

**CRISPR/Cas9-mediated genetic resource for unknown kinase and phosphatase genes in *Drosophila***

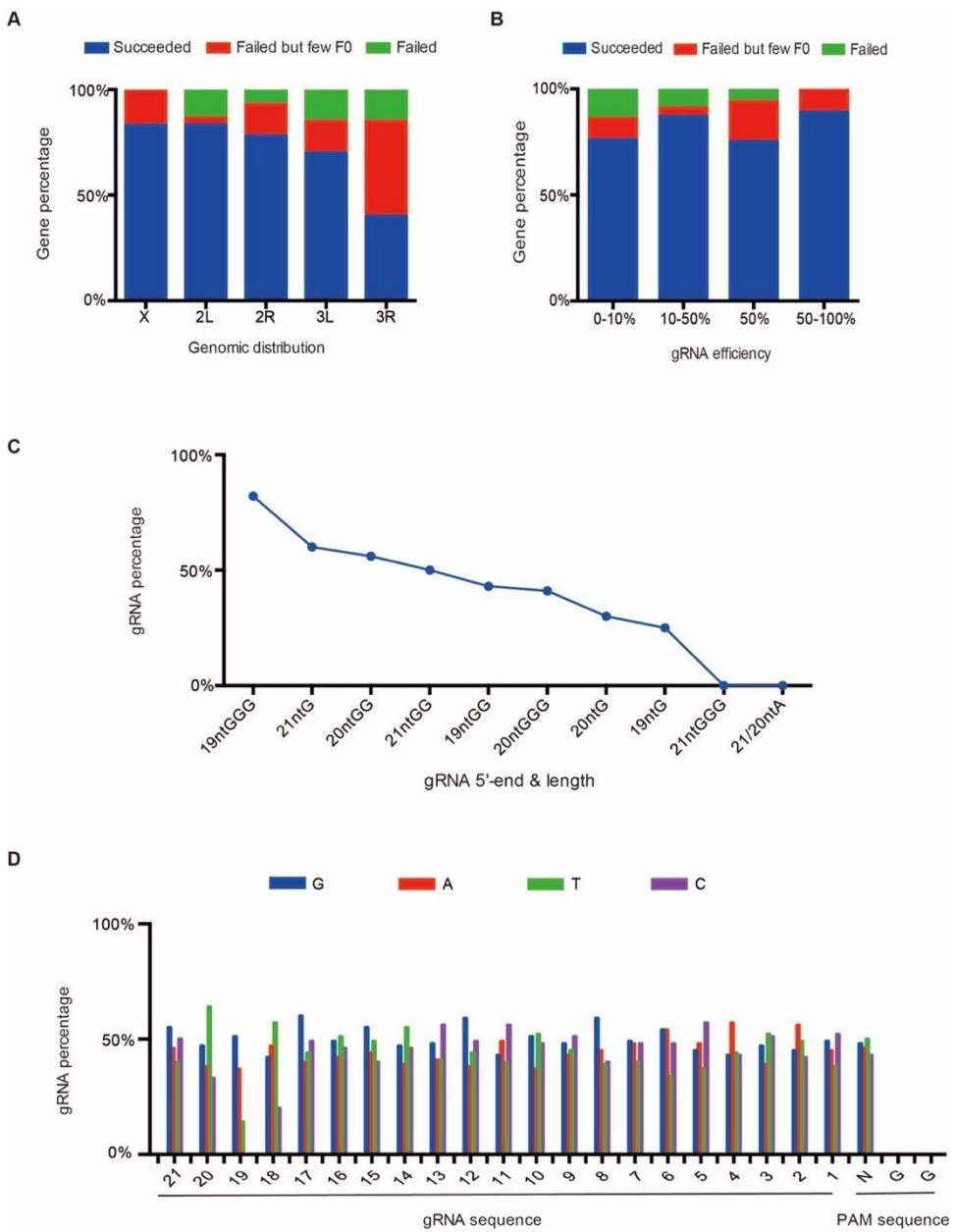
Menghua Wu<sup>1,2</sup>, Xuedi Zhang<sup>2</sup>, Wei Wei<sup>1</sup>, Li Long<sup>1</sup>, Sainan An<sup>3</sup> and Guanjun Gao<sup>2,1,\*</sup>

<sup>1</sup> School of Life Sciences, Tsinghua University, Beijing, 100084, PR China

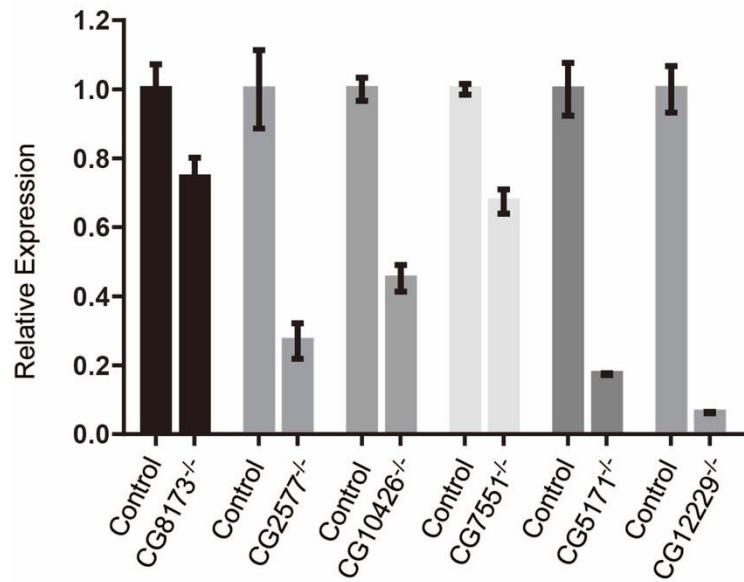
<sup>2</sup> School of Life Science and Technology, ShanghaiTech University, Shanghai, 201210, PR China

<sup>3</sup> National Institute of Biological Sciences, Beijing, 102206, PR China

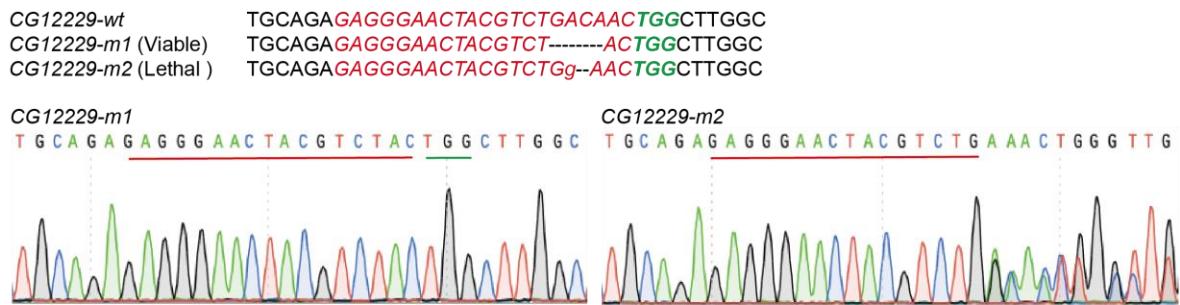
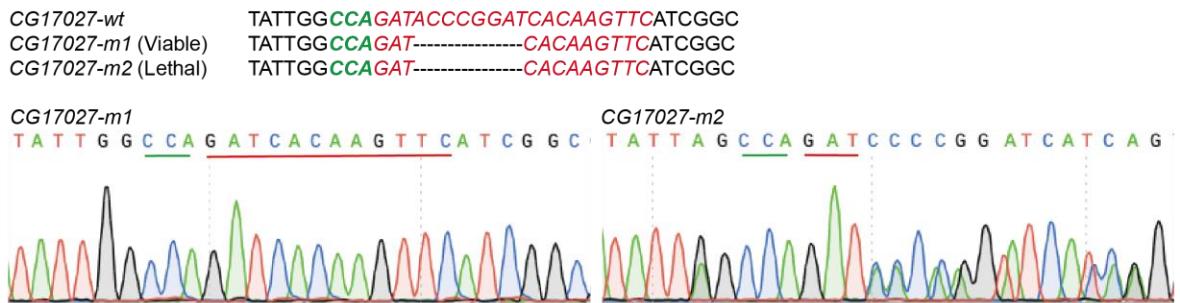
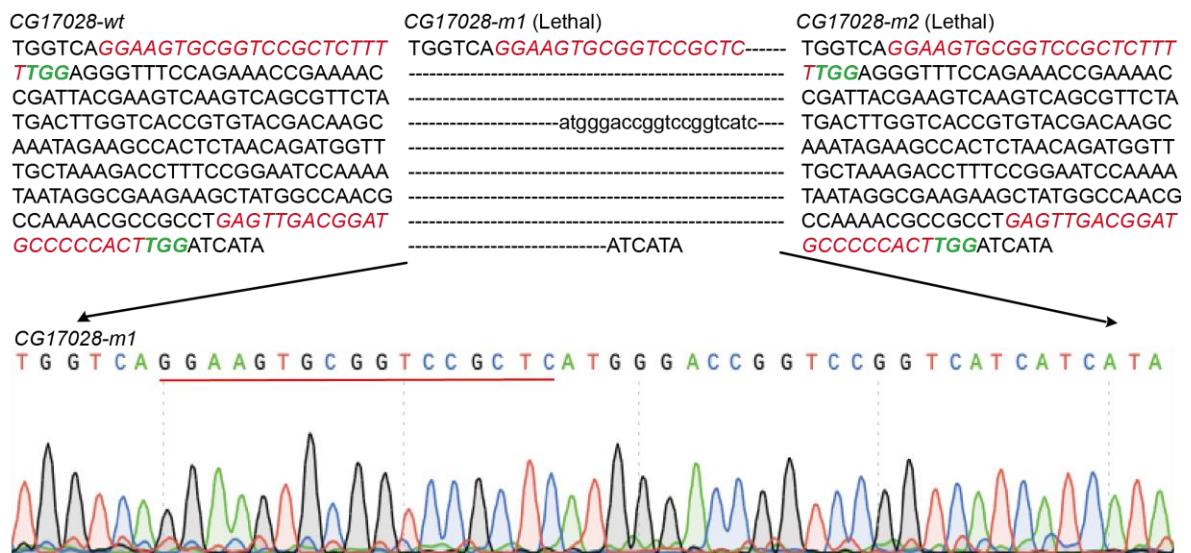
\* Corresponding: gaogj@shanghaitech.edu.cn



**Supplementary Figure 1. CRISPR/Cas9-mediated mutagenesis efficiency.** (A) Mutant yield of different genomic subgroups classified by whether stable mutants were successfully generated. The high percentage of too few F0s in group 3R might be due to the injection of FRT82B flies. (B) The gene percentage of different levels of gRNA efficiency by whether stable mutants were generated. The gRNA efficiency was defined based on a T7EI assay activity with dead injected F0 larvae and classified by different levels of activity (Supplementary Figure 1C). (C) The gRNA percentage of different 5'-end "G"s by whether mutations at the gRNA recognition site were detected. (D) The gRNA percentage at different positions in the gRNA and PAM sequence by whether mutations at the gRNA recognition site were detected. Twenty-one nt of the gRNA sequence was calculated, and the original genomic sequence was added in the case of 19-20 nt gRNA, with the data at positions 21 and 20 as a reference.



**Supplementary Figure 2. Random qRT-PCR verification of our resource.** CG8173, CG2577, CG10426, CG7551, CG5171 and CG12229 mRNA levels were quantified by qRT-PCR for control, CG8173<sup>-/-</sup>, CG2577<sup>-/-</sup>, CG10426<sup>-/-</sup>, CG7551<sup>-/-</sup>, CG5171<sup>-/-</sup> and CG12229<sup>-/-</sup>, respectively. Error bars represent the means  $\pm$  SD values of three independent experiments.

**A****B****C**

**Supplementary Figure 3. Abnormal lethal events in the CRISPR/Cas9 resource.** (A, B) Example frameshift viable and lethal allele sequences for the same gene. Red area, predicted gRNA recognition site. Green area, PAM sequence. (C) Large deletion of CG17028-*m1* sequenced by gel purification of the lower PCR product from heterozygous F2. All DNA sequences were obtained from the flybase website (flybase.org) and the alignments were performed by CLUSTALW.

### Supplementary Note 1: Targeted indel mutations mediated by Cas9/gRNA at 385 mutant alleles for 105 genes.

Note: wt, wild-type DNA sequence; m#, mutation line# DNA sequence. Deletions are shown as red dashes and insertions as highlighted in blue and lowercase letters. The change of DNA length (in nucleotides) caused by each mutation is indicated as purple (+, insertion; -, deletion). Note that some alterations have both insertions and deletions of nucleotides and in these cases the alterations are enumerated in the brackets. All DNA sequences were obtained from the flybase website (flybase.org) and the alignments were performed by CLUSTALW.

