

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)	41752	41752	41751	41751
Total length (>= 5000 bp)	41752	41752	41751	41751
Total length (>= 10000 bp)	41752	41752	41751	41751
Total length (>= 25000 bp)	41752	41752	41751	41751
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	41752	41752	41751	41751
Total length	41752	41752	41751	41751
Reference length	41757	41757	41757	41757
GC (%)	38.98	38.98	38.98	38.98
Reference GC (%)	38.98	38.98	38.98	38.98
N50	41752	41752	41751	41751
NG50	41752	41752	41751	41751
N75	41752	41752	41751	41751
NG75	41752	41752	41751	41751
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 (%)	99.988	99.988	99.986	99.986
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	41752	41752	41751	41751
Total aligned length	41752	41752	41751	41751
NA50	41752	41752	41751	41751
NGA50	41752	41752	41751	41751
NA75	41752	41752	41751	41751
NGA75	41752	41752	41751	41751
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

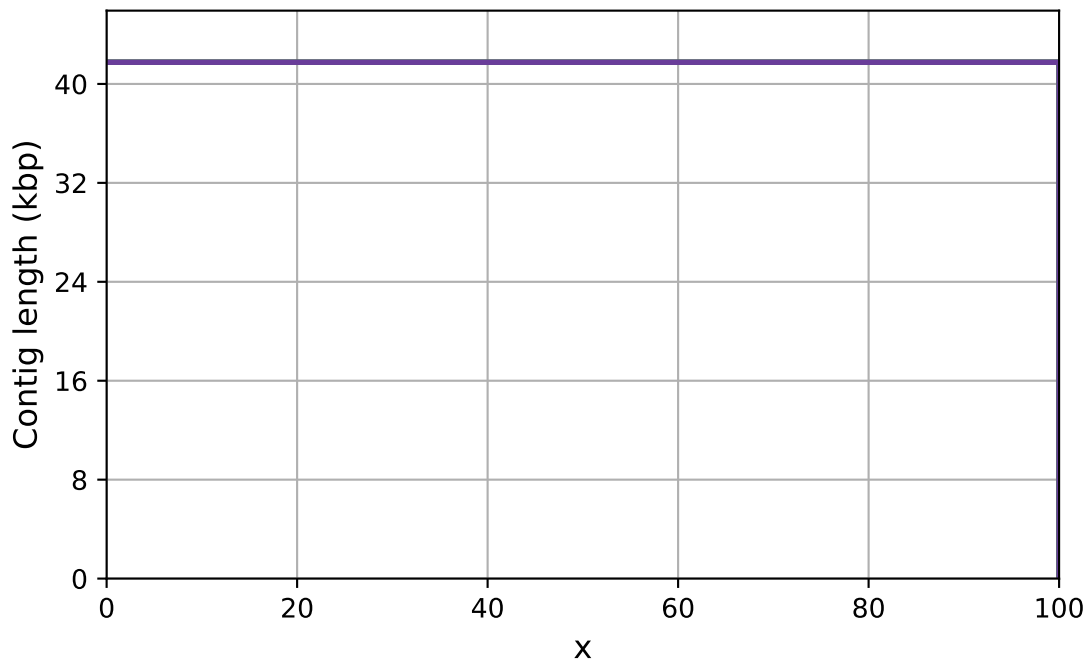
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

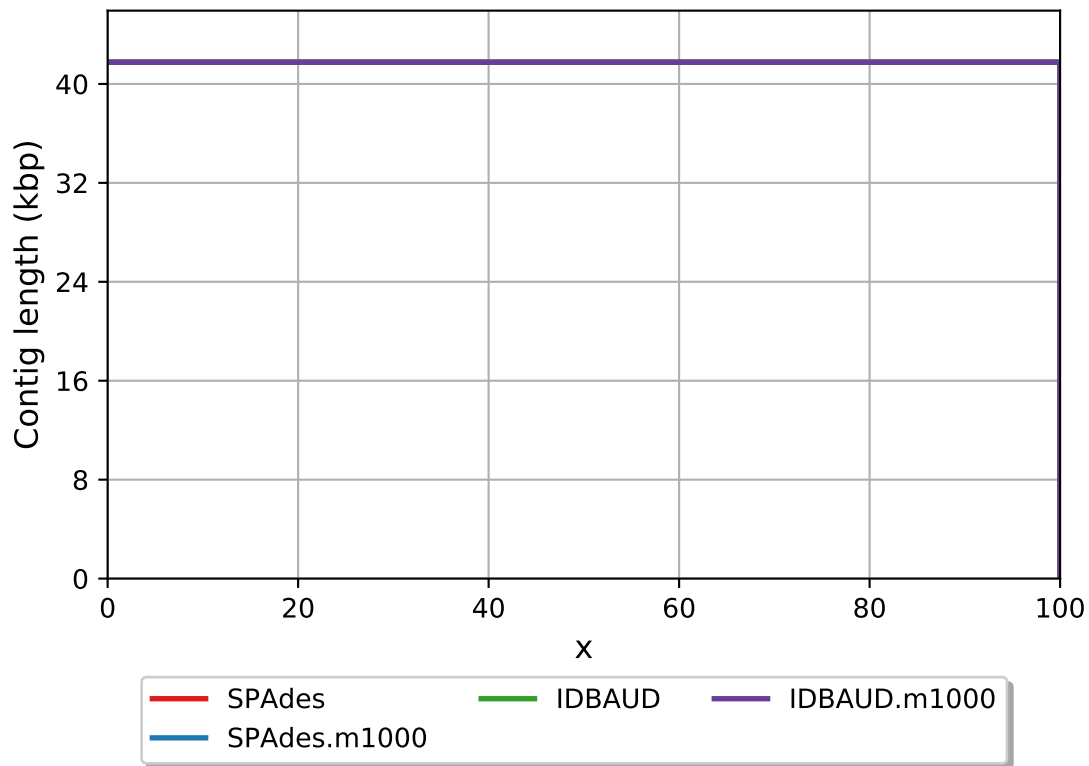
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

