

Report

	final.contigs
# contigs (>= 1000 bp)	439
# contigs (>= 5000 bp)	65
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1295987
Total length (>= 5000 bp)	456089
Total length (>= 10000 bp)	43150
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	668
Largest contig	21323
Total length	1456996
Reference length	1822564
GC (%)	35.77
Reference GC (%)	35.13
N50	3204
NG50	2413
N90	936
NG90	-
L50	134
LG50	199
L90	455
LG90	-
# misassemblies	16
# misassembled contigs	14
Misassembled contigs length	57471
# local misassemblies	27
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	0 + 176 part
Unaligned length	328270
Genome fraction (%)	54.898
Duplication ratio	1.070
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7623.90
# indels per 100 kbp	280.30
Largest alignment	18187
Total aligned length	1071013
NA50	1725
NGA50	923
NA90	-
NGA90	-
LA50	217
LGA50	361
LA90	-
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

	final.contigs
# misassemblies	16
# contig misassemblies	16
# c. relocations	11
# c. translocations	5
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	14
Misassembled contigs length	57471
# possibly misassembled contigs	167
# possible misassemblies	189
# local misassemblies	27
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	1
# unaligned mis. contigs	8
# mismatches	81653
# indels	3002
# indels (<= 5 bp)	2774
# indels (> 5 bp)	228
Indels length	9839

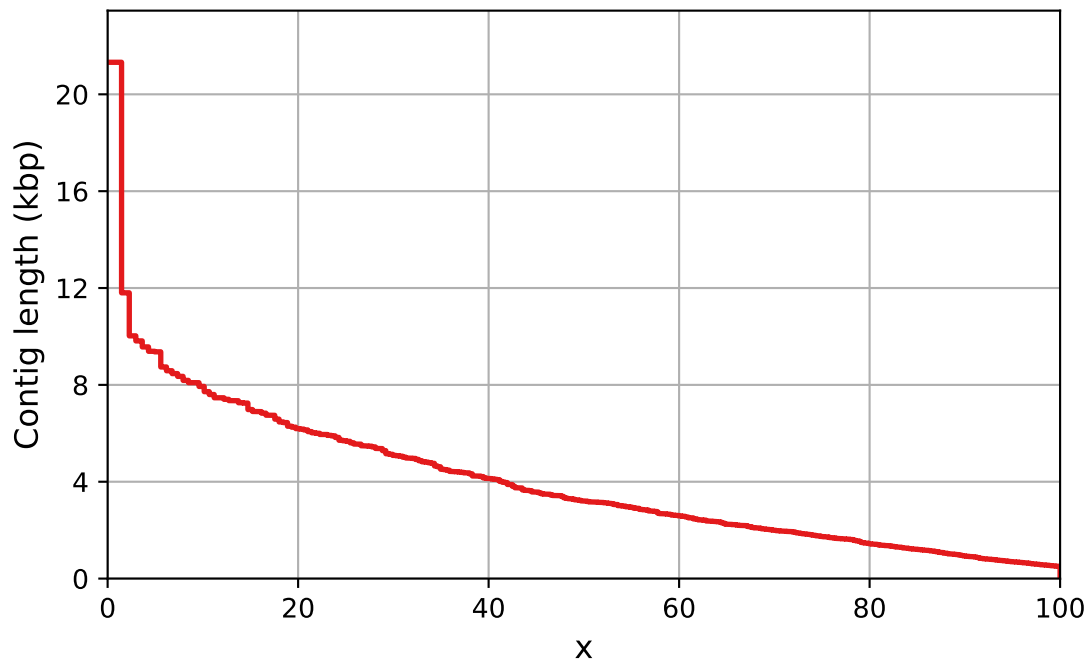
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	176
Partially unaligned length	328270
# N's	0

