

**Table S6: Genome assembly validation by transcripts mapping**

		>0%Aligned		>%50 aligned		>%80 aligned	
Transcripts length	Total transcripts	Number of transcripts	Percentage (%)	Number of transcripts	Percentage (%)	Number of transcripts	Percentage (%)
>500 bp	39,106	38,520	98.50	38,174	97.62	37,460	95.79
>1000 bp	18,184	17,966	98.80	17,786	97.81	17,421	95.80

The male and female transcriptomes were from eleven mixed tissues respectively. Then the sequencing short reads were assembled to transcripts. Transcripts were mapped to *L. crocea* genome by BLAT to validate completeness of genome assembly.