Report

	Getorganelle	Fast_Plast	NOVOPlasty
# contigs (>= 0 bp)	1	394	1
# contigs (>= 1000 bp)	1	42	1
# contigs (>= 5000 bp)	1	5	1
# contigs (>= 10000 bp)	1	3	1
# contigs (>= 25000 bp)	1	1	1
# contigs (>= 50000 bp)	1	0	1
Total length (>= 0 bp)	154051	275275	152695
Total length (>= 1000 bp)	154051	137804	152695
Total length (>= 5000 bp)	154051	65796	152695
Total length (>= 10000 bp)	154051	50479	152695
Total length (>= 25000 bp)	154051	25153	152695
Total length (>= 50000 bp)	154051	0	152695
# contigs	1	94	1
Largest contig	154051	25153	152695
Total length	154051	172591	152695
Reference length	152695	152695	152695
GC (%)	39.15	40.88	39.14
Reference GC (%)	39.14	39.14	39.14
N50	154051	3018	152695
NG50	154051	4007	152695
N75	154051	1196	152695
NG75	154051	1703	152695
L50	1	11	1
LG50	1	8	1
L75	1	35	1
LG75	1	24	1
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	2	4	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	3	0
# unaligned contigs	0 + 1 part	38 + 10 part	0 + 0 part
Unaligned length	1356	38444	0
Genome fraction (%)	100.000	80.575	100.000
Duplication ratio	1.000	1.090	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	6.55	311.30	0.00
# indels per 100 kbp	0.00	15.44	0.00
Largest alignment	152695	25153	152695
Total aligned length	152695	130545	152695
NA50	152695	2717	152695
NGA50	152695	4007	152695
NA75	152695	161	152695
NGA75	152695	1222	152695
LA50	1	11	1
LGA50	1	8	1
LA75	1	49	1
LGA75	1	26	1

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

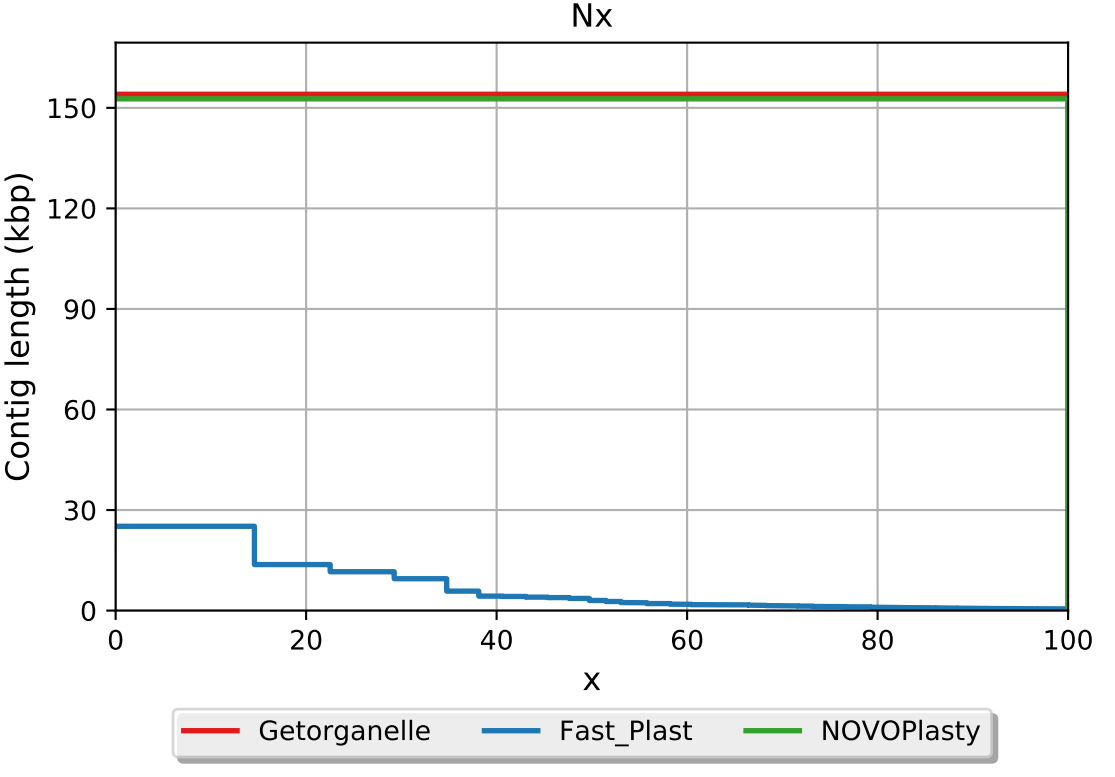
	Getorganelle	Fast_Plast	NOVOPlasty
# misassemblies	0	0	0
# contig misassemblies	0	0	0
# c. relocations	0	0	0
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	2	4	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	3	0
# mismatches	10	383	0
# indels	0	19	0
# indels (<= 5 bp)	0	14	0
# indels (> 5 bp)	0	5	0
Indels length	0	86	0

