

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	20	20	34	34
# contigs (>= 5000 bp)	19	19	23	23
# contigs (>= 10000 bp)	18	18	21	21
# contigs (>= 25000 bp)	16	16	20	20
# contigs (>= 50000 bp)	15	15	19	19
Total length (>= 1000 bp)	3155235	3155235	3132828	3132828
Total length (>= 5000 bp)	3151471	3151471	3099904	3099904
Total length (>= 10000 bp)	3144377	3144377	3083383	3083383
Total length (>= 25000 bp)	3113952	3113952	3059686	3059686
Total length (>= 50000 bp)	3069648	3069648	3018238	3018238
# contigs	22	20	54	34
Largest contig	607162	607162	416193	416193
Total length	3156903	3155235	3146798	3132828
Reference length	3192235	3192235	3192235	3192235
GC (%)	28.26	28.25	28.25	28.24
Reference GC (%)	28.36	28.36	28.36	28.36
N50	252692	252692	195357	195357
NG50	252692	252692	195357	195357
N75	140564	140564	113556	113556
NG75	140564	140564	113556	113556
L50	5	5	6	6
LG50	5	5	6	6
L75	9	9	12	12
LG75	9	9	12	12
# misassemblies	5	5	0	0
# misassembled contigs	3	3	0	0
Misassembled contigs length	658560	658560	0	0
# local misassemblies	2	2	28	28
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	3	3	3	3
# 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 (%)	98.728	98.703	98.504	98.116
Duplication ratio	1.002	1.001	1.001	1.000
# N's per 100 kbp	10.29	10.30	5.34	5.36
# mismatches per 100 kbp	14.06	14.06	0.35	0.22
# indels per 100 kbp	1.59	1.59	0.19	0.19
Largest alignment	361152	361152	416094	416094
Total aligned length	3152060	3150392	3146337	3132367
NA50	215436	215436	195357	195357
NGA50	215436	215436	195357	195357
NA75	140564	140564	113556	113556
NGA75	140564	140564	113556	113556
LA50	6	6	6	6
LGA50	6	6	6	6
LA75	11	11	12	12
LGA75	11	11	12	12

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

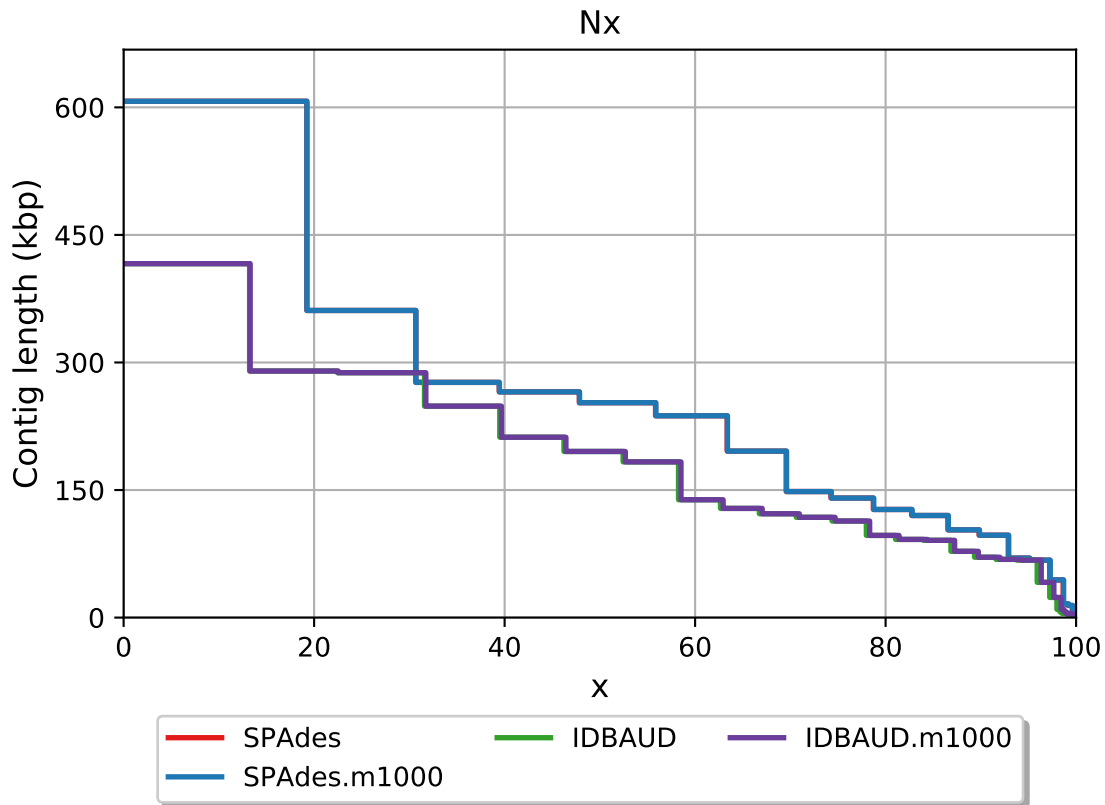
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	5	5	0	0
# contig misassemblies	5	5	0	0
# c. relocations	5	5	0	0
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	3	3	0	0
Misassembled contigs length	658560	658560	0	0
# possibly misassembled contigs	0	0	0	0
# possible misassemblies	0	0	0	0
# local misassemblies	2	2	28	28
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	3	3	3	3
# unaligned mis. contigs	0	0	0	0
# mismatches	443	443	11	7
# indels	50	50	6	6
# indels (<= 5 bp)	43	43	3	3
# indels (> 5 bp)	7	7	3	3
Indels length	209	209	92	92

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).