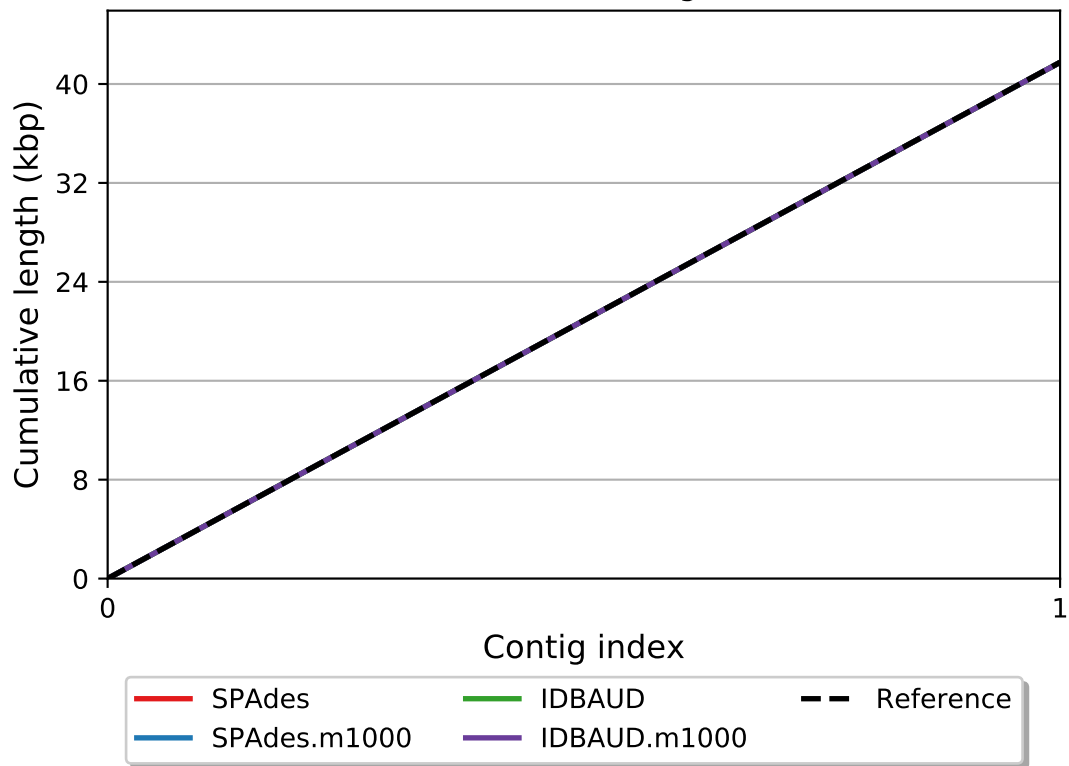


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

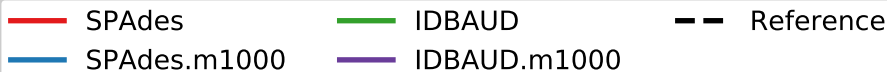
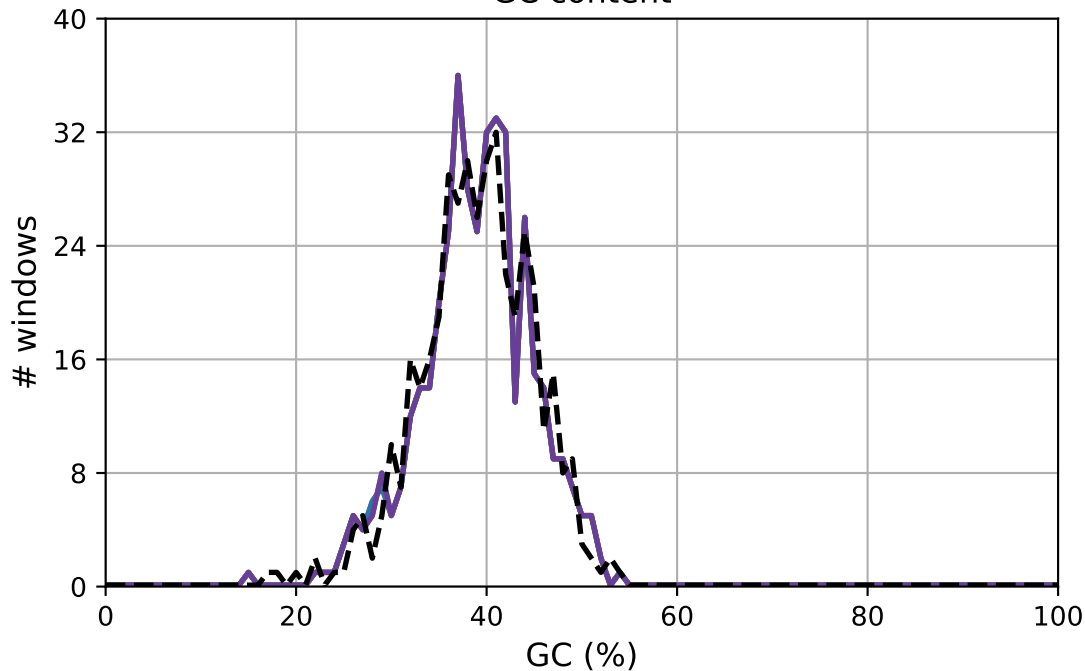
NGx



