

Report

	contigs
# contigs (>= 1000 bp)	163
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	225965
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	681
Largest contig	3906
Total length	579983
Reference length	2382730
GC (%)	36.93
Reference GC (%)	36.87
N50	868
NG50	-
N90	559
NG90	-
auN	1021.9
auNG	248.7
L50	232
LG50	-
L90	571
LG90	-
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	8110
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 4 part
Unaligned length	6351
Genome fraction (%)	23.878
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1868.80
# indels per 100 kbp	40.67
Largest alignment	3900
Total aligned length	570419
NA50	844
NGA50	-
NA90	544
NGA90	-
auNA	968.8
auNGA	235.8
LA50	241
LGA50	-
LA90	588
LGA90	-

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	6
# contig misassemblies	6
# c. relocations	1
# c. translocations	5
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	8110
# possibly misassembled contigs	2
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	10660
# indels	232
# indels (<= 5 bp)	213
# indels (> 5 bp)	19
Indels length	779

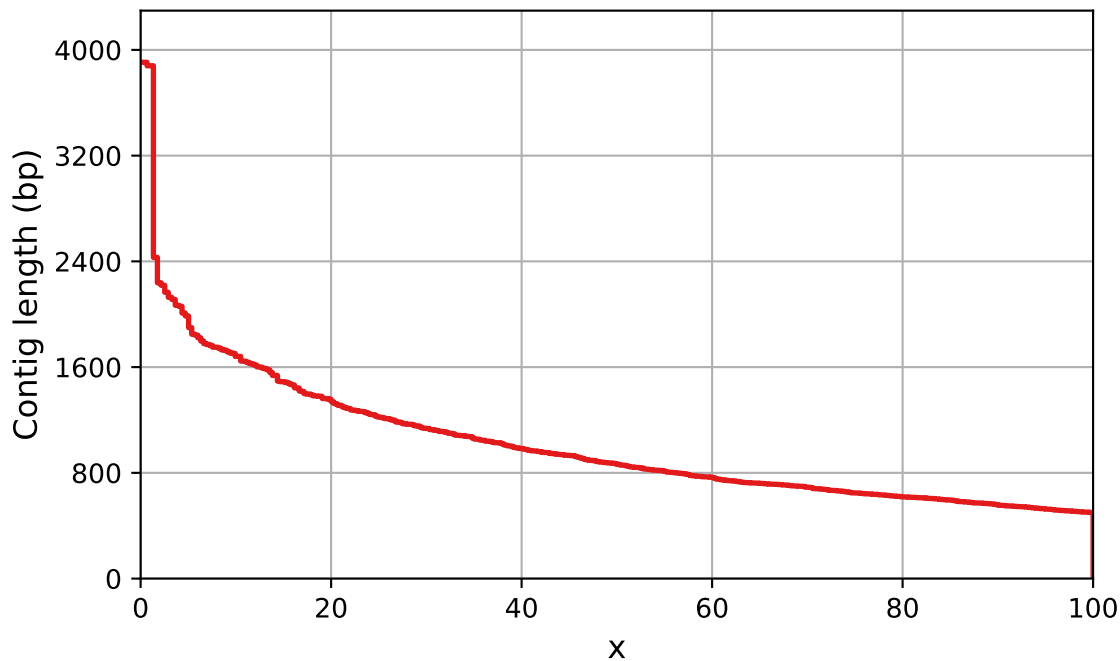
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	contigs
# fully unaligned contigs	1
Fully unaligned length	2112
# partially unaligned contigs	4
Partially unaligned length	4239
# N's	0

