Report

	reads_r_dbg_k35
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1132
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	880
Total length	880
Reference length	1040
GC (%)	51.82
Reference GC (%)	51.25
N50	880
NG50	880
N90	880
NG90	-
auN	880.0
auNG	744.6
L50	1
LG50	1
L90	1
LG90	-
# 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 (%)	84.615
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	880
Total aligned length	880
NA50	880
NGA50	880
NA90	880
NGA90	-
auNA	880.0
auNGA	744.6
LA50	1
LGA50	1
LA90	1
LGA90	-

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

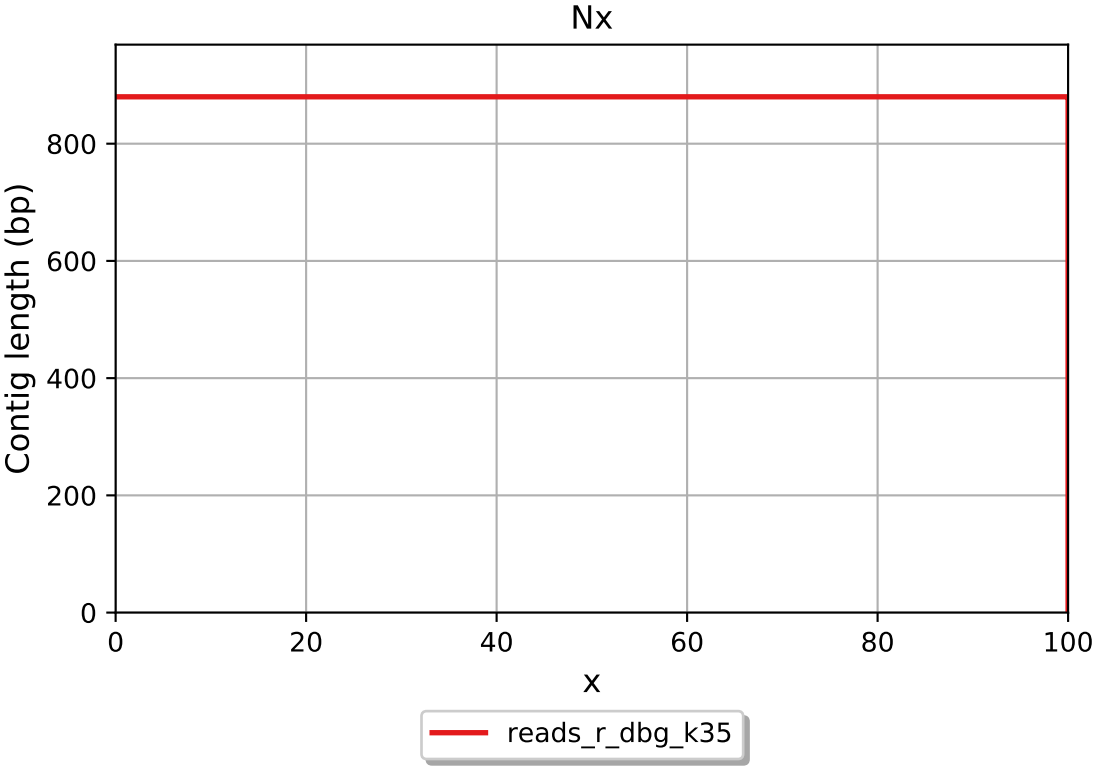
	reads_r_dbg_k35
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. 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

