

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	66	66	80	80
# contigs (>= 5000 bp)	53	53	58	58
# contigs (>= 10000 bp)	48	48	51	51
# contigs (>= 25000 bp)	36	36	39	39
# contigs (>= 50000 bp)	19	19	17	17
Total length (>= 1000 bp)	2719422	2719422	2704186	2704186
Total length (>= 5000 bp)	2688705	2688705	2653992	2653992
Total length (>= 10000 bp)	2646609	2646609	2599943	2599943
Total length (>= 25000 bp)	2447736	2447736	2400700	2400700
Total length (>= 50000 bp)	1798849	1798849	1575272	1575272
# contigs	68	66	88	80
Largest contig	160826	160826	160549	160549
Total length	2721086	2719422	2709902	2704186
Reference length	2812094	2812094	2812094	2812094
GC (%)	50.68	50.67	50.68	50.68
Reference GC (%)	50.72	50.72	50.72	50.72
N50	76915	76915	60464	62565
NG50	72233	72233	60464	60464
N75	42612	42612	38758	38758
NG75	41256	41256	36434	36434
L50	12	12	14	13
LG50	13	13	14	14
L75	25	25	28	28
LG75	26	26	30	30
# misassemblies	6	6	1	1
# misassembled contigs	6	6	1	1
Misassembled contigs length	301882	301882	76722	76722
# local misassemblies	3	3	13	13
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	11	11	10	10
# 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 (%)	96.612	96.552	96.228	96.038
Duplication ratio	1.002	1.002	1.001	1.001
# N's per 100 kbp	92.76	92.81	98.42	98.62
# mismatches per 100 kbp	3.61	3.61	0.07	0.00
# indels per 100 kbp	0.15	0.15	0.15	0.15
Largest alignment	160826	160826	160549	160549
Total aligned length	2718558	2716894	2707235	2701519
NA50	72107	72107	59254	59254
NGA50	71964	71964	57702	57702
NA75	38782	38782	38758	38758
NGA75	36903	36903	36185	36185
LA50	12	12	14	14
LGA50	13	13	15	15
LA75	26	26	28	28
LGA75	28	28	30	30

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

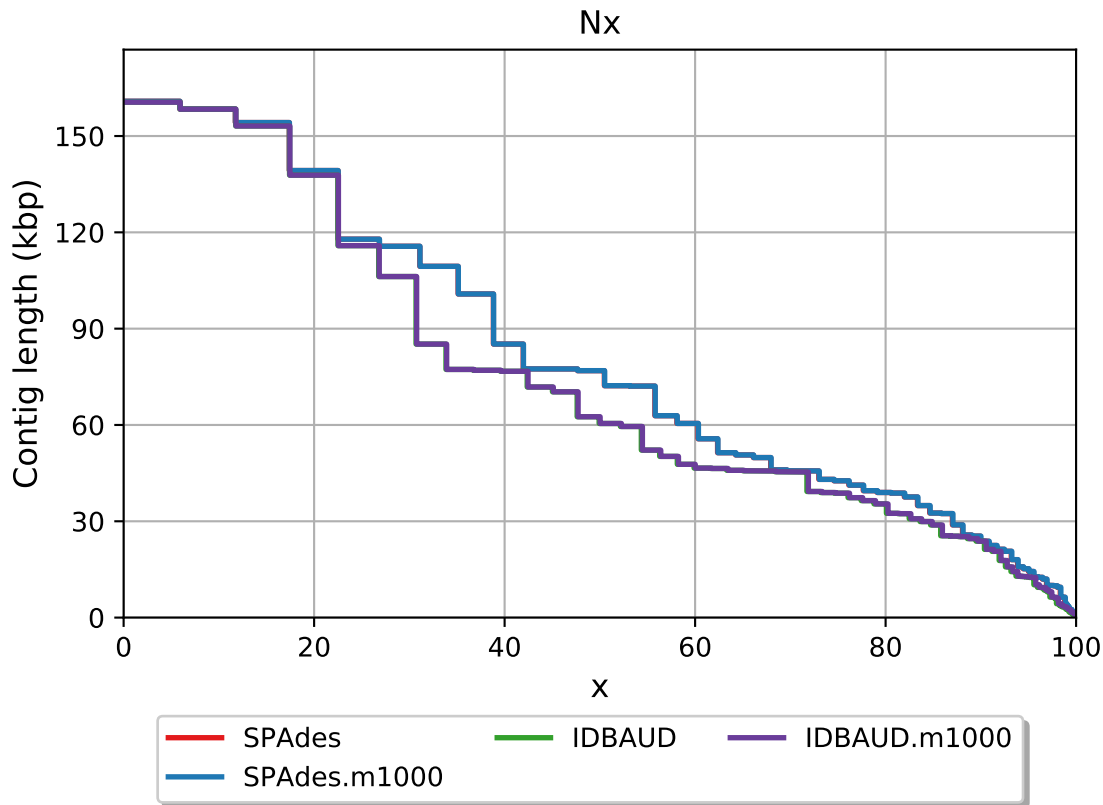
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	6	6	1	1
# contig misassemblies	6	6	1	1
# c. relocations	6	6	1	1
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	6	6	1	1
Misassembled contigs length	301882	301882	76722	76722
# possibly misassembled contigs	0	0	0	0
# possible misassemblies	0	0	0	0
# local misassemblies	3	3	13	13
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	11	11	10	10
# unaligned mis. contigs	0	0	0	0
# mismatches	98	98	2	0
# indels	4	4	4	4
# indels (<= 5 bp)	2	2	2	2
# indels (> 5 bp)	2	2	2	2
Indels length	136	136	163	163

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).

