Report

	spades_noerror
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29482
Total length (>= 1000 bp)	29482
Total length (>= 5000 bp)	29482
Total length (>= 10000 bp)	29482
Total length (>= 25000 bp)	29482
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29482
Total length	29482
Reference length	30119
GC (%)	41.26
Reference GC (%)	41.24
N50	29482
NG50	29482
N90	29482
NG90	29482
auN	29482.0
auNG	28858.5
L50	1
LG50	1
L90	1
LG90	1
# 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 (%)	97.885
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	29482
Total aligned length	29482
NA50	29482
NGA50	29482
NA90	29482
NGA90	29482
auNA	29482.0
auNGA	28858.5
LA50	1
LGA50	1
LA90	1
LGA90	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

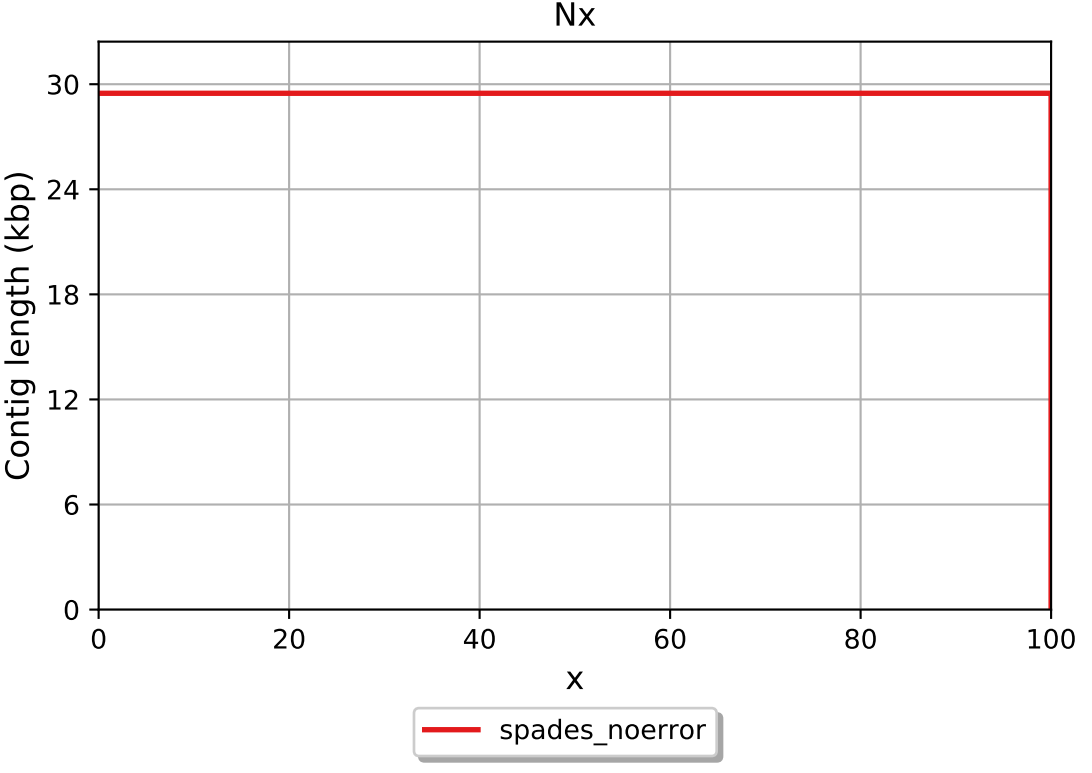
	spades_noerror
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext.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

