

## Report

	Getorganelle_1	Fast_Plant.fsa
# contigs (>= 0 bp)	1	1
# contigs (>= 1000 bp)	1	1
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	1	1
Total length (>= 0 bp)	154478	154473
Total length (>= 1000 bp)	154478	154473
Total length (>= 5000 bp)	154478	154473
Total length (>= 10000 bp)	154478	154473
Total length (>= 25000 bp)	154478	154473
Total length (>= 50000 bp)	154478	154473
# contigs	1	1
Largest contig	154478	154473
Total length	154478	154473
Reference length	154478	154478
GC (%)	36.29	36.29
Reference GC (%)	36.29	36.29
N50	154478	154473
NG50	154478	154473
N75	154478	154473
NG75	154478	154473
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	1	0
# misassembled contigs	1	0
Misassembled contigs length	154478	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	82.998	100.000
Duplication ratio	1.205	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.65
# indels per 100 kbp	0.00	0.65
Largest alignment	110434	154473
Total aligned length	154478	154473
NA50	110434	154473
NGA50	110434	154473
NA75	44044	154473
NGA75	44044	154473
LA50	1	1
LGA50	1	1
LA75	2	1
LGA75	2	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

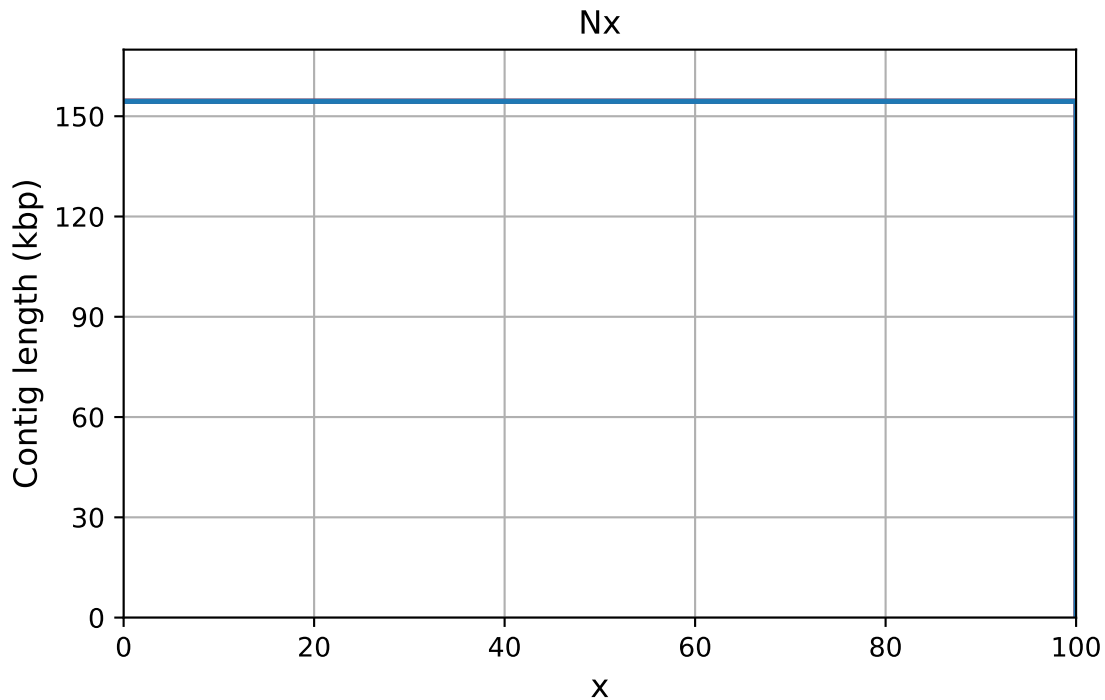
	Getorganelle_1	Fast_Plust.fsa
# misassemblies	1	0
# contig misassemblies	1	0
# c. relocations	1	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	0
Misassembled contigs length	154478	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	0	1
# indels	0	1
# indels (<= 5 bp)	0	1
# indels (> 5 bp)	0	0
Indels length	0	5

