Supplementary Table S2. Overview of the transcriptome sequencing data and quality check.

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
EF_1	45.44	43.87	6.58	97.66	92.62	96.54
EF_2	45.44	43.85	6.58	98.09	93.91	96.5
EF_3	41.27	39.34	5.9	97.84	93.09	95.32
MF_1	45.44	44.31	6.65	97.56	92.31	97.51
MF_2	47.19	45.06	6.76	98.21	94.28	95.49
MF_3	45.44	43.85	6.58	98.14	94.07	96.5
WF_1	45.44	44.12	6.62	97.59	92.45	97.1
WF_2	45.44	44.15	6.62	98.07	93.8	97.16
WF_3	47.19	44.92	6.74	98.5	95.19	95.19