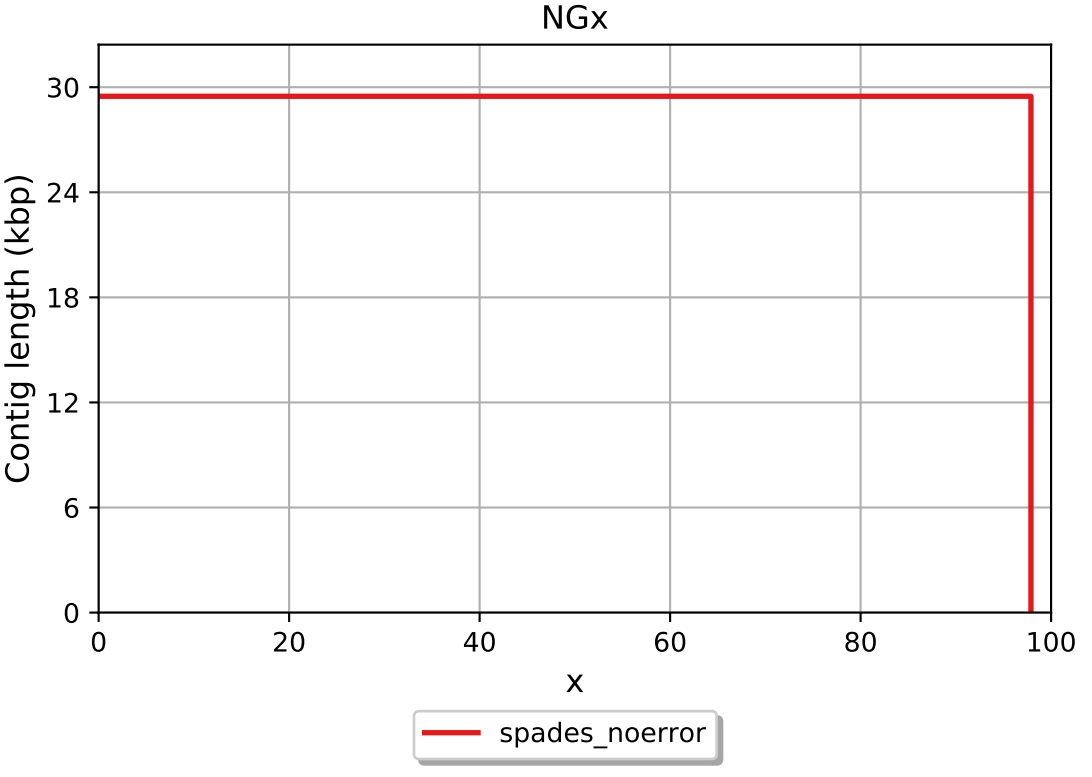
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

