

1. mkg-r/mkg-r2

5'breakpoint

mau-mkg-r -TGGTAAATATCAAGTTTTTCGGCA AAAGCCGTTTTTCCGAATTCGGTCATTAATAATC  
 mau-mkg-r2 TTAGAAAATTCCCAATTTT-GCCC AAAGCCGTTTTTCCCAATTTCTGCCATAAATAATC  
**SAR\_DM**  
 mau-mkg-r CGTTTTTTTGCCTCAACTTTAAAAATAATTGTCTGAATATGGAATGCCCTATCTCGTTGT  
 mau-mkg-r2 AGTTTTTTTACGAAAACTTTTAAAAATAATTGTCTGTATATGGAAT-----GTTGA  
  
 mau-mkg-r GCTCGTATTAAAATCCCAATCGGAACTGTAGCCACAAATGGAATTTCTATTTTTTGGCC  
 mau-mkg-r2 GCTCGTAATTAATTTCCAATC-AAACTGTGTTCAAAAATGCAAAATTTCTATTTTTTGGCC  
  
 mau-mkg-r ATTTTTTGCAAATTTTGATGATGTTACCCCTTTCCAAAAATGCGAAAATTGACCCAAAAA  
 mau-mkg-r2 ATTTTTTGCAAATTTTGATGATGTTACCCCTTTCTAAAAATGCAAAAATTGACCCAAAAA  
  
 mau-mkg-r TTAATTTTCTAAATTTCTTCAAAAAGTGATAGGGATTGTTAGCACTTGGTAAATATCTGC  
 mau-mkg-r2 TTAATTTTCTAAATTTCTTCAAAAAGTTATAGGGATTGTTAGCAC-TGGTAAATAGCTGC  
  
 mau-mkg-r TCAAAACAGTTATTCTTTCTTTATCAGCATTTTTAGCCAAGTTATGGTGGGAACCCC  
 mau-mkg-r2 TCAAAACAGTTATTCTTTCTTTATCAGCATTTTTAGCCAAGTTATGGTGGGAACCCC  
  
 mau-mkg-r TCCAAAATAAATACGCATTTTATAAATAATTAAGCAATTAAGTTTTAAAGTAAAAGCT  
 mau-mkg-r2 TCCAAAATAAATACGCATTTTATAAATAATTAAGCAATTAAGTTTTAAAGTAAAAGCT  
  
 mau-mkg-r TCACAAATTTTTATTATAATTATAGGGGCGGTAAATGAAGTAGTAATTGTTCAAAGGAT  
 mau-mkg-r2 TCACAAATTTTTATTATAATTATAGGGGCGGTAAATGAAGTAGTAATTGTTCAAAGGAT  
  
 mau-mkg-r AACGCTTTAATTCGATTTTCGTACGCAGATTGTAAGAAAGAGTAGTCGACTGAAATTCTA  
 mau-mkg-r2 AACGCTTTAATTCGATTTTCGTACGCAGATTGTAAGAAAGAGTAGTCGACTGAAATTCTA  
  
 mau-mkg-r AAAAAATTCACATCTAAGGAACATTTTGACCTGCCATATGTGAACTGTCAAAAACAATACTT  
 mau-mkg-r2 AAAAAATTCACATCTAAGGAACATTTTGACCTGCCATATGTGAACTGTCAAAAACAATACTT  
  
 mau-mkg-r CTTTATTGAGACGTTACAAAGTGAGCTAGTAAGAAATCGTAGCTGTCACAGAAAAAAACC  
 mau-mkg-r2 CTTTATTGAGACGTTACAAAGTGAGCTAGTAAGAAATCGTAGCTGTCACAGAAAAAAACC  
  
 mau-mkg-r TGTCTACATTTTTTTGATTCTTCTTTTTGCGTAAATAAAAAA **ATG** TCGGCCTCTGCATCGG  
 mau-mkg-r2 TGTCTACATTTTTTTGATTCTTCTTTTTGCGTAAATAAAAAA **ATG** TCGGCCTCTGCATCGG  
  
 mau-mkg-r AATCAACTTCTCCGCTGGGGATGGTGACGGTAATCTTGTGCTTTGCATGGTATGCGGTG  
 mau-mkg-r2 AATCAACTTCTCCGCTGGGGATGGTGACGGTAATCTTGTGCTTTGCATGGTATGCGGTG  
  
 mau-mkg-r CCCCCTTCCAGAGTACGCAGGATTGCCCTTGCCCACGCGCTGCTCAAGCATGGCAGCAAGC  
 mau-mkg-r2 CCCCCTTCCAGAGTACGCAGGATTGCCCTTGCCCACGCGCTGCTCAAGCATGGCAGCAAGC  
  
 mau-mkg-r TCCAGAAGCAACTGCGAAAGCGATTGAACGCCATTACCACGATATTTAACAGCGCACAAA  
 mau-mkg-r2 TCCAGAAGCAACTGCGAAAGCGATTGAACGCCATTACCACGATATTTAACAGCGCACAAA  
  
 mau-mkg-r GCCAATCCGAACGCCATGAGCTGCGGGAGGCTCTCGAGAAGTCCAAGCCCGGGCGGGCACC  
 mau-mkg-r2 GCCAATCCGAACGCCATGAGCTGCGGGAGGCTCTCGAGAAGTCCAAGCCCGGGCGGGCACC  
  
 mau-mkg-r TGCGCACCGTATTGAATATCTTTGCTGTTGATCTCGAAAAGATGAAAACCTGCTTCGAGC  
 mau-mkg-r2 TGCGCACCGTATTGAATATCTTTGCTGTTGATCTCGAAAAGATGAAAACCTGCTTCGAGC  
  
 mau-mkg-r ACGTCCGCAACTGCATAGAGAAGGAGATGAAGGGCAAGGTTAGGGTGTTCGCCCTTTGGTT  
 mau-mkg-r2 ACGTCCGCAACTGCATAGAGAAGGAGATGAAGGGCAAGGTTAGGGTGTTCGCCCTTTGGTT  
  
 mau-mkg-r CACTGGTGACTGGTTTAGCATTGAAGGAGAGCGACCTGGATTTGTTTCTGGAGCCCAACG  
 mau-mkg-r2 CACTGGTGACTGGTTTAGCATTGAAGGAGAGCGACCTGGATTTGTTTATGGAGCCCAATG  
  
 mau-mkg-r GCAACCAGCCACCATTGTGCCATCAGTATCTATACAACAGGACTTCATACTTTTTACGAA  
 mau-mkg-r2 GCAACCAGCCACCATTGTGCCATCAGTATCTATACAACAGGACTTCATACTTTTTACGAA  
  
 mau-mkg-r GTTCCAAATGCTTTGCAGATGTGGTAACCATTGTCATGCCAGCGTGCCCATCATTAGAT  
 mau-mkg-r2 GTTCCAAATGCTTTGCAGATGTGGACACCATTGTCATGCCAGCGTGCCCATCATTAGAT  
  
 mau-mkg-r GTAAGCATCAGCTCACCGGACTGAACATAGACTTCAATATGTCAAATCCGAATGGCATAT  
 mau-mkg-r2 GTAAGCATCAGCTCACCGGACTGAACATAGACTTCAATATGTCAAATCCGAATGGCATAT

mau-mkg-r TTAACTCCCGATTTGTGGGCGAACTGATGCTTCGCAATGAGCGGATACGCGAGCTCAGCT  
 mau-mkg-r2 TTAACTCCCGATTTGTGGGCGAACTGATGCTTCGCAATGAGCGGATACGCGAGCTCAGCT  
  
 mau-mkg-r TATTTTTGAAAATCTGGGCCAAGAAGCTAAAATTGATTTGCAATGGCGGCATGACAAGCT  
 mau-mkg-r2 TATTTTTGAAAATCTGGGCCAAGAAGCTAAAATTGATTTGCAATGGCGGCATGACAAGCT  
  
 mau-mkg-r ATTGCTTAATATCCTTGATCATCGTAAACTTGCAAGTGAATCGAATAGTTCCATCCGTCA  
 mau-mkg-r2 ATTGCTTAATATCCTTGATCATCGTAAACTTGCAAGTGAATCGAATAGTTCCATCCGTCA  
  
 mau-mkg-r AACAGCTCCAGTCACTCTGTCCACCGGTTATTTTGTGCGGGCGTTAACTTTGCCTACAGCC  
 mau-mkg-r2 AACAGCTCCAGTCACTCTGTCCACCGGTTATTTTGTGCGGGCGTTAACTTTGCCTACAGCC  
  
 mau-mkg-r TGGACCTAACGCCGCCGATTACAGAACGGCTCACCACGCTGGATTTACTTAAAACTTCT  
 mau-mkg-r2 TGGACCTAACGCCGCCGATTACAGAACGGCTCACCACGCTGGATTTACTTAAAACTTCT  
  
 mau-mkg-r TCATATACTACAGCACTGTCAACTTTGACAAAAGTTTATTGAGTCCGTTTCTGGGCGGCT  
 mau-mkg-r2 TCATATACTACAGCACTGTCAACTTTGACAAAAGTTTATTGAGTCCGTTTCTGGGCGGCT  
  
 mau-mkg-r GTGTGGACAAGGAGACAACACTGGGCATACCAGGAGGATTTCCCGAGTACGATGAGCAAC  
 mau-mkg-r2 GTGTGGACAAGGAGACAACACTGGGCATACCAGGAGGATTTCCCGAGTACGATGAGCAAC  
  
 mau-mkg-r AGAAGCTCGTGCATGATGCAACAGGTGAGCCGCCACACGCTTCCAGCTGGATAGAGTTA  
 mau-mkg-r2 AGAAGCTCGTGCATGATGCAACAGGTGAGCCGCCACACGCTTCCAGCTGGATAGAGTTA  
  
 mau-mkg-r TGTGCGTACAGGATCCCTTCGAGCTGAACCGCAACGTGGCCAAATCAGTGTCCATTGCAA  
 mau-mkg-r2 TGTGCGTACAGGATCCCTTCGAGCTGAACCGCAACGTGGCCAAATCAGTGTCCATTGC-A  
  
 mau-mkg-r ATTTATTTTACTTTAGACAATGCCTAGTCCTGGCTGCTCAAGCATGCAGCGATCAGGAAC  
 mau-mkg-r2 ATTTATTTTACTTTAGACAATGCCTAGTCCTGGCTGCTCAAGCATGCAGCGATCAGGAAC  
  
 mau-mkg-r TAACTTCGCAACCAGAGAAGCTATACGACTACCTATTATTTGGCCTGGCGGATAAGTTAG  
 mau-mkg-r2 TAACTTCGCAACCAGAGAAGCTATACGACTACCTATTATTTGGCCTGGCGGATAAGTTAG  
  
 mau-mkg-r TAGCCGACAAGATAGTGGCAGATAAAAAGATGGCAGATTCAATGCCAAATTGAAAACAGAT  
 mau-mkg-r2 TAGCCGACAAGATAGTGGCAGATAAAAAGATGGCAGATTCAATGCCAAATTGAAAACAGAT  
 Stop Codon  
 mau-mkg-r CT TAA TGACTTACACTTTTCACACATTCAATTACTTGAATTTACAATATCACTATAGACT  
 mau-mkg-r2 CT TAA TGACTTACACTTTTCACACATTCAATTACTTGAATTTACAATATCACTATAGACT  
  
 mau-mkg-r AAACATAACACTAAACTAATAAACTAAACTAATAAAAGTTGACTAAACTTTTTCTTGGCA  
 mau-mkg-r2 AAACATAACACTAAACTAATAAACTAAACTAATAAAAGTTGACTAAACTTTTTCTTGGCA  
  
 mau-mkg-r AAAGTCTCTTGGAGCAGGGAGAAATATTTACAAGGGCAACAAAGCTTACTTAAATCATT  
 mau-mkg-r2 AAAGTCTCTTGGAGCAGGGAGAAATATTTACAAGGGCAACAAAGCTTACTTAAATCATT  
  
 mau-mkg-r TACAAGGTGTGTCTGAATAATAAAGAAGTTATAATTGATGGCCAGTTATCCAGCGCGTC  
 mau-mkg-r2 TACAAGGTGTGTCTGAATAATAAAGAAGTTATAATTGATGGCCAGTTATCCAGCGCGTC  
  
 mau-mkg-r TGAAGAAGGTCTGATCGTGACAGCGCCACTGTGGTTCAAAGCACTCATTAAAGATCCTGCG  
 mau-mkg-r2 TGAAGAAGGTCTGATCGTGACAGCGCCACTGTGGTTCAAAGCACTCATTAAAGATCCTGCG  
  
 mau-mkg-r TCTATTCTGCGAAAGAAGCTGCGCGAGCGAGTGTCCCTGTATCGGTGCCCAATTGGC  
 mau-mkg-r2 TCTATTCTGCGAAAGAAGCTGCGCGAGCGAGTGTCCCTGTATCGGTGCCCAATTGGC  
 3' breakpoint  
 mau-mkg-r GCTGCACGTGCCGCGCAAGACGCTGCCCTTCAGTTGGGTGGCAGCTGGAGGTCGATCG  
 mau-mkg-r2 GCTGCACGTGCCGCGCAAGACGCTGCCCTTCAGTTGGGTGGCAGCTGGAGGTCGATCG

