

Precision Breast Cancer Medicine: early stage triple negative breast cancer -a review of molecular characterisation, therapeutic targets and future trends

Karen Pinilla Alba^{1, 2, 3}, Lynsey M. Drewett^{1, 2}, Rebecca Lucey^{1, 2}, Jean E. Abraham^{1, 2, 3*}

¹Cambridge Breast Cancer Research Unit, University of Cambridge, Department of Oncology, United Kingdom, ²Cambridge University Hospitals NHS Foundation Trust, United Kingdom, ³Cancer Research UK Cambridge Centre, Cancer Research UK Cambridge Institute, University of Cambridge, United Kingdom

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Abstract

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Personalised approaches to the management of all solid tumours are increasing rapidly along with wider accessibility for clinicians. Advances in tumour characterisation and targeted therapies have placed triple negative breast cancers (TNBC) at the forefront of this approach. TNBC is a highly heterogeneous disease with a variety of histopathological features and is driven by distinct molecular alterations. The ability to tailor individualised and effective treatments for each patient based on the particular importance in this group due to the high risk of distant recurrence and death.

The mainstay of treatment across all subtypes of TNBC has historically been cytotoxic chemotherapy which is often associated with off-target tissue toxicity and drug resistance. Neoadjuvant chemotherapy is commonly used as it allows close monitoring of early treatment response and provides valuable prognostic information. Patients who achieve a complete pathological response after neoadjuvant chemotherapy are known to have significantly improved long-term outcomes. Conversely, poor responders are known to face a higher risk of relapse and death. The identification of those subgroups that are more likely to benefit from breakthroughs in the personalised approach is one of the challenges of the current era where several targeted therapies are available.

The aim of this review is to present an overview of contemporary practice, and promising future trends in the management of early TNBC. Platinum chemotherapy, DNA damage response (DDR) inhibitors, immune checkpoint inhibitors, inhibitors of the PI3K-AKT-mTOR, and Androgen receptor (AR) pathways are some of the increasingly studied therapies which will be reviewed. We will also discuss the growing evidence for less-developed agents and predictive biomarkers that are likely to contribute to the forthcoming advances in this field. Finally, we will propose a framework for the personalised management of TNBC based upon the integration of clinico-pathological and molecular features to ensure that long term outcomes are optimised.

Contribution to the field

Triple negative breast cancer (TNBC) accounts for 15% of all breast cancers. It affects younger patients, has an aggressive natural history, and presents at an advanced stage. It is a highly heterogeneous disease and exhibits a wide variety of features that can be characterised based upon genetics and pathology, at both the tissue and the molecular level. These features have evolved over time and with increasing understanding of the biological landscape of the disease, although they are not exploited in the clinical setting. This review describes the development of this multifaceted categorisation and draws upon it to focus on current and promising future treatment approaches. The evidence base for well-established chemotherapy regimens is reviewed. Newer treatments and clinical trial progress to date is summarised. We argue that the current therapeutic options for TNBC are limited. Patients diagnosed with early stage disease will far too frequently have limited response to routinely prescribed treatment and face poor long-term outcomes. We highlight the importance of the personalised approach to managing the disease and propose a framework to guide the clinician towards developing a bespoke treatment pathway for every patient diagnosed with early stage TNBC.

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5 **Karen Pinilla Alba^{1,2,3}, Lynsey M Drewett^{1,2}, Rebecca Lucey^{1,2}, Jean E Abraham^{1,2,3}**

6 ¹ Precision Breast Cancer Institute, University of Cambridge, Department of Oncology, Cambridge,
7 UK, ² Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK; ³ Cancer Research
8 UK Cambridge Centre, Cancer Research UK Cambridge Institute, University of Cambridge,
9 Cambridge, UK.

10 **Correspondence:**

11 Professor Jean Abraham
12 ja344@medschl.cam.ac.uk
13

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15

16 **1. Introduction**

17 Breast cancer (BC) is the most common cancer affecting women and is the leading cause of cancer-related
18 death in women worldwide¹. Triple negative breast cancers (TNBC), a highly heterogeneous subtype,
19 represent approximately 15% of all breast cancers². TNBC behaves aggressively, has a poorer prognosis,
20 and a higher risk of distant relapse and death relative to other BC subtypes². Genomic and transcriptomic
21 data has enhanced our ability to understand the TNBC taxonomy and enabled the identification of new
22 therapeutic targets. The development of new therapeutic options and optimisation of personalised
23 management strategies is critical in improving outcomes for affected patients.

24 This review aims to provide an overview of contemporary practice in the treatment of early-stage TNBC
25 and to highlight promising future directions. The growing evidence for newer therapies predicted to
26 contribute to forthcoming advances in this field will be discussed. Finally, a framework for the personalised
27 management of TNBC based upon the integration of clinical and molecular features will be discussed.

28 **2. Diagnosis and clinical presentation**

29 TNBC is characterised by the absence of oestrogen (ER) and progesterone (PR) receptor expression, in
30 addition to the absence of HER2 amplification as measured by immunohistochemistry or fluorescence in
31 situ hybridisation. TNBC is disproportionately seen in younger women, as well as Hispanic and African
32 American populations³. Disease-free intervals following primary treatment of early-stage (I-III) TNBC are
33 often short. The recurrence rate for is 25%, with the highest risk of recurrence in the first three years after
34 diagnosis, and a median time to relapse after surgery of 18.8 months⁴. Metastatic TNBC (mTNBC) exhibits
35 a more aggressive phenotype than other BC subtypes, as demonstrated by a shorter chemotherapy response
36 duration, and a shorter overall survival (OS) (median 13.3 months)⁵.

37 3. TNBC heterogeneity

38 TNBC is a heterogeneous disease with significant inter- and intra-tumour heterogeneity^{6,7,8}. Multiple efforts
39 have focused on adequately addressing this biological complexity to enable the tailoring of therapeutic
40 options to individual tumour characteristics.

41 3.1. Histological subtypes

42 The current clinical definition of TNBC encompasses multiple histological subtypes. Approximately 85%
43 of TNBC are morphologically defined as invasive carcinoma of no special type (IC-NST). The remaining
44 TNBCs are less common tumours of special type which are collectively associated with a worse prognosis⁹.
45 Individual special types display distinct pathological and molecular characteristics and prognoses. Tumours
46 of indolent course include adenoid cystic, secretory and tubular carcinomas. Medullary histology is
47 associated with a good prognosis and high response rates to chemotherapy, whereas metaplastic tumours
48 show differentiation toward squamous epithelium with mesenchymal components and are frequently
49 chemoresistant¹⁰. An accurate histological examination marks the first step towards the identification of key
50 mechanistic features that could be exploited to direct treatment (Table 1).

51 *Table 1: Histological special subtypes of TNBC*

52 3.2. Molecular subtypes

53 Numerous efforts to build upon the molecular classification of TNBC have been proposed (Table 2). Here
54 we review the most recognised classifiers that utilise genomic and transcriptomic data and summarise their
55 predictive value when tested in early TNBC clinical cohorts. Many other classification approaches have
56 been proposed (Table S1), with the absence of clinical evidence for treatment response limiting their use.

57 3.2.1. Intrinsic subtypes

58 Breast cancers can be classified into six intrinsic molecular subtypes by gene expression (GE) profiling^{17,18}
59 as follows: Luminal A, Luminal B, Her2 enriched, Normal-like, Basal-like, and Claudin low. Each subtype
60 is identified within the TNBC group as defined by immunohistochemistry. Basal-like tumours are most
61 frequent (50%-75%), however, they are not exclusive to the TNBC phenotype¹⁸. The claudin-low subtype
62 represents 25-40% of TNBC and was more recently introduced¹⁹.

63 Basal-like tumours are characterised by the presence of cytokeratins typically expressed by the basal layer
64 of the skin, widespread genomic instability, high proliferation markers, loss of function of *BRCA1*, and
65 dysregulation of *MYC* and *RBI* pathways¹⁸. Claudin-low tumours have several features in common with
66 basal-like tumours but are uniquely characterised by low levels of cell adhesion proteins, enrichment of
67 mesenchymal traits and stem cell features²⁰. Luminal tumours overexpress a 'luminal signature' containing
68 *ESR1*, *GATA3*, *FOXA1*, *XBPI* and *MYB*. Her2 amplification concomitantly with overexpression of *HER2*-
69 amplicon-associated genes defines the Her2 enriched subtype²¹.

70 Intrinsic subtypes provide independent predictive information regarding response to neoadjuvant
71 chemotherapy (NACT) when considering all subtypes of breast cancer, although not consistently for the
72 TNBC cohort when viewed in isolation. Claudin-low tumours are associated with lower pathological
73 complete response (pCR) rates in comparison to basal-like subtypes²¹. In a subgroup analysis of the
74 BrighTNess trial, pCR rates were higher for basal-like vs. non-basal tumours (52.3% vs 35.4%, p=0.003)²¹.
75 In contrast, no difference in pCR rate was observed with the addition of carboplatin for patients with basal-
76 like TNBC vs non-basal TNBC in the CALGB40603 study²². These results illustrate that the predictive value
77 often linked to the basal-like subtypes has not always been reproduced in the early setting of TNBC, making
78 intrinsic subtypes a less reliable biomarker of response within this group.

79 3.2.2. Lehmann/Pietenpol subtypes

80 Lehmann et al. selected clustering analyses to identify six TNBC subtypes displaying unique GE patterns
81 and ontologies. Each subtype was characterised by the activation of specific signalling pathways that led to
82 a selective response to targeted therapies in vivo²³. Additional histopathological quantification and laser-
83 capture microdissection prompted a refined classification with only four tumour-specific subtypes
84 (TNBCtype-4). The original immunomodulatory and mesenchymal stem-like subtypes were deemed to
85 originate from infiltrating lymphocytes and tumour-associated stromal cells; therefore, excluding the impact
86 of these elements into the classification. The new approach demonstrated differences in clinical baseline
87 characteristics and both local and distant disease progression²⁴. Basal-like 1 (BL1) revealed increased
88 markers of proliferation, and elevated expression of the DNA damage response (DDR) genes. Basal-like 2
89 (BL2) were characterised by features of basal/myoepithelial origin and activation of growth factor pathways
90 such as *EGF*, *NGF*, *MET*, *Wnt/β-catenin*, and *IGF1R*. The mesenchymal (M) subtype displays activation of
91 pathways involved in epithelial–mesenchymal transition (EMT), cellular differentiation, and growth
92 pathways. Luminal androgen receptor (LAR) tumours are characterised by a high expression of androgen
93 receptor (*AR*) and downstream *AR* targets, and enrichment of pathways involved in steroid synthesis,
94 porphyrin metabolism, and androgen/oestrogen metabolism²⁵.

95 A retrospective analysis from the validation cohort of the TNBC subtype classification presented by Masuda
96 et al showed that the likelihood of pCR with NACT was subtype dependent. BL1 had the highest pCR rate;
97 BL2 and LAR had the lowest. TNBC subtypes demonstrated improved pCR predictions as compared to
98 intrinsic subtypes (basal-like vs. non-basal)²⁵. In a retrospective analysis of clinically annotated microarray
99 datasets of BC patients, TNBC type-4 subtyping was not associated with significant differences in pCR in
100 the TNBC subgroup. However, the overall incidence of pCR for the subtypes demonstrates trends similar
101 to those observed in previous studies. BL1 displayed the greatest pCR rate (41%) and LAR and BL2
102 displayed the lowest (29% and 18% respectively). BL1 patients had significantly higher pCR rates compared
103 with other subtypes (49% vs. 31% $p=0.04$)²⁴. Santonja et.al explored the performance of Lehmann subtypes
104 and their association with pCR in 125 TNBC patients treated with neoadjuvant anthracyclines and/or taxanes
105 with and without carboplatin and their results were consistent with previous reports²⁶. The pCR rate for
106 carboplatin containing regimens was highest for BL1 tumours (80% vs 23%, $p=0.027$). LAR tumours had
107 the lowest pCR rate to all treatments (14.3% vs 42.7%, $p=0.045$).