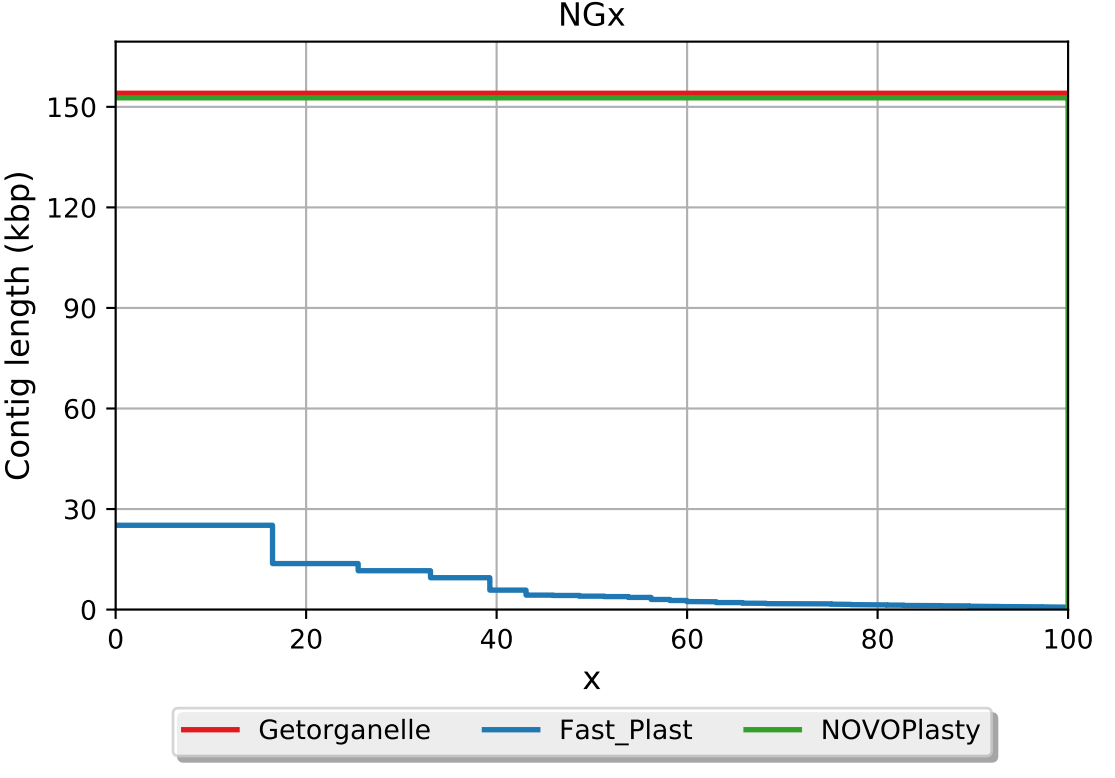
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

