Report

	B8_RB11_racon3
# contigs (>= 0 bp)	24
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	24
# contigs (>= 10000 bp)	23
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	21
Total length (>= 0 bp)	15184803
Total length (>= 1000 bp)	15184803
Total length (>= 5000 bp)	15184803
Total length (>= 10000 bp)	15175098
Total length (>= 25000 bp)	15150983
Total length (>= 50000 bp)	15150983
# contigs	24
Largest contig	1349481
Total length	15184803
Reference length	15074320
GC (%)	48.03
Reference GC (%)	48.02
N50	989449
NG50	989449
N75	718653
NG75	718653
L50	7
LG50	7
L75	12
LG75	12
# misassemblies	144
# misassembled contigs	19
Misassembled contigs length	14892783
# local misassemblies	159
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 21 part
Unaligned length	519580
Genome fraction (%)	97.144
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	423.59
# indels per 100 kbp	186.21
Largest alignment	951516
Total aligned length	14660834
NA50	239738
NGA50	240170
NA75	135509
NGA75	143691
LA50	19
LGA50	18
LA75	40
LGA75	39

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

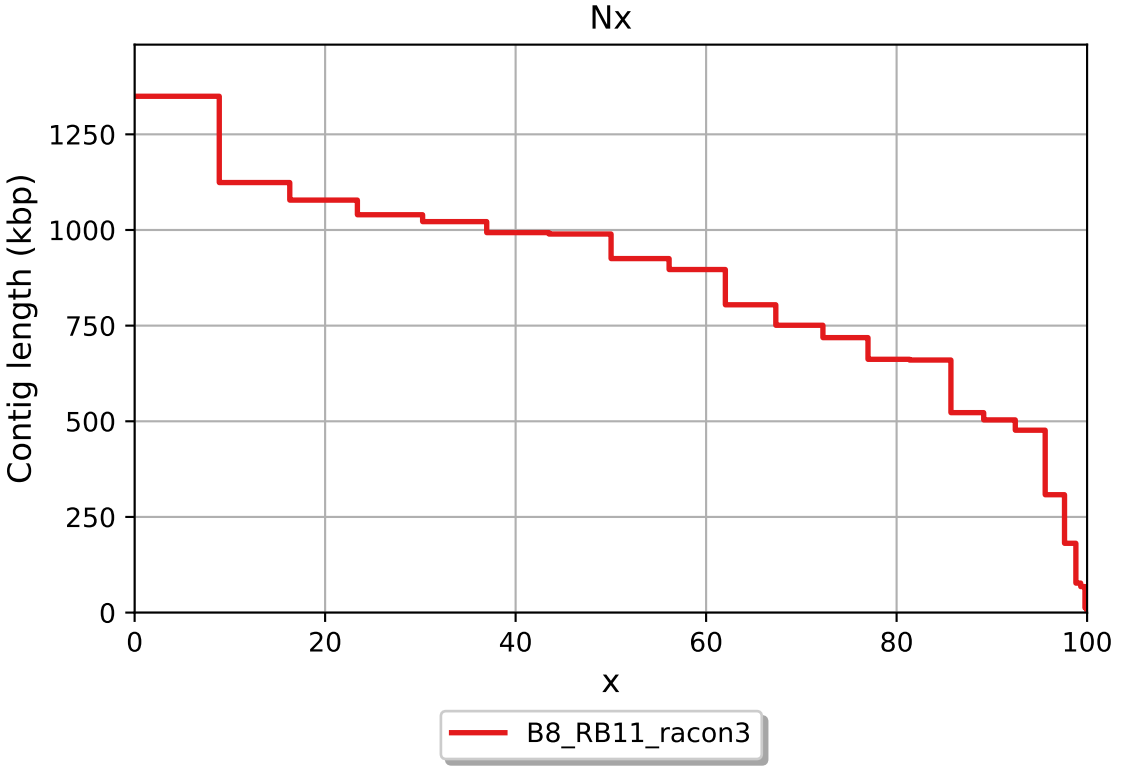
	B8_RB11_racon3
# misassemblies	144
# contig misassemblies	144
# c. relocations	81
# c. translocations	49
# c. inversions	14
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	19
Misassembled contigs length	14892783
# local misassemblies	159
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	61881
# indels	27202
# indels (<= 5 bp)	24576
# indels (> 5 bp)	2626
Indels length	78832

