Report

	final.contigs
# contigs (>= 1000 bp)	869
# contigs (>= 5000 bp)	361
# contigs (>= 10000 bp)	115
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4864468
Total length (>= 5000 bp)	3480378
Total length (>= 10000 bp)	1767563
Total length (>= 25000 bp)	227736
Total length (>= 50000 bp)	0
# contigs	963
Largest contig	32238
Total length	4932310
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.22
N50	7581
NG50	7673
N75	4546
NG75	4664
L50	196
LG50	191
L75	407
LG75	395
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	6669
Genome fraction (%)	99.630
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.20
# indels per 100 kbp	0.00
Largest alignment	32238
NA50	7581
NGA50	7673
NA75	4511
NGA75	4653
LA50	196
LGA50	191
LA75	408
LGA75	396

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).
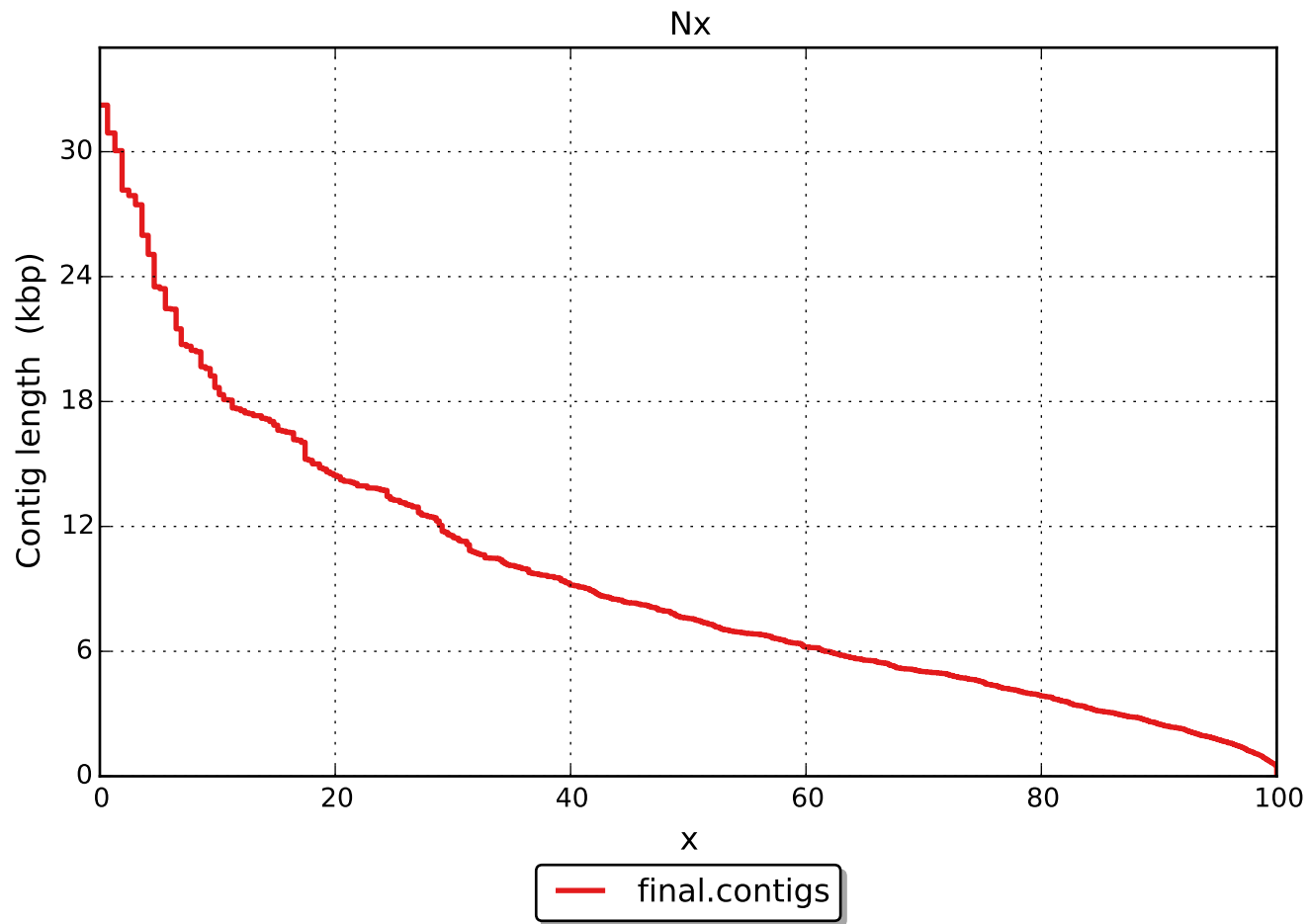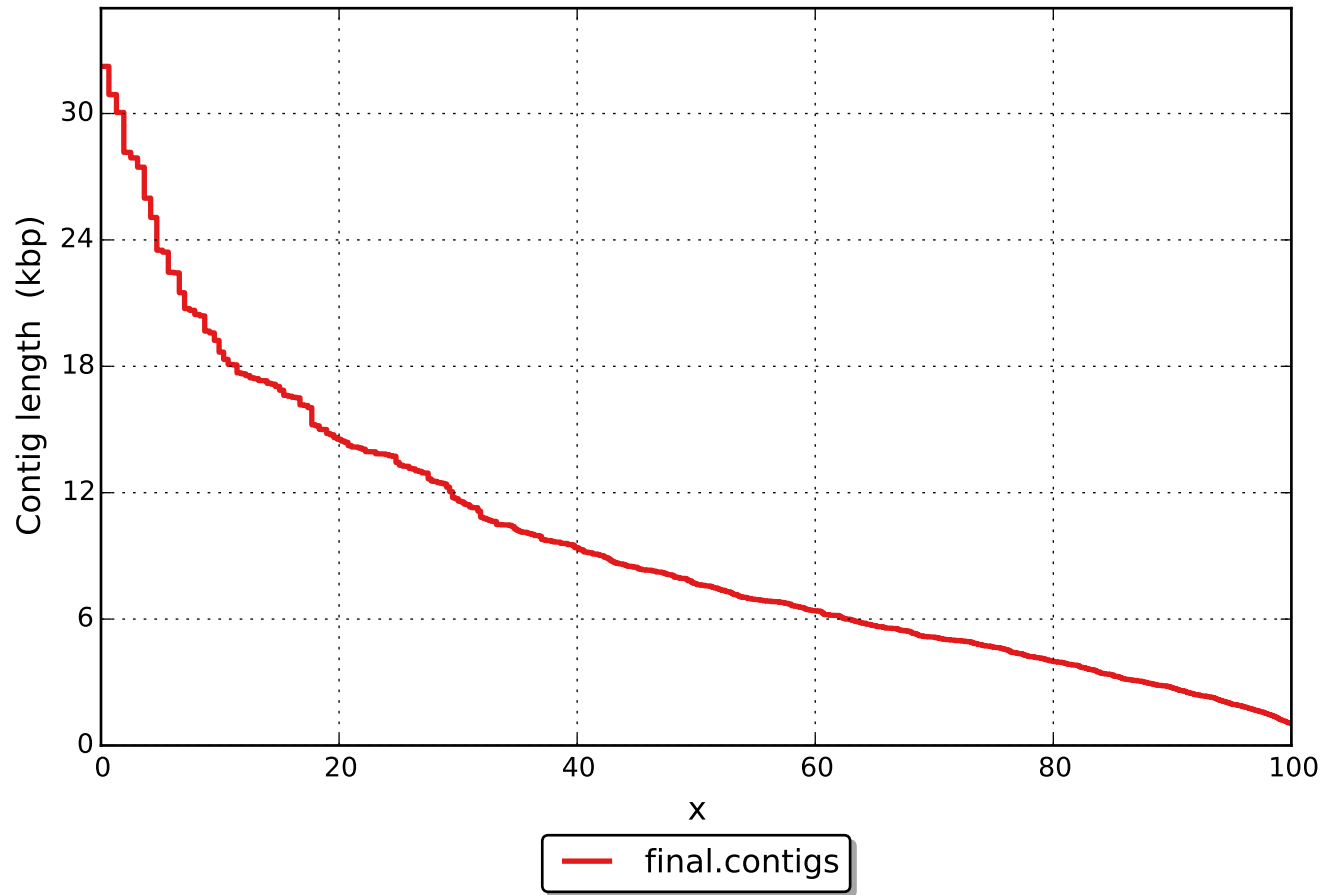
Misassemblies report

