

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	167
# contigs ( $\geq 1000$ bp)	27
# contigs ( $\geq 5000$ bp)	16
# contigs ( $\geq 10000$ bp)	8
# contigs ( $\geq 25000$ bp)	6
# contigs ( $\geq 50000$ bp)	6
Total length ( $\geq 0$ bp)	3135716
Total length ( $\geq 1000$ bp)	3111330
Total length ( $\geq 5000$ bp)	3077772
Total length ( $\geq 10000$ bp)	3020239
Total length ( $\geq 25000$ bp)	2999016
Total length ( $\geq 50000$ bp)	2999016
# contigs	31
Largest contig	1439166
Total length	3113949
Reference length	3168410
GC (%)	37.63
Reference GC (%)	37.70
N50	835679
NG50	835679
N75	293214
NG75	293214
L50	2
LG50	2
L75	3
LG75	3
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	212823
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	1 + 6 part
Unaligned length	43098
Genome fraction (%)	96.809
Duplication ratio	1.001
# N's per 100 kbp	1187.56
# mismatches per 100 kbp	10.79
# indels per 100 kbp	4.86
Largest alignment	1418045
Total aligned length	3070843
NA50	831530
NGA50	831530
NA75	292528
NGA75	292528
LA50	2
LGA50	2
LA75	3
LGA75	3

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).

## Misassemblies report

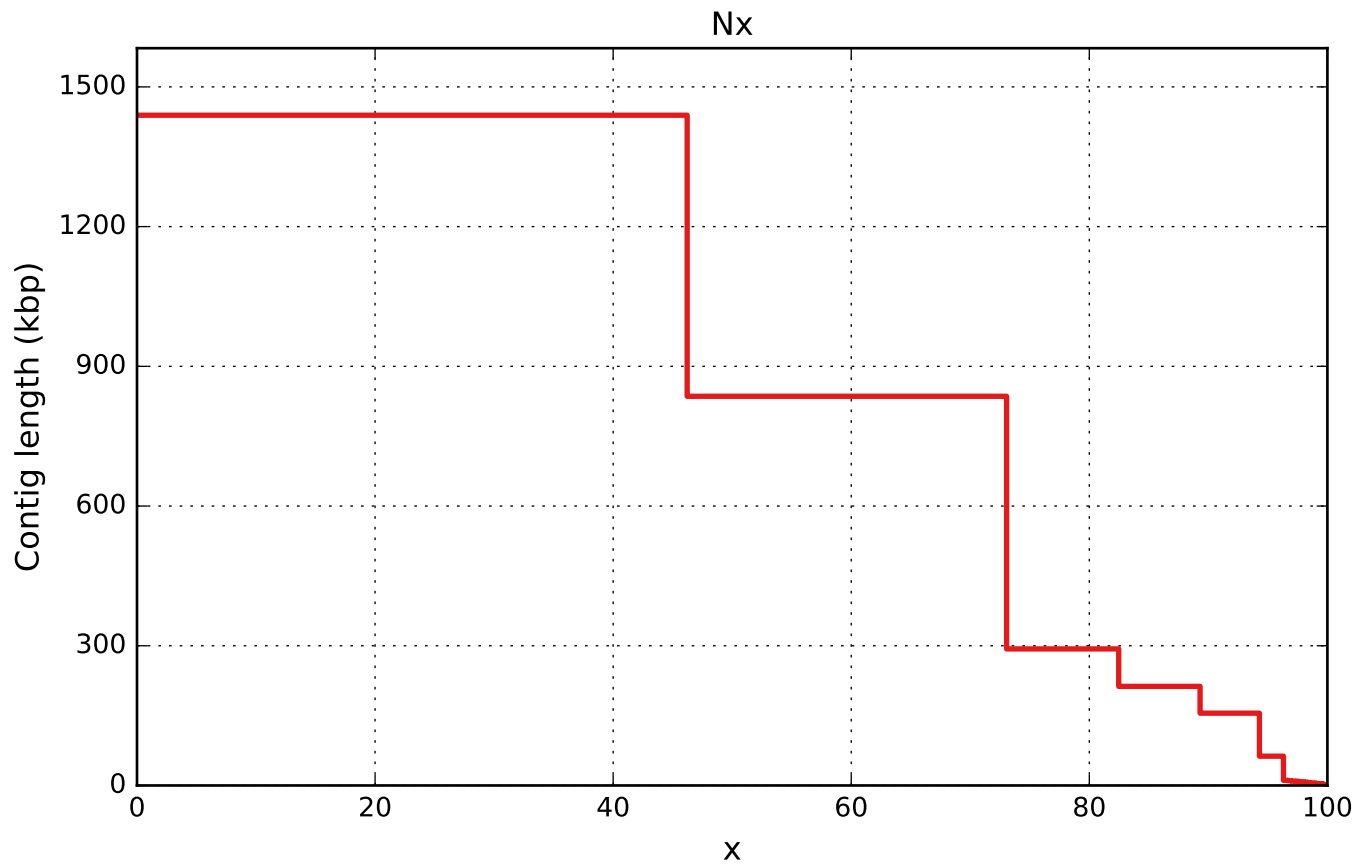
	scaffolds
# misassemblies	1
# relocations	0
# translocations	1
# inversions	0
# misassembled contigs	1
Misassembled contigs length	212823
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	331
# indels	149
# indels ( $\leq 5$ bp)	137
# indels ( $> 5$ bp)	12
Indels length	527

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).

