

Report

	SRR33190466_closedgap	SRR33190466.consensus	ref_SRR33190466
# contigs (>= 0 bp)	1	1	1
# contigs (>= 1000 bp)	1	1	1
# contigs (>= 5000 bp)	1	1	1
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	1	1	1
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	29647	29856	29903
Total length (>= 1000 bp)	29647	29856	29903
Total length (>= 5000 bp)	29647	29856	29903
Total length (>= 10000 bp)	29647	29856	29903
Total length (>= 25000 bp)	29647	29856	29903
Total length (>= 50000 bp)	0	0	0
# contigs	1	1	1
Largest contig	29647	29856	29903
Total length	29647	29856	29903
Reference length	29903	29903	29903
GC (%)	37.86	37.81	37.82
Reference GC (%)	37.97	37.97	37.97
N50	29647	29856	29903
NG50	29647	29856	29903
N90	29647	29856	29903
NG90	29647	29856	29903
auN	29647.0	29856.0	29903.0
auNG	29393.2	29809.1	29903.0
L50	1	1	1
LG50	1	1	1
L90	1	1	1
LG90	1	1	1
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	99.338	98.689	99.368
Duplication ratio	0.998	0.998	1.000
# N's per 100 kbp	3.37	1108.65	892.89
# mismatches per 100 kbp	428.39	427.64	447.60
# indels per 100 kbp	43.85	37.33	6.73
Largest alignment	29646	29464	29714
Total aligned length	29646	29464	29714
NA50	29646	29464	29714
NGA50	29646	29464	29714
NA90	29646	29464	29714
NGA90	29646	29464	29714
auNA	29645.0	29077.1	29526.2
auNGA	29391.2	29031.4	29526.2
LA50	1	1	1
LGA50	1	1	1
LA90	1	1	1
LGA90	1	1	1

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

	SRR33190466_closedgap	SRR33190466.consensus	ref_SRR33190466
# misassemblies	0	0	0
# contig misassemblies	0	0	0
# c. relocations	0	0	0
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	127	126	133
# indels	13	11	2
# indels (<= 5 bp)	6	5	2
# indels (> 5 bp)	7	6	0
Indels length	91	79	2

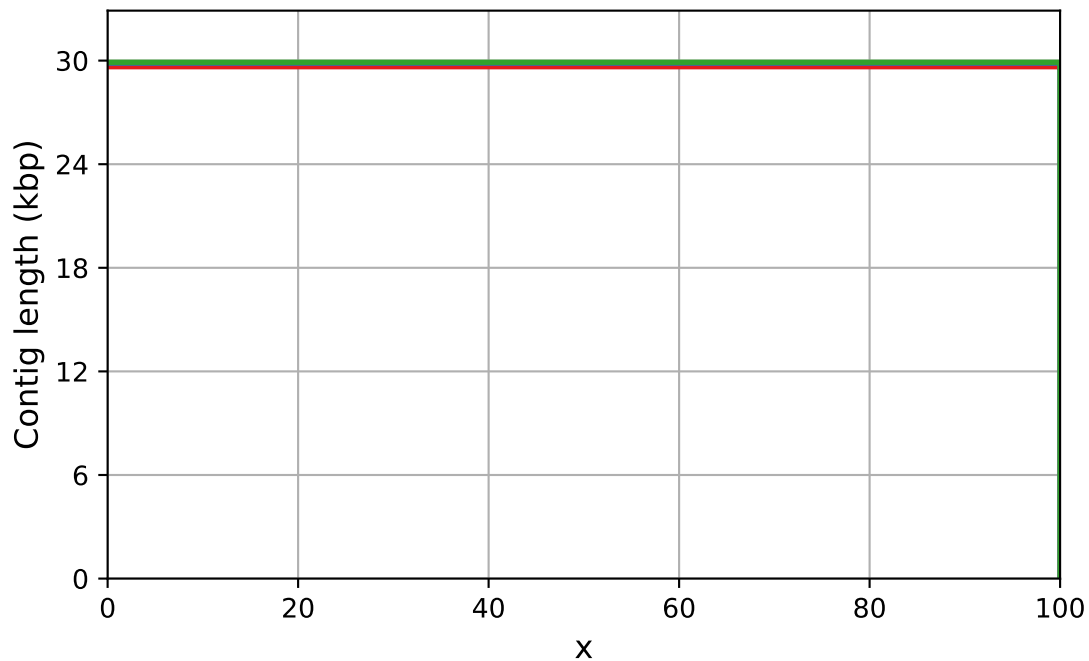
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR33190466_closedgap	SRR33190466.consensus	ref_SRR33190466
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	1	331	267

