Report

|	final.contigs
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4551877
Total length (>= 5000 bp)	4497397
Total length (>= 10000 bp)	4454018
Total length (>= 25000 bp)	4174547
Total length (>= 50000 bp)	3607181
# contigs	113
Largest contig	249259
Total length	4562633
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	105838
NG50	105838
N75	56775
NG75	54945
L50	14
LG50	14
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.241
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.87
# indels per 100 kbp	8.93
Largest alignment	249259
NA50	105838
NGA50	105838
NA75	56775
NGA75	54945
LA50	14
LGA50	14
LA75	29
LGA75	30

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	10
# mismatches	2639
# indels	407
# short indels	406
# long indels	1
Indels length	680

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).
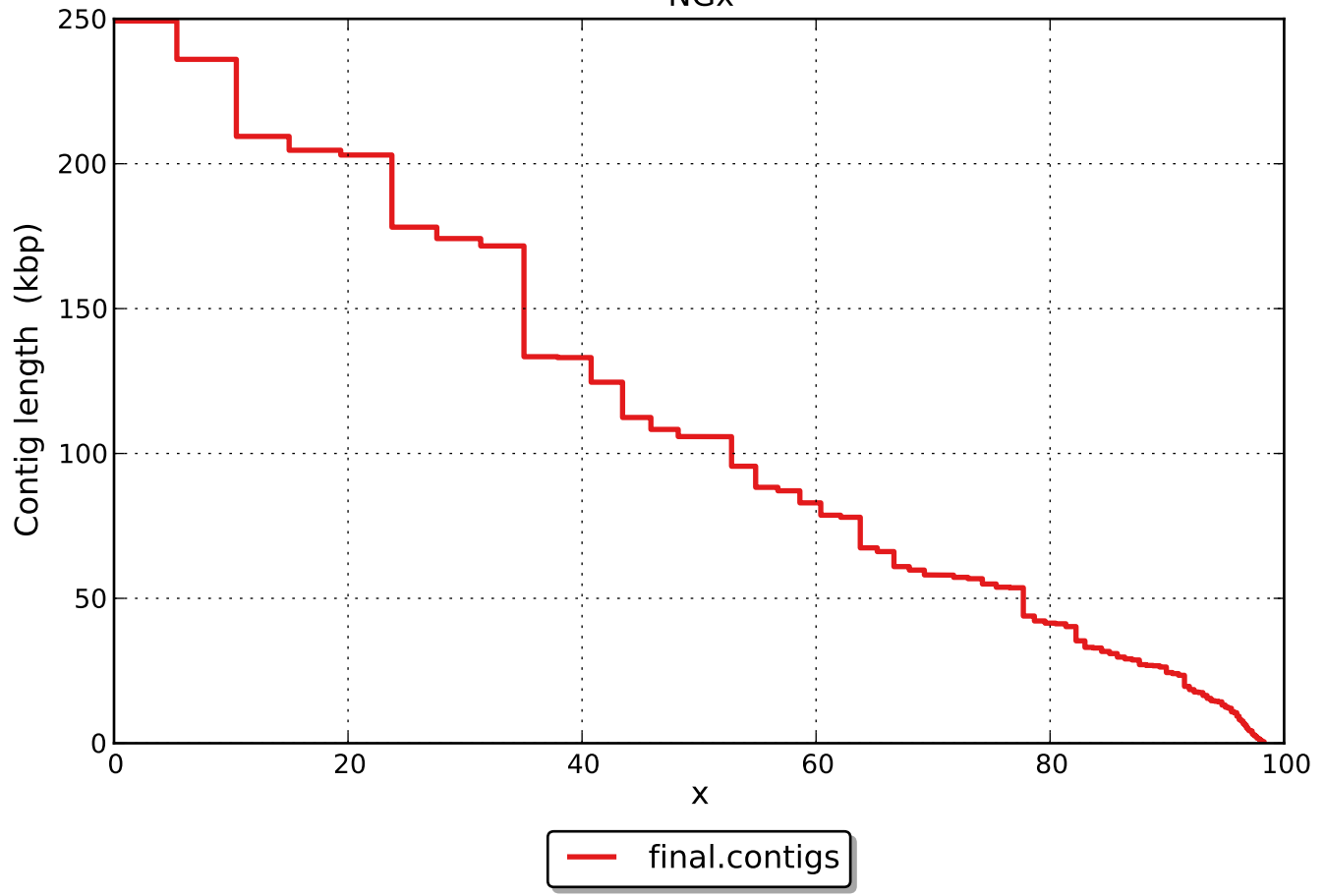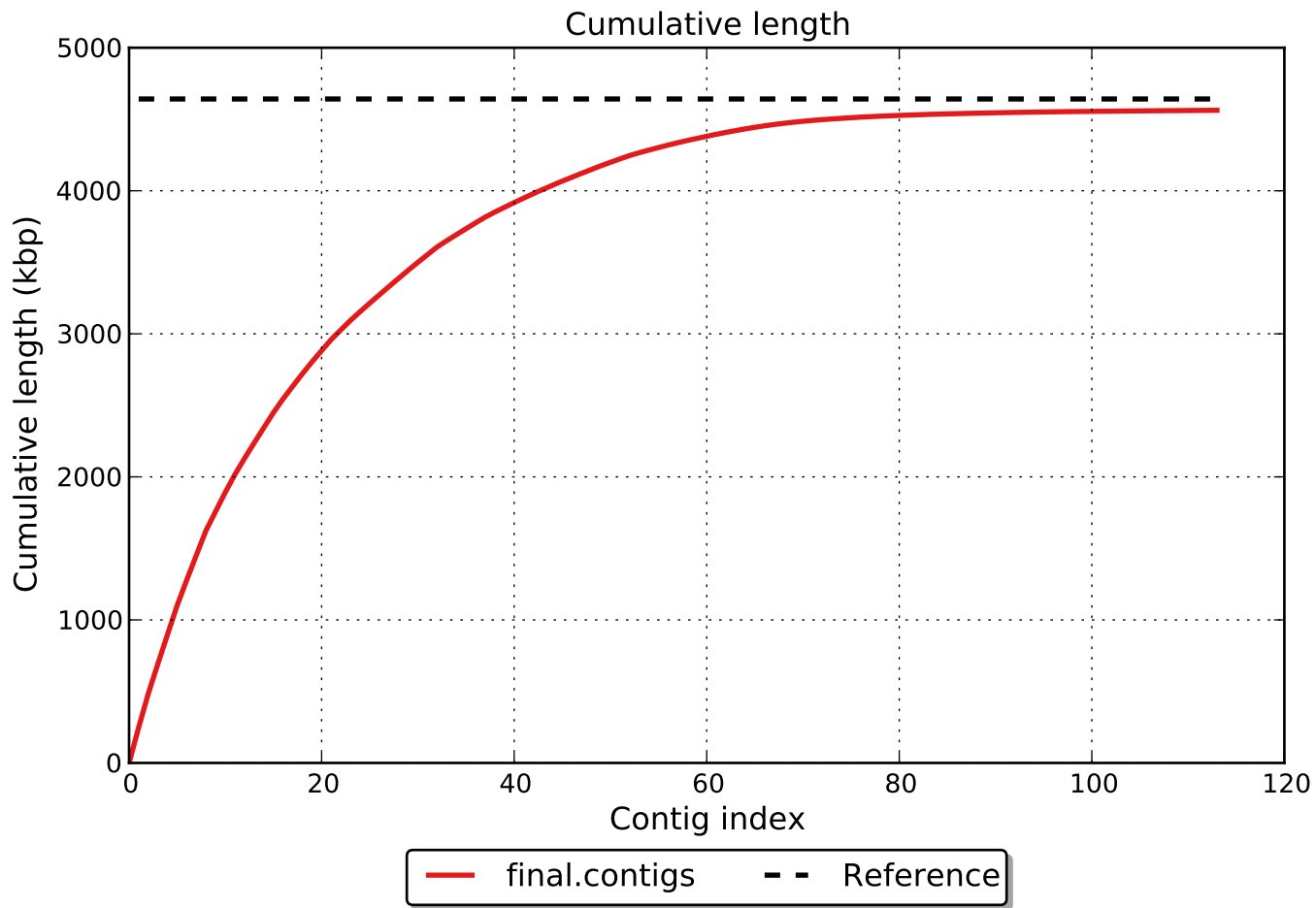
Unaligned report

	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).
