

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	20	20	28	28
# contigs (>= 5000 bp)	19	19	28	28
# contigs (>= 10000 bp)	18	18	26	26
# contigs (>= 25000 bp)	16	16	22	22
# contigs (>= 50000 bp)	14	14	20	20
Total length (>= 1000 bp)	3385048	3385048	3364116	3364116
Total length (>= 5000 bp)	3383820	3383820	3364116	3364116
Total length (>= 10000 bp)	3377476	3377476	3352267	3352267
Total length (>= 25000 bp)	3337359	3337359	3283160	3283160
Total length (>= 50000 bp)	3240313	3240313	3208464	3208464
# contigs	20	20	32	28
Largest contig	835083	835083	349674	349674
Total length	3385048	3385048	3367044	3364116
Reference length	3401021	3401021	3401021	3401021
GC (%)	57.38	57.38	57.38	57.38
Reference GC (%)	57.33	57.33	57.33	57.33
N50	292112	292112	179580	179580
NG50	292112	292112	179580	179580
N75	179785	179785	122163	122163
NG75	179785	179785	112474	112474
L50	3	3	7	7
LG50	3	3	7	7
L75	7	7	12	12
LG75	7	7	13	13
# misassemblies	34	34	33	33
# misassembled contigs	10	10	12	12
Misassembled contigs length	2798925	2798925	2352497	2352497
# local misassemblies	162	162	203	203
# scaffold gap ext. mis.	2	2	0	0
# scaffold gap loc. mis.	10	10	0	0
# unaligned mis. contigs	2	2	5	5
# unaligned contigs	0 + 19 part	0 + 19 part	0 + 28 part	0 + 27 part
Unaligned length	678518	678518	696108	695354
Genome fraction (%)	79.506	79.506	78.497	78.446
Duplication ratio	1.001	1.001	1.000	1.000
# N's per 100 kbp	12.41	12.41	0.00	0.00
# mismatches per 100 kbp	3934.40	3934.40	3904.55	3905.19
# indels per 100 kbp	102.99	102.99	95.22	95.17
Largest alignment	217526	217526	211653	211653
Total aligned length	2706138	2706138	2670437	2668531
NA50	71400	71400	61461	61461
NGA50	71400	71400	61461	61461
NA75	18990	18990	16627	16627
NGA75	18239	18239	11981	11981
LA50	15	15	17	17
LGA50	15	15	17	17
LA75	34	34	40	40
LGA75	35	35	42	42

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

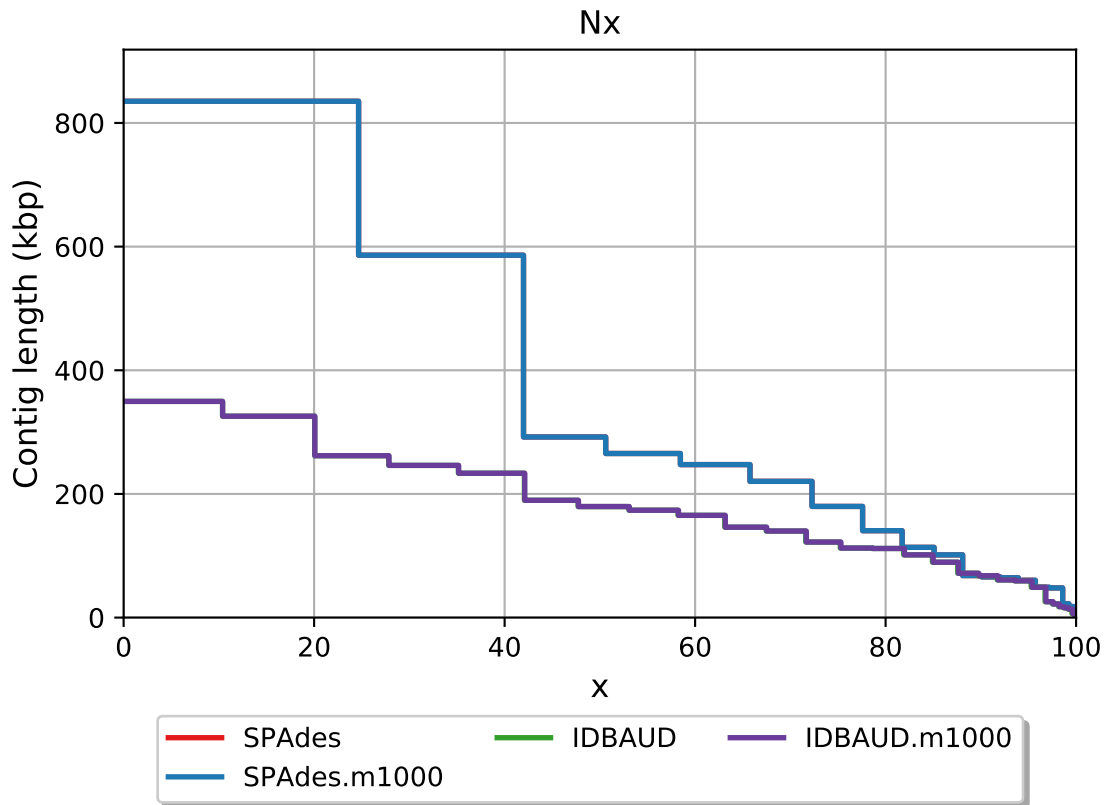
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	34	34	33	33
# contig misassemblies	33	33	33	33
# c. relocations	33	33	33	33
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	1	1	0	0
# s. relocations	1	1	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	10	10	12	12
Misassembled contigs length	2798925	2798925	2352497	2352497
# possibly misassembled contigs	17	17	24	23
# possible misassemblies	259	259	264	263
# local misassemblies	162	162	203	203
# scaffold gap ext. mis.	2	2	0	0
# scaffold gap loc. mis.	10	10	0	0
# unaligned mis. contigs	2	2	5	5
# mismatches	106387	106387	104240	104189
# indels	2785	2785	2542	2539
# indels (<= 5 bp)	2521	2521	2325	2322
# indels (> 5 bp)	264	264	217	217
Indels length	8122	8122	6961	6958

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).

