

# Report

	scaffolds
# contigs (>= 1000 bp)	364
# contigs (>= 5000 bp)	241
# contigs (>= 10000 bp)	154
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4454441
Total length (>= 5000 bp)	4103011
Total length (>= 10000 bp)	3446895
Total length (>= 25000 bp)	1653950
Total length (>= 50000 bp)	574446
# contigs	393
Largest contig	95483
Total length	4476694
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	18571
NG50	17843
N75	10727
NG75	9817
L50	69
LG50	73
L75	146
LG75	158
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	156454
# local misassemblies	12
# unaligned contigs	0 + 2 part
Unaligned length	531
Genome fraction (▼)	96.280
Duplication ratio	1.002
# N's per 100 kbp	267.38
# mismatches per 100 kbp	99.51
# indels per 100 kbp	22.69
Largest alignment	95385
NA50	18206
NGA50	17408
NA75	10403
NGA75	9705
LA50	70
LGA50	75
LA75	149
LGA75	161

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

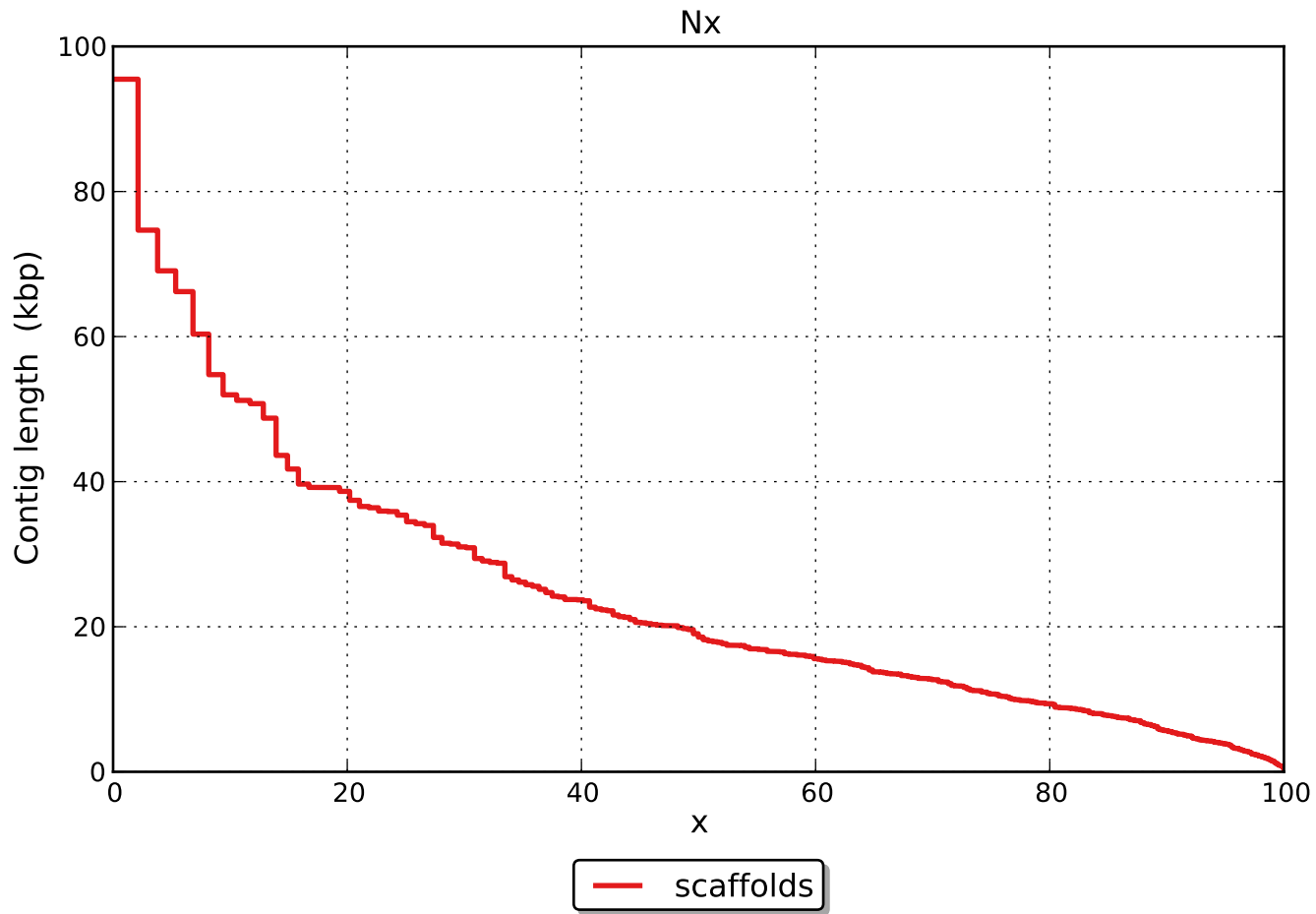
	scaffolds
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	156454
# local misassemblies	12
# mismatches	4447
# indels	1014
# short indels	683
# long indels	331
Indels length	6037

