Report

	final.contigs
# contigs (>= 0 bp)	55818
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp) # contigs (>= 10000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16992122
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	550
Largest contig	778
Total length	297680
Reference length	4641652
GC (%)	51.06
Reference GC (%)	50.79
N50	531
N75	511
L50	260
L75	403
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	12 + 2 part
Unaligned length	6497
Genome fraction (%)	6.056
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2062.68
# indels per 100 kbp	0.71
Largest alignment	778
NA50	531
NGA50	-
NA75	510
LA50	261
LA75	404
	-

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	5798
# indels	2
# short indels	2
# long indels	0
Indels length	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).

Unaligned report

	final.contigs
# fully unaligned contigs	12
Fully unaligned length	6187
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	310
# 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).















