

Supplementary Material

MicroRNA High Throughput Loss-of-Function Screening Reveals an Oncogenic Role for miR-21-5p in Hodgkin Lymphoma

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Table S1. Overview of the miRZIP constructs pool in high throughput screen

No.	miRZIP construct	miRNA expression	No.	miRZIP construct	miRNA expression
1	miRZIP-21-5p	Top 10 in cHL	33	miRZIP-100-5p	Not different
2	miRZIP-92a-3p	Top 10 in cHL	34	miRZIP-106a-5p	Not different
3	miRZIP-142-5p	Top 10 in cHL	35	miRZIP-106b-5p	Not different
4	miRZIP-155-5p	Top 10 in cHL	36	miRZIP-125a-5p	Not different
5	miRZIP-30e-5p	Top 10 in cHL	37	miRZIP-142-3p	Not different
6	miRZIP-27b-3p	Top 10 in cHL	38	miRZIP-146a-5p	Not different
7	miRZIP-181a-5p	Top 10 in cHL	39	miRZIP-146b-5p	Not different
8	miRZIP-9-5p	Increased in cHL	40	miRZIP-182a-5p	Not different
9	miRZIP-23a-3p	Increased in cHL	41	miRZIP-183-5p	Not different
10	miRZIP-24-3p	Increased in cHL	42	miRZIP-190-5p	Not different
11	miRZIP-27a-3p	Increased in cHL	43	miRZIP-205-5p	Not different
12	miRZIP-92b-3p	Increased in cHL	44	miRZIP-301b	Not different
13	miRZIP-196a-5p	Increased in cHL	45	miRZIP-320a-3p	Not different
14	miRZIP-345-5p	Increased in cHL	46	miRZIP-324-3p	Not different
15	miRZIP-378a-3p	Increased in cHL	47	miRZIP-330b-5p	Not different
16	miRZIP-615-3p	Increased in cHL	48	miRZIP-449a-5p	Not different
17	miRZIP-625-5p	Increased in cHL	49	miRZIP-4454	Not different
18	miRZIP-150-5p	Decreased in cHL	50	miRZIP-let-7b-5p	Not different
19	miRZIP-15a-5p	Not different	51	miRZIP-let-7e-5p	Not different
20	miRZIP-16-5p	Not different	52	miRZIP-let-7f-2-3p	Not different
21	miRZIP-17-5p	Not different	53	miRZIP-144-3p	Not expressed
22	miRZIP-18a-5p	Not different	54	miRZIP-431-3p	Not expressed
23	miRZIP-19a-3p	Not different	55	miRZIP-494-3p	Not expressed
24	miRZIP-19b-1-3p	Not different	56	miRZIP-500a-5p	Not expressed
25	miRZIP-20a-5p	Not different	57	miRZIP-892b	Not expressed
26	miRZIP-21-3p	Not different	58	miRZIP-4455	Not expressed
27	miRZIP-23b-3p	Not different	59	miRZIP-NT1	Negative control
28	miRZIP-25-3p	Not different	60	miRZIP-NT2	Negative control
29	miRZIP-26a-5p	Not different	61	miRZIP-NT3	Negative control
30	miRZIP-29a-3p	Not different	62	miRZIP-NT4	Negative control
31	miRZIP-34a-5p	Not different	63	miRZIP-NT5	Negative control
32	miRZIP-99b-5p	Not different			

