Report

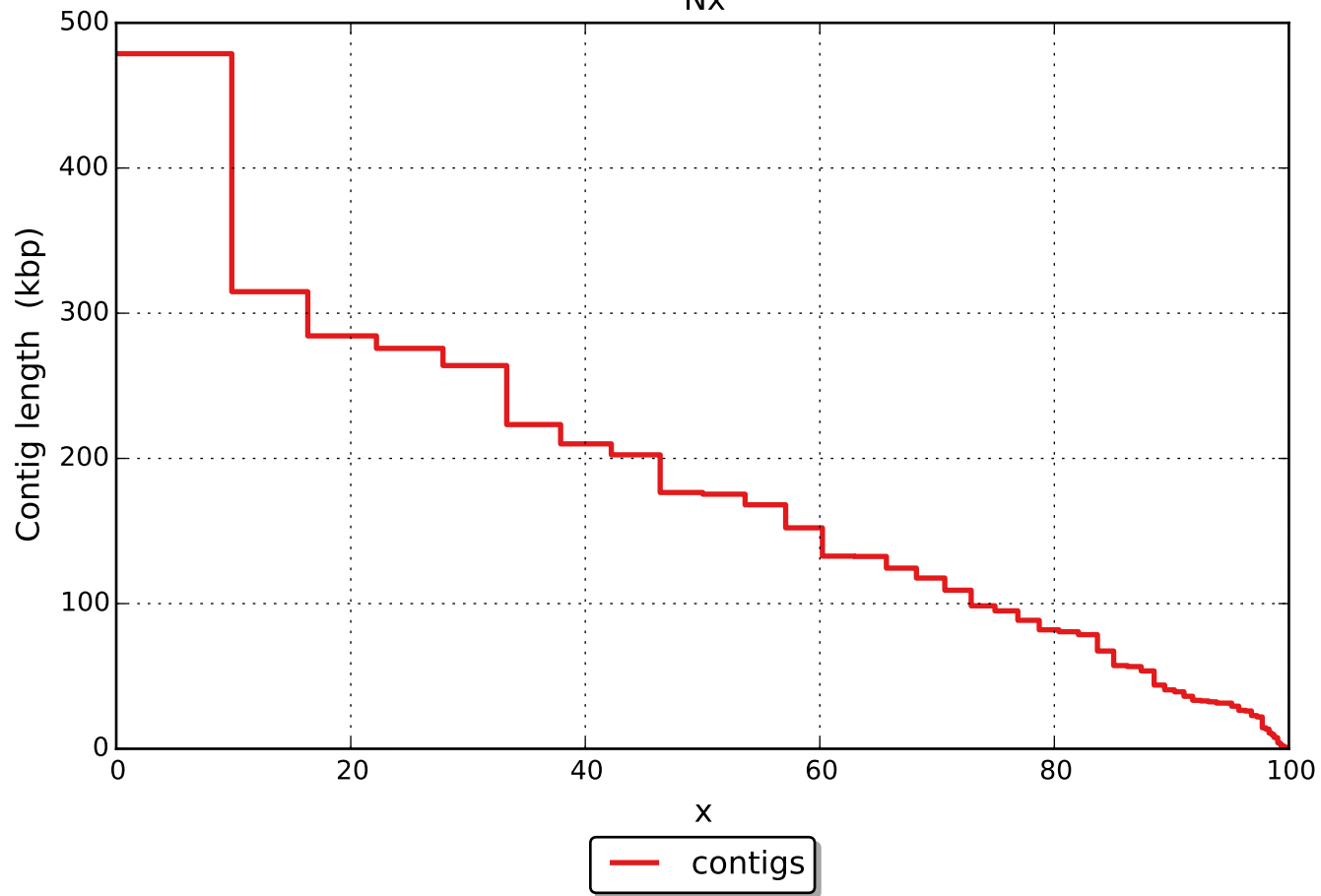|	contigs
# contigs (>= 1000 bp)	63
# contigs (>= 5000 bp)	47
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4845535
Total length (>= 5000 bp)	4812099
Total length (>= 10000 bp)	4786865
Total length (>= 25000 bp)	4703153
Total length (>= 50000 bp)	4299936
# contigs	79
Largest contig	478751
Total length	4858252
Reference length	4641652
GC (%)	50.66
Reference GC (%)	50.79
N50	176518
NG50	176518
N75	94985
NG75	109215
L50	9
LG50	9
L75	19
LG75	17
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	302439
Genome fraction (%)	97.885
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	125.10
# indels per 100 kbp	0.51
Largest alignment	314840
NA50	168040
NGA50	168040
NA75	80607
NGA75	88484
LA50	11
LGA50	11
LA75	22
LGA75	20

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
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	5684
# indels	23
# short indels	22
# long indels	1
Indels length	34

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).
