Report

	lv4_k1500_kf3_tt1000
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	230733
Total length (>= 1000 bp)	230733
Total length (>= 5000 bp)	230733
Total length (>= 10000 bp)	230733
Total length (>= 25000 bp)	230733
Total length (>= 50000 bp)	0
# contigs	8
Largest contig	29360
Total length	230733
Reference length	29903
GC (%)	39.64
Reference GC (%)	37.97
N50	28799
NG50	29360
N90	28339
NG90	29360
auN	28845.0
auNG	222569.6
L50	4
LG50	1
L90	8
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	6 + 0 part
Unaligned length	173277
Genome fraction (%)	96.375
Duplication ratio	1.994
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1004.25
# indels per 100 kbp	0.00
Largest alignment	28789
Total aligned length	57456
NA50	-
NGA50	28789
NA90	-
NGA90	28789
auNA	7153.7
auNGA	55198.6
LA50	-
LGA50	1
LA90	-
LGA90	1

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

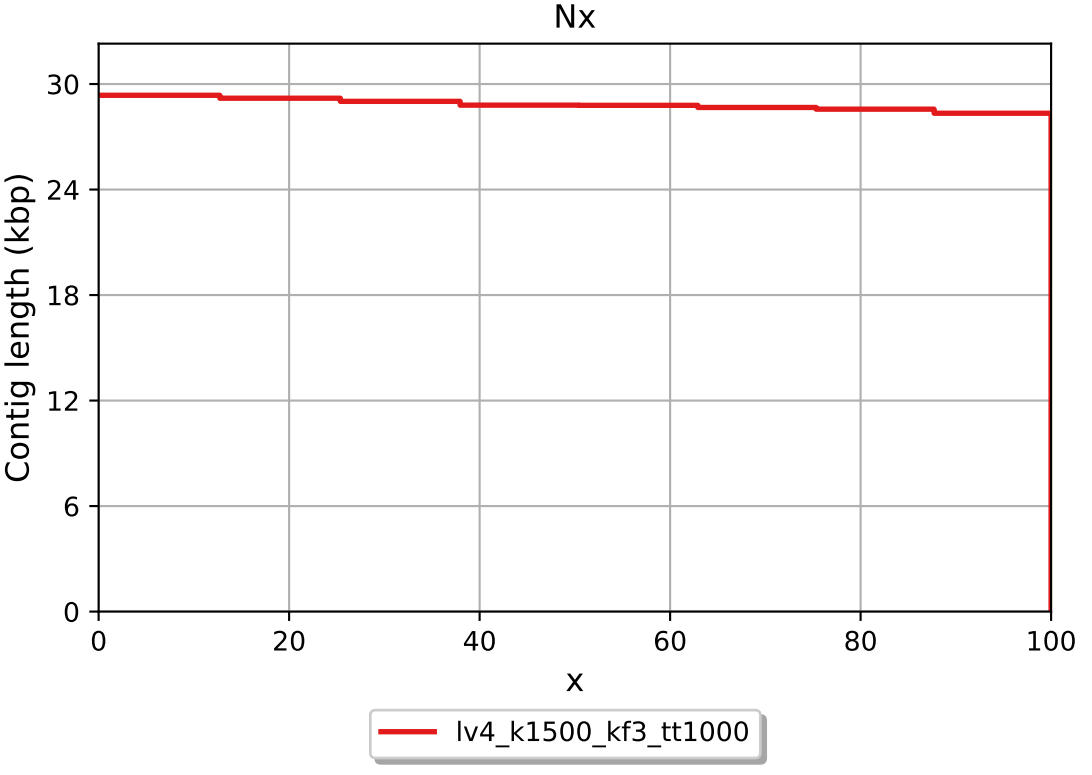
	lv4_k1500_kf3_tt1000
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	577
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