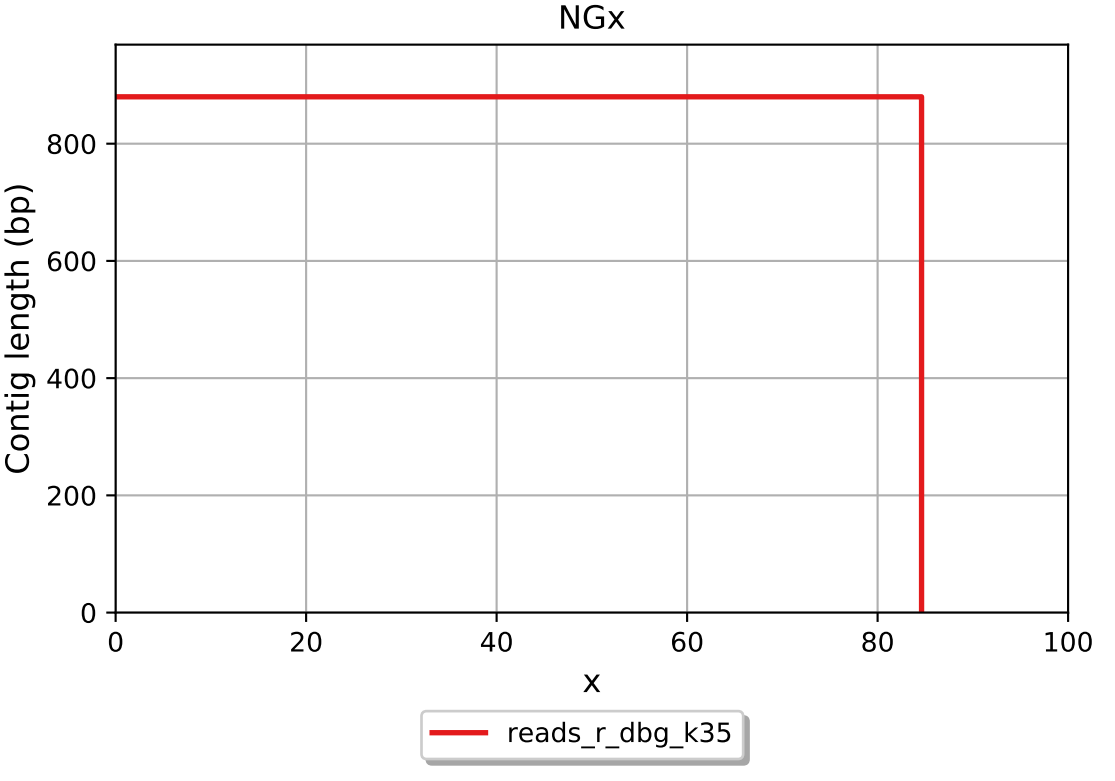
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

