Report

	final.contigs
# contigs (>= 0 bp)	1113
# contigs (>= 1000 bp)	921
Total length (>= 0 bp)	5256451
Total length (>= 1000 bp)	5119805
# contigs	1113
Largest contig	36412
Total length	5256451
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	8097
NG50	7667
N75	4263
NG75	3865
L50	203
LG50	217
L75	423
LG75	464
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.467
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.59
# indels per 100 kbp	0.12
Largest alignment	36412
NA50	8097
NGA50	7667
NA75	4263
NGA75	3865
LA50	203
LGA50	217
LA75	423
LGA75	464

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).
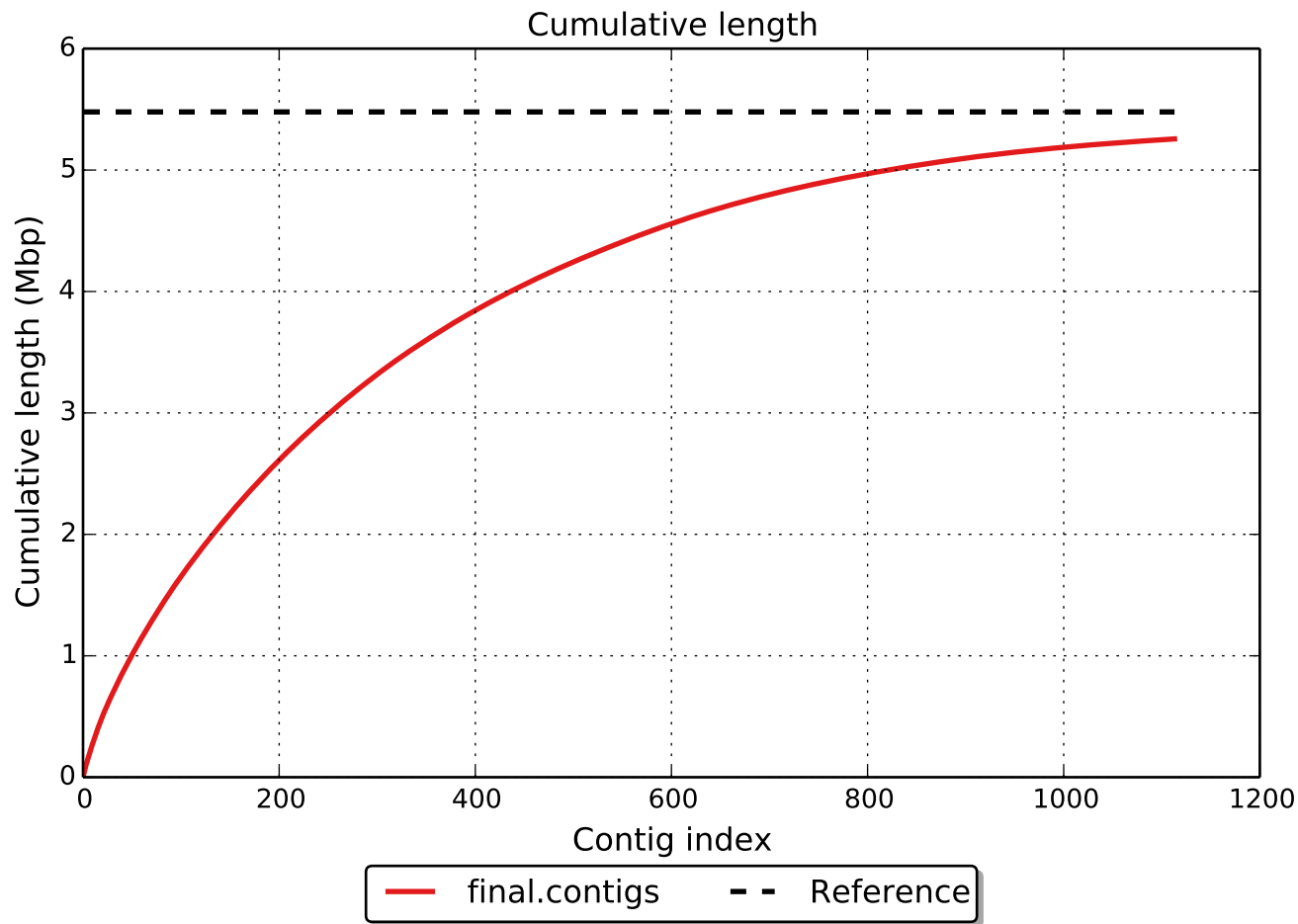
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	807
# indels	6
# short indels	4
# long indels	2
Indels length	33

