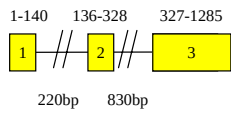
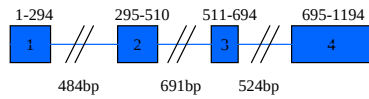


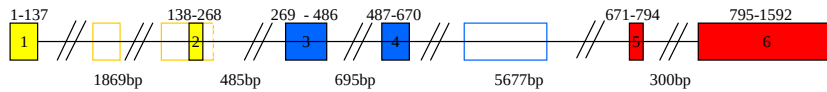
Additional Data File 3.



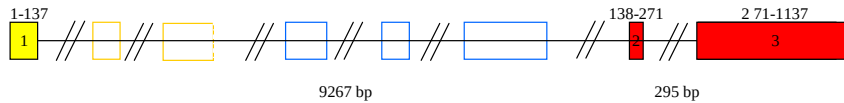
Ssty 1



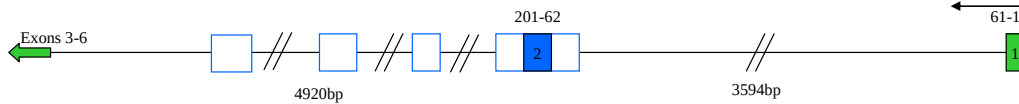
Asty



AK016790



AK015935



BU936708

Figure. Diagram of the intron/exon structure of *Ssty1* and *Asty* loci, together with the two structurally identical ‘recombinant’ loci that, based on sequence matching with BLAST, apparently encode the transcripts AK016790 and AK015935. Also shown is the locus encoding transcript BU936708 that includes part of *Asty* exon 4 transcribed in the antisense direction. The numbers above each locus refer to the base positions of the transcript sequence. The number of base pairs between each transcribed exon is given below each locus. The unfilled coloured outlines show the positions of the *Ssty1* and *Asty* exons in the original loci. In the ‘recombinant’ loci *Ssty1* exon 3 is incomplete. For details see the clustal alignment below.

Ssty1 exon positions **Asty** exon positions exons in clones Homology breakdown after *Asty*

ref NT_099035.1 MmY_98672_33_5	GTGTAGCTTTGGCTGTTAGGAAAATCACTCTGTAGAATAG-ACTAGCCTT	969
ref NT_078929.2 MmY_78994_33_4	GTGTAGCTTTGGCTGTTAGGAAAATCACTCTGTAGAATAG-ACTAGCCTT	971
ref NT_099035.1 MmY_98672_33_c	ACATACATATGGGCCTCAAATATAACACTCCATTTCGTGAGCGTTAGATCA	987
ref NT_099026.1 MmY_98663_33_c	GTGTAGCTTTGGCTGTTAGGAAAATCACTTTGTAGAATAG-ACTAGCCTT	925
	** * *** * * * * ***** * ** ***	
ref NT_099035.1 MmY_98672_33_5	TATCTCACTAAGGTTTGCCTCC-----CTCTGCCTC-TTGAGTACTAGG	1012
ref NT_078929.2 MmY_78994_33_4	TATCTCACTAAGGTTTGCCTCC-----CTCTGCCTC-TTGAGTACTAGG	1014
ref NT_099035.1 MmY_98672_33_c	TTTCTCTCCAAACATGGTCTCTAGGAAATTATACTTCACTTAATTCTGCC	1037
ref NT_099026.1 MmY_98663_33_c	TATCTCACTAAGGTTTGCCTCC-----CTCTGCCTC-TTGAGTACTAGG	968
	* ***** * ** * * *** * * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	ATTTAAGACTTGGGTCACTAACACCTCCTATTAACCTTCTGATTTGATTGT	1062
ref NT_078929.2 MmY_78994_33_4	ATTTAAGACTTGGGTCACTAACACCTCCTATTAACCTTCTGATTTGATTGT	1064
ref NT_099035.1 MmY_98672_33_c	CTGCATTAACAGAGCCTGAAACATAGGTCATCTATCCTTCCTACCATCCT	1087
ref NT_099026.1 MmY_98663_33_c	ATTAAAGATTTGGGTTACTACCATCTCCTATTAACCTTCTGATTTGATTGT	1018
	* * * * * * ** ** * * * ** *	
ref NT_099035.1 MmY_98672_33_5	TTGTTTTGTTTTTTGTTTGTTTT-TCATTTTTGTTTTTTTTTGTTTTGTTT	1111
ref NT_078929.2 MmY_78994_33_4	TTGTTTTGTTTTTTGTTTGTTTT-TCATTTTTTTTTTGTTTTGTTT--GTT	1111
ref NT_099035.1 MmY_98672_33_c	TCATGCAAACACCCATATAACTGATGATAAGCTTCAAGAGTGCTTAGAGA	1137
ref NT_099026.1 MmY_98663_33_c	TTGTTTTGTTTTGT-TCTGTTTG-----TTTTTCTTTTTTGATT--TT	1058
	* * * * * * ** **	
ref NT_099035.1 MmY_98672_33_5	TGTTTGTTTGTTTGTTTGTTTGTTTTTGTTGTTGTTTTTTGTTTAAGTTGTT	1161
ref NT_078929.2 MmY_78994_33_4	TGTTTGTTTGTTTGTTT-TTTGTTGTTGTTGTTTTTTGTTTAAGTTGTT	1160
ref NT_099035.1 MmY_98672_33_c	CTTACATTCATGC-CTGATGCATAATGCTTGATTGCTGCCAGGCTTACC	1186
ref NT_099026.1 MmY_98663_33_c	TGTTTGATGTTT--TGTTTGTTTTTGTTGGTTTTTTGTTTTAGTTGTT	1106
	* * * * * * * *** ** ** **	
ref NT_099035.1 MmY_98672_33_5	AATGTTGTTGCTGATTTGGAGACATGGTTCCTTTGTCTACCACTGGCTGC	1211
ref NT_078929.2 MmY_78994_33_4	AATGTTGTTGCTGATTTGGAGACATGGTTCCTTTGTCTACCACTGGCTGC	1210
ref NT_099035.1 MmY_98672_33_c	AAGGTGTATGTGAAGATGG-GACTCTTCTACGTTTTGAAGCAGTTCTACC	1235
ref NT_099026.1 MmY_98663_33_c	AATGTTGTAGCTGATTTGGAGACATTTTTCTTTGTCTATCACTGGCTGC	1156
	** ** * * *** *** * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	CCTGGAACCTCACTTTGTAGACCAGGCTGGTCTCTAAGTC---AGAAATC	1257
ref NT_078929.2 MmY_78994_33_4	CCTGGAACCTCACTTTGTAGACCAGGCTGGTCTCTAAGTC---AGAAATC	1256
ref NT_099035.1 MmY_98672_33_c	TCTCCTGCTTAAG--GTAGGCTAGGTCACTCCCTTAACCCTAAAGAGGTT	1283
ref NT_099026.1 MmY_98663_33_c	CCTGGAACCTCACTTTGTAGACCAGGCTGGTCTCTAAGTC---AGAAATC	1202
	** ** * ***** * *** ** * * * *** *	
ref NT_099035.1 MmY_98672_33_5	TGCCTTATCCTGCCTTCTGAATGCTGAGTTTAAATGCTTGTTGCCACCATA	1307
ref NT_078929.2 MmY_78994_33_4	TGCCTTATCCTGCCTTCTGAATGCTGAGTTTAAATGCTTGTTGCCACCATA	1306
ref NT_099035.1 MmY_98672_33_c	GGGGACATTAAGCAGACTCTAATTCTGCTTTAATCTTCTACTCCTAAACA	1333
ref NT_099026.1 MmY_98663_33_c	TGCCTGACCCTGCCTTCTGAAAGCTGGGATTAATGTGTGTGCCACTATA	1252
	* * ** ** * **** * ** * *	
ref NT_099035.1 MmY_98672_33_5	GCTGGATTATGAACTTCTTATTTGGATCAAATTAAGTTTAGAAGCCCCAAA	1357
ref NT_078929.2 MmY_78994_33_4	GCTGGATTATGAACTTCTTATTTGGATCAAATTAAGTTTAGAAGCCCCAAA	1356
ref NT_099035.1 MmY_98672_33_c	TCAATACT-TAGACCACTAATTTGTGTCCATTATATCAAATGCACCT	1382
ref NT_099026.1 MmY_98663_33_c	GCTGGATTATGAGCTTCTTATTTTGATTAAATTAAGTTTAGAAGCCCCAAA	1302
	* * * * * ** ***** * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	CATGTTTAGCATAGCCTTCTTGACCTACTCAAAAATTCCATTAGAGAAGA	1407
ref NT_078929.2 MmY_78994_33_4	CATGTTTAGCATAGCCTTCTTGACCTACTCAAAAATTCCATTAGAGAAGA	1406
ref NT_099035.1 MmY_98672_33_c	C-TGTATACATGAGGGTCCAATATCTGTCTTGTAAGCTTGATGGGCCTGA	1431
ref NT_099026.1 MmY_98663_33_c	CATGTTTAGCATAACCTTCTTGACCTGCTCAAAAATTCCATTAGAGAAGA	1352
	* *** ** * * * * ** ** * * **	

ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

AAGATTTCTCAGGTAAGGGATGCCACCTCGCCAGAGCCCTGGTTGGCA
AAGATTTCTCAGGTAAGGGATGCCACCTCGCCAGAGCCCTGGTTGGCA
CCAAGTGTCTAAGATTAC - - TTCCAAACTTCTTCTGTTACAAATATTCTG
AGTATTTCTCAGGTGAGGGATGCCACCTCGCCAGAGCCCTGGTTGGCA

1941
1948
1952
1891

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

GAGCGGTACAACACAAATTTAAGGGTAAAGATGGCTCTGAGGACAAGTGG
GAGCGGTACAACACAAATTTAAGGGTAAAGATGGCTCTGAGGACAAGTGG
GAGACATTCCTC - CATTCAAGAAAATTGGCCTTGCTCTTATGTCATCTGA
GAGCGGTACAACACAAATTTGAGAGGAAAGATGGCTCTGAGGTCAAGTGG

1991
1998
2001
1941

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

AGGAGGGTTATGCTAGCCCAGGTGCCAATCATGAAGGATTTGTTTTACAG
AGGAGGGTTGTGCTAGCCCAGGTGCCAATCATGAAGGATTTGTTTTACAG
CTAAAGGTT - TCATAGACCAAA - GATAACCATCCA - - ACCTGT - - TGGAA
AGGGGGGTGGTGTGCTAGCCCAGGTGCCAATCATGAAGGATTTGTTTTACAT

2041
2048
2045
1991

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

TAC - TACAAGAAGAATCCAGCTCTCTACTTCTATCAGCTCCTGGATGACT
TACCTACAAGAAGGATCCAGCTCTCTACTTCTATCAGCTCCTGGATGACT
TAC - - - TGAACAATTGCTGCCTGCT - - TTCCACATACCACATAAAATAT
TACCTACAAGAAGGATCCAGCTCTCTATGCTTATCAGCTCCTGGATGACT

2090
2098
2090
2041

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

ACAAGAAAGGGAACCTCCACATCATTCCAGACACTCCTCTG - GCTGAGGA
ACAAGAAAGGGAACCTCCACATCATTCCAGAAACTCCTCTG - GCTGAGGA
GTGGATATCCTAAATTCTGCAAAAAAAAAAAAAAGATTTGTAAGCTGATCA
ACAAGGAAGGTAACCTCCACATGATTCCAGACACTCCTCCG - GCTGAGGA

2139
2147
2140
2090

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

AAGATCAGGAGATGACAGTGATGTGTTGATAGGTAAGTGGGTGCAGTACA
GAGATCAGGAGATGACAGTGATGTGTTGATAGGTAAGTGGGTGCAGTACA
AGCAATACTGTGACTCCCTCTTCTCCAGA - AGGTATTTGCATTTTCACCA
GAGATCAGGAGATGACAGTGATGTGTTGATTGGTAAGTGGGTGGAGTACA

2189
2197
2189
2140

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

CCA - GAAAAGGTGGTTCCAAATAGTTTCAGAAAGGTTGTTTACCAAATTCT
CCA - GAAAAGGTGGTTCCAAATAGTTTCAGAAAGGTTGTTTACCAAATTCT
ATGTGAAATGGTATTTCTTATTTATTGAAAATAGCCAGAGATTTTACACT
CCA - GAAAAGATGGTTCCAAAAAGTTTCGGAAGGTTGTTTACCAAGTTCT

