**Supplementary Table 5**: results of enrichment analysis for the genes located in the regions of variants with suggestive p values (p<5e-06) for association the phenotypes of interest in the meta-analysis. N genes=n genes in each set; N overlap=n genes that overlap with the genes of interest (those in the regions carrying polymorphisms with suggestive associations); adj. p=FDR corrected p value. Gene sets were downloaded from [http.//www.broadinstitute.org/gsea/](http://www.broadinstitute.org/gsea/). For further methodological details see (Watanabe et al., 2017).

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phenotype** | **Category** | **Gene Set** | **N genes** | **N overlap** | **p** | **Adj. p** | **Genes** |
| TRD vs. response | GO molecular function | GO\_DOUBLE\_STRANDED\_DNA\_BINDING | 757 | 7 | 2.746E-08 | 1.396E-05 | SOX13,ZNF548,ZNF772,ZNF419,ZNF773,ZNF549,ZIK1 |
| GO molecular function | GO\_NUCLEIC\_ACID\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY | 1180 | 8 | 4.189E-08 | 1.396E-05 | SOX13,ZNF548,ZNF772,ZNF419,ZNF773,ZNF549,ZIK1,ZNF134 |
| GO molecular function | GO\_REGULATORY\_REGION\_NUCLEIC\_ACID\_BINDING | 810 | 7 | 4.648E-08 | 1.396E-05 | SOX13,ZNF548,ZNF772,ZNF419,ZNF773,ZNF549,ZIK1 |
| GO molecular function | GO\_SEQUENCE\_SPECIFIC\_DNA\_BINDING | 1019 | 7 | 2.738E-07 | 6.166E-05 | SOX13,ZNF548,ZNF772,ZNF419,ZNF773,ZNF549,ZIK1 |
| Symptom improv. | GO biological process | GO\_NEGATIVE\_REGULATION\_OF\_MUSCLE\_CELL\_APOPTOTIC\_PROCESS | 30 | 3 | 3.418E-08 | 1.516E-04 | ADCYAP1,HMGCR,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_MUSCLE\_CELL\_APOPTOTIC\_PROCESS | 43 | 3 | 1.524E-07 | 3.381E-04 | ADCYAP1,HMGCR,HEY2 |
| GO biological process | GO\_DETECTION\_OF\_CALCIUM\_ION | 14 | 2 | 4.658E-07 | 6.887E-04 | SYT1,KCNMB2 |
| GO biological process | GO\_REGULATION\_OF\_BLOOD\_CIRCULATION | 295 | 5 | 7.411E-07 | 7.703E-04 | CACNA1C,ADCYAP1,KCNMB2,HMGCR,HEY2 |
| GO biological process | GO\_NEGATIVE\_REGULATION\_OF\_STRIATED\_MUSCLE\_CELL\_APOPTOTIC\_PROCESS | 17 | 2 | 8.682E-07 | 7.703E-04 | HMGCR,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_STRIATED\_MUSCLE\_CELL\_APOPTOTIC\_PROCESS | 22 | 2 | 1.959E-06 | 1.448E-03 | HMGCR,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_PEPTIDE\_TRANSPORT | 254 | 4 | 8.371E-06 | 5.305E-03 | CACNA1C,ADCYAP1,RBCK1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_SYSTEM\_PROCESS | 506 | 5 | 1.656E-05 | 9.184E-03 | CACNA1C,ADCYAP1,KCNMB2,HMGCR,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_VASODILATION | 48 | 2 | 2.158E-05 | 1.064E-02 | ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_SYNAPTIC\_TRANSMISSION\_GLUTAMATERGIC | 50 | 2 | 2.442E-05 | 1.083E-02 | SYT1,ADCYAP1 |
| GO biological process | GO\_VASCULAR\_PROCESS\_IN\_CIRCULATORY\_SYSTEM | 163 | 3 | 3.200E-05 | 1.204E-02 | ADCYAP1,KCNMB2,HMGCR |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_MUSCLE\_TISSUE\_DEVELOPMENT | 55 | 2 | 3.257E-05 | 1.204E-02 | HMGCR,HEY2 |
