

Report	contigs
# contigs (>= 0 bp)	390
# contigs (>= 1000 bp)	185
# contigs (>= 5000 bp)	129
# contigs (>= 10000 bp)	105
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	5067454
Total length (>= 1000 bp)	5021069
Total length (>= 5000 bp)	4888841
Total length (>= 10000 bp)	4711104
Total length (>= 25000 bp)	3989190
Total length (>= 50000 bp)	2895752
# contigs	185
Largest contig	232547
Total length	5021069
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	59969
NG50	69659
N90	15177
NG90	21836
auN	71987.6
auNG	77872.0
L50	26
LG50	23
L90	91
LG90	71
# total reads	2212976
# left	1106488
# right	1106488
Mapped (%)	99.87
Reference mapped (%)	72.95
Properly paired (%)	93.94
Reference properly paired (%)	70.7
Avg. coverage depth	63
Reference avg. coverage depth	50
Coverage >= 1x (%)	100.0
Reference coverage >= 1x (%)	92.1
# misassemblies	70
# misassembled contigs	44
Misassembled contigs length	2869551
# local misassemblies	57
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	9
# unaligned mis. contigs	2
# unaligned contigs	39 + 80 part
Unaligned length	832924
Genome fraction (%)	90.119
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1245.73
# indels per 100 kbp	27.50
Largest alignment	136731
Total aligned length	4181156
NA50	32722
NGA50	35155
NA90	-
NGA90	380
auNA	39074.0
auNGA	42268.0
LA50	46
LGA50	40
LA90	-
LGA90	199

All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Reads report

	contigs
# total reads	2212976
# left	1106488
# right	1106488
# mapped	2210065
Mapped (%)	99.87
# properly paired	2078770
Properly paired (%)	93.94
# singletons	3156
Singletons (%)	0.14
# misjoint mates	67756
Misjoint mates (%)	3.06
Avg. coverage depth	63
Coverage >= 1x (%)	100.0
Coverage >= 5x (%)	99.24
Coverage >= 10x (%)	97.79
# reference mapped	1614325
Reference mapped (%)	72.95
# reference properly paired	1564680
Reference properly paired (%)	70.7
# reference singletons	19816
Reference singletons (%)	0.9
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	50
Reference coverage >= 1x (%)	92.1
Reference coverage >= 5x (%)	91.48
Reference coverage >= 10x (%)	90.58

All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

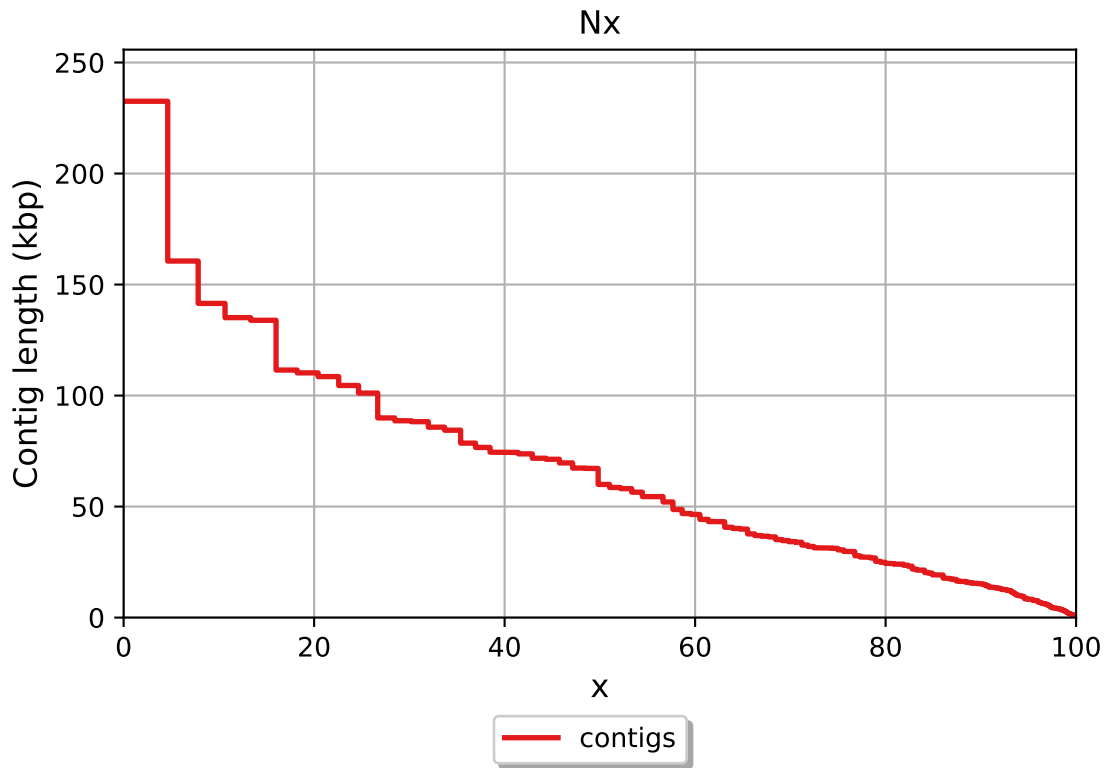
	contigs
# misassemblies	70
# contig misassemblies	70
# c. relocations	70
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	44
Misassembled contigs length	2869551
# local misassemblies	57
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	9
# unaligned mis. contigs	2
# mismatches	52086
# indels	1150
# indels (<= 5 bp)	955
# indels (> 5 bp)	195
Indels length	14591

