
PD41302	3	72.1	2	25457231	25457231	G	A	0.006	DNMT3A	p.Q886X	Nonsense
PD41302	4	77.3	2	25457231	25457231	G	A	0.004	DNMT3A	p.Q886X	Nonsense
PD41302	1	64.8	2	25469937	25469937	T	A	0.006	DNMT3A	p.I369F	Missense
PD41302	2	68.0	2	25469937	25469937	T	A	0.006	DNMT3A	p.I369F	Missense
PD41302	3	72.1	2	25469937	25469937	T	A	0.010	DNMT3A	p.I369F	Missense
PD41302	4	77.3	2	25469937	25469937	T	A	0.011	DNMT3A	p.I369F	Missense
PD41302	1	64.8	4	106196999	106197000	CA	C	0.009	TET2	p.H1778fs	Frameshift
PD41302	2	68.0	4	106196999	106197000	CA	C	0.010	TET2	p.H1778fs	Frameshift
PD41302	3	72.1	4	106196999	106197000	CA	C	0.022	TET2	p.H1778fs	Frameshift
PD41302	4	77.3	4	106196999	106197000	CA	C	0.054	TET2	p.H1778fs	Frameshift
PD41303	1	68.4	2	25457225	25457225	G	T	0.001	DNMT3A	p.L888M	Missense
PD41303	2	71.5	2	25457225	25457225	G	T	0.005	DNMT3A	p.L888M	Missense
PD41303	3	75.0	2	25457225	25457225	G	T	0.000	DNMT3A	p.L888M	Missense
PD41303	4	77.9	2	25457225	25457225	G	T	0.000	DNMT3A	p.L888M	Missense
PD41303	5	82.2	2	25457225	25457225	G	T	0.000	DNMT3A	p.L888M	Missense
PD41303	1	68.4	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense
PD41303	2	71.5	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense
PD41303	3	75.0	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense
PD41303	4	77.9	9	5073770	5073770	G	T	0.000	JAK2	p.V617F	Missense
PD41303	5	82.2	9	5073770	5073770	G	T	0.054	JAK2	p.V617F	Missense
PD41303	1	68.4	12	12037498	12037498	G	A	0.003	ETV6	p.A377T	Missense
PD41303	2	71.5	12	12037498	12037498	G	A	0.002	ETV6	p.A377T	Missense
PD41303	3	75.0	12	12037498	12037498	G	A	0.292	ETV6	p.A377T	Missense
PD41303	4	77.9	12	12037498	12037498	G	A	0.372	ETV6	p.A377T	Missense
PD41303	5	82.2	12	12037498	12037498	G	A	0.361	ETV6	p.A377T	Missense
PD41303	1	68.4	16	67662315	67662315	A	T	0.000	CTCF	p.K521X	Nonsense
PD41303	2	71.5	16	67662315	67662315	A	T	0.001	CTCF	p.K521X	Nonsense
PD41303	3	75.0	16	67662315	67662315	A	T	0.000	CTCF	p.K521X	Nonsense
PD41303	4	77.9	16	67662315	67662315	A	T	0.000	CTCF	p.K521X	Nonsense
PD41303	5	82.2	16	67662315	67662315	A	T	0.010	CTCF	p.K521X	Nonsense
PD41303	1	68.4	X	133511716	133511716	T	A	0.001	PHF6	p.N23K	Missense
PD41303	2	71.5	X	133511716	133511716	T	A	0.000	PHF6	p.N23K	Missense
PD41303	3	75.0	X	133511716	133511716	T	A	0.005	PHF6	p.N23K	Missense
PD41303	4	77.9	X	133511716	133511716	T	A	0.010	PHF6	p.N23K	Missense
PD41303	5	82.2	X	133511716	133511716	T	A	0.009	PHF6	p.N23K	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41303	1	68.4	X	39922997	39922997	C	A	0.000	BCOR	p.V1203V	Synonymous
PD41303	2	71.5	X	39922997	39922997	C	A	0.004	BCOR	p.V1203V	Synonymous
PD41303	3	75.0	X	39922997	39922997	C	A	0.002	BCOR	p.V1203V	Synonymous
PD41303	4	77.9	X	39922997	39922997	C	A	0.000	BCOR	p.V1203V	Synonymous
PD41303	5	82.2	X	39922997	39922997	C	A	0.000	BCOR	p.V1203V	Synonymous
PD41304	1	62.7	4	106155428	106155428	A	G	0.012	TET2	p.K110R	Missense
PD41304	2	65.7	4	106155428	106155428	A	G	0.015	TET2	p.K110R	Missense
PD41304	3	69.4	4	106155428	106155428	A	G	0.023	TET2	p.K110R	Missense
PD41304	4	72.3	4	106155428	106155428	A	G	0.019	TET2	p.K110R	Missense
PD41304	5	77.6	4	106155428	106155428	A	G	0.019	TET2	p.K110R	Missense
PD41305	1	56.8	9	139412372	139412372	G	T	0.014	NOTCH1	p.H425N	Missense
PD41305	2	59.9	9	139412372	139412372	G	T	0.012	NOTCH1	p.H425N	Missense
PD41305	3	63.7	9	139412372	139412372	G	T	0.017	NOTCH1	p.H425N	Missense
PD41305	4	66.4	9	139412372	139412372	G	T	0.018	NOTCH1	p.H425N	Missense
PD41305	5	71.1	9	139412372	139412372	G	T	0.014	NOTCH1	p.H425N	Missense
PD41305	1	56.8	17	74732959	74732959	G	T	0.001	SRSF2	p.P95H	Missense
PD41305	2	59.9	17	74732959	74732959	G	T	0.002	SRSF2	p.P95H	Missense
PD41305	3	63.7	17	74732959	74732959	G	T	0.004	SRSF2	p.P95H	Missense
PD41305	4	66.4	17	74732959	74732959	G	T	0.004	SRSF2	p.P95H	Missense
PD41305	5	71.1	17	74732959	74732959	G	T	0.050	SRSF2	p.P95H	Missense
PD41306	1	75.0	2	198266834	198266834	T	C	0.000	SF3B1	p.K700E	Missense
PD41306	2	78.2	2	198266834	198266834	T	C	0.002	SF3B1	p.K700E	Missense
PD41306	3	81.6	2	198266834	198266834	T	C	0.003	SF3B1	p.K700E	Missense
PD41306	4	85.5	2	198266834	198266834	T	C	0.014	SF3B1	p.K700E	Missense
PD41306	1	75.0	4	106180891	106180892	AG	A	0.000	TET2	p.R1307fs	Frameshift
PD41306	2	78.2	4	106180891	106180892	AG	A	0.001	TET2	p.R1307fs	Frameshift
PD41306	3	81.6	4	106180891	106180892	AG	A	0.001	TET2	p.R1307fs	Frameshift
PD41306	4	85.5	4	106180891	106180892	AG	A	0.005	TET2	p.R1307fs	Frameshift
PD41306	1	75.0	4	106193788	106193788	T	G	0.002	TET2	p.V1417G	Missense
PD41306	2	78.2	4	106193788	106193788	T	G	0.008	TET2	p.V1417G	Missense
PD41306	3	81.6	4	106193788	106193788	T	G	0.010	TET2	p.V1417G	Missense
PD41306	4	85.5	4	106193788	106193788	T	G	0.009	TET2	p.V1417G	Missense
PD41306	1	75.0	17	58740665	58740665	C	T	0.000	PPM1D	p.Q524X	Nonsense
PD41306	2	78.2	17	58740665	58740665	C	T	0.006	PPM1D	p.Q524X	Nonsense
PD41306	3	81.6	17	58740665	58740665	C	T	0.002	PPM1D	p.Q524X	Nonsense
PD41306	4	85.5	17	58740665	58740665	C	T	0.005	PPM1D	p.Q524X	Nonsense
PD41306	1	75.0	20	31023093	31023093	A	T	0.008	ASXL1	p.R860X	Nonsense
PD41306	2	78.2	20	31023093	31023093	A	T	0.008	ASXL1	p.R860X	Nonsense
PD41306	3	81.6	20	31023093	31023093	A	T	0.007	ASXL1	p.R860X	Nonsense
PD41306	4	85.5	20	31023093	31023093	A	T	0.007	ASXL1	p.R860X	Nonsense
PD41306	1	75.0	X	129148990	129148990	C	T	0.005	BCORL1	p.Q748X	Nonsense
PD41306	2	78.2	X	129148990	129148990	C	T	0.011	BCORL1	p.Q748X	Nonsense
PD41306	3	81.6	X	129148990	129148990	C	T	0.010	BCORL1	p.Q748X	Nonsense
PD41306	4	85.5	X	129148990	129148990	C	T	0.014	BCORL1	p.Q748X	Nonsense
PD41307	1	58.4	2	25463318	25463318	C	T	0.000	DNMT3A	p.E725E	Synonymous
PD41307	2	61.6	2	25463318	25463318	C	T	0.003	DNMT3A	p.E725E	Synonymous
PD41307	3	65.5	2	25463318	25463318	C	T	0.008	DNMT3A	p.E725E	Synonymous
PD41307	4	68.1	2	25463318	25463318	C	T	0.002	DNMT3A	p.E725E	Synonymous
PD41307	5	72.5	2	25463318	25463318	C	T	0.005	DNMT3A	p.E725E	Synonymous
PD41308	1	56.2	2	25466799	25466799	C	T	0.011	DNMT3A	p.R635Q	Missense
PD41308	2	59.2	2	25466799	25466799	C	T	0.006	DNMT3A	p.R635Q	Missense
PD41308	3	62.2	2	25466799	25466799	C	T	0.003	DNMT3A	p.R635Q	Missense
PD41308	4	65.5	2	25466799	25466799	C	T	0.008	DNMT3A	p.R635Q	Missense
PD41308	5	69.7	2	25466799	25466799	C	T	0.005	DNMT3A	p.R635Q	Missense
PD41310	1	62.6	2	198265574	198265574	G	A	0.002	SF3B1	p.A861A	Synonymous
PD41310	2	65.2	2	198265574	198265574	G	A	0.000	SF3B1	p.A861A	Synonymous
PD41310	3	69.0	2	198265574	198265574	G	A	0.005	SF3B1	p.A861A	Synonymous
PD41310	4	71.9	2	198265574	198265574	G	A	0.001	SF3B1	p.A861A	Synonymous
PD41310	5	76.2	2	198265574	198265574	G	A	0.013	SF3B1	p.A861A	Synonymous
PD41310	1	62.6	2	25464574	25464575	CC	C	0.005	DNMT3A	p.G646fs	Frameshift
PD41310	2	65.2	2	25464574	25464575	CC	C	0.005	DNMT3A	p.G646fs	Frameshift
PD41310	3	69.0	2	25464574	25464575	CC	C	0.001	DNMT3A	p.G646fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41310	4	71.9	2	25464574	25464575	CC	C	0.007	DNMT3A	p.G646fs	Frameshift
PD41310	5	76.2	2	25464574	25464575	CC	C	0.003	DNMT3A	p.G646fs	Frameshift
PD41310	1	62.6	X	15343247	15343248	TT	T	0.000	PIGA	p.H292fs	Frameshift
PD41310	2	65.2	X	15343247	15343248	TT	T	0.000	PIGA	p.H292fs	Frameshift
PD41310	3	69.0	X	15343247	15343248	TT	T	0.004	PIGA	p.H292fs	Frameshift
PD41310	4	71.9	X	15343247	15343248	TT	T	0.000	PIGA	p.H292fs	Frameshift
PD41310	5	76.2	X	15343247	15343248	TT	T	0.004	PIGA	p.H292fs	Frameshift
PD41310	1	62.6	X	15349587	15349587	G	A	0.000	PIGA	p.L156F	Missense
PD41310	2	65.2	X	15349587	15349587	G	A	0.000	PIGA	p.L156F	Missense
PD41310	3	69.0	X	15349587	15349587	G	A	0.000	PIGA	p.L156F	Missense
PD41310	4	71.9	X	15349587	15349587	G	A	0.005	PIGA	p.L156F	Missense
PD41310	5	76.2	X	15349587	15349587	G	A	0.001	PIGA	p.L156F	Missense
PD41311	1	76.8	17	7578457	7578457	C	T	0.000	TP53	p.R119H	Missense
PD41311	2	79.8	17	7578457	7578457	C	T	0.008	TP53	p.R119H	Missense
PD41311	3	85.5	17	7578457	7578457	C	T	0.003	TP53	p.R119H	Missense
PD41311	1	76.8	20	31022839	31022839	T	G	0.115	ASXL1	p.L775X	Nonsense
PD41311	2	79.8	20	31022839	31022839	T	G	0.192	ASXL1	p.L775X	Nonsense
PD41311	3	85.5	20	31022839	31022839	T	G	0.282	ASXL1	p.L775X	Nonsense
PD41311	1	76.8	X	53438972	53438972	G	T	0.000	SMC1A	p.G340G	Synonymous
PD41311	2	79.8	X	53438972	53438972	G	T	0.004	SMC1A	p.G340G	Synonymous
PD41311	3	85.5	X	53438972	53438972	G	T	0.000	SMC1A	p.G340G	Synonymous
PD41312	1	55.1	7	148514377	148514377	A	G	0.000	EZH2	p.I449I	Synonymous
PD41312	2	58.1	7	148514377	148514377	A	G	0.000	EZH2	p.I449I	Synonymous
PD41312	3	61.7	7	148514377	148514377	A	G	0.000	EZH2	p.I449I	Synonymous
PD41312	4	64.5	7	148514377	148514377	A	G	0.000	EZH2	p.I449I	Synonymous
PD41312	5	68.7	7	148514377	148514377	A	G	0.006	EZH2	p.I449I	Synonymous
PD41312	1	55.1	11	118342893	118342893	T	C	0.001	KMT2A	p.L340P	Missense
PD41312	2	58.1	11	118342893	118342893	T	C	0.001	KMT2A	p.L340P	Missense
PD41312	3	61.7	11	118342893	118342893	T	C	0.002	KMT2A	p.L340P	Missense
PD41312	4	64.5	11	118342893	118342893	T	C	0.003	KMT2A	p.L340P	Missense
PD41312	5	68.7	11	118342893	118342893	T	C	0.009	KMT2A	p.L340P	Missense
PD41312	1	55.1	17	58740456	58740457	CT	C	0.014	PPM1D	p.A454fs	Frameshift
PD41312	2	58.1	17	58740456	58740457	CT	C	0.012	PPM1D	p.A454fs	Frameshift
PD41312	3	61.7	17	58740456	58740457	CT	C	0.011	PPM1D	p.A454fs	Frameshift
PD41312	4	64.5	17	58740456	58740457	CT	C	0.014	PPM1D	p.A454fs	Frameshift
PD41312	5	68.7	17	58740456	58740457	CT	C	0.019	PPM1D	p.A454fs	Frameshift
PD41312	1	55.1	X	129146572	129146575	TGAG	T	0.001	BCORL1	p.36_36del	Inframe
PD41312	2	58.1	X	129146572	129146575	TGAG	T	0.002	BCORL1	p.36_36del	Inframe
PD41312	3	61.7	X	129146572	129146575	TGAG	T	0.004	BCORL1	p.36_36del	Inframe
PD41312	4	64.5	X	129146572	129146575	TGAG	T	0.003	BCORL1	p.36_36del	Inframe
PD41312	5	68.7	X	129146572	129146575	TGAG	T	0.001	BCORL1	p.36_36del	Inframe
PD41313	1	72.2	2	198266606	198266606	C	G	0.002	SF3B1	p.A744P	Missense
PD41313	2	75.3	2	198266606	198266606	C	G	0.009	SF3B1	p.A744P	Missense
PD41313	3	79.2	2	198266606	198266606	C	G	0.011	SF3B1	p.A744P	Missense
PD41313	4	81.7	2	198266606	198266606	C	G	0.012	SF3B1	p.A744P	Missense
PD41313	5	85.9	2	198266606	198266606	C	G	0.005	SF3B1	p.A744P	Missense
PD41313	1	72.2	13	28588600	28588600	C	T	0.001	FLT3	p.A950T	Missense
PD41313	2	75.3	13	28588600	28588600	C	T	0.001	FLT3	p.A950T	Missense
PD41313	3	79.2	13	28588600	28588600	C	T	0.000	FLT3	p.A950T	Missense
PD41313	4	81.7	13	28588600	28588600	C	T	0.001	FLT3	p.A950T	Missense
PD41313	5	85.9	13	28588600	28588600	C	T	0.007	FLT3	p.A950T	Missense
PD41313	1	72.2	X	133559255	133559255	A	G	0.000	PHF6	p.G331G	Synonymous
PD41313	2	75.3	X	133559255	133559255	A	G	0.000	PHF6	p.G331G	Synonymous
PD41313	3	79.2	X	133559255	133559255	A	G	0.006	PHF6	p.G331G	Synonymous
PD41313	4	81.7	X	133559255	133559255	A	G	0.000	PHF6	p.G331G	Synonymous
PD41313	5	85.9	X	133559255	133559255	A	G	0.000	PHF6	p.G331G	Synonymous
PD41315	1	71.5	2	25457242	25457242	C	T	0.003	DNMT3A	p.R882H	Missense
PD41315	2	75.4	2	25457242	25457242	C	T	0.003	DNMT3A	p.R882H	Missense
PD41315	3	79.7	2	25457242	25457242	C	T	0.010	DNMT3A	p.R882H	Missense
PD41315	4	84.3	2	25457242	25457242	C	T	0.007	DNMT3A	p.R882H	Missense
PD41315	1	71.5	2	25467485	25467485	C	T	0.019	DNMT3A	p.D531N	Missense
PD41315	2	75.4	2	25467485	25467485	C	T	0.028	DNMT3A	p.D531N	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41315	3	79.7	2	25467485	25467485	C	T	0.037	DNMT3A	p.D531N	Missense
PD41315	4	84.3	2	25467485	25467485	C	T	0.052	DNMT3A	p.D531N	Missense
PD41315	1	71.5	4	106156676	106156677	AG	A	0.001	TET2	p.Q526fs	Frameshift
PD41315	2	75.4	4	106156676	106156677	AG	A	0.002	TET2	p.Q526fs	Frameshift
PD41315	3	79.7	4	106156676	106156677	AG	A	0.004	TET2	p.Q526fs	Frameshift
PD41315	4	84.3	4	106156676	106156677	AG	A	0.006	TET2	p.Q526fs	Frameshift
PD41316	1	68.7	4	106190828	106190828	C	G	0.010	TET2	p.S1369X	Nonsense
PD41316	2	71.8	4	106190828	106190828	C	G	0.013	TET2	p.S1369X	Nonsense
PD41316	3	76.6	4	106190828	106190828	C	G	0.010	TET2	p.S1369X	Nonsense
PD41316	4	80.3	4	106190828	106190828	C	G	0.019	TET2	p.S1369X	Nonsense
PD41316	1	68.7	4	106196825	106196825	A	T	0.000	TET2	p.K1720X	Nonsense
PD41316	2	71.8	4	106196825	106196825	A	T	0.001	TET2	p.K1720X	Nonsense
PD41316	3	76.6	4	106196825	106196825	A	T	0.008	TET2	p.K1720X	Nonsense
PD41316	4	80.3	4	106196825	106196825	A	T	0.004	TET2	p.K1720X	Nonsense
PD41316	1	68.7	7	101847807	101847807	T	C	0.005	CUX1	p.L1015P	Missense
PD41316	2	71.8	7	101847807	101847807	T	C	0.000	CUX1	p.L1015P	Missense
PD41316	3	76.6	7	101847807	101847807	T	C	0.000	CUX1	p.L1015P	Missense
PD41316	4	80.3	7	101847807	101847807	T	C	0.000	CUX1	p.L1015P	Missense
PD41316	1	68.7	20	31023388	31023388	C	G	0.001	ASXL1	p.S958X	Nonsense
PD41316	2	71.8	20	31023388	31023388	C	G	0.005	ASXL1	p.S958X	Nonsense
PD41316	3	76.6	20	31023388	31023388	C	G	0.000	ASXL1	p.S958X	Nonsense
PD41316	4	80.3	20	31023388	31023388	C	G	0.001	ASXL1	p.S958X	Nonsense
PD41316	1	68.7	X	39923646	39923646	C	T	0.005	BCOR	p.A1149T	Missense
PD41316	2	71.8	X	39923646	39923646	C	T	0.000	BCOR	p.A1149T	Missense
PD41316	3	76.6	X	39923646	39923646	C	T	0.000	BCOR	p.A1149T	Missense
PD41316	4	80.3	X	39923646	39923646	C	T	0.000	BCOR	p.A1149T	Missense
PD41317	1	70.3	2	25457249	25457249	T	C	0.004	DNMT3A	p.M880V	Missense
PD41317	2	73.3	2	25457249	25457249	T	C	0.001	DNMT3A	p.M880V	Missense
PD41317	3	77.3	2	25457249	25457249	T	C	0.004	DNMT3A	p.M880V	Missense
PD41317	5	84.9	2	25457249	25457249	T	C	0.011	DNMT3A	p.M880V	Missense
PD41318	1	72.7	2	25463229	25463229	A	G	0.008	DNMT3A	p.F755S	Missense
PD41318	2	75.8	2	25463229	25463229	A	G	0.007	DNMT3A	p.F755S	Missense
PD41318	3	80.7	2	25463229	25463229	A	G	0.005	DNMT3A	p.F755S	Missense
PD41318	1	72.7	4	106155695	106155695	T	A	0.001	TET2	p.L199X	Nonsense
PD41318	2	75.8	4	106155695	106155695	T	A	0.001	TET2	p.L199X	Nonsense
PD41318	3	80.7	4	106155695	106155695	T	A	0.007	TET2	p.L199X	Nonsense
PD41318	1	72.7	X	123220523	123220523	T	A	0.006	STAG2	p.I1060I	Synonymous
PD41318	2	75.8	X	123220523	123220523	T	A	0.004	STAG2	p.I1060I	Synonymous
PD41318	3	80.7	X	123220523	123220523	T	A	0.005	STAG2	p.I1060I	Synonymous
PD41319	1	63.6	16	3786663	3786663	G	A	0.000	CREBBP	p.I1516I	Synonymous
PD41319	2	66.7	16	3786663	3786663	G	A	0.001	CREBBP	p.I1516I	Synonymous
PD41319	3	71.5	16	3786663	3786663	G	A	0.009	CREBBP	p.I1516I	Synonymous
PD41319	4	75.8	16	3786663	3786663	G	A	0.014	CREBBP	p.I1516I	Synonymous
PD41320	1	63.3	X	154317557	154317557	G	A	0.007	BRCC3	p.M141I	Missense
PD41320	2	66.4	X	154317557	154317557	G	A	0.009	BRCC3	p.M141I	Missense
PD41320	3	70.6	X	154317557	154317557	G	A	0.003	BRCC3	p.M141I	Missense
PD41320	4	73.3	X	154317557	154317557	G	A	0.009	BRCC3	p.M141I	Missense
PD41320	5	77.3	X	154317557	154317557	G	A	0.006	BRCC3	p.M141I	Missense
PD41321	1	63.8	2	25463239	25463239	A	C	0.001	DNMT3A	p.F752V	Missense
PD41321	2	66.6	2	25463239	25463239	A	C	0.004	DNMT3A	p.F752V	Missense
PD41321	4	73.3	2	25463239	25463239	A	C	0.006	DNMT3A	p.F752V	Missense
PD41321	5	77.1	2	25463239	25463239	A	C	0.004	DNMT3A	p.F752V	Missense
PD41321	1	63.8	4	106182983	106182983	C	A	0.019	TET2	p.A1341E	Missense
PD41321	2	66.6	4	106182983	106182983	C	A	0.017	TET2	p.A1341E	Missense
PD41321	4	73.3	4	106182983	106182983	C	A	0.026	TET2	p.A1341E	Missense
PD41321	5	77.1	4	106182983	106182983	C	A	0.023	TET2	p.A1341E	Missense
PD41321	1	63.8	4	106196276	106196276	C	T	0.004	TET2	p.Q1537X	Nonsense
PD41321	2	66.6	4	106196276	106196276	C	T	0.004	TET2	p.Q1537X	Nonsense
PD41321	4	73.3	4	106196276	106196276	C	T	0.026	TET2	p.Q1537X	Nonsense
PD41321	5	77.1	4	106196276	106196276	C	T	0.017	TET2	p.Q1537X	Nonsense
PD41321	1	63.8	X	15808631	15808631	G	A	0.000	ZRSR2	p.E5K	Missense
PD41321	2	66.6	X	15808631	15808631	G	A	0.007	ZRSR2	p.E5K	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41321	4	73.3	X	15808631	15808631	G	A	0.000	ZRSR2	p.E5K	Missense
PD41321	5	77.1	X	15808631	15808631	G	A	0.000	ZRSR2	p.E5K	Missense
PD41321	1	63.8	X	44942775	44942775	C	A	0.000	KDM6A	p.L1171I	Missense
PD41321	2	66.6	X	44942775	44942775	C	A	0.002	KDM6A	p.L1171I	Missense
PD41321	4	73.3	X	44942775	44942775	C	A	0.006	KDM6A	p.L1171I	Missense
PD41321	5	77.1	X	44942775	44942775	C	A	0.000	KDM6A	p.L1171I	Missense
PD41322	1	67.4	4	106158275	106158275	C	G	0.001	TET2	p.S1059X	Nonsense
PD41322	2	70.4	4	106158275	106158275	C	G	0.003	TET2	p.S1059X	Nonsense
PD41322	3	75.8	4	106158275	106158275	C	G	0.004	TET2	p.S1059X	Nonsense
PD41322	4	80.0	4	106158275	106158275	C	G	0.023	TET2	p.S1059X	Nonsense
PD41323	1	64.5	4	106157560	106157560	C	T	0.010	TET2	p.Q821X	Nonsense
PD41323	2	67.5	4	106157560	106157560	C	T	0.001	TET2	p.Q821X	Nonsense
PD41323	3	71.0	4	106157560	106157560	C	T	0.004	TET2	p.Q821X	Nonsense
PD41323	4	74.4	4	106157560	106157560	C	T	0.002	TET2	p.Q821X	Nonsense
PD41323	5	78.7	4	106157560	106157560	C	T	0.001	TET2	p.Q821X	Nonsense
PD41323	1	64.5	20	57429332	57429332	A	T	0.006	GNAS	p.K338X	Nonsense
PD41323	2	67.5	20	57429332	57429332	A	T	0.003	GNAS	p.K338X	Nonsense
PD41323	3	71.0	20	57429332	57429332	A	T	0.004	GNAS	p.K338X	Nonsense
PD41323	4	74.4	20	57429332	57429332	A	T	0.004	GNAS	p.K338X	Nonsense
PD41323	5	78.7	20	57429332	57429332	A	T	0.010	GNAS	p.K338X	Nonsense
PD41324	1	71.8	11	119149280	119149280	G	A	0.012	CBL	p.V430M	Missense
PD41324	2	74.8	11	119149280	119149280	G	A	0.002	CBL	p.V430M	Missense
PD41324	3	79.7	11	119149280	119149280	G	A	0.005	CBL	p.V430M	Missense
PD41325	1	74.0	4	106156060	106156060	C	T	0.000	TET2	p.Q321X	Nonsense
PD41325	2	76.5	4	106156060	106156060	C	T	0.001	TET2	p.Q321X	Nonsense
PD41325	3	82.4	4	106156060	106156060	C	T	0.008	TET2	p.Q321X	Nonsense
PD41325	4	85.4	4	106156060	106156060	C	T	0.004	TET2	p.Q321X	Nonsense
PD41325	1	74.0	4	106193719	106193719	A	G	0.001	TET2	c.4183-2A>G	Splice site
PD41325	2	76.5	4	106193719	106193719	A	G	0.005	TET2	c.4183-2A>G	Splice site
PD41325	3	82.4	4	106193719	106193719	A	G	0.011	TET2	c.4183-2A>G	Splice site
PD41325	4	85.4	4	106193719	106193719	A	G	0.017	TET2	c.4183-2A>G	Splice site
PD41325	1	74.0	11	119149247	119149247	T	A	0.007	CBL	p.C419S	Missense
PD41325	2	76.5	11	119149247	119149247	T	A	0.008	CBL	p.C419S	Missense
PD41325	3	82.4	11	119149247	119149247	T	A	0.011	CBL	p.C419S	Missense
PD41325	4	85.4	11	119149247	119149247	T	A	0.025	CBL	p.C419S	Missense
PD41326	1	69.9	11	119155715	119155715	C	A	0.000	CBL	p.Q490K	Missense
PD41326	2	72.4	11	119155715	119155715	C	A	0.006	CBL	p.Q490K	Missense
PD41326	3	78.2	11	119155715	119155715	C	A	0.000	CBL	p.Q490K	Missense
PD41326	4	81.3	11	119155715	119155715	C	A	0.001	CBL	p.Q490K	Missense
PD41328	1	62.5	7	101926051	101926051	C	T	0.012	CUX1	p.A648A	Synonymous
PD41328	2	65.5	7	101926051	101926051	C	T	0.008	CUX1	p.A648A	Synonymous
PD41328	3	70.1	7	101926051	101926051	C	T	0.003	CUX1	p.A648A	Synonymous
PD41328	4	73.7	7	101926051	101926051	C	T	0.005	CUX1	p.A648A	Synonymous
PD41328	5	76.8	7	101926051	101926051	C	T	0.001	CUX1	p.A648A	Synonymous
PD41330	1	72.8	2	25463577	25463577	T	A	0.008	DNMT3A	p.D702V	Missense
PD41330	2	76.9	2	25463577	25463577	T	A	0.007	DNMT3A	p.D702V	Missense
PD41330	3	80.4	2	25463577	25463577	T	A	0.005	DNMT3A	p.D702V	Missense
PD41330	4	84.8	2	25463577	25463577	T	A	0.003	DNMT3A	p.D702V	Missense
PD41330	1	72.8	4	106194039	106194039	C	T	0.002	TET2	p.Q1501X	Nonsense
PD41330	2	76.9	4	106194039	106194039	C	T	0.004	TET2	p.Q1501X	Nonsense
PD41330	3	80.4	4	106194039	106194039	C	T	0.004	TET2	p.Q1501X	Nonsense
PD41330	4	84.8	4	106194039	106194039	C	T	0.009	TET2	p.Q1501X	Nonsense
PD41330	1	72.8	4	55561875	55561875	G	T	0.000	KIT	p.A89S	Missense
PD41330	2	76.9	4	55561875	55561875	G	T	0.000	KIT	p.A89S	Missense
PD41330	3	80.4	4	55561875	55561875	G	T	0.000	KIT	p.A89S	Missense
PD41330	4	84.8	4	55561875	55561875	G	T	0.009	KIT	p.A89S	Missense
PD41331	1	70.6	4	106156139	106156139	C	A	0.002	TET2	p.A347E	Missense
PD41331	3	78.3	4	106156139	106156139	C	A	0.000	TET2	p.A347E	Missense
PD41331	4	82.6	4	106156139	106156139	C	A	0.008	TET2	p.A347E	Missense
PD41331	1	70.6	X	15808637	15808637	A	G	0.005	ZRSR2	p.M7V	Missense
PD41331	3	78.3	X	15808637	15808637	A	G	0.014	ZRSR2	p.M7V	Missense
PD41331	4	82.6	X	15808637	15808637	A	G	0.023	ZRSR2	p.M7V	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41332	1	73.2	X	39932838	39932838	A	G	0.003	BCOR	p.S587S	Synonymous
PD41332	3	80.8	X	39932838	39932838	A	G	0.000	BCOR	p.S587S	Synonymous
PD41332	4	85.2	X	39932838	39932838	A	G	0.000	BCOR	p.S587S	Synonymous
PD41333	1	67.1	4	106190849	106190849	A	C	0.000	TET2	p.D1376A	Missense
PD41333	2	71.3	4	106190849	106190849	A	C	0.002	TET2	p.D1376A	Missense
PD41333	3	74.4	4	106190849	106190849	A	C	0.014	TET2	p.D1376A	Missense
PD41333	4	79.5	4	106190849	106190849	A	C	0.018	TET2	p.D1376A	Missense
PD41333	1	67.1	X	44922970	44922970	C	T	0.033	KDM6A	p.Q663X	Nonsense
PD41333	2	71.3	X	44922970	44922970	C	T	0.025	KDM6A	p.Q663X	Nonsense
PD41333	3	74.4	X	44922970	44922970	C	T	0.028	KDM6A	p.Q663X	Nonsense
PD41333	4	79.5	X	44922970	44922970	C	T	0.014	KDM6A	p.Q663X	Nonsense
PD41334	1	68.7	1	1735936	1735936	C	G	0.087	GNB1	p.D118H	Missense
PD41334	2	72.1	1	1735936	1735936	C	G	0.123	GNB1	p.D118H	Missense
PD41334	3	76.5	1	1735936	1735936	C	G	0.182	GNB1	p.D118H	Missense
PD41334	4	80.6	1	1735936	1735936	C	G	0.241	GNB1	p.D118H	Missense
PD41334	1	68.7	2	25466800	25466800	G	A	0.007	DNMT3A	p.R635W	Missense
PD41334	2	72.1	2	25466800	25466800	G	A	0.014	DNMT3A	p.R635W	Missense
PD41334	3	76.5	2	25466800	25466800	G	A	0.011	DNMT3A	p.R635W	Missense
PD41334	4	80.6	2	25466800	25466800	G	A	0.015	DNMT3A	p.R635W	Missense
PD41334	1	68.7	X	44918491	44918491	G	A	0.104	KDM6A	c.975-1G>A	Splice site
PD41334	2	72.1	X	44918491	44918491	G	A	0.108	KDM6A	c.975-1G>A	Splice site
PD41334	3	76.5	X	44918491	44918491	G	A	0.093	KDM6A	c.975-1G>A	Splice site
PD41334	4	80.6	X	44918491	44918491	G	A	0.051	KDM6A	c.975-1G>A	Splice site
PD41336	1	79.7	3	128205210	128205210	G	T	0.008	GATA2	p.A77A	Synonymous
PD41336	3	87.3	3	128205210	128205210	G	T	0.005	GATA2	p.A77A	Synonymous
PD41336	1	79.7	17	58740749	58740749	C	T	0.009	PPM1D	p.R552X	Nonsense
PD41336	3	87.3	17	58740749	58740749	C	T	0.019	PPM1D	p.R552X	Nonsense
PD41337	1	62.0	2	25462071	25462071	A	G	0.006	DNMT3A	p.M779T	Missense
PD41337	2	65.0	2	25462071	25462071	A	G	0.012	DNMT3A	p.M779T	Missense
PD41337	3	68.4	2	25462071	25462071	A	G	0.011	DNMT3A	p.M779T	Missense
PD41337	4	71.4	2	25462071	25462071	A	G	0.022	DNMT3A	p.M779T	Missense
PD41337	5	75.8	2	25462071	25462071	A	G	0.020	DNMT3A	p.M779T	Missense
PD41337	1	62.0	X	154317597	154317597	T	C	0.003	BRCC3	p.S155P	Missense
PD41337	2	65.0	X	154317597	154317597	T	C	0.008	BRCC3	p.S155P	Missense
PD41337	3	68.4	X	154317597	154317597	T	C	0.021	BRCC3	p.S155P	Missense
PD41337	4	71.4	X	154317597	154317597	T	C	0.020	BRCC3	p.S155P	Missense
PD41337	5	75.8	X	154317597	154317597	T	C	0.024	BRCC3	p.S155P	Missense
PD41338	1	62.0	2	25463517	25463517	C	T	0.004	DNMT3A	p.G722D	Missense
PD41338	3	68.5	2	25463517	25463517	C	T	0.006	DNMT3A	p.G722D	Missense
PD41338	4	71.5	2	25463517	25463517	C	T	0.003	DNMT3A	p.G722D	Missense
PD41338	5	75.8	2	25463517	25463517	C	T	0.005	DNMT3A	p.G722D	Missense
PD41338	1	62.0	4	106190860	106190860	C	T	0.016	TET2	p.H1380Y	Missense
PD41338	3	68.5	4	106190860	106190860	C	T	0.018	TET2	p.H1380Y	Missense
PD41338	4	71.5	4	106190860	106190860	C	T	0.013	TET2	p.H1380Y	Missense
PD41338	5	75.8	4	106190860	106190860	C	T	0.008	TET2	p.H1380Y	Missense
PD41338	1	62.0	9	139418389	139418389	G	T	0.000	NOTCH1	p.N61K	Missense
PD41338	3	68.5	9	139418389	139418389	G	T	0.000	NOTCH1	p.N61K	Missense
PD41338	4	71.5	9	139418389	139418389	G	T	0.002	NOTCH1	p.N61K	Missense
PD41338	5	75.8	9	139418389	139418389	G	T	0.010	NOTCH1	p.N61K	Missense
PD41338	1	62.0	17	7577551	7577551	C	T	0.002	TP53	p.G205S	Missense
PD41338	3	68.5	17	7577551	7577551	C	T	0.007	TP53	p.G205S	Missense
PD41338	4	71.5	17	7577551	7577551	C	T	0.015	TP53	p.G205S	Missense
PD41338	5	75.8	17	7577551	7577551	C	T	0.019	TP53	p.G205S	Missense
PD41338	1	62.0	X	39914765	39914765	G	A	0.002	BCOR	p.P1499S	Missense
PD41338	3	68.5	X	39914765	39914765	G	A	0.003	BCOR	p.P1499S	Missense
PD41338	4	71.5	X	39914765	39914765	G	A	0.009	BCOR	p.P1499S	Missense
PD41338	5	75.8	X	39914765	39914765	G	A	0.005	BCOR	p.P1499S	Missense
PD41339	1	71.9	1	1735980	1735980	C	A	0.000	GNB1	p.C103F	Missense
PD41339	2	74.9	1	1735980	1735980	C	A	0.008	GNB1	p.C103F	Missense
PD41339	3	79.4	1	1735980	1735980	C	A	0.002	GNB1	p.C103F	Missense
PD41339	4	83.7	1	1735980	1735980	C	A	0.001	GNB1	p.C103F	Missense
PD41339	1	71.9	4	106194058	106194059	AG	A	0.034	TET2	p.Q1507fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41339	2	74.9	4	106194058	106194059	AG	A	0.047	TET2	p.Q1507fs	Frameshift
PD41339	3	79.4	4	106194058	106194059	AG	A	0.110	TET2	p.Q1507fs	Frameshift
PD41339	4	83.7	4	106194058	106194059	AG	A	0.064	TET2	p.Q1507fs	Frameshift
PD41339	1	71.9	17	7577565	7577565	T	C	0.001	TP53	p.N200S	Missense
PD41339	2	74.9	17	7577565	7577565	T	C	0.002	TP53	p.N200S	Missense
PD41339	3	79.4	17	7577565	7577565	T	C	0.007	TP53	p.N200S	Missense
PD41339	4	83.7	17	7577565	7577565	T	C	0.014	TP53	p.N200S	Missense
PD41340	1	73.8	2	198268468	198268468	A	G	0.000	SF3B1	p.T520T	Synonymous
PD41340	2	76.9	2	198268468	198268468	A	G	0.002	SF3B1	p.T520T	Synonymous
PD41340	3	81.4	2	198268468	198268468	A	G	0.007	SF3B1	p.T520T	Synonymous
PD41340	4	85.7	2	198268468	198268468	A	G	0.000	SF3B1	p.T520T	Synonymous
PD41340	1	73.8	4	106164772	106164772	C	T	0.008	TET2	p.R1214W	Missense
PD41340	2	76.9	4	106164772	106164772	C	T	0.009	TET2	p.R1214W	Missense
PD41340	3	81.4	4	106164772	106164772	C	T	0.027	TET2	p.R1214W	Missense
PD41340	4	85.7	4	106164772	106164772	C	T	0.023	TET2	p.R1214W	Missense
PD41341	1	67.8	2	198266834	198266834	T	C	0.008	SF3B1	p.K700E	Missense
PD41341	2	70.7	2	198266834	198266834	T	C	0.004	SF3B1	p.K700E	Missense
PD41341	3	74.2	2	198266834	198266834	T	C	0.012	SF3B1	p.K700E	Missense
PD41341	4	76.9	2	198266834	198266834	T	C	0.005	SF3B1	p.K700E	Missense
PD41341	5	81.2	2	198266834	198266834	T	C	0.011	SF3B1	p.K700E	Missense
PD41341	1	67.8	2	25458574	25458574	A	C	0.006	DNMT3A	c.2597+2T>G	Splice site
PD41341	2	70.7	2	25458574	25458574	A	C	0.006	DNMT3A	c.2597+2T>G	Splice site
PD41341	3	74.2	2	25458574	25458574	A	C	0.005	DNMT3A	c.2597+2T>G	Splice site
PD41341	4	76.9	2	25458574	25458574	A	C	0.004	DNMT3A	c.2597+2T>G	Splice site
PD41341	5	81.2	2	25458574	25458574	A	C	0.003	DNMT3A	c.2597+2T>G	Splice site
PD41341	1	67.8	2	25463586	25463586	C	T	0.003	DNMT3A	p.G699D	Missense
PD41341	2	70.7	2	25463586	25463586	C	T	0.002	DNMT3A	p.G699D	Missense
PD41341	3	74.2	2	25463586	25463586	C	T	0.007	DNMT3A	p.G699D	Missense
PD41341	4	76.9	2	25463586	25463586	C	T	0.001	DNMT3A	p.G699D	Missense
PD41341	5	81.2	2	25463586	25463586	C	T	0.003	DNMT3A	p.G699D	Missense
PD41341	1	67.8	2	25469990	25469991	AA	A	0.002	DNMT3A	p.C351fs	Frameshift
PD41341	2	70.7	2	25469990	25469991	AA	A	0.010	DNMT3A	p.C351fs	Frameshift
PD41341	3	74.2	2	25469990	25469991	AA	A	0.005	DNMT3A	p.C351fs	Frameshift
PD41341	4	76.9	2	25469990	25469991	AA	A	0.008	DNMT3A	p.C351fs	Frameshift
PD41341	5	81.2	2	25469990	25469991	AA	A	0.012	DNMT3A	p.C351fs	Frameshift
PD41341	1	67.8	2	25470545	25470545	A	T	0.004	DNMT3A	p.I310N	Missense
PD41341	2	70.7	2	25470545	25470545	A	T	0.005	DNMT3A	p.I310N	Missense
PD41341	3	74.2	2	25470545	25470545	A	T	0.004	DNMT3A	p.I310N	Missense
PD41341	4	76.9	2	25470545	25470545	A	T	0.015	DNMT3A	p.I310N	Missense
PD41341	5	81.2	2	25470545	25470545	A	T	0.003	DNMT3A	p.I310N	Missense
PD41341	1	67.8	4	106155264	106155268	CTCT	C	0.002	TET2	p.S56fs	Frameshift
PD41341	2	70.7	4	106155264	106155268	CTCT	C	0.004	TET2	p.S56fs	Frameshift
PD41341	3	74.2	4	106155264	106155268	CTCT	C	0.007	TET2	p.S56fs	Frameshift
PD41341	4	76.9	4	106155264	106155268	CTCT	C	0.003	TET2	p.S56fs	Frameshift
PD41341	5	81.2	4	106155264	106155268	CTCT	C	0.013	TET2	p.S56fs	Frameshift
PD41341	1	67.8	4	106194070	106194070	T	A	0.007	TET2	p.L1511X	Nonsense
PD41341	2	70.7	4	106194070	106194070	T	A	0.020	TET2	p.L1511X	Nonsense
PD41341	3	74.2	4	106194070	106194070	T	A	0.022	TET2	p.L1511X	Nonsense
PD41341	4	76.9	4	106194070	106194070	T	A	0.022	TET2	p.L1511X	Nonsense
PD41341	5	81.2	4	106194070	106194070	T	A	0.024	TET2	p.L1511X	Nonsense
PD41341	1	67.8	20	57484420	57484420	C	A	0.009	GNAS	p.R844S	Missense
PD41341	2	70.7	20	57484420	57484420	C	A	0.016	GNAS	p.R844S	Missense
PD41341	3	74.2	20	57484420	57484420	C	A	0.018	GNAS	p.R844S	Missense
PD41341	4	76.9	20	57484420	57484420	C	A	0.025	GNAS	p.R844S	Missense
PD41341	5	81.2	20	57484420	57484420	C	A	0.050	GNAS	p.R844S	Missense
PD41341	1	67.8	20	31024823	31024824	CA	C	0.001	ASXL1	p.K1437fs	Frameshift
PD41341	2	70.7	20	31024823	31024824	CA	C	0.004	ASXL1	p.K1437fs	Frameshift

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41341	3	74.2	20	31024823	31024824	CA	C	0.004	ASXL1	p.K1437fs	Frameshift
PD41341	4	76.9	20	31024823	31024824	CA	C	0.006	ASXL1	p.K1437fs	Frameshift
PD41341	5	81.2	20	31024823	31024824	CA	C	0.029	ASXL1	p.K1437fs	Frameshift
PD41342	1	58.4	2	25463229	25463229	A	G	0.002	DNMT3A	p.F755S	Missense
PD41342	2	61.4	2	25463229	25463229	A	G	0.002	DNMT3A	p.F755S	Missense
PD41342	3	64.9	2	25463229	25463229	A	G	0.007	DNMT3A	p.F755S	Missense
PD41342	4	67.6	2	25463229	25463229	A	G	0.009	DNMT3A	p.F755S	Missense
PD41342	5	71.9	2	25463229	25463229	A	G	0.013	DNMT3A	p.F755S	Missense
PD41343	1	75.9	2	25462075	25462075	C	G	0.009	DNMT3A	p.V778L	Missense
PD41343	2	78.9	2	25462075	25462075	C	G	0.004	DNMT3A	p.V778L	Missense
PD41343	3	83.0	2	25462075	25462075	C	G	0.005	DNMT3A	p.V778L	Missense
PD41343	1	75.9	7	101740759	101740760	AT	A	0.000	CUX1	p.F129fs	Frameshift
PD41343	2	78.9	7	101740759	101740760	AT	A	0.006	CUX1	p.F129fs	Frameshift
PD41343	3	83.0	7	101740759	101740760	AT	A	0.000	CUX1	p.F129fs	Frameshift
PD41343	1	75.9	X	39932138	39932138	C	T	0.008	BCOR	p.V821M	Missense
PD41343	2	78.9	X	39932138	39932138	C	T	0.006	BCOR	p.V821M	Missense
PD41343	3	83.0	X	39932138	39932138	C	T	0.003	BCOR	p.V821M	Missense
PD41344	1	67.8	4	106190860	106190860	C	G	0.002	TET2	p.H1380D	Missense
PD41344	2	70.7	4	106190860	106190860	C	G	0.003	TET2	p.H1380D	Missense
PD41344	3	74.2	4	106190860	106190860	C	G	0.009	TET2	p.H1380D	Missense
PD41344	4	76.9	4	106190860	106190860	C	G	0.011	TET2	p.H1380D	Missense
PD41344	5	80.9	4	106190860	106190860	C	G	0.007	TET2	p.H1380D	Missense
PD41344	1	67.8	17	7578265	7578265	A	G	0.001	TP53	p.I156T	Missense
PD41344	2	70.7	17	7578265	7578265	A	G	0.002	TP53	p.I156T	Missense
PD41344	3	74.2	17	7578265	7578265	A	G	0.002	TP53	p.I156T	Missense
PD41344	4	76.9	17	7578265	7578265	A	G	0.002	TP53	p.I156T	Missense
PD41344	5	80.9	17	7578265	7578265	A	G	0.007	TP53	p.I156T	Missense
PD41344	1	67.8	17	58740467	58740467	C	T	0.000	PPM1D	p.R458X	Nonsense
PD41344	2	70.7	17	58740467	58740467	C	T	0.001	PPM1D	p.R458X	Nonsense
PD41344	3	74.2	17	58740467	58740467	C	T	0.001	PPM1D	p.R458X	Nonsense
PD41344	4	76.9	17	58740467	58740467	C	T	0.003	PPM1D	p.R458X	Nonsense
PD41344	5	80.9	17	58740467	58740467	C	T	0.007	PPM1D	p.R458X	Nonsense
PD41344	1	67.8	17	58740543	58740544	CT	C	0.000	PPM1D	p.T483fs	Frameshift
PD41344	2	70.7	17	58740543	58740544	CT	C	0.000	PPM1D	p.T483fs	Frameshift
PD41344	3	74.2	17	58740543	58740544	CT	C	0.002	PPM1D	p.T483fs	Frameshift
PD41344	4	76.9	17	58740543	58740544	CT	C	0.013	PPM1D	p.T483fs	Frameshift
PD41344	5	80.9	17	58740543	58740544	CT	C	0.039	PPM1D	p.T483fs	Frameshift
PD41344	1	67.8	17	58740708	58740710	TAG	T	0.000	PPM1D	p.L538fs	Frameshift
PD41344	2	70.7	17	58740708	58740710	TAG	T	0.000	PPM1D	p.L538fs	Frameshift
PD41344	3	74.2	17	58740708	58740710	TAG	T	0.003	PPM1D	p.L538fs	Frameshift
PD41344	4	76.9	17	58740708	58740710	TAG	T	0.011	PPM1D	p.L538fs	Frameshift
PD41344	5	80.9	17	58740708	58740710	TAG	T	0.006	PPM1D	p.L538fs	Frameshift
PD41344	1	67.8	20	31021637	31021637	C	T	0.011	ASXL1	p.Q546X	Nonsense
PD41344	2	70.7	20	31021637	31021637	C	T	0.017	ASXL1	p.Q546X	Nonsense
PD41344	3	74.2	20	31021637	31021637	C	T	0.013	ASXL1	p.Q546X	Nonsense
PD41344	4	76.9	20	31021637	31021637	C	T	0.011	ASXL1	p.Q546X	Nonsense
PD41344	5	80.9	20	31021637	31021637	C	T	0.007	ASXL1	p.Q546X	Nonsense
PD41345	2	85.6	4	106156502	106156502	A	G	0.008	TET2	p.H468R	Missense
PD41345	3	92.1	4	106156502	106156502	A	G	0.002	TET2	p.H468R	Missense
PD41345	2	85.6	4	106157761	106157761	C	T	0.034	TET2	p.Q888X	Nonsense
PD41345	3	92.1	4	106157761	106157761	C	T	0.124	TET2	p.Q888X	Nonsense
PD41345	2	85.6	17	74732960	74732960	G	C	0.025	SRSF2	p.P95A	Missense
PD41345	3	92.1	17	74732960	74732960	G	C	0.020	SRSF2	p.P95A	Missense
PD41345	2	85.6	21	44514777	44514777	T	C	0.004	U2AF1	p.Q84R	Missense
PD41345	3	92.1	21	44514777	44514777	T	C	0.030	U2AF1	p.Q84R	Missense
PD41346	2	72.1	9	139400990	139400990	T	A	0.029	NOTCH1	p.K1335X	Nonsense
PD41346	3	75.8	9	139400990	139400990	T	A	0.022	NOTCH1	p.K1335X	Nonsense
PD41346	4	83.2	9	139400990	139400990	T	A	0.315	NOTCH1	p.K1335X	Nonsense
PD41346	2	72.1	17	74732959	74732959	G	T	0.001	SRSF2	p.P95H	Missense
PD41346	3	75.8	17	74732959	74732959	G	T	0.002	SRSF2	p.P95H	Missense
PD41346	4	83.2	17	74732959	74732959	G	T	0.320	SRSF2	p.P95H	Missense
PD41346	2	72.1	20	31022319	31022319	G	T	0.025	ASXL1	p.E602X	Nonsense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41346	3	75.8	20	31022319	31022319	G	T	0.018	ASXL1	p.E602X	Nonsense
PD41346	4	83.2	20	31022319	31022319	G	T	0.243	ASXL1	p.E602X	Nonsense
PD41347	2	70.3	4	106156069	106156069	C	T	0.009	TET2	p.Q324X	Nonsense
PD41347	3	76.7	4	106156069	106156069	C	T	0.007	TET2	p.Q324X	Nonsense
PD41347	4	81.4	4	106156069	106156069	C	T	0.004	TET2	p.Q324X	Nonsense
PD41347	2	70.3	4	106158025	106158029	C	CAGAT	0.051	TET2	p.Q976fs	Frameshift
PD41347	3	76.7	4	106158025	106158029	C	CAGAT	0.072	TET2	p.Q976fs	Frameshift
PD41347	4	81.4	4	106158025	106158029	C	CAGAT	0.084	TET2	p.Q976fs	Frameshift
PD41347	2	70.3	17	7578506	7578506	G	T	0.000	TP53	p.P103T	Missense
PD41347	3	76.7	17	7578506	7578506	G	T	0.009	TP53	p.P103T	Missense
PD41347	4	81.4	17	7578506	7578506	G	T	0.001	TP53	p.P103T	Missense
PD41347	2	70.3	X	129149996	129149996	G	A	0.000	BCORL1	p.R1083Q	Missense
PD41347	3	76.7	X	129149996	129149996	G	A	0.001	BCORL1	p.R1083Q	Missense
PD41347	4	81.4	X	129149996	129149996	G	A	0.008	BCORL1	p.R1083Q	Missense
PD41528	2	76.1	2	198267371	198267371	G	T	0.002	SF3B1	p.H662Q	Missense
PD41528	3	81.4	2	198267371	198267371	G	T	0.020	SF3B1	p.H662Q	Missense
PD41528	4	85.5	2	198267371	198267371	G	T	0.045	SF3B1	p.H662Q	Missense
PD41528	2	76.1	2	25467428	25467428	C	T	0.089	DNMT3A	p.G550R	Missense
PD41528	3	81.4	2	25467428	25467428	C	T	0.048	DNMT3A	p.G550R	Missense
PD41528	4	85.5	2	25467428	25467428	C	T	0.022	DNMT3A	p.G550R	Missense
PD41528	2	76.1	4	106196457	106196458	TC	T	0.106	TET2	p.F1597fs	Frameshift
PD41528	3	81.4	4	106196457	106196458	TC	T	0.209	TET2	p.F1597fs	Frameshift
PD41528	4	85.5	4	106196457	106196458	TC	T	0.201	TET2	p.F1597fs	Frameshift
PD41528	2	76.1	4	106197285	106197285	T	C	0.034	TET2	p.I1873T	Missense
PD41528	3	81.4	4	106197285	106197285	T	C	0.028	TET2	p.I1873T	Missense
PD41528	4	85.5	4	106197285	106197285	T	C	0.007	TET2	p.I1873T	Missense
PD41528	2	76.1	17	7577572	7577572	T	C	0.000	TP53	p.M198V	Missense
PD41528	3	81.4	17	7577572	7577572	T	C	0.023	TP53	p.M198V	Missense
PD41528	4	85.5	17	7577572	7577572	T	C	0.024	TP53	p.M198V	Missense
PD41528	2	76.1	X	44913131	44913131	C	T	0.004	KDM6A	p.A269V	Missense
PD41528	3	81.4	X	44913131	44913131	C	T	0.000	KDM6A	p.A269V	Missense
PD41528	4	85.5	X	44913131	44913131	C	T	0.000	KDM6A	p.A269V	Missense
PD41529	2	73.9	1	1747229	1747229	T	C	0.006	GNB1	p.K57E	Missense
PD41529	3	77.4	1	1747229	1747229	T	C	0.007	GNB1	p.K57E	Missense
PD41529	4	81.3	1	1747229	1747229	T	C	0.025	GNB1	p.K57E	Missense
PD41529	2	73.9	4	106157431	106157431	C	T	0.009	TET2	p.Q778X	Nonsense
PD41529	3	77.4	4	106157431	106157431	C	T	0.004	TET2	p.Q778X	Nonsense
PD41529	4	81.3	4	106157431	106157431	C	T	0.002	TET2	p.Q778X	Nonsense
PD41529	2	73.9	12	112926270	112926270	C	T	0.012	PTPN11	p.T468M	Missense
PD41529	3	77.4	12	112926270	112926270	C	T	0.008	PTPN11	p.T468M	Missense
PD41529	4	81.3	12	112926270	112926270	C	T	0.014	PTPN11	p.T468M	Missense
PD41529	2	73.9	16	67662314	67662314	G	T	0.002	CTCF	p.E520D	Missense
PD41529	3	77.4	16	67662314	67662314	G	T	0.001	CTCF	p.E520D	Missense
PD41529	4	81.3	16	67662314	67662314	G	T	0.009	CTCF	p.E520D	Missense
PD41530	2	74.3	4	106164071	106164071	C	G	0.006	TET2	p.P1194R	Missense
PD41530	3	78.0	4	106164071	106164071	C	G	0.005	TET2	p.P1194R	Missense
PD41530	4	80.9	4	106164071	106164071	C	G	0.011	TET2	p.P1194R	Missense
PD41530	2	74.3	4	106164764	106164764	G	A	0.025	TET2	p.C1211Y	Missense
PD41530	3	78.0	4	106164764	106164764	G	A	0.036	TET2	p.C1211Y	Missense
PD41530	4	80.9	4	106164764	106164764	G	A	0.087	TET2	p.C1211Y	Missense
PD41530	2	74.3	4	106193967	106193968	GA	G	0.017	TET2	p.E1477fs	Frameshift
PD41530	3	78.0	4	106193967	106193968	GA	G	0.029	TET2	p.E1477fs	Frameshift
PD41530	4	80.9	4	106193967	106193968	GA	G	0.030	TET2	p.E1477fs	Frameshift
PD41530	2	74.3	4	106197241	106197243	CAT	C	0.004	TET2	p.I1859fs	Frameshift
PD41530	3	78.0	4	106197241	106197243	CAT	C	0.006	TET2	p.I1859fs	Frameshift
PD41530	4	80.9	4	106197241	106197243	CAT	C	0.013	TET2	p.I1859fs	Frameshift
PD41532	3	76.1	12	25398281	25398281	C	T	0.007	KRAS	p.G13D	Missense
PD41532	4	79.3	12	25398281	25398281	C	T	0.005	KRAS	p.G13D	Missense
PD41532	5	84.4	12	25398281	25398281	C	T	0.000	KRAS	p.G13D	Missense

Sample ID	Study Phase	Age	Chr	Start	End	WT	MT	VAF	Gene	Protein	Effect
PD41532	3	76.1	17	7577545	7577545	T	C	0.001	TP53	p.M207V	Missense
PD41532	4	79.3	17	7577545	7577545	T	C	0.005	TP53	p.M207V	Missense
PD41532	5	84.4	17	7577545	7577545	T	C	0.009	TP53	p.M207V	Missense
PD41532	3	76.1	20	31022277	31022277	C	T	0.054	ASXL1	p.Q588X	Nonsense
PD41532	4	79.3	20	31022277	31022277	C	T	0.038	ASXL1	p.Q588X	Nonsense
PD41532	5	84.4	20	31022277	31022277	C	T	0.048	ASXL1	p.Q588X	Nonsense
PD42295	2	73.3	17	7577120	7577120	C	T	0.001	TP53	p.R234H	Missense
PD42295	3	77.2	17	7577120	7577120	C	T	0.000	TP53	p.R234H	Missense
PD42295	4	81.2	17	7577120	7577120	C	T	0.012	TP53	p.R234H	Missense
PD42296	2	77.9	2	25457224	25457224	A	G	0.016	DNMT3A	p.L888P	Missense
PD42296	3	83.1	2	25457224	25457224	A	G	0.043	DNMT3A	p.L888P	Missense
PD42297	2	75.5	2	25463184	25463184	G	A	0.006	DNMT3A	p.S770L	Missense
PD42297	3	81.3	2	25463184	25463184	G	A	0.016	DNMT3A	p.S770L	Missense
PD42297	4	84.8	2	25463184	25463184	G	A	0.025	DNMT3A	p.S770L	Missense
PD42297	2	75.5	4	106156301	106156317	CATCACAATTGCTTCTT	C	0.026	TET2	p.P401fs	Frameshift
PD42297	3	81.3	4	106156301	106156317	CATCACAATTGCTTCTT	C	0.155	TET2	p.P401fs	Frameshift
PD42297	4	84.8	4	106156301	106156317	CATCACAATTGCTTCTT	C	0.308	TET2	p.P401fs	Frameshift
PD42297	2	75.5	4	106164866	106164866	A	G	0.006	TET2	p.Y1245C	Missense
PD42297	3	81.3	4	106164866	106164866	A	G	0.148	TET2	p.Y1245C	Missense
PD42297	4	84.8	4	106164866	106164866	A	G	0.338	TET2	p.Y1245C	Missense

Table 9 | dN/dS ratios for missense / truncating mutations in CH genes [dN/dS ratios (and corresponding genes) with q-values < 0.1 are highlighted in yellow]

gene_name	n_syn	n_mis	n_non	n_spl	n_ind	dNdS_missense	p_dNdS_missense	q_dNdS_missense	dNdS_truncating	p_dNdS_truncating	q_dNdS_truncating	p_global_cv	qglobal_cv
DNMT3A	4	116	28	23	27	20.56	0.00E+00	0.00E+00	79.10	0.00E+00	0.00E+00	0.00E+00	0.00E+00
TET2	1	77	68	4	75	7.60	0.00E+00	0.00E+00	71.66	0.00E+00	0.00E+00	0.00E+00	0.00E+00
TP53	1	31	3	0	0	12.90	0.00E+00	0.00E+00	11.40	2.52E-03	1.87E-02	0.00E+00	0.00E+00
SF3B1	3	40	1	1	0	5.77	0.00E+00	0.00E+00	2.33	2.94E-01	7.56E-01	0.00E+00	0.00E+00
PPM1D	1	4	19	0	11	1.12	8.26E-01	8.80E-01	58.70	0.00E+00	0.00E+00	0.00E+00	0.00E+00
ASXL1	6	6	13	2	13	0.71	3.80E-01	6.03E-01	20.35	3.66E-15	4.76E-14	1.33E-13	1.15E-12
JAK2	0	12	0	0	0	21.29	1.19E-12	1.23E-11	0.00	6.98E-01	7.80E-01	2.63E-10	1.95E-09
SRSF2	0	15	0	0	2	8.23	1.26E-09	1.09E-08	0.00	6.84E-01	7.80E-01	3.50E-08	2.27E-07
CBL	1	19	1	4	2	3.84	1.65E-06	1.22E-05	9.43	2.38E-04	2.48E-03	9.05E-08	5.23E-07
BRCC3	0	8	2	1	2	4.62	5.50E-04	2.60E-03	10.81	2.95E-03	1.92E-02	9.06E-05	4.71E-04
KRAS	0	8	0	0	0	8.63	6.52E-06	4.24E-05	0.00	6.25E-01	7.56E-01	3.86E-04	1.82E-03
CTCF	1	10	3	1	0	2.38	1.64E-02	5.69E-02	10.27	7.29E-04	6.32E-03	1.79E-03	7.77E-03
GNB1	2	9	0	0	0	4.35	3.86E-04	2.23E-03	0.00	4.76E-01	7.56E-01	1.08E-02	4.31E-02
U2AF1	0	8	0	0	0	4.78	4.35E-04	2.26E-03	0.00	5.31E-01	7.56E-01	1.25E-02	4.63E-02
BCORL1	7	16	3	0	5	1.55	1.02E-01	2.21E-01	3.98	5.14E-02	2.97E-01	6.74E-02	2.34E-01
IDH2	0	3	0	0	0	9.68	4.10E-03	1.78E-02	0.00	8.83E-01	8.97E-01	8.25E-02	2.68E-01
GATA2	4	0	1	0	0	0.00	1.25E-02	4.65E-02	5.10	1.99E-01	6.90E-01	9.59E-02	2.88E-01
PTPN11	0	9	0	0	0	2.79	8.59E-03	3.44E-02	0.00	3.47E-01	7.56E-01	9.95E-02	2.88E-01
KDM6A	3	12	1	2	2	1.66	1.07E-01	2.23E-01	3.00	1.07E-01	5.06E-01	1.41E-01	3.87E-01
IDH1	0	3	0	0	0	5.45	2.16E-02	7.03E-02	0.00	8.02E-01	8.51E-01	2.54E-01	6.61E-01
SMC1A	3	12	0	0	0	1.79	6.69E-02	1.68E-01	0.00	1.84E-01	6.85E-01	2.75E-01	6.81E-01
KMT2A	1	5	2	0	1	1.12	8.05E-01	8.80E-01	5.17	6.73E-02	3.50E-01	3.00E-01	7.02E-01
PHF6	2	5	0	1	0	2.76	5.18E-02	1.52E-01	3.32	3.17E-01	7.56E-01	3.10E-01	7.02E-01
U2AF2	0	7	0	0	0	2.26	5.78E-02	1.58E-01	0.00	4.32E-01	7.56E-01	3.78E-01	7.85E-01
KIT	1	5	0	0	0	2.75	5.28E-02	1.52E-01	0.00	5.48E-01	7.56E-01	3.91E-01	7.85E-01
BCOR	7	14	0	0	1	1.40	2.35E-01	4.36E-01	0.00	2.20E-01	6.93E-01	3.93E-01	7.85E-01
ZRSR2	1	6	0	0	0	2.28	7.64E-02	1.81E-01	0.00	3.65E-01	7.56E-01	4.11E-01	7.92E-01
GNAS	2	12	1	0	0	1.78	6.79E-02	1.68E-01	1.98	5.39E-01	7.56E-01	4.47E-01	8.29E-01
EZH2	3	7	1	0	1	1.73	1.82E-01	3.51E-01	1.71	6.23E-01	7.56E-01	4.67E-01	8.38E-01
JAK3	1	4	0	0	0	2.73	8.52E-02	1.93E-01	0.00	5.92E-01	7.56E-01	5.17E-01	8.75E-01
PRPF40B	3	6	0	0	1	1.20	6.66E-01	7.87E-01	0.00	2.27E-01	6.93E-01	5.39E-01	8.75E-01
ETV6	1	4	0	0	1	1.53	4.29E-01	6.38E-01	0.00	4.53E-01	7.56E-01	5.54E-01	8.75E-01
CREBBP	5	11	3	0	1	0.78	3.85E-01	6.03E-01	1.92	3.08E-01	7.56E-01	5.81E-01	8.75E-01
CUX1	6	11	1	1	2	1.20	5.52E-01	7.00E-01	2.04	3.68E-01	7.56E-01	5.87E-01	8.75E-01
PTEN	0	3	0	0	1	1.46	5.38E-01	7.00E-01	0.00	4.65E-01	7.56E-01	5.89E-01	8.75E-01
SMC3	2	7	0	0	0	1.19	6.56E-01	7.87E-01	0.00	1.51E-01	6.34E-01	6.88E-01	9.63E-01
PIGA	1	3	0	0	1	1.14	8.30E-01	8.80E-01	0.00	5.51E-01	7.56E-01	7.01E-01	9.63E-01
RAD21	1	3	0	1	1	0.96	9.49E-01	9.68E-01	2.29	4.65E-01	7.56E-01	7.03E-01	9.63E-01
STAG2	3	7	0	0	0	1.10	7.97E-01	8.80E-01	0.00	1.59E-01	6.34E-01	7.26E-01	9.68E-01
MPL	1	1	0	0	0	5.60	1.79E-01	3.51E-01	0.00	8.97E-01	8.97E-01	7.69E-01	9.97E-01
SF3A1	1	3	0	0	0	0.66	4.47E-01	6.45E-01	0.00	3.03E-01	7.56E-01	8.01E-01	9.97E-01
CSF3R	1	3	0	0	0	2.01	2.79E-01	4.99E-01	0.00	5.77E-01	7.56E-01	8.30E-01	9.97E-01
SF1	0	3	0	0	0	0.68	4.74E-01	6.66E-01	0.00	3.90E-01	7.56E-01	8.70E-01	9.97E-01
CSF1R	1	0	0	0	0	0.00	2.88E-01	4.99E-01	0.00	7.47E-01	8.10E-01	8.72E-01	9.97E-01
FLT3	1	3	0	0	0	1.71	3.94E-01	6.03E-01	0.00	4.93E-01	7.56E-01	8.79E-01	9.97E-01
NRAS	0	2	0	0	0	2.01	3.78E-01	6.03E-01	0.00	6.24E-01	7.56E-01	9.07E-01	9.97E-01
WT1	1	4	0	0	0	1.17	7.64E-01	8.80E-01	0.00	4.18E-01	7.56E-01	9.46E-01	9.97E-01
NOTCH1	9	15	1	1	0	0.86	5.40E-01	7.00E-01	1.55	5.61E-01	7.56E-01	9.50E-01	9.97E-01
RUNX1	0	3	0	0	0	0.94	9.13E-01	9.50E-01	0.00	4.73E-01	7.56E-01	9.71E-01	9.97E-01
BRAF	0	0	0	0	0	0.00	5.37E-01	7.00E-01	0.00	8.48E-01	8.82E-01	9.81E-01	9.97E-01
CALR	1	1	0	0	0	1.59	6.66E-01	7.87E-01	0.00	7.05E-01	7.80E-01	9.88E-01	9.97E-01
CEBPA	1	3	0	0	0	1.02	9.71E-01	9.71E-01	0.00	6.94E-01	7.80E-01	9.97E-01	9.97E-01

Table 10 | Prediction of future VAF trajectories

Sample ID	Sex	Study Phase	Age	Chr	Start	WT	MT	VAF Observed	VAF Predicted	Gene	Protein	Effect
PD41305	M	6	73.4	17	76736877	G	T	0.074	0.113	SRSF2	p.P95H	Missense
PD41246	F	6	92.5	9	5073770	G	T	0.147	0.138	JAK2	p.V617F	Missense
PD34511	F	6	91.9	2	197402110	T	C	0.104	0.124	SF3B1	p.K700E	Missense
PD34511	F	6	91.9	2	197402759	C	A	0.065	0.101	SF3B1	p.R625L	Missense
PD41276	M	6	79.4	2	197402110	T	C	0.009	0.015	SF3B1	p.K700E	Missense
PD41276	M	6	79.4	2	197402635	C	G	0.342	0.435	SF3B1	p.K666N	Missense
PD41081	M	6	84.3	21	43094667	T	G	0.118	0.088	U2AF1	p.Q157P	Missense
PD41285	M	6	79.5	2	197402110	T	C	0.010	0.006	SF3B1	p.K700E	Missense
PD34493	M	6	83.8	2	197402635	C	A	0.106	0.093	SF3B1	p.K666N	Missense
PD34493	M	6	83.8	21	43094667	T	C	0.211	0.166	U2AF1	p.Q157R	Missense
PD41103	M	6	91.7	2	25234373	C	T	0.321	0.379	DNMT3A	p.R882H	Missense
PD41082	F	6	73.9	1	1815790	T	C	0.042	0.019	GNB1	p.K57E	Missense
PD41082	F	6	73.9	2	197402635	C	A	0.162	0.121	SF3B1	p.K666N	Missense
PD41075	M	6	88.2	17	76736877	G	A	0.117	0.194	SRSF2	p.P95L	Missense
PD41161	F	6	89.7	17	76736877	G	T	0.040	0.103	SRSF2	p.P95H	Missense

Table 11a | Growth coefficients for all clones

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41102	SRSF2-SRSF2:NM_003016:exon1:c.43_44GA	SRSF2	0.031	0.002	-0.048	0.105	0.153	0.001	0.094	0.213	0.000	0.000	0.000	0.000	0.153	0.001	0.103	0.203	-9.04	-4.95	0.184
PD41345	SRSF2-P95A	SRSF2	-0.030	0.002	-0.126	0.059	0.153	0.001	0.094	0.213	-0.046	0.003	-0.164	0.059	0.107	0.003	0.019	0.196	-10.33	-1.89	0.077
PD41345	TET2nt-H468R	TET2	-0.021	0.003	-0.120	0.083	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-11.57	-3.53	0.077
PD41345	TET2t-Q888X	TET2	0.067	0.001	-0.004	0.131	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.23	-4.55	0.148
PD41345	U2AF1-Q157R	U2AF1	-0.007	0.002	-0.101	0.084	0.193	0.002	0.101	0.289	0.154	0.004	0.036	0.285	0.348	0.003	0.260	0.435	-20.29	-10.63	0.341
PD41073	DNMT3Ant-L637V	DNMT3A	-0.001	0.001	-0.067	0.064	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.37	-0.93	0.037
PD41073	DNMT3At-F640fs	DNMT3A	0.008	0.002	-0.085	0.098	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-9.07	-3.81	0.060
PD41073	PPM1D-E476X	PPM1D	0.012	0.002	-0.080	0.102	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.45	-4.18	0.106
PD41073	TET2t-Q1553fs	TET2	-0.004	0.002	-0.103	0.077	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.36	-4.19	0.077
PD41269	DNMT3Ant-S638C	DNMT3A	0.035	0.002	-0.043	0.107	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.97	-4.42	0.073
PD34501	TET2t-N811fs	TET2	0.007	0.002	-0.081	0.108	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.80	-3.43	0.088
PD34496	DNMT3At-C557X	DNMT3A	-0.028	0.002	-0.104	0.047	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.23	-2.91	0.023
PD41296	SF3B1-H662Y	SF3B1	-0.062	0.002	-0.139	0.016	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-7.60	-3.90	0.054
PD34487	ASXL1-Q1251X	ASXL1	0.050	0.002	-0.031	0.127	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.53	-5.34	0.147
PD34487	TET2nt-H1380Y	TET2	0.005	0.002	-0.082	0.082	0.098	0.000	0.078	0.116	-0.053	0.001	-0.122	0.020	0.045	0.001	-0.010	0.109	-6.92	-2.91	0.050
PD34485	TP53nt-R248W	TP53	-0.024	0.002	-0.119	0.068	0.049	0.000	0.013	0.087	0.019	0.004	-0.097	0.136	0.068	0.003	-0.029	0.166	-8.02	-2.27	0.044
PD41289	DNMT3Ant-V675A	DNMT3A	0.056	0.001	-0.002	0.111	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.06	-3.80	0.093
PD41114	DNMT3Ant-R736H	DNMT3A	-0.016	0.002	-0.098	0.062	0.038	0.000	0.021	0.055	0.060	0.002	-0.021	0.135	0.098	0.002	0.032	0.162	-5.91	-3.92	0.082
PD41114	JAK2-V617F	JAK2	-0.045	0.002	-0.136	0.039	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-6.75	-4.19	0.093
PD41227	CBLnt-I361S	CBL	-0.012	0.002	-0.092	0.062	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-6.69	-3.78	0.032
PD41227	DNMT3Ant-G302S	DNMT3A	-0.045	0.001	-0.104	0.028	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.89	-2.66	-0.007
PD41312	PPM1D-A454fs	PPM1D	-0.037	0.001	-0.100	0.024	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-4.62	-3.30	0.056
PD41239	ASXL1-G828fs	ASXL1	0.056	0.001	0.001	0.117	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-4.32	-1.85	0.153
PD41239	SRSF2-P95H	SRSF2	-0.051	0.002	-0.136	0.031	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-10.46	-6.44	0.396
PD41239	TET2nt-T1883K	TET2	0.088	0.002	-0.018	0.174	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.39	-6.11	0.186
PD41108	DNMT3Ant-R326P	DNMT3A	0.018	0.001	-0.037	0.078	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.12	-3.34	0.056
PD41108	DNMT3Ant-S669F	DNMT3A	0.028	0.001	-0.029	0.092	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.65	-3.71	0.066
PD41108	DNMT3At-NM_175629:exon12:c.1474+1G>-	DNMT3A	0.047	0.001	-0.029	0.117	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.22	-4.92	0.098
PD41108	TET2t-S675X	TET2	0.007	0.001	-0.064	0.078	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.18	-4.70	0.087
PD34497	TET2t-NM_001127208:exon9:c.4182+2->T	TET2	0.082	0.001	0.040	0.131	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.74	-3.07	0.163
PD34497	TET2t-P1155fs	TET2	-0.015	0.002	-0.100	0.080	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.64	-3.88	0.066

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34497	TET2t-R544X	TET2	-0.017	0.002	-0.098	0.064	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.69	-3.45	0.064
PD41243	DNMT3Ant-I780T	DNMT3A	0.012	0.002	-0.074	0.101	0.038	0.000	0.021	0.055	0.046	0.003	-0.065	0.169	0.084	0.003	-0.007	0.183	-8.99	-3.59	0.096
PD41243	DNMT3Ant-M880V	DNMT3A	-0.004	0.002	-0.099	0.074	0.038	0.000	0.021	0.055	0.024	0.003	-0.075	0.139	0.062	0.003	-0.029	0.150	-9.27	-2.84	0.058
PD41243	DNMT3At-Q615X	DNMT3A	-0.017	0.001	-0.094	0.061	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.51	-2.07	0.035
PD41243	DNMT3At-Y436X	DNMT3A	0.000	0.002	-0.079	0.083	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.03	-3.18	0.052
PD34484	DNMT3At-F640fs	DNMT3A	-0.056	0.001	-0.133	0.014	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.45	-2.32	-0.004
PD41249	DNMT3At-L504fs	DNMT3A	0.008	0.002	-0.064	0.097	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.34	-4.18	0.060
PD41249	TET2nt-C1221S	TET2	-0.020	0.002	-0.116	0.082	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.16	-3.94	0.077
PD41532	ASXL1-Q588X	ASXL1	-0.054	0.001	-0.123	0.018	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-5.20	-1.49	0.043
PD41532	KRAS-G13D	KRAS	-0.034	0.002	-0.130	0.060	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-10.18	-3.29	0.048
PD41532	TP53nt-M246V	TP53	0.017	0.002	-0.074	0.104	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-8.95	-3.84	0.066
PD41163	DNMT3Ant-R882C	DNMT3A	0.006	0.002	-0.082	0.088	0.038	0.000	0.021	0.055	-0.020	0.003	-0.126	0.085	0.017	0.003	-0.070	0.109	-5.12	-0.02	0.023
PD41163	TET2nt-H1912R	TET2	-0.007	0.003	-0.115	0.091	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.60	-4.45	0.091
PD34475	TET2t-R1404X	TET2	0.056	0.000	0.018	0.097	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.42	-3.78	0.137
PD41112	CBLnt-C396W	CBL	-0.003	0.001	-0.080	0.069	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-7.68	-3.36	0.041
PD41112	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	-0.037	0.002	-0.120	0.039	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-10.26	-5.12	0.106
PD41112	DNMT3Ant-R882H	DNMT3A	-0.067	0.001	-0.139	0.004	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-4.71	-1.35	-0.014
PD41528	DNMT3Ant-G550R	DNMT3A	-0.092	0.000	-0.128	-0.045	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-1.76	0.00	-0.054
PD41528	SF3B1-H662Q	SF3B1	0.047	0.002	-0.047	0.126	0.116	0.001	0.067	0.157	0.027	0.003	-0.075	0.124	0.142	0.002	0.062	0.224	-11.31	-5.62	0.189
PD41528	TET2nt-I1873T	TET2	-0.096	0.002	-0.185	-0.022	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-5.81	-0.89	0.006
PD41528	TET2t-F1597fs	TET2	0.014	0.001	-0.035	0.062	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.39	-1.89	0.095
PD41528	TP53nt-M237V	TP53	0.041	0.002	-0.051	0.122	0.049	0.000	0.013	0.087	0.078	0.003	-0.034	0.183	0.128	0.003	0.042	0.217	-11.58	-5.41	0.169
PD41175	DNMT3Ant-D686E	DNMT3A	0.000	0.001	-0.069	0.063	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.04	-2.96	0.038
PD41175	GNB1-A248T	GNB1	0.027	0.003	-0.076	0.122	0.101	0.001	0.032	0.175	0.000	0.000	0.000	0.000	0.101	0.001	0.038	0.160	-12.78	-6.13	0.127
PD41175	PPM1D-W427X	PPM1D	-0.001	0.002	-0.079	0.077	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-8.65	-4.63	0.092
PD41192	DNMT3Ant-R326C	DNMT3A	0.099	0.001	0.054	0.146	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-3.90	-2.04	0.137
PD41192	DNMT3Ant-V687L	DNMT3A	-0.040	0.002	-0.135	0.049	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.38	-2.63	-0.002
PD41192	SF3B1-T798I	SF3B1	-0.034	0.002	-0.134	0.050	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-10.65	-4.81	0.081
PD41302	DNMT3Ant-I369F	DNMT3A	0.005	0.002	-0.073	0.081	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.08	-3.31	0.043
PD41302	DNMT3At-Q886X	DNMT3A	-0.001	0.002	-0.080	0.081	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.12	-4.03	0.051
PD41302	TET2t-H1778fs	TET2	0.048	0.001	-0.015	0.116	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.42	-4.00	0.129
PD42297	DNMT3Ant-S770L	DNMT3A	0.018	0.002	-0.060	0.098	0.038	0.000	0.021	0.055	0.054	0.001	-0.012	0.120	0.092	0.001	0.038	0.145	-8.94	-3.89	0.110
PD42297	TET2nt-Y1245C	TET2	0.225	0.001	0.158	0.284	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-11.21	-7.79	0.323
PD42297	TET2t-P401fs	TET2	0.191	0.001	0.136	0.243	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.45	-6.60	0.272

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41149	DNMT3At-NM_175629:exon9:c.1015-2A>G	DNMT3A	0.000	0.002	-0.076	0.081	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.95	-3.97	0.052
PD41149	DNMT3At-NM_175629:exon11:c.1429+1G>A	DNMT3A	0.047	0.002	-0.035	0.125	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.80	-5.03	0.099
PD41167	DNMT3At-S770X	DNMT3A	0.007	0.001	-0.046	0.057	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.74	-2.77	0.058
PD34505	TET2t-W1847X	TET2	0.031	0.002	-0.047	0.121	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.43	-3.43	0.112
PD41122	DNMT3At-R458fs	DNMT3A	0.062	0.001	-0.002	0.120	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.75	-4.28	0.114
PD41115	CTCFt-S488X	CTCF	-0.004	0.002	-0.085	0.079	0.084	0.002	-0.005	0.171	0.000	0.000	0.000	0.000	0.084	0.002	0.008	0.159	-9.63	-4.40	0.080
PD41115	SRSF2-P95L	SRSF2	-0.018	0.002	-0.090	0.070	0.153	0.001	0.094	0.213	-0.015	0.002	-0.110	0.067	0.138	0.001	0.077	0.199	-9.46	-4.99	0.121
PD41226	DNMT3Ant-R201C	DNMT3A	0.018	0.001	-0.059	0.087	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.56	-4.32	0.056
PD41226	DNMT3Ant-V636M	DNMT3A	-0.021	0.001	-0.090	0.050	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.21	-3.13	0.017
PD42296	DNMT3Ant-L888P	DNMT3A	0.030	0.002	-0.052	0.122	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.90	-2.28	0.068
PD41235	SRSF2-P95L	SRSF2	0.022	0.002	-0.072	0.121	0.153	0.001	0.094	0.213	-0.015	0.002	-0.110	0.067	0.138	0.001	0.077	0.199	-12.89	-6.48	0.160
PD41235	TET2t-C973fs	TET2	0.035	0.001	-0.034	0.116	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.54	-5.12	0.116
PD41235	TET2t-E692X	TET2	-0.055	0.001	-0.124	0.021	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.96	-2.73	0.026
PD34533	TP53nt-F212V	TP53	0.010	0.002	-0.076	0.097	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-8.55	-3.80	0.060
PD34521	CTCFnt-T563I	CTCF	0.004	0.002	-0.095	0.090	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-8.53	-3.64	0.067
PD34521	JAK2-V617F	JAK2	-0.099	0.001	-0.164	-0.025	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-3.72	-0.86	0.038
PD41245	BRCC3nt-G152R	BRCC3	-0.014	0.002	-0.103	0.084	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-7.93	-2.40	0.026
PD41221	DNMT3Ant-R882H	DNMT3A	-0.016	0.002	-0.087	0.062	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-7.47	-0.59	0.038
PD41221	TET2nt-Y1902H	TET2	0.001	0.002	-0.089	0.093	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-13.01	-4.67	0.099
PD41221	TET2t-Q888X	TET2	0.014	0.002	-0.072	0.097	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-11.76	-4.42	0.095
PD41221	TET2t-Q916X	TET2	-0.029	0.002	-0.105	0.045	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.78	-2.04	0.052
PD41221	U2AF1-Q157P	U2AF1	0.011	0.003	-0.086	0.126	0.193	0.002	0.101	0.289	0.063	0.004	-0.052	0.188	0.256	0.003	0.175	0.343	-22.46	-10.43	0.267
PD34575	DNMT3Ant-I769M	DNMT3A	-0.028	0.002	-0.126	0.063	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-8.90	-2.27	0.010
PD34575	PPM1D-N477fs	PPM1D	0.025	0.002	-0.059	0.104	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-10.95	-5.50	0.119
PD34575	SF3B1-K666N	SF3B1	-0.005	0.002	-0.094	0.079	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-12.05	-5.80	0.144
PD41099	IDH1-H133R	IDH1	-0.019	0.002	-0.099	0.064	0.107	0.004	-0.016	0.220	0.000	0.000	0.000	0.000	0.107	0.004	0.010	0.204	-8.24	-4.34	0.088
PD41099	SRSF2-P95R	SRSF2	-0.047	0.002	-0.130	0.027	0.153	0.001	0.094	0.213	0.000	0.000	0.000	0.000	0.153	0.001	0.103	0.203	-8.34	-5.04	0.106
PD41099	TP53nt-R273G	TP53	0.036	0.003	-0.066	0.136	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-9.54	-5.54	0.085
PD41185	DNMT3Ant-I705T	DNMT3A	0.002	0.002	-0.076	0.077	0.038	0.000	0.021	0.055	0.019	0.002	-0.061	0.095	0.057	0.002	-0.007	0.122	-3.81	-1.88	0.059
PD41310	DNMT3At-G646fs	DNMT3A	-0.027	0.002	-0.103	0.054	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.70	-3.89	0.025
PD41074	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	-0.029	0.001	-0.092	0.026	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.10	-2.64	0.022
PD34579	CBLnt-Q409R	CBL	-0.019	0.003	-0.122	0.074	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-12.01	-3.70	0.024

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34579	DNMT3Ant-I833V	DNMT3A	-0.010	0.002	-0.086	0.068	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.30	-1.99	0.028
PD34569	CBLt-Q691fs	CBL	-0.026	0.002	-0.114	0.062	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-10.42	-4.91	0.117
PD34569	DNMT3Ant-I898T	DNMT3A	-0.025	0.002	-0.104	0.068	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.59	-2.13	0.013
PD34569	DNMT3At-W698X	DNMT3A	0.056	0.001	-0.012	0.121	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.12	-2.87	0.107
PD34569	SF3B1-K666N	SF3B1	-0.060	0.001	-0.125	0.010	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-5.75	-2.55	0.090
PD41129	DNMT3Ant-A662G	DNMT3A	0.023	0.001	-0.047	0.096	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.30	-3.68	0.061
PD41152	ASXL1-NM_015338:exon11:c.1719+2T>C	ASXL1	-0.018	0.003	-0.125	0.081	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-12.08	-5.68	0.078
PD41135	DNMT3Ant-S638F	DNMT3A	0.008	0.002	-0.086	0.099	0.038	0.000	0.021	0.055	0.042	0.003	-0.067	0.154	0.079	0.003	-0.010	0.171	-7.19	-4.06	0.087
PD41135	DNMT3At-G654fs	DNMT3A	0.003	0.001	-0.062	0.073	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.82	-3.83	0.054
PD41135	TET2t-Q749X	TET2	-0.011	0.001	-0.083	0.059	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.33	-4.11	0.070
PD34571	PPM1D-R429fs	PPM1D	0.013	0.002	-0.069	0.095	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.27	-4.27	0.107
PD41176	PPM1D-E226X	PPM1D	-0.034	0.002	-0.132	0.058	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-12.15	-4.45	0.060
PD41176	TET2nt-A1876G	TET2	-0.004	0.002	-0.077	0.077	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.10	-4.68	0.094
PD34580	DNMT3Ant-R659H	DNMT3A	0.022	0.001	-0.047	0.107	0.038	0.000	0.021	0.055	-0.034	0.002	-0.119	0.043	0.004	0.002	-0.063	0.074	-4.54	-1.44	0.026
PD34504	DNMT3At-NM_175629:exon16:c.1852-1G>A	DNMT3A	0.025	0.002	-0.054	0.107	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.05	-4.62	0.077
PD41347	TET2t-Q324X	TET2	-0.033	0.002	-0.124	0.060	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.90	-3.31	0.048
PD41347	TET2t-Q976fs	TET2	-0.021	0.001	-0.068	0.030	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.26	-2.11	0.060
PD41347	TP53nt-P142T	TP53	0.012	0.002	-0.075	0.098	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-9.14	-4.28	0.061
PD41222	TET2nt-H1380Y	TET2	-0.063	0.002	-0.153	0.040	0.098	0.000	0.078	0.116	-0.053	0.001	-0.122	0.020	0.045	0.001	-0.010	0.109	-7.17	-3.87	-0.018
PD41142	CBLnt-L380P	CBL	-0.026	0.002	-0.110	0.063	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-7.59	-1.73	0.017
PD41142	DNMT3At-R771X	DNMT3A	-0.030	0.002	-0.111	0.047	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.17	-2.13	0.021
PD41142	SF3B1-K666N	SF3B1	0.009	0.002	-0.079	0.096	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-12.10	-6.36	0.159
PD41142	TET2t-R544X	TET2	-0.015	0.002	-0.108	0.068	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.77	-3.97	0.066
PD34550	CTCFnt-V361I	CTCF	-0.024	0.002	-0.113	0.069	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-8.03	-3.24	0.039
PD34550	TET2t-G1719fs	TET2	0.011	0.002	-0.059	0.091	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.56	-4.49	0.092
PD41139	DNMT3Ant-L819V	DNMT3A	0.004	0.001	-0.043	0.056	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-3.32	-2.25	0.042
PD41139	TET2nt-C1271S	TET2	-0.056	0.002	-0.140	0.033	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.86	-4.22	0.042
PD41211	CBLnt-I383M	CBL	0.020	0.002	-0.067	0.114	0.044	0.001	-0.016	0.091	0.071	0.004	-0.060	0.185	0.114	0.004	0.010	0.220	-13.33	-5.69	0.134
PD41211	TET2nt-H1380Y	TET2	0.095	0.001	0.020	0.162	0.098	0.000	0.078	0.116	-0.053	0.001	-0.122	0.020	0.045	0.001	-0.010	0.109	-8.09	-5.24	0.140
PD41191	TET2t-L920X	TET2	-0.019	0.002	-0.113	0.075	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.50	-3.31	0.062
PD41191	TET2t-S473fs	TET2	-0.014	0.003	-0.111	0.089	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.08	-4.04	0.067
PD41191	TET2t-W1847X	TET2	-0.016	0.001	-0.080	0.051	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-3.31	-0.80	0.064
PD41265	DNMT3At-NM_175629:exon20:c.2323-2A>G	DNMT3A	0.026	0.001	-0.026	0.075	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.01	-3.07	0.078

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41265	DNMT3At-NM_175629:exon9:c.1015-2A>T	DNMT3A	-0.062	0.001	-0.119	-0.012	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.98	-2.08	-0.010
PD41265	PTPN11-R502L	PTPN11	-0.037	0.002	-0.119	0.039	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-9.55	-5.74	0.144
PD41331	TET2nt-A347E	TET2	0.001	0.002	-0.091	0.085	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.86	-5.15	0.099
PD41130	CTCFnt-H347R	CTCF	0.001	0.002	-0.084	0.081	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-7.70	-2.84	0.064
PD41130	PPM1D-N448fs	PPM1D	-0.001	0.001	-0.051	0.046	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-3.63	-1.45	0.093
PD41181	DNMT3Ant-R736C	DNMT3A	0.023	0.002	-0.065	0.107	0.038	0.000	0.021	0.055	0.032	0.002	-0.048	0.104	0.070	0.001	0.007	0.132	-8.66	-4.19	0.093
PD41181	DNMT3At-NM_175629:exon21:c.2478+1G>A	DNMT3A	0.018	0.001	-0.058	0.087	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.88	-3.53	0.069
PD34577	DNMT3Ant-Q886R	DNMT3A	-0.034	0.002	-0.115	0.053	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.90	-1.46	0.003
PD34577	DNMT3At-R320X	DNMT3A	0.008	0.001	-0.037	0.061	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-2.61	-0.01	0.059
PD34526	DNMT3Ant-R882C	DNMT3A	-0.013	0.002	-0.096	0.079	0.038	0.000	0.021	0.055	-0.020	0.003	-0.126	0.085	0.017	0.003	-0.070	0.109	-6.88	-0.59	0.005
PD41304	TET2nt-K110R	TET2	-0.047	0.001	-0.104	0.009	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.17	-3.17	0.051
PD41123	ASXL1-Q1350X	ASXL1	-0.081	0.001	-0.127	-0.034	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-3.45	-1.88	0.016
PD41123	DNMT3At-W314X	DNMT3A	0.058	0.001	-0.007	0.124	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.84	-4.21	0.109
PD41160	DNMT3Ant-R635W	DNMT3A	0.069	0.001	0.002	0.139	0.038	0.000	0.021	0.055	0.014	0.001	-0.052	0.079	0.051	0.001	0.000	0.104	-4.71	-3.41	0.120
PD41160	TET2t-R1455fs	TET2	0.071	0.001	0.015	0.133	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.18	-3.96	0.152
PD41144	DNMT3Ant-R736C	DNMT3A	0.020	0.002	-0.056	0.102	0.038	0.000	0.021	0.055	0.032	0.002	-0.048	0.104	0.070	0.001	0.007	0.132	-9.40	-4.27	0.090
PD41144	SF3B1-K666N	SF3B1	0.018	0.002	-0.062	0.091	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-12.12	-7.20	0.167
PD34479	DNMT3Ant-I705T	DNMT3A	-0.020	0.002	-0.116	0.072	0.038	0.000	0.021	0.055	0.019	0.002	-0.061	0.095	0.057	0.002	-0.007	0.122	-7.28	-3.13	0.036
PD41188	GNB1-K57M	GNB1	-0.013	0.002	-0.091	0.067	0.101	0.001	0.032	0.175	0.000	0.000	0.000	0.000	0.101	0.001	0.038	0.160	-7.46	-3.00	0.088
PD41188	PTPN11-G363R	PTPN11	0.004	0.002	-0.091	0.100	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-12.56	-6.73	0.185
PD41188	TET2nt-R1926G	TET2	0.017	0.002	-0.072	0.118	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.40	-4.76	0.115
PD34527	TET2nt-C1298Y	TET2	0.134	0.001	0.084	0.190	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.43	-6.07	0.232
PD34527	TET2nt-V1417F	TET2	-0.025	0.002	-0.111	0.061	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.57	-4.52	0.073
PD34527	TET2t-Q674X	TET2	0.151	0.001	0.098	0.200	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.57	-6.22	0.232
PD34527	TP53nt-R175G	TP53	0.002	0.001	-0.067	0.074	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-6.22	-3.32	0.052
PD41218	DNMT3Ant-G332R	DNMT3A	-0.039	0.000	-0.076	-0.002	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-1.89	-0.01	-0.002
PD41218	DNMT3Ant-R729G	DNMT3A	-0.018	0.002	-0.109	0.060	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.64	-2.16	0.020
PD41218	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	0.009	0.002	-0.076	0.093	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.67	-3.43	0.060
PD41218	TET2t-Y1649X	TET2	0.010	0.002	-0.072	0.097	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.63	-5.05	0.091
PD34514	DNMT3Ant-G511E	DNMT3A	-0.004	0.001	-0.070	0.071	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.28	-2.89	0.033
PD34514	DNMT3Ant-R635W	DNMT3A	-0.035	0.001	-0.097	0.039	0.038	0.000	0.021	0.055	0.014	0.001	-0.052	0.079	0.051	0.001	0.000	0.104	-4.49	-1.85	0.017