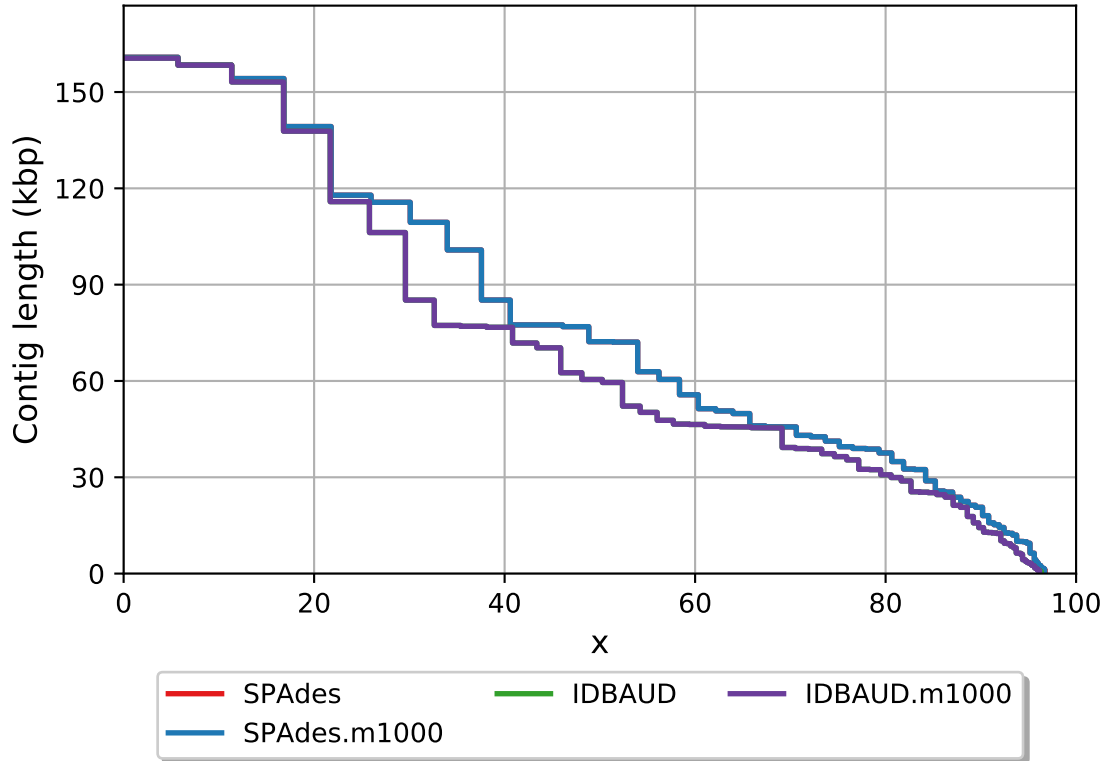
Unaligned report

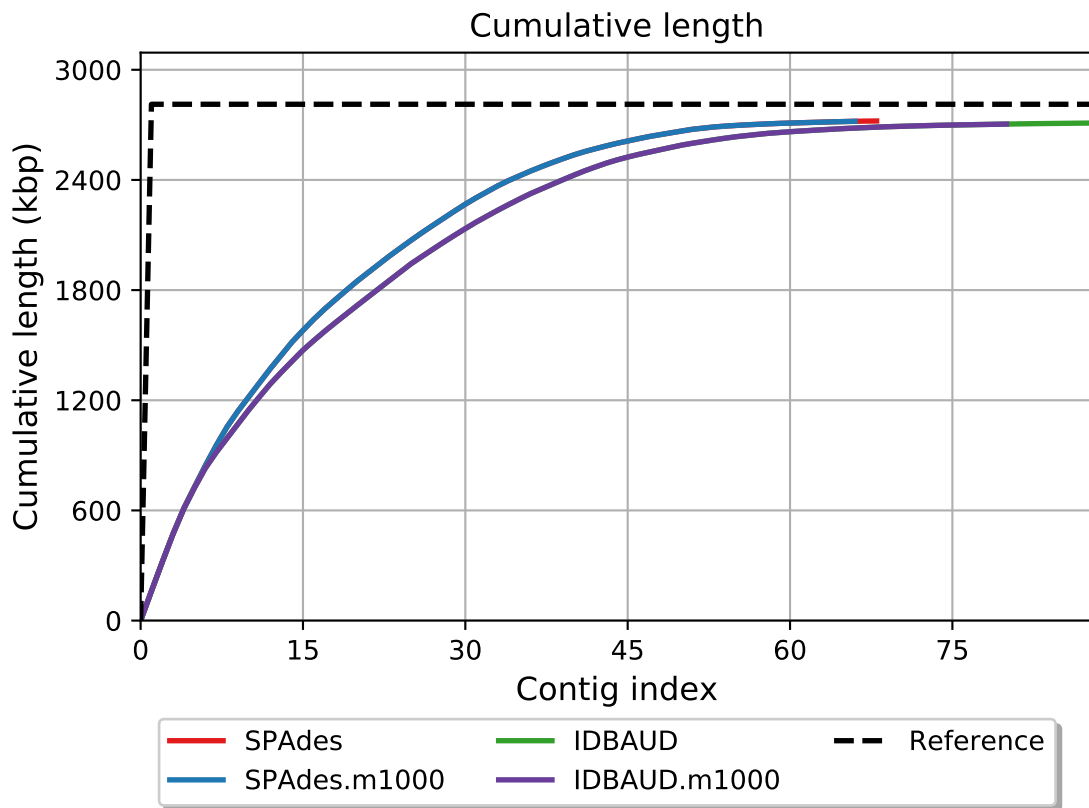
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	2524	2524	2667	2667

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).

