

Table 1: All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Assembly	ma.T0	ma.T1	ref_ma
# contigs (≥ 0 bp)	5276	4698	8017
# contigs (≥ 1000 bp)	37	36	73
# contigs (≥ 5000 bp)	4	0	3
# contigs (≥ 10000 bp)	0	0	0
# contigs (≥ 25000 bp)	0	0	0
# contigs (≥ 50000 bp)	0	0	0
Total length (≥ 0 bp)	998182	921129	1635713
Total length (≥ 1000 bp)	86695	67562	157811
Total length (≥ 5000 bp)	24070	0	20505
Total length (≥ 10000 bp)	0	0	0
Total length (≥ 25000 bp)	0	0	0
Total length (≥ 50000 bp)	0	0	0
# contigs	140	175	204
Largest contig	7771	4781	7844
Total length	157407	160489	251304
Reference length	119667750	119667750	119667750
GC (%)	35.36	35.13	34.16
Reference GC (%)	36.06	36.06	36.06
N50	1149	906	1405
N75	734	642	812
L50	30	50	47
L75	75	104	108
# misassemblies	2	0	1
# misassembled contigs	2	0	1
Misassembled contigs length	1854	0	1122
# local misassemblies	9	2	5
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	7	7	8
# unaligned contigs	13 + 27 part	24 + 23 part	12 + 26 part
Unaligned length	67535	61353	59304
Genome fraction (%)	0.072	0.080	0.155
Duplication ratio	1.039	1.039	1.039
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	352.45	199.22	121.72
# indels per 100 kbp	224.18	220.19	127.67
Largest alignment	¹ 2847	2102	7092
Total aligned length	86584	95909	187332
NA50	413	530	804
NGA50	-	-	-
LA50	99	104	78