

Report

	contigs
# contigs (>= 0 bp)	3890
# contigs (>= 1000 bp)	2142
# contigs (>= 5000 bp)	167
# contigs (>= 10000 bp)	30
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6650658
Total length (>= 1000 bp)	5595221
Total length (>= 5000 bp)	1442170
Total length (>= 10000 bp)	548810
Total length (>= 25000 bp)	209168
Total length (>= 50000 bp)	0
# contigs	3234
Largest contig	36324
Total length	6395901
Reference length	6264404
GC (%)	65.70
Reference GC (%)	66.56
N50	2657
NG50	2715
N75	1456
NG75	1503
L50	663
LG50	638
L75	1486
LG75	1420
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	29335
# local misassemblies	22
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	216 + 68 part
Unaligned length	970716
Genome fraction (%)	86.378
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	414.17
# indels per 100 kbp	8.39
Largest alignment	15466
Total aligned length	5419362
NA50	1972
NGA50	2007
NA75	921
NGA75	979
LA50	925
LGA50	892
LA75	2105
LGA75	2002

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	10
# contig misassemblies	10
# c. relocations	10
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	29335
# local misassemblies	22
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	22411
# indels	454
# indels (<= 5 bp)	394
# indels (> 5 bp)	60
Indels length	1470

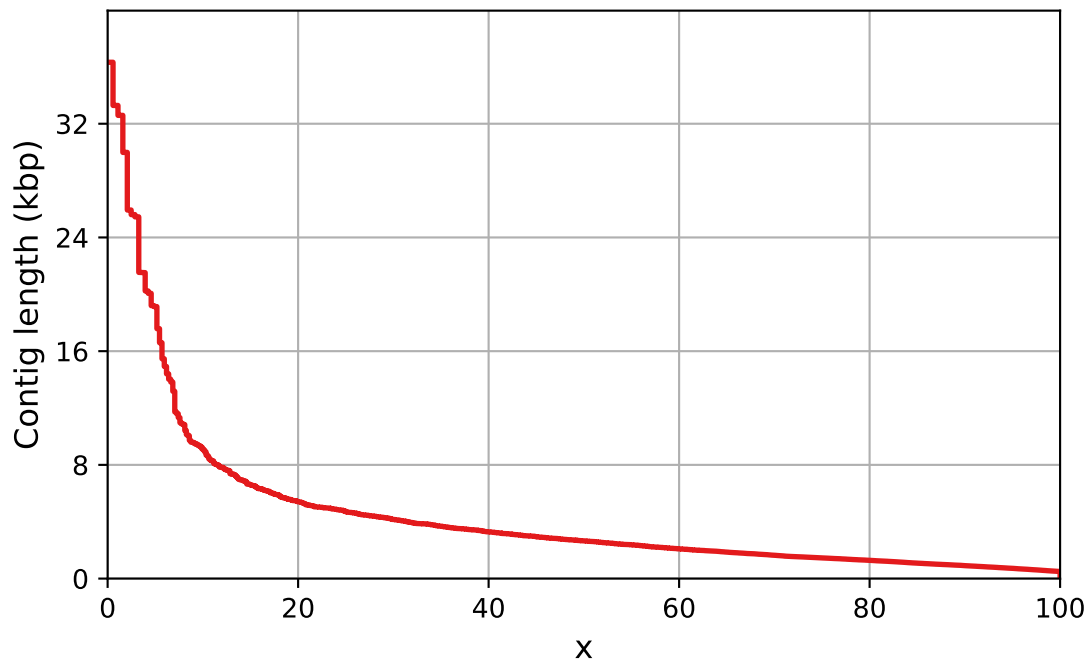
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	contigs
# fully unaligned contigs	216
Fully unaligned length	686865
# partially unaligned contigs	68
Partially unaligned length	283851
# N's	0