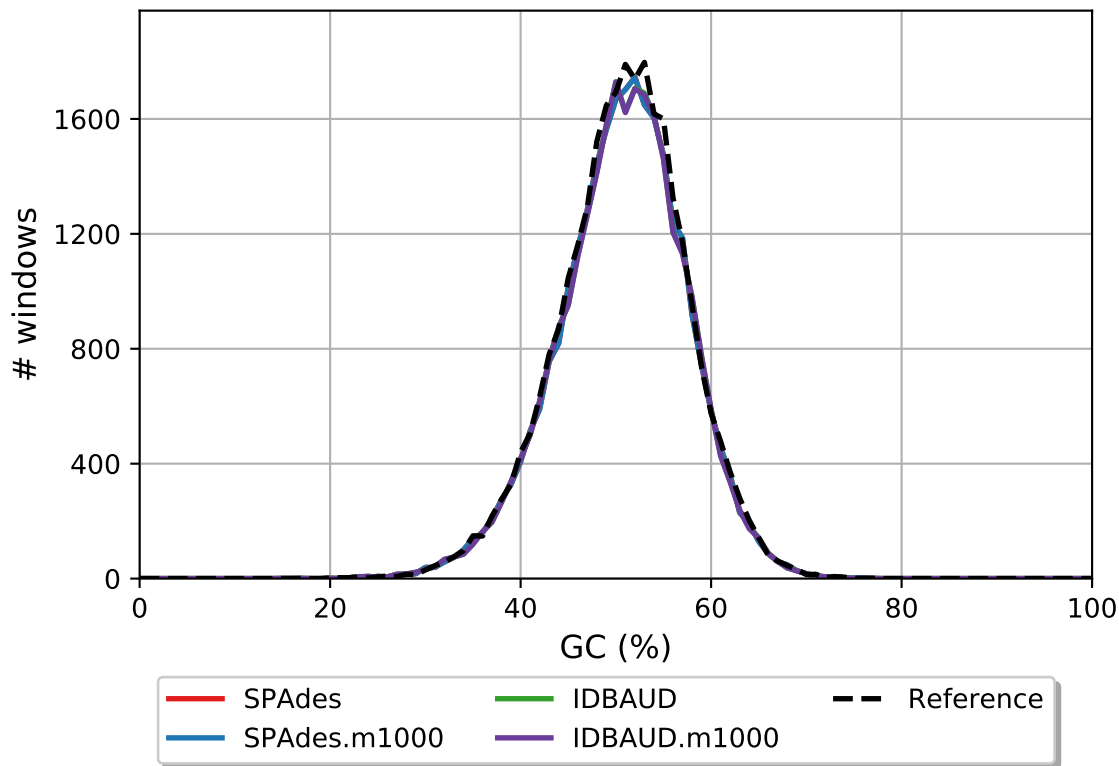


NGx

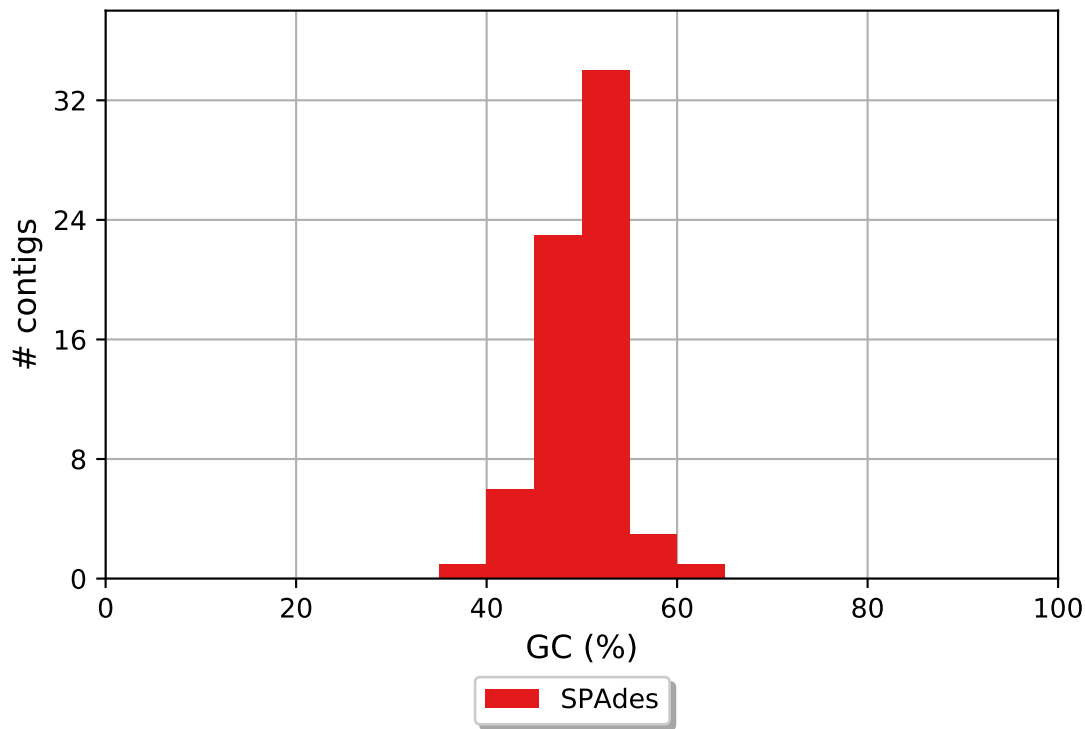




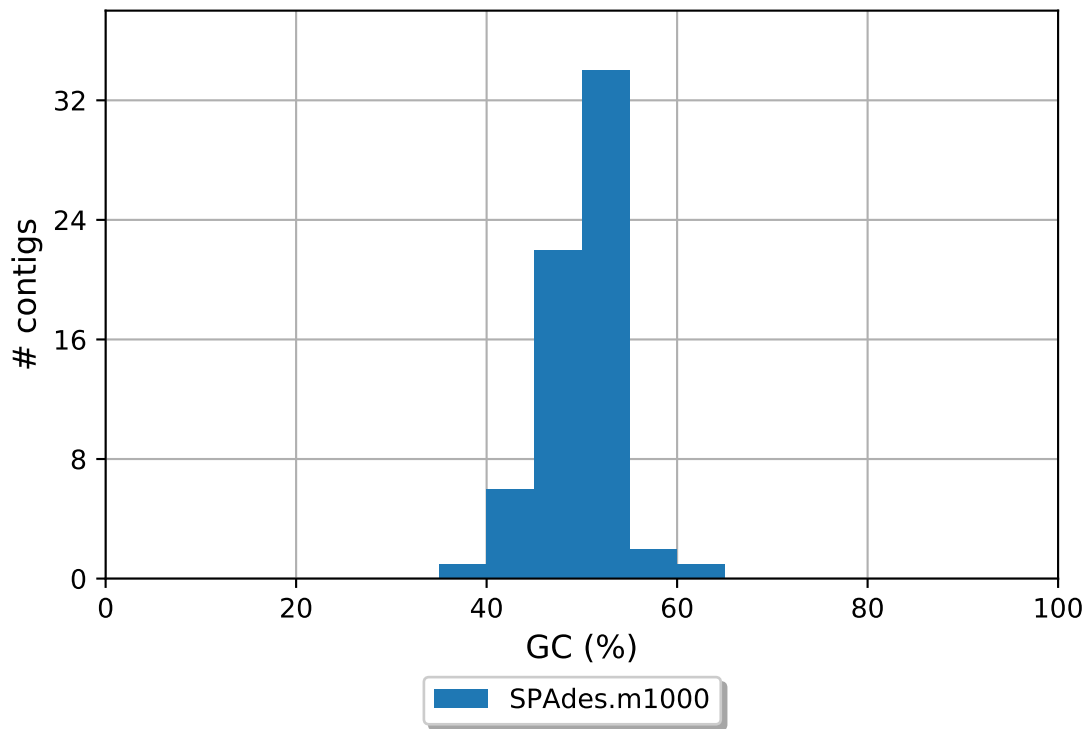
GC content