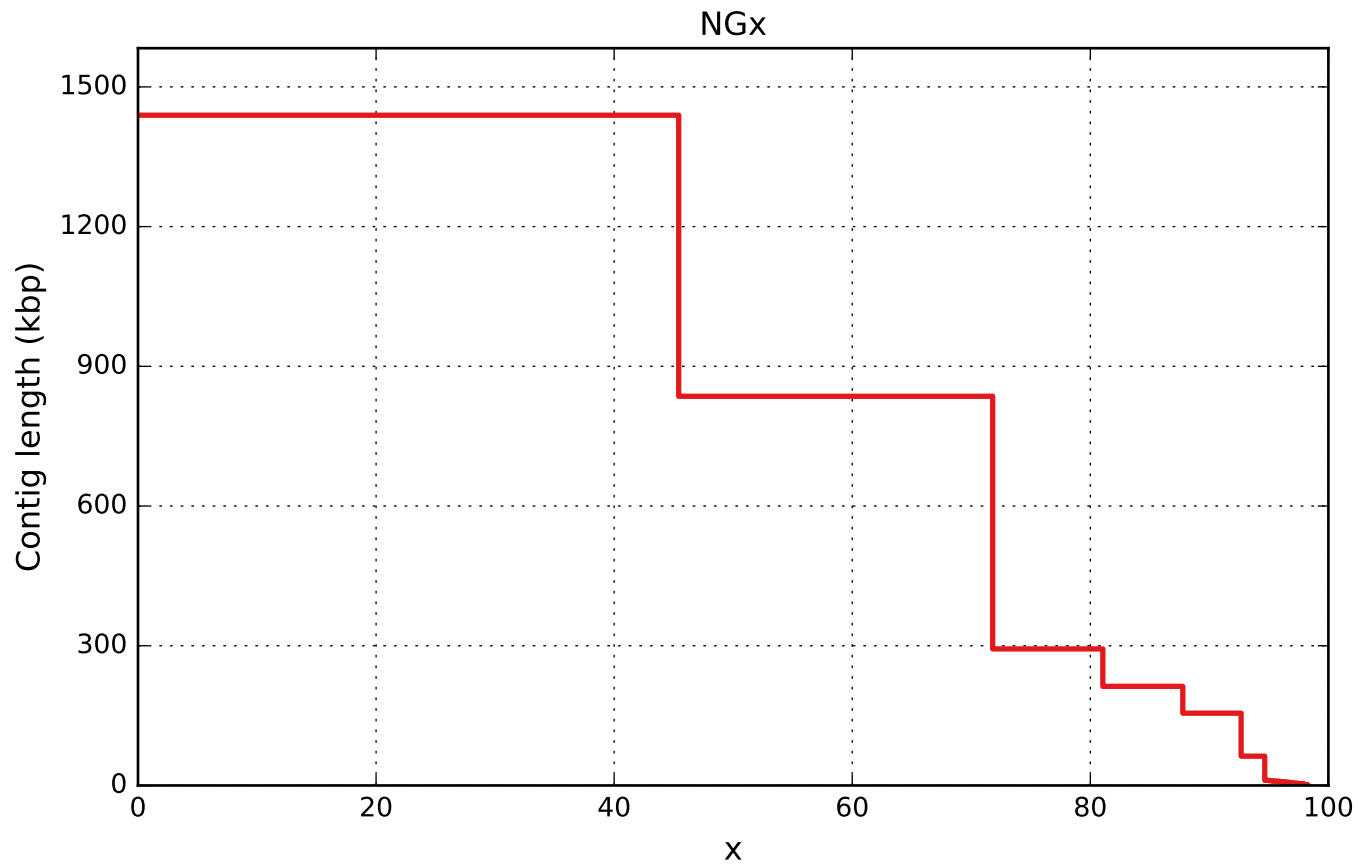
## Unaligned report

	scaffolds
# fully unaligned contigs	1
Fully unaligned length	3214
# partially unaligned contigs	6
Partially unaligned length	39884
# N's	36980

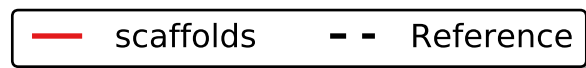
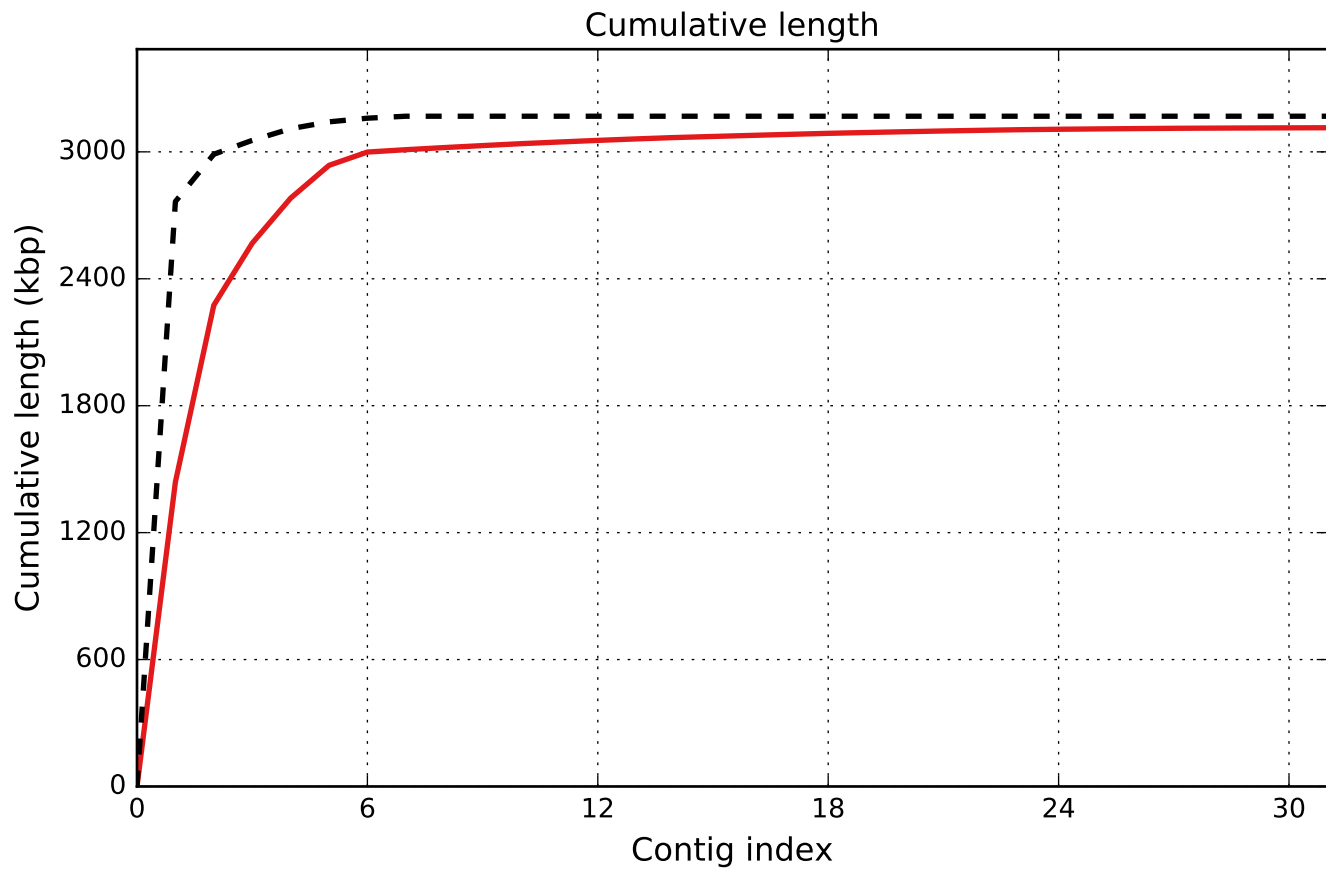
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

