Report

	contigs_reads_r_k35	contigs_reads_r_k45
# contigs (>= 0 bp)	4	1
# contigs (>= 1000 bp)	0	1
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	1136	1040
Total length (>= 1000 bp)	0	1040
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	4	1
Largest contig	914	1040
Total length	1136	1040
Reference length	1040	1040
GC (%)	50.79	51.25
Reference GC (%)	51.25	51.25
N50	914	1040
NG50	914	1040
N90	134	1040
NG90	134	1040
auN	754.6	1040.0
auNG	824.3	1040.0
L50	1	1
LG50	1	1
L90	2	1
LG90	2	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 0 part	0 + 0 part
Unaligned length	88	0
Genome fraction (%)	100.000	100.000
Duplication ratio	1.008	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
Largest alignment	914	1040
Total aligned length	1048	1040
NA50	914	1040
NGA50	914	1040
NA90	134	1040
NGA90	134	1040
auNA	751.2	1040.0
auNGA	820.5	1040.0
LA50	1	1
LGA50	1	1
LA90	2	1
LGA90	2	1

All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

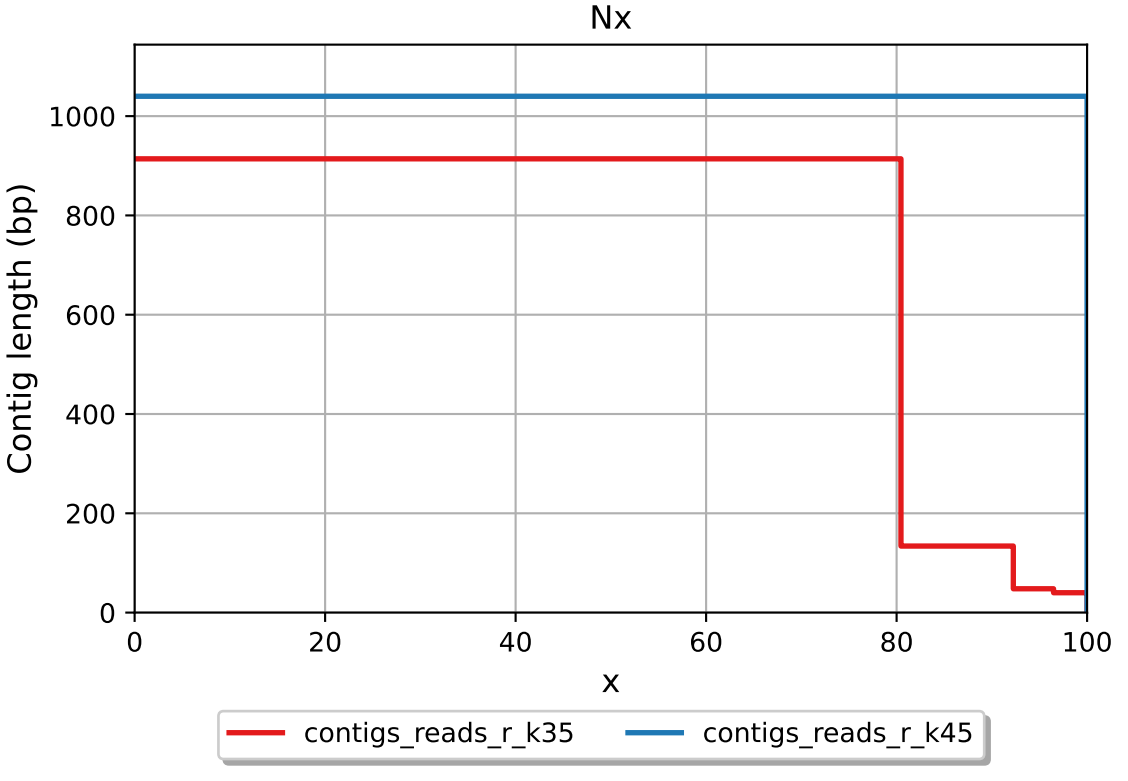
	contigs_reads_r_k35	contigs_reads_r_k45
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	0	0
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

