

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)	42263	42263	42261	42261
Total length (>= 5000 bp)	42263	42263	42261	42261
Total length (>= 10000 bp)	42263	42263	42261	42261
Total length (>= 25000 bp)	42263	42263	42261	42261
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	42263	42263	42261	42261
Total length	42263	42263	42261	42261
Reference length	42271	42271	42271	42271
GC (%)	64.89	64.89	64.89	64.89
Reference GC (%)	64.89	64.89	64.89	64.89
N50	42263	42263	42261	42261
NG50	42263	42263	42261	42261
N75	42263	42263	42261	42261
NG75	42263	42263	42261	42261
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	99.976	99.976
Duplication ratio	1.000	1.000	1.000	1.000
# 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	42263	42263	42261	42261
Total aligned length	42263	42263	42261	42261
NA50	42263	42263	42261	42261
NGA50	42263	42263	42261	42261
NA75	42263	42263	42261	42261
NGA75	42263	42263	42261	42261
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	0	0	0	0
# indels (<= 5 bp)	0	0	0	0
# indels (> 5 bp)	0	0	0	0
Indels length	0	0	0	0

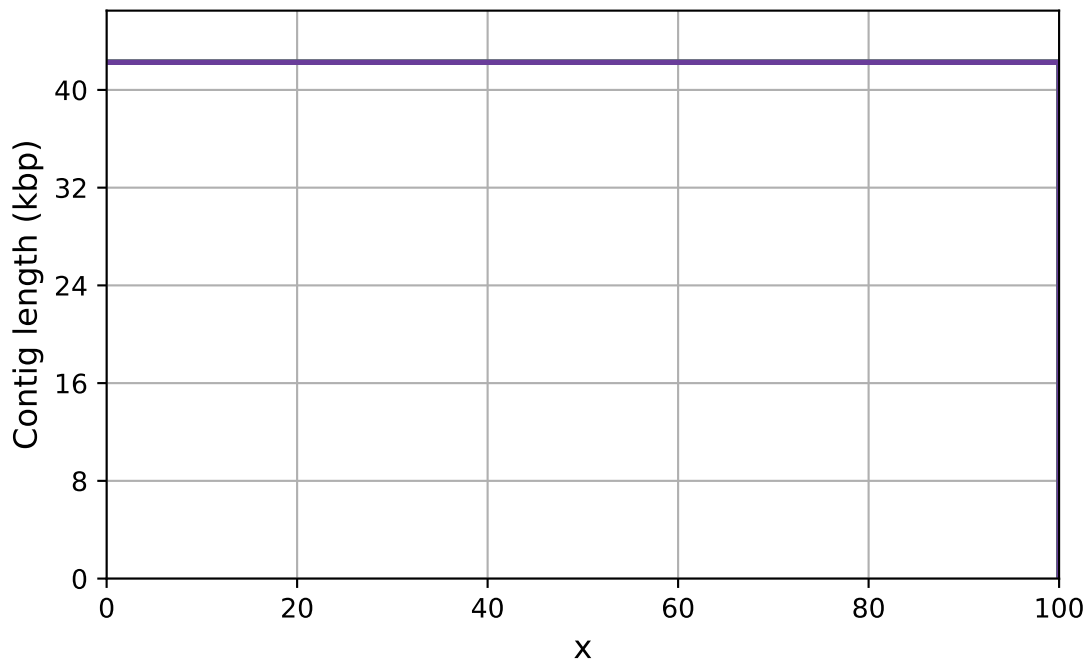
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

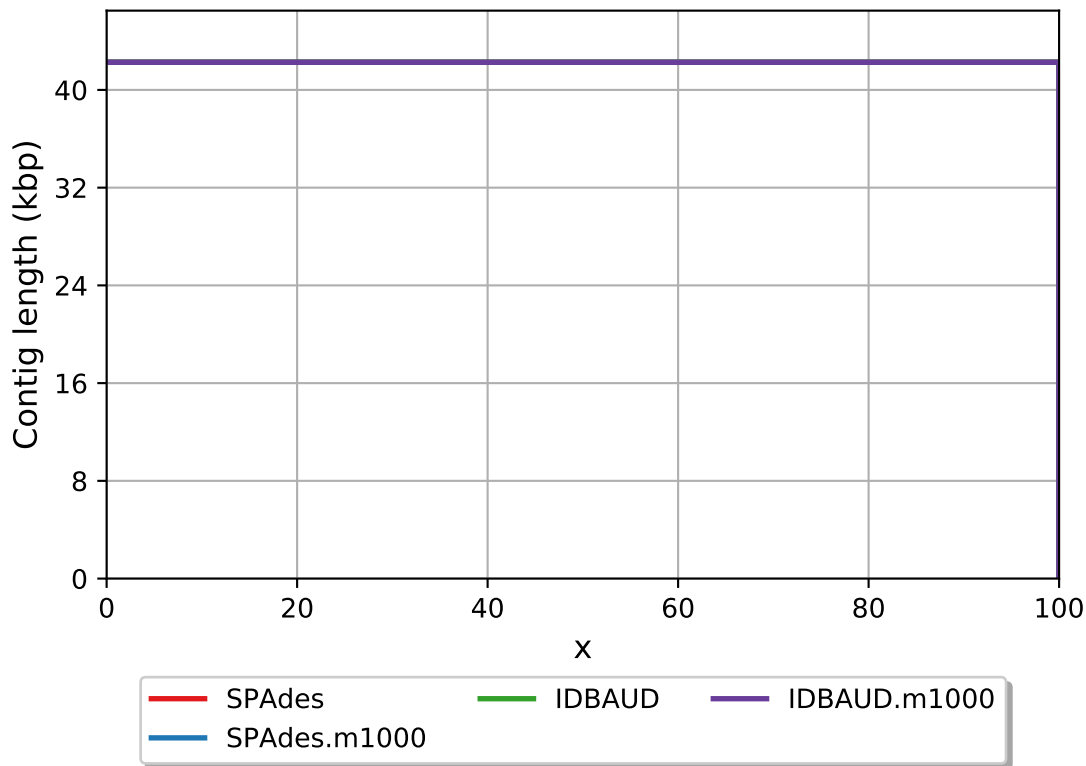
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

