

Report

	contigs
# contigs (>= 0 bp)	474
# contigs (>= 1000 bp)	162
# contigs (>= 5000 bp)	91
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	2976324
Total length (>= 1000 bp)	2910007
Total length (>= 5000 bp)	2735728
Total length (>= 10000 bp)	2559150
Total length (>= 25000 bp)	2008803
Total length (>= 50000 bp)	1402695
# contigs	191
Largest contig	114283
Total length	2929089
Reference length	2919198
GC (%)	37.64
Reference GC (%)	37.88
N50	49767
NG50	49767
N75	19960
NG75	20562
L50	19
LG50	19
L75	43
LG75	42
# misassemblies	70
# misassembled contigs	42
Misassembled contigs length	1909199
# local misassemblies	29
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	67 + 42 part
Unaligned length	538779
Genome fraction (%)	81.566
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	359.33
# indels per 100 kbp	13.90
Largest alignment	78437
Total aligned length	2383583
NA50	23387
NGA50	23387
NA75	7355
NGA75	7688
LA50	36
LGA50	36
LA75	88
LGA75	87

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

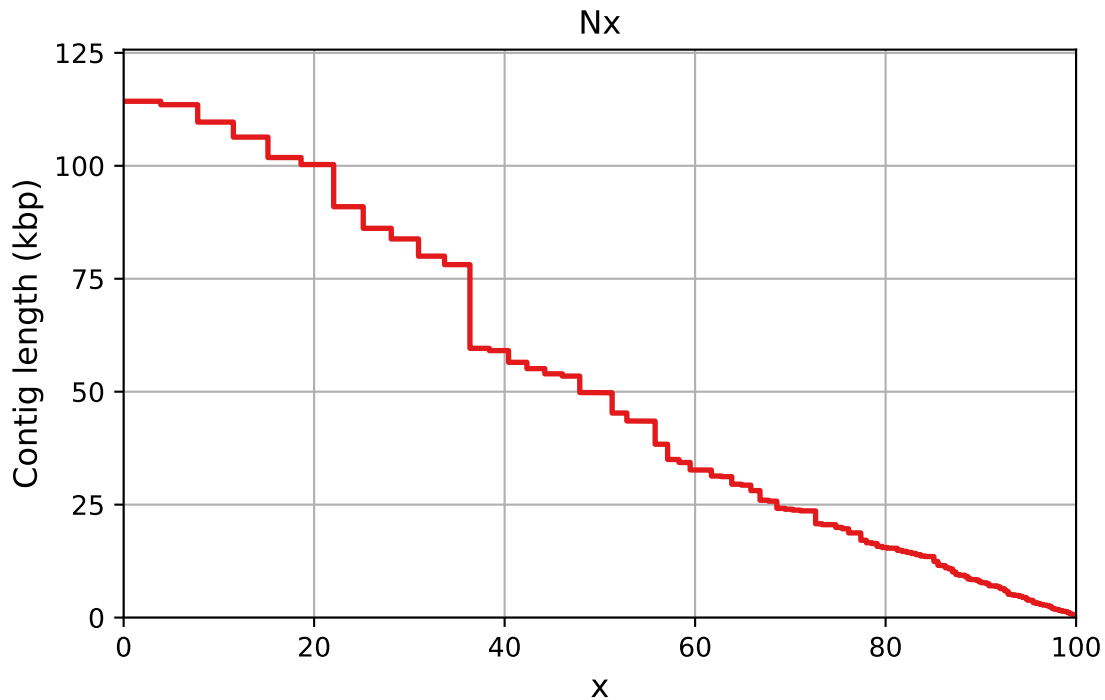
	contigs
# misassemblies	70
# contig misassemblies	70
# c. relocations	69
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	42
Misassembled contigs length	1909199
# local misassemblies	29
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	8556
# indels	331
# indels (<= 5 bp)	298
# indels (> 5 bp)	33
Indels length	1273

