

## 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)	26191	26191	25903	25903
Total length (>= 5000 bp)	26191	26191	25903	25903
Total length (>= 10000 bp)	26191	26191	25903	25903
Total length (>= 25000 bp)	26191	26191	25903	25903
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	26191	26191	25903	25903
Total length	26191	26191	25903	25903
Reference length	26111	26111	26111	26111
GC (%)	46.31	46.31	46.32	46.32
Reference GC (%)	46.31	46.31	46.31	46.31
N50	26191	26191	25903	25903
NG50	26191	26191	25903	25903
N75	26191	26191	25903	25903
NG75	26191	26191	25903	25903
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	0	0	0	0
# 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 (%)	99.981	99.981	99.203	99.203
Duplication ratio	1.003	1.003	1.000	1.000
# N's per 100 kbp	381.81	381.81	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	0.00
# indels per 100 kbp	3.83	3.83	3.86	3.86
Largest alignment	26191	26191	25903	25903
Total aligned length	26191	26191	25903	25903
NA50	26191	26191	25903	25903
NGA50	26191	26191	25903	25903
NA75	26191	26191	25903	25903
NGA75	26191	26191	25903	25903
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	0	0	0	0
# 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	1	1	1	1
# indels (<= 5 bp)	0	0	0	0
# indels (> 5 bp)	1	1	1	1
Indels length	85	85	8	8

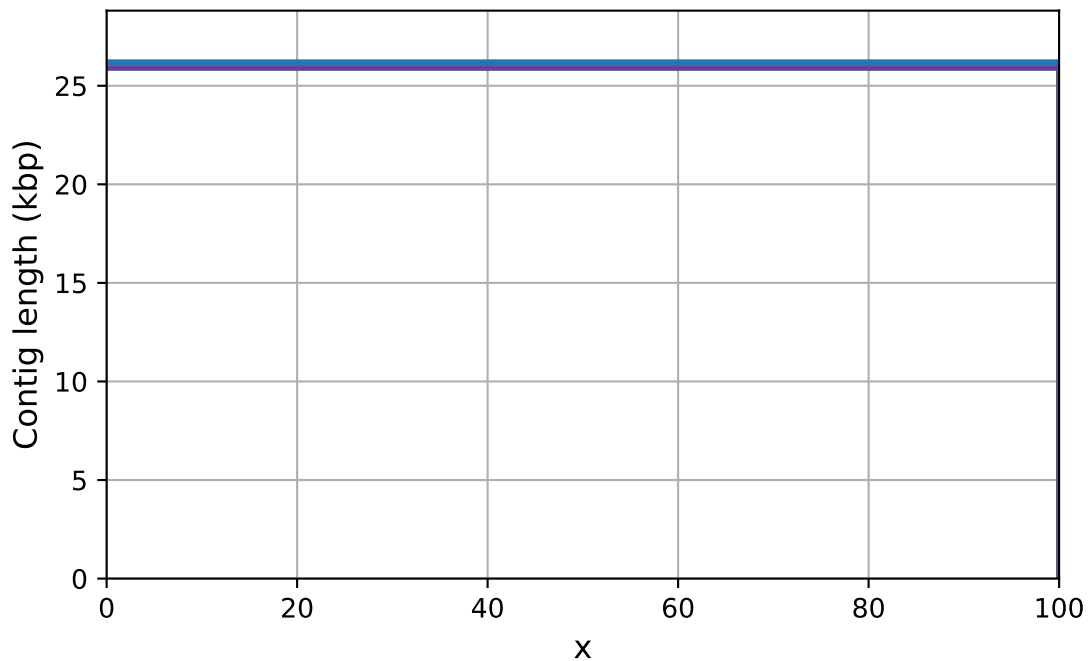
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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	100	100	0	0

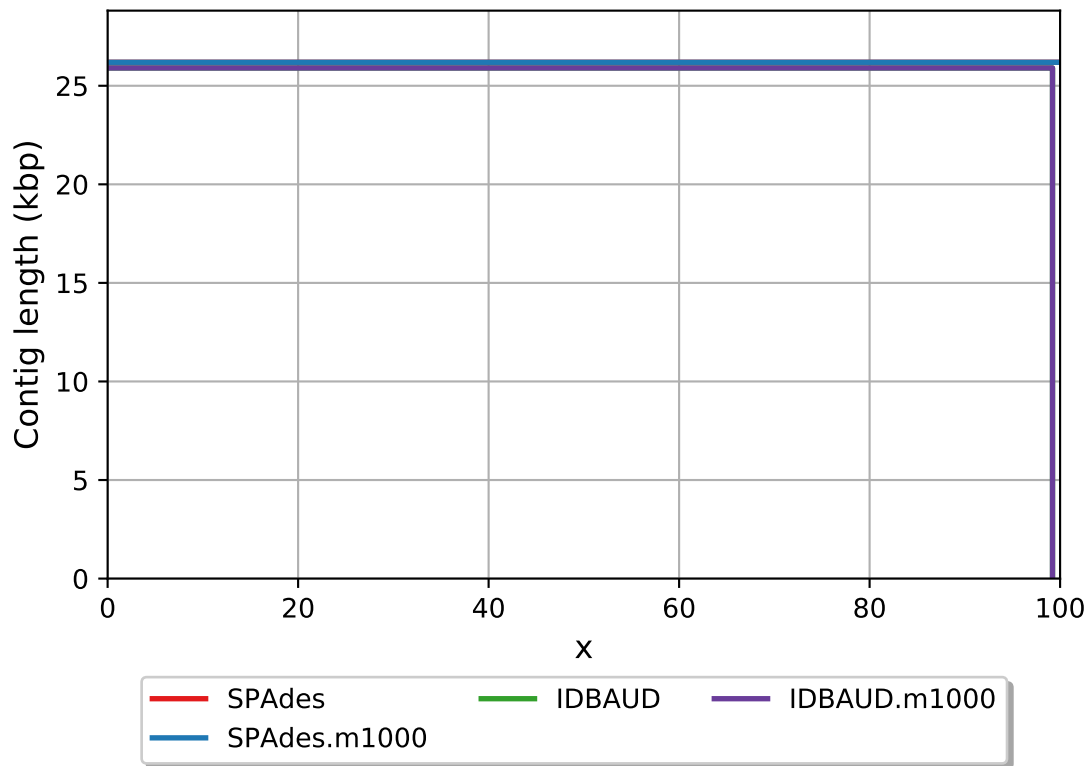
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

