

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)	45694	45694	45671	45671
Total length (>= 5000 bp)	45694	45694	45671	45671
Total length (>= 10000 bp)	45694	45694	45671	45671
Total length (>= 25000 bp)	45694	45694	45671	45671
Total length (>= 50000 bp)	0	0	0	0
# contigs	1	1	1	1
Largest contig	45694	45694	45671	45671
Total length	45694	45694	45671	45671
Reference length	48216	48216	48216	48216
GC (%)	54.90	54.90	54.89	54.89
Reference GC (%)	54.85	54.85	54.85	54.85
N50	45694	45694	45671	45671
NG50	45694	45694	45671	45671
N75	45694	45694	45671	45671
NG75	45694	45694	45671	45671
L50	1	1	1	1
LG50	1	1	1	1
L75	1	1	1	1
LG75	1	1	1	1
# misassemblies	1	1	1	1
# misassembled contigs	1	1	1	1
Misassembled contigs length	45694	45694	45671	45671
# 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 (%)	94.518	94.518	94.518	94.518
Duplication ratio	1.003	1.003	1.002	1.002
# 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	33301	33301	36304	36304
Total aligned length	45694	45694	45671	45671
NA50	33301	33301	36304	36304
NGA50	33301	33301	36304	36304
NA75	12393	12393	36304	36304
NGA75	12393	12393	36304	36304
LA50	1	1	1	1
LGA50	1	1	1	1
LA75	2	2	1	1
LGA75	2	2	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	1	1	1	1
# contig misassemblies	1	1	1	1
# c. relocations	1	1	1	1
# 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	1	1	1	1
Misassembled contigs length	45694	45694	45671	45671
# 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

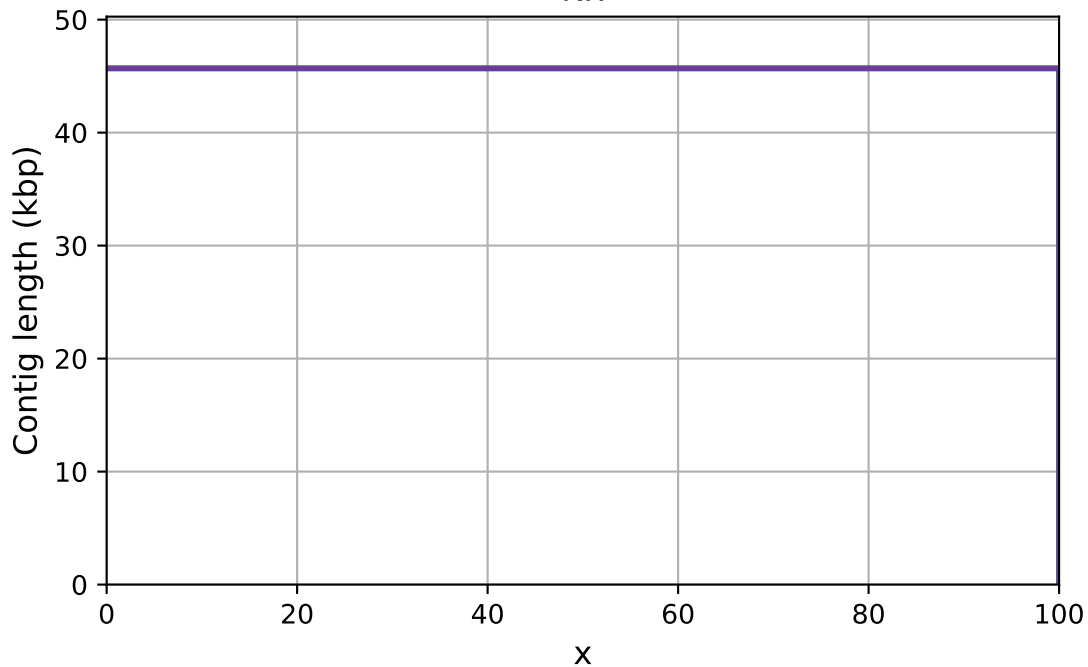
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

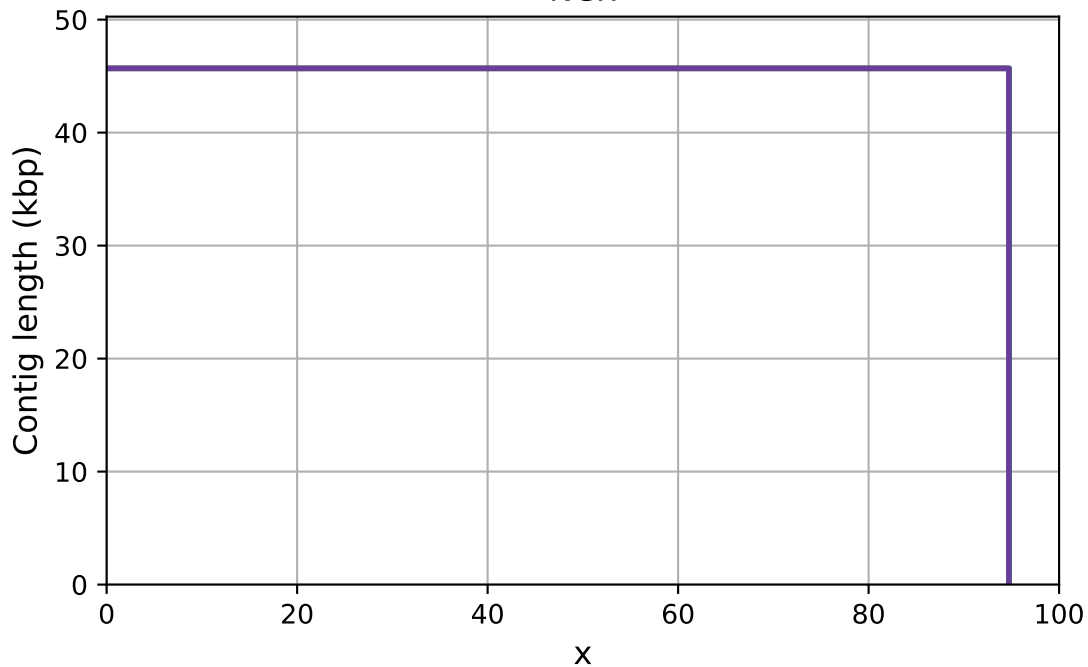
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