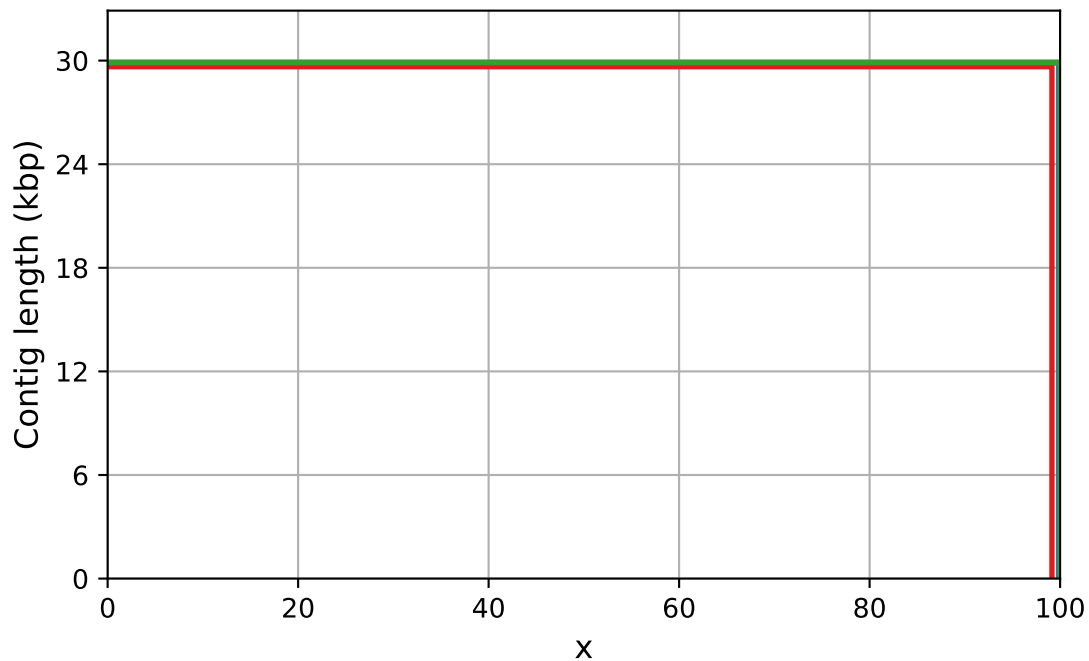
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