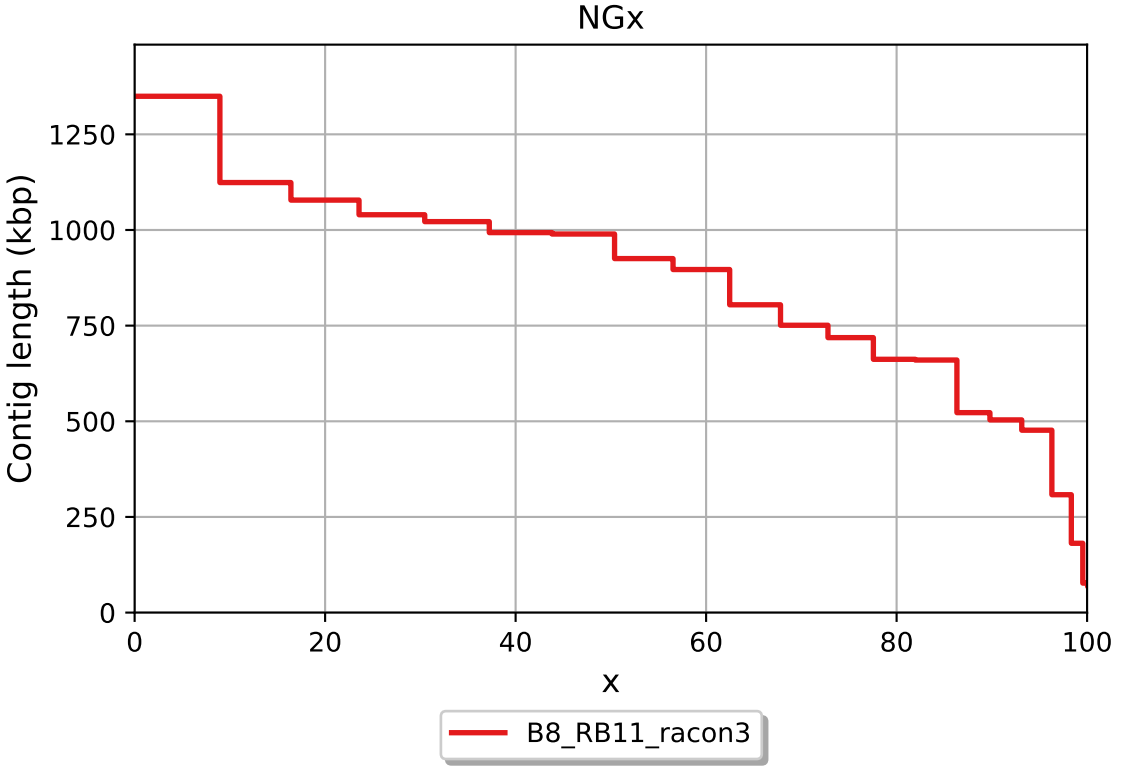
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

