Report

	final.contigs
# contigs (>= 0 bp)	12705
# contigs (>= 0 bp) # contigs (>= 1000 bp)	1533
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6815779
Total length (>= 1000 bp)	2896074
Total length (>= 5000 bp)	108627
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2833
Largest contig	7697
Total length	3817960
Reference length	4641652
N50	1618
N75	1021
L50	763
L75	1501
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	250
Genome fraction (%)	80.904
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.42
# indels per 100 kbp	0.00
Largest alignment	7697
NA50	1618
NA75	1021
LA50	763
LA75	1501

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	429
# 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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	250
# 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).









