**SUPPLEMENTAL TABLES**

**Supplemental Table 1. Strain names for the 191 TS-EL mutant alleles.**

|  |  |  |  |
| --- | --- | --- | --- |
| Strain\*  (original genetic background) | Strain1  (after N2 outcross 1x) | TS allele | Affected gene |
| EU847 | EU30582 | *or388* | *let-19* |
| EU851 | EU31422 | *or392* | *klp-18* |
| CZ45061 | EU31362 | *or428* | *glp-1* |
| CZ45051 | EU31372 | *or448* | *glp-1* |
| CZ41151 | EU31382 | *or488* | *glp-1* |
| CZ40771 | EU30652 | *or542* | *chaf-1* |
| CZ43851 | EU30552 | *or566* | *let-19* |
| EU1120 | EU30892 | *or614* | *zwl-1* |
| EU1631 | EU2974 | *or789* | *emb-5* |
| EU1632 |  | *or790* |  |
| EU1636 |  | *or794* |  |
| EU1638 | EU3009 | *or796* |  |
| EU1647 | EU3175 | ***or805*** |  |
| EU1655 | EU3110 | *or813* |  |
| EU1688 |  | *or826* |  |
| EU1676 |  | *or834* |  |
| EU1681 | EU2994 | *or839* | *sart-3* |
| EU1693 |  | *or851* |  |
| EU1695 |  | *or853* |  |
| EU1706 | EU2995 | ***or862*** | *emb-5* |
| EU1711 | EU31392 | ***or867*** |  |
| EU1713 |  | *or869* |  |
| EU1714 | EU3039 | *or870* | *klp-18* |
| EU1717 | EU3064 | *or873* |  |
| EU1720 | EU2973 | *or876* |  |
| EU1723 |  | *or879* |  |
| EU1727 | EU3111 | *or883* |  |
| EU1737 |  | *or893* |  |
| EU1738 |  | *or894* |  |
| EU1739 |  | *or895* |  |
| EU1740 | EU3040 | *or896* |  |
| EU1742 |  | *or898* |  |
| EU1750 | EU3193 | *or906* |  |
| EU1751 |  | *or907* |  |
| EU1753 |  | *or909* |  |
| EU1758 | EU3001 | *or914* | *gad-1* |
| EU1763 | EU2955 | *or919* | *mom-4* |
| EU1765 | EU32172 | *or921* | *nap-1* |
| EU1766 | EU3176 | ***or922*** |  |
| EU1780 | EU2954 | *or936* | *cdc-25.2* |
| EU1795 |  | *or951* |  |
| EU1798 |  | *or954* |  |
| EU1802 | EU3011 | *or958* |  |
| EU1808 | EU3041 | *or960* |  |
| EU1815 |  | *or967* |  |
| EU1816 |  | *or968* |  |
| EU1822 |  | *or974* |  |
| EU1823 | EU30862 | *or975* | *emb-5* |
| EU1829 |  | *or981* |  |
| EU1832 |  | *or984* |  |
| EU1839 | EU3053 | ***or991*** |  |
| EU1843 | EU3002 | *or995* |  |
| EU1850 | EU31632 | ***or1002*** | *zim-3* |
| EU1851 |  | *or1003* |  |
| EU1852 | EU3042 | *or1004* |  |
| EU1853 | EU3177 | *or1005* | *let-19* |
| EU1854 | EU3194 | *or1006* |  |
| EU1856 |  | *or1008* |  |
| EU1865 |  | *or1016* |  |
| EU1837 |  | *or1024* |  |
| EU1874 |  | *or1025* |  |
| EU1882 |  | *or1033* |  |
| EU1883 |  | *or1034* |  |
| EU1899 | EU2958 | *or1050* |  |
| EU1901 |  | *or1052* |  |
| EU1913 | EU3211 | *or1064* |  |
| EU1920 |  | *or1071* |  |
| EU1931 |  | *or1081* |  |
| EU1933 | EU3012 | *or1083* |  |
| EU1935 | EU2992 | *or1085* | *lrr-1* |
| EU1944 |  | *or1094* |  |
| EU1947 | EU2961 | *or1097* | *emb-5* |
| EU1948 |  | *or1098* |  |
| EU1951 |  | *or1101* |  |
| EU1956 | EU2849 | ***or1106*** | *zim-3* |
| EU1957 | EU3204 | ***or1107*** |  |
| EU1958 | EU2963 | *or1108* | *drsh-1* |
| EU1959 | EU3043 | *or1109* |  |
| EU1960 |  | *or1110* |  |
| EU1963 | EU2957 | *or1113* | *let-19* |
| EU1964 |  | *or1114* |  |
| EU1965 |  | *or1115* |  |
| EU1968 | EU2968 | *or1118* | *apx-1* |
| EU1971 | EU3072 | *or1121* |  |
| EU1972 | EU3195 | *or1122* |  |
| EU1976 |  | *or1126* |  |
| EU1982 |  | *or1132* |  |
| EU1987 |  | *or1136* |  |