CG10702-wt

GGCAACATGCTGGCGTTGGCCTCATGTTCTGGCGCTATATGTCCCGTGCACCGAA.....ATGTTCCC  
GCACCTGACCGTC

CG10702-m1

GGCAACATGCTGGCGTTGGCCTCATG-----CACCTGACCGTC [-258]

CG10702-m2

GGCAACATGCTGGCGTTGGCCTCATG-----CACCTGACCGTC [-258]

CG10702-m3

GGCAACATG-----aCATaTaTaTGGCGCTATATGTCCCGTGCACCGAA.....ATGTTCCCGCACCTGACC  
GTC [-20,+4]

CG11221-wt

TCGATCCTCGGCGACGGTGGTAGCACCAAC.....AGCGTGAGCCGCCGGAGCAGCATCTACAAGAACCG  
GACAAGAATGACGGCGGACAGATCCATCTCATTCCGGACGTGGAGCTGCCGCTGATGACCTT

CG11221-m1

TCGATCCTCGGCGACGGTGGTAGCACCAAC.....AGCGTGAGCCGCCGGAGCAGCATCTACAAGAACCG  
GACAAGAATGACGGCGGACAG-----ATTCCGGATGTGGAGCTGCCGCTGATGACCTT [-9]

CG11221-m2

TCGATCCTCGG-----TGGTAGCACCAAC.....AGCGTGAGCCGCCGGAGCAGCATCTACAAGAACCGGACA  
AGAATGACGGCGGACAGATCCATCTCATTCCGGACGTGGAGCTGCCGCTGATGACCTT [-6]

CG11221-m4

TCGATCCTCGG---ACGGTGGTAGCACCAAC.....AGCGTGAGCCGCCGGAGCAGCATCTACAAGAACCGGACA  
CAAGAATGACGGCGGACAGATCCATCT-----CCGGATGTGGAGCTGCCGCTGATGACCTT [-7]

CG11221-m6

TCGATCCTCGGCGACGGTGGTAGCACCAAC.....AGCGTGAGCCGCCGGAGCAGCATCTACAAGAACCG  
GACAAGAATGACGGCGGACAGATCCtTCg-ATTCCGGACGTGGAGCTGCCGCTGATGACCTT [-3,+2]

CG14006-wt

AGCCCCACATCCAGGAAGGACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTG  
CAGATAGCCGCTGGCGAAGATTACACTCAGTATAAAGGAGCCACCGTGCG

CG14006-m1

AGCCCCAC-----GGAAGGACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTGCA  
GATAGCCGCTGGCGAAGATTACACTCAGTATAAAGGAGCCACCGTGCG [-5]

CG14006-m2

AGCCCCACATC---GAAGGACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTGCA  
GATAGCCGCTGGCGAAGATTACACTCAGTATAAAGGAGCCACCGTGCG [-3]

CG14006-m3

AGCCCCACATCCAG-----ACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTGCAG  
ATAGCCGCTGGCGAAGATTACACTCAGTATAAAGGAGCCACCGTGCG [-5]

CG14006-m4

AGCCCCACAT--GGAAGGACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTGCA  
GATAGCCGCTGGCGAAGATTACACTCAGTATAAAGGAGCCACCGTGCG [-3]

CG14006-m5

AGCCCCACATCCAGGAAGGACAGACGCTGCTTAACATGCTGTACGTGAACAACCAGGTCC.....TGCGCCTG  
CAGATAGCCGCTGGCGAAGATTACACTCAcTATAAtcGGAGCCACCGTGCG [+4,-2]

CG17010-wt

CCGGCTTACGCAGCCCTTCAAATGGAAAGAAGCTGGATGTGGTTCTCGGGACGGCAAACATCGAAT  
ATAT

CG17010-m1

CCGGCTTACGCAGCCCTTCAAATGGAAAGAAGCTGGATGTGGTTG---TCGGGACGGAAACATCGAATAT  
AT [-3]

CG17010-m2

CCGGCTTACGCAGCCCTTCAAATGGAAAGAAGCTGGATGTGGTTGTCTT-----CAAACATCGAATATAT [-  
8]

CG17010-m3

CCGGCTTACGCAGCCCTTCAAATGGAAAGAAGCTGGATGTGGTTCTCGG-ACGGCAAACATCGAATA  
TAT [-1]

CG2964-wt

CATGTCGTTGTCGCCGAAATCCGTGCTAAAGGAGGGCTCCACACAGCTGAGCCACATCTG.....CAACGAGG  
CGCTGGAGAGGATTCATAGGAGACGGGCAAATCCGAACGGTCGCCATTGC

CG2964-m1

CATGT-----CGGGCCAATCCGAACGGTCGC

CATTG C [-267]

CG2964-m2

CATGTCGTTGTCGCCGAAATCCGTGCTAAAGGAGGGCTCCACACAGCTGAGCCACATCTG.....CAACGAGG  
CGCTGGAGAGGATTCATAGA---CGGGCCAATCCGAACGGTCGCCATTGC [-3]

CG2964-m3

CATGTCGTTGTCGCCGAAATCCGTGCTAAAGGAGGGCTCCACACAGCTGAGCCACATCTG.....CAACGAGG  
CGCTGGAGAGGATTCAT-----CGGGCCAATCCGAACGGTCGCCATTGC [-6]

CG2964-m4

CATGTCGTTGTCGCCGAAATCCGTGCTAAAGGAGGGCTCCACACAGCTGAGCCACATCTG.....CAACGAGG  
CGCTGGAGAGGATTCATAA-GAGACGGGCAAATCCGAACGGTCGCCATTGC [-1]

CG31714-wt

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA.....CTCCTATT  
CCTCGTCCAGTCCAGGATGCGGGGGTATGCTAAAGG--CGCCATGGCAACAT

CG31714-m1

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA.....CTCCTATT  
CCTCGTCCAGTCCAGGATGCGGGGGTATGCTAAAGG--CGCCATGGCAACAT [-2]

CG31714-m2

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA-----  
-----GGCAACAT [-193]

CG31714-m3

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA.....CTCCTATT  
CCTCGTCCAGTCCAGGATGC-----CATGGCAACAT [-21]

CG31714-m4

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA.....CTCCTATT  
CCTCGTCCAGTCCAGGATGCGGGGGTATG-----CaCCATGGCAACAT [-10,+1]

CG31714-m5

GCTGCTGACGCTCCTGCTGCCGGCGGTCTGCCACACCAGACGCCTCCAGATGCAGACCA.....CTCCTATT  
CCTCGTCCAGTCCAGGATGCGGGGGTATGCaTAcAGG--ATGttGCAACAT [-7,+4]

CG3277-wt

GAAATCACAGAGCTGACCACAAATGTCACGCTCTACATGGAGAAAATACCACGCCTACAGGTGCGA

CG3277-m1

GAAATCACAGAGCTGACCACAAATGTCACGCTCTACATGGAGAAAATACCACG-----TGCAGA [-8]

CG34380-wt

ACCAACGCCAACAGCAGCCGCTCCCCGCCCTCCATGCCGCCGGGGGGCTGGACGCTGTGCCTCTGGACG  
CTGGTGATGCCAGCGGCTGTTAATGCTAACGTACCGACGACGATGGCA

CG34380-m1

ACCAACGCCAACAGCAGCCGCTCCCCGCCCTCCATGCCGCCGGGGGGCTGGACGCTGTGCCTCTGGACG  
CTGGTGATCGC---GGCTGTTAATGCTAACGTACCGACGACGATGGCA [-4]

CG34380-m2

ACCAACGCCAACAGCAGCCGCTCCCCGCCCTCCATGCCGCCGGGGGGCTGGACGCTGTGCC-----  
-AGCGGCTGTTAATGCTAACGTACCGACGACGATGGCA [-20]

CG3544-wt

TGGACATGCTGATGGACTGTTAGTGAAACAGGGAGCGGATATGCACACGGTGGTCTATTGCCGGAGCT  
GCTCAGCAGCACGGTTGCGTC.....CGGACGTGCAGGTCCGTGAAATGGAGCACACCGTCG

CG3544-m1

TGGACATGCTGATGGACTGTTAGTGAACACAGGGAGCGGATATGC---CGGTGGTCTCTATTGCCGGAGCTG  
 CTCAGCAGCACGGTTCGTC.....CGGACGTGCAGGTCCGTGAAATGGAGCACACCGTCG **[+3]**  
 CG3544-m2  
 TGGACATGCTGATGGACTGTTAGTGAACACAGGGAGCGGATATGCACAaCGGTGGTCTCTATTGCCGGAGC  
 TGCTCAGCAGCACGGTTCGTC.....CGGACGTGCAGGTCCGTGAAATGGAGCACACCGTCG **[+1]**  
 CG3544-m3  
 TGGACATGCTGATGGACTGTTAGTGAACACAGGGAGCGGATAT-----  
 --CGAGGTCCGTGAAATGGAGCACACCGTCG **[+177]**  
 CG3544-m4  
 TGGACAT---AT---C-----C-GG-----CACGGTGGTCTCTATTGCCGGAGCTGCTCAGCAGCACGGTTG  
 CGTC.....CGGACGTGCAGGTCCGTGAAATGGAGCACACCGTCG **[+33]**  
 CG3544-m5  
 TGGACATGCTGATGGACTGTTAGTGAACACAGGGAGCGGATATGCACAItTGGTCTCTATTGCCGGAGCTG  
 CTCAGCAGCACGGTTCGTC.....CGGACGTGCAGGTCCGTGAAATGGAGCACACCGTCG **[+3,-2]**

**CG4629-wt**  
 CGACGACGACGCCCTGACAATTGTCAGCCGCCACGCCACTCCGCCCTACCAGCGGCTACCAAGGC  
 GCTGCAATGCGATCCCGCTCGGCCACGAGGTGAGTGCAAATTGAA  
 CG4629-m1  
 CGACGACGACGCCCTGACAATTGTCAGCCGtggAGCCCccACTCCGCCCTACCAGCGGCTACCAAGG  
 CGCTGCAATGCGATCCCGCTCGGCCACGAGGTGAGTGCAAATTGAA **[+7,-4]**  
 CG4629-m2  
 CGACGACGACGCCCTGACAATTGTCAGCCGCCACC---ACTCCGCCCTACCAGCGGCTACCAAG---GCT  
 GCAATGCGATCCCGCTCGGCCACGAGGTGAGTGCAAATTGAA **[+6]**  
 CG4629-m3  
 CGACGACGACGCCCTGACAATTGTCAGCCGtggAGCCCccACTCCGCCCTACCAGCGGCTACCAAG-G  
 GCTGCAATGCGATCCCGCTCGGCCACGAGGTGAGTGCAAATTGAA **[+7,-5]**  
 CG4629-m4  
 CGACGACGACGCCCTGACAATTGTCAGCCGCCAC-----TCCGCCCTACCAGCGGCTACCAAGGGC-TG  
 CAATGCGATCCCGCTCGGCCACGAGGTGAGTGCAAATTGAA **[+8]**

**CG4839-wt**  
 GCCGAAAATGGCAGCGCAAACAATGGCGTCCAGGAGCGGAAGTTCCGCACCAA.....AGCGGGTGCAGCCG  
 GGTGC  
 CG4839-m1  
 GCCGAAAA-----CAATGGCGTCCAGGAGAGGAAGTTCCGCACCAA.....AGCGGGTgcgctgCAGCCGGG  
 TGC **[+12,+6]**  
 CG4839-m2  
 GCCGAAAATGGCA-----TCCAGGAGAGGAAGTTCCGCACCAA.....AGCGGGTgcgctgCAGCCGGGTG  
 C **[+15,+6]**

**CG5790-wt**  
 AAAGTCGGGACCAACATGGATTGTGCTAATACGAATTAGAATCGGCAGGGAAAGA.....CCGGAACTATGC  
 CTTCCGTTCGGGCACTAACCATCATTCTAGGCATCAACAGCTCCTTC  
 CG5790-m1  
 AAAGTCGGGAC---CATGGATTGTGCTAATACGAATTAGAATCGGCAGGGAAAGA.....CCGGAACTATGCCT  
 TCCGTTCGGGCACTAACCATCATTCTAGGCATCAACAGCTCCTTC **[+3]**  
 CG5790-m2  
 AAAGTCGGGACtcACATGGATTGTGCTAATACGAATTAGAATCGGCAGGGAAAGA.....CCGGAACTATG  
 CCTTCCG-----GCACTAACCATCATTCTAGGCATCAACAACTCCTTC **[+4,-6]**  
 CG5790-m3  
 AAAGTCGGGACttagCACATGGATTGTGCTAATACGAATTAGAATCGGCAGGGAAAGA.....CCGGAACTATG  
 CCTTCCG-----GGCACTAACCATCATTCTAGGCATCAACAACTCCTTC **[+4,-5]**  
 CG5790-m4  
 AAAGTCGGGACttagCACATGGATTGTGCTAATACGAATTAGAATCGGCAGGGAAAGAGTT.....GAACATGCC  
 T-----aGGC-----ATAGACTAGGCATCAACAACTCCTTC **[+4,-19]**  
 CG5790-m5  
 AAAGTCGGGCAtaaAcGGGcTGTGCTAATACGAATTAGAATCGGCAGGGAAAGA.....CCGGAACTATGCCTTC  
 CGTTCCGGCACTAACCATCATTCTAGGCATCAACAGCTCCTTC **[+7,+4]**

