Report

	contigs
# contigs (>= 0 bp)	251
# contigs (>= 1000 bp)	201
# contigs (>= 5000 bp)	146
# contigs (>= 10000 bp)	119
# contigs (>= 25000 bp)	65
# contigs (>= 50000 bp)	22
Total length (>= 0 bp)	4580233
Total length (>= 1000 bp)	4567035
Total length (>= 5000 bp)	4424775
Total length (>= 10000 bp)	4223737
Total length (>= 25000 bp)	3304393
Total length (>= 50000 bp)	1760731
# contigs	209
Largest contig	169368
Total length	4573239
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	41451
NG50	40157
N75	21792
NG75	21375
L50	34
LG50	35
L75	71
LG75	73
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	46624
# local misassemblies	6
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.134
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17.61
# indels per 100 kbp	0.44
Largest alignment	167852
NA50	40157
NGA50	39814
NA75	21697
NGA75	21112
LA50	34
LGA50	35
LA75	72
LGA75	75

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).
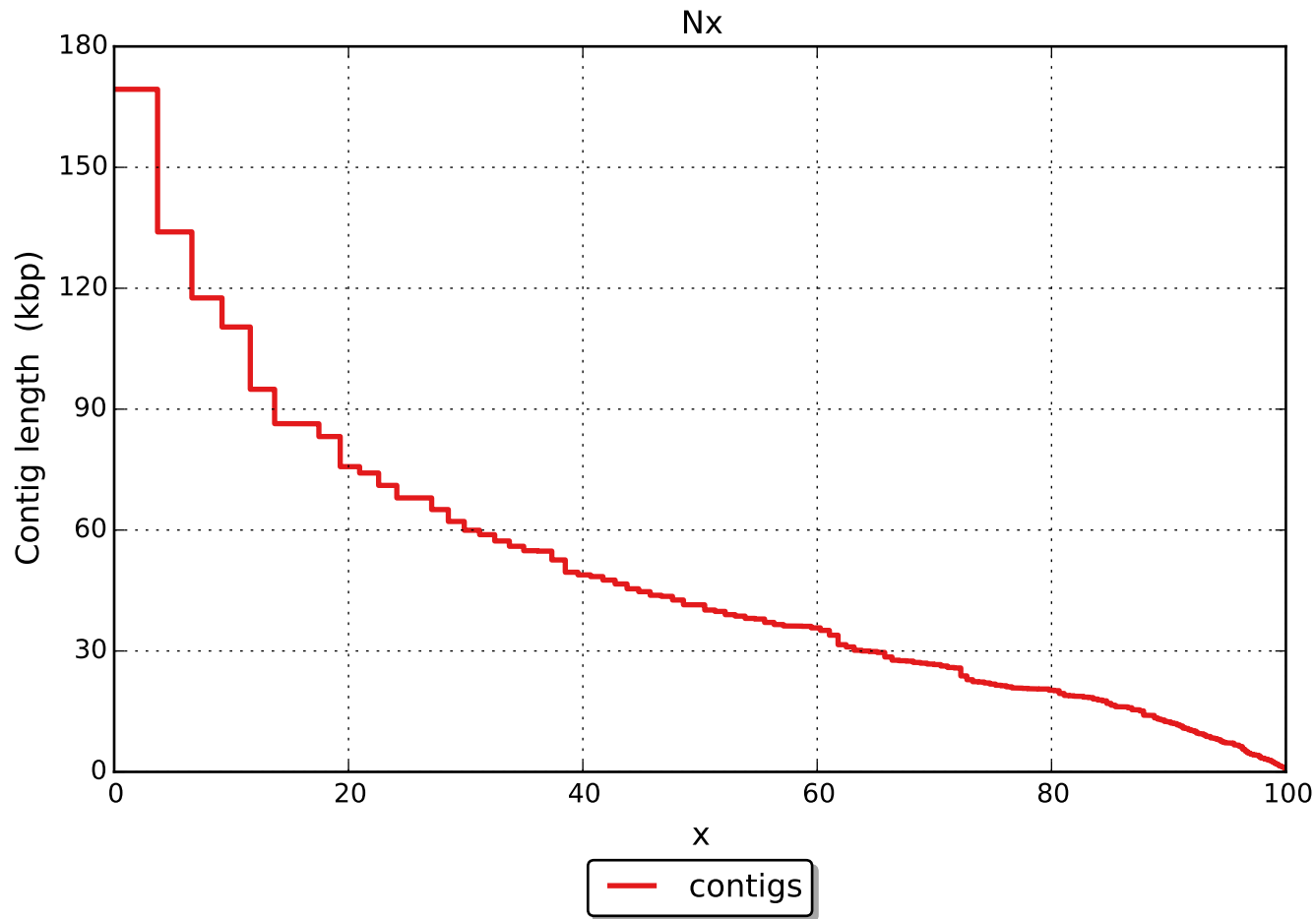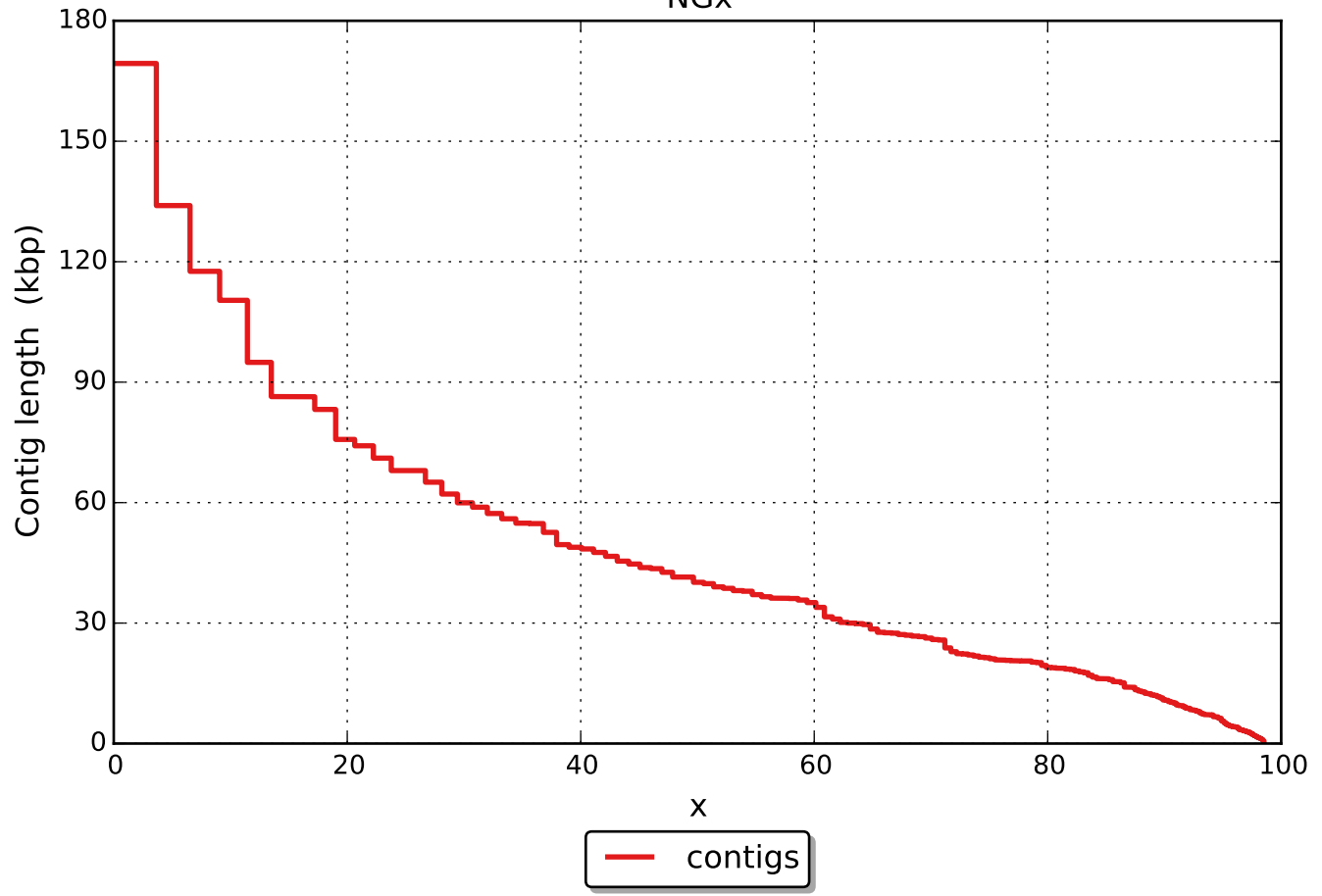
Misassemblies report

