

Supplementary Table 2A. Negative correlations involving differentially expressed miRNAs between pPCL and MM patients and putative target transcripts

microRNA ^a	RefSeq ID	Gene symbol ^b	No. of algorithms predicting the target gene	Correlation coefficient	microRNA ^a	RefSeq ID	Gene symbol ^b	No. of algorithms predicting the target gene	Correlation coefficient
	NM_001001342	BLOC1S2*	5	-0.52		NM_020918	GPAM*	7	-0.58
	NM_173809	BLOC1S2*	5	-0.52		NM_016395	PTPLAD1*	5	-0.62
	NM_014661	FAM63B*	5	-0.53		NM_003617	RGS9*	6	-0.54
<i>hsa-lei-7a</i>	NM_001017368	RFEL*	5	-0.57		NM_003262	SEC62*	5	-0.54
	NM_057178	RFEL*	5	-0.57		NM_001859	SLC31A1*	5	-0.59
	NM_006290	TNFAIP3*	5	-0.54		NM_017919	STX11*	5	-0.54
<i>hsa-miR-1224-5p</i>	NM_017896	C20orf11	5	-0.53	hsa-miR-330-3p	NM_018837	SULF2*	5	-0.62
	NM_007032	TRIOBP	5	-0.56		NM_198596	SULF2*	5	-0.62
	NM_000962	PTGS1	5	-0.54		NM_006956	ZNF12	5	-0.53
	NM_080591	PTGS1	5	-0.54		NM_016265	ZNF12	5	-0.53
	NM_181701	OSOX2	5	-0.57		NM_001042510	ZNF706*	6	-0.55
hsa-miR-125b	NM_001040454	SLC26A6	5	-0.57		NM_001042511	ZNF706*	6	-0.55
	NM_022911	SLC26A6	5	-0.57		NM_016096	ZNF706*	6	-0.55
	NM_022918	TMEM135*	6	-0.52		NM_001083314	CHMP1A*	5	-0.59
<i>hsa-miR-139-3p</i>	NM_015651	PHF19*	5	-0.53		NM_002768	CHMP1A*	5	-0.59
	NM_004717	DGKI*	5	-0.52	<i>hsa-miR-370</i>	NM_003901	SGPL1	5	-0.52
hsa-miR-140-5p	NM_006699	MAN1A2*	6	-0.52		NM_007032	TRIOBP	5	-0.57
	NM_004232	SOC34*	5	-0.58		NM_004231	ATP6V1F*	5	-0.69
hsa-miR-18a	NM_153686	LCORL	5	-0.59		NM_014275	MGAT4B*	5	-0.56
	NM_003328	TYX	5	-0.53	<i>hsa-miR-423-5p</i>	NM_054013	MGAT4B*	5	-0.58
	NM_00107701	MIER1	5	-0.52		NM_020679	MIF4GD*	5	-0.53
hsa-miR-19a	NM_00107703	MIER1	5	-0.52		NM_000262	NAGA	5	-0.52
	NM_020948	MIER1	6	-0.52		NM_001042368	RALGDS*	5	-0.56
	NM_001042546	ATPAF1*	5	-0.52		NM_006266	RALGDS*	5	-0.56
	NM_022745	ATPAF1*	5	-0.52		NM_003564	TAGLN2*	5	-0.53
	NM_138426	GLCCI1*	5	-0.59		NM_001031695	RBM9*	5	-0.54
hsa-miR-21	NM_001013406	KRIT1*	5	-0.54	hsa-miR-464	NM_001082576	RBM9*	5	-0.54
	NM_004912	KRIT1*	7	-0.54		NM_001082577	RBM9*	5	-0.54
	NM_194454	KRIT1*	7	-0.54		NM_001082578	RBM9*	5	-0.54
	NM_194455	KRIT1*	6	-0.54		NM_004232	SOC34*	5	-0.52
	NM_194456	KRIT1*	7	-0.54		NM_030884	MAP4*	5	-0.52
	NM_000125	ESR1	6	-0.52		NM_001025247	TAF5L*	5	-0.55
<i>hsa-miR-222</i>	NM_002862	PYGB	5	-0.53		NM_005112	WDR1*	5	-0.52
	NM_015374	SUN2*	5	-0.56		NM_017491	WDR1*	5	-0.52
<i>hsa-miR-223</i>	NM_005909	MAP1B	5	-0.55	hsa-miR-628-5p	NM_001083962	TCF4*	5	-0.61
	NM_001105	ACVR1*	7	-0.52		NM_001119	ADD1	5	-0.52
	NM_001080433	CCDC85A	6	-0.52		NM_014189	ADD1	5	-0.52
hsa-miR-301a	NM_001031695	RBM9*	5	-0.53		NM_014190	ADD1	5	-0.52
	NM_001082576	RBM9*	5	-0.53		NM_00109571	CADPS2	5	-0.56
	NM_001082578	RBM9*	5	-0.53		NM_002508	NID1	5	-0.56
	NM_014309	RBM9*	5	-0.53		NM_017896	C20orf11	5	-0.55
	NM_004799	ZFYVE9*	5	-0.52		NM_000195	HPS1*	5	-0.52
	NM_001105	ACVR1*	6	-0.52		NM_030927	TSPAN14*	6	-0.53
hsa-miR-301b	NM_018638	ETNK1*	5	-0.54		NM_004309	ARHGDI4*	5	-0.54
	NM_003705	SLC25A12	5	-0.52		NM_014146	LAT2	5	-0.53
	NM_174916	UBR1*	5	-0.52		NM_032463	LAT2	5	-0.53
	NM_198401	ANKRD46*	5	-0.62		NM_022763	FNDC3B	6	-0.53
	NM_032012	C9orf8*	5	-0.60		NM_001023570	IOCB1*	5	-0.54
	NM_144718	CCDC52*	5	-0.54		NM_001023571	IOCB1*	5	-0.54
hsa-miR-330-3p	NM_001008493	ENAH	6	-0.58		NM_014766	SCRN1	5	-0.56
	NM_018212	ENAH	6	-0.58		NM_052931	SLAMF6*	6	-0.52
	NM_182705	FAM107B*	5	-0.55		NM_152527	SLC16A14	6	-0.57

