Report

	final.contigs
# contigs (>= 0 bp)	1069
# contigs (>= 1000 bp)	616
# contigs (>= 5000 bp)	445
# contigs (>= 10000 bp)	314
# contigs (>= 25000 bp)	112
# contigs (>= 50000 bp)	19
Total length (>= 0 bp)	9392114
Total length (>= 1000 bp)	9234051
Total length (>= 5000 bp)	8729784
Total length (>= 10000 bp)	7723955
Total length (>= 25000 bp)	4360174
Total length (>= 50000 bp)	1190778
# contigs	645
Largest contig	80531
Total length	9255494
Reference length	9283304
N50	23990
N75	13625
L50	123
L75	249
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	1 + 0 part
Unaligned length	503
Genome fraction (%)	99.066
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.98
# indels per 100 kbp	0.03
Largest alignment	80531
NA50	23990
NA75	13625
LA50	123
LA75	249

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).
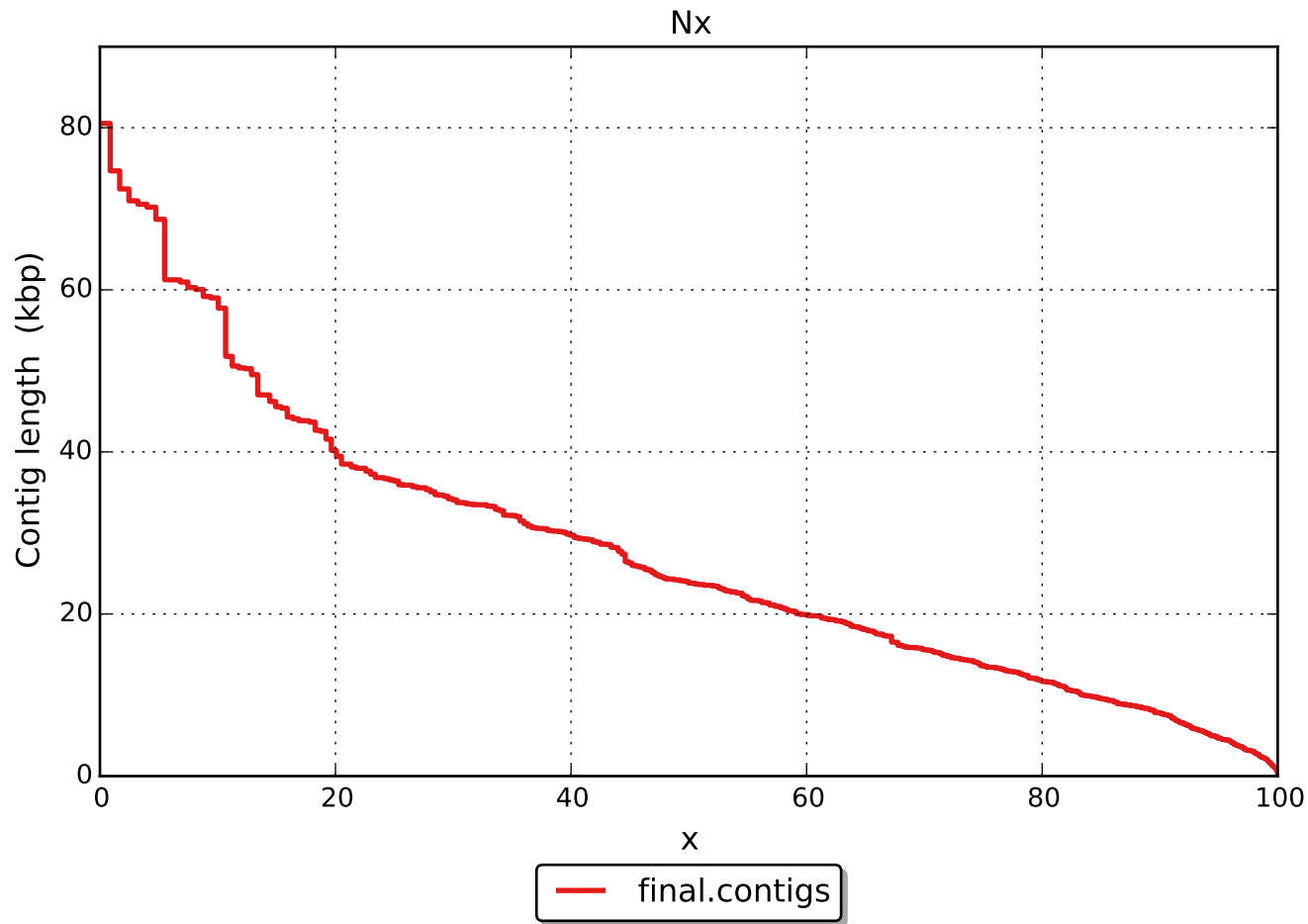
Misassemblies report

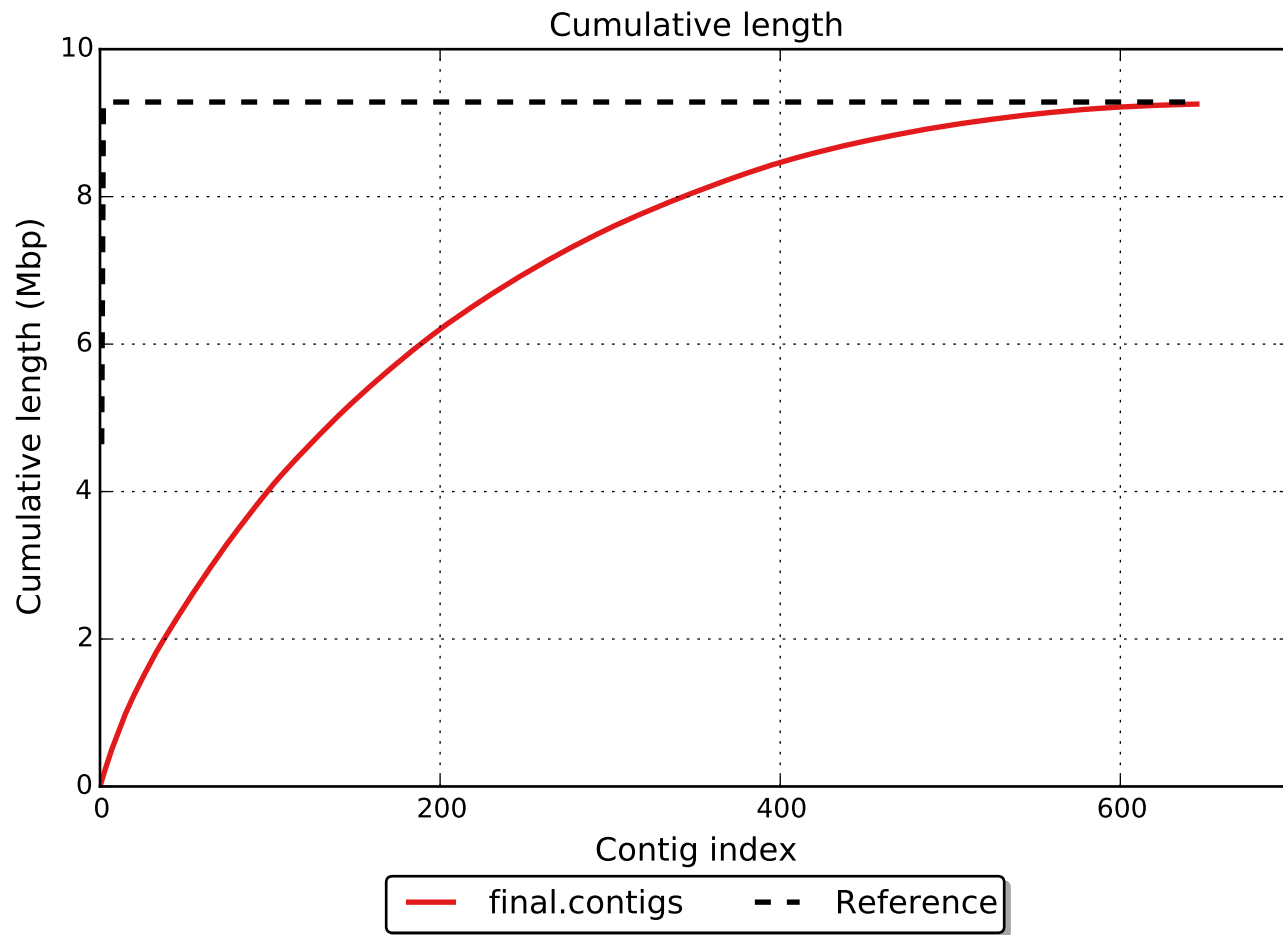|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	918
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).
