Supplemental Material – Table S3.
RNA-related Cellular Functions Enriched in the Regulatory Network *(Fig.2A)***.**

Gene Ontology Term[1]		p_{BH} [2]
GO:0003723	RNA binding	1.1×10^{-16}
GO:0003676	nucleic acid binding	6.3×10^{-9}
GO:0005634	nucleus	1.5×10^{-6}
GO:0010467	gene expression	1.6×10^{-4}
GO:0030530	hnRNP complex	4.0×10^{-4}
GO:0008380	RNA splicing	8.7×10^{-4}
GO:0006396	RNA processing	0.0010
GO:0006397	mRNA processing	0.0017
GO:0016071	mRNA metabolic process	0.0031
GO:0005730	nucleolus	0.0193
GO:0005840	ribosome	0.0275
GO:0016070	RNA metabolic process	0.0517

Notes:

1 Enrichment of RNA-related Gene Ontology (GO) terms among human proteins in the regulatory network, discovered by DAVID analysis (ref. 26).

2 Significance estimated by Benjamini-Hochberg test for false discovery (p_{BH}).