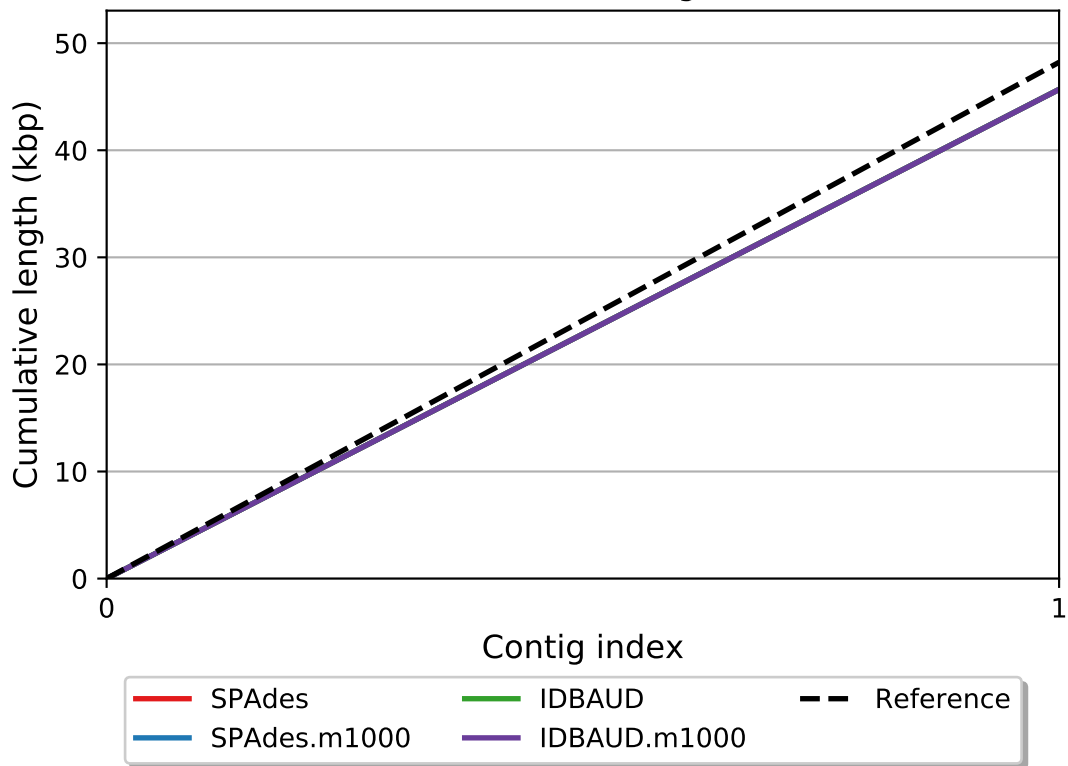
— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

