

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	77	77	107	107
# contigs (>= 5000 bp)	63	63	79	79
# contigs (>= 10000 bp)	54	54	58	58
# contigs (>= 25000 bp)	34	34	36	36
# contigs (>= 50000 bp)	21	21	20	20
Total length (>= 1000 bp)	3287348	3287348	3262809	3262809
Total length (>= 5000 bp)	3251406	3251406	3196762	3196762
Total length (>= 10000 bp)	3185513	3185513	3036439	3036439
Total length (>= 25000 bp)	2842311	2842311	2695548	2695548
Total length (>= 50000 bp)	2329050	2329050	2089356	2089356
# contigs	79	77	125	107
Largest contig	252961	252961	224974	224974
Total length	3288651	3287348	3275131	3262809
Reference length	3402093	3402093	3402093	3402093
GC (%)	62.05	62.05	62.05	62.06
Reference GC (%)	62.05	62.05	62.05	62.05
N50	84984	84984	72199	72199
NG50	77276	77276	63231	63231
N75	46347	46347	36862	40508
NG75	44579	44579	31243	31243
L50	11	11	13	13
LG50	12	12	14	14
L75	24	24	29	28
LG75	26	26	31	31
# misassemblies	11	11	0	0
# misassembled contigs	11	11	0	0
Misassembled contigs length	644512	644512	0	0
# local misassemblies	2	2	23	23
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	14	14	3	3
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 1 part	0 + 0 part	0 + 0 part
Unaligned length	933	933	0	0
Genome fraction (%)	96.454	96.432	96.160	95.818
Duplication ratio	1.002	1.002	1.001	1.001
# N's per 100 kbp	90.19	90.22	19.97	20.04
# mismatches per 100 kbp	7.25	7.25	0.09	0.06
# indels per 100 kbp	0.30	0.30	0.00	0.00
Largest alignment	252595	252595	223855	223855
Total aligned length	3284335	3283032	3273357	3261035
NA50	83605	83605	72199	72199
NGA50	77276	77276	63231	63231
NA75	41927	41927	36862	40508
NGA75	35935	35935	31205	31205
LA50	11	11	13	13
LGA50	12	12	14	14
LA75	26	26	29	28
LGA75	28	28	32	32

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

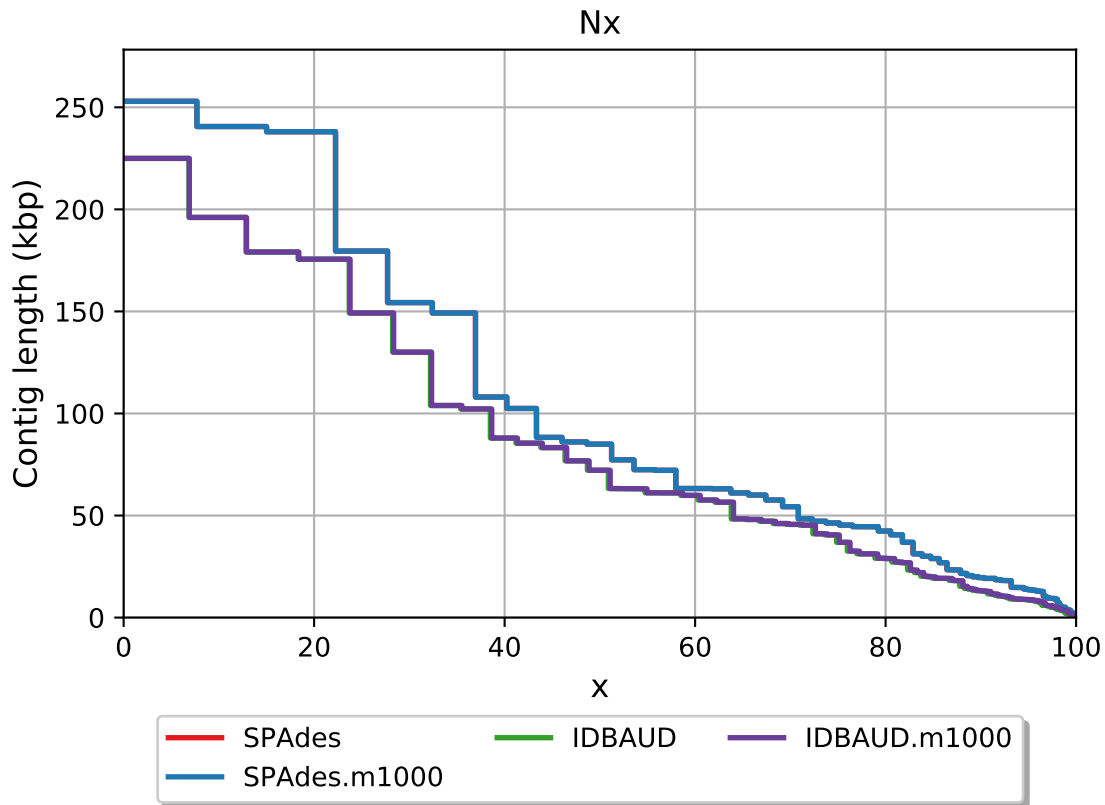
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	11	11	0	0
# contig misassemblies	9	9	0	0
# c. relocations	9	9	0	0
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	2	2	0	0
# s. relocations	2	2	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	11	11	0	0
Misassembled contigs length	644512	644512	0	0
# possibly misassembled contigs	0	0	0	0
# possible misassemblies	0	0	0	0
# local misassemblies	2	2	23	23
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	14	14	3	3
# unaligned mis. contigs	0	0	0	0
# mismatches	238	238	3	2
# indels	10	10	0	0
# indels (<= 5 bp)	7	7	0	0
# indels (> 5 bp)	3	3	0	0
Indels length	164	164	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).

