Report

	sortie_sequencage1
# contigs (>= 0 bp)	586
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	62259
Total length (>= 1000 bp)	45261
Total length (>= 5000 bp)	45261
Total length (>= 10000 bp)	45261
Total length (>= 25000 bp)	45261
Total length (>= 50000 bp)	0
# contigs	586
Largest contig	45261
Total length	62259
Reference length	48576
GC (%)	50.53
Reference GC (%)	49.87
N50	45261
NG50	45261
N75	39
NG75	45261
L50	1
LG50	1
L75	38
LG75	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	1
# unaligned contigs	585 + 1 part
Unaligned length	41105
Genome fraction (%)	43.505
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	331.24
# indels per 100 kbp	0.00
Largest alignment	429
Total aligned length	21154
NGA50	-

All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

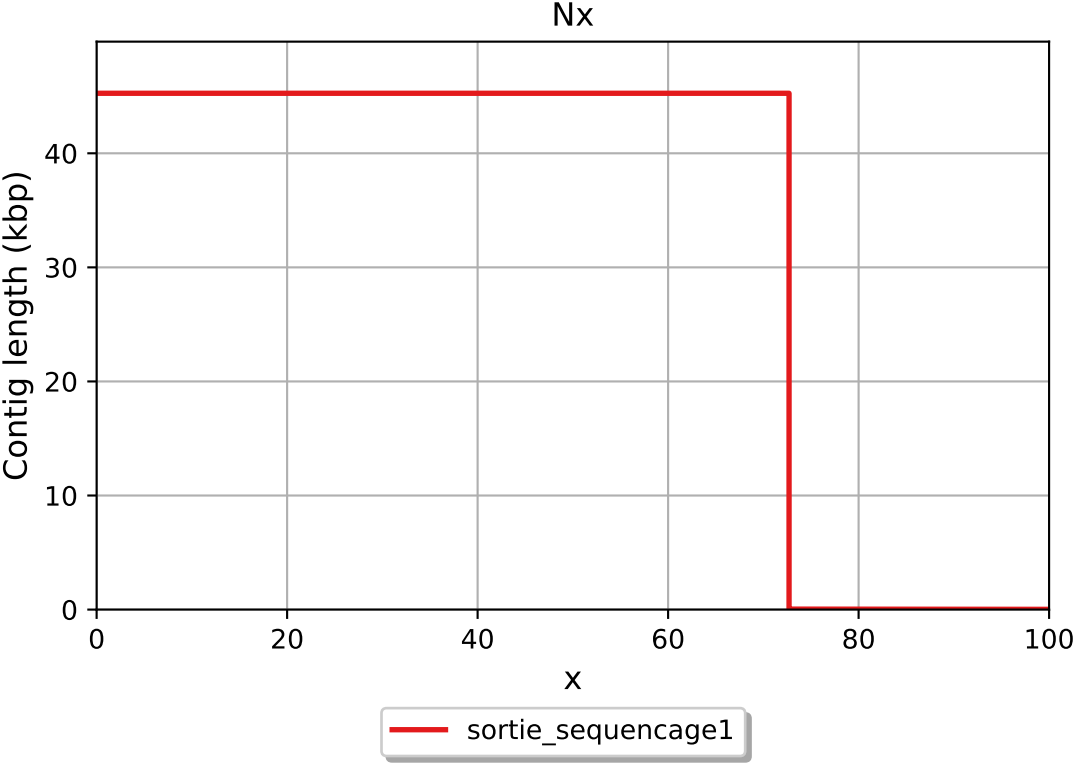
	sortie_sequencage1
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	70
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

