

Report

	contigs_SRR15131330_spades_fasta
# contigs (≥ 0 bp)	913
# contigs (≥ 1000 bp)	141
Total length (≥ 0 bp)	1943393
Total length (≥ 1000 bp)	1817445
# contigs	156
Largest contig	56016
Total length	1828630
Reference length	2191149
GC (%)	36.69
Reference GC (%)	37.07
N50	20442
NG50	17352
N90	5672
NG90	-
auN	23868.1
auNG	19919.2
L50	28
LG50	38
L90	89
LG90	-
# misassemblies	108
# misassembled contigs	59
Misassembled contigs length	1137891
# local misassemblies	23
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 47 part
Unaligned length	152190
Genome fraction (%)	82.051
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	586.51
# indels per 100 kbp	51.76
Largest alignment	46871
Total aligned length	1667312
NA50	11161
NGA50	8874
NA90	822
NGA90	-
auNA	15071.2
auNGA	12577.7
LA50	44
LGA50	63
LA90	214
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_SRR15131330_spades_fasta
# misassemblies	108
# contig misassemblies	108
# c. relocations	108
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	59
Misassembled contigs length	1137891
# local misassemblies	23
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9779
# indels	863
# indels (<= 5 bp)	669
# indels (> 5 bp)	194
Indels length	6259

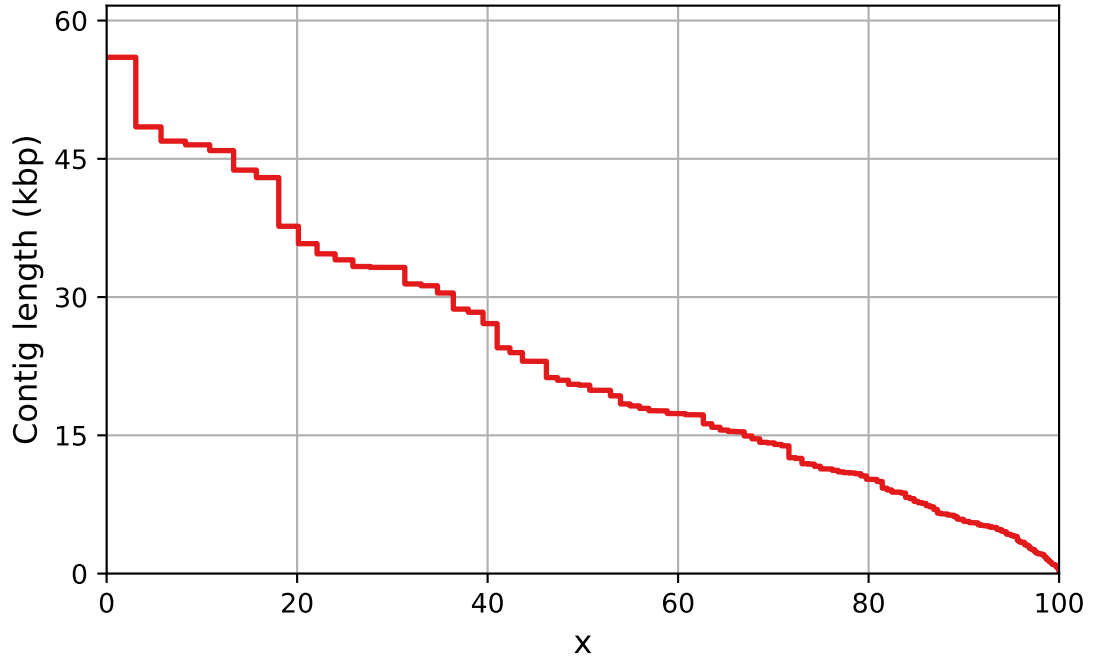
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	contigs_SRR15131330_spades_fasta
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	47
Partially unaligned length	152190
# N's	0

