**Supplementary Table 2. 84 significantly enriched pathways shared between schizophrenia and smoking behaviors.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Pathway ID** | **Description** | **SCZ P-value** | **CPD P-value** | **Ever smoking P-value** | **Former smoking P-value** | **Age at smoking initiation P-value** |
| GO:0014069 | Postsynaptic density | 0 | **1.43E-13** | **1.21E-09** | **1.50E-06** | **3.09E-06** |
| GO:0005891 | Voltage-gated calcium channel complex | 3.04E-14 | 0.1377  | **0.0091**  | 0.0225  | **0.0027**  |
| GO:0005245 | Voltage-gated calcium channel activity | 4.66E-13 | 0.0400  | **0.0006**  | **0.0008**  | **0.0004**  |
| GO:0045211 | Postsynaptic membrane | 7.44E-13 | **4.97E-11** | **1.10E-10** | **5.92E-09** | **5.52E-06** |
| GO:0043025 | Neuronal cell body | 1.39E-11 | **1.67E-07** | **1.68E-05** | **0.0001**  | 0.0083  |
| GO:0005244 | Voltage-gated ion channel activity | 1.21E-09 | 0.0094  | **4.73E-05** | **8.13E-07** | **7.19E-06** |
| GO:0045202 | Synapse | 3.01E-09 | **2.76E-13** | **6.88E-15** | **1.91E-09** | **4.88E-08** |
| GO:0030425 | Dendrite | 9.46E-09 | **1.34E-07** | **0.0043**  | **0.0011**  | **0.0001**  |
| GO:0007268 | Synaptic transmission | 3.22E-08 | **8.03E-10** | **1.85E-11** | **3.22E-11** | **9.84E-06** |
| GO:0007411 | Axon guidance | 5.89E-08 | **8.28E-06** | **6.04E-12** | **8.10E-12** | **3.64E-09** |
| GO:0015464 | Acetylcholine receptor activity | 7.92E-08 | **0** | 0.3912  | 0.0131  | 0.0937  |
| hsa04720 | Long-term potentiation | 1.79E-07 | 0.0991  | **0.0003**  | **0.0087**  | **0.0002**  |
| GO:0005001 | Transmembrane receptor protein tyrosine phosphatase activity | 7.21E-07 | **0.0010**  | **5.50E-08** | **0.0086**  | **7.84E-05** |
| GO:0006816 | Calcium ion transport | 7.31E-07 | 0.0133  | **1.75E-05** | **0.0001**  | **2.01E-06** |
| GO:0042734 | Presynaptic membrane | 1.33E-06 | 0.0186  | **3.12E-06** | **0.0004**  | **0.0003**  |
| GO:0006112 | Energy reserve metabolic process | 1.33E-06 | 0.0333  | **3.53E-05** | 0.0684  | **4.26E-05** |
| hsa05414 | Dilated cardiomyopathy | 3.13E-06 | 0.0237  | **2.76E-05** | 0.0270  | **0.0025**  |
| GO:0043197 | Dendritic spine | 4.34E-06 | **0.0009**  | **0.0007**  | **0.0011**  | **0.0048**  |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 5.15E-06 | 0.0550  | **0.0026**  | 0.0231  | 0.0163  |
| hsa04010 | MAPK signaling pathway | 8.24E-06 | 0.0081  | **0.0009**  | **0.0076**  | **0.0006**  |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 1.06E-05 | **0.0025**  | **4.17E-06** | **1.36E-05** | **0.0008**  |
| GO:0060079 | regulation of excitatory postsynaptic membrane potential | 1.13E-05 | **0** | 0.2769  | **5.17E-06** | 0.0407  |
| GO:0050796 | regulation of insulin secretion | 1.38E-05 | 0.0071  | **0.0031**  | 0.1553  | **0.0003**  |
| R-HSA-2467813 | Separation of Sister Chromatids | 2.18E-05 | **4.89E-06** | 0.1230  | 0.8301  | 0.6372  |
| GO:0048041 | focal adhesion assembly | 6.84E-05 | 0.0410  | 0.4262  | 0.1181  | **0.0052**  |
| GO:0004889 | nicotinic acetylcholine-activated cation-selective channel activity | 6.89E-05 | **0** | 0.3010  | 0.0280  | 0.1518  |