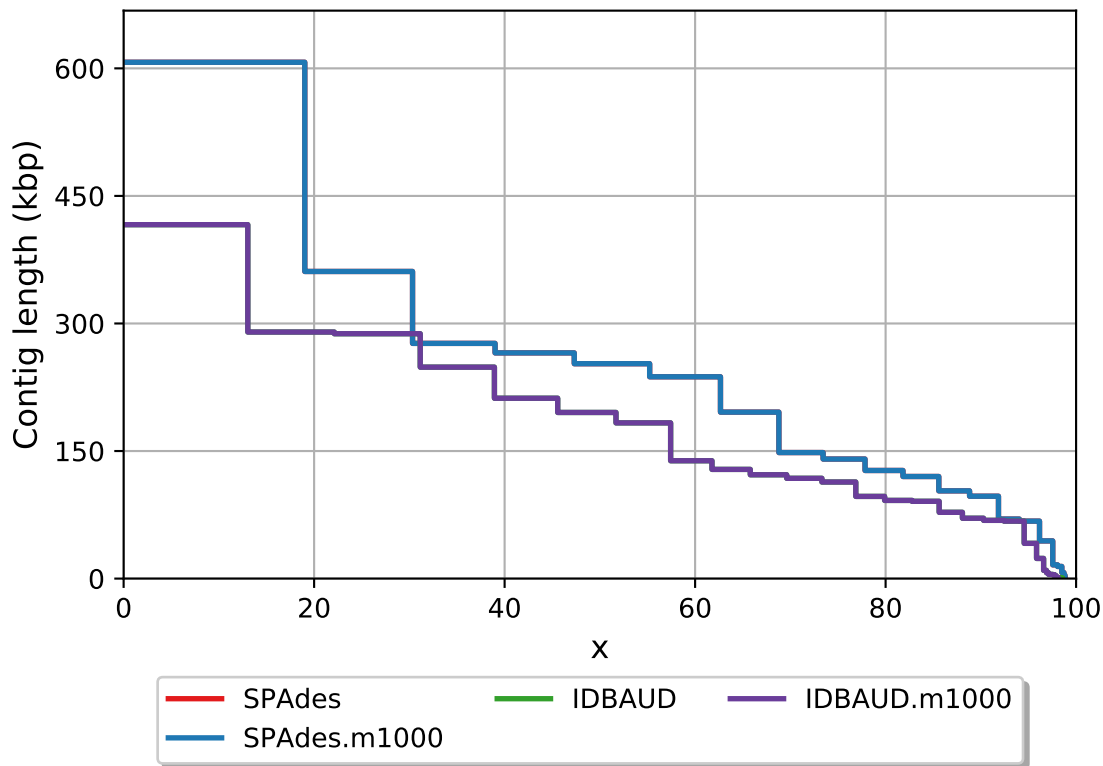
Unaligned report

	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	325	325	168	168

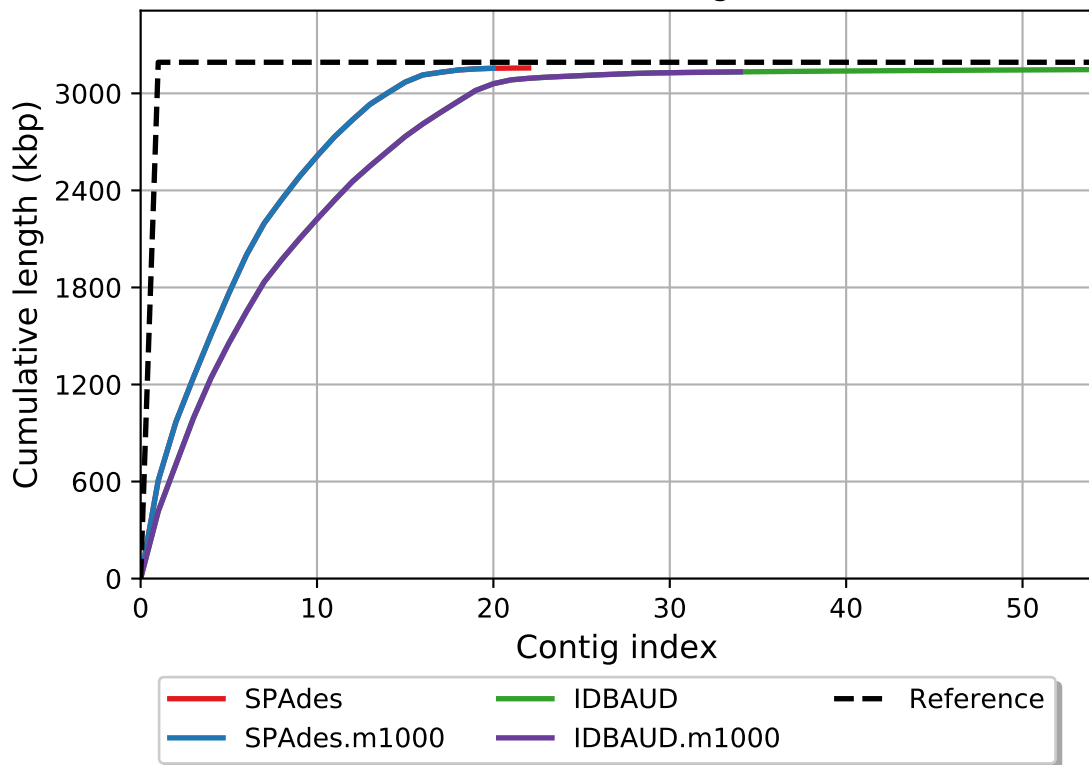
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



