

**Table S7. GO analyses of downregulated mRNAs in the ceRNA network**

id	term	category	p Value	Enrichment _score	Gene
GO:0090131	mesenchyme migration	BP	0.000	19.15	ACTA2; ACTG2; ACTC1
GO:0009952	anterior/posterior pattern specification	BP	0.000	5.39	EMX2; TGFBR1; HOXB3; HOXB2; HOXB5; MSX1; HOXC6; HOXA7; HOXC9; HOXC11; HOXC4; HOXC10; HOXA10; HOXB6; HOXA5; HOXC8; HOXA6; HOXA3
GO:0006936	muscle contraction	BP	0.000	4.61	CACNA1H; TPM1; SORBS1; TACR2; CKMT2; SLC8A1; ACTA2; SLC6A8; TRDN; TPM2; SLMAP; SNTA1; CALD1; MYL9; TLN1; LMOD1; GNAO1; MYL6; ITGA1
GO:0002027	regulation of heart rate	BP	0.000	8.21	SLC8A1; PDE4D; BVES; POPDC2; ANK2; EPAS1; SNTA1; DMD; GPD1L
GO:0007507	heart development	BP	0.000	3.68	CACNA1C; CC2D2A; PDLIM3; RBM20; TGFB2; SHOX2; BVES; HDAC9; NTRK3; ARMC4; SRF; TGFBR1; KCNAB1; CRIP1; ITGA3; KCNJ8; FOXL1; HEXIM1; ALPK3; HAND2
GO:0060065	uterus development	BP	0.000	15.32	TGFB2; MYOCD; HOXA10; SRC

GO:0007517	muscle organ development	BP	0.000	4.32	CACNA1H; UNC45A; MRAS; AEBP1; ITGA7; SPEG; BVES; SMTN; MKX; USP2; ITGB1BP2; MSX1; DMD; LAMA5
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	BP	0.000	9.57	ATP1A2; CACNA1C; SLC8A1; ANK2; PLN; DMD
GO:0030878	thyroid gland development	BP	0.000	9.57	TGFB2; THRA; SRF; HOXB3; HOXA5; HOXA3
GO:0002576	platelet degranulation	BP	0.000	4.00	ALDOA; ACTN1; FLNA; ITIH4; LEFTY2; PCDH7; ACTN4; ITIH3; PDGFA; WDR1; TLN1; HABP4; CDC37L1; APOOL
GO:0030018	Z disc	CC	0.000	6.45	CACNA1C; ATP2B4; LDB3; ACTN1; SYNPO; FLNA; SLC8A1; PDLIM3; NOS1AP; FLNC; PPP1R12A; DST; SORBS2; SYNC; PALLD; PPP1R12B; NEXN; FBXO32; FHOD3; SYNPO2; ITGB1BP2; ACTN4; AHNAK2; ANK2; MYOM1; DMD; DNAJB6; MYOZ2; PARVA; JPH2; PGM5; FBXL22

GO:0005925	focal adhesion	CC	0.000	3.41	NFASC; ZYX; ILK; FBLIM1; SORBS1; DIXDC1; ACTB; ACTN1; CORO1C; FLNA; FLNC; FBLN7; NHS; LIMS2; PPP1R12A; DST; SORBS2; ANXA6; FHL1; PALLD; NEXN; KLF11; CSRP1; PIP5K1C; GNA12; SYNPO2; CNN1; TNS1; ACTN4; SVIL; CSPG4; ITGA3; SDC4; VASP; VCL; ACTC1; PDLIM7; RRAS; TLN1; RSU1; NCKAP1; RAB21; TES; PARVA; PGM5; ITGA1; ENAH
GO:0001725	stress fiber	CC	0.000	7.47	ZYX; ILK; TPM1; FBLIM1; SORBS1; ROR1; ACTB; ACTN1; ACTA2; MYH10; DAAM1; SYNPO2; ACTN4; PDLIM7; PGM5; ENAH

GO:0015629	actin cytoskeleton	CC	0.000	3.76	ALDOA; PDLIM5; SPTB; ACTB; CORO1C; SYNPO; FLNA; PDLIM3; ACTA2; PPP1R12A; DST; PALLD; SMTN; CDC42EP3; ARHGAP6; FILIP1; TPM2; SVIL; HSPB7; CORO6; AMPH; VASP; VCL; CALD1; PDLIM7; CAPZA2; MACF1; STK38L; MSRB1; MYOZ2; ENAH
GO:0043034	costamere	CC	0.000	11.26	ILK; FLNC; SVIL; AHNAK2; ANK2; SDC4; VCL; DMD; SYNM; PGM5
GO:0042383	sarcolemma	CC	0.000	5.19	SLC8A1; FLNC; DTNA; SYNC; BVES; SLMAP; POPDC2; AHNAK2; ANK2; SNTA1; VCL; DMD; KCNB1; KCNJ8; SYNM; PGM5

