Report

	lv2_k300_kf2
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	58825
Total length (>= 1000 bp)	58825
Total length (>= 5000 bp)	58825
Total length (>= 10000 bp)	58825
Total length (>= 25000 bp)	58825
Total length (>= 50000 bp)	0
# contigs	2
Largest contig	29719
Total length	58825
Reference length	29903
GC (%)	39.16
Reference GC (%)	37.97
N50	29719
NG50	29719
N90	29106
NG90	29719
auN	29415.7
auNG	57866.4
L50	1
LG50	1
L90	2
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	1 + 0 part
Unaligned length	29106
Genome fraction (%)	99.385
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	29719
Total aligned length	29719
NA50	29719
NGA50	29719
NA90	-
NGA90	29719
auNA	15014.3
auNGA	29536.1
LA50	1
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

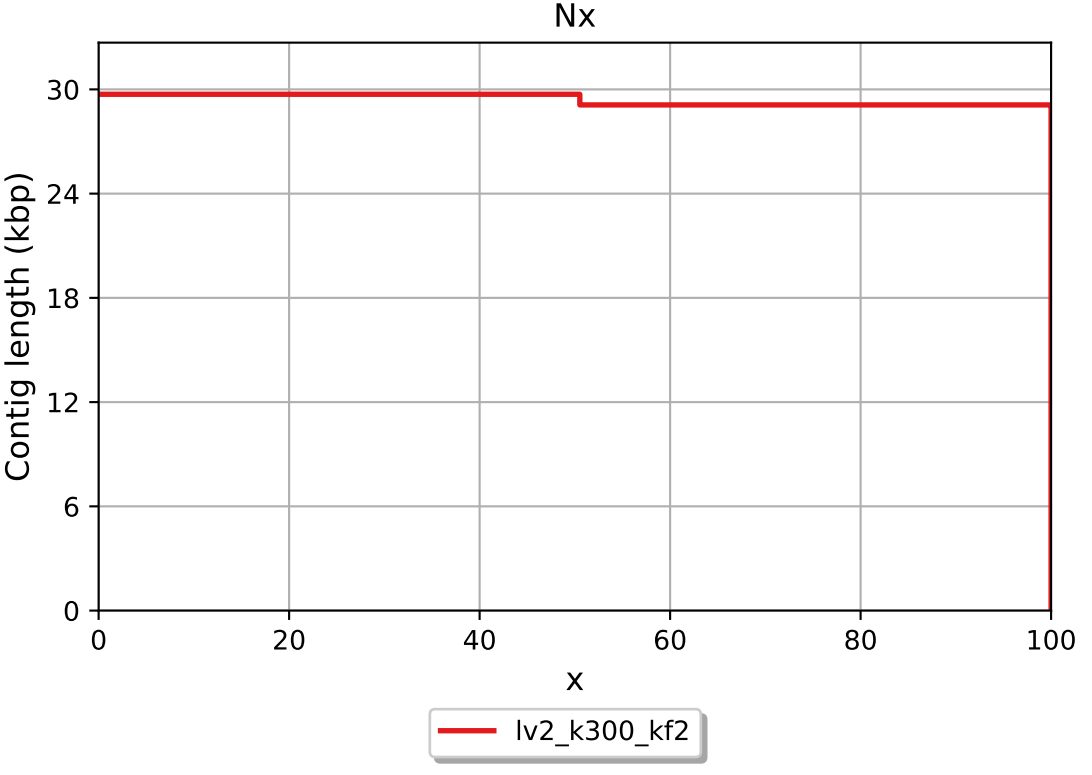
	lv2_k300_kf2
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	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

