

Report	SRRoutput
# contigs (>= 0 bp)	22
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	12051270
Total length (>= 1000 bp)	12051270
Total length (>= 5000 bp)	12051270
Total length (>= 10000 bp)	12051270
Total length (>= 25000 bp)	11978000
Total length (>= 50000 bp)	11945303
# contigs	22
Largest contig	1495363
Total length	12051270
Reference length	12157105
Estimated reference length	-
GC (%)	38.32
Reference GC (%)	38.15
N50	802231
NG50	802231
N90	348143
NG90	348143
auN	852710.3
auNG	845286.9
L50	6
LG50	6
L90	14
LG90	14
# total reads	-
# left	-
# right	-
Mapped (%)	-
Reference mapped (%)	-
Properly paired (%)	-
Reference properly paired (%)	-
Avg. coverage depth	-
Reference avg. coverage depth	-
Coverage >= 1x (%)	-
Reference coverage >= 1x (%)	-
# large blocks misassemblies	-
# misassemblies	86
# misassembled contigs	18
Misassembled contigs length	11372283
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	-
# possible TEs	-
# unaligned mis. contigs	0
# unaligned contigs	0 + 14 part
Unaligned length	70803
Genome fraction (%)	96.901
Duplication ratio	1.015
Avg contig read support	-
# N's per 100 kbp	0.00
# mismatches per 100 kbp	211.81
# indels per 100 kbp	21.60
# genomic features	-
# operons	-
Complete BUSCO (%)	-
Partial BUSCO (%)	-
# predicted genes (unique)	-
# predicted genes (>= 0 bp)	-
# predicted genes (>= 300 bp)	-
# predicted genes (>= 1500 bp)	-
# predicted genes (>= 3000 bp)	-
# predicted rRNA genes	-
Largest alignment	765542
Total aligned length	11956409
NA50	267325
NGA50	267325
NA90	107862
NGA90	95271
auNA	349090.8
auNGA	346051.8
LA50	13
LGA50	13
LA90	41
LGA90	42
K-mer-based compl. (%)	-
K-mer-based cor. length (%)	-
K-mer-based mis. length (%)	-

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

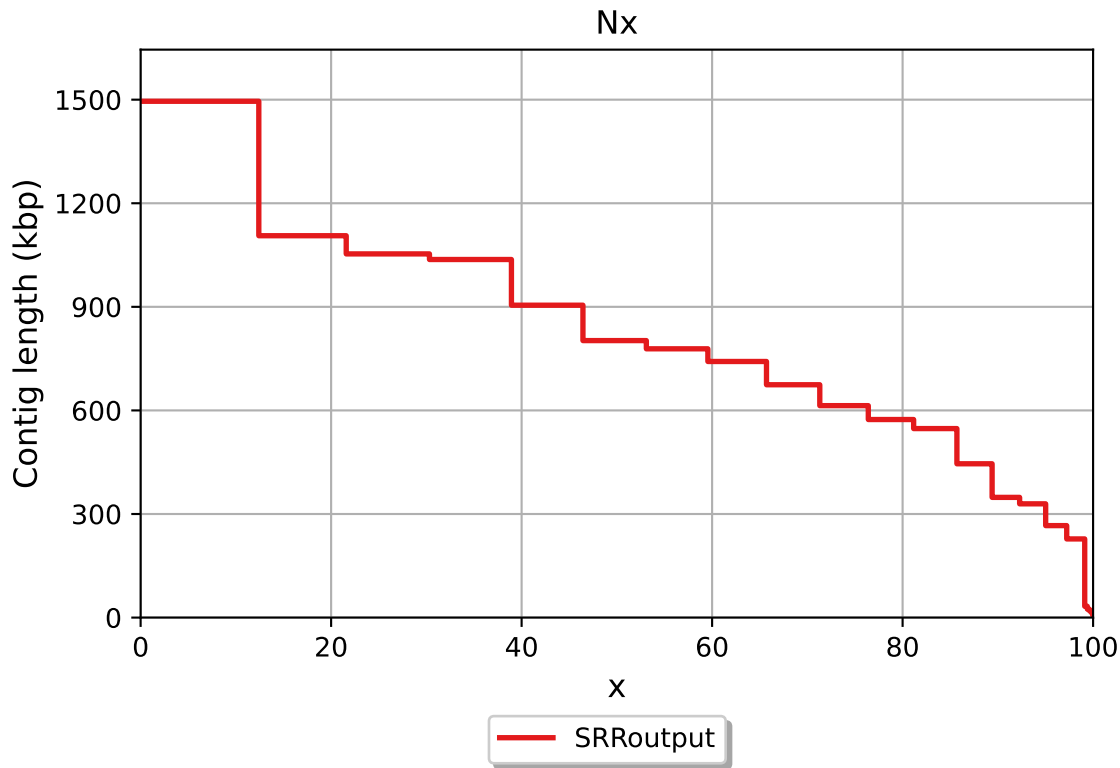
	SRRoutput
# misassemblies	86
# contig misassemblies	86
# c. relocations	33
# c. translocations	53
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	18
Misassembled contigs length	11372283
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	-
# possible TEs	-
# unaligned mis. contigs	0
# mismatches	25325
# indels	2582
# indels (<= 5 bp)	2219
# indels (> 5 bp)	363
Indels length	13736