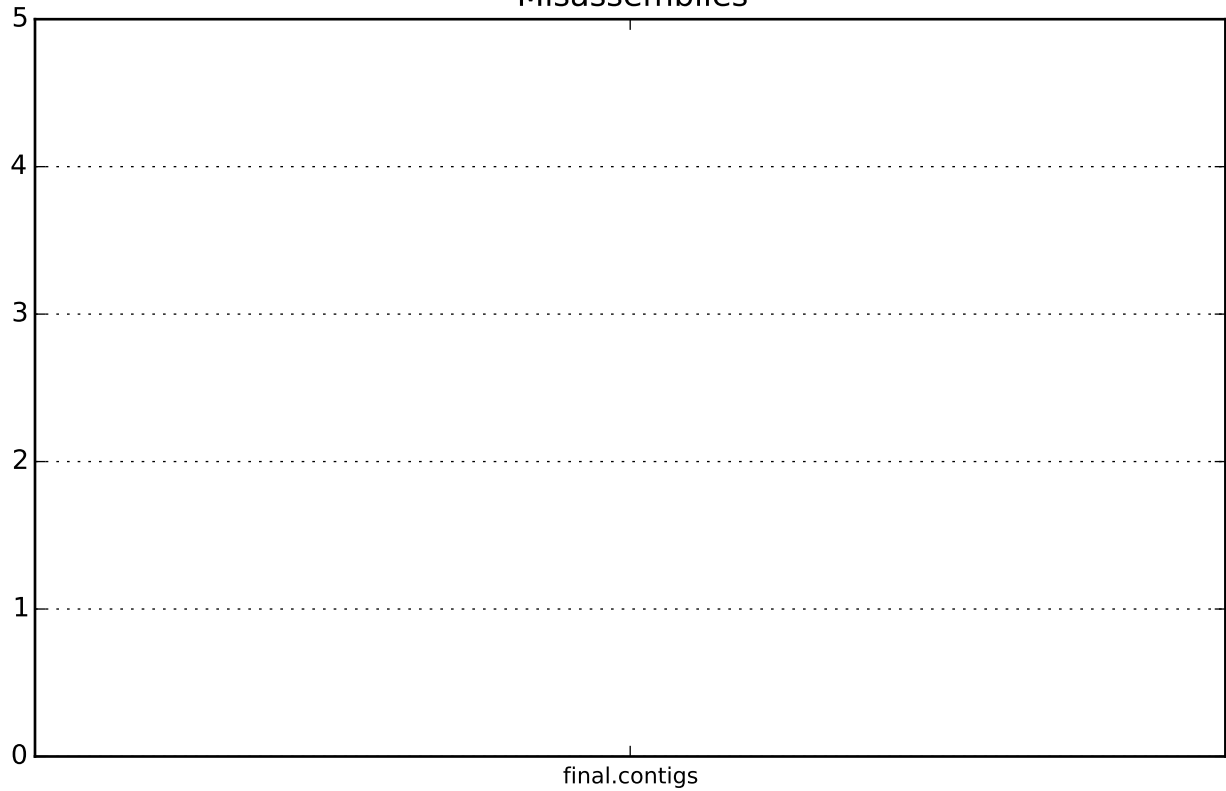
Unaligned report

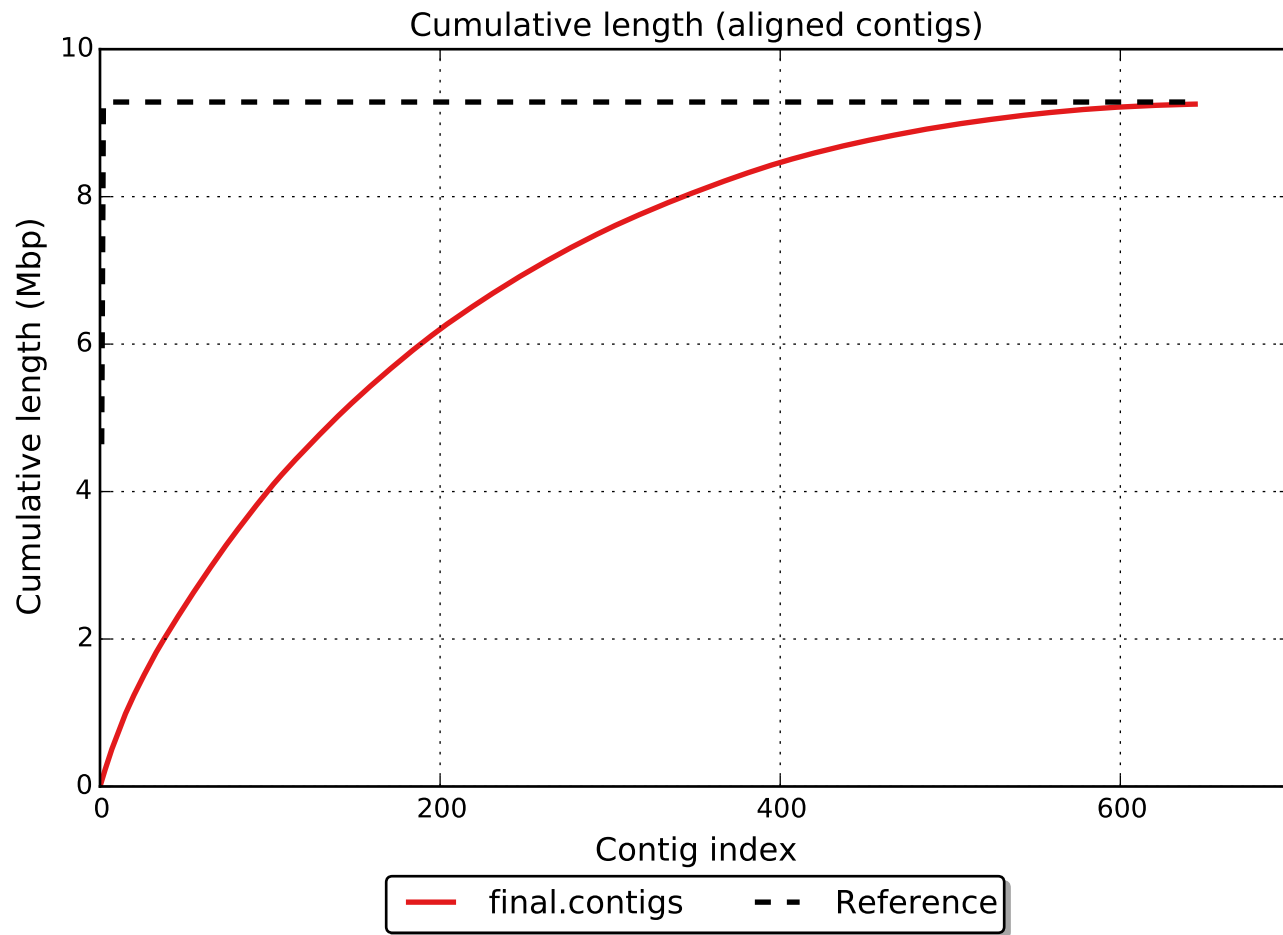|	final.contigs
# fully unaligned contigs	1
Fully unaligned length	503
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)