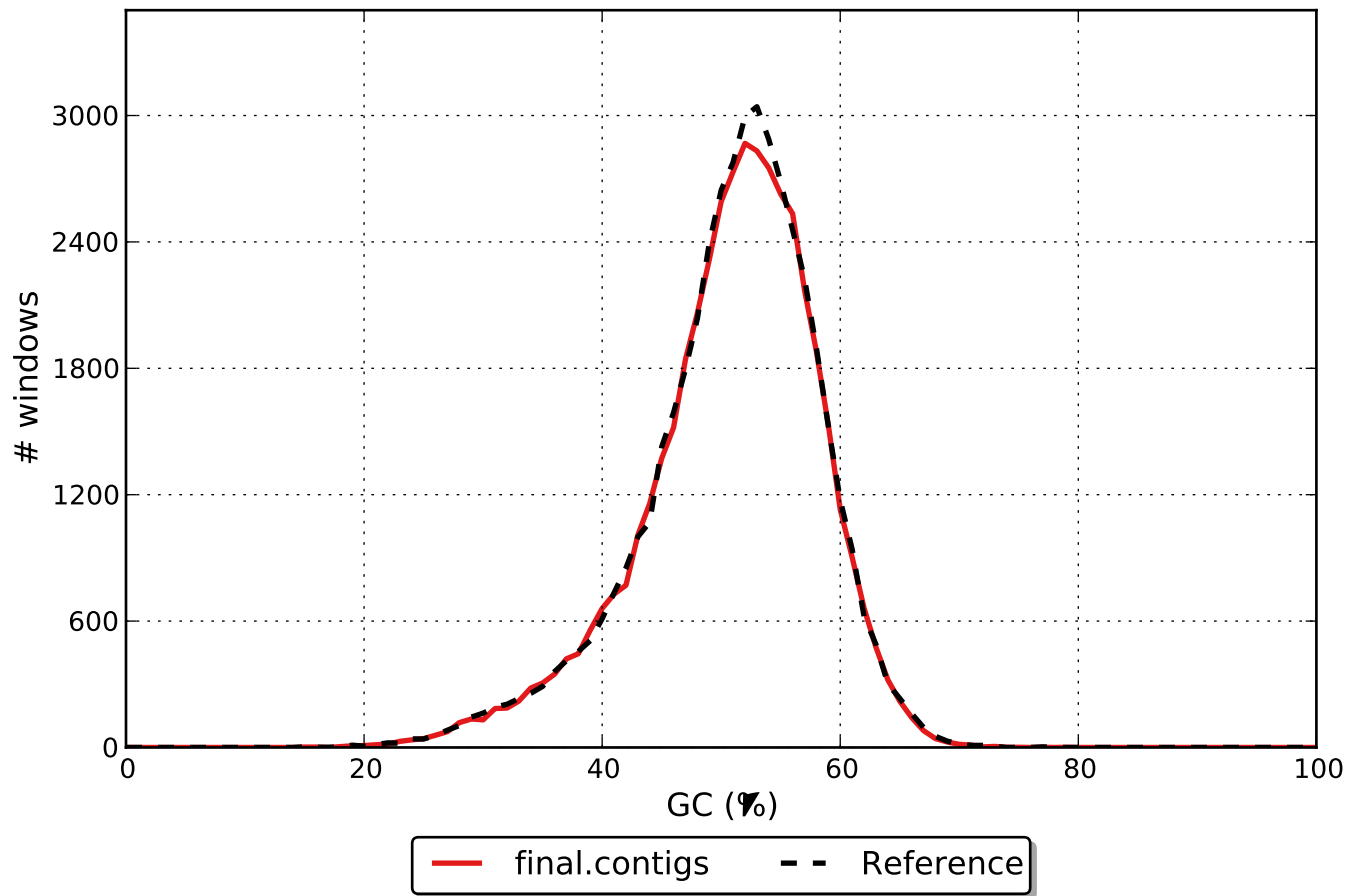