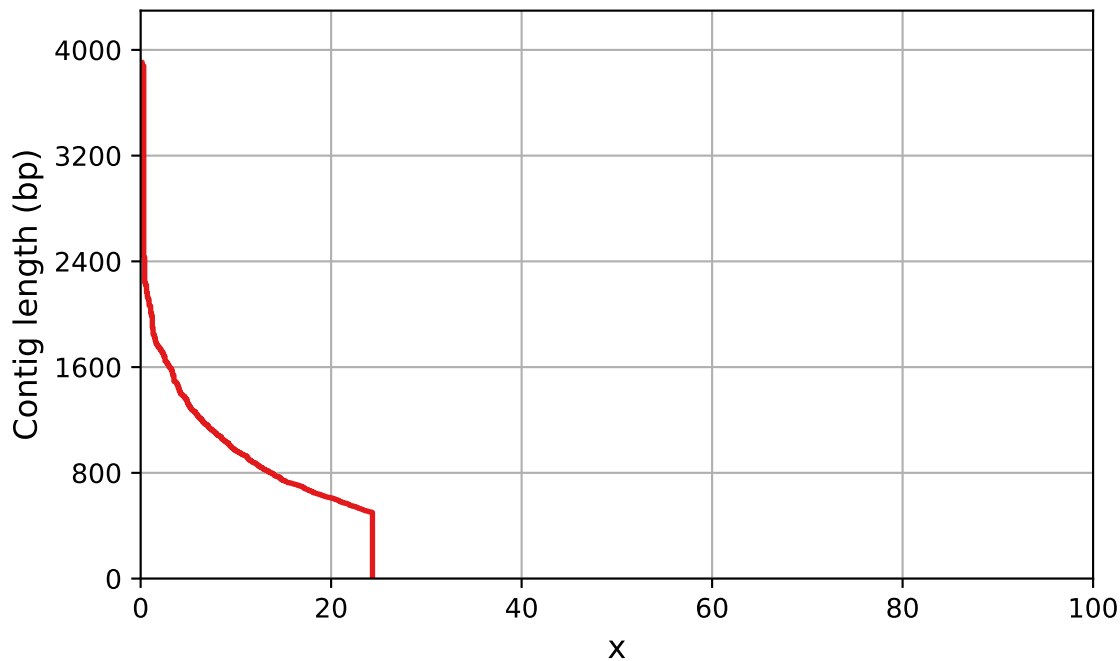
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