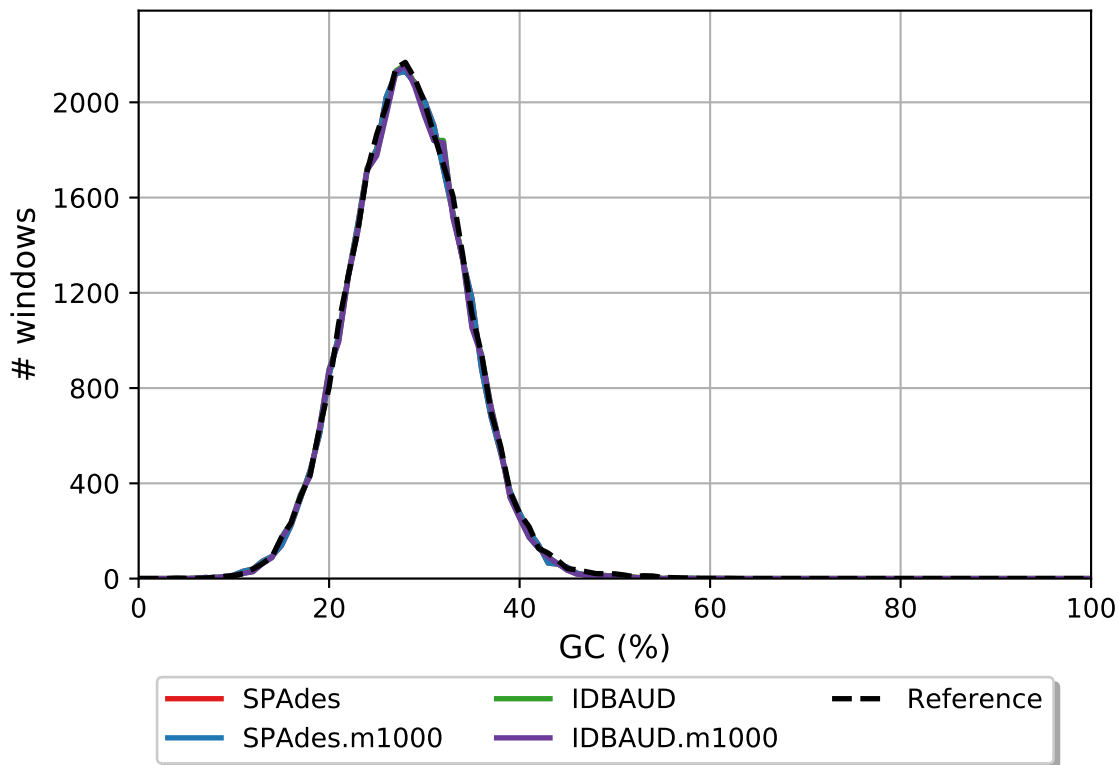
NGx



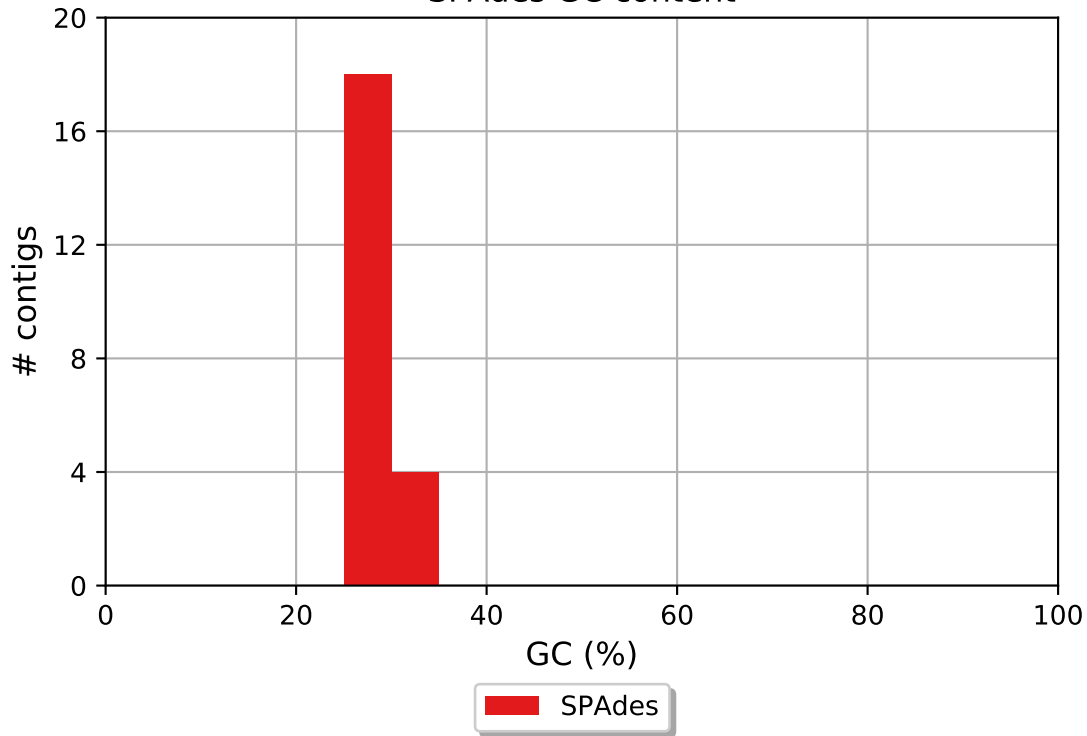
Cumulative length



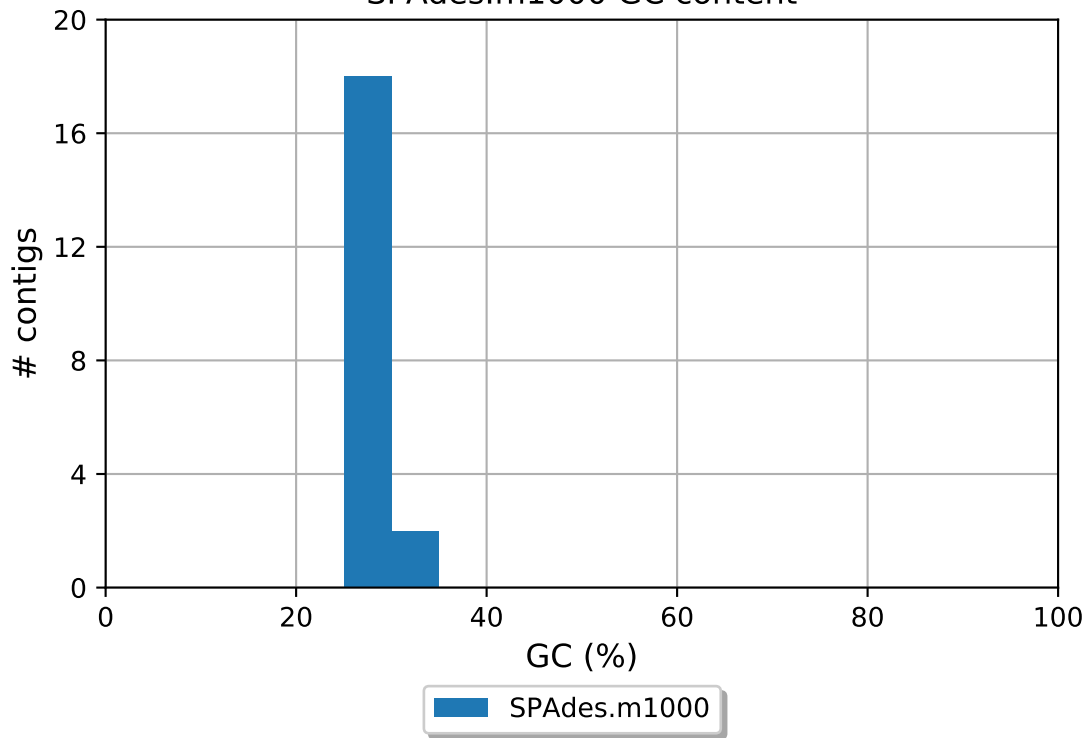