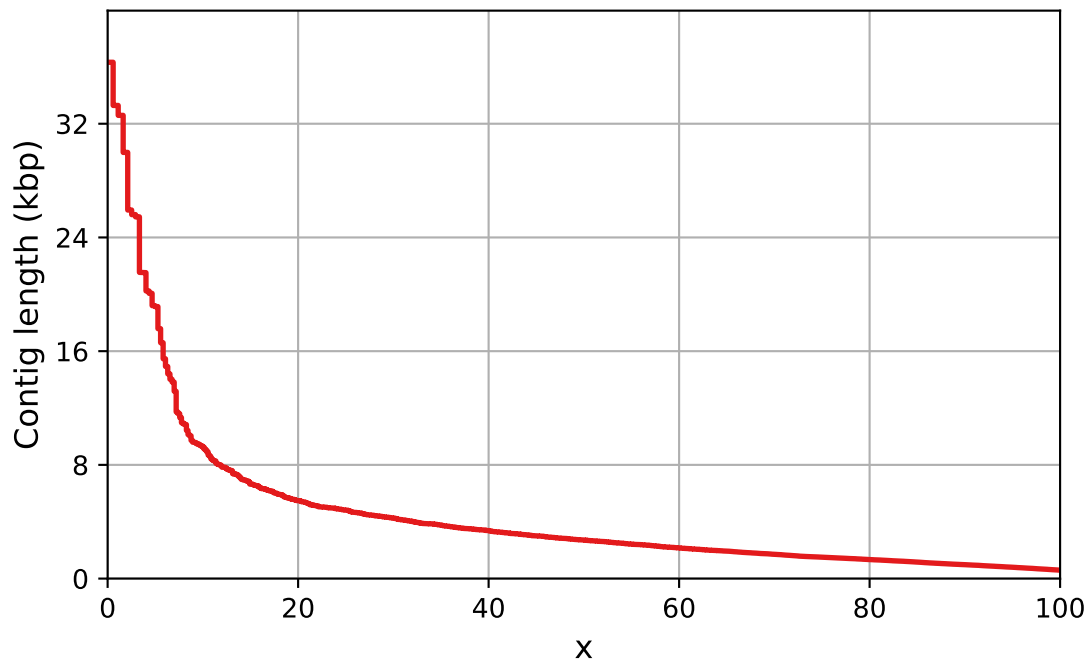
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