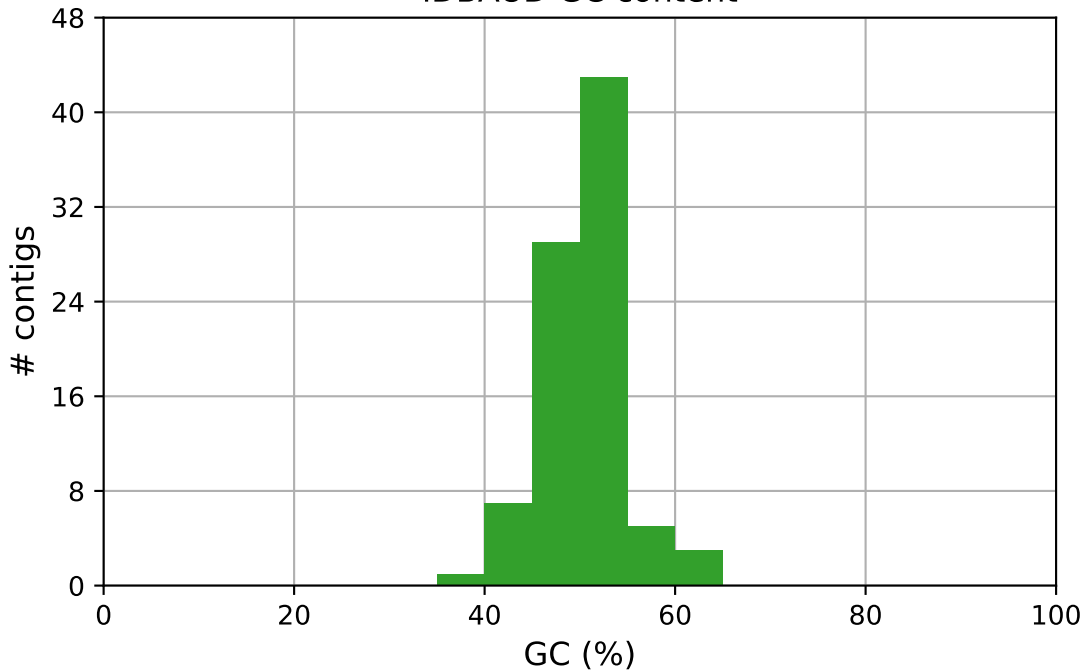
SPAdes GC content



SPAdes.m1000 GC content

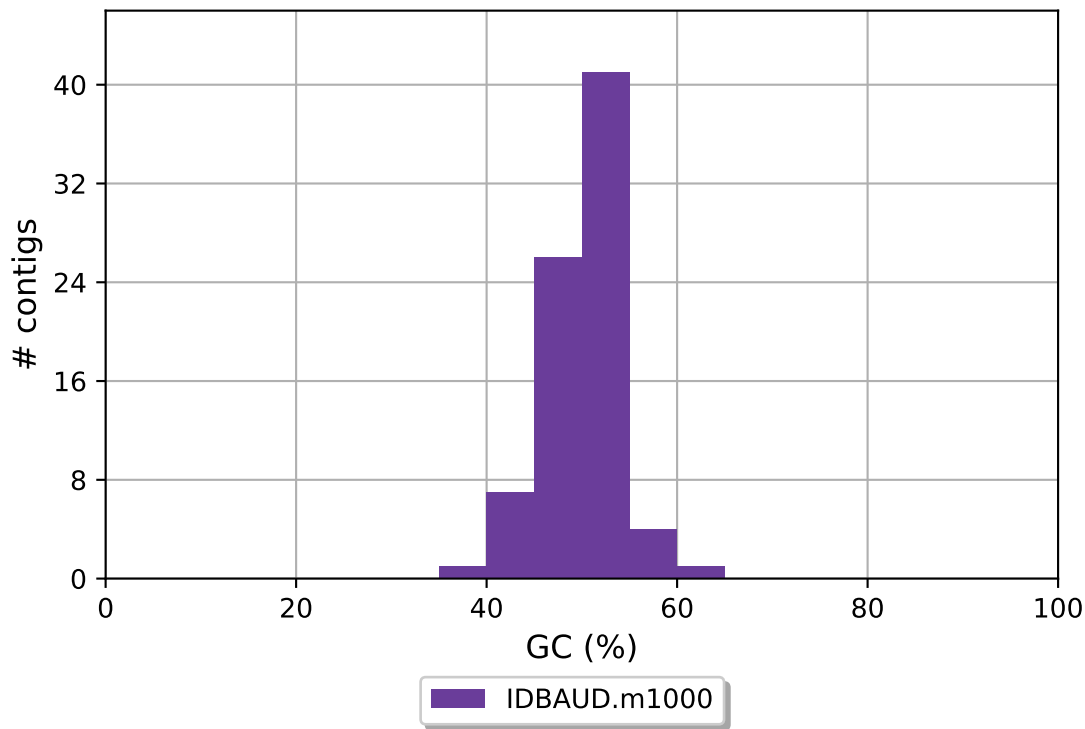


IDBAUD GC content