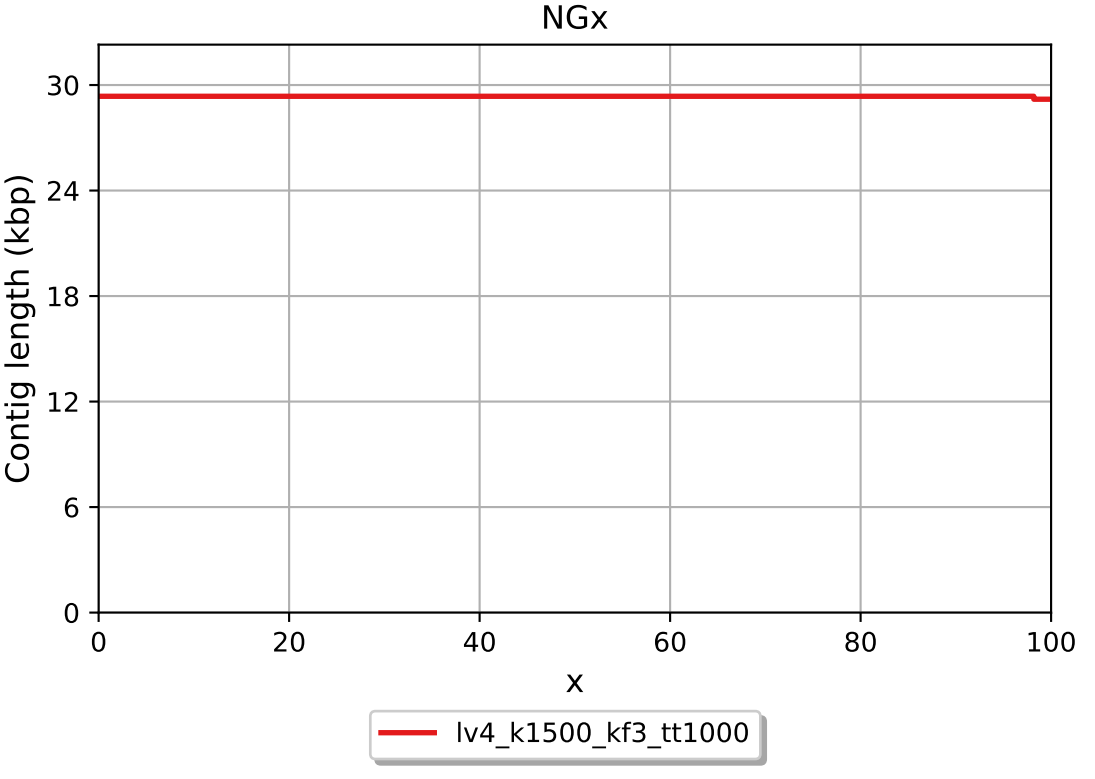
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