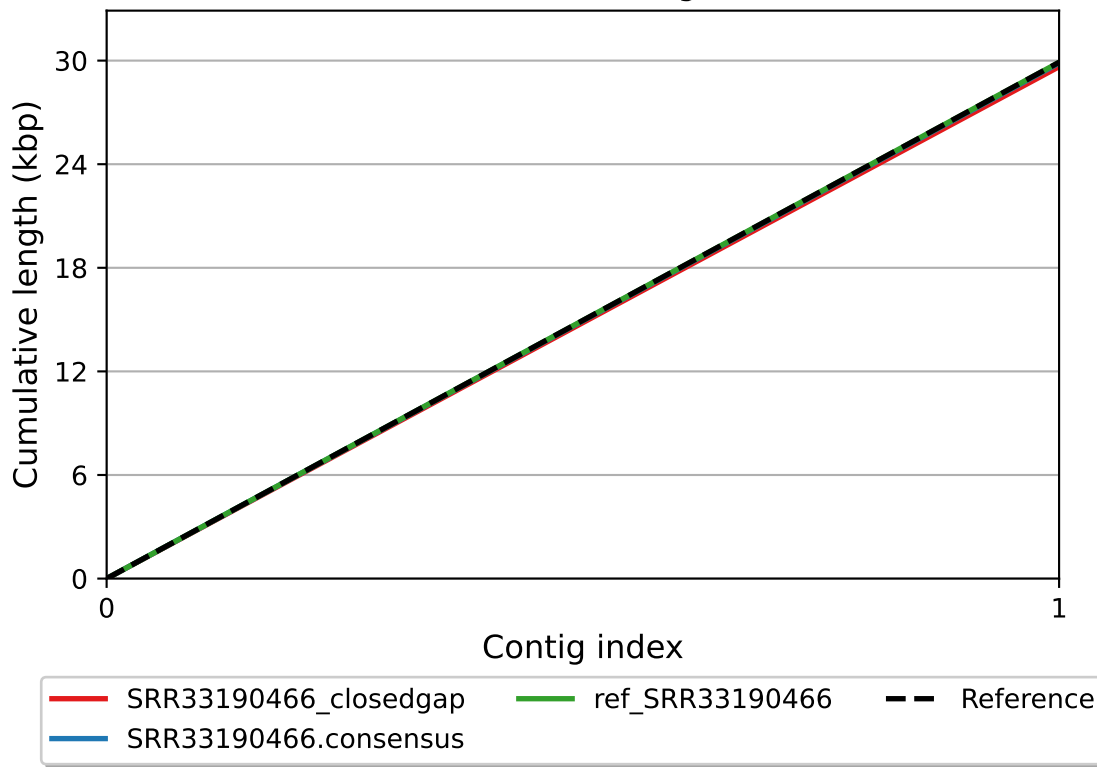
SRR33190466_closedgap SRR33190466.consensus ref_SRR33190466

