Report

	SPAdes_reads_ampliados_coincidentes_02__Contigs
# contigs (>= 0 bp)	12
# contigs (>= 1000 bp)	3
Total length (>= 0 bp)	16935
Total length (>= 1000 bp)	15564
# contigs	3
Largest contig	6320
Total length	15564
Reference length	15948
GC (%)	47.81
Reference GC (%)	48.10
N50	5355
NG50	5355
N90	3889
NG90	3889
auN	5380.5
auNG	5251.0
L50	2
LG50	2
L90	3
LG90	3
# total reads	542938
# left	271513
# right	271425
Mapped (%)	98.73
Reference mapped (%)	100.28
Properly paired (%)	96.38
Reference properly paired (%)	100.0
Avg. coverage depth	5004
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 (%)	96.965
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3944.41
# indels per 100 kbp	12.87
Largest alignment	6320
Total aligned length	15541
NA50	5332
NGA50	5332
NA90	3889
NGA90	3889
auNA	5364.7
auNGA	5235.6
LA50	2
LGA50	2
LA90	3
LGA90	3

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_02__Contigs
# total reads	542938
# left	271513
# right	271425
# mapped	536020
Mapped (%)	98.73
# properly paired	523258
Properly paired (%)	96.38
# singletons	295
Singletons (%)	0.05
# misjoint mates	9890
Misjoint mates (%)	1.82
Avg. coverage depth	5004
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

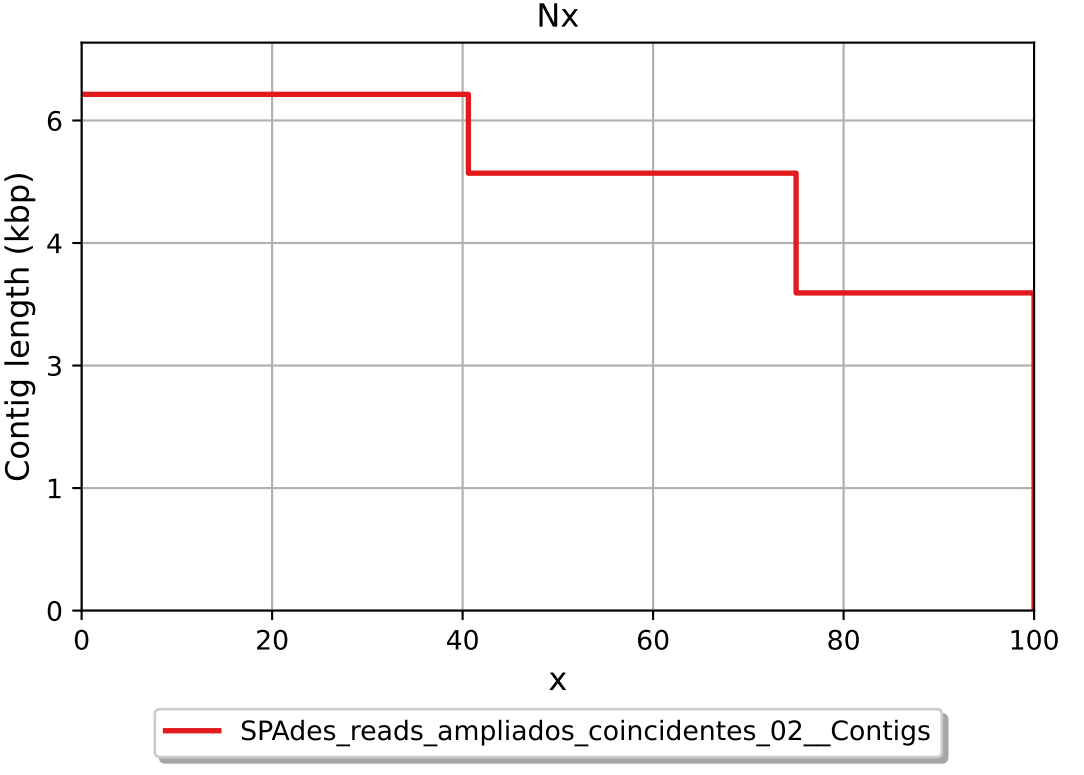
	SPAdes_reads_ampliados_coincidentes_02__Contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	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

