Report

	final.contigs
# contigs (>= 1000 bp)	1506
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2275600
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4246
Largest contig	4818
Total length	4207973
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	1057
NG50	953
N75	746
NG75	626
L50	1340
LG50	1663
L75	2522
LG75	3236
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	112
Genome fraction (%)	82.007
Duplication ratio	1.056
# N's per 100 kbp	0.00
# mismatches per 100 kbp	137.90
# indels per 100 kbp	0.28
Largest alignment	4818
NA50	1057
NGA50	953
NA75	744
NGA75	626
LA50	1340
LGA50	1663
LA75	2523
LGA75	3238

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	5
# relocations	3
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# mismatches	5493
# indels	11
# short indels	11
# long indels	0
Indels length	11

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	112
# 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).

