**CG7094-wt**  
 GCCCATTGGGTCCGGTCTCGCGATATATCTCGGACTAACGATCACGGATGGATCCGAGGTGGCCA  
 TTAAGGTGGAGAAGAACGATGCCAAGTACCGCAGCTGATATACGAGGC  
 CG7094-m1  
 GCCCATTGGGTCCGGTCTCGCGATATATCTCGGACTAACGATCACGGATGGATCCGAGGcaaGCAT  
 -----GCCAAGTACCCGAGCTGATATACGAGGC **[+22,+3]**  
 CG7094-m2

GCCCATTGGGTCCGGGCTTCGGC-T-CTC-CT-TC-T-CC-TTAAGGTGGAGAAGAACG  
 ATGCCAAGTACCCCGCAGCTGATATAACGAGGC **[-35,+1]**  
 CG7094-m3  
 GCCCATTGGGTCCGGGCTTCGGCAGATATATCTCGGACTAACGATCACGGATGGATCCGA-CATTAA  
 GGTGGAGAAGAACGATGCCAAGTACCCCGCAGCTGATATAACGAGGC **[-6]**  
 CG7094-m4  
 GCCCATTGGGTCCGGGCTTCGGCAGATATATCTCGGACTAACGATCACGGATGGATCCGAGGTG-----  
 GTGGCGAAGAACGATGCCAAGTACCCCGCAGCTGATATAACGAGGC **[-9]**  
 CG7094-m5  
 GCCCATTGGGTCCGGGCTTCGGCAGATATATCTCGGACTAACGATCACGGATGGATCCGAGGTG-----  
 -GAGAAGAACGATGCCAAGTACCCCGCAGCTGATATAACGAGGC **[-12]**  
 CG7094-m6  
 GCCCATTGGGTCCGGGCTTCGGCAGATATATCTCGGACTAACGATCACGGATGGATCC-A-CC-TAA  
 GGTGGAGAAGAACGATGCCAAGTACCCCGCAGCTGATATAACGAGGC **[-7]**

CG7236-wt  
 TCAGTCGGCTGGCGAGGGCTCCTACGGTGTGGTCTACAAGTGCCGGATCGGGAAACGG  
 CG7236-m1  
 TCAGTCGGCTGGCGA-CT-GG-G-CTACAgGTGCCGGATCGGGAAACGG **[-13]**  
 CG7236-m2  
 TCAGTCGGCTGG-----GTGTGGTCTACAAGTGCCGGATCGGGAAACGG **[-15]**  
 CG7236-m3  
 TCAGTCGGCTGGCGAGGGCTC---GGTGTGGTCTACAAGTGCCGGATCGGGAAACGG **[-4]**

CG9222-wt  
 GTGGTACCCCTTTAATGGCGACATCTCCAGAAGAAAAAACGATCAAGGCGGAGG.....ACTCGGGTCGTC  
 GTCAGGAGCAGAAGGTCTACACCTTCAGTGACCGGCCACCACAACCAAGCCACCGGCACCATCCGGA  
 CG9222-m1  
 GTGGTACCCCTTTAATGGCGACATCTCCAGAAGAAAAAACGATCAAGGCGGAGG.....ACTCGGGTCGTC  
 TCAGGAGCAGAAGGTCTACACCTTCAGTGACCGGCCACCACAACCAAGCCACCGGCACCATCCGGA **[-1]**  
 CG9222-m2  
 GTGGTACCCCTTTAATGGCGACATCTCCAGAAGAAAAAACGATCAAGGCGGAGG.....ACTCGGGTCGTC-  
 -----TACACCTTCAGTGACCGGCCACCACAACCAAGCCACCGGCACCATCCGGA **[-17]**

CG9541-wt  
 TTTGTTTAGGCGCCCCGGTAGTGGCAAGGTACCCATTGCGATACCTCATGCAGGAG  
 CG9541-m1  
 TTTGTTTAG-----TGGCAAGGTACCCATTGCGATACCTCATGCAGGAG **[-13]**  
 CG9541-m2  
 TTTGTTTAGGCGCCCCGGT-GTGGCAAGGTACCCATTGCGATACCTCATGCAGGAG **[-1]**

CG10376-wt  
 GGTGGTCAGCCGGAGTTGTGTAACTCGTACGGCCAATGAGACATACAAAGTGTCCGGCGAGGAGCGTCAT  
 GCCGAATTGGTCTCAGCTATTG  
 CG10376-m1  
 GGTGGTCAGCCGGAGTTGTGTAACTCGTACGGCCAatTGtAtgtacgGACATACAAAGTGTCCGGCGAGGAGCGT  
 CATGCCGAATTGGTCTCAGCTATTG **[+7]**  
 CG10376-m2  
 GGTGGTCAGCCGGAGTTGTGTAACTCGTACGGCCAatTGGcCgTACATACAAAGTGTCCGGCGAGGAGCGTCA  
 TGCCGAATTGGTCTCAGCTATTG **[+3]**  
 CG10376-m3  
 GGTGGTCAGCCGGAGTTGTGTAACTCGTACGGCCA-----GGAGCGTCATGCCGAATTGGTCTC  
 AGCTATTG **[-25]**  
 CG10376-m4  
 GGTGGTCAGCCGGAGTTGTGTAACTCGTACGGC-----CATACAAAGTGTCCGGCGAGGAGCGTCATGCCG  
 AATTGGTCTCAGCTATTG **[-8]**

CG15385-wt  
 TCGCCAAGTACAGAGAACGCTGTGCTCCGGCTCAGCTGCAGCGTTGGATGATGGCGGCATCTGGAG  
 GGTTGGAAGCTTCAGGGCGTGTCTGGTCATCAGGCACGGGGATCGGG  
 CG15385-m1  
 TCGCCAAGTACAGAGAACGCTGTGCTCCGGCTCAGCTGCAGCGTTGGAG-----GGGTTGGAAG  
 CTTCAGGGCGTGTCTGGTCATCAGGCACGGGGATCGGG **[-18]**  
 CG15385-m2  
 TCGCCAAGTACAGAGAACGCTGTGCTCCGGCTCAGCTGCAGCGTTGGATGATGGCGG-TTGGAG  
 GTTGGAAAGCTTCAGGGCGTGTCTGGTCATCAGGCACGGGGATCGGG **[-4]**

CG15385-m3

TCGCCAAGTACAGAGAACGCTGTGCTCCGGCTCAGCTGCAGCGTTGGATGGCG-----GGTTG  
GAAGCTTCAGGGCGTGCTCCTGGCATCAGGCACGGGATCGGG [-11]

CG16771-wt

GTTTCGAAAACTCAGCGATGTGGACATGACGGAAGTGCAGCTGAACAATTGGATGACTC

CG16771-m1

GTTTCGAAAACTCAGCGATGTGGACATGACGGAAGTGCAGCTG---AATTGGATGACTC [-3]

CG16771-m2

GTTTCGAAAACTCAGCGATGTGGACATGACGGAAGTGCAGCTGA---AATTGGATGACTC [-2]

CG17124-wt

AACGAGAAGGGGGCGGAGGTGAAGGAGCGGCGGGAGAAGTTCTCACGGCCAAGTACGGT

CG17124-m1

AACG-G-----T-ACG-----GTACGGT [-44]

CG17124-m2

AACGAG---GGGGCGGAGGTGAAGGAGCGGCGGGAGAAGTTCTCACGGCCAAGTACGGT [-2]

CG17124-m3

AACG-----GT [-54]

CG17124-m4

AACGA---GGGGCGGAGGTGAAGGAGCGGCGGGAGAAGTT-----G-----GTACGGT [-14]

CG17124-m5

AACGAGgtGGGG-CGGAGGTGAAGGAGCGGCGGGAGAAGTTCTCACGGCCAAGTACGGT [-3,+2]

CG5171-wt

ACCTGTAATTAGTAATCTCGAGGGATTTGCGAATAATTACCTGGTAAGTCGGAGTTAT.....AGCGAAGACC  
AAAATGCCGTGGAACTGGAGGCCACTGCACAAGATAGCCAAGCATTCCCAGT

CG5171-m1

ACCTGTAATTAGTAATCTCGAGGGATTTGCGAATAATTACCTGGTAAGTCGGAGTTAT.....AGCGAAGACC  
AAAATGCCGTGGAACTGGAGGCCACTGCACAAGATAGCCAAGCA-CCCAAAGT [-1]

CG5171-m2

ACCTGTAATTAGTAATCTCGAGGGATTTGCGAATAA-----GTCGGAGTTAT.....AGCGAAGACCAAAATG  
CCCGTGGAACTGGAGGCCACTGCACAAGATAGCCAAGCATTCCCAGT [-13]

CG5171-m3

ACCTGTAATTAGTAATCTCGAGGGATTTGCGAATAATTACCTGGTAAGTCGGAGTTAT.....AGCGAAGACC  
AAAATGCCGTGGAACTGGAGGCCACTGCACAAGATAGCC-----CAAAGT [-8]

CG5171-m4

ACCTGTAATTAGTAATCTCGAGGGATTTGCGAATAATTACCTGGTAAGTCGGAGTTAT.....AGCGAAGACC  
AAAATGCCGTGGAACTGGAGGCCACTGCACAAGATAGCCAAGCAaTCCCAGT [+1]

CG5177-wt

AGAAGGCACCATTGCTGAAGAAGGAGGAGGACTACGTGAAGGCCCTCGAGGGGTGAGTT.....GCTCACC  
GAGGAGCTGCCGTACGCCAAGGATACCGAGATCAACATCAAGAAACTGGC

CG5177-m1

AGAAGGCACCA-----AGGATACCGAGATCAACATC  
AAAGAAACTGGC [-198]

CG6380-wt

CACATGATCATCGACGAACCAAAGACACCCCTCGTCTTGAGGAGGATTGCCAAAGGAGTTGGATACAAAT  
GCCCTGATCGAAAAGTTGAGACACACATCAAAGTCAGAAATGCCGGCA

CG6380-m1

CACATGATCATCGACGAACCAAAGACACCCCTCGTCTTGAGGAGGATTGCCAAAG---TTGGATACAAATGC  
TTGAGACACACATCAAAGTCAGAAATGCCGGCA [-29]

CG6380-m2

CACATGATCATCGACGAACCAAAGACACCCCTCGTCTTGAGGAGGATTGCCAAAG---TTGGATACAAATGC  
CCTGATCGAAAAGTTGAGACACACATCAAAGTCAGAAATGCCGGCA [-3]

CG6380-m3

CACATGATCATCGACGAACCAAAGACACCCCTCGTCTTGAGGAGGATTGCCAAAGGAtacaaaGTTGGATAC  
AAATGCCCTGATCGAAAAGTTGAGACACACATCAAAGTCAGAAATGCCGGCA [+6]

CG7115-wt

CTCTATTGCAAGCGGTAGATGTGTGGAGTCGCAGCATCCTGGGACGCATCCAGGCAACCCTCGGTGCCA  
GAAG

CG7115-m1

CTCTATTGCAAGCGGTAGATGTGTGGAGTCGCAGCATCCTGGGACGCATCC-----TgGGTCGCCAGAAG  
[-10,+1]

CG7115-m2

CTCTATTGCAAGCGGTAGATGTGTGGAGTCGCAGCATCCTGtttaGaGctAaaaatagCaagttaaaataagGCTAgTC  
 CgttAtcaactgaaaaagtGGCACCGaGTCGCCAGAAG [+45]  
 CG7115-m3  
 CTCTATTGCAAGCGGTAGATGTGTGGAGTCGCAGCATCCTGGG-----CCTCGGTGCCAGAAG [-15]  
 CG7115-m4  
 CTCTATTGCAAGCGGTAGATGTGTGGAGTCGCAGCA-----GA---A---GG-----CCTCGGTGCCAGAAG [-17]

CG7180-wt  
 GCAGAGGAAAAGCCGAGCCATCGTCTCCATACCGAACACCATAAACTGAGTATGCTCAA  
 CG7180-m1  
 GCAGAGGAAAAGCCGAGCCATC-----CATACCGAACACCATAAACTGAGTATGCTCAA [-5]  
  