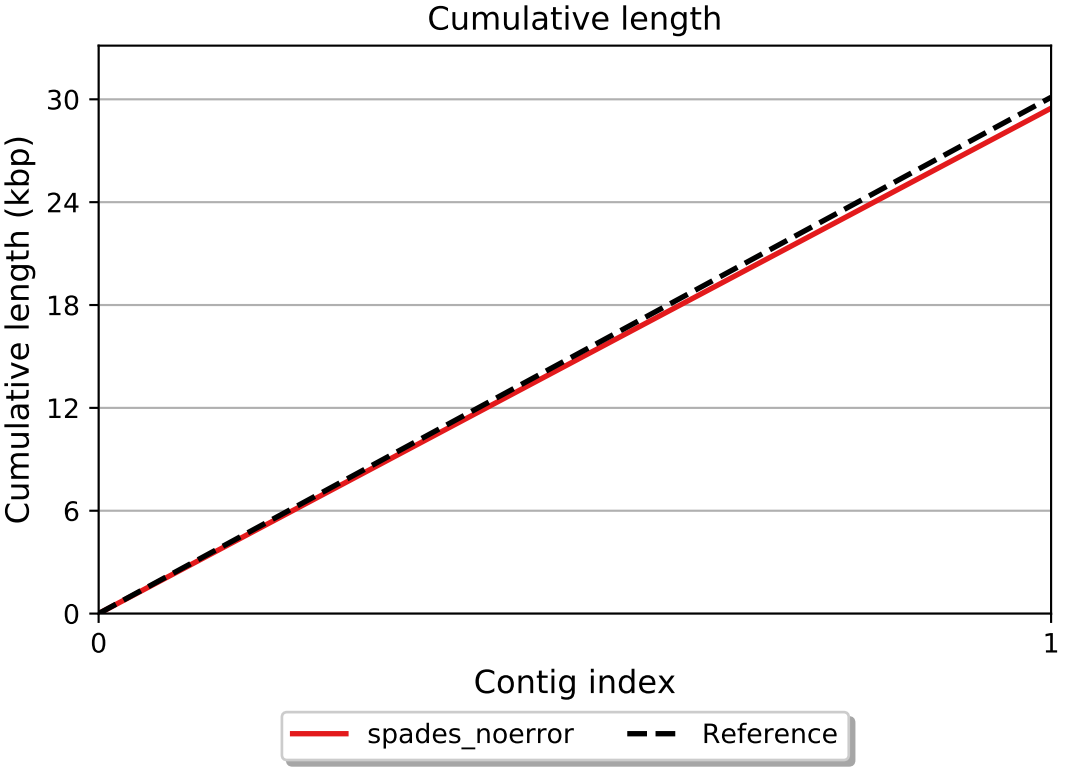
Unaligned report

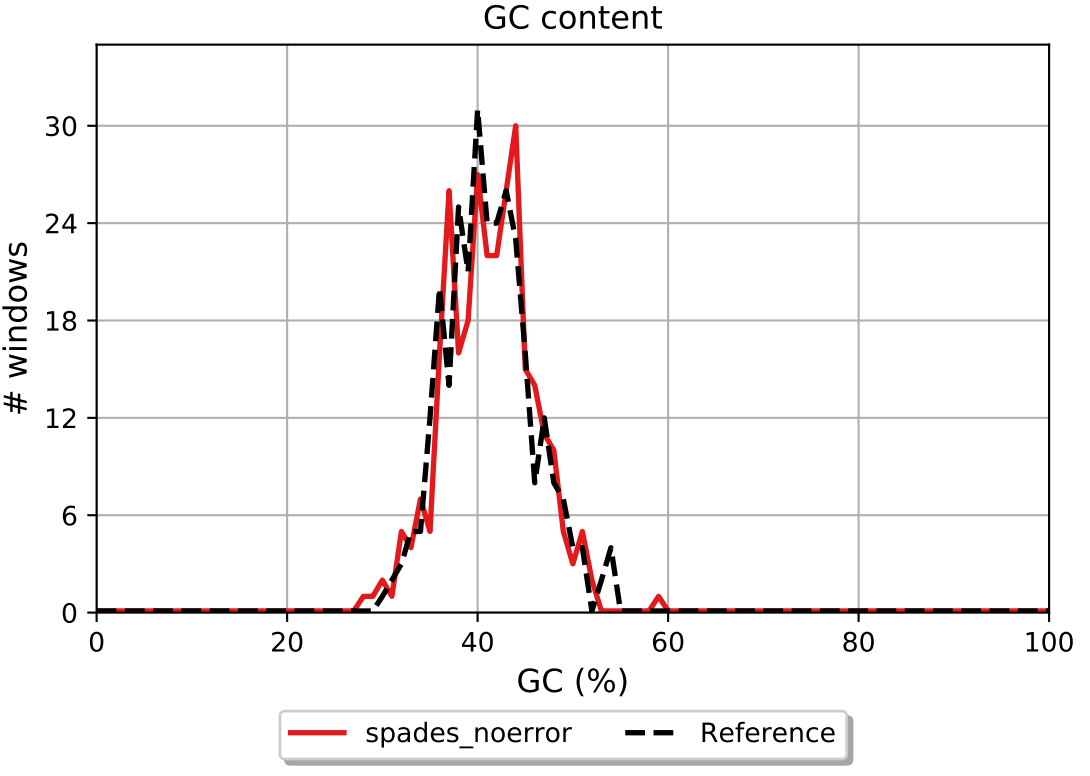
	spades_noerror
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

