Report

	final conting
#	final.contigs
# contigs (>= 1000 bp)	1753
# contigs (>= 5000 bp)	28
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3469843
Total length (>= 5000 bp)	174905
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3133
Largest contig	9656
Total length	4468356
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1738
NG50	1693
N75	1059
NG75	997
L50	825
LG50	875
L75	1638
LG75	1765
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.511
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.56
# indels per 100 kbp	
	0.05 9656
Largest alignment	
NA50	1738
NGA50	1693
NA75	1059
NGA75	997
LA50	825
LGA50	875
LA75	1638
LGA75	1765

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	625
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).