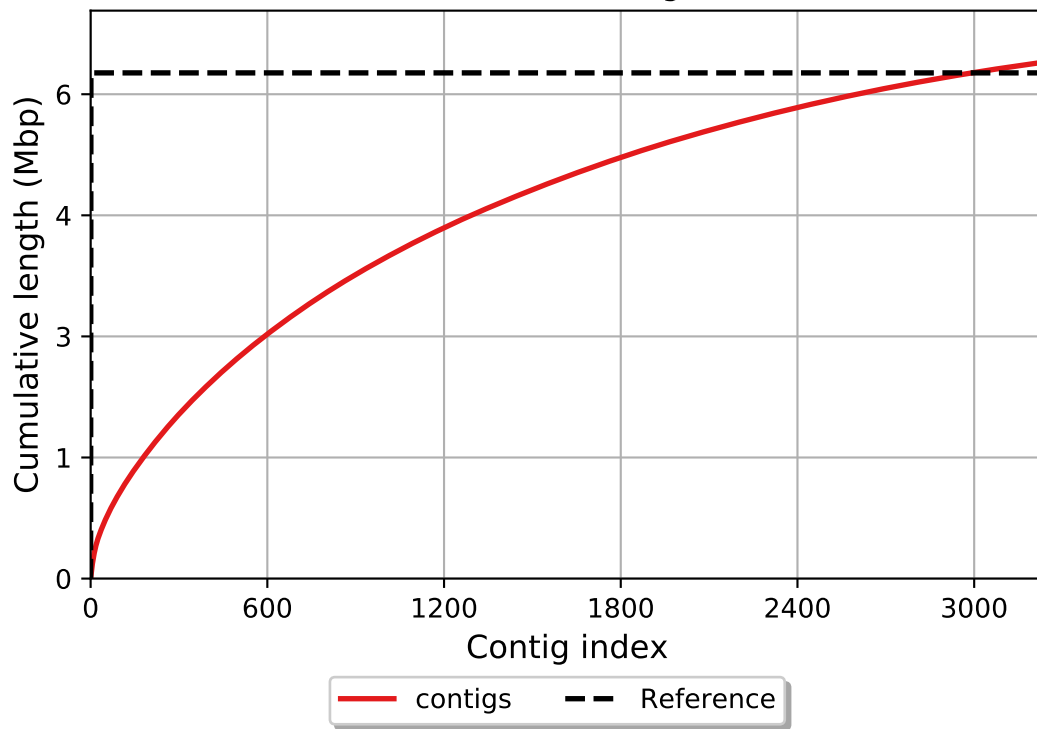
contigs

NGx

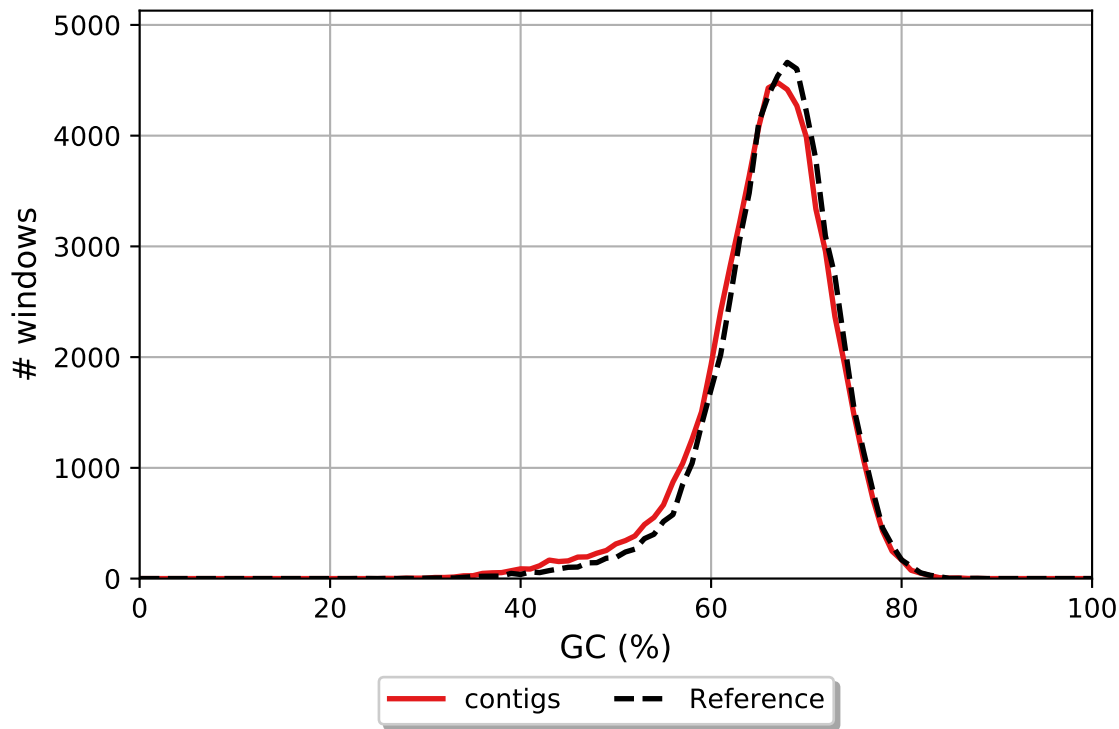


contigs

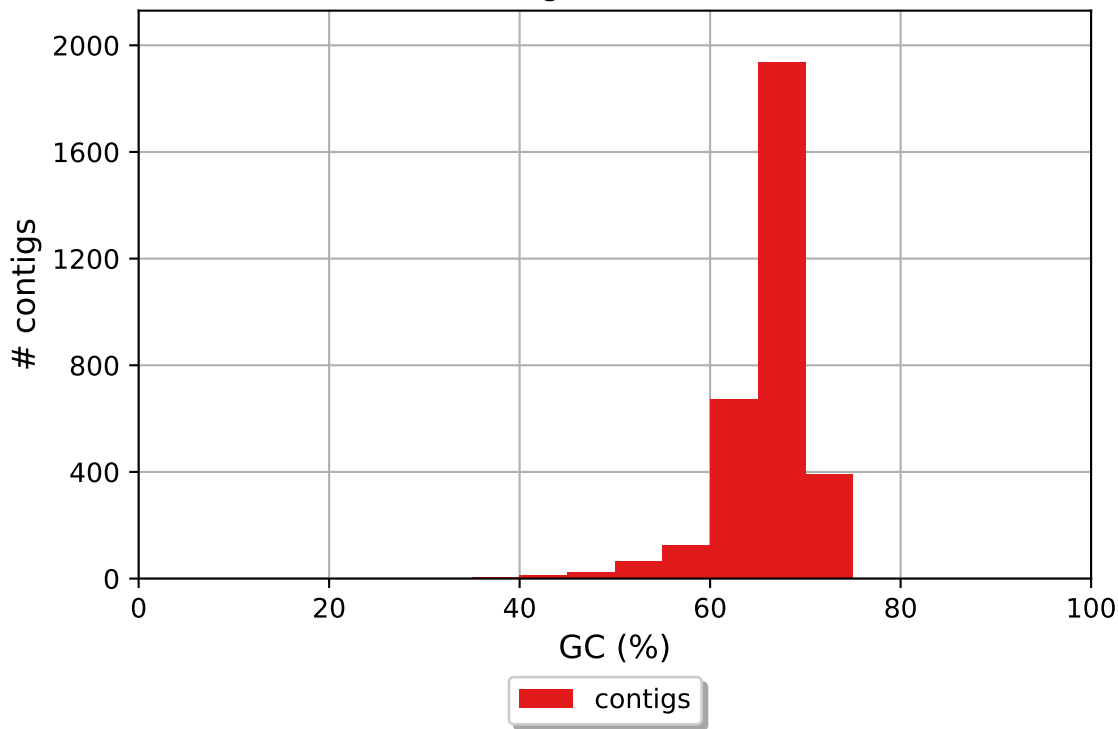