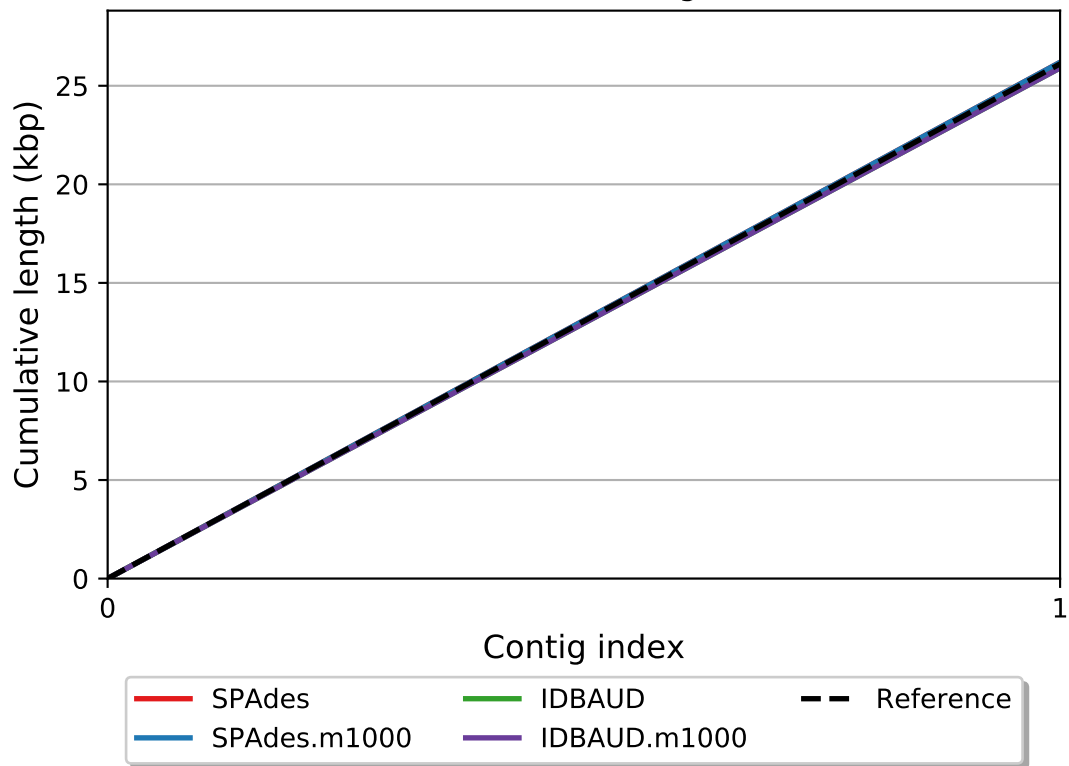


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— SPAdes.m1000

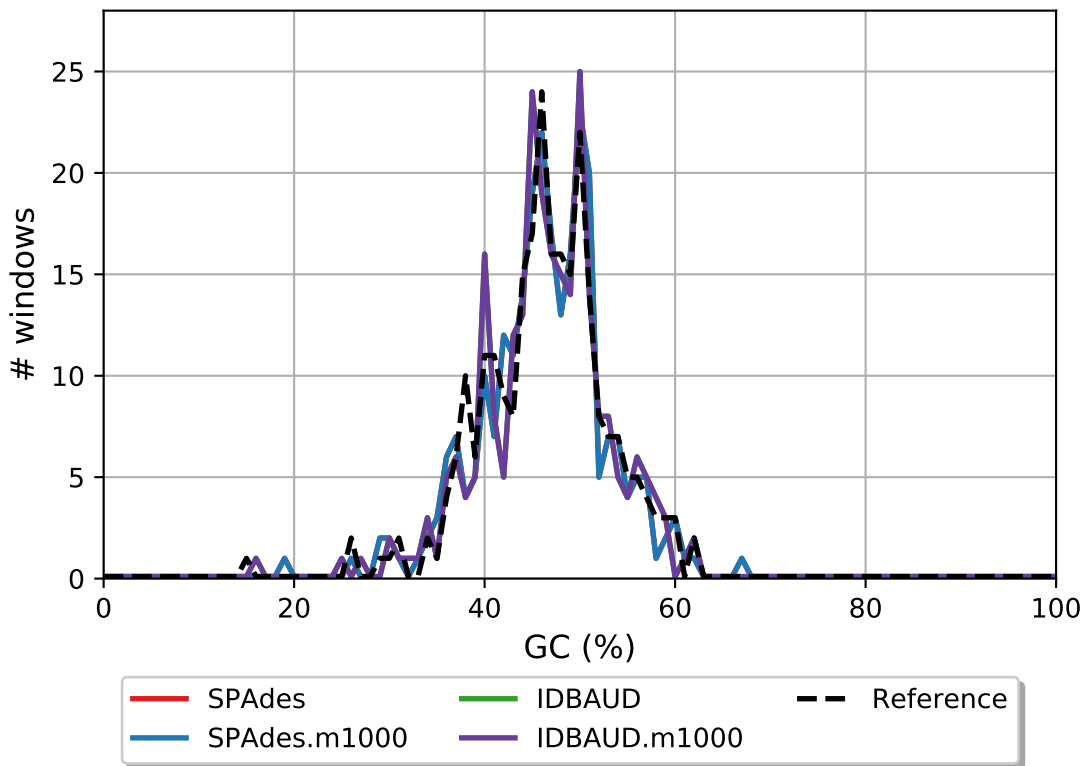