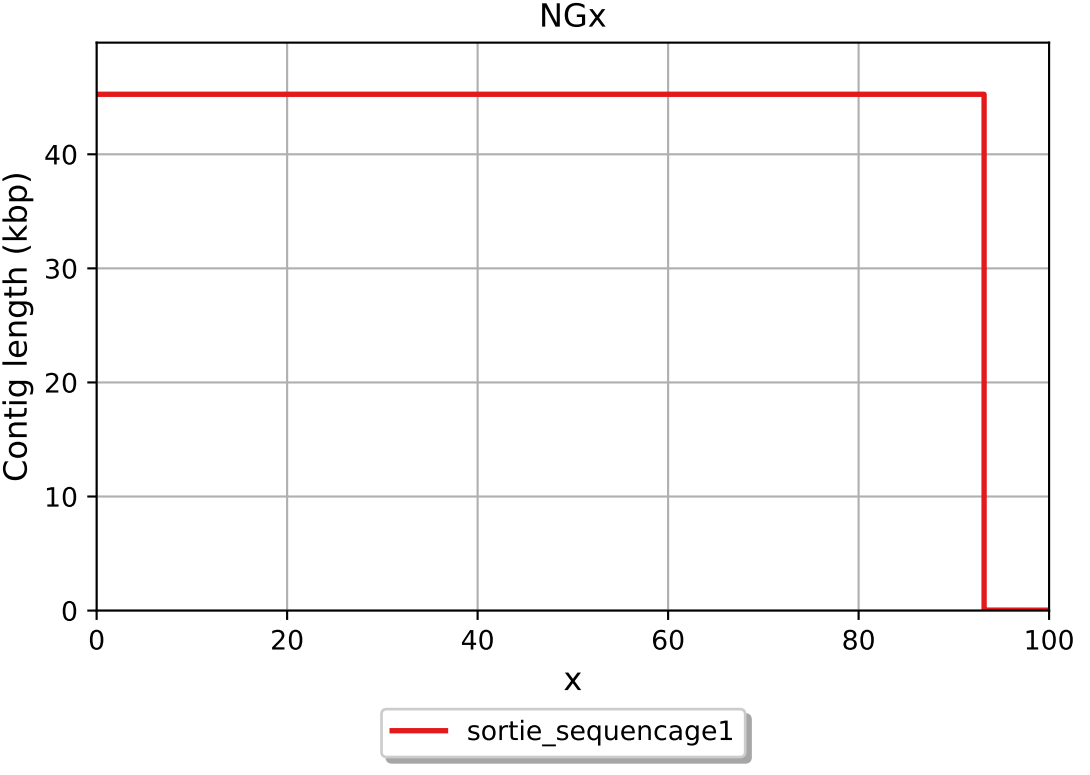
All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