108 3.2.3. Burstein subtypes

109 Burstein and colleagues applied non-negative matrix factorisation clustering to identify four distinct TNBC
110 subtypes characterised by key molecular features and prognosis: LAR, mesenchymal, basal-like
111 immunosuppressed (BLIS), and basal-like immune-activated (BLIA). BLIS and BLIA showed the best and
112 worst clinical outcomes, respectively. LAR and mesenchymal subtypes revealed significant overlap with
113 Lehmann's classification. Burstein's subtypes based on immune signalling (BLIA, BLIS) revealed a
114 combination of BL1 and BL2 subtypes²⁷.

115 3.2.4. FUSCC classification.

116 Liu et al. developed a classification system based on the transcriptome profiles of both messenger RNAs
117 and long non-coding RNAs to divide TNBC into four distinct clusters. Cluster A: immunomodulatory
118 subtype, Cluster B: luminal androgen receptor subtype (LAR), Cluster C: mesenchymal-like subtype, and
119 Cluster D: basal-like and immune-suppressed (BLIS) subtype. No significant difference in prognosis was
120 found between the four subtypes. Tumours classified as BLIS subtype experienced poorer relapse-free
121 survival (RFS) compared to all other subtypes^{28,29}. Further classification of BLIS tumours based on their
122 homologous recombination deficiency (HRD) status³⁰ showed that high-HRD BLIS TNBCs and low-HRD
123 BLIS TNBCs exhibited distinctive genomic characteristics and prognoses. Patients with tumours defined as
124 low-HRD had a worse prognosis than those in the high-HRD subgroup (5-year RFS of 73% and 95%,
125 respectively, $p = 0.002$)²⁹.

126

3.2.5. Integrative Clusters

127 Combining GE and DNA copy number analysis within the METABRIC dataset further expanded the
128 taxonomy of breast cancer³¹. Eleven Integrative Clusters (IntClust) with distinctive copy number profiles
129 and clinical outcomes were identified. TNBC are most frequently classified as IntClust 4ER- or IntClust 10.
130 Rueda et al. showed that patients with tumours classified as IntClust 10 (n=222) have a low probability of
131 late relapse (five years after diagnosis); while those classified as IntClust4ER- (n=73) show a persistent and
132 increasing risk of relapse or cancer-related death after 5 years. Classification by immunohistochemistry or
133 intrinsic subtypes did not segregate this risk³². The predictive value of IntClust to define response to NACT
134 is yet to be fully established.

135

3.2.6. Prado-Vasquez classification

136 Prado-Vasquez et al developed a probabilistic graphical model to classify the cellular component of tumours
137 into four groups based on the ‘stem cell hypothesis’, defined based upon the grade of development of the
138 cells from which they derived: Luminal (LAR), basal, claudin-high (CLDN-high), and claudin-low (CLDN-
139 low). The sparse k-means method was used to define high or low immune activity, and to classify the tumour
140 as Immune metanode positive or negative. Immune metanode activity was prognostic overall, and
141 particularly in the Luminal group defined by the cellular classification and TNBC type4 -LAR³³.
142

143 Combining molecular knowledge with patient management is an increasingly accepted practice across
144 tumour types. In early TNBC, a lack of reproducibility and the absence of a unified approach have led to
145 the continuous use of unselected clinical strategies that remain insufficient. Stable commonalities among
146 the classification methods of molecular subtyping in TNBC suggest the presence of clear biological groups
147 suitable for personalised therapeutic interventions. For instance, luminal-like and mesenchymal tumours are
148 consistently identified across the methods with decent overlap and reproducible outcome data. Moreover,
149 most methods include a measurement of the interaction between tumours and immune response, highlighting
150 the importance of considering this element a key component of the TNBC taxonomy. Overall, these efforts
151 provide the basis to understand how the molecular complexity of TNBC influences outcomes. Considering
152 treatment response as the result of dynamic network interaction, rather than focusing on individual static
153 components, is likely to have more predictive power. But even with reproducible and reliable classification
154 delivering this in a clinical timeframe suitable for neoadjuvant therapy decision-making remains a challenge.

155

Table 2: Common TNBC Classification Methods *Most prevalent intrinsic subtypes in TNBC listed

Summary Box 1 - Biological and clinical features of TNBC

- **TNBC is characterised by the absence of ER, PR and HER2 expression and is associated with high early response rates to treatment and poor prognosis.**
- **TNBC is a heterogeneous disease with a high level of inter and intra tumour heterogeneity.**
- **Multiple TNBC classifications that split TNBC tumours based on unique molecular features have been described but have yet to be incorporated into routine clinical practice.**

156

4. Overall approach to the treatment of early stage TNBC

157 Therapeutic options for early TNBC were traditionally limited to cytotoxic chemotherapy, surgery and
158 radiotherapy. Significant advances in basic and clinical research have led to tangible improvements in the
159 current therapeutic arsenal. Pembrolizumab immunotherapy has now been approved by the FDA for use in
160 combination with chemotherapy for high-risk early-stage TNBC following survival data from the
161 KEYNOTE-522 trial³⁴. This has established immunotherapy as a new standard of care in the United States,
162 and it is anticipated to reach clinical practice in other countries in the near future. Similarly, the recent FDA

163 approval of Olaparib for the adjuvant treatment of high-risk germline *BRCA(gBRCA)* carriers following
164 results of the OlympiA trial is expected to reshape clinical practice³⁵. These encouraging developments
165 highlight the importance of a personalised treatment approach and focus attention on the unresolved
166 challenges of appropriate patient selection and derived toxicity.

167 Closing the gap between pre-clinical advances and the clinical setting remains a lengthy and challenging
168 process.

169 **4.1. (Neo)adjuvant Chemotherapy**

170 The effect of polychemotherapy compared with no chemotherapy across all BC subtypes was assessed as
171 part of the 2012 Early Breast Cancer Trialists' Collaborative Group (EBCTCG) meta-analysis of 32,000
172 patients. This showed a ~50% reduction in 2-year recurrence and 20-25% reduction in BC³⁶. Chemotherapy
173 is particularly important in managing TNBC as these tumours demonstrate a better response as compared to
174 other subtypes of BC and the importance of achieving and optimising early treatment response in these
175 tumours is well recognised.

176 **4.1.1. Anthracyclines**

177 Anthracyclines target cell proliferation pathways by interacting with DNA gyrase and leading to DNA
178 double-strand breaks (DSBs). The ABC trials proved the addition of an anthracycline to taxane and
179 cyclophosphamide improved patient outcomes, with the greatest benefit in high-risk patients; those with
180 lymph node involvement or hormone-negative disease³⁷. More recently, a large meta-analysis by Braybrooke
181 et al. found an 18% reduction in 10-year recurrence risk with the addition of anthracycline to taxane
182 chemotherapy, as compared to taxane alone³⁸. There are multiple anthracycline-taxane based regimens now
183 in use, with evidence to support one "optimal" standard of care regimen for TNBC lacking³⁹.

184 Anthracycline-free chemotherapy regimens are considered when cardiotoxicity is a concern, and routine use
185 of such regimens for treatment de-escalation is an area of increasing interest⁴⁰. Evidence regarding efficacy
186 as standard treatment for TNBC is conflicting, although a recent meta-analysis has established
187 anthracycline-free chemotherapy to be acceptable for lower risk, early-stage HER2-negative BC³⁹.

188 *Table 3: Major clinical trials evaluating adjuvant anthracycline-free chemotherapy regimens for patients with stage I-III TNBC*

189 **4.1.2. Microtubule Targeting Agents**

190 Taxanes inhibit cell division by stabilising microtubules, preventing depolymerisation, spindle formation,
191 and progression through the cell cycle. Paclitaxel and docetaxel are regularly used to treat early-stage
192 TNBC. An EBCTCG meta-analysis showed the addition of taxane to anthracycline resulted in a
193 proportional reduction in mortality rates of 15–20%⁴¹. The European Cooperative Trial in Operable Breast
194 Cancer (ECTO) also demonstrated significant improvements in RFS and distant RFS⁴². Although this
195 evidence is not unique to TNBC, these studies provide the strongest evidence to support taxane use in this
196 cohort. BL1 and BL2 tumours appear to derive an increased benefit from this drug class⁴⁶.

197 There are several novel alternatives to traditional taxanes under investigation. Nab-paclitaxel is a solvent-
198 free albumin-bound nanoparticle formulation of paclitaxel. It potentially enables higher intra-tumoural
199 taxane concentrations, better efficacy and improved tolerability. The GeparSepto⁴⁷ and ETNA trials⁴⁸ showed
200 conflicting results with a significant difference in pCR rates seen only in GeparSepto (Table S2) which may
201 reflect the relative dose intensities used.

202 Etoposides are a promising alternative to taxanes in development. These novel potent microtubule
203 stabilisers can bypass common resistance mechanisms seen with taxanes, such as drug efflux pumps and β -
204 tubulin. In the early setting, the phase 3 TITAN trial has shown similar efficacy, and reduced rates of
205 peripheral neuropathy, dose modifications and discontinuation with Ixabepilone in comparison with
206 paclitaxel⁵⁰.

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4.1.3. Platinum salts

208 The clinical activity of platinum agents has been significantly associated with a DDR vulnerability in both
209 sporadic and *gBRCA*-associated TNBC. Carboplatin is increasingly used in neoadjuvant regimens,
210 improving both pCR and long term outcomes⁵¹. Please see section 5.1.

211

4.1.4. Capecitabine

212 Capecitabine is an oral prodrug of the antimetabolite 5-fluorouracil. Capecitabine is not currently
213 recommended in clinical guidelines for the neoadjuvant or adjuvant treatment of TNBC, though it is
214 selectively used as a post neoadjuvant treatment for residual TNBC. Evidence for use in the adjuvant setting
215 is accumulating, but in most cases studies have not incorporated the molecular features of the TNBC cohort
216 into the planned analysis for response assessment. The recent phase 3 CBCSG-010 trial for unselected
217 patients with TNBC with concomitant use of capecitabine 1,000 mg/m² and standard anthracycline-taxane
218 adjuvant chemotherapy (ACT) established a significant 5-year disease free survival (DFS) benefit⁵². This is
219 supported by the FINXX trial⁵³ and the Ye et al. meta-analysis which demonstrated improved DFS and OS
220 with a tolerable increase in toxicity⁵⁴.

221

4.2. Bone modifying agents

222 Adjuvant bisphosphonates are recommended for breast cancer patients with low-oestrogen status at high
223 risk of relapse to decrease skeletal metastases and improve OS and DFS, as evidenced by the AZURE trial
224 and EBCTCG meta-analysis, both of which included patients of all BC subtypes^{55,56}. While the majority of
225 evidence for bone modifying agents in TNBC comes from studies of patients receiving ACT, benefit is also
226 likely to be derived in the neoadjuvant setting⁵⁷. A subgroup analysis of patients receiving neoadjuvant ZA
227 alongside NACT in the AZURE trial led to improved pCR rates⁵⁸. The role of RANK-L remains under
228 investigation. The D-CARE trial of adjuvant denosumab showed no improvement in bone metastases free
229 survival, invasive disease free survival (iDFS) or OS in high-risk early breast cancer. This suggests the
230 mechanisms by which bisphosphonates act against the metastatic potential of BC cells are broader and more
231 sustained than the known effects on bone cell function⁵⁹.

