

Table S6. GO analyses of upregulated mRNAs in the ceRNA network

id	term	category	p Value	Enrichment _score	Gene
GO:0050974	detection of mechanical stimulus involved in sensory perception	BP	0.000	35.44	ASIC2; SERPINE2; PIEZO2
GO:0030198	extracellular matrix organization	BP	0.000	3.94	COL5A2; COL10A1; ITGA4; DMP1; EGFL6; COL11A1; ADAMTS9; FBN2; MATN3; ICAM5; LAMA1; PRDX4; NDNF; CRISPLD2; COL27A1
GO:0051127	positive regulation of actin nucleation	BP	0.000	21.26	FMN1; SCIN; MAGEL2
GO:0001501	skeletal system development	BP	0.000	4.53	COL5A2; COL10A1; RUNX2; PAPSS2; SH3PXD2B; MEPE; CDH11; ADAMTS4; MATN3; GDF11; ALX4
GO:0032956	regulation of actin cytoskeleton organization	BP	0.000	6.70	CDK10; EPHA5; SH3BP1; EFNA5; VANGL2; ARHGEF19; SIGLEC15
GO:0097264	self proteolysis	BP	0.000	17.72	TENM2; TENM3; TENM4

GO:0050861	positive regulation of B cell receptor signaling pathway	BP	0.000	17.72	LYN; NFAM1; CMTM3
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.000	4.81	LYN; LTK; GRAP; MATK; TEC; INSR; DOK5; GRAPL
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	BP	0.000	5.91	SMAGP; TENM2; TENM3; CADM1; JAML; TENM4
GO:0032793	positive regulation of CREB transcription factor activity	BP	0.000	10.63	LRP8; PRKD2; EPHA5
GO:0005886	plasma membrane	CC	0.000	1.58	ADORA2A; CACNA1D; CACNA1E; ITGA4; BMF; RGS10; RHBDF2; LSP1; LRP8; SH3KBP1; SMAGP; ELMO1; TRO; SLC4A8; CD68; GLRA3; PRKD2; TENM2; SIRPB1; MCC; ASIC2; CADM1; JAML; OBSCN; GNG4; TENM4; FMN1; LYN; SCIN; CCR2; CEP55; DPEP1;

GO:0005887	integral component of plasma membrane	CC	0.000	1.78	ADORA2A; LRRC55; SMAGP; TRO; SLC4A8; GLRA3; TENM2; TENM3; TMEM150C; SIRPB1; ASIC2; CADM1; TENM4; SLC6A6; LTK; CEMIP2; MFSD2A; RASGRP3; SLCO2B1; LPAR6; TPBG; SLC1A3; TRPV4; SLC4A10; CNPY2; TFR2; LRRC8E; CALCRL;
GO:0005578	proteinaceous extracellular matrix	CC	0.000	2.74	COL10A1; LRRC55; DMP1; MEPE; EMID1; ADAMTS9; ADAMTS4; LRRN1; COL24A1; FBN2; MATN3; OMD; LAMA1; LRFN1; NDNF; CRISPLD2
GO:0032045	guanyl-nucleotide exchange factor complex	CC	0.000	10.63	ELMO1; RASGRP3; KNDC1

GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	CC	0.000	4.43	LYN; KCNAB2; STAC3; GRAP; MATK; TEC; GRAPL
GO:0043204	perikaryon	CC	0.000	3.58	PDE9A; GLRA3; CPNE5; NAIP; KNDC1; EFNA2; CNTNAP2; RTN4RL1; RTN4RL2
GO:0005581	collagen trimer	CC	0.000	4.73	COL10A1; EMID1; COL24A1; FCN1; C1QTNF6; COLEC12
GO:0005912	adherens junction	CC	0.000	4.52	FMN1; TRPV4; FRMD4A; SH3BP1; EFNA5; FRMD4B
GO:0005856	cytoskeleton	CC	0.001	2.13	KAZN; SH3KBP1; FGD3; KCNAB2; SSH2; ARHGAP39; FRMD4A; SHROOM2; MAP2K6; TEC; FRMD4B; APBB1IP; TMSB10; COTL1; SPIRE2; CDC42EP5; NEK8

GO:0043005	neuron projection	CC	0.001	2.47	SH3KBP1; SLC4A8; TENM2; TENM3; TENM4; STMN1; SLC1A3; STON2; CPNE5; NAIP; CYGB; RTN4RL2
GO:0070915	lysophosphatidic acid receptor activity	MF	0.000	35.44	LPAR6; LPAR4; LPAR3
GO:0005201	extracellular matrix structural constituent	MF	0.000	6.03	COL5A2; MEPE; COL11A1; COL24A1; FBN2; MATN3; LAMA1; COL27A1
GO:0050839	cell adhesion molecule binding	MF	0.000	6.70	ITGA4; SMAGP; TENM2; TENM3; CADM1; JAML; TENM4
GO:0046875	ephrin receptor binding	MF	0.000	8.86	LYN; PIK3CG; EFNA2; EFNB3; EFNA5
GO:0004715	non-membrane spanning protein tyrosine kinase activity	MF	0.000	5.91	PRAG1; LYN; GRAP; MATK; TEC; GRAPL
GO:0008301	DNA binding, bending	MF	0.000	8.86	TOP2A; LEF1; HMGB3
GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	MF	0.000	8.86	DPEP1; LEF1; NAIP
GO:0004714	transmembrane receptor protein tyrosine kinase activity	MF	0.000	8.18	LTK; EPHB4; INSRR

GO:0008237	metallopeptidase activity	MF	0.000	4.34	ANPEP; CNDP2; ADAM28; ADAMTS9; ADAMTS4; ENPEP
GO:0008569	ATP-dependent microtubule motor activity, minus-end-directed	MF	0.001	7.09	DNAH14; DNAH8; KIF25