	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	1026
# 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).
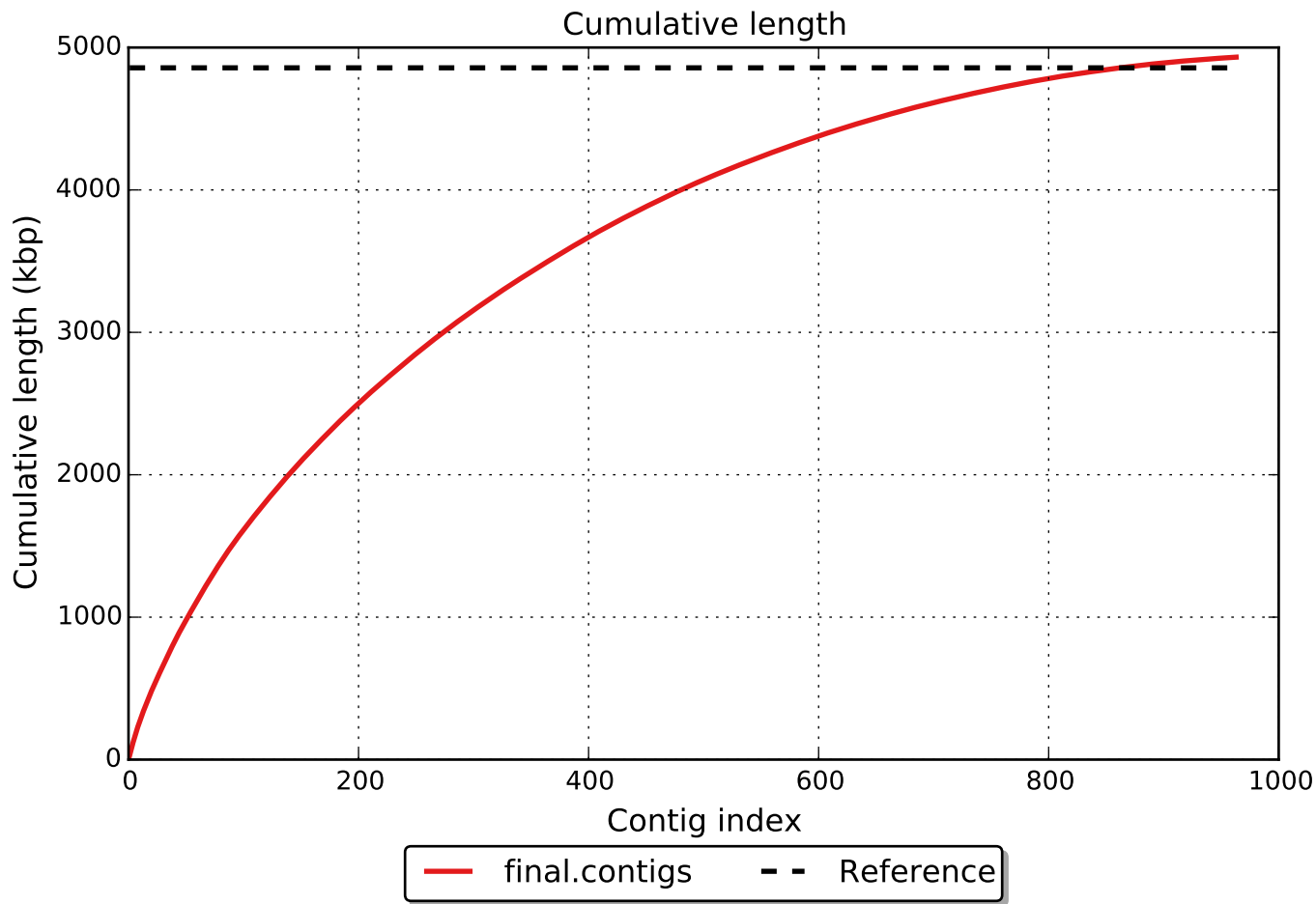
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	6669
# N's	0

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