

## Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	47019	47019	46996	46996
Total length (>= 5000 bp)	47019	47019	46996	46996
Total length (>= 10000 bp)	47019	47019	46996	46996
Total length (>= 25000 bp)	47019	47019	46996	46996
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	47019	47019	46996	46996
Total length	47019	47019	46996	46996
Reference length	47325	47325	47325	47325
GC (%)	39.28	39.28	39.25	39.25
Reference GC (%)	39.23	39.23	39.23	39.23
N50	47019	47019	46996	46996
NG50	47019	47019	46996	46996
N75	47019	47019	46996	46996
NG75	47019	47019	46996	46996
L50	1	1	1	1
LG50	1	1	1	1
L75	1	1	1	1
LG75	1	1	1	1
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	1	1	1
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	99.098	99.098	99.098	99.098
Duplication ratio	1.003	1.003	1.002	1.002
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	47019	47019	46996	46996
Total aligned length	47019	47019	46996	46996
NA50	47019	47019	46996	46996
NGA50	47019	47019	46996	46996
NA75	47019	47019	46996	46996
NGA75	47019	47019	46996	46996
LA50	1	1	1	1
LGA50	1	1	1	1
LA75	1	1	1	1
LGA75	1	1	1	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

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	0	0	0	0
# contig misassemblies	0	0	0	0
# c. relocations	0	0	0	0
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# possibly misassembled contigs	0	0	0	0
# possible misassemblies	0	0	0	0
# local misassemblies	1	1	1	1
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	0	0	0	0
# indels	0	0	0	0
# indels (<= 5 bp)	0	0	0	0
# indels (> 5 bp)	0	0	0	0
Indels length	0	0	0	0

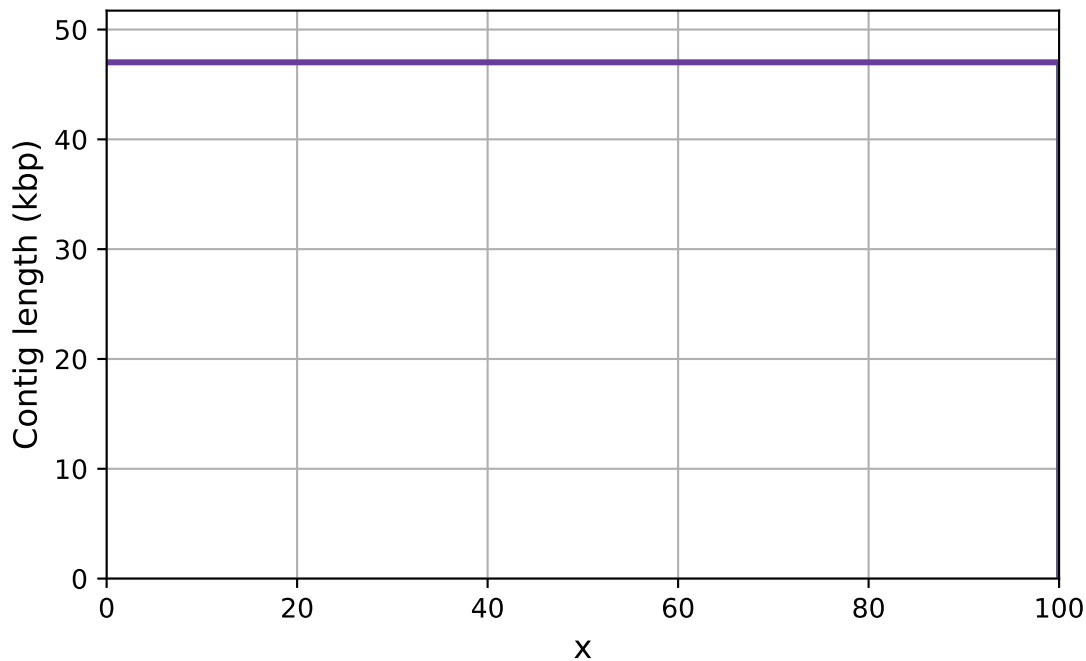
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

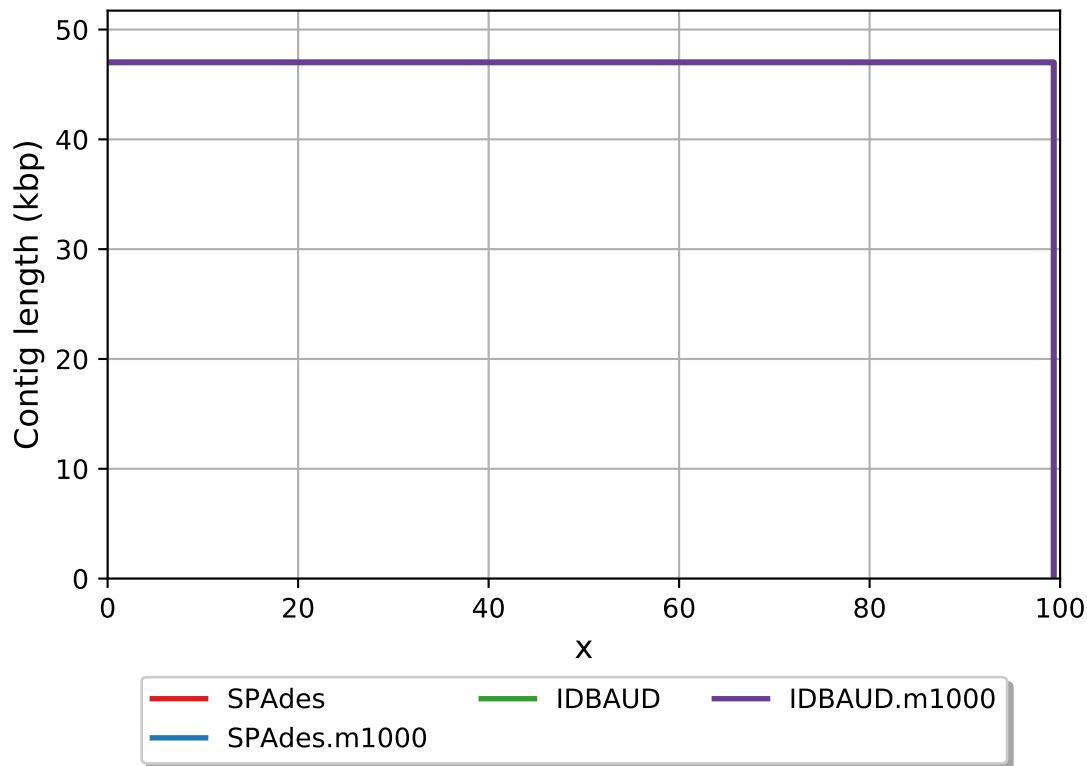
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