| EU1996 | EU2993 | *or1140* |  |
| EU2013 | EU3003 | *or1145* |  |
| EU2016 | EU3044 | *or1148* |  |
| EU2021 | EU3212 | *or1153* |  |
| EU2022 | EU2976 | *or1154* | *emb-5* |
| EU2023 |  | *or1155* |  |
| EU2031 |  | *or1163* |  |
| EU2032 |  | *or1164* |  |
| EU2049 | EU2979 | *or1181* |  |
| EU2051 |  | *or1183* |  |
| EU2054 |  | *or1186* |  |
| EU2060 | EU3196 | *or1192* |  |
| EU2061 | EU2841 | ***or1193*** | *rib-1* |
| EU2063 | EU2972 | ***or1195*** |  |
| EU2065 |  | *or1197* |  |
| EU2066 | EU3143 | *or1198* |  |
| EU2070 | EU3133 | *or1202* |  |
| EU2080 |  | *or1212* |  |
| EU2082 | EU3112 | *or1214* |  |
| EU2084 | EU3090 | *or1216* |  |
| EU2086 | EU3213 | *or1218* |  |
| EU2087 | EU3148 | ***or1219*** |  |
| EU2089 |  | *or1221* |  |
| EU2090 | EU3178 | *or1222* |  |
| EU2097 |  | *or1229* |  |
| EU2099 | EU2977 | *or1231* |  |
| EU2105 | EU3013 | *or1237* | *fntb-1* |
| EU2110 |  | *or1242* |  |
| EU2125 |  | *or1257* |  |
| EU2127 | EU3149 | *or1259* |  |
| EU2132 |  | *or1264* |  |
| EU2154 |  | *or1286* |  |
| EU2158 |  | *or1290* |  |
| EU2162 | EU3192 | *or1294* |  |
| EU2164 |  | *or1296* |  |
| EU2167 |  | *or1299* |  |
| EU2168 |  | *or1300* |  |
| EU2169 |  | *or1301* |  |
| EU2170 |  | *or1302* |  |
| EU2177 |  | *or1309* |  |
| EU2180 | EU2843 | ***or1312*** | *hlh-1* |
| EU2182 |  | *or1314* |  |
| EU2198 | EU32182 | ***or1330*** | *emb-4* |
| EU2206 |  | *or1338* |  |
| EU2210 |  | *or1342* |  |
| EU2222 | EU3113 | ***or1354*** |  |
| EU2263 |  | *or1395* |  |
| EU2272 | EU32072 | *or1404* |  |
| EU2275 |  | *or1407* |  |
| EU2292 | EU3046 | *or1424* |  |
| EU2294 |  | *or1426* |  |
| EU2295 |  | *or1427* |  |
| EU2303 |  | *or1435* |  |
| EU2341 |  | *or1473* |  |
| EU2356 |  | *or1488* |  |
| EU2379 | EU3114 | *or1511* |  |
| EU2400 |  | *or1524* |  |
| EU2402 |  | *or1526* |  |
| EU2415 |  | *or1539* |  |
| EU2416 |  | *or1540* |  |
| EU2478 |  | *or1599* |  |
| EU2481 |  | *or1602* |  |
| EU2531 |  | *or1647* |  |
| EU2552 |  | *or1665* |  |
| EU2554 |  | *or1667* |  |
| EU2555 |  | *or1668* |  |
| EU2559 | EU3063 | *or1672* |  |
| EU2574 | EU2844 | ***or1688*** | *rib-2* |
| EU2575 |  | *or1689* |  |
| EU2576 |  | *or1690* |  |
| EU2585 |  | *or1699* |  |
| EU2588 | EU3165 | *or1702* |  |
| EU2592 |  | *or1706* |  |
| EU2610 | EU3116 | ***or1723*** | *emb-9* |
| EU2616 |  | *or1729* |  |
| EU2620 | EU3198 | *or1733* |  |
| EU2624 |  | *or1737* |  |
| EU2625 |  | *or1738* |  |
| EU2626 |  | *or1739* |  |
| EU2627 |  | *or1740* |  |
| EU2629 | EU3015 | *or1742* |  |
| EU2639 | EU3199 | ***or1752*** |  |
| EU2641 | EU3134 | *or1754* |  |
| EU2642 | EU3078 | *or1755* |  |
| EU2643 |  | *or1756* |  |
| EU2645 | EU3181 | *or1758* |  |
| EU2650 | EU3147 | *or1763* |  |
| EU2652 | EU2839 | *or1765* |  |
| EU2653 | EU3200 | *or1766* |  |
| EU2668 | EU3135 | *or1781* |  |
| EU2669 |  | *or1782* |  |
| EU2671 |  | *or1784* |  |
| EU2672 |  | *or1785* |  |
| EU2674 |  | *or1787* |  |
| EU2678 |  | *or1791* |  |
| EU2684 |  | *or1797* |  |
| EU2687 |  | *or1800* |  |
| EU2733 |  | *or1835* |  |
| EU2787 |  | *or1889* |  |
| EU2792 |  | *or1894* |  |
| EU2793 |  | *or1895* |  |
| EU2811 |  | *or1911* |  |
| EU2832 |  | *or1932* |  |