GO:0005886	plasma membrane	CC	0.000	1.39	ADRA1B; ADRA2C; ATP1A2; CACNA1C; CACNB2; GUCY1A2; HTR1B; PTGIR; ATP2B4; NFASC; CACNA1H; CSDE1; FAT3; SH3D19; FAM168B; TTC7B; RAP1A; ZYX; AKTIP; ITM2C; ILK; RGS7BP; CABP1; KCNIP3; SORBS1; TACR2; SLC38A1; SDK1; LRRC4B; DGKG; MYO1C; DMPK; ROR1; STRN3; MRAS; ENTPD1; PRKG1; MRGPRF; ITPR1; ACTB; ACTN1; PLXNA4; FLNA; ARHGEF25; SLC8A1; MICAL3; MAPT; PTGER3; FLNC;
GO:0014069	postsynaptic density	CC	0.000	3.07	CACNA1C; PLCB4; PDLIM5; CABP1; CPEB1; ITPR1; ACTB; SYNPO; NCS1; ANKS1B; CAMK2G; DNAJC6; IGSF9B; MPP2; GRIK5; MAGI2; SYNDIG1; MAP1B; ANK2; DMD; CAP2; MACF1; PJA2; NLGN1; SYT11; SRC
GO:0005884	actin filament	CC	0.000	4.99	TPM1; FLNA; PLS3; PALLD; ARHGAP6; TPM2; DAPK3; ACTC1; LMOD1; RHOQ; GNG12; SRC

GO:0005901	caveola	CC	0.000	5.27	ADRA1B; ATP1A2; ATP2B4; NOS1AP; TRPC4; BVES; TGFBR1; AKAP6; CAVIN1; EHD2; SRC
GO:0033745	L-methionine-(R)-S-oxide reductase activity	MF	0.000	19.15	MSRB3; MSRB2; MSRB1
GO:0003779	actin binding	MF	0.000	3.33	ALDOA; PDLIM5; SPTB; SORBS1; DIXDC1; SYNPO; MICAL3; DST; MICAL1; PALLD; DAAM2; SMTN; MYH10; DAAM1; FHOD3; SYNPO2; CNN1; TNS1; MYO18B; ACTN4; SNTA1; VASP; YWHAH; DMD; CALD1; CAPZA2; CAP2; MACF1; LMOD1; MSRB2; STK38L; MSRB1; MYOZ2; MYO3A; PARVA; SPTBN4; MYLK; PLEKHH2; ENAH
GO:0051015	actin filament binding	MF	0.000	3.86	CACNB2; DSTN; TPM1; SPTB; MYO1C; ACTN1; CORO1C; FLNA; CTNNA3; FLNC; PLS3; NEXN; MYH10; TPM2; MYO1D; ADSSL1; ACTN4; SVIL; CORO6; VCL; MYOM1; WDR1; TLN1; MACF1; SHROOM3

GO:0005516	calmodulin binding	MF	0.000	3.15	CACNA1C; ATP2B4; PNCK; MYO1C; STRN3; SLC8A1; RRAD; AEBP1; WFS1; PDE1C; CAMK2G; MYH10; CFAP221; CNN1; MYO1D; SNTA1; CALD1; AKAP5; GEM; NDUFAF4; SLC8A2; MYO3A; CAMKK1; MAP6; MYLK
GO:0050998	nitric-oxide synthase binding	MF	0.000	10.64	ATP2B4; ACTB; NOS1AP; SNTA1; DMD
GO:0044325	ion channel binding	MF	0.000	3.43	KCNIP3; ACTN1; FLNA; SLC8A1; FHL1; PDE4D; TRDN; KCNAB1; ACTN4; ANK2; SNTA1; YWHAH; AKAP6; KCNB1; RIMS3; GPD1L; SRC
GO:0008307	structural constituent of muscle	MF	0.000	4.91	TPM1; PDLIM3; NEXN; SMTN; TPM2; MYOM1; DMD; MYL9; SYNM; MYL6
GO:0030898	actin-dependent ATPase activity	MF	0.000	9.57	MYO1C; MYH10; MYO1D; MYO3A; MYL6

GO:0045296	cadherin binding	MF	0.000	2.44	ALDOA; UNC45A; FLNA; CTNNA3; PHLDB2; KLC2; TRPC4; LRRFIP1; PFKP; CHMP2B; COBLL1; EHD1; CCT8; MPP7; VASP; VCL; ARHGAP1; CALD1; KIF5B; TLN1; MACF1; TES; PARVA; ESYT2; MICALL1; VASN; ERC1; SRC
GO:0008017	microtubule binding	MF	0.000	2.60	KATNAL1; MTUS2; MAP9; KIF13A; MAPT; DYNC1I1; TRAF3IP1; MAPRE2; REEP1; MAP7D3; CLIP3; SUN2; CLIP1; DNM1L; CCSER2; SGIP1; MAP1B; KIF5B; KIF1C; TPPP; MACF1; MID2; MTCL1; MAP6