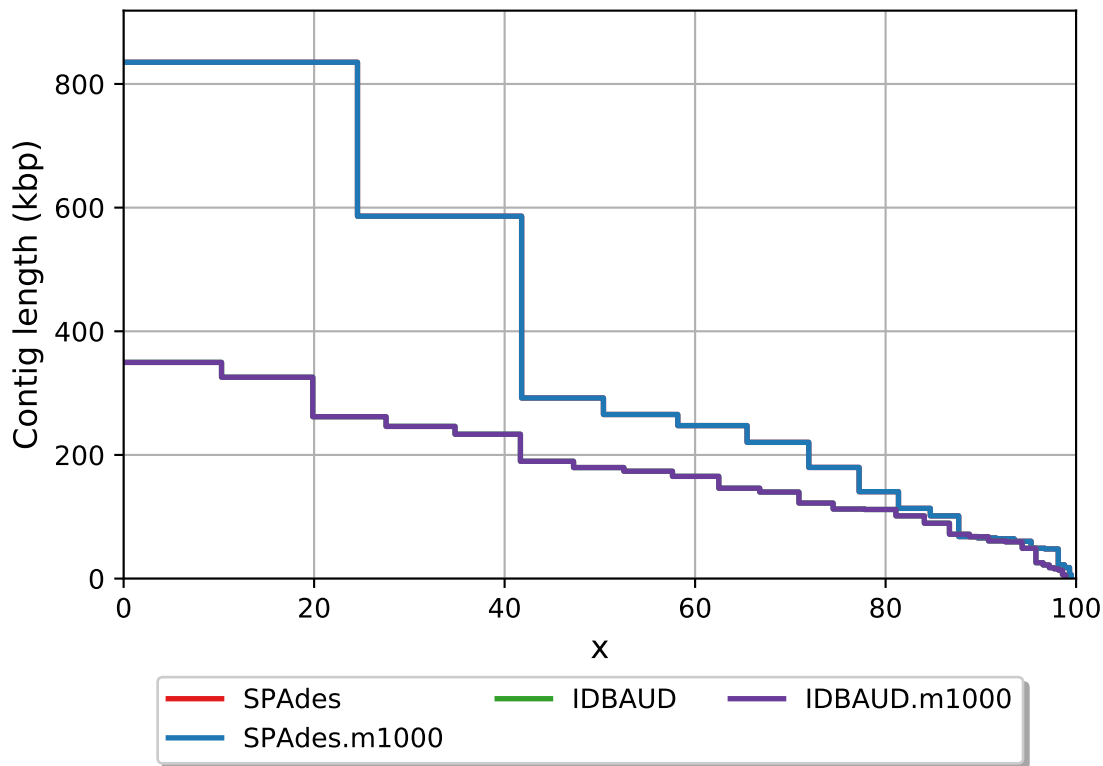
Unaligned report

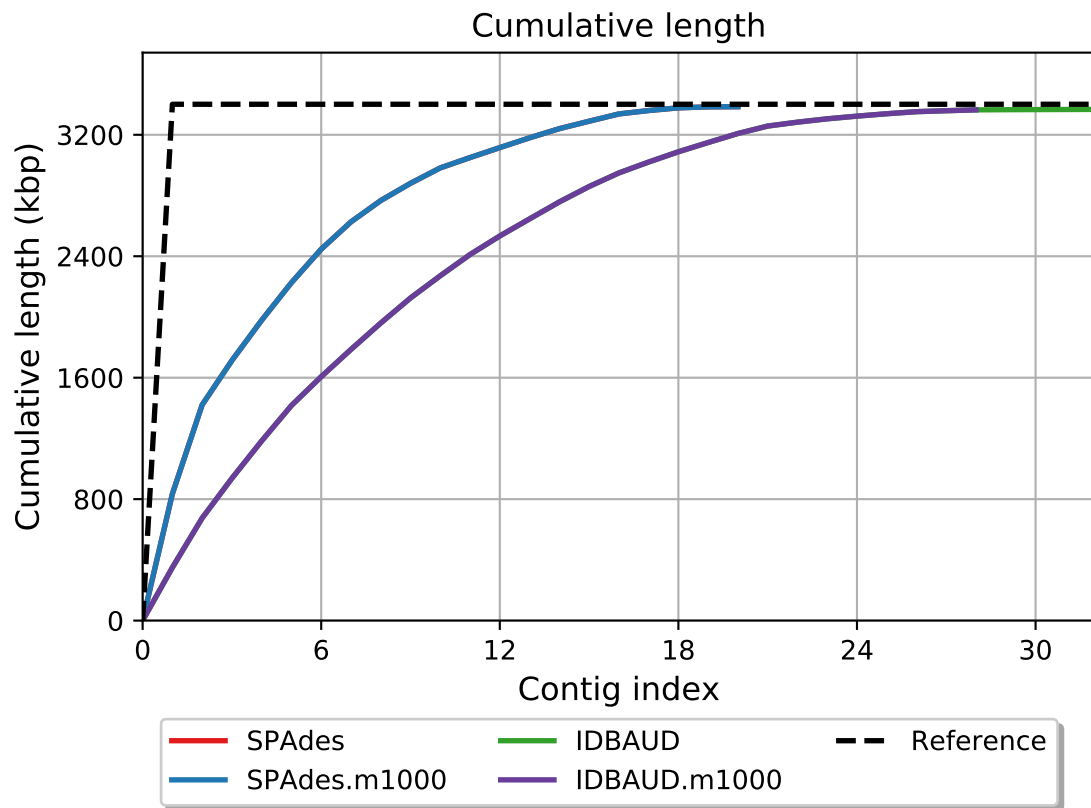
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	19	19	28	27
Partially unaligned length	678518	678518	696108	695354
# N's	420	420	0	0

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).

