Report

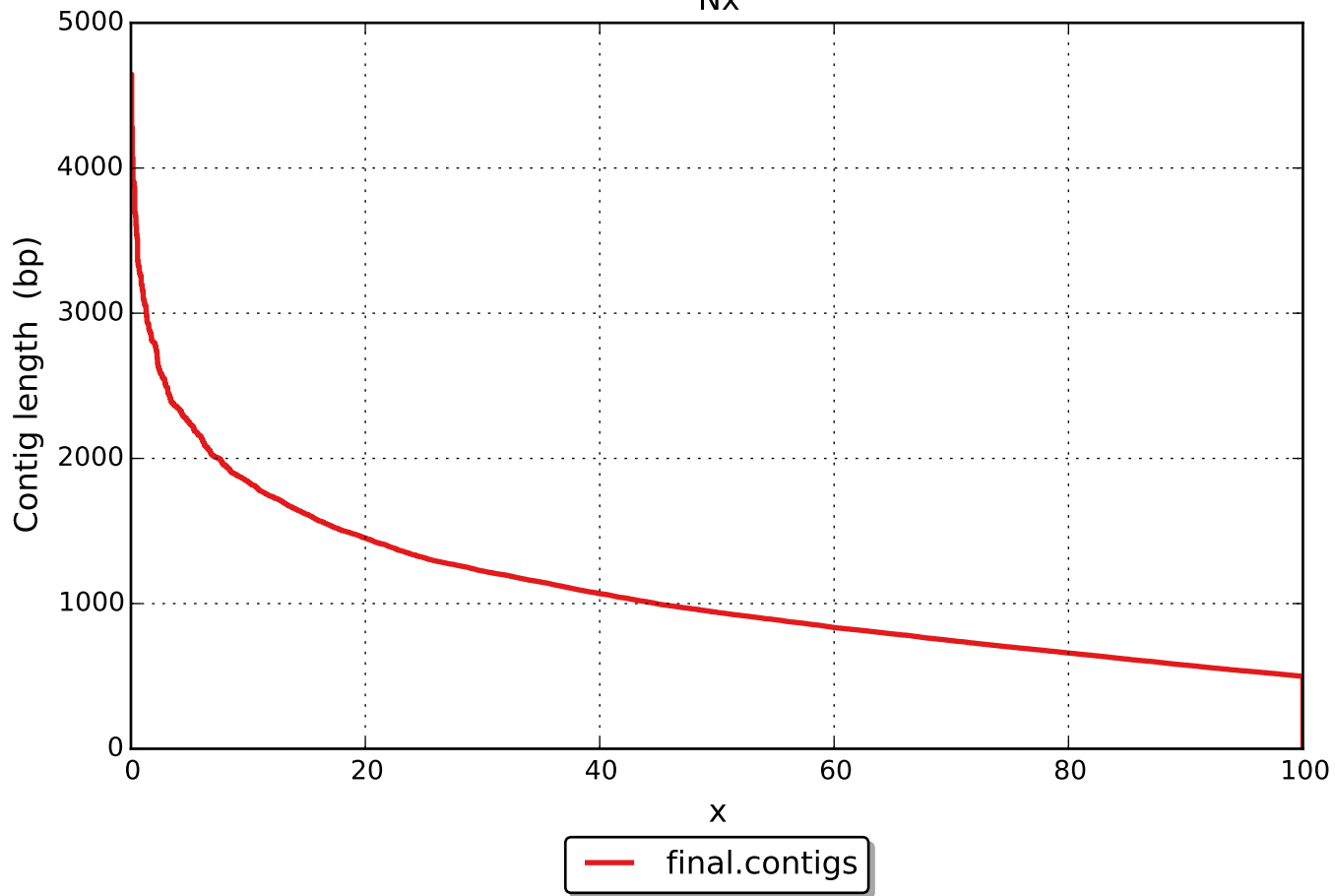|	final.contigs
# contigs (>= 0 bp)	14726
# contigs (>= 1000 bp)	2379
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9842040
Total length (>= 1000 bp)	3383178
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8290
Largest contig	4645
Total length	7541761
