

Report

	contigs
# contigs (≥ 0 bp)	93
# contigs (≥ 1000 bp)	35
# contigs (≥ 5000 bp)	30
# contigs (≥ 10000 bp)	26
# contigs (≥ 25000 bp)	24
# contigs (≥ 50000 bp)	16
Total length (≥ 0 bp)	3120505
Total length (≥ 1000 bp)	3108348
Total length (≥ 5000 bp)	3094555
Total length (≥ 10000 bp)	3063664
Total length (≥ 25000 bp)	3023149
Total length (≥ 50000 bp)	2779505
# contigs	38
Largest contig	522651
Total length	3110131
Reference length	2919198
GC (%)	37.58
Reference GC (%)	37.88
N50	161982
NG50	270437
N75	117395
NG75	123278
L50	5
LG50	4
L75	10
LG75	9
# misassemblies	167
# misassembled contigs	17
Misassembled contigs length	2652852
# local misassemblies	38
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	8 + 23 part
Unaligned length	572038
Genome fraction (%)	83.922
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	395.41
# indels per 100 kbp	19.14
Largest alignment	137660
Total aligned length	2537443
NA50	23522
NGA50	24553
NA75	3158
NGA75	9304
LA50	34
LGA50	30
LA75	98
LGA75	75

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

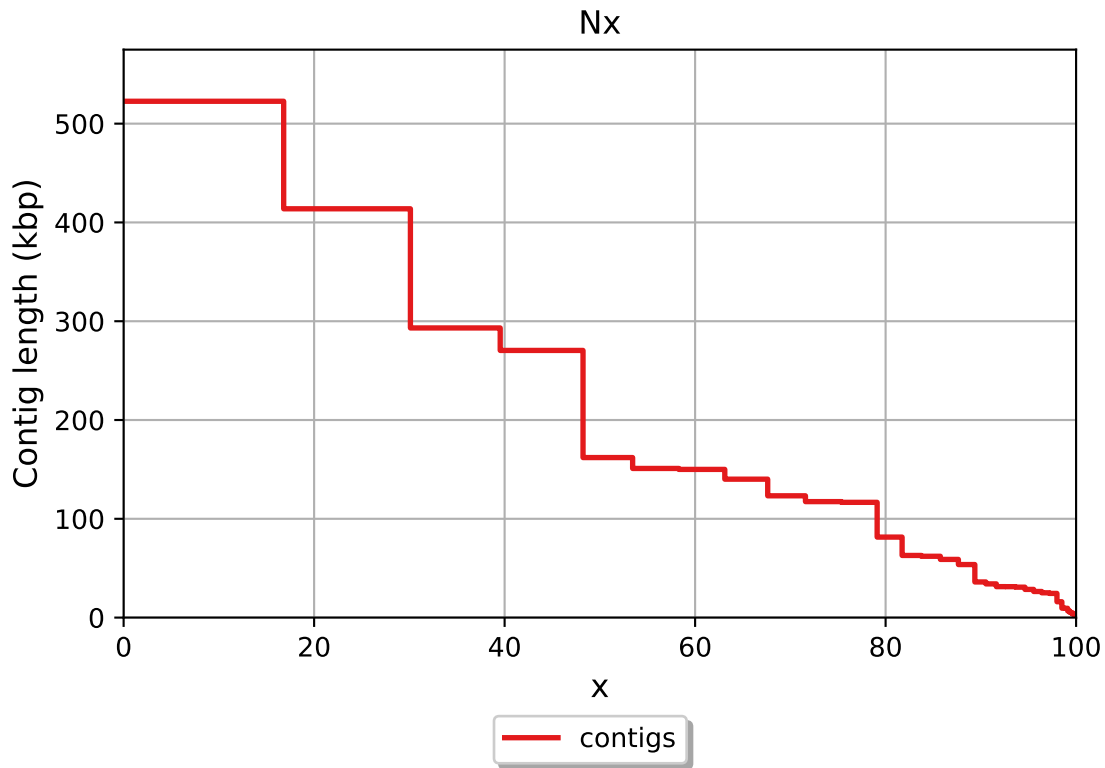
	contigs
# misassemblies	167
# contig misassemblies	167
# c. relocations	156
# c. translocations	8
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	17
Misassembled contigs length	2652852
# local misassemblies	38
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	9687
# indels	469
# indels (<= 5 bp)	430
# indels (> 5 bp)	39
Indels length	1632

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).

