

Report

	scaffolds
# contigs (≥ 0 bp)	71
# contigs (≥ 1000 bp)	18
# contigs (≥ 5000 bp)	16
# contigs (≥ 10000 bp)	14
# contigs (≥ 25000 bp)	13
# contigs (≥ 50000 bp)	10
Total length (≥ 0 bp)	3121385
Total length (≥ 1000 bp)	3111126
Total length (≥ 5000 bp)	3104566
Total length (≥ 10000 bp)	3089939
Total length (≥ 25000 bp)	3077556
Total length (≥ 50000 bp)	2985873
# contigs	19
Largest contig	711421
Total length	3111645
Reference length	2919198
GC (%)	37.65
Reference GC (%)	37.88
N50	485854
NG50	485854
N75	204006
NG75	245525
L50	3
LG50	3
L75	6
LG75	5
# misassemblies	178
# misassembled contigs	8
Misassembled contigs length	2718970
# local misassemblies	38
# scaffold gap ext. mis.	1
# scaffold gap loc. mis.	1
# unaligned mis. contigs	5
# unaligned contigs	5 + 14 part
Unaligned length	559967
Genome fraction (%)	84.244
Duplication ratio	1.038
# N's per 100 kbp	27.67
# mismatches per 100 kbp	390.85
# indels per 100 kbp	14.72
Largest alignment	137660
Total aligned length	2549641
NA50	24276
NGA50	26795
NA75	4045
NGA75	9362
LA50	31
LGA50	27
LA75	90
LGA75	69

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

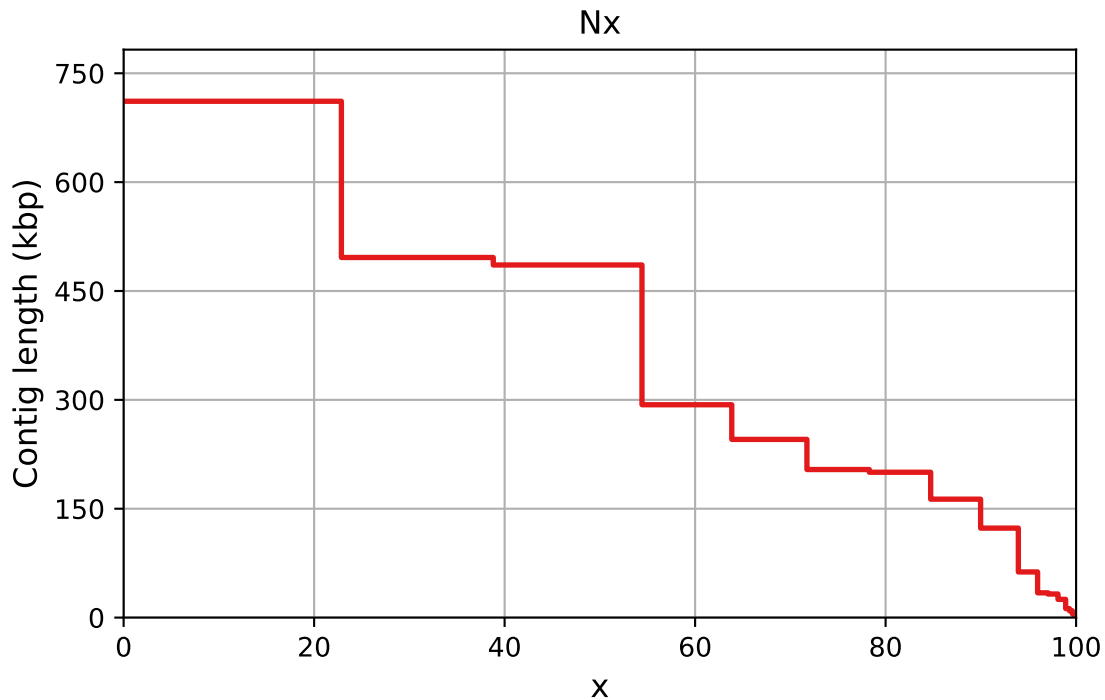
	scaffolds
# misassemblies	178
# contig misassemblies	177
# c. relocations	165
# c. translocations	9
# c. inversions	3
# scaffold misassemblies	1
# s. relocations	1
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	2718970
# local misassemblies	38
# scaffold gap ext. mis.	1
# scaffold gap loc. mis.	1
# unaligned mis. contigs	5
# mismatches	9612
# indels	362
# indels (<= 5 bp)	325
# indels (> 5 bp)	37
Indels length	1446

