

TABLE S1. Length distribution of raw data

Raw Reads	Raw Data(bp)	Q20(%)	Q30(%)	GC(%)	Reads Len.(bp)
58,881,563	11,776,3112,600	97.52	93.11	43.90	101

TABLE S2. Length distribution of assembled contigs, transcripts, and unigenes

	Total Length (bp)	Sequence No.	Max Length (bp)	Average Length (bp)	N50	>N50 Reads No.
Contigs	98,418,921	316,703	16,007	310.76	522	38,638
Transcripts	141,535,320	145,857	16,008	970	1,636	27,911
Unigenes	54,594,810	39,625	16,008	1,378	1,971	9,484