Table 1: Statistics for the best assembled accession.

	Subsection	Species	Accession	# contigs (>= 1kb)	Largest contig (Mb)	Contigs >= 1 kb	Contigs >= 25 kb	Contigs >= 50kb	Total length	Genome Size (GS)	% Genome Covered	N50	% N	# Gene Models	# BUSCOs	% recovered	# partial BUSCO
affold Statistics	Austroamericana	G. raimondii	Paterson 2012	1,033	70.71	761.41	754.80		761.41	880	86.5%	62.18	2%				
	Austroamericana	G. raimondii	D5-8	1,431	53.83	589.99	585.87	585.79	592.04	880	67.3%	48.45	14%	30,475	1,339	93%	27
	Caducibracteata	G. armourianum	D2-1-6	13,359	55.08	645.03	600.41	599.97	671.70	856	78.5%	47.59	15%	28,845	1,124	78%	55
	Caducibracteata	G. harknessii	JFW	20,602	52.42	615.99	541.69	540.67	643.05	910	70.7%	43.64	7%	36,068	1,294	90%	51
	Caducibracteata	G. turneri	D10-7	18,841	49.15	742.21	654.97	601.54	774.62	910	85.1%	33.33	2%	45,244	1,366	95%	17
	Erioxylum	G. aridum	DRD-185	21,813	52.48	619.71	552.02	551.45	648.51	919	70.6%	42.90	8%	35,142	1,285	89%	47
	Erioxylum	G. lobatum	D7-157	22,383	53.83	625.55	555.17	554.44	654.85	934	70.1%	43.64	8%	35,572	1,310	91%	41
	Erioxylum	G. laxum	D9-4	16,668	60.54	689.25	623.49	621.55	720.31	934	77.1%	48.55	13%	32,375	1,321	92%	37
	Erioxylum	G. schwendimanii	D11-1	18,906	52.32	623.31	526.16	513.54	651.41	929	70.1%	40.29	5%	38,314	1,348	94%	25
Š	Houzingenia	G. thurberi	D1-35	15,309	47.60	582.19	505.27	498.80	605.21	841	72.0%	37.86	4%	37,553	1,342	93%	26
	Houzingenia	G. trilobum	D8-8	14,099	44.53	562.98	483.41	474.98	586.05	851	68.9%	36.15	5%	36,663	1,321	92%	43
	Integrifolia	G. davidsonii	D3D-27	16,779	48.06	603.64	517.19	506.66	629.89	910	69.2%	38.65	3%	38,755	1,237	86%	41
	Integrifolia	G. klotzschianum	D3K-57	16,881	46.26	569.35	495.76	492.77	596.12	880	67.7%	37.84	5%	37,444	1,332	93%	37
	Selera	G. gossypioides	D6-5	23,734	42.78	554.55	446.85	441.62	585.41	841	69.6%	33.53	4%	26,492	1,133	79%	41