

Report

	SPAdes_reads_ampliados_coincidentes_Contigs
# contigs (>= 0 bp)	20
# contigs (>= 1000 bp)	5
Total length (>= 0 bp)	17762
Total length (>= 1000 bp)	15636
# contigs	5
Largest contig	5355
Total length	15636
Reference length	15948
GC (%)	47.78
Reference GC (%)	48.10
N50	4397
NG50	4397
N90	1572
NG90	1572
auN	3830.1
auNG	3755.1
L50	2
LG50	2
L90	5
LG90	5
# total reads	543207
# left	271650
# right	271557
Mapped (%)	99.57
Reference mapped (%)	100.28
Properly paired (%)	92.12
Reference properly paired (%)	100.0
Avg. coverage depth	4978
Reference avg. coverage depth	4960
Coverage >= 1x (%)	100.0
Reference coverage >= 1x (%)	99.44
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.934
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3926.22
# indels per 100 kbp	12.81
Largest alignment	5332
Total aligned length	15613
NA50	4397
NGA50	4397
NA90	1572
NGA90	1572
auNA	3814.4
auNGA	3739.7
LA50	2
LGA50	2
LA90	5
LGA90	5

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).

Reads report

	SPAdes_reads_ampliados_coincidentes_Contigs
# total reads	543207
# left	271650
# right	271557
# mapped	540861
Mapped (%)	99.57
# properly paired	500424
Properly paired (%)	92.12
# singletons	314
Singletons (%)	0.06
# misjoint mates	32744
Misjoint mates (%)	6.03
Avg. coverage depth	4978
Coverage >= 1x (%)	100.0
Coverage >= 5x (%)	99.93
Coverage >= 10x (%)	99.9
# reference mapped	543506
Reference mapped (%)	100.28
# reference properly paired	541972
Reference properly paired (%)	100.0
# reference singletons	0
Reference singletons (%)	0.0
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	4960
Reference coverage >= 1x (%)	99.44
Reference coverage >= 5x (%)	99.43
Reference coverage >= 10x (%)	99.4

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

	SPAdes_reads_ampliados_coincidentes__Contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	613
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

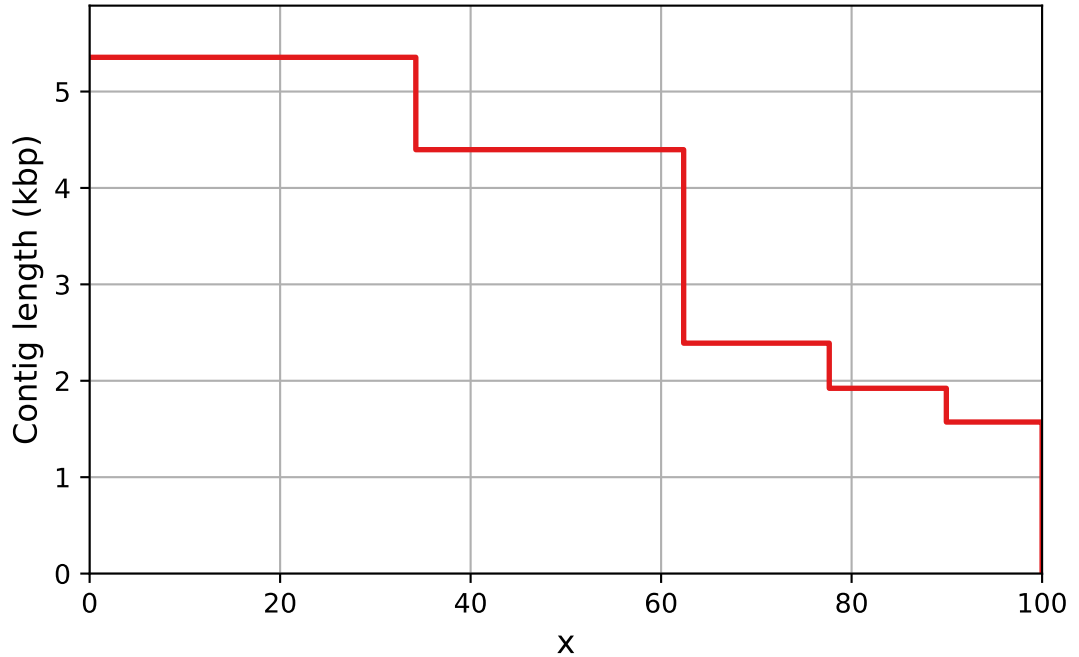
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SPAdes_reads_ampliados_coincidentes__Contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