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

## Unaligned report

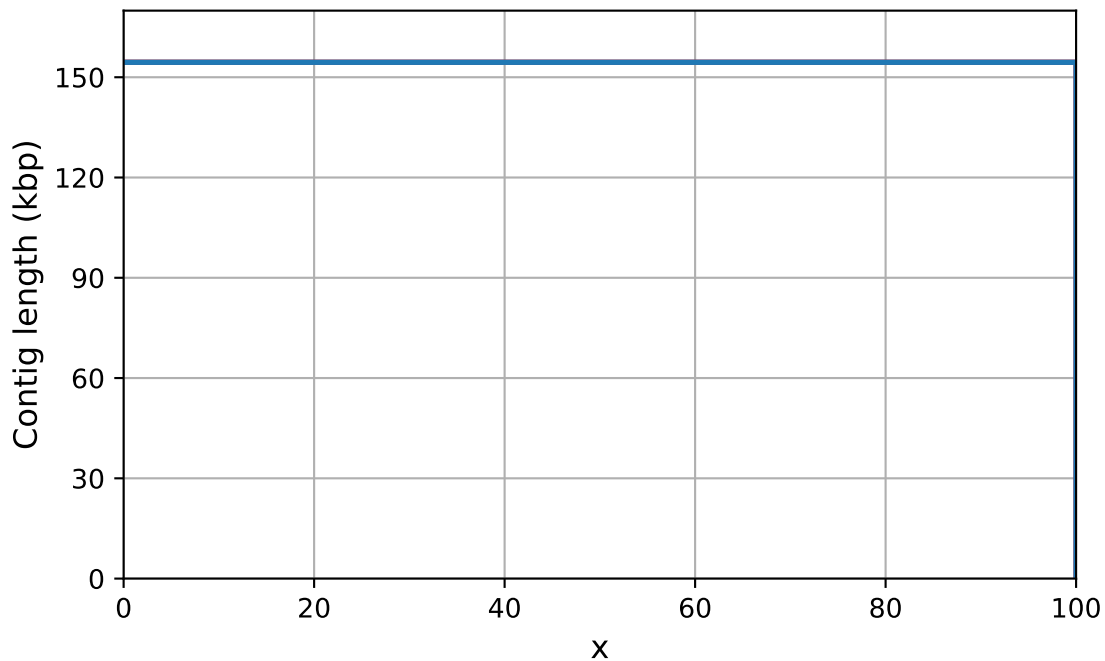
	Getorganelle_1	Fast_Plant.fsa
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