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

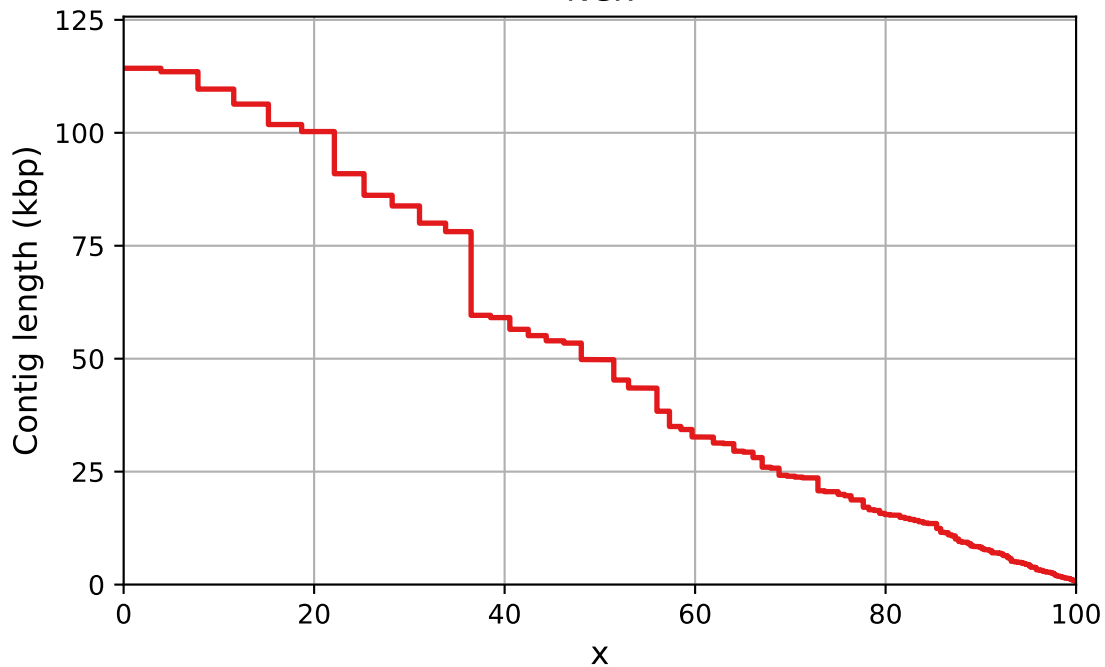
	contigs
# fully unaligned contigs	67
Fully unaligned length	250118
# partially unaligned contigs	42
Partially unaligned length	288661
# N's	0

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).