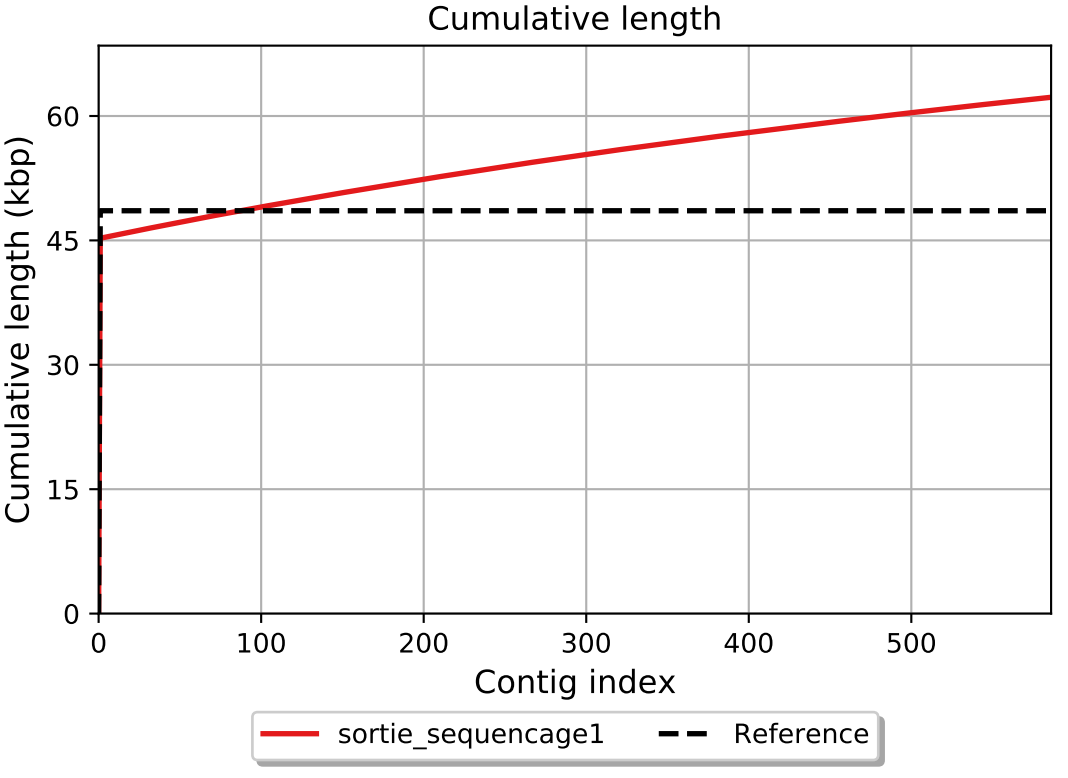
Unaligned report

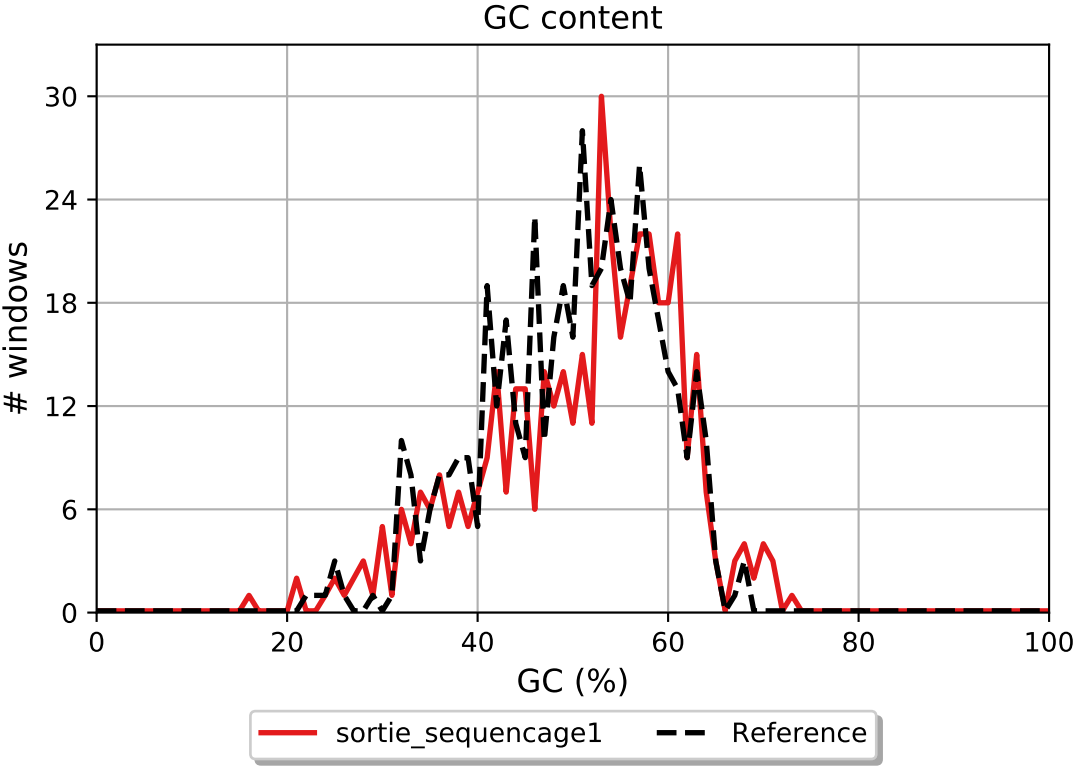
	sortie_sequencage1
# fully unaligned contigs	585
Fully unaligned length	16998
# partially unaligned contigs	1
Partially unaligned length	24107
# N's	0