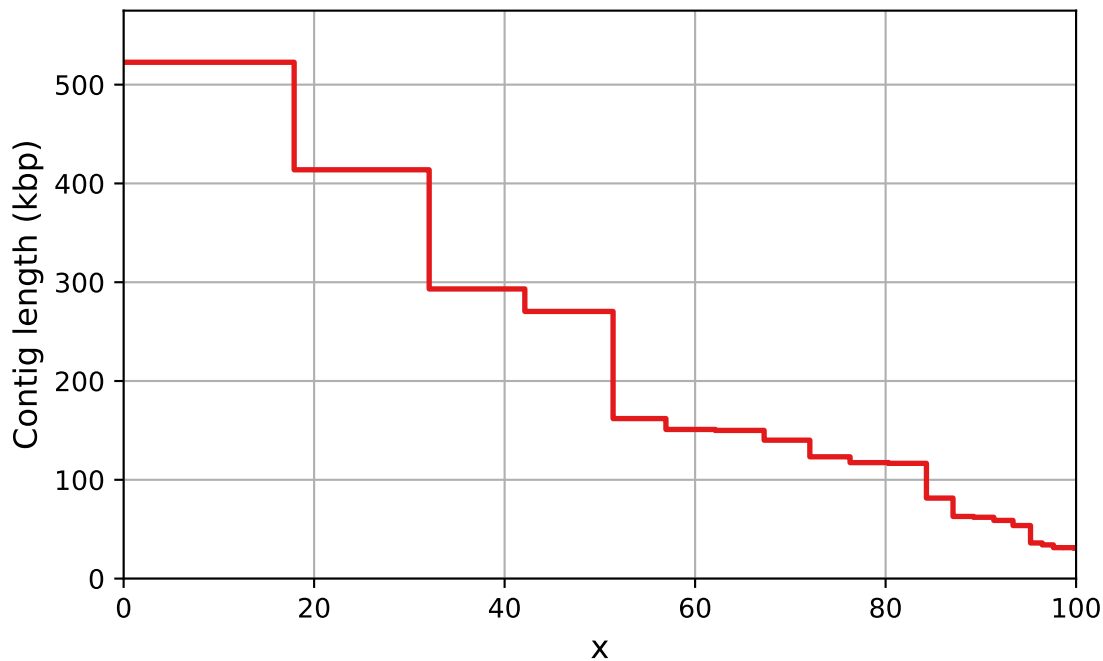
Unaligned report

	contigs
# fully unaligned contigs	8
Fully unaligned length	31981
# partially unaligned contigs	23
Partially unaligned length	540057
# N's	0

