

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1
# contigs (>= 10000 bp)	0	0	0	0
# contigs (>= 25000 bp)	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	7678	7678	7678	7678
Total length (>= 5000 bp)	7678	7678	7678	7678
Total length (>= 10000 bp)	0	0	0	0
Total length (>= 25000 bp)	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	7678	7678	7678	7678
Total length	7678	7678	7678	7678
Reference length	7679	7679	7679	7679
GC (%)	59.36	59.36	59.36	59.36
Reference GC (%)	59.37	59.37	59.37	59.37
N50	7678	7678	7678	7678
NG50	7678	7678	7678	7678
N75	7678	7678	7678	7678
NG75	7678	7678	7678	7678
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 (%)	99.987	99.987	99.987	99.987
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	7678	7678	7678	7678
Total aligned length	7678	7678	7678	7678
NA50	7678	7678	7678	7678
NGA50	7678	7678	7678	7678
NA75	7678	7678	7678	7678
NGA75	7678	7678	7678	7678
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

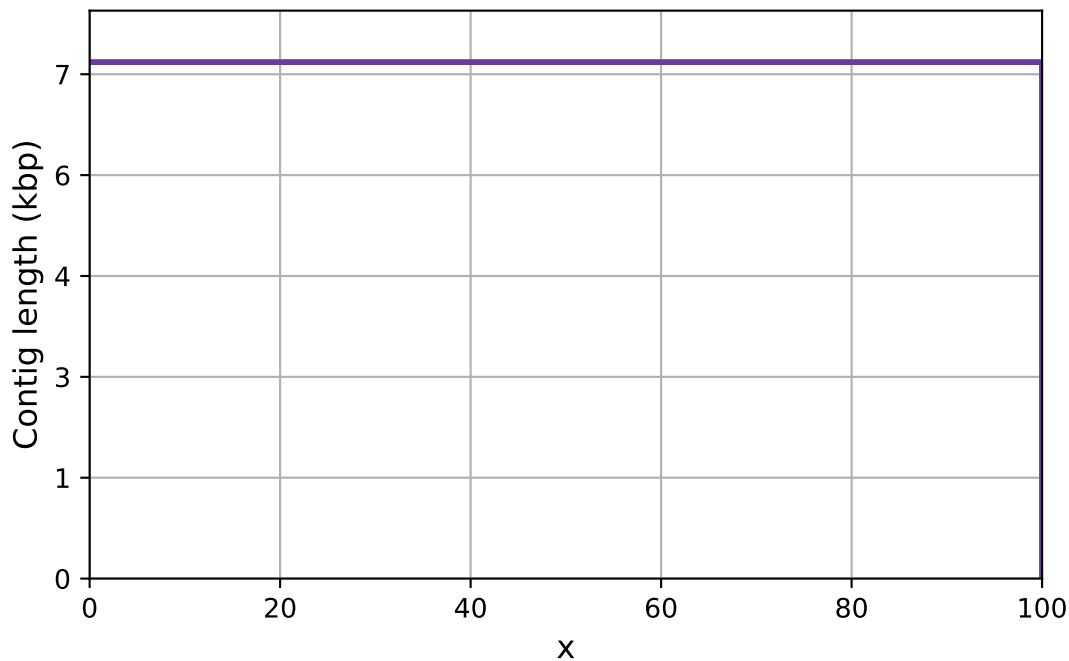
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

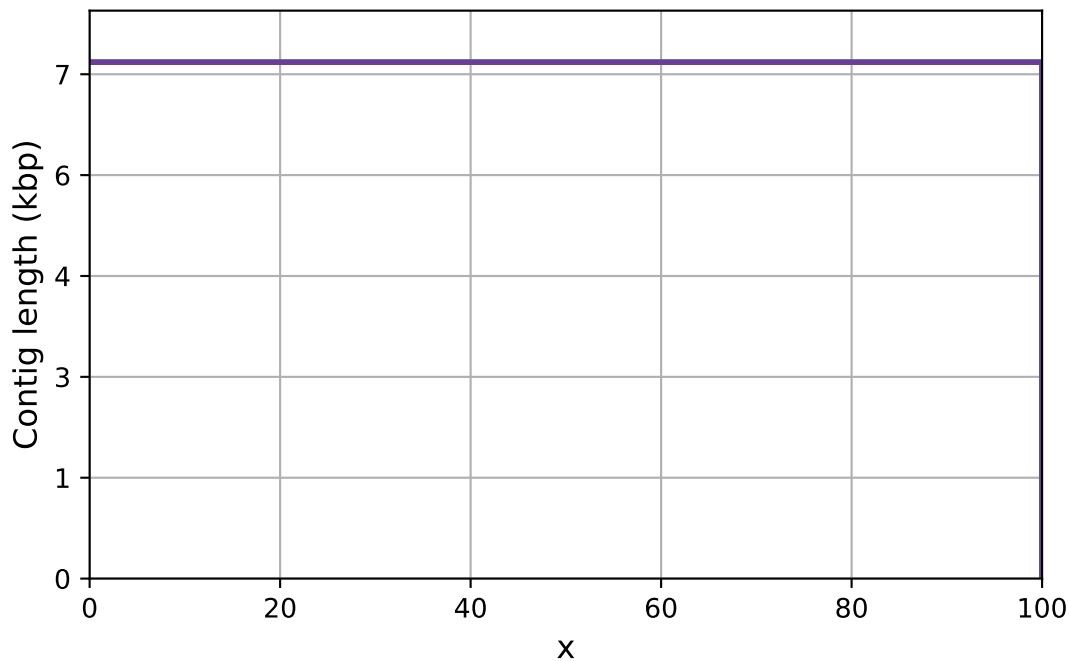
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



