Report

	reads_hiseq_5k_dbg_k40
# contigs (>= 0 bp)	97
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	32995
Total length (>= 1000 bp)	21980
Total length (>= 5000 bp)	5605
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	18
Largest contig	5605
Total length	27044
Reference length	30119
GC (%)	41.23
Reference GC (%)	41.24
N50	2608
NG50	2608
N90	587
NG90	-
auN	2787.2
auNG	2502.6
L50	4
LG50	4
L90	13
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	3 + 0 part
Unaligned length	1126
Genome fraction (%)	85.398
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	5598
Total aligned length	25911
NA50	2608
NGA50	2608
NA90	587
NGA90	-
auNA	2768.3
auNGA	2485.7
LA50	4
LGA50	4
LA90	13
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

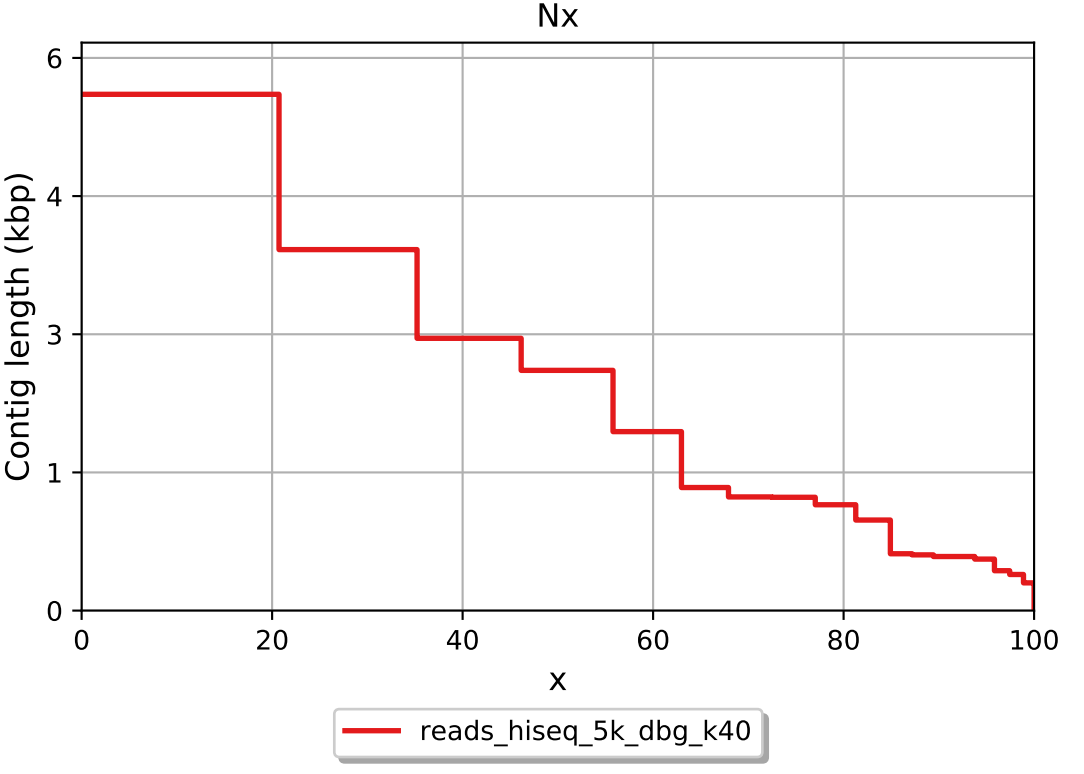
	reads_hiseq_5k_dbg_k40
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

