

Table S1. Patients Characteristics

Characteristics	Colorectal cancer (n=20)
Gender	
Male	12
Female	8
Age at diagnosis	
Mean±SD	60±12
Median (range)	56 (32-81)
Clinical stage	
I	4
II	11
III	5
Nodal status	
Positive	12
Negative	8
Tumor location	
Rectum	10
Distal colon	4
Proximal colon	6
Histology	
Adenocarcinoma	15
Mucous adenocarcinoma	5
signet-ring cell carcinoma	0

Supplementary Table S2: Primers for miRNA* RT-qPCR

miR_name	Forward primer	Reverse primer
hsa-miR-425-3p	gcatcgggaatgcgtgt	agtttttttttttttggcgga
hsa-miR-2277-3p	cagcgcctgcct	agtttttttttttttcgagcca
hsa-miR-1247-3p	cgggaacgtcgagac	ccagtttttttttttctcca
hsa-miR-505-5p	ggggagccaggaagt	gtccagtttttttttttaacatca
hsa-miR-642a-3p	gcagagacacattggagag	ggccagtttttttttttgttc
hsa-miR-766-5p	cagaggaggaattggtgct	ggccagtttttttttttagac
hsa-miR-664a-5p	cagactgctagggaaaatg	gtccagtttttttttttccaatc
hsa-miR-877-5p	gtagaggagatggcgca	ggccagtttttttttttgttc
hsa-miR-10a-3p	gcgcagcaaatcgtatc	ggccagtttttttttttatcc
hsa-miR-7854-3p	gaggtgaccgcagatg	ggccagtttttttttttcttc
hsa-miR-10b-3p	cgccagcagattcgattc	ggccagtttttttttttatcc
hsa-miR-191-3p	ctgcgcttgatttcgt	ccagtttttttttttgggga
hsa-miR-466-5p	cagtgtgtgcatgtgtg	ggccagttttttttttatatac
hsa-miR-6720-5p	agttccagccctgtag	cagtttttttttttttacgcgg
hsa-miR-219a-1-3p	gcagagagttgagtctggac	ccagttttttttttttacggga
hsa-miR-550a-3-5p	gagtgctgaggaggt	ggccagtttttttttttctct
hsa-miR-4796-3p	cgcagtaaatggcagagt	ggccagtttttttttttgttc
hsa-miR-628-3p	gcagttctagtaagagtggca	gtccagtttttttttttcgac
hsa-miR-1304-3p	gcagtctcactgtagcatc	cagttttttttttttggggttc
hsa-miR-29c-5p	accgatttctcctgggtg	ggccagtttttttttttctga
hsa-miR-556-3p	gcgcagatattaccattagctc	ggccagtttttttttttaagatg
hsa-miR-627-3p	gcagctcttttttgagactc	ggccagtttttttttttagtg
hsa-miR-98-3p	gcgcagctatacaactactac	ggccagtttttttttttagga
hsa-miR-548a-5p	gcagaaaagtaattgcggtct	ggccagtttttttttttacc
hsa-miR-10399-5p	gcgcagaattacagattgct	gtccagtttttttttttctga
hsa-miR-33a-5p	cgagggtcattgtagt	gtccagtttttttttttgaat
hsa-miR-15b-3p	cgccagcgaatcattattgc	aggccagtttttttttttagag
hsa-miR-2467-5p	gtgaggctctgttagcctt	ccagtttttttttttagacca
hsa-miR-548aa	cgcaaaaaccacaactactttg	gtccagtttttttttttgtgc
hsa-miR-31-3p	gtgctatgccacaatattgc	ggccagtttttttttttgatg
hsa-miR-23b-5p	gggttctgcatgct	caggccagtttttttttttaaac
hsa-miR-548ae-5p	cgcaaaaagtaattgtggt	tccagttttttttttttggca
hsa-miR-26b-3p	cagcctgtctccattactg	gtccagtttttttttttgagc
hsa-miR-454-3p	cgccagtagtccaatattgct	gtccagtttttttttttaacct
hsa-miR-10399-3p	gtctctcgacaagctgt	ggccagtttttttttttaacct
hsa-miR-29a-3p	cgccagtagcaccatctga	tccagtttttttttttaaccga
hsa-miR-10401-3p	aggacctcgcctgc	gtccagtttttttttttggc
hsa-miR-577	gcgcaggtagataaaatattggt	ggccagtttttttttttcag

Supplementary Table S4: miRNAs set of higher level in the exosomes and higher level inside the cells (SW620 vs. NCM460, Exo|Cell).