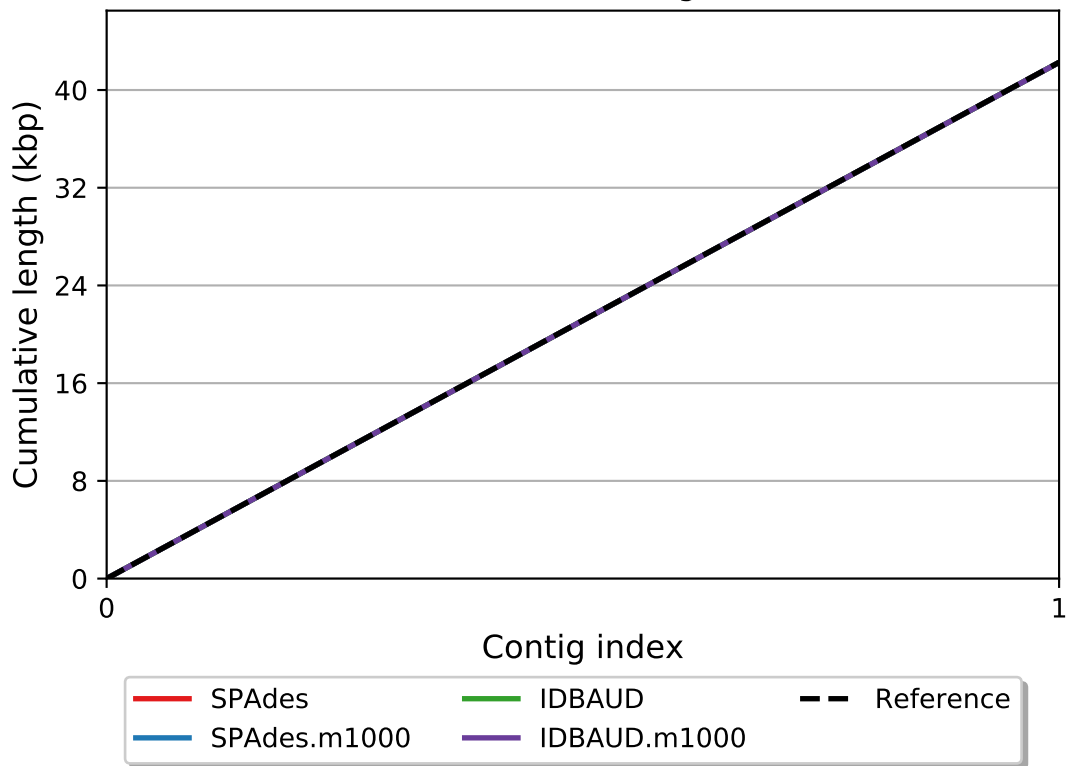


SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

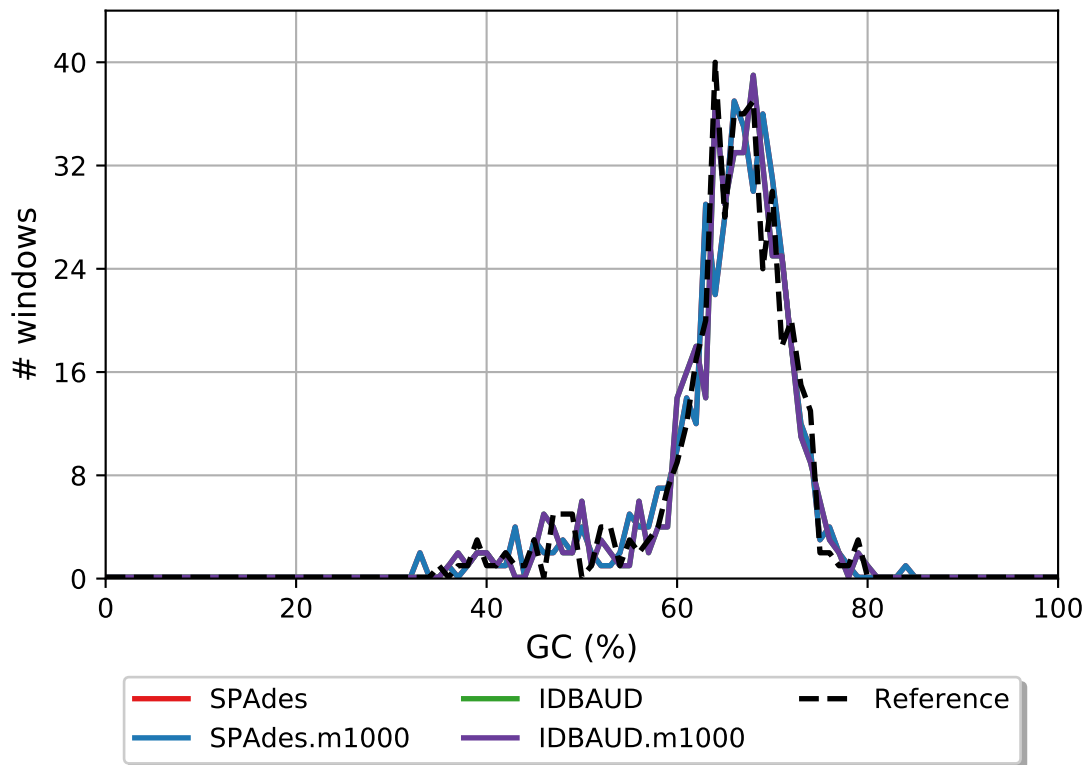
NGx