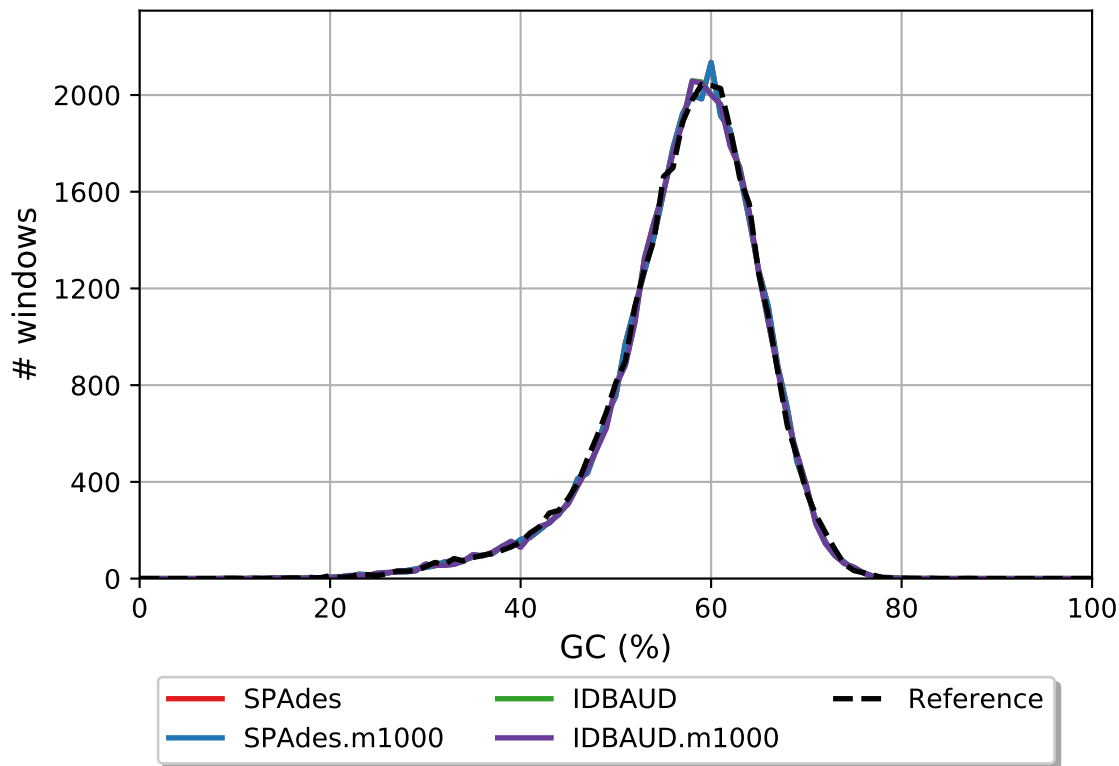


NGx

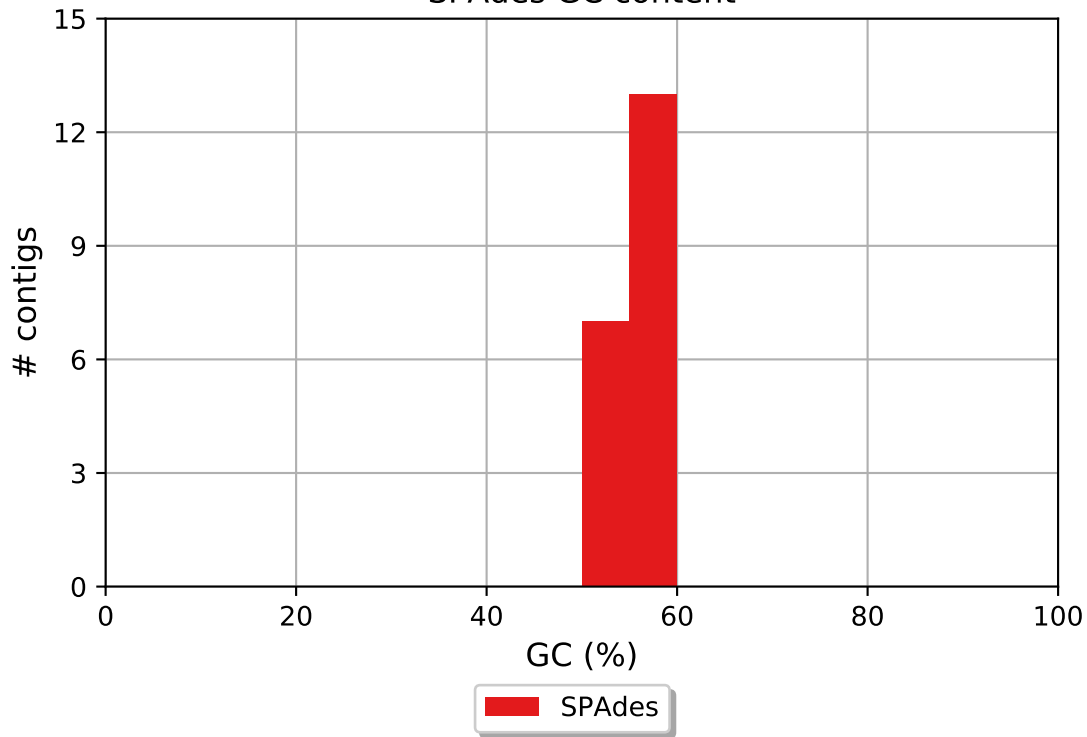




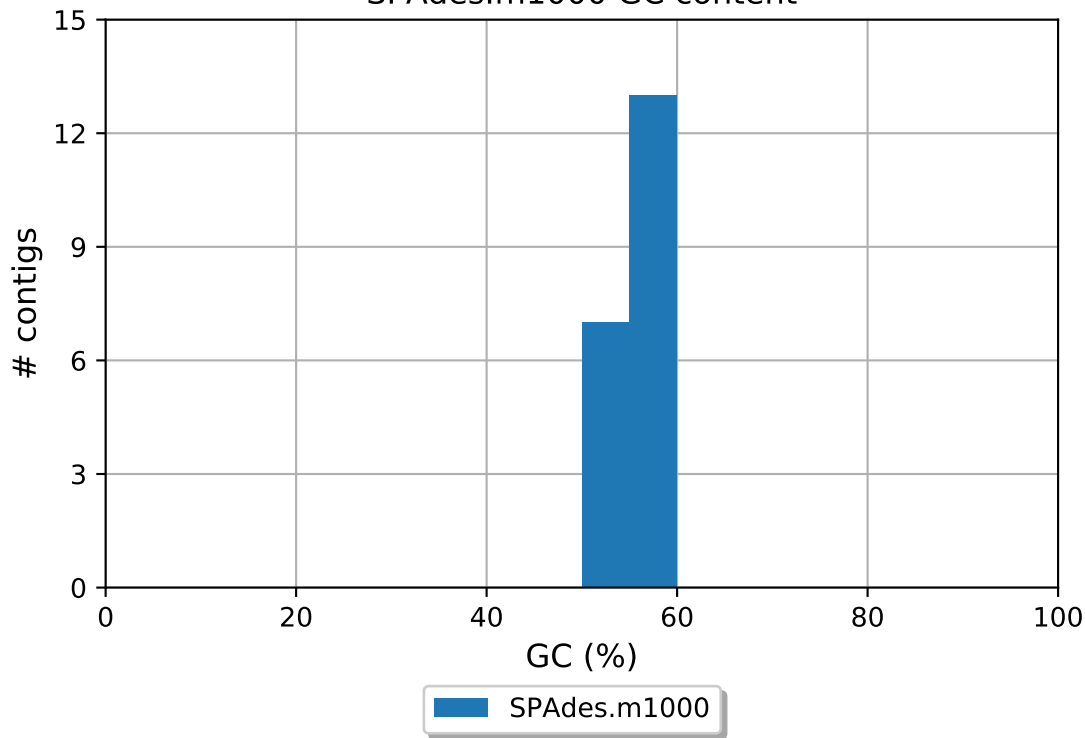
GC content