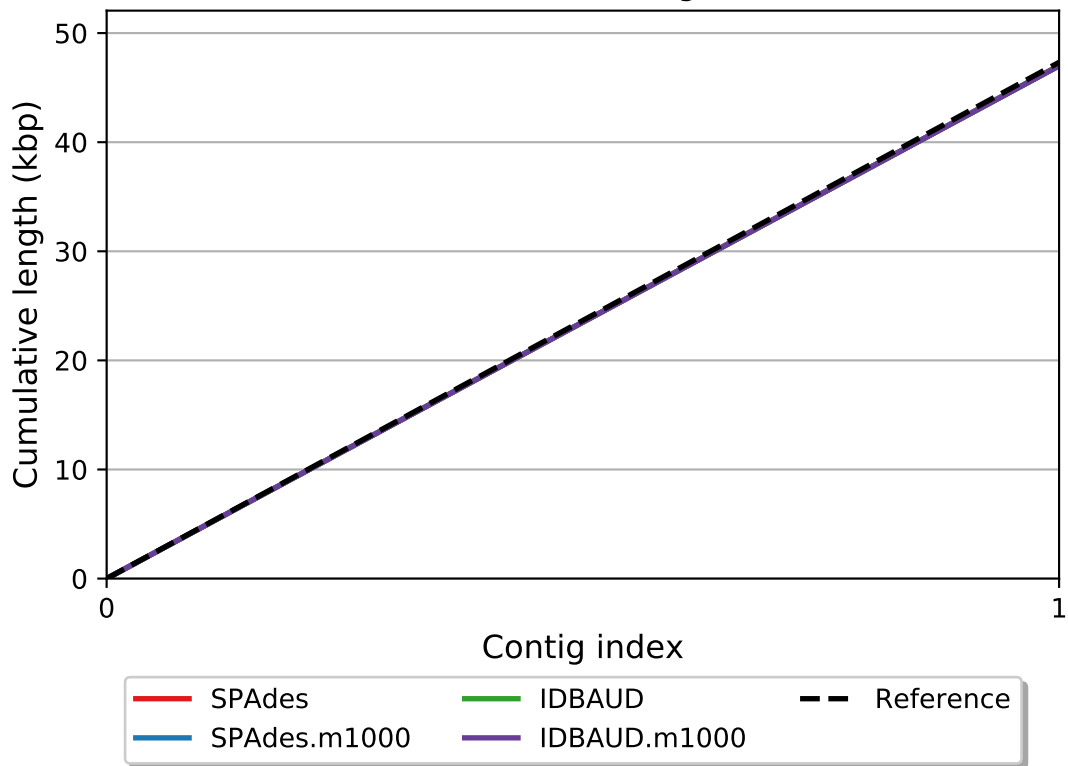


— SPAdes — IDBAUD — IDBAUD.m1000  
— SPAdes.m1000

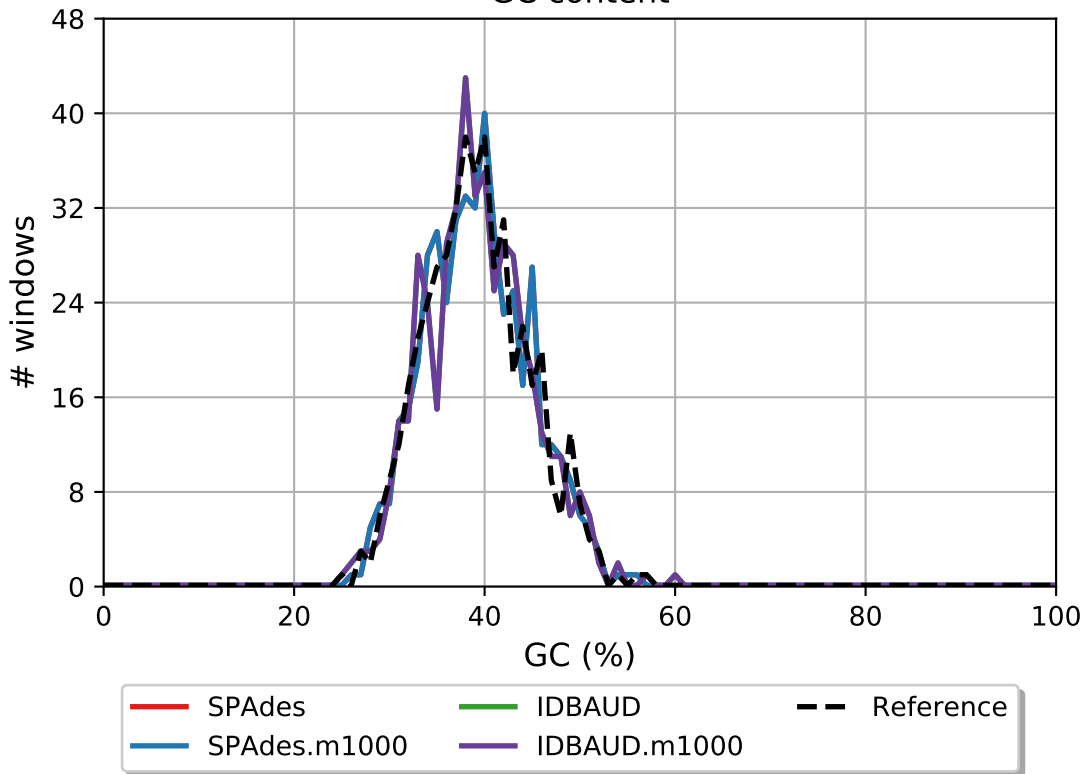