## 2. CG3101/CG3101-r

sim-CG3101 -----  
 sim-CG3101-r AATGCAAATATGAAAATACCTTTCTGAGCTCGTAATTAATTTCCAATCGAACTGTAATA  
  
 sim-CG3101 -----  
 sim-CG3101-r AGAAATAGGAATTCTATTTTTAATCAATTTTATACGTTTTGGCAAAGCGGTTTTCTGAA  
**SAR\_DM SAR\_DM**  
 sim-CG3101 ----- AACATAATTGCCTGAATATG  
 sim-CG3101-r TTTCGGGCATAAAAATAATTAGTATTTTGGGCACAGCACAAAAAATATTTGTTCAAAATAAT  
 5' breakpoint  
 sim-CG3101 GAATGC CATAACATCGTTGAGCTCGTAATTAATTTCCAATCAAAGTGTGTTCAAACATGG  
 sim-CG3101-r GAAAGT CATAGCTCGTCGATATCGTTATTAATTTCCAATCAAAGTGTGTTCAAATAATG  
  
 sim-CG3101 ATATTCAAATTTTTTGCCATTTT-----  
 sim-CG3101-r AAATTCTAATTTTTTCGCCATTTTTTGCAAATTTTGATGATGTTACCCCTTACAAAAAATG

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sim-CG3101 -----
sim-CG3101-r CTAAAATTGATTCAAAAATTAATTTTCCTAAATTCCTTCAAAAAGTGATAGGGATCGTTAG

sim-CG3101 -----TTTTAGCCAA
sim-CG3101-r CAC TGGTAATTAGCTGCTCAAAACAGTTATTCCTTTCTTCTTATGAGCATTTTTAGCCAA

sim-CG3101 GTTATGGTGGGAACCCCTTCGAAAATAAATACGCATTTTATAAATAATTAAGGTAATTAAG
sim-CG3101-r GTTATGGTGGGAACCCCTCGAAAATAAATACGCATTTTATAAATAATTAAGGTAATTAAG

sim-CG3101 GTTTTTAAAGTAAAAGCTTCACAAATTTTTATTATAATTATAGGGGCGGTAAATGAAGTA
sim-CG3101-r GTTTTTAAAGTAAAAGCTTCACAAATTTTTATTATAATTATAGGGGCGGTAAATGAAGTA

sim-CG3101 GTAATTGTTCAAAGGATAACGCCTTAATTCGATTGCGTATGCAGATTGTAAAGTAGTCGA
sim-CG3101-r GTAATTGTTCAAAGGATAACGCCTTAATTCGATTTCGTATGCAGATTGTAAAGTAGTCGA

sim-CG3101 CTGAAATTCAAAAAATTCAGATCTAAGGAACATTTTGACCTGCCATATGAGAACTGTCA
sim-CG3101-r CTGAAATCTAAAAAATGCAGATCTAAGGAACATTTTGAC-----

sim-CG3101 AAACAATACTTCTTTATTGAGACGTTACAAAGTGAGCTAGTAAGAAATCGTAGCTGTCC
sim-CG3101-r -----CTTTATTGAGACGTTACAAAGTGAGCTA-TAAGAAATCGTAGCTGTCC
Exon4
sim-CG3101 AGAAAAAACCTGTCTAAATTTTTTGATTCTTGATG GCGGTTATACAGCGCTCTGAAG
sim-CG3101-r AAAAAAACCTGTCTAAATTTTTTGATTCTTGATG GCGGTTATACAGCGCTCTGAAG

sim-CG3101 AAGGTCTGATCGTGACAGCGCCACTGTGGTTCAAAGCACTCATTAAAGATCCTGCGTCTA
sim-CG3101-r AAGGTCTGATCGTGACAGCGCCACTGTGGTTCAAAGCACTCATTAAAGATCCTGCGTCTA

sim-CG3101 TTCGTGCGAAAGAAGCTGCGCGAGCGAGTGTACTGTATCGGTGCCTCAATTGGCGCTG
sim-CG3101-r TTCGTGCGAAAGAAGCTGCGCGAGCGAGTGTACTGTATCGGTGCCTCAATTGGCGCTG

sim-CG3101 CCCCTTCACTTGGGTGGCAGCTGGAGGTCGATCACGACACATCGTTGCTCAGCTGACGC
sim-CG3101-r CCCCTTCACTTGGGTGGCAGCTGGAGGTCGATCACGACACATCGTTGCTCAGCTGCCGC

sim-CG3101 CAATCGATGATGAATCGTGAGGACAAGCTGCTGGCCAATATCATGGATGTGAGCGATGGA
sim-CG3101-r CAATCGATGATGAATCGTGAGGACAAGCTGCTGGCCAATATCATGGATGTGAGCGATGGA

sim-CG3101 TCCGGATCCAGTTCAGAAACTGGATCAGAAATGTGTCCAACAGTCAAAAAGCCAGGATA
sim-CG3101-r TCCGGATCCAGTTCAGAAACTGGATCAGAAATGTGTCCAACAATAAAAAACCAGGATA

sim-CG3101 ATCAGCGCCGTCACCAGTTGGGCGATAATAATACCGCGGACAACAACAGAACCATCACG
sim-CG3101-r ATCAGCGCCGTCACCAGTTGGGCGATAATAATACCGCGGACAACAACAGAACCATCACG

sim-CG3101 TACGCCACCACAGCCTCTGGAGCAGCTAACGGCGCCACCACCAATGGGGGCAGACAGTTT
sim-CG3101-r TACGCCACCACAGCCTCTGGAGCAGCTAACGGCGCCACCACCAATGGGGGCAGACAGTTT

sim-CG3101 TTGAACCCGCCAGCAGCTCCTCATCCGACATGAGTATCGATGATAGTCTCGATGGTCAG
sim-CG3101-r TTGAACCCGCCAGCAGCTCCTCATCCGACATGAGTATCGATGATAGTACTGATGGTCAG

sim-CG3101 GAGGGCGATTCCAAGTCCATTATCAGATTGTCCAGATGATAAAGCAGGGCGGACTCCGT
sim-CG3101-r GAGGGCGATTCCAAGTCCATTATCAGATTGTCCAGATGGTGAAGCAGGGCGGACTCCGT

sim-CG3101 GGTCTGTTTGGAGGAGTACGCGGTCATTCGGAATAGGCCGCCGAGGGCACCTTCTGGCAT
sim-CG3101-r GGTCTGTTTGGAGGAGTACGCGGTCATTCGGAATAGGCCGCCGAGGGCACCTTCTGGCAT
Exon4
sim-CG3101 TCAAG GTAGGTCAAATGAAATCTTCATTCTAGATCACTGATAATTAACGTTCTTATATTC
sim-CG3101-r TCGAG GTAGGTCAAATGAAATCTTCATTCTAGACCACTGATAATTAACGTTCTTATATTC
Exon5
sim-CG3101 TCGCAG AATGCATGCCAATCTGACCAAGAATCGCTTCGCAGACGTCCTCTGCTACGATCA
sim-CG3101-r TCGCAG AATGCATGCCAATCTGACCAAGAATCGCTTCGCAGACGTCCTCTGCTACGATCA

sim-CG3101 AAATCGAGTGGTTCTGACACACGAAGACGGCGACGAGGCGTCGGATTACATAAATGCGAA
sim-CG3101-r AAATCGAGTGGTTCTGACACACGAAGACGGCGACGAGGCGTCGGATTACATAAATGCGAA
Exon5
sim-CG3101 CTTTCGTCGATGGCTACAAAGAAAATAGTGCCTATATAACAACCTCAAG GTAAGCGATGATG
sim-CG3101-r CTTTCGTCGATGGCTACAAAGAAAATAGTGCCTATATAACAACCTCAAG GTAAGCGATGGTG
Exon6
sim-CG3101 ACACACTAAATCATATGCATAAACTATATGCTAATGGAGTTAACTCCGCCAG GTCCATTA
sim-CG3101-r ACACACTAATCATATGCATAAACTATATGCTAATGGAGTTAACTCCGCCAG GTCCATTA

sim-CG3101 CCAAACACATGCAAGGACTTTTGGCGCATGATCTGGGAACAACATTGTTTACTTATAGTG
sim-CG3101-r CCAAACACATGCAAGGACTTTTGGCGCATGATCTGGGAACAACATTGTTTACTTATAGTG

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sim-CG3101 CATTGGTAATTAGCTGCTCAAAACAGTTATTCTTACATCTATATGACAATTTTCAGCCAA  
sim-CG3101-r CATTGGTAATTAGCTGCTCAAAACAGTTATTCTTTCATCTTTATGACAATTTTCAGCGAA

sim-CG3101 GATATGACGAAAATTCCGTTTGTAAATTAACACGTTTTTGGCAAAGCGGTTTTTCCGAAT  
sim-CG3101-r GGTATGACCATAATTCCATTTGTAATATCAAGTTTTTGGCAAAGCTGTTTTTCCGAAT

sim-CG3101 TTCCGGTAGTCAAATAATCAGTTTTTCCGACACAACCTGAAATTTAATTGTCCAAATCTGG  
sim-CG3101-r TTCCGGTAGTCAACTAATCAGATTTTTTCGACACAACCTTAAAAATAATTGTCCAAATATGA

sim-CG3101 AATGCTATACCTCGCTGAACTTGTAAATTAATTTCCAATCAAACCTGTGTTCAAAAATGCA  
sim-CG3101-r AATGCCATATCTCGTTGTGTTGTAATTAATTTCCAATCGAACTGTATCCACAAATGGA

sim-CG3101 AATTCATTTTTTCCCATTTTTTGCAAATTTTGATGATGTTACCCCTTACAAAAAATGC  
sim-CG3101-r AATTCATTTTTTGGCAATTTTTTGCAAATTTTGATGATGTTACCCCTTACAAAAAATGC

sim-CG3101 AAAAATTCACCCAAAAATTAATTTTCTAAATTTCTTCAAAAAGTGATAGGGATTGTTAGC  
sim-CG3101-r AAAAATTCACCCAAAAATTAATTTTCTAAATTTCTTCAAAAAGTGATAGGGATCGTTAGC

sim-CG3101 ACTGGTAATTAGCTGCTCAAAACAGTTATTCTTCTTCATTATGAGCATT 3'breakpoint  
sim-CG3101-r ATTGGTAATTAGCTGCTCAAAACAGTTATTCTTTCATCTTTATGAGCATT -----

sim-CG3101 TTATGACTAAAATTCATTCGAAAAGTTTTGGATTTTTCGAAAATCTGGATCCAAAATCC  
sim-CG3101-r -----

sim-CG3101 GTAATCTGGATTGCAAACCTGTCCAAATCTGGATTGCATTCCCTCGTTGAGCTTGTATT  
sim-CG3101-r -----

sim-CG3101 AAA  
sim-CG3101-r ---

### 3. kep1/CG3875

mel-kep1 -----  
mel-CG3875 GGAAGCGTTCCGACCATATTAAGTATATTCTTGATATATTATATGAATATCTTAA  
**DNAREP1\_DM**

mel-kep1 -----  
mel-CG3875 TTAGATATATTCTTGATCAGAATCAATATCAACTGTCTGCTCTCTGTAGGAACGTCGAG

mel-kep1 -----  
mel-CG3875 ATCCAGAAACTATAAAAGCTACAATGTTGAGATAAGGGTCACAGCTTCCCGAGACATAG

mel-kep1 -----  
mel-CG3875 TCCGAGCCTTTGTTGAACCATGTACCACGCCACTCTAACGCCACAAACATAATGGGCA  
5'breakpoint

mel-kep1 --  
mel-CG3875 CGACATTTAAACAATCACTATTGAATTAATAAGTTGGCAGCCCGAAAACCTCACACG  
AC CGACATTTAAACAATCACTATAGCACTGAAAAAGCTGACAACCT-CAAACCTCATACG  
Transcription Start Position

mel-kep1 CTTGGC |  
mel-CG3875 AGCTCTGCCATTATTTAGTTTCATTGGTGTACATACTGTTTTTCAGTCTACACC  
TTTGGC | AGCTCGGCCAGCATTTTCAGTTTCATTGATATACAGAACATTGTTTCAGTCTACATC  
Start Codon

mel-kep1 -ATTTTTAATTGT-AATTTTCTGTAAGATTGTT |  
mel-CG3875 ATG ATAAAAATGGAAACCCCAAGCGA  
AATTTTGAATTGTGAATATTCGGTAAAGATTAT | GTG ATAAAAATGGAAACCCCAAGCGA

mel-kep1 GTTTACTGAGAAACAG-----CCACCCACCCACGATC-----ACCAGCCGCG  
mel-CG3875 GTTTACTGAGGAACAGAACCAAGACCAACCCACCCAGGACCAACCTACCTACCAGCCGCG

mel-kep1 TCTTAACGAGGTGGCCAAAAGTTTCTCGCCGATTTGGACGAGGAGCGCCAGCGATTGTC  
mel-CG3875 TCTGAACGAGGTGGCCAAAAGTTTCTCGCCGATTTGGACGAGGAGCGCAAGCGATTGTC

Exon1  
mel-kep1 CGCGGACTTTCCACTTTGCGCACTGCTAATCGACGAA |  
mel-CG3875 CGCGGAGTTTCCACTTTGCGCTCTGCTAATCGACGAA | GTAAAAATCAATTTGGCCCTTTT  
GTAAAAATCAATTTGGCTC-TTT

Exon2  
mel-kep1 ACAGGGTATTTTAATGGTACTAATCCCAATATTCGAC |  
mel-CG3875 ACAGGGTATTTTAATGGTACTTATCCCAATATTCGAC | CTGTGGACCGTGTCTACTGCACT  
CTGTGGACCGTGTCTTCTCCACT

mel-kep1 GGTCGTATTTCCCGGAAAAGAGTTTCTACGCAGACGTGTACAAGCAGAAGCCGATGAAGATT  
mel-CG3875 GGTCGTATTTCCCGGAAAAGAGTTTCTACGCAGACGTGTACCACCAGAGGCCGATGAAGATT

Exon2  
mel-kep1 ACCCAAAAGGTCTTCGTGCCCGTAAAGCAGTATCCCAAG |  
mel-CG3875 ACCCAAAAGGTCTTCGTGCCCGTAAATAAGTTTCCCAAG | GTGGG-TTTATAACAATTAGCT  
GTGGGTTTACACAATTAGTT

Exon3  
mel-kep1 GTCTCTCCGTTTCGAAAATAAATCCGTACCCTTGCGCAG |  
mel-CG3875 GTCTCTCCGTTTCGAAAATAAATCCGTACCCTTGCGCAG | TCAACTTCACTGGCAAGAT