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34514	DNMT3Ant-R729W	DNMT3A	-0.044	0.000	-0.085	-0.004	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-2.28	-0.51	-0.006
PD34514	JAK2-V617F	JAK2	0.019	0.002	-0.066	0.112	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-12.30	-7.05	0.157
PD41318	DNMT3Ant-F755S	DNMT3A	-0.015	0.002	-0.112	0.079	0.038	0.000	0.021	0.055	0.007	0.003	-0.092	0.116	0.045	0.003	-0.041	0.135	-7.94	-1.98	0.030
PD41318	TET2t-L199X	TET2	0.009	0.002	-0.078	0.106	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.41	-5.02	0.090
PD41271	PPM1D-E475X	PPM1D	0.005	0.002	-0.083	0.094	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.83	-4.94	0.098
PD41271	PPM1D-N477fs	PPM1D	0.016	0.002	-0.071	0.101	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-11.31	-6.25	0.109
PD34543	IDH1-R132H	IDH1	-0.032	0.002	-0.124	0.057	0.107	0.004	-0.016	0.220	0.171	0.004	0.037	0.302	0.278	0.003	0.195	0.362	-14.87	-6.72	0.246
PD34543	JAK2-V617F	JAK2	-0.146	0.001	-0.199	-0.088	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-3.04	0.00	-0.009
PD34543	SRSF2-P95H	SRSF2	-0.006	0.002	-0.103	0.086	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-23.13	-14.65	0.441
PD34543	TET2t-M1734fs	TET2	-0.109	0.000	-0.140	-0.072	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-2.01	0.00	-0.028
PD34511	DNMT3At-P385fs	DNMT3A	0.015	0.001	-0.042	0.069	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.93	-2.09	0.066
PD34511	SF3B1-K700E	SF3B1	-0.012	0.001	-0.085	0.057	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-6.07	-2.67	0.087
PD34511	SF3B1-R625L	SF3B1	-0.018	0.001	-0.091	0.055	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-6.77	-2.99	0.098
PD41120	ASXL1-S1014fs	ASXL1	-0.019	0.001	-0.101	0.054	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-7.27	-4.81	0.078
PD41120	TET2t-Q1534X	TET2	0.005	0.002	-0.073	0.089	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.14	-4.65	0.086
PD41120	TET2t-Q744X	TET2	-0.035	0.002	-0.115	0.042	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.69	-4.29	0.046
PD41093	BRCC3nt-L153P	BRCC3	0.007	0.002	-0.094	0.093	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-10.33	-3.69	0.047
PD34540	SF3B1-G742D	SF3B1	0.025	0.002	-0.070	0.119	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-9.95	-5.64	0.140
PD34540	TET2t-N1328fs	TET2	-0.007	0.001	-0.077	0.068	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.03	-3.36	0.074
PD34506	TP53nt-R273L	TP53	-0.048	0.002	-0.130	0.042	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-5.86	-2.60	0.001
PD41275	DNMT3At-NM_175629:exon14:c.1555-1G>T	DNMT3A	0.003	0.002	-0.077	0.085	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.89	-3.96	0.055
PD41275	TET2nt-I1873T	TET2	-0.005	0.001	-0.075	0.072	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-7.37	-4.60	0.097
PD41157	TET2t-Q649X	TET2	0.005	0.001	-0.057	0.071	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.51	-3.42	0.086
PD41127	TET2nt-A1876V	TET2	-0.014	0.002	-0.093	0.071	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.02	-4.17	0.084
PD41127	TET2nt-I1873T	TET2	0.000	0.002	-0.074	0.081	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-8.78	-4.02	0.102
PD41117	TET2nt-A394T	TET2	0.014	0.002	-0.080	0.105	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-11.52	-5.98	0.111
PD41117	TET2nt-I1873T	TET2	0.186	0.001	0.117	0.255	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-12.02	-8.25	0.288
PD41117	TET2nt-R1366H	TET2	-0.037	0.001	-0.083	0.011	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.13	-2.65	0.061
PD41118	BRCC3t-NM_001018055:exon2:c.140+1G>A	BRCC3	0.054	0.002	-0.025	0.141	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-9.46	-4.93	0.111
PD41118	DNMT3Ant-K367N	DNMT3A	-0.046	0.001	-0.118	0.023	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.97	-1.76	-0.008
PD41118	DNMT3At-NM_175629:exon12:c.1430-1G>-	DNMT3A	0.011	0.002	-0.078	0.086	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.30	-4.27	0.063

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41118	DNMT3At-P385fs	DNMT3A	-0.036	0.000	-0.073	0.001	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-2.35	-0.87	0.016
PD41118	TET2t-K188fs	TET2	-0.055	0.001	-0.124	0.009	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.53	-2.49	0.026
PD41118	TET2t-Q185fs	TET2	-0.047	0.001	-0.121	0.019	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.90	-2.69	0.033
PD41177	DNMT3Ant-S770L	DNMT3A	-0.006	0.001	-0.073	0.072	0.038	0.000	0.021	0.055	0.054	0.001	-0.012	0.120	0.092	0.001	0.038	0.145	-5.55	-2.83	0.085
PD41177	DNMT3At-Q515X	DNMT3A	0.019	0.002	-0.070	0.100	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.41	-3.79	0.071
PD41308	DNMT3Ant-R635Q	DNMT3A	-0.017	0.002	-0.101	0.067	0.038	0.000	0.021	0.055	-0.026	0.002	-0.100	0.057	0.012	0.002	-0.053	0.078	-5.26	-3.32	-0.006
PD34531	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	-0.069	0.002	-0.149	0.012	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-9.61	-3.58	0.074
PD34531	DNMT3At-NM_175629:exon18:c.2173+1G>A	DNMT3A	0.004	0.000	-0.029	0.041	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.21	-1.13	0.056
PD34531	PPM1D-Q524X	PPM1D	-0.070	0.001	-0.124	-0.015	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-5.33	-1.93	0.024
PD41145	TET2t-R550X	TET2	-0.050	0.002	-0.132	0.046	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.28	-4.33	0.031
PD41171	ASXL1-P808fs	ASXL1	0.047	0.002	-0.049	0.120	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-10.07	-6.12	0.144
PD34554	CTCFnt-S461P	CTCF	0.024	0.002	-0.071	0.115	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-10.72	-4.42	0.087
PD34554	DNMT3At-F734fs	DNMT3A	-0.002	0.002	-0.093	0.092	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.52	-3.33	0.050
PD34554	DNMT3At-W860X	DNMT3A	-0.010	0.002	-0.104	0.084	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.78	-3.40	0.042
PD34554	TET2nt-TET2:NM_001127208:exon7:c.3852_3854del:p.1284_1285del	TET2	0.009	0.001	-0.060	0.090	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.32	-3.22	0.106
PD34554	TET2t-G1313fs	TET2	0.031	0.001	-0.034	0.097	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.76	-4.13	0.112
PD34554	TET2t-H650fs	TET2	-0.075	0.001	-0.129	-0.014	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-3.77	-0.75	0.006
PD41143	DNMT3Ant-I705T	DNMT3A	0.018	0.002	-0.070	0.105	0.038	0.000	0.021	0.055	0.019	0.002	-0.061	0.095	0.057	0.002	-0.007	0.122	-8.07	-3.56	0.075
PD41143	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	0.024	0.001	-0.040	0.095	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.21	-3.00	0.076
PD41143	TET2t-C1271fs	TET2	-0.043	0.002	-0.128	0.035	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.46	-2.61	0.038
PD41132	GNB1-K57E	GNB1	-0.038	0.002	-0.112	0.039	0.101	0.001	0.032	0.175	-0.014	0.002	-0.100	0.084	0.087	0.001	0.032	0.144	-6.98	-3.87	0.050
PD41132	TET2t-K1533X	TET2	-0.021	0.002	-0.101	0.062	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.45	-4.27	0.060
PD41084	JAK2-V617F	JAK2	-0.005	0.001	-0.071	0.060	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-9.05	-5.17	0.133
PD41124	TET2t-C1271X	TET2	-0.003	0.002	-0.088	0.070	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.26	-5.39	0.078
PD41124	TET2t-K944X	TET2	-0.001	0.002	-0.084	0.074	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.19	-4.72	0.080
PD41124	TET2t-Q317X	TET2	-0.034	0.001	-0.114	0.034	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.40	-3.16	0.047
PD41124	TP53nt-R181P	TP53	-0.013	0.002	-0.092	0.062	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-7.48	-3.26	0.036
PD41194	DNMT3Ant-I769V	DNMT3A	-0.024	0.002	-0.106	0.051	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.66	-2.62	0.014
PD41194	SF3B1-R549H	SF3B1	0.034	0.002	-0.058	0.120	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-11.75	-6.42	0.150

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41194	TET2t-Q618fs	TET2	0.131	0.001	0.083	0.181	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.58	-6.04	0.212
PD41194	TP53nt-R282W	TP53	-0.002	0.002	-0.092	0.087	0.049	0.000	0.013	0.087	-0.027	0.003	-0.145	0.078	0.023	0.003	-0.065	0.112	-7.86	-2.36	0.020
PD41128	DNMT3Ant-L647R	DNMT3A	0.041	0.002	-0.042	0.125	0.038	0.000	0.021	0.055	-0.005	0.002	-0.104	0.081	0.032	0.002	-0.046	0.110	-6.73	-1.55	0.073
PD41128	TET2nt-R1261C	TET2	-0.022	0.002	-0.115	0.061	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.30	-3.39	0.076
PD34547	CTCFnt-H425R	CTCF	0.015	0.002	-0.079	0.102	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-12.83	-5.25	0.078
PD34547	DNMT3Ant-G726D	DNMT3A	-0.018	0.002	-0.104	0.069	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.65	-2.64	0.020
PD34547	DNMT3Ant-S638F	DNMT3A	0.004	0.002	-0.085	0.090	0.038	0.000	0.021	0.055	0.042	0.003	-0.067	0.154	0.079	0.003	-0.010	0.171	-9.47	-3.18	0.083
PD34547	DNMT3At-NM_175629:exon22:c.2479-2A>C	DNMT3A	-0.008	0.002	-0.084	0.080	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.22	-3.45	0.044
PD41184	DNMT3Ant-A910V	DNMT3A	-0.005	0.002	-0.092	0.077	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.08	-2.08	0.033
PD41184	DNMT3Ant-P804L	DNMT3A	0.017	0.002	-0.074	0.111	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.38	-3.02	0.055
PD41184	DNMT3Ant-R659H	DNMT3A	-0.034	0.002	-0.107	0.043	0.038	0.000	0.021	0.055	-0.034	0.002	-0.119	0.043	0.004	0.002	-0.063	0.074	-3.38	-0.08	-0.030
PD41184	DNMT3At-NM_175629:exon8:c.1014+1G>A	DNMT3A	0.005	0.002	-0.072	0.086	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.79	-2.15	0.057
PD41291	JAK2-V617F	JAK2	0.179	0.001	0.119	0.240	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-12.20	-8.97	0.316
PD41291	SF3B1-K666R	SF3B1	-0.020	0.002	-0.104	0.070	0.116	0.001	0.067	0.157	-0.047	0.004	-0.177	0.082	0.069	0.004	-0.041	0.177	-9.18	-2.71	0.048
PD41291	TP53t-C124X	TP53	-0.016	0.002	-0.099	0.064	-0.056	0.002	-0.144	0.026	0.000	0.000	0.000	0.000	-0.056	0.002	-0.130	0.016	-1.96	0.00	-0.072
PD41134	TET2t-K753fs	TET2	-0.038	0.002	-0.123	0.035	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.15	-3.19	0.043
PD41293	DNMT3Ant-Y724C	DNMT3A	0.022	0.001	-0.046	0.089	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.58	-3.71	0.060
PD41293	TET2t-Q185fs	TET2	0.012	0.001	-0.061	0.079	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.08	-4.04	0.093
PD41131	TP53nt-G187S	TP53	-0.047	0.002	-0.128	0.030	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-7.05	-2.53	0.003
PD41336	PPM1D-R552X	PPM1D	0.002	0.002	-0.088	0.091	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.00	-3.52	0.095
PD41276	CBLt-W190X	CBL	0.033	0.002	-0.047	0.117	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-9.07	-5.65	0.176
PD41276	SF3B1-K666N	SF3B1	0.097	0.001	0.047	0.148	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-4.81	-3.61	0.247
PD41276	SF3B1-K700E	SF3B1	0.020	0.002	-0.070	0.102	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-8.19	-4.85	0.118
PD34570	DNMT3At-R484fs	DNMT3A	-0.008	0.003	-0.113	0.085	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.60	-3.81	0.043
PD34570	TET2t-M1028fs	TET2	-0.057	0.001	-0.123	0.009	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.93	-1.85	0.024
PD41155	DNMT3Ant-S770P	DNMT3A	0.003	0.002	-0.084	0.090	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.78	-2.82	0.041
PD41155	PTPN11-G507A	PTPN11	-0.024	0.002	-0.113	0.077	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-10.96	-5.62	0.157
PD41253	PPM1D-N477fs	PPM1D	0.029	0.001	-0.040	0.096	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.15	-5.82	0.123
PD41253	TET2t-N338fs	TET2	0.029	0.001	-0.016	0.082	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.74	-4.41	0.110
PD41254	KRAS-F78L	KRAS	-0.011	0.002	-0.098	0.076	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-9.88	-5.10	0.071
PD41136	TET2t-Q531fs	TET2	-0.071	0.001	-0.121	-0.028	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-3.37	-1.87	0.010
PD41136	TET2t-Q548X	TET2	-0.059	0.001	-0.108	-0.016	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-3.34	-1.86	0.022
PD34556	DNMT3Ant-F868L	DNMT3A	-0.037	0.001	-0.108	0.034	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.14	-1.89	0.001

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34556	DNMT3At-W860X	DNMT3A	0.042	0.002	-0.044	0.126	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-10.55	-5.19	0.094
PD34556	GNB1-L117M	GNB1	-0.003	0.002	-0.091	0.089	0.101	0.001	0.032	0.175	0.000	0.000	0.000	0.000	0.101	0.001	0.038	0.160	-12.69	-5.59	0.098
PD34556	PPM1D-E451X	PPM1D	0.030	0.002	-0.053	0.103	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-11.06	-5.97	0.123
PD34556	TET2t-N837fs	TET2	0.007	0.002	-0.078	0.088	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.87	-5.61	0.088
PD34556	TET2t-T1086fs	TET2	0.036	0.002	-0.042	0.129	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-11.17	-5.78	0.117
PD41241	DNMT3Ant-P904L	DNMT3A	-0.005	0.002	-0.088	0.081	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.01	-2.95	0.033
PD41214	IDH2-R140Q	IDH2	-0.044	0.002	-0.128	0.052	0.000	0.000	0.000	0.000	0.118	0.002	0.024	0.211	0.118	0.002	0.040	0.201	-9.73	-4.32	0.074
PD41214	TET2t-Q1834X	TET2	0.041	0.001	-0.035	0.116	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.09	-4.74	0.122
PD41237	CBLnt-L399H	CBL	0.026	0.002	-0.077	0.111	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-10.21	-4.91	0.069
PD41237	CTCFt-Y392X	CTCF	-0.029	0.002	-0.112	0.063	0.084	0.002	-0.005	0.171	0.000	0.000	0.000	0.000	0.084	0.002	0.008	0.159	-9.14	-3.29	0.054
PD41237	TET2t-Q917X	TET2	0.067	0.001	-0.001	0.139	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.29	-4.95	0.148
PD41315	DNMT3Ant-D531N	DNMT3A	0.027	0.001	-0.035	0.088	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.64	-2.78	0.064
PD41315	DNMT3Ant-R882H	DNMT3A	0.004	0.002	-0.080	0.090	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-8.13	-3.51	0.057
PD41315	TET2t-Q526fs	TET2	0.004	0.002	-0.077	0.088	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.01	-4.83	0.085
PD41148	CBLnt-R420Q	CBL	-0.007	0.002	-0.094	0.077	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-8.14	-3.23	0.037
PD41148	TET2t-L346fs	TET2	0.023	0.001	-0.053	0.098	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.52	-3.73	0.104
PD41298	TET2t-I274fs	TET2	-0.038	0.001	-0.104	0.030	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.76	-3.35	0.043
PD41294	DNMT3Ant-R379H	DNMT3A	-0.008	0.001	-0.082	0.062	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.83	-2.87	0.029
PD41294	TET2t-Q321X	TET2	-0.014	0.001	-0.070	0.055	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.33	-3.60	0.067
PD34562	ASXL1-C856fs	ASXL1	-0.018	0.002	-0.106	0.069	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.61	-3.57	0.078
PD34562	IDH1-R132H	IDH1	0.073	0.002	-0.012	0.153	0.107	0.004	-0.016	0.220	0.171	0.004	0.037	0.302	0.278	0.003	0.195	0.362	-14.41	-8.80	0.351
PD34562	PPM1D-S446X	PPM1D	-0.027	0.003	-0.117	0.078	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.85	-3.78	0.066
PD34562	SF3B1-K666R	SF3B1	0.008	0.003	-0.098	0.111	0.116	0.001	0.067	0.157	-0.047	0.004	-0.177	0.082	0.069	0.004	-0.041	0.177	-10.82	-2.66	0.077
PD34562	SRSF2-95_103del	SRSF2	0.031	0.001	-0.041	0.097	0.153	0.001	0.094	0.213	0.000	0.000	0.000	0.000	0.153	0.001	0.103	0.203	-6.68	-3.36	0.184
PD41300	ASXL1-Q491X	ASXL1	-0.046	0.000	-0.081	-0.012	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-1.89	-0.78	0.050
PD41234	KRAS-Q22L	KRAS	0.007	0.002	-0.085	0.088	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-10.00	-4.99	0.089
PD41234	TET2nt-A1863V	TET2	0.025	0.001	-0.045	0.088	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.12	-4.76	0.123
PD41297	CTCFnt-D710Y	CTCF	0.006	0.002	-0.081	0.097	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-9.30	-4.13	0.069
PD41297	TET2nt-L1418P	TET2	-0.010	0.002	-0.098	0.075	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.75	-4.45	0.088
PD41303	CTCFt-K521X	CTCF	0.020	0.003	-0.072	0.118	0.084	0.002	-0.005	0.171	0.000	0.000	0.000	0.000	0.084	0.002	0.008	0.159	-11.28	-5.65	0.104
PD41303	DNMT3Ant-L888M	DNMT3A	-0.031	0.002	-0.117	0.064	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-9.21	-4.14	0.007
PD41303	JAK2-V617F	JAK2	0.094	0.002	-0.002	0.181	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-12.18	-7.75	0.231
PD34482	SF3B1-L712F	SF3B1	-0.035	0.002	-0.134	0.055	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-11.84	-5.59	0.081
PD41325	CBLnt-C419S	CBL	0.022	0.002	-0.056	0.116	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-7.53	-3.07	0.066
PD41325	TET2t-NM_001127208:exon10:c.4183-2A>G	TET2	0.026	0.002	-0.065	0.101	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.09	-4.59	0.107

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41325	TET2t-Q321X	TET2	0.022	0.002	-0.068	0.111	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.44	-5.43	0.103
PD41326	CBLnt-Q490K	CBL	-0.002	0.003	-0.101	0.095	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-9.66	-4.00	0.042
PD41301	CBLt-NM_005188:exon15:c.2252-2A>G	CBL	0.062	0.002	-0.017	0.148	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-8.76	-5.91	0.205
PD41233	ASXL1-H630fs	ASXL1	0.055	0.000	0.016	0.093	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-3.56	-2.57	0.152
PD41233	JAK2-V617F	JAK2	-0.047	0.001	-0.113	0.014	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-5.56	-3.55	0.090
PD41233	PTPN11-N308D	PTPN11	0.185	0.001	0.112	0.256	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-9.01	-6.76	0.366
PD41233	TP53t-Q317X	TP53	-0.045	0.002	-0.126	0.039	-0.056	0.002	-0.144	0.026	0.000	0.000	0.000	0.000	-0.056	0.002	-0.130	0.016	-6.56	-2.79	-0.100
PD41233	U2AF1-R156H	U2AF1	-0.021	0.002	-0.113	0.067	0.193	0.002	0.101	0.289	0.000	0.000	0.000	0.000	0.193	0.002	0.114	0.269	-10.01	-6.08	0.173
PD41146	TET2t-E1178fs	TET2	-0.015	0.000	-0.051	0.027	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.57	-2.62	0.066
PD41146	TET2t-N374fs	TET2	0.006	0.001	-0.052	0.070	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.70	-3.47	0.087
PD41146	TET2t-Q866X	TET2	-0.022	0.002	-0.104	0.062	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.50	-3.92	0.059
PD41306	ASXL1-R860X	ASXL1	-0.032	0.002	-0.112	0.052	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.16	-3.46	0.065
PD41306	PPM1D-Q524X	PPM1D	0.012	0.002	-0.080	0.094	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-10.43	-5.33	0.105
PD41306	SF3B1-K700E	SF3B1	0.035	0.002	-0.056	0.121	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-11.03	-5.60	0.134
PD41306	TET2nt-V1417G	TET2	-0.002	0.002	-0.085	0.076	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.97	-4.48	0.096
PD41306	TET2t-R1307fs	TET2	0.024	0.002	-0.078	0.121	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-11.34	-5.88	0.105
PD41077	BRCC3nt-H127P	BRCC3	0.022	0.002	-0.060	0.114	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-8.07	-3.86	0.062
PD41077	DNMT3Ant-E477K	DNMT3A	-0.020	0.001	-0.068	0.024	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-2.17	-0.45	0.018
PD41077	DNMT3At-A462fs	DNMT3A	0.036	0.002	-0.051	0.117	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.24	-4.70	0.088
PD41311	ASXL1-L775X	ASXL1	0.048	0.001	-0.011	0.107	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-5.87	-2.90	0.145
PD41311	TP53nt-R158H	TP53	0.011	0.002	-0.081	0.116	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-10.01	-3.94	0.060
PD41140	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	-0.039	0.001	-0.089	0.011	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.24	-2.08	0.012
PD41140	PTPN11-T219N	PTPN11	0.003	0.003	-0.096	0.107	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-10.77	-6.45	0.185
PD34428	CBLnt-V430M	CBL	0.011	0.002	-0.077	0.099	0.044	0.001	-0.016	0.091	-0.021	0.004	-0.134	0.097	0.023	0.003	-0.068	0.116	-6.61	-1.69	0.033
PD34428	DNMT3Ant-R635W	DNMT3A	-0.030	0.002	-0.115	0.066	0.038	0.000	0.021	0.055	0.014	0.001	-0.052	0.079	0.051	0.001	0.000	0.104	-7.74	-2.23	0.021
PD34428	PPM1D-C407fs	PPM1D	0.019	0.002	-0.073	0.110	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-12.84	-6.51	0.113
PD41087	ASXL1-E906X	ASXL1	0.020	0.002	-0.073	0.113	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.57	-5.45	0.117
PD41087	SRSF2-P95H	SRSF2	0.120	0.002	0.042	0.204	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-13.35	-10.18	0.567
PD41087	SRSF2-P95L	SRSF2	0.030	0.002	-0.050	0.101	0.153	0.001	0.094	0.213	-0.015	0.002	-0.110	0.067	0.138	0.001	0.077	0.199	-7.28	-4.86	0.168
PD41087	SRSF2-Y44H	SRSF2	0.056	0.002	-0.026	0.134	0.153	0.001	0.094	0.213	0.000	0.000	0.000	0.000	0.153	0.001	0.103	0.203	-9.44	-6.17	0.210
PD41087	TET2t-S1015fs	TET2	-0.241	0.001	-0.294	-0.193	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-1.76	-0.44	-0.160
PD34573	DNMT3Ant-W210C	DNMT3A	0.016	0.002	-0.069	0.105	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-8.86	-3.98	0.054
PD41183	TET2t-Q745X	TET2	0.020	0.002	-0.059	0.089	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.96	-4.33	0.101
PD34559	SF3B1-A744D	SF3B1	-0.036	0.001	-0.097	0.035	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-6.66	-2.07	0.080

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34559	SF3B1-G740R	SF3B1	-0.025	0.001	-0.091	0.050	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-8.07	-3.13	0.091
PD34559	TET2nt-T1393A	TET2	0.011	0.002	-0.072	0.099	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.64	-4.47	0.109
PD34559	TET2t-C1211fs	TET2	-0.011	0.002	-0.097	0.066	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.05	-3.20	0.070
PD34523	CTCFt-NM_006565:exon4:c.782-2A>G	CTCF	0.033	0.002	-0.061	0.118	0.084	0.002	-0.005	0.171	0.000	0.000	0.000	0.000	0.084	0.002	0.008	0.159	-8.96	-3.87	0.117
PD34523	TET2nt-Q909K	TET2	-0.027	0.003	-0.127	0.076	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.58	-4.41	0.071
PD34523	TET2t-Q1537X	TET2	0.023	0.002	-0.060	0.104	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.24	-3.93	0.104
PD41159	SF3B1-K700E	SF3B1	-0.006	0.001	-0.080	0.062	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-6.08	-4.15	0.093
PD41203	TET2nt-R1359H	TET2	0.006	0.002	-0.081	0.098	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.04	-4.17	0.103
PD41203	TET2t-P413fs	TET2	0.068	0.001	-0.002	0.134	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.82	-4.33	0.149
PD41203	TET2t-S1586fs	TET2	0.000	0.003	-0.091	0.101	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.58	-4.29	0.081
PD41203	TP53nt-R282W	TP53	-0.003	0.002	-0.092	0.086	0.049	0.000	0.013	0.087	-0.027	0.003	-0.145	0.078	0.023	0.003	-0.065	0.112	-6.93	-0.88	0.020
PD34494	DNMT3At-NM_175629:exon8:c.856-1G>A	DNMT3A	-0.012	0.002	-0.104	0.077	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-10.58	-3.47	0.039
PD34494	PPM1D-K511X	PPM1D	0.008	0.001	-0.059	0.074	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-8.03	-3.49	0.102
PD34494	TET2nt-E1178G	TET2	-0.061	0.001	-0.134	0.010	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.68	-1.54	0.037
PD41150	DNMT3Ant-I780T	DNMT3A	-0.002	0.002	-0.105	0.093	0.038	0.000	0.021	0.055	0.046	0.003	-0.065	0.169	0.084	0.003	-0.007	0.183	-9.57	-2.72	0.082
PD41150	DNMT3Ant-L754H	DNMT3A	-0.001	0.002	-0.082	0.085	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.24	-2.92	0.036
PD41150	TET2t-N281fs	TET2	-0.005	0.002	-0.095	0.081	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.10	-4.15	0.076
PD41320	BRCC3nt-M142I	BRCC3	-0.021	0.002	-0.101	0.059	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-6.07	-3.18	0.019
PD41151	DNMT3Ant-F732L	DNMT3A	0.044	0.001	-0.018	0.105	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.95	-1.94	0.082
PD41151	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	-0.019	0.002	-0.119	0.069	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.68	-2.70	0.033
PD41151	TET2t-H193fs	TET2	-0.021	0.002	-0.105	0.068	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.12	-3.38	0.060
PD41151	TET2t-K1488fs	TET2	-0.009	0.002	-0.104	0.078	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.58	-3.70	0.072
PD41151	TET2t-Q831fs	TET2	-0.005	0.002	-0.088	0.069	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.55	-3.53	0.076
PD34509	TET2t-I1230fs	TET2	-0.029	0.001	-0.089	0.047	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.16	-2.32	0.052
PD41339	GNB1-C103F	GNB1	-0.006	0.002	-0.092	0.077	0.101	0.001	0.032	0.175	0.000	0.000	0.000	0.000	0.101	0.001	0.038	0.160	-10.86	-5.09	0.094
PD41339	TET2t-Q1507fs	TET2	-0.010	0.001	-0.055	0.037	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.77	-2.58	0.071
PD41339	TP53nt-N239S	TP53	0.035	0.002	-0.049	0.115	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-8.51	-4.19	0.084
PD41166	DNMT3Ant-Y660C	DNMT3A	0.009	0.002	-0.065	0.085	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.77	-2.82	0.047
PD41166	TET2nt-M1333R	TET2	0.011	0.002	-0.068	0.085	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.01	-4.95	0.109
PD41313	SF3B1-A744P	SF3B1	-0.017	0.002	-0.104	0.072	0.116	0.001	0.067	0.157	-0.043	0.003	-0.150	0.053	0.073	0.003	-0.010	0.155	-8.02	-2.91	0.056
PD41260	ASXL1-H630fs	ASXL1	0.024	0.001	-0.022	0.077	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-5.76	-3.77	0.121
PD41260	DNMT3Ant-R736C	DNMT3A	-0.035	0.002	-0.110	0.042	0.038	0.000	0.021	0.055	0.032	0.002	-0.048	0.104	0.070	0.001	0.007	0.132	-5.90	-2.83	0.035
PD34565	TET2nt-L1311Q	TET2	-0.036	0.001	-0.102	0.033	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.65	-3.59	0.062

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34565	TET2nt-S817F	TET2	0.008	0.002	-0.074	0.077	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.35	-4.85	0.105
PD41197	DNMT3Ant-R771Q	DNMT3A	-0.006	0.002	-0.081	0.081	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.74	-3.02	0.031
PD41197	DNMT3Ant-Y735C	DNMT3A	-0.008	0.001	-0.072	0.067	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.49	-2.58	0.029
PD41197	DNMT3At-E469X	DNMT3A	0.044	0.001	-0.018	0.104	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.28	-3.75	0.096
PD34513	DNMT3At-R887X	DNMT3A	-0.030	0.002	-0.113	0.057	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.82	-3.06	0.022
PD41174	TP53nt-R248W	TP53	0.030	0.002	-0.060	0.121	0.049	0.000	0.013	0.087	0.019	0.004	-0.097	0.136	0.068	0.003	-0.029	0.166	-8.37	-4.40	0.098
PD41324	CBLnt-V430M	CBL	-0.014	0.002	-0.109	0.076	0.044	0.001	-0.016	0.091	-0.021	0.004	-0.134	0.097	0.023	0.003	-0.068	0.116	-7.77	-1.58	0.008
PD41081	DNMT3At-Q696fs	DNMT3A	0.003	0.002	-0.081	0.074	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.30	-3.93	0.054
PD41081	TP53nt-R273H	TP53	-0.001	0.002	-0.081	0.089	0.049	0.000	0.013	0.087	0.049	0.003	-0.069	0.160	0.098	0.003	0.006	0.190	-7.61	-3.98	0.097
PD41081	U2AF1-Q157P	U2AF1	-0.004	0.002	-0.086	0.082	0.193	0.002	0.101	0.289	0.063	0.004	-0.052	0.188	0.256	0.003	0.175	0.343	-11.22	-6.94	0.253
PD41295	DNMT3At-NM_175629:exon22:c.2597+1G>A	DNMT3A	-0.015	0.001	-0.080	0.056	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.99	-2.63	0.037
PD41330	DNMT3Ant-D702V	DNMT3A	-0.027	0.002	-0.106	0.055	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.79	-2.62	0.011
PD41330	TET2t-Q1501X	TET2	0.006	0.002	-0.080	0.088	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.90	-4.46	0.087
PD41274	ASXL1-L1266fs	ASXL1	-0.063	0.002	-0.147	0.017	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-6.89	-3.82	0.034
PD41244	DNMT3Ant-D702G	DNMT3A	0.017	0.002	-0.071	0.096	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.86	-3.22	0.055
PD41244	DNMT3Ant-R882H	DNMT3A	-0.016	0.002	-0.104	0.068	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-7.13	-2.52	0.038
PD41244	DNMT3Ant-Y660H	DNMT3A	-0.006	0.002	-0.091	0.079	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.20	-2.45	0.032
PD41244	DNMT3At-K589X	DNMT3A	-0.010	0.002	-0.100	0.077	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.89	-2.79	0.041
PD41244	DNMT3At-P777fs	DNMT3A	0.005	0.001	-0.061	0.078	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.71	-2.66	0.057
PD41285	DNMT3At-E856fs	DNMT3A	0.068	0.001	0.013	0.126	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.90	-4.03	0.119
PD41285	DNMT3At-NM_175629:exon9:c.1122+1G>-	DNMT3A	-0.010	0.001	-0.084	0.060	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.03	-4.45	0.041
PD41285	SF3B1-K700E	SF3B1	-0.020	0.002	-0.099	0.062	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-7.99	-4.76	0.079
PD41285	TET2nt-P288R	TET2	-0.021	0.002	-0.098	0.063	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.72	-3.94	0.076
PD41286	DNMT3Ant-L653F	DNMT3A	0.042	0.001	-0.003	0.088	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.00	-2.66	0.080
PD41286	DNMT3At-Q415X	DNMT3A	-0.005	0.001	-0.058	0.048	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.26	-2.67	0.047
PD41161	BRCC3t-H127fs	BRCC3	-0.003	0.002	-0.082	0.080	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-9.14	-4.08	0.055
PD41161	DNMT3At-W330X	DNMT3A	0.011	0.001	-0.057	0.076	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.67	-2.34	0.063
PD41161	SRSF2-P95H	SRSF2	-0.028	0.002	-0.129	0.064	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-19.62	-12.35	0.419
PD41161	TET2t-P1410fs	TET2	0.011	0.002	-0.067	0.088	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.17	-5.07	0.092
PD41161	TET2t-P1644fs	TET2	0.001	0.001	-0.071	0.076	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.29	-4.39	0.082
PD41161	TET2t-S1039X	TET2	0.016	0.002	-0.063	0.094	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.20	-4.98	0.097
PD41344	ASXL1-Q546X	ASXL1	-0.070	0.001	-0.142	0.003	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-5.91	-2.70	0.026
PD41344	PPM1D-L538fs	PPM1D	0.026	0.001	-0.043	0.101	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.08	-5.80	0.120
PD41344	PPM1D-R458X	PPM1D	0.022	0.002	-0.053	0.104	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.58	-5.74	0.115

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41344	PPM1D-T483fs	PPM1D	0.124	0.002	0.050	0.206	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-10.43	-6.96	0.218
PD41344	TET2nt-H1380D	TET2	-0.008	0.001	-0.079	0.073	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.86	-4.55	0.090
PD41344	TP53nt-I195T	TP53	0.016	0.002	-0.071	0.114	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-8.41	-4.54	0.065
PD41154	DNMT3At-L723fs	DNMT3A	-0.050	0.002	-0.129	0.034	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.35	-3.43	0.002
PD41154	SRSF2-P95A	SRSF2	0.017	0.002	-0.067	0.108	0.153	0.001	0.094	0.213	-0.046	0.003	-0.164	0.059	0.107	0.003	0.019	0.196	-6.60	-3.82	0.124
PD34558	ASXL1-Q1063fs	ASXL1	-0.057	0.001	-0.118	0.005	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-6.45	-3.04	0.040
PD34558	SF3B1-K666N	SF3B1	-0.017	0.002	-0.104	0.071	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-11.67	-6.40	0.133
PD41190	ASXL1-NM_015338:exon12:c.1720-2A>C	ASXL1	0.055	0.001	0.011	0.095	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-4.29	-2.79	0.152
PD41190	CBLt-P433fs	CBL	0.012	0.002	-0.075	0.096	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-10.53	-6.13	0.155
PD41190	TET2nt-H1881R	TET2	-0.038	0.002	-0.120	0.042	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.21	-3.65	0.060
PD41190	TET2nt-T1372I	TET2	0.072	0.000	0.028	0.112	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-4.44	-3.01	0.170
PD41278	DNMT3Ant-W860R	DNMT3A	-0.018	0.001	-0.092	0.051	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.97	-3.59	0.020
PD41278	PPM1D-C478X	PPM1D	0.026	0.002	-0.049	0.107	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-8.04	-5.28	0.120
PD41156	SF3B1-K666M	SF3B1	0.135	0.002	0.054	0.217	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-11.86	-7.53	0.251
PD34486	KRAS-T58I	KRAS	-0.004	0.002	-0.091	0.072	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-7.68	-3.31	0.078
PD41162	TET2nt-T97K	TET2	-0.035	0.003	-0.144	0.069	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.93	-4.93	0.063
PD34517	DNMT3Ant-S770L	DNMT3A	-0.015	0.002	-0.104	0.061	0.038	0.000	0.021	0.055	0.054	0.001	-0.012	0.120	0.092	0.001	0.038	0.145	-6.68	-3.13	0.076
PD34517	DNMT3At-E427fs	DNMT3A	-0.027	0.002	-0.109	0.050	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.11	-3.02	0.025
PD34517	DNMT3At-Y370X	DNMT3A	-0.017	0.001	-0.076	0.048	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.33	-2.13	0.035
PD34517	KRAS-G12C	KRAS	0.015	0.002	-0.074	0.111	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-11.77	-5.92	0.097
PD34517	TP53nt-L336V	TP53	-0.017	0.002	-0.107	0.080	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-7.69	-3.52	0.032
PD34578	DNMT3At-E21fs	DNMT3A	0.032	0.002	-0.049	0.117	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.42	-4.15	0.083
PD34578	PPM1D-S403fs	PPM1D	-0.034	0.002	-0.117	0.055	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-6.80	-3.30	0.059
PD41257	KRAS-I84T	KRAS	0.033	0.001	-0.038	0.114	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-7.13	-4.32	0.116
PD34551	PPM1D-R581X	PPM1D	-0.035	0.002	-0.123	0.057	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-6.54	-3.18	0.059
PD41085	DNMT3Ant-F732S	DNMT3A	0.014	0.002	-0.070	0.082	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.79	-4.07	0.052
PD41088	CBLnt-R149Q	CBL	0.016	0.002	-0.073	0.101	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-10.22	-2.30	0.060
PD41088	TP53nt-V272M	TP53	-0.027	0.002	-0.120	0.056	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-9.08	-1.01	0.022
PD41169	TET2t-Q1542X	TET2	0.006	0.002	-0.080	0.094	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.76	-4.31	0.087
PD41169	U2AF1-Q157R	U2AF1	0.010	0.002	-0.084	0.096	0.193	0.002	0.101	0.289	0.154	0.004	0.036	0.285	0.348	0.003	0.260	0.435	-17.23	-10.04	0.357
PD41219	PPM1D-E476X	PPM1D	0.006	0.002	-0.078	0.088	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.90	-5.30	0.100
PD41164	DNMT3Ant-A410T	DNMT3A	-0.013	0.002	-0.100	0.079	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.42	-2.69	0.024
PD41164	DNMT3At-A525fs	DNMT3A	0.012	0.002	-0.067	0.084	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.03	-3.77	0.063
PD34538	ASXL1-R1171fs	ASXL1	-0.021	0.002	-0.097	0.062	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-9.31	-4.49	0.075
PD34538	PPM1D-R572X	PPM1D	-0.015	0.001	-0.090	0.055	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-8.54	-4.23	0.078
PD34538	SF3B1-H662Q	SF3B1	-0.036	0.002	-0.125	0.045	0.116	0.001	0.067	0.157	0.027	0.003	-0.075	0.124	0.142	0.002	0.062	0.224	-10.06	-4.36	0.106

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41165	DNMT3Ant-I705T	DNMT3A	-0.001	0.002	-0.083	0.093	0.038	0.000	0.021	0.055	0.019	0.002	-0.061	0.095	0.057	0.002	-0.007	0.122	-9.35	-3.38	0.056
PD41165	DNMT3At-Q249X	DNMT3A	-0.026	0.002	-0.110	0.050	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.38	-2.55	0.025
PD41165	TET2nt-R1359S	TET2	0.048	0.001	-0.025	0.125	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.88	-6.31	0.146
PD41165	TET2t-F681fs	TET2	-0.035	0.001	-0.103	0.040	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.43	-3.20	0.046
PD41165	TET2t-V1054fs	TET2	-0.009	0.002	-0.093	0.063	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.61	-4.91	0.072
PD41165	TP53nt-M237V	TP53	-0.022	0.002	-0.108	0.067	0.049	0.000	0.013	0.087	0.078	0.003	-0.034	0.183	0.128	0.003	0.042	0.217	-11.22	-4.39	0.105
PD41236	TET2t-L1916fs	TET2	-0.034	0.001	-0.105	0.043	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.72	-3.67	0.047
PD34548	DNMT3Ant-F331V	DNMT3A	0.025	0.002	-0.051	0.115	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-8.28	-3.60	0.063
PD34548	TET2t-K1254fs	TET2	-0.001	0.002	-0.088	0.084	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.02	-4.22	0.080
PD41334	DNMT3Ant-R635W	DNMT3A	-0.005	0.002	-0.083	0.075	0.038	0.000	0.021	0.055	0.014	0.001	-0.052	0.079	0.051	0.001	0.000	0.104	-6.32	-2.89	0.046
PD41334	GNB1-D118H	GNB1	0.023	0.001	-0.049	0.093	0.101	0.001	0.032	0.175	0.000	0.000	0.000	0.000	0.101	0.001	0.038	0.160	-4.13	-2.47	0.124
PD41316	ASXL1-S958X	ASXL1	-0.027	0.002	-0.112	0.061	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-9.55	-5.08	0.070
PD41316	TET2t-K1720X	TET2	0.019	0.002	-0.072	0.108	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.52	-5.30	0.100
PD41316	TET2t-S1369X	TET2	-0.017	0.001	-0.086	0.054	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.48	-3.40	0.064
PD34539	TET2t-Q1553fs	TET2	0.040	0.001	-0.032	0.104	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.44	-5.24	0.121
PD41092	JAK2-V617F	JAK2	0.096	0.001	0.036	0.151	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-5.58	-3.93	0.234
PD41323	TET2t-Q821X	TET2	-0.047	0.002	-0.124	0.032	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.42	-4.06	0.034
PD34576	SF3B1-K666N	SF3B1	-0.025	0.001	-0.099	0.054	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-7.72	-4.26	0.124
PD34576	TET2t-Q1687X	TET2	-0.004	0.002	-0.097	0.079	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.03	-4.09	0.077
PD34515	DNMT3At-NM_175629:exon18:c.2083-2A>G	DNMT3A	0.000	0.002	-0.090	0.093	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.25	-2.61	0.051
PD34525	DNMT3At-V441fs	DNMT3A	-0.002	0.002	-0.078	0.082	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.05	-3.38	0.050
PD41529	CTCFnt-E520D	CTCF	0.011	0.002	-0.090	0.095	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-9.38	-3.89	0.073
PD41529	GNB1-K57E	GNB1	0.019	0.002	-0.072	0.104	0.101	0.001	0.032	0.175	-0.014	0.002	-0.100	0.084	0.087	0.001	0.032	0.144	-8.74	-3.76	0.106
PD41529	PTPN11-T472M	PTPN11	-0.025	0.002	-0.117	0.062	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-9.97	-4.64	0.156
PD41529	TET2t-Q778X	TET2	-0.027	0.002	-0.121	0.071	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.33	-3.29	0.054
PD34566	PTPN11-P495L	PTPN11	-0.012	0.002	-0.095	0.085	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-10.98	-6.19	0.169
PD34566	TET2nt-G1288V	TET2	0.005	0.002	-0.090	0.094	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.43	-5.02	0.103
PD34566	TET2nt-H1416R	TET2	-0.039	0.002	-0.115	0.040	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.99	-3.44	0.059
PD34566	TP53nt-R175H	TP53	-0.048	0.002	-0.135	0.033	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-7.46	-3.25	0.001
PD41106	ASXL1-Q1294fs	ASXL1	0.029	0.001	-0.047	0.100	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-9.50	-5.86	0.125
PD41106	DNMT3Ant-G843D	DNMT3A	0.005	0.000	-0.036	0.049	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-3.70	-2.02	0.043
PD41106	DNMT3Ant-L637Q	DNMT3A	0.011	0.002	-0.066	0.088	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.61	-4.13	0.049
PD41106	DNMT3Ant-Y908C	DNMT3A	0.043	0.001	-0.035	0.112	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.25	-4.06	0.081
PD41106	TET2nt-Q1414E	TET2	0.043	0.001	-0.031	0.118	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.73	-5.34	0.140
PD41321	DNMT3Ant-F752V	DNMT3A	0.008	0.001	-0.067	0.082	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.95	-4.05	0.045
PD41321	TET2nt-A1341E	TET2	-0.044	0.001	-0.113	0.032	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.39	-2.73	0.054

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41321	TET2t-Q1537X	TET2	0.021	0.001	-0.055	0.092	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.89	-4.04	0.102
PD41080	TET2nt-H1868Y	TET2	-0.061	0.001	-0.113	-0.002	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-4.20	-2.57	0.037
PD41080	TET2t-G422fs	TET2	-0.034	0.001	-0.096	0.022	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.22	-3.34	0.047
PD41080	TET2t-Q232X	TET2	-0.025	0.002	-0.120	0.052	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.00	-4.17	0.056
PD41080	TP53nt-C176F	TP53	-0.034	0.001	-0.106	0.038	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-5.44	-3.06	0.015
PD34495	BRCC3nt-R83C	BRCC3	0.001	0.001	-0.071	0.072	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-4.22	-0.11	0.041
PD34495	PPM1D-P531fs	PPM1D	-0.007	0.002	-0.093	0.088	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-10.16	-3.37	0.086
PD34495	TET2t-I1105fs	TET2	-0.023	0.002	-0.117	0.070	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.57	-2.77	0.058
PD41119	DNMT3Ant-D768G	DNMT3A	-0.023	0.002	-0.102	0.054	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.27	-2.95	0.015
PD41255	ASXL1-Q396X	ASXL1	0.000	0.001	-0.053	0.047	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-4.47	-2.77	0.096
PD34489	ASXL1-S852X	ASXL1	-0.070	0.001	-0.114	-0.017	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-3.95	-0.10	0.027
PD34489	CBLnt-R420G	CBL	0.026	0.002	-0.069	0.114	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-11.52	-2.86	0.070
PD34489	TET2t-A1769fs	TET2	-0.021	0.002	-0.109	0.057	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.23	-2.57	0.060
PD34489	TET2t-Q461fs	TET2	0.012	0.002	-0.075	0.106	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-13.63	-5.26	0.093
PD42295	TP53nt-R273H	TP53	0.012	0.002	-0.086	0.104	0.049	0.000	0.013	0.087	0.049	0.003	-0.069	0.160	0.098	0.003	0.006	0.190	-11.02	-4.14	0.110
PD34500	PPM1D-W427X	PPM1D	0.010	0.002	-0.077	0.098	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-10.01	-3.83	0.104
PD34545	DNMT3At-E294X	DNMT3A	-0.006	0.002	-0.097	0.078	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.75	-2.68	0.046
PD34545	DNMT3At-NM_175629:exon15:c.1851+1G>A	DNMT3A	0.013	0.001	-0.060	0.078	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.84	-2.00	0.065
PD34545	TET2nt-S1898F	TET2	0.003	0.002	-0.089	0.100	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.08	-4.39	0.101
PD34545	TET2nt-T1399P	TET2	-0.014	0.002	-0.101	0.070	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.17	-3.87	0.084
PD34545	TET2t-Q1523X	TET2	-0.008	0.002	-0.088	0.072	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.53	-2.83	0.072
PD41238	SF3B1-K700E	SF3B1	0.008	0.002	-0.099	0.094	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-9.72	-4.33	0.107
PD41238	TP53nt-V272G	TP53	0.004	0.002	-0.088	0.096	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-8.18	-3.28	0.053
PD41322	TET2t-S1059X	TET2	0.036	0.002	-0.066	0.113	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.35	-4.61	0.117
PD41266	TET2nt-S1290L	TET2	0.056	0.002	-0.028	0.147	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.42	-5.73	0.154
PD41266	TET2t-E808X	TET2	0.000	0.002	-0.074	0.077	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.20	-4.99	0.081
PD41266	TET2t-L1819X	TET2	-0.042	0.001	-0.105	0.024	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.45	-2.92	0.039
PD41266	TET2t-Y1766X	TET2	0.030	0.002	-0.051	0.108	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.14	-5.85	0.111
PD34541	BRCC3nt-C157R	BRCC3	-0.001	0.002	-0.089	0.088	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-11.65	-5.16	0.039
PD34541	DNMT3At-W330X	DNMT3A	0.003	0.002	-0.076	0.078	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.20	-3.88	0.055
PD34541	TET2nt-D1981N	TET2	-0.054	0.002	-0.136	0.034	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.44	-4.16	0.044
PD34541	TET2nt-P1367L	TET2	-0.021	0.002	-0.102	0.055	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.99	-4.30	0.076
PD34541	TET2t-L1740X	TET2	-0.057	0.002	-0.143	0.031	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.75	-3.60	0.024
PD41083	DNMT3At-W330X	DNMT3A	0.034	0.002	-0.051	0.113	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-9.51	-4.62	0.085
PD41083	TET2t-Q618X	TET2	-0.043	0.002	-0.129	0.032	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.58	-3.56	0.038

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34481	SF3B1-K666N	SF3B1	0.048	0.002	-0.022	0.129	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-10.76	-6.39	0.197
PD41193	CBLt-NM_005188:exon9:c.1228-1G>A	CBL	0.064	0.002	-0.021	0.146	0.143	0.001	0.082	0.208	0.000	0.000	0.000	0.000	0.143	0.001	0.088	0.197	-8.93	-5.38	0.207
PD41193	IDH2-R140Q	IDH2	0.063	0.002	-0.015	0.157	0.000	0.000	0.000	0.000	0.118	0.002	0.024	0.211	0.118	0.002	0.040	0.201	-6.71	-4.40	0.181
PD41193	TET2nt-I1873T	TET2	-0.112	0.001	-0.173	-0.051	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-2.36	-0.87	-0.010
PD41101	TET2t-Q1068X	TET2	0.026	0.001	-0.033	0.088	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.91	-4.54	0.107
PD41178	ASXL1-R693X	ASXL1	0.014	0.001	-0.056	0.083	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-7.88	-4.49	0.110
PD41178	PPM1D-L484fs	PPM1D	-0.015	0.001	-0.064	0.028	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-4.05	-2.29	0.078
PD41230	ASXL1-S993fs	ASXL1	0.004	0.002	-0.090	0.087	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-9.29	-5.41	0.101
PD41230	BRCC3t-C240X	BRCC3	0.046	0.002	-0.049	0.138	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-9.73	-4.97	0.103
PD41230	CBLnt-C404Y	CBL	0.008	0.002	-0.076	0.083	0.044	0.001	-0.016	0.091	-0.020	0.002	-0.108	0.066	0.023	0.002	-0.047	0.092	-5.21	-2.49	0.031
PD34502	DNMT3Ant-V830A	DNMT3A	0.004	0.001	-0.056	0.060	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-4.88	-2.29	0.042
PD34502	TET2nt-R1878P	TET2	-0.010	0.002	-0.094	0.069	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.56	-4.44	0.087
PD34502	TET2t-K1049fs	TET2	-0.040	0.002	-0.129	0.058	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.20	-3.35	0.041
PD34502	TP53nt-Y220C	TP53	-0.005	0.002	-0.091	0.092	0.049	0.000	0.013	0.087	0.011	0.004	-0.111	0.117	0.060	0.003	-0.033	0.153	-9.42	-3.51	0.055
PD41202	SF3B1-A604T	SF3B1	-0.017	0.002	-0.118	0.074	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-12.39	-5.58	0.099
PD41202	SF3B1-K666N	SF3B1	-0.030	0.002	-0.131	0.061	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-11.23	-5.82	0.120
PD41079	BRCC3t-W286X	BRCC3	-0.043	0.001	-0.123	0.026	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-5.29	-0.68	0.014
PD41079	DNMT3Ant-F755S	DNMT3A	-0.013	0.002	-0.098	0.077	0.038	0.000	0.021	0.055	0.007	0.003	-0.092	0.116	0.045	0.003	-0.041	0.135	-9.38	-1.77	0.032
PD41079	DNMT3At-NM_175629:exon14:c.1667+1G>A	DNMT3A	0.017	0.002	-0.070	0.118	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-9.75	-3.94	0.069
PD34568	CTCFnt-T204I	CTCF	0.013	0.002	-0.075	0.094	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-8.82	-4.50	0.076
PD41337	BRCC3nt-S156P	BRCC3	0.038	0.001	-0.033	0.110	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-5.77	-3.66	0.078
PD41337	DNMT3Ant-M779T	DNMT3A	0.025	0.001	-0.042	0.098	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.61	-3.35	0.063
PD41338	DNMT3Ant-G722D	DNMT3A	-0.011	0.002	-0.100	0.071	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.55	-3.44	0.026
PD41338	TET2nt-H1380Y	TET2	-0.045	0.002	-0.120	0.035	0.098	0.000	0.078	0.116	-0.053	0.001	-0.122	0.020	0.045	0.001	-0.010	0.109	-4.95	-2.40	0.000
PD41338	TP53nt-G244S	TP53	0.037	0.002	-0.036	0.120	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-6.67	-3.99	0.086
PD41078	DNMT3Ant-R635Q	DNMT3A	0.010	0.001	-0.066	0.084	0.038	0.000	0.021	0.055	-0.026	0.002	-0.100	0.057	0.012	0.002	-0.053	0.078	-1.75	-0.72	0.021
PD41078	TET2nt-G1275E	TET2	-0.061	0.001	-0.133	0.012	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.81	-3.17	0.037
PD41078	TP53nt-C242F	TP53	0.014	0.001	-0.050	0.089	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-6.49	-4.00	0.064
PD41340	TET2nt-R1214W	TET2	0.000	0.001	-0.070	0.076	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.83	-3.83	0.098
PD41199	BRCC3nt-L308P	BRCC3	-0.019	0.001	-0.088	0.059	0.040	0.001	-0.023	0.099	0.000	0.000	0.000	0.000	0.040	0.001	-0.012	0.092	-5.85	-2.07	0.021
PD41199	DNMT3Ant-L647R	DNMT3A	-0.044	0.002	-0.134	0.037	0.038	0.000	0.021	0.055	-0.005	0.002	-0.104	0.081	0.032	0.002	-0.046	0.110	-7.41	-1.64	-0.011
PD41530	TET2nt-C1211Y	TET2	0.046	0.002	-0.035	0.126	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.51	-3.68	0.144
PD41530	TET2nt-P1194R	TET2	0.002	0.003	-0.096	0.096	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.93	-4.08	0.099
PD41530	TET2t-E1477fs	TET2	0.001	0.002	-0.073	0.082	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.67	-2.89	0.082

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41530	TET2t-I1859fs	TET2	0.013	0.002	-0.074	0.104	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.81	-4.40	0.094
PD41341	ASXL1-K1437fs	ASXL1	0.056	0.002	-0.017	0.138	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.95	-5.59	0.152
PD41341	DNMT3Ant-G699D	DNMT3A	-0.009	0.002	-0.102	0.080	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.73	-3.57	0.028
PD41341	DNMT3Ant-I310N	DNMT3A	-0.014	0.001	-0.087	0.061	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.57	-3.35	0.024
PD41341	DNMT3At-C351fs	DNMT3A	0.015	0.001	-0.061	0.089	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.17	-3.88	0.066
PD41341	DNMT3At-NM_175629:exon22:c.2597+2T>G	DNMT3A	-0.035	0.001	-0.112	0.038	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.75	-3.43	0.016
PD41341	SF3B1-K700E	SF3B1	-0.030	0.002	-0.104	0.046	0.116	0.001	0.067	0.157	-0.017	0.001	-0.082	0.054	0.099	0.001	0.050	0.147	-7.41	-3.67	0.069
PD41341	TET2t-L1511X	TET2	-0.013	0.001	-0.072	0.049	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.95	-3.27	0.068
PD41341	TET2t-S56fs	TET2	0.007	0.001	-0.065	0.083	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.04	-4.76	0.088
PD34469	DNMT3Ant-V675M	DNMT3A	0.003	0.002	-0.077	0.092	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.92	-3.23	0.041
PD34469	DNMT3At-V341fs	DNMT3A	-0.009	0.002	-0.089	0.079	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.64	-2.99	0.043
PD34469	SF3B1-K666T	SF3B1	0.064	0.002	-0.033	0.150	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-9.36	-5.31	0.180
PD41342	DNMT3Ant-F755S	DNMT3A	0.031	0.002	-0.049	0.124	0.038	0.000	0.021	0.055	0.007	0.003	-0.092	0.116	0.045	0.003	-0.041	0.135	-6.34	-3.88	0.076
PD34493	SF3B1-K666N	SF3B1	-0.052	0.001	-0.109	0.001	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-5.43	-3.31	0.098
PD34493	U2AF1-Q157R	U2AF1	0.035	0.002	-0.055	0.123	0.193	0.002	0.101	0.289	0.154	0.004	0.036	0.285	0.348	0.003	0.260	0.435	-14.36	-9.72	0.382
PD41343	DNMT3Ant-V778L	DNMT3A	-0.012	0.002	-0.095	0.086	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.39	-2.59	0.025
PD41267	DNMT3Ant-S75F	DNMT3A	0.016	0.003	-0.079	0.117	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-11.40	-4.84	0.054
PD41267	DNMT3At-G550fs	DNMT3A	-0.032	0.002	-0.126	0.064	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.49	-2.29	0.020
PD34549	DNMT3At-E664X	DNMT3A	0.002	0.003	-0.095	0.102	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.70	-3.73	0.054
PD34549	PPM1D-T483fs	PPM1D	0.022	0.002	-0.069	0.119	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.49	-5.38	0.115
PD34483	DNMT3Ant-C387W	DNMT3A	0.028	0.002	-0.065	0.114	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-8.68	-4.56	0.066
PD34483	TET2t-I274fs	TET2	-0.023	0.001	-0.094	0.049	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.25	-3.04	0.058
PD34512	DNMT3Ant-K361E	DNMT3A	-0.027	0.002	-0.118	0.064	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.75	-2.09	0.011
PD34512	TET2nt-L1872P	TET2	-0.039	0.002	-0.127	0.061	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.78	-2.73	0.059
PD34512	U2AF1-Q157P	U2AF1	0.012	0.002	-0.075	0.100	0.193	0.002	0.101	0.289	0.063	0.004	-0.052	0.188	0.256	0.003	0.175	0.343	-14.26	-7.22	0.268
PD41270	DNMT3At-E578X	DNMT3A	0.007	0.001	-0.059	0.071	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.38	-3.64	0.059
PD41270	DNMT3At-R598X	DNMT3A	0.011	0.001	-0.036	0.060	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.71	-2.56	0.062
PD41270	TP53nt-R248Q	TP53	0.056	0.002	-0.017	0.133	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-6.90	-4.78	0.105
PD34492	SF3B1-D621N	SF3B1	0.015	0.002	-0.077	0.106	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-12.44	-5.89	0.131
PD34492	TET2t-R1216X	TET2	-0.006	0.002	-0.086	0.075	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.27	-3.90	0.075
PD41121	TET2t-S792X	TET2	0.020	0.002	-0.073	0.111	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.44	-4.51	0.101
PD41209	DNMT3At-Q485X	DNMT3A	-0.011	0.001	-0.084	0.065	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.74	-3.23	0.040
PD41209	DNMT3At-S839fs	DNMT3A	-0.035	0.001	-0.092	0.017	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.87	-2.18	0.016
PD41256	TET2t-Q1624X	TET2	0.033	0.001	-0.044	0.105	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.70	-4.38	0.114
PD41256	TET2t-T1554fs	TET2	0.028	0.002	-0.063	0.112	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-11.49	-6.13	0.109
PD41248	CBLnt-I383M	CBL	-0.004	0.002	-0.096	0.080	0.044	0.001	-0.016	0.091	0.071	0.004	-0.060	0.185	0.114	0.004	0.010	0.220	-9.29	-2.93	0.110

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41248	KRAS-T50I	KRAS	0.030	0.002	-0.059	0.123	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-8.86	-3.93	0.112
PD41248	PTPN11-R265Q	PTPN11	-0.042	0.002	-0.116	0.034	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-7.66	-3.76	0.139
PD41248	TET2t-T759fs	TET2	0.023	0.002	-0.071	0.114	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.46	-5.66	0.104
PD41089	DNMT3Ant-R326S	DNMT3A	-0.030	0.001	-0.099	0.034	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.93	-2.60	0.007
PD41086	SF3B1-A744P	SF3B1	0.007	0.002	-0.081	0.096	0.116	0.001	0.067	0.157	-0.043	0.003	-0.150	0.053	0.073	0.003	-0.010	0.155	-8.49	-3.53	0.079
PD41086	TET2nt-Q1699R	TET2	-0.041	0.002	-0.122	0.042	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.25	-3.35	0.056
PD41223	TET2t-Q976X	TET2	-0.021	0.002	-0.095	0.056	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.41	-4.18	0.060
PD41103	DNMT3Ant-R882H	DNMT3A	0.119	0.001	0.060	0.183	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-6.21	-4.34	0.173
PD41095	DNMT3Ant-L295P	DNMT3A	0.004	0.002	-0.072	0.084	0.038	0.000	0.021	0.055	0.063	0.002	-0.030	0.150	0.101	0.002	0.025	0.176	-7.42	-4.30	0.105
PD34567	PPM1D-R458X	PPM1D	-0.080	0.001	-0.137	-0.024	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-4.59	-2.17	0.014
PD41082	GNB1-K57E	GNB1	0.036	0.002	-0.048	0.110	0.101	0.001	0.032	0.175	-0.014	0.002	-0.100	0.084	0.087	0.001	0.032	0.144	-6.73	-4.63	0.123
PD41082	SF3B1-K666N	SF3B1	0.089	0.001	0.029	0.156	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-6.61	-4.85	0.239
PD41082	TET2nt-L1322Q	TET2	0.034	0.002	-0.052	0.117	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.93	-5.53	0.132
PD41082	TET2nt-Q1274R	TET2	-0.020	0.001	-0.079	0.040	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.20	-3.68	0.078
PD41082	TET2t-H435fs	TET2	0.039	0.001	-0.028	0.106	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.52	-4.67	0.120
PD41082	TET2t-Q1542X	TET2	0.025	0.001	-0.044	0.099	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.75	-4.69	0.106
PD41082	TET2t-Q1825X	TET2	-0.009	0.000	-0.035	0.016	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-0.20	0.00	0.072
PD41082	TET2t-S315fs	TET2	0.033	0.001	-0.019	0.086	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.11	-3.79	0.114
PD34529	SF3B1-A1117S	SF3B1	0.003	0.002	-0.084	0.096	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-11.57	-5.78	0.119
PD34563	DNMT3Ant-M761V	DNMT3A	0.002	0.002	-0.080	0.085	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.80	-3.53	0.039
PD34563	TP53t-W146X	TP53	0.046	0.002	-0.045	0.138	-0.056	0.002	-0.144	0.026	0.000	0.000	0.000	0.000	-0.056	0.002	-0.130	0.016	-7.88	-2.52	-0.010
PD41067	DNMT3At-Y284X	DNMT3A	0.012	0.001	-0.042	0.060	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-3.82	-2.32	0.063
PD34553	SF3B1-K666N	SF3B1	-0.037	0.001	-0.084	0.012	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-2.55	-1.35	0.113
PD34553	TET2t-L532X	TET2	-0.031	0.002	-0.121	0.045	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.68	-4.10	0.050
PD41268	JAK2-V617F	JAK2	-0.023	0.001	-0.094	0.048	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-6.23	-4.14	0.114
PD41317	DNMT3Ant-M880V	DNMT3A	0.009	0.002	-0.079	0.101	0.038	0.000	0.021	0.055	0.024	0.003	-0.075	0.139	0.062	0.003	-0.029	0.150	-8.85	-3.68	0.072
PD34519	PPM1D-S446fs	PPM1D	0.007	0.002	-0.071	0.087	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.28	-5.48	0.101
PD41272	SF3B1-K666N	SF3B1	-0.022	0.001	-0.094	0.041	0.116	0.001	0.067	0.157	0.034	0.001	-0.025	0.089	0.150	0.000	0.117	0.182	-8.48	-4.95	0.128
PD34499	JAK2-V617F	JAK2	-0.042	0.002	-0.120	0.035	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-9.34	-4.97	0.095
PD34499	TET2nt-C1135Y	TET2	-0.009	0.001	-0.083	0.069	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.65	-4.87	0.089
PD34499	TET2nt-H269N	TET2	-0.036	0.002	-0.132	0.047	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.09	-4.82	0.061
PD34499	TET2nt-I1873T	TET2	0.031	0.001	-0.022	0.087	0.098	0.000	0.078	0.116	0.004	0.001	-0.053	0.059	0.102	0.001	0.058	0.146	-4.20	-2.67	0.133
PD34499	TET2nt-L1210P	TET2	0.116	0.001	0.050	0.175	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.25	-6.94	0.214
PD34499	TET2t-L1447fs	TET2	0.008	0.001	-0.054	0.072	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.08	-4.88	0.089
PD34499	TET2t-Q417X	TET2	0.010	0.002	-0.072	0.094	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.39	-5.07	0.091
PD34499	TET2t-S675X	TET2	-0.037	0.001	-0.107	0.042	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.51	-3.61	0.044
PD34499	TET2t-Y1294fs	TET2	0.108	0.001	0.048	0.163	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.64	-6.54	0.189

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41098	TET2nt-T621N	TET2	0.001	0.002	-0.085	0.081	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.25	-4.93	0.099
PD41098	TET2t-L230fs	TET2	0.023	0.002	-0.063	0.119	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-12.64	-6.70	0.104
PD41273	CTCFnt-K592N	CTCF	-0.018	0.002	-0.102	0.072	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-9.24	-5.16	0.045
PD34546	PTPN11-L126S	PTPN11	-0.003	0.002	-0.097	0.096	0.181	0.001	0.119	0.248	0.000	0.000	0.000	0.000	0.181	0.001	0.126	0.237	-13.87	-7.01	0.179
PD41333	TET2nt-D1376A	TET2	0.046	0.002	-0.031	0.125	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.77	-5.38	0.144
PD41105	TET2nt-Q70R	TET2	-0.009	0.001	-0.066	0.047	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.03	-2.81	0.089
PD41105	TET2t-P101fs	TET2	-0.007	0.001	-0.056	0.049	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.82	-2.77	0.074
PD41113	DNMT3Ant-R882H	DNMT3A	-0.013	0.002	-0.085	0.070	0.038	0.000	0.021	0.055	0.016	0.001	-0.040	0.076	0.054	0.001	0.007	0.103	-7.80	-3.03	0.041
PD34536	DNMT3At-K343fs	DNMT3A	0.007	0.002	-0.078	0.079	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-7.45	-3.93	0.058
PD34536	TET2nt-C1221Y	TET2	-0.012	0.002	-0.091	0.062	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-8.57	-4.80	0.086
PD34510	TET2t-V1432fs	TET2	-0.021	0.002	-0.097	0.060	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.04	-3.39	0.060
PD41216	DNMT3Ant-P700L	DNMT3A	-0.027	0.002	-0.106	0.046	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-6.57	-2.16	0.010
PD41216	TET2t-NM_001127208:exon8:c.3955-2A>G	TET2	0.015	0.002	-0.066	0.117	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.01	-4.74	0.096
PD41216	TET2t-S509X	TET2	-0.029	0.001	-0.077	0.020	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.54	-1.86	0.052
PD41217	DNMT3At-NM_175629:exon17:c.2082+2T>G	DNMT3A	-0.014	0.001	-0.079	0.042	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-5.53	-2.74	0.037
PD41217	DNMT3At-R320X	DNMT3A	-0.043	0.001	-0.106	0.012	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-4.27	-1.74	0.009
PD41247	CBLnt-Q379R	CBL	0.001	0.002	-0.089	0.106	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-8.73	-2.76	0.045
PD41247	IDH2-R140Q	IDH2	0.012	0.002	-0.091	0.096	0.000	0.000	0.000	0.000	0.118	0.002	0.024	0.211	0.118	0.002	0.040	0.201	-11.75	-4.84	0.130
PD41247	SF3B1-G1082V	SF3B1	-0.005	0.002	-0.104	0.085	0.116	0.001	0.067	0.157	0.000	0.000	0.000	0.000	0.116	0.001	0.078	0.153	-13.00	-5.72	0.111
PD41247	TET2t-T1331fs	TET2	0.019	0.002	-0.070	0.103	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.18	-4.39	0.100
PD41305	SRSF2-P95H	SRSF2	-0.045	0.002	-0.131	0.043	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-10.31	-7.11	0.402
PD41242	TET2nt-L1332P	TET2	0.112	0.001	0.046	0.180	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-9.63	-6.40	0.210
PD41242	TET2t-I274fs	TET2	0.125	0.001	0.055	0.189	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.02	-6.90	0.206
PD41242	TET2t-K603X	TET2	0.020	0.003	-0.082	0.129	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-10.69	-5.80	0.101
PD41242	TET2t-S1481fs	TET2	-0.041	0.000	-0.075	-0.009	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-1.52	-0.24	0.040
PD41242	TET2t-S1798X	TET2	0.023	0.002	-0.058	0.105	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.01	-5.27	0.104
PD41070	DNMT3Ant-R379C	DNMT3A	0.005	0.001	-0.068	0.072	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.91	-3.35	0.043
PD41070	TET2nt-L1322P	TET2	-0.022	0.002	-0.109	0.063	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-6.94	-3.64	0.076
PD41071	TET2t-K1197X	TET2	0.005	0.002	-0.075	0.084	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.28	-4.74	0.086
PD41071	TET2t-K664fs	TET2	-0.007	0.002	-0.086	0.077	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.21	-4.86	0.074
PD41071	TP53nt-P72S	TP53	-0.009	0.001	-0.081	0.057	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-5.96	-3.07	0.040
PD41346	ASXL1-E602X	ASXL1	0.153	0.001	0.097	0.213	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-8.92	-6.13	0.250
PD41346	SRSF2-P95H	SRSF2	0.085	0.002	0.008	0.163	0.153	0.001	0.094	0.213	0.294	0.002	0.209	0.379	0.447	0.001	0.388	0.508	-17.22	-12.63	0.532
PD41104	DNMT3Ant-N838D	DNMT3A	0.019	0.000	-0.010	0.051	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-1.11	0.00	0.056

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD41104	GNB1-K57E	GNB1	-0.023	0.001	-0.093	0.044	0.101	0.001	0.032	0.175	-0.014	0.002	-0.100	0.084	0.087	0.001	0.032	0.144	-1.40	0.00	0.064
PD41240	TET2t-E566X	TET2	-0.023	0.002	-0.105	0.059	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-7.39	-3.15	0.058
PD41240	TET2t-I274fs	TET2	-0.030	0.003	-0.119	0.073	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.54	-3.90	0.051
PD41224	TET2nt-G1361R	TET2	-0.004	0.002	-0.091	0.075	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-10.75	-5.32	0.094
PD41225	DNMT3Ant-R882S	DNMT3A	0.051	0.001	0.005	0.099	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-5.90	-3.62	0.089
PD41125	CTCFnt-Q65H	CTCF	-0.021	0.003	-0.124	0.074	0.063	0.002	-0.013	0.137	0.000	0.000	0.000	0.000	0.063	0.002	-0.002	0.127	-9.61	-4.14	0.042
PD34491	PPM1D-E539X	PPM1D	-0.024	0.002	-0.112	0.060	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-9.39	-3.18	0.069
PD34503	ASXL1-I641fs	ASXL1	-0.060	0.000	-0.097	-0.025	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-2.91	-1.51	0.037
PD34503	DNMT3Ant-L295P	DNMT3A	0.012	0.002	-0.074	0.095	0.038	0.000	0.021	0.055	0.063	0.002	-0.030	0.150	0.101	0.002	0.025	0.176	-9.72	-5.03	0.113
PD34503	TET2t-Q1828X	TET2	0.010	0.001	-0.065	0.081	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.47	-4.80	0.091
PD34542	TET2nt-G1861V	TET2	-0.083	0.001	-0.135	-0.034	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-4.02	-2.02	0.015
PD34542	U2AF1-S34F	U2AF1	0.018	0.002	-0.076	0.107	0.193	0.002	0.101	0.289	0.000	0.000	0.000	0.000	0.193	0.002	0.114	0.269	-13.43	-7.34	0.212
PD41107	DNMT3Ant-S770L	DNMT3A	0.001	0.002	-0.093	0.095	0.038	0.000	0.021	0.055	0.054	0.001	-0.012	0.120	0.092	0.001	0.038	0.145	-9.51	-4.35	0.092
PD41107	TET2nt-H1219Y	TET2	-0.003	0.001	-0.063	0.058	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-5.77	-2.72	0.095
PD34537	CBLnt-V363M	CBL	-0.018	0.002	-0.104	0.085	0.044	0.001	-0.016	0.091	0.000	0.000	0.000	0.000	0.044	0.001	-0.004	0.087	-10.41	-3.16	0.026
PD41262	DNMT3Ant-R736H	DNMT3A	0.031	0.002	-0.045	0.105	0.038	0.000	0.021	0.055	0.060	0.002	-0.021	0.135	0.098	0.002	0.032	0.162	-4.77	-2.84	0.129
PD41262	DNMT3At-Q842X	DNMT3A	-0.016	0.002	-0.096	0.068	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.44	-4.03	0.035
PD41262	TET2t-T1091fs	TET2	0.034	0.000	-0.005	0.075	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.97	-3.15	0.115
PD41075	SRSF2-P95L	SRSF2	-0.035	0.002	-0.115	0.037	0.153	0.001	0.094	0.213	-0.015	0.002	-0.110	0.067	0.138	0.001	0.077	0.199	-5.24	-2.60	0.103
PD41186	TP53nt-L348F	TP53	-0.008	0.002	-0.110	0.077	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-11.72	-4.92	0.041
PD41280	CBLnt-C404Y	CBL	-0.005	0.002	-0.087	0.078	0.044	0.001	-0.016	0.091	-0.020	0.002	-0.108	0.066	0.023	0.002	-0.047	0.092	-6.53	-3.72	0.019
PD41280	TET2t-L1819fs	TET2	-0.006	0.002	-0.081	0.070	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.92	-4.46	0.075
PD34561	TET2nt-C1289F	TET2	0.028	0.001	-0.025	0.087	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.76	-4.75	0.126
PD34561	TET2t-G898X	TET2	0.032	0.001	-0.032	0.110	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.74	-4.85	0.113
PD41110	PPM1D-K549X	PPM1D	-0.012	0.001	-0.073	0.047	0.094	0.000	0.064	0.123	0.000	0.000	0.000	0.000	0.094	0.000	0.069	0.119	-5.90	-3.78	0.082
PD41208	KRAS-A146T	KRAS	-0.015	0.001	-0.084	0.062	0.082	0.001	0.019	0.140	0.000	0.000	0.000	0.000	0.082	0.001	0.032	0.132	-6.07	-3.18	0.068
PD41182	ASXL1-K1025fs	ASXL1	0.040	0.001	-0.025	0.104	0.097	0.000	0.074	0.121	0.000	0.000	0.000	0.000	0.097	0.000	0.076	0.117	-10.97	-5.50	0.137
PD41182	TET2t-G563X	TET2	-0.018	0.002	-0.110	0.076	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-11.57	-3.03	0.063
PD41196	DNMT3Ant-S770L	DNMT3A	0.014	0.001	-0.065	0.084	0.038	0.000	0.021	0.055	0.054	0.001	-0.012	0.120	0.092	0.001	0.038	0.145	-6.29	-3.70	0.106
PD41231	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	-0.036	0.002	-0.116	0.045	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-6.22	-1.63	0.015
PD41246	JAK2-V617F	JAK2	0.048	0.001	-0.023	0.119	0.000	0.000	0.000	0.000	0.137	0.000	0.097	0.174	0.137	0.000	0.104	0.169	-10.05	-5.78	0.185
PD41246	TET2nt-N1266S	TET2	-0.018	0.002	-0.099	0.064	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.71	-3.03	0.080
PD41287	BRCC3t-T166fs	BRCC3	-0.033	0.002	-0.106	0.054	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-6.57	-3.79	0.025
PD41288	TP53nt-Y220C	TP53	0.008	0.002	-0.075	0.102	0.049	0.000	0.013	0.087	0.011	0.004	-0.111	0.117	0.060	0.003	-0.033	0.153	-6.30	-4.09	0.068
PD34520	TET2nt-C1271G	TET2	-0.035	0.002	-0.121	0.049	0.098	0.000	0.078	0.116	0.000	0.000	0.000	0.000	0.098	0.000	0.082	0.114	-7.96	-3.41	0.063

PID	Site	Gene	Unknown Cause Effect _mean	Unknown Cause Effect _Var	Unknown Cause Effect _Q05	Unknown Cause Effect _Q95	Gene Effect _mean	Gene Effect _Var	Gene Effect _Q05	Gene Effect _Q95	Site Effect _mean	Site Effect _Var	Site Effect _Q05	Site Effect _Q95	Genetic Effect _mean	Genetic Effect _Var	Genetic Effect _Q05	Genetic Effect _Q95	Offset _Q05	Offset _Q95	Full Effect Mean
PD34520	TET2t-NM_001127208:exon5:c.3501-2A>C	TET2	0.017	0.001	-0.033	0.062	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.31	-2.04	0.098
PD41229	TET2t-N528fs	TET2	-0.055	0.001	-0.108	-0.012	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-4.19	-2.63	0.026
PD34477	DNMT3Ant-Y793N	DNMT3A	-0.005	0.002	-0.090	0.080	0.038	0.000	0.021	0.055	0.000	0.000	0.000	0.000	0.038	0.000	0.023	0.052	-7.26	-3.75	0.033
PD34477	TET2t-Q962X	TET2	-0.066	0.001	-0.143	0.002	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-5.68	-2.74	0.015
PD34477	TET2t-T621fs	TET2	0.012	0.002	-0.062	0.104	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-8.51	-5.13	0.093
PD34477	TP53nt-P151R	TP53	-0.019	0.002	-0.101	0.053	0.049	0.000	0.013	0.087	0.000	0.000	0.000	0.000	0.049	0.000	0.018	0.080	-6.27	-3.21	0.030
PD34488	CBLnt-C404Y	CBL	-0.007	0.002	-0.096	0.069	0.044	0.001	-0.016	0.091	-0.020	0.002	-0.108	0.066	0.023	0.002	-0.047	0.092	-7.75	-2.90	0.016
PD34488	SRSF2-R47P	SRSF2	-0.092	0.001	-0.168	-0.022	0.153	0.001	0.094	0.213	0.000	0.000	0.000	0.000	0.153	0.001	0.103	0.203	-8.33	-3.40	0.061
PD34488	TET2t-S402X	TET2	0.003	0.002	-0.086	0.079	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-9.48	-4.65	0.084
PD41264	BRCC3t-NM_001018055:exon7:c.548+1G>A	BRCC3	-0.001	0.002	-0.083	0.091	0.058	0.001	-0.009	0.118	0.000	0.000	0.000	0.000	0.058	0.001	0.003	0.112	-7.89	-3.25	0.057
PD41264	DNMT3At-C586fs	DNMT3A	0.009	0.002	-0.084	0.098	0.052	0.000	0.034	0.068	0.000	0.000	0.000	0.000	0.052	0.000	0.037	0.067	-8.93	-4.47	0.061
PD41264	TET2t-NM_001127208:exon7:c.3804-2A>G	TET2	0.001	0.001	-0.063	0.065	0.081	0.000	0.069	0.093	0.000	0.000	0.000	0.000	0.081	0.000	0.070	0.091	-6.07	-3.04	0.082

Table 11b | Age at onset estimates for all clones

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41102	SRSF2-SRSF2:NM_003016:exon1:c.43_44GA	SRSF2	74.53	36.1	16.8	23.1	27.8	37.9	44.7	46.3	48.3
PD41345	SRSF2-P95A	SRSF2	85.61	17.7	-1.0	-1.0	-1.0	12.8	42.2	47.5	51.7
PD41345	TET2nt-H468R	TET2	85.61	30.4	-1.0	-1.0	-1.0	34.4	54.5	57.8	61.9
PD41345	TET2t-Q888X	TET2	85.61	31.8	4.2	14.4	19.5	34.0	43.6	45.4	48.0
PD41345	U2AF1-Q157R	U2AF1	92.11	67.9	59.7	62.6	64.2	68.5	71.8	72.7	73.7
PD41073	DNMT3Ant-L637V	DNMT3A	77.53	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41073	DNMT3At-F640fs	DNMT3A	84.47	17.8	-1.0	-1.0	-1.0	16.1	38.6	42.6	46.9
PD41073	PPM1D-E476X	PPM1D	80.68	26.9	-1.0	-1.0	3.2	30.0	44.0	46.4	49.4
PD41073	TET2t-Q1553fs	TET2	84.47	22.0	-1.0	-1.0	-1.0	24.3	41.9	45.3	48.4
PD41269	DNMT3Ant-S638C	DNMT3A	68.92	10.1	-1.0	-1.0	-1.0	6.4	24.9	27.8	31.6
PD34501	TET2t-N811fs	TET2	79.5	18.1	-1.0	-1.0	-1.0	18.0	37.6	40.8	44.6
PD34496	DNMT3At-C557X	DNMT3A	69.07	2.4	-1.0	-1.0	-1.0	-1.0	5.9	13.5	20.0
PD41296	SF3B1-H662Y	SF3B1	66.64	9.3	-1.0	-1.0	-1.0	-1.0	25.8	30.7	36.0
PD34487	ASXL1-Q1251X	ASXL1	74.67	31.6	7.6	15.6	21.3	34.1	41.8	43.4	45.2
PD34487	TET2nt-H1380Y	TET2	68.14	7.2	-1.0	-1.0	-1.0	-1.0	21.6	27.9	33.0
PD34485	TP53nt-R248W	TP53	71.31	11.3	-1.0	-1.0	-1.0	-1.0	31.1	36.4	42.0
PD41289	DNMT3Ant-V675A	DNMT3A	68.04	8.8	-1.0	-1.0	-1.0	6.9	20.2	23.4	26.7
PD41114	DNMT3Ant-R736H	DNMT3A	59.72	6.5	-1.0	-1.0	-1.0	-0.5	18.1	22.1	25.9
PD41114	JAK2-V617F	JAK2	63.57	13.3	-1.0	-1.0	-1.0	12.7	27.9	31.3	34.3
PD41227	CBLnt-I361S	CBL	69.21	5.6	-1.0	-1.0	-1.0	-1.0	17.4	22.8	28.7
PD41227	DNMT3Ant-G302S	DNMT3A	62.23	-0.3	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41312	PPM1D-A454fs	PPM1D	55.07	0.1	-1.0	-1.0	-1.0	-1.0	-1.0	2.4	7.6
PD41239	ASXL1-G828fs	ASXL1	73.56	9.8	-1.0	-1.0	-1.0	9.3	19.0	21.7	24.5
PD41239	SRSF2-P95H	SRSF2	73.56	48.2	42.5	43.9	44.8	48.5	51.3	52.0	52.9
PD41239	TET2nt-T1883K	TET2	81.16	42.5	24.8	31.4	35.2	44.3	50.2	51.4	53.0
PD41108	DNMT3Ant-R326P	DNMT3A	60.87	0.4	-1.0	-1.0	-1.0	-1.0	-1.0	4.1	9.9
PD41108	DNMT3Ant-S669F	DNMT3A	64.09	2.4	-1.0	-1.0	-1.0	-1.0	8.3	13.3	18.4
PD41108	DNMT3At-NM_175629:exon12:c.1474+1G>-	DNMT3A	70.78	17.7	-1.0	-1.0	-1.0	19.7	30.8	33.0	35.6
PD41108	TET2t-S675X	TET2	70.78	15.2	-1.0	-1.0	-1.0	15.8	30.2	32.9	35.3
PD34497	TET2t-NM_001127208:exon9:c.4182+2->T	TET2	68.31	16.4	2.5	7.2	9.4	17.2	23.1	24.6	26.2
PD34497	TET2t-P1155fs	TET2	74.33	13.4	-1.0	-1.0	-1.0	9.9	31.0	34.0	38.1
PD34497	TET2t-R544X	TET2	68.31	6.6	-1.0	-1.0	-1.0	-1.0	20.2	24.6	29.4
PD41243	DNMT3Ant-I780T	DNMT3A	77.43	19.0	-1.0	-1.0	-1.0	19.8	38.2	41.6	45.7
PD41243	DNMT3Ant-M880V	DNMT3A	80.23	16.6	-1.0	-1.0	-1.0	11.8	38.7	43.2	47.6
PD41243	DNMT3At-Q615X	DNMT3A	77.43	2.9	-1.0	-1.0	-1.0	-1.0	7.4	15.6	24.1
PD41243	DNMT3At-Y436X	DNMT3A	77.43	10.5	-1.0	-1.0	-1.0	-0.7	28.5	33.8	37.9
PD34484	DNMT3At-F640fs	DNMT3A	68.53	0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	7.2
PD41249	DNMT3At-L504fs	DNMT3A	74.36	10.1	-1.0	-1.0	-1.0	2.9	26.0	30.4	35.0
PD41249	TET2nt-C1221S	TET2	67.7	15.3	-1.0	-1.0	-1.0	13.3	33.5	37.5	41.4
PD41532	ASXL1-Q588X	ASXL1	76.12	0.5	-1.0	-1.0	-1.0	-1.0	-1.0	2.9	11.5
PD41532	KRAS-G13D	KRAS	76.12	20.3	-1.0	-1.0	-1.0	17.9	43.6	49.5	55.3
PD41532	TP53nt-M246V	TP53	84.42	17.9	-1.0	-1.0	-1.0	16.6	38.1	41.7	46.0
PD41163	DNMT3Ant-R882C	DNMT3A	78.37	2.4	-1.0	-1.0	-1.0	-1.0	5.7	14.1	22.6
PD41163	TET2nt-H1912R	TET2	78.37	28.8	-1.0	-1.0	-1.0	32.6	48.2	51.4	54.3
PD34475	TET2t-R1404X	TET2	65.82	15.4	0.6	4.9	7.7	16.1	22.5	24.4	26.7
PD41112	CBLnt-C396W	CBL	80.57	9.1	-1.0	-1.0	-1.0	-1.0	25.4	30.7	35.5
PD41112	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	84.23	31.5	-1.0	-1.0	12.0	35.2	47.6	50.3	53.3
PD41112	DNMT3Ant-R882H	DNMT3A	73.69	-0.5	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41528	DNMT3Ant-G550R	DNMT3A	76.11	0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41528	SF3B1-H662Q	SF3B1	81.36	42.7	20.9	28.9	33.5	45.3	52.0	53.5	55.4
PD41528	TET2nt-I1873T	TET2	76.11	1.3	-1.0	-1.0	-1.0	-1.0	-1.0	7.1	17.4

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41528	TET2t-F1597fs	TET2	76.11	1.3	-1.0	-1.0	-1.0	-1.0	4.6	8.6	12.9
PD41528	TP53nt-M237V	TP53	81.36	41.0	9.6	22.4	29.0	44.4	52.8	54.5	56.7
PD41175	DNMT3Ant-D686E	DNMT3A	69.45	1.8	-1.0	-1.0	-1.0	-1.0	3.4	10.4	18.8
PD41175	GNB1-A248T	GNB1	83.17	47.7	16.6	28.2	35.0	50.3	60.2	63.0	67.4
PD41175	PPM1D-W427X	PPM1D	77.43	21.6	-1.0	-1.0	-1.0	23.7	38.5	41.2	44.1
PD41192	DNMT3Ant-R326C	DNMT3A	70.7	5.8	-1.0	-1.0	-1.0	4.4	13.7	15.9	18.6
PD41192	DNMT3Ant-V687L	DNMT3A	70.7	8.2	-1.0	-1.0	-1.0	-1.0	24.1	30.9	38.6
PD41192	SF3B1-T798I	SF3B1	73.69	33.6	-1.0	-1.0	9.2	37.8	51.8	55.1	59.6
PD41302	DNMT3Ant-I369F	DNMT3A	64.75	2.7	-1.0	-1.0	-1.0	-1.0	8.5	14.0	21.7
PD41302	DNMT3At-Q886X	DNMT3A	72.07	8.7	-1.0	-1.0	-1.0	-0.5	23.4	27.7	32.8
PD41302	TET2t-H1778fs	TET2	64.75	17.9	-1.0	-1.0	4.2	19.5	28.9	31.0	33.8
PD42297	DNMT3Ant-S770L	DNMT3A	75.54	22.4	-1.0	-1.0	-1.0	24.7	39.8	42.6	46.0
PD42297	TET2nt-Y1245C	TET2	75.54	50.7	45.5	46.7	47.9	50.8	53.7	54.3	55.0
PD42297	TET2t-P401fs	TET2	75.54	45.1	39.0	40.7	41.8	45.4	48.3	49.1	50.0
PD41149	DNMT3At-NM_175629:exon9:c.1015-2A>G	DNMT3A	69.92	7.3	-1.0	-1.0	-1.0	-1.0	21.5	26.0	31.0
PD41149	DNMT3At-NM_175629:exon11:c.1429+1G>A	DNMT3A	76.9	20.4	-1.0	-1.0	-1.0	22.9	34.7	37.1	39.6
PD41167	DNMT3At-S770X	DNMT3A	65.39	-0.2	-1.0	-1.0	-1.0	-1.0	-1.0	0.7	5.7
PD34505	TET2t-W1847X	TET2	66.62	12.8	-1.0	-1.0	-1.0	12.2	26.5	29.6	33.6
PD41122	DNMT3At-R458fs	DNMT3A	68.71	16.7	-1.0	-1.0	2.6	17.8	27.9	30.2	33.4
PD41115	CTCFt-S488X	CTCF	87.99	24.2	-1.0	-1.0	-1.0	26.6	44.1	47.2	50.6
PD41115	SRSF2-P95L	SRSF2	75.81	29.6	-1.0	5.1	13.5	32.4	44.2	46.3	49.0
PD41226	DNMT3Ant-R201C	DNMT3A	70.1	5.9	-1.0	-1.0	-1.0	-1.0	17.4	21.9	26.6
PD41226	DNMT3Ant-V636M	DNMT3A	60.09	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	3.6
PD42296	DNMT3Ant-L888P	DNMT3A	77.88	6.9	-1.0	-1.0	-1.0	-1.0	20.3	25.4	31.8
PD41235	SRSF2-P95L	SRSF2	81.53	50.7	27.5	36.3	42.0	52.5	60.2	62.6	66.9
PD41235	TET2t-C973fs	TET2	77.37	26.8	-1.0	4.3	11.9	29.6	39.4	41.6	44.3
PD41235	TET2t-E692X	TET2	68.7	1.5	-1.0	-1.0	-1.0	-1.0	1.9	9.2	16.3
PD34533	TP53nt-F212V	TP53	82.95	14.7	-1.0	-1.0	-1.0	9.9	34.2	38.7	43.3
PD34521	CTCFnt-T563I	CTCF	79.82	16.0	-1.0	-1.0	-1.0	13.7	35.8	40.0	43.6
PD34521	JAK2-V617F	JAK2	71.74	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41245	BRCC3nt-G152R	BRCC3	74.4	9.9	-1.0	-1.0	-1.0	-1.0	28.4	34.6	39.5
PD41221	DNMT3Ant-R882H	DNMT3A	93.69	5.3	-1.0	-1.0	-1.0	-1.0	17.5	26.0	33.6
PD41221	TET2nt-Y1902H	TET2	101.45	45.9	-1.0	5.3	23.2	52.7	65.2	67.9	70.5
PD41221	TET2t-Q888X	TET2	98.32	35.3	-1.0	-1.0	5.7	40.8	55.6	58.1	61.5
PD41221	TET2t-Q916X	TET2	93.69	9.8	-1.0	-1.0	-1.0	-1.0	29.3	34.9	41.9
PD41221	U2AF1-Q157P	U2AF1	98.32	76.4	64.8	69.0	71.5	77.6	81.8	82.8	84.1
PD34575	DNMT3Ant-I769M	DNMT3A	81.78	14.9	-1.0	-1.0	-1.0	0.4	37.8	45.2	53.1
PD34575	PPM1D-N477fs	PPM1D	90.88	36.8	-1.0	11.3	20.7	40.9	51.2	53.4	55.8
PD34575	SF3B1-K666N	SF3B1	85.15	44.1	12.1	24.8	31.7	47.8	56.3	58.2	60.4
PD41099	IDH1-H133R	IDH1	76.54	19.1	-1.0	-1.0	-1.0	20.4	36.4	39.8	43.3
PD41099	SRSF2-P95R	SRSF2	68.18	24.3	-1.0	-1.0	5.8	27.3	38.5	40.8	43.5
PD41099	TP53nt-R273G	TP53	76.54	32.7	-1.0	6.7	16.2	35.1	46.2	49.9	55.5
PD41185	DNMT3Ant-I705T	DNMT3A	69.55	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41310	DNMT3At-G646fs	DNMT3A	62.58	4.3	-1.0	-1.0	-1.0	-1.0	14.2	19.4	25.9
PD41074	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	67.01	-0.4	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-0.8
PD34579	CBLnt-Q409R	CBL	76.61	50.6	-1.0	12.2	24.5	55.1	76.6	76.6	76.6
PD34579	DNMT3Ant-I833V	DNMT3A	76.61	1.9	-1.0	-1.0	-1.0	-1.0	3.3	11.8	19.7
PD34569	CBLt-Q691fs	CBL	77.69	30.3	-1.0	-1.0	9.3	34.3	46.1	48.7	52.0
PD34569	DNMT3Ant-I898T	DNMT3A	74.68	2.5	-1.0	-1.0	-1.0	-1.0	6.6	14.6	21.5
PD34569	DNMT3At-W698X	DNMT3A	74.68	9.4	-1.0	-1.0	-1.0	7.2	21.9	25.3	29.1
PD34569	SF3B1-K666N	SF3B1	74.68	5.4	-1.0	-1.0	-1.0	-1.0	16.2	20.2	24.5
PD41129	DNMT3Ant-A662G	DNMT3A	67.92	4.6	-1.0	-1.0	-1.0	-1.0	15.3	19.7	24.6
PD41152	ASXL1-NM_015338:exon11:c.1719+2T>C	ASXL1	65.63	43.8	3.5	15.4	26.5	46.8	64.7	65.6	65.6

