Figure S2 Amino acid changes in the Fz coding sequence caused by GC:AT and AT:GC base pair changes. First line indicates the codon number, the second line is the wild-type amino acid in one letter code, the third line shows the wild-type codon, the fourth line shows the amino acid change produced by a GC:AT change of the nucleotide indicated immediately above, the fifth line shows the amino acid change produced by an AT:GC change of the nucleotide indicated immediately above. Amino acid changes underlined are Stop codons and those predicted by the SIFT method (Ng and Henikoff 2001) to alter protein activity (i.e. those with a SIFT value of ≤0.05). GC:AT transpositions at 50 nucleotide positions result in Stop codons (nonsense mutations), and at 187 nucleotide positions result in amino acid changes (missense mutations) predicted to be deleterious by the SIFT method. AT:GC transpositions at 240 nucleotide positions result in amino acid changes (missense mutations) predicted to be deleterious by the SIFT method.