Reference length	9714864
N50	939
N75	702
L50	2780
L75	5107
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	4784
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	79.472
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	281.78
# indels per 100 kbp	0.08
Largest alignment	4645
NA50	939
NA75	701
LA50	2781
LA75	5108

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	4
# relocations	3
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	4784
# local misassemblies	3
# mismatches	21755
# indels	6
# short indels	6
# long indels	0
Indels length	6

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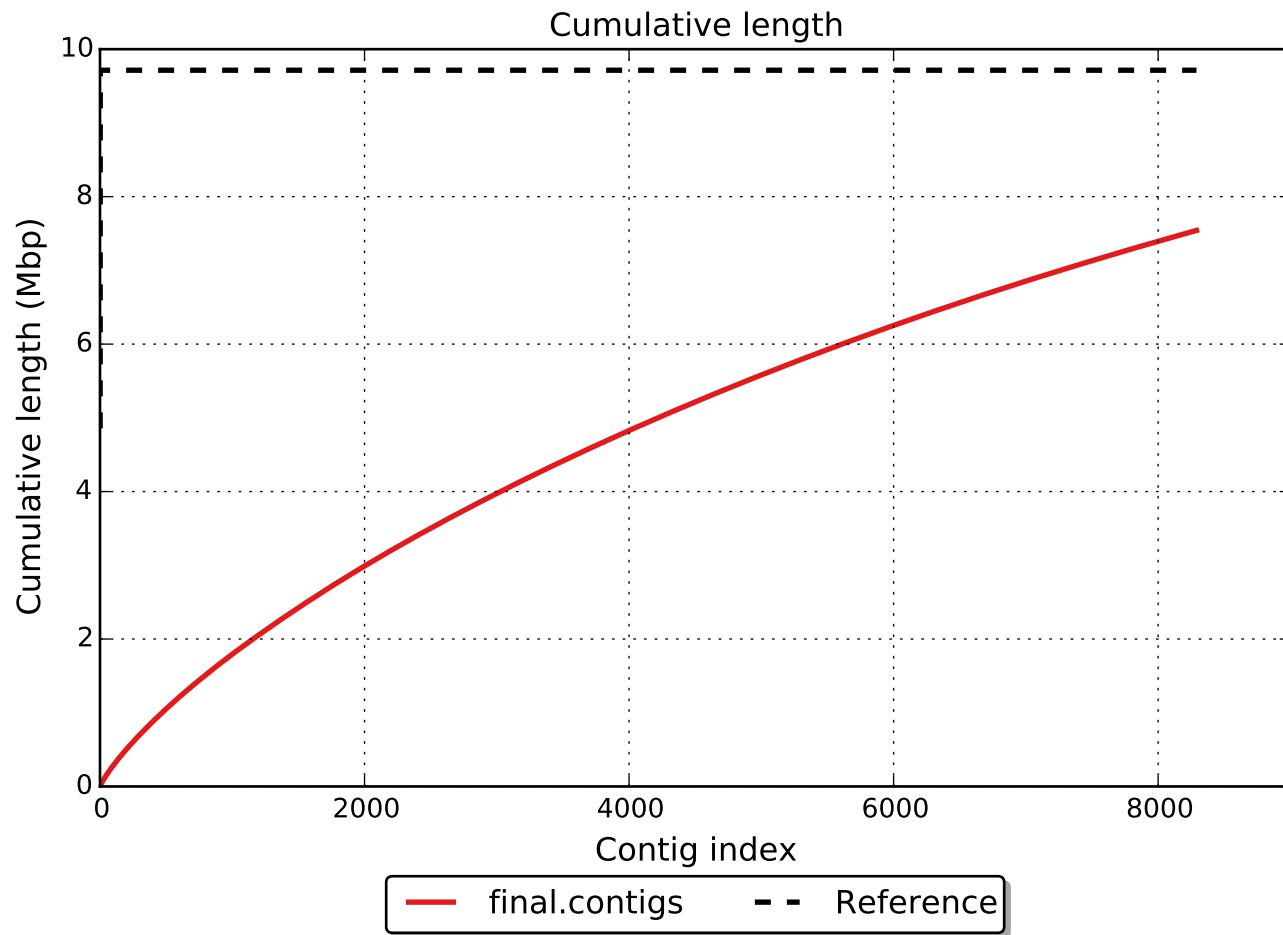(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
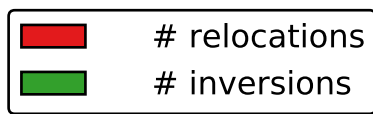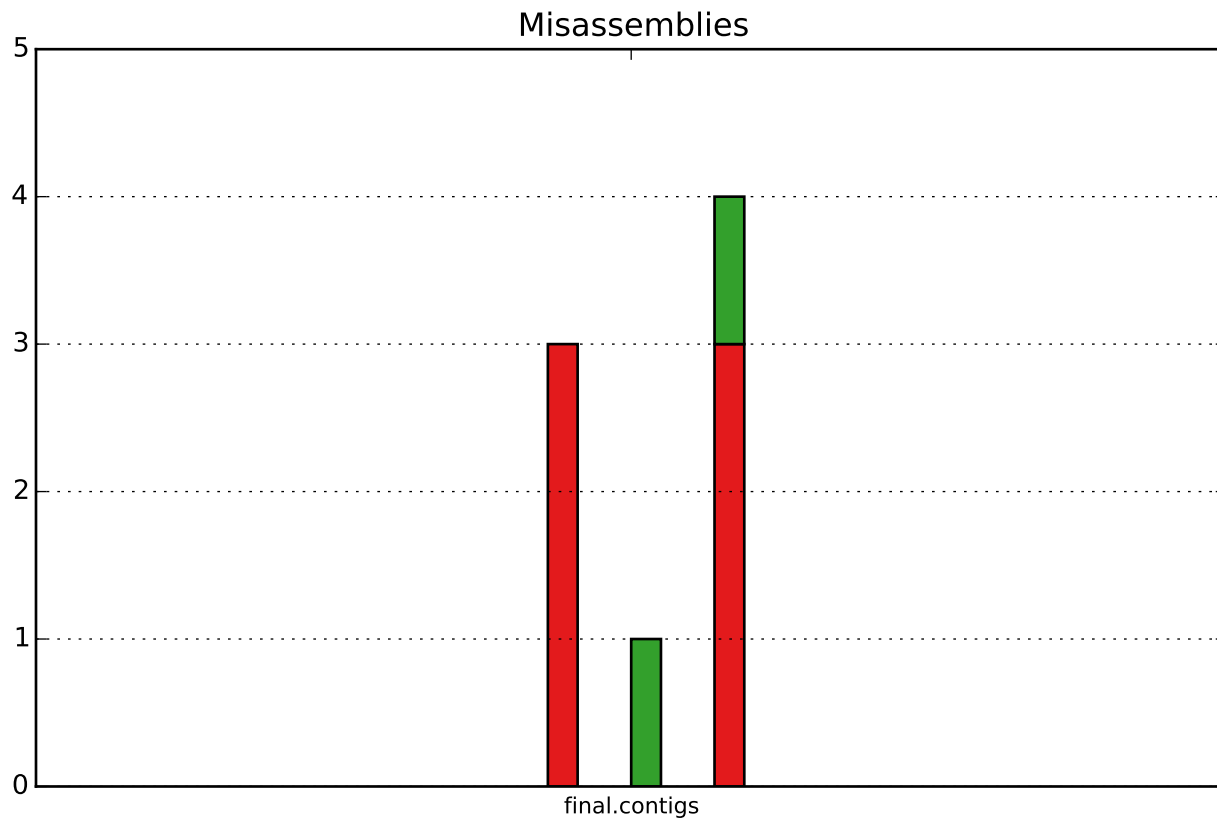
Unaligned report

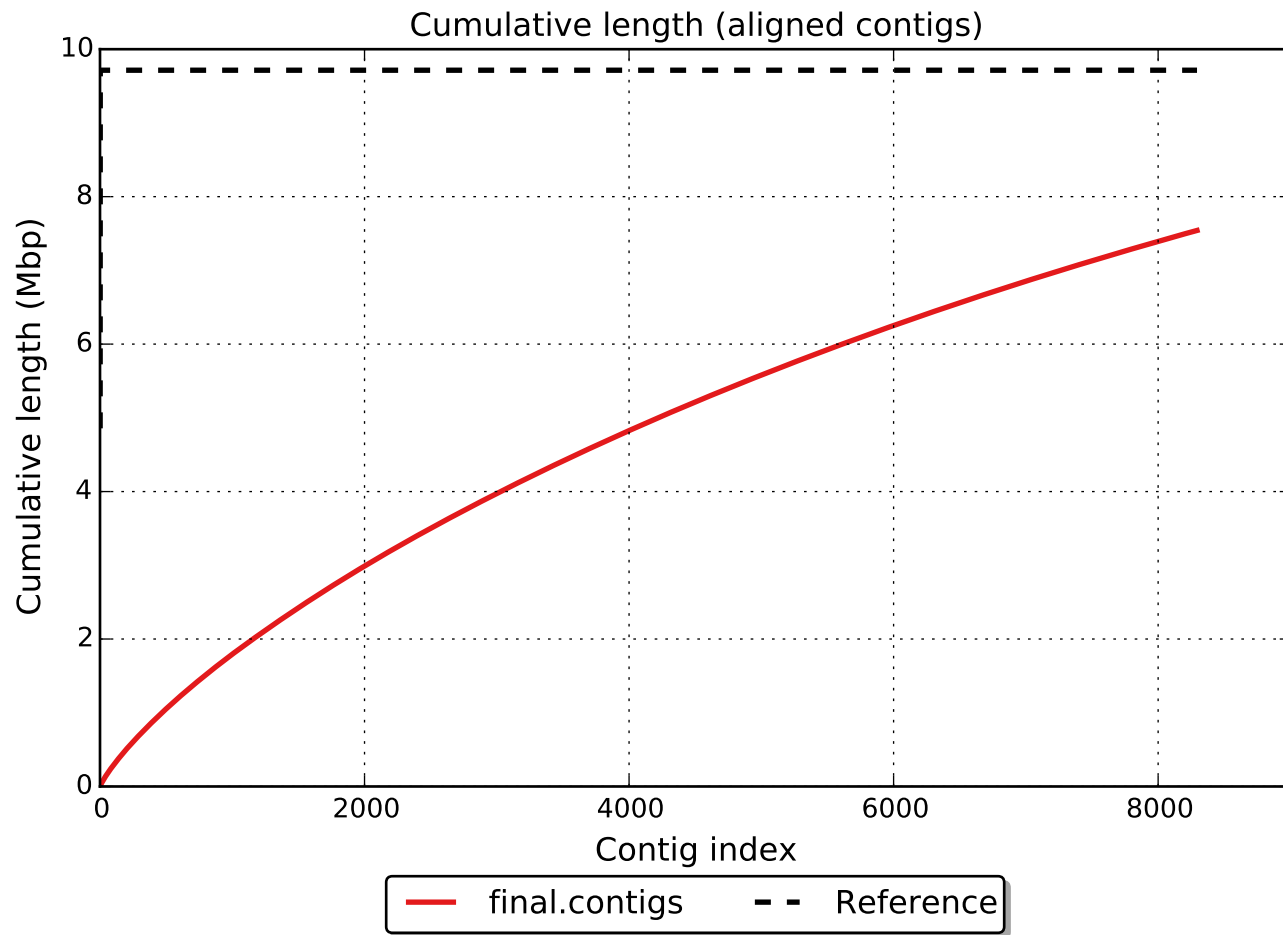|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Cumulative length (aligned contigs)