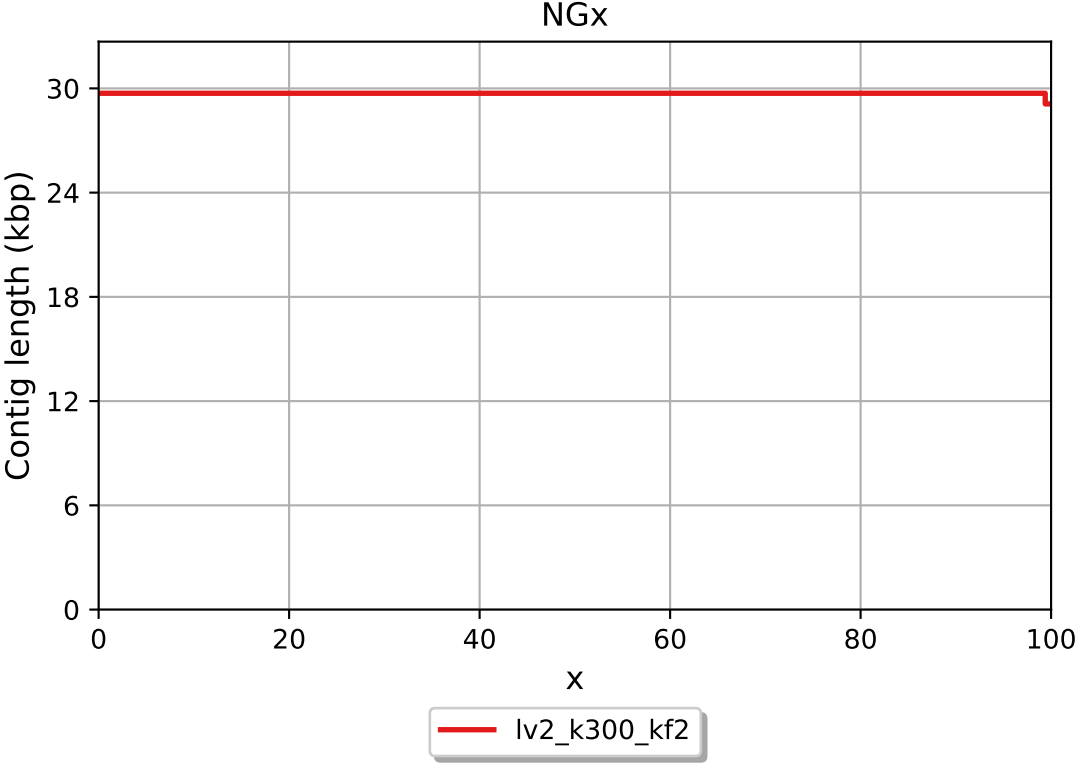
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

