Report

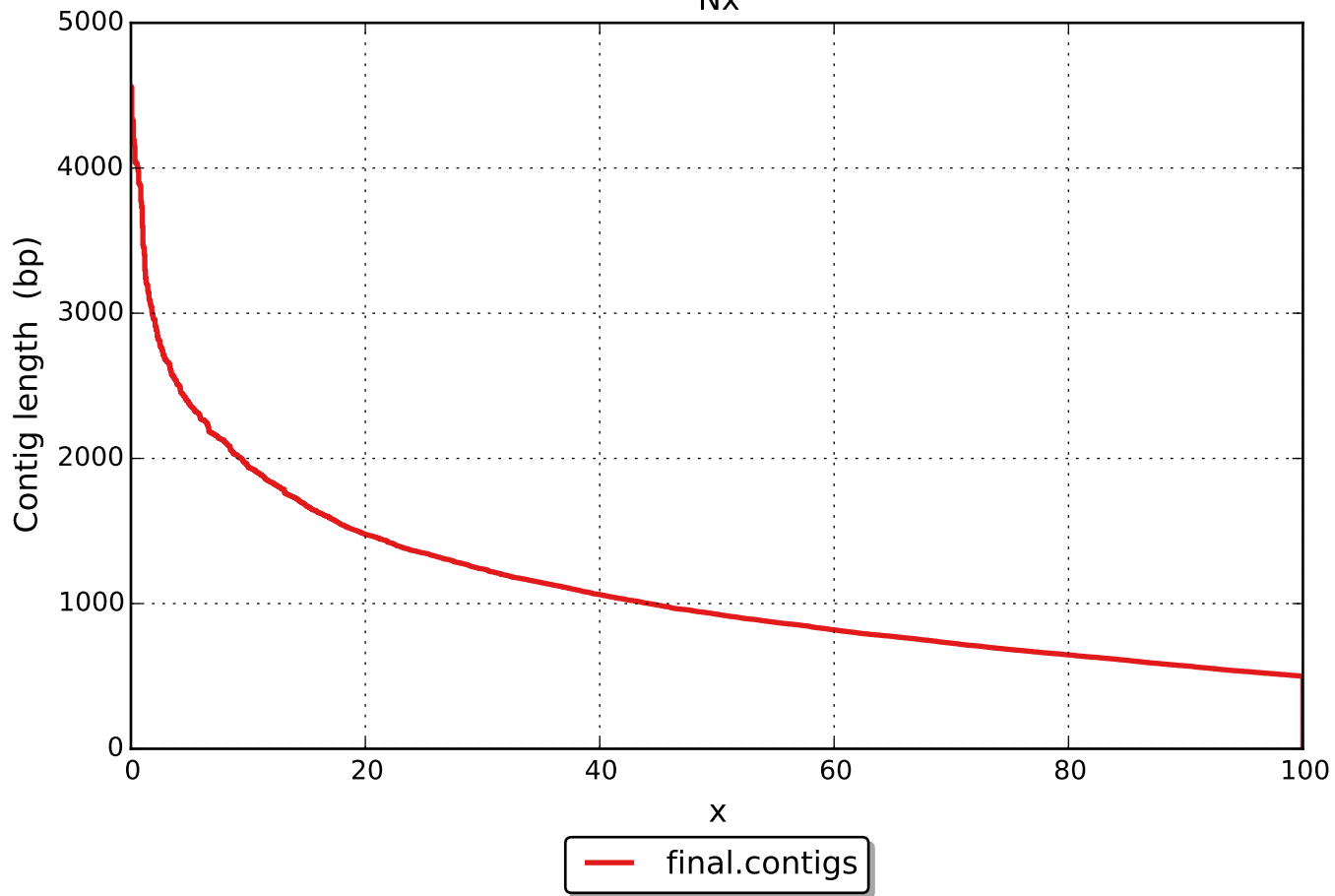|	final.contigs
# contigs (>= 0 bp)	13452
# contigs (>= 1000 bp)	1916
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8646576
Total length (>= 1000 bp)	2797361
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6990
Largest contig	4559
