

Table S2

Quality of transcriptomic data.

Samples	Raw reads	Clean reads	Clean bases (Gb)	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)	Mapping ratio (%)
T_1	45988332	44135614	6.62	0.03	97.94	93.95	43.45	87.66
T_2	44417148	42770534	6.42	0.03	97.95	93.94	42.85	86.84
T_3	44607896	43458038	6.52	0.03	97.95	93.98	43.57	87.09
STS_1	54142434	52131192	7.82	0.03	97.9	93.77	44.67	87.89
STS_2	54342808	53193934	7.98	0.03	97.85	93.67	44.59	87.13
STS_3	50404382	48865720	7.33	0.03	98.11	94.29	44.5	87.92