Report

	final.contigs
# contigs (>= 0 bp)	4134
# contigs (>= 1000 bp)	1865
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4910941
Total length (>= 1000 bp)	3548413
Total length (>= 5000 bp)	113410
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3301
Largest contig	6813
Total length	4584558
Reference length	4641652
N50	1664
N75	1050
L50	884
L75	1758
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	9298
# local misassemblies	5
# unaligned contigs	0 + 16 part
Unaligned length	729
Genome fraction (%)	92.589
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	503.90
# indels per 100 kbp	9.89
Largest alignment	6813
NA50	1659
NA75	1048
LA50	884
LA75	1761

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	6
# relocations	5
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	9298
# local misassemblies	5
# mismatches	21656
# indels	425
# short indels	423
# long indels	2
Indels length	640

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).
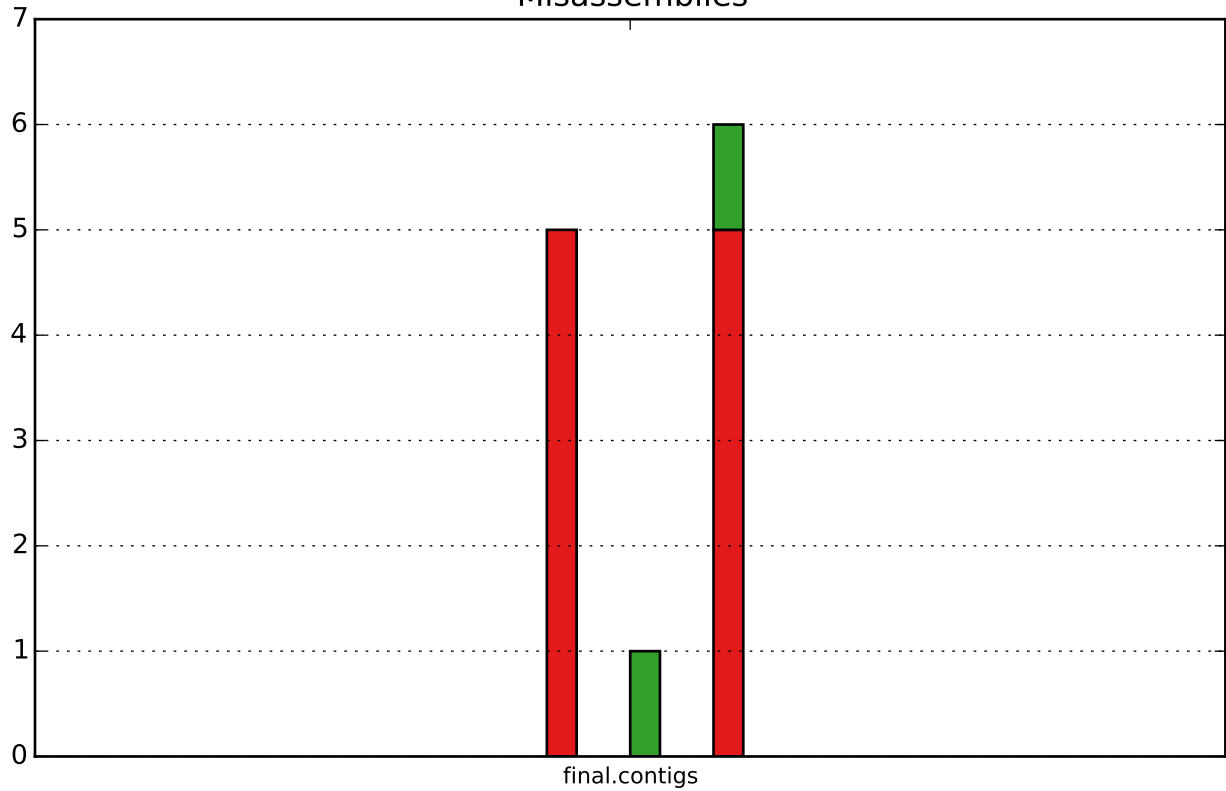
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
# with misassembly	0
# both parts are significant	0
Partially unaligned length	729
# 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).
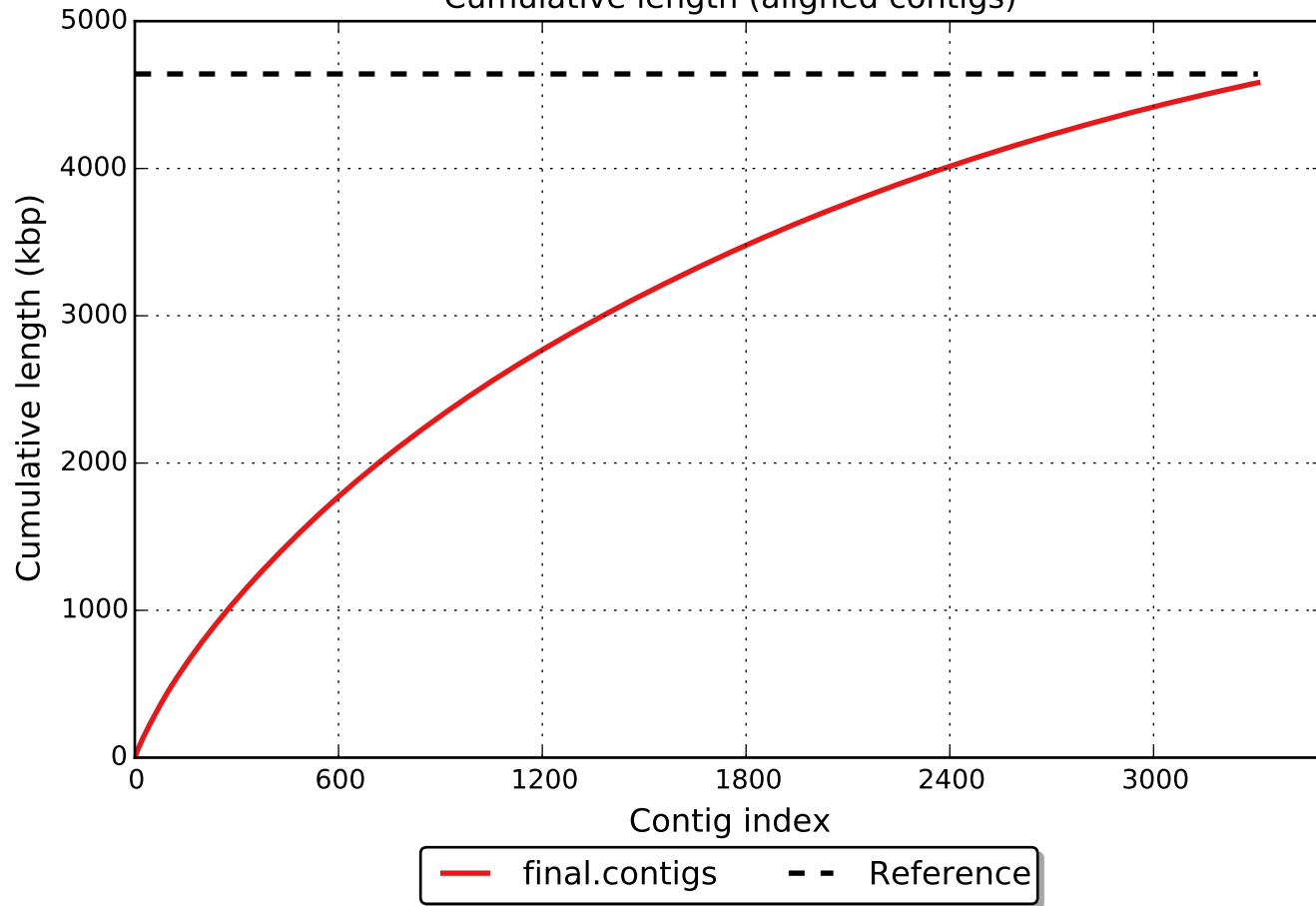
Nx