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

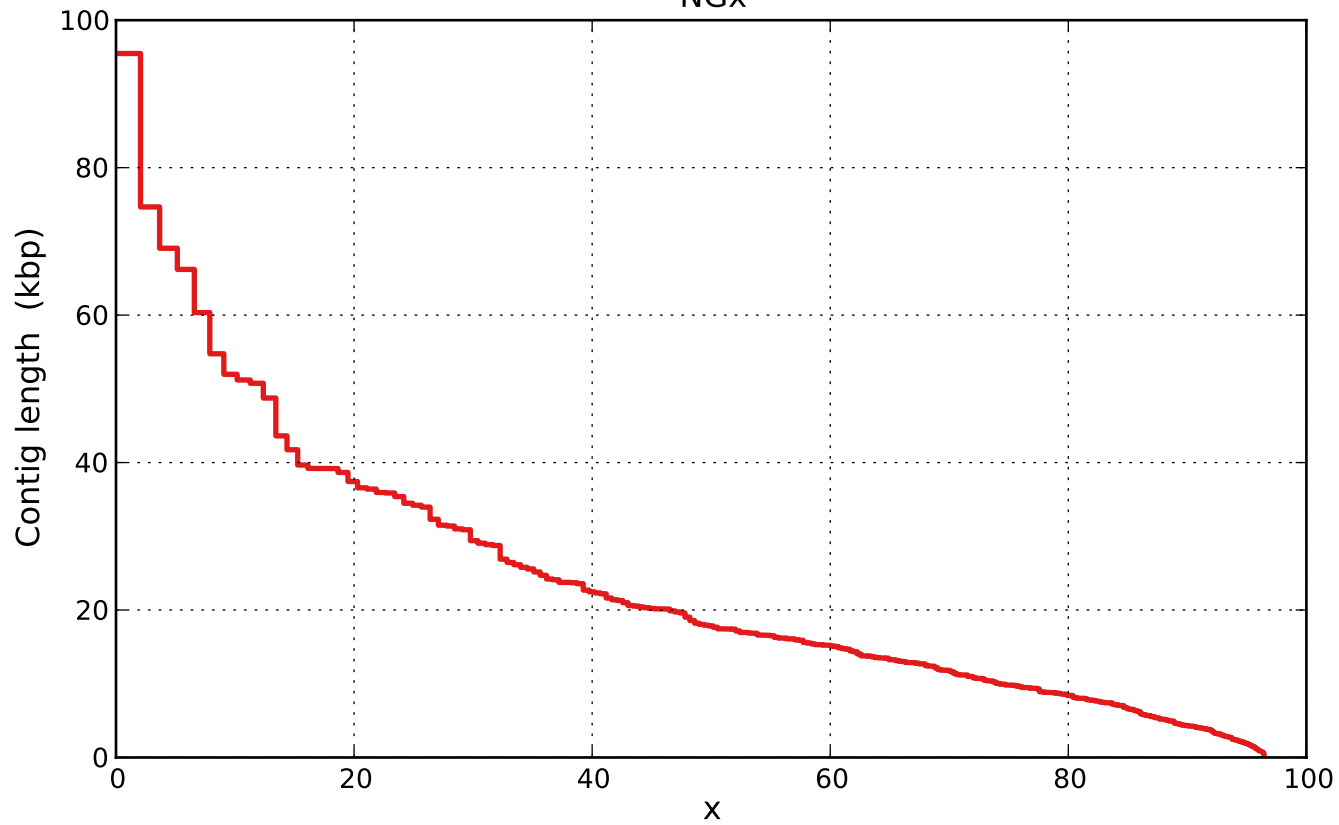
## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	531
# N's	11970