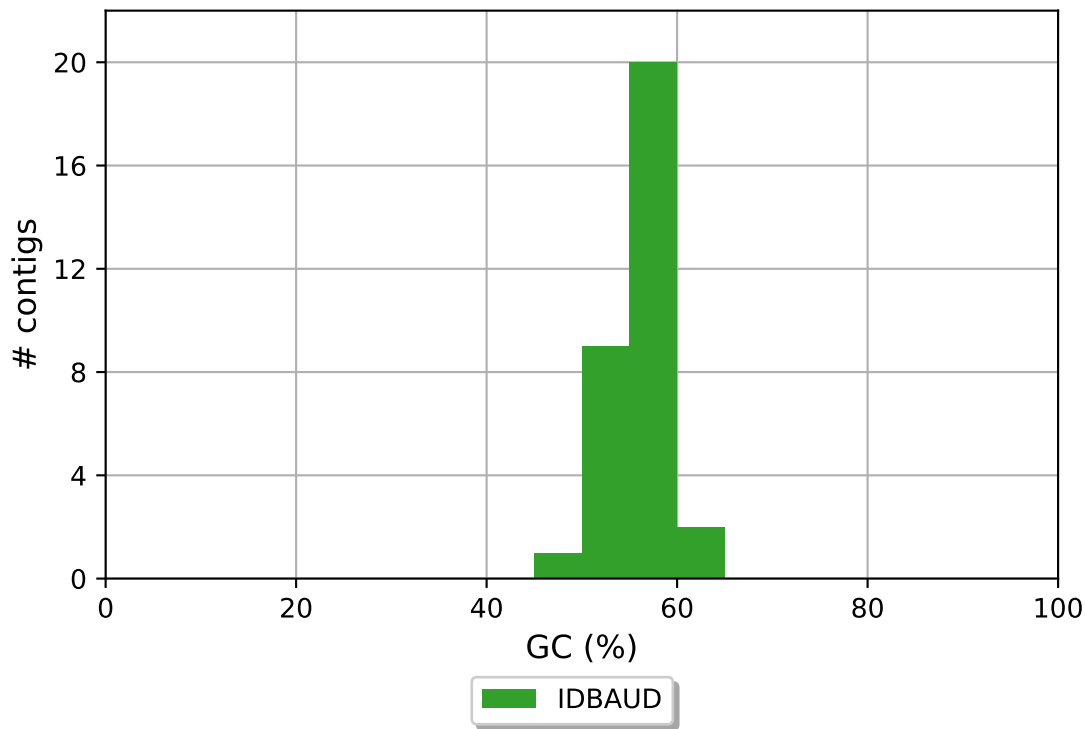
SPAdes GC content



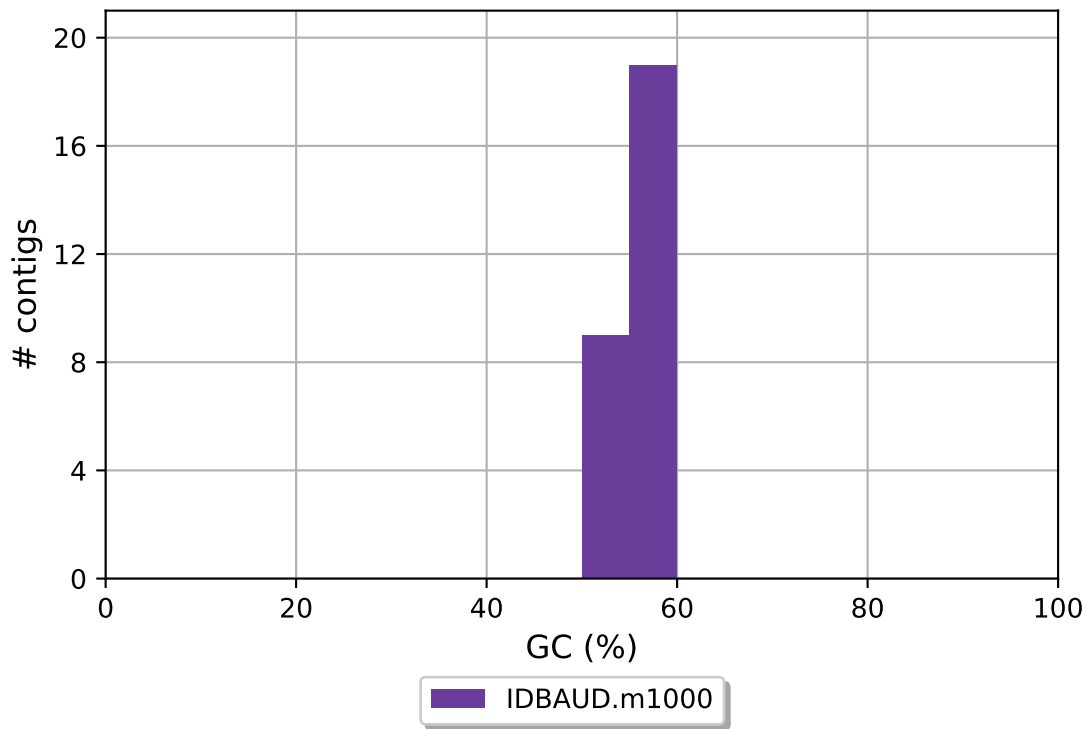
SPAdes.m1000 GC content