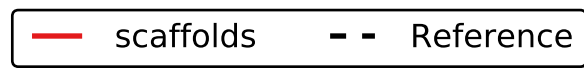
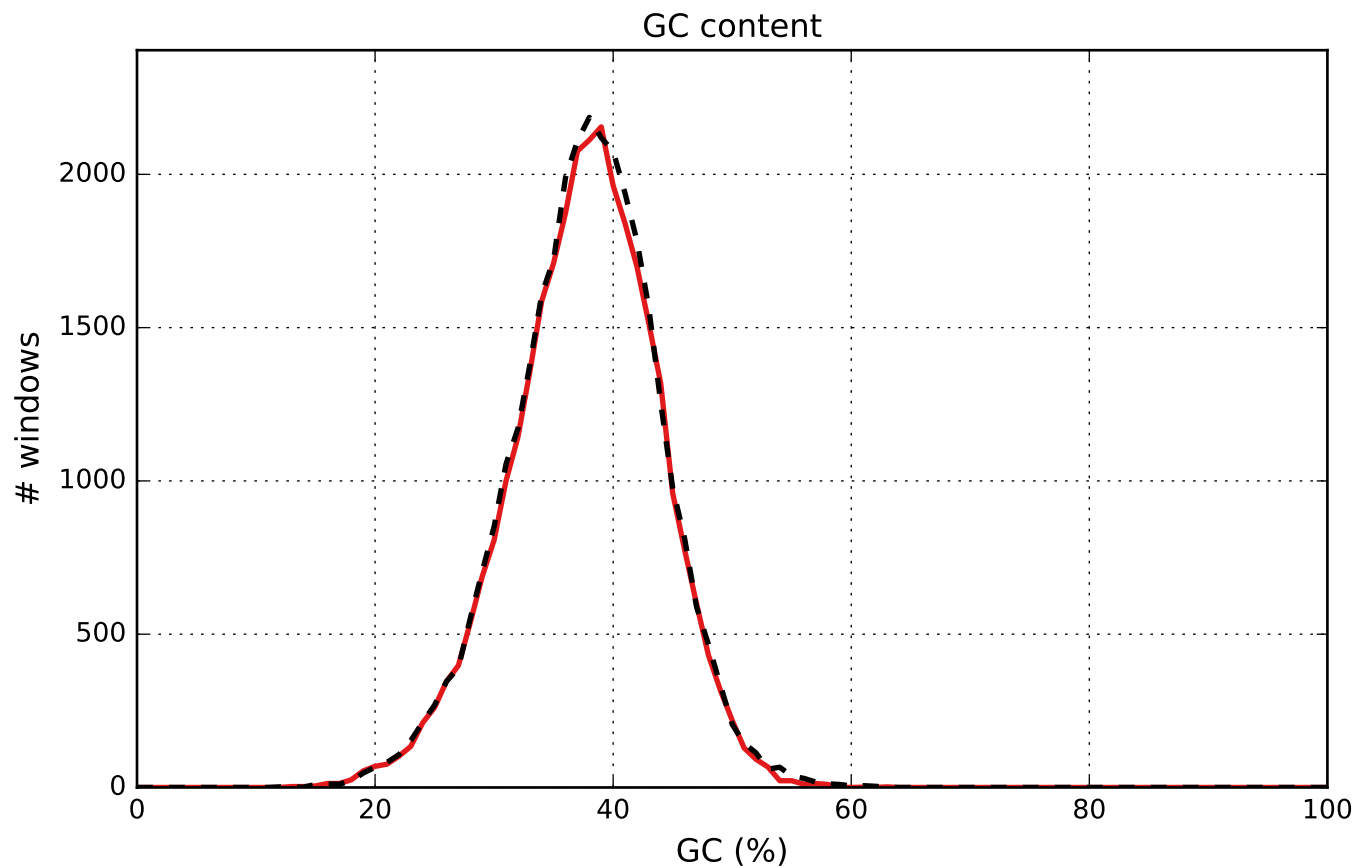


