Report

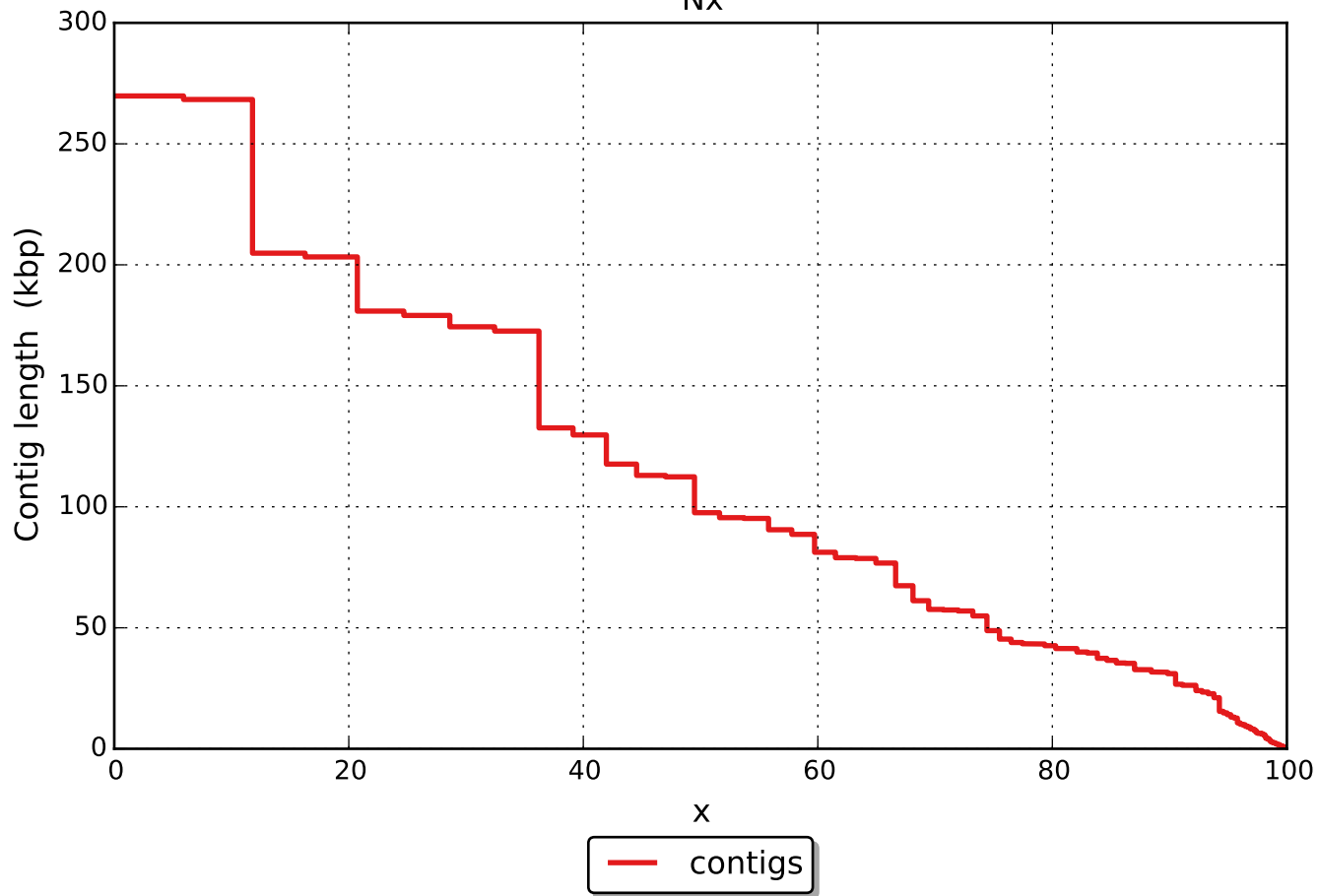|	contigs
# contigs (>= 0 bp)	2070
# contigs (>= 1000 bp)	105
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	5037214
Total length (>= 1000 bp)	4549861
Total length (>= 5000 bp)	4481629
Total length (>= 10000 bp)	4392475
Total length (>= 25000 bp)	4210120
Total length (>= 50000 bp)	3396749
# contigs	127
Largest contig	269780
Total length	4564243
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	97563
NG50	97563
N75	48827
NG75	45329
L50	14
LG50	14
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	1 + 1 part
Unaligned length	538
Genome fraction (%)	98.179
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.88
# indels per 100 kbp	0.22
Largest alignment	269780
NA50	97563
NGA50	97563
NA75	48827
NGA75	45329
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).
