Report

	final.contigs
# contigs (>= 1000 bp)	430
# contigs (>= 5000 bp)	283
# contigs (>= 10000 bp)	177
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	4665832
Total length (>= 5000 bp)	4226853
Total length (>= 10000 bp)	3451345
Total length (>= 25000 bp)	1198293
Total length (>= 50000 bp)	119867
# contigs	450
Largest contig	66558
Total length	4680923
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	16126
NG50	16358
N75	9775
NG75	9889
L50	92
LG50	90
L75	183
LG75	181
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.902
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.50
# indels per 100 kbp	0.00
Largest alignment	66558
NA50	16126
NGA50	16358
NA75	9775
NGA75	9889
LA50	92
LGA50	90
LA75	183
LGA75	181

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).
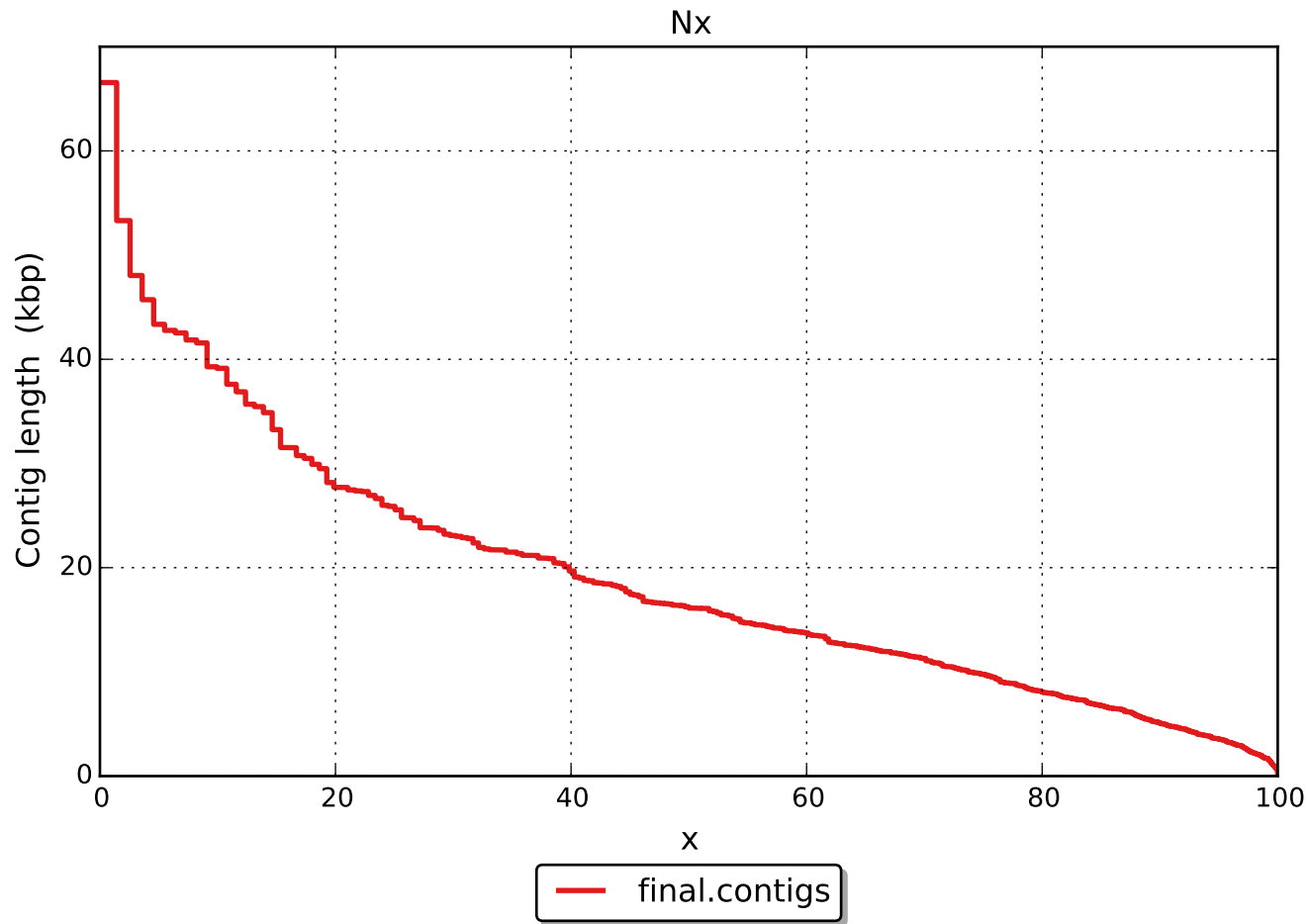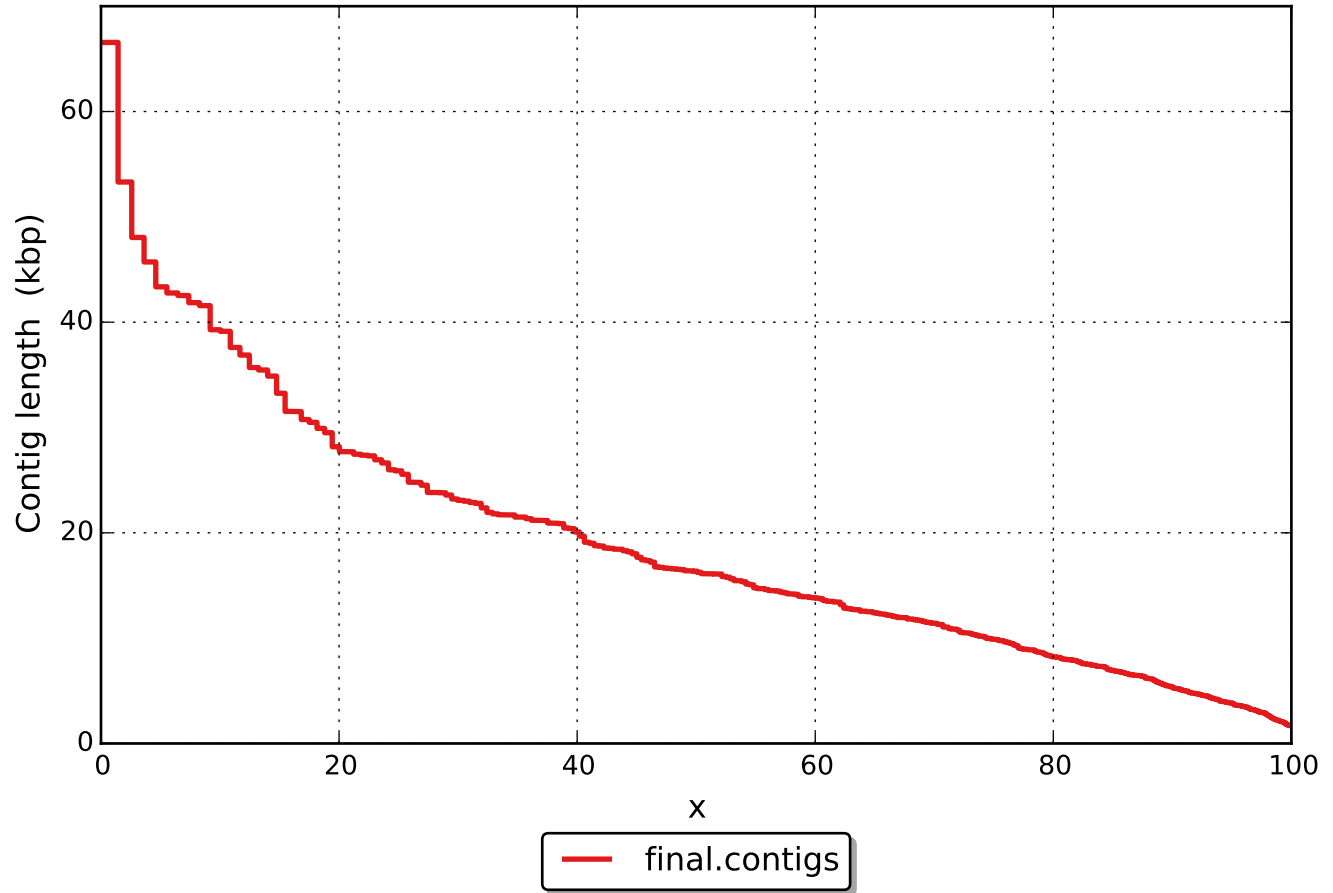
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	487
# 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).
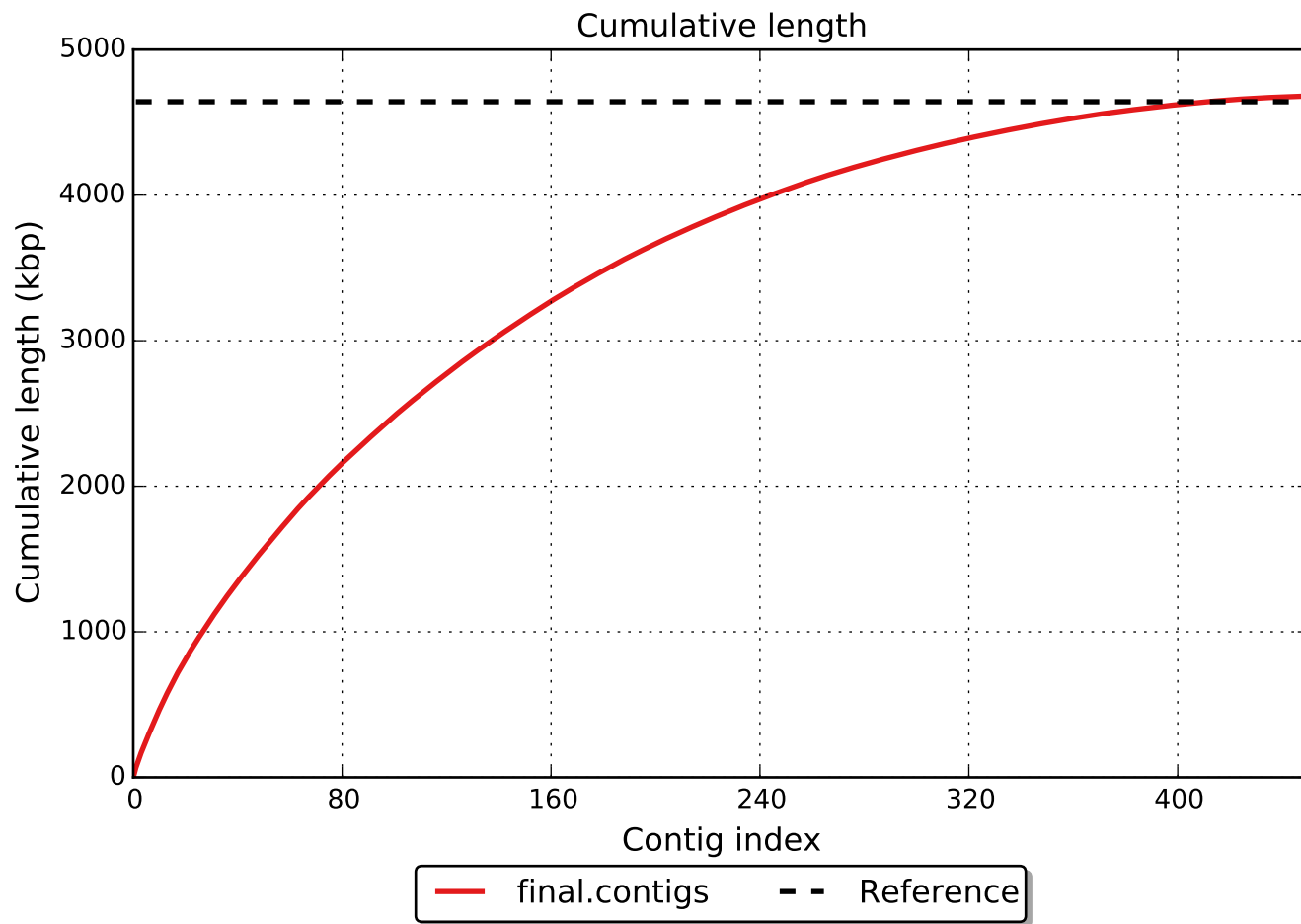
Unaligned report

	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).