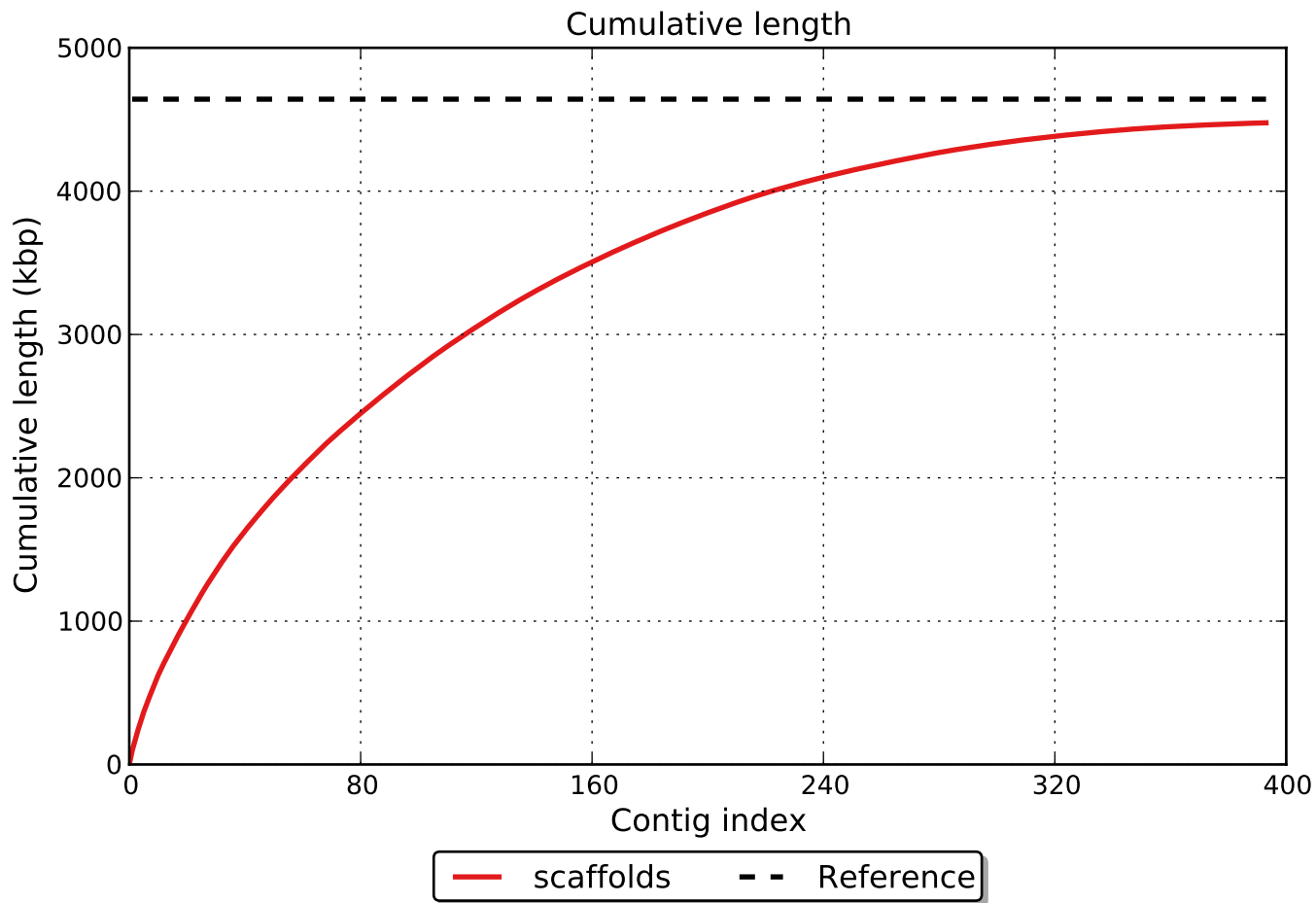
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