All statistics are based on contigs of size ≥ 1000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

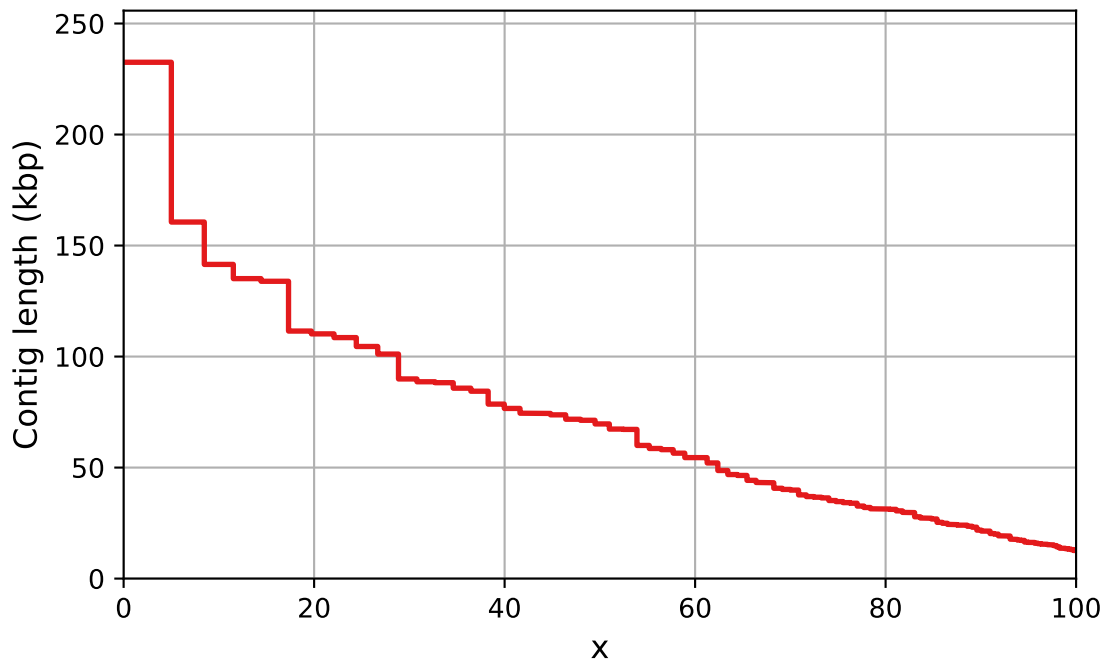
Unaligned report

	contigs
# fully unaligned contigs	39
Fully unaligned length	262638
# partially unaligned contigs	80
Partially unaligned length	570286
# N's	0

All statistics are based on contigs of size ≥ 1000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

