Report

	final.contigs
# contigs (>= 1000 bp)	1828
# contigs (>= 5000 bp)	57
# contigs (>= 3000 bp) # contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
-	
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3843133
Total length (>= 5000 bp)	349017
Total length (>= 10000 bp)	14787
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2906
Largest contig	14787
Total length	4629653
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	1977
NG50	1967
N75	1238
NG75	1236
L50	757
LG50	760
L75	1496
LG75	1503
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.394
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.36
# indels per 100 kbp	0.14
Largest alignment	14787
NA50	1977
NGA50	1967
NA75	1238
NGA75	1236
LA50	757
LGA50	760
LA75	1496
LGA75	1503
25,775	1 1505

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	0
# mismatches	2584
# 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	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).