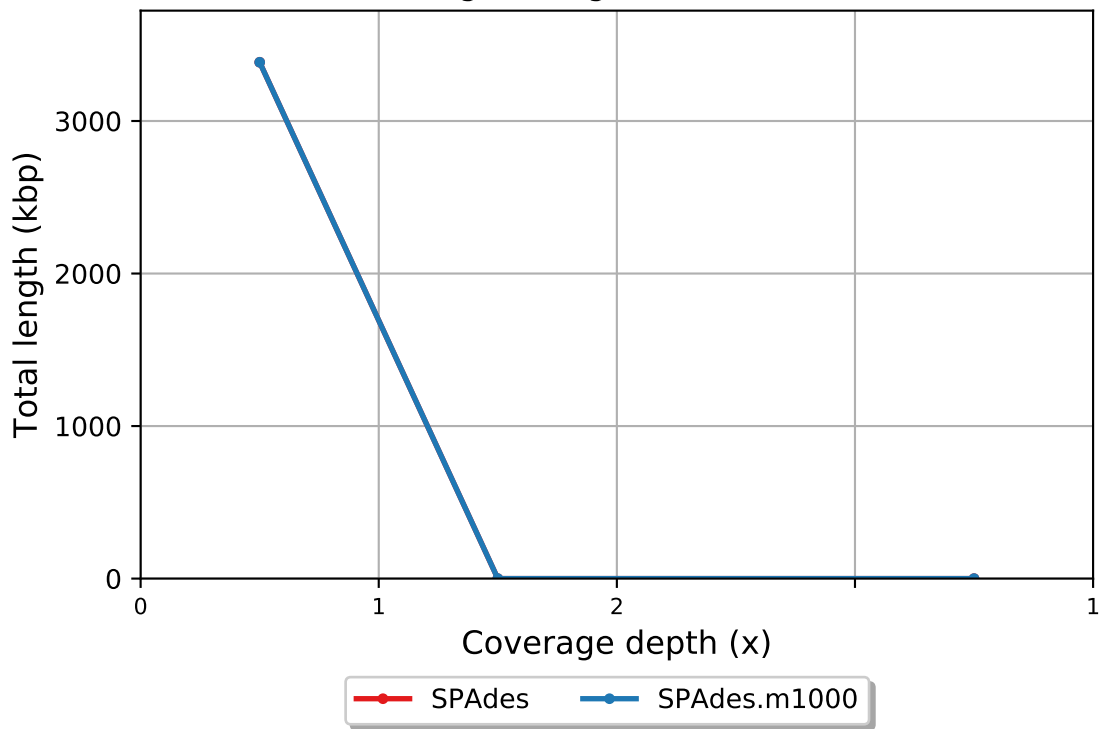
IDBAUD GC content



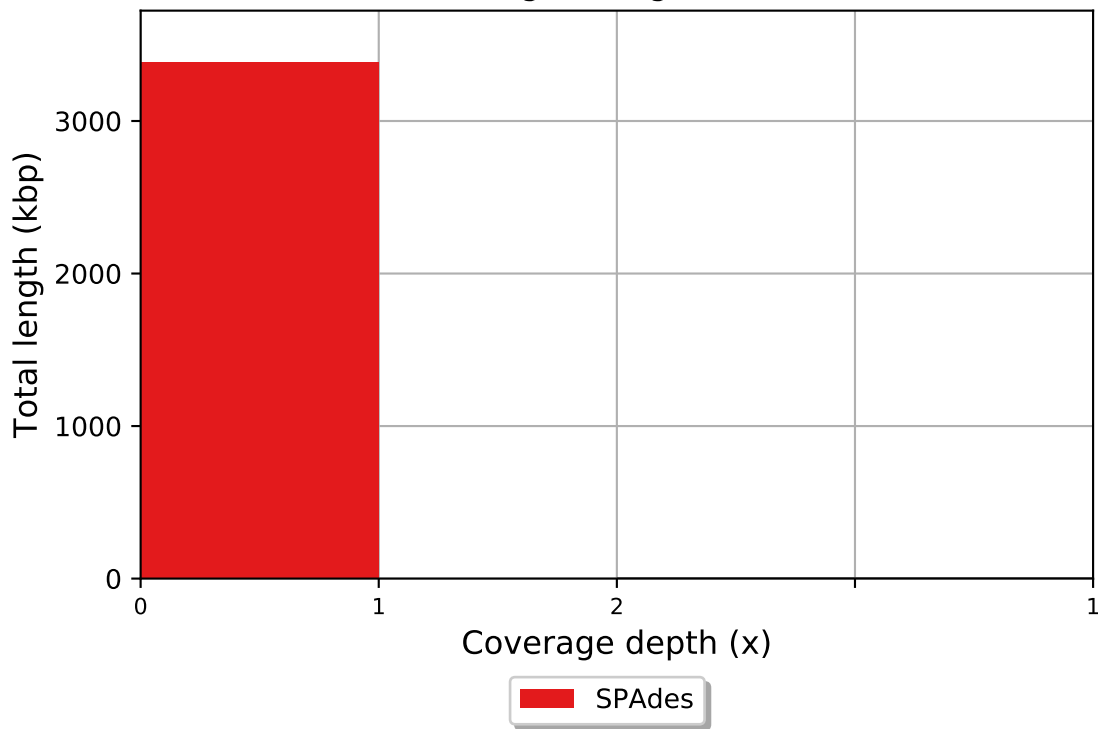
IDBAUD.m1000 GC content



