Report

	final.contigs
# contigs (>= 1000 bp)	1106
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1642138
Total length (>= 5000 bp)	10187
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3450
Largest contig	5185
Total length	3287719
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	999
NG50	763
N75	719
L50	1108
LG50	1883
L75	2079
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	18308
# local misassemblies	3
# unaligned contigs	0 + 5 part
Unaligned length	315
Genome fraction (%)	68.646
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	967.77
# indels per 100 kbp	0.78
Largest alignment	5185
NA50	998
NGA50	762
NA75	719
LA50	1111
LGA50	1888
LA75	2084

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	11
# relocations	11
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	11
Misassembled contigs length	18308
# local misassemblies	3
# mismatches	30836
# indels	25
# short indels	25
# long indels	0
Indels length	35

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	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	315
# 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).