# NGx



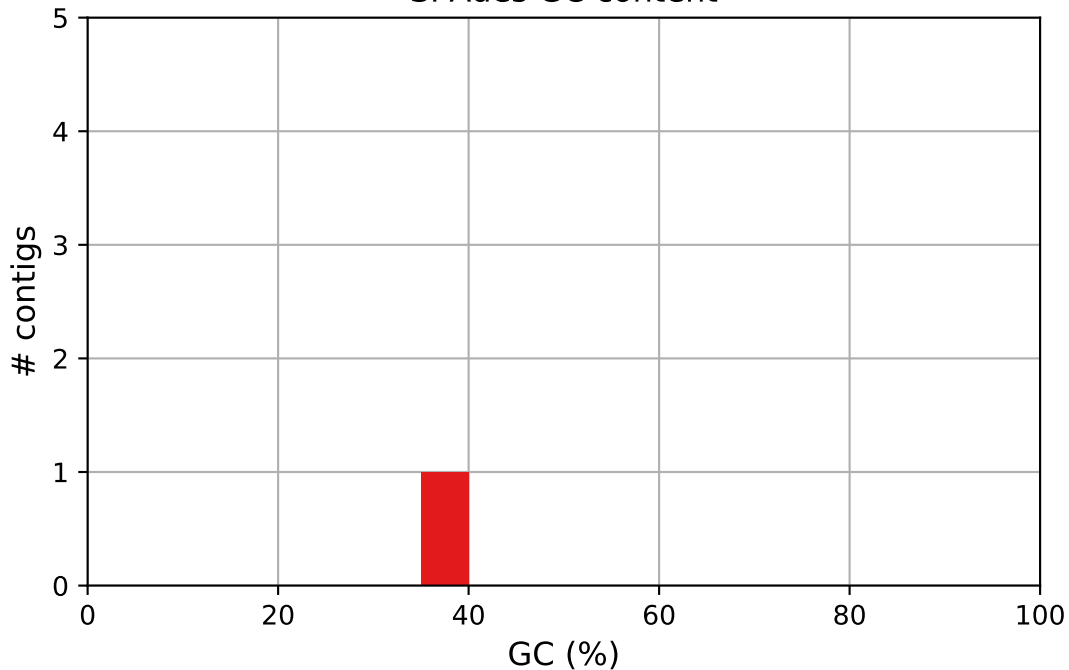
Cumulative length



## GC content



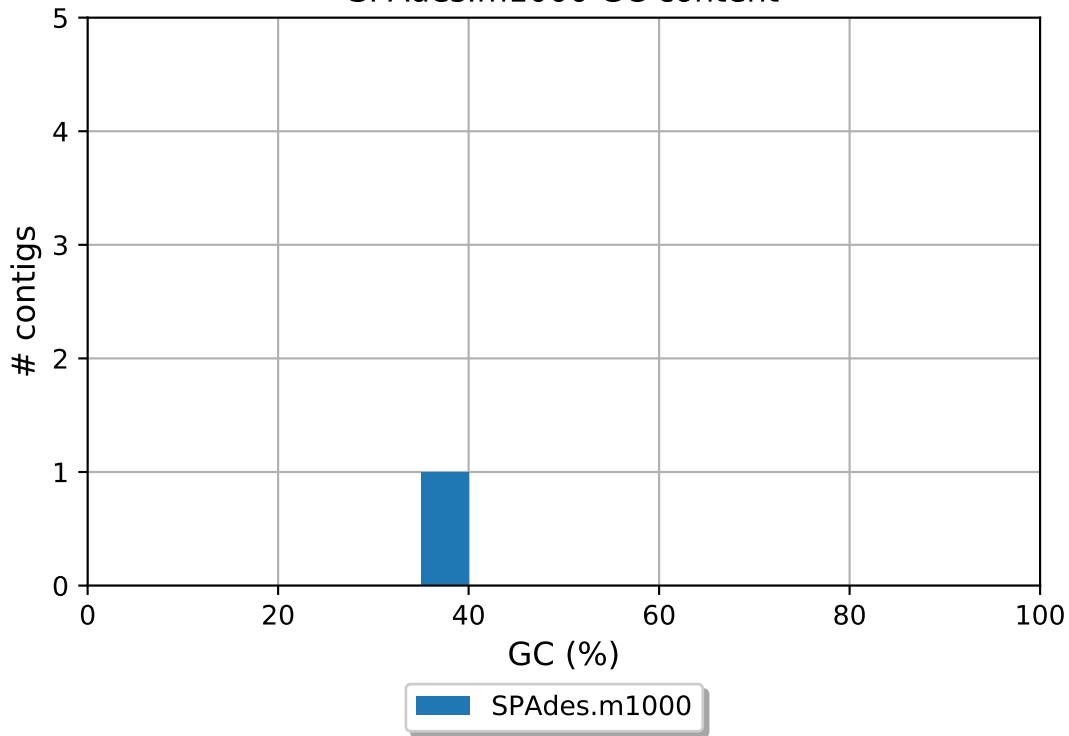