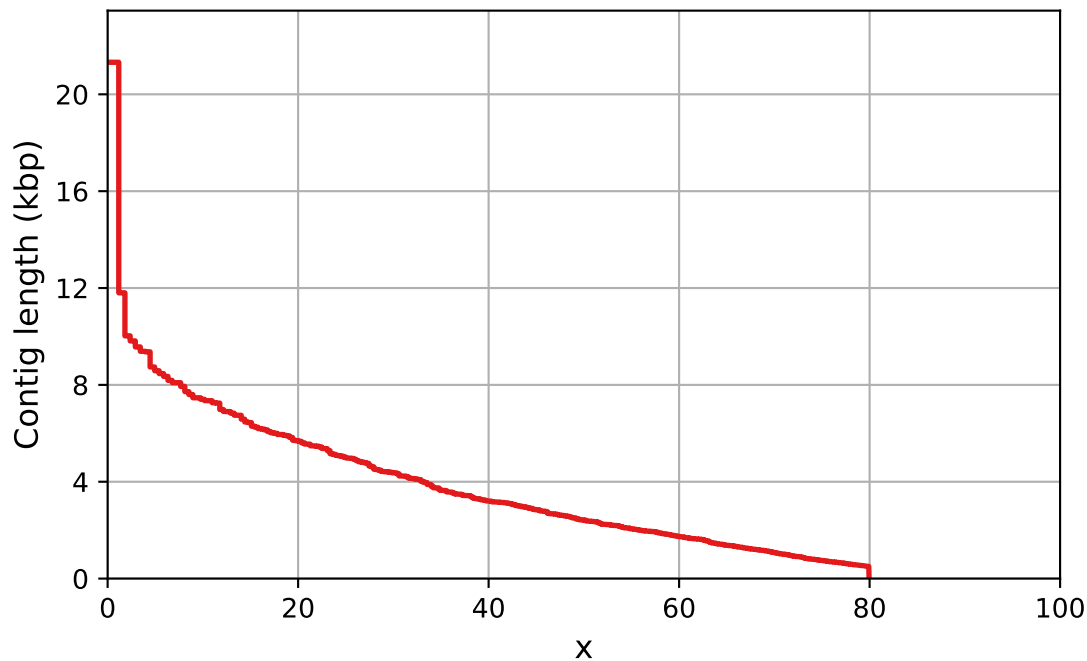
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