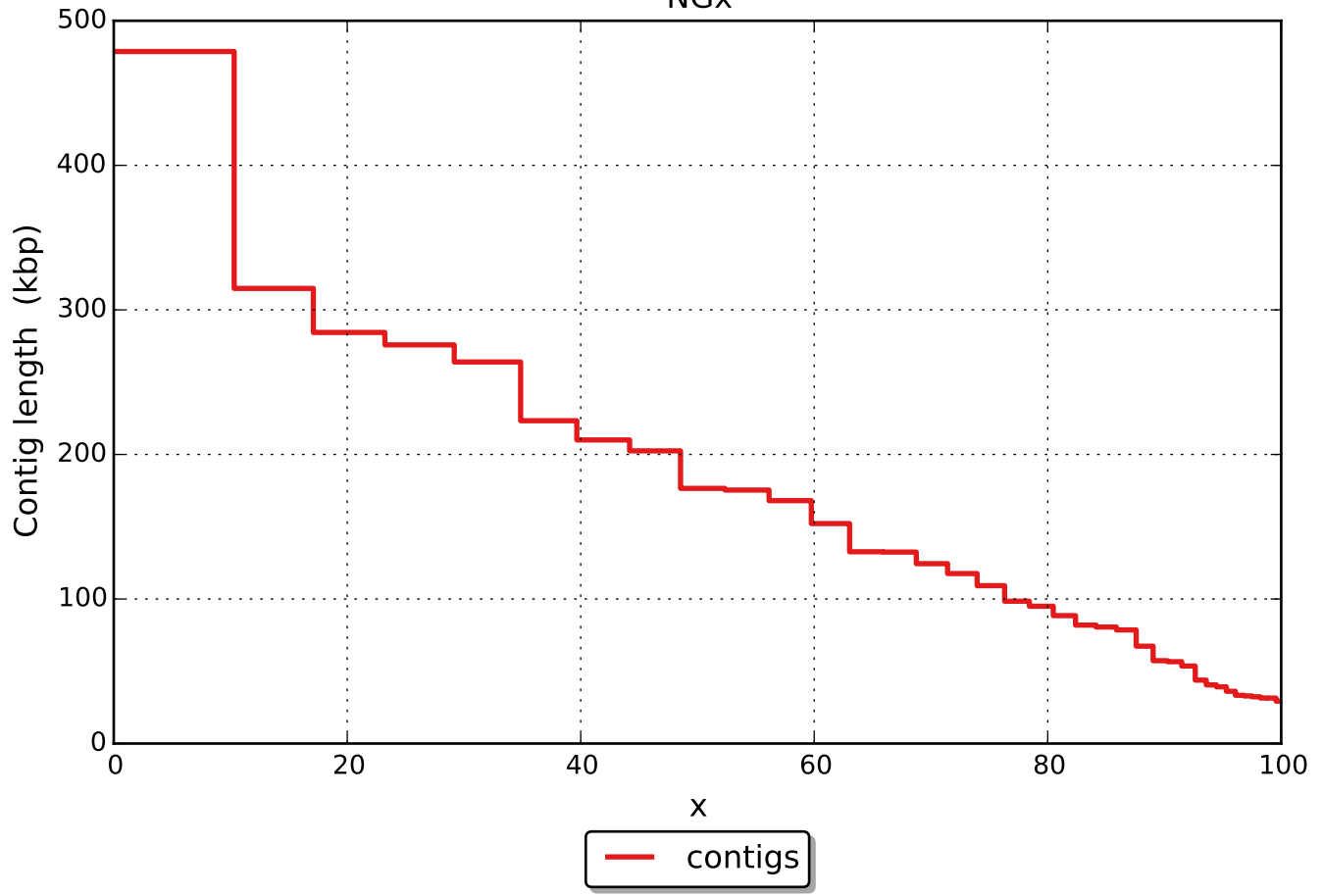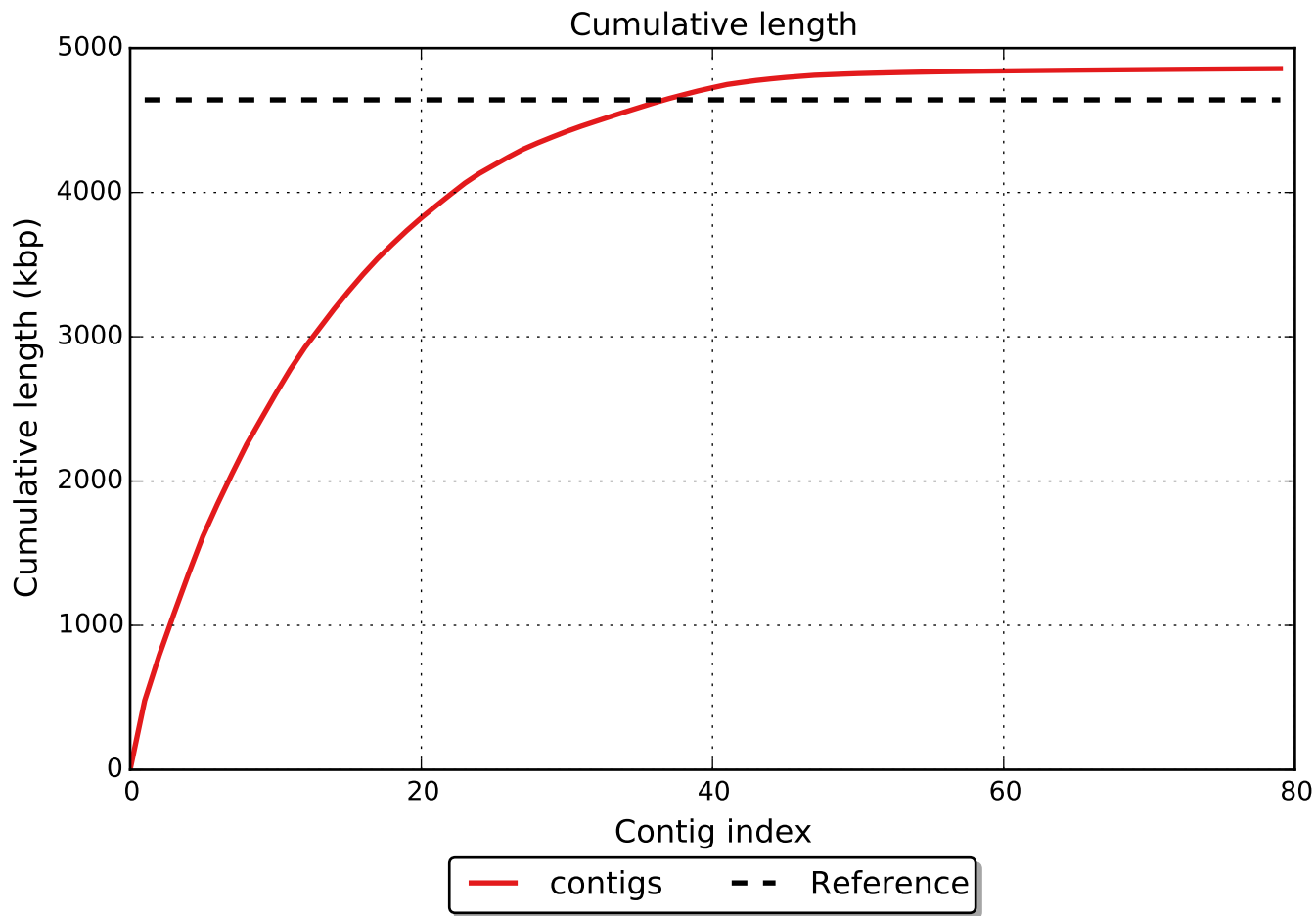
Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	1
# both parts are significant	1
Partially unaligned length	302439
# 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).
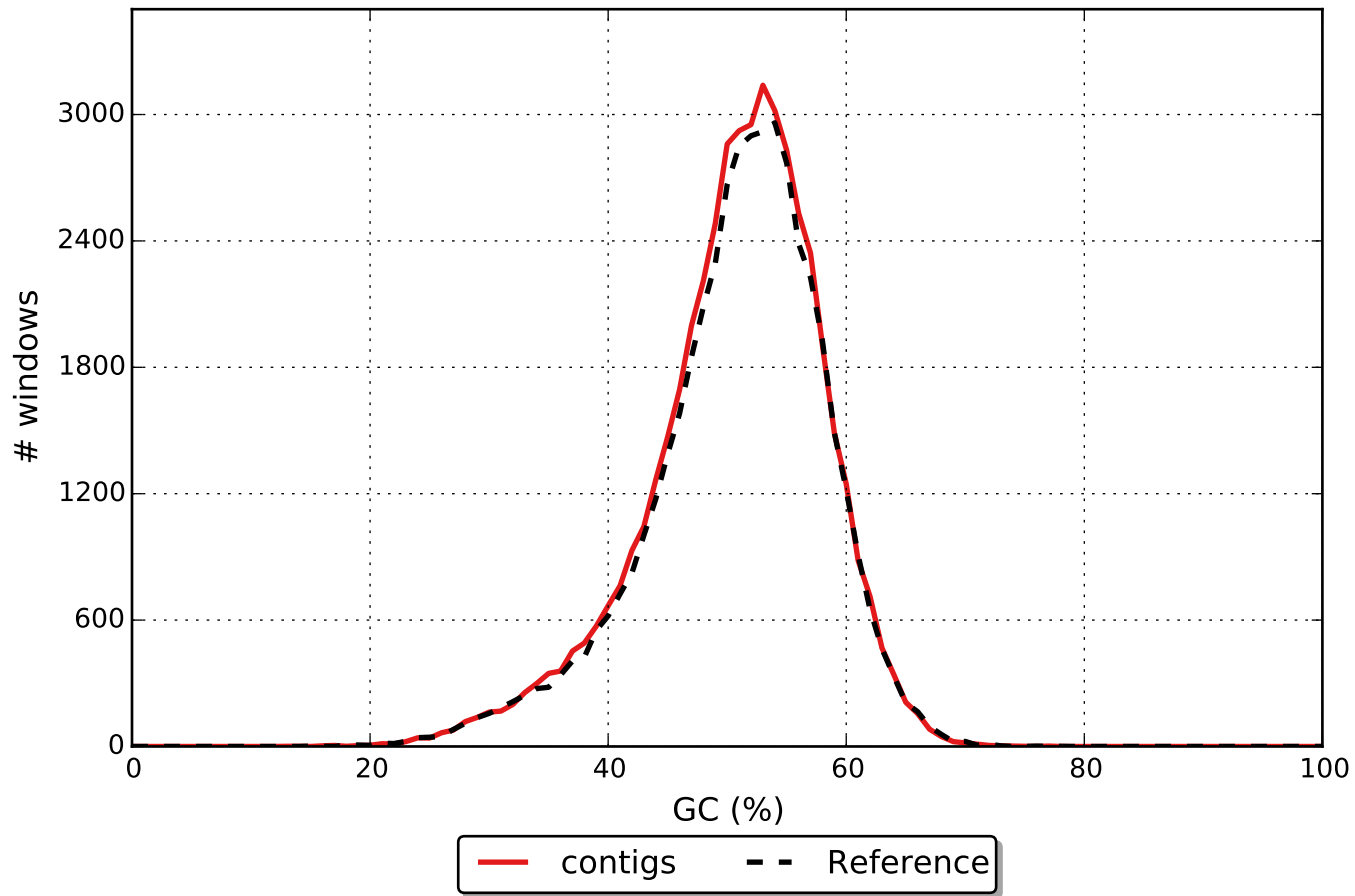