**Mapping QTLRs affecting Marek’s Disease resistance on chicken Chromosome Z**

**Supplemental**

**Table S1.** QTLR genes.

| **QTLR** | **Gene stable ID version** | **Gene name** | **Gene description** | **Start** | **End** |
| --- | --- | --- | --- | --- | --- |
| F6-1 | ENSGALG00000033353.2 | RIT2 | Ras like without CAAX 2 | 3,471,974 | 3,658,288 |
| F6-1 | ENSGALG00000053587.1 |  |  | 3,831,101 | 3,888,531 |
| F6-1 | ENSGALG00000053587.1 |  |  | 3,831,101 | 3,888,531 |
| F6-1 | ENSGALG00000035773.2 | PIK3C3 | phosphatidylinositol 3-kinase catalytic subunit type 3 | 3,984,326 | 4,085,724 |
| F6-1 | ENSGALG00000035773.2 | PIK3C3 | phosphatidylinositol 3-kinase catalytic subunit type 3 | 3,984,326 | 4,085,724 |
| F6-1 | ENSGALG00000035773.2 | PIK3C3 | phosphatidylinositol 3-kinase catalytic subunit type 3 | 3,984,326 | 4,085,724 |
| F6-1 | ENSGALG00000035773.2 | PIK3C3 | phosphatidylinositol 3-kinase catalytic subunit type 3 | 3,984,326 | 4,085,724 |
| F6-1 | ENSGALG00000035773.2 | PIK3C3 | phosphatidylinositol 3-kinase catalytic subunit type 3 | 3,984,326 | 4,085,724 |
| F6-1 | ENSGALG00000046722.1 |  |  | 4,109,272 | 4,122,240 |
| F6-1 | ENSGALG00000046722.1 |  |  | 4,109,272 | 4,122,240 |
| F6-1 | ENSGALG00000027997.2 |  |  | 4,192,457 | 4,192,635 |
| F6-1 | ENSGALG00000050161.1 |  |  | 4,342,321 | 4,353,388 |
| F6-1 | ENSGALG00000050161.1 |  |  | 4,342,321 | 4,353,388 |
| F6-1 | ENSGALG00000050161.1 |  |  | 4,342,321 | 4,353,388 |
| F6-1 | ENSGALG00000047964.1 |  |  | 5,328,479 | 5,331,064 |
| F6-1 | ENSGALG00000050555.1 |  |  | 5,408,840 | 5,410,258 |
| F6-1 | ENSGALG00000054065.1 |  |  | 5,670,782 | 5,680,806 |
| F6-1 | ENSGALG00000054065.1 |  |  | 5,670,782 | 5,680,806 |
| F6-1, P-1 | ENSGALG00000038930.3 |  |  | 6,156,148 | 6,256,742 |
| F6-1, P-1 | ENSGALG00000055071.1 |  |  | 6,412,831 | 6,424,558 |
| F6-1, P-1 | ENSGALG00000046768.1 |  |  | 6,473,573 | 6,492,274 |
| F6-1, P-1 | ENSGALG00000046768.1 |  |  | 6,473,573 | 6,492,274 |
| F6-1, P-1 | ENSGALG00000050344.1 | CELF4 | CUGBP Elav-like family member 4 | 6,768,902 | 6,793,723 |
| F6-1, P-1 | ENSGALG00000002413.6 |  |  | 6,770,918 | 6,823,825 |
| F6-1, P-1 | ENSGALG00000048972.1 |  |  | 6,831,508 | 6,876,170 |
| F6-1, P-1 | ENSGALG00000002419.7 | KIAA1328 | KIAA1328 | 6,945,983 | 7,102,689 |
| F6-1, P-1 | ENSGALG00000026547.4 | TPGS2 | tubulin polyglutamylase complex subunit 2 | 7,102,975 | 7,126,925 |
| F6-1, P-1 | ENSGALG00000018534.5 | AQP7 | aquaporin 7 | 7,124,552 | 7,137,256 |
| F6-1, P-1 | ENSGALG00000026884.3 |  | phospholipase A2 inhibitor and LY6/PLAUR domain containing | 7,161,279 | 7,165,204 |
| F6-1, P-1 | ENSGALG00000002452.6 | AQP3 | aquaporin 3 (Gill blood group) | 7,195,127 | 7,209,340 |
| F6-1, P-1 | ENSGALG00000030730.2 | NOL6 | nucleolar protein 6 | 7,254,427 | 7,288,141 |
| F6-1, P-1 | ENSGALG00000030730.2 | NOL6 | nucleolar protein 6 | 7,254,427 | 7,288,141 |
| F6-1, P-1 | ENSGALG00000001668.7 | UBE2R2 | ubiquitin conjugating enzyme E2 R2 | 7,304,134 | 7,356,093 |
| F6-1, P-1 | ENSGALG00000013809.6 |  | AD012Z | 7,358,700 | 7,496,820 |
| F6-1, P-1 | ENSGALG00000013809.6 |  | AD012Z | 7,358,700 | 7,496,820 |
| F6-1, P-1 | ENSGALG00000005759.5 | IFNW1 | interferon omega 1 | 7,372,029 | 7,372,640 |
| F6-1, P-1 | ENSGALG00000046996.1 | IFN-A | interferon type A1/A2-like | 7,377,531 | 7,378,293 |
| F6-1, P-1 | ENSGALG00000047630.1 | IFN-A | interferon type A1/A2-like | 7,381,503 | 7,382,265 |
| F6-1, P-1 | ENSGALG00000054396.1 |  | interferon type A1/A2-like | 7,385,475 | 7,386,237 |
| F6-1, P-1 | ENSGALG00000053752.1 | IFN-A | interferon type A1/A2-like | 7,387,284 | 7,388,046 |
| F6-1, P-1 | ENSGALG00000054368.1 |  | interferon type A1/A2-like | 7,391,261 | 7,392,023 |
| F6-1, P-1 | ENSGALG00000048874.1 | IFN-A | interferon | 7,395,233 | 7,395,995 |
| F6-1, P-1 | ENSGALG00000044725.2 |  | interferon type A1/A2-like | 7,399,231 | 7,399,942 |
| F6-1, P-1 | ENSGALG00000050924.1 | IFN-A | interferon type A1/A2-like | 7,401,271 | 7,402,033 |
| F6-1, P-1 | ENSGALG00000033669.2 |  |  | 7,405,294 | 7,405,874 |
| F6-1, P-1 | ENSGALG00000052209.1 |  | interferon type A1/A2-like | 7,410,282 | 7,411,044 |
| F6-1, P-1 | ENSGALG00000053207.1 |  | interferon type A1/A2-like | 7,414,251 | 7,415,013 |
| F6-1, P-1 | ENSGALG00000054104.1 |  | interferon type A3-like | 7,421,956 | 7,422,718 |
| F6-1, P-1 | ENSGALG00000025660.2 |  | small nucleolar RNA SNORD121A | 7,438,822 | 7,438,906 |
| F6-1, P-1 | ENSGALG00000025641.2 |  | small nucleolar RNA SNORD121A | 7,441,643 | 7,441,726 |
| F6-1, P-1 | ENSGALG00000005800.6 | DCAF12L2 | DDB1 and CUL4 associated factor 12 like 2 | 7,510,336 | 7,540,872 |
| F6-1, P-1 | ENSGALG00000021378.6 | UBAP1 | ubiquitin associated protein 1 | 7,543,736 | 7,574,787 |
| F6-1, P-1 | ENSGALG00000053307.1 |  |  | 7,575,708 | 7,578,512 |
| F6-1, P-1 | ENSGALG00000005806.6 | KIF24 | kinesin family member 24 | 7,583,295 | 7,612,042 |
| F6-1, P-1 | ENSGALG00000005806.6 | KIF24 | kinesin family member 24 | 7,583,295 | 7,612,042 |
| F6-1, P-1 | ENSGALG00000027295.3 | NUDT2 | nudix hydrolase 2 | 7,613,662 | 7,620,056 |
| F6-1, P-1 | ENSGALG00000027295.3 | NUDT2 | nudix hydrolase 2 | 7,613,662 | 7,620,056 |
| F6-1, P-1 | ENSGALG00000045636.2 |  | uncharacterized LOC427400 | 7,621,689 | 7,637,215 |
| F6-1, P-1 | ENSGALG00000025921.3 |  | LOC431653 | 7,645,535 | 7,647,631 |
| F6-1, P-1 | ENSGALG00000005814.6 |  | KIAA1161 | 7,654,557 | 7,656,593 |
| F6-1, P-1 | ENSGALG00000005821.6 | FAM219A | family with sequence similarity 219 member A | 7,677,351 | 7,715,763 |
| F6-1, P-1 | ENSGALG00000005821.6 | FAM219A | family with sequence similarity 219 member A | 7,677,351 | 7,715,763 |
| F6-1, P-1 | ENSGALG00000005821.6 | FAM219A | family with sequence similarity 219 member A | 7,677,351 | 7,715,763 |
| F6-1, P-1 | ENSGALG00000005831.7 | DNAI1 | dynein axonemal intermediate chain 1 | 7,780,562 | 7,905,039 |
| F6-1, P-1 | ENSGALG00000005831.7 | DNAI1 | dynein axonemal intermediate chain 1 | 7,780,562 | 7,905,039 |
| F6-1, P-1 | ENSGALG00000005831.7 | DNAI1 | dynein axonemal intermediate chain 1 | 7,780,562 | 7,905,039 |
| F6-1, P-1 | ENSGALG00000005831.7 | DNAI1 | dynein axonemal intermediate chain 1 | 7,780,562 | 7,905,039 |
| F6-1, P-1 | ENSGALG00000030845.2 | ENHO | energy homeostasis associated | 7,905,544 | 7,906,945 |
| F6-1, P-1 | ENSGALG00000038723.2 | RPP25L | ribonuclease P/MRP 25kDa subunit-like | 7,909,086 | 7,911,236 |
| F6-1, P-1 | ENSGALG00000038723.2 | RPP25L | ribonuclease P/MRP 25kDa subunit-like | 7,909,086 | 7,911,236 |
| F6-1, P-1 | ENSGALG00000021365.6 | DCTN3 | dynactin subunit 3 | 7,913,360 | 7,921,570 |
| F6-1, P-1 | ENSGALG00000005839.6 | ARID3C | AT-rich interaction domain 3C | 7,926,291 | 7,938,483 |
| F6-1, P-1 | ENSGALG00000028996.3 | SIGMAR1 | sigma non-opioid intracellular receptor 1 | 7,940,896 | 7,943,905 |
| F6-1, P-1 | ENSGALG00000028996.3 | SIGMAR1 | sigma non-opioid intracellular receptor 1 | 7,940,896 | 7,943,905 |
| F6-1, P-1 | ENSGALG00000028996.3 | SIGMAR1 | sigma non-opioid intracellular receptor 1 | 7,940,896 | 7,943,905 |
| F6-1, P-1 | ENSGALG00000026195.3 | GALT | galactose-1-phosphate uridylyltransferase | 7,943,944 | 7,946,758 |
| F6-1, P-1 | ENSGALG00000026195.3 | GALT | galactose-1-phosphate uridylyltransferase | 7,943,944 | 7,946,758 |
| F6-1, P-1 | ENSGALG00000028140.3 | CNTFR | ciliary neurotrophic factor receptor | 8,134,527 | 8,304,301 |
| F6-1, P-1 | ENSGALG00000028140.3 | CNTFR | ciliary neurotrophic factor receptor | 8,134,527 | 8,304,301 |