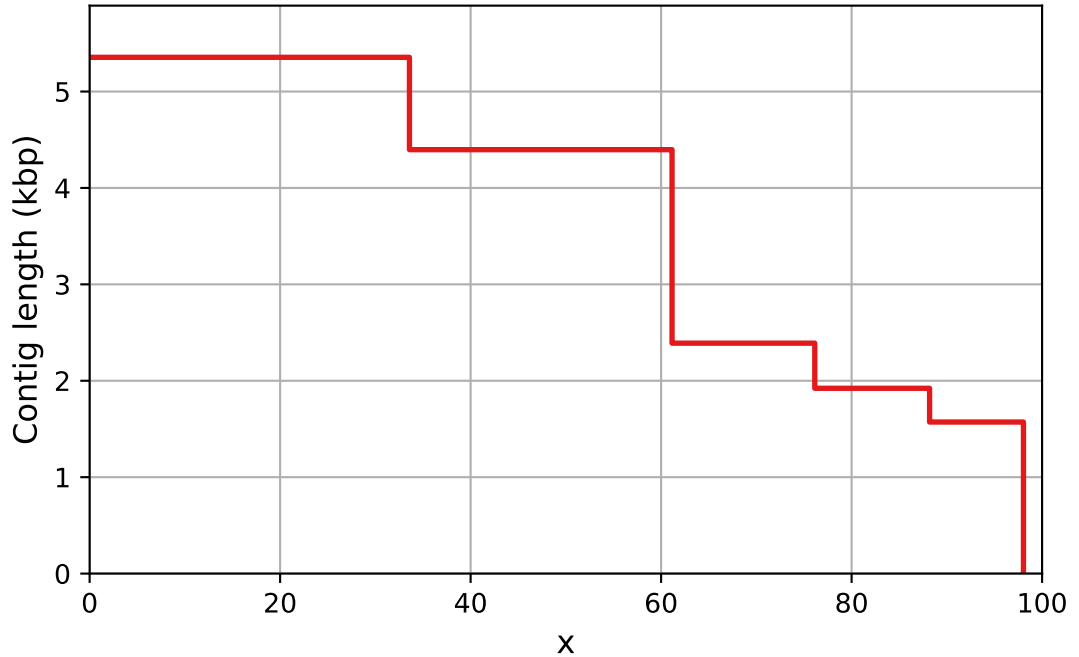
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



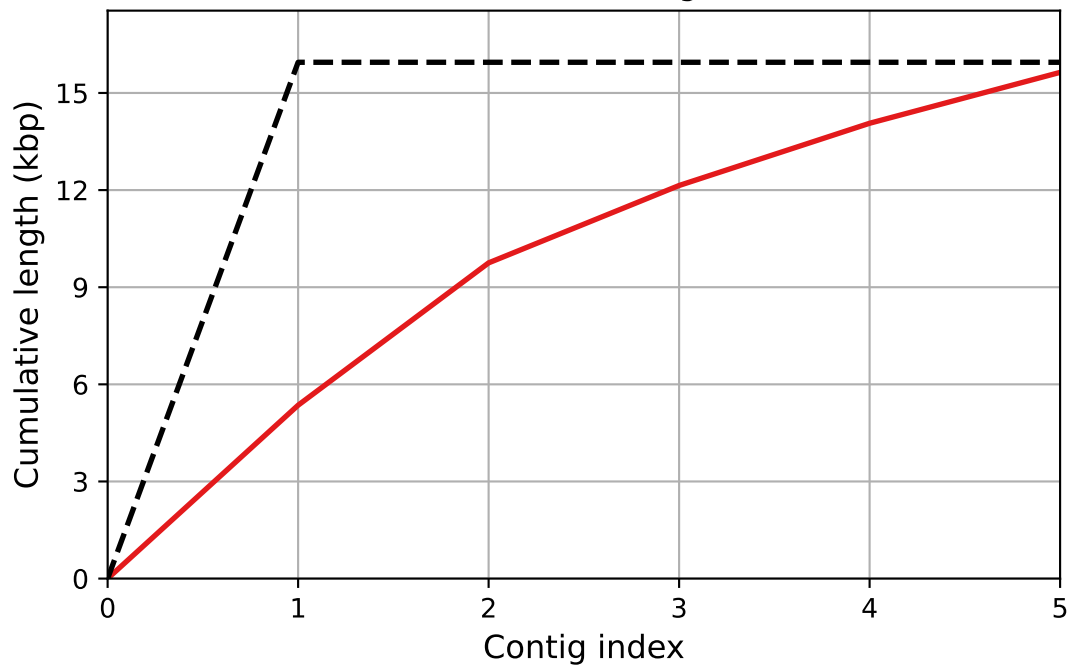
SPAdes_reads_ampliados_coincidentes_Contigs