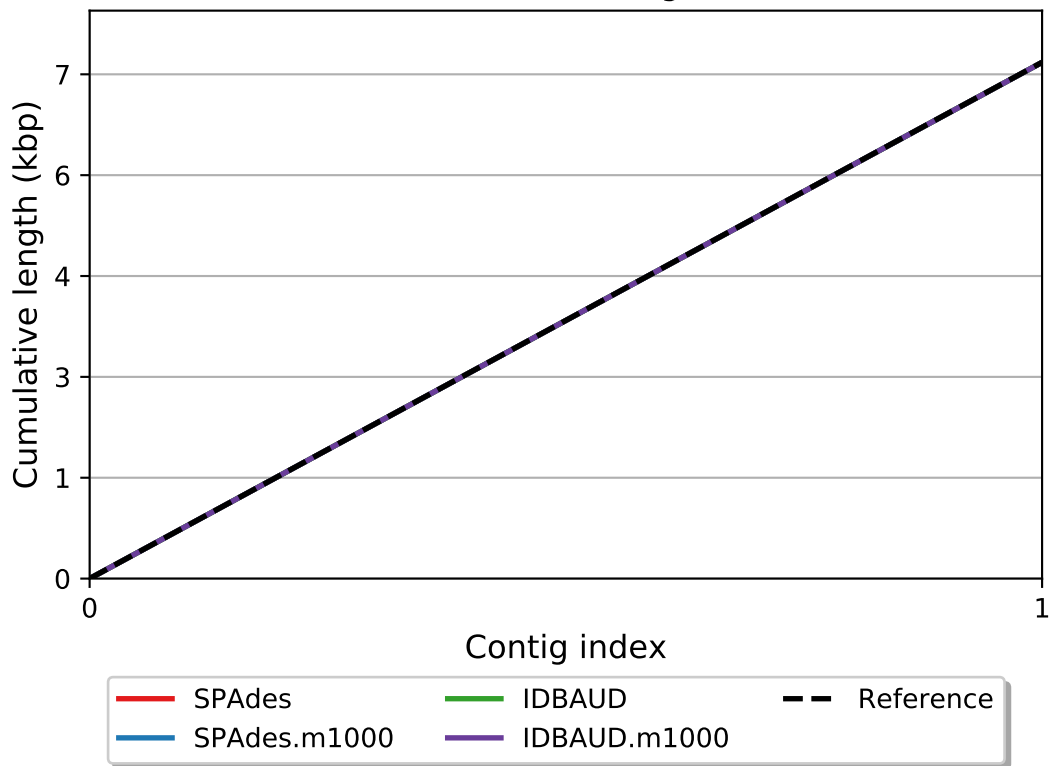
— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