Total length	6321706
Reference length	9283304
N50	927
N75	684
L50	2295
L75	4288
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 4 part
Unaligned length	255
Genome fraction (%)	64.658
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	261.81
# indels per 100 kbp	0.05
Largest alignment	4559
NA50	927
NA75	684
LA50	2295
LA75	4289

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	1
# mismatches	15715
# indels	3
# short indels	3
# long indels	0
Indels length	3

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
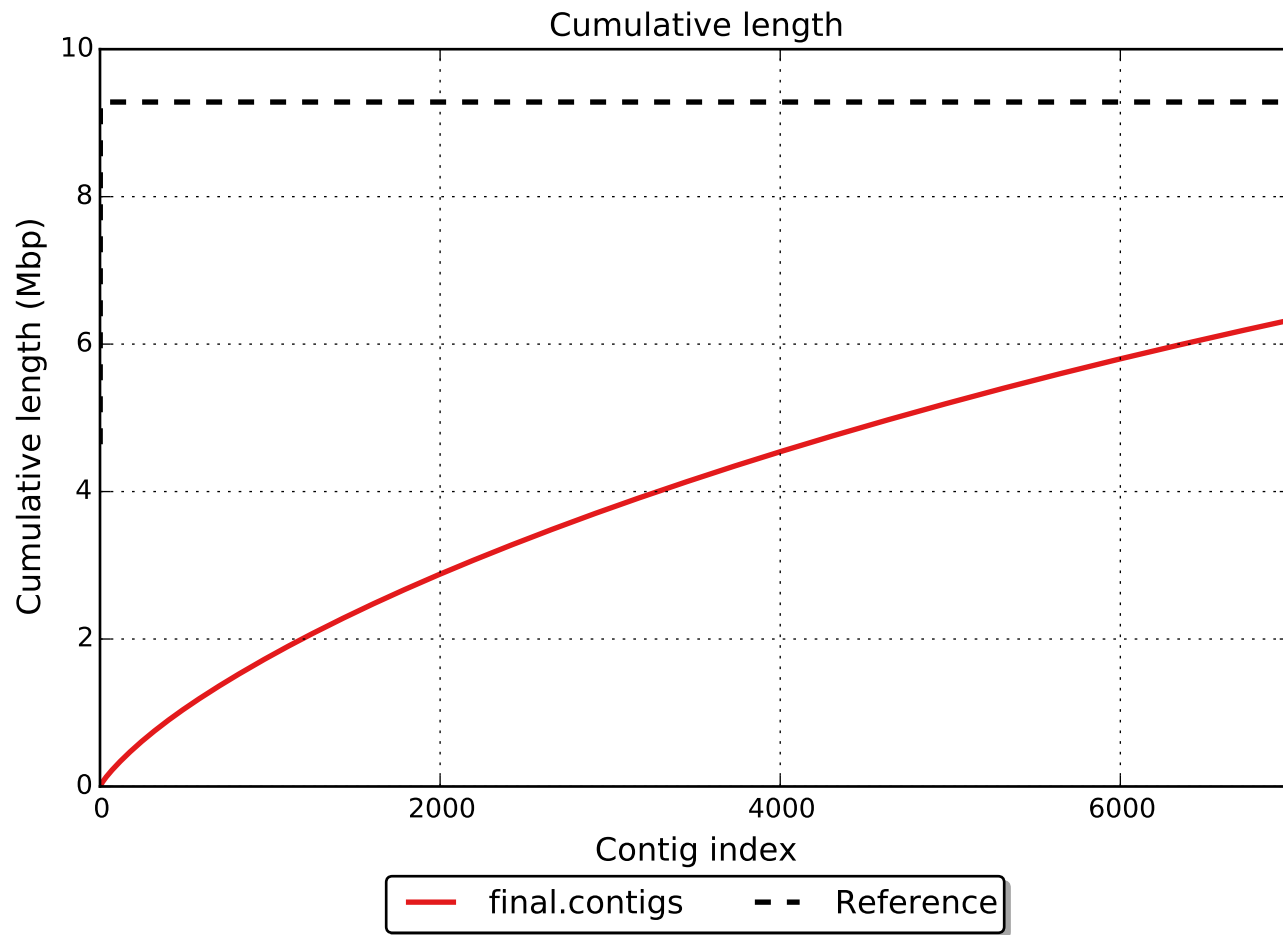(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