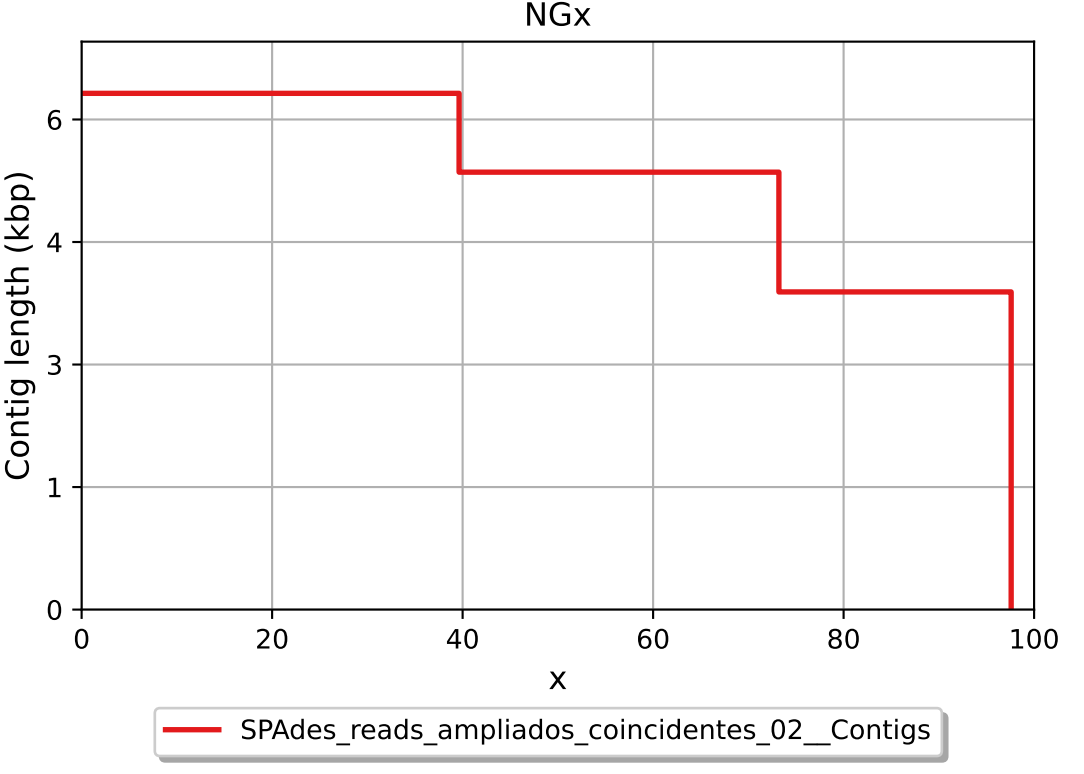
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