2238
2246
2239
2189

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

AGCCAATCCTTC - ACATTCAATTTACATTTGCAAAGTGTCACAGAAATG
AGCCAATCCTTC - ACATTCAATTTACATTTGCAAAGTGTCACAGAAATG
TTTTACAAGTAG - GTTTAGAATTGCACATTTGCAAAGTGTCACAGAAATG
AGCCAATCCTTCGGTGTACTTTATCAAGTTT - CATGGTGACATCCATATC

2287
2295
2288
2238

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ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

C - TGCTTATGACCAGAGTGCTTAAACTTCCTTATTCT - - - - - CATGAA
C - TGCTTATGACCAGAGTGCTTAAACTTCCTTATTCT - - - - - CATGAA
C - TGCTTATGACCAGAATGCTTAAACTTCCTTATTCT - - - - - CATGAA
TATGTCTAT - ACTATGGTGCCAAAGATTCTTGAAGTTGAAAAATCATAAA

2329
2337
2330
2287

* * * * * * * * * * * * * * *

ref|NT_099035.1|MmY_98672_33_5
ref|NT_078929.2|MmY_78994_33_4
ref|NT_099035.1|MmY_98672_33_c
ref|NT_099026.1|MmY_98663_33_c

GTTT - GTCACATTACCTC - - - - - CTTGATGAAGGGCACAACCATCCTAC
GTTT - GTCACATTACCTC - - - - - CTTGATGAAGGGCACAACCATCCTAC
GTTT - GCCACATTACCTC - - - - - TTT - ATGAAGGGCACAACCATCCTAC
GTACAGAAACGTAAACATATAGGACTGGAAGAAAAAAAAAGTTTTTTTTT

2372
2380
2372
2337

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ref NT_099035.1 MmY_98672_33_5	TTCTGTG-----CAAAATTGCCCAAGCTCCTCCCC-TATCTTACTT--	2412
ref NT_078929.2 MmY_78994_33_4	TTCTGTG-----CAAAATTGCCCAAGCTCCTCCCC-TATCTTACTT--	2420
ref NT_099035.1 MmY_98672_33_c	TTCTGTG-----CAAACTGCCCAAGCTCCTCCCC-TATCTTACTT--	2412
ref NT_099026.1 MmY_98663_33_c	TCCTGTGTTGGCTACATAAGGGTCTTTGATAATCCAGTATCTTTGCCAA * ***** ** ** * * * * * *****	2387
ref NT_099035.1 MmY_98672_33_5	TAGGAAGATTTAGACATTACAAACAGAGA--GTACTCCAACCTGTGTTG	2459
ref NT_078929.2 MmY_78994_33_4	TAGGAAGATTTAGACATTACAAACAGAGA--GTACTCCAACCTGTGTTG	2467
ref NT_099035.1 MmY_98672_33_c	TAGGAAGATTTATACATTACAAACAGAGA--GTGCTCCAACCTGTGTGG	2459
ref NT_099026.1 MmY_98663_33_c	TAAATGTGTTTTGTTCT AAAAATGTAAATGTGTGACATGACATGCTGTG ** * * * * * * * * * * * * *	2437
ref NT_099035.1 MmY_98672_33_5	AGC--ACAGTGTGTTTGAGGAAATCCCCCAGATTC--ACCATCTTCCCA-	2504
ref NT_078929.2 MmY_78994_33_4	AGC--ACAGTGTGTTTGAGGAAATCCCCCAGATTC--ACCATCTTCCCA-	2512
ref NT_099035.1 MmY_98672_33_c	AGC--ACAGTGTGTTTGAGGAAATCCCCCAGATTC--TCCATCTTCCCA-	2504
ref NT_099026.1 MmY_98663_33_c	AGTGAACAATTTGCTGGACGAGATGGCCTACAGTGGAAGAAGTCAAAAT * * * * * * * * * * * * * * *	2487
ref NT_099035.1 MmY_98672_33_5	---GTGTATGTCCTACCTATAAATTCTAATT-TCCATGGTCTGGGAAGC	2549
ref NT_078929.2 MmY_78994_33_4	---GTGTATGTCCTACCTATAAATTCTAATT-TCCATGGTCTGGGAAGC	2557
ref NT_099035.1 MmY_98672_33_c	---GTGTATGTCCTACTTATAAATTCTAATT-TCCGTGGTCTGGAAAGC	2549
ref NT_099026.1 MmY_98663_33_c	GAAGATGAAAGTTTCATTTTCAGGCGGTGAACAGTACATACACCTAAAATC * * * * * * * * * * * * * * *	2537
ref NT_099035.1 MmY_98672_33_5	AC-TGTTCTGATCTAAGAGATTTCTGAACACTCTGGACTGAAATCCCAAA	2598
ref NT_078929.2 MmY_78994_33_4	AC-TGTTCTGACCTAAGAGATTTCTGAACACTCTGGACTGAAATCCCAAA	2606
ref NT_099035.1 MmY_98672_33_c	AC-TGTTCTGGCCTAAGAGATTTCTGAACACTCTGGACTGAAATCCCAAA	2598
ref NT_099026.1 MmY_98663_33_c	ATACATGCTAAAATGAACAGCTTCTCTGGTCTGCATTCCGAATAAGGAAT * * * * * * * * * * * * * *	2587
ref NT_099035.1 MmY_98672_33_5	CAGAA--GAGTATCAAGGTAAGGGTAAATCAGATTACTATCTTTGTTTT	2645
ref NT_078929.2 MmY_78994_33_4	CAGAA--GAGTATCAAGGTAAGGGTAAATCAGATTACTATCTTTGTTTT	2653
ref NT_099035.1 MmY_98672_33_c	CAGAA--GAGTATCAAGGTAAGGGTAAATCAGTTTACTATCTTTGTTTT	2645
ref NT_099026.1 MmY_98663_33_c	TGGAGATGGAACTTTGAGGAGCAGGGATGGCAGAAAAAGATGGATGTTTA * * * * * * * * * * * * * *	2637
ref NT_099035.1 MmY_98672_33_5	GT--TACCTTAG ACAGAGACATCATGGCC ---TCCATGCAGAGGAATG	2688
ref NT_078929.2 MmY_78994_33_4	GT--TACCTTAGAGAGAGACATCATGGCC---TCCATGCAGAGGAATG	2696
ref NT_099035.1 MmY_98672_33_c	AT--TACCTTAAACAGAGACATCCTGGCC---TCCATGCAGATGAATG	2688
ref NT_099026.1 MmY_98663_33_c	GTAAGTAGGGGAGAAGGACAGGACATAGGTAGAACCCTCTGATGTGAAGAC * * * * * * * * * * * * * *	2687
ref NT_099035.1 MmY_98672_33_5	TGTGGATGGACATATATTTAAGGAAGACACTAAACCAGAAAAATACCACAT	2738
ref NT_078929.2 MmY_78994_33_4	TGTGGATGGACATATATTTAAGGAAGACACTAAACCAGAAAAATACCACAT	2746
ref NT_099035.1 MmY_98672_33_c	TGTGGATGGACATATATTTAAGGAAGACACTAAACCAGAAAAATACTACAT	2738
ref NT_099026.1 MmY_98663_33_c	TGAAGGAGAAACAAAATTTGGGGAAAGTGGGACATTTAAATTAATGTG- * * * * * * * * * * * * * *	2736
ref NT_099035.1 MmY_98672_33_5	TACACCCTCTTAAAGACTTCTAAGATTGTTGTCATGCCTACCACAGACA	2788
ref NT_078929.2 MmY_78994_33_4	TACACCCTCTTAAAGACTTCTAAGATTGTTGTCATGCCTACCACAGACA	2796
ref NT_099035.1 MmY_98672_33_c	TGCACCCTCTTAAAAAATTCTAAGATTGTTGTCATGACTACCACTGAAA	2788
ref NT_099026.1 MmY_98663_33_c	---GCCTTGTTCACAAAGGTGAAACCTAGAAAAC-TGATTGAAATAGAC- * * * * * * * * * * * * * *	2781
ref NT_099035.1 MmY_98672_33_5	TTCAGATGATGTGATTCTTGATTGTGATTTTCATGTTTGGAGCTGATGAA	2838
ref NT_078929.2 MmY_78994_33_4	TTCAGATGATGTGATTCTTGATTGTGATTTTCATGTTTGGAGCTGATGAA	2846
ref NT_099035.1 MmY_98672_33_c	TTCAGATGATGTGATTCTTGATTGTGATTTTCATGTTTGGAGCTGATGAA	2838
ref NT_099026.1 MmY_98663_33_c	-TCAGAAATCAGAGAAATCAGGTTTTCTTTGAATAATGACACTTAAAGAA ***** * * * * * * * * * *	2830

