Report

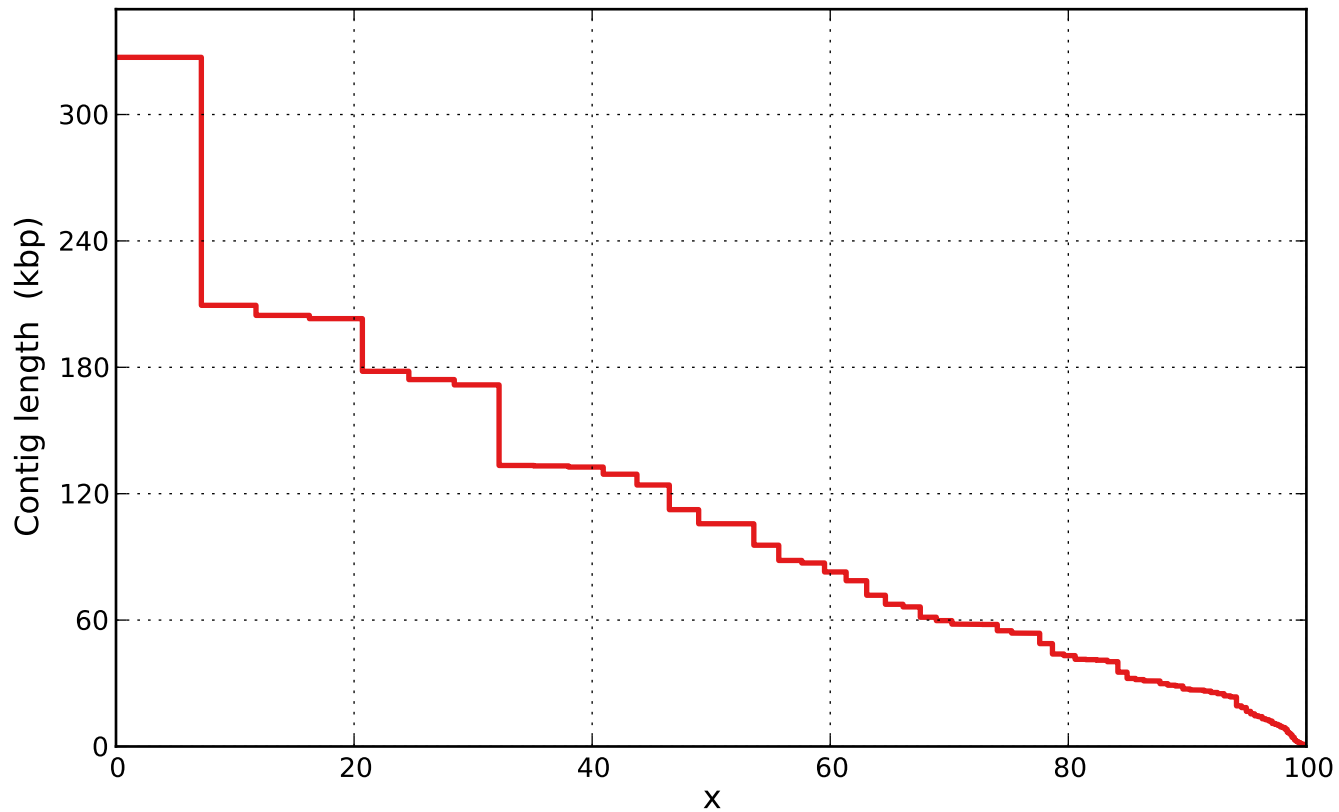|	final.contigs
# contigs (>= 0 bp)	141
# contigs (>= 1000 bp)	97
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4572769
Total length (>= 1000 bp)	4554509
Total length (>= 5000 bp)	4507427
Total length (>= 10000 bp)	4462528
Total length (>= 25000 bp)	4246976
Total length (>= 50000 bp)	3540315
# contigs	109
Largest contig	327146
Total length	4562531
Reference length	4641652
N50	105738
N75	54941
L50	14
L75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	51
Genome fraction (%)	98.245
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.83
# indels per 100 kbp	9.32
Largest alignment	327146
NA50	105738
NA75	54941
LA50	14
LA75	29

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	4
# mismatches	2637
# indels	425
# short indels	424
# long indels	1
Indels length	667

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).