| GO biological process | GO\_CIRCULATORY\_SYSTEM\_PROCESS | 365 | 4 | 4.782E-05 | 1.294E-02 | CACNA1C,ADCYAP1,KCNMB2,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_PEPTIDE\_SECRETION | 207 | 3 | 8.118E-05 | 1.294E-02 | CACNA1C,ADCYAP1,HMGCR |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT | 230 | 3 | 1.220E-04 | 1.377E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_REGULATION\_OF\_HEART\_RATE | 86 | 2 | 1.242E-04 | 1.377E-02 | CACNA1C,HEY2 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_BLOOD\_CIRCULATION | 93 | 2 | 1.566E-04 | 1.456E-02 | ADCYAP1,HEY2 |
| GO biological process | GO\_ACTION\_POTENTIAL | 94 | 2 | 1.617E-04 | 1.456E-02 | CACNA1C,KCNMB2 |
| GO biological process | GO\_REGULATION\_OF\_HORMONE\_SECRETION | 260 | 3 | 1.953E-04 | 1.456E-02 | CACNA1C,ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_MUSCLE\_TISSUE\_DEVELOPMENT | 102 | 2 | 2.059E-04 | 1.456E-02 | HMGCR,HEY2 |
| GO biological process | GO\_NEGATIVE\_REGULATION\_OF\_PROTEIN\_COMPLEX\_ASSEMBLY | 105 | 2 | 2.243E-04 | 1.531E-02 | LDLRAD4,HEY2 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_SYNAPTIC\_TRANSMISSION | 110 | 2 | 2.573E-04 | 1.642E-02 | SYT1,ADCYAP1 |
| GO biological process | GO\_REGULATION\_OF\_CELL\_DEVELOPMENT | 831 | 5 | 2.597E-04 | 1.642E-02 | SYT1,ADCYAP1,LDLRAD4,ENC1,HEY2 |
| GO biological process | GO\_MUSCLE\_SYSTEM\_PROCESS | 281 | 3 | 2.628E-04 | 1.642E-02 | CACNA1C,COL4A3BP,HEY2 |
| GO biological process | GO\_RESPONSE\_TO\_CALCIUM\_ION | 115 | 2 | 2.932E-04 | 1.698E-02 | SYT1,KCNMB2 |
| GO biological process | GO\_REGULATION\_OF\_NEURON\_DIFFERENTIATION | 550 | 4 | 3.268E-04 | 1.743E-02 | SYT1,ADCYAP1,ENC1,HEY2 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_CELL\_PROJECTION\_ORGANIZATION | 300 | 3 | 3.371E-04 | 1.743E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_NEURON\_DIFFERENTIATION | 304 | 3 | 3.544E-04 | 1.790E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_MULTICELLULAR\_ORGANISMAL\_SIGNALING | 123 | 2 | 3.573E-04 | 1.790E-02 | CACNA1C,KCNMB2 |
| GO biological process | GO\_REGULATION\_OF\_G\_PROTEIN\_COUPLED\_RECEPTOR\_PROTEIN\_SIGNALING\_PATHWAY | 126 | 2 | 3.834E-04 | 1.849E-02 | ADCYAP1,CAMKMT |
| GO biological process | GO\_RESPONSE\_TO\_ETHANOL | 136 | 2 | 4.795E-04 | 1.962E-02 | ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_MEMBRANE\_POTENTIAL | 343 | 3 | 5.591E-04 | 2.148E-02 | CACNA1C,ADCYAP1,KCNMB2 |
| GO biological process | GO\_NEUROTRANSMITTER\_TRANSPORT | 153 | 2 | 6.758E-04 | 2.418E-02 | SYT1,SV2C |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_DEVELOPMENTAL\_GROWTH | 154 | 2 | 6.887E-04 | 2.425E-02 | SYT1,HEY2 |
| GO biological process | GO\_NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_WOUNDING | 155 | 2 | 7.018E-04 | 2.451E-02 | ADCYAP1,HMGCR |