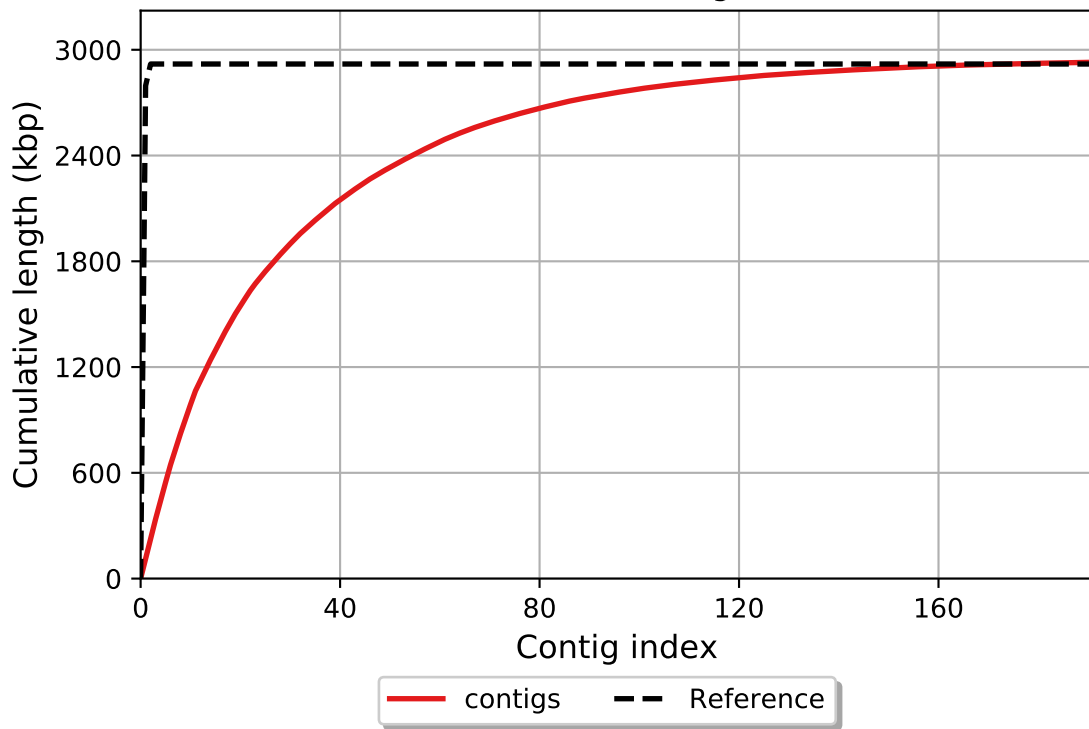
contigs

NGx

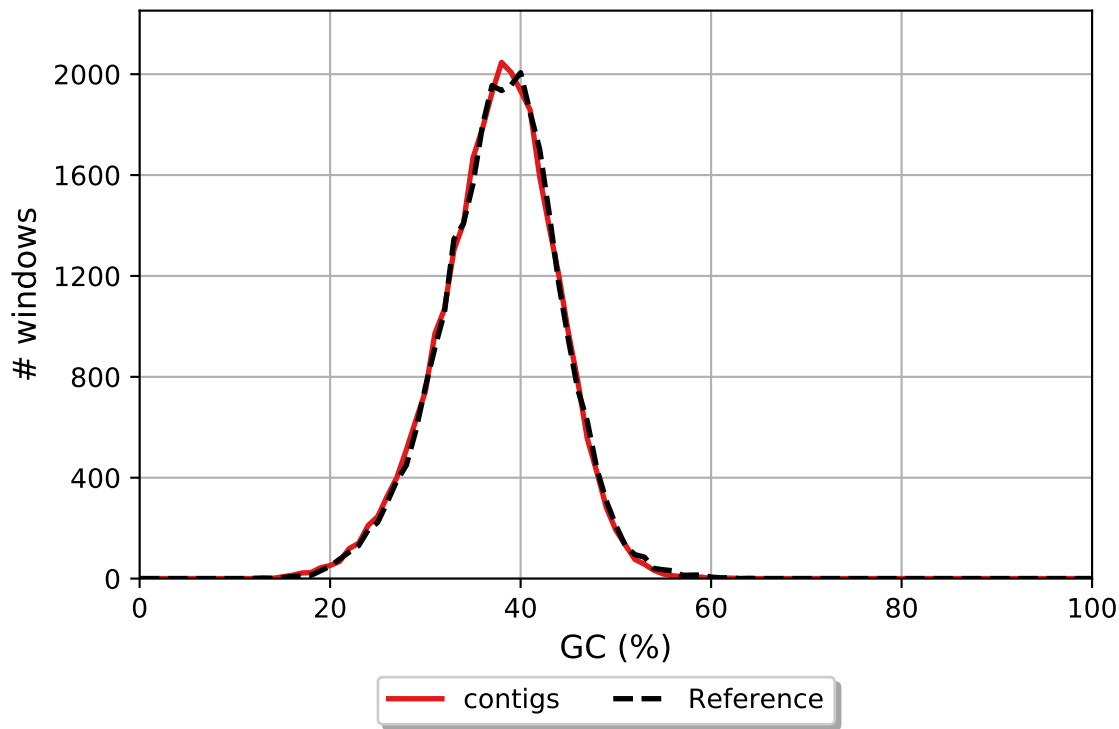


