Report

	reads_hiseq_5k_olc
# contigs (>= 0 bp)	214
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	106594
Total length (>= 1000 bp)	39436
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	99
Largest contig	3650
Total length	79074
Reference length	30119
GC (%)	41.26
Reference GC (%)	41.24
N50	965
NG50	2742
N90	378
NG90	1661
auN	1431.2
auNG	3757.5
L50	21
LG50	5
L90	76
LG90	11
# 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	48 + 0 part
Unaligned length	18572
Genome fraction (%)	96.902
Duplication ratio	2.072
# N's per 100 kbp	0.00
# mismatches per 100 kbp	302.57
# indels per 100 kbp	0.00
Largest alignment	3650
Total aligned length	60482
NA50	965
NGA50	2742
NA90	-
NGA90	1661
auNA	1337.6
auNGA	3511.6
LA50	21
LGA50	5
LA90	-
LGA90	11

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

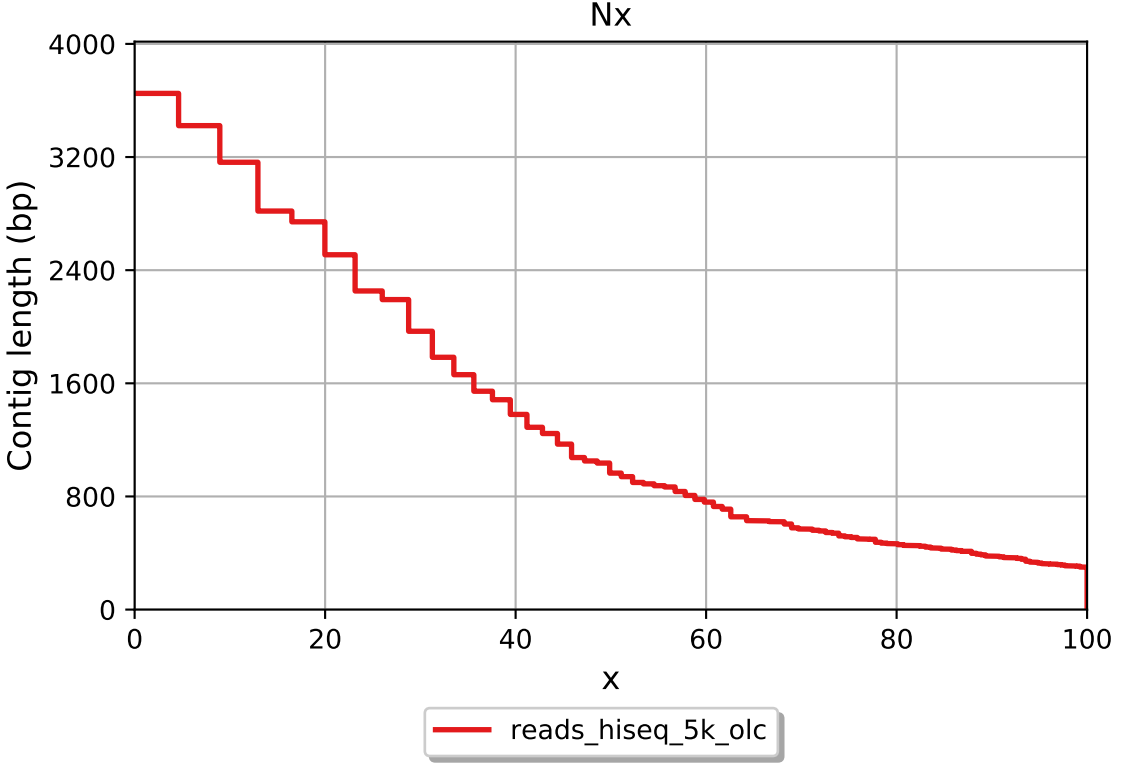
	reads_hiseq_5k_olc
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	183
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