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).

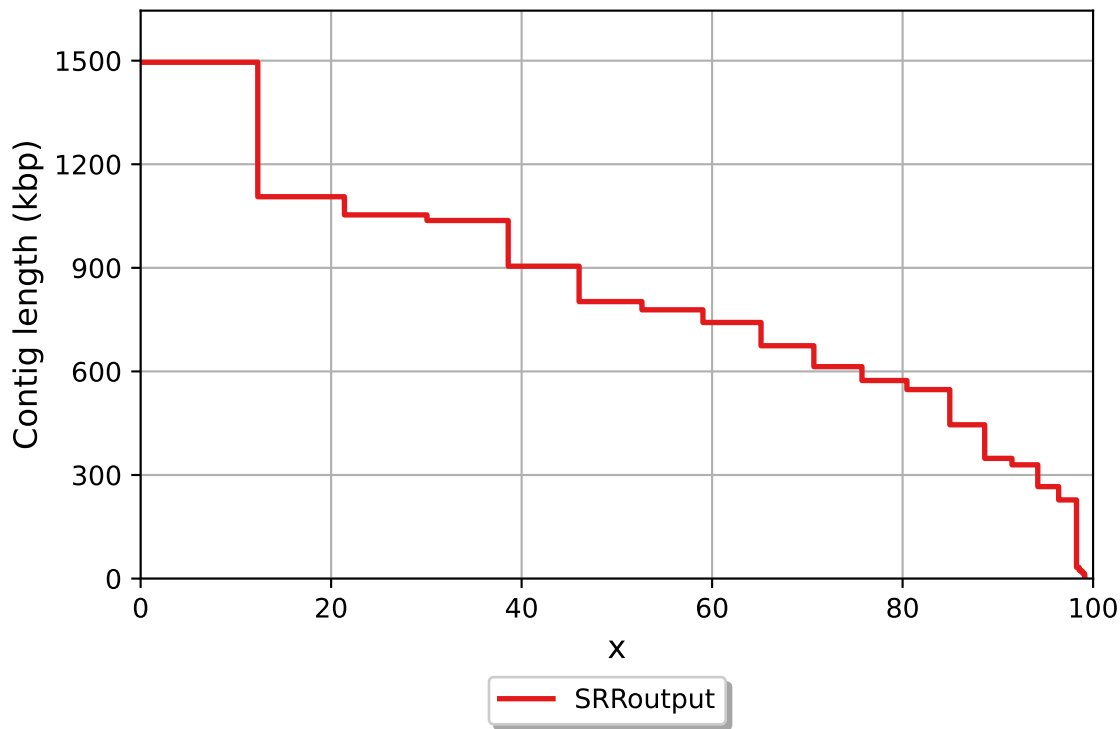
Unaligned report

	SRRoutput
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	70803
# N's	0

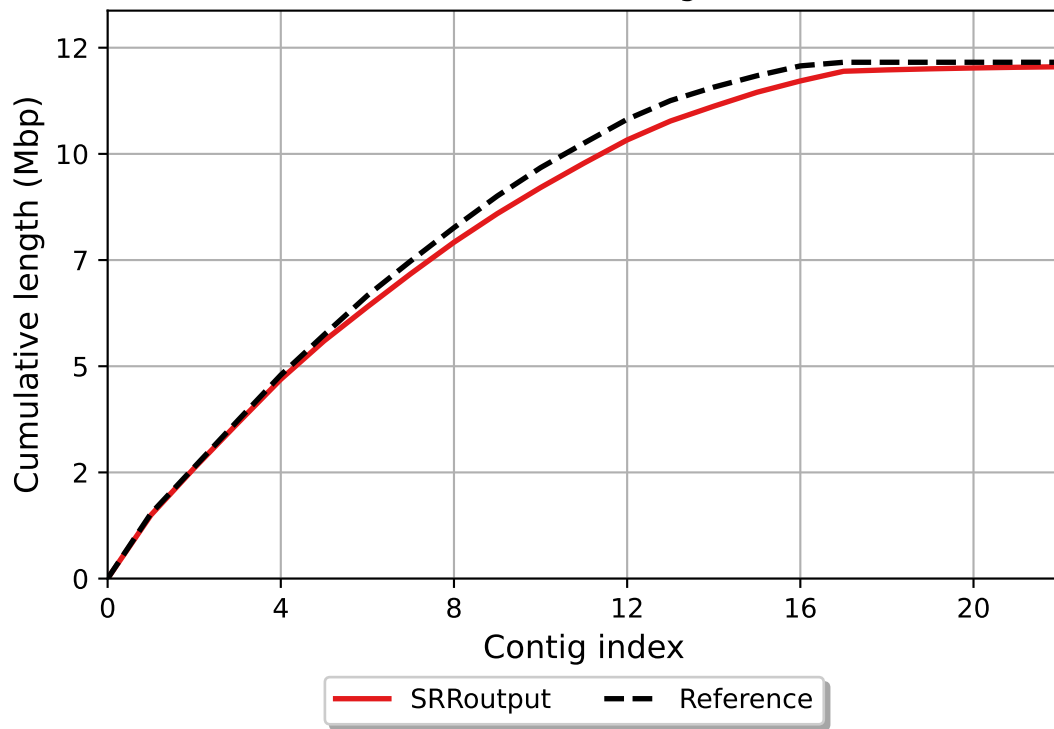
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



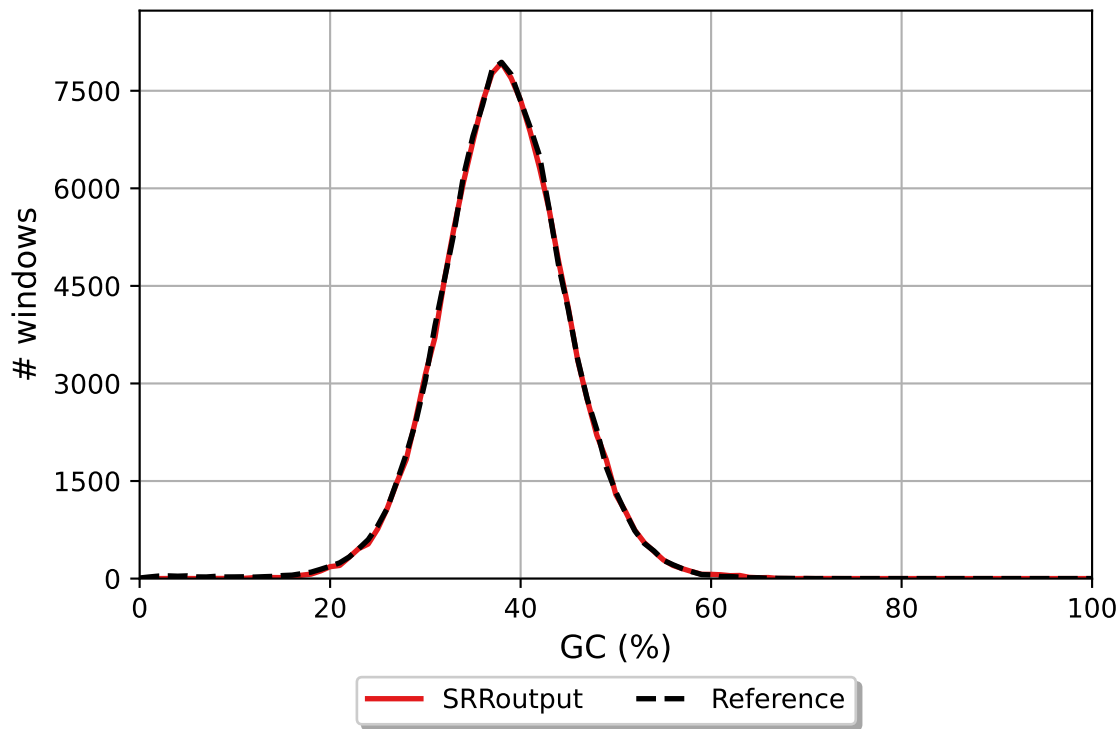
NGx



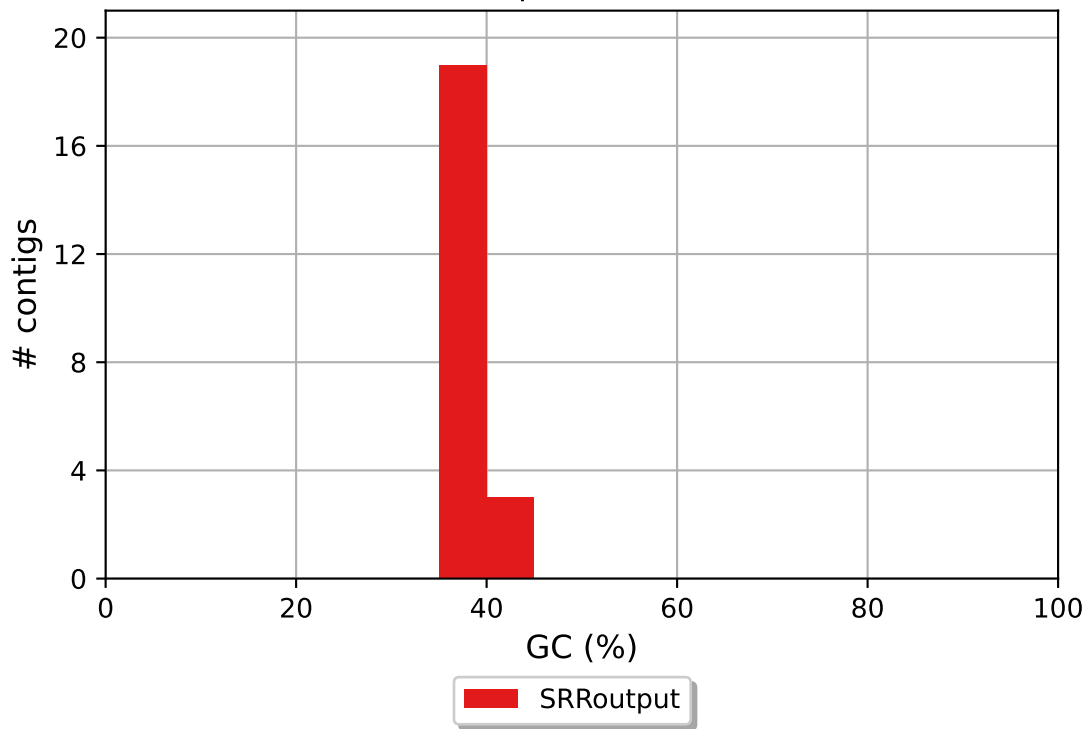
Cumulative length