NGx



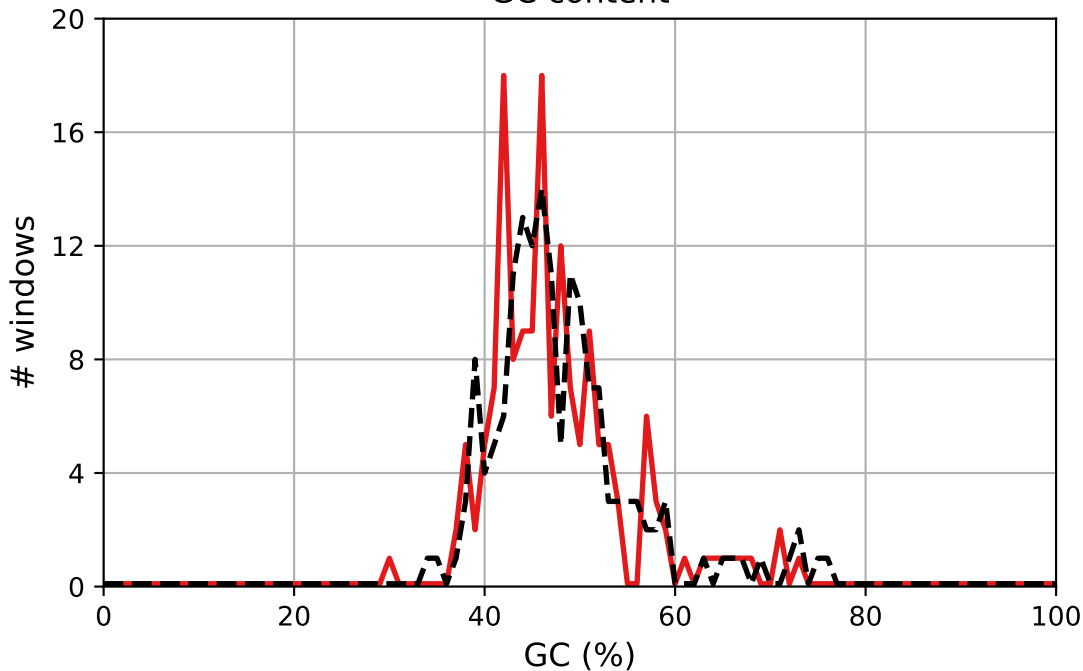
SPAdes_reads_ampliados_coincidentes_Contigs