High in exosome and high in cell (HEHC)											
miR_name	miR_seq	up/down	fold_change(SW_620/NCM_460)(Exo Cell)	log2(fold_change)	pvalue(chi_square_2x2)	pvalue(fisher_test)	NCM_460(norm)	SW_620(norm)	NCM_460(raw)	SW_620(raw)	Expression level
hsa-miR-425-3p_L+1R-1[81] *	CATCGGGAATGTCGTGTCCGCC	up up	2.82 3.20	1.49 1.68	1.25E-74 1.52E-76	2.57E-76 1.20E-78	280 213	789 682	72 392	509 1,505	middle middle
hsa-miR-2277-3p_R+1 *	TGACAGCGCCCTGCCTGGCTCG	up up	inf 11.72	inf 3.55	1.95E-05 9.25E-38	3.95E-06 7.81E-42	0 15	16 172	0 27	10 380	middle middle
hsa-miR-1247-3p_L-3 ^[82] *	CGGGAACGTCGAGACTGGAGC	up up	inf 2.65	inf 1.41	2.89E-06 1.06E-02	3.83E-07 1.64E-02	0 6	19 16	0 11	12 35	middle middle
hsa-miR-505-5p_R+1 ^[83] *	GGGAGCCAGGAAGTATTGATGTT	up up	inf 4.95	inf 2.31	5.25E-18 1.75E-08	2.44E-22 5.97E-09	0 9	64 46	0 17	41 101	middle middle
hsa-miR-1343-3p	CTCCTGGGGCCCGCACTCTCGC	up up	inf 2.41	inf 1.27	2.53E-03 2.43E-08	1.99E-03 2.04E-08	0 35	8 85	0 65	5 188	middle middle
hsa-miR-628-5p ^[84, 85]	ATGCTGACATATTACTAGAGG	up up	inf 2.04	inf 1.03	6.58E-08 2.20E-06	3.61E-09 2.80E-06	0 39	25 79	0 71	16 174	middle middle
hsa-miR-642a-3p_R-1 ^[86] *	AGACACATTTGGAGAGGGAAC	up up	inf inf	inf inf	5.25E-18 1.38E-12	2.44E-22 3.85E-15	0 0	64 42	0 0	41 92	middle middle
hsa-miR-766-5p_R-1 ^[87] *	AGGAGGAATTGGTGCTGGTCT	up up	inf inf	inf inf	3.53E-04 1.95E-02	1.93E-04 1.92E-02	0 0	11 5	0 0	7 10	middle middle
hsa-miR-664a-5p_R-2 ^[88] *	ACTGGCTAGGGAAAATGATTGG	up up	inf inf	inf inf	1.35E-15 1.69E-06	5.81E-19 3.01E-07	0 0	54 19	0 0	35 42	middle middle
hsa-miR-877-5p_R+3 ^[89] *	GTAGAGGAGATGGCGCAGGGGAC	up up	inf 2.59	inf 1.37	4.17E-53 7.54E-26	2.87E-68 6.56E-26	0 107	200 276	0 196	129 609	middle middle
hsa-miR-10a-3p_R-1	CAAATTCGTATCTAGGG	up up	3.44 2.97	1.78 1.57	0.00E+00 6.06E-	4.47E-274 3.5	677 198	2,332 589	174 364	1,504 1,3	middle mi