Contig length (kbp)

x

final.contigs
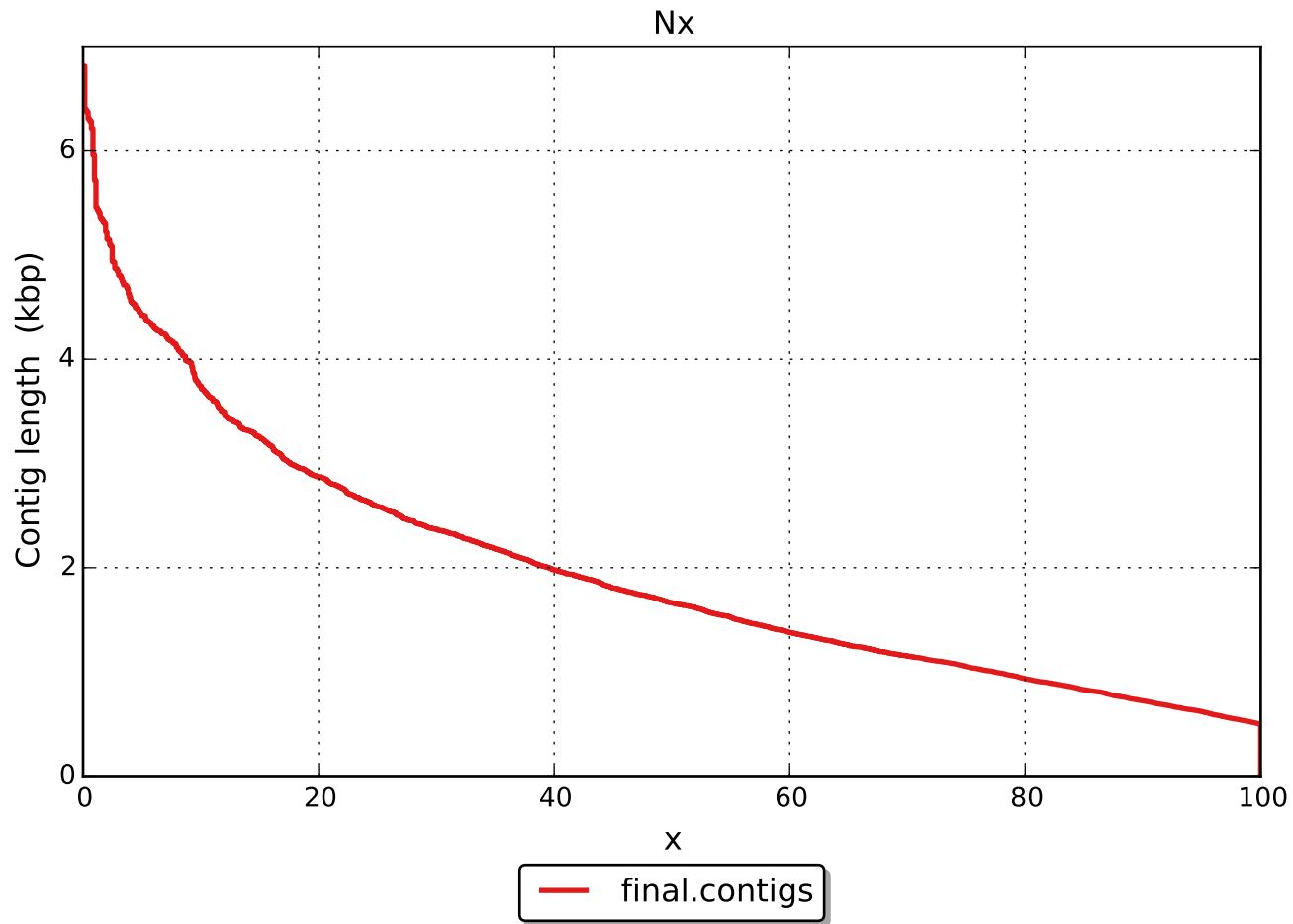