

## Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	77	77	318	318
# contigs (>= 5000 bp)	63	63	187	187
# contigs (>= 10000 bp)	55	55	97	97
# contigs (>= 25000 bp)	37	37	15	15
# contigs (>= 50000 bp)	19	19	0	0
Total length (>= 1000 bp)	2891525	2891525	2722765	2722765
Total length (>= 5000 bp)	2853115	2853115	2373105	2373105
Total length (>= 10000 bp)	2805887	2805887	1691909	1691909
Total length (>= 25000 bp)	2487703	2487703	494222	494222
Total length (>= 50000 bp)	1774770	1774770	0	0
# contigs	80	77	401	318
Largest contig	186282	186282	48097	48097
Total length	2893768	2891525	2782995	2722765
Reference length	2918353	2918353	2918353	2918353
GC (%)	32.67	32.66	32.72	32.71
Reference GC (%)	32.87	32.87	32.87	32.87
N50	73068	73068	12075	12488
NG50	73068	73068	11545	11545
N75	40938	40938	7657	7769
NG75	39011	39011	6794	6794
L50	14	14	70	67
LG50	14	14	75	75
L75	28	28	142	137
LG75	29	29	156	156
# misassemblies	35	34	29	23
# misassembled contigs	23	22	28	22
Misassembled contigs length	1466831	1465856	213655	209090
# local misassemblies	50	50	150	149
# scaffold gap ext. mis.	3	3	0	0
# scaffold gap loc. mis.	41	41	3	3
# unaligned mis. contigs	5	5	5	5
# unaligned contigs	1 + 31 part	1 + 31 part	2 + 43 part	2 + 41 part
Unaligned length	250170	250170	180663	179335
Genome fraction (%)	90.288	90.221	88.775	86.872
Duplication ratio	1.003	1.003	1.004	1.003
# N's per 100 kbp	182.67	182.81	23.32	23.84
# mismatches per 100 kbp	414.89	414.51	414.51	418.03
# indels per 100 kbp	24.37	24.35	14.71	14.87
Largest alignment	158591	158591	45850	45850
Total aligned length	2635482	2633546	2597002	2538455
NA50	41226	41226	10121	10346
NGA50	40832	40832	9773	9773
NA75	20074	20074	5596	6048
NGA75	19668	19668	4885	4885
LA50	20	20	79	76
LGA50	21	21	86	86
LA75	44	44	166	158
LGA75	45	45	185	185

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

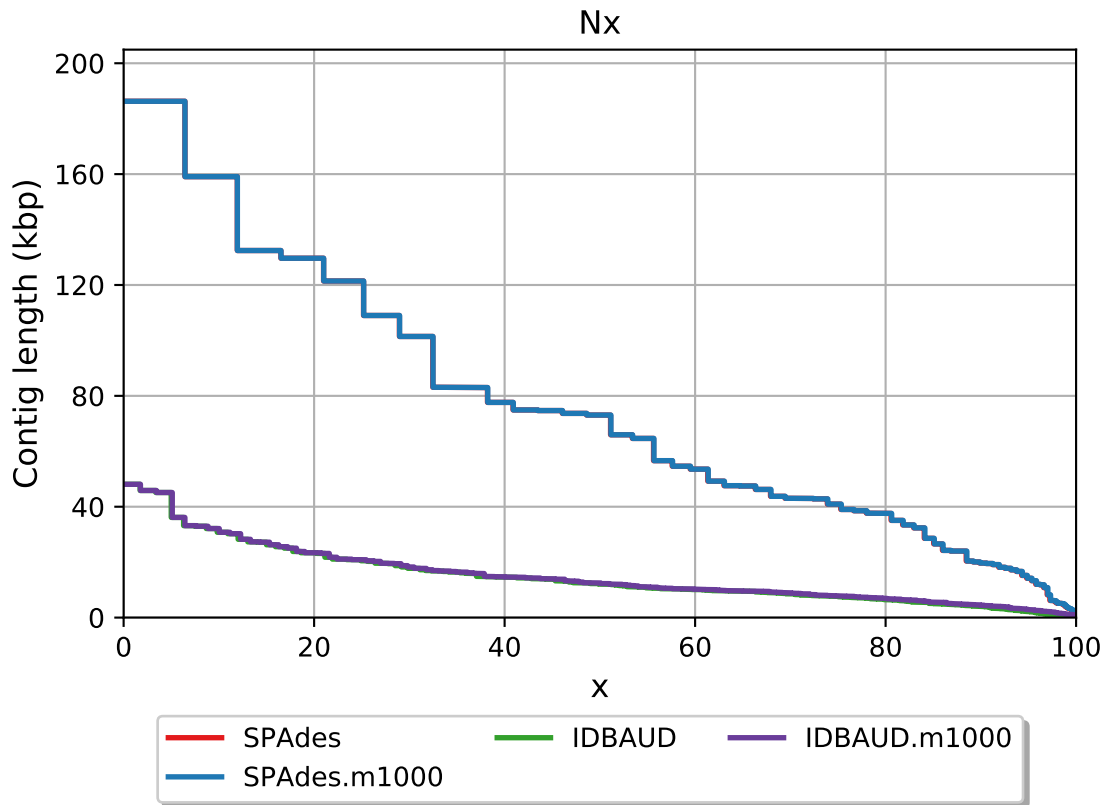
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	35	34	29	23
# contig misassemblies	33	32	29	23
# c. relocations	33	32	27	22
# c. translocations	0	0	0	0
# c. inversions	0	0	2	1
# scaffold misassemblies	2	2	0	0
# s. relocations	2	2	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	23	22	28	22
Misassembled contigs length	1466831	1465856	213655	209090
# possibly misassembled contigs	26	26	40	38
# possible misassemblies	70	70	63	61
# local misassemblies	50	50	150	149
# scaffold gap ext. mis.	3	3	0	0
# scaffold gap loc. mis.	41	41	3	3
# unaligned mis. contigs	5	5	5	5
# mismatches	10932	10914	10739	10598
# indels	642	641	381	377
# indels (<= 5 bp)	379	379	323	319
# indels (> 5 bp)	263	262	58	58
Indels length	6252	6232	2721	2717