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mel-CG3875      GTCCCTCCGTCGGCAAATAAAATCCGTACCCTTGCGCAG TTCAACTTCGCTCGGAAGAT
mel-kep1        CCTGGGGCCCAAGGGCAATTCGCTGCGTCGCCCTCAGGAGGAGACCCAGTGCAAGATTGC
mel-CG3875      CCTGGGGCCCAAGGGGAACTCGGTGCGTCGCCCTAAAGGAGGAGACCAACTGCAAGATTGT
mel-kep1        CATTAAAGGGTCGCAGTTCGATCCGCGATCGTAACAAAGAAGAGCAGCTGCGCAGCACAGG
mel-CG3875      CATCAAGGGTCGCAGCTCGATGCGCGATCGTAACAAAGAGGAGGAGCTGCGCAGCTCAGG
mel-kep1        CGACCCGAGATATGCTCATCTTCAGAAGGACCTATTTTTGGAGGTCAGCACGGTGGCCAC
mel-CG3875      CGACCCGAGATATGCCCATCTTCACAAGGATCTCTTTTTGGAGGTCAGCGCGGTGGCCCC
mel-kep1        TCCGGCGGAGTGCTATGCCCGCATAGCCTACGCTCTGGCCGAGATCCGTAAGTATCTTAT
mel-CG3875      TCCGGCGGAGTGCTATGCACGGATAGCCTACGCCCTGGCCGAGATCCGTAAGTACCTCAT
mel-kep1        TCCAGACAAGAACGACGAGGTTTACACGAACAGCTGCGCGAGCTGATGGAAATGGATCC
mel-CG3875      TCCAGACGACAACGACGATGTTTGGCACGAGCAGCAGCGCGAGCTGATGGAAATGAATCC
mel-kep1        CGAGTCAGCCAAAAACATTCACGGACCGAATCTGGAGGCCTACAG GTA-----ATCTTA
mel-CG3875      CGAGTCGGCCAAGAAAAGTAACGGACTCAATATGGCGCCTACAG GTAATGGTCATCTTA
mel-kep1        CACCCTATGCA-----
mel-CG3875      TTCTCTCTGCATACCGATGCAACTTGACTTACTTGACAAGCAAGTTAAGCATGTGGTATC
mel-kep1        -----GCCTTTGGGCATGAGAATAAAAAATA---TATTATTTTGCAG ATCTGTCTTC
mel-CG3875      CATCTGCTTGCCATTGGGCA-AAGGGTAAAAATCCATTGTTATTTTGCAG ATCGATCTTC
mel-kep1        GACAAGAAGTTTGGAGGCAACAGCAATGGGGCTCCCAAATACATCAACCTGATTAAGAGA
mel-CG3875      GACAAGACGATTGGAGGCAACAGGAATGGGGCTCCCAAGTACAACAACCAGATTAGGCGA
mel-kep1        GCTGCGGAAAATCCGCCCGA GTAAGTTACTTGTAAAGTATAATTTTGTATTATTTAATGA
mel-CG3875      GTTACGGAAAATCCGCGCGA GTAAGTTACTTGTAAAGTATAATTTTGTATCATTTAATGA
mel-kep1        CCCCACCAGGAGTAATGGAACCGAGAGTCCTCGCGTCATAGTAGTGCCTTAAATCCTAGC
mel-CG3875      CCAAACCAGGAGTTA-----CCGCGTCCTAGTAGTTCCTTAAATCCTAGC
mel-kep1        CAACATCTGTAAACCCAGCAATTAACATTTTCATTTTATAG AGTCGACGATGTGGAGGA
mel-CG3875      CAACATGCGTTGAGCCAGCAACTAACATTTTCATCTTTATAG AGTCGCCGATATGGAGGA
mel-kep1        GGTGGCCTATGAGT---ATGAACATCGTATGCCCCCAAGCGTCCGCCTACGGGCTATGA
mel-CG3875      GGTGGAATATGATTATGATGAACATCGTATGCCCCCAGTCGTCGGTCTTTGGGCTTTGA
mel-kep1        GTACAGCAAAAC GTAAGTTAATCCCAAGCATGCATTCTTTATTTGGGTAGTGCCGGGGTCT
mel-CG3875      GTATAGCAAAAC GTAAGT-----
mel-kep1        ATGACATAAGATCGATTTTTTCCCTGAATGCACCAGTTTTTTGGGATGCACCTTTGACAG
mel-CG3875      -----
mel-kep1        GAACTTTGGGTTATAGATTAGATTAGATCATACTATCAAACCAATAACTGTGATTGAGC
mel-CG3875      -----GTT-----ATTAGATTATAATATCAAATCAATAATCG-----
mel-kep1        AAGCTCTCAGATCAAATAATAATACTACTGGAATGATTAATATTATGCAACGATTCACT
mel-CG3875      -----AAGCTATGTAATATACTAGAAATGAATAATATTATGAAACTAATAAAT
mel-kep1        CCTTTATAGTAATTACATACACGCATAAAATACTACAAATAATAATCAACCAATTTTATA
mel-CG3875      AAATAATAAATAATAATAATAATAATAATCAATACAAATAATAATCAACCAATTTTATA
mel-kep1        G CACGTCCATCAATAATACCGACAAACGCGGCGCATATAAACG-----TCCATATCCG
mel-CG3875      G CACCTCCATCAATGACAGCGACAAACGCTACGCCATTTAAACGTGCATATCCGTATCCG
mel-kep1        ACTGACATGAAACGTATGCGCGAACCGCCCATCAAGTCCTATAAGCCCAATCCGTATACA
mel-CG3875      ACTGACATGAATCGTAGCGCGAACCGCCCATCAAGTCATATAAGCCCAATCCGTATACA
mel-kep1        ATACTTAAAAA-ATATAAA TAA TAGAGCTCCGGTTGATTTTCGTCGCACACCGCTATAAA
mel-CG3875      ATACTTAACAAATATATAAA TAA TAGAGCGCCAAGTGATTTTCGTCGCACAACCGCTATAAT
mel-kep1        TGAAAACAAAGGACAATGCTTACGTTATAAAATCCATGCT-GGGAGCACATTGAAAATAC
mel-CG3875      TGAAAACAAAGGACAATGCTTACGTTGTAATAATCCATGCCGGGGAACTCATGGAA-----
mel-kep1        TTTAATCAAGAAGAAAGCAGCATTCAAAATGATGCTATCAATTAATAAACATTAATATTT
mel-CG3875      -----AAGAAGAAAGCAGCATTCAAAATGATGCTATCAATGAATAAA-----TT
mel-kep1        ATAAAACGCGCACTTGCGCTATCAATTCCACAAACAATATTAATCTTAAATTTGTATAT

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mel-CG4021      TTCAGCCTACATCAATTTTAAATTGTGATTTTTTCGCTAAAGATTGTT ATGGAATAAATGGA
mel-kep1       AACCCCAAGCGAGTTTACTGAGAAACAGCCACCACC---CACGATCACCAGCCGCGTCT
mel-CG4021     AAACCCCAAGCGAGATTACTGAGGAACAGCCAACCTACCACACACGAGTACCAGCCGCGTCT

mel-kep1       TAACGAGGTGGCCAAAAGTTTTCTCGCCGATTTGGACGAGGAGCGCCAGCGATTGTCCGC
mel-CG4021     GAACGAGATAGCCAAAAGTTTTCTCGCCGATTTGGACGAGGAGCGCCAGCGTTTGTCCGC

                                Exon1
mel-kep1       GGACTTTCCTACTTTGCGCACTGCTAATCGACGAGG GTAAAATCAATTTGGCCCTTTTACA
mel-CG4021     GGAGTTTCCACTTTGCGCACTGCTAATCGACGAGG GTAAAATCAATTCGTCCC-TTTACA

                                Exon2
mel-kep1       GGG-TATTTTAAATGGTACTAATCCCAATATTGCAG GTGGGACCGTGTCTACTGCACTG
mel-CG4021     GGGTATATTTTATTTGGTACTAATCCCAA-ATTGCAG CTAGGGACCGTGTCTACGCCACTG

mel-kep1       GTCGTATTCCCAGAAAAGAGTTCTACGCAGACGTGTACAAGCAGAAGCCGATGAAGATTA
mel-CG4021     GTCGTATTCCCAGCAAGGAACCTACGCAGACGTGTACCGGCAGAAGCCGATGAAGATTA

                                Exon2
mel-kep1       CCCAAAAGGTCTTCGTGCCCGTAAAGCAGTATCCCAA GTGGG-TTTATACAATTAGCTG
mel-CG4021     TTCAAAAGGTCTTCGTGCCCGTTAACCCAGTATCCCAA GTGGGTTTTATACAATTAAGT

                                Exon3
mel-kep1       TCCTTCCGTTTCGAAAAATAAATCCGTACCCTTGCGCAG TTCAACTTCCTGGCAAGATC
mel-CG4021     TCCCCTATGTCCGCAAAAATAAATCCGTACCCTTGCGCAG TTCAACTTCCTGGCAAGATC

mel-kep1       CTGGGGCCCAAGGGCAATTCGCTGCGTTCGCTTCAGGAGGAGACCCAGTGAAGATTGCC
mel-CG4021     CTGGGGCCCAAGGGGAACCTCGCTGCGTTCGCTTCAGGAGGAGACCCAGTGAAGATTGCC

mel-kep1       ATTAAGGGTTCGAGTTCGATCCGCGATCGTAACAAAAGAGCAGCTGCGCAGCACAGGC
mel-CG4021     CTCAAGGGTTCGAGTTCGATGCGCGATCGTAACAAAAGAGGAAGAGCTGCGCA-----GC

mel-kep1       GACCCGAGATATGCTCATCTTCAGAAGGACCTATTTTTGGAGGTCAGCACGGTGGCCACT
mel-CG4021     GACCCAAGATATGCCCATCTTCAGAAGAATCTTTCTGGAGGTCAGCACGGTGGCCATA

mel-kep1       CCGGCGGAGTGCTATGCCCGCATAGCCTACGCTTGCCGAGATCCGTAAGTATCTTATT
mel-CG4021     CCGGCGGAGTGCCATTTCCCGCATAGCCTACGCTTGCCGAGATTCGTAAGTATCTGATT

mel-kep1       CCAGACAAGAACGACGAGGTTTCACACGAACAGCTGCGCGAGCTGATGGAATGGATCCC
mel-CG4021     CCAGACAATAACGACGAGGTTTCGACGAGCAGCTGCGCGAGCTGATGGAATAGATCCC

                                Exon3
mel-kep1       GAGTCAGCCAAAACATTACGCGACCGAATCTGGAGGCCTACAG GTA-----ATCTTAC
mel-CG4021     GAGTCGCGCAAGAACTTTAAGGGACTCAATCTGGAGGCGTACAG GTAATACCGATCTGAT

mel-kep1       ACCCT-----ATGCAGCCTTTGGGCATGA-----GAATAAAAAATATATTAT
mel-CG4021     ATCCTTCGCTTGCCATTAGTACAATTTTAAAGTCTAGATTAATTAATAAAAAATCTATTAT

                                Exon4
mel-kep1       TTTGCAGTATCTGTCTTCGACAAGAAGTTTGGAGGCAACAGCAATGGGGCTCCCAAATACA
mel-CG4021     TTTGCAGTATCTGTCTTCGACAAGAAGTTTGGAGGCAACAGCAATGGGGCTCTAAGTACA

                                Exon4
mel-kep1       TCAACCTGATTAAGAGAGCTGCGGAAAATCCGCCCCA GTAAGTACTTGTAAAGTATAAT
mel-CG4021     TCAATCTGATTAAGCGGGTTGCGGAAAATCCGTCCAA GTAAGTACTT-----GTATAAT

mel-kep1       TTTGTATTATTTAATGACCCACCAGGAGTAATGGAACCGAGAGTCTCGCGTCATAGTA
mel-CG4021     TATGTATCATTTAATGACACCAATAG-----GTATCCCCGCTCCAAGTA

                                Exon5
mel-kep1       GTGCCTTAAATCCTAGCCAACATCTGTTAACCAGCAATTAACATTTTCATTTTATAGT A
mel-CG4021     GTTCCTTGAATCCTAG-----TCAGCAACTAACATTTTCATCTTTATAGT A

mel-kep1       GTCGACGATGTGGAGGAGGTGGCCTATGAGT---ATGAACATCGTATGCCCCCAAGCGT
mel-CG4021     GTCGCGGATATGGAGCAGGTGGACTATGATTATGATGAACATCATATGCCCCCAATTCAT