ref NT_099035.1 MmY_98672_33_5	GGAGAAAGTACCTGGAATGTCCTAGAATTCTCAAG-GTATCAATCAGTGT	2887
ref NT_078929.2 MmY_78994_33_4	GGAGAAAGTACCTGGAATGTCCTAGAATTCTCAAG-GTATCAATCAGTGT	2895
ref NT_099035.1 MmY_98672_33_c	GGAGTAAGTACCTGGAATGTCCTATAATTCTCAAG-GTATCAATCAGTGT	2887
ref NT_099026.1 MmY_98663_33_c	ACCTGTCTTACATTTTAAGATTTATTATCTTTACTTATGTGGGTGGGGAT	2880
	*** * * * * *	
ref NT_099035.1 MmY_98672_33_5	TCAATTTCTGCTCAATAGTGCTG-CAGACATAGGAATA-ACAGGATAAAA	2935
ref NT_078929.2 MmY_78994_33_4	TCAATTTCTGCTCAATAGTGCTG-CAGACATAGGAATA-ACAGGATAAAA	2943
ref NT_099035.1 MmY_98672_33_c	TCAATTTCTGATCAATAGTGCTG-CAGACATAGGAATA-ACAGGATAAAA	2935
ref NT_099026.1 MmY_98663_33_c	ATGGTATGTGCTTTTGAGTACAGGTGAACACAGAGACATGCATTGTCAGG	2930
	* * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	CTATTCTATACAATCCTATGAAGCTCCTATC-ACCATC--CTCCTATTTT	2982
ref NT_078929.2 MmY_78994_33_4	CTATTCTATACAATCCTATGAAGCTCCTATC-ACCATC--CTCCTATTTT	2990
ref NT_099035.1 MmY_98672_33_c	CTATTCTATACAATCCTATGAAGCTCCTATC-ACCATC--ATCCTATTTT	2982
ref NT_099026.1 MmY_98663_33_c	TCCCCTGGAGCTGACATTAAAGGTGATTATTTGCCATTGGATATGAATTC	2980
	* * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	AGAGAATCTTAGATCTATCACTAATCCTGAGACAGGCAGAAACAATTCTT	3032
ref NT_078929.2 MmY_78994_33_4	AGAGAATCTTAGATCTATCACTAATCCTGAGACAGGCAGAAACAATTCTT	3040
ref NT_099035.1 MmY_98672_33_c	AGAGAATCTTAGCTCTATCACAAATCCCGAGACCAGCAGAAACAATTCTT	3032
ref NT_099026.1 MmY_98663_33_c	AAGAAACC--AAATCCATTTT--TCTTGTGGT--GCAAAAGTGCTTGTT	3023
	* * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	CTCCTGCACATAGGAGT--ACTGCATATGTCTCCCCTTACCCAAAGTAT	3079
ref NT_078929.2 MmY_78994_33_4	CTCCTGCACATAGGGGT--ACTGCATATGTCTCCCCTTACCGAAAGTAT	3087
ref NT_099035.1 MmY_98672_33_c	CTCCTGCACATAGGGGT--ACTTCATATGTCTCCCCTTACCCAAAGTAT	3079
ref NT_099026.1 MmY_98663_33_c	ACCATTGATTCATCTCTCTAATCCCATAAAGATATCTTTTTTAAGAAATC	3073
	* * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	TCAACTTACTGT-CTTTTACTGAATTGGCTTTTACTACTATAC--CTGAAA	3126
ref NT_078929.2 MmY_78994_33_4	TCAACTTACTGT-CTTTTACTGAATTGGCTTTTACTACTATAC--CTGAAA	3134
ref NT_099035.1 MmY_98672_33_c	TCCACTTACTGTTCTTTTACTGAATTGGCTTTTACTACTATAC--CTGAAA	3127
ref NT_099026.1 MmY_98663_33_c	CAAAATTCACATGCATAAAACAGACCAGATTGAAGATAAGAAAGTTCTAA	3123
	* * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	TATTCCACTTTTACCAAAGGATCTACCAGCCCTCCCTGTTCTAATAGAG	3176
ref NT_078929.2 MmY_78994_33_4	TATTCCACTTTTACCAAAGGATCTACCAGCCCTCCCTGTTCTAATAGAG	3184
ref NT_099035.1 MmY_98672_33_c	TATTCCACTTTTACCAAAGGATCTTCCAGCCCTCCCTGTTCTAATAGAG	3177
ref NT_099026.1 MmY_98663_33_c	T-TGATGGTGACCATTAAAAGCAATAAGGGACACACAAAGAGTAGAGGAC	3172
	* * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	AGCTACAGTCCACCACTATCCAA--AGGGTTCTCAGACATT---CTAA	3219
ref NT_078929.2 MmY_78994_33_4	AGCTACAGTCCACCAATATCCAA--AGGGTTCTCAGACATT---CTAA	3227
ref NT_099035.1 MmY_98672_33_c	AGCTACCGTCCACCAATATCCAA--AGGGTTCTCAGACATT---CTAA	3220
ref NT_099026.1 MmY_98663_33_c	ACTGAGAGACAAATGAATTCTAAGTTAGAGTTCTCAAAAAGTTAAGCTGG	3222
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ref NT_099035.1 MmY_98672_33_5	ATATGCCCTGTGGGAGTAAACTTACTAAGTCTATTTAA-TTGGGCC---	3265
ref NT_078929.2 MmY_78994_33_4	ATATGCCCTGTGGGAGTAAACTTACTAAGTCTATTTAA-TTGGGCC---	3273
ref NT_099035.1 MmY_98672_33_c	ATATGCCCTGTGGGAGTAAACTTACTAAGTCTATTTAA-TTGGGCC---	3266
ref NT_099026.1 MmY_98663_33_c	AGACACAGGAAGAAGAGAAATTTAAGGAAATAGTCAAACCTGGGCCATA	3272
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ref NT_099035.1 MmY_98672_33_5	-TCAGATC--CTTCTGCTTTGACCAAAAGGATTTCAATCTGCTGACTCTG	3312
ref NT_078929.2 MmY_78994_33_4	-TCAGATC--CTTCTGCTTTGACCAAAAGGATTTCAATCTACTGACTCTG	3320
ref NT_099035.1 MmY_98672_33_c	-TCAGATC--CTTCTGCTTTGACCAAAAGGATTTCAATCTACTGACTCTG	3313
ref NT_099026.1 MmY_98663_33_c	TCCACATTGGCTTCTTTGTTTTCTTAACAAATAGCCAGCCTGTCATTACA	3322
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ref NT_099035.1 MmY_98672_33_5	CTACCCAAC-CAAACATACTAGTTTACCTG-TACAA-AGGGGATTTAGAT	3851
ref NT_078929.2 MmY_78994_33_4	CTACCCAAC-CAAACATACTAGTTTACCTG-TACAA-AGGGGATTTAGAT	3858
ref NT_099035.1 MmY_98672_33_c	CTACCCAAC-CAAACATACTAGTTTACCTG-TACAA-AGGGGTTTTAGAT	3851
ref NT_099026.1 MmY_98663_33_c	GTAACCAATGCATATATGCTGACCTCTTTTCTACGCCAGTTGACATGGGT	3855
	** **** ** * * * * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	TTCCAATTTCTCACAAAGATACCC-----CTCTTACCATTGA	3888
ref NT_078929.2 MmY_78994_33_4	TTCCAATTTCTCACAAAGATACCC-----CTCTTACCATTGA	3895
ref NT_099035.1 MmY_98672_33_c	TTCCAATTTCTCACAAAGATGCCCTCGTGTATTTCCCCTCTGACCATTGG	3901
ref NT_099026.1 MmY_98663_33_c	TTCAAA- -TGTTATGAGTTTCCCCACTGT- -GTGGGTCACTTTTTGAGGA	3901
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ref NT_099035.1 MmY_98672_33_5	GTTCTATCTATTTTTTCATGGCTCATAGGGTCTCATTTCTTCCAATGTC	3938
ref NT_078929.2 MmY_78994_33_4	GTTCTATCTATTTTTTCATGGCTCATAGGGTCTCATTTCTTCCAATGTC	3945
ref NT_099035.1 MmY_98672_33_c	GGTCTATCTATTTTTTCATGGCTCATAGGGTCTCATTTCTTCCAATGTC	3951
ref NT_099026.1 MmY_98663_33_c	GCCCGTGTACTTCATGGAGGTCTGCCTGGGTTCATCTATACTCTCAGAG	3951
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ref NT_099035.1 MmY_98672_33_5	CATTACTGGCTCACTTCTGACCACTAGCCATACATCTCTGATTAGTGTTG	3988
ref NT_078929.2 MmY_78994_33_4	CATTACTGGCTCACTTCTGACCACTAGCCATACATCTCTGATTAGTGTTG	3995
ref NT_099035.1 MmY_98672_33_c	CATTACCACTCACCTCTGACCACTAGCCATACATCTCTGATTAGTGTTG	4001
ref NT_099026.1 MmY_98663_33_c	-GTTTGGAGGCA	4000
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ref NT_099035.1 MmY_98672_33_5	GGGGTGTTCTCGGTATGA-CACTAAGGCCAACAAATAGT-GCCTACATGCC	4036
ref NT_078929.2 MmY_78994_33_4	GGGGTGTTCTCGGTATGA-CACTAAGGCCAACAAATAGT-GCCTACATGCC	4043
ref NT_099035.1 MmY_98672_33_c	GGGATGTTCTCGGTATGA-CAATAAGGCCAACAGTAGT-GCCTACATGCC	4049
ref NT_099026.1 MmY_98663_33_c	GGAATGCCATGGACTCAGTCATTACAATTTTCTCTCTAGAATAAGTTTG	4050
	** ** * * * * * * * * * *	
ref NT_099035.1 MmY_98672_33_5	ATTTCTGAATAATTGGATCTTAAATTCCACCATTGTCCAAGTGTA	4085
ref NT_078929.2 MmY_78994_33_4	ATTTCTGAATAATTGGATCTTAAATTCCACCATTGTCCAAGTGTA	4092
ref NT_099035.1 MmY_98672_33_c	ATTTTTGAAAAATTGGATCTTAAATTCCACCTCTGTCCAAGGGTACT-TC	4098
ref NT_099026.1 MmY_98663_33_c	TATGCTTCAGCATTTGATAATAATCTCTATTGTTGATTAATTTAATATC	4100
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ref NT_099035.1 MmY_98672_33_5	TGAAAGACTTTTCTCATTACATGGGGTCTCTACAGTAGCATCTTTGTTCA	4135
ref NT_078929.2 MmY_78994_33_4	TGAAAGACTTTTCTCATTACATGGGGTCTCTACAGTAGCATCTTTGTTCA	4142
ref NT_099035.1 MmY_98672_33_c	AGAAAGACCTTTTCTCATTACATGGGTTCTCTATAGTAGCTTCTTTATTCA	4148
ref NT_099026.1 MmY_98663_33_c	TGGGAGAGTTTCTGCAGTA-ACTGATTCTCTTAGGGATTAGTTGCTGTGA	4149
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ref NT_099035.1 MmY_98672_33_5	TCAGGCCTCTAGTTGTACCTTCTGGCCTAAGCAGATCTTATACTTCACTT	4185
ref NT_078929.2 MmY_78994_33_4	TCAGGCCTCTAGTTGTACCTTCTGGCCTAAGCAGGTTTTATACTTCAATT	4192
ref NT_099035.1 MmY_98672_33_c	ACAGGCCTCTGGTTGTACCTTCTGGCC-AAGCAGGTCTTACACTTCACTT	4197
ref NT_099026.1 MmY_98663_33_c	AAAGACACCATGTCAAAGGCCA- - -CTCATAAGAGCCAACATTTCA-TT	4194
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ref NT_099035.1 MmY_98672_33_5	AAAGAGATGCCAAATTTACACAATGTAGACAAAGATGCATTGAGCATTC-	4234
ref NT_078929.2 MmY_78994_33_4	AAAGAGATGCCAAATTTACACAATGTAGACAAAGATGCATTGAGCATTC-	4241
ref NT_099035.1 MmY_98672_33_c	AAAGAGATGCCACATTTACACAATGTAGACAAAAAGGATTTGAGCATTC-	4246
ref NT_099026.1 MmY_98663_33_c	AGTGCTTTTCTACATTT-CATTACACGTTCAGAGATTTACTCCACGATCA	4243
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ref NT_099035.1 MmY_98672_33_5	TCATACTCATTAATATAACATTCCTCCCCTCAGGTTTGAAGTCTCCAGAG	4284
ref NT_078929.2 MmY_78994_33_4	TCATACTCATTAATATAACATTCCTCCCCTCAGGTTTGAAGTCTCCAGAG	4291
ref NT_099035.1 MmY_98672_33_c	TCATACTCATCAATATAACATTCCTCCCCTCAGGTTTGAAGTCTCCAGAG	4296
ref NT_099026.1 MmY_98663_33_c	TCAAGGCAGAAAATATGGCACT-----GTCT-AGGCAGACATGG	4281
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ref NT_099035.1 MmY_98672_33_5	CTGT - -GTTATTTTTCCACCAGATGACAGTTTCATTTGAGGTCATTTGAAA	4816
ref NT_078929.2 MmY_78994_33_4	CTGT - -GTTATTTTTCCACCAGATGACAGTTTCATTTGAGGTCATTTGAAA	4823
ref NT_099035.1 MmY_98672_33_c	CTGT - -GTTATTTTTCCACCAGTTGACAGTTTCATTTGAGGTAATTTGGAA	4828
ref NT_099026.1 MmY_98663_33_c	TTAACAACAATGTGGAAGTATAAGCTGAATACAACCTTTGCTATGGAATT	4820
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ref NT_099035.1 MmY_98672_33_5	CA -TCGTTCTTACTATGTGTCTTTAAAA -GATATATTTTGGAGCTGAGG	4864
ref NT_078929.2 MmY_78994_33_4	GA -TCATTCCTTACTATGTGTCTTTAAAA -GATATATTTTGGAGCTGAGG	4871
ref NT_099035.1 MmY_98672_33_c	GT -TCGTTCTTACTATGTGTCTTTAAAA -GATATATTTTGGAGCTGAGG	4876
ref NT_099026.1 MmY_98663_33_c	TGCTCTTTGGACATGGTGGATCCTTACAACAATAAACATAGTAAGACATT	4870
	** ** * ** ** *** ** *** * * * *	
ref NT_099035.1 MmY_98672_33_5	GGTATGGCTGAATATCTT -CAGCACAATAAACACCTTCTATAACATTACT	4913
ref NT_078929.2 MmY_78994_33_4	GGTATGGCTGAATATCTT -CAGCACAATAAACACCTTCTATAACATTACT	4920
ref NT_099035.1 MmY_98672_33_c	GGTATGGCTGAATATCTT -CAGCACAATAAATACCTTCTGTAACGTTACT	4925
ref NT_099026.1 MmY_98663_33_c	CATA -GGAAAAATGTCTAACAGTGCCAATGCCACTAATCTTAAACCAC -	4918
	** ** *** *** *** * * ** *** **	
ref NT_099035.1 MmY_98672_33_5	ATCTAGTGGATTATAAGTATCAGGTTGT -ACACAGTAGTAAC -TAAAATA	4961
ref NT_078929.2 MmY_78994_33_4	ATCTAGTGGATTATAAGTATCAGGTTGT -ACACAGTAGTAAC -TAAAATA	4968
ref NT_099035.1 MmY_98672_33_c	ATCTAGTGTATTATAAGTATCAGGTTGT -ACACAGTAGTAAG -TAAAATA	4973
ref NT_099026.1 MmY_98663_33_c	AAATAATAATGTGTAGACATTTTATTTTATTTTAAAGGTAAGATATACTC	4968
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ref NT_099035.1 MmY_98672_33_5	ATGGACAA -TTTGAGA - -AAGATTTTAGGGTGAAATCTCTCATAATATA	5007
ref NT_078929.2 MmY_78994_33_4	ATGGACAA -TTTGAGA - -AAGATTTTAGGGTGAAATCTCTCATAATATA	5014
ref NT_099035.1 MmY_98672_33_c	ATGGACAAGTTTGAGA - -AAGATTTTAGGGTGTAATCTCTCATAATATA	5020
ref NT_099026.1 MmY_98663_33_c	GTGTACCTACCTGAGATGTAATTGTTCTAGTTTGCTTCTTTCTCACTATG	5018
	** ** ***** ** ** * * *** ** * ***	
ref NT_099035.1 MmY_98672_33_5	CAGAAAA - - -AAAAGGAAAT - -CCTAGATATTAA - - -TCAAATCTAT	5046
ref NT_078929.2 MmY_78994_33_4	CAGAAAA - - -AAA -GGAAAT - -CCTAGATATTAA - - -TCAAATCTAT	5052
ref NT_099035.1 MmY_98672_33_c	CACAAAA - - -AGA - - -AAAT - -CCTAGATATTAA - - -TCAAATCTAT	5056
ref NT_099026.1 MmY_98663_33_c	TAGAATACTACAATCAAAAATAAATTGGAAATAGAAGTGTTATAGTCTAT	5068
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ref NT_099035.1 MmY_98672_33_5	-GCACACCAAATGAACATTGTGGGTTTTGTGGGTT -TGTTTGTATATGTC	5094
ref NT_078929.2 MmY_78994_33_4	-GCACACCAAATGAACATTGTGGGTTTTGTGGGTT -TGTTTGTATATGTC	5100
ref NT_099035.1 MmY_98672_33_c	-GCACACCAAATGAACATTATGAGTTTTGTGGATT -TGTTTTTATATGTC	5104
ref NT_099026.1 MmY_98663_33_c	CACCGAGGAAGACAAAACAGGAAGTTGTATCAGTAACAGCAAAAAACAGC	5118
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ref NT_099035.1 MmY_98672_33_5	TTTGTAGTTCGAATGTCCAACCTTTATGTCTTAATTGATGATTGTAAACA	5144
ref NT_078929.2 MmY_78994_33_4	TTTGTAGTTCGAATGTCCAACCTTTATGTCTTAATTGATGATTGTAAACA	5150
ref NT_099035.1 MmY_98672_33_c	TTTGTAGTTCGAATGTCCAACCTTTATGTCTTAATTGAGGATTGTAAACA	5154
ref NT_099026.1 MmY_98663_33_c	TTATTGGCTTGC - - -CACTGTCTTAGTCACTCTTTTATTGAT -GTGAAGA	5164
	** * * * * * *** * ** ** *** * * *	
ref NT_099035.1 MmY_98672_33_5	GTGCTCAGAGTGTGTGCATGTGAATTAAGGGCACCATGTCTTTAGTGTT	5194
ref NT_078929.2 MmY_78994_33_4	GTGCTCAGAGTGTGTGCATGTGAATTAAGGGCACCATGTCTTTAGTGTT	5200
ref NT_099035.1 MmY_98672_33_c	ATGCTCAGGGTGTATGTGTGTGAGTTAAAGGGCACCATGTCTTTAGTGTT	5204
ref NT_099026.1 MmY_98663_33_c	GATACCATTGGATAAGGCAACTATTAGAAAACAAAACATTTAACTAGAGGC	5214
	** * * * *** * *** * *** *	
ref NT_099035.1 MmY_98672_33_5	TAGATTAA - -TTTCACATATCTGTCTATCTGTC -ATCTATG - - - -TATG	5236
ref NT_078929.2 MmY_78994_33_4	TACATTAA - -TTTCACATAT - -AATTATCTGTCTATCTGT - - - -CATC	5240
ref NT_099035.1 MmY_98672_33_c	TAGATTAA - -TATCACATATC - -ATTATCTGTCTATCCATCA - -TCTATA	5248
ref NT_099026.1 MmY_98663_33_c	TTGCTTACATTTTCAGAAGTTTGGTCATTCACCAAGGGAGGGATCCCATC	5264
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ref NT_099035.1 MmY_98672_33_5	TATGTATGTATGTATGTATGTATGTA-TGAAGTAATGATTGAA---TGT	5281
ref NT_078929.2 MmY_78994_33_4	TATGTATGTATGTATGTATGTATGTA-TGAAGTAATGATTGAA---TGT	5285
ref NT_099035.1 MmY_98672_33_c	TATGTATGTATGTATGTTTGTATGTA-TGAAGTAATGATTGAA---TGT	5293
ref NT_099026.1 MmY_98663_33_c	ACTGGAGCAATAGAGAACTATTGATCCTTAAGCAAAGAGAGAGATTCTGC	5314
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ref NT_099035.1 MmY_98672_33_5	ATTTATATAGATATGTATGCAACT--ATTTCTCTATCATCTACCTATC--	5327
ref NT_078929.2 MmY_78994_33_4	ATTTATATAGATATGTATGCAACT--ATTTCTCTATCATCTACCTATC--	5331
ref NT_099035.1 MmY_98672_33_c	ATTTATATAGATATGTATGCAACT--ATTTCTCTATCATCTACCAATCAC	5341
ref NT_099026.1 MmY_98663_33_c	CATTGCTTTGGCTTCTTGAAAACCAAACCCATCCTTGTTGACACATC-C	5363
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ref NT_099035.1 MmY_98672_33_5	TCTCTCTCTTTCTATTTCTCTCACCCTCTTTCTCTGTTTATCTCTTATGC	5377
ref NT_078929.2 MmY_78994_33_4	TCTCTCTCTTTCTATTTCTCTCACCCTCTTTCTCTGTTTATCTCTTATGC	5381
ref NT_099035.1 MmY_98672_33_c	TCTTTCTCTTTCTATTTCTCTCACCCTCTCTCTCTGTTTATCTCTTATGC	5391
ref NT_099026.1 MmY_98663_33_c	ACTTCCTCCAATGAAGCCACACATTCTCTTATTCCTTCTAATCTTTAAAC	5413
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ref NT_099035.1 MmY_98672_33_5	--ATGAATATATGCATGCATGTAGCTAGGTAGGTGTG-GTATTTTAAATG	5424
ref NT_078929.2 MmY_78994_33_4	--ATGAATATATGCATGCATGTAGCTAGGTAGGTGTG-GTATTTTAAATG	5428
ref NT_099035.1 MmY_98672_33_c	--ATGAATATATGTATGCATGTAGCTAGGTAGGTGTG-GTAGTTTTAATG	5438
ref NT_099026.1 MmY_98663_33_c	TCACTGCCACTTCCCAGTGACTAAGTATTCATATATATGTGTCTATAGAG	5463
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ref NT_099035.1 MmY_98672_33_5	TAATTATTT--CCCATCGGCCCATAGGCTGTATTAGGATGAT-----TA	5466
ref NT_078929.2 MmY_78994_33_4	TAATTGGTT--CCCATCGGCCCATAGGCTGTATTAGGATGAT-----TA	5470
ref NT_099035.1 MmY_98672_33_c	TAATTGGTT--CCCATCGGCCCATAGGCTGTATTAGGGTGAG-----TA	5480
ref NT_099026.1 MmY_98663_33_c	AACTTTCTTATTCAAACCTACCAATTTTCTATGGCTTGATCATCTTTTATT	5513
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ref NT_099035.1 MmY_98672_33_5	ACCTTGTTGGA--CTAGGTGTTTCCTTGTTGGAG-GAAGGGTGTC--CT	5511
ref NT_078929.2 MmY_78994_33_4	ACCTTGTTGGA--CTAGGTGTTTCCTTGTTGGAG-GAAGGGTGTC--CT	5515
ref NT_099035.1 MmY_98672_33_c	ACCTTGATGGA--CTAGGTGTTTCCTTGTTGGAG-GAAAGGTGTC--CT	5525
ref NT_099026.1 MmY_98663_33_c	ATTTTAGTACAGTCTAAAAGGCTCCCAATTAAATGACTACTGTTGAGCT	5563
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ref NT_099035.1 MmY_98672_33_5	GGAGGAGGTGGGTGGTCTCACACATGTTCAAGTTAGTTATGCACAGTAGG	5561
ref NT_078929.2 MmY_78994_33_4	GGAGGAGGTGGGTGGTCTCACACATGTTCAAGTTAGTTATGCCAGTAGG	5565
ref NT_099035.1 MmY_98672_33_c	GGAAGAGGTGGGTGGTCTCATTATGTTCAAGTTA---TGCCAGTAGG	5571
ref NT_099026.1 MmY_98663_33_c	TAGCCACAGTGGTGGGCCCTCCACATC--AATCA-TTACCCAAGAAAAAT	5610
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ref NT_099035.1 MmY_98672_33_5	GCTCTGTGTGTTTGCTGTCTCTGTCTTTCCAAGAGTAGCTGTGATAGA	5611
ref NT_078929.2 MmY_78994_33_4	GCTCTGTGTGTTTGCTGTCTCTGTCTTTCCAAGAGTAGCTGTGATAGA	5615
ref NT_099035.1 MmY_98672_33_c	GTTCTGTGTGTTTGTTGTCTGTTTGTCTTTCCAAGAGTAGCTGTGATAGT	5621
ref NT_099026.1 MmY_98663_33_c	ATCCTATAGACTTACCTAATAACCAAGTGAATAGAGACAGATCT--TCAA	5658
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ref NT_099035.1 MmY_98672_33_5	GTGTTCAGTGATTCAAGGAGGGGATGTTGGTTAGATGGCATATAAAGCAG	5661
ref NT_078929.2 MmY_78994_33_4	GTGTTCAGTGATTCAAGGAGGGGATGTTGGTTAGATGGCATATAAAGCAG	5665
ref NT_099035.1 MmY_98672_33_c	GTGTTCAGTGATTCAAGGAGGGGATGTTGGTTAGATGGCATATAAAGCAG	5671
ref NT_099026.1 MmY_98663_33_c	TTGCTCTCTCTCTCAGGTAT--CCGTTGATTGTCAAGATTGGGAAAAAA	5706
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ref NT_099035.1 MmY_98672_33_5	GCAAGACACCTT-TACATACATGGTAGAAGAAGCA-AGCTTTAAGAAGCA	5709
ref NT_078929.2 MmY_78994_33_4	GCAAGACACATT-TACATACATGTTAGAAGAAGCA-AGCTTTAAGAAGCA	5713
ref NT_099035.1 MmY_98672_33_c	GCAAGACACATT-TACATACATGGTAGAAGAAGCA-AACTTTAAGAAGCA	5719
ref NT_099026.1 MmY_98663_33_c	TAAAGTCCCATCACAGGAATATTTTACTGACTCCACAACCTACCCAAACA	5756
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ref NT_099035.1 MmY_98672_33_5	TTAAAAGAATCACAAAACCTAACTTTTATATAAAAAACCTATCATCCCTTT	6230
ref NT_078929.2 MmY_78994_33_4	TTAAAAGAATCACAAAACCTAACTTTTATATAAAAAACCTATCATCCCTTT	6244
ref NT_099035.1 MmY_98672_33_c	TTAAAAGAATCACAAAACCTAACTTTTATGTAAAAACCTATCATCCCTTT	6259
ref NT_099026.1 MmY_98663_33_c	ATAATTTAATGATTCTAACACATTTTACCTCCATTCCATT - - TCCCCTC	6277
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ref NT_099035.1 MmY_98672_33_5	CTACTTTGAATCCTCAGGGTGCACATCTGTTTACCTAACCATGTTTTTCTT	6280
ref NT_078929.2 MmY_78994_33_4	CTACTTTGAATCCTCAGGGTGCACATCTGTTTACCTAACCATGTTTTTCTT	6294
ref NT_099035.1 MmY_98672_33_c	CTACTTTGAATCCTCAGGGTGCACATCTGTTTACCTAACCATGTCTTTCTT	6309
ref NT_099026.1 MmY_98663_33_c	ATTTTCTGCTTCTTCATATGATATTGCAATCTATTAAA - ATACAGTACTG	6326
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ref NT_099035.1 MmY_98672_33_5	AAATCATATCAGGAATCAGAATGAGGAAATAGGTACAAGGAAATAATAAT	6330
ref NT_078929.2 MmY_78994_33_4	AAATCATATCAGGAATCAGAATGAGGAAATAGGTACAAGGAAATAATAAT	6344
ref NT_099035.1 MmY_98672_33_c	AAATCATATCAGGAATCAGAATGAGGAAATAGGTATAAGGAAATAATAAT	6359
ref NT_099026.1 MmY_98663_33_c	AAGGCAGAGGGAGGATCAGTGTGGGAA - - - GCTGCAAAGTTCTT - TAAT	6371
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ref NT_099035.1 MmY_98672_33_5	CATCTGAACACCAGCCTGACTTT - - - GAAAAAAAAAAGGCATGTTTTTT	6376
ref NT_078929.2 MmY_78994_33_4	CATCTGAACACCAGCCTGACTTT - - - GAAAAAAAAAAGGCATGTTTTTT	6390
ref NT_099035.1 MmY_98672_33_c	CATCTGAACACCAGCCTGACTTTTGAAAAAAAAAAAGGCATGCTTTTTC	6409
ref NT_099026.1 MmY_98663_33_c	TCTA-AAACAACAGATACACTGTC - - TGAATATTCCAGATACAACCTTTT	6417
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ref NT_099035.1 MmY_98672_33_5	GTAGTAATTCTT - - TTCAAGATTGTGGTTGAAGTATTAATC - GCATCAGC	6423
ref NT_078929.2 MmY_78994_33_4	GTAGTAATTCTT - - TCCAAGATTGTGGTTGAAGTATTAATC - GCATCAGC	6437
ref NT_099035.1 MmY_98672_33_c	GTAGTAATTCTT - - TCCAAGATCGTGATTGAAGTATTAATCTGAATCAGC	6457
ref NT_099026.1 MmY_98663_33_c	- TGGTAACCTTTGGGTCTACTGTTAGCATGAAATTTCTAGAAAAAAAAAAC	6466
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ref NT_099035.1 MmY_98672_33_5	TGCAATCCTTGAG - - AAAGTTCGATCTAAATAACACTGTGGGTGGCAATG	6471
ref NT_078929.2 MmY_78994_33_4	TGCAATCCTTGAG - - AAAGTTCGATCTAAATAACACTGTGGGTGGCAATG	6485
ref NT_099035.1 MmY_98672_33_c	TGCAATCCTTGAG - - AAAGTTAGATCTAAATAACACTGTGGGTGGCAATG	6505
ref NT_099026.1 MmY_98663_33_c	TTAAAGAATTAAGCCATGGTTCCTCTGGACCAGAGAGTTTAGTATCACTA	6516
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ref NT_099035.1 MmY_98672_33_5	ATATTGCCAGTGAGGGGCTGGAACCCCCCTTAAATTTTTCATACAATCCA	6521
ref NT_078929.2 MmY_78994_33_4	ATATTGCCAGTGAGGGGCTGGAACCCCCCTTAAATTTTTCATACAATCCA	6535
ref NT_099035.1 MmY_98672_33_c	ATATTGCCAGTGAGGGGCTGGAACCCCCCTTAAATTTTTCATACAATCCA	6555
ref NT_099026.1 MmY_98663_33_c	ATGAGTCATATTCATG - - - TCAATCATTTTCATCACTGTTACAAGATGCC	6563
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ref NT_099035.1 MmY_98672_33_5	TAGATTATGAGGAATGTGATGTGAGGGCAGCAAGTAGGGAGAACTCTAC	6571
ref NT_078929.2 MmY_78994_33_4	TAGATTATGAGGAATGTGATGTGAGGGCAGCAAGTAGGGAGAACTCTAC	6585
ref NT_099035.1 MmY_98672_33_c	TAGATTATGAGGGATGTGATGTGAGGGCAGCAAGTAGAGAGAACTCTAC	6605
ref NT_099026.1 MmY_98663_33_c	TAG - CAACAAGGAAAACAGGTCCATGGTCACAAG - AGTATGAAA - - - - -	6605
	*** * *** * * * **** * ****	
ref NT_099035.1 MmY_98672_33_5	AACAGCATGAGTGGTAACAGAGTGGTACCAGCTTTTAAGTGTTTAAGAGT	6621
ref NT_078929.2 MmY_78994_33_4	AACAGCATGAGTGGTAACAGAGTGGTACCAGCTTTTAAGTGTTTAAGAGT	6635
ref NT_099035.1 MmY_98672_33_c	AACAGCATGAGTGGTAACAGAGTGGTACCAGCTTTTAAGTGTTTAAGAGT	6655
ref NT_099026.1 MmY_98663_33_c	- GGGGCATGAATG - - AGCACAATTGT - CCAATTTATTGGCAGCCAGTAA	6651
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ref NT_099035.1 MmY_98672_33_5	GGTAAGAGCTTTTAAGTGTTTACCTCACCAAGAATCCATCAAAGCCCTG	6671
ref NT_078929.2 MmY_78994_33_4	GGTAAGAGATTTTAAGTGTTTACCTCACCAAGAATCCATCAAAGCCCTG	6685
ref NT_099035.1 MmY_98672_33_c	GGTAAGAGCTTTTAAGTGTTTACCTCACCAAGAATCCATCAAAGCCCTG	6705
ref NT_099026.1 MmY_98663_33_c	CATCA - ACACAGGAAGCGACCAAATAACAATAACACCTTCCAAGAC - - - A	6697
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ref NT_099035.1 MmY_98672_33_5	TATTTTGGAGGTAAAATGTACATTCTGGGGAGCCCCTCTGCCATGCTTAA	6721
ref NT_078929.2 MmY_78994_33_4	TATTTTGGAGGTAAAATGTACATTCTGGGGAGCCCCTCTGCCATGCTTAA	6735
ref NT_099035.1 MmY_98672_33_c	TATTTTGGAGGTAAAATGTACATTCTGGGGAGCCCCTCTGCCATGCTTAA	6755
ref NT_099026.1 MmY_98663_33_c	TGTTCCCAATG-ACCACGTTCTT- -TACAAGTTTCTCACCCCTTCCATG	6744
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ref NT_099035.1 MmY_98672_33_5	TATTCTAATAAAATTAATAAATAATTAATTTCTCATTTAATAGACCCTG	6771
ref NT_078929.2 MmY_78994_33_4	TATTCTAATAAAATTAATAAATAATTAATTTCTCATTTAATAGACCCTG	6785
ref NT_099035.1 MmY_98672_33_c	TATTCTAGTAAAATTAATAAATAATTAATTTCTCATTTAATAGACCCTG	6805
ref NT_099026.1 MmY_98663_33_c	CACACCCATCAATCAACGCATAGATTAAAGCCCTCA- -GGGTCCAATCAC	6792
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ref NT_099035.1 MmY_98672_33_5	CTTACAGTCCCTCCAAATTTTACTCCCCACGGTTCTTTTACTACCTCCCA	6821
ref NT_078929.2 MmY_78994_33_4	CTTACAGTCCCCCAAATTTTACTCCCCACGGTTCTTTTACTACCTCCCA	6835
ref NT_099035.1 MmY_98672_33_c	CTTACAGTCCCCCAAATTTTACTCCCCACGGTTCTTTTACTACCTCCCA	6855
ref NT_099026.1 MmY_98663_33_c	TTTTCAGATTGAGTATATTGTTCTACCTATGAACATTGTACTTCGGGCCA	6842
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ref NT_099035.1 MmY_98672_33_5	---TCCTCTCCAGTTCCTCC-----CCCTTTCGGTCATCATTCATCAAA	6862
ref NT_078929.2 MmY_78994_33_4	---TCCTCTCCAGTTCCTCC-----CCCTTTCGGTCATCATTCATCAAA	6876
ref NT_099035.1 MmY_98672_33_c	---TCCTCTCCAGTTCCTCC-----ACCTTTCGGTCATCATTCATCAAA	6896
ref NT_099026.1 MmY_98663_33_c	AAACCTTCATCAAAGACCCAGGACAGACATTTCAAACCCATTTACCACA	6892
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ref NT_099035.1 MmY_98672_33_5	TATTTCTCTTTCAAATATCTCTTCCTG----CATTTCTTATTCAACCC	6907
ref NT_078929.2 MmY_78994_33_4	TATTTCTCTTTCAAATATCTCTTCCTG----CATTTCTTATTCAACCC	6921
ref NT_099035.1 MmY_98672_33_c	TATTTCTCTTTCAAATATCTCTTCCTG----CATTTCTTATTCAACCC	6941
ref NT_099026.1 MmY_98663_33_c	GCATTCTTTATGCTACACAAAGTGATAGGATCTATCTGTCTCTTTAAGGG	6942
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ref NT_099035.1 MmY_98672_33_5	CATCTCCCTCCACCA- -TGCCACCTGATCTTCTCCTTCTTGCCACCTTT	6955
ref NT_078929.2 MmY_78994_33_4	CATCTCCCTCCACCA- -TGCCACCTGATCTTCTCCTTCTTGCCACCTTT	6969
ref NT_099035.1 MmY_98672_33_c	CATCTCCCTCCACCA- -TGCCACCTGATCTTCTCCTTCTTGCCACCTTT	6989
ref NT_099026.1 MmY_98663_33_c	TATCTCTATCAAGCAGTTCCAAAAGGAAAATGTCCAGGTAAACAGCATCA	6992
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ref NT_099035.1 MmY_98672_33_5	GTACACTAATAAA-TCCATTCTATTTCTCCATACCATGGGCATCCATGTA	7004
ref NT_078929.2 MmY_78994_33_4	GTACACTAATAAA-TCCATTCTATTTCTCCATACCATGGGCATCCATGTA	7018
ref NT_099035.1 MmY_98672_33_c	GTCCACTAATAAAATCCATTCTATATCCCCATACCATGGGCATCCATGTA	7039
ref NT_099026.1 MmY_98663_33_c	GCACCTCCAGGAG- -CTTTTATAAATGTGAGT-TCAAGAAGAGCAAAAT-	7038
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ref NT_099035.1 MmY_98672_33_5	TGCACCCAAGTCC-TTCCTCTATACCTAACTTCACTGGATCTACAGATTG	7053
ref NT_078929.2 MmY_78994_33_4	TGCACCCAAGTCC-TTCCTCTATACCTAACTTCACTGGATCTACAGATTG	7067
ref NT_099035.1 MmY_98672_33_c	TGCACCCAAGTCCCTTCTCTATACCTAACTTCACTGGATCTACAGATTG	7089
ref NT_099026.1 MmY_98663_33_c	TGCAATGAAATTTAAGGGTCTTTGTCCCGCATCTCTGCATCTTAAACCA	7088
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ref NT_099035.1 MmY_98672_33_5	TAGACAGGCCATCACATATGTAATGTTGAATGTCTTAATGTTTCTATTGC	7103
ref NT_078929.2 MmY_78994_33_4	TAGACAGGCCATCACATATGTAATGTTGAATGTCTTAATGTTTCTATTGC	7117
ref NT_099035.1 MmY_98672_33_c	TAGACAGGCCATCACATATGTAATGTAGAATGTGTTAATCTTTCTATTGC	7139
ref NT_099026.1 MmY_98663_33_c	TAGGGTGAACA-CAGAAATGTAG-GTCAAAAGTGTGAATTTACCTATAC	7136
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ref NT_099035.1 MmY_98672_33_5	TGTCACCAAAAACTATAAC- -CCAAGCACAAAGTTGGGGAGGGTAGGACTT	7151
ref NT_078929.2 MmY_78994_33_4	TGTCACCAAAAACTATAAC- -CCAAGCACAAAGTTGGGGAGGGTAGGACTT	7165
ref NT_099035.1 MmY_98672_33_c	TGTCACCAAAAACTATAAC- -CCAAGCACAAAGTTTGGGGAGGGTAGGACTT	7187
ref NT_099026.1 MmY_98663_33_c	TACAATAATTGGGATGATTTCTAGCCATCTCTACGTTCTGTCTGTTACG	7186
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ref NT_099035.1 MmY_98672_33_5	ATTTGCAATGTGGGTACTGTAAGGAAAAGAGACACTGAGCAAGAGACTGC	7201
ref NT_078929.2 MmY_78994_33_4	ATTTGCAATGTGGGTACTGTAAGGAAAAGAGACACTGAGCAAGAGACTGC	7215
ref NT_099035.1 MmY_98672_33_c	ATTTG GTTTACAC-TTCTTCATTGCTATTTCATCATCTGAAGACAGACAGA	7236
ref NT_099026.1 MmY_98663_33_c	GAGTCCACCAAGTCTGCCTCAAGGCATATTG-CATAGTGTGAAATAGTGC	7235
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ref NT_099035.1 MmY_98672_33_5	CCCAAGAAAGAGACAGATACCAGACCACCTAAGTCCTTTTCTCAGAGGAT	7251
ref NT_078929.2 MmY_78994_33_4	CCCAAGAAAGAGACAGATACCAGACCACCTAAGTCCTTTTCTCAGAGGAT	7265
ref NT_099035.1 MmY_98672_33_c	AC--AGGAACTGAAATGGGCCAGGAACCTAGAGGCAGGAGCT--AATAC	7281
ref NT_099026.1 MmY_98663_33_c	CAGCAGTTGATTGCAAACAACACTATGTGTTGACTTGCATGT--AAAAT	7282
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ref NT_099035.1 MmY_98672_33_5	GATGACTACATGATATGGGGAA--CAGACAC-CCTACGTGACACTAGGG	7297
ref NT_078929.2 MmY_78994_33_4	GATGACTACATGATATGGGGAA--CAGACAC-CCTACGTGACACTAGGG	7311
ref NT_099035.1 MmY_98672_33_c	AGAGACCA--GGGATGGGTG--CTCCTGC-CACGCACACCAGTCGAG	7323
ref NT_099026.1 MmY_98663_33_c	GAGACATGTATAATATAGACACATTTGTACATACACACATACTCACAGAA	7332
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ref NT_099035.1 MmY_98672_33_5	TAACCCAGCTGTGGAAGAGACCCTTATGGCTTCCCTTCATGATATC-AG	7346
ref NT_078929.2 MmY_78994_33_4	TAACCCAGCTGTGGAAGAGACCCTTATGGCTTCCCTTCATGATATC-AG	7360
ref NT_099035.1 MmY_98672_33_c	TCAGCTTGACAGGCCTAGAGGCCTGGAAG----CACTCATGA-----	7361
ref NT_099026.1 MmY_98663_33_c	AGAGGCAAGCAGTAGAGGAGCTTTGTCTTAGGAACCTCATGGAAGAGAT	7382
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ref NT_099035.1 MmY_98672_33_5	AGCAGAGTTTTT-----AGTCCTGACAGAGCCACTGGAGAAATTGA	7387
ref NT_078929.2 MmY_78994_33_4	AGCAGAGTTTTT-----AGTCCTGACAGAGCCACTGGAGAAATTGA	7401
ref NT_099035.1 MmY_98672_33_c	GGCAAAGAGTTT-----CACGGAAGCTCACCTTCTGGAGTTTGGC	7402
ref NT_099026.1 MmY_98663_33_c	GGTAGAAATCTTGTAAGGCAGAGAGGTCACTGAGACACTGTCTCTACTGC	7432
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ref NT_099035.1 MmY_98672_33_5	GGACCCAGAAATCCTTAGTATTCGGGGCTACTGGTCAGAAACCATACTCT	7437
ref NT_078929.2 MmY_78994_33_4	GGACCCAGAAATCCTTAGTATTCGGGGCTACTGGTCAGAAACCATACTCT	7451
ref NT_099035.1 MmY_98672_33_c	CTTCTCATTAACCC--ATATACTAATCCCCTATTCCCGCGTTAG--TC	7446
ref NT_099026.1 MmY_98663_33_c	ACAAAATCAGGCCAGTCTTCCTTGCATCCCTAAGTGGTATGGTATCACTA	7482
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ref NT_099035.1 MmY_98672_33_5	TAGACCA--CTGATAAGAAAGTTAATCTATGAATAAGCCAAGTAACTCAT	7485
ref NT_078929.2 MmY_78994_33_4	TAGACCA--CTGATAAGAAAGTTAATCTATGAATAAGCCAAGTAACTCAT	7499
ref NT_099035.1 MmY_98672_33_c	TGGTGTA-TGGATCCACGTGCTCTCTTTTAGTGTTATCTTATTATAAGT	7494
ref NT_099026.1 MmY_98663_33_c	TCCATCATCCCCATCTGAGAATATATGGACTATTGATGAAGGGTGGAGAA	7532
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ref NT_099035.1 MmY_98672_33_5	TCCTCCCTCATCATTCCTCAAGCCCCACCACATTGTTG--TGGAGAGAC	7532
ref NT_078929.2 MmY_78994_33_4	TCCTCCCTCATCATTCCTCAAGCCCCACCACATTGTTG--TGGAGAGAT	7546
ref NT_099035.1 MmY_98672_33_c	TCTTTTAAAGATTGAATTCTGATATAGCTAAGCTTTCG--CCA--GT	7537
ref NT_099026.1 MmY_98663_33_c	TCAGTTTTTCATCAAAGGTAAGGCTTTTGTATGTGATAGGTTTGCCATGCT	7582
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ref NT_099035.1 MmY_98672_33_5	ATACTAG-----CATATTTAAAATCCCAAATAAGCTGCTCTTTGGAAGG	7576
ref NT_078929.2 MmY_78994_33_4	ATACTAG-----CATATTTAAAATCCCAAATAAGCTGCTCTTTGGAAGG	7590
ref NT_099035.1 MmY_98672_33_c	GTTCCAA-----TATCCTAGAAAGTCCT-TGAGCTGACCATGGGCTTG	7579
ref NT_099026.1 MmY_98663_33_c	CTACTGGTAGCCCCATGTCCAAGAGTTTA-TGGGCAACACAATTGATT	7630
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ref NT_099035.1 MmY_98672_33_5	AACTTCAATC---CCTTGGAAGCCTGTCCC-TATAAATTTAACTTTAA	7621
ref NT_078929.2 MmY_78994_33_4	AACTTCAATC---CCTTGGAAGCCTGTCCC-TATAAATTTAACTTTAA	7635
ref NT_099035.1 MmY_98672_33_c	GATTTTCAGTAAGAATGTTGCCTATTCAATGGCATTGGAATGCGCTCTGG	7629
ref NT_099026.1 MmY_98663_33_c	GAATTGGGTTGTATCAAAGGGGAGAAAAGTAGACTTGAACCTGGGAGGAT	7680
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ref NT_099035.1 MmY_98672_33_5	AATTAGAAGAAGAATATAGATTACATGAGTCTCAA - - GCCCCGTCAAGAA	7669
ref NT_078929.2 MmY_78994_33_4	AATTAGAAGAAGAATATAGATTACATGAGTCTCAA - - GCCCCGTCAAGAA	7683
ref NT_099035.1 MmY_98672_33_c	TATTATACTACCCCTTTGAATAAAAAGCTAAGTCAGT - GCCCTACACAGAA	7678
ref NT_099026.1 MmY_98663_33_c	GATTAAGGTGGAATGGGTCTGGTTTTGGTCTGGGAGGAGTTATCAAGAG	7730
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ref NT_099035.1 MmY_98672_33_5	AAGTACTAGAATGGACCTATTTAGAGAGATATCCAACAGCCT - - GGGCAG	7717
ref NT_078929.2 MmY_78994_33_4	AAGTACTAGAATGGACCTATTTAGAGAGATATCCAACAGCCT - - GGGCAG	7731
ref NT_099035.1 MmY_98672_33_c	ATTTATCATCAT - - - CTAGGAAGAAGGAAGTTTGAGACCTA - - AGGAGG	7722
ref NT_099026.1 MmY_98663_33_c	AATTGG - AAAGTGAATTCCATCAAAAAATTGTATGAAGTTCTCAAGGAAT	7779
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ref NT_099035.1 MmY_98672_33_5	AGACTGGTGGTATAATTGAGACAA - AAATGG - TGTCCCCCCCCATCATTG	7765
ref NT_078929.2 MmY_78994_33_4	AGACTGGTGGTATAATTGAGACAA - AAATGG - TGTCCCCCCC - ATCATTG	7778
ref NT_099035.1 MmY_98672_33_c	AAGCAGAGTACATACTTAGAACTATAGATAGCTGAGTTCCACCCATATAC	7772
ref NT_099026.1 MmY_98663_33_c	TAATTAATGTAGTTCTTAATATAC - - AATGTCTGTACTGAACATATACAG	7827
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ref NT_099035.1 MmY_98672_33_5	-----TGACATTGAAAACCTGGTGAG-----ATTCTTTTCGGGGTACA - AC	7804
ref NT_078929.2 MmY_78994_33_4	-----TGACATTGAAAACCTGGTGAG-----ATTCTTTTCGGGGTACA - AC	7817
ref NT_099035.1 MmY_98672_33_c	-----ACGTATTTACAATGGCCTAG-----GGGGAAGGTGGTCTATA - - C	7810
ref NT_099026.1 MmY_98663_33_c	ACCACTTATATTTCAATCTCCTAAATAGCAACTCATTTTATAGCACTTAC	7877
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ref NT_099035.1 MmY_98672_33_5	AATACACCATGAGCAAAG - - AGGCCAGTGAGGGCATCAGACCTC - - ACCT	7850
ref NT_078929.2 MmY_78994_33_4	AATACACCATGAGCAAAG - - AGGCCAGTGAGGGCATCAGACCTC - - ACCT	7863
ref NT_099035.1 MmY_98672_33_c	AATAGACTA - AAATAGGA - - ACTATAGCAAGGTCACGAA - - - - - GCCA	7850
ref NT_099026.1 MmY_98663_33_c	ATTACATTACGTGCAAAAGTAATCCAGAGATTATTTAAAATAAAGAAGGA	7927
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ref NT_099035.1 MmY_98672_33_5	TCAAAGGCT - - - - CTTAGAAGTAGGCGTGTTTGGTCCTTTGTCAGTCTTC	7896
ref NT_078929.2 MmY_78994_33_4	TCAAAGGCT - - - - CTTAGAAGTAGGCGTGTTTGGTCCTTTGTCAGTCTTC	7909
ref NT_099035.1 MmY_98672_33_c	TTGACTTCT - - - - TCTAAGACTATG - - - - - TGGATCTTTGGTGGAGTTC	7890
ref NT_099026.1 MmY_98663_33_c	TCAGGGGATATGGCCAGAGACAATGCCATGTGTGTGTTCAAACATTAC	7977
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ref NT_099035.1 MmY_98672_33_5	CTGGAATACTCTGTTGCTACCAGTTAAAAAGCAAGGCTTTGCCACCTGGC	7946
ref NT_078929.2 MmY_78994_33_4	CTGGAATACTCTGTTGCTACCAGTTAAAAAGCAAGGCTTTGCCACCTGGC	7959
ref NT_099035.1 MmY_98672_33_c	TTTTTGATCCAGTTGTTAACAGTGAA - - - - - TTTTATC - CCAGGT	7930
ref NT_099026.1 MmY_98663_33_c	CTACAACAC - CAGTGCTTATGATTTTGG - - - - GAGGGGCAGAGACAGGAA	8022
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ref NT_099035.1 MmY_98672_33_5	ACTCCCTAATAATCCCCCTTACTAAAGAGACTGGGACTTTCTCATGGAC	7996
ref NT_078929.2 MmY_78994_33_4	ACTCCCTAATAATCCCCCTTACTAAAGAGACTGGGACTTTCTCATGGAC	8009
ref NT_099035.1 MmY_98672_33_c	GTTTCCTGTGAGACCTTCTGAGTTTTTATTCCCTCCGTTTTCTGTAAGAAT	7980
ref NT_099026.1 MmY_98663_33_c	GATGACTGTGGCTTCTGAAAGCCAGCCTCACTACCAGCTCAGCAAGAAA	8072
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ref NT_099035.1 MmY_98672_33_5	CCAATATATGGGGAGGCCTTTAAAAAGATTAAAAAATCGTGCTTAGTGC -	8045
ref NT_078929.2 MmY_78994_33_4	CCCATATATGGGGAGGCCTTTAAAAAGATTAAAGATCGTGCTTAGTGC -	8058
ref NT_099035.1 MmY_98672_33_c	CCAGTA - - - - - ACCTCTTTGTACCTT - - - - GCTTGTGTGTCACCC -	8016
ref NT_099026.1 MmY_98663_33_c	CCCAGTCACAAGGGGATAAGTTATGGAGGAAAAGAGTAGATCACACTATA	8122
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ref NT_099035.1 MmY_98672_33_5	CTCAGCCCTAGTCCTGACAGATGTGACCGAGCCATTCACTCT - CTATTTA	8094
ref NT_078929.2 MmY_78994_33_4	CTCAGCCCTAGTCCTGACAGATGTGACCGAGCCATTCACTCT - CTATTTA	8107
ref NT_099035.1 MmY_98672_33_c	AACTTCCCTATTCTCTTC - - - TGT - ATAAAAAGTTTGATGCT - CAATTTG	8061
ref NT_099026.1 MmY_98663_33_c	CCCTTCCCTAGCCTCTGAACCTAC - - CTGTACAGTTCTCTATGCAGACTC	8170
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ref NT_099035.1 MmY_98672_33_5	G - ATAAAAGAG - CAGAAATAGTGAGATAGGTCCTTAAGCTCTGGGG	8142
ref NT_078929.2 MmY_78994_33_4	G - ATAAAAGAG - CAGAAATAGTGAGATAGGTCCTGAAGCTAAGCTCTGGGG	8155
ref NT_099035.1 MmY_98672_33_c	ACACATTACATTAGATTCTACACAACCTCTCCTCTGTGTATCTGTCTAT	8111
ref NT_099026.1 MmY_98663_33_c	ACATAAATATGATTAAAATATGCAAGAGGTTATTTTGCATAGCTTATATT	8220
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ref NT_099035.1 MmY_98672_33_5	ACATAGAAAAGAC - TTGTGGCCTACTTGTAACCTTAAAGCTCTGACCC	8191
ref NT_078929.2 MmY_78994_33_4	ACATAGAAAAGAC - TTGTGGCCTACTTGTAACCTTAAAGCTCTGACCC	8204
ref NT_099035.1 MmY_98672_33_c	CATTTTCATCCAAT - GCTTTGCCCACCTGTGACTAGAGATCCGTTCCACGG	8160
ref NT_099026.1 MmY_98663_33_c	CAAAAGCAATGTTGTTTTAGACTAGAAACCTGAGGACTTTATATCATTAT	8270
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ref NT_099035.1 MmY_98672_33_5	AATGCCCAGTGGATGGCCGTCTTTCTTAAAGATATCAATACTTCTCAAA	8241
ref NT_078929.2 MmY_78994_33_4	AATGCCCAGTGGATGGCCGTCTTTCTTAAAGATATCAATACTTCTCAAA	8254
ref NT_099035.1 MmY_98672_33_c	A - -GACAA-AGGTGCCCAGAAATGTCTGCAGCATTCTGCTTAGTGCCTAG-	8193
ref NT_099026.1 MmY_98663_33_c	AGTTCCTGGAGCAAACCTCCAAGATATAGATGATGGGTATATCTTCTTAC	8320
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ref NT_099035.1 MmY_98672_33_5	GATGCTGACAACTGACTCTAGGTCAAGGAACTATAGTAGTAGCCCCCCT	8291
ref NT_078929.2 MmY_78994_33_4	GATGCTGACAACTGACTCTAGGTCAAGGAACTATAGTAGTAGCCCCCCT	8304
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TGTGC - - - AAAGGAAACCTCAGTTAAGTGTGTGTGTGTCAGTGACTCCAAA	8366
ref NT_099035.1 MmY_98672_33_5	CTGCCCCCATGCCTTAGAAAGCATTGTTAGGCAGCTGCCAGATTGCTGGA	8341
ref NT_078929.2 MmY_78994_33_4	CTGCCCCCATGCCTTAGAAAGCATTGTTAGGCAGCTGCCAGATTGCTGGA	8354
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CAGCTTTCTCCTCTATGTTCTTTATATAGCA - - - - TAGAATGATCTG	8411
ref NT_099035.1 MmY_98672_33_5	TGACTAATGCTCACAGGACCCATTATCAGAGCCTCTTTCTGACTGAGAGA	8391
ref NT_078929.2 MmY_78994_33_4	TGACTAATGCTCACAGGACCCATTATCAGAGCCTCTTTCTGACTGAGAGA	8404
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TAAATAATGAAAATATGAACG - - - - CAAAGCTTTTTTGTGATTTAAGGC	8456
ref NT_099035.1 MmY_98672_33_5	GTGTAGAGAGAGTGTAATTTGCACCCCTGCTATCCTGAATCCTTCCACCT	8441
ref NT_078929.2 MmY_78994_33_4	GTGTAGAGAGAGTGTAATTTGCACCCCTGCTATCCTGAATCCTTCCACCT	8454
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TTGTGTTAAATCATA - TTTATAAC - - - ATTGTATTAAAT - - - - GGAAG	8497
ref NT_099035.1 MmY_98672_33_5	TGCTGCCTGAAGCTGACAACTCCCTACCAGTGAAGGTGTATAGACATCCT	8491
ref NT_078929.2 MmY_78994_33_4	TGCTTCCTGAAGCTGACATCTCCCTACCAGTGAAGGTGTATAGACATCCT	8504
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TGAAATCTTCAGCTCTCAGGAACAATACAGTCAAT - CCTATAGGCTTCTG	8546
ref NT_099035.1 MmY_98672_33_5	GGCAGAAGAAACCAAACTAAGAAAGAAGTCATTGACCAGCCATGGTCAG	8541
ref NT_078929.2 MmY_78994_33_4	GGCAGAAGAAACCAAACTAAGAAAGAAGTCATTGACCAGCCATGGTCAG	8554
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TTTTG - - - - - CTCCATTGTGAGCAAA - - - ATTAATTGCACATCAACAG	8586
ref NT_099035.1 MmY_98672_33_5	GTTGCCCAATTGGTACACAGATGGTATCAGCTTTTTTGATTGAAGGTAAA	8591
ref NT_078929.2 MmY_78994_33_4	GTTGCCCAATTGGTACACAGATGGTATCAGCTTTTTTGATTGAAGGTAAA	8604
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GTCCCACTTTTAACTAAATCAGGGAGAAGGGCTATGTTTCCGTACAAA	8636