| F6-1, P-1 | ENSGALG00000028140.3 | CNTFR | ciliary neurotrophic factor receptor | 8,134,527 | 8,304,301 |
| F6-1, P-1 | ENSGALG00000028140.3 | CNTFR | ciliary neurotrophic factor receptor | 8,134,527 | 8,304,301 |
| F6-1, P-1 | ENSGALG00000028140.3 | CNTFR | ciliary neurotrophic factor receptor | 8,134,527 | 8,304,301 |
| F6-1 | ENSGALG00000005848.8 | IL11RA | interleukin 11 receptor subunit alpha | 8,328,565 | 8,349,086 |
| F6-1 | ENSGALG00000005848.8 | IL11RA | interleukin 11 receptor subunit alpha | 8,328,565 | 8,349,086 |
| F6-1 | ENSGALG00000005848.8 | IL11RA | interleukin 11 receptor subunit alpha | 8,328,565 | 8,349,086 |
| F6-1 | ENSGALG00000005848.8 | IL11RA | interleukin 11 receptor subunit alpha | 8,328,565 | 8,349,086 |
| F6-1 | ENSGALG00000028256.3 | CCL19 | C-C motif chemokine ligand 19 | 8,363,698 | 8,366,694 |
| F6-1 | ENSGALG00000046192.2 | CCL21 | c-C motif chemokine 26-like | 8,370,305 | 8,373,001 |
| F6-1 | ENSGALG00000050776.1 |  |  | 8,389,062 | 8,461,689 |
| F6-1 | ENSGALG00000050776.1 |  |  | 8,389,062 | 8,461,689 |
| F6-1 | ENSGALG00000050776.1 |  |  | 8,389,062 | 8,461,689 |
| F6-1 | ENSGALG00000048171.1 |  |  | 8,416,911 | 8,465,130 |
| F6-1 | ENSGALG00000048171.1 |  |  | 8,416,911 | 8,465,130 |
| F6-1 | ENSGALG00000048171.1 |  |  | 8,416,911 | 8,465,130 |
| F6-1 | ENSGALG00000045914.2 |  |  | 8,425,829 | 8,456,048 |
| F6-1 | ENSGALG00000045914.2 |  |  | 8,425,829 | 8,456,048 |
| F6-1 | ENSGALG00000045914.2 |  |  | 8,425,829 | 8,456,048 |
| F6-1 | ENSGALG00000001900.6 | PHF24 | PHD finger protein 24 | 8,501,025 | 8,509,540 |
| F6-1 | ENSGALG00000001918.6 | DNAJB5 | DnaJ heat shock protein family (Hsp40) member B5 | 8,525,124 | 8,538,233 |
| F6-1 | ENSGALG00000001918.6 | DNAJB5 | DnaJ heat shock protein family (Hsp40) member B5 | 8,525,124 | 8,538,233 |
| F6-1 | ENSGALG00000001918.6 | DNAJB5 | DnaJ heat shock protein family (Hsp40) member B5 | 8,525,124 | 8,538,233 |
| F6-1 | ENSGALG00000001986.7 | VCP | valosin containing protein | 8,540,925 | 8,562,119 |
| F6-1 | ENSGALG00000002009.5 | FANCG | Fanconi anemia complementation group G | 8,563,543 | 8,574,697 |
| F6-1 | ENSGALG00000002023.5 | PIGO | phosphatidylinositol glycan anchor biosynthesis class O | 8,577,948 | 8,591,196 |
| F6-1 | ENSGALG00000025775.2 | gga-mir-6649 | gga-mir-6649 | 8,585,251 | 8,585,389 |
| F6-1 | ENSGALG00000002064.7 | STOML2 | stomatin like 2 | 8,592,089 | 8,597,473 |
| F6-1 | ENSGALG00000002069.6 | FAM214B | family with sequence similarity 214 member B | 8,598,884 | 8,606,934 |
| F6-1 | ENSGALG00000002069.6 | FAM214B | family with sequence similarity 214 member B | 8,598,884 | 8,606,934 |
| F6-1 | ENSGALG00000002069.6 | FAM214B | family with sequence similarity 214 member B | 8,598,884 | 8,606,934 |
| F6-1 | ENSGALG00000002165.6 | UNC13B | unc-13 homolog B | 8,647,537 | 8,854,699 |
| F6-1 | ENSGALG00000002326.6 |  | ATPase phospholipid transporting 8B4 (putative) | 8,885,670 | 8,943,726 |
| F6-1 | ENSGALG00000002326.6 |  | ATPase phospholipid transporting 8B4 (putative) | 8,885,670 | 8,943,726 |
| F6-1 | ENSGALG00000002371.6 | RUSC2 | RUN and SH3 domain containing 2 | 8,966,773 | 9,000,212 |
| F6-1 | ENSGALG00000002371.6 | RUSC2 | RUN and SH3 domain containing 2 | 8,966,773 | 9,000,212 |
| F6-1 | ENSGALG00000028411.3 |  |  | 9,006,673 | 9,015,300 |
| F6-1 | ENSGALG00000028411.3 |  |  | 9,006,673 | 9,015,300 |
| F6-1 | ENSGALG00000021355.5 |  | receptor-type tyrosine-protein phosphatase S-like | 9,015,759 | 9,024,777 |
| F6-1 | ENSGALG00000021355.5 |  | receptor-type tyrosine-protein phosphatase S-like | 9,015,759 | 9,024,777 |
| F6-1 | ENSGALG00000027747.2 | TROJANZ | phosphotyrosine phosphatase kappa-like-Z | 9,025,003 | 9,030,333 |
| F6-1 | ENSGALG00000045280.2 |  | uncharacterized LOC100858953 | 9,032,707 | 9,039,475 |
| F6-1 | ENSGALG00000045280.2 |  | uncharacterized LOC100858953 | 9,032,707 | 9,039,475 |
| F6-1 | ENSGALG00000027658.3 | TESK1 | testis-specific kinase 1 | 9,047,866 | 9,055,667 |
| F6-1 | ENSGALG00000027658.3 | TESK1 | testis-specific kinase 1 | 9,047,866 | 9,055,667 |
| F6-1 | ENSGALG00000005194.4 | CD72 | CD72 molecule | 9,056,639 | 9,060,366 |
| F6-1 | ENSGALG00000005194.4 | CD72 | CD72 molecule | 9,056,639 | 9,060,366 |
| F6-1 | ENSGALG00000005194.4 | CD72 | CD72 molecule | 9,056,639 | 9,060,366 |
| F6-1 | ENSGALG00000021353.5 |  | CD72 antigen-like | 9,061,604 | 9,064,699 |
| F6-1 | ENSGALG00000021353.5 |  | CD72 antigen-like | 9,061,604 | 9,064,699 |
| F6-1 | ENSGALG00000002383.7 | CD72AG | CD72 antigen | 9,066,022 | 9,069,155 |
| F6-1 | ENSGALG00000029035.4 |  | C-type lectin domain family 5, member A | 9,069,756 | 9,071,860 |
| F6-1 | ENSGALG00000040221.2 |  | undifferentiated embryonic cell transcription factor 1-like | 9,072,456 | 9,075,192 |
| F6-1 | ENSGALG00000002386.6 | TMEM8B | transmembrane protein 8B | 9,080,563 | 9,084,664 |
| F6-1 | ENSGALG00000025868.3 | TAF1C | TATA-box binding protein associated factor, RNA polymerase I subunit C-Z | 9,087,724 | 9,092,161 |
| F6-1 | ENSGALG00000027418.3 |  | histidine triad nucleotide binding protein 1 | 9,092,401 | 9,093,974 |
| F6-1 | ENSGALG00000027418.3 |  | histidine triad nucleotide binding protein 1 | 9,092,401 | 9,093,974 |
| F6-1 | ENSGALG00000027418.3 |  | histidine triad nucleotide binding protein 1 | 9,092,401 | 9,093,974 |
| F6-1 | ENSGALG00000027630.3 | NPR2 | natriuretic peptide receptor 2 | 9,096,779 | 9,106,881 |
| F6-1 | ENSGALG00000027630.3 | NPR2 | natriuretic peptide receptor 2 | 9,096,779 | 9,106,881 |
| F6-1 | ENSGALG00000028118.3 | MSMP | microseminoprotein, prostate associated | 9,113,971 | 9,115,313 |
| F6-1 | ENSGALG00000002394.7 | RGP1 | RGP1 homolog, RAB6A GEF complex partner 1 | 9,116,265 | 9,126,065 |
| F6-1 | ENSGALG00000002394.7 | RGP1 | RGP1 homolog, RAB6A GEF complex partner 1 | 9,116,265 | 9,126,065 |
| F6-1 | ENSGALG00000002412.6 | GBA2 | glucosylceramidase beta 2 | 9,126,064 | 9,135,875 |
| F6-1 | ENSGALG00000002412.6 | GBA2 | glucosylceramidase beta 2 | 9,126,064 | 9,135,875 |
| F6-1 | ENSGALG00000021848.4 |  | avidin-like | 9,136,599 | 9,137,711 |
| F6-1 | ENSGALG00000021848.4 |  | avidin-like | 9,136,599 | 9,137,711 |
| F6-1 | ENSGALG00000021848.4 |  | avidin-like | 9,136,599 | 9,137,711 |
| F6-1 | ENSGALG00000026655.3 |  | avidin-related protein 2-like | 9,145,291 | 9,146,416 |
| F6-1 | ENSGALG00000026655.3 |  | avidin-related protein 2-like | 9,145,291 | 9,146,416 |
| F6-1 | ENSGALG00000026655.3 |  | avidin-related protein 2-like | 9,145,291 | 9,146,416 |
| F6-1 | ENSGALG00000028039.3 | AVR2 | avidin related protein 2 | 9,149,010 | 9,150,157 |
| F6-1 | ENSGALG00000028039.3 | AVR2 | avidin related protein 2 | 9,149,010 | 9,150,157 |
| F6-1 | ENSGALG00000028039.3 | AVR2 | avidin related protein 2 | 9,149,010 | 9,150,157 |
| F6-1 | ENSGALG00000023622.4 |  | avidin-related protein 4/5-like | 9,152,592 | 9,154,039 |
| F6-1 | ENSGALG00000025945.3 | AVD | avidin | 9,164,659 | 9,166,088 |
| F6-1 | ENSGALG00000025945.3 | AVD | avidin | 9,164,659 | 9,166,088 |
| F6-1 | ENSGALG00000002523.6 | CREB3 | cAMP responsive element binding protein 3 like 4 | 9,167,587 | 9,172,144 |
| F6-1 | ENSGALG00000002548.7 | TLN1 | talin 1 | 9,172,857 | 9,204,072 |
| F6-1 | ENSGALG00000002548.7 | TLN1 | talin 1 | 9,172,857 | 9,204,072 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000025842.4 | TPM2 | tropomyosin 2 | 9,207,127 | 9,219,170 |
| F6-1 | ENSGALG00000002578.7 |  | aph-1 homolog B, gamma-secretase subunit | 9,221,379 | 9,225,735 |
| F6-1 | ENSGALG00000021340.6 | CA9 | carbonic anhydrase 9 | 9,225,475 | 9,236,423 |