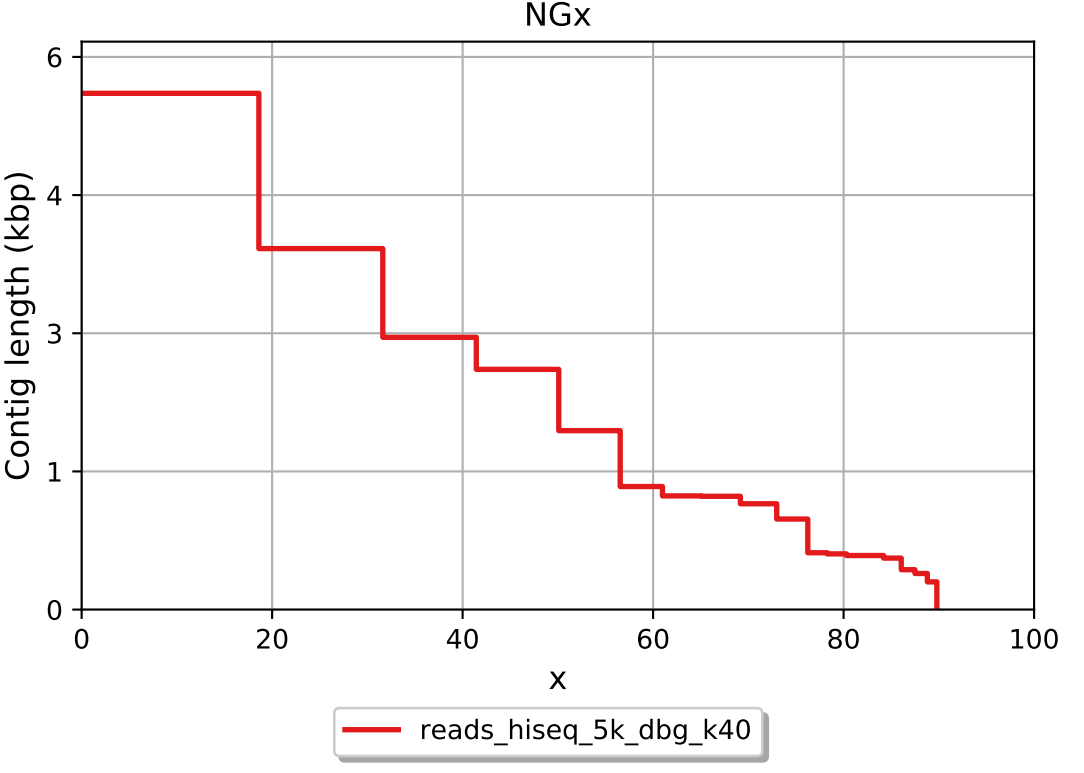
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