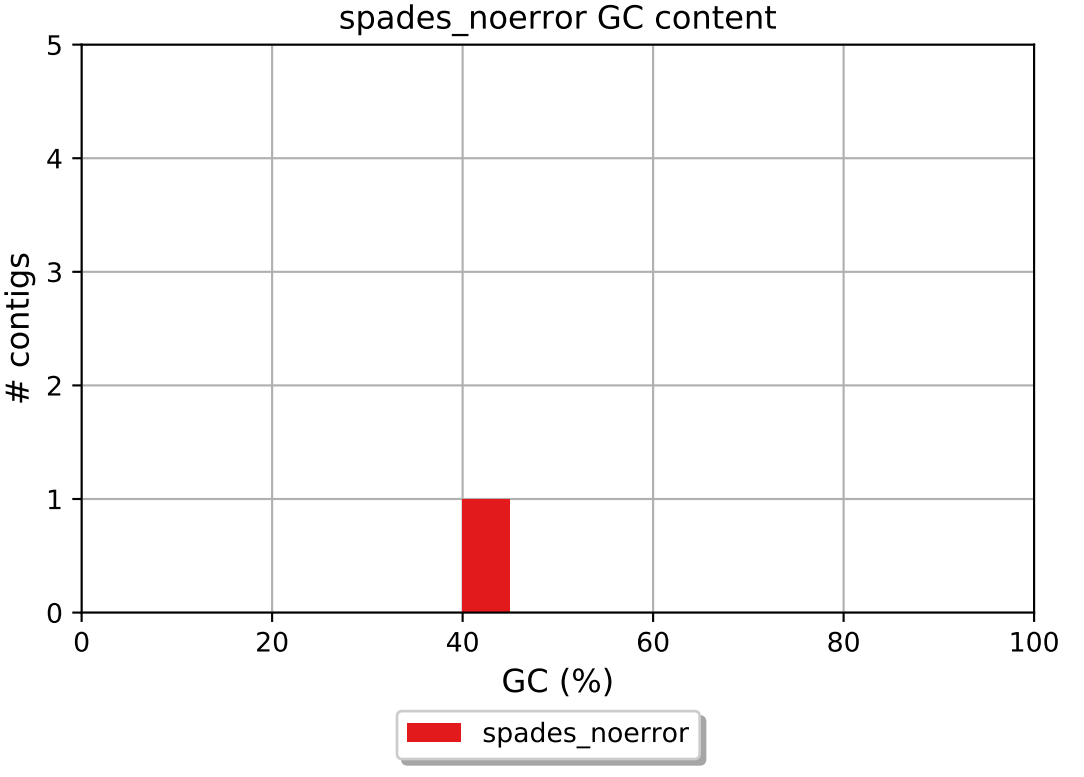
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