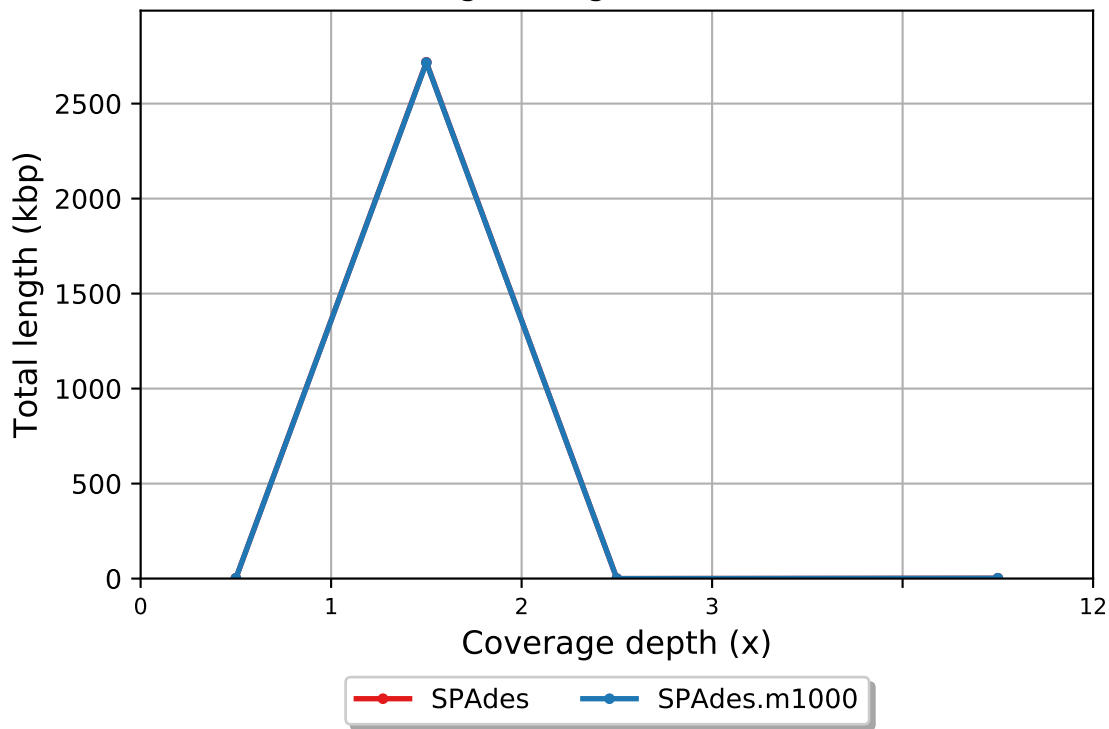


IDBAUD

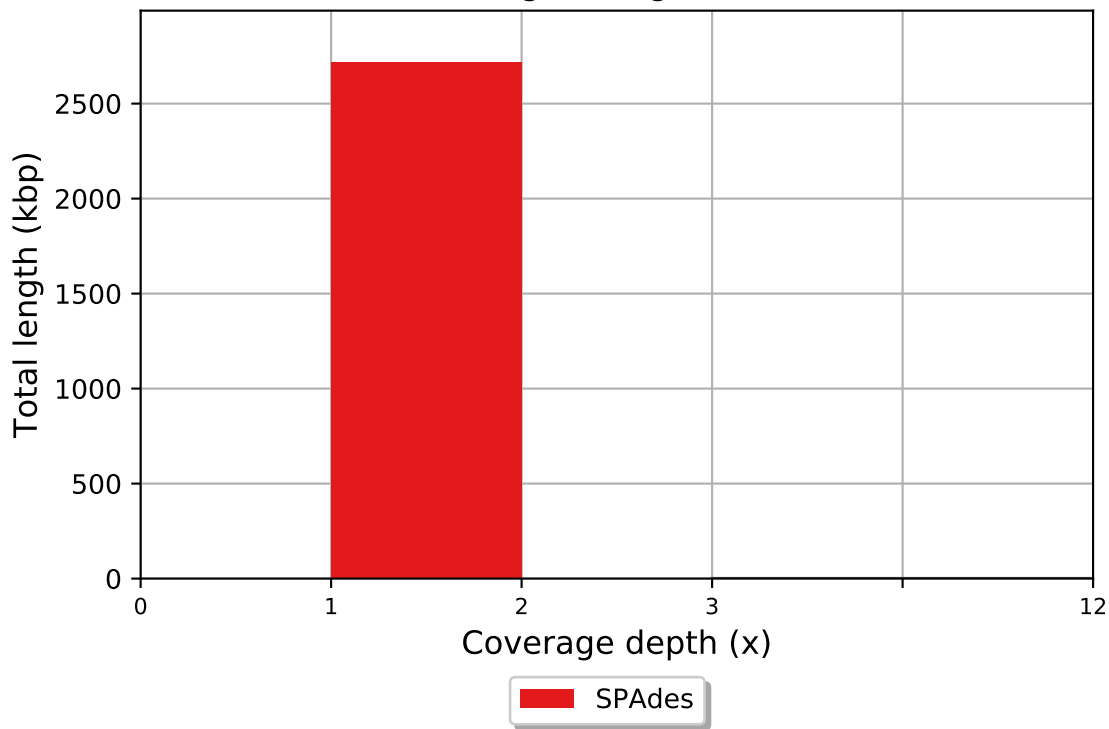
IDBAUD.m1000 GC content