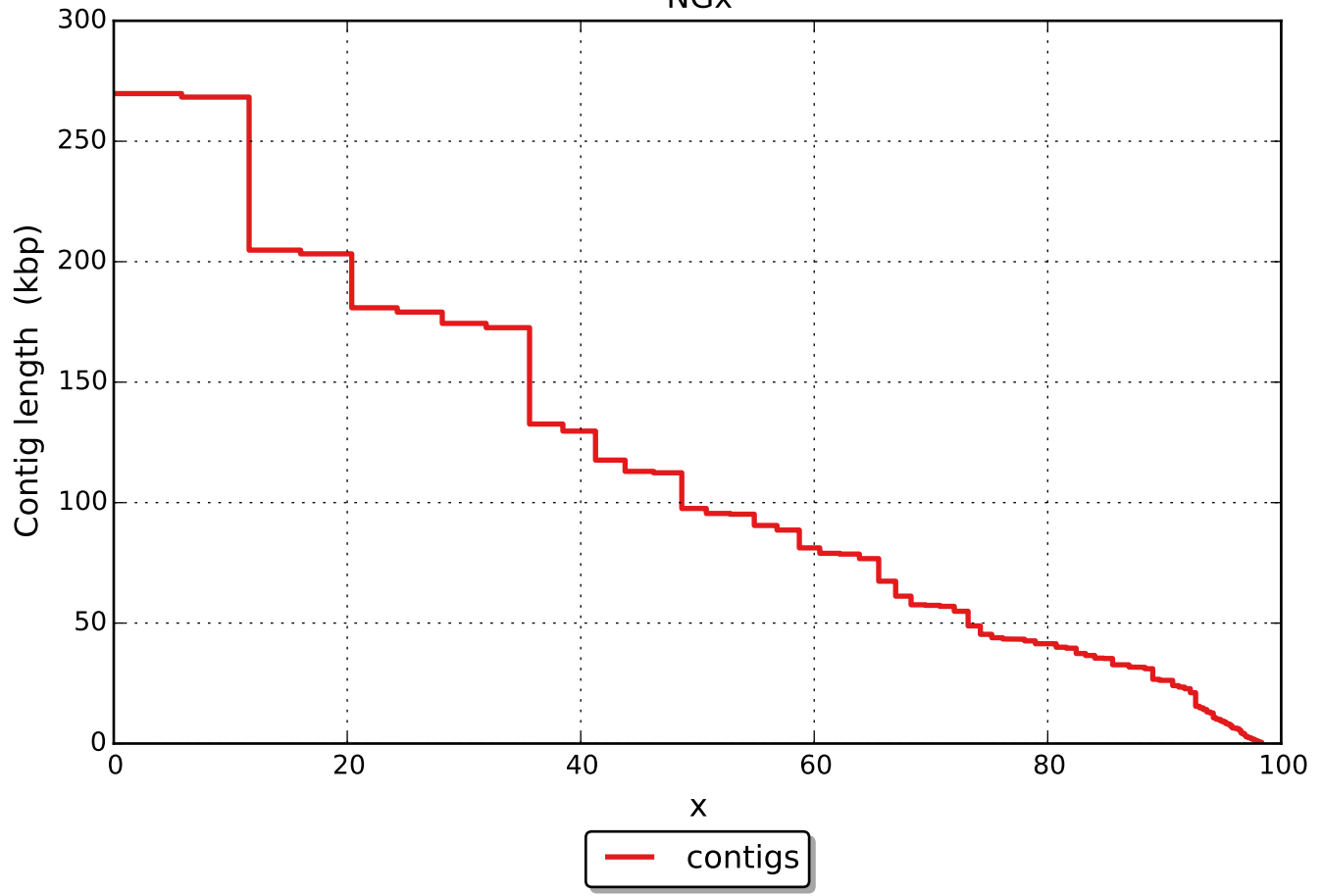
Misassemblies report

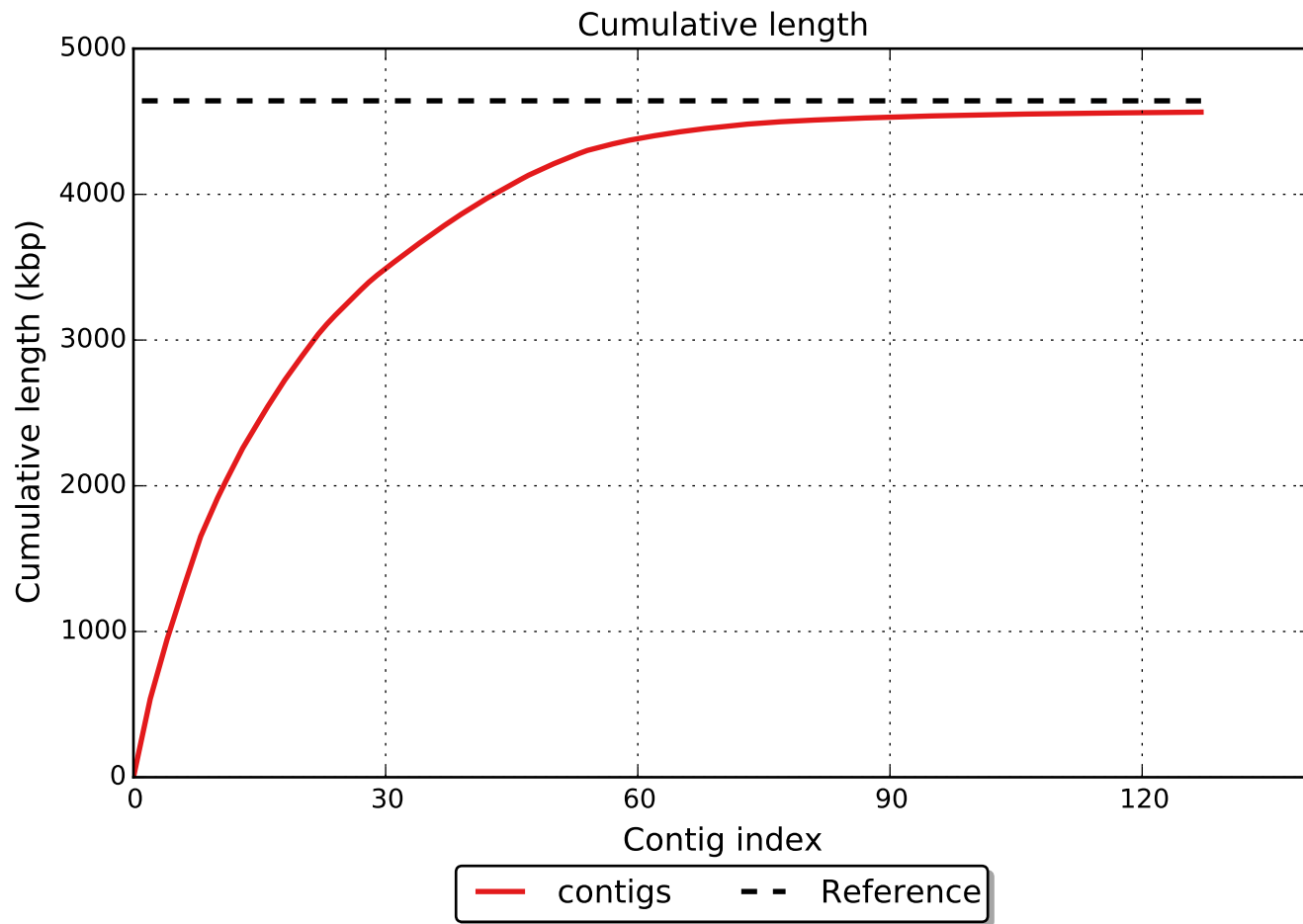|	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	496
# indels	10
# short indels	10
# long indels	0
Indels length	11

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