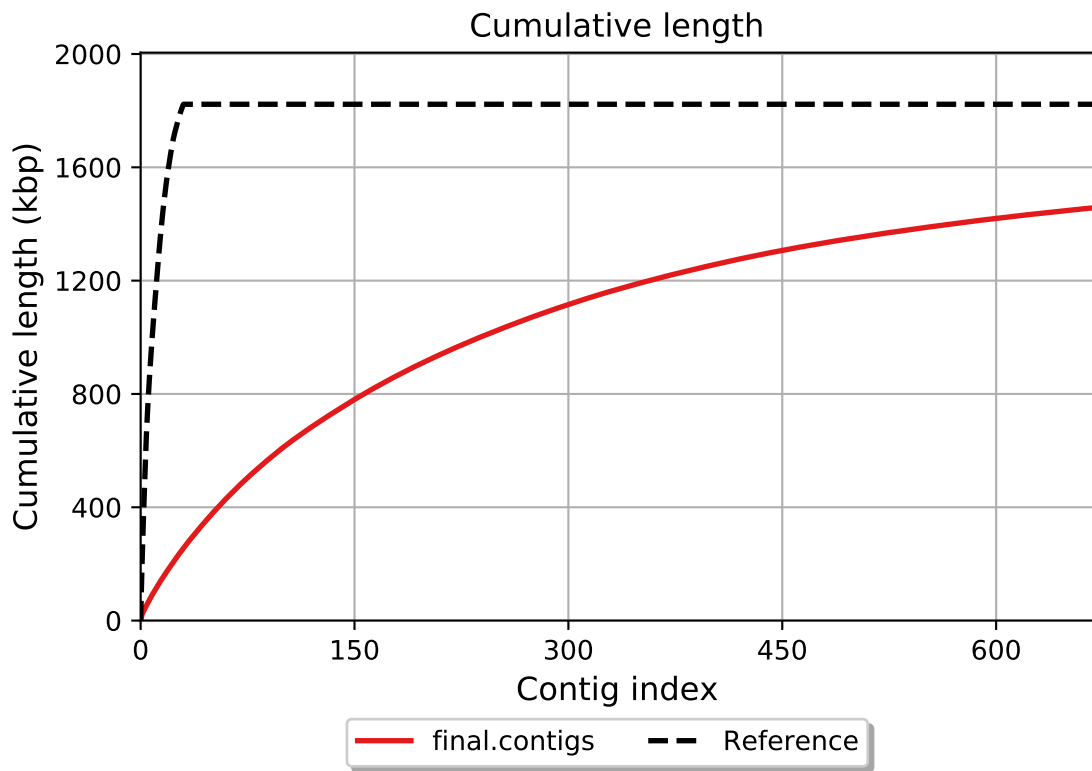


— final.contigs

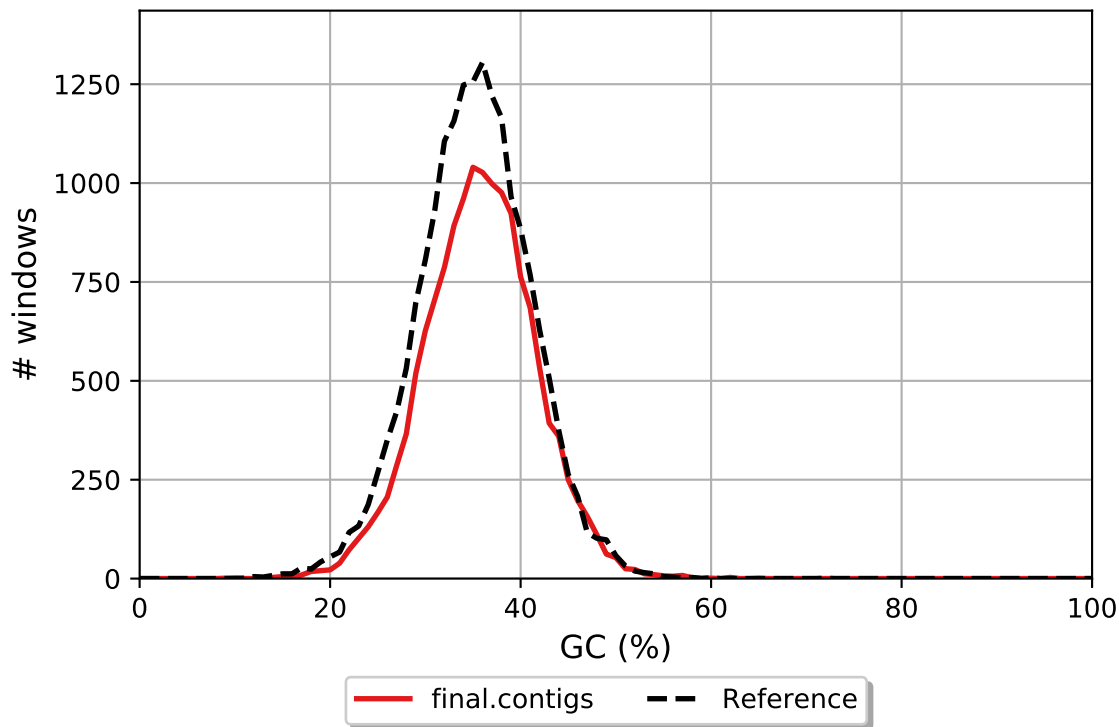
NGx



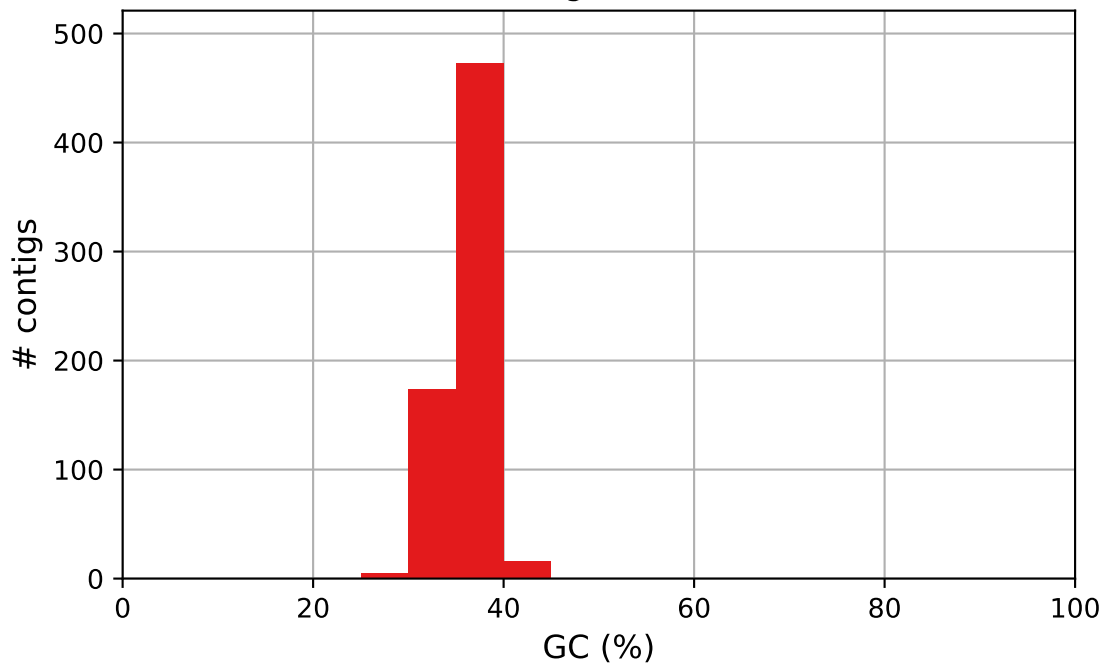
