Report

# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp)	final.contigs 1721 89
# contigs (>= 5000 bp) # contigs (>= 10000 bp)	
# contigs (>= 10000 bp)	
3 `	2
	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4015400
Total length (>= 5000 bp)	559709
Total length (>= 10000 bp)	24013
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2583
Largest contig	12951
Total length	4645350
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	2301
NG50	2301
N75	1403
NG75	1404
L50	635
LG50	635
L75	1278
LG75	1276
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.822
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.49
# indels per 100 kbp	0.00
Largest alignment	12951
NA50	2301
NGA50	2301
NA75	1403
NGA75	1404
LA50	635
LGA50	635
	1270
LA75	1278

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	157
# 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).















