

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	3	3	4	4
# contigs (>= 5000 bp)	3	3	3	3
# contigs (>= 10000 bp)	3	3	1	1
# contigs (>= 25000 bp)	2	2	1	1
# contigs (>= 50000 bp)	1	1	0	0
Total length (>= 1000 bp)	126775	126775	51294	51294
Total length (>= 5000 bp)	126775	126775	47909	47909
Total length (>= 10000 bp)	126775	126775	31309	31309
Total length (>= 25000 bp)	115606	115606	31309	31309
Total length (>= 50000 bp)	73675	73675	0	0
# contigs	3	3	5	4
Largest contig	73675	73675	31309	31309
Total length	126775	126775	52064	51294
Reference length	41941	41941	41941	41941
GC (%)	33.34	33.34	36.23	36.25
Reference GC (%)	35.98	35.98	35.98	35.98
N50	73675	73675	31309	31309
NG50	73675	73675	31309	31309
N75	41931	41931	8824	8824
NG75	73675	73675	8824	8824
L50	1	1	1	1
LG50	1	1	1	1
L75	2	2	2	2
LG75	1	1	2	2
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	2	2
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	1	1
# unaligned mis. contigs	1	1	0	0
# unaligned contigs	0 + 2 part	0 + 2 part	0 + 2 part	0 + 2 part
Unaligned length	83738	83738	10800	10800
Genome fraction (%)	99.976	99.976	96.481	95.112
Duplication ratio	1.026	1.026	1.020	1.015
# N's per 100 kbp	179.85	179.85	508.99	516.63
# mismatches per 100 kbp	40.54	40.54	14.83	15.04
# indels per 100 kbp	2.38	2.38	0.00	0.00
Largest alignment	41931	41931	31067	31067
Total aligned length	42809	42809	40999	40229
NA50	-	-	31067	31067
NGA50	41931	41931	31067	31067
NA75	-	-	8824	8824
NGA75	41931	41931	8824	8824
LA50	-	-	1	1
LGA50	1	1	1	1
LA75	-	-	2	2
LGA75	1	1	2	2

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	2	2
# possible misassemblies	0	0	2	2
# local misassemblies	0	0	2	2
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	1	1
# unaligned mis. contigs	1	1	0	0
# mismatches	17	17	6	6
# indels	1	1	0	0
# indels (<= 5 bp)	1	1	0	0
# indels (> 5 bp)	0	0	0	0
Indels length	3	3	0	0

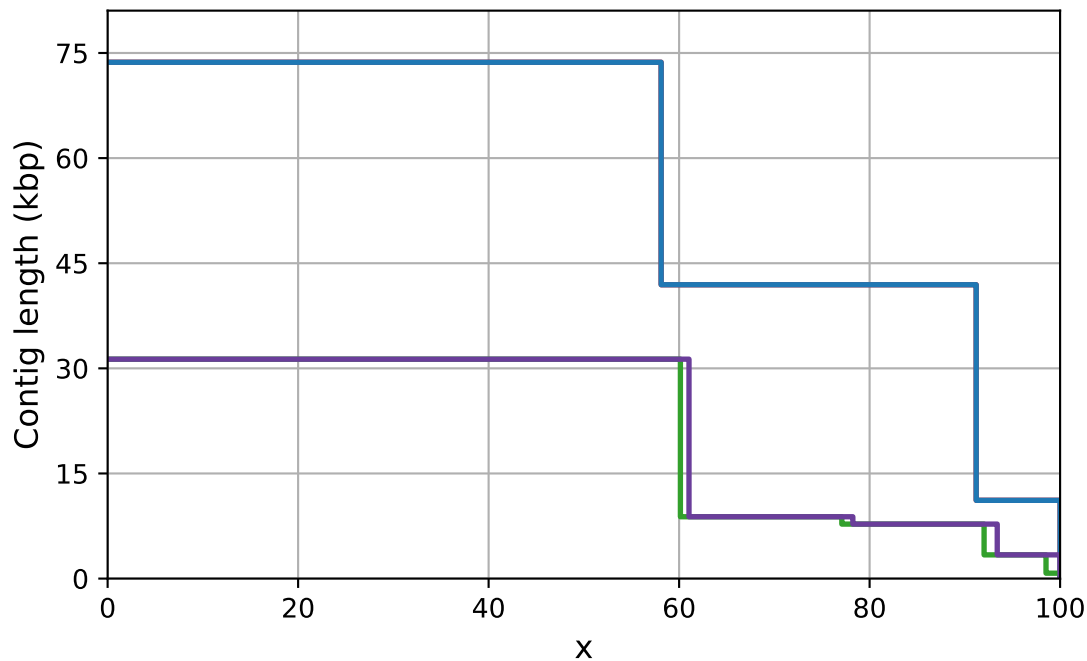
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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	2	2	2	2
Partially unaligned length	83738	83738	10800	10800
# N's	228	228	265	265

