Report

	final conting
# conting (> = 0 bn)	final.contigs
# contigs (>= 0 bp)	13973
# contigs (>= 1000 bp)	1785
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8354300
Total length (>= 1000 bp)	2532780
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5903
Largest contig	4533
Total length	5401180
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	957
NG50	1054
N75	699
NG75	795
L50	1957
LG50	1579
L75	3617
LG75	2852
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4764 + 21 part
Unaligned length	3935374
Genome fraction (%)	30.977
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	676.08
# indels per 100 kbp	0.49
Largest alignment	4533
NGA50	-
	<u> </u>

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9721
# indels	7
# short indels	7
# long indels	0
Indels length	7

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	4764
Fully unaligned length	3928498
# partially unaligned contigs	21
# with misassembly	1
# both parts are significant	0
Partially unaligned length	6876
# 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).















