

Report

	scaffolds
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	5
# contigs (≥ 10000 bp)	5
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	5
Total length (≥ 1000 bp)	1462865
Total length (≥ 5000 bp)	1461795
Total length (≥ 10000 bp)	1461795
Total length (≥ 25000 bp)	1461795
Total length (≥ 50000 bp)	1461795
# contigs	6
Largest contig	768359
Total length	1462865
Reference length	4641652
GC (%)	50.04
Reference GC (%)	50.78
N50	768359
N75	176518
L50	1
L75	3
# misassemblies	14
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	0
# unaligned contigs	0 + 4 part
Unaligned length	686848
Genome fraction (%)	13.215
Duplication ratio	1.265
# N's per 100 kbp	1.16
# mismatches per 100 kbp	1408.86
# indels per 100 kbp	1.47
Largest alignment	111117
NGA50	-

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

	scaffolds
# misassemblies	14
# relocations	10
# translocations	0
# inversions	4
# possibly misassembled contigs	3
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	0
# mismatches	8642
# indels	9
# short indels	9
# long indels	0
Indels length	12

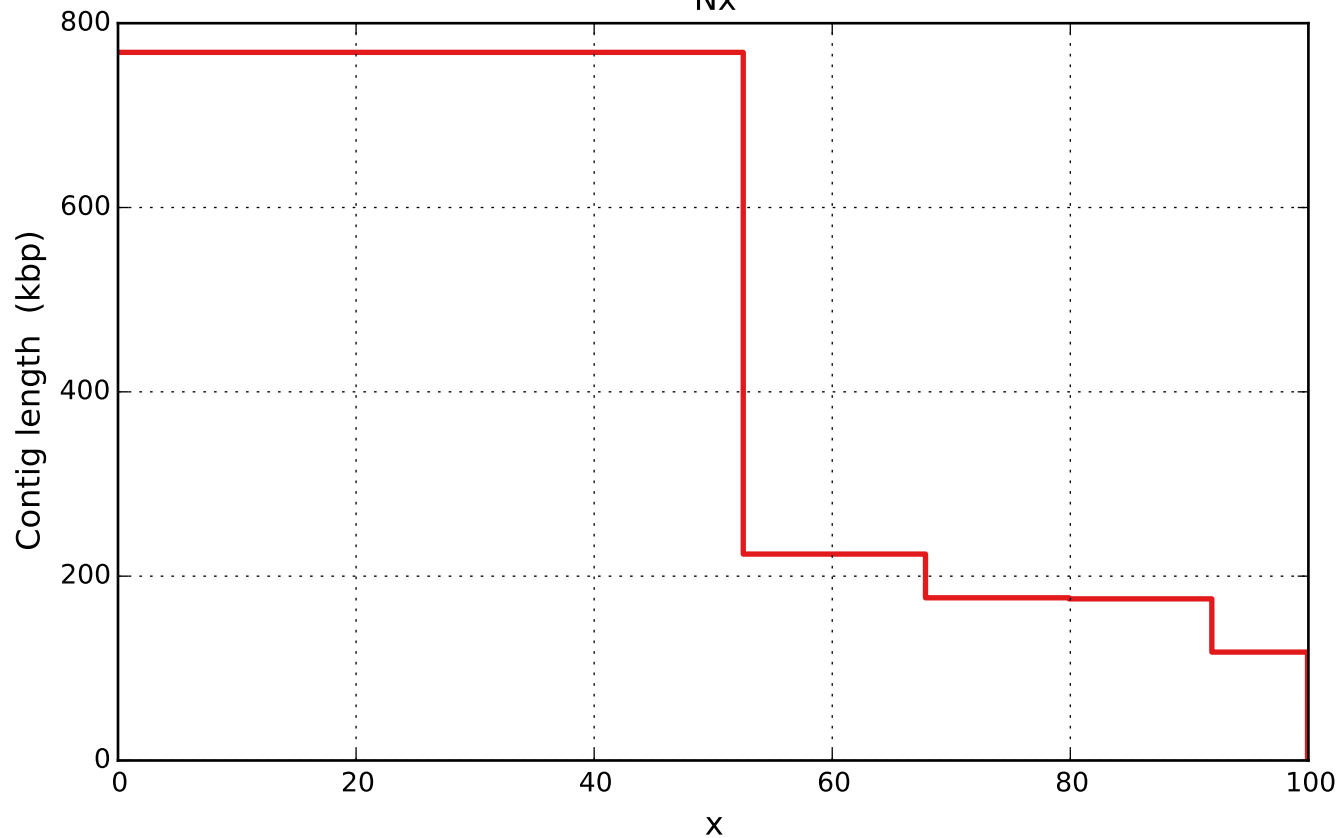
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	1
# both parts are significant	2
Partially unaligned length	686848
# N's	17