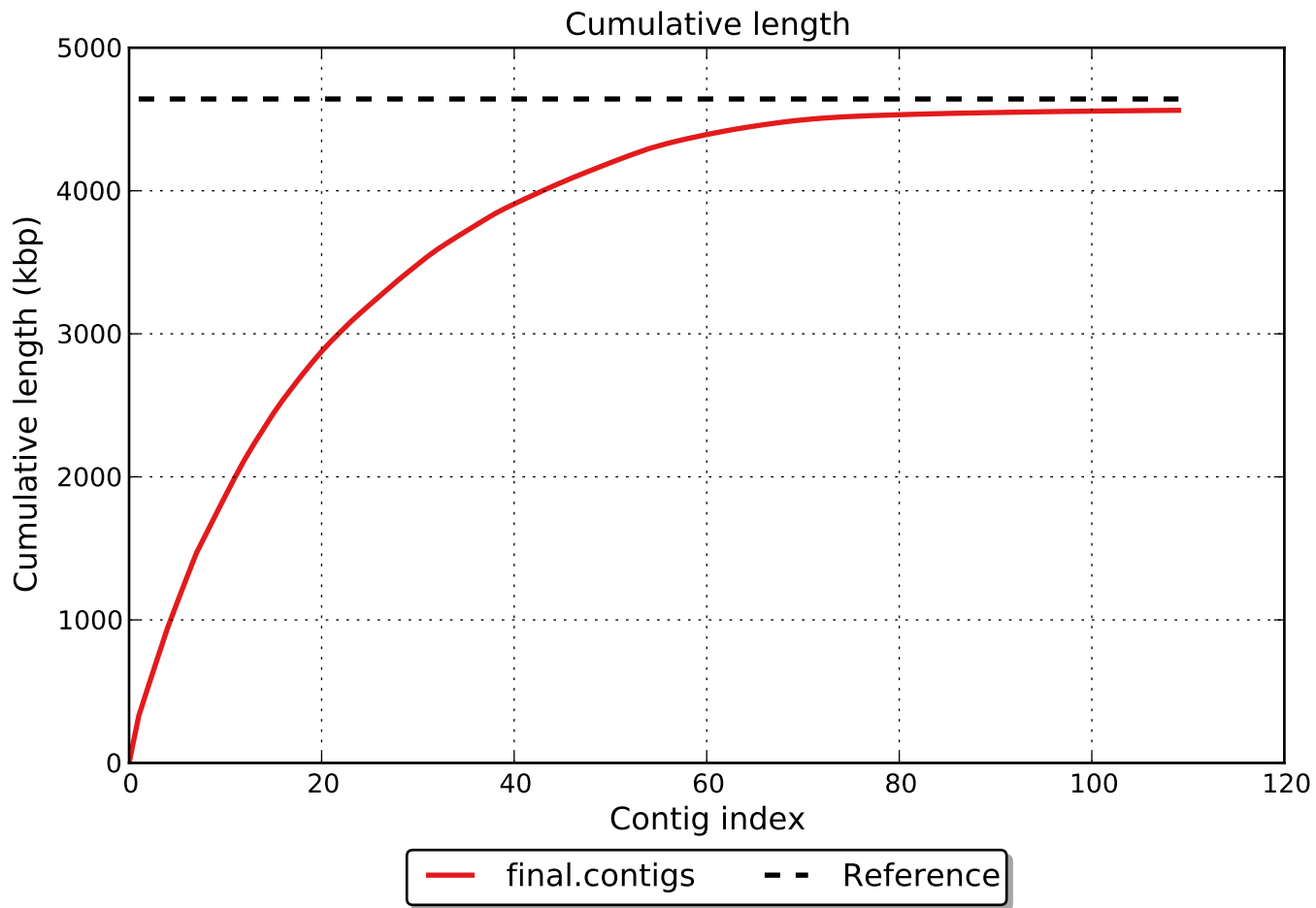
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	51
# N's	0

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