# NGx



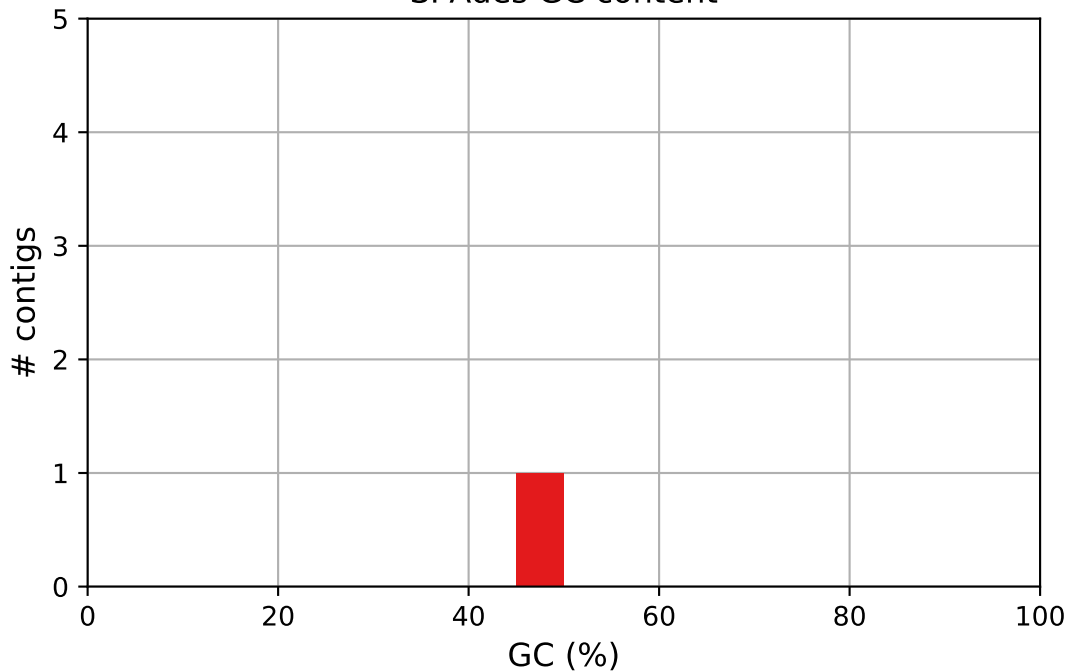
Cumulative length



GC content

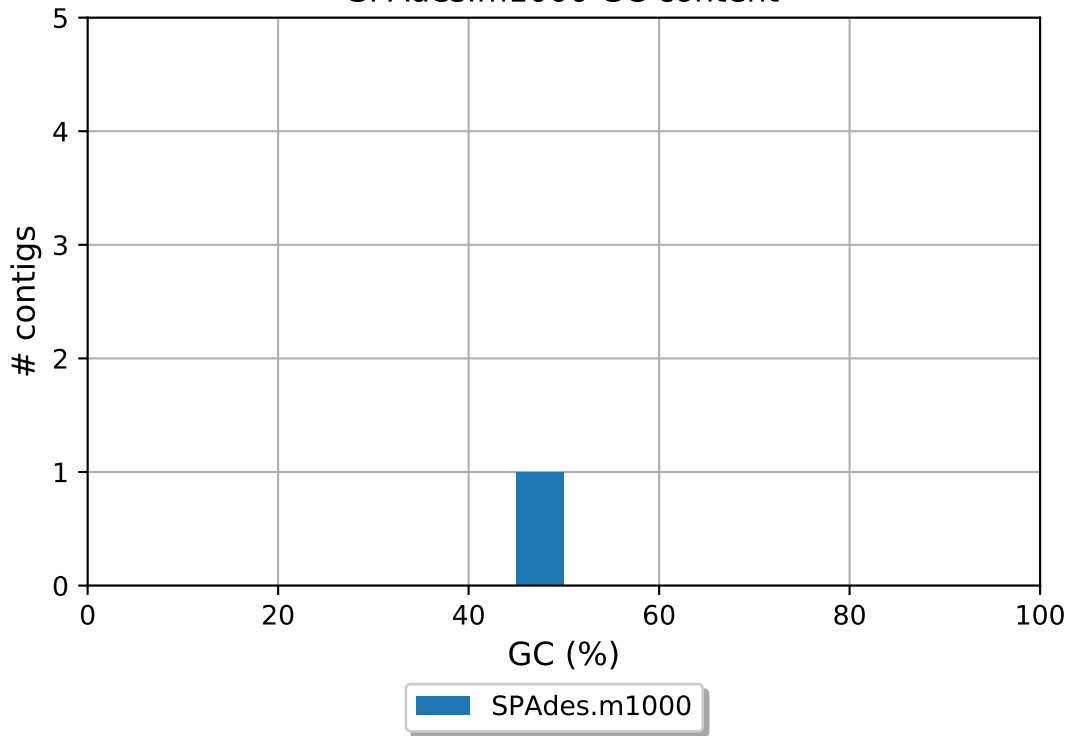


# SPAdes GC content

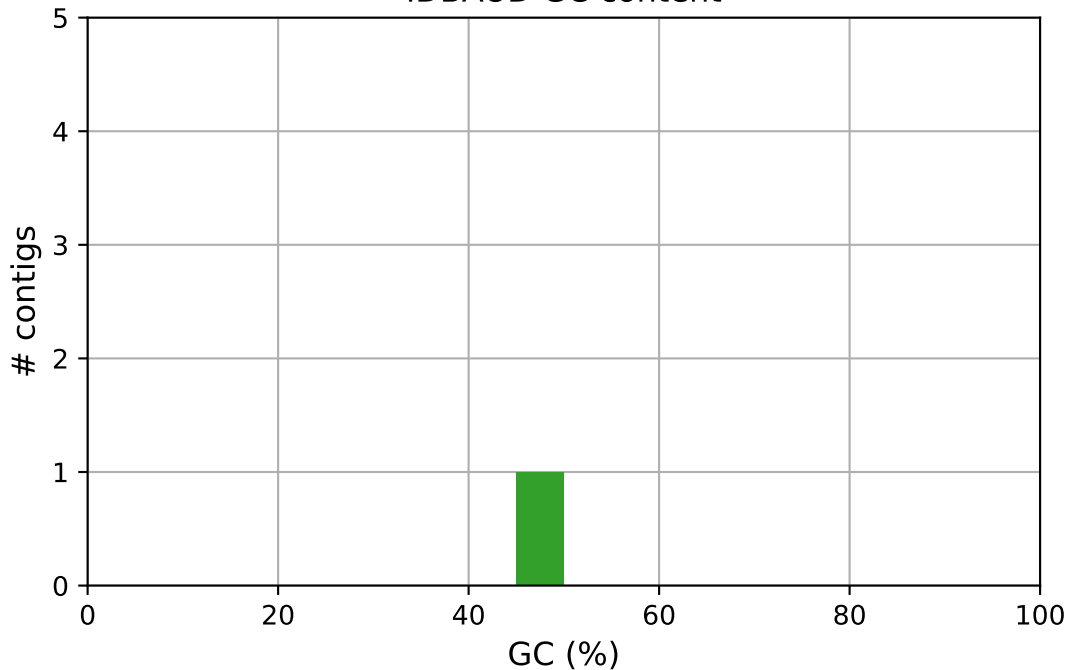