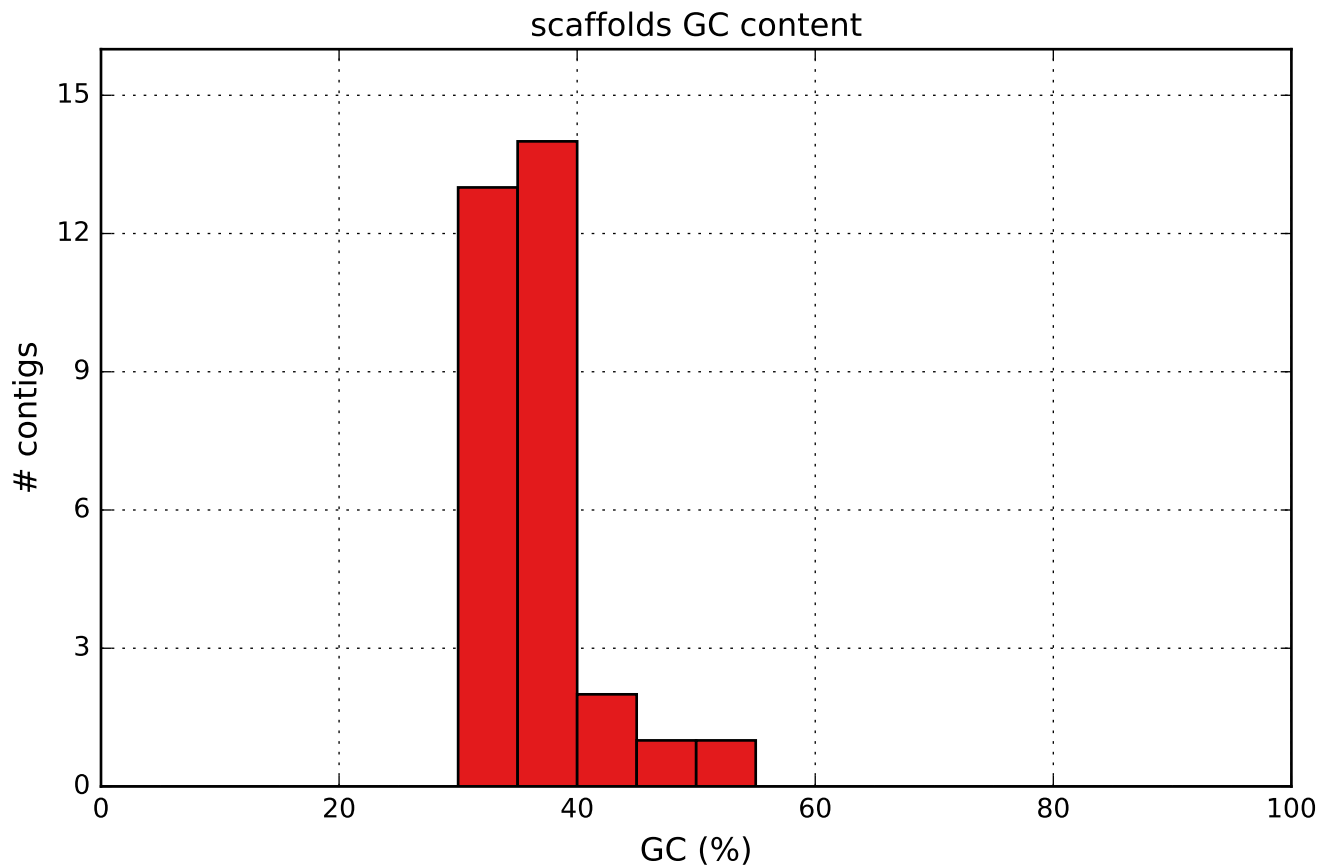
scaffolds



— scaffolds



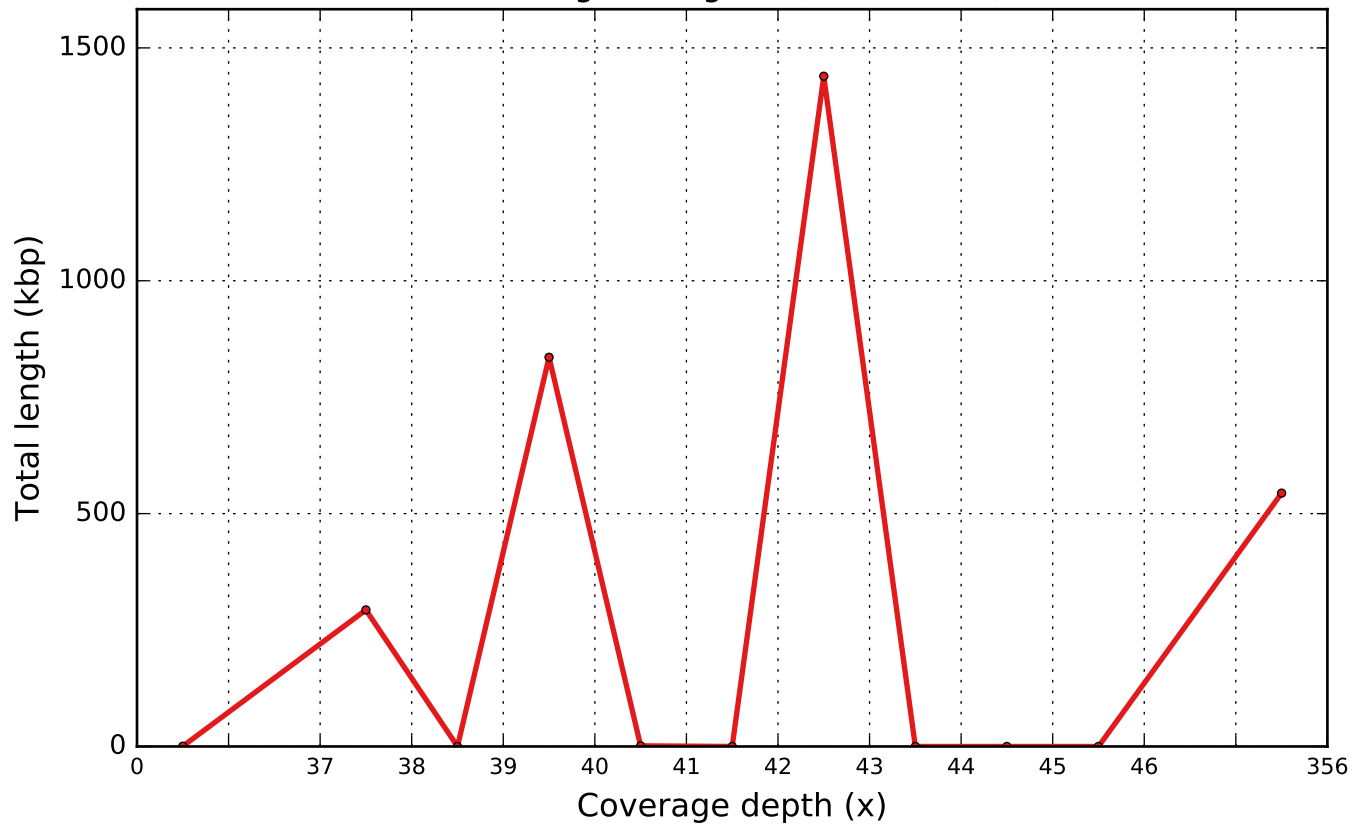