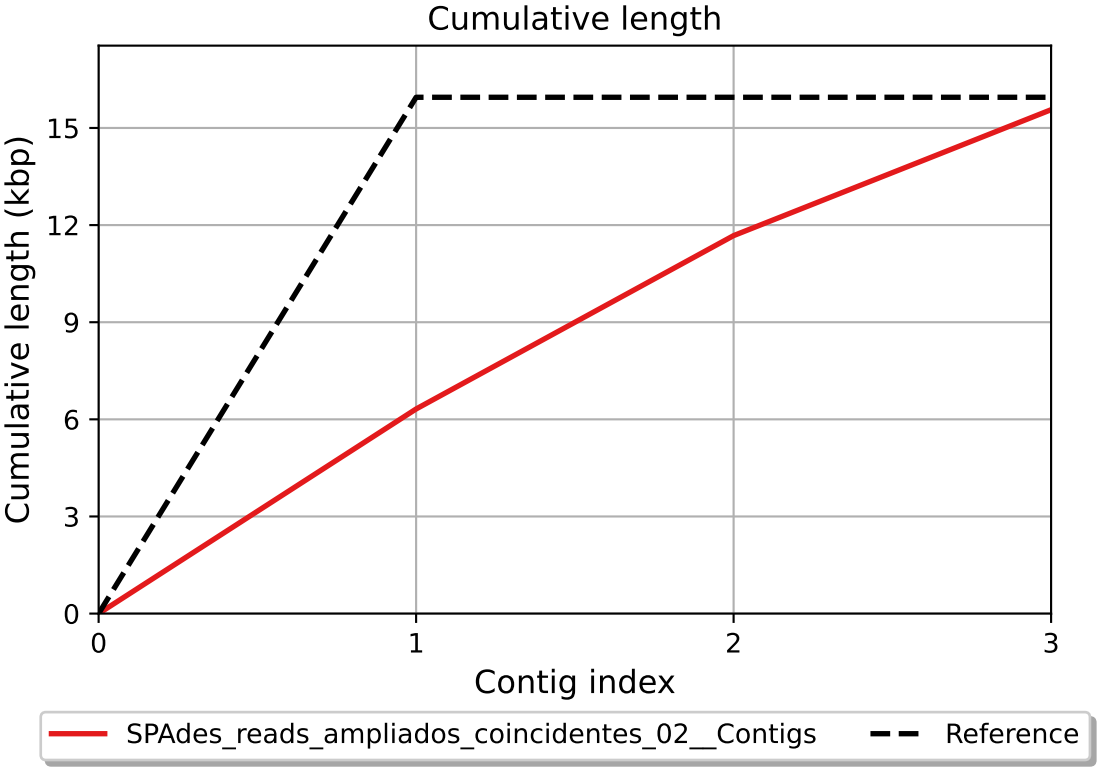
Unaligned report

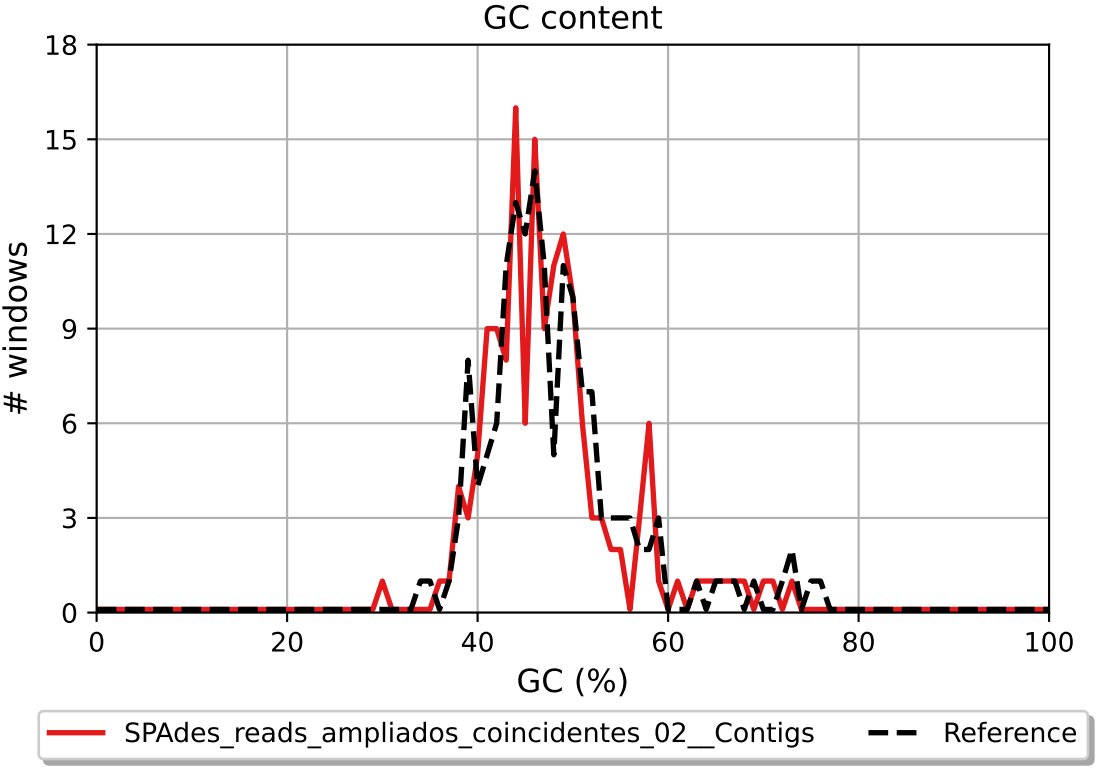
	SPAdes_reads_ampliados_coincidentes_02__Contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