| F6-1 | ENSGALG00000037611.2 |  | myosin IIIA-like | 9,259,275 | 9,283,017 |
| F6-1 | ENSGALG00000037611.2 |  | myosin IIIA-like | 9,259,275 | 9,283,017 |
| F6-1 | ENSGALG00000002599.5 | ARHGEF39 | rho guanine nucleotide exchange factor 39 | 9,282,572 | 9,296,247 |
| F6-1 | ENSGALG00000002605.5 | MRPL17 | mitochondrial ribosomal protein L17 | 9,297,716 | 9,298,745 |
| F6-1 | ENSGALG00000027785.3 | CCBE1 | collagen and calcium binding EGF domains 1 | 9,303,582 | 9,323,467 |
| F6-1 | ENSGALG00000052480.1 |  |  | 9,414,544 | 9,419,141 |
| F6-1 | ENSGALG00000017952.2 | U6 | U6 spliceosomal RNA | 9,439,172 | 9,439,274 |
| F6-1 | ENSGALG00000035325.2 | PMAIP1 | phorbol-12-myristate-13-acetate-induced protein 1 | 9,445,555 | 9,446,532 |
| F6-1 | ENSGALG00000048029.1 |  |  | 9,447,204 | 9,450,366 |
| F6-1 | ENSGALG00000048029.1 |  |  | 9,447,204 | 9,450,366 |
| F6-1 | ENSGALG00000002854.6 | PDZD2 | PDZ domain containing 2 | 9,455,347 | 9,647,483 |
| F6-1 | ENSGALG00000002854.6 | PDZD2 | PDZ domain containing 2 | 9,455,347 | 9,647,483 |
| F6-1 | ENSGALG00000002854.6 | PDZD2 | PDZ domain containing 2 | 9,455,347 | 9,647,483 |
| F6-1 | ENSGALG00000002854.6 | PDZD2 | PDZ domain containing 2 | 9,455,347 | 9,647,483 |
| F6-1 | ENSGALG00000002854.6 | PDZD2 | PDZ domain containing 2 | 9,455,347 | 9,647,483 |
| F6-1 | ENSGALG00000047625.1 |  |  | 9,589,180 | 9,602,788 |
| F6-1 | ENSGALG00000028267.4 |  | golgi phosphoprotein 3 | 9,666,788 | 9,696,930 |
| F6-1 | ENSGALG00000003168.6 | MTMR12 | myotubularin related protein 12 | 9,711,679 | 9,742,308 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000014784.6 | MAST4 | microtubule associated serine/threonine kinase family member 4 | 21,008,217 | 21,296,403 |
| F6-2 | ENSGALG00000023411.4 | CD180 | CD180 molecule | 21,298,598 | 21,307,258 |
| F6-2 | ENSGALG00000023411.4 | CD180 | CD180 molecule | 21,298,598 | 21,307,258 |
| F6-2 | ENSGALG00000027398.2 | 5S\_rRNA | 5S ribosomal RNA | 21,328,741 | 21,328,853 |
| F6-2 | ENSGALG00000047586.1 |  |  | 21,375,203 | 21,406,692 |
| F6-2 | ENSGALG00000047586.1 |  |  | 21,375,203 | 21,406,692 |
| F6-2 | ENSGALG00000047586.1 |  |  | 21,375,203 | 21,406,692 |
| F6-2 | ENSGALG00000051141.1 |  |  | 21,410,315 | 21,414,779 |
| F6-2 | ENSGALG00000047121.1 |  |  | 21,514,091 | 21,529,002 |
| F6-2 | ENSGALG00000052422.1 |  |  | 21,553,771 | 21,569,265 |
| F6-2 | ENSGALG00000052422.1 |  |  | 21,553,771 | 21,569,265 |
| F6-2 | ENSGALG00000014786.6 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | 21,600,456 | 21,657,260 |
| F6-2 | ENSGALG00000014786.6 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | 21,600,456 | 21,657,260 |
| F6-2 | ENSGALG00000014786.6 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | 21,600,456 | 21,657,260 |
| F6-2 | ENSGALG00000014786.6 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | 21,600,456 | 21,657,260 |
| F6-2 | ENSGALG00000014786.6 | PIK3R1 | phosphoinositide-3-kinase regulatory subunit 1 | 21,600,456 | 21,657,260 |
| F6-2 | ENSGALG00000055083.1 |  |  | 21,642,595 | 21,642,648 |
| F6-2 | ENSGALG00000050639.1 |  |  | 21,696,285 | 21,700,466 |
| F6-2 | ENSGALG00000050639.1 |  |  | 21,696,285 | 21,700,466 |
| F6-2 | ENSGALG00000053270.1 |  |  | 21,748,962 | 21,756,431 |
| F6-2 | ENSGALG00000053270.1 |  |  | 21,748,962 | 21,756,431 |
| F6-2 | ENSGALG00000054494.1 |  |  | 21,843,033 | 21,864,499 |
| F6-2 | ENSGALG00000014787.7 | SLC30A5 | solute carrier family 30 member 5 | 21,885,739 | 21,906,410 |
| F6-2 | ENSGALG00000014787.7 | SLC30A5 | solute carrier family 30 member 5 | 21,885,739 | 21,906,410 |
| F6-2 | ENSGALG00000014788.5 | CENPH | centromere protein H | 21,910,292 | 21,917,147 |
| F6-2 | ENSGALG00000014789.5 | MRPS36 | mitochondrial ribosomal protein S36 | 21,916,343 | 21,924,487 |
| F6-2 | ENSGALG00000014789.5 | MRPS36 | mitochondrial ribosomal protein S36 | 21,916,343 | 21,924,487 |
| F6-2 | ENSGALG00000014790.7 | CDK7 | cyclin dependent kinase 7 | 21,927,561 | 21,950,303 |
| F6-2 | ENSGALG00000014798.7 | SERINC5 | serine incorporator 5 | 21,970,233 | 22,007,388 |
| F6-2 | ENSGALG00000014798.7 | SERINC5 | serine incorporator 5 | 21,970,233 | 22,007,388 |
| F6-2 | ENSGALG00000014798.7 | SERINC5 | serine incorporator 5 | 21,970,233 | 22,007,388 |
| F6-2 | ENSGALG00000014804.7 | THBS4 | thrombospondin 4 | 22,015,511 | 22,053,757 |
| F6-2 | ENSGALG00000014804.7 | THBS4 | thrombospondin 4 | 22,015,511 | 22,053,757 |
| F6-2 | ENSGALG00000014807.7 | MTX3 | metaxin 3 | 22,058,070 | 22,068,952 |
| F6-2 | ENSGALG00000014807.7 | MTX3 | metaxin 3 | 22,058,070 | 22,068,952 |
| F6-2 | ENSGALG00000014807.7 | MTX3 | metaxin 3 | 22,058,070 | 22,068,952 |
| F6-2 | ENSGALG00000026553.3 | CMYA5 | cardiomyopathy associated 5 | 22,126,658 | 22,173,992 |
| F6-2 | ENSGALG00000014810.7 | TENT2 | poly(A) RNA polymerase D4, non-canonical | 22,175,870 | 22,214,446 |
| F6-2 | ENSGALG00000014813.6 | HOMER1 | homer scaffolding protein 1 | 22,241,850 | 22,331,531 |
| F6-2 | ENSGALG00000014813.6 | HOMER1 | homer scaffolding protein 1 | 22,241,850 | 22,331,531 |
| F6-2 | ENSGALG00000014819.5 | JMY | junction mediating and regulatory protein, p53 cofactor | 22,345,907 | 22,404,480 |
| F6-2 | ENSGALG00000050556.1 |  | translation initiation factor IF-2-like | 22,406,010 | 22,413,931 |
| F6-2 | ENSGALG00000050556.1 |  | translation initiation factor IF-2-like | 22,406,010 | 22,413,931 |
| F6-2 | ENSGALG00000050556.1 |  | translation initiation factor IF-2-like | 22,406,010 | 22,413,931 |
| F6-2 | ENSGALG00000004518.6 | BHMT2 | betaine--homocysteine S-methyltransferase 2 | 22,436,116 | 22,452,194 |
| F6-2 | ENSGALG00000004491.6 | DMGDH | dimethylglycine dehydrogenase | 22,452,215 | 22,497,335 |
| F6-2 | ENSGALG00000004438.6 | ARSB | arylsulfatase B | 22,502,339 | 22,568,346 |
| F6-2 | ENSGALG00000054348.1 |  |  | 22,582,992 | 22,593,599 |
| F6-2 | ENSGALG00000004437.6 | LHFPL2 | lipoma HMGIC fusion partner-like 2 | 22,593,889 | 22,715,686 |
| F6-2 | ENSGALG00000004437.6 | LHFPL2 | lipoma HMGIC fusion partner-like 2 | 22,593,889 | 22,715,686 |
| F6-2 | ENSGALG00000043918.2 |  |  | 22,706,176 | 22,714,516 |
| F6-2 | ENSGALG00000004425.7 | SCAMP1 | secretory carrier membrane protein 1 | 22,721,122 | 22,759,474 |
| F6-2 | ENSGALG00000004425.7 | SCAMP1 | secretory carrier membrane protein 1 | 22,721,122 | 22,759,474 |
| F6-2 | ENSGALG00000004390.5 | AP3B1 | adaptor related protein complex 3 beta 1 subunit | 22,789,928 | 22,948,747 |
| F6-2 | ENSGALG00000004390.5 | AP3B1 | adaptor related protein complex 3 beta 1 subunit | 22,789,928 | 22,948,747 |
| F6-2 | ENSGALG00000051662.1 |  |  | 22,902,220 | 22,904,751 |
| F6-2 | ENSGALG00000054660.1 |  |  | 22,955,085 | 22,959,339 |
| F6-2 | ENSGALG00000054660.1 |  |  | 22,955,085 | 22,959,339 |
| F6-2 | ENSGALG00000004353.6 | TBCA | tubulin folding cofactor A | 23,086,355 | 23,119,037 |
| F6-2 | ENSGALG00000004353.6 | TBCA | tubulin folding cofactor A | 23,086,355 | 23,119,037 |
| F6-2 | ENSGALG00000026744.3 | OTP | orthopedia homeobox | 23,138,813 | 23,145,672 |
| F6-2 | ENSGALG00000004350.7 | WDR41 | WD repeat domain 41 | 23,183,991 | 23,205,580 |
| F6-2 | ENSGALG00000004350.7 | WDR41 | WD repeat domain 41 | 23,183,991 | 23,205,580 |
| F6-2 | ENSGALG00000004339.6 |  | phosphodiesterase 8B | 23,210,259 | 23,289,222 |
| F6-2 | ENSGALG00000050330.1 |  |  | 23,294,173 | 23,294,224 |
| F6-2 | ENSGALG00000025649.2 |  | small nucleolar RNA SNORA47 | 23,310,532 | 23,310,661 |
| F6-2 | ENSGALG00000004311.5 | AGGF1 | angiogenic factor with G-patch and FHA domains 1 | 23,312,434 | 23,332,349 |
