**Table S1.** Overrepresentation of significant SNPs excluding previously reported[5-9](#_ENREF_5)genes ± 0.5Mb and the APOE region as above.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| interval α | N SNPs | Est. N of independent sig. SNPs | Expected N SNPs (mean±SD) | RatioEst/Exp | p-value |
|
| 0 < p ≤ 10-6 | 9 | 8 | 4±2.0 | 2.03 | 0.015 |
| 10-6 < p ≤ 10-5 | 133 | 61 | 33±6.4 | 1.83 | 1.6x10-5 |
| 10-5 < p ≤ 10-4 | 1515 | 868 | 334±20 | 2.20 | 2.8x10-154 |
| 10-4 < p ≤ 10-3 | 8562 | 5044 | 3339±64 | 1.51 | 3.0x10-157 |
| 10-3 < p ≤ 0.01 | 66524 | 36772 | 33386±201 | 1.10 | 1.3x10-63 |
| 0.01 < p ≤ 0.1 | 630948 | 330229 | 324707±602 | 1.02 | 4.6x10-20 |
| 0.1 < p ≤ 0.2 | 698604 | 370270 | 347297±945 | 1.07 | 1.4x10-130 |
| 0.2 < p ≤ 0.3 | 692171 | 382472 | 347330±1143 | 1.10 | 1.6x10-207 |
| 0.3 < p ≤ 0.4 | 696887 | 393565 | 345110±1257 | 1.14 | <10-256 |
| 0.4 < p ≤ 0.5 | 701195 | 401522 | 350385±1310 | 1.15 | <10-256 |

Exp = expected, signif = significant. SD = standard deviation, Est = estimated number[21](#_ENREF_21) of independent SNPs. The number of significant SNPs in the intervals are counted while adjusting individual SNP p-values for genomic control λ=1.087.