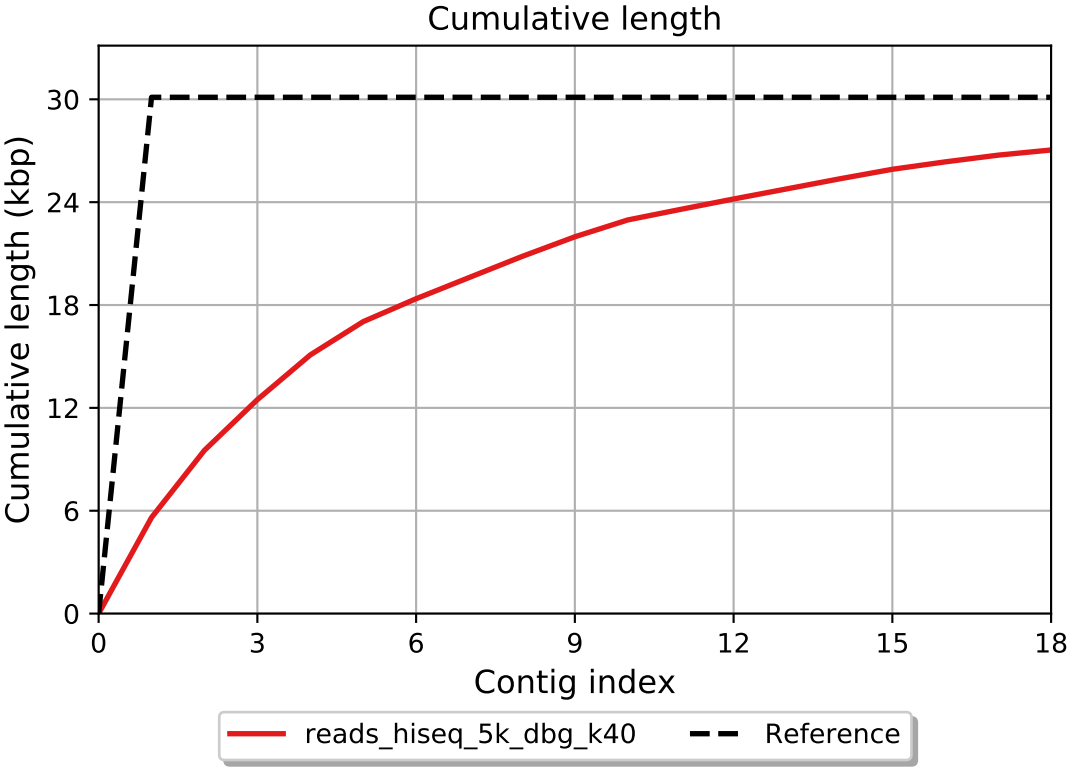
Unaligned report

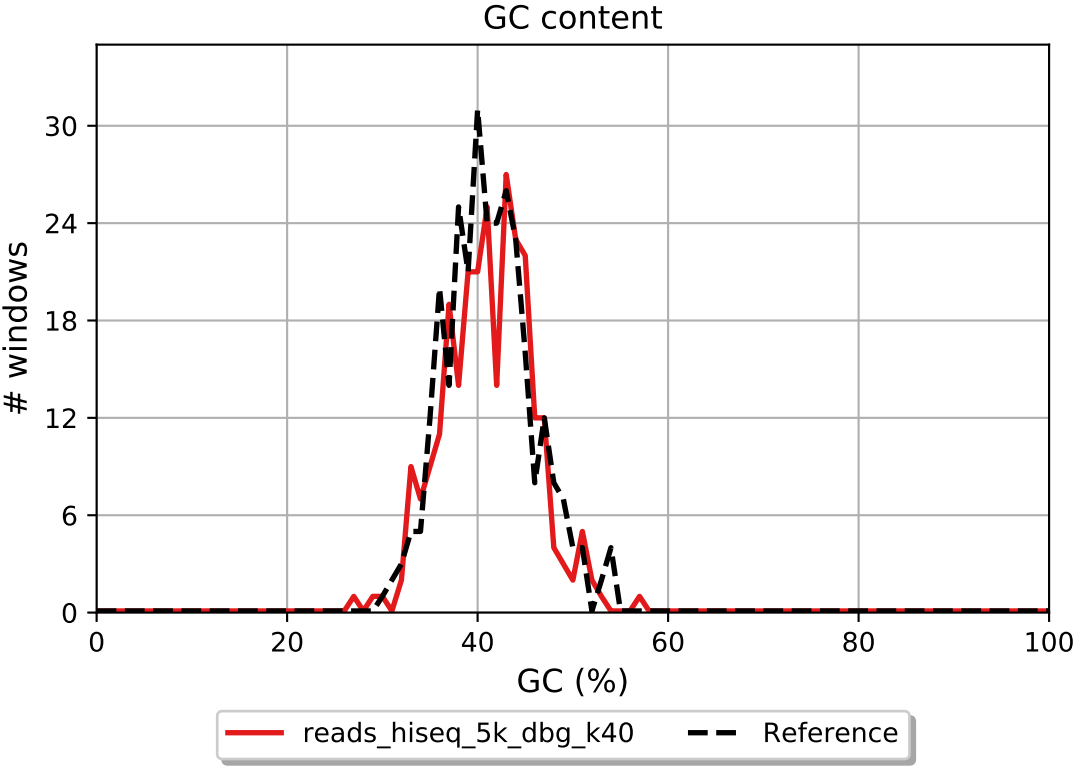
	reads_hiseq_5k_dbg_k40
# fully unaligned contigs	3
Fully unaligned length	1126
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

