

**Table S10. Summary of sequence data used for genome assembly**

<b>Platform</b>	<b>PacBio (HiFi)</b>	
	SMRT cell 1	SMRT cell 2
Number of reads	2.0M	2.2M
Yield (bp)	27.6 GB	26.4 GB
Read quality (median)	Q33	Q33
Coverage	72.40051191	69.18795232