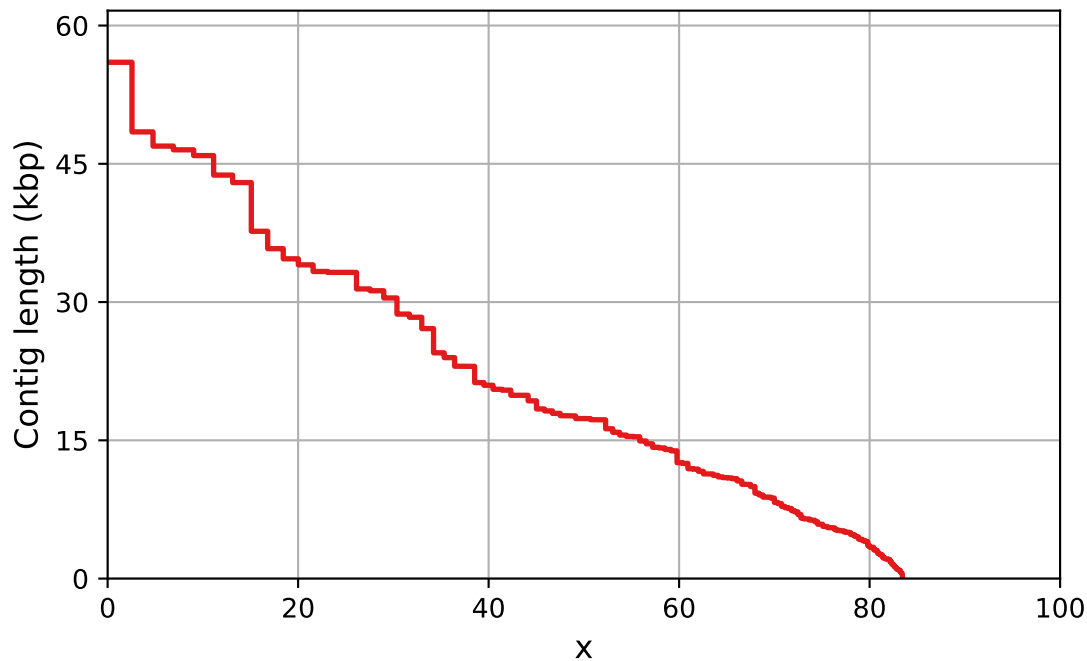
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