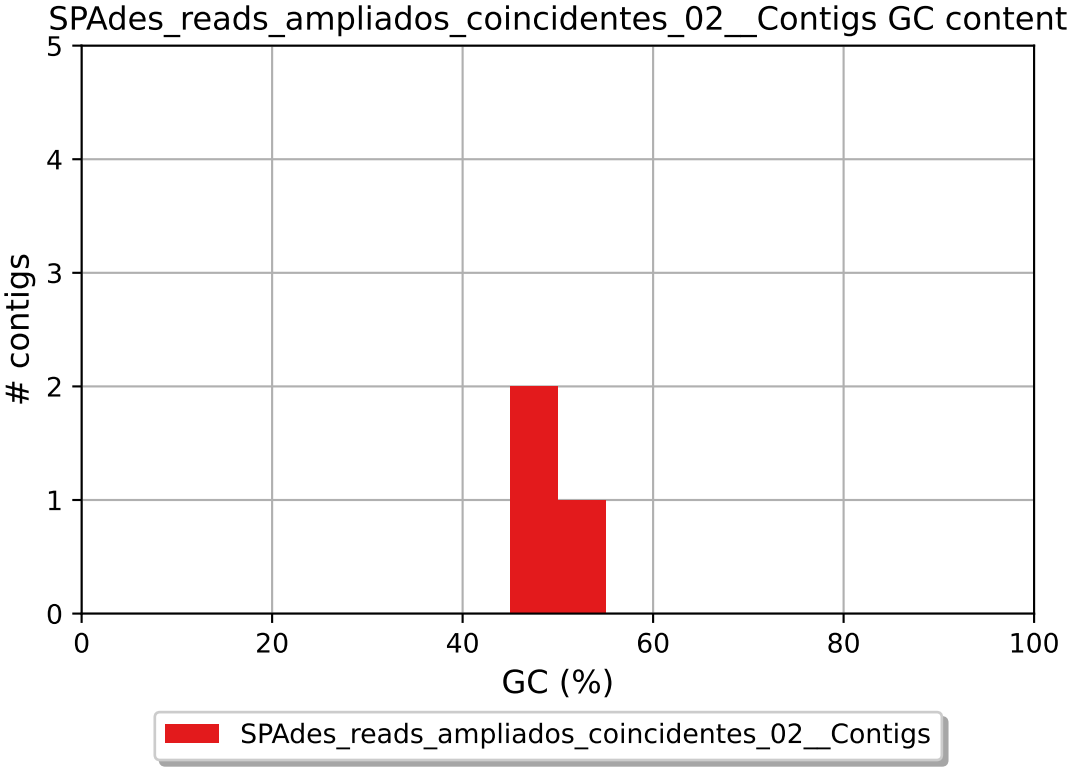
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

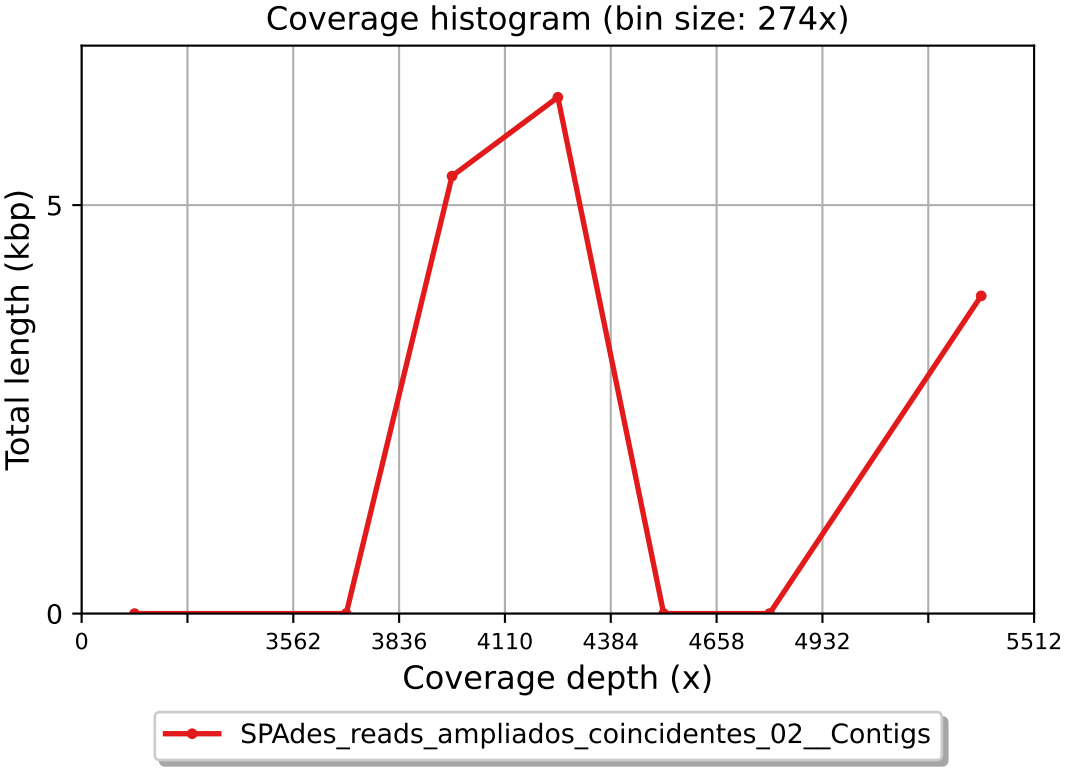

Nx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
SPAdes_reads_ampliados_coincidentes_02__Contigs