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

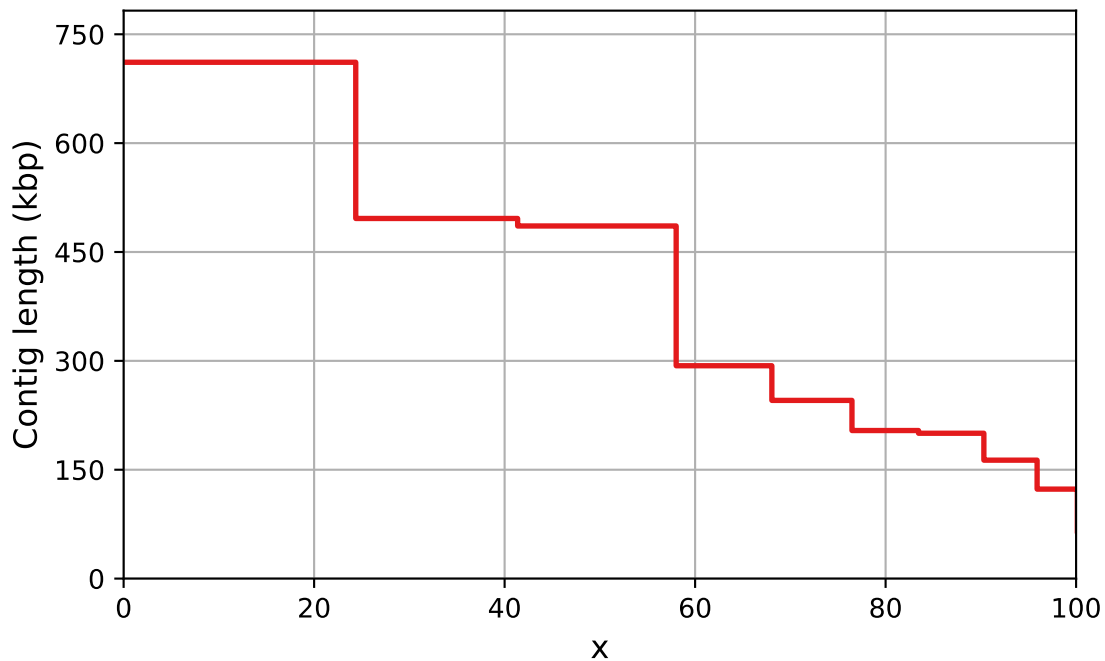
	scaffolds
# fully unaligned contigs	5
Fully unaligned length	21706
# partially unaligned contigs	14
Partially unaligned length	538261
# N's	861

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).



