

Supplementary Table 1: 20 best miRNAs targets by their CRC relationship.

Protein name	Target Gene	UNIPROT_AC	CRC effector*	#miRNA	miRNA ID
Hypoxia-inducible factor 1-alpha	HIF1A	Q16665	1	1	hsa-miR-18a-5p
Programmed cell death protein 1	PDCD1	Q15116	1	1	hsa-miR-15b-5p
Methylcytosine dioxygenase TET1	TET1	Q8NFU7	1	1	hsa-miR-29a-3p
Insulin-like growth factor I	IGF1	P05019	1	1	hsa-miR-29a-3p
ETS domain-containing protein Elk-4	ELK4	P28324	0	1	hsa-miR-15b-5p
Mothers against decapentaplegic homolog 2	SMAD2	Q15796	1	1	hsa-miR-18a-5p
Adenine phosphoribosyltransferase	APRT	P07741	0	1	hsa-miR-15b-5p
Connective tissue growth factor	CTGF	P29279	0	1	hsa-miR-18a-5p
Protein C-ets-2	ETS2	P15036	1	1	hsa-miR-18a-5p
Glycogen synthase kinase-3 beta	GSK3B	P49841	1	1	hsa-miR-15b-5p
Vascular endothelial growth factor A	VEGFA	P15692	1	3	hsa-miR-335-5p, hsa-miR-29a-3p, hsa-miR-15b-5p
Cellular tumor antigen p53	TP53	P04637	1	3	hsa-miR-19b-3p, hsa-miR-19a-3p, hsa-miR-18a-5p
SprT-like domain-containing protein Spartan	SPRTN	Q9H040	0	1	hsa-miR-29a-3p

Tyrosine-protein kinase ABL1	ABL1	P00519	0	1	hsa-miR-29a-3p
Tubulin beta chain	TUBB	P07437	0	1	hsa-miR-15b-5p
UV excision repair protein RAD23 homolog B	RAD23B	P54727	0	1	hsa-miR-15b-5p
Apoptosis-stimulating of p53 protein 1	PPP1R13B	Q96KQ4	0	1	hsa-miR-29a-3p
Transducin-like enhancer protein 3	TLE3	Q04726	1	1	hsa-miR-18a-5p
Activin receptor type-2A	ACVR2A	P27037	1	1	hsa-miR-15b-5p
Low affinity immunoglobulin gamma Fc region receptor II-b	FCGR2B	P31994	0	1	hsa-miR-18a-5p
Note: 0=No efector; 1= Effector					

Supplementary Table 2: TPMS scores of distinct miRNA targets grouped by physiopathological process.

Physiopathological process	High	Medium	Low	L/HM ratio
Tissue invasion and metastasis (EMT)	104 (3.3%)	631 (20.1%)	2400 (76.6%)	3.3
Sustained angiogenesis	13 (0.4%)	172 (5.5%)	2950 (94.1%)	15.9
Immune system suppression/resistance	33 (1.1%)	59 (1.9%)	3043 (97.1%)	33.1
Cell growth and proliferation	9 (0.3%)	296 (9.4%)	2830 (90.3%)	9.2
Inflammation	1 (0.0%)	260 (8.3%)	2874 (91.7%)	11
Proteins related to epigenetic instability	2 (0.1%)	168 (5.4%)	2965 (94.6%)	17.4
Evading apoptosis	0 (0.0%)	87 (2.8%)	3048 (97.2%)	34.6
Note: The last column contains the arithmetical ratio – low/(high+medium).				