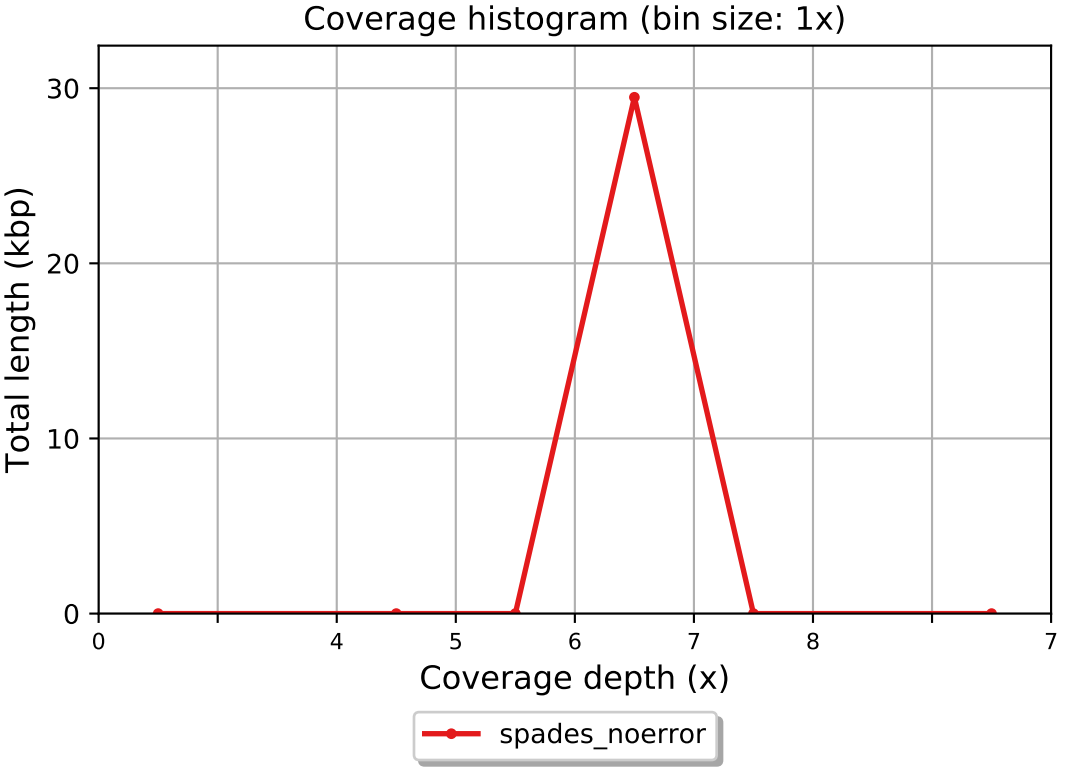

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_noerror

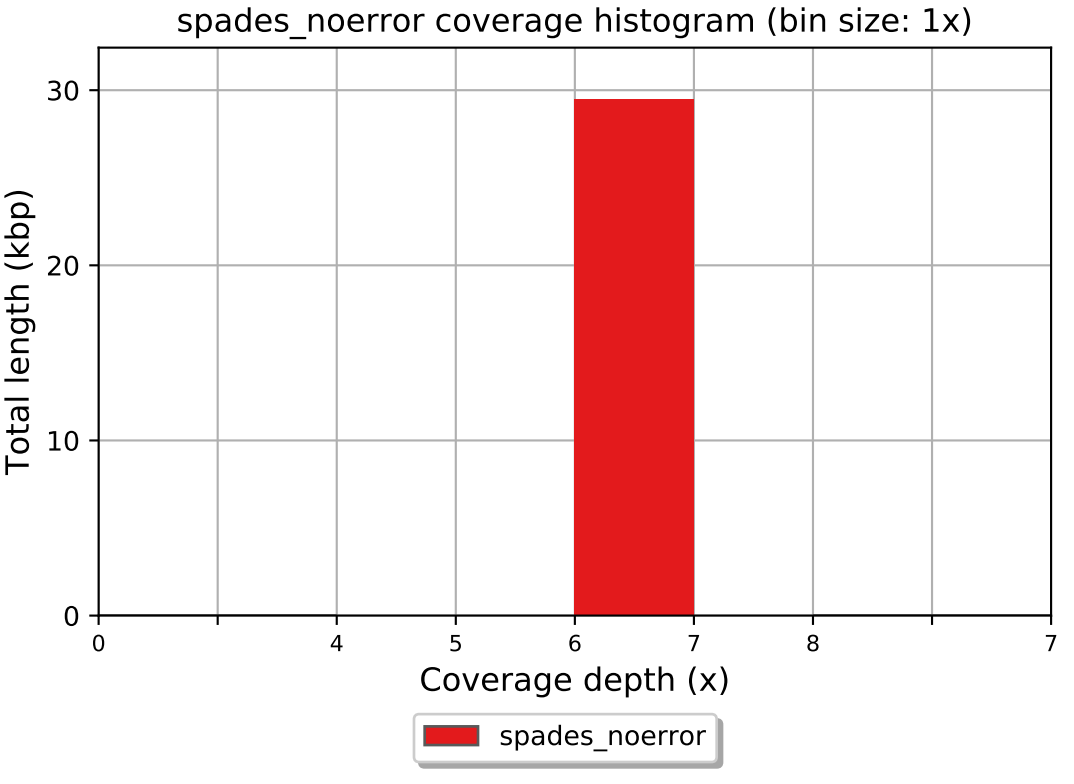

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