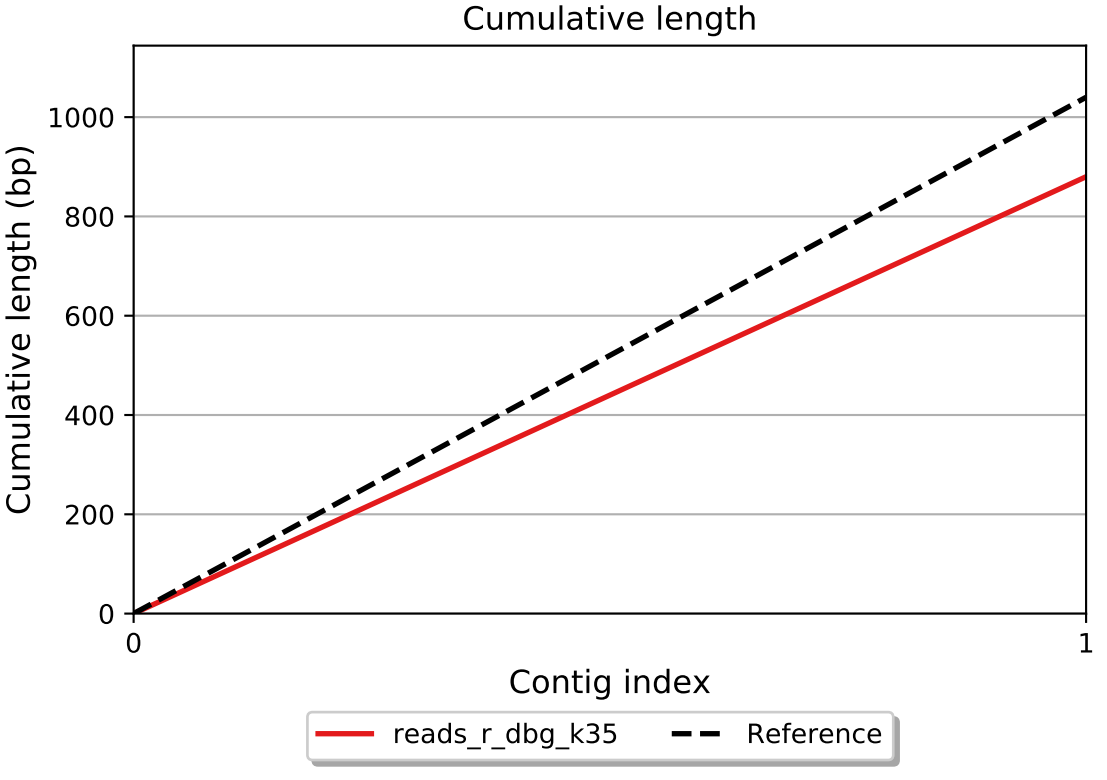
Unaligned report

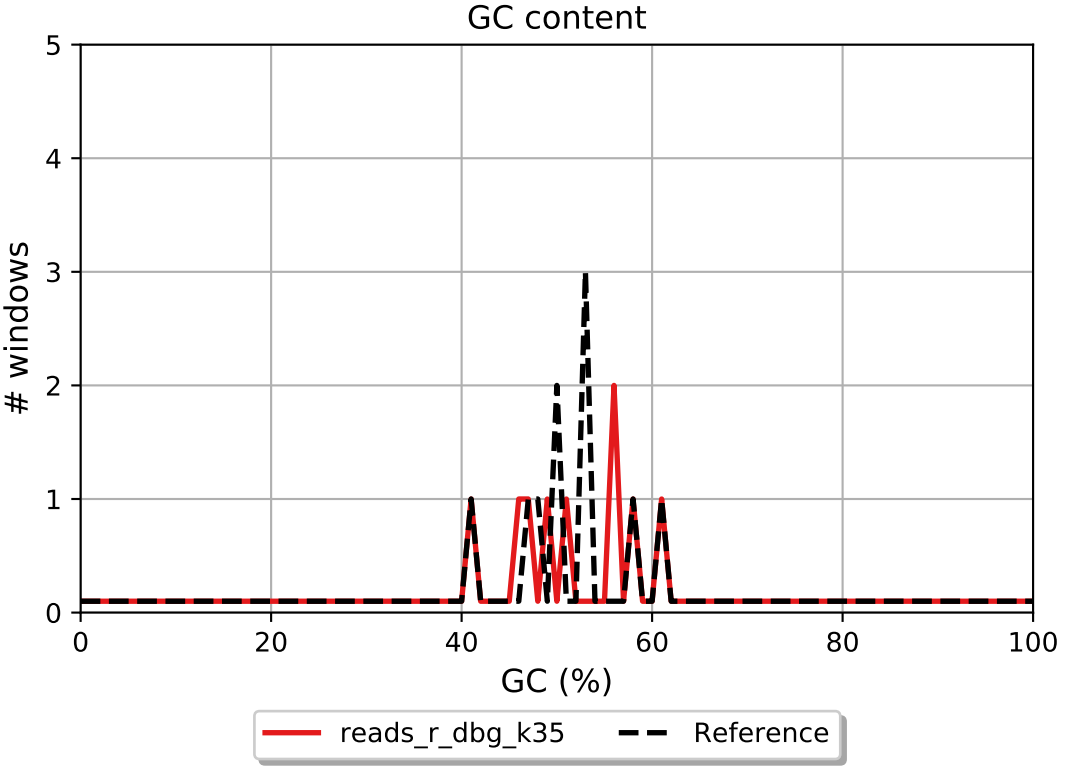
	reads_r_dbg_k35
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