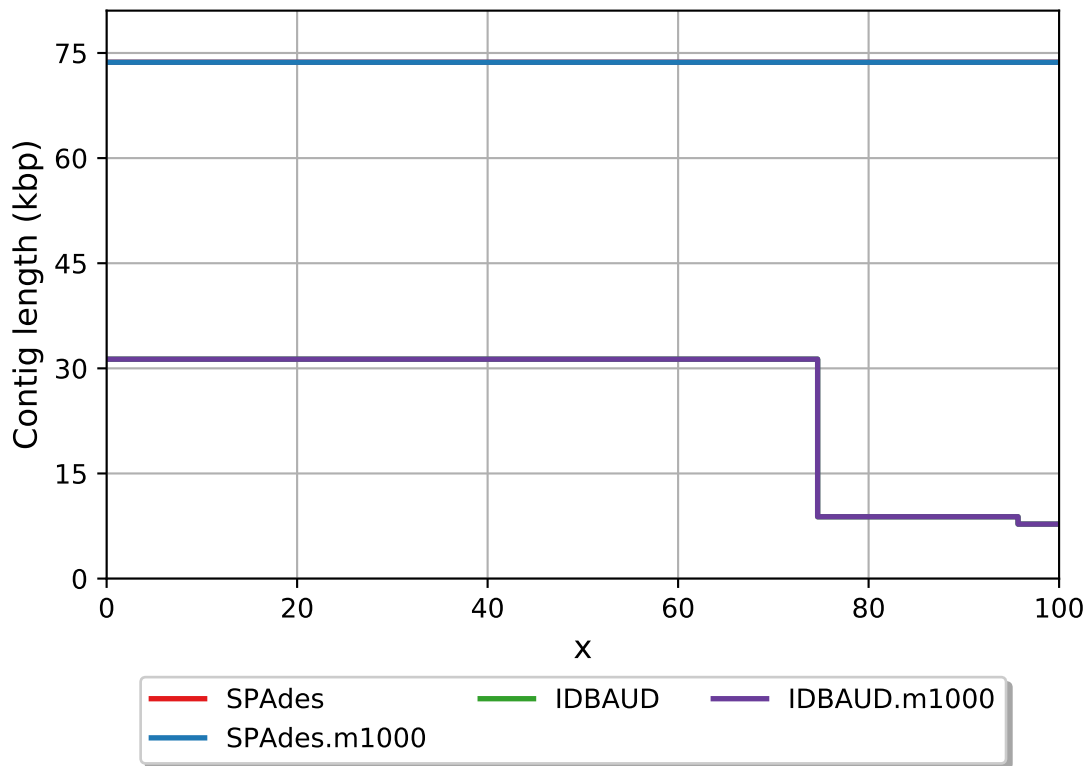
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