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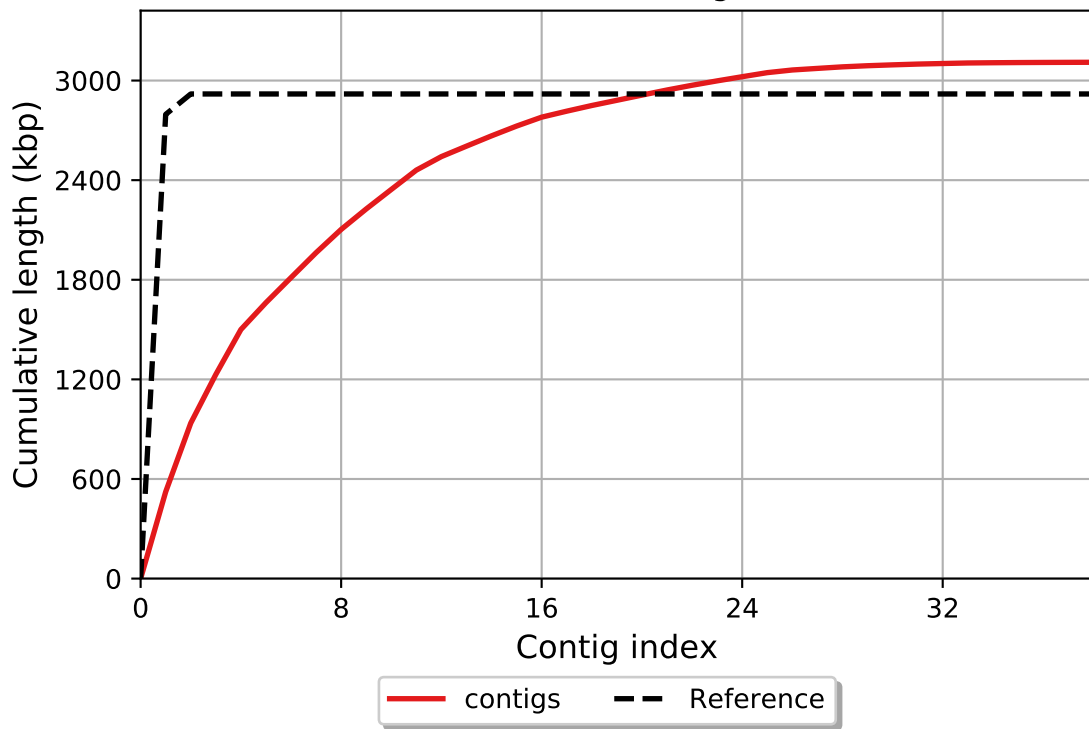


