Report

	final conting
#	final.contigs
# contigs (>= 1000 bp)	1830
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4127099
Total length (>= 5000 bp)	425185
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2724
Largest contig	9591
Total length	4790571
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	2241
NG50	2215
N75	1372
NG75	1328
L50	694
LG50	709
L75	1373
LG75	1411
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0 + 0 part
Genome fraction (%)	95.323
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.80
# indels per 100 kbp	0.00
Largest alignment	9591
NA50	2241
NGA50	2215
NA75	1372
NGA75	1328
LA50	694
LGA50	709
	709 1373

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	0
# mismatches	315
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Unaligned report

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