Cumulative length

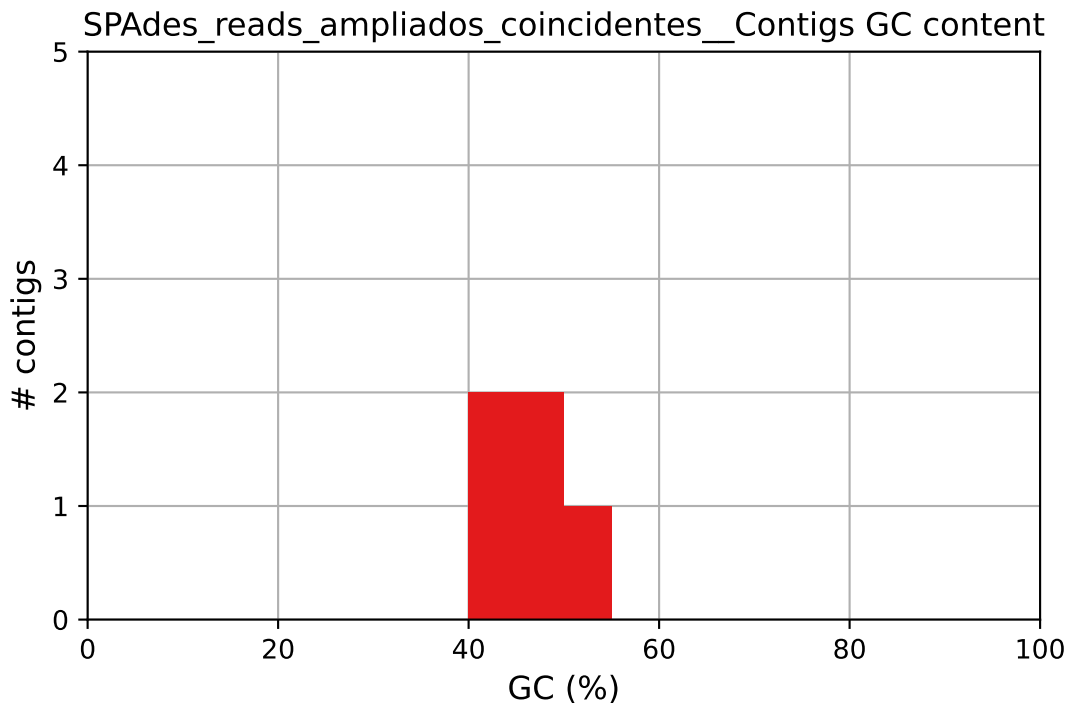


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GC content

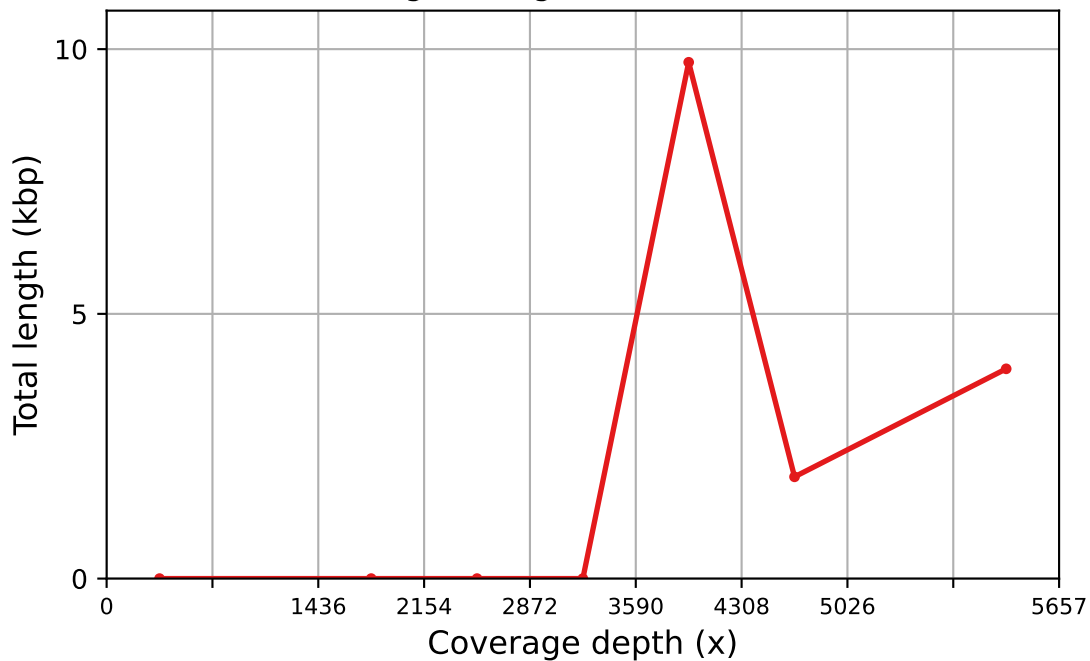


