## Report

	final.contigs
# contigs (>= 1000 bp)	275
# contigs (>= 5000 bp)	212
# contigs (>= 10000 bp)	153
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4662751
Total length (>= 5000 bp)	4475089
Total length (>= 10000 bp)	4004223
Total length (>= 25000 bp)	2571490
-	
Total length (>= 50000 bp)	716301 282
# contigs	
Largest contig	74679
Total length	4667619
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	28606
NG50	28919
N75	15380
NG75	15512
L50	59
LG50	58
L75	113
LG75	112
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.960
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.42
# indels per 100 kbp	0.00
Largest alignment	74679
NA50	28606
NGA50	28919
NA75	15380
NGA75	15512
LA50	59
LGA50	58
LA75	113
LGA75	112

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	437
# 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).















