

Supplemental Table S3: Genome estimation statistics of four *Macadamia* species through K-mer analysis (using Jellyfish tool) and flow cytometry.

Methods to estimate genome size	Parameters	<i>M. janseni</i>	<i>M. ternifolia</i>	<i>M. integrifolia</i>	<i>M. tetraphylla</i>
K-mer analysis	Length	643 Mb	662 Mb	676 Mb	653 Mb
	Heterozygous	0.66%	0.99%	1.55%	1.33%
	Unique	69.10%	63.70%	63.20%	63.50%
	Kcov	16.3	7.74	9.33	6.76
	err	0.35%	0.14%	2.27%	0.15%
	Dup	0.65%	0.26%	0.65%	0.49%
Flow cytometry	Length	769 Mb	775 Mb	747 Mb	796 Mb
	Coefficient of variation	1.19%	0.49%	0.80%	0.62%