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



— Getorganelle\_1      — Fast\_Plant.fsa

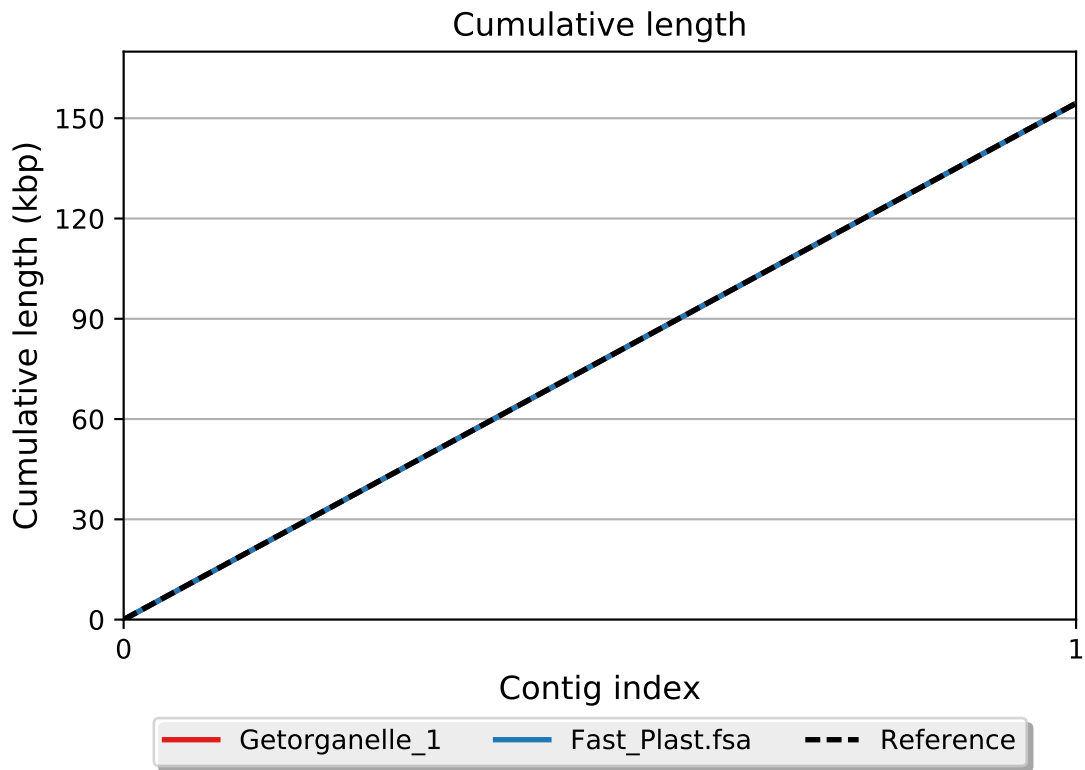