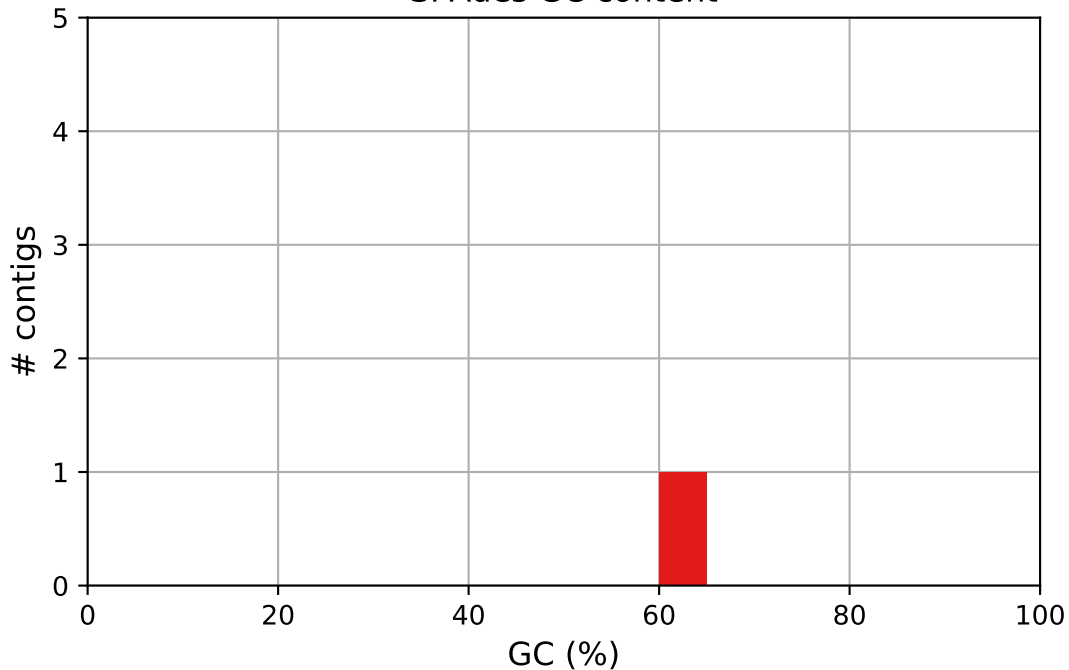
Cumulative length



GC content

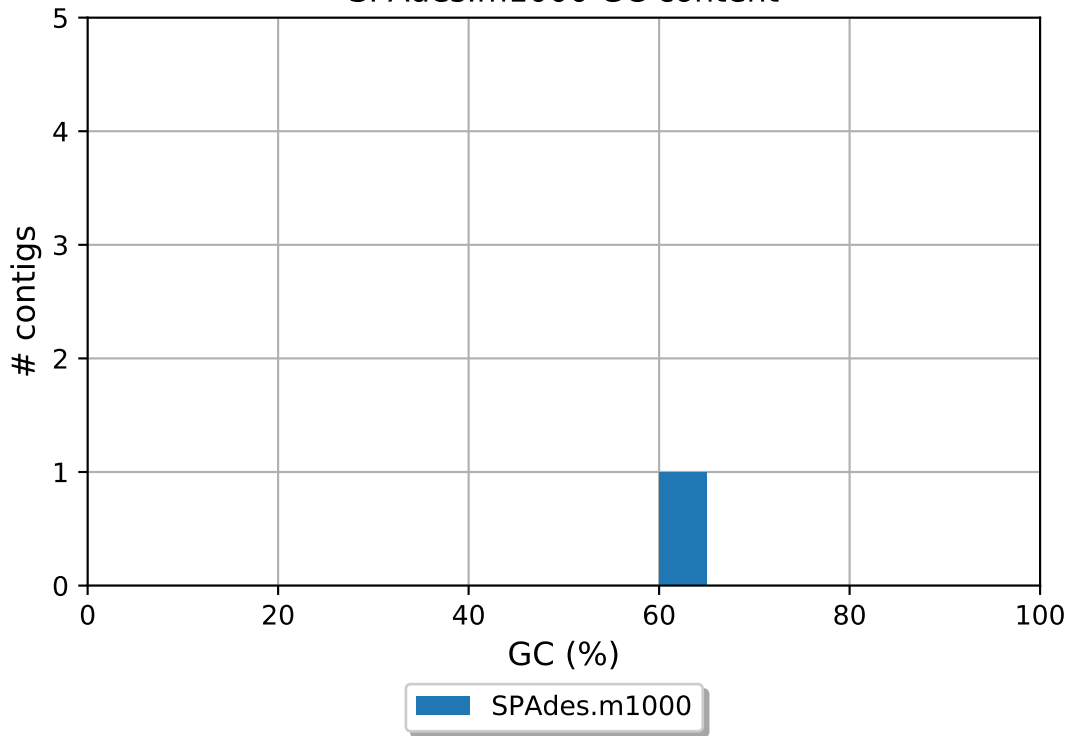


SPAdes GC content

