Report

	final.contigs
# contigs (>= 0 bp)	506
# contigs (>= 1000 bp)	371
# contigs (>= 5000 bp)	312
# contigs (>= 10000 bp)	252
# contigs (>= 25000 bp)	133
# contigs (>= 50000 bp)	45
Total length (>= 0 bp)	9257110
Total length (>= 1000 bp)	9208467
Total length (>= 5000 bp)	9039652
Total length (>= 10000 bp)	8588599
Total length (>= 25000 bp)	6463224
Total length (>= 50000 bp)	3403962
# contigs	394
Largest contig	177974
Total length	9225256
Reference length	9283304
N50	37676
N75	22685
L50	73
L75	152
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.080
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	0.00
Largest alignment	177974
NA50	37676
NA75	22582
LA50	73
LA75	153

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).
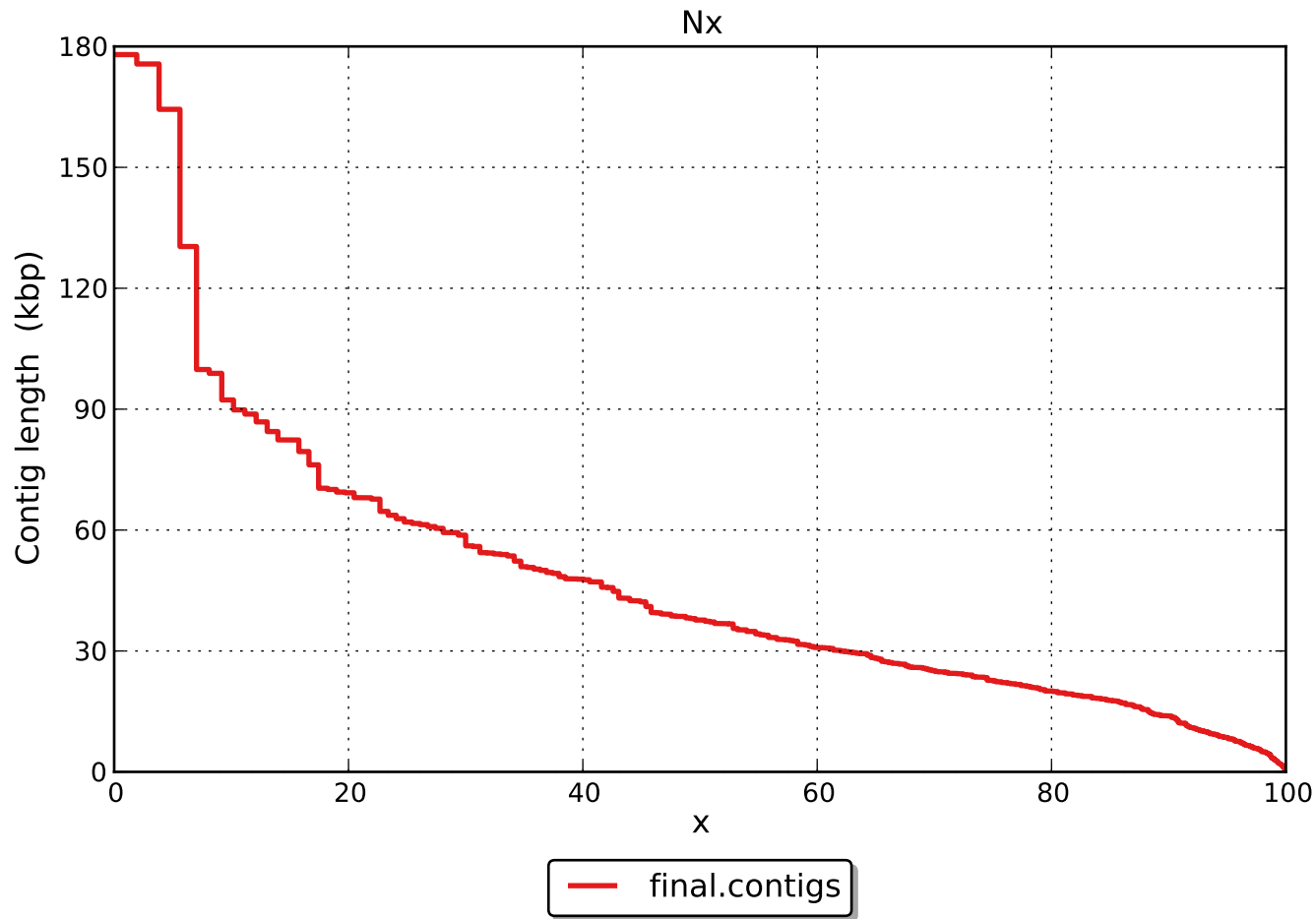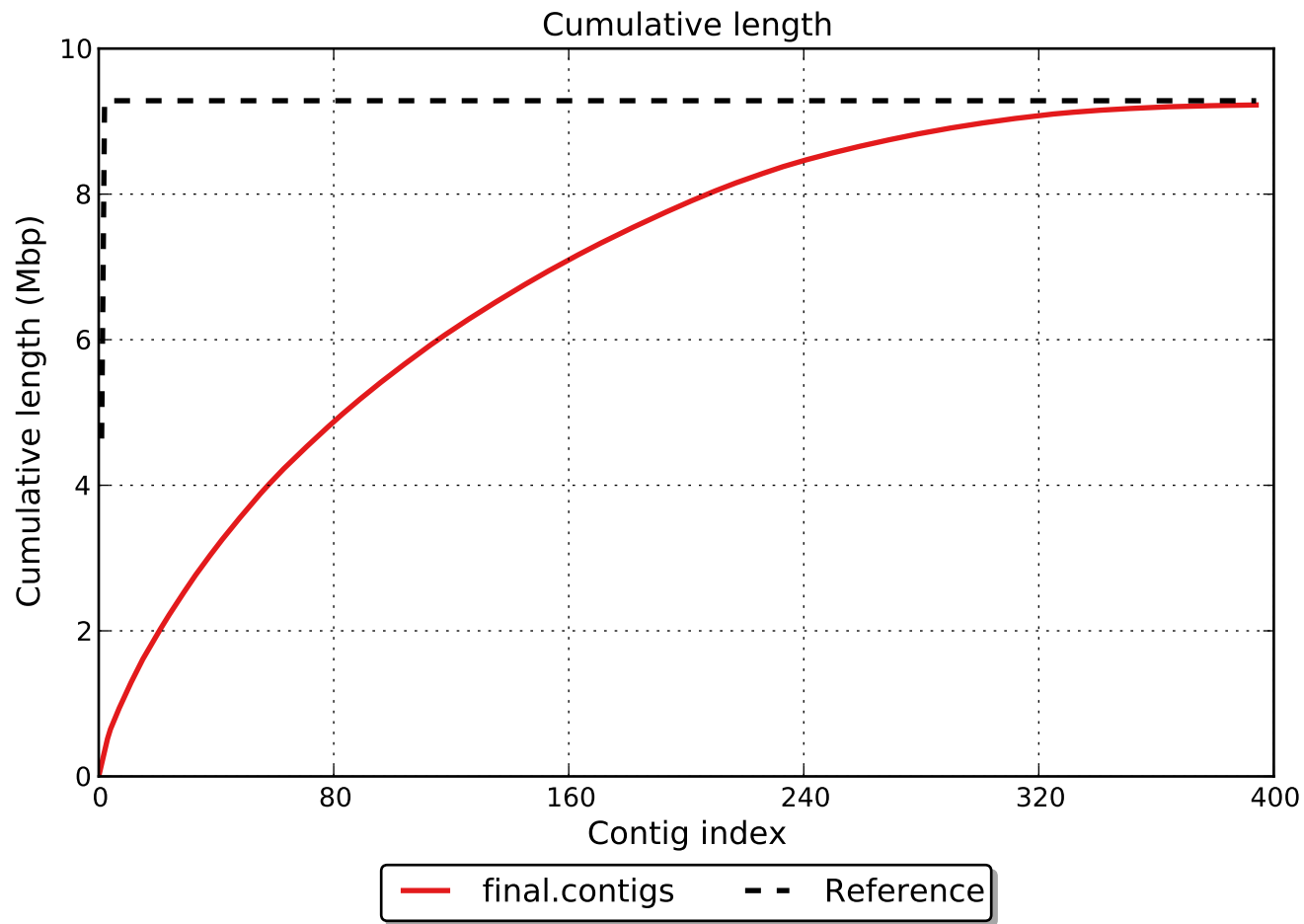
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	0

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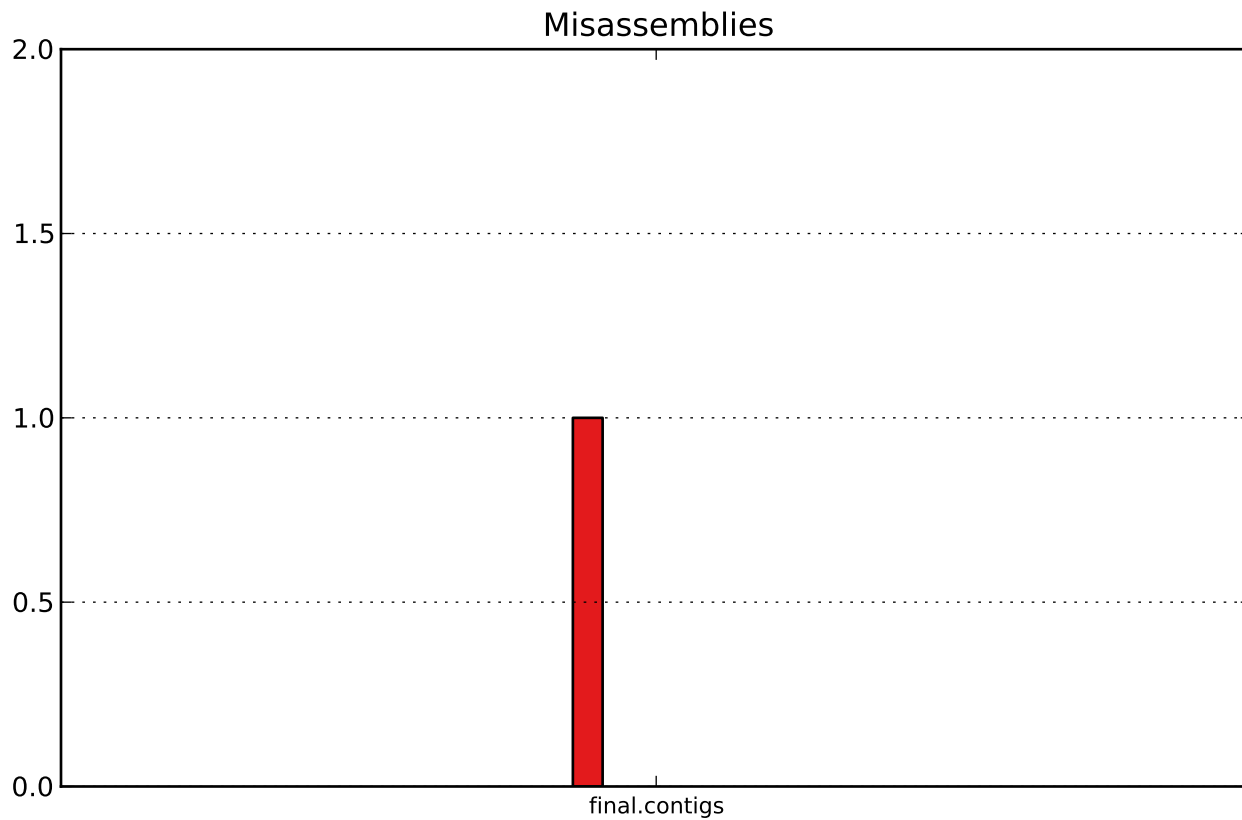(