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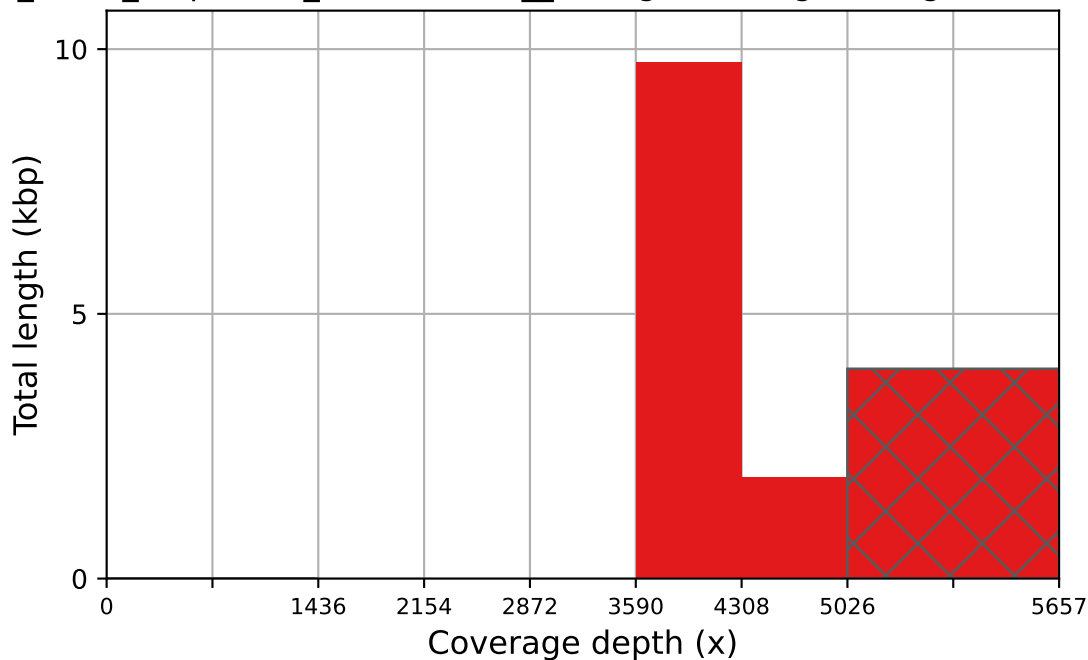
SPAdes_reads_ampliados_coincidentes__Contigs

Coverage histogram (bin size: 718x)