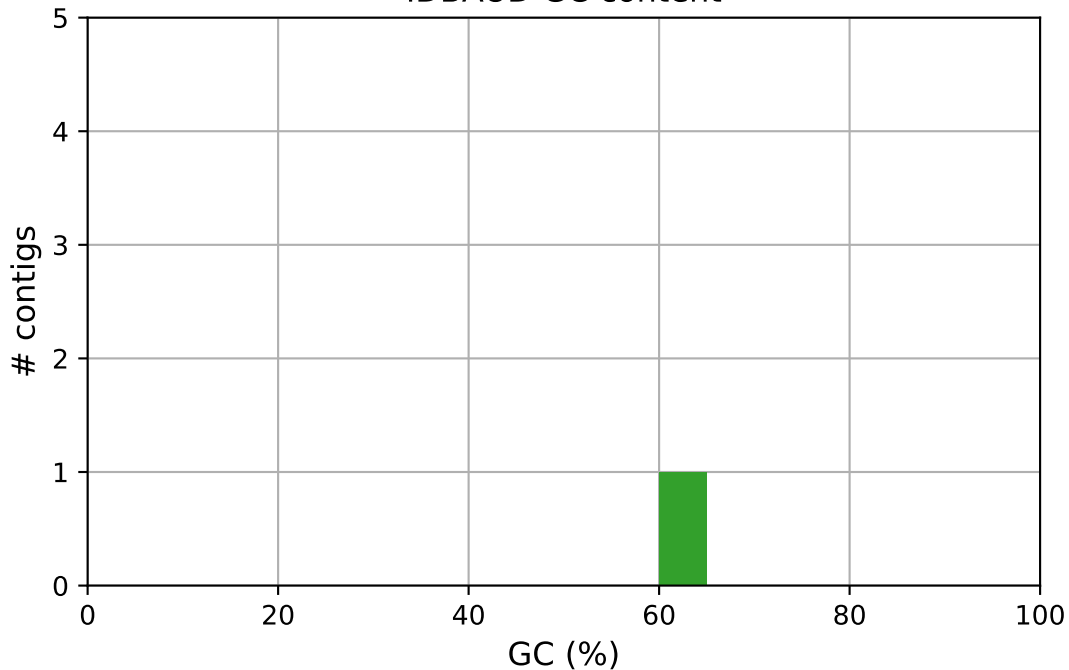


SPAdes

SPAdes.m1000 GC content

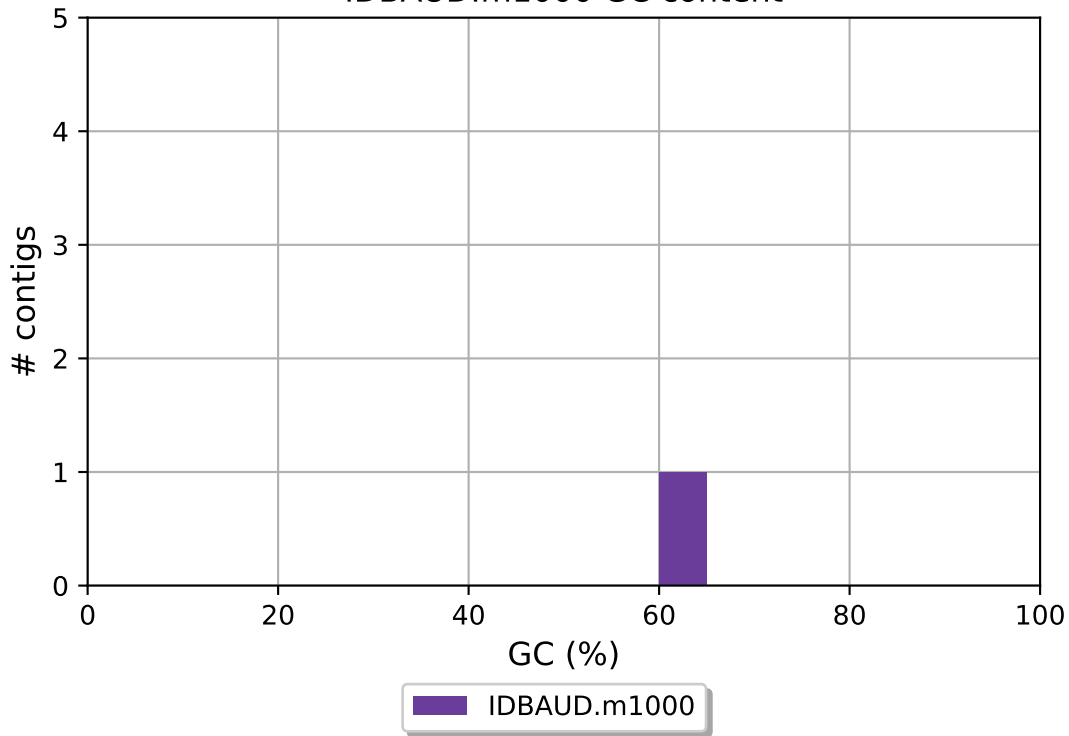


IDBAUD GC content