                                Exon5
mel-kep1       CCGCCTACGGGCTATGAGTACAGCAAAA GTAAGTAAATCCCAAGCATGCATTCTTTATTT
mel-CG4021     CTGCCACGGGCTATGAGTACAGCATAC GTAAGT-----GTG-----TT

mel-kep1       GGGTAGTGCC---GGGGTCTATGACATAAGATCGATTTTTCCCTGAATGCACCAGTTTTT
mel-CG4021     TGGTAGTGCTTGGGGTCTATTACA-----

mel-kep1       TGGGATGCACCTTTGACAGGAACCTTGGGTTATAGATTAGATTAGATCATACTATCAAAA
mel-CG4021     -----

mel-kep1       CCAATAACTGTGATTGAGCAAGCTCTCAGATCAAATATATAACTGGAATGATTTAA
mel-CG4021     --AATAA-----

mel-kep1       TATTATGCAACGATTCACCTTTATAGTAATTACATACACGCATAAAATACTACAAATA

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mel-CG4021 -----ATTACAAATA
mel-kep1      Exon6
mel-CG4021    ATAATCAACCAATTTTATAG CACGTCCATCAATAATACCGACAAACGCAGCGCATATAA
mel-kep1      ACGTCCA-----TATCCGACTGACATGAAACGTATGCGCGAACCGCCCATCAAAGTCTA
mel-CG4021    ACGTCCATATCCGTATCCGACTGACATGAAACCTGTGCGCGAACCGCCCATAAAAGTTCTA
mel-kep1      Stop Codon
mel-CG4021    TAAGCCCAATCCGTATACAATACTTAAAAAATATAAA TAA TAGAGCTCCGGTTGATTTCG
mel-kep1      TCGCACACCGCTATAAATGAAAAACAAGGACAATGCTTACGTTATAAAATCCATGCTGGG
mel-CG4021    -----GGCACCTACGTTATGAAATCTATGCTTGG
mel-kep1      AGCACATTGAAAATACTTTAATCAAGAAGAAAGCAGCATTCAAAATGATGCTATCAATTA
mel-CG4021    AGCACAGT-----AAGAAAGCTGCATTCAAAATGATGCTATCAATGA
mel-kep1      3' breakpoint
mel-CG4021    ATAAACATTAATATTTATA
mel-kep1      -----
mel-CG4021    CTTTCCTTACTTCGTAAAAAACGTTAATAAAATGATACGTATACCC AAAATAATAACTAA
DNAREP1_DM
mel-kep1      -----
mel-CG4021    TATATAACATTTTTCAAAGTGTGGCGTGGCAGTTCTGGACGGTTGGGTGCCTTGGAG
mel-kep1      -----
mel-CG4021    TGGGCGTGGCAACATGAATTAAAAAAATTGCGCTTCGTCTATAGTTAAACGCTTCCTTC
mel-kep1      -----
mel-CG4021    TGCCTGTTACATACTTCCAACGAACGGGTATAACTATTATTACTC
6. kep1/CR9337
sch-kep1      -----
sch-CR9337    TTATACCGTTACTCGTAGATTAAGGGTATACTAGATTCCTTTAAAGTATGTAAGG
DNAREP1_DM
sch-kep1      -----
sch-CR9337    TATATGTAAGTATATATATTTCTTCAGAATCGATGTCTGTCCTTCCGTATGAACGTTGA
sch-kep1      -----
sch-CR9337    GATGCCAGGAACATATAAAGATAGAAGGTAACGATTAGGAACACAGATTCTAGAGACATA
sch-kep1      -----
sch-CR9337    GATGCAGCGCAAGTTTGTGAACCGTGTCCCATGCTCTAACTCTAACGCCACAAAGCGC
sch-kep1      -----
sch-CR9337    CCAAACCTGACACGCCACAACACTATATCTAATTTTTCATTTTATTATTTTGTTCAC
sch-kep1      -----
sch-CR9337    TTTCTACCGGTATTCAAAATATATTAATAATCTCGTTTGGAAATAAACTGGAGAATCT
sch-kep1      -----
sch-CR9337    CGACTATAGCATTCATGTTTTTAATCTGATGGGTAAGTAGCCTAAGTGTACCAGAGACCA
sch-kep1      -----
sch-CR9337    TGGTGGTGTTCAGTTTCTGCACATAATGGGATACCCGACATTTAAACAATCAGTTTTCAGC
5' breakpoint      Transcription Start Position
sch-kep1      -----
sch-CR9337    ACTGAAAAATATGCCTC AAAACTTCATACGGTTGAC AGCTCTGGCACCATTTTAGTTCAT
sch-kep1      TGATATACATACTGTTTTTCAGTCTAC----GTTTTAATTGTAATTTTTCGGTAAGGATT
sch-CR9337    TGATATACAAAGCGTTATTCAGTCTACATCAATTTTAATTGTGATTTTTTGGTAAAGATT
sch-kep1      Start Codon
sch-CR9337    GTT ATG ATAAAAATGGAACCCCAAGCGAGTTTGTGAGAAGCAGCCTCCTACCCACGAC
sch-kep1      GTT ACG ATAAAAATGGAACCTCAAGCGAGTTAACTGAGAAAGAGCCACTTACCCACGAC
sch-kep1      CACCAGCCGCGTCTGAACGAGGTGGCCAAAAGTTTCTGGCCGATTTGGACGAGGAGCGC
sch-CR9337    CACCAGCCGCGTCTGAACGAGGTGGCCAAAAGTTTCTGGCCGATTTGGACGAGGAGCGC
sch-kep1      Exon1
sch-CR9337    CAGCGATTGTCCGCGGACTTTCCACTTTGCGCACTGCTAATCGACGAG GTAAAAATCAAT
AAGCGATTGTCCGCGGAGTTTCCACTTTGCGCACTGCTAATCGCCGAGG GTAAAAATCAAT
Exon2

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sch-kep1 TCGGCTCTTTACAGGGTATATTAATGGTACTAATCCCACATTGCAG CTGTGGACCGCGTC  
sch-CR9337 TCGGTCCTTTACAGGGTATTTTAATAGTACTAATCCCACATTGCAG CTGTGGACCGGTGC

sch-kep1 TACTGCACTGGTCGTATTCCCGGCAAGGAGTTCTACGCAGACGTGTACAAGCAGAAGCCG  
sch-CR9337 TACGGCACTGGCCGTATTCCCGGCAAGGAGTTATACGCAGACGTGTACAACCAAAAGCCG

sch-kep1 ATGAAGATTACACAAAAGGTATTCGTGCCCGTAAAGCAGTATCCCAAG GTGGGTTTTATA  
sch-CR9337 ATGAAGATTACCAAAACGGTCTTTGTGCCCGTAAATCAGTATCCCAAG GTGGGTTTTGAA

sch-kep1 CAATTAAGTGTCCCTCCGTCCCCAAAATAAATCCGTATCCTTGCGCAG TTCAACTTCAC  
sch-CR9337 CAATTAGCTGTCCATCCCGTCCGCAAAATGAATCCTTACCCTTGCGCAG TTCAACTTCAT

sch-kep1 TGGCAAGATCCTGGGGCCCAAGGGCAACTCGCTGCGTCGCCTTCAGGAGGAGACCCAGTG  
sch-CR9337 TGGCAAGATCCTGGGGCCCAAGGGGAAGTTCGTGCGTCGCCTTCAGGAGGAGACCCAGTG

sch-kep1 CAAGATTGCCATTAAGGGTTCGCGTTTCGATCCGCGATCGTAACAAAGAGGAGCAGCTGCG  
sch-CR9337 CAAGATTGCCATCAAGGGTTCGCGTTTCGATGCGCGATCGTAACAAAGAGGAGCAGTTGCG

sch-kep1 CAGCACAGGCGATCCGAGATATGCCCATCTTCAGAAGGATCTATTCCTGGAGGTCAGCAC  
sch-CR9337 CAGCACAGGTGACCCGAGATATGCCCATCTTCAGAAGAATCTCTTTCTGGAGGTCAGCAC

sch-kep1 GGTGGCCACTCCGGCGGAGTGCATGCCCCGATAGCTTACGCCCTGGCCGAGATCCGTAA  
sch-CR9337 GGTGGCAACCCGGCGGAGTGCATGTCCGCATAGCCTACGCCCTGGCCGAGATCCGTAA

sch-kep1 GTATCTTATTCCAGACAAGAACGACGAGGTTTCGCACGAGCAGCTGCGCGAGCTGATGGA  
sch-CR9337 GTATCTTATTCCAGACAAGAACGACGCGGTTTCGCACGAGCAGCTGCGCGTGTGAAGGA

sch-kep1 AATGGATCCCGAGTCGGCCAAAACATTACGGACCC---AATCTGGAGGCTTACAG GTA  
sch-CR9337 AATGGATCCCGAGTCGGCCAAAACAGTAACGGACTCTGGAGTCTGGAGGCTACAG GTA

sch-kep1 AGGGGGATGTTTTACCCTATGCATACCGATGCGGTTTGCCT-----TTGG  
sch-CR9337 ATGGGGAT-----CCCTCTGCATACCGATGTAACCTGACTTACTTGACAAGCGAGTTGA

sch-kep1 GCAT-----AAGAATAAAAAATGTA---TTATTTTGCA  
sch-CR9337 GCATGTGGTATACAAAGGCTTGATATTGGGCAAGGAGTAAAAATCTATTGTTATTTTGCA

sch-kep1 GATCTGTCTTCGACAAGAAATTTGGAGGCAACAGCAATGGGGCTCCCAAGTATATCAACC  
sch-CR9337 GATCTGTCTTCGACAAGAAATTTGGAGGCAACAGCAATGGGGCTCTCACGTACATCAACC

sch-kep1 TGATTAAGCGAGCTGCGGAAAATCCGCCG GTAAGTTACTTGTAAGTATAAATTTTGTA  
sch-CR9337 CGATTAAGCGAGTTGCGGAAAATCCACCCG GTAAGTTACTTGTAAGTATAAATTTTGTA

sch-kep1 TAATTTAATGACCCACCAGGAGTTATGGACCTGAGAGTCCCTCGCGTTATAGTAGTGCA  
sch-CR9337 TCATTTAATGTCC-----TTGTTCTTTGAATCCTACC-----CA

sch-kep1 ATATGTGTTAACCCAGCAACTAACATTTTCGATCTTTATAAGTTCGACGATGTGGAGGAGG  
sch-CR9337 ACATGCGTTGAGCCAGCAACTAACATTTTCGATCTTTATAAGTTCGACGATGTGGAGGAGG

sch-kep1 TGGCCTATGAGTATGAACATCGTATGCCCCCAAGCGTCCCTACTGGCTATGAGTACA  
sch-CR9337 TGGTCTATG-----ATCTTATGCCCCCAGTCATCCGCCCTACGAGCTATGAGTACA

sch-kep1 GCAAAAGTGAAGTTGATCCCAAGCATGCATTCCTTTATTTGGGTAGTGCCGGGGTCTATAAA  
sch-CR9337 GGAACGTAAG-----TATTT-GGTAGTGCCGGGGTCCAT-TA

sch-kep1 CATAATATAGATTTCCCCCTAAAGGCACTTCGCCAGTTTTTGGGGATTTGGGTTATAGAT  
sch-CR9337 CATAAGATTGTTTT---ATGGGATGCATCT-----TTGACGGGAAGTTGGGATTTAGAT

sch-kep1 TAGATCATACTATCAA----AACCAATAACAGTGATTGAGCAAGCTCTCAGATCAAAC  
sch-CR9337 ACGAT--TATTATCGAGTATTAAGTACAACAGTGAATGATCAAGATCTCAGATCAAAC

sch-kep1 ATATAATACACTGGAATGAT-----TAATATTATGCAACGATTCACCTCTTTATAGT  
sch-CR9337 ATATAATACACTACAATGACTAATATTATAATATTATACAACGATTAACCTCTTTATAGT

sch-kep1 AATTACATACACGCATAAATTACTACAATAATAATCAACCAATTTTATAAG CACGTCCAT  
sch-CR9337 AATTACATACACGCATAAATTACTACTAATAATAATCAACCAATTTTATAAG CATTTCAT

sch-kep1 CAATAATACCGACAAACGCTGCGGCATATAAACGTCCATATCCG-----ACTGACATGA  
sch-CR9337 TAAAAATACCGAAAACGAGTGGCATATAAACGTCCATATCCGTATCTTACTGACATGA

sch-kep1 AACGTATGCGCGAACCGCCCATCAAGTCCATAAGCCCAATCCGTATACAATACTTAAAA  
sch-CR9337 AATTTATGCGCGAACCGCCCATCAAGAAGTTTAAAGCCCAATCCTTTTA-----AACG

Stop Codon

sch-kep1 AATATAAA **TAA** TAGAGCTCCGGTTGATTTTCGTCGCACACCGCTATAAATGAAAACAAAGG  
sch-CR9337 GACTTAAG TTA -----

sch-kep1 ACAATGCTTAAAAATCCATGCTGGGAGCACATTGAAAATACTTTAATCAAGAAGAAAGCAG  
sch-CR9337 -----TAAAATCCATGATGGGAGCACATTGAAAATACTTTAAACAAGATGGAAGCAG

sch-kep1 CATTCAAAATGATGCTATCAATGAATAAACATTAACATTTATAAAAACGCGCACTTGCGCT  
sch-CR9337 ATTTCAA-----AATGAATAAATATTAACATTTATAAAAACCGCACTTGCGCT

sch-kep1 ATCAATTTCCACAAACAATATTAACCTTAAATTTTATTCCCATAAATATGTTAAACTGT  
sch-CR9337 ATCAAATCCTACAAACAATATTAATCTTAATTATTTATTTCCCTAATTATGTTGAGCTGT

sch-kep1 TGGCATGCCTTTTCTGGACCATTCAACAGATAATAAGTCAAATAATTCCTATTATGTTT  
sch-CR9337 TGGCATG-----CCCATTATGTTT

sch-kep1 AAATTATGATTTCTGAGTTCGTAATTTT---TTATGAATTAATAAATGTAATAAAAGG  
sch-CR9337 AAATTAAAA--TCCTGCGTTTGTAAATTTTCTATTATAAATTAACAC--TAATAAATA  
Polyadenylation Site

sch-kep1 ATACGCATTGAATGAATTTAATAAATTTCTCAGCAATCACTCTCTAACTATGCCCGATTCTT  
sch-CR9337 AAACATCATTGAAT--ATTTTATAAATTT-----CAATCCGA TCTAATTATGCCCG-----

sch-kep1 TTAATGACTCGACCCCTCATTATAATGAATA--TGCATTACGTAATTAACAATTGT  
sch-CR9337 -----ATTTACAATCAATATTTGCATTACCTAATTAACAATTAA

sch-kep1 CTCCTAGCAGTAGAATCAAG--AGTTATATATCTAATAAATAAAAACGGTACGAACTTA  
sch-CR9337 CATACTAGCATTAAAAAGTTAGCTAGTTATATTTCTAA-AAAATGAATTGA-----

sch-kep1 TCACATTGTTTAAATCAAAAAAAAAAAAAACGAAATGAAGATTACATCAAGACATTTAAGTG  
sch-CR9337 --ACATCCTTTTATC-----AGATGAATCAAAGTGAAGATCGCATCAAGATACTTAAGTG

sch-kep1 CGTCTAAAAATAAGTTAATAACAATTATAAATTTATAAATGAACAAAAAAGAACATTG  
sch-CR9337 CTTTTAAAAATAATTTATAATCCATCATAATTTATAAATGAAC-AAGAGAGAACAATA  
3' breakpoint

sch-kep1 AATAAACATATAAAGAGTTTGCATAACTAAAATATTTTCAGGTTTTT-----  
sch-CR9337 AATAAACATATAAAGAGTTTGCATAACTAAAATATTTTCAGGTTTTT AGGCAAAGTATTA

