**Integrated genetic and methylomic analyses identify shared biology between autism and autistic traits**

**Supplementary Note**

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**Supplementary Figure 1: Histograms of SCDC and CCC scores in the samples used in the MWAS**



Kernel density plots of SCDC scores (n = 701) and CCC scores (n = 666) in the sample used for the MWAS analyses.

**Supplementary Figure 2: Manhattan plot and qq-plot of the MWAS for the CCC scores**

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*A: Manhattan plot of the CCC MWAS. B: Quantile-Quantile plot of the CCC MWAS*

**Supplementary Table 1: Sample information and participant demographics**

|  |  |  |
| --- | --- | --- |
|  | **SCDC** | **CCC** |
| **Mean** | 14.65 (3.44) | 151.83 (6.77) |
| **Sample size** | 701 | 666 |
| **Males**  | 341 | 323 |
| **Whitecells**  | 575 | 543 |
| **Bcell** | 0.16 (0.03) | 0.16 (0.03) |
| **CD3T** | 0.019 (0.05) | 0.019 (0.05) |
| **CD4T** | 0.16 (0.04) | 0.16 (0.05) |
| **CD8T** | 0.06 (0.03) | 0.06 (0.04) |
| **Gran** | 0.46 (0.08) | 0.46 (0.09) |
| **Mono** | 0.10 (0.03) | 0.10 (0.03) |
| **NK** | 0.14 (0.03) | 0.14 (0.03) |

*This table provides sample information and participant demographics. We provide the mean values and , in paranthesis, standard deviation for the mean scores, and cell proportions for participants included in the SCDC and the CCC MWAS.*

**Supplementary Table 2: List of CpGs with P < 0.0001 in the SCDC MWAS**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Name | Chromosome | Position | Gene symbol | Gene Region | BETA | SE | P |
| cg00156802 | chrX | 19358457 | chrX:19361726-19362479 |  | -0.81768 | 0.2024 | 5.35E-05 |
| cg03098447 | chr17 | 7210075 | EIF5A;EIF5A;EIF5A | TSS1500;TSS1500;TSS1500 | 2.499287 | 0.641473 | 9.77E-05 |
| cg03202738 | chr4 | 1.56E+08 | NPY2R | TSS200 | 3.25216 | 0.791181 | 3.95E-05 |
| cg05125693 | chr10 | 94051830 | CPEB3;MARCH5 | TSS1500;Body | 2.865308 | 0.724334 | 7.63E-05 |
| cg05877109 | chr14 | 23775794 | BCL2L2 | TSS1500 | 2.574715 | 0.583753 | 1.03E-05 |
| cg07640800 | chr2 | 80529315 | LRRTM1;CTNNA2;CTNNA2 | 3'UTR;Body;Body | 1.673823 | 0.381845 | 1.17E-05 |
| cg10894566 | chr15 | 89905901 | chr15:89904822-89906050 | 5.931252 | 1.379222 | 1.70E-05 |
| cg11228785 | chr5 | 1.79E+08 | ADAMTS2;ADAMTS2 | Body;Body | 1.080653 | 0.275089 | 8.55E-05 |
| cg11416605 | chrX | 63267928 | chrX:63263904-63264129 |  | 1.233394 | 0.296407 | 3.17E-05 |
| cg11490681 | chr17 | 77460916 | HRNBP3 | 5'UTR | 0.591558 | 0.151996 | 9.94E-05 |
| cg13448605 | chr1 | 38100467 | RSPO1;RSPO1 | 1stExon;5'UTR | 11.17919 | 2.843069 | 8.42E-05 |
| cg14379490 | chr9 | 96221055 | FAM120A | Body | -1.78917 | 0.35686 | 5.34E-07 |
| cg15925695 | chr11 | 1.12E+08 | DIXDC1;DIXDC1 | TSS200;Body | 2.998837 | 0.745251 | 5.72E-05 |
| cg17185953 | chr1 | 53387522 | ECHDC2 | TSS200 | 3.780007 | 0.964301 | 8.86E-05 |
| cg19478343 | chr20 | 49620679 | KCNG1 | Body | -1.6772 | 0.402575 | 3.10E-05 |
| cg19984781 | chr6 | 30710898 | FLOT1 | TSS1500 | 0.932476 | 0.237908 | 8.87E-05 |
| cg25165908 | chr12 | 1.11E+08 | CUX2 | Body | -1.17914 | 0.299162 | 8.10E-05 |
| cg25377985 | chr4 | 1.48E+08 | TTC29 | TSS1500 | 1.876305 | 0.464107 | 5.28E-05 |
| cg27314761 | chr2 | 1.97E+08 | SLC39A10;SLC39A10 | 5'UTR;5'UTR | -1.07153 | 0.248946 | 1.68E-05 |