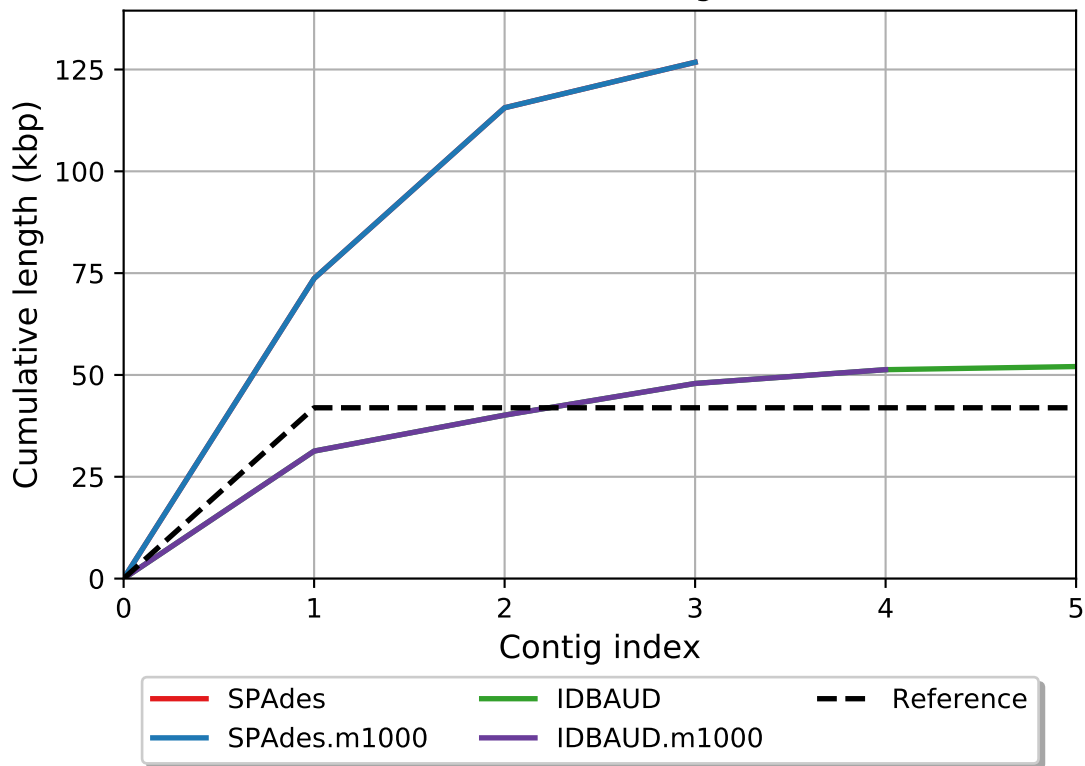


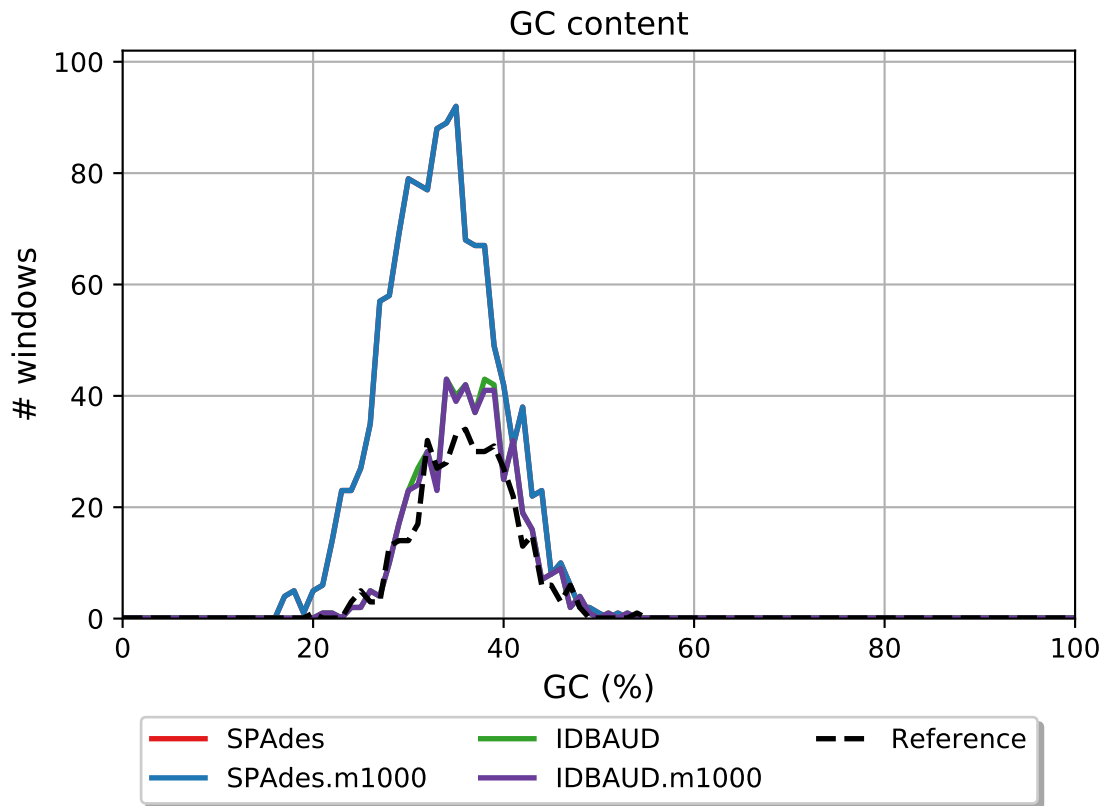
SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

