Report

	final.contigs
# contigs (>= 0 bp)	12427
# contigs (>= 1000 bp)	3510
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10500382
Total length (>= 1000 bp)	5716048
Total length (>= 5000 bp)	11285
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8004
Largest contig	5697
Total length	8926482
Reference length	9714864
N50	1235
N75	836
L50	2378
L75	4582
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	4628
# local misassemblies	1
# unaligned contigs	1 + 3 part
Unaligned length	697
Genome fraction (%)	88.371
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	121.29
# indels per 100 kbp	0.09
Largest alignment	5697
NA50	1235
NA75	836
LA50	2379
LA75	4583

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).
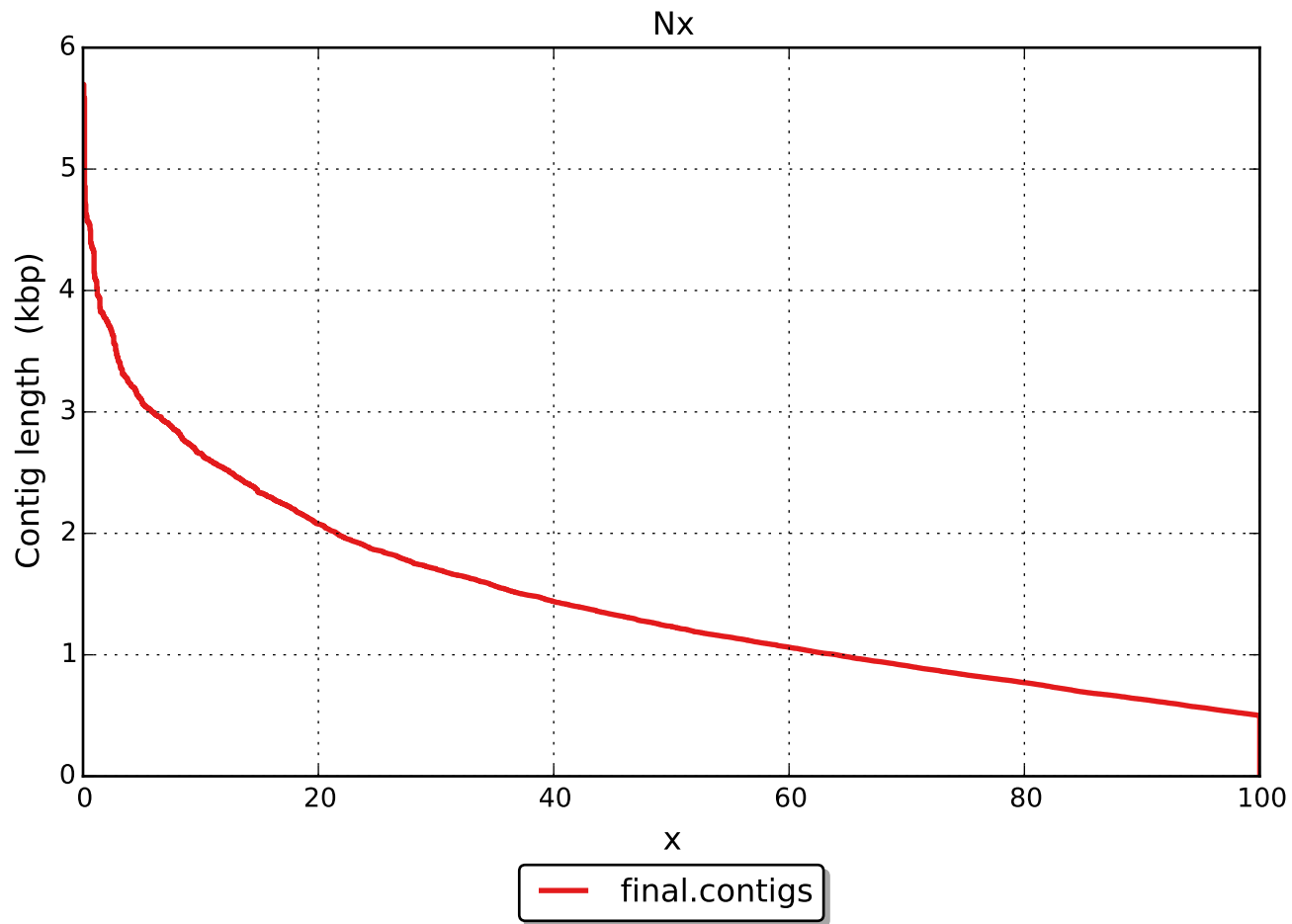
Misassemblies report