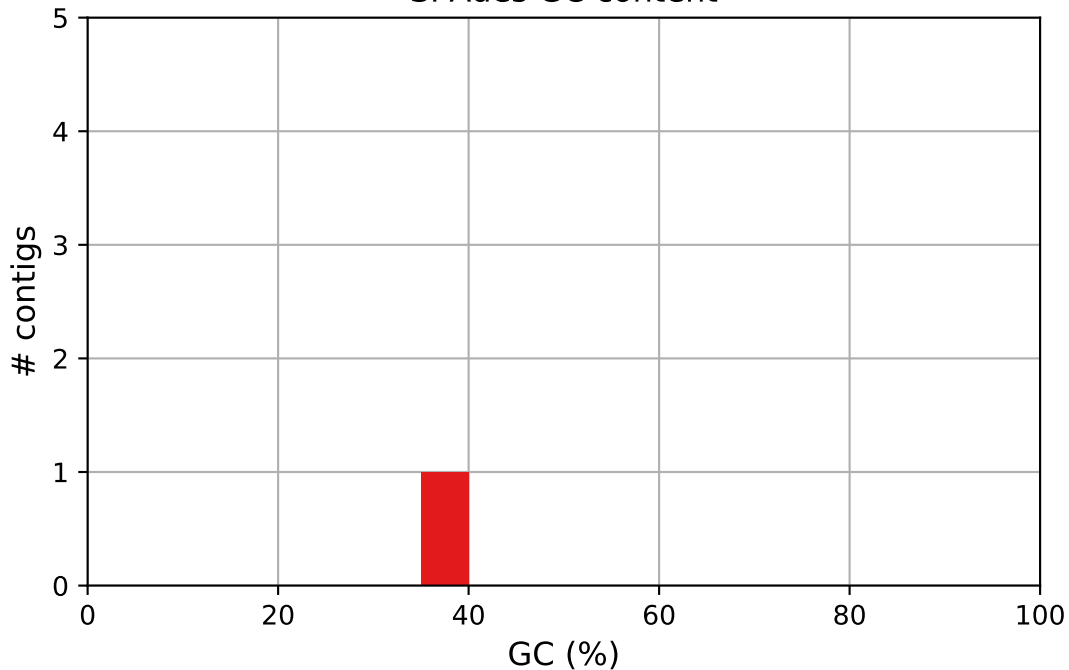
Cumulative length



GC content

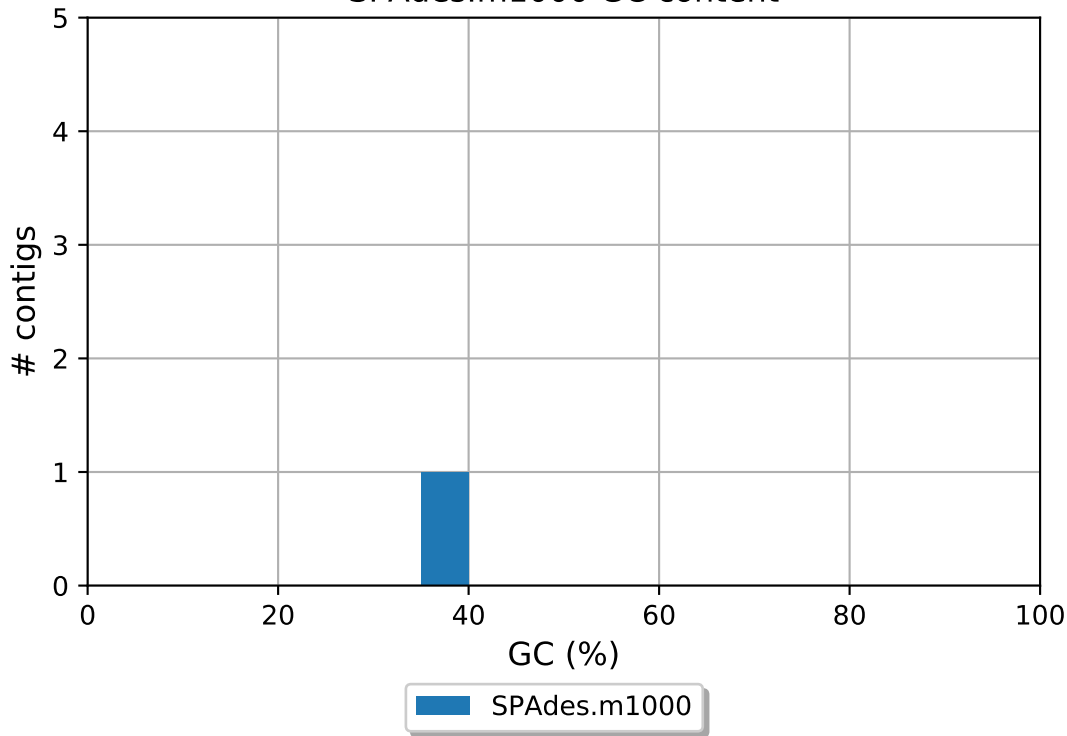


SPAdes GC content

