Supplementary Table S3:

Putative binding sites of the miR-338-5p and miR-421 for the indicated target genes, related to **Fig. 3**, **4** and **5**. List of predicted miR-338-5p and miR-421 binding sites on the 3' UTR of the indicated target genes, as detected by miRanda (http://www.microrna.org), where mirSVR score predicts the strength of interaction between miRNA and target gene.

Sn. No.	Gene	MiR-338-5p binding site	mirSVR score	MiR-421 binding site	mirSVR score
1.	CDK1	3'gugaGUCGUGGUCCUAU - AACAa 5' : 25: 5' guuaUAUCAACA - GAUAGUUGUg 3'	-1.0732		
2.	CDK6	3' guGAGUCGU GGUCCUAUAACAa 5' : : : 2860: 5' cuCAUAGCAAGUUAAAAUAUUGUg 3'	-0.0060	3' cgcggGUUAAUUACAGACAACUa 5' : 7944: 5' gggaaCAGGCAGU- ACUGUUGAg 3'	-0.0010
	CDK6	3'guGAGU -CGUGGUCCUAUAACAa 5' : : 4067: 5' ucUUUAUGAACAAUAUAUUGUa 3'	-0.0423	3' cgcGGGUUAAUUACAGACAACUa 5' : : 9942: 5' uuuUUCAA AAUUGGUGUUGAa 3'	-0.0006
3.	МСМЗ	3' gugagucgugguccUAUAACAa 5' : 481: 5' guuaaggugaauauGUAUUGUa 3'	-0.0678	3' cgcggguuaauuacagACAACUa 5' 525: 5' agaugaauauccgagaUGUUGAa 3'	-0.0616
4.	МСМ10	3' gugagucgugguccuAUAACAa 5' 1146: 5' guaaauugguuggaauUAUUGUa 3'	-0.0710	3' cgCGGGUUAAUUACAGAC - AACUa 5' : : 74: 5'uuGUCC - AUUGAUUCCUGAUUGAc 3'	-0.1004
	МСМ10	3'gugAGUCGU- GGU CCUAUAACAa 5' : : 1669: 5' cagUCAGUAUUCACGUGUAUAUUGUu 3'	-0.6754	3' cgcggguuAAUUACAGACAACUa 5' : 1107: 5'auuugaccUAAGUGAAUGUUGAu 3'	-0.0127
5.	CCNA2			3' cgcggguuaauuacagACAACUa 5' 1130: 5' agcaaaccucuauaagUGUUGAg 3'	-0.0657
6.	CCNE2	3' gugagucgugguccuAUAACAa 5' 1203: 5' aagaaacuauacauuUAUUGUu 3'	-0.0323		
7.	EPCAM	3' guGAGUCGUGGUCCUAU-AACAa 5' : : : 104: 5' agUUUAACAUCA - UAUAUUUGUa 3'	-1.2590		
8.	c-Kit	3' gugaGUCGUGGUCCUAUA-ACAa 5' : 1087: 5'gggcCAGUAUCUAUAUAUGUGUa 3'	-0.8710	3' cgcgggUUAAUUACAGAC-AACUa 5' 	-0.4369
	c-Kit	3' gugagucgugguccUAUAACaa 5' 1937: 5'ggcuuuuuuuguaaAUAUUGaa 3'	-0.2657	3′ cgcGGGUUAAUUACA GACAACUa 5′ : : : : 2091: 5′ auuCCUGUAUGUUGUCCAAUUGUUGAc 3′	-0.0291
9.	SOX2	3' gugagucgugguccuAUAACAa 5' 899: 5'auauuucuguaaauuUAUUGUg3'	-0.4237		
10.	SOX9	3' guGAGUCGUGGUCCUAUAACAa 5' : : 1491: 5' cuUUGGGCUGCCUUAUAUUGUg 3'	-0.1917	3' cgcggguuaauuacAGACAACua 5' 1226: 5' aaaggguauggucaUCUGUUGuu 3'	-0.1024
	SOX9	3' gugagucgugguccuAUAACAa 5' 1981: 5' uuuuuuuuuguauauUAUUGUu 3'	-0.2106	3' cgcGGGUUAAUUACAGACAACUa 5' : : : : : 1376: 5' uuuCUUUGUU-GUUUUUGUUGAa 3'	-0.0908
11.	ABCG2	3' gugAGU-CGUGGUCCUAUAA- CAa 5' 	-0.3691		
12.	TET1	3' gugagucgugguccuAUAACAa 5' : 655: 5' auaguauaagaauccUAUUGUc 3'	-0.0772	3' cgcgggUUAAUUACAGACAACUa 5' : 1126: 5' agaaaaAAAAAAUUCUUGUUGAa 3'	-0.0497
	TET1	3'guGAGUCGU-GGUCCUAU-AACAa 5' : 1083: 5'aaCUAAGUAGACA-GAUAUUUGUa 3'	-0.3136	3' cgcgggUUAAUUACAGACAACUa 5' : : 1763: 5' caaguaGAUUUCUGCUUGUUGAa 3'	-0.0435