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41135	DNMT3Ant-S638F	DNMT3A	66.66	13.5	-1.0	-1.0	-1.0	11.1	30.6	33.7	37.1
PD41135	DNMT3At-G654fs	DNMT3A	62.99	2.6	-1.0	-1.0	-1.0	-1.0	8.2	13.6	19.3
PD41135	TET2t-Q749X	TET2	62.99	6.3	-1.0	-1.0	-1.0	-1.0	18.2	23.0	26.9
PD34571	PPM1D-R429fs	PPM1D	82.68	26.8	-1.0	-1.0	4.2	30.2	42.7	45.4	48.6
PD41176	PPM1D-E226X	PPM1D	71.43	42.1	-1.0	-1.0	11.1	47.7	67.9	71.4	71.4
PD41176	TET2nt-A1876G	TET2	79.54	24.2	-1.0	-1.0	0.6	26.0	41.2	44.4	47.7
PD34580	DNMT3Ant-R659H	DNMT3A	72.39	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34504	DNMT3At-NM_175629:exon16:c.1852-1G>A	DNMT3A	77.19	17.3	-1.0	-1.0	-1.0	18.1	34.5	37.2	40.5
PD41347	TET2t-Q324X	TET2	70.29	9.6	-1.0	-1.0	-1.0	-1.0	26.6	32.5	38.8
PD41347	TET2t-Q976fs	TET2	70.29	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	1.3
PD41347	TP53nt-P142T	TP53	76.73	23.4	-1.0	-1.0	-1.0	24.9	43.0	46.8	51.7
PD41222	TET2nt-H1380Y	TET2	55.47	9.8	-1.0	-1.0	-1.0	-1.0	27.3	35.4	52.3
PD41142	CBLnt-L380P	CBL	79.19	6.0	-1.0	-1.0	-1.0	-1.0	19.3	26.4	35.2
PD41142	DNMT3At-R771X	DNMT3A	79.19	5.1	-1.0	-1.0	-1.0	-1.0	15.3	22.5	31.1
PD41142	SF3B1-K666N	SF3B1	86.6	48.0	27.4	34.1	38.5	50.6	57.4	59.0	60.7
PD41142	TET2t-R544X	TET2	86.6	25.1	-1.0	-1.0	-1.0	28.6	46.2	49.6	53.1
PD34550	CTCFnt-V361I	CTCF	67.17	12.7	-1.0	-1.0	-1.0	5.7	31.4	37.4	42.1
PD34550	TET2t-G1719fs	TET2	71.18	16.7	-1.0	-1.0	-1.0	18.0	32.3	34.8	37.6
PD41139	DNMT3Ant-L819V	DNMT3A	56.27	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41139	TET2nt-C1271S	TET2	56.27	6.4	-1.0	-1.0	-1.0	-1.0	19.5	24.9	30.7
PD41211	CBLnt-I383M	CBL	90.36	45.4	2.6	19.5	30.2	50.3	60.0	62.0	64.2
PD41211	TET2nt-H1380Y	TET2	75.58	30.6	14.0	19.1	22.4	32.1	39.0	40.4	42.1
PD41191	TET2t-L920X	TET2	70.5	9.6	-1.0	-1.0	-1.0	0.7	25.2	31.0	36.1
PD41191	TET2t-S473fs	TET2	70.5	18.5	-1.0	-1.0	-1.0	18.3	39.0	42.7	47.5
PD41191	TET2t-W1847X	TET2	70.5	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-0.1
PD41265	DNMT3At-NM_175629:exon20:c.2323-2A>G	DNMT3A	63.94	1.7	-1.0	-1.0	-1.0	-1.0	6.4	10.7	14.3
PD41265	DNMT3At-NM_175629:exon9:c.1015-2A>T	DNMT3A	63.94	-0.1	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41265	PTPN11-R502L	PTPN11	79.1	35.4	9.4	19.8	25.1	38.0	45.9	47.7	49.9
PD41331	TET2nt-A347E	TET2	82.63	32.0	-1.0	0.2	12.0	35.7	47.5	50.1	52.9
PD41130	CTCFnt-H347R	CTCF	76.22	10.4	-1.0	-1.0	-1.0	0.7	28.3	32.3	37.2
PD41130	PPM1D-N448fs	PPM1D	76.22	-0.2	-1.0	-1.0	-1.0	-1.0	-1.0	1.5	6.4
PD41181	DNMT3Ant-R736C	DNMT3A	78.01	21.4	-1.0	-1.0	-1.0	23.9	39.8	42.7	45.5
PD41181	DNMT3At-NM_175629:exon21:c.2478+1G>A	DNMT3A	73.14	8.0	-1.0	-1.0	-1.0	-0.8	22.1	26.8	30.9
PD34577	DNMT3Ant-Q886R	DNMT3A	80.05	3.5	-1.0	-1.0	-1.0	-1.0	7.1	17.9	28.1
PD34577	DNMT3At-R320X	DNMT3A	80.05	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34526	DNMT3Ant-R882C	DNMT3A	80.19	4.8	-1.0	-1.0	-1.0	-1.0	16.8	24.5	32.5
PD41304	TET2nt-K110R	TET2	62.74	0.1	-1.0	-1.0	-1.0	-1.0	-1.0	1.8	8.6
PD41123	ASXL1-Q1350X	ASXL1	64.59	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41123	DNMT3At-W314X	DNMT3A	64.59	15.8	-1.0	-1.0	-1.0	16.6	28.2	31.0	34.0
PD41160	DNMT3Ant-R635W	DNMT3A	54.7	8.4	-1.0	-1.0	-1.0	7.8	17.9	20.2	22.6
PD41160	TET2t-R1455fs	TET2	57.71	18.1	2.8	7.7	10.5	19.3	25.2	26.9	28.7
PD41144	DNMT3Ant-R736C	DNMT3A	83.79	23.5	-1.0	-1.0	-1.0	25.6	42.4	45.4	48.5
PD41144	SF3B1-K666N	SF3B1	88.17	50.3	34.8	39.6	43.1	51.9	57.8	59.1	60.7
PD34479	DNMT3Ant-I705T	DNMT3A	66.48	8.0	-1.0	-1.0	-1.0	-1.0	23.8	29.0	34.4
PD41188	GNB1-K57M	GNB1	73.23	12.3	-1.0	-1.0	-1.0	8.6	29.0	33.1	37.1
PD41188	PTPN11-G363R	PTPN11	81.45	49.8	32.3	37.9	41.9	51.8	57.9	59.4	61.0
PD41188	TET2nt-R1926G	TET2	76.28	27.7	-1.0	-1.0	5.0	31.6	43.7	45.9	48.6
PD34527	TET2nt-C1298Y	TET2	67.77	40.9	34.0	36.0	37.3	41.3	44.6	45.4	46.5
PD34527	TET2nt-V1417F	TET2	67.77	18.2	-1.0	-1.0	-1.0	19.0	36.6	39.6	43.6
PD34527	TET2t-Q674X	TET2	74.52	41.2	34.7	36.3	37.7	41.5	44.8	45.7	46.8
PD34527	TP53nt-R175G	TP53	67.77	3.0	-1.0	-1.0	-1.0	-1.0	10.2	15.5	21.8
PD41218	DNMT3Ant-G332R	DNMT3A	79.26	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41218	DNMT3Ant-R729G	DNMT3A	79.26	5.6	-1.0	-1.0	-1.0	-1.0	18.1	26.4	34.6

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41218	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	79.26	14.8	-1.0	-1.0	-1.0	10.3	34.6	39.0	43.0
PD41218	TET2t-Y1649X	TET2	89.99	33.1	-1.0	-1.0	9.8	37.9	50.5	53.3	56.6
PD34514	DNMT3Ant-G511E	DNMT3A	70.21	1.7	-1.0	-1.0	-1.0	-1.0	2.6	10.2	19.2
PD34514	DNMT3Ant-R635W	DNMT3A	70.21	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34514	DNMT3Ant-R729W	DNMT3A	70.21	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34514	JAK2-V617F	JAK2	84.7	49.6	31.0	38.2	41.6	51.4	58.4	59.8	61.9
PD41318	DNMT3Ant-F755S	DNMT3A	72.72	10.1	-1.0	-1.0	-1.0	-1.0	28.9	34.4	41.8
PD41318	TET2t-L199X	TET2	80.71	26.6	-1.0	-1.0	-1.0	30.3	43.9	46.5	49.3
PD41271	PPM1D-E475X	PPM1D	86.93	31.5	-1.0	-1.0	11.8	35.6	46.9	49.6	52.2
PD41271	PPM1D-N477fs	PPM1D	86.93	43.1	10.9	24.1	31.4	46.5	55.2	57.5	59.8
PD34543	IDH1-R132H	IDH1	84.12	54.9	40.9	45.3	48.1	55.9	62.0	63.5	65.5
PD34543	JAK2-V617F	JAK2	84.12	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34543	SRSF2-P95H	SRSF2	93.6	72.4	67.9	69.0	69.9	72.6	75.0	75.5	76.1
PD34543	TET2t-M1734fs	TET2	84.12	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34511	DNMT3At-P385fs	DNMT3A	74.63	0.3	-1.0	-1.0	-1.0	-1.0	-1.0	3.1	9.9
PD34511	SF3B1-K700E	SF3B1	74.63	6.3	-1.0	-1.0	-1.0	-1.0	19.1	22.6	26.7
PD34511	SF3B1-R625L	SF3B1	74.63	11.5	-1.0	-1.0	-1.0	9.3	26.4	30.0	33.3
PD41120	ASXL1-S1014fs	ASXL1	68.57	12.6	-1.0	-1.0	-1.0	11.2	26.7	30.1	34.1
PD41120	TET2t-Q1534X	TET2	68.57	13.9	-1.0	-1.0	-1.0	14.0	28.7	31.7	34.6
PD41120	TET2t-Q744X	TET2	68.57	5.6	-1.0	-1.0	-1.0	-1.0	16.0	22.5	27.6
PD41093	BRCC3nt-L153P	BRCC3	86.96	25.7	-1.0	-1.0	-1.0	27.9	49.0	53.0	57.7
PD34540	SF3B1-G742D	SF3B1	76.34	36.5	7.2	19.2	26.0	39.3	47.3	49.1	51.6
PD34540	TET2t-N1328fs	TET2	65.8	5.0	-1.0	-1.0	-1.0	-1.0	15.2	19.5	25.0
PD34506	TP53nt-R273L	TP53	66.45	1.2	-1.0	-1.0	-1.0	-1.0	-1.0	6.4	14.7
PD41275	DNMT3At-NM_175629:exon14:c.1555-1G>T	DNMT3A	77.35	7.7	-1.0	-1.0	-1.0	-1.0	21.8	26.2	30.7
PD41275	TET2nt-I1873T	TET2	69.11	16.5	-1.0	-1.0	-1.0	17.5	31.2	33.9	37.2
PD41157	TET2t-Q649X	TET2	60.88	4.7	-1.0	-1.0	-1.0	-1.0	15.2	19.3	23.0
PD41127	TET2nt-A1876V	TET2	75.37	20.1	-1.0	-1.0	-1.0	21.4	38.6	42.3	46.0
PD41127	TET2nt-I1873T	TET2	78.4	22.4	-1.0	-1.0	-1.0	25.0	40.6	43.1	45.8
PD41117	TET2nt-A394T	TET2	85.91	42.2	4.7	18.9	27.4	46.1	55.8	58.0	60.6
PD41117	TET2nt-I1873T	TET2	82.14	52.5	47.0	48.4	49.5	52.8	55.6	56.3	57.3
PD41117	TET2nt-R1366H	TET2	72.75	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	2.7	9.1
PD41118	BRCC3t-NM_001018055:exon2:c.140+1G>A	BRCC3	78.49	29.1	-1.0	-1.0	10.0	32.8	44.1	46.6	49.5
PD41118	DNMT3Ant-K367N	DNMT3A	69.1	-0.4	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41118	DNMT3At-NM_175629:exon12:c.1430-1G>-	DNMT3A	78.49	14.3	-1.0	-1.0	-1.0	11.9	31.8	36.3	41.5
PD41118	DNMT3At-P385fs	DNMT3A	69.1	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41118	TET2t-K188fs	TET2	69.1	0.3	-1.0	-1.0	-1.0	-1.0	-1.0	0.4	9.1
PD41118	TET2t-Q185fs	TET2	69.1	1.5	-1.0	-1.0	-1.0	-1.0	0.1	8.8	16.5
PD41177	DNMT3Ant-S770L	DNMT3A	67.88	4.6	-1.0	-1.0	-1.0	-1.0	14.4	18.7	22.9
PD41177	DNMT3At-Q515X	DNMT3A	75.3	11.1	-1.0	-1.0	-1.0	6.5	27.1	32.0	36.2
PD41308	DNMT3Ant-R635Q	DNMT3A	56.21	0.7	-1.0	-1.0	-1.0	-1.0	-1.0	1.3	9.8
PD34531	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	80.49	20.5	-1.0	-1.0	-1.0	20.7	42.7	46.8	50.7
PD34531	DNMT3At-NM_175629:exon18:c.2173+1G>A	DNMT3A	80.49	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34531	PPM1D-Q524X	PPM1D	80.49	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41145	TET2t-R550X	TET2	65.16	14.6	-1.0	-1.0	-1.0	8.8	34.3	39.1	44.2
PD41171	ASXL1-P808fs	ASXL1	81.76	39.4	16.5	26.0	30.8	41.7	48.8	50.5	52.4
PD34554	CTCFnt-S461P	CTCF	85.39	29.5	-1.0	-1.0	-1.0	33.9	49.2	52.6	55.9
PD34554	DNMT3At-F734fs	DNMT3A	76.08	13.9	-1.0	-1.0	-1.0	7.1	34.4	39.2	43.9
PD34554	DNMT3At-W860X	DNMT3A	79.47	14.1	-1.0	-1.0	-1.0	5.6	35.2	40.2	45.8
PD34554	TET2nt-TET2:NM_00112720	TET2	76.08	15.3	-1.0	-1.0	-1.0	15.5	30.2	33.4	36.9

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
	8:exon7:c.3852_3854 del:p.1284_1285del										
PD34554	TET2t-G1313fs	TET2	76.08	19.7	-1.0	-1.0	-0.2	21.8	33.9	36.6	39.5
PD34554	TET2t-H650fs	TET2	76.08	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41143	DNMT3Ant-I705T	DNMT3A	74.58	14.4	-1.0	-1.0	-1.0	11.1	32.9	36.8	40.7
PD41143	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	71.23	5.5	-1.0	-1.0	-1.0	-1.0	17.1	21.6	26.5
PD41143	TET2t-C1271fs	TET2	71.23	3.1	-1.0	-1.0	-1.0	-1.0	8.5	16.6	24.8
PD41132	GNB1-K57E	GNB1	65.79	6.8	-1.0	-1.0	-1.0	-1.0	20.5	25.9	31.3
PD41132	TET2t-K1533X	TET2	69.49	10.1	-1.0	-1.0	-1.0	2.7	25.7	30.5	36.1
PD41084	JAK2-V617F	JAK2	78.65	30.8	5.9	14.0	19.7	33.0	41.7	43.6	46.3
PD41124	TET2t-C1271X	TET2	83.99	31.9	-1.0	-1.0	9.9	35.6	48.6	51.9	54.9
PD41124	TET2t-K944X	TET2	80.47	22.6	-1.0	-1.0	-1.0	25.3	40.6	43.7	47.1
PD41124	TET2t-Q317X	TET2	74.1	7.2	-1.0	-1.0	-1.0	-1.0	22.2	28.4	33.5
PD41124	TP53nt-R181P	TP53	74.1	7.1	-1.0	-1.0	-1.0	-1.0	22.0	27.6	34.9
PD41194	DNMT3Ant-I769V	DNMT3A	72.29	2.7	-1.0	-1.0	-1.0	-1.0	7.3	15.4	23.9
PD41194	SF3B1-R549H	SF3B1	84.67	44.9	20.3	29.3	34.8	47.5	55.5	57.1	59.3
PD41194	TET2t-Q618fs	TET2	72.29	39.9	32.5	34.4	36.0	40.3	44.0	45.0	46.3
PD41194	TP53nt-R282W	TP53	75.53	8.8	-1.0	-1.0	-1.0	-1.0	25.9	33.6	41.2
PD41128	DNMT3Ant-L647R	DNMT3A	81.73	6.9	-1.0	-1.0	-1.0	-1.0	21.2	26.7	31.8
PD41128	TET2nt-R1261C	TET2	81.73	18.8	-1.0	-1.0	-1.0	18.8	39.7	43.0	47.1
PD34547	CTCFnt-H425R	CTCF	85.62	51.4	9.3	22.2	32.8	53.7	69.7	76.6	85.6
PD34547	DNMT3Ant-G726D	DNMT3A	75.6	8.7	-1.0	-1.0	-1.0	-1.0	25.7	30.9	37.0
PD34547	DNMT3Ant-S638F	DNMT3A	78.63	20.5	-1.0	-1.0	-1.0	20.8	42.1	46.0	49.5
PD34547	DNMT3At-NM_175629:exon22:c.2479-2A>C	DNMT3A	78.63	10.4	-1.0	-1.0	-1.0	-1.0	28.5	33.6	39.4
PD41184	DNMT3Ant-A910V	DNMT3A	72.98	2.2	-1.0	-1.0	-1.0	-1.0	5.0	12.8	21.5
PD41184	DNMT3Ant-P804L	DNMT3A	72.98	7.4	-1.0	-1.0	-1.0	-1.0	22.9	28.3	33.4
PD41184	DNMT3Ant-R659H	DNMT3A	72.98	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41184	DNMT3At-NM_175629:exon8:c.1014+1G>A	DNMT3A	72.98	2.4	-1.0	-1.0	-1.0	-1.0	7.2	14.4	22.1
PD41291	JAK2-V617F	JAK2	77.7	53.8	49.7	50.6	51.3	53.9	56.2	56.8	57.5
PD41291	SF3B1-K666R	SF3B1	82.88	16.9	-1.0	-1.0	-1.0	12.2	39.2	43.7	49.6
PD41291	TP53t-C124X	TP53	74.31	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41134	TET2t-K753fs	TET2	80.21	11.6	-1.0	-1.0	-1.0	-0.6	31.2	36.2	41.1
PD41293	DNMT3Ant-Y724C	DNMT3A	62.87	2.2	-1.0	-1.0	-1.0	-1.0	7.8	12.4	17.5
PD41293	TET2t-Q185fs	TET2	62.87	9.1	-1.0	-1.0	-1.0	6.6	21.1	24.5	28.3
PD41131	TP53nt-G187S	TP53	72.68	5.0	-1.0	-1.0	-1.0	-1.0	14.0	21.3	31.8
PD41336	PPM1D-R552X	PPM1D	79.66	21.1	-1.0	-1.0	-1.0	22.7	40.6	43.9	47.3
PD41276	CBLt-W190X	CBL	69.28	37.3	21.0	26.8	30.5	38.8	44.9	46.2	48.0
PD41276	SF3B1-K666N	SF3B1	62.24	29.3	24.0	25.3	26.2	29.5	32.3	33.1	33.8
PD41276	SF3B1-K700E	SF3B1	69.28	24.2	-1.0	-1.0	7.9	26.9	37.9	40.3	43.0
PD34570	DNMT3At-R484fs	DNMT3A	80.99	15.1	-1.0	-1.0	-1.0	10.3	35.0	40.3	45.5
PD34570	TET2t-M1028fs	TET2	70.67	-0.4	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	1.8
PD41155	DNMT3Ant-S770P	DNMT3A	71.54	5.2	-1.0	-1.0	-1.0	-1.0	17.3	23.2	30.0
PD41155	PTPN11-G507A	PTPN11	71.54	40.3	11.0	23.7	30.2	43.3	51.3	52.9	54.9
PD41253	PPM1D-N477fs	PPM1D	78.92	34.0	10.3	19.4	24.2	36.3	44.2	45.9	48.0
PD41253	TET2t-N338fs	TET2	68.62	16.7	-1.0	-1.0	4.3	17.8	26.7	29.1	32.4
PD41254	KRAS-F78L	KRAS	73	30.0	-1.0	-1.0	5.0	33.9	47.3	50.0	54.2
PD41136	TET2t-Q531fs	TET2	63.45	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41136	TET2t-Q548X	TET2	63.45	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34556	DNMT3Ant-F868L	DNMT3A	76.01	0.7	-1.0	-1.0	-1.0	-1.0	-1.0	0.8	12.0
PD34556	DNMT3At-W860X	DNMT3A	86.18	33.9	-1.0	-1.0	12.9	38.1	50.8	53.1	56.4
PD34556	GNB1-L117M	GNB1	86.18	50.1	12.8	26.4	35.7	54.0	64.0	66.8	70.5
PD34556	PPM1D-E451X	PPM1D	86.18	43.4	15.5	24.6	31.6	46.5	54.8	56.7	58.8
PD34556	TET2t-N837fs	TET2	90.45	37.1	-1.0	7.1	17.7	41.6	52.9	55.8	58.4
PD34556	TET2t-T1086fs	TET2	90.45	39.3	1.9	16.7	25.5	43.0	52.6	54.8	57.5
PD41241	DNMT3Ant-P904L	DNMT3A	74	5.8	-1.0	-1.0	-1.0	-1.0	18.9	24.5	30.6

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41214	IDH2-R140Q	IDH2	75.07	22.9	-1.0	-1.0	-1.0	24.2	43.6	46.9	51.2
PD41214	TET2t-Q1834X	TET2	67.33	24.4	-1.0	1.8	9.3	26.7	37.4	39.7	41.9
PD41237	CBLnt-L399H	CBL	82.06	31.6	-1.0	-1.0	8.1	34.2	50.0	53.4	57.8
PD41237	CTCFt-Y392X	CTCF	78.21	18.3	-1.0	-1.0	-1.0	16.5	39.4	44.3	49.0
PD41237	TET2t-Q917X	TET2	74.51	30.7	8.5	15.3	20.0	33.0	40.9	42.7	44.3
PD41315	DNMT3Ant-D531N	DNMT3A	71.47	2.0	-1.0	-1.0	-1.0	-1.0	6.4	12.0	17.8
PD41315	DNMT3Ant-R882H	DNMT3A	79.69	13.0	-1.0	-1.0	-1.0	5.9	32.6	36.9	40.7
PD41315	TET2t-Q526fs	TET2	84.34	23.8	-1.0	-1.0	-1.0	26.7	41.0	43.7	46.7
PD41148	CBLnt-R420Q	CBL	76.61	10.5	-1.0	-1.0	-1.0	-1.0	29.5	34.7	40.4
PD41148	TET2t-L346fs	TET2	73.58	16.6	-1.0	-1.0	-1.0	17.3	31.3	35.2	38.3
PD41298	TET2t-I274fs	TET2	62.83	1.4	-1.0	-1.0	-1.0	-1.0	2.2	9.0	17.5
PD41294	DNMT3Ant-R379H	DNMT3A	66.49	1.3	-1.0	-1.0	-1.0	-1.0	0.7	7.7	15.6
PD41294	TET2t-Q321X	TET2	66.49	4.3	-1.0	-1.0	-1.0	-1.0	13.5	18.5	24.3
PD34562	ASXL1-C856fs	ASXL1	77.65	16.3	-1.0	-1.0	-1.0	14.8	35.7	39.6	44.1
PD34562	IDH1-R132H	IDH1	80.77	57.1	50.7	52.4	53.6	57.5	60.5	61.2	62.0
PD34562	PPM1D-S446X	PPM1D	77.65	24.1	-1.0	-1.0	-1.0	26.0	45.5	49.3	53.1
PD34562	SF3B1-K666R	SF3B1	84.43	27.6	-1.0	-1.0	-1.0	31.4	49.8	52.8	56.0
PD34562	SRSF2-95_103del	SRSF2	77.65	25.7	8.0	13.8	17.4	27.1	34.0	35.6	38.0
PD41300	ASXL1-Q491X	ASXL1	67.43	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41234	KRAS-Q22L	KRAS	78.91	29.2	-1.0	-1.0	3.4	33.2	46.6	49.1	52.0
PD41234	TET2nt-A1863V	TET2	73.58	25.5	-1.0	4.4	12.0	28.0	37.6	40.0	42.4
PD41297	CTCFnt-D710Y	CTCF	82.43	24.8	-1.0	-1.0	-1.0	27.4	44.4	47.4	51.0
PD41297	TET2nt-L1418P	TET2	78.57	20.9	-1.0	-1.0	-1.0	22.9	38.0	41.4	44.8
PD41303	CTCFt-K521X	CTCF	82.16	41.0	0.7	17.4	26.0	44.6	54.6	56.7	59.4
PD41303	DNMT3Ant-L888M	DNMT3A	71.54	28.3	-1.0	-1.0	-1.0	29.2	53.1	67.2	71.5
PD41303	JAK2-V617F	JAK2	82.16	51.6	42.3	45.5	47.4	52.3	56.2	57.0	58.3
PD34482	SF3B1-L712F	SF3B1	71.54	45.2	0.9	17.5	27.8	49.4	61.4	64.8	70.6
PD41325	CBLnt-C419S	CBL	73.99	10.0	-1.0	-1.0	-1.0	0.3	27.2	31.7	36.7
PD41325	TET2t-NM_001127208:exon10:c.4183-2A>G	TET2	82.35	25.6	-1.0	-1.0	3.2	28.7	41.8	44.4	47.2
PD41325	TET2t-Q321X	TET2	82.35	34.4	-1.0	3.4	14.8	38.9	50.5	52.6	55.1
PD41326	CBLnt-Q490K	CBL	72.38	27.9	-1.0	-1.0	-1.0	30.1	50.1	54.6	63.8
PD41301	CBLt-NM_005188:exon15:c.2252-2A>G	CBL	69.24	39.1	26.8	30.8	33.5	40.3	45.1	46.0	47.4
PD41233	ASXL1-H630fs	ASXL1	60.06	8.6	-1.0	0.4	2.6	8.9	14.2	15.8	17.4
PD41233	JAK2-V617F	JAK2	63.61	5.5	-1.0	-1.0	-1.0	0.0	15.9	19.2	22.8
PD41233	PTPN11-N308D	PTPN11	67.43	46.2	42.6	43.5	44.2	46.2	48.4	49.0	49.6
PD41233	TP53t-Q317X	TP53	60.06	14.6	-1.0	-1.0	-1.0	-1.0	48.6	60.1	60.1
PD41233	U2AF1-R156H	U2AF1	74.4	40.5	20.5	27.1	32.0	43.1	49.4	50.8	52.1
PD41146	TET2t-E1178fs	TET2	72.93	-0.5	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	2.6
PD41146	TET2t-N374fs	TET2	72.93	9.0	-1.0	-1.0	-1.0	4.8	22.2	26.0	30.4
PD41146	TET2t-Q866X	TET2	76.27	13.8	-1.0	-1.0	-1.0	9.3	32.9	37.0	42.8
PD41306	ASXL1-R860X	ASXL1	75.03	12.6	-1.0	-1.0	-1.0	7.1	30.8	36.0	40.5
PD41306	PPM1D-Q524X	PPM1D	78.19	34.2	-1.0	4.2	15.1	38.3	49.7	51.9	54.7
PD41306	SF3B1-K700E	SF3B1	85.47	39.8	1.3	19.0	27.7	43.5	52.6	54.5	56.6
PD41306	TET2nt-V1417G	TET2	78.19	22.7	-1.0	-1.0	-1.0	25.0	40.3	43.4	46.5
PD41306	TET2t-R1307fs	TET2	85.47	39.3	-1.0	13.4	23.2	43.9	53.7	56.1	58.6
PD41077	BRCC3nt-H127P	BRCC3	76.12	13.8	-1.0	-1.0	-1.0	10.8	32.1	36.0	40.4
PD41077	DNMT3Ant-E477K	DNMT3A	69.31	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41077	DNMT3At-A462fs	DNMT3A	76.12	20.4	-1.0	-1.0	-1.0	22.9	36.1	39.3	42.1
PD41311	ASXL1-L775X	ASXL1	76.76	14.9	-1.0	-1.0	2.3	15.6	25.0	27.6	30.7
PD41311	TP53nt-R158H	TP53	79.8	25.7	-1.0	-1.0	-1.0	28.3	48.1	51.0	55.1
PD41140	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	58.14	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41140	PTPN11-T219N	PTPN11	67.74	44.8	28.5	34.5	38.0	46.3	51.9	53.6	55.5
PD34428	CBLnt-V430M	CBL	74.15	3.6	-1.0	-1.0	-1.0	-1.0	11.3	17.7	27.5
PD34428	DNMT3Ant-R635W	DNMT3A	74.15	7.8	-1.0	-1.0	-1.0	-1.0	24.5	31.8	38.5
PD34428	PPM1D-C407fs	PPM1D	85.31	52.6	24.6	34.3	40.3	53.8	65.5	69.6	76.5

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41087	ASXL1-E906X	ASXL1	75.36	28.5	-1.0	4.5	14.0	31.6	41.0	43.2	45.3
PD41087	SRSF2-P95H	SRSF2	71.09	55.4	53.3	53.8	54.1	55.5	56.7	57.1	57.4
PD41087	SRSF2-P95L	SRSF2	67.75	29.8	14.1	19.2	22.4	31.1	37.2	38.8	40.5
PD41087	SRSF2-Y44H	SRSF2	71.09	42.3	30.7	34.7	36.8	43.3	47.8	49.0	50.3
PD41087	TET2t-S1015fs	TET2	61.02	NA	NA	NA	NA	NA	NA	NA	NA
PD34573	DNMT3Ant-W210C	DNMT3A	87.26	17.0	-1.0	-1.0	-1.0	13.6	37.4	41.4	46.3
PD41183	TET2t-Q745X	TET2	65.37	15.2	-1.0	-1.0	-1.0	16.1	29.9	32.3	34.8
PD34559	SF3B1-A744D	SF3B1	85.03	6.2	-1.0	-1.0	-1.0	-1.0	18.6	23.5	29.1
PD34559	SF3B1-G740R	SF3B1	85.03	15.0	-1.0	-1.0	-1.0	13.8	32.0	36.2	40.4
PD34559	TET2nt-T1393A	TET2	85.03	31.3	-1.0	-1.0	8.5	35.5	49.0	51.6	55.0
PD34559	TET2t-C1211fs	TET2	85.03	16.2	-1.0	-1.0	-1.0	13.5	36.9	41.1	46.0
PD34523	CTCFt-NM_006565:exon4:c.782-2A>G	CTCF	75.79	22.7	-1.0	-1.0	-1.0	25.4	40.5	43.1	46.1
PD34523	TET2nt-Q909K	TET2	75.79	31.7	-1.0	-1.0	-1.0	35.9	52.4	55.3	59.7
PD34523	TET2t-Q1537X	TET2	75.79	19.7	-1.0	-1.0	-1.0	21.2	36.8	39.7	42.5
PD41159	SF3B1-K700E	SF3B1	58.8	9.6	-1.0	-1.0	-1.0	7.6	22.2	25.1	28.8
PD41203	TET2nt-R1359H	TET2	76.41	22.6	-1.0	-1.0	-1.0	24.9	40.9	43.5	46.7
PD41203	TET2t-P413fs	TET2	76.41	26.1	0.3	8.4	15.0	28.4	36.9	39.0	41.2
PD41203	TET2t-S1586fs	TET2	79.32	24.0	-1.0	-1.0	-1.0	27.4	43.4	46.3	49.6
PD41203	TP53nt-R282W	TP53	76.41	6.2	-1.0	-1.0	-1.0	-1.0	20.0	26.9	33.3
PD34494	DNMT3At-NM_175629:exon8:c.856-1G>A	DNMT3A	87.76	29.7	-1.0	-1.0	-1.0	32.8	53.8	57.5	63.1
PD34494	PPM1D-K511X	PPM1D	84.81	17.4	-1.0	-1.0	-1.0	17.7	33.6	36.6	40.2
PD34494	TET2nt-E1178G	TET2	84.81	3.0	-1.0	-1.0	-1.0	-1.0	9.4	16.1	25.0
PD41150	DNMT3Ant-I780T	DNMT3A	78.09	22.1	-1.0	-1.0	-1.0	23.9	42.7	46.9	50.9
PD41150	DNMT3Ant-L754H	DNMT3A	74.69	6.3	-1.0	-1.0	-1.0	-1.0	19.7	24.8	31.4
PD41150	TET2t-N281fs	TET2	83.14	20.1	-1.0	-1.0	-1.0	21.4	39.0	42.6	46.6
PD41320	BRCC3nt-M142I	BRCC3	63.34	1.6	-1.0	-1.0	-1.0	-1.0	2.2	10.0	18.4
PD41151	DNMT3Ant-F732L	DNMT3A	74.92	1.6	-1.0	-1.0	-1.0	-1.0	5.4	10.4	15.1
PD41151	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	74.92	7.7	-1.0	-1.0	-1.0	-1.0	24.2	29.5	36.5
PD41151	TET2t-H193fs	TET2	74.92	12.1	-1.0	-1.0	-1.0	5.1	29.9	34.1	40.0
PD41151	TET2t-K1488fs	TET2	78.4	17.1	-1.0	-1.0	-1.0	15.9	36.2	40.0	44.5
PD41151	TET2t-Q831fs	TET2	74.92	10.8	-1.0	-1.0	-1.0	4.1	27.5	31.7	35.8
PD34509	TET2t-I1230fs	TET2	70.35	0.7	-1.0	-1.0	-1.0	-1.0	-1.0	5.7	13.4
PD41339	GNB1-C103F	GNB1	74.94	33.5	-1.0	-1.0	9.7	37.9	51.0	54.0	56.6
PD41339	TET2t-Q1507fs	TET2	71.91	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	3.7	8.0
PD41339	TP53nt-N239S	TP53	79.44	19.5	-1.0	-1.0	-1.0	20.7	37.9	41.0	44.5
PD41166	DNMT3Ant-Y660C	DNMT3A	72.72	4.8	-1.0	-1.0	-1.0	-1.0	16.3	21.4	27.6
PD41166	TET2nt-M1333R	TET2	77.42	27.1	-1.0	0.8	9.1	30.4	41.8	44.2	46.6
PD41313	SF3B1-A744P	SF3B1	75.25	11.4	-1.0	-1.0	-1.0	1.7	30.1	35.3	41.1
PD41260	ASXL1-H630fs	ASXL1	66.31	13.1	-1.0	-1.0	1.1	13.8	22.6	25.0	27.7
PD41260	DNMT3Ant-R736C	DNMT3A	66.31	1.6	-1.0	-1.0	-1.0	-1.0	3.0	10.0	18.2
PD34565	TET2nt-L1311Q	TET2	67.02	5.1	-1.0	-1.0	-1.0	-1.0	16.3	20.6	25.8
PD34565	TET2nt-S817F	TET2	74.11	22.6	-1.0	-1.0	3.4	24.8	37.2	39.5	42.7
PD41197	DNMT3Ant-R771Q	DNMT3A	73.16	7.6	-1.0	-1.0	-1.0	-1.0	22.5	28.7	37.4
PD41197	DNMT3Ant-Y735C	DNMT3A	73.16	1.7	-1.0	-1.0	-1.0	-1.0	1.0	10.4	19.5
PD41197	DNMT3At-E469X	DNMT3A	73.16	12.8	-1.0	-1.0	-1.0	11.8	27.2	30.4	34.9
PD34513	DNMT3At-R887X	DNMT3A	71.02	4.6	-1.0	-1.0	-1.0	-1.0	14.7	21.2	28.6
PD41174	TP53nt-R248W	TP53	71.04	21.1	-1.0	-1.0	-1.0	23.5	38.0	41.1	43.9
PD41324	CBLnt-V430M	CBL	71.78	10.3	-1.0	-1.0	-1.0	-1.0	29.1	35.6	42.0
PD41081	DNMT3At-Q696fs	DNMT3A	81.45	8.5	-1.0	-1.0	-1.0	-1.0	24.0	28.2	33.5
PD41081	TP53nt-R273H	TP53	66.95	15.8	-1.0	-1.0	-1.0	16.2	31.5	35.0	38.6
PD41081	U2AF1-Q157P	U2AF1	73.94	48.3	39.7	42.0	43.7	48.8	52.8	54.1	55.5
PD41295	DNMT3At-NM_175629:exon22:c.2597+1G>A	DNMT3A	64.32	0.0	-1.0	-1.0	-1.0	-1.0	-1.0	-0.7	7.4
PD41330	DNMT3Ant-D702V	DNMT3A	72.82	3.4	-1.0	-1.0	-1.0	-1.0	8.7	16.9	25.6

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41330	TET2t-Q1501X	TET2	84.82	22.4	-1.0	-1.0	-1.0	25.3	39.9	42.4	45.8
PD41274	ASXL1-L1266fs	ASXL1	61.63	6.1	-1.0	-1.0	-1.0	-1.0	19.2	23.3	30.3
PD41244	DNMT3Ant-D702G	DNMT3A	70.56	6.0	-1.0	-1.0	-1.0	-1.0	19.1	23.9	29.6
PD41244	DNMT3Ant-R882H	DNMT3A	70.56	6.4	-1.0	-1.0	-1.0	-1.0	20.0	26.5	33.6
PD41244	DNMT3Ant-Y660H	DNMT3A	70.56	2.3	-1.0	-1.0	-1.0	-1.0	5.9	14.0	21.5
PD41244	DNMT3At-K589X	DNMT3A	70.56	5.9	-1.0	-1.0	-1.0	-1.0	18.8	25.1	30.2
PD41244	DNMT3At-P777fs	DNMT3A	70.56	2.0	-1.0	-1.0	-1.0	-1.0	6.0	12.1	19.1
PD41285	DNMT3At-E856fs	DNMT3A	65.15	13.7	-1.0	-1.0	-0.5	14.3	25.0	26.8	29.0
PD41285	DNMT3At-NM_175629:exon9:c.1122+1G>-	DNMT3A	72.14	7.1	-1.0	-1.0	-1.0	-1.0	19.9	25.2	30.6
PD41285	SF3B1-K700E	SF3B1	72.14	18.0	-1.0	-1.0	-1.0	18.8	34.6	38.2	41.3
PD41285	TET2nt-P288R	TET2	62.45	9.3	-1.0	-1.0	-1.0	3.4	24.4	27.8	31.3
PD41286	DNMT3Ant-L653F	DNMT3A	61.28	-0.3	-1.0	-1.0	-1.0	-1.0	-1.0	0.6	4.6
PD41286	DNMT3At-Q415X	DNMT3A	61.28	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41161	BRCC3t-H127fs	BRCC3	76.31	18.2	-1.0	-1.0	-1.0	16.2	38.9	43.4	47.4
PD41161	DNMT3At-W330X	DNMT3A	73.22	1.9	-1.0	-1.0	-1.0	-1.0	5.7	11.1	18.6
PD41161	SRSF2-P95H	SRSF2	85.94	66.5	61.9	63.1	64.0	66.7	69.0	69.5	70.2
PD41161	TET2t-P1410fs	TET2	85.94	25.2	-1.0	-1.0	0.7	28.6	42.0	44.8	47.3
PD41161	TET2t-P1644fs	TET2	76.31	15.7	-1.0	-1.0	-1.0	15.1	32.2	35.5	39.9
PD41161	TET2t-S1039X	TET2	85.94	25.9	-1.0	-1.0	3.3	29.2	42.3	44.8	47.7
PD41344	ASXL1-Q546X	ASXL1	67.82	1.2	-1.0	-1.0	-1.0	-1.0	-0.2	8.1	15.9
PD41344	PPM1D-L538fs	PPM1D	76.88	32.2	5.7	15.5	21.0	34.7	43.4	45.5	47.4
PD41344	PPM1D-R458X	PPM1D	80.87	33.5	-1.0	12.5	20.0	36.9	46.0	48.1	50.3
PD41344	PPM1D-T483fs	PPM1D	76.88	46.5	37.1	39.9	42.0	47.3	51.3	52.2	53.5
PD41344	TET2nt-H1380D	TET2	74.19	17.5	-1.0	-1.0	-1.0	18.0	32.4	35.7	39.3
PD41344	TP53nt-I195T	TP53	80.87	17.2	-1.0	-1.0	-1.0	16.9	35.0	39.1	43.5
PD41154	DNMT3At-L723fs	DNMT3A	59.14	3.0	-1.0	-1.0	-1.0	-1.0	7.8	14.9	24.4
PD41154	SRSF2-P95A	SRSF2	66.18	16.6	-1.0	-1.0	-1.0	17.7	30.0	32.8	35.9
PD34558	ASXL1-Q1063fs	ASXL1	72.87	1.8	-1.0	-1.0	-1.0	-1.0	3.4	12.4	19.6
PD34558	SF3B1-K666N	SF3B1	86.81	44.9	19.5	28.5	34.3	47.8	56.0	57.7	59.6
PD41190	ASXL1-NM_015338:exon12:c.1720-2A>C	ASXL1	66.32	11.7	-1.0	1.2	4.1	12.1	18.6	20.3	22.1
PD41190	CBLt-P433fs	CBL	79.73	40.5	17.6	25.0	31.0	43.1	50.4	51.9	53.8
PD41190	TET2nt-H1881R	TET2	66.32	8.3	-1.0	-1.0	-1.0	-0.8	23.6	27.9	32.4
PD41190	TET2nt-T1372I	TET2	66.32	16.8	5.9	9.0	10.9	17.3	22.5	24.0	25.5
PD41278	DNMT3Ant-W860R	DNMT3A	61.72	1.1	-1.0	-1.0	-1.0	-1.0	-1.0	6.4	13.6
PD41278	PPM1D-C478X	PPM1D	76.91	27.1	-1.0	8.8	14.7	29.3	38.2	40.2	42.6
PD41156	SF3B1-K666M	SF3B1	80.82	50.8	42.4	44.7	46.4	51.4	55.2	56.2	57.4
PD34486	KRAS-T58I	KRAS	72.68	12.4	-1.0	-1.0	-1.0	8.7	29.4	33.6	37.6
PD41162	TET2nt-T97K	TET2	68.4	28.3	-1.0	-1.0	-0.3	30.4	48.0	51.7	58.3
PD34517	DNMT3Ant-S770L	DNMT3A	67.38	8.4	-1.0	-1.0	-1.0	-0.6	23.6	27.5	32.2
PD34517	DNMT3At-E427fs	DNMT3A	67.38	1.5	-1.0	-1.0	-1.0	-1.0	1.5	9.1	17.8
PD34517	DNMT3At-Y370X	DNMT3A	67.38	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34517	KRAS-G12C	KRAS	76.72	46.1	14.1	24.0	31.8	47.7	60.9	66.5	76.7
PD34517	TP53nt-L336V	TP53	67.38	10.9	-1.0	-1.0	-1.0	0.0	29.1	34.1	39.4
PD34578	DNMT3At-E21fs	DNMT3A	70.13	13.2	-1.0	-1.0	-1.0	11.6	29.2	32.7	36.4
PD34578	PPM1D-S403fs	PPM1D	67.63	6.2	-1.0	-1.0	-1.0	-1.0	19.2	24.4	30.0
PD41257	KRAS-I84T	KRAS	70.8	19.0	-1.0	-1.0	1.3	20.9	32.0	34.3	37.1
PD34551	PPM1D-R581X	PPM1D	65.74	6.3	-1.0	-1.0	-1.0	-1.0	19.4	25.2	30.0
PD41085	DNMT3Ant-F732S	DNMT3A	70.31	6.8	-1.0	-1.0	-1.0	-1.0	20.2	24.5	28.9
PD41088	CBLnt-R149Q	CBL	99.15	21.8	-1.0	-1.0	-1.0	20.5	47.1	51.0	56.1
PD41088	TP53nt-V272M	TP53	90.39	13.1	-1.0	-1.0	-1.0	-1.0	36.7	43.1	51.8
PD41169	TET2t-Q1542X	TET2	77.93	21.5	-1.0	-1.0	-1.0	23.9	39.5	42.6	45.7
PD41169	U2AF1-Q157R	U2AF1	83.43	62.9	56.8	58.3	59.8	63.3	66.0	66.7	67.5
PD41219	PPM1D-E476X	PPM1D	84.06	31.2	-1.0	1.8	13.4	34.7	46.4	48.6	51.0
PD41164	DNMT3Ant-A410T	DNMT3A	68.02	3.1	-1.0	-1.0	-1.0	-1.0	8.9	16.1	24.1
PD41164	DNMT3At-A525fs	DNMT3A	71.11	8.8	-1.0	-1.0	-1.0	-0.1	24.4	28.0	32.3
PD34538	ASXL1-R1171fs	ASXL1	77.49	21.9	-1.0	-1.0	-1.0	23.3	41.2	44.5	48.1

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD34538	PPM1D-R572X	PPM1D	81.27	18.1	-1.0	-1.0	-1.0	18.7	36.4	39.6	43.0
PD34538	SF3B1-H662Q	SF3B1	81.27	27.9	-1.0	-1.0	1.0	31.4	46.2	49.1	52.0
PD41165	DNMT3Ant-I705T	DNMT3A	88.84	18.6	-1.0	-1.0	-1.0	16.7	40.0	44.1	49.2
PD41165	DNMT3At-Q249X	DNMT3A	78.3	5.9	-1.0	-1.0	-1.0	-1.0	17.9	25.0	34.8
PD41165	TET2nt-R1359S	TET2	82.21	41.7	21.6	27.8	32.4	43.7	51.0	52.8	54.9
PD41165	TET2t-F681fs	TET2	75.31	6.4	-1.0	-1.0	-1.0	-1.0	20.0	26.2	32.4
PD41165	TET2t-V1054fs	TET2	82.21	25.9	-1.0	-1.0	-1.0	28.9	44.3	47.4	50.9
PD41165	TP53nt-M237V	TP53	82.21	31.7	-1.0	-1.0	0.6	36.7	51.4	54.3	57.4
PD41236	TET2t-L1916fs	TET2	75.45	9.0	-1.0	-1.0	-1.0	-1.0	25.8	30.9	37.0
PD34548	DNMT3Ant-F331V	DNMT3A	82.15	12.1	-1.0	-1.0	-1.0	4.8	30.2	35.1	40.4
PD34548	TET2t-K1254fs	TET2	82.15	20.8	-1.0	-1.0	-1.0	22.0	40.5	43.7	47.2
PD41334	DNMT3Ant-R635W	DNMT3A	68.72	3.6	-1.0	-1.0	-1.0	-1.0	11.7	17.7	25.4
PD41334	GNB1-D118H	GNB1	68.72	4.6	-1.0	-1.0	-1.0	2.5	11.7	13.8	16.2
PD41316	ASXL1-S958X	ASXL1	71.81	25.7	-1.0	-1.0	-1.0	28.9	44.5	47.6	51.1
PD41316	TET2t-K1720X	TET2	76.64	29.6	-1.0	-1.0	9.8	33.5	45.0	47.3	49.8
PD41316	TET2t-S1369X	TET2	68.7	5.6	-1.0	-1.0	-1.0	-1.0	17.4	22.5	27.0
PD34539	TET2t-Q1553fs	TET2	78.89	28.5	-0.7	10.2	17.1	31.0	39.9	41.8	44.0
PD41092	JAK2-V617F	JAK2	61.14	29.9	23.1	24.8	26.1	30.1	33.9	35.0	36.1
PD41323	TET2t-Q821X	TET2	64.54	7.7	-1.0	-1.0	-1.0	-1.0	22.7	27.9	34.9
PD34576	SF3B1-K666N	SF3B1	70.06	21.9	-1.0	-1.0	4.8	24.5	35.4	38.0	40.8
PD34576	TET2t-Q1687X	TET2	76.66	15.6	-1.0	-1.0	-1.0	14.9	33.0	36.2	40.1
PD34515	DNMT3At-NM_175629:exon18:c.2083-2A>G	DNMT3A	74.8	7.3	-1.0	-1.0	-1.0	-1.0	21.6	27.4	33.8
PD34525	DNMT3At-V441fs	DNMT3A	71.55	6.3	-1.0	-1.0	-1.0	-1.0	19.5	24.5	29.7
PD41529	CTCFnt-E520D	CTCF	81.29	23.8	-1.0	-1.0	-1.0	26.3	43.0	46.5	49.9
PD41529	GNB1-K57E	GNB1	73.86	21.3	-1.0	-1.0	-1.0	23.6	38.5	41.1	45.0
PD41529	PTPN11-T472M	PTPN11	73.86	34.8	-1.0	12.6	20.7	38.5	48.1	50.0	52.1
PD41529	TET2t-Q778X	TET2	73.86	14.5	-1.0	-1.0	-1.0	9.8	34.3	38.6	43.0
PD34566	PTPN11-P495L	PTPN11	81.29	42.3	21.0	27.4	33.2	44.7	52.1	53.6	55.2
PD34566	TET2nt-G1288V	TET2	76.99	28.0	-1.0	-1.0	7.1	31.4	43.1	45.7	48.8
PD34566	TET2nt-H1416R	TET2	67.58	7.2	-1.0	-1.0	-1.0	-1.0	21.5	26.0	30.7
PD34566	TP53nt-R175H	TP53	67.58	7.8	-1.0	-1.0	-1.0	-1.0	23.3	29.8	39.0
PD41106	ASXL1-Q1294fs	ASXL1	81.87	35.7	11.8	19.8	25.4	38.3	46.2	47.7	50.3
PD41106	DNMT3Ant-G843D	DNMT3A	66.48	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41106	DNMT3Ant-L637Q	DNMT3A	81.87	11.3	-1.0	-1.0	-1.0	3.7	28.7	32.4	36.8
PD41106	DNMT3Ant-Y908C	DNMT3A	74.3	12.0	-1.0	-1.0	-1.0	9.9	27.4	31.0	34.4
PD41106	TET2nt-Q1414E	TET2	76.94	32.2	9.0	17.4	22.1	34.4	42.6	44.4	46.2
PD41321	DNMT3Ant-F752V	DNMT3A	73.34	6.1	-1.0	-1.0	-1.0	-1.0	18.6	23.7	29.1
PD41321	TET2nt-A1341E	TET2	63.83	1.3	-1.0	-1.0	-1.0	-1.0	1.6	9.4	16.2
PD41321	TET2t-Q1537X	TET2	73.34	14.1	-1.0	-1.0	-1.0	14.5	27.6	30.4	34.4
PD41080	TET2nt-H1868Y	TET2	60.63	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41080	TET2t-G422fs	TET2	60.63	0.3	-1.0	-1.0	-1.0	-1.0	-1.0	2.9	9.1
PD41080	TET2t-Q232X	TET2	63.8	8.0	-1.0	-1.0	-1.0	-1.0	22.3	26.8	31.4
PD41080	TP53nt-C176F	TP53	60.63	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	-0.7	8.0
PD34495	BRCC3nt-R83C	BRCC3	82.92	-0.4	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	1.2
PD34495	PPM1D-P531fs	PPM1D	82.92	24.9	-1.0	-1.0	-1.0	26.7	45.8	49.5	53.9
PD34495	TET2t-I1105fs	TET2	82.92	18.5	-1.0	-1.0	-1.0	14.6	42.0	47.1	51.9
PD41119	DNMT3Ant-D768G	DNMT3A	69.84	2.3	-1.0	-1.0	-1.0	-1.0	2.4	11.8	21.0
PD41255	ASXL1-Q396X	ASXL1	62.96	2.0	-1.0	-1.0	-1.0	-1.0	7.5	11.0	14.8
PD34489	ASXL1-S852X	ASXL1	93.92	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34489	CBLnt-R420G	CBL	103.1	25.9	-1.0	-1.0	-1.0	27.4	50.8	55.3	60.5
PD34489	TET2t-A1769fs	TET2	93.92	19.4	-1.0	-1.0	-1.0	15.4	44.5	49.5	54.7
PD34489	TET2t-Q461fs	TET2	103.1	48.0	-1.0	4.9	24.4	53.9	68.0	70.7	73.5
PD42295	TP53nt-R273H	TP53	81.19	33.8	-1.0	-1.0	10.1	38.7	51.4	53.5	56.2
PD34500	PPM1D-W427X	PPM1D	86	28.6	-1.0	-1.0	0.4	32.6	46.9	49.5	52.9
PD34545	DNMT3At-E294X	DNMT3A	79.26	8.1	-1.0	-1.0	-1.0	-1.0	24.9	31.5	36.2
PD34545	DNMT3At-NM_175629:exon15:c.1851+1G>A	DNMT3A	79.26	2.7	-1.0	-1.0	-1.0	-1.0	9.1	14.9	20.9

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD34545	TET2nt-S1898F	TET2	79.26	27.0	-1.0	-1.0	-1.0	31.3	45.3	48.3	51.9
PD34545	TET2nt-T1399P	TET2	79.26	21.0	-1.0	-1.0	-1.0	22.3	40.9	44.3	47.5
PD34545	TET2t-Q1523X	TET2	79.26	9.6	-1.0	-1.0	-1.0	2.0	25.3	29.4	35.3
PD41238	SF3B1-K700E	SF3B1	81.3	26.8	-1.0	-1.0	-1.0	31.1	44.2	47.1	50.2
PD41238	TP53nt-V272G	TP53	77.51	11.2	-1.0	-1.0	-1.0	1.0	29.6	34.3	40.4
PD41322	TET2t-S1059X	TET2	80.02	25.7	-1.0	0.3	10.4	28.2	38.7	40.9	43.8
PD41266	TET2nt-S1290L	TET2	80.24	37.1	15.1	24.5	28.8	39.4	46.2	47.6	49.7
PD41266	TET2t-E808X	TET2	80.24	19.0	-1.0	-1.0	-1.0	20.2	35.5	38.3	40.9
PD41266	TET2t-L1819X	TET2	65.07	0.6	-1.0	-1.0	-1.0	-1.0	-1.0	3.5	11.8
PD41266	TET2t-Y1766X	TET2	80.24	31.8	-1.0	12.6	18.8	34.9	43.7	45.4	47.8
PD34541	BRCC3nt-C157R	BRCC3	74.03	46.5	-1.0	11.3	23.8	49.1	74.0	74.0	74.0
PD34541	DNMT3At-W330X	DNMT3A	74.03	7.6	-1.0	-1.0	-1.0	-1.0	21.6	26.5	31.6
PD34541	TET2nt-D1981N	TET2	74.03	14.8	-1.0	-1.0	-1.0	7.9	35.4	40.3	45.6
PD34541	TET2nt-P1367L	TET2	70.2	14.8	-1.0	-1.0	-1.0	13.7	31.7	35.4	38.7
PD34541	TET2t-L1740X	TET2	66.98	9.3	-1.0	-1.0	-1.0	-1.0	26.6	32.6	39.4
PD41083	DNMT3At-W330X	DNMT3A	89.6	25.9	-1.0	-1.0	-1.0	29.1	43.0	46.1	50.1
PD41083	TET2t-Q618X	TET2	77.48	13.2	-1.0	-1.0	-1.0	3.2	33.3	38.4	45.1
PD34481	SF3B1-K666N	SF3B1	79.63	45.0	31.7	35.6	38.3	46.3	52.0	53.2	54.6
PD41193	CBLt-NM_005188:exon9:c.1228-1G>A	CBL	72.25	38.5	24.0	28.5	31.6	39.9	45.5	47.0	48.4
PD41193	IDH2-R140Q	IDH2	67.02	27.6	13.9	17.7	20.7	28.6	34.6	36.1	37.9
PD41193	TET2nt-I1873T	TET2	64	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41101	TET2t-Q1068X	TET2	70.34	17.0	-1.0	-1.0	2.6	18.0	28.8	31.4	34.3
PD41178	ASXL1-R693X	ASXL1	70.32	20.9	-1.0	-1.0	2.3	23.3	34.8	37.3	40.1
PD41178	PPM1D-L484fs	PPM1D	70.32	-0.5	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	3.0
PD41230	ASXL1-S993fs	ASXL1	81.25	30.5	-1.0	5.2	14.0	34.3	44.4	46.8	49.2
PD41230	BRCC3t-C240X	BRCC3	81.25	30.0	-1.0	-1.0	9.1	34.2	46.2	48.2	51.2
PD41230	CBLnt-C404Y	CBL	66.89	-0.1	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	5.8
PD34502	DNMT3Ant-V830A	DNMT3A	71.14	-0.3	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	3.5
PD34502	TET2nt-R1878P	TET2	78.46	20.4	-1.0	-1.0	-1.0	22.5	38.3	41.2	44.2
PD34502	TET2t-K1049fs	TET2	74.11	19.5	-1.0	-1.0	-1.0	17.2	41.5	46.6	53.3
PD34502	TP53nt-Y220C	TP53	74.11	20.6	-1.0	-1.0	-1.0	21.6	42.0	46.1	49.8
PD41202	SF3B1-A604T	SF3B1	71.93	46.1	10.9	23.5	30.5	48.0	63.2	67.4	71.9
PD41202	SF3B1-K666N	SF3B1	68.94	41.7	4.5	19.6	28.1	45.7	54.8	56.9	59.8
PD41079	BRCC3t-W286X	BRCC3	78.71	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	7.8
PD41079	DNMT3Ant-F755S	DNMT3A	78.71	18.2	-1.0	-1.0	-1.0	13.2	42.9	47.7	52.5
PD41079	DNMT3At-NM_175629:exon14:c.1667+1G>A	DNMT3A	84.11	22.3	-1.0	-1.0	-1.0	23.7	43.0	46.4	51.0
PD34568	CTCFnt-T204I	CTCF	79.49	21.1	-1.0	-1.0	-1.0	22.4	39.7	43.1	46.2
PD41337	BRCC3nt-S156P	BRCC3	64.99	4.7	-1.0	-1.0	-1.0	-1.0	14.4	18.4	22.6
PD41337	DNMT3Ant-M779T	DNMT3A	61.98	2.8	-1.0	-1.0	-1.0	-1.0	10.2	14.8	19.5
PD41338	DNMT3Ant-G722D	DNMT3A	68.45	3.8	-1.0	-1.0	-1.0	-1.0	11.7	18.9	25.2
PD41338	TET2nt-H1380Y	TET2	62.04	0.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	3.3
PD41338	TP53nt-G244S	TP53	68.45	9.8	-1.0	-1.0	-1.0	6.4	23.7	27.3	31.1
PD41078	DNMT3Ant-R635Q	DNMT3A	62.81	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41078	TET2nt-G1275E	TET2	62.81	1.4	-1.0	-1.0	-1.0	-1.0	1.2	9.8	17.2
PD41078	TP53nt-C242F	TP53	65.94	6.5	-1.0	-1.0	-1.0	-1.0	18.9	23.0	26.8
PD41340	TET2nt-R1214W	TET2	73.83	16.7	-1.0	-1.0	-1.0	17.2	32.8	36.1	39.5
PD41199	BRCC3nt-L308P	BRCC3	73.41	0.8	-1.0	-1.0	-1.0	-1.0	-1.0	2.0	14.4
PD41199	DNMT3Ant-L647R	DNMT3A	73.41	8.2	-1.0	-1.0	-1.0	-1.0	25.3	31.5	40.8
PD41530	TET2nt-C1211Y	TET2	74.29	22.9	-1.0	0.0	9.1	25.1	34.8	37.3	39.9
PD41530	TET2nt-P1194R	TET2	74.29	22.4	-1.0	-1.0	-1.0	24.7	40.8	43.5	46.3
PD41530	TET2t-E1477fs	TET2	74.29	8.0	-1.0	-1.0	-1.0	0.4	22.4	26.7	31.3
PD41530	TET2t-I1859fs	TET2	77.98	20.6	-1.0	-1.0	-1.0	22.5	38.4	41.6	44.9
PD41341	ASXL1-K1437fs	ASXL1	76.94	35.1	15.3	21.6	26.1	37.1	44.4	45.9	47.7
PD41341	DNMT3Ant-G699D	DNMT3A	74.22	7.8	-1.0	-1.0	-1.0	-1.0	23.1	29.5	37.1
PD41341	DNMT3Ant-I310N	DNMT3A	70.73	2.5	-1.0	-1.0	-1.0	-1.0	7.1	14.5	21.8
PD41341	DNMT3At-C351fs	DNMT3A	70.73	9.4	-1.0	-1.0	-1.0	2.8	24.0	28.8	32.7

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41341	DNMT3At-NM_175629:exon22:c.2597+2T>G	DNMT3A	67.75	3.1	-1.0	-1.0	-1.0	-1.0	8.6	16.4	23.2
PD41341	SF3B1-K700E	SF3B1	67.75	10.6	-1.0	-1.0	-1.0	3.9	26.5	31.1	35.4
PD41341	TET2t-L1511X	TET2	67.75	3.7	-1.0	-1.0	-1.0	-1.0	12.4	17.4	22.1
PD41341	TET2t-S56fs	TET2	74.22	18.0	-1.0	-1.0	-1.0	19.3	33.4	36.4	40.1
PD34469	DNMT3Ant-V675M	DNMT3A	70.56	5.8	-1.0	-1.0	-1.0	-1.0	18.4	24.1	29.8
PD34469	DNMT3At-V341fs	DNMT3A	70.56	4.5	-1.0	-1.0	-1.0	-1.0	14.4	20.9	27.4
PD34469	SF3B1-K666T	SF3B1	73.57	36.3	15.6	22.9	28.1	38.5	45.1	46.7	48.5
PD41342	DNMT3Ant-F755S	DNMT3A	64.9	9.4	-1.0	-1.0	-1.0	4.3	23.7	27.3	31.2
PD34493	SF3B1-K666N	SF3B1	66.25	5.5	-1.0	-1.0	-1.0	0.9	14.6	17.7	21.5
PD34493	U2AF1-Q157R	U2AF1	76.62	56.9	52.3	53.3	54.4	57.1	59.6	60.3	60.9
PD41343	DNMT3Ant-V778L	DNMT3A	75.93	6.7	-1.0	-1.0	-1.0	-1.0	20.3	27.6	34.7
PD41267	DNMT3Ant-S75F	DNMT3A	83.77	40.6	-1.0	-1.0	12.9	42.5	63.0	72.9	83.8
PD41267	DNMT3At-G550fs	DNMT3A	75.01	7.4	-1.0	-1.0	-1.0	-1.0	22.9	29.6	35.8
PD34549	DNMT3At-E664X	DNMT3A	72.47	12.9	-1.0	-1.0	-1.0	7.1	31.4	35.4	38.7
PD34549	PPM1D-T483fs	PPM1D	75.7	31.3	-1.0	5.7	15.4	34.9	45.1	47.1	49.2
PD34483	DNMT3Ant-C387W	DNMT3A	80.01	16.9	-1.0	-1.0	-1.0	16.6	35.5	39.1	42.9
PD34483	TET2t-I274fs	TET2	69.7	4.2	-1.0	-1.0	-1.0	-1.0	14.4	19.9	24.4
PD34512	DNMT3Ant-K361E	DNMT3A	79.8	5.9	-1.0	-1.0	-1.0	-1.0	18.8	26.3	35.1
PD34512	TET2nt-L1872P	TET2	79.8	12.9	-1.0	-1.0	-1.0	3.9	33.8	38.7	44.1
PD34512	U2AF1-Q157P	U2AF1	79.8	54.7	42.5	46.6	49.3	55.8	60.4	61.7	63.0
PD41270	DNMT3At-E578X	DNMT3A	60.87	1.7	-1.0	-1.0	-1.0	-1.0	5.6	11.0	16.4
PD41270	DNMT3At-R598X	DNMT3A	57.68	-0.8	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41270	TP53nt-R248Q	TP53	67.76	17.1	-1.0	-1.0	-1.0	18.7	29.8	32.2	34.8
PD34492	SF3B1-D621N	SF3B1	87.95	44.8	7.2	23.1	31.7	48.4	58.4	60.4	62.7
PD34492	TET2t-R1216X	TET2	84.08	20.5	-1.0	-1.0	-1.0	22.1	41.7	44.7	48.2
PD41121	TET2t-S792X	TET2	85.17	32.4	-1.0	-1.0	9.1	36.9	49.8	52.3	54.9
PD41209	DNMT3At-Q485X	DNMT3A	62.95	1.7	-1.0	-1.0	-1.0	-1.0	4.6	10.8	18.4
PD41209	DNMT3At-S839fs	DNMT3A	62.95	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41256	TET2t-Q1624X	TET2	80.76	24.7	-1.0	-1.0	5.3	27.8	39.1	42.2	45.3
PD41256	TET2t-T1554fs	TET2	87.81	42.2	4.9	19.8	28.8	46.3	55.7	57.8	60.1
PD41248	CBLnt-I383M	CBL	73.46	23.3	-1.0	-1.0	-1.0	25.8	42.6	46.0	49.0
PD41248	KRAS-T50I	KRAS	76.59	23.5	-1.0	-1.0	-1.0	27.0	40.9	43.4	46.3
PD41248	PTPN11-R265Q	PTPN11	73.46	22.4	-1.0	-1.0	6.0	24.6	35.7	38.1	40.8
PD41248	TET2t-T759fs	TET2	81.01	37.3	-1.0	13.2	22.9	40.9	50.8	53.1	55.9
PD41089	DNMT3Ant-R326S	DNMT3A	70.51	0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	9.7
PD41086	SF3B1-A744P	SF3B1	73.36	15.5	-1.0	-1.0	-1.0	12.6	35.1	38.7	42.4
PD41086	TET2nt-Q1699R	TET2	73.36	12.5	-1.0	-1.0	-1.0	3.7	31.6	37.5	42.3
PD41223	TET2t-Q976X	TET2	64.67	6.4	-1.0	-1.0	-1.0	-1.0	17.7	22.7	28.0
PD41103	DNMT3Ant-R882H	DNMT3A	74.38	26.3	17.2	19.3	20.9	26.6	31.6	32.7	34.1
PD41095	DNMT3Ant-L295P	DNMT3A	68.36	17.4	-1.0	-1.0	-1.0	18.7	32.3	34.9	38.6
PD34567	PPM1D-R458X	PPM1D	68.97	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41082	GNB1-K57E	GNB1	63.49	18.8	-1.0	-1.0	2.9	20.9	31.0	33.2	35.6
PD41082	SF3B1-K666N	SF3B1	63.49	34.8	27.5	29.6	30.9	35.3	38.5	39.4	40.5
PD41082	TET2nt-L1322Q	TET2	70.96	28.3	3.3	12.8	18.4	30.5	38.1	39.8	41.6
PD41082	TET2nt-Q1274R	TET2	59.7	2.7	-1.0	-1.0	-1.0	-1.0	9.5	12.9	16.9
PD41082	TET2t-H435fs	TET2	63.49	18.5	-1.0	0.5	6.0	20.0	29.1	31.0	33.3
PD41082	TET2t-Q1542X	TET2	66.64	16.3	-1.0	-1.0	-1.0	17.7	28.6	30.8	33.4
PD41082	TET2t-Q1825X	TET2	56.51	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41082	TET2t-S315fs	TET2	59.7	9.1	-1.0	-1.0	-1.0	8.7	18.6	20.4	23.2
PD34529	SF3B1-A1117S	SF3B1	81.9	43.7	5.2	23.1	32.1	47.1	56.6	58.9	60.8
PD34563	DNMT3Ant-M761V	DNMT3A	81.64	9.2	-1.0	-1.0	-1.0	-1.0	24.9	31.5	38.6
PD34563	TP53t-W146X	TP53	86.79	13.4	-1.0	-1.0	-1.0	-1.0	32.5	38.8	47.4
PD41067	DNMT3At-Y284X	DNMT3A	61.64	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34553	SF3B1-K666N	SF3B1	65.52	-0.5	-1.0	-1.0	-1.0	-1.0	-1.0	-0.1	2.8
PD34553	TET2t-L532X	TET2	65.52	11.2	-1.0	-1.0	-1.0	4.5	27.9	32.7	37.4
PD41268	JAK2-V617F	JAK2	63.84	13.9	-1.0	-1.0	-1.0	14.3	26.0	28.6	31.1
PD41317	DNMT3Ant-M880V	DNMT3A	84.92	19.2	-1.0	-1.0	-1.0	19.8	38.4	42.2	46.4
PD34519	PPM1D-S446fs	PPM1D	77.52	29.8	-1.0	2.4	12.2	33.5	44.2	46.1	48.6

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41272	SF3B1-K666N	SF3B1	72.9	28.3	2.3	11.2	15.9	30.4	39.6	41.5	43.6
PD34499	JAK2-V617F	JAK2	77.62	26.4	-1.0	-1.0	1.6	29.7	43.1	46.2	49.2
PD34499	TET2nt-C1135Y	TET2	77.62	21.5	-1.0	-1.0	-1.0	23.6	38.0	40.8	44.0
PD34499	TET2nt-H269N	TET2	73.77	30.5	-1.0	-1.0	-1.0	34.1	49.9	53.5	58.1
PD34499	TET2nt-I1873T	TET2	70.69	6.5	-1.0	-1.0	-1.0	5.9	13.2	15.3	17.8
PD34499	TET2nt-L1210P	TET2	77.62	46.0	37.4	39.9	41.3	46.5	50.8	51.7	52.7
PD34499	TET2t-L1447fs	TET2	80.73	20.2	-1.0	-1.0	-1.0	22.2	34.3	37.4	40.5
PD34499	TET2t-Q417X	TET2	80.73	26.8	-1.0	-1.0	1.9	30.4	44.0	46.7	49.4
PD34499	TET2t-S675X	TET2	70.69	6.6	-1.0	-1.0	-1.0	-1.0	19.8	26.2	32.8
PD34499	TET2t-Y1294fs	TET2	80.73	43.8	34.0	37.0	38.7	44.5	48.7	49.6	50.9
PD41098	TET2nt-T621N	TET2	83.52	26.7	-1.0	-1.0	6.1	29.8	42.1	44.7	47.9
PD41098	TET2t-L230fs	TET2	83.52	54.9	30.6	38.2	43.6	55.2	67.6	72.8	82.5
PD41273	CTCFnt-K592N	CTCF	66.75	27.5	-1.0	-1.0	-1.0	29.9	46.0	50.3	63.2
PD34546	PTPN11-L126S	PTPN11	74.38	54.2	35.9	42.1	46.3	55.7	63.1	65.2	69.0
PD41333	TET2nt-D1376A	TET2	74.35	32.5	9.1	17.0	22.5	34.8	42.6	44.2	46.0
PD41105	TET2nt-Q70R	TET2	77.19	5.9	-1.0	-1.0	-1.0	-1.0	16.6	21.0	25.0
PD41105	TET2t-P101fs	TET2	77.19	3.4	-1.0	-1.0	-1.0	-1.0	11.8	16.3	20.5
PD41113	DNMT3Ant-R882H	DNMT3A	74.02	8.2	-1.0	-1.0	-1.0	-1.0	24.7	30.0	36.8
PD34536	DNMT3At-K343fs	DNMT3A	68.59	10.0	-1.0	-1.0	-1.0	3.3	25.8	30.0	34.5
PD34536	TET2nt-C1221Y	TET2	77.71	21.6	-1.0	-1.0	-1.0	23.8	37.8	40.8	43.8
PD34510	TET2t-V1432fs	TET2	70.04	7.2	-1.0	-1.0	-1.0	-1.0	20.5	26.7	32.0
PD41216	DNMT3Ant-P700L	DNMT3A	74.88	2.2	-1.0	-1.0	-1.0	-1.0	4.2	11.8	21.5
PD41216	TET2t-NM_001127208:exon8:c.3955-2A>G	TET2	83.67	27.1	-1.0	-1.0	-1.0	30.7	44.8	47.5	51.8
PD41216	TET2t-S509X	TET2	74.88	-0.6	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	0.6
PD41217	DNMT3At-NM_175629:exon17:c.2082+2T>G	DNMT3A	69	0.2	-1.0	-1.0	-1.0	-1.0	-1.0	0.4	9.7
PD41217	DNMT3At-R320X	DNMT3A	69	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41247	CBLnt-Q379R	CBL	79.87	14.3	-1.0	-1.0	-1.0	5.7	35.7	40.1	45.1
PD41247	IDH2-R140Q	IDH2	84.26	40.9	-1.0	13.7	25.9	45.7	55.7	57.6	60.0
PD41247	SF3B1-G1082V	SF3B1	79.87	48.4	9.2	24.9	34.2	50.8	63.4	67.8	75.1
PD41247	TET2t-T1331fs	TET2	79.87	24.9	-1.0	-1.0	-1.0	27.9	43.2	45.5	48.1
PD41305	SRSF2-P95H	SRSF2	71.09	49.0	44.6	45.9	46.7	49.3	51.4	52.0	52.7
PD41242	TET2nt-L1332P	TET2	75.9	43.3	33.1	36.3	38.3	44.0	48.4	49.5	50.6
PD41242	TET2t-I274fs	TET2	75.9	44.9	35.8	38.3	40.1	45.6	49.7	50.8	52.0
PD41242	TET2t-K603X	TET2	82.08	37.5	1.5	14.9	22.7	40.6	51.5	54.1	56.6
PD41242	TET2t-S1481fs	TET2	69	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41242	TET2t-S1798X	TET2	82.08	27.3	-1.0	-1.0	9.3	30.7	42.2	44.8	47.1
PD41070	DNMT3Ant-R379C	DNMT3A	64.67	2.1	-1.0	-1.0	-1.0	-1.0	6.0	12.1	18.1
PD41070	TET2nt-L1322P	TET2	64.67	8.8	-1.0	-1.0	-1.0	1.6	23.1	27.8	33.0
PD41071	TET2t-K1197X	TET2	76.04	19.9	-1.0	-1.0	-1.0	21.9	35.4	38.8	42.0
PD41071	TET2t-K664fs	TET2	80.77	18.8	-1.0	-1.0	-1.0	20.1	35.1	38.2	42.1
PD41071	TP53nt-P72S	TP53	65.65	2.1	-1.0	-1.0	-1.0	-1.0	5.1	11.7	19.5
PD41346	ASXL1-E602X	ASXL1	72.08	42.9	35.8	37.5	39.1	43.2	46.7	47.6	48.6
PD41346	SRSF2-P95H	SRSF2	83.15	61.5	58.9	59.6	60.1	61.6	62.9	63.3	63.8
PD41104	DNMT3Ant-N838D	DNMT3A	76.23	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41104	GNB1-K57E	GNB1	76.23	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD41240	TET2t-E566X	TET2	74.94	8.3	-1.0	-1.0	-1.0	-1.0	23.3	29.5	34.3
PD41240	TET2t-I274fs	TET2	74.94	19.6	-1.0	-1.0	-1.0	18.0	41.4	45.9	50.3
PD41224	TET2nt-G1361R	TET2	92.38	35.5	-1.0	4.6	14.4	40.0	52.0	54.6	57.5
PD41225	DNMT3Ant-R882S	DNMT3A	69.8	5.6	-1.0	-1.0	-1.0	1.2	15.3	18.7	22.3
PD41125	CTCFnt-Q65H	CTCF	64.5	24.7	-1.0	-1.0	-1.0	26.6	45.4	49.7	55.4
PD34491	PPM1D-E539X	PPM1D	83.96	18.0	-1.0	-1.0	-1.0	15.7	39.9	43.9	48.3
PD34503	ASXL1-I641fs	ASXL1	70.83	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34503	DNMT3Ant-L295P	DNMT3A	80.88	31.2	-1.0	1.4	13.2	34.9	45.9	48.1	50.7
PD34503	TET2t-Q1828X	TET2	80.88	21.1	-1.0	-1.0	-1.0	23.2	36.4	39.6	42.7
PD34542	TET2nt-G1861V	TET2	66.16	-0.7	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34542	U2AF1-S34F	U2AF1	81.49	53.5	40.1	45.3	48.1	54.7	59.8	61.2	62.8

PID	Site	Gene	Age At Study Entry	Age At Onset Mean	Age At Onset _Q05	Age At Onset _Q10	Age At Onset _Q16	Age At Onset _Q50	Age At Onset _Q84	Age At Onset _Q90	Age At Onset _Q95
PD41107	DNMT3Ant-S770L	DNMT3A	82.68	24.4	-1.0	-1.0	-1.0	27.1	43.5	46.5	49.4
PD41107	TET2nt-H1219Y	TET2	73.57	5.9	-1.0	-1.0	-1.0	-1.0	16.8	20.8	24.8
PD34537	CBLnt-V363M	CBL	73.71	26.9	-1.0	-1.0	-1.0	24.9	54.2	63.4	73.7
PD41262	DNMT3Ant-R736H	DNMT3A	70.82	8.6	-1.0	-1.0	-1.0	8.3	17.2	19.2	21.7
PD41262	DNMT3At-Q842X	DNMT3A	74	13.8	-1.0	-1.0	-1.0	6.7	33.1	38.7	44.9
PD41262	TET2t-T1091fs	TET2	70.82	6.8	-1.0	-1.0	-1.0	5.8	15.0	17.4	20.4
PD41075	SRSF2-P95L	SRSF2	70.69	5.6	-1.0	-1.0	-1.0	0.0	15.7	19.9	23.5
PD41186	TP53nt-L348F	TP53	76.14	43.3	-1.0	3.8	15.8	45.9	72.0	76.1	76.1
PD41280	CBLnt-C404Y	CBL	70.26	3.9	-1.0	-1.0	-1.0	-1.0	12.7	18.7	25.0
PD41280	TET2t-L1819fs	TET2	75.36	11.3	-1.0	-1.0	-1.0	9.0	26.2	29.3	32.5
PD34561	TET2nt-C1289F	TET2	71.97	25.5	2.0	10.0	14.9	27.2	35.7	37.7	40.2
PD34561	TET2t-G898X	TET2	79.23	26.2	-1.0	4.6	11.8	28.5	39.0	41.4	45.0
PD41110	PPM1D-K549X	PPM1D	62.9	5.4	-1.0	-1.0	-1.0	-1.0	15.6	19.5	24.0
PD41208	KRAS-A146T	KRAS	64.74	4.7	-1.0	-1.0	-1.0	-1.0	14.8	20.1	26.2
PD41182	ASXL1-K1025fs	ASXL1	92.51	40.1	12.2	22.5	28.5	42.8	52.2	53.6	56.0
PD41182	TET2t-G563X	TET2	92.51	31.7	-1.0	-1.0	-1.0	36.0	57.5	61.0	65.1
PD41196	DNMT3Ant-S770L	DNMT3A	63.98	11.9	-1.0	-1.0	-1.0	11.1	25.5	28.4	30.9
PD41231	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	76.64	1.8	-1.0	-1.0	-1.0	-1.0	0.1	9.7	21.2
PD41246	JAK2-V617F	JAK2	76.54	41.5	25.3	30.7	34.2	43.1	49.1	50.5	51.9
PD41246	TET2nt-N1266S	TET2	76.54	11.8	-1.0	-1.0	-1.0	6.4	28.9	33.1	39.0
PD41287	BRCC3t-T166fs	BRCC3	67.8	4.7	-1.0	-1.0	-1.0	-1.0	14.1	20.9	27.3
PD41288	TP53nt-Y220C	TP53	64.4	8.9	-1.0	-1.0	-1.0	2.0	23.6	27.5	31.3
PD34520	TET2nt-C1271G	TET2	73.07	12.4	-1.0	-1.0	-1.0	6.9	30.3	34.1	39.8
PD34520	TET2t-NM_001127208:exon5:c.3501-2A>C	TET2	73.07	1.7	-1.0	-1.0	-1.0	-1.0	6.8	10.3	13.6
PD41229	TET2t-N528fs	TET2	62.5	-0.9	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0	-1.0
PD34477	DNMT3Ant-Y793N	DNMT3A	75.28	7.6	-1.0	-1.0	-1.0	-1.0	21.9	27.8	34.1
PD34477	TET2t-Q962X	TET2	65.55	0.9	-1.0	-1.0	-1.0	-1.0	-1.0	3.6	14.6
PD34477	TET2t-T621fs	TET2	79.59	23.8	-1.0	-1.0	4.0	26.5	38.6	41.3	44.1
PD34477	TP53nt-P151R	TP53	65.55	3.1	-1.0	-1.0	-1.0	-1.0	10.3	15.9	22.6
PD34488	CBLnt-C404Y	CBL	76.94	7.4	-1.0	-1.0	-1.0	-1.0	23.5	30.1	38.0
PD34488	SRSF2-R47P	SRSF2	73.8	12.0	-1.0	-1.0	-1.0	3.6	31.4	36.2	41.4
PD34488	TET2t-S402X	TET2	88.07	26.2	-1.0	-1.0	-1.0	29.8	44.4	47.1	50.5
PD41264	BRCC3t-NM_001018055:exon7:c.548+1G>A	BRCC3	70.84	11.3	-1.0	-1.0	-1.0	3.6	29.2	33.8	38.9
PD41264	DNMT3At-C586fs	DNMT3A	81.35	20.0	-1.0	-1.0	-1.0	20.1	38.9	42.5	46.9
PD41264	TET2t-NM_001127208:exon7:c.3804-2A>G	TET2	70.84	5.1	-1.0	-1.0	-1.0	-1.0	15.3	19.8	24.9

Table 12 | Inherited genotypes of*JAK2*-V617F positive individuals at 12 loci previously shown to confer an increased risk of MPN or *JAK2*-V617F-driven CH

Sample ID	rs1548483 (T=risk)	rs7705526 (A=risk)	rs2853677 (G=risk)	rs58270997 (T=risk)	rs7310615 (C=risk)	rs59384377 (T=risk)	46_1 haplotype* (GGCC=risk)	rs621940 (G=risk)	rs1800056 (C=risk)
PD41246	CC	CA	GA	-	-	AT	GGCC	CG	TT
PD34543	CC	AA	GG	CT	GG	AT	GGCC	CG	TC
PD41084	CC	CA	GA	CC	GG	AA	TCTT	CC	TT
PD41092	CC	CA	GA	CC	GG	AA	TCTT	CG	TT
PD41268	CC	CA	GA	CT	CG	AA	TCTT	CC	TT
PD34499	CC	CA	GA	CT	CG	AA	TCTT	CC	TT
PD41114	CT	CC	GA	CT	CG	AA	TCTT	CG	TT
PD34521	CC	CA	GA	CC	GG	AA	TCTT	CC	TT
PD34514	CC	CA	AA	CT	CG	AA	TCTT	CC	TT
PD41291	CT	CC	AA	CC	GG	AT	GGCC	CG	TT
PD41303	CT	CA	GA	CT	GG	AA	TCTT	CC	TT
PD41233	CC	CA	GG	CC	GG	AA	TCTT	CG	TC

* The 46/1 haplotype is characterised by four SNPs in complete linkage disequilibrium: rs3780367, rs10974944, rs12343867, rs1159782

Table 13 | Somatic mutations identified in TwinsUK cohort

Sample ID	Family ID	Chr	Position	WT	MT	WT Count	MT Count	VAF	Gene	Protein	Effect
PD42446b	1	4	106157058	C	-	3384	39	0.012	TET2	p.F653fs	frameshift
PD42349b	2	2	25463571	ACCAG	-	2207	15	0.007	DNMT3A	p.L703fs	frameshift
PD42350b	2	2	25466797	C	T	2015	11	0.005	DNMT3A	p.V636M	missense
PD42350b	2	2	198266834	T	C	1976	101	0.049	SF3B1	p.K700E	missense
PD42320b	3	2	25458692	G	-	1560	149	0.087	DNMT3A	p.F827fs	frameshift
PD42320b	3	4	106155102	G	-	1963	12	0.006	TET2	p.M1fs	frameshift
PD42320b	3	4	106157845	C	T	2305	202	0.081	TET2	p.Q916X	stopgain
PD42320b	3	4	106180860	T	TTTG	2220	193	0.08	TET2	p.N1296fs	in-frame
PD42329b	4	1	1747229	T	C	2085	23	0.011	GNB1	p.K57E	missense
PD42329b	4	4	106157522	AAGTA	-	2103	39	0.018	TET2	p.E808fs	frameshift
PD42306c	5	2	25468910	G	A	2272	12	0.005	DNMT3A	p.Q485X	stopgain
PD42365b	6	2	25463182	G	A	2060	134	0.061	DNMT3A	p.R771X	stopgain
PD42365b	6	20	31022937	C	-	2700	34	0.012	ASXL1	p.P808fs	frameshift
PD42393b	6	2	25464537	C	T	2323	18	0.008	DNMT3A	p.R659H	missense
PD42358b	7	2	25457192	G	C	1978	23	0.012	DNMT3A	p.R899G	missense
PD42358b	7	2	25466800	G	A	1792	36	0.02	DNMT3A	p.R635W	missense
PD42363b	7	2	25463507	A	C	1807	108	0.056	DNMT3A	c.2173+2T>G	splicing
PD42430b	8	4	106197411	CTCT	-	2779	28	0.01	TET2	p.A1915fs	frameshift
PD42399b	9	1	1747229	T	C	2681	26	0.01	GNB1	p.K57E	missense
PD42399b	9	2	198267361	T	C	2104	495	0.19	SF3B1	p.K666E	missense
PD42370b	10	17	7577120	C	T	2137	14	0.007	TP53	p.R273H	missense
PD42437b	11	2	25462068	A	G	1743	240	0.121	DNMT3A	p.I780T	missense
PD42396b	12	2	25463196	TT	-	1949	26	0.013	DNMT3A	p.K766fs	frameshift
PD42396b	12	2	25463508	C	T	1699	13	0.008	DNMT3A	c.2173+1G>A	splicing
PD42423b	12	2	25470498	G	A	1663	512	0.235	DNMT3A	p.R326C	missense
PD42366b	13	2	25464468	A	C	2382	12	0.005	DNMT3A	p.M682R	missense
PD42402b	13	2	25463181	C	G	1750	29	0.016	DNMT3A	p.R771P	missense
PD42453b	14	4	106155334	AC	-	2495	23	0.009	TET2	p.T79fs	frameshift
PD42463b	15	2	25463286	C	T	1581	18	0.011	DNMT3A	p.R736H	missense
PD42452b	16	2	25469936	A	C	2035	48	0.023	DNMT3A	p.I369S	missense
PD42336b	17	4	106162555	G	A	2260	51	0.022	TET2	p.V1157M	missense
PD42360b	17	2	25457174	G	C	2147	148	0.065	DNMT3A	p.L905V	missense
PD42464b	18	2	25470914	C	A	1363	13	0.009	DNMT3A	p.E283X	stopgain
PD42367b	19	2	25467128	A	T	2114	21	0.01	DNMT3A	p.C583S	missense
PD42367b	19	4	106157809	C	T	2129	16	0.007	TET2	p.Q904X	stopgain
PD42367b	19	4	106182938	T	A	1453	9	0.006	TET2	p.L1326X	stopgain
PD42435b	19	2	25463237	G	T	2156	21	0.01	DNMT3A	p.F752L	missense
PD42435b	19	2	25463286	C	T	1951	38	0.019	DNMT3A	p.R736H	missense
PD42435b	19	4	106193931	C	T	2690	16	0.006	TET2	p.R1465X	stopgain
PD42357c	20	11	119149284	T	C	2101	15	0.007	CBL	p.V431A	missense
PD42357c	20	17	7578522	T	A	2372	12	0.005	TP53	p.Q136H	missense
PD42362c	20	2	25467408	C	T	2483	25	0.01	DNMT3A	c.1667+1G>A	splicing
PD42362c	20	4	106156540	C	T	2971	40	0.013	TET2	p.Q481X	stopgain
PD42328c	21	2	25463538	A	-	2157	29	0.013	DNMT3A	p.I715fs	frameshift
PD42328c	21	2	25464573	A	T	2199	16	0.007	DNMT3A	p.L647H	missense
PD42334c	21	2	25462020	C	T	1731	18	0.01	DNMT3A	p.G796D	missense
PD42334c	21	2	25463184	G	T	1670	127	0.071	DNMT3A	p.S770X	stopgain
PD42327b	22	2	25462014	A	C	1909	10	0.005	DNMT3A	p.L798R	missense
PD42327b	22	4	106157317	C	T	2634	26	0.01	TET2	p.Q740X	stopgain
PD42465b	23	2	25466797	C	G	1620	9	0.006	DNMT3A	p.V636L	missense
PD42465b	23	2	25469918	A	-	1578	8	0.006	DNMT3A	c.3284+1->GT	splicing
PD42465b	23	X	154306952	AT	-	1755	10	0.006	BRCC3	p.H126fs	frameshift
PD42344b	24	2	25459804	C	T	1190	8	0.007	DNMT3A	c.2478+1G>A	splicing
PD42344b	24	4	106164913	C	T	1660	15	0.009	TET2	p.R1261C	missense
PD42344b	24	4	106196705	C	T	2964	18	0.006	TET2	p.Q1680X	stopgain
PD42467b	24	2	25462086	T	C	1975	20	0.01	DNMT3A	c.2323-2A>G	splicing
PD42467b	24	2	25463508	C	T	2019	16	0.008	DNMT3A	c.2173+1G>A	splicing
PD42467b	24	2	25469945	C	A	2385	17	0.007	DNMT3A	p.R366L	missense

Sample ID	Family ID	Chr	Position	WT	MT	WT Count	MT Count	VAF	Gene	Protein	Effect
PD42467b	24	4	106155605	A	-	2544	31	0.012	TET2	p.H169fs	frameshift
PD42467b	24	21	44524456	G	A	2272	25	0.011	U2AF1	p.S34F	missense
PD42381b	25	2	25458577	T	C	1801	14	0.008	DNMT3A	p.R866G	missense
PD42381b	25	2	25458669	G	A	1701	61	0.035	DNMT3A	p.T835M	missense
PD42381b	25	2	25462086	T	G	1402	163	0.104	DNMT3A	c.2323-2A>C	splicing
PD42416b	26	2	25463287	G	C	2022	27	0.013	DNMT3A	p.R736G	missense
PD42395b	27	2	25463541	G	C	2579	21	0.008	DNMT3A	p.S714C	missense
PD42395b	27	2	25470483	A	C	2762	34	0.012	DNMT3A	p.F331V	missense
PD42395b	27	2	198266612	C	T	2119	26	0.012	SF3B1	p.G742S	missense
PD42395b	27	17	7577539	G	C	2773	17	0.006	TP53	p.R248G	missense
PD42438b	27	4	106190786	C	T	2327	46	0.019	TET2	p.A1355V	missense
PD42414b	28	17	40475068	G	C	2243	18	0.008	STAT3	p.S614R	missense
PD42414b	28	20	31021187	C	T	2085	262	0.112	ASXL1	p.Q396X	stopgain
PD42414b	28	20	31022441	A	AG	2365	564	0.193	ASXL1	p.G642fs	frameshift
PD42379b	29	2	25463562	C	T	1674	104	0.059	DNMT3A	p.G707D	missense
PD42422b	29	4	106164794	G	T	2237	66	0.029	TET2	p.C1221F	missense
PD42346b	30	2	25457243	G	A	2475	33	0.013	DNMT3A	p.R882C	missense
PD42346b	30	2	25463247	C	T	2347	26	0.011	DNMT3A	p.R749H	missense
PD42351b	30	2	25457231	G	A	2197	19	0.009	DNMT3A	p.Q886X	stopgain
PD42351b	30	2	25467083	G	A	2321	12	0.005	DNMT3A	p.R598X	stopgain
PD42380b	31	4	106182926	T	G	1366	43	0.031	TET2	p.L1322R	missense
PD42380b	31	4	106193931	C	T	2267	19	0.008	TET2	p.R1465X	stopgain
PD42411b	32	2	25468934	C	T	2093	11	0.005	DNMT3A	c.1430-1G>A	splicing
PD42411b	32	4	106196850	A	-	2461	16	0.006	TET2	p.E1728fs	frameshift
PD42392b	33	2	25463271	G	T	2180	20	0.009	DNMT3A	p.A741E	missense
PD42392b	33	2	25467083	G	A	2351	50	0.021	DNMT3A	p.R598X	stopgain
PD42403b	33	2	25467083	G	A	2334	12	0.005	DNMT3A	p.R598X	stopgain
PD42403b	33	4	106156744	AC	-	2703	30	0.011	TET2	p.T549fs	frameshift
PD42384b	34	4	106155948	G	-	2541	25	0.01	TET2	p.E283fs	frameshift
PD42384b	34	11	119148924	A	G	2027	48	0.023	CBL	p.K382E	missense
PD42303b	35	2	25467448	C	T	2351	31	0.013	DNMT3A	p.G543D	missense
PD42308b	36	4	106155749	C	-	2203	26	0.012	TET2	p.S217fs	frameshift
PD42308b	36	17	7577538	C	A	2225	22	0.01	TP53	p.R248L	missense
PD42308b	36	17	58740749	C	T	2389	17	0.007	PPM1D	p.R552X	stopgain
PD42314b	36	2	25467072	C	-	2600	58	0.022	DNMT3A	p.W601fs	frameshift
PD42338b	37	4	106157029	C	T	2568	23	0.009	TET2	p.Q644X	stopgain
PD42342b	37	2	25470516	G	A	2748	50	0.018	DNMT3A	p.R320X	stopgain
PD42316b	38	2	25458684	A	C	2343	22	0.009	DNMT3A	p.V830G	missense
PD42316b	38	2	25462065	T	C	2102	23	0.011	DNMT3A	p.D781G	missense
PD42316b	38	2	25469138	C	T	2788	40	0.014	DNMT3A	p.W440X	stopgain
PD42354c	39	2	25467498	G	T	2186	19	0.009	DNMT3A	p.Y526X	stopgain
PD42354c	39	17	7577539	G	A	2274	14	0.006	TP53	p.R248W	missense
PD42359c	39	2	25467072	C	T	2358	59	0.024	DNMT3A	p.W601X	stopgain
PD42359c	39	2	25469139	C	T	2482	34	0.014	DNMT3A	p.W440X	stopgain
PD42359c	39	4	106164067	T	C	2105	314	0.13	TET2	p.C1193R	missense
PD42440b	40	2	25463236	A	G	2309	15	0.006	DNMT3A	p.W753R	missense
PD42462b	40	2	25470029	T	C	1990	38	0.019	DNMT3A	c.1015-2A>G	splicing
PD42385b	41	2	25463297	A	C	1936	16	0.008	DNMT3A	p.F732L	missense
PD42454b	42	4	106196208	T	-	1890	18	0.009	TET2	p.L1514fs	frameshift
PD42405b	43	4	106157788	C	T	2994	67	0.022	TET2	p.Q897X	stopgain
PD42405b	43	4	106183003	C	-	1897	13	0.007	TET2	p.Q1348fs	frameshift
PD42418b	43	2	25469027	A	T	1473	924	0.385	DNMT3A	c.1429+2T>A	splicing
PD42418b	43	11	119148917	A	C	1877	10	0.005	CBL	p.Q379H	missense
PD42418b	43	X	154299845	G	T	2387	16	0.007	BRCC3	p.E15X	stopgain
PD42418b	43	X	154348331	G	A	2191	20	0.009	BRCC3	p.W286X	stopgain
PD42368b	44	4	106155440	A	-	2258	19	0.008	TET2	p.Q114fs	frameshift
PD42412b	45	4	106156540	C	T	2855	22	0.008	TET2	p.Q481X	stopgain
PD42413b	46	2	25468150	A	-	1662	204	0.109	DNMT3A	p.F509fs	frameshift
PD42413b	46	4	106197317	A	G	2577	224	0.08	TET2	p.T1884A	missense
PD42433b	46	4	106190828	C	G	1969	91	0.044	TET2	p.S1369X	stopgain

Sample ID	Family ID	Chr	Position	WT	MT	WT Count	MT Count	VAF	Gene	Protein	Effect
PD42352b	47	2	25463286	C	A	1907	13	0.007	DNMT3A	p.R736L	missense
PD42352b	47	17	7578253	C	T	1972	18	0.009	TP53	p.G199E	missense
PD42317b	48	2	25467436	A	C	1693	610	0.265	DNMT3A	p.L547R	missense
PD42317b	48	4	106197140	C	T	2657	54	0.02	TET2	p.Q1825X	stopgain
PD42317b	48	17	7578372	A	T	2084	46	0.022	TP53	p.D186E	missense
PD42323b	48	4	106157054	A	-	2711	24	0.009	TET2	p.Q652fs	frameshift
PD42323b	48	4	106180816	G	A	2252	324	0.126	TET2	p.G1282S	missense
PD42323b	48	4	106196771	C	T	2758	36	0.013	TET2	p.Q1702X	stopgain
PD42323b	48	20	31022983	T	A	2418	358	0.129	ASXL1	p.L823X	stopgain
PD42356b	49	X	44928974	C	T	2182	14	0.006	KDM6A	p.Q692X	stopgain
PD42361b	49	X	44928974	C	T	2261	17	0.007	KDM6A	p.Q692X	stopgain
PD42450b	50	2	25458627	G	-	2449	244	0.091	DNMT3A	p.P849fs	frameshift
PD42410b	51	2	25457192	G	A	2131	56	0.026	DNMT3A	p.R899C	missense
PD42410b	51	2	25458670	T	C	1823	52	0.028	DNMT3A	p.T835A	missense
PD42406b	52	20	57484420	C	A	1902	25	0.013	GNAS	p.R844S	missense
PD42325b	53	2	25498395	TCTCC	-	1847	54	0.029	DNMT3A	p.K154fs	frameshift
PD42355b	53	2	25463301	A	T	1706	127	0.069	DNMT3A	p.F731Y	missense
PD42355b	53	2	198266834	T	C	2122	14	0.007	SF3B1	p.K700E	missense
PD42373b	54	4	106156080	A	-	2772	153	0.052	TET2	p.S327fs	frameshift
PD42302b	55	4	106164913	C	T	1303	7	0.005	TET2	p.R1261C	missense
PD42302b	55	17	58740439	T	-	2024	12	0.006	PPM1D	p.N448fs	frameshift
PD42331b	55	2	198267491	C	G	2106	85	0.039	SF3B1	p.E622D	missense
PD42331b	55	4	106155628	C	-	2298	225	0.089	TET2	p.P177fs	frameshift
PD42331b	55	4	106156264	A	T	2560	14	0.005	TET2	p.K389X	stopgain
PD42331b	55	17	7577538	C	T	2355	25	0.011	TP53	p.R248Q	missense
PD42331b	55	17	74732959	G	C	2481	16	0.006	SRSF2	p.P95R	missense
PD42428b	56	17	58740665	C	T	2319	13	0.006	PPM1D	p.Q524X	stopgain
PD42307b	57	17	58740450	T	-	1688	103	0.057	PPM1D	p.V452fs	frameshift
PD42307b	57	X	44942035	G	GT	679	63	0.085	KDM6A	c.3284+1->GT	splicing
PD42315b	58	4	106182984	ACCTGATGCATAT	-	1725	10	0.006	TET2	p.A1341fs	frameshift
PD42339b	59	2	25464490	C	T	2533	15	0.006	DNMT3A	p.V675M	missense
PD42339b	59	2	25467109	T	-	2775	81	0.028	DNMT3A	p.K589fs	frameshift
PD42339b	59	2	25467198	G	T	2606	17	0.006	DNMT3A	p.C559X	stopgain
PD42339b	59	4	106162508	A	-	2007	12	0.006	TET2	p.E1141fs	frameshift
PD42305b	60	4	106158411	TATA	-	2176	80	0.036	TET2	p.F1104fs	frameshift
PD42311b	60	2	25466793	A	G	1707	10	0.006	DNMT3A	p.L637P	missense
PD42311b	60	4	106155921	C	-	2466	54	0.021	TET2	p.I274fs	frameshift
PD42337b	61	17	58740691	A	-	2779	19	0.007	PPM1D	p.T532fs	frameshift
PD42341b	61	2	25466794	G	C	1901	25	0.013	DNMT3A	p.L637V	missense
PD42426b	62	2	25463289	T	C	2020	122	0.057	DNMT3A	p.Y735C	missense
PD42426b	62	4	106162585	A	T	2142	14	0.006	TET2	p.R1167W	missense
PD42448b	62	17	7577141	C	T	2293	18	0.008	TP53	p.G266E	missense
PD42439b	63	2	25463300	G	T	2069	14	0.007	DNMT3A	p.F731L	missense
PD42324b	64	2	25466797	C	T	1809	113	0.059	DNMT3A	p.V636M	missense
PD42460b	65	2	25470002	A	G	2609	15	0.006	DNMT3A	p.L347P	missense
PD42460b	65	17	58740546	T	A	2298	21	0.009	PPM1D	p.L484X	stopgain
PD42432b	66	4	106193782	T	C	2202	144	0.061	TET2	p.L1415P	missense
PD42313b	67	4	106197285	T	C	2369	553	0.189	TET2	p.I1873T	missense
PD42313b	67	X	39930892	C	A	1464	8	0.005	BCOR	p.E1017X	stopgain
PD42319b	67	2	25463308	G	A	1944	32	0.016	DNMT3A	p.R729W	missense
PD42319b	67	4	106155778	G	GA	2606	196	0.07	TET2	p.E227fs	frameshift
PD42319b	67	9	5073770	G	T	1576	102	0.061	JAK2	p.V617F	missense

Table 14 | Modelling of genetic and environmental influences on CH

A

		Age- and Sex-adjusted model			Sex only-adjusted model		
Model	Comparison	Minus2LL	AIC	p-value	Minus2LL	AIC	p-value
Sat	*NA*	353.2	83.2	*NA*	356.9	84.9	NA
Sat	ACE	355.3	79.3	0.55	358.1	80.1	0.75
ACE	AE	355.3	77.3	0.93	358.1	78.1	1
ACE	CE	355.8	77.8	0.49	359	79	0.35
ACE	E	360.6	80.6	0.07	364.1	82.1	0.05

B

		Age- and Sex-adjusted model		Sex only-adjusted model	
Model	Factor	ML Estimate	95% CI	ML Estimate	95% CI
AE	A	0.33	0.049 – 0.55	0.34	0.07 – 0.56
	E	0.67	0.45 – 0.95	0.66	0.44 – 0.93
ACE	A	0.29	8.5E-07 – 0.55	0.34	2.9E-08 – 0.56
	C	0.03	1.5E-05 – 0.44	1.20E-13	1.2E-13 – 0.44
	E	0.68	0.46 – 0.96	0.66	0.44 – 0.94

Maximum likelihood model fitting was applied to estimate A (additive genetic), C (shared environmental) and E (unique environmental) contributions to CH, using the openMX R package2. For this analysis CH was represented by maximum VAF per individual; zero in the absence of CH, and rising with increasingly large clonal size. Prior to model fitting, a log transformation was applied to the maximum VAF measurements. Modelling was performed adjusting for (i) both age and gender, and (ii) gender alone.