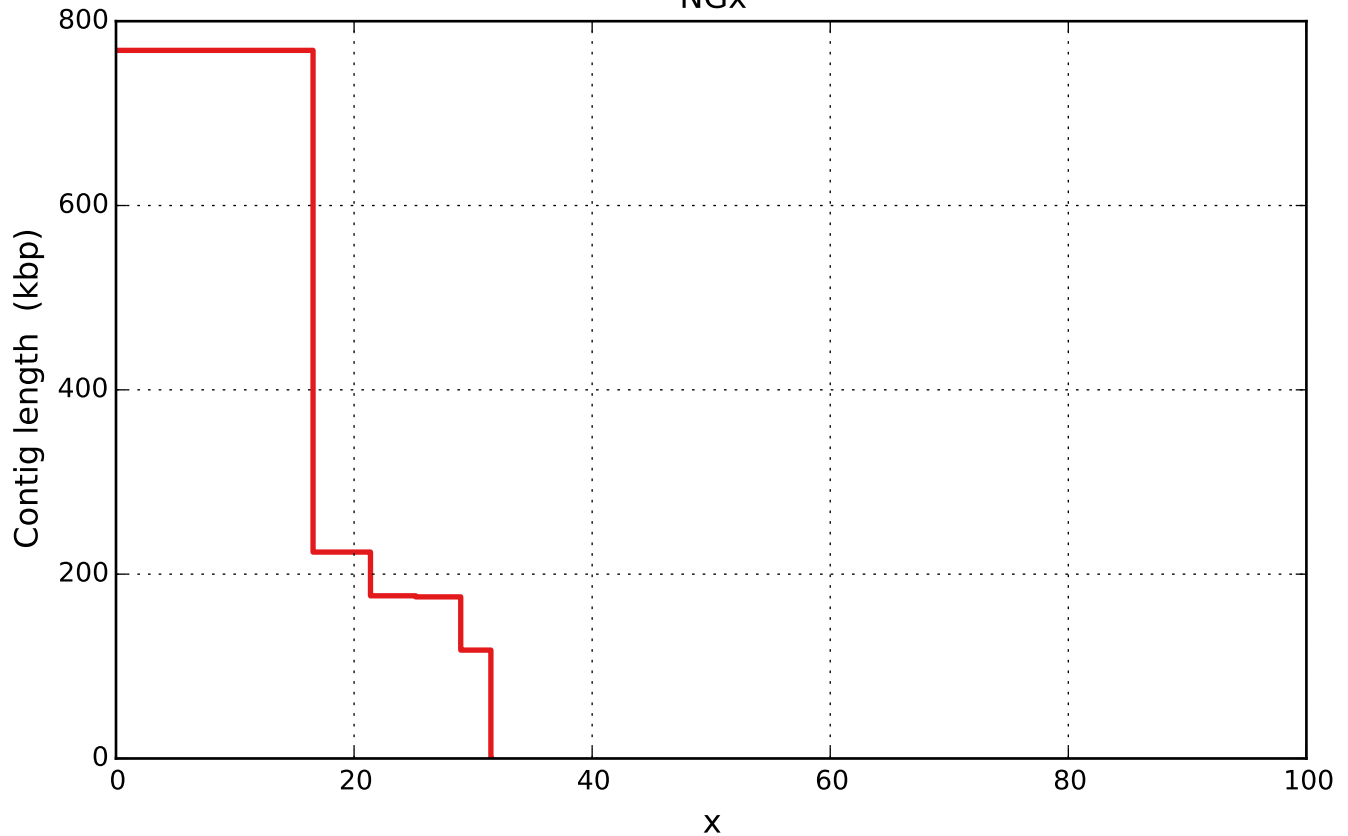
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