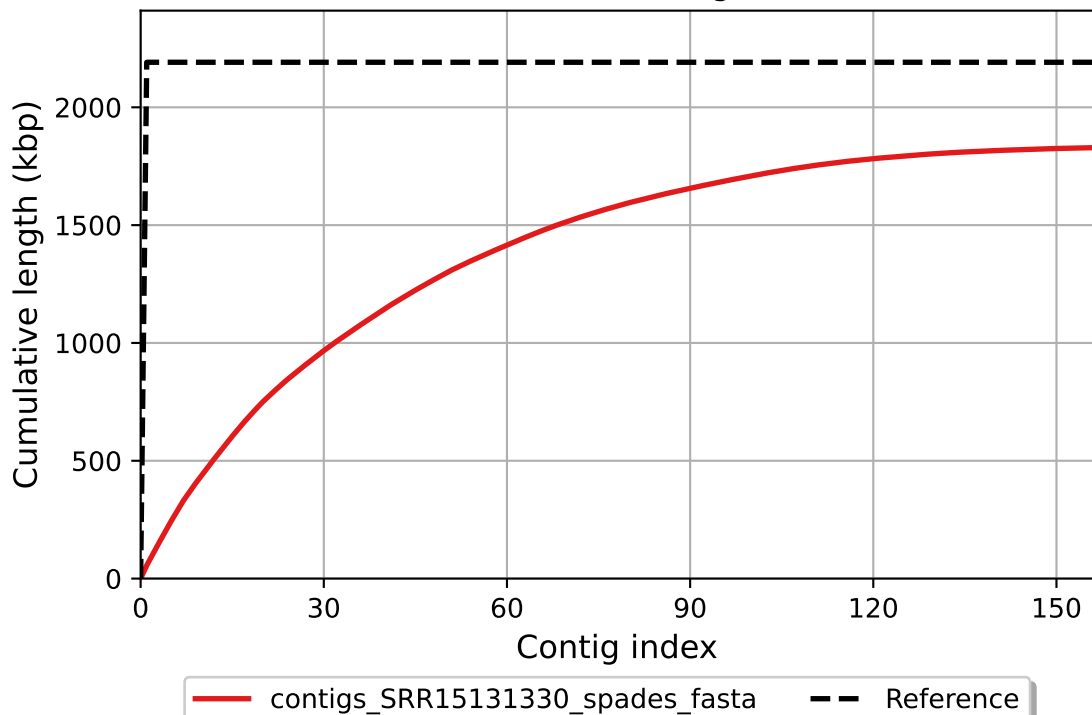
— contigs_SRR15131330_spades_fasta

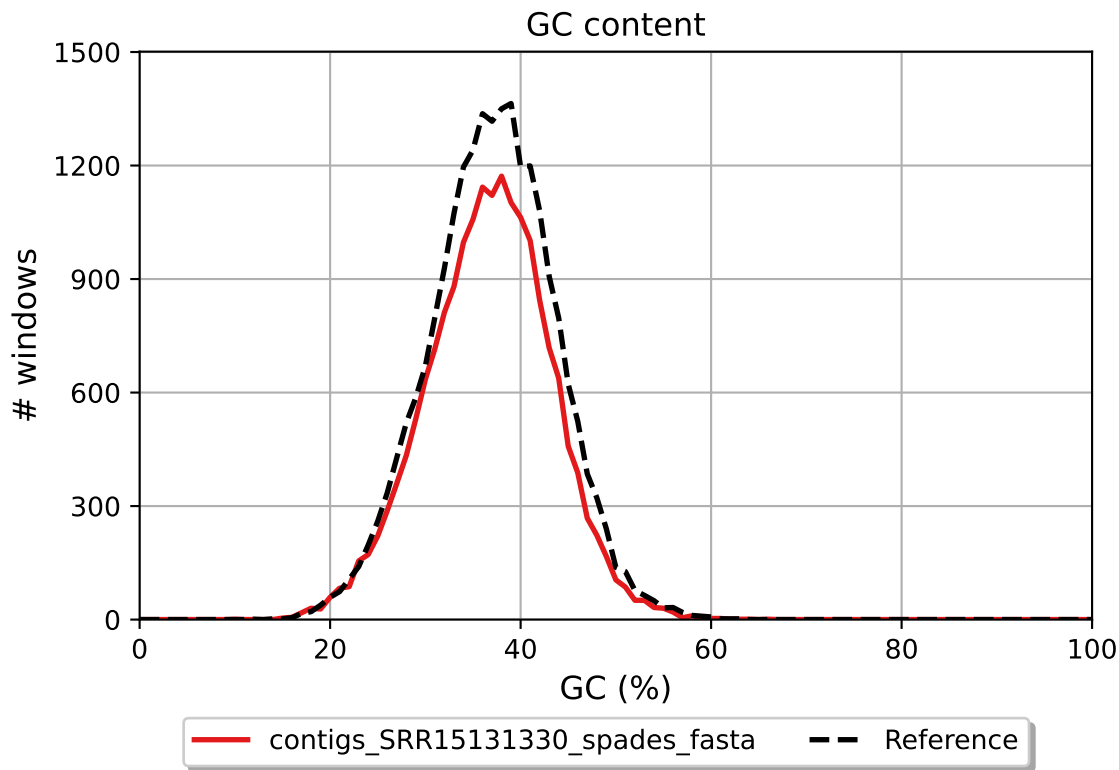
NGx