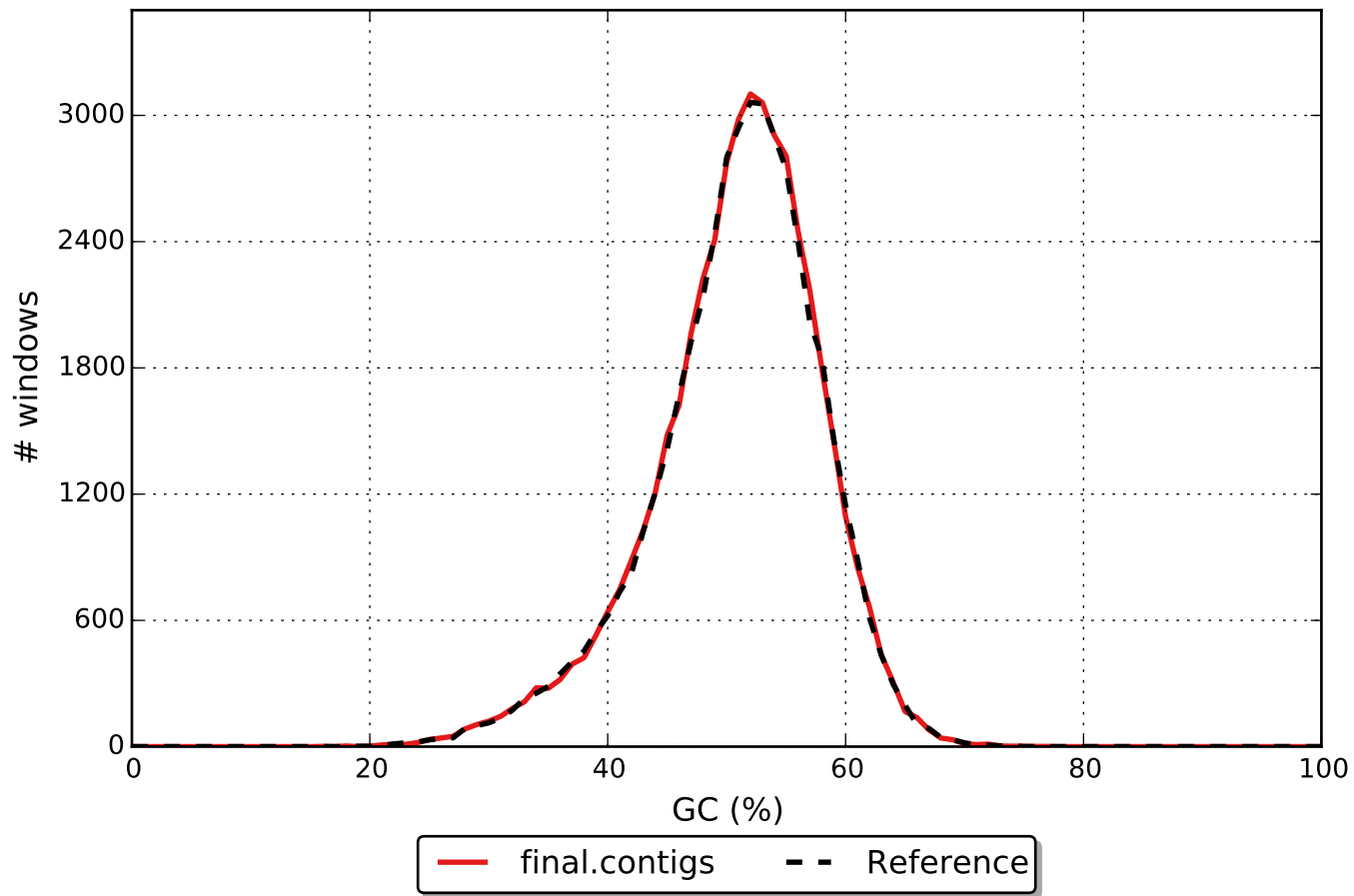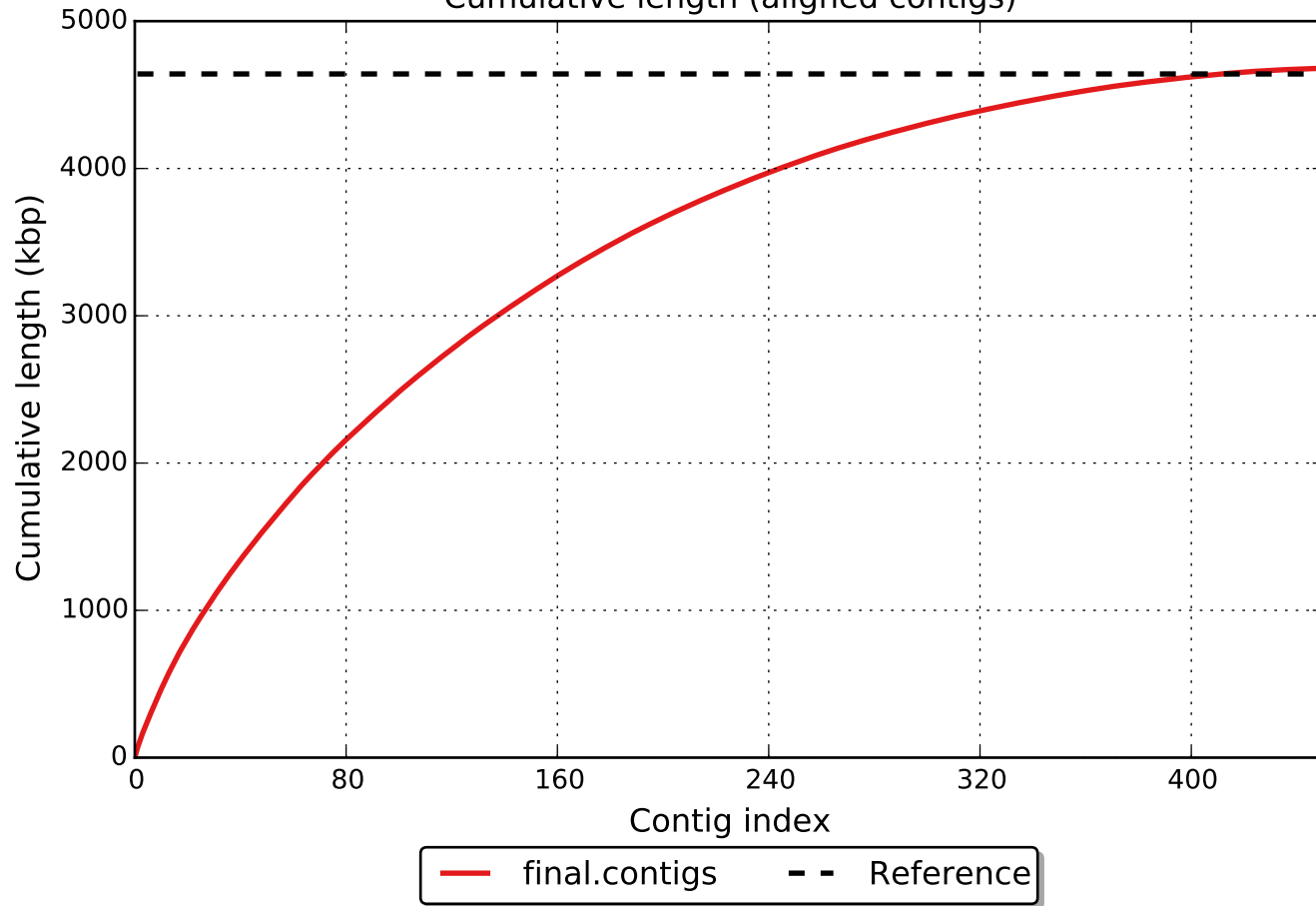