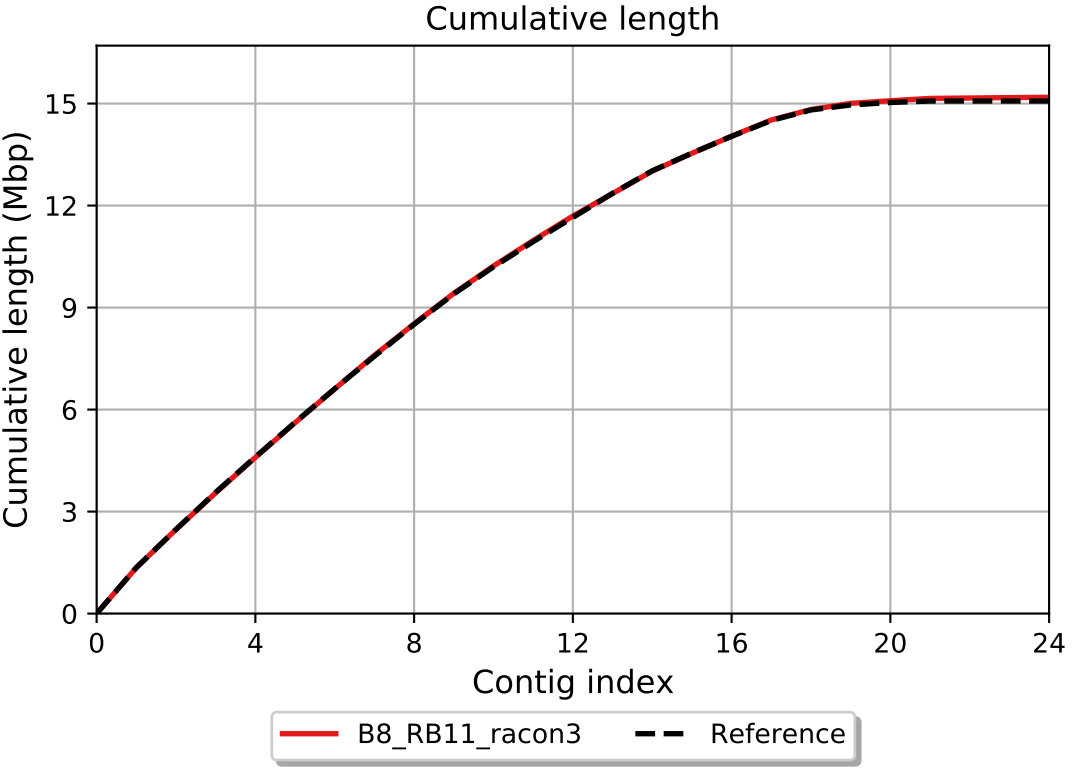
Unaligned report

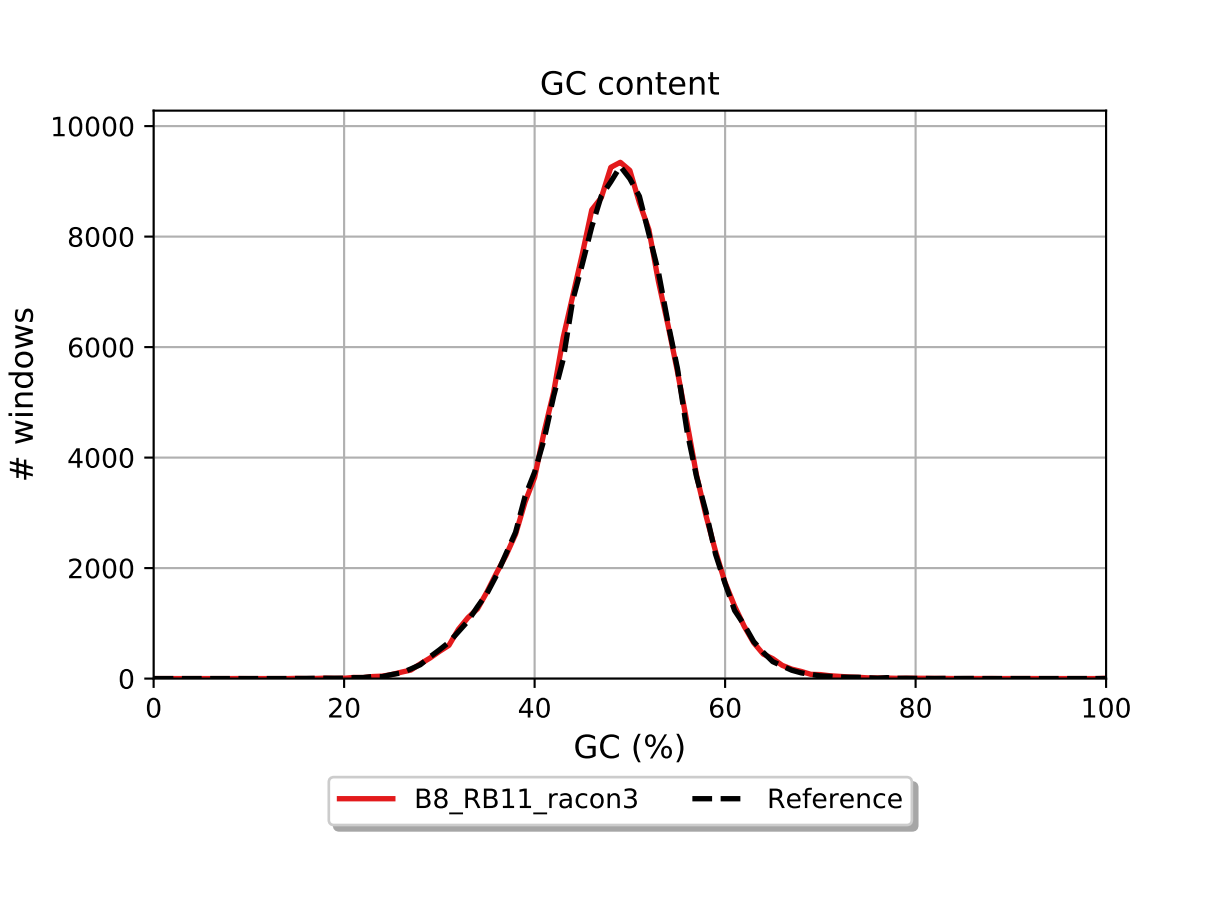
	B8_RB11_racon3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	21