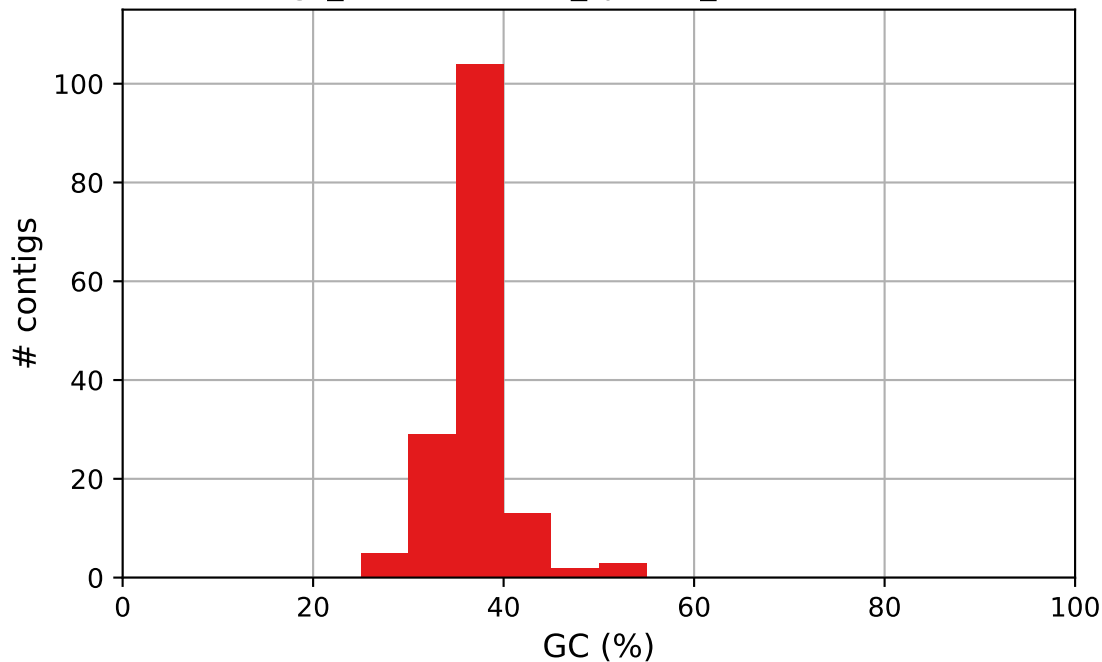
— contigs_SRR15131330_spades_fasta

Cumulative length



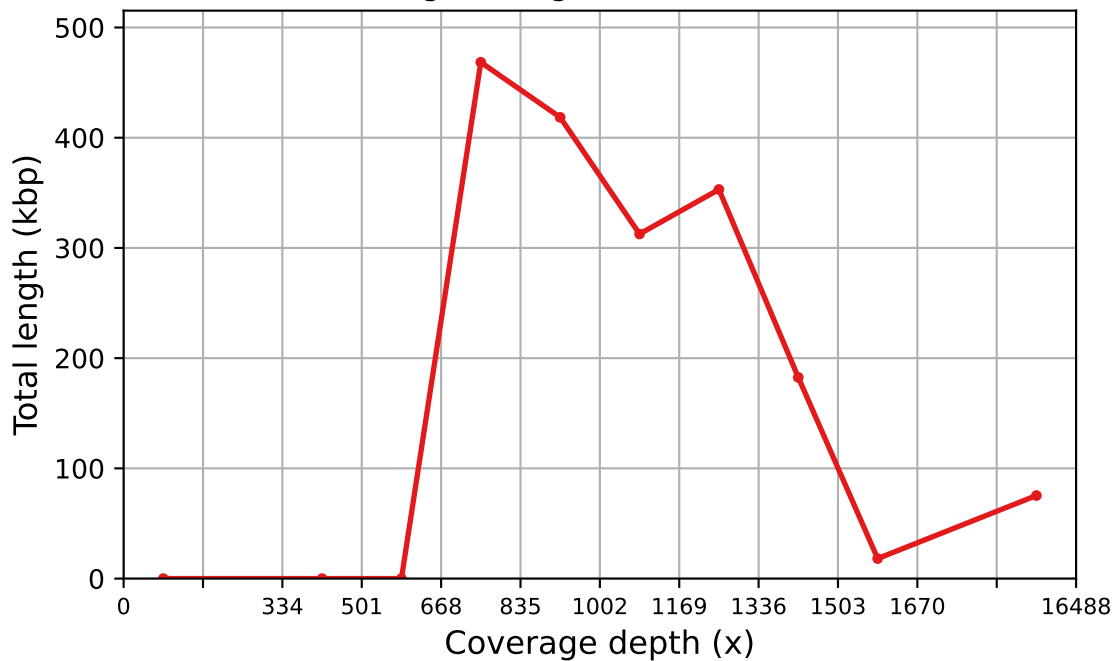