\* = original genetic background includes: *lin-2*(*e1309*)*X*; *ojIs1[pie-1::gfp::beta-tbb-2]*; *ruIs32[unc-119*(*+*) *pie-1::GFP::H2B]*; *?Is?[?::gfp::ph]* (may contain *unc-119* (*eds*)) *III*

1 = after N2 outcross 1x, the new strain may contain the following: *ojIs1[pie-1::gfp::beta-tbb-2]*; *ruIs32[unc-119*(*+*) *pie-1::GFP::H2B]*; *?Is?[?::gfp::ph]* (may contain *unc-119* (*eds*)) *III*

2 = after N2 outcross 2x, the new strain may contain the following: *ojIs1[pie-1::gfp::beta-tbb-2]*; *ruIs32[unc-119*(*+*) *pie-1::GFP::H2B]*; *?Is?[?::gfp::ph]* (may contain *unc-119* (*eds*)) *III*

**Bold** denotes the mutant allele has a penetrant elongation defect after late upshift

**Supplemental Table 2. Strains used for complementation tests (alphabetical by gene).**

|  |  |  |
| --- | --- | --- |
| Genotype | Strain | Available |
| *apx-1*(*or545ts*) *V* | EU1013 | BB Lab |
| *cdc-25.2*(*g52ts*) *V* | GG52 | CGC |
| *chaf-1*(*n5453*) *I/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | MT20434 | CGC |
| *dcr-1*(*ok247*) *III/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | PD8753 | CGC |
| *drsh-1*(*ok369*) *I/ hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | VC1138 | CGC |
| *emb-4*(*hc60ts*) *V* | MJ60 | CGC |
| *emb-5*(*hc61ts*) *III* | GS1369 | CGC |
| *emb-9*(*hc70ts*) *III* | MJ70 | CGC |
| *fntb-1*(*ok590*) *V/nT1 [qIs51]* (*IV;V*) | VC399 | CGC |
| *gad-1*(*ct226ts*) *dpy-11*(*e224*) *V* | BW1943 | CGC |
| *gad-1*(*ok573*) *V/nT1* (*IV;V*) | VC327 | CGC |
| *glp-1*(*q46*) *III/ hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | JK4862 | CGC |
| *hlh-1*(*cc561ts*) *II* | PD4605 | CGC |
| *klp-18*(*ok2519*) *IV/nT1 [qIs51]* (*IV;V*) | VC1915 | CGC |
| *let-19*(*os33*)*/mIn1 [dpy-10*(*e128*) *mIs14] II* | HS458 | CGC |
| *lrr-1*(*ok3435*)*/mIn1 [mIs14 dpy-10*(*e128*)*] II* | VC2646 | CGC |
| *dpy-5*(*e61*) *mom-4*(*or39*) *I/hT1* (*I;III*)*; him-5*(*e1490*) *V* | EU424 | BB Lab |
| *mua-3*(*rh195ts*) *III* | OT136 | CGC |
| *nap-1*(*tm1278*) *IV/nT1 [qIs51]* (*IV;V*) | EU1626 | NBRC |
| *pab-1*(*ok1656*) *I/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | VC1191 | CGC |
| *rib-1*(*ok556*) *IV/nT1* (*IV;V*) | VC302 | CGC |
| *rib-2*(*gk318*) *III/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | VC733 | CGC |
| *rpn-1*(*ok2259*) *IV/nT1 [qIs51]* (*IV;V*) | VC1720 | CGC |
| *sart-3*(*tm6688*) *IV/nT1* (*IV;V*) | FX16561 | NBRP |
| *tag-307*(*gk418*) *III/mT1 [dpy-10*(*e128*)*]* (*II;III*) | VC890 | CGC |
| *teg-4*(*ok883*) *I/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | VC658 | CGC |
| *ttn-1*(*gk171*) *V/nT1* (*IV;V*) | VC313 | CGC |
| *vab-10*(*mc44*)*/unc-75*(*e950*) *unc-101*(*m1*) *I* | ML653 | CGC |
| *zfp-1*(*ok554*) *III* | RB774 | CGC |
| *unc-24*(*e138*) *zim-3*(*tm2303ts*) *IV* | CA448 | CGC |
| *zwl-1*(*ok2378*) *I/hT2 [bli-4*(*e937*) *let-?*(*q782*) *qIs48]* (*I;III*) | VC2705 | CGC |

BB Lab = Bruce Bowerman’s laboratory

CGC = Caenorhabditis Genetics Center, University of Minnesota, Twin Cities, Minnesota

NBRP = National Bioresource Project, Department of Physiology, Tokyo women’s Medical University School of Medicine, Tokyo, Japan