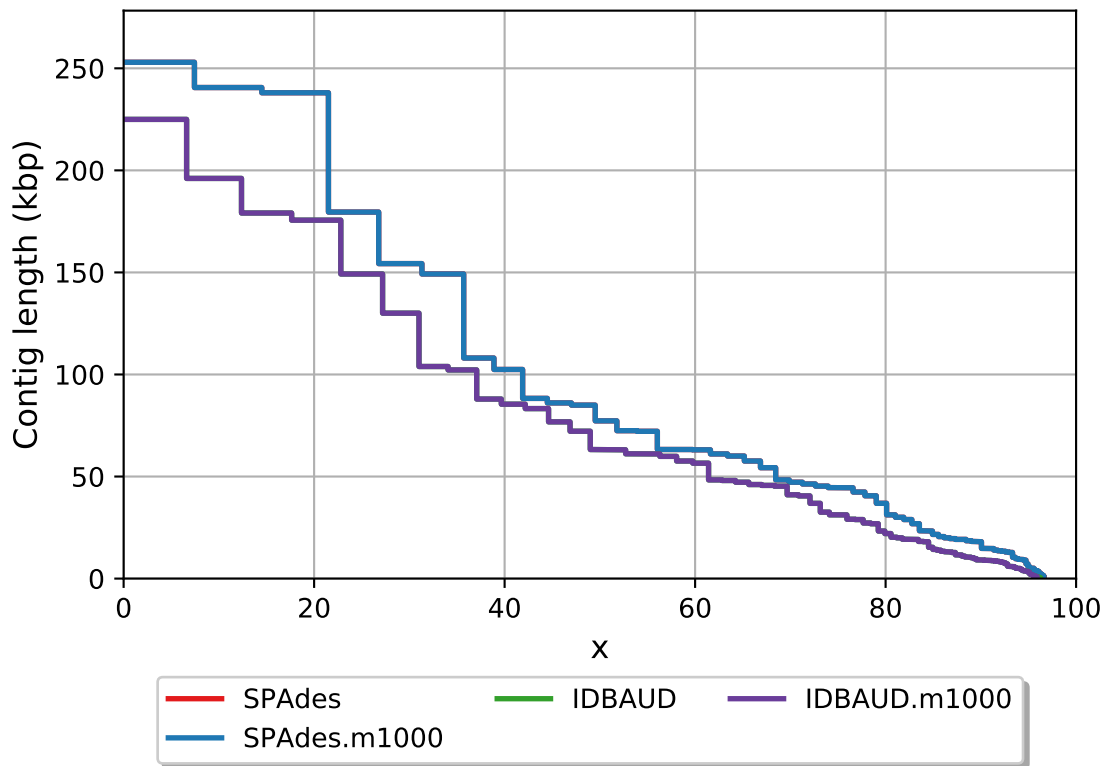
Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	1	1	0	0
Partially unaligned length	933	933	0	0
# N's	2966	2966	654	654

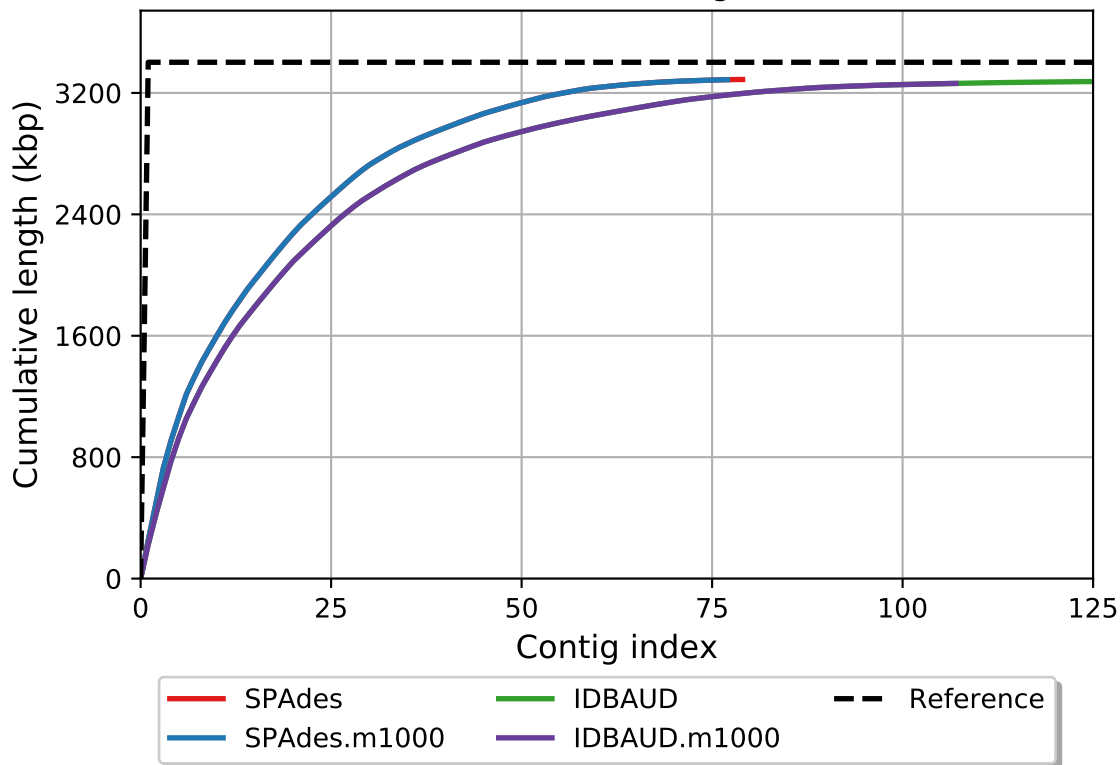
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