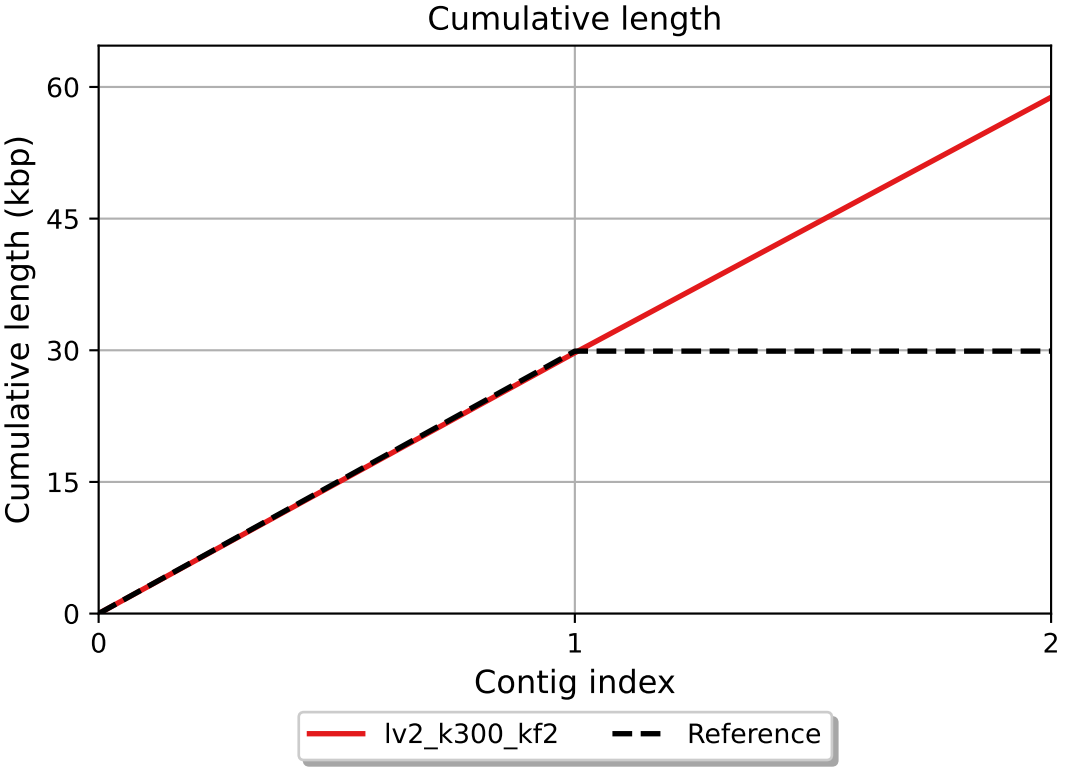
Unaligned report

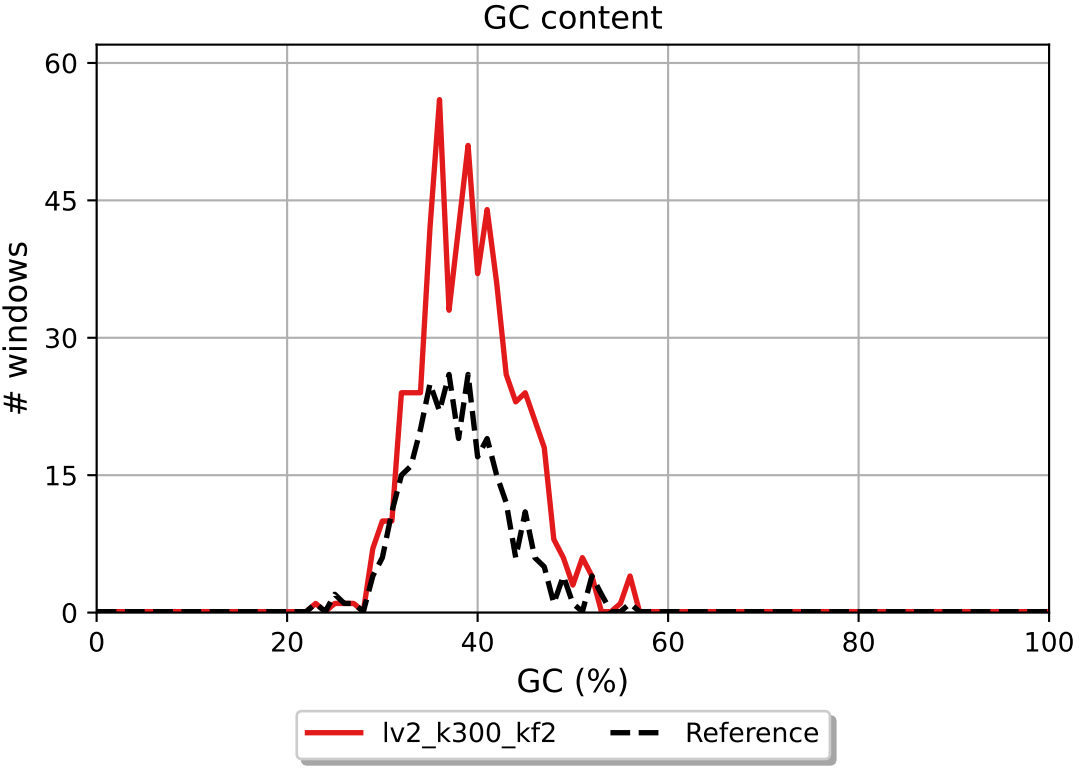
	lv2_k300_kf2
# fully unaligned contigs	1
Fully unaligned length	29106
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