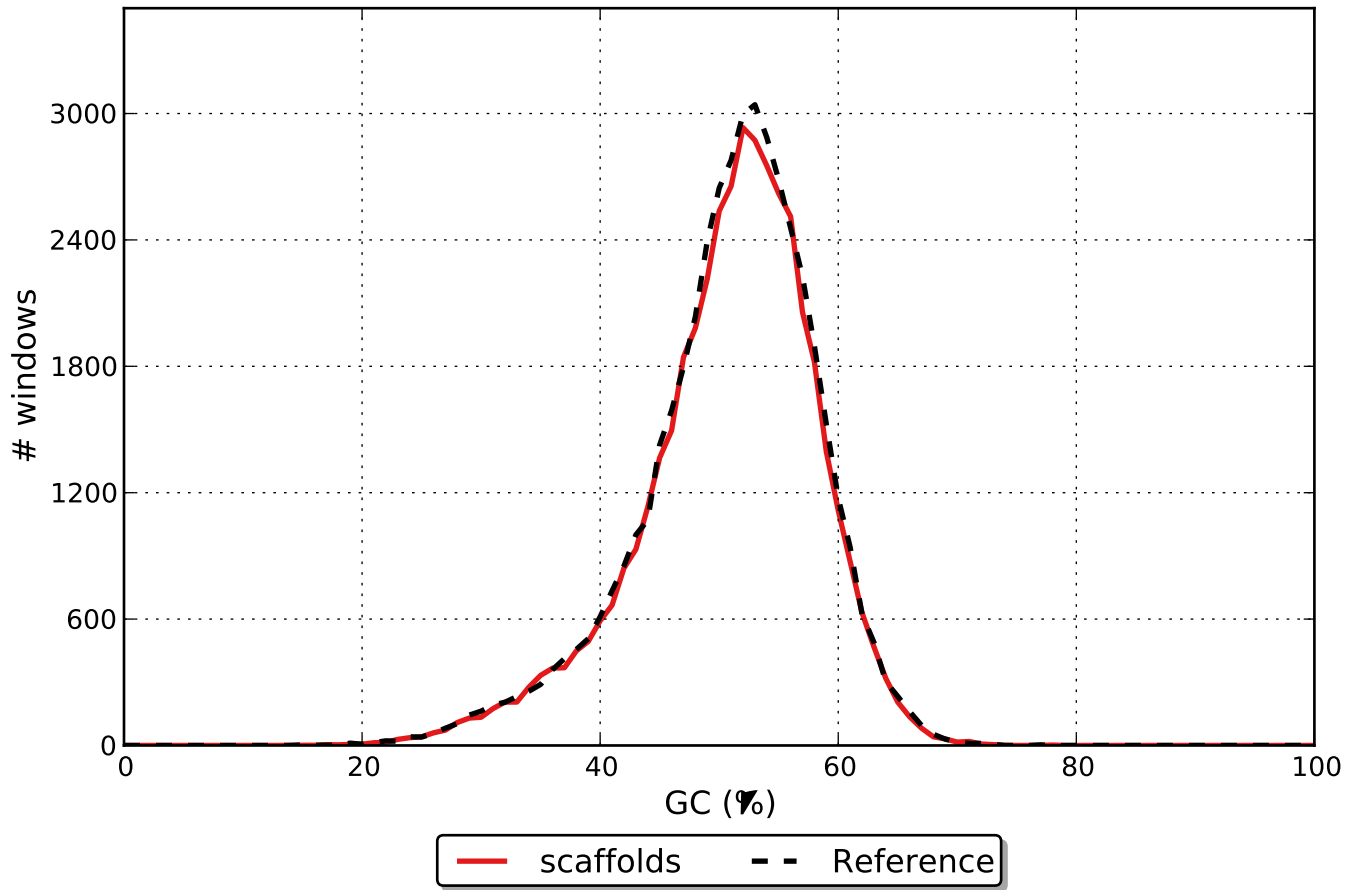
NGx