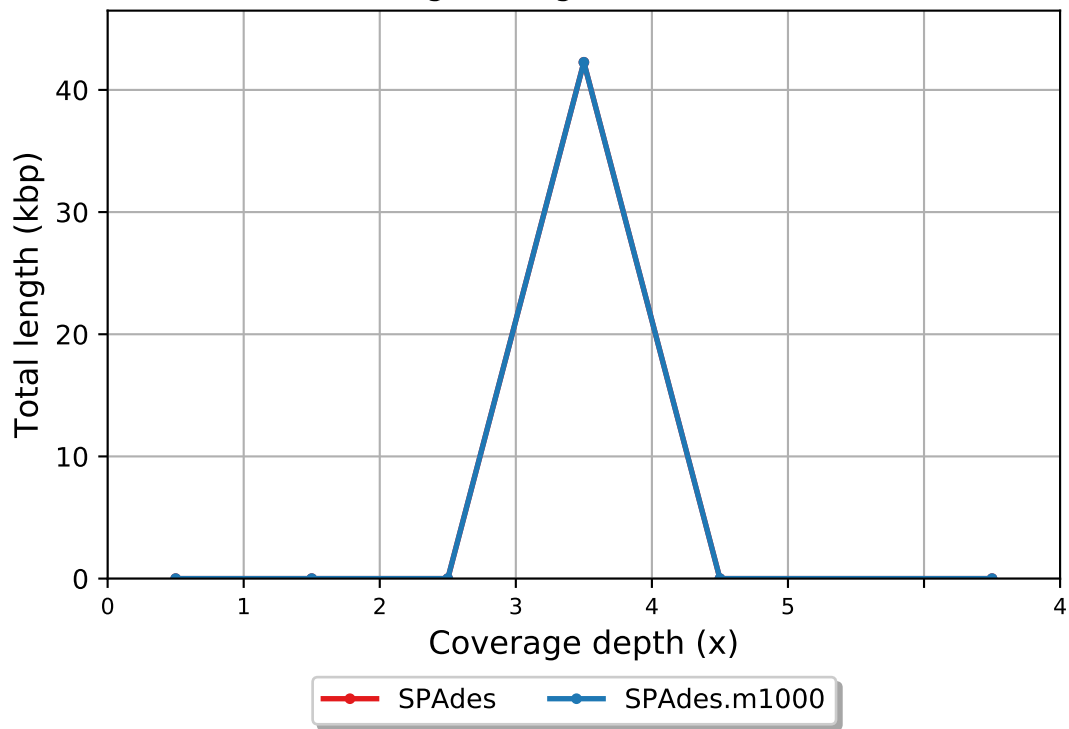


IDBAUD

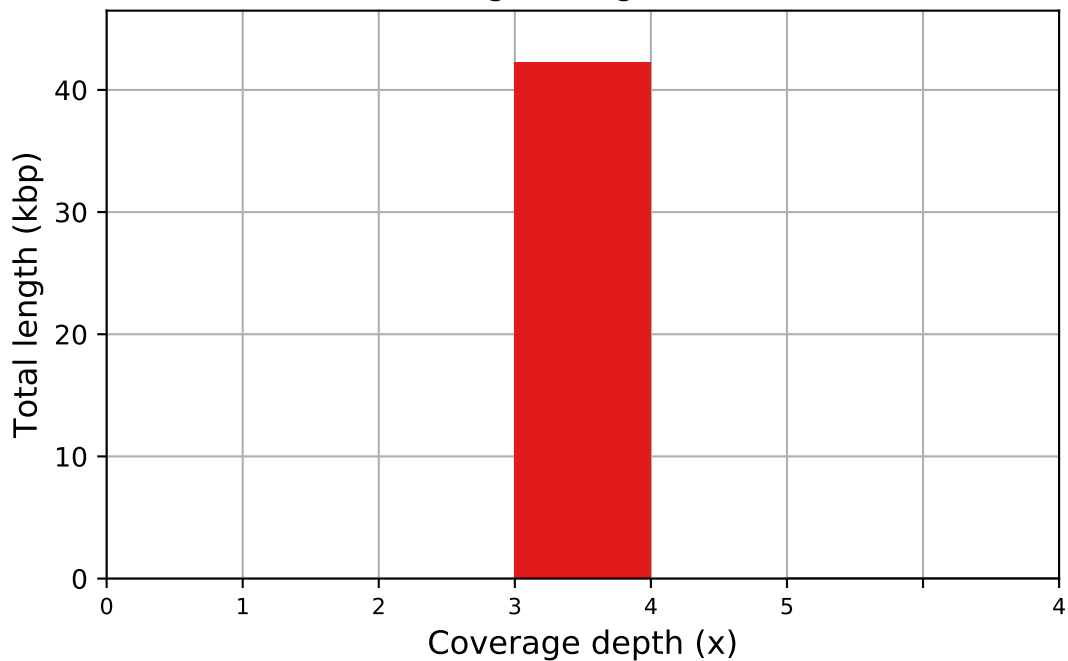
IDBAUD.m1000 GC content



Coverage histogram (bin size: 1x)