# NGx



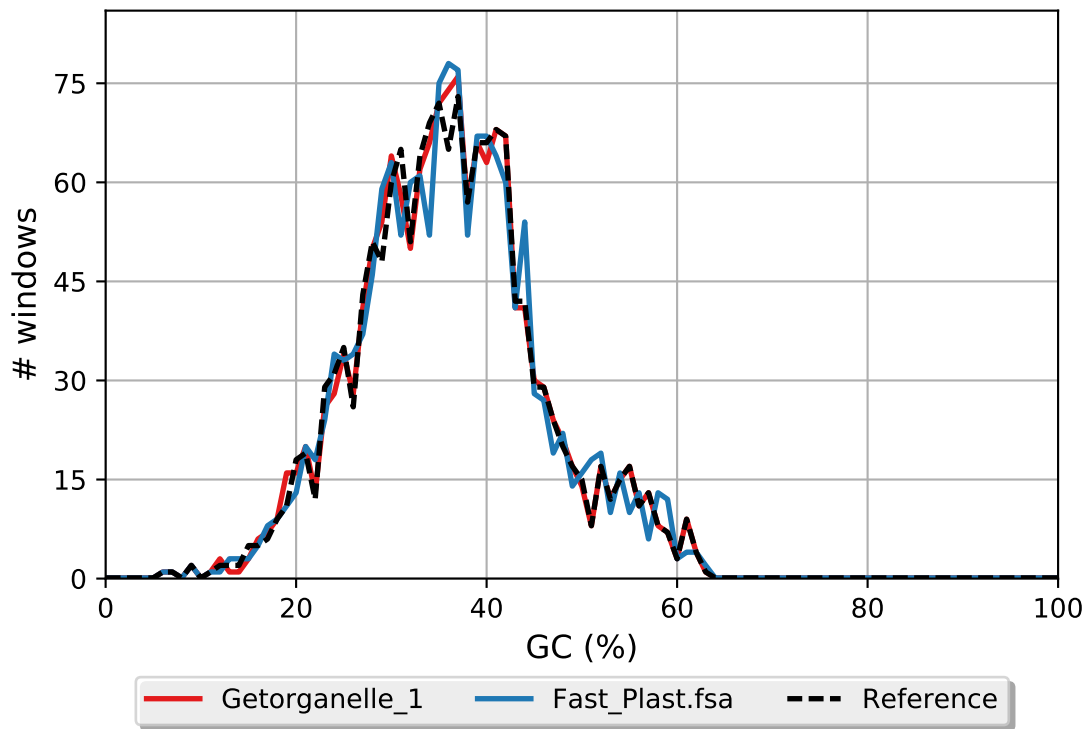
Getorganelle\_1



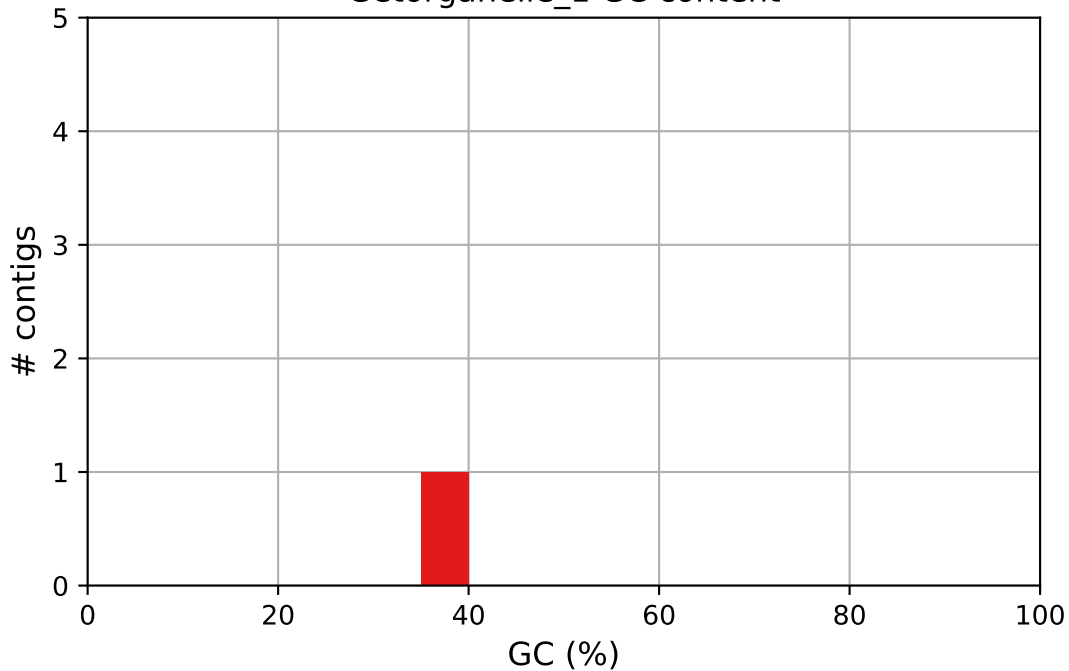
Fast\_Plust.fsa