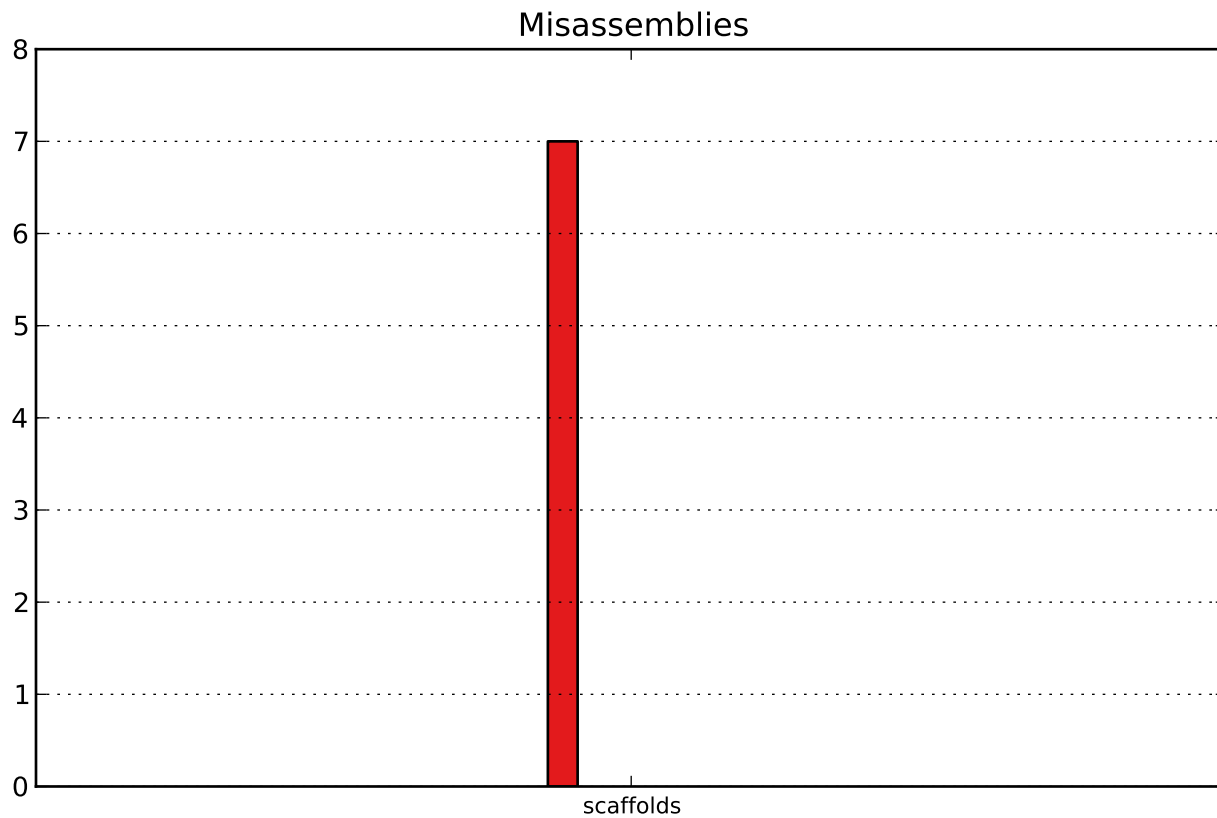


— scaffolds



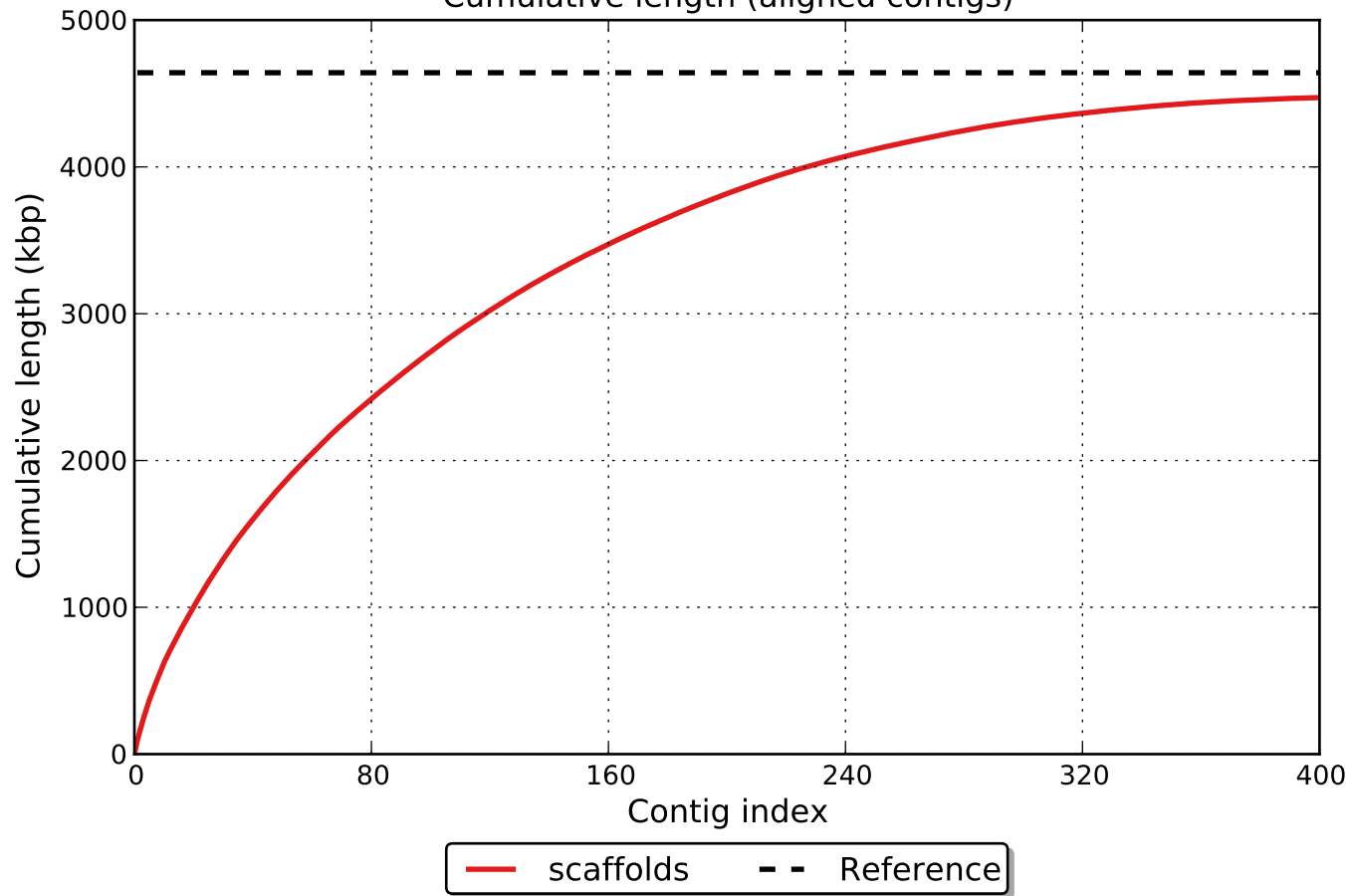