sch-kep1 -----  
sch-CR9337 ATTTGTATACCCGTTAGTCGCAAAGTAAAAGGGTCTACCAGATTTCGTTGAAACTATGTA  
**DNAREP1\_DM**

sch-kep1 -----  
sch-CR9337 ACTGGTAGAAGAAAGCGTTTGTGGACCATATATCATGCCCACTCCAACGCCCAAAAC

sch-kep1 -----  
sch-CR9337 CGCACAAATCTGTCATGCCTAGACTTTAGAAAAATGTGTTGATATTTTTTTCATAATTTG

sch-kep1 -----  
sch-CR9337 CAAAAACTGTTTGCCTACTCCAGTCTAACGCCCTAAAGTCGCCGAATGCCCACTTTT

sch-kep1 -----  
sch-CR9337 GAACAATTTTAAAAATTTTTTCCAATTTTATTCCGCAATATTTATCGATATACCAGAAAA

sch-kep1 -----  
sch-CR9337 ATTACGAAATTCGCGTTTTGCATTCACTAGCTGAGTAACGGGTAAGTTGCTATAGCAT

sch-kep1 -----  
sch-CR9337 TTCTCTCTTGCTT

**7. CR9337/CR33318**

sch-CR9337 **DNAREP1\_DM**  
mel-CR33318 TTATACCCGTTACTCGTAGATTTAAAAGGGTATACTAGATTCCCTTTAAAAGTATGTAAAAG  
-----

sch-CR9337 TATATGTAAAAGTATATATATTTCTTCAGAATCGATGTCTGTCTTCCGTATGAACGTTGA  
mel-CR33318 -----

sch-CR9337 GATGCCAGGAACATAAAAAGATAGAAGGTAACGATTAGGAACACAGATTCTAGAGACATA  
mel-CR33318 -----

sch-CR9337 GATGCAGCGCAAGTTTGTGTAACCGTGTCCCATGCTCTAACTCTAACGCCCAAAAGCGC  
mel-CR33318 -----AACTTTTTGCCACGCC--ACTCTAACGCC--TAAAGTCG  
**DNAREP1\_DM**

sch-CR9337 CCAAACTGACACGCCCAACACTATATCTAATTTTTTCAATTTTATTATTTGTTTTCC-

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mel-CR33318      CCAAACCTTGCACGTCCAC-ACTTTAGAAC-AATTTTT--TTATTTATTTTATTACCCA
sch-CR9337       ATTTCTACCGGTATTCCAAATA--TATTTAAATATCTCGTTT-----TGGA
mel-CR33318      ATATCTACCGATATCCCAGAAAATTATGAACTTCCGCGTTGCATTACACTAGCTGA

sch-CR9337       ATA-----AACTGGAGAATCTCGACTATAGCAT----TCATGTTTTTAATCT
mel-CR33318      GTAACGGTTACCTGATAGTCGGGGAACATAGACTATAGCATTATCTCTTGGTTTTTAATCT

sch-CR9337       GATG-----GGTAAGTAGCCTAAGTGTACCAGAG-----
mel-CR33318      GATGTAGCTTAAGTATGACTGTAAATGTCTAAAGTAAGGCTGAGTTAATAAACGCTTAA

sch-CR9337       -----ACCATGG-
mel-CR33318      ACAAATGTATGTATGTTTCATCTTTGGATATACATATTTGCTTTTGGGGAACAACTACGGA

sch-CR9337       -----TGGTGTTCAGTTTTCTGCAC-----ATAATGGGATACCCG
mel-CR33318      TATGGTTATCTTTCCACGGGTCTATTTTTTATATTTTTTAACTAAGGATTGGCGACTGG
          5' breakpoint
sch-CR9337       ACATTTAA CAATCACTTTAGCACTGAAAAATAT---GCCTCAAAACTTCAAACGGTTG
mel-CR33318      ACGTGTGTT CAATCACTATAGCACTGAAAAAGTTGGCAGCCTCAAAACTTCAAACTTTTG

sch-CR9337       GCAGGTCTGCCATCATTTTAGTTCAGTATATACAAAGCGTTATTCAGTCTACATCAATT
mel-CR33318      GCAGGTCTCC---CTTTTTAAGTCACTGATATATAATTCTTTATTCAGTCTACATCAATT
          Start Codon
sch-CR9337       TTAATTGTGATTTTTTGGTAAAGATTGTTACGATAAAA ATG GAAACCTCAAGCGAGTTAA
mel-CR33318      TCAATTGTGATTTTTTCGGTAAATATTGTTACGATAAAA ATG GGAACAGCAAGCGCGTTAC

sch-CR9337       CTGAGAAAGAGCCACTTACCCACGACCACCAGCCGCGTCTGAACGAGGTGGCCAAAAGT
mel-CR33318      CTTTGAAACAGCCACCTTCCCACGACCACCAGCCGCGTCTGAACGAGGTGACCCAAAAGT

sch-CR9337       TTCTCGCCGATTTGGACGAGGAGCGGAAGCGATTGTCCGCGGAGTTTCCACTTTGCGCAC
mel-CR33318      TTCTCGCCGATTTGGTGCAGGAGAGCCAGTATTGTCCGCGGAGTTTCCACTTTGCGCAC
          Exon1
sch-CR9337       TGCTAATCGCCGAGG GTAAAAACAATTCGGTCTTTACAGGGTATTTAATAGTACTAAT
mel-CR33318      TGCTAATTGCCGAGG GTAAAAACAATTCGGCCCTTTACAGGGTATTTAATGGTATTAAT

          Exon2
sch-CR9337       CCCACATTGCAG CTGTGGACCGTGTCTACGGCACTGGCCGTTATCCCAGCAAGGAGTTAT
mel-CR33318      CCCACATTGCAG CTGTGGACCGTGTCTATGGCACTGGACGTTATCCCAGCAAGGAGTTAT

sch-CR9337       ACGCAGACGTGTACAACCAAAAGCCGATGAAGATTACCCAAACGGTCTTTGTGCCGTTA
mel-CR33318      ACGCAGACGTGTACAAGCAGAAGCCGATAAAGATTACCCAAACGGTCTTCGTGCCGTTA
          Exon2
sch-CR9337       ATCAGTATCCCAAG GTGGGTTTTGA-ACAATTAGCTGTCCATCCCAGTCCGCAAAATGAAT
mel-CR33318      ATCAGTATCCCAAG GTGGTTTTTTATACAATTAGCTATCCACTCCGACCGCAAAATGAAT

          Exon3
sch-CR9337       CCTTACCCTTGCGCAG TTCAACTTCACTGGCAAGATCCTGGGGCCAAGGGGAAGTCTGTT
mel-CR33318      CCTTACACTTGCGCAG TTCAACTTCACTGGCAAGATCCTGGGGACCAAGGGGAAT-----

sch-CR9337       GCGTCGCCTTCAGGAGGAGACCAGTGAAGATTGCCATCAAGGGTCGCGGTTTCGATGCG
mel-CR33318      -----

sch-CR9337       CGATCGTAACAAAGAGGAGCAGTTGCGCAGCACAGGTGACCCGAGATATGCCATCTTTCA
mel-CR33318      -----

sch-CR9337       GAAGAACTCTTTCTGGAGGTCAGCACGGTGGCCAACCCGGCGGAGTGCTATGTCCGCAT
mel-CR33318      -----

sch-CR9337       AGCCTACGCCCTGGCCGAGATCCGTAAGTATCTTATTCCAGACAAGAACGACGCGGTTTT
mel-CR33318      -----

sch-CR9337       GCACGAGCAGCTGCGCGTGTGAAGGAAATGGATCCCAGTCCGCCAAGAACAGTAACGG
mel-CR33318      -----

          Exon3
sch-CR9337       ACTCTGGAGTCTGGAGGTTCTACAG GTAATGGGGATCCCTCTGCATACCGATGTAAGTTGA
mel-CR33318      -----

sch-CR9337       CTTACTTGACAAGCGAGTTGAGCATGTGGTATACAAAGGCTTGATATTGGGCAAGGAGTA
mel-CR33318      -----

          Exon4
sch-CR9337       AAAATCTATTGTTATTTTGCAG ATCTGTCTCGACAAGAAGTTGGGAGGCAACAGCAATG
mel-CR33318      -----

          Exon4
sch-CR9337       GGGCTCTCACGTACATCAACCCGATTAAGCGAGTTGCGGGAAATCCACCCCA GTAAGTTA

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mel-CR33318      --GCTCT-----
sch-CR9337      CTTGTAAAGTATTATTTTGTATCATTTAATGTCCTTGTTCCTTTGAATCCTACCCAACATG
mel-CR33318      -----
sch-CR9337      CGTTGAGCCAGCAACTAACATTTTGTATCTTTATAGAGTCGACGATGTGGAGGAGGTGGTC
mel-CR33318      -----
sch-CR9337      TATGATCTTATGCCCCCAGTCATCCGCCTACGAGCTATGAGTACAGGAAATGTAAGTAT
mel-CR33318      -----
sch-CR9337      TTGGTAGTGCCGGGGTCCATTACATAAGATTGTTTTATGGGATGCATCTTTGACGGGAAC
mel-CR33318      -----
sch-CR9337      TTGGGATTTAGATACGATTATTATCGAGTATTAAGTACGACAACAGTGAATGATCAAGATCT
mel-CR33318      -----
sch-CR9337      CAGATCAAACATATAATACTACAATGACTAATATTATAATATTATAACAACGATTAAC
mel-CR33318      -----
sch-CR9337      TTCTTTATAGTAATTACATACACGCATAAAATTAATAATAATAATCAACCAATTTTAT
mel-CR33318      -----
sch-CR9337      AGCATTTCATTAAAAATACCGAAAACGCAGTGGCATATAAACGTCCATATCCGTATCT
mel-CR33318      -----
sch-CR9337      TACTGACATGAAATTTATGCGCGAACCGCCATCAAGAACTTAAGCCCAATCCTTTTAA
mel-CR33318      -----
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mel-CR33318      -----
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sch-CR9337      GCCCATTATG-TTTAAATTAATACTCGCTTTGTAATTTTCTATTATAAAATTAAAACAC
mel-CR33318      -----
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mel-CR33318      -----
sch-CR9337      CCCGATTTACAATCAATATTTGCATTACCTAATTAACAATTAACATACTAGCATTAAAA
mel-CR33318      -----
sch-CR9337      GTTAGCTAGTTATATTTCTAAAAAATGAATTGA-----
mel-CR33318      -----
sch-CR9337      -ACATCCTTTTATCAGATGAATCAAAGTGAAGATCGCATCAAGATACTTAAGTGCTTTTA
mel-CR33318      -----
sch-CR9337      AAAATAATTTTATAATCCATCATAATTTTATAAATGAACAAGAGAGAACAATAAATAAAC
mel-CR33318      -----
sch-CR9337      ATATAAAGAGTTTGCATAACTAAAATATTTTCAGGTTTTTTTAGGCAAAGTATTAATTTGTA
mel-CR33318      -----
sch-CR9337      DNAREP1_DM
mel-CR33318      TACCCGTTAGTCGCAAAGTAAAAGGGTCTACCAGATTCGTTGAAAACATATGTAAGTGGTA
mel-CR33318      -----
sch-CR9337      GAAGAAAGCGTTTGTGACCCATATTATCATGCCCACTCCAACGCCACAAACCGCACAA
mel-CR33318      -----
sch-CR9337      ATCTGTCATGCCTAGACTTTAGAAAAATGTGTTGATATTTTTTTCATAATTTGCAAAAAA
mel-CR33318      -----
sch-CR9337      CTGTTTGCCACTCCCAGTCTAACGCCCTAAAGTCGCCGAATGCCACACTTTTGAACAAT
mel-CR33318      -----
sch-CR9337      TTTAAAAATTTTTTCCAATTTTATTCGCAATATTTATCGATATACCAGAAAAATTACGA

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mel-CR33318 -----
sch-CR9337 AATTCGCGTTTTGCATTCATACTAGCTGAGTAACGGGTAACCTTGCTATAGCATTTCTCTC
mel-CR33318 -----
sch-CR9337 TTGCTT
mel-CR33318 -----