| GO biological process | GO\_SECOND\_MESSENGER\_MEDIATED\_SIGNALING | 160 | 2 | 7.696E-04 | 2.579E-02 | CACNA1C,ADCYAP1 |
| GO biological process | GO\_SINGLE\_ORGANISM\_BEHAVIOR | 383 | 3 | 8.450E-04 | 2.645E-02 | ADCYAP1,SEZ6L,HMGCR |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_ERK1\_AND\_ERK2\_CASCADE | 170 | 2 | 9.173E-04 | 2.731E-02 | ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_SECRETION | 694 | 4 | 9.426E-04 | 2.775E-02 | CACNA1C,SYT1,ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT | 404 | 3 | 1.031E-03 | 2.942E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_REGULATION\_OF\_NERVOUS\_SYSTEM\_DEVELOPMENT | 746 | 4 | 1.303E-03 | 3.469E-02 | SYT1,ADCYAP1,ENC1,HEY2 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_NERVOUS\_SYSTEM\_DEVELOPMENT | 434 | 3 | 1.343E-03 | 3.469E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_DEVELOPMENTAL\_PROCESS | 1135 | 5 | 1.356E-03 | 3.469E-02 | SYT1,ADCYAP1,ENC1,HMGCR,HEY2 |
| GO biological process | GO\_CELL\_CELL\_SIGNALING | 757 | 4 | 1.390E-03 | 3.469E-02 | CACNA1C,SYT1,ADCYAP1,KCNMB2 |
| GO biological process | GO\_REGULATION\_OF\_CYTOSOLIC\_CALCIUM\_ION\_CONCENTRATION | 202 | 2 | 1.507E-03 | 3.654E-02 | CACNA1C,ADCYAP1 |
| GO biological process | GO\_HEART\_MORPHOGENESIS | 212 | 2 | 1.731E-03 | 3.918E-02 | COL4A3BP,HEY2 |
| GO biological process | GO\_HEART\_DEVELOPMENT | 465 | 3 | 1.731E-03 | 3.918E-02 | CACNA1C,COL4A3BP,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_ANATOMICAL\_STRUCTURE\_SIZE | 465 | 3 | 1.731E-03 | 3.918E-02 | ADCYAP1,KCNMB2,HMGCR |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_CELL\_DEVELOPMENT | 469 | 3 | 1.786E-03 | 3.982E-02 | SYT1,ADCYAP1,ENC1 |
| GO biological process | GO\_REGULATION\_OF\_HORMONE\_LEVELS | 475 | 3 | 1.872E-03 | 4.062E-02 | CACNA1C,ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_MULTICELLULAR\_ORGANISMAL\_DEVELOPMENT | 1663 | 6 | 1.877E-03 | 4.062E-02 | SYT1,ADCYAP1,LDLRAD4,ENC1,HMGCR,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_HEART\_CONTRACTION | 221 | 2 | 1.949E-03 | 4.176E-02 | CACNA1C,HEY2 |
| GO biological process | GO\_MUSCLE\_CONTRACTION | 232 | 2 | 2.238E-03 | 4.569E-02 | CACNA1C,COL4A3BP |
| GO biological process | GO\_NITROGEN\_COMPOUND\_TRANSPORT | 499 | 3 | 2.240E-03 | 4.569E-02 | SYT1,ADCYAP1,COL4A3BP |
| GO biological process | GO\_POSITIVE\_REGULATION\_OF\_GROWTH | 234 | 2 | 2.293E-03 | 4.624E-02 | SYT1,HEY2 |
| GO biological process | GO\_MUSCLE\_CELL\_DIFFERENTIATION | 235 | 2 | 2.321E-03 | 4.631E-02 | HMGCR,HEY2 |
| GO biological process | GO\_SYSTEM\_PROCESS | 1726 | 6 | 2.328E-03 | 4.631E-02 | CACNA1C,ADCYAP1,KCNMB2,HMGCR,COL4A3BP,HEY2 |
| GO biological process | GO\_REGULATION\_OF\_ERK1\_AND\_ERK2\_CASCADE | 236 | 2 | 2.349E-03 | 4.652E-02 | ADCYAP1,HMGCR |
| GO biological process | GO\_REGULATION\_OF\_CELLULAR\_LOCALIZATION | 1271 | 5 | 2.422E-03 | 4.775E-02 | CACNA1C,SYT1,ADCYAP1,RBCK1,HMGCR |