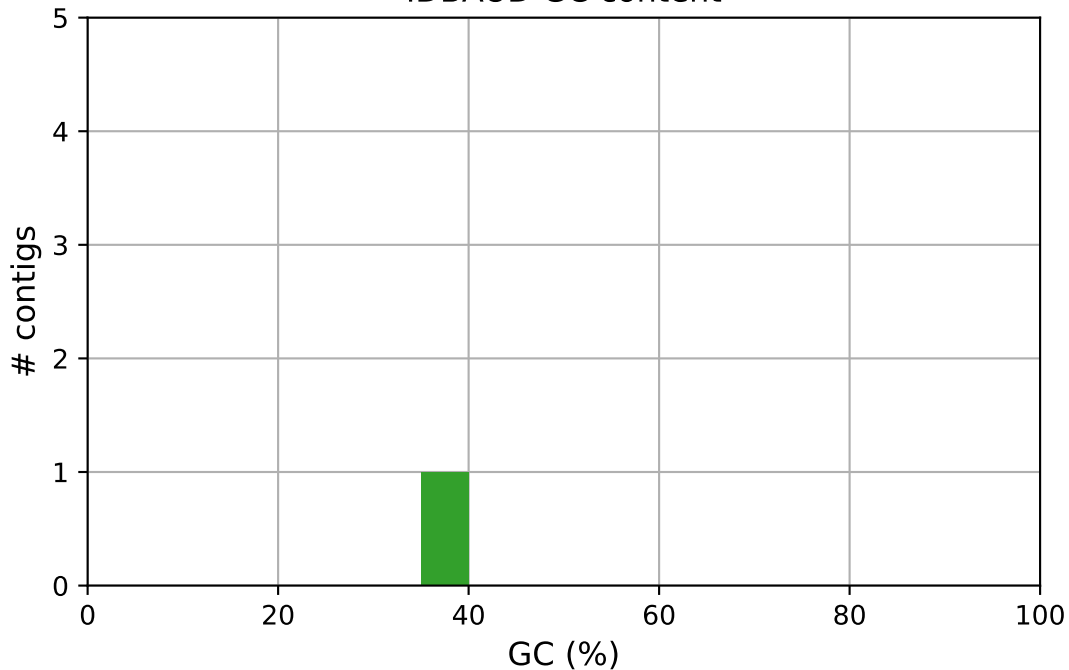


SPAdes

SPAdes.m1000 GC content

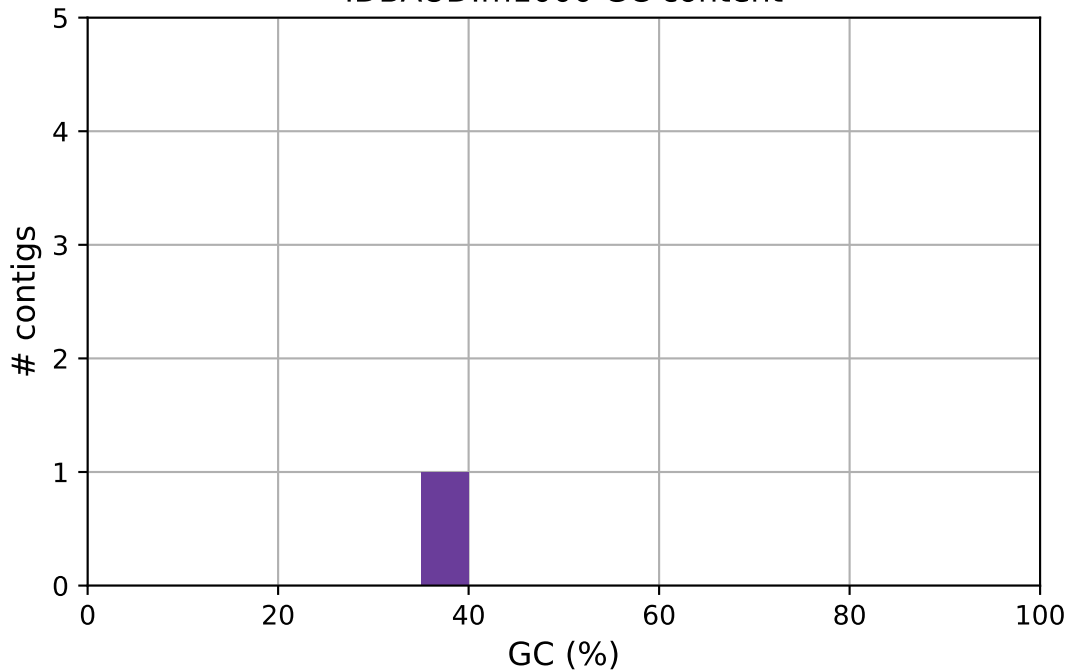