Table S2. Insert sequences of the custom miRZIP constructs in the pool

miRZIP construct	Sense sequence (5'-GATCC-Insert-TTTTG-3')	Antisense sequence (5'-AATTCAAAAA-Insert-G-3')
miRZIP-21-3p	GCAACACCGGTGATGGACTATCTTCTGTCAAGACAGCCCACGTGACTGGTGTG	CAACACCAGTCGATGGGCTGTCGACAGGAAGATACTGCACCGGTGTTGC
miRZIP-23b-3p	GATCACATGCCAGGGACTAACCTTCTGTCAAGGTAAATCCCTGGCAATGTGAT	ATCACATTGCCAGGGATTACCTGACAGGAAGGTTAGCCTGGCGATGTGATC
miRZIP-27a-3p	GTTCACAGCGGCTAACGTCCCACCTTCTGTCAAGCGGAACCTAGCCACTGTGAA	TTCACAGTGGCTAACGTCCCGCTGACAGGAAGGTGGGACTTAGCCGCTGTGAAC
miRZIP-92b-3p	GTATTGCAATCGTCCGGACTACCTTCTGTCAAGGGAGGCCGGACGTGACAAT	TATTGCACTCGTCCCGCTCCGTACAGGAAGGTAGTCGGGACGATTGCAAATAC
miRZIP-99b-5p	GCACCCGTGAAACCGACCTGAGCTTCTGTCAAGCGAAGGTGGTTCTACGGGTG	CACCCGTAGAACCGACCTTGCCTGACAGGAAGCTCAGGGTCGTTGACCGGGTGC
miRZIP-100-5p	GAACCCGTGGATCGAACCTCGCCTTCTGTCAAGCACAAGTTCGGATCTACGGGT	AACCGTAGATCCGAACTTGTGCTGACAGGAAGCGCAGGTTGGATCCACGGGTTG
miRZIP-144-3p	GTACAGTACAGATGATAATCTTCTGTCAAGAGTACATCATCTACTGT	TACAGTATAGATGATGACTCTGACAGGAAGATTATATCATCTGACTGTAC
miRZIP-146b-5p	GTGAGAACGGAATCCATAGACTTCTGTCAAGAGCCTATGGAATTCACTTCA	TGAGAACTGAATTCCATAGGCTCTGACAGGAAGAGTCTATGGAATTCCGTTTCAC
miRZIP-150-5p	GTCTCCAGCCCTTGTACAAGCGCTTCTGTCAAGCACTGGTACAAGGGTTGGGAGA	TCTCCCAACCTTGTACCACTGTCGACAGGAAGCGCTGTACAAGGGCTGGGAGAC
miRZIP-183-5p	GTATGGCAATGGTAGAACCCAATCTTCTGTCAAGAGTGAATTCTACCGTGCATA	TATGGCACTGGTAGAACCTACTGTCGACAGGAAGATTGGATTCTACCATGCCATAC
miRZIP-190-5p	GTGATATGTTGATATTAAGTCGCTTCTGTCAAGCACCTAAATATCAAACATATCA	TGATATGTTGATATTAAGGTTGCTGACAGGAAGCGACTTAATATCAAGCATATCAC
miRZIP-205-5p	GTCCTCACTCCACCGGAATCCGCTTCTGTCAAGCAGACTCCGGTGGAAATGAAGGA	TCCTTCATTCCACCGGAGTCTGTCGACAGGAAGCGGATTCCGGTGGAGTGAAGGAC
miRZIP-301b-3p	GCAGTGCACTGATATTGTCATCCTTCTGTCAAGGTTGACAATATCATTGCACTG	CAGTGCAATGATATTGTCAAAGCTGACAGGAAGGATTGGACAATATCAGTGCACTG
miRZIP-324-3p	GAUTGCCAAGGTGCTACTAGCTTCTGTCAAGCCAGCAGCACCTGGGGCAGT	ACTGCCCCAGGTGCTGTCGGCTGACAGGAAGCTAGTAGCACCTTGGGCAGTC
miRZIP-330b-5p	GTCTCTGGACCTGTCTCAGACCTTCTGTCAAGGCCCTAAAGACACAGGCCAGAGA	TCTCTGGGCTGTCTTAGGCCTGACAGGAAGGTCTGAGACACAGGTCCAGAGAC