ref NT_099035.1 MmY_98672_33_5	AGAAAAGTGGTGCCAGCAGTGGTCAACGGAAAAGAAACC-ATCCGTGTAA	8640
ref NT_078929.2 MmY_78994_33_4	AGAAAAGTGGTGCCAGCAGTGGTCAACGGAAAAGAAACC-ATCCGTGTAA	8653
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	T---AAGTAATGTCAAT-GTGATTATTCAAGTAGAAATCTGGCAGGGTTA	8682
ref NT_099035.1 MmY_98672_33_5	GCAGCTTTACTGAAGAAATGACAGTCCAGAGAGAAGAGCTAATCAC-ACA	8689
ref NT_078929.2 MmY_78994_33_4	GCAGCTTTACTGAAGAAATGACAGTCCAGAGAGAAGAGCTAATCAC-ACA	8702
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GGATGCGTTTGGCTTATGTGATAGTGATGACTGATTAGTCTCTTGTTATG	8732
ref NT_099035.1 MmY_98672_33_5	TACCCAAGCCTTGCAGCTGGCCATAGAAAAGAACATCAATATCTAAACAG	8739
ref NT_078929.2 MmY_78994_33_4	TACCCAAGCCTTGCAGCTGGCCATAGAAAAGAACATCAATATCTAAACAG	8752
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CAAATAACCCTTACCTCTG----AGAAAAGACAAGTAATGATATAAAAT	8777
ref NT_099035.1 MmY_98672_33_5	ACAGCATGTA-TGCCTTTGCCACATGCATGGTAGTATCTGTAGAAAAAGG	8788
ref NT_078929.2 MmY_78994_33_4	ACAGCATGTA-TGCCTTTGCCACATGCATGGTAGTATCTGTAGAAAAAGG	8801
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ATACTATGAAGTGACATGGACACTTAT-TACTAGATTTTCATTTTC-----	8821
ref NT_099035.1 MmY_98672_33_5	ATGCTACTCACTTCTACTGGGGAAGATATTTAAAAATAAAAAGGAAACCTT	8838
ref NT_078929.2 MmY_78994_33_4	ATGCTACTCACTTCTACTGGGGAAGATATTTAAAAATAAAAAGGAAACCTT	8851
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	-CTTTACATACTTTAGTTGTTTGAAAAATTGTGGCCACAG--AAGCTC	8867
ref NT_099035.1 MmY_98672_33_5	GAGACTATTAGAAGCCATACACTTTGCAAAAAACTGGACATCATACATTG	8888
ref NT_078929.2 MmY_78994_33_4	GAGACTATTAGAAGCCATACACTTTGCAAAAAACTGGACATCATACATTG	8901
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AAA--TATTCAAAGGTGTTAGTTTTCCAGGTGGTGAGATGTTAAGAA--A	8913
ref NT_099035.1 MmY_98672_33_5	CCATTGTCACCACAAAGTCCATGAGGCCATAGTGAAGGGAAATCTGATGC	8938
ref NT_078929.2 MmY_78994_33_4	CCATTGTCACCACAAAGTCCATGAGGCCATAGTGAAGGGAAATCTGATGC	8951
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GAATT-----AGAATT--TGAATTTTTA-TTAAAGGAGATTTG----	8948
ref NT_099035.1 MmY_98672_33_5	CTGAACTGACTGGCCTAAAAAAAAATAAATGAATAAAATAAAGAACGTGA	8988
ref NT_078929.2 MmY_78994_33_4	CTGAACTGACTGGCCTAAAAAAAA-TAAATGAATAAAATAAAGAACGTGA	9000
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	-----TCACTATTCTTTGAAATATCAAA--AATCCATCAGGCTCTCTCT	8990
ref NT_099035.1 MmY_98672_33_5	AGACCATTATAAACTCAAAG--ATGCAGGCTTTGACTATACTCCAGAAGA	9036
ref NT_078929.2 MmY_78994_33_4	AGACCATTATAAACTCAAAG--ATGCAGGCTTTGACTATACTCCAGAAGA	9048
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CTCTCATTCTTAATCTCTCCTCATTCTCTCTCTATCTCTGTCTCTTTGTC	9040
ref NT_099035.1 MmY_98672_33_5	TCAGAAATTAACAGGCAAAATACCTGATATATGTGGGTGTACTACCCGGG	9086
ref NT_078929.2 MmY_78994_33_4	TCAGAAATTAACAGGCAAAATACCTGATATATGTGGGTGTACTACCCGGG	9098
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TCTATCTCTGTCTCTCTC--TCTCTGTTTCAT-TCTCTGTTTCTCTCTGT	9087