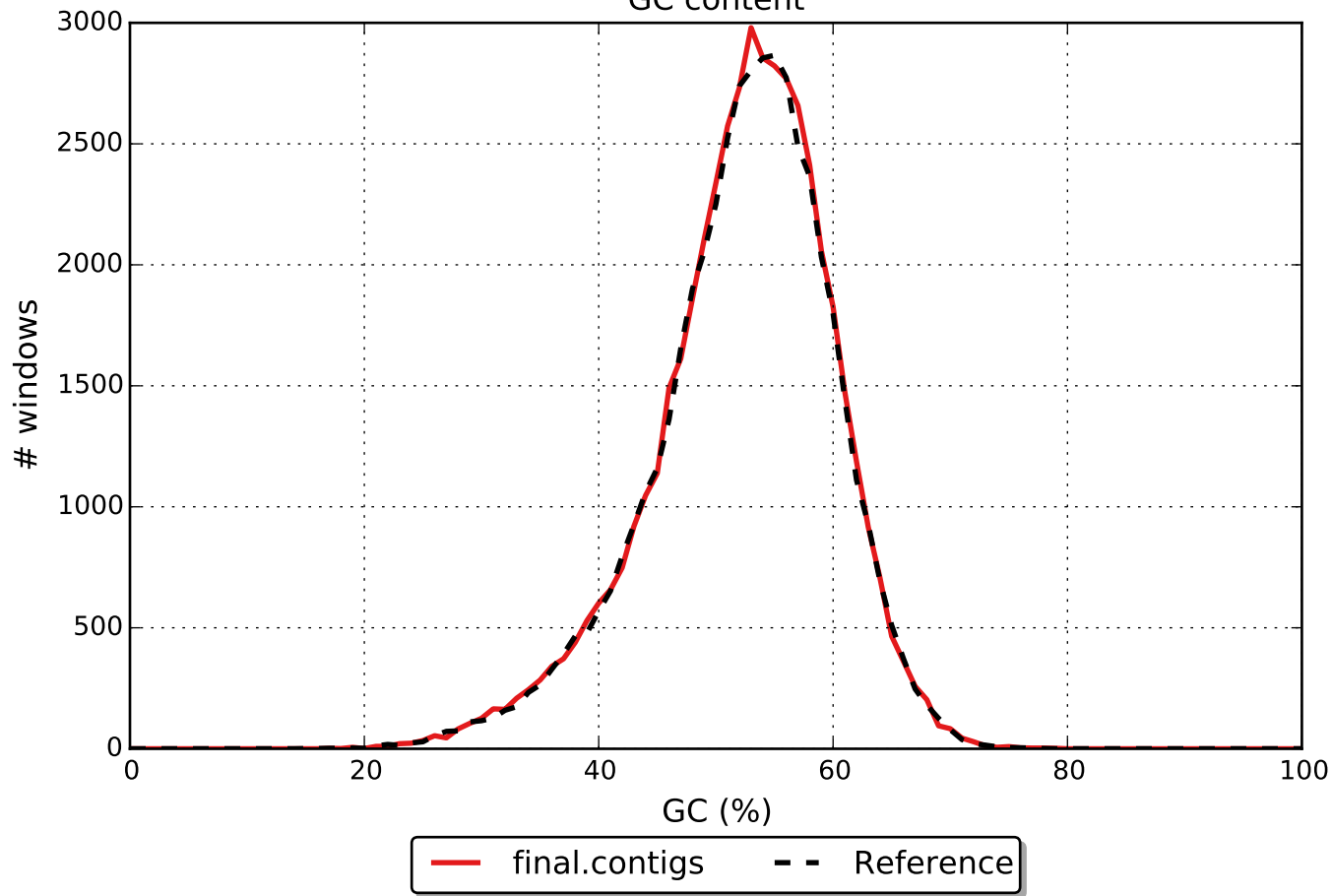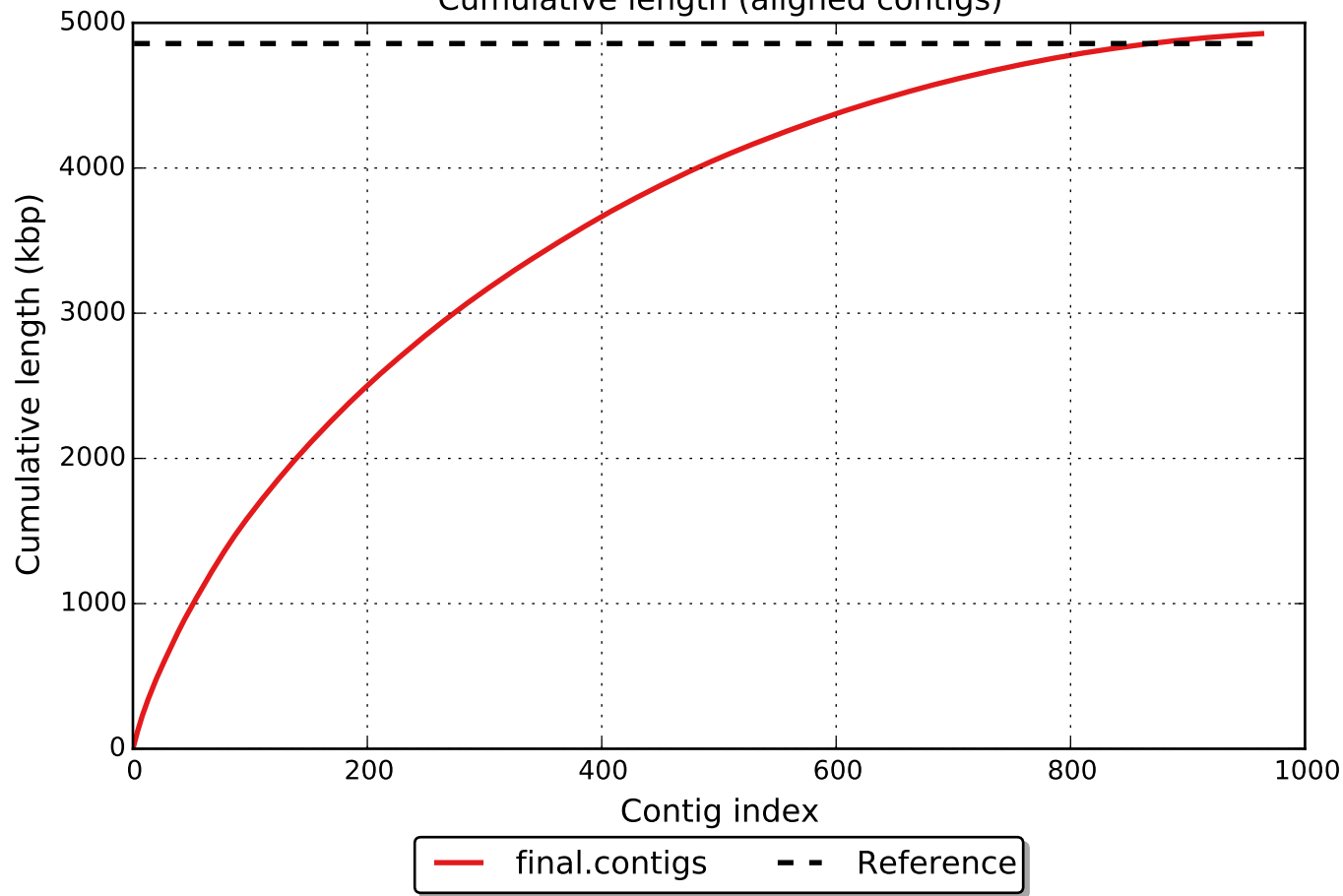(