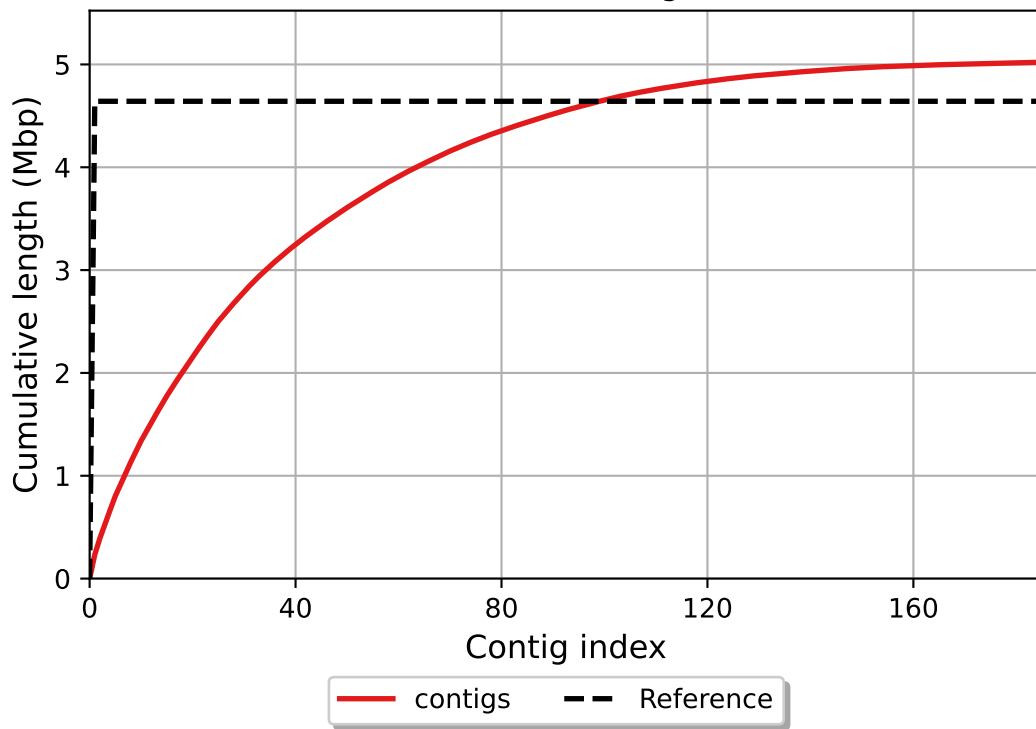


NGx

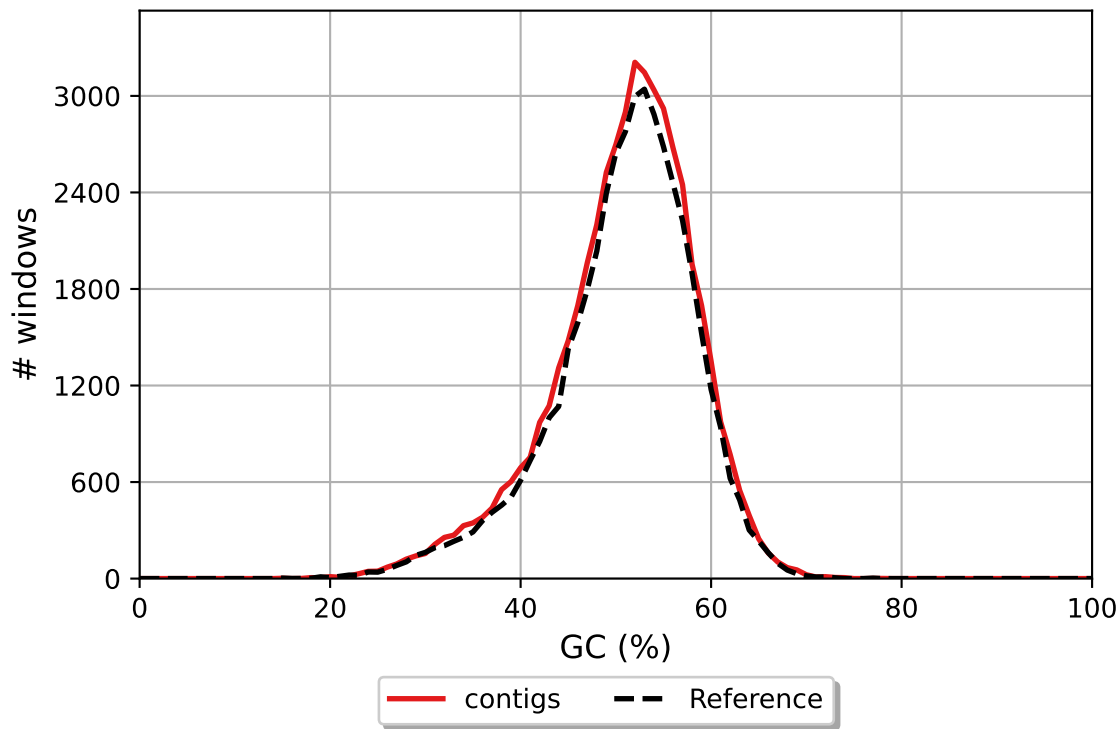


contigs

