

Supplemental Tables:

Supplemental Table 1 GO functional annotation of biological process for miR-198 target

genes

GO ID	GO term	Count (%)	P value	Gene symbol
GO:0007167	enzyme linked receptor protein signaling pathway	20(1.3)	1.82E-10	MTSS1, MPZL1, FUT8, NLK, CBL, MET, SMAD2, PTEN, SRC, etc.
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	15(1.0)	1.23E-08	MTSS1, MPZL1, CBL, MET, PTEN, SRC, NTRK3, DDR1, CTGF, etc.
GO:0006928	cell motion	20(1.3)	4.06E-08	PVR, MTSS1, TLN1, FUT8, FOXJ1, MET, ZEB2, PTEN, SRC, etc.
GO:0016477	cell migration	14(0.9)	1.10E-06	PVR, FUT8, FOXJ1, MET, ZEB2, PTEN, SRC, ULK1, ITGA5, etc.
GO:0042127	regulation of cell proliferation	23(1.5)	1.59E-06	CTBP2, FOXJ1, CSF1, TNFRSF8, CDK6, SMAD2, BCL2L1, CDK4, etc.
GO:0051674	localization of cell	14(0.9)	3.59E-06	PVR, FUT8, FOXJ1, MET, ZEB2, PTEN, SRC, ULK1, ITGA5, etc.
GO:0048870	cell motility	14(0.9)	3.59E-06	PVR, FUT8, FOXJ1, MET, ZEB2, PTEN, SRC, ULK1, ITGA5, etc.
GO:0042325	regulation of phosphorylation	17(1.1)	3.90E-06	CSF1, MET, ZEB2, PTEN, SPDYA, PPP1R9B, SPRY2, YWHAG, etc.
GO:0051174	regulation of phosphorus metabolic process	17(1.1)	6.48E-06	CSF1, MET, ZEB2, PTEN, SPDYA, PPP1R9B, SPRY2, YWHAG, etc.
GO:0019220	regulation of phosphate metabolic process	17(1.1)	6.48E-06	CSF1, MET, ZEB2, PTEN, SPDYA, PPP1R9B, SPRY2, YWHAG, etc.
GO:0006468	protein amino acid	20(1.3)	6.91E-06	NLK, MET, STK17B, CDK6, SMAD2,

	phosphorylation			CDK4, SRC, PAK6, NTRK3, etc.
GO:0045859	regulation of protein kinase activity	14(0.9)	1.26E-05	SPDYA, SPRY2, YWHAG, CDKN2B, CCND2, CSF1, MET, CD4, etc.
GO:0006793	phosphorus metabolic process	24(1.5)	1.46E-05	INPPL1, NLK, MET, STK17B, CDK6, SMAD2, CDK4, PTEN, etc.
GO:0006796	phosphate metabolic process	24(1.5)	1.46E-05	INPPL1, NLK, MET, STK17B, CDK6, SMAD2, CDK4, PTEN, SRC, etc.
GO:0043549	regulation of kinase activity	14(0.9)	1.82E-05	SPDYA, SPRY2, YWHAG, CDKN2B, CCND2, CSF1, MET, CD4, etc.
GO:0051338	regulation of transferase activity	14(0.9)	2.80E-05	SPDYA, SPRY2, YWHAG, CDKN2B, CCND2, CSF1, MET, CD4, etc.
GO:0010033	response to organic substance	19(1.2)	7.07E-05	PPARA, SMAD2, BCL2L1, PTEN, SRC, DDR1, HDAC4, CDKN2B, etc.
GO:0016310	phosphorylation	20(1.3)	8.49E-05	NLK, MET, STK17B, CDK6, SMAD2, CDK4, SRC, PAK6, NTRK3, etc.
GO:0001952	regulation of cell-matrix adhesion	5(0.3)	9.11E-05	DDR1, CSF1, CDK6, THBS1, PTEN
GO:0008285	negative regulation of cell proliferation	13(0.8)	9.32E-05	DDR1, HDAC4, CTBP2, CDKN2B, BTG2, FOXJ1, TNFRSF8, etc.
GO:0032268	regulation of cellular protein metabolic process	14(0.9)	3.18E-04	CSF1, ZEB2, CDK4, HDAC4, PPP1R9B, CCND2, SERPINA5, etc.
GO:0051329	interphase of mitotic cell cycle	7(0.4)	3.19E-04	SPDYA, CDKN2B, CCND2, POLD1, CDK6, BIRC5, CDK4
GO:0051325	interphase	7(0.4)	3.72E-04	SPDYA, CDKN2B, CCND2, POLD1, CDK6, BIRC5, CDK4
GO:0010810	regulation of cell-substrate adhesion	5(0.3)	7.43E-04	DDR1, CSF1, CDK6, THBS1, PTEN
GO:0045860	positive regulation of protein kinase activity	9(0.6)	8.77E-04	SPDYA, CCND2, CSF1, MET, ZEB2, CD4, EGF, THBS1, FRS2