# SPAdes GC content



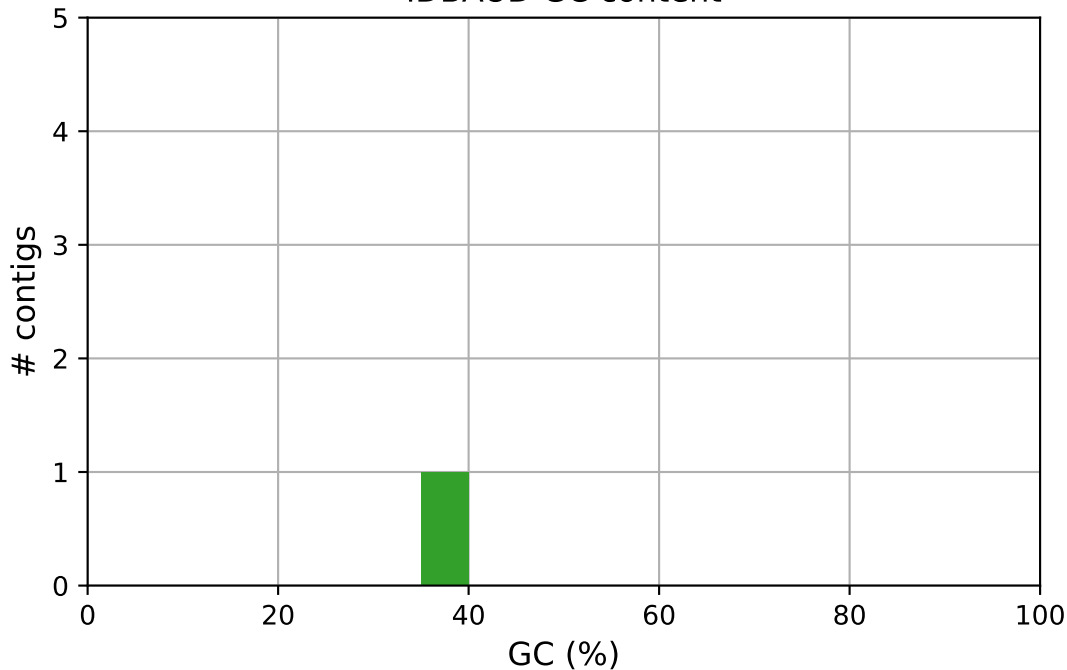
SPAdes



SPAdes.m1000 GC content

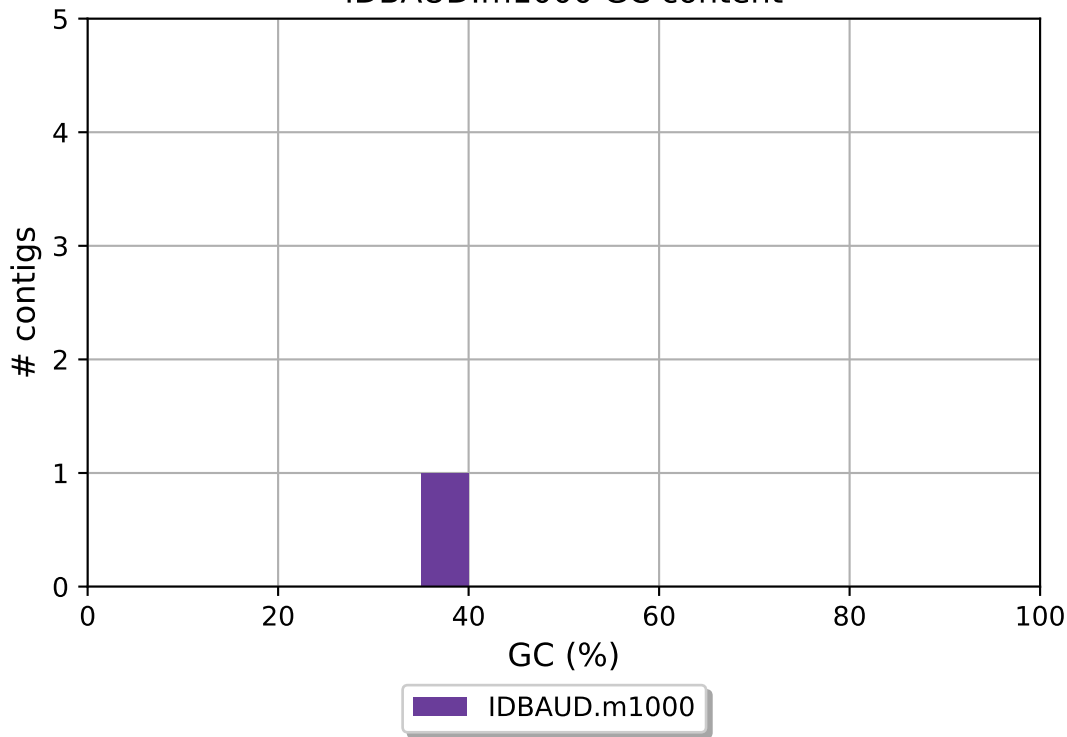