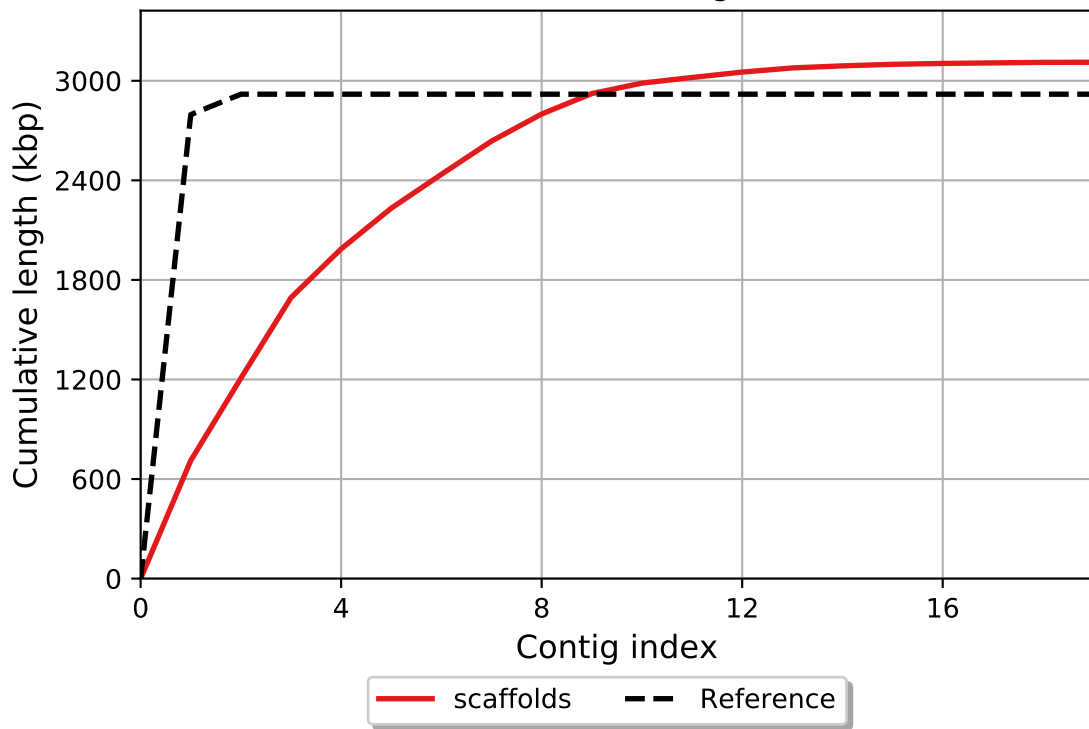
— scaffolds

NGx

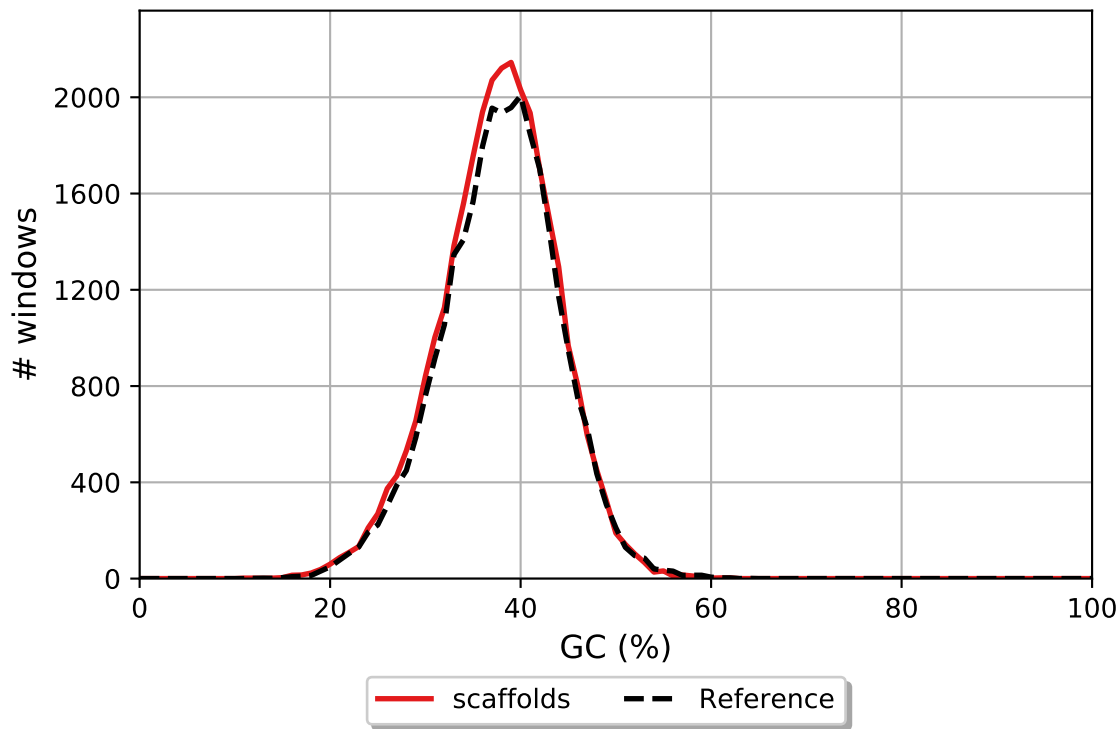