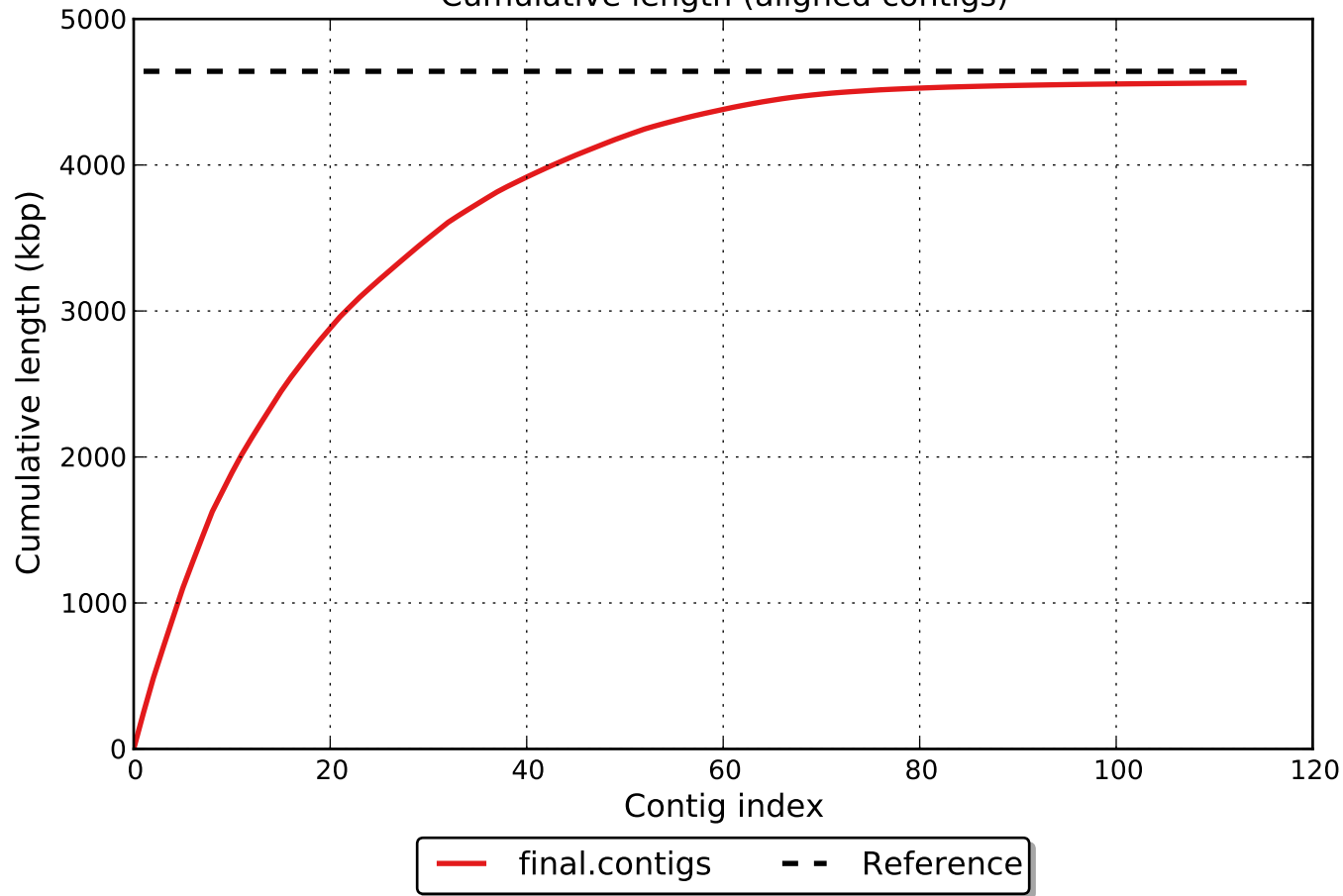
NGx
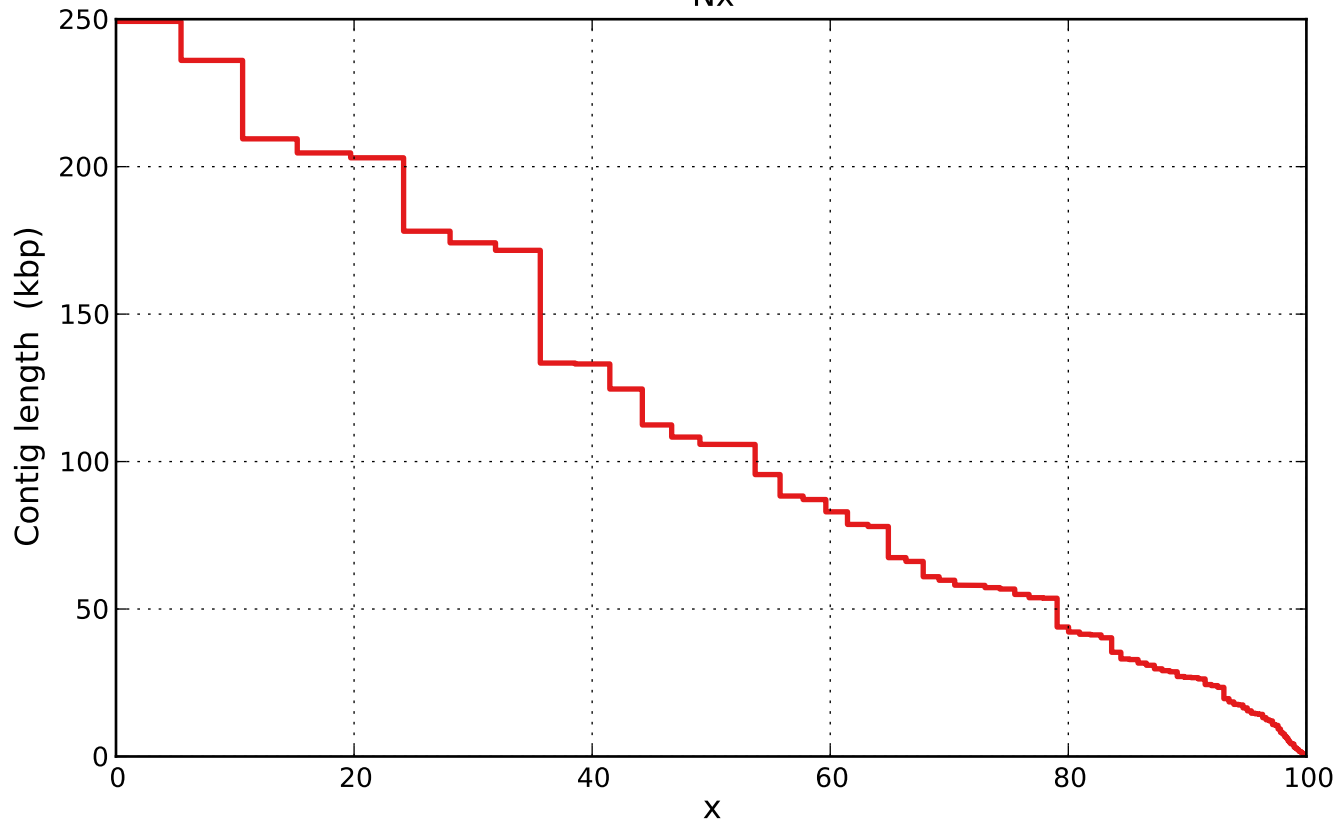
