

Supplemental Table S1. Gene Ontology analysis using the GOTERM_BP5 dataset with DAVID.

GO ID	GOTERM_BP5	<i>p</i> -value
<i>PolyA site</i>		
GO:0031644	Regulation of neurological system process*	6.99E-04
GO:0051969	Regulation of transmission of nerve impulse*	7.59E-04
GO:0050804	Regulation of synaptic transmission*	1.02E-03
GO:0016568	Chromatin modification	1.74E-03
GO:0043271	Negative regulation of ion transport	3.81E-03
<i>TSS</i>		
GO:0031328	Positive regulation of cellular biosynthetic process	4.56E-04
GO:0009891	Positive regulation of biosynthetic process	4.56E-04
GO:0051254	Positive regulation of RNA metabolic process	5.26E-04
GO:0010629	Negative regulation of gene expression	6.11E-04
GO:0045893	Positive regulation of transcription, DNA-dependent	6.59E-04
<i>Gene expression</i>		
GO:0007186	G-protein coupled receptor protein signaling pathway	2.32E-04
GO:0006355	Regulation of transcription, DNA-dependent	2.66E-04
GO:0051252	Regulation of RNA metabolic process	3.15E-04
GO:0007166	Cell surface receptor linked signal transduction	1.66E-03
GO:0021510	Spinal cord development*	2.47E-03

Fus-knockdown-mediated shifts in PolyA sites, shifts in TSSs, and changes in gene expressions are collated, respectively. Combined sets of the top and bottom 1000 genes are analyzed using the GOTERM_BP5 dataset with DAVID. For background, 12,522 PolyA sites and 7,677 TSSs, which are detected in PolyA-seq and CAGE-seq, respectively, are used. For gene expression analysis, 571 differentially expressed genes ($p < 0.01$) in the collation of 12,834 genes expressed in N2A cells (FKPM > 0.1) are similarly analyzed.

GO terms with the five best *p*-values in each category are indicated.

*GO terms with neuron-specific functionalities.