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

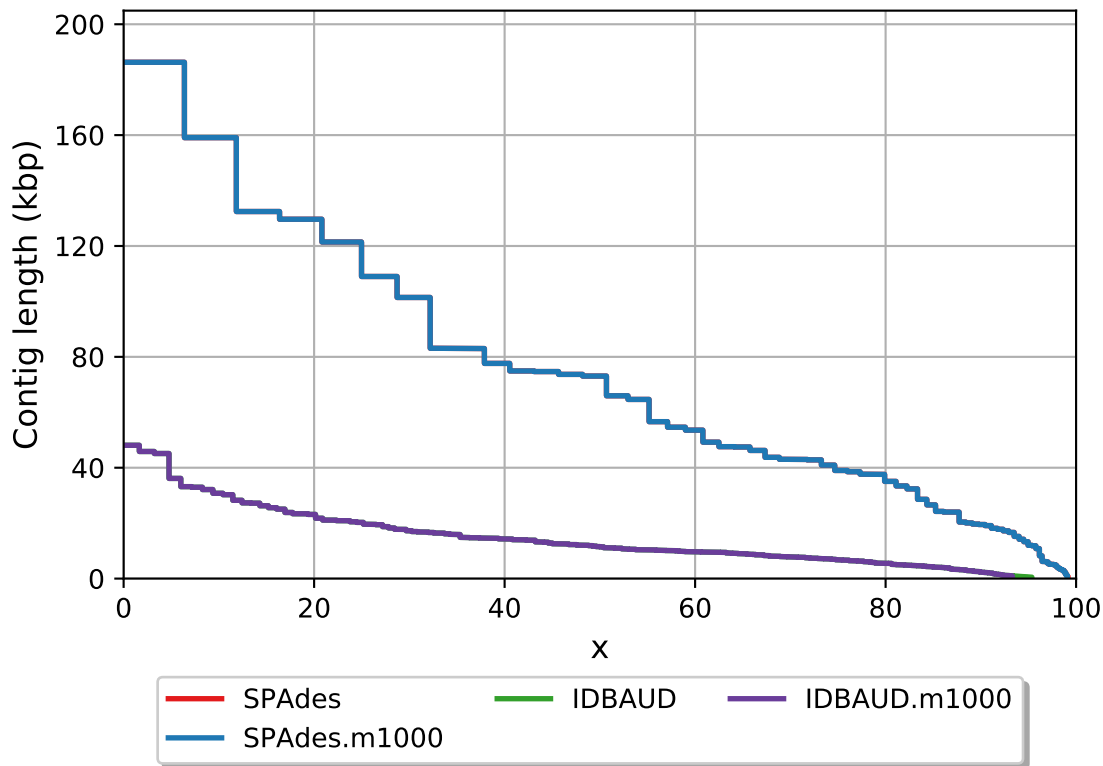
## Unaligned report

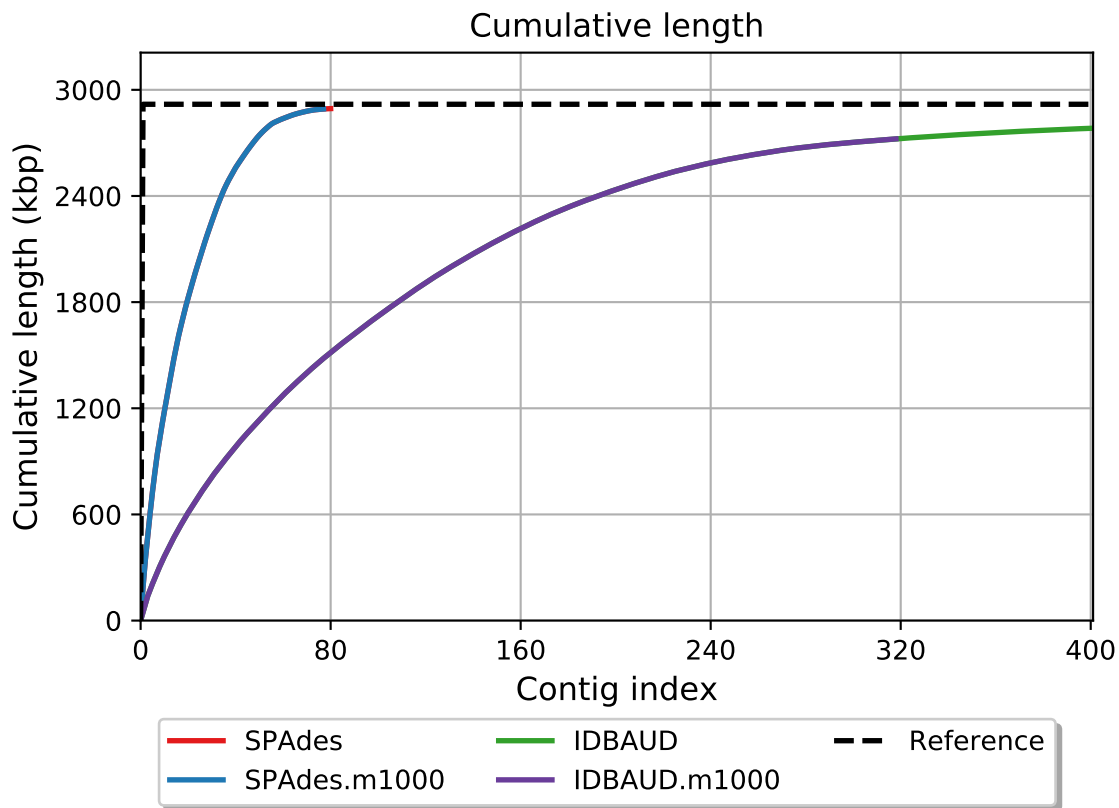
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	1	1	2	2
Fully unaligned length	2206	2206	5789	5789
# partially unaligned contigs	31	31	43	41
Partially unaligned length	247964	247964	174874	173546
# N's	5286	5286	649	649

