**Table S4 Detailed results for the MAGENTA analysis (GWAS enrichment)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Database** | **Term** | **Description** | **No. genes\*** | **Exp. no.****enriched genes** | **Obs. no.****enriched genes** | **Nominal *P*** |
| GO | GO:0031981 | nuclear lumen  | 1834 | 92 | 115 | 1.6x10-3 |
| GO:0006351 | transcription  | 2626 | 131 | 137 | 1.5x10-1 |
| GO:0005654 | nucleoplasm  | 1286 | 64 | 79 | 1.8x10-2 |
| GO:0005730 | nucleolus  | 629 | 31 | 44 | 1.4x10-2 |
| GO:0016568 | chromatin modification  | 438 | 22 | 31 | 2.6x10-2 |
| GO:0003723 | RNA binding  | 1294 | 65 | 77 | 4.0x10-2 |
| GO:0004386 | helicase activity  | 138 | 7 | 15 | 3.0x10-3 |
| GO:0010975 | neuron projection development  | 238 | 12 | 12 | 5.4x10-1 |
| GO:0007268 | synaptic transmission  | 638 | 32 | 32 | 5.0x10-1 |
| GO:0030182 | neuron differentiation  | 1015 | 51 | 63 | 3.0x10-2 |
| GO:0006397 | mRNA processing | 388 | 19 | 21 | 3.8x10-1 |
| GO:0005681 | spliceosomal complex | 143 | 7 | 9 | 2.9x10-1 |
| INTERPRO |  IPR001650 | DNA/RNA helicase, C-terminal | 102 | 5 | 12 | 4.3x10-3 |
| IPR014001 | DEAD-like helicase, N-terminal | 104 | 5 | 12 | 5.8x10-3 |
| RNA Helicase | Pre-mRNA Splicing  | 14 genes | 12 | 3 | 2 | 1.2x10-1 |
| Pre-mRNA Splicing | 7 genes | 7 | 2 | 0 | 1.0x10-1 |

\*the number of genes analyzed by MAGENTA.

Exp. no. enriched genes=expected number of genes with gene P values < 95th percentile in entire genome.

Obs. no. enriched genes=observed number of genes with gene P values < 95th percentile in entire genome.