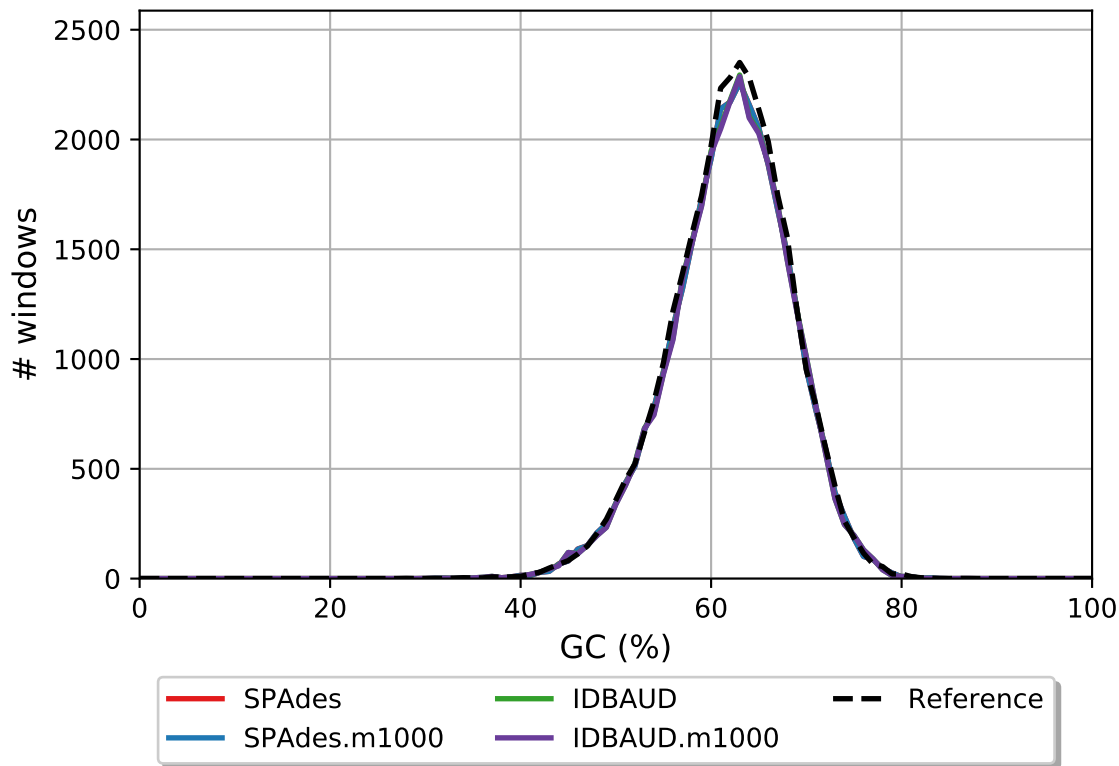
NGx



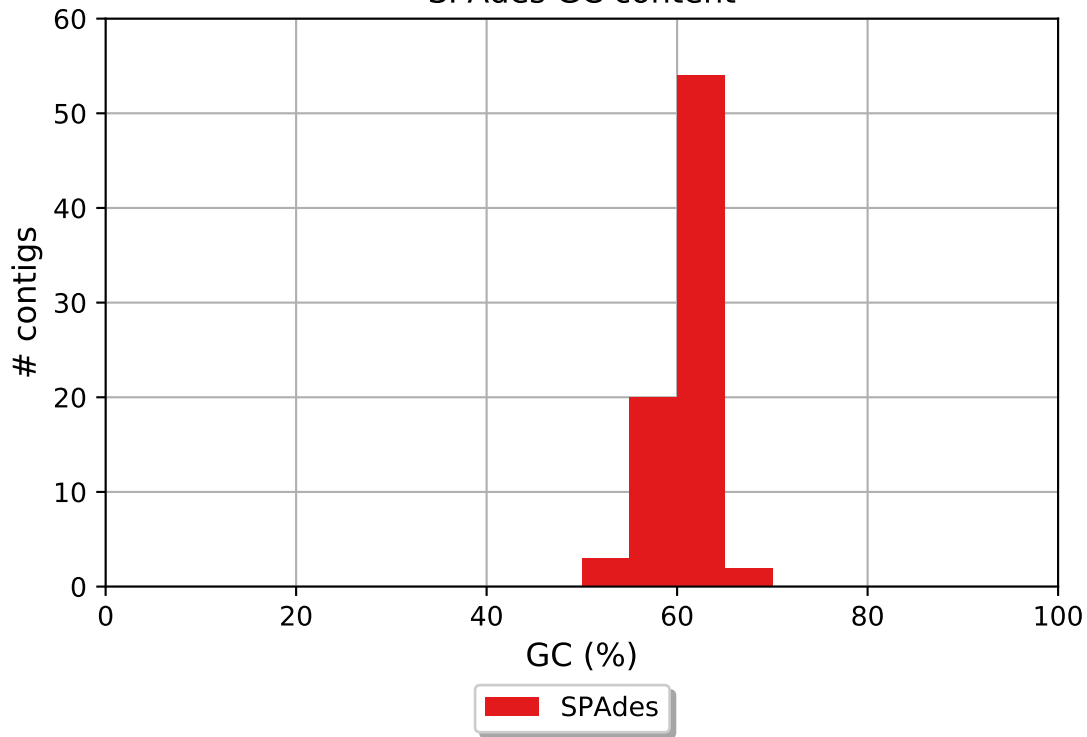
Cumulative length



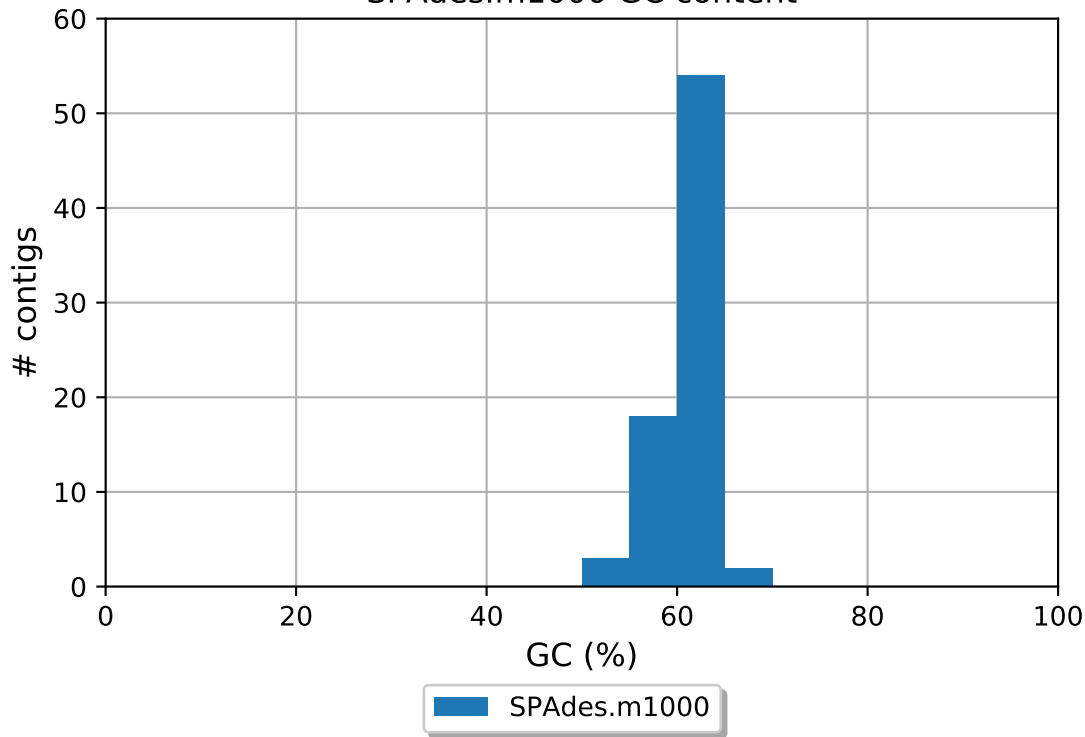