GO:0001932	regulation of protein amino acid phosphorylation	8(0.5)	9.21E-04	PPP1R9B, CCND2, ZEB2, CD4, TNK2, EGF, BMPR1A, CBS
GO:0033674	positive regulation of kinase activity	9(0.6)	1.10E-03	SPDYA, CCND2, CSF1, MET, ZEB2, CD4, EGF, THBS1, FRS2
GO:0022403	cell cycle phase	12(0.8)	1.21E-03	SPDYA, CDKN2B, CCND2, FANCD2, POLD1, CDK6, PAFAH1B1, etc.
GO:0051347	positive regulation of transferase activity	9(0.6)	1.40E-03	SPDYA, CCND2, CSF1, MET, ZEB2, CD4, EGF, THBS1, FRS2
GO:0022402	cell cycle process	14(0.9)	1.62E-03	CDK6, BIRC5, CDK4, RAD52, SPDYA, PPP1R9B, CDKN2B, etc.
GO:0043405	regulation of MAP kinase activity	7(0.4)	1.66E-03	SPRY2, MET, ZEB2, EGF, THBS1, FRS2, CBS
GO:0042327	positive regulation of phosphorylation	6(0.4)	1.76E-03	CCND2, CD4, TNK2, EGF, THBS1, BMPR1A
GO:0010562	positive regulation of phosphorus metabolic process	6(0.4)	2.02E-03	CCND2, CD4, TNK2, EGF, THBS1, BMPR1A
GO:0045937	positive regulation of phosphate metabolic process	6(0.4)	2.02E-03	CCND2, CD4, TNK2, EGF, THBS1, BMPR1A
GO:0051726	regulation of cell cycle	10(0.6)	2.89E-03	SPDYA, PPP1R9B, CDKN2B, CCND2, CDK6, BIRC5, H2AFX, EGF, CDK4, PTEN
GO:0035295	tube development	8(0.5)	3.61E-03	SPRY2, SP1, CTGF, HOXB13, ZEB2, SMAD2, EGF, BMPR1A
GO:0007155	cell adhesion	15(1.0)	3.88E-03	PVR, MTSS1, TLN2, INPPL1, PCDH9, SRC, DDR1, CTGF, etc.
GO:0022610	biological adhesion	15(1.0)	3.93E-03	PVR, MTSS1, TLN2, INPPL1, PCDH9, SRC, DDR1, CTGF, etc.
GO:0008284	positive regulation of cell proliferation	11(0.7)	3.99E-03	SPDYA, HDAC4, CCND2, CSF1, CDK6, BCL2L1, MST1R, EGF, etc.