contigs

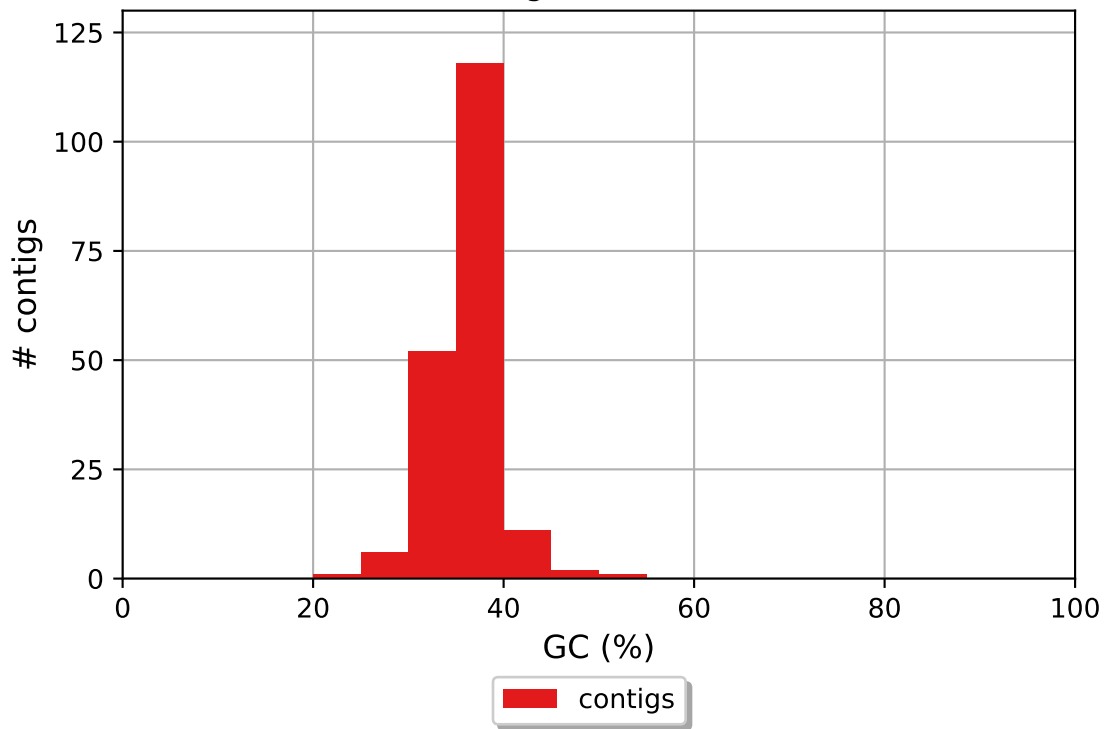
Cumulative length



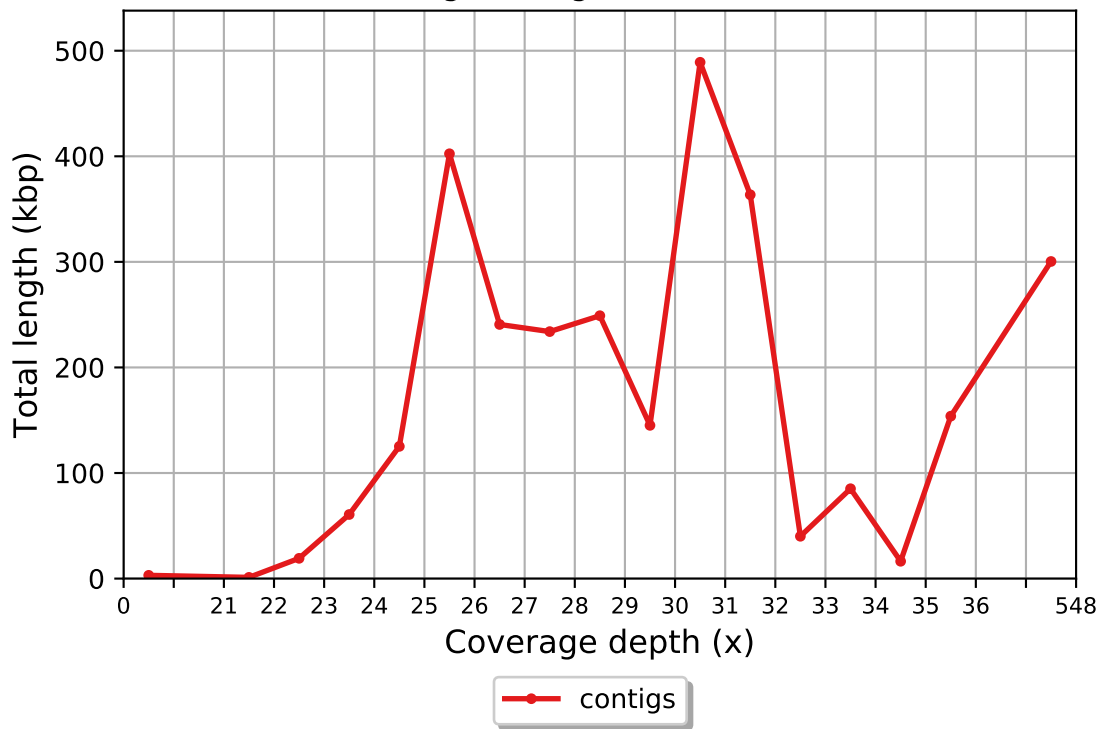