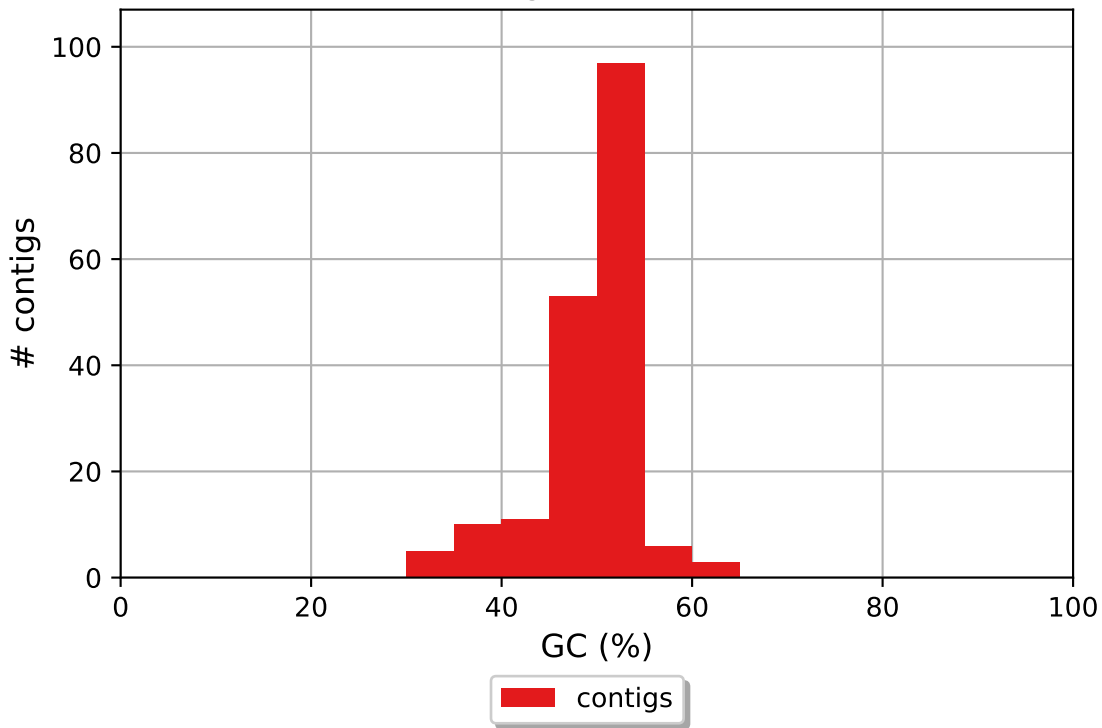
Cumulative length



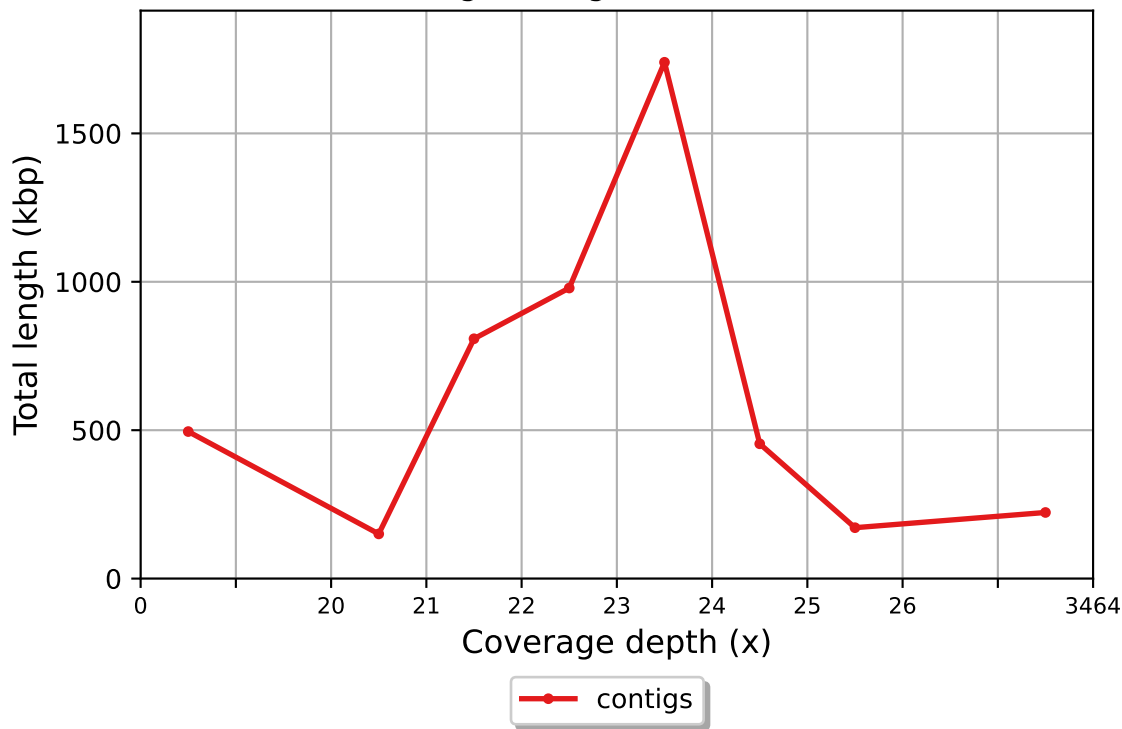
GC content