ref NT_099035.1 MmY_98672_33_5	GAGTCTCTAGGACCAAGATGGTTGCTCTGTCCTGCCCACAATAGAAAGGT	9136
ref NT_078929.2 MmY_78994_33_4	GAGTCTCTAGGACCAAGATGGTTGCTCTGTCCTGCCCACAATAGAAAGGT	9148
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CTCTGCTTGTTGTCTGTAGTATTGCA-TGTGAGCTCTCAGATACTGCTCT	9136
ref NT_099035.1 MmY_98672_33_5	AACAATATGTCTCCAATCTAAACCACCTCATGCACTTGGAATTGAGAAG	9186
ref NT_078929.2 MmY_78994_33_4	AACAATATGTCTCCAATCTAAACCACCTCATGCACTTGGAATTGAGAAG	9198
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ACACATGTGTGCCTGCCTGTTGCCATGGTGTGTACCATGATGTCCTGGAG	9186
ref NT_099035.1 MmY_98672_33_5	--GTCAAAGAAAATGTTGAGAGCTCAAAGTCAATGTTATAAGATTGCCA	9234
ref NT_078929.2 MmY_78994_33_4	--GTCAAAGAAAATGTTGAGAGCTCAAAGTCAATGTTATAAGATTGCCA	9246
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TCGCCTTCTGAAACTGTAAGACCGCAATTAAATATTTTCATCTTATAATTT	9236
ref NT_099035.1 MmY_98672_33_5	GATGTTGCCAGGGGATTGTTAAT-GAATGCCAAGCATG-TGCCCTCACC	9282
ref NT_078929.2 MmY_78994_33_4	GATGTTGCCAGGGGATTGTTAAT-GAATGCCAAGCATG-TGCCCTCACC	9294
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GGTGTGGTCATGTCTCACATCAATAGAACAGTAACCAAGACATCCATATT	9286
ref NT_099035.1 MmY_98672_33_5	ATTGCTGGGCACCACAAGAACACCCCCCCC-AGAAGGTGGATAAAGAGTTG	9331
ref NT_078929.2 MmY_78994_33_4	ATTGCTGGGCACCACAAGAACACCCCCCCCAGAAGGTGGATAAAGAGTTG	9344
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CCAGTTTATTTTTTCAATCATTCTGTACTT-----ATTTCAATAAAGTTA	9331
ref NT_099035.1 MmY_98672_33_5	ACT---GGCCATGAGCATACTGAAAAGTAGACTTTACTGAAGTTAAACCA	9378
ref NT_078929.2 MmY_78994_33_4	ACT---GGCCATGAGCATACTGAAAAGTAGACTTTACTGAAGTTAAACCA	9391
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CCTTTTGTCCATTGAAAAGTTTTAAGAATACTTTTAAAGGTCTGAACAA	9381
ref NT_099035.1 MmY_98672_33_5	GCCAAGTACAGTAATAAATATCTATTTGTTTTTTTGTAACACCTTTTCA	9428
ref NT_078929.2 MmY_78994_33_4	GCCAAGTACAGTAATAAATATCTATTTGTTTTTTTGTAACACCTTTTCA	9441
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AT--AGTGC--CAGTAGGAGTGGCACTGTTAGTAGGTGTGGCCTTTTTGA	9427
ref NT_099035.1 MmY_98672_33_5	GGCTTGGTCTGAAGCCTTCCCACTAATAACAAGAACACCCATGCCATGGG	9478
ref NT_078929.2 MmY_78994_33_4	GGCTTGGTCTGAAGCCTTCCCACTAATAACAAGAACACCCATGCCATGGG	9491
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AGTATGTGTGA-----CCCTGTTGG-AGTAGATGTAGCCTTGTTGGAGG	9470
ref NT_099035.1 MmY_98672_33_5	AAAGAAGATATTAGAGGAAAATTTCTCAAGATTTGGCATCTCTAAGGTAC	9528
ref NT_078929.2 MmY_78994_33_4	AAAGAAGATATTAGAGGAAAGTTTCCCAAGATTTGGCATCTGTAAGGTAC	9541
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AAATGTAACACTGTGCTTGTGGACTTTGAGATCGGCTATGCTTAAGCTGT	9520
ref NT_099035.1 MmY_98672_33_5	TTTCATCAGACAATGGCCCCTCCTTCATTGTCCAGGTAAGCCAAGGGTTA	9578
ref NT_078929.2 MmY_78994_33_4	TTTCATCAGACAATGGCCCCTCCTTCATTGTCCAGGTAAGCCAAGGGTTA	9591
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CCCCAGTGTGGCACACAGTCTCCATC-TTCTACCTGTGTATCAAGATGTA	9569