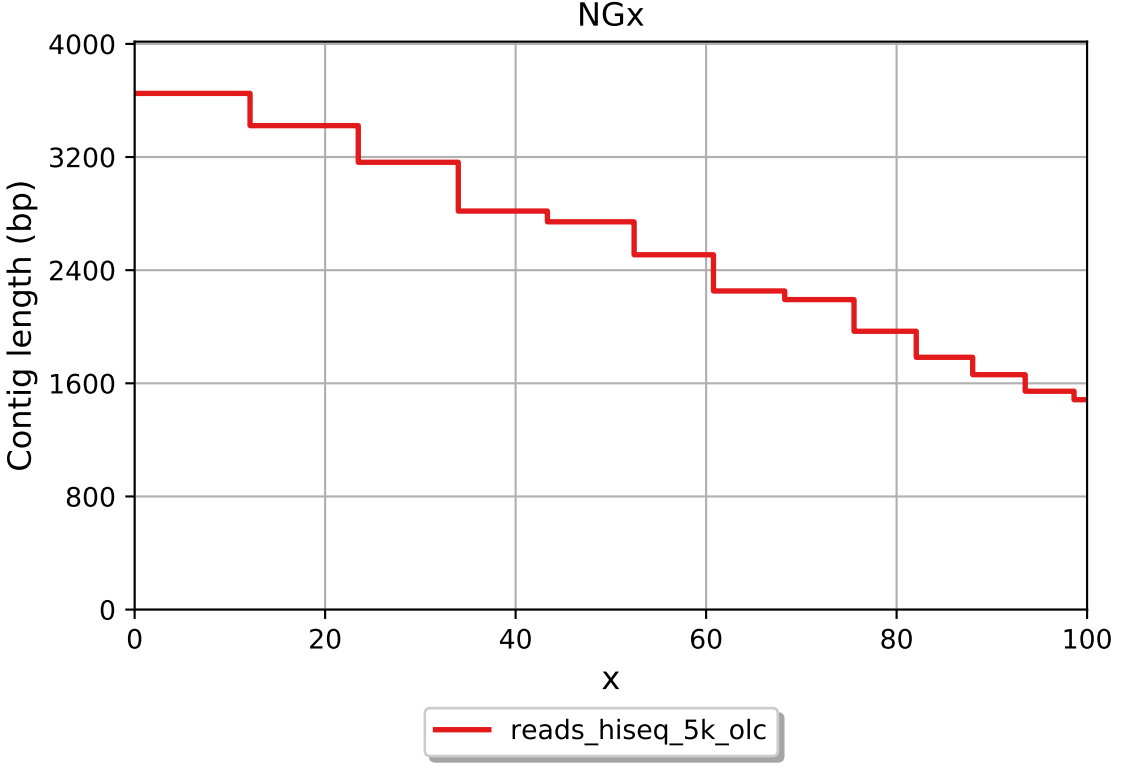
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