| hsa04912 | GnRH signaling pathway | 7.76E-05 | **0.0056**  | **8.06E-05** | **0.0042**  | **0.0001**  |
| GO:0005516 | calmodulin binding | 9.23E-05 | **0.0008**  | **4.99E-06** | **1.23E-06** | 0.0122  |
| GO:0008066 | glutamate receptor activity | 9.41E-05 | **0.0040**  | 0.0142  | **0.0007**  | **0.0001**  |
| GO:0030315 | T-tubule | 9.87E-05 | 0.1611  | **0.0055**  | 0.1042  | **0.0024**  |
| GO:0045296 | cadherin binding | 1.44E-04 | **0.0028**  | **0.0008**  | **0.0004**  | **5.83E-05** |
| cxcr4Pathway | CXCR4 Signaling Pathway | 1.49E-04 | **0.0013**  | 0.070  | 0.0196  | 0.2016  |
| GO:0005892 | nicotinic acetylcholine-gated receptor-channel complex | 2.03E-04 | **0** | 0.3836  | 0.0592  | 0.1342  |
| GO:0005096 | GTPase activator activity | 2.60E-04 | **0.0002**  | **4.91E-05** | **0.0007**  | 0.0069  |
| GO:0001764 | neuron migration | 2.78E-04 | 0.1975  | **0.0028**  | 0.0115  | 0.0854  |
| GO:0048167 | regulation of synaptic plasticity | 3.55E-04 | **0.0034**  | 0.0765  | **0.0020**  | 0.0991  |
| GO:0046982 | protein heterodimerization activity | 3.99E-04 | **0.0011**  | **0.0003**  | **0.0047**  | 0.0703  |
| R-HSA-5632684 | Hedgehog 'on' state | 4.04E-04 | **6.71E-12** | 0.8588  | 0.6504  | 0.5780  |
| GO:0004697 | protein kinase C activity | 4.76E-04 | 0.2579  | **0.0023**  | 0.0110  | **6.67E-05** |
| GO:0001508 | regulation of action potential | 4.88E-04 | **0** | 0.0716  | 0.0262  | 0.1443  |
| GO:0007156 | homophilic cell adhesion | 4.91E-04 | **0.0011**  | **1.48E-05** | **2.00E-07** | **1.50E-07** |
| GO:0005216 | ion channel activity | 5.09E-04 | **2.95E-13** | **0.0001**  | **1.29E-05** | **0.0001**  |
| GO:0051056 | regulation of small GTPase mediated signal transduction | 5.30E-04 | **0.0002**  | **1.14E-06** | **4.88E-05** | **0.0002**  |
| hsa04020 | Calcium signaling pathway | 5.96E-04 | **0.0056**  | **2.74E-10** | **2.38E-06** | **2.99E-06** |
| GO:0015297 | antiporter activity | 6.05E-04 | 0.1069  | 0.1549  | **0.0016**  | 0.0107  |
| GO:0006813 | potassium ion transport | 7.43E-04 | **0.0038**  | **2.73E-06** | **0.0017**  | **9.14E-05** |
| GO:0005234 | extracellular-glutamate-gated ion channel activity | 9.05E-04 | **0.0043**  | 0.0588  | **0.0050**  | **0.0037**  |
| biopeptidesPathway | Bioactive Peptide Induced Signaling Pathway | 0.00105 | 0.2457  | 0.2987  | **0.0057**  | 0.0545  |
| GO:0007413 | axonal fasciculation | 0.0011 | 0.1479  | 0.0300  | **0.0083**  | 0.1062  |
| GO:0007420 | brain development | 0.0011 | 0.0204  | **0.0038**  | **0.0040**  | 0.0295  |
| GO:0007626 | locomotory behavior | 0.00115 | **9.36E-14** | **0.0032**  | **3.10E-05** | **0.0030**  |
| gpcrPathway | Signaling Pathway from G-Protein Families | 0.00131 | 0.0139  | 0.0399  | 0.2843  | **0.0036**  |
| GO:0008013 | beta-catenin binding | 0.00151 | 0.0250  | **0.0015**  | **0.0002**  | 0.0082  |
| GO:0001701 | in utero embryonic development | 0.00157 | 0.0332  | **0.0005**  | 0.0448  | 0.2770  |
| GO:0008076 | voltage-gated potassium channel complex | 0.00163 | 0.0209  | **0.0004**  | **0.0036**  | **0.0046**  |