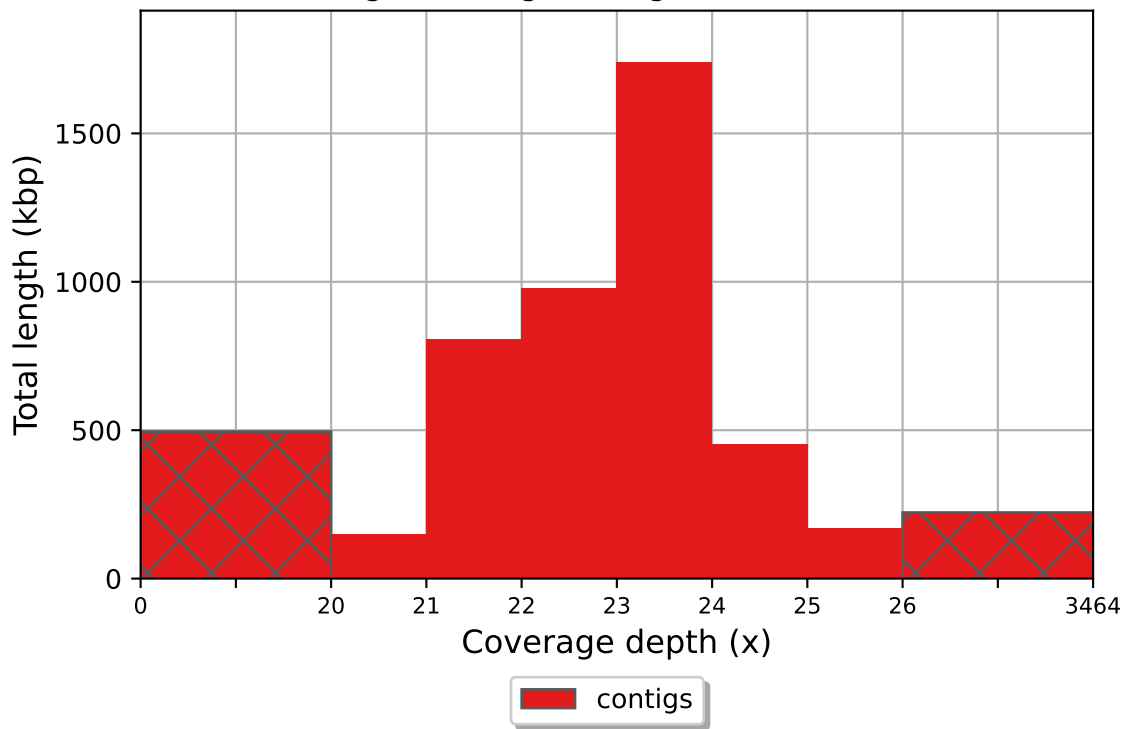
contigs GC content



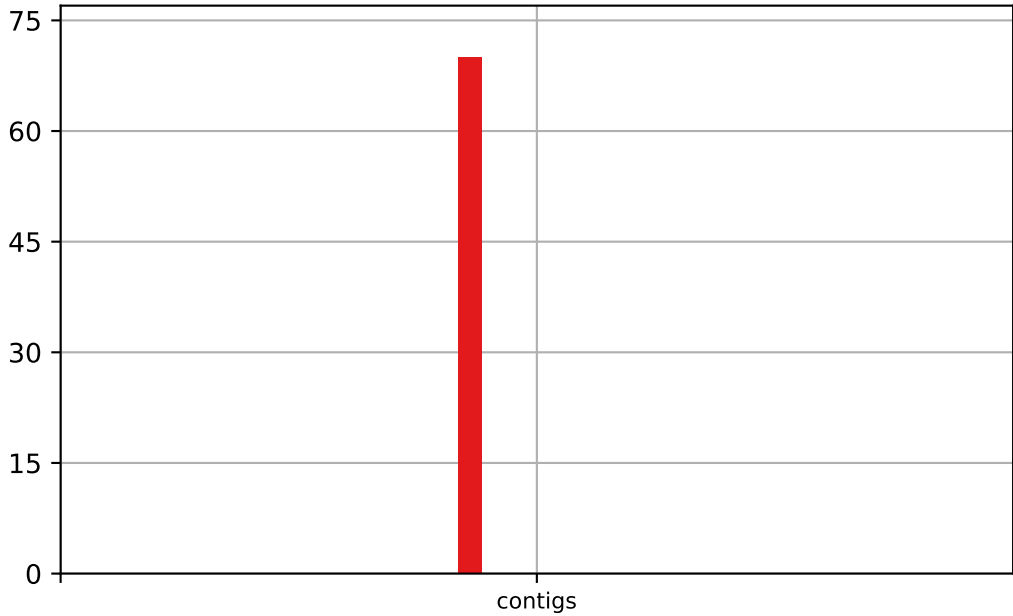