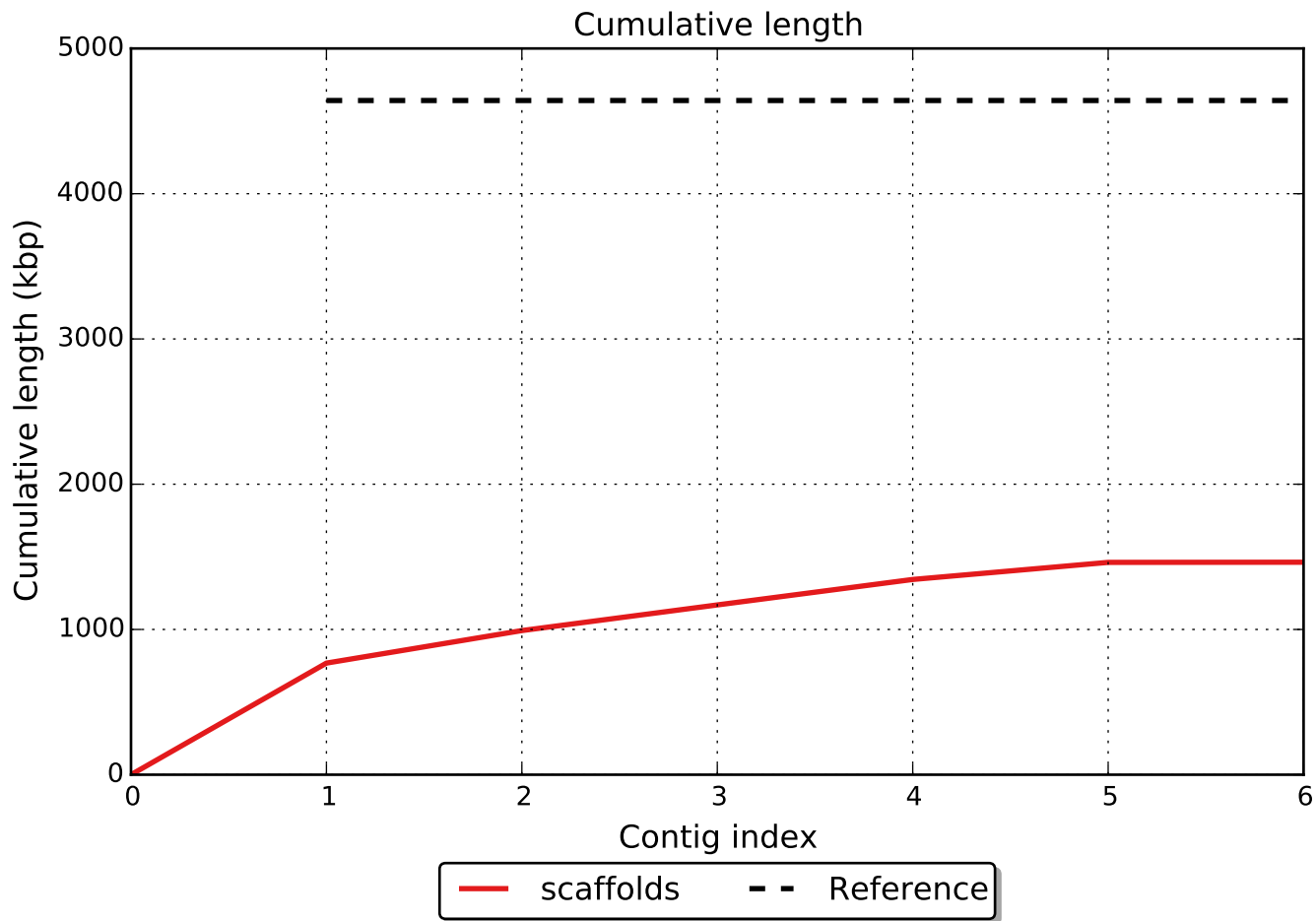


— scaffolds