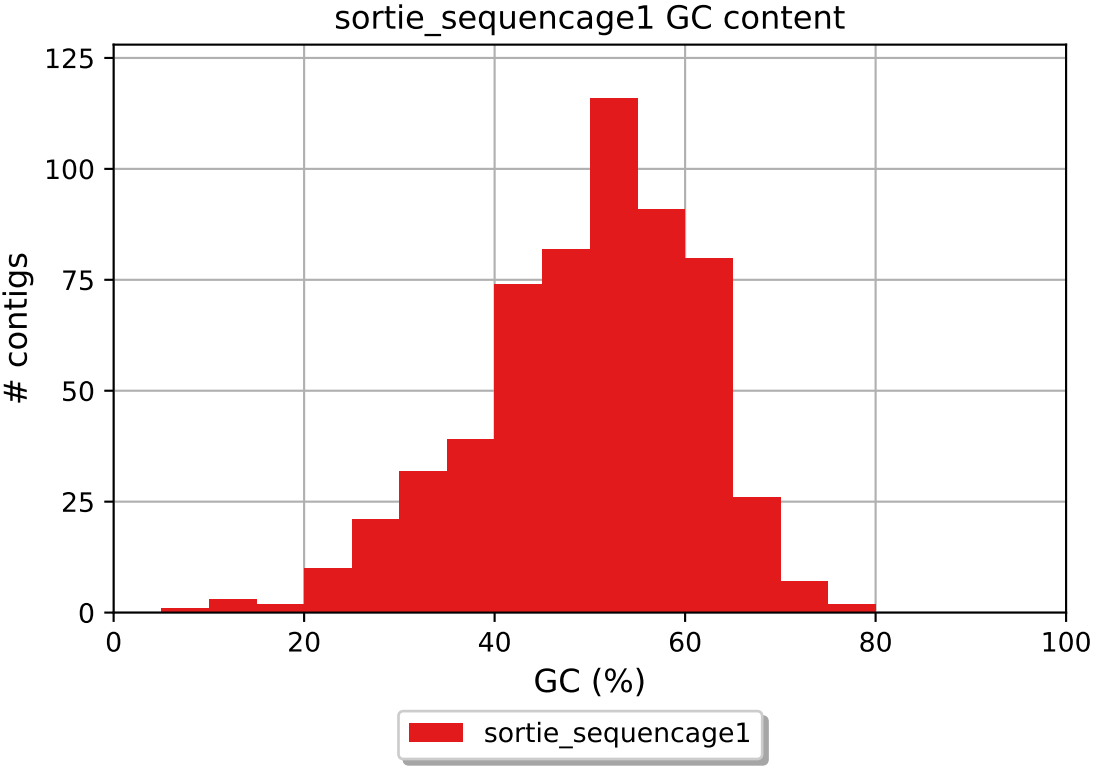
All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