Cumulative length



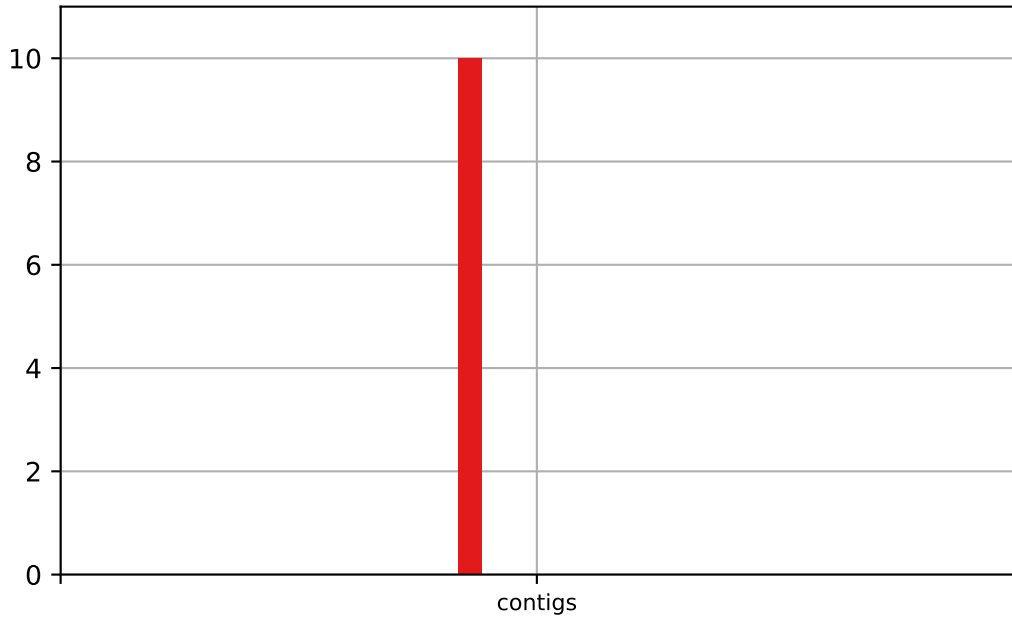
GC content



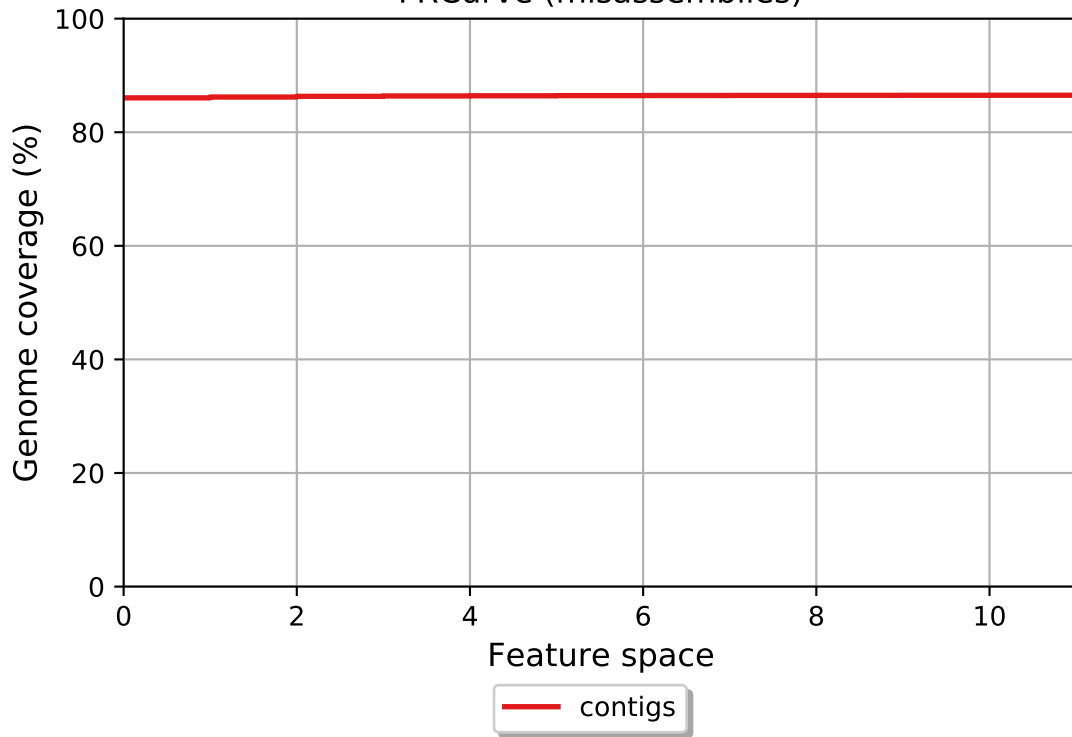