miRZIP-345-5p	GGCTGACTACTAGTCCAGAGCCCCCTCTGTCAAGGAGCCCTGGACTAGGAGTCAGC	GCTGACTCTAGTCCAGGGCTCTGACAGGAAGGGCTCTGACTAGTCAGGCC
miRZIP-431-3p	GCAGGTGCGCTTGCAGGGATTATCTTCTGTCAAGAGAACCCCTGCAAGACGACCTG	CAGGTGCTTGCAGGGCTCTGACAGGAAGAGATAACCTGCAAGGCCAGCTGC
miRZIP-449a-5p	GTGGCAGTATATTGTTAGTGTACCTTCTGTCAAGCAGCTAACATACTGCCA	TGGCAGTGTATTGTTAGCTGGCTGACAGGAAGATCATCTAACATAACTGCCAC
miRZIP-500a-5p	GTAATCCTCGCTACCTGGCGAAACTTCTGTCACTCTCACCCAGGTGCAAGGGATTA	TAATCCTTGCTACCTGGGTGAGACTGACAGGAAGTTGCCAGGTAGCGAGGATTAC
miRZIP-615-3p	GTCCGAGCATGGGCTCCATCCTTCTGTCAAGAAGAGGGAGACCCAGGCTCGGA	TCGGAGCCTGGGCTCCCTTCTGACAGGAAGGGATGGAGACCCATGCTGGAC
miRZIP-625-5p	GAGGGGGACAGTTCTATGTACCTTCTGTCAAGGACTATAGAACCTTCCCCCT	AGGGGAAAGTTCTATAGTCCCTGACAGGAAGGTACGATAGAACTGCCCCCTC
miRZIP-892b-3p	GCACTGGCCCTTCTGGATATACCTTCTGTCACTTACCCAGAAAGGAGCCAGTG	CACTGGCTCTTCTGGTAGACTGACAGGAAGTATCCAGAAAGGGGCCAGTGC
miRZIP-4454	GGGATCCGCGTCACCGAACACTTCTGTCACTGGTGGCGTACTCGGATCC	GGATCCGAGTCACGGCACCCTGACAGGAAGTTCCGTGACGCCAGTCCC
miRZIP-4455	GAGGGGTGATGTGCTCTTCTGTCAAGAAAACACACACACCT	AGGGTGTGTGTTCTGACAGGAAGAGAACATACACCCCTC
miRZIP-let7e-5p	GTGAGGTAAGAGGTTGACAGCTTCTGTCAAGAACTATACACCTTCTACCTCA	TGAGGTAGGAGGTTGATAGTCTGACAGGAAGAGCTGACACCTTACCTCAC
miRZIP-let-7f-2-3P	GCTATACAATCTACTGTCTTACCTCTGTCAAGAGAACAGACTAGACTGTATAG	CTATACAGTCTACTGTCTTCTGACAGGAAGATAAGGACAGTAGATTGTATAGC
miRZIP-NT1	CAAGCTGACCTGAAAGTCTTCAAGAGAGAACCTCAGGGTCAGCTT	CAAGCTGACCTGAAAGTCTCTGACAGGAAGACTCAGGGTCAGCTT
miRZIP-NT2	GCTAAGGTCAAGTCGCCCCGATCTTCTGTCAAGAGCGAGGGCGACTTAACCTTAGG	CCTAAGGTAAAGTCGCCCTCGCTCTGACAGGAAGATGGGGGCGACTTGACCTTAGC
miRZIP-NT3	GCAACAAGGTGAAGAGCACCCACCCCTTCTGTCAAGGAGTTGGTGTCTTCATCTGTTG	CAACAAGATGAAGAGCACCAACTCTGACAGGAAGGGGGTGGGTGCTTCACCTGTTGC
miRZIP-NT4	GCTAAGGTAAAGTCGCCCTCGCTTCAAGAGAACAGCAGGGCGACTAACCTTAGG	CCTAAGGTAAAGTCGCCCTCGCTCTGAAAGCGAGGGCGACTAACCTTAGC
miRZIP-NT5	GCAACAAGATGAAGAGCACCAACTCTCAAGAGAGTTGTTCTACTTCTGTTGAG	CTAACACCAGAGAAGTAGAACAACTCTTGAAGAGTTGGTGTCTTCATCTGTTGC