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
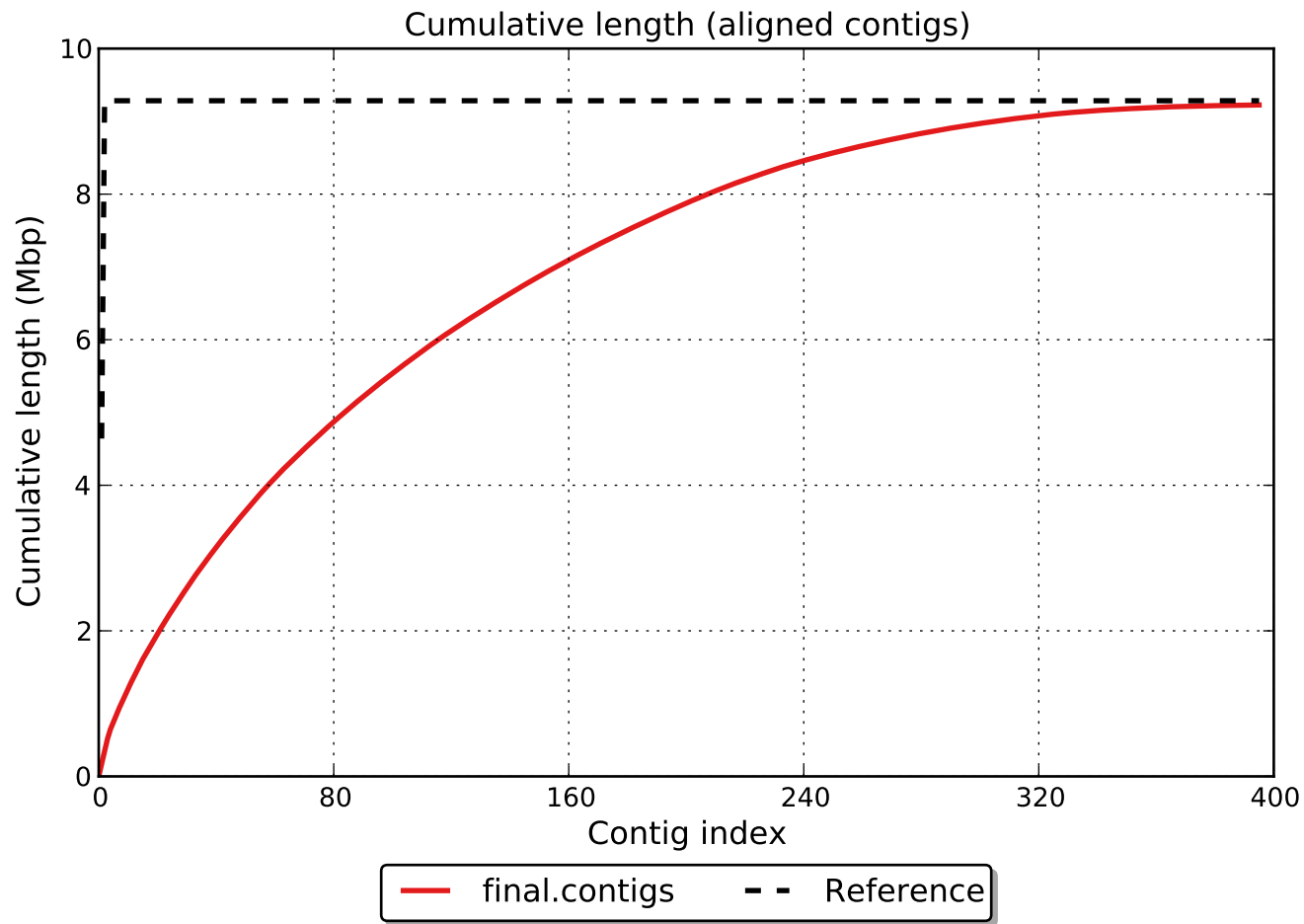
Unaligned report

	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
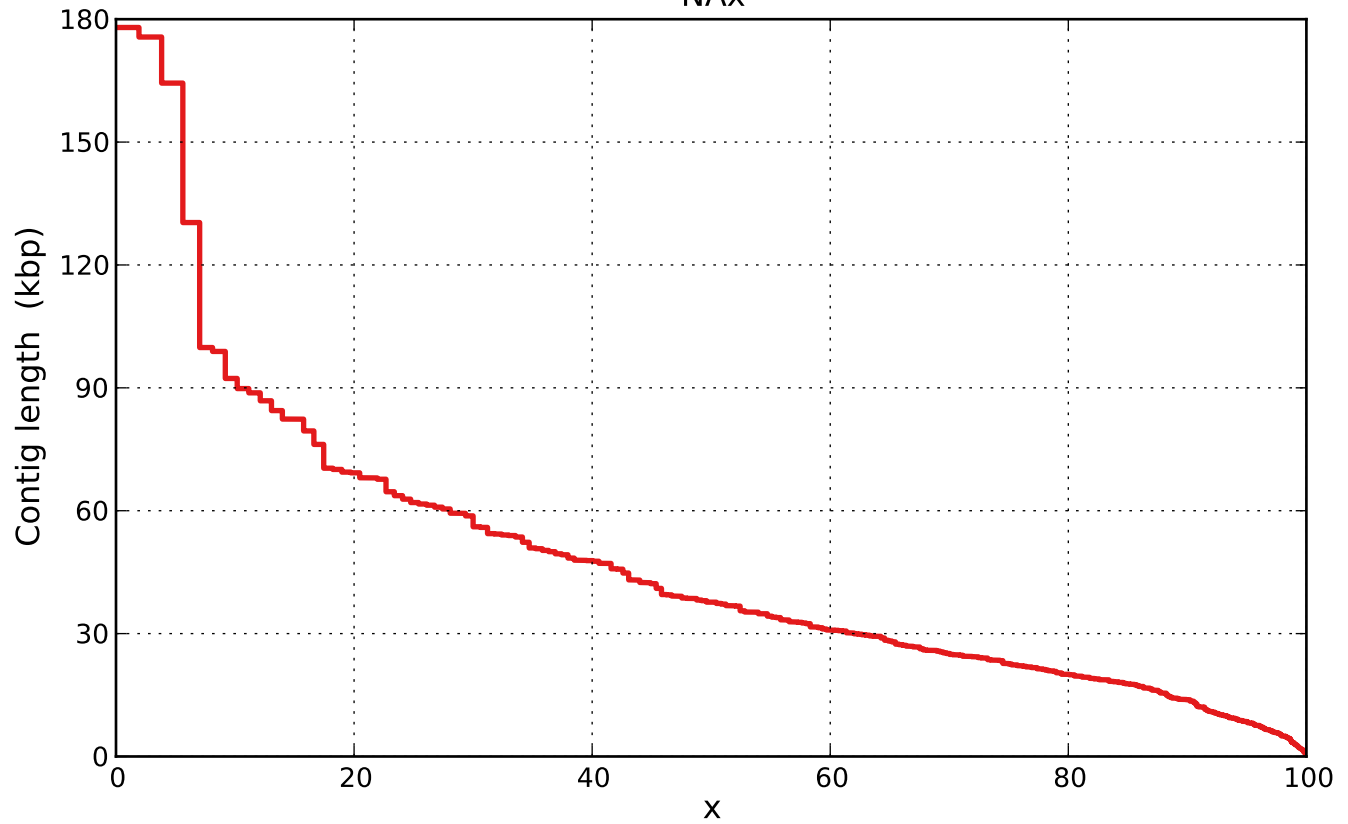(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)