

Supplementary Table 5: Composition of small RNA libraries. We sequenced small RNA from the hot (H) and cold (C) evolved populations at multiple time points (hot at generations 22, 44 and 108; cold at generations 22 and 54) and assessed the abundance of reads mapping to TEs (i.e.: siRNAs and piRNAs), miRNAs, tRNAs, rRNAs and mRNAs. For each set of small RNAs we also estimated the fraction of reads mapping to the sense strand. t. [M.]: total number of reads in million; m. [M.]: mapped reads in million

sample	t. [M.]	m. [M.]	abundance [%]					fraction sense [%]				
			TE	miRNA	tRNA	rRNA	mRNA	TE	miRNA	tRNA	rRNA	mRNA
H1-22	16.2	9.63	27.2	62.0	0.8	4.3	5.6	52.6	100.0	99.9	100.0	51.6
H1-44	13.8	6.50	15.8	40.4	21.5	9.5	12.8	23.9	100.0	100.0	100.0	81.5
H1-108	12.7	6.76	27.2	60.5	1.1	4.4	6.9	25.2	100.0	99.9	99.9	35.0
H3-22	13.6	6.05	18.4	63.1	7.2	2.7	8.5	26.8	100.0	100.0	99.9	67.6
H3-44	14.1	7.68	15.8	40.0	24.5	7.8	11.9	25.5	100.0	100.0	100.0	79.2
H3-108	14.7	7.17	18.0	70.2	1.6	5.7	4.6	25.1	100.0	99.9	100.0	42.1
H5-22	14.6	7.60	22.2	65.7	2.7	2.3	7.1	26.4	100.0	100.0	99.8	51.4
H5-44	13.5	7.08	24.6	49.7	6.9	10.6	8.2	23.6	100.0	100.0	100.0	58.4
H5-108	15.2	7.64	25.9	60.0	1.1	6.5	6.5	25.0	100.0	99.8	100.0	37.3
C1-22	12.7	5.03	17.4	51.0	11.8	9.0	10.8	24.9	100.0	100.0	100.0	75.9
C1-54	12.2	6.07	25.5	61.7	1.2	5.8	5.9	24.6	100.0	99.9	99.9	40.5
C3-22	18.4	7.49	16.1	50.0	8.4	10.6	14.9	23.5	100.0	100.0	100.0	83.3
C3-54	14.4	7.81	23.7	61.9	1.8	6.6	6.0	24.7	100.0	99.9	100.0	42.6
C5-22	17.7	7.32	18.7	56.3	5.8	12.0	7.2	24.5	100.0	100.0	100.0	64.2
C5-54	16.7	8.53	21.8	62.8	1.8	8.2	5.3	23.1	100.0	99.9	100.0	38.2