Report

	final.contigs
# contigs (>= 0 bp)	6466
# contigs (>= 1000 bp)	3363
# contigs (>= 5000 bp)	222
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9882619
Total length (>= 1000 bp)	8267530
Total length (>= 5000 bp)	1401787
Total length (>= 10000 bp)	65584
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4740
Largest contig	13353
Total length	9288600
Reference length	9283304
N50	2555
N75	1543
L50	1169
L75	2324
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# unaligned contigs	1 + 2 part
Unaligned length	852
Genome fraction (%)	96.460
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.60
# indels per 100 kbp	0.01
Largest alignment	13353
NA50	2554
NA75	1542
LA50	1169
LA75	2325

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).
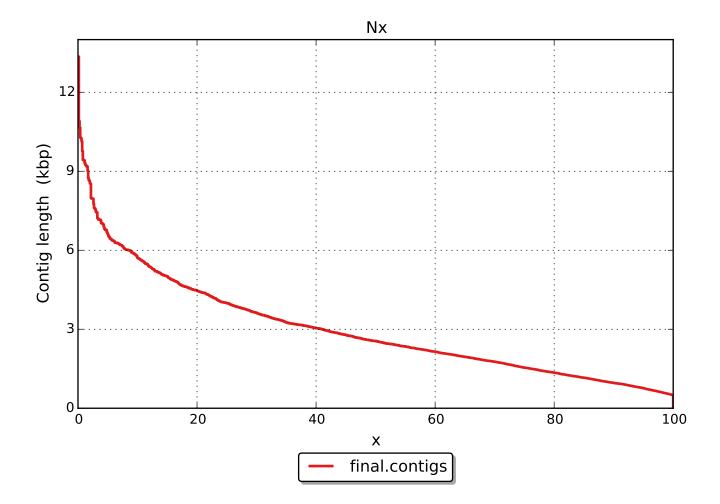
Misassemblies report

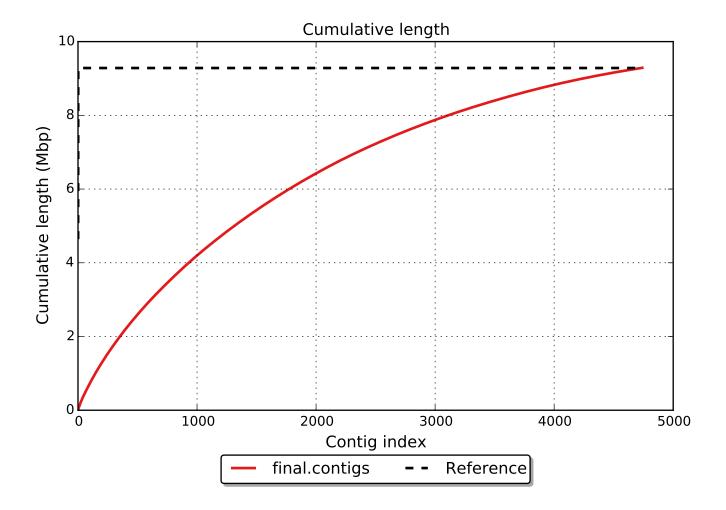|	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# mismatches	4710
# indels	1
# short indels	1
# long indels	0
Indels length	1

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	1
Fully unaligned length	555
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	297
# 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).
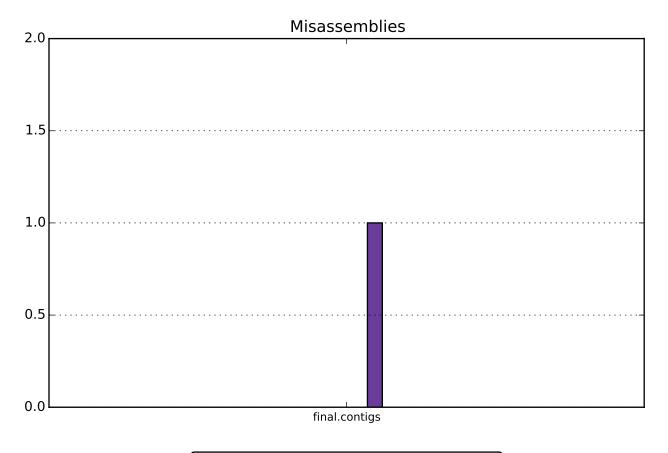
Nx

Contig length (kbp)

x

— final.contigs

Cumulative length

Cumulative length (Mbp) vs Contig index

Legend: final.contigs, Reference

Cumulative length (aligned contigs)