

Additional file 1. Summary of small RNA sequences in 8 samples

Classification	Total	Female				Male			
		Brain	Heart	Liver	Muscle	Brain	Heart	Liver	Muscle
Raw Illumina GA reads	23366676	2688206	5596759	969577	3096459	1623849	4606782	516456	4268588
High quality reads after filtering single read sequences	19424182	2299762	4752051	783321	2437464	1460197	3819237	450480	3421670
Non-redundant sequences after filtering single read sequences	402321	141184	228117	84301	212667	78611	212343	46967	181443
Reads with perfect match to genome (%)	11708847 (60%)	1467218 (64%)	2861627 (60%)	439337 (56%)	2019463 (59%)	967322 (66%)	2291015 (60%)	252526 (56%)	1410339 (58%)
Non-redundant sequences with perfect match to genome (%)	66541 (17%)	29916 (21%)	44722 (20%)	23695 (28%)	49572 (23%)	13344 (17%)	43545 (21%)	13274 (28%)	45815 (25%)
Reads homology to miRBase miRNA (%)	12470982 (64%)	1619412 (70%)	3284065 (69%)	441943 (56%)	1168793 (48%)	1265741 (87%)	2361307 (62%)	329407 (73%)	2000314 (58%)
Non-redundant sequences homology to miRBase miRNA	78922	36880	47515	17609	30156	30511	42957	14049	38641
Reads originated from rRNA/tRNA/other ncRNAs (%)	4754931 (24%)	427621 (19%)	1028406 (22%)	211652 (27%)	939435 (39%)	35455 (2%)	1035338 (27%)	39073 (9%)	1037951 (30%)
Reads originated from mRNA (%)	37401 (0.2%)	2763 (0.1%)	5671 (0.1%)	2478 (0.3%)	6903 (0.3%)	989 (0.1%)	5567 (0.1%)	831 (0.2%)	12199 (0.4%)
Reads originated from repeats (%)	85655 (0.4%)	7492 (0.3%)	16568 (0.3%)	4109 (0.5%)	18463 (0.8%)	1018 (0.1%)	19471 (0.5%)	1154 (0.3%)	17380 (0.5%)
MiRNA species	193	186	179	164	175	184	180	164	177