**Supplemental Table 3. Embryonic lethality and genetic characterization of penetrant L4 upshifted TS-EL mutants.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| TS allele | Gene | % EL at 15°C (n) | % EL at 26°C (n) | Heterozygous  % EL at 26°C (n) | Segregation frequency (n) |
| *or388* | *let-19* | 10.3 (755) | 100.0 (509) | 5.7 (475) | 25.0 (80) |
| *or392* | *klp-18* | 2.6 (460) | 99.6 (455) | 2.8 (246) | 22.5 (80) |
| *or428* | *glp-1* | 0.9 (441) | 100.0 (373) | 2.8 (538) | 25.0 (80) |
| *or448* | *glp-1* | 0.4 (521) | 99.7 (395) | 10.1 (495) | 27.5 (80) |
| *or488* | *glp-1* | 6.9 (595) | 99.8 (550) | 4.3 (234) | 21.3 (80) |
| *or542* | *chaf-1* | 0.8 (593) | 100.0 (635) | 0.7 (416) | 29.1 (79) |
| *or566* | *let-19* | 5.7 (436) | 100.0 (236) | 2.6 (380) | 23.1 (78) |
| *or614* | *zwl-1* | 13.5 (208) | 99.0 (244) | 1.2 (568) | 23.1 (78) |
| *or789* | *emb-5* | 0.0 (305) | 100.0 (252) | 3.1 (540) | 29.9 (77) |
| *or813* |  | 18.3 (689) | 95.4 (474) | 9.8 (357) | 21.3 (80) |
| *or839* | *sart-3* | 1.4 (424) | 92.5 (415) | 0.7 (431) | 13.8 (80) |
| *or870* | *klp-18* | 2.2 (682) | 99.7 (395) | 6.4 (607) | 14.6 (82) |
| *or883* |  | 4.4 (274) | 94.4 (445) | 1.5 (652) | 18.8 (80) |
| *or896* |  | 5.7 (367) | 98.7 (313) | 12.3 (447) | 21.3 (80) |
| *or906* |  | 65.5 (383) | 92.1 (721) | 15.0 (812) | 21.3 (80) |
| *or914* | *gad-1* | 4.0 (346) | 99.6 (270) | 0.5 (205) | 23.8 (80) |
| *or919* | *mom-4* | 9.1 (285) | 100.0 (187) | 0.8 (399) | 26.8 (71) |
| *or921* | *np-1* | 45.3 (988) | 99.3 (2436) | 24.2 (1223) | 32.5 (80) |
| *or936*† | *cdc-25.2* | 0.2 (416) | 100.0 (520) | 30.6 (447) | 24.4 (78) |
| *or958* |  | 4.6 (460) | 99.1 (333) | 6.1 (750) | 27.5 (80) |
| *or960* |  | 36.7 (1241) | 95.3 (1409) | 0.6 (365) | 19.2 (73) |
| *or975* | *emb-5* | 0.2 (418) | 100.0 (335) | 5.2 (478) | 26.4 (72) |
| *or1005* | *let-19* | 12.9 (855) | 100.0 (517) | 2.7 (1128) | 22.5 (80) |
| *or1006* |  | 20.2 (933) | 97.4 (534) | 14.5 (1519) | 30.0 (80) |
| *or1064* |  | 0.3 (327) | 99.7 (342) | 26.8 (448) | 37.5 (80) |
| *or1083* |  | 4.6 (410) | 96.7 (457) | 9.3 (248) | 22.5 (80) |
| *or1085* | *lrr-1* | 0.2 (422) | 99.5 (435) | 0.6 (357) | 31.5 (73) |
| *or1097* | *emb-5* | 0.4 (564) | 100.0 (350) | 16.4 (501) | 13.9 (79) |
| *or1108* | *drsh-1* | 8.9 (338) | 100.0 (260) | 2.2 (504) | 22.1 (77) |