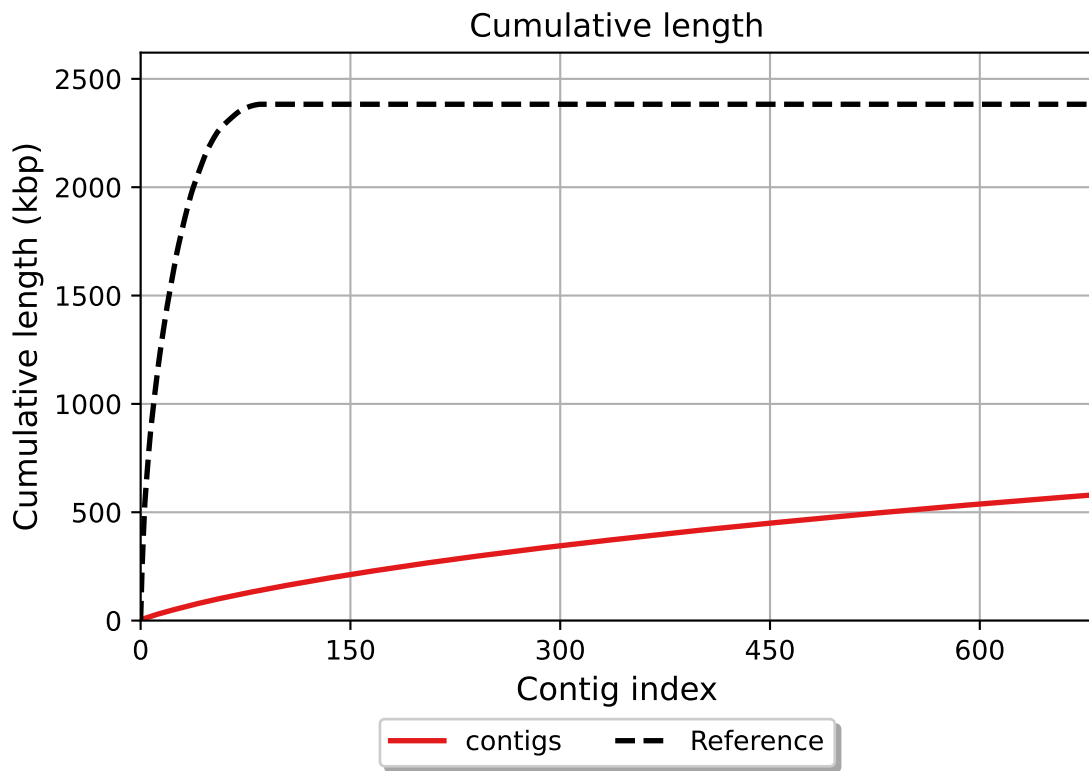


— contigs

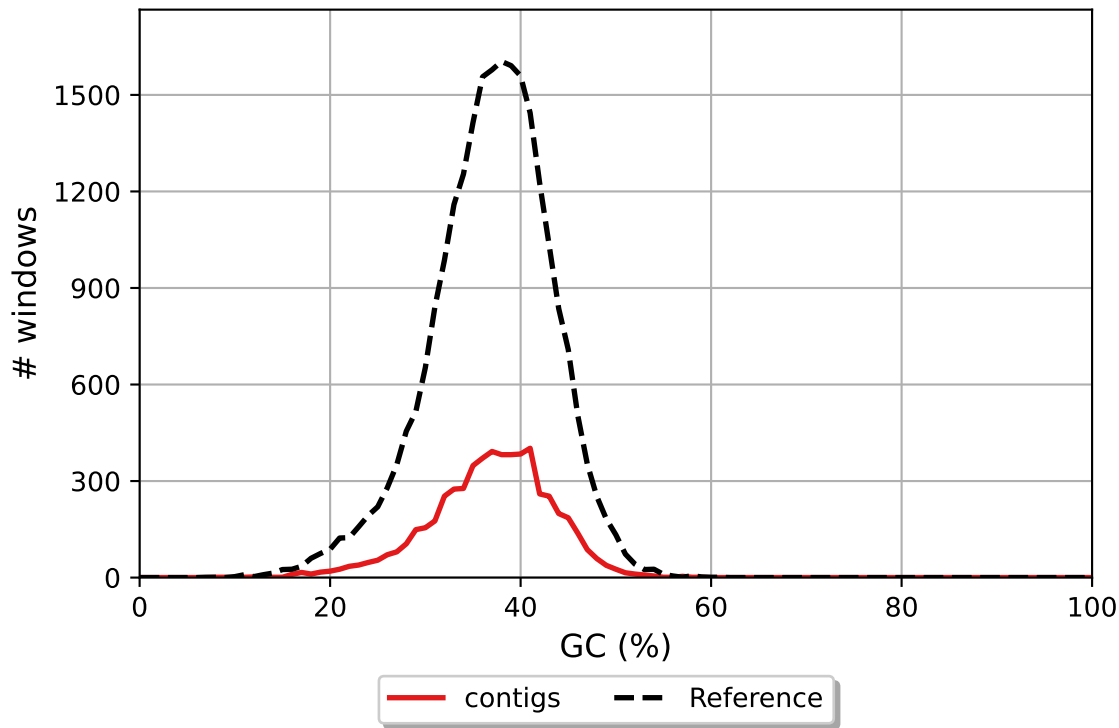
NGx



