Supplemental Table S2. Gene Ontology analysis using the Panther_BP_ALL dataset with DAVID.

GO ID	GO_Term Panther_BP_ALL	*p*-value
PolyA site		
BP00166	Neuronal activities	3.83E-05
BP00167	Synaptic transmission	6.28E-04
BP00193	Developmental processes	8.14E-04
BP00102	Signal transduction	0.00469
BP00120	Cell adhesion-mediated signaling	0.0069
TSS		
BP00273	Chromatin packaging and remodeling	4.66E-07
BP00133	Nuclear transport	0.00148
BP00031	Nucleoside, nucleotide and nucleic acid metabolism	0.00152
BP00120	Cell adhesion-mediated signaling	0.00458
Gene expression		
BP00203	Cell cycle	0.00017
BP00282	Mitosis	0.00079
BP00289	Other metabolism	0.00255
BP00001	Carbohydrate metabolism	0.00811

The method of DAVID analysis and the analyzed data are identical to those in Supplemental Table S1 except that the GO term dataset is Panther_BP_ALL.

GO terms with the *p*-values less than 0.01 are indicated.