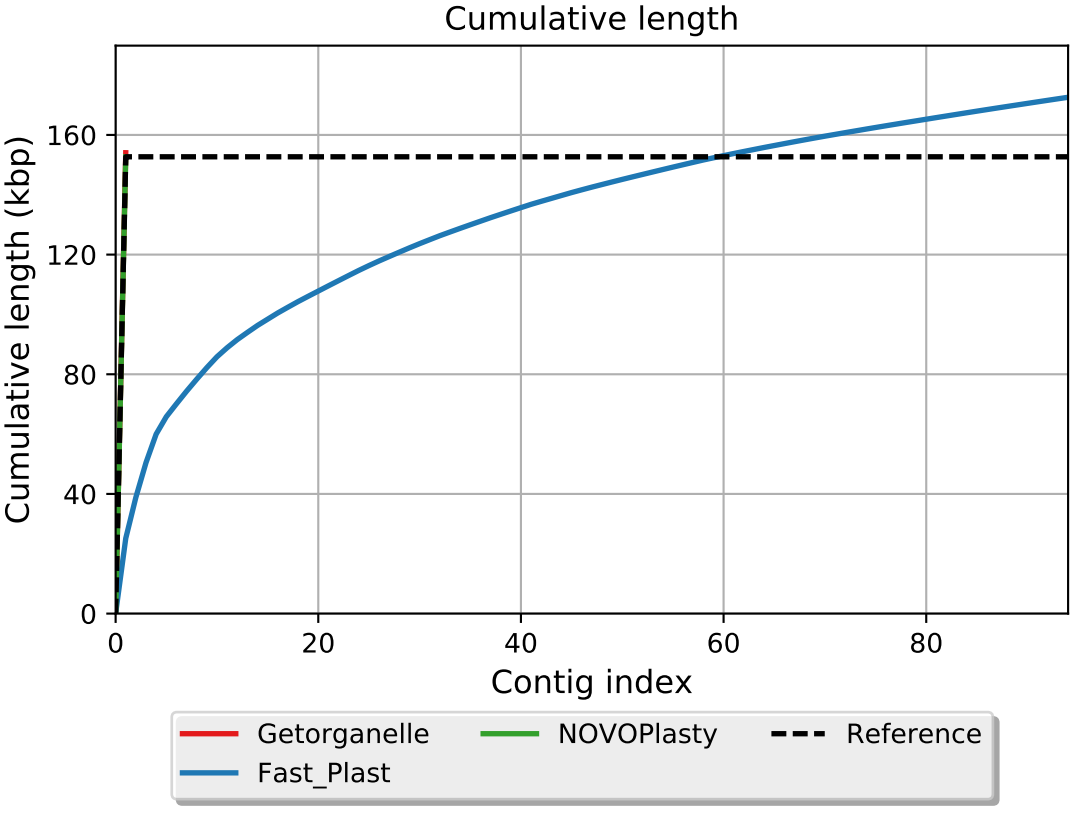
Unaligned report

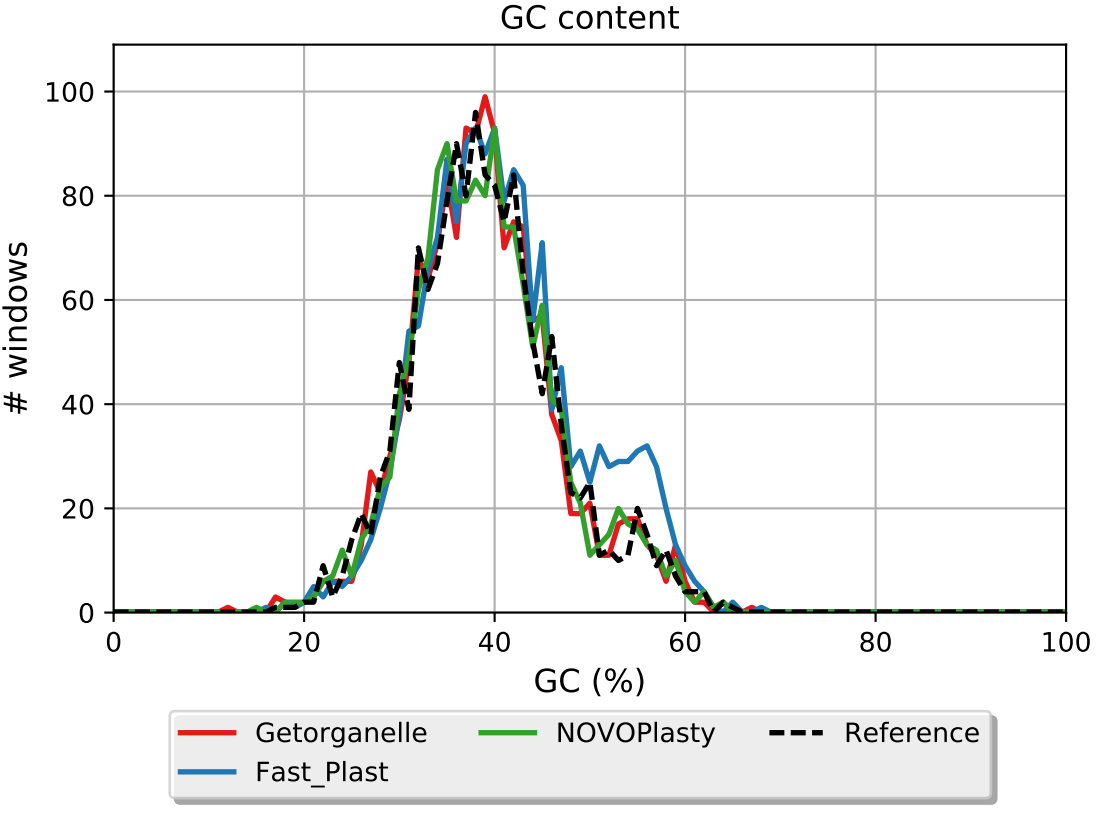
	Getorganelle	Fast_Plast	NOVOPlasty
# fully unaligned contigs	0	38	0
Fully unaligned length	0	29246	0
# partially unaligned contigs	1	10	0
Partially unaligned length	1356	9198	0
# N's	0	0	0

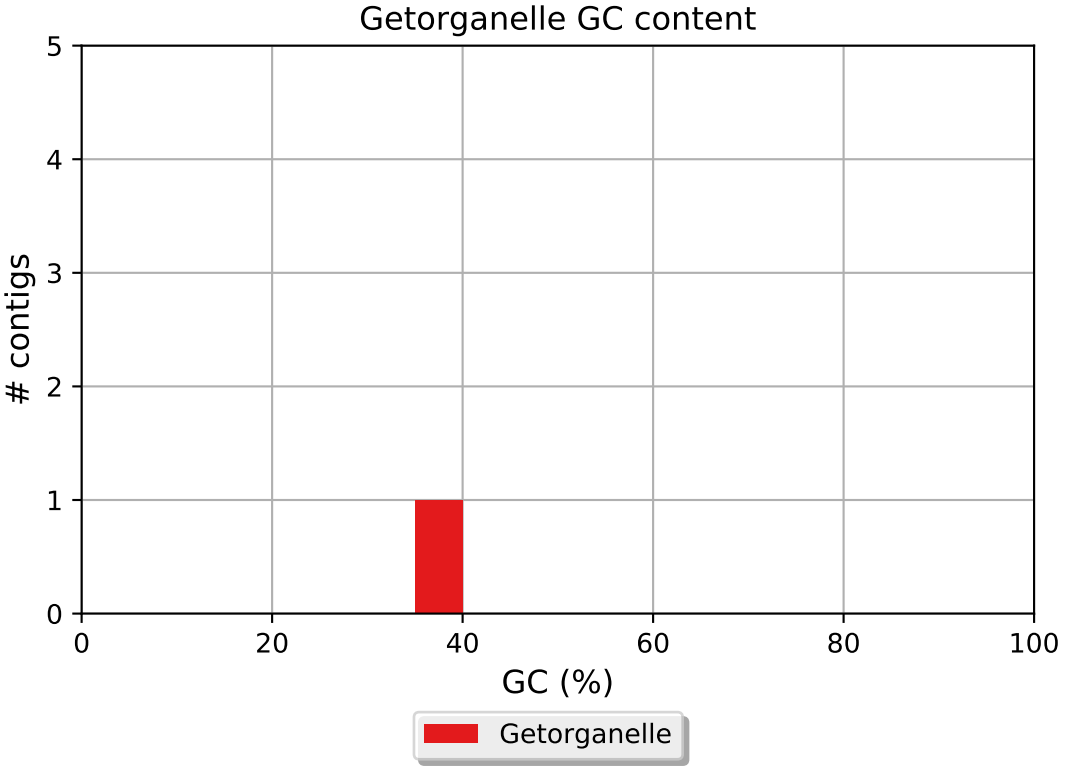
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