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

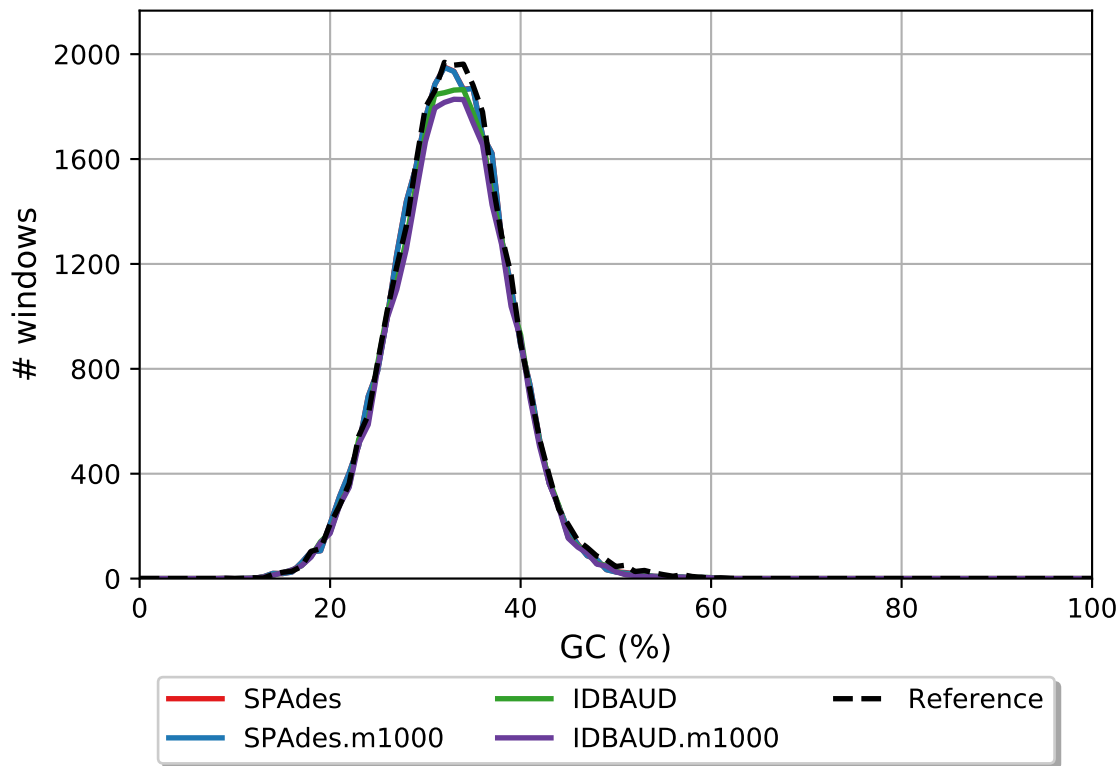


