Report

	reads_r_dbg_k40
# contigs (>= 0 bp)	5
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1188
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	946
Total length	946
Reference length	1040
GC (%)	51.16
Reference GC (%)	51.25
N50	946
NG50	946
N90	946
NG90	946
auN	946.0
auNG	860.5
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 (%)	91.058
Duplication ratio	0.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	105.71
Largest alignment	946
Total aligned length	946
NA50	946
NGA50	946
NA90	946
NGA90	946
auNA	946.0
auNGA	860.5
LA50	1
LGA50	1
LA90	1
LGA90	1

All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

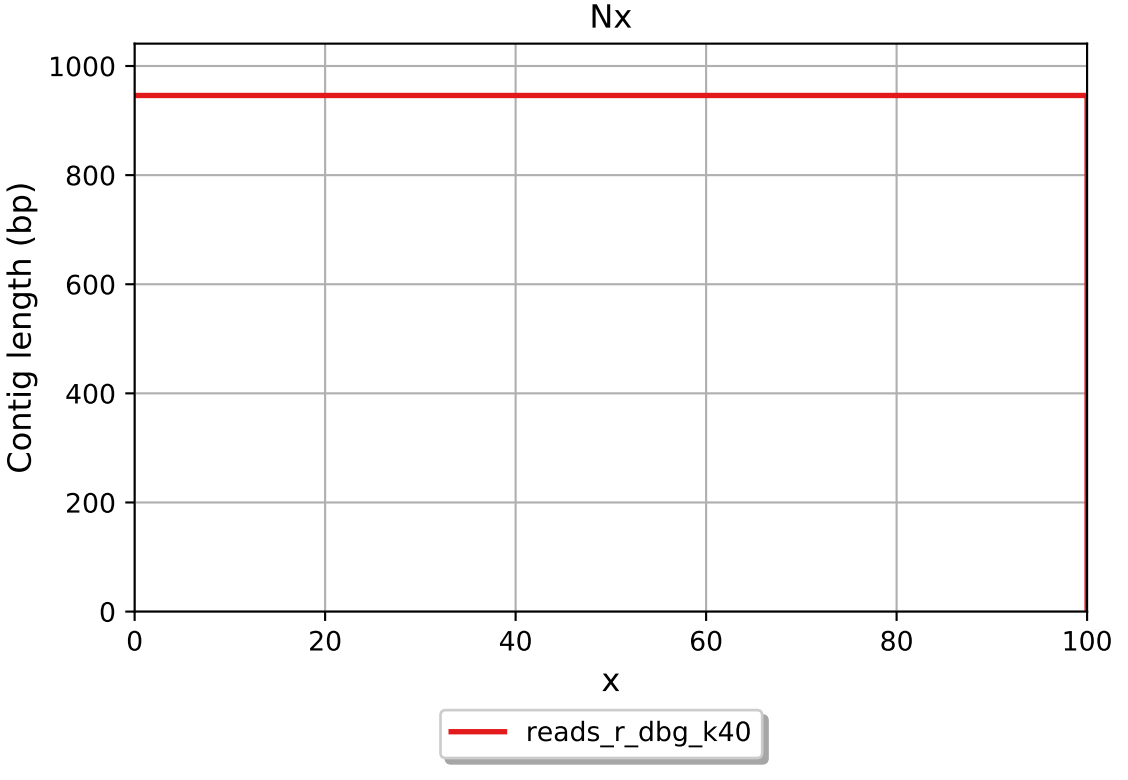
	reads_r_dbg_k40
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