A. Cholesky decomposition of a saturated ACE model reveals that the best fit model includes additive genetic and unique environmental factors (AE model). Minus2LL, minus 2*log-likelihood; AIC, Akaike Information Criterion; Sat, saturated.

B. Results of AE and ACE modelling, showing the proportion of variance (ML, maximum-likelihood) explained by individual factors. Since the best fit model is AE, these results are highlighted in bold. In summary, heritability is estimated at approximately one-third, whereas the influence of unique environmental factors is estimated at approximately two-thirds.

Table 15 | Historical and observed growth rates for all clones.

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historical Growth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD34562	ASXL1-C856fs	ASXL1	0.004	0.078	0.156	0.078	0.056	0.095	0.163	0.100
PD41087	ASXL1-E906X	ASXL1	0.035	0.118	0.198	0.117	0.052	0.121	0.200	0.122
PD41239	ASXL1-G828fs	ASXL1	0.107	0.152	0.203	0.153	0.127	0.156	0.205	0.159
PD41260	ASXL1-H630fs	ASXL1	0.082	0.121	0.161	0.121	0.092	0.123	0.162	0.124
PD41233	ASXL1-H630fs	ASXL1	0.125	0.151	0.180	0.152	0.127	0.152	0.180	0.152
PD34503	ASXL1-I641fs	ASXL1	0.014	0.037	0.062	0.037	0.093	0.093	0.093	0.093
PD41182	ASXL1-K1025fs	ASXL1	0.082	0.137	0.189	0.137	0.085	0.138	0.189	0.138
PD41341	ASXL1-K1437fs	ASXL1	0.088	0.152	0.218	0.152	0.089	0.152	0.218	0.153
PD41274	ASXL1-L1266fs	ASXL1	-0.036	0.033	0.102	0.034	0.042	0.072	0.121	0.075
PD41311	ASXL1-L775X	ASXL1	0.099	0.145	0.194	0.145	0.110	0.147	0.195	0.149
PD41190	ASXL1-NM_015338:exon12:c.1720-2A>C	ASXL1	0.120	0.151	0.185	0.152	0.122	0.152	0.185	0.153
PD41171	ASXL1-P808fs	ASXL1	0.069	0.145	0.214	0.144	0.072	0.145	0.214	0.145
PD34558	ASXL1-Q1063fs	ASXL1	-0.011	0.040	0.094	0.040	0.059	0.076	0.113	0.079
PD34487	ASXL1-Q1251X	ASXL1	0.078	0.148	0.215	0.147	0.081	0.148	0.215	0.148
PD41106	ASXL1-Q1294fs	ASXL1	0.061	0.126	0.190	0.125	0.066	0.126	0.191	0.126
PD41123	ASXL1-Q1350X	ASXL1	-0.020	0.016	0.052	0.016	0.088	0.088	0.088	0.088
PD41255	ASXL1-Q396X	ASXL1	0.057	0.096	0.139	0.096	0.096	0.112	0.147	0.115
PD41344	ASXL1-Q546X	ASXL1	-0.034	0.025	0.089	0.026	0.059	0.074	0.117	0.080
PD41532	ASXL1-Q588X	ASXL1	-0.016	0.043	0.102	0.043	0.078	0.092	0.130	0.097
PD34538	ASXL1-R1171fs	ASXL1	0.007	0.075	0.143	0.075	0.044	0.086	0.147	0.089
PD41178	ASXL1-R693X	ASXL1	0.050	0.111	0.170	0.110	0.069	0.115	0.172	0.116
PD41306	ASXL1-R860X	ASXL1	-0.004	0.064	0.139	0.065	0.053	0.085	0.147	0.090
PD41120	ASXL1-S1014fs	ASXL1	0.013	0.078	0.143	0.078	0.050	0.087	0.149	0.091
PD34489	ASXL1-S852X	ASXL1	-0.009	0.026	0.068	0.027	0.079	0.084	0.105	0.088
PD41316	ASXL1-S958X	ASXL1	-0.002	0.071	0.148	0.070	0.025	0.079	0.152	0.082
PD41230	ASXL1-S993fs	ASXL1	0.026	0.101	0.174	0.101	0.045	0.105	0.176	0.106
PD41245	BRCC3nt-G152R	BRCC3	-0.065	0.025	0.116	0.026	0.040	0.074	0.140	0.080
PD41077	BRCC3nt-H127P	BRCC3	-0.019	0.061	0.144	0.062	0.045	0.086	0.155	0.091
PD41093	BRCC3nt-L153P	BRCC3	-0.050	0.047	0.142	0.047	0.021	0.074	0.153	0.078
PD41199	BRCC3nt-L308P	BRCC3	-0.039	0.021	0.087	0.021	0.062	0.078	0.114	0.083
PD41320	BRCC3nt-M142I	BRCC3	-0.051	0.020	0.088	0.019	0.052	0.073	0.113	0.077
PD34495	BRCC3nt-R83C	BRCC3	-0.013	0.040	0.098	0.041	0.088	0.101	0.132	0.104
PD41337	BRCC3nt-S156P	BRCC3	0.024	0.078	0.133	0.078	0.073	0.096	0.141	0.100
PD41230	BRCC3t-C240X	BRCC3	0.013	0.103	0.192	0.103	0.045	0.110	0.194	0.114
PD41161	BRCC3t-H127fs	BRCC3	-0.027	0.055	0.134	0.055	0.034	0.074	0.141	0.079
PD41264	BRCC3t-NM_001018055:exon7:c.548+1G>A	BRCC3	-0.026	0.057	0.143	0.057	0.053	0.088	0.158	0.094
PD41287	BRCC3t-T166fs	BRCC3	-0.044	0.025	0.097	0.025	0.040	0.068	0.122	0.073
PD41079	BRCC3t-W286X	BRCC3	-0.052	0.015	0.082	0.014	0.069	0.083	0.114	0.087
PD41112	CBLnt-C396W	CBL	-0.027	0.041	0.104	0.041	0.043	0.070	0.116	0.074
PD41280	CBLnt-C404Y	CBL	-0.059	0.019	0.097	0.019	0.044	0.069	0.123	0.075
PD34488	CBLnt-C404Y	CBL	-0.057	0.016	0.093	0.016	0.034	0.061	0.121	0.067
PD41230	CBLnt-C404Y	CBL	-0.025	0.032	0.086	0.031	0.068	0.082	0.117	0.086
PD41325	CBLnt-C419S	CBL	-0.006	0.065	0.139	0.066	0.060	0.090	0.149	0.096
PD41227	CBLnt-I361S	CBL	-0.038	0.031	0.105	0.032	0.042	0.071	0.121	0.075
PD41211	CBLnt-I383M	CBL	0.025	0.135	0.242	0.134	0.047	0.138	0.244	0.140
PD41248	CBLnt-I383M	CBL	-0.004	0.111	0.223	0.110	0.065	0.128	0.231	0.136
PD41142	CBLnt-L380P	CBL	-0.062	0.018	0.097	0.017	0.047	0.069	0.125	0.076
PD41237	CBLnt-L399H	CBL	-0.021	0.069	0.154	0.069	0.026	0.080	0.162	0.085
PD41247	CBLnt-Q379R	CBL	-0.048	0.043	0.136	0.045	0.041	0.085	0.154	0.088
PD41326	CBLnt-Q490K	CBL	-0.053	0.042	0.132	0.042	0.019	0.065	0.143	0.072
PD41088	CBLnt-R149Q	CBL	-0.022	0.060	0.140	0.060	0.041	0.081	0.149	0.086
PD34489	CBLnt-R420G	CBL	-0.012	0.071	0.149	0.070	0.047	0.087	0.159	0.093
PD41148	CBLnt-R420Q	CBL	-0.046	0.037	0.119	0.037	0.040	0.073	0.135	0.078
PD34537	CBLnt-V363M	CBL	-0.064	0.026	0.117	0.026	0.018	0.063	0.137	0.068

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD34428	CBLnt-V430M	CBL	-0.045	0.033	0.109	0.033	0.064	0.085	0.146	0.092
PD41324	CBLnt-V430M	CBL	-0.109	0.008	0.124	0.008	0.044	0.082	0.165	0.090
PD41301	CBLt-NM_005188:exon15:c.2252-2A>G	CBL	0.126	0.205	0.283	0.205	0.126	0.205	0.283	0.205
PD41112	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	0.035	0.105	0.180	0.106	0.052	0.108	0.181	0.112
PD34531	CBLt-NM_005188:exon15:c.2434+1G>A	CBL	0.004	0.073	0.145	0.074	0.049	0.088	0.151	0.093
PD41193	CBLt-NM_005188:exon9:c.1228-1G>A	CBL	0.127	0.206	0.293	0.207	0.128	0.206	0.293	0.207
PD41190	CBLt-P433fs	CBL	0.069	0.154	0.240	0.155	0.072	0.154	0.240	0.156
PD34569	CBLt-Q691fs	CBL	0.034	0.117	0.203	0.117	0.058	0.121	0.205	0.125
PD41276	CBLt-W190X	CBL	0.105	0.175	0.247	0.176	0.106	0.176	0.247	0.177
PD41297	CTCFnt-D710Y	CTCF	-0.026	0.069	0.159	0.069	0.028	0.084	0.167	0.089
PD41529	CTCFnt-E520D	CTCF	-0.028	0.074	0.172	0.073	0.039	0.092	0.179	0.099
PD41130	CTCFnt-H347R	CTCF	-0.013	0.063	0.136	0.064	0.059	0.091	0.149	0.096
PD34554	CTCFnt-S461P	CTCF	-0.009	0.087	0.185	0.087	0.037	0.098	0.188	0.104
PD34568	CTCFnt-T204I	CTCF	-0.015	0.076	0.164	0.076	0.041	0.091	0.170	0.096
PD34521	CTCFnt-T563I	CTCF	-0.026	0.067	0.164	0.067	0.050	0.094	0.175	0.101
PD34550	CTCFnt-V361I	CTCF	-0.054	0.039	0.138	0.039	0.038	0.078	0.159	0.085
PD34523	CTCFt-NM_006565:exon4:c.782-2A>G	CTCF	0.034	0.117	0.201	0.117	0.071	0.127	0.204	0.131
PD41115	CTCFt-S488X	CTCF	-0.003	0.079	0.162	0.080	0.043	0.089	0.166	0.095
PD41237	CTCFt-Y392X	CTCF	-0.045	0.056	0.153	0.054	0.040	0.083	0.165	0.090
PD41164	DNMT3Ant-A410T	DNMT3A	-0.048	0.023	0.100	0.024	0.054	0.079	0.134	0.084
PD41129	DNMT3Ant-A662G	DNMT3A	0.001	0.060	0.122	0.061	0.061	0.086	0.134	0.091
PD41184	DNMT3Ant-A910V	DNMT3A	-0.037	0.033	0.104	0.033	0.063	0.082	0.137	0.090
PD34483	DNMT3Ant-C387W	DNMT3A	-0.010	0.065	0.140	0.066	0.037	0.080	0.146	0.085
PD41315	DNMT3Ant-D531N	DNMT3A	0.014	0.065	0.116	0.064	0.075	0.092	0.132	0.096
PD41175	DNMT3Ant-D686E	DNMT3A	-0.016	0.038	0.095	0.038	0.059	0.076	0.118	0.080
PD41244	DNMT3Ant-D702G	DNMT3A	-0.019	0.055	0.123	0.055	0.058	0.085	0.136	0.089
PD41330	DNMT3Ant-D702V	DNMT3A	-0.058	0.010	0.079	0.011	0.044	0.063	0.109	0.068
PD41119	DNMT3Ant-D768G	DNMT3A	-0.051	0.016	0.082	0.015	0.046	0.067	0.111	0.071
PD34548	DNMT3Ant-F331V	DNMT3A	-0.007	0.062	0.135	0.063	0.052	0.085	0.145	0.090
PD41151	DNMT3Ant-F732L	DNMT3A	0.032	0.081	0.133	0.082	0.094	0.110	0.150	0.114
PD41085	DNMT3Ant-F732S	DNMT3A	-0.012	0.051	0.116	0.052	0.047	0.077	0.128	0.080
PD41321	DNMT3Ant-F752V	DNMT3A	-0.019	0.045	0.107	0.045	0.041	0.070	0.119	0.074
PD41079	DNMT3Ant-F755S	DNMT3A	-0.072	0.031	0.140	0.032	0.033	0.079	0.159	0.086
PD41318	DNMT3Ant-F755S	DNMT3A	-0.074	0.029	0.135	0.030	0.051	0.086	0.168	0.095
PD41342	DNMT3Ant-F755S	DNMT3A	-0.008	0.077	0.160	0.076	0.064	0.103	0.170	0.108
PD34556	DNMT3Ant-F868L	DNMT3A	-0.060	0.001	0.059	0.001	0.045	0.058	0.088	0.061
PD41227	DNMT3Ant-G302S	DNMT3A	-0.061	-0.008	0.047	-0.007	0.050	0.070	0.099	0.071
PD34514	DNMT3Ant-G511E	DNMT3A	-0.024	0.033	0.090	0.033	0.057	0.073	0.117	0.077
PD41341	DNMT3Ant-G699D	DNMT3A	-0.046	0.028	0.106	0.028	0.034	0.064	0.123	0.070
PD41338	DNMT3Ant-G722D	DNMT3A	-0.045	0.026	0.100	0.026	0.045	0.071	0.130	0.077
PD34547	DNMT3Ant-G726D	DNMT3A	-0.057	0.021	0.094	0.020	0.035	0.065	0.114	0.069
PD41106	DNMT3Ant-G843D	DNMT3A	0.011	0.043	0.077	0.043	0.088	0.095	0.105	0.096
PD41341	DNMT3Ant-I310N	DNMT3A	-0.037	0.023	0.086	0.024	0.046	0.066	0.111	0.071
PD41302	DNMT3Ant-I369F	DNMT3A	-0.022	0.042	0.106	0.043	0.059	0.080	0.128	0.084
PD34479	DNMT3Ant-I705T	DNMT3A	-0.054	0.036	0.130	0.036	0.049	0.086	0.159	0.092
PD41185	DNMT3Ant-I705T	DNMT3A	0.025	0.059	0.096	0.059	0.093	0.102	0.119	0.103
PD41143	DNMT3Ant-I705T	DNMT3A	-0.008	0.074	0.155	0.075	0.056	0.097	0.165	0.102
PD41165	DNMT3Ant-I705T	DNMT3A	-0.030	0.056	0.140	0.056	0.038	0.079	0.151	0.084
PD34575	DNMT3Ant-I769M	DNMT3A	-0.071	0.009	0.089	0.010	0.016	0.054	0.113	0.059
PD41194	DNMT3Ant-I769V	DNMT3A	-0.053	0.015	0.081	0.014	0.044	0.065	0.109	0.069
PD41243	DNMT3Ant-I780T	DNMT3A	0.021	0.095	0.175	0.096	0.064	0.108	0.182	0.115

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41150	DNMT3Ant-I780T	DNMT3A	-0.029	0.083	0.195	0.082	0.051	0.106	0.205	0.114
PD34579	DNMT3Ant-I833V	DNMT3A	-0.037	0.027	0.091	0.028	0.060	0.078	0.119	0.082
PD34569	DNMT3Ant-I898T	DNMT3A	-0.060	0.013	0.088	0.013	0.053	0.075	0.123	0.079
PD34512	DNMT3Ant-K361E	DNMT3A	-0.065	0.011	0.086	0.011	0.042	0.064	0.120	0.070
PD41118	DNMT3Ant-K367N	DNMT3A	-0.066	-0.009	0.053	-0.008	0.060	0.071	0.100	0.073
PD41095	DNMT3Ant-L295P	DNMT3A	0.030	0.105	0.183	0.105	0.068	0.113	0.189	0.118
PD34503	DNMT3Ant-L295P	DNMT3A	0.035	0.114	0.189	0.113	0.053	0.116	0.191	0.119
PD41106	DNMT3Ant-L637Q	DNMT3A	-0.018	0.050	0.114	0.049	0.035	0.068	0.120	0.073
PD41073	DNMT3Ant-L637V	DNMT3A	-0.017	0.037	0.091	0.037	0.084	0.097	0.127	0.100
PD41128	DNMT3Ant-L647R	DNMT3A	0.003	0.073	0.142	0.073	0.076	0.103	0.161	0.108
PD41199	DNMT3Ant-L647R	DNMT3A	-0.104	-0.012	0.083	-0.011	0.035	0.064	0.120	0.069
PD41286	DNMT3Ant-L653F	DNMT3A	0.044	0.080	0.116	0.080	0.093	0.105	0.132	0.107
PD41150	DNMT3Ant-L754H	DNMT3A	-0.037	0.036	0.110	0.036	0.051	0.077	0.126	0.081
PD41139	DNMT3Ant-L819V	DNMT3A	0.002	0.042	0.082	0.042	0.097	0.102	0.122	0.104
PD41303	DNMT3Ant-L888M	DNMT3A	-0.071	0.006	0.088	0.007	0.011	0.047	0.101	0.051
PD42296	DNMT3Ant-L888P	DNMT3A	-0.006	0.068	0.141	0.068	0.070	0.098	0.159	0.103
PD34563	DNMT3Ant-M761V	DNMT3A	-0.031	0.039	0.110	0.039	0.040	0.068	0.125	0.073
PD41337	DNMT3Ant-M779T	DNMT3A	0.001	0.063	0.122	0.063	0.071	0.092	0.134	0.096
PD41317	DNMT3Ant-M880V	DNMT3A	-0.022	0.073	0.161	0.072	0.048	0.092	0.168	0.098
PD41243	DNMT3Ant-M880V	DNMT3A	-0.038	0.057	0.150	0.058	0.047	0.088	0.161	0.094
PD41216	DNMT3Ant-P700L	DNMT3A	-0.057	0.011	0.077	0.010	0.047	0.065	0.104	0.069
PD41184	DNMT3Ant-P804L	DNMT3A	-0.022	0.054	0.132	0.055	0.058	0.088	0.150	0.093
PD41241	DNMT3Ant-P904L	DNMT3A	-0.040	0.032	0.107	0.033	0.050	0.077	0.125	0.081
PD34577	DNMT3Ant-Q886R	DNMT3A	-0.067	0.004	0.072	0.003	0.042	0.062	0.114	0.067
PD41226	DNMT3Ant-R201C	DNMT3A	-0.005	0.056	0.117	0.056	0.049	0.078	0.128	0.082
PD41192	DNMT3Ant-R326C	DNMT3A	0.100	0.137	0.175	0.137	0.119	0.142	0.178	0.144
PD41108	DNMT3Ant-R326P	DNMT3A	0.009	0.056	0.103	0.056	0.072	0.088	0.119	0.091
PD41089	DNMT3Ant-R326S	DNMT3A	-0.049	0.007	0.063	0.007	0.046	0.064	0.093	0.066
PD41070	DNMT3Ant-R379C	DNMT3A	-0.018	0.043	0.102	0.043	0.059	0.079	0.118	0.083
PD41294	DNMT3Ant-R379H	DNMT3A	-0.030	0.029	0.088	0.029	0.057	0.075	0.113	0.079
PD41308	DNMT3Ant-R635Q	DNMT3A	-0.084	-0.006	0.075	-0.006	0.058	0.079	0.115	0.081
PD41160	DNMT3Ant-R635W	DNMT3A	0.065	0.121	0.173	0.120	0.094	0.128	0.175	0.131
PD34428	DNMT3Ant-R635W	DNMT3A	-0.060	0.020	0.108	0.021	0.044	0.073	0.136	0.079
PD34514	DNMT3Ant-R635W	DNMT3A	-0.029	0.016	0.062	0.017	0.070	0.080	0.099	0.081
PD41334	DNMT3Ant-R635W	DNMT3A	-0.020	0.046	0.114	0.046	0.062	0.085	0.134	0.090
PD34580	DNMT3Ant-R659H	DNMT3A	-0.031	0.026	0.081	0.026	0.078	0.092	0.120	0.095
PD41184	DNMT3Ant-R659H	DNMT3A	-0.092	-0.032	0.039	-0.030	0.079	0.094	0.106	0.092
PD41218	DNMT3Ant-R729G	DNMT3A	-0.052	0.019	0.090	0.020	0.042	0.066	0.114	0.071
PD41260	DNMT3Ant-R736C	DNMT3A	-0.028	0.034	0.099	0.035	0.062	0.083	0.123	0.086
PD41181	DNMT3Ant-R736C	DNMT3A	0.011	0.094	0.177	0.093	0.053	0.104	0.181	0.108
PD41144	DNMT3Ant-R736C	DNMT3A	0.012	0.090	0.166	0.090	0.053	0.098	0.171	0.104
PD41262	DNMT3Ant-R736H	DNMT3A	0.090	0.129	0.164	0.129	0.108	0.132	0.166	0.134
PD41114	DNMT3Ant-R736H	DNMT3A	0.018	0.082	0.149	0.082	0.071	0.100	0.157	0.105
PD41197	DNMT3Ant-R771Q	DNMT3A	-0.036	0.031	0.100	0.031	0.035	0.067	0.119	0.070
PD34526	DNMT3Ant-R882C	DNMT3A	-0.084	0.002	0.097	0.005	0.054	0.080	0.133	0.085
PD41163	DNMT3Ant-R882C	DNMT3A	-0.064	0.019	0.123	0.023	0.083	0.109	0.176	0.115
PD41112	DNMT3Ant-R882H	DNMT3A	-0.066	-0.014	0.038	-0.014	0.057	0.066	0.078	0.068
PD41244	DNMT3Ant-R882H	DNMT3A	-0.045	0.038	0.122	0.038	0.056	0.083	0.147	0.090
PD41103	DNMT3Ant-R882H	DNMT3A	0.145	0.172	0.201	0.173	0.145	0.172	0.201	0.173
PD41113	DNMT3Ant-R882H	DNMT3A	-0.030	0.040	0.111	0.041	0.048	0.075	0.130	0.080
PD41221	DNMT3Ant-R882H	DNMT3A	-0.028	0.037	0.107	0.038	0.060	0.080	0.129	0.086
PD41315	DNMT3Ant-R882H	DNMT3A	-0.024	0.056	0.138	0.057	0.048	0.083	0.146	0.089
PD41225	DNMT3Ant-R882S	DNMT3A	0.051	0.089	0.128	0.089	0.078	0.097	0.131	0.100
PD41269	DNMT3Ant-S638C	DNMT3A	0.009	0.074	0.137	0.073	0.054	0.088	0.143	0.092
PD41135	DNMT3Ant-S638F	DNMT3A	-0.001	0.086	0.178	0.087	0.062	0.107	0.189	0.114
PD34547	DNMT3Ant-S638F	DNMT3A	-0.012	0.082	0.184	0.083	0.056	0.105	0.196	0.111
PD41108	DNMT3Ant-S669F	DNMT3A	0.017	0.065	0.117	0.066	0.067	0.085	0.128	0.090
PD41267	DNMT3Ant-S75F	DNMT3A	-0.030	0.054	0.139	0.054	0.022	0.072	0.145	0.076
PD41196	DNMT3Ant-S770L	DNMT3A	0.044	0.106	0.167	0.106	0.079	0.115	0.171	0.119
PD41107	DNMT3Ant-S770L	DNMT3A	0.003	0.092	0.181	0.092	0.048	0.105	0.184	0.109

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD42297	DNMT3Ant-S770L	DNMT3A	0.034	0.109	0.186	0.110	0.067	0.118	0.191	0.122
PD41177	DNMT3Ant-S770L	DNMT3A	0.031	0.085	0.141	0.085	0.083	0.105	0.150	0.109
PD34517	DNMT3Ant-S770L	DNMT3A	-0.002	0.075	0.157	0.076	0.069	0.103	0.170	0.109
PD41155	DNMT3Ant-S770P	DNMT3A	-0.035	0.041	0.117	0.041	0.054	0.081	0.134	0.087
PD41226	DNMT3Ant-V636M	DNMT3A	-0.041	0.018	0.073	0.017	0.062	0.075	0.111	0.080
PD41289	DNMT3Ant-V675A	DNMT3A	0.046	0.094	0.140	0.093	0.074	0.101	0.143	0.104
PD34469	DNMT3Ant-V675M	DNMT3A	-0.034	0.042	0.113	0.041	0.050	0.078	0.131	0.083
PD41192	DNMT3Ant-V687L	DNMT3A	-0.080	-0.002	0.078	-0.002	0.012	0.054	0.102	0.056
PD41343	DNMT3Ant-V778L	DNMT3A	-0.051	0.025	0.102	0.025	0.042	0.069	0.123	0.074
PD34502	DNMT3Ant-V830A	DNMT3A	-0.006	0.042	0.090	0.042	0.074	0.086	0.118	0.090
PD34573	DNMT3Ant-W210C	DNMT3A	-0.024	0.053	0.127	0.054	0.034	0.074	0.135	0.078
PD41278	DNMT3Ant-W860R	DNMT3A	-0.042	0.021	0.078	0.020	0.048	0.068	0.104	0.071
PD41166	DNMT3Ant-Y660C	DNMT3A	-0.017	0.046	0.112	0.047	0.058	0.081	0.129	0.086
PD41244	DNMT3Ant-Y660H	DNMT3A	-0.040	0.032	0.104	0.032	0.062	0.080	0.129	0.086
PD41293	DNMT3Ant-Y724C	DNMT3A	0.006	0.060	0.116	0.060	0.067	0.089	0.132	0.093
PD41197	DNMT3Ant-Y735C	DNMT3A	-0.027	0.028	0.090	0.029	0.059	0.076	0.110	0.080
PD34477	DNMT3Ant-Y793N	DNMT3A	-0.041	0.033	0.108	0.033	0.036	0.069	0.120	0.073
PD41106	DNMT3Ant-Y908C	DNMT3A	0.019	0.081	0.144	0.081	0.060	0.094	0.148	0.098
PD41077	DNMT3At-A462fs	DNMT3A	0.015	0.090	0.158	0.088	0.050	0.097	0.162	0.100
PD41164	DNMT3At-A525fs	DNMT3A	-0.001	0.064	0.129	0.063	0.056	0.086	0.138	0.090
PD41341	DNMT3At-C351fs	DNMT3A	0.001	0.066	0.129	0.066	0.056	0.084	0.136	0.088
PD34496	DNMT3At-C557X	DNMT3A	-0.041	0.022	0.089	0.023	0.052	0.073	0.113	0.076
PD41264	DNMT3At-C586fs	DNMT3A	-0.019	0.061	0.140	0.061	0.031	0.076	0.147	0.080
PD34545	DNMT3At-E294X	DNMT3A	-0.027	0.046	0.122	0.046	0.053	0.083	0.138	0.087
PD34517	DNMT3At-E427fs	DNMT3A	-0.042	0.024	0.092	0.025	0.057	0.076	0.124	0.081
PD41197	DNMT3At-E469X	DNMT3A	0.045	0.095	0.149	0.096	0.072	0.103	0.153	0.106
PD41270	DNMT3At-E578X	DNMT3A	0.005	0.058	0.116	0.059	0.070	0.089	0.135	0.094
PD34549	DNMT3At-E664X	DNMT3A	-0.031	0.053	0.140	0.054	0.042	0.080	0.148	0.087
PD41285	DNMT3At-E856fs	DNMT3A	0.073	0.118	0.167	0.119	0.085	0.121	0.167	0.123
PD41073	DNMT3At-F640fs	DNMT3A	-0.019	0.060	0.141	0.060	0.037	0.079	0.147	0.084
PD34484	DNMT3At-F640fs	DNMT3A	-0.067	-0.005	0.061	-0.004	0.055	0.069	0.096	0.072
PD34554	DNMT3At-F734fs	DNMT3A	-0.029	0.050	0.131	0.050	0.040	0.075	0.141	0.081
PD41267	DNMT3At-G550fs	DNMT3A	-0.060	0.019	0.101	0.020	0.041	0.069	0.127	0.074
PD41310	DNMT3At-G646fs	DNMT3A	-0.042	0.025	0.093	0.025	0.038	0.068	0.114	0.070
PD41135	DNMT3At-G654fs	DNMT3A	-0.002	0.053	0.111	0.054	0.063	0.083	0.128	0.087
PD34536	DNMT3At-K343fs	DNMT3A	-0.010	0.061	0.124	0.058	0.051	0.080	0.131	0.084
PD41244	DNMT3At-K589X	DNMT3A	-0.036	0.041	0.119	0.041	0.056	0.085	0.136	0.089
PD41249	DNMT3At-L504fs	DNMT3A	-0.007	0.059	0.130	0.060	0.046	0.077	0.139	0.083
PD41154	DNMT3At-L723fs	DNMT3A	-0.067	0.001	0.073	0.002	0.021	0.061	0.108	0.064
PD34545	DNMT3At-NM_175629:exon15:c.1851+1G>A	DNMT3A	0.007	0.065	0.123	0.065	0.079	0.098	0.138	0.102
PD34504	DNMT3At-NM_175629:exon16:c.1852-1G>A	DNMT3A	0.010	0.077	0.145	0.077	0.046	0.087	0.149	0.090
PD41074	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	-0.026	0.022	0.071	0.022	0.064	0.076	0.099	0.078
PD41218	DNMT3At-NM_175629:exon16:c.1936+1G>A	DNMT3A	-0.012	0.061	0.131	0.060	0.050	0.086	0.141	0.089
PD41217	DNMT3At-NM_175629:exon17:c.2082+2T>G	DNMT3A	-0.016	0.038	0.089	0.037	0.067	0.078	0.111	0.083
PD34515	DNMT3At-NM_175629:exon18:c.2083-2A>G	DNMT3A	-0.026	0.052	0.126	0.051	0.057	0.084	0.145	0.091
PD41265	DNMT3At-NM_175629:exon20:c.2323-2A>G	DNMT3A	0.034	0.078	0.120	0.078	0.082	0.097	0.128	0.101

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41181	DNMT3At-NM_175629:exon21:c.2478+1G>A	DNMT3A	0.006	0.069	0.131	0.069	0.061	0.090	0.139	0.094
PD34547	DNMT3At-NM_175629:exon22:c.2479-2A>C	DNMT3A	-0.028	0.044	0.115	0.044	0.042	0.072	0.127	0.077
PD41295	DNMT3At-NM_175629:exon22:c.2597+1G>A	DNMT3A	-0.020	0.036	0.094	0.037	0.073	0.088	0.124	0.092
PD41341	DNMT3At-NM_175629:exon22:c.2597+2T>G	DNMT3A	-0.048	0.016	0.080	0.016	0.041	0.064	0.102	0.067
PD34494	DNMT3At-NM_175629:exon8:c.856-1G>A	DNMT3A	-0.040	0.039	0.119	0.039	0.016	0.061	0.126	0.066
PD41184	DNMT3At-NM_175629:exon8:c.1014+1G>A	DNMT3A	-0.009	0.057	0.126	0.057	0.077	0.097	0.144	0.103
PD41149	DNMT3At-NM_175629:exon9:c.1015-2A>G	DNMT3A	-0.013	0.051	0.120	0.052	0.049	0.081	0.131	0.084
PD41265	DNMT3At-NM_175629:exon9:c.1015-2A>T	DNMT3A	-0.056	-0.010	0.035	-0.010	0.015	0.080	0.099	0.068
PD41285	DNMT3At-NM_175629:exon9:c.1122+1G>-	DNMT3A	-0.021	0.042	0.105	0.041	0.033	0.064	0.116	0.068
PD41231	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	-0.053	0.015	0.083	0.015	0.056	0.073	0.121	0.079
PD41151	DNMT3At-NM_175629:exon10:c.1123-1G>A	DNMT3A	-0.045	0.032	0.113	0.033	0.046	0.076	0.138	0.081
PD41140	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	-0.027	0.012	0.054	0.012	0.105	0.106	0.108	0.106
PD41143	DNMT3At-NM_175629:exon10:c.1279+1G>A	DNMT3A	0.019	0.075	0.136	0.076	0.074	0.096	0.147	0.101
PD41149	DNMT3At-NM_175629:exon11:c.1429+1G>A	DNMT3A	0.031	0.099	0.165	0.099	0.054	0.104	0.168	0.107
PD41108	DNMT3At-NM_175629:exon12:c.1474+1G>-	DNMT3A	0.035	0.100	0.160	0.098	0.058	0.105	0.162	0.106
PD41118	DNMT3At-NM_175629:exon12:c.1430-1G>-	DNMT3A	-0.006	0.062	0.132	0.063	0.039	0.074	0.140	0.080
PD41275	DNMT3At-NM_175629:exon14:c.1555-1G>T	DNMT3A	-0.017	0.054	0.124	0.055	0.052	0.085	0.135	0.088
PD41079	DNMT3At-NM_175629:exon14:c.1667+1G>A	DNMT3A	-0.009	0.069	0.148	0.069	0.040	0.082	0.154	0.087
PD34511	DNMT3At-P385fs	DNMT3A	0.021	0.067	0.112	0.066	0.086	0.098	0.131	0.102
PD41244	DNMT3At-P777fs	DNMT3A	-0.002	0.058	0.115	0.057	0.073	0.091	0.136	0.096
PD41165	DNMT3At-Q249X	DNMT3A	-0.042	0.025	0.092	0.025	0.042	0.065	0.120	0.070
PD41286	DNMT3At-Q415X	DNMT3A	0.003	0.047	0.090	0.047	0.082	0.093	0.124	0.096
PD41209	DNMT3At-Q485X	DNMT3A	-0.025	0.040	0.104	0.040	0.062	0.081	0.122	0.085
PD41177	DNMT3At-Q515X	DNMT3A	-0.003	0.072	0.145	0.071	0.056	0.090	0.153	0.095
PD41243	DNMT3At-Q615X	DNMT3A	-0.027	0.035	0.097	0.035	0.058	0.077	0.131	0.082
PD41081	DNMT3At-Q696fs	DNMT3A	-0.012	0.053	0.119	0.054	0.048	0.077	0.129	0.081

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41262	DNMT3At-Q842X	DNMT3A	-0.036	0.035	0.107	0.035	0.016	0.058	0.117	0.062
PD41302	DNMT3At-Q886X	DNMT3A	-0.020	0.052	0.120	0.051	0.042	0.077	0.131	0.080
PD34577	DNMT3At-R320X	DNMT3A	0.022	0.058	0.103	0.059	0.109	0.118	0.151	0.123
PD41217	DNMT3At-R320X	DNMT3A	-0.041	0.009	0.058	0.009	0.074	0.082	0.109	0.086
PD41122	DNMT3At-R458fs	DNMT3A	0.064	0.113	0.164	0.114	0.078	0.116	0.165	0.118
PD34570	DNMT3At-R484fs	DNMT3A	-0.039	0.042	0.130	0.043	0.027	0.069	0.144	0.075
PD41270	DNMT3At-R598X	DNMT3A	0.023	0.062	0.101	0.062	0.093	0.103	0.125	0.106
PD41142	DNMT3At-R771X	DNMT3A	-0.048	0.020	0.091	0.021	0.048	0.070	0.113	0.074
PD34513	DNMT3At-R887X	DNMT3A	-0.049	0.021	0.096	0.022	0.042	0.069	0.122	0.074
PD41167	DNMT3At-S770X	DNMT3A	0.014	0.059	0.100	0.058	0.079	0.090	0.117	0.093
PD41209	DNMT3At-S839fs	DNMT3A	-0.029	0.016	0.061	0.016	0.081	0.086	0.095	0.087
PD34469	DNMT3At-V341fs	DNMT3A	-0.027	0.042	0.114	0.043	0.058	0.082	0.130	0.087
PD34525	DNMT3At-V441fs	DNMT3A	-0.017	0.049	0.115	0.050	0.056	0.082	0.130	0.085
PD41123	DNMT3At-W314X	DNMT3A	0.054	0.109	0.166	0.109	0.075	0.113	0.168	0.116
PD41083	DNMT3At-W330X	DNMT3A	0.013	0.087	0.155	0.085	0.044	0.093	0.157	0.095
PD34541	DNMT3At-W330X	DNMT3A	-0.009	0.055	0.119	0.055	0.052	0.078	0.131	0.083
PD41161	DNMT3At-W330X	DNMT3A	0.008	0.063	0.116	0.063	0.075	0.090	0.134	0.095
PD34569	DNMT3At-W698X	DNMT3A	0.052	0.107	0.162	0.107	0.088	0.117	0.166	0.121
PD34554	DNMT3At-W860X	DNMT3A	-0.037	0.042	0.123	0.042	0.033	0.068	0.137	0.074
PD34556	DNMT3At-W860X	DNMT3A	0.019	0.094	0.166	0.094	0.040	0.098	0.167	0.100
PD41067	DNMT3At-Y284X	DNMT3A	0.022	0.064	0.101	0.063	0.092	0.101	0.136	0.106
PD34517	DNMT3At-Y370X	DNMT3A	-0.016	0.034	0.085	0.035	0.081	0.094	0.117	0.096
PD41243	DNMT3At-Y436X	DNMT3A	-0.018	0.051	0.121	0.052	0.049	0.081	0.133	0.085
PD41175	GNB1-A248T	GNB1	0.025	0.128	0.225	0.127	0.044	0.132	0.226	0.134
PD41334	GNB1-D118H	GNB1	0.090	0.124	0.156	0.124	0.110	0.129	0.158	0.131
PD41082	GNB1-K57E	GNB1	0.052	0.124	0.192	0.123	0.072	0.127	0.194	0.130
PD41104	GNB1-K57E	GNB1	0.043	0.062	0.095	0.064	0.128	0.134	0.142	0.135
PD41132	GNB1-K57E	GNB1	-0.018	0.049	0.120	0.050	0.049	0.077	0.134	0.083
PD41529	GNB1-K57E	GNB1	0.020	0.106	0.192	0.106	0.065	0.118	0.197	0.122
PD41188	GNB1-K57M	GNB1	0.009	0.088	0.165	0.088	0.071	0.109	0.174	0.113
PD41099	IDH1-H133R	IDH1	-0.009	0.088	0.183	0.088	0.052	0.105	0.190	0.110
PD34543	IDH1-R132H	IDH1	0.163	0.243	0.341	0.246	0.163	0.243	0.341	0.246
PD41214	IDH2-R140Q	IDH2	-0.018	0.071	0.169	0.074	0.038	0.089	0.180	0.096
PD41247	IDH2-R140Q	IDH2	0.020	0.131	0.238	0.130	0.049	0.136	0.239	0.139
PD41193	IDH2-R140Q	IDH2	0.128	0.180	0.236	0.181	0.128	0.180	0.236	0.181
PD41246	JAK2-V617F	JAK2	0.120	0.186	0.249	0.185	0.121	0.186	0.249	0.186
PD34543	JAK2-V617F	JAK2	-0.044	-0.012	0.037	-0.009	0.077	0.083	0.092	0.084
PD41084	JAK2-V617F	JAK2	0.080	0.133	0.186	0.133	0.084	0.134	0.187	0.134
PD34499	JAK2-V617F	JAK2	0.028	0.095	0.163	0.095	0.049	0.100	0.165	0.103
PD41114	JAK2-V617F	JAK2	0.017	0.093	0.173	0.093	0.064	0.107	0.179	0.112
PD34521	JAK2-V617F	JAK2	-0.017	0.038	0.094	0.038	0.095	0.105	0.127	0.106
PD34514	JAK2-V617F	JAK2	0.079	0.154	0.239	0.157	0.080	0.155	0.239	0.157
PD41208	KRAS-A146T	KRAS	0.002	0.069	0.133	0.068	0.069	0.092	0.146	0.098
PD41254	KRAS-F78L	KRAS	-0.009	0.072	0.148	0.071	0.025	0.079	0.152	0.083
PD34517	KRAS-G12C	KRAS	0.003	0.097	0.192	0.097	0.036	0.105	0.195	0.108
PD41532	KRAS-G13D	KRAS	-0.046	0.047	0.142	0.048	0.029	0.075	0.159	0.081
PD41257	KRAS-I84T	KRAS	0.054	0.115	0.178	0.116	0.072	0.119	0.181	0.122
PD41234	KRAS-Q22L	KRAS	0.004	0.089	0.175	0.089	0.036	0.096	0.178	0.101
PD41248	KRAS-T50I	KRAS	0.019	0.113	0.201	0.112	0.064	0.125	0.204	0.127
PD34486	KRAS-T58I	KRAS	0.008	0.078	0.148	0.078	0.062	0.095	0.155	0.100
PD41312	PPM1D-A454fs	PPM1D	0.004	0.056	0.109	0.056	0.080	0.095	0.128	0.098
PD34428	PPM1D-C407fs	PPM1D	0.034	0.111	0.195	0.113	0.044	0.114	0.196	0.117
PD41278	PPM1D-C478X	PPM1D	0.053	0.119	0.190	0.120	0.063	0.120	0.190	0.122
PD34556	PPM1D-E451X	PPM1D	0.056	0.124	0.190	0.123	0.061	0.125	0.190	0.124
PD41271	PPM1D-E475X	PPM1D	0.023	0.100	0.171	0.098	0.045	0.104	0.172	0.105
PD41219	PPM1D-E476X	PPM1D	0.024	0.101	0.170	0.100	0.048	0.104	0.172	0.106
PD41073	PPM1D-E476X	PPM1D	0.026	0.106	0.181	0.106	0.058	0.112	0.185	0.116
PD34491	PPM1D-E539X	PPM1D	-0.005	0.069	0.145	0.069	0.050	0.088	0.153	0.093
PD34494	PPM1D-K511X	PPM1D	0.048	0.101	0.155	0.102	0.074	0.108	0.158	0.111
PD41110	PPM1D-K549X	PPM1D	0.033	0.081	0.134	0.082	0.071	0.095	0.140	0.099

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41178	PPM1D-L484fs	PPM1D	0.045	0.079	0.110	0.078	0.094	0.102	0.123	0.104
PD41344	PPM1D-L538fs	PPM1D	0.059	0.120	0.185	0.120	0.063	0.120	0.185	0.121
PD41130	PPM1D-N448fs	PPM1D	0.058	0.093	0.130	0.093	0.109	0.119	0.141	0.121
PD41271	PPM1D-N477fs	PPM1D	0.033	0.110	0.186	0.109	0.039	0.111	0.186	0.111
PD41253	PPM1D-N477fs	PPM1D	0.065	0.123	0.180	0.123	0.068	0.123	0.180	0.124
PD34575	PPM1D-N477fs	PPM1D	0.047	0.119	0.188	0.119	0.058	0.121	0.189	0.122
PD34495	PPM1D-P531fs	PPM1D	0.007	0.085	0.167	0.086	0.050	0.096	0.171	0.101
PD34531	PPM1D-Q524X	PPM1D	-0.019	0.024	0.066	0.024	0.060	0.069	0.088	0.071
PD41306	PPM1D-Q524X	PPM1D	0.028	0.106	0.182	0.105	0.046	0.109	0.183	0.110
PD34571	PPM1D-R429fs	PPM1D	0.031	0.108	0.176	0.107	0.062	0.113	0.178	0.116
PD34567	PPM1D-R458X	PPM1D	-0.029	0.013	0.057	0.014	0.064	0.074	0.100	0.077
PD41344	PPM1D-R458X	PPM1D	0.043	0.115	0.187	0.115	0.053	0.117	0.187	0.118
PD41336	PPM1D-R552X	PPM1D	0.018	0.095	0.171	0.095	0.061	0.106	0.175	0.111
PD34538	PPM1D-R572X	PPM1D	0.014	0.079	0.140	0.078	0.051	0.091	0.145	0.093
PD34551	PPM1D-R581X	PPM1D	-0.017	0.058	0.141	0.059	0.064	0.093	0.155	0.100
PD34578	PPM1D-S403fs	PPM1D	-0.011	0.058	0.134	0.059	0.062	0.090	0.151	0.095
PD34519	PPM1D-S446fs	PPM1D	0.032	0.101	0.171	0.101	0.047	0.104	0.171	0.106
PD34562	PPM1D-S446X	PPM1D	-0.016	0.067	0.152	0.066	0.035	0.084	0.157	0.089
PD34549	PPM1D-T483fs	PPM1D	0.030	0.115	0.198	0.115	0.050	0.120	0.200	0.121
PD41344	PPM1D-T483fs	PPM1D	0.150	0.219	0.283	0.218	0.150	0.219	0.283	0.218
PD34500	PPM1D-W427X	PPM1D	0.024	0.104	0.181	0.104	0.058	0.112	0.185	0.115
PD41175	PPM1D-W427X	PPM1D	0.028	0.092	0.161	0.092	0.053	0.098	0.165	0.102
PD41188	PTPN11-G363R	PTPN11	0.092	0.185	0.276	0.185	0.095	0.185	0.276	0.186
PD41155	PTPN11-G507A	PTPN11	0.066	0.156	0.248	0.157	0.077	0.156	0.248	0.159
PD34566	PTPN11-P495L	PTPN11	0.085	0.168	0.257	0.169	0.087	0.169	0.258	0.170
PD41248	PTPN11-R265Q	PTPN11	0.070	0.139	0.209	0.139	0.089	0.143	0.210	0.145
PD41265	PTPN11-R502L	PTPN11	0.067	0.144	0.219	0.144	0.072	0.144	0.219	0.145
PD41140	PTPN11-T219N	PTPN11	0.088	0.183	0.280	0.185	0.090	0.183	0.280	0.185
PD41529	PTPN11-T472M	PTPN11	0.068	0.156	0.246	0.156	0.080	0.158	0.247	0.160
PD34529	SF3B1-A1117S	SF3B1	0.037	0.118	0.199	0.119	0.048	0.119	0.199	0.122
PD34559	SF3B1-A744D	SF3B1	0.026	0.080	0.135	0.080	0.078	0.100	0.144	0.104
PD41086	SF3B1-A744P	SF3B1	0.001	0.079	0.159	0.079	0.059	0.099	0.167	0.104
PD41313	SF3B1-A744P	SF3B1	-0.027	0.054	0.138	0.056	0.051	0.085	0.153	0.091
PD34492	SF3B1-D621N	SF3B1	0.049	0.130	0.216	0.131	0.058	0.132	0.216	0.134
PD34559	SF3B1-G740R	SF3B1	0.034	0.092	0.151	0.091	0.070	0.103	0.156	0.106
PD34540	SF3B1-G742D	SF3B1	0.057	0.140	0.226	0.140	0.065	0.141	0.226	0.143
PD41528	SF3B1-H662Q	SF3B1	0.105	0.190	0.272	0.189	0.107	0.191	0.272	0.190
PD34538	SF3B1-H662Q	SF3B1	0.026	0.105	0.189	0.106	0.059	0.113	0.194	0.117
PD41296	SF3B1-H662Y	SF3B1	-0.012	0.052	0.124	0.054	0.048	0.079	0.137	0.084
PD34493	SF3B1-K666N	SF3B1	0.059	0.097	0.139	0.098	0.086	0.107	0.143	0.110
PD41082	SF3B1-K666N	SF3B1	0.186	0.240	0.292	0.239	0.186	0.240	0.292	0.239
PD41272	SF3B1-K666N	SF3B1	0.076	0.128	0.179	0.128	0.082	0.129	0.179	0.130
PD34575	SF3B1-K666N	SF3B1	0.067	0.145	0.222	0.144	0.072	0.146	0.222	0.146
PD34569	SF3B1-K666N	SF3B1	0.035	0.090	0.145	0.090	0.086	0.108	0.152	0.112
PD41142	SF3B1-K666N	SF3B1	0.084	0.159	0.235	0.159	0.085	0.159	0.235	0.160
PD41144	SF3B1-K666N	SF3B1	0.098	0.166	0.237	0.167	0.098	0.166	0.237	0.167
PD34558	SF3B1-K666N	SF3B1	0.056	0.132	0.209	0.133	0.063	0.132	0.209	0.134
PD34576	SF3B1-K666N	SF3B1	0.061	0.125	0.191	0.124	0.077	0.128	0.194	0.130
PD34481	SF3B1-K666N	SF3B1	0.131	0.197	0.263	0.197	0.132	0.197	0.263	0.198
PD34562	SF3B1-K666R	SF3B1	-0.050	0.078	0.205	0.077	0.044	0.108	0.222	0.118
PD34469	SF3B1-K666T	SF3B1	0.100	0.181	0.263	0.180	0.102	0.181	0.263	0.181
PD34511	SF3B1-K700E	SF3B1	0.031	0.086	0.145	0.087	0.082	0.108	0.153	0.112
PD41276	SF3B1-K700E	SF3B1	0.046	0.117	0.195	0.118	0.063	0.121	0.196	0.125
PD41285	SF3B1-K700E	SF3B1	0.006	0.079	0.156	0.079	0.045	0.091	0.161	0.095
PD41306	SF3B1-K700E	SF3B1	0.045	0.135	0.217	0.134	0.059	0.137	0.218	0.138
PD41159	SF3B1-K700E	SF3B1	0.028	0.094	0.161	0.093	0.069	0.107	0.166	0.110
PD41238	SF3B1-K700E	SF3B1	0.016	0.108	0.199	0.107	0.055	0.116	0.201	0.120
PD41341	SF3B1-K700E	SF3B1	-0.002	0.068	0.137	0.069	0.058	0.091	0.151	0.095
PD41194	SF3B1-R549H	SF3B1	0.066	0.149	0.234	0.150	0.070	0.150	0.234	0.151
PD34511	SF3B1-R625L	SF3B1	0.034	0.098	0.158	0.098	0.078	0.112	0.164	0.115

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41345	SRSF2-P95A	SRSF2	-0.021	0.074	0.182	0.077	0.062	0.104	0.196	0.114
PD41154	SRSF2-P95A	SRSF2	0.050	0.123	0.202	0.124	0.080	0.131	0.205	0.135
PD41305	SRSF2-P95H	SRSF2	0.317	0.401	0.489	0.402	0.317	0.401	0.489	0.402
PD34543	SRSF2-P95H	SRSF2	0.348	0.440	0.537	0.441	0.348	0.440	0.537	0.441
PD41239	SRSF2-P95H	SRSF2	0.318	0.394	0.481	0.396	0.318	0.394	0.481	0.396
PD41161	SRSF2-P95H	SRSF2	0.321	0.418	0.520	0.419	0.321	0.418	0.520	0.419
PD41115	SRSF2-P95L	SRSF2	0.055	0.120	0.187	0.121	0.068	0.122	0.188	0.124
PD41075	SRSF2-P95L	SRSF2	0.049	0.103	0.158	0.103	0.094	0.117	0.164	0.122
PD41235	SRSF2-P95L	SRSF2	0.061	0.159	0.257	0.160	0.070	0.161	0.257	0.162
PD41099	SRSF2-P95R	SRSF2	0.036	0.106	0.180	0.106	0.053	0.110	0.181	0.112
PD34488	SRSF2-R47P	SRSF2	-0.006	0.059	0.131	0.061	0.050	0.081	0.139	0.086
PD41102	SRSF2-NM_003016:exon1:c.43_44GA	SRSF2	0.113	0.184	0.256	0.184	0.115	0.184	0.256	0.185
PD41321	TET2nt-A1341E	TET2	-0.005	0.053	0.115	0.054	0.075	0.093	0.141	0.098
PD41234	TET2nt-A1863V	TET2	0.065	0.123	0.181	0.123	0.072	0.124	0.182	0.125
PD41176	TET2nt-A1876G	TET2	0.031	0.092	0.162	0.094	0.052	0.097	0.163	0.101
PD41127	TET2nt-A1876V	TET2	0.012	0.083	0.158	0.084	0.052	0.095	0.163	0.099
PD41331	TET2nt-A347E	TET2	0.022	0.100	0.174	0.099	0.040	0.104	0.176	0.106
PD41117	TET2nt-A394T	TET2	0.031	0.113	0.187	0.111	0.041	0.115	0.188	0.115
PD34499	TET2nt-C1135Y	TET2	0.026	0.089	0.151	0.089	0.050	0.094	0.153	0.097
PD41530	TET2nt-C1211Y	TET2	0.076	0.144	0.209	0.144	0.095	0.147	0.210	0.149
PD41249	TET2nt-C1221S	TET2	-0.004	0.076	0.163	0.077	0.053	0.092	0.171	0.099
PD34536	TET2nt-C1221Y	TET2	0.020	0.085	0.149	0.086	0.047	0.092	0.151	0.095
PD34520	TET2nt-C1271G	TET2	-0.010	0.064	0.134	0.063	0.050	0.083	0.145	0.088
PD41139	TET2nt-C1271S	TET2	-0.031	0.041	0.118	0.042	0.041	0.073	0.136	0.079
PD34561	TET2nt-C1289F	TET2	0.079	0.125	0.172	0.126	0.082	0.126	0.172	0.127
PD34527	TET2nt-C1298Y	TET2	0.190	0.232	0.276	0.232	0.190	0.232	0.276	0.232
PD41333	TET2nt-D1376A	TET2	0.077	0.144	0.211	0.144	0.080	0.145	0.211	0.145
PD34541	TET2nt-D1981N	TET2	-0.031	0.042	0.123	0.044	0.025	0.063	0.130	0.069
PD34494	TET2nt-E1178G	TET2	-0.024	0.036	0.098	0.037	0.061	0.079	0.124	0.083
PD41078	TET2nt-G1275E	TET2	-0.024	0.037	0.098	0.037	0.061	0.080	0.126	0.085
PD34566	TET2nt-G1288V	TET2	0.029	0.103	0.179	0.103	0.052	0.108	0.182	0.110
PD41224	TET2nt-G1361R	TET2	0.021	0.094	0.164	0.094	0.041	0.097	0.166	0.099
PD34542	TET2nt-G1861V	TET2	-0.025	0.015	0.057	0.015	0.076	0.088	0.110	0.090
PD41107	TET2nt-H1219Y	TET2	0.045	0.094	0.147	0.095	0.085	0.109	0.154	0.113
PD41344	TET2nt-H1380D	TET2	0.028	0.089	0.152	0.090	0.056	0.095	0.153	0.099
PD34487	TET2nt-H1380Y	TET2	-0.033	0.050	0.135	0.050	0.059	0.090	0.157	0.097
PD41222	TET2nt-H1380Y	TET2	-0.114	-0.019	0.081	-0.018	0.012	0.054	0.127	0.060
PD41211	TET2nt-H1380Y	TET2	0.100	0.140	0.179	0.140	0.101	0.140	0.179	0.140
PD41338	TET2nt-H1380Y	TET2	-0.066	-0.001	0.068	0.000	0.066	0.080	0.108	0.083
PD34566	TET2nt-H1416R	TET2	-0.006	0.058	0.126	0.059	0.058	0.086	0.140	0.091
PD41080	TET2nt-H1868Y	TET2	-0.006	0.036	0.082	0.037	0.082	0.094	0.116	0.095
PD41190	TET2nt-H1881R	TET2	-0.010	0.061	0.129	0.060	0.057	0.085	0.141	0.091
PD41163	TET2nt-H1912R	TET2	0.006	0.091	0.179	0.091	0.043	0.101	0.184	0.104
PD34499	TET2nt-H269N	TET2	-0.013	0.061	0.138	0.061	0.019	0.073	0.141	0.075
PD41345	TET2nt-H468R	TET2	-0.007	0.075	0.165	0.077	0.036	0.089	0.170	0.093
PD41275	TET2nt-I1873T	TET2	0.035	0.095	0.161	0.097	0.060	0.101	0.165	0.106
PD41127	TET2nt-I1873T	TET2	0.027	0.102	0.178	0.102	0.060	0.111	0.181	0.114
PD41117	TET2nt-I1873T	TET2	0.235	0.287	0.344	0.288	0.235	0.287	0.344	0.288
PD34499	TET2nt-I1873T	TET2	0.107	0.132	0.161	0.133	0.114	0.134	0.161	0.135
PD41528	TET2nt-I1873T	TET2	-0.066	0.005	0.082	0.006	0.059	0.080	0.128	0.085
PD41304	TET2nt-K110R	TET2	0.005	0.051	0.099	0.051	0.074	0.086	0.118	0.090
PD34565	TET2nt-L1311Q	TET2	0.008	0.063	0.116	0.062	0.061	0.082	0.128	0.086
PD41070	TET2nt-L1322P	TET2	0.007	0.076	0.151	0.076	0.064	0.096	0.162	0.102
PD41082	TET2nt-L1322Q	TET2	0.059	0.133	0.203	0.132	0.064	0.133	0.204	0.133
PD41242	TET2nt-L1332P	TET2	0.153	0.209	0.267	0.210	0.153	0.209	0.267	0.210
PD41297	TET2nt-L1418P	TET2	0.014	0.087	0.161	0.088	0.052	0.096	0.164	0.101
PD34512	TET2nt-L1872P	TET2	-0.020	0.058	0.142	0.059	0.051	0.085	0.157	0.092
PD41166	TET2nt-M1333R	TET2	0.046	0.109	0.173	0.109	0.061	0.112	0.174	0.114

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41246	TET2nt-N1266S	TET2	0.013	0.078	0.153	0.080	0.065	0.097	0.162	0.102
PD41530	TET2nt-P1194R	TET2	0.015	0.100	0.183	0.099	0.059	0.109	0.187	0.115
PD34541	TET2nt-P1367L	TET2	0.011	0.076	0.141	0.076	0.052	0.088	0.146	0.092
PD41285	TET2nt-P288R	TET2	0.008	0.076	0.145	0.076	0.063	0.097	0.153	0.100
PD41082	TET2nt-Q1274R	TET2	0.028	0.079	0.127	0.078	0.076	0.095	0.135	0.099
PD41106	TET2nt-Q1414E	TET2	0.077	0.140	0.205	0.140	0.079	0.140	0.205	0.141
PD41086	TET2nt-Q1699R	TET2	-0.014	0.056	0.131	0.056	0.048	0.080	0.141	0.085
PD41105	TET2nt-Q70R	TET2	0.043	0.088	0.136	0.089	0.081	0.101	0.142	0.105
PD34523	TET2nt-Q909K	TET2	-0.014	0.070	0.160	0.071	0.026	0.082	0.165	0.087
PD41340	TET2nt-R1214W	TET2	0.032	0.097	0.160	0.098	0.067	0.105	0.165	0.109
PD41128	TET2nt-R1261C	TET2	-0.001	0.078	0.151	0.076	0.053	0.093	0.157	0.098
PD41203	TET2nt-R1359H	TET2	0.028	0.102	0.182	0.103	0.061	0.111	0.186	0.116
PD41165	TET2nt-R1359S	TET2	0.085	0.146	0.210	0.146	0.086	0.146	0.211	0.147
PD34502	TET2nt-R1878P	TET2	0.015	0.088	0.158	0.087	0.051	0.097	0.160	0.100
PD41188	TET2nt-R1926G	TET2	0.035	0.115	0.194	0.115	0.058	0.120	0.196	0.123
PD41266	TET2nt-S1290L	TET2	0.076	0.154	0.225	0.154	0.081	0.155	0.226	0.155
PD34545	TET2nt-S1898F	TET2	0.019	0.102	0.181	0.101	0.053	0.110	0.185	0.113
PD34565	TET2nt-S817F	TET2	0.041	0.104	0.170	0.105	0.063	0.108	0.171	0.112
PD41190	TET2nt-T1372I	TET2	0.138	0.169	0.201	0.170	0.138	0.169	0.201	0.170
PD34559	TET2nt-T1393A	TET2	0.038	0.109	0.183	0.109	0.059	0.113	0.184	0.116
PD34545	TET2nt-T1399P	TET2	0.012	0.083	0.158	0.084	0.051	0.096	0.162	0.100
PD41098	TET2nt-T621N	TET2	0.028	0.099	0.168	0.099	0.053	0.104	0.170	0.107
PD34554	TET2nt-TET2:NM_001127208:exon7:c.3852_3854del:p.1284_1285del	TET2	0.044	0.107	0.167	0.106	0.078	0.115	0.171	0.118
PD34527	TET2nt-V1417F	TET2	0.000	0.073	0.144	0.073	0.043	0.087	0.149	0.090
PD41306	TET2nt-V1417G	TET2	0.027	0.095	0.168	0.096	0.057	0.103	0.171	0.107
PD41221	TET2nt-Y1902H	TET2	0.020	0.099	0.179	0.099	0.040	0.102	0.180	0.104
PD34489	TET2t-A1769fs	TET2	-0.008	0.060	0.130	0.060	0.045	0.078	0.139	0.084
PD34559	TET2t-C1211fs	TET2	0.004	0.070	0.137	0.070	0.052	0.085	0.143	0.090
PD41143	TET2t-C1271fs	TET2	-0.028	0.038	0.106	0.038	0.060	0.080	0.135	0.086
PD41124	TET2t-C1271X	TET2	0.010	0.079	0.143	0.078	0.030	0.082	0.145	0.084
PD41235	TET2t-C973fs	TET2	0.052	0.116	0.179	0.116	0.065	0.118	0.180	0.119
PD41146	TET2t-E1178fs	TET2	0.034	0.066	0.099	0.066	0.085	0.092	0.109	0.094
PD41530	TET2t-E1477fs	TET2	0.017	0.082	0.148	0.082	0.073	0.100	0.158	0.106
PD41240	TET2t-E566X	TET2	-0.013	0.058	0.131	0.058	0.058	0.087	0.143	0.092
PD41235	TET2t-E692X	TET2	-0.036	0.026	0.089	0.026	0.057	0.074	0.114	0.078
PD41266	TET2t-E808X	TET2	0.016	0.080	0.146	0.081	0.045	0.089	0.149	0.092
PD41528	TET2t-F1597fs	TET2	0.054	0.095	0.134	0.095	0.101	0.113	0.144	0.117
PD41165	TET2t-F681fs	TET2	-0.012	0.046	0.106	0.046	0.051	0.074	0.121	0.078
PD34554	TET2t-G1313fs	TET2	0.057	0.112	0.169	0.112	0.073	0.116	0.170	0.118
PD34550	TET2t-G1719fs	TET2	0.029	0.092	0.156	0.092	0.057	0.100	0.160	0.103
PD41080	TET2t-G422fs	TET2	-0.002	0.047	0.096	0.047	0.068	0.083	0.119	0.086
PD41182	TET2t-G563X	TET2	-0.016	0.065	0.143	0.063	0.031	0.079	0.146	0.082
PD34561	TET2t-G898X	TET2	0.056	0.112	0.172	0.113	0.069	0.114	0.173	0.116
PD41302	TET2t-H1778fs	TET2	0.074	0.130	0.184	0.129	0.088	0.132	0.186	0.133
PD41151	TET2t-H193fs	TET2	-0.012	0.058	0.131	0.060	0.049	0.083	0.142	0.087
PD41082	TET2t-H435fs	TET2	0.061	0.120	0.177	0.120	0.076	0.122	0.177	0.124
PD34554	TET2t-H650fs	TET2	-0.042	0.006	0.057	0.006	0.081	0.091	0.107	0.093
PD34495	TET2t-I1105fs	TET2	-0.022	0.057	0.140	0.058	0.045	0.081	0.151	0.087
PD34509	TET2t-I1230fs	TET2	-0.005	0.051	0.109	0.052	0.078	0.092	0.128	0.097
PD41530	TET2t-I1859fs	TET2	0.019	0.093	0.172	0.094	0.057	0.104	0.176	0.109
PD34483	TET2t-I274fs	TET2	-0.006	0.058	0.120	0.058	0.066	0.089	0.132	0.093
PD41242	TET2t-I274fs	TET2	0.148	0.207	0.263	0.206	0.148	0.207	0.263	0.206
PD41240	TET2t-I274fs	TET2	-0.032	0.050	0.135	0.051	0.030	0.075	0.144	0.080
PD41298	TET2t-I274fs	TET2	-0.012	0.043	0.101	0.043	0.061	0.079	0.121	0.083
PD34502	TET2t-K1049fs	TET2	-0.038	0.042	0.122	0.041	0.021	0.067	0.131	0.071
PD41071	TET2t-K1197X	TET2	0.020	0.087	0.152	0.086	0.049	0.095	0.155	0.096

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD34548	TET2t-K1254fs	TET2	0.007	0.079	0.153	0.080	0.048	0.091	0.159	0.096
PD41151	TET2t-K1488fs	TET2	-0.002	0.072	0.147	0.072	0.048	0.087	0.153	0.092
PD41132	TET2t-K1533X	TET2	-0.006	0.060	0.131	0.060	0.046	0.080	0.140	0.084
PD41316	TET2t-K1720X	TET2	0.023	0.101	0.177	0.100	0.041	0.105	0.179	0.107
PD41118	TET2t-K188fs	TET2	-0.029	0.025	0.083	0.026	0.065	0.079	0.117	0.083
PD41242	TET2t-K603X	TET2	0.023	0.100	0.187	0.101	0.037	0.102	0.190	0.106
PD41071	TET2t-K664fs	TET2	0.007	0.074	0.142	0.074	0.040	0.082	0.146	0.086
PD41134	TET2t-K753fs	TET2	-0.023	0.042	0.111	0.043	0.041	0.070	0.126	0.074
PD41124	TET2t-K944X	TET2	0.013	0.081	0.147	0.080	0.046	0.088	0.149	0.091
PD34499	TET2t-L1447fs	TET2	0.038	0.090	0.142	0.089	0.054	0.093	0.143	0.095
PD41341	TET2t-L1511X	TET2	0.018	0.068	0.120	0.068	0.071	0.090	0.129	0.094
PD34541	TET2t-L1740X	TET2	-0.049	0.023	0.100	0.024	0.024	0.060	0.118	0.064
PD41280	TET2t-L1819fs	TET2	0.010	0.075	0.140	0.075	0.053	0.090	0.145	0.093
PD41266	TET2t-L1819X	TET2	-0.014	0.038	0.094	0.039	0.066	0.081	0.120	0.086
PD41236	TET2t-L1916fs	TET2	-0.015	0.046	0.113	0.047	0.044	0.070	0.124	0.075
PD41318	TET2t-L199X	TET2	0.016	0.089	0.169	0.090	0.042	0.099	0.171	0.101
PD41148	TET2t-L346fs	TET2	0.043	0.104	0.166	0.104	0.071	0.109	0.169	0.114
PD34553	TET2t-L532X	TET2	-0.022	0.050	0.121	0.050	0.040	0.073	0.132	0.078
PD41191	TET2t-L920X	TET2	-0.016	0.062	0.142	0.062	0.056	0.089	0.154	0.095
PD34570	TET2t-M1028fs	TET2	-0.032	0.024	0.081	0.024	0.073	0.087	0.111	0.089
PD34540	TET2t-N1328fs	TET2	0.012	0.074	0.137	0.074	0.073	0.097	0.147	0.101
PD41150	TET2t-N281fs	TET2	0.000	0.077	0.150	0.076	0.044	0.090	0.155	0.093
PD41253	TET2t-N338fs	TET2	0.070	0.110	0.150	0.110	0.078	0.111	0.150	0.112
PD41146	TET2t-N374fs	TET2	0.039	0.086	0.138	0.087	0.072	0.098	0.144	0.100
PD41229	TET2t-N528fs	TET2	-0.014	0.027	0.065	0.026	0.075	0.085	0.110	0.087
PD34501	TET2t-N811fs	TET2	0.008	0.088	0.167	0.088	0.060	0.104	0.174	0.109
PD34556	TET2t-N837fs	TET2	0.017	0.088	0.156	0.088	0.033	0.092	0.157	0.093
PD41325	TET2t-NM_001127208:exon10:c.4183-2A>G	TET2	0.035	0.106	0.178	0.107	0.062	0.112	0.182	0.115
PD34520	TET2t-NM_001127208:exon5:c.3501-2A>C	TET2	0.058	0.098	0.138	0.098	0.101	0.116	0.145	0.119
PD41264	TET2t-NM_001127208:exon7:c.3804-2A>G	TET2	0.029	0.082	0.137	0.082	0.078	0.099	0.146	0.104
PD41216	TET2t-NM_001127208:exon8:c.3955-2A>G	TET2	0.023	0.096	0.172	0.096	0.050	0.102	0.177	0.106
PD34497	TET2t-NM_001127208:exon9:c.4182+2->T	TET2	0.126	0.164	0.199	0.163	0.128	0.164	0.199	0.164
PD41105	TET2t-P101fs	TET2	0.031	0.073	0.118	0.074	0.076	0.093	0.128	0.097
PD34497	TET2t-P1155fs	TET2	-0.010	0.066	0.146	0.066	0.052	0.092	0.153	0.096
PD41161	TET2t-P1410fs	TET2	0.026	0.092	0.159	0.092	0.047	0.097	0.160	0.099
PD41161	TET2t-P1644fs	TET2	0.022	0.081	0.142	0.082	0.055	0.091	0.147	0.094
PD42297	TET2t-P401fs	TET2	0.227	0.272	0.316	0.272	0.227	0.272	0.316	0.272
PD41203	TET2t-P413fs	TET2	0.090	0.150	0.204	0.149	0.096	0.151	0.204	0.151
PD41101	TET2t-Q1068X	TET2	0.057	0.107	0.159	0.107	0.072	0.109	0.160	0.112
PD41330	TET2t-Q1501X	TET2	0.015	0.087	0.158	0.087	0.050	0.096	0.160	0.098
PD34545	TET2t-Q1523X	TET2	0.006	0.073	0.139	0.072	0.064	0.092	0.150	0.097
PD41120	TET2t-Q1534X	TET2	0.019	0.084	0.156	0.086	0.055	0.094	0.160	0.099
PD34523	TET2t-Q1537X	TET2	0.033	0.103	0.175	0.104	0.066	0.113	0.178	0.117
PD41321	TET2t-Q1537X	TET2	0.041	0.102	0.165	0.102	0.071	0.110	0.169	0.113
PD41082	TET2t-Q1542X	TET2	0.047	0.105	0.168	0.106	0.064	0.109	0.170	0.112
PD41169	TET2t-Q1542X	TET2	0.012	0.088	0.161	0.087	0.050	0.097	0.167	0.101
PD41073	TET2t-Q1553fs	TET2	-0.004	0.077	0.155	0.077	0.047	0.091	0.160	0.095
PD34539	TET2t-Q1553fs	TET2	0.064	0.121	0.177	0.121	0.070	0.122	0.177	0.123
PD41256	TET2t-Q1624X	TET2	0.052	0.115	0.177	0.114	0.071	0.118	0.179	0.120
PD34576	TET2t-Q1687X	TET2	0.003	0.078	0.148	0.077	0.053	0.091	0.155	0.096
PD34503	TET2t-Q1828X	TET2	0.031	0.091	0.150	0.091	0.056	0.096	0.152	0.099

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41118	TET2t-Q185fs	TET2	-0.024	0.033	0.093	0.033	0.062	0.079	0.119	0.083
PD41293	TET2t-Q185fs	TET2	0.038	0.092	0.152	0.093	0.071	0.102	0.158	0.107
PD41080	TET2t-Q232X	TET2	-0.016	0.055	0.127	0.056	0.049	0.081	0.142	0.086
PD41124	TET2t-Q317X	TET2	-0.016	0.047	0.108	0.047	0.049	0.071	0.120	0.076
PD41325	TET2t-Q321X	TET2	0.023	0.103	0.180	0.103	0.045	0.108	0.181	0.109
PD41294	TET2t-Q321X	TET2	0.016	0.067	0.122	0.067	0.066	0.087	0.131	0.091
PD41347	TET2t-Q324X	TET2	-0.028	0.046	0.129	0.048	0.049	0.082	0.142	0.087
PD34499	TET2t-Q417X	TET2	0.021	0.089	0.162	0.091	0.044	0.095	0.165	0.099
PD34489	TET2t-Q461fs	TET2	0.017	0.093	0.173	0.093	0.035	0.097	0.175	0.099
PD41315	TET2t-Q526fs	TET2	0.015	0.086	0.153	0.085	0.047	0.093	0.156	0.096
PD41136	TET2t-Q531fs	TET2	-0.029	0.010	0.048	0.010	0.089	0.098	0.104	0.097
PD41194	TET2t-Q618fs	TET2	0.173	0.212	0.252	0.212	0.173	0.212	0.252	0.212
PD41083	TET2t-Q618X	TET2	-0.032	0.037	0.107	0.038	0.028	0.062	0.122	0.066
PD41157	TET2t-Q649X	TET2	0.031	0.085	0.145	0.086	0.080	0.103	0.151	0.108
PD34527	TET2t-Q674X	TET2	0.189	0.231	0.275	0.232	0.189	0.231	0.275	0.232
PD41183	TET2t-Q745X	TET2	0.039	0.100	0.165	0.101	0.067	0.108	0.167	0.112
PD41135	TET2t-Q749X	TET2	0.011	0.070	0.131	0.070	0.061	0.087	0.139	0.092
PD41529	TET2t-Q778X	TET2	-0.029	0.055	0.135	0.054	0.040	0.081	0.149	0.086
PD41151	TET2t-Q831fs	TET2	0.011	0.075	0.143	0.076	0.061	0.093	0.150	0.097
PD41146	TET2t-Q866X	TET2	-0.012	0.059	0.130	0.059	0.042	0.076	0.137	0.081
PD41345	TET2t-Q888X	TET2	0.091	0.149	0.206	0.148	0.095	0.149	0.207	0.150
PD41221	TET2t-Q888X	TET2	0.023	0.096	0.164	0.095	0.049	0.103	0.166	0.104
PD41221	TET2t-Q916X	TET2	-0.012	0.053	0.118	0.052	0.057	0.080	0.130	0.086
PD41237	TET2t-Q917X	TET2	0.089	0.149	0.207	0.148	0.092	0.149	0.207	0.149
PD34477	TET2t-Q962X	TET2	-0.044	0.013	0.078	0.015	0.055	0.073	0.117	0.078
PD41347	TET2t-Q976fs	TET2	0.020	0.060	0.102	0.060	0.088	0.098	0.122	0.101
PD41223	TET2t-Q976X	TET2	-0.004	0.060	0.127	0.060	0.055	0.084	0.135	0.088
PD34492	TET2t-R1216X	TET2	0.006	0.075	0.144	0.075	0.048	0.090	0.150	0.093
PD41306	TET2t-R1307fs	TET2	0.021	0.105	0.186	0.105	0.039	0.108	0.187	0.109
PD41160	TET2t-R1455fs	TET2	0.103	0.153	0.201	0.152	0.107	0.154	0.201	0.153
PD34497	TET2t-R544X	TET2	-0.006	0.064	0.133	0.064	0.063	0.089	0.144	0.094
PD41142	TET2t-R544X	TET2	-0.010	0.066	0.139	0.066	0.031	0.078	0.144	0.081
PD41145	TET2t-R550X	TET2	-0.042	0.031	0.105	0.031	0.017	0.057	0.121	0.061
PD41161	TET2t-S1039X	TET2	0.029	0.096	0.163	0.097	0.052	0.101	0.165	0.104
PD41322	TET2t-S1059X	TET2	0.043	0.117	0.187	0.117	0.066	0.120	0.189	0.123
PD41316	TET2t-S1369X	TET2	0.004	0.065	0.124	0.064	0.065	0.088	0.136	0.093
PD41203	TET2t-S1586fs	TET2	-0.002	0.082	0.164	0.081	0.043	0.094	0.167	0.098
PD41242	TET2t-S1798X	TET2	0.034	0.105	0.176	0.104	0.053	0.108	0.177	0.110
PD41082	TET2t-S315fs	TET2	0.070	0.113	0.158	0.114	0.086	0.117	0.159	0.119
PD34488	TET2t-S402X	TET2	0.012	0.083	0.153	0.084	0.044	0.091	0.155	0.094
PD41191	TET2t-S473fs	TET2	-0.016	0.066	0.152	0.067	0.038	0.086	0.160	0.091
PD41216	TET2t-S509X	TET2	0.012	0.051	0.094	0.052	0.083	0.093	0.111	0.095
PD41341	TET2t-S56fs	TET2	0.024	0.089	0.151	0.088	0.054	0.095	0.154	0.098
PD34499	TET2t-S675X	TET2	-0.018	0.045	0.107	0.044	0.047	0.071	0.124	0.076
PD41108	TET2t-S675X	TET2	0.025	0.088	0.149	0.087	0.053	0.097	0.152	0.099
PD41121	TET2t-S792X	TET2	0.021	0.102	0.177	0.101	0.050	0.107	0.178	0.110
PD34556	TET2t-T1086fs	TET2	0.045	0.116	0.191	0.117	0.052	0.117	0.191	0.119
PD41262	TET2t-T1091fs	TET2	0.082	0.115	0.148	0.115	0.097	0.119	0.150	0.120
PD41247	TET2t-T1331fs	TET2	0.022	0.100	0.177	0.100	0.056	0.109	0.179	0.112
PD41256	TET2t-T1554fs	TET2	0.032	0.109	0.185	0.109	0.041	0.110	0.185	0.111
PD34477	TET2t-T621fs	TET2	0.026	0.092	0.163	0.093	0.049	0.097	0.165	0.100
PD41248	TET2t-T759fs	TET2	0.026	0.105	0.182	0.104	0.043	0.108	0.183	0.109
PD41165	TET2t-V1054fs	TET2	0.007	0.072	0.137	0.072	0.034	0.078	0.139	0.081
PD34510	TET2t-V1432fs	TET2	-0.006	0.060	0.127	0.060	0.057	0.084	0.141	0.090
PD34505	TET2t-W1847X	TET2	0.042	0.111	0.185	0.112	0.081	0.120	0.190	0.126
PD41191	TET2t-W1847X	TET2	0.010	0.064	0.119	0.064	0.108	0.119	0.152	0.123
PD34499	TET2t-Y1294fs	TET2	0.139	0.189	0.237	0.189	0.139	0.189	0.237	0.189
PD41218	TET2t-Y1649X	TET2	0.019	0.091	0.164	0.091	0.041	0.096	0.166	0.098
PD41266	TET2t-Y1766X	TET2	0.042	0.111	0.177	0.111	0.049	0.112	0.177	0.113
PD41080	TP53nt-C176F	TP53	-0.049	0.015	0.078	0.015	0.061	0.077	0.112	0.081

PID	Site	Gene	Observed Growth Q05	Observed Growth Q50	Observed Growth Q95	Observed Growth Mean	Historica lGrowth Q05	Historical Growth Q50	Historical Growth Q95	Historical Growth Mean
PD41078	TP53nt-C242F	TP53	0.002	0.064	0.122	0.064	0.057	0.083	0.131	0.087
PD34533	TP53nt-F212V	TP53	-0.019	0.059	0.140	0.060	0.044	0.082	0.151	0.087
PD41131	TP53nt-G187S	TP53	-0.069	0.003	0.072	0.003	0.031	0.055	0.099	0.059
PD41338	TP53nt-G244S	TP53	0.021	0.086	0.151	0.086	0.067	0.100	0.158	0.105
PD41344	TP53nt-I195T	TP53	-0.013	0.065	0.143	0.065	0.037	0.079	0.150	0.084
PD34517	TP53nt-L336V	TP53	-0.055	0.033	0.119	0.032	0.031	0.071	0.135	0.075
PD41528	TP53nt-M237V	TP53	0.075	0.169	0.262	0.169	0.083	0.171	0.262	0.171
PD41165	TP53nt-M237V	TP53	0.010	0.105	0.205	0.105	0.048	0.115	0.209	0.120
PD41532	TP53nt-M246V	TP53	-0.015	0.066	0.146	0.066	0.044	0.085	0.156	0.090
PD41339	TP53nt-N239S	TP53	0.009	0.083	0.162	0.084	0.050	0.096	0.167	0.100
PD34477	TP53nt-P151R	TP53	-0.038	0.031	0.098	0.030	0.052	0.074	0.116	0.078
PD41071	TP53nt-P72S	TP53	-0.020	0.040	0.100	0.040	0.059	0.078	0.122	0.082
PD41311	TP53nt-R158H	TP53	-0.027	0.059	0.152	0.060	0.027	0.079	0.157	0.083
PD34527	TP53nt-R175G	TP53	-0.005	0.051	0.109	0.052	0.062	0.083	0.123	0.086
PD34566	TP53nt-R175H	TP53	-0.075	0.001	0.078	0.001	0.016	0.052	0.105	0.055
PD41124	TP53nt-R181P	TP53	-0.030	0.035	0.102	0.036	0.044	0.068	0.119	0.073
PD41270	TP53nt-R248Q	TP53	0.041	0.105	0.173	0.105	0.062	0.110	0.174	0.113
PD41174	TP53nt-R248W	TP53	0.003	0.098	0.194	0.098	0.056	0.111	0.199	0.116
PD34485	TP53nt-R248W	TP53	-0.060	0.043	0.150	0.044	0.054	0.095	0.178	0.102
PD41099	TP53nt-R273G	TP53	-0.004	0.088	0.169	0.085	0.029	0.095	0.171	0.096
PD41081	TP53nt-R273H	TP53	0.030	0.097	0.168	0.097	0.066	0.107	0.172	0.111
PD42295	TP53nt-R273H	TP53	-0.014	0.112	0.232	0.110	0.045	0.125	0.236	0.130
PD34506	TP53nt-R273L	TP53	-0.069	0.001	0.077	0.001	0.052	0.075	0.118	0.079
PD41203	TP53nt-R282W	TP53	-0.080	0.020	0.121	0.020	0.062	0.090	0.155	0.097
PD41194	TP53nt-R282W	TP53	-0.071	0.021	0.115	0.020	0.042	0.073	0.147	0.081
PD41238	TP53nt-V272G	TP53	-0.028	0.052	0.132	0.053	0.046	0.083	0.152	0.088
PD41088	TP53nt-V272M	TP53	-0.054	0.021	0.099	0.022	0.036	0.064	0.124	0.070
PD41288	TP53nt-Y220C	TP53	-0.025	0.069	0.164	0.068	0.061	0.101	0.177	0.107
PD34502	TP53nt-Y220C	TP53	-0.052	0.055	0.160	0.055	0.034	0.087	0.172	0.092
PD41233	TP53t-Q317X	TP53	-0.193	-0.101	-0.005	-0.100	0.006	0.033	0.104	0.037
PD34563	TP53t-W146X	TP53	-0.109	-0.009	0.085	-0.010	0.013	0.055	0.111	0.058
PD41081	U2AF1-Q157P	U2AF1	0.182	0.251	0.330	0.253	0.182	0.251	0.330	0.253
PD41221	U2AF1-Q157P	U2AF1	0.156	0.267	0.379	0.267	0.156	0.267	0.379	0.267
PD34512	U2AF1-Q157P	U2AF1	0.171	0.267	0.367	0.268	0.171	0.267	0.367	0.268
PD34493	U2AF1-Q157R	U2AF1	0.305	0.381	0.463	0.382	0.305	0.381	0.463	0.382
PD41345	U2AF1-Q157R	U2AF1	0.232	0.341	0.448	0.341	0.232	0.341	0.448	0.341
PD41169	U2AF1-Q157R	U2AF1	0.250	0.356	0.471	0.357	0.250	0.356	0.471	0.357
PD41233	U2AF1-R156H	U2AF1	0.073	0.173	0.270	0.173	0.080	0.174	0.270	0.174
PD34542	U2AF1-S34F	U2AF1	0.110	0.210	0.317	0.212	0.112	0.210	0.317	0.212

Table 16a | Somatic variants identified in the AML cohort

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11216a	2	25457173	25457173	A	G	0.591	DNMT3A	Missense	p.L905P
PD7806a	2	25457176	25457176	G	A	0.254	DNMT3A	Missense	p.P904L
PD11014a	2	25457176	25457176	G	A	0.451	DNMT3A	Missense	p.P904L
PD9272a	2	25457177	25457177	G	C	0.765	DNMT3A	Missense	p.P904A
PD10933a	2	25457180	25457181	CG	C	0.5	DNMT3A	Frameshift	p.F902fs
PD8419a	2	25457191	25457191	C	T	0.421	DNMT3A	Missense	p.R899H
PD8570a	2	25457194	25457194	A	G	0.419	DNMT3A	Missense	p.I898T
PD9350a	2	25457209	25457209	C	G	0.259	DNMT3A	Missense	p.W893S
PD8473a	2	25457209	25457209	C	G	0.4	DNMT3A	Missense	p.W893S
PD7991a	2	25457231	25457231	G	C	0.545	DNMT3A	Missense	p.Q886E
PD8005a	2	25457242	25457242	C	A	0.529	DNMT3A	Missense	p.R882L
PD8170a	2	25457242	25457242	C	G	0.0984	DNMT3A	Missense	p.R882P
PD11100a	2	25457242	25457242	C	G	0.125	DNMT3A	Missense	p.R882P
PD11163a	2	25457242	25457242	C	G	0.253	DNMT3A	Missense	p.R882P
PD7791a	2	25457242	25457242	C	G	0.364	DNMT3A	Missense	p.R882P
PD8057a	2	25457242	25457242	C	G	0.5	DNMT3A	Missense	p.R882P
PD9328a	2	25457242	25457242	C	G	0.722	DNMT3A	Missense	p.R882P
PD11234a	2	25457242	25457242	C	T	0.0879	DNMT3A	Missense	p.R882H
PD11179a	2	25457242	25457242	C	T	0.13	DNMT3A	Missense	p.R882H
PD11140a	2	25457242	25457242	C	T	0.19	DNMT3A	Missense	p.R882H
PD8394a	2	25457242	25457242	C	T	0.212	DNMT3A	Missense	p.R882H
PD7828a	2	25457242	25457242	C	T	0.22	DNMT3A	Missense	p.R882H
PD10931a	2	25457242	25457242	C	T	0.22	DNMT3A	Missense	p.R882H
PD8495a	2	25457242	25457242	C	T	0.236	DNMT3A	Missense	p.R882H
PD10930a	2	25457242	25457242	C	T	0.25	DNMT3A	Missense	p.R882H
PD8372a	2	25457242	25457242	C	T	0.25	DNMT3A	Missense	p.R882H
PD11268a	2	25457242	25457242	C	T	0.266	DNMT3A	Missense	p.R882H
PD8177a	2	25457242	25457242	C	T	0.269	DNMT3A	Missense	p.R882H
PD8276a	2	25457242	25457242	C	T	0.277	DNMT3A	Missense	p.R882H
PD8267a	2	25457242	25457242	C	T	0.286	DNMT3A	Missense	p.R882H
PD11272a	2	25457242	25457242	C	T	0.286	DNMT3A	Missense	p.R882H
PD10880a	2	25457242	25457242	C	T	0.288	DNMT3A	Missense	p.R882H
PD8295a	2	25457242	25457242	C	T	0.294	DNMT3A	Missense	p.R882H
PD11231a	2	25457242	25457242	C	T	0.3	DNMT3A	Missense	p.R882H
PD8430a	2	25457242	25457242	C	T	0.307	DNMT3A	Missense	p.R882H
PD8071a	2	25457242	25457242	C	T	0.308	DNMT3A	Missense	p.R882H
PD11269a	2	25457242	25457242	C	T	0.311	DNMT3A	Missense	p.R882H
PD8435a	2	25457242	25457242	C	T	0.33	DNMT3A	Missense	p.R882H
PD7796a	2	25457242	25457242	C	T	0.337	DNMT3A	Missense	p.R882H
PD7732a	2	25457242	25457242	C	T	0.347	DNMT3A	Missense	p.R882H
PD7720a	2	25457242	25457242	C	T	0.36	DNMT3A	Missense	p.R882H
PD11184a	2	25457242	25457242	C	T	0.362	DNMT3A	Missense	p.R882H
PD7967a	2	25457242	25457242	C	T	0.362	DNMT3A	Missense	p.R882H
PD11029a	2	25457242	25457242	C	T	0.364	DNMT3A	Missense	p.R882H
PD8456a	2	25457242	25457242	C	T	0.364	DNMT3A	Missense	p.R882H
PD7835a	2	25457242	25457242	C	T	0.366	DNMT3A	Missense	p.R882H
PD10865a	2	25457242	25457242	C	T	0.367	DNMT3A	Missense	p.R882H
PD7759a	2	25457242	25457242	C	T	0.367	DNMT3A	Missense	p.R882H
PD7705a	2	25457242	25457242	C	T	0.368	DNMT3A	Missense	p.R882H
PD8185a	2	25457242	25457242	C	T	0.375	DNMT3A	Missense	p.R882H
PD8060a	2	25457242	25457242	C	T	0.379	DNMT3A	Missense	p.R882H
PD9201a	2	25457242	25457242	C	T	0.381	DNMT3A	Missense	p.R882H
PD10921a	2	25457242	25457242	C	T	0.385	DNMT3A	Missense	p.R882H
PD11108a	2	25457242	25457242	C	T	0.385	DNMT3A	Missense	p.R882H
PD8424a	2	25457242	25457242	C	T	0.387	DNMT3A	Missense	p.R882H
PD8274a	2	25457242	25457242	C	T	0.392	DNMT3A	Missense	p.R882H
PD9232a	2	25457242	25457242	C	T	0.393	DNMT3A	Missense	p.R882H
PD10984a	2	25457242	25457242	C	T	0.393	DNMT3A	Missense	p.R882H
PD8157a	2	25457242	25457242	C	T	0.395	DNMT3A	Missense	p.R882H
PD8016a	2	25457242	25457242	C	T	0.395	DNMT3A	Missense	p.R882H

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11038a	2	25457242	25457242	C	T	0.397	DNMT3A	Missense	p.R882H
PD8301a	2	25457242	25457242	C	T	0.397	DNMT3A	Missense	p.R882H
PD11229a	2	25457242	25457242	C	T	0.4	DNMT3A	Missense	p.R882H
PD7964a	2	25457242	25457242	C	T	0.4	DNMT3A	Missense	p.R882H
PD7989a	2	25457242	25457242	C	T	0.4	DNMT3A	Missense	p.R882H
PD7737a	2	25457242	25457242	C	T	0.404	DNMT3A	Missense	p.R882H
PD8187a	2	25457242	25457242	C	T	0.404	DNMT3A	Missense	p.R882H
PD8384a	2	25457242	25457242	C	T	0.405	DNMT3A	Missense	p.R882H
PD7988a	2	25457242	25457242	C	T	0.406	DNMT3A	Missense	p.R882H
PD9373a	2	25457242	25457242	C	T	0.41	DNMT3A	Missense	p.R882H
PD8176a	2	25457242	25457242	C	T	0.41	DNMT3A	Missense	p.R882H
PD7610a	2	25457242	25457242	C	T	0.411	DNMT3A	Missense	p.R882H
PD8329a	2	25457242	25457242	C	T	0.411	DNMT3A	Missense	p.R882H
PD7995a	2	25457242	25457242	C	T	0.412	DNMT3A	Missense	p.R882H
PD10918a	2	25457242	25457242	C	T	0.412	DNMT3A	Missense	p.R882H
PD7956a	2	25457242	25457242	C	T	0.415	DNMT3A	Missense	p.R882H
PD10853a	2	25457242	25457242	C	T	0.422	DNMT3A	Missense	p.R882H
PD9215a	2	25457242	25457242	C	T	0.424	DNMT3A	Missense	p.R882H
PD9341a	2	25457242	25457242	C	T	0.424	DNMT3A	Missense	p.R882H
PD8253a	2	25457242	25457242	C	T	0.426	DNMT3A	Missense	p.R882H
PD11113a	2	25457242	25457242	C	T	0.429	DNMT3A	Missense	p.R882H
PD8263a	2	25457242	25457242	C	T	0.429	DNMT3A	Missense	p.R882H
PD10928a	2	25457242	25457242	C	T	0.431	DNMT3A	Missense	p.R882H
PD7864a	2	25457242	25457242	C	T	0.433	DNMT3A	Missense	p.R882H
PD7667a	2	25457242	25457242	C	T	0.437	DNMT3A	Missense	p.R882H
PD11098a	2	25457242	25457242	C	T	0.439	DNMT3A	Missense	p.R882H
PD11170a	2	25457242	25457242	C	T	0.441	DNMT3A	Missense	p.R882H
PD7961a	2	25457242	25457242	C	T	0.441	DNMT3A	Missense	p.R882H
PD8436a	2	25457242	25457242	C	T	0.445	DNMT3A	Missense	p.R882H
PD8568a	2	25457242	25457242	C	T	0.446	DNMT3A	Missense	p.R882H
PD7994a	2	25457242	25457242	C	T	0.449	DNMT3A	Missense	p.R882H
PD7868a	2	25457242	25457242	C	T	0.453	DNMT3A	Missense	p.R882H
PD7815a	2	25457242	25457242	C	T	0.458	DNMT3A	Missense	p.R882H
PD11232a	2	25457242	25457242	C	T	0.462	DNMT3A	Missense	p.R882H
PD10965a	2	25457242	25457242	C	T	0.462	DNMT3A	Missense	p.R882H
PD8380a	2	25457242	25457242	C	T	0.462	DNMT3A	Missense	p.R882H
PD10950a	2	25457242	25457242	C	T	0.462	DNMT3A	Missense	p.R882H
PD8244a	2	25457242	25457242	C	T	0.462	DNMT3A	Missense	p.R882H
PD11150a	2	25457242	25457242	C	T	0.463	DNMT3A	Missense	p.R882H
PD10895a	2	25457242	25457242	C	T	0.463	DNMT3A	Missense	p.R882H
PD11282a	2	25457242	25457242	C	T	0.463	DNMT3A	Missense	p.R882H
PD8208a	2	25457242	25457242	C	T	0.467	DNMT3A	Missense	p.R882H
PD11145a	2	25457242	25457242	C	T	0.467	DNMT3A	Missense	p.R882H
PD8190a	2	25457242	25457242	C	T	0.467	DNMT3A	Missense	p.R882H
PD10993a	2	25457242	25457242	C	T	0.468	DNMT3A	Missense	p.R882H
PD8553a	2	25457242	25457242	C	T	0.47	DNMT3A	Missense	p.R882H
PD7657a	2	25457242	25457242	C	T	0.47	DNMT3A	Missense	p.R882H
PD7905a	2	25457242	25457242	C	T	0.474	DNMT3A	Missense	p.R882H
PD11071a	2	25457242	25457242	C	T	0.475	DNMT3A	Missense	p.R882H
PD11217a	2	25457242	25457242	C	T	0.476	DNMT3A	Missense	p.R882H
PD7745a	2	25457242	25457242	C	T	0.478	DNMT3A	Missense	p.R882H
PD9197a	2	25457242	25457242	C	T	0.478	DNMT3A	Missense	p.R882H
PD8290a	2	25457242	25457242	C	T	0.478	DNMT3A	Missense	p.R882H
PD10794a	2	25457242	25457242	C	T	0.478	DNMT3A	Missense	p.R882H
PD9226a	2	25457242	25457242	C	T	0.479	DNMT3A	Missense	p.R882H
PD11077a	2	25457242	25457242	C	T	0.48	DNMT3A	Missense	p.R882H
PD8192a	2	25457242	25457242	C	T	0.48	DNMT3A	Missense	p.R882H
PD10941a	2	25457242	25457242	C	T	0.481	DNMT3A	Missense	p.R882H
PD7804a	2	25457242	25457242	C	T	0.482	DNMT3A	Missense	p.R882H
PD8021a	2	25457242	25457242	C	T	0.482	DNMT3A	Missense	p.R882H
PD8127a	2	25457242	25457242	C	T	0.482	DNMT3A	Missense	p.R882H
PD8266a	2	25457242	25457242	C	T	0.482	DNMT3A	Missense	p.R882H