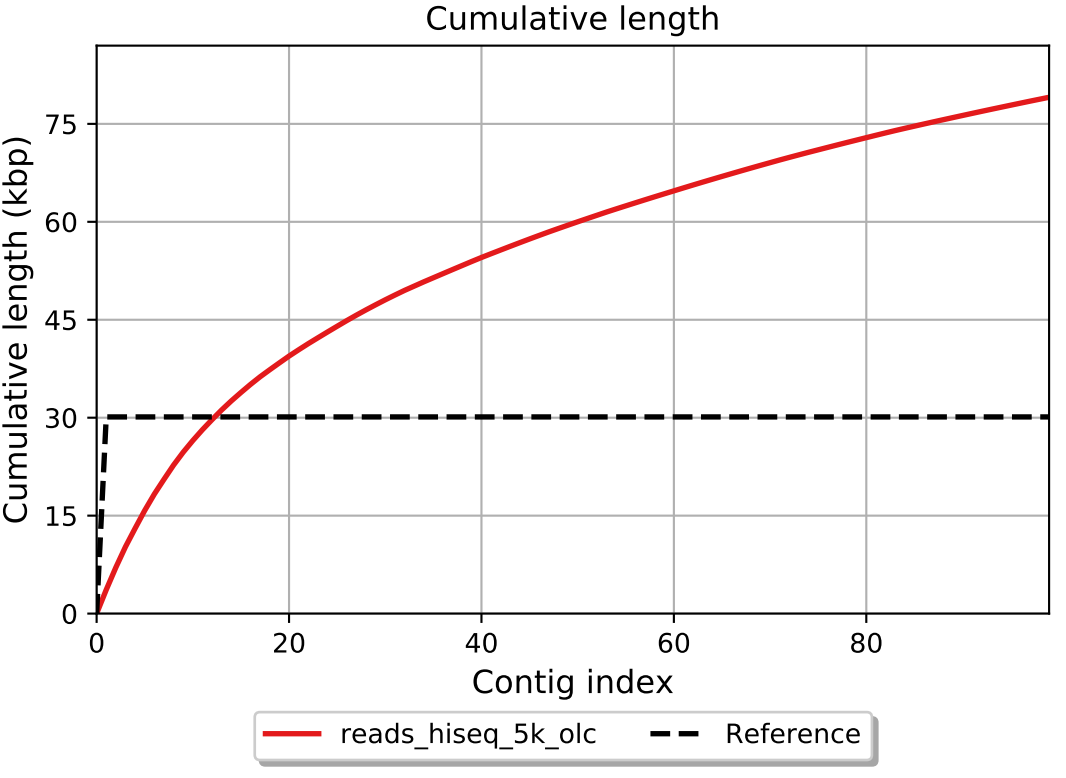
Unaligned report

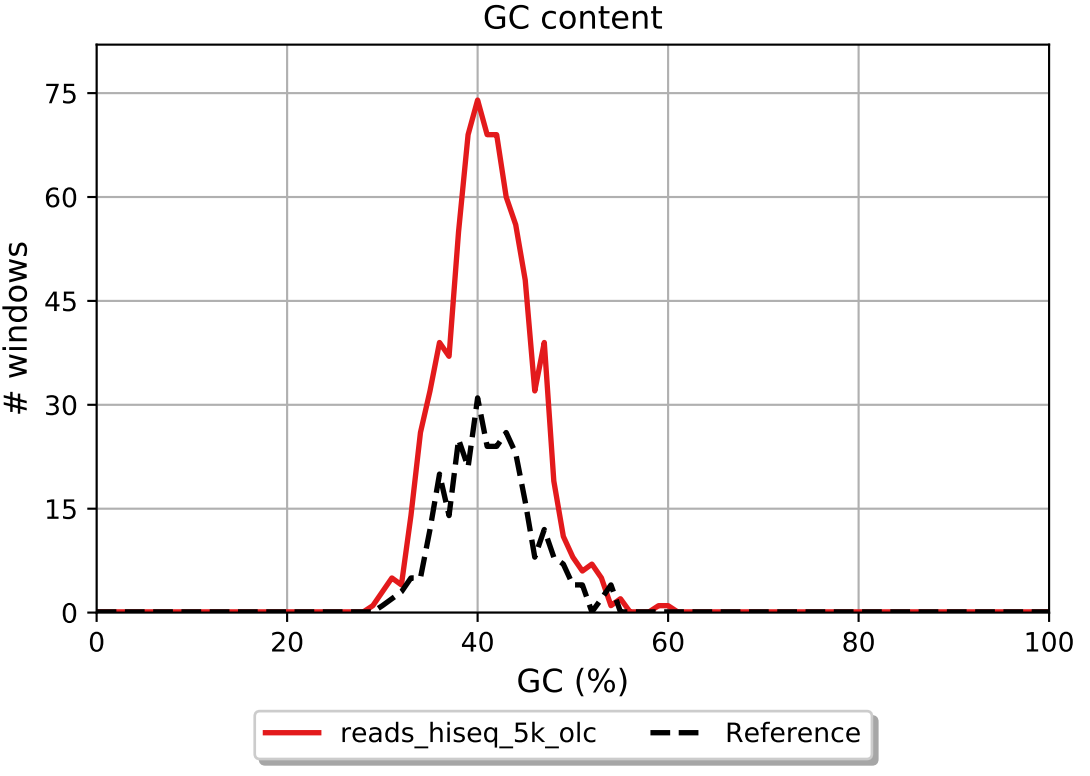
	reads_hiseq_5k_olc
# fully unaligned contigs	48
Fully unaligned length	18572
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