Partially unaligned length	519580
# N's	0

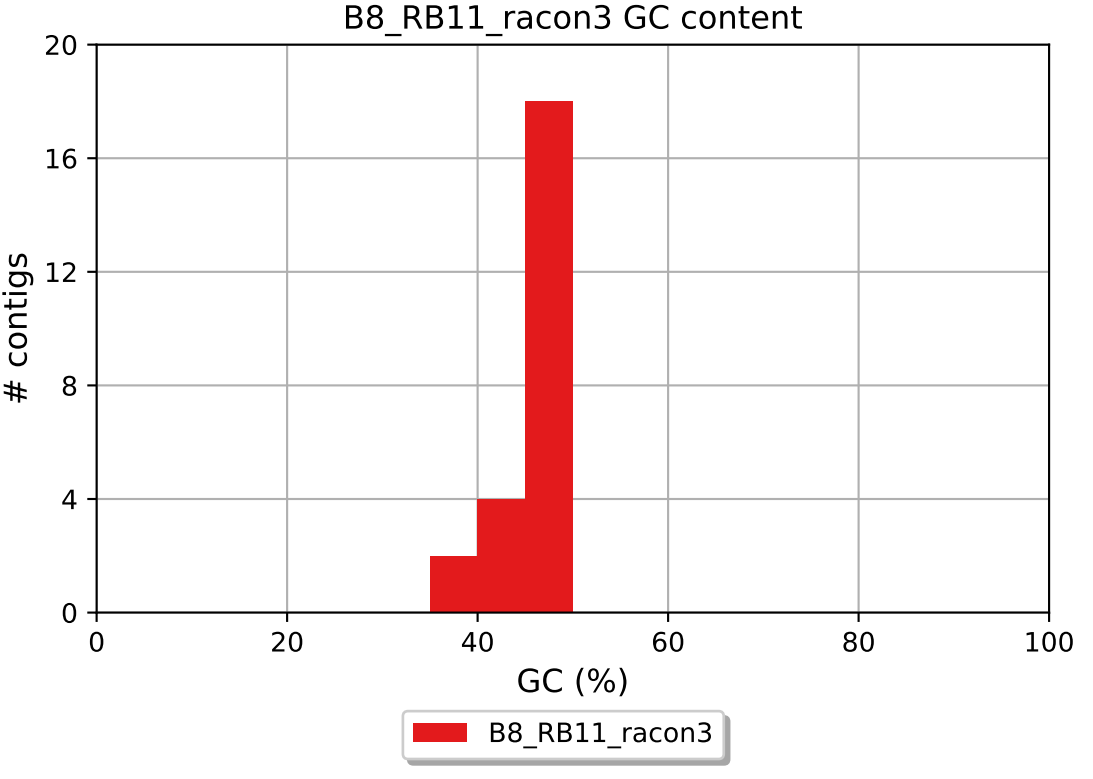
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