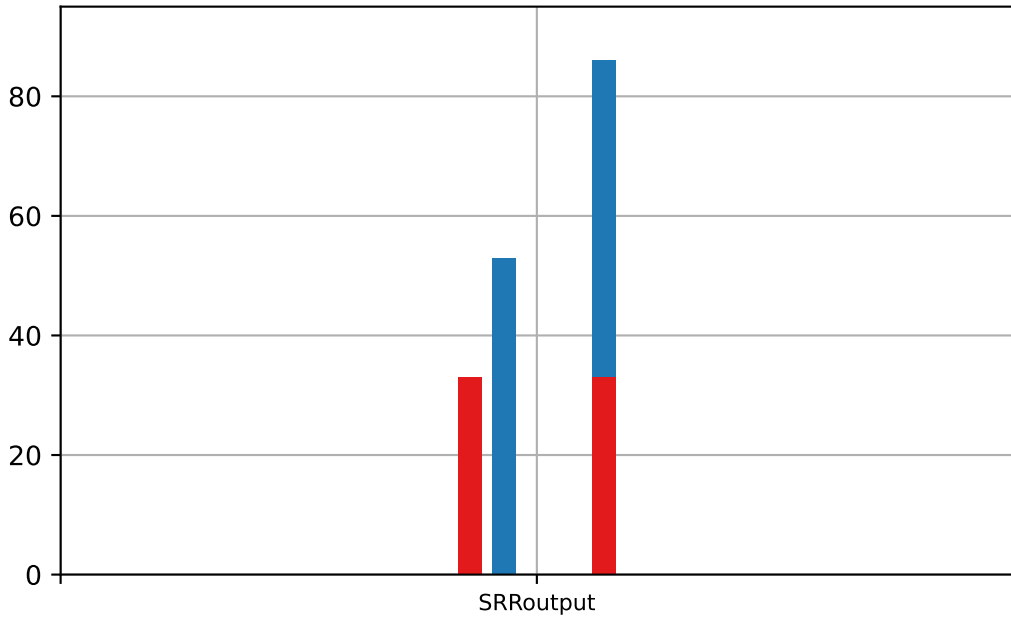
GC content



SRRoutput GC content



Misassemblies