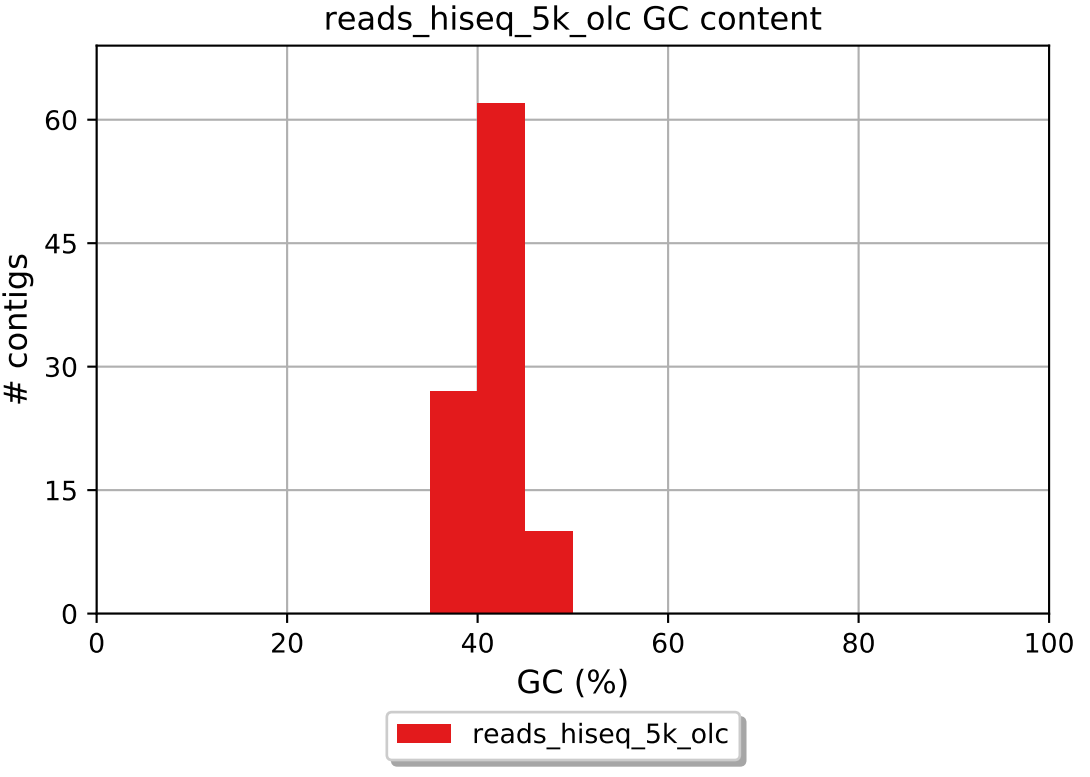
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