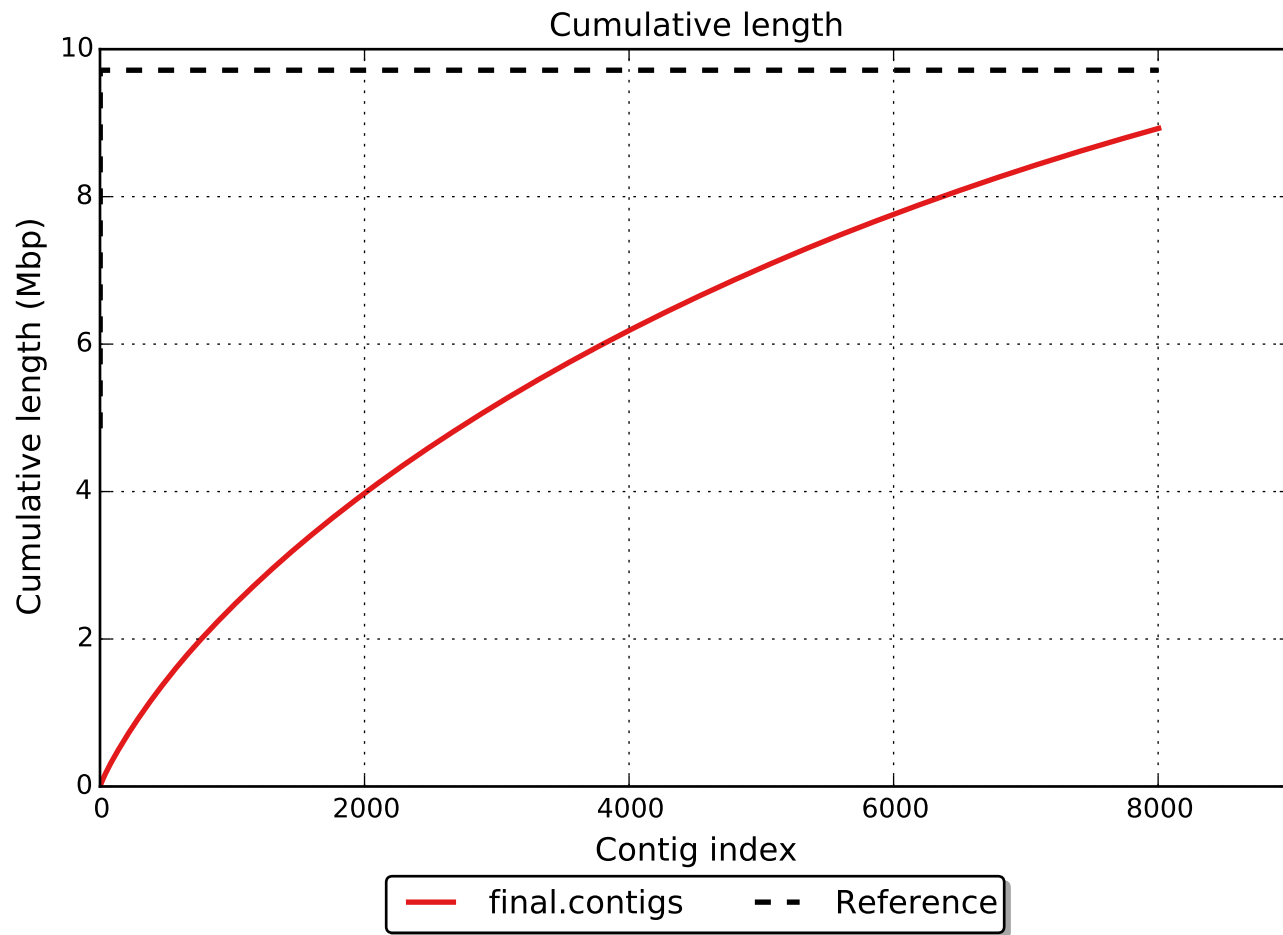|	final.contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	4628
# local misassemblies	1
# mismatches	10413
# indels	8
# short indels	8
# long indels	0
Indels length	8

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	509
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	188
# 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).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs