Report

	final.contigs
# contigs (>= 0 bp)	464
# contigs (>= 1000 bp)	136
# contigs (>= 5000 bp)	111
# contigs (>= 10000 bp)	98
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4659121
Total length (>= 1000 bp)	4547414
Total length (>= 5000 bp)	4479948
Total length (>= 10000 bp)	4379149
Total length (>= 25000 bp)	3733533
Total length (>= 50000 bp)	2766902
# contigs	153
Largest contig	229997
Total length	4559533
Reference length	4641652
N50	58023
N75	31670
L50	24
L75	48
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.353
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.04
# indels per 100 kbp	0.07
Largest alignment	229997
NA50	58023
NA75	31670
LA50	24
LA75	48

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	3
# mismatches	139
# 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

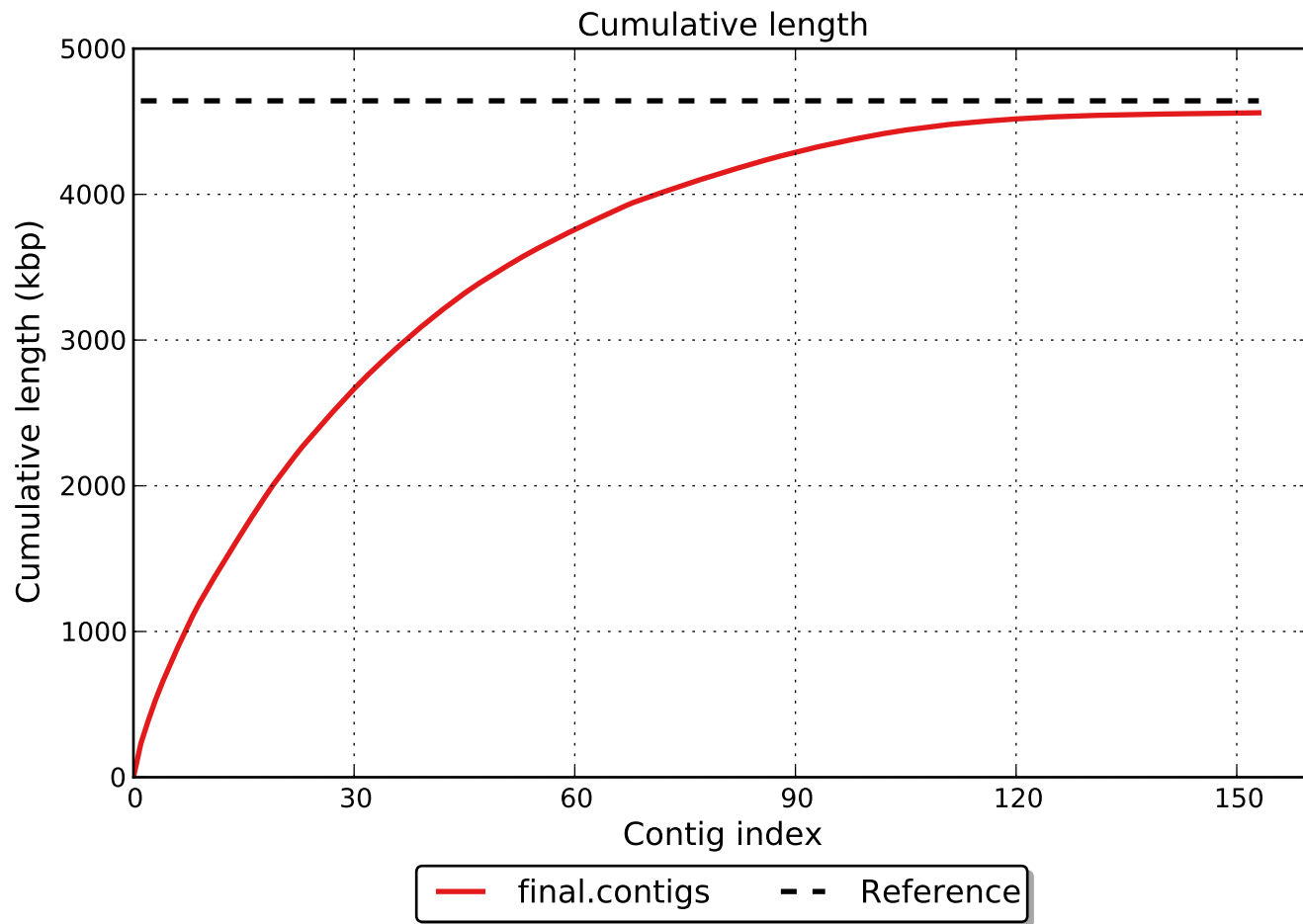|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).
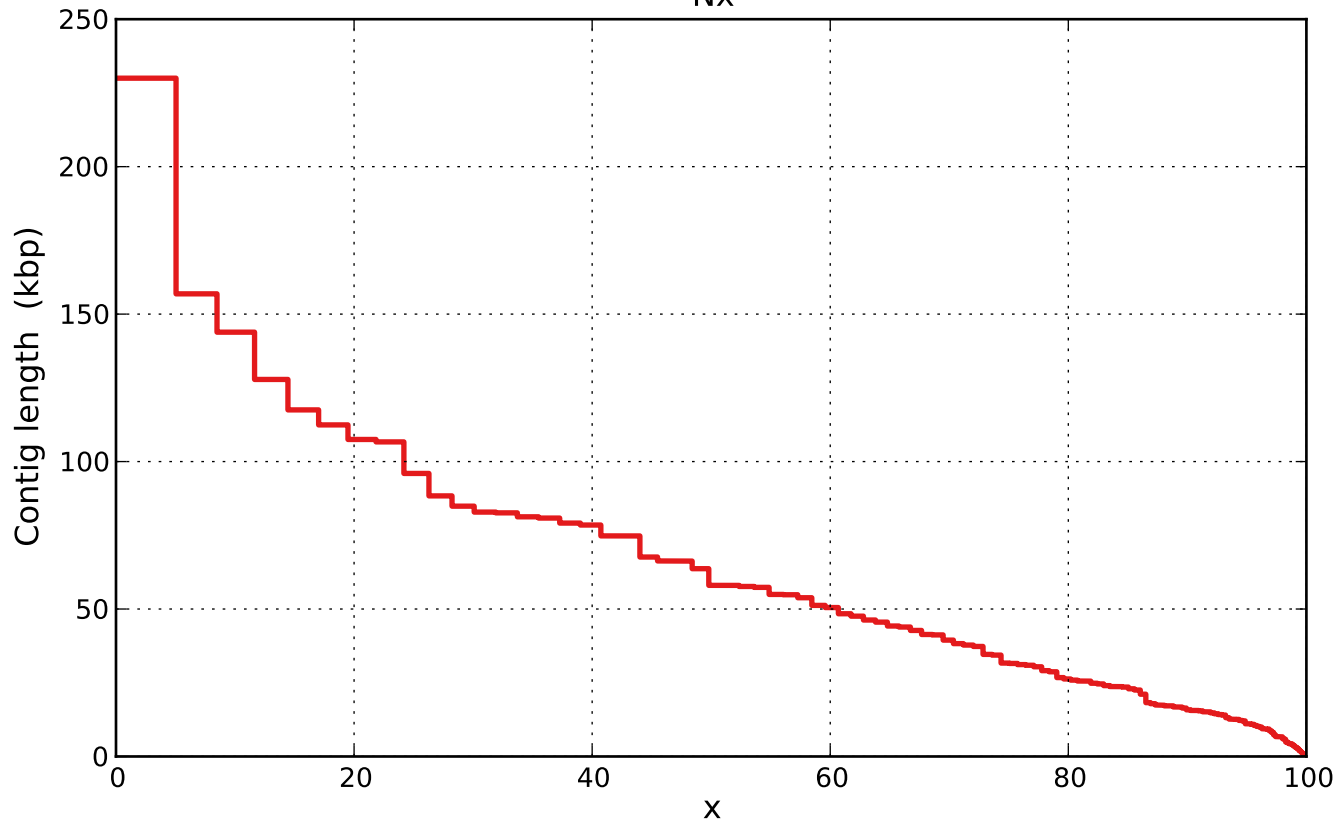
Cumulative length
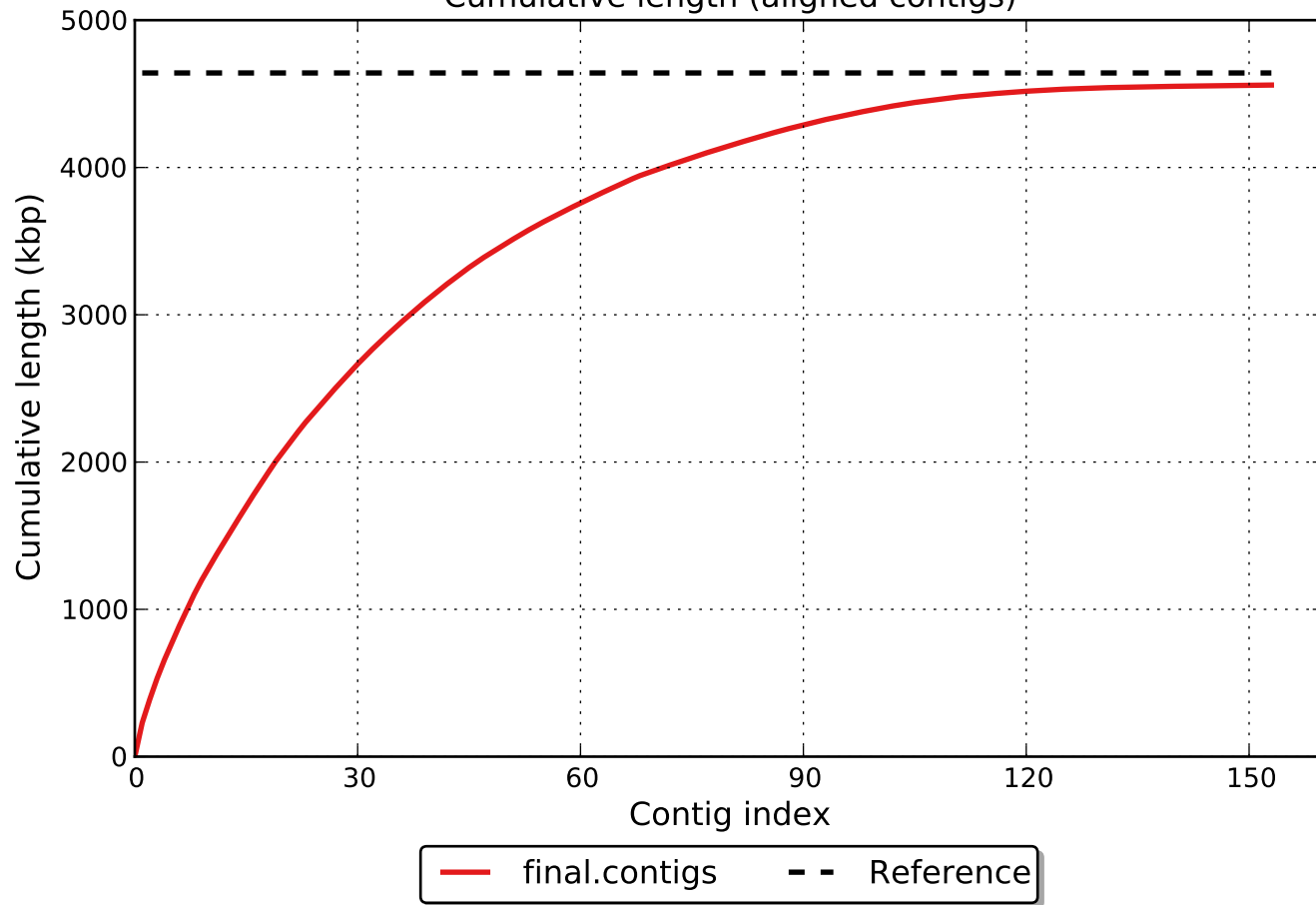
Misassemblies

final.contigs

Cumulative length (aligned contigs)