

Table S2 Summary of transcriptome sequencing data.

	T1_1	T1_2	T1_3	T2_1	T2_2	T2_3	T4_1	T4_2	T4_3
Total Bases Count (Gb)	8.78	9.10	7.04	8.26	8.49	8.64	8.00	9.96	8.65
Average Read Length (Gb)	150	150	150	150	150	150	150	150	150
Q10 Bases Count (Gb)	8.78	9.1	7.04	8.26	8.49	8.64	8.00	9.96	8.65
Q10 Bases Ratio (%)	100	100	100	100	100	100	100	100	100
Q20 Bases Count (Gb)	8.58	8.89	6.87	8.07	8.3	8.44	7.81	9.76	8.46
Q20 Bases Ratio (%)	97.70	97.68	97.55	97.59	97.73	97.72	97.65	97.99	97.78
Q30 Bases Count (Gb)	8.22	8.52	6.57	7.72	7.96	8.10	7.48	9.40	8.12
Q30 Bases Ratio (%)	93.65	93.63	93.31	93.43	93.74	93.74	93.52	94.36	93.85
N Bases Count (Mb)	0.21	0.21	0.16	0.20	0.20	0.19	0.18	0.24	0.20
N Bases Ratio (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GC Bases Count (Gb)	4.07	4.21	3.24	3.84	3.96	4.08	3.80	4.68	4.07
GC Bases Ratio (%)	46.34	46.25	46.10	46.43	46.62	47.24	47.58	47.01	47.08