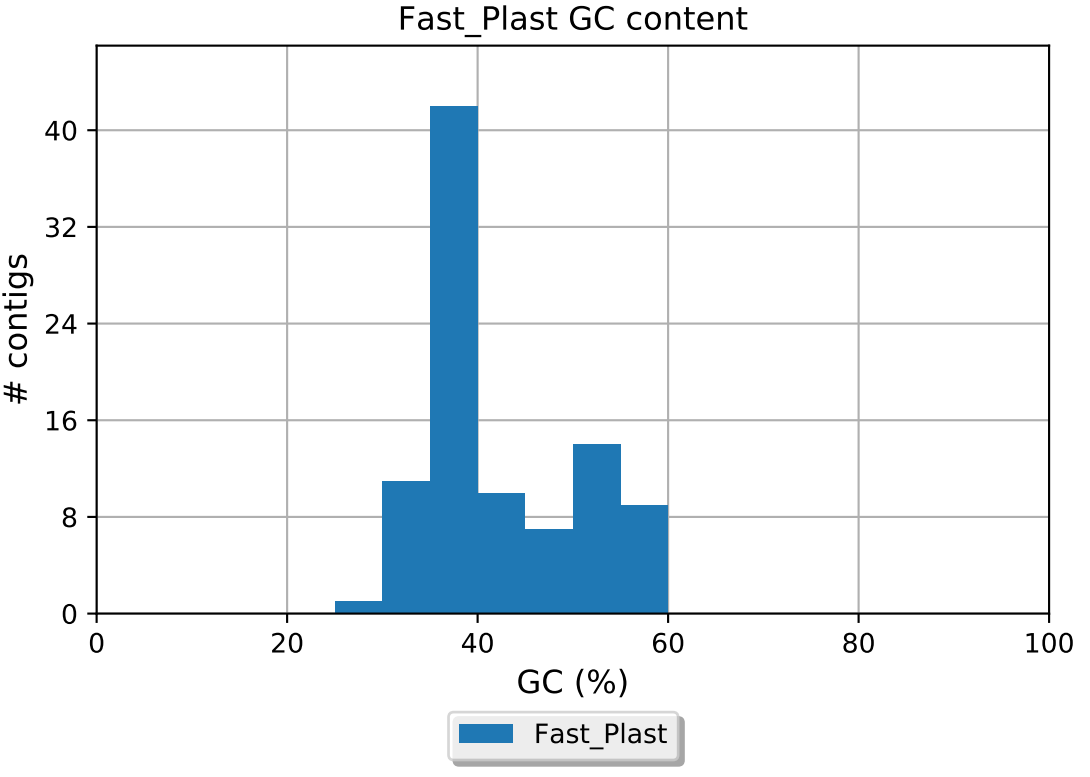

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
Getorganelle
Fast_Plast
NOVOPlasty

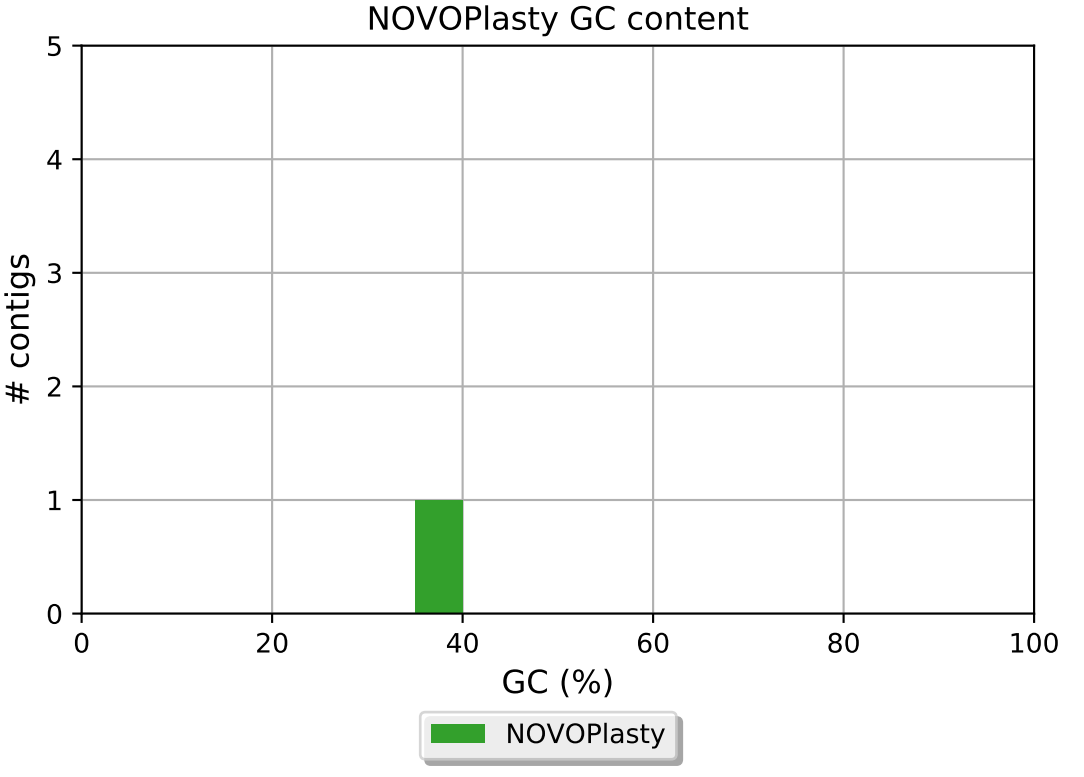

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
Getorganelle
Fast_Plast
NOVOPlasty