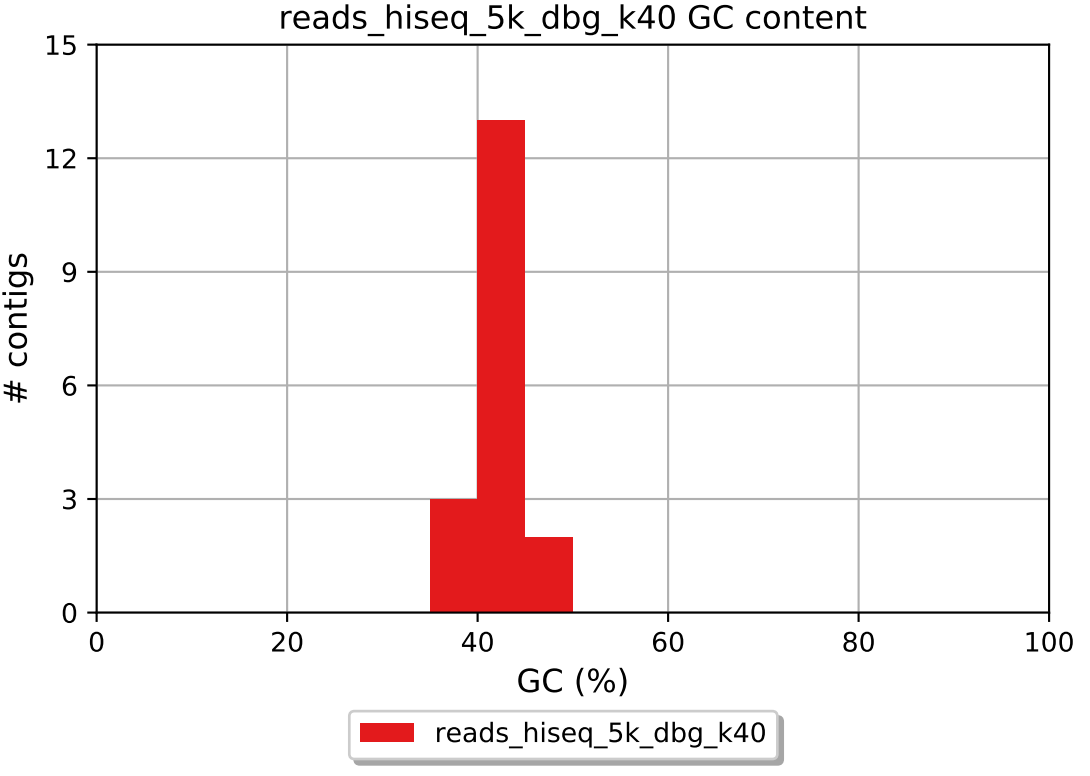
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