# GC content



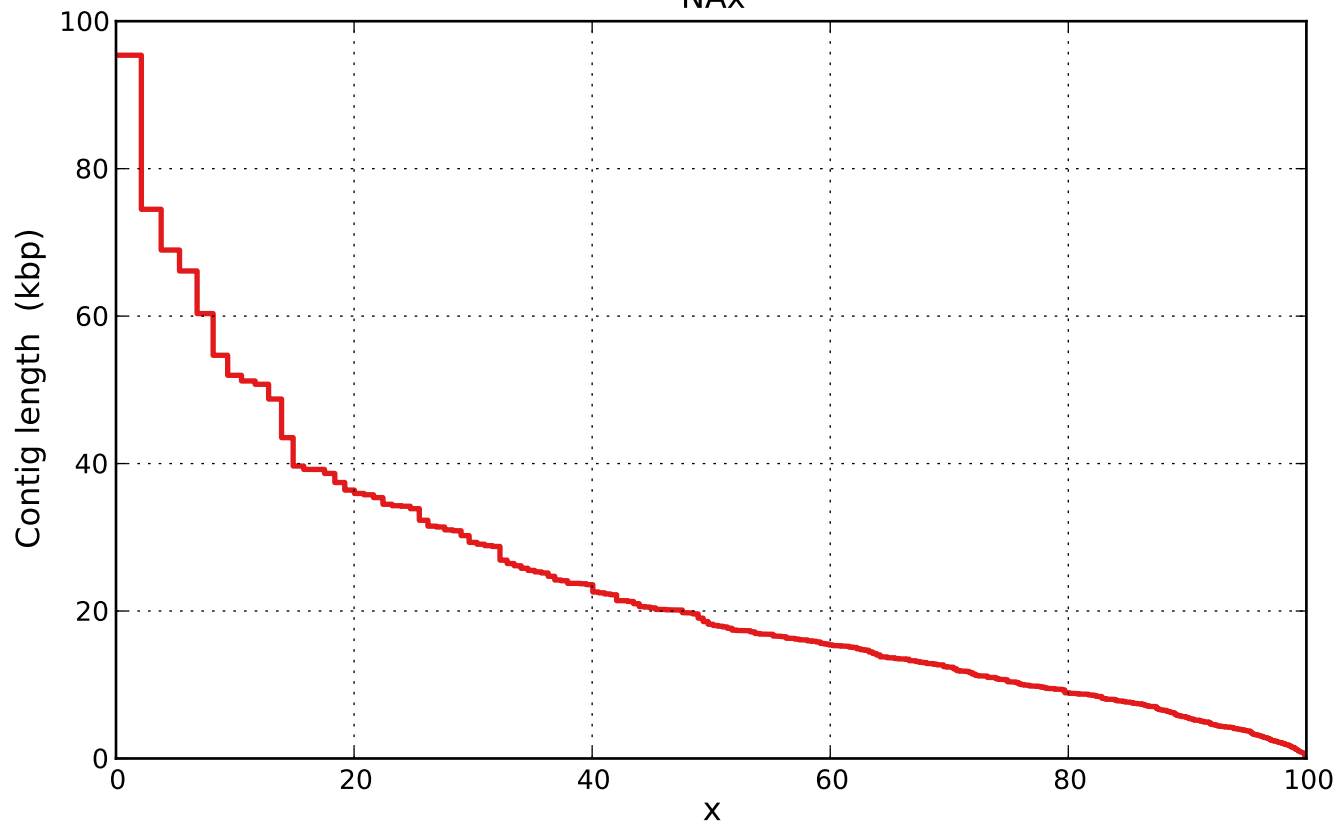




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