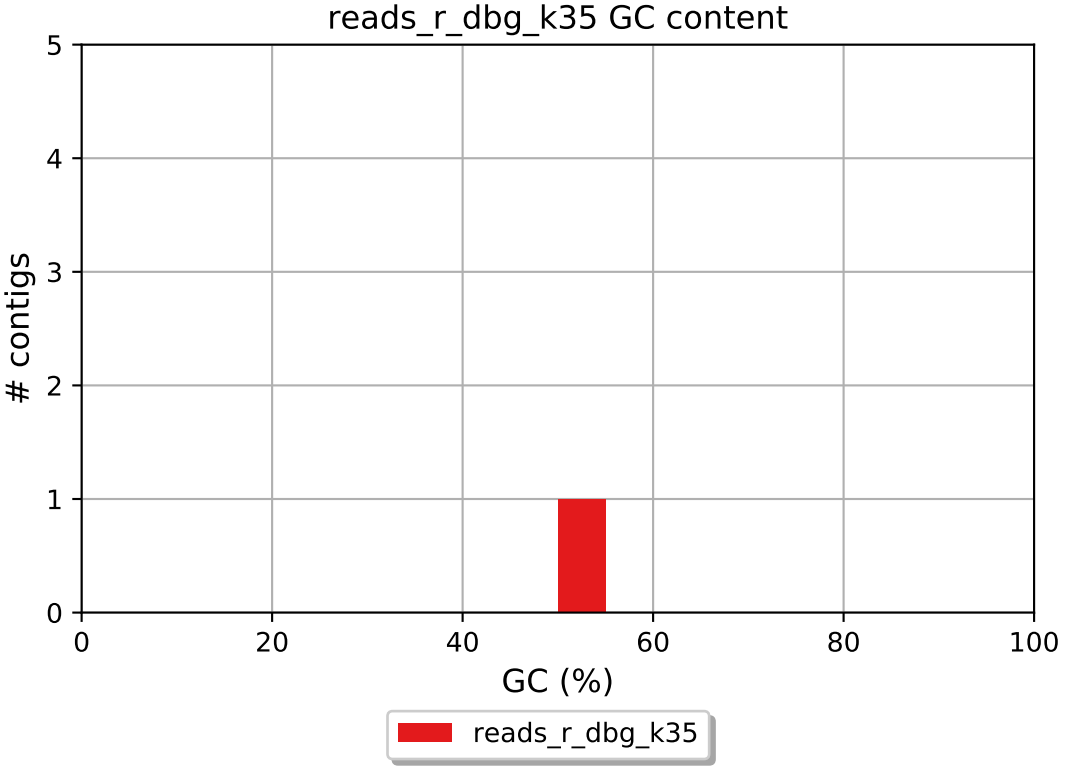
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

