

Table S1. Predicted pathway based on two-fold deregulated genes.

Pathways/Processes/Diseases	Database KEGG Gene Ontology	Freq. (Network vs Genome)	P-Value (FDR Corrected)	Genes
KEGG-Pathway-hsa03040: Spliceosome - Homo sapiens (human)	KEGG	33.3%(6/18) 1.4% (131/9324)	2.44E-05	SNRNP70SNRPAEFTUD2U2AF2SNRNP200SF3B3
GO-BP-0006397:mRNA processing	Gene Ontology	27.8%(5/18) 1.1% (104/9324)	1.32E-04	SNRNP70SRPK1RNPS1U2AF2SNRNP200
GO-BP-0006396:RNA processing	Gene Ontology	33.3%(6/18) 2.3% (216/9324)	1.56E-04	SNRNP70SRPK1RNPS1U2AF2SNRNP200SRRT
GO-BP-0000377:RNA splicing	Gene Ontology		2.78E-04	SNRNP70RNPS1U2AF2SNRNP200
GO-BP-0000398:mRNA splicing	Gene Ontology		2.23E-04	SNRNP70RNPS1U2AF2SNRNP200
GO-BP-0000375:RNA splicing	Gene Ontology		1.98E-04	SNRNP70RNPS1U2AF2SNRNP200
GO-BP-0016071:mRNA metabolic process	Gene Ontology	27.8%(5/18) 1.5% (143/9324)	1.81E-04	SNRNP70SRPK1RNPS1U2AF2SNRNP200
GO-BP-0008380:RNA splicing	Gene Ontology	22.2%(4/18) 1.1% (100/9324)	9.34E-04	SNRNP70RNPS1U2AF2SNRNP200
GO-BP-0050684:regulation of mRNA processing	Gene Ontology	16.7%(3/18) 0.5% (46/9324)	2.13E-03	SRPK1RNPS1U2AF2
GO-BP-0043484:regulation of RNA splicing	Gene Ontology	16.7%(3/18) 0.6% (56/9324)	3.46E-03	SNRNP70RNPS1U2AF2
GO-BP-0048025:negative regulation of mRNA splicing	Gene Ontology		3.83E-03	RNPS1U2AF2
GO-BP-0050686:negative regulation of mRNA processing	Gene Ontology	11.1%(2/18) 0.1% (12/9324)	4.21E-03	RNPS1U2AF2
KEGG-Pathway-hsa03013: RNA transport - Homo sapiens (human)	KEGG	22.2%(4/18) 1.8% (164/9324)	3.94E-03	PNNSRRM1RNPS1GEMIN4
GO-BP-0033119:negative regulation of RNA splicing	Gene Ontology	11.1%(2/18) 0.2% (15/9324)	5.72E-03	RNPS1U2AF2
KEGG-Pathway-hsa05168: Herpes simplex infection - Homo sapiens (human)	KEGG	22.2%(4/18) 2.0% (188/9324)	5.76E-03	CSNK2A1CSNK2BSRPK1USP7
KEGG-Pathway-hsa03015: mRNA surveillance pathway - Homo sapiens (human)	KEGG	16.7%(3/18) 1.0% (91/9324)	9.07E-03	PNNSRRM1RNPS1
GO-BP-0048024:regulation of mRNA splicing	Gene Ontology		1.92E-02	RNPS1U2AF2
KEGG-Pathway-hsa04310: Wnt signaling pathway - Homo sapiens (human)	KEGG	16.7%(3/18) 1.5% (139/9324)	2.74E-02	CSNK2A1CSNK2BDVL2
GO-BP-0002009:morphogenesis of an epithelium	Gene Ontology	11.1%(2/18) 0.5% (49/9324)	4.54E-02	CSNK2BDVL2