— scaffolds

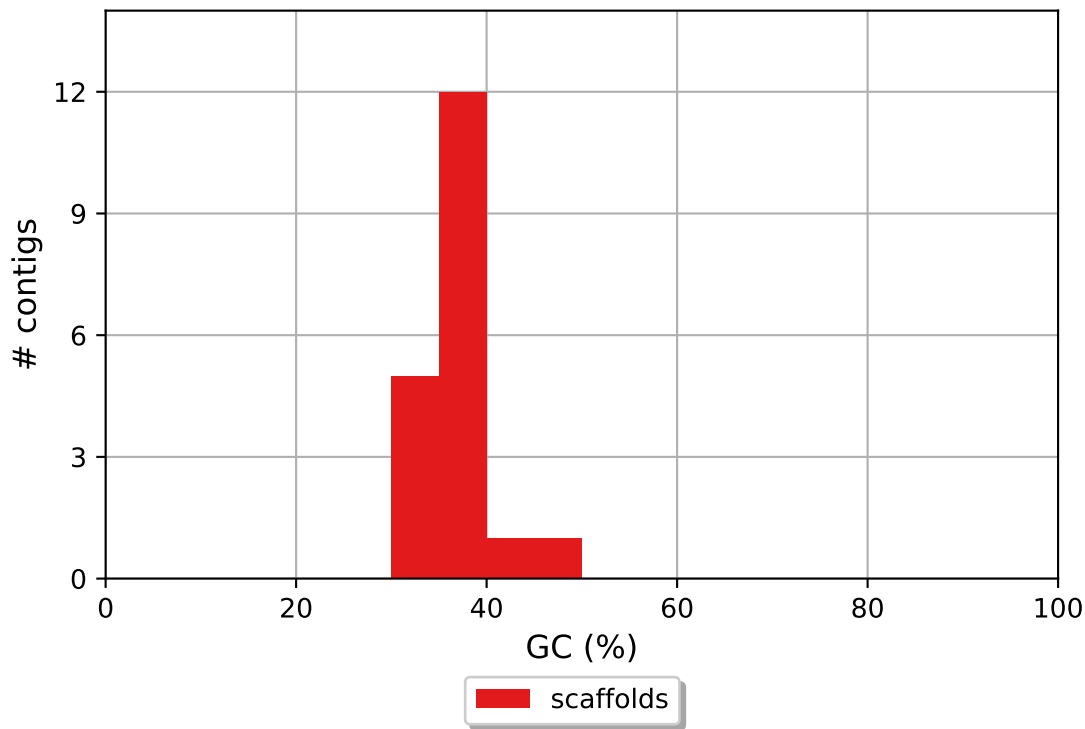
Cumulative length



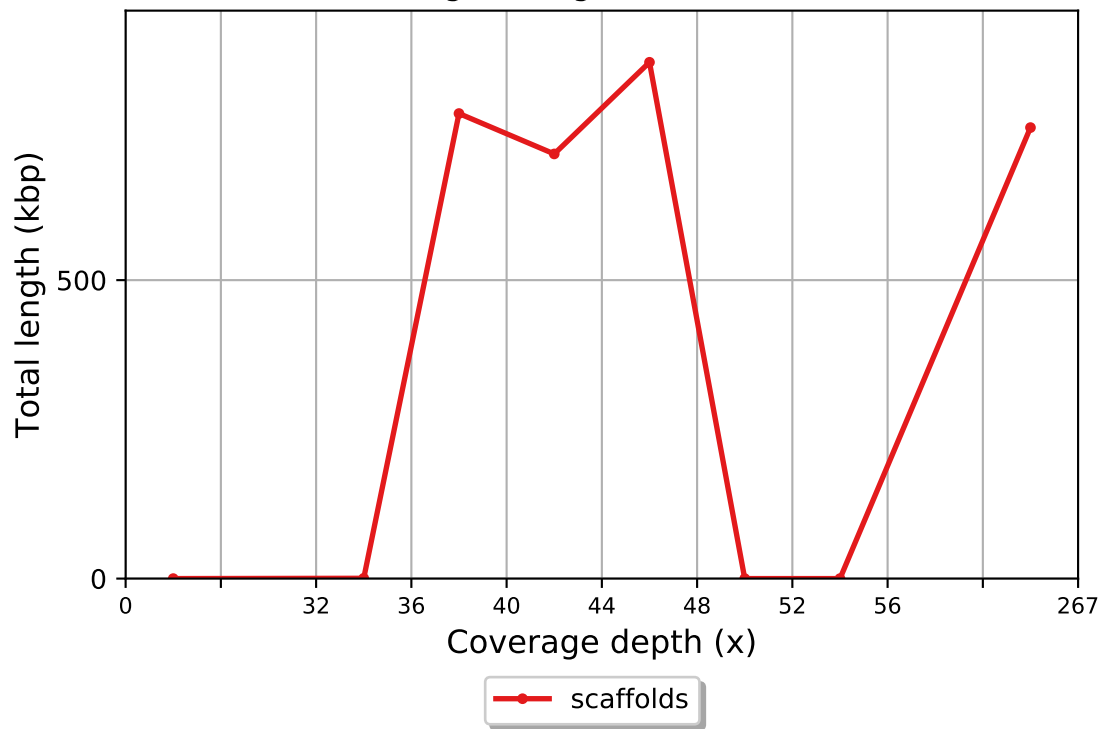