Summary Box 2 - Standard of care treatments in TNBC

- Sequential anthracycline-taxane based regimens are considered standard of care.**
- Anthracycline-free chemotherapies are considered for lower risk tumours or in patients where cardiotoxicity is a concern.**
- Taxane-free chemotherapy or use of an alternative microtubule stabiliser is considered in patients with peripheral neuropathy or taxane hypersensitivity reactions.**
- Bisphosphonates are recommended for the treatment of operable breast cancer of all subtypes in patients with low oestrogen states, whether natural or induced. They should particularly be considered in patients at high risk of relapse or treatment-related bone loss.**

232

4.3. Treatment Schedule

233

4.3.1. Neoadjuvant vs. Adjuvant Chemotherapy

234 Chemotherapy can be delivered in the adjuvant or neoadjuvant setting with no significant difference in long-
235 term outcomes, as illustrated by the NSABP B-18, EORTC 10902, and IBBGS trials⁶⁰⁻⁶². More recently, an
236 EBCTCG meta-analysis demonstrated no significant difference in distant recurrence or death between
237 NACT and ACT but a more frequent local recurrence rate⁶³. A TNBC specific meta-analysis suggested
238 NACT is associated with a comparable DFS but worse OS than ACT⁶⁴, perhaps explained by patients with
239 higher disease burden being more likely to receive NACT. In this meta-analysis patients that achieved pCR,

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240 had superior OS and DFS compared to those treated with ACT. This evidence does not support the
241 suggestion that NACT promotes cancer cell dissemination⁶⁵.

242 Advantages of NACT include downstaging tumours resulting in increased rates of breast-conserving surgery
243 and associated improved cosmesis and reductions in postoperative lymphoedema. In addition, it allows
244 assessment of treatment response, provides valuable prognostic information⁶⁶, guides choice of post-surgical
245 treatment, and allows for ineffective treatment to be ceased to avoid unnecessary toxicity. NACT also
246 provides an ideal platform for translational research, assessment of biomarkers, and genetic testing⁶⁷.

247 The same Anthracycline/Taxane-based regimens are typically used in NACT and ACT. Whether the
248 scheduling of these combinations has any effect on efficacy has been a matter of extensive research. The
249 evidence suggests using taxanes and anthracyclines sequentially increases efficacy and decreases toxicity⁶⁸.
250 There is some evidence to show administration of taxane chemotherapy before anthracyclines is associated
251 with improved pCR rates⁶⁹.

252 **4.3.2. Dose-dense and metronomic chemotherapy**

253 There has been increasing interest in personalising treatment schedules to take patient and tumour
254 characteristics into account. Dose-dense NACT is now a widely accepted treatment strategy for high-risk
255 TNBC in order to prevent cancer cell repopulation⁷⁰. It has been consistently shown to improve rates of pCR,
256 breast-conserving surgery, and recurrence in hormone-low BC^{71,72}. Although this regimen has not translated
257 into a significant survival benefit⁷², this approach should be considered in selected patients with a high
258 disease burden. Dose-dense ACT improves DFS and OS rates in patients with low hormone receptor levels,
259 although this is accompanied by increased toxicity and patients need to be selected carefully⁷³.

260 At the other end of the spectrum, metronomic chemotherapy is given at minimum biologically effective
261 dose either continuously or with minimal extended breaks from treatment to reduce severe toxicity. It is
262 thought to have angiogenic, stroma targeting, and immunostimulatory effects⁷⁴. It has been investigated as a
263 single approach as well as being used in combination to intensify standard chemotherapy. It may have a role
264 as a maintenance therapy for high-risk patients or for use by patients who would not otherwise be able to
265 tolerate the adverse effects of standard treatments. The SYSUCC-001 study showed significant
266 improvement in 5-year DFS with 1 year of maintenance capecitabine⁷⁵. The IBCSG 22-00 trial confirmed
267 a 7.9% reduction in the absolute risk of relapse in patients with node-positive TNBC⁷⁶ after 1 year of low
268 dose capecitabine and methotrexate maintenance treatment, although no improvement in DFS was observed.

269 **4.4. Assessing Response to NACT**

270 Residual Cancer Burden (RCB) is a prognostic score which classifies tumour response to chemotherapy
271 using a numeric score based on four characteristics of surgical outcome: primary tumour bed dimensions,
272 cellularity fraction of invasive cancer, size of largest metastasis, and number of positive lymph nodes⁶⁷. Four
273 prognostic categories were established (Table 4). It has been shown NACT achieves a pCR in slightly over
274 a third of patients with TNBC and these patients enjoy excellent long term survival outcomes⁷⁷. Higher rates
275 of pCR following NACT are seen in TNBC, as compared to other subtypes, despite the high rate of disease
276 relapse in this cohort. This is believed to derive from poor outcomes in patients with residual chemotherapy-
277 resistant disease⁷⁸. RCB after NACT can accurately predict both event-free survival (EFS) and DFS and is
278 commonly used as a surrogate outcome in clinical trials⁷⁹.

279 Liquid biopsies for circulating tumour DNA (ctDNA) measurement is a promising dynamic approach to
280 assess for residual disease and to predict treatment response in real-time⁸⁰. Fragments of DNA released by
281 apoptosed or necrosed tumour cells can be longitudinally measured in patients' blood samples. Detection of
282 high ctDNA levels at the time of surgery has been associated with reduced DFS and OS rates and clearance
283 of ctDNA during NACT has been associated with improved outcomes across all BC subtypes⁸¹. Clinical
284 trials that incorporate this approach for patient selection are imminent.

285 *Table 4: Residual cancer burden categories*

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4.5. Post Neoadjuvant Treatments

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Patients with residual disease at surgery are often considered for further systemic therapy. Current treatment options in this setting following NACT include capecitabine and Poly ADP-ribose polymerase inhibitors (PARPi) for *gBRCA* carriers.

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The Create-X trial demonstrated that six to eight cycles of capecitabine improved 5-year DFS and OS as compared to no further therapy, especially in the TNBC cohort⁸². In contrast, the GEICAM/2003-11_CIBOMA/2004-01 trial failed to show a statistically significant increase in DFS with the use of eight cycles of adjuvant capecitabine²⁹. Of note, a pre-planned analysis of this study showed that the non-basal TNBC cohort derived most benefit from receiving capecitabine⁸³. Significant differences in study populations limit direct comparisons between these two studies. Create-X enrolled an Asian population who are known to be highly efficient metabolizers of fluoropyrimidines, all of whom had high-risk pathologically-assessed residual disease. In contrast, GEICAM/CIBOMA accrued patients from Europe and South America, only 80% of whom had residual disease. Meta-analyses on the topic have concluded upon an overall improvement in DFS and OS with capecitabine⁸⁴ and opinion from the St Gallen international conference found 87% of experts would offer capecitabine to patients with residual TNBC in the post-neoadjuvant setting⁸⁵. Differences in outcomes on a population level and issues with toxicity have led to capecitabine being offered on a case-specific basis rather than as standard of care⁸⁶. The GEICAM/CIBOMA data indicates that more detailed investigation is needed of exactly which TNBC sub-types would benefit from capecitabine.

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Table 5: Major clinical trials evaluating capecitabine in patients with stage I-III TNBC

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The OlympiA trial recruited 1836 patients with HER2 negative cancers, 82% classified as TNBC, and showed that 52 weeks of adjuvant Olaparib was associated with a significant DFS improvement in patients with *gBRCA1/2* mutations (3-year iDFS 85.9% for Olaparib vs 77.1% for placebo)⁸⁵. A 32% reduction in the risk of death versus placebo (HR=0.68; 95% CI 0.50-0.91; p=0.0091) led to the recent FDA approval for Olaparib in this setting.

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The optimal treatment for residual disease after NACT remains a matter for debate, particularly for *gBRCA* carriers with high-risk TNBC. A direct comparison between adjuvant Olaparib and capecitabine is not available. The theoretical advantage for Olaparib use includes targeting a known tumour susceptibility in a selected population, leading to improved response, and improved tolerability as compared to standard cytotoxics. Interestingly, a phase 2 trial that assessed the value of molecularly targeted postneoadjuvant treatment vs clinician's choice in TNBC patients with residual disease did not demonstrate superiority of this approach⁸⁷. Despite the limitations in regards to the primary outcome, an example was set for biomarker-driven clinical trials and the use of ctDNA in optimising the selection of biomarker-treatment partners. Patient preference and financial issues clearly also need to be considered in this setting.

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Summary Box 3 - Key concepts in the current treatment of TNBC

-Chemotherapy can be given in the adjuvant or neoadjuvant setting and the same regimens are typically used. Long-term survival outcomes are similar.

-Advantages of NACT include a rapid evaluation of tumour response, prognostication using RCB scoring, and improved surgical outcomes.

-RCB is strongly associated with long term outcomes in TNBC

-Patients with TNBC who are at increased risk of relapse after chemotherapy in the neoadjuvant setting benefit from adjuvant capecitabine. Patients in the *gBRCA* subgroup benefit from PARP inhibitors.

-Sequential liquid biopsies to assess ctDNA level represents a possibility for monitoring treatment response in real-time.

321

322 **5. Targetable molecular pathways**

323 Much progress has been made to define and treat TNBC according to aberrations on the molecular
324 level, although the derivation and use of biomarkers to select patients for specific treatments has
325 been somewhat lacking. In order to make further progress, the identification of predictive
326 biomarkers must be a central focus of our research and once secure, used to guide and to select
327 patients most likely to derive benefit from targeted treatments.

328 Tables S3, S4 and S5 summarise ongoing trials contributing to the use of molecularly targeted
329 treatment for early TNBC

330 **5.1. DNA damage response (DDR)**

331 TNBCs are frequently deficient in DDR pathways and exhibit high chromosomal instability^{7,88}. Repair of
332 DNA double-strand breaks (DSBs) relies on the homologous recombination (HR) pathway. Dysfunctional
333 activity of genes involved in this pathway compromises the ability of cells to mend DSBs, thereby inducing
334 Homologous Recombination Deficiency (HRD)⁸⁹.

335 HRD can occur via numerous mechanisms, all resulting in similar phenotypic and genotypic features to
336 those of *BRCA* mutant tumours; an observation that has been termed ‘*BRCA*-ness’. Phenotypic and
337 molecular similarities between *BRCA*-associated BC and sporadic TNBC have led to the application of
338 similar therapeutic interventions in both groups. In patients with *BRCA* mutations and *BRCA*ness features,
339 a compromised DDR pathway facilitates increased sensitivity to drugs such as platinum and PARPi, based
340 on the concept of synthetic lethality⁹⁰.

341 Approximately 10-20% of TNBC harbour *gBRCA* mutations, and 70% of *gBRCA1* and 16% of *gBRCA2*-
342 associated tumours are classified as TNBC⁹¹. Somatic *BRCA* mutations are uncommon in sporadic TNBC^{6,18,29}.
343 *BRCA1* and 2 mutations, and hypermethylation of *BRCA1* promoter, only account for some TNBCs that
344 exhibit functional evidence of HRD. Around 40% of BCs are identifiable as HRD in the absence of these
345 changes⁹². Dysfunctional *BRCA* pathways are frequently enabled by other mechanisms, for example, *RAD51*
346 and *PALB2* mutations can confer a *BRCA*-ness phenotype⁹².

347 **5.1.1. Therapeutic approaches**

348 **5.1.1.1. Platinum agents**

349 The cytotoxic activity of platinum is mediated by the formation of platinum–DNA adducts that interfere
350 with DNA replication and transcription, activating DNA-damage recognition and repair, cell-cycle arrest,
351 and apoptosis.

