Report

	final.contigs
# contigs (>= 1000 bp)	1574
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2387361
Total length (>= 5000 bp)	16451
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4062
Largest contig	6221
Total length	4141631
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1111
NG50	1024
N75	769
NG75	663
L50	1274
LG50	1509
L75	2395
LG75	2920
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	13721
# local misassemblies	3
# unaligned contigs	0 + 17 part
Unaligned length	541
Genome fraction (%)	83.504
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	844.67
# indels per 100 kbp	10.19
Largest alignment	6221
NA50	1106
NGA50	1021
NA75	766
NGA75	662
LA50	1278
LGA50	1513
LA75	2402
LGA75	2928

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	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	13721
# local misassemblies	3
# mismatches	32739
# indels	395
# short indels	394
# long indels	1
Indels length	547

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	17
# with misassembly	0
# both parts are significant	0
Partially unaligned length	541
# 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).

