*	GAAT				62	6E-63				00	ddle
hsa-mir-4454-p5	TCCGAGTCACGGCACC AAA	up up	7.45 66.37	2.90 6.05	0.00E+00 0.00E+00	3.51E-267 0.00E+00	183 111	1,363 7,335	47 203	879 16,180	high high
hsa-miR-361-5p ^[90-102]	TTATCAGAATCTCCAGG GGTAC	up up	2.69 2.02	1.43 1.01	0.00E+00 0.00E+00	0.00E+00 0.00E+00	2,771 3,505	7,457 7,076	712 6,438	4,809 15,609	high high
hsa-miR-7854-3p_R+1 *	TGAGGTGACCGCAGAT GGGAAG	up up	inf inf	inf inf	5.25E-18 5.20E-05	2.44E-22 1.57E-05	0 0	64 14	0 0	41 30	middle middle
hsa-miR-98-5p ^[103-105]	TGAGGTAGTAAGTTGTA TTGTT	up up	6.28 2.04	2.65 1.03	0.00E+00 0.00E+00	0.00E+00 0.00E+00	599 4,226	3,764 8,633	154 7,762	2,427 19,043	high high
hsa-miR-10b-3p_L-1 ^[106,107] *	CAGATTTCGATTCTAGGG GAAT	up up	inf inf	inf inf	1.12E-06 1.05E-08	1.76E-07 5.42E-10	0 0	20 27	0 0	13 60	middle middle
hsa-miR-425-5p ^[108-115]	AATGACACGATCACTCC CGTTGA	up up	2.67 2.50	1.42 1.32	0.00E+00 0.00E+00	9.89E-146 0.00E+00	611 2,181	1,630 5,443	157 4,006	1,051 12,007	high high
hsa-miR-466_R-1_1ss22 AC ^[116-119]	ATACACATACACGCAAC ACACC	up up	inf inf	inf inf	1.95E-05 9.30E-06	3.95E-06 3.23E-06	0 0	16 16	0 0	10 36	middle middle
hsa-miR-191-3p_L-1 *	CTGCGCTTGGATTTCGT CCCC	up up	inf 2.44	inf 1.29	1.34E-04 8.62E-03	8.86E-05 1.11E-02	0 8	12 19	0 14	8 41	middle middle
hsa-mir-466-p5 *	TGTGTTGCATGTGTGTAT ATGT	up up	inf inf	inf inf	2.06E-24 1.72E-03	1.91E-30 1.80E-03	0 0	88 8	0 0	57 18	middle middle
hsa-miR-664a-3p ^[120]	TATTCATTATCCCCAGC CTACA	up up	inf 3.03	inf 1.60	2.57E-08 4.86E-24	1.66E-09 2.36E-24	0 71	26 214	0 130	17 473	middle middle
hsa-miR-4286_R+1 ^[121]	ACCCCACTCCTGGTACC A	up up	inf 2.68	inf 1.42	3.34E-17 2.42E-35	5.47E-21 8.48E-36	0 137	60 368	0 252	39 812	middle middle
hsa-miR-6720-5p_R+1 *	TTCCAGCCCTGGTAGGC GCCGCGT	up up	inf 3.26	inf 1.71	9.39E-04 9.59E-04	9.13E-04 1.95E-03	0 7	9 21	0 12	6 47	middle middle
hsa-miR-196a-5p ^[36,122]	TAGGTAGTTTCATGTTG	up up	5.35 2.99	2.42 1.58	0.00E+00 0.00E+00	0.00E+00 0.00E+00	699 1,823	3,734 5,44	180 3,349	2,408 12,	high high