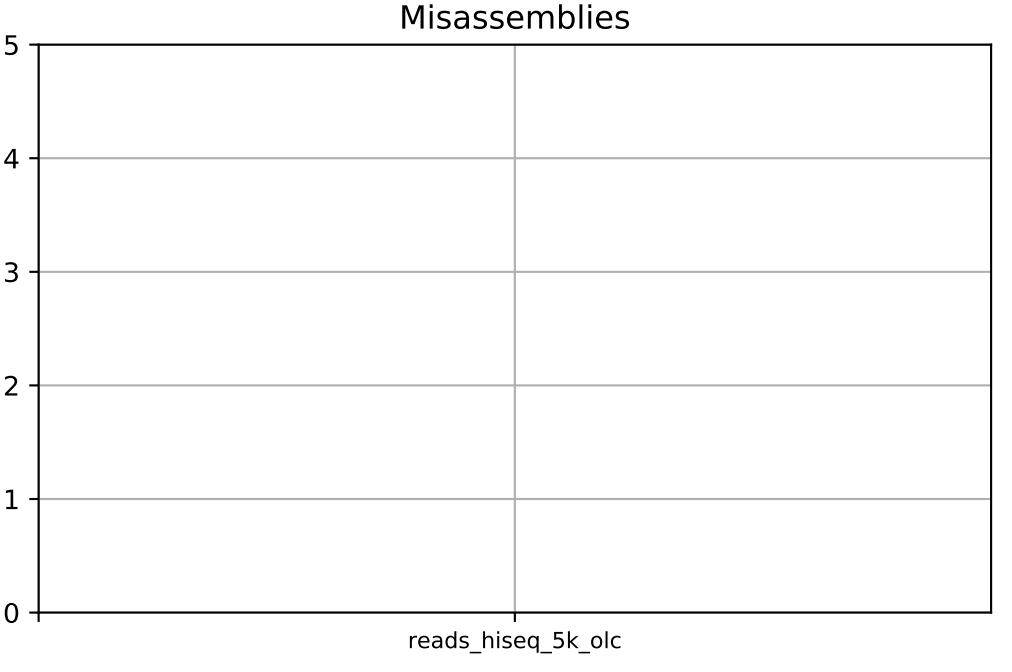

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
reads_hiseq_5k_olc

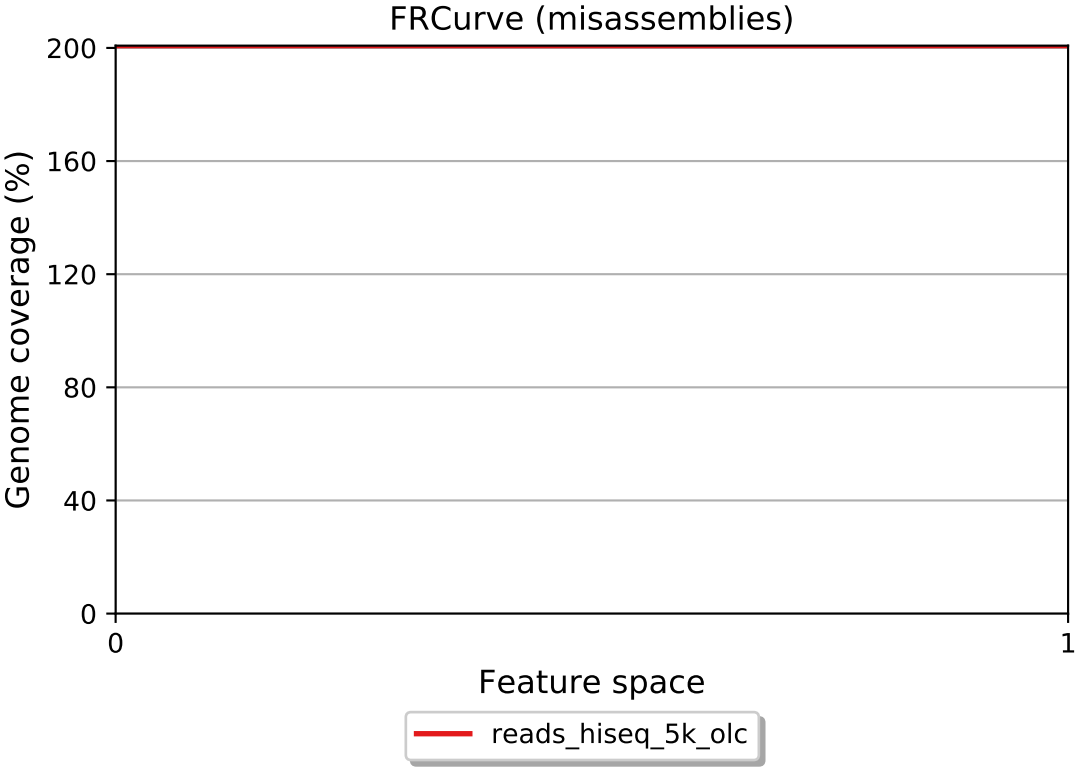

NGx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
