

Supplemental Table S1: Top Five Enriched Gene Ontology Terms & Candidate OMIM Genes Among High Scoring Genes

GO Annotation Term	Genes (N)	Genes Expected (N)	Enrichment	Genes without OMIM CNS-Related Phenotypes
Biological Processes				
Positive regulation of protein localization to Cajal body (GO:1904871)	9	0.7	13.0*	<i>CCT2, CCT3, CCT4, CCT7, CCT8, CCT6A, DKC1, TCP1</i>
Positive regulation of establishment of protein localization to telomere (GO:1904851)	9	0.8	11.7*	<i>CCT2, CCT3, CCT4, CCT7, CCT8, CCT6A, DKC1, TCP1</i>
Axo-dendritic protein transport (GO:0099640)	10	1.0	10.0*	<i>DLG2, KIF5B, MAP1A, TERF2, SFPQ</i>
Alternative mRNA splicing, via spliceosome (GO:0000380)	13	1.3	9.9***	<i>CELF4, DDX5, DDX17, DHX9, HNRNPM, RBM17, SFPQ, SFSWAP, SLU7, SRSF1</i>
Positive regulation of telomerase RNA localization to Cajal body (GO:1904874)	11	1.2	9.5**	<i>CCT2, CCT3, CCT4, CCT7, CCT8, CCT6A, DKC1, RUVBL1, RUVBL2, TCP1</i>
Cellular Component				
nBAF complex (GO:0071565)	12	1.2	10.4***	<i>DPF1, SMARCC1</i>
Proteasome regulatory particle, base subcomplex (GO:0008540)	9	0.9	9.8**	<i>PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD1, PSMD2, PSMD4</i>
Chaperonin-containing T-complex (GO:0005832)	8	0.9	9.5*	<i>CCT2, CCT3, CCT4, CCT7, CCT8, CCT6A, TCP1</i>
NuRD complex (GO:0016581)	11	1.2	8.9**	<i>MTA3, HDAC2, RBBP7, MBD3, ZBTB7A, MTA1, CHD5, RBBP4</i>
Proteasome regulatory particle (GO:0005838)	15	1.7	8.9***	<i>PSMC4, PSMC6, PSMD6, PSMD14, PSMD2, PSMD11, PSMC3, PSMC1, PSMD13, PSMC2, ADRM1, PSMD1, PSMD3, PSMD4, PSMC5</i>
Molecular Function				
Protein kinase A catalytic subunit binding (GO:0034236)	10	1.0	10.0**	<i>CSK, EZR, GSK3B, GSK3A, PRKAR1B, PRKAR2B, PJA2</i>
Tau-protein kinase activity (GO:0050321)	14	1.7	8.3**	<i>TTBK1, GSK3B, TAOK2, GSK3A, BRSK1, MARK4, FYN, BRSK2, ROCK2, TAOK1, MARK2</i>
Microtubule plus-end binding (GO:0051010)	10	1.2	8.1*	<i>CLASP1, CLASP2, CLIP1, CLIP2, MAPRE1, MAPRE2, NUMA1</i>
Pre-mRNA binding (GO:0036002)	21	2.9	7.4***	<i>CELF1, CELF2, CELF4, CELF5, DDX5, HNRNPL, PRPF8, RBM22, RBM4, SF1, SRSF2, SLU7, TRA2B, U2AF2</i>
Lysine-acetylated histone binding (GO:0070577)	11	1.5	7.2*	<i>CARM1, BRD2, BRD3, BRD4, BRD7, ZMYND8</i>

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$; p -values for Chi-squared testing uses Bonferroni correction for multiple testing for Biological processes (9,050 unique tests), Cellular Component (1,472 unique tests), Molecular Function (2,811 unique tests); **bold** genes appear two or more times in this table