Sn. No.	Gene	MiR-338-5p binding site	mirSVR score	MiR-421 binding site	mirSVR score
13.	SUZ12	3' guGAGUCGUGGUCCUAU - AACAa 5' : 124: 5' auUUCA ACAAGGAUAUUUGUa 3'	-0.6815	3' cgcgggUUAAUUACAGACAACUa 5' 1775: 5'uaauaaAAUUACU-UCUGUUGAg 3'	-1.2313
	SUZ12	3' gugAGUCGUGG - UCCUAUAACaa 5' : :: 1172: 5' uuaUUAUCCUUAAAGAUAUUGca 3'	-0.3337	3' cgcGGGUUAAUUACAGAC - AACUa 5' :: 1775: 5'uucUUCAUCUUAUGCCUGUUUGAg 3'	-0.5071
14.	AEBP2	3'gugagucguggUCCUAUAACAa 5' 582: 5' aauaauauugaAGGAUAUUGUa 3'	-0.5066	3' cgcGGGUUAA UUACAGA - CAACUa 5' : : : 2436: 5' guuUUCGAUUCCUUUGUCUAGUUGAc 3'	-0.2690
	AEBP2	3' gugagucgugguccUAUAACAa 5' : 423: 5' uguguaacuuguuaGUAUUGUa 3'	-0.5066		
15.	RBBP4	3' gugagUCGUGGU CCUAUAACAa 5' : : : : 4232: 5' uuuaaGGCAUUAAUUAGUAUUGUu 3'	-0.0009	3' cgcggguuaauuacagACAACUa 5' 1775: 5' uuugauacugauuacaUGUUGAg 3'	-0.0051
16.	RBBP7	3' gugaguCGUG GUCCUAUAACAa 5' : : 49: 5' uguugcGUACUGUAUCAUAUUGUa3'	-1.0487	3' cgCGGGUUAAUUAC AGACAACUa 5' : : 6:5' aaGUACGAGAAAUGUUUCUGUUGA3'	-1.3579
17.	HDAC2	3' gugaGUCGUGGUCCUAUAACAa 5' : : 4642: 5' aaaaUAGAACUAUCAUAUUGUa 3'	-0.1439	3' cgcGGGUUAAUUACAGACAACUa 5' : : : 2001: 5' uauUCUGAUCUACCCCUGUUGAc 3'	-0.0284
	HDAC2	3'guGAGUCGUGGUCCUAUAACAa 5' : 860: 5'caUUCAGCAACUACUUAUUGUa 3'	-0.0005		
18.	MTF2	3′ gugAGUCGUGGU - CCUAUAACAa 5′ :: :: 152: 5′ cugUCAAUGUUAUGGAUAUUGUa 3′	-0.3136	3' cgcGGGUUAAUUACAGACAACUa 5' 1704: 5' uaaCACACAGAGUUUGUGUUGAu 3'	-0.1805
	MTF2	3' gugagucgugguccUAUAACaa 5' 469: 5' ugaaagacuguaaaAUAUUGaa 3'	-0.3521		