GC content



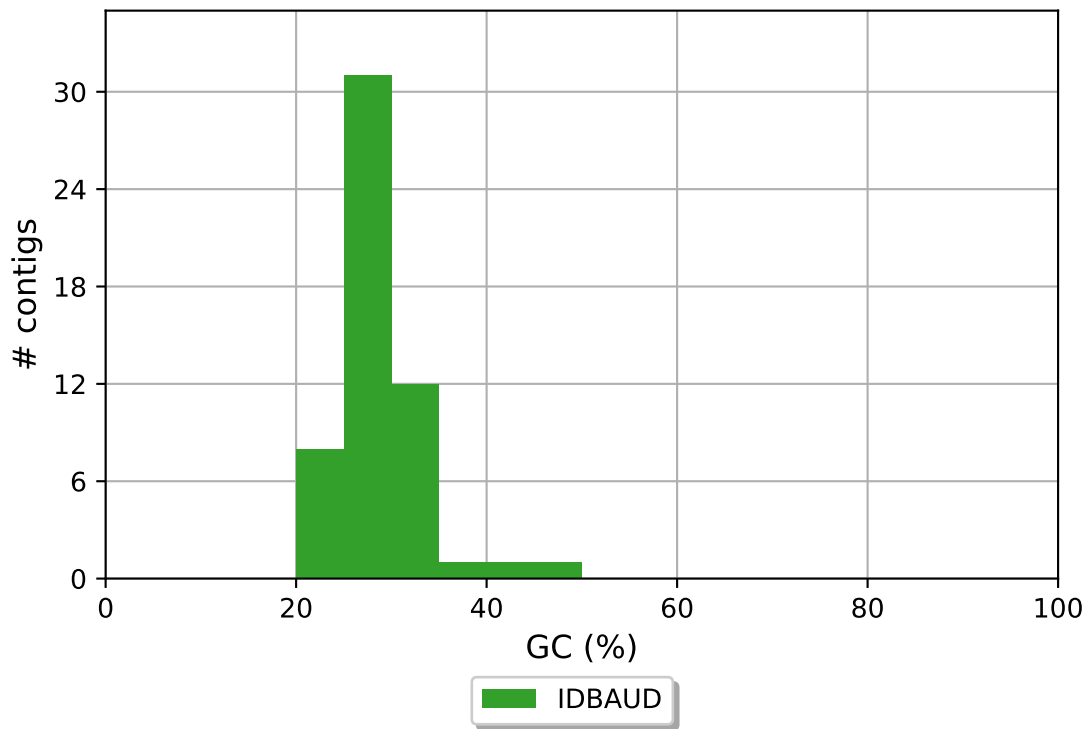
SPAdes GC content



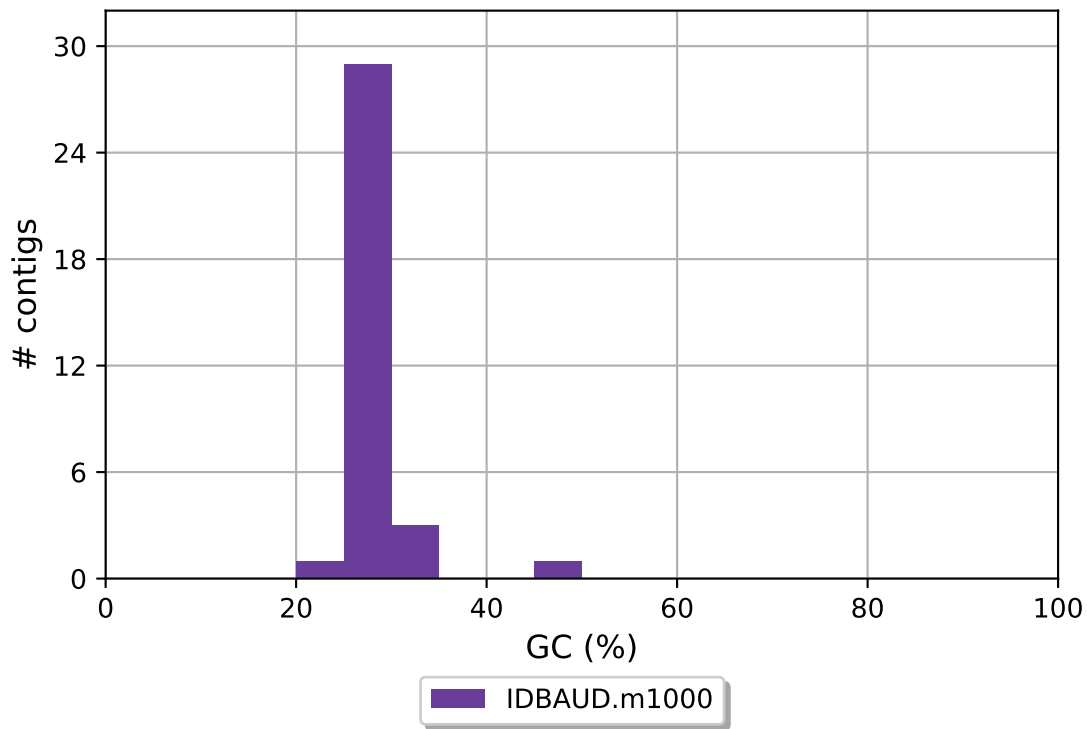
SPAdes.m1000 GC content