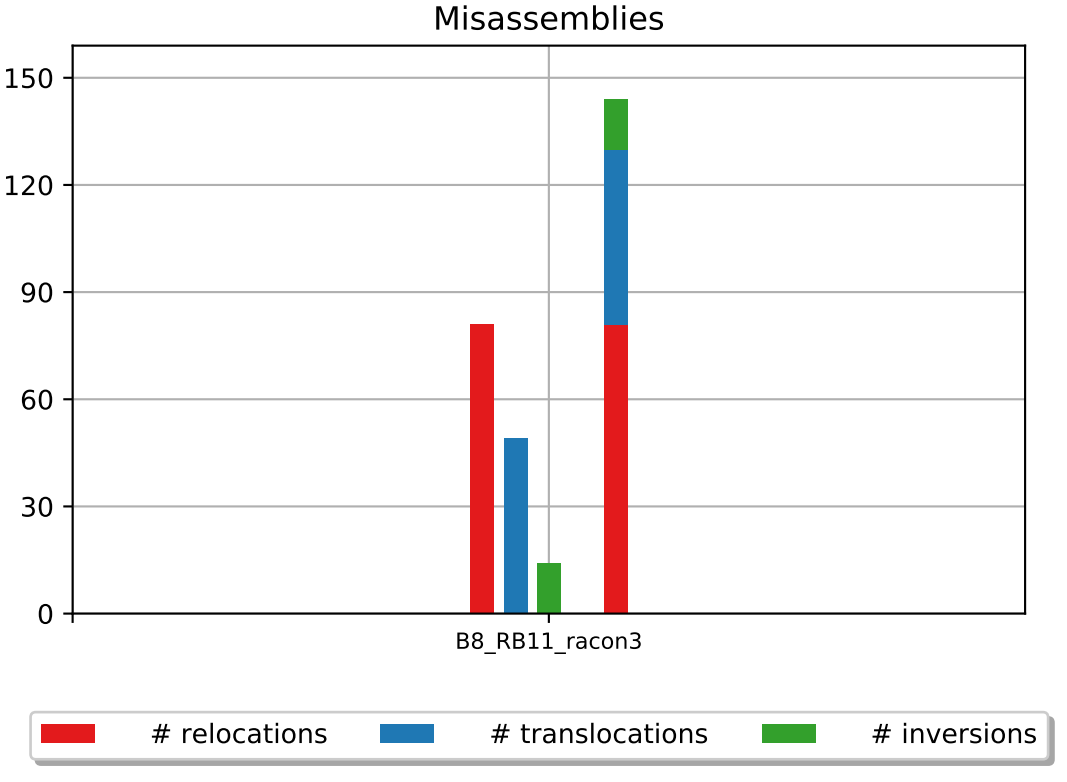

Nx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
B8_RB11_racon3

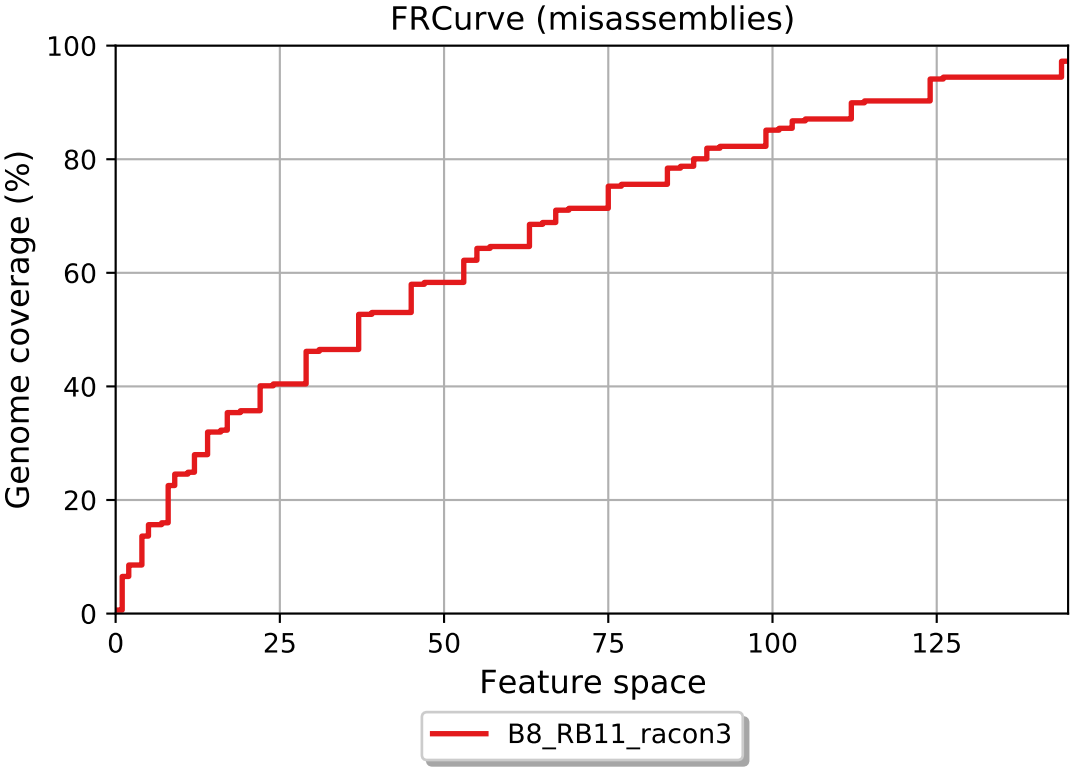

NGx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