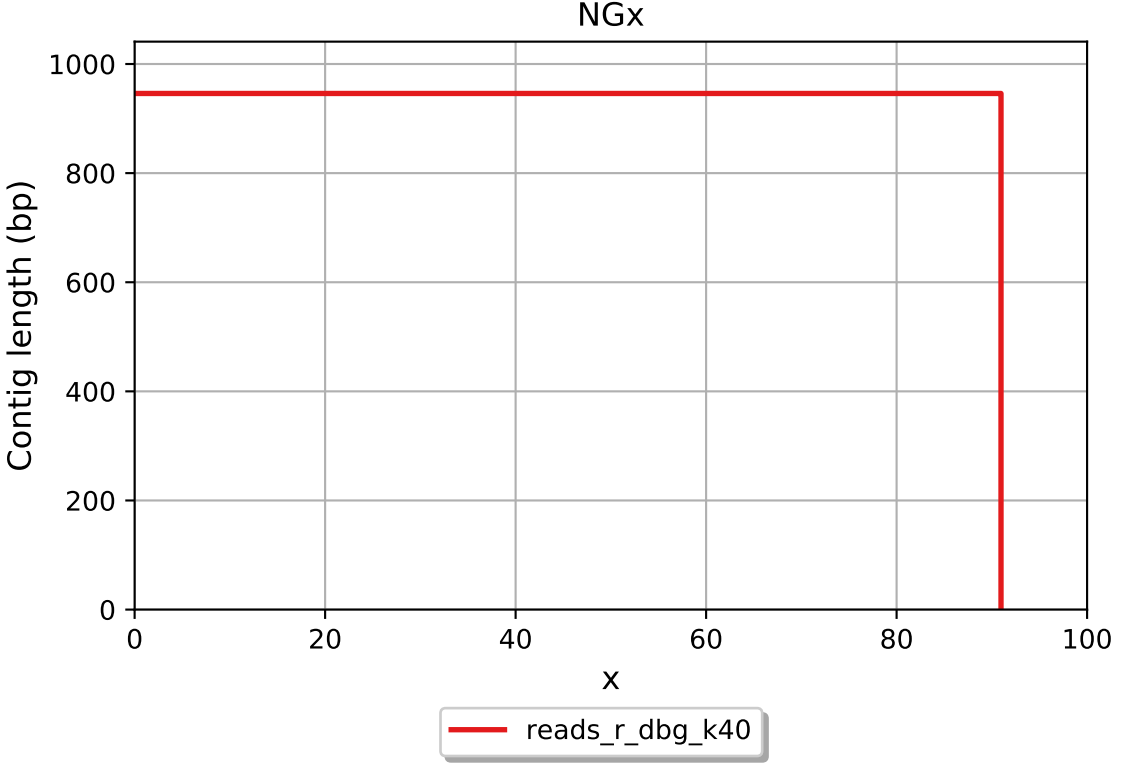
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