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7881a	2	25457242	25457242	C	T	0.483	DNMT3A	Missense	p.R882H
PD7627a	2	25457242	25457242	C	T	0.485	DNMT3A	Missense	p.R882H
PD10829a	2	25457242	25457242	C	T	0.486	DNMT3A	Missense	p.R882H
PD8449a	2	25457242	25457242	C	T	0.487	DNMT3A	Missense	p.R882H
PD7911a	2	25457242	25457242	C	T	0.489	DNMT3A	Missense	p.R882H
PD9253a	2	25457242	25457242	C	T	0.489	DNMT3A	Missense	p.R882H
PD7904a	2	25457242	25457242	C	T	0.491	DNMT3A	Missense	p.R882H
PD11262a	2	25457242	25457242	C	T	0.5	DNMT3A	Missense	p.R882H
PD10882a	2	25457242	25457242	C	T	0.506	DNMT3A	Missense	p.R882H
PD8346a	2	25457242	25457242	C	T	0.507	DNMT3A	Missense	p.R882H
PD8538a	2	25457242	25457242	C	T	0.511	DNMT3A	Missense	p.R882H
PD8322a	2	25457242	25457242	C	T	0.511	DNMT3A	Missense	p.R882H
PD11144a	2	25457242	25457242	C	T	0.515	DNMT3A	Missense	p.R882H
PD7805a	2	25457242	25457242	C	T	0.517	DNMT3A	Missense	p.R882H
PD8131a	2	25457242	25457242	C	T	0.519	DNMT3A	Missense	p.R882H
PD7779a	2	25457242	25457242	C	T	0.52	DNMT3A	Missense	p.R882H
PD7936a	2	25457242	25457242	C	T	0.524	DNMT3A	Missense	p.R882H
PD8370a	2	25457242	25457242	C	T	0.524	DNMT3A	Missense	p.R882H
PD8065a	2	25457242	25457242	C	T	0.525	DNMT3A	Missense	p.R882H
PD8159a	2	25457242	25457242	C	T	0.528	DNMT3A	Missense	p.R882H
PD8423a	2	25457242	25457242	C	T	0.528	DNMT3A	Missense	p.R882H
PD7776a	2	25457242	25457242	C	T	0.53	DNMT3A	Missense	p.R882H
PD8578a	2	25457242	25457242	C	T	0.531	DNMT3A	Missense	p.R882H
PD10919a	2	25457242	25457242	C	T	0.533	DNMT3A	Missense	p.R882H
PD8494a	2	25457242	25457242	C	T	0.533	DNMT3A	Missense	p.R882H
PD9326a	2	25457242	25457242	C	T	0.539	DNMT3A	Missense	p.R882H
PD7754a	2	25457242	25457242	C	T	0.548	DNMT3A	Missense	p.R882H
PD7662a	2	25457242	25457242	C	T	0.55	DNMT3A	Missense	p.R882H
PD8152a	2	25457242	25457242	C	T	0.551	DNMT3A	Missense	p.R882H
PD8574a	2	25457242	25457242	C	T	0.553	DNMT3A	Missense	p.R882H
PD8134a	2	25457242	25457242	C	T	0.574	DNMT3A	Missense	p.R882H
PD7631a	2	25457242	25457242	C	T	0.579	DNMT3A	Missense	p.R882H
PD7744a	2	25457242	25457242	C	T	0.59	DNMT3A	Missense	p.R882H
PD10966a	2	25457242	25457242	C	T	0.594	DNMT3A	Missense	p.R882H
PD8294a	2	25457242	25457242	C	T	0.595	DNMT3A	Missense	p.R882H
PD7976a	2	25457242	25457242	C	T	0.6	DNMT3A	Missense	p.R882H
PD7906a	2	25457242	25457242	C	T	0.603	DNMT3A	Missense	p.R882H
PD9385a	2	25457242	25457242	C	T	0.697	DNMT3A	Missense	p.R882H
PD11003a	2	25457242	25457242	C	T	0.917	DNMT3A	Missense	p.R882H
PD7935a	2	25457243	25457243	G	A	0.273	DNMT3A	Missense	p.R882C
PD7833a	2	25457243	25457243	G	A	0.304	DNMT3A	Missense	p.R882C
PD7612a	2	25457243	25457243	G	A	0.319	DNMT3A	Missense	p.R882C
PD8416a	2	25457243	25457243	G	A	0.321	DNMT3A	Missense	p.R882C
PD8395a	2	25457243	25457243	G	A	0.324	DNMT3A	Missense	p.R882C
PD9220a	2	25457243	25457243	G	A	0.326	DNMT3A	Missense	p.R882C
PD9202a	2	25457243	25457243	G	A	0.333	DNMT3A	Missense	p.R882C
PD8506a	2	25457243	25457243	G	A	0.333	DNMT3A	Missense	p.R882C
PD8445a	2	25457243	25457243	G	A	0.337	DNMT3A	Missense	p.R882C
PD8334a	2	25457243	25457243	G	A	0.344	DNMT3A	Missense	p.R882C
PD8557a	2	25457243	25457243	G	A	0.345	DNMT3A	Missense	p.R882C
PD9268a	2	25457243	25457243	G	A	0.361	DNMT3A	Missense	p.R882C
PD8309a	2	25457243	25457243	G	A	0.398	DNMT3A	Missense	p.R882C
PD10917a	2	25457243	25457243	G	A	0.4	DNMT3A	Missense	p.R882C
PD9337a	2	25457243	25457243	G	A	0.408	DNMT3A	Missense	p.R882C
PD8412a	2	25457243	25457243	G	A	0.412	DNMT3A	Missense	p.R882C
PD7803a	2	25457243	25457243	G	A	0.424	DNMT3A	Missense	p.R882C
PD8328a	2	25457243	25457243	G	A	0.427	DNMT3A	Missense	p.R882C
PD8544a	2	25457243	25457243	G	A	0.429	DNMT3A	Missense	p.R882C
PD8357a	2	25457243	25457243	G	A	0.442	DNMT3A	Missense	p.R882C
PD8353a	2	25457243	25457243	G	A	0.444	DNMT3A	Missense	p.R882C
PD8165a	2	25457243	25457243	G	A	0.446	DNMT3A	Missense	p.R882C
PD9235a	2	25457243	25457243	G	A	0.446	DNMT3A	Missense	p.R882C

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10850a	2	25457243	25457243	G	A	0.446	DNMT3A	Missense	p.R882C
PD8236a	2	25457243	25457243	G	A	0.451	DNMT3A	Missense	p.R882C
PD8213a	2	25457243	25457243	G	A	0.455	DNMT3A	Missense	p.R882C
PD8550a	2	25457243	25457243	G	A	0.46	DNMT3A	Missense	p.R882C
PD7893a	2	25457243	25457243	G	A	0.462	DNMT3A	Missense	p.R882C
PD8046a	2	25457243	25457243	G	A	0.462	DNMT3A	Missense	p.R882C
PD11045a	2	25457243	25457243	G	A	0.484	DNMT3A	Missense	p.R882C
PD8275a	2	25457243	25457243	G	A	0.494	DNMT3A	Missense	p.R882C
PD11251a	2	25457243	25457243	G	A	0.5	DNMT3A	Missense	p.R882C
PD8113a	2	25457243	25457243	G	A	0.5	DNMT3A	Missense	p.R882C
PD11260a	2	25457243	25457243	G	A	0.516	DNMT3A	Missense	p.R882C
PD11286a	2	25457243	25457243	G	A	0.516	DNMT3A	Missense	p.R882C
PD8375a	2	25457243	25457243	G	A	0.523	DNMT3A	Missense	p.R882C
PD8582a	2	25457243	25457243	G	A	0.525	DNMT3A	Missense	p.R882C
PD10795a	2	25457243	25457243	G	A	0.532	DNMT3A	Missense	p.R882C
PD11218a	2	25457243	25457243	G	A	0.536	DNMT3A	Missense	p.R882C
PD8448a	2	25457243	25457243	G	A	0.544	DNMT3A	Missense	p.R882C
PD8374a	2	25457243	25457243	G	A	0.548	DNMT3A	Missense	p.R882C
PD7656a	2	25457243	25457243	G	A	0.552	DNMT3A	Missense	p.R882C
PD11004a	2	25457243	25457243	G	A	0.559	DNMT3A	Missense	p.R882C
PD8558a	2	25457243	25457243	G	A	0.565	DNMT3A	Missense	p.R882C
PD9252a	2	25457243	25457243	G	A	0.568	DNMT3A	Missense	p.R882C
PD11072a	2	25457243	25457243	G	A	0.569	DNMT3A	Missense	p.R882C
PD10975a	2	25457243	25457243	G	A	0.579	DNMT3A	Missense	p.R882C
PD10847a	2	25457243	25457243	G	A	0.597	DNMT3A	Missense	p.R882C
PD10824a	2	25457243	25457243	G	A	0.633	DNMT3A	Missense	p.R882C
PD7634a	2	25457243	25457243	G	A	0.882	DNMT3A	Missense	p.R882C
PD10820a	2	25457243	25457243	G	A	0.951	DNMT3A	Missense	p.R882C
PD7685a	2	25457243	25457243	G	T	0.371	DNMT3A	Missense	p.R882S
PD10947a	2	25457243	25457243	G	T	0.44	DNMT3A	Missense	p.R882S
PD8004a	2	25457243	25457243	G	T	0.446	DNMT3A	Missense	p.R882S
PD8316a	2	25457243	25457243	G	T	0.455	DNMT3A	Missense	p.R882S
PD10807a	2	25457243	25457243	G	T	0.463	DNMT3A	Missense	p.R882S
PD11162a	2	25457243	25457243	G	T	0.467	DNMT3A	Missense	p.R882S
PD11093a	2	25457243	25457243	G	T	0.556	DNMT3A	Missense	p.R882S
PD7655a	2	25457243	25457243	G	T	0.566	DNMT3A	Missense	p.R882S
PD9327a	2	25457243	25457243	G	T	0.567	DNMT3A	Missense	p.R882S
PD11284a	2	25457247	25457247	C	G	0.395	DNMT3A	Missense	p.M880I
PD10992a	2	25457259	25457259	G	T	0.422	DNMT3A	Missense	p.D876E
PD8139a	2	25457285	25457285	A	C	0.474	DNMT3A	Missense	p.F868V
PD11281a	2	25458584	25458584	T	G	0.465	DNMT3A	Missense	p.E863D
PD10840a	2	25458595	25458595	A	G	0.4	DNMT3A	Missense	p.W860R
PD7781a	2	25458595	25458595	A	G	0.855	DNMT3A	Missense	p.W860R
PD8148a	2	25458618	25458619	AT	A	0.212	DNMT3A	Nonsense	p.M852X
PD7678a	2	25458619	25458619	T	C	0.444	DNMT3A	Missense	p.M852V
PD8206a	2	25458620	25458622	GAA	G	0.35	DNMT3A	Frameshift	p.F851fs
PD11285a	2	25458627	25458627	G	A	0.321	DNMT3A	Missense	p.P849L
PD8430a	2	25458628	25458628	G	GA	0.041	DNMT3A	Frameshift	p.F848fs
PD9322a	2	25458635	25458635	C	T	0.149	DNMT3A	Synonymous	p.Q846Q
PD10904a	2	25458647	25458647	C	A	0.44	DNMT3A	Missense	p.Q842H
PD9216a	2	25458649	25458649	G	A	0.456	DNMT3A	Nonsense	p.Q842X
PD10816a	2	25458649	25458649	G	A	0.484	DNMT3A	Nonsense	p.Q842X
PD8382a	2	25458656	25458656	G	A	0.555	DNMT3A	Synonymous	p.S839S
PD8084a	2	25458661	25458661	T	C	0.381	DNMT3A	Missense	p.N838D
PD11190a	2	25458669	25458669	G	A	0.45	DNMT3A	Missense	p.T835M
PD9273a	2	25458669	25458669	G	A	0.462	DNMT3A	Missense	p.T835M
PD9378a	2	25458687	25458687	T	A	0.379	DNMT3A	Missense	p.K829I
PD11281a	2	25458695	25458695	C	A	0.455	DNMT3A	Splice site	c.2479-1G>T
PD9357a	2	25458696	25458696	T	C	0.104	DNMT3A	Splice site	c.2479-2A>G
PD8541a	2	25458696	25458696	T	C	0.236	DNMT3A	Splice site	c.2479-2A>G
PD10987a	2	25459820	25459821	AT	A	0.434	DNMT3A	Frameshift	p.H821fs

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8203a	2	25459860	25459874	GTGGATGCCAACGGC	G	0.294	DNMT3A	Frameshift	p.R803fs
PD8472a	2	25459873	25459873	G	A	0.0812	DNMT3A	Missense	p.P804S
PD8180a	2	25461999	25461999	C	T	0.923	DNMT3A	Missense	p.R803K
PD8419a	2	25462000	25462000	T	C	0.304	DNMT3A	Missense	p.R803G
PD7850a	2	25462000	25462000	T	G	0.5	DNMT3A	Synonymous	p.R803R
PD7880a	2	25462006	25462006	T	C	0.351	DNMT3A	Missense	p.M801V
PD10812a	2	25462020	25462020	C	A	0.359	DNMT3A	Missense	p.G796V
PD11202a	2	25462022	25462022	C	A	0.394	DNMT3A	Missense	p.W795C
PD11073a	2	25462032	25462032	C	T	0.333	DNMT3A	Missense	p.R792H
PD10881a	2	25462068	25462068	A	G	0.34	DNMT3A	Missense	p.I780T
PD8011a	2	25462068	25462068	A	G	0.432	DNMT3A	Missense	p.I780T
PD9318a	2	25462077	25462077	G	C	0.371	DNMT3A	Missense	p.P777R
PD9364a	2	25462080	25462080	T	A	0.137	DNMT3A	Missense	p.N776I
PD10852a	2	25463169	25463169	A	C	0.489	DNMT3A	Splice site	c.2322+2T>G
PD11020a	2	25463171	25463171	C	A	0.465	DNMT3A	Missense	p.E774D
PD9361a	2	25463175	25463175	A	C	0.32	DNMT3A	Missense	p.L773R
PD7908a	2	25463176	25463176	G	T	0.476	DNMT3A	Missense	p.L773I
PD8252a	2	25463182	25463182	G	A	0.443	DNMT3A	Nonsense	p.R771X
PD11131a	2	25463184	25463184	G	A	0.418	DNMT3A	Missense	p.S770L
PD10904a	2	25463184	25463184	G	C	0.457	DNMT3A	Missense	p.S770W
PD9202a	2	25463184	25463184	G	GCG	0.259	DNMT3A	Frameshift	p.S770fs
PD7909a	2	25463184	25463184	G	T	0.442	DNMT3A	Nonsense	p.S770X
PD9278a	2	25463195	25463197	CTT	C	0.467	DNMT3A	Frameshift	p.K766fs
PD9255a	2	25463214	25463217	GCCA	G	0.545	DNMT3A	Inframe	p.759_760del
PD10906a	2	25463248	25463248	G	A	0.391	DNMT3A	Missense	p.R749C
PD8297a	2	25463248	25463248	G	A	0.509	DNMT3A	Missense	p.R749C
PD8063a	2	25463263	25463264	TG	T	0.349	DNMT3A	Frameshift	p.P743fs
PD7928a	2	25463287	25463287	G	A	0.552	DNMT3A	Missense	p.R736C
PD8417a	2	25463287	25463287	G	A	0.556	DNMT3A	Missense	p.R736C
PD11107a	2	25463287	25463287	G	A	0.929	DNMT3A	Missense	p.R736C
PD10810a	2	25463289	25463289	T	C	0.5	DNMT3A	Missense	p.Y735C
PD11195a	2	25463289	25463289	T	C	0.571	DNMT3A	Missense	p.Y735C
PD9339a	2	25463296	25463296	C	CA	0.514	DNMT3A	Frameshift	p.F732fs
PD10992a	2	25463532	25463532	T	C	0.475	DNMT3A	Missense	p.N717S
PD8091a	2	25463535	25463535	A	T	0.426	DNMT3A	Missense	p.V716D
PD8381a	2	25463541	25463541	G	C	0.109	DNMT3A	Missense	p.S714C
PD10897a	2	25463541	25463541	G	C	0.339	DNMT3A	Missense	p.S714C
PD7643a	2	25463541	25463541	G	C	0.42	DNMT3A	Missense	p.S714C
PD11016a	2	25463541	25463541	G	C	0.451	DNMT3A	Missense	p.S714C
PD9239a	2	25463541	25463541	G	C	0.647	DNMT3A	Missense	p.S714C
PD8543a	2	25463542	25463542	A	G	0.382	DNMT3A	Missense	p.S714P
PD11135a	2	25463544	25463545	AG	A	0.296	DNMT3A	Frameshift	p.L713fs
PD8038a	2	25463551	25463551	T	A	0.882	DNMT3A	Missense	p.N711Y
PD11057a	2	25463562	25463562	C	A	0.433	DNMT3A	Missense	p.G707V
PD8407a	2	25463568	25463568	A	G	0.364	DNMT3A	Missense	p.I705T
PD7716a	2	25463577	25463577	T	A	0.857	DNMT3A	Missense	p.D702V
PD8493a	2	25463579	25463579	G	A	0.469	DNMT3A	Synonymous	p.F701F
PD10988a	2	25463586	25463586	C	T	0.439	DNMT3A	Missense	p.G699D
PD7855a	2	25463587	25463587	C	T	0.464	DNMT3A	Missense	p.G699S
PD8314a	2	25463595	25463596	TG	T	0.345	DNMT3A	Frameshift	p.Q696fs
PD8268a	2	25464444	25464444	A	C	0.3	DNMT3A	Missense	p.V690G
PD7694a	2	25464450	25464450	C	T	0.538	DNMT3A	Missense	p.R688H
PD10841a	2	25464457	25464457	C	G	0.48	DNMT3A	Missense	p.D686H
PD10899a	2	25464469	25464470	TG	T	0.442	DNMT3A	Frameshift	p.I681fs
PD8474a	2	25464475	25464475	T	TC	0.085	DNMT3A	Frameshift	p.G679fs
PD8323a	2	25464487	25464487	G	A	0.457	DNMT3A	Missense	p.R676W
PD11171a	2	25464507	25464507	G	A	0.409	DNMT3A	Missense	p.S669F
PD10816a	2	25464514	25464515	CA	C	0.52	DNMT3A	Frameshift	p.C666fs
PD8469a	2	25464528	25464528	G	C	0.388	DNMT3A	Missense	p.A662G
PD11192a	2	25464534	25464534	T	C	0.5	DNMT3A	Missense	p.Y660C

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10812a	2	25464547	25464548	GA	G	0.333	DNMT3A	Frameshift	p.I655fs
PD11014a	2	25464549	25464568	ATGCCCAAGTCCTTCAGCAC	ACG	0.152	DNMT3A	Frameshift	c.1945_1963CG
PD11086a	2	25464554	25464554	C	G	0.516	DNMT3A	Missense	p.L653F
PD8504a	2	25464565	25464565	G	C	0.4	DNMT3A	Missense	p.L650V
PD7757a	2	25466782	25466782	C	CA	0.333	DNMT3A	Frameshift	p.F640fs
PD8427a	2	25466799	25466799	C	T	0.258	DNMT3A	Missense	p.R635Q
PD8216a	2	25467095	25467096	GC	G	0.304	DNMT3A	Frameshift	p.G593fs
PD8489a	2	25467132	25467132	C	T	0.893	DNMT3A	Nonsense	p.W581X
PD7743a	2	25467408	25467408	C	T	0.444	DNMT3A	Splice site	c.1667+1G>A
PD7931a	2	25467411	25467411	G	T	0.476	DNMT3A	Nonsense	p.C555X
PD8543a	2	25467415	25467415	C	T	0.5	DNMT3A	Missense	p.C554Y
PD7644a	2	25467425	25467425	T	TTCCGCACATGAGC	0.155	DNMT3A	Frameshift	p.G550fs
PD11073a	2	25467428	25467428	C	T	0.457	DNMT3A	Missense	p.G550R
PD7689a	2	25467436	25467436	A	C	0.593	DNMT3A	Missense	p.L547R
PD8030a	2	25467436	25467436	A	T	0.562	DNMT3A	Missense	p.L547H
PD11261a	2	25467437	25467437	G	A	0.344	DNMT3A	Missense	p.L547F
PD10896a	2	25467448	25467448	C	A	0.475	DNMT3A	Missense	p.G543V
PD10961a	2	25467465	25467465	G	A	0.565	DNMT3A	Synonymous	p.C537C
PD11064a	2	25467481	25467484	CCGT	C	0.417	DNMT3A	Inframe	p.531_532del
PD7977a	2	25467495	25467495	C	G	0.404	DNMT3A	Missense	p.Q527H
PD7632a	2	25468140	25468150	TCCTCCAACGA	T	0.353	DNMT3A	Frameshift	p.F509fs
PD7654a	2	25468174	25468174	T	C	0.342	DNMT3A	Missense	p.N501S
PD7627a	2	25468174	25468174	T	C	0.512	DNMT3A	Missense	p.N501S
PD8261a	2	25468174	25468174	T	C	0.525	DNMT3A	Missense	p.N501S
PD7680a	2	25468187	25468187	A	C	0.5	DNMT3A	Missense	p.C497G
PD10986a	2	25468888	25468888	C	T	0.333	DNMT3A	Splice site	c.1474+1G>A
PD8460a	2	25468929	25468933	CCGCT	C	0.351	DNMT3A	Frameshift	p.E477fs
PD8279a	2	25469027	25469027	A	G	0.424	DNMT3A	Splice site	c.1429+2T>C
PD10901a	2	25469118	25469118	G	GG	0.152	DNMT3A	Frameshift	p.A447fs
PD10981a	2	25469153	25469153	C	CA	0.355	DNMT3A	Frameshift	p.V435fs
PD9364a	2	25469173	25469173	T	A	0.308	DNMT3A	Nonsense	p.K429X
PD10843a	2	25470002	25470002	A	G	0.36	DNMT3A	Missense	p.L347P
PD8294a	2	25470010	25470010	C	T	0.158	DNMT3A	Synonymous	p.L344L
PD9365a	2	25470011	25470011	A	G	0.625	DNMT3A	Missense	p.L344P
PD11064a	2	25470475	25470475	G	GAGGTCCG	0.211	DNMT3A	Frameshift	p.D333fs
PD9248a	2	25470493	25470493	C	T	0.346	DNMT3A	Nonsense	p.W327X
PD11052a	2	25470516	25470516	G	A	0.541	DNMT3A	Nonsense	p.R320X
PD11165a	2	25470516	25470516	G	A	0.556	DNMT3A	Nonsense	p.R320X
PD8282a	2	25470603	25470629	CAAAGCCCCGGCCGTCCTGGAGCCCCA	C	0.128	DNMT3A	Inframe	p.286_290del
PD11271a	2	25470959	25470959	C	G	0.604	DNMT3A	Missense	p.D268H
PD8422a	2	25471005	25471005	G	GG	0.051	DNMT3A	Frameshift	p.D252fs
PD11283a	2	25471064	25471065	GC	G	0.545	DNMT3A	Frameshift	p.G232fs
PD7812a	2	25472558	25472558	C	T	0.589	DNMT3A	Missense	p.V14M
PD11036a	2	25497955	25497955	C	G	0.524	DNMT3A	Missense	p.G165A
PD9306a	2	25498398	25498398	C	T	0.0714	DNMT3A	Missense	p.E155K
PD7780a	2	25505485	25505485	C	T	0.621	DNMT3A	Synonymous	p.G91G
PD7950a	2	198257063	198257066	GTTC	G	0.418	SF3B1	Inframe	p.1292_1293del
PD7861a	2	198257107	198257107	C	T	0.6	SF3B1	Missense	p.A1279T
PD7756a	2	198257135	198257135	G	A	0.245	SF3B1	Synonymous	p.Y1269Y
PD8133a	2	198257138	198257138	A	G	0.53	SF3B1	Synonymous	p.I1268I
PD8554a	2	198257166	198257166	C	T	0.237	SF3B1	Missense	p.R1259Q
PD8284a	2	198257174	198257174	G	A	0.0446	SF3B1	Synonymous	p.H1256H
PD9355a	2	198257768	198257768	C	T	0.0631	SF3B1	Synonymous	p.Q1228Q

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7901a	2	198260882	198260882	C	T	0.0471	SF3B1	Missense	p.G1146E
PD10795a	2	198260945	198260945	G	A	0.0511	SF3B1	Missense	p.P1125L
PD9262a	2	198263198	198263198	G	A	0.142	SF3B1	Missense	p.R1041C
PD9313a	2	198263204	198263204	C	T	0.168	SF3B1	Missense	p.V1039I
PD9384a	2	198263207	198263207	G	A	0.0389	SF3B1	Missense	p.L1038F
PD8533a	2	198263286	198263287	TG	T	0.076	SF3B1	Frameshift	p.P1011fs
PD11245a	2	198264822	198264823	CA	C	0.048	SF3B1	Frameshift	p.L990fs
PD9272a	2	198265078	198265078	A	G	0.457	SF3B1	Synonymous	p.C933C
PD7634a	2	198265081	198265081	G	T	0.0248	SF3B1	Synonymous	p.I932I
PD7607a	2	198265129	198265129	T	C	0.505	SF3B1	Synonymous	p.T916T
PD11136a	2	198265508	198265508	A	G	0.458	SF3B1	Synonymous	p.D883D
PD11135a	2	198265515	198265515	G	A	0.0754	SF3B1	Missense	p.A881V
PD8280a	2	198266224	198266224	T	C	0.0823	SF3B1	Missense	p.D799G
PD9257a	2	198266494	198266494	T	C	0.188	SF3B1	Missense	p.D781G
PD8133a	2	198266508	198266508	T	A	0.444	SF3B1	Missense	p.E776D
PD7802a	2	198266512	198266512	C	A	0.411	SF3B1	Missense	p.R775L
PD7682a	2	198266538	198266538	A	C	0.59	SF3B1	Synonymous	p.T766T
PD8331a	2	198266611	198266611	C	T	0.392	SF3B1	Missense	p.G742D
PD8372a	2	198266805	198266805	A	T	0.439	SF3B1	Synonymous	p.I709I
PD11139a	2	198266817	198266817	A	AGCA	0.177	SF3B1	Inframe	p.S705delinsMR
PD8385a	2	198266831	198266831	C	A	0.223	SF3B1	Missense	p.V701F
PD8487a	2	198266834	198266834	T	C	0.0157	SF3B1	Missense	p.K700E
PD7970a	2	198266834	198266834	T	C	0.0508	SF3B1	Missense	p.K700E
PD8258a	2	198266834	198266834	T	C	0.0634	SF3B1	Missense	p.K700E
PD7706a	2	198266834	198266834	T	C	0.138	SF3B1	Missense	p.K700E
PD9220a	2	198266834	198266834	T	C	0.291	SF3B1	Missense	p.K700E
PD8411a	2	198266834	198266834	T	C	0.292	SF3B1	Missense	p.K700E
PD8300a	2	198266834	198266834	T	C	0.304	SF3B1	Missense	p.K700E
PD7731a	2	198266834	198266834	T	C	0.362	SF3B1	Missense	p.K700E
PD9313a	2	198266834	198266834	T	C	0.396	SF3B1	Missense	p.K700E
PD9344a	2	198266834	198266834	T	C	0.408	SF3B1	Missense	p.K700E
PD11128a	2	198266834	198266834	T	C	0.423	SF3B1	Missense	p.K700E
PD7951a	2	198266834	198266834	T	C	0.45	SF3B1	Missense	p.K700E
PD8077a	2	198266834	198266834	T	C	0.506	SF3B1	Missense	p.K700E
PD8420a	2	198266834	198266834	T	C	0.513	SF3B1	Missense	p.K700E
PD9311a	2	198266840	198266840	G	A	0.116	SF3B1	Nonsense	p.Q698X
PD10923a	2	198267311	198267311	A	G	0.522	SF3B1	Synonymous	p.H682H
PD9384a	2	198267342	198267342	G	A	0.328	SF3B1	Missense	p.A672V
PD9359a	2	198267359	198267359	C	A	0.369	SF3B1	Missense	p.K666N
PD9246a	2	198267359	198267359	C	A	0.408	SF3B1	Missense	p.K666N
PD9372a	2	198267359	198267359	C	A	0.431	SF3B1	Missense	p.K666N
PD7947a	2	198267359	198267359	C	A	0.472	SF3B1	Missense	p.K666N
PD11237a	2	198267359	198267359	C	G	0.093	SF3B1	Missense	p.K666N
PD10987a	2	198267359	198267359	C	G	0.535	SF3B1	Missense	p.K666N
PD11136a	2	198267359	198267359	C	G	0.548	SF3B1	Missense	p.K666N
PD11099a	2	198267359	198267359	C	G	0.782	SF3B1	Missense	p.K666N
PD7972a	2	198267360	198267360	T	G	0.333	SF3B1	Missense	p.K666T
PD11263a	2	198267360	198267360	T	G	0.629	SF3B1	Missense	p.K666T
PD7975a	2	198267371	198267371	G	C	0.261	SF3B1	Missense	p.H662Q
PD8113a	2	198267373	198267373	G	A	0.43	SF3B1	Missense	p.H662Y
PD11193a	2	198267483	198267483	C	A	0.0973	SF3B1	Missense	p.R625L
PD9297a	2	198267484	198267484	G	A	0.0731	SF3B1	Missense	p.R625C
PD11144a	2	198267484	198267484	G	A	0.0797	SF3B1	Missense	p.R625C
PD8105a	2	198267484	198267484	G	A	0.335	SF3B1	Missense	p.R625C
PD7779a	2	198267525	198267525	G	A	0.4	SF3B1	Missense	p.S611F
PD7634a	2	198267713	198267713	G	A	0.0764	SF3B1	Missense	p.A589V
PD8500a	2	198269843	198269843	T	C	0.0387	SF3B1	Missense	p.K499R
PD11120a	2	198269873	198269873	G	A	0.121	SF3B1	Missense	p.P489L
PD8445a	2	198274561	198274561	T	A	0.486	SF3B1	Synonymous	p.P279P
PD11214a	2	198274589	198274589	C	T	0.556	SF3B1	Missense	p.R270Q
PD10910a	2	198274610	198274610	G	A	0.488	SF3B1	Missense	p.A263V
PD9337a	2	198281465	198281465	C	G	0.495	SF3B1	Missense	p.E222D

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8270a	2	198281565	198281565	G	T	0.488	SF3B1	Missense	p.A189E
PD8078a	2	198283299	198283299	A	G	0.488	SF3B1	Synonymous	p.P143P
PD11154a	2	198285794	198285794	G	A	0.507	SF3B1	Missense	p.P87S
PD11151a	2	198285806	198285806	C	T	0.0469	SF3B1	Missense	p.G83R
PD8500a	2	198288548	198288548	G	A	0.129	SF3B1	Missense	p.A60V
PD8141a	2	198288551	198288551	G	T	0.0813	SF3B1	Missense	p.A59D
PD11175a	2	198288573	198288573	C	T	0.0307	SF3B1	Missense	p.A52T
PD10812a	2	198288590	198288590	C	T	0.024	SF3B1	Missense	p.G46E
PD7757a	2	209113112	209113112	C	A	0.126	IDH1	Missense	p.R132L
PD8056a	2	209113112	209113112	C	A	0.354	IDH1	Missense	p.R132L
PD7837a	2	209113112	209113112	C	T	0.0554	IDH1	Missense	p.R132H
PD8314a	2	209113112	209113112	C	T	0.0781	IDH1	Missense	p.R132H
PD10921a	2	209113112	209113112	C	T	0.0811	IDH1	Missense	p.R132H
PD8282a	2	209113112	209113112	C	T	0.11	IDH1	Missense	p.R132H
PD9197a	2	209113112	209113112	C	T	0.116	IDH1	Missense	p.R132H
PD10918a	2	209113112	209113112	C	T	0.117	IDH1	Missense	p.R132H
PD11029a	2	209113112	209113112	C	T	0.129	IDH1	Missense	p.R132H
PD8188a	2	209113112	209113112	C	T	0.144	IDH1	Missense	p.R132H
PD7791a	2	209113112	209113112	C	T	0.151	IDH1	Missense	p.R132H
PD8539a	2	209113112	209113112	C	T	0.157	IDH1	Missense	p.R132H
PD8412a	2	209113112	209113112	C	T	0.19	IDH1	Missense	p.R132H
PD7943a	2	209113112	209113112	C	T	0.196	IDH1	Missense	p.R132H
PD8256a	2	209113112	209113112	C	T	0.198	IDH1	Missense	p.R132H
PD11057a	2	209113112	209113112	C	T	0.256	IDH1	Missense	p.R132H
PD8538a	2	209113112	209113112	C	T	0.258	IDH1	Missense	p.R132H
PD8294a	2	209113112	209113112	C	T	0.283	IDH1	Missense	p.R132H
PD8544a	2	209113112	209113112	C	T	0.293	IDH1	Missense	p.R132H
PD11285a	2	209113112	209113112	C	T	0.297	IDH1	Missense	p.R132H
PD8004a	2	209113112	209113112	C	T	0.299	IDH1	Missense	p.R132H
PD8091a	2	209113112	209113112	C	T	0.299	IDH1	Missense	p.R132H
PD7803a	2	209113112	209113112	C	T	0.321	IDH1	Missense	p.R132H
PD8095a	2	209113112	209113112	C	T	0.333	IDH1	Missense	p.R132H
PD11038a	2	209113112	209113112	C	T	0.355	IDH1	Missense	p.R132H
PD8033a	2	209113112	209113112	C	T	0.374	IDH1	Missense	p.R132H
PD8029a	2	209113112	209113112	C	T	0.383	IDH1	Missense	p.R132H
PD7991a	2	209113112	209113112	C	T	0.392	IDH1	Missense	p.R132H
PD7645a	2	209113112	209113112	C	T	0.394	IDH1	Missense	p.R132H
PD11202a	2	209113112	209113112	C	T	0.399	IDH1	Missense	p.R132H
PD9386a	2	209113112	209113112	C	T	0.401	IDH1	Missense	p.R132H
PD11042a	2	209113112	209113112	C	T	0.409	IDH1	Missense	p.R132H
PD9328a	2	209113112	209113112	C	T	0.415	IDH1	Missense	p.R132H
PD8159a	2	209113112	209113112	C	T	0.418	IDH1	Missense	p.R132H
PD11010a	2	209113112	209113112	C	T	0.419	IDH1	Missense	p.R132H
PD7804a	2	209113112	209113112	C	T	0.422	IDH1	Missense	p.R132H
PD11125a	2	209113112	209113112	C	T	0.425	IDH1	Missense	p.R132H
PD8274a	2	209113112	209113112	C	T	0.43	IDH1	Missense	p.R132H
PD8355a	2	209113112	209113112	C	T	0.431	IDH1	Missense	p.R132H
PD7707a	2	209113112	209113112	C	T	0.433	IDH1	Missense	p.R132H
PD8371a	2	209113112	209113112	C	T	0.437	IDH1	Missense	p.R132H
PD8436a	2	209113112	209113112	C	T	0.438	IDH1	Missense	p.R132H
PD7644a	2	209113112	209113112	C	T	0.44	IDH1	Missense	p.R132H
PD7855a	2	209113112	209113112	C	T	0.447	IDH1	Missense	p.R132H
PD10803a	2	209113112	209113112	C	T	0.448	IDH1	Missense	p.R132H
PD8491a	2	209113112	209113112	C	T	0.45	IDH1	Missense	p.R132H
PD11063a	2	209113112	209113112	C	T	0.453	IDH1	Missense	p.R132H
PD8275a	2	209113112	209113112	C	T	0.455	IDH1	Missense	p.R132H
PD11196a	2	209113112	209113112	C	T	0.457	IDH1	Missense	p.R132H
PD10847a	2	209113112	209113112	C	T	0.468	IDH1	Missense	p.R132H
PD11059a	2	209113112	209113112	C	T	0.491	IDH1	Missense	p.R132H
PD8202a	2	209113112	209113112	C	T	0.492	IDH1	Missense	p.R132H
PD10855a	2	209113112	209113112	C	T	0.492	IDH1	Missense	p.R132H
PD11076a	2	209113112	209113112	C	T	0.498	IDH1	Missense	p.R132H

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD9373a	2	209113112	209113112	C	T	0.527	IDH1	Missense	p.R132H
PD7888a	2	209113112	209113112	C	T	0.528	IDH1	Missense	p.R132H
PD10957a	2	209113112	209113112	C	T	0.532	IDH1	Missense	p.R132H
PD8493a	2	209113112	209113112	C	T	0.847	IDH1	Missense	p.R132H
PD8320a	2	209113113	209113113	G	A	0.0615	IDH1	Missense	p.R132C
PD11238a	2	209113113	209113113	G	A	0.104	IDH1	Missense	p.R132C
PD11181a	2	209113113	209113113	G	A	0.162	IDH1	Missense	p.R132C
PD11140a	2	209113113	209113113	G	A	0.183	IDH1	Missense	p.R132C
PD11028a	2	209113113	209113113	G	A	0.247	IDH1	Missense	p.R132C
PD8288a	2	209113113	209113113	G	A	0.253	IDH1	Missense	p.R132C
PD11002a	2	209113113	209113113	G	A	0.274	IDH1	Missense	p.R132C
PD11163a	2	209113113	209113113	G	A	0.294	IDH1	Missense	p.R132C
PD10976a	2	209113113	209113113	G	A	0.338	IDH1	Missense	p.R132C
PD9280a	2	209113113	209113113	G	A	0.339	IDH1	Missense	p.R132C
PD11107a	2	209113113	209113113	G	A	0.349	IDH1	Missense	p.R132C
PD8336a	2	209113113	209113113	G	A	0.362	IDH1	Missense	p.R132C
PD8213a	2	209113113	209113113	G	A	0.368	IDH1	Missense	p.R132C
PD10842a	2	209113113	209113113	G	A	0.378	IDH1	Missense	p.R132C
PD9215a	2	209113113	209113113	G	A	0.385	IDH1	Missense	p.R132C
PD8487a	2	209113113	209113113	G	A	0.4	IDH1	Missense	p.R132C
PD11232a	2	209113113	209113113	G	A	0.402	IDH1	Missense	p.R132C
PD11266a	2	209113113	209113113	G	A	0.402	IDH1	Missense	p.R132C
PD8016a	2	209113113	209113113	G	A	0.406	IDH1	Missense	p.R132C
PD8146a	2	209113113	209113113	G	A	0.416	IDH1	Missense	p.R132C
PD8546a	2	209113113	209113113	G	A	0.416	IDH1	Missense	p.R132C
PD7857a	2	209113113	209113113	G	A	0.417	IDH1	Missense	p.R132C
PD11227a	2	209113113	209113113	G	A	0.419	IDH1	Missense	p.R132C
PD9332a	2	209113113	209113113	G	A	0.424	IDH1	Missense	p.R132C
PD11101a	2	209113113	209113113	G	A	0.425	IDH1	Missense	p.R132C
PD8263a	2	209113113	209113113	G	A	0.431	IDH1	Missense	p.R132C
PD8438a	2	209113113	209113113	G	A	0.434	IDH1	Missense	p.R132C
PD8180a	2	209113113	209113113	G	A	0.442	IDH1	Missense	p.R132C
PD7768a	2	209113113	209113113	G	A	0.442	IDH1	Missense	p.R132C
PD11007a	2	209113113	209113113	G	A	0.442	IDH1	Missense	p.R132C
PD8489a	2	209113113	209113113	G	A	0.443	IDH1	Missense	p.R132C
PD8499a	2	209113113	209113113	G	A	0.45	IDH1	Missense	p.R132C
PD8368a	2	209113113	209113113	G	A	0.457	IDH1	Missense	p.R132C
PD9378a	2	209113113	209113113	G	A	0.462	IDH1	Missense	p.R132C
PD11251a	2	209113113	209113113	G	A	0.472	IDH1	Missense	p.R132C
PD7992a	2	209113113	209113113	G	A	0.473	IDH1	Missense	p.R132C
PD8488a	2	209113113	209113113	G	A	0.482	IDH1	Missense	p.R132C
PD11040a	2	209113113	209113113	G	A	0.485	IDH1	Missense	p.R132C
PD11087a	2	209113113	209113113	G	A	0.498	IDH1	Missense	p.R132C
PD7979a	2	209113113	209113113	G	A	0.5	IDH1	Missense	p.R132C
PD7980a	2	209113113	209113113	G	A	0.514	IDH1	Missense	p.R132C
PD8407a	2	209113113	209113113	G	A	0.541	IDH1	Missense	p.R132C
PD7841a	2	209113113	209113113	G	A	0.56	IDH1	Missense	p.R132C
PD9241a	2	209113113	209113113	G	C	0.373	IDH1	Missense	p.R132G
PD11223a	2	209113113	209113113	G	C	0.409	IDH1	Missense	p.R132G
PD11265a	2	209113113	209113113	G	C	0.411	IDH1	Missense	p.R132G
PD9234a	2	209113113	209113113	G	C	0.462	IDH1	Missense	p.R132G
PD7680a	2	209113113	209113113	G	T	0.379	IDH1	Missense	p.R132S
PD8011a	2	209113113	209113113	G	T	0.485	IDH1	Missense	p.R132S
PD8313a	2	209113320	209113320	C	T	0.0612	IDH1	Missense	p.A63T
PD9328a	4	106155174	106155174	C	T	0.027	TET2	Synonymous	p.C25C
PD8225a	4	106155202	106155202	C	T	0.0714	TET2	Nonsense	p.Q35X
PD11258a	4	106155306	106155306	C	T	0.0356	TET2	Synonymous	p.S69S
PD8346a	4	106155307	106155314	CAGAATAG	C	0.293	TET2	Frameshift	p.Q70fs
PD8329a	4	106155308	106155308	A	C	0.24	TET2	Missense	p.Q70P
PD11155a	4	106155317	106155317	G	A	0.05	TET2	Missense	p.R73H
PD8284a	4	106155351	106155351	G	A	0.0436	TET2	Synonymous	p.G84G

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8348a	4	106155422	106155422	A	T	0.515	TET2	Missense	p.Q108L
PD11257a	4	106155495	106155496	TC	T	0.324	TET2	Frameshift	p.P133fs
PD11258a	4	106155499	106155499	G	A	0.0699	TET2	Missense	p.G134S
PD8008a	4	106155507	106155507	C	T	0.0436	TET2	Synonymous	p.S136S
PD7722a	4	106155579	106155579	T	TA	0.353	TET2	Frameshift	p.K161fs
PD11175a	4	106155681	106155681	C	T	0.0275	TET2	Synonymous	p.D194D
PD8019a	4	106155700	106155700	A	T	0.0258	TET2	Nonsense	p.K201X
PD7769a	4	106155843	106155843	C	A	0.497	TET2	Missense	p.H248Q
PD8126a	4	106155878	106155879	TG	T	0.362	TET2	Frameshift	p.L260fs
PD10841a	4	106155888	106155888	G	GC	0.387	TET2	Frameshift	p.I264fs
PD8464a	4	106155916	106155916	C	T	0.489	TET2	Nonsense	p.Q273X
PD7663a	4	106155920	106155921	TC	T	0.273	TET2	Frameshift	p.I274fs
PD8208a	4	106155920	106155921	TC	T	0.408	TET2	Frameshift	p.I274fs
PD11280a	4	106155935	106155935	C	CAGAC	0.195	TET2	Frameshift	p.T279fs
PD8225a	4	106155948	106155948	G	A	0.0473	TET2	Synonymous	p.E283E
PD11194a	4	106155970	106155970	G	A	0.0275	TET2	Missense	p.V291M
PD9300a	4	106155992	106155992	C	T	0.0496	TET2	Missense	p.A298V
PD11212a	4	106155993	106155994	TG	T	0.423	TET2	Frameshift	p.D299fs
PD9274a	4	106156000	106156000	G	A	0.0207	TET2	Missense	p.A301T
PD8451a	4	106156003	106156005	GAT	G	0.402	TET2	Frameshift	p.D302fs
PD11240a	4	106156040	106156041	GT	G	0.427	TET2	Frameshift	p.C314fs
PD11193a	4	106156062	106156062	A	G	0.0323	TET2	Synonymous	p.Q321Q
PD9253a	4	106156077	106156077	A	G	0.561	TET2	Synonymous	p.K326K
PD8370a	4	106156079	106156079	C	G	0.49	TET2	Nonsense	p.S327X
PD7690a	4	106156103	106156105	CTG	C	0.632	TET2	Frameshift	p.P335fs
PD11130a	4	106156143	106156143	T	A	0.0216	TET2	Synonymous	p.S348S
PD8538a	4	106156144	106156144	G	A	0.0202	TET2	Missense	p.G349S
PD11243a	4	106156160	106156160	C	G	0.461	TET2	Nonsense	p.S354X
PD8076a	4	106156246	106156246	C	T	0.133	TET2	Nonsense	p.Q383X
PD10981a	4	106156270	106156270	T	TT	0.27	TET2	Frameshift	p.S391fs
PD7692a	4	106156279	106156279	G	A	0.0275	TET2	Missense	p.A394T
PD11133a	4	106156312	106156316	CTTCT	C	0.404	TET2	Frameshift	p.L405fs
PD11260a	4	106156348	106156348	C	T	0.391	TET2	Nonsense	p.Q417X
PD11254a	4	106156363	106156363	G	T	0.494	TET2	Nonsense	p.G422X
PD7769a	4	106156384	106156384	G	A	0.517	TET2	Missense	p.G429R
PD9385a	4	106156402	106156402	C	T	0.0861	TET2	Missense	p.H435Y
PD7837a	4	106156468	106156468	G	A	0.0555	TET2	Missense	p.A457T
PD8585a	4	106156485	106156485	T	C	0.472	TET2	Synonymous	p.S462S
PD7801a	4	106156512	106156512	C	T	0.507	TET2	Synonymous	p.S471S
PD11141a	4	106156513	106156513	C	T	0.0273	TET2	Missense	p.P472S
PD11198a	4	106156523	106156523	T	TG	0.357	TET2	Frameshift	p.M475fs
PD9377a	4	106156537	106156537	C	T	0.0548	TET2	Missense	p.P480S
PD9271a	4	106156570	106156570	C	T	0.0507	TET2	Nonsense	p.Q491X
PD8430a	4	106156599	106156599	G	A	0.0476	TET2	Synonymous	p.L500L
PD11254a	4	106156613	106156615	CAA	C	0.362	TET2	Frameshift	p.T505fs
PD11165a	4	106156624	106156638	TCAGAACACCTCAAG	T	0.572	TET2	Frameshift	p.S509fs
PD9222a	4	106156625	106156625	C	T	0.0342	TET2	Missense	p.S509L
PD11272a	4	106156628	106156630	AAC	A	0.053	TET2	Frameshift	p.E510fs
PD7666a	4	106156630	106156630	C	T	0.0398	TET2	Missense	p.H511Y
PD11244a	4	106156655	106156657	TTG	T	0.473	TET2	Frameshift	p.F519fs
PD10971a	4	106156675	106156675	C	T	0.548	TET2	Nonsense	p.Q526X
PD11222a	4	106156693	106156693	T	C	0.0259	TET2	Synonymous	p.L532L
PD8006a	4	106156729	106156729	C	T	0.23	TET2	Nonsense	p.R544X
PD8158a	4	106156776	106156777	TC	T	0.297	TET2	Nonsense	p.L560X
PD11228a	4	106156782	106156783	AC	A	0.041	TET2	Frameshift	p.P562fs
PD9323a	4	106156805	106156805	C	T	0.0503	TET2	Missense	p.A569V
PD7810a	4	106156824	106156824	G	A	0.494	TET2	Synonymous	p.A575A
PD11287a	4	106156845	106156849	TGAGG	T	0.343	TET2	Frameshift	p.E583fs
PD7655a	4	106156890	106156890	C	A	0.462	TET2	Synonymous	p.S597S
PD11258a	4	106156924	106156925	TC	T	0.16	TET2	Frameshift	p.S609fs

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8006a	4	106156965	106156965	G	GA	0.133	TET2	Frameshift	p.K623fs
PD10943a	4	106156991	106156991	C	CA	0.815	TET2	Frameshift	p.S631fs
PD9323a	4	106157008	106157008	G	A	0.088	TET2	Missense	p.E637K
PD7791a	4	106157008	106157008	G	T	0.0487	TET2	Nonsense	p.E637X
PD10822a	4	106157011	106157011	A	G	0.474	TET2	Missense	p.M638V
PD8231a	4	106157059	106157059	C	T	0.496	TET2	Nonsense	p.Q654X
PD8351a	4	106157208	106157208	G	GA	0.329	TET2	Frameshift	p.N704fs
PD11163a	4	106157217	106157217	G	T	0.0215	TET2	Missense	p.Q706H
PD9358a	4	106157233	106157233	C	T	0.0852	TET2	Missense	p.P712S
PD11148a	4	106157251	106157252	CT	C	0.419	TET2	Frameshift	p.L718fs
PD8256a	4	106157257	106157257	C	T	0.167	TET2	Nonsense	p.Q720X
PD10933a	4	106157322	106157322	C	CTAAAC	0.267	TET2	Frameshift	p.Q742fs
PD10919a	4	106157332	106157332	C	T	0.457	TET2	Nonsense	p.Q745X
PD10886a	4	106157335	106157336	CA	C	0.338	TET2	Frameshift	p.Q746fs
PD11250a	4	106157345	106157352	AAATAAAG	A	0.256	TET2	Frameshift	p.Q749fs
PD11284a	4	106157367	106157368	AC	A	0.393	TET2	Frameshift	p.L757fs
PD11116a	4	106157401	106157401	G	A	0.0474	TET2	Missense	p.D768N
PD10861a	4	106157404	106157404	C	T	0.493	TET2	Nonsense	p.Q769X
PD10924a	4	106157407	106157407	C	CA	0.283	TET2	Frameshift	p.Q770fs
PD11222a	4	106157443	106157443	G	A	0.0284	TET2	Missense	p.E782K
PD8152a	4	106157469	106157469	G	A	0.496	TET2	Synonymous	p.Q790Q
PD8469a	4	106157473	106157474	TC	T	0.392	TET2	Nonsense	p.S792X
PD8469a	4	106157477	106157478	AA	A	0.224	TET2	Frameshift	p.K793fs
PD7613a	4	106157480	106157480	C	G	0.447	TET2	Nonsense	p.S794X
PD11198a	4	106157527	106157527	C	T	0.373	TET2	Nonsense	p.Q810X
PD8452a	4	106157527	106157527	C	T	0.873	TET2	Nonsense	p.Q810X
PD7844a	4	106157540	106157540	G	A	0.504	TET2	Missense	p.R814H
PD11124a	4	106157552	106157556	CTTAT	C	0.853	TET2	Frameshift	p.P818fs
PD8211a	4	106157620	106157621	GT	G	0.488	TET2	Frameshift	p.V841fs
PD9350a	4	106157677	106157677	C	T	0.0423	TET2	Nonsense	p.Q860X
PD8305a	4	106157677	106157677	C	T	0.411	TET2	Nonsense	p.Q860X
PD8309a	4	106157755	106157756	CA	C	0.8	TET2	Frameshift	p.Q886fs
PD7656a	4	106157809	106157809	C	T	0.367	TET2	Nonsense	p.Q904X
PD8200a	4	106157834	106157834	C	CA	0.447	TET2	Frameshift	p.A912fs
PD9286a	4	106157834	106157834	C	T	0.706	TET2	Missense	p.A912V
PD11150a	4	106157845	106157845	C	T	0.231	TET2	Nonsense	p.Q916X
PD7842a	4	106157845	106157845	C	T	0.274	TET2	Nonsense	p.Q916X
PD8423a	4	106157845	106157845	C	T	0.486	TET2	Nonsense	p.Q916X
PD10894a	4	106157846	106157846	A	AA	0.327	TET2	Frameshift	p.Q916fs
PD8334a	4	106157863	106157863	C	T	0.0361	TET2	Missense	p.H922Y
PD7879a	4	106157883	106157884	TC	T	0.534	TET2	Frameshift	p.P929fs
PD9364a	4	106157916	106157916	G	A	0.0733	TET2	Synonymous	p.Q939Q
PD8575a	4	106157921	106157921	C	T	0.0405	TET2	Missense	p.P941L
PD10879a	4	106157944	106157945	CA	C	0.345	TET2	Frameshift	p.H949fs
PD8354a	4	106157945	106157945	A	G	0.514	TET2	Missense	p.H949R
PD8500a	4	106157948	106157948	C	T	0.0461	TET2	Missense	p.A950V
PD7711a	4	106157961	106157961	G	A	0.416	TET2	Nonsense	p.W954X
PD7958a	4	106157971	106157971	C	T	0.118	TET2	Nonsense	p.Q958X
PD11189a	4	106157971	106157971	C	T	0.382	TET2	Nonsense	p.Q958X
PD11072a	4	106157986	106157986	C	T	0.433	TET2	Nonsense	p.Q963X
PD8280a	4	106157991	106157993	AAC	A	0.382	TET2	Frameshift	p.T965fs
PD10863a	4	106158004	106158005	CA	C	0.428	TET2	Frameshift	p.Q969fs
PD8203a	4	106158008	106158009	CT	C	0.454	TET2	Frameshift	p.T970fs
PD8349a	4	106158082	106158082	A	C	0.508	TET2	Missense	p.T995P
PD10818a	4	106158135	106158135	A	G	0.491	TET2	Synonymous	p.P1012P
PD11243a	4	106158137	106158138	CT	C	0.049	TET2	Frameshift	p.P1013fs
PD10944a	4	106158156	106158157	GC	G	0.436	TET2	Frameshift	p.Q1020fs
PD9322a	4	106158175	106158175	G	A	0.0657	TET2	Missense	p.E1026K
PD9297a	4	106158186	106158187	GC	G	0.097	TET2	Frameshift	p.Q1030fs
PD10904a	4	106158238	106158238	A	AA	0.396	TET2	Frameshift	p.T1047fs
PD8008a	4	106158289	106158289	G	A	0.0373	TET2	Missense	p.V1064I

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11241a	4	106158299	106158299	G	C	0.539	TET2	Missense	p.R1067T
PD8227a	4	106158301	106158301	C	T	0.388	TET2	Nonsense	p.Q1068X
PD8483a	4	106158313	106158313	G	A	0.275	TET2	Missense	p.A1072T
PD11172a	4	106158316	106158316	G	A	0.0597	TET2	Missense	p.E1073K
PD9296a	4	106158338	106158338	C	T	0.0608	TET2	Missense	p.A1080V
PD8065a	4	106158357	106158359	TTC	T	0.287	TET2	Frameshift	p.S1087fs
PD9330a	4	106158371	106158371	C	T	0.0777	TET2	Missense	p.T1091I
PD8479a	4	106158404	106158404	A	AAGG	0.359	TET2	Inframe	p.N1102delinsNR
PD9318a	4	106158419	106158419	C	T	0.0661	TET2	Missense	p.S1107L
PD8417a	4	106158429	106158430	AT	A	0.379	TET2	Frameshift	p.L1111fs
PD8454a	4	106158470	106158470	T	TGT	0.178	TET2	Frameshift	p.V1124fs
PD11199a	4	106158541	106158541	G	C	0.452	TET2	Missense	p.V1148L
PD8187a	4	106162481	106162494	CTATTATCTCAAC A	C	0.202	TET2	Splice site	
PD7936a	4	106162495	106162495	G	A	0.351	TET2	Splice site	c.3410-1G>A
PD11164a	4	106162498	106162499	CA	C	0.76	TET2	Frameshift	p.Q1138fs
PD7770a	4	106162529	106162529	A	G	0.511	TET2	Missense	p.Y1148C
PD8384a	4	106162567	106162567	A	G	0.502	TET2	Missense	p.R1161G
PD11127a	4	106164016	106164016	A	G	0.356	TET2	Missense	p.R1176G
PD11086a	4	106164021	106164022	TG	T	0.384	TET2	Frameshift	p.E1178fs
PD11241a	4	106164048	106164063	AGGCAAAAGTTCTCAG	A	0.273	TET2	Inframe	p.1187_1191del
PD11283a	4	106164061	106164061	C	T	0.444	TET2	Nonsense	p.Q1191X
PD8170a	4	106164068	106164068	G	A	0.108	TET2	Missense	p.C1193Y
PD10930a	4	106164071	106164071	C	G	0.31	TET2	Missense	p.P1194R
PD8466a	4	106164071	106164071	C	T	0.031	TET2	Missense	p.P1194L
PD8101a	4	106164080	106164080	A	G	0.464	TET2	Missense	p.K1197R
PD8423a	4	106164082	106164083	TG	T	0.394	TET2	Frameshift	p.W1198fs
PD8001a	4	106164726	106164726	G	A	0.429	TET2	Splice site	c.3595-1G>A
PD7613a	4	106164767	106164767	T	C	0.418	TET2	Missense	p.L1212S
PD10809a	4	106164778	106164778	C	T	0.0619	TET2	Nonsense	p.R1216X
PD8231a	4	106164778	106164778	C	T	0.315	TET2	Nonsense	p.R1216X
PD11230a	4	106164779	106164779	G	A	0.436	TET2	Missense	p.R1216Q
PD7754a	4	106164794	106164794	G	A	0.517	TET2	Missense	p.C1221Y
PD7857a	4	106164839	106164840	TC	T	0.446	TET2	Frameshift	p.I1236fs
PD8083a	4	106164887	106164887	T	C	0.312	TET2	Missense	p.L1252P
PD9228a	4	106164897	106164897	C	G	0.531	TET2	Nonsense	p.Y1255X
PD11251a	4	106164906	106164906	C	T	0.466	TET2	Synonymous	p.L1258L
PD11240a	4	106164913	106164913	C	T	0.458	TET2	Missense	p.R1261C
PD8154a	4	106164916	106164916	C	T	0.342	TET2	Missense	p.R1262W
PD9326a	4	106164917	106164917	G	A	0.331	TET2	Missense	p.R1262Q
PD8410a	4	106164923	106164923	C	T	0.531	TET2	Missense	p.A1264V
PD11153a	4	106164936	106164936	G	A	0.445	TET2	Splice site	c.3803+1G>A
PD7873a	4	106164937	106164937	T	C	0.329	TET2	Splice site	c.3803+2T>C
PD8431a	4	106180783	106180783	T	TG	0.529	TET2	Frameshift	p.C1271fs
PD8403a	4	106180787	106180860	CCTGTCAGGGGCTGGATCCAGAAACCTGTGGTGCCTCCTTCTCTTTTGGTTGTTCATGGAGCATGTACTACAAT	C	0.057	TET2	Frameshift	p.A1272fs
PD7770a	4	106180790	106180790	G	A	0.478	TET2	Missense	p.C1273Y
PD11231a	4	106180790	106180790	G	T	0.12	TET2	Missense	p.C1273F
PD11233a	4	106180790	106180790	G	T	0.51	TET2	Missense	p.C1273F
PD8497a	4	106180797	106180797	G	GG	0.043	TET2	Frameshift	p.L1276fs
PD11120a	4	106180816	106180816	G	T	0.51	TET2	Missense	p.G1282C

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD9273a	4	106180817	106180817	G	GTGC	0.203	TET2	Inframe	p.G1282delinsGC
PD9339a	4	106180864	106180865	TG	T	0.804	TET2	Frameshift	p.C1298fs
PD8297a	4	106180866	106180866	T	G	0.385	TET2	Missense	p.C1298W
PD11072a	4	106180869	106180869	G	C	0.5	TET2	Missense	p.K1299N
PD8441a	4	106180873	106180873	G	T	0.46	TET2	Missense	p.A1301S
PD8554a	4	106180927	106180927	G	A	0.167	TET2	Splice site	c.3954+1G>A
PD11148a	4	106180927	106180927	G	T	0.674	TET2	Splice site	c.3954+1G>T
PD8290a	4	106180927	106180927	G	T	0.922	TET2	Splice site	c.3954+1G>T
PD10928a	4	106182915	106182915	G	A	0.28	TET2	Splice site	c.3955-1G>A
PD9331a	4	106182917	106182917	A	T	0.448	TET2	Missense	p.E1319V
PD8588a	4	106182926	106182926	T	A	0.426	TET2	Missense	p.L1322Q
PD8454a	4	106182940	106182940	C	T	0.267	TET2	Nonsense	p.Q1327X
PD8451a	4	106182940	106182940	C	T	0.452	TET2	Nonsense	p.Q1327X
PD8493a	4	106182981	106182981	T	C	0.0377	TET2	Synonymous	p.L1340L
PD7710a	4	106190765	106190765	A	G	0.445	TET2	Splice site	c.4045-2A>G
PD10960a	4	106190766	106190766	G	A	0.381	TET2	Splice site	c.4045-1G>A
PD7656a	4	106190776	106190776	G	A	0.418	TET2	Missense	p.E1352K
PD8337a	4	106190781	106190783	CAG	C	0.068	TET2	Frameshift	p.R1354fs
PD8108a	4	106190786	106190786	C	T	0.381	TET2	Missense	p.A1355V
PD8444a	4	106190794	106190815	TGCCGTCTGGGTCTGAAGGAAG	T	0.145	TET2	Inframe	p.1358_1365del
PD11113a	4	106190797	106190797	C	T	0.0858	TET2	Missense	p.R1359C
PD11021a	4	106190797	106190797	C	T	0.361	TET2	Missense	p.R1359C
PD10989a	4	106190798	106190798	G	A	0.0345	TET2	Missense	p.R1359H
PD8465a	4	106190808	106190808	G	A	0.0603	TET2	Synonymous	p.L1362L
PD8082a	4	106190824	106190824	T	G	0.46	TET2	Missense	p.F1368V
PD7886a	4	106190831	106190831	G	A	0.401	TET2	Missense	p.G1370E
PD11218a	4	106190846	106190846	T	TT	0.385	TET2	Frameshift	p.L1375fs
PD10819a	4	106190852	106190852	T	C	0.463	TET2	Missense	p.F1377S
PD9355a	4	106190853	106190853	C	T	0.0269	TET2	Synonymous	p.F1377F
PD11244a	4	106190857	106190857	G	C	0.485	TET2	Missense	p.A1379P
PD11153a	4	106190860	106190860	C	T	0.03	TET2	Missense	p.H1380Y
PD8486a	4	106190860	106190860	C	T	0.487	TET2	Missense	p.H1380Y
PD11217a	4	106190861	106190861	A	C	0.481	TET2	Missense	p.H1380P
PD8279a	4	106193719	106193719	A	G	0.947	TET2	Splice site	c.4183-2A>G
PD10985a	4	106193730	106193730	C	CT	0.065	TET2	Frameshift	p.L1398fs
PD11119a	4	106193748	106193748	C	T	0.32	TET2	Nonsense	p.R1404X
PD8001a	4	106193748	106193748	C	T	0.475	TET2	Nonsense	p.R1404X
PD8090a	4	106193749	106193749	G	A	0.302	TET2	Missense	p.R1404Q
PD8413a	4	106193785	106193785	A	G	0.893	TET2	Missense	p.H1416R
PD10924a	4	106193787	106193787	G	T	0.395	TET2	Missense	p.V1417F
PD10875a	4	106193794	106193795	CT	C	0.434	TET2	Frameshift	p.P1419fs
PD11284a	4	106193796	106193796	T	TTA	0.455	TET2	Frameshift	p.L1420fs
PD7756a	4	106193801	106193801	C	T	0.367	TET2	Synonymous	p.Y1421Y
PD11203a	4	106193809	106193810	CT	C	0.494	TET2	Frameshift	p.S1424fs
PD7822a	4	106193822	106193823	GT	G	0.505	TET2	Frameshift	p.F1429fs
PD10904a	4	106193853	106193853	A	T	0.483	TET2	Nonsense	p.K1439X
PD7707a	4	106193871	106193871	C	T	0.0369	TET2	Nonsense	p.Q1445X
PD8208a	4	106193872	106193872	A	G	0.432	TET2	Missense	p.Q1445R
PD10865a	4	106193892	106193892	C	T	0.414	TET2	Nonsense	p.R1452X
PD9234a	4	106193894	106193894	A	T	0.0423	TET2	Synonymous	p.R1452R
PD11155a	4	106193932	106193932	G	A	0.0573	TET2	Missense	p.R1465Q
PD10898a	4	106194042	106194043	AC	A	0.442	TET2	Frameshift	p.T1502fs
PD8464a	4	106194063	106194063	A	T	0.464	TET2	Nonsense	p.K1509X
PD11046a	4	106194070	106194070	T	A	0.651	TET2	Nonsense	p.L1511X
PD9308a	4	106194073	106194073	C	T	0.868	TET2	Missense	p.A1512V
PD8513a	4	106196248	106196248	G	GC	0.042	TET2	Frameshift	p.P1528fs
PD11153a	4	106196252	106196252	C	T	0.646	TET2	Nonsense	p.Q1529X
PD10865a	4	106196267	106196267	C	T	0.448	TET2	Nonsense	p.Q1534X
PD11149a	4	106196295	106196295	G	A	0.0688	TET2	Missense	p.R1543K

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11005a	4	106196296	106196296	A	AC	0.358	TET2	Frameshift	p.P1544fs
PD11212a	4	106196300	106196300	C	T	0.442	TET2	Nonsense	p.Q1545X
PD7807a	4	106196382	106196382	G	A	0.563	TET2	Missense	p.R1572Q
PD8095a	4	106196394	106196394	T	A	0.0519	TET2	Missense	p.V1576D
PD11222a	4	106196412	106196412	C	T	0.0347	TET2	Missense	p.S1582F
PD7842a	4	106196424	106196424	C	A	0.13	TET2	Nonsense	p.S1586X
PD8293a	4	106196427	106196427	A	AT	0.281	TET2	Frameshift	p.D1587fs
PD11018a	4	106196443	106196443	C	T	0.444	TET2	Synonymous	p.T1592T
PD11147a	4	106196457	106196458	TC	T	0.41	TET2	Frameshift	p.F1597fs
PD8244a	4	106196479	106196479	T	C	0.0202	TET2	Synonymous	p.A1604A
PD10824a	4	106196482	106196483	AG	A	0.396	TET2	Frameshift	p.G1606fs
PD11195a	4	106196519	106196519	T	TA	0.121	TET2	Nonsense	p.Y1618_P1619 delinsX
PD7871a	4	106196556	106196556	C	G	0.423	TET2	Nonsense	p.S1630X
PD8095a	4	106196561	106196561	C	T	0.0231	TET2	Nonsense	p.Q1632X
PD11250a	4	106196586	106196587	AC	A	0.396	TET2	Frameshift	p.D1640fs
PD8533a	4	106196619	106196619	C	T	0.712	TET2	Missense	p.P1651L
PD8162a	4	106196670	106196670	C	T	0.0331	TET2	Missense	p.S1668F
PD8046a	4	106196690	106196692	ATC	A	0.045	TET2	Frameshift	p.I1675fs
PD11242a	4	106196695	106196695	T	TCCAA	0.135	TET2	Frameshift	p.T1677fs
PD11134a	4	106196771	106196771	C	T	0.025	TET2	Nonsense	p.Q1702X
PD7756a	4	106196823	106196823	G	A	0.42	TET2	Missense	p.G1719E
PD7775a	4	106196846	106196850	CATGA	C	0.314	TET2	Frameshift	p.H1727fs
PD8533a	4	106196851	106196851	G	T	0.0221	TET2	Missense	p.E1728D
PD11253a	4	106196856	106196856	A	G	0.0255	TET2	Missense	p.D1730G
PD9377a	4	106196863	106196863	C	T	0.0273	TET2	Synonymous	p.H1732H
PD9383a	4	106196915	106196915	G	A	0.0464	TET2	Missense	p.D1750N
PD8498a	4	106196927	106196927	G	C	0.621	TET2	Missense	p.G1754R
PD8532a	4	106196946	106196946	C	G	0.0203	TET2	Missense	p.S1760C
PD8294a	4	106196965	106196965	C	T	0.113	TET2	Synonymous	p.Y1766Y
PD10875a	4	106196967	106196967	G	GT	0.044	TET2	Frameshift	p.S1767fs
PD11146a	4	106196997	106196999	TTC	T	0.356	TET2	Frameshift	p.L1777fs
PD8244a	4	106197111	106197111	G	A	0.0333	TET2	Missense	p.G1815D
PD8420a	4	106197118	106197118	C	CA	0.335	TET2	Frameshift	p.K1818fs
PD9374a	4	106197140	106197140	C	T	0.554	TET2	Nonsense	p.Q1825X
PD10933a	4	106197149	106197149	C	T	0.539	TET2	Nonsense	p.Q1828X
PD8036a	4	106197190	106197190	G	A	0.0825	TET2	Synonymous	p.E1841E
PD11149a	4	106197195	106197195	A	G	0.355	TET2	Missense	p.N1843S
PD9355a	4	106197200	106197200	G	T	0.396	TET2	Nonsense	p.E1845X
PD10863a	4	106197208	106197208	G	GG	0.373	TET2	Frameshift	p.S1848fs
PD7958a	4	106197210	106197210	C	G	0.351	TET2	Nonsense	p.S1848X
PD8533a	4	106197232	106197232	G	T	0.445	TET2	Synonymous	p.L1855L
PD8335a	4	106197244	106197244	T	G	0.543	TET2	Missense	p.I1859M
PD8214a	4	106197245	106197245	G	T	0.479	TET2	Missense	p.G1860W
PD7756a	4	106197250	106197250	A	T	0.0882	TET2	Synonymous	p.G1861G
PD11133a	4	106197271	106197271	T	TG	0.45	TET2	Frameshift	p.G1869fs
PD7881a	4	106197282	106197282	T	G	0.0653	TET2	Missense	p.L1872R
PD9232a	4	106197282	106197282	T	G	0.482	TET2	Missense	p.L1872R
PD8174a	4	106197285	106197285	T	C	0.0284	TET2	Missense	p.I1873T
PD11231a	4	106197285	106197285	T	C	0.0523	TET2	Missense	p.I1873T
PD8581a	4	106197285	106197285	T	C	0.252	TET2	Missense	p.I1873T
PD7655a	4	106197285	106197285	T	C	0.37	TET2	Missense	p.I1873T
PD10886a	4	106197285	106197285	T	C	0.452	TET2	Missense	p.I1873T
PD7695a	4	106197299	106197299	C	T	0.0764	TET2	Missense	p.R1878C
PD8242a	4	106197305	106197305	C	T	0.0584	TET2	Synonymous	p.L1880L
PD8019a	4	106197317	106197317	A	G	0.386	TET2	Missense	p.T1884A
PD9271a	4	106197336	106197336	A	AA	0.614	TET2	Frameshift	p.N1890fs
PD11174a	4	106197354	106197354	G	C	0.908	TET2	Missense	p.R1896T
PD8560a	4	106197377	106197377	C	T	0.0281	TET2	Missense	p.H1904Y
PD8208a	4	106197378	106197378	A	G	0.472	TET2	Missense	p.H1904R
PD8444a	4	106197402	106197402	A	G	0.414	TET2	Missense	p.H1912R
PD8512a	4	106197423	106197423	C	T	0.0468	TET2	Missense	p.A1919V

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD9214a	4	106197441	106197441	C	T	0.0354	TET2	Missense	p.A1925V
PD7968a	4	106197552	106197552	C	T	0.462	TET2	Missense	p.P1962L
PD11212a	4	106197552	106197552	C	T	0.49	TET2	Missense	p.P1962L
PD10932a	4	106197552	106197552	C	T	0.542	TET2	Missense	p.P1962L
PD8244a	4	106197563	106197563	C	T	0.0638	TET2	Missense	p.R1966C
PD9214a	4	106197576	106197576	C	T	0.0307	TET2	Missense	p.S1970F
PD8465a	4	106197581	106197581	G	A	0.0488	TET2	Missense	p.A1972T
PD10930a	4	106197611	106197614	TCCA	TT	0.203	TET2	Frameshift	c.5945_5947T
PD11227a	9	5069969	5069969	G	A	0.0429	JAK2	Missense	p.V520I
PD11165a	9	5072510	5072510	G	A	0.482	JAK2	Missense	p.G554S
PD7988a	9	5072549	5072549	G	T	0.48	JAK2	Missense	p.V567L
PD9311a	9	5072570	5072570	C	A	0.0974	JAK2	Missense	p.H574N
PD11210a	9	5072600	5072600	G	A	0.0291	JAK2	Missense	p.D584N
PD7764a	9	5073770	5073770	G	T	0.0432	JAK2	Missense	p.V617F
PD10991a	9	5073770	5073770	G	T	0.0537	JAK2	Missense	p.V617F
PD7942a	9	5073770	5073770	G	T	0.0753	JAK2	Missense	p.V617F
PD11193a	9	5073770	5073770	G	T	0.142	JAK2	Missense	p.V617F
PD8481a	9	5073770	5073770	G	T	0.349	JAK2	Missense	p.V617F
PD8487a	9	5073770	5073770	G	T	0.445	JAK2	Missense	p.V617F
PD8531a	9	5073770	5073770	G	T	0.55	JAK2	Missense	p.V617F
PD10963a	9	5073770	5073770	G	T	0.653	JAK2	Missense	p.V617F
PD9296a	9	5073770	5073770	G	T	0.838	JAK2	Missense	p.V617F
PD7845a	9	5073770	5073770	G	T	0.856	JAK2	Missense	p.V617F
PD7968a	9	5073770	5073770	G	T	0.993	JAK2	Missense	p.V617F
PD8580a	9	5073770	5073770	G	T	1	JAK2	Missense	p.V617F
PD7779a	11	119103241	119103241	G	A	0.1	CBL	Synonymous	p.Q93Q
PD9384a	11	119103255	119103255	T	C	0.54	CBL	Missense	p.I98T
PD8156a	11	119142470	119142470	A	G	0.486	CBL	Missense	p.I157V
PD8501a	11	119142496	119142496	A	G	0.528	CBL	Synonymous	p.L165L
PD8283a	11	119142562	119142562	G	A	0.513	CBL	Synonymous	p.A187A
PD9312a	11	119144721	119144721	C	T	0.607	CBL	Missense	p.T245I
PD8210a	11	119144723	119144723	C	T	0.137	CBL	Nonsense	p.R246X
PD9205a	11	119145557	119145557	C	T	0.048	CBL	Missense	p.L255F
PD9380a	11	119145571	119145571	C	T	0.104	CBL	Synonymous	p.N259N
PD9376a	11	119145622	119145622	A	G	0.0585	CBL	Synonymous	p.E276E
PD8548a	11	119145629	119145629	G	A	0.0478	CBL	Missense	p.A279T
PD9383a	11	119145661	119145661	C	T	0.111	CBL	Synonymous	p.G289G
PD7634a	11	119146739	119146739	G	A	0.204	CBL	Missense	p.G301D
PD11153a	11	119148466	119148466	G	A	0.128	CBL	Splice site	c.1008-1G>A
PD9298a	11	119148534	119148534	G	A	0.0471	CBL	Missense	p.D359N
PD7774a	11	119148874	119148874	A	T	0.416	CBL	Splice site	c.1096-2A>T
PD10845a	11	119148875	119148875	G	C	0.918	CBL	Splice site	c.1096-1G>C
PD11254a	11	119148880	119148880	A	C	0.475	CBL	Missense	p.Q367P
PD8101a	11	119148890	119148893	ATAC	A	0.267	CBL	Inframe	p.371_371del
PD11243a	11	119148891	119148891	T	C	0.334	CBL	Missense	p.Y371H
PD11153a	11	119148892	119148892	A	G	0.188	CBL	Missense	p.Y371C
PD7937a	11	119148907	119148907	C	T	0.32	CBL	Missense	p.S376F
PD11022a	11	119148919	119148919	T	C	0.121	CBL	Missense	p.L380P
PD8210a	11	119148919	119148919	T	C	0.174	CBL	Missense	p.L380P
PD10972a	11	119148919	119148919	T	C	0.521	CBL	Missense	p.L380P
PD8030a	11	119148919	119148919	T	C	0.876	CBL	Missense	p.L380P
PD8056a	11	119148929	119148929	A	G	0.287	CBL	Missense	p.I383M
PD11024a	11	119148958	119148958	T	A	0.47	CBL	Missense	p.I393N
PD10871a	11	119148962	119148962	G	A	0.528	CBL	Synonymous	p.E394E
PD9348a	11	119148974	119148974	C	A	0.496	CBL	Missense	p.H398Q
PD8393a	11	119148976	119148976	T	A	0.316	CBL	Missense	p.L399H
PD10806a	11	119148982	119148982	G	C	0.229	CBL	Missense	p.C401S
PD10801a	11	119148982	119148982	G	C	0.35	CBL	Missense	p.C401S
PD8385a	11	119148990	119148990	T	A	0.68	CBL	Missense	p.C404S
PD10894a	11	119148991	119148991	G	A	0.52	CBL	Missense	p.C404Y
PD11153a	11	119149219	119149219	G	A	0.548	CBL	Splice site	c.1228-1G>A
PD9297a	11	119149245	119149245	T	C	0.0972	CBL	Missense	p.F418S

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD9214a	11	119149248	119149248	G	A	0.708	CBL	Missense	p.C419Y
PD8278a	11	119149248	119149248	G	A	0.942	CBL	Missense	p.C419Y
PD8006a	11	119149251	119149251	G	A	0.0643	CBL	Missense	p.R420Q
PD7975a	11	119149251	119149251	G	A	0.242	CBL	Missense	p.R420Q
PD10894a	11	119149251	119149251	G	A	0.48	CBL	Missense	p.R420Q
PD8094a	11	119149304	119149304	G	A	0.0702	CBL	Missense	p.G438R
PD7619a	11	119149313	119149313	A	T	0.543	CBL	Missense	p.S441C
PD8425a	11	119149346	119149346	T	TC	0.043	CBL	Frameshift	p.S452fs
PD8026a	11	119149374	119149374	A	ATGA	0.269	CBL	Nonsense	p.E461delinsEX
PD8373a	11	119155759	119155759	G	A	0.431	CBL	Synonymous	p.P504P
PD8533a	11	119155760	119155760	C	A	0.0956	CBL	Missense	p.Q505K
PD8550a	11	119155779	119155779	C	T	0.0288	CBL	Missense	p.S511L
PD11137a	11	119155983	119155983	C	T	0.425	CBL	Missense	p.R550W
PD8186a	11	119156046	119156046	G	A	0.0891	CBL	Missense	p.D571N
PD9323a	11	119156070	119156070	C	T	0.263	CBL	Missense	p.P579S
PD8465a	11	119156072	119156072	C	T	0.108	CBL	Synonymous	p.P579P
PD9383a	11	119156089	119156089	G	A	0.121	CBL	Missense	p.R585H
PD9335a	11	119156209	119156209	C	T	0.0338	CBL	Missense	p.P625L
PD8070a	11	119156246	119156246	C	T	0.468	CBL	Synonymous	p.L637L
PD8465a	11	119158563	119158563	G	A	0.03	CBL	Missense	p.S648N
PD9209a	11	119167664	119167664	A	T	0.489	CBL	Missense	p.Q691H
PD9309a	11	119168142	119168142	G	A	0.032	CBL	Missense	p.M734I
PD9324a	11	119168165	119168165	C	T	0.0337	CBL	Missense	p.P742L
PD8502a	11	119168172	119168172	C	A	0.434	CBL	Synonymous	p.I744I
PD8501a	11	119170275	119170275	G	A	0.043	CBL	Synonymous	p.R835R
PD8192a	11	119170290	119170290	T	G	0.49	CBL	Missense	p.C840W
PD9345a	11	119170338	119170338	G	A	0.0535	CBL	Synonymous	p.Q856Q
PD10897a	11	119170354	119170354	G	A	0.245	CBL	Missense	p.E862K
PD11283a	11	119170354	119170354	G	A	0.443	CBL	Missense	p.E862K
PD10921a	11	119170358	119170358	A	G	0.462	CBL	Missense	p.N863S
PD11151a	11	119170359	119170359	C	T	0.507	CBL	Synonymous	p.N863N
PD9376a	11	119170370	119170370	A	G	0.103	CBL	Missense	p.Q867R
PD9310a	11	119170431	119170431	G	A	0.0613	CBL	Missense	p.M887I
PD9222a	11	119170432	119170432	G	A	0.071	CBL	Missense	p.A888T
PD9323a	11	119170475	119170475	C	T	0.0292	CBL	Missense	p.A902V
PD10949a	12	25362842	25362842	C	A	0.087	KRAS	Missense	p.V152F
PD7737a	12	25368380	25368380	T	G	0.474	KRAS	Missense	p.M189L
PD10945a	12	25368405	25368405	A	T	0.478	KRAS	Nonsense	p.C180X
PD8214a	12	25378561	25378561	G	A	0.0574	KRAS	Missense	p.A146V
PD8052a	12	25378561	25378561	G	A	0.258	KRAS	Missense	p.A146V
PD8061a	12	25378561	25378561	G	A	0.458	KRAS	Missense	p.A146V
PD9299a	12	25378562	25378562	C	T	0.0291	KRAS	Missense	p.A146T
PD8489a	12	25378562	25378562	C	T	0.437	KRAS	Missense	p.A146T
PD8061a	12	25378562	25378562	C	T	0.439	KRAS	Missense	p.A146T
PD8452a	12	25378562	25378562	C	T	0.602	KRAS	Missense	p.A146T
PD8318a	12	25378647	25378647	T	A	0.0465	KRAS	Missense	p.K117N
PD8239a	12	25378647	25378647	T	A	0.59	KRAS	Missense	p.K117N
PD11164a	12	25378647	25378647	T	G	0.224	KRAS	Missense	p.K117N
PD7912a	12	25378647	25378647	T	G	0.274	KRAS	Missense	p.K117N
PD10903a	12	25380194	25380194	T	C	0.809	KRAS	Synonymous	p.K88K
PD7699a	12	25380275	25380275	T	A	0.223	KRAS	Missense	p.Q61H
PD8460a	12	25380275	25380275	T	G	0.0529	KRAS	Missense	p.Q61H
PD8544a	12	25380275	25380275	T	G	0.0865	KRAS	Missense	p.Q61H
PD7732a	12	25380275	25380275	T	G	0.117	KRAS	Missense	p.Q61H
PD7865a	12	25380275	25380275	T	G	0.211	KRAS	Missense	p.Q61H
PD8255a	12	25380275	25380275	T	G	0.293	KRAS	Missense	p.Q61H
PD10989a	12	25380275	25380275	T	G	0.504	KRAS	Missense	p.Q61H
PD11017a	12	25380276	25380276	T	G	0.743	KRAS	Missense	p.Q61P
PD8044a	12	25380285	25380285	G	A	0.178	KRAS	Missense	p.T58I
PD8224a	12	25380285	25380285	G	A	0.367	KRAS	Missense	p.T58I
PD7756a	12	25398240	25398240	G	A	0.222	KRAS	Missense	p.H27Y
PD10832a	12	25398281	25398281	C	T	0.0481	KRAS	Missense	p.G13D

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10814a	12	25398281	25398281	C	T	0.0524	KRAS	Missense	p.G13D
PD10857a	12	25398281	25398281	C	T	0.0553	KRAS	Missense	p.G13D
PD8329a	12	25398281	25398281	C	T	0.0565	KRAS	Missense	p.G13D
PD10996a	12	25398281	25398281	C	T	0.0568	KRAS	Missense	p.G13D
PD7660a	12	25398281	25398281	C	T	0.0583	KRAS	Missense	p.G13D
PD9278a	12	25398281	25398281	C	T	0.063	KRAS	Missense	p.G13D
PD8167a	12	25398281	25398281	C	T	0.0635	KRAS	Missense	p.G13D
PD11141a	12	25398281	25398281	C	T	0.0656	KRAS	Missense	p.G13D
PD7832a	12	25398281	25398281	C	T	0.0861	KRAS	Missense	p.G13D
PD8078a	12	25398281	25398281	C	T	0.104	KRAS	Missense	p.G13D
PD8572a	12	25398281	25398281	C	T	0.116	KRAS	Missense	p.G13D
PD7818a	12	25398281	25398281	C	T	0.117	KRAS	Missense	p.G13D
PD11057a	12	25398281	25398281	C	T	0.159	KRAS	Missense	p.G13D
PD10938a	12	25398281	25398281	C	T	0.182	KRAS	Missense	p.G13D
PD8134a	12	25398281	25398281	C	T	0.208	KRAS	Missense	p.G13D
PD10859a	12	25398281	25398281	C	T	0.216	KRAS	Missense	p.G13D
PD8587a	12	25398281	25398281	C	T	0.223	KRAS	Missense	p.G13D
PD8332a	12	25398281	25398281	C	T	0.23	KRAS	Missense	p.G13D
PD10967a	12	25398281	25398281	C	T	0.32	KRAS	Missense	p.G13D
PD10862a	12	25398281	25398281	C	T	0.323	KRAS	Missense	p.G13D
PD8041a	12	25398281	25398281	C	T	0.335	KRAS	Missense	p.G13D
PD8077a	12	25398281	25398281	C	T	0.384	KRAS	Missense	p.G13D
PD8313a	12	25398281	25398281	C	T	0.555	KRAS	Missense	p.G13D
PD10970a	12	25398284	25398284	C	A	0.0252	KRAS	Missense	p.G12V
PD8018a	12	25398284	25398284	C	A	0.0376	KRAS	Missense	p.G12V
PD8332a	12	25398284	25398284	C	A	0.0411	KRAS	Missense	p.G12V
PD10859a	12	25398284	25398284	C	A	0.0655	KRAS	Missense	p.G12V
PD8329a	12	25398284	25398284	C	A	0.16	KRAS	Missense	p.G12V
PD8184a	12	25398284	25398284	C	A	0.23	KRAS	Missense	p.G12V
PD8334a	12	25398284	25398284	C	A	0.231	KRAS	Missense	p.G12V
PD9299a	12	25398284	25398284	C	A	0.304	KRAS	Missense	p.G12V
PD10899a	12	25398284	25398284	C	A	0.432	KRAS	Missense	p.G12V
PD8265a	12	25398284	25398284	C	A	0.551	KRAS	Missense	p.G12V
PD7801a	12	25398284	25398284	C	G	0.0844	KRAS	Missense	p.G12A
PD9279a	12	25398284	25398284	C	G	0.16	KRAS	Missense	p.G12A
PD9265a	12	25398284	25398284	C	G	0.189	KRAS	Missense	p.G12A
PD8590a	12	25398284	25398284	C	G	0.233	KRAS	Missense	p.G12A
PD7655a	12	25398284	25398284	C	G	0.239	KRAS	Missense	p.G12A
PD10935a	12	25398284	25398284	C	G	0.259	KRAS	Missense	p.G12A
PD8542a	12	25398284	25398284	C	G	0.289	KRAS	Missense	p.G12A
PD7859a	12	25398284	25398284	C	G	0.318	KRAS	Missense	p.G12A
PD10960a	12	25398284	25398284	C	T	0.0333	KRAS	Missense	p.G12D
PD8041a	12	25398284	25398284	C	T	0.0443	KRAS	Missense	p.G12D
PD8018a	12	25398284	25398284	C	T	0.0451	KRAS	Missense	p.G12D
PD10948a	12	25398284	25398284	C	T	0.0591	KRAS	Missense	p.G12D
PD8044a	12	25398284	25398284	C	T	0.06	KRAS	Missense	p.G12D
PD10890a	12	25398284	25398284	C	T	0.0618	KRAS	Missense	p.G12D
PD11013a	12	25398284	25398284	C	T	0.067	KRAS	Missense	p.G12D
PD8323a	12	25398284	25398284	C	T	0.0717	KRAS	Missense	p.G12D
PD7783a	12	25398284	25398284	C	T	0.0719	KRAS	Missense	p.G12D
PD11036a	12	25398284	25398284	C	T	0.0774	KRAS	Missense	p.G12D
PD7619a	12	25398284	25398284	C	T	0.085	KRAS	Missense	p.G12D
PD7985a	12	25398284	25398284	C	T	0.0972	KRAS	Missense	p.G12D
PD10976a	12	25398284	25398284	C	T	0.103	KRAS	Missense	p.G12D
PD10955a	12	25398284	25398284	C	T	0.15	KRAS	Missense	p.G12D
PD7868a	12	25398284	25398284	C	T	0.252	KRAS	Missense	p.G12D
PD8366a	12	25398284	25398284	C	T	0.259	KRAS	Missense	p.G12D
PD8275a	12	25398284	25398284	C	T	0.28	KRAS	Missense	p.G12D
PD10851a	12	25398284	25398284	C	T	0.286	KRAS	Missense	p.G12D
PD11021a	12	25398284	25398284	C	T	0.349	KRAS	Missense	p.G12D
PD8084a	12	25398284	25398284	C	T	0.357	KRAS	Missense	p.G12D
PD9334a	12	25398284	25398284	C	T	0.359	KRAS	Missense	p.G12D

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10961a	12	25398284	25398284	C	T	0.367	KRAS	Missense	p.G12D
PD8115a	12	25398284	25398284	C	T	0.376	KRAS	Missense	p.G12D
PD8251a	12	25398285	25398285	C	A	0.0913	KRAS	Missense	p.G12C
PD7863a	12	25398285	25398285	C	G	0.0536	KRAS	Missense	p.G12R
PD10928a	12	25398285	25398285	C	G	0.259	KRAS	Missense	p.G12R
PD7949a	12	25398285	25398285	C	T	0.0872	KRAS	Missense	p.G12S
PD11089a	12	25398285	25398285	C	T	0.0988	KRAS	Missense	p.G12S
PD10790a	12	25398285	25398285	C	T	0.113	KRAS	Missense	p.G12S
PD11275a	12	25398285	25398285	C	T	0.255	KRAS	Missense	p.G12S
PD8569a	12	25398295	25398295	T	C	0.513	KRAS	Synonymous	p.V8V
PD11127a	12	112884113	112884113	A	G	0.464	PTPN11	Synonymous	p.A16A
PD7631a	12	112888158	112888158	C	G	0.211	PTPN11	Missense	p.N58K
PD9278a	12	112888163	112888163	G	C	0.091	PTPN11	Missense	p.G60A
PD11261a	12	112888163	112888163	G	T	0.0791	PTPN11	Missense	p.G60V
PD8427a	12	112888163	112888163	G	T	0.0864	PTPN11	Missense	p.G60V
PD8249a	12	112888163	112888163	G	T	0.0984	PTPN11	Missense	p.G60V
PD10793a	12	112888163	112888163	G	T	0.131	PTPN11	Missense	p.G60V
PD10996a	12	112888163	112888163	G	T	0.212	PTPN11	Missense	p.G60V
PD10857a	12	112888163	112888163	G	T	0.364	PTPN11	Missense	p.G60V
PD10827a	12	112888163	112888163	G	T	0.423	PTPN11	Missense	p.G60V
PD8491a	12	112888165	112888165	G	A	0.299	PTPN11	Missense	p.D61N
PD10844a	12	112888165	112888165	G	A	0.343	PTPN11	Missense	p.D61N
PD11093a	12	112888165	112888165	G	C	0.056	PTPN11	Missense	p.D61H
PD11206a	12	112888165	112888165	G	C	0.361	PTPN11	Missense	p.D61H
PD7939a	12	112888165	112888165	G	C	0.398	PTPN11	Missense	p.D61H
PD8012a	12	112888165	112888165	G	T	0.484	PTPN11	Missense	p.D61Y
PD10831a	12	112888165	112888165	G	T	0.488	PTPN11	Missense	p.D61Y
PD8568a	12	112888166	112888166	A	G	0.39	PTPN11	Missense	p.D61G
PD11038a	12	112888166	112888166	A	T	0.0903	PTPN11	Missense	p.D61V
PD9377a	12	112888166	112888166	A	T	0.092	PTPN11	Missense	p.D61V
PD8544a	12	112888166	112888166	A	T	0.101	PTPN11	Missense	p.D61V
PD7924a	12	112888166	112888166	A	T	0.348	PTPN11	Missense	p.D61V
PD7855a	12	112888166	112888166	A	T	0.471	PTPN11	Missense	p.D61V
PD8012a	12	112888166	112888166	A	T	0.496	PTPN11	Missense	p.D61V
PD7889a	12	112888168	112888168	T	G	0.0667	PTPN11	Missense	p.Y62D
PD8495a	12	112888189	112888189	G	A	0.0634	PTPN11	Missense	p.E69K
PD7672a	12	112888189	112888189	G	A	0.14	PTPN11	Missense	p.E69K
PD8192a	12	112888189	112888189	G	A	0.229	PTPN11	Missense	p.E69K
PD11022a	12	112888195	112888195	T	C	0.0744	PTPN11	Missense	p.F71L
PD8184a	12	112888197	112888197	T	A	0.153	PTPN11	Missense	p.F71L
PD11236a	12	112888198	112888198	G	A	0.0541	PTPN11	Missense	p.A72T
PD9307a	12	112888198	112888198	G	A	0.0746	PTPN11	Missense	p.A72T
PD11139a	12	112888198	112888198	G	A	0.143	PTPN11	Missense	p.A72T
PD8005a	12	112888198	112888198	G	A	0.178	PTPN11	Missense	p.A72T
PD11159a	12	112888198	112888198	G	A	0.194	PTPN11	Missense	p.A72T
PD8256a	12	112888198	112888198	G	A	0.198	PTPN11	Missense	p.A72T
PD8096a	12	112888198	112888198	G	A	0.29	PTPN11	Missense	p.A72T
PD7946a	12	112888198	112888198	G	A	0.376	PTPN11	Missense	p.A72T
PD11133a	12	112888199	112888199	C	A	0.373	PTPN11	Missense	p.A72D
PD8330a	12	112888199	112888199	C	A	0.471	PTPN11	Missense	p.A72D
PD8090a	12	112888199	112888199	C	G	0.125	PTPN11	Missense	p.A72G
PD11059a	12	112888199	112888199	C	G	0.202	PTPN11	Missense	p.A72G
PD9354a	12	112888199	112888199	C	T	0.0417	PTPN11	Missense	p.A72V
PD7662a	12	112888199	112888199	C	T	0.0868	PTPN11	Missense	p.A72V
PD8587a	12	112888199	112888199	C	T	0.0955	PTPN11	Missense	p.A72V
PD10807a	12	112888199	112888199	C	T	0.112	PTPN11	Missense	p.A72V
PD9237a	12	112888199	112888199	C	T	0.177	PTPN11	Missense	p.A72V
PD8427a	12	112888199	112888199	C	T	0.183	PTPN11	Missense	p.A72V
PD8409a	12	112888199	112888199	C	T	0.235	PTPN11	Missense	p.A72V
PD7936a	12	112888199	112888199	C	T	0.254	PTPN11	Missense	p.A72V
PD10885a	12	112888199	112888199	C	T	0.35	PTPN11	Missense	p.A72V
PD9350a	12	112888199	112888199	C	T	0.396	PTPN11	Missense	p.A72V