NGx

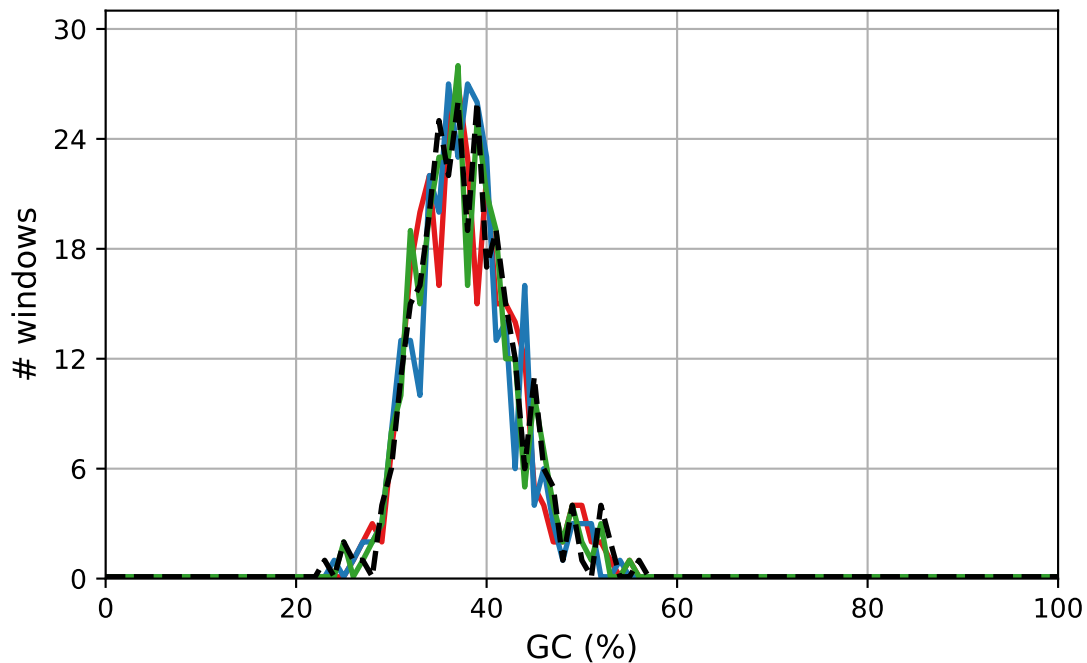


— SRR33190466_closedgap — SRR33190466.consensus — ref_SRR33190466

Cumulative length

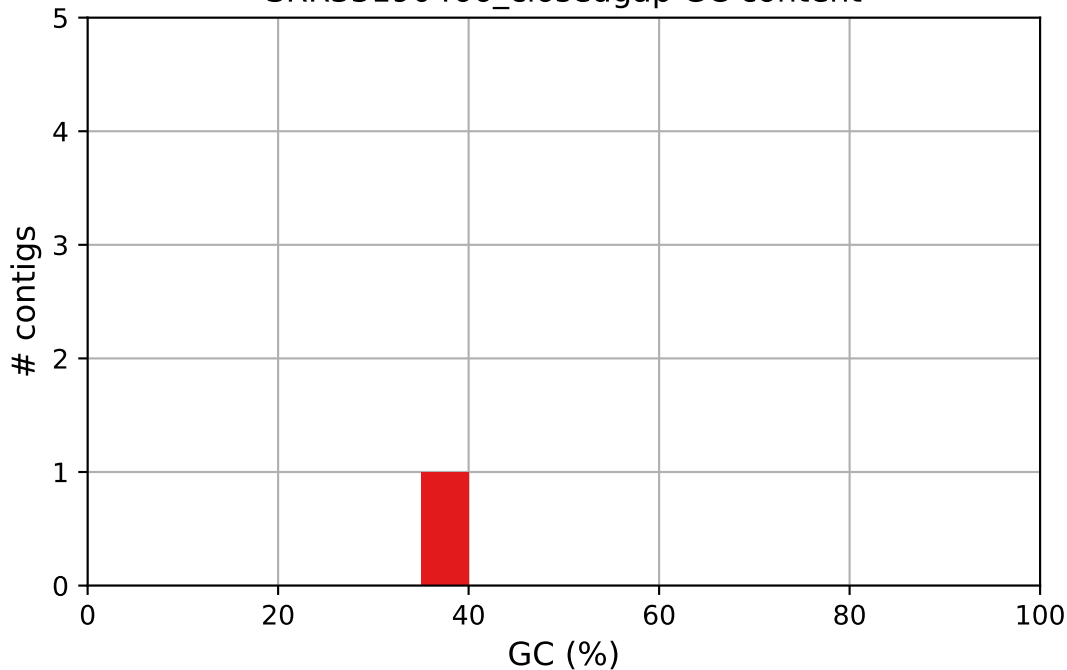