GO:0032270	positive regulation of cellular protein metabolic process	8(0.5)	4.93E-03	HDAC4, CCND2, CSF1, CD4, TNK2, CDK4, THBS1, BMPR1A
GO:0001701	in utero embryonic development	7(0.4)	4.99E-03	FUT8, SP1, APBA2, SMAD2, BCL2L1, CAPN2, MLL2
GO:0031399	regulation of protein modification process	9(0.6)	4.99E-03	HDAC4, PPP1R9B, CCND2, ZEB2, CD4, TNK2, EGF, BMPR1A, CBS
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	4(0.3)	5.05E-03	PEG10, CDKN2B, SMAD2, THBS1
GO:0042981	regulation of apoptosis	16(1.0)	5.35E-03	CYCS, STK17B, TNFRSF8, BIRC5, BCL2L1, ARHGEF9, PTEN, etc.
GO:0009725	response to hormone stimulus	10(0.6)	5.67E-03	PPARA, BTG2, CCND2, MSI1, SORT1, BCL2L1, PTPN1, THBS1, PTEN, SRC
GO:0010553	negative regulation of specific transcription from RNA polymerase II promoter	4(0.3)	5.81E-03	HDAC4, PPARA, FOXJ1, NCOR2
GO:0043067	regulation of programmed cell death	16(1.0)	5.85E-03	CYCS, STK17B, TNFRSF8, BIRC5, BCL2L1, ARHGEF9, PTEN, etc.
GO:0010941	regulation of cell death	16(1.0)	6.05E-03	CYCS, STK17B, TNFRSF8, BIRC5, BCL2L1, ARHGEF9, PTEN, etc.
GO:0051247	positive regulation of protein metabolic process	8(0.5)	6.18E-03	HDAC4, CCND2, CSF1, CD4, TNK2, CDK4, THBS1, BMPR1A
GO:0044093	positive regulation of molecular function	13(0.8)	6.19E-03	SPDYA, HDAC4, VCP, CCND2, FOXJ1, CSF1, CYCS, MET, etc.
GO:0019058	viral infectious cycle	4(0.3)	6.64E-03	CTBP2, PVRL2, CD4, HMGA1
GO:0043085	positive regulation of catalytic activity	12(0.8)	6.88E-03	SPDYA, VCP, CCND2, FOXJ1, CSF1, MET, CYCS, ZEB2, CD4, EGF, etc.
GO:0006915	apoptosis	13(0.8)	7.62E-03	PEA15, PEG10, VCP, BAG3, CYCS, STK17B, TNFRSF18, BIRC5, etc.

GO:0030155	regulation of cell adhesion	6(0.4)	7.71E-03	DDR1, CSF1, CDK6, THBS1, PTEN, SRC
GO:0009952	anterior/posterior pattern formation	6(0.4)	8.43E-03	HOXA1, BTG2, ZEB2, SMAD2, FRS2, BMPR1A
GO:0012501	programmed cell death	13(0.8)	8.52E-03	PEA15, PEG10, VCP, BAG3, CYCS, STK17B, TNFRSF18, BIRC5, etc.
GO:0014902	myotube differentiation	3(0.2)	8.77E-03	SORT1, ADAM12, CAPN2
GO:0032582	negative regulation of gene-specific transcription	4(0.3)	9.01E-03	HDAC4, PPARA, FOXJ1, NCOR2

Note: GO, Gene Ontology.

Supplemental Table 2 GO functional annotation of cellular component for miR-198 target

genes.

GO ID	GO term	Count (%)	P value	Gene symbol
GO:0043233	organelle lumen	34(2.2)	5.11E-06	POLR2E, HOXB13, DGCR8, GPSM2, CD4, H2AFX, OGT, THBS1, etc.
GO:0031974	membrane-enclosed lumen	34(2.2)	7.82E-06	POLR2E, HOXB13, DGCR8, GPSM2, CD4, H2AFX, OGT, THBS1, etc.
GO:0031981	nuclear lumen	29(1.9)	1.07E-05	POLR2E, HOXB13, DGCR8, GPSM2, H2AFX, OGT, MYB, NOVA1, etc.
GO:0005829	cytosol	26(1.7)	5.67E-05	TLN1, INPPL1, CBL, CYCS, BIRC5, SMAD2, BCL2L1, ARHGEF9, etc.
GO:0070013	intracellular organelle lumen	31(2.0)	6.56E-05	POLR2E, HOXB13, DGCR8, GPSM2, CD4, H2AFX, OGT, MYB, etc.
GO:0001726	ruffle	6(0.4)	2.19E-04	MTSS1, TLN1, TLN2, ITGA5, ARHGAP1, CDK6
GO:0005886	plasma membrane	49(3.1)	3.18E-04	PVR, HDLBP, TLN1, MPZL1, MSR1, TLN2, CSF1, HFE, TNFRSF8, etc.
GO:0005654	nucleoplasm	18(1.2)	8.06E-04	CTBP2, ADARB1, POLR2E, HOXB13, SMAD2, DACH1, RAD52, CDK4, etc.
GO:0005901	caveola	5(0.3)	8.60E-04	CBL, SLC2A1, CACNA1C, SRC, BMPR1A
GO:0031252	cell leading edge	7(0.4)	9.53E-04	MTSS1, TLN1, TLN2, ITGA5, ARHGAP1, CDK6, PAFAH1B1
GO:0015629	actin cytoskeleton	9(0.6)	1.66E-03	PPP1R9B, MTSS1, TLN2, INPPL1, STK17B, SPTBN1, MST1R, BMF, TPM3
GO:0000307	cyclin-dependent protein	3(0.2)	3.50E-03	CCND2, CDK6, CDK4