GC content



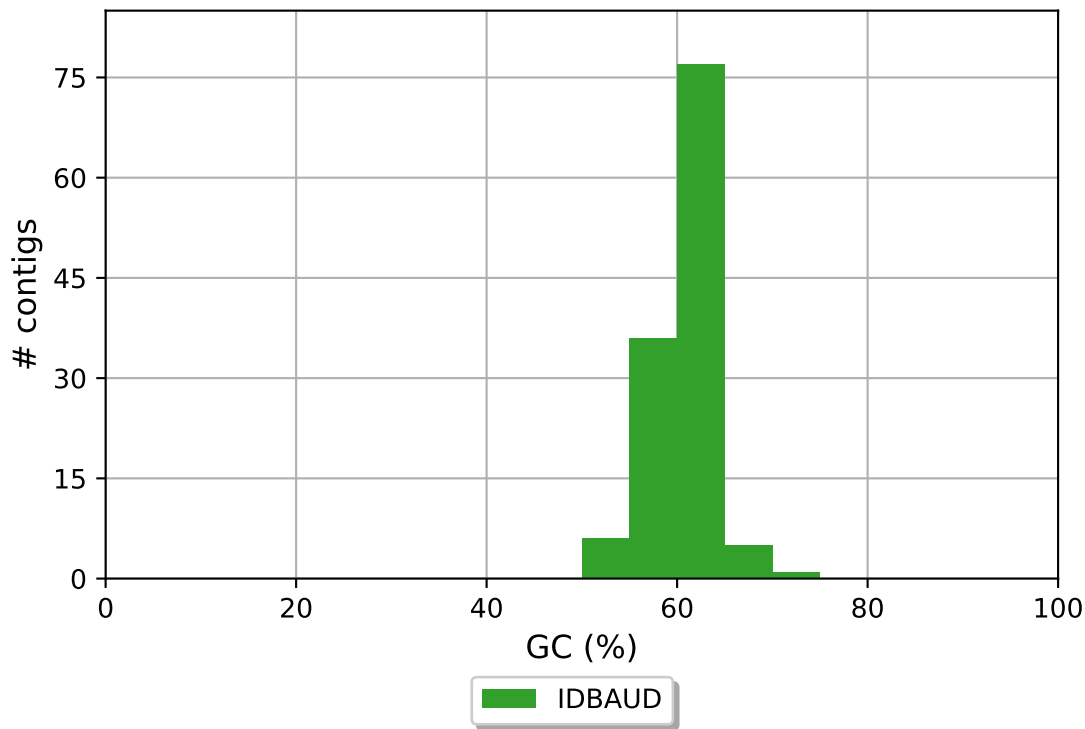
SPAdes GC content



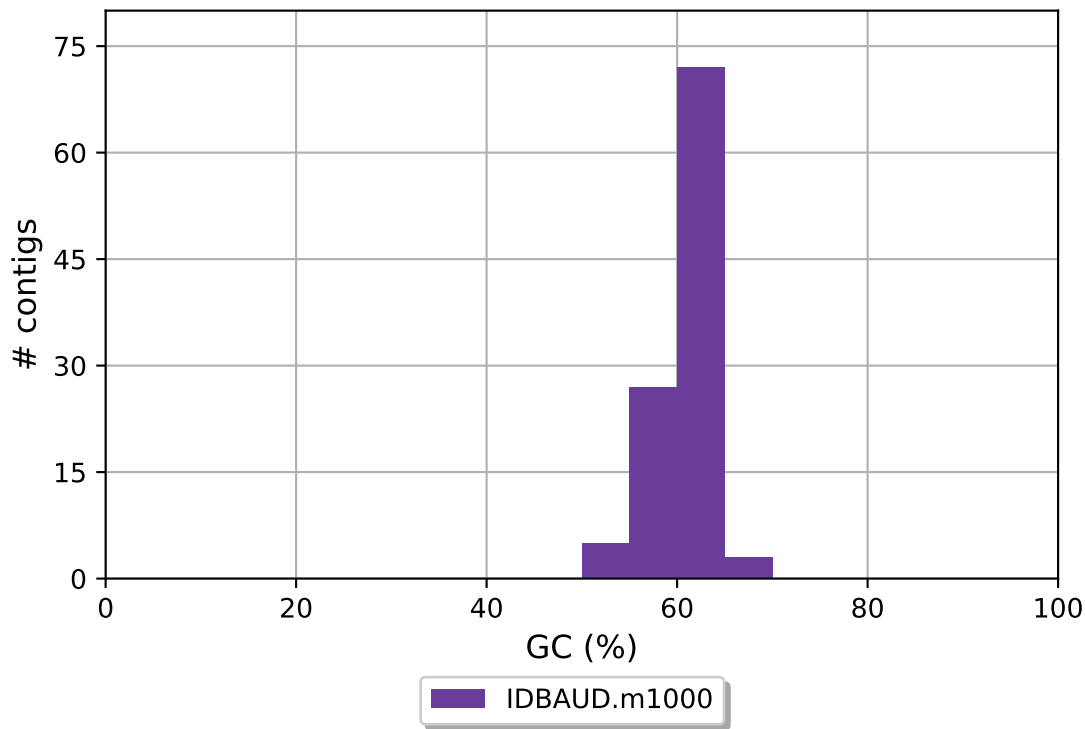
SPAdes.m1000 GC content