# IDBAUD GC content

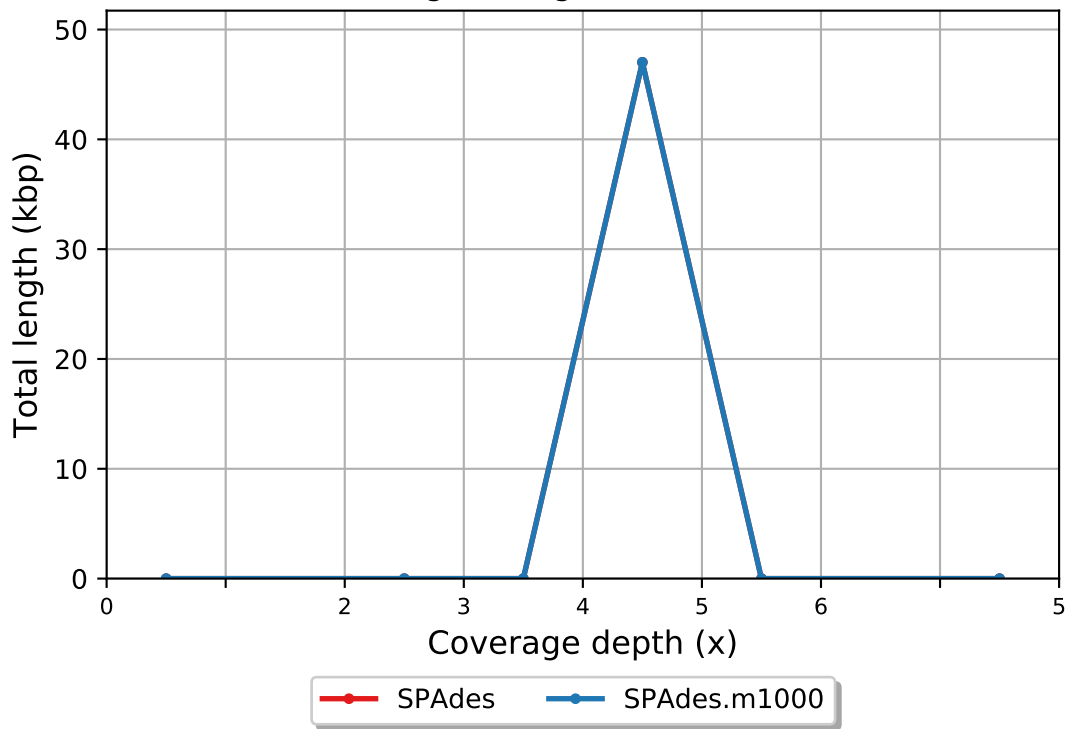


IDBAUD

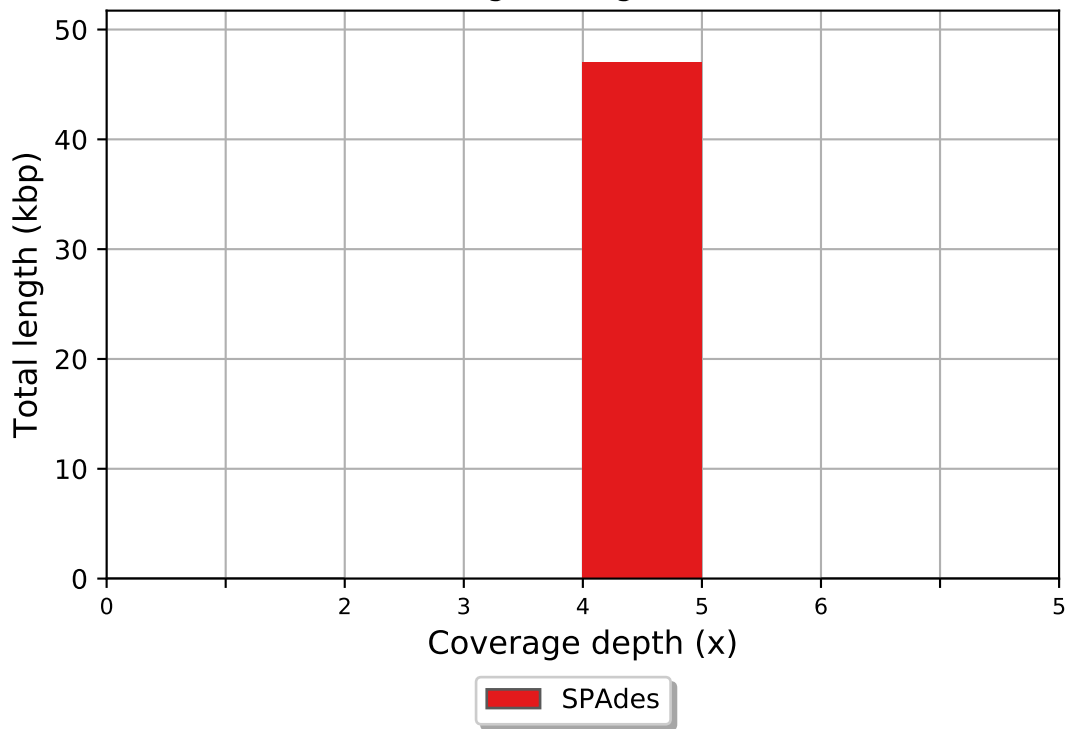
IDBAUD.m1000 GC content



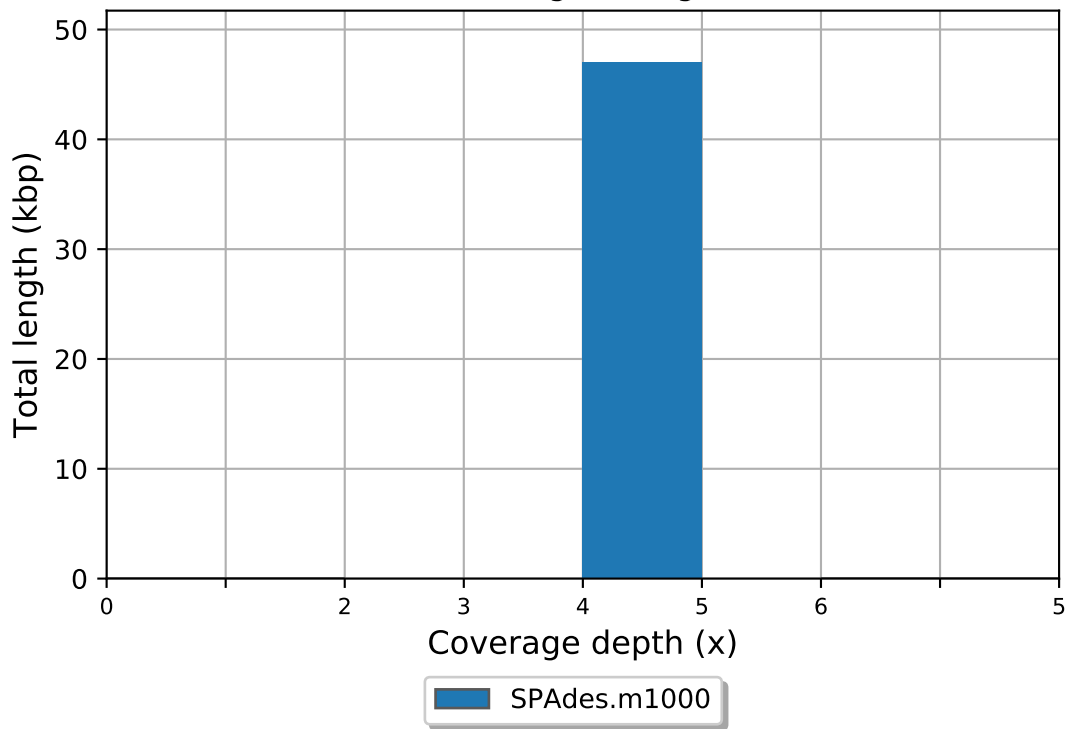