IDBAUD GC content



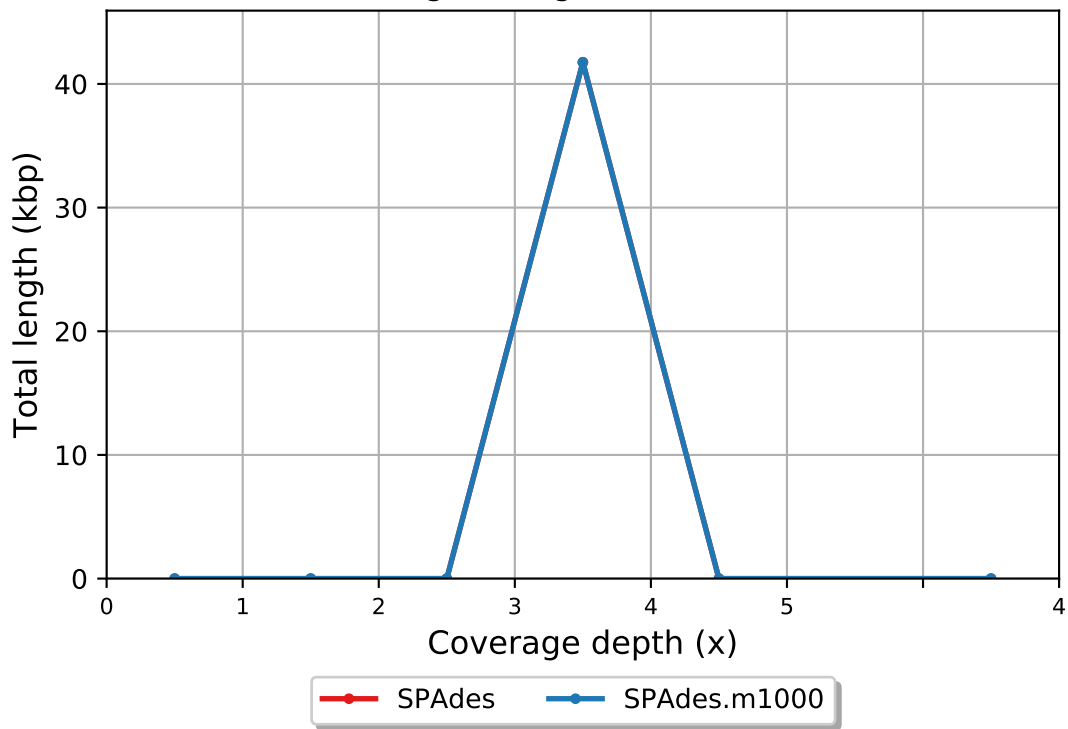
IDBAUD

IDBAUD.m1000 GC content

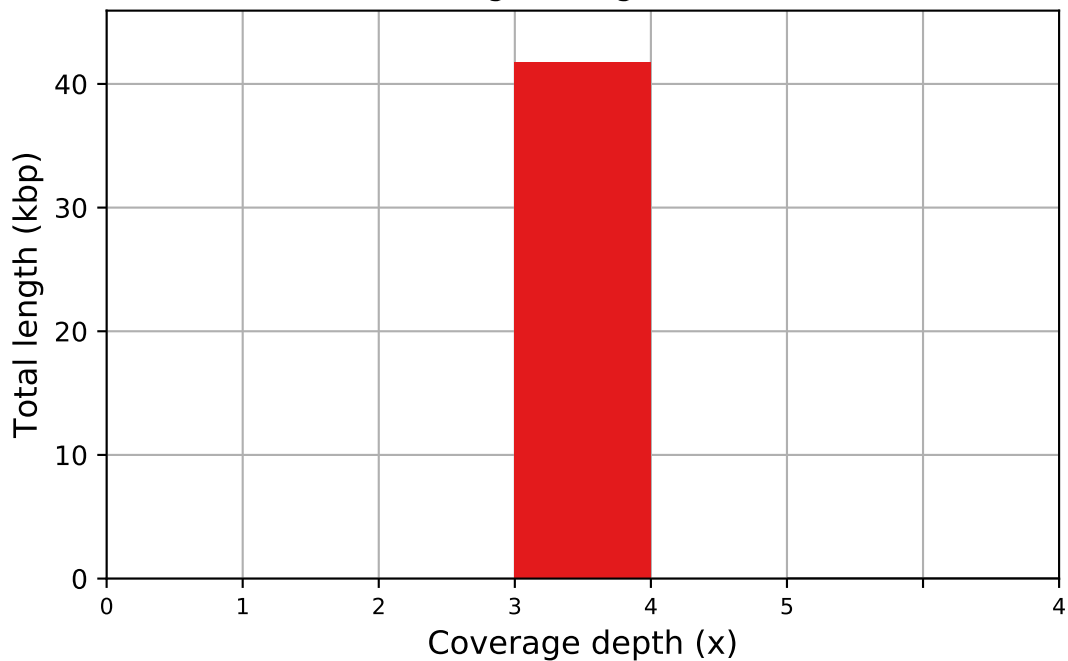