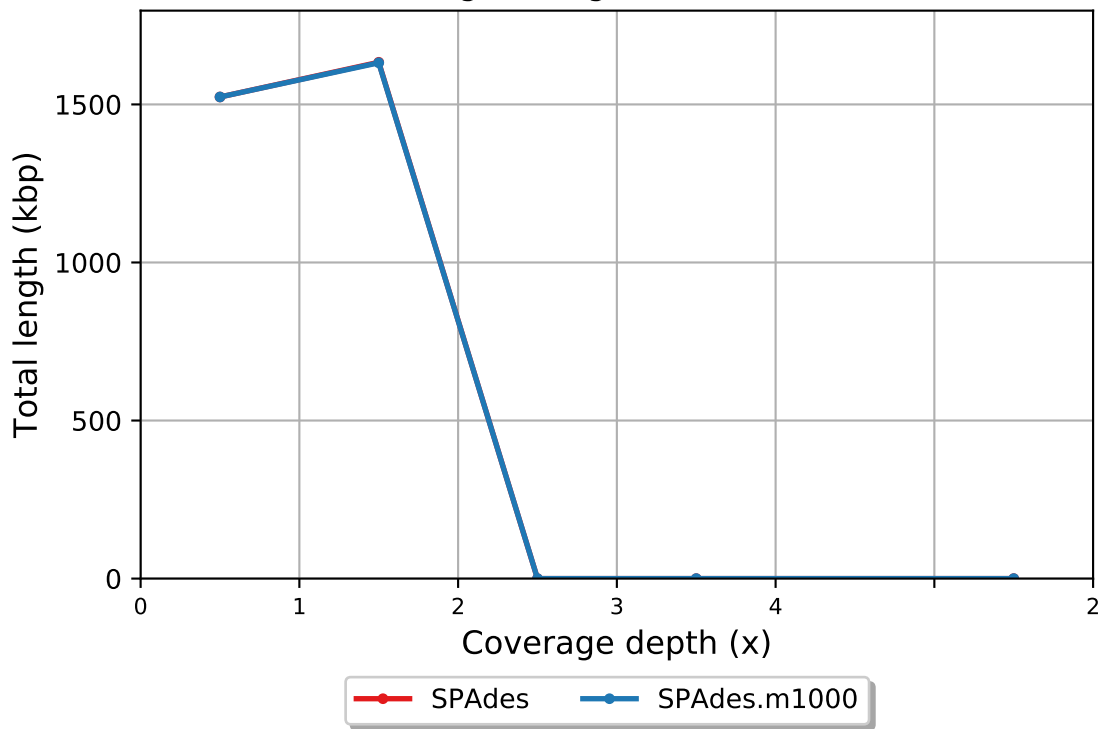
IDBAUD GC content



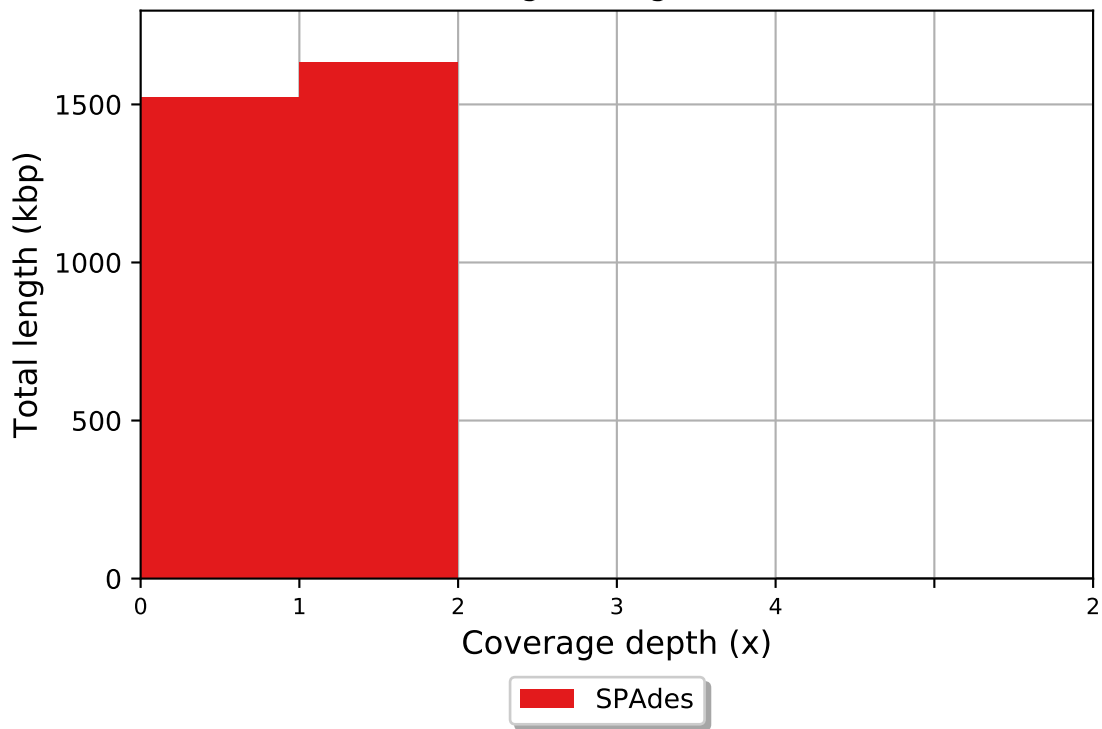
IDBAUD.m1000 GC content