 scaffolds

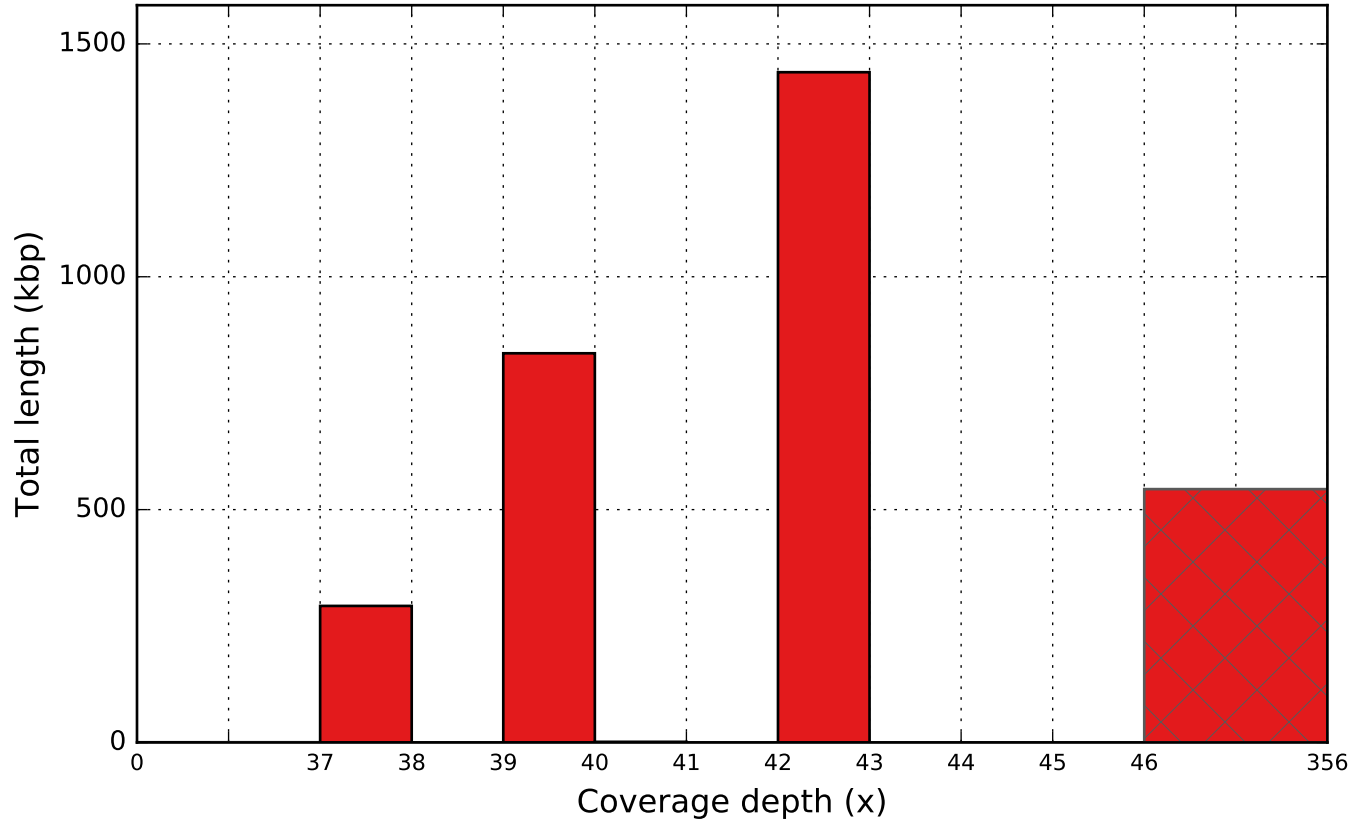


Coverage histogram (bin size: 1x)