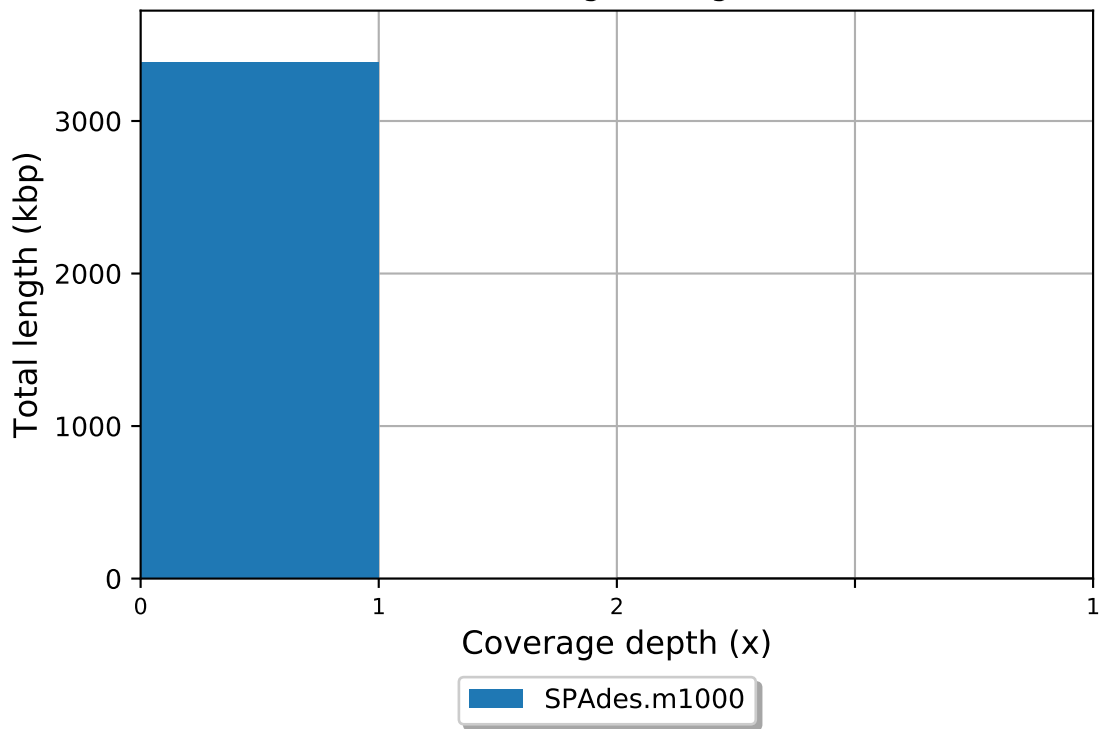
Coverage histogram (bin size: 1x)



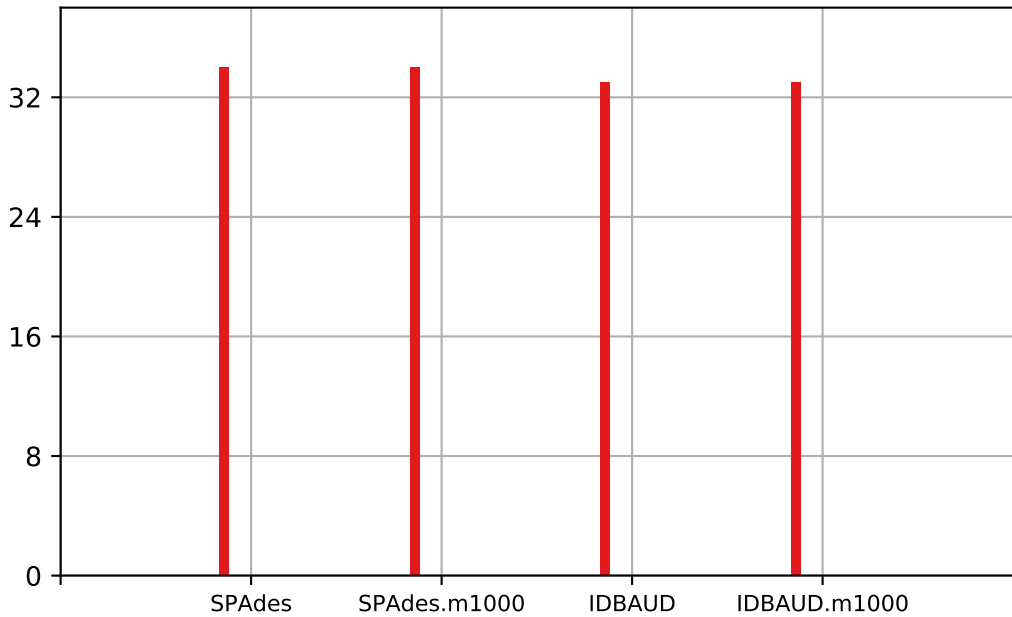
SPAdes coverage histogram (bin size: 1x)