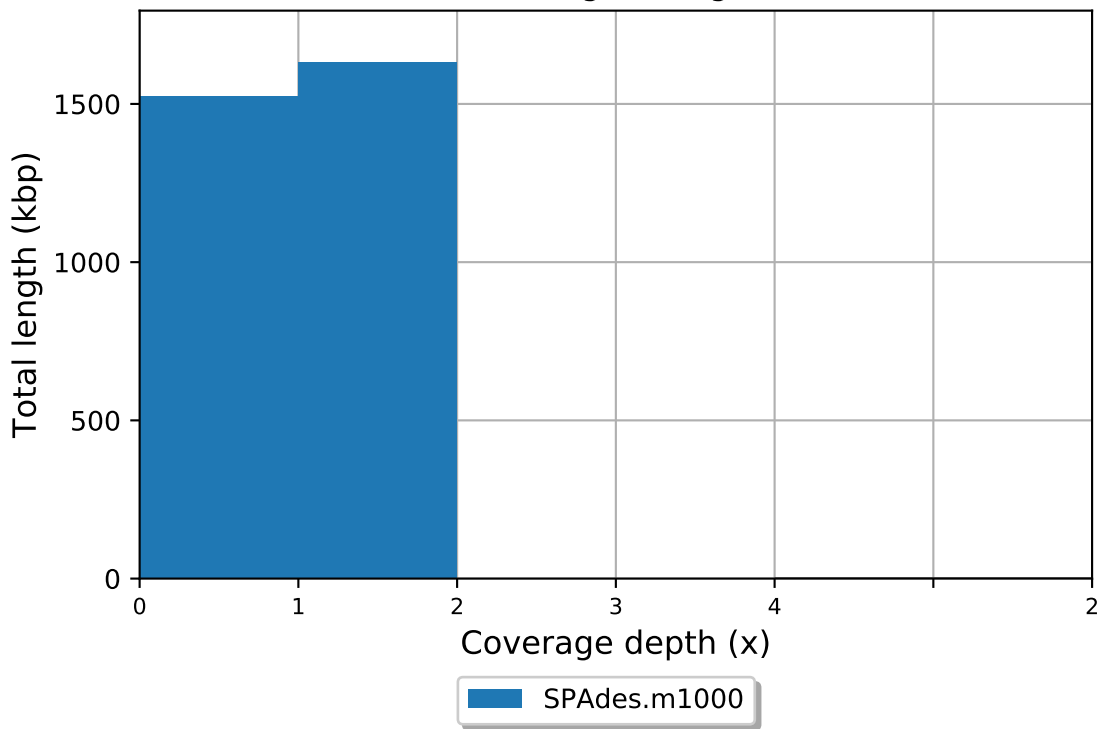
Coverage histogram (bin size: 1x)



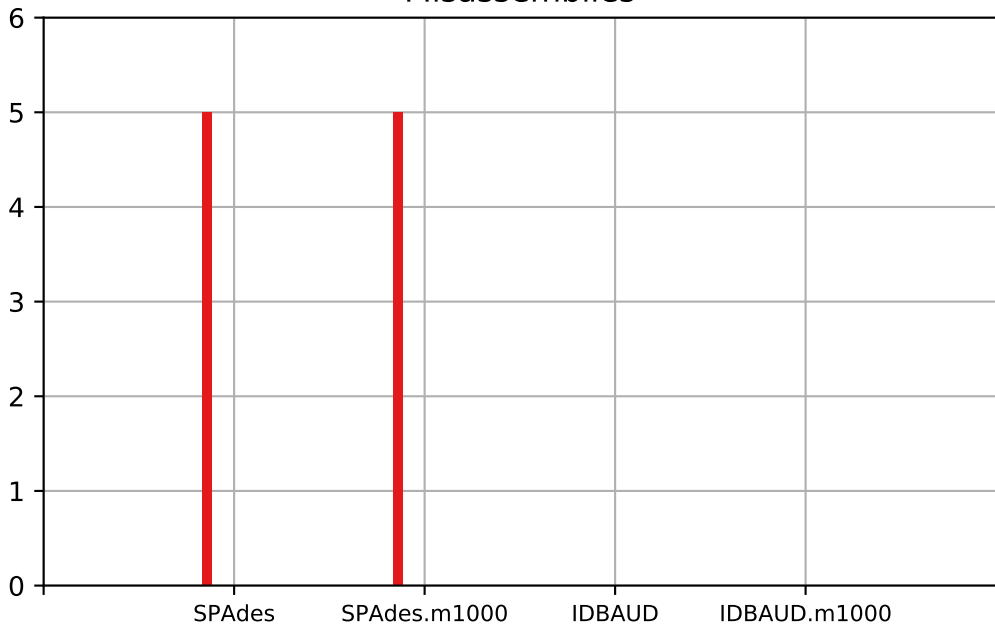
SPAdes coverage histogram (bin size: 1x)