contigs GC content



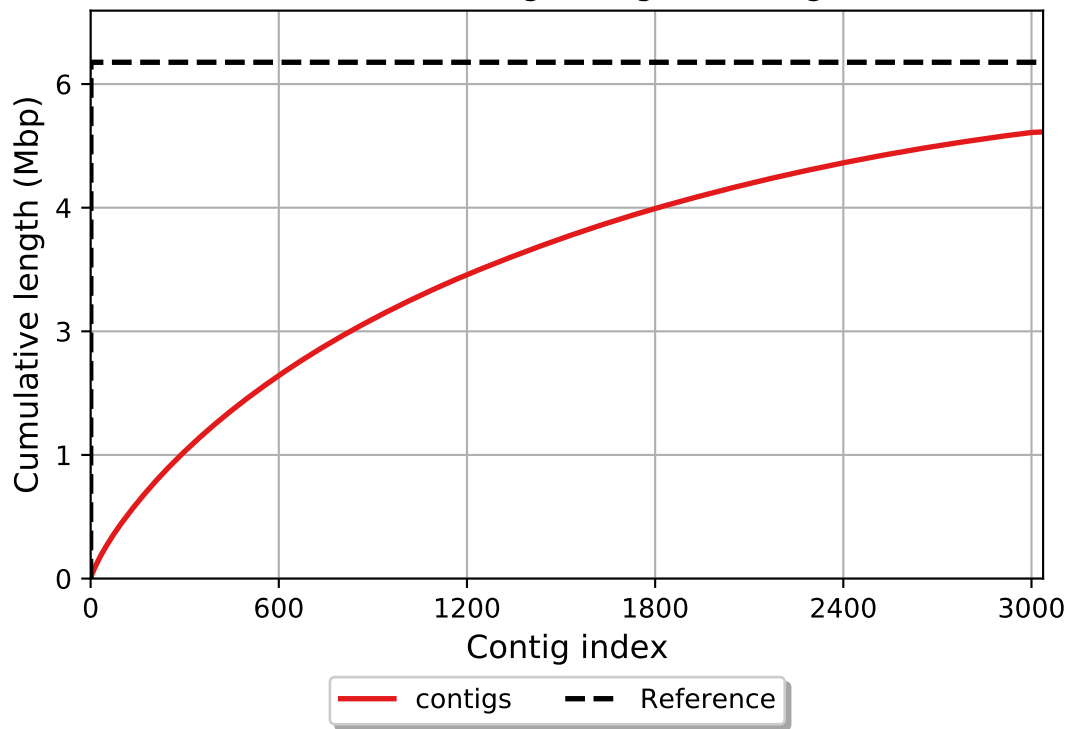
Misassemblies



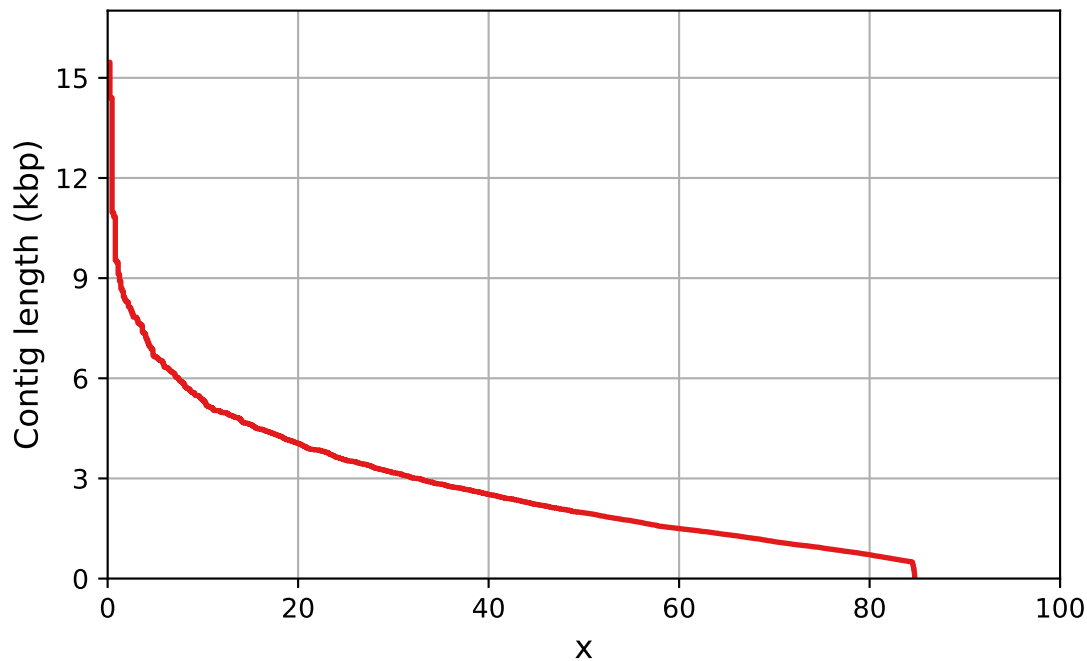