Coverage histogram (bin size: 1x)



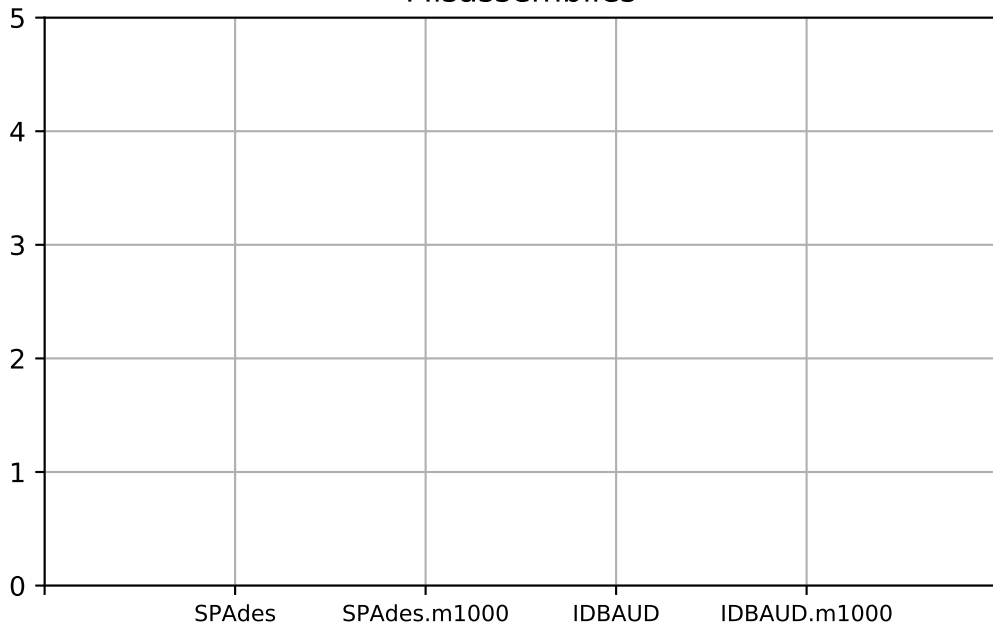
SPAdes coverage histogram (bin size: 1x)



