Table S4

Binding characteristics of MHV68 miRNA-host mRNA hybrids selected for validation.

Transcript	miRNA	Binding Sites	Number of Interactions	Region Targeted	Seed binding*	3' Binding+	Visual Representation of Binding^	EBV Target?	KSHV Target?
Arid1a	6-3p	1	130	3' UTR	seed 7m1	strong	UGAAACUGUG...UGAGGUGGUUU |||||| ⁞ ||||||||||| CAUUUGACCUAAGACUCCACCAAA	✓	✓
Ctsl	8-5p	1	112	3' UTR	other	strong	CACUCACUGGGGGUUUGGUC |||| |⁞⁞|||||||||| GAGUUAUUCCCAAACCAG	✓	
Ewsr1	7-5p	1	91	CDS	seed 7	moderate	AAAGGUGGAGGUGCGGUAACCU |||⁞|||||||||||| AUUCUACCUCCACGCCACU	✓	✓
Fus	5-5p	1	26	CDS	seed 6	moderate	AGAGUUGAGAUC.GGGUCGUCU |||||| |||| ACUCAACGAACAACCCAUAUCA	✓	✓
Ifitm3	7-5p	2	4	5' UTR-CDS	seed 7	moderate	AAAG.GUGGA....GGUGCGGUAACC ||| |||| ||||||| CUUCACACCAAGUACCACGCCUC	✓	
Phc3	6-3p	1	5	CDS	seed 6	strong	UGAAACUGUGUGAGGUGGUUUU |||||| |⁞ |||||||| CCUUUGAAAUCCUCCACCACUU	✓	✓
Foxj3	12-3p	2	5	3' UTR	other	strong	UUUGGUGUGGGAGUCCU.ACCCCUU ||| |||||| ||||| CAAACAA..UCAGGAAUGGGGUU	✓	✓
Kdm5b	1-3p	3	71	3' UTR	seed 7	weak	UAGAAAUGGC..CGUACUUCCUUU |||||||⁞|| ||| ATCUUUAUCGUGGCACAU	✓	✓
Trp53inp1	5-5p	1	5	5' UTR	other	moderate	AGAGUUGAGAUC.GGGTCGUC ||||| ⁞⁞|| |⁞ GCUCUCUAAUUUCA.CGUG		

* Indicates the complementarity within the miRNA seed sequence (miRNA nt 2-8): "seed 6" indicates complementarity of 6 consecutive nt within the seed sequence, "seed 7" indicates complementarity of all 7 nt, "seed 7m1" indicates 1 mismatch within the 7 nt seed, "other" indicates complementarity to less than 6 nt.

+ Indicates the extent of complementarity within the 3' portion of the miRNA (those nts downstream of the seed sequence).

^ Top strand is miRNA sequence, bottom strand is mRNA target sequence. Vertical lines between nucleotides indicates base pairing and dashed lines represent G:U wobble pairing. Dots between nucleotides represent a stretch of nucleotides on the opposing side which contains a bulge.