GC content



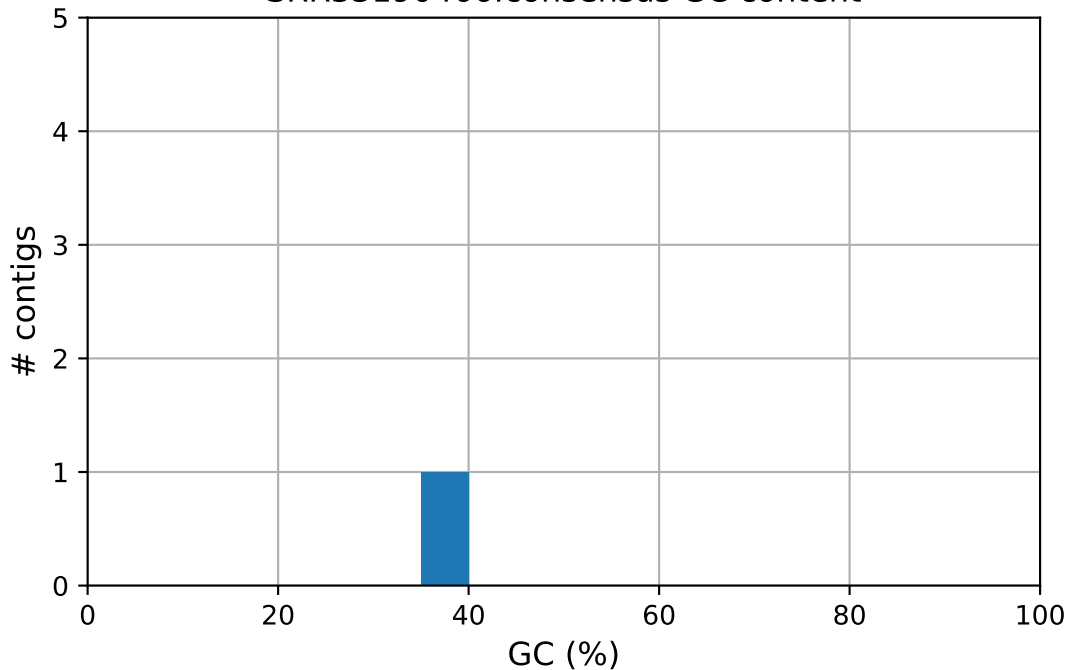
— SRR33190466_closedgap — ref_SRR33190466 - - Reference
— SRR33190466.consensus

