

Report

	contigs
# contigs (≥ 0 bp)	4083
# contigs (≥ 1000 bp)	5
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1219476
Total length (≥ 1000 bp)	10099
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	134
Largest contig	3668
Total length	86117
Reference length	4641652
GC (%)	51.39
Reference GC (%)	50.79
N50	580
N75	537
L50	54
L75	93
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	6431
# local misassemblies	0
# unaligned contigs	1 + 1 part
Unaligned length	652
Genome fraction (%)	1.835
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1090.98
# indels per 100 kbp	2.35
Largest alignment	3605
NA50	577
NGA50	-
NA75	534
LA50	55
LA75	94

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	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	6431
# local misassemblies	0
# mismatches	929
# indels	2
# short indels	2
# long indels	0
Indels length	2

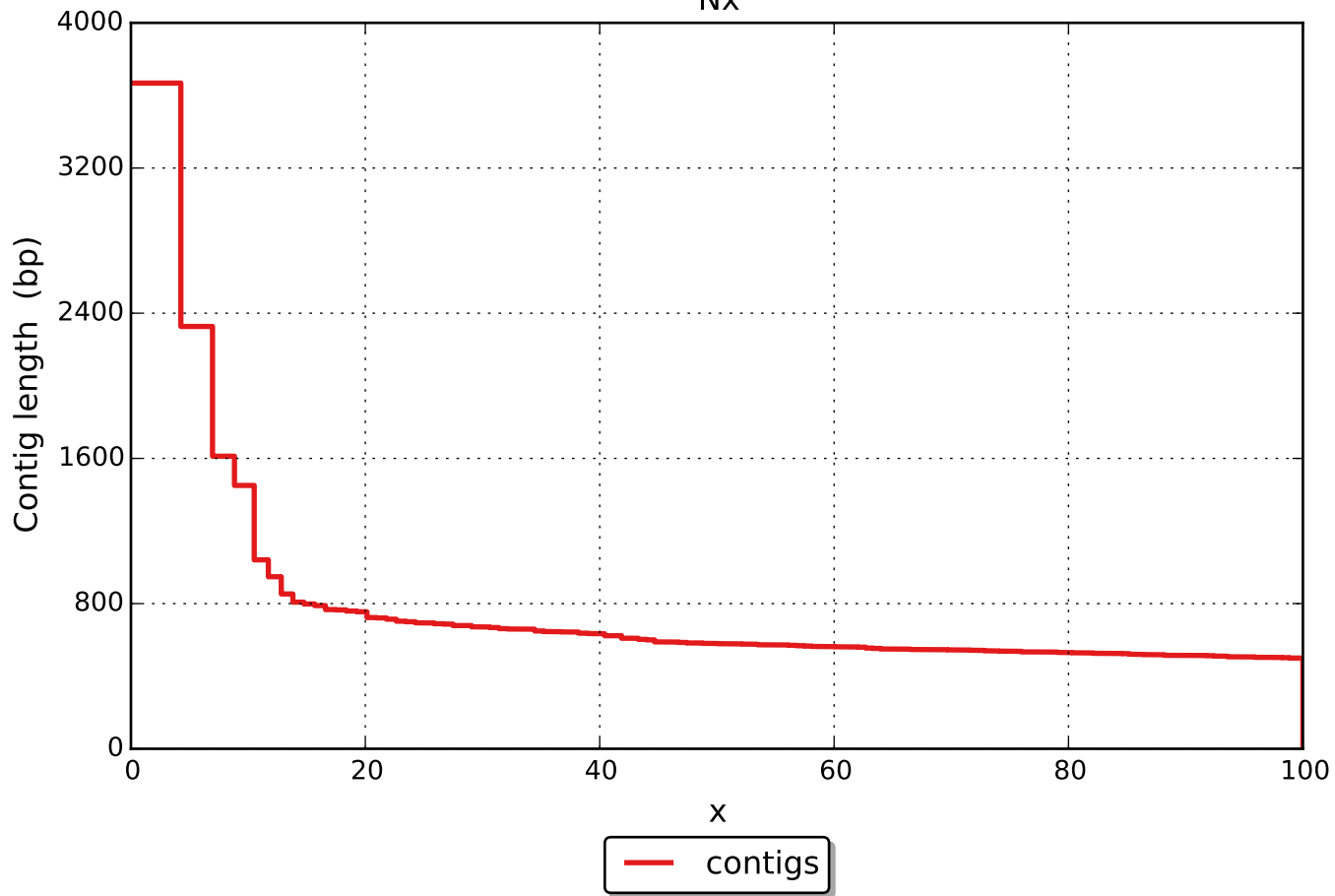
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