NGx

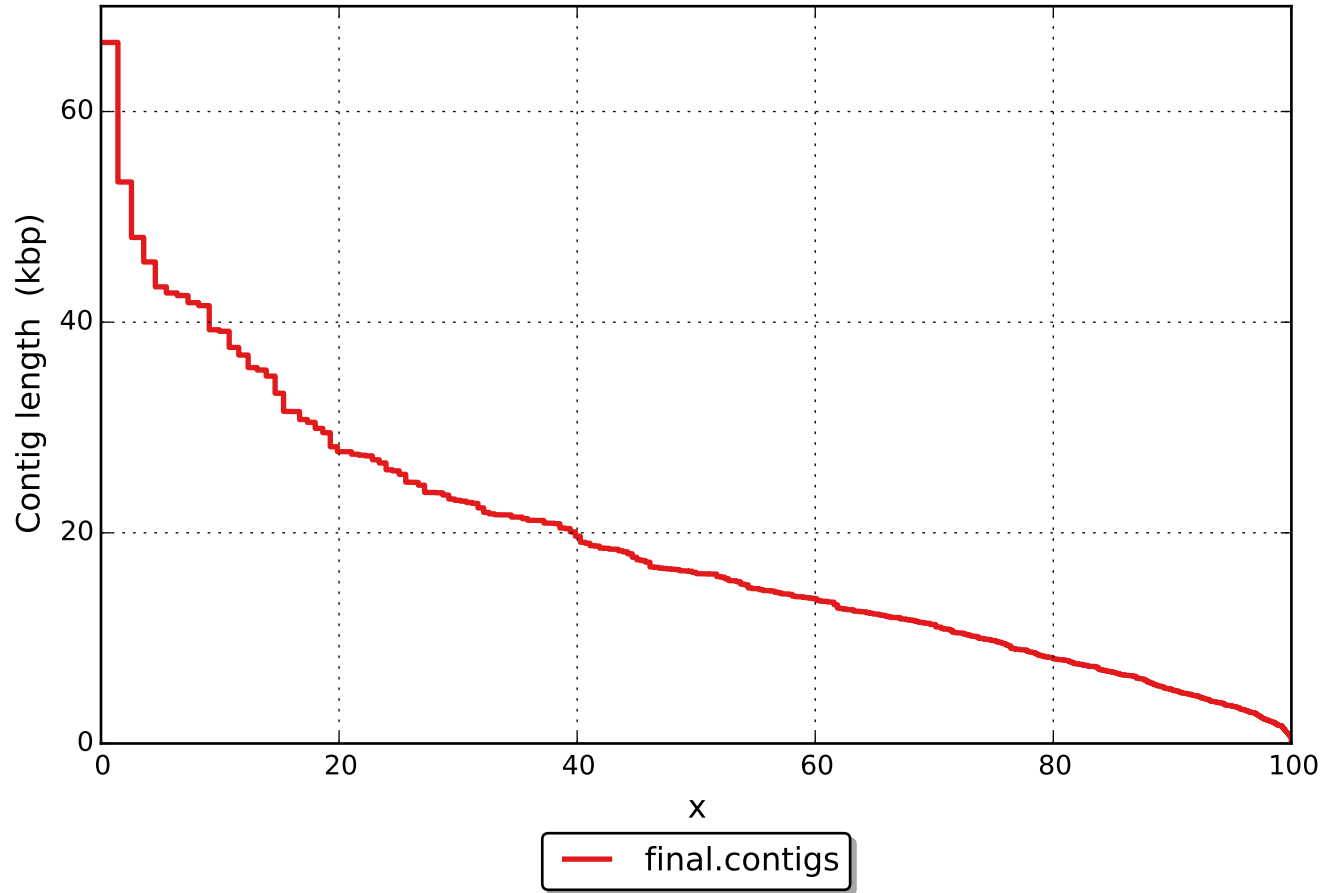Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs

NGAx