NGx

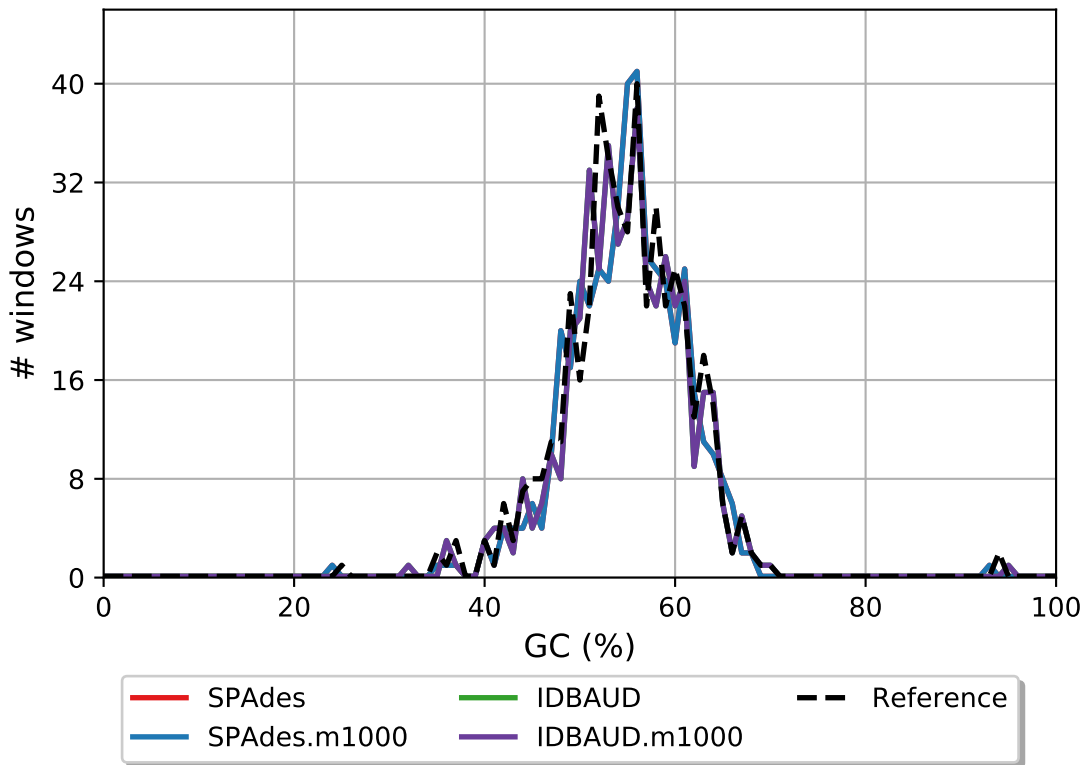


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

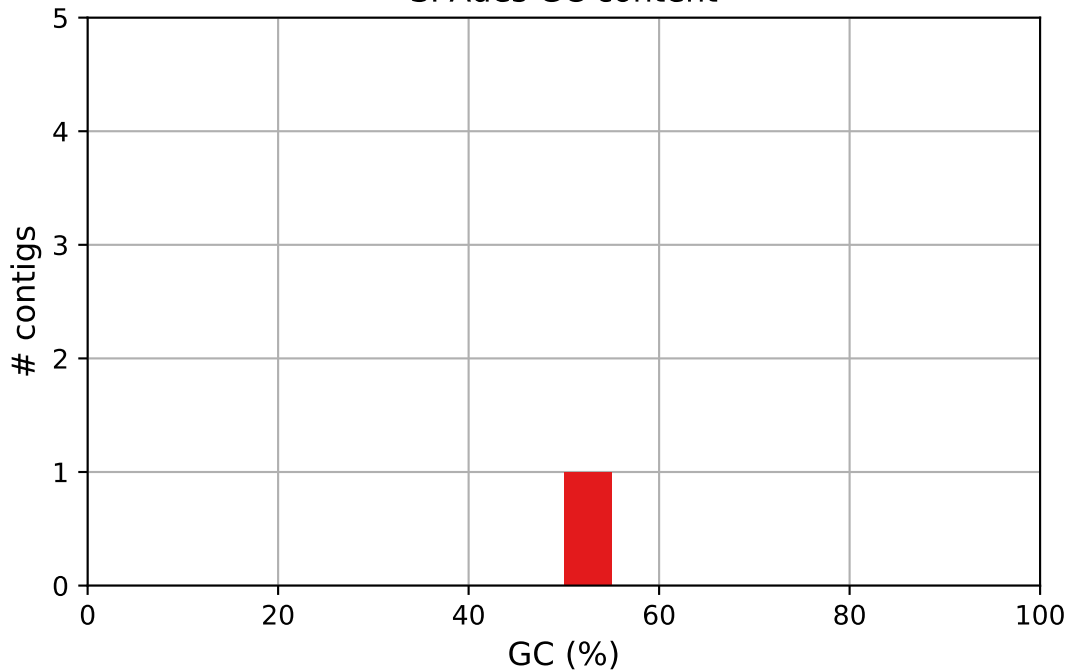
Cumulative length



GC content

