## Report

	final.contigs
# contigs (>= 0 bp)	10015
# contigs (>= 1000 bp)	3621
# contigs (>= 5000 bp)	34
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10040043
Total length (>= 1000 bp)	6609169
Total length (>= 5000 bp)	206120
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6795
Largest contig	8916
Total length	8911858
Reference length	9283304
N50	1531
N75	982
L50	1889
L75	3697
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	3
# unaligned contigs	1 + 0 part
Unaligned length	515
Genome fraction (%)	91.496
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	72.69
# indels per 100 kbp	0.12
Largest alignment	8916
NA50	1529
NA75	982
LA50	1889
LA75	3698

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	3
# mismatches	6174
# indels	10
# short indels	10
# long indels	0
Indels length	10

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	1
Fully unaligned length	515
# 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).