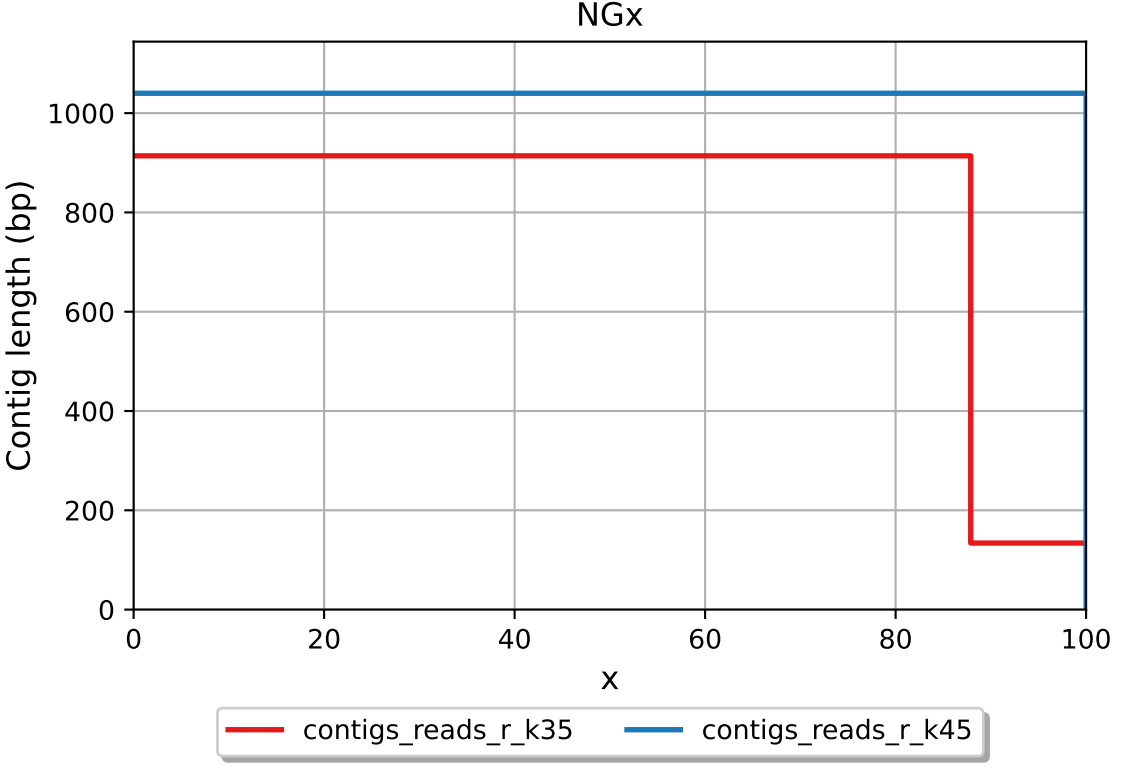
All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