NGx

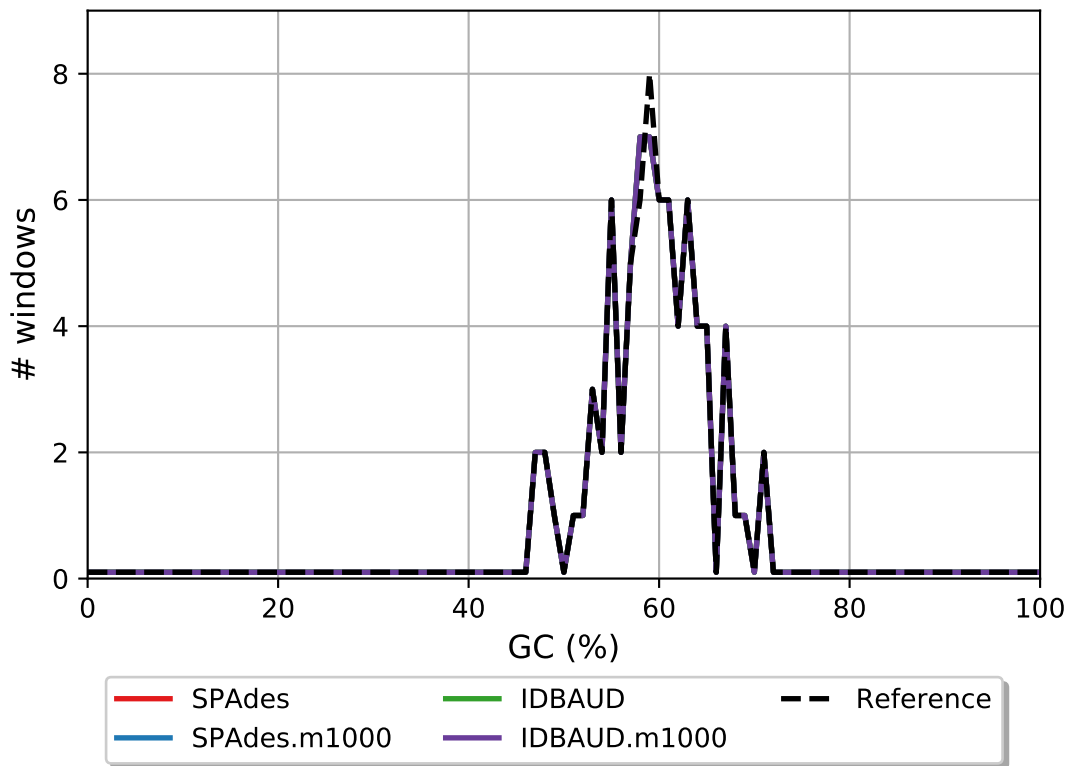


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

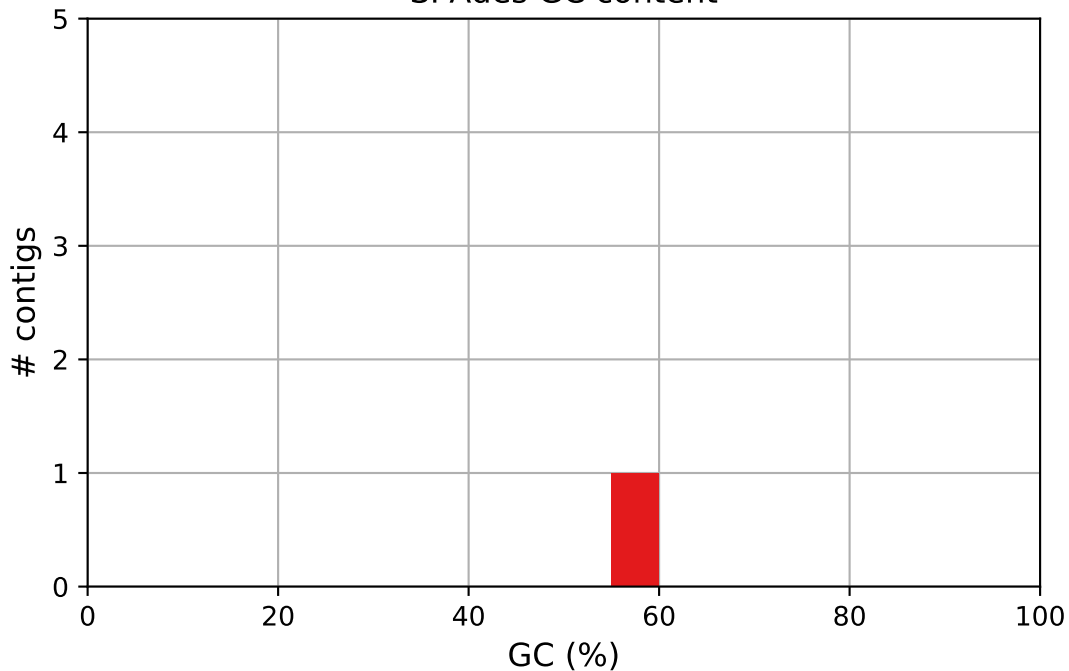
Cumulative length



GC content