_noerror


Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
spades_noerror
Reference

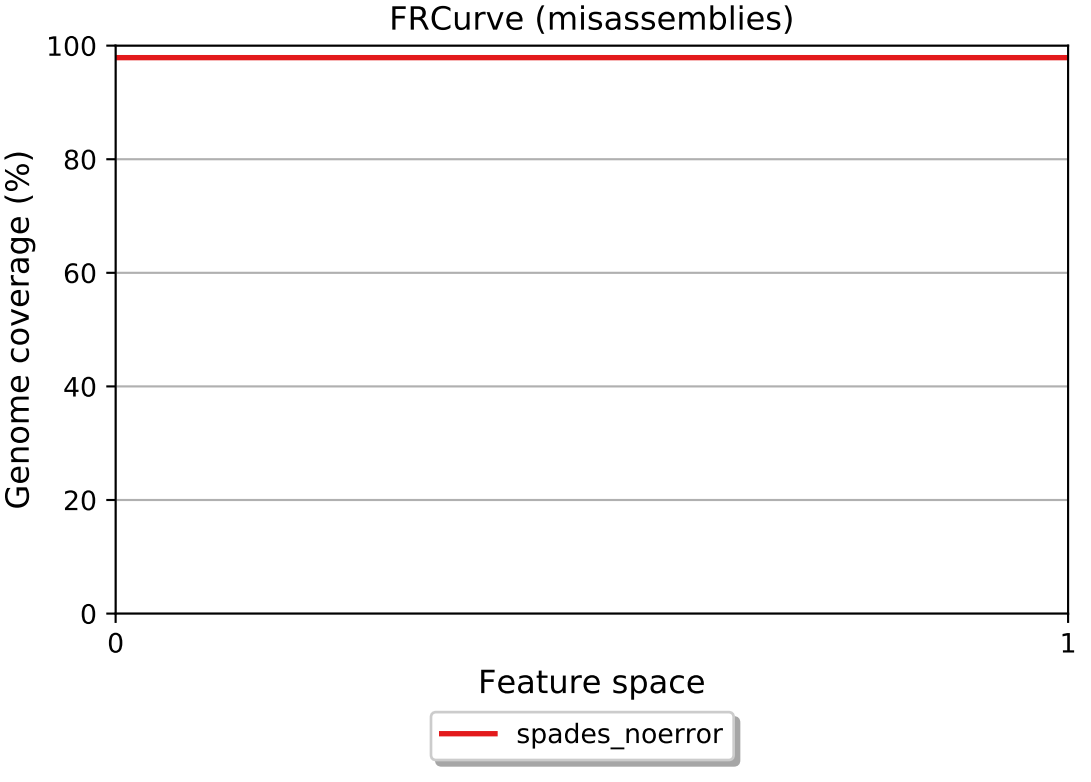

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