 CG10082-wt TTTCTTGGGGATTGGGGATGGGAGATTCTGACTTGTGTCATATCAGAACATGTT  
 CAAATATAAACAGCCCGAC.....CCACAGCAGCAGCAGCAGCAG.....GTTGCAGTTGCCAGTGGA  
 TCCAGCTTCTGCAACAAGGCTCAT  
 CG10082-m1  
 TTTCTTGGGGATTGGGGATGGGAGATTCTGACTTGTGTCATATCAGAACATGTTCAAATATAACAA  
 GCCGCGAC.....CCACAGCAGCAG-----CAGCAc.....GTTGCAGTTGCCAGTGGAATCCAGCTTCTGCAAC  
 AAGGCTCAT [-7,+1]  
 CG10082-m2  
 TTTCTTGGGG-----G-----  
 -----ACAAGGCTCAT [-244]  
 CG10082-m3  
 TTTCTTGGGG-----CACCAGCTCGGTGCCACTTTCAAGTTGATAACGGACTAGCCTTATTTAACTTGCTAT  
 TTCTAGCTCTAAACATCCCCAAGAAATATACCTATAGTGGTCGTATTAAGG-----CTCGGACAAGGCT  
 CAT [-125]  
 CG10082-m4  
 T-----AACAAAGG-----  
 -----CTCAT [-253]

CG10459-wt  
 TGTGGTCGGTATCCTAACGCCACGATGCCAACAGATCCTGGCCAGTGGCGGTGCAGACTGCA  
 CG10459-m1  
 TGTGGTCGGTATCC-----GATGCCAACAGATCCTGGCCAGTGGCGGTGCAGACTGCA [-9]  
 CG10459-m2  
 TGTGGTCGGTATCC-----TGCCAAGATCCTGGCCAGTGGCGGTGCAGACTGCA [-11]

CG1344-wt  
 ACTAAAAGGAATACTTGTGAGGAAAATGCGGTGGAGACTAATCAATTGGACAGTT.....TCAGACCTCTAG  
 ATGAGGTGCTGGCCCAGCAGACTGACATTGAAGTCTGCCTAGG  
 CG1344-m1  
 ACTAAAAGGAATACTTGTGAGG-----ACTGACATTGAAGTC  
 TGCCTAGG [-340]  
 CG1344-m2  
 ACTAAAAGGAATACTTGTGAGGAAAATGCGGTGGAGACTAATCAATTGGACAGTT.....TCAGACCTCT  
 -----GACATTGAAGTCTGCCTAGG [-25]  
 CG1344-m3  
 ACTAAAAGGAATACTTGTGAGGAAtAcTTGCGGTGGAGACTAATCAATTGGACAGTT.....TCAGACCTCTA  
 GATGAGGTGCTGGCCCAGCAGACTGACATTGAAGTCTGCCTAGG [+2]

CG17528-wt  
 AGGCTCTATTATCGAAAAGACGAATCAACCACATAATGTTAGGAAGATAAACTACA  
 CG17528-m1  
 AGGCTCTATTATCGAAAAGACGAATCAACCACATAAaT-----AGATAAACTACA [-8,+2]

CG3216-wt  
 GGGCTCTGGACTGGCTCGGACATGTACTTCCAGGACGACGTAATCGCTTATTGGAC  
 CG3216-m1  
 GGGCTCTG-----CGGACATGTACTTCCAGGACGACGTAATCGCTTATTGGAC [-9]  
 CG3216-m2  
 GGGCTCTG-----GCTCGGGACATGTACTTCCAGGACGACGTAATCGCTTATTGGAC [-5]

CG33671-wt  
 GCTGGAGGACAGCCAGGTGGCAAGTTCAACTGGAGGCCCTAACTGCACACT  
 CG33671-m1  
 GCTGGAGGACAGCCAGGTGGCAAG-----GCCCTTAACTGCACACT [-13]

CG33671-m2

GCTGGAGGACAGCCAGGTGGCAAGTTTcCAcCTGGAGGtgtagGCCCTTAAGTCACACT [+7,-1]

CG3494-wt

GTGACGGATTGAACAGCCCCCAGGCTGCAGGGAGGAAAGGAAGCGGAAGCGGATGGGAGTC.....CTCAAAT  
CAGCGAGGTGCCCATGGAGGTATTCGAGGCAGCTCAGCAGGAGCTAGTGAA

CG3494-m1

GTGACGGATTGAACAGCCCCTAGGCTGCAGGGAGGAAAGGAAGCGGAAGCAGATGGGAGTC.....CTCAGAT  
CA---AG---GtC---AG---A---TCGAGGCAGCTCAGCAGGAGCTAGTGAA [-14,+2]

CG3499-m2

GTGACGGATTGAACAGCCCCCAGGCTGCAGGGAGGAAAG-----GAAGCGGATGGGAGTC.....CTCAAATCAG  
CGAGGTGCCCATGGAGGTATTCGAGGCAGCTCAGCAGGAGCTAGTGAA [-6]

CG3494-m3

GTGACGGATTGAACAGCCCCCAGGCTGCAGGGAGGAAAG-----GAAGCGGATGGGAGTC.....CTCAGATCAG  
CGAGGTGCCCATGGAGGTAgcTTCGAGGCAGCTCAGCAGGAGCTAGTGAA [-6,+2]

CG3608-wt

TTTGTGCAGACCATGAAGGTACTTCACTCCGATGCGCCGCAAAACCCCATTGAGGACCTG

CG3608-m1

TTTGTGCAGAC---AAc---ACTTCACTCCGATGCGCCGCAAAACCCCATTGAGGACCTG [-7,+1]

CG3608-m2

TTTGTGCAGA-----AGGTACTTCACTCCGATGCGCCGCAAAACCCCATTGAGGACCTG [-6]

CG4945-wt

CTACTGGTGGAGCATCGGGGATCACAGACGGAGATGGTCCTGAAAGCTGTACCCAAACCA.....CAGGAGTA  
TGCTCCACTAGGTGGTAACCTCTATAATAACAATATTATATATCTATATA

CG4945-m1

CTACTGGTGGAGCATCGGG-----GATGGTCCTGAAAGCTGTACCCAAACCA.....CAGGAGTATGCTCCA  
CTAGGTGGTA--TCCTATAACTAACAAATATTATATATCTATATA [-15]

CG4945-m2

CTACTGGTGGAGCATCGGG-----ACGGGAGATGGTCCTGAAAGCTGTACCCAAACCA.....CAGGAGTA  
TGCTCCACTAGGTGGG--ACTCCTATAATAACAATATTATATATCTATATA [-2]

CG4945-m3

CTACTGGTGGAGCATCGGG-----ACGGGAGATGGTCCTGAAAGCTGTACCCAAACCA.....CAGGAGTATGC  
TCCACTAGGTGGTA--TCCTATAACTAACAAATATTATATATCTATATA [-9]

CG5757-wt

GCGCGGGAAAACGTGGAGCGTTGATAATATTGAAGGATGTGATCGAAGTGGAAAGACCA

CG5757-m1

GCGCGGGAAAACGTGGAGCGTTGATAATATTgTGAAGGATGTGATCGAAGTGGAAAGACCA [+1]

CG8179-wt

ATCGGGAAAGGATGGCCGGCGCAAGGTACGGAGTGCAGTCAGTGCACGGAGCAGTGG

CG8179-m1

ATCGGGAAAGGAT-----CGCAAGGTACGGAGTGCAGTCAGTGCACGGAGCAGTGG [-6]

CG8726-wt

TATGCTCTGCCTGCGAACGACACTACGTGGTCGCTGGTGGAAAGTATGGTGCCATAGGTATGCT

CG8726-m1

TATGCTCTGCCTGCGAACGACACTACGTGGTCGCTGGTGGAAAGTATGGTGCCA--GGTATGCT [-2]

CG8726-m2

TATGCTCTGCCTGCGAACGACACTACGTGGTCGCTGGTGGAAAGTATGGTGCCAT-GGTATGCT [-1]

CG8878-wt

ACGCAAGCGAAAGCGTTCTCGCGTCAAGGCCGCCAGAAGCGCCAGCGCTTGAGTGGTGGTCCAGCAGC  
GCCAATGGCTTC

CG8878-m1

ACGCAAGCGAAAGCGTTCTCGCGTCAAGGCCGCCAGAAGCGCCAGCG-----CGCCAATGGCTT  
C [-20]

CG8878-m2

ACGCAAGCGAAAGCGTTCTGCG-----GTGGTCCAGCGCCAGCGCCAATGGCTTC [-34]

CG8878-m3

ACGCAAGCGA-----TG-G-----CC-----TG-Ga-----TG-GTCCAGCGCCAGCGCCAATGGCTTC [-39,+1]

CG8878-m4

ACGCAAGCGAAAGCGTTCTCGCGTCAAGGCCGCCAGAAGCGCCAGC-C-----GTGGTCCAGCGCCAGCGCCA  
ATGGCTTC [-8]

CG10417-wt

TAGCCGTTGGAGCTAGCTCTATGCAAGGATGGCGGAACAGCCAAGAGGTAAATTGAGATG  
CG10417-m1  
TAGCCGTTGGAGCTAGCTCTAT---AGGATGGCGGAACAGCCAAGAGGTAAATTGAGATG [-3]  
CG10417-m2  
TAGCCGTTGGAGCTAGCTCTAT---GGATGGCGGAACAGCCAAGAGGTAAATTGAGATG [-4]  
CG10417-m3  
TAGCCGTTGGAGCTAGCTCTATGC---ATGGCGGAACAGCCAAGAGGTAAATTGAGATG [-4]  
CG10417-m4  
TAGCCGTTGGAGCTAGCTCTAaGC--GGATGGCGGAACAGCCAAGAGGTAAATTGAGATG [-3,+1]

CG3290-wt

ACAGTCACAGCTGCTCGCATCCTGAAAGGACAACGCCAAGGAAACACTGGGGAGGAGTCC  
CG3290-m1  
ACAGTCACAGCTGCTCGCATCCTAAAAGGACAACGCCA----CACTGGGGAGGAGTCC [-5]

CG3292-wt

TAGCCATTAGCCTGGTGTATGCACCCCTGGTGGCCACCTCCTGGCTGCTTCATAG.....CGCGAAGGAAA  
CCTTATCGACCAAATGCCATGGCAAGGGAAAACCCGGACCAGAGGAGGAAGAA  
CG3292-m1  
TAGCCATTAG-CTGGTGTATGCACCCCTGGTGGCCACCTCCTGGCTGCTTCATAG.....CGCGAAGGAAA  
CTTATCGACCAAATGCCATGGCAAGGGAAAACCCGGACC ggtcctcc AGAGGAGGAGAAGAA [-1,+8]  
CG3292-m2  
TAGCCATTAGCCTGGTGTATGCACCCCTGGTGGCCACCTCCTGGCTGCTTCATAG.....CGCGAAGGAAA  
CCTTATCGACCAAATGCCATGGCAAGGGAAAACCCGGACC-GAGGAGGAGAAGAA [1]  
CG3292-m3  
TAGCCA-----AGAAGAA [-2  
32]  
CG3292-m4  
TAGCCATTAGCCTGGTGTATGCACCCCTGGTGGCCACCTCCTGGCTGCTTCATAG.....CGCGAAGGAAA  
CCTTATCGACCAAATGCCATGGCAAGGGAAAACCCG T-CC-GGAGGAGAAGAA [-5,+1]

CG3530-wt

AGCTTCCCTTGAGCACGACAGGATCTCGCTACTCATCCGCTGCAAGACCTTCCTCTCCG.....AAGGATGAT  
TTCCCCAAGAACGCTGGCTGGGATTACTTAAACTGGAGGCGGAGTTCAAG  
CG3530-m1  
AG-----CACGACAGGATCTCGCTACTCATCCGCTGCAAGACCTTCCTCTCCG.....AAGGATGATTTCCC  
CAAGAACGCTGGCTGGGATTACTTAAACTGGAGGCGGAGTTCAAG [-11]  
CG3530-m2  
AGCTTCCCTTGAGCACGACAGGATCTCGCTACTCATCCGCTGCAAGACCTTCCTCTCCG.....AAGGATGAT  
TTCCCCAAGAACGCTGGCTGGGATTACTTAAACTG-GCGGAGTTCAAG [-3]