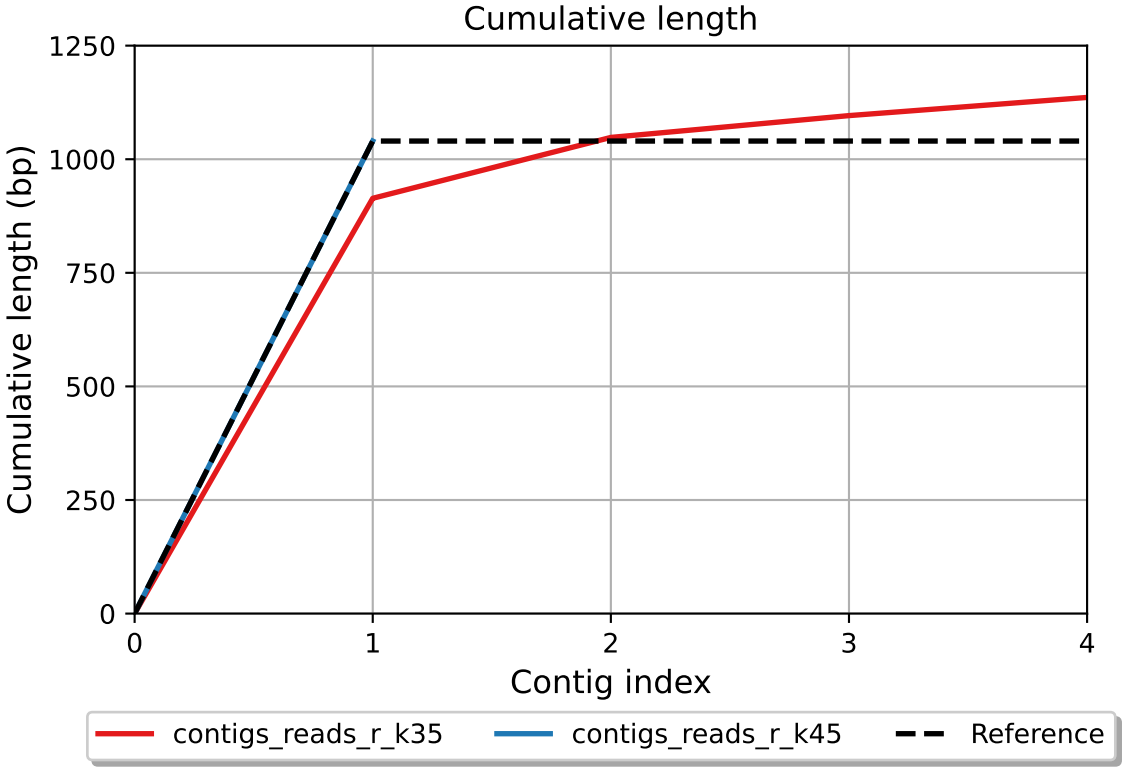
Unaligned report

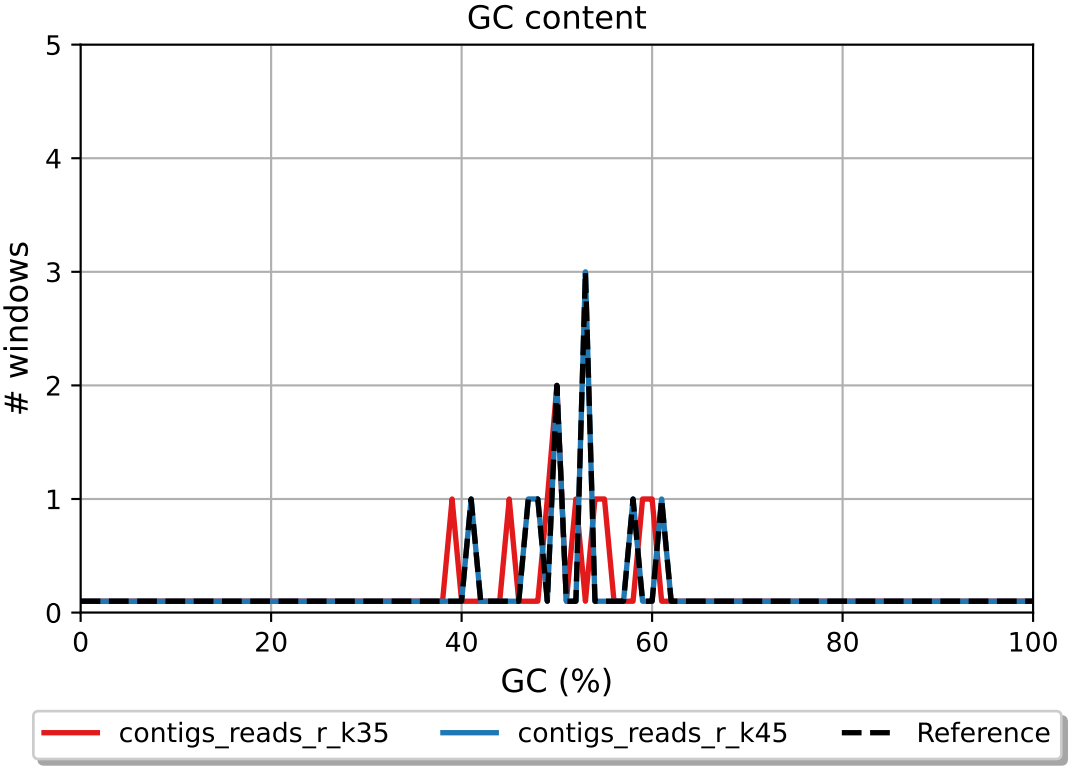
	contigs_reads_r_k35	contigs_reads_r_k45
# fully unaligned contigs	2	0
Fully unaligned length	88	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

