

Table 1 Summary of the transcriptome assembly and annotation

Reads	Total Raw Reads	837.99M
	Total Clean Reads	622.96M
	Clean Nucleotides (nt)	148.06G
	Reads length (nt)	126 x 2
	Q20 percentage	99.5%
	GC percentage	52%
	Total Number	94,063
Contigs	Total Length (nt)	152,960,919
	Mean Length (nt)	1,626
	Median Length (nt)	1,189
	N50 (nt)	2,470
	Total Number	49,135
Unigenes	Total Length (nt)	75,064,073
	Mean Length (nt)	1,527
	Median Length (nt)	959
	N50 (nt)	2,668
	L50 number	8,949
	Min Unigene Length (nt)	201
	Max Unigene Length (nt)	16,999
	Average Depth (×)	803 x
	NCBI-nr	33,909 (69.01%)
	NCBI-nt	41,045 (83.54%)
Unigene Annotation	KEGG	5,625(11.45%)
	Swiss-Prot	23,976 (48.80%)
	PFAM	23,713 (48.26%)
	GO	24,108 (49.06%)
	COG	10,313 (20.99%)
	At least one Database	43,061 (87.64%)