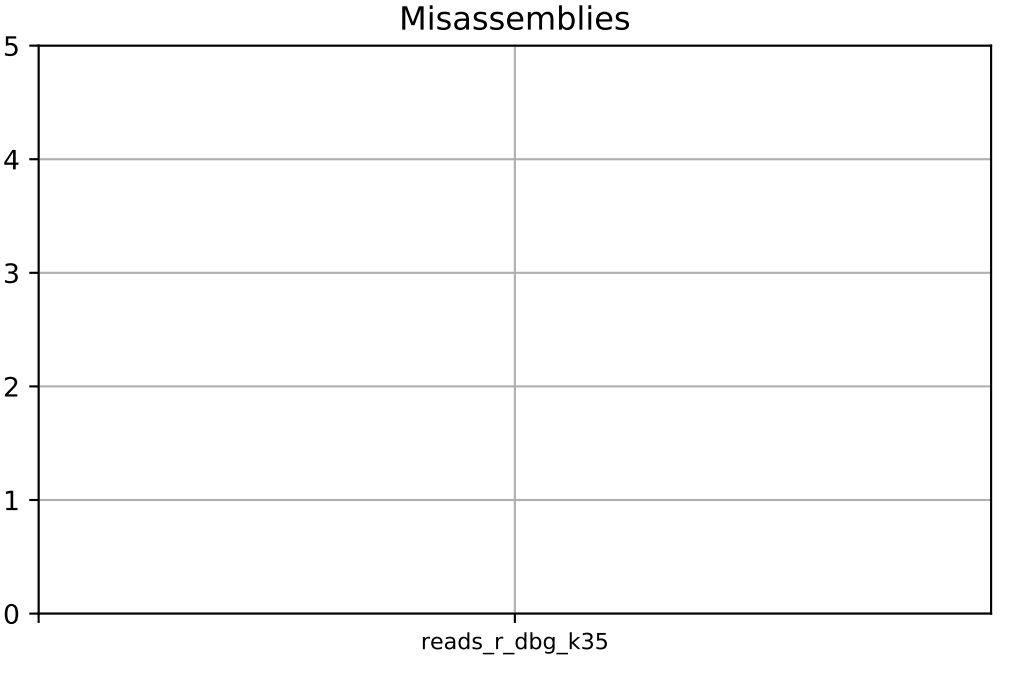

Nx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
reads_r_dbg_k35

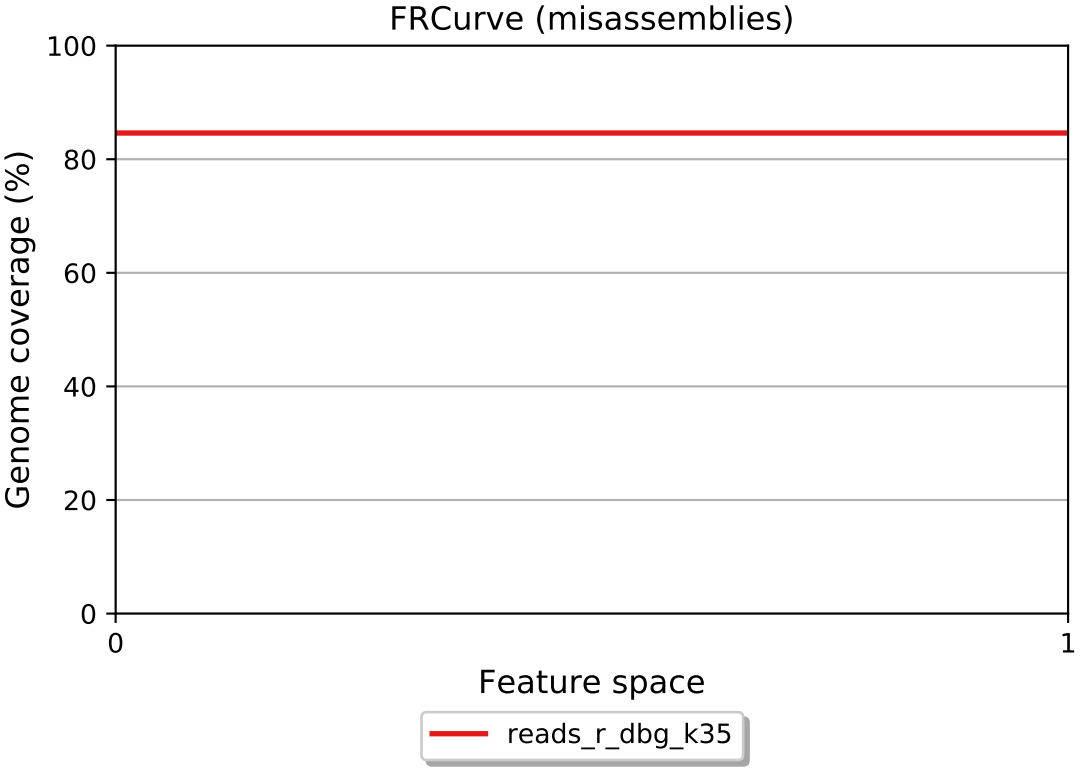

NGx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
