Report

Report	
	AJ055.MiniCL
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	5634250
Total length (>= 1000 bp)	5634250
Total length (>= 5000 bp)	5634250
Total length (>= 10000 bp)	5634250
Total length (>= 25000 bp)	5634250
Total length (>= 50000 bp)	5634250
# contigs	16
Largest contig	1138302
Total length	5634250
Reference length	5504133
GC (%)	57.13
Reference GC (%)	57.38
N50	470381
NG50	470381
N75	298434
NG75	298434
L50	4
LG50	4
L75	7
LG75	7
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	166422
Genome fraction (%)	98.626
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.91
# indels per 100 kbp	639.88
Largest alignment	1138217
Total aligned length	5467427
NA50	470380
NGA50	470380
NA75	298434
NGA75	298434
LA50	4
LGA50	4
LA75	7
LGA75	7
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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.MiniCL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	1895
# indels	34736
# indels (<= 5 bp)	34577
# indels (> 5 bp)	159
Indels length	46912

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.MiniCL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	166422
# 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).



