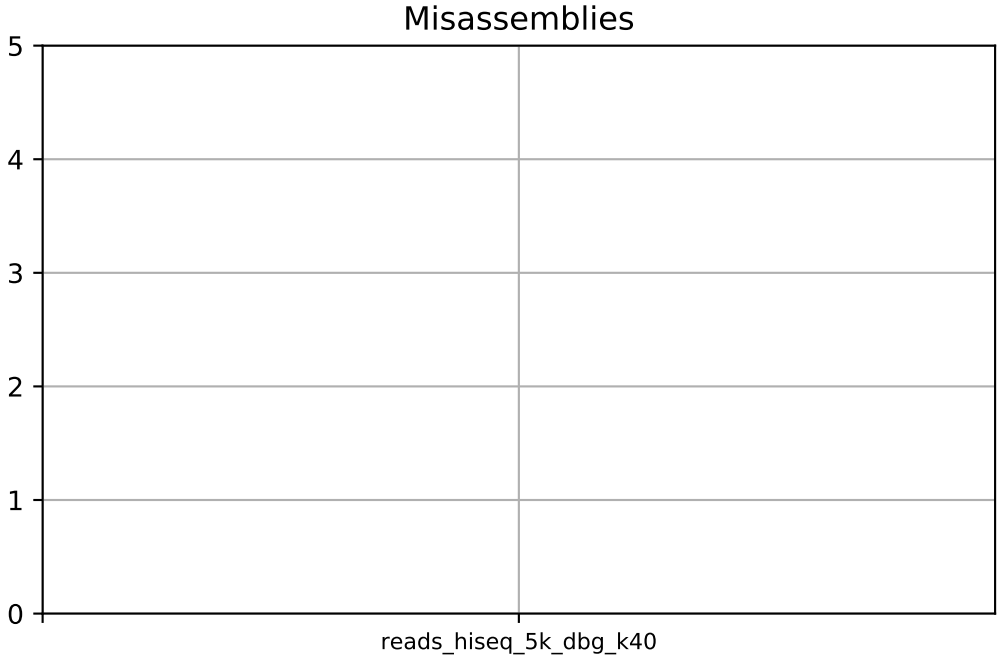

Nx
Contig length (kbp)
6
4
3
1
0
0
20
40
60
80
100
x
reads_hiseq_5k_dbg_k40

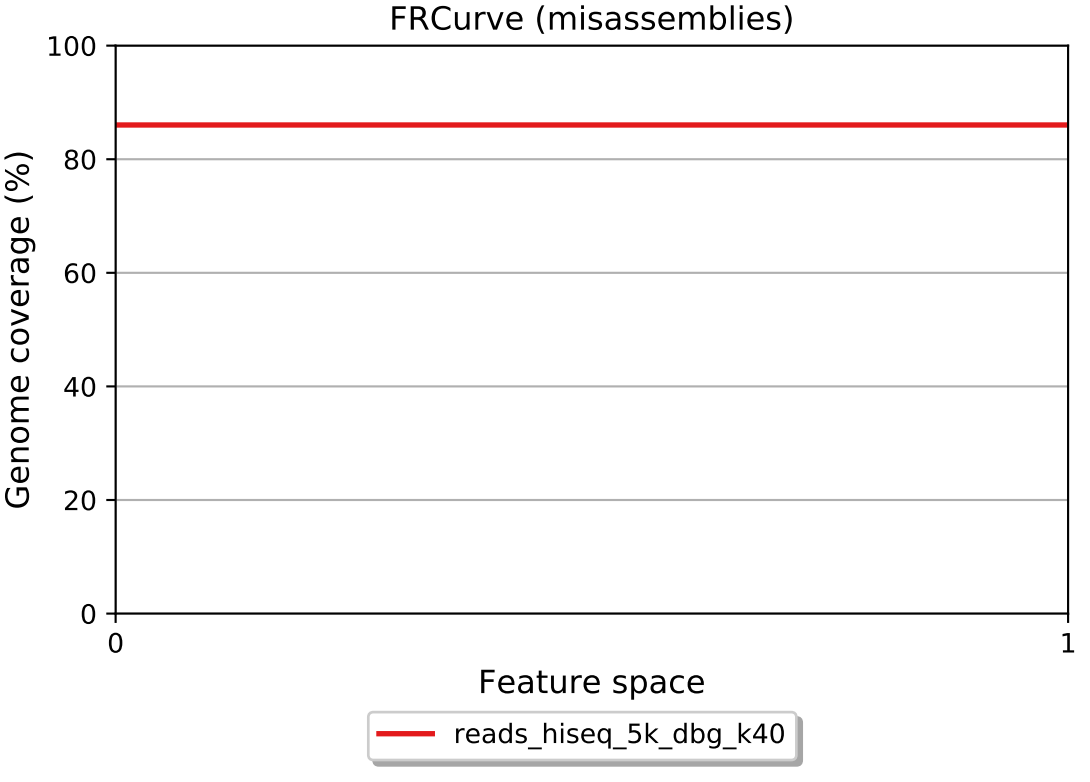

NGx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