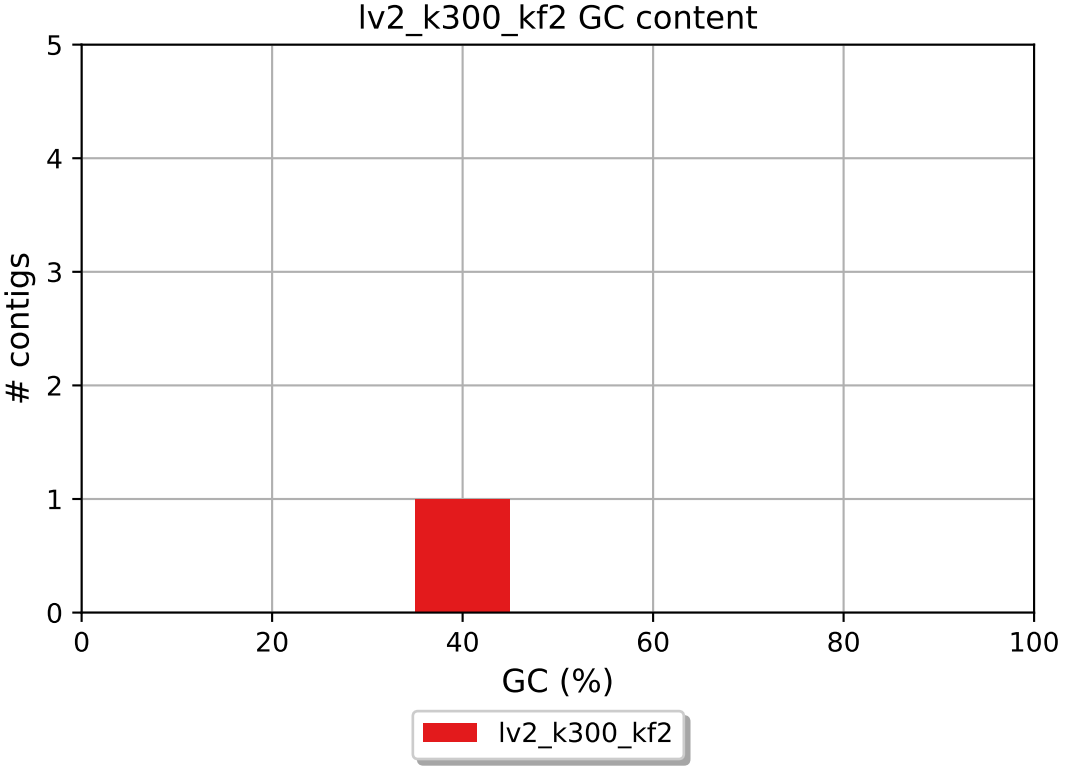
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