IDBAUD.m1000

Coverage histogram (bin size: 1x)

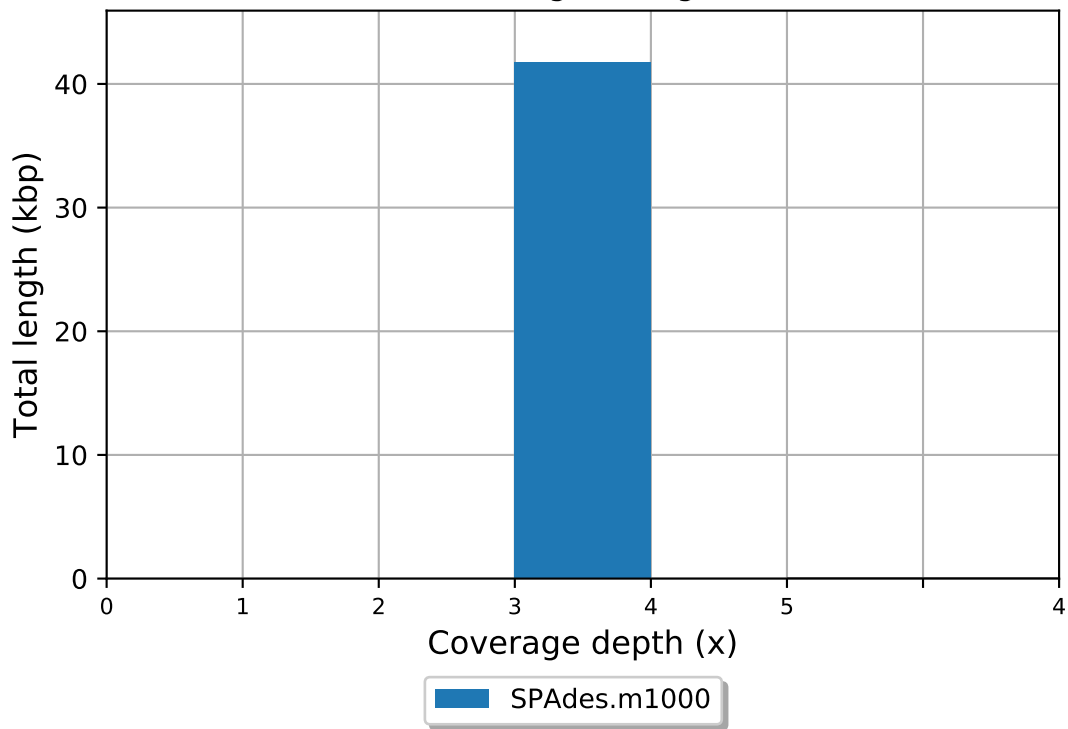


SPAdes coverage histogram (bin size: 1x)