| GO biological process | GO\_BEHAVIOR | 512 | 3 | 2.459E-03 | 4.827E-02 | ADCYAP1,SEZ6L,HMGCR |
| GO biological process | GO\_NEGATIVE\_REGULATION\_OF\_CELL\_DEATH | 867 | 4 | 2.528E-03 | 4.837E-02 | ADCYAP1,RBCK1,HMGCR,HEY2 |
| GO cell component | GO\_EXOCYTIC\_VESICLE\_MEMBRANE | 55 | 2 | 3.257E-05 | 1.116E-02 | SYT1,SV2C |
| GO cell component | GO\_TERMINAL\_BOUTON | 64 | 2 | 5.138E-05 | 1.116E-02 | SYT1,ADCYAP1 |
| GO cell component | GO\_PRESYNAPSE | 282 | 3 | 2.664E-04 | 2.207E-02 | SYT1,ADCYAP1,SV2C |
| GO cell component | GO\_NEURON\_PROJECTION\_TERMINUS | 129 | 2 | 4.108E-04 | 2.809E-02 | SYT1,ADCYAP1 |
| GO cell component | GO\_SYNAPSE\_PART | 607 | 4 | 5.138E-04 | 2.809E-02 | CACNA1C,SYT1,ADCYAP1,SV2C |
| GO cell component | GO\_EXOCYTIC\_VESICLE | 141 | 2 | 5.328E-04 | 2.809E-02 | SYT1,SV2C |
| GO cell component | GO\_TRANSPORT\_VESICLE\_MEMBRANE | 146 | 2 | 5.897E-04 | 2.850E-02 | SYT1,SV2C |
| GO cell component | GO\_CATION\_CHANNEL\_COMPLEX | 166 | 2 | 8.562E-04 | 3.820E-02 | CACNA1C,KCNMB2 |
| GO cell component | GO\_SYNAPSE | 751 | 4 | 1.342E-03 | 4.716E-02 | CACNA1C,SYT1,ADCYAP1,SV2C |
| GO cell component | GO\_EXCITATORY\_SYNAPSE | 196 | 2 | 1.382E-03 | 4.716E-02 | CACNA1C,SYT1 |
| GO molecular function | GO\_PHOSPHATIDYLINOSITOL\_PHOSPHATE\_BINDING | 116 | 2 | 3.008E-04 | 1.862E-02 | SYT1,COL4A3BP |
| GO molecular function | GO\_HORMONE\_RECEPTOR\_BINDING | 167 | 2 | 8.712E-04 | 2.804E-02 | ADCYAP1,NCOA7 |
| GO molecular function | GO\_CALMODULIN\_BINDING | 178 | 2 | 1.048E-03 | 2.980E-02 | CACNA1C,SYT1 |
| GO molecular function | GO\_PHOSPHATIDYLINOSITOL\_BINDING | 198 | 2 | 1.423E-03 | 3.664E-02 | SYT1,COL4A3BP |
| GO molecular function | GO\_ORGANIC\_ACID\_BINDING | 207 | 2 | 1.617E-03 | 3.821E-02 | SYT1,EGLN3 |
| TRD vs. others | GO biological process | go regulation of dna templated transcription in response to stress | 67 | 2 | 4.73E-06 | 1.06E-02 | NEDD4,EGLN2 |
| GO biological process | go intracellular steroid hormone receptor signaling pathway | 71 | 2 | 5.63E-06 | 1.06E-02 | NEDD4,EGLN2 |
| GO biological process | go steroid hormone mediated signaling pathway | 124 | 2 | 3.01E-05 | 1.27E-02 | NEDD4,EGLN2 |
| GO biological process | go hormone mediated signaling pathway | 157 | 2 | 6.09E-05 | 1.77E-02 | NEDD4,EGLN2 |
| GO biological process | go intracellular receptor signaling pathway | 167 | 2 | 7.32E-05 | 2.00E-02 | NEDD4,EGLN2 |
| GO biological process | go cellular response to steroid hormone stimulus | 217 | 2 | 1.59E-04 | 2.85E-02 | NEDD4,EGLN2 |
| GO biological process | go positive regulation of protein catabolic process | 262 | 2 | 2.77E-04 | 3.89E-02 | NEDD4,EGLN2 |
| GO cell component | go actin based cell projection | 179 | 2 | 9.00E-05 | 1.05E-02 | NEDD4,LOXHD1 |
| GO cell component | go perinuclear region of cytoplasm | 642 | 3 | 2.18E-04 | 1.59E-02 | NEDD4,RAB4B,PKHD1 |
| GO molecular function | go organic acid binding | 207 | 2 | 1.38E-04 | 1.40E-02 | NEDD4,EGLN2 |