reads_hiseq_5k_dbg_k40

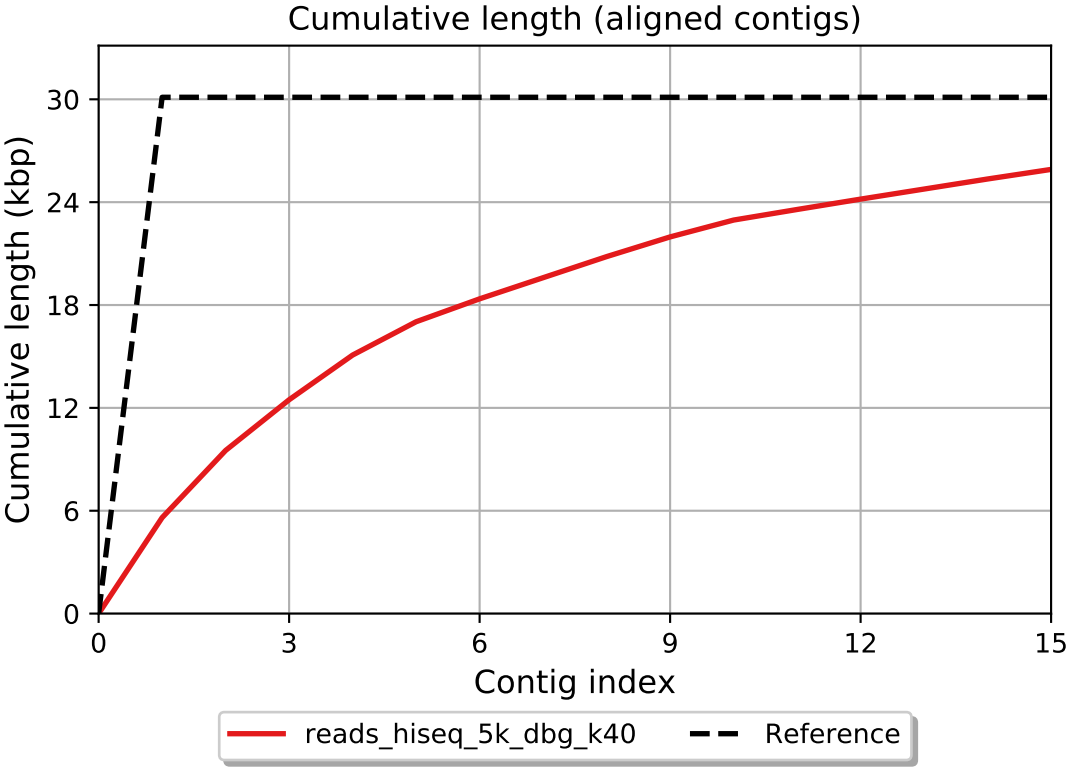

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
3
6
9
12
15
18
Contig index
reads_hiseq_5k_dbg_k40
Reference