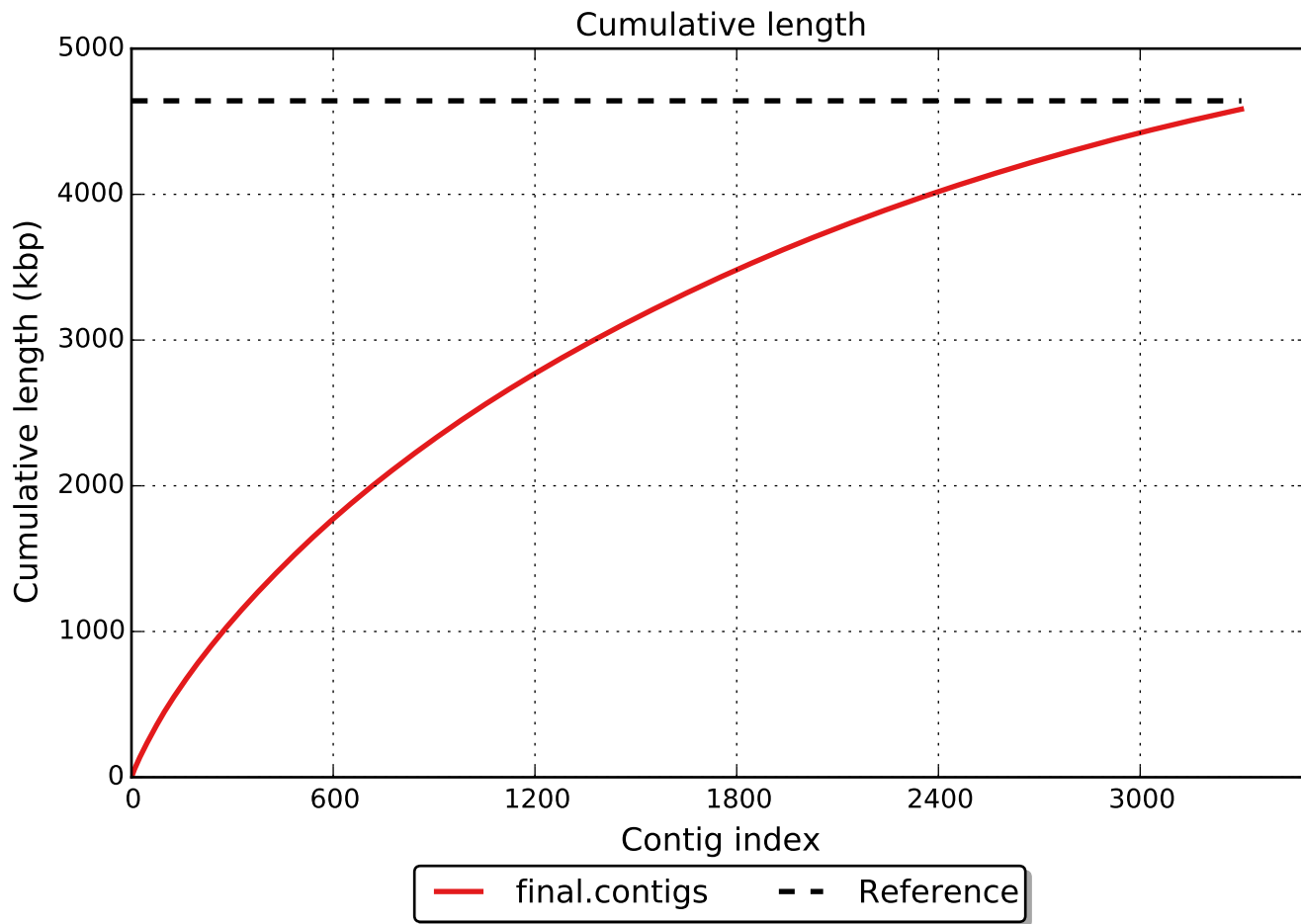
Cumulative length

Misassemblies

Cumulative length (aligned contigs)