## Report

	final.contigs
# contigs (>= 1000 bp)	1511
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2639292
Total length (>= 5000 bp)	63112
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3781
Largest contig	6821
Total length	4204524
Reference length	4857432
GC (%)	52.15
Reference GC (%)	52.22
N50	1265
NG50	1104
N75	791
NG75	639
L50	1034
LG50	1311
L75	2093
LG75	2785
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	98
Genome fraction (%)	79.853
Duplication ratio	1.084
# N's per 100 kbp	0.00
# mismatches per 100 kbp	546.18
# indels per 100 kbp	0.05
Largest alignment	6821
NA50	1265
NGA50	1104
NA75	791
NGA75	639
LA50	1034
LGA50	1311
LA75	2093
LGA75	2786

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	21185
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	98
# 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).