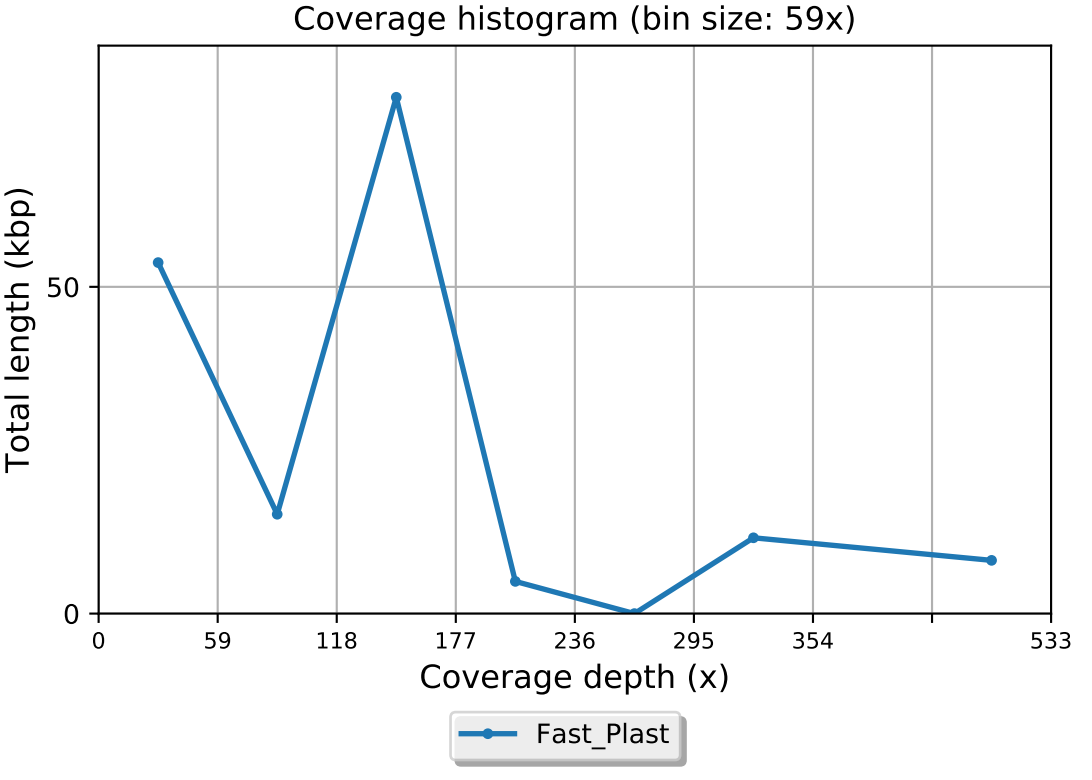

Cumulative length
Cumulative length (kbp)
160
120
80
40
0
0
20
40
60
80
Contig index
Getorganelle
NOVOPlasty
Reference
Fast_Plast

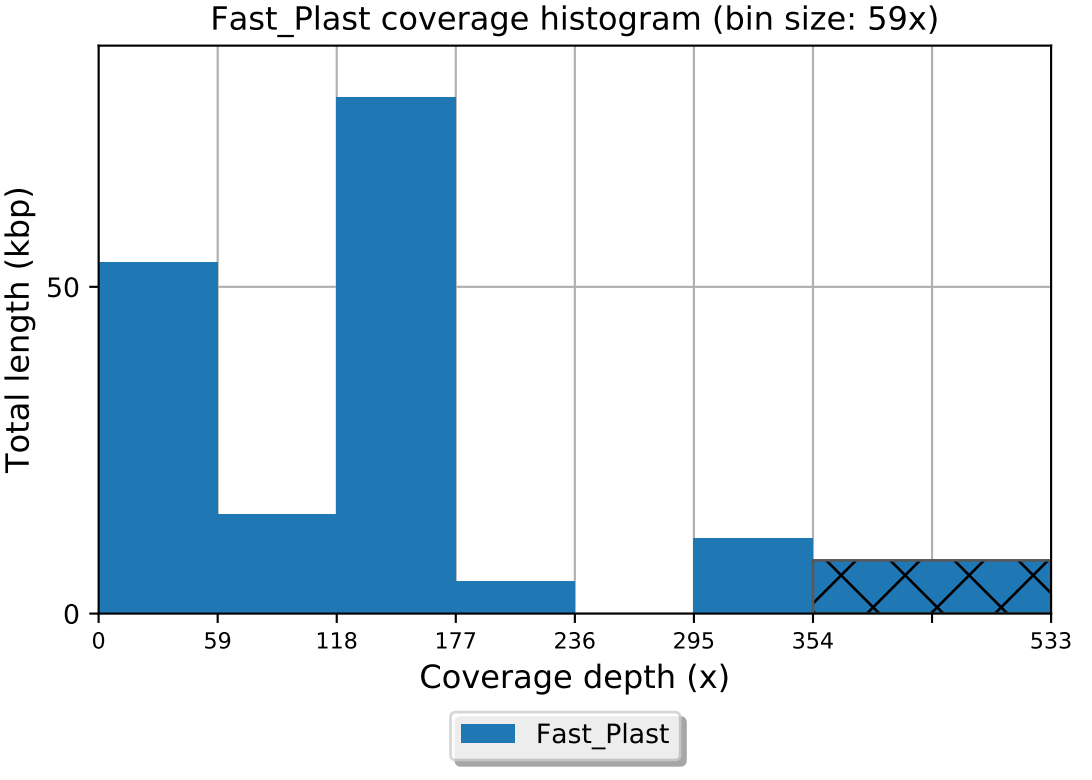

GC content
windows
GC (%)
0
20
40
60
80
100
Getorganelle
NOVOPlasty
Reference
Fast_Plast

