Report

	final.contigs
# contigs (>= 0 bp)	4321
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1948663
Total length (>= 1000 bp)	33234
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1129
Largest contig	1965
Total length	712668
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.79
N50	608
N75	550
L50	480
L75	790
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	2351
# local misassemblies	0
# unaligned contigs	88 + 11 part
Unaligned length	52147
Genome fraction (%)	14.037
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3281.06
# indels per 100 kbp	2.00
Largest alignment	1965
NA50	602
NGA50	-
NA75	538
LA50	484
LA75	797

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	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	2351
# local misassemblies	0
# mismatches	21377
# indels	13
# short indels	13
# long indels	0
Indels length	13

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	88
Fully unaligned length	50044
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2103
# 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).

Nx

NGx

Contig length (bp)

x

final.contigs

Cumulative length

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)

NAx

Contig length (bp) vs x

— final.contigs

NGAx