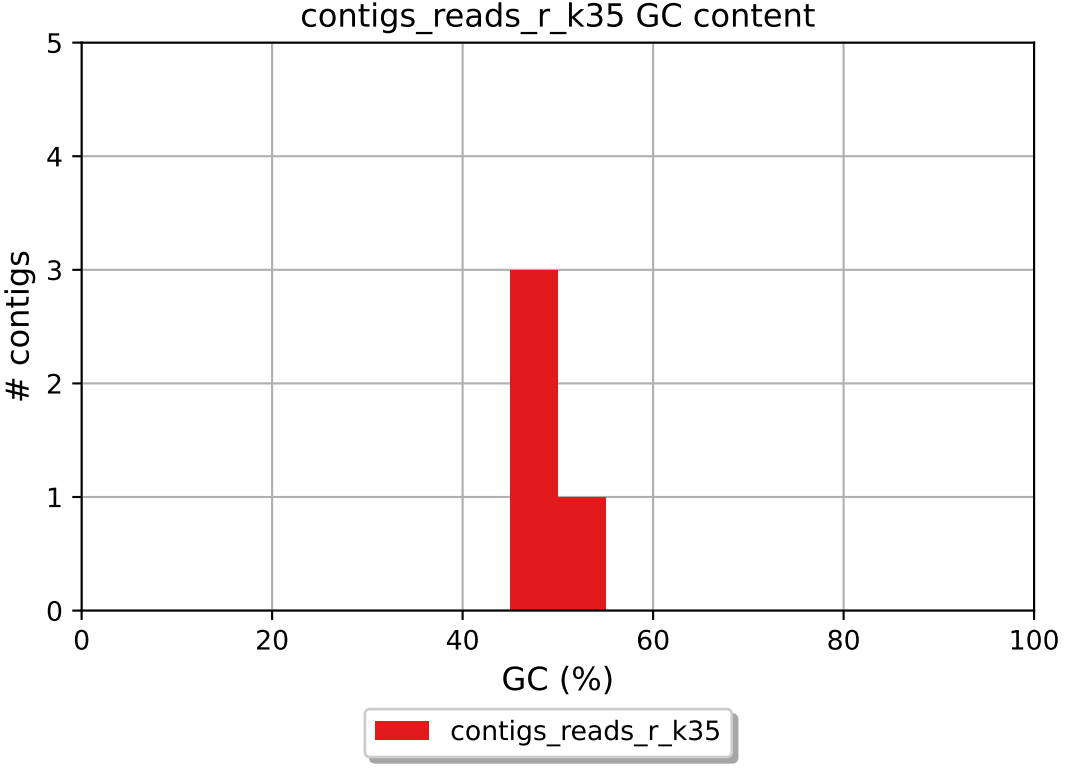
All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

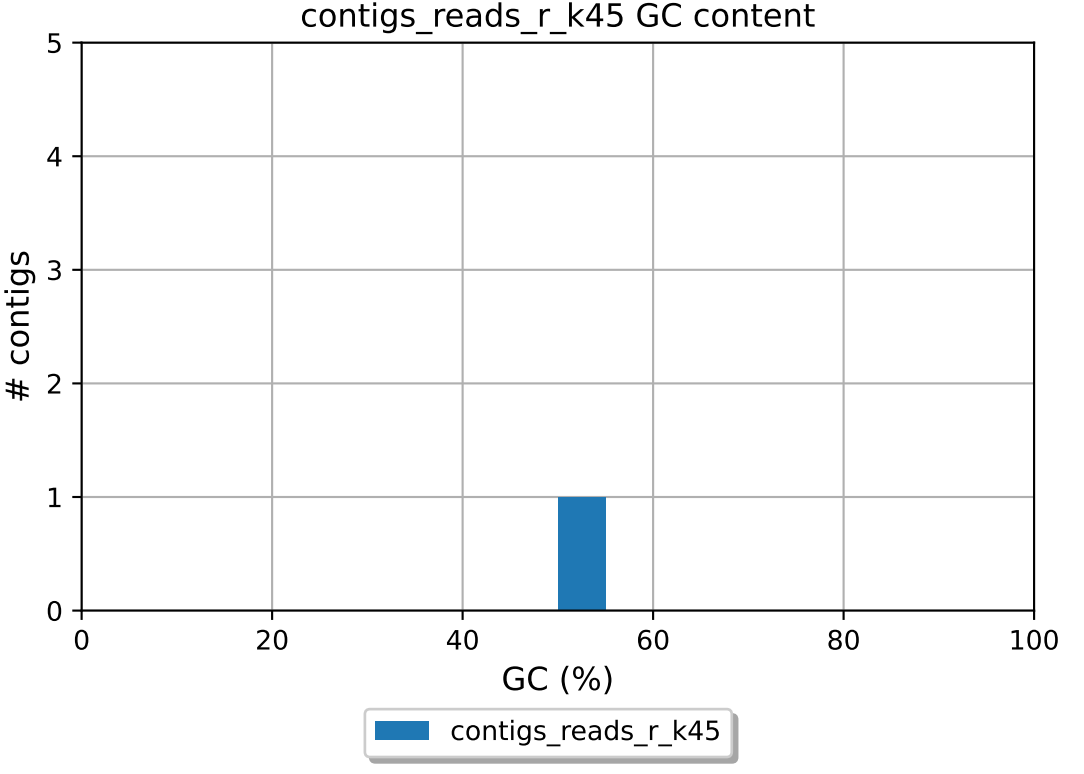

Nx
Contig length (bp)
0
200
400
600
800
1000
0
20
40
60
80
100
x
contigs_reads_r_k35
contigs_reads_r_k45