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

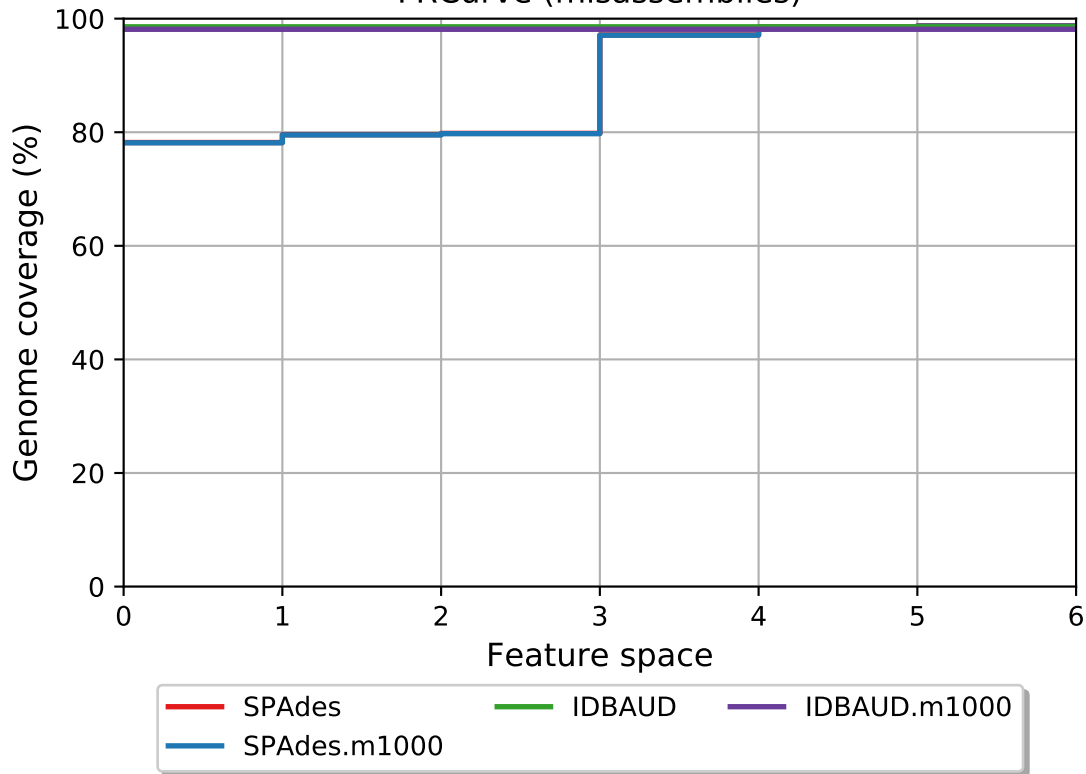


Misassemblies

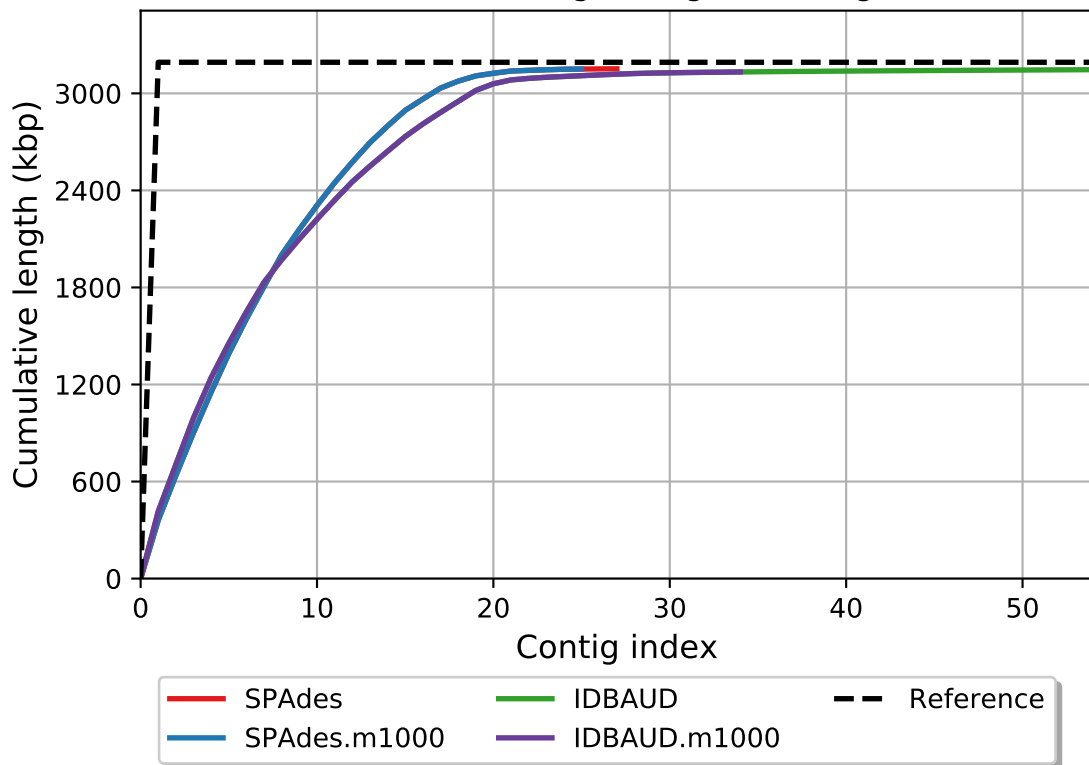


 # relocations

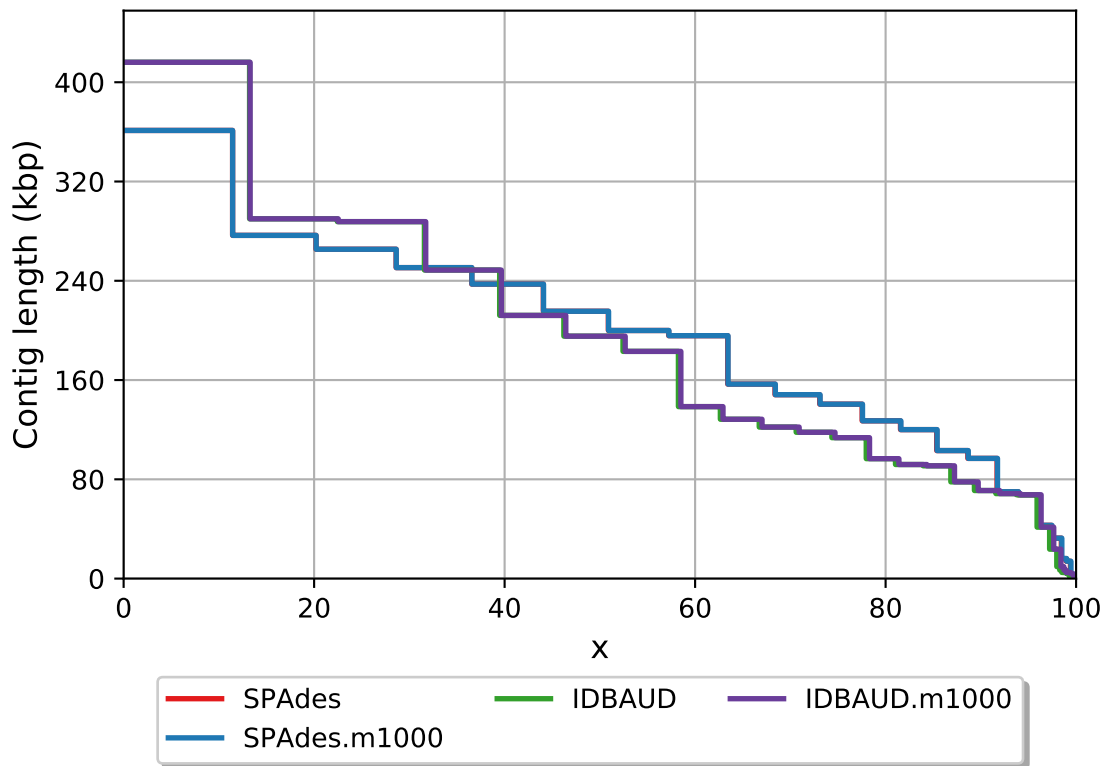
FRCurve (misassemblies)