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**8. CR9337/CR9337-r**

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                    5'breakpoint
sch-CR9337 TTATACCCGTTACTCGTAGATTTAAAAGGGTATACTAGATTCCTTTAAAAGTATGTAAAAG
sch-CR9337-r TTATACCCGTTACTCGCAGAGTAAAAGGGTATACTAGATTCGTTGAAAAGTATGTAAACG
                    DNAREP1_DM
sch-CR9337 -----TATATGTAAAAGTATATATATCTTCAGAAATCGATGTCT
sch-CR9337-r ACAGAAGAGAGCGTTCCCGACCATAT--AAAGTATATATATCTTCAGAAATCGATGTCT
sch-CR9337 GTCCTTCCGTATGAACGTTGAGATGCCAGGAACATAAAAAGATAGAAGGTAACGATTAGG
sch-CR9337-r GTCCTTCCGTATGAACGTTGAGATGCCAGGAACATAAAAAGATAGAAGGTAACGATTAGG
sch-CR9337 AACACAGATTCTAGAGACATAGATGCAGCGCAAGTTTGTGAACCGTGTCCCATGCTCTA
sch-CR9337-r AACACAGATTCTAGAGACATAGATGCAGCGCAAGTTTGTGAACCGTGTCCCATGCTCTA
sch-CR9337 ACTCTAACGCCCCACAAAGCGCCCAAACTGACACGCCCCACAACACTATATCTAATTTTTTC
sch-CR9337-r ACTCTAACGCCCCACAAAGCGCCCAAACTGACACGCCCCACAACACTATATCTAATTTTTTC
sch-CR9337 ATTTTATTATTTTGTGTTTTCCATTTCTACCGGTATTCCAAAATATATTTAAAATATCTCGTT
sch-CR9337-r ATTTTATTATTTTGTGTTTTCCATTTCTACCGGTATTCCAAAATATATTTAAAATATCTCGTT
sch-CR9337 TTGAATAAACTGGAGAATCTCGACTATAGCATTCATGTTTTTAATCTGATGGGTAAGTA
sch-CR9337-r TTGAATAAACTGGAGAATCTCGACTATAGCATTCATGTTTTTAATCTGATGGGTAAGTA
sch-CR9337 GCCTAAGTGTACCAGAGACCATGGTGGTGTTCAGTTTTCTGCACATAATGGGATACCCGA
sch-CR9337-r GCCTAAGTGTACCAGAGACCATGGTGGTGTTCAGTTTTCTGCACATAATGGGATACCCGA
sch-CR9337 CATTTAAACAATCACTTTAGCACTGAAAAATATGCCTCAAACTTCAACCGTTGGCAGG
sch-CR9337-r CATTTAAACAATCACTTTAGCACTGAAAAATATGCCTCAAACTTCAACCGTTGGCAGG
sch-CR9337 TCTGCCATCATTTTAGTTCACTGATATACAAAGCGTTATTCAGTCTACATCAATTTTAAT
sch-CR9337-r TCTGCCATCATTTTAGTTCACTGATATACAAAGCGTTATTCAGTCTACATCAATTTTAAT
                    Start Codon
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sch-CR9337-r TGTGATTTTTTGGTAAAGATTGTTACGATAAAAATG ATG GAAACCTCAAGCGAGTTAACTGAG
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sch-CR9337-r AAAGAGCCACTTACCCACGACCACCAGCCGCTCTGAACGAGGTGGCCCAAAAGTTTCTC
sch-CR9337 GCCGATTTGGACGAGGAGCGGAAGCGATTGTCCGCGGAGTTTCCACTTTGCGCACTGCTA
sch-CR9337-r GCCGATTTGGACGAGGAGCGGAAGCGATTGTCCGCGGAGTTTCCACTTTGCGCACTGCTA
                    Exon1
sch-CR9337 ATCGCCGAGG GTAAAATCAATTCGGTCTTTACAGGGTATTTAATAGTACTAATCCAC
sch-CR9337-r ATCGCCGAGG GTAAAATCAATTCGGCCCTTTACAGGGTATTTAATAGTACTAATCCAC
                    Exon2
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sch-CR9337-r ATTCAG CTGTGGACCGTGTCTACAGCACTGGTCTGATTTCCCGCAAGGAGTTATACGCA
sch-CR9337 GACGTGTACAACAAAAGCCGATGAAGATTACCCAAACGGTCTTTGTGCCGTTAATCAG
sch-CR9337-r GACGTGTACAACAAAAGCCGATGAAGATTACCCAAACGGTCTTTGTGCCGTTAATCAG
                    Exon2
sch-CR9337 TATCCCAAG GTGGGTTTTGAACAATTAGCTGTCCATCCCGTCCGCAAAATGAATCCTTAC
sch-CR9337-r TATCCCAAG GTGGGTTTTGAACAATTAGCTGTCCATCCCGTCCGCAAAATGAATCCTTAC
                    Exon3
sch-CR9337 CCTTGCGCAG TCAACTTCATTGGCAAGATCCTGGGGCCCAAGGGGAACCTGTTGCGTGC
sch-CR9337-r CCTTGCGCAG TCAACTTCATTGGCAAGATCCTGGGGCCCAAGGGGAACCTGTTGCGTGC
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sch-CR9337-r CCTTCAGGAGGAGACCCAGTGCAAGATTGCCATCAAGGGTCGCGGTTTCGATGCGCGATCG
sch-CR9337 TAACAAAGAGGAGCAGTTGCGCAGCACAGGTGACCCGAGATATGCCATCTTCAGAAGAA
sch-CR9337-r TAACAAAGAGGAGCAGTTGCGCAGCACAGGTGACCCGAGATATGCCATCTTCAGAAGAA
sch-CR9337 TCTCTTTCTGGAGGTCAGCACGGTGGCCAACCCGGCGGAGTCTATGTCCGCATAGCCTA

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sch-CR9337-r TCTCTTTCTGGAGGTCAGCACGGTGGCCAACCCGGCGGAGTGCTATGTCCGCATAGCCTA

sch-CR9337 CGCCCTGGCCGAGATCCGTAAGTATCTTATTTCCAGACAAGAACGACGCGTTTCGCACGA  
sch-CR9337-r CGCCCTGGCCGAGATCCGTTGAGTATCTTATTTCCAGACAAGAACGACGCGTTTCGCACGA

sch-CR9337 GCAGCTGCGCGTGTCTGAAGGAAATGGATCCCGAGTCCGCCAAGAACAGTAACGGACTCTG  
sch-CR9337-r GCAGCTGCGCGAGCTGAAGGAAATGGAACCCGAGTCCGCCAAGAACAGTAACGGACTCTG

Exon3

sch-CR9337 GAGTCTGGAGGTCTACAG GTAATGGGGATCCCTCTGCATACCGATGTAACCTGACTTACT  
sch-CR9337-r GAGTCTGGAGGTCTACAG GTAATGGGGATCCCTCTGCATACCGATGTAACCTGACTTACT

sch-CR9337 TGACAAGCGAGTTGAGCATGTGGTATACAAAGGCTTGATATTTGGGCAAGGAGTAAAAATC  
sch-CR9337-r TGACAAGCGAGTTGAGCATGTGGTATACAAAGGCTTGATATTTGGGCAAGGAGTAAAAATC

Exon4

sch-CR9337 TATTGTTATTTTGCAG ATCTGTCTCGACAAGAAGTTGGGAGGCAACAGCAATGGGGCTC  
sch-CR9337-r TATTGTTATTTTGCAG ATCTGTCTCGACAAGAAGTTGGGAGGCAACAGCAATGGGGCTC

Exon4

sch-CR9337 TCACGTACATCAACCCGATTAAGCGAGTTGCGGGAAATCCACCCGA GTAAGTTACTTGTA  
sch-CR9337-r TCACGTACATCAACCCGATTAAGCGAGTTGCGGGAAATCCACCCGA GTAAGTTACTTGTA

sch-CR9337 AAGTATTATTTTGTATCATTTAATGTCCTTGTCTTTGAATCCTACCCAACATGCGTTGA  
sch-CR9337-r AAGTATTATTTTGTATCATTTAATGTCCTTGTCTTTGAATCCTACCCAACATGCGTTGA

Exon5

sch-CR9337 GCCAGCAACTAACATTTTGTATCTTTATAG AGTCGACGATGTGGAGGAGTGGTCTATGAT  
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Exon5

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sch-CR9337-r CTTATGCCCCCAGTCATCCGCCTACGAGCTATGAGTACAGGAAAC GTAAGTATTTGGTA

sch-CR9337 GTGCCGGGGTCCATTACATAAGATTGTTTTATGGGATGCATCTTTGACGGGAACTTGGGA  
sch-CR9337-r GTGCCGTGGTCCATTACATAAGATTGTTTTATGGGATGCATCTTTGACGGGAACTTGGGA

sch-CR9337 TTTAGATACGATTATTATCGAGTATTAAGTACAAACAGTGAATGATCAAGATCTCAGATC  
sch-CR9337-r TTTAGATACGATTATTATCGAGTATTAAGTACAAACAGTGAATGAGCAAGATCTCAGATC

sch-CR9337 AAATATATAATACTACTACAATGACTAATATTATAATATTATACAACGATTAACCTCTTT  
sch-CR9337-r AAATATATAATACTACTACAATGACTAATATTATAATATTATACAACGATTAACCTCTTT

Exon6

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sch-CR9337 TCCATTAATAATACCGGAAAACGCGAGTGGCATATAAACGTCATATCCGTATCTTACTGA  
sch-CR9337-r TCCATTAATAATACCGGAAAACGCGAGTGGCATATAAACGTCATATCCGTATCTTACTGA

sch-CR9337 CATGAAATTTATGCGCGAACC GCCCATCAAGAACTTTAAGCCCAATCCTTTTAAACGGAC  
sch-CR9337-r CATGAAATTTATGCGCGAACC GCCCATCAAGAACTTTAAGCCCAATCCTTTTAAACGGAC

Stop Codon

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sch-CR9337-r T TAA GTTATAAAATCCATGATGGGAGCACATTGAAAATACTTTAAACCAGATGGAAGCAG

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sch-CR9337-r ATTTCAAATGAATAAATATTAACATTTATAAAAAACCCACTTGCCTATCAAATCCTAC

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sch-CR9337 TATGTTTAAATTA--AAATCCTGCGTTTGTAAATTTTCTATTATAAATTAACAACTAATA  
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sch-CR9337 AAATAAACTCATTGAATATTTTATAAATCAATCCGATCTAATTATGCCGATTTACAA  
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sch-CR9337 TCAATATTTGCATTACCTAATTAACAATTAACATACTAGCATTAAGTTAGCTAGTTA  
sch-CR9337-r TCAATATATGCATTACCTAATTAACAATTAACA-CTAGCATTAAGTTAGCTAGTTA

sch-CR9337 TATTTCTAAAAAATGAATTGA-----ACATCCTTTTA  
sch-CR9337-r TATATCT-AAAAATAAATTTGGTAATTACATAAAACGGTACGAACTTATCACATCCTTTTA

sch-CR9337 TCAGATGAATCAAAGTGAAGATCGCATCAAGATACTTAAGTGCTTTTAAAAATAATTTCA  
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sch-CR9337 TAATCCATCATAATTTTATAAATGAACAAGAGAGAACAATAAATAAACATATAAAGAGTT



sch-CR9337-r TAAACCATTATAATTTTATAAATGAACACGAAAGAACATTAATAAA-----  
 sch-CR9337 TGCATAACTAAAATATTTTCAGGTTTTTTAGGCAAAGTATTAATTTGTATACCCGTTAGTC  
 sch-CR9337-r ---ATAACTAAAATATTTTCAGG-TTTTTAAGCAAAGTATTCATTTTTATACCCGTTA---  
 sch-CR9337 GCAAAGTAAAAGGCTACCAGATTCGTTGAAAACATGTAAGTGGTAGAAGAAAGCG **3' breakpoint**  
 sch-CR9337-r -----AAGAGGGTATATAAGATTCGTTGAAAACATTTTAAACAGGTAGAAGGAAGCGT C  
 sch-CR9337 T-----GTTGACCC-----  
 sch-CR9337-r TCCGACCATATGATCAGAATCAATAGCCGAGTCGATCTAGCCACATCTGTCCGCCTGCC  
 sch-CR9337 -----ATATTATCATGCCC  
 sch-CR9337-r TTCTGTCCGTATGCACGTCGAGATCTCAGGAAGCTAGAAAAGCTAGAAGGTTGCCACGCC  
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 sch-CR9337-r ACTCCAACGCCACAAACCGC-CATACCTGCCACGCCAACATCGTTGAAGAATTTGTGG-  
 sch-CR9337 TATTTTTTTCATAATTTGCAAAAACTGT-TTGCCACTCCCAGTCTAACGCCCTAAAGTC  
 sch-CR9337-r -TGTTTTTCTTAATCT-----AATCCGCTTGTAATTT-----TCTA-----TACATTC  
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 sch-CR9337-r GCCAAAAAAAAAAAGCATACTTCTGAAAAA-----AAATGTAATTTTTTCTCATTTTAT  
 sch-CR9337 TCCGCAATATTTATCGATATACCAGAAAAATTACGAAATTCGCGTTTTGCATTCATACTA  
 sch-CR9337-r TTCCCAA-----TATCCAAATCCAGAAAAATGATGAAA-----TTTCGCATTCACACTT  
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 sch-CR9337-r GCTGAGTAACGGGTA-----

**9. CG7692/CG9902**

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 mel-CG7692 -----  
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 mel-CG7692 -----  
 mel-CG9902 TACCAACGAATCTCGTATACCCTTCTGGTCTATAGTAAGTGTTTTGTATTCTTGTCTTCT  
 5' breakpoint  
 mel-CG7692 -----  
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 mel-CG7692 CCTAGCGAGTTCACCTTCCCCATTACAGCAATTACAGCTAGTCTCGTGGTTTTAGCGAGTAC  
 mel-CG9902 CTTAGCGAATGCACCTTCCACATTTAGCAAATACGCCTAGCCTTACAGTTTAGCGAGTAT  
 mel-CG7692 ATGAACCTCG---AGATAGCGCTGCCACTAT-GTTTAAAACCATCCACTTACGGTAATCG  
 mel-CG9902 ATGAACCTCGTGTAGACAGCGTTGCCCTTTTCGATTAA---CATCGATTTACAGTAATCG  
 Transcription Start Position  
 mel-CG7692 GCGTCAGCTGTTG-----**CAAGCTAAATAAACTAAGTACAAGCCGGCTGA**  
 mel-CG9902 GGTTACAGCTGTTGTTGCTTGAACCTT CAAGCTAAATTAATAAATCGAAACCGGCAAA  
 Start Codon  
 mel-CG7692 AAAAC-AAATCGACTTTTTCGAGGATGTGCATGAATTAGGTACTGCGGA **ATG** GATCTAA  
 mel-CG9902 AAAAAGGAAATCGACTTGACATAGCATTGCCATGAATTAAGTGTGCAAA ATG GATATAA  
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 Exon1  
 mel-CG7692 ACGATGAGTTCTCGCG **G** GTAAGGACACGCTTTGGACATATATCTGAACTCCCTGTTTTA  
 mel-CG9902 ACGACGAGTTTTTCGGCG GTAAGGACTTGCTTTGTACATAAATCCTTATGCACAGTTTTTC

mel-CG7692 ATGGCTTAAATCTTGA-TCTACAG  Exon2  
 mel-CG9902 ATTGCTTAAATCTTGGTTTTATAG AAAATGTTTGTATTCTGCAATGCGCACAGCGATGTG

mel-CG7692 GATGTGTTTGTAGCTAATGGGCAATGACCGTTGTGCGAGTTAATCTACGGATGGGAGGTG  
 mel-CG9902 GATGTGTTTGTAGCTAATGGGCGATGACCGTTGTGCGAGTTACTCTACGGATGGGAGGTG