# NGx

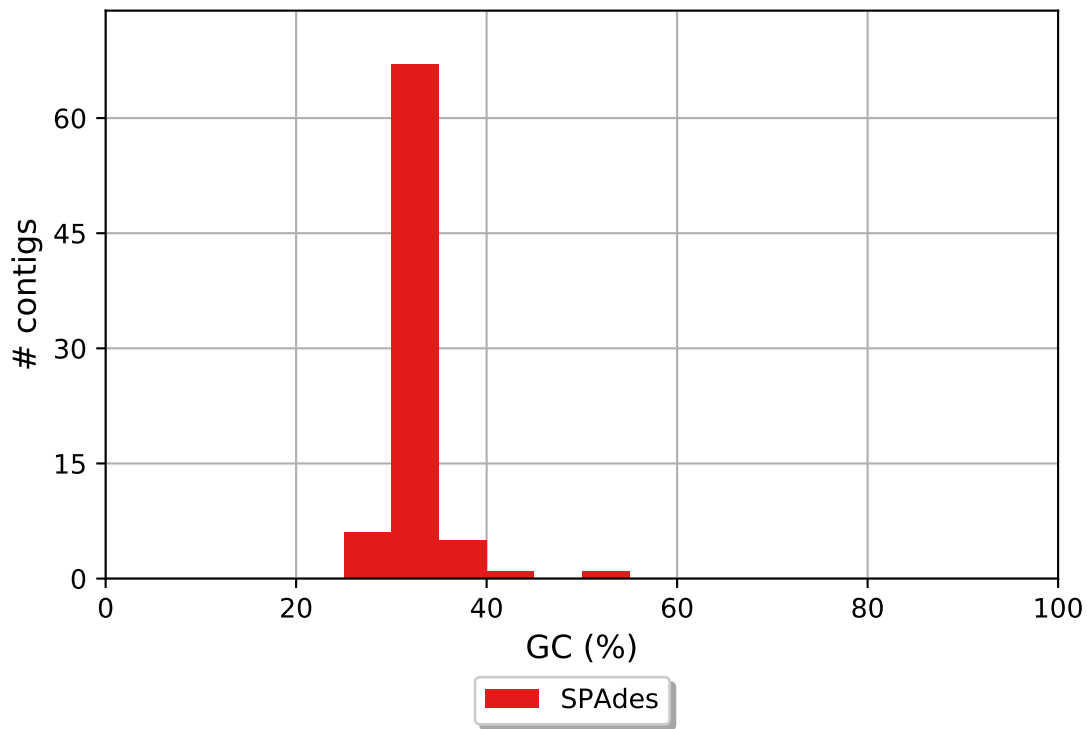




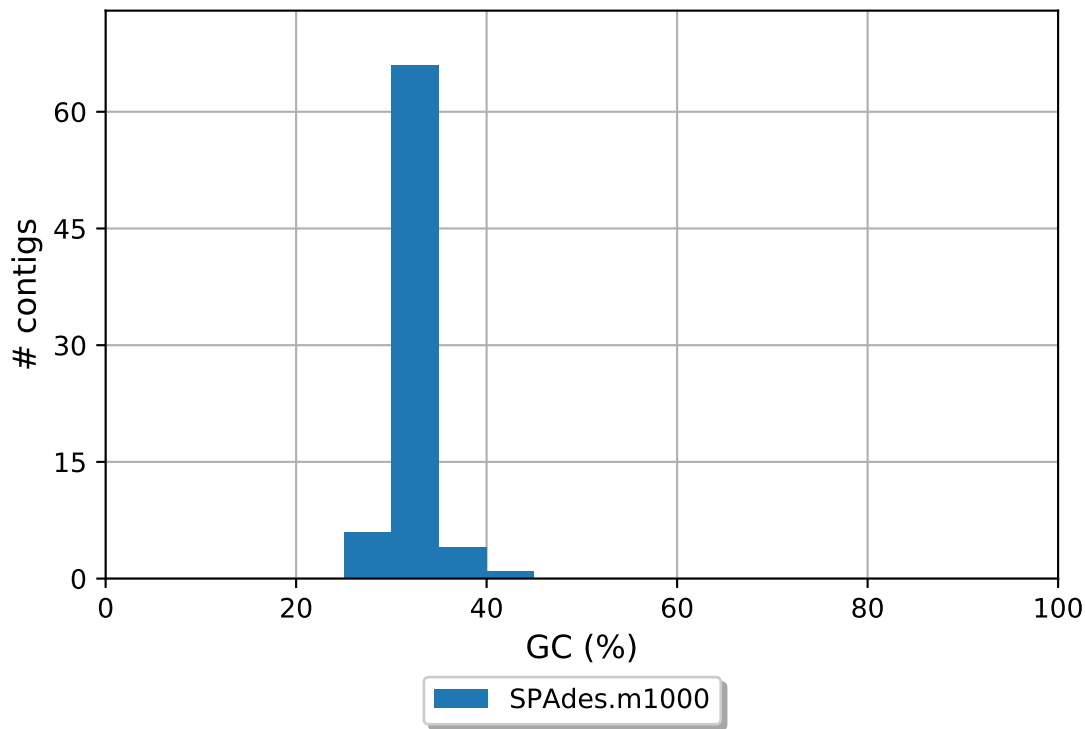
GC content