	kinase holoenzyme complex			
GO:0008287	protein serine/threonine phosphatase complex	4(0.3)	4.27E-03	SPDYA, PPP1R9B, CYCS, PPP2R5E
GO:0044459	plasma membrane part	30(1.9)	5.20E-03	TLN1, MPZL1, MSR1, TLN2, HFE, BCL2L1, SRC, CNR1, SLC2A1, etc.
GO:0044451	nucleoplasm part	12(0.8)	5.81E-03	SPDYA, HDAC4, CTBP2, POLR2E, HOXB13, SMAD2, DACH1, OGT, etc.
GO:0045121	membrane raft	6(0.4)	6.45E-03	CBL, SLC2A1, CD4, CACNA1C, SRC, BMPR1A
GO:0005938	cell cortex	6(0.4)	7.03E-03	PPP1R9B, INPPL1, GPSM2, SPTBN1, PAFAH1B1, MAPRE1
GO:0030863	cortical cytoskeleton	4(0.3)	7.55E-03	PPP1R9B, INPPL1, SPTBN1, MAPRE1
GO:0005881	cytoplasmic microtubule	3(0.2)	9.39E-03	PAFAH1B1, BIRC5, MAPRE1

Note: GO, Gene Ontology.

Supplemental Table 3 GO functional annotation of molecular function for miR-198 target

genes.

GO ID	GO term	Count (%)	P value	Gene symbol
GO:0019899	enzyme binding	21(1.3)	1.55E-08	NLK, BIRC5, SMAD2, HMGA1, SPDYA, HDAC4, PPP1R9B, etc.
GO:0019904	protein domain specific binding	13(0.8)	2.54E-05	PPARA, MTSS1, TLN1, YWHAG, FUT8, VCP, INPPL1, NLK, etc.
GO:0004672	protein kinase activity	16(1.0)	1.94E-04	PAK6, NTRK3, DDR1, POLR2E, ULK1, NLK, MET, NEK8, etc.
GO:0017124	SH3 domain binding	6(0.4)	1.38E-03	MTSS1, FUT8, INPPL1, CBL, ARHGAP1, ADAM12
GO:0004713	protein tyrosine kinase activity	7(0.4)	2.99E-03	NTRK3, DDR1, MET, TNK2, MST1R, MAP2K7, SRC
GO:0019900	kinase binding	7(0.4)	4.33E-03	SPDYA, YWHAG, CDKN2B, CCND2, SLC2A1, CD4, MAP2K7
GO:0032403	protein complex binding	7(0.4)	6.70E-03	ULK1, ITGA5, CTGF, SPTBN1, PTPN1, THBS1, FRS2
GO:0004857	enzyme inhibitor activity	8(0.5)	8.43E-03	PPP1R9B, YWHAG, CDKN2B, SERPINF2, SERPINA5, BIRC5, BCL2L1, TNK2
GO:0019901	protein kinase binding	6(0.4)	8.53E-03	SPDYA, YWHAG, CDKN2B, CCND2, CD4, MAP2K7

Note: GO, Gene Ontology.