SPAdes

SPAdes.m1000 GC content

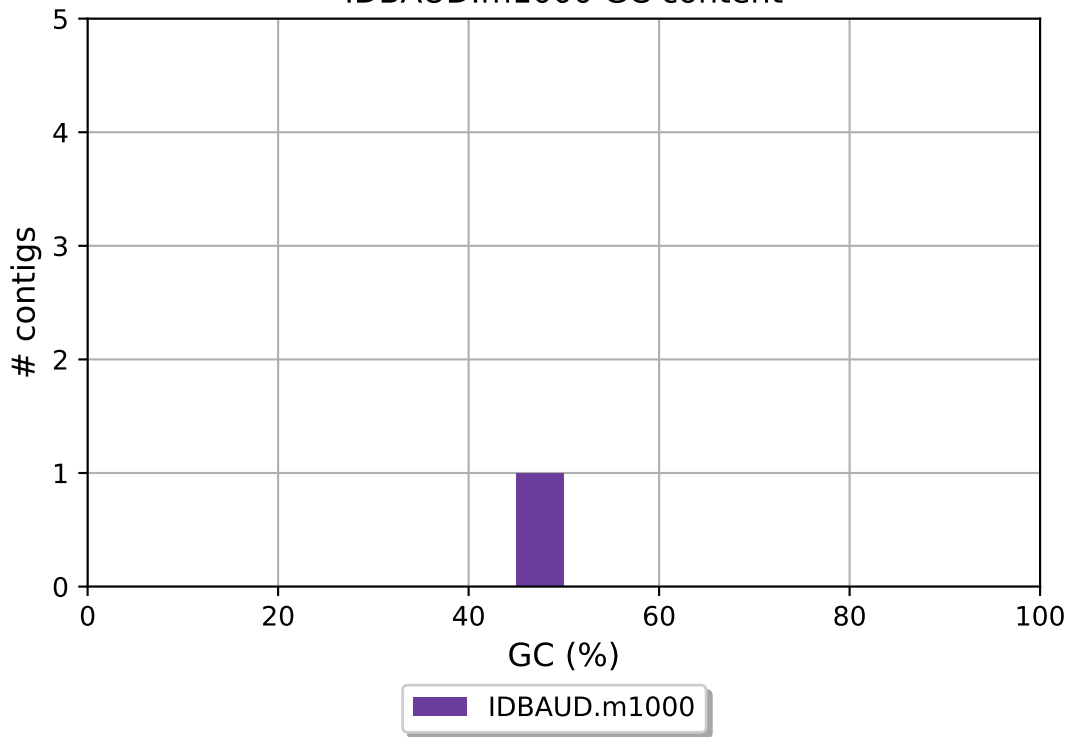


# IDBAUD GC content

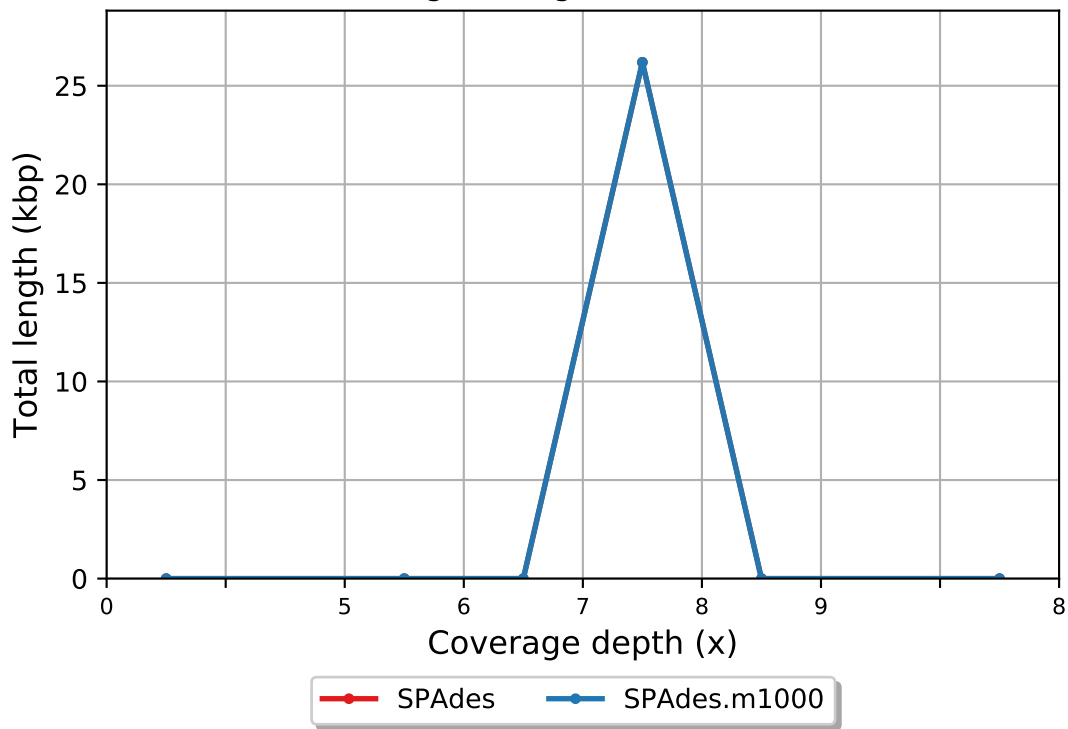


IDBAUD