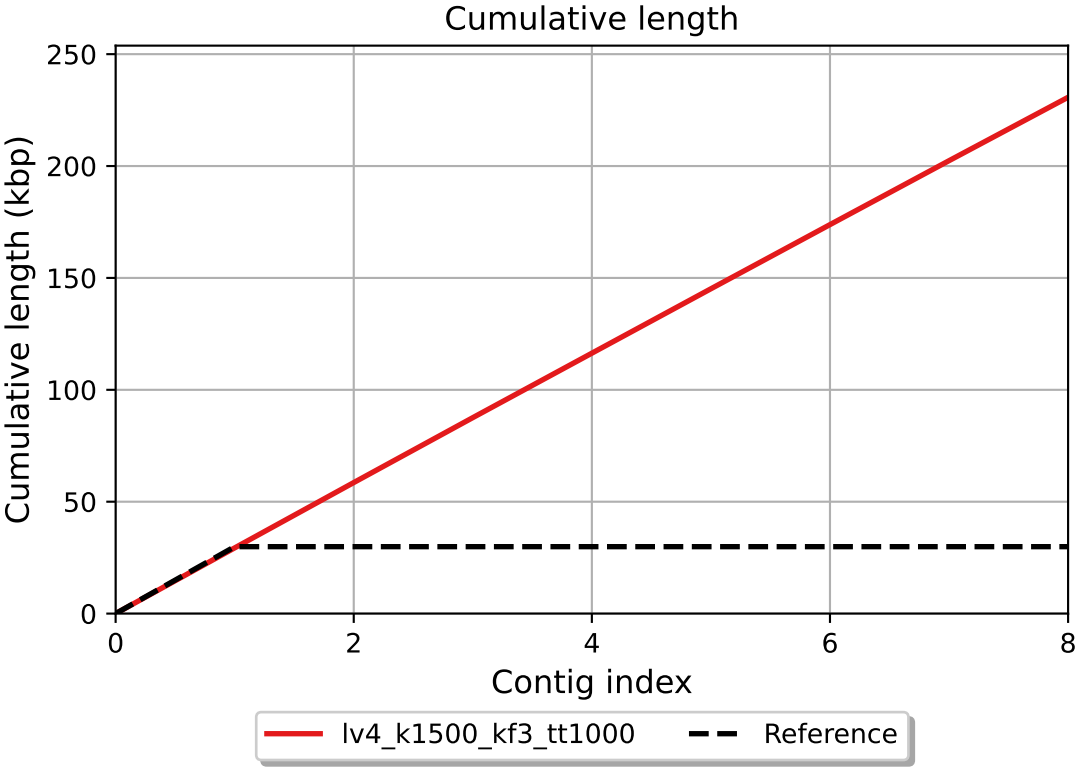
Unaligned report

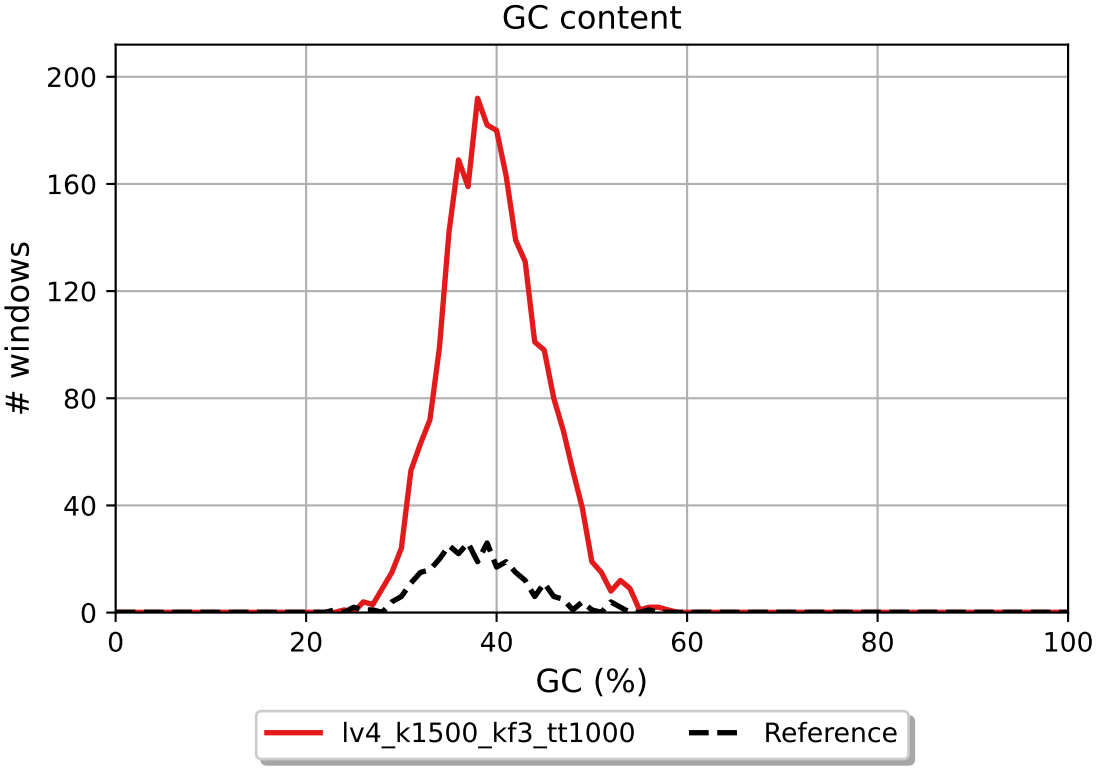
	lv4_k1500_kf3_tt1000
# fully unaligned contigs	6
Fully unaligned length	173277
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