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

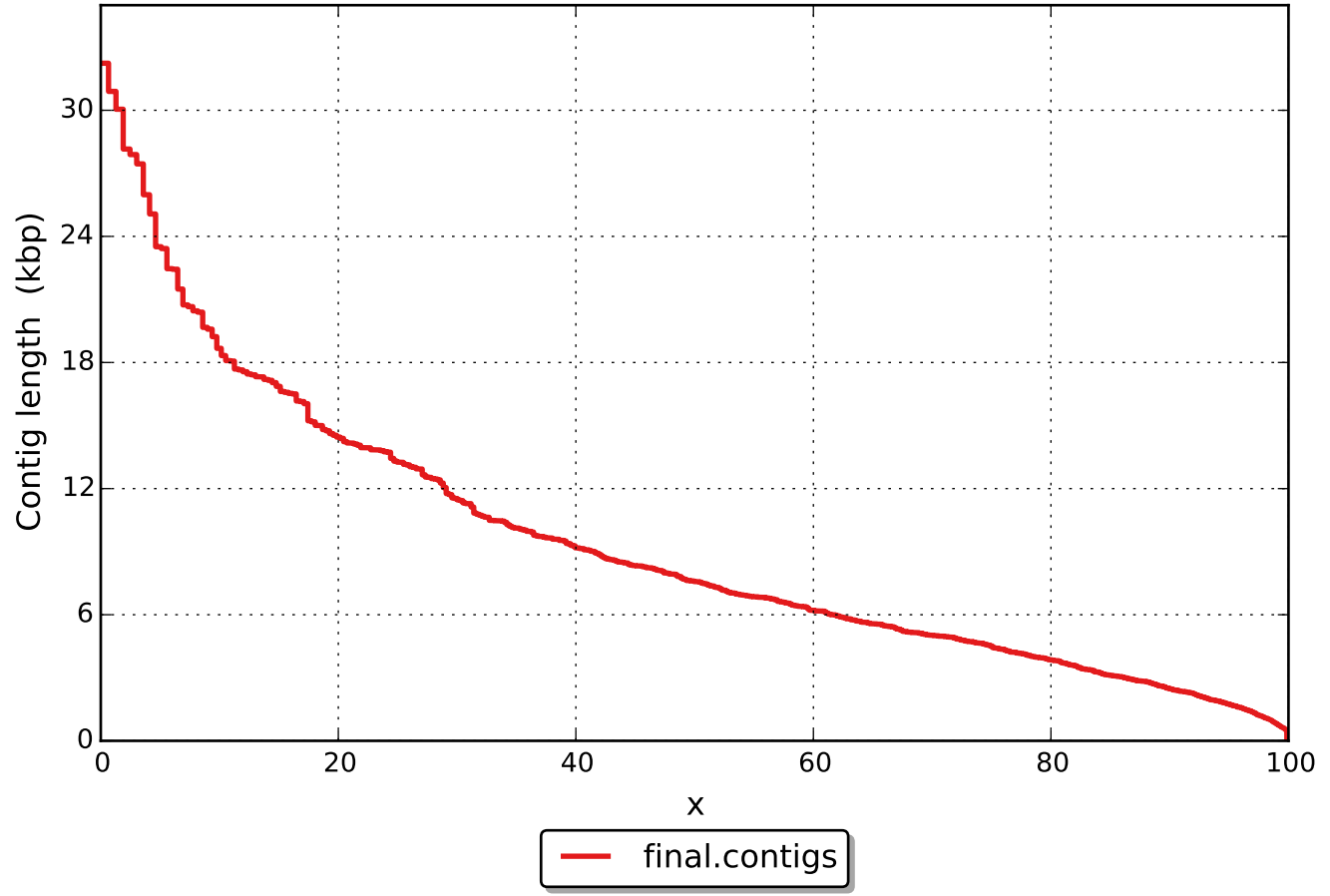Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx