

Table S1. Sequence alterations of *egl-15* alleles

Allele	Wild-type sequence	Mutant sequence	Alteration
<i>n1456</i>	CACAAAGTGTGGCCA	CACAAAGTCTGGCC	Q268Ochre
<i>n1460</i>	ATCACAG attatctgg	ATCACAA attatctgg	exon 7 splice acceptor
<i>n1784</i>	TCAGTAAGAT ttgcctca	TCAATAAGAT ttgcctca	exon 7 splice donor
<i>n2210</i>	AAAGTTGGAAGTGC ^A	AAAGTTGAAAGTGC ^A	G374E
<i>n2202</i>	CTCACTGGGGATGGTA	CTCACTGAGGATGGTA	G492R
<i>n2205</i>	CTCACTGGGGATGGTA	CTCACTGGAGATGGTA	G492E
<i>n1459</i>	CAATGTAATT tgggaaa	CAATATAATT tgggaaa	Exon 11 splice donor
<i>n1475</i>	AGTTTGGAAAGCAAC	AGTTTGAAAAGCAAC	W655Opal
<i>n1775</i>	GCTCACGAAAAAGAG	GCTCACAAAAAAGAG	E680K
<i>n1783</i>	GCTGGTCCGCTTATG	GCTGGTCTGCTTATG	P714L
<i>n1476</i>	AATATCGGATTTGGA	AATATCGAATTTGGA	D815N
<i>n1454</i>	TTAAATGGATGGCTTT	TTAAATGAATGGCTTT	W840Opal
<i>n1478</i>	CATGCCTGAACCTCTAT	CATGCCTTAACCTCTAT	E882Ochre
<i>n1455</i>	GGATACAGGTGAAAA	GGATACAAGTGAAAA	R892I
<i>n1780</i>	GCAGAATGGAGGCCACC	GCAGAATAGAGGCCACC	M893I
<i>n1477ts</i>	TTGGATTGGATGTTAA	TTGGATTGAATGTTAA	W930Opal
<i>n2217</i>	CAGTTTGGGAAGTTGA	CAGTTTGAGAAGTTGA	W633Opal
<i>n2182</i>	GAGGGAGCATTGGAG	GAGGGAGTATTGGAG	A650V
<i>n2189</i>	CCCTATCCAACGATTGC	CCCTATCTAACGATTGC	P876L
<i>n2184</i>	AAAGAAGGATACAGGT	AAAGAAGAATACAGGT	G890E
<i>n2203</i>	GACACTTGGTGGAACT	GACACTTAGTGGAACT	G871S
<i>n2206</i>	TTGGATTGGATGTTAA	TTGGATTAGATGTTAA	W930Amber
<i>n1457</i>	CCAGGATCAATTTC	CCAGGATTAATTTC	Q948Ochre
<i>ay1</i>	TTTCAG atccactaa	TTTCAA atccactaa	Exon 5A splice acceptor
<i>n484</i>	GCGGATGGGAGAAGAT	GCGGATGAGAGAAGAT	W167(5A) Opal
<i>n1458</i>	TCGATTGGCTCACTGA	TCGATTGACTCACTGA	W135(5A) Opal

Sequence alterations of *egl-15* alleles flanked by genomic sequence; altered nucleotides are indicated in bold with italics. Coding sequences are depicted in upper case letters, intronic sequences in lowercase and a vertical line represents exon-intron boundaries. Amino acid alterations resulting from the mutation are shown in the far-right column.