

**Table S1** Summary of sequencing data quality

Sample	Raw Reads	Clean reads	Clean bases	Error(%)	Q20(%)	Q30(%)	GC(%)
A_1	48882404	48300674	7.25G	0.03	97.18	92.18	44.92
A_2	43846336	42986032	6.45G	0.03	95.24	93.14	44.41
A_3	57210364	55979060	8.4G	0.03	95.47	93.45	44.76
B_1	54257518	53353704	8G	0.03	94.93	92.76	44.38
B_2	48333432	47773134	7.17G	0.03	97.08	92.01	44.48
B_3	70107204	68709184	10.31G	0.03	96.31	94.35	45.23
C_1	45429078	44870166	6.73G	0.03	97.14	92.13	45.16
C_2	51137978	50283984	7.54G	0.03	97.18	92.23	44.38
C_3	59574510	58446284	8.77G	0.03	96.33	94.36	44.31
D_1	46570886	45692200	6.85G	0.03	95.38	93.34	45.24
D_2	46536406	45590504	6.84G	0.03	97.15	92.08	44.65
D_3	54457980	53217126	7.98G	0.03	95.25	93.18	44.51
E_1	52938882	51914108	7.79G	0.03	95.41	93.37	44.34
E_2	75908614	74100432	11.12G	0.03	94.89	92.73	46.52
E_3	44781362	44144740	6.62G	0.03	97.11	92.01	44.16
F_1	55636566	54614738	8.19G	0.03	96.61	91.04	44.71
F_2	54514410	53578788	8.04G	0.03	97.58	93.13	45.46
F_3	61489712	60443538	9.07G	0.03	97.18	92.12	45.56

**Table S2** List of splicing length distribution

Nucleotides Length(bp)	Transcripts	Unigenes
200-500	270,563	123,318
500-1000	150,345	139,092
1000-2000	125,279	123,842
>2000	58,731	58,613
Total	604,918	444,865
Min Length	201	201
Mean Length	890	1,094
Median Length	574	818
Max Length	14,246	14,246
N50	1,374	1,512
N90	373	529