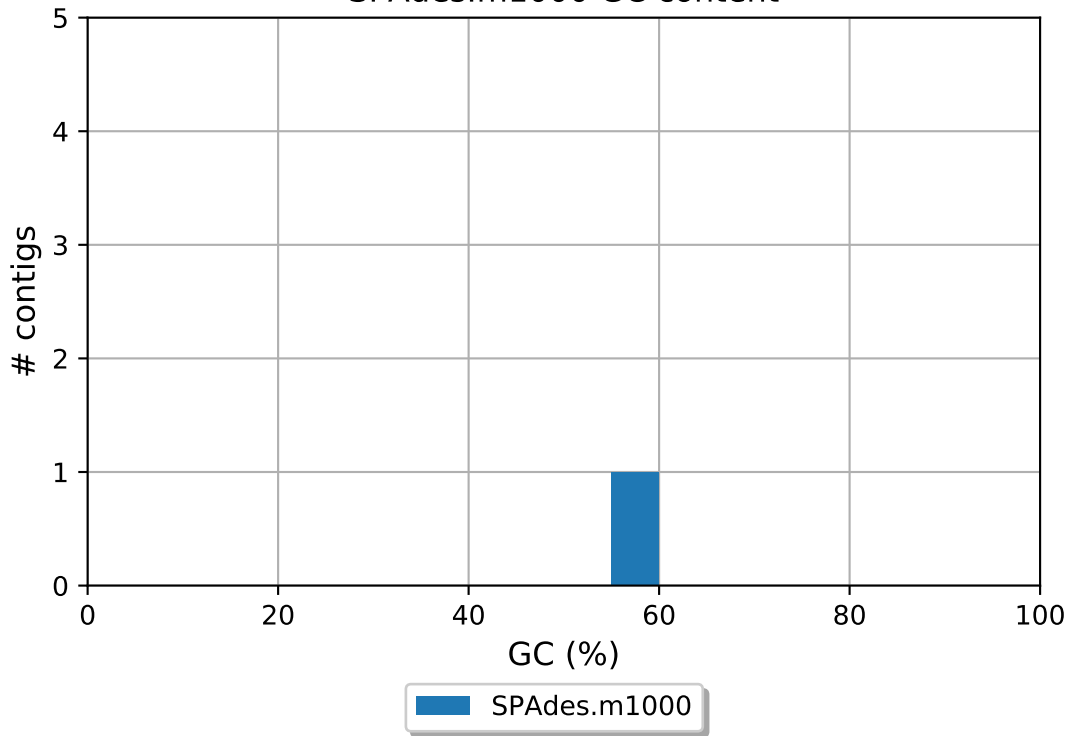


SPAdes GC content

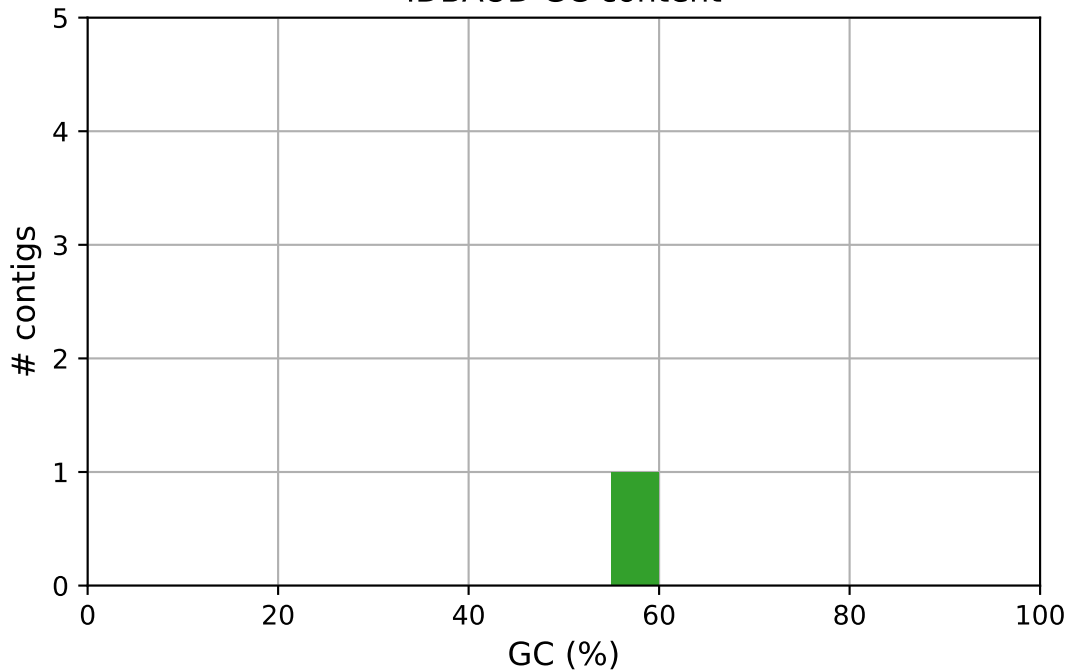


SPAdes

SPAdes.m1000 GC content

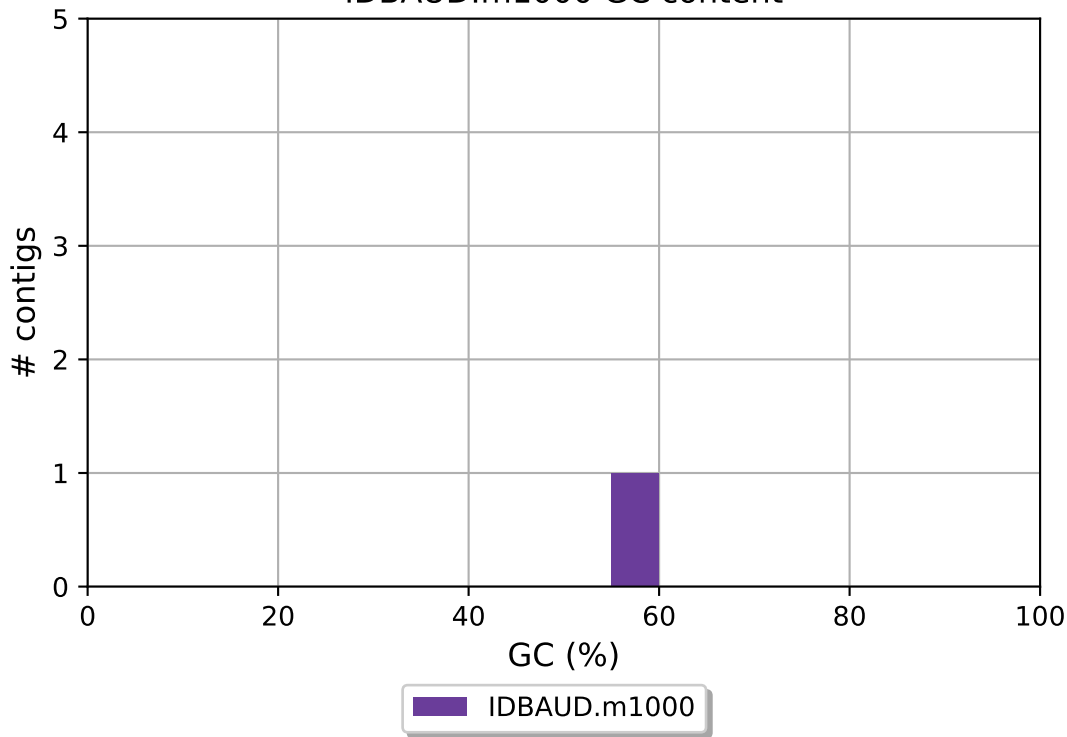


