Table S1. GO enrichment analysis of aberrantly expressed RBPs.

	GO term	**p value**	**FDR**
Up-regulated RBPs	ncRNA processing	5.72E-38	7.63E-35
	RNA splicing	1.75E-37	1.17E-34
	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	1.67E-28	5.58E-26
	mRNA splicing, via spliceosome	1.67E-28	5.58E-26
	RNA splicing, via transesterification reactions	2.26E-28	6.03E-26
	RNA 3'-end processing	2.32E-22	5.16E-20
	RNA catabolic process	3.33E-21	6.34E-19
	tRNA processing	3.95E-21	6.58E-19
	tRNA metabolic process	6.40E-21	9.48E-19
	mRNA catabolic process	3.36E-18	4.47E-16
	spliceosomal complex	1.76E-21	2.50E-19
	cytoplasmic ribonucleoprotein granule	2.58E-14	1.84E-12
	ribonucleoprotein granule	6.79E-14	3.22E-12
	small nuclear ribonucleoprotein complex	1.08E-13	3.84E-12
	Sm-like protein family complex	4.86E-13	1.38E-11
	spliceosomal snRNP complex	8.47E-13	2.00E-11
	catalytic step 2 spliceosome	2.74E-12	5.56E-11
	U2-type spliceosomal complex	4.29E-12	7.62E-11
	ribosome	2.47E-11	3.90E-10
	U2-type precatalytic spliceosome	4.67E-11	6.64E-10
	catalytic activity, acting on RNA	3.11E-29	5.07E-27
	mRNA 3'-UTR binding	5.18E-15	4.23E-13
	catalytic activity, acting on a tRNA	8.47E-12	4.61E-10
	endoribonuclease activity	1.36E-10	5.53E-09
	ribonucleoprotein complex binding	3.53E-10	1.15E-08
	ribonuclease activity	5.63E-10	1.53E-08
	RNA helicase activity	1.24E-09	2.68E-08
	tRNA binding	1.31E-09	2.68E-08
	snRNA binding	2.47E-09	4.47E-08
	endoribonuclease activity, producing 5'-phosphomonoesters	3.40E-09	5.54E-08
Down-regulated RBPs	regulation of translation	3.73E-24	5.28E-21
	regulation of cellular amide metabolic process	1.64E-22	1.16E-19
	RNA phosphodiester bond hydrolysis	8.66E-16	4.09E-13
	negative regulation of translation	6.39E-15	2.26E-12
	negative regulation of cellular amide metabolic process	2.91E-14	8.25E-12
	defense response to virus	5.50E-14	1.16E-11
	regulation of mRNA metabolic process	5.75E-14	1.16E-11
	RNA catabolic process	2.03E-13	3.35E-11
	nucleic acid phosphodiester bond hydrolysis	2.13E-13	3.35E-11

	response to virus	7.82E-13	1.11E-10
	cytoplasmic ribonucleoprotein granule	1.91E-12	2.15E-10
	ribonucleoprotein granule	3.97E-12	2.23E-10
	P-body	3.38E-08	1.06E-06
	CCR4-NOT complex	3.78E-08	1.06E-06
	ribosome	7.18E-08	1.62E-06
	ribosomal subunit	1.84E-07	3.45E-06
	organellar ribosome	8.05E-07	1.13E-05
	mitochondrial ribosome	8.05E-07	1.13E-05
	organellar large ribosomal subunit	1.03E-06	1.17E-05
	mitochondrial large ribosomal subunit	1.03E-06	1.17E-05
	catalytic activity, acting on RNA	2.76E-22	4.27E-20
	single-stranded RNA binding	8.03E-20	6.21E-18
	double-stranded RNA binding	2.21E-18	1.14E-16
	ribonuclease activity	3.98E-14	1.40E-12
	mRNA 3'-UTR binding	4.52E-14	1.40E-12
	nuclease activity	9.97E-12	2.57E-10
	mRNA 3'-UTR AU-rich region binding	3.46E-10	7.65E-09
	AU-rich element binding	6.16E-10	1.19E-08
	translation regulator activity	7.19E-09	1.24E-07
	endonuclease activity	1.64E-08	2.53E-07