Report

Report	
	AJ292.MiniCL
# contigs (>= 0 bp)	6
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	6
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	6
Total length (>= 0 bp)	5414604
Total length (>= 1000 bp)	5414604
Total length (>= 5000 bp)	5414604
Total length (>= 10000 bp)	5414604
Total length (>= 25000 bp)	5414604
Total length (>= 50000 bp)	5414604
# contigs	6
Largest contig	1660035
Total length	5414604
Reference length	5445112
GC (%)	57.57
Reference GC (%)	57.62
N50	1327492
NG50	1327492
N75	720527
NG75	720527
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	1029778
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	3766
Genome fraction (%)	98.916
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17.79
# indels per 100 kbp	409.22
Largest alignment	1660035
Total aligned length	5410760
NA50	1327480
NGA50	1327480
NA75	638853
NGA75	
	638853
LA50	2
LGA50	2
LA75	4
LGA75	4

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

	AJ292.MiniCL
# misassemblies	3
# relocations	1
# translocations	0
# inversions	2
# misassembled contigs	2
Misassembled contigs length	1029778
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	958
# indels	22041
# indels (<= 5 bp)	21973
# indels (> 5 bp)	68
Indels length	30126

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

Unaligned report

	AJ292.MiniCL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	3766
# 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).



