IDBAUD GC content

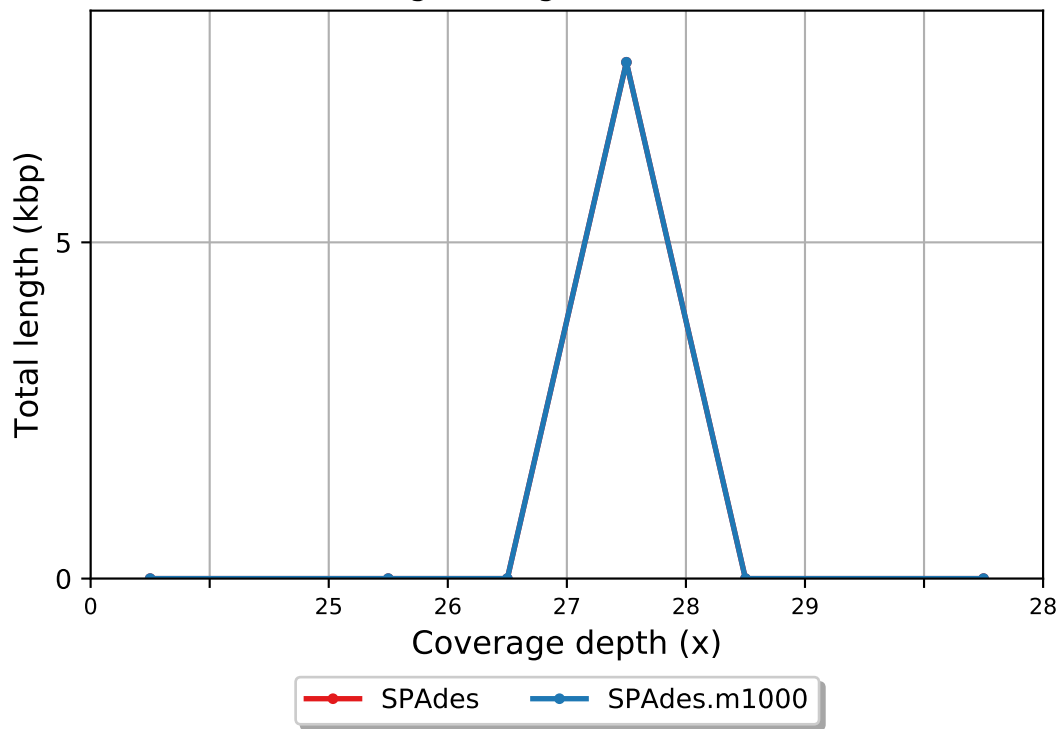


IDBAUD

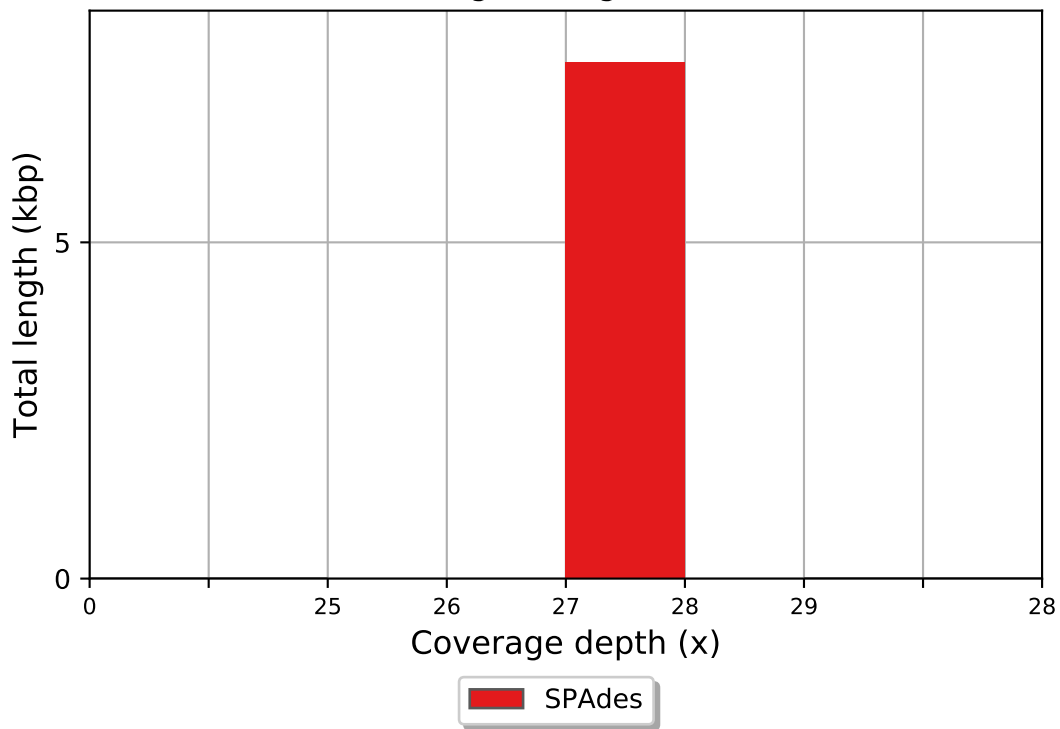
IDBAUD.m1000 GC content



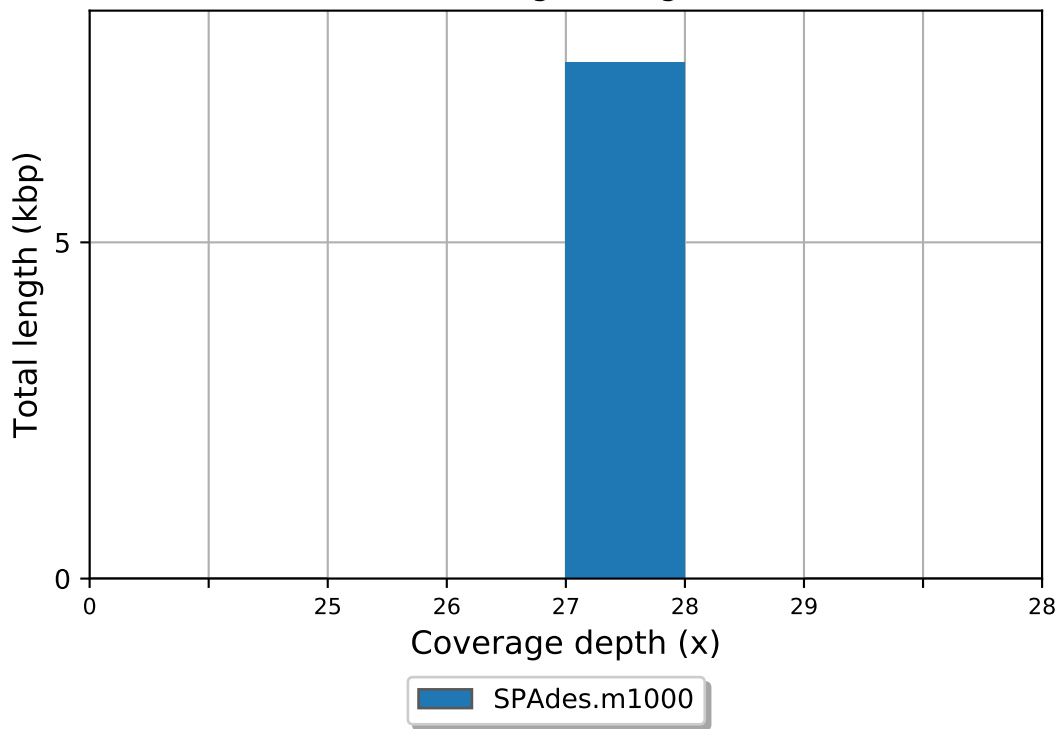