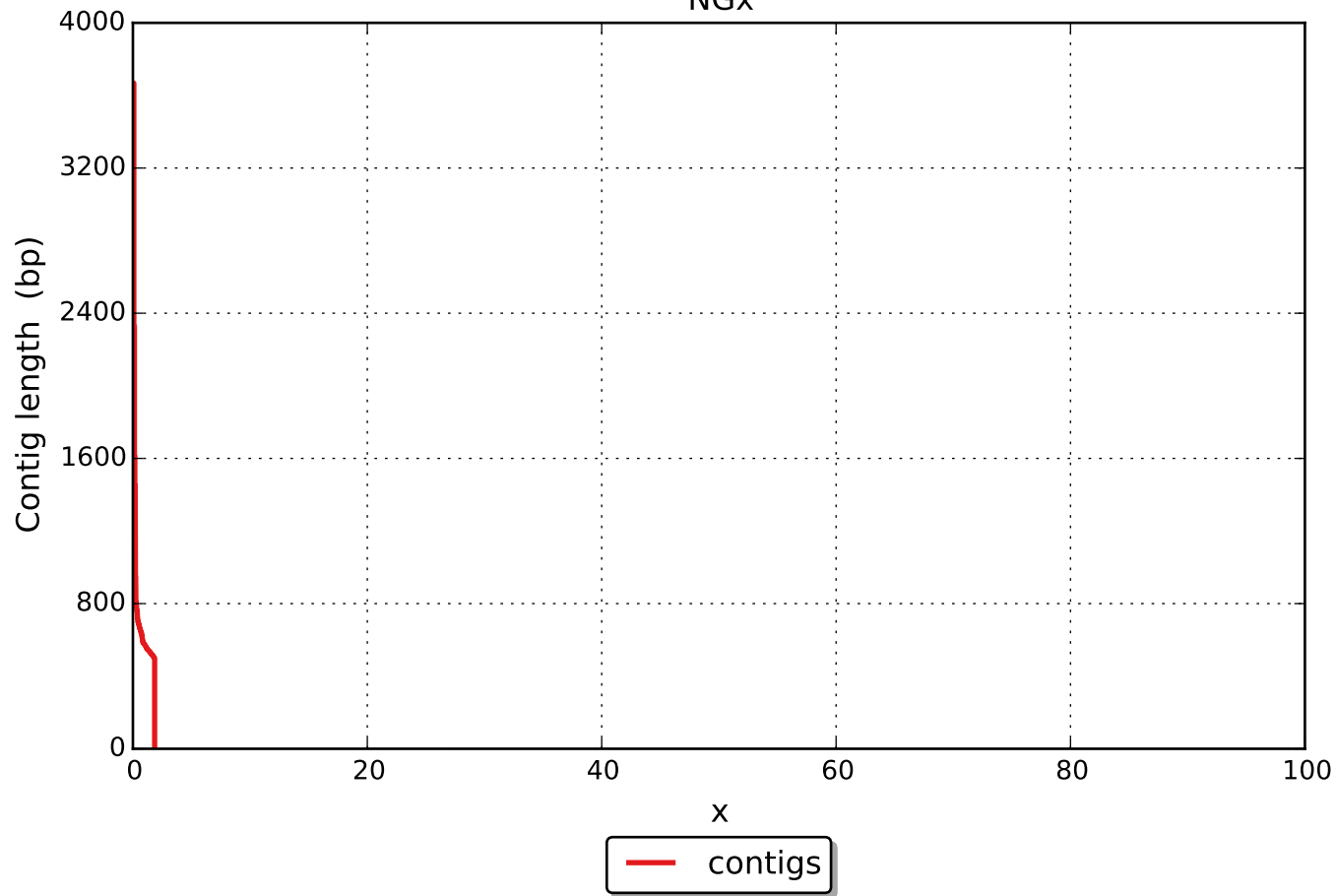
	contigs
# fully unaligned contigs	1
Fully unaligned length	589
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	63
# N's	0