NGx

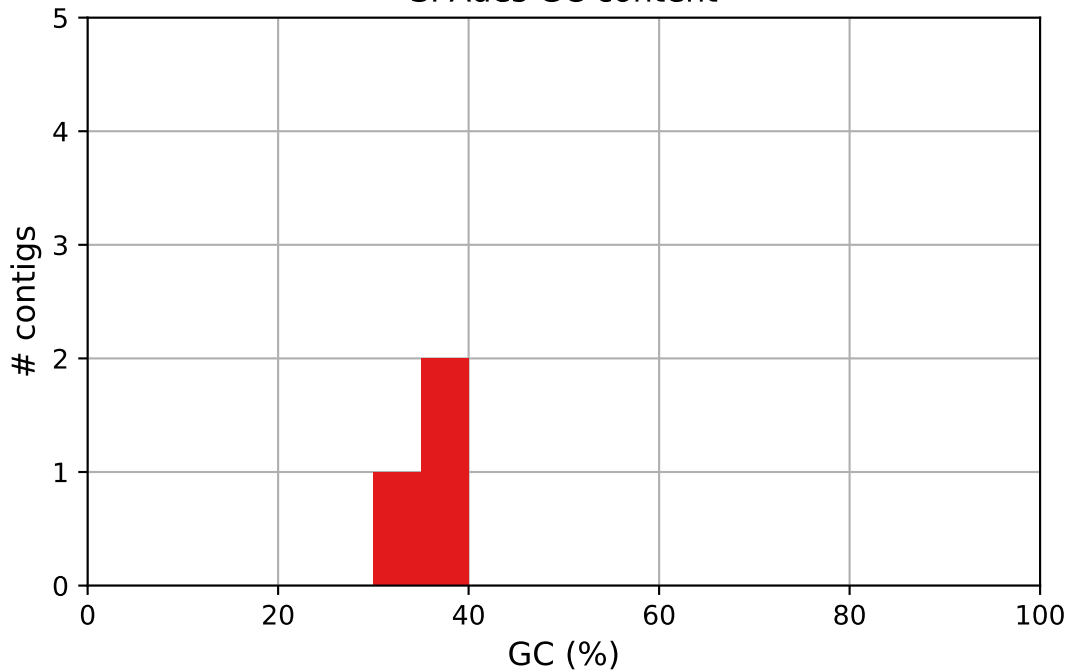


Cumulative length



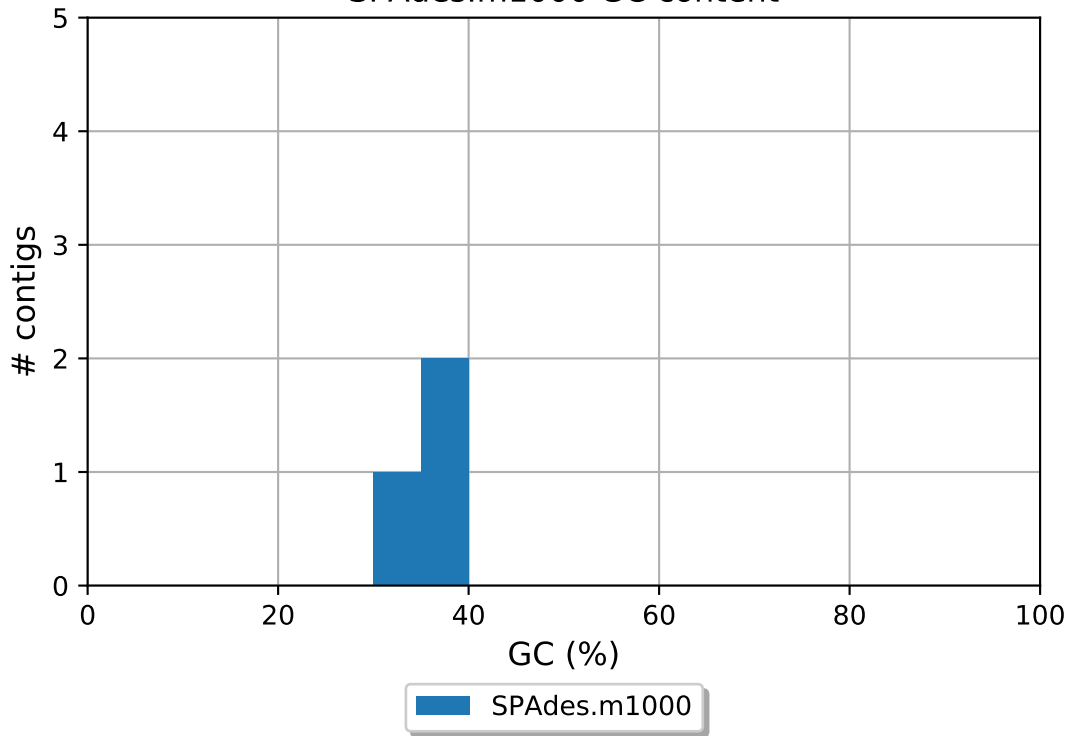


SPAdes GC content

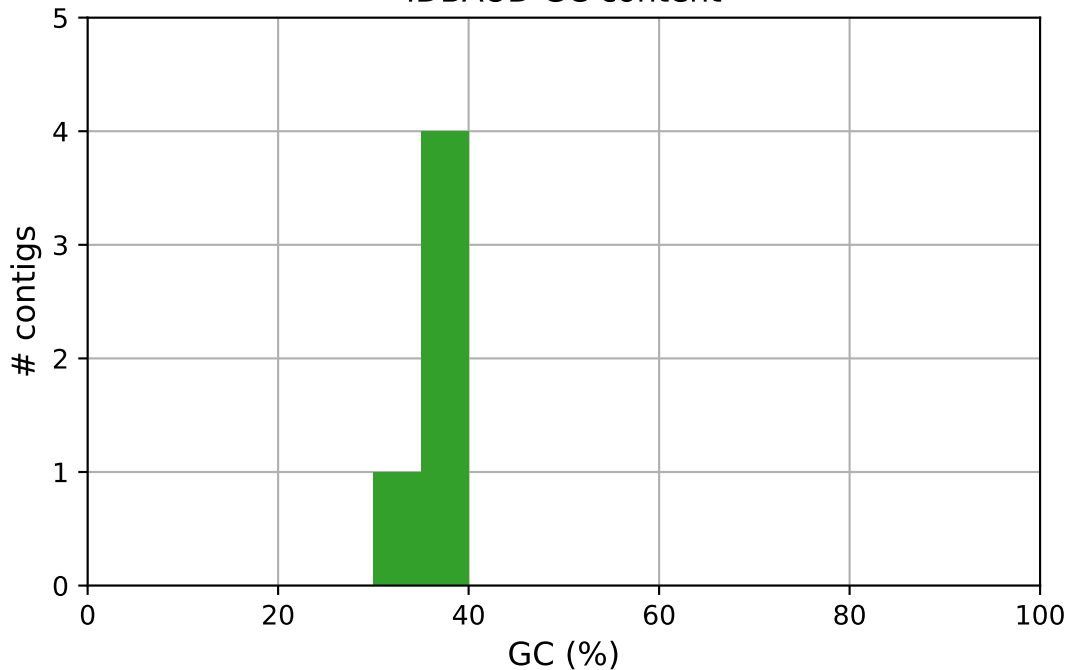