Table S3. An overview of the EV-BC pool infected samples before normalization

KM-H2 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	65.3%	2,000,000	116,841 (92.7%)	93,267 (92.4%)	135,002 (92.5%)
D13	78.5%	2,000,000	157,463 (92.4%)	183,180 (92.4%)	149,366 (92.5%)
D21	72.1%	2,000,000	160,855 (93.0%)	148,527 (93.0%)	176,961 (92.9%)
KM-H2 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	69.7%	2,000,000	55,124 (92.0%)	120,749 (92.9%)	140,012 (92.9%)
D13	77.3%	2,000,000	160,190 (92.6%)	137,003 (92.7%)	123,926 (92.7%)
D21	63.9%	2,000,000	81,761 (92.2%)	101,287 (92.8%)	89,748 (92.5%)
L540 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	77.3%	1,270,000	109,080 (92.3%)	120,355 (92.3%)	135,186 (92.4%)
D13	60.1%	1,200,000	111,375 (92.5%)	121,134 (92.1%)	107,458 (92.4%)
D21	90.8%	1,320,000	122,168 (92.2%)	89,641 (92.5%)	95,989 (91.8%)
L540 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	77.9%	1,010,000	139,801 (92.7%)	92,307 (93.0%)	115,886 (91.8%)
D13	57.4%	1,100,000	133,505 (92.2%)	278,249 (92.6%)	158,827 (92.4%)
D21	90.9%	1,160,000	79,069 (92.0%)	128,486 (92.4%)	159,826 (92.3%)
L428 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	83.6%	1,300,000	195,864 (92.4%)	59,529 (92.5%)	77,294 (92.9%)
D13	85.9%	1,300,000	57,553 (92.4%)	42,761 (92.8%)	80,383 (93.1%)
D21	77.4%	1,150,000	55,336 (91.9%)	85,659 (92.8%)	57,249 (93.5%)
L428 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	87.2%	1,300,000	100,314 (92.4%)	166,946 (93.1%)	132,859 (92.7%)
D13	83.0%	1,300,000	217,973 (93.1%)	72,161 (93.0%)	80,173 (92.4%)
D21	72.4%	1,100,000	208,992 (92.3%)	138,774 (92.0%)	180,581 (92.7%)

Table S4. An overview of the miRZIP pool infected samples before normalization

KM-H2 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	60.5%	1,460,000	61,693 (92.1%)	59,553 (92.0%)	78,131 (92.8%)
D13	65.3%	1,500,000	109,879 (92.0%)	112,420 (91.9%)	149,119 (92.3%)
D21	78.2%	1,700,000	44,537 (91.7%)	49,198 (91.9%)	63,269 (92.0%)
KM-H2 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	72.5%	1,500,000	41,723 (92.2%)	35,819 (91.8%)	51,558 (91.9%)
D13	60.9%	1,500,000	216,082 (91.8%)	47,324 (92.7%)	87,926 (92.7%)
D21	74.1%	1,660,000	106,071 (92.4%)	101,032 (92.3%)	68,881 (92.4%)
L540 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	81.6%	1,130,000	66,263 (93.0%)	55,346 (92.4%)	67,447 (92.6%)
D13	61.9%	1,200,000	62,293 (91.5%)	46,964 (92.4%)	62,648 (92.5%)
D21	91.5%	1,310,000	73,223 (92.6%)	133,582 (92.4%)	36,687 (92.1%)
L540 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	79.2%	1,380,000	54,683 (92.7%)	33,272 (92.2%)	36,651 (91.9%)
D13	66.9%	1,200,000	37,460 (91.4%)	50,030 (91.8%)	59,321 (92.3%)
D21	92.9%	1,320,000	67,277 (92.1%)	192,478 (90.5%)	51,751 (92.1%)
L428 1 st	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	89.7%	1,300,000	83,930 (92.4%)	86,752 (92.7%)	77,874 (92.1%)
D13	91.2%	1,300,000	75,433 (92.3%)	50,638 (92.5%)	73,552 (92.5%)
D21	76.1%	1,300,000	98,908 (92.7%)	89,004 (92.4%)	95,505 (92.2%)
L428 2 nd	GFP%	Sorted cells	Mapped read counts and percentage		
			PCR 1 (%)	PCR 2 (%)	PCR 3 (%)
D5	90.6%	1,300,000	85,798 (92.4%)	99,018 (92.5%)	76,480 (92.1%)
D13	94.4%	1,300,000	197,295 (92.8%)	111,294 (92.3%)	151,994 (91.6%)
D21	88.1%	1,080,000	105,527 (92.7%)	104,211 (92.4%)	92,298 (92.2%)