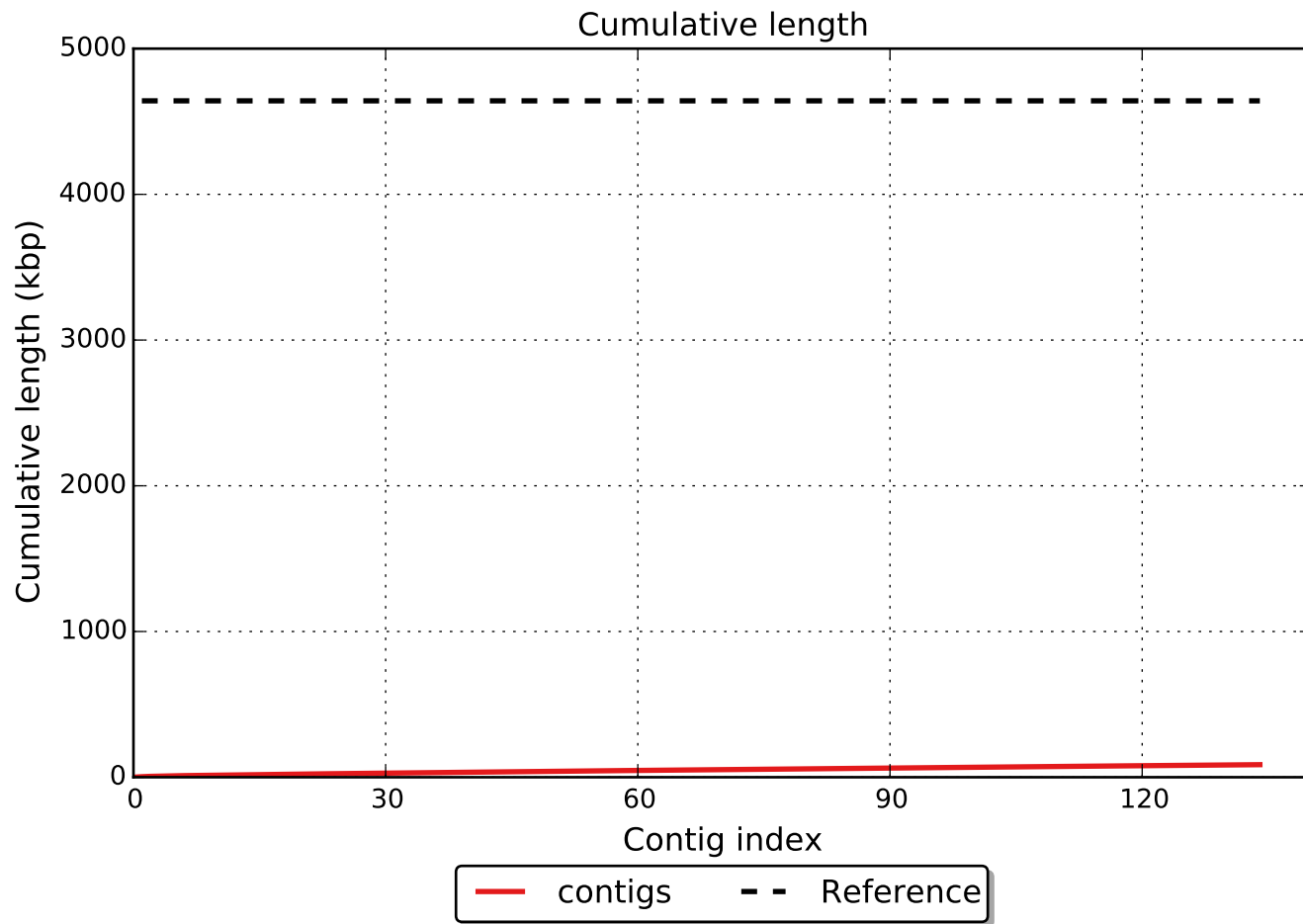
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