SPAdes

SPAdes.m1000 GC content

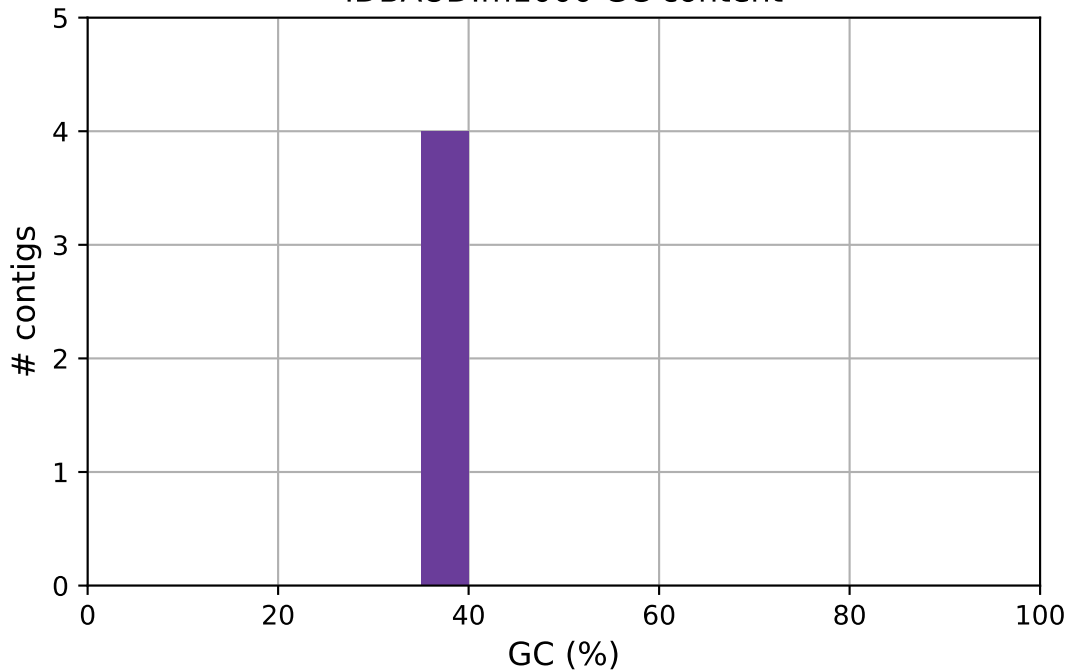


IDBAUD GC content



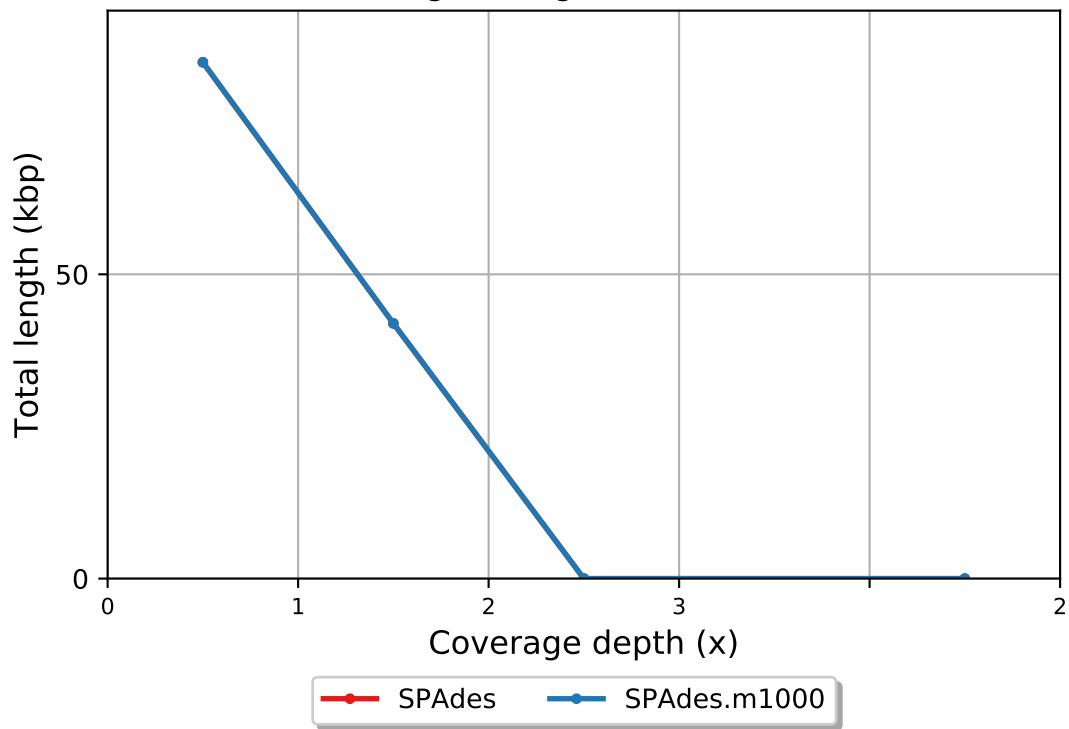
IDBAUD