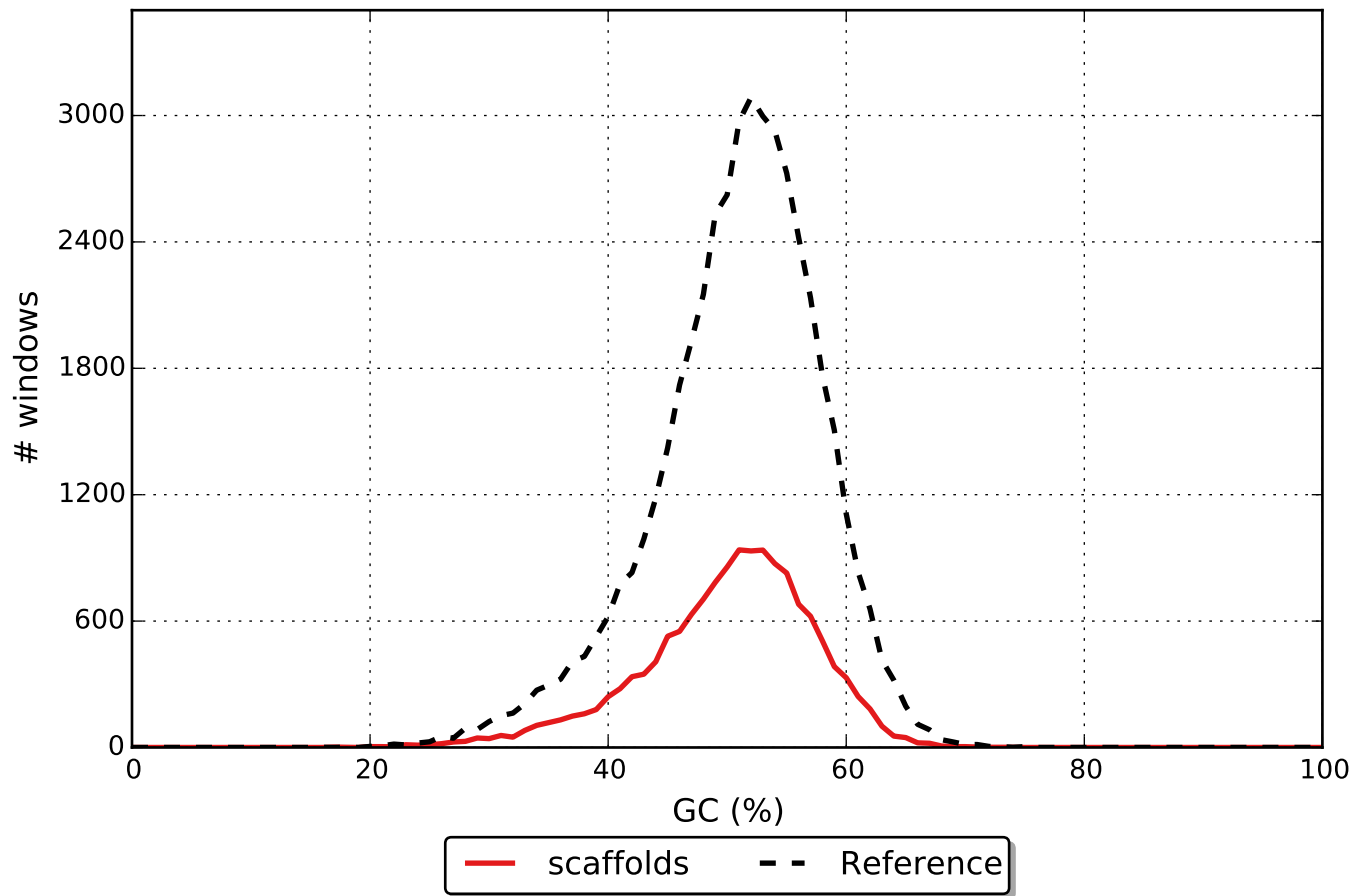
NGx

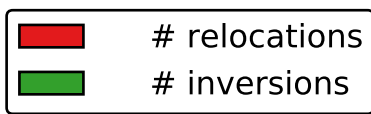
