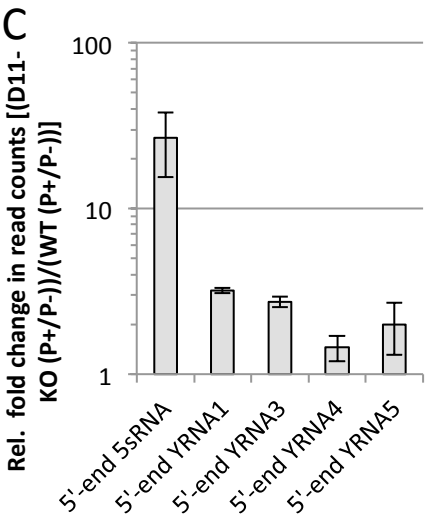
A

miRNA	Sequence	Read count/million reads (Rep 1, Rep 2)				Ratio (P+/P-) (Rep1, Rep2)	
		WT P-	WT P+	DUSP11-KO P-	DUSP11-KO P+	WT	D11-KO
BLV-miR-B5-5p	AAGGAAGGTTGTGGCTCAGAGGT	19870, 2760	31915, 1810	1847, 242	2410, 278	1.61, 0.66	1.30, 1.15
BV-miR-B5-3p	CTCGGACCGCAACCTCCCTTTC	1417, 1150	1390, 1021	1489, 1392	1138, 1233	0.98, 0.89	0.76, 0.89
BLV-miR-B2-5p	ACATGACTGAGTGTAGCGCAGA	10658, 7713	6436, 5647	2748, 738	2863, 1202	0.60, 0.73	1.04, 1.63
BLV-miR-B2-3p	TGCGTGTCACTCAGTCATTTT	1187, 4927	706, 5456	2153, 7850	2387, 6837	0.59, 1.11	1.11, 0.87
hsa-miR-10a-5p	TACCCTGTAGATCCGAATTTGTG	33070, 58933	31966, 59910	59056, 85080	45142, 68320	0.78, 1.02	0.68, 0.80
hsa-miR-92a-3p	TATTGCACTTGTCCCGGCCTGT	27074, 39940	20769, 28441	29323, 37787	22237, 28101	0.62, 0.71	0.68, 0.74
hsa-miR-25-3p	CATTGCACTTGTCTCGGTCTGA	2182930243	16034, 21166	23487, 27384	17877, 21400	0.60, 0.70	0.68, 0.78
hsa-miR-148a-3p	TCAGTGCACTACAGAACTTTGT	13923, 51391	10898, 54253	57100, 71919	26603, 59109	0.64, 1.06	0.42, 0.82
hsa-miR-7-5p	TGGAAGACTAGUGATTTTGTTGT	11061, 21296	11484, 19415	25732, 22770	17479, 19595	0.84, 0.91	0.61, 0.86

B

RNA	Sequence	Rep 1, Rep 2	
		Ratio WT (P+/P-)	Ratio D11KO (P+/P-)
5'-end 5sRNA	GTCTACGGCCATACCACCCTGAACGC	4.82, 3.38	49.1, 51.0
3'-end 5sRNA	ACCGGGTGCTGTAGGCTTT	0.73, 0.72	0.69, 0.22
5'-end YRNA1	GGCTGGTCCGAAGGTAGTGAGTTATCTCAATT	2.23, 3.12	6.58, 3.12
3'-end YRNA1	CTTCTCACTACTGCACTTGACTAGTCTT	0.91, 0.77	0.88, 0.23
5'-end YRNA3	GGCTGGTCCGAGTGCAGTGGTGTTTACAAC	0.62, 0.76	3.32, 0.87
3'-end YRNA3	CTCCCACTGCTTCACTTGACTAGCCTT	0.42, 0.68	0.92, 0.25
5'-end YRNA4	GGCTGGTCCGATGGTAGTGGGTTATCAGAACT	1.88, 1.85	3.65, 1.66
3'-end YRNA4	CCCCCACTGCTAAATTTGACTGGCTT	0.42, 0.54	0.84, 0.27
5'-end YRNA5	AGTTGGTCCGAGTGTTGTGGGTTATT	28.07, 7.07	70.43, 6.03
3'-end YRNA5	CTTGACTAGCTTGCTGTTT	0.51, 0.93	1.25, 0.26

C



D

5S rRNA	Sequence	Pumilio2-SRR048967	Pumilio2-SRR048968	AGO1-SRR048973.	AGO2-SRR048974	AGO2-SRR048975	AGO-3-SRR048976.	AGO3-SRR048977	AGO4-SRR048978	AGO4-SRR048979	AGO2-miR-124-SRR048980	AGO2-miR-7-SRR048981
5'-end	GTCTACGGCCATACCACCCTGAACGC	0	0	0	0	0	0	0	0	0	0	0
5'-end	GTCTACGGCCATACCACCCTGAAC	0	0	4	0	0	4	0	0	20	1	2
5'-end	GTCTACGGCCATACCACCCT	0	0	0	0	0	7	0	0	3	2	2
5'-end	GTCTACGGCCATACCACCCTGAACG	0	1	25	0	0	19	0	2	32	6	9
5'-end	GTCTACGGCCATACCACCCTGA	0	0	1	0	0	1	0	0	7	1	0
5'-end	GTCTACGGCCATACCACCCTG	0	0	70	0	1	32	0	3	6	17	20
Freq.	GTCTACGGCCATACCACCCTG…	1.00	1.00	0.69	0.99	1.00	0.59	1.00	1.00	1.00	0.90	0.96
	GTCTACGGCCACACCACCCTG…	0.00	0.00	0.31	0.01	0.00	0.41	0.00	0.00	0.00	0.10	0.04

Supplemental Figure 3. Small RNA sequencing of host and BLV small RNAs in WT and DUSP11-KO cells.
(A) Small RNA read counts from RNA treated with (P+) or without (P-) RNA-5'-polyphosphatase prior to library preparation from parental (WT) and DUSP11-KO HEK293T cells. The read counts for the most abundant miRNAs that perfectly mapped to the 5p arm or the 3p arm of BLV B2 and B5 pre-miRNAs in parental (WT) and DUSP11-KO HEK293T cells are shown in the table. The read counts for five host miRNAs, which are generally the 5 most abundant miRNAs in each small RNA library, are shown in the table. The read counts were normalized to reads per million total reads in each library. Two independent replicates are shown in the table separated by the comma. The ratio of phosphatase pre-treated to untreated (P+/P-) for both the WT and D11-KO cells is shown in the table. (B) Ratios of the total read counts (P+/P-) of the generally most abundant small RNA (18-32 nts) that maps to either the 5'-end or 3'-end of the 5s rRNA and the Y-RNAs (Supplemental Data 1). (C) Graph showing the average ratio (P+/P-) of the RNAs in (B). Ratios were normalized to the 3p arm. The DUSP11-KO ratios were then normalized to the WT ratio. (D) Meta analysis of PAR-CLIP data (Hafner et al., 2010). The read counts for the 5'-end derivative of the 5S rRNA are shown for indicated immunoprecipitated negative control (Pumilio) and the indicated AGO proteins. The transition (T to C) frequency observed at nucleotide 12 (highlight in red) of RNAs that map to the 5'-end of the 5S rRNA is shown for each library.