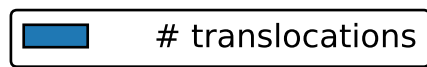
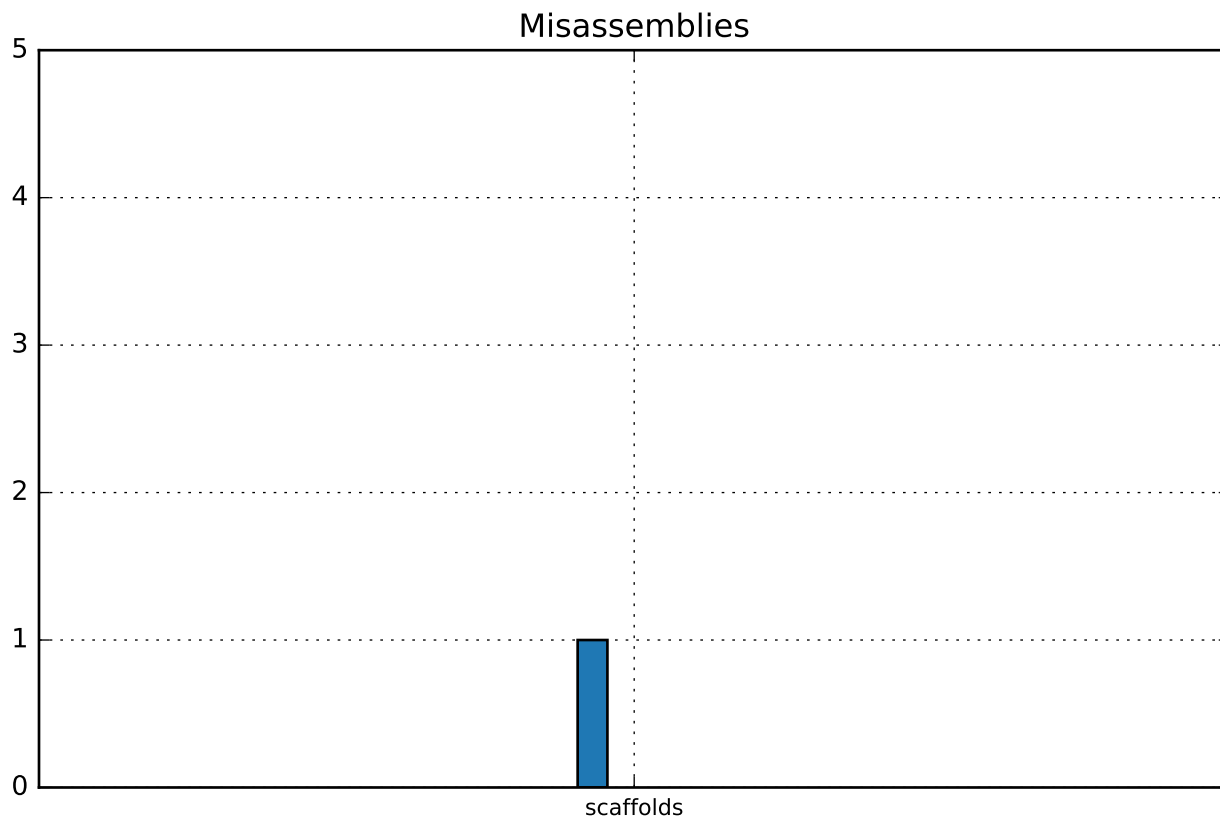


—•— scaffolds

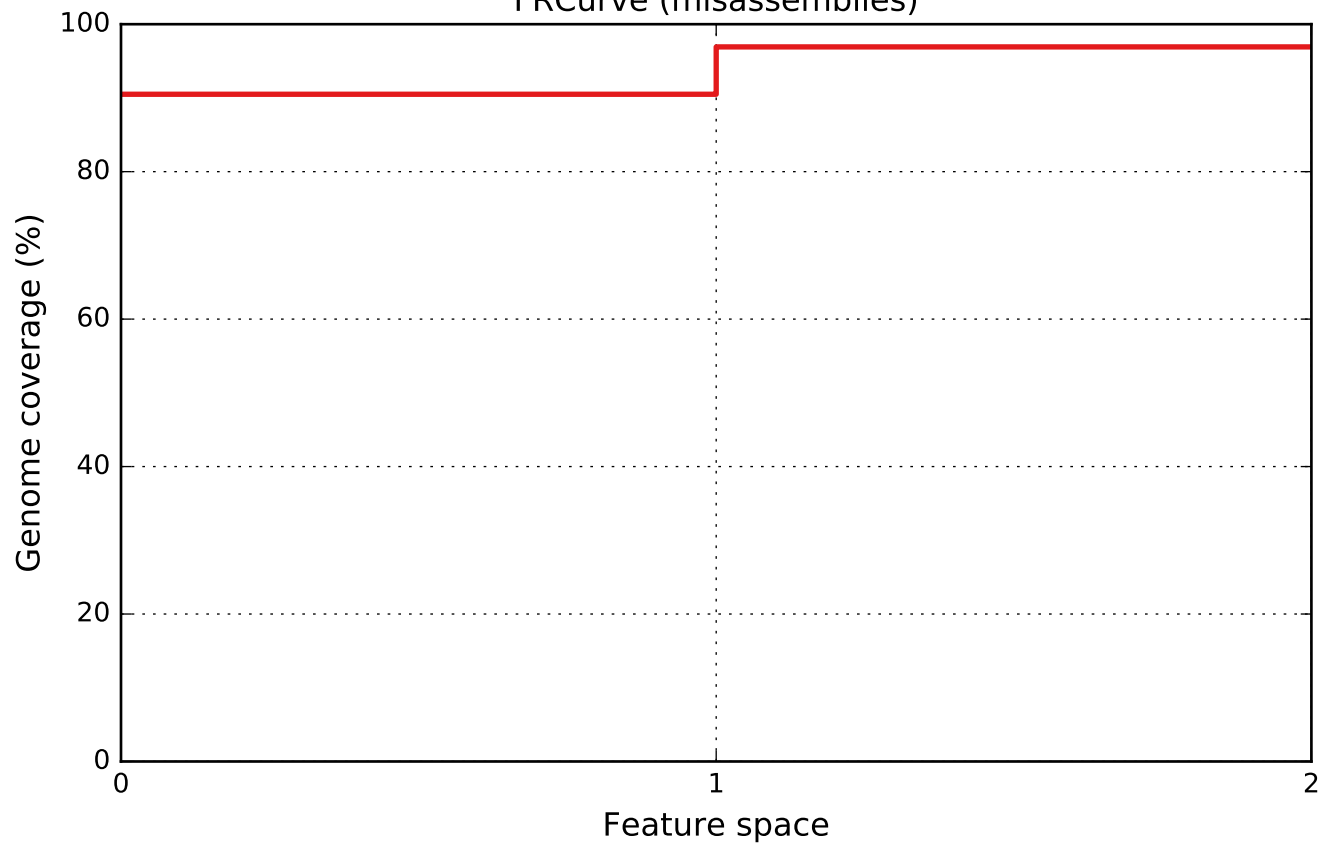
scaffolds coverage histogram (bin size: 1x)