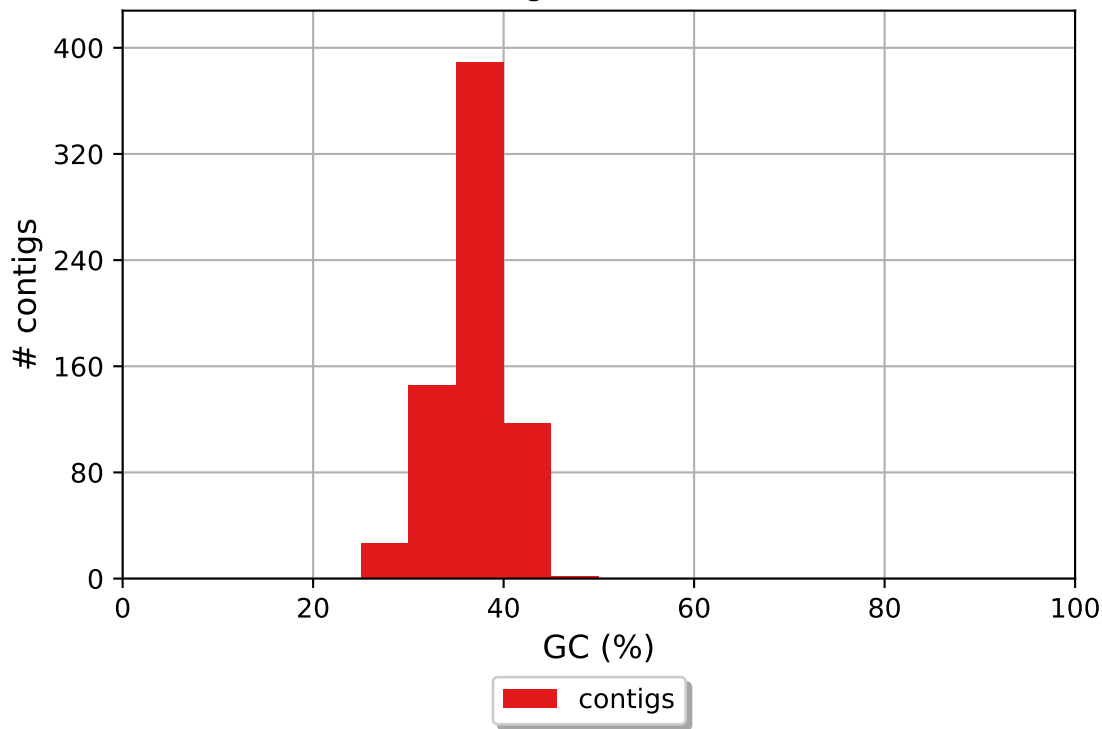
— contigs



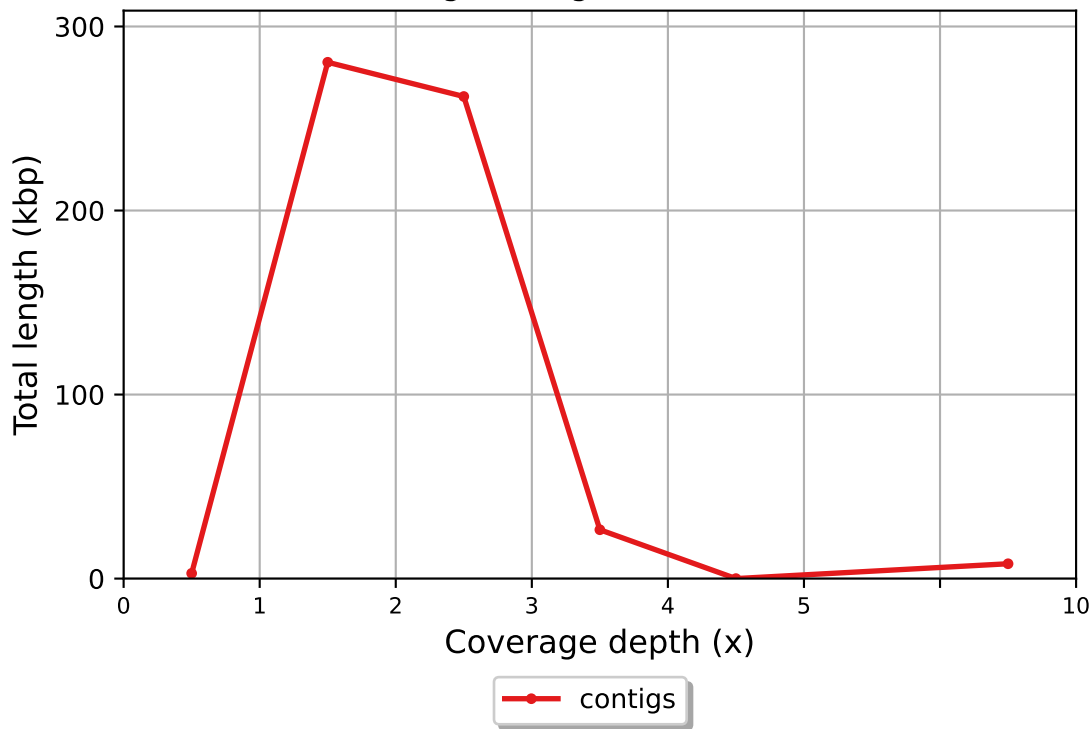
GC content