IDBAUD.m1000 GC content

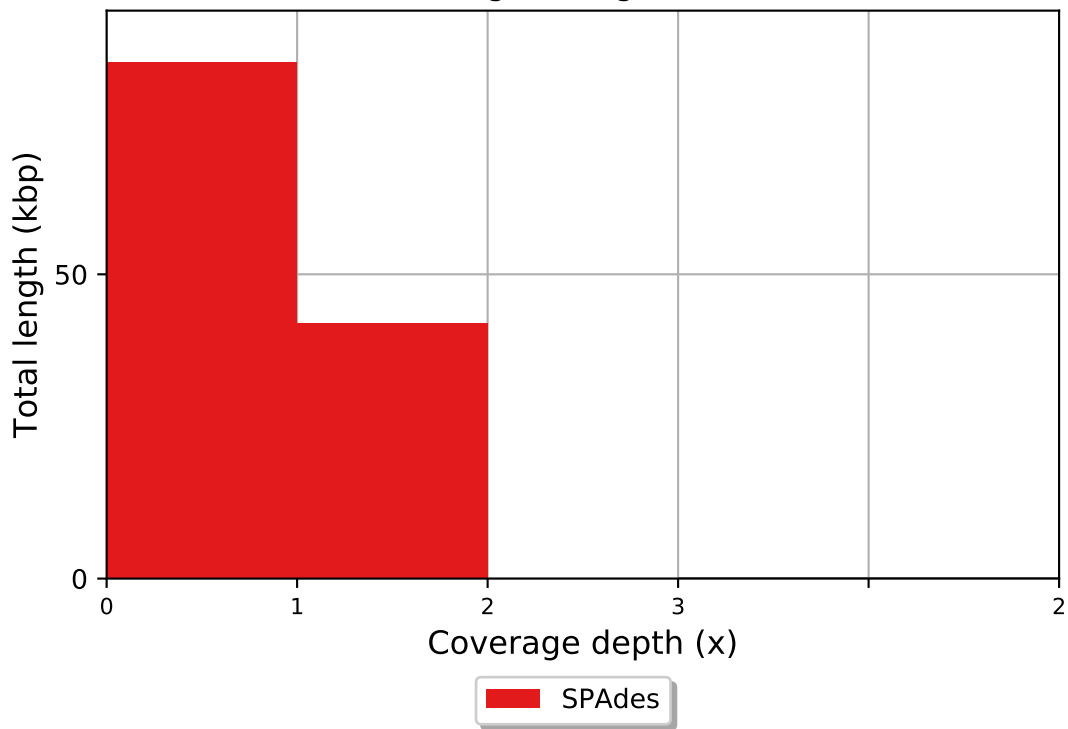


IDBAUD.m1000

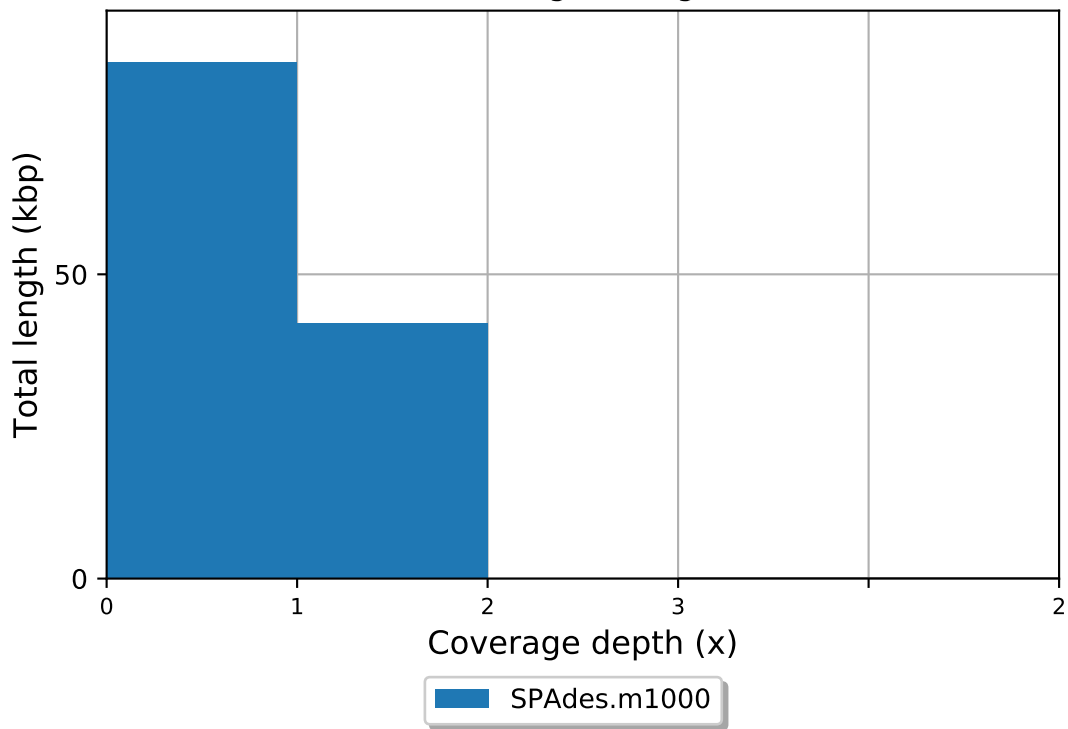
Coverage histogram (bin size: 1x)