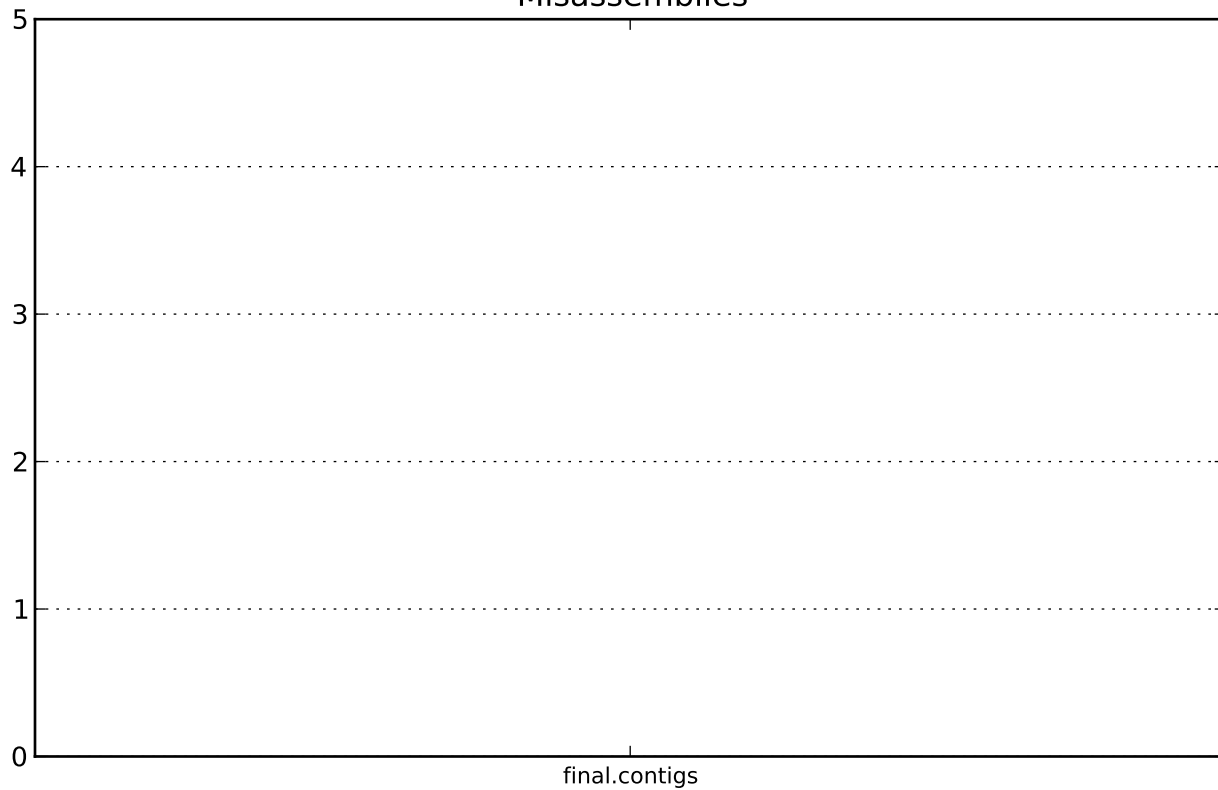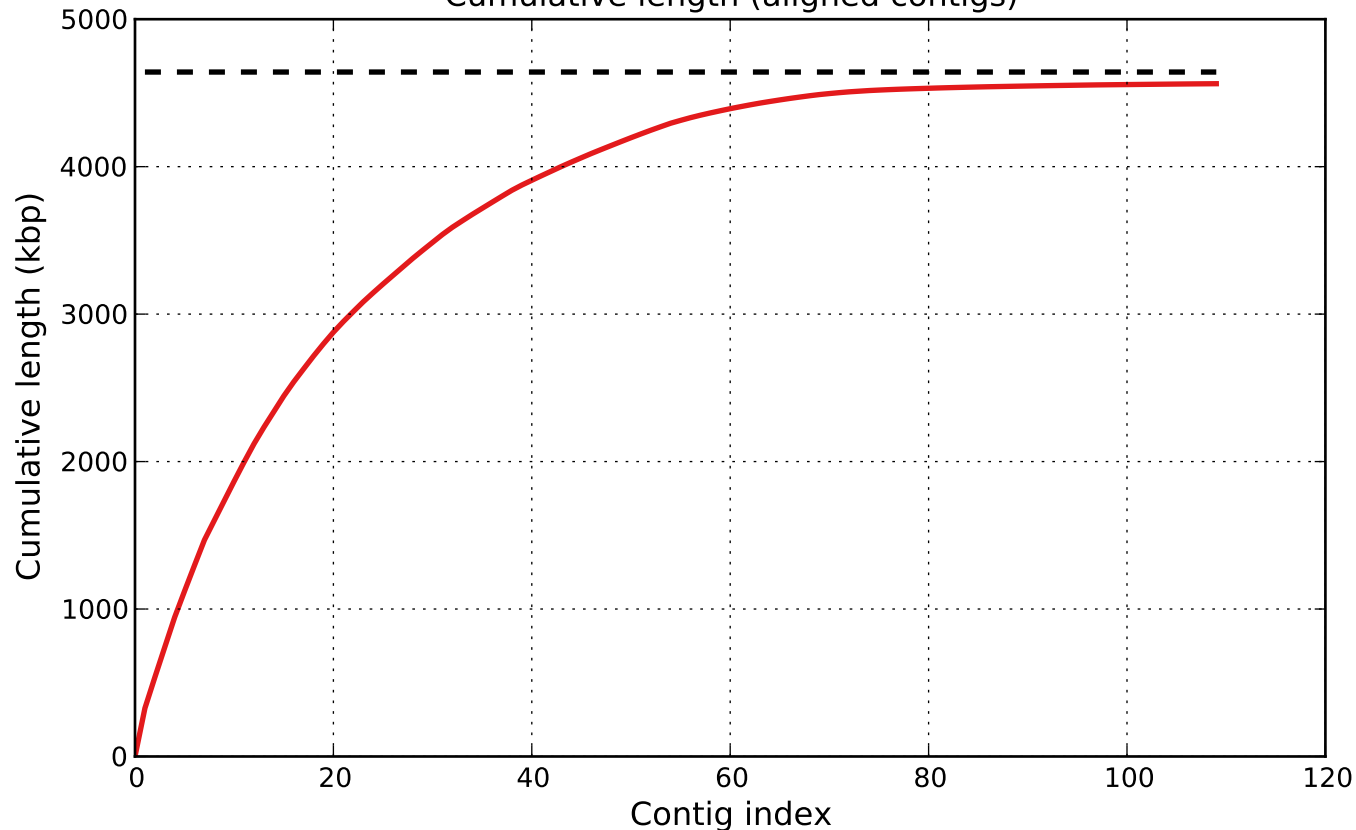(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)