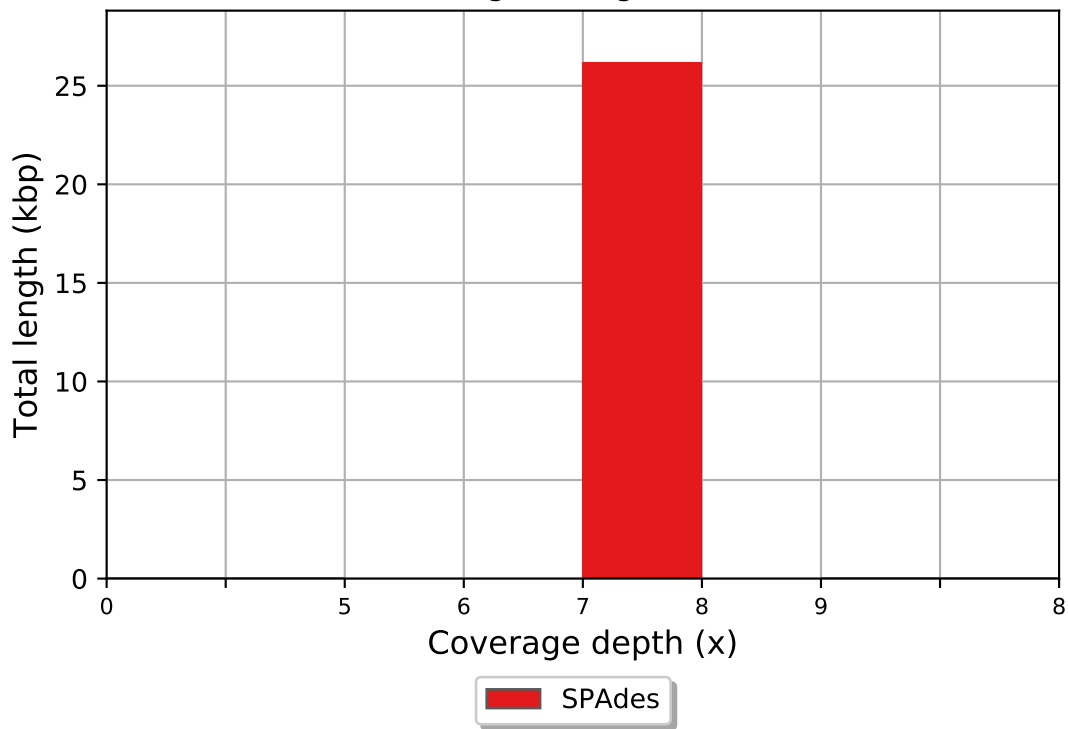
IDBAUD.m1000 GC content



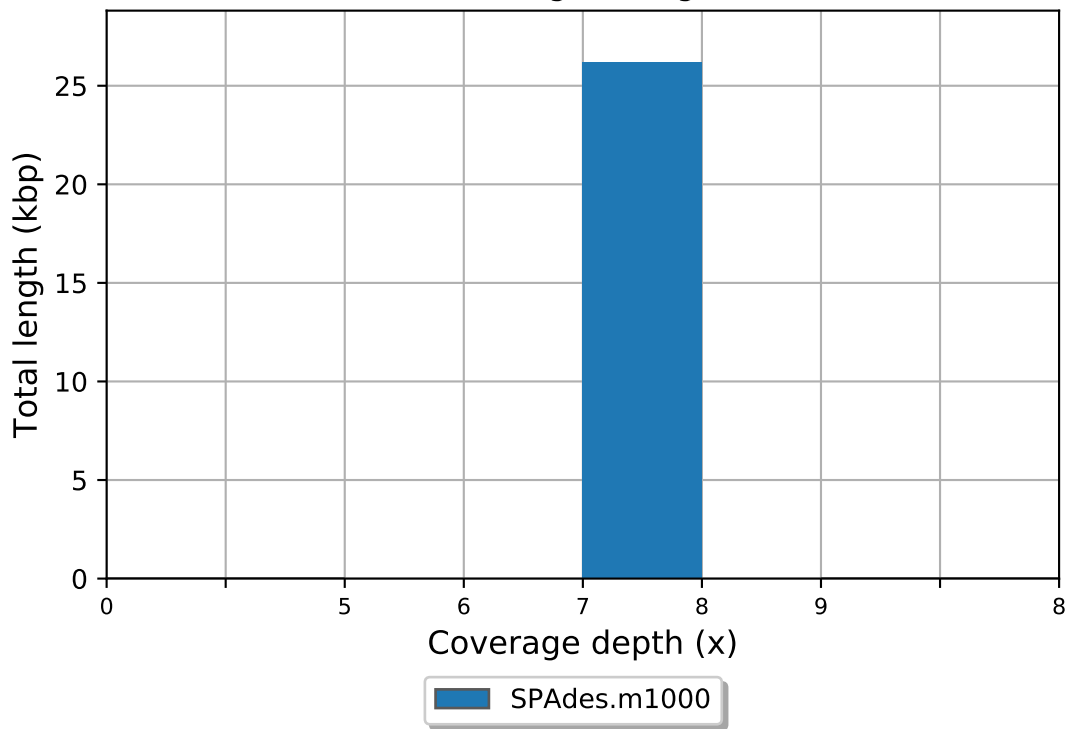
Coverage histogram (bin size: 1x)