GC content



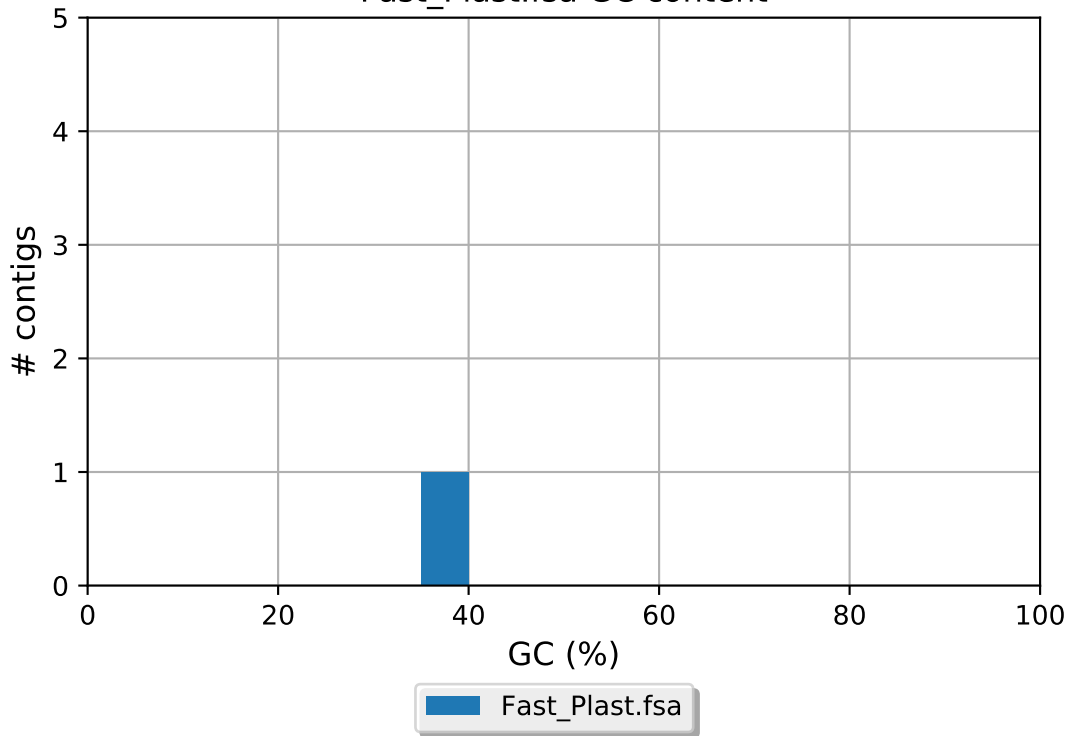
Getorganelle\_1 GC content



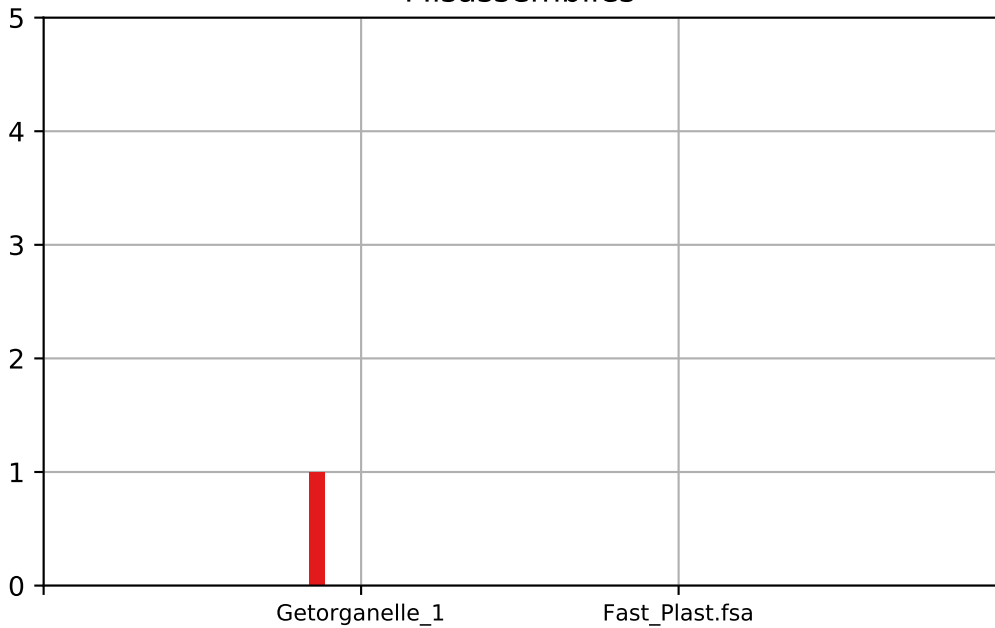