contigs_SRR15131330_spades_fasta GC content



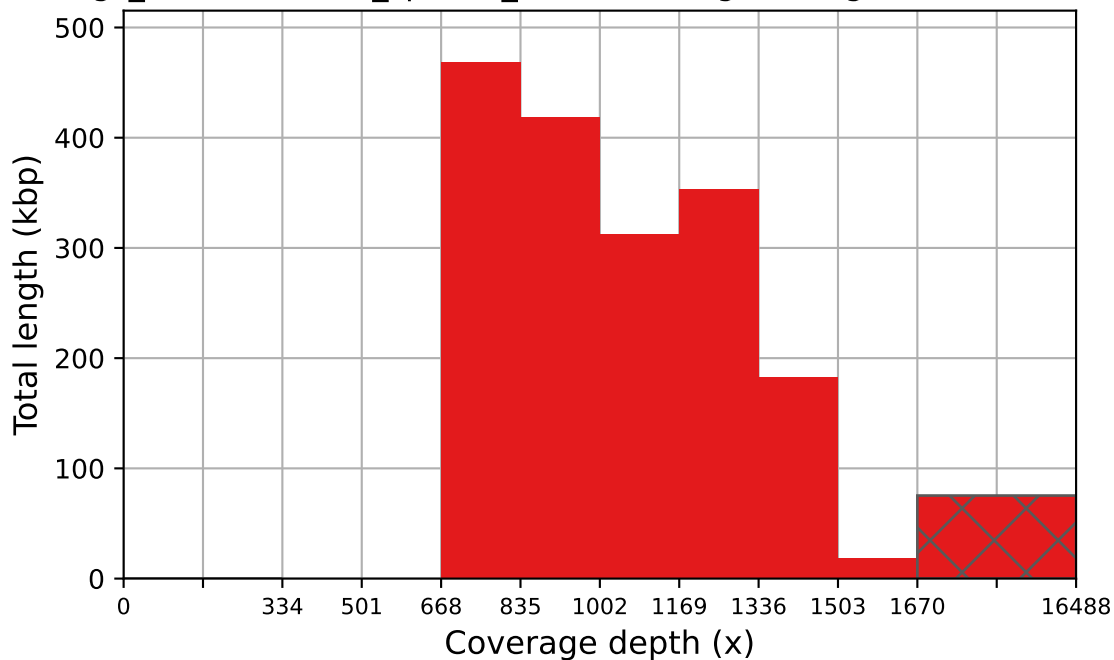
contigs_SRR15131330_spades_fasta

Coverage histogram (bin size: 167x)