GC content



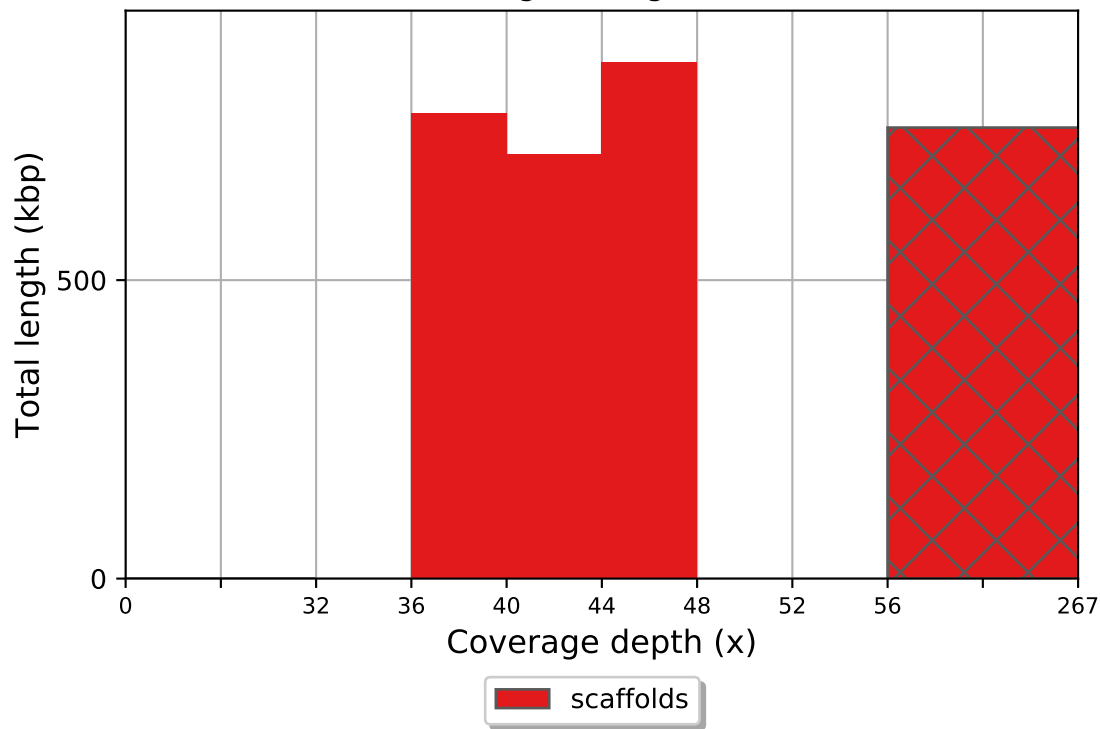
scaffolds GC content