| *or1109* |  | 49.9 (395) | 95.3 (555) | 1.7 (357) | 20.0 (80) |
| *or1113* | *let-19* | 4.1 (410) | 100.0 (643) | 6.2 (420) | 24.4 (78) |
| *or1118* | *apx-1* | 50.4 (272) | 100.0 (360) | 2.0 (455) | 17.7 (79) |
| *or1121* |  | 0.3 (391) | 99.0 (405) | 1.7 (530) | 26.3 (80) |
| *or1122*† |  | 6.1 (411) | 96.3 (491) | 33.5 (346) | 20.0 (80) |
| *or1136*† |  | 23.8 (420) | 100.0 (619) | 1.8 (740) | 10.2 (59) |
| *or1140* |  | 2.4 (456) | 99.5 (206) | 1.4 (513) | 37.5 (80) |
| *or1145* |  | 0.8 (379) | 99.7 (346) | 0.5 (189) | 30.0 (80) |
| *or1153*† |  | 1.1 (359) | 93.2 (1017) | 29.4 (585) | 25.6 (90) |
| *or1154* | *emb-5* | 1.0 (386) | 100.0 (290) | 9.7 (401) | 27.5 (80) |
| *or1181* |  | 3.9 (332) | 100.0 (430) | 1.1 (447) | 28.2 (78) |
| *or1183*† |  | 23.3 (771) | 100.0 (801) | 2.0 (453) | 9.0 (78) |
| *or1186* |  | 1.9 (539) | 94.2 (486) | 7.2 (374) | 20.0 (80) |
| *or1192* |  | 27.7 (748) | 98.9 (379) | 12.6 (422) | 27.5 (80) |
| *or1198* |  | 0.4 (281) | 100.0 (309) | 2.4 (739) | 25.3 (79) |
| *or1202* |  | 2.1 (568) | 100.0 (434) | 3.5 (367) | 21.1 (114) |
| *or1214* |  | 14.4 (360) | 94.4 (250) | 2.5 (678) | 24.4 (90) |
| *or1216* |  | 1.4 (419) | 99.7 (324) | 2.5 (471) | 17.3 (75) |
| *or1218*† |  | 0.9 (316) | 100.0 (814) | 25.4 (1933) | 7.4 (285) |
| *or1222* |  | 1.3 (400) | 100.0 (451) | 26.7 (1086) | 28.8 (80) |
| *or1237* | *fntb-1* | 30.1 (379) | 93.5 (217) | 4.5 (332) | 30.4 (79) |
| *or1259* |  | 5.5 (271) | 92.0 (224) | 0.4 (518) | 26.3 (80) |
| *or1294* |  | 5.7 (262) | 100.0 (541) | 19.3 (409) | 30.0 (80) |
| *or1404* |  | 1.0 (973) | 98.1 (586) | 11.2 (1784) | 24.7 (166) |
| *or1511* |  | 1.2 (564) | 100.0 (341) | 1.1 (467) | 28.8 (80) |
| *or1702* |  | 0.8 (735) | 100.0 (490) | 7.8 (396) | 28.2 (78) |
| *or1733* |  | 73.9 (376) | 97.4 (736) | 25.9 (1447) | 30.0 (80) |
| *or1742* |  | 13.5 (490) | 83.8 (290) | 2.7 (294) | 17.5 (160) |
| *or1754* |  | 1.2 (497) | 100.0 (464) | 21.9 (534) | 28.0 (50) |
| *or1755* |  | 59.2 (196) | 84.5 (239) | 7.2 (454) | 32.5 (80) |
| *or1758*† |  | 4.1 (469) | 100.0 (412) | 40.5 (422) | 26.7 (90) |
| *or1763* |  | 1.9 (534) | 100.0 (279) | 16.1 (417) | 29.9 (87) |
| *or1766* |  | 6.1 (474) | 97.0 (429) | 16.0 (357) | 18.2 (80) |
| *or1781* |  | 21.2 (609) | 100.0 (600) | 25.5 (1695) | 24.0 (50) |