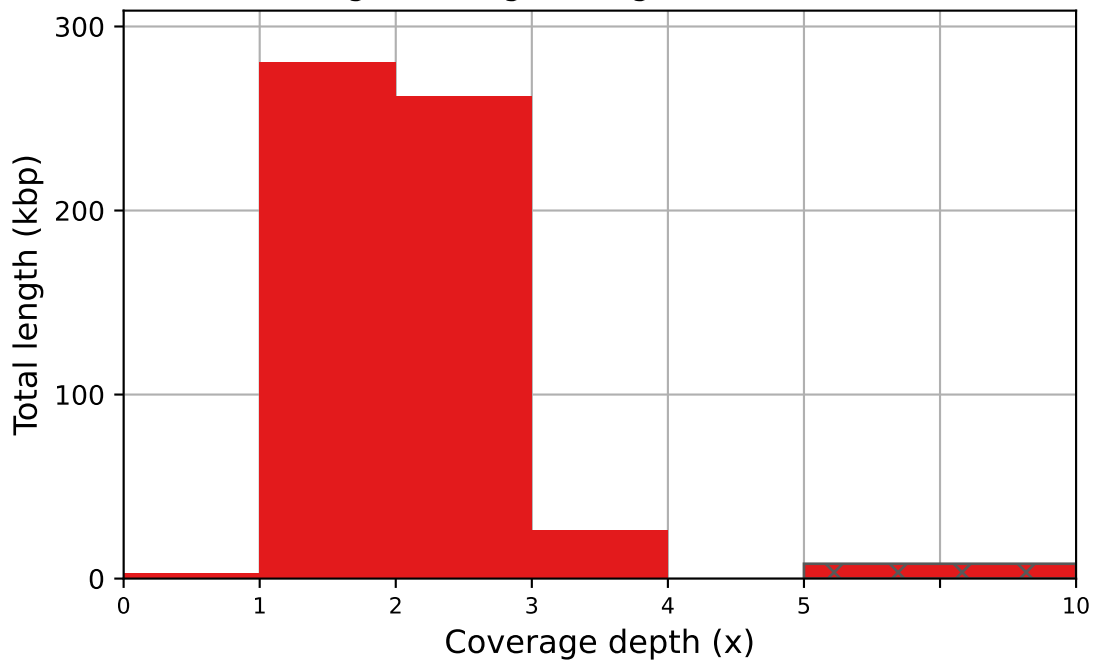
contigs GC content



Coverage histogram (bin size: 1x)