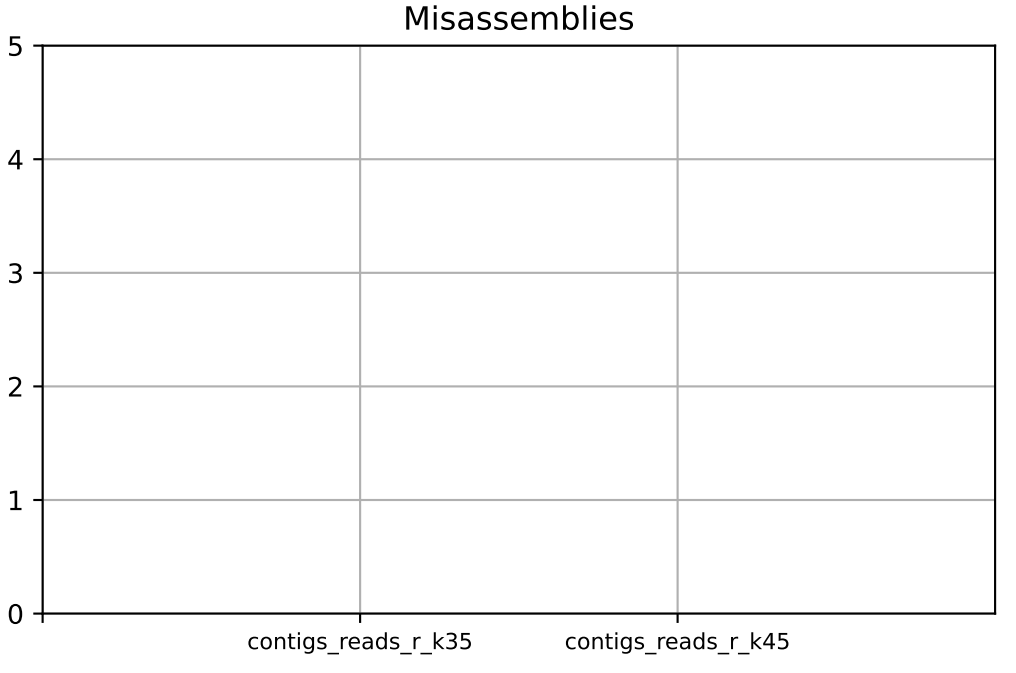

NGx
Contig length (bp)
0
200
400
600
800
1000
0
20
40
60
80
100
x
contigs_reads_r_k35
contigs_reads_r_k45

