

Supplemental Table S3. Gene ontology analysis using the Panther_BP_ALL dataset of differentially expressed transcripts between primary motor neurons and primary cortical neurons.

GO ID	GO_Term Panther_BP_ALL	P-value
<i>PolyA site</i>		
BP00167	Synaptic transmission	9.07E-07
BP00166	Neuronal activities	1.76E-06
BP00125	Intracellular protein traffic	8.51E-06
BP00168	Neurotransmitter release	3.81E-05
BP00127	Regulated exocytosis	2.56E-04
BP00126	Exocytosis	3.13E-04
BP00136	Other intracellular protein traffic	5.68E-04
<i>Gene expression</i>		
BP00193	Developmental processes	4.50E-12
BP00246	Ectoderm development	6.78E-09
BP00274	Cell communication	3.52E-08
BP00199	Neurogenesis	5.48E-07
BP00108	Receptor protein tyrosine kinase signaling pathway	1.63E-06
BP00102	Signal transduction	1.28E-04
BP00248	Mesoderm development	1.86E-04
BP00285	Cell structure and motility	1.88E-04
BP00111	Intracellular signaling cascade	2.03E-04
BP00201	Skeletal development	4.32E-04
BP00166	Neuronal activities	7.85E-04
BP00019	Lipid, fatty acid and steroid metabolism	0.00183
BP00064	Protein phosphorylation	0.00338
BP00275	Extracellular matrix protein-mediated signaling	0.00361
BP00167	Synaptic transmission	0.00392
BP00112	Calcium mediated signaling	0.00398
BP00287	Cell motility	0.00465
BP00063	Protein modification	0.00485
BP00286	Cell structure	0.00598
BP00224	Cell proliferation and differentiation	0.00627
BP00122	Ligand-mediated signaling	0.00744

One hundred and twenty-two polyA sites and 910 genes are differentially expressed (fold change > 1.8, $p < 0.1$ by t-test) between these two cell types. GO terms with the p -values less than 0.01 are indicated.