**Appendix 4.** Details of the single variants most strongly associated with extreme case/control status based on a) the largest beta coefficient (β, suggesting risk variants), and b) the smallest beta coefficient (suggesting protective variants). P-values of variants from exome-chip analysis of 33,976 cases and controls are also reported [1].

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Rs ID** | **Position** | **Minor** **allele** | **Major** **allele** | **MAF****cases** | **MAF****controls** | **P-value** | **β** | **Nearest gene** | **Location/** **function** | **Exome chip** **p-value** |
| a) | rs12673849 | 7:149562275 | T | C | 0.09 | 0 | 9.48x10-5 | 4.53 | *ZNF862* | UTR3 | 0.33 |
|  | rs117051141 | 7:149573187 | T | C | 0.09 | 0 | 9.48x10-5 | 4.53 | *ATP6V0E2* | intronic | 0.34 |
|  | rs7799802 | 7:149577330 | A | G | 0.09 | 0 | 9.48x10-5 | 4.53 | *ATP6V0E2* | UTR3 | 0.36 |
|  | rs113889337 | 11:73362985 | G | A | 0.04 | 0 | 1.51x10-3 | 4.21 | *PLEKHB1* | intronic | 0.64 |
|  | rs33927012 | 1:17354297 | G | A | 0.04 | 0 | 2.42x10-3 | 4.04 | *SDHB* | nonsynonymous neutral | 0.77 |
|  | rs11928501 | 3:73118221 | C | A | 0.05 | 0 | 1.64x10-3 | 4.01 | *PPP4R2* | intergenic | 0.41 |
|  | rs11866635 | 16:1391132 | T | C | 0.07 | 0 | 3.14x10-3 | 3.97 | *BAIAP3* | synonymous | 0.13 |
|  | rs8055112 | 16:1397698 | A | G | 0.07 | 0 | 3.14x10-3 | 3.97 | *BAIAP3* | intronic | 0.15 |
|  | rs12103312 | 16:1398602 | A | G | 0.07 | 0 | 3.14x10-3 | 3.97 | *BAIAP3* | UTR3 | 0.15 |
|  | rs141133909 | 6:74161604 | T | C | 0.08 | 0 | 3.12x10-3 | 3.93 | *MB21D1* | nonsynonymous, damaging | 0.23 |
| b) | rs117615621 | 17:4455266 | T | G | 0 | 0.06 | 2.97x10-3 | -3.78 | *MYBBP1A* | nonsynonymous, damaging | 0.18 |
|  | rs78378263 | 11:48387526 | T | G | 0.45 | 0.50 | 4.53x10-3 | -3.75 | *OR4C45,**OR4A47* | intergenic | NA |
|  | rs17110157 | 1:84948540 | G | A | 0 | 0.07 | 1.47x10-3 | -3.75 | *RPF1* | intronic | 0.38 |
|  | rs76421103 | 1:84971819 | A | G | 0 | 0.07 | 1.47x10-3 | -3.75 | *GNG5* | UTR5 | 0.40 |
|  | rs11801891 | 1:85020637 | T | G | 0 | 0.07 | 1.47x10-3 | -3.75 | *SPATA1,**CTBS* | UTR3 | 0.29 |
|  | rs1043493 | 1:85020649 | T | C | 0 | 0.07 | 1.47x10-3 | -3.70 | *SPATA1,**CTBS* | UTR3 | 0.29 |
|  | rs11570461 | 17:45259022 | T | G | 0 | 0.06 | 2.78x10-3 | -3.70 | *CDC27* | intronic | 0.77 |
|  | rs144597450 | 3:150398311 | A | C | 0 | 0.04 | 4.06x10-3 | -3.69 | *FAM194A* | nonsynonymous, neutral | 0.23 |
|  | rs144036725 | 2:204825416 | T | C | 0 | 0.06 | 3.89x10-3 | -3.66 | *ICOS* | UTR3 | NA |
|  | rs7528067 | 1:84961108 | A | G | 0 | 0.06 | 2.78x10-3 | -3.75 | *RPF1* | nonsynonymous, neutral | 0.40 |

1. Fritsche LG, Igl W, Bailey JNC, Grassmann F, Sengupta S, Bragg-Gresham JL, Burdon KP, Hebbring SJ, Wen C, Gorski M. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat.Genet. 2016; 48:134-43.