B8_RB11_racon3

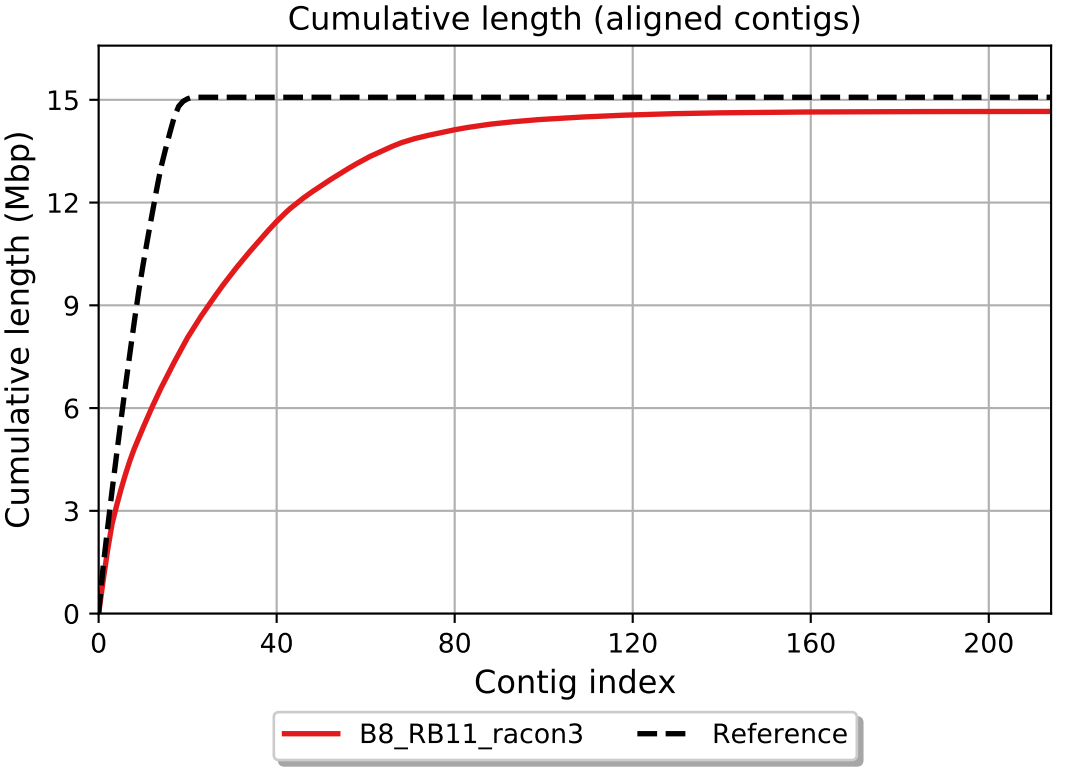

Cumulative length
Cumulative length (Mbp)
0
3
6
9
12
15
0
4
8
12
16
20
24
Contig index
B8_RB11_racon3
Reference