CG6805-wt

TGGCACCAACCAC TTGTCCGGATAACCAGCTGCCGATATCTATGTAATCGGATTCCAGGAGGTGAGCACCA  
CACCGCAGGTGCTAAAATCTTCAATGACGATCCGTGGGTGCTGAAGAT  
CG6805-m1  
TGGCACCAACCAC TTGTCCGGATAACCAGCTGCCGATATCTATGTAATCGGATTCCAGGAGGTGAGCACCA---  
-GCAGGTGCTAAAATCTTCAATGACGATCCGTGGGTGCTGAAGAT [-5]  
CG6805-m2  
TGGCACCAACCAC TTGTCCGGATAACCAGCTGCCGATATCTATGTAATCGGATTCCAGGAGGTGAGCACCA---  
-GCAGGTGCTAAAATCTTCAATGACGATCCGTGGGTGCTGAAGAT [-4]  
CG6805-m3  
TGGCACCAACCAC TTGTCCGGATAACCAGCTGCCGATATCTATGTAATCG-----GAGGT-----GCAGGTG  
CTAAAATCTTCAATGACGATCCGTGGGTGCTGAAGAT [-20]

CG12484-wt

CACACGCTGGGTCTTACAACGAGGGCTCTGGGATAAACATCACGTGCGTGGCCATCGGC  
CG12484-m1  
CACACGCTGGGTCTTACAACGAGGGCTCTGGGATAAACAT---TGCCTGGCCATCGGC [-4]  
CG12484-m2  
CACACGCTGGGTCTTACAACGAGGGCTCTGGGATAAACATCA-TGCCTGGCCATCGGC [-2]  
CG12484-m3  
CACACGCTGGGTCTTACAACGAGGGCTCTGGGATAAACATCA G-GCGTGGCCATCGGC [-2,+1]  
CG12484-m4  
CACACGCTGGGTCTTACAACGAGGGCTCTGGGATAAACATCAC-TGCCTGGCCATCGGC [-1]

CG33672-wt  
 CGAACGACGGCTGGCGGAAGTTAGCTAGGCCGTAATCGTATGCCAGCCTTCAGCGGAAGACCCCTTC  
 TCCAGAAGCATAGATTAGTTAACTCAACGCTTGCGAAGAACTGAAAGA  
 CG33672-m1  
 CGAACGACGGCTGGCGGAAGTTAGCTAGGCCGTAATCGTATGCCAGCCTTCAG-GGCAAGACCCCTTC  
 CCAGAAGCATAGATTAGTTAACTCAACGCTTGCGAAGAACTGAAAGA [-2]  
 CG33672-m2  
 CGAACGACGGCTGGCGGAAGTTAGCTAGGCCGTAATCGTATGCCAGCCTTCAG-GGCAAGACCCCTTC  
 TCCAGAAGCATAGATTAGTTAACTCAACGCTTGCGAAGAACTGAAAGA [-1]

CG34318-wt  
 CTGCAGGAGGTGAAACCGATTACAGGCCCTGCAACGACGTGGCCAGCGTCCTT  
 CG34318-m1  
 CTGCAGGAGGTGAAAC-----ACAGGCCTGCAACGACGTGGCCAGCGTCCTT [-6]  
 CG34318-m2  
 CTGCAGGAGGTGAAACCGAaaCgaaACAGGCCTGCAACGACGTGGCCAGCGTCCTT [+6,-2]  
 CG34318-m3  
 CTGCAGGAGGTGAAACCG-TTg-CAGGCCTGCAACGACGTGGCCAGCGTCCTT [-3,+1]

CG10738-wt  
 GACGACTCAGGGATCGGGTCATTCCCTCAGTCGTCGTGGCCGAAACTTACG  
 CG10738-m1  
 GACGA-TCAGGGATCGGGTCATTCCCTCAGTCGTCGTGGCCGAAACTTACG [-1]  
 CG10738-m2  
 GACGAatCccgaTCAGGGATCGGGTCATTCCCTCAGTCGTCGTGGCCGAAACTTACG [+6]

CG11811-wt  
 GGGCGCTAGCAGCAGCAGCAGCAGTAGCAGTAGCAGTCAGCGGCATCCTAACGAGCA  
 CG11811-m1  
 GGGCGCTAGCAGCAGCAGCAGCAGcggcagTAGCAGTGCAGCGGCATCCTAACGAGCA [+6]

CG12229-wt  
 CTACGTCTGACAACCTGGCTGGCTCTGGAGATTAACGGCGAGTGCTGTCGCGTTGGGAGA  
 CG12229-m1  
 CTACGTCT-----GGCTGGCTCTGGAGATTAACGGCGAGTGCTGTCGCGTTGGGAGA [-7]  
 CG12229-m2  
 CTACGTCT---ACTGGCTGGCTCTGGAGATTAACGGCGAGTGCTGTCGCGTTGGGAGA [-4]  
 CG12229-m3  
 CTACGTCTG-gAACTGGCTGGCTCTGGAGATTAACGGCGAGTGCTGTCGCGTTGGGAGA [-2,+1]

CG12289-wt  
 GACTACGTGACCACCATGGATAAGGTCGACTTCCAGTGCACAGGTGCAGCACCCAGAAT  
 CG12289-m1  
 GACTACGT-----GACAGGTGCAGCACCCAGAAT [-31]

CG1271-wt  
 ATGCGAAGTCCGGGATCGCGGTGGATGCTGTAAGTGATTGATCTCAAGT  
 CG1271-m1  
 ATcGGtccAAtcGaTCGGGATCGCGGTGGATGCTGTAAGTGATTGATCTCAAGT [+7]

CG34455-wt  
 GTTCGATGTGGATCCACTGAACCTGGTCCAGTCTCCAATCATACGGCTACAAGACCT  
 CG34455-m1  
 GTTCGATGTGGATCCACTG-----GGTCCAGTCTCCAATCATACGGCTACAAGACCT [-5]

CG7328-wt  
 CGTGACCACATGGGAGCTATCCTATGGAGGACACCGATCGCGATGCCGGATGGGTT  
 CG7328-m1  
 CGTGACCACATGGGAGCTATCCTATGGAGGACACCGATCGCGATGCCGGATGGGTT [-13]  
 CG7328-m2  
 CGTGACCACATGGGAGCTATCCTATGGAGGACACCGATCGGC-TGCCTGGATGGGTT [-2]

CG7551-wt  
 ATACTGGATTGCGGGTGGCAAGGCCTCGAACAACTGTACTGTTTGGCCAATCTGGCGT.....CTTGAAGA  
 GTCGTGGCATATTATCGACAACTGTCCAACCTGTGACCAGGGTGCACCCCTT  
 CG7551-m1

ATACTGGAT---CGGTGGCAAGGCCTCGAACAACTGTACTGTTTGGCCAATCTGGCGT.....CTTGAAGAGT  
 CGTGGCATATTATCGACAACACTGTCCAACCTGTGACCAGGGTGCACCCCT [-3]  
 CG7551-m2  
 ATACTGGATTTCGCGGTGGCAAGGCCTCGAACAACTGTACTGTTTGGCCAATCTGGCGT.....CTTGAAGA  
 GTCGCGGCATCATTATCGACAACACTGTCCAACC---ACCAGGGTGCACCCCT [-4]  
 CG7551-m3  
 ATACTGGATTC-CGGTGGCAAGGCCTCGAACAACTGTACTGTTTGGCCAATCTGGCGT.....CTTGAAGAG  
 TCGTGGCATCATTATCGACAACCTGTGACCAGGGTGCACCCCT [-1]

CG7616-wt  
 ATGGCCTGCGAGAGGCGAATGTCCAGAAAGGCGGTGTCCTGTATTGCGATTTAGTCTTT  
 CG7616-m1  
 ATGGCCTGCGAGAGGCGAATGTCCA---AGGCGGTGTCCTGTATTGCGATTTAGTCTTT [-3]

CG10089-wt  
 CGCGAAGGCAACGTACTCATCCACTGCCTGGCGGGGATGTGCGCTCGGTGACCGTGGCGTGGCCTATA  
 TCATGACGGCCACACACCTGAACCTGAAGGAGGCCTTAAGGTGGT  
 CG10089-m1  
 CGCGAAGGCAACGTACTCATCCACTGCCTGGCGGGGATGTGCGCTCGG-----GTGGCGTGGCCTATATCA  
 TGACGGCCACACACCTGAACCTGAAGGAGGCCTTAAGGTGGT [-6]  
 CG10089-m2  
 CGCGAAGGCAACGTACTCATCCACTGCCTGGCGGGGATGTGCGCTCGG---CGTGGCCTataGGCCTATA  
 TCATGACGGCCACACACCTGAACCTGAAGGAGGCCTTAAGGTGGT [-4,+5]  
 CG10089-m3  
 CGCGAAGGCAACGTACTCATCCACTGCCTGGCGGGGATGTGCGCTCGG-----CATGACGGCC  
 ACACACCTGAACCTGAAGGAGGCCTTAAGGTGGT [-21]  
 CG10089-m4  
 CGCGAAGGCAACGTACTCATCCACTGCCTGGCGGGGATGTGCGCTCGG---CCGTGGCCGTGGCCTATATC  
 ATGACGGCCACACACCTGAACCTGAAGGAGGCCTTAAGGTGGT [-3]  
 CG10089-m5  
 CGCGAAGGCAACGTACTCATCCACTGCCTG-----GCCTATATCATGACGGCCACACACC  
 TGAACCTGAAGGAGGCCTTAAGGTGGT [-33]

CG10426-wt  
 GCTGAGCAAGCGACCTAGTAAGGTGGAGCC.....GCGATGGAGGAGCCGACGTGGTATGCCCGCAAGTC

CG10426-m1  
 GCTGAGCAAGCGACCTA---AGGTGGAGCC.....GCGATGGAGGAGCCGACGTGGTATGCCCGCAAGTC [-3]  
 CG10426-m2  
 GCTGAGCAAGCGACCTA---AGGTGGAGCC.....GCGATGGAGGAGCCGACGTGGTatggtttagagctagaatagcaagttaaa  
 ataaggctagtcgttatcaactgaaaaagtggcacgcgtcggtctagtcggTGCGCGCAAGTC [-3,+80]  
 CG10426-m3  
 GCTGAGCAAGCGACCT---AAGGTGGAGGCC.....GCGATGGAGGAGCCGACGTGGT-----GGCGCAAGTC [-7]  
 CG10426-m4  
 GCTGAGCAAGCGACCTAG-----TGGAGCC.....GCGATGGAGGAGCCGACGTG-----GCGCAAGTC [-13]

CG10592-wt  
 ACTTCGAGGCCCTCGACGAGGAGCTGGACACACGATTCTGGCACGATAAGGCCAATCGATTCTGGCCGAT  
 AAGCTGGCCGGCATAAAAGCTAACGAGAACCGCGCCAAGAACGTGA  
 CG10592-m1  
 ACTTCGAGGCCCTCGACGAGGAGCTGG-----GCACGATAAGGCCAATCGATTCTGGCCGATAAGCTGGCG  
 GCCATAAAAGCTAACGAGAACCGCGCCAAGAACGTGA [-20]  
 CG10592-m2  
 ACTTCGAGGCCCTCGACGAGGAGCTGG-----CACGATAAGGCCAATCGATTCTGGCCGATAAGCT  
 GGCGGCCATAAAAGCTAACGAGAACCGCGCCAAGAACGTGA [-11]  
 CG10592-m3  
 ACTTCGAGGCCCTCGACGAGGAGCTGG-----ACGATAAGGCCAATCGATTCTGGCCGATAAGCTGG  
 CCGGCCATAAAAGCTAACGAGAACCGCGCCAAGAACGTGA [-15]  
 CG10592-m4  
 ACTTCGAGGCCCTCGACGAGGAGCTGGACACACGA---C---AC-----  
 ---AAGAACGTGA [-72]

CG11425-wt  
 TCTGCGGCCCGCCCATCCGCCTCCTGGTGGACCTGGCCTGCTGGCCTACTTATTGTCC  
 CG11425-m1  
 TCTGCGGCCCGCCCATCCG---CCTGGTGGACCTGGCCTGCTGGCCTACTTATTGTCC [-3]

CG11426-wt  
 CGGCTCACGGGACCGTCATCGGATGCCGGATGACGCAGCGCCTGCTCGTGGAGCTCCT.....GCCGGTA  
 ATGCTCGGCTGATCGTGGGCTGCTCCGGCCCTGGTCATGGTGGTGGTGGA

CG11426-m1  
 CGGCTCACGGGACCGTCATCGGATGCCGGATGACGCAGCGCCTGCTCGTGGAGCTCCT.....GCCGGTA  
 ATGCTCG-----GCCCTCCGGCCCTGGTCATGGTGGTGGTGGA [-12]

CG11426-m2  
 CGGCTCACGGGACCGTCATCGGATGCCGGATGACGCAGCGCCTGCTCGTGGAGCTCCT.....GCCGGTA  
 ATGCTCG-----TGGGCCTGCTCCGGCCCTGGTCATGGTGGTGGTGGA [-9]

CG11426-m3  
 CGGCTCACGGGACCGTCATCG-----GATGACGCAGCGCCTGCTCGTGGAGCTCCT.....GCCGGTAATGC  
 TCGGCCTGATCGTGGCCTGCTCCGGCCCTGGTCATGGTGGTGGTGGA [-8]

CG11437-wt  
 TCTTCGACCCGCTCAATCTCAGTGTGAAAATGTGCGGAATCCGAACACCGCTCCCT.....TATCCCTAT  
 CGCCAGCCCTGGCTGACCAAGGTCCACCTACGATCGCAGTGGTTGCTCTG

CG11437-m1  
 TCTTCGACCCGCTCAATCTCAGTGTGAAAATGTGCGGAATCCG-----CGTCTCCTC.....TATCCCTATCGC  
 CAGCCCTGGCTGACCAAGGTCCACCTACGATCGCAGTGGTTGCTCTG [-6]

CG11437-m2  
 TCTTCGACCCGCTCAATCTCAGTGTGAAAATGTGCGGAATCCGAt---GGTCTCCTC.....TATCCCTATCG  
 CCAGCCCTGGCTGACCAAGGTCCACCTACGATCGCAGTGGTTGCTCTG [-4,+1]

CG11437-m3  
 TCTTCGACCCGCTCAATCTCAGTGTGAAAATGTGCGGAATCCGAACACCGCTCCCT.....TATCCCTAT  
 CGCCAGCC---GCTGACCAAGGTCCACCTACGATCGCAGTGGTTGCTCTG [-3]

CG11437-m4  
 TCTTCGACCCGCTCAATCTCAGTGTGAAAATGTGCGGAATCCGAACACCGCTCCCT.....TATCCCTAT  
 CGCCAGCCa---GCTGACCAAGGTCCACCTACGATCGCAGTGGTTGCTCTG [-3,+!]