NGx

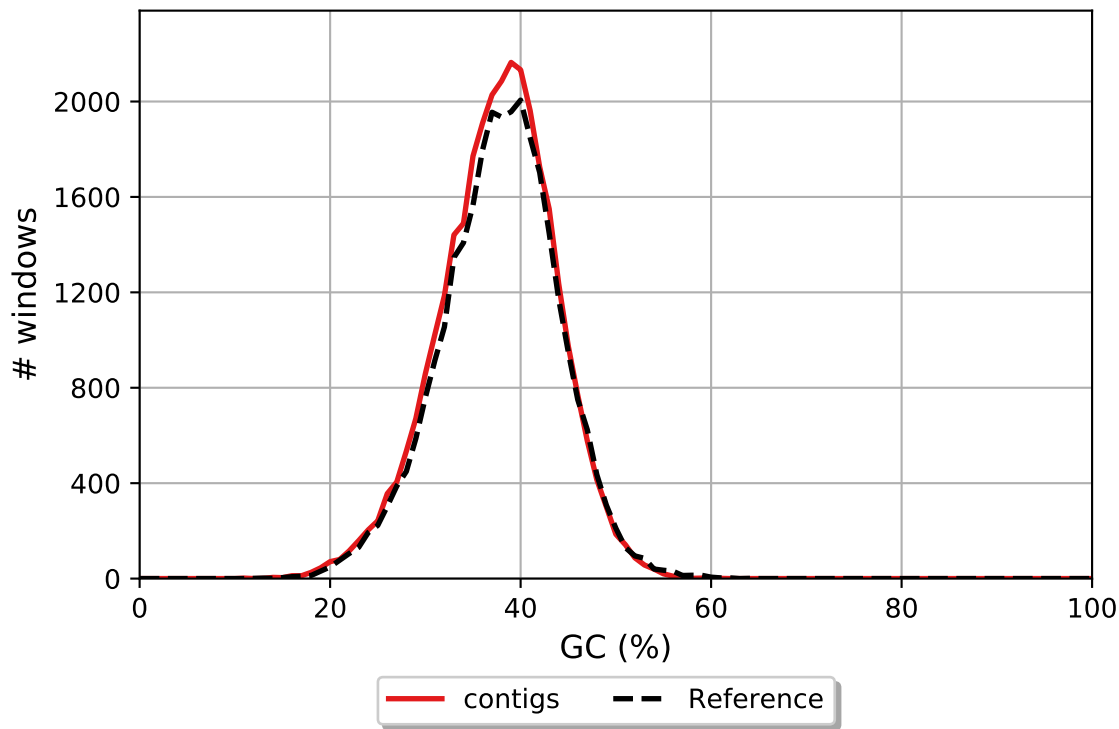


contigs

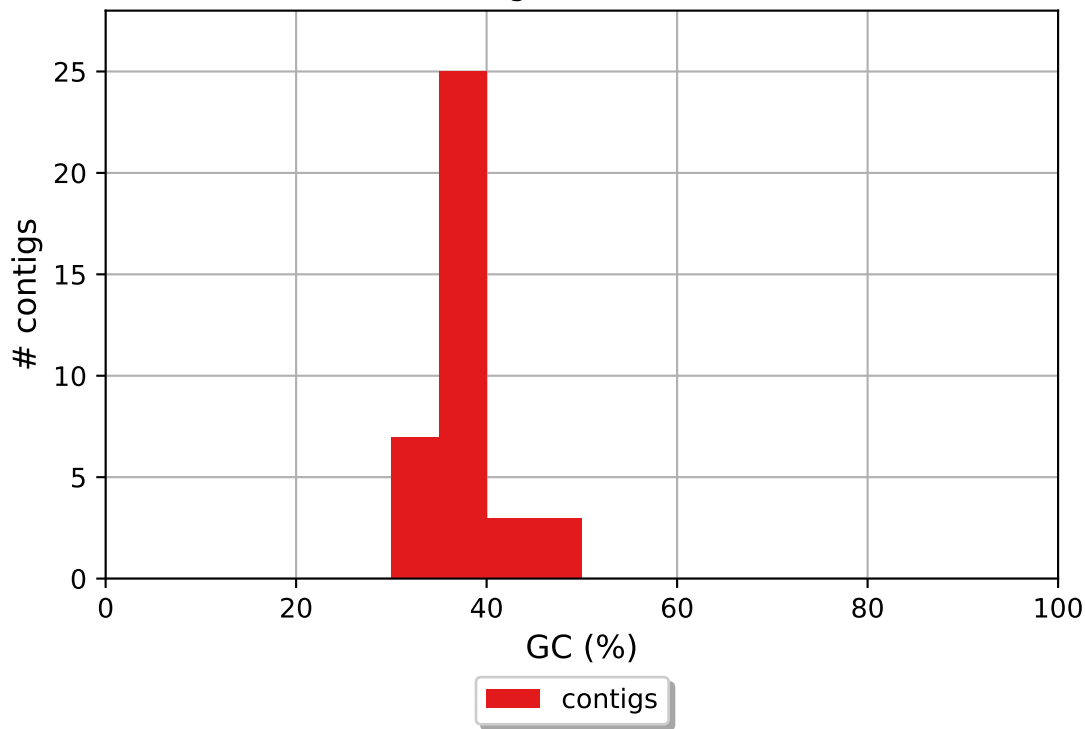
Cumulative length