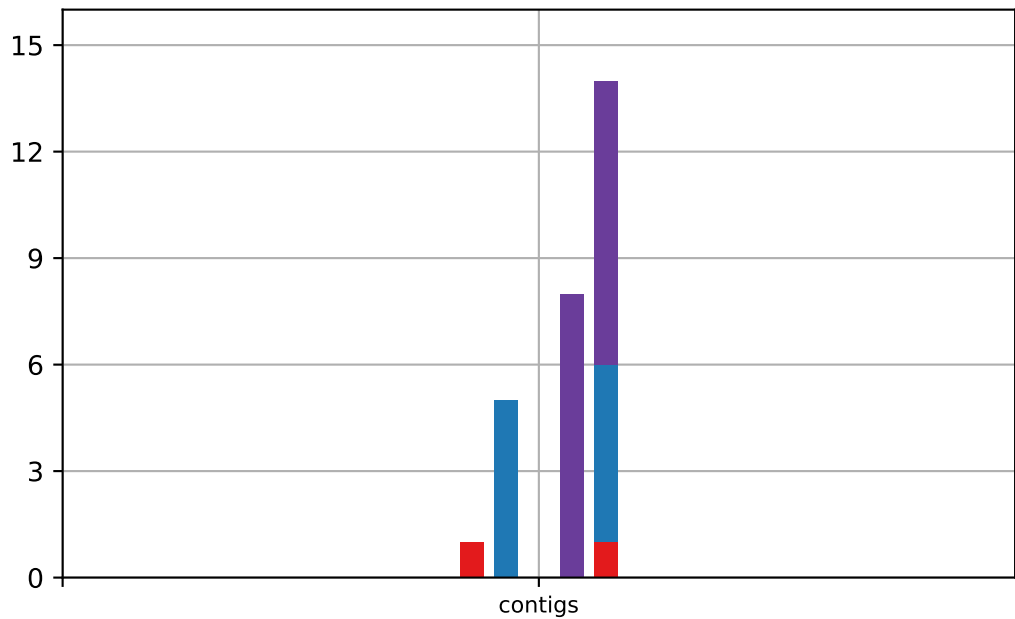


contigs coverage histogram (bin size: 1x)