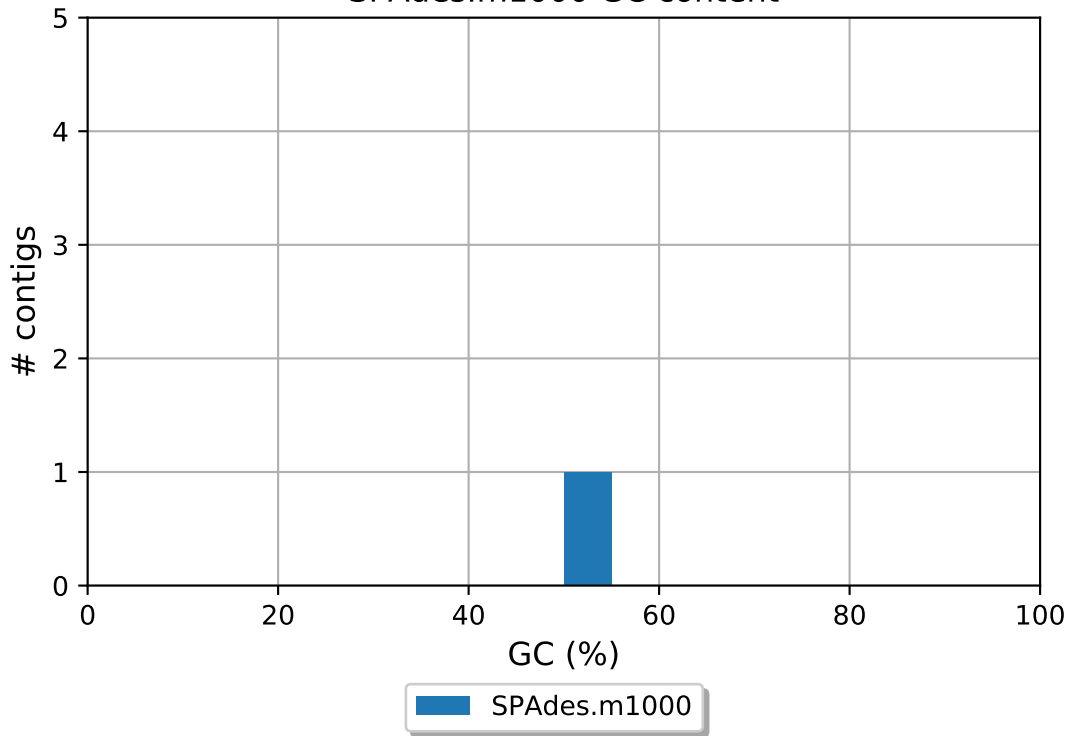


SPAdes GC content

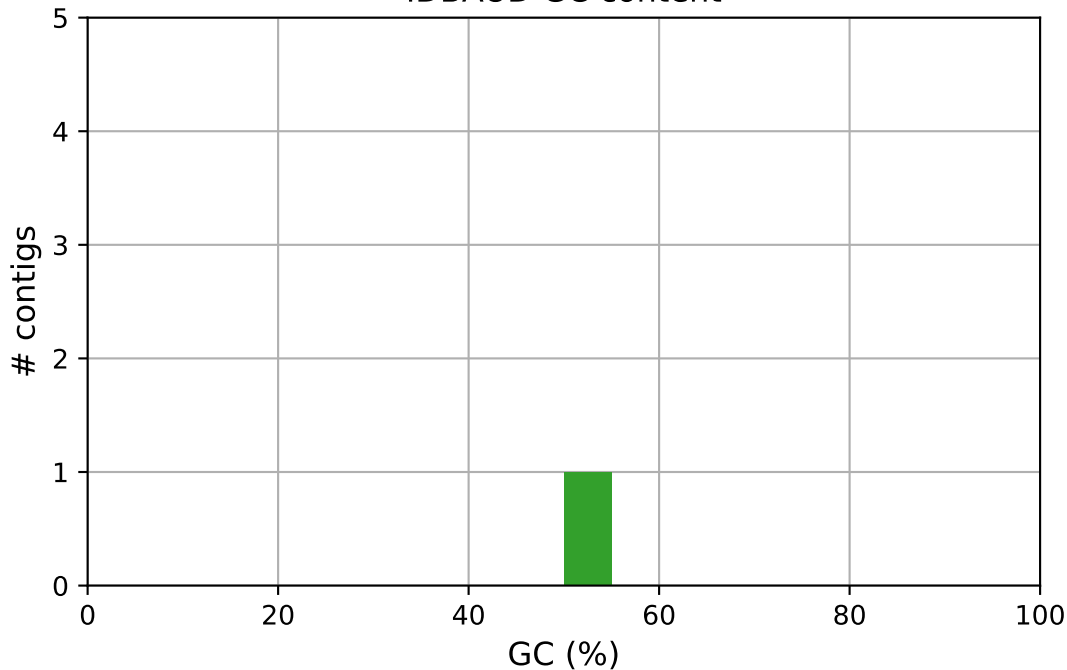


SPAdes

SPAdes.m1000 GC content

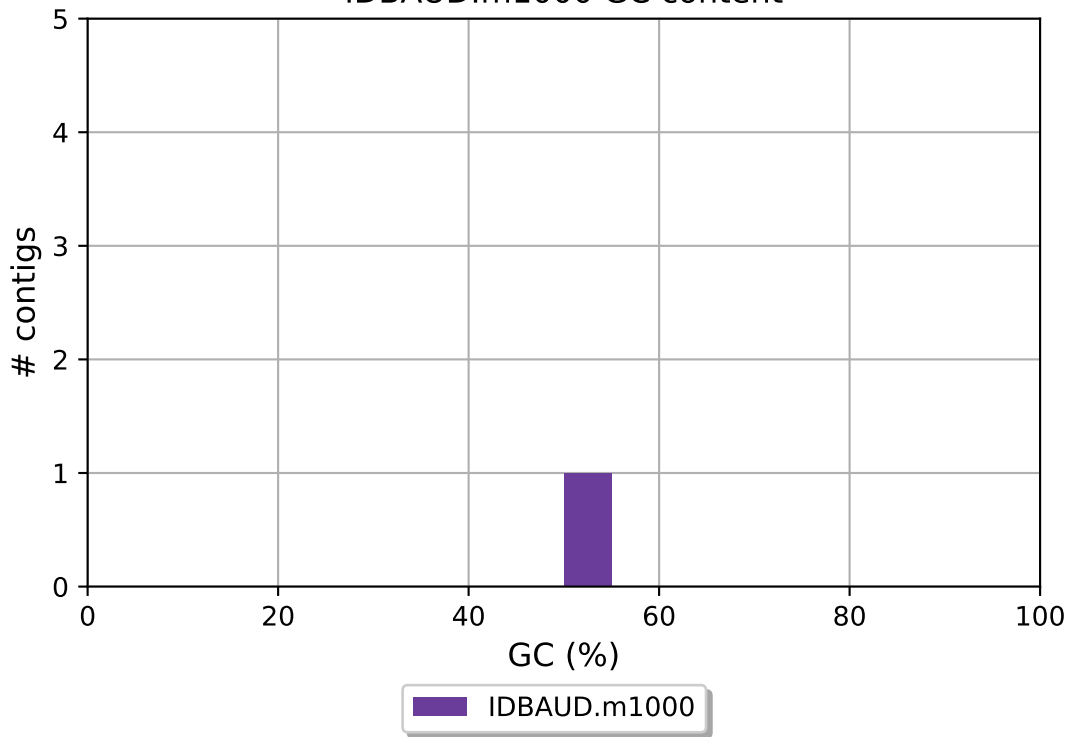