GC content



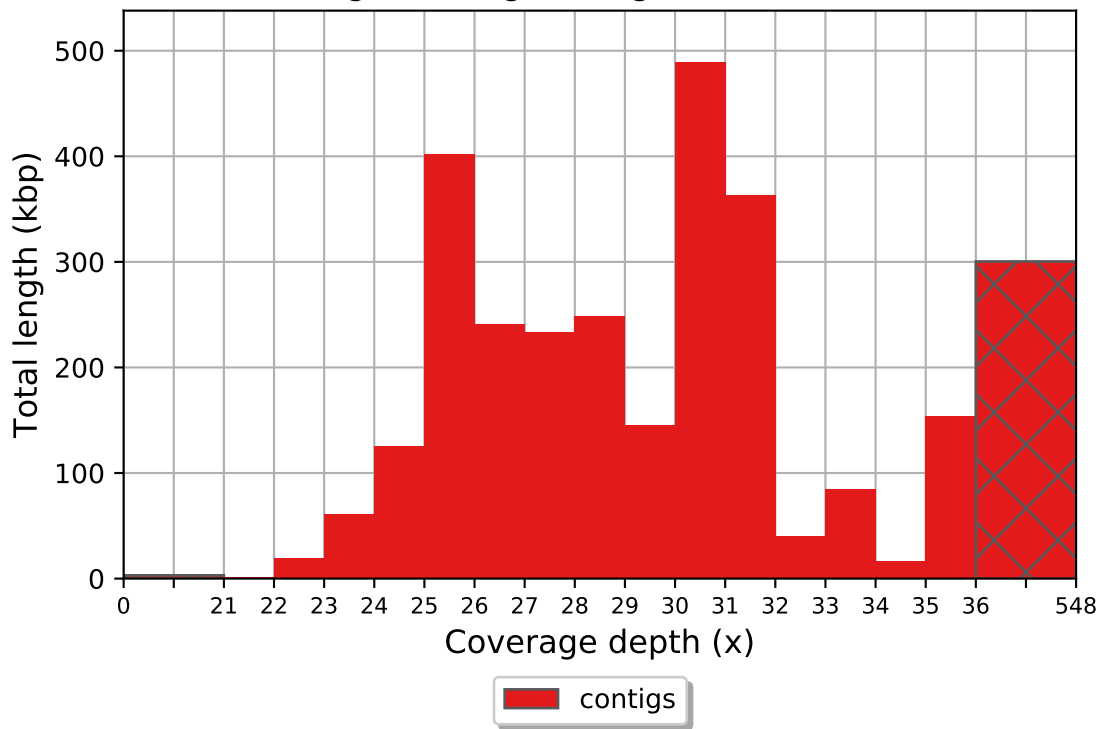
contigs GC content



