Here are the answers concerning our recently published manuscript (FBrf0250351 Gavory et al., 2021, PLoS Genet. 17(8): e1009730).

1)    eIF3b[S-4212] allele produces an inframe deletion of 39 nucleotides and leads to the loss of 14 amino acids (VSSWKVKEDTGFNM). See below for exact position.

reference: GTGGGATCCCACTGGACGCTACGTTGTGACTGG-~~TGTCTCGTCATGGAAGGTGAAAGAGGATACCGGCTTCAACATG~~-TACACGTTCCAGGGCCGCATCATCAAGCGTACC
mutant   : GTGGGATCCCACTGGACGCTACGTTGTGACTGG-----------------------------AC--GC----------TACACGTTCCAGGGCCGCATCATCAAGCGTACC
           |                                                                                                             |
           chr2R:13,425,760                                                                               chr2R:13,425,868

reference  540 WDPTGRYVVTGVSSWKVKEDTGFNMYTFQGRIIKRT

mutant     540 WDPTGRYVVTG-------------RYTFQGRIIKRT

2)    Rae1[E-1896] allele produces a deletion of 22 nucleotides leading to a frameshift and insertion of a STOP codon 20 amino acid downstream. See below for exact position.

Reference:  TACTGCGCCGATGTGGAGTATCCGATGGCCG-~~TGGTGGGCACGGCCAACAGAGG~~-ACTCATCATATACTCGCTGCAGAATAGCCCAACCGAGTACAAGCGGCAGGAGA

Mutant:     TACTGCGCCGATGTGGAGTATCCGATGGCCG------------------------ACTCATCATATACTCGCTGCAGAATAGCCCAACCGAGTACAAGCGGCAGGAGA

            |                                                                                                          |
           chr2R:21,659,414                                                                               chr2R:21,659,279

Reference: 156  YCADVEYPMAVVGTANRGLIIYSLQNSPTEYKRQESPLKYQHR

Mutant:    156  YCADVEYPMADSSYTRCRIAQPSTSGRRVR\*STSTVPFPFSGT

3)    emb[E-1836] produces a G to A transition (Position 8405915) in the acceptor splice site between intron 2 and 3

8405493 **CCCCATCCTGTCCAAAGTGCGATTCATTATGATCTCGCGCATGGCCAAGCCGGAGGAGGT** 8405552

8405553 **GCTGGTGGTGGAGAACGAAAACGGGGAAGTGGTGCGCGAGTTCATGAAGGACACAAACTC** 8405612

8405613 **AATAAACCTGTACAAGAACATGCGCGAAACGCTGGTCTTTCTTACCCATTTGGACTCTGT** 8405672

8405673 **GGACACGGACCGCATCATGACGCTAAAGCTGCTTAATCAGGTGAACGGATCGGAATTCTC** 8405732

8405733 **TTGGAAGAACCTGAACACGTTGTGCTGGGCCATTGGTTCCATATCCG**GTGAGCCATTTTT 8405792

8405793 GGTGTTTTATTCCCAGTCTGTACTTGGTTTTTATAAATCACAAACATTCATTCCTGATTA 8405852

8405853 TCATGGACCACCATTATTTCCGAGTATAACCCTATTTTTTTTTGTGCTTTTATCACTCTT 8405912

8405913 CAG**GTGCTTTTTGTGAAGAGGACGAAAAACGGTTCCTGGTCACCGTGATCAAGGATCTAT** 8405972

8405973 **TAGGCCTGTGCGAACAGAAGAAGGGCAAGGACAACAAGGCCATTATTGCCTCCAATATCA** 8406032

8406033 **TGTATGTGGTGGGACAGTATCCACGCTTCCTGCGCGCCCATTGGAAGTTCCTCAAGACGG** 8406092

8406093 **TGGTAAACAAACTCTTCGAATTTATGCACGAAACGCACGATGGTGTCCAGGATATGGCAT** 8406152

4)    Tryptophan nonsense mutations tara[S-1192], Mmp2[S-2288], Rae1[E-558] and Rae1[E-992] are TGG to TAG.