IDBAUD GC content

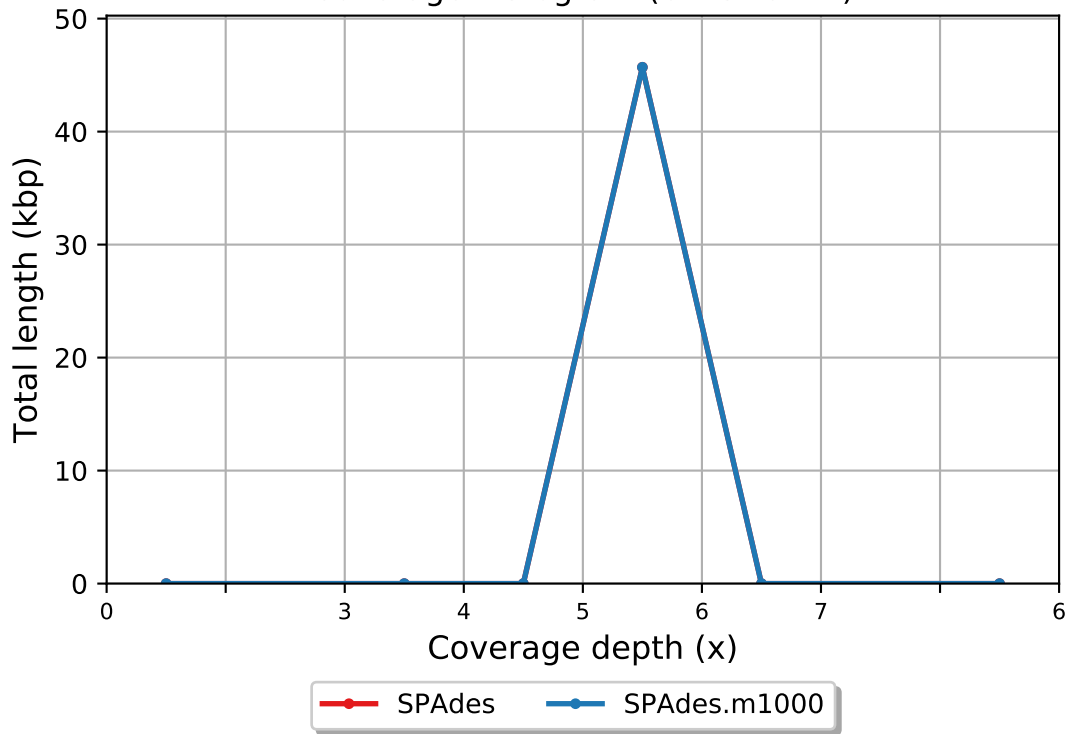


IDBAUD

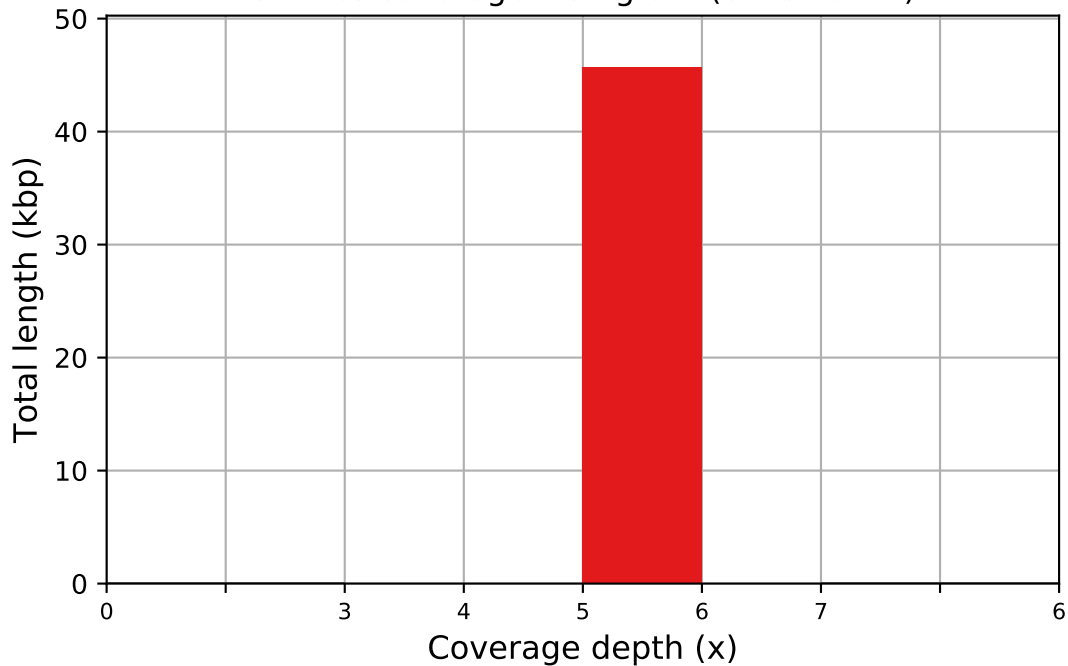
IDBAUD.m1000 GC content



Coverage histogram (bin size: 1x)