	TTGGG				+00	E+00		8		017	
hsa-miR-219a-1-3p_R+ 1 *	AGAGTTGAGTCTGGAC GTCCCGT	up up	inf 2.68	inf 1.42	9.39E-04 1.91E-02	9.13E-04 3.08E-02	0 5	9 13	0 9	6 29	middle middle
hsa-miR-4659a-3p	TTTCTTCTAGACATGG CAACG	up up	inf 3.61	inf 1.85	3.53E-04 1.03E-02	1.93E-04 8.41E-03	0 3	11 12	0 6	7 26	middle middle
hsa-miR-550a-3-5p_R+ 1 ^[123] *	AGTGCCTGAGGGAGTA AGAGA	up up	inf inf	inf inf	2.11E-09 2.32E-03	7.39E-11 1.80E-03	0 0	30 8	0 0	20 17	middle middle
hsa-miR-212-3p ^[124, 125]	TAACAGTCTCCAGTCAC GGCC	up up	inf 3.59	inf 1.84	7.49E-06 3.63E-09	1.82E-06 1.37E-09	0 17	17 63	0 32	11 138	middle middle
hsa-miR-130b-3p ^[126]	CAGTGCAATGATGAAA GGGCAT	up up	2.40 3.12	1.26 1.64	4.46E-85 4.28E-55	2.64E-86 3.43E-56	459 160	1,103 498	118 293	711 1,098	middle middle
hsa-let-7i-5p ^[127]	TGAGGTAGTAGTTTGTG CTGTT	up up	2.95 2.00	1.56 1.00	0.00E+00 0.00E+00	0.00E+00 0.00E+00	13,624 15,844	40,214 31,705	3,501 29,101	25,933 69,935	high high
hsa-miR-4796-3p_R-1 *	TAAAGTGGCAGAGTATA GACA	up up	inf inf	inf inf	3.53E-04 2.95E-04	1.93E-04 1.68E-04	0 0	11 11	0 0	7 24	middle middle
hsa-miR-6720-3p	CGCGCCTGCAGGA GGTAGA	up up	inf 4.60	inf 3.87	1.12E-06 8.15E-28	1.76E-07 2.10E-31	0 8	20 119	0 15	13 263	middle middle
hsa-mir-1304-p5	CGGTTTGAGGCTACAGT GAGAT	up up	4.02 5.71	2.01 2.51	1.00E-23 6.25E-50	1.69E-24 4.76E-53	43 52	172 295	11 95	111 651	middle middle
hsa-miR-132-3p ^[128]	TAACAGTCTACAGCCAT GGTCG	up up	2.44 2.16	1.28 1.11	1.70E-67 2.42E-41	2.08E-68 1.75E-41	350 268	853 580	90 492	550 1,279	middle middle
hsa-miR-1247-5p ^[129-131]	ACCCGTCCCCTCGTCC CCGGA	up up	inf 3.78	inf 1.92	0.00E+00 1.79E-55	2.56E-276 1.71E-57	0 112	816 424	0 206	526 936	middle middle
hsa-miR-628-3p_L+1 ^[132, 133] *	TTCTAGTAAGAGTGGCA GTCGA	up up	2.19 2.67	1.13 1.42	8.32E-05 6.97E-26	9.21E-05 4.49E-26	23 100	51 266	6 183	33 587	middle middle
hsa-miR-190b-5p	TGATATGTTGATATTGG	up up	inf inf	inf inf	5.16E-24 5.42E-	4.17E-30 6.21	0 0	87 21	0 0	56 46	middle mi

	GTTG				07	E-08					ddle
hsa-miR-1304-3p_1ss13 CA *	TCTCACTGTAGCATCGA ACCCC	up up	2.46 3.05	1.30 1.61	6.63E-28 7.51E- 79	3.26E-28 9.31 E-81	136 242	335 737	35 444	216 1,625	middle mi ddle
hsa-miR-504-5p	AGACCCTGGTCTGCACT CTATC	up up	inf inf	inf inf	2.89E-06 6.36E- 10	3.83E-07 1.04 E-11	0 0	19 32	0 0	12 70	middle mi ddle

*: passenger strand

Supplementary Table S5: miRNAs set of higher level in the exosomes but lower level inside the cells (SW620 vs. NCM460, Exo|Cell).