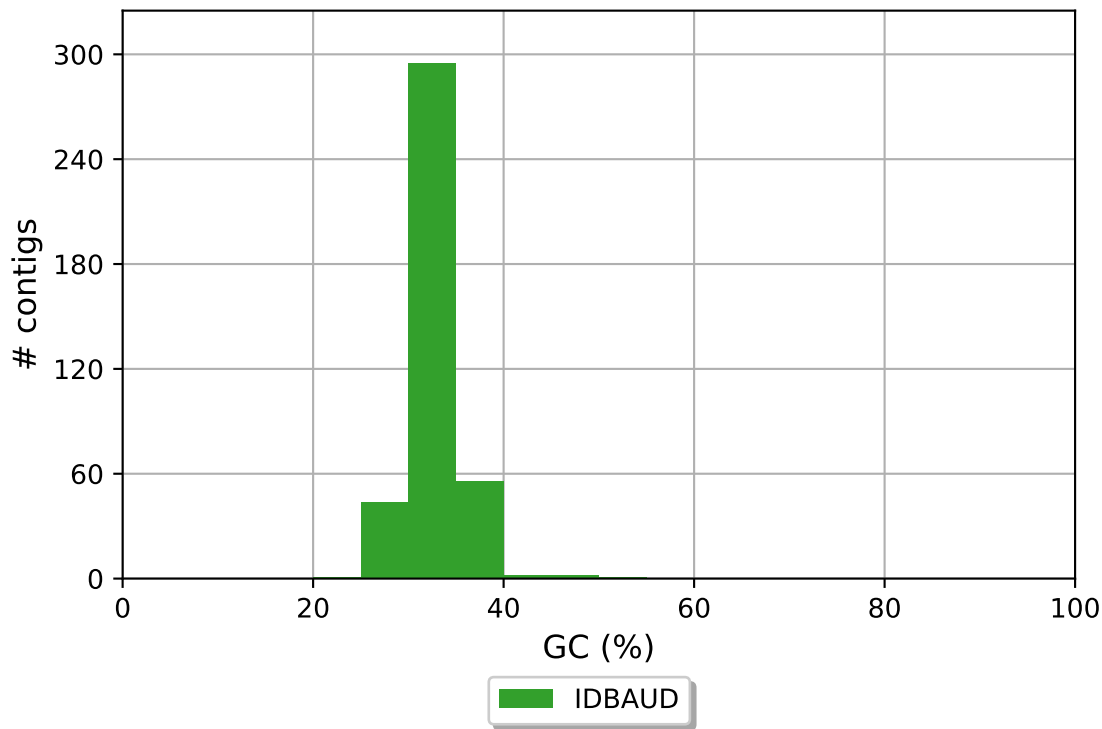
SPAdes GC content



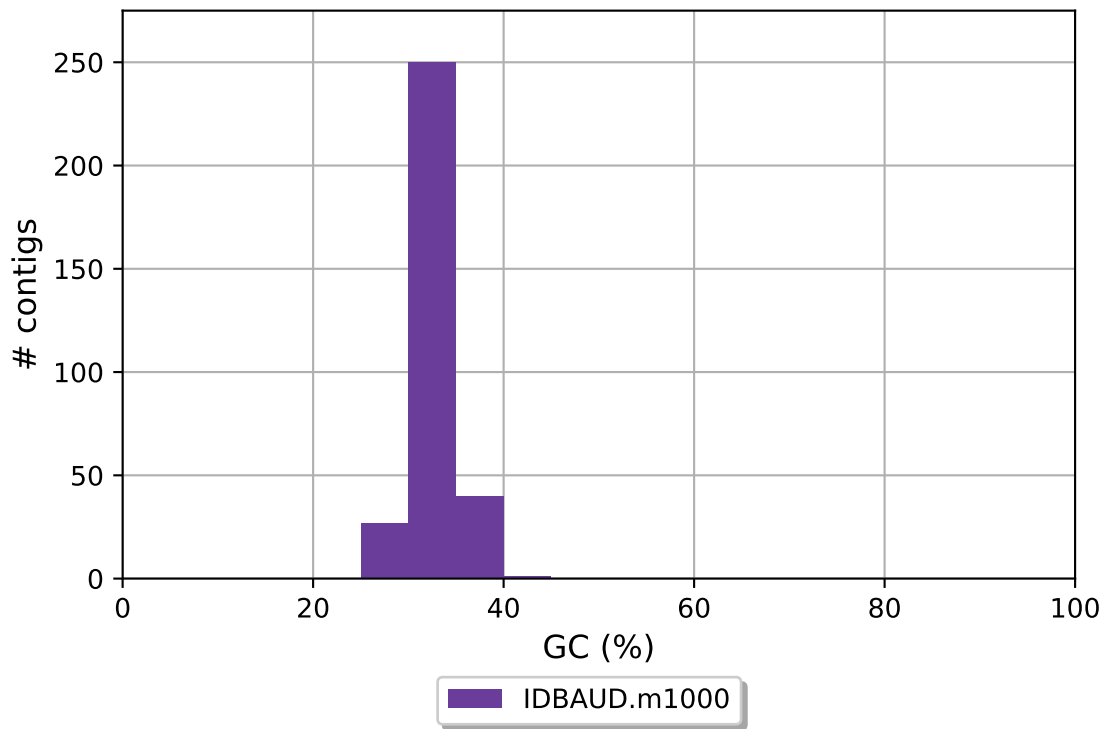
SPAdes.m1000 GC content