| F6-2 | ENSGALG00000014994.6 | CRHBP | corticotropin releasing hormone binding protein | 23,367,125 | 23,375,581 |
| F6-2 | ENSGALG00000014989.6 | S100Z | S100 calcium binding protein Z | 23,387,539 | 23,392,421 |
| F6-2 | ENSGALG00000014984.6 | F2RL1 | F2R like trypsin receptor 1 | 23,413,354 | 23,422,556 |
| F6-2 | ENSGALG00000014983.6 | F2R | coagulation factor II thrombin receptor | 23,447,817 | 23,454,784 |
| F6-2 | ENSGALG00000048150.1 |  |  | 23,455,217 | 23,458,422 |
| F6-2 | ENSGALG00000048150.1 |  |  | 23,455,217 | 23,458,422 |
| F6-2 | ENSGALG00000014978.6 | IQGAP2 | IQ motif containing GTPase activating protein 2 | 23,461,532 | 23,577,608 |
| F6-2 | ENSGALG00000014978.6 | IQGAP2 | IQ motif containing GTPase activating protein 2 | 23,461,532 | 23,577,608 |
| F6-2 | ENSGALG00000014978.6 | IQGAP2 | IQ motif containing GTPase activating protein 2 | 23,461,532 | 23,577,608 |
| F6-2 | ENSGALG00000014978.6 | IQGAP2 | IQ motif containing GTPase activating protein 2 | 23,461,532 | 23,577,608 |
| F6-2 | ENSGALG00000014978.6 | IQGAP2 | IQ motif containing GTPase activating protein 2 | 23,461,532 | 23,577,608 |
| F6-2 | ENSGALG00000023379.4 | F2RL2 | coagulation factor II thrombin receptor like 2 | 23,491,652 | 23,495,738 |
| F6-2 | ENSGALG00000014967.6 | SV2C | synaptic vesicle glycoprotein 2C | 23,595,088 | 23,689,449 |
| P-2 | ENSGALG00000015032.6 | CD274 | CD274 molecule | 27,663,890 | 27,681,451 |
| P-2 | ENSGALG00000015032.6 | CD274 | CD274 molecule | 27,663,890 | 27,681,451 |
| P-2 | ENSGALG00000015032.6 | CD274 | CD274 molecule | 27,663,890 | 27,681,451 |
| P-2 | ENSGALG00000015032.6 | CD274 | CD274 molecule | 27,663,890 | 27,681,451 |
| P-2 | ENSGALG00000015032.6 | CD274 | CD274 molecule | 27,663,890 | 27,681,451 |
| P-2 | ENSGALG00000031794.2 | PDCD1LG2 | programmed cell death 1 ligand 2 | 27,685,252 | 27,700,855 |
| P-2 | ENSGALG00000031794.2 | PDCD1LG2 | programmed cell death 1 ligand 2 | 27,685,252 | 27,700,855 |
| P-2 | ENSGALG00000031794.2 | PDCD1LG2 | programmed cell death 1 ligand 2 | 27,685,252 | 27,700,855 |
| P-2 | ENSGALG00000031794.2 | PDCD1LG2 | programmed cell death 1 ligand 2 | 27,685,252 | 27,700,855 |
| P-2 | ENSGALG00000027292.2 | gga-mir-6669 | gga-mir-6669 | 27,711,357 | 27,711,464 |
| P-2 | ENSGALG00000015036.6 | RIC1 | RIC1 homolog, RAB6A GEF complex partner 1 | 27,712,512 | 27,762,665 |
| P-2 | ENSGALG00000015036.6 | RIC1 | RIC1 homolog, RAB6A GEF complex partner 1 | 27,712,512 | 27,762,665 |
| P-2 | ENSGALG00000000438.6 | ERMP1 | endoplasmic reticulum metallopeptidase 1 | 27,771,796 | 27,786,843 |
| P-2 | ENSGALG00000015045.6 |  | monocarboxylate transporter 2-like | 27,800,576 | 27,810,305 |
| F6-3 | ENSGALG00000005416.5 | TTC39B | tetratricopeptide repeat domain 39B | 31,833,333 | 31,861,093 |
| F6-3 | ENSGALG00000005416.5 | TTC39B | tetratricopeptide repeat domain 39B | 31,833,333 | 31,861,093 |
| F6-3 | ENSGALG00000015105.6 | PSIP1 | PC4 and SFRS1 interacting protein 1 | 31,937,116 | 31,971,222 |
| F6-3 | ENSGALG00000052632.1 |  |  | 31,940,763 | 31,942,282 |
| F6-3 | ENSGALG00000015103.5 | CCDC171 | coiled-coil domain containing 171 | 31,978,142 | 32,207,290 |
| F6-3 | ENSGALG00000015103.5 | CCDC171 | coiled-coil domain containing 171 | 31,978,142 | 32,207,290 |
| F6-3 | ENSGALG00000015103.5 | CCDC171 | coiled-coil domain containing 171 | 31,978,142 | 32,207,290 |
| F6-3 | ENSGALG00000053886.1 |  |  | 32,223,128 | 32,226,544 |
| F6-3 | ENSGALG00000054332.1 |  |  | 32,263,422 | 32,278,000 |
| F6-3 | ENSGALG00000054261.1 |  |  | 32,274,970 | 32,281,085 |
| F6-3 | ENSGALG00000025350.2 | gga-mir-1779 | gga-mir-1779 | 32,310,284 | 32,310,375 |
| F6-3 | ENSGALG00000015101.6 | BNC2 | basonuclin 2 | 32,350,839 | 32,692,210 |
| F6-3 | ENSGALG00000015101.6 | BNC2 | basonuclin 2 | 32,350,839 | 32,692,210 |
| F6-3 | ENSGALG00000015101.6 | BNC2 | basonuclin 2 | 32,350,839 | 32,692,210 |
| F6-3 | ENSGALG00000054671.1 |  |  | 32,745,113 | 32,745,143 |
| F6-3 | ENSGALG00000028298.3 | CNTLN | centlein, centrosomal protein | 32,755,378 | 32,945,968 |
| F6-3 | ENSGALG00000028298.3 | CNTLN | centlein, centrosomal protein | 32,755,378 | 32,945,968 |
| F6-3 | ENSGALG00000015096.7 | SH3GL2 | SH3 domain containing GRB2 like 2, endophilin A1 | 32,971,787 | 33,062,636 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000020554.5 | ADAMTSL1 | ADAMTS like 1 | 33,117,991 | 33,546,156 |
| F6-3 | ENSGALG00000052548.1 |  |  | 33,153,703 | 33,189,587 |
| F6-3 | ENSGALG00000015071.6 | FOCAD | focadhesin | 34,160,694 | 34,260,169 |
| F6-3 | ENSGALG00000015071.6 | FOCAD | focadhesin | 34,160,694 | 34,260,169 |
| F6-3 | ENSGALG00000028142.3 | HACD4 | 3-hydroxyacyl-CoA dehydratase 4 | 34,263,630 | 34,278,183 |
| F6-3 | ENSGALG00000015062.5 | IFNK | interferon kappa-like 1 | 34,282,011 | 34,285,224 |
| F6-3 | ENSGALG00000051843.1 |  | sperm-associated antigen 4 protein-like | 34,293,089 | 34,427,349 |
| F6-3 | ENSGALG00000051843.1 |  | sperm-associated antigen 4 protein-like | 34,293,089 | 34,427,349 |
| F6-3 | ENSGALG00000051843.1 |  | sperm-associated antigen 4 protein-like | 34,293,089 | 34,427,349 |
| F6-3 | ENSGALG00000051843.1 |  | sperm-associated antigen 4 protein-like | 34,293,089 | 34,427,349 |
| F6-3 | ENSGALG00000051843.1 |  | sperm-associated antigen 4 protein-like | 34,293,089 | 34,427,349 |
| F6-3 | ENSGALG00000050028.1 | gga-mir-7482-6 | gga-mir-7482-2 | 34,300,413 | 34,300,469 |
| F6-3 | ENSGALG00000047600.1 |  |  | 34,305,315 | 34,336,138 |
| F6-3 | ENSGALG00000047600.1 |  |  | 34,305,315 | 34,336,138 |
| F6-3 | ENSGALG00000054049.1 | gga-mir-7482-6 | gga-mir-7482-2 | 34,315,494 | 34,315,550 |
| F6-3 | ENSGALG00000048442.1 | gga-mir-7482-1 | gga-mir-7482-2 | 34,330,880 | 34,330,936 |
| F6-3 | ENSGALG00000053918.1 | gga-mir-7482-1 | gga-mir-7482-2 | 34,346,218 | 34,346,274 |
| F6-3 | ENSGALG00000055107.1 | gga-mir-7482-1 | gga-mir-7482-2 | 34,406,920 | 34,406,976 |
| F6-3 | ENSGALG00000048217.1 | gga-mir-7482-3 | gga-mir-7482-2 | 34,421,954 | 34,422,010 |
| F6-3 | ENSGALG00000054345.1 | RFKL | riboflavin kinase-like | 34,447,841 | 34,452,877 |
| F6-3 | ENSGALG00000054345.1 | RFKL | riboflavin kinase-like | 34,447,841 | 34,452,877 |
| F6-3 | ENSGALG00000015107.6 | PIP5K1B | phosphatidylinositol-4-phosphate 5-kinase type 1 beta | 34,485,673 | 34,580,466 |
| F6-3 | ENSGALG00000015107.6 | PIP5K1B | phosphatidylinositol-4-phosphate 5-kinase type 1 beta | 34,485,673 | 34,580,466 |
| F6-3 | ENSGALG00000015107.6 | PIP5K1B | phosphatidylinositol-4-phosphate 5-kinase type 1 beta | 34,485,673 | 34,580,466 |
| F6-3 | ENSGALG00000015107.6 | PIP5K1B | phosphatidylinositol-4-phosphate 5-kinase type 1 beta | 34,485,673 | 34,580,466 |
| F6-3 | ENSGALG00000015108.6 | FXN | frataxin | 34,582,882 | 34,592,944 |
| F6-3 | ENSGALG00000015109.6 | TJP2 | tight junction protein 2 | 34,597,386 | 34,662,316 |
| F6-3 | ENSGALG00000015109.6 | TJP2 | tight junction protein 2 | 34,597,386 | 34,662,316 |
| F6-3 | ENSGALG00000055034.1 |  |  | 34,597,613 | 34,597,652 |
| F6-3 | ENSGALG00000025512.2 | gga-mir-1556 | gga-mir-1556 | 34,656,766 | 34,656,851 |
| F6-3 | ENSGALG00000015110.6 | FAM189A2 | family with sequence similarity 189 member A2 | 34,698,424 | 34,709,646 |
| F6-3 | ENSGALG00000015110.6 | FAM189A2 | family with sequence similarity 189 member A2 | 34,698,424 | 34,709,646 |
| F6-3 | ENSGALG00000015111.6 | APBA1 | amyloid beta precursor protein binding family A member 1 | 34,714,860 | 34,792,783 |
| F6-3 | ENSGALG00000015111.6 | APBA1 | amyloid beta precursor protein binding family A member 1 | 34,714,860 | 34,792,783 |