scaffolds

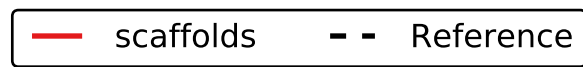
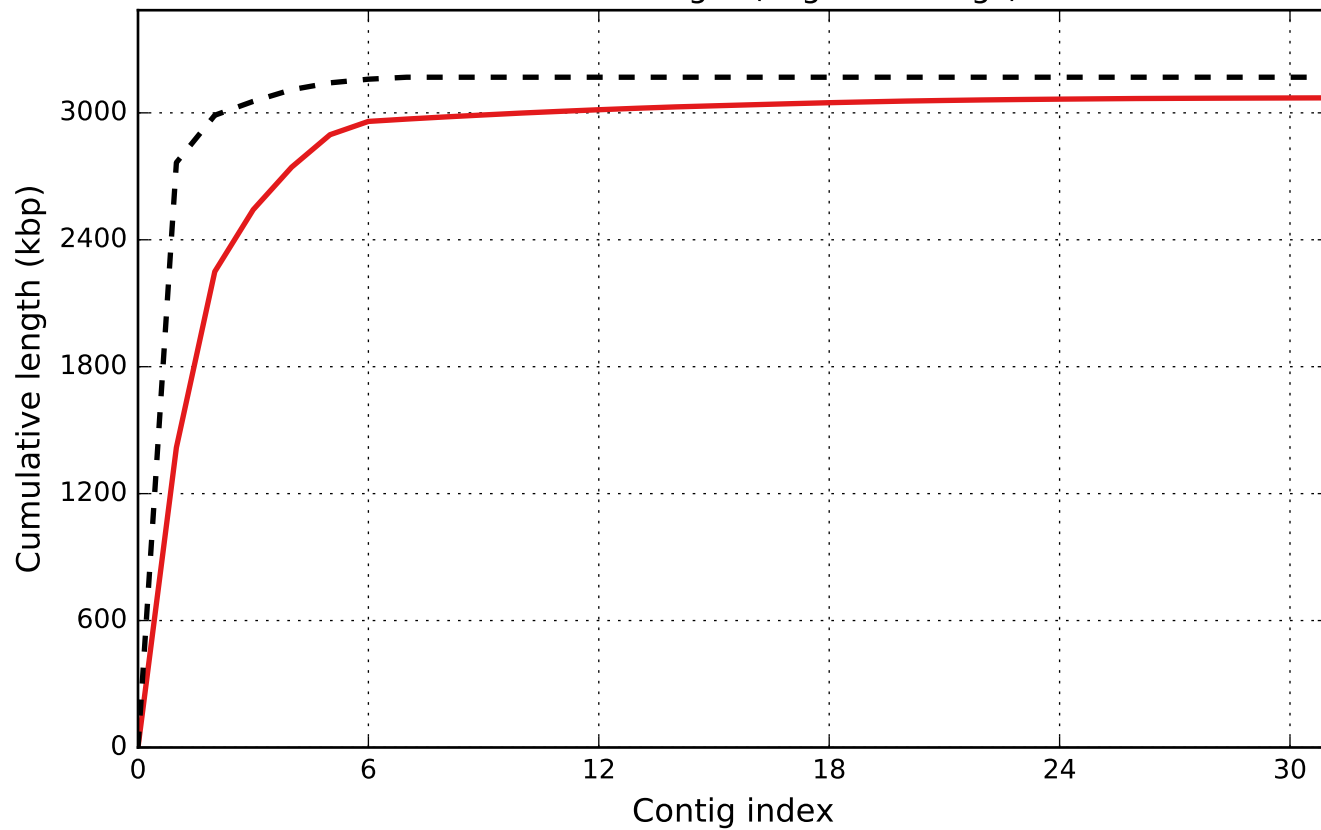