— final.contigs



GC content

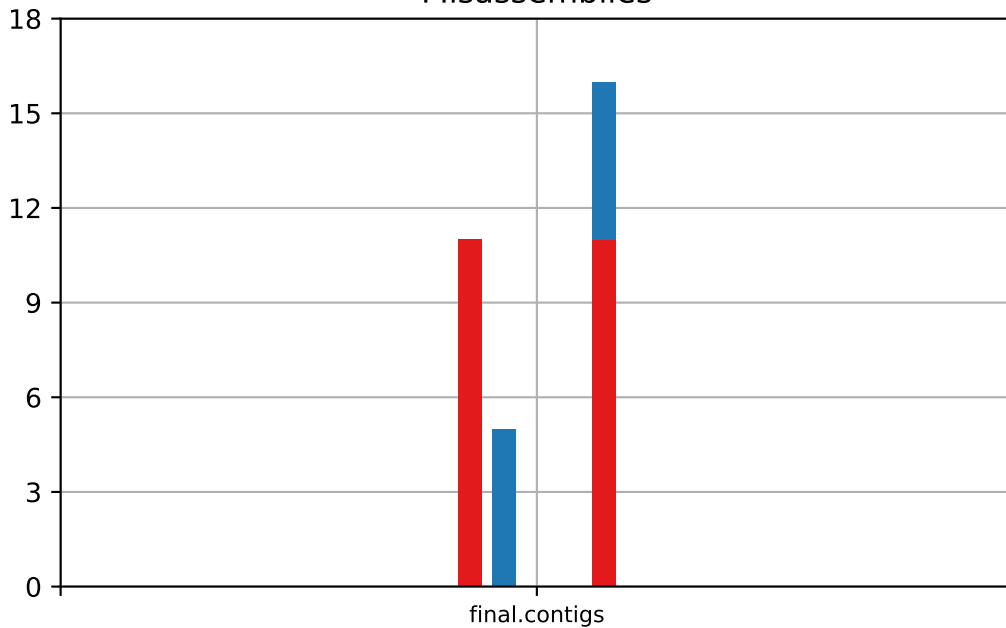


final.contigs GC content



final.contigs

Misassemblies