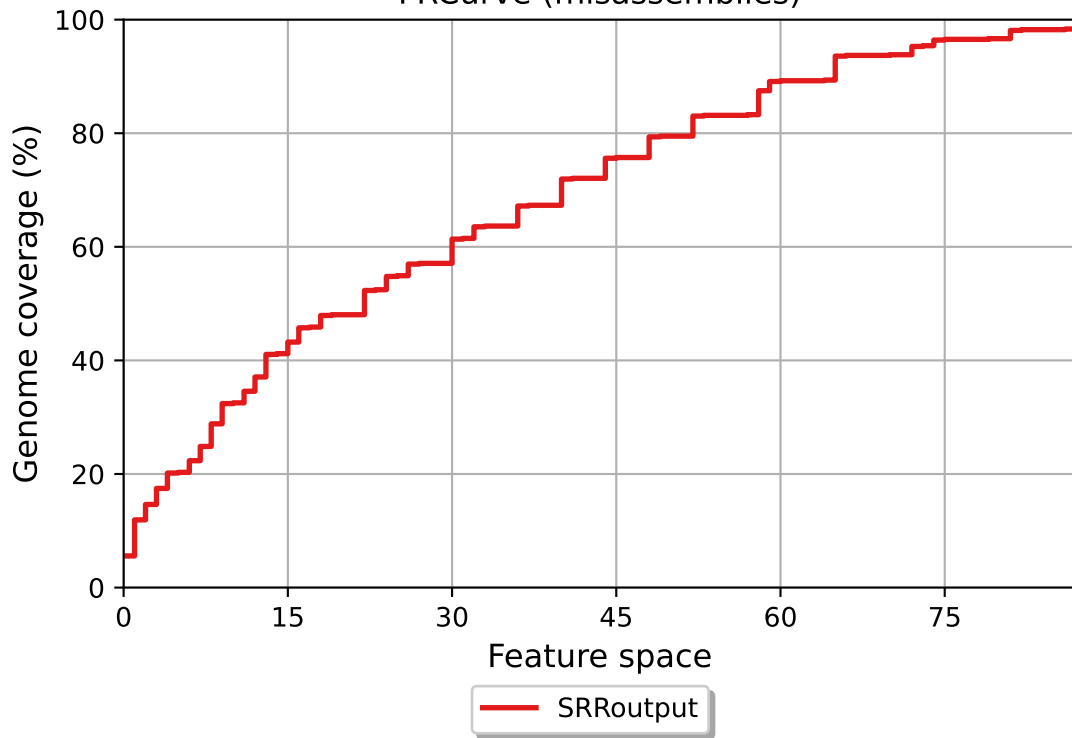


relocations

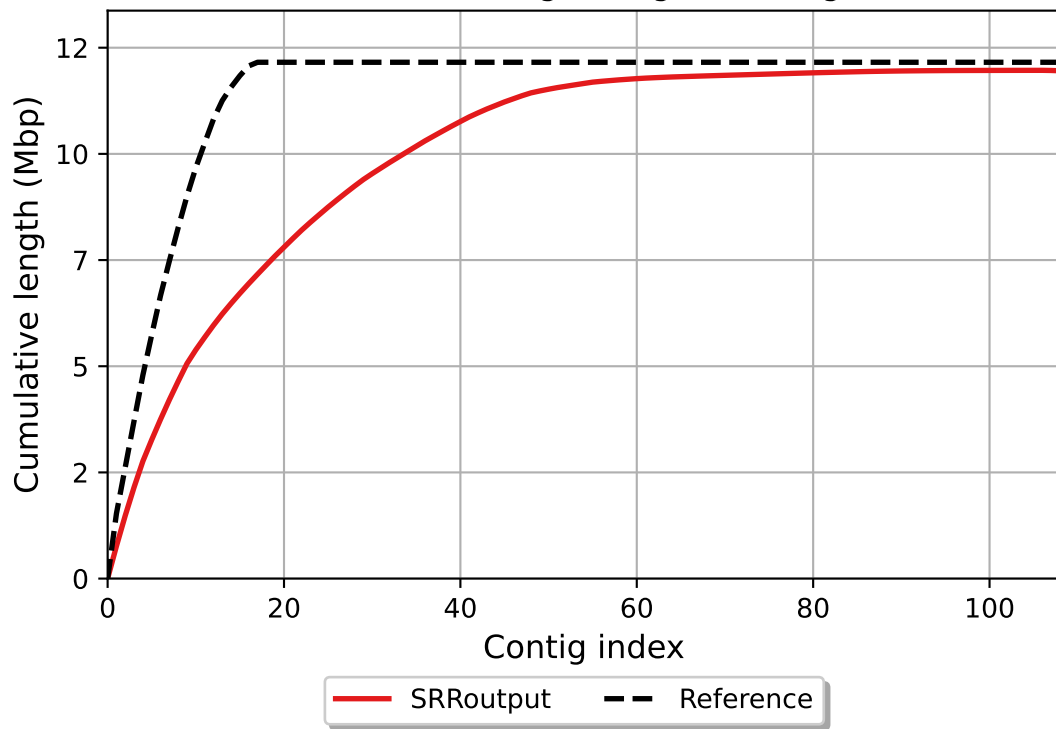


translocations