^aUp-regulated miRNAs in pPCL are in bold, down-regulated miRNAs in pPCL are in italic. ^bDifferentially expressed genes between the same pPCL and MM samples (SAM, q-value=0) are marked with an asterisk.

Supplementary Table 2B. Most significant GO Biological Processes

GO Term	Target genes	%*	P
negative regulation of protein complex disassembly	<i>TRIOBP, MAP1B, MAP4, ADD1</i>	5.80%	0.001
regulation of protein complex disassembly	<i>TRIOBP, MAP1B, MAP4, ADD1</i>	5.80%	0.001
negative regulation of cytoskeleton organization	<i>TRIOBP, MAP1B, MAP4, ADD1</i>	5.80%	0.001
negative regulation of cellular component organization	<i>TRIOBP, MAP1B, MAP4, ARHGDI1A, ADD1</i>	7.25%	0.002
negative regulation of organelle organization	<i>TRIOBP, MAP1B, MAP4, ADD1</i>	5.80%	0.004
negative regulation of cellular process	<i>IQCB1, TRIOBP, PTGS1, MAP1B, ESR1, SOCS4, RBM9, CHMP1A, RGS5, MAP4, TCF4, TNFAIP3, ARHGDI1A, ACVR1, ADD1</i>	21.74%	0.004
establishment of localization in cell	<i>SLC25A12, ENAH, LAT2, CADPS2, ZFYVE9, STX17, SCRNI, SUN2, RFFL, SEC62</i>	14.49%	0.006
negative regulation of biological process	<i>IQCB1, TRIOBP, PTGS1, MAP1B, ESR1, SOCS4, RBM9, CHMP1A, RGS5, MAP4, TCF4, TNFAIP3, ARHGDI1A, ACVR1, ADD1</i>	21.74%	0.01
cellular localization	<i>SLC25A12, ENAH, LAT2, CADPS2, ZFYVE9, STX17, SCRNI, SUN2, RFFL, SEC62</i>	14.49%	0.01
regulation of cytoskeleton organization	<i>TRIOBP, MAP1B, MAP4, ADD1</i>	5.80%	0.017
barbed-end actin filament capping	<i>TRIOBP, ADD1</i>	2.90%	0.020
regulation of protein polymerization	<i>TRIOBP, MAP1B, ADD1</i>	4.35%	0.030
N-glycan processing	<i>MGAT4B, MANTA2</i>	2.90%	0.035
estrogen receptor signaling pathway	<i>ESR1, RBM9</i>	2.90%	0.043
regulation of protein complex assembly	<i>TRIOBP, MAP1B, ADD1</i>	4.35%	0.050

*% indicates the percentage of target genes in the class relative to the total number of target genes.