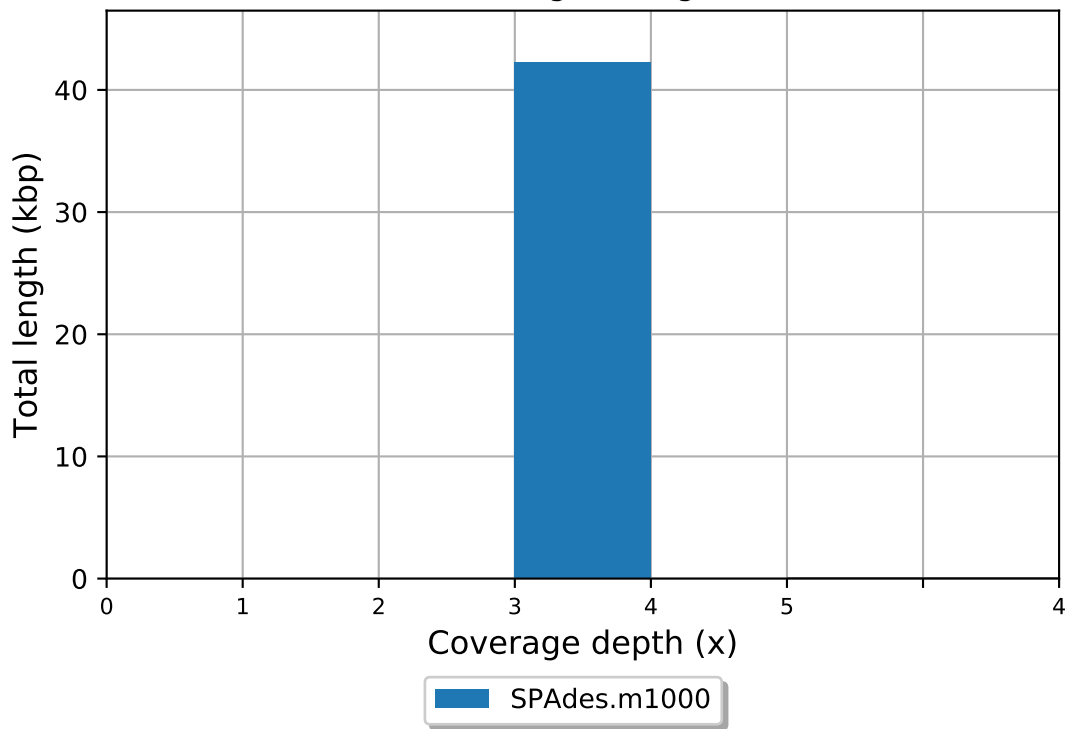


SPAdes coverage histogram (bin size: 1x)