| GO:0016477 | cell migration | 0.002 | **0.0034**  | 0.3172  | 0.2692  | 0.0396  |
| GO:0006812 | cation transport | 0.0020 | 0.3269  | 0.0701  | **0.0001**  | **0.0018**  |
| GO:0005085 | guanyl-nucleotide exchange factor activity | 0.00214 | 0.0070  | **3.88E-07** | **0.0002**  | **3.62E-05** |
| GO:0030426 | growth cone | 0.00220 | 0.1866  | **0.0001**  | 0.0142  | 0.0300  |
| GO:0048011 | nerve growth factor receptor signaling pathway | 0.00238 | 0.1766  | **0.0056**  | **8.20E-05** | **7.36E-05** |
| GO:0046928 | regulation of neurotransmitter secretion | 0.00242 | **0** | 0.6366  | **0.0009**  | 0.2304  |
| GO:0023034 | intracellular signaling pathway | 0.00253 | 0.0446  | **0.0002**  | **1.39E-06** | **0.0001**  |
| GO:0042493 | response to drug | 0.00321 | **4.14E-07** | 0.0360  | 0.0314  | 0.2751  |
| GO:0007205 | activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway | 0.00327 | 0.5082  | **0.0064**  | 0.2543  | 0.2388  |
| GO:0009986 | cell surface | 0.00339 | 0.0082  | **0.0007**  | 0.0518  | 0.0075  |
| GO:0031225 | anchored to membrane | 0.00352 | 0.0965  | 0.1650  | **0.0025**  | 0.0086  |
| GO:0030165 | PDZ domain binding | 0.00378 | 0.0238  | **0.0005**  | 0.0208  | 0.0094  |
| GO:0019228 | regulation of action potential in neuron | 0.00411 | 0.0172  | 0.2668  | **0.0017**  | **2.56E-05** |
| hsa04730 | Long-term depression | 0.00417 | **7.10E-05** | **0.0012**  | **2.85E-06** | **0.0009**  |
| agrPathway | Agrin in Postsynaptic Differentiation | 0.00427 | 0.0111  | 0.0213  | **0.0063**  | **0.0004**  |
| edg1Pathway | Phospholipids as signalling intermediaries | 0.00481 | 0.0505  | **0.0047**  | 0.0236  | 0.0264  |
| calcineurinPathway | Effects of calcineurin in Keratinocyte Differentiation | 0.00499 | 0.0461  | 0.2350  | 0.2321  | **0.0017**  |
| GO:0007409 | axonogenesis | 0.0050 | 0.0225  | **3.39E-05** | **0.0067**  | **0.0027**  |
| GO:0004629 | phospholipase C activity | 0.00506 | 0.2683  | 0.0704  | **0.0004**  | 0.4306  |
| R-HSA-4641258 | Degradation of DVL | 0.00512 | **9.19E-14** | 0.8883  | 0.5507  | 0.2936  |
| fcer1Pathway | Fc Epsilon Receptor I Signaling in Mast Cells | 0.00513 | 0.1880  | 0.3738  | 0.2656  | **0.0002**  |
| GO:0007264 | small GTPase mediated signal transduction | 0.00538 | 0.1142  | **0.0024**  | 0.0510  | **0.0007**  |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 0.00604 | **2.00E-14** | 0.3257  | 0.2802  | 0.7022  |
| sppaPathway | Aspirin Blocks Signaling Pathway Involved in Platelet Activation | 0.00623 | **0.0010**  | **0.0047**  | **0.0050**  | 0.0179  |
| R-HSA-1234176 | Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha | 0.00627 | **7.39E-14** | 0.5995  | 0.6921  | 0.4570  |
| GO:0007194 | negative regulation of adenylate cyclase activity | 0.0064 | 0.1784  | **0.0044**  | 0.0520  | 0.0978  |
| GO:0016529 | sarcoplasmic reticulum | 0.0065 | 0.0701  | **0.0008**  | 0.2641  | 0.0639  |
| hsa04270 | Vascular smooth muscle contraction | 0.00656 | 0.0132  | **1.46E-05** | **3.24E-05** | **4.05E-06** |
| GO:0048511 | rhythmic process | 0.00661 | 0.2534  | **0.00083** | 0.0365  | **0.0023**  |