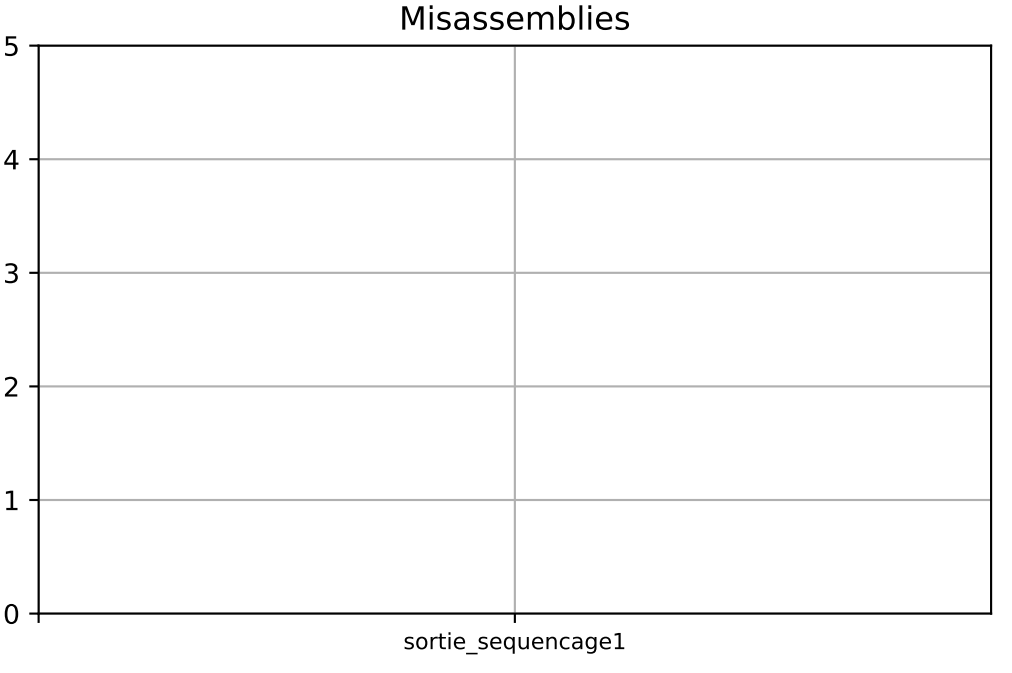

Nx
Contig length (kbp)
0
10
20
30
40
0
20
40
60
80
100
x
sortie_sequencage1

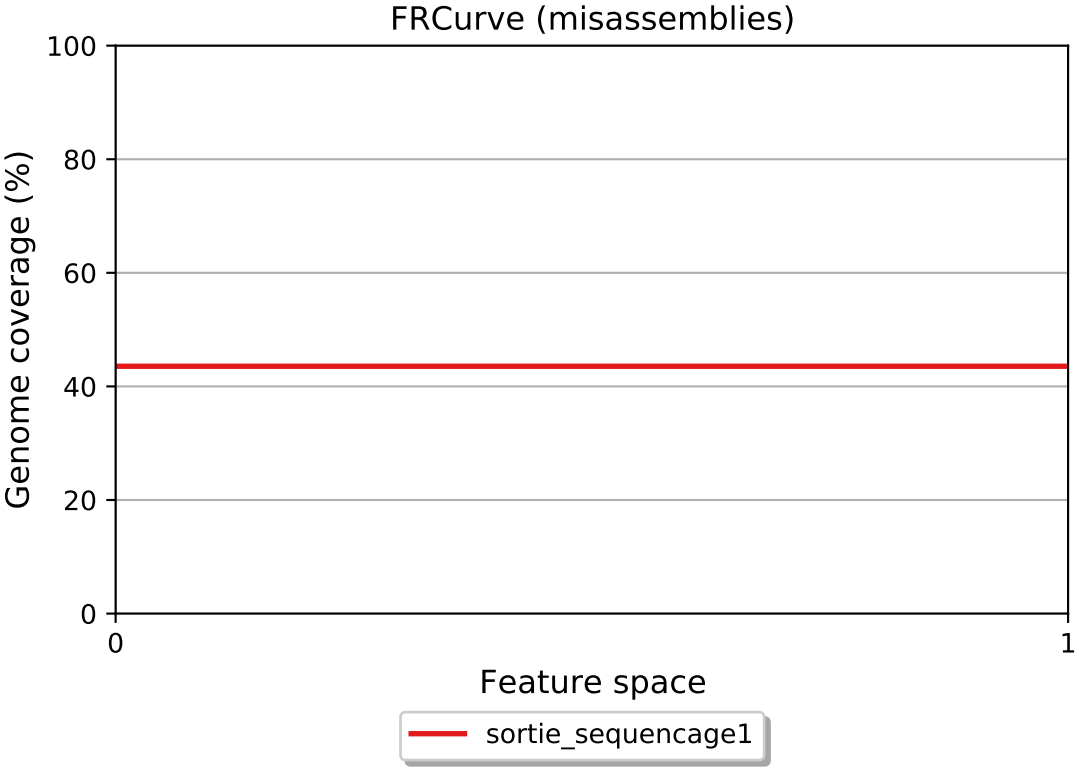

NGx
Contig length (kbp)
0
10
20
30
40
0