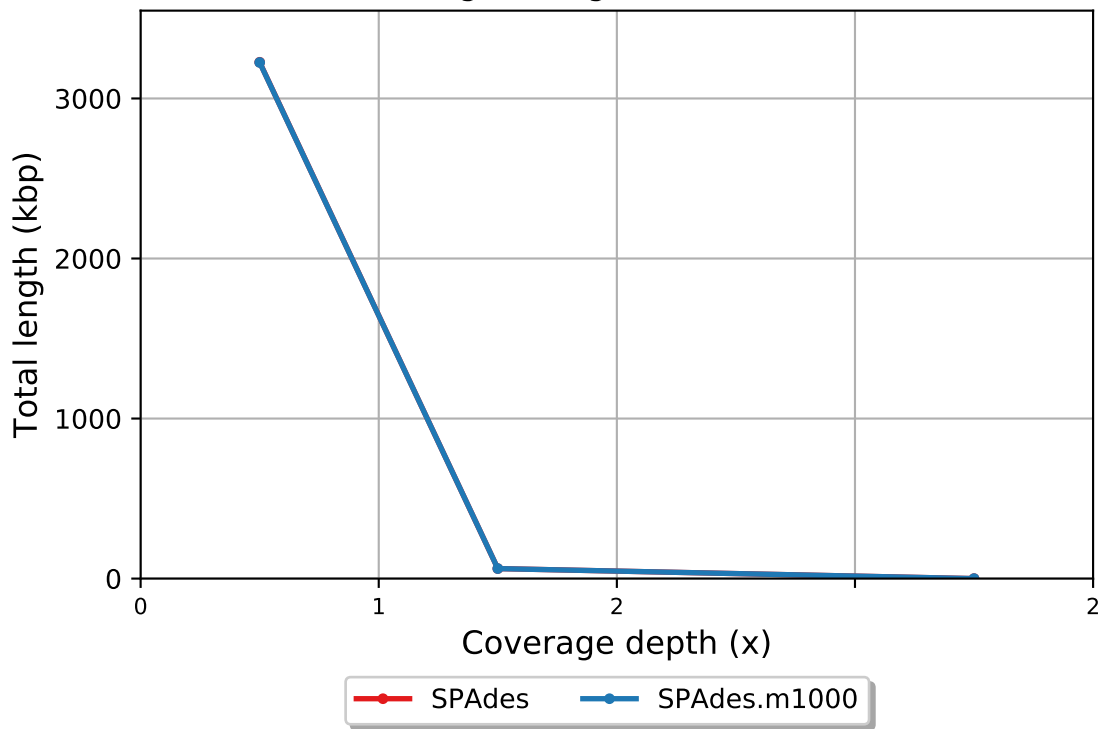
IDBAUD GC content



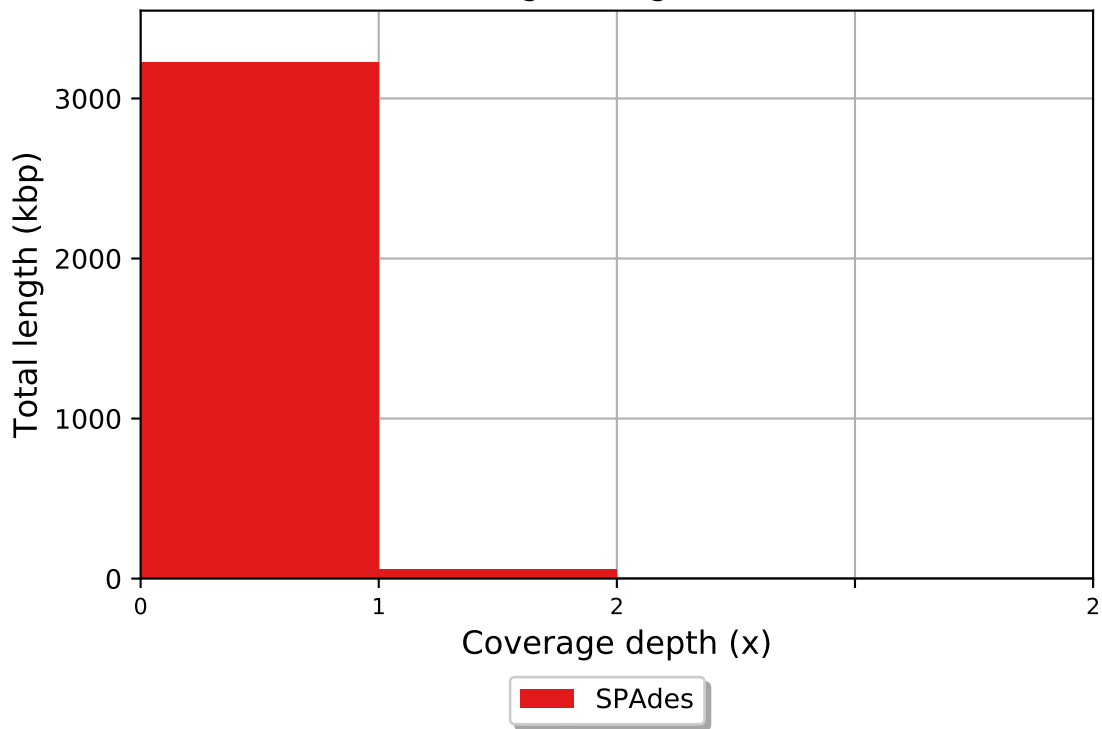
IDBAUD.m1000 GC content