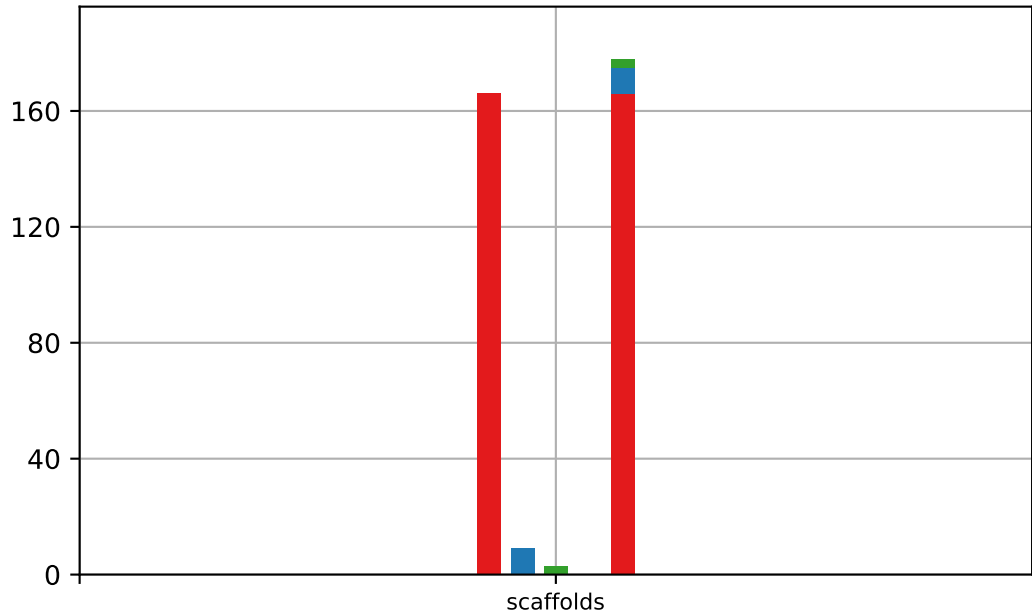
Coverage histogram (bin size: 4x)



scaffolds coverage histogram (bin size: 4x)