20
40
60
80
100
x
sortie_sequencage1

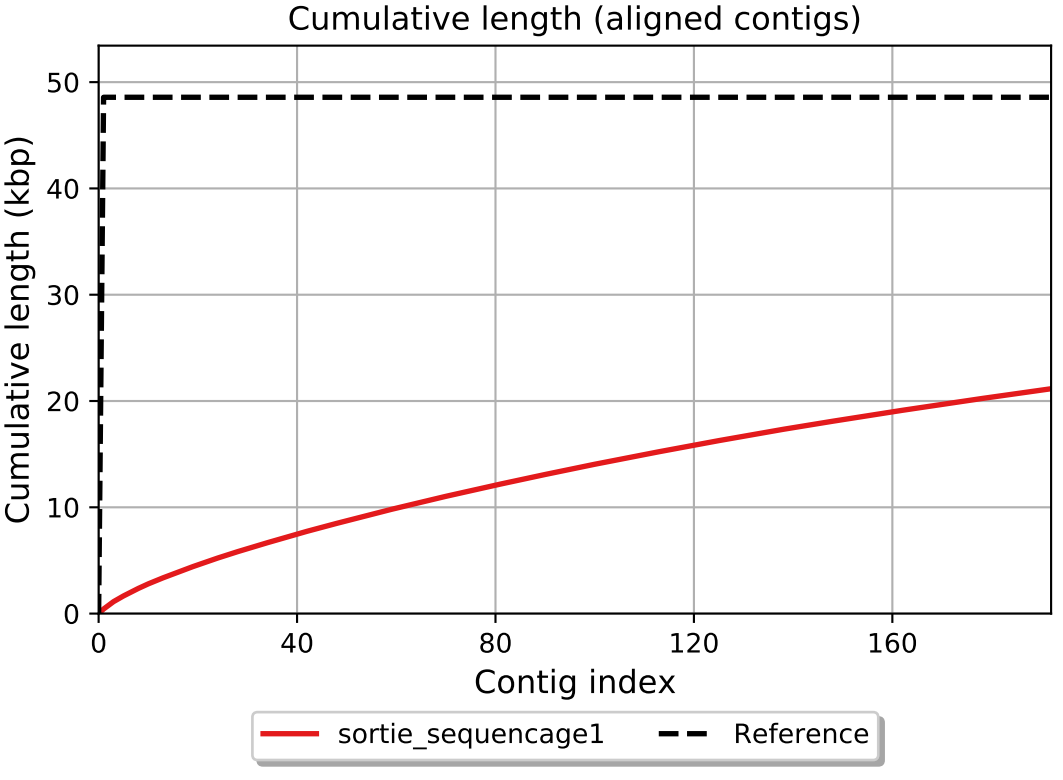

Cumulative length
Cumulative length (kbp)
0
15
30
45
60
0
100
200
300
400
500
Contig index
sortie_sequencage1
Reference

