## Report

	final.contigs
# contigs (>= 1000 bp)	1795
	31
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp) # contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	
Total length (>= 5000 bp)	3556937 190855
Total length (>= 10000 bp)	190833
Total length (>= 10000 bp)  Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3148
Largest contig	
Total length	9656
	4532931
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	1751
NG50	1717
N75	1083
NG75	1040
L50	829
LG50	861
L75	1644
LG75	1721
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.020
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.83
# indels per 100 kbp	0.00
Largest alignment	9656
NA50	1751
NGA50	1717
NA75	1083
NGA75	1040
LA50	829
LGA50	861
LA75	1644
LGA75	1721

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	298
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## 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).















