

Report

	scaffolds
# contigs (≥ 1000 bp)	33
# contigs (≥ 5000 bp)	29
# contigs (≥ 10000 bp)	28
# contigs (≥ 25000 bp)	26
# contigs (≥ 50000 bp)	22
Total length (≥ 1000 bp)	4848847
Total length (≥ 5000 bp)	4841052
Total length (≥ 10000 bp)	4832527
Total length (≥ 25000 bp)	4805122
Total length (≥ 50000 bp)	4643282
# contigs	45
Largest contig	472565
Total length	4857430
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.78
N50	305624
NG50	305624
N75	201240
NG75	214400
L50	7
LG50	7
L75	12
LG75	11
# misassemblies	15
# misassembled contigs	2
Misassembled contigs length	401494
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	222
Genome fraction (%)	98.834
Duplication ratio	1.059
# N's per 100 kbp	0.21
# mismatches per 100 kbp	526.65
# indels per 100 kbp	1.05
Largest alignment	472565
NA50	304586
NGA50	304586
NA75	156700
NGA75	183277
LA50	7
LGA50	7
LA75	13
LGA75	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).

Misassemblies report

	scaffolds
# misassemblies	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	2
Misassembled contigs length	401494
# local misassemblies	3
# mismatches	24160
# indels	48
# short indels	48
# long indels	0
Indels length	50

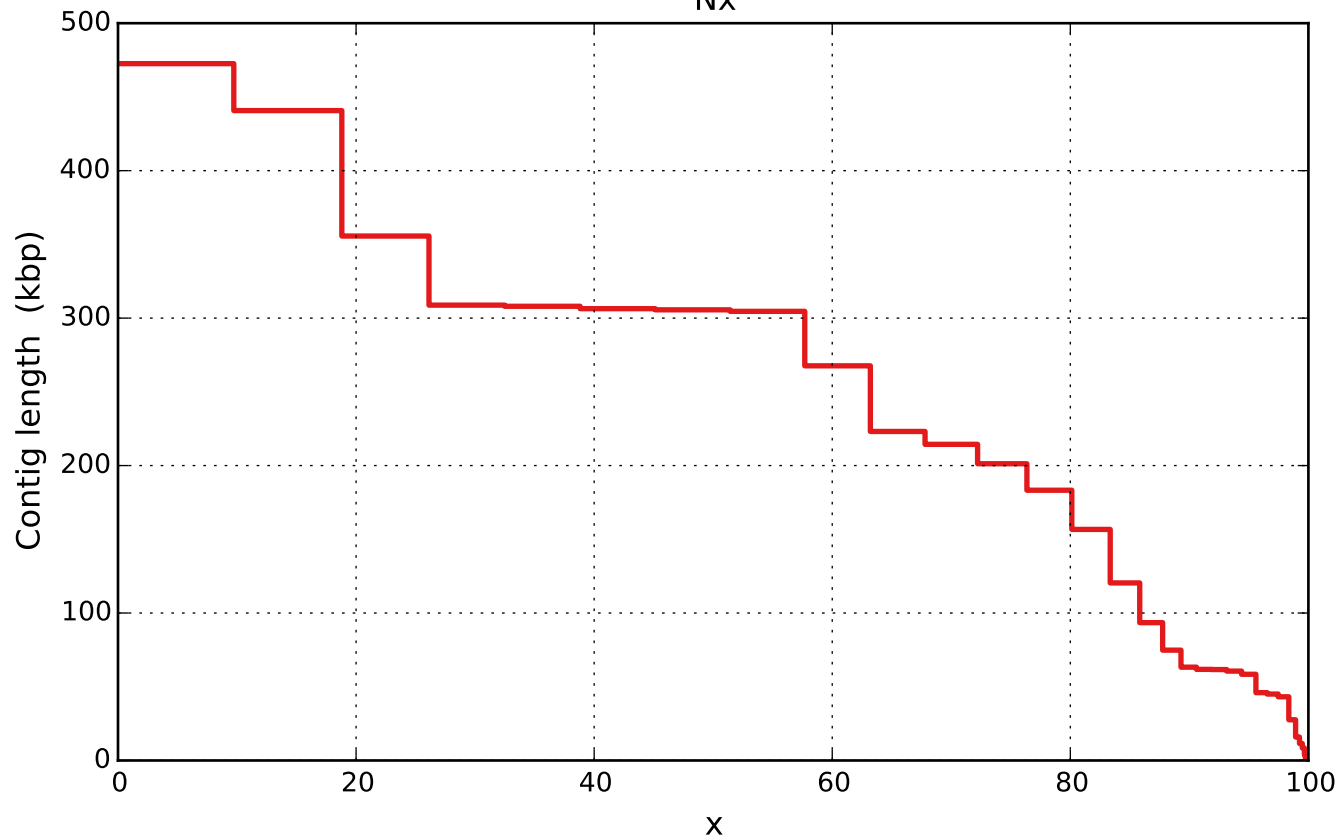