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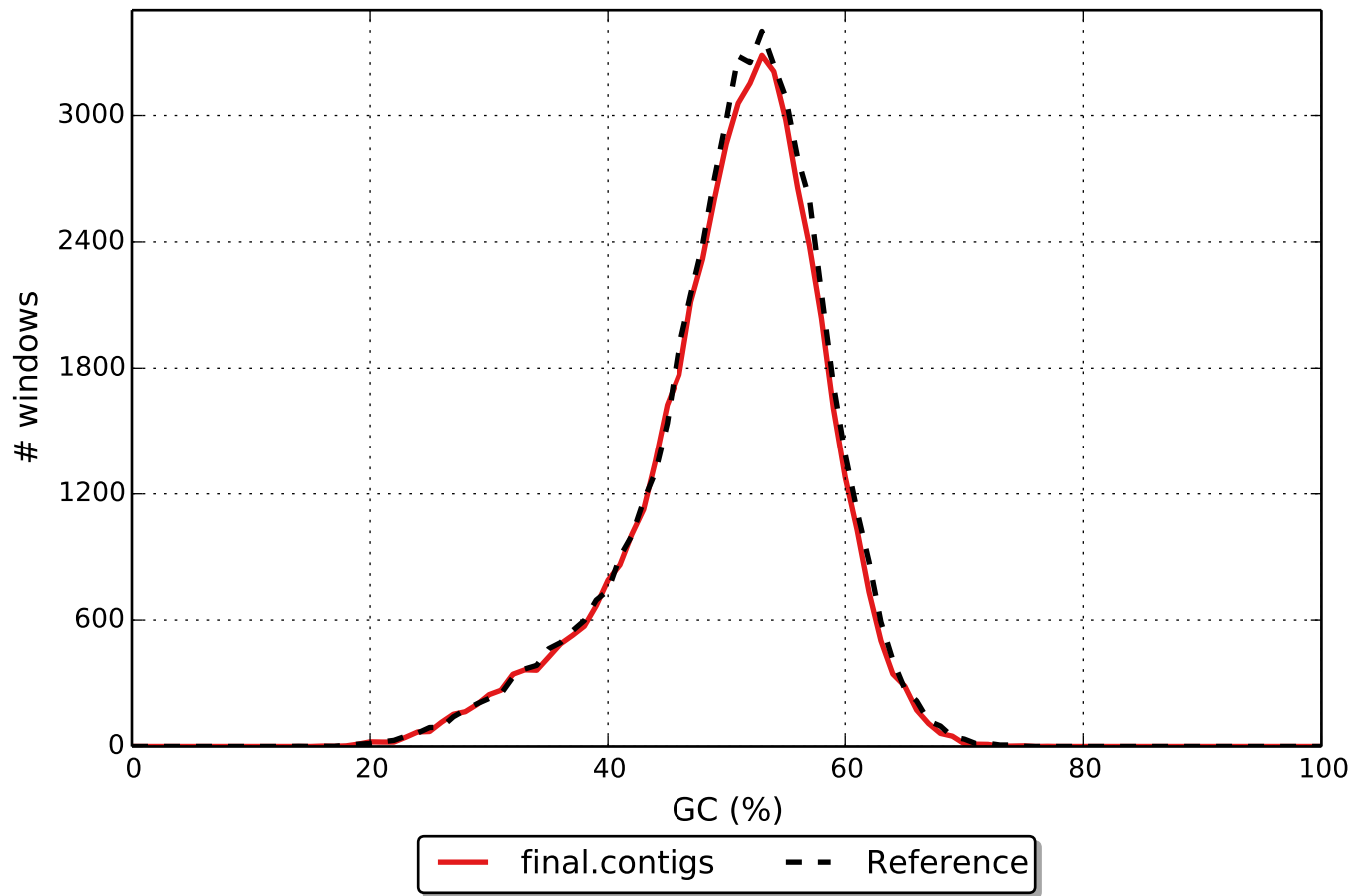
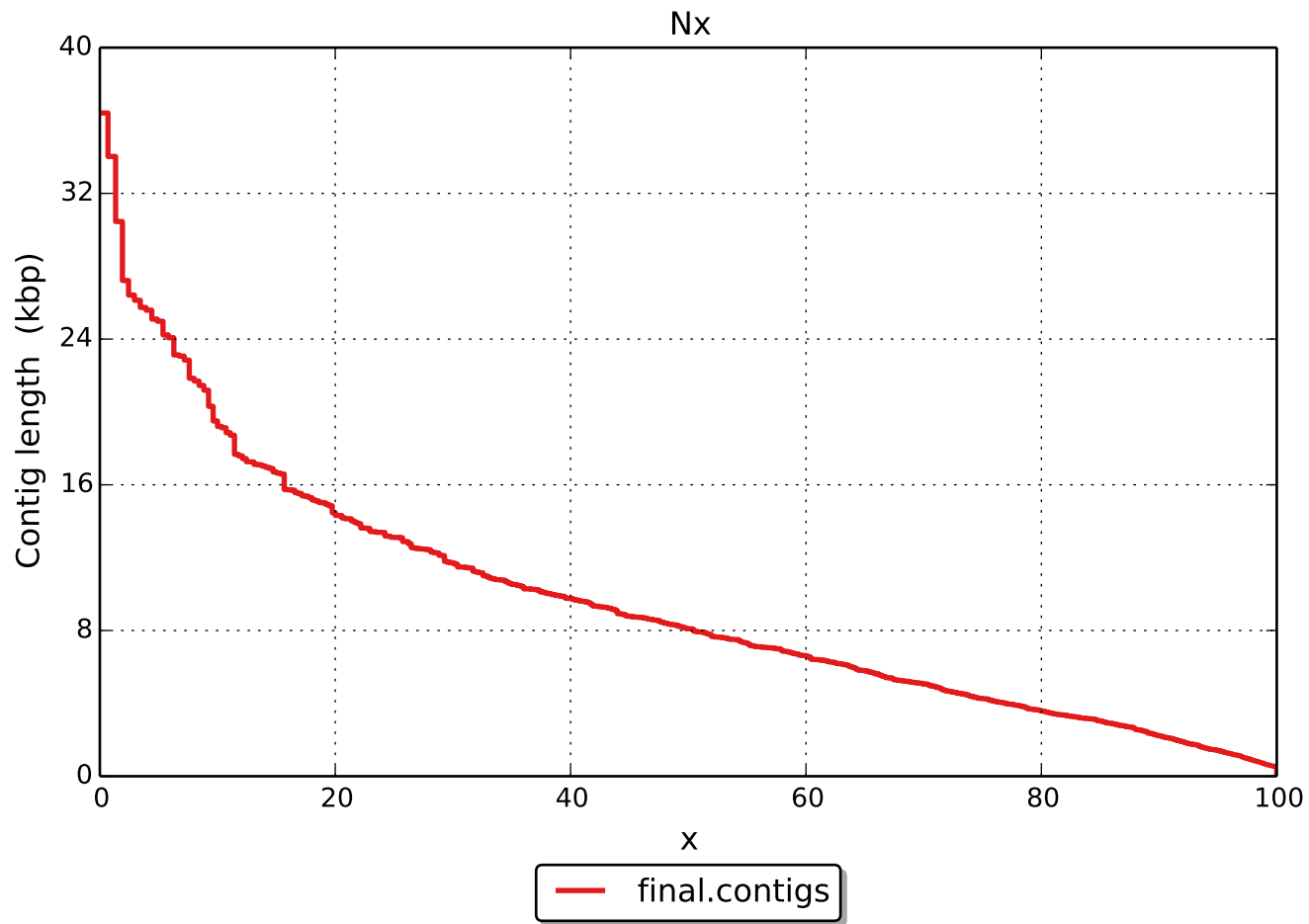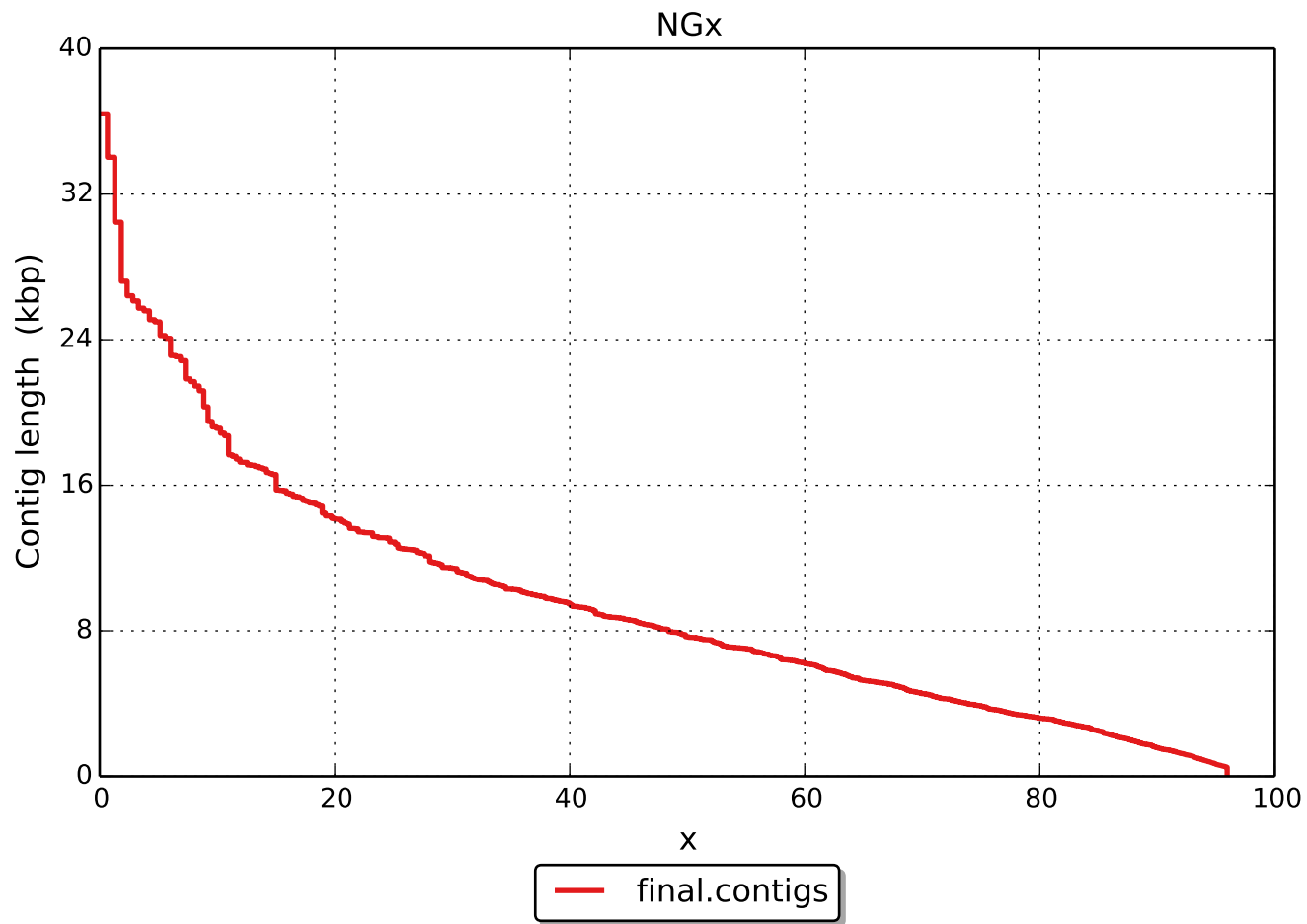|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).