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	46624
# local misassemblies	6
# mismatches	802
# indels	20
# short indels	20
# long indels	0
Indels length	27

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).
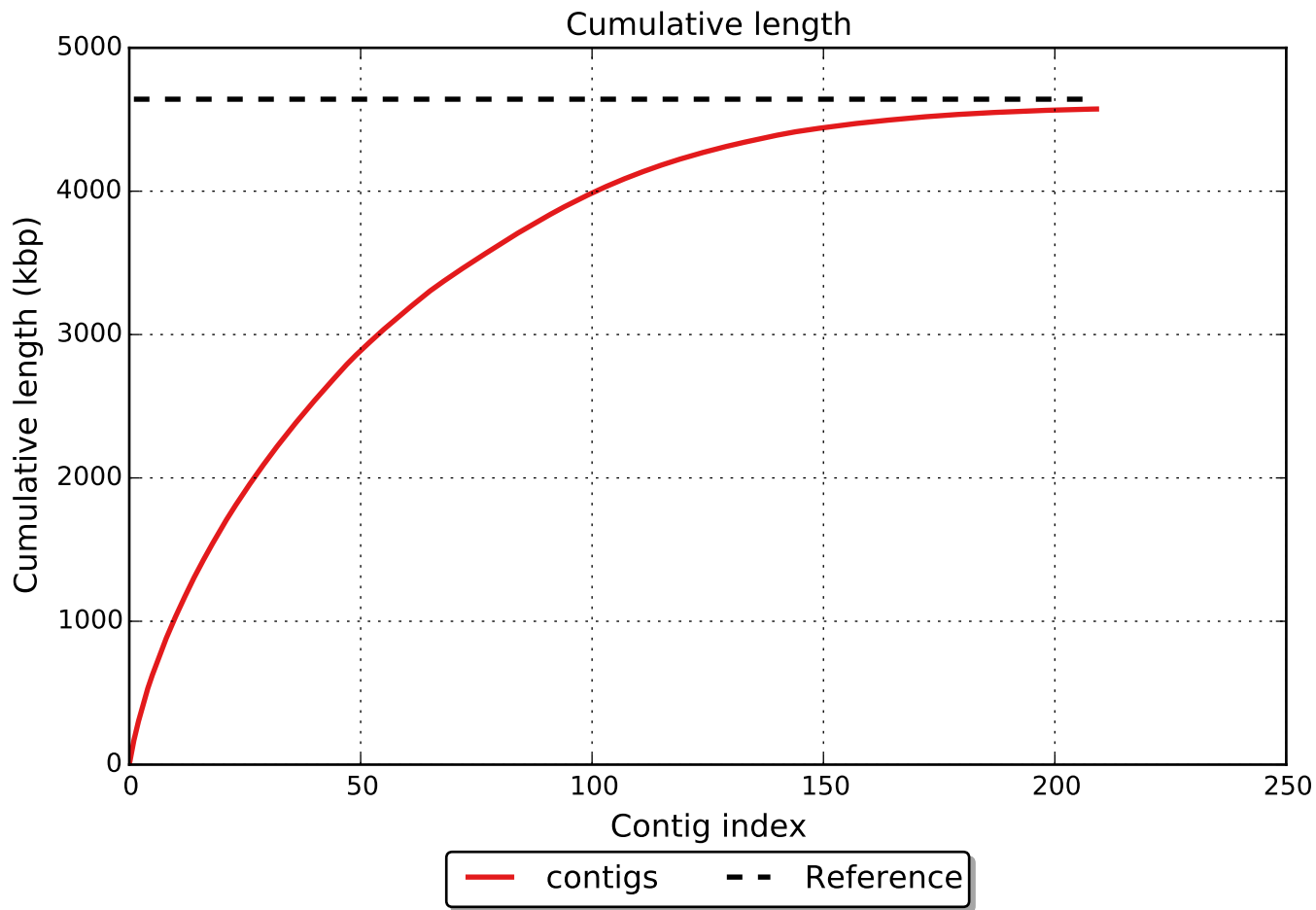
Unaligned report