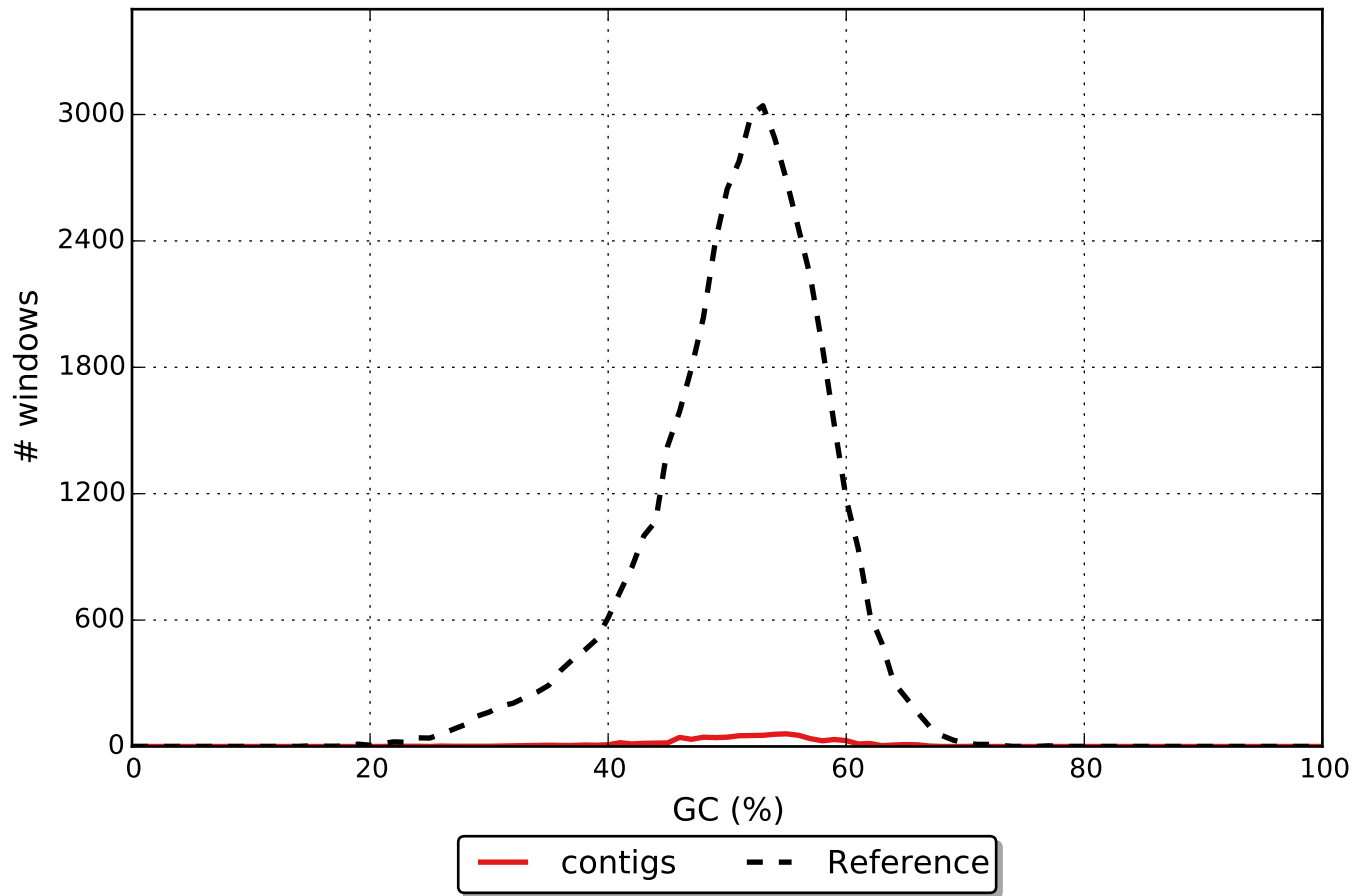