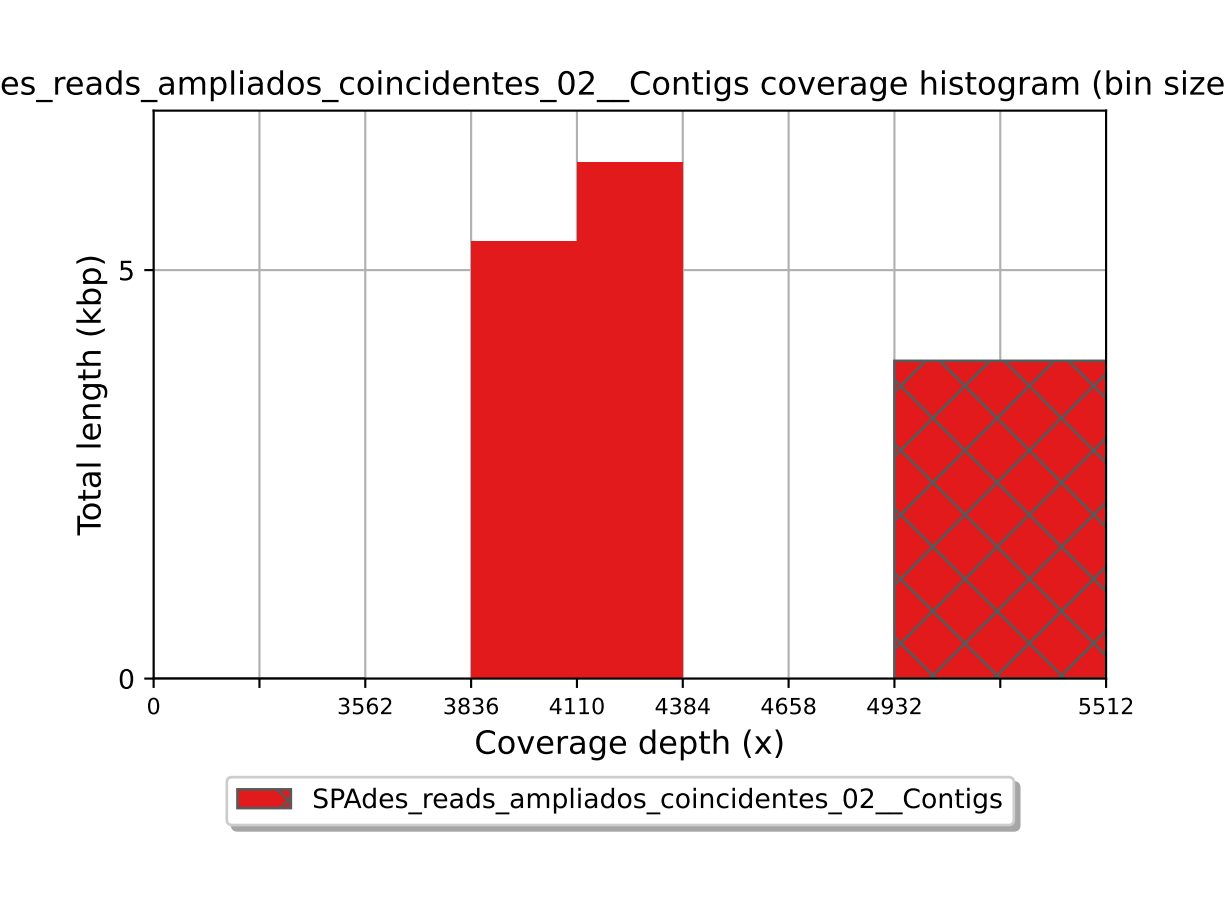

NGx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
SPAdes_reads_ampliados_coincidentes_02__Contigs