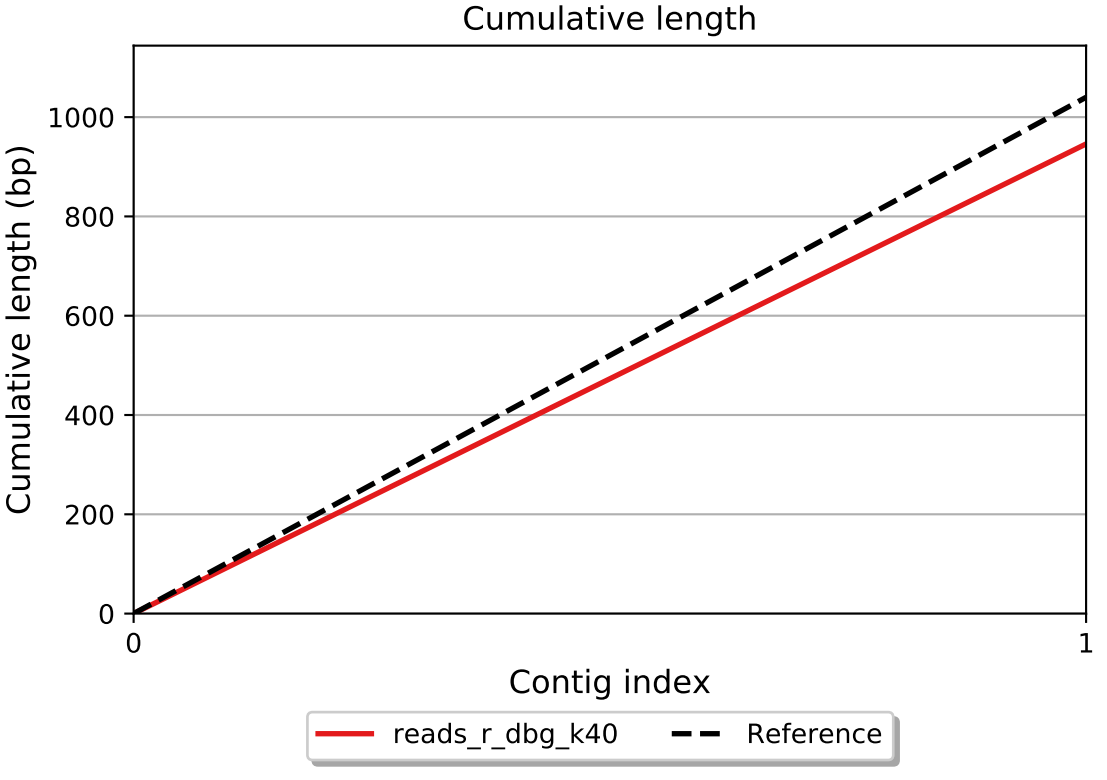
Unaligned report

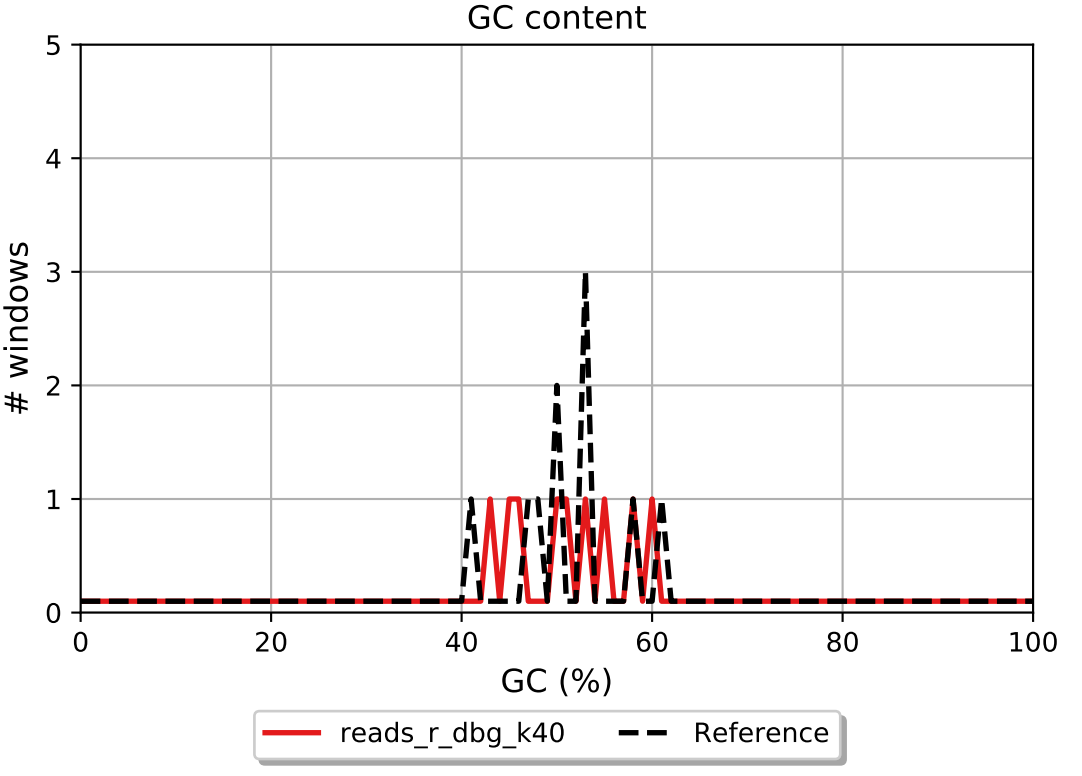
	reads_r_dbg_k40
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