352 Platinum-containing regimens have not been regarded as standard of care in the treatment of TNBC in most
353 guidelines to date. Several trials have investigated the addition of platinum agents to standard chemotherapy
354 for this subgroup based on the potential increased susceptibility of TNBC to DNA-damaging compounds²⁵
355 (Table 6). Improved pCR rates with the addition of carboplatin have been a consistent finding, with
356 confirmed EFS benefit in two large randomised studies, GeparSixto and BrighTNess^{93–99}. These results have
357 led to the inclusion of carboplatin within neoadjuvant regimens for high-risk TNBC in an American Society
358 of Clinical Oncology guideline⁹⁹.

359 Combining carboplatin with anthracycline/taxane NACT increases haematological and gastrointestinal
360 toxicity, which in turn has implications for patient selection. Predictive biomarkers to identify those patients
361 deriving the most benefit from the addition of platinum, for example, *gBRCA* mutations, have been
362 investigated. Single-agent cisplatin has shown conflicting results in *BRCA* carriers¹⁰⁰. The PARTNER

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363 (NCT03150576) trial includes a cohort of *gBRCA* mutated patients¹⁰¹ and will help to elucidate the effect of
364 platinum and PARPi in this subgroup.

365 There is currently no routine indication for platinum agents in the post-neoadjuvant setting. The EA1131
366 study (NCT02445391) was closed early as neither cisplatin nor carboplatin were able to demonstrate non-
367 inferiority or superiority over capecitabine, and toxicity rates were higher¹⁰².

368 *Table 6: Major interventional clinical trials involving platinum agents in patients with stage I-III TNBC*

369 5.1.1.2. PARP inhibition

370 Poly ADP-ribose polymerase (PARP) activity is crucial for maintaining the correct fork speed and fidelity
371 of DNA synthesis. PARP1 is involved in the response to single-strand DNA (ssDNA) damage and maintains
372 genome integrity via base excision repair. PARP1 is also a critical early event for DNA DSBs repair
373 activation and regulation of resection¹⁶¹. PARP inhibition causes replication stress, induces ssDNA breaks
374 and affects the normal regulation of p53 and its downstream effectors¹⁰⁶. In tumours that have deficiencies
375 in the HR pathway, the accumulation of DSBs originating from primary ssDNA breaks leads to cell cycle
376 arrest and death¹⁰⁷.

377 Robust evidence now supports the efficacy of single-agent PARPi in BC patients with *gBRCA* mutations
378 who have received prior chemotherapy^{108,109}. A variety of PARPi and combinations have now been explored
379 in both patients with *gBRCA* mutations and sporadic (non-*BRCA*) TNBC in the early setting.

380 Evidence to date for the use of **Olaparib** is promising, both as monotherapy and in combination with
381 chemotherapy, immunotherapy, or radiotherapy. In the neoadjuvant setting, Olaparib was given as
382 monotherapy in 32 patients with unselected TNBC for up to 10 weeks before chemotherapy¹¹⁰ with overall
383 objective response rate 56.3% vs 51.9% among patients not harbouring *gBRCA1/2* or germline *PALB2*
384 mutations. A numerical enrichment of somatic HR mutations and *BRCA1* methylation in the responding
385 group suggests favourable activity of Olaparib here. Other trials in the neoadjuvant setting combine Olaparib
386 with chemotherapy. GePAROLA included patients with HER2-negative BC and HRD, delivering paclitaxel
387 with Olaparib or carboplatin followed by epirubicin and cyclophosphamide¹¹¹. No formal testing between the
388 arms was planned but increased benefit from Olaparib was observed in young (<40 years) and HR-positive
389 patients. In the TNBC subgroup, pCR rate was 56.0% with olaparib and 59.3% with carboplatin. PARTNER
390 is a phase 3 trial that assesses the addition of Olaparib to neoadjuvant platinum-based chemotherapy in the
391 treatment of TNBC and *gBRCA* derived tumours. Preliminary safety results show that the combination of
392 Olaparib and platinum has an acceptable and manageable toxicity profile¹¹². In the I-SPY2 trial, research arm
393 patients received Olaparib and Durvalumab with paclitaxel then doxorubicin and cyclophosphamide¹¹³ which
394 increased pCR in the TNBC group (27%–47%), Immune-rich tumours had greater sensitivity to this
395 treatment. The adjuvant phase 1 RadioPARP trial for patients with inflammatory, locoregionally advanced
396 or mTNBC, or patients with residual disease after surgery for TNBC, sought to evaluate safety and dosing
397 for Olaparib in combination with radiotherapy¹¹⁴. Olaparib was escalated to the maximum target dose of 200
398 mg twice daily with no dose-limiting toxicity.

399 **Talazoparib** has been reviewed in the neoadjuvant setting as monotherapy and in combination with
400 chemotherapy. TALA was a pilot study that recruited 20 patients with operable BC and a *BRCA* mutation
401 to receive Talazoparib monotherapy for 6 months¹¹⁵. Despite the small sample size, this trial showed an
402 encouraging pCR rate of 53% and RCB-0/I of 63%, with a manageable safety profile. In the I-SPY2 trial,
403 Talazoparib combined with irinotecan for HER2 negative patients had limited activity beyond that seen with
404 standard treatment¹¹⁶.

405 **Veliparib** has also been evaluated in the neoadjuvant setting in the I-SPY2 trial¹¹⁷. The addition of Veliparib
406 to carboplatin containing chemotherapy increased pCR rate in the TNBC group from 26% to 51%. This
407 combination was further assessed in the phase 3 BrighTNess trial in 634 patients with TNBC⁹⁸ where no
408 additional benefit for Veliparib above that achieved by adding carboplatin, regardless of *BRCA* mutation
409 status, was found. A key limitation of this study is the low dose of Veliparib, less than half of that used in

410 the BROCADE-3 study in the advanced disease setting¹¹⁸. Veliparib has been combined with radiotherapy
411 for inflammatory or locoregionally recurrent TNBC which resulted in significant local toxicity¹¹⁹.

412 Both Talazoparib and Olaparib are effective as monotherapy in patients that carry *gBRCA* mutations. Given
413 the low dose of Veliparib used in the BrighTNess trial, and taking into account individual PARPi differences
414 in PARP trapping capacity, the potential summative benefit from the addition of platinum to PARPi cannot
415 be excluded. This encourages further investigation into the role of other PARPi such as Olaparib and
416 Talazoparib, and the great potential for combination therapy, as demonstrated by ongoing trials in Table S3.

417 5.1.1.3. Other DDR agents

418 The ATR inhibitor **Ceralasertib** (AZD6738) is being investigated as monotherapy in chemotherapy-
419 resistant TNBC as part of a pre-surgical window of opportunity and post-surgical biomarker study
420 (NCT03740893, PHOENIX), reviewing the change in mean proliferation index between baseline and post-
421 treatment. PARTNERING is a phase 2 sub-study for the PARTNER trial that offers Durvalumab in
422 combination with AZD6738 to patients with evidence of residual disease after completion of NACT and
423 before surgery. WEE 1 inhibitors have not yet been reviewed in the early TNBC setting.

424 **Table S3** summarises the major incomplete clinical trials involving DDR agents in patients with stage I-III
425 TNBC.

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Summary Box 4 - DNA damage response: treatment strategies

- There is strong evidence to support the addition of platinum agents to NACT to improve patient outcomes, especially in high risk and *gBRCA* carriers.
- Improvements in pCR and EFS rates with platinum chemotherapy combinations need to be balanced against additive chemotherapy toxicities.
- PARP inhibition causes replication stress, induces ssDNAs breaks and affects the normal regulation of p53 and its downstream effectors.
- Encouraging evidence supports the efficacy of single agent PARPi in BC patients with *gBRCA* mutations who have no prior chemotherapy exposure.
- The group of patients with TNBC most likely to benefit from PARP inhibition in the neoadjuvant setting is yet to be established.
- Olaparib improves DFS in *gBRCA* carriers with high risk HER2 negative disease following neoadjuvant or adjuvant chemotherapy.

427 5.1.2. Predictive biomarkers of DDR agents

428 5.1.2.1. *BRCA* mutations

429 The predictive value of both *gBRCA* and somatic *BRCA* mutations for response to platinum and PARPi has
430 been validated in large clinical trials that include patients with ovarian and metastatic BC^{109,115}. The role of
431 *BRCA* status as an independent predictive biomarker for the TNBC population in the neoadjuvant setting is
432 still unclear with studies showing conflicting results. In a secondary analysis of the GeparSixto trial ($n=50$)¹²⁰,
433 *gBRCA* mutations were predictive of higher pCR rates and carboplatin did not increase this further. In the
434 CALGB 40603 trial, pCR rates in patients with *gBRCA* mutations were similar to the overall population,
435 and this outcome was not altered by the addition of carboplatin¹²¹.

436 *BRCA1/2* mutation carriers with TNBC subtype in the I-SPY 2 trial were significantly more likely to achieve
437 a pCR than non-*BRCA* TNBC (predicted pCR of 75% vs 29%)¹²² and a greater response was seen for patients
438 with a *BRCA*-ness signature¹¹⁷. Subgroup analysis of the BrighTNess trial did not show a difference in pCR
439 rate based on *BRCA* status⁴⁶. However, in the GeparOcto trial¹²³ *gBRCA* mutation carriers gained greater

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440 benefit from platinum (68.1% vs 45.7%, $p=0.005$), particularly in the TNBC subgroup (74.3% vs 47%,
441 $p=0.005$).

442 In the PETREMAC trial, in which patients received olaparib monotherapy before chemotherapy,
443 pathogenic mutations (germline or somatic) in the HR pathways and/or *BRCA1* promoter methylation were
444 associated with Olaparib overall response (OR) 88.9%¹²⁴. Although pCR rates in the GeparOLA trial for
445 *gBRCA1/2* carriers were significantly higher than in non-carriers (62.7% vs 41.3%, $P=0.047$), exploratory
446 analysis revealed no difference between treatment arms if somatic or germline *BRCA1/2* mutation were
447 detected¹²⁵.

448 5.1.2.2. HRD by gene sets analysis and functional assays

449 Several attempts to simplify and systematically identify common molecular changes associated with
450 defective HR have been published. The evaluation of DNA damage repair-related genes by either gene
451 expression or by the presence of mutations has shown a positive association with response. Confirmation of
452 the predictive value of these individual efforts has not always been accomplished given the underlying
453 heterogeneity of some of these variations. (Table 7).

454 5.1.2.3. HRD by genomic scars and mutational signatures.

455 The detection of mutational signatures uniquely identifying patterns of defective HR repair is the subject of
456 several studies. Vollebergh et.al assessed whether array comparative genomic hybridisation patterns could
457 predict the benefit of intensified carboplatin-based chemotherapy¹²⁶. A HRD score defined by an unweighted
458 sum of loss of heterozygosity, telomeric allelic imbalance, large-scale transition, and *BRCA1/2* mutations
459 has been tested in TNBC treated with platinum, and used to aid patient selection in PARPi trials^{127,128}. In the
460 absence of *gBRCA* mutations, a high HRD score was associated with higher pCR rates irrespective of the
461 use of carboplatin. Microhomology-mediated indels, HRD index, single base substitution signature 3,
462 rearrangement signature 3 and 5, and genomic instability markers of HRD are aggregated into the HRDetect
463 score⁹². The prognostic value of HRDetect has been demonstrated in two retrospective clinical cohorts and
464 further evaluation of its predictive power in randomised clinical trials is awaited.

465 HRD is yet to be used to guide in the clinical management of TNBC despite its theoretical significance. The
466 absence of a standardised definition of HRD beyond *gBRCA* mutation and the lack of prospective clinical
467 trial data, currently limit clinical utility.