reads_hiseq_5k_olc

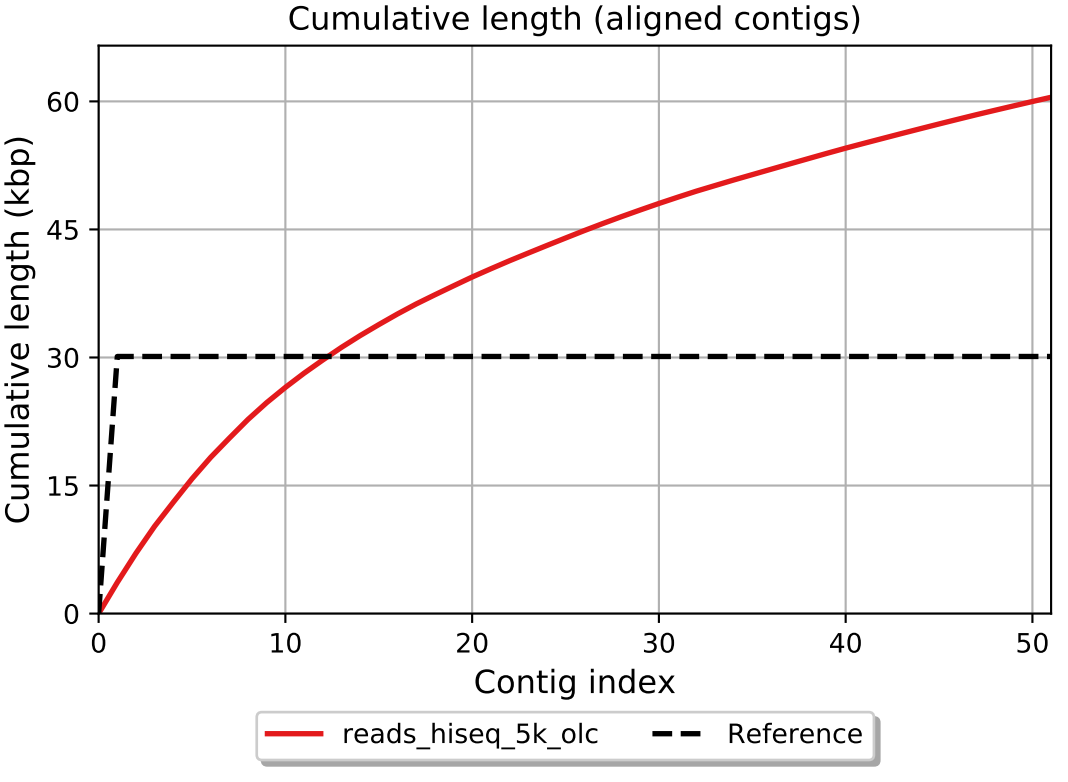

Cumulative length
Cumulative length (kbp)
0
15
30
45
60
75
0
20
40
60
80
Contig index
reads_hiseq_5k_olc
Reference