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7796a	12	112888199	112888199	C	T	0.4	PTPN11	Missense	p.A72V
PD9379a	12	112888210	112888210	G	A	0.0392	PTPN11	Missense	p.E76K
PD8014a	12	112888210	112888210	G	A	0.0476	PTPN11	Missense	p.E76K
PD8294a	12	112888210	112888210	G	A	0.0635	PTPN11	Missense	p.E76K
PD8225a	12	112888210	112888210	G	A	0.0833	PTPN11	Missense	p.E76K
PD9385a	12	112888210	112888210	G	A	0.105	PTPN11	Missense	p.E76K
PD8004a	12	112888210	112888210	G	A	0.249	PTPN11	Missense	p.E76K
PD10970a	12	112888210	112888210	G	A	0.294	PTPN11	Missense	p.E76K
PD8236a	12	112888210	112888210	G	A	0.365	PTPN11	Missense	p.E76K
PD9209a	12	112888210	112888210	G	A	0.443	PTPN11	Missense	p.E76K
PD11169a	12	112888210	112888210	G	A	0.443	PTPN11	Missense	p.E76K
PD7767a	12	112888210	112888210	G	A	0.478	PTPN11	Missense	p.E76K
PD11031a	12	112888210	112888210	G	C	0.497	PTPN11	Missense	p.E76Q
PD11247a	12	112888211	112888211	A	C	0.161	PTPN11	Missense	p.E76A
PD11128a	12	112888211	112888211	A	C	0.285	PTPN11	Missense	p.E76A
PD8446a	12	112888211	112888211	A	C	0.317	PTPN11	Missense	p.E76A
PD9259a	12	112888211	112888211	A	G	0.0242	PTPN11	Missense	p.E76G
PD8370a	12	112888211	112888211	A	G	0.0314	PTPN11	Missense	p.E76G
PD8124a	12	112888211	112888211	A	G	0.086	PTPN11	Missense	p.E76G
PD10923a	12	112888211	112888211	A	G	0.209	PTPN11	Missense	p.E76G
PD10997a	12	112888211	112888211	A	G	0.239	PTPN11	Missense	p.E76G
PD8271a	12	112888211	112888211	A	G	0.347	PTPN11	Missense	p.E76G
PD11097a	12	112888211	112888211	A	G	0.403	PTPN11	Missense	p.E76G
PD8196a	12	112888211	112888211	A	G	0.47	PTPN11	Missense	p.E76G
PD7752a	12	112888211	112888211	A	T	0.0913	PTPN11	Missense	p.E76V
PD11047a	12	112888220	112888220	A	G	0.0874	PTPN11	Missense	p.Q79R
PD7803a	12	112888220	112888220	A	G	0.34	PTPN11	Missense	p.Q79R
PD8512a	12	112888242	112888242	G	A	0.08	PTPN11	Synonymous	p.G86G
PD8313a	12	112888284	112888284	T	A	0.0824	PTPN11	Nonsense	p.Y100X
PD8571a	12	112891081	112891081	G	A	0.194	PTPN11	Missense	p.E139K
PD7672a	12	112891083	112891083	G	C	0.208	PTPN11	Missense	p.E139D
PD8512a	12	112891093	112891093	C	T	0.13	PTPN11	Missense	p.H143Y
PD8500a	12	112891143	112891143	G	A	0.179	PTPN11	Synonymous	p.E159E
PD8266a	12	112891152	112891152	C	T	0.424	PTPN11	Synonymous	p.D162D
PD8501a	12	112892385	112892385	T	G	0.0554	PTPN11	Synonymous	p.V181V
PD8493a	12	112892473	112892473	C	T	0.0779	PTPN11	Nonsense	p.Q211X
PD7648a	12	112910785	112910785	G	A	0.423	PTPN11	Missense	p.R265Q
PD8373a	12	112910809	112910809	A	G	0.524	PTPN11	Missense	p.N273S
PD8498a	12	112910818	112910818	A	G	0.0458	PTPN11	Missense	p.K276R
PD8291a	12	112910844	112910844	T	C	0.124	PTPN11	Missense	p.F285L
PD7873a	12	112915455	112915455	T	C	0.287	PTPN11	Missense	p.F285S
PD10973a	12	112915455	112915455	T	C	0.394	PTPN11	Missense	p.F285S
PD11195a	12	112915480	112915480	C	T	0.544	PTPN11	Synonymous	p.H293H
PD8242a	12	112915523	112915523	A	G	0.132	PTPN11	Missense	p.N308D
PD8082a	12	112915523	112915523	A	G	0.458	PTPN11	Missense	p.N308D
PD8078a	12	112915523	112915523	A	G	0.489	PTPN11	Missense	p.N308D
PD9294a	12	112915532	112915532	A	G	0.455	PTPN11	Missense	p.M311V
PD8475a	12	112919946	112919946	C	T	0.49	PTPN11	Synonymous	p.N387N
PD8155a	12	112919947	112919947	G	A	0.455	PTPN11	Missense	p.V388I
PD9311a	12	112924363	112924363	G	A	0.114	PTPN11	Missense	p.D437N
PD8280a	12	112924416	112924416	G	A	0.146	PTPN11	Synonymous	p.P454P
PD9377a	12	112926249	112926249	C	G	0.346	PTPN11	Missense	p.A461G
PD8557a	12	112926249	112926249	C	G	0.445	PTPN11	Missense	p.A461G
PD7634a	12	112926258	112926258	G	A	0.289	PTPN11	Missense	p.G464D
PD11123a	12	112926265	112926265	A	G	0.422	PTPN11	Synonymous	p.T466T
PD8440a	12	112926315	112926315	G	A	0.0319	PTPN11	Splice site	c.1459+1G>A
PD9291a	12	112926852	112926852	C	T	0.0233	PTPN11	Missense	p.P491L
PD8472a	12	112926852	112926852	C	T	0.122	PTPN11	Missense	p.P491L
PD7923a	12	112926852	112926852	C	T	0.134	PTPN11	Missense	p.P491L
PD9302a	12	112926852	112926852	C	T	0.281	PTPN11	Missense	p.P491L
PD11010a	12	112926852	112926852	C	T	0.358	PTPN11	Missense	p.P491L
PD9386a	12	112926884	112926884	T	C	0.287	PTPN11	Missense	p.S502P

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8332a	12	112926884	112926884	T	C	0.415	PTPN11	Missense	p.S502P
PD10833a	12	112926884	112926884	T	G	0.261	PTPN11	Missense	p.S502A
PD11125a	12	112926884	112926884	T	G	0.321	PTPN11	Missense	p.S502A
PD9221a	12	112926885	112926885	C	T	0.0226	PTPN11	Missense	p.S502L
PD8328a	12	112926885	112926885	C	T	0.0305	PTPN11	Missense	p.S502L
PD7903a	12	112926885	112926885	C	T	0.0348	PTPN11	Missense	p.S502L
PD11072a	12	112926885	112926885	C	T	0.0359	PTPN11	Missense	p.S502L
PD8048a	12	112926885	112926885	C	T	0.0366	PTPN11	Missense	p.S502L
PD7837a	12	112926885	112926885	C	T	0.144	PTPN11	Missense	p.S502L
PD11199a	12	112926885	112926885	C	T	0.188	PTPN11	Missense	p.S502L
PD11113a	12	112926885	112926885	C	T	0.23	PTPN11	Missense	p.S502L
PD7927a	12	112926885	112926885	C	T	0.282	PTPN11	Missense	p.S502L
PD9358a	12	112926885	112926885	C	T	0.382	PTPN11	Missense	p.S502L
PD8213a	12	112926885	112926885	C	T	0.434	PTPN11	Missense	p.S502L
PD9213a	12	112926885	112926885	C	T	0.449	PTPN11	Missense	p.S502L
PD7986a	12	112926887	112926887	G	A	0.367	PTPN11	Missense	p.G503R
PD7730a	12	112926888	112926888	G	A	0.0771	PTPN11	Missense	p.G503E
PD11072a	12	112926888	112926888	G	C	0.0583	PTPN11	Missense	p.G503A
PD8225a	12	112926888	112926888	G	C	0.109	PTPN11	Missense	p.G503A
PD10805a	12	112926888	112926888	G	C	0.444	PTPN11	Missense	p.G503A
PD7947a	12	112926888	112926888	G	C	0.451	PTPN11	Missense	p.G503A
PD8038a	12	112926888	112926888	G	T	0.05	PTPN11	Missense	p.G503V
PD8389a	12	112926888	112926888	G	T	0.0517	PTPN11	Missense	p.G503V
PD8370a	12	112926888	112926888	G	T	0.067	PTPN11	Missense	p.G503V
PD8173a	12	112926888	112926888	G	T	0.158	PTPN11	Missense	p.G503V
PD7744a	12	112926888	112926888	G	T	0.16	PTPN11	Missense	p.G503V
PD7683a	12	112926888	112926888	G	T	0.17	PTPN11	Missense	p.G503V
PD8439a	12	112926888	112926888	G	T	0.378	PTPN11	Missense	p.G503V
PD9239a	12	112926900	112926900	C	A	0.121	PTPN11	Missense	p.T507K
PD8004a	12	112926910	112926910	G	C	0.126	PTPN11	Missense	p.Q510H
PD8251a	12	112926910	112926910	G	C	0.291	PTPN11	Missense	p.Q510H
PD7991a	12	112926910	112926910	G	T	0.203	PTPN11	Missense	p.Q510H
PD9312a	12	112926973	112926973	A	G	0.0281	PTPN11	Synonymous	p.E531E
PD9300a	12	112939965	112939965	G	A	0.0884	PTPN11	Synonymous	p.G539G
PD7643a	12	112940006	112940006	C	T	0.513	PTPN11	Missense	p.T553M
PD8451a	12	112942532	112942532	C	T	0.464	PTPN11	Synonymous	p.N582N
PD11273a	15	90631837	90631837	C	A	0.08	IDH2	Missense	p.R172S
PD11234a	15	90631838	90631838	C	T	0.0889	IDH2	Missense	p.R172K
PD11278a	15	90631838	90631838	C	T	0.0938	IDH2	Missense	p.R172K
PD8062a	15	90631838	90631838	C	T	0.125	IDH2	Missense	p.R172K
PD7743a	15	90631838	90631838	C	T	0.2	IDH2	Missense	p.R172K
PD11269a	15	90631838	90631838	C	T	0.211	IDH2	Missense	p.R172K
PD8343a	15	90631838	90631838	C	T	0.217	IDH2	Missense	p.R172K
PD10901a	15	90631838	90631838	C	T	0.231	IDH2	Missense	p.R172K
PD7741a	15	90631838	90631838	C	T	0.25	IDH2	Missense	p.R172K
PD8161a	15	90631838	90631838	C	T	0.25	IDH2	Missense	p.R172K
PD11166a	15	90631838	90631838	C	T	0.261	IDH2	Missense	p.R172K
PD9201a	15	90631838	90631838	C	T	0.278	IDH2	Missense	p.R172K
PD7720a	15	90631838	90631838	C	T	0.312	IDH2	Missense	p.R172K
PD11014a	15	90631838	90631838	C	T	0.317	IDH2	Missense	p.R172K
PD11131a	15	90631838	90631838	C	T	0.326	IDH2	Missense	p.R172K
PD10882a	15	90631838	90631838	C	T	0.347	IDH2	Missense	p.R172K
PD11004a	15	90631838	90631838	C	T	0.356	IDH2	Missense	p.R172K
PD8214a	15	90631838	90631838	C	T	0.357	IDH2	Missense	p.R172K
PD7907a	15	90631838	90631838	C	T	0.366	IDH2	Missense	p.R172K
PD7885a	15	90631838	90631838	C	T	0.385	IDH2	Missense	p.R172K
PD10839a	15	90631838	90631838	C	T	0.387	IDH2	Missense	p.R172K
PD7850a	15	90631838	90631838	C	T	0.393	IDH2	Missense	p.R172K
PD8364a	15	90631838	90631838	C	T	0.407	IDH2	Missense	p.R172K
PD11253a	15	90631838	90631838	C	T	0.412	IDH2	Missense	p.R172K
PD10992a	15	90631838	90631838	C	T	0.421	IDH2	Missense	p.R172K
PD10965a	15	90631838	90631838	C	T	0.447	IDH2	Missense	p.R172K

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11035a	15	90631838	90631838	C	T	0.452	IDH2	Missense	p.R172K
PD7913a	15	90631838	90631838	C	T	0.467	IDH2	Missense	p.R172K
PD7976a	15	90631838	90631838	C	T	0.475	IDH2	Missense	p.R172K
PD8040a	15	90631838	90631838	C	T	0.486	IDH2	Missense	p.R172K
PD10810a	15	90631838	90631838	C	T	0.487	IDH2	Missense	p.R172K
PD9316a	15	90631838	90631838	C	T	0.489	IDH2	Missense	p.R172K
PD10816a	15	90631838	90631838	C	T	0.5	IDH2	Missense	p.R172K
PD10941a	15	90631838	90631838	C	T	0.5	IDH2	Missense	p.R172K
PD11003a	15	90631838	90631838	C	T	0.5	IDH2	Missense	p.R172K
PD11144a	15	90631838	90631838	C	T	0.512	IDH2	Missense	p.R172K
PD10849a	15	90631838	90631838	C	T	0.596	IDH2	Missense	p.R172K
PD8252a	15	90631838	90631838	C	T	0.596	IDH2	Missense	p.R172K
PD8147a	15	90631838	90631838	C	T	0.625	IDH2	Missense	p.R172K
PD11074a	15	90631838	90631838	C	T	0.633	IDH2	Missense	p.R172K
PD8295a	15	90631839	90631839	T	A	0.268	IDH2	Missense	p.R172W
PD8244a	15	90631934	90631934	C	T	0.0488	IDH2	Missense	p.R140Q
PD7715a	15	90631934	90631934	C	T	0.0645	IDH2	Missense	p.R140Q
PD8472a	15	90631934	90631934	C	T	0.0722	IDH2	Missense	p.R140Q
PD10843a	15	90631934	90631934	C	T	0.082	IDH2	Missense	p.R140Q
PD11057a	15	90631934	90631934	C	T	0.0952	IDH2	Missense	p.R140Q
PD10825a	15	90631934	90631934	C	T	0.106	IDH2	Missense	p.R140Q
PD11236a	15	90631934	90631934	C	T	0.129	IDH2	Missense	p.R140Q
PD10974a	15	90631934	90631934	C	T	0.148	IDH2	Missense	p.R140Q
PD8412a	15	90631934	90631934	C	T	0.156	IDH2	Missense	p.R140Q
PD11029a	15	90631934	90631934	C	T	0.16	IDH2	Missense	p.R140Q
PD8091a	15	90631934	90631934	C	T	0.161	IDH2	Missense	p.R140Q
PD8187a	15	90631934	90631934	C	T	0.162	IDH2	Missense	p.R140Q
PD10918a	15	90631934	90631934	C	T	0.176	IDH2	Missense	p.R140Q
PD10897a	15	90631934	90631934	C	T	0.213	IDH2	Missense	p.R140Q
PD10954a	15	90631934	90631934	C	T	0.219	IDH2	Missense	p.R140Q
PD9220a	15	90631934	90631934	C	T	0.227	IDH2	Missense	p.R140Q
PD8441a	15	90631934	90631934	C	T	0.234	IDH2	Missense	p.R140Q
PD8193a	15	90631934	90631934	C	T	0.235	IDH2	Missense	p.R140Q
PD11184a	15	90631934	90631934	C	T	0.25	IDH2	Missense	p.R140Q
PD8282a	15	90631934	90631934	C	T	0.25	IDH2	Missense	p.R140Q
PD7631a	15	90631934	90631934	C	T	0.25	IDH2	Missense	p.R140Q
PD8307a	15	90631934	90631934	C	T	0.259	IDH2	Missense	p.R140Q
PD9254a	15	90631934	90631934	C	T	0.26	IDH2	Missense	p.R140Q
PD8424a	15	90631934	90631934	C	T	0.278	IDH2	Missense	p.R140Q
PD9253a	15	90631934	90631934	C	T	0.286	IDH2	Missense	p.R140Q
PD8060a	15	90631934	90631934	C	T	0.293	IDH2	Missense	p.R140Q
PD11268a	15	90631934	90631934	C	T	0.296	IDH2	Missense	p.R140Q
PD8015a	15	90631934	90631934	C	T	0.304	IDH2	Missense	p.R140Q
PD9248a	15	90631934	90631934	C	T	0.314	IDH2	Missense	p.R140Q
PD8153a	15	90631934	90631934	C	T	0.318	IDH2	Missense	p.R140Q
PD8473a	15	90631934	90631934	C	T	0.318	IDH2	Missense	p.R140Q
PD11094a	15	90631934	90631934	C	T	0.32	IDH2	Missense	p.R140Q
PD8317a	15	90631934	90631934	C	T	0.328	IDH2	Missense	p.R140Q
PD7670a	15	90631934	90631934	C	T	0.333	IDH2	Missense	p.R140Q
PD8057a	15	90631934	90631934	C	T	0.339	IDH2	Missense	p.R140Q
PD10872a	15	90631934	90631934	C	T	0.342	IDH2	Missense	p.R140Q
PD8218a	15	90631934	90631934	C	T	0.342	IDH2	Missense	p.R140Q
PD8241a	15	90631934	90631934	C	T	0.343	IDH2	Missense	p.R140Q
PD11231a	15	90631934	90631934	C	T	0.35	IDH2	Missense	p.R140Q
PD11114a	15	90631934	90631934	C	T	0.364	IDH2	Missense	p.R140Q
PD8228a	15	90631934	90631934	C	T	0.364	IDH2	Missense	p.R140Q
PD10939a	15	90631934	90631934	C	T	0.365	IDH2	Missense	p.R140Q
PD9340a	15	90631934	90631934	C	T	0.365	IDH2	Missense	p.R140Q
PD11244a	15	90631934	90631934	C	T	0.375	IDH2	Missense	p.R140Q
PD7824a	15	90631934	90631934	C	T	0.377	IDH2	Missense	p.R140Q
PD10820a	15	90631934	90631934	C	T	0.379	IDH2	Missense	p.R140Q
PD11226a	15	90631934	90631934	C	T	0.381	IDH2	Missense	p.R140Q

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8291a	15	90631934	90631934	C	T	0.394	IDH2	Missense	p.R140Q
PD8506a	15	90631934	90631934	C	T	0.4	IDH2	Missense	p.R140Q
PD11122a	15	90631934	90631934	C	T	0.407	IDH2	Missense	p.R140Q
PD11190a	15	90631934	90631934	C	T	0.419	IDH2	Missense	p.R140Q
PD7946a	15	90631934	90631934	C	T	0.42	IDH2	Missense	p.R140Q
PD11145a	15	90631934	90631934	C	T	0.421	IDH2	Missense	p.R140Q
PD8118a	15	90631934	90631934	C	T	0.424	IDH2	Missense	p.R140Q
PD10973a	15	90631934	90631934	C	T	0.425	IDH2	Missense	p.R140Q
PD10905a	15	90631934	90631934	C	T	0.426	IDH2	Missense	p.R140Q
PD10997a	15	90631934	90631934	C	T	0.437	IDH2	Missense	p.R140Q
PD11176a	15	90631934	90631934	C	T	0.437	IDH2	Missense	p.R140Q
PD7621a	15	90631934	90631934	C	T	0.441	IDH2	Missense	p.R140Q
PD7781a	15	90631934	90631934	C	T	0.443	IDH2	Missense	p.R140Q
PD7982a	15	90631934	90631934	C	T	0.444	IDH2	Missense	p.R140Q
PD10988a	15	90631934	90631934	C	T	0.444	IDH2	Missense	p.R140Q
PD11024a	15	90631934	90631934	C	T	0.452	IDH2	Missense	p.R140Q
PD8550a	15	90631934	90631934	C	T	0.452	IDH2	Missense	p.R140Q
PD9239a	15	90631934	90631934	C	T	0.455	IDH2	Missense	p.R140Q
PD10999a	15	90631934	90631934	C	T	0.455	IDH2	Missense	p.R140Q
PD7977a	15	90631934	90631934	C	T	0.455	IDH2	Missense	p.R140Q
PD9292a	15	90631934	90631934	C	T	0.458	IDH2	Missense	p.R140Q
PD7956a	15	90631934	90631934	C	T	0.463	IDH2	Missense	p.R140Q
PD8578a	15	90631934	90631934	C	T	0.464	IDH2	Missense	p.R140Q
PD11216a	15	90631934	90631934	C	T	0.467	IDH2	Missense	p.R140Q
PD11186a	15	90631934	90631934	C	T	0.467	IDH2	Missense	p.R140Q
PD7643a	15	90631934	90631934	C	T	0.468	IDH2	Missense	p.R140Q
PD8079a	15	90631934	90631934	C	T	0.475	IDH2	Missense	p.R140Q
PD9249a	15	90631934	90631934	C	T	0.48	IDH2	Missense	p.R140Q
PD8044a	15	90631934	90631934	C	T	0.481	IDH2	Missense	p.R140Q
PD8494a	15	90631934	90631934	C	T	0.484	IDH2	Missense	p.R140Q
PD8253a	15	90631934	90631934	C	T	0.485	IDH2	Missense	p.R140Q
PD8131a	15	90631934	90631934	C	T	0.486	IDH2	Missense	p.R140Q
PD9268a	15	90631934	90631934	C	T	0.488	IDH2	Missense	p.R140Q
PD11170a	15	90631934	90631934	C	T	0.489	IDH2	Missense	p.R140Q
PD8172a	15	90631934	90631934	C	T	0.489	IDH2	Missense	p.R140Q
PD11117a	15	90631934	90631934	C	T	0.5	IDH2	Missense	p.R140Q
PD7988a	15	90631934	90631934	C	T	0.5	IDH2	Missense	p.R140Q
PD8023a	15	90631934	90631934	C	T	0.5	IDH2	Missense	p.R140Q
PD8328a	15	90631934	90631934	C	T	0.5	IDH2	Missense	p.R140Q
PD8219a	15	90631934	90631934	C	T	0.51	IDH2	Missense	p.R140Q
PD7909a	15	90631934	90631934	C	T	0.513	IDH2	Missense	p.R140Q
PD7739a	15	90631934	90631934	C	T	0.514	IDH2	Missense	p.R140Q
PD8583a	15	90631934	90631934	C	T	0.515	IDH2	Missense	p.R140Q
PD11276a	15	90631934	90631934	C	T	0.517	IDH2	Missense	p.R140Q
PD8176a	15	90631934	90631934	C	T	0.529	IDH2	Missense	p.R140Q
PD10983a	15	90631934	90631934	C	T	0.531	IDH2	Missense	p.R140Q
PD8185a	15	90631934	90631934	C	T	0.532	IDH2	Missense	p.R140Q
PD8112a	15	90631934	90631934	C	T	0.537	IDH2	Missense	p.R140Q
PD9350a	15	90631934	90631934	C	T	0.538	IDH2	Missense	p.R140Q
PD8052a	15	90631934	90631934	C	T	0.541	IDH2	Missense	p.R140Q
PD11261a	15	90631934	90631934	C	T	0.545	IDH2	Missense	p.R140Q
PD10891a	15	90631934	90631934	C	T	0.55	IDH2	Missense	p.R140Q
PD8376a	15	90631934	90631934	C	T	0.55	IDH2	Missense	p.R140Q
PD11134a	15	90631934	90631934	C	T	0.56	IDH2	Missense	p.R140Q
PD10966a	15	90631934	90631934	C	T	0.568	IDH2	Missense	p.R140Q
PD8144a	15	90631934	90631934	C	T	0.578	IDH2	Missense	p.R140Q
PD11229a	15	90631934	90631934	C	T	0.583	IDH2	Missense	p.R140Q
PD7981a	15	90631934	90631934	C	T	0.588	IDH2	Missense	p.R140Q
PD11054a	15	90631934	90631934	C	T	0.595	IDH2	Missense	p.R140Q
PD11159a	15	90631934	90631934	C	T	0.6	IDH2	Missense	p.R140Q
PD7942a	15	90631934	90631934	C	T	0.629	IDH2	Missense	p.R140Q
PD8008a	15	90631934	90631934	C	T	0.629	IDH2	Missense	p.R140Q

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11162a	15	90631934	90631934	C	T	0.63	IDH2	Missense	p.R140Q
PD11032a	15	90631934	90631934	C	T	0.643	IDH2	Missense	p.R140Q
PD8554a	15	90631934	90631934	C	T	0.857	IDH2	Missense	p.R140Q
PD8571a	15	90631935	90631935	G	A	0.556	IDH2	Missense	p.R140W
PD9307a	15	90631935	90631935	G	C	0.367	IDH2	Missense	p.R140G
PD11144a	15	90631946	90631946	T	C	0.237	IDH2	Missense	p.N136S
PD11020a	17	7572954	7572955	GA	G	0.524	TP53	Frameshift	p.F346fs
PD8472a	17	7573005	7573005	G	A	0.0237	TP53	Synonymous	p.H329H
PD7740a	17	7573931	7573931	A	C	0.459	TP53	Missense	p.S327A
PD11258a	17	7573973	7573973	C	T	0.085	TP53	Missense	p.D313N
PD9227a	17	7574003	7574003	G	A	0.439	TP53	Nonsense	p.R303X
PD8552a	17	7574004	7574004	G	GA	0.252	TP53	Frameshift	p.F302fs
PD8310a	17	7574034	7574034	C	T	0.875	TP53	Splice site	c.731-1G>A
PD11169a	17	7576852	7576852	C	T	0.899	TP53	Splice site	c.597+1G>A
PD9227a	17	7576928	7576928	T	C	0.0135	TP53	Splice site	c.524-2A>G
PD9384a	17	7577055	7577055	G	A	0.186	TP53	Missense	p.P256S
PD7867a	17	7577090	7577090	C	T	0.486	TP53	Missense	p.R244H
PD9258a	17	7577091	7577091	G	A	0.377	TP53	Missense	p.R244C
PD10826a	17	7577091	7577091	G	A	0.464	TP53	Missense	p.R244C
PD10965a	17	7577091	7577091	G	A	0.523	TP53	Missense	p.R244C
PD11020a	17	7577094	7577094	G	A	0.386	TP53	Missense	p.R243W
PD11194a	17	7577097	7577097	C	T	0.891	TP53	Missense	p.D242N
PD9355a	17	7577106	7577106	G	A	0.271	TP53	Missense	p.P239S
PD9260a	17	7577112	7577112	C	G	0.0549	TP53	Missense	p.A237P
PD8333a	17	7577114	7577114	C	T	0.86	TP53	Missense	p.C236Y
PD7836a	17	7577115	7577115	A	G	0.343	TP53	Missense	p.C236R
PD8418a	17	7577120	7577120	C	T	0.0886	TP53	Missense	p.R234H
PD7717a	17	7577120	7577120	C	T	0.382	TP53	Missense	p.R234H
PD11226a	17	7577120	7577120	C	T	0.804	TP53	Missense	p.R234H
PD8189a	17	7577121	7577121	G	A	0.133	TP53	Missense	p.R234C
PD8312a	17	7577121	7577121	G	A	0.693	TP53	Missense	p.R234C
PD11200a	17	7577121	7577121	G	A	0.75	TP53	Missense	p.R234C
PD11012a	17	7577121	7577121	G	A	0.907	TP53	Missense	p.R234C
PD7806a	17	7577124	7577124	C	T	0.147	TP53	Missense	p.V233M
PD7829a	17	7577124	7577124	C	T	0.356	TP53	Missense	p.V233M
PD11135a	17	7577130	7577130	A	G	0.0588	TP53	Missense	p.F231L
PD7814a	17	7577138	7577138	C	G	0.257	TP53	Missense	p.R228P
PD9237a	17	7577139	7577139	G	A	0.467	TP53	Missense	p.R228W
PD9227a	17	7577142	7577142	C	G	0.447	TP53	Missense	p.G227R
PD7752a	17	7577144	7577144	A	G	0.903	TP53	Missense	p.L226P
PD10831a	17	7577148	7577148	G	GGACCAGGGGGAG	0.609	TP53	Inframe	p.N224delinsNSPWS
PD11178a	17	7577153	7577153	C	A	0.426	TP53	Missense	p.G223V
PD8145a	17	7577508	7577508	T	G	0.23	TP53	Missense	p.E219A
PD7682a	17	7577521	7577521	T	C	0.528	TP53	Missense	p.I215V
PD9283a	17	7577529	7577529	A	C	0.145	TP53	Missense	p.I212S
PD10808a	17	7577534	7577534	C	A	0.442	TP53	Missense	p.R210S
PD9260a	17	7577538	7577538	C	T	0.13	TP53	Missense	p.R209Q
PD9230a	17	7577538	7577538	C	T	0.772	TP53	Missense	p.R209Q
PD11085a	17	7577538	7577538	C	T	0.775	TP53	Missense	p.R209Q
PD11068a	17	7577538	7577538	C	T	0.782	TP53	Missense	p.R209Q
PD10963a	17	7577538	7577538	C	T	0.849	TP53	Missense	p.R209Q
PD8227a	17	7577538	7577538	C	T	0.876	TP53	Missense	p.R209Q
PD8537a	17	7577538	7577538	C	T	0.938	TP53	Missense	p.R209Q
PD11026a	17	7577539	7577539	G	A	0.0293	TP53	Missense	p.R209W
PD10931a	17	7577539	7577539	G	A	0.466	TP53	Missense	p.R209W
PD8099a	17	7577539	7577539	G	A	0.622	TP53	Missense	p.R209W
PD11015a	17	7577547	7577547	C	T	0.226	TP53	Missense	p.G206D
PD11288a	17	7577547	7577547	C	T	0.528	TP53	Missense	p.G206D
PD11138a	17	7577556	7577556	C	G	0.295	TP53	Missense	p.C203S
PD7795a	17	7577559	7577559	G	A	0.0645	TP53	Missense	p.S202F

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10990a	17	7577559	7577559	G	A	0.0829	TP53	Missense	p.S202F
PD7931a	17	7577559	7577559	G	A	0.717	TP53	Missense	p.S202F
PD7744a	17	7577559	7577559	G	A	0.838	TP53	Missense	p.S202F
PD7869a	17	7577559	7577559	G	T	0.688	TP53	Missense	p.S202Y
PD8227a	17	7577565	7577565	T	C	0.0287	TP53	Missense	p.N200S
PD11223a	17	7577566	7577566	T	C	0.554	TP53	Missense	p.N200D
PD11175a	17	7577566	7577566	T	C	0.937	TP53	Missense	p.N200D
PD9217a	17	7577568	7577568	C	T	0.961	TP53	Missense	p.C199Y
PD11168a	17	7577570	7577570	C	T	0.155	TP53	Missense	p.M198I
PD7966a	17	7577570	7577570	C	T	0.735	TP53	Missense	p.M198I
PD8054a	17	7577570	7577570	C	T	0.78	TP53	Missense	p.M198I
PD11056a	17	7577571	7577571	A	T	0.957	TP53	Missense	p.M198K
PD8311a	17	7577577	7577577	T	C	0.66	TP53	Missense	p.N196S
PD8319a	17	7577577	7577577	T	C	0.824	TP53	Missense	p.N196S
PD8485a	17	7577580	7577580	T	C	0.689	TP53	Missense	p.Y195C
PD10919a	17	7578182	7578182	G	A	0.043	TP53	Missense	p.P184S
PD8577a	17	7578190	7578190	T	C	0.312	TP53	Missense	p.Y181C
PD11044a	17	7578190	7578190	T	C	0.337	TP53	Missense	p.Y181C
PD9270a	17	7578190	7578190	T	C	0.412	TP53	Missense	p.Y181C
PD11257a	17	7578190	7578190	T	C	0.64	TP53	Missense	p.Y181C
PD11154a	17	7578190	7578190	T	C	0.727	TP53	Missense	p.Y181C
PD9211a	17	7578191	7578191	A	G	0.64	TP53	Missense	p.Y181H
PD8440a	17	7578196	7578196	A	C	0.333	TP53	Missense	p.V179G
PD11066a	17	7578204	7578204	A	C	0.116	TP53	Missense	p.S176R
PD11213a	17	7578204	7578204	A	C	0.285	TP53	Missense	p.S176R
PD10856a	17	7578206	7578206	T	C	0.0176	TP53	Missense	p.S176G
PD11257a	17	7578208	7578208	T	C	0.0751	TP53	Missense	p.H175R
PD8018a	17	7578211	7578211	C	T	0.023	TP53	Missense	p.R174Q
PD11143a	17	7578212	7578212	G	A	0.873	TP53	Nonsense	p.R174X
PD8390a	17	7578236	7578236	A	C	0.0991	TP53	Missense	p.Y166D
PD9260a	17	7578262	7578262	C	T	0.141	TP53	Missense	p.R157Q
PD11102a	17	7578265	7578265	A	T	0.495	TP53	Missense	p.I156N
PD9267a	17	7578266	7578266	T	A	0.86	TP53	Missense	p.I156F
PD9345a	17	7578266	7578267	TA	T	0.065	TP53	Frameshift	p.L155fs
PD11160a	17	7578272	7578272	G	T	0.693	TP53	Missense	p.H154N
PD11213a	17	7578290	7578290	C	T	0.201	TP53	Splice site	c.164-1G>A
PD11178a	17	7578368	7578377	CACCATCGCT	C	0.443	TP53	Frameshift	p.S146fs
PD11137a	17	7578394	7578394	T	C	0.876	TP53	Missense	p.H140R
PD10909a	17	7578403	7578403	C	A	0.702	TP53	Missense	p.C137F
PD11000a	17	7578404	7578404	A	T	0.774	TP53	Missense	p.C137S
PD8457a	17	7578406	7578406	C	T	0.15	TP53	Missense	p.R136H
PD9312a	17	7578406	7578406	C	T	0.229	TP53	Missense	p.R136H
PD9379a	17	7578406	7578406	C	T	0.282	TP53	Missense	p.R136H
PD9291a	17	7578406	7578406	C	T	0.695	TP53	Missense	p.R136H
PD9259a	17	7578406	7578406	C	T	0.727	TP53	Missense	p.R136H
PD10903a	17	7578406	7578406	C	T	0.771	TP53	Missense	p.R136H
PD8576a	17	7578406	7578406	C	T	0.914	TP53	Missense	p.R136H
PD9368a	17	7578413	7578413	C	A	0.887	TP53	Missense	p.V134L
PD8578a	17	7578427	7578427	T	G	0.943	TP53	Missense	p.H129P
PD9369a	17	7578433	7578433	G	GACTGCTTGT	0.333	TP53	Inframe	p.S127delinsTSSS
PD10840a	17	7578437	7578437	G	A	0.368	TP53	Nonsense	p.Q126X
PD7983a	17	7578437	7578437	G	A	0.915	TP53	Nonsense	p.Q126X
PD11168a	17	7578440	7578440	T	C	0.17	TP53	Missense	p.K125E
PD7698a	17	7578440	7578440	T	C	0.571	TP53	Missense	p.K125E
PD9216a	17	7578442	7578442	T	C	0.627	TP53	Missense	p.Y124C
PD7735a	17	7578442	7578442	T	C	0.968	TP53	Missense	p.Y124C
PD8548a	17	7578454	7578454	G	A	0.0526	TP53	Missense	p.A120V
PD11215a	17	7578457	7578458	CG	C	0.167	TP53	Frameshift	p.R119fs
PD9310a	17	7578457	7578457	C	G	0.0805	TP53	Missense	p.R119P
PD8557a	17	7578457	7578457	C	T	0.05	TP53	Missense	p.R119H
PD11153a	17	7578477	7578477	G	T	0.0339	TP53	Synonymous	p.P112P

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7924a	17	7578490	7578491	AC	A	0.881	TP53	Frameshift	p.V108fs
PD9355a	17	7578492	7578492	C	T	0.0268	TP53	Nonsense	p.W107X
PD11154a	17	7578492	7578492	C	T	0.0779	TP53	Nonsense	p.W107X
PD9309a	17	7578493	7578493	C	T	0.169	TP53	Nonsense	p.W107X
PD8280a	17	7578503	7578503	C	T	0.087	TP53	Missense	p.V104M
PD7711a	17	7578511	7578511	G	T	0.427	TP53	Missense	p.T101N
PD8496a	17	7578530	7578530	A	T	0.544	TP53	Missense	p.F95I
PD9260a	17	7578535	7578535	T	C	0.388	TP53	Missense	p.K93R
PD8122a	17	7578535	7578535	T	C	0.786	TP53	Missense	p.K93R
PD8560a	17	7578540	7578540	G	A	0.102	TP53	Synonymous	p.L91L
PD11030a	17	7578542	7578542	G	C	0.125	TP53	Missense	p.L91V
PD11277a	17	7578542	7578542	G	C	0.585	TP53	Missense	p.L91V
PD7949a	17	7578555	7578555	C	T	0.892	TP53	Splice site	c.259-1G>A
PD8026a	17	7578556	7578556	T	C	0.759	TP53	Splice site	c.259-2A>G
PD7762a	17	7579315	7579326	GCAAGTCACAGA	GTGGAGCC	0.176	TP53	Frameshift	c.244_254GGCTCCA
PD11247a	17	7579358	7579358	C	A	0.364	TP53	Missense	p.R71L
PD11264a	17	7579361	7579361	A	C	0.438	TP53	Missense	p.F70C
PD11215a	17	7579366	7579366	G	GT	0.19	TP53	Nonsense	p.Y68_G69delinsX
PD11168a	17	7579372	7579372	G	A	0.065	TP53	Synonymous	p.G66G
PD8484a	17	7579470	7579470	C	T	0.0718	TP53	Missense	p.V34M
PD8083a	17	7579527	7579527	A	G	0.161	TP53	Missense	p.F15L
PD7968a	17	7579528	7579528	C	T	0.966	TP53	Nonsense	p.W14X
PD11152a	17	7579533	7579533	G	A	0.839	TP53	Nonsense	p.Q13X
PD9220a	17	7579551	7579551	A	G	0.0516	TP53	Missense	p.S7P
PD7662a	17	7579882	7579882	C	T	0.518	TP53	Missense	p.E11K
PD11151a	17	7579888	7579888	T	C	0.147	TP53	Missense	p.S9G
PD7675a	17	74732406	74732406	C	T	0.148	SRSF2	Missense	p.R168K
PD11122a	17	74732471	74732471	G	A	0.507	SRSF2	Synonymous	p.R146R
PD7958a	17	74732959	74732959	G	A	0.25	SRSF2	Missense	p.P95L
PD8451a	17	74732959	74732959	G	A	0.444	SRSF2	Missense	p.P95L
PD10872a	17	74732959	74732959	G	A	0.688	SRSF2	Missense	p.P95L
PD11258a	17	74732959	74732959	G	C	0.136	SRSF2	Missense	p.P95R
PD7824a	17	74732959	74732959	G	C	0.312	SRSF2	Missense	p.P95R
PD11101a	17	74732959	74732959	G	C	0.412	SRSF2	Missense	p.P95R
PD10902a	17	74732959	74732959	G	C	0.471	SRSF2	Missense	p.P95R
PD11209a	17	74732959	74732959	G	C	0.5	SRSF2	Missense	p.P95R
PD11255a	17	74732959	74732959	G	C	0.571	SRSF2	Missense	p.P95R
PD10949a	17	74732959	74732959	G	T	0.267	SRSF2	Missense	p.P95H
PD11019a	17	74732959	74732959	G	T	0.3	SRSF2	Missense	p.P95H
PD8383a	17	74732959	74732959	G	T	0.3	SRSF2	Missense	p.P95H
PD7659a	17	74732959	74732959	G	T	0.312	SRSF2	Missense	p.P95H
PD9224a	17	74732959	74732959	G	T	0.333	SRSF2	Missense	p.P95H
PD7715a	17	74732959	74732959	G	T	0.333	SRSF2	Missense	p.P95H
PD8146a	17	74732959	74732959	G	T	0.462	SRSF2	Missense	p.P95H
PD9253a	17	74732959	74732959	G	T	0.5	SRSF2	Missense	p.P95H
PD8068a	17	74732959	74732959	G	T	0.533	SRSF2	Missense	p.P95H
PD8477a	17	74732959	74732959	G	T	0.591	SRSF2	Missense	p.P95H
PD11005a	17	74733073	74733073	A	T	0.25	SRSF2	Missense	p.F57Y
PD8426a	17	74733073	74733073	A	T	0.463	SRSF2	Missense	p.F57Y
PD11167a	20	30954269	30954269	G	A	0.0206	ASXL1	Missense	p.S47N
PD8533a	20	30956873	30956873	G	T	0.0625	ASXL1	Nonsense	p.G67X
PD8367a	20	31015932	31015932	A	G	0.49	ASXL1	Missense	p.K85R
PD9286a	20	31015963	31015964	TA	T	0.267	ASXL1	Frameshift	p.T96fs
PD9383a	20	31016036	31016036	A	G	0.37	ASXL1	Missense	p.S120G
PD8485a	20	31017142	31017142	C	T	0.51	ASXL1	Missense	p.A158V
PD11258a	20	31017161	31017161	G	A	0.0646	ASXL1	Synonymous	p.K164K
PD8488a	20	31017724	31017724	G	A	0.552	ASXL1	Missense	p.D196N
PD8280a	20	31017790	31017790	C	T	0.106	ASXL1	Missense	p.R218C
PD8502a	20	31019198	31019198	C	T	0.275	ASXL1	Missense	p.R265C
PD8145a	20	31019406	31019406	G	A	0.147	ASXL1	Synonymous	p.L301L
PD8560a	20	31019451	31019451	G	A	0.436	ASXL1	Synonymous	p.A316A

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11207a	20	31021163	31021163	G	A	0.345	ASXL1	Missense	p.V388I
PD8493a	20	31021172	31021172	G	A	0.286	ASXL1	Missense	p.E391K
PD11234a	20	31021215	31021215	A	T	0.543	ASXL1	Missense	p.D405V
PD9246a	20	31021219	31021219	G	A	0.306	ASXL1	Synonymous	p.G406G
PD7767a	20	31021250	31021250	C	T	0.427	ASXL1	Nonsense	p.R417X
PD11143a	20	31021260	31021260	C	T	0.116	ASXL1	Missense	p.A420V
PD8454a	20	31021283	31021283	C	T	0.208	ASXL1	Nonsense	p.Q428X
PD8502a	20	31021304	31021304	G	GG	0.062	ASXL1	Frameshift	p.V435fs
PD11264a	20	31021371	31021372	AC	A	0.388	ASXL1	Frameshift	p.D457fs
PD8473a	20	31021433	31021433	G	A	0.479	ASXL1	Missense	p.G478S
PD10862a	20	31021466	31021466	C	T	0.509	ASXL1	Missense	p.R489W
PD10996a	20	31021472	31021472	C	T	0.473	ASXL1	Nonsense	p.Q491X
PD7852a	20	31021542	31021544	CTG	C	0.243	ASXL1	Frameshift	p.T514fs
PD11143a	20	31021587	31021587	A	T	0.305	ASXL1	Missense	p.Q529L
PD7775a	20	31021590	31021590	C	T	0.5	ASXL1	Missense	p.A530V
PD9308a	20	31022264	31022264	G	A	0.46	ASXL1	Nonsense	p.W583X
PD11209a	20	31022277	31022277	C	T	0.461	ASXL1	Nonsense	p.Q588X
PD11153a	20	31022277	31022277	C	T	0.586	ASXL1	Nonsense	p.Q588X
PD9265a	20	31022284	31022284	C	CTT	0.381	ASXL1	Frameshift	p.T590fs
PD8334a	20	31022332	31022332	G	A	0.146	ASXL1	Missense	p.R606Q
PD9205a	20	31022341	31022342	CT	C	0.395	ASXL1	Frameshift	p.T609fs
PD8144a	20	31022346	31022346	G	A	0.596	ASXL1	Missense	p.A611T
PD11255a	20	31022366	31022366	T	TT	0.433	ASXL1	Frameshift	p.K618fs
PD8420a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.098	ASXL1	Frameshift	p.H630fs
PD8457a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.122	ASXL1	Frameshift	p.H630fs
PD9381a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.122	ASXL1	Frameshift	p.H630fs
PD8583a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.143	ASXL1	Frameshift	p.H630fs
PD9218a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.148	ASXL1	Frameshift	p.H630fs
PD8107a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.172	ASXL1	Frameshift	p.H630fs
PD11089a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.182	ASXL1	Frameshift	p.H630fs
PD10790a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.2	ASXL1	Frameshift	p.H630fs
PD8108a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.2	ASXL1	Frameshift	p.H630fs
PD11124a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.229	ASXL1	Frameshift	p.H630fs
PD8153a	20	31022402	31022425	TCACCA CTGCCA TAGAGA GGCGGC	T	0.273	ASXL1	Frameshift	p.H630fs
PD8112a	20	31022402	31022425	TCACCA CTGCCA	T	0.293	ASXL1	Frameshift	p.H630fs

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
				TAGAGAGGCGGC					
PD9210a	20	31022525	31022525	G	GCC	0.435	ASXL1	Frameshift	p.A671fs
PD9332a	20	31022575	31022575	G	GT	0.529	ASXL1	Frameshift	p.C687fs
PD7913a	20	31022592	31022592	C	T	0.0943	ASXL1	Nonsense	p.R693X
PD7715a	20	31022592	31022592	C	T	0.377	ASXL1	Nonsense	p.R693X
PD7846a	20	31022592	31022592	C	T	0.418	ASXL1	Nonsense	p.R693X
PD11027a	20	31022592	31022592	C	T	0.429	ASXL1	Nonsense	p.R693X
PD7857a	20	31022592	31022592	C	T	0.444	ASXL1	Nonsense	p.R693X
PD7942a	20	31022592	31022592	C	T	0.467	ASXL1	Nonsense	p.R693X
PD11147a	20	31022592	31022592	C	T	0.478	ASXL1	Nonsense	p.R693X
PD8068a	20	31022592	31022592	C	T	0.489	ASXL1	Nonsense	p.R693X
PD11183a	20	31022592	31022592	C	T	0.567	ASXL1	Nonsense	p.R693X
PD9365a	20	31022593	31022593	G	A	0.107	ASXL1	Missense	p.R693Q
PD8447a	20	31022600	31022600	A	AG	0.373	ASXL1	Frameshift	p.L696fs
PD8504a	20	31022646	31022646	A	G	0.46	ASXL1	Missense	p.T711A
PD11259a	20	31022661	31022662	GC	G	0.157	ASXL1	Frameshift	p.A716fs
PD11065a	20	31022736	31022737	GA	G	0.324	ASXL1	Frameshift	p.D741fs
PD8470a	20	31022741	31022741	G	A	0.0321	ASXL1	Synonymous	p.G742G
PD10946a	20	31022757	31022757	C	T	0.518	ASXL1	Nonsense	p.Q748X
PD8028a	20	31022760	31022760	C	T	0.0778	ASXL1	Missense	p.L749F
PD10915a	20	31022768	31022768	T	TG	0.061	ASXL1	Frameshift	p.A752fs
PD11181a	20	31022777	31022778	TG	T	0.11	ASXL1	Frameshift	p.G755fs
PD11268a	20	31022777	31022778	TG	T	0.265	ASXL1	Frameshift	p.G755fs
PD9197a	20	31022794	31022794	A	G	0.0611	ASXL1	Missense	p.Q760R
PD9282a	20	31022800	31022800	T	TT	0.315	ASXL1	Frameshift	p.L762fs
PD7859a	20	31022839	31022839	T	G	0.274	ASXL1	Nonsense	p.L775X
PD7986a	20	31022847	31022847	C	T	0.3	ASXL1	Nonsense	p.Q778X
PD7990a	20	31022872	31022872	G	A	0.5	ASXL1	Missense	p.R786K
PD7712a	20	31022875	31022875	C	A	0.46	ASXL1	Missense	p.T787N
PD8345a	20	31022895	31022899	ACTTC	A	0.479	ASXL1	Frameshift	p.T794fs
PD7691a	20	31022904	31022904	G	T	0.385	ASXL1	Nonsense	p.E797X
PD9230a	20	31022915	31022920	TGAGGA	T	0.316	ASXL1	Frameshift	p.E801fs
PD7686a	20	31022915	31022918	TGAG	T	0.378	ASXL1	Inframe	p.801_801del
PD8114a	20	31022936	31022937	TC	T	0.439	ASXL1	Frameshift	p.P808fs
PD8401a	20	31022938	31022938	C	A	0.462	ASXL1	Missense	p.P808H
PD9253a	20	31022938	31022938	C	A	0.576	ASXL1	Missense	p.P808H
PD11241a	20	31022987	31022988	GA	G	0.393	ASXL1	Frameshift	p.K825fs
PD11246a	20	31022988	31022988	A	T	0.462	ASXL1	Nonsense	p.K825X
PD11060a	20	31023000	31023000	C	T	0.158	ASXL1	Nonsense	p.Q829X
PD8419a	20	31023073	31023073	C	T	0.395	ASXL1	Missense	p.P853L
PD7634a	20	31023136	31023136	C	T	0.0638	ASXL1	Missense	p.P874L
PD8214a	20	31023208	31023208	G	A	0.471	ASXL1	Nonsense	p.W898X
PD11119a	20	31023294	31023294	G	T	0.417	ASXL1	Nonsense	p.G927X
PD8153a	20	31023335	31023335	G	A	0.47	ASXL1	Synonymous	p.L940L
PD8353a	20	31023359	31023359	G	A	0.385	ASXL1	Synonymous	p.E948E
PD8463a	20	31023395	31023395	G	A	0.351	ASXL1	Nonsense	p.W960X
PD9328a	20	31023401	31023401	G	A	0.0466	ASXL1	Synonymous	p.V962V
PD10949a	20	31023436	31023436	A	AA	0.259	ASXL1	Frameshift	p.Y974fs
PD8493a	20	31023460	31023460	A	AA	0.052	ASXL1	Frameshift	p.K982fs
PD8580a	20	31023510	31023510	A	C	0.442	ASXL1	Missense	p.T999P
PD9306a	20	31023569	31023569	T	A	0.0537	ASXL1	Synonymous	p.T1018T
PD8103a	20	31023694	31023694	T	A	0.121	ASXL1	Missense	p.V1060D
PD11259a	20	31023728	31023728	G	A	0.409	ASXL1	Synonymous	p.A1071A
PD8465a	20	31023783	31023783	A	T	0.0582	ASXL1	Nonsense	p.R1090X
PD7931a	20	31023866	31023866	C	A	0.414	ASXL1	Synonymous	p.P1117P
PD8558a	20	31023893	31023893	C	T	0.549	ASXL1	Synonymous	p.H1126H
PD9357a	20	31023916	31023916	C	T	0.404	ASXL1	Missense	p.P1134L
PD8442a	20	31023920	31023920	A	G	0.478	ASXL1	Synonymous	p.Q1135Q
PD8069a	20	31023957	31023957	C	T	0.329	ASXL1	Missense	p.R1148C
PD9365a	20	31024018	31024018	G	A	0.0787	ASXL1	Missense	p.S1168N
PD9234a	20	31024184	31024184	T	G	0.532	ASXL1	Synonymous	p.S1223S

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD9220a	20	31024239	31024239	G	A	0.0745	ASXL1	Missense	p.D1242N
PD11132a	20	31024308	31024308	G	T	0.482	ASXL1	Missense	p.D1265Y
PD8133a	20	31024384	31024384	C	T	0.325	ASXL1	Missense	p.A1290V
PD9306a	20	31024521	31024521	G	A	0.217	ASXL1	Missense	p.G1336R
PD9250a	20	31024661	31024661	C	G	0.543	ASXL1	Synonymous	p.A1382A
PD10895a	20	31024914	31024914	C	T	0.0629	ASXL1	Missense	p.L1467F
PD9330a	20	31024959	31024959	G	A	0.0784	ASXL1	Missense	p.A1482T
PD11271a	20	31025008	31025008	C	T	0.435	ASXL1	Missense	p.T1498M
PD8083a	20	31025102	31025102	A	T	0.229	ASXL1	Synonymous	p.G1529G
PD8298a	21	44513269	44513269	G	A	0.456	U2AF1	Synonymous	p.G222G
PD7795a	21	44514769	44514769	T	TCTCATA	0.062	U2AF1	Inframe	p.E159delinsDMR
PD7992a	21	44514777	44514777	T	C	0.404	U2AF1	Missense	p.Q157P
PD8084a	21	44514777	44514777	T	C	0.424	U2AF1	Missense	p.Q157P
PD8258a	21	44514777	44514777	T	C	0.433	U2AF1	Missense	p.Q157P
PD8415a	21	44514777	44514777	T	G	0.0519	U2AF1	Missense	p.Q157P
PD7986a	21	44514777	44514777	T	G	0.392	U2AF1	Missense	p.Q157P
PD8325a	21	44514777	44514777	T	G	0.4	U2AF1	Missense	p.Q157P
PD11241a	21	44514777	44514777	T	G	0.4	U2AF1	Missense	p.Q157P
PD11027a	21	44514777	44514777	T	G	0.485	U2AF1	Missense	p.Q157P
PD8143a	21	44514780	44514780	C	T	0.0323	U2AF1	Missense	p.R156H
PD7771a	21	44514780	44514780	C	T	0.0448	U2AF1	Missense	p.R156H
PD8586a	21	44514780	44514780	C	T	0.158	U2AF1	Missense	p.R156H
PD7831a	21	44514780	44514780	C	T	0.228	U2AF1	Missense	p.R156H
PD8358a	21	44514780	44514780	C	T	0.328	U2AF1	Missense	p.R156H
PD7942a	21	44514780	44514780	C	T	0.444	U2AF1	Missense	p.R156H
PD8228a	21	44514780	44514780	C	T	0.448	U2AF1	Missense	p.R156H
PD9283a	21	44514878	44514878	C	T	0.27	U2AF1	Synonymous	p.A123A
PD7756a	21	44520618	44520618	G	A	0.377	U2AF1	Synonymous	p.L48L
PD7756a	21	44521522	44521522	G	T	0.226	U2AF1	Synonymous	p.I51I
PD10846a	21	44524453	44524453	C	A	0.199	U2AF1	Missense	p.R35L
PD8061a	21	44524453	44524453	C	A	0.507	U2AF1	Missense	p.R35L
PD11257a	21	44524456	44524456	G	A	0.0274	U2AF1	Missense	p.S34F
PD8273a	21	44524456	44524456	G	A	0.125	U2AF1	Missense	p.S34F
PD11088a	21	44524456	44524456	G	A	0.271	U2AF1	Missense	p.S34F
PD8567a	21	44524456	44524456	G	A	0.272	U2AF1	Missense	p.S34F
PD9247a	21	44524456	44524456	G	A	0.286	U2AF1	Missense	p.S34F
PD10956a	21	44524456	44524456	G	A	0.343	U2AF1	Missense	p.S34F
PD7885a	21	44524456	44524456	G	A	0.358	U2AF1	Missense	p.S34F
PD8290a	21	44524456	44524456	G	A	0.363	U2AF1	Missense	p.S34F
PD9206a	21	44524456	44524456	G	A	0.397	U2AF1	Missense	p.S34F
PD11026a	21	44524456	44524456	G	A	0.401	U2AF1	Missense	p.S34F
PD11146a	21	44524456	44524456	G	A	0.402	U2AF1	Missense	p.S34F
PD10996a	21	44524456	44524456	G	A	0.429	U2AF1	Missense	p.S34F
PD10842a	21	44524456	44524456	G	A	0.434	U2AF1	Missense	p.S34F
PD8084a	21	44524456	44524456	G	A	0.435	U2AF1	Missense	p.S34F
PD8508a	21	44524456	44524456	G	A	0.435	U2AF1	Missense	p.S34F
PD10804a	21	44524456	44524456	G	A	0.444	U2AF1	Missense	p.S34F
PD7950a	21	44524456	44524456	G	A	0.446	U2AF1	Missense	p.S34F
PD8129a	21	44524456	44524456	G	A	0.474	U2AF1	Missense	p.S34F
PD7711a	21	44524456	44524456	G	A	0.487	U2AF1	Missense	p.S34F
PD11283a	21	44524456	44524456	G	A	0.488	U2AF1	Missense	p.S34F
PD7722a	21	44524456	44524456	G	T	0.404	U2AF1	Missense	p.S34Y
PD11275a	21	44524456	44524456	G	T	0.449	U2AF1	Missense	p.S34Y
PD9205a	21	44524474	44524474	C	T	0.0876	U2AF1	Missense	p.R28H
PD10924a	5	170837543	170837543	C	CTCTG	27.8	NPM1	Frameshift	p.W288fs*12
PD10971a	5	170837543	170837543	C	CTCTG	4.46	NPM1	Frameshift	p.W288fs*12
PD11047a	5	170837543	170837543	C	CTCTG	24.1	NPM1	Frameshift	p.W288fs*12
PD11093a	5	170837543	170837543	C	CTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD11159a	5	170837543	170837543	C	CTCTG	44	NPM1	Frameshift	p.W288fs*12
PD11195a	5	170837543	170837543	C	CTCTG	33.9	NPM1	Frameshift	p.W288fs*12
PD7662a	5	170837543	170837543	C	CTCTG	28.1	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7732a	5	170837543	170837543	C	CTCTG	28.9	NPM1	Frameshift	p.W288fs*12
PD7737a	5	170837543	170837543	C	CTCTG	25	NPM1	Frameshift	p.W288fs*12
PD7855a	5	170837543	170837543	C	CTCTG	34	NPM1	Frameshift	p.W288fs*12
PD7893a	5	170837543	170837543	C	CTCTG	31.5	NPM1	Frameshift	p.W288fs*12
PD7937a	5	170837543	170837543	C	CTCTG	19.6	NPM1	Frameshift	p.W288fs*12
PD8083a	5	170837543	170837543	C	CTCTG	23.8	NPM1	Frameshift	p.W288fs*12
PD8148a	5	170837543	170837543	C	CTCTG	13.9	NPM1	Frameshift	p.W288fs*12
PD8256a	5	170837543	170837543	C	CTCTG	26.6	NPM1	Frameshift	p.W288fs*12
PD8271a	5	170837543	170837543	C	CTCTG	24.3	NPM1	Frameshift	p.W288fs*12
PD8282a	5	170837543	170837543	C	CTCTG	29.5	NPM1	Frameshift	p.W288fs*12
PD8288a	5	170837543	170837543	C	CTCTG	19.6	NPM1	Frameshift	p.W288fs*12
PD8294a	5	170837543	170837543	C	CTCTG	24.8	NPM1	Frameshift	p.W288fs*12
PD8313a	5	170837543	170837543	C	CTCTG	20.5	NPM1	Frameshift	p.W288fs*12
PD8413a	5	170837543	170837543	C	CTCTG	29.6	NPM1	Frameshift	p.W288fs*12
PD8419a	5	170837543	170837543	C	CTCTG	34.7	NPM1	Frameshift	p.W288fs*12
PD8425a	5	170837543	170837543	C	CTCTG	29.3	NPM1	Frameshift	p.W288fs*12
PD8448a	5	170837543	170837543	C	CTCTG	27	NPM1	Frameshift	p.W288fs*12
PD8456a	5	170837543	170837543	C	CTCTG	32.9	NPM1	Frameshift	p.W288fs*12
PD8493a	5	170837543	170837543	C	CTCTG	18.2	NPM1	Frameshift	p.W288fs*12
PD8504a	5	170837543	170837543	C	CTCTG	30.7	NPM1	Frameshift	p.W288fs*12
PD9365a	5	170837543	170837543	C	CTCTG	32.3	NPM1	Frameshift	p.W288fs*12
PD7848a	5	170837544	170837544	T	TCTGC	22.4	NPM1	Frameshift	p.W288fs*12
PD7923a	5	170837544	170837544	T	TCTGC	3.85	NPM1	Frameshift	p.W288fs*12
PD8004a	5	170837544	170837544	T	TTTGC	22.9	NPM1	Frameshift	p.W288fs*12
PD7821a	5	170837545	170837545	C	CTGCA	35.5	NPM1	Frameshift	p.W288fs*12
PD8386a	5	170837547	170837547	G	GCAGA	7.29	NPM1	Frameshift	p.W288fs*12
PD8260a	5	170837547	170837547	G	GCAGG	31.4	NPM1	Frameshift	p.W288fs*12
PD10886a	5	170837547	170837547	G	GCATG	27.6	NPM1	Frameshift	p.W288fs*12
PD10966a	5	170837547	170837547	G	GCATG	35.9	NPM1	Frameshift	p.W288fs*12
PD10977a	5	170837547	170837547	G	GCATG	32.4	NPM1	Frameshift	p.W288fs*12
PD10999a	5	170837547	170837547	G	GCATG	41.2	NPM1	Frameshift	p.W288fs*12
PD11112a	5	170837547	170837547	G	GCATG	29.5	NPM1	Frameshift	p.W288fs*12
PD11125a	5	170837547	170837547	G	GCATG	42	NPM1	Frameshift	p.W288fs*12
PD11245a	5	170837547	170837547	G	GCATG	30.1	NPM1	Frameshift	p.W288fs*12
PD7690a	5	170837547	170837547	G	GCATG	30.8	NPM1	Frameshift	p.W288fs*12
PD7707a	5	170837547	170837547	G	GCATG	24	NPM1	Frameshift	p.W288fs*12
PD7837a	5	170837547	170837547	G	GCATG	23.6	NPM1	Frameshift	p.W288fs*12
PD7901a	5	170837547	170837547	G	GCATG	27.6	NPM1	Frameshift	p.W288fs*12
PD7944a	5	170837547	170837547	G	GCATG	29.5	NPM1	Frameshift	p.W288fs*12
PD7955a	5	170837547	170837547	G	GCATG	32.3	NPM1	Frameshift	p.W288fs*12
PD8030a	5	170837547	170837547	G	GCATG	33.3	NPM1	Frameshift	p.W288fs*12
PD8036a	5	170837547	170837547	G	GCATG	28.9	NPM1	Frameshift	p.W288fs*12
PD8073a	5	170837547	170837547	G	GCATG	23.5	NPM1	Frameshift	p.W288fs*12
PD8225a	5	170837547	170837547	G	GCATG	26.9	NPM1	Frameshift	p.W288fs*12
PD8269a	5	170837547	170837547	G	GCATG	36.8	NPM1	Frameshift	p.W288fs*12
PD8298a	5	170837547	170837547	G	GCATG	32.7	NPM1	Frameshift	p.W288fs*12
PD8363a	5	170837547	170837547	G	GCATG	34.3	NPM1	Frameshift	p.W288fs*12
PD8379a	5	170837547	170837547	G	GCATG	27.6	NPM1	Frameshift	p.W288fs*12
PD8403a	5	170837547	170837547	G	GCATG	31.8	NPM1	Frameshift	p.W288fs*12
PD8464a	5	170837547	170837547	G	GCATG	32.3	NPM1	Frameshift	p.W288fs*12
PD8469a	5	170837547	170837547	G	GCATG	32.4	NPM1	Frameshift	p.W288fs*12
PD8470a	5	170837547	170837547	G	GCATG	37.7	NPM1	Frameshift	p.W288fs*12
PD9252a	5	170837547	170837547	G	GCATG	28.6	NPM1	Frameshift	p.W288fs*12
PD9374a	5	170837547	170837547	G	GCATG	37.3	NPM1	Frameshift	p.W288fs*12
PD11059a	5	170837547	170837547	G	GCCAG	26.2	NPM1	Frameshift	p.W288fs*12
PD7760a	5	170837547	170837547	G	GCCAG	19.1	NPM1	Frameshift	p.W288fs*12
PD7761a	5	170837547	170837547	G	GCCAG	7.95	NPM1	Frameshift	p.W288fs*12
PD10914a	5	170837547	170837547	G	GCCGA	22.2	NPM1	Frameshift	p.W288fs*12
PD10945a	5	170837547	170837547	G	GCCGG	24.7	NPM1	Frameshift	p.W288fs*12
PD8160a	5	170837547	170837547	G	GCCGG	31	NPM1	Frameshift	p.W288fs*12
PD8581a	5	170837547	170837547	G	GCCGG	13.6	NPM1	Frameshift	p.W288fs*12
PD10855a	5	170837547	170837547	G	GCCTG	37.5	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10880a	5	170837547	170837547	G	GCCTG	17.5	NPM1	Frameshift	p.W288fs*12
PD10885a	5	170837547	170837547	G	GCCTG	28.7	NPM1	Frameshift	p.W288fs*12
PD10978a	5	170837547	170837547	G	GCCTG	22	NPM1	Frameshift	p.W288fs*12
PD10980a	5	170837547	170837547	G	GCCTG	31.9	NPM1	Frameshift	p.W288fs*12
PD11005a	5	170837547	170837547	G	GCCTG	16.2	NPM1	Frameshift	p.W288fs*12
PD11038a	5	170837547	170837547	G	GCCTG	30.6	NPM1	Frameshift	p.W288fs*12
PD11176a	5	170837547	170837547	G	GCCTG	31.7	NPM1	Frameshift	p.W288fs*12
PD7643a	5	170837547	170837547	G	GCCTG	33.8	NPM1	Frameshift	p.W288fs*12
PD7645a	5	170837547	170837547	G	GCCTG	34.3	NPM1	Frameshift	p.W288fs*12
PD7689a	5	170837547	170837547	G	GCCTG	33.1	NPM1	Frameshift	p.W288fs*12
PD7917a	5	170837547	170837547	G	GCCTG	31.4	NPM1	Frameshift	p.W288fs*12
PD7934a	5	170837547	170837547	G	GCCTG	50	NPM1	Frameshift	p.W288fs*12
PD7967a	5	170837547	170837547	G	GCCTG	19.2	NPM1	Frameshift	p.W288fs*12
PD8021a	5	170837547	170837547	G	GCCTG	26.3	NPM1	Frameshift	p.W288fs*12
PD8082a	5	170837547	170837547	G	GCCTG	29.6	NPM1	Frameshift	p.W288fs*12
PD8090a	5	170837547	170837547	G	GCCTG	25.3	NPM1	Frameshift	p.W288fs*12
PD8091a	5	170837547	170837547	G	GCCTG	15.9	NPM1	Frameshift	p.W288fs*12
PD8092a	5	170837547	170837547	G	GCCTG	29	NPM1	Frameshift	p.W288fs*12
PD8177a	5	170837547	170837547	G	GCCTG	23.9	NPM1	Frameshift	p.W288fs*12
PD8183a	5	170837547	170837547	G	GCCTG	18.2	NPM1	Frameshift	p.W288fs*12
PD8404a	5	170837547	170837547	G	GCCTG	30.9	NPM1	Frameshift	p.W288fs*12
PD9273a	5	170837547	170837547	G	GCCTG	32.6	NPM1	Frameshift	p.W288fs*12
PD9278a	5	170837547	170837547	G	GCCTG	31.1	NPM1	Frameshift	p.W288fs*12
PD9283a	5	170837547	170837547	G	GCCTG	25	NPM1	Frameshift	p.W288fs*12
PD9334a	5	170837547	170837547	G	GCCTG	31.3	NPM1	Frameshift	p.W288fs*12
PD7899a	5	170837547	170837547	G	GCGCC	27.8	NPM1	Frameshift	p.W288fs*12
PD9292a	5	170837547	170837547	G	GCGTG	33.3	NPM1	Frameshift	p.W288fs*12
PD10953a	5	170837547	170837547	G	GCTTG	31.3	NPM1	Frameshift	p.W288fs*12
PD8275a	5	170837547	170837547	G	GCTTG	31.1	NPM1	Frameshift	p.W288fs*12
PD8324a	5	170837547	170837547	G	GCTTG	22.8	NPM1	Frameshift	p.W288fs*12
PD8588a	5	170837547	170837547	G	GCTTG	15.8	NPM1	Frameshift	p.W288fs*12
PD10959a	5	170837547	170837547	G	GTAGG	13.5	NPM1	Frameshift	p.W288fs*12
PD10870a	5	170837547	170837547	G	GTATG	42.7	NPM1	Frameshift	p.W288fs*12
PD10972a	5	170837547	170837547	G	GTATG	29.4	NPM1	Frameshift	p.W288fs*12
PD11098a	5	170837547	170837547	G	GTATG	31.3	NPM1	Frameshift	p.W288fs*12
PD11206a	5	170837547	170837547	G	GTATG	30.2	NPM1	Frameshift	p.W288fs*12
PD8367a	5	170837547	170837547	G	GTATG	29.2	NPM1	Frameshift	p.W288fs*12
PD8398a	5	170837547	170837547	G	GTATG	35.4	NPM1	Frameshift	p.W288fs*12
PD8431a	5	170837547	170837547	G	GTCAG	16.8	NPM1	Frameshift	p.W288fs*12
PD9255a	5	170837547	170837547	G	GTCAG	21.8	NPM1	Frameshift	p.W288fs*12
PD8003a	5	170837547	170837547	G	GTCAT	26	NPM1	Frameshift	p.W288fs*12
PD10907a	5	170837547	170837547	G	GTCGG	26.5	NPM1	Frameshift	p.W288fs*12
PD7628a	5	170837547	170837547	G	GTCGG	31.5	NPM1	Frameshift	p.W288fs*12
PD10794a	5	170837547	170837547	G	GTCTG	31.2	NPM1	Frameshift	p.W288fs*12
PD10795a	5	170837547	170837547	G	GTCTG	36.6	NPM1	Frameshift	p.W288fs*12
PD10798a	5	170837547	170837547	G	GTCTG	13.1	NPM1	Frameshift	p.W288fs*12
PD10803a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD10807a	5	170837547	170837547	G	GTCTG	31.8	NPM1	Frameshift	p.W288fs*12
PD10824a	5	170837547	170837547	G	GTCTG	24.7	NPM1	Frameshift	p.W288fs*12
PD10829a	5	170837547	170837547	G	GTCTG	24.4	NPM1	Frameshift	p.W288fs*12
PD10832a	5	170837547	170837547	G	GTCTG	32.5	NPM1	Frameshift	p.W288fs*12
PD10841a	5	170837547	170837547	G	GTCTG	31.6	NPM1	Frameshift	p.W288fs*12
PD10843a	5	170837547	170837547	G	GTCTG	22.9	NPM1	Frameshift	p.W288fs*12
PD10844a	5	170837547	170837547	G	GTCTG	38.6	NPM1	Frameshift	p.W288fs*12
PD10847a	5	170837547	170837547	G	GTCTG	40.7	NPM1	Frameshift	p.W288fs*12
PD10850a	5	170837547	170837547	G	GTCTG	23.1	NPM1	Frameshift	p.W288fs*12
PD10852a	5	170837547	170837547	G	GTCTG	31.3	NPM1	Frameshift	p.W288fs*12
PD10853a	5	170837547	170837547	G	GTCTG	18.8	NPM1	Frameshift	p.W288fs*12
PD10862a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD10891a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD10895a	5	170837547	170837547	G	GTCTG	26.3	NPM1	Frameshift	p.W288fs*12
PD10896a	5	170837547	170837547	G	GTCTG	42	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD10897a	5	170837547	170837547	G	GTCTG	21.2	NPM1	Frameshift	p.W288fs*12
PD10899a	5	170837547	170837547	G	GTCTG	37.6	NPM1	Frameshift	p.W288fs*12
PD10905a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD10910a	5	170837547	170837547	G	GTCTG	26.4	NPM1	Frameshift	p.W288fs*12
PD10917a	5	170837547	170837547	G	GTCTG	36.3	NPM1	Frameshift	p.W288fs*12
PD10918a	5	170837547	170837547	G	GTCTG	31.5	NPM1	Frameshift	p.W288fs*12
PD10921a	5	170837547	170837547	G	GTCTG	29.2	NPM1	Frameshift	p.W288fs*12
PD10925a	5	170837547	170837547	G	GTCTG	27.2	NPM1	Frameshift	p.W288fs*12
PD10930a	5	170837547	170837547	G	GTCTG	13.9	NPM1	Frameshift	p.W288fs*12
PD10934a	5	170837547	170837547	G	GTCTG	28.6	NPM1	Frameshift	p.W288fs*12
PD10939a	5	170837547	170837547	G	GTCTG	25.8	NPM1	Frameshift	p.W288fs*12
PD10940a	5	170837547	170837547	G	GTCTG	28.3	NPM1	Frameshift	p.W288fs*12
PD10943a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD10944a	5	170837547	170837547	G	GTCTG	20.7	NPM1	Frameshift	p.W288fs*12
PD10947a	5	170837547	170837547	G	GTCTG	40.6	NPM1	Frameshift	p.W288fs*12
PD10950a	5	170837547	170837547	G	GTCTG	35.6	NPM1	Frameshift	p.W288fs*12
PD10954a	5	170837547	170837547	G	GTCTG	33	NPM1	Frameshift	p.W288fs*12
PD10957a	5	170837547	170837547	G	GTCTG	38.3	NPM1	Frameshift	p.W288fs*12
PD10964a	5	170837547	170837547	G	GTCTG	23.1	NPM1	Frameshift	p.W288fs*12
PD10967a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD10973a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD10975a	5	170837547	170837547	G	GTCTG	36.2	NPM1	Frameshift	p.W288fs*12
PD10981a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD10984a	5	170837547	170837547	G	GTCTG	26.8	NPM1	Frameshift	p.W288fs*12
PD10988a	5	170837547	170837547	G	GTCTG	30	NPM1	Frameshift	p.W288fs*12
PD10993a	5	170837547	170837547	G	GTCTG	20.3	NPM1	Frameshift	p.W288fs*12
PD10997a	5	170837547	170837547	G	GTCTG	27.2	NPM1	Frameshift	p.W288fs*12
PD11002a	5	170837547	170837547	G	GTCTG	22.8	NPM1	Frameshift	p.W288fs*12
PD11010a	5	170837547	170837547	G	GTCTG	40	NPM1	Frameshift	p.W288fs*12
PD11016a	5	170837547	170837547	G	GTCTG	27.6	NPM1	Frameshift	p.W288fs*12
PD11029a	5	170837547	170837547	G	GTCTG	22.7	NPM1	Frameshift	p.W288fs*12
PD11037a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD11045a	5	170837547	170837547	G	GTCTG	35.1	NPM1	Frameshift	p.W288fs*12
PD11048a	5	170837547	170837547	G	GTCTG	41.3	NPM1	Frameshift	p.W288fs*12
PD11052a	5	170837547	170837547	G	GTCTG	33	NPM1	Frameshift	p.W288fs*12
PD11054a	5	170837547	170837547	G	GTCTG	20.3	NPM1	Frameshift	p.W288fs*12
PD11057a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD11071a	5	170837547	170837547	G	GTCTG	26.9	NPM1	Frameshift	p.W288fs*12
PD11072a	5	170837547	170837547	G	GTCTG	34.4	NPM1	Frameshift	p.W288fs*12
PD11073a	5	170837547	170837547	G	GTCTG	36.6	NPM1	Frameshift	p.W288fs*12
PD11077a	5	170837547	170837547	G	GTCTG	32.8	NPM1	Frameshift	p.W288fs*12
PD11095a	5	170837547	170837547	G	GTCTG	29.9	NPM1	Frameshift	p.W288fs*12
PD11101a	5	170837547	170837547	G	GTCTG	21.9	NPM1	Frameshift	p.W288fs*12
PD11103a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD11108a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD11113a	5	170837547	170837547	G	GTCTG	34.4	NPM1	Frameshift	p.W288fs*12
PD11115a	5	170837547	170837547	G	GTCTG	32.1	NPM1	Frameshift	p.W288fs*12
PD11117a	5	170837547	170837547	G	GTCTG	36.6	NPM1	Frameshift	p.W288fs*12
PD11122a	5	170837547	170837547	G	GTCTG	33.5	NPM1	Frameshift	p.W288fs*12
PD11133a	5	170837547	170837547	G	GTCTG	48.8	NPM1	Frameshift	p.W288fs*12
PD11148a	5	170837547	170837547	G	GTCTG	20.3	NPM1	Frameshift	p.W288fs*12
PD11150a	5	170837547	170837547	G	GTCTG	8.97	NPM1	Frameshift	p.W288fs*12
PD11162a	5	170837547	170837547	G	GTCTG	29.2	NPM1	Frameshift	p.W288fs*12
PD11165a	5	170837547	170837547	G	GTCTG	21.7	NPM1	Frameshift	p.W288fs*12
PD11172a	5	170837547	170837547	G	GTCTG	27.7	NPM1	Frameshift	p.W288fs*12
PD11174a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD11186a	5	170837547	170837547	G	GTCTG	40.4	NPM1	Frameshift	p.W288fs*12
PD11187a	5	170837547	170837547	G	GTCTG	24.4	NPM1	Frameshift	p.W288fs*12
PD11190a	5	170837547	170837547	G	GTCTG	32.4	NPM1	Frameshift	p.W288fs*12
PD11192a	5	170837547	170837547	G	GTCTG	28.6	NPM1	Frameshift	p.W288fs*12
PD11196a	5	170837547	170837547	G	GTCTG	36.8	NPM1	Frameshift	p.W288fs*12
PD11202a	5	170837547	170837547	G	GTCTG	30.3	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD11212a	5	170837547	170837547	G	GTCTG	41.2	NPM1	Frameshift	p.W288fs*12
PD11217a	5	170837547	170837547	G	GTCTG	34.6	NPM1	Frameshift	p.W288fs*12
PD11218a	5	170837547	170837547	G	GTCTG	25.9	NPM1	Frameshift	p.W288fs*12
PD11221a	5	170837547	170837547	G	GTCTG	17.3	NPM1	Frameshift	p.W288fs*12
PD11231a	5	170837547	170837547	G	GTCTG	10.8	NPM1	Frameshift	p.W288fs*12
PD11233a	5	170837547	170837547	G	GTCTG	39.7	NPM1	Frameshift	p.W288fs*12
PD11240a	5	170837547	170837547	G	GTCTG	34.4	NPM1	Frameshift	p.W288fs*12
PD11243a	5	170837547	170837547	G	GTCTG	18.4	NPM1	Frameshift	p.W288fs*12
PD11244a	5	170837547	170837547	G	GTCTG	27.5	NPM1	Frameshift	p.W288fs*12
PD11248a	5	170837547	170837547	G	GTCTG	5.79	NPM1	Frameshift	p.W288fs*12
PD11250a	5	170837547	170837547	G	GTCTG	35.1	NPM1	Frameshift	p.W288fs*12
PD11254a	5	170837547	170837547	G	GTCTG	26.8	NPM1	Frameshift	p.W288fs*12
PD11261a	5	170837547	170837547	G	GTCTG	36.7	NPM1	Frameshift	p.W288fs*12
PD11265a	5	170837547	170837547	G	GTCTG	24.6	NPM1	Frameshift	p.W288fs*12
PD11280a	5	170837547	170837547	G	GTCTG	36.4	NPM1	Frameshift	p.W288fs*12
PD11286a	5	170837547	170837547	G	GTCTG	28.6	NPM1	Frameshift	p.W288fs*12
PD7610a	5	170837547	170837547	G	GTCTG	45.6	NPM1	Frameshift	p.W288fs*12
PD7612a	5	170837547	170837547	G	GTCTG	38.9	NPM1	Frameshift	p.W288fs*12
PD7627a	5	170837547	170837547	G	GTCTG	21.1	NPM1	Frameshift	p.W288fs*12
PD7631a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD7634a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD7644a	5	170837547	170837547	G	GTCTG	23.4	NPM1	Frameshift	p.W288fs*12
PD7655a	5	170837547	170837547	G	GTCTG	43.8	NPM1	Frameshift	p.W288fs*12
PD7656a	5	170837547	170837547	G	GTCTG	39	NPM1	Frameshift	p.W288fs*12
PD7657a	5	170837547	170837547	G	GTCTG	31.6	NPM1	Frameshift	p.W288fs*12
PD7661a	5	170837547	170837547	G	GTCTG	8.02	NPM1	Frameshift	p.W288fs*12
PD7667a	5	170837547	170837547	G	GTCTG	31.9	NPM1	Frameshift	p.W288fs*12
PD7670a	5	170837547	170837547	G	GTCTG	34.2	NPM1	Frameshift	p.W288fs*12
PD7672a	5	170837547	170837547	G	GTCTG	35.2	NPM1	Frameshift	p.W288fs*12
PD7677a	5	170837547	170837547	G	GTCTG	23.6	NPM1	Frameshift	p.W288fs*12
PD7678a	5	170837547	170837547	G	GTCTG	34.2	NPM1	Frameshift	p.W288fs*12
PD7680a	5	170837547	170837547	G	GTCTG	37.6	NPM1	Frameshift	p.W288fs*12
PD7683a	5	170837547	170837547	G	GTCTG	34.7	NPM1	Frameshift	p.W288fs*12
PD7685a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD7687a	5	170837547	170837547	G	GTCTG	33.6	NPM1	Frameshift	p.W288fs*12
PD7705a	5	170837547	170837547	G	GTCTG	24.7	NPM1	Frameshift	p.W288fs*12
PD7709a	5	170837547	170837547	G	GTCTG	20.2	NPM1	Frameshift	p.W288fs*12
PD7739a	5	170837547	170837547	G	GTCTG	24	NPM1	Frameshift	p.W288fs*12
PD7745a	5	170837547	170837547	G	GTCTG	32.9	NPM1	Frameshift	p.W288fs*12
PD7754a	5	170837547	170837547	G	GTCTG	15.5	NPM1	Frameshift	p.W288fs*12
PD7759a	5	170837547	170837547	G	GTCTG	30	NPM1	Frameshift	p.W288fs*12
PD7787a	5	170837547	170837547	G	GTCTG	35.8	NPM1	Frameshift	p.W288fs*12
PD7791a	5	170837547	170837547	G	GTCTG	30.5	NPM1	Frameshift	p.W288fs*12
PD7796a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD7800a	5	170837547	170837547	G	GTCTG	14.1	NPM1	Frameshift	p.W288fs*12
PD7802a	5	170837547	170837547	G	GTCTG	30.6	NPM1	Frameshift	p.W288fs*12
PD7803a	5	170837547	170837547	G	GTCTG	33.6	NPM1	Frameshift	p.W288fs*12
PD7804a	5	170837547	170837547	G	GTCTG	35.4	NPM1	Frameshift	p.W288fs*12
PD7810a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD7815a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD7828a	5	170837547	170837547	G	GTCTG	18.9	NPM1	Frameshift	p.W288fs*12
PD7830a	5	170837547	170837547	G	GTCTG	27.7	NPM1	Frameshift	p.W288fs*12
PD7833a	5	170837547	170837547	G	GTCTG	21.9	NPM1	Frameshift	p.W288fs*12
PD7834a	5	170837547	170837547	G	GTCTG	32.4	NPM1	Frameshift	p.W288fs*12
PD7835a	5	170837547	170837547	G	GTCTG	32.4	NPM1	Frameshift	p.W288fs*12
PD7842a	5	170837547	170837547	G	GTCTG	18.3	NPM1	Frameshift	p.W288fs*12
PD7849a	5	170837547	170837547	G	GTCTG	32.7	NPM1	Frameshift	p.W288fs*12
PD7868a	5	170837547	170837547	G	GTCTG	34.8	NPM1	Frameshift	p.W288fs*12
PD7872a	5	170837547	170837547	G	GTCTG	36	NPM1	Frameshift	p.W288fs*12
PD7881a	5	170837547	170837547	G	GTCTG	28.1	NPM1	Frameshift	p.W288fs*12
PD7888a	5	170837547	170837547	G	GTCTG	41.9	NPM1	Frameshift	p.W288fs*12
PD7904a	5	170837547	170837547	G	GTCTG	36.4	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7905a	5	170837547	170837547	G	GTCTG	17.1	NPM1	Frameshift	p.W288fs*12
PD7909a	5	170837547	170837547	G	GTCTG	24	NPM1	Frameshift	p.W288fs*12
PD7911a	5	170837547	170837547	G	GTCTG	26.3	NPM1	Frameshift	p.W288fs*12
PD7914a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD7918a	5	170837547	170837547	G	GTCTG	34.9	NPM1	Frameshift	p.W288fs*12
PD7922a	5	170837547	170837547	G	GTCTG	32.7	NPM1	Frameshift	p.W288fs*12
PD7927a	5	170837547	170837547	G	GTCTG	23.1	NPM1	Frameshift	p.W288fs*12
PD7928a	5	170837547	170837547	G	GTCTG	36.8	NPM1	Frameshift	p.W288fs*12
PD7935a	5	170837547	170837547	G	GTCTG	10.4	NPM1	Frameshift	p.W288fs*12
PD7936a	5	170837547	170837547	G	GTCTG	29.4	NPM1	Frameshift	p.W288fs*12
PD7945a	5	170837547	170837547	G	GTCTG	46.4	NPM1	Frameshift	p.W288fs*12
PD7946a	5	170837547	170837547	G	GTCTG	34.6	NPM1	Frameshift	p.W288fs*12
PD7956a	5	170837547	170837547	G	GTCTG	35	NPM1	Frameshift	p.W288fs*12
PD7961a	5	170837547	170837547	G	GTCTG	27.4	NPM1	Frameshift	p.W288fs*12
PD7964a	5	170837547	170837547	G	GTCTG	32.1	NPM1	Frameshift	p.W288fs*12
PD7974a	5	170837547	170837547	G	GTCTG	27.8	NPM1	Frameshift	p.W288fs*12
PD7979a	5	170837547	170837547	G	GTCTG	39	NPM1	Frameshift	p.W288fs*12
PD7990a	5	170837547	170837547	G	GTCTG	30.4	NPM1	Frameshift	p.W288fs*12
PD7991a	5	170837547	170837547	G	GTCTG	36.8	NPM1	Frameshift	p.W288fs*12
PD8005a	5	170837547	170837547	G	GTCTG	24.5	NPM1	Frameshift	p.W288fs*12
PD8006a	5	170837547	170837547	G	GTCTG	38.8	NPM1	Frameshift	p.W288fs*12
PD8007a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD8022a	5	170837547	170837547	G	GTCTG	18.5	NPM1	Frameshift	p.W288fs*12
PD8023a	5	170837547	170837547	G	GTCTG	42.5	NPM1	Frameshift	p.W288fs*12
PD8024a	5	170837547	170837547	G	GTCTG	28.9	NPM1	Frameshift	p.W288fs*12
PD8031a	5	170837547	170837547	G	GTCTG	34.2	NPM1	Frameshift	p.W288fs*12
PD8033a	5	170837547	170837547	G	GTCTG	33	NPM1	Frameshift	p.W288fs*12
PD8038a	5	170837547	170837547	G	GTCTG	33.7	NPM1	Frameshift	p.W288fs*12
PD8040a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8044a	5	170837547	170837547	G	GTCTG	26.9	NPM1	Frameshift	p.W288fs*12
PD8046a	5	170837547	170837547	G	GTCTG	34.6	NPM1	Frameshift	p.W288fs*12
PD8053a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8056a	5	170837547	170837547	G	GTCTG	20.2	NPM1	Frameshift	p.W288fs*12
PD8057a	5	170837547	170837547	G	GTCTG	38.6	NPM1	Frameshift	p.W288fs*12
PD8060a	5	170837547	170837547	G	GTCTG	31.9	NPM1	Frameshift	p.W288fs*12
PD8063a	5	170837547	170837547	G	GTCTG	19.4	NPM1	Frameshift	p.W288fs*12
PD8065a	5	170837547	170837547	G	GTCTG	31.1	NPM1	Frameshift	p.W288fs*12
PD8071a	5	170837547	170837547	G	GTCTG	22.2	NPM1	Frameshift	p.W288fs*12
PD8079a	5	170837547	170837547	G	GTCTG	32.3	NPM1	Frameshift	p.W288fs*12
PD8087a	5	170837547	170837547	G	GTCTG	36	NPM1	Frameshift	p.W288fs*12
PD8095a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD8098a	5	170837547	170837547	G	GTCTG	20.4	NPM1	Frameshift	p.W288fs*12
PD8117a	5	170837547	170837547	G	GTCTG	40.4	NPM1	Frameshift	p.W288fs*12
PD8120a	5	170837547	170837547	G	GTCTG	33.8	NPM1	Frameshift	p.W288fs*12
PD8123a	5	170837547	170837547	G	GTCTG	31.6	NPM1	Frameshift	p.W288fs*12
PD8127a	5	170837547	170837547	G	GTCTG	34.4	NPM1	Frameshift	p.W288fs*12
PD8131a	5	170837547	170837547	G	GTCTG	29.1	NPM1	Frameshift	p.W288fs*12
PD8152a	5	170837547	170837547	G	GTCTG	27.4	NPM1	Frameshift	p.W288fs*12
PD8158a	5	170837547	170837547	G	GTCTG	20.2	NPM1	Frameshift	p.W288fs*12
PD8159a	5	170837547	170837547	G	GTCTG	28.4	NPM1	Frameshift	p.W288fs*12
PD8165a	5	170837547	170837547	G	GTCTG	26.1	NPM1	Frameshift	p.W288fs*12
PD8171a	5	170837547	170837547	G	GTCTG	11.4	NPM1	Frameshift	p.W288fs*12
PD8172a	5	170837547	170837547	G	GTCTG	30.3	NPM1	Frameshift	p.W288fs*12
PD8174a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8176a	5	170837547	170837547	G	GTCTG	38.8	NPM1	Frameshift	p.W288fs*12
PD8179a	5	170837547	170837547	G	GTCTG	28.6	NPM1	Frameshift	p.W288fs*12
PD8187a	5	170837547	170837547	G	GTCTG	20.2	NPM1	Frameshift	p.W288fs*12
PD8190a	5	170837547	170837547	G	GTCTG	38	NPM1	Frameshift	p.W288fs*12
PD8192a	5	170837547	170837547	G	GTCTG	39.5	NPM1	Frameshift	p.W288fs*12
PD8193a	5	170837547	170837547	G	GTCTG	22.2	NPM1	Frameshift	p.W288fs*12
PD8204a	5	170837547	170837547	G	GTCTG	13.2	NPM1	Frameshift	p.W288fs*12
PD8208a	5	170837547	170837547	G	GTCTG	34.7	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8210a	5	170837547	170837547	G	GTCTG	33.7	NPM1	Frameshift	p.W288fs*12
PD8211a	5	170837547	170837547	G	GTCTG	34.3	NPM1	Frameshift	p.W288fs*12
PD8213a	5	170837547	170837547	G	GTCTG	18.6	NPM1	Frameshift	p.W288fs*12
PD8218a	5	170837547	170837547	G	GTCTG	21.9	NPM1	Frameshift	p.W288fs*12
PD8224a	5	170837547	170837547	G	GTCTG	34.5	NPM1	Frameshift	p.W288fs*12
PD8231a	5	170837547	170837547	G	GTCTG	29.4	NPM1	Frameshift	p.W288fs*12
PD8235a	5	170837547	170837547	G	GTCTG	33.7	NPM1	Frameshift	p.W288fs*12
PD8236a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD8244a	5	170837547	170837547	G	GTCTG	26.8	NPM1	Frameshift	p.W288fs*12
PD8251a	5	170837547	170837547	G	GTCTG	28.2	NPM1	Frameshift	p.W288fs*12
PD8253a	5	170837547	170837547	G	GTCTG	33.5	NPM1	Frameshift	p.W288fs*12
PD8257a	5	170837547	170837547	G	GTCTG	27.4	NPM1	Frameshift	p.W288fs*12
PD8267a	5	170837547	170837547	G	GTCTG	28.1	NPM1	Frameshift	p.W288fs*12
PD8274a	5	170837547	170837547	G	GTCTG	35.4	NPM1	Frameshift	p.W288fs*12
PD8276a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8279a	5	170837547	170837547	G	GTCTG	31.2	NPM1	Frameshift	p.W288fs*12
PD8285a	5	170837547	170837547	G	GTCTG	29.5	NPM1	Frameshift	p.W288fs*12
PD8291a	5	170837547	170837547	G	GTCTG	25.6	NPM1	Frameshift	p.W288fs*12
PD8293a	5	170837547	170837547	G	GTCTG	22.1	NPM1	Frameshift	p.W288fs*12
PD8297a	5	170837547	170837547	G	GTCTG	37.5	NPM1	Frameshift	p.W288fs*12
PD8301a	5	170837547	170837547	G	GTCTG	34.4	NPM1	Frameshift	p.W288fs*12
PD8303a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8307a	5	170837547	170837547	G	GTCTG	12	NPM1	Frameshift	p.W288fs*12
PD8309a	5	170837547	170837547	G	GTCTG	35.9	NPM1	Frameshift	p.W288fs*12
PD8314a	5	170837547	170837547	G	GTCTG	30.8	NPM1	Frameshift	p.W288fs*12
PD8316a	5	170837547	170837547	G	GTCTG	31.9	NPM1	Frameshift	p.W288fs*12
PD8322a	5	170837547	170837547	G	GTCTG	37.3	NPM1	Frameshift	p.W288fs*12
PD8323a	5	170837547	170837547	G	GTCTG	35.8	NPM1	Frameshift	p.W288fs*12
PD8326a	5	170837547	170837547	G	GTCTG	10.8	NPM1	Frameshift	p.W288fs*12
PD8327a	5	170837547	170837547	G	GTCTG	18.7	NPM1	Frameshift	p.W288fs*12
PD8328a	5	170837547	170837547	G	GTCTG	27.9	NPM1	Frameshift	p.W288fs*12
PD8329a	5	170837547	170837547	G	GTCTG	23.5	NPM1	Frameshift	p.W288fs*12
PD8334a	5	170837547	170837547	G	GTCTG	23.7	NPM1	Frameshift	p.W288fs*12
PD8346a	5	170837547	170837547	G	GTCTG	27	NPM1	Frameshift	p.W288fs*12
PD8353a	5	170837547	170837547	G	GTCTG	30.8	NPM1	Frameshift	p.W288fs*12
PD8365a	5	170837547	170837547	G	GTCTG	35.5	NPM1	Frameshift	p.W288fs*12
PD8368a	5	170837547	170837547	G	GTCTG	25.7	NPM1	Frameshift	p.W288fs*12
PD8371a	5	170837547	170837547	G	GTCTG	32.1	NPM1	Frameshift	p.W288fs*12
PD8372a	5	170837547	170837547	G	GTCTG	19.5	NPM1	Frameshift	p.W288fs*12
PD8374a	5	170837547	170837547	G	GTCTG	39.7	NPM1	Frameshift	p.W288fs*12
PD8375a	5	170837547	170837547	G	GTCTG	29.6	NPM1	Frameshift	p.W288fs*12
PD8380a	5	170837547	170837547	G	GTCTG	36.6	NPM1	Frameshift	p.W288fs*12
PD8387a	5	170837547	170837547	G	GTCTG	16.5	NPM1	Frameshift	p.W288fs*12
PD8393a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD8394a	5	170837547	170837547	G	GTCTG	10.2	NPM1	Frameshift	p.W288fs*12
PD8399a	5	170837547	170837547	G	GTCTG	31.3	NPM1	Frameshift	p.W288fs*12
PD8400a	5	170837547	170837547	G	GTCTG	3.45	NPM1	Frameshift	p.W288fs*12
PD8407a	5	170837547	170837547	G	GTCTG	29.8	NPM1	Frameshift	p.W288fs*12
PD8412a	5	170837547	170837547	G	GTCTG	25.7	NPM1	Frameshift	p.W288fs*12
PD8416a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD8417a	5	170837547	170837547	G	GTCTG	29.5	NPM1	Frameshift	p.W288fs*12
PD8424a	5	170837547	170837547	G	GTCTG	19.3	NPM1	Frameshift	p.W288fs*12
PD8430a	5	170837547	170837547	G	GTCTG	33.6	NPM1	Frameshift	p.W288fs*12
PD8435a	5	170837547	170837547	G	GTCTG	23.1	NPM1	Frameshift	p.W288fs*12
PD8436a	5	170837547	170837547	G	GTCTG	29.9	NPM1	Frameshift	p.W288fs*12
PD8438a	5	170837547	170837547	G	GTCTG	28.4	NPM1	Frameshift	p.W288fs*12
PD8441a	5	170837547	170837547	G	GTCTG	15.5	NPM1	Frameshift	p.W288fs*12
PD8444a	5	170837547	170837547	G	GTCTG	24.1	NPM1	Frameshift	p.W288fs*12
PD8445a	5	170837547	170837547	G	GTCTG	26.7	NPM1	Frameshift	p.W288fs*12
PD8446a	5	170837547	170837547	G	GTCTG	22.9	NPM1	Frameshift	p.W288fs*12
PD8460a	5	170837547	170837547	G	GTCTG	28.3	NPM1	Frameshift	p.W288fs*12
PD8472a	5	170837547	170837547	G	GTCTG	37.2	NPM1	Frameshift	p.W288fs*12