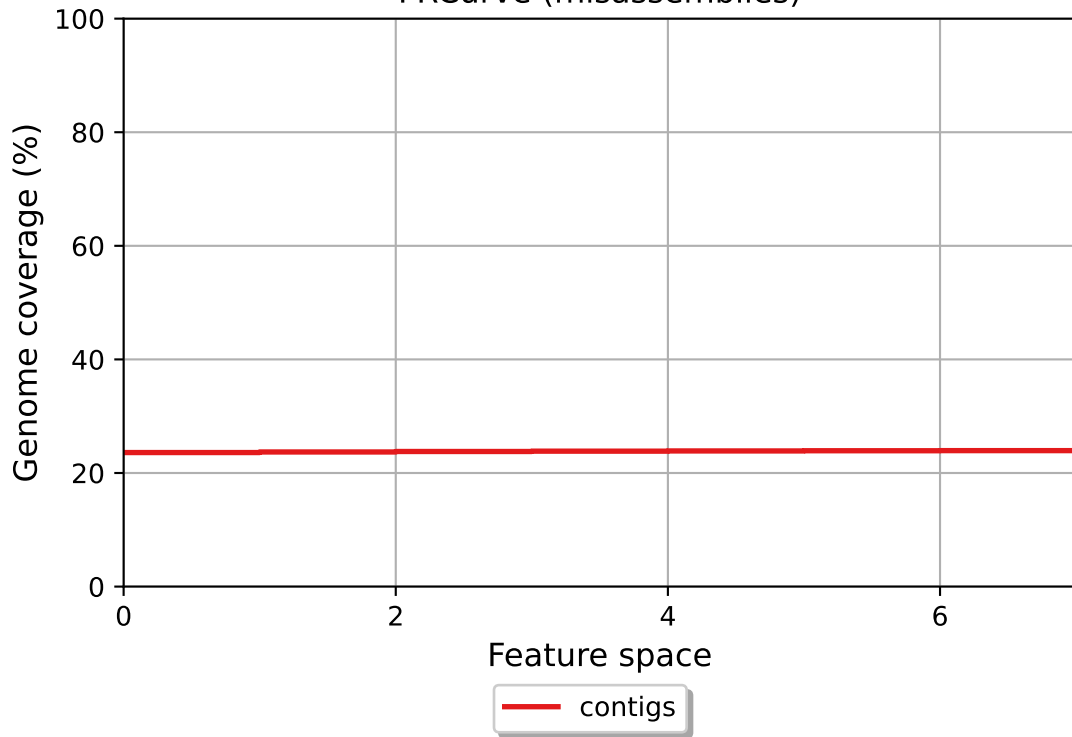
contigs

Misassemblies

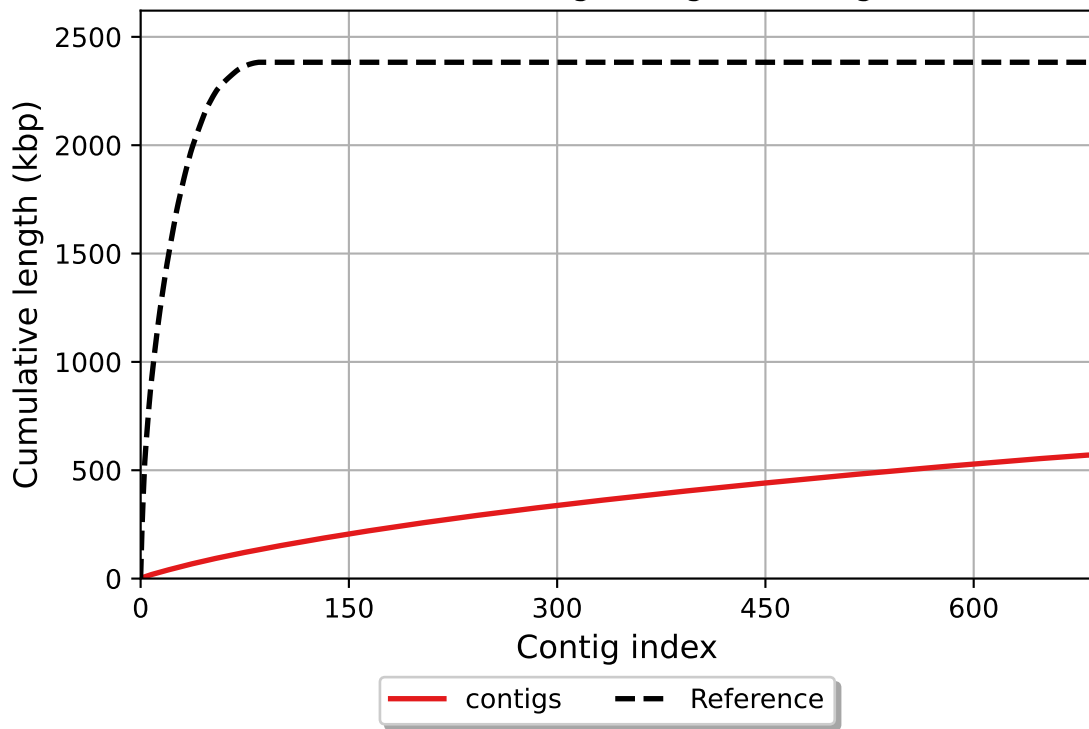


relocations # translocations # interspecies translocations