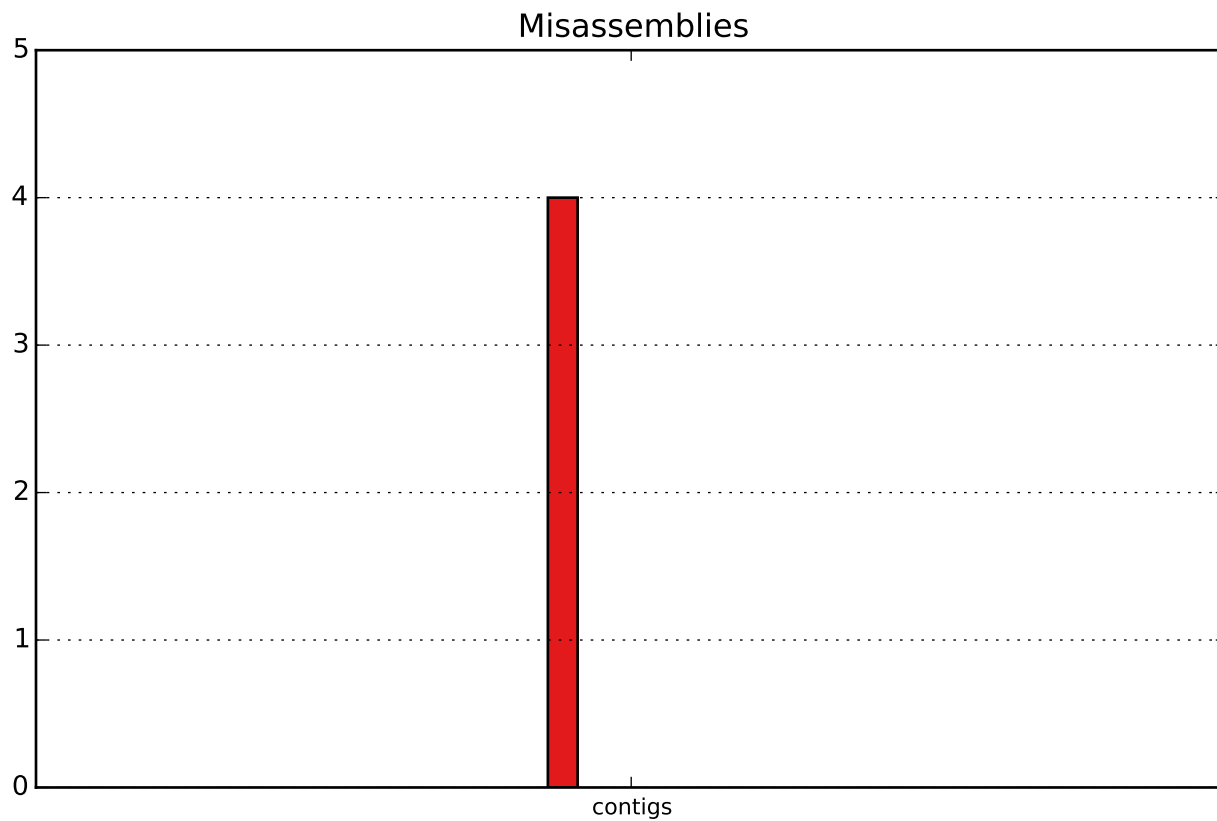
NGx



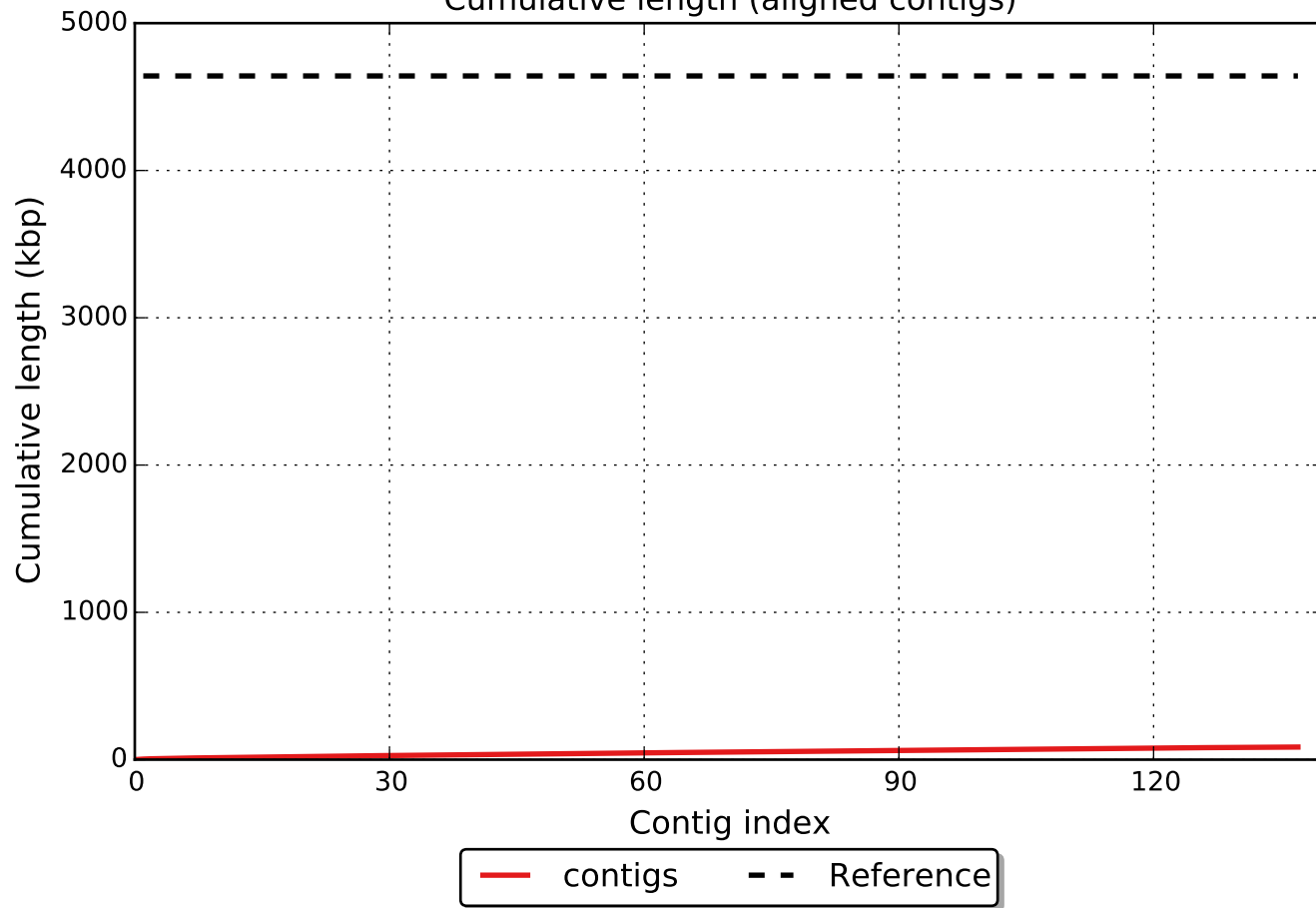