† = removed from further study (either because the allele is a multi-loci mutant or is dominant)

**Supplemental Table 4. Sequence alterations in the late upshifted causal TS-EL mutants.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| LG | Gene | Transcript | TS allele | Nucleotide mutated1 | Nucleotide change | Codon mutated | Amino acid change | Length of protein |
| V | *emb-4* | Y80D3A.2a | *or1330\** | 2900 | atc > aAtc | 967 | I > N | 1467 |
| III | *emb-5* | T04A8.14 | *or862* | 2593 | T > C | 865 | S > P | 1521 |
| III | *emb-9* | K04H4.1a | *or1723* | 3509 | G > A | 1170 | G > E | 1759 |
| II | *hlh-1* | B0304.1b | *or1312* | 586 | C > T | 196 | L > F | 324 |
| IV | *rib-1* | F12F6.3a | *or1193* | 377 | A > T | 126 | H > L | 382 |
| III | *rib-2* | K01G5.6.1 | *or1688* | 710 | T > A | 237 | V > D | 814 |
| IV | *zim-3* | T07G12.11a | *or1002* | 1607 | T > G | 536 | I > S | 581 |
| *or1106*¥ | 597 | T > A | 199 | Y > stop |

LG = Linkage group

1 = Mutated nucleotide positions are given for the spliced form of the gene

a = isoform a, b = isoform b

Nature of mutations: all are missense mutations, except: \* = insertion causing a frameshift and a likely early stop at codon 1004, and ¥ = nonsense