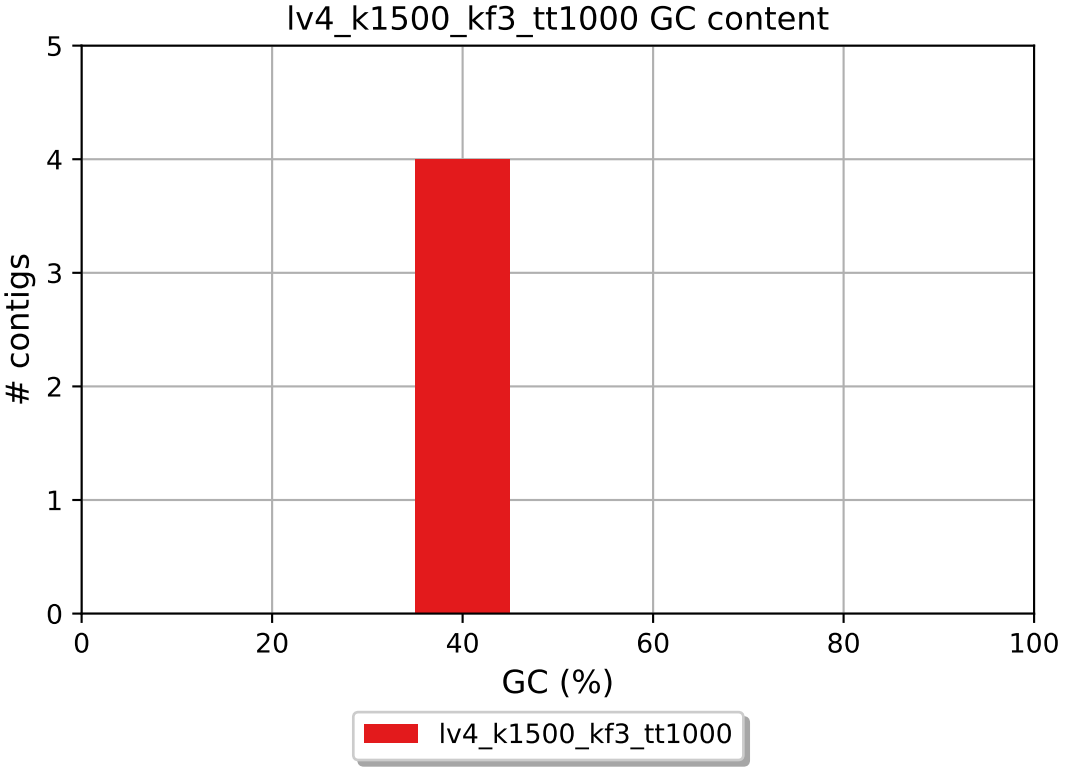
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

