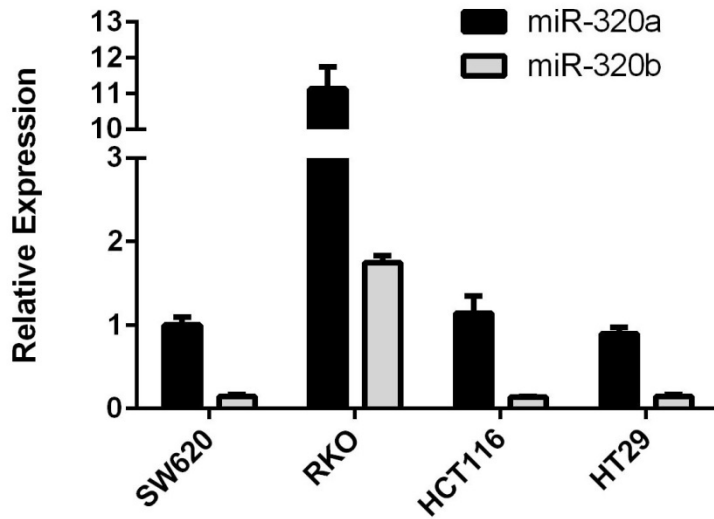


Supplemental Figure1. Insufficient specificity of TaqMan assay (Applied Biosystems, Life technologies) in distinguishing microRNA-320b from microRNA-320a by quantitative Real-time PCR. The TaqMan assay with both the TaqMan-miR320a probe and the TaqMan-miR-320b probe showed the significant increase of microRNA-320a and microRNA-320b expression, at 48 hours following microRNA-320a and microRNA-320b mimics transfection, respectively. (***) $p < 0.001$). For TaqMan assay RT-qPCR, microRNAs are first specific reverse transcribed by stem-loop specific reverse transcription primers at 3'-terminal, then elongated by one microRNA-specific primer and a second universal primer with TaqMan probe. (TaqMan miR-320a assay ID : 002277, TaqMan miR-320b assay ID : 002844, Applied Biosystems, Life technologies)



Supplemental Figure2. The microRNA-320a and microRNA-320b expression in SW620, RKO, HCT116 and HT29, by quantitative Real-time PCR, using TaqMan assay(Applied Biosystems, Life Technologies). RKO colon cells have high expression level of microRNA-320 whereas SW620 colon cells show low expression of microRNA-320.

	CRC with metastasis (n=20)	CRC without metastasis (n=27)	p value
Age (years)	56.6±9.9	58.7±10.9	0.5*
Gender (Female)	6(30%)	11(40.7%)	0.45§
Tumor localization			
Colon	15(75%)	15(55.6%)	0.17§
Rectum	5(25%)	12(44.4%)	
Lymph nodes harvested	15±6.5	15.4±5.6	0.86*
Tumor differentiation			
Well	2(10%)	3(11.1%)	0.37§
Moderately	16(80%)	17(63.0%)	
Poorly/Undifferentiation	2(10%)	7(25.9%)	
pT classification			
pT1	0(0%)	0(0%)	0.09§
pT2	0(0%)	3(11.1%)	
pT3	18(90%)	24(88.9%)	
pT4	2(10%)	0(0%)	
pN classification			
pN0	11(55%)	17(63.0%)	0.02§
pN1	4(20%)	10(37.0%)	
pN2	5(25%)	0(0%)	
Lymphatic/vascular invasion	5(25%)	0(0%)	0.01 Ø
Perineural invasion	4(20%)	1(3.7%)	0.15 Ø

Supplemental Table 1. Basic demographic and clinicopathologic features of CRC patients with or without metastasis. The table showed that there is no statistically significant difference in the basic demographic and clinicopathologic features between the patients with or without metastasis. Data are shown as mean ± standard deviation or *n* (%). * Student's test. §, χ^2 test. Ø, Fisher test.

miRNA	Fold change	p-value
Down-regulated		
hsa-miR-15b-5p	-1.48	0.03319
hsa-miR-192-5p	-2.06	0.02678
hsa-miR-196a-5p	-1.65	0.00997
hsa-miR-200b-3p	-2.10	0.00938
hsa-miR-200c-3p	-1.91	0.02077
hsa-miR-20a-5p	-1.44	0.03405
hsa-miR-20b-5p	-1.47	0.01799
hsa-miR-223-3p	-1.97	0.00616
hsa-miR-501-3p	-1.33	0.04455
hsa-miR-95	-1.84	0.01798
Up-regulated		
hcmv-miR-UL70-3p	2.52	0.00124
hsa-miR-1183	2.63	0.02259
hsa-miR-1224-5p	1.84	0.04782
hsa-miR-1308*	1.55	0.01774
hsa-miR-135b-5p	1.71	0.01997
hsa-miR-154-5p	3.09	0.01102
hsa-miR-1826*	1.37	0.01977
hsa-miR-221-3p	1.48	0.01011
hsa-miR-296-5p	2.17	0.02152
hsa-miR-299-5p	4.44	0.01505
hsa-miR-301b	1.80	0.01179
hsa-miR-320b	1.42	0.00355
hsa-miR-33b-3p	3.57	0.04770
hsa-miR-342-5p	2.01	0.01538
hsa-miR-371a-5p	2.28	0.01380
hsa-miR-409-3p	5.32	0.03073
hsa-miR-410	3.70	0.01658
hsa-miR-486-5p	3.59	0.00018
hsa-miR-497-5p	1.75	0.02651
hsa-miR-500a-5p	4.04	0.03861
hsa-miR-572	1.77	0.01424
hsa-miR-622	1.70	0.03515
hsa-miR-630	3.57	0.03949
hsa-miR-654-3p	5.09	0.00225
hsa-miR-923*	3.06	0.00018
hsa-miR-939	1.36	0.03482
kshv-miR-K12-10b	2.94	0.03003

Supplemental Table 2. Dysregulated microRNAs in microRNA microarray. Fold change (Metastasis vs Non-metastasis) ≥ 1 , t-test unpaired p-value ≤ 0.05 . * Dead miRNA entry in miRBase(v.21)