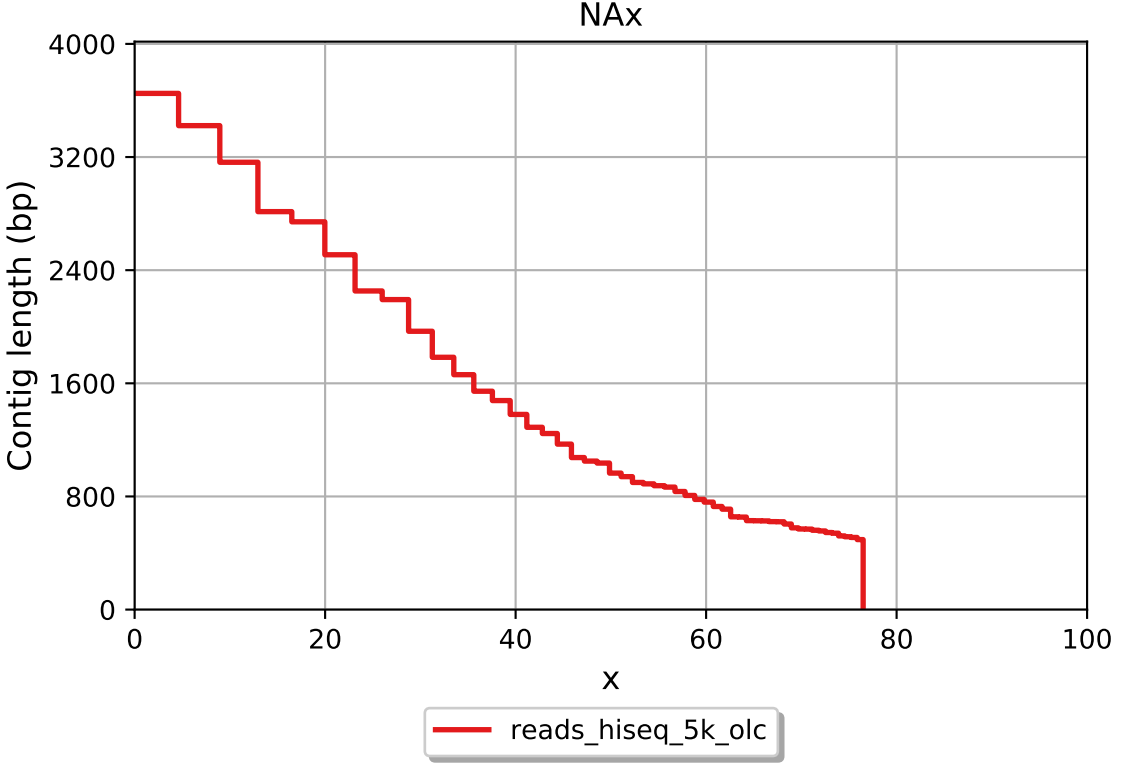

GC content
windows
GC (%)
0
15
30
45
60
75
0
20
40
60
80
100
reads_hiseq_5k_olc
Reference

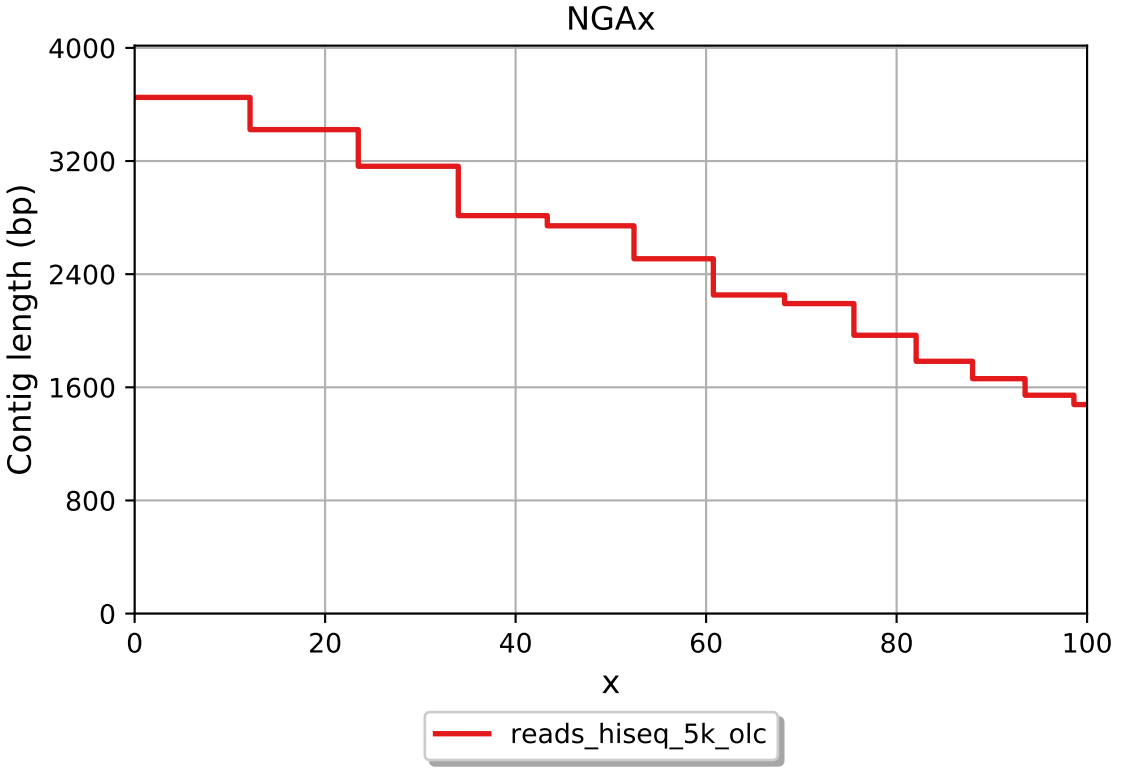

reads_hiseq_5k_olc GC content
contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
reads_hiseq_5k_olc


Misassemblies
5
4
3
2
1
0
reads_hiseq_5k_olc


FRCurve (misassemblies)
200
160
120
80
40
0
Genome coverage (%)
0
1
Feature space
reads_hiseq_5k_olc


Cumulative length (aligned contigs)
Cumulative length (kbp)
60
45
30
15
0
0
10
20
30
40
50
Contig index
reads_hiseq_5k_olc
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
reads_hiseq_5k_olc


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
reads_hiseq_5k_olc