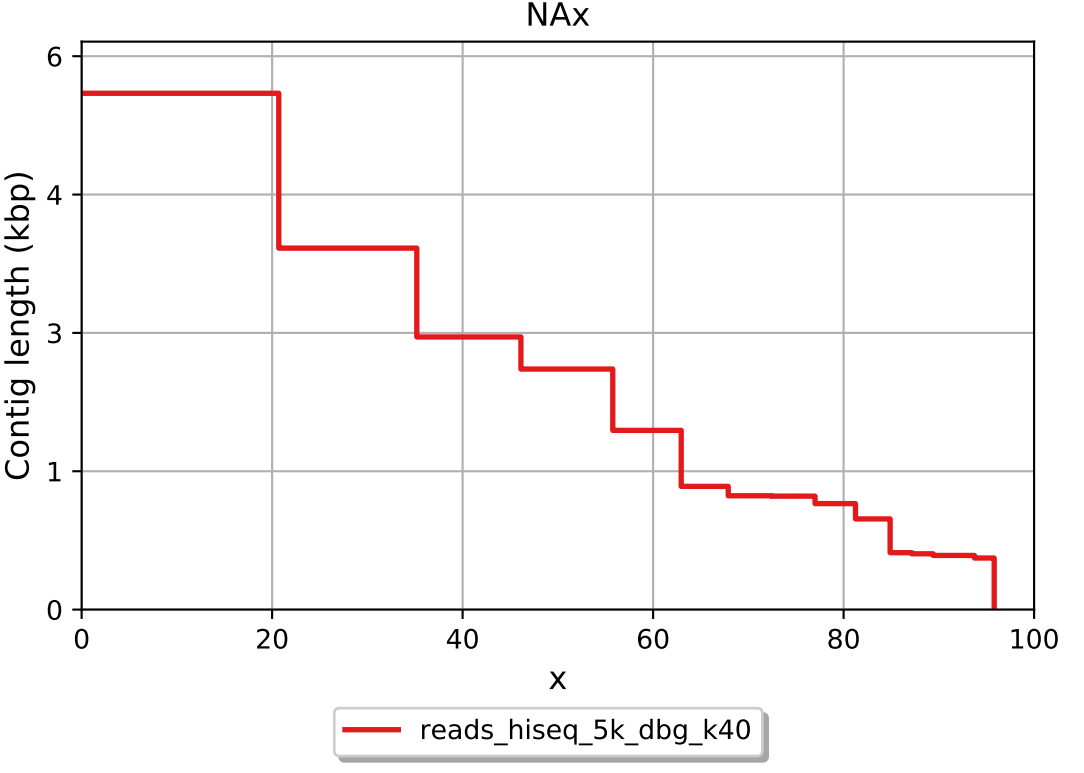

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
reads_hiseq_5k_dbg_k40
Reference

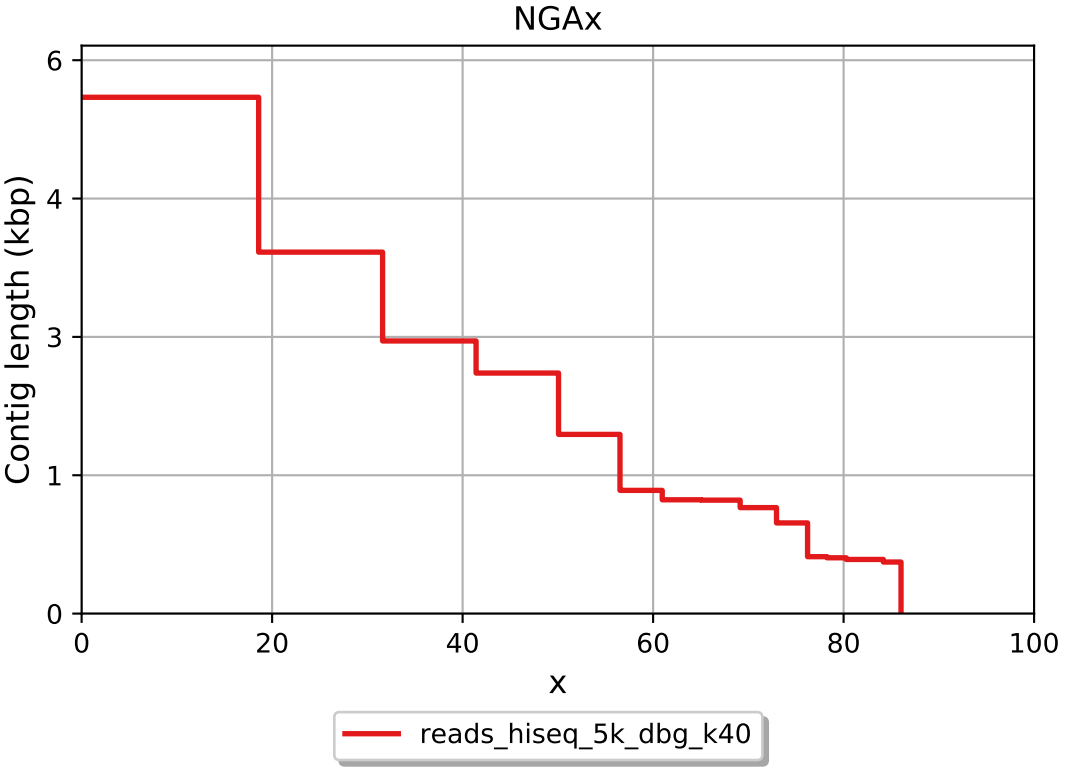

reads_hiseq_5k_dbg_k40 GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
reads_hiseq_5k_dbg_k40


Misassemblies
5
4
3
2
1
0
reads_hiseq_5k_dbg_k40


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
reads_hiseq_5k_dbg_k40


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
3
6
9
12
15
Contig index
reads_hiseq_5k_dbg_k40
Reference


NAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
reads_hiseq_5k_dbg_k40


NGAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
reads_hiseq_5k_dbg_k40