**Supplementary Table 3: Results of the gene-set analyses for the SCDC MWAS (top 50 gene sets)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ID | Description | Size | pvalue | padj |
| GO:0022626 | cytosolic ribosome | 261 | 9.12E-05 | 0.17 |
| GO:0002181 | cytoplasmic translation | 119 | 0.000442 | 0.40 |
| GO:0000184 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 155 | 0.000639 | 0.40 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 308 | 0.001124 | 0.51 |
| GO:0003735 | structural constituent of ribosome | 256 | 0.001618 | 0.51 |
| GO:0022625 | cytosolic large ribosomal subunit | 140 | 0.002153 | 0.51 |
| GO:0030183 | B cell differentiation | 128 | 0.002483 | 0.51 |
| GO:0042100 | B cell proliferation | 105 | 0.002731 | 0.51 |
| GO:0022618 | ribonucleoprotein complex assembly | 293 | 0.002934 | 0.51 |
| GO:0010927 | cellular component assembly involved in morphogenesis | 125 | 0.003083 | 0.51 |
| GO:0032279 | asymmetric synapse | 268 | 0.004005 | 0.51 |
| GO:0006805 | xenobiotic metabolic process | 146 | 0.004308 | 0.51 |
| GO:0098984 | neuron to neuron synapse | 271 | 0.004424 | 0.51 |
| GO:0019210 | kinase inhibitor activity | 115 | 0.004464 | 0.51 |
| GO:0099572 | postsynaptic specialization | 263 | 0.004754 | 0.51 |
| GO:0004860 | protein kinase inhibitor activity | 110 | 0.004758 | 0.51 |
| GO:0005840 | ribosome | 484 | 0.005194 | 0.51 |
| GO:0034728 | nucleosome organization | 278 | 0.005454 | 0.51 |
| GO:0042113 | B cell activation | 318 | 0.005769 | 0.51 |
| GO:0006898 | receptor-mediated endocytosis | 381 | 0.006104 | 0.51 |
| GO:0022627 | cytosolic small ribosomal subunit | 112 | 0.006365 | 0.51 |
| GO:0050670 | regulation of lymphocyte proliferation | 238 | 0.006579 | 0.51 |
| GO:0045047 | protein targeting to ER | 113 | 0.006649 | 0.51 |
| GO:0072599 | establishment of protein localization to endoplasmic reticulum | 117 | 0.006713 | 0.51 |
| GO:0014069 | postsynaptic density | 261 | 0.006767 | 0.51 |
| GO:0048675 | axon extension | 128 | 0.008435 | 0.61 |
| GO:0032944 | regulation of mononuclear cell proliferation | 241 | 0.009089 | 0.64 |
| GO:0046651 | lymphocyte proliferation | 303 | 0.010073 | 0.64 |
| GO:0031503 | protein-containing complex localization | 348 | 0.010266 | 0.64 |
| GO:0070972 | protein localization to endoplasmic reticulum | 144 | 0.010555 | 0.64 |
| GO:0070663 | regulation of leukocyte proliferation | 253 | 0.0109 | 0.64 |
| GO:0031901 | early endosome membrane | 146 | 0.011318 | 0.64 |
| GO:0050671 | positive regulation of lymphocyte proliferation | 153 | 0.011383 | 0.64 |
| GO:0009897 | external side of plasma membrane | 303 | 0.012647 | 0.64 |
| GO:0015935 | small ribosomal subunit | 170 | 0.012804 | 0.64 |
| GO:0070665 | positive regulation of leukocyte proliferation | 163 | 0.013243 | 0.64 |
| GO:1902936 | phosphatidylinositol bisphosphate binding | 111 | 0.01341 | 0.64 |
| GO:0051291 | protein heterooligomerization | 124 | 0.01344 | 0.64 |
| GO:0000786 | nucleosome | 154 | 0.013598 | 0.64 |
| GO:0044445 | cytosolic part | 441 | 0.014362 | 0.64 |
| GO:0032943 | mononuclear cell proliferation | 307 | 0.014697 | 0.64 |
| GO:0044391 | ribosomal subunit | 393 | 0.014809 | 0.64 |
| GO:1905897 | regulation of response to endoplasmic reticulum stress | 102 | 0.014985 | 0.64 |
| GO:0044815 | DNA packaging complex | 166 | 0.015002 | 0.64 |
| GO:2001237 | negative regulation of extrinsic apoptotic signaling pathway | 114 | 0.015159 | 0.64 |
| GO:0031623 | receptor internalization | 108 | 0.016557 | 0.66 |
| GO:0032946 | positive regulation of mononuclear cell proliferation | 156 | 0.016599 | 0.66 |
| GO:0050864 | regulation of B cell activation | 176 | 0.01669 | 0.66 |
| GO:0034614 | cellular response to reactive oxygen species | 177 | 0.01728 | 0.66 |
| GO:0035690 | cellular response to drug | 363 | 0.017447 | 0.66 |