

Table S4. Fold changes of miRNAs among three proliferative model systems*

miRNA	LAT Y136F vs HP	LATY136F vs H poly	HP vs H poly
mmu-miR-150	2.05125	1.45025	-1.41441
mmu-miR-181a	-1.24194	-17.0887	-13.7597
mmu-miR-669f	-3.08868	-3.41972	-1.10718
mmu-miR-29c	2.09182	1.41124	-1.48226
mmu-miR-155	2.33373	2.1416	-1.08971
mmu-miR-467f	-1.70784	-2.56578	-1.50236
mmu-miR-466a/b-3p	-3.14156	-3.20508	-1.02022
mmu-miR-361	5.07191	1.91212	-2.65251
mmu-miR-547	-2.15841	-1.94257	1.11111
mmu-miR-1949	-1.95502	-2.56314	-1.31106
mmu-miR-345-3p	-2.40861	-1.17877	2.04333
mmu-miR-101b	1.37158	2.24132	1.63412
mmu-miR-340-5p	-1.79564	-2.19813	-1.22415
mmu-miR-148a	1.29683	3.54754	2.73555
mmu-miR-139-5p	-5.58714	-4.64108	1.20385
mmu-miR-132	3.93657	2.68011	-1.46881
mmu-miR-539	-2.09499	-1.42408	1.47111
mmu-miR-125a-5p	5.4581	2.03884	-2.67706
mmu-miR-130b	1.71777	2.339	1.36164

*Fold differences of miRNAs with Nanostring counts that passed the minimum intensity filter. miRNAs are ordered by rows according to expression in C57BL/6 naïve CD4⁺ T cells beginning with highest expression on the top. LAT Y136F indicates LAT Y136F CD4⁺ T cells, B6 HP indicates C57BL/6 CD4⁺ T cells undergoing homeostatic proliferation and B6 H poly indicates C57BL/6 CD4⁺ T cells from *H. polygyrus*-infected mice.