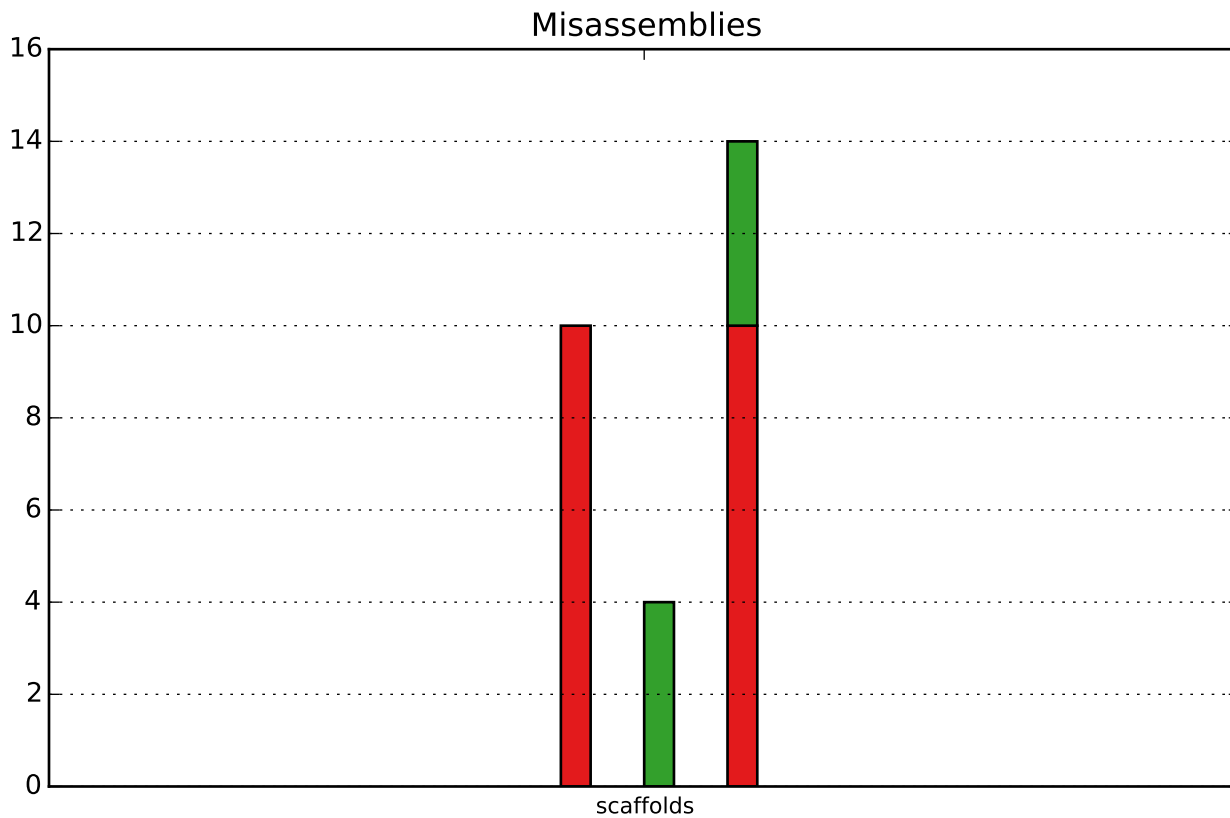