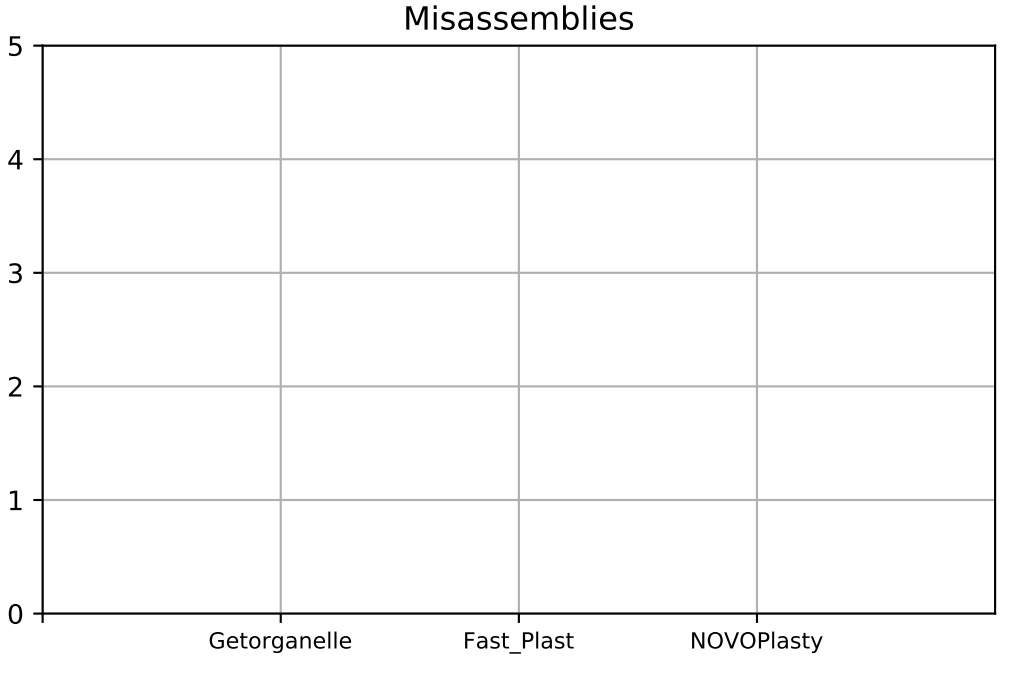

Getorganelle GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Getorganelle

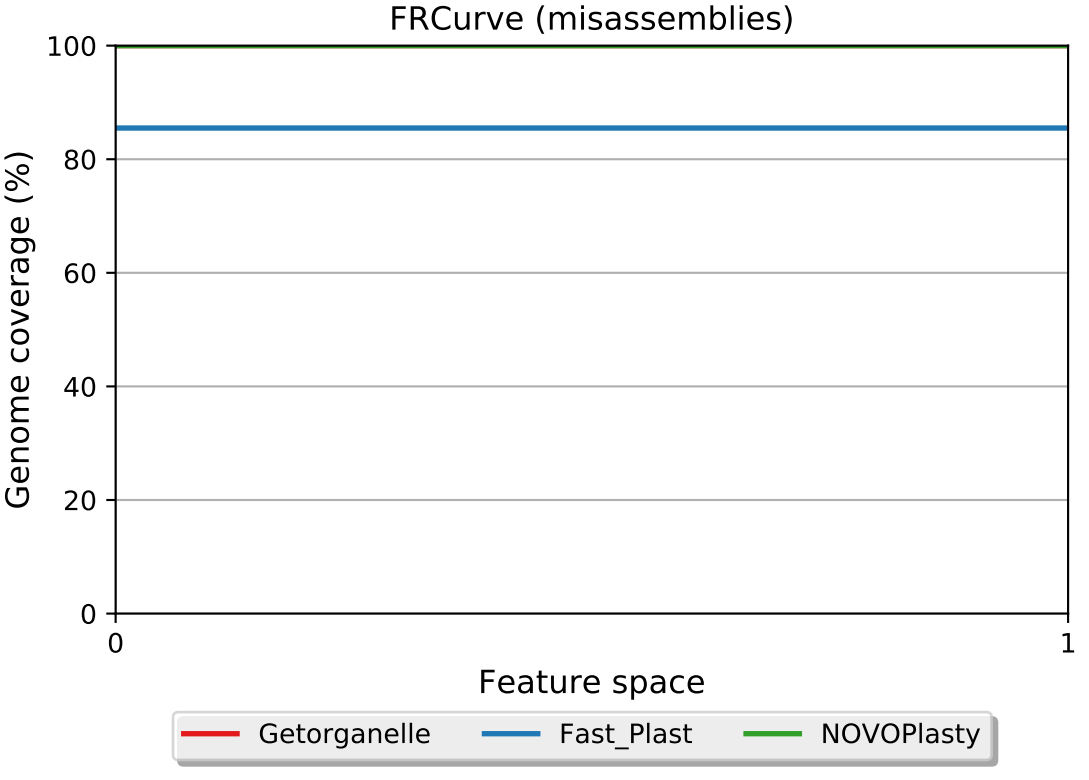

Fast_Plast GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
Fast_Plast