Coverage histogram (bin size: 1x)



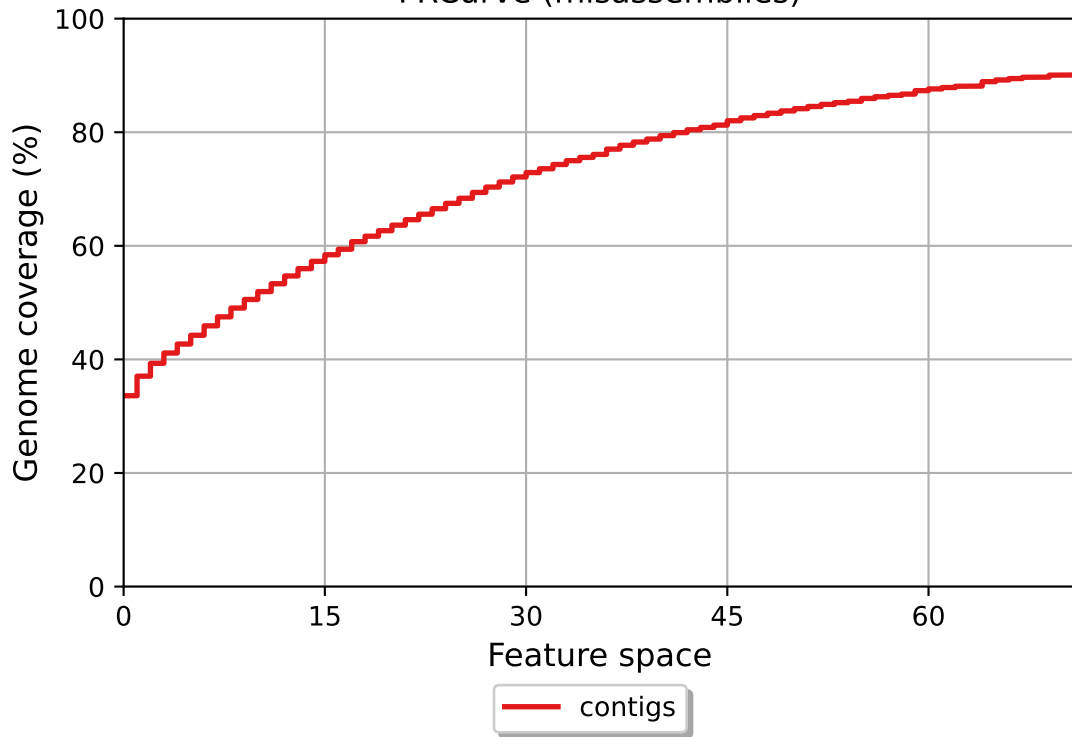
contigs coverage histogram (bin size: 1x)