CG11438-wt  
 GTCCAAGTATTCAAGCTGGCCCGCGGGTTCTGCGACCTGCTGATCTGGTGGCCCTCAGCGTGGCCAGT  
 GTGCTCTCCACAAGATGGGGCGTCCCTCCGGCGCGCTTCTGTGG

CG11438-m1  
 GTCCAAGTATTCAAGCTGGCCCGCGGGTTCTGCGACCTGCTGATCTGGTGGCCCTCAGCGTGGCCAGT  
 G-----GGCGTCCCTCCGGCGCGCTTCTGTGG [-18]

CG11438-m2  
 GTCCAAGTATTCAAGCTGGCCCGCGGGTTCTGCGACCTGCTGATCTGGTGGCCCTCAGCGTGGCCAGT  
 GTGCTCTCCACAcTGGAAGCTGGTGAAG---CCGGCGCGGCTTCTGTGG [-8,+7]

CG11438-m3  
 GTCCAAGTATTCAAGCTGGCCCGCGGGTTCTGCGACCTGCTGATCTGGTGGCCCTCAGCGTGGCCAGT  
 CAAGATGGGGCGTCCCTCCGGCGCGGCTTCTGTGG [-19]

CG11597-wt  
 GGTCAGTTGAGGATCTGCTCCACCTGCTGGAATTGGCGGTTCGTGCAGGAGCATCGC

CG11597-m1  
 GGTCAGTTGAGGATCTGCTCCACCTGCTGGAATTGGCGGTTCG-TGCAGGAGCATCGC [-1]

CG17027-wt  
 ACTTTCTCATGGAGAAAATATTGGCCAGATAACCGGATCACAAGTTCATGGCGAGGAGG

CG17027-m1  
 ACTTTCTCATGGAGAAAATATTGGCCAG-----ATCACAAGTTCATGGCGAGGAGG [-8]

CG17027-m2  
 ACTTTCTCATGGAGAAAATATTGG-----CCCGGATCACAAGTTCATGGCGAGGAGG [-7]

CG17028-wt  
 TCGGGTCCGCTC.....ATCATAGATCCC

CG17028-m1  
 TCGGGTCCGCTC-----ATGGGACCGGTCCGGTCATC-----ATCATAGATCCC [-181]

CG17029-wt  
 TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGGGATTGGTGGCCGCC  
 CCCGAATCCCTGATCATTGGCGAGGAGGAGTCGGCAGTTTCAC

CG17029-m1  
 TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGG-----TGGCCGCCTTCCC  
 GAATCCCTGATCATTGGCGAGGAGGAGTCGGCAGTTTCAC [-6]

CG17029-m2

TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGG<sup>tggcc</sup>GATTGGTGGCCGC  
CTTCCCAGAACCTGATCATTGGCGAGGAGTCGGCAGTTCAC **[+5]**

CG17029-m3

TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGG<sup>cA</sup>-----CCGCCTTCCCG  
AATCCCTGATCATTGGCGAGGAGTCGGCAGTTCAC **[+8,+1]**

CG17029-m4

TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGG<sup>tttgact</sup>GATTGGTGGCCG  
CCTTCCCAGAACCTGATCATTGGCGAGGAGTCGGCAGTTTC **[+7]**

CG17029-m5

TTCTACGACCTGGTGACCGTGACGATAAGCAAATCGAGGATTTGACCGAGG-----ATTGGTGGCCGCCTTC  
CCGAATCCCTGATCATTGGCGAGGAGTCGGCAGTTCAC **[+2]**

CG17746-wt

CAACACACTCCACACCGCACACCATAAACGCCAATGGGTCAAGACTCTATCGAACCGGTGA.....TGCAG  
GGGTGGCGCATCAACATGGAGGACTCGCACACCCACATCCTCTCGCTGCCGGACG

CG17746-m1

CAACACACTCCACACCCACACCCATAAACGCCAATGGGTCAAGACTCTATCG-----GTGA.....TGCAGGGG  
TGGCGCATCAA-----CTCGCACACCCACATCCTCTCGCTGCCGGACG **[+15]**

CG17746-m2

CAACACACTCCACACCGCACACCATAAACGCCAATGGGTCAAGACTCTATCGAACCGGTGA.....TGC-----  
TGG-----ACTCGCACACCCACATCCTCTCGCTGCCGGACG **[+21]**

CG17746-m3

CAACACACTCCACACCGCACACCATAAACGCCAATGGGTCAAGACTCTATCGAACCGGTGA.....TGCAG  
GGGTGGCG-----CATGGAGGACTCGCACACCCACATCCTCTCGCTGCCGGACG **[+6]**

CG17746-m4

CAACACACTCCACACCGCACACCATAAACGCCAATGGGTCAAGACTCTATCGAACCGGTGA.....TGCAG  
GGGTGGCGCATCA-----ACTCGCACACCCACATCCTCTCGCTGCCGGACG **[+9]**

CG5150-wt

GAGTCTTAAGTTCTGGATTGCCTCGGTCTGCTGACCGTCGTTGGGTG.....GAGGCGAGGAGTTGAAGC  
TCTCCTTCGAAGAATTCCCCTTACCGGACTATCGAAAACCT

CG5150-m1

GAGTCTTAAGTTCTGGATTGCCTCGGTCTGCTGACCGTCGTTGGGTG.....GAGGCGAGGAGTTGAAGC  
TCTCCTTCGAAGAATTCCCC-----CCGGACTATCGAAAACCT **[+4]**

CG5150-m2

GAGTCTTAAGTTCTGGATTGCCTCGGTCTGCTGACCGTCGTCG-----.....A  
CCGGACTATCGAAAACCT **[+287]**

CG5150-m3

GAGTCTTAAGTTCTGGATTGCCTCGGTCTGCTGACCGTCGTTGGGTG.....GAGGCGAGGAGTTGAAGC  
TCTCCTTCGAAGAATTCCCCTT<sup>tcc</sup>CCGGACTATCGAAAACCT **[+3,-1]**

CG5150-m4

GAGTCTTAAGTTCTGGATTGCCTCGGTCTGCTGACCGTCGTTGGGTG.....GAGGCGAGGAGTTGAAGC  
TCTCCTTCGA-----AACCT **[+26]**

CG9238-wt

AAGCCATATATAAAATGATTCGCACAGTCGCCCATATTCAAGTCACAGTCACAGTCCACCCGTTA

CG9238-m1

AAGCCATATATAAAATGATTCGCACAG-----TCCACCCGTTA **[+21]**

CG9389-wt

GGAAACGCGGCTACCCGATTGGCTGGAGGATCACGAGGCCACTCAGCAGGATGCCGGGTGAACAC  
A.....GTCATCGGAGGAATCAGAGAAACCGTCCCACCTGCTGCTGCATCGCGCCTCCAGC

CG9389-m1

GGAAACGCGGCTACCCGATTGGCTGGAGGATCACGAGGCCACTCAGCAGGATGCCGGGTGAACAC  
AATCAGAGAAACCGTCCCACCTGCTGCTGCATCGCGCCTCCAGC **[+25]**

CG9389-m2

GGAAACGCGGCTACCCGATTGGCTGGAGGATCACGAGGCCACTCAGCAGGATGCCGGGTGAACAC  
A.....GTCATCGGAGGAATCAGAGAAACCGTCCCACCT-----GCATCGCGCCTCCAGC **[+6]**

CG9391-wt

ACAACTGGACGTGGAAAAGTGCTTAGAGGTGGCCAGCAACCTGGTTCCGAAGCCGGAA

CG9391-m1

ACAACTGGACGTGGAAAAG-----AGGTGGCCAGCAACCTGGTTCCGAAGCCGGAA **[+7]**

CG9391-m2

ACAACTGGACGTGGAAAAG-----GTGGCCAGCAACCTGGTTCCGAAGCCGGAA **[+9]**

CG9449-wt  
 CACCCGACGGCATTGTCTCGCATGACGGGCGGACTAATTGCATCGCGGTATAATCTG  
 CG9449-m1  
 CACCCGACGGCATTGTCTCGCATGACGGGCGGACTAATT-----GCGGTATAATCTG [-6]  
 CG9449-m2  
 CACCCGACGGCATTGTCTCGCATGACGGGCGGACTAATT---CGGCGGTATAATCTG [-4]  
 CG9449-m3  
 CACCCGACGGCATTGTCTCGCATTGTCGG-----CGGTATAATCTG [-18]

CG9451-wt  
 GAAGTGCCGCAGG AAGTCACGGAAGGTCTGGGATGTCTCTCAAAGCTCAGC.....ACCTACGAGCCCTT  
 CGGTTGGGAGCACTCACCAATGTTAGTACTTATCAAACATAAACAGACTATTATCGAAGCTA  
 CG9451-m1  
 GAAGTGCCGCAGGAAG-----.....TACATCACTGTTAGTACTTATC  
 AACACATAAACAAAGACTATTATCGAAGCTA [-1001]  
 CG9451-m2  
 GAAGTGCCGCAGGAAG-----.....TACGTCACTGTTAGTACTTATC  
 AACACATAAACAAAGACTATTATCGAAGCTA [-1001]  
 CG9451-m3  
 GAAGTGCCGCAGGcAAGTCACtAAaGcTgatGtGATGTCCTCAAAGCTCAGC.....ACCTACGAG-----C  
 ACTCACCAATGTTAGTACTTATCAA-CAT--AACAGACTATTATCGAAGCTA [-28,+9]

CG34140-wt  
 TCTATACAGTCATATAGTAACCGTAACTTCAGAACAGACGCCGGTGTACGCCCTGCA  
 CG34140-m1  
 TCTATACAGTCATATAGTAACCGTAACTTCAGAACAC-----CGCCCTGCA [-14]

CG5946-wt  
 GTGCCACTGCCGTGGGTGTGGTAGCCGTACTGCCGGCGCCCTGATCGTCACTATCTGCTGAATAAGAA  
 GTCCACGAAACCACGCCGGAACCCAATCGCACCGCTGGCTCGCACACTGTGGATCCCAATGA  
 CG5946-m1  
 GTGCCACTGCCGTGGGTGTGGTAGCCG-----GCGCCCTGATCGTCACTATCTGCTGAATAAGAAGTCC  
 ACGAAACCACGCCGGAACCCAATCG-----CTCGGCTCGCACACTGTGGATCCCAATGA [-14]

CG10177-wt  
 TCGGGGTGTGCTTCCTGCGGAACGGAGATAGACACTTCAAGGGCGTTAATTGGTCATCT  
 CG10177-m1  
 TCGGGGTGTGCTTCCTG-----GAGATAGACACTTCAGGGCGTTAATTGGTCATCT [-8]  
 CG10177-m2  
 TCGGGGTGTGCTTCCTG--GAACGGAGATAGACACTTCAAGGGCGTTAATTGGTCATCT [-2]  
 CG10177-m3  
 TCGGGGTGTG-----CGGAGATAGACACTTCAGGGCGTTAATTGGTCATCT [-12]