mel-CG7692 TGCCATCTGCCACCAGGGATTCCGAGTCCTTAAAGGACCCAGCGCTGCGTCACATGGTG  
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
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mel-CG7692 ATTGGTGAAGTGGCAATTTCAACTGGTCTGACGTTCTGCAGTTCCAGACAAGGCCCTGG  
 mel-CG9902 ATTGGTGAAGTGGCAATATCAACTGGTCTGACGTTCTGCAGTTCCAGACAAGGCCCTGG

mel-CG7692 AGCCTGCCCTACCTGCAGCAGCTATTCCTTAACCTGAAGCTGAACAAACACCACGCCATC  
 mel-CG9902 AGCCTGCCCTACCTGCATCAGCTATTTCTTAACCTGGAGCTGAATAAACAACACGGCATC



mel-CG7692 GAGCACCCAGTTCCGCGGCATCAGGAGAA  Exon2  
 mel-CG9902 GAACACAAAGTTCAAGCGGCATCAGGAGAA  GCAAGCAATTACTATTTTTCCGAAGGAT



mel-CG7692 TTATCTAATCATAGTC-AATTTCTTAG  Exon3  
 mel-CG9902 TCATCTAATCATTTGCCCTATTTCTTAG  AAGTTGCTTTCCTGATACAGGAAGGGATATCTC

mel-CG7692 TGGCCCTGCTGCGGCTAATACAGCTCTTTAATGCCGGCAACTTTGAGGCCGTGAAACAGC  
 mel-CG9902 TGGCCCTGCTGCGACTAATCCAGCTCTTTAATGCCGGCAACTTTGAGGCCGTGAAACAGC

mel-CG7692 TGGCGCTTCGGATGCTGGCTGCTTGGGTGAAAGCACACGAAAATGATCAATTTGTGTCCT  
 mel-CG9902 TGGCGCTTCGGATGCTAGCTGCTTGGGTGAAAATCCACGAAAATGCACCATTTGTGTCCT

mel-CG7692 TTGAAGGGGATAAAAACTCAATTACACTAATCGGTCATCTATACCTCTTGACTGTTTTTG  
 mel-CG9902 TTAAAGGGGATGAAAACACAATTACACTAATCGGTCATGTATGCTCTTGCCGCTTTTTG

mel-CG7692 TAAGAGATGAAAATCGAGGCTTTGTAATAGATAAATTT  Exon3  
 mel-CG9902 TTAGGGATGATAATCAAGGCTTTGTAATAGATAAATTT  GTAAGGAAAACATACATGATA-

mel-CG7692 ---CAACATATC-AAACACAATGTCATCATAAAACCACTCCTTAG  Exon4  
 mel-CG9902 AACTAACATAACAAAATAAATGTCGTCATAAAACCACTCCTTAG  ATGTACAACATACGG

mel-CG7692 TTCTATACCCAGATCATGCAGGAAGCTTCGATGTTACATGACATTAACCTTACGCCAGCT  
 mel-CG9902 TTCTATGTCCAGATCATGGAGGAATTTTCGAGTCACATGATATTAACCTTACGCCAGCT

mel-CG7692 CGGCTTATTGCCACGTTTTCGCTGCGTCTTCAACTCGGAAAAATGGGTTCTTTGAGCAA  
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mel-CG7692 ATTGGGTTTAGGAAATTCAAATTCAGTCTGGTCACTTCATTGCGCGTCATGCTGGAGGTC  
 mel-CG9902 ATTGCATTTAGGAAATTCAAATTCAGTCTGGTCACTTCATTGCGCGTCATGCTGGAGGTC

mel-CG7692 TACGCCAGCTATGTGCTTGGGAATCTCCTGATGGAGCTCCAGGCGCTCAACGAACACGAT  
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 mel-CG9902 TTCTGGAGCACCTGCCACAGTTCAAAGAGCTAATGGATCGCTATGTAGAGGAGCGAGAG

mel-CG7692 AGCAGCGAGCGCTTCTTCTAGAGGAACTCAAGAAGAAGGAAAACCAGCGAAAACAGCCAC  
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mel-CG7692 TTTCAACCACATGTAGTAGAGCTAAATCTCAACTACCAGCAGCAGATATGCAAGGGAAAC  
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mel-CG7692 CGAGCCAGCAACATAGGCGACTACAAGAAGTGTGATGACGACGAACAGATTCAGCCTGAG  
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mel-CG7692 GTGGACGAAGAACAAGATAGACAAATAGATCCGGTGTTCAAAATGTACCAAACAATGAG  
 mel-CG9902 GTGGCGAAGAACAAGATAGACAAATAGATCCGGTTTTTCAAATGTACCAAACAATGAG

mel-CG7692 GAAGTTTTGAGCTTTGTGTACAACTGCTGGCAGAGCG  Exon4  
 mel-CG9902 GAAGTTTTGAGCTTTGTGTACAAATGCTGGCAGAGCG  GTAAGTGTGAGAACTATGAA

Exon5

me1-CG7692 AAGGAATTCCTGTACTAAACACAGTGCCTTC---ATGTAG AATTTTTCAGGATGGACATT  
me1-CG9902 AAGCGAAAACCTTACTAAGCACCGCGCTTTTTTAATTTAG AATTTTTCAGGCTGGAGATT

me1-CG7692 TGCTAAGATTGCCCTGCTGCTGAAGATCATTGGACAACAGTTGAATGCAATTGAAATATG  
me1-CG9902 TGCTAAGATTGCTCTGCTGCTGAAAATTATTGGGCAACAAATAAATGCATTAGAAATGTG

me1-CG7692 GAAATATCATCCCGGATTAACAGTTGATTTTTATGCTTAATTTGGAGCAAAAGATGTGCGGA  
me1-CG9902 GAGATATCATCCCGGGTTAACCGTTGATTTTTATGCTCGATTTGGAGCAAAAGATGTCTGC

me1-CG7692 AAACATATGCTGACCTAGCCAAGGTATTCTCCGAACATGGGTTTATGGAGGCAGAATTCTG  
me1-CG9902 AAACATATGCTGACCTAGCCAATTTGTTCTCTGACCATGGATTTATGGAGGCAGAATTCTG

me1-CG7692 GCTTACGGCTTTCTACCTCCACCCACATCATCAAATTATAACGAAGTGAGGCGCTGTTC  
me1-CG9902 GCTGACTGCTTTCTACCTCCACCCACATCATCAAATTATAACGAAGTAAAGCGCTGTTC

me1-CG7692 GCGTATTAAGAAAAACGGCAGGAGGACGACTTGCTACCTGCTACGACACCACAGAACGT  
me1-CG9902 GTGGATCATGAAAAATCGACAGGAGGAGGGCGGGCTCCCTGCTCCAGCGATTGGCAACGT

me1-CG7692 CAAGTACGAACCTGCTGAGCTCCACCATCGATGTGGACGAGATTGTAAAAATAACGAACCA  
me1-CG9902 CAAGTACGAACCTGCTGAGCTCCACCATCGATGTGCACCAGATTATGACCATAACAAACCA

me1-CG7692 TTACGATCCAGTGGCCGACTACGATCCGATACACAAATCGCTGCAGGCGTTGCGGCTTCC  
me1-CG9902 TGAAGATCCAGTGTCCGACTACGATCCAATAAACGAGTCGCTGAAGGCGTTGCGTCTACC

me1-CG7692 CCGCAGCATGATCCAAGACCTTCTGACCGTGGTCTTCCAACCACGAATAAACGATACTC  
me1-CG9902 CAGCAACATGACCAAGGATCTTCTGACCGTGGTCTTCCAACCACGACATAAAACAATACTC

me1-CG7692 ATGGGCTCTCGATTGGCACACGCTACACGAGCGTTGCCATGCCCTTCTCAAAGCCCGGA  
me1-CG9902 ATGGGCTCTCGATTGGCAAACGCTAGACGAGCGTTGCAGTGCCCTACTCAAAGCCAGGA

me1-CG7692 CCTCAAGAGAAAAATTTGTGTCTCTTAACATGGCCGAAGCTGGCGACGATTTGAAGTACCT  
me1-CG9902 CCTGAAGAGAAAAATTTGTGTCTCTTAACATGGCCGAATCATGCGACGACTTGAAGTATCT

me1-CG7692 CCAGATCGACTATGCCAAATACAGGGATCGCCCTCAGTTGGACTATGGCACCATAGAAGA  
me1-CG9902 CCAGATCGACTATGCCAAGTACAGGGATCGACCACAGTTGGACTATGGCACCATAGAAGA

me1-CG7692 GGGCTACGAAAATGCGGTTAATCTCCAGAGGCTGAGGAAGAAGCTGAACAAACGTCAGC  
me1-CG9902 GGGCTACGAAAATGAGACTAATCTCTCGAATGCAGCTGGAAAGGCTGAATCAACACCAGC

me1-CG7692 AGTGGATGATGAAGCAGAGAAAGCCAAGGAGCAGAAAAAGCGGCGACCCGCAAAACGCAA  
me1-CG9902 AGTGCATGATAAAGCAGAGAAAGCCAAGGAGCTGAAAATGCGGCGACACGCAAAACGCAA

me1-CG7692 AATTTGGGACGAAAG GTTAGCAACAAAATCGTTTTCTTTTGGAGCCACTTCCTTTCATAATA  
me1-CG9902 ATGTTGGTATGAAG GTTAGCAACGAAAATCTTTTTCTTTTGGAGCAACTTTCATATAAGATT

me1-CG7692 ACTAATAATTCAGTCATACTAATAATTTCAATTTAAAATCCC-----  
me1-CG9902 A-----GATTCAGTCAAACCTAATGAATTTTAAATCCCACAGTTTCGGAAGACGAG

me1-CG7692 -----  
me1-CG9902 GAAGAGGCTGCCTCAAGTGATTCGAGAGCCAGCTACACAGGAAATGGCCGCCGAACACAG

me1-CG7692 -----  
me1-CG9902 ATTAGAGCCGACGATTCATCCAAAGCTAATGGTCGCCGACTGGGATTAGAGCCGCA

me1-CG7692 -----  
me1-CG9902 GCCATTGCAGCCAATATCAAATTTGCTGAAATGTCTTTCCAGAGACATCGAATAGGCGC

me1-CG7692 -----  
me1-CG9902 TTTTCTACACAGCCCGTCGTCAGGAACAGCCAAAAATCGCCGTCAGCCTAAAAAACAA

Exon6

me1-CG7692 ---ACAG TAGTATTTTCGGAAGACGAGGAGGAGGCTGCCAAGCGATTTCGGAGCCCTAC  
me1-CG9902 AAAACAG TATTGTTTTCGAAAGAAGAGGATGAGGTTTCTCAAGTGATTTCGGAGCCCTGT

me1-CG7692 TACACAGGAAATGGCCGCCGACTCGGGTTAGGGCGGCAGCCATGGTAGCCAATGCCATG  
me1-CG9902 TACACAGGAAATGGCCGCCGACTCAGATGAGAGCCGACGCAATTCAGCCAAGGCCAAA

me1-CG7692 TTGTCTGACA-----  
me1-CG9902 TTGTCTGAAATCTCCTCTCCAGAGACATCGAATAAGCACTTTTCTACACGGTCCATCGTC

me1-CG7692 -----  
me1-CG9902 AACGAGCAGCCAAGAATCGCAGTCCAGTCTCGAAAAACAAAAGCAGTAATGTTTTCGAAA

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mel-CG7692 -----
mel-CG9902 GACGGGGATGAGACTTCCTCAAGCGATTTCGGAGCACTGCTACACCAGAAATGGCCACCTG

mel-CG7692 -----TGGATCGAAGT
mel-CG9902 AATCGGATTAGAGCCGCAGCCATTTCAGCCAAAGCCAATTTGCCTGAATTGGATCGAAAA

mel-CG7692 GTGCGCGGTGGGCGACGATCGAGCTCTCCAGAGACATCACATCACCAATTTTCATACGCAG
mel-CG9902 GTGAGCGGTGGGCGACGATCGATCTTTCAGAGGCATCGGGTAATCACTTTGTTACACAG

mel-CG7692 CCCGTCGTCGAGGAGCAGCCAAAAATCGCAGTCCAGCCTCCAAAACAACTGTGTCTACAA
mel-CG9902 CCCGTCGTCGCGGAGCAGCCAAAAATCGCAGTTCAGCCGAAAAATCAAC-----

mel-CG7692 GAAACATCTGCGCGTGTGCGAAAAGCGTACGATTAGCGAACTGATGGAGTCACGACCCAAA
mel-CG9902 -----AAAAGCGTACAATTGCCGAGCTGATGAAGTCACGACCCATG

mel-CG7692 TTTACCAACGAAACCGTCCGTTTAAAGCCGATCGCCGACATATGGAGTTTCAAGAAGGAA
mel-CG9902 TTTACCAACGAAACGAAAGGATTTAAGCCGATCGCCGACATATGGAGTTTTCAGCAAGGAA

mel-CG7692 GAGCTGCAGAATGTGGTAGAAGACAGCAGCAGCATGATAGAGTGCAGCTCGATATTAAC
mel-CG9902 GAGCTAGAGAATGTGGTTAGCGGGCCCAACGACATGATAGAGTGCAGCTCGATTATAGCC

mel-CG7692 AAATTCAAAATCTTGAAGGCCCTCAAATGGCCAAAGCTGCAAAAAGCCGCGTGCAGCCA
mel-CG9902 AAAATGAAGTTATTGAAGGACCTCAAATGGCGAAATCTGCAAAAAGCAGCCGGACAGCCA

mel-CG7692 TGTTCCAGCTTGTTCAAATATCGTTTCGCACGGGATCGGAAACTGAAAGCGTAAACTCA
mel-CG9902 TGTTACAGC-----TCGTTTCGCACAGGATCAGAAACTGAAAGCGTGAATTCC

mel-CG7692 GAAACTTCCACGATGGCTACCCACGACTTCAACGAGGAGGAGTTCAGCGAAGTTCTACC
mel-CG9902 GAAACTTCCACGATGGCTACACAGCAATTTAACGAGAAGGGGACCCTGTAGTTCCCCC

