Supplementary Table 2S

Composite P-Values for *GenMapp* Biopathway Analyses of Various Gene Clusters

				Stratum Oriens				Stratum Pyramidale				Stratum Radiatum			
				CA3/2		CA1		CA3/2		CA1		CA3/2		CA1	
	N_i	N_t	%	BD	SZ	BD	SZ	BD	SZ	BD	SZ	BD	SZ	BD	SZ
Synaptic Function															
Acetylcholine Synthesis	0	7	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Calcium Channels	1	28	0.04	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
GPCRDB Class C Metabotropic glutamate pheromone	3	15	0.2	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Ion channel activity	15	116	0.13	4.45E-21	3.35E-20	5.11E-38	2.47E-11	NC	NC	NC	NC	NC	NC	NC	NC
Monoamine GPCRs	0	35	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Peptide GPCRs	6	71	0.08	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Potassium channel activity	20	132	0.13	2.05E-37	1.86E-29	1.93E-42	5.73E-14	NC	NC	NC	NC	NC	NC	NC	NC
Potassium ion transport	26	156	0.17	9.01E-51	2.27E-39	7.55E-47	6.77E-14	NC	NC	5.71E-10	NC	NC	NC	NC	NC
Synaptic transmission	49	241	0.2	2.64E-87	2.74E-54	5.61E-91	6.39E-22	NC	NC	NC	NC	NC	NC	NC	NC
Voltage-gated ion channel activity	24	167	0.14	1.64E-44	3.19E-28	1.27E-68	2.60E-20	NC	7.56E-10	NC	NC	NC	NC	NC	NC
Signaling															
Apoptosis	5	45	0.11	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Catecholamine Biosynthesis	0	4	0	NC	NC	8.27E-99	NC	NC	NC	NC	NC	NC	NC	NC	NC
Cell Cycle Regulation	39	187	0.21	1.79E-81	8.27E-67	3.31E-92	1.43E-22	NC	NC	1.62E-11	NC	NC	NC	NC	3.13E-13
G Protein Signaling	15	80	0.19	2.54E-29	9.92E-16	4.96E-41	NC	NC	NC	NC	NC	NC	NC	NC	NC
G13 Signaling Pathway	3	33	0.09	NC	1.07E-19	1.90E-13	NC	NC	NC	NC	NC	NC	NC	NC	NC
Glucocorticoid & Mineralocorticoid Metabolism	0	12	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Glycogen Metabolism	2	35	0.06	NC	NC	1.50E-18	NC	NC	NC	NC	NC	NC	NC	NC	NC
Glycolysis and Gluconeogenesis	7	45	0.16	NC	6.61E-27	8.55E-38	NC	NC	NC	NC	NC	NC	NC	NC	NC
MAPK Cascade	0	30	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
S1P Signaling	12	48	0.24	1.29E-12	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Second-messenger-mediated signaling	34	160	0.21	2.86E-63	8.40E-46	1.24E-53	1.25E-11	NC	NC	NC	NC	NC	NC	NC	NC
Small ligand GPCRs	3	16	0.19	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
TGF Beta Signaling Pathway	18	123	0.15	6.84E-22	2.92E-15	6.05E-29	1.45E-11	NC	NC	NC	NC	NC	NC	NC	NC
Wnt signaling	4	72	0.06	1.04E-10	6.92E-10	7.98E-26	NC	NC	NC	NC	NC	NC	NC	NC	NC
Metabolism															
Cholesterol Biosynthesis	4	19	0.21	NC	NC	6.75E-23	NC	NC	NC	NC	NC	NC	NC	NC	NC
Electron Transport Chain	9	105	0.09	3.46E-18	1.89E-49	3.74E-62	NC	NC	NC	NC	NC	NC	NC	NC	3.47E-36
Inflammatory Response Pathway	2	32	0.06	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Krebs-TCA Cycle	6	31	0.19	NC	3.87E-11	3.91E-29	NC	NC	NC	NC	NC	NC	NC	NC	NC
Nucleotide GPCRs	2	12	0.17	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Nucleotide Metabolism	2	16	0.13	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Oxidative Stress	5	28	0.17	2.02E-10	NC	1.90E-11	NC	NC	NC	NC	NC	NC	NC	NC	NC
Pentose Phosphate Pathway	1	7	0.14	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Proteasome Degradation	4	43	0.09	NC	4.16E-21	8.37E-34	NC	NC	NC	NC	NC	NC	NC	NC	NC
Steroid Biosynthesis	0	35	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Transcription/Translation															
Response to DNA damage stimulus	39	206	0.16	9.76E-69	2.58E-38	1.41E-89	3.05E-23	NC	NC	NC	NC	NC	NC	NC	NC
Ribosomal Proteins	10	88	0.11	1.83E-17	1.15E-13	2.57E-58	NC	NC	NC	NC	NC	3.15E-13	NC	NC	NC
Translation Factors	14	51	0.27	6.43E-37	3.49E-12	1.57E-51	NC	NC	NC	NC	NC	NC	NC	NC	NC
tRNA Synthetases	3	21	0.14	NC	NC	6.36E-23	NC	NC	NC	NC	NC	NC	NC	NC	NC
Other															
Blood Clotting Cascade	3	20	0.15	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Calcium regulation in cardiac cells	37	149	0.25	7.23E-67	1.15E-72	NC	6.66E-19	NC	NC	1.03E-14	NC	NC	NC	NC	2.04E-27
Heme Biosynthesis	3	9	0.33	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Matrix Metalloproteinases	0	0	0	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Neurogenesis	55	237	0.23	1.45E-109	1.42E-77	1.57E-117	4.22E-36	NC	NC	NC	NC	NC	NC	NC	4.91E-14
Nuclear Receptors	9	42	0.21	4.66E-22	3.67E-18	8.39E-16	NC	NC	NC	NC	NC	NC	NC	NC	NC
Orphan GPCRs	4	16	0.25	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Ovarian Infertility Genes	5	31	0.16	7.17E-11	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC	NC
Positive regulation of apoptosis	26	130	0.2	9.40E-45	8.14E-34	2.61E-85	3.91E-14	NC	NC	NC	NC	NC	NC	NC	NC

For SO of CA3/2 in SZs N_T = Total number of genes in biopathway/cluster; N_i = number of genes meeting p = 0.05 inclusionary criterion; % = N_i/ N_T . The alpha level of significance was Pc = $10^{-10;}$ NC = No Change