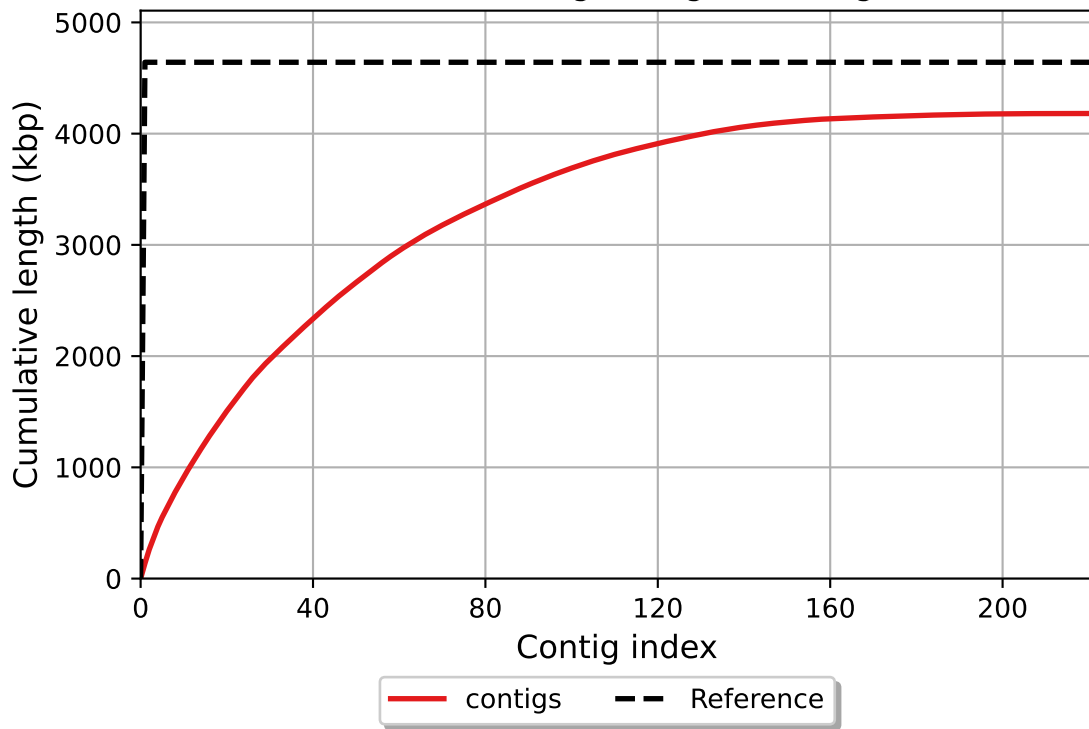
Misassemblies



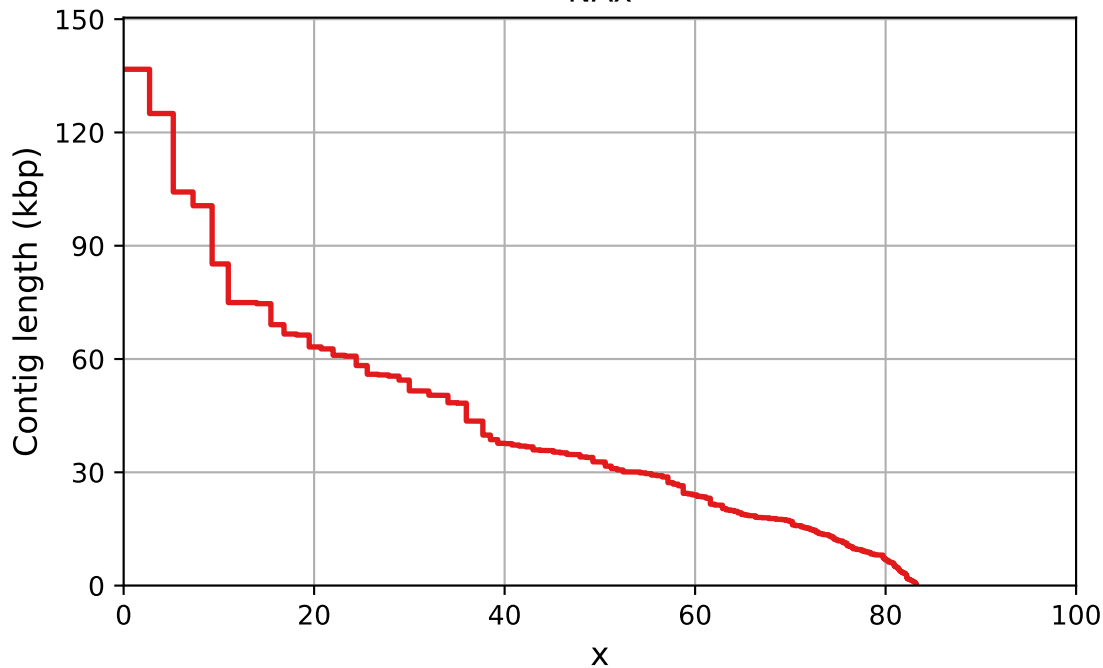
FRCurve (misassemblies)