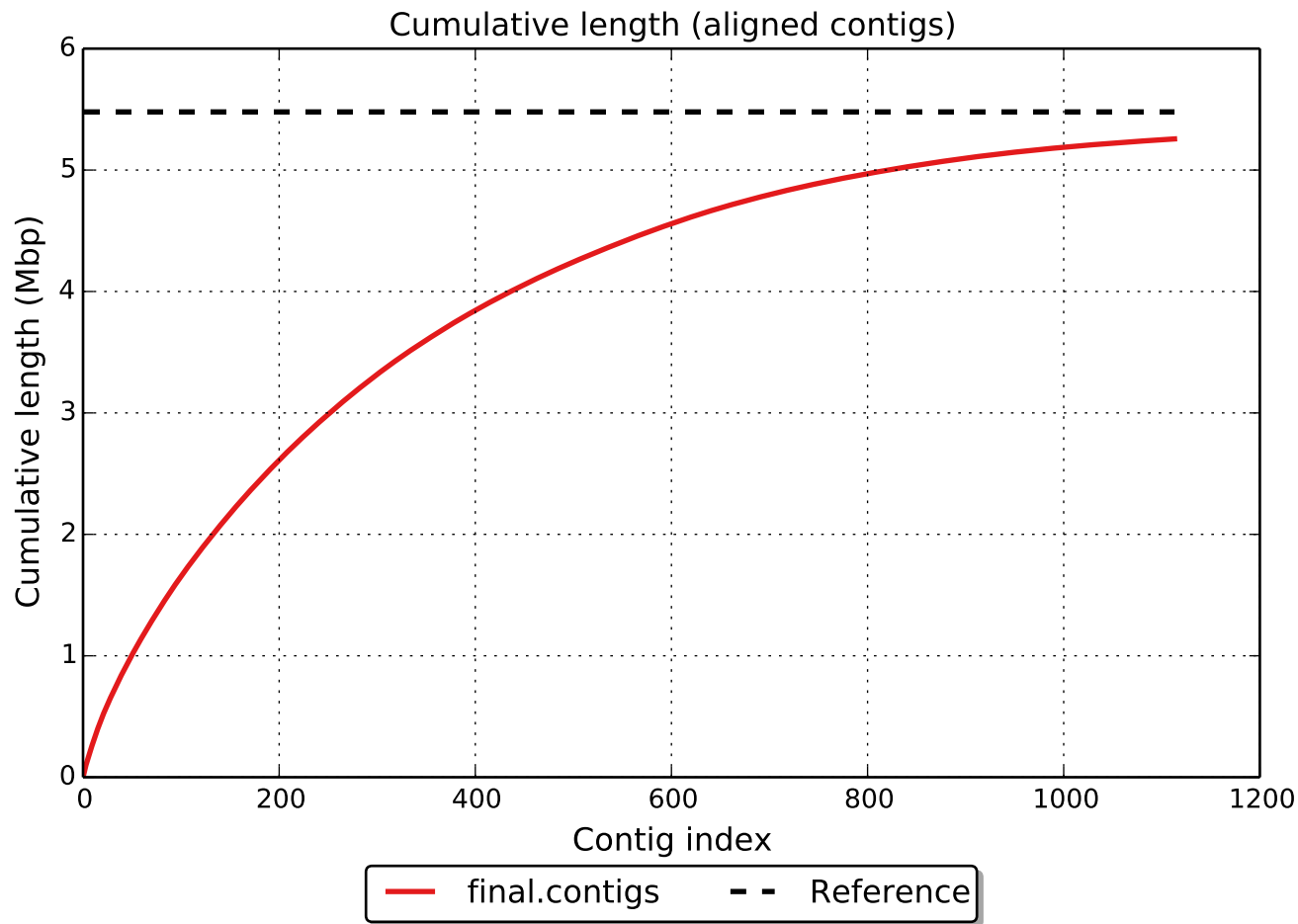
Cumulative length

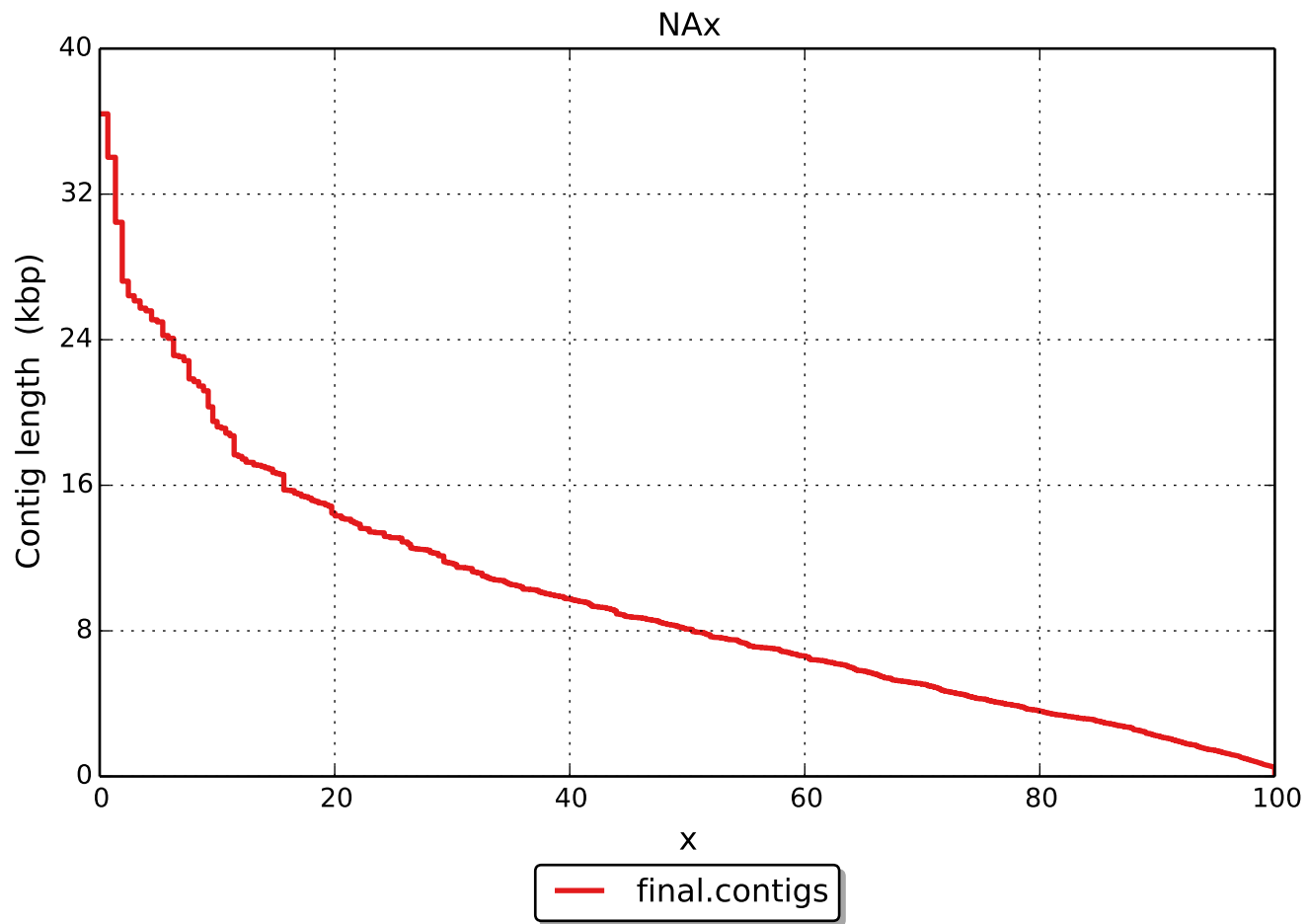Cumulative length (Mbp) vs Contig index

final.contigs — Reference

Nx

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx