

**S2 Table. Inferred genome properties based on k-mer content**

	<b>Heterozygosity</b>	<b>Haploid length</b>	<b>Repeat Length</b>	<b>Unique Length</b>	<b>Read Error Rate</b>
Minimum	0.0302	~249 Mb	105.6 Mb	143.2 Mb	0.00151
Maximum	0.0306	~249.2 Mb	105.7 Mb	143.4 Mb	0.00151