468 *Table 7: HRD related biomarkers and its association with treatment response.*

469 5.1.2.4. Tumour mutational burden

470 An increased number of tumour mutations could be correlated with an enhanced response to drugs causing
471 DNA damage. For example, somatic hypermutation was shown to be an independent factor for estimating
472 the risk of platinum sensitivity in high-grade serous ovarian cancer (OR=3.616, $p=0.002$)¹³². A higher tumour
473 mutational burden (TMB) has been observed in BCs that harbour DDR gene mutations¹³³, although
474 correlation with response to platinum is not yet established. Contrastingly, in the PETREMAC trial, no
475 difference in TMB was observed between responders and non-responders, or *BRCA* carriers versus non-
476 carriers¹⁰⁷.

Summary Box 5 - DNA damage response: biomarkers

-The role of *BRCA* status as an independent predictive biomarker among the TNBC population in the neoadjuvant setting is unclear

-Overall, alterations in DNA damage repair-related genes by either gene expression or presence of mutations has shown a positive association with response to NACT and/or PARPi.

-Mutational signatures predictive of *BRCA1/BRCA2* deficiency or a '*BRCA*-ness status' have shown a trend to positive association with response to platinum chemotherapy. However, these

results are signature specific and should be considered preliminary. Data from randomised clinical trials that prospectively assess the value of these biomarkers is awaited.
-Higher TMB has been observed in BC tumours that harbour DDR gene mutations. Correlation with response to platinum agents is not yet established.

478 5.2. Immune response

479 Although BC is largely considered an immune quiescent cancer type¹³⁴, increasing evidence suggests that a
480 range of tumour immunogenicity is present. TNBC is characterised by increased immune activation and
481 wide immune heterogeneity compared to other BC subtypes¹³⁵.

482 5.2.1. Therapeutic approaches

483 Tumours evade detection and eradication by the immune system through the dysregulation of pathways
484 controlled by immune checkpoints. Immunotherapy harnesses the patient's immune system to target
485 malignant cells using Immune checkpoint inhibitors (ICI), Chimeric antigen receptor T cells or cancer
486 vaccines. ICIs release the immune system from tumour-induced inhibitory signals, allowing an effective
487 anti-tumour response. They include monoclonal antibodies (mAbs) against cytotoxic T lymphocyte-
488 associated antigen-4 (CTLA-4), programmed cell death-1 (PD-1), and programmed cell death ligand-1 (PD-
489 L1).

490 5.2.1.1. Monoclonal antibodies against PD-1

491 **Pembrolizumab** is the most well-established and successful anti-PD-1 ICI in operable TNBC. The addition
492 of Pembrolizumab to NACT has shown increases in pCR rate across several RCTs including the
493 KEYNOTE-173 and I-SPY 2 trials^{136,137}. These successes led to the landmark phase 3 KEYNOTE-522 trial
494 which has culminated in the FDA approval for use of Pembrolizumab in high-risk early-stage TNBC, the
495 first regulatory approval for an immunotherapy agent in this setting. Pembrolizumab is now considered a
496 standard of care treatment in the United States for patients fitting trial eligibility criteria.

497
498 KEYNOTE-522 evaluated neoadjuvant Pembrolizumab in combination with carboplatin/paclitaxel and
499 anthracycline-based NACT, and then adjuvantly as monotherapy, in high-risk early TNBC. pCR rate
500 improved by 7.5% (95% CI: 1.6% to 13.4%) with the addition of Pembrolizumab, and after a median follow
501 up of 39.1 months, 36-month EFS improved from 77% to 85% (HR: 0.63; 95% CI, 0.48 to 0.82; P<0.001).
502 OS data remains immature at the time of analysis³⁴. High-risk patients derived the greatest benefit with higher
503 absolute improvements in pCR in stage III and node-positive disease. There are some limitations to this
504 study. With this trial design, it is not possible to elucidate the relative contributions of the neoadjuvant and
505 adjuvant treatment phases on these EFS results. Concern has been raised at the rate of serious adverse events
506 (77% incidence of grade ≥ 3 events in the immunotherapy group), and immunotherapy related adverse effects
507 (irAE) (affecting 33.5% of patients on this trial) due to their protracted nature. It is therefore imperative to
508 detect predictive biomarkers to facilitate the selection of patients likely to derive the most benefit from
509 immunotherapy and treatment de-escalation strategies. No predictive biomarkers were identified on this
510 trial. Improvement in pCR rate was seen regardless of PD-L1 status³⁸. Patients on the Pembrolizumab arm
511 that achieved pCR derived a modest survival benefit (approximately 2%), as compared to 10% in the cohort
512 of patients with residual disease at surgery. This suggests that the value of adjuvant Pembrolizumab as a
513 monotherapy may be small in the group who achieved pCR. Removal of the adjuvant portion of treatment
514 based on response at surgery could represent a potential treatment de-escalation strategy that requires further
515 exploration.

516 5.2.1.2. Monoclonal antibodies against PD-L1

517
518 **Atezolizumab**, **Durvalumab** and **Avelumab** are the most established anti-PD-L1 ICIs being investigated
519 in operable TNBC, although results from trials have been inconsistent. pCR rate improved from 41% to

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520 58% with the addition of Atezolizumab to anthracycline/taxane-based chemotherapy in Impassion031⁴⁹.
521 Secondary endpoints (EFS, DFS and OS) are expected later this year, however, this trial is not powered to
522 show survival differences. The phase 3 NeoTRIPaPDL1 trial failed to show a significant pCR advantage
523 with the addition of Atezolizumab to neoadjuvant carboplatin and nab-paclitaxel⁴⁰, although EFS was the
524 primary endpoint and this data is not yet available. These incongruent results are likely to reflect the higher
525 risk patient population in NeoTRIPaPDL1 and the difference in the chemotherapy backbone. Results from
526 the TONIC trial suggest anthracycline chemotherapy, used in Impassion031, leads to a potentiation of the
527 effects of immunotherapy¹⁴¹. These insights should inform the choice of chemotherapy backbone in the
528 design of future immunotherapy trials.

529
530 GeparNUEVO assessed Durvalumab in addition to anthracycline/taxane-based NACT. This showed a non-
531 significant 9% improvement in pCR rate. Improvements in 3y iDFS and 3y OS were also seen, though this
532 trial was not powered to definitively assess long term survival differences. An underpowered subgroup
533 analysis showed a particular benefit in patients who received Durvalumab alone for two weeks prior to
534 NACT, suggesting immunological interactions with priming in this window phase^{142,143}. While the small
535 patient cohort included in GeparNUEVO has cumulated in statistically non-significant pCR and iDFS
536 benefits, the results are similar to those from KEYNOTE-522. This is despite lacking a platinum agent and
537 an adjuvant treatment phase. These represent potential treatment de-escalation avenues that could benefit
538 from further exploration. Discrepancy between the magnitude of benefit for pCR rate and survival seen
539 across both trials suggests pCR to be a poor surrogate marker for long term survival in immunotherapy trials
540 in operable TNBC. Published and ongoing trials of ICI have been summarised in **Tables 8 and 9**.

541
542 The use of ICIs in TNBC is an area of active research, although it is at an early stage, and long-term outcome
543 data remain immature for the majority of the neoadjuvant trials. Concern regarding the use of pCR as a
544 primary endpoint upon which to grant regulatory approval for neoadjuvant Pembrolizumab was cited by the
545 FDA, and long-term survival data is of particular interest¹⁴⁴. There is a paucity of data available to guide use
546 of pembrolizumab in the adjuvant or post-neoadjuvant setting, particularly in combination with agents such
547 capecitabine or Olaparib used in more contemporary practice. This represents a challenge when adopting
548 Pembrolizumab as standard of care treatment and results of trials investigating these issues are highly
549 anticipated.

550
551 *Table 8: Major neoadjuvant trials of immune checkpoint inhibitors in patients with stage I-III TNBC*

552 *Table 9: Major adjuvant trials of immune checkpoint inhibitors in patients with stage I-III TNBC. Ongoing trials*
553 *evaluating PARP inhibitors in combination with immunotherapy can be found in supplementary table 3.*

554 **5.2.1.3. Cancer Vaccines**

555 Cancer vaccines utilise tumour associated antigens to stimulate CD4+ and CD8+ T cells, inducing the
556 patient's immune system to target cancer cells that were previously successfully evading immune
557 suppression. They have yet to show success in late-stage clinical trials or to receive regulatory approval for
558 TNBC. Clinical trials evaluating cancer vaccines in non-metastatic TNBC are listed in **Table S4**.

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Summary Box 6 - Immune response: treatment strategies

- Immunotherapy is of particular interest in TNBC due to the higher degree of immune activation seen in comparison to other BC types.
- TNBC is a heterogeneous disease that exhibits various degrees of immunogenicity.
- Several early stage BC trials have established PD-1 and PD-L1 ICIs as a promising treatment option in combination with chemotherapy.

- Pembrolizumab has been granted FDA approval in the neoadjuvant setting for high-risk early-stage TNBC in combination with chemotherapy and to continue as monotherapy in the adjuvant setting (KEYNOTE-522).

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5.2.2. Predictive biomarkers of ICI response

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5.2.2.1. PD-L1

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PD-L1 expression is higher in TNBC compared with non-TNBC¹³⁶ and quantification is currently performed using five distinct FDA-approved companion diagnostic tests across tumour types. Variety in assays, scoring systems, and cut-off values renders the interpretation of its predictive value challenging¹⁴⁰. Increased pCR rate in PD-L1+ early-stage TNBC is seen, but rather confusingly, ICI benefit independent of PD-L1 status has been consistently described^{138,143,148,149}. In the GeparNUEVO trial, pCR rate was increased in PD-L1+ tumours in all therapy groups but PD-L1 did not predict ICI response¹⁴³. Similar results were observed in the KEYNOTE-522 and Impassion 031 trials.

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5.2.2.2. Tumour mutational burden

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High tumour mutational burden precipitates enhanced immunogenicity by increasing the number of tumour antigenic peptides or neoantigens that can be recognised by T-cells¹⁵⁰. Based on this hypothesis, high TMB has been correlated with an increased response to ICI^{151,152} independently of PD-L1 expression¹⁵³. The FDA granted accelerated approval of Pembrolizumab as monotherapy for advanced tumours that exhibit high TMB (defined as ≥ 10 mut/Mb) in 2020¹⁵⁴. More recently, it has been shown that the association of TMB with response to ICI relies on a positive correlation between CD8+ T-cell level and neoantigen load, and differs across tumour types¹⁵¹.

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The role of mutational load as an independent predictive biomarker of ICI response is yet to be defined in TNBC¹⁵⁵ due to limited data availability and differences among TMB quantification methods. In the GeparNUEVO trial, TMB was higher in patients with pCR (median 1.87 versus 1.39 mut/MB), and both continuous TMB and immune GE profile independently predicted pCR. In comparison, no difference in pCR rate was observed in patients with high TMB who received ICI when compared to other targeted therapies in the ARTEMIS trial (NCT02276443).

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5.2.2.3. Tumour infiltrating lymphocytes (TILs)

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Both intra-tumoural TILs (iTILs) and stromal TILs (sTILs) have prognostic and predictive roles in the treatment of early TNBC, and have also been evaluated in this setting as a biomarker of immunotherapy response. In the GeparNUEVO trial¹⁴¹, sTILs prior to therapy predicted a higher pCR rate overall, and in both therapy groups, but were not predictive of Durvalumab response. The increase in iTILs in post-window samples compared with pre-therapeutic samples was predictive of pCR, yet the treatment interaction test did not reach significance ($P = 0.085$). High TILs were significantly associated with Olaparib response in the PETREMACT trial¹¹⁰. Criscitiello et al used a LASSO penalised regression model to develop a 4-gene signature to predict high and low TILs after NACT. High TILs signature was associated with improved long-term outcomes independent of pCR¹⁵⁴. Overall, increased TILs are associated with a more favourable response to NACT and improved long-term outcomes^{156,157}.