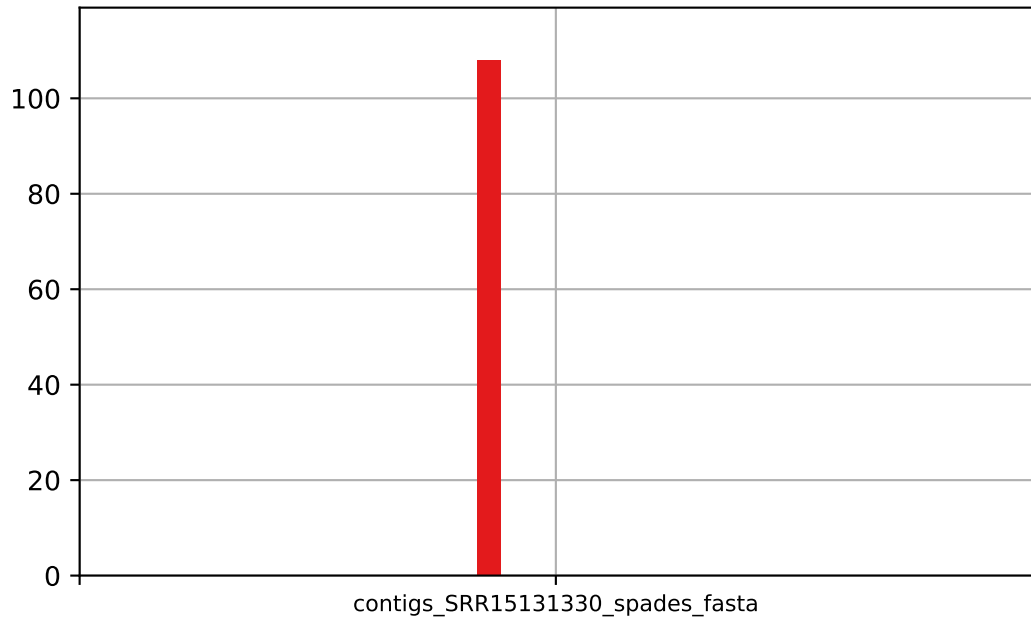


contigs_SRR15131330_spades_fasta

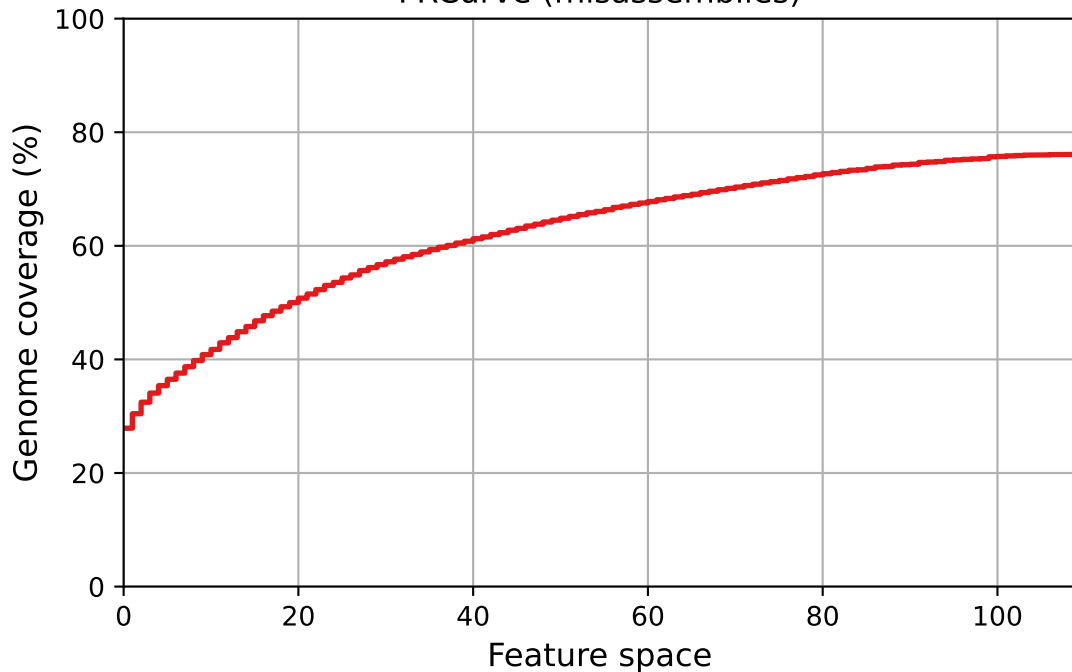
contigs_SRR15131330_spades_fasta coverage histogram (bin size: 167x)