Misassemblies



relocations

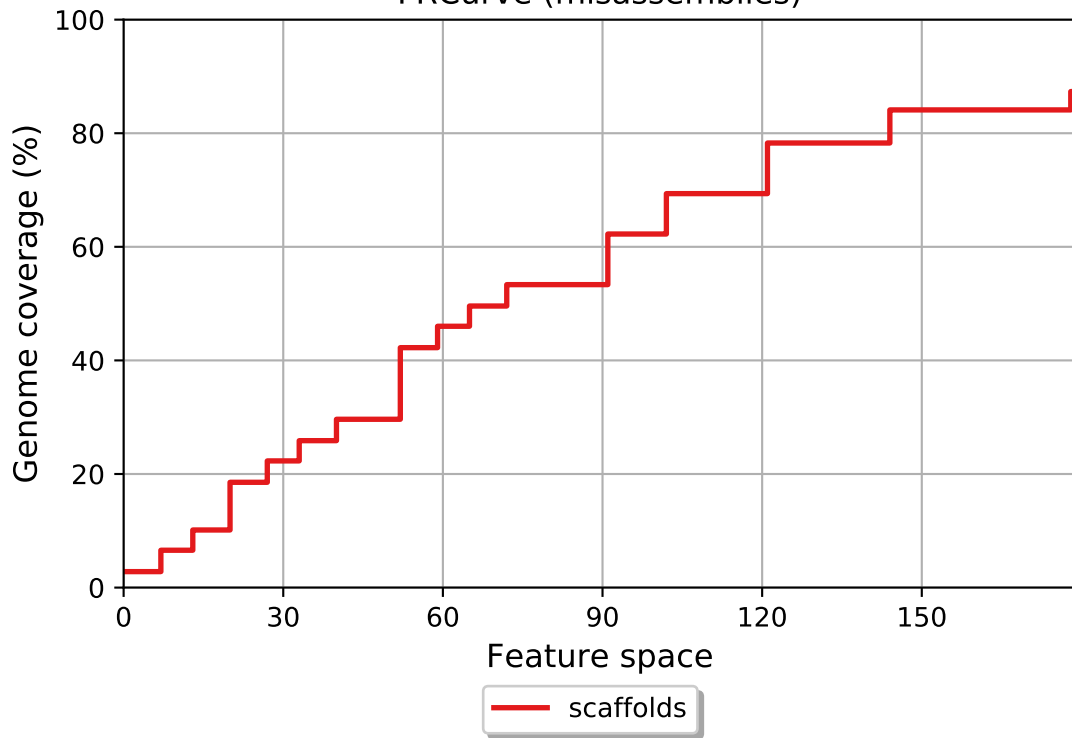


translocations

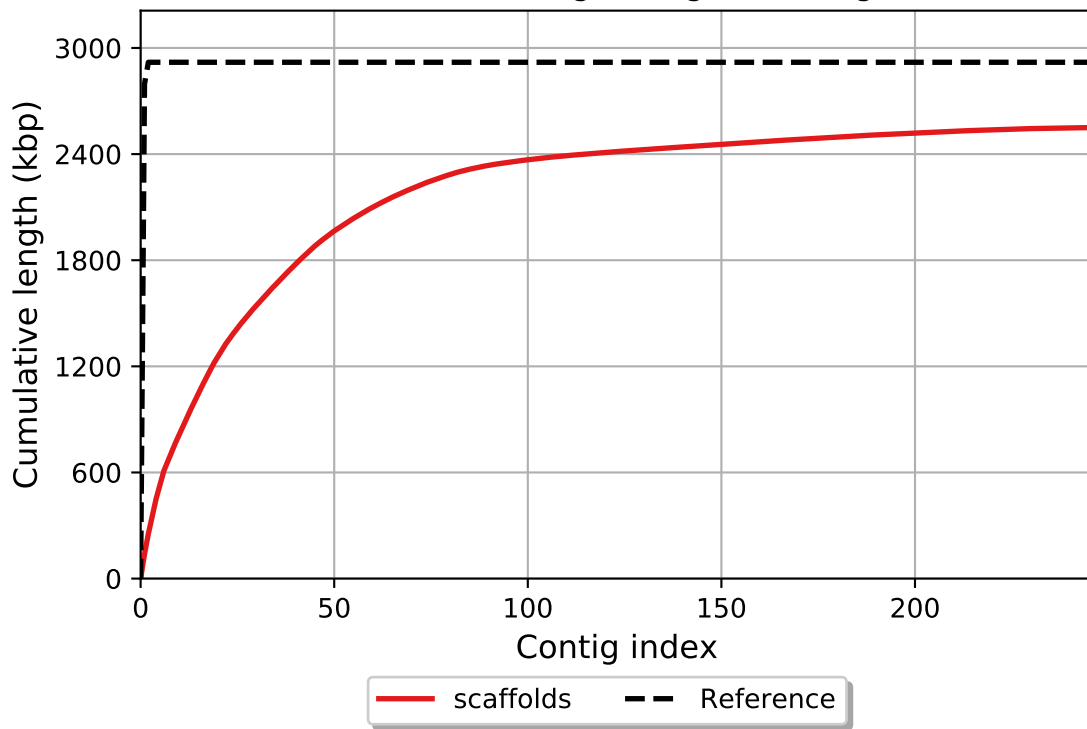


inversions

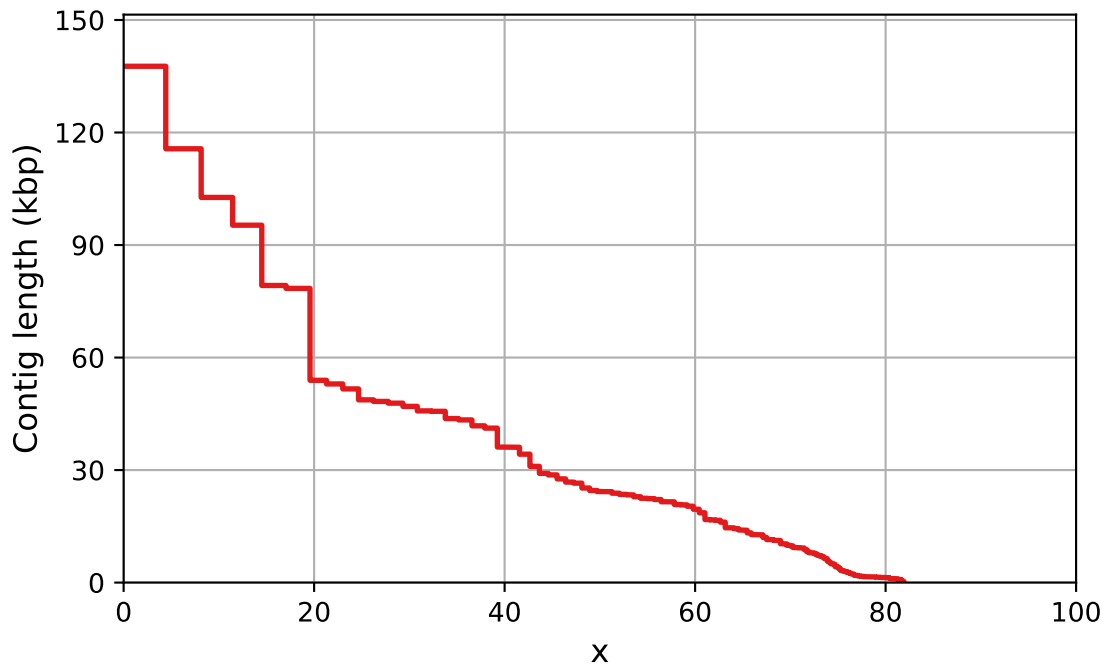