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5.2.2.4. Immune signatures

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GE immune signatures have been extensively used to describe profiles of immune infiltration and immune cell type that impact on the prognosis of many tumour types including TNBC¹⁵⁸⁻¹⁶¹. Few studies have tested the value of GE immune signatures in the prediction of chemotherapy response in the early setting of TNBC. Sharma et al¹⁶², evaluated the performance of a DNA damage immune response signature and sTILs as prognostic markers in patients with TNBC treated with adjuvant doxorubicin and cyclophosphamide. in the

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601 SWOG 9313 trial. DDIR was associated with improved OS and DFS, and was moderately correlated with
602 sTILs density ($\geq 20\%$ v, $<20\%$). Lv et al. identified CXCL9 and CXCL13 as prognostic biomarkers in
603 TNBC using network analysis. Further testing in two neoadjuvant data sets confirmed its predictive value
604 in the response to chemotherapy¹⁶³. Exploratory analysis of the GeparNUEVO trial revealed that predefined
605 TIL and IFN-gamma signatures were associated with increased pCR rate, without specificity for
606 Durvalumab response. The expression of six genes required for immune cell function were significantly
607 correlated with pCR and showed a positive test for interaction with Durvalumab plus NACT¹⁶⁴. Further
608 evaluation of the interactions between tumour and immune system, as well as its architectural heterogeneity,
609 will provide a more accurate estimation of the individual predictive potential to be derived from immune
610 signatures.

611 5.2.2.5. Microsatellite instability status

612 Pembrolizumab monotherapy received FDA approval in 2017 for the treatment of advanced mismatch repair
613 deficient solid tumours¹⁶⁵. Although only a small proportion of breast cancers are defined as Microsatellite
614 Instable, tumours with defects in the mismatch repair pathways are known to have highly upregulated
615 expression of multiple immune checkpoints and increased sensitivity to ICI¹⁶⁶. The introduction of new
616 strategies to facilitate the identification of this biomarker in a low frequency cohort like TNBC remains a
617 challenge.

Summary Box 7 - Immune response: Biomarkers

- **Response to ICIs appears to be independent of PD-L1 status in early TNBC.**
- **High TMB has been correlated with an increased likelihood of response to ICI, particularly in tumours where CD8+ T-cell levels are positively correlated with neoantigen load.**
- **The role of mutational load as an independent predictive biomarker of ICI response is yet to be defined in TNBC.**
- **Increased TILs are associated with a more favourable response to NACT and long-term outcomes.**
- **Modest positive association of GE immune signatures with ICI response have been reported.**
- **The interaction between TMB and GE immune signatures has been shown to be as a promising independent predictor of pCR.**
- **The dynamics of immune activation after treatment are strongly associated with long term outcome, independently of response rate.**
- **Tumours with defects in the mismatch repair pathways are known to have highly upregulated expression of multiple immune checkpoints and increased sensitivity to ICI.**

618 5.3. PIK3CA/AKT1/PTEN pathway

619 Dysregulation of the PI3K/AKT/mTOR pathway is often observed in TNBC^{18,29}, and remains a promising
620 target for the future treatment of this BC subtype. Pathway activation is predominantly via *PIK3CA*
621 mutations (~9-18%), loss of *PTEN* (~35%) or *INPP4B* (~30%), and amplification of *PIK3CA* (~43%). The
622 frequency of PI3K/AKT/mTOR pathway activation and its spectrum varies by TNBC subtype^{18,29}, and is
623 strongly associated with the LAR subtype across classifiers.

624 5.3.1. Alpha-specific PI3K inhibitors

625 In unselected TNBC, response to PIK3CA inhibitors remains low. The BELLE-4 study evaluated the
626 efficacy of **Buparlisib** in the locally advanced setting for patients with HER2 negative BC in combination
627 with paclitaxel versus placebo and observed no benefit from PIK3CA inhibition¹⁶⁷. Worse outcomes were
628 observed in the TNBC cohort treated with the PIK3CA inhibitor and lack of benefit was independent of
629 *PIK3CA* mutation or PTEN loss by immunohistochemistry¹⁶⁷. Shorter treatment duration in the buparlisib

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630 arm due to adverse events, and longer progression free survival (PFS) in the placebo arm than anticipated,
631 are possible explanations for the worse outcomes in this subgroup. The global lack of activity is possibly
632 due to inadequate patient selection and the absence of an accurate biomarker. Parallel pathway activation
633 could also explain a resistance mechanism that requires addressing.

634 5.3.2. AKT inhibitors

635 **Ipatasertib** was reviewed in the neoadjuvant setting in combination with paclitaxel for TNBC patients in
636 the FAIRLANE trial⁶⁸. Adding ipatasertib did not significantly increase the pCR rate compared with
637 paclitaxel alone and this effect was independent of *PIK3CA/AKT1/PTEN* or *PTEN* low status. Complete
638 clinical response was absent in the placebo-treated group in patients with tumours defined as LAR subtype,
639 but was observed in 50% of those treated with ipatasertib. This difference was not evident in pCR rates.
640 Elevated immune scores were more strongly associated with improved outcomes in paclitaxel-
641 treated compared to ipatasertib-treated patients, highlighting the key interaction with the immune system.
642 All ipatasertib-treated patients with low immune scores and complete clinical response had
643 *PIK3CA/AKT1/PTEN*-altered tumours. **MK2206** has been trialled in the neoadjuvant setting in the I-SPY2
644 trial for stage 2-3 BC of any subtype⁶⁹. Patients received paclitaxel chemotherapy with or without MK2206,
645 then AC. pCR for the TNBC group was 40.2% with MK2206 vs. 22.4% without. Following assessment for
646 biomarkers in the AKT pathway in the TNBC subgroup, higher levels of phosphorylated AKT and its
647 substrates were paradoxically associated with reduced response to MK-2206.

648 5.3.3. MTOR inhibitors

649 **Everolimus** has been reviewed in the neoadjuvant setting for patients with TNBC in combination with
650 cisplatin and paclitaxel²⁶, and in combination with docetaxel, 5-fluorouracil, epirubicin and
651 cyclophosphamide⁷⁰. No improvement in response rate has been demonstrated.

652 The exact contribution of drugs targeting the *PIK3CA/AKT1/PTEN* pathway in early TNBC as not yet
653 been defined. The complexity of the immune microenvironment and parallel molecular alterations can
654 obscure an accurate estimation of clinical benefit if they are not both in some way accounted for. It is
655 important to trial these therapies in a way that reduces these confounders and separates the TNBC subtypes
656 to determine their individual response. Current approaches include combining alpelisib with nab-paclitaxel
657 in the neoadjuvant setting (NCT04216472) for anthracycline refractory TNBC with *PIK3CA* or *PTEN*
658 alterations, with exploratory objectives to assess biomarkers of response and resistance to alpelisib and nab-
659 paclitaxel combination.

660 **Table S5** summarises ongoing trials that target this pathway in early TNBC.

661 5.4. AR pathway

662 AR expression is found in approximately 10-35% of TNBCs as detected by immunohistochemistry^{171,172}. The
663 LAR molecular subtype derived from GE accounts for 20-40% of TNBC and is characterised by the
664 activation of AR, ER, prolactin, and ErbB4 signalling. Tumours defined as LAR subtype typically contain
665 a higher number of *PIK3CA* mutations and pCR rate following NACT is significantly lower compared to
666 other subtypes.

667 There is a paucity of data for drugs targeting the AR pathway in the early TNBC setting. **Enzalutamide** has
668 been trialled as monotherapy¹⁷³, and in combination with *PIK3CAi* in the advanced setting with modest
669 benefit⁷⁴. Other AR pathway targeted drugs, for example, **Abiraterone** and **Bicalutamide**, have been
670 reviewed in the advanced setting with modest results^{175,176}. Although overall benefit remains limited, it is
671 unclear if this derives from inadequate patient selection or analogous pathway activation. Results from four
672 trials in the early TNBC setting are highly anticipated.

673 **Table S5** summarises ongoing trials that target this pathway in early TNBC.

674 5.5. Receptor tyrosine kinase family

675 5.5.1. HER2

676 Approximately 35% of TNBC as defined by immunohistochemistry could be classified as HER2-low¹⁷⁸.
677 Somatic ERBB2 mutations occur in approximately 3% of TNBC⁵, and a subset of TNBC tumours are
678 classified as HER2 enriched by gene expression. This biological heterogeneity has expanded therapeutic
679 opportunities in this population of patients. In an exploratory analysis of a cohort of the I-SPY2 trial,
680 activation of HER2-EGFR was identified as a positive predictor of pCR in 49 TNBC patients treated with a
681 pan-HER inhibitor¹⁷⁷. A significant correlation between response to HER2 inhibition and HER2 pathway
682 activation has been demonstrated in TNBC cell lines¹⁷⁹.

683 **Neratinib** has been investigated in the neoadjuvant setting for high-risk clinical stage II or III BC. The pCR
684 rate overall in the I-SPY 2 trial was 37.5% in the neratinib arm, and among patients demonstrating
685 phosphorylation of *HER2* or *EGFR* (i.e., biomarker-positive for *EGFR* Y1173 or *ERBB2* Y1248), it rose to
686 63%¹⁸⁰. Encouraging results in the HER2-low-expressing refractory BC setting with **Trastuzumab**
687 **Deruxtecan** (OR 37%)¹⁸¹ and **Trastuzumab Duocarmazine** (OR 40%)¹⁸² now require translation into the
688 early setting. These trials illustrate the importance of identifying patients categorised as TNBC who are
689 more accurately defined as HER2 low. (**Table S5**)

690 5.5.2. VEGF

691 *VEGF* promotes angiogenesis, invasion, and increases vascular permeability, and is an essential element in
692 TNBC formation, progression, and metastasis. VEGF-A expression is higher in TNBC compared with other
693 BC subtypes¹⁸³, and enhanced angiogenic potential is associated with poor prognosis in BC¹⁸⁴. Targeting of
694 *VEGF* has been extensively tested in TNBC, but no clear predictive biomarkers of treatment response have
695 been identified.

696 Trials targeting VEGF in the neoadjuvant TNBC setting have shown disappointing results to date with no
697 difference in DFS or OS. The addition of **Bevacizumab** significantly increased the rate of pCR among
698 patients with Her2 negative disease in some studies¹⁸⁵⁻¹⁸⁸. The ARTemis and GeparQuinto trials reported
699 increased benefit primarily in the TNBC subgroup. In the adjuvant setting, the BEATRICE trial added
700 Bevacizumab to anthracycline and/or taxane-based chemotherapy⁹⁶ and no difference in iDFS or OS between
701 treatment groups was found. The underlying reason for the lack of treatment effect with these drugs is poorly
702 understood. It is possible that a fundamental flaw in either the drug or the signalling pathway is being
703 overlooked. Attempts to overcome drug resistance using novel agents and combinations are ongoing (**Table**
704 **S5**).

705 5.5.3. FGFR

706 The fibroblast growth factor receptor family includes *FGFR1-4*. Signalling through this pathway regulates
707 cell survival, proliferation and differentiation. Genes that encode for these receptors are amplified in ~10%
708 of BC¹⁷. Although *FGFR1* is the most frequent genomic alteration in all subtypes of BC, amplification, and
709 overexpression of FGFR2 is more frequently observed among TNBC (~4%). Basal BC with elevated *MET*
710 and *FGFR1* signatures is associated with poor relapse free survival²⁹¹. The interplay between MET and FGFR
711 has been shown to regulate cancer stem cells in mesenchymal subtypes²⁹².