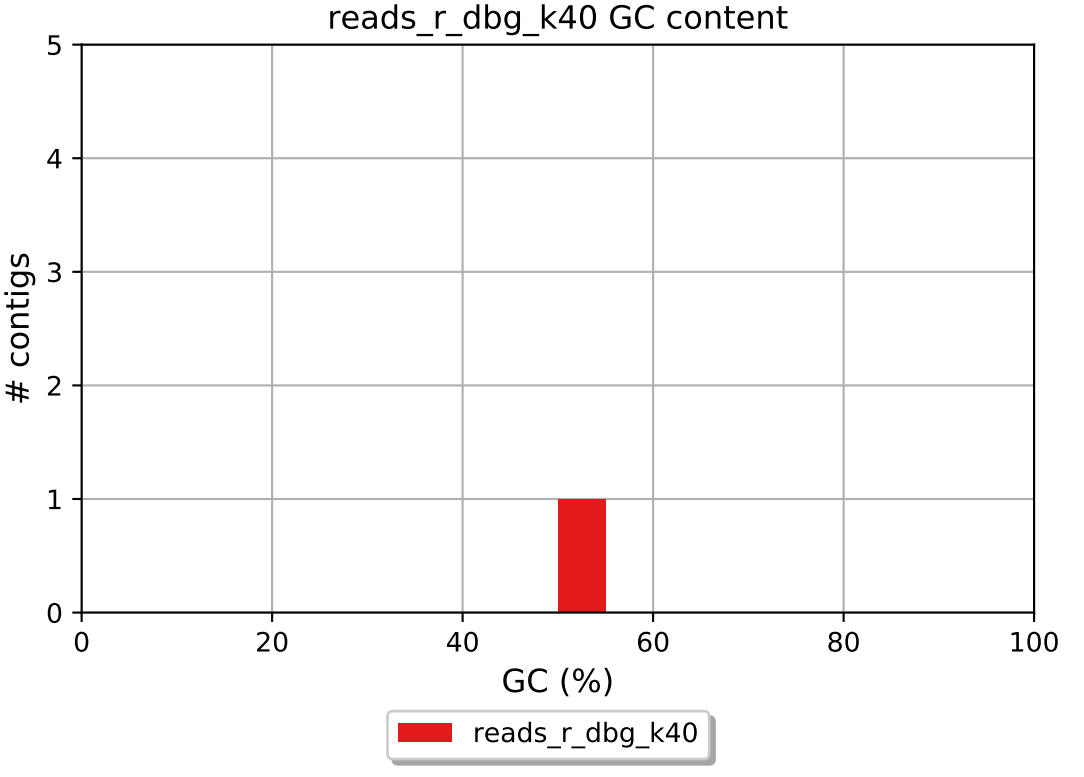
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