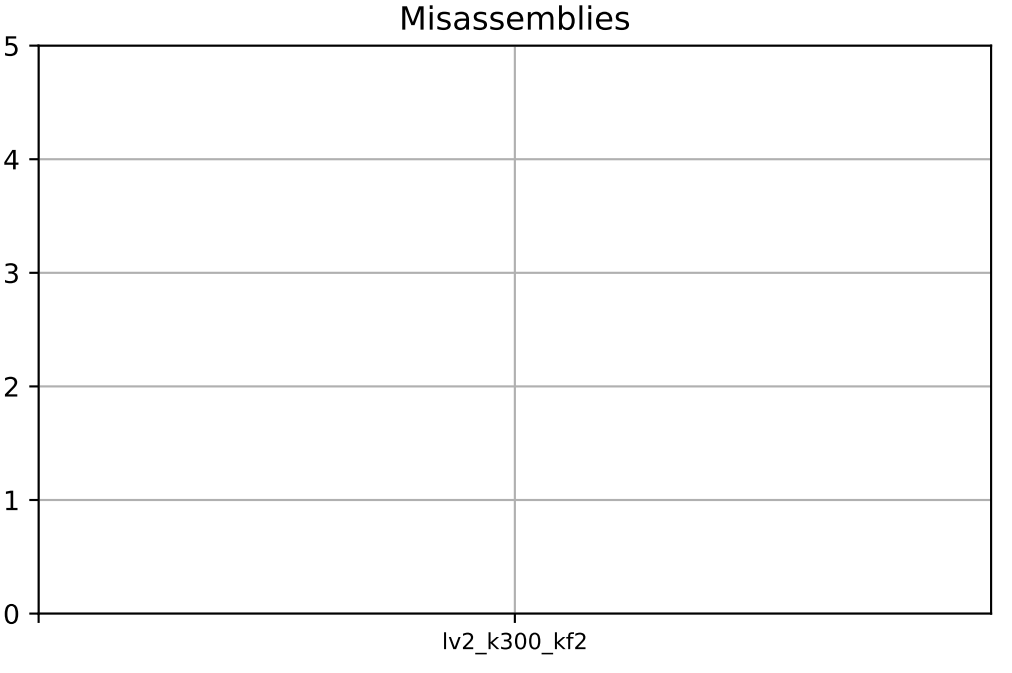

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv2_k300_kf2

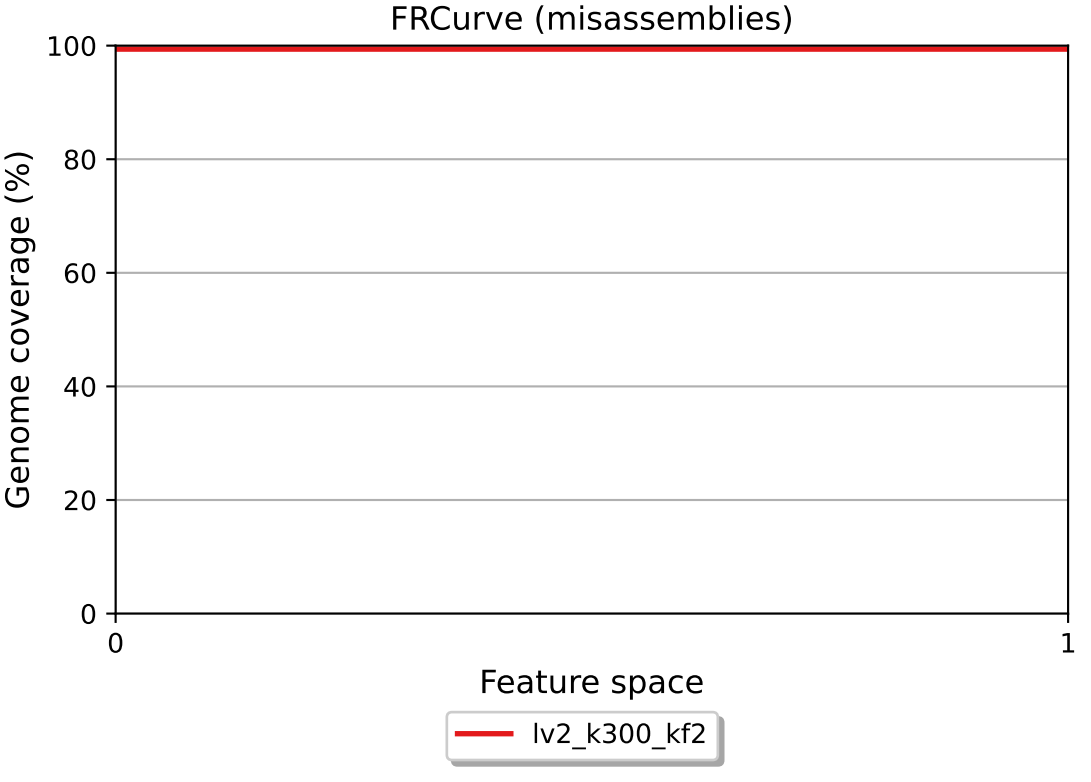

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv2_k300_kf2

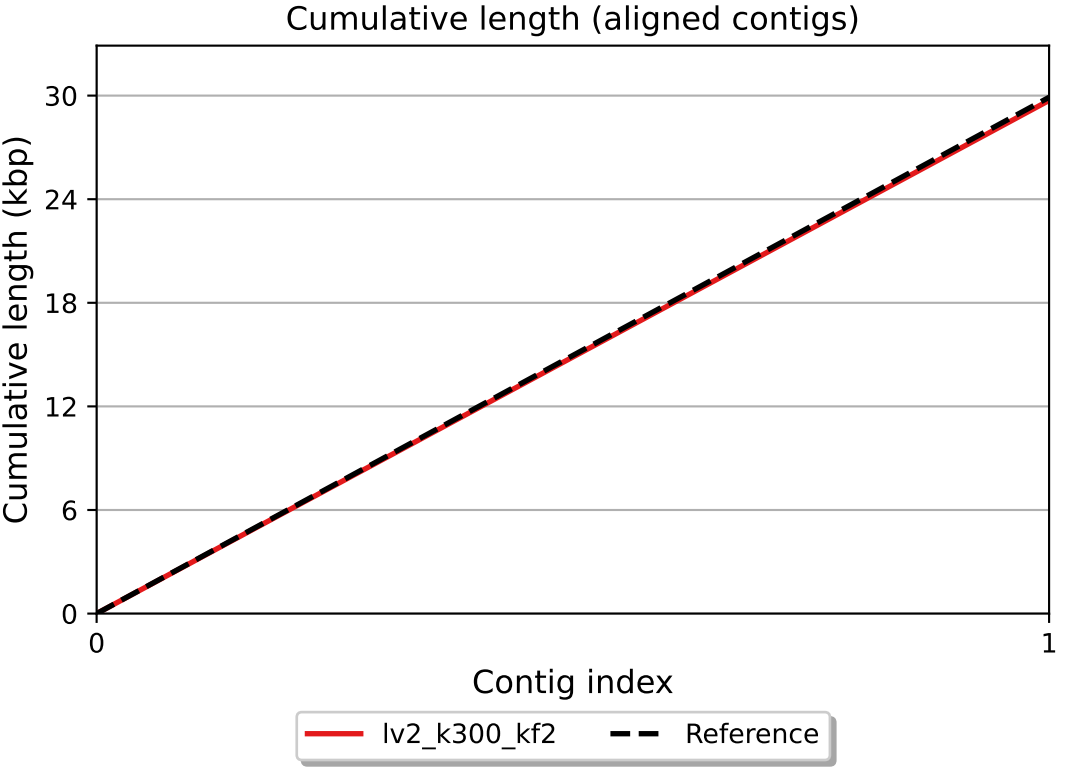

Cumulative length
Cumulative length (kbp)
60
45
30
15
0
0
1
2
Contig index
lv2_k300_kf2
Reference