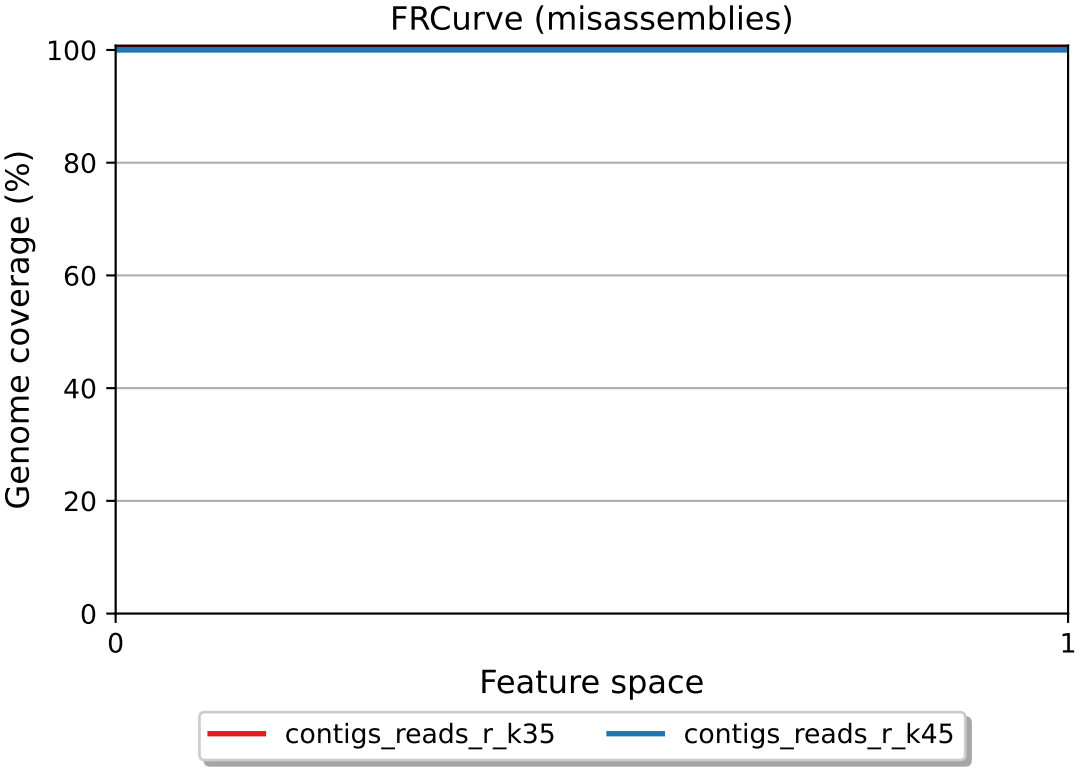

Cumulative length
Cumulative length (bp)
1250
1000
750
500
250
0
0
1
2
3
4
Contig index
contigs_reads_r_k35
contigs_reads_r_k45
Reference

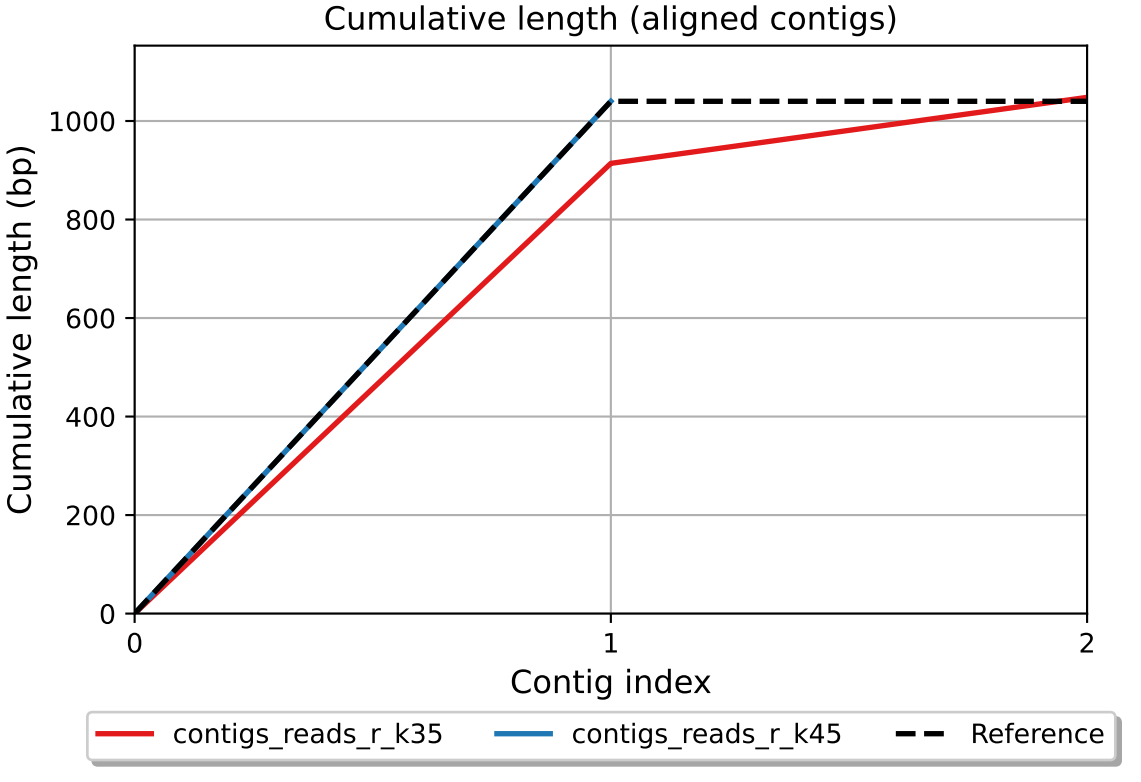

GC content
windows
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs_reads_r_k35
contigs_reads_r_k45
Reference

