

**Supplementary Table 3: Integration Sites**

ET insertion	Chromosome & Position	Nearest Gene and description	Insertion position vs nearest gene
<i>et10.1</i>	Ch10: bp21,730,662	Novel predicted gene, Similar to mannose receptor, C type 2	4th intron
<i>et10.4</i>	Ch2: bp43,825,248	zgc:110183 unknown function	1.5kb upstream
<i>et30.4</i>	Ch22: bp3,944,788	zgc:110764 Mitochondrial import inner membrane translocase	12.2kb downstream
<i>et58.1</i>	Ch20: bp25,029,937	rtn1b reticulon 1-like	1st intron
<i>et204</i>	Ch11: bp44,796,716	pax7 paired box gene 7	4th intron
<i>et206</i> *	Ch10: bp11,016,855	Mrrf mitochondrial ribosome recycling factor	5.5kb downstream
<i>et208</i> **	Ch9: bp22,786 on CT030044.6	unknown	unknown

Supplementary Table 3: Insertion sites resulting in enhancer trap patterns of interest.

For each enhancer trap insertion shown, the chromosome and location on the chromosome are indicated. The nearest gene or predicted gene is identified, along with the insertion's proximity to that gene.

\*The genomic region flanking insertion *et206* is most strongly aligned with the indicated location on chromosome 10, but is also highly similar to the region flanking chromosome 4, bp42,770,860

\*\**et208* was localized to a sequenced genomic clone, but could not be linked to an assembled genomic contig, and is therefore not linked to a nearest gene.