Report

	final.contigs
# contigs (>= 0 bp)	5326
# contigs (>= 1000 bp)	809
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3611011
Total length (>= 1000 bp)	1111056
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3188
Largest contig	4425
Total length	2765777
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	891
NG50	606
N75	674
L50	1098
LG50	2377
L75	1991
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	12815
# local misassemblies	0
# unaligned contigs	1591 + 11 part
Unaligned length	1310413
Genome fraction (%)	31.148
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	626.71
# indels per 100 kbp	0.21
Largest alignment	3996
NA50	535
NGA50	-
LA50	1457

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	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	12815
# local misassemblies	0
# mismatches	9061
# indels	3
# short indels	3
# long indels	0
Indels length	3

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	1591
Fully unaligned length	1306403
# partially unaligned contigs	11
# with misassembly	1
# both parts are significant	0
Partially unaligned length	4010
# 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).

