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD8473a	5	170837547	170837547	G	GTCTG	21.5	NPM1	Frameshift	p.W288fs*12
PD8479a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD8486a	5	170837547	170837547	G	GTCTG	32.1	NPM1	Frameshift	p.W288fs*12
PD8491a	5	170837547	170837547	G	GTCTG	27.9	NPM1	Frameshift	p.W288fs*12
PD8494a	5	170837547	170837547	G	GTCTG	31.4	NPM1	Frameshift	p.W288fs*12
PD8495a	5	170837547	170837547	G	GTCTG	24.4	NPM1	Frameshift	p.W288fs*12
PD8512a	5	170837547	170837547	G	GTCTG	31.6	NPM1	Frameshift	p.W288fs*12
PD8536a	5	170837547	170837547	G	GTCTG	30.3	NPM1	Frameshift	p.W288fs*12
PD8538a	5	170837547	170837547	G	GTCTG	17.1	NPM1	Frameshift	p.W288fs*12
PD8539a	5	170837547	170837547	G	GTCTG	28.1	NPM1	Frameshift	p.W288fs*12
PD8540a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8544a	5	170837547	170837547	G	GTCTG	16.1	NPM1	Frameshift	p.W288fs*12
PD8546a	5	170837547	170837547	G	GTCTG	29.4	NPM1	Frameshift	p.W288fs*12
PD8551a	5	170837547	170837547	G	GTCTG	23.5	NPM1	Frameshift	p.W288fs*12
PD8553a	5	170837547	170837547	G	GTCTG	22.3	NPM1	Frameshift	p.W288fs*12
PD8557a	5	170837547	170837547	G	GTCTG	40	NPM1	Frameshift	p.W288fs*12
PD8558a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD8562a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD8568a	5	170837547	170837547	G	GTCTG	33	NPM1	Frameshift	p.W288fs*12
PD8570a	5	170837547	170837547	G	GTCTG	30.2	NPM1	Frameshift	p.W288fs*12
PD8574a	5	170837547	170837547	G	GTCTG	31.4	NPM1	Frameshift	p.W288fs*12
PD8582a	5	170837547	170837547	G	GTCTG	23.1	NPM1	Frameshift	p.W288fs*12
PD9197a	5	170837547	170837547	G	GTCTG	34	NPM1	Frameshift	p.W288fs*12
PD9214a	5	170837547	170837547	G	GTCTG	36.9	NPM1	Frameshift	p.W288fs*12
PD9226a	5	170837547	170837547	G	GTCTG	37.3	NPM1	Frameshift	p.W288fs*12
PD9232a	5	170837547	170837547	G	GTCTG	28.4	NPM1	Frameshift	p.W288fs*12
PD9234a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD9239a	5	170837547	170837547	G	GTCTG	29.7	NPM1	Frameshift	p.W288fs*12
PD9240a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD9241a	5	170837547	170837547	G	GTCTG	34.8	NPM1	Frameshift	p.W288fs*12
PD9248a	5	170837547	170837547	G	GTCTG	18.6	NPM1	Frameshift	p.W288fs*12
PD9254a	5	170837547	170837547	G	GTCTG	24.1	NPM1	Frameshift	p.W288fs*12
PD9268a	5	170837547	170837547	G	GTCTG	34	NPM1	Frameshift	p.W288fs*12
PD9272a	5	170837547	170837547	G	GTCTG	29.4	NPM1	Frameshift	p.W288fs*12
PD9284a	5	170837547	170837547	G	GTCTG	35.6	NPM1	Frameshift	p.W288fs*12
PD9301a	5	170837547	170837547	G	GTCTG	38.4	NPM1	Frameshift	p.W288fs*12
PD9302a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD9307a	5	170837547	170837547	G	GTCTG	27	NPM1	Frameshift	p.W288fs*12
PD9323a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD9326a	5	170837547	170837547	G	GTCTG	28.8	NPM1	Frameshift	p.W288fs*12
PD9327a	5	170837547	170837547	G	GTCTG	25	NPM1	Frameshift	p.W288fs*12
PD9335a	5	170837547	170837547	G	GTCTG	37.4	NPM1	Frameshift	p.W288fs*12
PD9339a	5	170837547	170837547	G	GTCTG	32	NPM1	Frameshift	p.W288fs*12
PD9340a	5	170837547	170837547	G	GTCTG	30.6	NPM1	Frameshift	p.W288fs*12
PD9341a	5	170837547	170837547	G	GTCTG	37.8	NPM1	Frameshift	p.W288fs*12
PD9350a	5	170837547	170837547	G	GTCTG	39.1	NPM1	Frameshift	p.W288fs*12
PD9355a	5	170837547	170837547	G	GTCTG	na	NPM1	Frameshift	p.W288fs*12
PD9358a	5	170837547	170837547	G	GTCTG	33.3	NPM1	Frameshift	p.W288fs*12
PD9361a	5	170837547	170837547	G	GTCTG	28.9	NPM1	Frameshift	p.W288fs*12
PD9373a	5	170837547	170837547	G	GTCTG	34.8	NPM1	Frameshift	p.W288fs*12
PD9377a	5	170837547	170837547	G	GTCTG	27.4	NPM1	Frameshift	p.W288fs*12
PD9383a	5	170837547	170837547	G	GTCTG	71.7	NPM1	Frameshift	p.W288fs*12
PD9385a	5	170837547	170837547	G	GTCTG	55.4	NPM1	Frameshift	p.W288fs*12
PD11100a	5	170837547	170837547	G	GTGTG	6.2	NPM1	Frameshift	p.W288fs*12
PD10881a	5	170837547	170837547	G	GTTTG	27.8	NPM1	Frameshift	p.W288fs*12
PD8157a	5	170837547	170837547	G	GTTTG	19.8	NPM1	Frameshift	p.W288fs*12
PD8206a	5	170837551	170837551	G	GAGAA	35.8	NPM1	Frameshift	p.W290fs*10
PD7730a	5	170837551	170837551	G	GAGGA	32.1	NPM1	Frameshift	p.W290fs*10
PD7805a	5	170837551	170837551	G	GAGGA	32.8	NPM1	Frameshift	p.W290fs*10
PD8238a	5	170837551	170837551	G	GAGGT	35.4	NPM1	Frameshift	p.W290fs*10
PD8455a	5	170837552	170837552	T	TG	0.51	NPM1	Frameshift	p.R291fs*8

Table 16b | Somatic variants identified in the MDS cohort

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6256a	2	25457159	25457159	C	G	0.5	DNMT3A	Missense	p.A910P
PD6107a	2	25457176	25457176	G	A	0.337	DNMT3A	Missense	p.P904L
PD6337a	2	25457180	25457180	C	T	0.716	DNMT3A	Missense	p.A903T
PD6971a	2	25457229	25457229	C	T	0.475	DNMT3A	Synonymous	p.Q886Q
PD6939a	2	25457230	25457230	T	C	0.371	DNMT3A	Missense	p.Q886R
PD5768a	2	25457242	25457242	C	G	0.238	DNMT3A	Missense	p.R882P
PD6968a	2	25457242	25457242	C	T	0.263	DNMT3A	Missense	p.R882H
PD6233a	2	25457242	25457242	C	T	0.3	DNMT3A	Missense	p.R882H
PD6482a	2	25457242	25457242	C	T	0.317	DNMT3A	Missense	p.R882H
PD6149a	2	25457242	25457242	C	T	0.324	DNMT3A	Missense	p.R882H
PD6974a	2	25457242	25457242	C	T	0.42	DNMT3A	Missense	p.R882H
PD6849a	2	25457242	25457242	C	T	0.432	DNMT3A	Missense	p.R882H
PD6520a	2	25457242	25457242	C	T	0.44	DNMT3A	Missense	p.R882H
PD5747a	2	25457242	25457242	C	T	0.449	DNMT3A	Missense	p.R882H
PD6288a	2	25457242	25457242	C	T	0.47	DNMT3A	Missense	p.R882H
PD6135a	2	25457242	25457242	C	T	0.483	DNMT3A	Missense	p.R882H
PD7079a	2	25457242	25457242	C	T	0.497	DNMT3A	Missense	p.R882H
PD6909a	2	25457243	25457243	G	A	0.123	DNMT3A	Missense	p.R882C
PD6311a	2	25457243	25457243	G	A	0.14	DNMT3A	Missense	p.R882C
PD7111a	2	25457243	25457243	G	A	0.167	DNMT3A	Missense	p.R882C
PD5732a	2	25457243	25457243	G	A	0.316	DNMT3A	Missense	p.R882C
PD6202a	2	25457243	25457243	G	A	0.362	DNMT3A	Missense	p.R882C
PD7088a	2	25457243	25457243	G	A	0.363	DNMT3A	Missense	p.R882C
PD6926a	2	25457243	25457243	G	A	0.413	DNMT3A	Missense	p.R882C
PD6163a	2	25457243	25457243	G	A	0.5	DNMT3A	Missense	p.R882C
PD5746a	2	25457243	25457243	G	T	0.182	DNMT3A	Missense	p.R882S
PD6123a	2	25457251	25457251	T	C	0.0269	DNMT3A	Missense	p.N879S
PD7084a	2	25457284	25457284	A	G	0.188	DNMT3A	Missense	p.F868S
PD6478a	2	25457291	25457291	T	C	0.41	DNMT3A	Splice site	
PD6197a	2	25458595	25458595	A	G	0.407	DNMT3A	Missense	p.W860R
PD6190a	2	25458604	25458604	C	T	0.0939	DNMT3A	Missense	p.D857N
PD6862a	2	25458627	25458627	G	A	0.301	DNMT3A	Missense	p.P849L
PD6912a	2	25458647	25458648	CT	C	0.03	DNMT3A	Frameshift	p.Q842fs
PD5755a	2	25458649	25458649	G	C	0.174	DNMT3A	Missense	p.Q842E
PD6111a	2	25458659	25458659	G	A	0.0823	DNMT3A	Synonymous	p.N838N
PD6083a	2	25458678	25458678	G	A	0.0886	DNMT3A	Missense	p.T832I
PD5736a	2	25458696	25458696	T	C	0.0663	DNMT3A	Splice site	
PD6973a	2	25459804	25459804	C	T	0.167	DNMT3A	Splice site	
PD6337a	2	25462010	25462010	G	A	0.0598	DNMT3A	Synonymous	p.P799P
PD6875a	2	25462012	25462012	G	A	0.413	DNMT3A	Missense	p.P799S
PD6941a	2	25462017	25462017	T	C	0.163	DNMT3A	Missense	p.N797S
PD6948a	2	25462018	25462018	T	C	0.255	DNMT3A	Missense	p.N797D
PD6118a	2	25462063	25462063	C	T	0.271	DNMT3A	Missense	p.A782T
PD7117a	2	25462068	25462068	A	G	0.376	DNMT3A	Missense	p.I780T
PD6195a	2	25462068	25462068	A	G	0.432	DNMT3A	Missense	p.I780T
PD5748a	2	25462076	25462076	A	G	0.435	DNMT3A	Synonymous	p.P777P
PD5763a	2	25463176	25463177	GA	G	0.042	DNMT3A	Frameshift	p.F772fs
PD6503a	2	25463182	25463182	G	A	0.239	DNMT3A	Nonsense	p.R771X
PD6138a	2	25463182	25463182	G	A	0.389	DNMT3A	Nonsense	p.R771X
PD6826a	2	25463182	25463182	G	A	0.774	DNMT3A	Nonsense	p.R771X
PD7045a	2	25463209	25463209	C	A	0.3	DNMT3A	Missense	p.G762C
PD6215a	2	25463247	25463247	C	A	0.349	DNMT3A	Missense	p.R749L
PD6538a	2	25463287	25463287	G	A	0.432	DNMT3A	Missense	p.R736C
PD6151a	2	25463289	25463289	T	C	0.444	DNMT3A	Missense	p.Y735C
PD6061a	2	25463296	25463297	CA	C	0.085	DNMT3A	Frameshift	p.F732fs
PD7119a	2	25463297	25463300	AAAG	A	0.114	DNMT3A	Inframe	p.731_732del
PD6108a	2	25463297	25463300	AAAG	A	0.064	DNMT3A	Inframe	p.731_732del
PD5742a	2	25463299	25463299	A	G	0.404	DNMT3A	Missense	p.F732L
PD6850a	2	25463303	25463304	GA	G	0.081	DNMT3A	Frameshift	p.L730fs
PD6794a	2	25463541	25463541	G	C	0.165	DNMT3A	Missense	p.S714C

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD5777a	2	25463585	25463586	GC	G	0.292	DNMT3A	Frameshift	p.G699fs
PD6295a	2	25464469	25464470	TG	T	0.221	DNMT3A	Frameshift	p.I681fs
PD5781a	2	25464576	25464576	C	T	0.197	DNMT3A	Missense	p.G646E
PD6256a	2	25466766	25466766	C	T	0.364	DNMT3A	Splice site	
PD7071a	2	25466774	25466774	G	C	0.233	DNMT3A	Missense	p.I643M
PD6960a	2	25466852	25466852	C	T	0.467	DNMT3A	Splice site	
PD6103a	2	25467077	25467077	C	T	0.243	DNMT3A	Missense	p.D600N
PD6266a	2	25467138	25467139	GT	G	0.535	DNMT3A	Frameshift	p.D579fs
PD6141a	2	25467436	25467436	A	C	0.514	DNMT3A	Missense	p.L547R
PD6939a	2	25467473	25467473	A	G	0.361	DNMT3A	Missense	p.S535P
PD6171a	2	25467498	25467498	G	T	0.25	DNMT3A	Nonsense	p.Y526X
PD6300a	2	25468150	25468152	AAG	A	0.35	DNMT3A	Frameshift	p.L508fs
PD6899a	2	25468174	25468174	T	C	0.409	DNMT3A	Missense	p.N501S
PD6793a	2	25468174	25468174	T	C	0.417	DNMT3A	Missense	p.N501S
PD6080a	2	25468174	25468174	T	C	0.523	DNMT3A	Missense	p.N501S
PD6337a	2	25469036	25469036	G	A	0.0323	DNMT3A	Synonymous	p.R474R
PD6523a	2	25469042	25469043	AT	A	0.54	DNMT3A	Frameshift	p.D472fs
PD6920a	2	25469089	25469091	GCT	G	0.161	DNMT3A	Frameshift	p.K456fs
PD7112a	2	25469114	25469114	G	T	0.468	DNMT3A	Nonsense	p.Y448X
PD6869a	2	25469148	25469149	GT	G	0.425	DNMT3A	Frameshift	p.T437fs
PD7087a	2	25469526	25469526	G	C	0.581	DNMT3A	Missense	p.F414L
PD5749a	2	25469528	25469529	AG	A	0.485	DNMT3A	Frameshift	p.G413fs
PD6061a	2	25469569	25469570	TC	T	0.146	DNMT3A	Frameshift	p.E400fs
PD6125a	2	25469603	25469603	C	T	0.566	DNMT3A	Missense	p.D389N
PD6142a	2	25469940	25469940	C	T	0.436	DNMT3A	Missense	p.A368T
PD6841a	2	25469945	25469945	C	G	0.231	DNMT3A	Missense	p.R366P
PD6081a	2	25469975	25469975	T	C	0.168	DNMT3A	Missense	p.Q356R
PD7036a	2	25469998	25469998	G	A	0.456	DNMT3A	Synonymous	p.S348S
PD6902a	2	25470004	25470004	C	A	0.13	DNMT3A	Synonymous	p.P346P
PD6175a	2	25470011	25470011	A	T	0.255	DNMT3A	Missense	p.L344Q
PD7017a	2	25470027	25470027	C	T	0.613	DNMT3A	Missense	p.V339M
PD6169a	2	25470468	25470469	AT	A	0.123	DNMT3A	Frameshift	p.K335fs
PD6852a	2	25470497	25470497	C	A	0.507	DNMT3A	Missense	p.R326L
PD6295a	2	25470518	25470519	CT	C	0.069	DNMT3A	Frameshift	p.S319fs
PD6799a	2	25470968	25470968	C	A	0.578	DNMT3A	Missense	p.V265L
PD6981a	2	25523033	25523033	G	A	0.115	DNMT3A	Missense	p.P51L
PD6298a	2	198257058	198257058	T	C	0.0356	SF3B1	Missense	p.Y1295C
PD6071a	2	198257079	198257079	T	G	0.0637	SF3B1	Missense	p.Y1288S
PD7095a	2	198257705	198257705	A	G	0.505	SF3B1	Synonymous	p.Y1249Y
PD7038a	2	198257870	198257870	G	A	0.469	SF3B1	Synonymous	p.H1194H
PD6910a	2	198257889	198257889	G	A	0.075	SF3B1	Missense	p.A1188V
PD7040a	2	198260882	198260882	C	T	0.0794	SF3B1	Missense	p.G1146E
PD6239a	2	198260883	198260883	C	T	0.333	SF3B1	Missense	p.G1146R
PD6061a	2	198260932	198260932	G	A	0.447	SF3B1	Synonymous	p.L1129L
PD6271a	2	198262741	198262741	G	A	0.532	SF3B1	Synonymous	p.V1078V
PD6786a	2	198263191	198263191	G	A	0.0413	SF3B1	Missense	p.A1043V
PD6881a	2	198265057	198265058	TA	T	0.029	SF3B1	Nonsense	p.L940X
PD6123a	2	198265063	198265063	C	T	0.224	SF3B1	Nonsense	p.W938X
PD6901a	2	198265085	198265085	T	A	0.063	SF3B1	Missense	p.Q931L
PD6133a	2	198265102	198265102	G	A	0.485	SF3B1	Synonymous	p.V925V
PD6931a	2	198266489	198266489	C	G	0.0496	SF3B1	Missense	p.E783Q
PD6123a	2	198266492	198266492	C	G	0.207	SF3B1	Missense	p.E782Q
PD6104a	2	198266494	198266494	T	C	0.143	SF3B1	Missense	p.D781G
PD7002a	2	198266494	198266494	T	C	0.185	SF3B1	Missense	p.D781G
PD6126a	2	198266494	198266494	T	C	0.467	SF3B1	Missense	p.D781G
PD6950a	2	198266562	198266562	A	G	0.461	SF3B1	Synonymous	p.D758D
PD6067a	2	198266605	198266605	G	A	0.0682	SF3B1	Missense	p.A744V
PD6339a	2	198266606	198266606	C	G	0.0609	SF3B1	Missense	p.A744P
PD6145a	2	198266606	198266606	C	G	0.328	SF3B1	Missense	p.A744P
PD6203a	2	198266606	198266606	C	G	0.411	SF3B1	Missense	p.A744P
PD6078a	2	198266606	198266606	C	T	0.0627	SF3B1	Missense	p.A744T
PD7077a	2	198266611	198266611	C	T	0.0708	SF3B1	Missense	p.G742D
PD6075a	2	198266713	198266713	C	T	0.0362	SF3B1	Missense	p.G740E

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6964a	2	198266713	198266713	C	T	0.043	SF3B1	Missense	p.G740E
PD6198a	2	198266714	198266714	C	T	0.0748	SF3B1	Missense	p.G740R
PD6990a	2	198266714	198266714	C	T	0.434	SF3B1	Missense	p.G740R
PD6881a	2	198266810	198266810	C	T	0.0465	SF3B1	Missense	p.A708T
PD6500a	2	198266831	198266831	C	A	0.341	SF3B1	Missense	p.V701F
PD6061a	2	198266831	198266831	C	T	0.129	SF3B1	Missense	p.V701I
PD6102a	2	198266834	198266834	T	C	0.0303	SF3B1	Missense	p.K700E
PD6846a	2	198266834	198266834	T	C	0.04	SF3B1	Missense	p.K700E
PD6248a	2	198266834	198266834	T	C	0.0511	SF3B1	Missense	p.K700E
PD6136a	2	198266834	198266834	T	C	0.0714	SF3B1	Missense	p.K700E
PD6129a	2	198266834	198266834	T	C	0.0734	SF3B1	Missense	p.K700E
PD7089a	2	198266834	198266834	T	C	0.0784	SF3B1	Missense	p.K700E
PD6331a	2	198266834	198266834	T	C	0.0812	SF3B1	Missense	p.K700E
PD6083a	2	198266834	198266834	T	C	0.087	SF3B1	Missense	p.K700E
PD6953a	2	198266834	198266834	T	C	0.0894	SF3B1	Missense	p.K700E
PD6333a	2	198266834	198266834	T	C	0.093	SF3B1	Missense	p.K700E
PD7090a	2	198266834	198266834	T	C	0.103	SF3B1	Missense	p.K700E
PD6298a	2	198266834	198266834	T	C	0.107	SF3B1	Missense	p.K700E
PD6993a	2	198266834	198266834	T	C	0.107	SF3B1	Missense	p.K700E
PD6991a	2	198266834	198266834	T	C	0.124	SF3B1	Missense	p.K700E
PD6259a	2	198266834	198266834	T	C	0.125	SF3B1	Missense	p.K700E
PD6522a	2	198266834	198266834	T	C	0.128	SF3B1	Missense	p.K700E
PD6850a	2	198266834	198266834	T	C	0.133	SF3B1	Missense	p.K700E
PD6265a	2	198266834	198266834	T	C	0.134	SF3B1	Missense	p.K700E
PD7021a	2	198266834	198266834	T	C	0.145	SF3B1	Missense	p.K700E
PD6199a	2	198266834	198266834	T	C	0.147	SF3B1	Missense	p.K700E
PD6938a	2	198266834	198266834	T	C	0.148	SF3B1	Missense	p.K700E
PD6891a	2	198266834	198266834	T	C	0.149	SF3B1	Missense	p.K700E
PD6311a	2	198266834	198266834	T	C	0.16	SF3B1	Missense	p.K700E
PD7011a	2	198266834	198266834	T	C	0.161	SF3B1	Missense	p.K700E
PD6338a	2	198266834	198266834	T	C	0.174	SF3B1	Missense	p.K700E
PD6315a	2	198266834	198266834	T	C	0.178	SF3B1	Missense	p.K700E
PD6831a	2	198266834	198266834	T	C	0.18	SF3B1	Missense	p.K700E
PD6079a	2	198266834	198266834	T	C	0.19	SF3B1	Missense	p.K700E
PD7022a	2	198266834	198266834	T	C	0.19	SF3B1	Missense	p.K700E
PD7108a	2	198266834	198266834	T	C	0.193	SF3B1	Missense	p.K700E
PD6839a	2	198266834	198266834	T	C	0.194	SF3B1	Missense	p.K700E
PD7024a	2	198266834	198266834	T	C	0.196	SF3B1	Missense	p.K700E
PD6337a	2	198266834	198266834	T	C	0.201	SF3B1	Missense	p.K700E
PD6153a	2	198266834	198266834	T	C	0.21	SF3B1	Missense	p.K700E
PD7111a	2	198266834	198266834	T	C	0.218	SF3B1	Missense	p.K700E
PD5780a	2	198266834	198266834	T	C	0.22	SF3B1	Missense	p.K700E
PD6905a	2	198266834	198266834	T	C	0.233	SF3B1	Missense	p.K700E
PD6851a	2	198266834	198266834	T	C	0.236	SF3B1	Missense	p.K700E
PD6094a	2	198266834	198266834	T	C	0.236	SF3B1	Missense	p.K700E
PD5781a	2	198266834	198266834	T	C	0.259	SF3B1	Missense	p.K700E
PD6336a	2	198266834	198266834	T	C	0.27	SF3B1	Missense	p.K700E
PD6948a	2	198266834	198266834	T	C	0.272	SF3B1	Missense	p.K700E
PD6295a	2	198266834	198266834	T	C	0.287	SF3B1	Missense	p.K700E
PD6151a	2	198266834	198266834	T	C	0.293	SF3B1	Missense	p.K700E
PD6304a	2	198266834	198266834	T	C	0.298	SF3B1	Missense	p.K700E
PD7077a	2	198266834	198266834	T	C	0.305	SF3B1	Missense	p.K700E
PD7075a	2	198266834	198266834	T	C	0.313	SF3B1	Missense	p.K700E
PD6540a	2	198266834	198266834	T	C	0.314	SF3B1	Missense	p.K700E
PD6989a	2	198266834	198266834	T	C	0.331	SF3B1	Missense	p.K700E
PD7029a	2	198266834	198266834	T	C	0.34	SF3B1	Missense	p.K700E
PD7076a	2	198266834	198266834	T	C	0.348	SF3B1	Missense	p.K700E
PD6065a	2	198266834	198266834	T	C	0.349	SF3B1	Missense	p.K700E
PD6536a	2	198266834	198266834	T	C	0.349	SF3B1	Missense	p.K700E
PD6961a	2	198266834	198266834	T	C	0.35	SF3B1	Missense	p.K700E
PD7088a	2	198266834	198266834	T	C	0.351	SF3B1	Missense	p.K700E
PD7104a	2	198266834	198266834	T	C	0.353	SF3B1	Missense	p.K700E
PD6497a	2	198266834	198266834	T	C	0.355	SF3B1	Missense	p.K700E

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6247a	2	198266834	198266834	T	C	0.359	SF3B1	Missense	p.K700E
PD6476a	2	198266834	198266834	T	C	0.369	SF3B1	Missense	p.K700E
PD6264a	2	198266834	198266834	T	C	0.373	SF3B1	Missense	p.K700E
PD6518a	2	198266834	198266834	T	C	0.377	SF3B1	Missense	p.K700E
PD6287a	2	198266834	198266834	T	C	0.378	SF3B1	Missense	p.K700E
PD6538a	2	198266834	198266834	T	C	0.378	SF3B1	Missense	p.K700E
PD7105a	2	198266834	198266834	T	C	0.382	SF3B1	Missense	p.K700E
PD6931a	2	198266834	198266834	T	C	0.384	SF3B1	Missense	p.K700E
PD6478a	2	198266834	198266834	T	C	0.388	SF3B1	Missense	p.K700E
PD6142a	2	198266834	198266834	T	C	0.39	SF3B1	Missense	p.K700E
PD7073a	2	198266834	198266834	T	C	0.395	SF3B1	Missense	p.K700E
PD7097a	2	198266834	198266834	T	C	0.396	SF3B1	Missense	p.K700E
PD6144a	2	198266834	198266834	T	C	0.4	SF3B1	Missense	p.K700E
PD6070a	2	198266834	198266834	T	C	0.401	SF3B1	Missense	p.K700E
PD7084a	2	198266834	198266834	T	C	0.402	SF3B1	Missense	p.K700E
PD6300a	2	198266834	198266834	T	C	0.404	SF3B1	Missense	p.K700E
PD7092a	2	198266834	198266834	T	C	0.407	SF3B1	Missense	p.K700E
PD6085a	2	198266834	198266834	T	C	0.408	SF3B1	Missense	p.K700E
PD6262a	2	198266834	198266834	T	C	0.408	SF3B1	Missense	p.K700E
PD6140a	2	198266834	198266834	T	C	0.409	SF3B1	Missense	p.K700E
PD6196a	2	198266834	198266834	T	C	0.415	SF3B1	Missense	p.K700E
PD7072a	2	198266834	198266834	T	C	0.415	SF3B1	Missense	p.K700E
PD6483a	2	198266834	198266834	T	C	0.418	SF3B1	Missense	p.K700E
PD6828a	2	198266834	198266834	T	C	0.421	SF3B1	Missense	p.K700E
PD6225a	2	198266834	198266834	T	C	0.423	SF3B1	Missense	p.K700E
PD7074a	2	198266834	198266834	T	C	0.423	SF3B1	Missense	p.K700E
PD7085a	2	198266834	198266834	T	C	0.43	SF3B1	Missense	p.K700E
PD6835a	2	198266834	198266834	T	C	0.432	SF3B1	Missense	p.K700E
PD6939a	2	198266834	198266834	T	C	0.439	SF3B1	Missense	p.K700E
PD6967a	2	198266834	198266834	T	C	0.439	SF3B1	Missense	p.K700E
PD6802a	2	198266834	198266834	T	C	0.441	SF3B1	Missense	p.K700E
PD6875a	2	198266834	198266834	T	C	0.441	SF3B1	Missense	p.K700E
PD6796a	2	198266834	198266834	T	C	0.443	SF3B1	Missense	p.K700E
PD6999a	2	198266834	198266834	T	C	0.443	SF3B1	Missense	p.K700E
PD5725a	2	198266834	198266834	T	C	0.446	SF3B1	Missense	p.K700E
PD6141a	2	198266834	198266834	T	C	0.447	SF3B1	Missense	p.K700E
PD6837a	2	198266834	198266834	T	C	0.448	SF3B1	Missense	p.K700E
PD6829a	2	198266834	198266834	T	C	0.45	SF3B1	Missense	p.K700E
PD6852a	2	198266834	198266834	T	C	0.455	SF3B1	Missense	p.K700E
PD7000a	2	198266834	198266834	T	C	0.456	SF3B1	Missense	p.K700E
PD6873a	2	198266834	198266834	T	C	0.46	SF3B1	Missense	p.K700E
PD6812a	2	198266834	198266834	T	C	0.464	SF3B1	Missense	p.K700E
PD7098a	2	198266834	198266834	T	C	0.47	SF3B1	Missense	p.K700E
PD6092a	2	198266834	198266834	T	C	0.472	SF3B1	Missense	p.K700E
PD6120a	2	198266834	198266834	T	C	0.478	SF3B1	Missense	p.K700E
PD6074a	2	198266834	198266834	T	C	0.481	SF3B1	Missense	p.K700E
PD6840a	2	198266834	198266834	T	C	0.489	SF3B1	Missense	p.K700E
PD6163a	2	198266834	198266834	T	C	0.492	SF3B1	Missense	p.K700E
PD6779a	2	198266834	198266834	T	C	0.492	SF3B1	Missense	p.K700E
PD6973a	2	198266834	198266834	T	C	0.5	SF3B1	Missense	p.K700E
PD6826a	2	198266834	198266834	T	C	0.509	SF3B1	Missense	p.K700E
PD6133a	2	198266834	198266834	T	C	0.535	SF3B1	Missense	p.K700E
PD7032a	2	198267353	198267353	T	C	0.494	SF3B1	Synonymous	p.V668V
PD5746a	2	198267359	198267359	C	G	0.129	SF3B1	Missense	p.K666N
PD6884a	2	198267359	198267359	C	G	0.416	SF3B1	Missense	p.K666N
PD6481a	2	198267359	198267359	C	G	0.461	SF3B1	Missense	p.K666N
PD6504a	2	198267359	198267359	C	G	0.49	SF3B1	Missense	p.K666N
PD7082a	2	198267360	198267360	T	A	0.424	SF3B1	Missense	p.K666M
PD6083a	2	198267360	198267360	T	C	0.0282	SF3B1	Missense	p.K666R
PD6150a	2	198267360	198267360	T	C	0.0299	SF3B1	Missense	p.K666R
PD6156a	2	198267360	198267360	T	C	0.0638	SF3B1	Missense	p.K666R
PD6927a	2	198267360	198267360	T	C	0.145	SF3B1	Missense	p.K666R
PD7106a	2	198267360	198267360	T	C	0.337	SF3B1	Missense	p.K666R

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7102a	2	198267360	198267360	T	C	0.346	SF3B1	Missense	p.K666R
PD6158a	2	198267360	198267360	T	C	0.405	SF3B1	Missense	p.K666R
PD6059a	2	198267360	198267360	T	C	0.441	SF3B1	Missense	p.K666R
PD6086a	2	198267360	198267360	T	C	0.451	SF3B1	Missense	p.K666R
PD6918a	2	198267360	198267360	T	C	0.454	SF3B1	Missense	p.K666R
PD6994a	2	198267360	198267360	T	C	0.487	SF3B1	Missense	p.K666R
PD6498a	2	198267360	198267360	T	C	0.498	SF3B1	Missense	p.K666R
PD6507a	2	198267360	198267360	T	G	0.288	SF3B1	Missense	p.K666T
PD6337a	2	198267360	198267360	T	G	0.348	SF3B1	Missense	p.K666T
PD7080a	2	198267360	198267360	T	G	0.378	SF3B1	Missense	p.K666T
PD6122a	2	198267360	198267360	T	G	0.481	SF3B1	Missense	p.K666T
PD6830a	2	198267361	198267361	T	G	0.43	SF3B1	Missense	p.K666Q
PD7001a	2	198267361	198267361	T	G	0.447	SF3B1	Missense	p.K666Q
PD6197a	2	198267361	198267361	T	G	0.489	SF3B1	Missense	p.K666Q
PD5779a	2	198267371	198267371	G	C	0.197	SF3B1	Missense	p.H662Q
PD6249a	2	198267371	198267371	G	C	0.216	SF3B1	Missense	p.H662Q
PD6934a	2	198267371	198267371	G	C	0.335	SF3B1	Missense	p.H662Q
PD6107a	2	198267371	198267371	G	C	0.344	SF3B1	Missense	p.H662Q
PD6250a	2	198267371	198267371	G	C	0.364	SF3B1	Missense	p.H662Q
PD6224a	2	198267371	198267371	G	C	0.377	SF3B1	Missense	p.H662Q
PD6221a	2	198267371	198267371	G	C	0.392	SF3B1	Missense	p.H662Q
PD7083a	2	198267371	198267371	G	C	0.406	SF3B1	Missense	p.H662Q
PD6501a	2	198267371	198267371	G	C	0.412	SF3B1	Missense	p.H662Q
PD6054a	2	198267371	198267371	G	C	0.454	SF3B1	Missense	p.H662Q
PD6296a	2	198267371	198267371	G	T	0.169	SF3B1	Missense	p.H662Q
PD7093a	2	198267371	198267371	G	T	0.301	SF3B1	Missense	p.H662Q
PD7078a	2	198267371	198267371	G	T	0.368	SF3B1	Missense	p.H662Q
PD7081a	2	198267371	198267371	G	T	0.394	SF3B1	Missense	p.H662Q
PD6062a	2	198267371	198267371	G	T	0.424	SF3B1	Missense	p.H662Q
PD7079a	2	198267371	198267371	G	T	0.508	SF3B1	Missense	p.H662Q
PD6299a	2	198267373	198267373	G	A	0.0961	SF3B1	Missense	p.H662Y
PD7087a	2	198267373	198267373	G	C	0.283	SF3B1	Missense	p.H662D
PD6995a	2	198267384	198267384	C	T	0.0341	SF3B1	Nonsense	p.W658X
PD6060a	2	198267421	198267421	G	A	0.0584	SF3B1	Missense	p.P646S
PD7010a	2	198267440	198267440	C	T	0.0537	SF3B1	Synonymous	p.L639L
PD7109a	2	198267481	198267481	T	C	0.27	SF3B1	Missense	p.N626D
PD6992a	2	198267483	198267483	C	A	0.0873	SF3B1	Missense	p.R625L
PD6521a	2	198267483	198267483	C	A	0.181	SF3B1	Missense	p.R625L
PD7100a	2	198267483	198267483	C	A	0.289	SF3B1	Missense	p.R625L
PD6959a	2	198267483	198267483	C	A	0.393	SF3B1	Missense	p.R625L
PD6149a	2	198267483	198267483	C	A	0.396	SF3B1	Missense	p.R625L
PD6131a	2	198267483	198267483	C	A	0.409	SF3B1	Missense	p.R625L
PD6091a	2	198267483	198267483	C	A	0.437	SF3B1	Missense	p.R625L
PD6297a	2	198267484	198267484	G	A	0.0426	SF3B1	Missense	p.R625C
PD6079a	2	198267484	198267484	G	A	0.0868	SF3B1	Missense	p.R625C
PD6155a	2	198267484	198267484	G	A	0.11	SF3B1	Missense	p.R625C
PD6511a	2	198267484	198267484	G	A	0.275	SF3B1	Missense	p.R625C
PD6148a	2	198267484	198267484	G	A	0.406	SF3B1	Missense	p.R625C
PD6289a	2	198267484	198267484	G	C	0.443	SF3B1	Missense	p.R625G
PD7111a	2	198267491	198267491	C	A	0.032	SF3B1	Missense	p.E622D
PD7110a	2	198267491	198267491	C	A	0.297	SF3B1	Missense	p.E622D
PD7099a	2	198267491	198267491	C	A	0.367	SF3B1	Missense	p.E622D
PD6490a	2	198267491	198267491	C	A	0.38	SF3B1	Missense	p.E622D
PD6492a	2	198267491	198267491	C	A	0.38	SF3B1	Missense	p.E622D
PD7095a	2	198267491	198267491	C	A	0.387	SF3B1	Missense	p.E622D
PD7112a	2	198267491	198267491	C	A	0.399	SF3B1	Missense	p.E622D
PD6165a	2	198267491	198267491	C	A	0.477	SF3B1	Missense	p.E622D
PD6878a	2	198267491	198267491	C	G	0.211	SF3B1	Missense	p.E622D
PD5788a	2	198267491	198267491	C	G	0.216	SF3B1	Missense	p.E622D
PD6482a	2	198267491	198267491	C	G	0.319	SF3B1	Missense	p.E622D
PD5787a	2	198267491	198267491	C	G	0.381	SF3B1	Missense	p.E622D
PD7086a	2	198267491	198267491	C	G	0.397	SF3B1	Missense	p.E622D
PD7091a	2	198267491	198267491	C	G	0.415	SF3B1	Missense	p.E622D

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7071a	2	198267491	198267491	C	G	0.462	SF3B1	Missense	p.E622D
PD6329a	2	198267705	198267705	C	T	0.309	SF3B1	Missense	p.E592K
PD6514a	2	198267705	198267705	C	T	0.361	SF3B1	Missense	p.E592K
PD6111a	2	198267710	198267710	C	T	0.43	SF3B1	Missense	p.R590K
PD6834a	2	198267751	198267751	C	T	0.518	SF3B1	Synonymous	p.V576V
PD6912a	2	198267753	198267753	C	T	0.0746	SF3B1	Missense	p.V576M
PD6509a	2	198269842	198269842	C	T	0.5	SF3B1	Synonymous	p.K499K
PD7007a	2	198272744	198272744	G	A	0.0895	SF3B1	Missense	p.A406V
PD6067a	2	198272804	198272804	C	T	0.11	SF3B1	Nonsense	p.W386X
PD6060a	2	198272839	198272839	G	A	0.181	SF3B1	Synonymous	p.H374H
PD6965a	2	198273269	198273269	G	A	0.1	SF3B1	Missense	p.P314L
PD6056a	2	198274559	198274559	C	T	0.278	SF3B1	Missense	p.G280D
PD6129a	2	198281599	198281599	C	A	0.201	SF3B1	Missense	p.A178S
PD6238a	2	198281627	198281627	A	G	0.49	SF3B1	Synonymous	p.I168I
PD6071a	2	198283282	198283282	G	A	0.0357	SF3B1	Missense	p.A149V
PD6914a	2	198285795	198285795	G	A	0.0426	SF3B1	Synonymous	p.A86A
PD6995a	2	198288572	198288572	G	T	0.0681	SF3B1	Missense	p.A52D
PD6780a	2	198288580	198288580	G	A	0.0163	SF3B1	Synonymous	p.S49S
PD6104a	2	198288581	198288581	C	T	0.0446	SF3B1	Missense	p.S49N
PD6790a	2	198288583	198288583	G	A	0.126	SF3B1	Synonymous	p.D48D
PD6083a	2	198288593	198288593	C	T	0.0337	SF3B1	Missense	p.G45D
PD6068a	2	198288617	198288617	C	T	0.00724	SF3B1	Missense	p.G37D
PD7039a	2	198288632	198288632	C	T	0.0279	SF3B1	Missense	p.G32D
PD6060a	2	198299714	198299714	T	C	0.0766	SF3B1	Missense	p.I4V
PD5735a	2	209113112	209113112	C	T	0.0117	IDH1	Missense	p.R132H
PD6533a	2	209113112	209113112	C	T	0.0427	IDH1	Missense	p.R132H
PD6179a	2	209113112	209113112	C	T	0.0468	IDH1	Missense	p.R132H
PD6904a	2	209113112	209113112	C	T	0.069	IDH1	Missense	p.R132H
PD6517a	2	209113112	209113112	C	T	0.117	IDH1	Missense	p.R132H
PD6823a	2	209113112	209113112	C	T	0.132	IDH1	Missense	p.R132H
PD7092a	2	209113112	209113112	C	T	0.16	IDH1	Missense	p.R132H
PD7009a	2	209113112	209113112	C	T	0.295	IDH1	Missense	p.R132H
PD6520a	2	209113112	209113112	C	T	0.381	IDH1	Missense	p.R132H
PD6514a	2	209113112	209113112	C	T	0.432	IDH1	Missense	p.R132H
PD6336a	2	209113113	209113113	G	A	0.0143	IDH1	Missense	p.R132C
PD6256a	2	209113113	209113113	G	A	0.0253	IDH1	Missense	p.R132C
PD6885a	2	209113113	209113113	G	A	0.0374	IDH1	Missense	p.R132C
PD6979a	2	209113113	209113113	G	A	0.122	IDH1	Missense	p.R132C
PD6985a	2	209113113	209113113	G	A	0.13	IDH1	Missense	p.R132C
PD6974a	2	209113113	209113113	G	A	0.169	IDH1	Missense	p.R132C
PD6958a	2	209113113	209113113	G	A	0.313	IDH1	Missense	p.R132C
PD6887a	2	209113113	209113113	G	A	0.416	IDH1	Missense	p.R132C
PD6271a	2	209113113	209113113	G	C	0.0283	IDH1	Missense	p.R132G
PD7014a	2	209113152	209113152	G	A	0.348	IDH1	Missense	p.R119W
PD6905a	2	209113320	209113320	C	T	0.0241	IDH1	Missense	p.A63T
PD6067a	2	209113354	209113354	G	A	0.0262	IDH1	Synonymous	p.A51A
PD6979a	4	106155135	106155135	C	T	0.078	TET2	Synonymous	p.N12N
PD6893a	4	106155166	106155166	C	T	0.0304	TET2	Missense	p.P23S
PD7035a	4	106155262	106155262	C	T	0.048	TET2	Missense	p.H55Y
PD6836a	4	106155264	106155264	C	T	0.0236	TET2	Synonymous	p.H55H
PD6934a	4	106155266	106155266	C	T	0.0221	TET2	Missense	p.S56F
PD6850a	4	106155318	106155319	TG	T	0.173	TET2	Nonsense	p.V74X
PD6780a	4	106155360	106155360	G	A	0.0203	TET2	Synonymous	p.K87K
PD7018a	4	106155406	106155406	C	G	0.523	TET2	Missense	p.L103V
PD6787a	4	106155409	106155410	TC	T	0.44	TET2	Frameshift	p.S104fs
PD6920a	4	106155428	106155428	A	G	0.171	TET2	Missense	p.K110R
PD7072a	4	106155471	106155472	CT	C	0.411	TET2	Frameshift	p.F125fs
PD6957a	4	106155495	106155496	TC	T	0.475	TET2	Frameshift	p.P133fs
PD6184a	4	106155506	106155506	G	A	0.0228	TET2	Missense	p.S136N
PD7010a	4	106155535	106155535	G	A	0.025	TET2	Missense	p.D146N
PD7008a	4	106155561	106155562	AG	A	0.018	TET2	Frameshift	p.A155fs
PD6252a	4	106155604	106155606	CAT	C	0.347	TET2	Frameshift	p.H169fs
PD6960a	4	106155608	106155609	AC	A	0.437	TET2	Frameshift	p.N170fs

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6953a	4	106155608	106155609	AC	A	0.017	TET2	Frameshift	p.N170fs
PD6110a	4	106155694	106155694	T	C	0.0214	TET2	Synonymous	p.L199L
PD6098a	4	106155710	106155710	C	T	0.0376	TET2	Missense	p.A204V
PD6790a	4	106155723	106155723	T	G	0.0265	TET2	Synonymous	p.P208P
PD6816a	4	106155731	106155731	C	T	0.068	TET2	Missense	p.A211V
PD7007a	4	106155748	106155749	TC	T	0.033	TET2	Frameshift	p.S217fs
PD6877a	4	106155748	106155749	TC	T	0.385	TET2	Frameshift	p.S217fs
PD7041a	4	106155751	106155752	GT	G	0.029	TET2	Frameshift	p.V218fs
PD6812a	4	106155773	106155774	TC	T	0.431	TET2	Frameshift	p.L225fs
PD6252a	4	106155860	106155861	GT	G	0.206	TET2	Frameshift	p.S254fs
PD6224a	4	106155920	106155921	TC	T	0.122	TET2	Frameshift	p.I274fs
PD6203a	4	106155920	106155921	TC	T	0.404	TET2	Frameshift	p.I274fs
PD6782a	4	106155928	106155928	G	A	0.0502	TET2	Missense	p.A277T
PD6225a	4	106155946	106155946	G	T	0.0282	TET2	Nonsense	p.E283X
PD6517a	4	106155946	106155946	G	T	0.45	TET2	Nonsense	p.E283X
PD6534a	4	106156042	106156043	TC	T	0.293	TET2	Frameshift	p.S315fs
PD6914a	4	106156054	106156054	C	A	0.0277	TET2	Missense	p.P319T
PD5726a	4	106156120	106156120	C	T	0.44	TET2	Nonsense	p.Q341X
PD7004a	4	106156130	106156131	CA	C	0.026	TET2	Frameshift	p.T344fs
PD6794a	4	106156139	106156139	C	T	0.0518	TET2	Missense	p.A347V
PD6302a	4	106156157	106156157	G	A	0.0752	TET2	Missense	p.C353Y
PD6245a	4	106156168	106156169	AG	A	0.403	TET2	Frameshift	p.S357fs
PD6246a	4	106156187	106156187	C	G	0.369	TET2	Missense	p.P363R
PD6872a	4	106156201	106156202	GA	G	0.245	TET2	Frameshift	p.E368fs
PD7116a	4	106156246	106156246	C	T	0.373	TET2	Nonsense	p.Q383X
PD6504a	4	106156262	106156263	CT	C	0.387	TET2	Frameshift	p.T388fs
PD6790a	4	106156279	106156279	G	T	0.0972	TET2	Missense	p.A394S
PD7035a	4	106156325	106156325	C	T	0.0353	TET2	Missense	p.P409L
PD6950a	4	106156333	106156334	CT	C	0.294	TET2	Frameshift	p.L412fs
PD6914a	4	106156339	106156339	C	T	0.0658	TET2	Nonsense	p.Q414X
PD6889a	4	106156348	106156348	C	T	0.874	TET2	Nonsense	p.Q417X
PD6973a	4	106156351	106156351	C	T	0.0972	TET2	Missense	p.L418F
PD5711a	4	106156353	106156354	TC	T	0.309	TET2	Frameshift	p.P419fs
PD6080a	4	106156358	106156358	C	G	0.227	TET2	Nonsense	p.S420X
PD6254a	4	106156360	106156361	GA	G	0.321	TET2	Frameshift	p.E421fs
PD7008a	4	106156366	106156366	A	T	0.348	TET2	Nonsense	p.K423X
PD7077a	4	106156381	106156381	G	A	0.024	TET2	Missense	p.G428S
PD6504a	4	106156399	106156399	C	T	0.451	TET2	Missense	p.H434Y
PD6124a	4	106156417	106156417	C	T	0.0296	TET2	Nonsense	p.Q440X
PD7035a	4	106156419	106156419	A	T	0.0294	TET2	Missense	p.Q440H
PD6982a	4	106156425	106156425	C	T	0.0293	TET2	Synonymous	p.N442N
PD6272a	4	106156453	106156454	GA	G	0.293	TET2	Frameshift	p.E452fs
PD5718a	4	106156468	106156468	G	A	0.0333	TET2	Missense	p.A457T
PD6910a	4	106156484	106156484	G	A	0.0296	TET2	Missense	p.S462N
PD6965a	4	106156497	106156497	T	C	0.0706	TET2	Synonymous	p.S466S
PD6060a	4	106156520	106156520	C	T	0.107	TET2	Missense	p.P474L
PD6857a	4	106156521	106156521	G	A	0.485	TET2	Synonymous	p.P474P
PD6811a	4	106156558	106156558	A	G	0.0607	TET2	Missense	p.R487G
PD5781a	4	106156578	106156579	AG	A	0.043	TET2	Frameshift	p.G494fs
PD5773a	4	106156578	106156579	AG	A	0.884	TET2	Frameshift	p.G494fs
PD6059a	4	106156627	106156627	G	T	0.432	TET2	Nonsense	p.E510X
PD6485a	4	106156657	106156657	G	A	0.511	TET2	Missense	p.G520S
PD6944a	4	106156661	106156661	G	A	0.164	TET2	Missense	p.S521N
PD7016a	4	106156664	106156664	G	A	0.0403	TET2	Missense	p.S522N
PD6124a	4	106156679	106156680	AC	A	0.032	TET2	Frameshift	p.D527fs
PD6877a	4	106156687	106156687	C	T	0.127	TET2	Nonsense	p.Q530X
PD6203a	4	106156687	106156687	C	T	0.444	TET2	Nonsense	p.Q530X
PD6995a	4	106156692	106156692	G	A	0.0227	TET2	Synonymous	p.Q531Q
PD6977a	4	106156711	106156712	CA	C	0.04	TET2	Frameshift	p.Q538fs
PD6129a	4	106156711	106156711	C	T	0.113	TET2	Nonsense	p.Q538X
PD6136a	4	106156726	106156726	G	A	0.0248	TET2	Missense	p.G543S
PD6206a	4	106156729	106156729	C	T	0.37	TET2	Nonsense	p.R544X
PD6194a	4	106156729	106156729	C	T	0.393	TET2	Nonsense	p.R544X

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6484a	4	106156729	106156729	C	T	0.454	TET2	Nonsense	p.R544X
PD7099a	4	106156744	106156745	AC	A	0.352	TET2	Frameshift	p.T549fs
PD7079a	4	106156776	106156776	T	A	0.463	TET2	Nonsense	p.Y559X
PD6068a	4	106156794	106156794	T	C	0.0544	TET2	Synonymous	p.I565I
PD7039a	4	106156795	106156795	G	A	0.111	TET2	Missense	p.E566K
PD6071a	4	106156823	106156823	C	T	0.062	TET2	Missense	p.A575V
PD6061a	4	106156851	106156851	A	G	0.0494	TET2	Synonymous	p.A584A
PD6086a	4	106156870	106156870	C	T	0.0748	TET2	Nonsense	p.Q591X
PD6265a	4	106156875	106156875	T	G	0.254	TET2	Nonsense	p.Y592X
PD6912a	4	106156902	106156902	C	A	0.0216	TET2	Synonymous	p.T601T
PD5747a	4	106156913	106156914	AC	A	0.331	TET2	Nonsense	p.Y605X
PD6995a	4	106156918	106156918	G	T	0.299	TET2	Nonsense	p.G607X
PD6900a	4	106156945	106156945	C	T	0.0303	TET2	Missense	p.P616S
PD6124a	4	106156963	106156963	C	T	0.311	TET2	Nonsense	p.Q622X
PD6317a	4	106157012	106157013	TG	T	0.039	TET2	Frameshift	p.M638fs
PD6824a	4	106157022	106157022	G	A	0.0386	TET2	Synonymous	p.G641G
PD7083a	4	106157053	106157053	C	T	0.346	TET2	Nonsense	p.Q652X
PD6790a	4	106157069	106157069	C	T	0.183	TET2	Missense	p.S657L
PD6228a	4	106157119	106157119	C	T	0.0379	TET2	Nonsense	p.Q674X
PD6867a	4	106157119	106157119	C	T	0.072	TET2	Nonsense	p.Q674X
PD6791a	4	106157119	106157119	C	T	0.482	TET2	Nonsense	p.Q674X
PD6824a	4	106157132	106157132	G	A	0.0619	TET2	Missense	p.G678D
PD6941a	4	106157155	106157155	A	T	0.227	TET2	Nonsense	p.R686X
PD7007a	4	106157160	106157160	A	T	0.0237	TET2	Synonymous	p.A687A
PD6883a	4	106157167	106157167	C	T	0.278	TET2	Nonsense	p.Q690X
PD7106a	4	106157167	106157167	C	T	0.311	TET2	Nonsense	p.Q690X
PD6787a	4	106157167	106157167	C	T	0.405	TET2	Nonsense	p.Q690X
PD6136a	4	106157189	106157189	C	T	0.0402	TET2	Missense	p.P697L
PD6964a	4	106157222	106157222	C	T	0.0284	TET2	Missense	p.S708L
PD6114a	4	106157251	106157252	CT	C	0.066	TET2	Frameshift	p.L718fs
PD5747a	4	106157251	106157252	CT	C	0.305	TET2	Frameshift	p.L718fs
PD6816a	4	106157257	106157257	C	T	0.0655	TET2	Nonsense	p.Q720X
PD6300a	4	106157257	106157257	C	T	0.0682	TET2	Nonsense	p.Q720X
PD6109a	4	106157278	106157278	G	A	0.0888	TET2	Missense	p.A727T
PD6301a	4	106157329	106157329	C	T	0.204	TET2	Nonsense	p.Q744X
PD6985a	4	106157335	106157335	C	T	0.069	TET2	Nonsense	p.Q746X
PD5750a	4	106157367	106157368	AC	A	0.753	TET2	Frameshift	p.L757fs
PD7116a	4	106157371	106157371	C	T	0.333	TET2	Nonsense	p.Q758X
PD6779a	4	106157375	106157377	CTT	C	0.256	TET2	Frameshift	p.T759fs
PD6258a	4	106157379	106157380	TC	T	0.433	TET2	Frameshift	p.P761fs
PD6793a	4	106157407	106157409	CAA	C	0.403	TET2	Frameshift	p.Q770fs
PD6507a	4	106157419	106157419	T	A	0.492	TET2	Missense	p.S774T
PD6108a	4	106157431	106157431	C	T	0.11	TET2	Nonsense	p.Q778X
PD6270a	4	106157450	106157451	GT	G	0.516	TET2	Frameshift	p.C784fs
PD6224a	4	106157455	106157455	C	T	0.0248	TET2	Missense	p.H786Y
PD7078a	4	106157467	106157467	C	T	0.414	TET2	Nonsense	p.Q790X
PD6071a	4	106157527	106157527	C	T	0.302	TET2	Nonsense	p.Q810X
PD6934a	4	106157556	106157556	T	C	0.0204	TET2	Synonymous	p.Y819Y
PD6801a	4	106157562	106157562	G	A	0.0265	TET2	Synonymous	p.Q821Q
PD6521a	4	106157572	106157573	TC	T	0.08	TET2	Nonsense	p.S825X
PD6270a	4	106157573	106157573	C	G	0.455	TET2	Nonsense	p.S825X
PD7082a	4	106157578	106157578	G	A	0.474	TET2	Missense	p.A827T
PD6192a	4	106157603	106157603	C	A	0.426	TET2	Nonsense	p.S835X
PD6539a	4	106157607	106157608	CA	C	0.109	TET2	Frameshift	p.N837fs
PD6540a	4	106157631	106157632	TA	T	0.013	TET2	Frameshift	p.K845fs
PD6539a	4	106157631	106157632	TA	T	0.21	TET2	Frameshift	p.K845fs
PD6194a	4	106157653	106157653	G	A	0.0201	TET2	Missense	p.E852K
PD6977a	4	106157692	106157692	A	T	0.0229	TET2	Missense	p.M865L
PD6124a	4	106157730	106157731	TC	T	0.272	TET2	Frameshift	p.L878fs
PD6200a	4	106157740	106157741	AG	A	0.241	TET2	Frameshift	p.R881fs
PD6201a	4	106157745	106157745	C	A	0.34	TET2	Nonsense	p.C882X
PD6801a	4	106157745	106157745	C	T	0.151	TET2	Synonymous	p.C882C
PD6189a	4	106157763	106157764	GA	G	0.399	TET2	Frameshift	p.K889fs

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD5789a	4	106157770	106157770	C	T	0.0439	TET2	Nonsense	p.Q891X
PD5788a	4	106157770	106157770	C	T	0.195	TET2	Nonsense	p.Q891X
PD6912a	4	106157776	106157776	G	A	0.153	TET2	Missense	p.A893T
PD6970a	4	106157827	106157827	C	T	0.393	TET2	Nonsense	p.Q910X
PD6801a	4	106157834	106157834	C	T	0.29	TET2	Missense	p.A912V
PD7039a	4	106157842	106157842	G	A	0.0371	TET2	Missense	p.A915T
PD6791a	4	106157845	106157845	C	T	0.261	TET2	Nonsense	p.Q916X
PD5776a	4	106157845	106157845	C	T	0.4	TET2	Nonsense	p.Q916X
PD7073a	4	106157845	106157845	C	T	0.408	TET2	Nonsense	p.Q916X
PD6480a	4	106157845	106157845	C	T	0.823	TET2	Nonsense	p.Q916X
PD6794a	4	106157848	106157848	C	T	0.0881	TET2	Nonsense	p.Q917X
PD6803a	4	106157889	106157889	G	A	0.027	TET2	Synonymous	p.V930V
PD7010a	4	106157892	106157893	TG	T	0.082	TET2	Frameshift	p.D932fs
PD6822a	4	106157908	106157909	CA	C	0.046	TET2	Frameshift	p.H937fs
PD6991a	4	106157908	106157908	C	G	0.522	TET2	Missense	p.H937D
PD6782a	4	106157928	106157928	G	A	0.0237	TET2	Synonymous	p.Q943Q
PD6067a	4	106157948	106157948	C	T	0.0326	TET2	Missense	p.A950V
PD6124a	4	106157952	106157952	T	G	0.538	TET2	Synonymous	p.A951A
PD6876a	4	106157995	106157995	C	T	0.243	TET2	Nonsense	p.Q966X
PD6950a	4	106157995	106157995	C	T	0.264	TET2	Nonsense	p.Q966X
PD6800a	4	106158017	106158018	GC	G	0.045	TET2	Frameshift	p.C973fs
PD7000a	4	106158049	106158049	G	T	0.397	TET2	Nonsense	p.E984X
PD6960a	4	106158051	106158052	AC	A	0.343	TET2	Frameshift	p.P985fs
PD6947a	4	106158060	106158060	C	A	0.404	TET2	Nonsense	p.C987X
PD6073a	4	106158064	106158064	C	T	0.0257	TET2	Missense	p.P989S
PD7008a	4	106158108	106158108	G	A	0.051	TET2	Nonsense	p.W1003X
PD6245a	4	106158108	106158109	GA	G	0.478	TET2	Frameshift	p.K1004fs
PD6867a	4	106158144	106158144	C	T	0.0526	TET2	Synonymous	p.S1015S
PD6856a	4	106158168	106158168	C	T	0.0228	TET2	Synonymous	p.S1023S
PD6057a	4	106158185	106158185	A	G	0.0321	TET2	Missense	p.E1029G
PD6301a	4	106158229	106158229	A	T	0.0203	TET2	Nonsense	p.K1044X
PD6296a	4	106158237	106158238	TA	T	0.065	TET2	Frameshift	p.T1047fs
PD6499a	4	106158256	106158256	C	T	0.441	TET2	Nonsense	p.Q1053X
PD6539a	4	106158258	106158259	AG	A	0.346	TET2	Nonsense	p.V1054X
PD7090a	4	106158268	106158268	G	T	0.12	TET2	Nonsense	p.E1057X
PD6125a	4	106158301	106158301	C	T	0.145	TET2	Nonsense	p.Q1068X
PD6893a	4	106158310	106158310	G	A	0.037	TET2	Missense	p.A1071T
PD6068a	4	106158326	106158326	G	A	0.0847	TET2	Missense	p.S1076N
PD6807a	4	106158362	106158362	C	A	0.448	TET2	Nonsense	p.S1088X
PD6073a	4	106158373	106158373	C	T	0.229	TET2	Missense	p.P1092S
PD6334a	4	106158385	106158386	AC	A	0.012	TET2	Frameshift	p.T1096fs
PD6299a	4	106158394	106158395	TC	T	0.028	TET2	Frameshift	p.S1099fs
PD6311a	4	106158407	106158408	AT	A	0.17	TET2	Frameshift	p.N1103fs
PD6264a	4	106158441	106158442	TC	T	0.057	TET2	Frameshift	p.P1115fs
PD6503a	4	106158477	106158478	TC	T	0.282	TET2	Frameshift	p.Q1127fs
PD6100a	4	106162507	106162507	G	A	0.0389	TET2	Missense	p.E1141K
PD6921a	4	106162532	106162532	C	T	0.0678	TET2	Missense	p.T1149I
PD7080a	4	106162537	106162537	C	T	0.0286	TET2	Synonymous	p.L1151L
PD5758a	4	106162544	106162544	C	T	0.0346	TET2	Missense	p.A1153V
PD6283a	4	106162552	106162552	A	T	0.497	TET2	Missense	p.N1156Y
PD6110a	4	106162559	106162559	C	A	0.134	TET2	Missense	p.A1158E
PD6275a	4	106162559	106162559	C	T	0.179	TET2	Missense	p.A1158V
PD5722a	4	106162561	106162561	G	C	0.304	TET2	Missense	p.A1159P
PD6056a	4	106162579	106162579	G	T	0.176	TET2	Nonsense	p.E1165X
PD5751a	4	106163989	106163989	A	C	0.439	TET2	Splice site	
PD6296a	4	106163990	106163990	G	A	0.0286	TET2	Splice site	
PD6803a	4	106164004	106164004	G	A	0.108	TET2	Missense	p.G1172S
PD6523a	4	106164013	106164013	A	T	0.551	TET2	Missense	p.I1175F
PD5777a	4	106164023	106164023	A	G	0.059	TET2	Missense	p.E1178G
PD6881a	4	106164025	106164025	A	G	0.126	TET2	Missense	p.R1179G
PD6232a	4	106164035	106164035	A	AGAA	0.301	TET2	Inframe	p.Y1182delinsYE
PD6123a	4	106164056	106164056	G	A	0.25	TET2	Missense	p.S1189N
PD6087a	4	106164060	106164060	T	G	0.488	TET2	Synonymous	p.S1190S

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6488a	4	106164068	106164068	G	A	0.0271	TET2	Missense	p.C1193Y
PD6143a	4	106164079	106164079	A	G	0.0221	TET2	Missense	p.K1197E
PD5785a	4	106164726	106164726	G	C	0.531	TET2	Splice site	
PD6282a	4	106164741	106164741	C	G	0.514	TET2	Missense	p.S1203R
PD6059a	4	106164757	106164758	CT	C	0.198	TET2	Frameshift	p.L1209fs
PD5726a	4	106164760	106164762	CTG	C	0.493	TET2	Frameshift	p.L1210fs
PD6834a	4	106164764	106164764	G	A	0.436	TET2	Missense	p.C1211Y
PD6261a	4	106164778	106164778	C	T	0.427	TET2	Nonsense	p.R1216X
PD6200a	4	106164787	106164787	C	G	0.169	TET2	Missense	p.H1219D
PD6199a	4	106164787	106164787	C	G	0.462	TET2	Missense	p.H1219D
PD6841a	4	106164794	106164794	G	A	0.219	TET2	Missense	p.C1221Y
PD6995a	4	106164800	106164800	C	T	0.15	TET2	Missense	p.A1223V
PD6141a	4	106164829	106164829	T	G	0.508	TET2	Missense	p.W1233G
PD5776a	4	106164839	106164842	TCCC	T	0.313	TET2	Inframe	p.1236_1237del
PD6799a	4	106164846	106164848	GTC	G	0.104	TET2	Frameshift	p.S1239fs
PD6111a	4	106164862	106164862	C	T	0.0727	TET2	Missense	p.L1244F
PD6834a	4	106164875	106164875	T	C	0.0883	TET2	Missense	p.L1248P
PD6192a	4	106164880	106164880	G	T	0.232	TET2	Nonsense	p.E1250X
PD7086a	4	106164886	106164887	CT	C	0.053	TET2	Frameshift	p.L1252fs
PD6110a	4	106164886	106164886	C	T	0.0307	TET2	Synonymous	p.L1252L
PD6928a	4	106164903	106164903	G	A	0.499	TET2	Synonymous	p.T1257T
PD6201a	4	106164913	106164913	C	T	0.468	TET2	Missense	p.R1261C
PD6189a	4	106164914	106164914	G	A	0.0325	TET2	Missense	p.R1261H
PD6881a	4	106164914	106164914	G	A	0.0667	TET2	Missense	p.R1261H
PD6200a	4	106164914	106164914	G	A	0.195	TET2	Missense	p.R1261H
PD5715a	4	106164914	106164914	G	A	0.341	TET2	Missense	p.R1261H
PD6199a	4	106164914	106164914	G	A	0.405	TET2	Missense	p.R1261H
PD6957a	4	106164920	106164920	G	A	0.463	TET2	Missense	p.C1263Y
PD6259a	4	106180774	106180774	A	C	0.0287	TET2	Splice site	
PD6798a	4	106180780	106180783	ACTT	A	0.012	TET2	Inframe	p.1270_1271del
PD6925a	4	106180784	106180784	G	A	0.374	TET2	Missense	p.C1271Y
PD6334a	4	106180792	106180794	CAG	C	0.376	TET2	Frameshift	p.Q1274fs
PD6545a	4	106180816	106180816	G	C	0.386	TET2	Missense	p.G1282R
PD6337a	4	106180817	106180817	G	A	0.166	TET2	Missense	p.G1282D
PD5740a	4	106180817	106180817	G	A	0.437	TET2	Missense	p.G1282D
PD5751a	4	106180823	106180826	CCTT	C	0.293	TET2	Inframe	p.1284_1285del
PD5715a	4	106180832	106180832	T	C	0.0985	TET2	Missense	p.F1287S
PD7010a	4	106180835	106180835	G	A	0.035	TET2	Missense	p.G1288D
PD7017a	4	106180835	106180835	G	A	0.0541	TET2	Missense	p.G1288D
PD7016a	4	106180835	106180835	G	A	0.0568	TET2	Missense	p.G1288D
PD7006a	4	106180835	106180835	G	A	0.322	TET2	Missense	p.G1288D
PD6479a	4	106180835	106180835	G	A	0.908	TET2	Missense	p.G1288D
PD6303a	4	106180835	106180835	G	T	0.1	TET2	Missense	p.G1288V
PD6808a	4	106180835	106180835	G	T	0.347	TET2	Missense	p.G1288V
PD6266a	4	106180840	106180840	T	C	0.462	TET2	Missense	p.S1290P
PD6301a	4	106180841	106180841	C	T	0.102	TET2	Missense	p.S1290L
PD6244a	4	106180845	106180845	G	T	0.459	TET2	Missense	p.W1291C
PD6537a	4	106180870	106180870	T	A	0.891	TET2	Missense	p.F1300I
PD6067a	4	106180893	106180893	G	A	0.0817	TET2	Synonymous	p.R1307R
PD6498a	4	106180901	106180901	A	C	0.454	TET2	Missense	p.K1310T
PD7090a	4	106180908	106180909	TG	T	0.275	TET2	Frameshift	p.G1313fs
PD7086a	4	106180926	106180926	G	C	0.468	TET2	Missense	p.E1318D
PD6523a	4	106182926	106182926	T	A	0.109	TET2	Missense	p.L1322Q
PD7085a	4	106182926	106182926	T	A	0.239	TET2	Missense	p.L1322Q
PD6808a	4	106182926	106182926	T	G	0.325	TET2	Missense	p.L1322R
PD6540a	4	106182928	106182928	G	T	0.0435	TET2	Nonsense	p.E1323X
PD6803a	4	106182949	106182949	T	C	0.0395	TET2	Missense	p.S1330P
PD6126a	4	106182956	106182956	T	C	0.265	TET2	Missense	p.L1332P
PD6211a	4	106182973	106182973	A	T	0.45	TET2	Nonsense	p.K1338X
PD6071a	4	106183006	106183006	G	C	0.0631	TET2	Splice site	
PD6103a	4	106190772	106190772	A	T	0.0441	TET2	Missense	p.E1350D
PD6054a	4	106190781	106190783	CAG	C	0.158	TET2	Frameshift	p.R1354fs
PD6276a	4	106190786	106190786	C	T	0.416	TET2	Missense	p.A1355V

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7002a	4	106190794	106190794	T	C	0.153	TET2	Missense	p.C1358R
PD7118a	4	106190794	106190794	T	G	0.373	TET2	Missense	p.C1358G
PD6142a	4	106190798	106190798	G	A	0.422	TET2	Missense	p.R1359H
PD6212a	4	106190807	106190807	T	C	0.0219	TET2	Missense	p.L1362P
PD6057a	4	106190817	106190817	C	T	0.0261	TET2	Synonymous	p.G1365G
PD6496a	4	106190818	106190818	C	T	0.0313	TET2	Missense	p.R1366C
PD5744a	4	106190830	106190830	G	A	0.904	TET2	Missense	p.G1370R
PD6288a	4	106190830	106190830	G	T	0.434	TET2	Missense	p.G1370W
PD6901a	4	106190832	106190832	G	A	0.134	TET2	Synonymous	p.G1370G
PD6325a	4	106190850	106190850	C	A	0.176	TET2	Missense	p.D1376E
PD7034a	4	106190852	106190852	T	C	0.141	TET2	Missense	p.F1377S
PD6841a	4	106190855	106190855	G	A	0.134	TET2	Missense	p.C1378Y
PD6516a	4	106190855	106190855	G	A	0.865	TET2	Missense	p.C1378Y
PD6910a	4	106190857	106190857	G	A	0.0298	TET2	Missense	p.A1379T
PD6513a	4	106190858	106190858	C	T	0.499	TET2	Missense	p.A1379V
PD6272a	4	106190860	106190860	C	T	0.323	TET2	Missense	p.H1380Y
PD5724a	4	106190860	106190860	C	T	0.444	TET2	Missense	p.H1380Y
PD6320a	4	106190860	106190860	C	T	0.463	TET2	Missense	p.H1380Y
PD6126a	4	106190873	106190873	A	G	0.0577	TET2	Missense	p.D1384G
PD6278a	4	106190876	106190876	T	TT	0.418	TET2	Frameshift	p.L1385fs
PD6334a	4	106190882	106190882	A	T	0.294	TET2	Missense	p.N1387I
PD7034a	4	106190887	106190887	C	T	0.106	TET2	Nonsense	p.Q1389X
PD7011a	4	106190898	106190898	C	G	0.281	TET2	Missense	p.S1392R
PD6160a	4	106190899	106190899	A	G	0.536	TET2	Missense	p.T1393A
PD6845a	4	106190900	106190900	C	T	0.113	TET2	Missense	p.T1393I
PD6189a	4	106190906	106190906	T	A	0.065	TET2	Splice site	
PD6527a	4	106193728	106193729	CT	C	0.442	TET2	Frameshift	p.T1397fs
PD6789a	4	106193748	106193748	C	T	0.259	TET2	Nonsense	p.R1404X
PD7106a	4	106193748	106193748	C	T	0.299	TET2	Nonsense	p.R1404X
PD6336a	4	106193748	106193748	C	T	0.393	TET2	Nonsense	p.R1404X
PD6123a	4	106193777	106193777	G	A	0.185	TET2	Synonymous	p.E1413E
PD6517a	4	106193787	106193787	G	T	0.406	TET2	Missense	p.V1417F
PD6806a	4	106193811	106193811	G	A	0.0317	TET2	Missense	p.D1425N
PD6985a	4	106193842	106193842	A	G	0.0569	TET2	Missense	p.Q1435R
PD6316a	4	106193844	106193844	G	T	0.0287	TET2	Nonsense	p.E1436X
PD6782a	4	106193856	106193856	C	T	0.0483	TET2	Missense	p.R1440W
PD6281a	4	106193892	106193892	C	T	0.429	TET2	Nonsense	p.R1452X
PD6217a	4	106193893	106193894	GA	G	0.028	TET2	Frameshift	p.R1452fs
PD6332a	4	106193939	106193941	GAA	G	0.3	TET2	Frameshift	p.K1468fs
PD6849a	4	106194010	106194011	AG	A	0.462	TET2	Frameshift	p.K1491fs
PD6970a	4	106194019	106194019	C	G	0.405	TET2	Nonsense	p.S1494X
PD5724a	4	106194057	106194057	C	T	0.327	TET2	Nonsense	p.Q1507X
PD5740a	4	106194058	106194059	AG	A	0.453	TET2	Frameshift	p.Q1507fs
PD6522a	4	106196207	106196208	CT	C	0.169	TET2	Frameshift	p.L1514fs
PD6206a	4	106196267	106196267	C	T	0.31	TET2	Nonsense	p.Q1534X
PD6509a	4	106196306	106196306	C	T	0.0377	TET2	Nonsense	p.Q1547X
PD6484a	4	106196328	106196330	CAG	C	0.403	TET2	Frameshift	p.T1554fs
PD6953a	4	106196332	106196332	G	A	0.024	TET2	Synonymous	p.E1555E
PD6153a	4	106196343	106196344	CT	C	0.006	TET2	Frameshift	p.S1559fs
PD6146a	4	106196379	106196379	G	A	0.0212	TET2	Missense	p.R1571K
PD7014a	4	106196420	106196420	A	T	0.0118	TET2	Missense	p.T1585S
PD6898a	4	106196433	106196434	AT	A	0.392	TET2	Nonsense	p.Y1589X
PD5786a	4	106196456	106196458	TTC	T	0.251	TET2	Frameshift	p.F1597fs
PD6848a	4	106196482	106196483	AG	A	0.327	TET2	Frameshift	p.G1606fs
PD6872a	4	106196491	106196491	T	G	0.367	TET2	Nonsense	p.Y1608X
PD6057a	4	106196492	106196492	T	A	0.125	TET2	Missense	p.L1609M
PD6295a	4	106196528	106196529	CT	C	0.269	TET2	Frameshift	p.L1621fs
PD6189a	4	106196546	106196546	C	T	0.0904	TET2	Nonsense	p.Q1627X
PD6812a	4	106196582	106196582	G	A	0.0247	TET2	Missense	p.V1639M
PD6868a	4	106196591	106196592	TG	T	0.424	TET2	Frameshift	p.C1642fs
PD6156a	4	106196597	106196597	C	T	0.0211	TET2	Missense	p.P1644S
PD6881a	4	106196603	106196603	C	T	0.0482	TET2	Synonymous	p.L1646L
PD6129a	4	106196621	106196621	C	T	0.0368	TET2	Nonsense	p.Q1652X

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6784a	4	106196637	106196637	A	T	0.0397	TET2	Missense	p.D1657V
PD7083a	4	106196650	106196650	T	A	0.312	TET2	Nonsense	p.Y1661X
PD5786a	4	106196654	106196655	AG	A	0.072	TET2	Frameshift	p.S1663fs
PD6874a	4	106196662	106196662	C	T	0.169	TET2	Synonymous	p.D1665D
PD6303a	4	106196726	106196728	CAG	C	0.076	TET2	Frameshift	p.Q1687fs
PD7090a	4	106196726	106196726	C	T	0.069	TET2	Nonsense	p.Q1687X
PD5777a	4	106196762	106196762	C	T	0.0223	TET2	Nonsense	p.Q1699X
PD6935a	4	106196771	106196771	C	T	0.0398	TET2	Nonsense	p.Q1702X
PD6782a	4	106196771	106196771	C	T	0.0443	TET2	Nonsense	p.Q1702X
PD6965a	4	106196771	106196771	C	T	0.105	TET2	Nonsense	p.Q1702X
PD6337a	4	106196771	106196771	C	T	0.158	TET2	Nonsense	p.Q1702X
PD6789a	4	106196775	106196775	G	GG	0.184	TET2	Frameshift	p.G1703fs
PD6096a	4	106196816	106196816	C	T	0.259	TET2	Missense	p.H1717Y
PD6973a	4	106196870	106196870	G	T	0.0453	TET2	Nonsense	p.G1735X
PD6305a	4	106196920	106196921	TA	T	0.347	TET2	Frameshift	p.K1752fs
PD6232a	4	106196921	106196921	A	T	0.51	TET2	Nonsense	p.K1752X
PD6985a	4	106197025	106197025	G	A	0.14	TET2	Synonymous	p.E1786E
PD7027a	4	106197041	106197041	C	T	0.447	TET2	Missense	p.H1792Y
PD6893a	4	106197074	106197074	G	A	0.0289	TET2	Missense	p.A1803T
PD6213a	4	106197094	106197095	TG	T	0.023	TET2	Frameshift	p.A1810fs
PD7093a	4	106197107	106197107	G	T	0.0381	TET2	Nonsense	p.G1814X
PD6224a	4	106197109	106197110	AG	A	0.031	TET2	Frameshift	p.G1815fs
PD6262a	4	106197114	106197114	T	G	0.415	TET2	Nonsense	p.L1816X
PD6824a	4	106197126	106197126	G	A	0.0445	TET2	Missense	p.S1820N
PD6794a	4	106197149	106197149	C	A	0.0298	TET2	Missense	p.Q1828K
PD6081a	4	106197196	106197196	C	T	0.0513	TET2	Synonymous	p.N1843N
PD6842a	4	106197222	106197223	AG	A	0.957	TET2	Frameshift	p.Q1852fs
PD6881a	4	106197247	106197247	G	A	0.0838	TET2	Synonymous	p.G1860G
PD6814a	4	106197272	106197272	G	A	0.043	TET2	Missense	p.G1869R
PD7081a	4	106197275	106197275	T	C	0.486	TET2	Missense	p.S1870P
PD6280a	4	106197285	106197285	T	C	0.0896	TET2	Missense	p.I1873T
PD6317a	4	106197285	106197285	T	C	0.0974	TET2	Missense	p.I1873T
PD6513a	4	106197285	106197285	T	C	0.487	TET2	Missense	p.I1873T
PD6779a	4	106197305	106197305	C	T	0.0255	TET2	Synonymous	p.L1880L
PD7081a	4	106197308	106197308	C	T	0.439	TET2	Missense	p.H1881Y
PD6081a	4	106197309	106197309	A	C	0.298	TET2	Missense	p.H1881P
PD6071a	4	106197313	106197313	C	T	0.0229	TET2	Synonymous	p.A1882A
PD6931a	4	106197317	106197317	A	G	0.402	TET2	Missense	p.T1884A
PD6280a	4	106197317	106197317	A	G	0.471	TET2	Missense	p.T1884A
PD6325a	4	106197318	106197318	C	T	0.156	TET2	Missense	p.T1884I
PD6060a	4	106197321	106197321	C	T	0.0399	TET2	Missense	p.P1885L
PD6056a	4	106197333	106197333	C	T	0.0572	TET2	Missense	p.P1889L
PD7118a	4	106197347	106197347	C	A	0.392	TET2	Missense	p.P1894T
PD6083a	4	106197348	106197348	C	T	0.0547	TET2	Missense	p.P1894L
PD6057a	4	106197348	106197348	C	T	0.16	TET2	Missense	p.P1894L
PD6118a	4	106197349	106197349	C	T	0.0741	TET2	Synonymous	p.P1894P
PD6123a	4	106197351	106197351	C	T	0.237	TET2	Missense	p.T1895I
PD6247a	4	106197371	106197371	T	C	0.347	TET2	Missense	p.Y1902H
PD7031a	4	106197377	106197377	C	T	0.0519	TET2	Missense	p.H1904Y
PD6935a	4	106197405	106197405	G	A	0.0977	TET2	Missense	p.G1913D
PD6282a	4	106197419	106197419	G	T	0.427	TET2	Nonsense	p.E1918X
PD6935a	4	106197423	106197423	C	T	0.0517	TET2	Missense	p.A1919V
PD6784a	4	106197440	106197440	G	A	0.0988	TET2	Missense	p.A1925T
PD6136a	4	106197442	106197442	C	T	0.0478	TET2	Synonymous	p.A1925A
PD6784a	4	106197474	106197474	G	A	0.0765	TET2	Missense	p.G1936D
PD6262a	4	106197491	106197491	C	T	0.179	TET2	Nonsense	p.Q1942X
PD6253a	4	106197552	106197552	C	T	0.484	TET2	Missense	p.P1962L
PD6295a	4	106197552	106197552	C	T	0.526	TET2	Missense	p.P1962L
PD6851a	4	106197557	106197557	T	C	0.192	TET2	Missense	p.Y1964H
PD6888a	4	106197600	106197601	TG	T	0.013	TET2	Frameshift	p.V1978fs
PD6060a	4	106197655	106197655	G	C	0.0205	TET2	Synonymous	p.G1996G
PD6111a	9	5069971	5069971	A	G	0.0634	JAK2	Synonymous	p.V520V
PD7035a	9	5069995	5069995	G	A	0.032	JAK2	Synonymous	p.R528R

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6790a	9	5069996	5069996	C	T	0.0478	JAK2	Missense	p.P529S
PD6118a	9	5072499	5072499	G	A	0.0301	JAK2	Missense	p.S550N
PD6973a	9	5072511	5072511	G	A	0.0929	JAK2	Missense	p.G554D
PD6056a	9	5072579	5072579	G	A	0.0356	JAK2	Missense	p.E577K
PD7021a	9	5073770	5073770	G	T	0.0264	JAK2	Missense	p.V617F
PD5724a	9	5073770	5073770	G	T	0.0354	JAK2	Missense	p.V617F
PD7024a	9	5073770	5073770	G	T	0.0496	JAK2	Missense	p.V617F
PD6229a	9	5073770	5073770	G	T	0.0648	JAK2	Missense	p.V617F
PD6337a	9	5073770	5073770	G	T	0.0655	JAK2	Missense	p.V617F
PD6799a	9	5073770	5073770	G	T	0.0909	JAK2	Missense	p.V617F
PD6191a	9	5073770	5073770	G	T	0.0927	JAK2	Missense	p.V617F
PD7085a	9	5073770	5073770	G	T	0.0973	JAK2	Missense	p.V617F
PD6957a	9	5073770	5073770	G	T	0.098	JAK2	Missense	p.V617F
PD6291a	9	5073770	5073770	G	T	0.102	JAK2	Missense	p.V617F
PD5788a	9	5073770	5073770	G	T	0.103	JAK2	Missense	p.V617F
PD7091a	9	5073770	5073770	G	T	0.143	JAK2	Missense	p.V617F
PD6835a	9	5073770	5073770	G	T	0.17	JAK2	Missense	p.V617F
PD6542a	9	5073770	5073770	G	T	0.18	JAK2	Missense	p.V617F
PD6973a	9	5073770	5073770	G	T	0.181	JAK2	Missense	p.V617F
PD6517a	9	5073770	5073770	G	T	0.216	JAK2	Missense	p.V617F
PD6972a	9	5073770	5073770	G	T	0.245	JAK2	Missense	p.V617F
PD6192a	9	5073770	5073770	G	T	0.268	JAK2	Missense	p.V617F
PD6305a	9	5073770	5073770	G	T	0.309	JAK2	Missense	p.V617F
PD6184a	9	5073770	5073770	G	T	0.33	JAK2	Missense	p.V617F
PD6338a	9	5073770	5073770	G	T	0.392	JAK2	Missense	p.V617F
PD6093a	9	5073770	5073770	G	T	0.399	JAK2	Missense	p.V617F
PD6949a	9	5073770	5073770	G	T	0.429	JAK2	Missense	p.V617F
PD6339a	9	5073770	5073770	G	T	0.471	JAK2	Missense	p.V617F
PD5737a	9	5073770	5073770	G	T	0.518	JAK2	Missense	p.V617F
PD6807a	9	5073770	5073770	G	T	0.524	JAK2	Missense	p.V617F
PD6336a	9	5073770	5073770	G	T	0.547	JAK2	Missense	p.V617F
PD5753a	9	5073770	5073770	G	T	0.569	JAK2	Missense	p.V617F
PD6928a	9	5073770	5073770	G	T	0.66	JAK2	Missense	p.V617F
PD5756a	11	119103313	119103315	GTT	G	0.024	CBL	Frameshift	p.F118fs
PD6200a	11	119142446	119142446	C	T	0.144	CBL	Nonsense	p.R149X
PD6123a	11	119142484	119142484	G	A	0.326	CBL	Missense	p.M161I
PD6056a	11	119142515	119142515	G	A	0.284	CBL	Missense	p.G172R
PD6848a	11	119142563	119142563	G	T	0.216	CBL	Nonsense	p.E188X
PD7079a	11	119142592	119142592	G	A	0.02	CBL	Splice site	
PD6953a	11	119144587	119144587	C	T	0.0327	CBL	Synonymous	p.V200V
PD6240a	11	119144596	119144597	GA	G	0.01	CBL	Frameshift	p.S204fs
PD6782a	11	119144599	119144599	C	T	0.0887	CBL	Synonymous	p.S204S
PD6240a	11	119144603	119144603	C	T	0.123	CBL	Nonsense	p.R206X
PD6787a	11	119144625	119144625	A	AA	0.342	CBL	Frameshift	p.H213fs
PD6497a	11	119144723	119144723	C	T	0.0293	CBL	Nonsense	p.R246X
PD6876a	11	119145564	119145564	A	G	0.219	CBL	Missense	p.N257S
PD6537a	11	119145587	119145587	C	T	0.485	CBL	Missense	p.H265Y
PD6156a	11	119145634	119145634	G	A	0.0799	CBL	Synonymous	p.R280R
PD6103a	11	119145661	119145661	C	T	0.472	CBL	Synonymous	p.G289G
PD5773a	11	119145665	119145665	T	A	0.0939	CBL	Splice site	
PD6893a	11	119146732	119146732	C	A	0.0273	CBL	Missense	p.R299S
PD6122a	11	119148486	119148486	C	T	0.0955	CBL	Nonsense	p.R343X
PD6197a	11	119148486	119148486	C	T	0.258	CBL	Nonsense	p.R343X
PD6255a	11	119148486	119148486	C	T	0.401	CBL	Nonsense	p.R343X
PD6965a	11	119148512	119148512	C	T	0.475	CBL	Synonymous	p.G351G
PD7039a	11	119148528	119148528	C	T	0.0649	CBL	Missense	p.P357S
PD6898a	11	119148537	119148537	C	G	0.0236	CBL	Missense	p.H360D
PD6311a	11	119148549	119148550	AC	A	0.015	CBL	Frameshift	p.T364fs
PD6823a	11	119148552	119148552	C	T	0.0306	CBL	Nonsense	p.Q365X
PD6278a	11	119148891	119148891	T	C	0.0635	CBL	Missense	p.Y371H
PD6178a	11	119148892	119148892	A	C	0.242	CBL	Missense	p.Y371S
PD6071a	11	119148904	119148904	G	A	0.0478	CBL	Missense	p.G375D
PD6898a	11	119148919	119148919	T	C	0.0234	CBL	Missense	p.L380P

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD7039a	11	119148919	119148919	T	C	0.2	CBL	Missense	p.L380P
PD6543a	11	119148919	119148919	T	G	0.227	CBL	Missense	p.L380R
PD6898a	11	119148922	119148922	G	A	0.48	CBL	Missense	p.C381Y
PD7090a	11	119148922	119148922	G	T	0.0401	CBL	Missense	p.C381F
PD7090a	11	119148930	119148930	T	C	0.0179	CBL	Missense	p.C384R
PD6072a	11	119148930	119148930	T	C	0.045	CBL	Missense	p.C384R
PD6945a	11	119148930	119148930	T	C	0.0594	CBL	Missense	p.C384R
PD6289a	11	119148931	119148931	G	A	0.0275	CBL	Missense	p.C384Y
PD6200a	11	119148931	119148931	G	A	0.0673	CBL	Missense	p.C384Y
PD6058a	11	119148931	119148931	G	A	0.158	CBL	Missense	p.C384Y
PD6199a	11	119148931	119148931	G	A	0.288	CBL	Missense	p.C384Y
PD6212a	11	119148947	119148947	G	T	0.1	CBL	Missense	p.K389N
PD7010a	11	119148948	119148948	G	T	0.0542	CBL	Missense	p.D390Y
PD6953a	11	119148958	119148958	T	G	0.0918	CBL	Missense	p.I393S
PD7011a	11	119148962	119148962	G	A	0.513	CBL	Synonymous	p.E394E
PD6277a	11	119148973	119148973	A	C	0.487	CBL	Missense	p.H398P
PD6979a	11	119148976	119148976	T	A	0.0757	CBL	Missense	p.L399H
PD6277a	11	119148990	119148990	T	G	0.224	CBL	Missense	p.C404G
PD6320a	11	119148991	119148991	G	A	0.0302	CBL	Missense	p.C404Y
PD6212a	11	119148991	119148991	G	A	0.123	CBL	Missense	p.C404Y
PD5789a	11	119148991	119148991	G	A	0.246	CBL	Missense	p.C404Y
PD6787a	11	119148991	119148991	G	A	0.255	CBL	Missense	p.C404Y
PD6500a	11	119148991	119148991	G	A	0.83	CBL	Missense	p.C404Y
PD6268a	11	119148992	119148992	T	G	0.801	CBL	Missense	p.C404W
PD6200a	11	119149002	119149002	T	A	0.0216	CBL	Missense	p.W408R
PD6192a	11	119149002	119149002	T	A	0.0301	CBL	Missense	p.W408R
PD6100a	11	119149002	119149002	T	A	0.0349	CBL	Missense	p.W408R
PD6099a	11	119149002	119149002	T	A	0.422	CBL	Missense	p.W408R
PD6106a	11	119149002	119149002	T	A	0.484	CBL	Missense	p.W408R
PD6784a	11	119149005	119149005	C	T	0.083	CBL	Nonsense	p.Q409X
PD6079a	11	119149242	119149242	C	T	0.17	CBL	Missense	p.P417L
PD6200a	11	119149248	119149248	G	A	0.149	CBL	Missense	p.C419Y
PD6283a	11	119149251	119149251	G	A	0.0611	CBL	Missense	p.R420Q
PD6255a	11	119149251	119149251	G	A	0.523	CBL	Missense	p.R420Q
PD6793a	11	119149251	119149251	G	A	0.846	CBL	Missense	p.R420Q
PD6950a	11	119149251	119149251	G	C	0.0223	CBL	Missense	p.R420P
PD6282a	11	119149251	119149251	G	T	0.0378	CBL	Missense	p.R420L
PD6212a	11	119149259	119149259	A	T	0.124	CBL	Missense	p.I423F
PD6780a	11	119149268	119149268	A	C	0.832	CBL	Missense	p.T426P
PD5773a	11	119149311	119149311	G	T	0.488	CBL	Missense	p.G440V
PD6881a	11	119149312	119149312	C	A	0.0476	CBL	Synonymous	p.G440G
PD6200a	11	119149329	119149329	G	A	0.0577	CBL	Missense	p.G446E
PD6122a	11	119155677	119155677	A	G	0.0907	CBL	Splice site	
PD6509a	11	119155710	119155710	C	T	0.454	CBL	Missense	p.A488V
PD6803a	11	119155743	119155743	G	A	0.0267	CBL	Missense	p.R499Q
PD6118a	11	119155802	119155802	G	A	0.0619	CBL	Missense	p.A519T
PD7017a	11	119155953	119155953	C	T	0.0576	CBL	Nonsense	p.R540X
PD6240a	11	119155953	119155953	C	T	0.0616	CBL	Nonsense	p.R540X
PD6902a	11	119155972	119155972	C	T	0.0326	CBL	Missense	p.P546L
PD6901a	11	119156025	119156025	C	T	0.0336	CBL	Missense	p.P564S
PD6289a	11	119156036	119156036	T	A	0.0566	CBL	Nonsense	p.C567X
PD6061a	11	119156045	119156045	C	T	0.0532	CBL	Synonymous	p.G570G
PD6805a	11	119156054	119156054	C	T	0.0242	CBL	Synonymous	p.P573P
PD6110a	11	119156089	119156089	G	A	0.0747	CBL	Missense	p.R585H
PD6914a	11	119156112	119156112	C	T	0.0487	CBL	Missense	p.R593W
PD6068a	11	119156187	119156187	C	T	0.173	CBL	Missense	p.H618Y
PD6973a	11	119158590	119158590	C	T	0.189	CBL	Missense	p.P657L
PD6104a	11	119158591	119158591	A	T	0.0795	CBL	Synonymous	p.P657P
PD6123a	11	119158647	119158647	T	C	0.0287	CBL	Missense	p.L676P
PD7098a	11	119167692	119167692	A	G	0.496	CBL	Missense	p.M701V
PD6973a	11	119168181	119168181	C	T	0.0977	CBL	Synonymous	p.S747S
PD7039a	11	119169103	119169103	G	A	0.0703	CBL	Missense	p.G763S
PD7013a	11	119170251	119170251	C	T	0.063	CBL	Synonymous	p.F827F

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6989a	11	119170256	119170256	G	A	0.496	CBL	Missense	p.R829Q
PD6328a	11	119170294	119170294	C	T	0.0331	CBL	Nonsense	p.Q842X
PD6910a	11	119170310	119170310	C	T	0.0424	CBL	Missense	p.A847V
PD7017a	11	119170311	119170311	C	T	0.0305	CBL	Synonymous	p.A847A
PD6118a	11	119170353	119170353	C	T	0.0676	CBL	Synonymous	p.I861I
PD6787a	11	119170356	119170356	G	A	0.0262	CBL	Synonymous	p.E862E
PD5718a	11	119170365	119170365	G	A	0.0337	CBL	Missense	p.M865I
PD6779a	11	119170426	119170426	G	A	0.0223	CBL	Missense	p.E886K
PD6479a	12	25378561	25378561	G	A	0.115	KRAS	Missense	p.A146V
PD7017a	12	25378637	25378637	G	A	0.0373	KRAS	Missense	p.P121S
PD6863a	12	25378643	25378643	C	T	0.101	KRAS	Missense	p.D119N
PD6276a	12	25378647	25378647	T	A	0.474	KRAS	Missense	p.K117N
PD7116a	12	25378647	25378647	T	G	0.0214	KRAS	Missense	p.K117N
PD6273a	12	25378647	25378647	T	G	0.348	KRAS	Missense	p.K117N
PD6072a	12	25380174	25380174	T	A	0.459	KRAS	Missense	p.H95L
PD7019a	12	25380279	25380279	C	T	0.0415	KRAS	Missense	p.G60D
PD6876a	12	25380280	25380280	C	G	0.24	KRAS	Missense	p.G60R
PD7010a	12	25398217	25398217	T	C	0.0457	KRAS	Synonymous	p.P34P
PD6955a	12	25398220	25398220	A	C	0.323	KRAS	Missense	p.D33E
PD6320a	12	25398220	25398220	A	T	0.0513	KRAS	Missense	p.D33E
PD6793a	12	25398262	25398262	C	G	0.0451	KRAS	Missense	p.L19F
PD6945a	12	25398262	25398262	C	G	0.0475	KRAS	Missense	p.L19F
PD6816a	12	25398276	25398276	C	T	0.227	KRAS	Missense	p.G15S
PD6153a	12	25398279	25398279	C	T	0.049	KRAS	Missense	p.V14I
PD6939a	12	25398281	25398281	C	T	0.0159	KRAS	Missense	p.G13D
PD6475a	12	25398282	25398282	C	A	0.442	KRAS	Missense	p.G13C
PD6894a	12	25398284	25398284	C	A	0.356	KRAS	Missense	p.G12V
PD6946a	12	25398284	25398284	C	T	0.0241	KRAS	Missense	p.G12D
PD6112a	12	25398284	25398284	C	T	0.0306	KRAS	Missense	p.G12D
PD5741a	12	25398284	25398284	C	T	0.0541	KRAS	Missense	p.G12D
PD6215a	12	25398284	25398284	C	T	0.153	KRAS	Missense	p.G12D
PD6913a	12	25398284	25398284	C	T	0.267	KRAS	Missense	p.G12D
PD7025a	12	25398285	25398285	C	T	0.0309	KRAS	Missense	p.G12S
PD6328a	12	112884123	112884123	C	T	0.0728	PTPN11	Synonymous	p.L20L
PD6123a	12	112884154	112884154	T	TT	0.067	PTPN11	Frameshift	p.L30fs
PD6946a	12	112884189	112884189	A	G	0.0336	PTPN11	Missense	p.T42A
PD6935a	12	112888155	112888155	G	A	0.0986	PTPN11	Synonymous	p.Q57Q
PD6335a	12	112888189	112888189	G	A	0.391	PTPN11	Missense	p.E69K
PD6788a	12	112888198	112888198	G	A	0.19	PTPN11	Missense	p.A72T
PD6884a	12	112888199	112888199	C	T	0.502	PTPN11	Missense	p.A72V
PD6263a	12	112888210	112888210	G	A	0.0368	PTPN11	Missense	p.E76K
PD6071a	12	112888247	112888248	TA	T	0.017	PTPN11	Frameshift	p.L88fs
PD6935a	12	112888288	112888288	C	T	0.523	PTPN11	Synonymous	p.L102L
PD6136a	12	112891010	112891010	G	A	0.227	PTPN11	Missense	p.G115E
PD6210a	12	112891117	112891117	G	A	0.0276	PTPN11	Missense	p.V151M
PD6794a	12	112891155	112891155	C	T	0.0848	PTPN11	Synonymous	p.G163G
PD6978a	12	112892398	112892398	C	T	0.475	PTPN11	Missense	p.R186W
PD6803a	12	112910782	112910782	G	A	0.0423	PTPN11	Missense	p.S264N
PD5757a	12	112910785	112910785	G	A	0.0351	PTPN11	Missense	p.R265Q
PD7032a	12	112910785	112910785	G	A	0.361	PTPN11	Missense	p.R265Q
PD5715a	12	112910793	112910793	G	A	0.251	PTPN11	Missense	p.G268S
PD6096a	12	112910839	112910840	TG	T	0.023	PTPN11	Frameshift	p.L283fs
PD6056a	12	112910843	112910843	C	G	0.00711	PTPN11	Synonymous	p.P284P
PD6963a	12	112915523	112915523	A	G	0.0424	PTPN11	Missense	p.N308D
PD6789a	12	112915523	112915523	A	G	0.195	PTPN11	Missense	p.N308D
PD6068a	12	112915713	112915713	C	T	0.0195	PTPN11	Missense	p.A329V
PD6995a	12	112915716	112915716	C	T	0.12	PTPN11	Missense	p.T330I
PD7001a	12	112919928	112919928	C	T	0.481	PTPN11	Synonymous	p.G381G
PD6926a	12	112924381	112924381	C	T	0.0893	PTPN11	Missense	p.H443Y
PD6805a	12	112924383	112924383	C	T	0.0693	PTPN11	Synonymous	p.H443H
PD7016a	12	112924384	112924384	C	T	0.111	PTPN11	Missense	p.H444Y
PD6113a	12	112926267	112926267	G	C	0.0383	PTPN11	Missense	p.G467A
PD6963a	12	112926852	112926852	C	A	0.047	PTPN11	Missense	p.P491H