	contigs
# fully unaligned contigs	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).
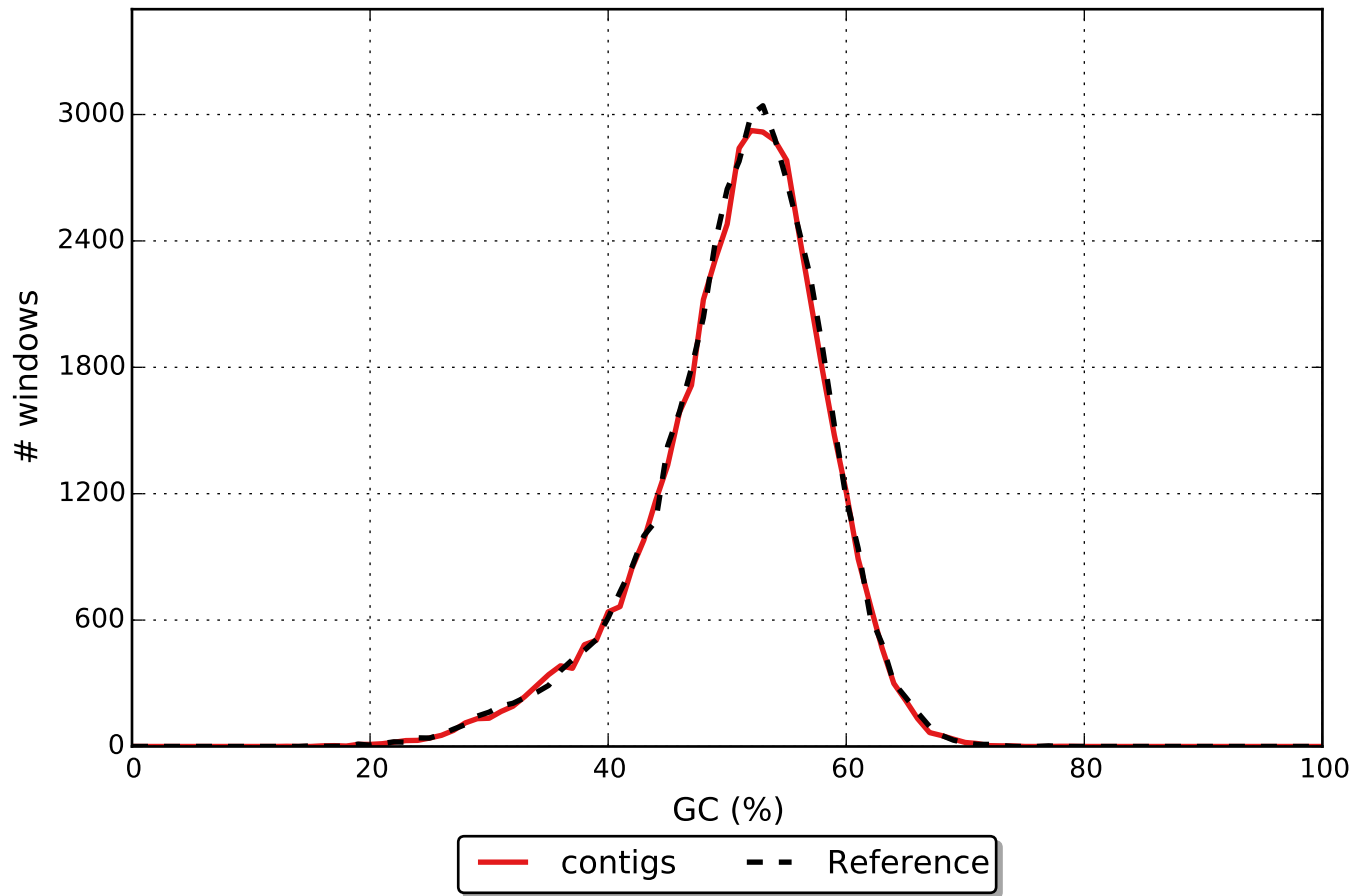