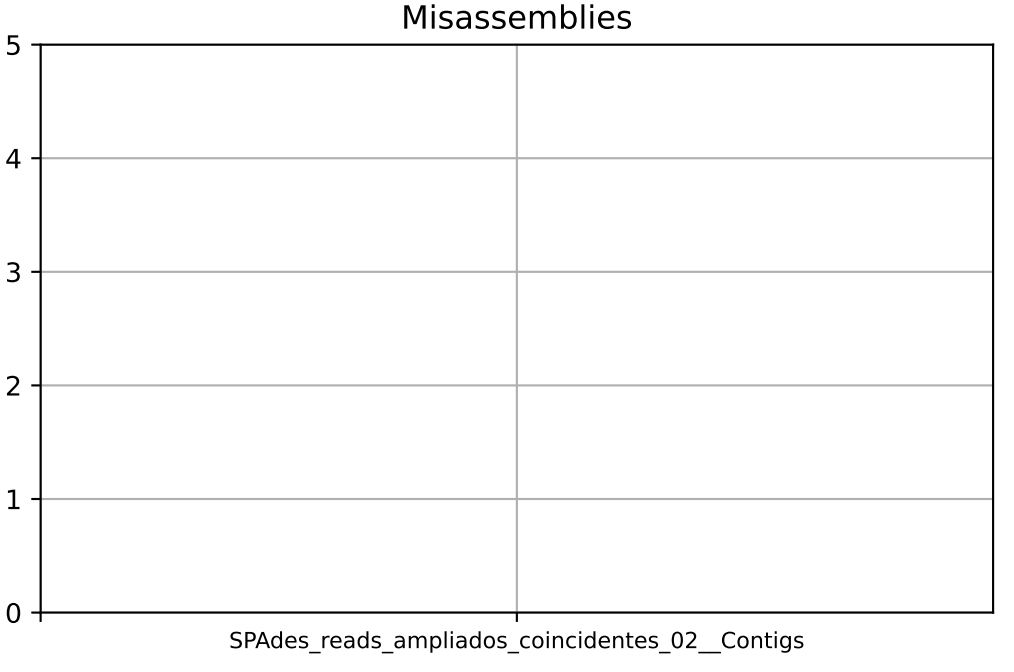

Cumulative length
Cumulative length (kbp)
0
3
6
9
12
15
0
1
2
3
Contig index
SPAdes_reads_ampliados_coincidentes_02__Contigs
Reference

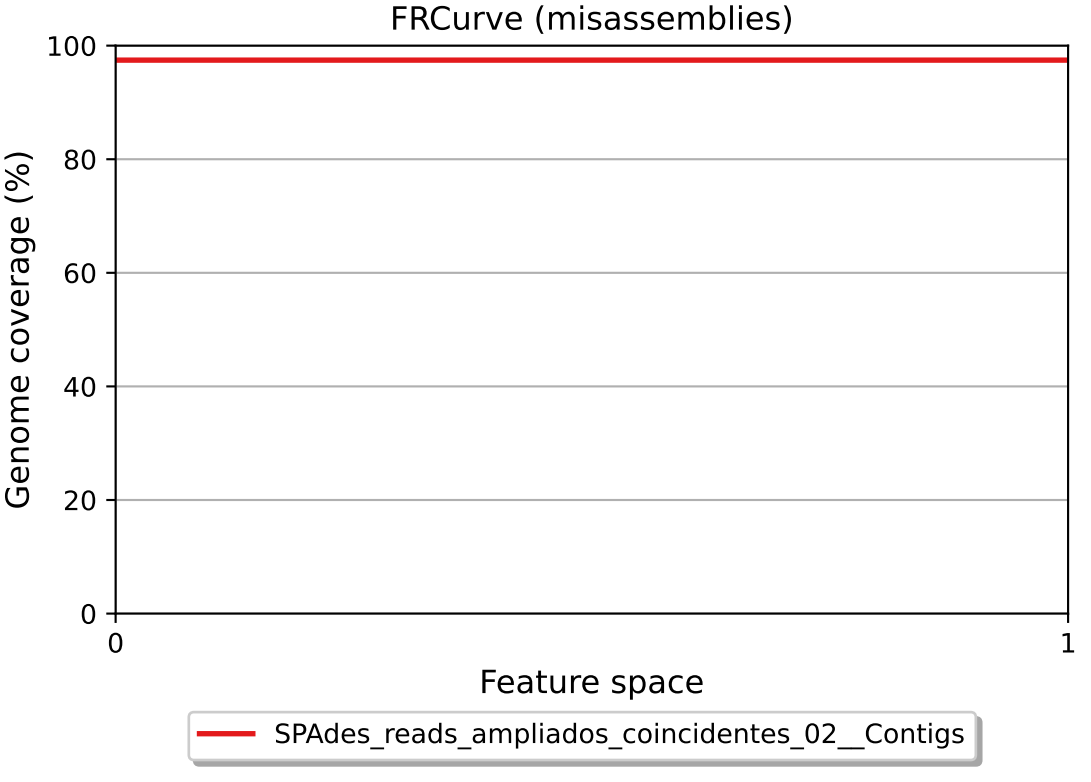

GC content
windows
GC (%)
0
3
6
9
12
15
18
0
20
40
60
80
100
SPAdes_reads_ampliados_coincidentes_02__Contigs
Reference