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	222
# N's	10

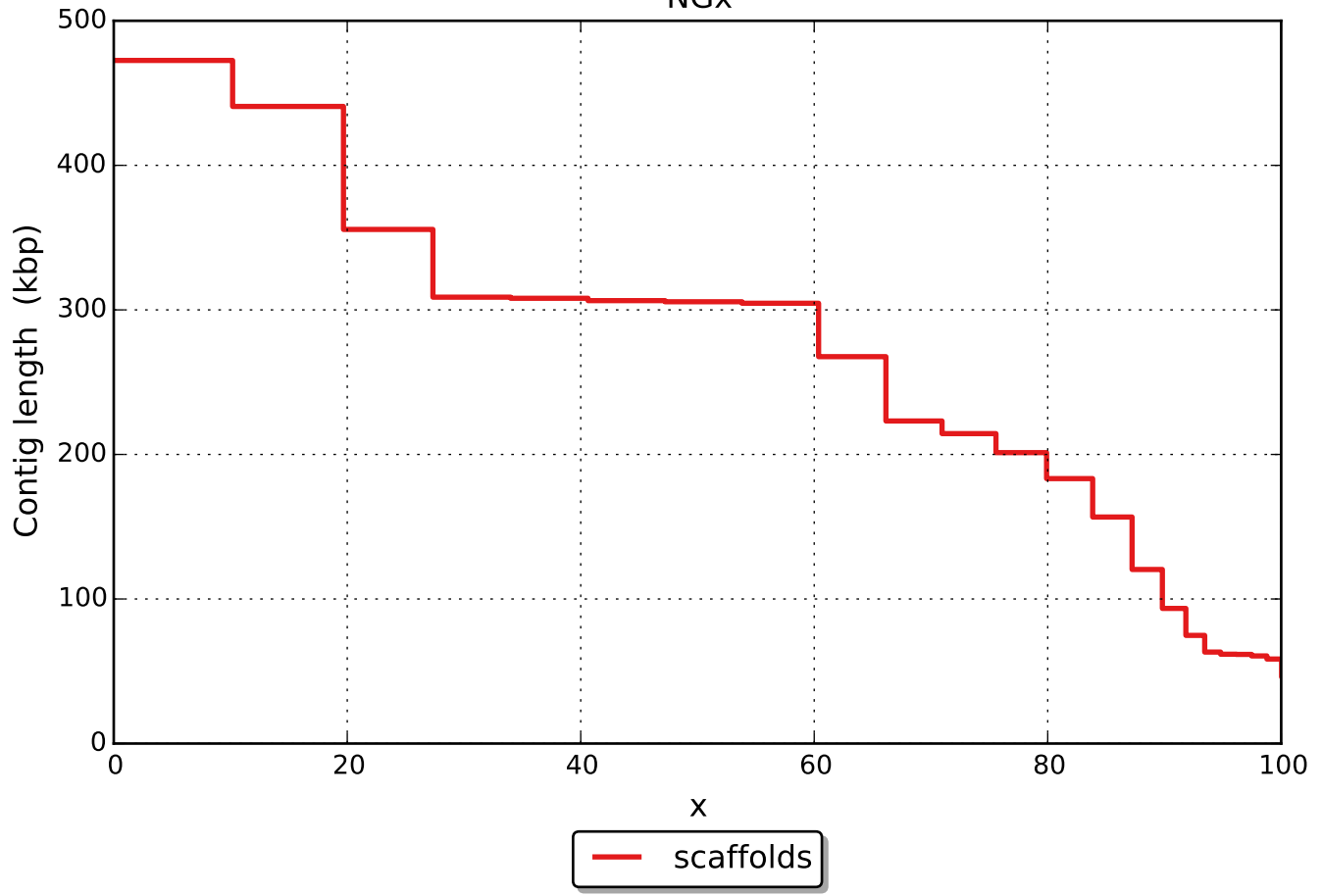
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

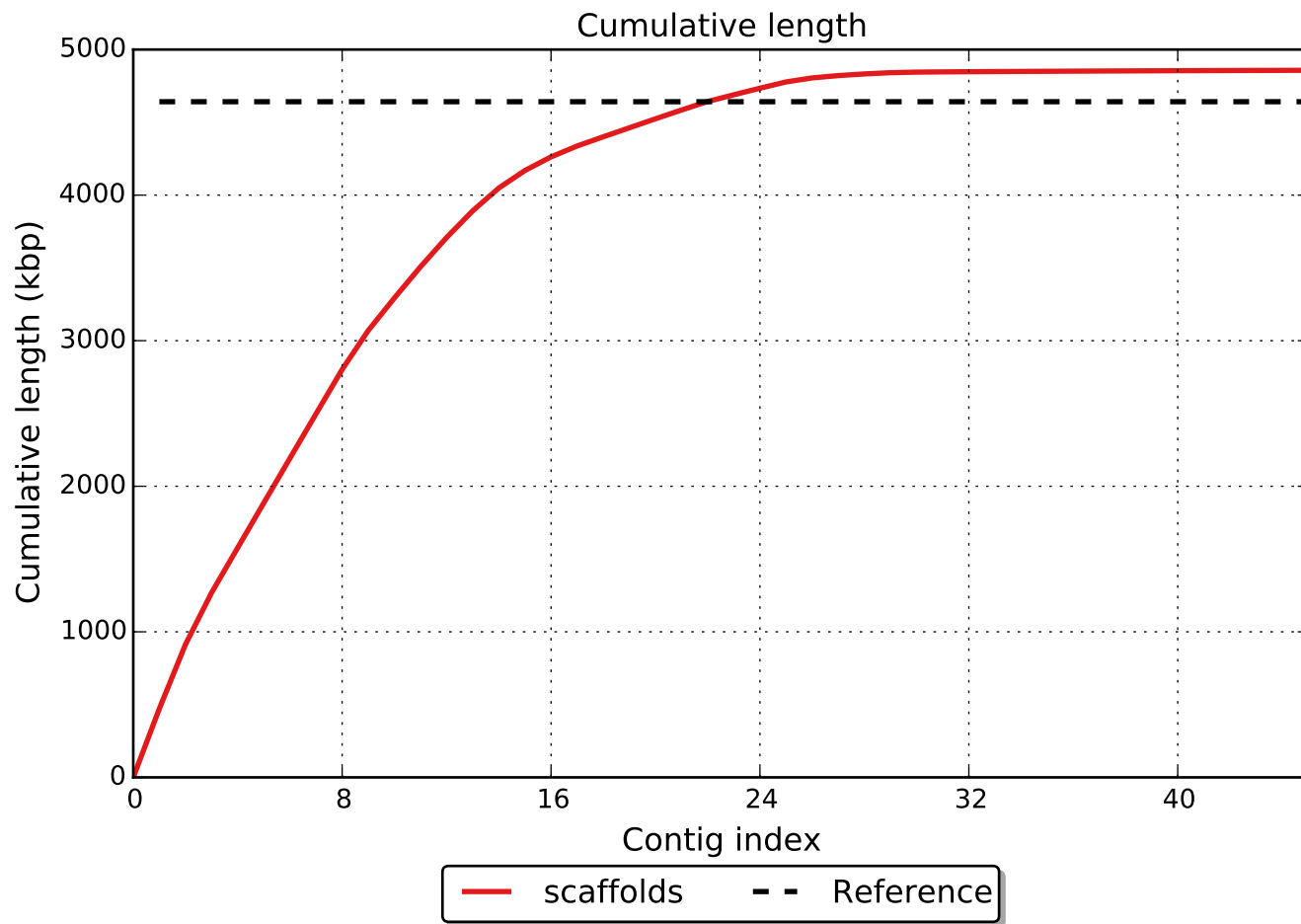
Nx



