

**Supplemental Table S1:** HiFiasm Contig Assembly Statistics and Benchmarking Universal Single Copy Gene (BUSCO) Completeness in four *Macadamia* Species

Contig Assembly	<i>M. jansanii</i>			<i>M. ternifolia</i>			<i>M. integrifolia</i>			<i>M. tetraphylla</i>		
	Hap 1	Hap2	Collapsed	Hap 1	Hap2	Collapsed	Hap 1	Hap2	Collapsed	Hap 1	Hap2	Collapsed
N50	24 Mb	14 Mb	46 Mb	27 Mb	23 Mb	47 Mb	10 Mb	9.8Mb	45 Mb	34 Mb	27 Mb	49 Mb
Length	816 Mb	776 Mb	826 Mb	810 Mb	783 Mb	827 Mb	813 Mb	797 Mb	824 Mb	821 Mb	806 Mb	839 Mb
Total Contigs	879	363	779	883	361	803	1254	484	1049	809	262	742
Contigs > 1Mb	72	96	30	55	64	28	116	115	27	55	56	27
Contigs >10Mb	25	21	19	21	23	18	20	18	17	23	19	18
BUSCO	97.8%	96.7%	97.9%	97.4%	97.7%	97.7%	97.2%	97.4%	97.6%	97.4%	97.6%	97.7%
Single BUSCO	84.0%	83.3%	84.1%	83.6%	84.0%	83.6%	83.7%	83.5%	83.9%	83.3%	83.8%	83.5%
Double busco	13.8%	13.4%	13.8%	13.8%	13.7%	14.1%	13.5%	13.9%	13.7%	14.1%	13.8%	14.2%
Fragmented	0.6%	0.7%	0.7%	0.8%	0.9%	0.8%	0.9%	0.7%	0.6%	0.8%	0.7%	0.7%
Missing	1.6%	2.6%	1.4%	1.8%	1.4%	1.5%	1.9%	1.9%	1.8%	1.8%	1.7%	1.6%