

Supplementary Table 1. Summary of RNA sequencing

Data	Total reads	Total read bases (bp)
Raw data	308,869,074	31,195,776,474
Trimming data	293,851,562	29,364,649,219 (trimming rate: 94.13%)

Supplementary Table 2. Summary of assembly

Data	Total transcripts	Length			
		Total assembled bases	Min.	Max.	Avg.
All transcript contig	57,610	21,900,725	201	19,035	380.15
Only longest isoform per 'gene'	45,525	16,394,934	201	19,035	360.13
Clutstered contig 'Unigene'	44,259	15,806,918	201	19,035	357.15

Supplementary Table 3. Annotation result

Data	Total Unigene	Nucleotide BLAST (version: 20180116)
Annotation result	44,259	16,354 (annotation rate: 36.95%)