mel-CG7692 GGTGTAAGTAAAGAGC---TAACACCTTCGCCGACCACAAAGTCTGATTTAACCATGGAC
mel-CG9902 GGTGAAGGTAAAGAGCAAAAAACACCTTCGCCGACCACAAACTCCGAATTAAGCACTGAA

mel-CG7692 CCAGAAGTGTTCAGCCCACTGGTGTAGACCAAGACGCATTTGATCCATGGGAGCCTAGAA
mel-CG9902 ACAGAAGTGTTCAGCCCACTGGTGTAGACCAAGACGCATTTGATCCATGACGCCCTAAAA

mel-CG7692 ACTACAAAAGTCCACAGAAAGACTCCGGAGTTTCTGTTTTTGACCAAGGAGCCCGTGAGA
mel-CG9902 ACTACAAAAGTCCACAGAAAGACTCCGGAGTTTCTGTTTTTGACCAAGGAGCCCGTGAGA

mel-CG7692 ACTGGACAACAGACCCAGGAGCCACTGGGAGATGCCTTAAAAACTAGTGACCTAAAACAG
mel-CG9902 ACTGGATAACAGACCCAGGAGTCCCGAGGATGTCATAGAAAAGTGTGATCTCAAACAG

mel-CG7692 GTCATCCCAAATGGACTGTTCAAAGTAGAGGGACTGGAAGCGAGACAGGCGCCGAAAAG
mel-CG9902 GTCCCCCTAAATAGCTGTTCAAAGTAGAGGGACTGGATGCAAGACAGGCGACAGGAAAAG

mel-CG7692 CCAAAACAAACTGGACAACCGCAACGGGATCTACCGAATACAAGAAAACAAAAGATAAG
mel-CG9902 CCAAAAAAAAAAGGAACAAACGGAACAGGATCTGCCAAATACTAGAAAACACAAGATAAG

mel-CG7692 3'breakpoint
mel-CG9902 CTT

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### 10. CG2952/CG2952-r

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5'breakpoint Start Codon
yak-CG2952 AAA|ATG GCCGACAAGAAGAATCTCCTCTGCTGTTTCGAGCATCCCACGGAGCCCGTCTTC
yak-CG2952-r AAA|ATG GCGACAAGAAGAATCTCCTCTTCTGTTTCGATCACCCGACGGAGCCCGTTTTTC

yak-CG2952 ATGGACAAGGGCGGCAACGGCACCTTGTTTCGATGTGCCCGCTCTACGTGACCGAGCGC
yak-CG2952-r ATGGACAAGGTGGCGATGGCACCATGTTCAATGTACCCGACCACTATCTGACCGATCAA

yak-CG2952 TACAGCAAGATGTGCAGAAACGTCCAGCGGCGGTTAGCGGTGG--GTTTCGAGAAGTGCG
yak-CG2952-r TACACGAAGATCTGCAAGAAGACGCAGTACCGAATTGGCGGTAGTAAAGCGAGAATGATA

yak-CG2952 TCCTGGTCAAGGAGATCGAGATCCAGATCTCAGCTGCCCATGAGACTGGGCCGTTCCG
yak-CG2952-r GACC--TCAAGGAGATCTCCATTCCTGATCTTAGCTTTCCCATGTCCTTGGGCCGTACCG

yak-CG2952 AGCAGTTCTCGCACTTCTGAAGTCCCACCGCCAGATGGCCAGCTCTTTGATCGATGTCT
yak-CG2952-r AGCAGTTCTCGCTGATGCTGAAATCCCACCGCCAGATGGCGGGCACTTGATCGAGGTCT

yak-CG2952 TCATCAAAATGCCACCGTAGATGAACTGCAGAGCGTGGCGGTGTACGCCAGAGATCGTG
yak-CG2952-r TTACCAAACTGCTTTCCTGGAGGATCTCCTAAGTGTGGCCGCTTTGCCAGGGATCGCG

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yak-CG2952 TCAATCCGGTGTCTTCAACTACGCCTTGTTCGGTGGCCATGCTCCATCGTCCGGACACCA  
 yak-CG2952-r TTAACGCTGTAATGTTTCATTATGCCCTATCGGTGGCTCTGCTCCATCGTCTGACACCC

yak-CG2952 AGGACCTGGGTCTGCCACCTTCGCGGAGATCTTCCAGATCACTTCATCGACTCGCAGA  
 yak-CG2952-r AGGGCCTAGATCTGCCATCCTTTGCGCAAAGCTTTCAGATCGATTTCATCGACTCGCAGG

yak-CG2952 TGATTTCGCAATATGCGCGAGGAGTCTTTTGTGGTGGAGCAGACCGCTGCCCGCTGCCCG  
 yak-CG2952-r TACTGCGCTCGGTACGCGAGCAATCGTTTCGTGGTGGAGGAATCGGAATCACGGGTTCCTA

yak-CG2952 TCGTTAATTCGGTCAAGTATAACGCCTCTGACTTCGACGTGGAGCACC GGCTGTGGTACT  
 yak-CG2952-r TTGTTGTTCCAGTTAACTATAACGCCTCCGATTTGGATCACGAGCACC GTCTGTGGTACT

yak-CG2952 TCCGCGAGGACTTGGGCGTCAACCTGCACCACTGGCACTGGCATCTGGTCTATCCCAT--  
 yak-CG2952-r TTCCGCGAGGATCTGGGCATCAATCTGCACCACTGGCACTGGCATCTCATCTATCCCATCG

yak-CG2952 -----AGATGCCCCCGACCGCAGCATCGTGGACAAGGACCGCCGTGGCGAGCTGTTCT  
 yak-CG2952-r AGATCAGCGATGGTGCCGATCGCCGGATAGTGGACAAGGATCGTCGTGGCGAGCTTTTCT

yak-CG2952 ACTACATGCACCAGCAGATCGTTGCCCGCTACAATGCCGAGCGGCTGAGCAACCACATGG  
 yak-CG2952-r ACTATATGCACCAGCAGGTGATGGCCCGCTACAACGCCGAGCGATTGAGCAATCACATGG

yak-CG2952 CCCGGGTGCAGCCGTTCAACAACCTAGACGAGCCATTGCCGAGGGCTACTTCCCAAGA  
 yak-CG2952-r CCCGGGTTTCAGCCGCTTAACGACTTGGATGAACCCATTGCCGAAGGCTACTTCCCAAGA

yak-CG2952 TGGACTCCATGGTGGCCAGCAGGGCGTATCCTCCGCGCTTCGACAACACCCGGCTGAGCG  
 yak-CG2952-r TGGACTCCACGGTGGCCAGTCCGGCCCTATCCTCCGCGATTTCGATAACACCAGCTGAGCG

yak-CG2952 ACGTAGATCGCCCCAACCAACAGTTGAGAGTGGGAATCGACGACATGAAGCGATGGCGCG  
 yak-CG2952-r ATGTGCACCGCCCGCCAACCAGATCAAAGTGGGGCTCAACGACATGAAGCGGTGGATCG

yak-CG2952 AGCGCATCTACGAGGCCATCCACCAGGGCTACGTTTTTGGAT GTGAGT-GCAGCTCTAGCT  
 yak-CG2952-r ATCGCATCTACCAAGCCATCCACCAGGGCTACGTTTTTGGAT GTGAGTCTTGGCCATTGTC  
Exon1

yak-CG2952 CTCTGAATGCCGGAATATAT----ACATATAGTTGGT-TCGTTGT-AG GATAACAATGA  
 yak-CG2952-r CTTTCAAT-----TATTTTTCATCAAGTACCTAATCTCATTTTCCAG ACAAACAATGA  
Exon2

yak-CG2952 AAAGATTGCCCTGGATGACGTGAAGGGGATCGACATCCTGGGCAACATCATAGAGGCCTC  
 yak-CG2952-r AAGGATTCAAGTTGGATGAAGTGAAGGGCATTGACTACCTCGGCAACATTATGAAGCCTC  
Exon2

yak-CG2952 CGCATTGACGCCCAACA GTACTCTGGTAAGCGATTTAGTTGCATAGACACATAGCATAAT  
 yak-CG2952-r CGTATTGTCGCCAATA CAGCACTGGTAAGA---TGAGCTACTTTGCCA-----  
Exon3

yak-CG2952 GGTAATCTCTTGAACAACAATTCCTAAATTTTCATCTCATCTGCAG TACGGCGACTTGCA  
 yak-CG2952-r -----CTCCTATGCA--TAGTACTAGAAT-ATCTAATCTGCAG TACGGTGTATGTGCA

yak-CG2952 CAACAAGGGGCACATGCTGATTGCGTACTCCCACGACCCAATCAACAAGCACCTGGAGTA  
 yak-CG2952-r CAACATGGGTACGTCTTGATCTCGTACTCCCACGATCCGACTAACAAGCATTTGGAGAA

yak-CG2952 TGCGGGCGTGATGGGGGACTCCTCCACCGCGATGCGCGATCCGATCTTCTACAAGTGGCA  
 yak-CG2952-r CCAGGGTGTGATGGGGGATTTACCCTGCGATGCGCGACCCAGTCTTCTACAAGTGGCA

yak-CG2952 CGCCTTCATAGACAACATTTTCCAGGAGCACAAGCGTCAGCTTACCCCTATGAGAAGAA  
 yak-CG2952-r CGCGTTTCATTGACAACATTTTCCAGGAGCACAAGGGGCGACTTCCGGCTACACCGAGGA

yak-CG2952 GGACCTAAGCTTTCGGACGTGCGCGTCCAGAGTATTGAAGTGGAGAGCCAGGGTAAGAT  
 yak-CG2952-r AGACCTGAGCTATCCCGGCATTACGGTTCAAAACATCAATGTGATTAGCCAGGATAGGAT

yak-CG2952 CAACAGGCTGACCACATTTCTGGCAGGAGTCCGATGTGGACATGTCCC GCGGCCTTGATTT  
 yak-CG2952-r CAACAGGATAACCACATTTCTGGCAGGAGTCCGATGTGGATATGTCCC GTGGCGTCTGACTT

yak-CG2952 CGTGCCGCGCGGCCACGTCCCTCGCTCGGTTACCCATCTGCAGCACCACCCATT CAGCTA  
 yak-CG2952-r TTTGCCCGTGGCAGTGTCTGCTCGATTACCCATCTGCAGCACAACCATT CACCTA

yak-CG2952 CACCATCAAGGTGGAGAACTCCAGCGAGGCCACGAGTATGGATACGTGCGCATCTTCAT  
 yak-CG2952-r CTCCATTAACATGGTCAACTCCACTGGAGCCCAAGTTCCGGCTACGTGCGCATCTTCAT

yak-CG2952 TGCGCCCAAGATGGATGATCGTAACAATCCCATGCCGCTGGAGGAGCAGCGTCTGATGAT  
 yak-CG2952-r GGGCCCAAGCTGGATGATCGTAACGCTCCCATGTTTATGGCAGATCAGCGCCGATGAT

yak-CG2952 GGTGGAGATGGACAAGTTCGTTGTTACCATGCCACCCGGAAGCCAAACTATTACCCGGAA  
 yak-CG2952-r GATTGAGCTGGACAAGTTTGGGATTTTCGATTCCACCCGGAACATAGGTTTGTACGCGA

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yak-CG2952      CTCCACGGAGTCGAGTGTCCACCATTCGGTTTTGAGCGCACCTTCCGGAACCTGGACCA---
yak-CG2952-r    CTCTACGGAATCGAGTGTAACCATTCCTTTAAGCGCACTTCCGCAATCTGGACAACAA

yak-CG2952      -----GCTGGAGGAGCTGGAGAATTTTCATGTGCGGCTGCGGCTGGCC
yak-CG2952-r    CCGTGGGGCTGCGAATTCTCCGAGGAGTTGGAGAACTTTTCTGCGGCTGCGGTTGGCC

yak-CG2952      CCAGCACATGTTGATTCCGAAAGGTCGGGCCGAGGGTCTGAGTTTCGAGCTCTTCGTCAT
yak-CG2952-r    CAATCACATGTTGGTCCCAAAGGGTCGTGTTGAGGGCATGAGCTTTGAGTTGTTTCGTCAT
                                Exon3
yak-CG2952      GGTTCCTCAACTACGAAGACGATAAG GTAAGGTGTCCTTAAAGTATACTGCTGCTGCCTCC
yak-CG2952-r    GATTCCTCAACTACGACAATGAAAGG GT-AGGTGTTCTCTAAGGGCTTTATGGACTTGTCC
                                Exon4
yak-CG2952      TGATCCCAACCCTCTTAACTCCTGCAG GTGGAACAGAAGGCAGCGGATTGTGCCTGCAGC
yak-CG2952-r    TGA-----CGTTTCACCTTCTCCAG GTTGACCAGACACTTGTGGGTAG---CTGCAGC

yak-CG2952      ATTGCCGCTTCCTACTGCGGACTGCGCGATCGCCTCTATCCGGACCGCAAGTCCATGGGC
yak-CG2952-r    GATGCCGCTTCCTACTGTGGAGTCCGCGATCGCCTTTACCCAGATCGCCGATCCATGGGC

yak-CG2952      TATCCCTTCGATCGCAGCATCCGCCGGGGTTCTGAGATGTTGGATAGGTTCCCTTACGCCC
yak-CG2952-r    TTCCCATTCGATCGCGTGCCTCGCATGAGTGCAGTTTTGCTGAAGGACTTCCTAACGCCC
                                3' breakpoint
yak-CG2952      AACATGCGCGCCGTCGAGGTCAATACCCATGAGTCCCGTACCGAAAAGCTTCC ---
yak-CG2952-r    AACATGAGCACTGTGGAAGTCAACATTACCCACGAGGACCGCACAGTAAAGCTTCC CAA

yak-CG2952      -----
yak-CG2952-r    TTGGCAAACCTTATCCTGATC TACATATATGTATCCATATATGTATATCTATATTATAGAT
                                (TATATG)n Simple-repeat

yak-CG2952      ----
yak-CG2952-r    GTAT

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