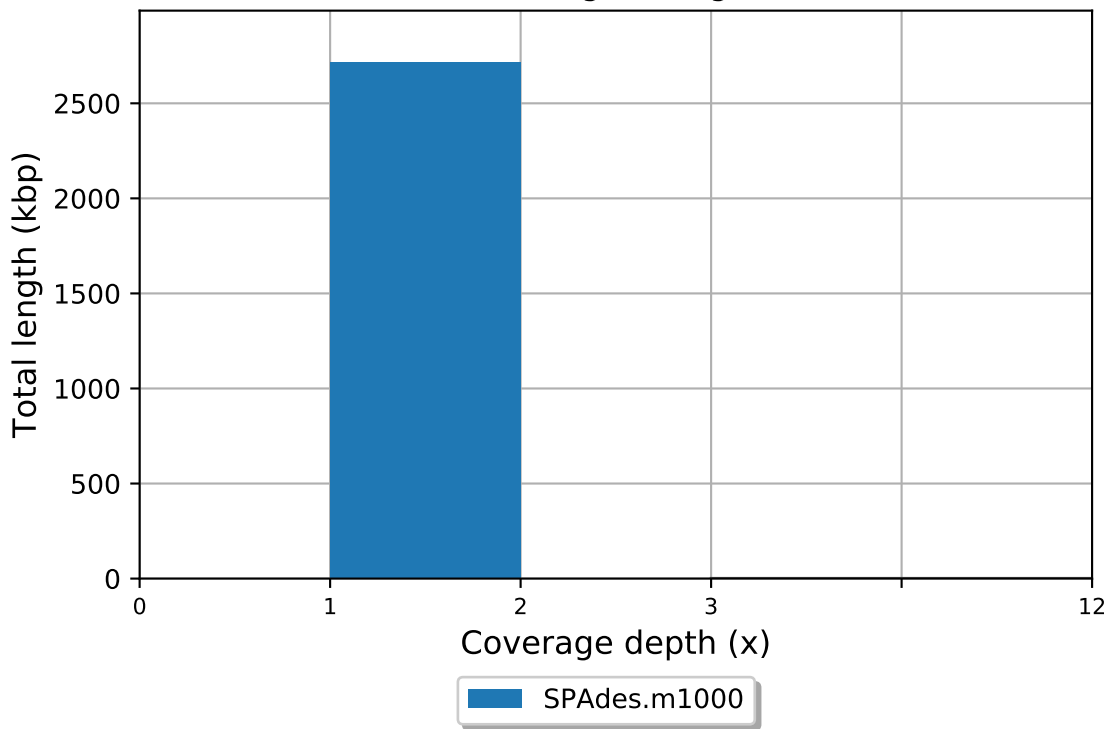
Coverage histogram (bin size: 1x)



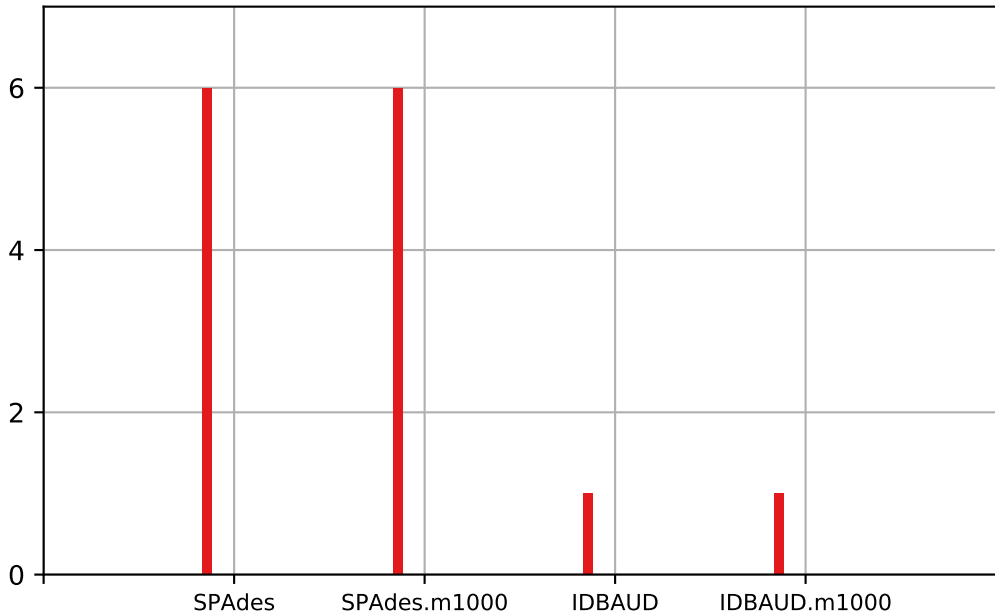
SPAdes coverage histogram (bin size: 1x)