reads_r_dbg_k35

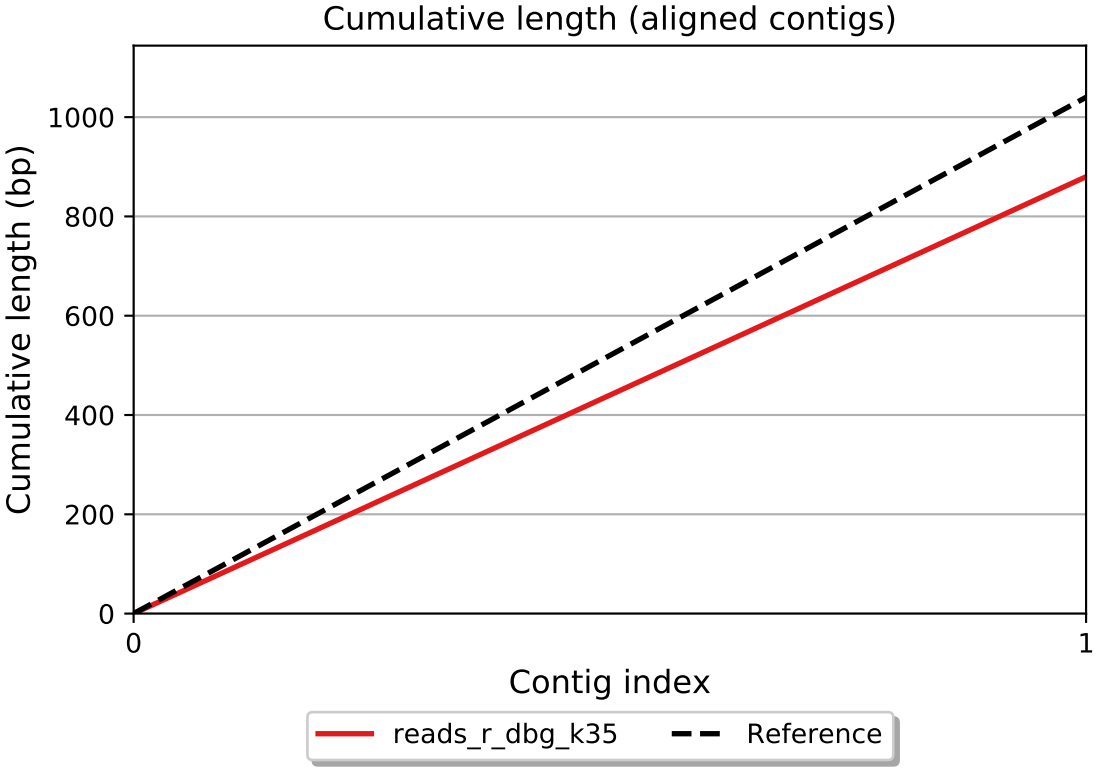

Cumulative length
Cumulative length (bp)
1000
800
600
400
200
0
0
1
Contig index
reads_r_dbg_k35
Reference

