Rei	oa	rt

Report	
	AJ055.CanuL
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	6
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	5728738
Total length (>= 1000 bp)	5728738
Total length (>= 5000 bp)	5722810
Total length (>= 10000 bp)	5722810
Total length (>= 25000 bp)	5707034
Total length (>= 50000 bp)	5678683
# contigs	9
Largest contig	3169885
Total length	5728738
Reference length	5504133
GC (%)	57.14
Reference GC (%)	57.38
N50	3169885
NG50	3169885
N75	1809348
NG75	1809348
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1809348
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	5 + 1 part
Unaligned length	221964
Genome fraction (%)	99.785
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.28
# indels per 100 kbp	165.41
	3169756
Largest alignment	5506645
Total aligned length NA50	3169756
NGA50	3169756
NA75	
	688559
NGA75	1120789
LA50	1
LGA50	1
LA75	3
LGA75	2

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).

Misassemblies report

	AJ055.CanuL
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1809348
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	345
# indels	9085
# indels (<= 5 bp)	9080
# indels (> 5 bp)	5
Indels length	9464

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).

Unaligned report

	AJ055.CanuL
# fully unaligned contigs	5
Fully unaligned length	50055
# partially unaligned contigs	1
Partially unaligned length	171909
# N's	0

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).





