CG12069-wt  
 AGCAAGCGCAGATGCACTTCAGTCCCAGGTGGACTACATTCTCATCCTGGACAAGTTGC  
 CG12069-m1  
 AGCAAGCGCAGATGCACTTCAGTCCCAGGTGGACTACATTCTC-----CTGGACAAGTTGC [-3]  
 CG12069-m2  
 AGCAAGCGCAGATGCACTTCAGTCCCAGGTGGACTACATTCTCA-----AGTTGC [-9]

CG14305-wt  
 GAAGTTGGATGTGGATGCACTGGCACAGCAGGGTACAATGTGGGTACAAGATCGCGAGGGTCTTA  
 TGCCACTGTTATAACCGCCGGTTATGCCGATGATGGACATGGAGTAC  
 CG14305-m1  
 GAAGTTGGATGTGGATGCACTGGCACAGCAGGGTACAATGTGGGTACAAGATC-----CGAGGGGTCTTATG  
 CCACTGTTATAACCGCCGGTTATGCCGATGATGGACATGGAGTAC [-2]  
 CG14305-m2  
 GAAGTTGGATGTGGATGCACTGGCACAGCAGGGTACAATGTGGGTACAAGATCG-----GGGTCTTATG  
 CACTGTTATAACCGCCGGTTATGCCGATGATGGACATGGAGTAC [-5]

CG1951-wt  
 TGACCGGGAGACCATGCTGGAAACACTGCGTCGCGGGGTTAACAGCTAACAAAAATTG  
 CG1951-m1  
 TGACCGGGAGACC-----TGGAAACACTGCGTCGCGGGGTTAACAGCTAACAAAAATTG [-4]  
 CG1951-m2  
 TGACCGGGAGACC-----CTGGAAACACTGCGTCGCGGGGTTAACAGCTAACAAAAATTG [-3]  
 CG1951-m3

TGACCGGGAGAC-----TGGAAACACTGCGTCGCCGGGTTAACAGCTAACAAAATTG [−5]

CG2246-wt

ACTGGTGACCTCTCTGCTCACTAATTATGTCTTTACCCCCAAAGGGATGCCAACATAATCATGG  
AGCTTCTGATTATGGCCTACGCCTGCAAGACTCCTCGGCTCGTCG

CG2246-m1

ACTGGTGACCTCTCTGCTCATTAATTATCTCTTTACCCCCAAAGa-GATGCCAACATAATCATGGA  
GCTTCTGATTATGGCCTACGCCTGCAAGACTCCTCGGCTCGTCG [−2,+1]

CG2246-m2

ACTGGTGACCTCTCTGCTCATTAATTATCTCTTTACCCCCAAAGa-GATGCCAACATA---TCATGGAG  
CTTCTGATTATGGCCTACGCCTGCAAGACTCCTCGGCTCGTCG [−5,+1]

CG31431-wt

TGTGGGCTTCAGCAGTCCCCTGTTGACTATACAGGTGAGTTAGTTCTTA

CG31431-m1

TGT<sub>cct</sub>GGCTTCAGCTGCCCCTGTTGACTATACAGGTGAGTTAGTTCTTA [+3,-1]

CG3809-wt

CTACCAGAGGAAACTTATGGGCTTGGCAACCCCCCTGCTGGACATCACCTGCACCGTTGAGGATAATGT  
GATCCTGGA

CG3809-m1

CTACCAGAGGAAACTTATGGGCTTGGCAACCCCCCTGCTGGACATCACCTGCAC--TTGAGGATAATGTGA  
TCCTGGA [-2]

CG10999-wt

CGCACGAAACAGGAGCAGGAGGTGCGTAGGCAGGGAGCTGATGAGCACGAAGTCAAGTGC

CG10999-m1

CGCACGAAACAGGAGCAGGAGGTGCG-----GGAGCTGATGAGCACGAAGTCAAGTGC [-6]

CG10999-m2

CGCACG-----GGAGCTGATGAGCACGAAGTCAAGTGC [-26]

CG12538-wt

GGTGGCTCTGGCGTGCTATTGAATTGAACAAGTGTCAAGCGTCAGCGTCAGGGGAAACAGCGTCGAAGCTGACGCT  
CCATGGTGTCCAATAAAACTACCAAAGCCCCCTCCCGCCG.....GAAACACAAATACTAGACGGC

CG12538-m1

GGT-----GTGCGGT-----TCCAATAAAACTACCAAAGCCCCCTC  
CCGCG.....GAAACACAAATACTAG<sub>tgtagctttggccgcga</sub>C [-67,+16]

CG12538-m2

GGTGGCTCTGGCGTGCTATTGAATTGAACAAGTGTCAAGCGTCAGCGTCAGGGGAAACAGCGTCGAAGCTGACGCT  
CCATGG-----CCCCTCCCGCCG.....GAAACACAAATACTAG<sub>tgtagctttggccgcga</sub>C [-23,+16]

CG12538-m3

GGTGGCTCTGGCGT-----GCTCCAATAAAACTACCAAAGCCCCCT  
CCCGCG.....GAAACACAAATACTAG<sub>tgtagctttggccgcga</sub>C [-64,+16]

CG12538-m4

GGTGGCTCTGGCGTGCTATTGAATTGAACAAGTGTCAAGCGTCAGCGTCAGGGGAAAC-----  
-----GCCCTCCCGCCG.....GAAACACAAATACTAG<sub>tgtagctttggccgcga</sub>C [-44,+16]

CG12746-wt

CGGGGAGCTGCTCTGGGTGATAGTGGCTCCCTTCTGGTCACTATGCCCTTACTG

CG12746-m1

CGGGGAGCTGCTCTGGGTGA-----ACTATGCCCTTACTG [-20]

CG14297-wt

CTTGCCTATTGCATGAAAAACTTACGTCAATTGCAAGGCAACTCGTCAGCTCCGATGCCGAGGTGA  
TTATGCAGAATCTGATGGTCAAGACGAGTCTACTGGGAGGTGGATAGTGCCGGTCTCAGGACATGGAAC  
ACT

CG14297-m1

CTTG--AT--GCA<sub>a</sub>GAAAAACTT<sub>cc</sub>ATCATTGCAAGGCAACTCGTCAGCTCCGATGCCGAGGTGATTAT  
GCAGAAT--GATGGTCAAGACGAGTCTACTGGGAGGTGGATAGTGCCGGTCTCAGGACATGGAAC<sub>tggac</sub>A  
CT [-10,+8]

CG14297-m2

CTTG--AT--G<sub>g</sub>A<sub>a</sub>GAAAAACTT<sub>cc</sub>ATCATTGCAAGGCAACTCGTCAGCTCCGATGCCGAGGTGATTAT  
GCAGAATCTGATGGTCAAGACGAGTCTACTGGGAGGTGGATAGTGCCGGTCTCAGGACATGGAAC<sub>tggac</sub>  
ACT [-9,+9]

CG2104-wt

GGCGTACTTACACTGATCACGTACTTGAACGATGTGAGCGCCGAGATACTGGGAATCCG  
CG2104-m1  
GGCGTACTTACACTGATCACGTACTTGAACGATGTGAGCGC-----AGGGAATCCG [-8]

CG31469-wt  
CACATGCCGGTCACCAATGGCGAGGCCATACTGAAGCATTGGTAGTGAACCGAATCTGCAGGACTGGT  
ATGTGGACAGTGCTGGCCTCAGGAGTTGGAACGTTGGCCTGGAGCCCC  
CG31469-m1  
CACATGCCGGTCACCAATGGCGAGGCCATACTGAAGCATTGGTAGTGAACCGAATC~~c~~TGCAGGACTGG  
TATGTGGACAGTGCTGGCCTCAGGAGTTGGAACGTTGGCCTGGAGCCCC [+1]

CG5361-wt GCAATGGTAACCACACAGCAGACCAAGGAGATTGCGAAATTATTGGCTGAAATCAAC  
CCAGGTGTTCC.....AGGTGGCAGCTCCCAGAAAATCT.....AATCAGCAGGATTGCGGAAGGTTATTAATG  
CAACGCAAGGCCGATAAGCA  
CG5361-m1  
GCAATGG-----CGACCTCCCAGAAAATCT.....AATCAGCA  
GGATTGGCGAAGGTTATTAATGCAACGCAAGGCCGATAAGCA [-189]  
CG5361-m2  
GCAATGGTAACCACACAGCAG-----GTGGCGACCTCCCAGAAAATC  
T.....AATCAGCAGGATTGCGGAAGGTTATTAATGCAACGCAAGGCCGATAAGCA [-171]  
CG5361-m3  
GCAATGGTAACCACACAGCAGAGAAGTGTGGTAAC-----  
--CTTCCTTGGCGAAGGTTATTAATGCAACGCAAGGCCGATAAGCA [-468]

CG6036-wt  
AGTCATCCATGAGTGAGTGGGATTCTGTGTG.....TCATGGGAATGGGCTGCGATACTGCGTAAGTCTATG  
CAAGGTTGGCGATTGAAATGGAGGATAGCCACTCGGCTGCTGCCGGCTGAAGGATCCCTCGAACGT  
CG6036-m1  
AGTCATCCATGAGTGAGTGGG~~gagtgggg~~ATTTCTGTGTG.....TCATGGGAATGGGCTGCGATACTGCGTAAGT  
TCTATGCAAGGTTGGC-AccT-----CCACTCGGCTGCTGCCGGCTGAAGGATCCCTCGAACGT [+10,  
-16]

CG13369-wt  
TAACAGACTACCCACAAGAGACTAGTGCAATTGCAGCAATGGCCCAAACGGAAGTGCTGGTGGCTCG  
GCCATCATTGACTTTATAAGGTAGGTGGCAGAGAAGGCTCGATCCCAA  
CG13369-m1  
TAACAGACTACCCACAAGAGACTAGTGCAATTGCAGCAATGGCCCAAACGGAAGTGCTGGTGGT--GCTCGG  
CCATCATTGACTTTATAAGGTAGGTGGCAGAGAAGGCTCGATCCCAA [-2]  
CG13369-m2  
TAACAGACTACCCACAAGAGACTAGTGCAATTGCAGCAATGGCCCAAACGGAAGTGCT-----CGGCCATC  
ATTGACTTTATAAGGTAGGTGGCAGAGAAGGCTCGATCCCAA [-11]  
CG13369-m3  
TAACAGACTACCCACAAGAGACTAGTGCAATTGCAGCAATGGCCCAAACGGAAGTGCTGGTGT--GCTCGG  
CATCATTGACTTTATAAGGTAGGTGGCAGAGAAGGCTCGATCCCAA [-3]

CG2577-wt  
TCCACAGTGGGAGCGGGTGGCCATCAAGGTGGAAAGCAGCAAGGTGCGCCATCCGAGCTCAACTA.....  
AGGCCGCCACGGTTGCCAAGGATTAGGTACTTCCACAAGGAGGACTACCAGGCGATGGTTATGGA  
TCTGC  
CG2577-m1  
TCCACAGTGGGAGCGGGTGG-----GG-GA-G-----  
-----CGATGGTTATGGATCTGC [-124]

CG32649-wt  
GGAATGGCCATCTTGAGCCTGCACAAGTCTCTCAATTGTAATCCACACC  
CG32649-m1  
GGAATGGCCATCTTGAGCCTGCACAAGTCTCTCAA~~g~~T~~cctcc~~TCGTAATCCACACC [+6]

CG32687-wt  
AGGAGAAGATCAGCCATGGAGGTGTACACGTGGACAGTTGGACACGGATTGCGGGAGCAGAAGACAC  
TGGACTTTGGCGTATGAGCCTGGACCTGGTCACGCTGGAGGATCACCTGGCCTGCCGCAGAAGGCTCT  
CG32687-m1  
AGGAGAAGATCAGCCATGGAGGTGTACACG-----CTGGA  
GGATCACCTGGCCTGCCGCAGAAGGCTCT [-75]  
CG32687-m2

AGGAGAAGATCAGCCATGG-----CACGCTGGIGGAT  
 CACCTGGCCTCGCCGCAGAAGGCTCT **[+82,+1]**  
 CG32687-m3  
 AGGAGAAGATCAGCCATGGAGGTGTACACG-----CCTGGACCTGGT  
 CACGCTGGAGGATCACCTGGCCTCGCCGCAGAAGGCTCT **[-59]**  
 CG32687-m4  
 AGGAGAAGATCAGCCATGGAGGTGTACACGTCGGAcgtAcacGTTGGACACGGATTGCGGGAGCAGAAG  
 ACACTGGACTTGGCCGTAT-AGCCTGGACCTGGTCACGCTGGAGGATCACCTGGCCTGCCGCAGAAGGC  
 TCT **[+6,-1]**