Cumulative length (aligned contigs)

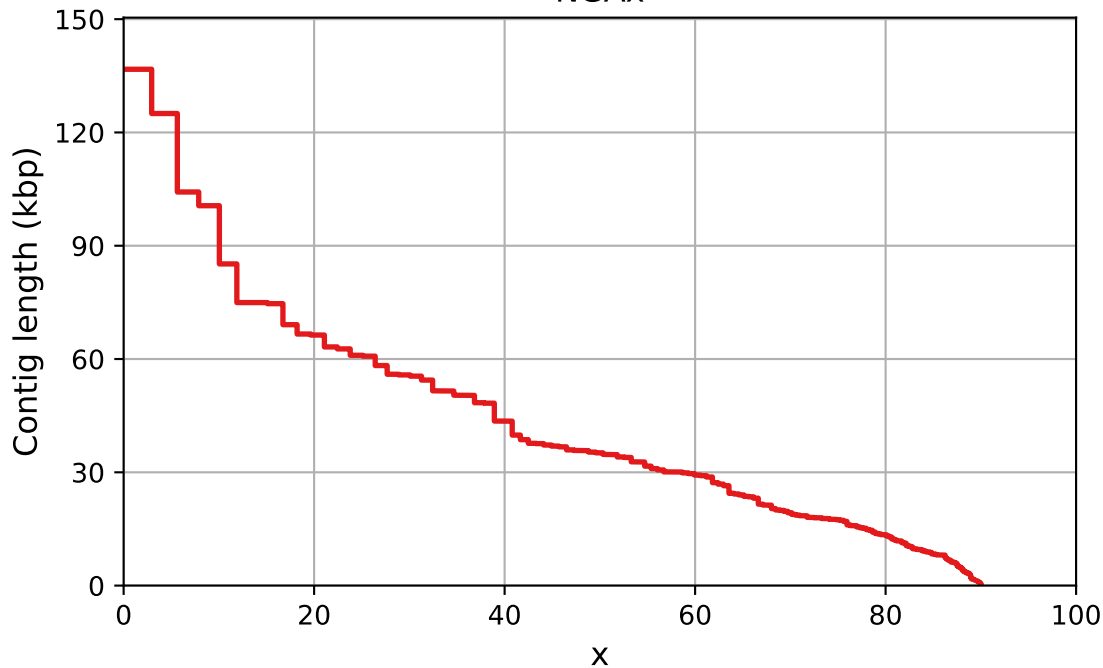


NAx



— contigs

NGAx



— contigs