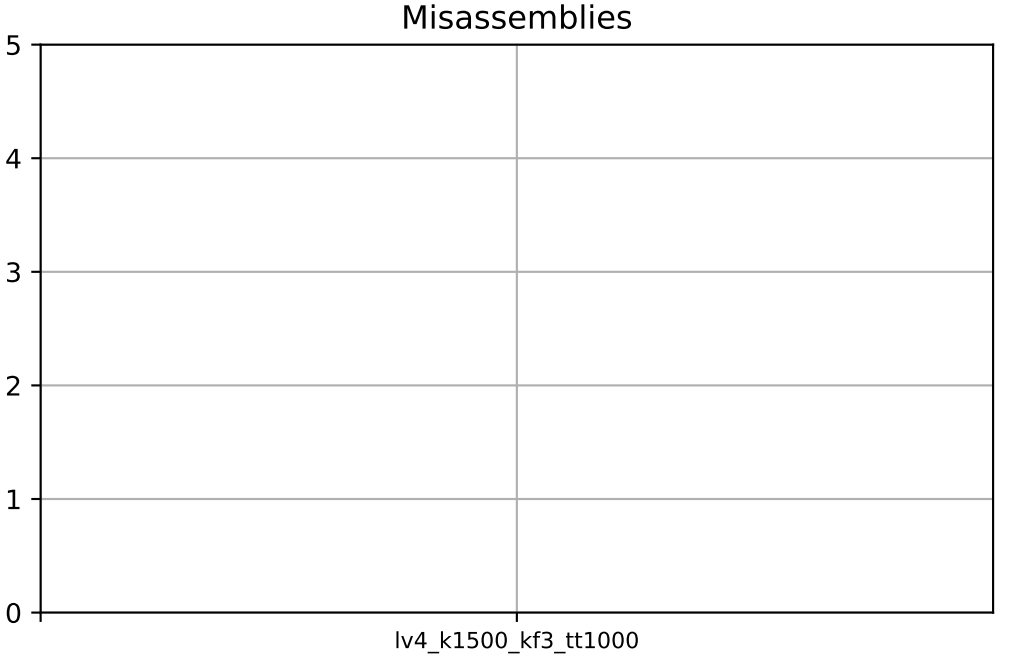

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv4_k1500_kf3_tt1000

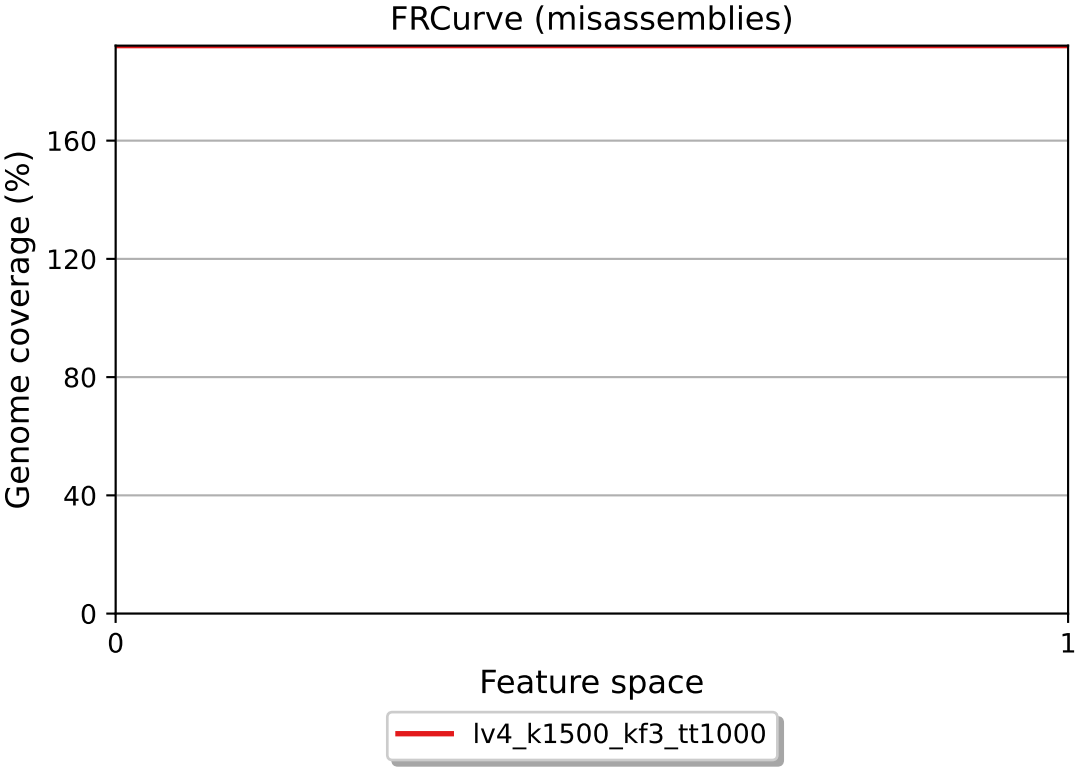

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv4_k1500_kf3_tt1000

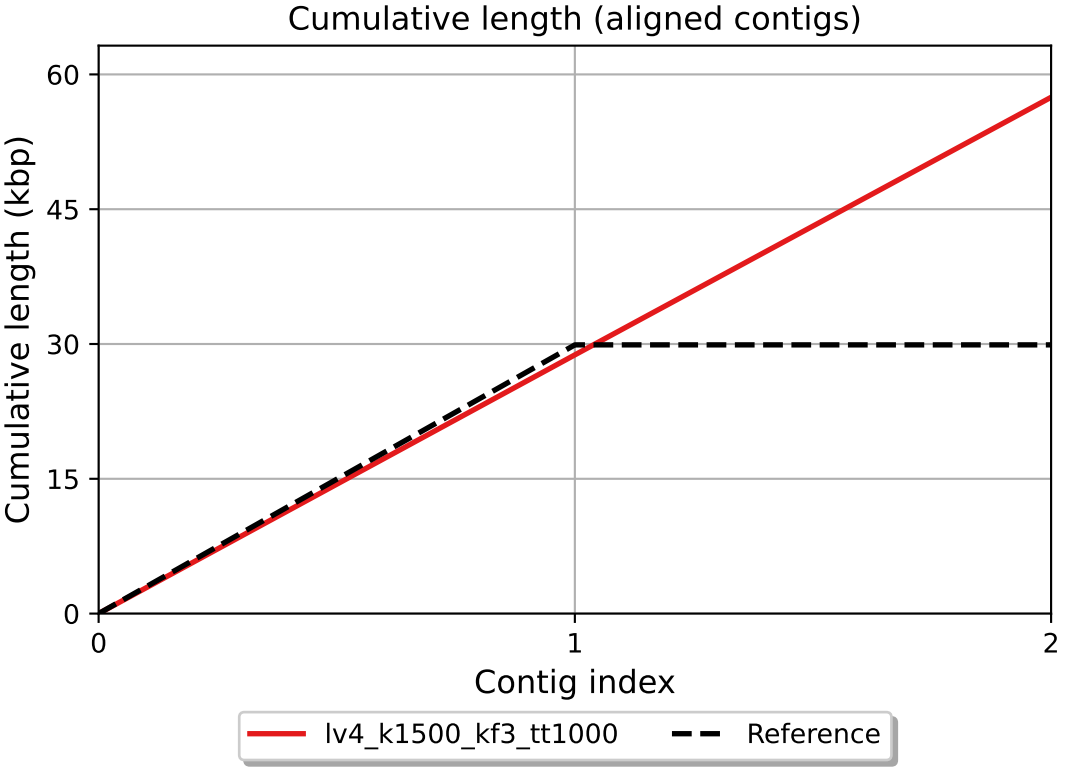

Cumulative length
Cumulative length (kbp)
250
200
150
100
50
0
0
2
4
6
8
Contig index
lv4_k1500_kf3_tt1000
Reference