Misassemblies

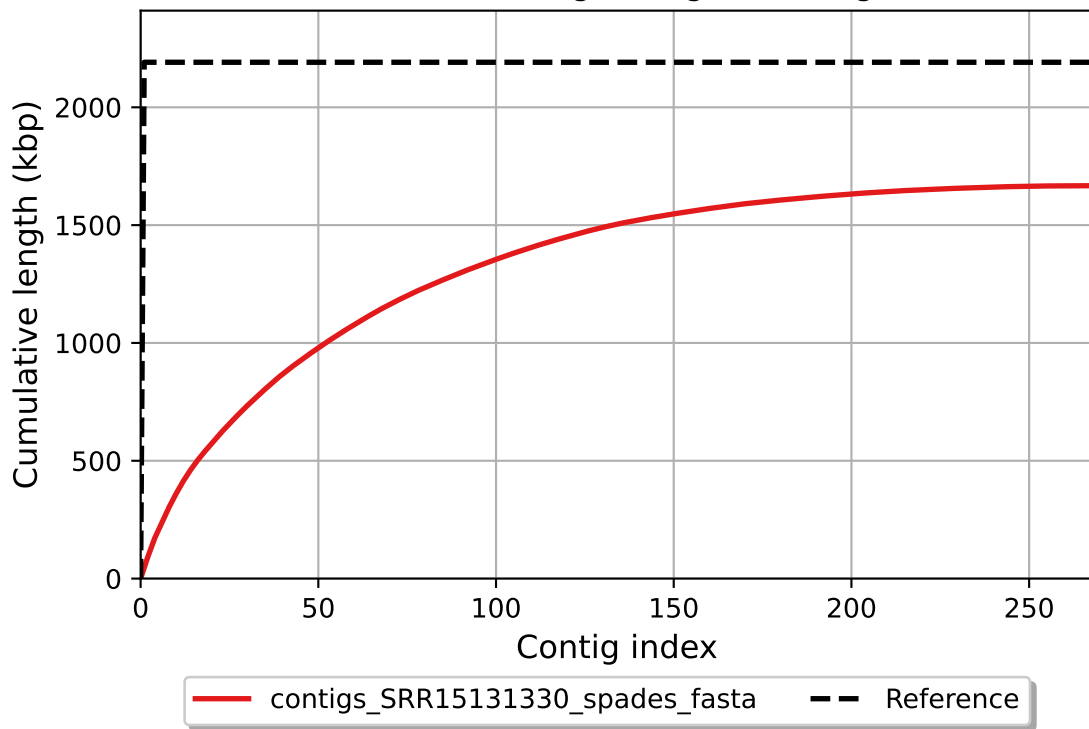


FRCurve (misassemblies)

