

Table S2 Summary of transcriptome and small RNA sequencing data

sample	RNA-Seq					Small RNA Sequencing				
	Raw reads	Clean reads	Valid%	Q30%	GC%	Raw reads	Lengh>30	Low_quality	Clean_reads	Q30(%)
CK1	20,331,308	19,184,623	94.36%	93.66%	45.03%	21,952,827	6,550,199	1,154	13,325,731	96.86
CK2	20,780,156	19,535,425	94.01%	93.04%	44.75%	24,163,572	4,242,635	751	16,105,323	97.11
CK3	20,063,749	19,108,715	95.24%	93.35%	44.79%	15,055,536	4,445,861	109	10,137,981	97.19
MeJA_1	22,516,698	21,246,757	94.36%	94.18%	45.00%	18,011,627	4,525,575	1,708	10,860,444	96.53
MeJA_2	20,558,249	19,398,764	94.36%	94.04%	44.65%	15,413,916	3,635,791	261	9,713,516	97.28
MeJA_3	21,877,359	20,678,480	94.52%	94.06%	44.23%	21,565,018	5,495,793	396	12,058,002	96.94