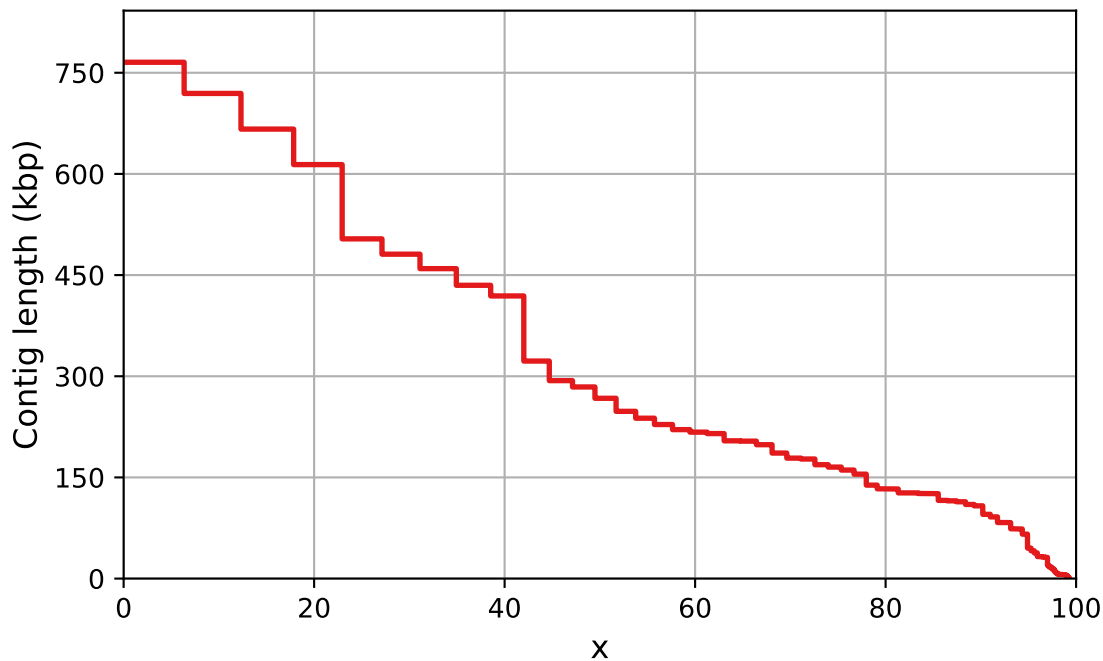
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



SRRoutput

NGAx

