

**Table S1** Summary of data output for each sample (LncRNA libraries)

Sample name	Raw reads	Clean reads	Raw bases(G)	Clean bases(G)	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
E120_1	95,136,750	94,162,346	14.27	14.12	0.01	97.99	94.87	48.39
E120_2	104,858,132	103,693,97	15.73	15.55	0.01	97.82	94.51	51.99
E120_3	109,873,850	108,854,76	16.48	16.33	0.01	97.91	94.75	51.99
E65_1	92,319,368	91,436,574	13.85	13.72	0.01	98.07	95.06	51.95
E65_2	95,265,442	94,404,738	14.29	14.16	0.01	98.1	95.11	52.43
E65_3	114,213,636	113,055,67	17.13	16.96	0.01	98.16	95.25	45.19
E90_1	91,771,374	90,803,258	13.77	13.62	0.03	97.33	92.59	48.6
E90_2	85,447,776	83,722,880	12.82	12.56	0.03	97.76	93.57	48.59
E90_3	85,950,416	84,254,962	12.89	12.64	0.03	97.69	93.43	50.76

**Table S2** Summary of data output for each sample (miRNA libraries)

Sample	Raw Reads	Clean Reads	Bases	Error rate	Q20	Q30	GC content
E120_3	24,594,694	24,108,334	1.230G	0.01%	98.94%	96.06%	49.94%
E120_2	23,480,919	22,890,002	1.174G	0.01%	98.84%	95.82%	50.29%
E120_1	19,106,255	17,689,794	0.955G	0.01%	98.14%	94.35%	50.08%
E90_2	18,281,030	17,152,251	0.914G	0.01%	98.21%	94.56%	48.92%
E90_3	16,751,062	15,648,767	0.838G	0.01%	98.22%	94.64%	49.43%
E90_1	11,090,195	10,186,863	0.555G	0.01%	98.52%	95.33%	49.55%
E65_2	21,689,760	21,261,809	1.084G	0.01%	98.85%	95.82%	49.50%
E65_3	28,099,273	27,418,451	1.405G	0.01%	98.71%	95.35%	50.09%
E65_1	21,919,844	21,424,462	1.096G	0.01%	98.87%	95.84%	50.39%