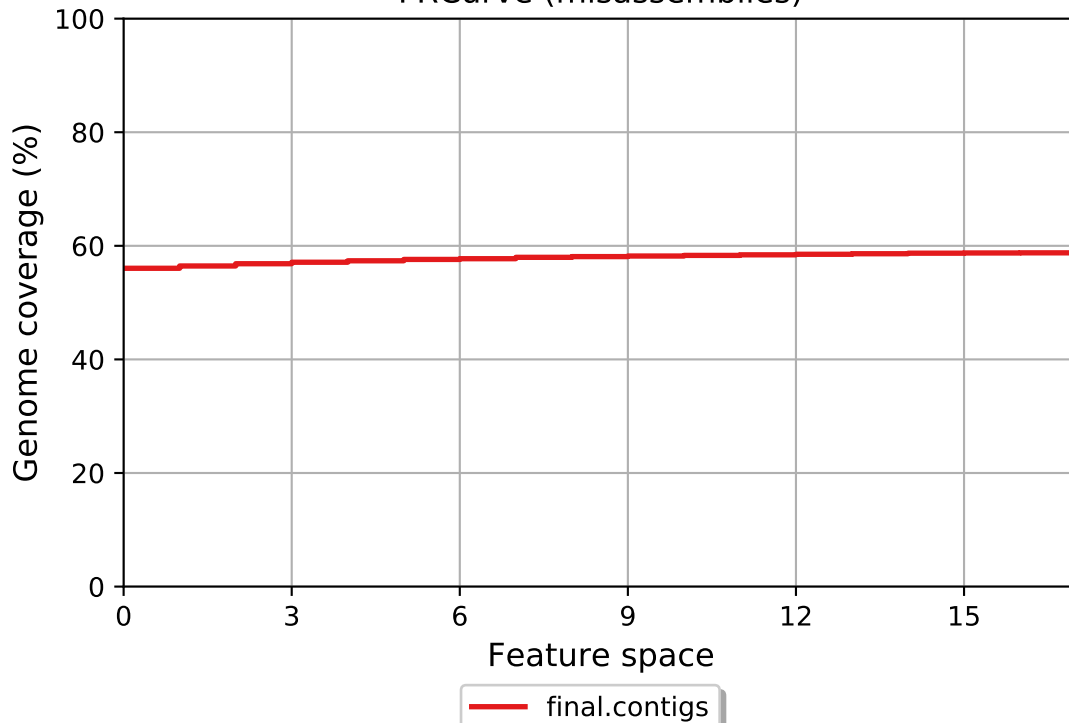


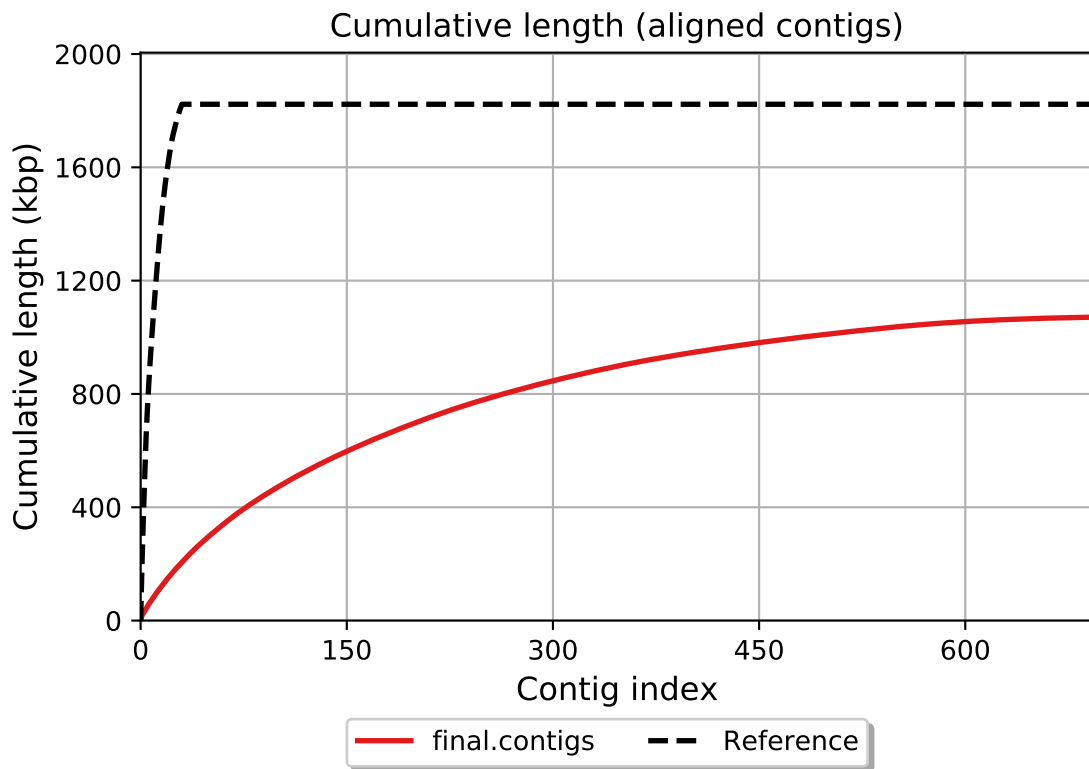
relocations



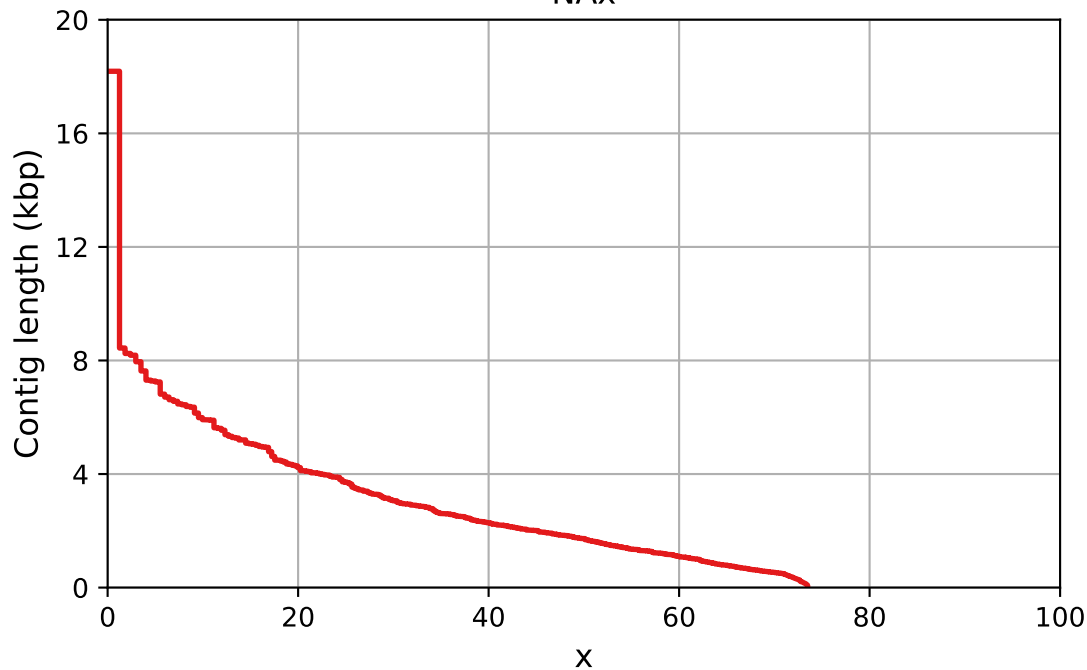
