Report

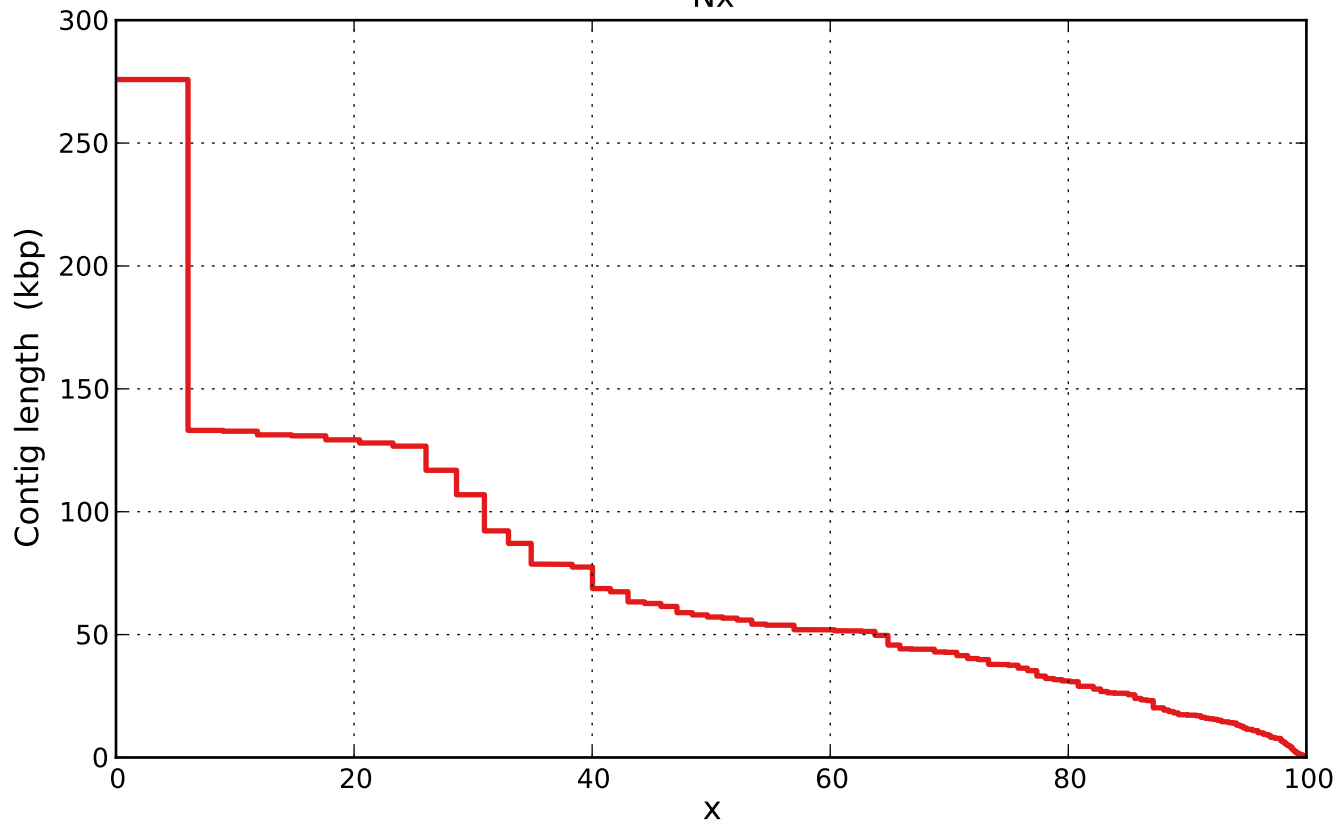|	final.contigs
# contigs (>= 0 bp)	182
# contigs (>= 1000 bp)	133
# contigs (>= 5000 bp)	105
# contigs (>= 10000 bp)	93
# contigs (>= 25000 bp)	62
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4569937
Total length (>= 1000 bp)	4547220
Total length (>= 5000 bp)	4487299
Total length (>= 10000 bp)	4395413
Total length (>= 25000 bp)	3903398
Total length (>= 50000 bp)	2908019
# contigs	153
Largest contig	275855
Total length	4560832
Reference length	4641652
N50	57159
N75	37529
L50	23
L75	47
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 2 part
Unaligned length	117
Genome fraction (%)	98.189
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.03
# indels per 100 kbp	9.33
Largest alignment	275855
NA50	57159
NA75	37529
LA50	23
LA75	47

