## Report

	final.contigs
# contigs (>= 1000 bp)	1855
# contigs (>= 5000 bp)	79
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4211773
Total length (>= 5000 bp)	469051
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2730
Largest contig	9591
Total length	4863070
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	2277
NG50	2279
N75	1384
NG75	1387
L50	696
LG50	694
L75	1378
LG75	1375
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.802
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.53
# indels per 100 kbp	0.00
Largest alignment	9591
NA50	2277
NGA50	2279
NA75	1384
NGA75	1387
LA50	696
	694
LGA50	
LGA50 LA75	1378

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	166
# 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).















