

**Supplemental Table S7.** Transcriptome sequencing data statistics

<b>sample name</b>	<b>ID</b>	<b>Clean reads</b>	<b>Clean bases</b>	<b>GC Content</b>	<b>%<math>\geq</math>Q30</b>
S1_rep1	T1	31,739,258	9,503,093,918	0.4563	0.9534
S1_rep2	T2	30,928,360	9,258,641,106	0.4575	0.9547
S1_rep3	T3	27,522,284	8,236,325,414	0.4582	0.9524
S2_rep1	T4	21,576,887	6,456,000,470	0.4611	0.9023
S2_rep2	T5	25,330,569	7,578,815,442	0.4603	0.9061
S2_rep3	T6	27,081,666	8,102,837,906	0.4620	0.9043
S3_rep1	T7	24,482,237	7,322,803,642	0.4623	0.9003
S3_rep2	T8	23,642,892	7,072,031,106	0.4591	0.9056
S3_rep3	T9	25,683,467	7,689,864,720	0.4598	0.9019
S4_rep1	T10	23,221,346	6,950,961,064	0.4606	0.9094
S4_rep2	T11	22,327,452	6,683,237,692	0.4601	0.9045
S4_rep3	T12	25,401,878	7,600,966,358	0.4598	0.9033
S5_rep1	T13	21,832,681	6,531,401,942	0.4595	0.9056
S5_rep2	T14	21,492,934	6,422,110,628	0.4600	0.9014
S5_rep3	T15	23,636,479	7,072,439,516	0.4590	0.8995
S6_rep1	T16	24,437,606	7,300,608,818	0.4590	0.9035
S6_rep2	T17	21,938,737	6,566,920,894	0.4597	0.9038
S6_rep3	T18	23038674	6894767462	0.4601	0.9029