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	9
# mismatches	2645
# indels	425
# short indels	425
# long indels	0
Indels length	597

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	117
# N's	0

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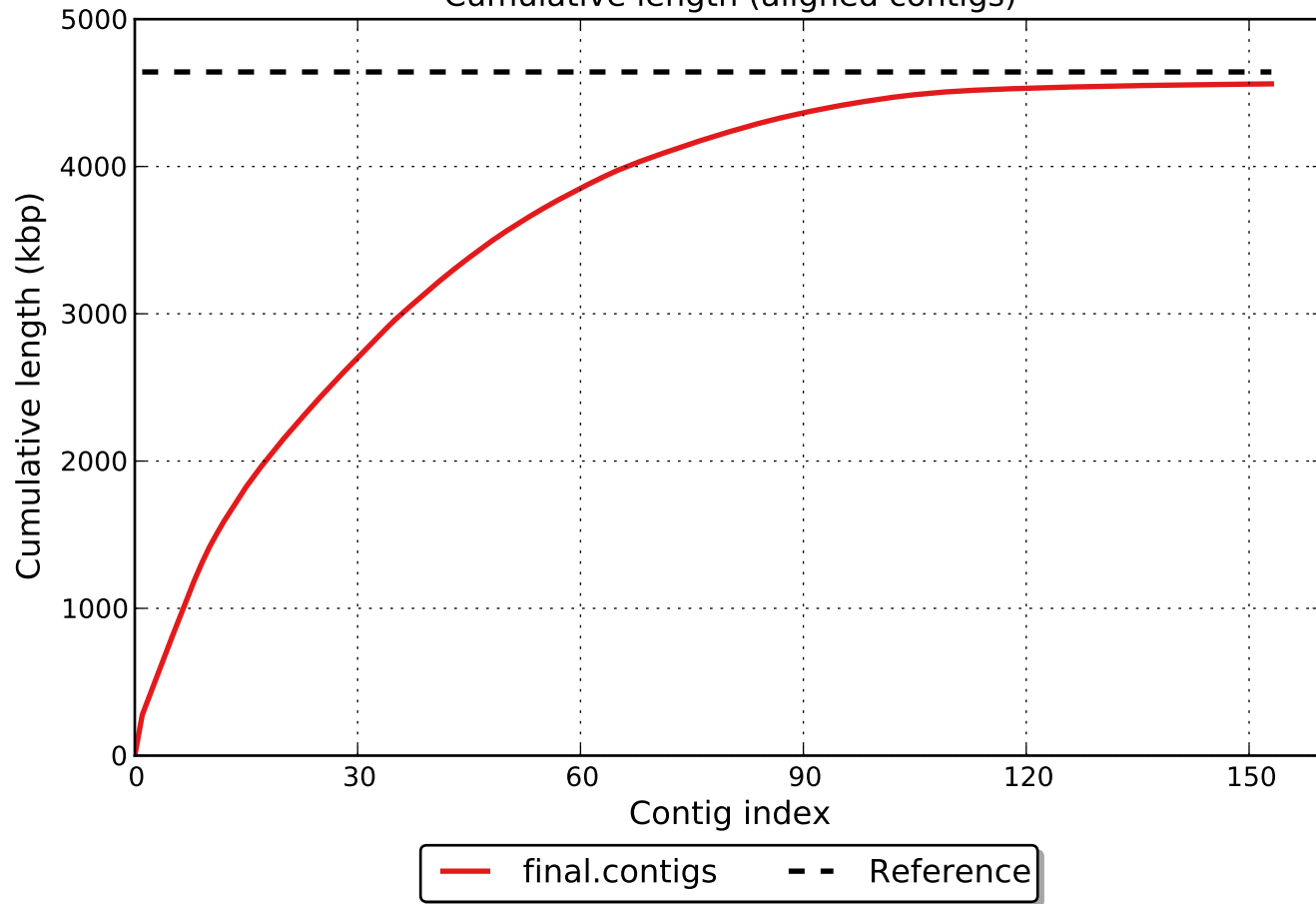(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