GC content

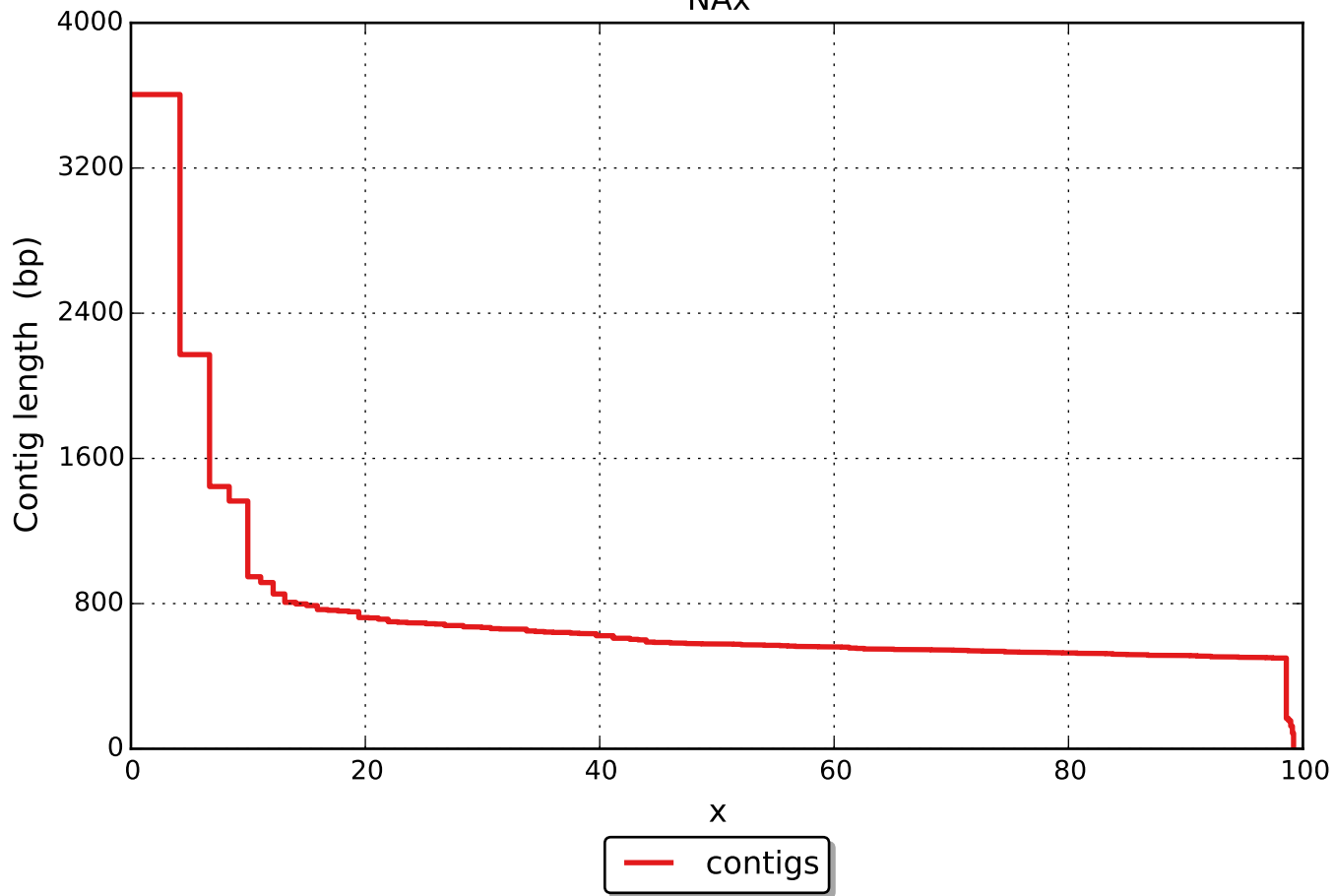




Cumulative length (aligned contigs)



NAx



NGAx