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

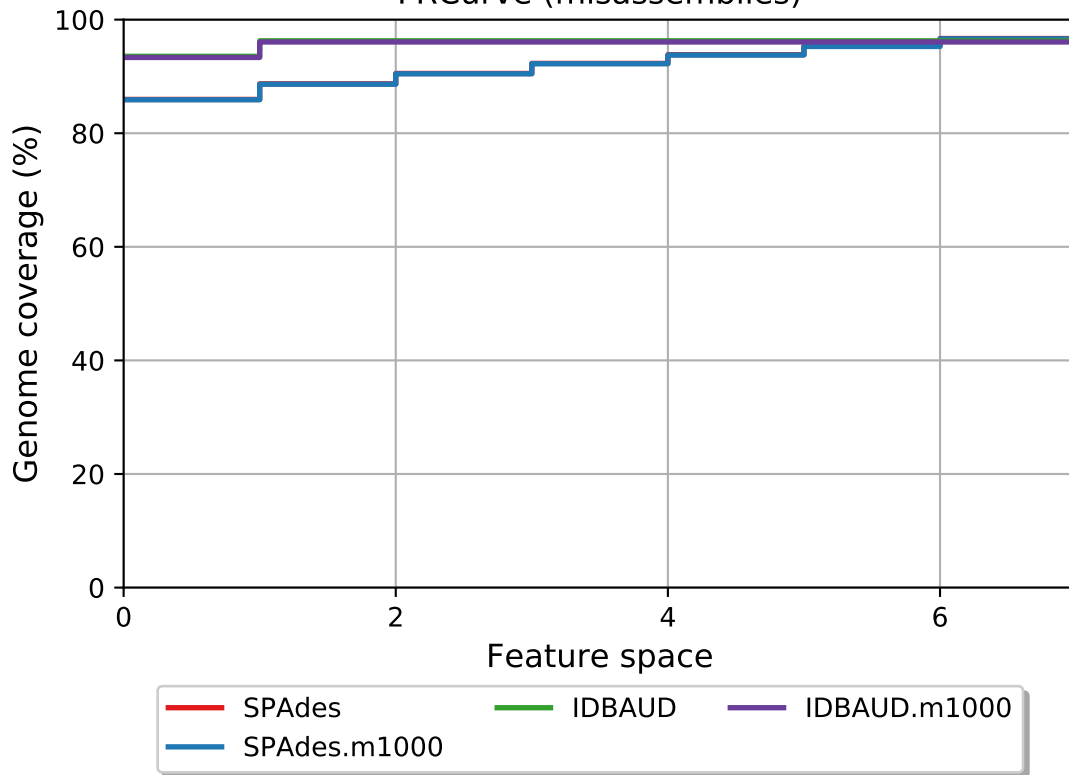


Misassemblies

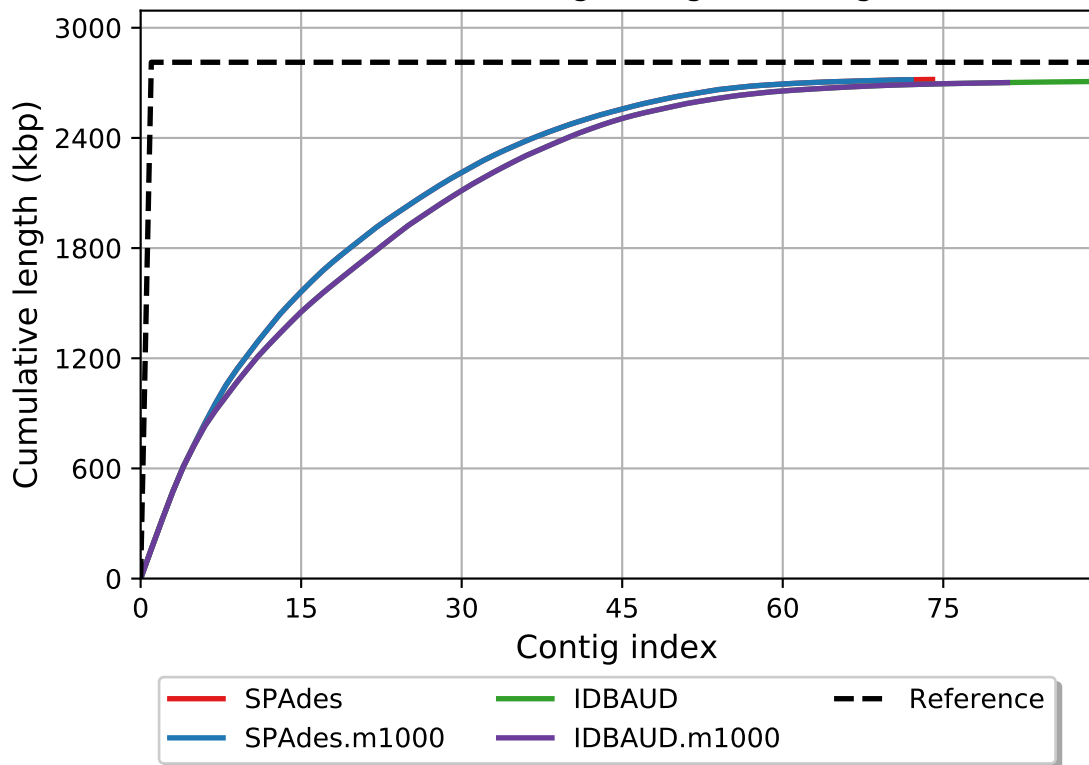


 # relocations

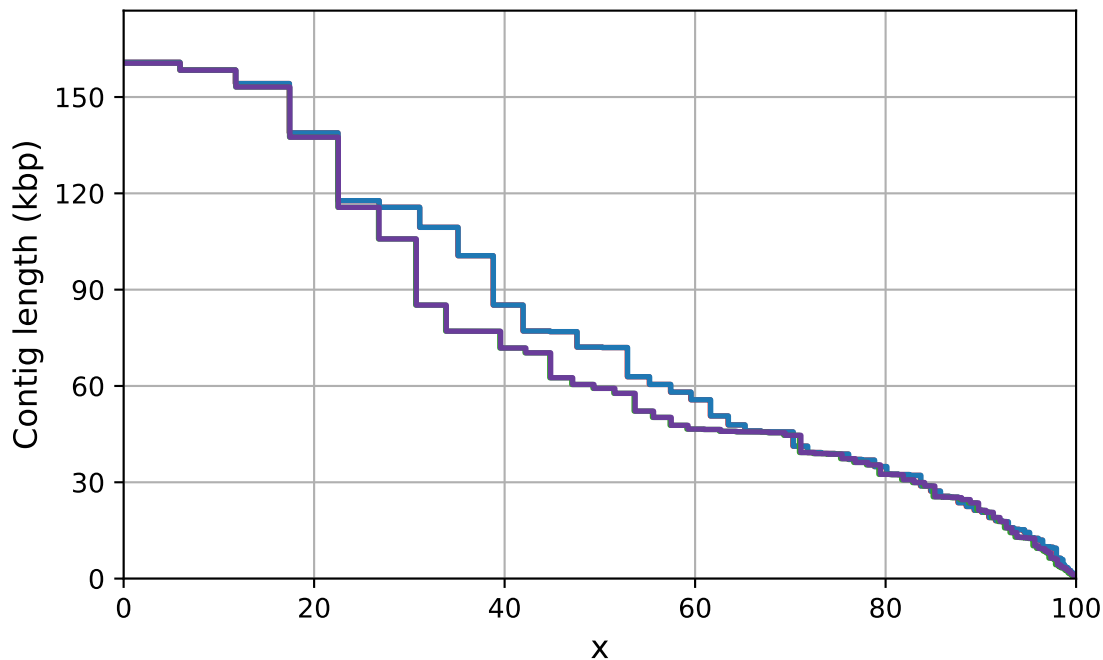
FRCurve (misassemblies)