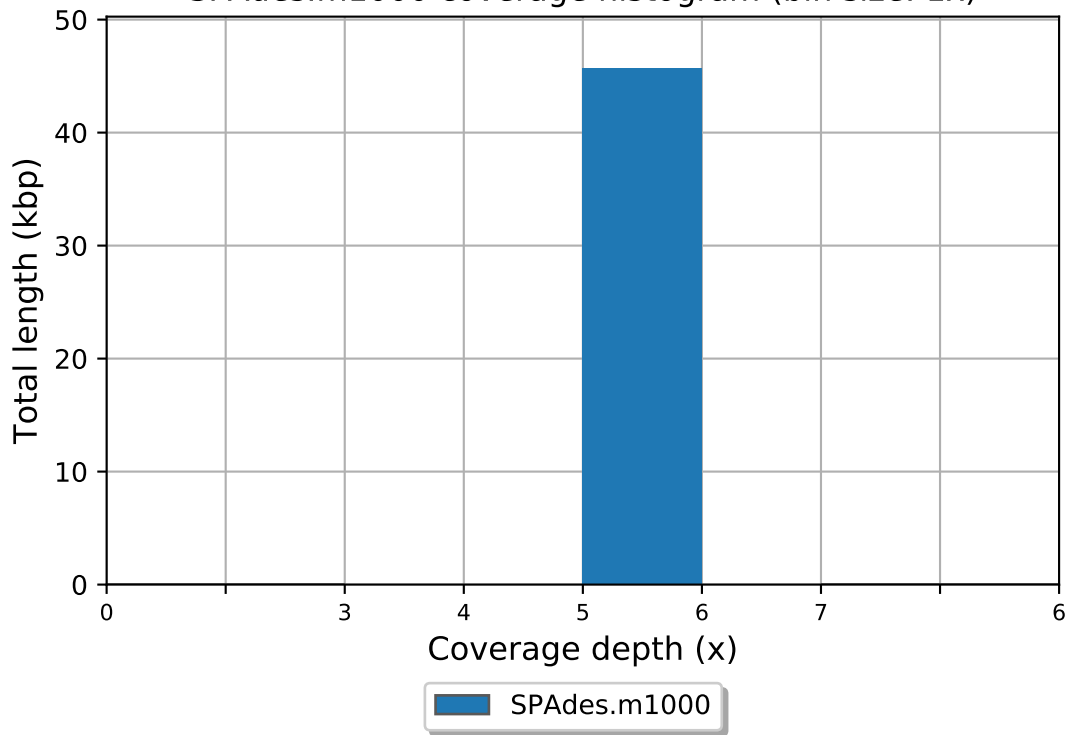


SPAdes coverage histogram (bin size: 1x)