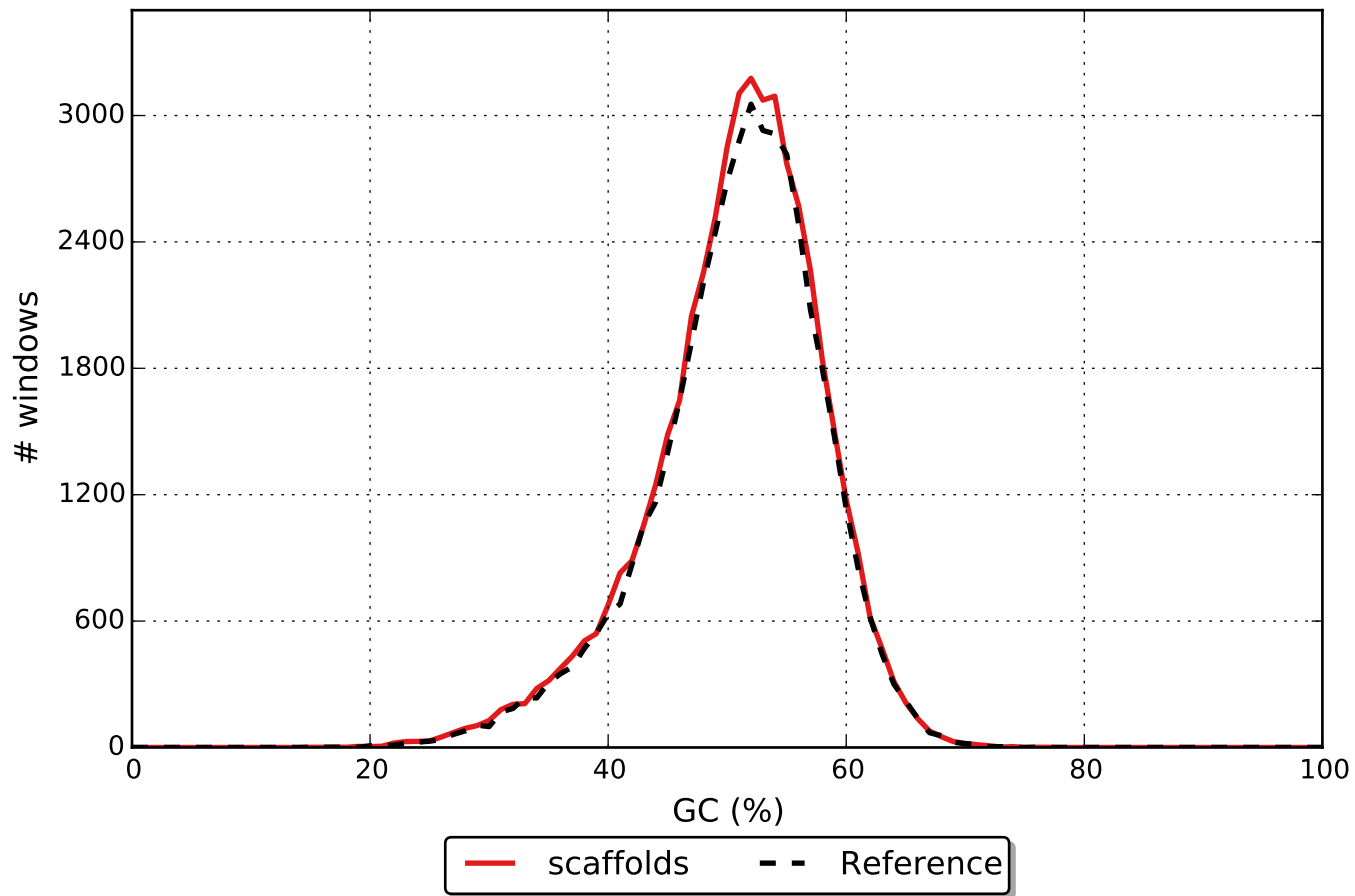
— scaffolds

NGx

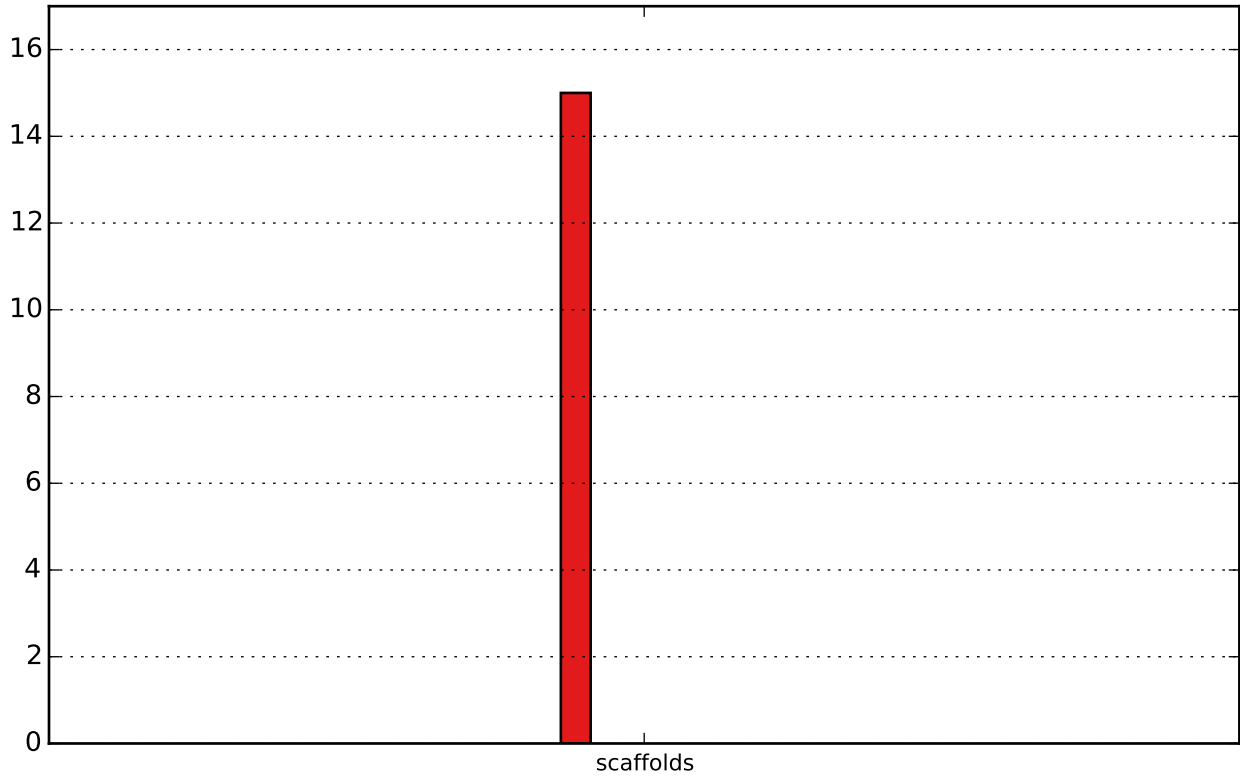




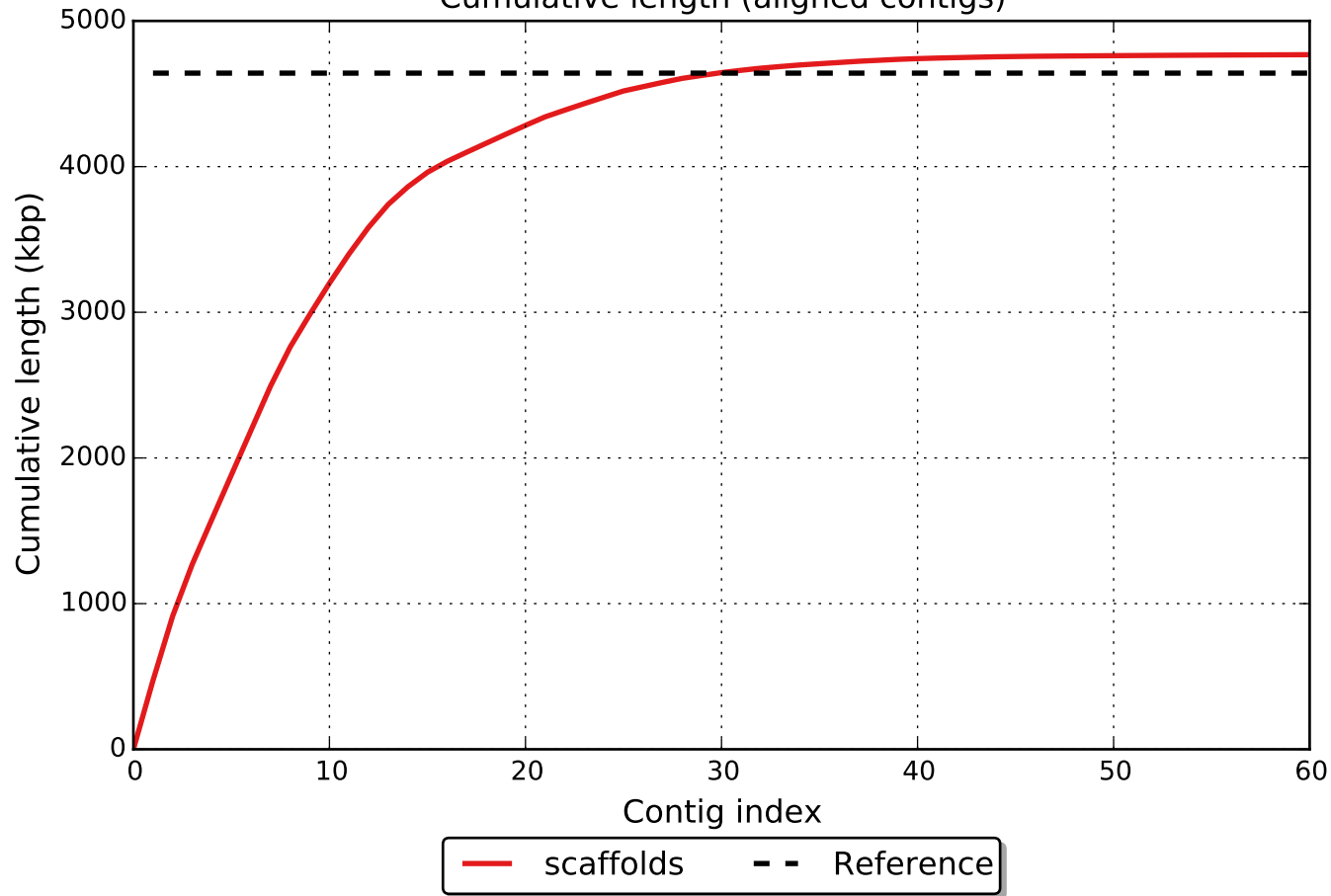
GC content



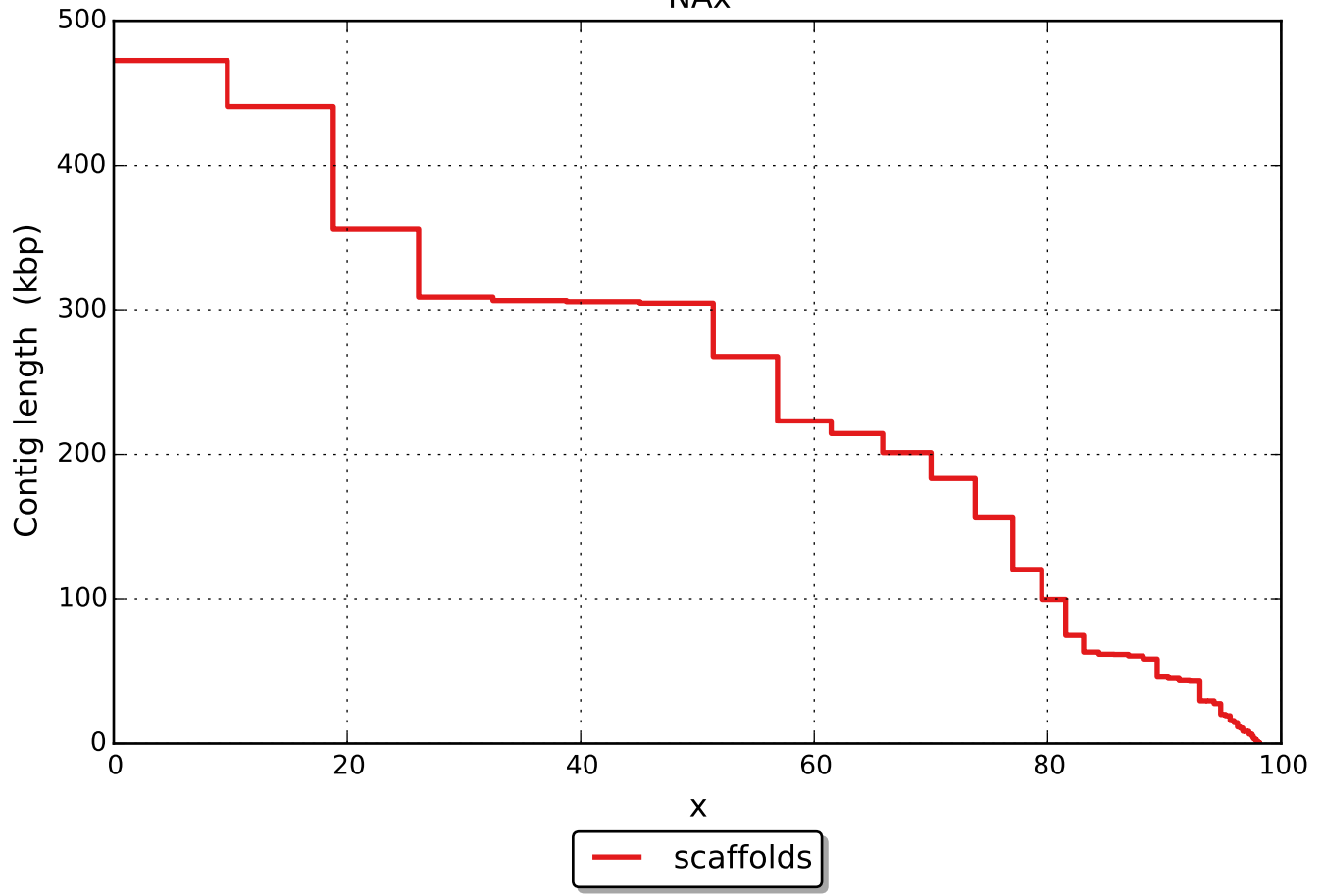
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

