

Table S1. The quality and quantity of transcriptome sequencing data.

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q20(%)	Clean Reads Q30(%)	Clean Reads Ratio (%)
Budst-1	75.12	68.87	10.33	98.84	96.07	91.69
Budst-2	75.12	68.82	10.32	98.72	95.77	91.62
Budst-3	75.12	68.8	10.32	98.76	95.87	91.58
Budpest1	75.12	68.87	10.33	98.74	95.81	91.69
Budpest2	75.11	68.26	10.24	98.73	95.97	90.88
Budpest3	75.12	68.36	10.25	98.71	95.75	91.01
Inbud-1	75.12	68.4	10.26	98.72	95.76	91.06
Inbud-2	78.38	71.77	10.77	98.68	95.64	91.56
Inbud-3	75.12	68.9	10.33	98.71	95.72	91.72
ST-1	73.48	67.24	10.09	98.88	96.43	91.51
ST-2	75.11	67.79	10.17	98.54	95.47	90.25
ST-3	75.12	68.93	10.34	98.75	95.84	91.76
PEST-1	75.12	68.45	10.27	98.73	95.79	91.13
PEST-2	75.12	68.91	10.34	98.74	95.81	91.73
PEST-3	78.38	71.6	10.74	98.69	95.68	91.35
InTE-1	75.12	69.05	10.36	98.75	95.87	91.92
InTE-2	75.11	68.41	10.26	98.76	96.06	91.08
InTE-3	75.11	68.13	10.22	98.51	95.38	90.7