## Report

	final.contigs
# contigs (>= 1000 bp)	1348
# contigs (>= 5000 bp)	282
# contigs (>= 10000 bp)	32
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4723851
Total length (>= 5000 bp)	2081637
Total length (>= 10000 bp)	414611
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1662
Largest contig	21956
Total length	4952692
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	4221
NG50	4297
N75	2533
NG75	2629
L50	369
LG50	358
L75	746
LG75	718
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3170
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.019
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.79
# indels per 100 kbp	0.04
Largest alignment	21956
NA50	4221
NGA50	4297
NA75	2533
NGA75	2628
LA50	369
LGA50	358
LA75	746
LGA75	718

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3170
# local misassemblies	0
# mismatches	1577
# 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	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).