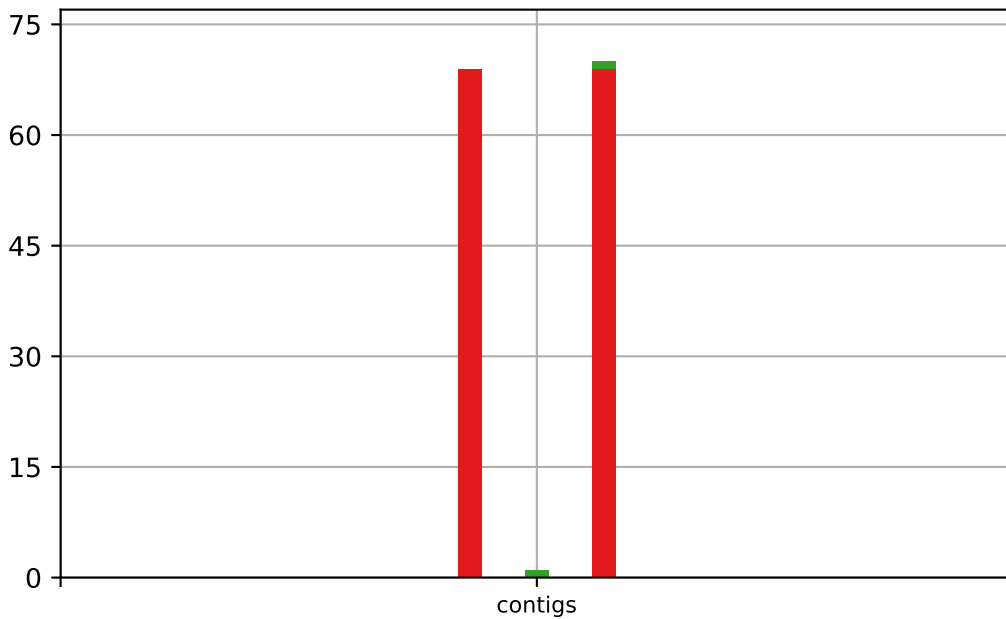
Coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)