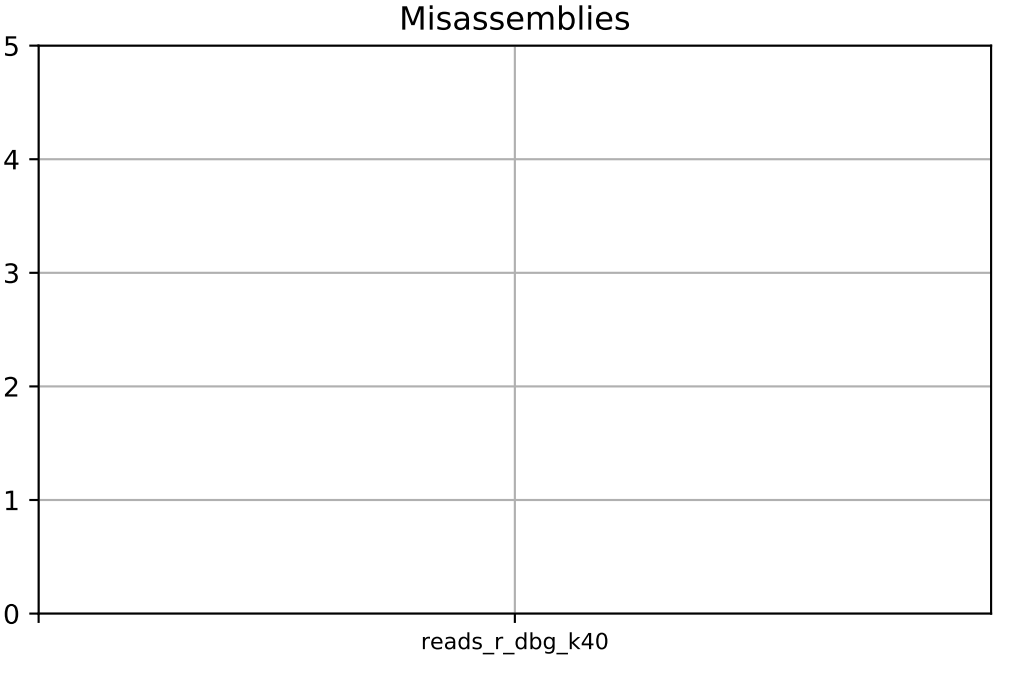

Nx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
reads_r_dbg_k40

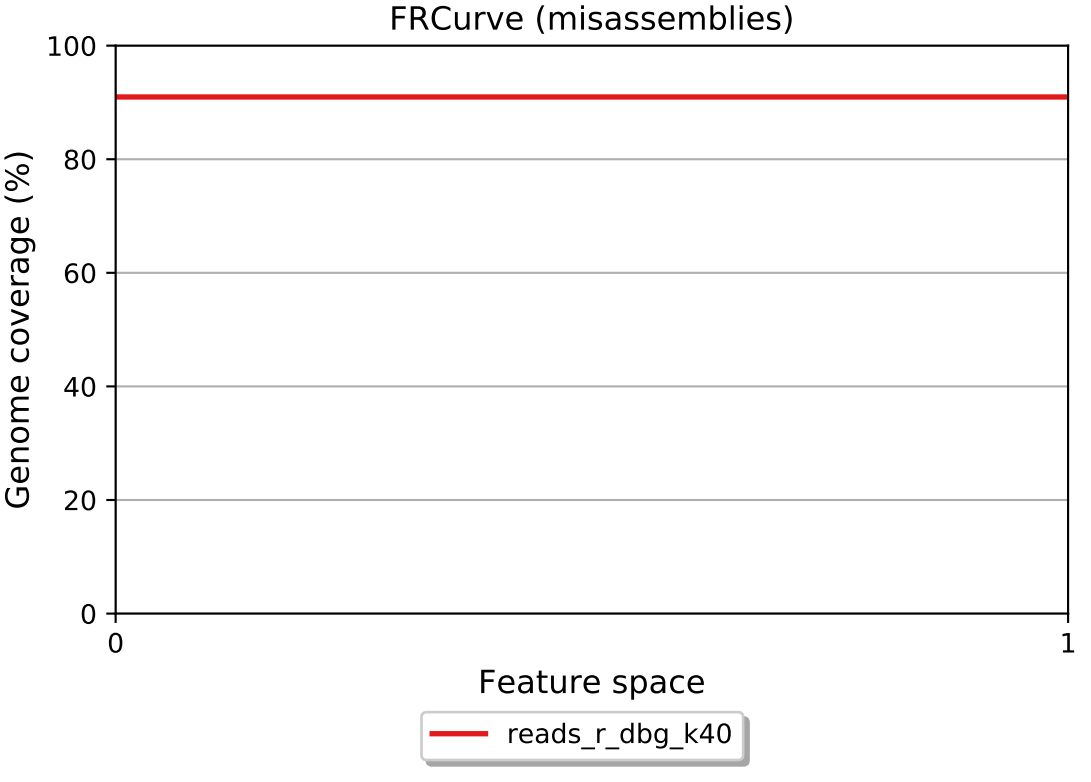

NGx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