Coverage histogram (bin size: 1x)



SPAdes coverage histogram (bin size: 1x)



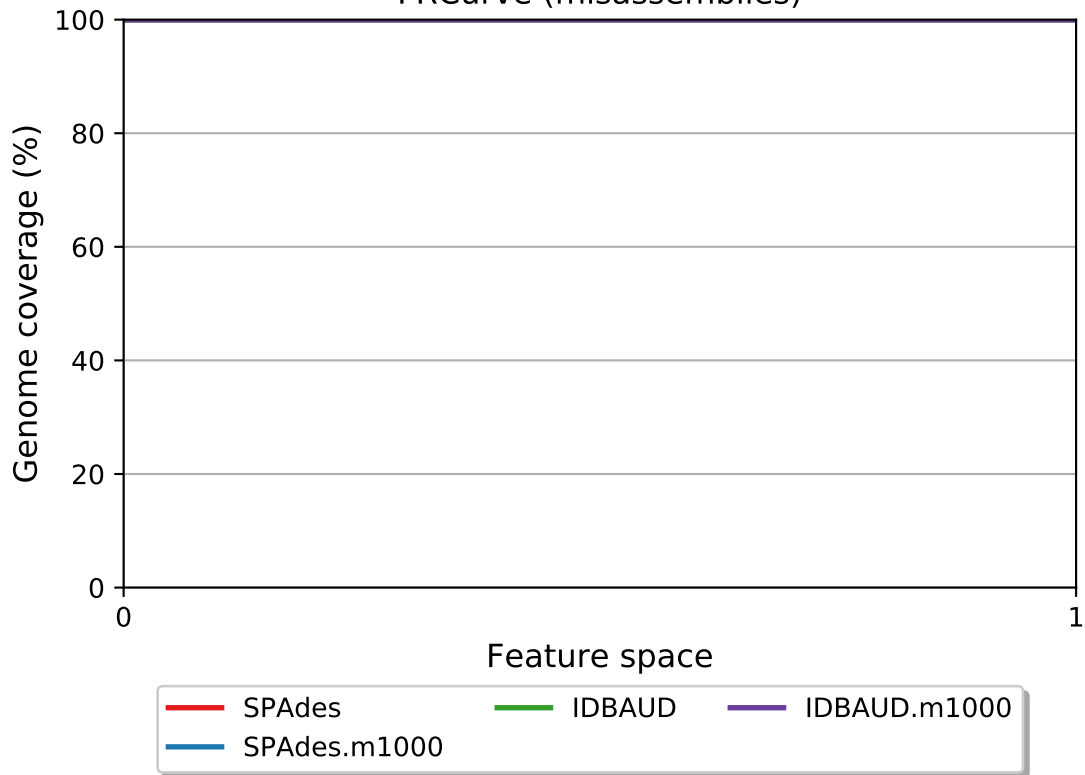
SPAdes.m1000 coverage histogram (bin size: 1x)