ref NT_099035.1 MmY_98672_33_5	GCCAGACAATGGGGGATTTCATTGGAAGATACATTGTTCTTACAGATTCCA	9628
ref NT_078929.2 MmY_78994_33_4	GCCAGACAATGGGGGATTTCATTGGAAGATACATTGTTCTTACAGATTCCA	9641
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	---AAACTCTCAGCTCCTTCTCTAGCATTGTGTCTGTCTGAATGCTTCCA	9616
ref NT_099035.1 MmY_98672_33_5	GACTTCAGGACAGGTAGAGTGGATGAATAGAGCATTAAAAGAAACCTTGA	9678
ref NT_078929.2 MmY_78994_33_4	GACTTCAGGACAGGTAGAGTGGATGAATAGAGCATTAAAAGAAACCTTGA	9691
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TATTTCCACTCATG-ATAATAATGGAGTAAACCTCTGAAAACAAGTT--A	9663
ref NT_099035.1 MmY_98672_33_5	CTAAATTGGTTTTAGAGACCTACAGAAAAGATTATGCAGCTCTTTTTTCCC	9728
ref NT_078929.2 MmY_78994_33_4	CTAAATTGGTTTTAGAGACCTACAGAAAAGATTATGCAGCTCTTTTTTCCC	9741
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CAAA---GTGTTCAAGAGTTACTGTGATCCTGGAGACTCTTCATGGCAA	9709
ref NT_099035.1 MmY_98672_33_5	TTTGCCTTGTCTGAGTATGGAACACCACAGGGAAATTTAAACTTACACC	9778
ref NT_078929.2 MmY_78994_33_4	TTTGCCTTGTCTGAGTATGGAACACCACAGGGAAATTTAAACTTACACC	9791
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TAAAACCCAACTAA-CACAAACACAAACATTCAAAAACACATTTGATAT	9758
ref NT_099035.1 MmY_98672_33_5	ATTCAAACTCCTCAACTTGGGACGCCCCTCCCTTTAA-CAGAAGCAGGTG	9827
ref NT_078929.2 MmY_78994_33_4	ATTCAAACTCCTCAACTTGGGACGCCCCTCCCTTTAAACAGAAGCAGGTG	9841
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TTTGACTATTCTTGGCCTAGGGAGTGGCACTACTGGGAGCTAATAACCTT	9808
ref NT_099035.1 MmY_98672_33_5	CAATGTTTGAACCTTGATGTTTCTTTTTTCAG AACCCCTCTA-----GCTC	9872
ref NT_078929.2 MmY_78994_33_4	CAATGTTTGAACCTTGATGTTTCTTTTTTCAG AACCCCTCTA-----GCTC	9886
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GTTGAAGTAAGTTTGGCCTTGTTGAAAGAAATTTATCTTTGTGAACATGG	9858
ref NT_099035.1 MmY_98672_33_5	ACTTGAAGGCTCTACAATTGGTCAGAAAAGATGCCTTGGAATGCTGAAA	9922
ref NT_078929.2 MmY_78994_33_4	ACTTGAAGGCCCTACAATTGGTCAGAAAAAATGCCTTGGAATGCTGAAA	9936
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ACTTTAATGCCCTCTGCCTAGCTGCCTGAAA-GCTAATCATTTCTAGCA	9907
ref NT_099035.1 MmY_98672_33_5	CACAATAAAAAACAAAAACAAAAACAAAAACAAAAACATACTAACC	9972
ref NT_078929.2 MmY_78994_33_4	CACAATAAAAAACAAAAACAAAAACAAAAACAAAAACATACTAACC	9986
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CCCTTCAGATGAAGATGTAGAACTCTCAGCTCCAAATGCACATGCCTGCC	9957
ref NT_099035.1 MmY_98672_33_5	AGGA----ACCATCTTCGTGCCACATAAATTTCAAACAGAAGATCCTGTC	10018
ref NT_078929.2 MmY_78994_33_4	AGGA----ACCATCTTCGTGCCACATAAATTTCAAACAGAAGATCCTGTC	10032
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AGGATCCTGCCATATTCCTACCTTGATGATAATGGACTGAATTTCTGAAC	10007
ref NT_099035.1 MmY_98672_33_5	CGGGTCCGGTGCCACCATTCTGGCAAACCTTGAACCTCAGATCAAAAGGATG	10068
ref NT_078929.2 MmY_78994_33_4	CGGGTCCGGTGCCACCATTCTGGCAAACCTTGAACCTCAGATCAAAAGGATG	10082
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CTG--TAAGCCAGGGTAAATTGAAAAGTGCTCTGCTGAT-AGTTGGTTG	10054