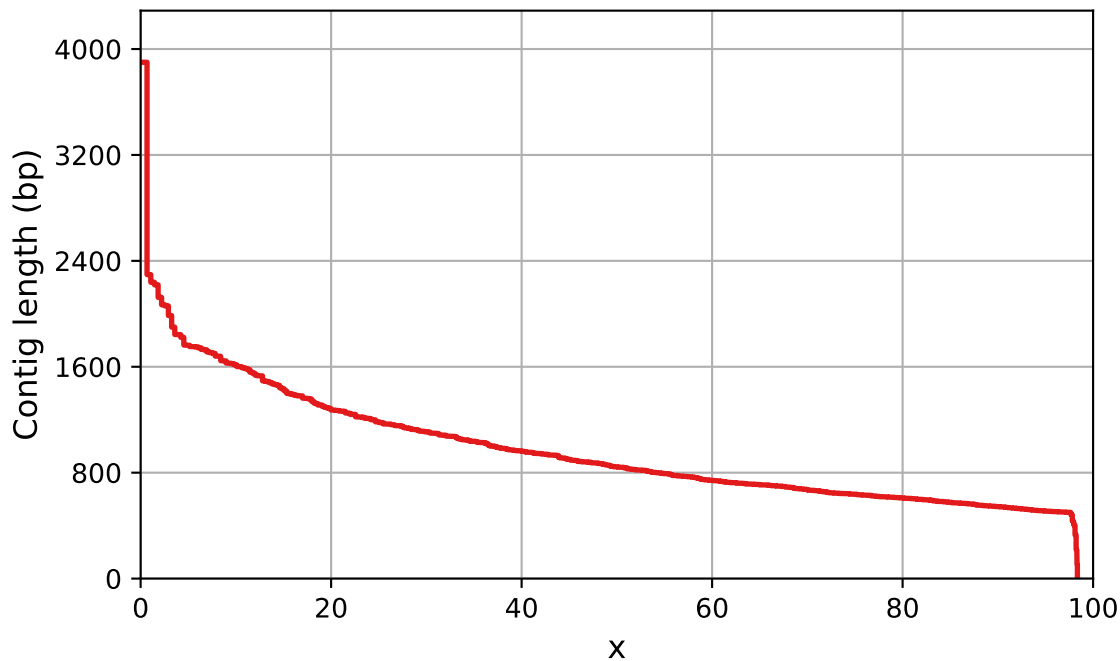
FRCurve (misassemblies)



Cumulative length (aligned contigs)

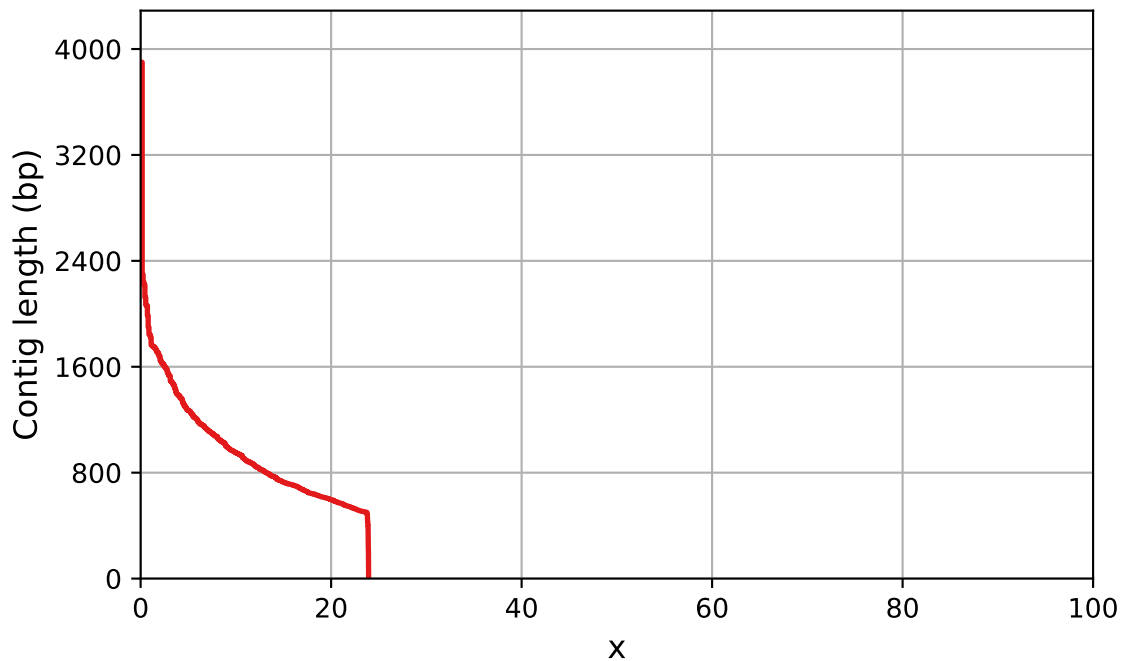


NAx



contigs

NGAx



— contigs