spades_noerror
Reference

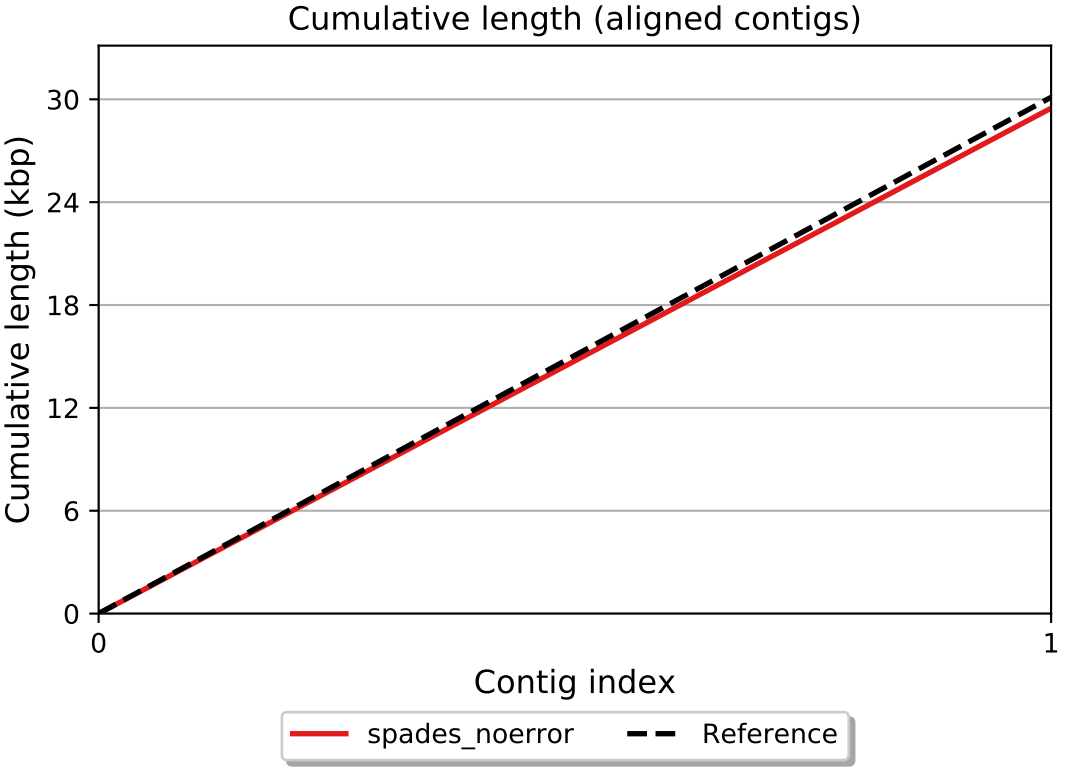

spades_noerror GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
spades_noerror