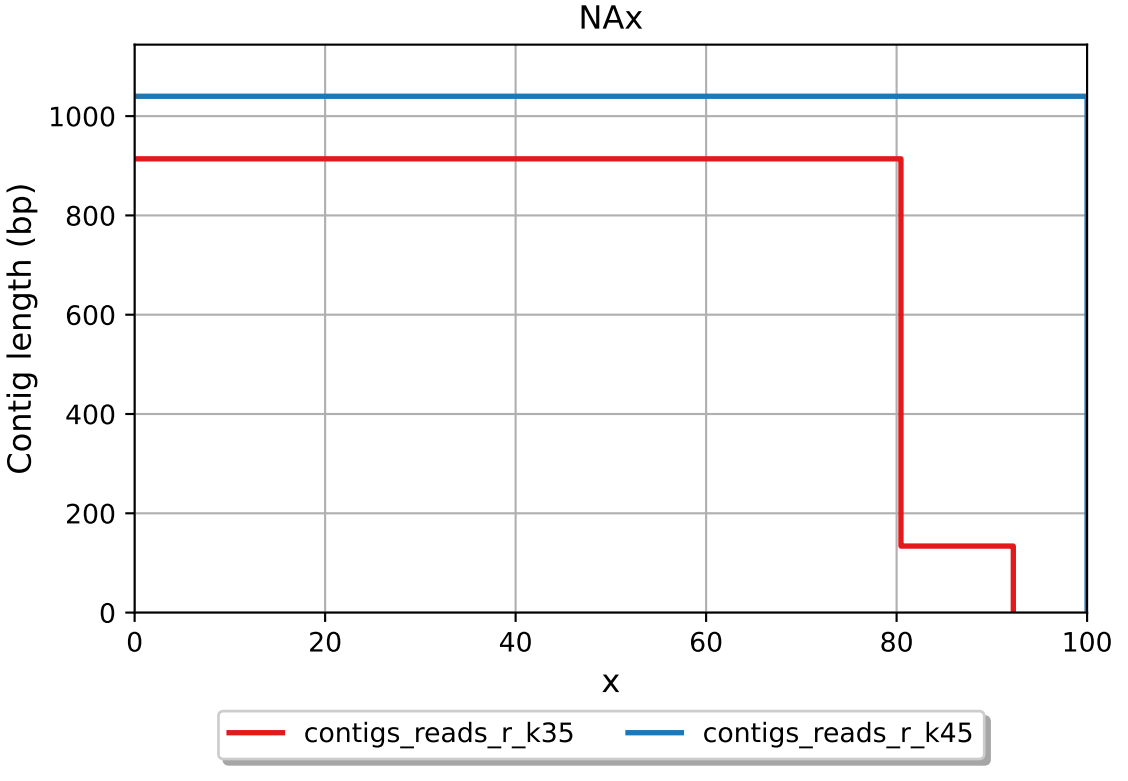

contigs_reads_r_k35 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs_reads_r_k35