	contigs
# fully unaligned contigs	1
Fully unaligned length	523
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	15
# 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).
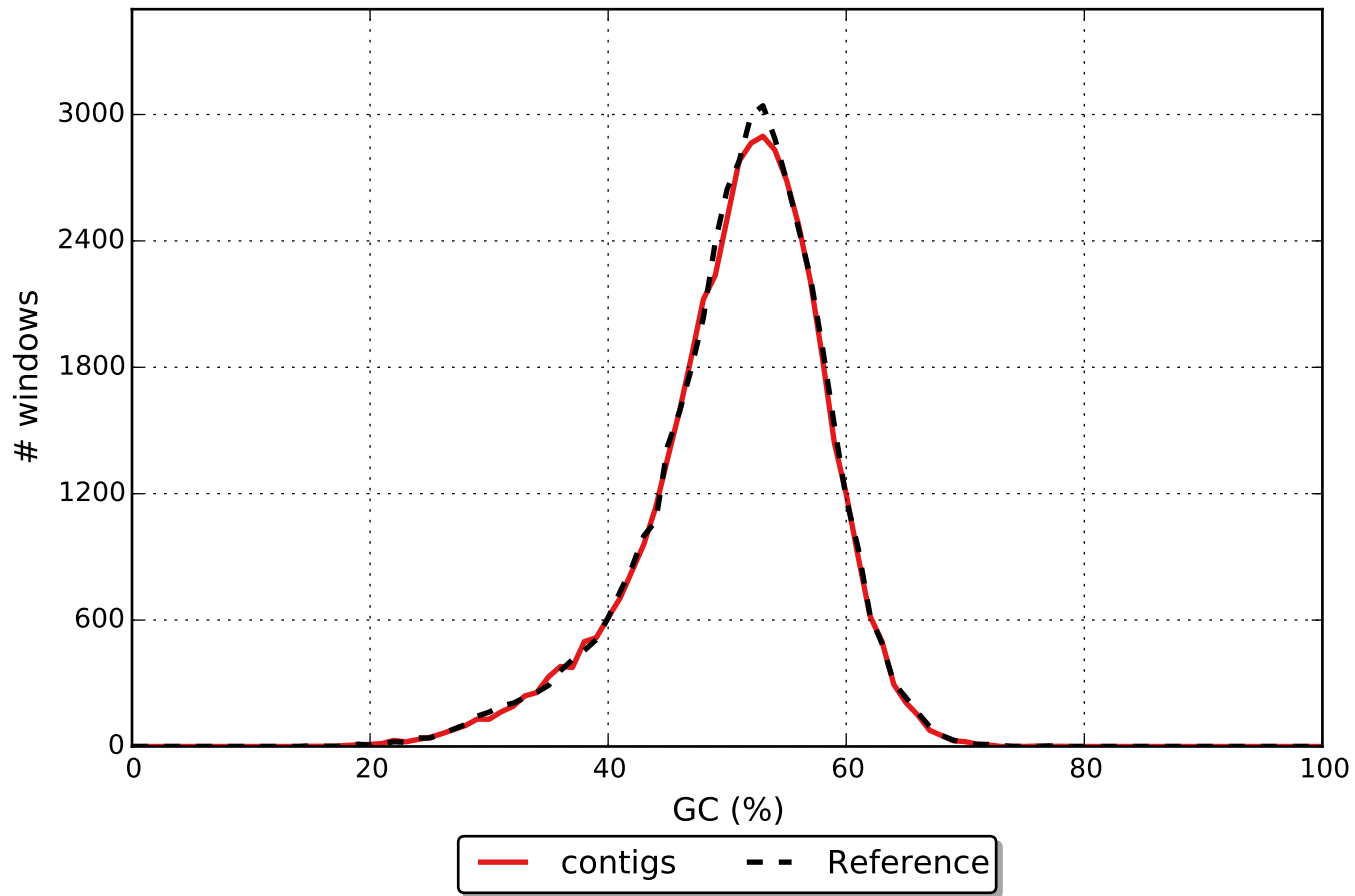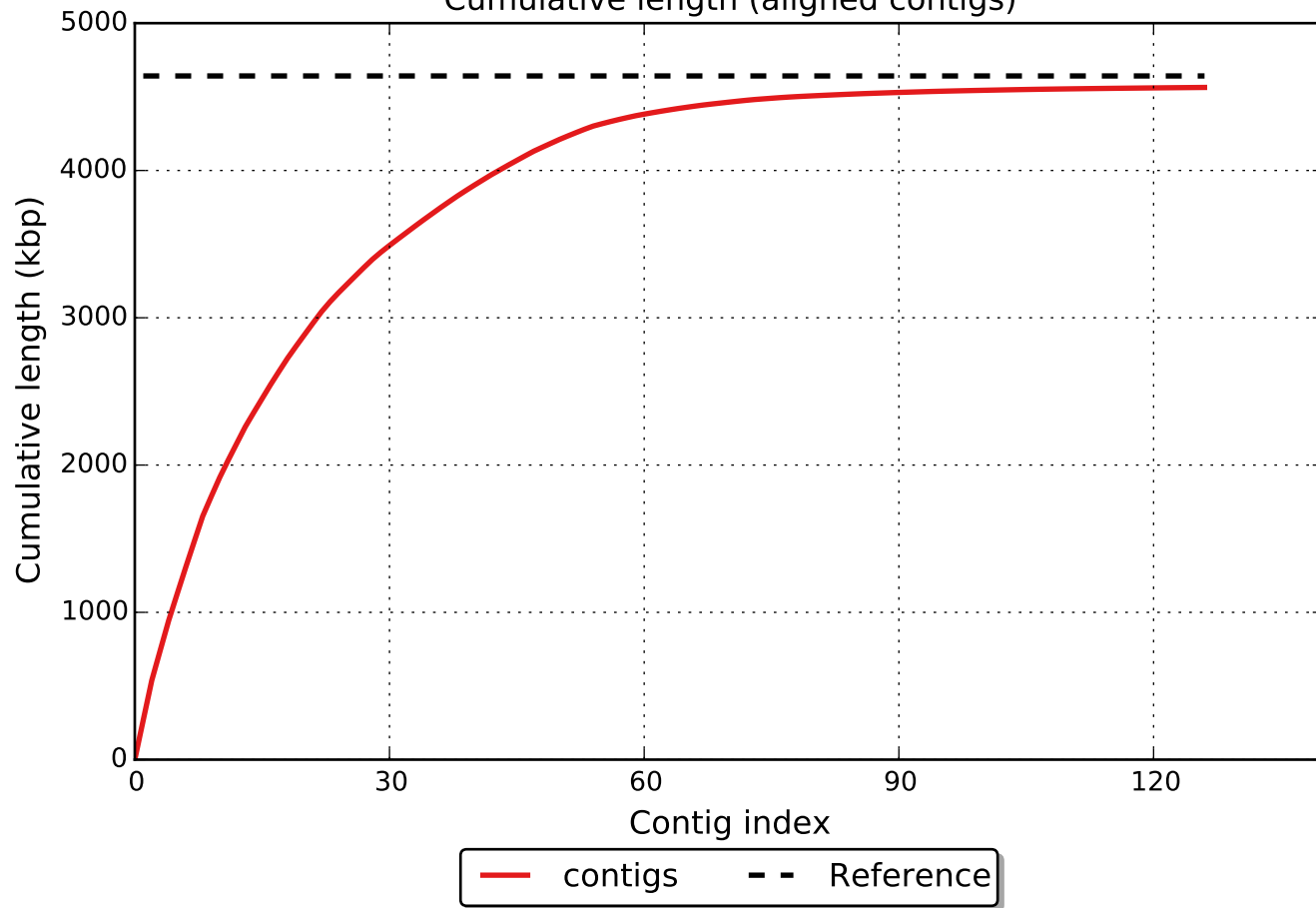
NGx