Cumulative length (aligned contigs)

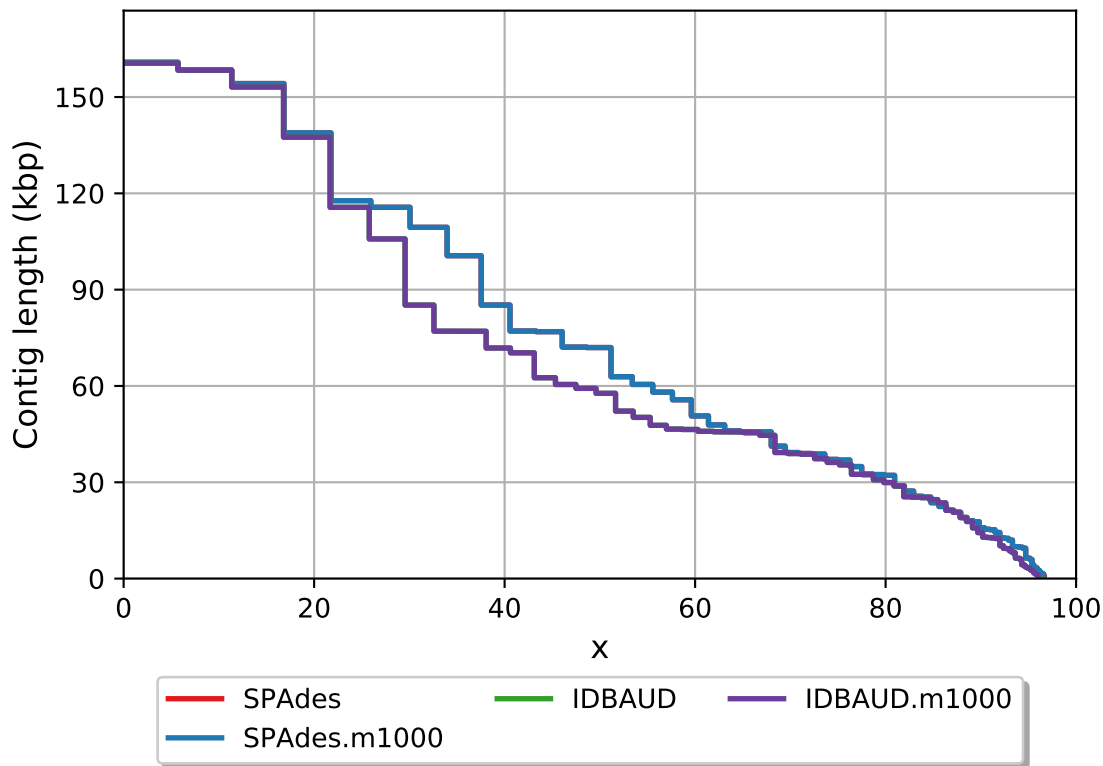


NAx

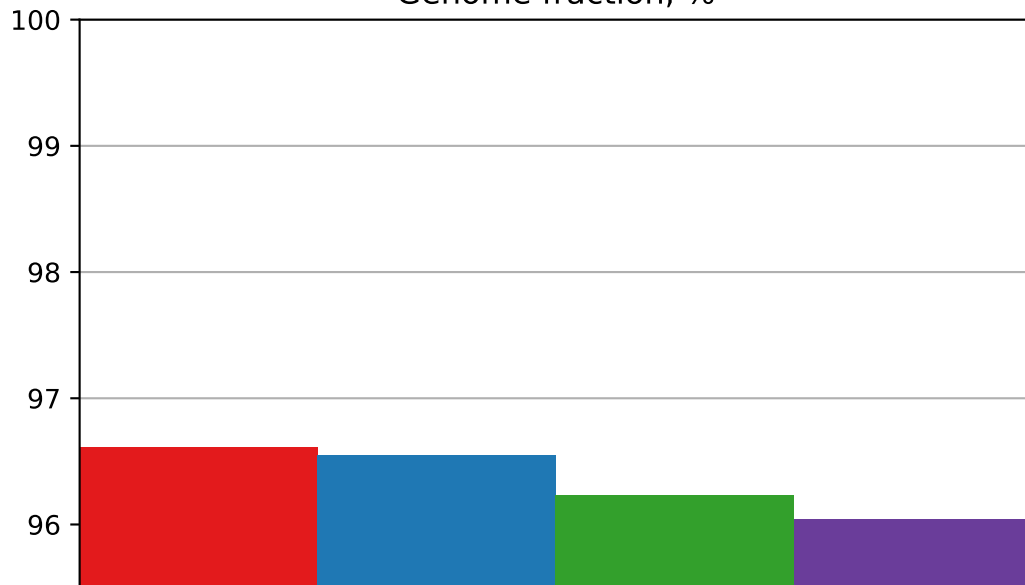


SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000