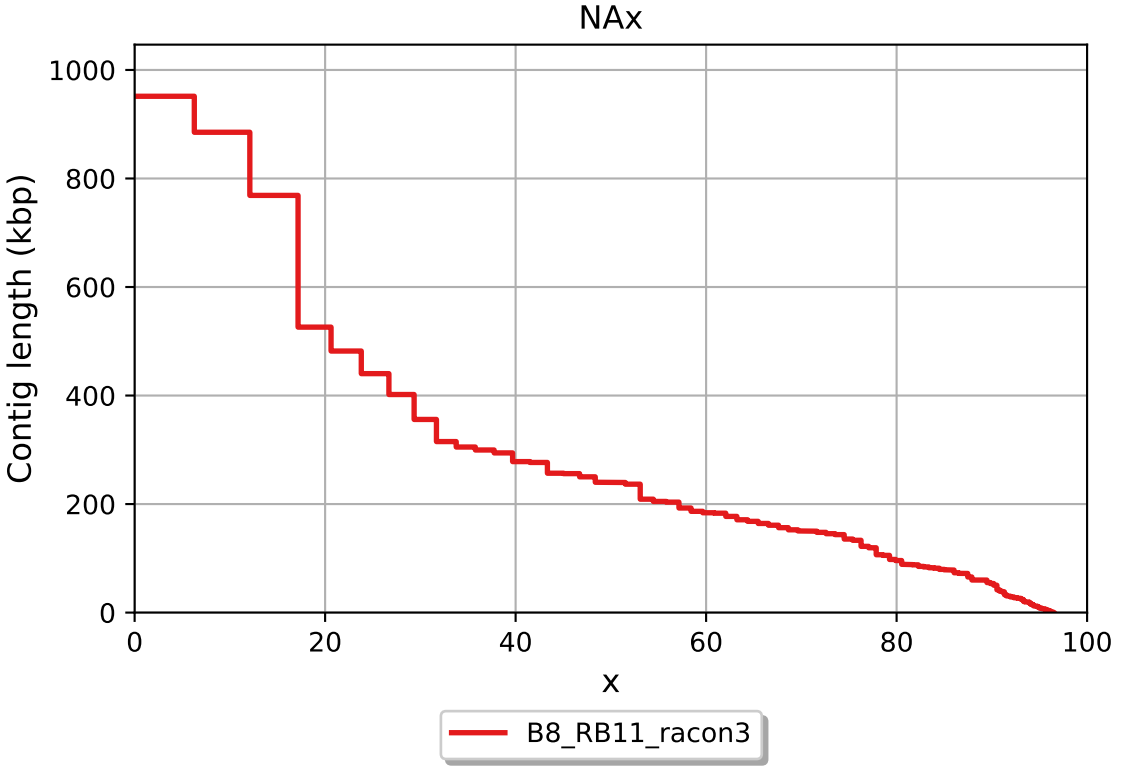

GC content
10000
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
B8_RB11_racon3
Reference

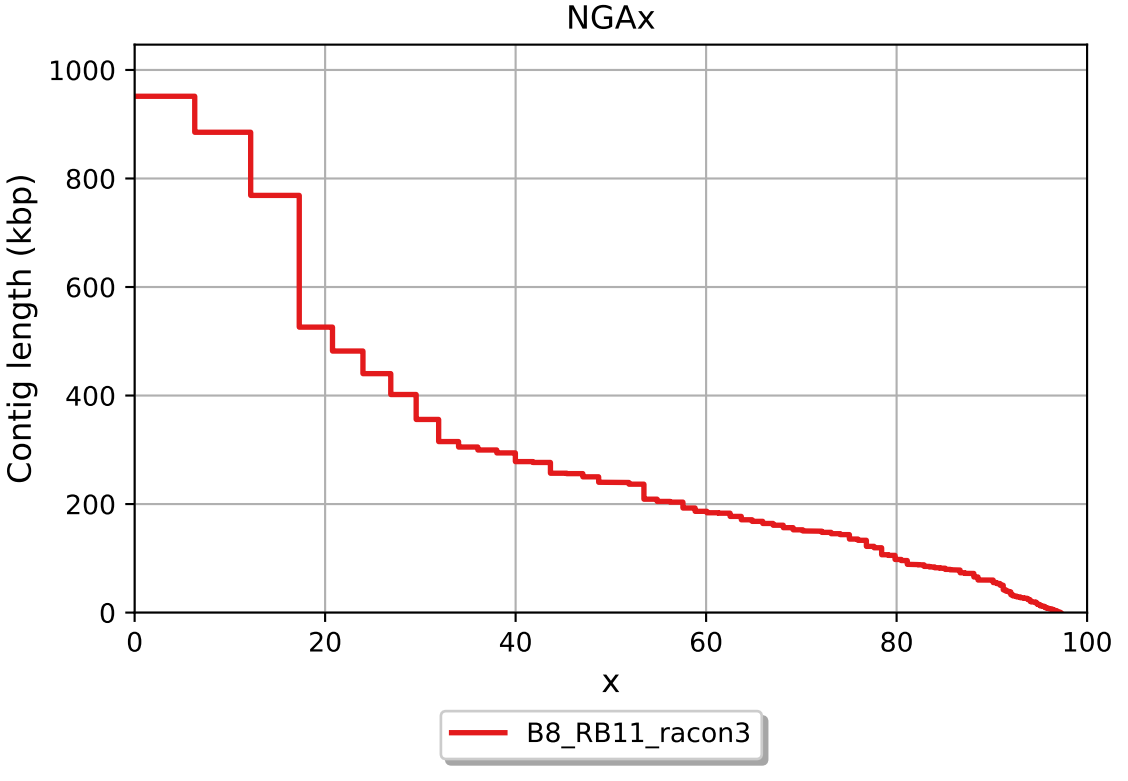

B8_RB11_racon3 GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
B8_RB11_racon3


Misassemblies
150
120
90
60
30
0
B8_RB11_racon3
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
25
50
75
100
125
Feature space
B8_RB11_racon3


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
3
6
9
12
15
0
40
80
120
160
200
Contig index
B8_RB11_racon3
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
B8_RB11_racon3


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
B8_RB11_racon3