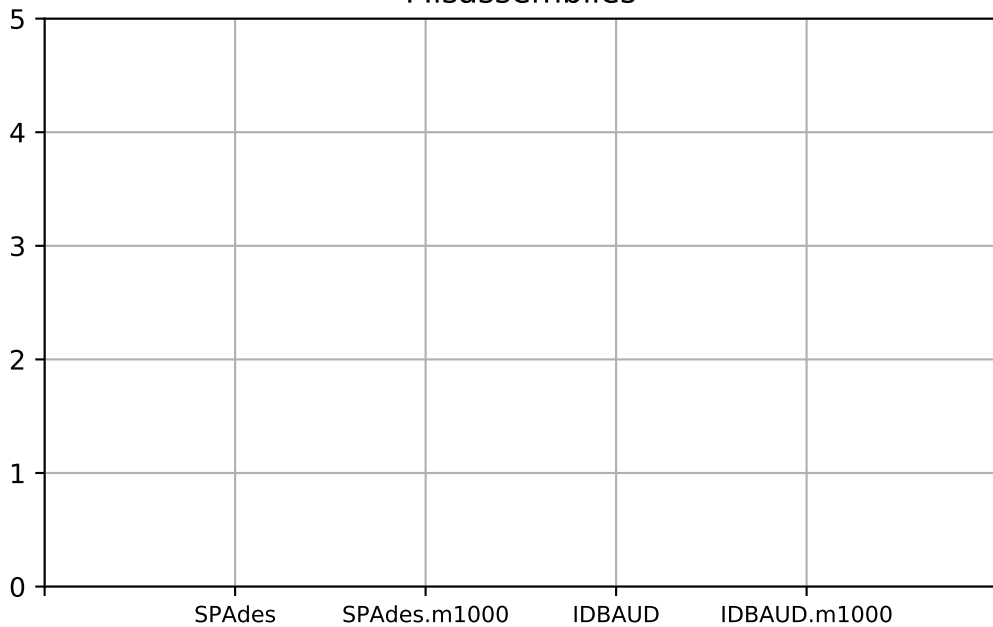
SPAdes coverage histogram (bin size: 1x)



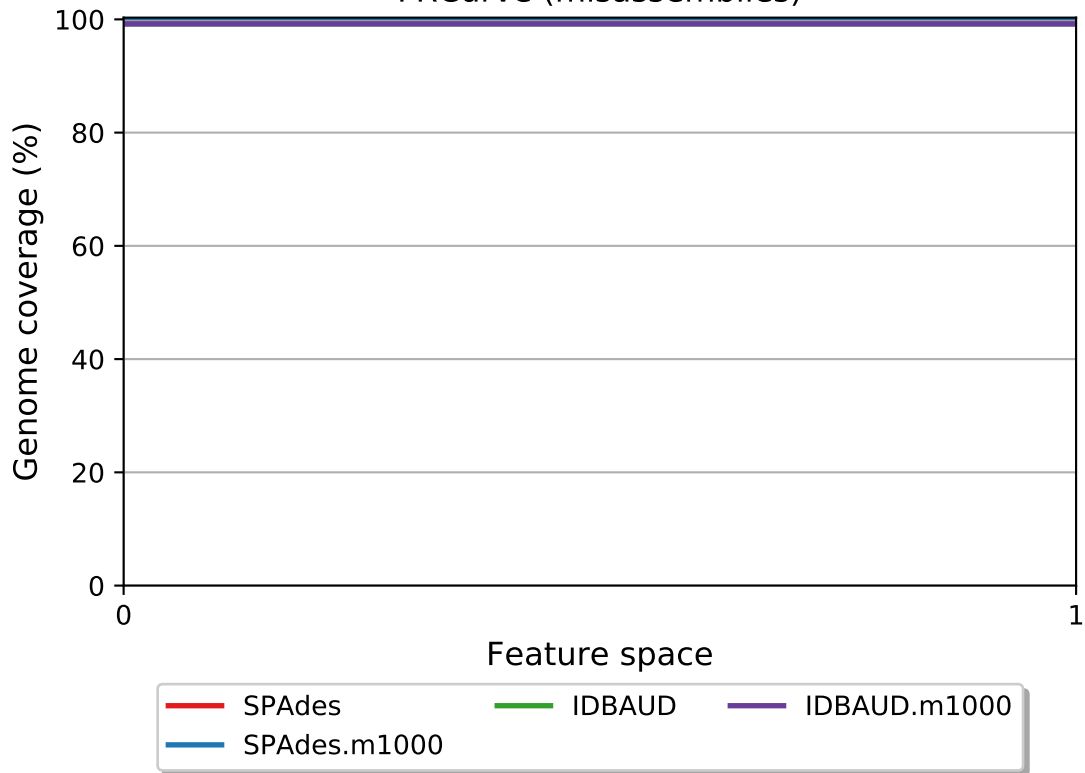
SPAdes.m1000 coverage histogram (bin size: 1x)