— scaffolds

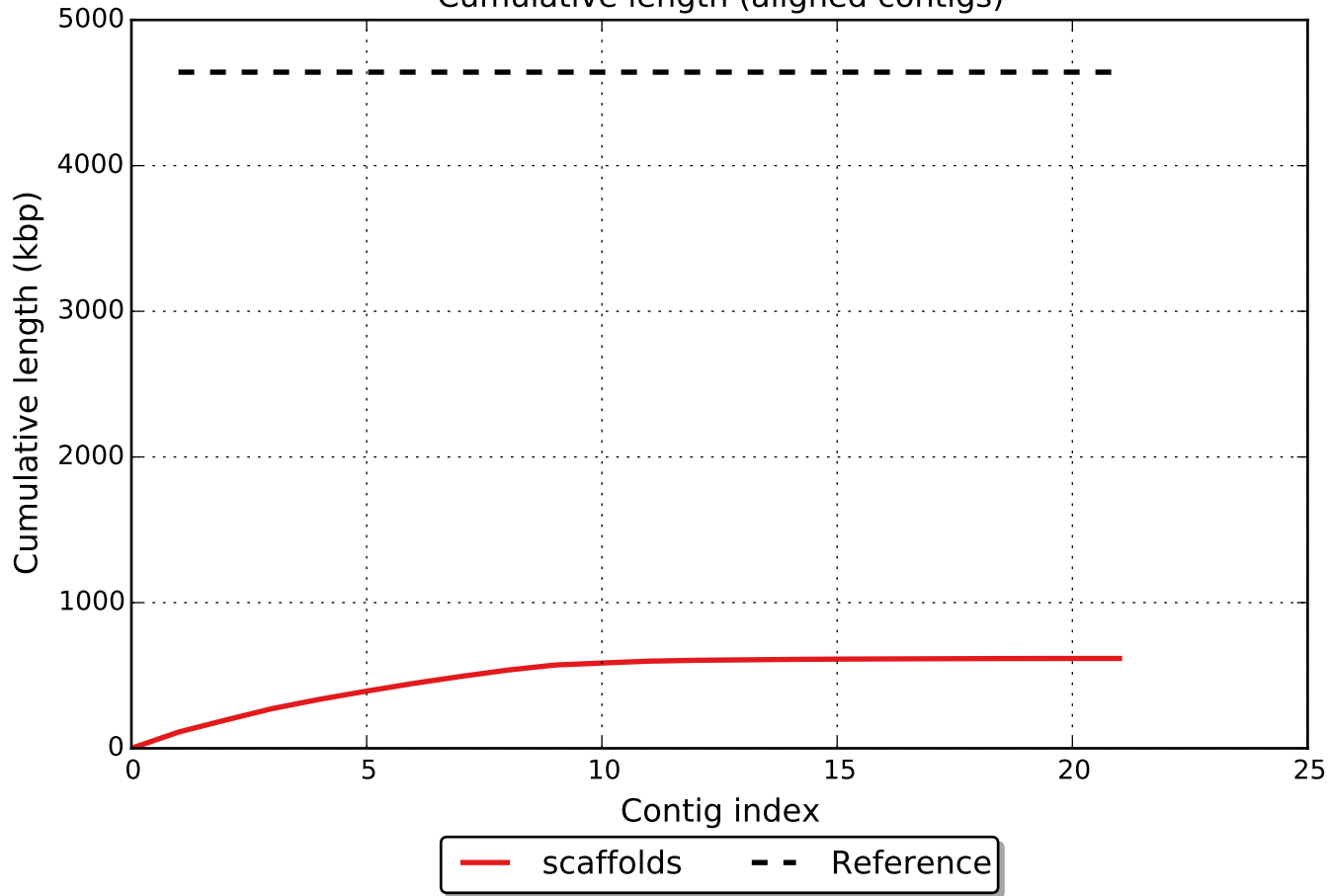


GC content