—●— SPAdes_reads_ampliados_coincidentes_Contigs

SPAdes_reads_ampliados_coincidentes__Contigs coverage histogram (bin size: 7

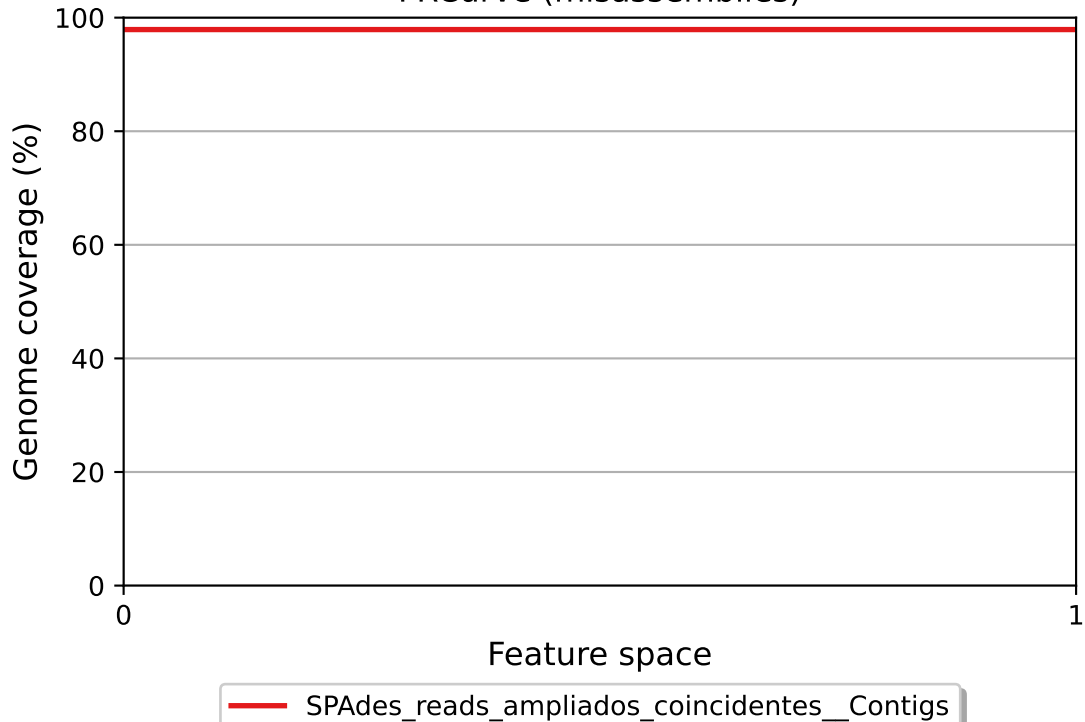


SPAdes_reads_ampliados_coincidentes__Contigs

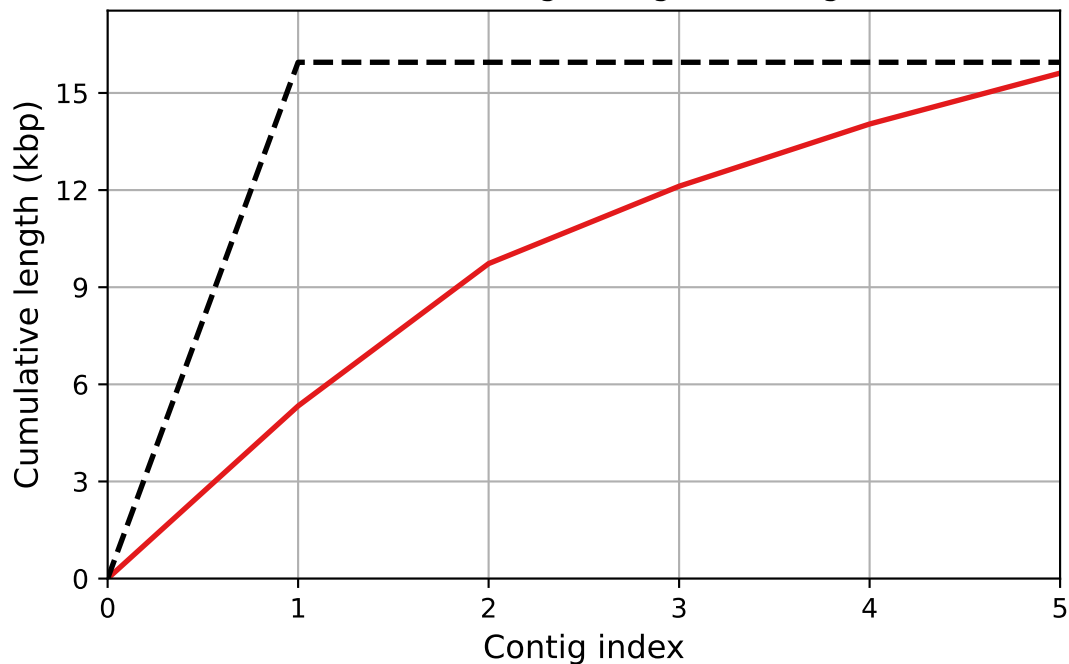
Misassemblies



FRCurve (misassemblies)