Misassemblies

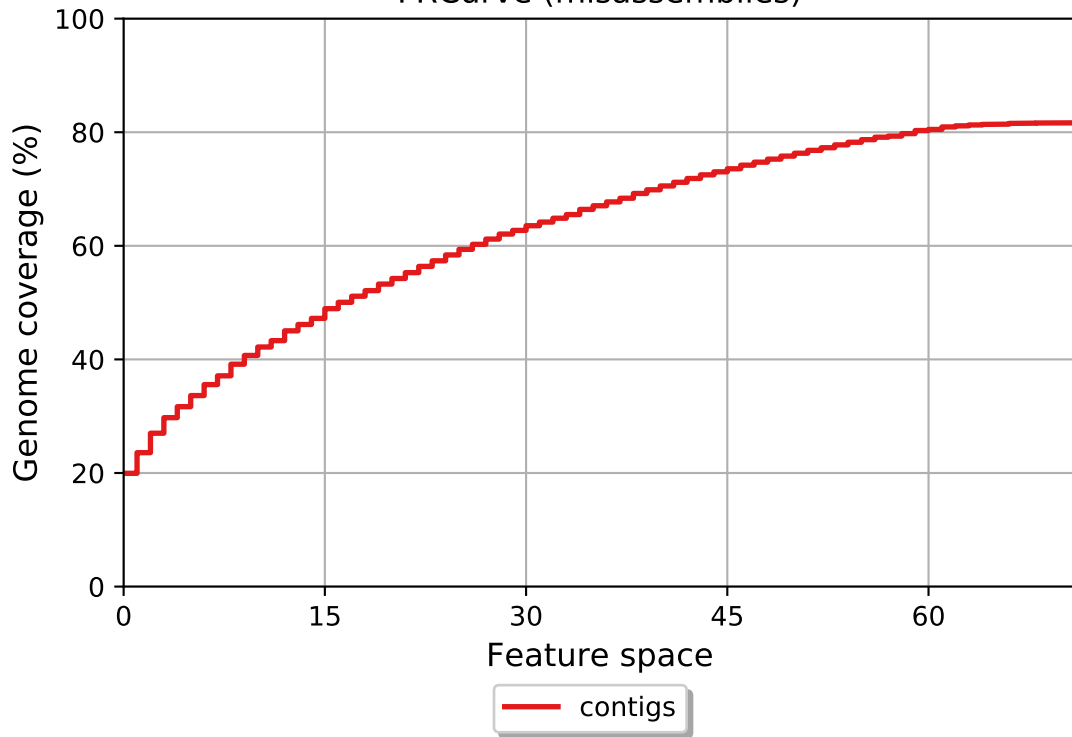


relocations

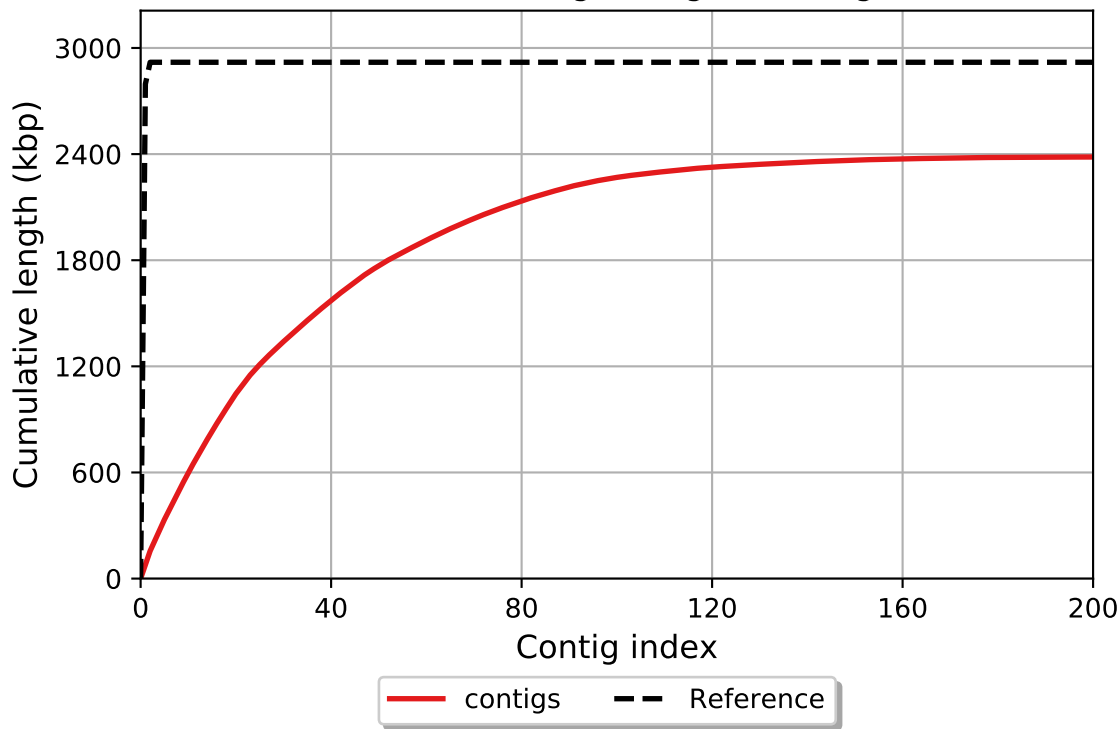


inversions

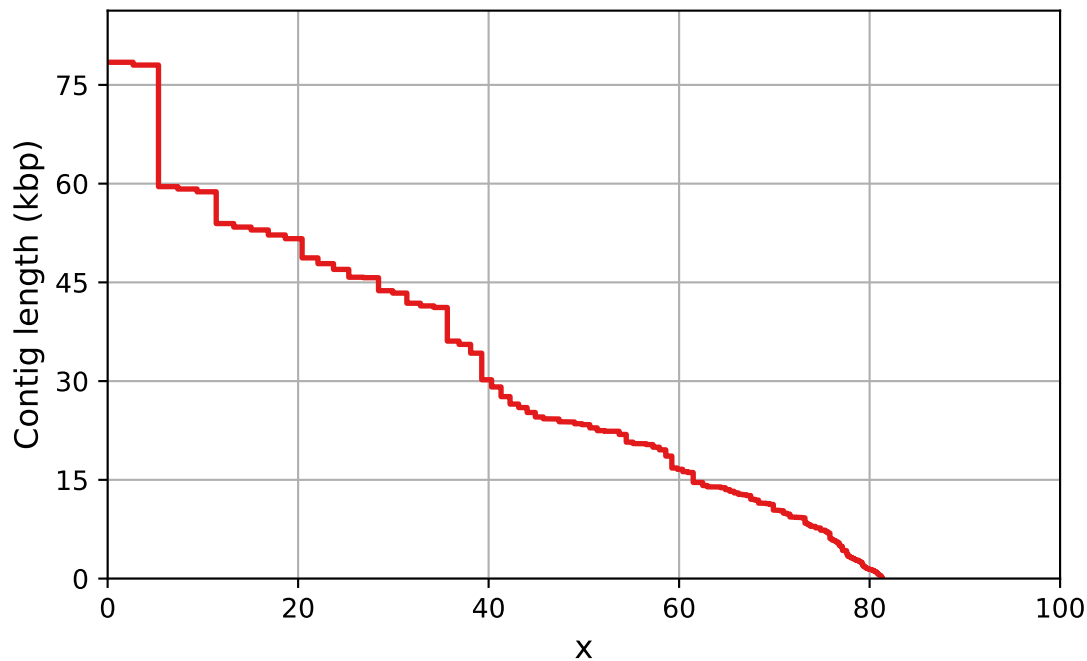