| F6-3 | ENSGALG00000015111.6 | APBA1 | amyloid beta precursor protein binding family A member 1 | 34,714,860 | 34,792,783 |
| F6-3 | ENSGALG00000015111.6 | APBA1 | amyloid beta precursor protein binding family A member 1 | 34,714,860 | 34,792,783 |
| F6-3 | ENSGALG00000015113.6 | PTAR1 | protein prenyltransferase alpha subunit repeat containing 1 | 34,812,638 | 34,839,726 |
| F6-3 | ENSGALG00000015113.6 | PTAR1 | protein prenyltransferase alpha subunit repeat containing 1 | 34,812,638 | 34,839,726 |
| F6-3 | ENSGALG00000015115.6 | MAMDC2 | MAM domain containing 2 | 34,893,638 | 34,957,995 |
| F6-3 | ENSGALG00000015115.6 | MAMDC2 | MAM domain containing 2 | 34,893,638 | 34,957,995 |
| F6-3 | ENSGALG00000025424.2 | gga-mir-1416 | gga-mir-1416 | 34,934,091 | 34,934,179 |
| F6-3 | ENSGALG00000015118.7 | SMC5 | structural maintenance of chromosomes 5 | 34,965,606 | 35,020,664 |
| F6-3 | ENSGALG00000015118.7 | SMC5 | structural maintenance of chromosomes 5 | 34,965,606 | 35,020,664 |
| F6-3 | ENSGALG00000015118.7 | SMC5 | structural maintenance of chromosomes 5 | 34,965,606 | 35,020,664 |
| F6-3 | ENSGALG00000027374.3 | KLF9 | Kruppel like factor 9 | 35,032,928 | 35,045,290 |
| F6-3 | ENSGALG00000045505.2 |  |  | 35,081,630 | 35,086,439 |
| F6-3 | ENSGALG00000045505.2 |  |  | 35,081,630 | 35,086,439 |
| F6-3 | ENSGALG00000045505.2 |  |  | 35,081,630 | 35,086,439 |
| F6-3 | ENSGALG00000015126.6 | TRPM3 | transient receptor potential cation channel subfamily M member 3 | 35,092,121 | 35,350,353 |
| F6-3 | ENSGALG00000015126.6 | TRPM3 | transient receptor potential cation channel subfamily M member 3 | 35,092,121 | 35,350,353 |
| F6-3 | ENSGALG00000045111.2 |  |  | 35,181,229 | 35,201,251 |
| F6-3 | ENSGALG00000045111.2 |  |  | 35,181,229 | 35,201,251 |
| F6-3 | ENSGALG00000026673.2 |  |  | 35,191,414 | 35,191,490 |
| F6-3 | ENSGALG00000028446.2 | gga-mir-204-1 | gga-mir-204-1 | 35,192,621 | 35,192,724 |
| P-3 | ENSGALG00000023089.5 | SSBP2 | single stranded DNA binding protein 2 | 63,726,084 | 63,891,888 |
| P-3 | ENSGALG00000015616.6 | ACOT12 | acyl-CoA thioesterase 12 | 63,906,538 | 63,937,293 |
| P-3 | ENSGALG00000015603.6 | ZCCHC9 | zinc finger CCHC-type containing 9 | 63,940,607 | 63,946,893 |
| P-3 | ENSGALG00000015603.6 | ZCCHC9 | zinc finger CCHC-type containing 9 | 63,940,607 | 63,946,893 |
| P-3 | ENSGALG00000015602.6 | CKMT2 | creatine kinase, mitochondrial 2 | 63,955,273 | 63,976,950 |
| P-3 | ENSGALG00000015598.6 | RASGRF2 | Ras protein specific guanine nucleotide releasing factor 2 | 63,986,799 | 64,109,277 |
| P-4 | ENSGALG00000008174.6 | MTAP | methylthioadenosine phosphorylase | 78,808,957 | 78,841,432 |
| P-4 | ENSGALG00000008174.6 | MTAP | methylthioadenosine phosphorylase | 78,808,957 | 78,841,432 |
| P-4 | ENSGALG00000034505.2 | CDKN2A | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) | 78,846,780 | 78,856,728 |
| P-4 | ENSGALG00000026137.4 | CDKN2B | cyclin dependent kinase inhibitor 2B | 78,858,726 | 78,862,135 |
| P-4 | ENSGALG00000054061.1 |  |  | 78,880,124 | 78,896,987 |
| P-4 | ENSGALG00000008188.6 | TRIM36 | tripartite motif containing 36 | 78,975,255 | 78,994,586 |
| P-4 | ENSGALG00000008197.6 | PGGT1B | protein geranylgeranyltransferase type I subunit beta | 79,004,881 | 79,039,363 |
| P-4 | ENSGALG00000008197.6 | PGGT1B | protein geranylgeranyltransferase type I subunit beta | 79,004,881 | 79,039,363 |
| P-4 | ENSGALG00000045092.2 | CCDC112 | coiled-coil domain containing 112 | 79,040,637 | 79,049,732 |
| P-4 | ENSGALG00000045092.2 | CCDC112 | coiled-coil domain containing 112 | 79,040,637 | 79,049,732 |
| P-4 | ENSGALG00000045092.2 | CCDC112 | coiled-coil domain containing 112 | 79,040,637 | 79,049,732 |
| P-4 | ENSGALG00000045092.2 | CCDC112 | coiled-coil domain containing 112 | 79,040,637 | 79,049,732 |
| P-4 | ENSGALG00000024749.2 | U2 | U2 spliceosomal RNA | 79,078,280 | 79,078,460 |
| P-4 | ENSGALG00000008204.4 | FEM1C | fem-1 homolog C | 79,117,516 | 79,130,913 |
| P-4 | ENSGALG00000008229.6 | ALDH7A1 | aldehyde dehydrogenase 7 family member A1 | 79,146,009 | 79,164,153 |
| P-4 | ENSGALG00000008237.6 | GRAMD2B | GRAM domain containing 3 | 79,172,117 | 79,205,381 |
| F6-4 | ENSGALG00000005337.7 | SNX2 | sorting nexin 2 | 81,461,079 | 81,494,229 |
| F6-4 | ENSGALG00000005337.7 | SNX2 | sorting nexin 2 | 81,461,079 | 81,494,229 |
| F6-4 | ENSGALG00000005337.7 | SNX2 | sorting nexin 2 | 81,461,079 | 81,494,229 |
| F6-4 | ENSGALG00000018874.4 | SNX24 | sorting nexin 24 | 81,496,699 | 81,572,966 |
| F6-4 | ENSGALG00000018874.4 | SNX24 | sorting nexin 24 | 81,496,699 | 81,572,966 |
| F6-4 | ENSGALG00000018874.4 | SNX24 | sorting nexin 24 | 81,496,699 | 81,572,966 |
| F6-4 | ENSGALG00000005346.7 | PPIC | peptidylprolyl isomerase C | 81,573,781 | 81,579,815 |
| F6-4 | ENSGALG00000053199.1 |  |  | 81,604,134 | 81,609,598 |
| F6-4 | ENSGALG00000053199.1 |  |  | 81,604,134 | 81,609,598 |
| F6-4 | ENSGALG00000005351.6 | PRDM6 | PR/SET domain 6 | 81,605,055 | 81,673,923 |
| F6-4 | ENSGALG00000047872.1 |  |  | 81,694,546 | 81,705,690 |
| F6-4 | ENSGALG00000005368.6 | CEP120 | centrosomal protein 120 | 81,708,876 | 81,746,900 |
| F6-4 | ENSGALG00000005368.6 | CEP120 | centrosomal protein 120 | 81,708,876 | 81,746,900 |
| F6-4 | ENSGALG00000005368.6 | CEP120 | centrosomal protein 120 | 81,708,876 | 81,746,900 |
| F6-4 | ENSGALG00000037184.2 | gga-mir-7483 | gga-mir-7483 | 81,752,893 | 81,752,949 |
| F6-4 | ENSGALG00000026300.3 |  |  | 81,753,560 | 81,755,457 |
| F6-4 | ENSGALG00000054942.1 |  |  | 81,765,424 | 81,795,194 |
| F6-4 | ENSGALG00000054942.1 |  |  | 81,765,424 | 81,795,194 |
| F6-4 | ENSGALG00000052152.1 |  |  | 81,784,395 | 81,788,678 |
| F6-4 | ENSGALG00000052152.1 |  |  | 81,784,395 | 81,788,678 |
| F6-4 | ENSGALG00000023036.5 |  |  | 81,787,829 | 81,793,027 |
| F6-4 | ENSGALG00000029118.3 |  | tRNA methyltransferase 10B | 81,795,195 | 81,801,734 |
| F6-4 | ENSGALG00000029118.3 |  | tRNA methyltransferase 10B | 81,795,195 | 81,801,734 |
| F6-4 | ENSGALG00000017558.7 |  | uncharacterized LOC768709 | 81,801,034 | 81,807,114 |
| F6-4 | ENSGALG00000017558.7 |  | uncharacterized LOC768709 | 81,801,034 | 81,807,114 |
| F6-4 | ENSGALG00000005390.6 | DCAF10 | DDB1 and CUL4 associated factor 10 | 81,806,718 | 81,819,704 |
| F6-4 | ENSGALG00000028340.3 |  |  | 81,822,686 | 81,831,505 |
| F6-4 | ENSGALG00000047056.1 |  |  | 81,830,390 | 81,831,844 |
| F6-4 | ENSGALG00000047056.1 |  |  | 81,830,390 | 81,831,844 |
| F6-4 | ENSGALG00000005395.7 | POLR1E | RNA polymerase I subunit E | 81,832,191 | 81,847,651 |
| F6-4 | ENSGALG00000005395.7 | POLR1E | RNA polymerase I subunit E | 81,832,191 | 81,847,651 |
| F6-4 | ENSGALG00000005354.6 | ZBTB5 | zinc finger and BTB domain containing 5 | 81,855,523 | 81,857,544 |
| F6-4 | ENSGALG00000005423.7 | GRHPR | glyoxylate and hydroxypyruvate reductase | 81,867,579 | 81,872,830 |
| F6-4 | ENSGALG00000028675.3 | ZCCHC7 | zinc finger CCHC-type containing 7 | 81,885,604 | 81,989,922 |
| F6-4 | ENSGALG00000028675.3 | ZCCHC7 | zinc finger CCHC-type containing 7 | 81,885,604 | 81,989,922 |
| F6-4 | ENSGALG00000028675.3 | ZCCHC7 | zinc finger CCHC-type containing 7 | 81,885,604 | 81,989,922 |
| F6-4 | ENSGALG00000028675.3 | ZCCHC7 | zinc finger CCHC-type containing 7 | 81,885,604 | 81,989,922 |
| F6-4 | ENSGALG00000028675.3 | ZCCHC7 | zinc finger CCHC-type containing 7 | 81,885,604 | 81,989,922 |
| F6-4 | ENSGALG00000051402.1 |  |  | 81,991,010 | 81,996,297 |
| F6-4 | ENSGALG00000051402.1 |  |  | 81,991,010 | 81,996,297 |