FRCurve (misassemblies)



Cumulative length (aligned contigs)

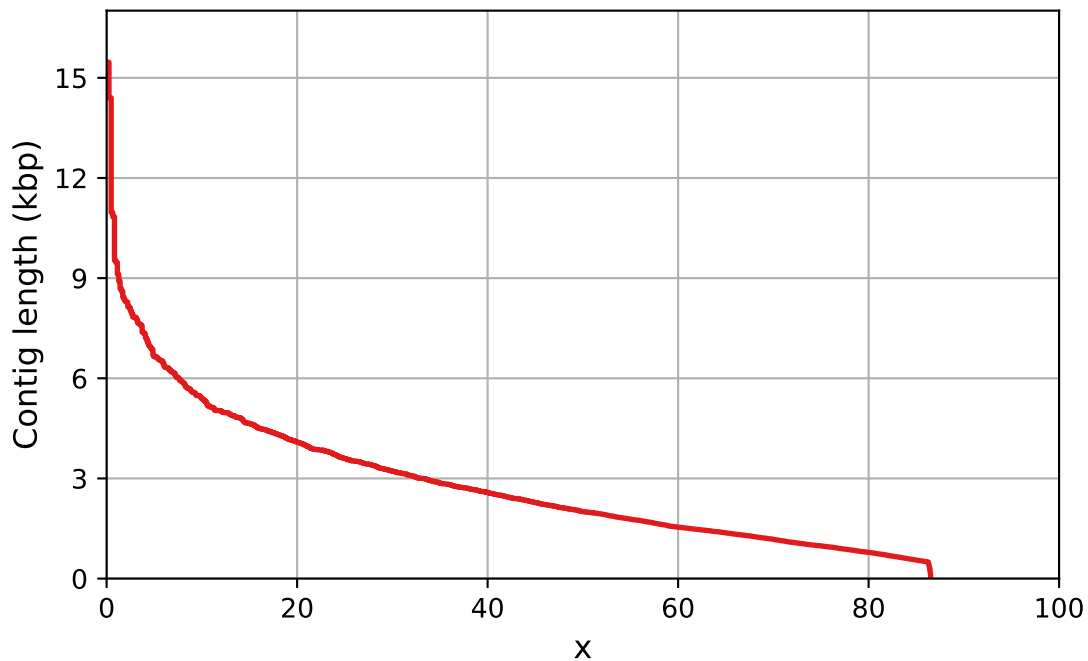


NAx



— contigs

NGAx



— contigs