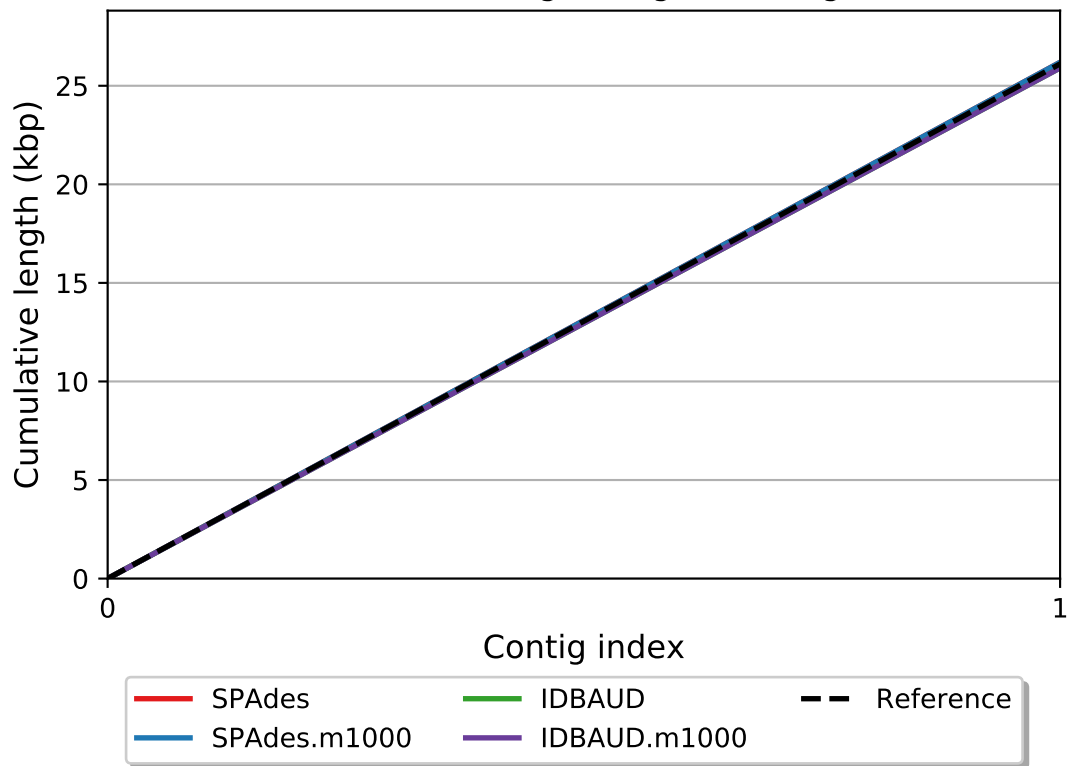
## Misassemblies



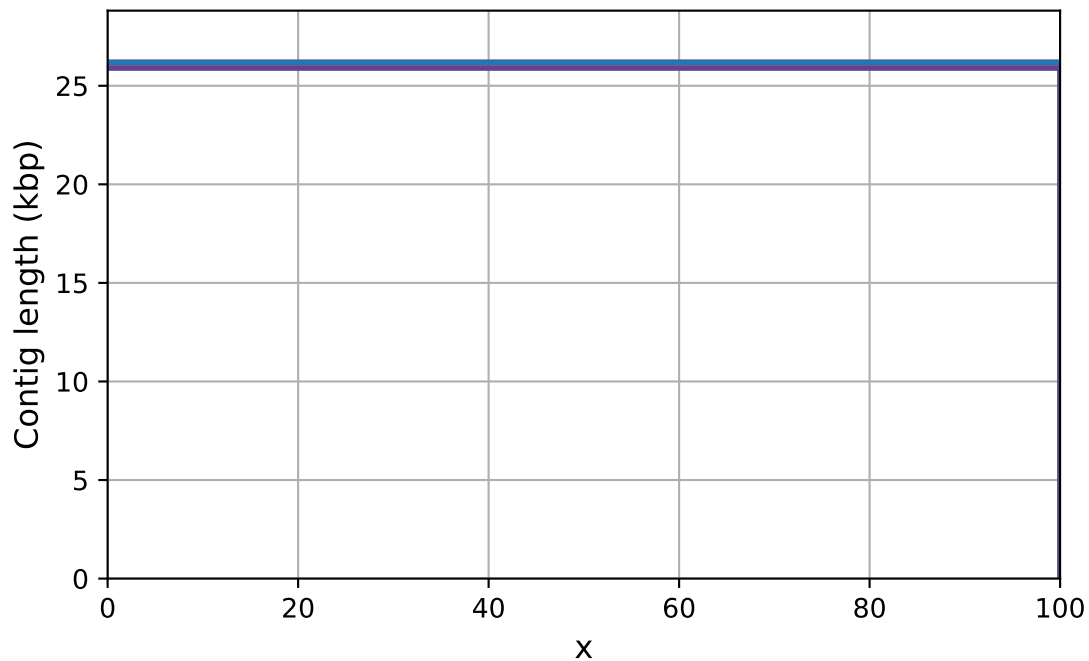
FRCurve (misassemblies)