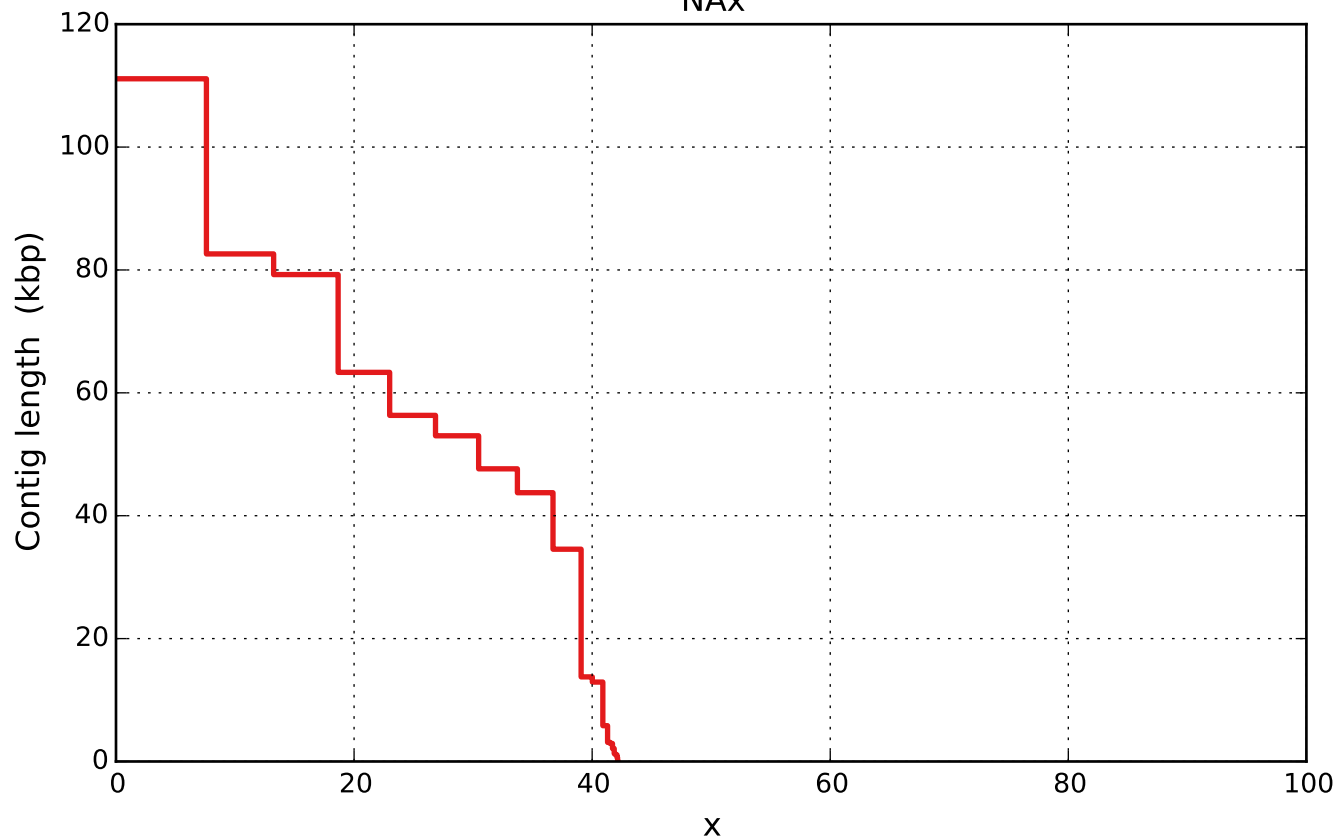




Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