High in exosome but low in cell (HELC)											
miR_name	miR_seq	up/down	fold_change(SW_620/NCM_460)(Exo Cell)	log2(fold_change)	pvalue(chi_square_2x2)	pvalue(fisher_test)	NCM_460(norm)	SW_620(norm)	NCM_460(raw)	SW_620(raw)	Expression level
hsa-miR-29c-5p_L-2R+3 ^[1] *	ACCGATTCTCCTGGTGTTCAGA	up down	inf 0.47	inf -1.10	2.53E-03 8.03E-03	1.99E-03 9.36E-03	0 64	8 30	0 118	5 66	middle middle
hsa-miR-375-3p ^[2]	TTTGTTTCGTTTCGGCTCGCGTGA	up down	4.17 0.11	2.06 -3.19	0.00E+00 4.38E-21	0.00E+00 1.98E-24	3,028 157	12,617 17	778 289	8,136 38	high high
hsa-miR-449a ^[3]	TGGCAGTGTATTGTTAGCTGGT	up down	inf 0.15	inf -2.75	1.34E-04 6.41E-03	8.86E-05 5.80E-03	0 15	12 2	0 28	8 5	middle middle
hsa-miR-590-3p	TAATTTTATGTATAAGCTAGT	up down	14.82 0.36	3.89 -1.46	2.23E-63 1.06E-56	4.25E-73 2.56E-59	19 1,313	288 479	5 2,412	186 1,056	middle middle
hsa-mir-3133-p3	TTGAGTTTAAAGATTCTTTAT	up down	inf inf	inf inf	5.09E-05 1.12E-04	1.87E-05 3.38E-05	0 18	14 0	0 33	9 0	middle middle
hsa-miR-9-3p ^[4]	ATAAAGCTAGATAACCGAAAGT	up down	3.25 0.05	1.70 -4.28	0.00E+00 3.39E-13	5.42E-98 1.27E-15	268 76	872 4	69 140	562 9	middle middle
hsa-miR-128-1-5p	CGGGGCCGTAGCACTGCTGAGA	up down	inf 0.38	inf -1.40	3.53E-04 1.92E-03	1.93E-04 1.49E-03	0 54	11 20	0 99	7 45	middle middle
hsa-miR-140-5p ^[5,6]	CAGTGGTTTACCTATGGTAG	up down	3.93 0.30	1.98 -1.73	0.00E+00 6.20E-44	5.22E-223 1.16E-46	428 746	1,684 225	110 1,370	1,086 496	middle middle
hsa-miR-556-3p_R-1 ^[7] *	ATATTACCATTAGCTCATCTT	up down	inf 0.21	inf -2.26	7.49E-06 1.49E-03	1.82E-06 9.00E-04	0 26	17 5	0 48	11 12	middle middle
hsa-miR-885-5p ^[8-10]	TCCATTACACTACCCTGCTCT	up down	inf inf	inf inf	9.39E-04 1.53E-02	9.13E-04 1.85E-02	0 7	9 0	0 13	6 0	low low
hsa-miR-627-3p_L+1 ^[11] *	CTCTTTTCTTTGAGACTCACT	up down	inf 0.10	inf -3.35	2.89E-06 3.04E-06	3.83E-07 1.77E-06	0 37	19 4	0 68	12 8	middle middle

hsa-mir-641-p3 ^[12, 13]	TGACTGTCCTATGCTTT CCT	up down	inf 0.09	inf -3.53	9.36E-11 1.51E-08	6.96E-13 3.54E-09	0 52	36 5	0 96	23 10	middle middle
hsa-miR-372-3p ^[14, 15]	AAAGTGCTGCGACATT GAGCGT	up down	2.72 -inf	1.45 -inf	3.65E-07 2.63E-03	2.25E-07 1.46E-03	23 11	64 0	6 20	41 0	middle middle
hsa-miR-576-5p ^[16, 17]	ATTCTAATTTCTCCACGT CTTT	up down	inf 0.18	inf -2.49	2.57E-08 4.85E-23	1.66E-09 1.79E-25	0 224	26 40	0 412	17 88	middle middle
hsa-miR-625-3p ^[18, 19]	GACTATAGAACTTCCCC CTCA	up down	16.65 0.36	4.06 -1.46	0.00E+00 6.61E-23	0.00E+00 1.01E-23	109 501	1,814 182	28 921	1,170 401	middle middle
hsa-miR-29b-3p ^[20, 21]	TAGCACCATTGAAATCA GTGTT	up down	2.55 0.48	1.35 -1.06	4.73E-62 2.23E-25	4.37E-63 6.23E-26	288 1,077	735 516	74 1,979	474 1,139	middle middle
hsa-miR-4521_R+4 *	GCTAAGGAAGTCCTGTG CTCAGTTTT	up down	inf 0.03	inf -5.00	2.53E-03 0.00E+00	1.99E-03 0.00E+00	0 4,653	8 145	0 8,545	5 320	high high
hsa-miR-98-3p_1ss22C T *	CTATACAACTTACTACTTT CCT	up down	inf 0.16	inf -2.65	2.17E-14 3.83E-26	1.30E-17 2.43E-29	0 239	50 38	0 439	32 84	middle middle
hsa-miR-19a-3p ^[22]	TGTGCAAATCTATGCAAA ACTGA	up down	3.35 0.35	1.75 -1.53	5.33E-88 8.61E-56	5.23E-91 1.10E-58	233 1,186	783 412	60 2,177	505 908	middle middle
hsa-miR-200b-5p ^[23-27]	CATCTTACTGGGCAGCAT TGGA	up down	3.02 -inf	1.59 -inf	3.64E-81 1.18E-47	3.44E-83 4.28E-67	265 253	799 0	68 465	515 0	middle middle
hsa-miR-30d-3p ^[28]	CTTTCAGTCAGATGTTTG CTGC	up down	3.49 0.10	1.80 -3.33	4.99E-14 6.66E-32	1.96E-14 4.41E-37	31 236	109 24	8 434	70 52	middle middle
hsa-miR-548a-5p_R+3 ^[29, 30] *	AAAAGTAATTGCGGTCTT TGGT	up down	inf 0.15	inf -2.70	2.53E-03 1.65E-03	1.99E-03 8.36E-04	0 21	8 3	0 38	5 7	middle middle
hsa-miR-548d-3p ^[31-33]	CAAAAACCACAGTTTCT TTTGC	up down	inf 0.22	inf -2.19	3.27E-02 1.67E-02	4.46E-02 1.01E-02	0 16	4 3	0 29	3 8	middle middle
hsa-miR-10399-5p_R+ 1 *	AATTACAGATTGTCTCAG AGAA	up down	inf 0.07	inf -3.77	2.57E-08 1.07E-06	1.66E-09 2.30E-07	0 37	26 3	0 68	17 6	middle middle