Cumulative length (aligned contigs)

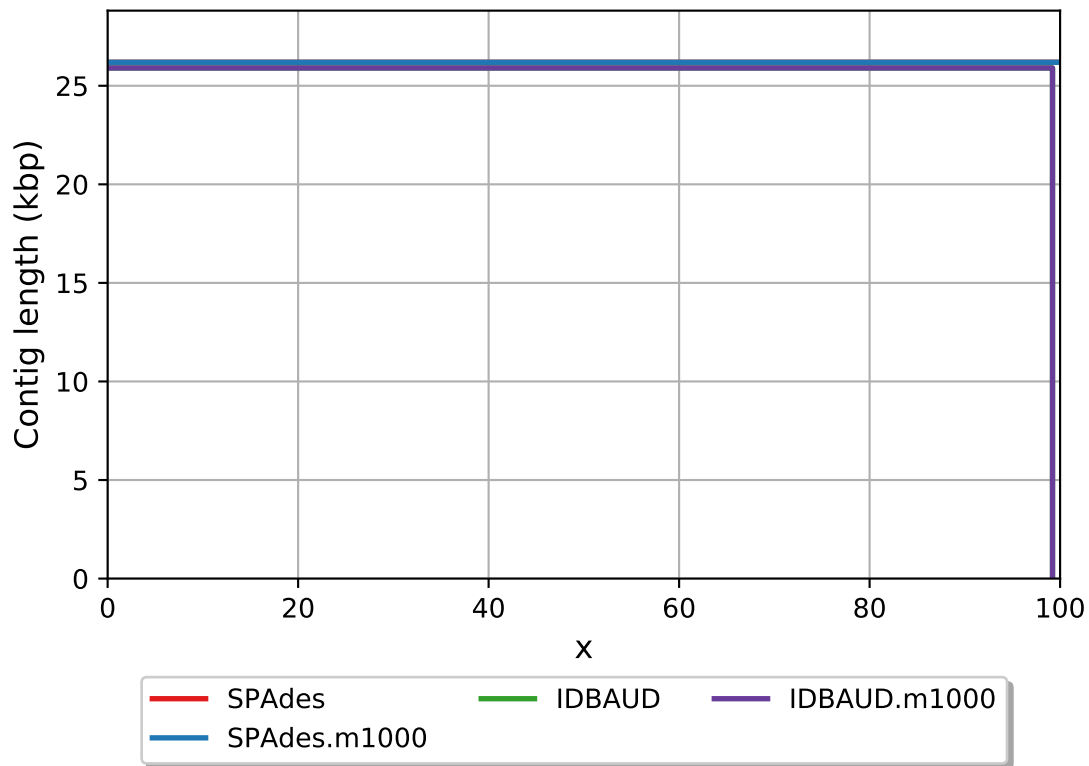


NAx

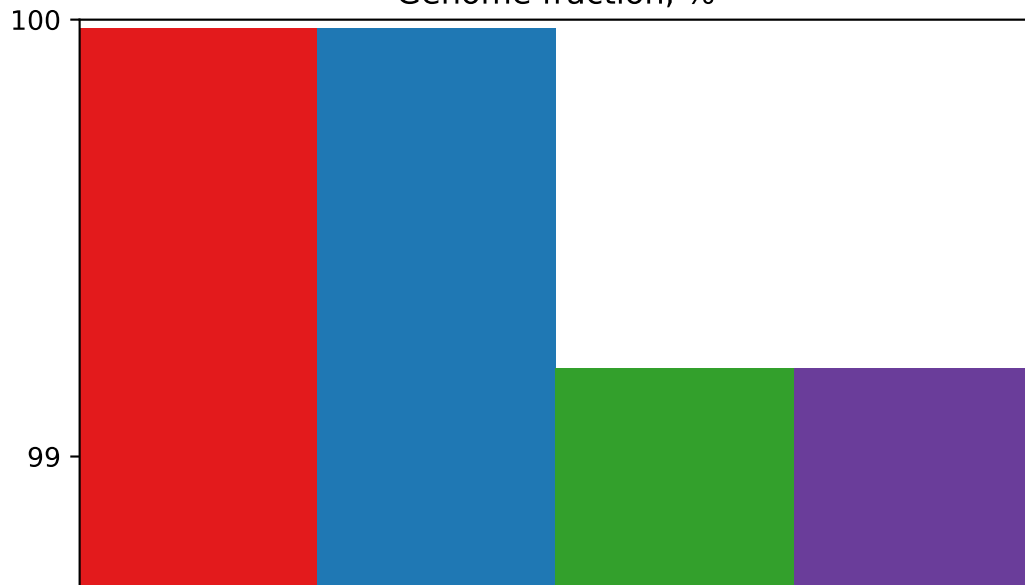


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— SPAdes.m1000

# NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000