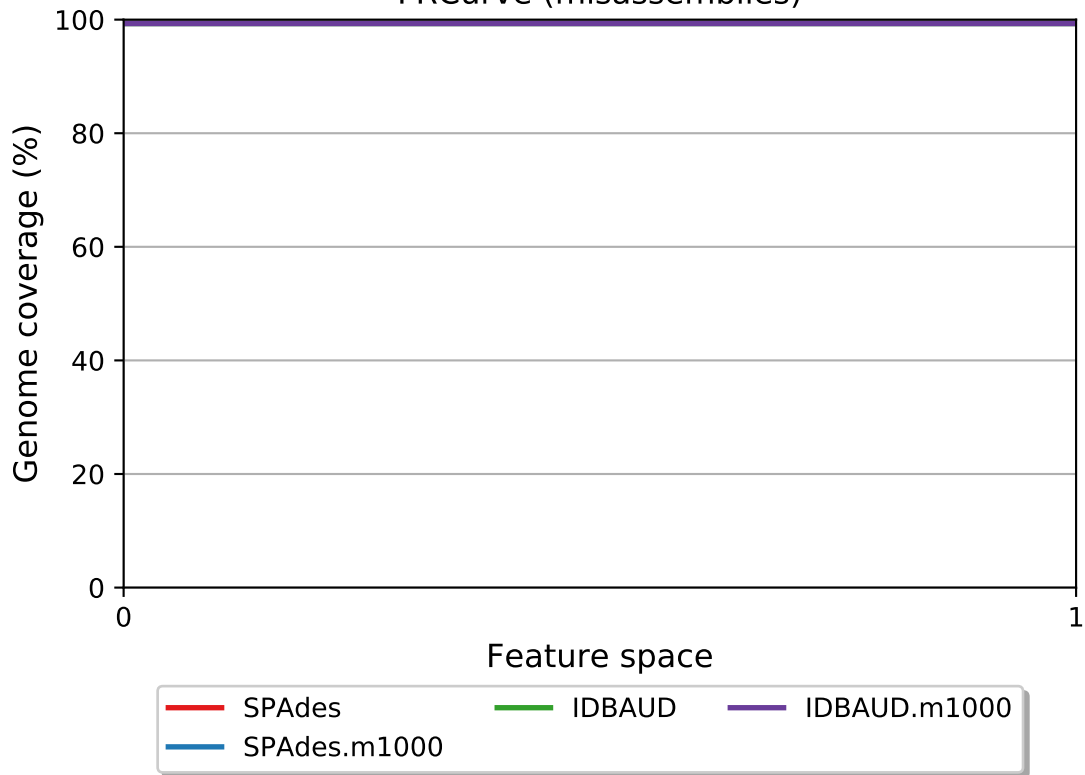
SPAdes.m1000 coverage histogram (bin size: 1x)



## Misassemblies

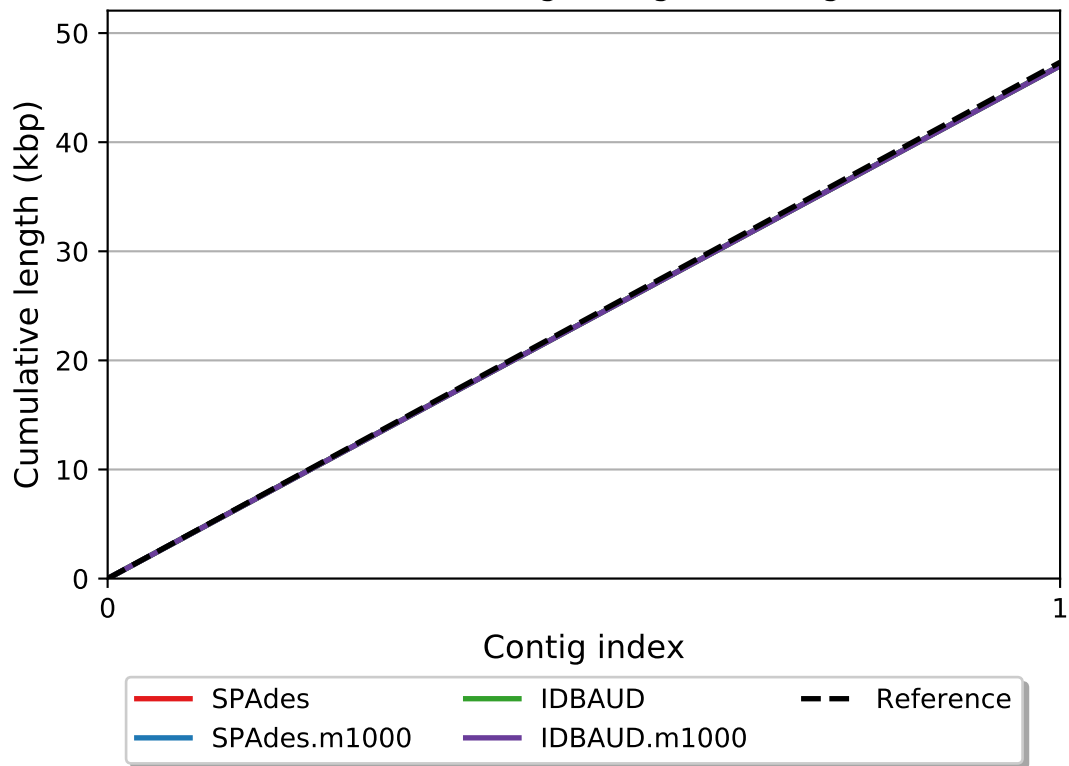


FRCurve (misassemblies)