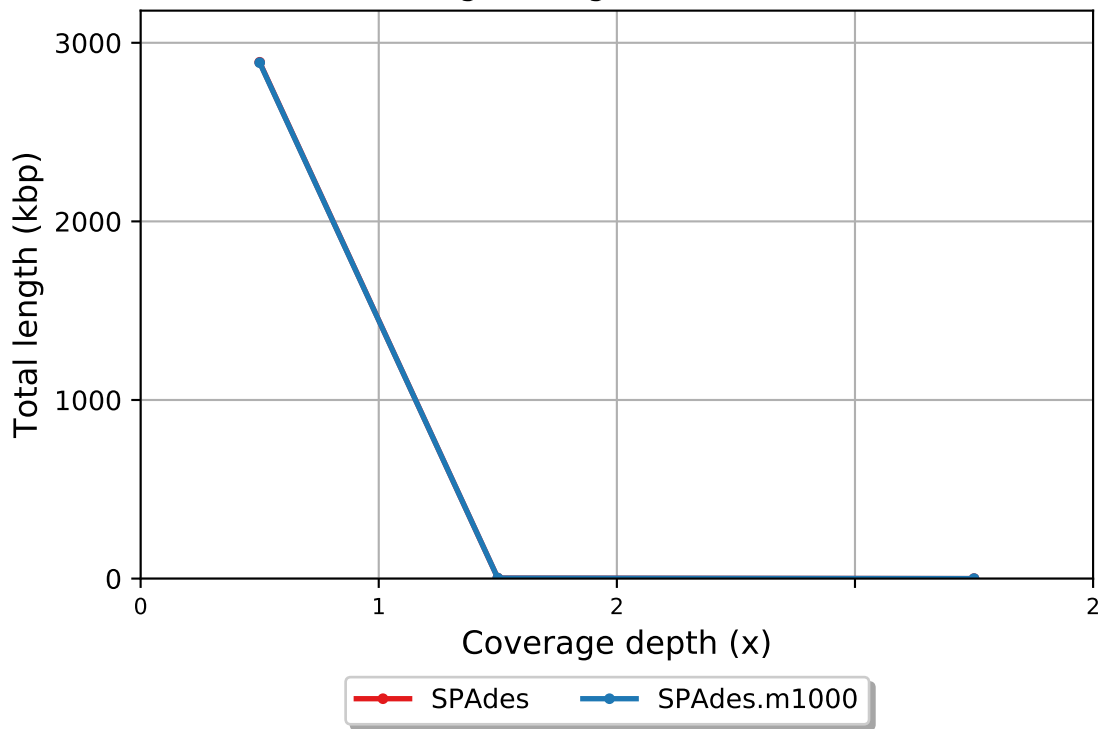
IDBAUD GC content



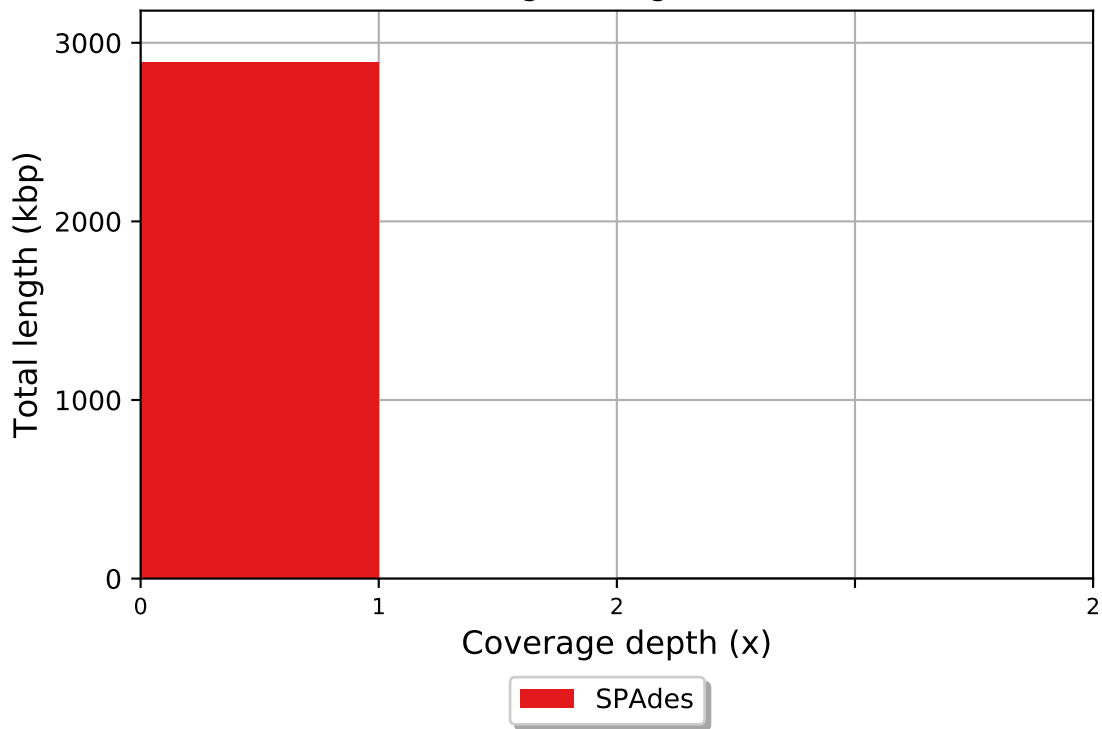