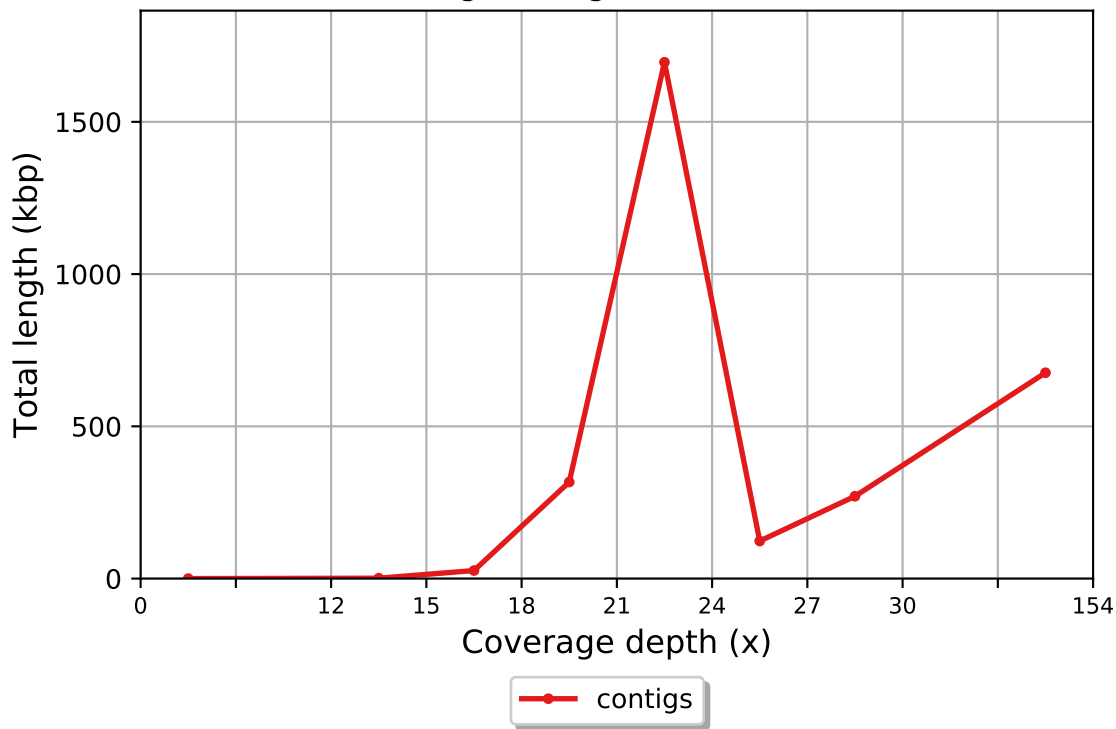
GC content



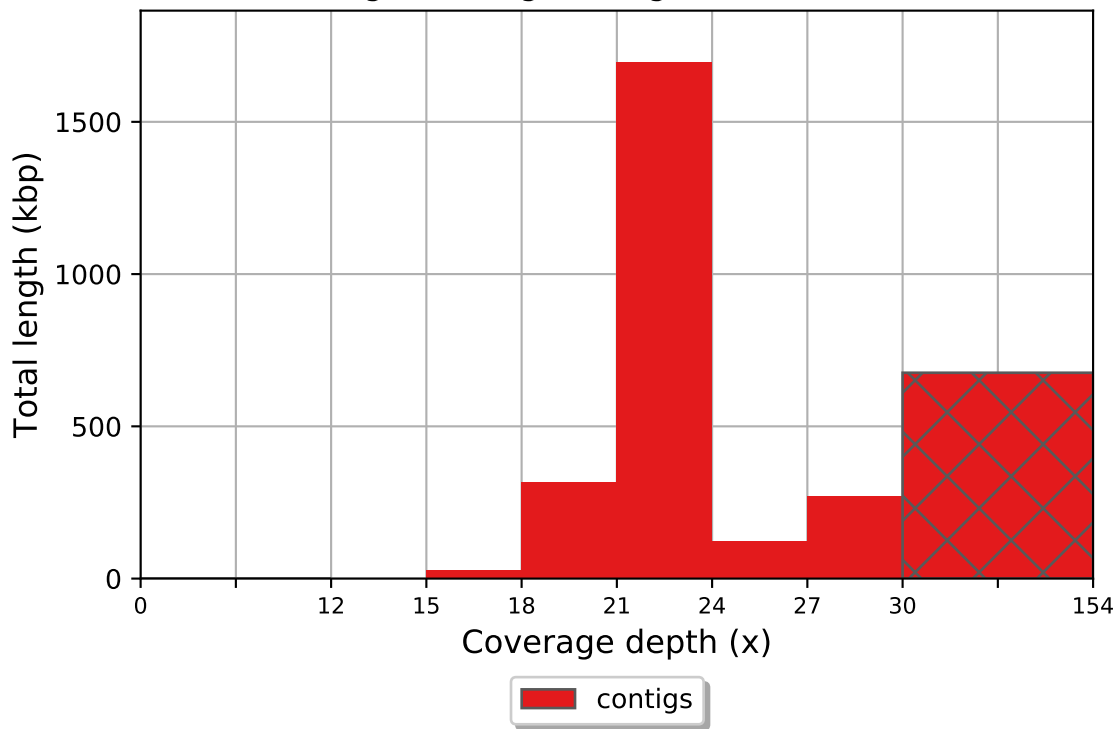
contigs GC content