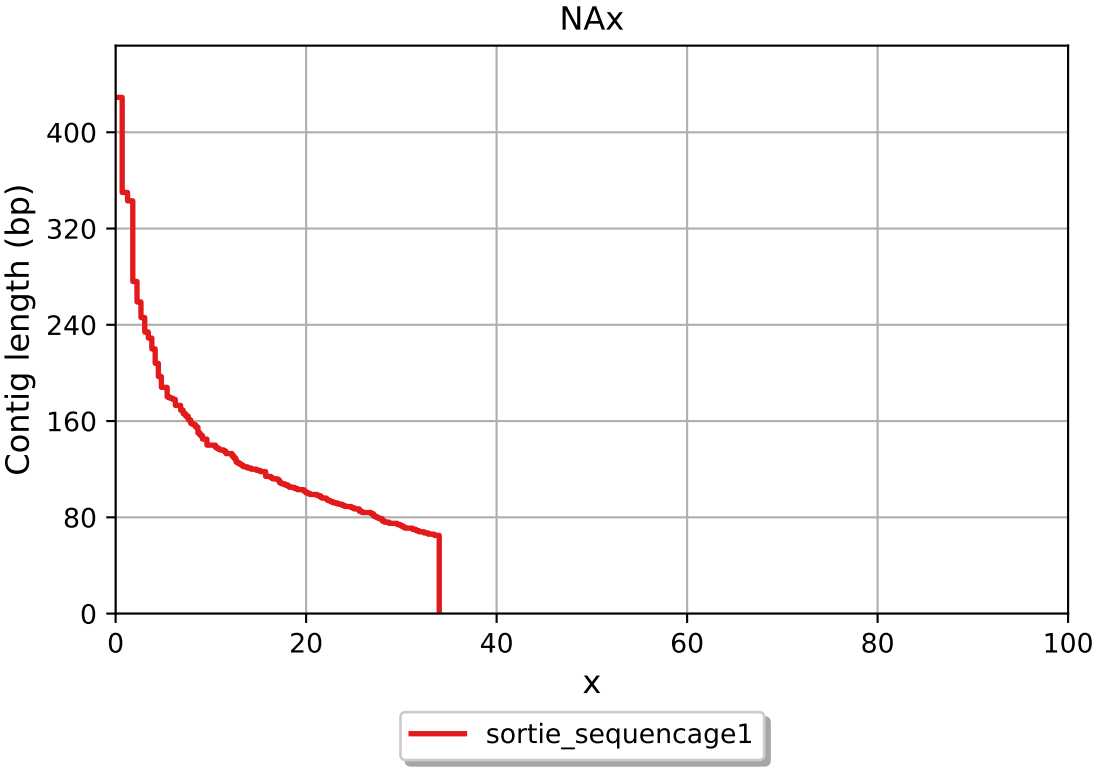

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
sortie_sequencage1
Reference

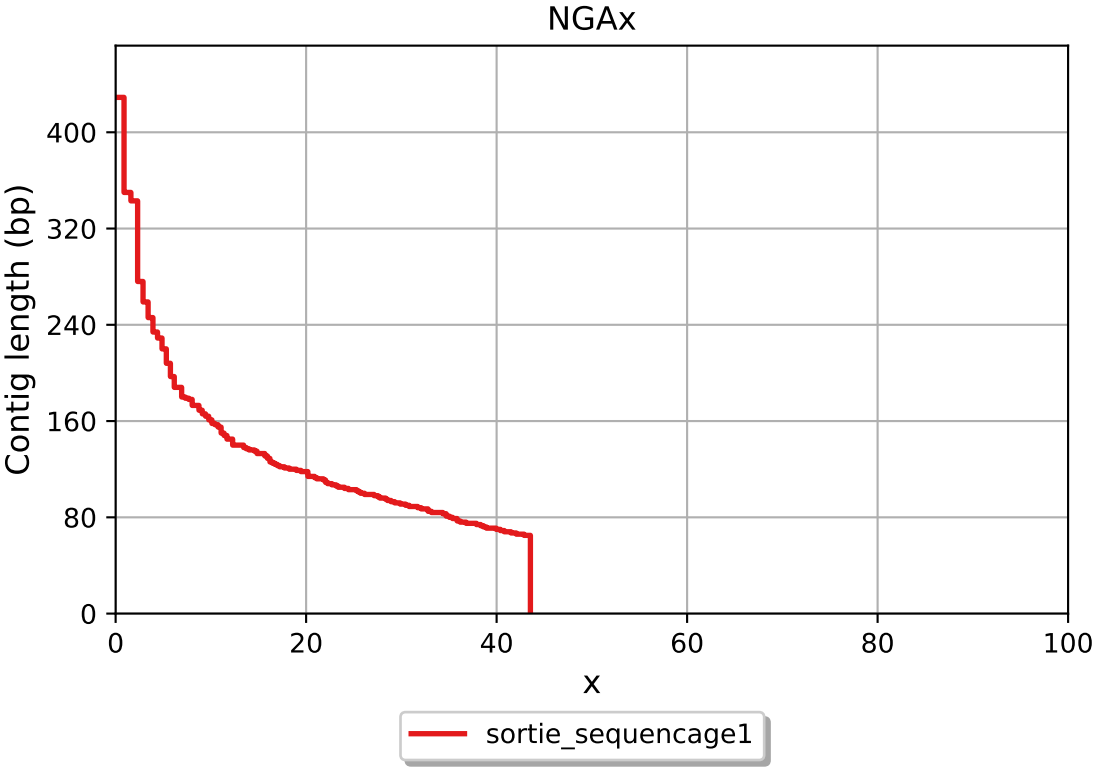

sortie_sequencage1 GC content
contigs
GC (%)
0
25
50
75
100
125
0
20
40
60
80
100
sortie_sequencage1


Misassemblies
5
4
3
2
1
0
sortie_sequencage1


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
sortie_sequencage1


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
10
20
30
40
50
0
40
80
120
160
Contig index
sortie_sequencage1
Reference


NAx
Contig length (bp)
400
320
240
160
80
0
0
20
40
60
80
100
x
sortie_sequencage1


NGAx
Contig length (bp)
400
320
240
160
80
0
0
20
40
60
80
100
x
sortie_sequencage1