final.contigs
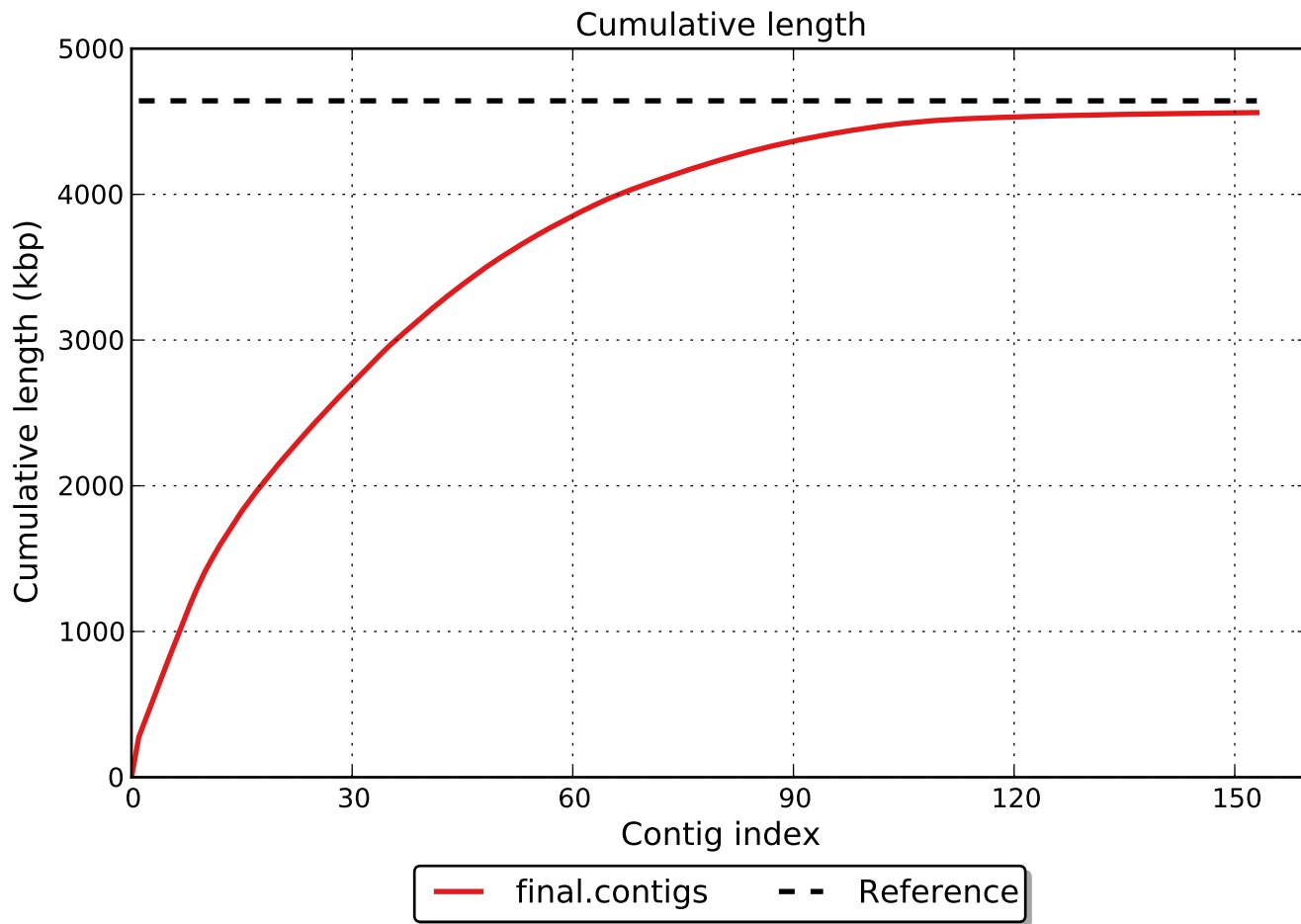
Cumulative length (aligned contigs)