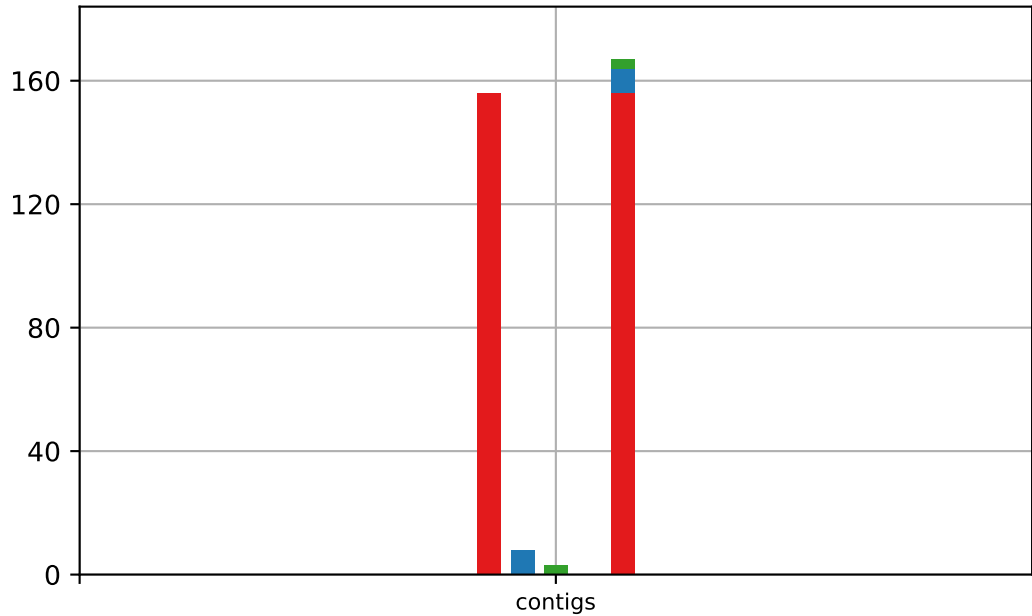
Coverage histogram (bin size: 3x)



contigs coverage histogram (bin size: 3x)