712 Trial data in this setting is limited to a small number of studies that do not select for TNBC, but in which
713 some response to this target has been seen. It seems likely that the correct biomarker has not yet been
714 identified. Ongoing trials for this target in the neoadjuvant setting include a window of opportunity trial
715 combining Lenvatinib and Pembrolizumab (NCT04427293).

716 5.5.4. EGFR

717 *EGFR* dysregulation is frequently reported in TNBC¹⁹¹ and enrichment for this pathway signalling is
718 predominantly observed in BL2 tumours¹⁹². In contrast to EGFR mutations, EGFR amplification is a
719 relatively frequent event (11% vs 23% respectively)^{193,17} and is considered an independent prognostic factor

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720 for poor disease-free survival¹⁹⁴. Several attempts to target this pathway with tyrosine kinase inhibitors and
721 mAbs in the context of mTNBC have been pursued without success. A limited number of trials have used
722 these therapies in the early setting.

723 **Cetuximab** has been trialled in combination with neoadjuvant docetaxel in a pilot phase two study including
724 stage II-IIIa TNBC¹⁹⁵. The pCR rate was 24% [95% CI: 7.3–40.7] and the pre-therapy ratio between CD8+
725 and FOXP3+ TILs equal or higher than 2.75 was predictive of pCR (43% versus 0%). **Panitumumab** and
726 the EGFR/HER2 inhibitor **Lapatinib** failed to demonstrate additional benefit in the advanced setting
727 independent of EGFR activation^{196,197}. The paucity of accurate biomarkers predictive of sensitive patients has
728 led to unsatisfactory outcomes and limited clinical utility despite increasing evidence for EGFR as the driver
729 of tumorigenesis in some TNBC.

730 **Table S5** summarises ongoing trials that target these pathways in early TNBC.

731 5.6. Other oncogenic targets

732 Inter-chromosomal rearrangements causing *NTRK* gene fusions can result in constitutive activation of TRK
733 proteins which act as oncogenic drivers through activation of cellular growth pathways. Results from early
734 phase trials that include advanced *NTRK* fusion-positive solid tumours support the use of **larotrectinib** and
735 **entrectinib** in this subgroup^{198,199}. *NTRK* gene fusions occur in low frequency (~0.3%) among all solid
736 tumours¹⁹⁹, however, a high prevalence is observed in a subgroup of TNBC¹⁶. The *ETV6-NTRK3* gene fusion
737 is frequently found in human secretory breast carcinoma¹⁶, and although the vast majority of these breast
738 tumours are treated with local treatments, targeting TRK signalling remains an option for cases of locally
739 advanced disease.

740 *Trop-2/TACSTD2* is a calcium signal transducer with extracellular, transmembrane, and intracellular
741 domains, and is overexpressed in many epithelial cancers including TNBC. It stimulates cancer cell growth
742 and it is implicated in various metabolic pathways. TROP-2 has also been found in stem cells of various
743 tissues, particularly in basal cells²⁰⁰. **Sacituzumab govitecan**, a humanised mAb that targets TROP2, has
744 shown a PFS and OS benefit in mTNBC²⁰¹. Trials are upcoming in the neoadjuvant setting (NeoSTAR,
745 NCT04230109), and recruiting in the adjuvant setting (GBG102-SASCIA NCT04595565 as monotherapy
746 and ASPRIA NCT04434040 in combination with immunotherapy) for patients with residual invasive
747 disease after NACT.

748 Dysregulation of the *NOTCH* pathway leads to aberrant self-renewal and transformation of mammary cancer
749 stem cells resulting in tumorigenesis²⁰². Inhibition of *NOTCH* signalling has been considered an attractive
750 strategy for the treatment of TNBC given its role in promoting EMT and cancer stem cell maintenance²⁰³.
751 Preclinical and clinical studies involving γ -secretase inhibitors and mAbs against *NOTCH* receptors have
752 explored its potential utility with encouraging results but toxicity has been limiting²⁰⁴. The subgroup of TNBC
753 achieving the best response to the targeting of this pathway remains undefined.

754 Activation of *RAS/MAPK* signalling is more frequent in TNBCs compared to other BC subtypes²⁰⁵. Although
755 canonical aberrations in the *RAS*, *RAF*, *MEK* or *ERK* genes are not found frequently in TNBC,
756 amplification or mutations in these genes are described in approximately 6% of BC overall^{18,206}. Other
757 mechanisms for *RAS/MAK* activation have also been described³¹⁹. *MEK* inhibitors have been trialled in
758 unselected mTNBC with modest results^{207,208}. Trials are underway in the locally advanced setting that select
759 for hyperactivation of *ERK* (NCT04494958) and *RAS* pathway mutations (NCT05111561).

760 Dysregulation of the *JAK/STAT3*, *cyclinD-CDK4/6-INK4-Rb-E2F*, *TGF- β* and *WNT/B-catenin* pathways
761 appears to be critical in TNBC development and progression. Clinical testing of the inhibition of these
762 pathways in TNBC is still immature.

763 **Table S5** summarises ongoing trials that target the above pathways in early TNBC.

764

Summary Box 8 - Other pathways: treatment strategies

- Targeted therapies should be directed with a biomarker to best determine efficacy in the TNBC population most likely to derive benefit.
- Dysregulation of the *PI3K/AKT/mTOR* pathway is often observed in TNBC. Efforts to target this pathway have inconsistently shown a modest benefit.
- Targeting AR has shown some clinical benefit and several trials are ongoing to further evaluate this. A standardised method to determine AR pathway activation is lacking.
- Overall benefit of targeting the *EGFR*, *VEGF* and *FGFR* pathways remains modest. Lack of predictive biomarkers that identify sensitive patients has limited the clinical utility of these drugs.
- Treatment directed towards HER2-low TNBC has provided new therapeutic opportunities in a proportion of patients with encouraging results from trials to date.
- Sacituzumab govitecan, a humanised mAb that targets TROP2, has shown a PFS and OS benefit in mTNBC. It remains to be seen if this success can be translated into the early TNBC setting.

765 Discussion

766 Improved understanding of tumour genomics, transcriptomics, epigenetics, and their interaction with the
767 tumour microenvironment has allowed a greater insight into the true diversity of TNBCs. In addition,
768 numerous advances in both preclinical and clinical research have directed the treatment of TNBC toward a
769 more personalised approach. Despite the introduction of an increasing number of novel strategies in the
770 clinical setting, approximately one third of patients diagnosed with early stage disease will have limited
771 response to primary treatment and face a poor long term outcome. The underlying complexity of TNBC and
772 the challenges in translating experimental science into the clinic could explain why current management
773 approaches remain insufficient. The current therapeutic landscape for early TNBC is severely limited when
774 compared to the large number of compounds in development. **Figure 1** shows the spectrum of agents with
775 known or potential activity in TNBC. Only a small proportion of these reach patient care, and the pace at
776 which these agents enter the early BC setting remains frustratingly slow. Immunotherapy and DDR agents
777 lead the field with encouraging results.

778 Predictive biomarkers are not routinely used in the clinical management of early sporadic TNBC. The use
779 of *gBRCA* mutations to select patients who could benefit from platinum-based chemotherapy and PARPi
780 demonstrates how a molecular alteration can aid patient selection for treatment. As yet there is no definitive
781 evidence to either support or refute the use of PARPi in the non-*gBRCA* TNBC population. An ongoing
782 neoadjuvant study (NCT03150576) that includes both sporadic TNBC and *BRCA*-associated tumours will
783 help to elucidate the value of *gBRCA* mutations in predicting response to the addition of PARPi to platinum-
784 based chemotherapy¹⁰². Furthermore, no biomarker predicted for benefit from Pembrolizumab in the
785 KEYNOTE-522 trial, despite the encouraging response rates shown. The expected role of PD-L1 as a
786 biomarker of response is not proven in the early setting^{138,143}. Substantial differences between the clonal
787 architecture and the microenvironment of primary and metastatic tumours^{210,211} suggest that the role of a given
788 biomarker should be evaluated separately in both early and advanced settings.

789 A single biomarker strategy is unlikely to be successful for such a heterogeneous disease considering the
790 large number of treatment strategies already tested and the increasing evidence of molecular complexity in
791 TNBC. **Figure 2** illustrates the variety of molecular components currently explored as potential biomarkers
792 of response and resistance. Several interactions across components also contribute to the challenge. As an
793 example, to adequately characterise the relationship between host immunity and tumour, a single
794 determination of the extent of immune activation is expected to be insufficient. Understanding how the
795 immune response modulates the intrinsic genomic architecture of the tumour, and the spatial and cellular
796

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797 distribution of immune cells in response to treatment appears to be crucial. Similarly, multiple pathway
798 signalling, a common finding in TNBC tumours, could result in the activation of compensatory feedback
799 loops that explain some mechanisms of tumour evasion and resistance when a single pathway inhibition is
800 applied²¹². An integrative approach including tumour architecture, microenvironment, and pathway
801 activation is more likely to succeed. A pragmatic example of how an immune-molecular profile directed
802 approach could be implemented is shown in **Figure 3**. Tumours could be classed as ‘hot’ (high immune
803 activation) or ‘cold’ (low immune activation) as well as ‘high-burden’ (high mutational/clonal burden) or
804 ‘low-burden’ (low mutational/clonal burden). Hot-high burden tumours are frequently highly proliferative
805 and more likely to exhibit high chromosomal instability. Increased response to cytotoxic and
806 immunotherapy agents is anticipated in this subgroup. The hot- low burden group represent a subgroup in
807 which clonal selection has been enforced by an active immune system. This good prognosis subgroup is
808 likely to require less intensive therapies with treatments focused on targeting key drivers. In sharp contrast,
809 cold tumours, require more comprehensive approaches that often include treatment escalation strategies. It
810 is possible that due to quiescent mechanisms of tumorigenesis cold tumours remain invisible to the immune
811 system. Therefore, sequential strategies that aim to enhance the immune system effect are essential in this
812 group. In cold-low burden tumours, targeted pathway inactivation followed by immune checkpoint
813 inhibition could potentially result in an augmented immune response achieving long-lasting control of the
814 disease. Cold-high burden tumours constitute a poor prognosis group with patent mechanisms of immune
815 evasion. Sequential strategies that include immunotherapy followed by either chemotherapy, pathway-
816 specific targeted agents, radiotherapy-targeted agent combinations are plausible options.

817
818 Response to NACT, measured as the amount of residual disease found at surgery, has recently been used as
819 a primary endpoint to test novel agents in the early setting. RCB is widely considered a prognostic factor
820 and is frequently used as a surrogate endpoint for long-term outcomes, particularly in this BC subgroup.
821 Although it is clear from a recent meta-analyses that RCB is a better endpoint than pCR, the identification
822 of the molecular characteristics that explain why some tumours do not follow the predicted outcomes
823 (recurrences after excellent responses or long-lasting EFS after residual disease) continues to present a
824 challenge. There is robust evidence that supports the association between RCB score and long-term outcome
825 in patients that have received NACT⁷⁹. Evidence for the predictive value of RCB in the context of targeted
826 therapy is lacking and requires further investigation^{67,168}. Multiple other methodologies to aid the
827 identification of patients with higher disease relapse risk are currently being explored. The post neoadjuvant
828 and adjuvant settings are an excellent opportunity to evaluate the contribution of dynamic biomarkers (e.g
829 RCB, TILs) to enable an accurate selection of patients that may benefit from escalating treatment strategies.
830 Pre- and post-treatment assessment of ctDNA and TME plus integration of traditional transcriptomic and
831 genomic signatures or classifications are some of the more promising approaches. Alternatively, innovative
832 adaptive trial designs that enable early response assessment and facilitate an early change in management
833 could minimise overtreatment and appropriately de-escalate or escalate therapy when appropriate.

