Report

	final.contigs
# contigs (>= 1000 bp)	1293
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1852001
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4395
Largest contig	4336
Total length	4020549
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.78
N50	952
NG50	859
N75	697
NG75	601
L50	1456
LG50	1799
L75	2695
LG75	3415
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 7 part
Unaligned length	750
Genome fraction (%)	80.152
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	282.87
# indels per 100 kbp	0.16
Largest alignment	4336
NA50	952
NGA50	859
NA75	697
NGA75	601
LA50	1456
LGA50	1799
LA75	2695
LGA75	3416

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	10524
# indels	6
# short indels	6
# long indels	0
Indels length	6

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	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	750
# 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).