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

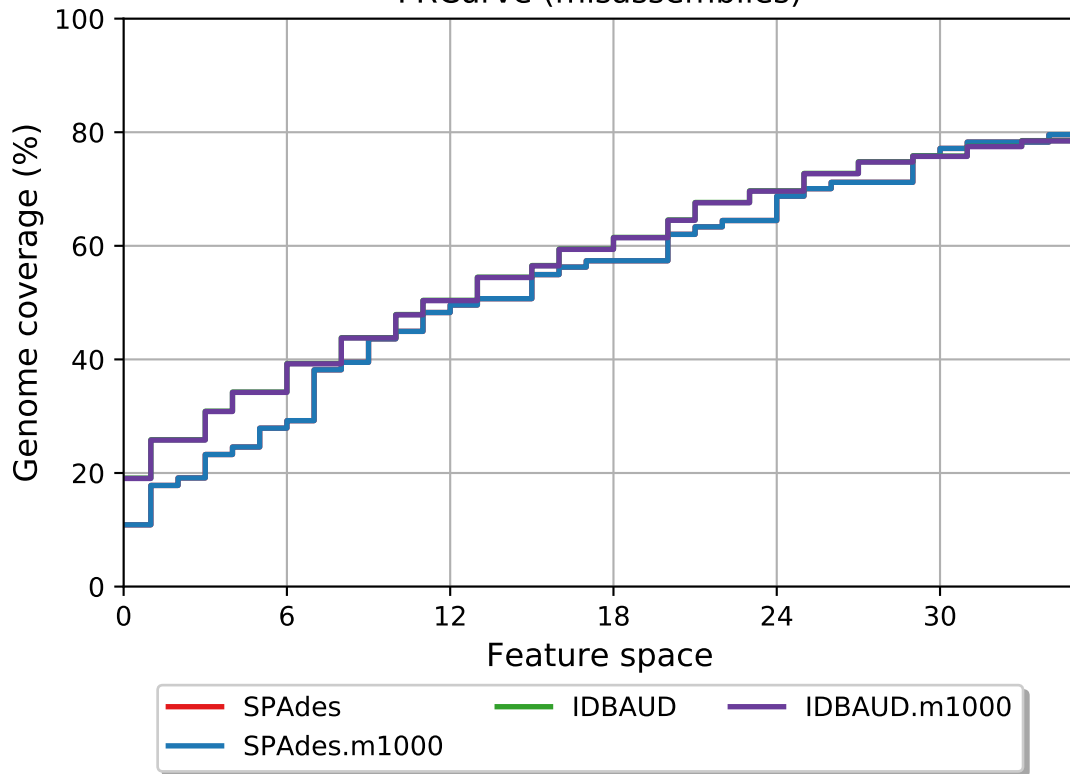


Misassemblies

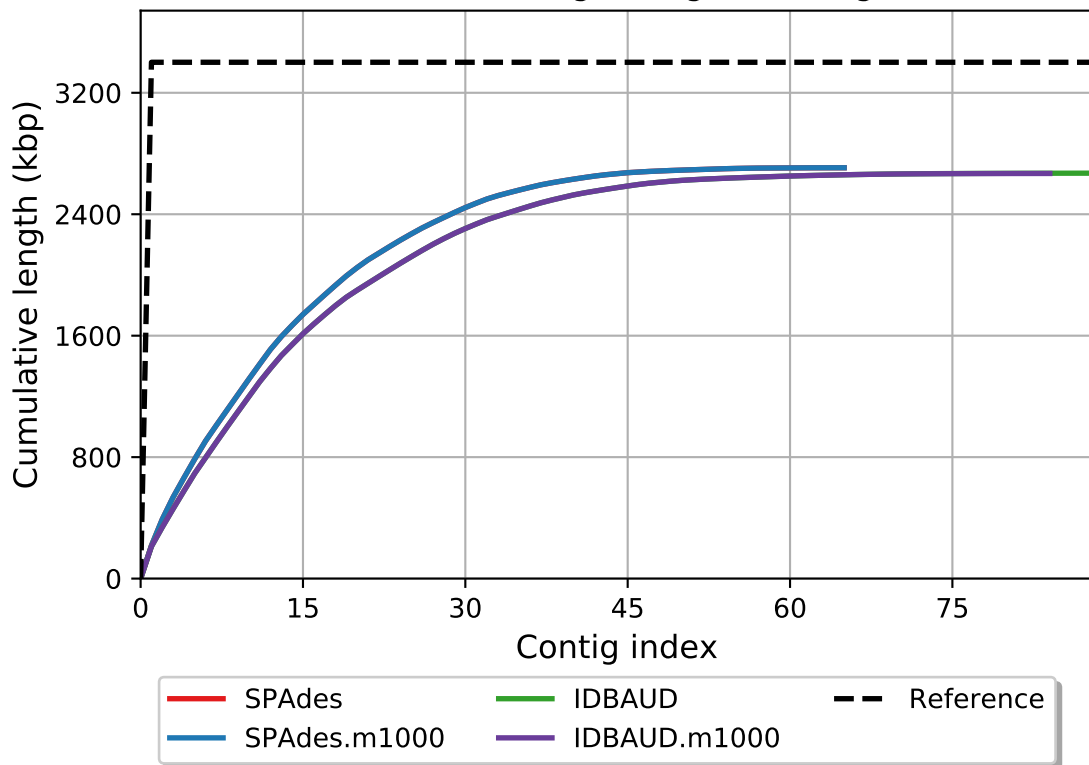


 # relocations

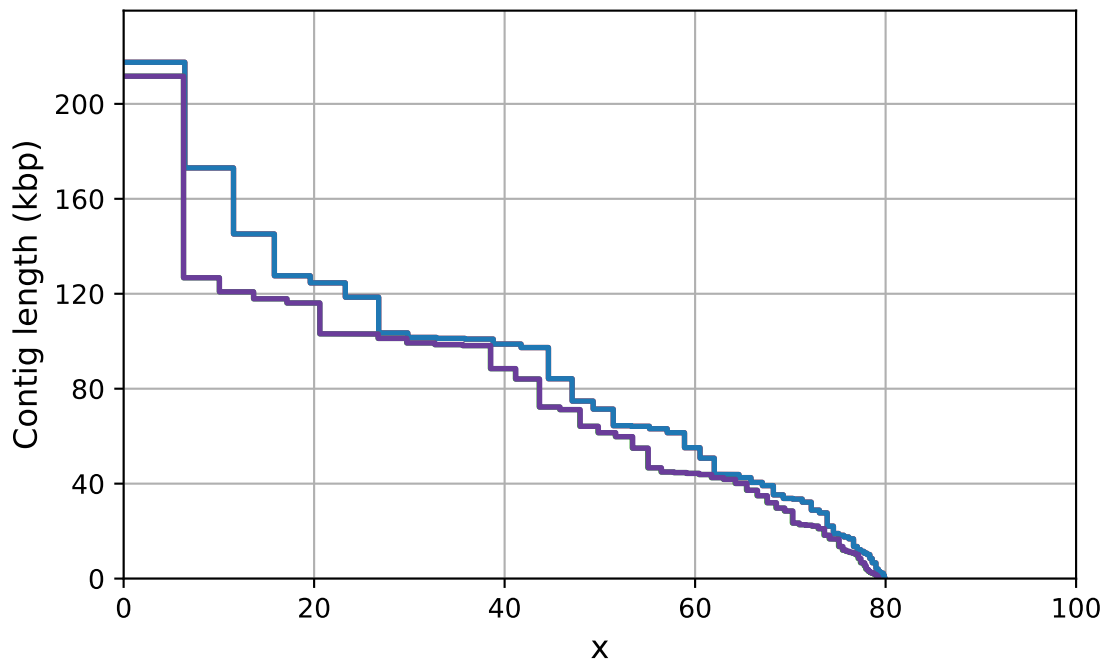