hsa-miR-34a-5p ^[34-36]	TGGCAGTGTCTTAGCTGG TTGT	up down	2.28 0.28	1.19 -1.84	0.00E+00 1.94E-43	6.26E-15 2.27E-46	918 666	2,097 186	236 1,224	1,352 410	middle middle
hsa-miR-135b-3p	ATGTAGGGCTAAAAGCCA TGGG	up down	inf 0.07	inf -3.92	1.31E-19 1.95E-06	2.29E-24 2.24E-07	0 34	70 2	0 63	45 5	middle middle
hsa-miR-33a-5p_R-1 ^[37-44] *	GTGCATTGTAGTTGCATT GC	up down	2.09 0.10	1.06 -3.29	1.41E-11 5.55E-10	1.40E-11 5.22E-11	78 66	163 7	20 122	105 15	middle middle
hsa-miR-181a-3p	ACCATCGACCGTTGATTG TACC	up down	2.68 0.01	1.42 -6.58	5.01E-19 2.06E-62	4.54E-19 2.97E-84	74 347	198 4	19 637	128 8	middle middle
hsa-miR-625-5p ^[45]	AGGGGAAAGTTCTATA GTCC	up down	9.39 0.35	3.23 -1.52	0.00E+00 3.72E-06	7.85E-11 2.31E-06	54 103	512 36	14 189	330 79	middle middle
hsa-miR-15b-3p_R-1 *	CGAATCATTATTGCTGC TCT	up down	3.73 0.37	1.90 -1.44	0.00E+00 4.14E-50	8.90E-97 2.11E-52	202 1,176	755 433	52 2,159	487 954	middle middle
hsa-miR-2467-5p_R+1 *	TGAGGCTCTGTAGCCTT GGCTCT	up down	inf 0.18	inf -2.46	2.53E-03 6.30E-03	1.99E-03 6.20E-03	0 17	8 3	0 32	5 7	middle middle
hsa-miR-548aa_L-1R-2 ^[46, 47] *	AAAACCACAATTACTTTT GCAC	up down	inf 0.38	inf -1.40	2.68E-05 5.63E-03	8.60E-06 5.60E-03	0 43	15 16	0 79	10 36	middle middle
hsa-miR-31-3p_R+1 ^[48] *	TGCTATGCCAACATATTG CCATC	up down	2.85 0.15	1.51 -2.70	3.71E-16 1.05E-81	1.39E-16 4.36E-93	54 766	155 117	14 1,406	100 259	middle middle
hsa-miR-374a-3p	CTATCAGATTGTATTGTA ATT	up down	6.69 0.32	2.74 -1.66	6.81E-24 3.41E-67	9.38E-26 3.08E-71	19 1,237	130 391	5 2,272	84 862	middle middle
hsa-miR-23b-5p_L-1 ^[49, 50] *	GGGTTCTGGCATGCTGA TTT	up down	inf 0.34	inf -1.55	1.37E-35 1.21E-03	2.65E-45 1.22E-03	0 49	132 17	0 90	85 37	middle middle
hsa-miR-548ae-5p_R+2 *	AAAAGTAATTGTGGTTTT TGCC	up down	2.68 0.32	1.42 -1.64	2.66E-04 3.81E-05	2.53E-04 4.18E-05	12 71	33 23	3 131	22 51	middle middle
hsa-miR-26b-3p_R+1 ^[51, 52] *	CCTGTTCTCCACTTGTG GCTC	up down	inf 0.47	inf -1.08	1.69E-07 1.61E-02	1.71E-08 1.43E-02	0 56	23 26	0 102	15 58	middle middle