Cumulative length
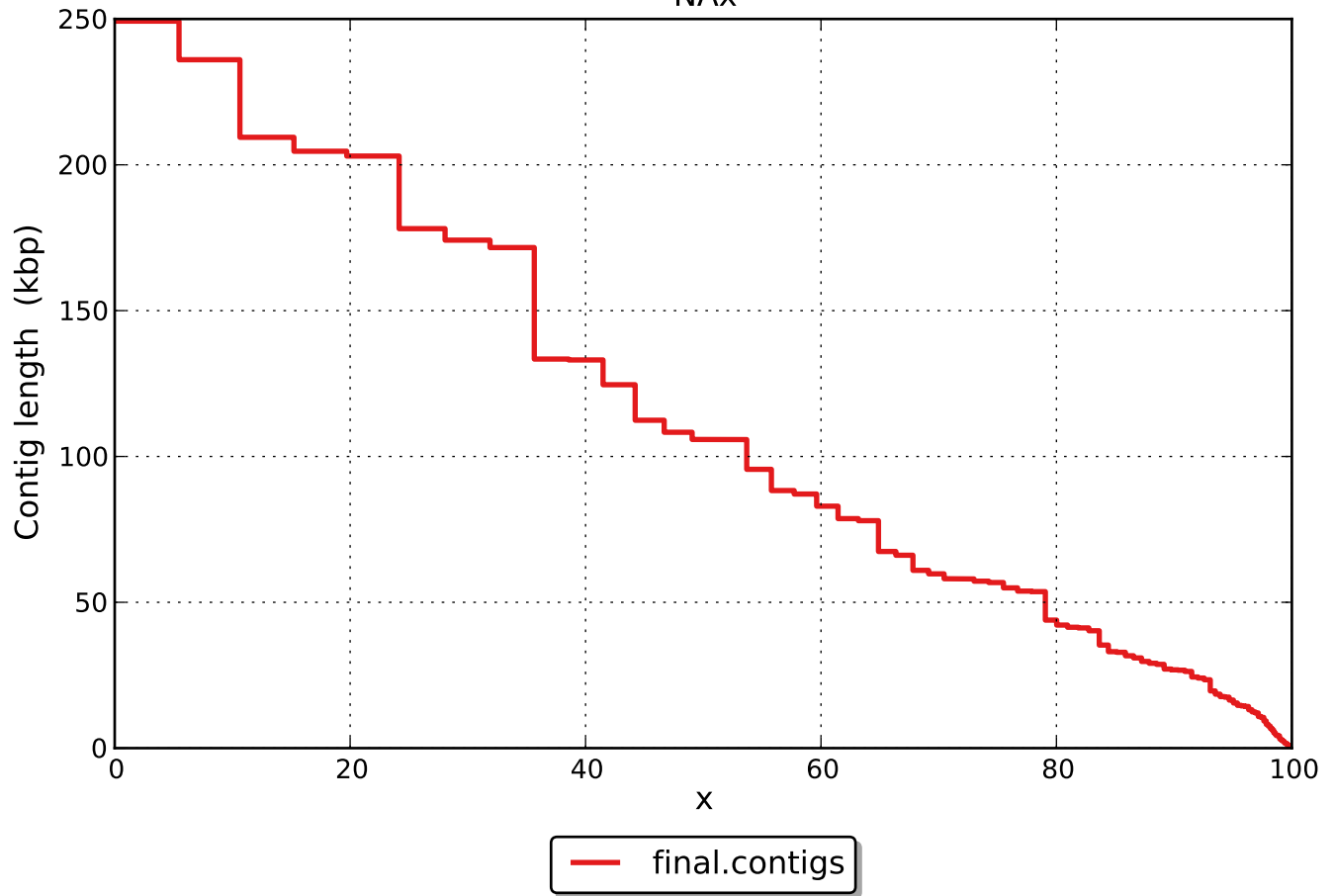
GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)