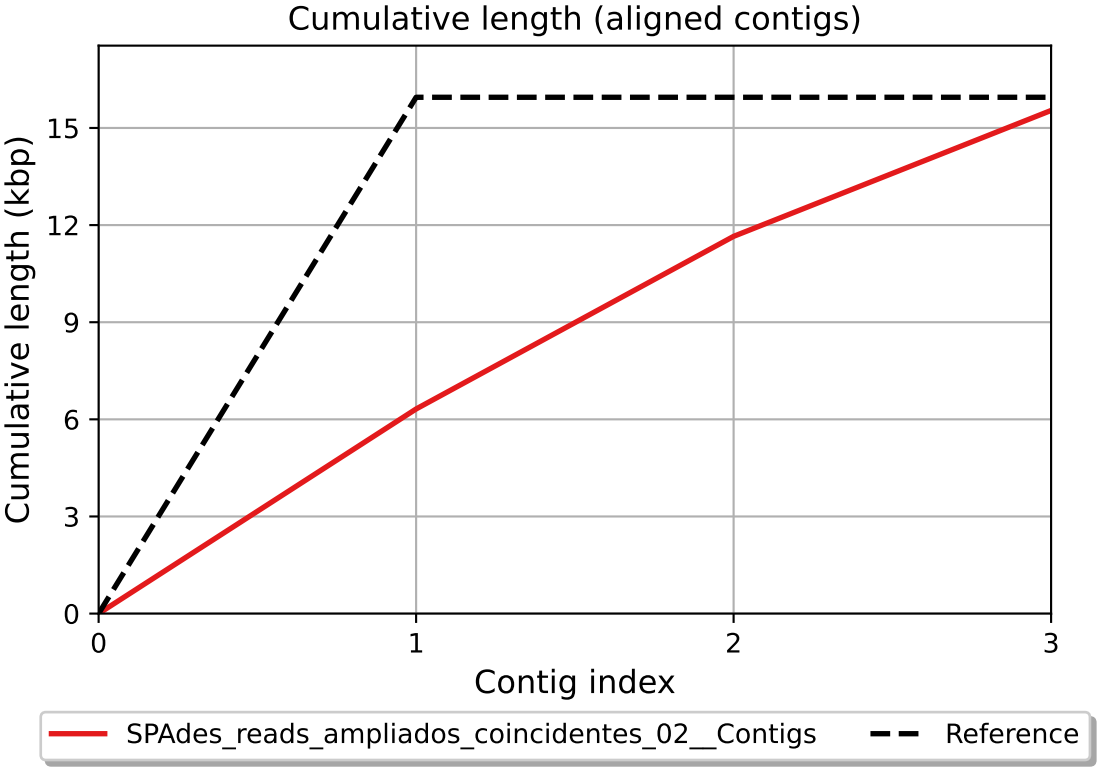

SPAdes_reads_ampliados_coincidentes_02__Contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SPAdes_reads_ampliados_coincidentes_02__Contigs