834
835 Several molecular predictors of response that incorporate a variety of ‘omic’ data to aid clinical decisions
836 have been developed. Limited clinical impact has been derived due to a lack of reproducibility, lengthy
837 timeline of results, and expense. The real-time delivery of genomic and transcriptomic results will facilitate
838 the implementation of adaptive trial designs and permit the investigation of novel and existing
839 biomarkers. There are multiple pan-cancer studies assessing the implementation of genomics and
840 transcriptomics into clinical care, for example, the UK 100,000 Genomes Project²¹³, the Dutch national
841 Centre for Personalised Cancer Treatment (CPCT) study²¹⁴, and the Personalised Onco-Genomics (POG)
842 Program²¹⁵. The Personalised Breast Cancer Programme (PBCP)²¹⁶ is a tumour-specific precision medicine
843 project that implements whole-genome sequencing data into the real-time treatment of early and advanced
844 breast cancer patients. This programme ensures the delivery of high quality annotated genomic data to
845 patients and clinicians while promoting hypothesis testing and tumour-specific analysis. It is clear that these
846 large-scale sequencing studies will add considerably to our understanding and enable better optimisation of
847 trial design, response prediction, prognostication, and biomarker discovery. These efforts, combined with

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848 the promising potential of novel agents and treatment combinations, gives us the exciting prospect of a
849 tailored treatment pathway for each patient diagnosed with early-stage TNBC.

850
851 The ultimate aim is that every patient diagnosed with early-stage TNBC has a bespoke treatment pathway
852 developed that fits their TNBC. The individualised use of preclinical models such as patient-derived
853 organoids or xenografts²¹⁶, and the implementation of advanced radiodiagnostic techniques²¹⁷ are pivotal to
854 achieving this goal. This type of integrated approach requires open and clear communication and
855 collaboration between basic scientists, clinicians, and other scientific disciplines, for example,
856 bioinformatics, mathematics, and physics, which will maximise the chance of success and ultimately
857 enhance patient benefit.

858
859 In conclusion, advances in tumour characterisation, real-time biomarker/genomic testing, trial design and
860 drug development provide the foundation for an era of precision therapeutic strategies in early TNBC. In
861 the development of complex strategies to integrate multi-modal data to derive individualised care plans, it
862 is important to consider the holistic needs of each patient to achieve a truly personalised approach.

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900 Acronyms

AR	Androgen receptor
BC	Breast cancer
BL1	Basal-like 1
BL2	Basal-like 2
BLIA	Basal-like immune activated
BLIS	Basal-like immunosuppressed
ctDNA	Circulating tumour DNA
DDR	DNA damage response
DFS	Disease free survival
DSBs	Double strand breaks
EBCTCG	Early Breast Cancer Trailist's Collaborative Group
EFS	Event free survival
EMT	Epithelial-mesenchymal transition
ER	Oestrogen receptor
gBRCA	Germline <i>BRCA</i>
GE	Gene expression
HR	Homologous recombination
HRD	Homologous recombination deficiency
ICI	Immune checkpoint inhibitors
iDFS	Invasive disease free survival
IntClust	Integrative Cluster
iTILs	Intratumoural TILs
LAR	Luminal androgen receptor
M	Mesenchymal -Lehmann subtype
mAbs	Monoclonal antibodies
mTNBC	Metastatic triple negative breast cancer
NACT	Neoadjuvant chemotherapy
OR	Overall response
OS	Overall survival
PARP	Poly ADP-ribose polymerase
PARPi	Poly ADP-ribose polymerase inhibitors
pCR	Pathological complete response
PD-1	Programmed cell death 1
PD-L1	Programmed cell death ligand-1
PFS	Progression free survival
PR	Progesterone receptor
RCB	Residual Cancer Burden

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RFS	Relapse-free survival
ssDNA	Single strand DNA
sTILs	Stromal TILs
TILs	Tumour infiltrating lymphocytes
TMB	Tumour mutational burden
TNBC	Triple negative breast cancer

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Tables

Provided in a separate file.

In review

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1807 **Conflict of Interest**

1808 The authors declare that the research was conducted in the absence of any commercial or financial
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1810 **Author Contributions**

1811 KP, LD, RL and JA each contributed to the design, literature review, writing, and editing of the
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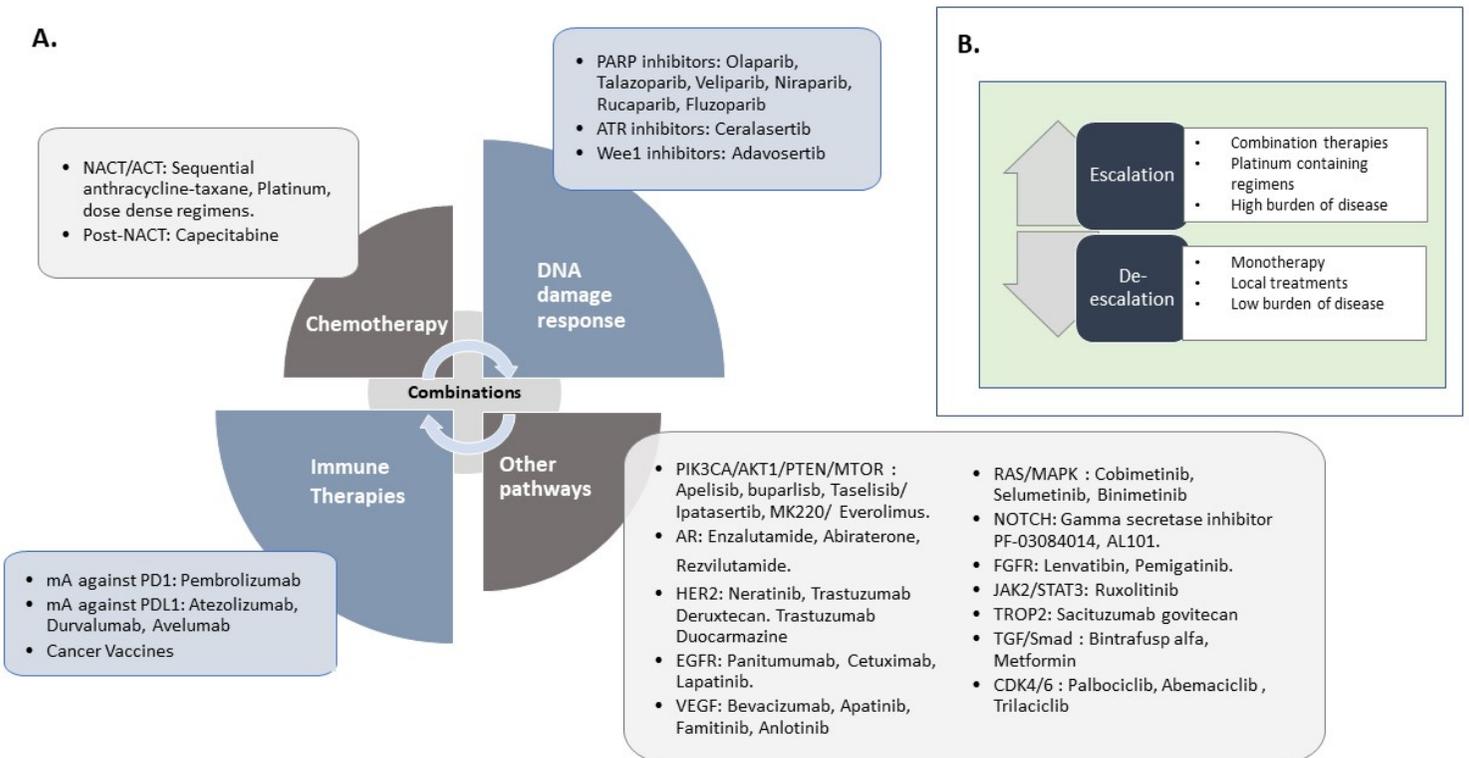
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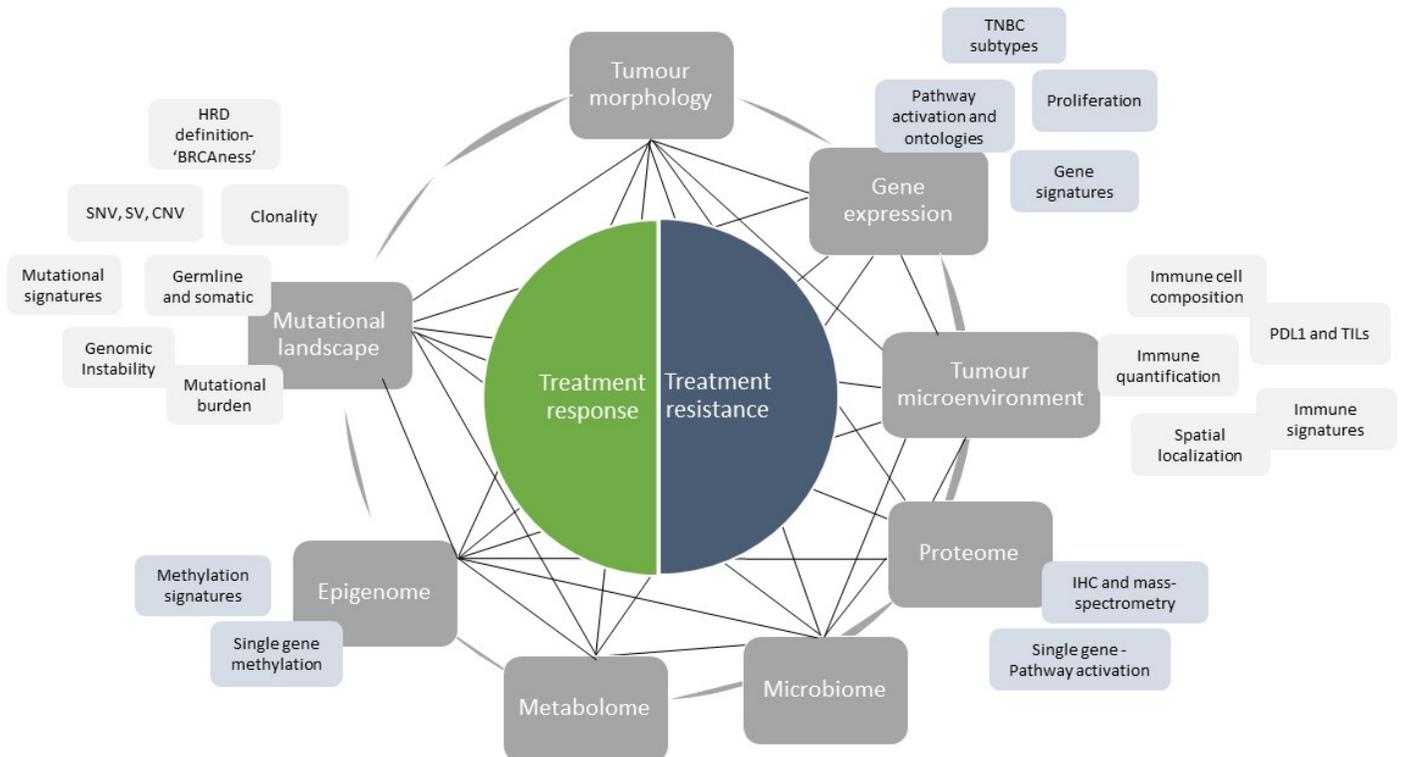
In review

Figure 1: Current therapeutic strategies in early TNBC. A. Treatment spectrum B. Treatment modalities for escalation and de-escalation.



In review

Figure 2: Biomarker landscape in TNBC.



In review

Figure 3: Proposed framework for the personalised treatment of early TNBC.

