

Table S1. The statistics of sequencing raw data from Pacific sequencing.

PacBio	Sample	Cells	Subreads Mean Length (Kb)	Subreads N50 (Kb)	Subreads Read Base (Gb)
	Amo-1	13	11.9	17.1	110.3
	Sample			AMO	
	Raw Paired-end Reads			654,107,968	
	Clean Paired-end Reads			649,325,992	
Hi-C	Clean Bases(bp)			92,123,475,893	
	Clean Paired-end Reads Rate (%)			99.27	
	Clean Q30 Bases Rate (%)			93.13	

Raw paired-end reads (bp): Number of reads obtained by Hi-C sequencing; Clean paired-end reads: Number of high-quality reads obtained after filtering; Clean bases (bp): Number of bases in clean data; Clean paired-end reads rate (%): The ratio of high-quality sequences obtained after filtering to raw paired-end reads; Clean Q30 bases rate (%): The ratio of bases with a sequencing quality value greater than 30 (error rate less than 0.1%) to the total bases in clean paired-end reads.