reads_r_dbg_k40

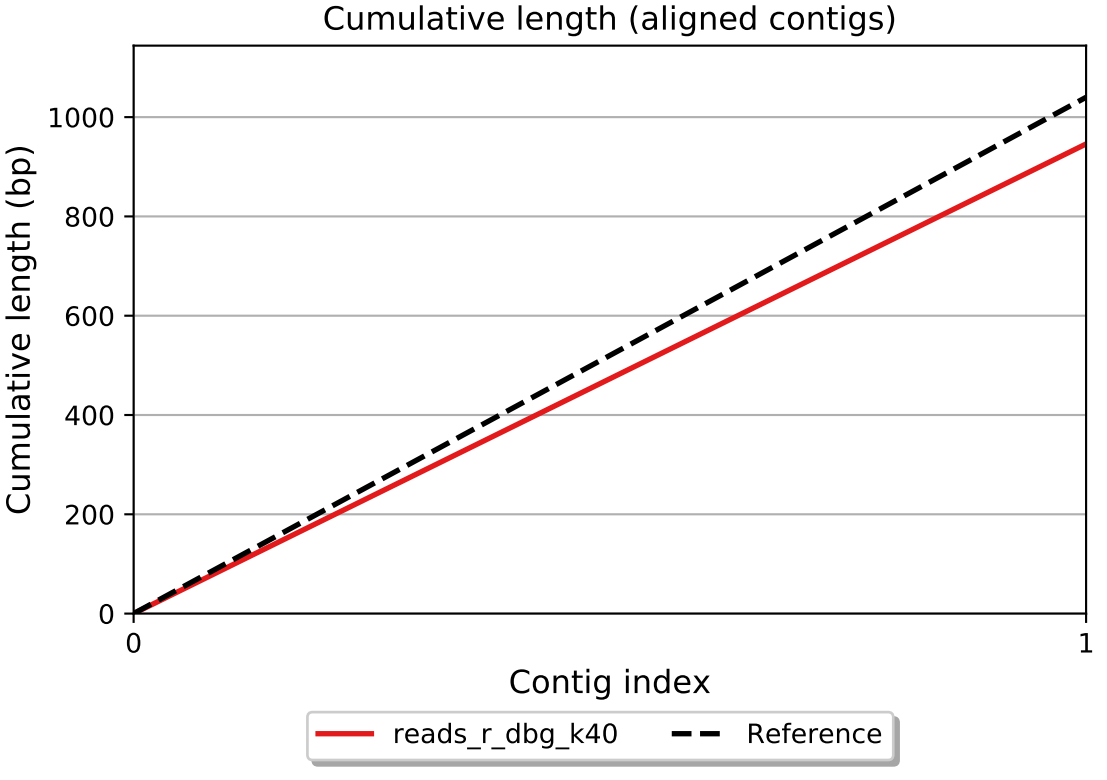

Cumulative length
Cumulative length (bp)
1000
800
600
400
200
0
0
1
Contig index
reads_r_dbg_k40
Reference

