

**Table S2 Statistics of the data generated by the transcriptome sequencing**

Sample	Reads	Q30 (%)	Clean Reads	Clean Reads (%)	Mapped Reads	Mapped Reads (%)
					Reads	(%)
L1	72450762	93.45	66073712	91.20	57422777	86.91
L2	56381628	93.41	53342500	94.60	46895904	87.91
L3	63665920	93.60	59348140	93.22	51850102	87.37
LM1	71196840	93.60	66226606	93.02	57819332	87.31
LM2	59676280	93.20	55606620	93.19	48404720	87.05
LM3	54808230	93.04	51414164	93.81	44890399	87.31
M1	61149972	93.42	56830012	92.94	49361326	86.86
M2	53828280	93.09	49746932	92.42	42944848	86.33
M3	70223978	93.58	64041340	91.20	55648237	86.89
HM1	60016574	93.89	55375358	92.27	48525787	87.63
HM2	59726742	94.05	55123066	92.29	48369413	87.75
HM3	53454620	93.29	49866530	93.29	43519347	87.27
H1	61523686	93.28	56956508	92.58	49679777	87.22%
H2	66583494	93.43	63092836	94.76	55189741	87.47%
H3	59603740	93.30	55324322	92.82	48429139	87.54%