CG4041-wt  
 AATTCCACACGTGCCAAGATTACAGATTCTACGGATAACACTCACTAATTCCACGACTGCC.....GAGTAT  
 CTGGGACTCTCACTGGAGGACTACGCCATGCGTCATCCACCGCTGGCATTGC  
 CG4041-m1  
 AATTCCACACGTGCCAAGATCACAGATTCTACGGATAACACTCACTAATTCCA-G--TGCC.....GAGTATC  
 TGGGACT<sup>ag</sup>TCACTGGAGGACTACGCCATGCGTCATCCACCGCTGGCATTGC **[-4,+2]**  
 CG4041-m2  
 AATTCCACACGTGCCAAGATCACAGATTCTACGGATAACACTCACTAATTCCA-G--TGCC.....GAGTATC  
 TGGGAA---TCACTGGAGGACTACGCCATGCGTCATCCACCGCTGGCATTGC **[-6]**

CG8173-wt  
 ATCAACGTGCCCATCGCCGATGATGAAGACCCTGGGCCACGGCACTGGGATCCGGTCTACCGCTTGG  
 ACCGCTCGCCTCGTCTCGCGAAATCCGCTGCCCTGGCCGTCAAG  
 CG8173-m1  
 ATCAACGTGCCGC-----TCGCCTCGTCTCGCGAAATCCGCTCGC  
 CCTGGGCCGTCAAG **[-62]**  
 CG8173-m2  
 ATCAACGTGCCCATCGCCGATGATGAAGACCCTGGGCCACGGCACTGGG-----CCGCTCGCC  
 TCGTCTCGCGAAATCCGCTGCCCTGGCCGTCAAG **[-19]**  
 CG8173-m3  
 ATCAACGTGCCCATCGCCGATGATGAAGACCCTGGGCCACGGCACTGGGATCCGGG  
 TCTACCGCTTGGACCGCTGCCCTCGTCTCGCGAAATCCGCTGCCCTGGCCGTcgcctcgctcgccgaaatccg  
 ctgcctcgAAAG **[+31]**  
 CG8173-m4  
 ATCAACGTGCCCATCGCCGATGATGAAGACCCTGGGCCACGGCACTGGGATCCGGTCTAC---TTGGAC  
 CGCTCGCCTCGTCTCGCGAAATCCGCTGCCCTGGCCGTCAAG **[-3]**

CG8565-wt  
 GCTCTCGATGATGGAATTGCCGGCAGAAAGCCGCCAAAATTAATAAGTATAGCGAACTTAGC  
 CG8565-m1  
 GCTCTCG-----GCCAAAATTAATAAGTATAGCGAACTTAGC **[-26]**  
 CG8565-m2  
 GCTC<sup>gga</sup>GATGAT---TcGCCG-Attc-GCCGGCCAAAATTAATAAGTATAGCGAACTTAGC **[-14,+7]**  
 CG8565-m3  
 GCTCTCGATGA-----GCCGGCCAAAATTAATAAGTATAGCGAACTTAGC **[-18]**

CG15743-wt  
 TCCATCAGGAGGAGCGGCCAGCGATCTACGGCATGCTGCGAGTGAGAATCCCAGCCGCG  
 CG15743-m1  
 TCCATCAGGAGGAGCGGCCAGCGA-CTACGGCATGCTGCGAGTGAGAATCCCAGCCGCG **[-1]**

CG1637-wt  
 ATCTGTCCTTGGAGGTGAGTGCATCTTCTTACTTTGCATTATGTAATTGCTCAC  
 CG1637-m1  
 ATCTG-----AGGTGAGTGCATCTTCTTACTTTGCATTATGTAATTGCTCAC **[-8]**  
 CG1637-m2  
 ATCT-----TTGGAGGTGAGTGCATCTTCTTACTTTGCATTATGTAATTGCTCAC **[-5]**

CG17598-wt  
 GTGCGGCCCATCATCGTGCCGCCAGACATCAACCTACTGCCCTGGGCCACCGGATACGCC  
 CG17598-m1  
 GTGCGGCCCATCATCGTGCCGCCAGACATCAACCTACTG-----GGGCACCGGATACGCC **[-5]**  
 CG17598-m2  
 GTGCGGCCCATCATCGTGCCGCCAGAC-----CCTGGGCCACCGGATACGCC **[-13]**

CG32812-wt  
 TCGTCAGCTAACCCCGTCCAACGTGTGACCACCAAGCAGGCCACAGGGCTGTCCGC  
 CG32812-m1

TCGTCAGCTCAACCgtGTtgaCCAActGTGTGACCACCAAGCAGGCCACAGGGCTGTCCGC [-2,+5]

CG32812-wt

CCTACGTTCCATTGGGATTAATCGAATCCGTACAGGTGCGAGATCTGTTCCAGCTGATTG

CG32812-m1

CCTACGTT-**Ac**TGGGATTAATCGAATCCGTACAGGTGCGAGATCTGTTCCAGCTGATTG [-2,+1]

CG42271-wt

TTGGTGTAAACTGCGTGGAAATTTACTGTTCTACCTCAAGGATAAGGACCCCAGTCAGCGGTGGCCGGCC  
TCCTGGTGTGGAGAACTGTCGTGCGCGATTCAAATGAGGAGCGTGA

CG42271-m1

TTGGTGTAAACTGCGTGGAAATTTACTGTTCTACCTCAAGGATAAGGACCCC---CAGCGGTGGCCGGCCTC  
CTGGTGTGGAGAACTGTCGTGCGCGATTCAAATGAGGAGCGTGA [-4]

CG42271-m2

TTGGTGTAAACTGCGTGGAAATTTACTGTTCTACCTCAAGGATAAGGACCC-----GCCCTCTGGTGC  
TGGAGAACTGTCGTGCGCGATTCAAATGAGGAGCGTGA [-16]

CG42271-m3

TTGGTGTAAACTGCGTGGAAATTTACTGTTCTACCTCAAGGAT-----T  
CAAATGAGGAGCGTGA [-59]

CG7378-wt

AACAGACACAGGCCGCCAGCTGCAGCGAGTCTGCACTAACGATGGCTCTAGCCG.....TTGATGGCA  
TCACCCACGTTCTGAACGCGGCCGAGGGATGTCGGTATGGTCAAGGTGGAC

CG7378-m1

AACAGACACAGGCCGCCAGCTGCAGCGAGTCTGCACTAACGATGGCTCTAGCCG.....TTGATGGCA  
TCACCCACGTTCTGAACGCGGCCGAGGGATGTCGGTATGGT---GGAC [-5]

CG7378-m2

AACAGAC**tcc**CAGGCCGCCAGCTGCAGCGAGTCTGCACTAACGATGGCTCTAGCCG.....TTGATGGC  
ATCACCCACGTTCTGAACGCGGCCGAGGGATGTCGGTATGG-----AC [-9,+3]

CG9784-wt

TCCGTGGACGCACAAGGCTAAGGAACTGCTACGCAACTACGACTATGTGGCCGTAAAGAC

CG9784-m1

TCCGTGGA-----AG--TAAGGAACTGCTACGCAACTACGACTATGTGGCCGTAAAGAC [-8]

## Supplementary Note 2. Detailed sequences for abnormal lethal events.

Note: wt, wild-type DNA/protein sequence; m#, mutation line# DNA/protein sequence. Deletions are shown as red dashes and insertions as highlighted in blue and lowercase letters. The change of DNA length (in nucleotides) caused by each mutation is indicated as purple (+, insertion; -, deletion). Note that some alterations have both insertions and deletions of nucleotides and in these cases the alterations are enumerated in the brackets. The DNA sequences are followed by the corresponding protein sequences. All DNA/protein sequences were obtained from the flybase website (flybase.org) and the alignments were performed by CLUSTALW.

CG12229-wt DNA sequence

ATG.....GGACACCAGAACATTGCGATATCGCGCATTCTGCAGAGAGGGAACTACGTCTGACAACGGCT  
TGGCTCTGGAGATTAACGGCGAGTGCTGCGCGTTGGGAGACTGAGGAACAACGTGCACC

CG12229-m1(viable) DNA sequence

ATG.....GGACACCAGAACATTGCGATATCGCGCATTCTGCAGAGAGGGAACTACGTCT---ACTGGCTTG  
GCTCTGGAGATTAACGGCGAGTGCTGCGCGTTGGGAGACTGAGGAACAACGTGCACC [-4]

CG12229-m2(lethal) DNA sequence

ATG.....GGACACCAGAACATTGCGATATCGCGCATTCTGCAGAGAGGGAACTACGTCTGg---AACTGGCTT  
GGCTCTGGAGATTAACGGCGAGTGCTGCGCGTTGGGAGACTGAGGAACAACGTGCAC [-3,+1]

CG12229-wt protein sequence

MPINQKEVTPQLDSQTGEDQGEQQEQPEDENRLEKFTVRLNGQHDLEQRLKDFKAACEAHEKHARRRKRYY  
HLGLVAKLVETTTHDELRRMLENGTYTFHVDTVGNKPDELKAILDTMIAISAHSAAEREELRLTTGLALEINGECCRV  
G.....

CG12229-m1(viable) protein sequence

MPINQKEVTPQLDSQTGEDQGEQQEQPEDENRLEKFTVRLNGQHDLEQRLKDFKAACEAHEKHARRRKRYY  
HLGLVAKLVETTTHDELRRMLENGTYTFHVDTVGNKPDELKAILDTMIAISAHSAAEREELRLLAWLWRLTASAVAL  
GD\*

CG12229-m2(lethal) protein sequence

MPINQKEVTPQLDSQTGEDQGEQQEQPEDENRLEKFTVRLNGQHDLEQRLKDFKAACEAHEKHARRRKRYY  
HLGLVAKLVETTTHDELRRMLENGTYTFHVDTVGNKPDELKAILDTMIAISAHSAAEREELRLEAWLWRLTASAVA  
LGD\*

CG17027-wt DNA sequence

AGTAAAACGTCTCAATCAAAGGCATTTCTACGACGTGGCACCGACTACGACAACAAGATTGAGGACTTT  
CTCATGGAGAAAATATTGCCAGATACCCGGATCACAGTTCATGGCGAGGAGACGGCTAACAAACAA  
CAACGTGT

CG17027-m1(viable) DNA sequence

AGTAAAACGTCTCAATCAAAGGCATTTCTACGACGTGGCACCGACTACGACAACAAGATTGAGGACTTT  
CTCATGGAGAAAATATTGCCAGAT-----CACAGTTCATGGCGAGGAGACGGCTAACAAACAA  
GTGT [-8]

CG17027-m2(lethal) DNA sequence

AGTAAAACGTCTCAATCAAAGGCATTTCTACGACGTGGCACCGACTACGACAACAAGATTGAGGACTTT  
CTCATGGAGAAAATATTGCCAGAT-----CACAGTTCATGGCGAGGAGACGGCTAACAAACAA  
GTGT [-8]

CG17027-wt protein sequence

MAGVSQADIEELYNFIHPLAIKAGEILMEGYEMASKNVSIKGDFYDVTDYDNKIEDFLMEKILARYPDHKFIGE  
E.....

CG17027-m1(viable) protein sequence

MAGVSQADIEELYNFIHPLAIKAGEILMEGYEMASKNVSIKGDFYDVTDYDNKIEDFLMEKILARSQVHRRGGDG\*

CG17027-m2(lethal) protein sequence

MAGVSQADIEELYNFIHPLAIKAGEILMEGYEMASKNVSIKGDFYDVTDYDNKIEDFLMEKILARSQVHRRGGDG\*

CG17028-wt DNA sequence

AGGAAGTGCCTCCGCTC.....ATCATAGATCCCATTGATGGCA

CG17028-m1(lethal) DNA sequence

AGGAAGTGCCTCCGCTC---.....ATGGGACCGGTCCGGTCATC.....---ATCATAGATCCCATTGATGGCA [-1,  
81]

CG17028-m2(lethal) DNA sequence

AGGAAGTGCCTCCGCTC.....ATCATAGATCCCATTGATGGCA [0]

CG17028-wt protein sequence

MSYRIGEEKLEVYYQVSLELVRKCGPLFLEGFQKPKTDYEVKSAYDLTVYDKQIEATLDGLLKTFPESKIIGEE  
AMANAKTPPELTADPTWIIDPIDGTNNYVRKIPHCCISVGLAINKE.....

CG17028-m1(*lethal*) protein sequence

MSYRIGEEKLEVYYQVSLELVRKCGPLMGPVRSSS\*

CG17028-m2(*lethal*) protein sequence

MSYRIGEEKLEVYYQVSLELVRKCGPLFLEGFQKPKTDYEVKSAYDLTVYDKQIEATLDGLLKTFPESKIIGEE  
AMANAKTPPELTADPTWIIDPIDGTNNYVRKIPHCCISVGLAINKE.....