

Supplementary Table 1. Summary of output statistics of transcriptome sequencing

Sample	Raw Reads	Clean reads	Clean bases	Q20(%)	GC(%)
F6h	52486552	50568290	7.59G	97.20	51.17
M6h	66248620	63809956	9.57G	97.10	50.91
F12h	57236690	54783724	8.22G	96.87	51.67
M12h	60949966	58627158	8.79G	97.14	51.29
F24h	54166678	52846538	7.93G	96.86	51.08
M24h	54053506	52694604	7.9G	96.16	48.88