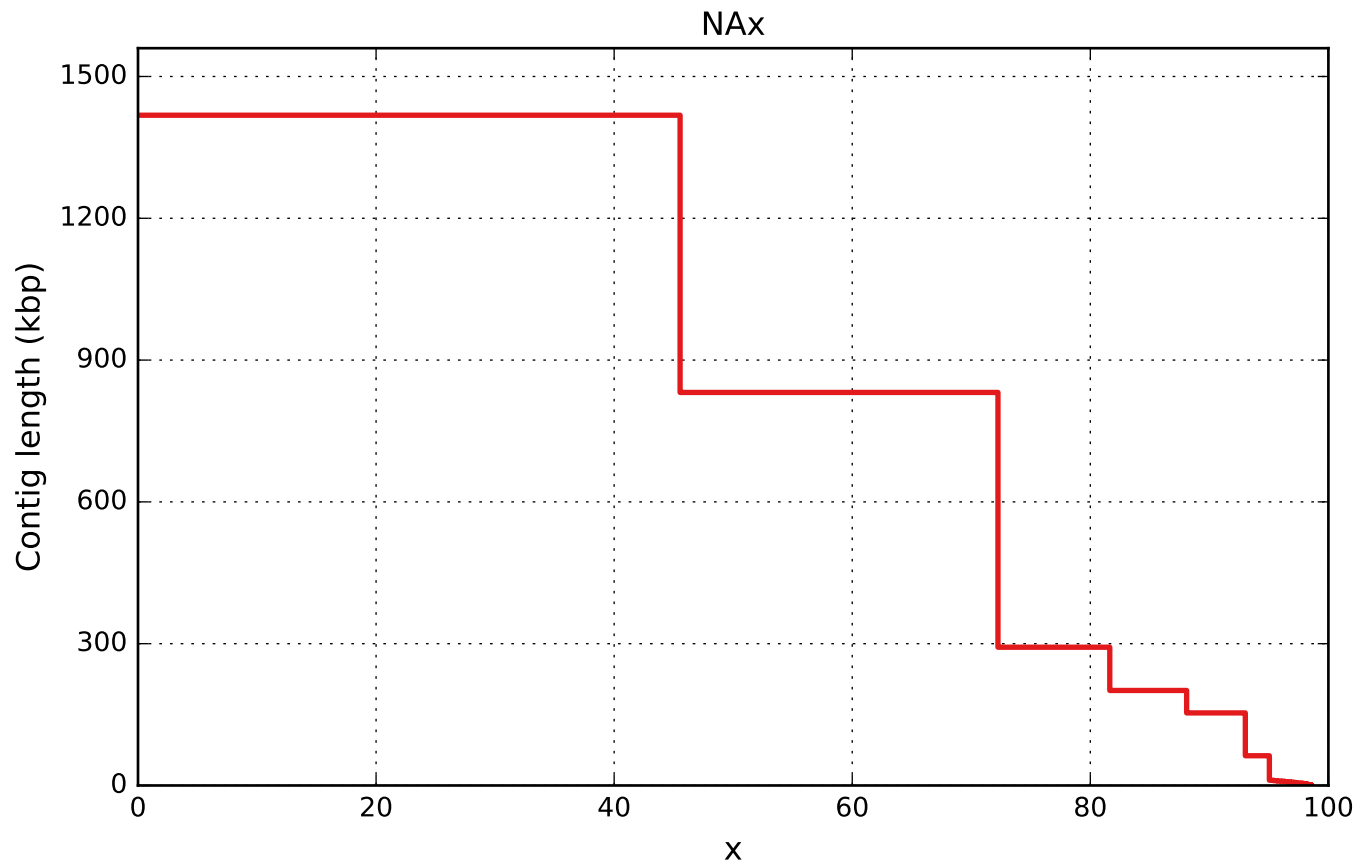
FRCurve (misassemblies)



— scaffolds

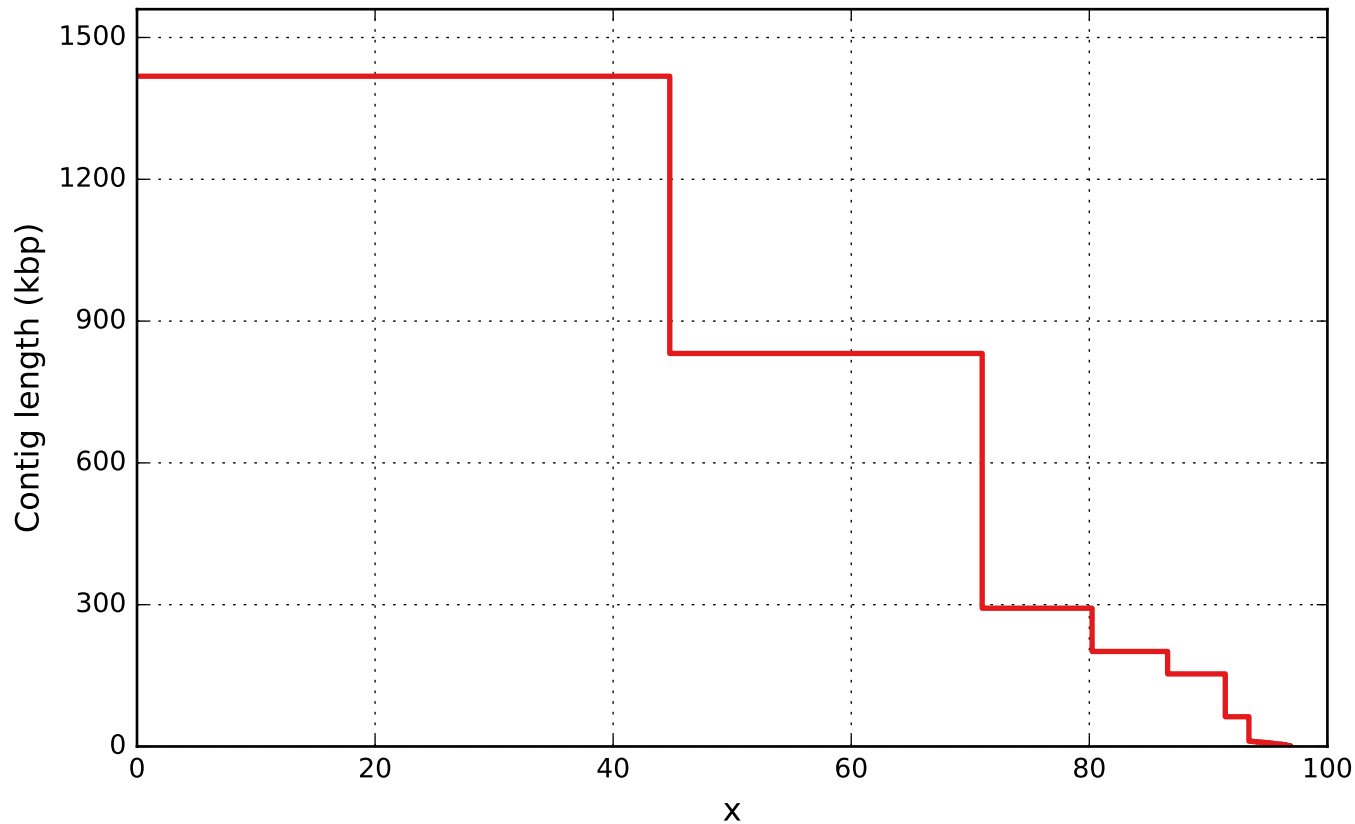
Cumulative length (aligned contigs)





— scaffolds

# NGAx



— scaffolds