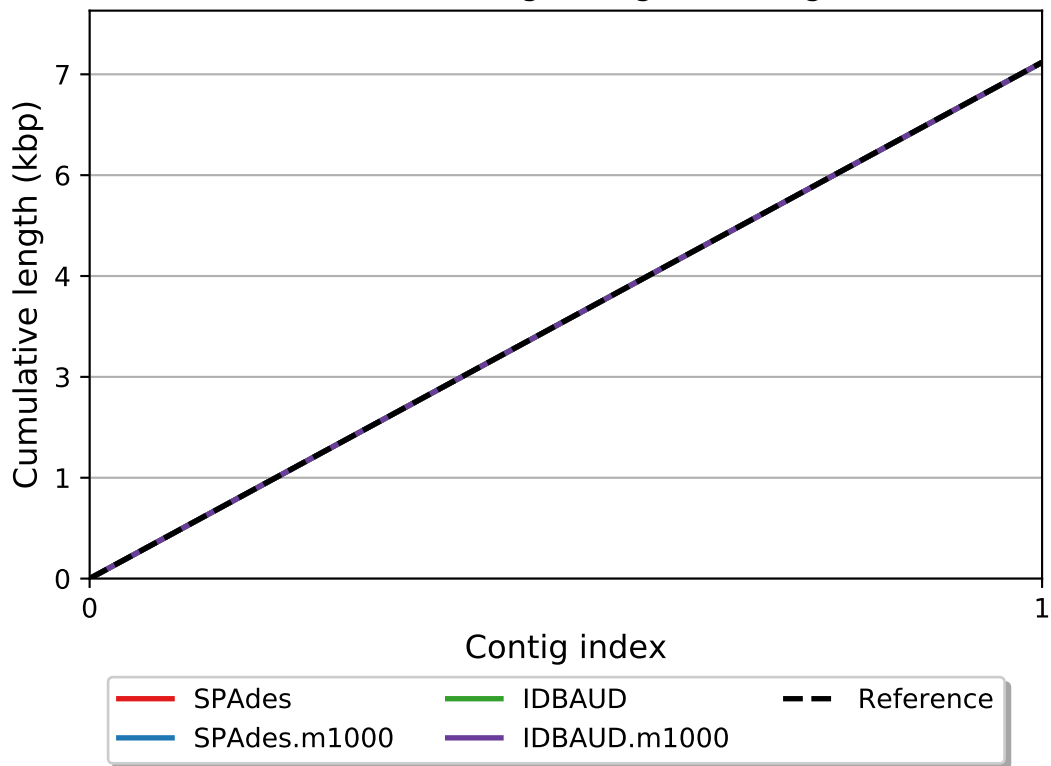
Misassemblies



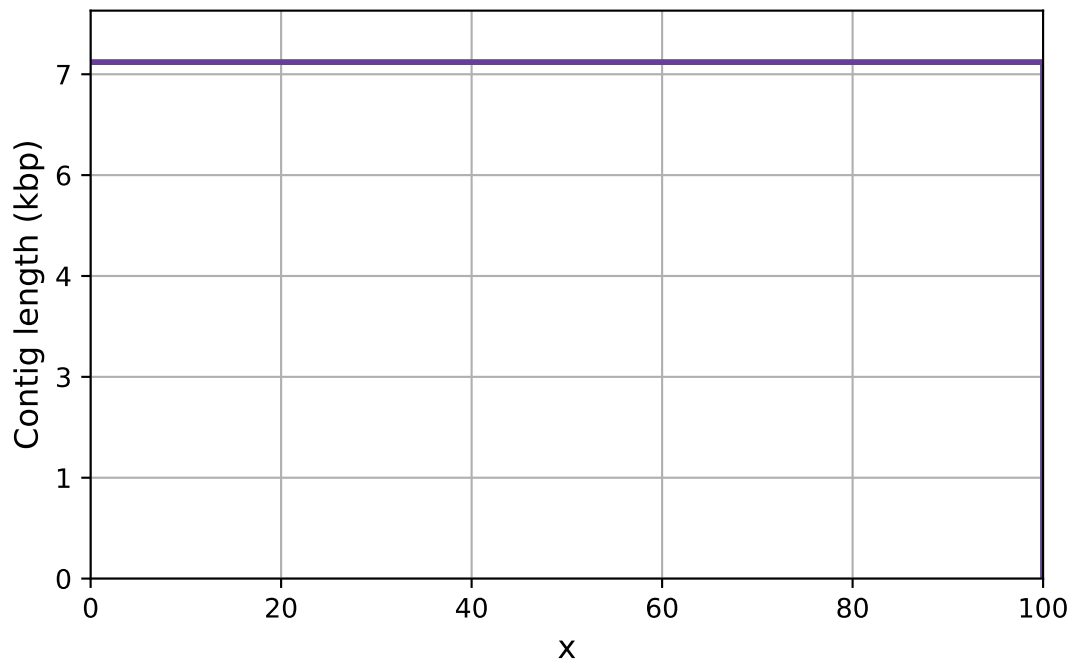
FRCurve (misassemblies)