SPAdes coverage histogram (bin size: 1x)



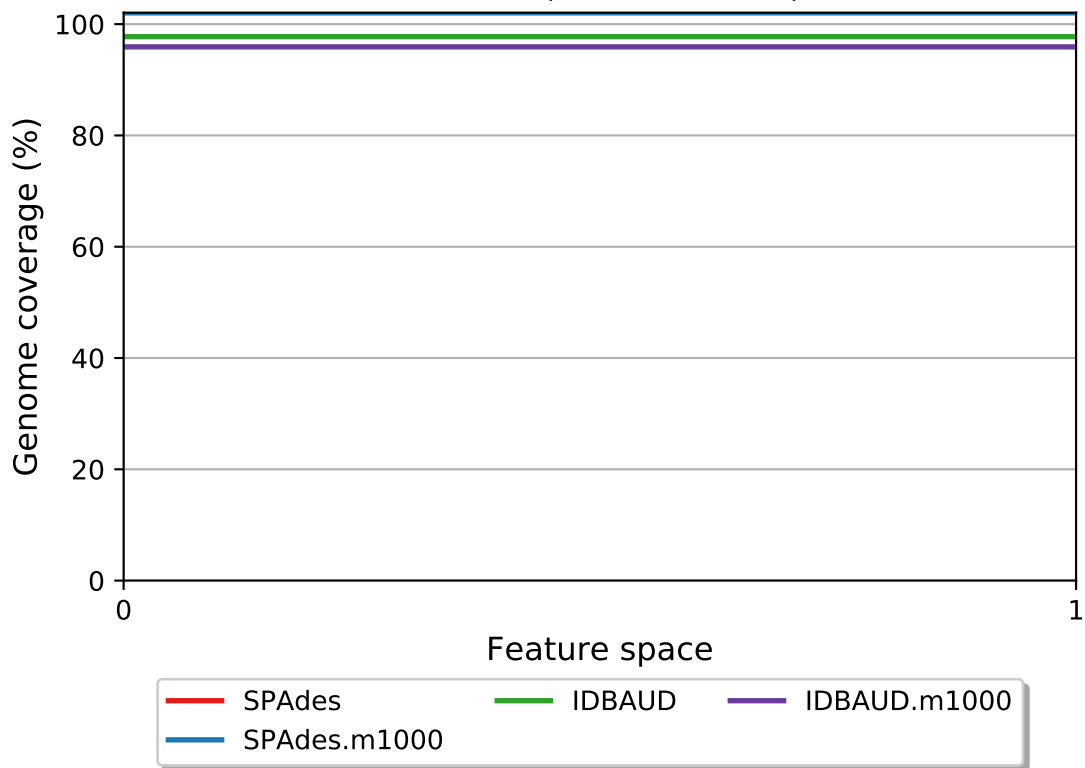
SPAdes.m1000 coverage histogram (bin size: 1x)