QTLR, QTLR serial number found by the F6 (Table 1) and the Pools (Table 3); Start, End, bp location on the GRCg6a reference of the first and last markers in the QTLR.

**Table S2.** Association tests of all markers and haplotypes in the QTLRs, by location (GRCg6a).

| **QTLR** | **Marker/**  **Haps** | **bp** | **Distance** | **Line** | | | | | | | | **Across Lines** | **Gene** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **WL1** | **WL2** | **WL3** | **WPR1** | **WPR2** | **WL4** | **WL5** | **RIR1** |
| F6-1 | 36053 | 3,605,367 |  |  |  |  |  |  |  |  |  |  | RIT2 |
| F6-1 | 36305 | 3,630,520 | 25,153 |  | 5.4E-01 |  |  |  |  |  | 2.9E-01 | 3.8E-01 | RIT2 |
| F6-1 | 40741 | 4,074,140 | 443,620 |  | 5.1E-01 |  |  |  | 8.0E-01 |  |  | 7.9E-01 | PIK3C3 |
| F6-1 | 43029 | 4,302,959 | 228,819 |  | 5.1E-01 |  |  |  |  |  | 1.2E-01 | 2.5E-01 |  |
| F6-1 | 46166 | 4,616,676 | 313,717 |  | 5.1E-01 |  |  |  |  |  | 9.4E-02 | 2.7E-01 |  |
| F6-1 | 49698 | 4,969,878 | 353,202 |  |  |  |  |  |  |  |  |  |  |
| F6-1 | 51533 | 5,153,327 | 183,449 |  | 5.1E-01 |  |  |  | 9.1E-01 |  | 9.4E-02 | 9.5E-01 |  |
| F6-1 | 51662 | 5,166,291 | 12,964 |  |  |  |  |  |  |  |  |  |  |
| F6-1 | 53289 | 5,328,932 | 162,641 |  |  |  |  |  |  |  |  |  |  |
| F6-1, P-1 | 60228 | 6,022,814 | 693,882 |  | 5.2E-01 |  |  |  |  |  | 9.6E-02 | 2.1E-01 |  |
| F6-1, P-1 | 61623 | 6,162,305 | 139,491 |  | 5.6E-01 |  |  |  |  |  | 1.1E-01 | 5.0E-02 | CELF4 |
| F6-1, P-1 | 63820 | 6,382,092 | 219,787 |  |  |  |  |  |  |  | 8.7E-02 | 9.2E-01 | CELF4 |
| F6-1, P-1 | 64741 | 6,474,175 | 92,083 |  | 6.5E-01 |  |  |  |  |  |  | 9.1E-03 | CELF4 |
| F6-1, P-1 | Haps A |  |  |  |  |  |  |  | 9.5E-01 |  | 1.1E-01 |  |  |
| F6-1, P-1 | 65507 | 6,550,716 | 76,541 |  |  |  |  |  |  |  |  |  | CELF4 |
| F6-1, P-1 | 66056 | 6,605,675 | 54,959 |  |  |  |  |  |  |  | 2.3E-01 | 7.7E-01 | CELF4 |
| F6-1, P-1 | 66834 | 6,683,420 | 77,745 |  |  |  |  |  |  |  | 1.9E-01 | 8.7E-01 | CELF4 |
| F6-1, P-1 | 68063 | 6,806,390 | 122,970 |  |  |  |  |  |  |  |  |  | CELF4 |
| F6-1, P-1 | 68223 | 6,822,355 | 15,965 |  |  |  |  |  |  |  |  | 7.5E-01 | CELF4 |
| F6-1, P-1 | 69120 | 6,912,085 | 89,730 |  |  |  |  |  |  |  |  |  | KIAA1328 |
| F6-1, P-1 | 69374 | 6,937,410 | 25,325 |  |  |  |  |  |  |  |  |  | KIAA1328 |
| F6-1, P-1 | 70632 | 7,063,264 | 125,854 |  | 1.6E-02 |  |  |  | 1.7E-02 |  | 1.3E-01 | 2.7E-01 | KIAA1328 |
| F6-1, P-1 | 71261 | 7,126,106 | 62,842 |  | 1.6E-02 |  |  |  | 2.3E-01 |  | 1.3E-01 | 8.5E-01 | AQP7 |
| F6-1, P-1 | 72526 | 7,252,666 | 126,560 |  |  |  |  |  |  |  |  |  |  |
| F6-1, P-1 | 73201 | 7,320,182 | 194,076 |  |  |  |  |  |  |  |  |  | UBE2R2 |
| F6-1, P-1 | 73638 | 7,363,803 | 43,621 |  |  |  |  |  |  |  |  |  | LOC407092 |
| F6-1, P-1 | 74454 | 7,445,437 | 81,634 |  |  |  |  |  | 1.5E-01 |  |  | 2.9E-01 | LOC407092 |
| F6-1, P-1 | 76350 | 7,635,023 | 189,586 |  |  |  |  |  | 3.9E-01 |  |  | 1.3E-01 | LOC427400 |
| F6-1, P-1 | 76508 | 7,650,818 | 15,795 |  |  |  |  |  |  |  |  |  |  |
| F6-1, P-1 | 80013 | 8,001,352 | 350,534 |  |  |  |  |  |  |  | 8.8E-01 | 2.9E-01 |  |
| F6-1, P-1 | Haps B |  |  |  | 1.6E-02 |  |  |  |  |  | 9.6E-01 |  |  |
| F6-1, P-1 | 83027 | 8,302,734 | 301,382 | 1.4E-01 |  | 1.7E-01 |  |  |  |  | 3.9E-01 | 9.4E-03 |  |
| F6-1 | 86041 | 8,604,115 | 301,381 | 1.2E-01 |  |  |  |  |  |  |  | 5.1E-01 |  |
| F6-1 | 89887 | 8,988,761 | 384,646 |  |  |  |  |  |  |  | 5.5E-01 | 9.3E-01 | RUSC2 |
| F6-1 | 89963 | 8,996,361 | 7,600 |  |  |  |  |  |  |  | 3.8E-01 | 6.5E-03 | RUSC2 |
| F6-1 | 91271 | 9,127,101 | 130,740 | 1.7E-01 |  |  |  |  |  |  | 5.9E-01 | 3.0E-02 | GBA2 |
| F6-1 | 93290 | 9,329,028 | 201,927 |  | 3.6E-02 |  |  |  | 6.8E-01 |  | 4.1E-01 | 6.0E-01 | CCBE1 |
| F6-1 | 95986 | 9,598,684 | 269,656 |  |  |  |  |  |  |  |  |  |  |
| F6-1 | 96619 | 9,661,956 | 63,272 |  |  |  |  |  |  |  |  | 5.5E-01 |  |
| F6-1 | 96957 | 9,695,793 | 33,837 |  |  |  |  |  |  |  | 6.7E-01 | 4.3E-01 | GOLPH3 |
| F6-1 | 97365 | 9,736,535 | 40,742 | 5.1E-01 | 7.0E-02 |  |  |  |  |  |  | 2.1E-01 | MTMR12 |
| F6-1 | Haps C |  |  |  | 3.9E-02 |  |  |  | 6.8E-01 |  |  |  |  |
| F6-2 | 21265 | 21,265,049 | 11,528,514 | 3.0E-01 |  |  |  |  | 9.7E-01 |  |  | 2.0E-01 | MAST4 |
| F6-2 | 21626 | 21,626,796 | 361,747 |  |  | 4.9E-01 |  |  | 7.0E-01 |  |  | 4.4E-01 | PIK3R1 |
| F6-2 | 21909 | 21,909,030 | 282,234 |  |  |  | 5.3E-02 |  |  |  | 1.5E-01 | 4.3E-02 |  |
| F6-2 | 22236 | 22,236,438 | 327,408 |  |  | 4.6E-01 |  |  |  |  | 2.2E-01 | 1.2E-01 |  |
| F6-2 | 22520 | 22,520,245 | 283,807 |  |  | 6.2E-01 | 5.3E-01 |  |  |  | 2.0E-01 | 9.7E-01 | ARSB |
| F6-2 | Haps A |  |  | 3.0E-01 |  |  |  |  | 9.5E-01 |  |  | 2.0E-01 |  |
| F6-2 | 22886 | 22,886,932 | 366,687 |  |  |  | 2.5E-01 |  |  |  |  | 8.3E-01 | AP3B1 |
| F6-2 | 22921 | 22,921,910 | 34,978 |  |  | 6.0E-01 | 4.1E-01 |  | 5.5E-01 |  | 9.4E-02 | 2.1E-01 | AP3B1 |
| F6-2 | 23017 | 23,017,033 | 95,123 |  |  |  | 4.4E-01 |  |  |  | 8.4E-01 | 5.7E-01 |  |
| F6-2 | 23073ta | 23,017,034 | 1 |  |  |  |  |  |  |  | 7.4E-01 | 6.8E-01 |  |
| F6-2 | 23073tg | 23,017,035 | 1 |  |  | 6.4E-01 |  |  |  |  |  | 5.3E-01 |  |
| F6-2 | 23073 | 23,073,692 | 56,657 |  | 9.6E-01 | 6.4E-01 |  |  | 2.8E-02 |  | 8.4E-01 | 3.2E-02 |  |
| F6-2 | 23086 | 23,086,227 | 12,535 |  | 9.6E-01 | 6.6E-01 | 2.9E-01 |  | 2.8E-02 |  | 8.1E-01 | 3.2E-01 |  |
| F6-2 | 23204 | 23,204,744 | 118,517 |  |  |  |  |  |  |  |  |  | PDE8B |
| F6-2 | Haps B |  |  |  | 9.6E-01 | 6.0E-01 |  |  |  |  |  |  |  |
| F6-2 | 23217 | 23,217,357 | 12,613 |  | 2.7E-02 | 4.7E-03 |  |  | 5.1E-01 |  | 2.0E-01 | 3.2E-01 | PDE8B |
| F6-2 | 23250 | 23,250,769 | 33,412 |  | 1.4E-01 | 2.4E-01 | 9.5E-01 |  | 5.1E-01 |  | 2.8E-01 | 4.2E-01 | PDE8B |