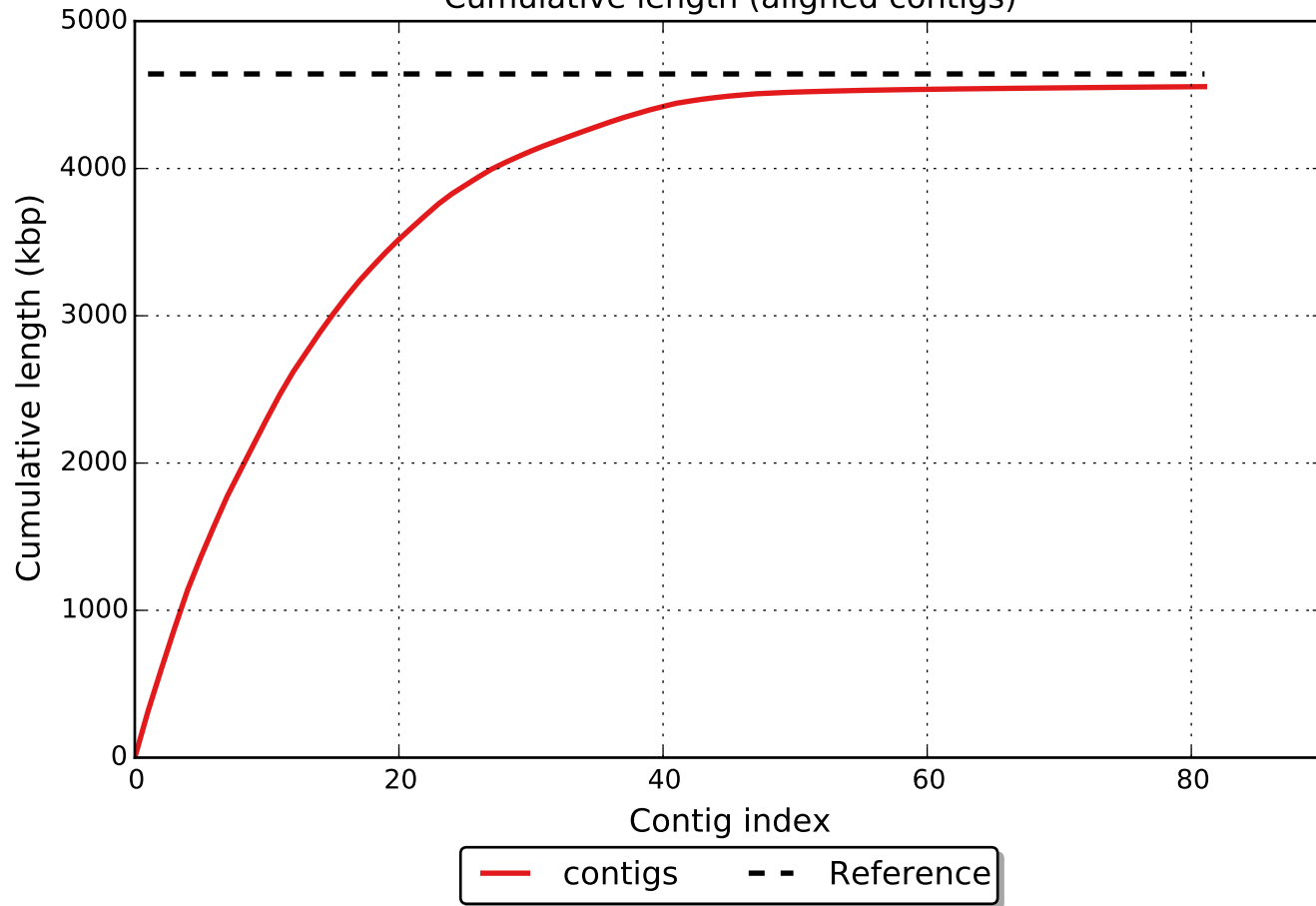
NGx

Cumulative length
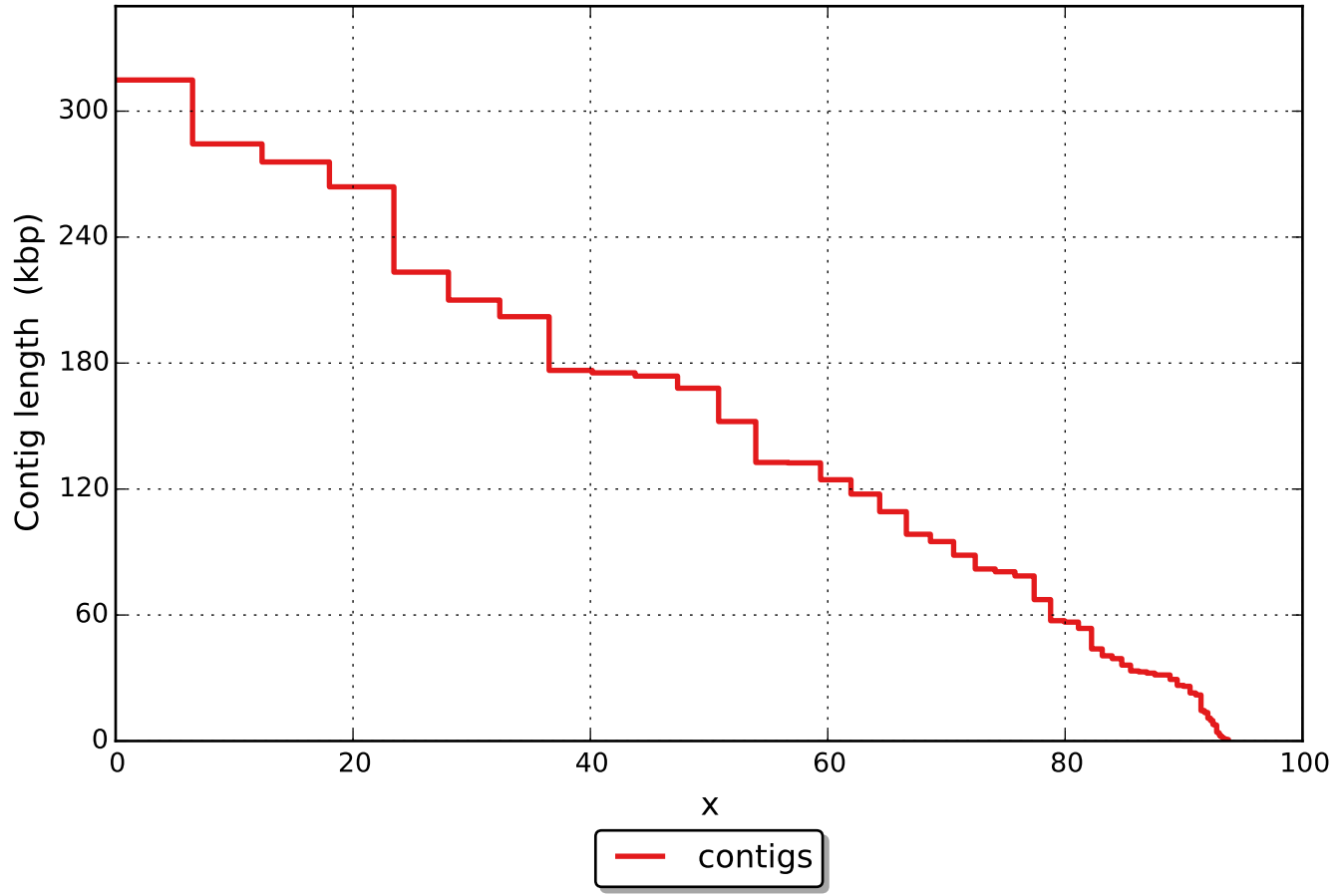
GC content

Misassemblies

contigs

Cumulative length (aligned contigs)

NAx