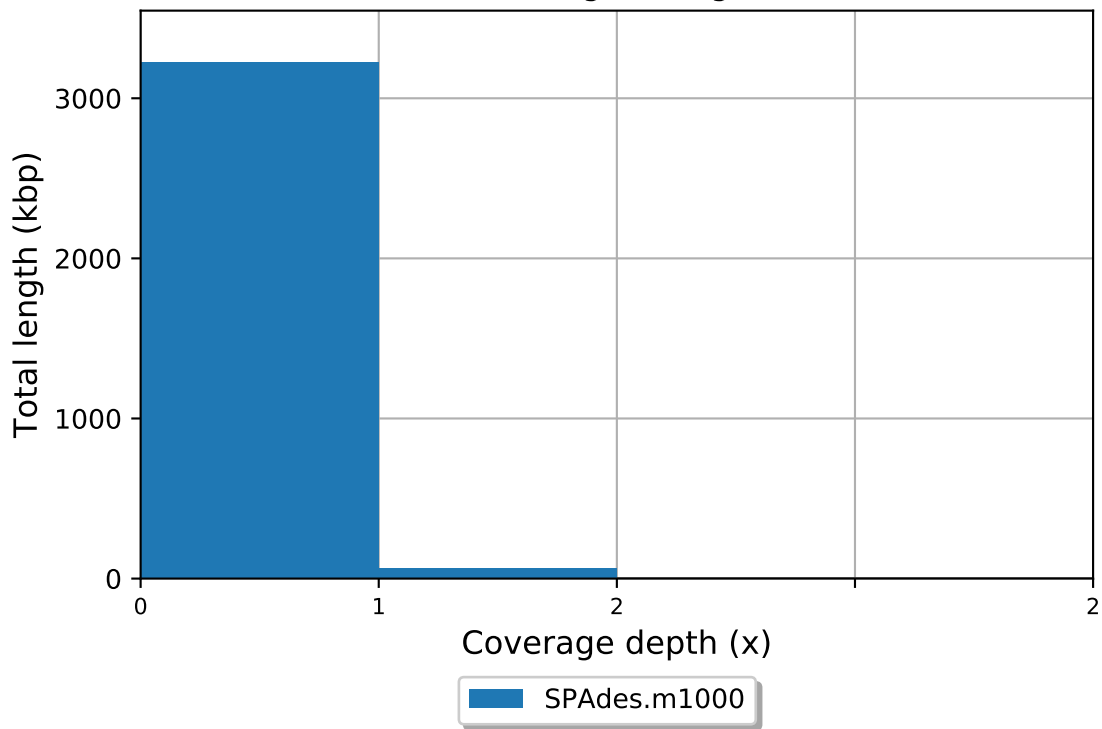
Coverage histogram (bin size: 1x)



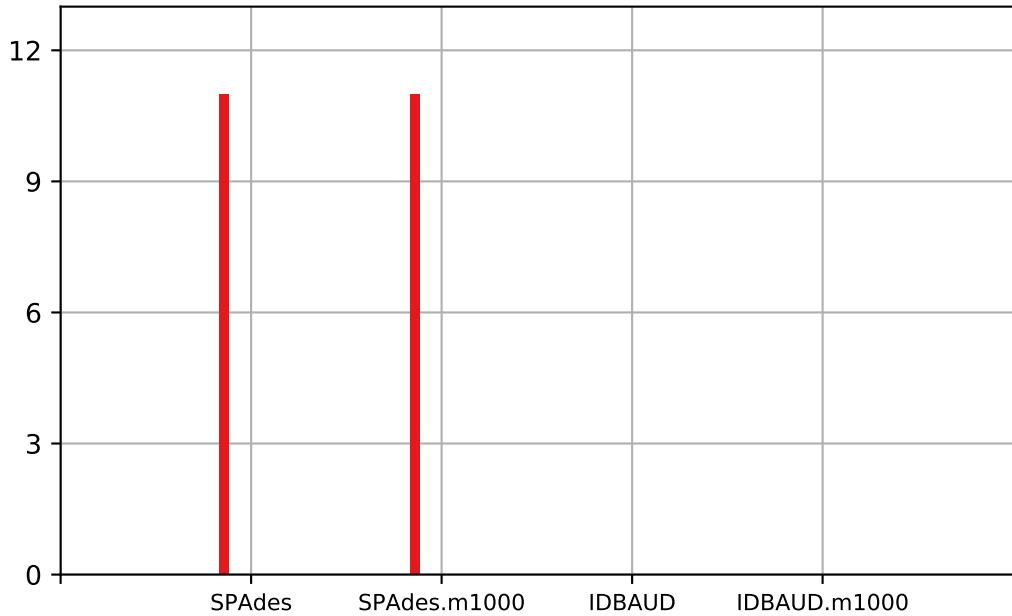
SPAdes coverage histogram (bin size: 1x)