IDBAUD.m1000 GC content



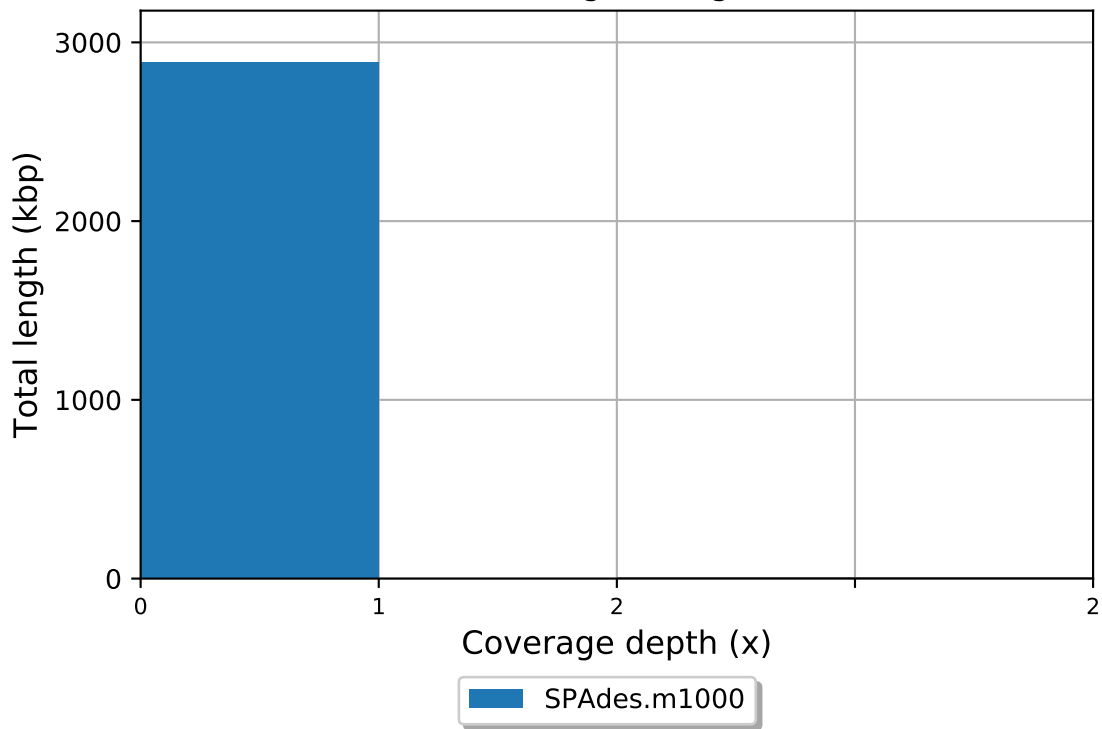
Coverage histogram (bin size: 1x)



