## Report

	final.contigs
# contigs (>= 0 bp)	8502
# contigs (>= 1000 bp)	237
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4390792
Total length (>= 1000 bp)	284621
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3595
Largest contig	2247
Total length	2468572
Reference length	4641652
GC (%)	50.66
Reference GC (%)	50.79
N50	669
NG50	518
N75	575
L50	1446
LG50	3305
L75	2444
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	3854
# local misassemblies	5
# unaligned contigs	82 + 31 part
Unaligned length	51301
Genome fraction (%)	48.998
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2656.21
# indels per 100 kbp	3.78
Largest alignment	2160
NA50	666
NGA50	511
NA75	570
LA50	1451
LGA50	3326
LA75	2455

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	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	3854
# local misassemblies	5
# mismatches	60411
# indels	86
# short indels	86
# long indels	0
Indels length	88

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	82
Fully unaligned length	47803
# partially unaligned contigs	31
# with misassembly	0
# both parts are significant	0
Partially unaligned length	3498
# 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).

