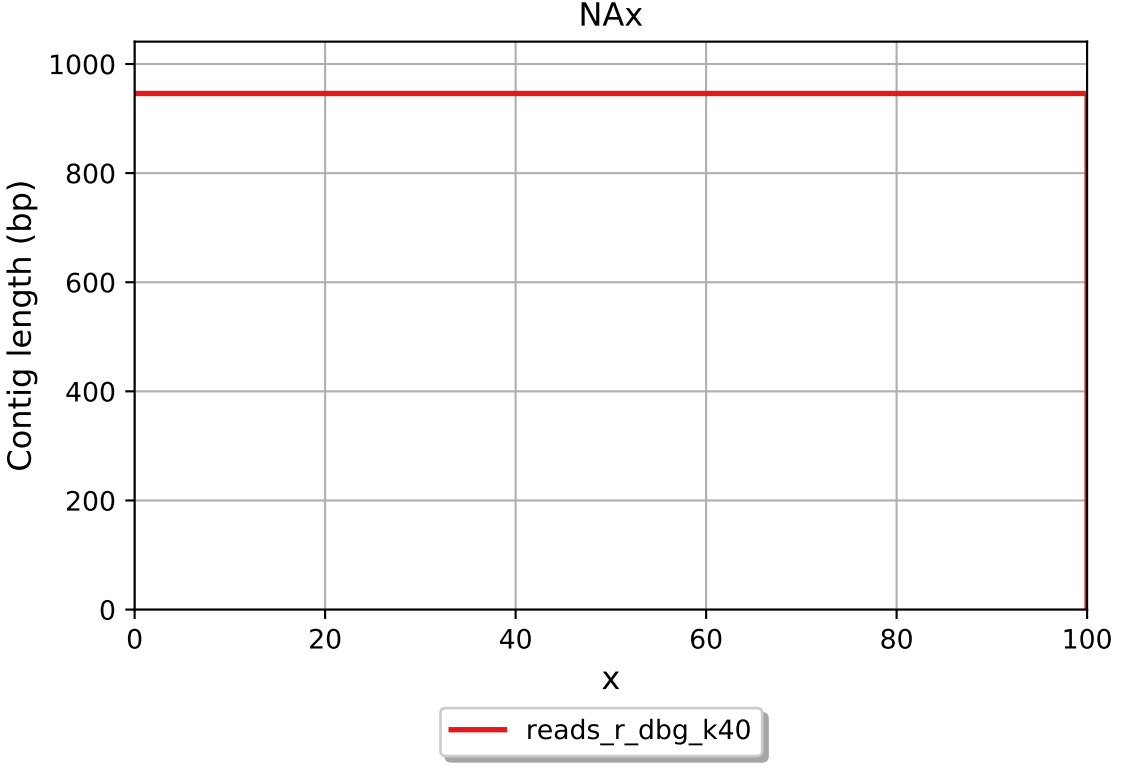

GC content
windows
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
reads_r_dbg_k40
Reference

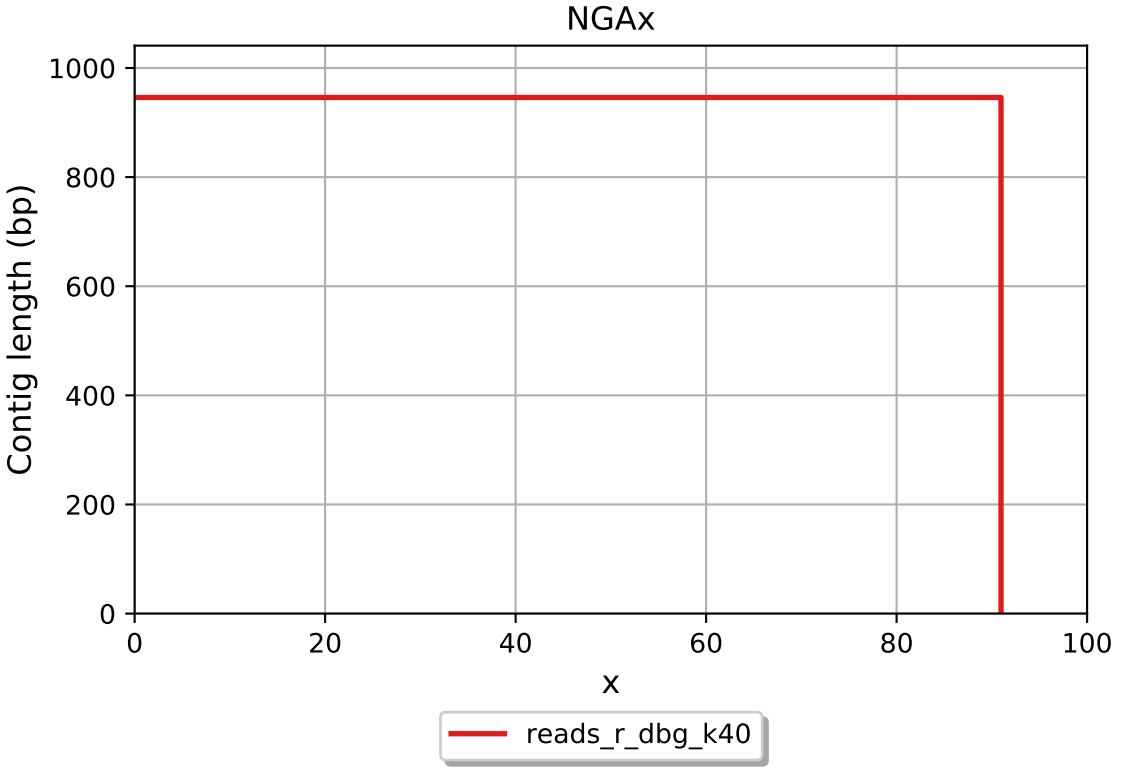

reads_r_dbg_k40 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
reads_r_dbg_k40


Misassemblies
5
4
3
2
1
0
reads_r_dbg_k40


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
reads_r_dbg_k40


Cumulative length (aligned contigs)
Cumulative length (bp)
1000
800
600
400
200
0
0
1
Contig index
reads_r_dbg_k40
Reference


NAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
reads_r_dbg_k40


NGAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
reads_r_dbg_k40