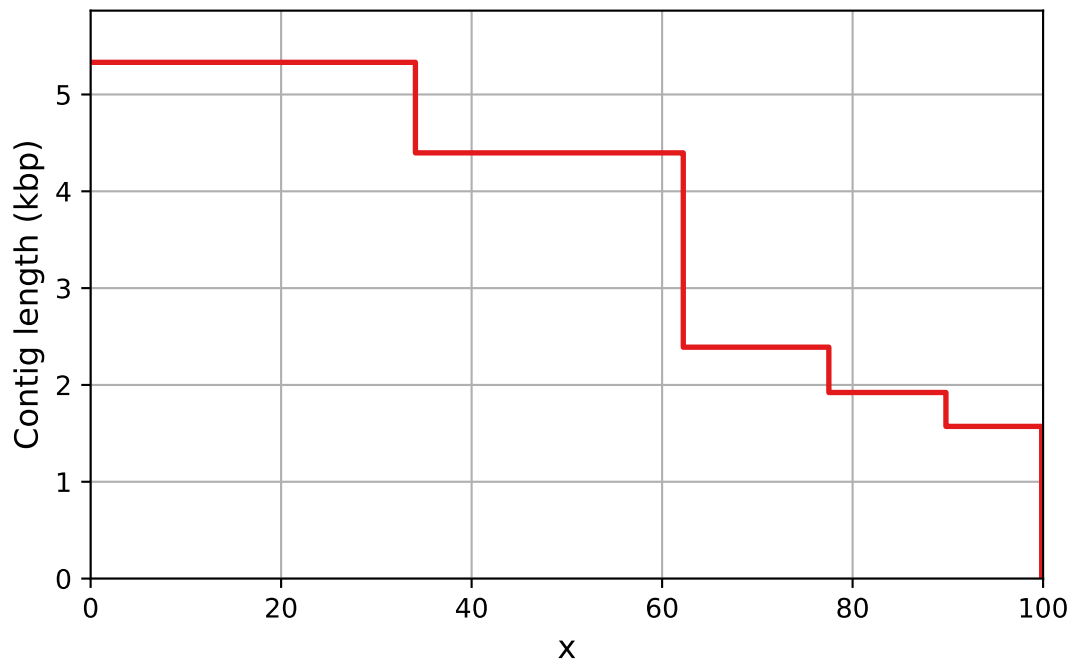


Cumulative length (aligned contigs)



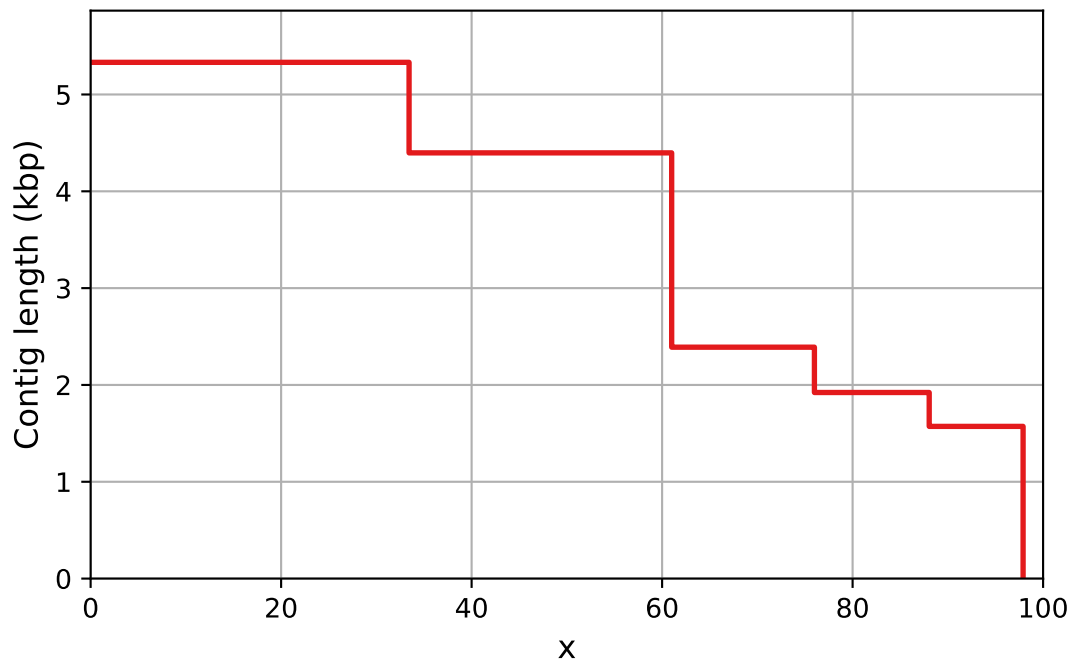
— SPAdes_reads_ampliados_coincidentes__Contigs - - Reference

NAx



— SPAdes_reads_ampliados_coincidentes__Contigs

NGAx



SPAdes_reads_ampliados_coincidentes__Contigs