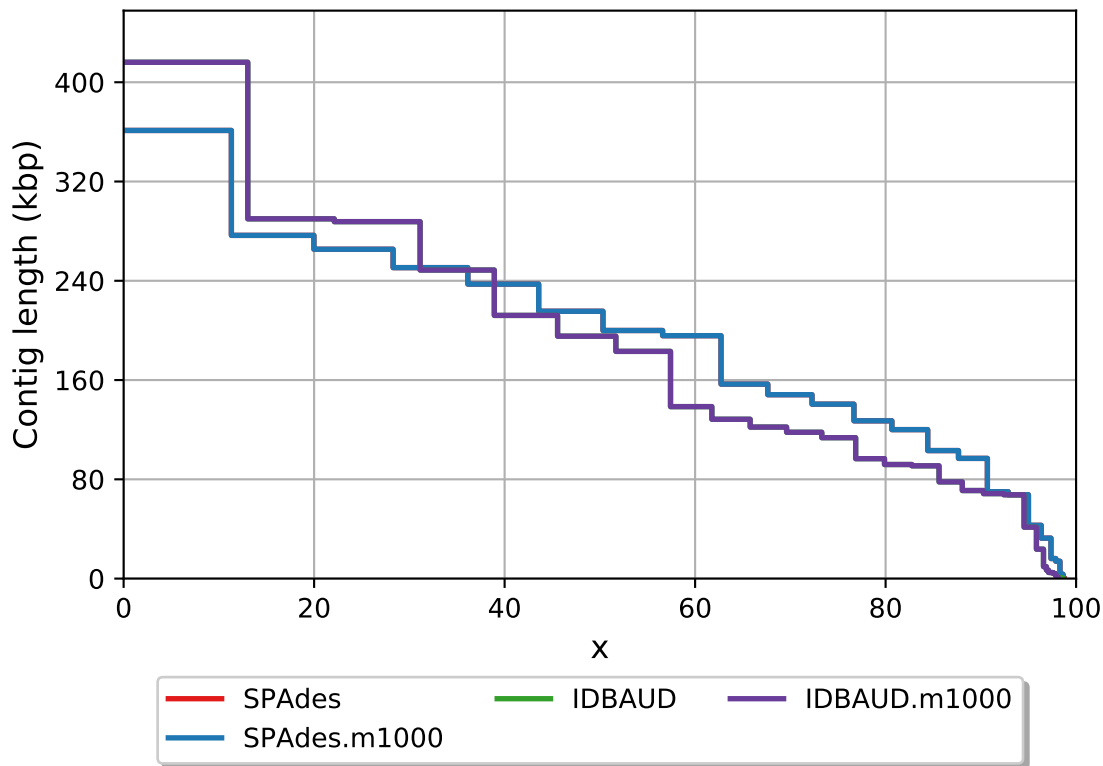
Cumulative length (aligned contigs)



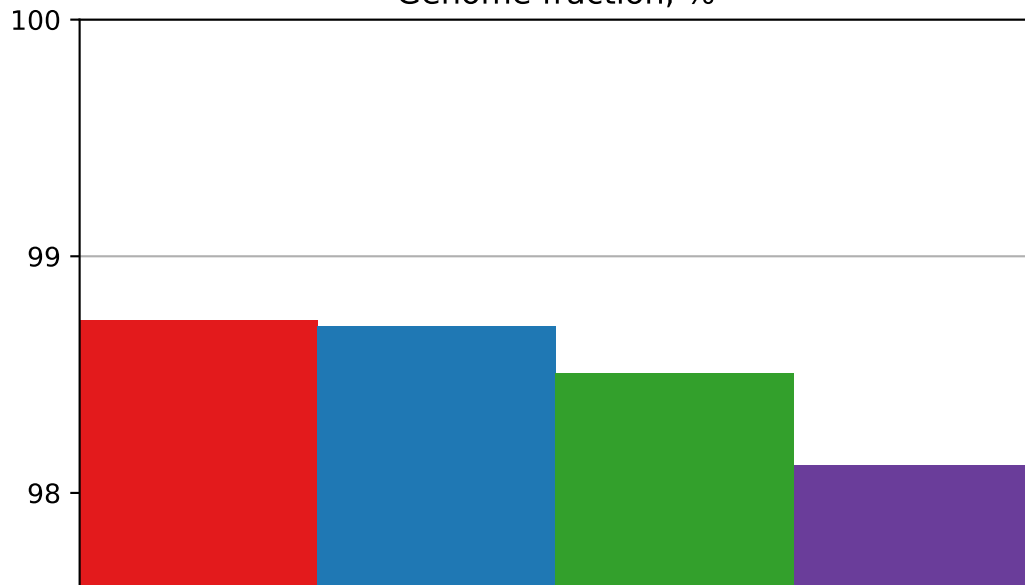
NAX



NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

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