SRR33190466_closedgap GC content



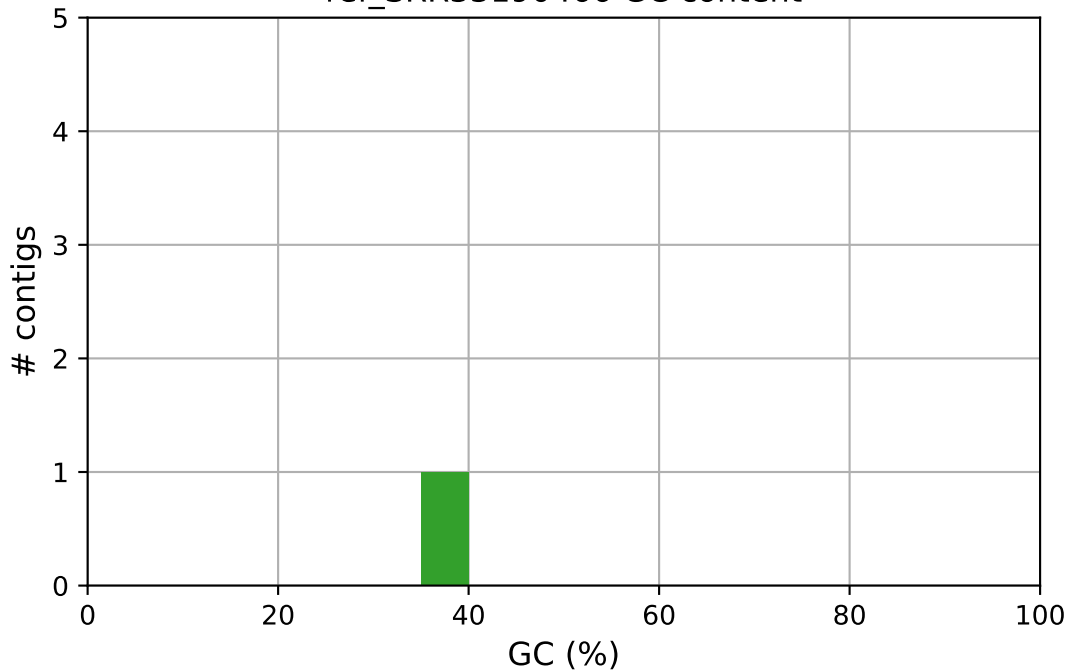
■ SRR33190466_closedgap

SRR33190466.consensus GC content



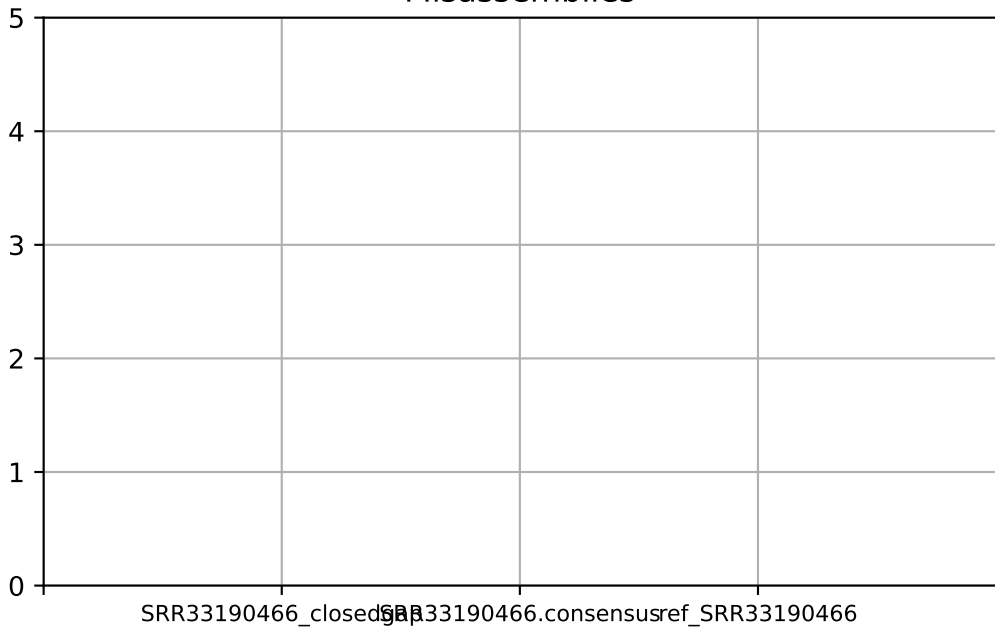
SRR33190466.consensus

ref_SRR33190466 GC content