ref NT_099035.1 MmY_98672_33_5	CTCCCTGGTGCTTCTGACAAGCCCTGCTGCCGCACCTCCAGCATGTAACC	10118
ref NT_078929.2 MmY_78994_33_4	CTCCCTGGTGCTTCTGACAAGCCCTGCTGCCGCACCTCCAGCATGTAACC	10132
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CTATTCCAGAAAGACCAAAAGTTATGACGTACCATCCAGAGTCTGAGAAT	10104
ref NT_099035.1 MmY_98672_33_5	GCTTCTGGCCTGCCATGGCCCACTGGCCTGGCACTGCTCACACACAGTGG	10168
ref NT_078929.2 MmY_78994_33_4	GCTTCTGGCCTGCCATGGCCCACTGGCCTGGC-----	10164
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ACATTGGTTTAGCTTCTAGCATTTGACAGAAAACAGGATTAACAAGATAA	10154
ref NT_099035.1 MmY_98672_33_5	GCACTGCACAGGATCCCCCCTTCTTCCCTCCTCCCACTGGCAAGAGTCTC	10218
ref NT_078929.2 MmY_78994_33_4	--ACTGCACAGGATCCCCCCTTCTTCCCTCCTCCCACTGGCAAGAGTCTC	10212
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TGAGAATATAAAACTTCC--TATTTCACTTAGAGACACATGGGTTAT	10201
ref NT_099035.1 MmY_98672_33_5	TTTCGTCTCATTCAAGGGGCTTCTGAGGTTCTCAATCTTACAAATCCTAA	10268
ref NT_078929.2 MmY_78994_33_4	TTTCGTCTCATTCAAGGGGCTTCTGAGGTTCTCAATCTTACAAATCCTAA	10262
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AGATCTGCGGAAGTCAAGGTTTCATGGGTGGT--ATGGTAGGGTGATTAG	10249
ref NT_099035.1 MmY_98672_33_5	AGCTGTGACCTCAGGTTGGCTTTATTTGGCAG--CTGG-GCCAGAGGTTT	10315
ref NT_078929.2 MmY_78994_33_4	AGCTGTGACCTCAGGTTGGCTTTATTTGCAG--CTGG-GCCAGAGGTTT	10309
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	TGTCTTTATATGAGTGCAGTGTCTGTTCCCAAGTCTGATGTCACACATAC	10299
ref NT_099035.1 MmY_98672_33_5	AATTTTCTAACTTATAAAATTAGAACTATGTACTAGAAGGAGTGGGAAAT	10365
ref NT_078929.2 MmY_78994_33_4	AATTTTCTAACTTATAAAATTAGAACTATGTACTAGAAGGAGTGGGAAAT	10359
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ACATATGTTAAGTAATGAGTAGAATATCTTCAACACTTGCTCTCTTAGA-	10348
ref NT_099035.1 MmY_98672_33_5	GTGAGACCC-----CAACTTAGAGCATTCTCCCTGGAAGGTGAAGCCCC	10410
ref NT_078929.2 MmY_78994_33_4	GTGAGAACC-----CAACTTAGAGCATTCTCCCTGGAAGGTGAAGCCCC	10404
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GTGAAACCCTCTCACCATTTTGACTAGTT-TGACTGGCCAATACACTATT	10397
ref NT_099035.1 MmY_98672_33_5	TGGACATTCTCCAAGCTTGATTCCCTGAGCTCTAAAAATACAGCCAGAA	10460
ref NT_078929.2 MmY_78994_33_4	TGGACATTGTCCAAGCTTGATTCCCTGAGCTCTAAAAATACAGCCAGAA	10454
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	GGGATATCTACCTGTCTCCA--CCCCACAGTGTTGCAGATATGAATAGAC	10445
ref NT_099035.1 MmY_98672_33_5	AGAAGCTCTATGTTCTCTACAGCCACCAAAAA-GCATTTTGGTTTCTGAG	10509
ref NT_078929.2 MmY_78994_33_4	AGAAGCTCTATGTTCTCTACAGCCACCAAAAA-GCATTTTGGTTTCTGAG	10503
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	AT--GTCTGGAATTTTACAGAGGTGCTGAGAATACATGAACTCCACTGAG	10493
ref NT_099035.1 MmY_98672_33_5	CCTTACAGCTAGAGATTGAAAAATTGGAGTTTTGCCAAG--GACATCTG	10556
ref NT_078929.2 MmY_78994_33_4	CCTTACAGCTAGAGATTGAAAAATTGGAGTTTTGCCAAG--GACATCTG	10550
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CCAACTTTCTAGCCCCCAGCAGGGTATTGTTTTTTGAAATCAATGATCAC	10543