Getorganelle\_1



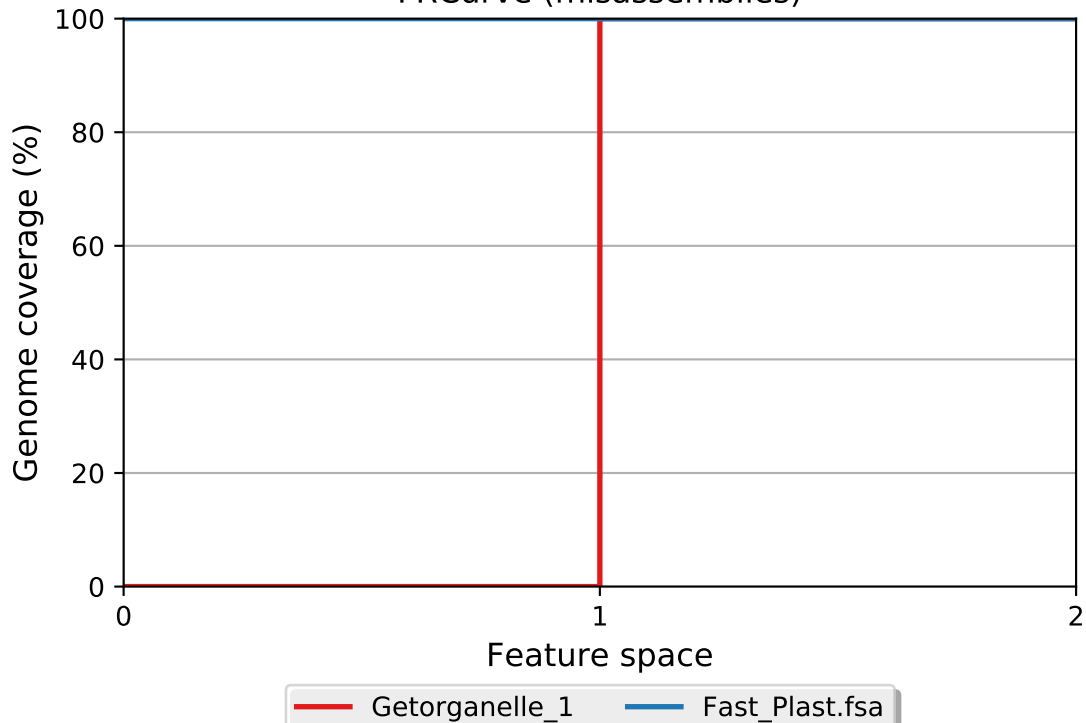
Fast\_Plust.fsa GC content



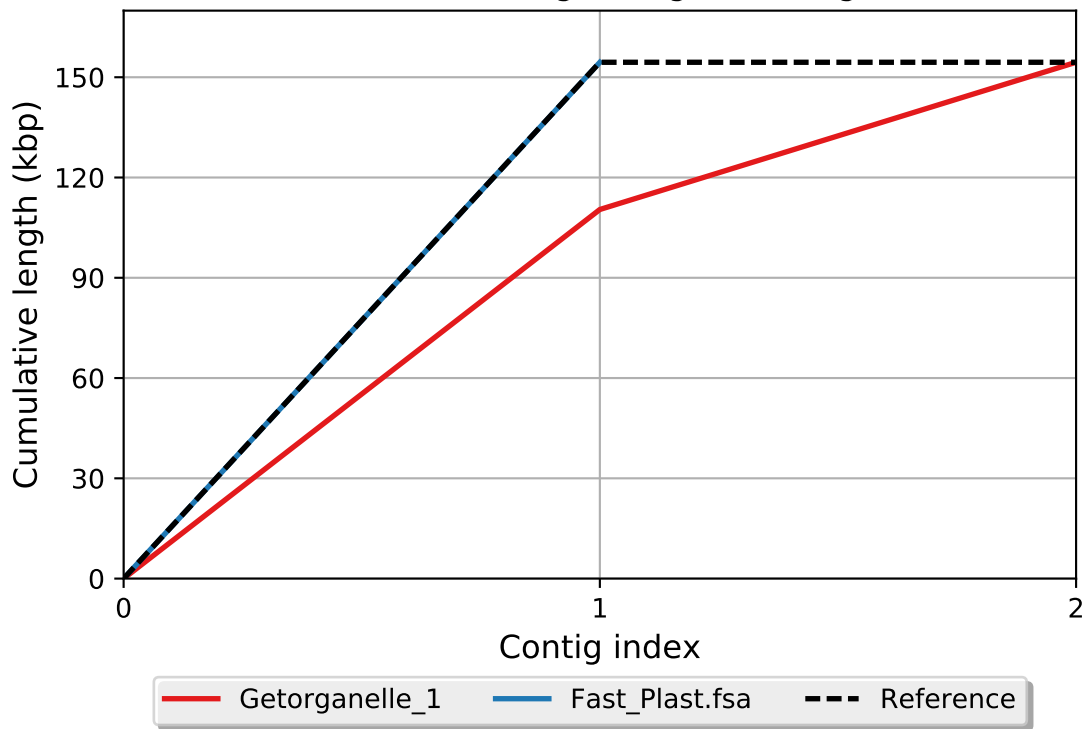