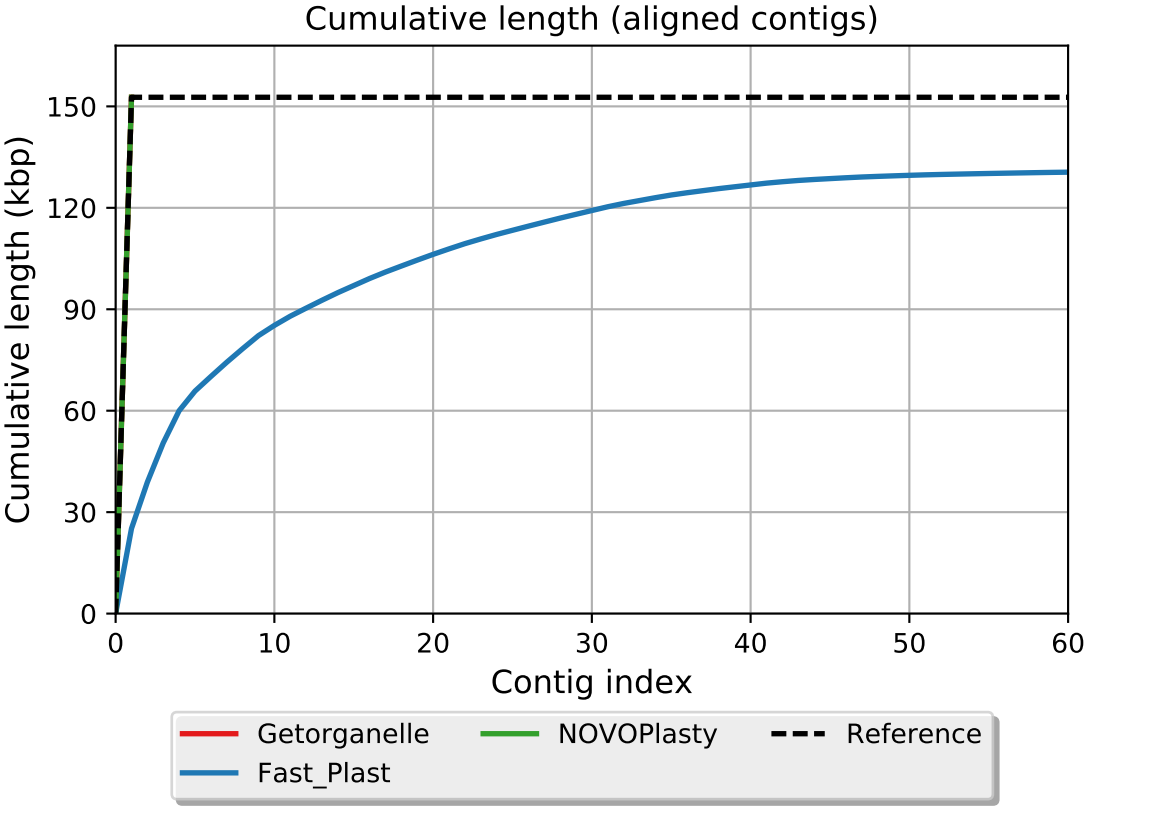

NOVOPlasty GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
NOVOPlasty

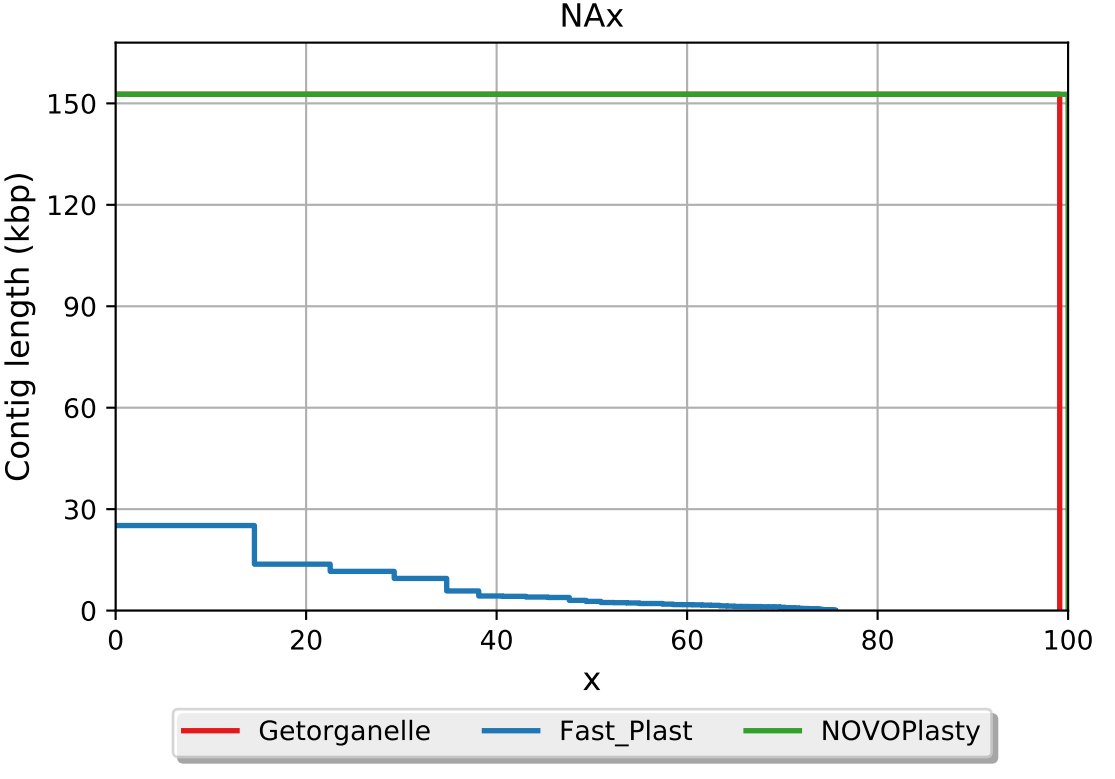

Coverage histogram (bin size: 59x)
Total length (kbp)
50
0
0
59
118
177
236
295
354
533
Coverage depth (x)
Fast_Plast