ref NT_099035.1 MmY_98672_33_5	GGCAGAGAAGAACATTCTCCCGACTCTTCCCAACTCTCCAAACTCTCCT	10606
ref NT_078929.2 MmY_78994_33_4	GGCAGAGAAGAACACTCTCCCGACTCTTCCCAACTCTCCAAACTCTCCT	10600
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	ATCAGTAGAGAA-ATGAAAACCAACATGACCCTGATATTCTACCTTACCT	10592
ref NT_099035.1 MmY_98672_33_5	CCCAACTCATCTCAATTCTCAGGTAGCTAATAAAAAACCCTCTTC-TGTC	10655
ref NT_078929.2 MmY_78994_33_4	CCCAACTCATCTCAATTCTCAGGTAGCTAATAAAAAACCCTCTTC-TGTC	10649
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CC-ACCTTACACCAATAAGTGAA-TGTTAAATATAAATTTAATTTATGTC	10640
ref NT_099035.1 MmY_98672_33_5	---ACATCTCAGAGTCATA-----	10671
ref NT_078929.2 MmY_78994_33_4	---ACATCTCAGAGTCATACGCCCTGCCCTGCACAGTGGAAGGAGTTTG	10696
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	CAAATGAATCCAGATTACATTCTAAT-----	10666
ref NT_099035.1 MmY_98672_33_5	-----	
ref NT_078929.2 MmY_78994_33_4	TCCTTAGCTAGCTGATAATAAACCTCTTACAGTTTGCA	10746
ref NT_099035.1 MmY_98672_33_c	-----	
ref NT_099026.1 MmY_98663_33_c	-----	