**Table S2.** Top associations between symptomatic (VL) or asymptomatic (DTH+) phenotypes and SNPs under linkage regions on chromosomes 9, 15 and 19. VL and DTH positive phenotypes were analysed as qualitative traits using LAMP. LOD and P-values indicate raw outputs from the program. The total number of LD blocks (961) was used to determine the modified Bonferroni corrected p-value. Locations of SNPs relative to genes, and their position relative to those gene, were based on proximity in the UCSC hg18 version of the human genome.

**Region SNP Trait LOD Pvalue correctedPval location relative**

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr9 | rs1470217 | VL | 4.23 | 5.9E-05 | 0.057 | TMEM215 APTX | intergenic |
| chr9 | rs1404195 | VL | 3.48 | 3.30E-04 | 0.317 | TMEM2 | upstream |
| chr9 | rs4879899 | VL | 3.34 | 4.50E-04 | 0.432 | ATP8B5P | intron |
| chr9 | rs16932295 | VL | 3.34 | 4.60E-04 | 0.442 | UNC13B | intron |
| chr9 | rs4879884 | VL | 3.27 | 5.40E-04 | 0.519 | UNC13B | intron |
| chr9 | rs872077 | VL | 3.22 | 6.00E-04 | 0.577 | PIP5K1B PRKACG | intergenic |
| chr9 | rs1880329 | VL | 3.01 | 9.80E-04 | 0.942 | TMEM2 | upstream |

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr15 | rs7176637 | VL | 3.57 | 2.70E-04 | 0.259 | C15orf60 | intron |
| chr15 | rs2680344 | VL | 3.34 | 4.60E-04 | 0.442 | HCN4 | intron |
| chr15 | rs10852160 | VL | 3.12 | 7.50E-04 | 0.721 | SLCO3A1 | upstream |
| chr15 | rs8027238 | VL | 3.02 | 9.60E-04 | 0.923 | KIAA1199 | intron |
| chr15 | rs16975142 | VL | 2.93 | 1.20E-03 | 1.153 | LOC145820 | upstream |

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr19 | rs8107014 | VL | 4.85 | 1.40E-05 | 0.013 | LTBP4 | intron |
| chr19 | rs7259067 | VL | 3.85 | 1.40E-04 | 0.135 | LTBP4 | intron |
| chr19 | rs11083560 | VL | 3.54 | 2.90E-04 | 0.279 | LTBP4 | intron |
| chr19 | rs2278242 | VL | 3.51 | 3.10E-04 | 0.298 | LTBP4 | intron |
| chr19 | rs2190837 | VL | 3.37 | 4.20E-04 | 0.404 | PSG5 | intron |
| chr19 | rs7246771 | VL | 3.11 | 7.70E-04 | 0.740 | PSG11 | downstream |
| chr19 | rs1864074 | VL | 3.1 | 7.90E-04 | 0.759 | LTBP4 | intron |

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr15 | rs12324805 | DTH positive | 3.69 | 2.00E-04 | 0.192 | MEX3B EFTUD1 | intron |
| chr15 | rs1266489 | DTH positive | 3.25 | 5.60E-04 | 0.538 | MAN2A2 | intron |
| chr15 | rs11072603 | DTH positive | 3.07 | 8.60E-04 | 0.826 | SCAPER | intron |
| chr15 | rs11073021 | DTH positive | 2.92 | 1.20E-03 | 1.153 | TMC3B MEX3B | intergenic |
| chr15 | rs6494904 | DTH positive | 2.77 | 1.70E-03 | 1.634 | THSD4 | intron |

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr19 | rs10402740 | DTH positive | 3.68 | 2.10E-04 | 0.202 | MAP3K10 | intron |
| chr19 | rs1010104 | DTH positive | 3.57 | 2.70E-04 | 0.259 | BAX | intron |
| chr19 | rs204538 | DTH positive | 3.44 | 3.70E-04 | 0.356 | ZNF229 | upstream |
| chr19 | rs2355720 | DTH positive | 3.43 | 3.80E-04 | 0.365 | FCGBP | intron |
| chr19 | rs1129156 | DTH positive | 3.2 | 6.30E-04 | 0.605 | MAP3K10 | exon |

| Region | SNP | Trait | LOD | Pvalue | correctedPval | location | relative |
|---|---|---|---|---|---|---|---|
| chr9 | rs6475870 | DTH positive | 3.53 | 2.90E-04 | 0.279 | TUSC1 LOC100506422 | intergenic |
| chr9 | rs10967916 | DTH positive | 2.8 | 1.60E-03 | 1.538 | MOB3B | intron |
| chr9 | rs10757915 | DTH positive | 2.64 | 2.30E-03 | 2.210 | LINGO2 | upstream |
| chr9 | rs4879913 | DTH positive | 2.54 | 2.90E-03 | 2.787 | CD72 | intron |
| chr9 | rs2298311 | DTH positive | 2.38 | 4.20E-03 | 4.036 | KIAA1045 | 3' utr |