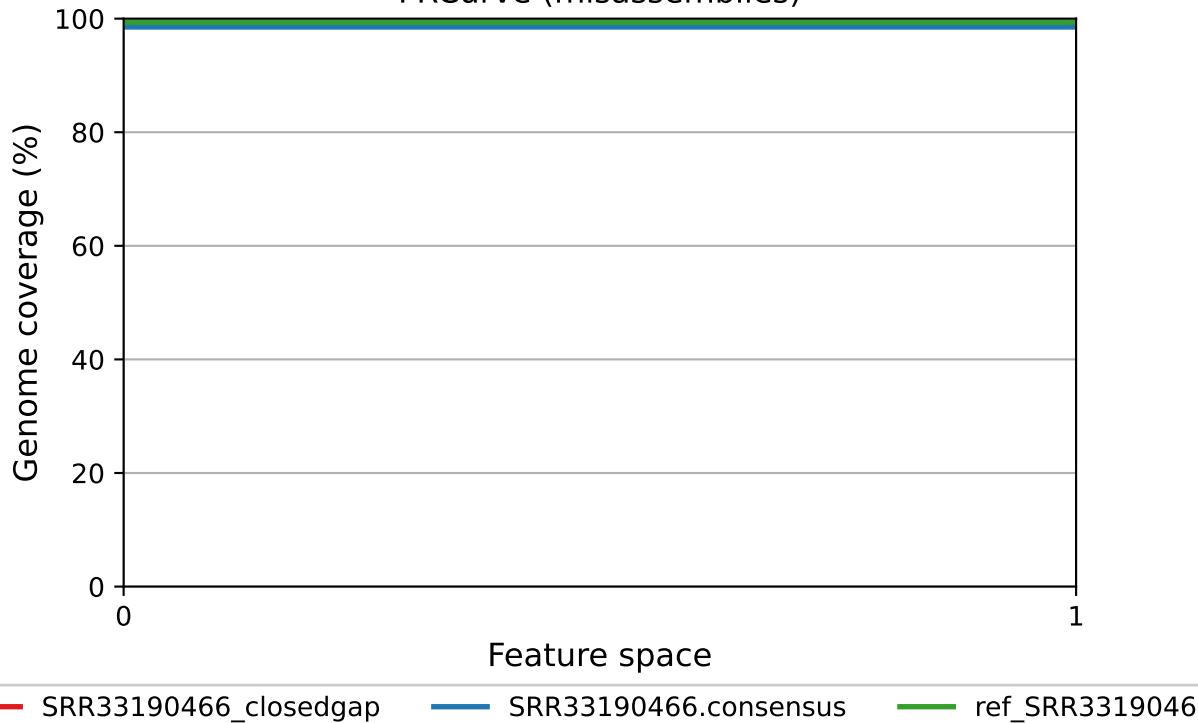


ref_SRR33190466

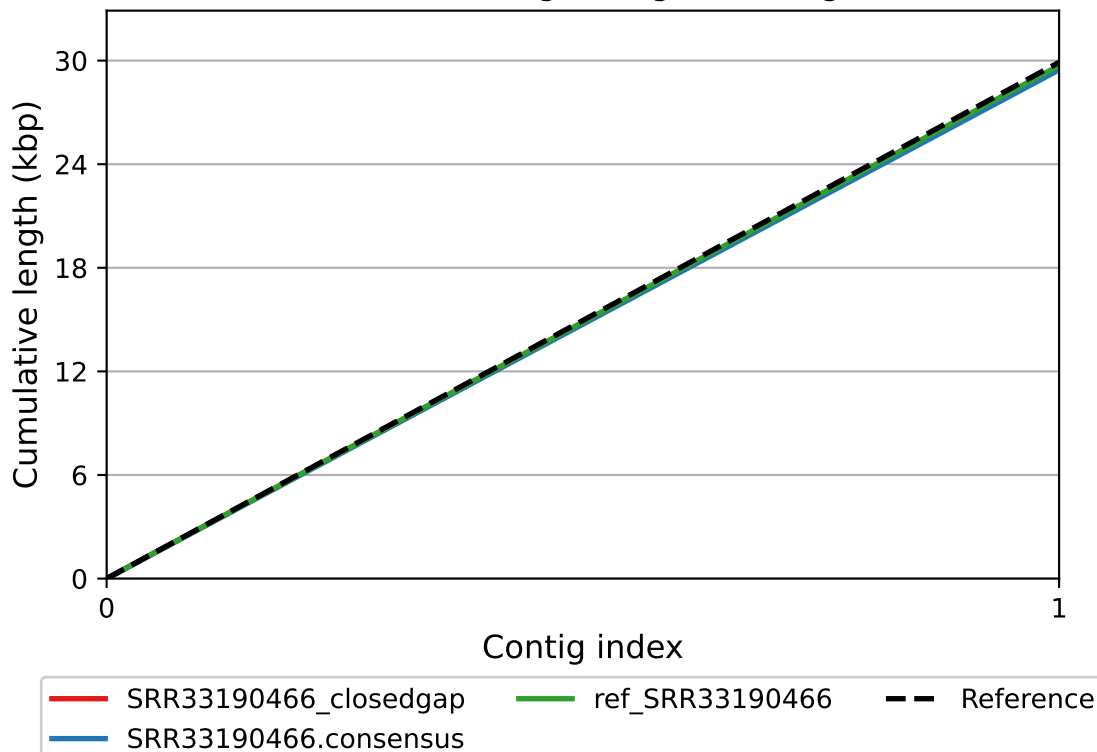
Misassemblies



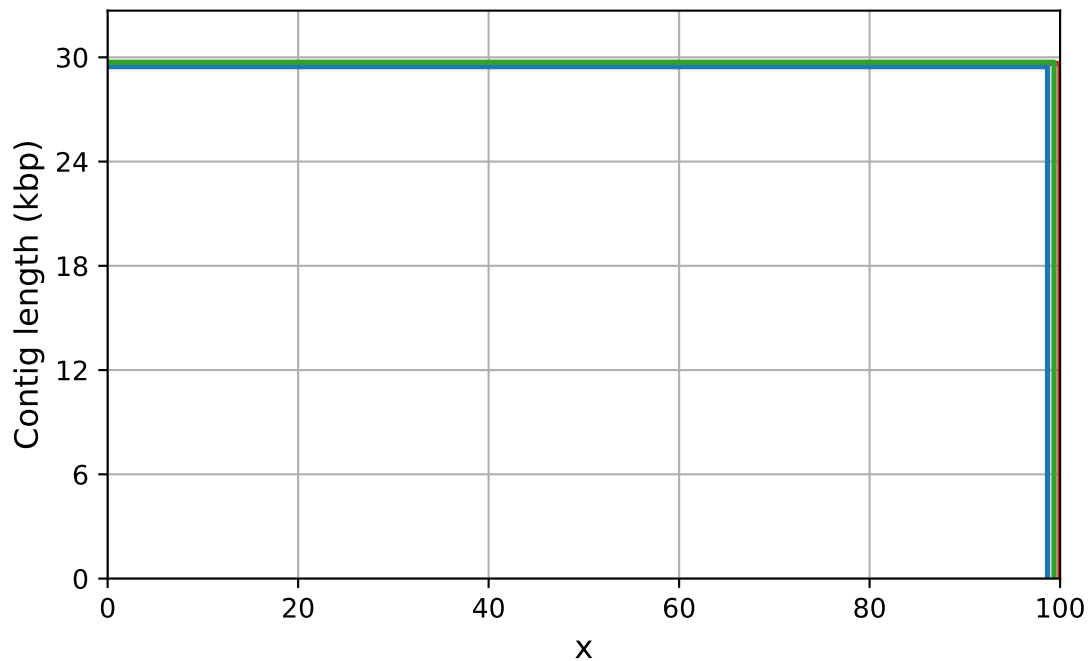
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

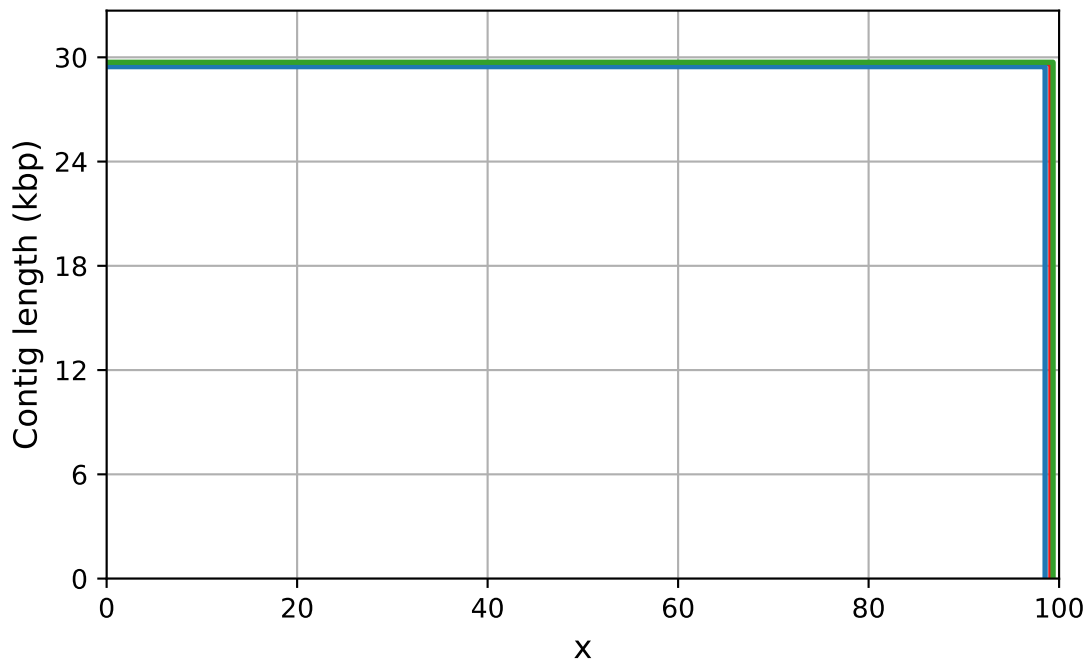


SRR33190466_closedgap

SRR33190466.consensus

ref_SRR33190466

NGAx



SRR33190466_closedgap SRR33190466.consensus ref_SRR33190466

Genome fraction, %

100

99

SRR33190466_closedgap SRR33190466.consensus ref_SRR33190466