FRCurve (misassemblies)



Cumulative length (aligned contigs)

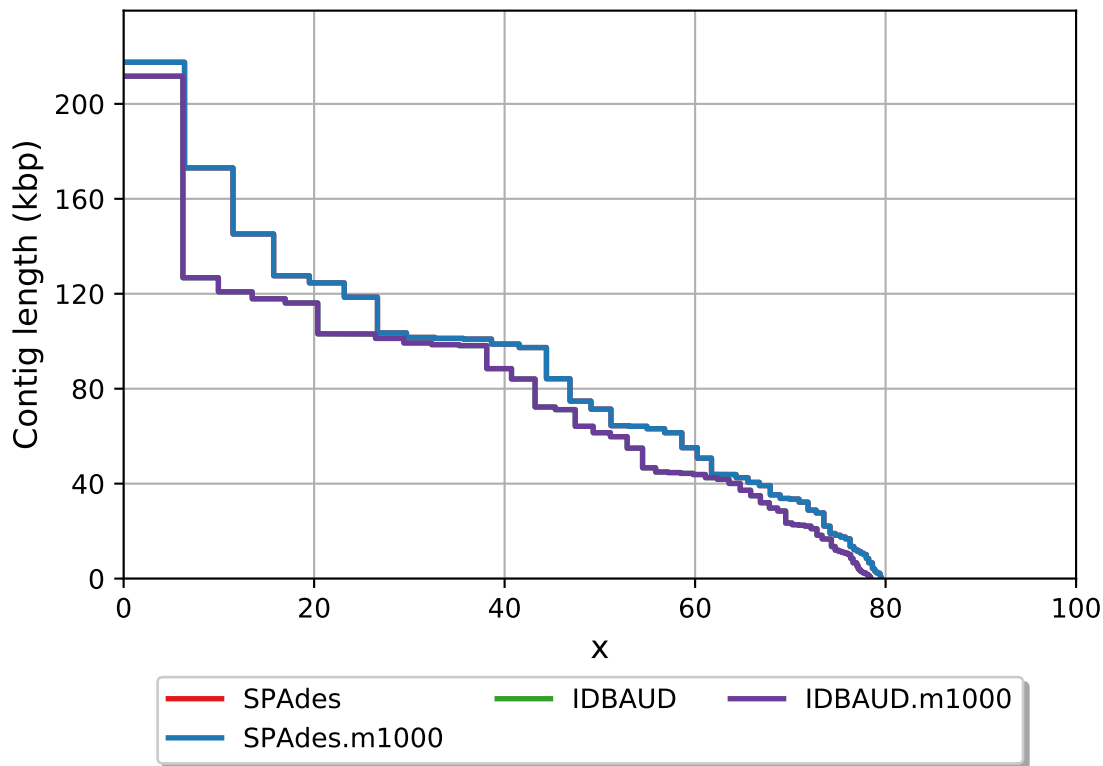


NAx

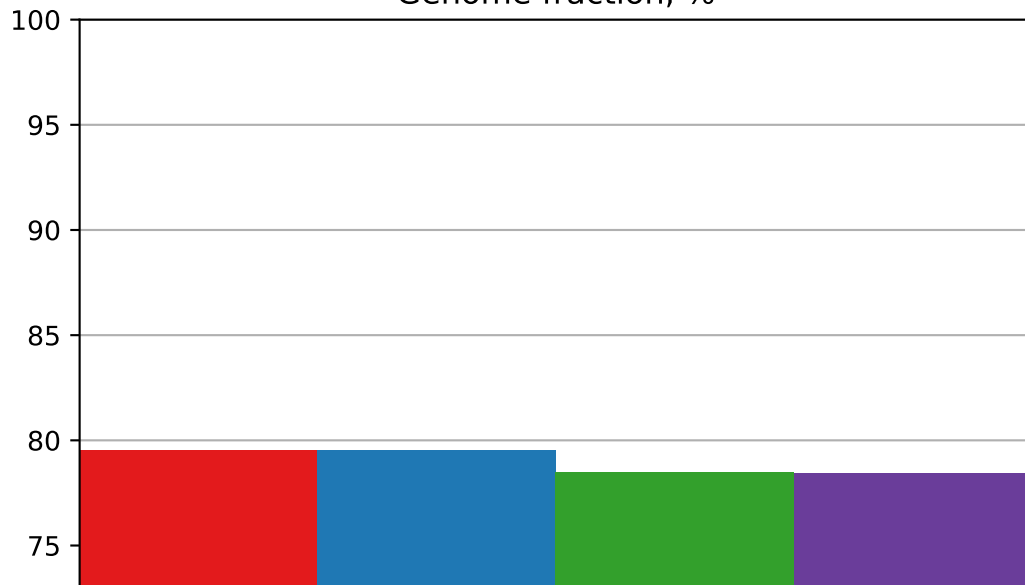


SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000