Cumulative length
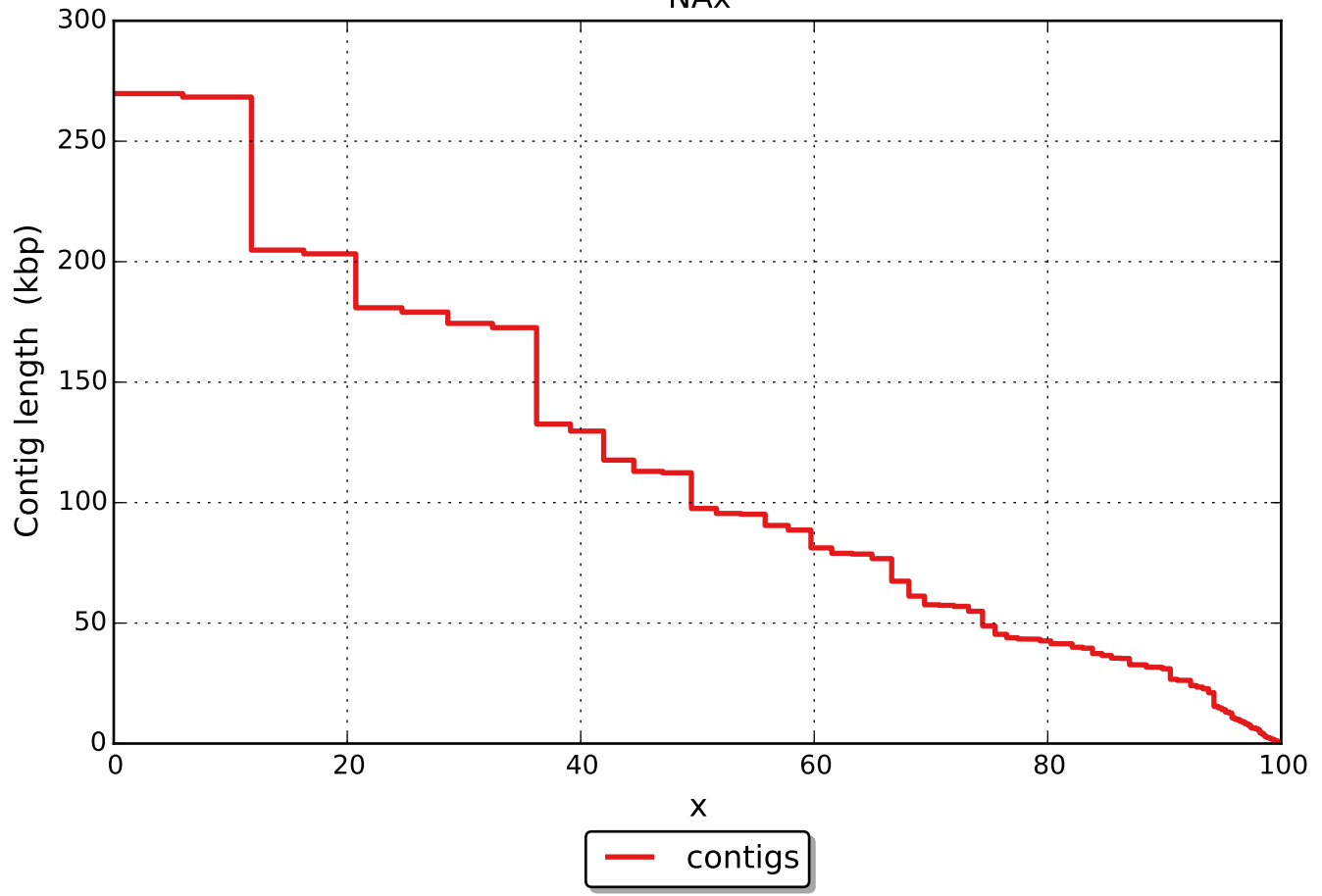
GC content

Misassemblies

contigs

Cumulative length (aligned contigs)