## Misassemblies



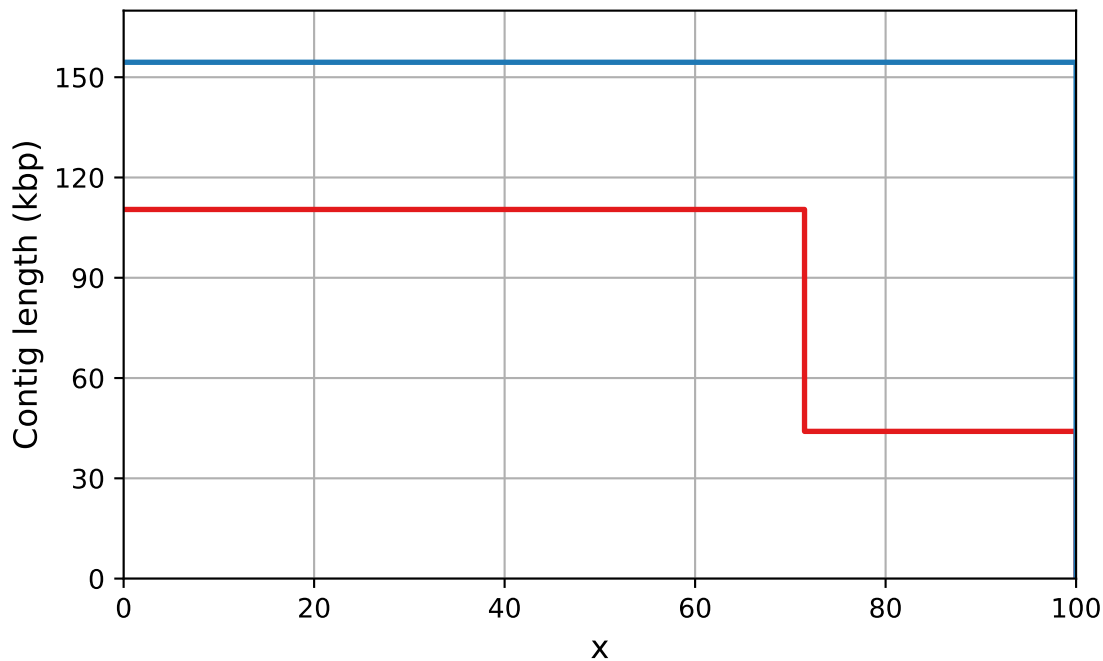
FRCurve (misassemblies)



Cumulative length (aligned contigs)