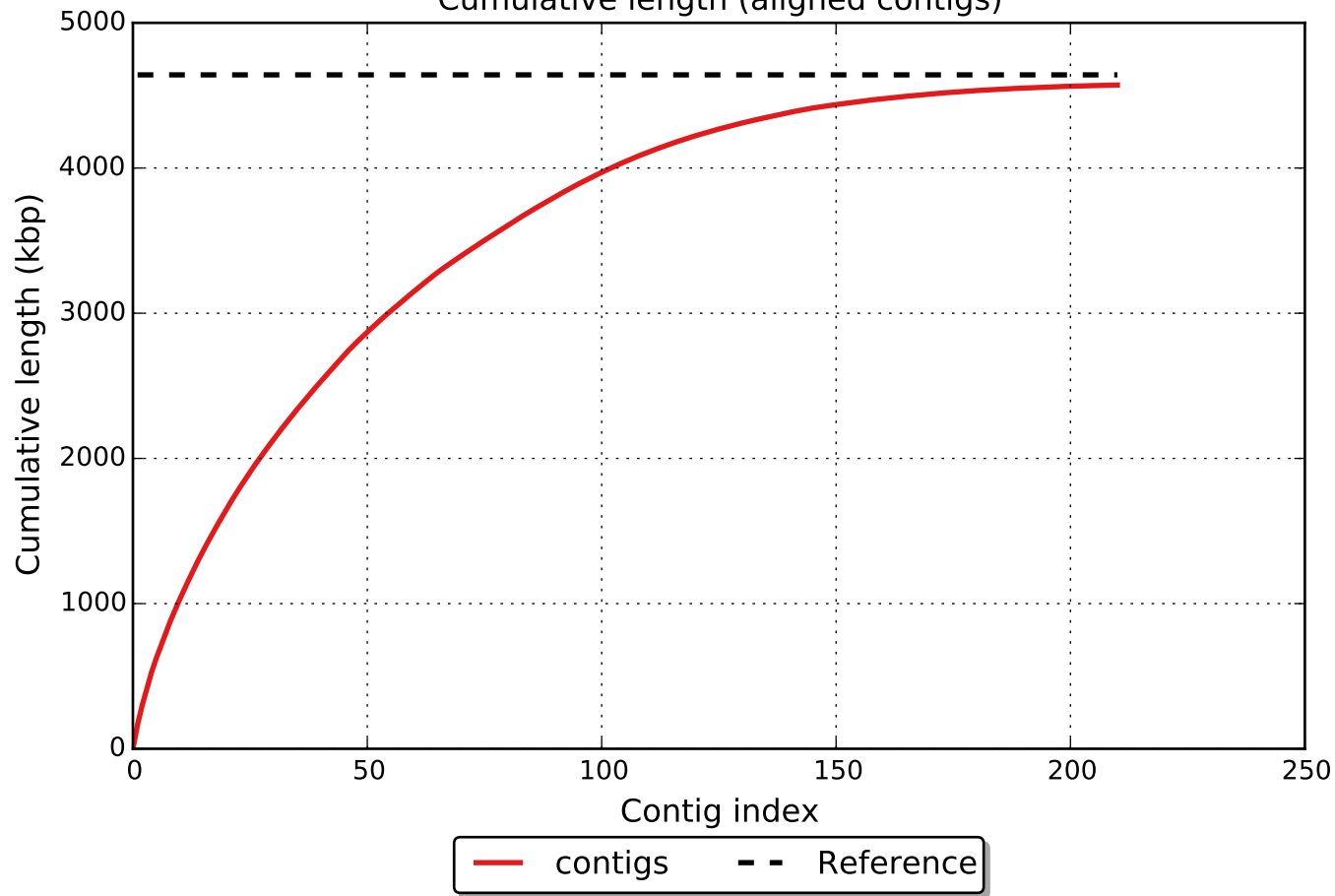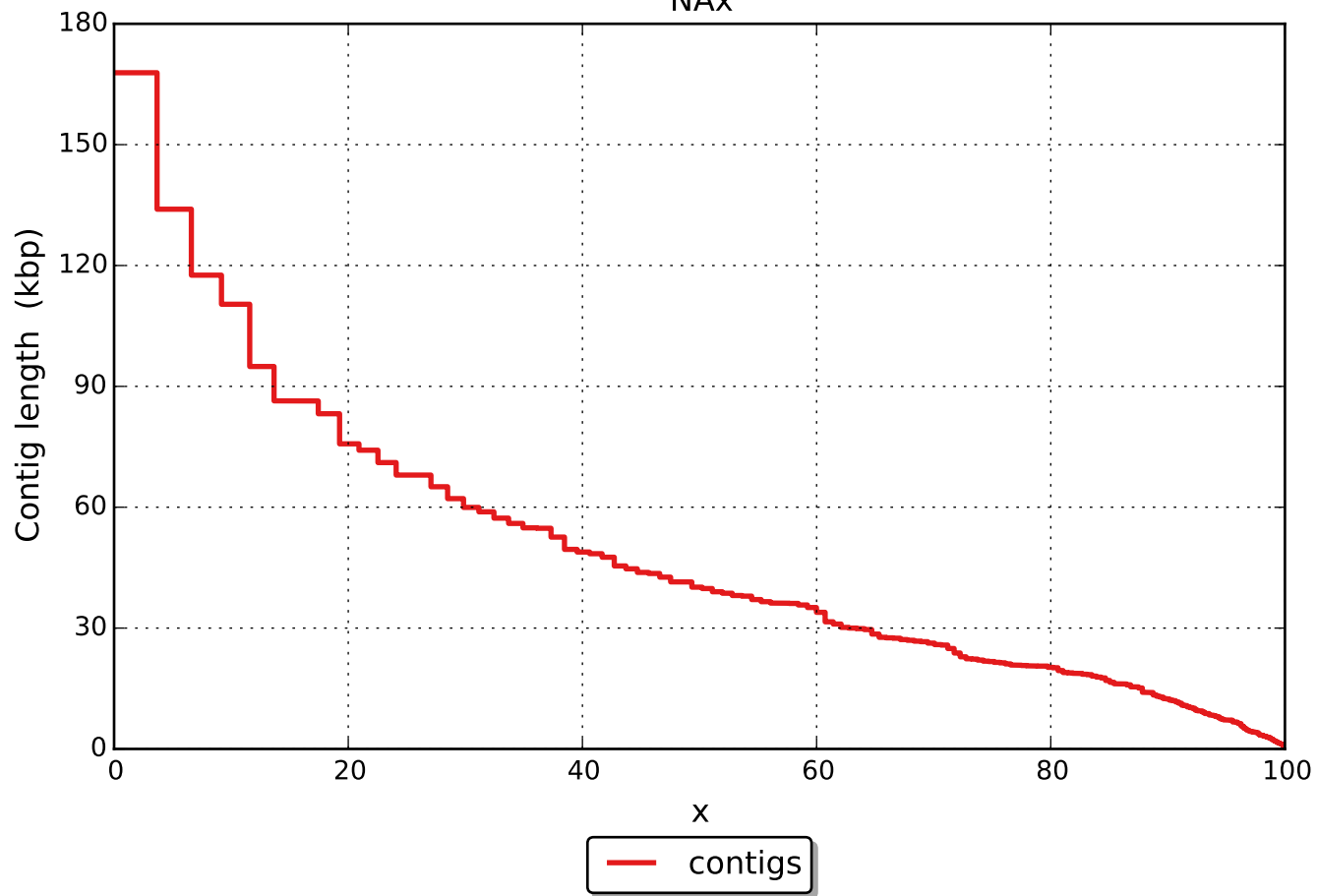
NGx

Contig length (kbp)

x

contigs

Cumulative length

GC content

windows

GC (%)

contigs — — Reference

Cumulative length (aligned contigs)