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6788a	12	112926885	112926885	C	T	0.139	PTPN11	Missense	p.S502L
PD6280a	12	112926887	112926887	G	C	0.11	PTPN11	Missense	p.G503R
PD6965a	12	112926900	112926900	C	T	0.0312	PTPN11	Missense	p.T507I
PD6905a	12	112926910	112926910	G	A	0.0383	PTPN11	Synonymous	p.Q510Q
PD6847a	12	112940006	112940006	C	T	0.484	PTPN11	Missense	p.T553M
PD7013a	12	112940057	112940057	C	T	0.0399	PTPN11	Missense	p.A570V
PD6284a	15	90631838	90631838	C	T	0.306	IDH2	Missense	p.R172K
PD6271a	15	90631838	90631838	C	T	0.328	IDH2	Missense	p.R172K
PD6792a	15	90631878	90631878	G	C	0.646	IDH2	Missense	p.R159G
PD7028a	15	90631934	90631934	C	T	0.204	IDH2	Missense	p.R140Q
PD6968a	15	90631934	90631934	C	T	0.219	IDH2	Missense	p.R140Q
PD6929a	15	90631934	90631934	C	T	0.234	IDH2	Missense	p.R140Q
PD6904a	15	90631934	90631934	C	T	0.25	IDH2	Missense	p.R140Q
PD6940a	15	90631934	90631934	C	T	0.252	IDH2	Missense	p.R140Q
PD6095a	15	90631934	90631934	C	T	0.279	IDH2	Missense	p.R140Q
PD5768a	15	90631934	90631934	C	T	0.315	IDH2	Missense	p.R140Q
PD6491a	15	90631934	90631934	C	T	0.325	IDH2	Missense	p.R140Q
PD6826a	15	90631934	90631934	C	T	0.351	IDH2	Missense	p.R140Q
PD6853a	15	90631934	90631934	C	T	0.362	IDH2	Missense	p.R140Q
PD6998a	15	90631934	90631934	C	T	0.386	IDH2	Missense	p.R140Q
PD5754a	15	90631934	90631934	C	T	0.388	IDH2	Missense	p.R140Q
PD6474a	15	90631934	90631934	C	T	0.398	IDH2	Missense	p.R140Q
PD6058a	15	90631934	90631934	C	T	0.398	IDH2	Missense	p.R140Q
PD6233a	15	90631934	90631934	C	T	0.421	IDH2	Missense	p.R140Q
PD6506a	15	90631934	90631934	C	T	0.438	IDH2	Missense	p.R140Q
PD6256a	15	90631934	90631934	C	T	0.482	IDH2	Missense	p.R140Q
PD5749a	15	90631934	90631934	C	T	0.489	IDH2	Missense	p.R140Q
PD6191a	15	90631934	90631934	C	T	0.5	IDH2	Missense	p.R140Q
PD6182a	15	90631934	90631934	C	T	0.509	IDH2	Missense	p.R140Q
PD6797a	15	90631934	90631934	C	T	0.6	IDH2	Missense	p.R140Q
PD6143a	15	90631935	90631935	G	C	0.0889	IDH2	Missense	p.R140G
PD6881a	17	7572976	7572976	G	T	0.0918	TP53	Missense	p.S339Y
PD6905a	17	7573977	7573977	G	A	0.0805	TP53	Synonymous	p.L311L
PD6901a	17	7574004	7574004	G	T	0.0413	TP53	Missense	p.F302L
PD7016a	17	7574017	7574017	C	T	0.0684	TP53	Missense	p.R298H
PD6083a	17	7574027	7574027	C	T	0.0674	TP53	Missense	p.G295R
PD6474a	17	7574030	7574030	G	A	0.451	TP53	Missense	p.R294C
PD6057a	17	7576558	7576558	G	A	0.0659	TP53	Synonymous	p.Y301Y
PD6811a	17	7576571	7576571	A	G	0.0465	TP53	Missense	p.L297S
PD6222a	17	7576578	7576578	G	A	0.0267	TP53	Missense	p.L295F
PD6293a	17	7576626	7576626	T	G	0.508	TP53	Frameshift	p.X303S
PD5745a	17	7576851	7576852	AC	A	0.355	TP53	Splice site	
PD6784a	17	7576852	7576852	C	A	0.101	TP53	Splice site	
PD6542a	17	7576888	7576888	T	A	0.0911	TP53	Nonsense	p.K281X
PD6541a	17	7576888	7576888	T	A	0.136	TP53	Nonsense	p.K281X
PD6906a	17	7576928	7576928	T	C	0.389	TP53	Splice site	
PD6851a	17	7577091	7577091	G	A	0.0393	TP53	Missense	p.R244C
PD6853a	17	7577091	7577091	G	A	0.517	TP53	Missense	p.R244C
PD6862a	17	7577097	7577097	C	A	0.204	TP53	Missense	p.D242Y
PD6097a	17	7577097	7577097	C	T	0.0538	TP53	Missense	p.D242N
PD7087a	17	7577101	7577101	C	T	0.0206	TP53	Synonymous	p.G240G
PD7116a	17	7577105	7577105	G	C	0.172	TP53	Missense	p.P239R
PD6087a	17	7577114	7577114	C	T	0.0784	TP53	Missense	p.C236Y
PD7038a	17	7577114	7577114	C	T	0.172	TP53	Missense	p.C236Y
PD6246a	17	7577120	7577120	C	T	0.0359	TP53	Missense	p.R234H
PD6236a	17	7577120	7577120	C	T	0.0973	TP53	Missense	p.R234H
PD7016a	17	7577120	7577120	C	T	0.254	TP53	Missense	p.R234H
PD5742a	17	7577120	7577120	C	T	0.341	TP53	Missense	p.R234H
PD6227a	17	7577120	7577120	C	T	0.798	TP53	Missense	p.R234H
PD5755a	17	7577121	7577121	G	A	0.13	TP53	Missense	p.R234C
PD6289a	17	7577121	7577121	G	A	0.314	TP53	Missense	p.R234C
PD6196a	17	7577124	7577124	C	T	0.0316	TP53	Missense	p.V233M
PD6981a	17	7577127	7577127	C	T	0.401	TP53	Missense	p.E232K

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6542a	17	7577130	7577130	A	C	0.106	TP53	Missense	p.F231V
PD6541a	17	7577130	7577130	A	C	0.194	TP53	Missense	p.F231V
PD6073a	17	7577507	7577507	T	A	0.162	TP53	Missense	p.E219D
PD6129a	17	7577507	7577507	T	A	0.246	TP53	Missense	p.E219D
PD6136a	17	7577507	7577507	T	A	0.289	TP53	Missense	p.E219D
PD6076a	17	7577507	7577507	T	A	0.309	TP53	Missense	p.E219D
PD6050a	17	7577507	7577507	T	A	0.464	TP53	Missense	p.E219D
PD6060a	17	7577507	7577507	T	A	0.478	TP53	Missense	p.E219D
PD6506a	17	7577521	7577522	TG	T	0.354	TP53	Frameshift	p.T214fs
PD6097a	17	7577529	7577529	A	C	0.0233	TP53	Missense	p.I212S
PD6096a	17	7577534	7577534	C	T	0.022	TP53	Synonymous	p.R210R
PD5739a	17	7577539	7577539	G	A	0.0179	TP53	Missense	p.R209W
PD6818a	17	7577539	7577539	G	A	0.171	TP53	Missense	p.R209W
PD6336a	17	7577539	7577539	G	A	0.306	TP53	Missense	p.R209W
PD5740a	17	7577539	7577539	G	A	0.445	TP53	Missense	p.R209W
PD6316a	17	7577539	7577539	G	C	0.0725	TP53	Missense	p.R209G
PD6159a	17	7577541	7577541	T	A	0.0714	TP53	Missense	p.N208I
PD6535a	17	7577548	7577548	C	T	0.312	TP53	Missense	p.G206S
PD7116a	17	7577550	7577550	C	T	0.112	TP53	Missense	p.G205D
PD5777a	17	7577551	7577551	C	A	0.074	TP53	Missense	p.G205C
PD6535a	17	7577559	7577559	G	A	0.399	TP53	Missense	p.S202F
PD6527a	17	7577568	7577568	C	T	0.0415	TP53	Missense	p.C199Y
PD6246a	17	7577568	7577568	C	T	0.378	TP53	Missense	p.C199Y
PD6192a	17	7577593	7577595	TAC	T	0.069	TP53	Frameshift	p.C190fs
PD5753a	17	7578190	7578190	T	C	0.102	TP53	Missense	p.Y181C
PD6522a	17	7578190	7578190	T	C	0.179	TP53	Missense	p.Y181C
PD7103a	17	7578190	7578190	T	C	0.337	TP53	Missense	p.Y181C
PD5752a	17	7578190	7578190	T	C	0.469	TP53	Missense	p.Y181C
PD6907a	17	7578203	7578203	C	T	0.328	TP53	Missense	p.V177M
PD6215a	17	7578203	7578203	C	T	0.381	TP53	Missense	p.V177M
PD6831a	17	7578208	7578208	T	C	0.131	TP53	Missense	p.H175R
PD6981a	17	7578212	7578212	G	A	0.0165	TP53	Nonsense	p.R174X
PD6822a	17	7578212	7578212	G	A	0.0359	TP53	Nonsense	p.R174X
PD7089a	17	7578217	7578217	G	A	0.0106	TP53	Missense	p.T172I
PD6782a	17	7578225	7578225	G	A	0.0394	TP53	Synonymous	p.D169D
PD6906a	17	7578234	7578234	A	T	0.402	TP53	Nonsense	p.Y166X
PD6215a	17	7578259	7578259	A	T	0.417	TP53	Missense	p.V158E
PD6502a	17	7578263	7578263	G	A	0.825	TP53	Nonsense	p.R157X
PD7104a	17	7578268	7578268	A	C	0.0479	TP53	Missense	p.L155R
PD7103a	17	7578268	7578268	A	C	0.363	TP53	Missense	p.L155R
PD6110a	17	7578281	7578281	G	A	0.019	TP53	Missense	p.P151S
PD7120a	17	7578388	7578388	C	T	0.473	TP53	Missense	p.R142H
PD6187a	17	7578395	7578395	G	C	0.129	TP53	Missense	p.H140D
PD6051a	17	7578431	7578431	G	A	0.0734	TP53	Nonsense	p.Q128X
PD6223a	17	7578440	7578440	T	C	0.0189	TP53	Missense	p.K125E
PD6235a	17	7578440	7578440	T	C	0.613	TP53	Missense	p.K125E
PD6803a	17	7578448	7578448	G	A	0.061	TP53	Missense	p.A122V
PD6982a	17	7578455	7578455	C	G	0.0409	TP53	Missense	p.A120P
PD7040a	17	7578457	7578457	C	T	0.0955	TP53	Missense	p.R119H
PD6917a	17	7578479	7578479	G	A	0.039	TP53	Missense	p.P112S
PD6794a	17	7578491	7578491	C	T	0.046	TP53	Missense	p.V108I
PD6067a	17	7578501	7578501	C	T	0.0294	TP53	Synonymous	p.V104V
PD6291a	17	7578542	7578542	G	C	0.0657	TP53	Missense	p.L91V
PD6285a	17	7578542	7578542	G	C	0.86	TP53	Missense	p.L91V
PD5742a	17	7579311	7579311	C	A	0.3	TP53	Splice site	
PD6219a	17	7579320	7579322	TCA	T	0.031	TP53	Frameshift	p.V83fs
PD7017a	17	7579334	7579334	G	A	0.208	TP53	Missense	p.T79I
PD6151a	17	7579358	7579358	C	G	0.159	TP53	Missense	p.R71P
PD7040a	17	7579373	7579373	C	A	0.112	TP53	Missense	p.G66V
PD6814a	17	7579378	7579378	G	A	0.078	TP53	Synonymous	p.Y64Y
PD6856a	17	7579576	7579576	G	A	0.0275	TP53	Synonymous	p.S37S
PD5768a	17	74732413	74732414	CG	C	0.031	SRSF2	Frameshift	p.S165fs
PD6256a	17	74732959	74732959	G	A	0.216	SRSF2	Missense	p.P95L

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6301a	17	74732959	74732959	G	A	0.233	SRSF2	Missense	p.P95L
PD6516a	17	74732959	74732959	G	A	0.237	SRSF2	Missense	p.P95L
PD5750a	17	74732959	74732959	G	A	0.24	SRSF2	Missense	p.P95L
PD6523a	17	74732959	74732959	G	A	0.256	SRSF2	Missense	p.P95L
PD6855a	17	74732959	74732959	G	A	0.3	SRSF2	Missense	p.P95L
PD6876a	17	74732959	74732959	G	A	0.31	SRSF2	Missense	p.P95L
PD6312a	17	74732959	74732959	G	A	0.326	SRSF2	Missense	p.P95L
PD6970a	17	74732959	74732959	G	A	0.357	SRSF2	Missense	p.P95L
PD6270a	17	74732959	74732959	G	A	0.375	SRSF2	Missense	p.P95L
PD5714a	17	74732959	74732959	G	A	0.4	SRSF2	Missense	p.P95L
PD6857a	17	74732959	74732959	G	A	0.4	SRSF2	Missense	p.P95L
PD6783a	17	74732959	74732959	G	A	0.407	SRSF2	Missense	p.P95L
PD5717a	17	74732959	74732959	G	A	0.409	SRSF2	Missense	p.P95L
PD6181a	17	74732959	74732959	G	A	0.409	SRSF2	Missense	p.P95L
PD5740a	17	74732959	74732959	G	A	0.447	SRSF2	Missense	p.P95L
PD7116a	17	74732959	74732959	G	A	0.455	SRSF2	Missense	p.P95L
PD6488a	17	74732959	74732959	G	A	0.462	SRSF2	Missense	p.P95L
PD6282a	17	74732959	74732959	G	A	0.471	SRSF2	Missense	p.P95L
PD6945a	17	74732959	74732959	G	A	0.481	SRSF2	Missense	p.P95L
PD6284a	17	74732959	74732959	G	A	0.55	SRSF2	Missense	p.P95L
PD6099a	17	74732959	74732959	G	C	0.13	SRSF2	Missense	p.P95R
PD6320a	17	74732959	74732959	G	C	0.219	SRSF2	Missense	p.P95R
PD6318a	17	74732959	74732959	G	C	0.226	SRSF2	Missense	p.P95R
PD6962a	17	74732959	74732959	G	C	0.25	SRSF2	Missense	p.P95R
PD6504a	17	74732959	74732959	G	C	0.31	SRSF2	Missense	p.P95R
PD5748a	17	74732959	74732959	G	C	0.343	SRSF2	Missense	p.P95R
PD6058a	17	74732959	74732959	G	C	0.359	SRSF2	Missense	p.P95R
PD6527a	17	74732959	74732959	G	C	0.395	SRSF2	Missense	p.P95R
PD5789a	17	74732959	74732959	G	C	0.4	SRSF2	Missense	p.P95R
PD6842a	17	74732959	74732959	G	C	0.407	SRSF2	Missense	p.P95R
PD6940a	17	74732959	74732959	G	C	0.412	SRSF2	Missense	p.P95R
PD5733a	17	74732959	74732959	G	C	0.444	SRSF2	Missense	p.P95R
PD6072a	17	74732959	74732959	G	C	0.444	SRSF2	Missense	p.P95R
PD6499a	17	74732959	74732959	G	C	0.462	SRSF2	Missense	p.P95R
PD7036a	17	74732959	74732959	G	T	0.108	SRSF2	Missense	p.P95H
PD5759a	17	74732959	74732959	G	T	0.16	SRSF2	Missense	p.P95H
PD7118a	17	74732959	74732959	G	T	0.171	SRSF2	Missense	p.P95H
PD5753a	17	74732959	74732959	G	T	0.179	SRSF2	Missense	p.P95H
PD6801a	17	74732959	74732959	G	T	0.231	SRSF2	Missense	p.P95H
PD6929a	17	74732959	74732959	G	T	0.244	SRSF2	Missense	p.P95H
PD6189a	17	74732959	74732959	G	T	0.257	SRSF2	Missense	p.P95H
PD5747a	17	74732959	74732959	G	T	0.258	SRSF2	Missense	p.P95H
PD7031a	17	74732959	74732959	G	T	0.286	SRSF2	Missense	p.P95H
PD6286a	17	74732959	74732959	G	T	0.321	SRSF2	Missense	p.P95H
PD6095a	17	74732959	74732959	G	T	0.333	SRSF2	Missense	p.P95H
PD7028a	17	74732959	74732959	G	T	0.333	SRSF2	Missense	p.P95H
PD6819a	17	74732959	74732959	G	T	0.342	SRSF2	Missense	p.P95H
PD6253a	17	74732959	74732959	G	T	0.344	SRSF2	Missense	p.P95H
PD6545a	17	74732959	74732959	G	T	0.344	SRSF2	Missense	p.P95H
PD6278a	17	74732959	74732959	G	T	0.355	SRSF2	Missense	p.P95H
PD6162a	17	74732959	74732959	G	T	0.368	SRSF2	Missense	p.P95H
PD6800a	17	74732959	74732959	G	T	0.368	SRSF2	Missense	p.P95H
PD6789a	17	74732959	74732959	G	T	0.375	SRSF2	Missense	p.P95H
PD6232a	17	74732959	74732959	G	T	0.381	SRSF2	Missense	p.P95H
PD6786a	17	74732959	74732959	G	T	0.382	SRSF2	Missense	p.P95H
PD6797a	17	74732959	74732959	G	T	0.387	SRSF2	Missense	p.P95H
PD6998a	17	74732959	74732959	G	T	0.409	SRSF2	Missense	p.P95H
PD6335a	17	74732959	74732959	G	T	0.431	SRSF2	Missense	p.P95H
PD5785a	17	74732959	74732959	G	T	0.432	SRSF2	Missense	p.P95H
PD6821a	17	74732959	74732959	G	T	0.476	SRSF2	Missense	p.P95H
PD6274a	17	74732959	74732959	G	T	0.533	SRSF2	Missense	p.P95H
PD6520a	17	74732959	74732959	G	T	0.571	SRSF2	Missense	p.P95H
PD6233a	17	74732960	74732960	G	A	0.769	SRSF2	Missense	p.P95S

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6283a	17	74732960	74732960	G	T	0.333	SRSF2	Missense	p.P95T
PD6255a	17	74732960	74732960	G	T	0.4	SRSF2	Missense	p.P95T
PD6809a	17	74732960	74732960	G	T	0.593	SRSF2	Missense	p.P95T
PD6236a	17	74733013	74733013	C	T	0.127	SRSF2	Missense	p.G77E
PD6075a	17	74733073	74733073	A	T	0.443	SRSF2	Missense	p.F57Y
PD6784a	20	30954240	30954240	C	T	0.0214	ASXL1	Synonymous	p.V37V
PD6912a	20	30954262	30954262	G	A	0.0283	ASXL1	Missense	p.E45K
PD6816a	20	31015939	31015939	C	T	0.0389	ASXL1	Synonymous	p.A87A
PD6060a	20	31015982	31015982	C	T	0.187	ASXL1	Missense	p.P102S
PD6912a	20	31016226	31016226	G	A	0.0228	ASXL1	Splice site	
PD6964a	20	31017181	31017181	G	A	0.0727	ASXL1	Missense	p.R171Q
PD6881a	20	31017227	31017227	T	C	0.0226	ASXL1	Synonymous	p.S186S
PD6123a	20	31019198	31019198	C	T	0.0476	ASXL1	Missense	p.R265C
PD6856a	20	31019254	31019254	G	A	0.0584	ASXL1	Synonymous	p.Q283Q
PD6874a	20	31019255	31019255	C	T	0.0394	ASXL1	Missense	p.L284F
PD7038a	20	31019390	31019390	G	A	0.0714	ASXL1	Missense	p.G296E
PD6912a	20	31019452	31019452	G	A	0.0605	ASXL1	Missense	p.A317T
PD6096a	20	31019460	31019460	C	T	0.201	ASXL1	Synonymous	p.S319S
PD6856a	20	31020711	31020711	G	A	0.055	ASXL1	Synonymous	p.R336R
PD6831a	20	31021124	31021124	G	A	0.388	ASXL1	Missense	p.V375M
PD6143a	20	31021206	31021206	G	A	0.524	ASXL1	Missense	p.R402Q
PD6843a	20	31021226	31021226	A	T	0.455	ASXL1	Nonsense	p.K409X
PD5760a	20	31021250	31021250	C	T	0.134	ASXL1	Nonsense	p.R417X
PD6943a	20	31021250	31021250	C	T	0.403	ASXL1	Nonsense	p.R417X
PD6915a	20	31021423	31021423	C	T	0.536	ASXL1	Synonymous	p.P474P
PD6110a	20	31021435	31021435	T	C	0.0634	ASXL1	Synonymous	p.G478G
PD6474a	20	31021439	31021439	G	T	0.463	ASXL1	Nonsense	p.E480X
PD6070a	20	31021472	31021472	C	T	0.0684	ASXL1	Nonsense	p.Q491X
PD6863a	20	31021499	31021499	G	A	0.0899	ASXL1	Missense	p.A500T
PD6856a	20	31021500	31021500	C	T	0.181	ASXL1	Missense	p.A500V
PD6806a	20	31021585	31021585	G	A	0.363	ASXL1	Synonymous	p.E528E
PD6901a	20	31021658	31021658	G	A	0.0909	ASXL1	Missense	p.E553K
PD6793a	20	31022402	31022425	TCACCAC TGCCATA GAGAGG CGGC	T	0.093	ASXL1	Frameshift	p.H630fs
PD6506a	20	31022402	31022425	TCACCAC TGCCATA GAGAGG CGGC	T	0.129	ASXL1	Frameshift	p.H630fs
PD5756a	20	31022402	31022425	TCACCAC TGCCATA GAGAGG CGGC	T	0.164	ASXL1	Frameshift	p.H630fs
PD6280a	20	31022428	31022430	CCA	C	0.36	ASXL1	Frameshift	p.T638fs
PD6477a	20	31022443	31022443	G	T	0.423	ASXL1	Missense	p.G643V
PD5754a	20	31022562	31022562	A	G	0.452	ASXL1	Missense	p.T683A
PD6790a	20	31022573	31022573	G	A	0.0762	ASXL1	Synonymous	p.K686K
PD6997a	20	31022592	31022592	C	T	0.0787	ASXL1	Nonsense	p.R693X
PD6477a	20	31022592	31022592	C	T	0.423	ASXL1	Nonsense	p.R693X
PD6256a	20	31022592	31022592	C	T	0.425	ASXL1	Nonsense	p.R693X
PD6277a	20	31022592	31022592	C	T	0.465	ASXL1	Nonsense	p.R693X
PD6129a	20	31022634	31022634	A	G	0.0299	ASXL1	Missense	p.T707A
PD6803a	20	31022637	31022637	C	T	0.0974	ASXL1	Nonsense	p.Q708X
PD6847a	20	31022672	31022672	G	A	0.0543	ASXL1	Synonymous	p.E719E
PD6164a	20	31022712	31022712	C	T	0.456	ASXL1	Nonsense	p.Q733X
PD6540a	20	31022715	31022716	AG	A	0.039	ASXL1	Frameshift	p.R734fs
PD6539a	20	31022715	31022716	AG	A	0.353	ASXL1	Frameshift	p.R734fs
PD6972a	20	31022723	31022724	AG	A	0.303	ASXL1	Frameshift	p.V737fs
PD6313a	20	31022759	31022760	AC	A	0.447	ASXL1	Frameshift	p.L749fs
PD6901a	20	31022783	31022783	C	T	0.372	ASXL1	Synonymous	p.D756D
PD6113a	20	31022792	31022792	C	T	0.143	ASXL1	Synonymous	p.C759C
PD6534a	20	31022793	31022793	C	T	0.238	ASXL1	Nonsense	p.Q760X
PD6104a	20	31022797	31022797	C	T	0.123	ASXL1	Missense	p.A761V
PD5776a	20	31022804	31022804	C	T	0.488	ASXL1	Synonymous	p.P763P

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6874a	20	31022824	31022824	C	T	0.258	ASXL1	Missense	p.S770L
PD7031a	20	31022835	31022835	A	T	0.225	ASXL1	Nonsense	p.R774X
PD6093a	20	31022847	31022847	C	T	0.391	ASXL1	Nonsense	p.Q778X
PD6786a	20	31022853	31022853	C	T	0.391	ASXL1	Nonsense	p.Q780X
PD6123a	20	31022862	31022862	C	T	0.029	ASXL1	Missense	p.P783S
PD6835a	20	31022898	31022899	TC	T	0.102	ASXL1	Frameshift	p.S795fs
PD6955a	20	31022902	31022902	G	A	0.233	ASXL1	Nonsense	p.W796X
PD7030a	20	31022904	31022904	G	T	0.0857	ASXL1	Nonsense	p.E797X
PD5748a	20	31022922	31022922	C	T	0.396	ASXL1	Nonsense	p.Q803X
PD6789a	20	31022936	31022937	TC	T	0.204	ASXL1	Frameshift	p.P808fs
PD6788a	20	31022936	31022937	TC	T	0.026	ASXL1	Frameshift	p.P808fs
PD6217a	20	31022936	31022937	TC	T	0.124	ASXL1	Frameshift	p.P808fs
PD6926a	20	31022938	31022938	C	A	0.524	ASXL1	Missense	p.P808H
PD6073a	20	31022960	31022960	G	A	0.0105	ASXL1	Synonymous	p.L815L
PD6783a	20	31022981	31022982	AT	A	0.25	ASXL1	Nonsense	p.L823X
PD6297a	20	31023013	31023014	GT	G	0.026	ASXL1	Frameshift	p.S833fs
PD6287a	20	31023087	31023087	C	T	0.442	ASXL1	Nonsense	p.Q858X
PD6511a	20	31023110	31023111	AT	A	0.015	ASXL1	Nonsense	p.L866X
PD6784a	20	31023124	31023124	G	A	0.0534	ASXL1	Missense	p.G870D
PD6163a	20	31023128	31023128	A	G	0.414	ASXL1	Synonymous	p.S871S
PD6056a	20	31023166	31023167	AC	A	0.007	ASXL1	Frameshift	p.N884fs
PD6169a	20	31023223	31023223	C	CGAAT	0.048	ASXL1	Frameshift	p.S903fs
PD6278a	20	31023300	31023303	GAGT	GGG	0.298	ASXL1	Frameshift	c.2786_2788GG
PD6894a	20	31023356	31023356	G	A	0.0882	ASXL1	Synonymous	p.E947E
PD6893a	20	31023401	31023401	G	A	0.0696	ASXL1	Synonymous	p.V962V
PD7010a	20	31023519	31023520	GC	G	0.044	ASXL1	Frameshift	p.A1002fs
PD7006a	20	31023519	31023520	GC	G	0.312	ASXL1	Frameshift	p.A1002fs
PD6110a	20	31023577	31023577	C	T	0.0508	ASXL1	Missense	p.A1021V
PD6910a	20	31023640	31023640	C	T	0.0459	ASXL1	Missense	p.P1042L
PD6123a	20	31023708	31023709	TG	T	0.017	ASXL1	Frameshift	p.W1065fs
PD6111a	20	31023777	31023777	C	T	0.0942	ASXL1	Nonsense	p.Q1088X
PD6790a	20	31023852	31023852	C	T	0.0396	ASXL1	Nonsense	p.Q1113X
PD6060a	20	31023866	31023866	C	T	0.351	ASXL1	Synonymous	p.P1117P
PD6271a	20	31023892	31023892	A	G	0.536	ASXL1	Missense	p.H1126R
PD6081a	20	31023960	31023960	A	T	0.0568	ASXL1	Missense	p.M1149L
PD6329a	20	31024025	31024026	AG	T	0.257	ASXL1	Frameshift	p.R1171fs
PD6854a	20	31024033	31024033	T	C	0.479	ASXL1	Missense	p.L1173S
PD6247a	20	31024084	31024084	G	A	0.478	ASXL1	Missense	p.R1190K
PD6136a	20	31024132	31024132	C	T	0.0671	ASXL1	Missense	p.A1206V
PD6488a	20	31024149	31024150	TC	T	0.418	ASXL1	Frameshift	p.S1212fs
PD6784a	20	31024208	31024208	C	T	0.0378	ASXL1	Synonymous	p.S1231S
PD6910a	20	31024474	31024474	C	T	0.0596	ASXL1	Missense	p.A1320V
PD6784a	20	31024584	31024584	G	A	0.172	ASXL1	Missense	p.A1357T
PD7016a	20	31024585	31024585	C	T	0.0752	ASXL1	Missense	p.A1357V
PD6056a	20	31024747	31024747	G	A	0.0379	ASXL1	Nonsense	p.W1411X
PD6109a	20	31024755	31024755	C	T	0.188	ASXL1	Missense	p.P1414S
PD6103a	20	31024910	31024911	AG	A	0.028	ASXL1	Frameshift	p.G1466fs
PD6941a	21	44513236	44513236	A	T	0.455	U2AF1	Missense	p.D233E
PD6056a	21	44514591	44514591	G	A	0.431	U2AF1	Missense	p.R189C
PD7020a	21	44514662	44514662	C	T	0.0512	U2AF1	Missense	p.R165Q
PD5723a	21	44514777	44514777	T	C	0.0295	U2AF1	Missense	p.Q157R
PD6872a	21	44514777	44514777	T	C	0.0484	U2AF1	Missense	p.Q157R
PD6196a	21	44514777	44514777	T	C	0.0563	U2AF1	Missense	p.Q157R
PD6197a	21	44514777	44514777	T	C	0.0661	U2AF1	Missense	p.Q157R
PD6474a	21	44514777	44514777	T	C	0.418	U2AF1	Missense	p.Q157R
PD6173a	21	44514777	44514777	T	C	0.444	U2AF1	Missense	p.Q157R
PD6160a	21	44514777	44514777	T	C	0.455	U2AF1	Missense	p.Q157R
PD5726a	21	44514777	44514777	T	C	0.504	U2AF1	Missense	p.Q157R
PD6283a	21	44514777	44514777	T	C	0.525	U2AF1	Missense	p.Q157R
PD6780a	21	44514777	44514777	T	C	0.619	U2AF1	Missense	p.Q157R
PD5784a	21	44514777	44514777	T	G	0.0262	U2AF1	Missense	p.Q157P
PD6168a	21	44514777	44514777	T	G	0.0642	U2AF1	Missense	p.Q157P
PD6088a	21	44514777	44514777	T	G	0.121	U2AF1	Missense	p.Q157P

Sample ID	Chr	Start	End	WT	MT	VAF	Gene	Effect	Protein
PD6988a	21	44514777	44514777	T	G	0.122	U2AF1	Missense	p.Q157P
PD5783a	21	44514777	44514777	T	G	0.124	U2AF1	Missense	p.Q157P
PD6909a	21	44514777	44514777	T	G	0.142	U2AF1	Missense	p.Q157P
PD6953a	21	44514777	44514777	T	G	0.194	U2AF1	Missense	p.Q157P
PD5732a	21	44514777	44514777	T	G	0.245	U2AF1	Missense	p.Q157P
PD6950a	21	44514777	44514777	T	G	0.264	U2AF1	Missense	p.Q157P
PD6534a	21	44514777	44514777	T	G	0.267	U2AF1	Missense	p.Q157P
PD6241a	21	44514777	44514777	T	G	0.299	U2AF1	Missense	p.Q157P
PD6515a	21	44514777	44514777	T	G	0.343	U2AF1	Missense	p.Q157P
PD6240a	21	44514777	44514777	T	G	0.369	U2AF1	Missense	p.Q157P
PD6246a	21	44514777	44514777	T	G	0.377	U2AF1	Missense	p.Q157P
PD6539a	21	44514777	44514777	T	G	0.392	U2AF1	Missense	p.Q157P
PD6093a	21	44514777	44514777	T	G	0.401	U2AF1	Missense	p.Q157P
PD6502a	21	44514777	44514777	T	G	0.403	U2AF1	Missense	p.Q157P
PD6853a	21	44514777	44514777	T	G	0.443	U2AF1	Missense	p.Q157P
PD5756a	21	44514777	44514777	T	G	0.45	U2AF1	Missense	p.Q157P
PD6167a	21	44514777	44514777	T	G	0.46	U2AF1	Missense	p.Q157P
PD6251a	21	44514777	44514777	T	G	0.463	U2AF1	Missense	p.Q157P
PD6188a	21	44514777	44514777	T	G	0.465	U2AF1	Missense	p.Q157P
PD6484a	21	44514777	44514777	T	G	0.466	U2AF1	Missense	p.Q157P
PD6506a	21	44514777	44514777	T	G	0.484	U2AF1	Missense	p.Q157P
PD6191a	21	44514777	44514777	T	G	0.486	U2AF1	Missense	p.Q157P
PD6986a	21	44514780	44514780	C	T	0.234	U2AF1	Missense	p.R156H
PD6794a	21	44514817	44514817	G	A	0.116	U2AF1	Synonymous	p.L144L
PD6934a	21	44514824	44514824	G	C	0.0565	U2AF1	Missense	p.H141Q
PD6900a	21	44514892	44514892	G	A	0.0286	U2AF1	Missense	p.R119C
PD6118a	21	44515578	44515578	T	C	0.299	U2AF1	Synonymous	p.G106G
PD6912a	21	44515805	44515806	TC	T	0.017	U2AF1	Frameshift	p.E83fs
PD7077a	21	44524446	44524446	G	A	0.0442	U2AF1	Missense	p.T9I
PD6155a	21	44524456	44524456	G	A	0.0652	U2AF1	Missense	p.S34F
PD6127a	21	44524456	44524456	G	A	0.0685	U2AF1	Missense	p.S34F
PD7012a	21	44524456	44524456	G	A	0.0708	U2AF1	Missense	p.S34F
PD6903a	21	44524456	44524456	G	A	0.107	U2AF1	Missense	p.S34F
PD5728a	21	44524456	44524456	G	A	0.136	U2AF1	Missense	p.S34F
PD6195a	21	44524456	44524456	G	A	0.248	U2AF1	Missense	p.S34F
PD6926a	21	44524456	44524456	G	A	0.354	U2AF1	Missense	p.S34F
PD6263a	21	44524456	44524456	G	A	0.391	U2AF1	Missense	p.S34F
PD5737a	21	44524456	44524456	G	A	0.397	U2AF1	Missense	p.S34F
PD7117a	21	44524456	44524456	G	A	0.424	U2AF1	Missense	p.S34F
PD6266a	21	44524456	44524456	G	A	0.436	U2AF1	Missense	p.S34F
PD6053a	21	44524456	44524456	G	A	0.465	U2AF1	Missense	p.S34F
PD6485a	21	44524456	44524456	G	A	0.465	U2AF1	Missense	p.S34F
PD6242a	21	44524456	44524456	G	A	0.475	U2AF1	Missense	p.S34F
PD6496a	21	44524456	44524456	G	A	0.488	U2AF1	Missense	p.S34F
PD6147a	21	44524456	44524456	G	A	0.553	U2AF1	Missense	p.S34F
PD6882a	21	44524456	44524456	G	T	0.0251	U2AF1	Missense	p.S34Y
PD6969a	21	44524456	44524456	G	T	0.401	U2AF1	Missense	p.S34Y
PD7039a	21	44524461	44524461	C	T	0.0542	U2AF1	Missense	p.G4D

Table 17a | Gene dN/dS in AML

gene_name	n_syn	n_mis	n_non	n_spl	n_ind	dNdS_missense	p_dNdS_missense	q_dNdS_missense	dNdS_truncating	p_dNdS_truncating	q_dNdS_truncating	pglobal_cv	qglobal_cv
ASXL1	16	39	26	0	23	1.07	8.08E-01	8.28E-01	6.96	7.00E-10	7.35E-09	3.33E-10	9.99E-10
CBL	14	50	1	4	3	1.81	3.52E-02	7.39E-02	1.12	8.32E-01	9.27E-01	1.40E-01	1.96E-01
DNMT3A	7	296	10	7	30	20.86	0.00E+00	0.00E+00	7.21	1.74E-06	9.14E-06	0.00E+00	0.00E+00
IDH1	0	108	0	0	0	168.52	0.00E+00	0.00E+00	0.00	8.03E-01	9.27E-01	0.00E+00	0.00E+00
IDH2	0	156	0	0	0	466.70	0.00E+00	0.00E+00	0.00	8.86E-01	9.30E-01	0.00E+00	0.00E+00
JAK2	0	17	0	0	0	27.57	2.75E-06	1.05E-05	0.00	6.96E-01	8.90E-01	8.00E-05	1.87E-04
KRAS	2	95	1	0	0	32.18	0.00E+00	0.00E+00	1.73	6.55E-01	8.88E-01	0.00E+00	0.00E+00
PTPN11	12	135	2	1	0	5.49	2.71E-13	1.27E-12	0.63	4.59E-01	7.89E-01	8.22E-15	3.14E-14
SF3B1	13	59	1	0	4	1.66	7.56E-02	1.38E-01	0.15	1.71E-02	5.53E-02	1.93E-03	3.85E-03
SRSF2	1	22	0	0	0	7.56	6.18E-04	1.73E-03	0.00	6.07E-01	8.88E-01	1.08E-02	2.06E-02
TET2	32	118	54	11	88	1.52	2.73E-02	6.38E-02	7.81	0.00E+00	0.00E+00	0.00E+00	0.00E+00
TP53	4	112	9	6	10	14.74	0.00E+00	0.00E+00	11.73	2.01E-07	1.21E-06	0.00E+00	0.00E+00
U2AF1	3	40	0	0	1	6.56	7.63E-06	2.29E-05	0.00	2.39E-01	4.57E-01	1.01E-05	2.48E-05

Table 17b | Gene dN/dS in MDS

gene_name	n_syn	n_mis	n_non	n_spl	n_ind	dNdS_missense	p_dNdS_missense	q_dNdS_missense	dNdS_truncating	p_dNdS_truncating	q_dNdS_truncating	pglobal_cv	qglobal_cv
ASXL1	20	31	22	1	18	0.68	1.78E-01	3.11E-01	6.82	1.67E-09	2.34E-08	1.22E-11	1.28E-10
CBL	15	66	13	3	4	2.14	3.37E-03	1.01E-02	4.84	2.06E-05	1.45E-04	3.46E-04	8.06E-04
DNMT3A	7	62	5	5	16	4.42	2.19E-06	1.02E-05	6.12	2.12E-04	9.89E-04	5.17E-06	1.67E-05
IDH1	1	21	0	0	0	13.03	1.94E-06	1.02E-05	0.00	7.12E-01	9.15E-01	9.95E-05	2.99E-04
IDH2	0	25	0	0	0	54.63	1.41E-12	1.97E-11	0.00	8.50E-01	9.15E-01	2.44E-10	2.05E-09
JAK2	2	33	0	0	0	13.85	1.43E-09	1.20E-08	0.00	4.72E-01	8.44E-01	4.02E-08	1.88E-07
KRAS	1	24	0	0	0	10.52	1.21E-05	4.63E-05	0.00	4.82E-01	8.44E-01	1.79E-04	5.02E-04
PTPN11	8	25	0	0	3	1.51	2.73E-01	4.25E-01	0.00	4.36E-02	1.41E-01	7.87E-02	1.65E-01
SF3B1	15	221	3	0	1	5.62	0.00E+00	0.00E+00	0.64	4.53E-01	8.44E-01	0.00E+00	0.00E+00
SRSF2	0	69	0	0	1	51.43	1.11E-16	2.33E-15	0.00	7.51E-01	9.15E-01	7.33E-15	1.03E-13
TET2	41	167	89	6	84	1.72	9.15E-04	2.96E-03	11.75	0.00E+00	0.00E+00	0.00E+00	0.00E+00
TP53	7	68	7	3	4	5.72	7.48E-09	5.23E-08	7.09	6.95E-05	3.65E-04	7.98E-08	3.35E-07
U2AF1	4	59	0	0	1	8.33	1.33E-09	1.20E-08	0.00	2.12E-01	5.23E-01	2.03E-09	1.42E-08

Table 17c | Site dN/dS in AML

chr	pos	ref	mut	gene	aa change	ref3 cod	mut3 cod	freq	mu	dnds	pval	qval	CI_low	CI_high
2	25457242	C	T	DNMT3A	R882H	CGC	CAC	144	0.0599	2403.5	8.923E-144	2.441E-138	2027.00	2829.71
15	90631934	C	T	IDH2	R140Q	CGG	CAG	112	0.0447	2506.3	3.508E-125	4.799E-120	2063.67	3015.72
2	209113112	C	T	IDH1	R132H	CGT	CAT	56	0.0489	1145.1	2.134E-61	6.485E-57	864.96	1486.95
2	25457243	G	A	DNMT3A	R882C	CCG	CTG	51	0.0299	1708.2	3.085E-66	1.055E-61	1271.90	2246.02
2	209113113	G	A	IDH1	R132C	TCG	TTG	43	0.0528	814.0	3.427E-46	7.813E-42	589.11	1096.48
15	90631838	C	T	IDH2	R172K	AGG	AAG	39	0.0242	1612.4	2.097E-54	5.736E-50	1146.57	2204.20
12	25398281	C	T	KRAS	G13D	GGC	GAC	24	0.0078	3088.8	1.460E-45	2.853E-41	1979.04	4595.85
12	25398284	C	T	KRAS	G12D	GGT	GAT	23	0.0477	482.6	2.553E-26	3.037E-22	305.90	724.06
21	44524456	G	A	U2AF1	S34F	TCT	TTT	20	0.0106	1878.8	1.635E-35	2.796E-31	1147.60	2901.59
2	198266834	T	C	SF3B1	K700E	GAA	GGA	14	0.0022	6355.9	9.574E-35	1.541E-30	3474.81	10664.07
9	5073770	G	T	JAK2	V617F	TGT	TTT	12	0.0044	2707.8	2.409E-26	2.996E-22	1399.14	4729.92
12	112926885	C	T	PTPN11	S502L	TCA	TTA	12	0.0084	1433.8	4.546E-23	4.784E-19	740.88	2504.59
12	112888199	C	T	PTPN11	A72V	GCC	GTC	11	0.0057	1916.0	4.976E-23	5.042E-19	956.44	3428.20
12	112888210	G	A	PTPN11	E76K	TGA	TAA	11	0.0061	1789.9	1.043E-22	1.019E-18	893.53	3202.71
12	25398284	C	A	KRAS	G12V	GGT	GTT	10	0.0119	840.9	6.178E-18	4.829E-14	403.25	1546.45
17	74732959	G	T	SRSF2	P95H	CCC	CAC	10	0.0017	5761.7	3.259E-26	3.566E-22	2762.98	10596.05
20	31022592	C	T	ASXL1	R693*	GCG	GTG	9	0.0235	383.0	1.104E-13	5.921E-10	175.14	727.10
2	25457243	G	T	DNMT3A	R882S	CCG	CAG	9	0.0032	2789.2	2.657E-21	2.345E-17	1275.42	5294.86
12	25398284	C	G	KRAS	G12A	GGT	GCT	8	0.0058	1374.7	4.894E-17	3.433E-13	593.49	2708.69
12	112888211	A	G	PTPN11	E76G	GAG	GGG	8	0.0017	4627.6	3.149E-21	2.692E-17	1997.88	9118.28
12	112888198	G	A	PTPN11	A72T	TGC	TAC	8	0.0053	1495.5	2.511E-17	1.808E-13	645.66	2946.78
12	112926888	G	T	PTPN11	G503V	GGG	GTG	7	0.0016	4373.4	5.891E-19	4.884E-15	1758.31	9010.78
12	112888163	G	T	PTPN11	G60V	GGT	GTT	7	0.0119	588.6	6.471E-13	3.219E-09	236.66	1212.81
17	7577538	C	T	TP53	R248Q	CGG	CAG	7	0.0447	156.6	4.613E-09	1.618E-05	62.98	322.75
17	7578406	C	T	TP53	R175H	CGC	CAC	7	0.0599	116.8	3.013E-08	9.699E-05	46.97	240.73
21	44514780	C	T	U2AF1	R156H	CGT	CAT	7	0.0489	143.1	8.259E-09	2.860E-05	57.55	294.91
2	25457242	C	G	DNMT3A	R882P	CGC	CCC	6	0.0027	2190.7	5.097E-15	3.099E-11	803.95	4768.26
12	25380275	T	G	KRAS	Q61H	AAG	ACG	6	0.0020	3052.5	7.022E-16	4.686E-12	1120.22	6644.04
12	112888166	A	T	PTPN11	D61V	GAT	GTT	6	0.0058	1039.2	4.329E-13	2.235E-09	381.38	2261.98
17	74732959	G	C	SRSF2	P95R	CCC	CGC	6	0.0010	5926.4	1.325E-17	9.795E-14	2174.87	12899.20
2	25463541	G	C	DNMT3A	S714C	TCC	TGC	5	0.0011	4504.4	1.170E-14	6.958E-11	1462.57	10511.80
12	112926852	C	T	PTPN11	P491L	CCC	CTC	5	0.0045	1115.2	1.221E-11	5.661E-08	362.09	2602.45
4	106197285	T	C	TET2	I1894T	ATT	ACT	5	0.0042	1183.4	9.094E-12	4.289E-08	384.25	2761.65
17	7578190	T	C	TP53	Y220C	TAT	TGT	5	0.0051	975.1	2.376E-11	1.032E-07	316.60	2275.45
21	44514777	T	G	U2AF1	Q157P	CAG	CCG	5	0.0008	6032.6	2.722E-15	1.692E-11	1958.78	14078.13
11	119148919	T	C	CBL	L380P	CTA	CCA	4	0.0023	1758.9	1.059E-10	4.457E-07	479.24	4503.48
2	209113113	G	C	IDH1	R132G	TCG	TGG	4	0.0032	1244.0	4.205E-10	1.667E-06	338.95	3185.11
12	25398285	C	T	KRAS	G12S	TGG	TAG	4	0.0047	855.9	1.858E-09	6.944E-06	233.20	2191.36
12	25378562	C	T	KRAS	A146T	AGC	AAC	4	0.0047	853.5	1.878E-09	6.944E-06	232.56	2185.35
12	112926888	G	C	PTPN11	G503A	GGG	GCG	4	0.0010	3819.6	4.802E-12	2.346E-08	1040.73	9779.82
2	198267359	C	G	SF3B1	K666N	AGA	ACA	4	0.0030	1336.3	3.163E-10	1.291E-06	364.10	3421.49
2	198267359	C	A	SF3B1	K666N	AGA	ATA	4	0.0068	585.1	8.380E-09	2.866E-05	159.42	1498.09
17	7577559	G	A	TP53	S241F	TCC	TTC	4	0.0030	1324.0	3.281E-10	1.320E-06	360.75	3390.02
17	7577121	G	A	TP53	R273C	GCG	GTG	4	0.0235	170.2	1.045E-06	2.696E-03	46.38	435.87
11	119149251	G	A	CBL	R420Q	CGA	CAA	3	0.0188	159.6	1.434E-05	2.823E-02	32.91	466.32
2	25468174	T	C	DNMT3A	N501S	AAT	AGT	3	0.0027	1101.7	4.721E-08	1.485E-04	227.20	3219.73
2	25463287	G	A	DNMT3A	R736C	CCG	CTG	3	0.0299	100.5	5.442E-05	9.134E-02	20.72	293.66
12	25378561	G	A	KRAS	A146V	GCA	GTA	3	0.0067	445.1	7.015E-07	1.845E-03	91.80	1300.87
12	112888211	A	C	PTPN11	E76A	GAG	GCG	3	0.0007	4096.3	9.279E-10	3.575E-06	844.75	11970.98
12	112888165	G	C	PTPN11	D61H	TGA	TCA	3	0.0010	2872.6	2.686E-09	9.691E-06	592.41	8395.09
12	112915523	A	G	PTPN11	N308D	AAA	AGA	3	0.0012	2585.0	3.684E-09	1.309E-05	533.08	7554.37
12	112888189	G	A	PTPN11	E69K	GGA	GAA	3	0.0041	740.5	1.545E-07	4.593E-04	152.71	2164.03
2	198267484	G	A	SF3B1	R625C	CCG	CTG	3	0.0299	100.5	5.442E-05	9.134E-02	20.72	293.66
17	74732959	G	A	SRSF2	P95L	CCC	CTC	3	0.0045	669.1	2.089E-07	6.016E-04	137.99	1955.41
4	106197552	C	T	TET2	P1983L	CCC	CTC	3	0.0045	669.1	2.089E-07	6.016E-04	137.99	1955.41
4	106157845	C	T	TET2	Q937*	TCA	TTA	3	0.0084	358.5	1.332E-06	3.375E-03	73.92	1047.56
17	7577570	C	T	TP53	M237I	TGT	TAT	3	0.0051	589.9	3.039E-07	8.661E-04	121.65	1723.92

chr	pos	ref	mut	gene	aa change	ref3 cod	mut3 cod	freq	mu	dnds	pval	qval	CI_low	CI_high
17	7577091	G	A	TP53	R283C	GCG	GTG	3	0.0235	127.7	2.736E-05	4.990E-02	26.33	373.12
17	7577539	G	A	TP53	R248W	CCG	CTG	3	0.0299	100.5	5.442E-05	9.134E-02	20.72	293.66
17	7577120	C	T	TP53	R273H	CGT	CAT	3	0.0489	61.3	2.186E-04	3.164E-01	12.65	179.27
21	44514777	T	C	U2AF1	Q157R	CAG	CGG	3	0.0027	1093.0	4.835E-08	1.503E-04	225.40	3194.24
20	31022938	C	A	ASXL1	P808H	CCT	CAT	2	0.0004	5475.5	1.951E-07	5.740E-04	663.10	19779.26
20	31022277	C	T	ASXL1	Q588*	TCA	TTA	2	0.0084	239.0	9.985E-05	1.561E-01	28.94	863.24
11	119148982	G	C	CBL	C401S	TGC	TCC	2	0.0011	1834.7	1.734E-06	4.274E-03	222.19	6627.59
11	119149248	G	A	CBL	C419Y	TGC	TAC	2	0.0053	373.9	4.119E-05	7.317E-02	45.28	1350.59
11	119170354	G	A	CBL	E862K	CGA	CAA	2	0.0188	106.4	4.875E-04	5.512E-01	12.88	384.27
2	25458595	A	G	DNMT3A	W860R	ATG	ACG	2	0.0012	1716.4	1.981E-06	4.592E-03	207.87	6200.39
2	25457209	C	G	DNMT3A	W893S	TGG	TCG	2	0.0019	1070.2	5.083E-06	1.086E-02	129.61	3866.04
2	25463289	T	C	DNMT3A	Y735C	TAC	TGC	2	0.0034	590.6	1.661E-05	3.201E-02	71.52	2133.29
2	25462068	A	G	DNMT3A	I780T	ATT	ACT	2	0.0042	473.4	2.579E-05	4.735E-02	57.33	1709.94
2	25458649	G	A	DNMT3A	Q842*	GCA	GTA	2	0.0067	296.8	6.509E-05	1.073E-01	35.94	1071.98
2	25458696	T	C	DNMT3A	.	TAG	TGG	2	0.0070	286.4	6.981E-05	1.125E-01	34.69	1034.66
2	25458669	G	A	DNMT3A	T835M	ACG	ATG	2	0.0197	101.7	5.324E-04	5.758E-01	12.31	367.21
2	25457176	G	A	DNMT3A	P904L	CCG	CTG	2	0.0299	67.0	1.188E-03	8.387E-01	8.11	241.99
2	25470516	G	A	DNMT3A	R320*	CCG	CTG	2	0.0299	67.0	1.188E-03	8.387E-01	8.11	241.99
2	25463248	G	A	DNMT3A	R749C	TCG	TTG	2	0.0528	37.9	3.471E-03	1.000E+00	4.59	136.77
2	209113112	C	A	IDH1	R132L	CGT	CTT	2	0.0029	687.0	1.229E-05	2.448E-02	83.20	2481.80
2	209113113	G	T	IDH1	R132S	TCG	TAG	2	0.0087	228.7	1.089E-04	1.683E-01	27.70	826.21
12	25378647	T	G	KRAS	K117N	AAT	ACT	2	0.0007	2983.2	6.567E-07	1.744E-03	361.28	10776.49
12	25378647	T	A	KRAS	K117N	AAT	ATT	2	0.0011	1789.9	1.822E-06	4.315E-03	216.77	6465.89
12	25398285	C	G	KRAS	G12R	TGG	TCG	2	0.0019	1070.2	5.083E-06	1.086E-02	129.61	3866.04
12	25380285	G	A	KRAS	T58I	ACA	ATA	2	0.0070	285.4	7.029E-05	1.125E-01	34.57	1031.10
12	112888199	C	A	PTPN11	A72D	GCC	GAC	2	0.0002	8610.3	7.895E-08	2.427E-04	1042.74	31103.28
12	112888199	C	G	PTPN11	A72G	GCC	GGC	2	0.0005	4113.2	3.457E-07	9.749E-04	498.12	14858.19
12	112926249	C	G	PTPN11	A461G	GCT	GGT	2	0.0006	3546.2	4.649E-07	1.259E-03	429.46	12810.03
12	112926910	G	C	PTPN11	Q510H	AGT	ACT	2	0.0010	1992.7	1.470E-06	3.690E-03	241.32	7198.27
12	112888165	G	T	PTPN11	D61Y	TGA	TTA	2	0.0011	1806.9	1.788E-06	4.290E-03	218.82	6527.12
12	112926884	T	G	PTPN11	S502A	GTC	GGC	2	0.0012	1703.3	2.011E-06	4.624E-03	206.28	6153.00
12	112926884	T	C	PTPN11	S502P	GTC	GCC	2	0.0020	998.7	5.835E-06	1.228E-02	120.95	3607.66
12	112888220	A	G	PTPN11	Q79R	CAG	CGG	2	0.0027	728.7	1.093E-05	2.216E-02	88.25	2632.22
12	112915455	T	C	PTPN11	F285S	GTT	GCT	2	0.0028	725.5	1.103E-05	2.219E-02	87.86	2620.73
12	112888165	G	A	PTPN11	D61N	TGA	TAA	2	0.0061	325.4	5.422E-05	9.134E-02	39.41	1175.62
2	198267360	T	G	SF3B1	K666T	AAG	ACG	2	0.0020	1017.5	5.622E-06	1.192E-02	123.22	3675.58
17	74733073	A	T	SRSF2	F57Y	TTC	TAC	2	0.0005	3708.9	4.251E-07	1.187E-03	449.17	13398.00
4	106197282	T	G	TET2	L1893R	CTC	CGC	2	0.0012	1665.6	2.103E-06	4.795E-03	201.71	6016.59
4	106157677	C	T	TET2	Q881*	CCA	CTA	2	0.0041	486.9	2.439E-05	4.508E-02	58.96	1758.71
4	106180790	G	T	TET2	C1294F	TGT	TTT	2	0.0044	451.3	2.835E-05	5.137E-02	54.65	1630.23
4	106182940	C	T	TET2	Q1348*	GCA	GTA	2	0.0067	296.8	6.509E-05	1.073E-01	35.94	1071.98
4	106157527	C	T	TET2	Q831*	ACA	ATA	2	0.0070	285.4	7.029E-05	1.125E-01	34.57	1031.10
4	106157971	C	T	TET2	Q979*	ACA	ATA	2	0.0070	285.4	7.029E-05	1.125E-01	34.57	1031.10
4	106190860	C	T	TET2	H1401Y	TCA	TTA	2	0.0084	239.0	9.985E-05	1.561E-01	28.94	863.24
4	106180927	G	T	TET2	.	GGT	GTT	2	0.0119	168.2	1.993E-04	2.960E-01	20.37	607.53
4	106164778	C	T	TET2	R1237*	GCG	GTG	2	0.0235	85.1	7.505E-04	7.466E-01	10.31	307.47
4	106190797	C	T	TET2	R1380C	CCG	CTG	2	0.0299	67.0	1.188E-03	8.387E-01	8.11	241.99
4	106193748	C	T	TET2	R1425*	TCG	TTG	2	0.0528	37.9	3.471E-03	1.000E+00	4.59	136.77
17	7578542	G	C	TP53	L130V	CCT	CGT	2	0.0007	2737.7	7.796E-07	2.031E-03	331.55	9889.63
17	7578204	A	C	TP53	S215R	GTG	GGG	2	0.0009	2241.9	1.162E-06	2.971E-03	271.50	8098.39
17	7578535	T	C	TP53	K132R	AAG	AGG	2	0.0021	956.0	6.366E-06	1.329E-02	115.78	3453.44
17	7577566	T	C	TP53	N239D	TAA	TGA	2	0.0029	685.5	1.235E-05	2.448E-02	83.01	2476.17
17	7578442	T	C	TP53	Y163C	TAC	TGC	2	0.0034	590.6	1.661E-05	3.201E-02	71.52	2133.29
17	7578492	C	T	TP53	W146*	GGG	GAG	2	0.0038	530.2	2.058E-05	3.922E-02	64.21	1915.34
17	7577577	T	C	TP53	N235S	AAC	AGC	2	0.0038	527.6	2.079E-05	3.922E-02	63.89	1905.81
17	7578437	G	A	TP53	Q165*	GCA	GTA	2	0.0067	296.8	6.509E-05	1.073E-01	35.94	1071.98
17	7578440	T	C	TP53	K164E	CAA	CGA	2	0.0073	273.7	7.635E-05	1.214E-01	33.15	988.88
17	7577547	C	T	TP53	G245D	GGC	GAC	2	0.0078	257.4	8.623E-05	1.364E-01	31.17	929.81
17	7577124	C	T	TP53	V272M	GGT	GAT	2	0.0477	42.0	2.869E-03	1.000E+00	5.08	151.58
21	44524456	G	T	U2AF1	S34Y	TCT	TAT	2	0.0016	1239.5	3.793E-06	8.235E-03	150.11	4477.50
21	44524453	C	A	U2AF1	R35L	CGG	CTG	2	0.0021	945.4	6.509E-06	1.329E-02	114.49	3415.05

Table 17d | Site dN/dS in MDS

chr	pos	ref	mut	gene	aachange	ref3_cod	mut3_cod	freq	mu	dnds	pval	qval	CI_low	CI_high
2	198266834	T	C	SF3B1	K700E	GAA	GGA	109	0.0291	3747.4	0.000E+00	0.000E+00	3076.97	4520.43
9	5073770	G	T	JAK2	V617F	TGT	TTT	29	0.0137	2123.5	1.404E-85	1.280E-80	1422.14	3049.70
17	74732959	G	T	SRSF2	P95H	CCC	CAC	28	0.0093	3017.3	5.832E-87	7.978E-82	2004.94	4360.77
21	44514777	T	G	U2AF1	Q157P	CAG	CCG	25	0.0054	4613.7	1.921E-82	1.314E-77	2985.73	6810.70
17	74732959	G	A	SRSF2	P95L	CCC	CTC	21	0.0126	1662.6	3.215E-60	1.759E-55	1029.16	2541.41
15	90631934	C	T	IDH2	R140Q	CGG	CAG	21	0.0185	1133.0	1.004E-56	4.579E-52	701.37	1731.97
21	44524456	G	A	U2AF1	S34F	TCT	TTT	16	0.0160	1001.7	9.520E-43	3.256E-38	572.57	1626.72
17	74732959	G	C	SRSF2	P95R	CCC	CGC	14	0.0044	3194.7	1.205E-44	4.708E-40	1746.59	5360.22
2	198267360	T	C	SF3B1	K666R	AAG	AGG	12	0.0051	2354.3	6.825E-37	2.075E-32	1216.48	4112.41
2	25457242	C	T	DNMT3A	R882H	CGC	CAC	11	0.0211	522.2	9.401E-27	2.068E-22	260.69	934.38
2	198267371	G	C	SF3B1	H662Q	ACA	AGA	10	0.0032	3161.3	2.883E-32	7.886E-28	1515.97	5813.76
21	44514777	T	C	U2AF1	Q157R	CAG	CGG	10	0.0046	2170.4	1.237E-30	3.077E-26	1040.79	3991.45
2	209113112	C	T	IDH1	R132H	CGT	CAT	10	0.0364	274.9	1.130E-21	1.932E-17	131.84	505.60
2	198267491	C	A	SF3B1	E622D	AGT	ATT	8	0.0037	2155.6	9.147E-25	1.788E-20	930.65	4247.44
2	25457243	G	A	DNMT3A	R882C	CCG	CTG	8	0.0224	357.8	1.561E-18	2.135E-14	154.48	705.03
2	209113113	G	A	IDH1	R132C	TCG	TTG	8	0.0482	166.0	7.112E-16	8.844E-12	71.66	327.06
2	198267491	C	G	SF3B1	E622D	AGT	ACT	7	0.0033	2095.7	9.369E-22	1.709E-17	842.60	4318.04
2	198267483	C	A	SF3B1	R625L	CGT	CTT	7	0.0096	727.0	1.541E-18	2.135E-14	292.30	1497.96
2	198267371	G	T	SF3B1	H662Q	ACA	AAA	6	0.0024	2465.8	2.920E-19	4.699E-15	904.91	5367.06
17	7577507	T	A	TP53	E258D	AAG	ATG	6	0.0027	2254.1	5.003E-19	7.605E-15	827.21	4906.18
11	119149002	T	A	CBL	W408R	CTG	CAG	5	0.0025	1993.3	8.341E-16	9.921E-12	647.23	4651.76
11	119148991	G	A	CBL	C404Y	TGT	TAT	5	0.0163	307.5	9.434E-12	9.559E-08	99.85	717.66
4	106164914	G	A	TET2	R1282H	CGC	CAC	5	0.0211	237.4	3.429E-11	3.191E-07	77.07	553.94
12	25398284	C	T	KRAS	G12D	GGT	GAT	5	0.0211	236.4	3.499E-11	3.191E-07	76.76	551.70
4	106180835	G	A	TET2	G1309D	GGT	GAT	5	0.0211	236.4	3.499E-11	3.191E-07	76.76	551.70
2	198267484	G	A	SF3B1	R625C	CCG	CTG	5	0.0224	223.6	4.615E-11	4.073E-07	72.61	521.88
17	7577120	C	T	TP53	R273H	CGT	CAT	5	0.0364	137.5	5.198E-10	4.063E-06	44.63	320.79
2	198267359	C	G	SF3B1	K666N	AGA	ACA	4	0.0009	4511.0	2.590E-14	2.952E-10	1229.09	11549.89
2	198267360	T	G	SF3B1	K666T	AAG	ACG	4	0.0018	2273.6	4.010E-13	4.220E-09	619.48	5821.28
17	7578190	T	C	TP53	Y220C	TAT	TGT	4	0.0060	665.7	5.436E-11	4.648E-07	181.39	1704.56
4	106196771	C	T	TET2	Q1723*	GCA	GTA	4	0.0113	354.6	6.722E-10	5.108E-06	96.63	908.04
4	106157845	C	T	TET2	Q937*	TCA	TTA	4	0.0122	327.7	9.212E-10	6.811E-06	89.29	839.11
11	119148931	G	A	CBL	C384Y	TGT	TAT	4	0.0163	246.0	2.891E-09	1.977E-05	67.03	629.91
20	31022592	C	T	ASXL1	R693*	GCG	GTG	4	0.0217	184.1	9.180E-09	5.642E-05	50.16	471.37
17	7577539	G	A	TP53	R248W	CCG	CTG	4	0.0224	178.9	1.029E-08	5.989E-05	48.75	458.07
2	198266606	C	G	SF3B1	A744P	GGC	GCC	3	0.0012	2485.0	2.939E-10	2.364E-06	512.47	7262.29
2	198267361	T	G	SF3B1	K666Q	TAA	TCA	3	0.0027	1129.8	3.123E-09	2.084E-05	233.00	3301.83
2	25468174	T	C	DNMT3A	N501S	AAT	AGT	3	0.0035	862.8	7.008E-09	4.565E-05	177.94	2521.60
11	119148930	T	C	CBL	C384R	ATG	ACG	3	0.0038	785.7	9.280E-09	5.642E-05	162.03	2296.09
2	198266494	T	C	SF3B1	D781G	GAT	GGT	3	0.0053	568.0	2.453E-08	1.342E-04	117.14	1660.00
4	106197285	T	C	TET2	I1894T	ATT	ACT	3	0.0072	415.7	6.251E-08	3.353E-04	85.72	1214.76
4	106157167	C	T	TET2	Q711*	CCA	CTA	3	0.0083	360.1	9.602E-08	4.865E-04	74.27	1052.50
17	74732960	G	T	SRSF2	P95T	CCC	CAC	3	0.0093	323.3	1.327E-07	6.367E-04	66.67	944.75
4	106157119	C	T	TET2	Q695*	GCA	GTA	3	0.0113	266.0	2.378E-07	1.103E-03	54.85	777.32
4	106190860	C	T	TET2	H1401Y	TCA	TTA	3	0.0122	245.8	3.012E-07	1.373E-03	50.69	718.31
11	119148486	C	T	CBL	R343*	ACG	ATG	3	0.0155	193.0	6.203E-07	2.571E-03	39.81	564.09
2	25463182	G	A	DNMT3A	R771*	GCG	GTG	3	0.0217	138.1	1.687E-06	6.593E-03	28.47	403.51
11	119149251	G	A	CBL	R420Q	CGA	CAA	3	0.0243	123.2	2.369E-06	8.795E-03	25.41	360.09
4	106156729	C	T	TET2	R565*	TCG	TTG	3	0.0482	62.2	1.805E-05	5.611E-02	12.84	181.91
4	106193748	C	T	TET2	R1425*	TCG	TTG	3	0.0482	62.2	1.805E-05	5.611E-02	12.84	181.91
17	7576888	T	A	TP53	K320*	GAA	GTA	2	0.0005	4044.7	1.223E-07	5.976E-04	489.84	14610.99
4	106155946	G	T	TET2	E304*	TGA	TTA	2	0.0005	3719.5	1.447E-07	6.823E-04	450.44	13435.94
12	25378647	T	G	KRAS	K117N	AAT	ACT	2	0.0009	2284.6	3.834E-07	1.719E-03	276.67	8252.59
12	112915523	A	G	PTPN11	N308D	AAA	AGA	2	0.0009	2248.3	3.958E-07	1.747E-03	272.27	8121.47
12	25398262	C	G	KRAS	L19F	TGA	TCA	2	0.0010	2065.7	4.688E-07	2.036E-03	250.17	7462.15
4	106164787	C	G	TET2	H1240D	CCA	CGA	2	0.0010	1972.4	5.143E-07	2.198E-03	238.87	7124.95
21	44524456	G	T	U2AF1	S34Y	TCT	TAT	2	0.0015	1352.2	1.094E-06	4.467E-03	163.75	4884.47
17	7578542	G	C	TP53	L130V	CCT	CGT	2	0.0016	1225.0	1.333E-06	5.284E-03	148.35	4425.12

chr	pos	ref	mut	gene	aachange	ref3_cod	mut3_cod	freq	mu	dnds	pval	qval	CI_low	CI_high
17	7577130	A	C	TP53	F270V	CTT	CGT	2	0.0020	993.6	2.025E-06	7.695E-03	120.33	3589.25
17	7578268	A	C	TP53	L194R	CTT	CGT	2	0.0020	993.6	2.025E-06	7.695E-03	120.33	3589.25
17	7578440	T	C	TP53	K164E	CAA	CGA	2	0.0024	830.4	2.898E-06	1.043E-02	100.57	2999.84
4	106182926	T	A	TET2	L1343Q	CTG	CAG	2	0.0025	797.3	3.144E-06	1.103E-02	96.56	2880.23
11	119148919	T	C	CBL	L380P	CTA	CCA	2	0.0031	638.4	4.902E-06	1.676E-02	77.31	2306.14
4	106197317	A	G	TET2	T1905A	AAC	AGC	2	0.0034	592.8	5.685E-06	1.920E-02	71.79	2141.29
4	106180835	G	T	TET2	G1309V	GGT	GTT	2	0.0070	286.5	2.428E-05	7.464E-02	34.69	1034.83
2	25462068	A	G	DNMT3A	I780T	ATT	ACT	2	0.0072	277.1	2.595E-05	7.887E-02	33.56	1001.02
4	106156687	C	T	TET2	Q551*	CCA	CTA	2	0.0083	240.1	3.454E-05	1.027E-01	29.08	867.31
2	198266713	C	T	SF3B1	G740E	GGA	GAA	2	0.0088	226.4	3.882E-05	1.130E-01	27.42	817.95
2	198267705	C	T	SF3B1	E592K	GGA	GAA	2	0.0088	226.4	3.882E-05	1.130E-01	27.42	817.95
15	90631838	C	T	IDH2	R172K	AGG	AAG	2	0.0092	216.7	4.238E-05	1.208E-01	26.24	782.68
2	198266714	C	T	SF3B1	G740R	AGG	AAG	2	0.0092	216.7	4.238E-05	1.208E-01	26.24	782.68
4	106157770	C	T	TET2	Q912*	ACA	ATA	2	0.0101	198.7	5.038E-05	1.406E-01	24.06	717.67
4	106157995	C	T	TET2	Q987*	ACA	ATA	2	0.0101	198.7	5.038E-05	1.406E-01	24.06	717.67
4	106157257	C	T	TET2	Q741*	GCA	GTA	2	0.0113	177.3	6.319E-05	1.746E-01	21.47	640.55
4	106197348	C	T	TET2	P1915L	CCC	CTC	2	0.0126	158.3	7.918E-05	2.103E-01	19.18	571.98
4	106197552	C	T	TET2	P1983L	CCC	CTC	2	0.0126	158.3	7.918E-05	2.103E-01	19.18	571.98
17	7577114	C	T	TP53	C275Y	TGT	TAT	2	0.0163	123.0	1.309E-04	3.285E-01	14.90	444.36
17	7577568	C	T	TP53	C238Y	TGT	TAT	2	0.0163	123.0	1.309E-04	3.285E-01	14.90	444.36
17	7578203	C	T	TP53	V216M	TGT	TAT	2	0.0163	123.0	1.309E-04	3.285E-01	14.90	444.36
4	106190855	G	A	TET2	C1399Y	TGT	TAT	2	0.0163	123.0	1.309E-04	3.285E-01	14.90	444.36
4	106180817	G	A	TET2	G1303D	GGT	GAT	2	0.0211	94.6	2.207E-04	5.344E-01	11.45	341.60
17	7577091	G	A	TP53	R283C	GCG	GTG	2	0.0217	92.0	2.329E-04	5.492E-01	11.15	332.52
17	7577121	G	A	TP53	R273C	GCG	GTG	2	0.0217	92.0	2.329E-04	5.492E-01	11.15	332.52
20	31021250	C	T	ASXL1	R417*	CCG	CTG	2	0.0224	89.5	2.465E-04	5.690E-01	10.83	323.14
12	112910785	G	A	PTPN11	R265Q	CGA	CAA	2	0.0243	82.1	2.919E-04	6.441E-01	9.95	296.73
11	119155953	C	T	CBL	R540*	TCG	TTG	2	0.0482	41.5	1.126E-03	1.000E+00	5.03	149.90
17	7578212	G	A	TP53	R213*	TCG	TTG	2	0.0482	41.5	1.126E-03	1.000E+00	5.03	149.90

Table 18a | Association of Age, Sex and presence/absence of CH (VAF>2%) with blood parameters

Trait	Gene	Effect Estimate	Effect StdErr	Effect Statistic	CI95_low	CI95_high	Model Statistic	Model pvalue	Model fdr	n data Points	n individuals
BASO	Age	0.000	0.000	3.119	0.000	0.001	9.320	2.27E-03	1.68E-02	977	251
EOS	Age	0.001	0.001	2.582	0.000	0.002	6.568	1.04E-02	4.51E-02	708	213
HB	Age	-0.044	0.005	-9.701	-0.053	-0.035	88.525	5.02E-21	5.02E-19	975	251
LYMPH	Age	-0.011	0.002	-4.943	-0.016	-0.007	24.106	9.12E-07	1.30E-05	975	251
MCV	Age	0.029	0.022	1.269	-0.016	0.072	1.609	2.05E-01	4.26E-01	975	251
MONO	Age	0.007	0.001	9.914	0.006	0.009	86.921	1.13E-20	5.65E-19	976	251
NEUT	Age	0.031	0.005	5.643	0.020	0.041	31.081	2.48E-08	4.71E-07	975	251
PLT	Age	-1.667	0.208	-8.022	-2.075	-1.260	61.837	3.73E-15	9.33E-14	974	251
RDW	Age	0.035	0.020	1.750	-0.004	0.074	3.027	8.19E-02	2.21E-01	436	173
WBC	Age	0.030	0.006	4.718	0.018	0.043	21.748	3.11E-06	3.71E-05	977	251
BASO	Sex	0.000	0.002	0.053	-0.004	0.004	0.003	9.58E-01	9.86E-01	977	251
EOS	Sex	0.044	0.013	3.383	0.019	0.070	11.143	8.44E-04	7.67E-03	708	213
HB	Sex	1.229	0.138	8.910	0.959	1.500	68.996	9.87E-17	3.29E-15	975	251
LYMPH	Sex	0.116	0.068	1.718	-0.016	0.248	2.932	8.69E-02	2.29E-01	975	251
MCV	Sex	2.948	1.172	2.515	0.650	5.245	6.247	1.24E-02	4.79E-02	975	251
MONO	Sex	0.104	0.018	5.754	0.069	0.140	30.825	2.82E-08	4.71E-07	976	251
NEUT	Sex	0.577	0.135	4.278	0.313	0.842	17.633	2.68E-05	2.68E-04	975	251
PLT	Sex	-19.053	6.812	-2.797	-32.404	-5.702	7.700	5.52E-03	3.45E-02	974	251
RDW	Sex	0.279	0.235	1.186	-0.182	0.740	1.397	2.37E-01	4.48E-01	436	173
WBC	Sex	0.838	0.176	4.756	0.493	1.183	21.610	3.34E-06	3.71E-05	977	251

Trait	Gene	Effect Estimate	Effect StdErr	Effect Statistic	CI95_low	CI95_high	Model Statistic	Model_p	Model_fdr	n data points with CH	n individuals with CH	n data points without CH	n individuals without CH
BASO	AllCH	-0.005	0.002	-2.521	-0.009	-0.001	6.315	1.20E-02	4.79E-02	653	168	322	83
EOS	AllCH	-0.036	0.014	-2.523	-0.063	-0.008	6.310	1.20E-02	4.79E-02	653	168	322	83
HB	AllCH	-0.052	0.148	-0.351	-0.341	0.238	0.123	7.26E-01	8.54E-01	653	168	324	83
LYMPH	AllCH	-0.034	0.072	-0.467	-0.175	0.108	0.218	6.40E-01	7.79E-01	653	168	322	83
MCV	AllCH	-0.611	1.249	-0.489	-3.058	1.837	0.239	6.25E-01	7.72E-01	653	168	324	83
MONO	AllCH	-0.053	0.020	-2.735	-0.091	-0.015	7.415	6.47E-03	3.46E-02	653	168	322	83
NEUT	AllCH	-0.218	0.145	-1.505	-0.502	0.066	2.257	1.33E-01	3.17E-01	653	168	322	83
PLT	AllCH	11.387	7.283	1.564	-2.886	25.660	2.436	1.19E-01	2.97E-01	652	168	323	83
RDW	AllCH	0.184	0.261	0.705	-0.327	0.695	0.495	4.82E-01	7.19E-01	112	90	55	45
WBC	AllCH	-0.359	0.189	-1.902	-0.729	0.011	3.598	5.79E-02	1.70E-01	653	168	324	83
BASO	ASXL1	-0.003	0.006	-0.517	-0.014	0.008	0.267	6.05E-01	7.72E-01	60	16	322	83
EOS	ASXL1	-0.053	0.030	-1.768	-0.111	0.006	3.091	7.87E-02	2.19E-01	60	16	322	83
HB	ASXL1	0.291	0.271	1.075	-0.240	0.822	1.150	2.84E-01	4.89E-01	60	16	324	83
LYMPH	ASXL1	-0.190	0.138	-1.370	-0.461	0.082	1.864	1.72E-01	3.88E-01	60	16	322	83
MCV	ASXL1	2.547	2.103	1.211	-1.575	6.670	1.455	2.28E-01	4.48E-01	60	16	324	83
MONO	ASXL1	-0.057	0.043	-1.324	-0.142	0.027	1.744	1.87E-01	3.97E-01	60	16	322	83
NEUT	ASXL1	-0.272	0.292	-0.933	-0.844	0.300	0.867	3.52E-01	5.96E-01	60	16	322	83
PLT	ASXL1	16.256	14.180	1.147	-11.535	44.048	1.306	2.53E-01	4.60E-01	60	16	323	83
RDW	ASXL1	-0.778	0.390	-1.995	-1.543	-0.014	3.867	4.92E-02	1.53E-01	12	10	55	45
WBC	ASXL1	-0.584	0.397	-1.471	-1.361	0.194	2.145	1.43E-01	3.33E-01	60	16	324	83
BASO	CBL	-0.005	0.010	-0.504	-0.023	0.014	0.253	6.15E-01	7.72E-01	18	5	322	83
EOS	CBL	-0.058	0.051	-1.156	-0.157	0.041	1.329	2.49E-01	4.60E-01	18	5	322	83
HB	CBL	0.485	0.436	1.113	-0.369	1.340	1.230	2.67E-01	4.69E-01	18	5	324	83
LYMPH	CBL	-0.119	0.243	-0.491	-0.596	0.357	0.240	6.24E-01	7.72E-01	18	5	322	83
MCV	CBL	0.482	3.584	0.134	-6.542	7.506	0.018	8.93E-01	9.56E-01	18	5	324	83
MONO	CBL	0.003	0.071	0.035	-0.137	0.142	0.001	9.72E-01	9.86E-01	18	5	322	83
NEUT	CBL	0.264	0.486	0.543	-0.689	1.216	0.294	5.88E-01	7.72E-01	18	5	322	83
PLT	CBL	12.929	21.830	0.592	-29.857	55.715	0.350	5.54E-01	7.72E-01	18	5	323	83
RDW	CBL	-0.548	0.692	-0.793	-1.904	0.807	0.625	4.29E-01	6.60E-01	3	3	55	45
WBC	CBL	0.078	0.669	0.116	-1.234	1.389	0.014	9.08E-01	9.56E-01	18	5	324	83
BASO	DNMT3A	-0.006	0.003	-1.970	-0.012	0.000	3.825	5.05E-02	1.53E-01	221	54	322	83
EOS	DNMT3A	-0.046	0.018	-2.603	-0.081	-0.011	6.657	9.88E-03	4.51E-02	221	54	322	83

Trait	Gene	Effect Estimate	Effect StdErr	Effect Statistic	CI95_low	CI95_high	Model Statistic	Model_p	Model_fdr	n data points with CH	n individuals with CH	n data points without CH	n individuals without CH
HB	DNMT3A	-0.012	0.181	-0.064	-0.367	0.344	0.004	9.49E-01	9.86E-01	221	54	324	83
LYMPH	DNMT3A	-0.110	0.092	-1.192	-0.290	0.071	1.413	2.35E-01	4.48E-01	221	54	322	83
MCV	DNMT3A	-0.466	1.496	-0.311	-3.399	2.467	0.097	7.56E-01	8.69E-01	221	54	324	83
MONO	DNMT3A	-0.079	0.026	-3.084	-0.130	-0.029	9.256	2.35E-03	1.68E-02	221	54	322	83
NEUT	DNMT3A	-0.344	0.181	-1.897	-0.699	0.011	3.551	5.95E-02	1.70E-01	221	54	322	83
PLT	DNMT3A	5.660	8.741	0.648	-11.472	22.792	0.419	5.17E-01	7.56E-01	220	54	323	83
RDW	DNMT3A	-0.192	0.299	-0.643	-0.778	0.394	0.411	5.22E-01	7.56E-01	37	28	55	45
WBC	DNMT3A	-0.591	0.246	-2.407	-1.072	-0.110	5.675	1.72E-02	6.10E-02	221	54	324	83
BASO	PPM1D	-0.005	0.009	-0.554	-0.021	0.012	0.307	5.80E-01	7.72E-01	25	6	322	83
EOS	PPM1D	-0.055	0.046	-1.190	-0.145	0.036	1.408	2.35E-01	4.48E-01	25	6	322	83
HB	PPM1D	0.255	0.411	0.620	-0.552	1.061	0.383	5.36E-01	7.66E-01	25	6	324	83
LYMPH	PPM1D	-0.079	0.222	-0.355	-0.513	0.356	0.126	7.23E-01	8.54E-01	25	6	322	83
MCV	PPM1D	7.928	3.290	2.410	1.479	14.377	5.628	1.77E-02	6.10E-02	25	6	324	83
MONO	PPM1D	0.001	0.065	0.016	-0.126	0.128	0.000	9.87E-01	9.87E-01	25	6	322	83
NEUT	PPM1D	0.135	0.452	0.298	-0.752	1.022	0.089	7.66E-01	8.70E-01	25	6	322	83
PLT	PPM1D	17.858	20.081	0.889	-21.501	57.217	0.787	3.75E-01	6.15E-01	25	6	323	83
RDW	PPM1D	-1.227	0.581	-2.111	-2.365	-0.088	4.272	3.88E-02	1.25E-01	5	3	55	45
WBC	PPM1D	-0.019	0.618	-0.030	-1.229	1.192	0.001	9.76E-01	9.86E-01	25	6	324	83
BASO	SF3B1	-0.001	0.006	-0.224	-0.013	0.011	0.050	8.23E-01	9.04E-01	53	12	322	83
EOS	SF3B1	-0.052	0.034	-1.533	-0.119	0.015	2.332	1.27E-01	3.09E-01	53	12	322	83
HB	SF3B1	0.135	0.295	0.458	-0.443	0.714	0.210	6.47E-01	7.79E-01	53	12	324	83
LYMPH	SF3B1	0.164	0.181	0.903	-0.192	0.519	0.813	3.67E-01	6.12E-01	53	12	322	83
MCV	SF3B1	5.903	2.386	2.474	1.226	10.579	5.923	1.49E-02	5.53E-02	53	12	324	83
MONO	SF3B1	-0.028	0.048	-0.580	-0.123	0.067	0.336	5.62E-01	7.72E-01	53	12	322	83
NEUT	SF3B1	0.040	0.348	0.116	-0.641	0.722	0.013	9.08E-01	9.56E-01	53	12	322	83
PLT	SF3B1	17.980	15.137	1.188	-11.689	47.648	1.402	2.36E-01	4.48E-01	53	12	323	83
RDW	SF3B1	0.708	0.419	1.692	-0.112	1.528	2.796	9.45E-02	2.42E-01	10	6	55	45
WBC	SF3B1	0.113	0.476	0.237	-0.821	1.046	0.056	8.13E-01	9.03E-01	53	12	324	83
BASO	SRSF2	-0.004	0.007	-0.558	-0.017	0.009	0.312	5.77E-01	7.72E-01	41	11	322	83
EOS	SRSF2	0.020	0.040	0.494	-0.059	0.099	0.243	6.22E-01	7.72E-01	41	11	322	83
HB	SRSF2	-0.282	0.335	-0.840	-0.938	0.375	0.702	4.02E-01	6.29E-01	41	11	324	83
LYMPH	SRSF2	-0.059	0.176	-0.334	-0.404	0.286	0.112	7.38E-01	8.58E-01	41	11	322	83
MCV	SRSF2	-2.010	2.703	-0.744	-7.307	3.288	0.551	4.58E-01	6.94E-01	41	11	324	83
MONO	SRSF2	-0.072	0.053	-1.362	-0.176	0.032	1.843	1.75E-01	3.88E-01	41	11	322	83
NEUT	SRSF2	-0.288	0.337	-0.855	-0.948	0.372	0.728	3.94E-01	6.25E-01	41	11	322	83
PLT	SRSF2	46.473	17.776	2.614	11.632	81.314	6.611	1.01E-02	4.51E-02	41	11	323	83
RDW	SRSF2	1.627	0.556	2.930	0.539	2.716	7.384	6.58E-03	3.46E-02	9	7	55	45
WBC	SRSF2	-0.406	0.474	-0.857	-1.334	0.522	0.732	3.92E-01	6.25E-01	41	11	324	83
BASO	TET2	-0.006	0.003	-2.289	-0.012	-0.001	5.156	2.32E-02	7.72E-02	306	65	322	83
EOS	TET2	-0.056	0.018	-3.212	-0.091	-0.022	10.041	1.53E-03	1.28E-02	306	65	322	83
HB	TET2	-0.201	0.179	-1.124	-0.553	0.150	1.255	2.63E-01	4.69E-01	306	65	324	83
LYMPH	TET2	0.017	0.093	0.180	-0.166	0.199	0.032	8.57E-01	9.32E-01	306	65	322	83
MCV	TET2	-0.756	1.461	-0.518	-3.619	2.107	0.268	6.05E-01	7.72E-01	306	65	324	83
MONO	TET2	-0.065	0.024	-2.758	-0.112	-0.019	7.494	6.19E-03	3.46E-02	306	65	322	83
NEUT	TET2	-0.451	0.160	-2.814	-0.765	-0.137	7.726	5.44E-03	3.45E-02	306	65	322	83
PLT	TET2	10.625	8.004	1.328	-5.062	26.313	1.757	1.85E-01	3.97E-01	306	65	323	83
RDW	TET2	0.080	0.295	0.271	-0.499	0.658	0.073	7.87E-01	8.84E-01	40	28	55	45
WBC	TET2	-0.575	0.219	-2.624	-1.005	-0.146	6.736	9.45E-03	4.51E-02	306	65	324	83

Table 18b | Association of clonal growth rate with blood parameters

Trait	Gene	Effect Estimate	Effect StdErr	Effect Statistic	CI95_low	CI95_high	Model Statistic	Model_p	Model_fdr	n data points with CH	n individuals with CH	n data points without CH	n individuals without CH
BASO	ASXL1	0.07	0.04	1.79	-0.01	0.16	3.11	7.78E-02	5.49E-01	60	16	322	83
EOS	ASXL1	-0.61	0.50	-1.22	-1.59	0.37	1.44	2.30E-01	7.29E-01	60	16	322	83
HB	ASXL1	-1.55	4.13	-0.38	-9.64	6.54	0.14	7.08E-01	9.26E-01	60	16	324	83
LYMPH	ASXL1	0.02	1.79	0.01	-3.48	3.53	0.00	9.89E-01	9.89E-01	60	16	322	83
MCV	ASXL1	-6.11	20.44	-0.30	-46.17	33.94	0.09	7.67E-01	9.26E-01	60	16	324	83
MONO	ASXL1	0.29	0.78	0.37	-1.25	1.83	0.14	7.11E-01	9.26E-01	60	16	322	83
NEUT	ASXL1	1.83	4.14	0.44	-6.28	9.94	0.20	6.59E-01	9.26E-01	60	16	322	83
PLT	ASXL1	-138.69	198.96	-0.70	-528.64	251.26	0.48	4.88E-01	9.26E-01	60	16	323	83
RDW	ASXL1	-3.91	11.87	-0.33	-27.18	19.35	0.10	7.49E-01	9.26E-01	12	10	55	45
WBC	ASXL1	1.77	5.22	0.34	-8.47	12.01	0.11	7.35E-01	9.26E-01	60	16	324	83
BASO	CBL	-0.01	0.10	-0.13	-0.22	0.19	0.02	8.99E-01	9.63E-01	18	5	322	83
EOS	CBL	1.89	0.85	2.24	0.24	3.55	4.64	3.12E-02	5.35E-01	18	5	322	83
HB	CBL	-4.21	9.89	-0.43	-23.60	15.17	0.18	6.71E-01	9.26E-01	18	5	324	83
LYMPH	CBL	1.87	5.91	0.32	-9.71	13.44	0.10	7.52E-01	9.26E-01	18	5	322	83
MCV	CBL	-40.93	79.39	-0.52	-196.54	114.67	0.26	6.07E-01	9.26E-01	18	5	324	83
MONO	CBL	0.15	1.84	0.08	-3.45	3.75	0.01	9.35E-01	9.63E-01	18	5	322	83
NEUT	CBL	8.19	13.20	0.62	-17.67	34.05	0.38	5.36E-01	9.26E-01	18	5	322	83
PLT	CBL	47.27	494.44	0.10	-921.80	1016.35	0.01	9.24E-01	9.63E-01	18	5	323	83
RDW	CBL	15.75	9.59	1.64	-3.04	34.54	1.63	2.02E-01	6.74E-01	3	3	55	45
WBC	CBL	12.61	18.92	0.67	-24.47	49.69	0.44	5.06E-01	9.26E-01	18	5	324	83
BASO	DNMT3A	-0.02	0.03	-0.67	-0.08	0.04	0.44	5.06E-01	9.26E-01	221	54	322	83
EOS	DNMT3A	-0.21	0.35	-0.61	-0.90	0.47	0.37	5.45E-01	9.26E-01	221	54	322	83
HB	DNMT3A	-10.76	3.34	-3.22	-17.31	-4.21	10.00	1.56E-03	1.09E-01	221	54	324	83
LYMPH	DNMT3A	-3.23	1.70	-1.90	-6.57	0.10	3.57	5.89E-02	5.49E-01	221	54	322	83
MCV	DNMT3A	-30.39	29.68	-1.02	-88.56	27.79	1.04	3.07E-01	8.59E-01	221	54	324	83
MONO	DNMT3A	-0.10	0.40	-0.25	-0.88	0.68	0.06	8.03E-01	9.26E-01	221	54	322	83
NEUT	DNMT3A	-5.53	3.10	-1.78	-11.60	0.55	3.14	7.63E-02	5.49E-01	221	54	322	83
PLT	DNMT3A	-170.13	144.33	-1.18	-453.01	112.76	1.38	2.39E-01	7.29E-01	220	54	323	83
RDW	DNMT3A	3.95	5.27	0.75	-6.38	14.28	0.55	4.57E-01	9.26E-01	37	28	55	45
WBC	DNMT3A	-9.02	4.11	-2.19	-17.08	-0.96	4.73	2.97E-02	5.35E-01	221	54	324	83
BASO	PPM1D	-0.03	0.05	-0.56	-0.12	0.07	0.31	5.77E-01	9.26E-01	25	6	322	83
EOS	PPM1D	-0.16	0.46	-0.35	-1.06	0.74	0.12	7.29E-01	9.26E-01	25	6	322	83
HB	PPM1D	-9.69	4.91	-1.97	-19.31	-0.07	3.62	5.72E-02	5.49E-01	25	6	324	83
LYMPH	PPM1D	-2.32	2.50	-0.93	-7.22	2.59	0.85	3.58E-01	8.94E-01	25	6	322	83
MCV	PPM1D	-21.50	41.28	-0.52	-102.41	59.40	0.27	6.03E-01	9.26E-01	25	6	324	83
MONO	PPM1D	0.80	0.85	0.94	-0.86	2.47	0.88	3.49E-01	8.94E-01	25	6	322	83
NEUT	PPM1D	3.64	7.37	0.49	-10.81	18.09	0.24	6.22E-01	9.26E-01	25	6	322	83
PLT	PPM1D	-84.53	241.62	-0.35	-558.11	389.04	0.12	7.27E-01	9.26E-01	25	6	323	83
RDW	PPM1D	-1.73	6.30	-0.27	-14.07	10.62	0.07	7.89E-01	9.26E-01	5	3	55	45
WBC	PPM1D	1.95	8.58	0.23	-14.86	18.76	0.05	8.20E-01	9.26E-01	25	6	324	83
BASO	SF3B1	0.04	0.04	0.86	-0.05	0.12	0.74	3.91E-01	9.26E-01	53	12	322	83
EOS	SF3B1	-0.05	0.56	-0.10	-1.15	1.04	0.01	9.22E-01	9.63E-01	53	12	322	83
HB	SF3B1	-2.63	5.13	-0.51	-12.69	7.42	0.26	6.09E-01	9.26E-01	53	12	324	83
LYMPH	SF3B1	-1.15	2.74	-0.42	-6.52	4.22	0.18	6.74E-01	9.26E-01	53	12	322	83
MCV	SF3B1	-37.64	39.95	-0.94	-115.93	40.66	0.88	3.49E-01	8.94E-01	53	12	324	83
MONO	SF3B1	-0.04	0.59	-0.06	-1.20	1.13	0.00	9.51E-01	9.65E-01	53	12	322	83
NEUT	SF3B1	2.83	4.70	0.60	-6.39	12.05	0.36	5.48E-01	9.26E-01	53	12	322	83
PLT	SF3B1	215.63	201.77	1.07	-179.84	611.09	1.13	2.88E-01	8.41E-01	53	12	323	83
RDW	SF3B1	2.61	14.05	0.19	-24.93	30.15	0.03	8.53E-01	9.46E-01	10	6	55	45
WBC	SF3B1	1.76	6.37	0.28	-10.73	14.25	0.08	7.83E-01	9.26E-01	53	12	324	83
BASO	SRSF2	-0.08	0.05	-1.56	-0.19	0.02	2.37	1.23E-01	5.49E-01	41	11	322	83
EOS	SRSF2	-1.27	0.76	-1.68	-2.76	0.22	2.49	1.15E-01	5.49E-01	41	11	322	83
HB	SRSF2	5.83	7.36	0.79	-8.59	20.25	0.61	4.36E-01	9.26E-01	41	11	324	83
LYMPH	SRSF2	-4.34	2.82	-1.54	-9.87	1.19	2.17	1.41E-01	5.49E-01	41	11	322	83
MCV	SRSF2	8.64	50.67	0.17	-90.66	107.95	0.03	8.65E-01	9.46E-01	41	11	324	83
MONO	SRSF2	1.52	1.05	1.45	-0.54	3.57	1.98	1.59E-01	5.57E-01	41	11	322	83
NEUT	SRSF2	-8.32	4.83	-1.72	-17.78	1.15	2.49	1.15E-01	5.49E-01	41	11	322	83

Trait	Gene	Effect Estimate	Effect StdErr	Effect Statistic	CI95_low	CI95_high	Model Statistic	Model_p	Model_fdr	n data points with CH	n individuals with CH	n data points without CH	n individuals without CH
PLT	SRSF2	-821.87	360.34	-2.28	-1528.12	-115.63	4.44	3.52E-02	5.35E-01	41	11	323	83
RDW	SRSF2	32.59	19.34	1.69	-5.31	70.49	2.48	1.15E-01	5.49E-01	9	7	55	45
WBC	SRSF2	-11.96	7.63	-1.57	-26.92	2.99	2.16	1.41E-01	5.49E-01	41	11	324	83
BASO	TET2	0.00	0.02	0.24	-0.03	0.04	0.06	8.10E-01	9.26E-01	306	65	322	83
EOS	TET2	-0.06	0.18	-0.34	-0.42	0.30	0.12	7.31E-01	9.26E-01	306	65	322	83
HB	TET2	-1.28	2.23	-0.57	-5.65	3.09	0.33	5.67E-01	9.26E-01	306	65	324	83
LYMPH	TET2	-1.54	1.08	-1.42	-3.67	0.58	2.02	1.56E-01	5.57E-01	306	65	322	83
MCV	TET2	8.91	18.91	0.47	-28.14	45.97	0.22	6.37E-01	9.26E-01	306	65	324	83
MONO	TET2	-0.37	0.23	-1.60	-0.82	0.08	2.53	1.11E-01	5.49E-01	306	65	322	83
NEUT	TET2	2.62	1.76	1.49	-0.82	6.07	2.21	1.38E-01	5.49E-01	306	65	322	83
PLT	TET2	129.60	84.98	1.53	-36.96	296.16	2.31	1.29E-01	5.49E-01	306	65	323	83
RDW	TET2	-8.08	3.82	-2.11	-15.58	-0.59	4.30	3.82E-02	5.35E-01	40	28	55	45
WBC	TET2	0.64	2.34	0.27	-3.95	5.23	0.08	7.84E-01	9.26E-01	306	65	324	83