Misassemblies



relocations

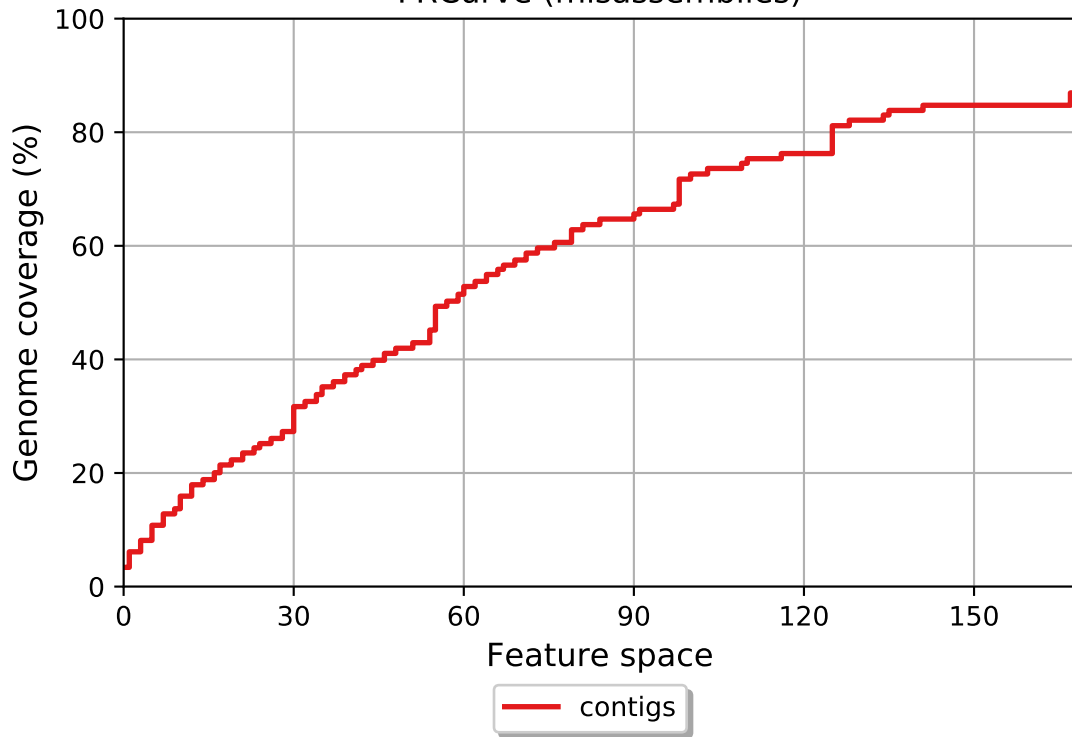


translocations

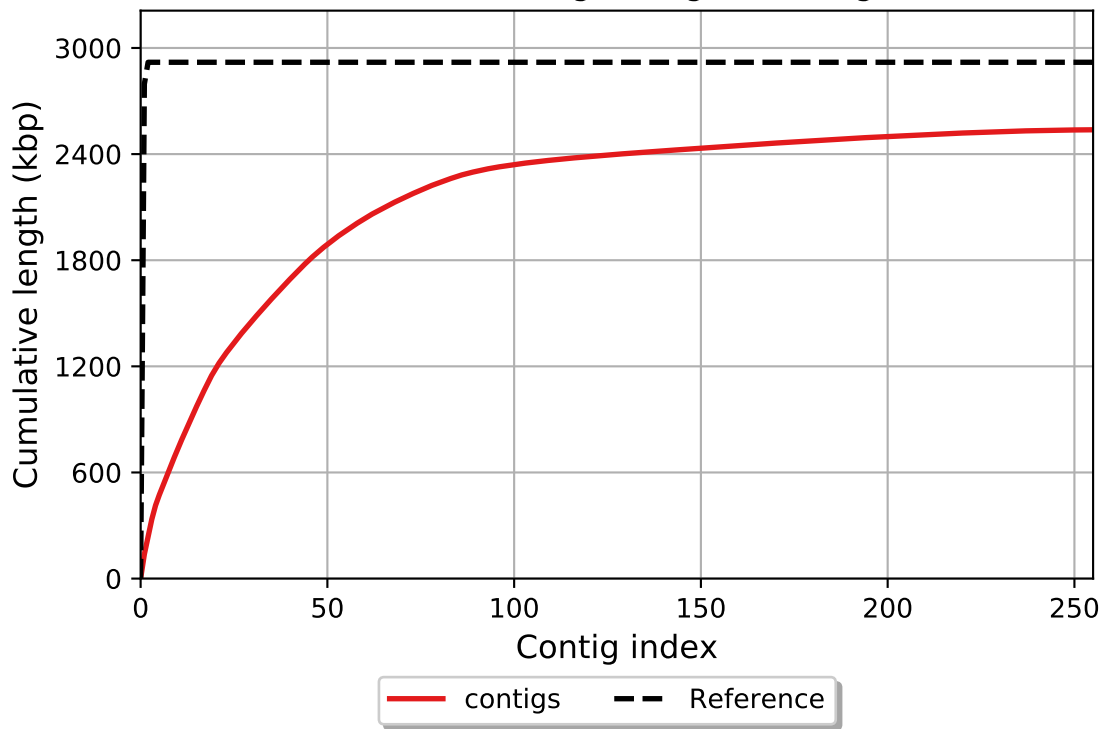


inversions