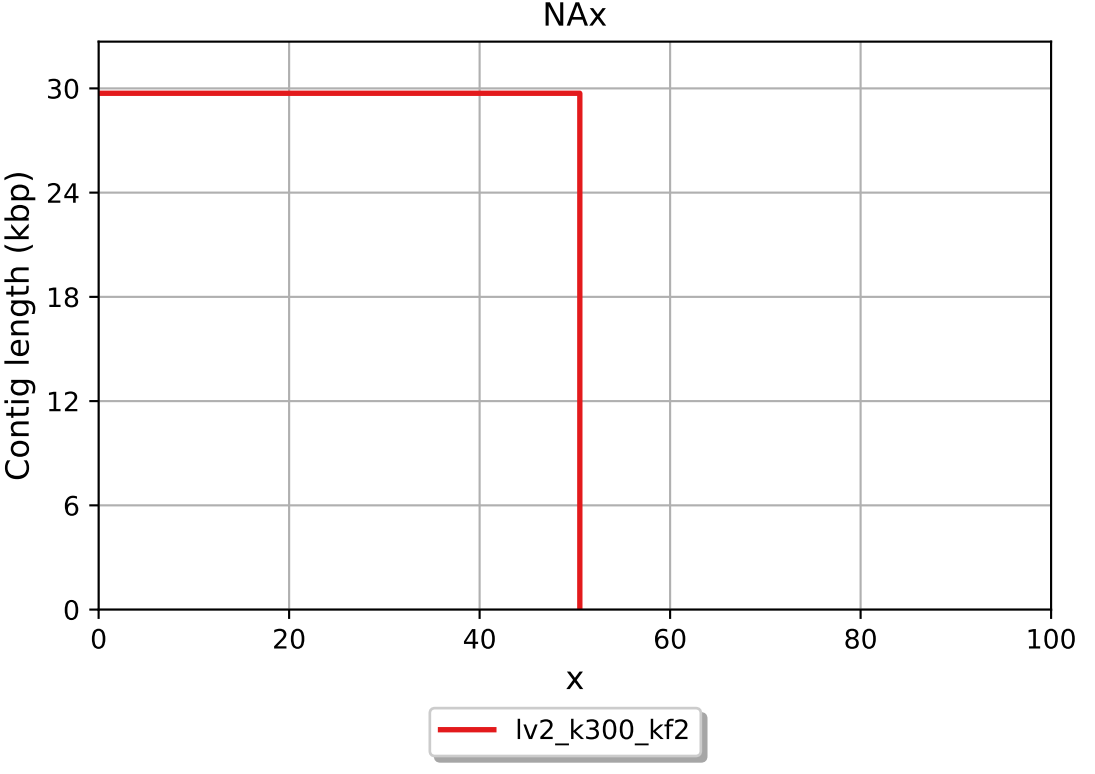

GC content
windows
GC (%)
0
15
30
45
60
0
20
40
60
80
100
lv2_k300_kf2
Reference

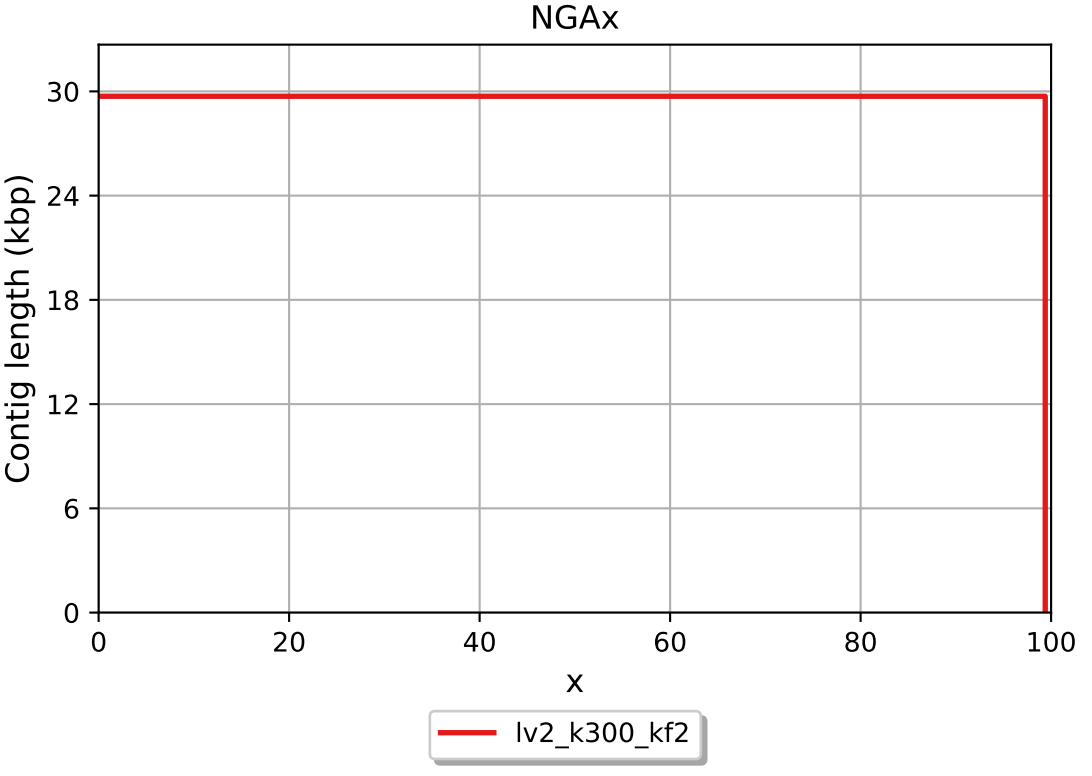

lv2_k300_kf2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
lv2_k300_kf2


Misassemblies
5
4
3
2
1
0
lv2_k300_kf2


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
lv2_k300_kf2


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
lv2_k300_kf2
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv2_k300_kf2


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
lv2_k300_kf2