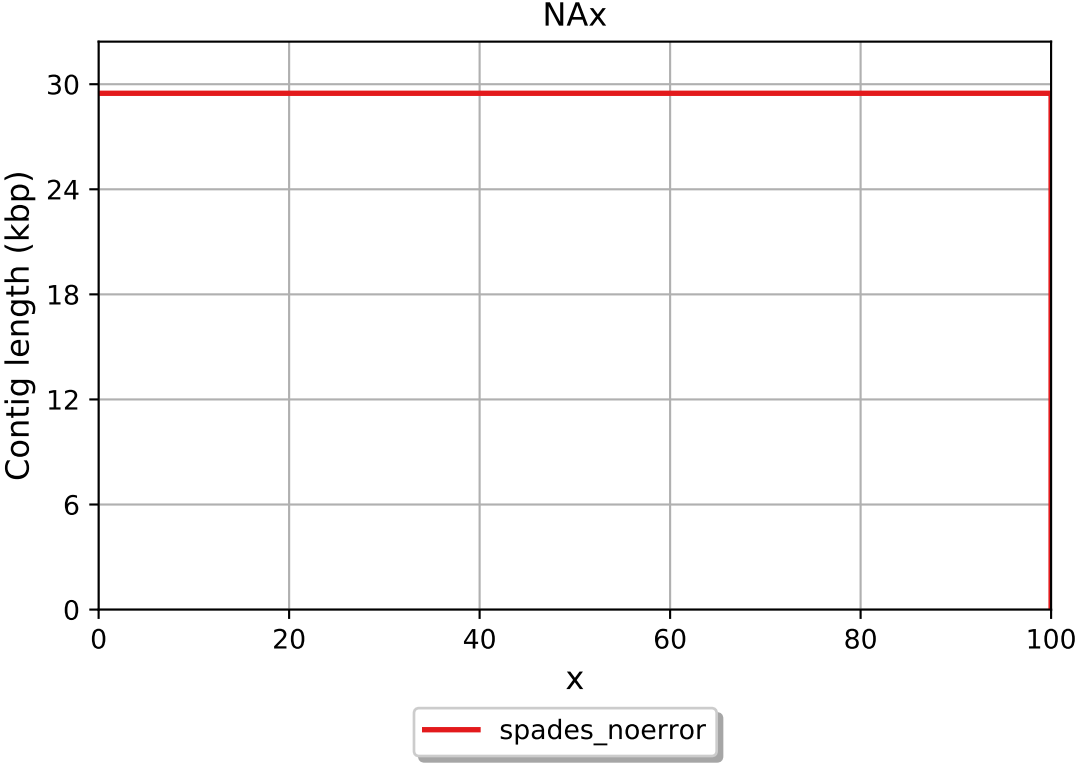

Coverage histogram (bin size: 1x)
Total length (kbp)
30
20
10
0
0
4
5
6
7
8
7
Coverage depth (x)
spades_noerror

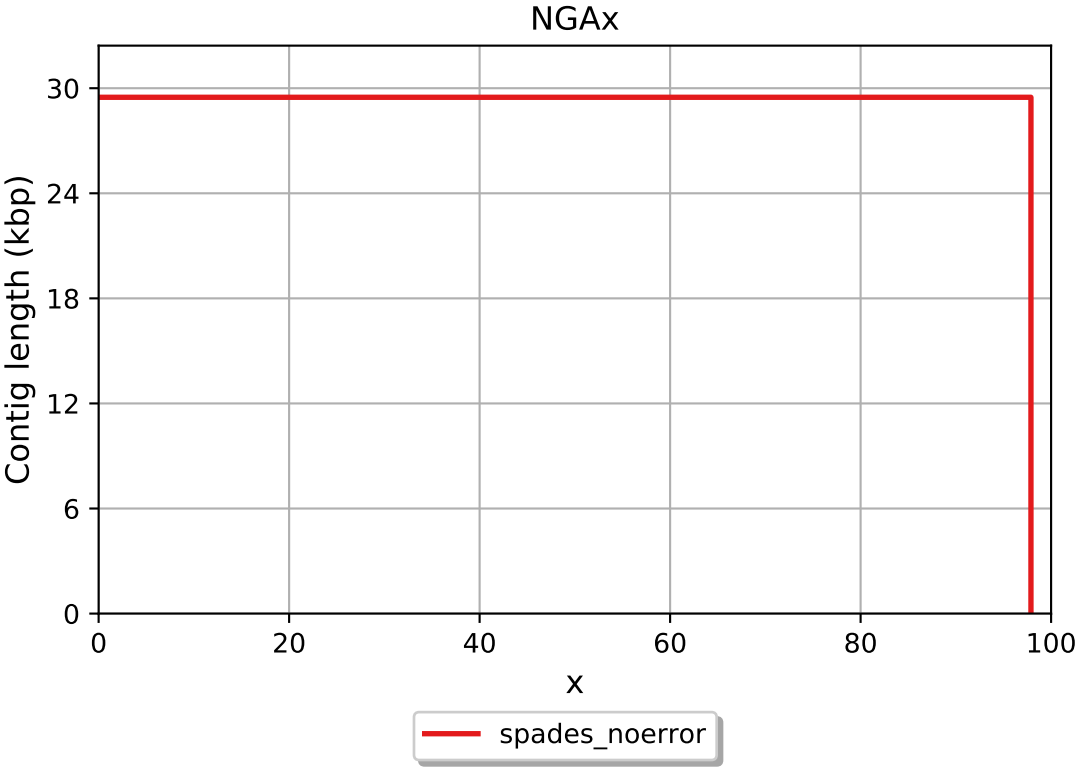

spades_noerror coverage histogram (bin size: 1x)
Total length (kbp)
30
20
10
0
0
4
5
6
7
8
7
Coverage depth (x)
spades_noerror

Misassemblies
5
4
3
2
1
0
spades_noerror


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
spades_noerror
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_noerror


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_noerror