Cumulative length (aligned contigs)

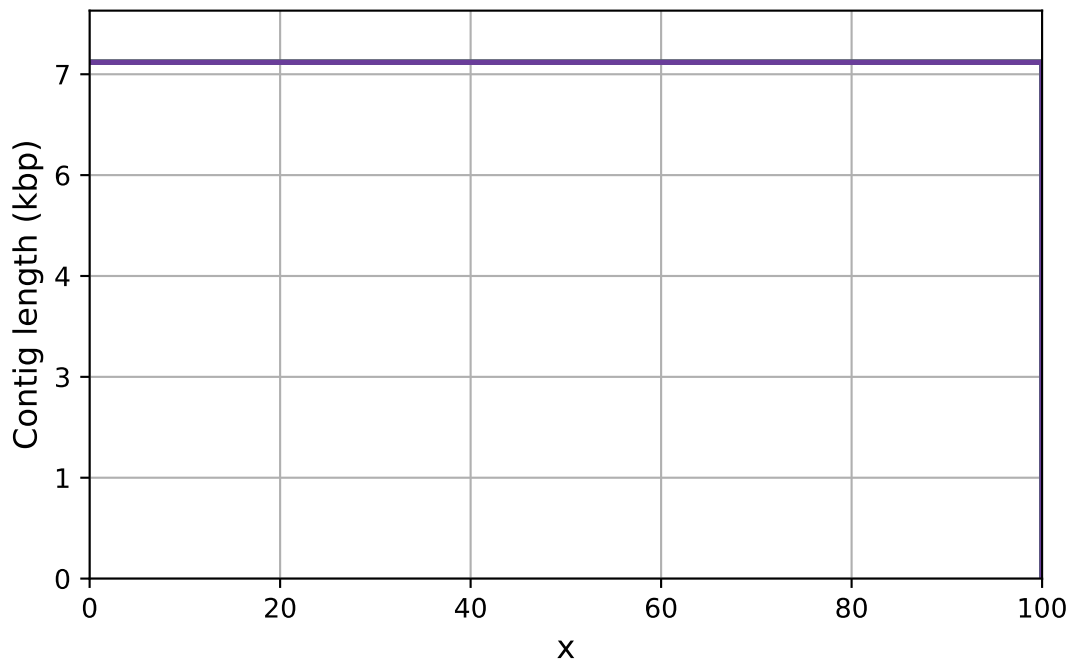


NAx

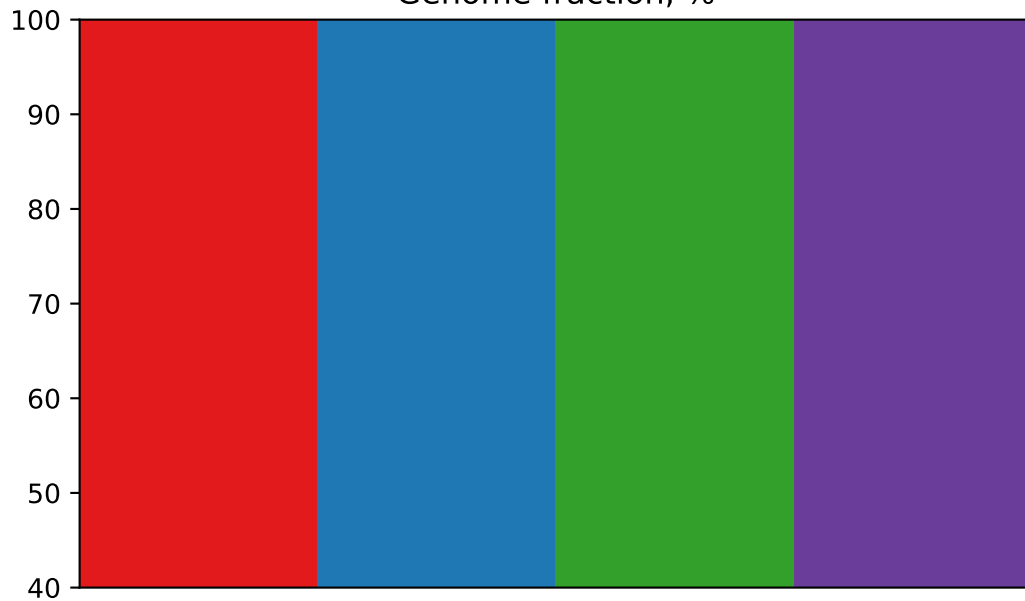


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000