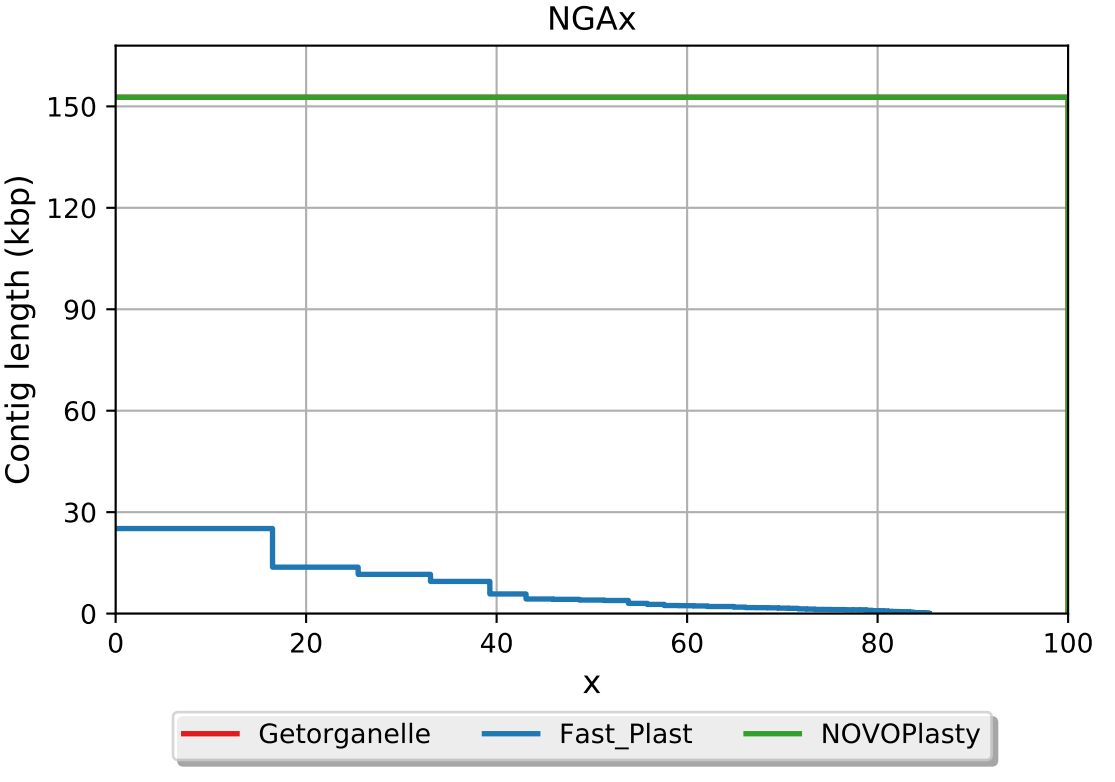

Fast_Plast coverage histogram (bin size: 59x)
Total length (kbp)
50
0
0
59
118
177
236
295
354
533
Coverage depth (x)
Fast_Plast

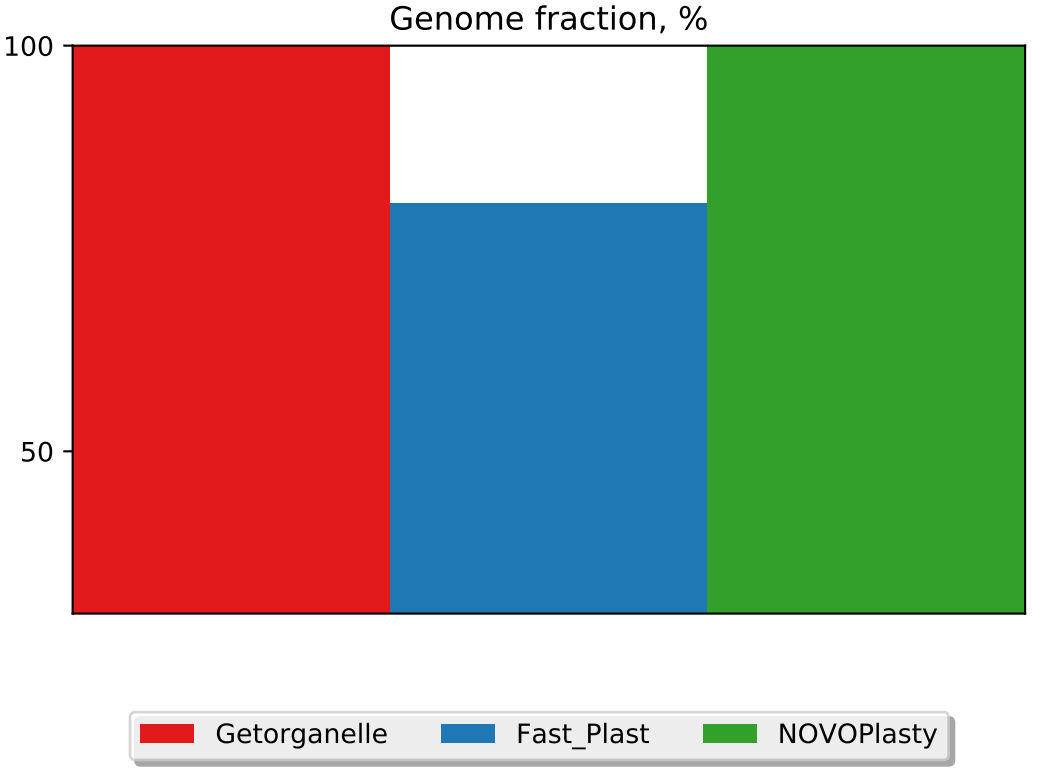

Misassemblies
5
4
3
2
1
0
Getorganelle
Fast_Plast
NOVOPlasty


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
150
120
90
60
30
0
0
10
20
30
40
50
60
Contig index
Getorganelle
NOVOPlasty
Reference
Fast_Plast


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
Getorganelle
Fast_Plast
NOVOPlasty


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
Getorganelle
Fast_Plast
NOVOPlasty


Genome fraction, %
100
50
Getorganelle
Fast_Plast
NOVOPlasty