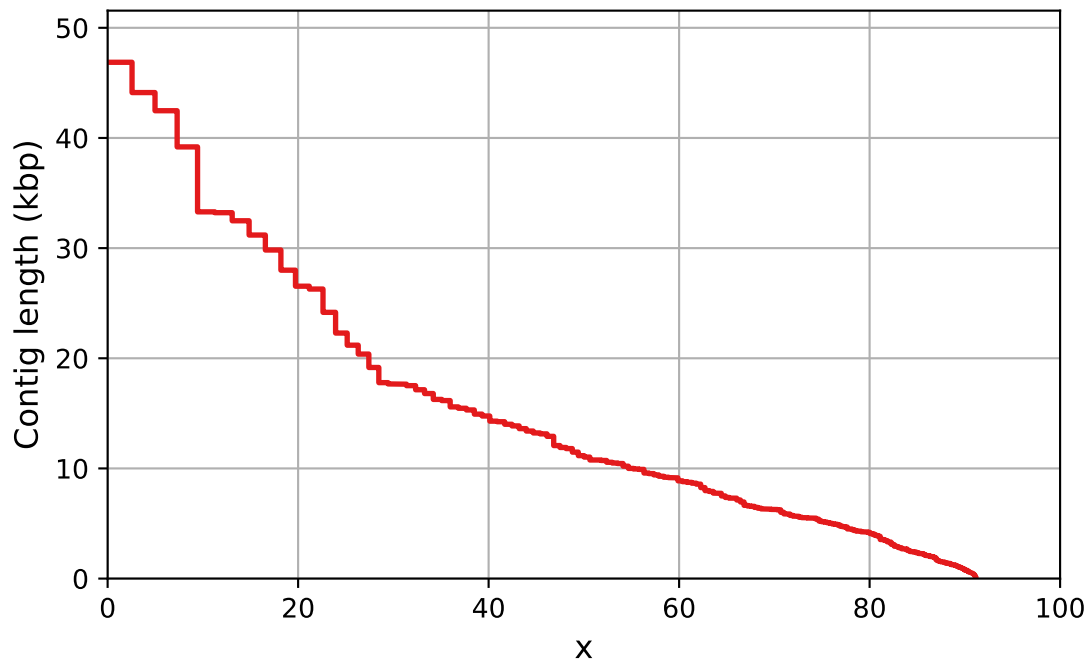


— contigs_SRR15131330_spades_fasta

Cumulative length (aligned contigs)

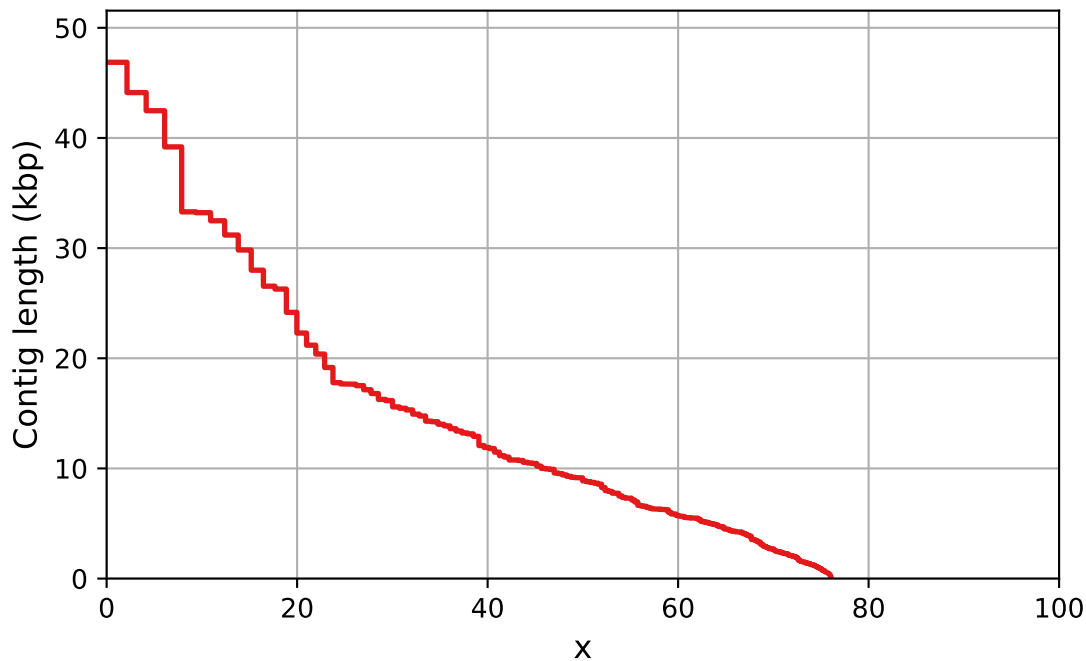


NAx



— contigs_SRR15131330_spades_fasta

NGAx



— contigs_SRR15131330_spades_fasta