translocations

FRCurve (misassemblies)



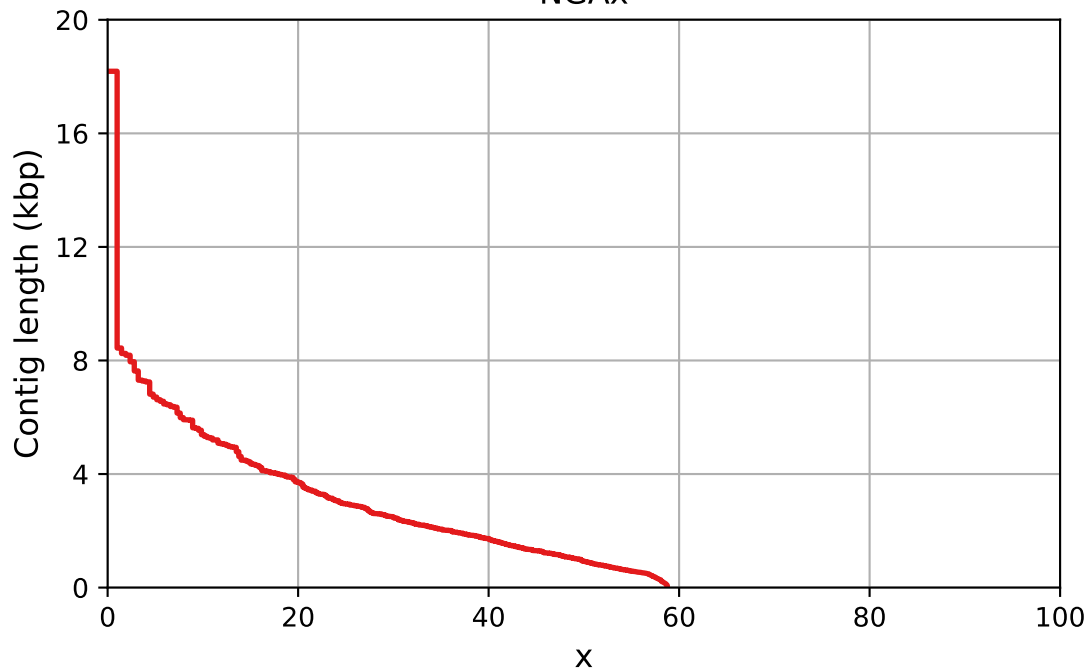


NAx



— final.contigs

NGAx



— final.contigs