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

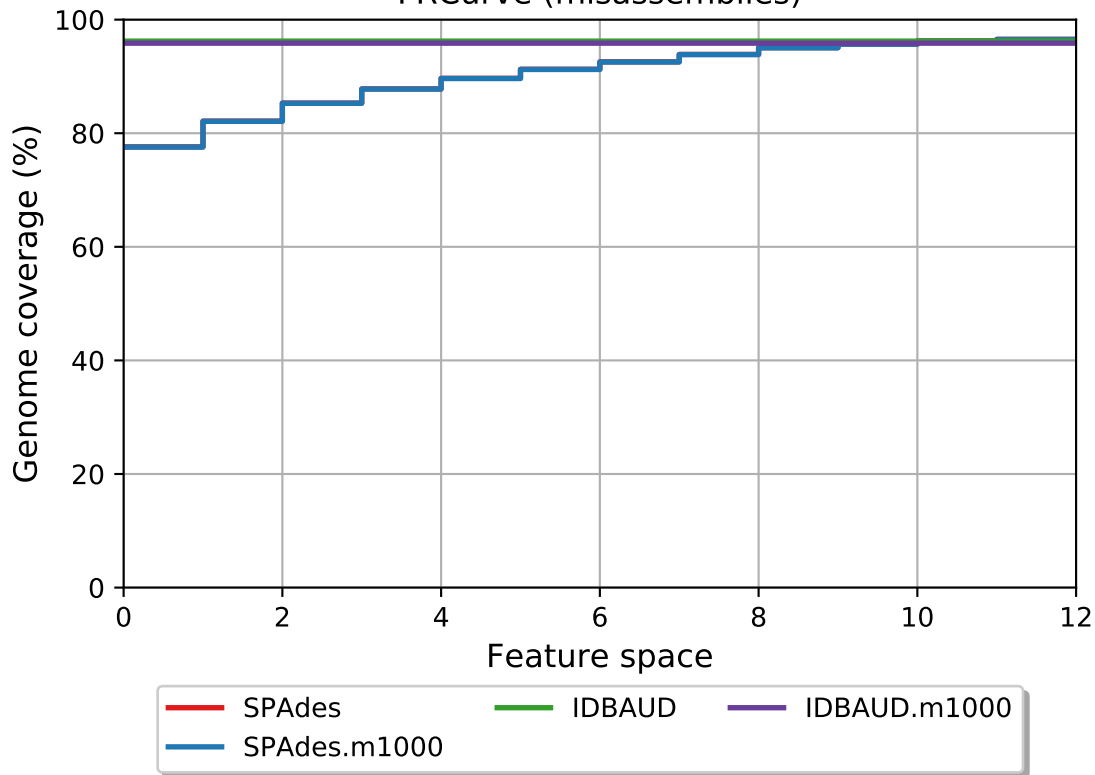


Misassemblies

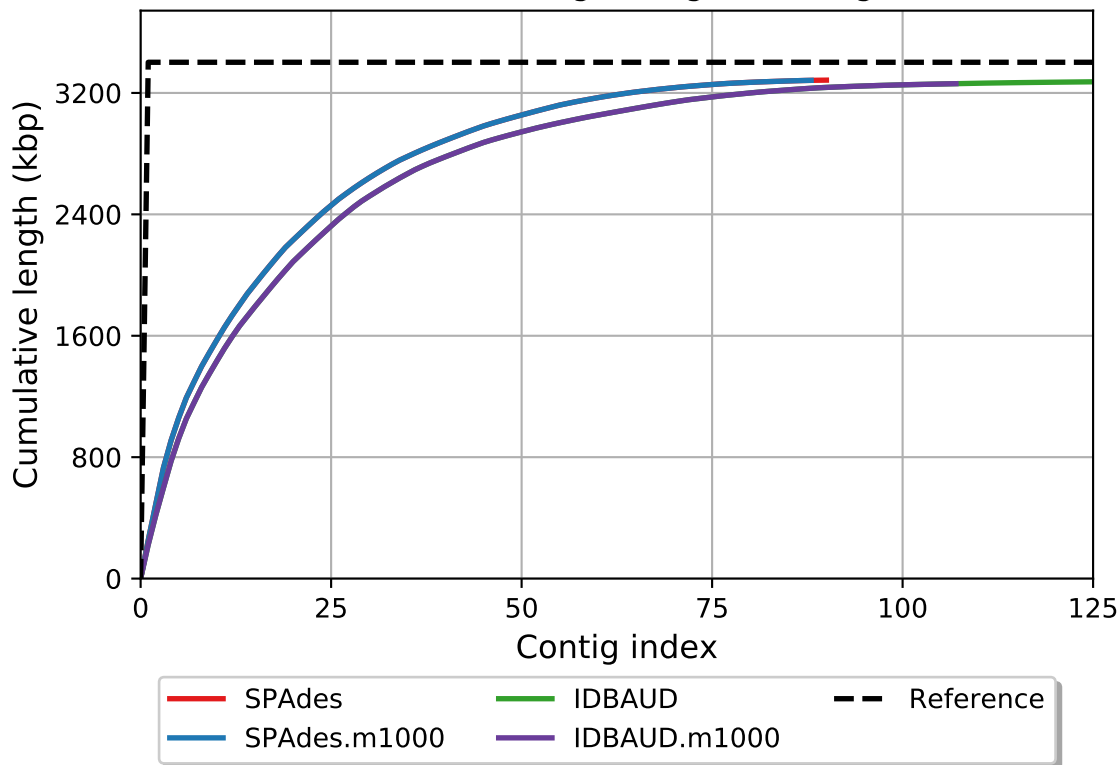


 # relocations

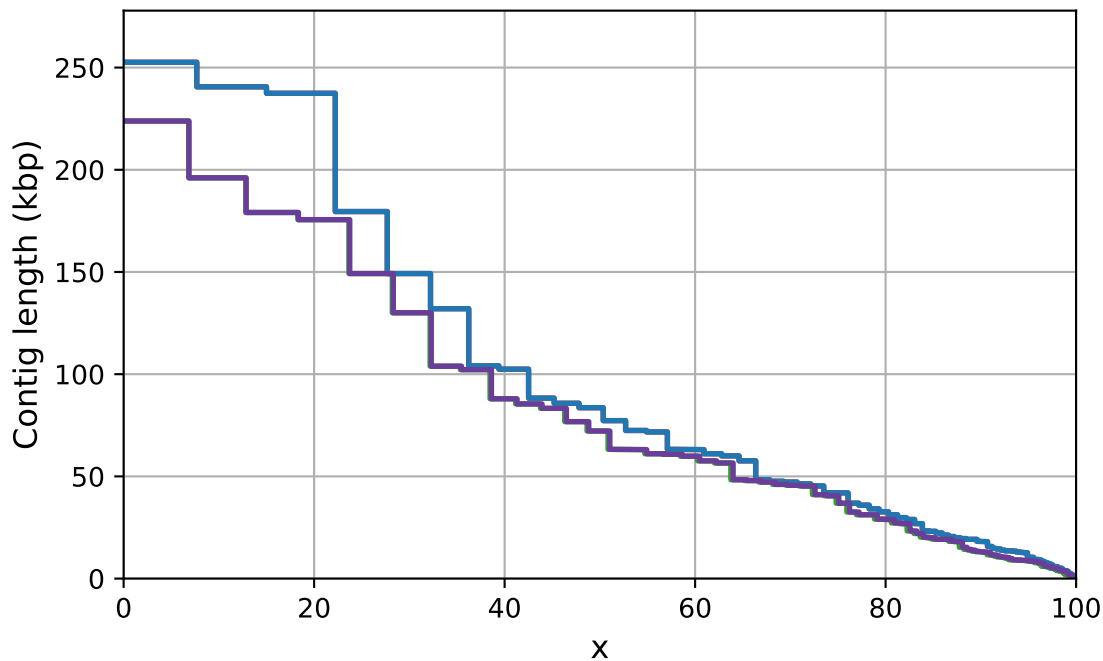
FRCurve (misassemblies)