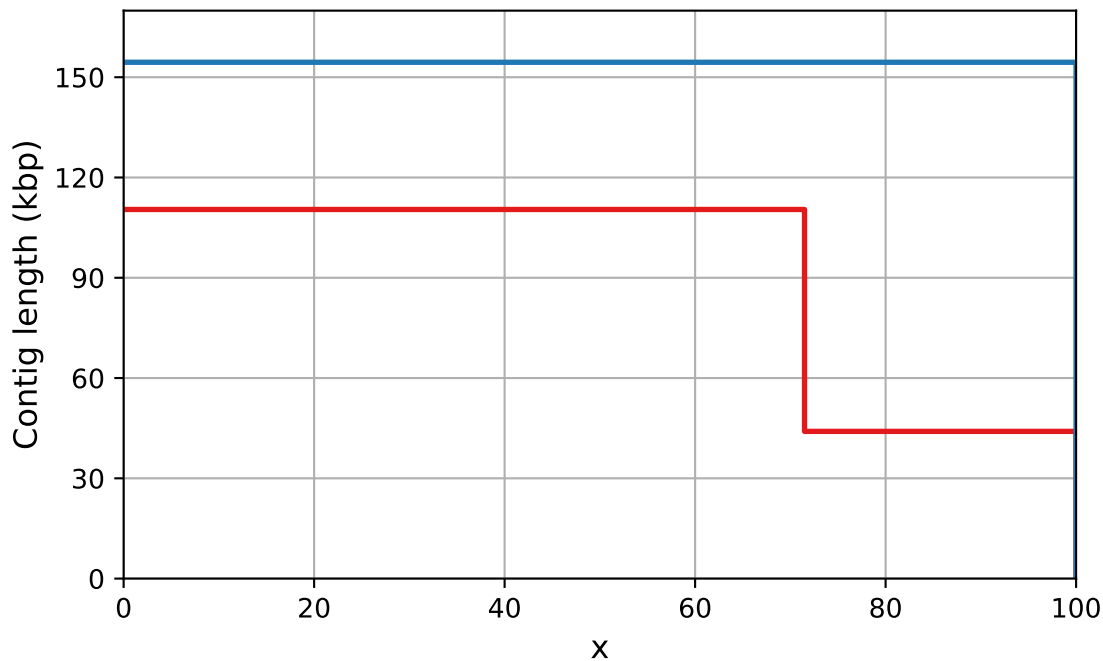


NAx



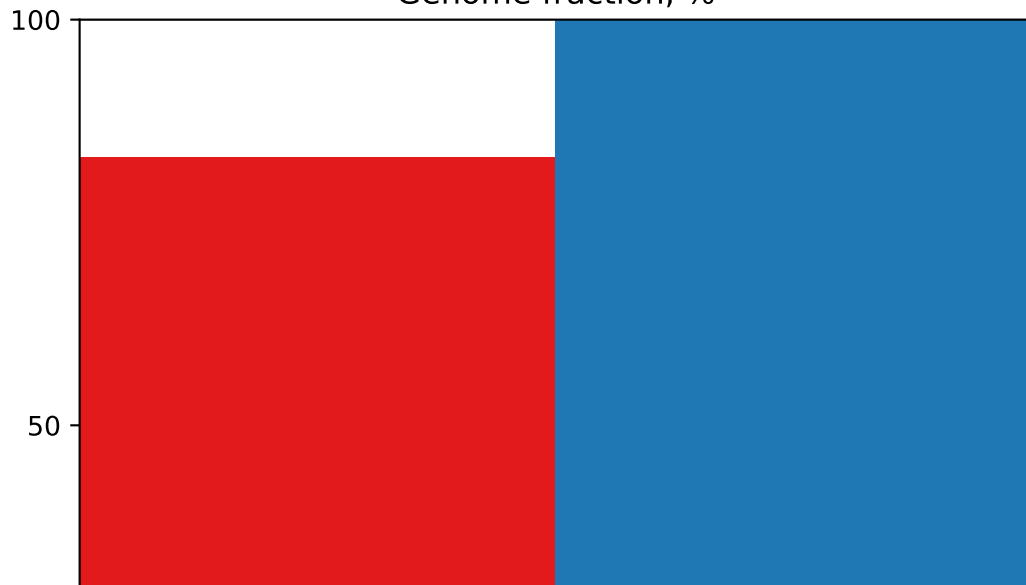
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# NGAx



— Getorganelle\_1 — Fast\_Plant.fsa

Genome fraction, %



Getorganelle\_1



Fast\_Plant.fsa