

Table S3. Lists the predicted targets among a large number of target genes

	p-value	Fold-change	UniqueID	target genes
1	0.0013755	105.5973394	hsa-miR-141	ACVR2B OAS2 VEZATIN
2	0.001418	70.01919698	hsa-miR-106a	TP53 HMGA2 KIAA0140 KIAA1196 KYNU
3	0.0034795	21.09042579	hsa-miR-200c	HMGA2 LYPLA2 LIN28B HRG22
4	4.40E-05	19.34663909	hsa-miR-96	PAPSS2 ARID3B LYPLA2
5	0.0002087	14.42281388	hsa-miR-378	OAS2 TP53 PAPSS2 KIAA0140 EMG1 LYPLA2 IQSEC2 KIAA1196 C14orf28 HRG22
6	0.006384	8.015188465	hsa-miR-604	TP53 PAPSS2 KIAA0140 RNF44 IQSEC2 KIAA1196 CTF D8 HRG22
7	0.0003038	7.806894621	hsa-miR-183	LYPLA2 IQSEC2 DLL1 D8
8	0.0004779	5.516431715	hsa-miR-107	ACVR2B OAS2 KIAA0140 LYPLA2 RNF44 DLL1 VEZATIN KIAA1196 TMPRSS3
9	0.0005951	4.955597325	hsa-miR-182*	
10	0.0004927	4.826474722	hsa-miR-182	OAS2 VEZATIN HRG22
11	3.70E-06	0.015905031	hsa-miR-299-5p	FAR1 RFX5 NAV3 PPP2R5A ENSG00000206323 CALU GOLGA1 SIAH1 ZDHC5 DST SP1 TARDBP FAM3B GNPTG
12	0.0005116	0.015549239	hsa-miR-134	TP53 IQSEC2 KIAA1196 HRG22
13	1.00E-07	0.014620055	hsa-miR-370	ACVR2B OAS2 HMGA2 PAPSS2 KIAA0140 ARID3B LYPLA2 RNF44 IQSEC2 DLL1 KIAA1196 TMPRSS3 LIN28B D8 HRG22
14	0.00304	0.01457168	hsa-miR-487b	GLCCI1 SNAP91 MYST4 AGA PCF11 RBM34 ZMYND8 EFHD2 C4ORF32 LY6G5B,CSNK2B CLIP1 DIABLO PAK7 ALDH1A3 16ORF68
15	4.03E-05	0.014021525	hsa-miR-379	ACVR2B VEZATIN C14orf28 LIN28B
16	2.40E-06	0.013965383	hsa-miR-655	INO80D RBMY2FP POU2F1 ZNF521 CPEB3 TBC1D3I,TBC1D3G CUGBP2 ADAMTS6 GPR162 CD47 C8ORF37 RBM26 SAMD12 DRGX C11ORF58
17	0.0004876	0.013661893	hsa-miR-409-3p	ACVR2B
18	6.17E-05	0.013622244	hsa-miR-494	ZNF207 RBM4B C5ORF32 NOVA1 ARHGAP5 LIF ENSG00000196908 C9ORF122 ZC3H7A ENSG00000204914 CXXC4 ENSG00000204917 SOCS6 MACC1
19	1.67E-05	0.012826702	hsa-miR-432	CALB2 OAS2 HMGA2 KYNU RNF44 IQSEC2 DLL1 VEZATIN KIAA1196 TMPRSS3 C14orf28 HRG22
20	0.0001018	0.008957157	hsa-miR-411	