FRCurve (misassemblies)



Cumulative length (aligned contigs)

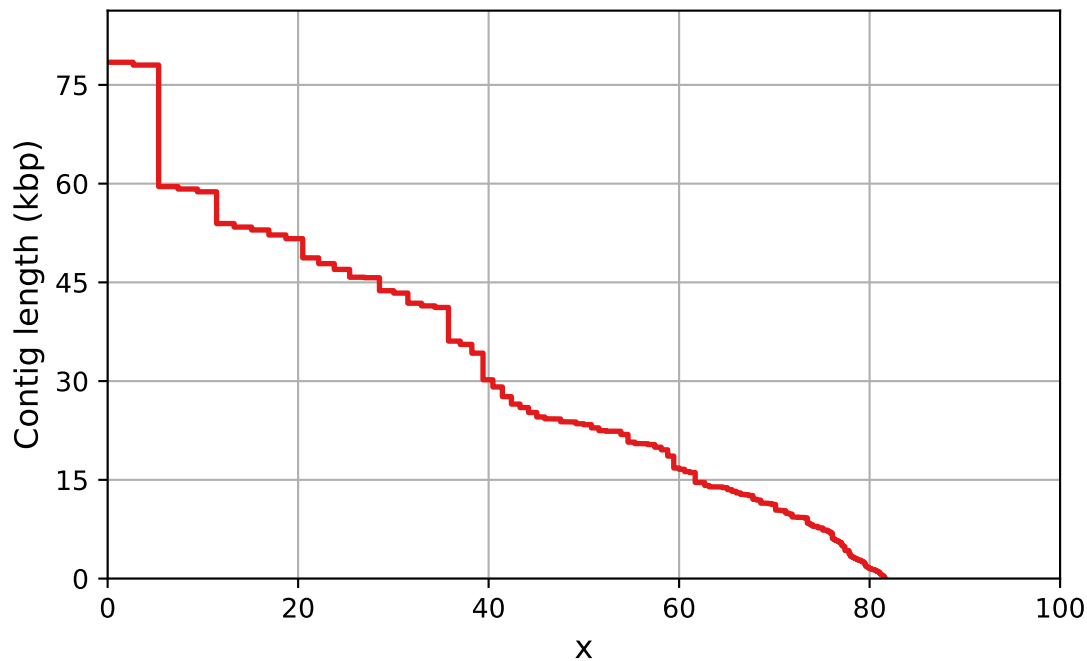


NAx



— contigs

NGAx



— contigs