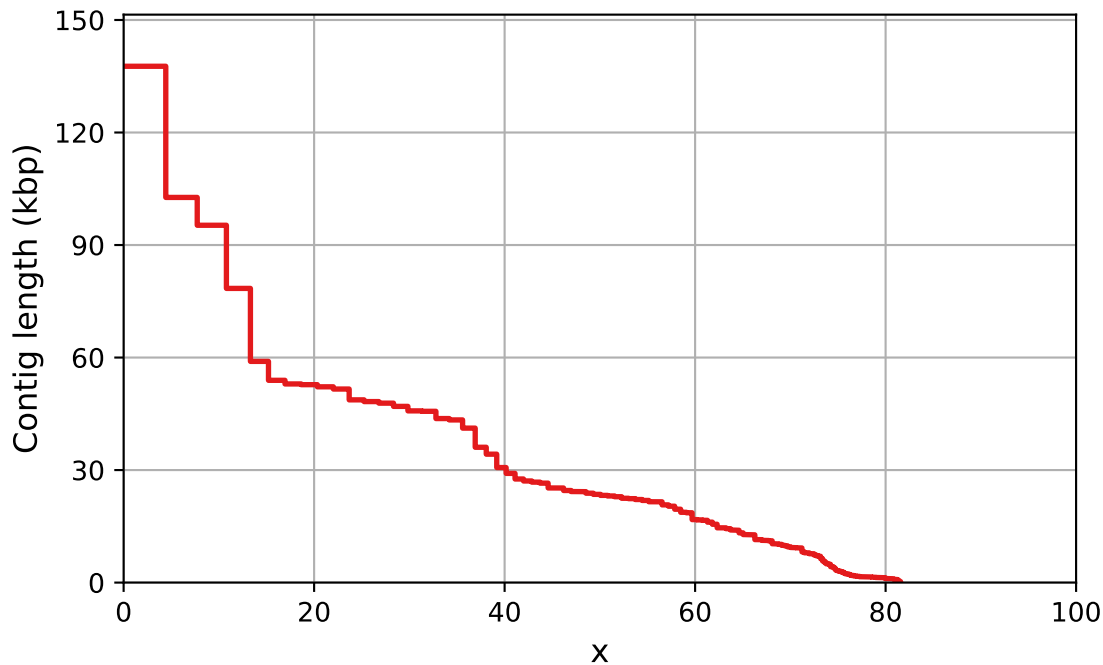
FRCurve (misassemblies)



Cumulative length (aligned contigs)

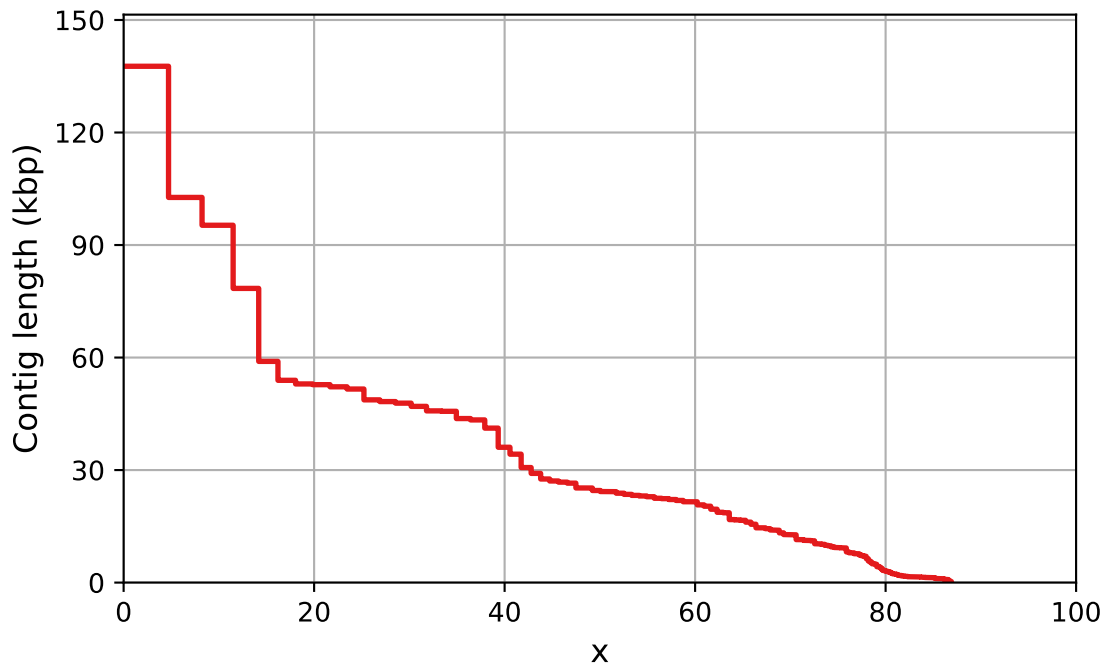


NAx



— contigs

NGAx



contigs