hsa-miR-9-5p ^[53-56]	TCTTTGGTTATCTAGCTGT ATGA	up down	4.06 0.01	2.02 -6.72	0.00E+00 1.39E-32	6.64E-119 2.68E-43	214 176	869 2	55 323	561 4	middle middle
hsa-miR-454-3p_R+1 ^[57-59] *	TAGTGCAATATTGCTTATA GGGTT	up down	inf 0.39	inf -1.36	1.12E-87 8.26E-47	7.34E-114 8.77E-49	0 1,220	335 474	0 2,240	216 1,046	middle middle
hsa-miR-499a-5p ^[60, 61]	TTAAGACTGCAGTGATG TTT	up down	111.34 0.24	6.80 -2.07	0.00E+00 9.89E-06	0.00E+00 1.14E-05	175 57	19,499 14	45 105	12,574 30	high high
hsa-miR-146a-5p ^[62-66]	TGAGAACTGAATCCATG GGTT	up down	12.56 0.04	3.65 -4.51	0.00E+00 0.00E+00	0.00E+00 3.59E-193	1,442 962	18,110 42	371 1,766	11,679 93	high high
hsa-mir-33a-p3	TGTTCTGGTGGTACCCAT G	up down	inf 0.25	inf -1.99	2.53E-03 1.53E-06	1.99E-03 6.63E-07	0 72	8 18	0 132	5 40	middle middle
hsa-miR-579-3p ^[67]	TTCATTTGGTATAAACCG CGATT	up down	inf 0.15	inf -2.70	9.36E-11 1.05E-21	6.96E-13 1.58E-24	0 192	36 29	0 352	23 65	middle middle
hsa-miR-548n	CAAAAGTAATTGTGGATT TTGT	up down	inf 0.25	inf -2.00	1.12E-06 5.15E-05	1.76E-07 4.18E-05	0 51	20 13	0 93	13 28	middle middle
hsa-miR-10399-3p_L+ 1_1ss22CT *	TCTCTCGACAAGCTGTA GGTT	up down	inf 0.08	inf -3.68	3.53E-04 2.67E-06	1.93E-04 6.93E-07	0 35	11 3	0 64	7 6	middle middle
hsa-miR-29a-3p_R-1 ^[68-72] *	TAGCACCATCTGAAATCG GTT	up down	2.09 0.44	1.06 -1.17	0.00E+00 0.00E+00	0.00E+00 0.00E+00	54,704 70,707	114,101 31,379	14,057 129,864	73,580 69,214	high high
hsa-miR-374b-3p	CTTAGCAGGTTGTATTAT CATT	up down	inf 0.43	inf -1.21	5.26E-30 2.37E-06	7.12E-38 2.34E-06	0 166	110 72	0 305	71 158	middle middle
hsa-miR-10401-3p_L+ 1R-1 *	GACCTCGCCGTCGCC CGCC	up down	10.46 0.48	3.39 -1.05	3.84E-66 1.11E-02	2.41E-74 1.12E-02	31 66	326 32	8 122	210 71	middle middle
hsa-miR-135b-5p ^[73, 74]	TATGGCTTTTCATTCTAT GTGA	up down	12.08 0.02	3.59 -5.37	0.00E+00 0.00E+00	0.00E+00 2.39E-217	245 977	2,962 24	63 1,795	1,910 52	middle middle
hsa-miR-577_L+1 ^[75-80] *	GTAGATAAAATATTGGTA CCTG	up down	inf -inf	inf -inf	0.00E+00 2.68E-27	2.86E-145 1.07E-37	0 141	428 0	0 259	276 0	middle middle

hsa-miR-192-3p	CTGCCAATCCATAGGTC ACAG	up down	inf -inf	inf -inf	6.05E-46 2.06E-03	8.21E-59 1.46E-03	0 11	172 0	0 21	111 0	middle m iddle
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*: passenger strand

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