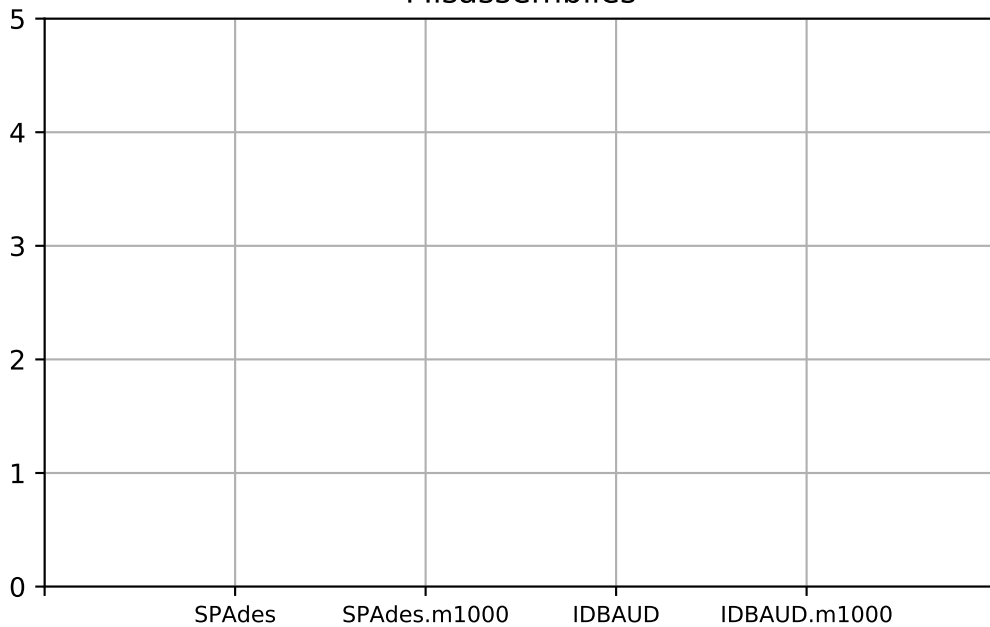


SPAdes

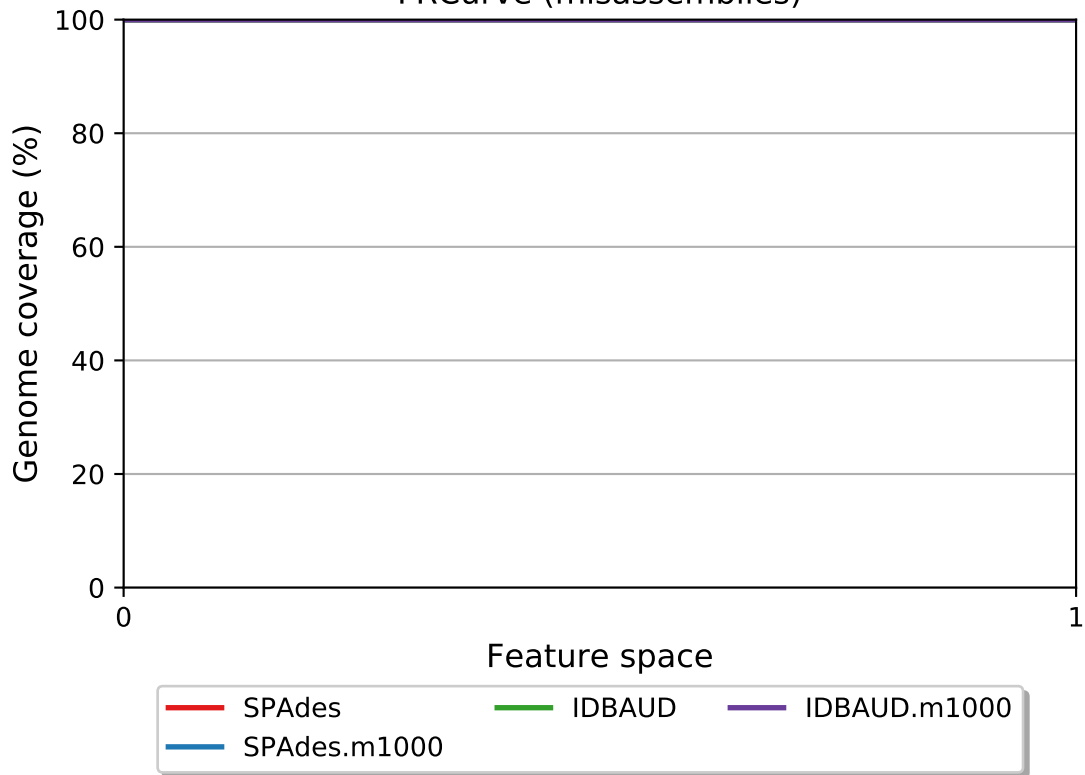
SPAdes.m1000 coverage histogram (bin size: 1x)