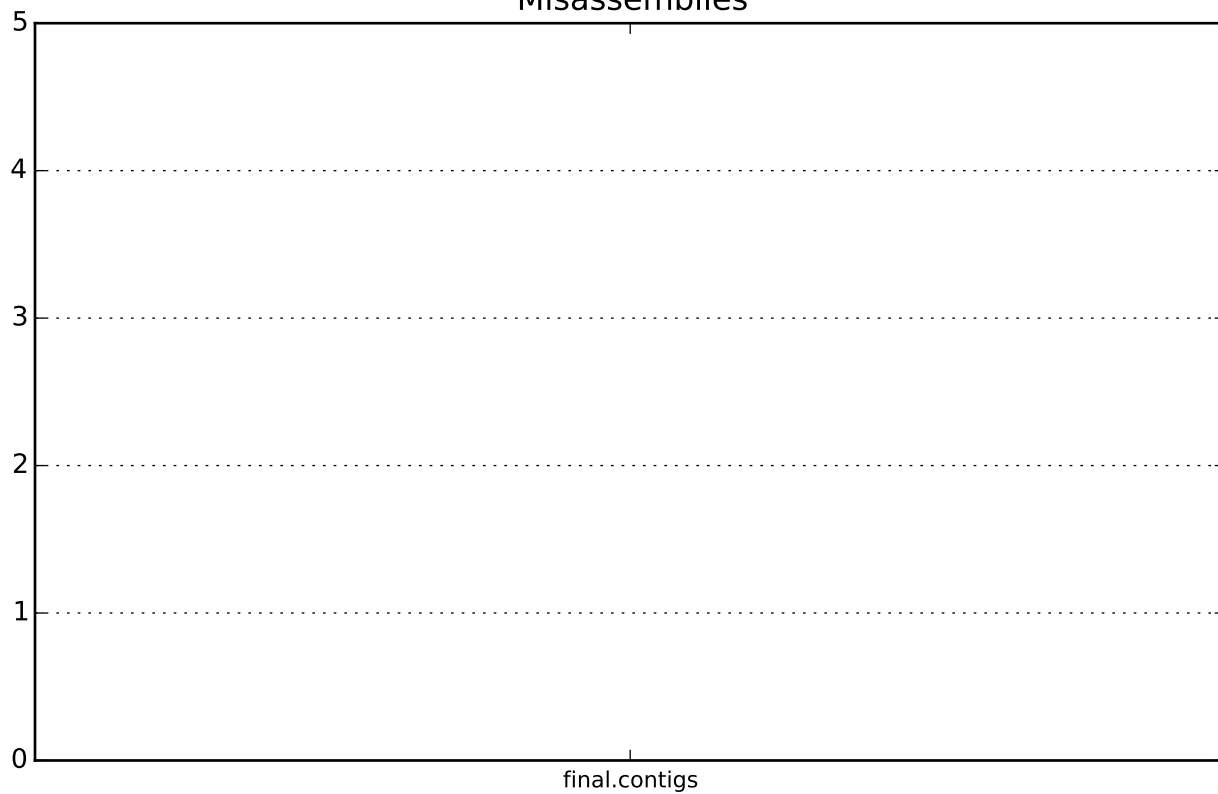|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	255
# N's	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
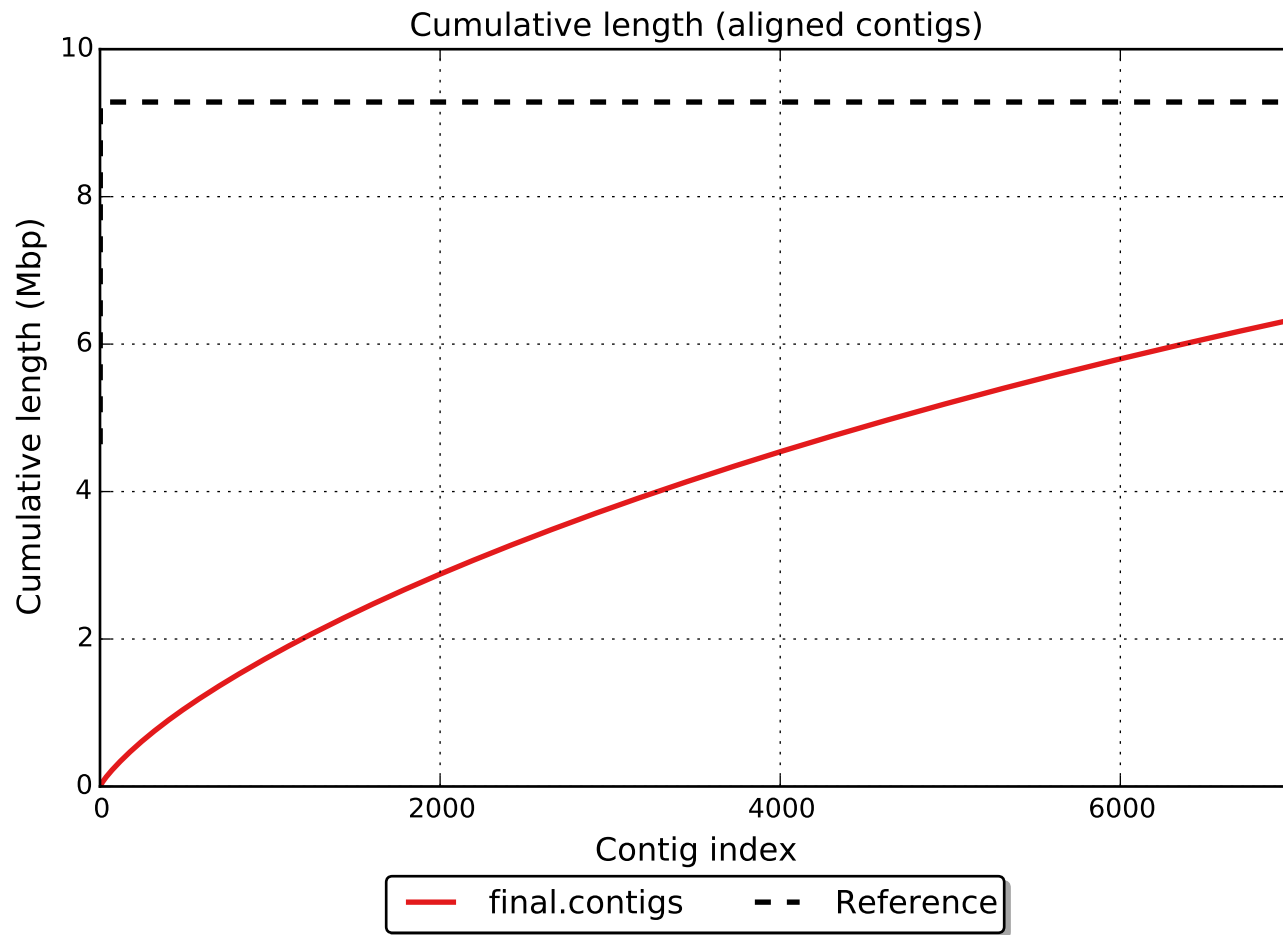(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)