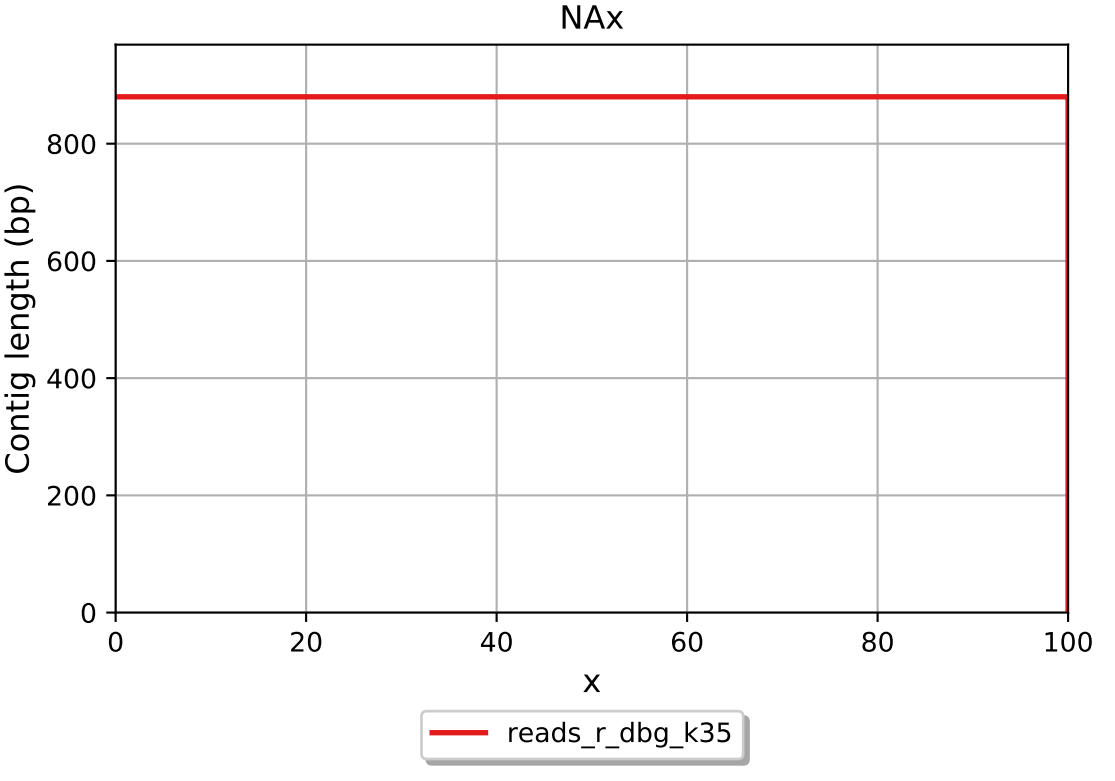

GC content
windows
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
reads_r_dbg_k35
Reference

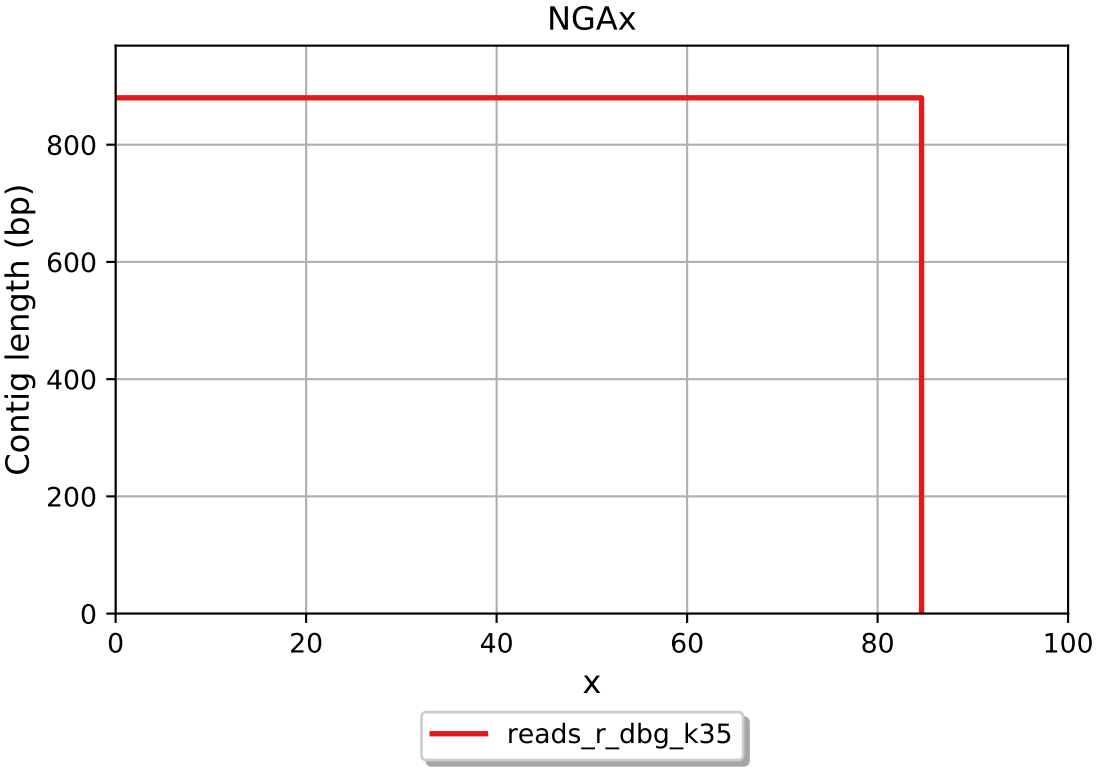

reads_r_dbg_k35 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
reads_r_dbg_k35


Misassemblies
5
4
3
2
1
0
reads_r_dbg_k35


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
reads_r_dbg_k35


Cumulative length (aligned contigs)
Cumulative length (bp)
1000
800
600
400
200
0
0
1
Contig index
reads_r_dbg_k35
Reference


NAx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
reads_r_dbg_k35


NGAx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
reads_r_dbg_k35