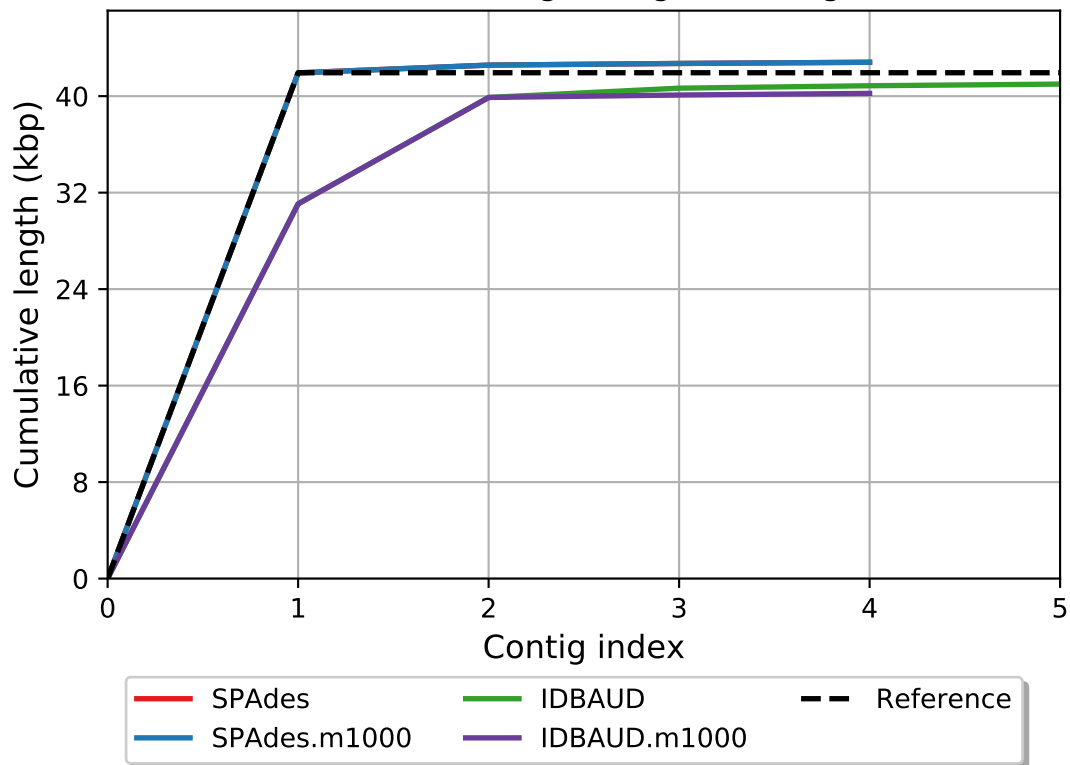
Misassemblies



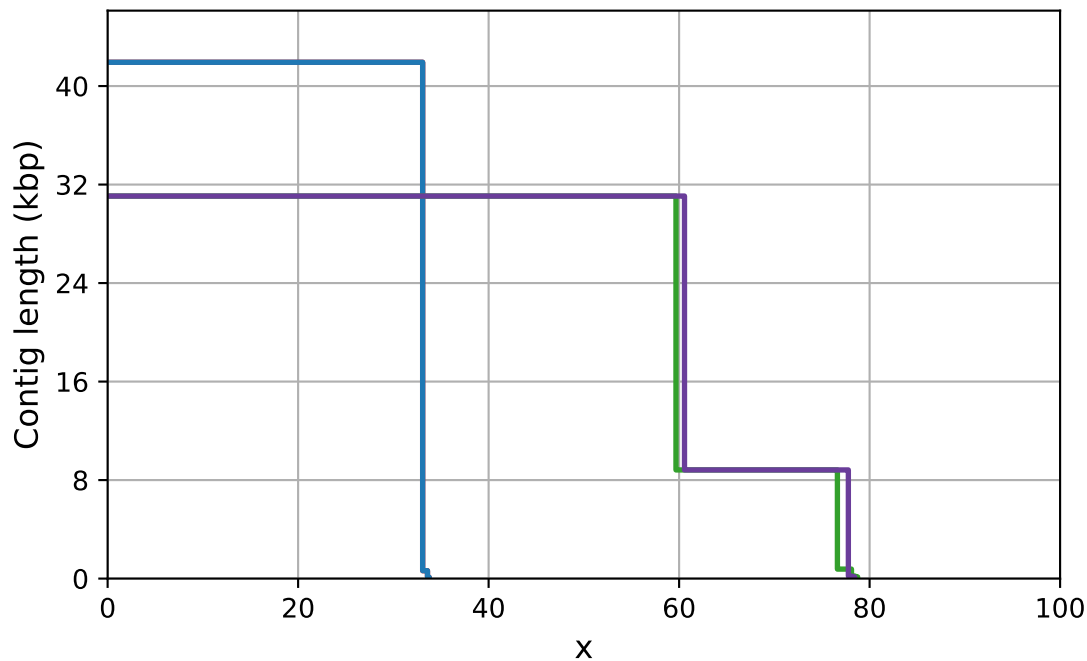
FRCurve (misassemblies)



Cumulative length (aligned contigs)

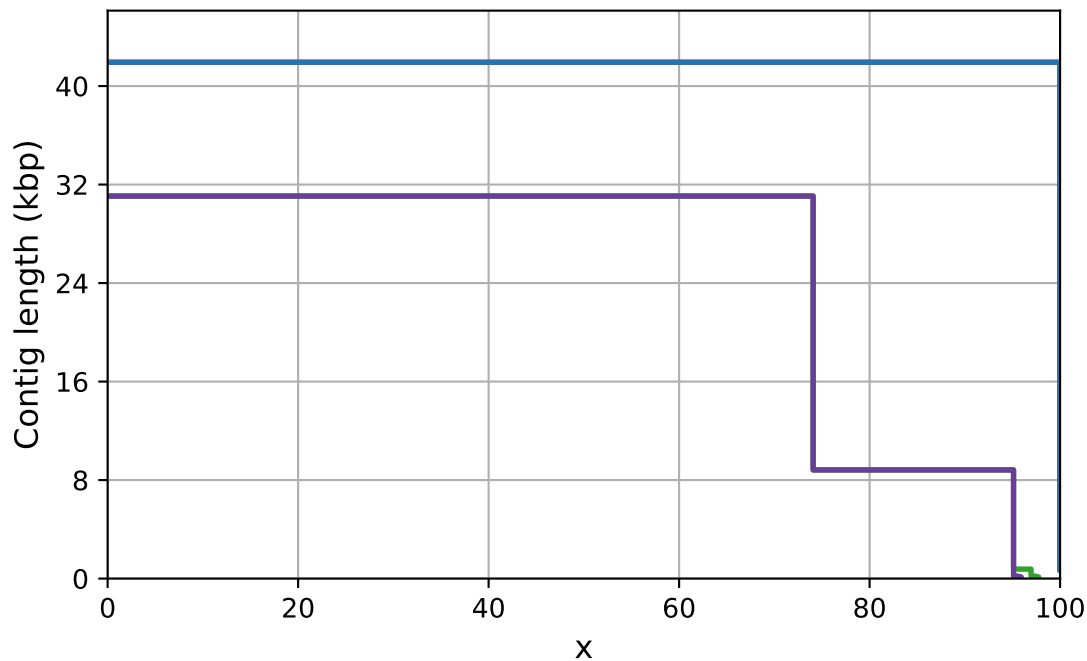


NAx



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

NGAx



SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