**Supplemental Table 5. Causal mutation identification for penetrant L4 upshifted TS-EL mutants.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TS allele | Tested | | Transheterozygote  % EL at 26°C (n) | |
| gene | allele |
| *or388* | ***let-19*** | *or566*ts | 100.0 | (688) |
| *eff-1* | *ok1021* | N/A | N/A |
| *or392* | ***klp-18*** | *ok2519* | 99.9 | (927) |
| *rpn-1* | *ok2259* | 0.5 | (662) |
| *or428* | ***glp-1*** | *q46* | 100.0 | (830) |
| *or448* | ***glp-1*** | *q46* | 100.0 | (486) |
| *tag-307* | *gk418* | 24.7 | (885) |
| *or488* | ***glp-1*** | *or448*ts | 99.4 | (966) |
| *or542* | ***chaf-1*** | *n5453* | 100.0 | (1351) |
| *or566* | ***let-19*** | *os33* | 100.0 | (505) |
| *or614* | ***zwl-1*** | *ok2378* | 100.0 | (218) |
| *or789* | ***emb-5*** | *or975*ts | 100.0 | (210) |
| *dcr-1* | *ok247* | 23.0 | (187) |
| *or839* | ***sart-3*** | *tm6688* | 97.0 | (2409) |
| *or870* | ***klp-18*** | *or392*ts | 99.9 | (1463) |
| *or914* | ***gad-1*** | *ok573* | 100.0 | (1434) |
| ***gad-1*** | *ct226*ts | 99.6 | (270) |
| *ttn-1* | *gk171* | 24.6 | (1122) |
| *or919* | ***mom-4*** | *or39* | 100.0 | (1106) |
| *vab-10* | *mc44* | 5.2 | (1790) |
| *or921* | ***nap-1*** | *tm1278* | 98.2 | (623) |
| *rpn-1* | *ok2259* | 10.7 | (657) |
| *rod-1* | *tm6186* | N/A | N/A |
| *or936* | ***cdc-25.2*** | *g52*ts | 100.0 | (1318) |
| *or975* | ***emb-5*** | *hc61*ts | 100.0 | (260) |
| *mua-3* | *rh195*ts | 6.1 | (2404) |
| *or1005* | ***let-19*** | *or566*ts | 100.0 | (262) |
| *or1085* | ***lrr-1*** | *ok3435* | 100.0 | (284) |
| *or1097* | ***emb-5*** | *hc61*ts | 100.0 | (372) |
| *acy-1* | *tm5028* | N/A | N/A |
| *or1108* | ***drsh-1*** | *ok369* | 99.9 | (1569) |
| *pab-1* | *ok1656* | 13.4 | (493) |
| *teg-4* | *ok883* | 1.6 | (1037) |
| *tlf-1* | *tm878* | N/A | N/A |
| *or1113* | ***let-19*** | *or566*ts | 100.0 | (773) |
| *or1118* | ***apx-1*** | *or545*ts | 100.0 | (417) |
| *chk-1* | *tm938* | N/A | N/A |
| *or1154* | ***emb-5*** | *or975*ts | 100.0 | (301) |
| *dcr-1* | *ok247* | 40.4 | (183) |
| *or1237* | ***fntb-1*** | *ok590* | 86.9 | (611) |
| *ttn-1* | *gk171* | 5.1 | (2778) |