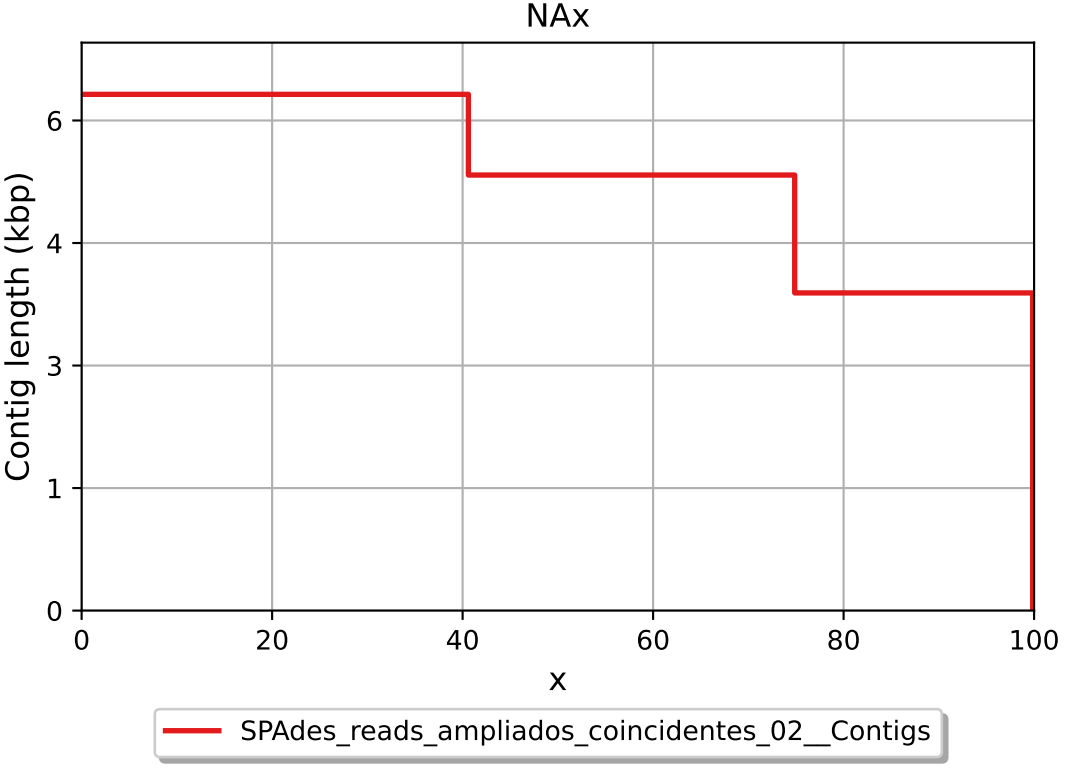

Coverage histogram (bin size: 274x)
Total length (kbp)
5
0
0
3562
3836
4110
4384
4658
4932
5512
Coverage depth (x)
SPAdes_reads_ampliados_coincidentes_02__Contigs

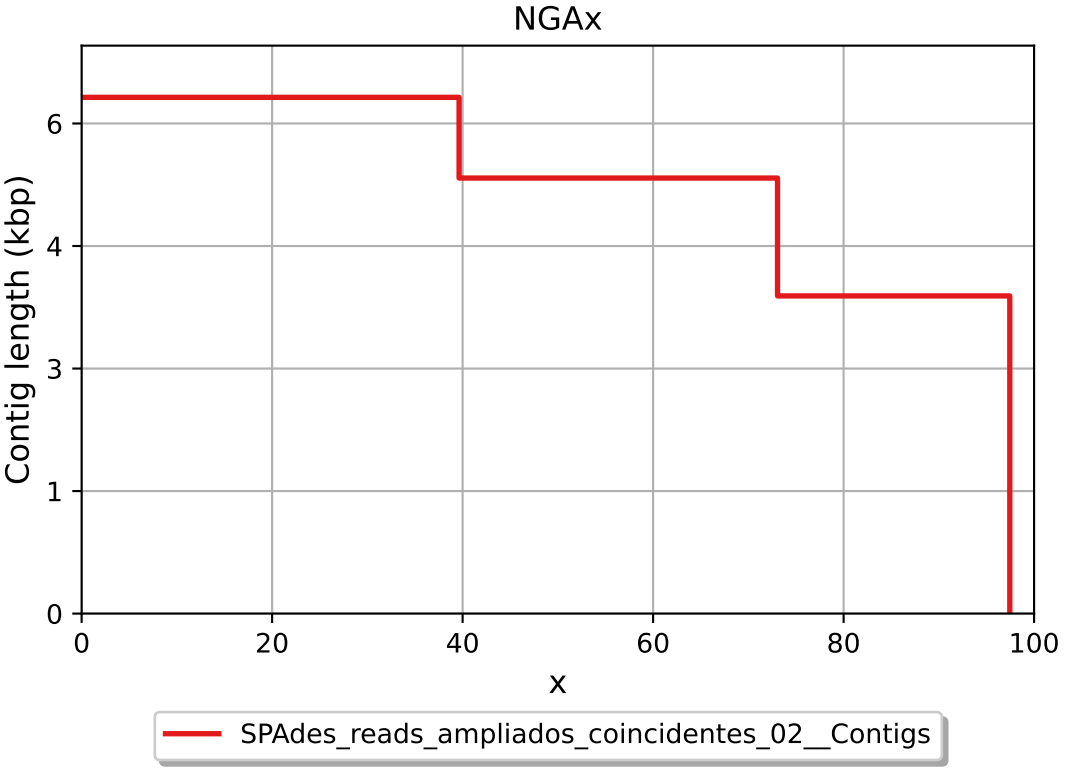

es_reads_ampliados_coincidentes_02__Contigs coverage histogram (bin size
Total length (kbp)
5
0
0
3562
3836
4110
4384
4658
4932
5512
Coverage depth (x)
SPAdes_reads_ampliados_coincidentes_02__Contigs


Misassemblies
5
4
3
2
1
0
SPAdes_reads_ampliados_coincidentes_02__Contigs


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
SPAdes_reads_ampliados_coincidentes_02__Contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
3
6
9
12
15
0
1
2
3
Contig index
SPAdes_reads_ampliados_coincidentes_02__Contigs
Reference


NAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
SPAdes_reads_ampliados_coincidentes_02__Contigs


NGAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
SPAdes_reads_ampliados_coincidentes_02__Contigs