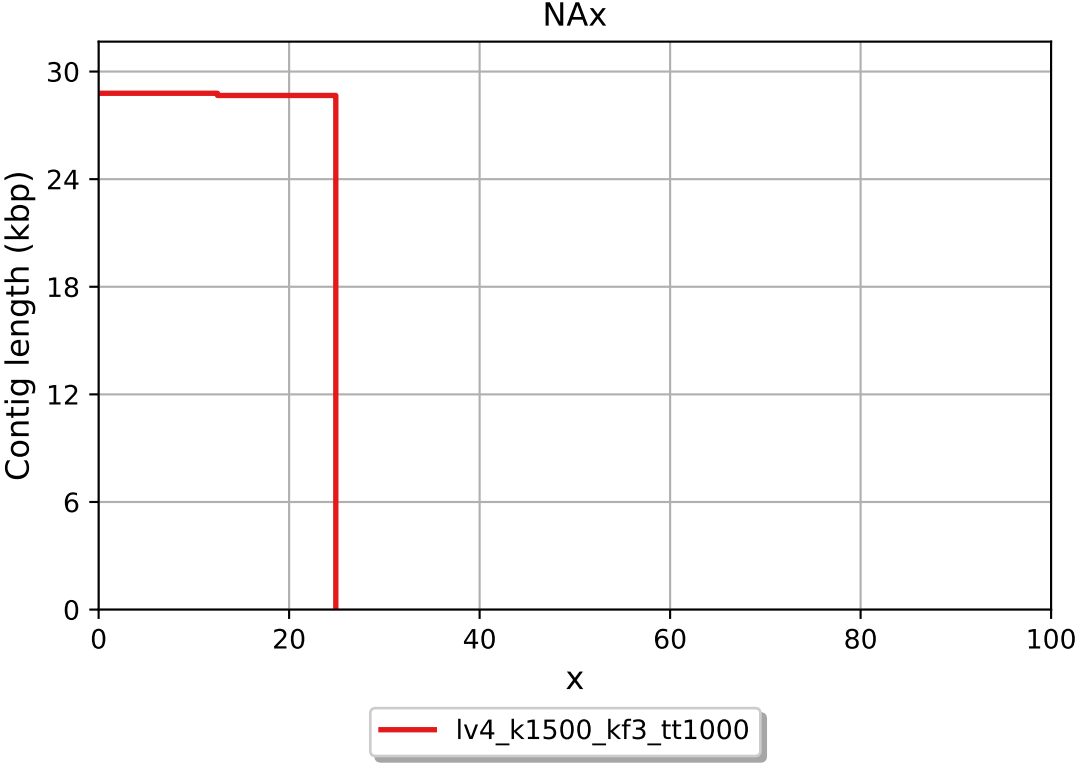

GC content
windows
GC (%)
0
20
40
60
80
100
0
40
80
120
160
200
lv4_k1500_kf3_tt1000
Reference

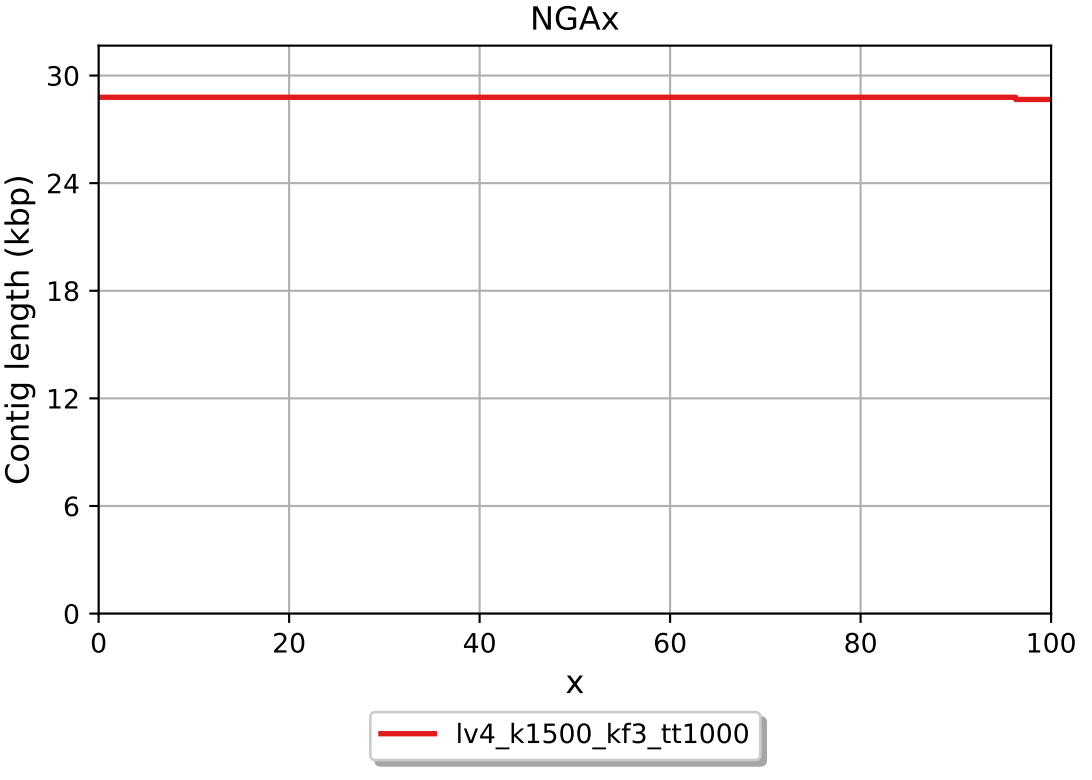

lv4_k1500_kf3_tt1000 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
lv4_k1500_kf3_tt1000


Misassemblies
5
4
3
2
1
0
lv4_k1500_kf3_tt1000


FRCurve (misassemblies)
Genome coverage (%)
160
120
80
40
0
0
1
Feature space
lv4_k1500_kf3_tt1000


Cumulative length (aligned contigs)
Cumulative length (kbp)
60
45
30
15
0
0
1
2
Contig index
lv4_k1500_kf3_tt1000
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv4_k1500_kf3_tt1000


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv4_k1500_kf3_tt1000