FRCurve (misassemblies)



Cumulative length (aligned contigs)

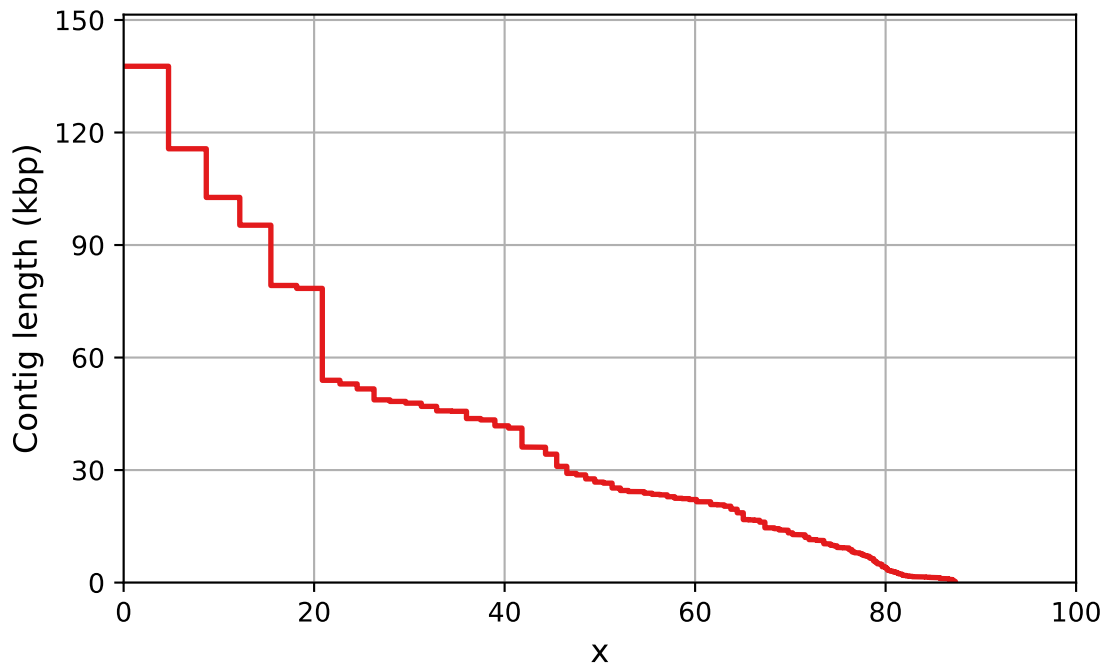


NAx



— scaffolds

NGAx



— scaffolds