| F6-2 | 23277 | 23,277,739 | 26,970 |  | 1.4E-01 | 2.3E-01 | 9.5E-01 |  | 4.9E-01 |  | 1.8E-01 | 9.6E-01 | PDE8B |
| F6-2 | 23556 | 23,556,398 | 278,659 |  |  |  |  |  |  |  |  |  | IQGAP2 |
| F6-2 | 23651 | 23,651,225 | 94,827 |  |  | 2.6E-01 |  |  | 1.6E-03 |  |  | 5.3E-01 | SV2C |
| F6-2 | Haps C |  |  |  |  |  | 9.4E-01 |  |  |  | 2.8E-01 | 5.8E-01 |  |
| P-2 | 26696 | 26,696,538 | 3,045,313 |  | 7.9E-01 |  |  |  |  |  |  | 6.2E-03 | RFX3 |
| P-2 | 26719 | 26,719,600 | 23,062 |  | 7.9E-01 |  |  |  |  |  |  | 6.2E-03 | RFX3 |
| P-2 | 26906 | 26,906,396 | 186,796 |  |  |  |  |  |  |  |  |  | GLIS3 |
| P-2 | 26939 | 26,939,448 | 33,052 |  |  |  |  |  |  |  |  |  | GLIS3 |
| P-2 | 27025 | 27,025,509 | 86,061 |  |  |  |  |  |  |  |  |  |  |
| P-2 | 27034 | 27,034,536 | 9,027 |  |  |  |  |  |  |  |  |  |  |
| P-2 | 27580 | 27,580,124 | 545,588 |  |  |  | 2.4E-01 | 1.9E-01 |  |  |  | 4.3E-01 | JAK2 |
| P-2 | 27710 | 27,710,563 | 130,439 |  | 7.3E-01 |  | 2.5E-01 | 2.6E-01 |  |  |  | 4.4E-01 | LOC112530672 |
| P-2 | 27849 | 27,849,293 | 138,730 |  |  |  | 2.0E-01 |  |  |  |  | 2.3E-01 | KIAA2026 |
| P-2 | 28046 | 28,046,457 | 197,164 |  | 8.1E-02 |  | 2.0E-01 | 3.0E-01 |  |  |  | 1.6E-03 | GLDC |
| P-2 | 28221 | 28,221,317 | 174,860 |  |  |  | 4.1E-01 | 3.5E-01 |  |  |  | 2.7E-01 | KDM4C |
| P-2 | Haps |  |  |  |  |  |  |  |  |  |  | 2.3E-05 |  |
| F6-3 | 31832 | 31,832,156 | 3,610,839 |  | 7.6E-01 | 4.6E-01 | 1.6E-01 | 3.4E-01 | 4.3E-02 |  |  | 9.1E-01 |  |
| F6-3 | 32118 | 32,118,038 | 285,882 |  | 7.7E-01 | 6.9E-01 |  |  | 6.5E-02 |  |  | 3.4E-01 | CCDC171 |
| F6-3 | 32381 | 32,381,617 | 263,579 |  |  |  | 5.6E-02 | 9.5E-02 |  |  |  | 2.3E-01 | BNC2 |
| F6-3 | 32731 | 32,731,634 | 350,017 |  |  | 1.2E-01 |  |  | 4.4E-01 |  |  | 7.7E-02 |  |
| F6-3 | 33216 | 33,216,121 | 484,487 |  |  |  |  |  |  |  |  |  | ADAMTSL1 |
| F6-3 | 33424 | 33,424,790 | 208,669 |  |  |  |  |  |  |  |  |  | ADAMTSL1 |
| F6-3 | 33582 | 33,582,800 | 158,010 |  |  |  |  |  |  |  |  |  |  |
| F6-3 | Haps A |  |  |  |  |  |  |  | 4.7E-01 |  |  | 6.1E-01 |  |
| F6-3 | 33661 | 33,661,217 | 78,417 |  |  |  |  | 4.4E-01 |  |  |  | 1.1E-01 |  |
| F6-3 | 33912 | 33,912,191 | 250,974 |  |  |  |  |  |  |  |  |  |  |
| F6-3 | 33962 | 33,962,980 | 50,789 |  |  |  |  | 3.2E-01 |  |  |  | 1.3E-01 |  |
| F6-3 | 34179 | 34,179,633 | 216,653 |  |  |  |  | 9.8E-01 |  |  |  | 3.2E-01 | FOCAD |
| F6-3 | 34513 | 34,513,217 | 333,584 |  |  |  |  |  |  |  |  |  |  |
| F6-3 | 34522 | 34,522,531 | 9,314 |  |  |  |  |  |  |  |  | 8.1E-01 |  |
| F6-3 | 34789 | 34,789,565 | 267,034 |  |  | 5.6E-01 |  | 6.5E-01 | 2.9E-01 |  |  | 3.4E-01 |  |
| F6-3 | 35054 | 35,054,652 | 265,087 |  | 5.3E-01 | 7.5E-01 |  | 9.8E-01 |  |  |  | 9.9E-01 |  |
| F6-3 | 35113 | 35,113,845 | 59,193 |  | 5.8E-01 | 6.7E-01 |  |  |  |  |  | 9.6E-01 | TRPM3 |
| F6-3 | 35323 | 35,323,399 | 209,554 |  | 4.6E-01 |  |  |  |  |  |  | 1.7E-01 | TRPM3 |
| F6-3 | 35383 | 35,383,364 | 59,965 |  |  |  |  |  |  |  |  | 6.7E-01 |  |
| F6-3 | Haps B |  |  |  |  |  |  |  | 2.9E-01 |  |  | 9.8E-01 |  |
| P-3 | 632931 | 63,293,165 | 27,002,440 | 8.7E-01 |  |  | 7.5E-01 |  | 6.7E-01 |  |  | 9.3E-01 |  |
| P-3 | 636773 | 63,677,398 | 384,233 | 1.1E-01 |  |  | 4.6E-01 | 4.6E-02 |  |  |  | 5.8E-01 |  |
| P-3 | 637662 | 63,766,213 | 88,815 |  |  |  |  |  | 6.6E-01 |  |  | 7.8E-01 | SSBP2 |
| P-3 | 637932 | 63,793,285 | 27,072 |  |  |  |  |  |  |  |  |  | SSBP2 |
| P-3 | 639060 | 63,906,067 | 112,782 |  |  |  | 4.0E-01 | 4.7E-02 |  |  |  | 9.7E-01 |  |
| P-3 | 639115 | 63,911,574 | 5,507 | 8.5E-01 |  |  | 5.0E-01 | 4.7E-02 | 6.5E-01 |  |  | 7.9E-01 | ACOT12 |
| P-3 | 640300 | 64,030,006 | 118,432 |  |  |  |  |  |  |  |  |  | RASGRF2 |
| P-3 | 640855 | 64,085,517 | 55,511 | 9.9E-01 |  |  |  |  | 7.0E-01 |  |  | 5.9E-01 | RASGRF2 |
| P-3 | 641390 | 64,139,066 | 53,549 | 9.7E-01 |  |  |  |  | 8.4E-01 |  |  | 7.4E-01 |  |
| P-3 | 642992 | 64,299,292 | 160,226 |  |  |  |  |  |  |  |  |  | FAM151B |
| P-3 | 645169 | 64,516,969 | 217,677 |  |  |  |  |  |  |  |  |  |  |
| P-3 | 645835 | 64,583,579 | 66,610 | 9.5E-01 |  |  | 9.9E-01 |  | 8.4E-01 |  |  | 4.0E-01 |  |
| P-3 | Haps |  |  |  |  |  |  |  |  |  |  | 4.4E-01 |  |
| P-4 | 73225 | 73,225,511 | 8,641,932 |  |  |  | 2.9E-02 | 6.3E-02 | 4.9E-01 |  |  | 4.0E-01 | GTF2H2 |
| P-4 | 73435 | 73,435,755 | 210,244 |  |  |  | 3.6E-02 | 2.9E-01 | 7.4E-01 |  |  | 9.8E-01 |  |
| P-4 | 78892 | 78,892,243 | 5,456,488 |  |  |  | 1.0E-08 | 1.7E-04 |  |  |  | 6.1E-12 |  |
| P-4 | 79212 | 79,212,166 | 319,923 |  | 9.9E-01 |  | 6.8E-09 | 8.7E-05 |  | 6.2E-01 | 1.4E-01 | 2.6E-07 |  |
| P-4 | 79463 | 79,463,296 | 251,130 |  |  |  | 7.2E-09 | 1.7E-04 |  |  |  | 4.2E-12 |  |
| P-4 | 79671 | 79,671,839 | 208,543 |  |  |  | 9.6E-09 | 1.7E-04 |  |  |  | 1.3E-13 |  |
| P-4 | 79878 | 79,878,110 | 206,271 | 1.5E-02 | 9.2E-01 |  | 2.4E-02 | 1.5E-03 |  |  |  | 4.4E-01 |  |
| P-4 | Haps |  |  |  |  |  |  |  | 7.2E-01 | 6.3E-01 | 4.6E-02 | 1.9E-03 |  |
| F6-4 | 81514 | 81,514,684 | 1,636,574 |  |  |  |  | 4.1E-01 |  |  | 1.3E-01 | 5.1E-01 |  |
| F6-4 | 81713 | 81,713,492 | 198,808 |  | 1.7E-02 |  | 1.5E-02 | 1.0E-01 | 2.3E-01 |  | 4.5E-01 | 2.5E-02 |  |
| F6-4 | 81750 | 81,750,092 | 36,600 |  | 1.6E-02 |  | 5.8E-02 | 1.9E-01 | 3.3E-01 |  |  | 3.5E-01 |  |
| F6-4 | 81795 | 81,795,629 | 45,537 |  |  |  | 1.6E-01 | 5.8E-01 |  |  |  | 8.8E-01 |  |
| F6-4 | 81840 | 81,840,502 | 44,873 | 7.7E-01 | 2.8E-01 |  | 5.1E-01 | 6.0E-02 | 7.6E-01 |  |  | 7.9E-01 |  |
| F6-4 | 81892 | 81,892,924 | 52,422 | 7.3E-01 | 2.8E-01 |  | 5.8E-01 | 3.5E-02 |  |  |  | 8.4E-01 |  |
| F6-4 | 82053 | 82,053,490 | 160,566 |  |  |  | 7.2E-01 |  |  |  |  | 7.8E-01 |  |
| F6-4 | 82142 | 82,142,145 | 88,655 |  |  |  |  |  |  |  |  |  |  |
| F6-4 | Haps |  |  |  |  |  |  |  |  |  | 4.1E-01 |  |  |

