## Report

	final.contigs
# contigs (>= 1000 bp)	1197
	0
# contigs (>= 5000 bp)  # contigs (>= 10000 bp)	0
# contigs (>= 10000 bp)	<del> </del>
# contigs (>= 25000 bp) # contigs (>= 50000 bp)	0
	0
Total length (>= 1000 bp)	1698098
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)  Total length (>= 50000 bp)	0
	0
# contigs	3919
Largest contig	4826
Total length	3626712
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	968
NG50	817
N75	714
NG75	536
L50	1315
LG50	1887
L75	2410
LG75	3638
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	74.292
Duplication ratio	1.052
# N's per 100 kbp	0.00
# mismatches per 100 kbp	89.90
# indels per 100 kbp	0.06
Largest alignment	4826
NA50	968
NGA50	817
NA75	714
NGA75	536
LA50	1315
LGA50	1888
LA75	2410
LGA75	3638
20,775	1 2020

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	3100
# 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).