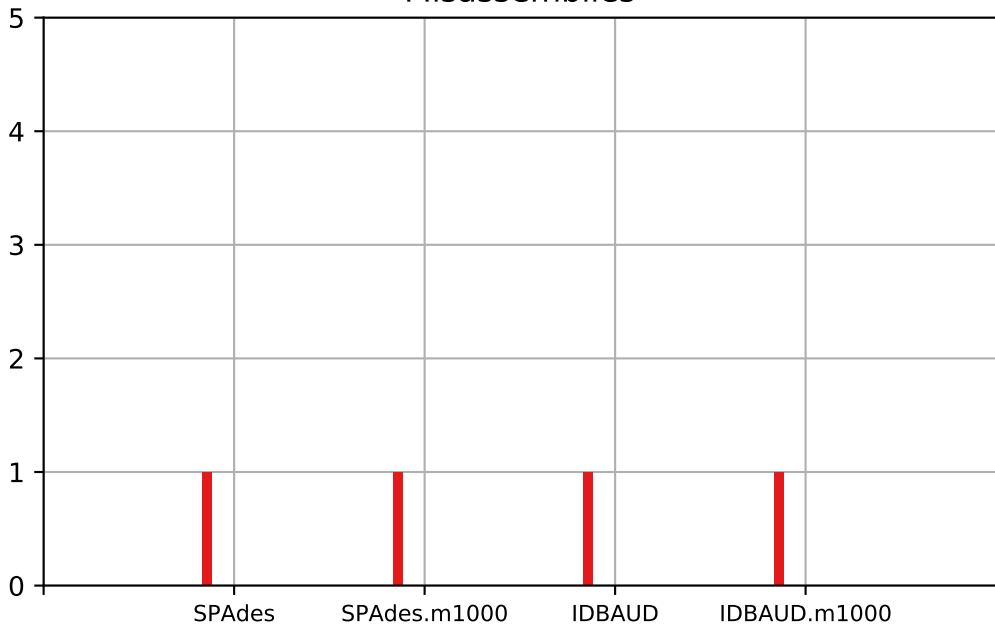


SPAdes

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

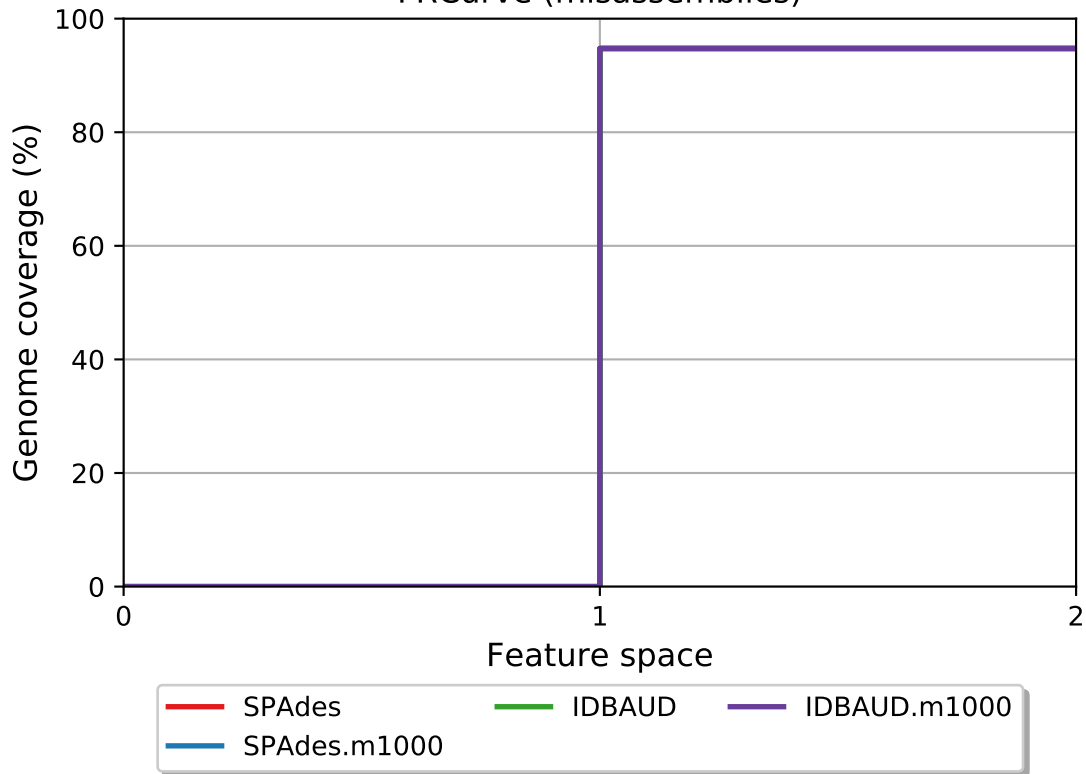


Misassemblies

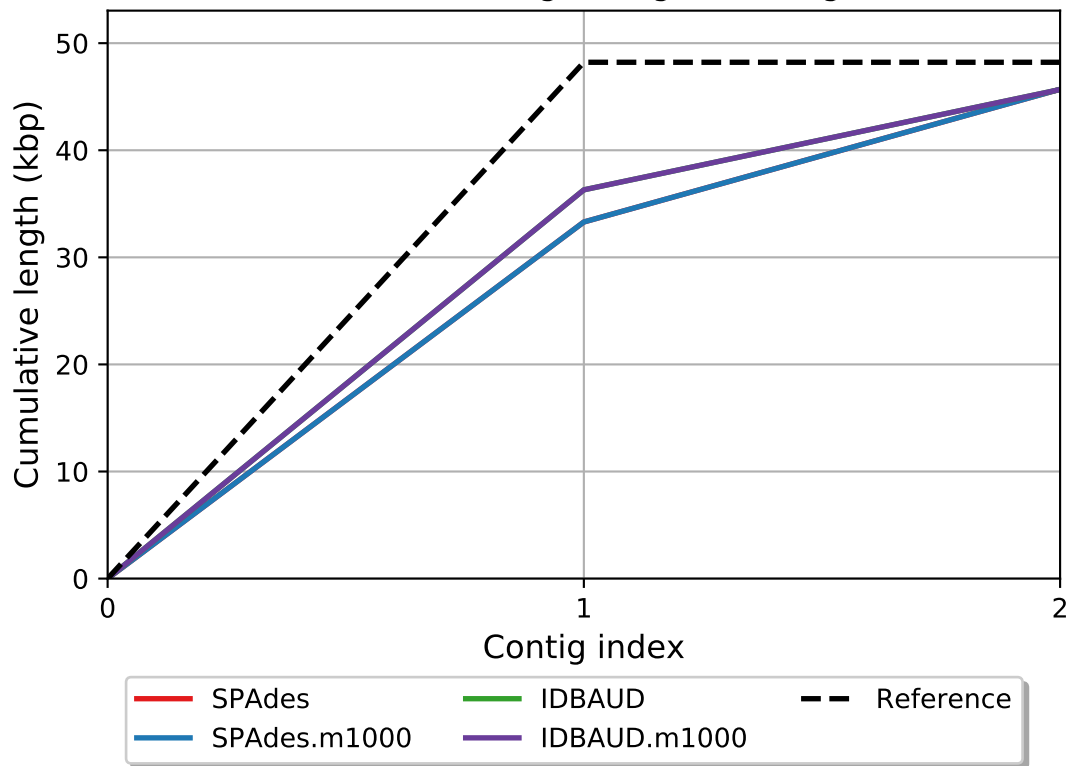


 # relocations

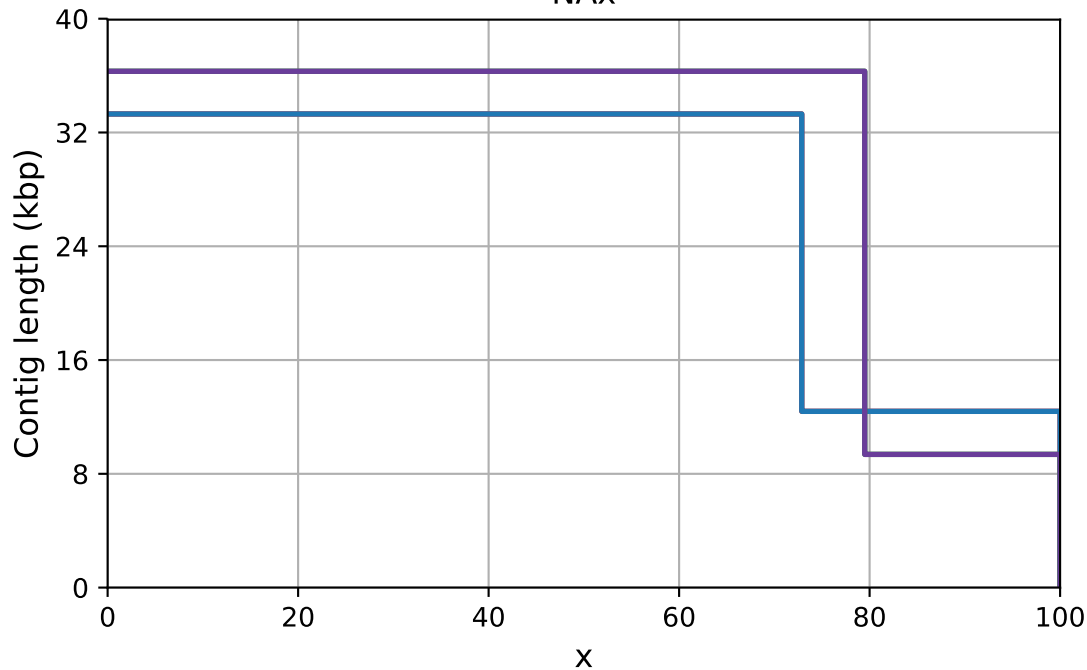
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAX

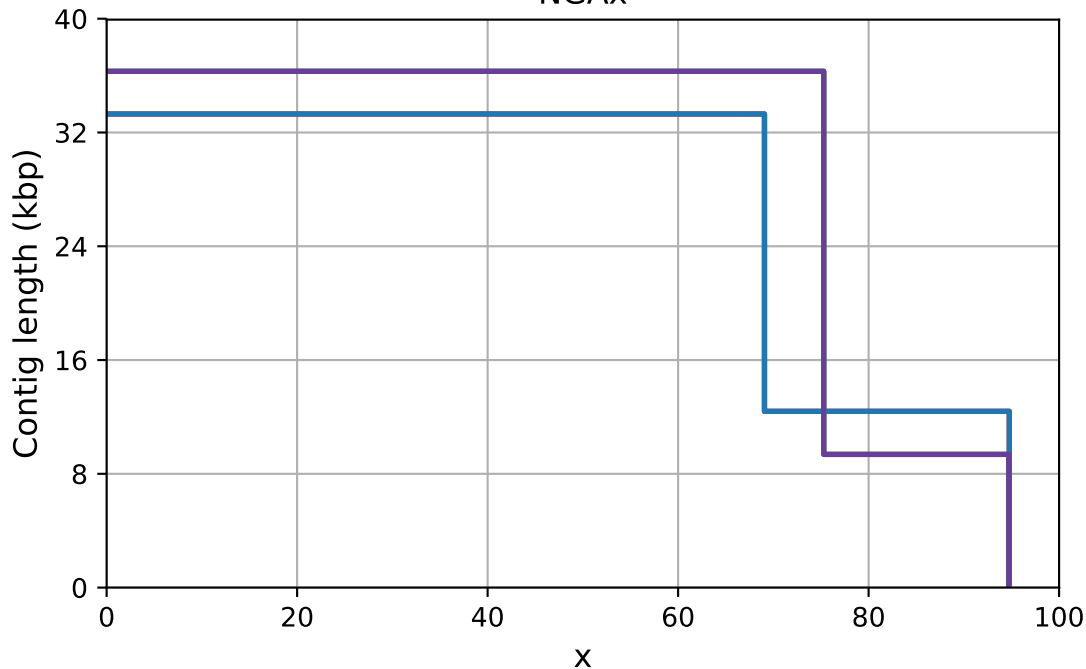


SPAdes
SPAdes.m1000

IDBAUD

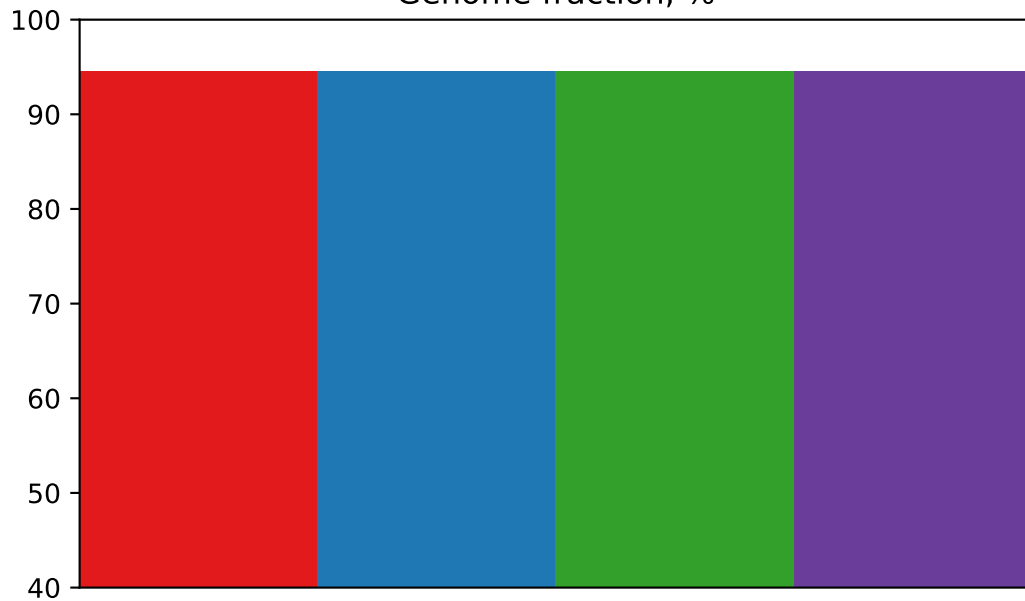
IDBAUD.m1000

NGAx



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

Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000