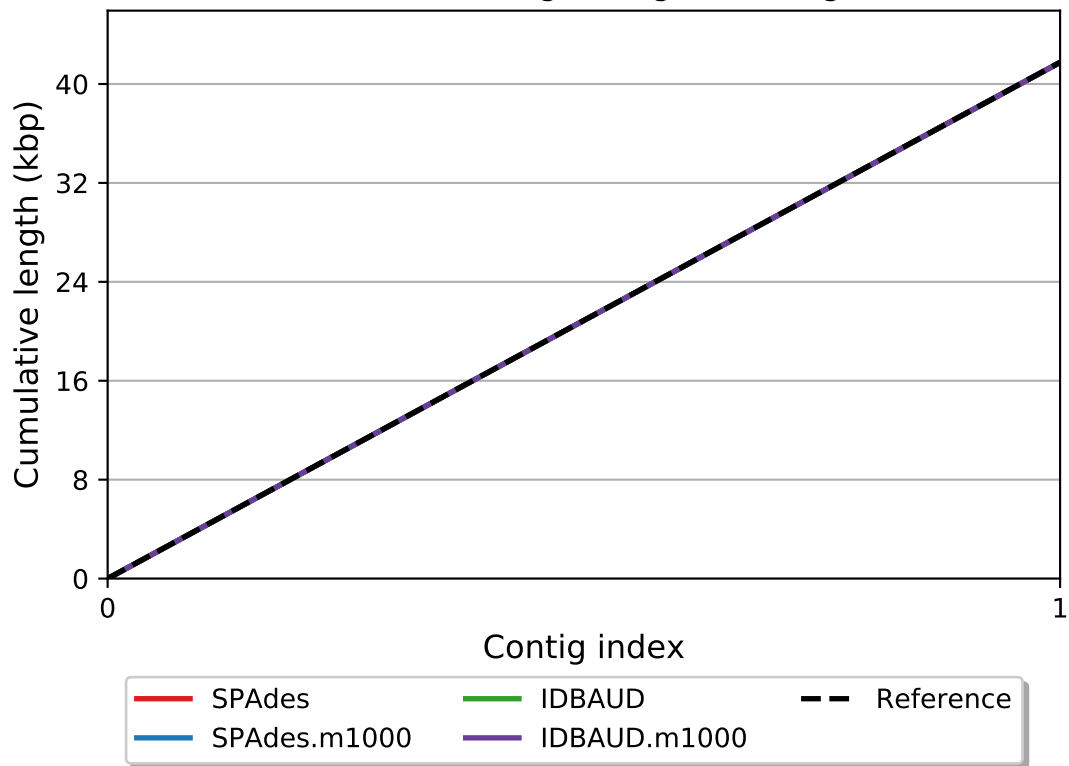
Misassemblies



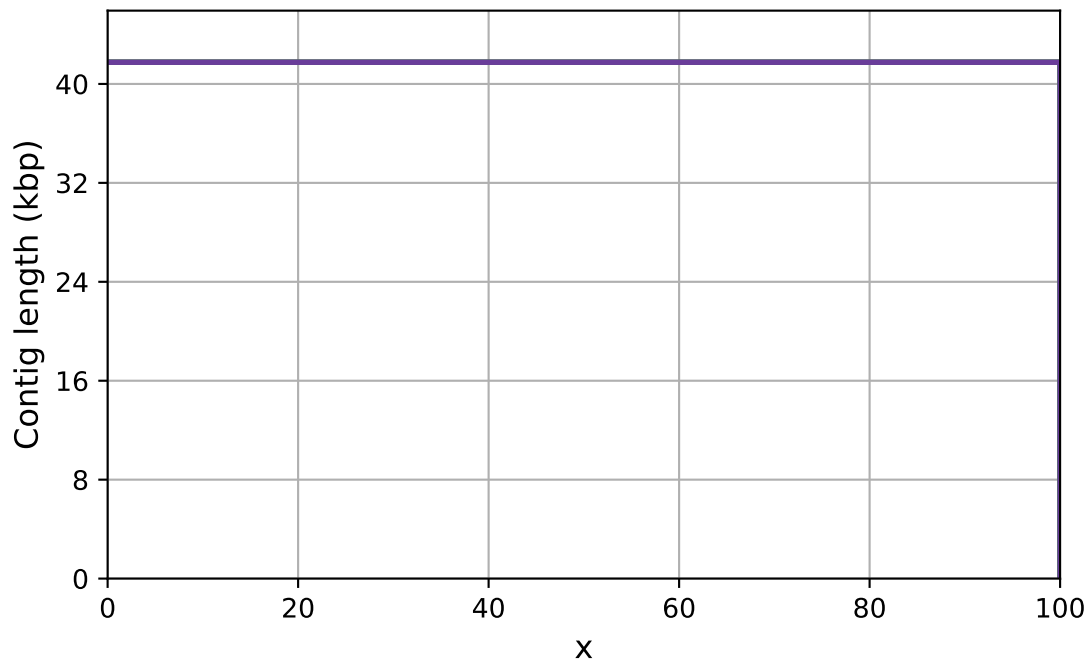
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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

NGAx