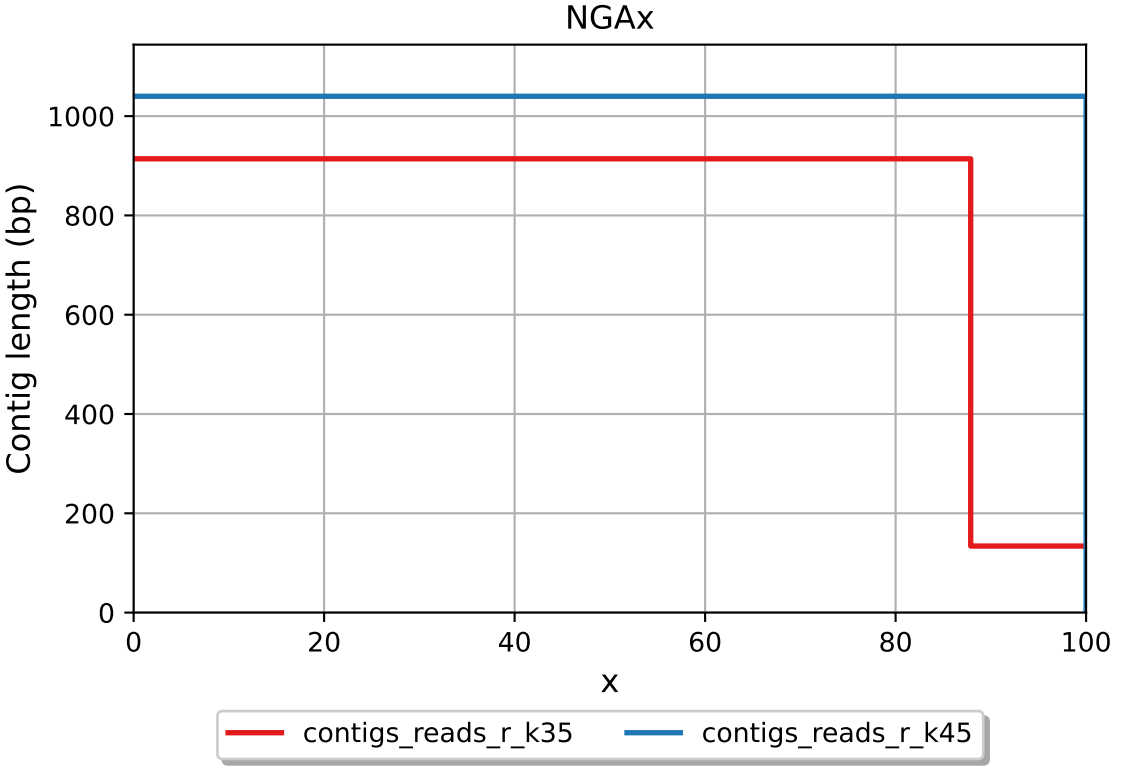

contigs_reads_r_k45 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs_reads_r_k45

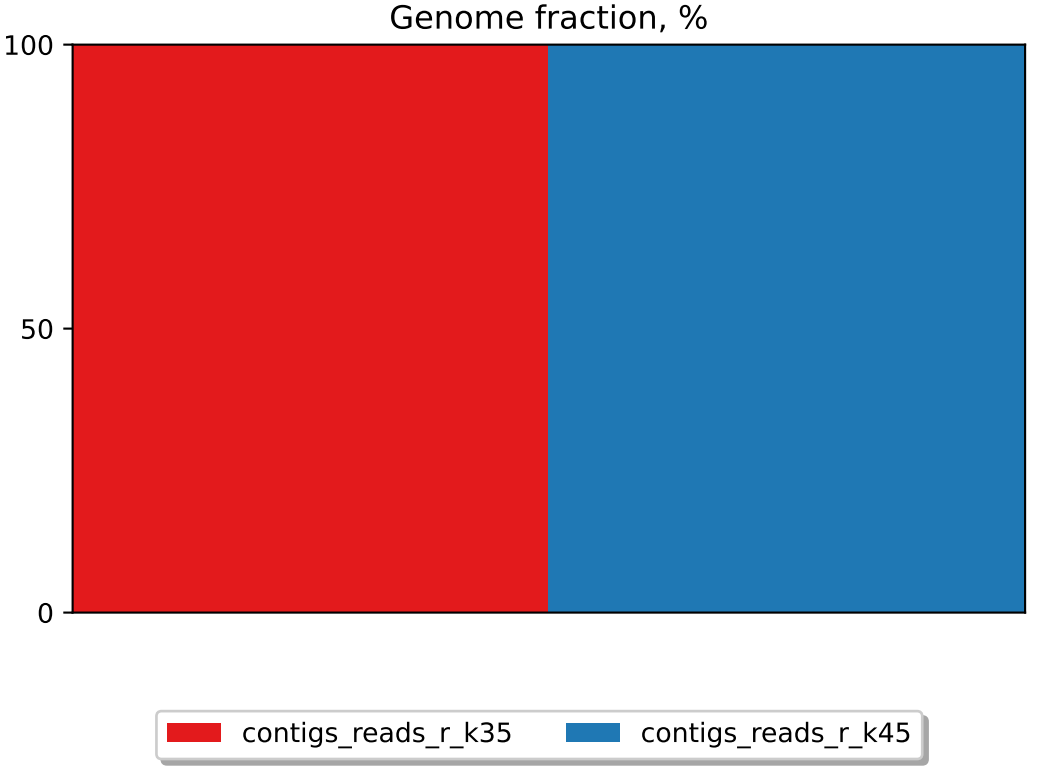

Misassemblies
5
4
3
2
1
0
contigs_reads_r_k35
contigs_reads_r_k45


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
contigs_reads_r_k35
contigs_reads_r_k45


Cumulative length (aligned contigs)
Cumulative length (bp)
0
200
400
600
800
1000
0
1
2
Contig index
contigs_reads_r_k35
contigs_reads_r_k45
Reference


NAx
Contig length (bp)
0
200
400
600
800
1000
0
20
40
60
80
100
x
contigs_reads_r_k35
contigs_reads_r_k45


NGAx
Contig length (bp)
0
200
400
600
800
1000
0
20
40
60
80
100
x
contigs_reads_r_k35
contigs_reads_r_k45


Genome fraction, %
100
50
0
contigs_reads_r_k35
contigs_reads_r_k45