**Bold** denotes the known mutation fails to complement the TS-EL allele

**Supplemental Table 6. Sequence alterations in the L4 upshifted causal TS-EL mutants.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| LG | Gene | Transcript | TS allele | Nucleotide mutated1 | Nucleotide change | Codon mutated | Amino acid change | Length of protein |
| V | *apx-1* | K08D9.3a | *or1118* | 322 | T > C | 108 | W > R | 515 |
| V | *cdc-25.2* | F16B4.8a | *or936* | 749 | T > C | 250 | I > T | 480 |
| I | *chaf-1* | T06D10.2a | *or542* | 1309 | G > A | 437 | A > T | 479 |
| I | *drsh-1* | F26E4.10a | *or1108* | 1760 | T > A | 587 | V > E | 1086 |
| III | *emb-5* | T04A8.14 | *or789* | 1364 | T > C | 455 | F > S | 1521 |
| *or975* | 1543 | G > A | 515 | A > T |
| *or1097* | 2036 | G > A | 679 | R > K |
| *or1154* | 1486 | T > C | 496 | Y > H |
| V | *fntb-1* | F23B12.6 | *or1237 ¥* | 270 | G > A | 90 | W > stop | 401 |
| V | *gad-1* | T05H4.14 | *or914* | 647 | A > T | 216 | D > V | 620 |
| III | *glp-1* | F02A9.6 | *or428* | 1204 | G > A | 402 | G > R | 1295 |
| *or448* | 161 | G > A | 54 | G > D |
| *or488* | 161 | G > A | 54 | G > D |
| IV | *klp-18* | C06G3.2 | *or392* | 2560 | G > A | 854 | V > M | 932 |
| *or870* | 904 | G > A | 302 | A > T |
| II | *let-19* | K08F8.6 | *or388* | 7127 | C > T | 2376 | P > L | 2862 |
| *or566* | 7127 | C > T | 2376 | P > L |
| *or1005* | 7127 | C > T | 2376 | P > L |
| *or1113* | 8254 | C > T | 2752 | P > S |
| II | *lrr-1* | F33G12.8 | *or1085* | 1000 | G > A | 334 | G > R | 453 |
| I | *mom-4* | F52F12.3 | *or919* | 443 | A > C | 148 | Y > S | 536 |
| IV | *nap-1* | D2096.8 | *or921* | 485 | T > C | 162 | F > S | 316 |
| IV | *sart-3* | B0035.12 | *or839* | 1328 | T > A | 443 | I > N | 836 |
| I | *zwl-1* | Y39G10AR.2a | *or614* | 854 | G > A | 285 | G > E | 630 |

LG = Linkage group

1 = Mutated nucleotide positions are given for the spliced form of the gene

a = isoform a

Nature of mutations: all are missense mutations, except: ¥ = nonsense

**Supplemental Table 7. Gene orthologs and functions for L4 upshifted causal TS-EL mutations.**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | TS allele | Human ortholog | Function |
| **Cell Division** (meiosis and/or mitosis) | | | |
| *klp-18* | *or392* | KLP2 | Kinesin motor protein |
| *or870* |
| *zwl-1* | *or614* | ZWILCH | Kinetochore protein |
| **Cell Cycle** | | | |
| *cdc-25.2* | *or936* | CDC25 | Phosphatase |
| *lrr-1* | *or1085* | LRR1 | Substrate recognition subunit of the cullin 2-RING E3 ubiquitin ligase CLR2 |
| **Gene Expression** (signaling/transcription factors) | | | |
| *apx-1* | *or1118* | Delta-like protein1 | Ligand for Notch signaling receptors |
| *emb-5* | *or789* | SPT6 | RNA polymerase II transcription elongation factor |
| *or975* |
| *or1097* |
| *or1154* |
| *gad-1* | *or914* | WDR70 | G protein, protein-protein interactions |
| *glp-1* | *or428* | Notch | Transmembrane receptor |
| *or448* |
| *or488* |
| *let-19* | *or388* | TRAP240 | Transcriptional co-activation subunit |
| *or566* |
| *or1005* |
| *or1113* |
| *mom-4* | *or919* | MAP3K7 | Map kinase |
| **Gene Expression** (nucleosome/chromatin regulation) | | | |
| *chaf-1* | *or542* | CHAF1A | Chromatin assembly factor subunit |
| *nap-1* | *or921* | NAP1L1 | Nucleosome assembly protein |
| **RNA Modification** | | | |
| *drsh-1* | *or1108* | Drosha | RNase III endoribonuclease |
| *sart-3* | *or839* | SART3 | RNA splicing |
| **Protein Modification** | | | |
| *fnt­b-1* | *or1237* | FNTB | Farnesyltransferase, beta subunit |