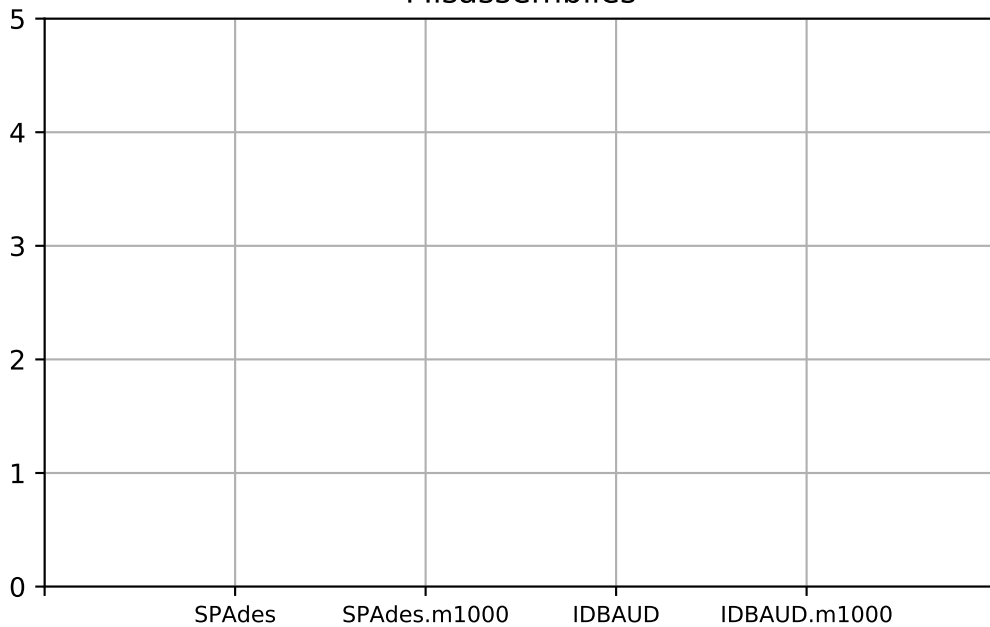


SPAdes

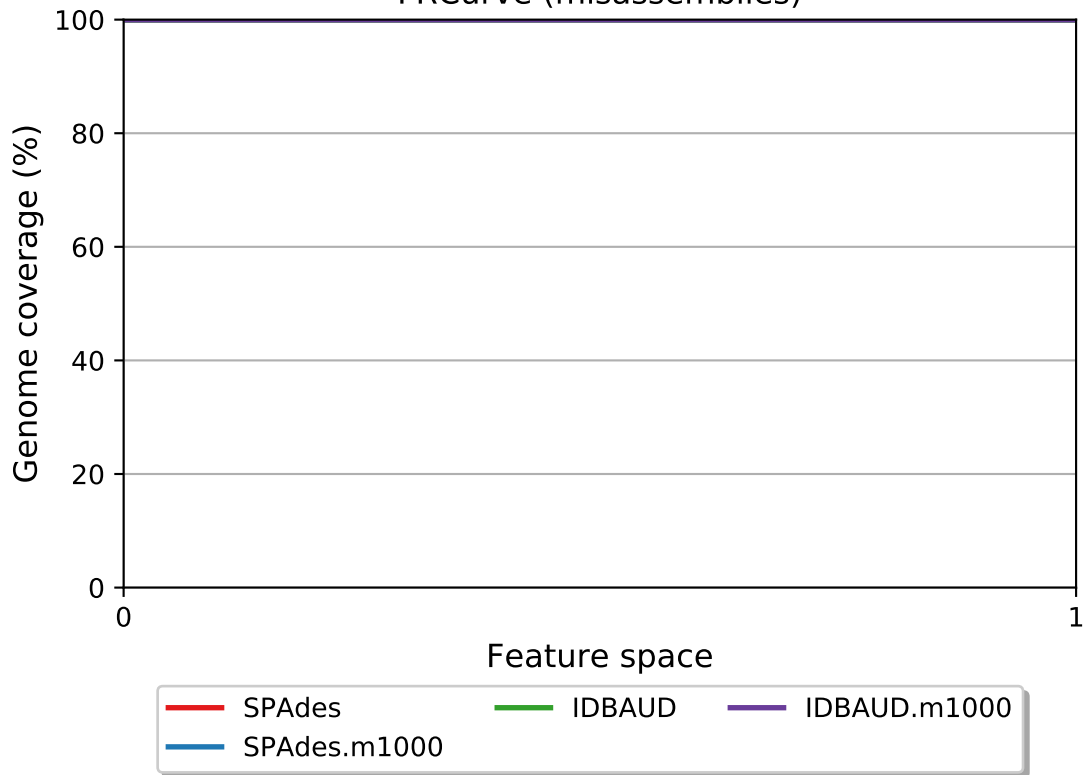
SPAdes.m1000 coverage histogram (bin size: 1x)



