Report

	final.contigs
# contigs (>= 1000 bp)	1698
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2802402
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3795
Largest contig	4997
Total length	4305266
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.78
N50	1285
NG50	1213
N75	854
NG75	767
L50	1127
LG50	1262
L75	2161
LG75	2474
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 4 part
Unaligned length	263
Genome fraction (%)	87.909
Duplication ratio	1.055
# N's per 100 kbp	0.00
# mismatches per 100 kbp	99.82
# indels per 100 kbp	0.12
Largest alignment	4997
NA50	1285
NGA50	1213
NA75	853
NGA75	767
LA50	1127
LGA50	1262
LA75	2162
LGA75	2474

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	4073
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	263
# 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).