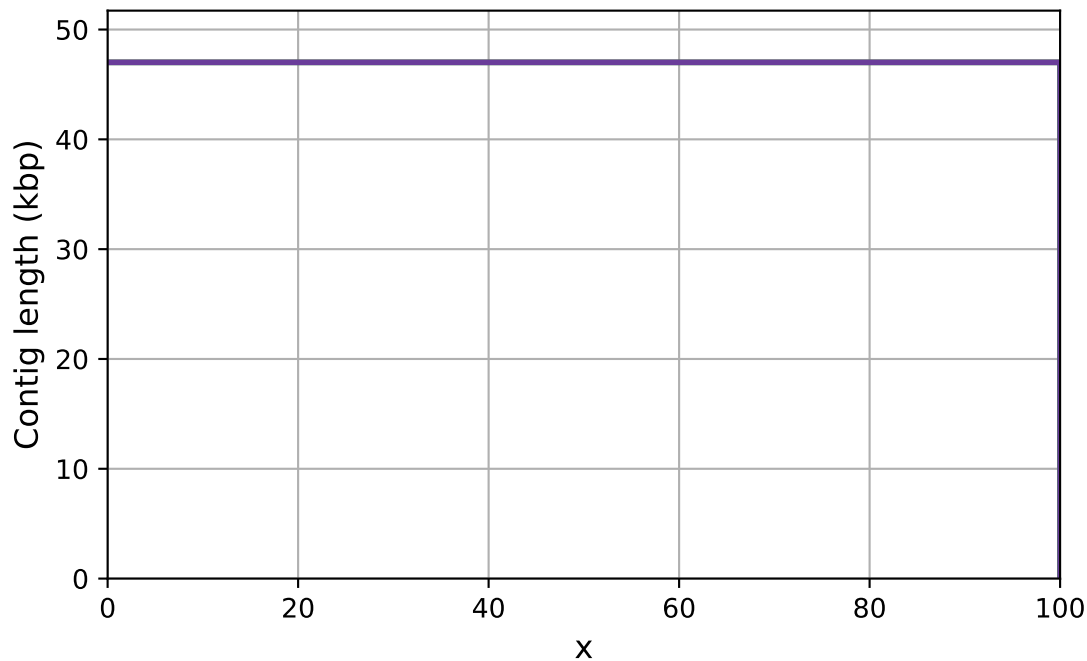




Cumulative length (aligned contigs)

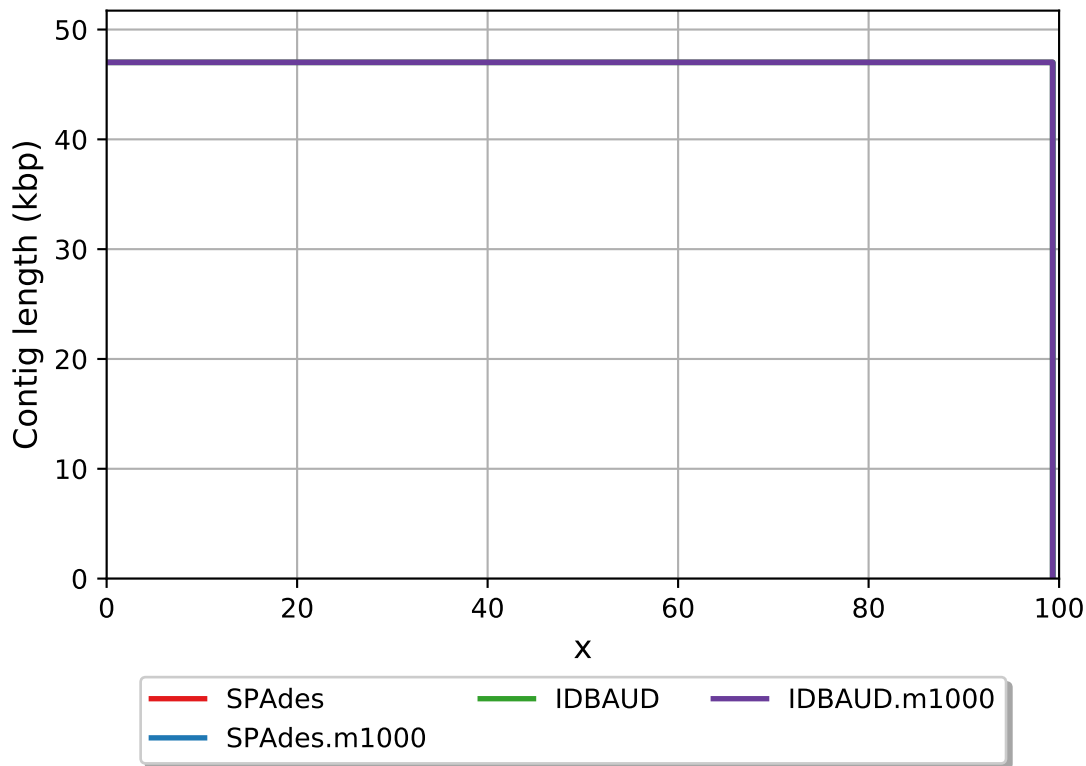


NAx



SPAdes IDBAUD IDBAUD.m1000  
SPAdes.m1000

## NGAx



Genome fraction, %

