**Appendix: Genome-wide Suggestive Variants from Single Variant Two-point Analysis**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **CHR** | **HLOD** | **rsID** | **POS** | **MAF** | **FUNCTION** | **GENE** |
| 9q33.2 | 2.56 | rs4837768 | 123170733 | 0.1816 | exonic | *CDK5RAP2* |
| 10q26.13 | 2.52 | rs2736923 | 124259062 | 0.3739 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2250511 | 124262419 | 0.3753 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2239587 | 124249309 | 0.3761 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2247430 | 124259750 | 0.3757 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2268349 | 124250384 | 0.3764 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2268350 | 124251060 | 0.3764 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2300434 | 124251697 | 0.3759 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2239586 | 124249235 | 0.3777 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs201902493 | 124258330 | 0.3772 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs1003079 | 124261348 | 0.3777 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2246731 | 124254180 | 0.3781 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs11200654 | 124254343 | 0.3773 | intronic | *HTRA1* |
| 10q26.13 | 2.52 | rs2268353 | 124254061 | 0.3785 | intronic | *HTRA1* |
| 10q26.13 | 2.49 | rs1048347 | 124096061 | 0.3928 | exonic | *BTBD16* |
| 10q24.33 | 2.48 | rs7071247 | 105257786 | 0.3296 | ncRNA\_intronic | *NEURL1-AS1* |
| 10q26.12 | 2.48 | rs3858340 | 121436286 | 0.2327 | exonic | *BAG3* |
| 9q31.3 | 2.46 | rs7030192 | 113169631 | 0.4114 | exonic | *SVEP1* |
| 14q11.2 | 2.46 | rs11625112 | 23596740 | 0.4218 | intronic | *SLC7A8* |
| 10q26.13 | 2.44 | rs2300432 | 124243189 | 0.3727 | intronic | *HTRA1* |
| 10q26.13 | 2.43 | rs2284666 | 124240785 | 0.367 | intronic | *HTRA1* |
| 10q26.13 | 2.43 | rs67307815 | 124240722 | 0.3665 | intronic | *HTRA1* |
| 10q26.13 | 2.43 | rs66884382 | 124240310 | 0.3657 | intronic | *HTRA1* |
| 9q33.1 | 2.41 | rs929589 | 122899590 | 0.2452 | intergenic | *BRINP1,MIR147A* |
| 10q26.13 | 2.4 | rs11200651 | 124246002 | 0.3794 | intronic | *HTRA1* |
| 10q26.13 | 2.4 | rs2268344 | 124244969 | 0.3773 | intronic | *HTRA1* |
| 10q26.13 | 2.36 | rs2268345 | 124245483 | 0.3528 | intronic | *HTRA1* |
| 12q21.33 | 2.27 | rs1949536 | 89490667 | 0.4375 | intergenic | *LOC728084,DUSP6* |
| 9q33.1 | 2.27 | rs7020782 | 119106881 | 0.2856 | exonic | *PAPPA* |
| 9q31.3 | 2.23 | rs7863519 | 113208250 | 0.444 | exonic | *SVEP1* |
| 20q12 | 2.21 | rs211835 | 38478566 | 0.4738 | intergenic | *LOC339568,LINC01370* |
| 9q31.1 | 2.2 | rs7023854 | 104291812 | 0.3387 | intergenic | *TMEM246,RNF20* |
| 10q26.13 | 2.14 | rs876790 | 124263535 | 0.4614 | intronic | *HTRA1* |
| 10q24.2 | 2.14 | rs2182169 | 100148004 | 0.4082 | intronic | *PYROXD2* |
| 14q24.2 | 2.12 | rs2280792 | 73711394 | 0.4579 | exonic | *PAPLN* |
| 6p21.32 | 2.1 | rs3106189 | 33282002 | 0.3844 | UTR5 | *TAPBP* |
| 6p21.32 | 2.1 | rs3106190\_ver3 | 33280629 | 0.3832 | intronic | *TAPBP* |
| 10q24.31 | 2.08 | rs2230804 | 101977883 | 0.4974 | exonic | *CHUK* |
| 10q26.11 | 2.06 | rs746832 | 122348065 | 0.4615 | ncRNA\_intronic | *MIR5694* |
| 14q24.3 | 2.06 | rs3784039 | 74489735 | 0.4302 | exonic | *CCDC176* |
| 9q33.1 | 2.05 | rs16909449 | 122861297 | 0.4799 | intergenic | *BRINP1,MIR147A* |
| 1p36.13 | 2.05 | rs3753827 | 20305887 | 0.4287 | intronic | *PLA2G2A* |
| 9q31.3 | 2.02 | rs2986671 | 113192655 | 0.4221 | exonic | *SVEP1* |
| 10q24.2 | 2.00 | rs2147896 | 100148176 | 0.3936 | exonic | *PYROXD2* |
| 12q21.33 | 2.00 | rs2279574 | 89745477 | 0.3959 | exonic | *DUSP6* |
| 3p26.1 | 1.99 | rs12638960 | 167171499 | 0.4157 | intronic | *SERPINI2* |
| 10q24.2 | 1.98 | rs2281636 | 101492403 | 0.333 | UTR5 | *COX15* |
| 9q33.1 | 1.98 | rs2104772 | 117808785 | 0.4268 | exonic | *TNC* |
| 12q21.32 | 1.97 | rs7980126 | 86716229 | 0.3617 | intronic | *MGAT4C* |
| 10q26.13 | 1.96 | rs2421028 | 124237338 | 0.4382 | intronic | *HTRA1* |
| 14q23.3 | 1.96 | rs7157792 | 77353103 | 0.2664 | intergenic | *LRRC74A,IRF2BPL* |
| 10q26.13 | 1.96 | rs4752700 | 124237612 | 0.4368 | intronic | *HTRA1* |
| 10q26.13 | 1.96 | rs4237540 | 124237498 | 0.4359 | intronic | *HTRA1* |
| 10q26.13 | 1.96 | rs760338 | 124238997 | 0.4362 | intronic | *HTRA1* |
| 1p31.3 | 1.93 | rs3762321 | 62253483 | 0.1474 | exonic | *INADL* |
| 6p21.32 | 1.93 | rs3130100 | 33283766 | 0.3969 | exonic | *ZBTB22* |
| 6p21.32 | 1.91 | rs2239842 | 33261871 | 0.2798 | intronic | *RGL2* |
| 10q24.2 | 1.91 | rs11190245 | 101451259 | 0.3598 | exonic | *ENTPD7* |
| 22q31.33 | 1.91 | rs4077129 | 50356693 | 0.221 | exonic | *PIM3* |
| 14q13.1 | 1.91 | rs33979974 | 33979974 | 0.4578 | intronic | *NPAS3* |

Table displaying the genome-wide significant and suggestive linkage signals from the single variant two-point linkage analysis sorted by HLOD. The genome-wide significance threshold is 3.3 and the genome-wide suggestive threshold is 1.9, as recommended by Lander and Kruglyak. CHR = chromosomal region, HLOD=heterogeneity LOD score, POS = position in basepairs of the SNP, MAF = minor allele frequency as calculated from the data set, FUNCTION = functional annotation of the SNP, GENE = genic location of the SNP or closest genes in the case of intergenic SNPs. Annotations performed by ANNOVAR.