Cumulative length (aligned contigs)

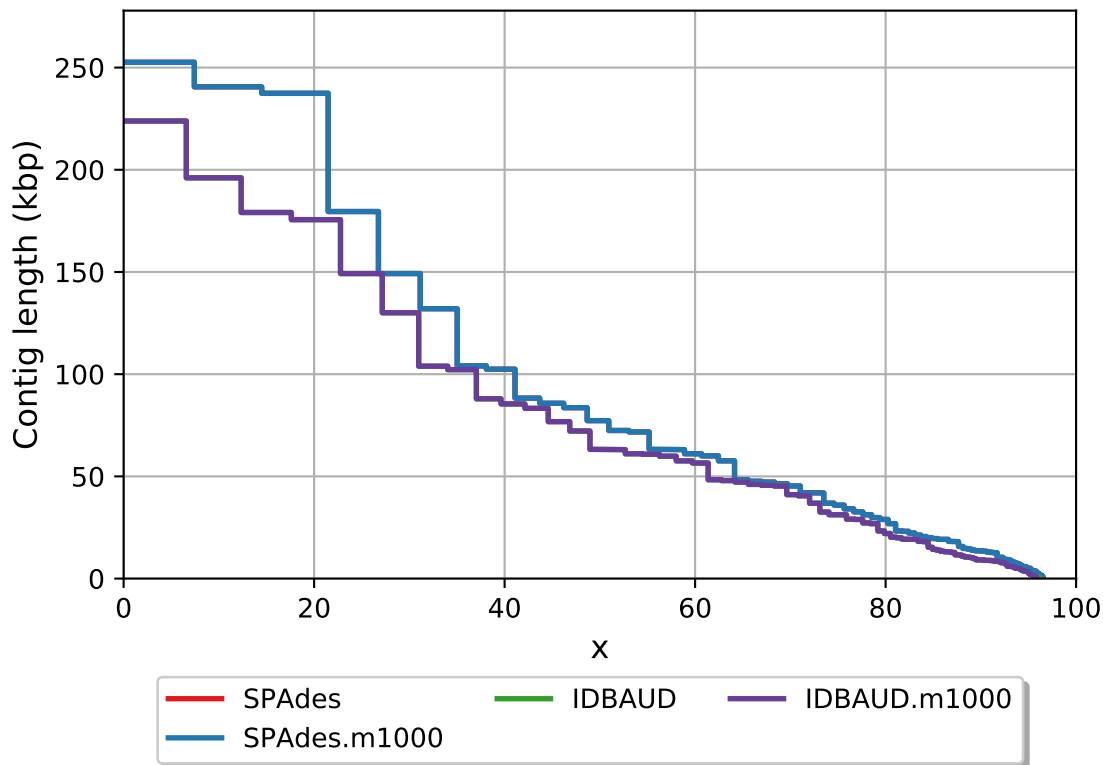


NAx

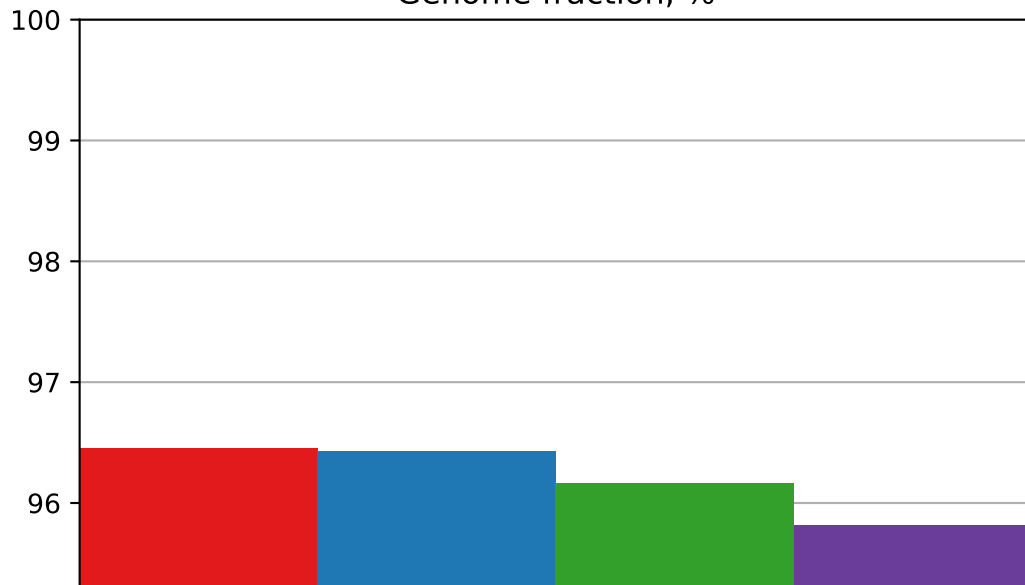


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000

NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000