QTLR: QTLR serial number found by the F6 (Table 1) and the Pools (Table 3); Marker/Haps, marker or haplotypes tested, where Haps are the haplotypes of all markers preceding this Haps and are downstream the previous Haps (for example, Haps B in the F6 + P-1 regions, includes Markers 65507 - 80013); bp, location on GGZ (haplotypes have no specific location); Distance, bp between markers; Line, test within a line; Across lines, test across all lines; pink highlight, P ≤ 0.05; Gene, a gene found in the QTLR (Table S1).

**Table S3.** Distribution of P values in the QTLRs.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **P** | **Markers + Haps** | | **%** | |
| **Lines** | **Ac Lines** | **Lines** | **Ac Lines** |
| ≤ 0.1 | 50 | 18 | 0.236 | 0.180 |
| >0.1 - ≤0.2 | 26 | 9 | 0.123 | 0.090 |
| >0.2 - ≤0.3 | 25 | 12 | 0.118 | 0.120 |
| >0.3 - ≤0.4 | 7 | 8 | 0.033 | 0.080 |
| >0.4 - ≤0.5 | 21 | 11 | 0.099 | 0.110 |
| >0.5 - ≤0.6 | 22 | 9 | 0.104 | 0.090 |
| >0.6 - ≤0.7 | 18 | 6 | 0.085 | 0.060 |
| >0.7 - ≤0.8 | 15 | 9 | 0.071 | 0.090 |
| >0.8 - ≤0.9 | 9 | 6 | 0.042 | 0.060 |
| >0.9 - ≤1.0 | 19 | 12 | 0.090 | 0.120 |
| Sum | 212 | 100 | 1.000 | 1.000 |

Markers + Haps, P values of the markers and haplotypes combined; %, proportions; Lines, tests within lines; Ac Lines, tests across lines.

**Table S4**. File Table 'S4 - QTLRs LD.pdf'. LD matrices found in seven of the eight pure lines by individual genotyping of QTLR genes (there was only one informative marker in Line WL5). Gene, QTLR gene (Tables S1 and S2); bp, location on GGZ; Dis., bp between markers; QTLR, QTLR serial number found by the F6 and the Pools (Tables 1 and 3); Marker, marker tested; LD values: red, r2 ≥ 0.7; pink, 0.15 ≥ r2 <0.7; white, r2 < 0.15; P, P-value of the Trend association test (Table S2): pink, P ≤ 0.05; white, P > 0.05. Different LD blocks have different colors.



**Appendix 1: Details of QTLR association and LD analyses**

Thorough examination of the distribution of the P-value locations and LD pattern, revealed some interesting observations. Three of the QTLRs are presented the main text. The rest are detailed below.

*1.1. QTLR P-2*

None of the 13 tests within lines was significant **(**Table S2), while three markers and the haplotypes (Haps) were highly significant in the Across Line tests (markers P = 3.2-1.6E-3; Haps P = 2.3E-5). The first two significant Across Lines markers (Markers 26696 and 26716) were informative only in Line WL2, where they were not significant. The downstream significant Marker 28046 was informative in three lines, where it approached significance in Line WL2, but not in Lines WPR1 or WPR2.

Such results suggest two possible causative elements distributing in some of the lines, which were not informative in the markers tested. One causative element located in the region of the *RFX3* gene (Regulatory Factor X3), which influences HLA Class II expression [50]. The second putative element located in the *GLDC* gene (Glycine Decarboxylase), which is located in a differential expressed region upon MD challenge identified by Chu et al. [49]. *GLDC* is involved in human encephalopathy [51] and neural tube defects [52].

*1.2. QTLR F6-3*

QTLR F6-3 was confirmed only in Line WL4 by a single marginal significant test and one test approaching significance (Table S2). Hence, taking a conservative approach, this confirmation of F6-3 should be taken with caution.

*1.3. QTLR P-3*

Unfortunately, Line WL2, where QTLR P-3 was identified, was found to have no informative markers in the examination of this QTLR (Table S2). All three markers tested in Line WPR2 were significant with very similar P-values. No other tested line was significant. The three significant markers in Line WPR2 formed a high LD block (Table S4), suggesting a single causative element. The first two markers are on either side of the *SSBP2* gene, and the third one is in the *ACOT12* gene. The putative tumour suppressor SSBP2 (Single Stranded DNA Binding Protein 2) has been linked with glioblastoma survival [53] and ACOT12 (Acyl-CoA Thioesterase 12) suppresses metastases [54] and has been linked to leukoencephalopathy [48] in human.

*1.4. QTLR F6-4*

Five significant tests were obtained in this QTLR (Table S2). Markers were significant in Lines WL2, WPR1 and Across Lines. Marker 81713 was significant in Lines WL2 and WPR1, and in the Across Lines test. The next marker, 81750, was significant in Line WL2 only, but approached significance in Line WPR1 (P = 5.8E-02). Another downstream marker, 81892, was significant only in Line WPR2. The two significant markers 81713 and 81750 were in the same high LD block in Line WL2 (Table S4), suggesting a single causative element distributing in this line. They did not have appreciable LD in Line WPR1, suggesting Marker 81713 - the one significant in three tests - to be closest to that causative element.