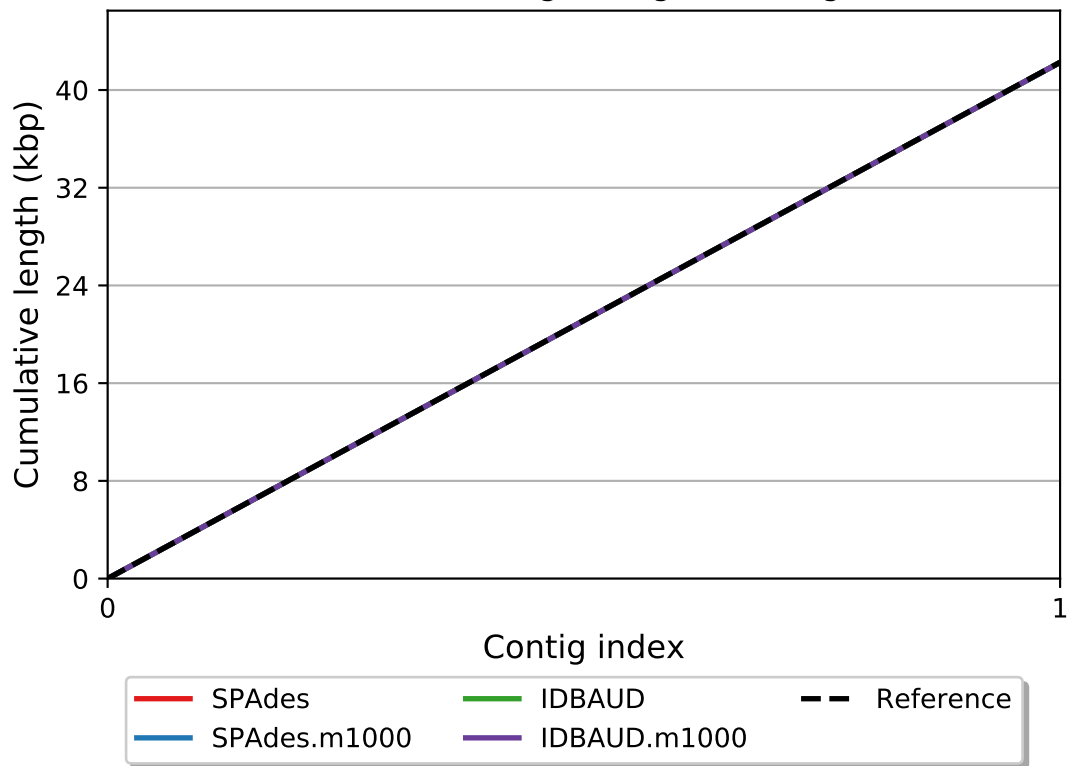
Misassemblies



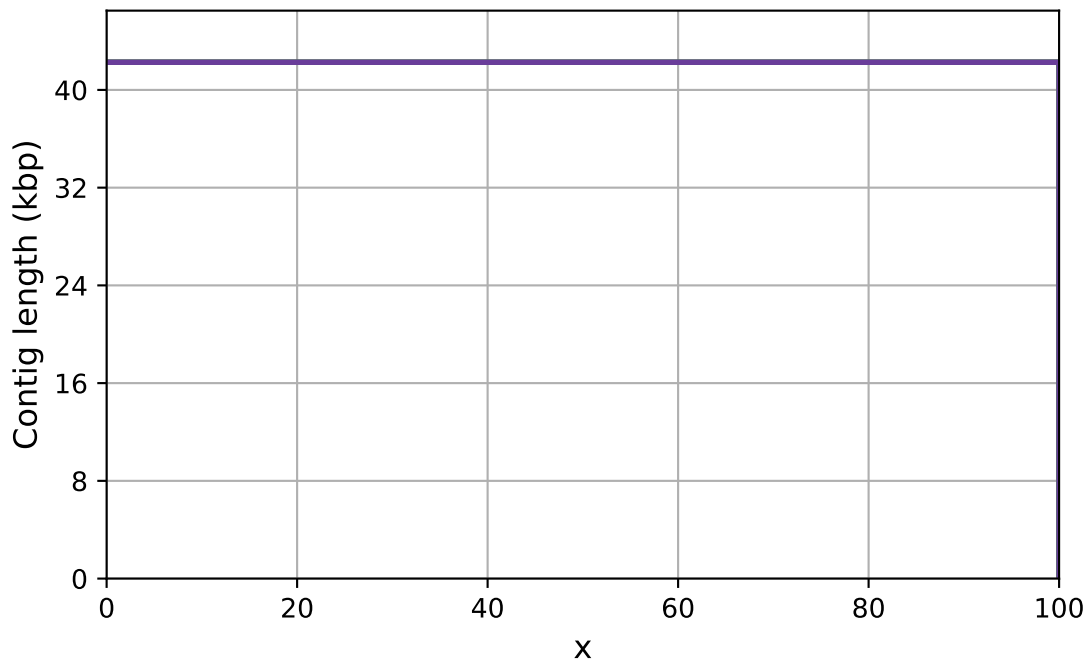
FRCurve (misassemblies)



Cumulative length (aligned contigs)

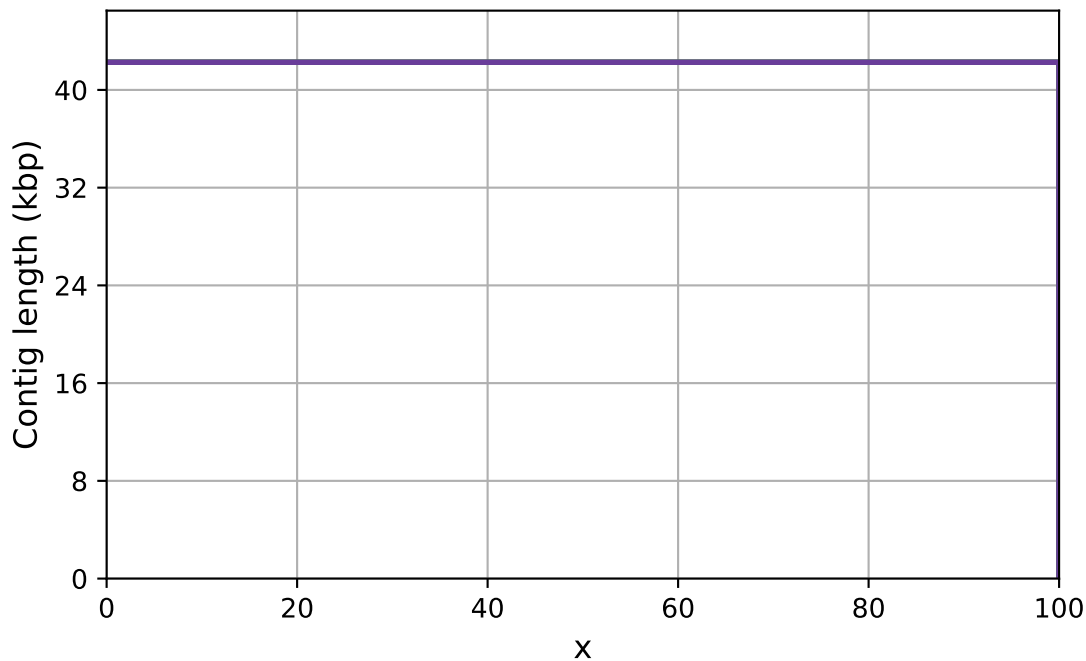


NAx



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

NGAx



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

Genome fraction, %