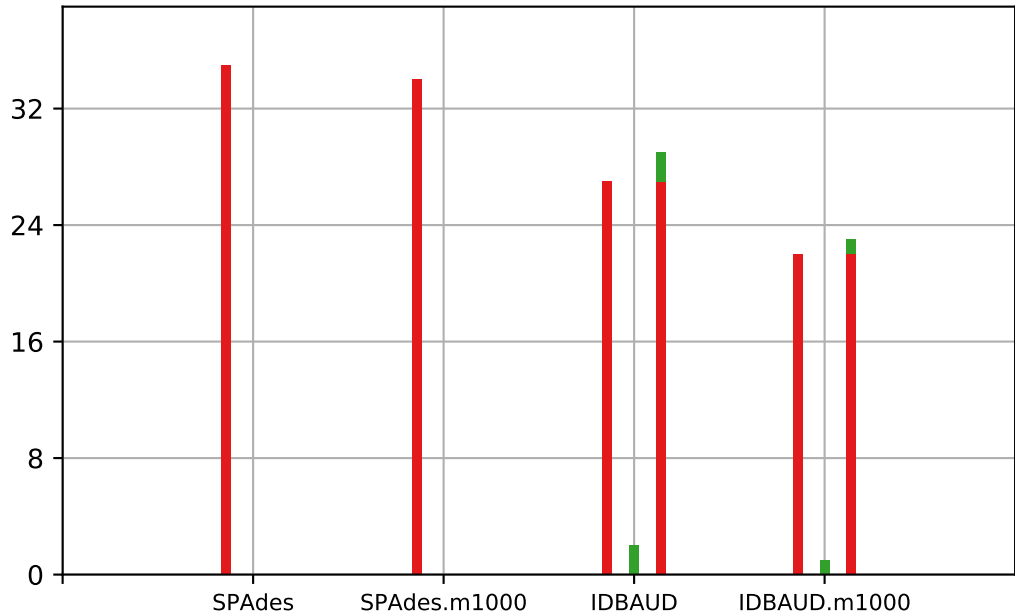
SPAdes coverage histogram (bin size: 1x)



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



## Misassemblies

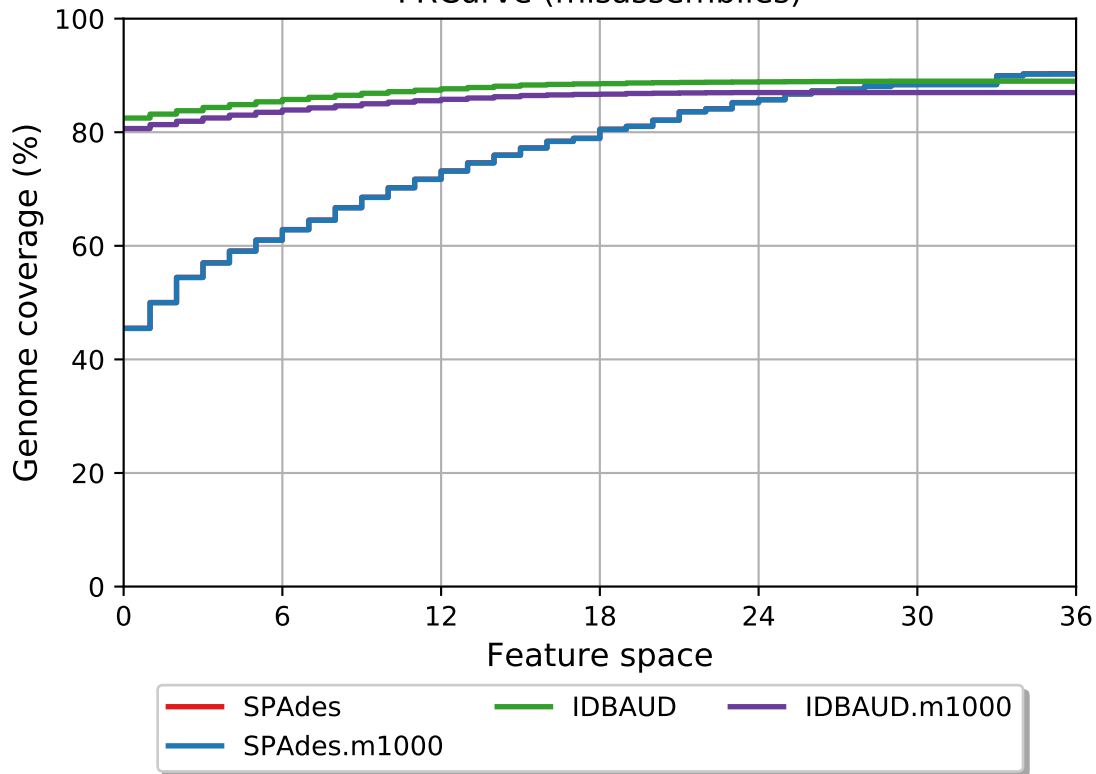


# relocations

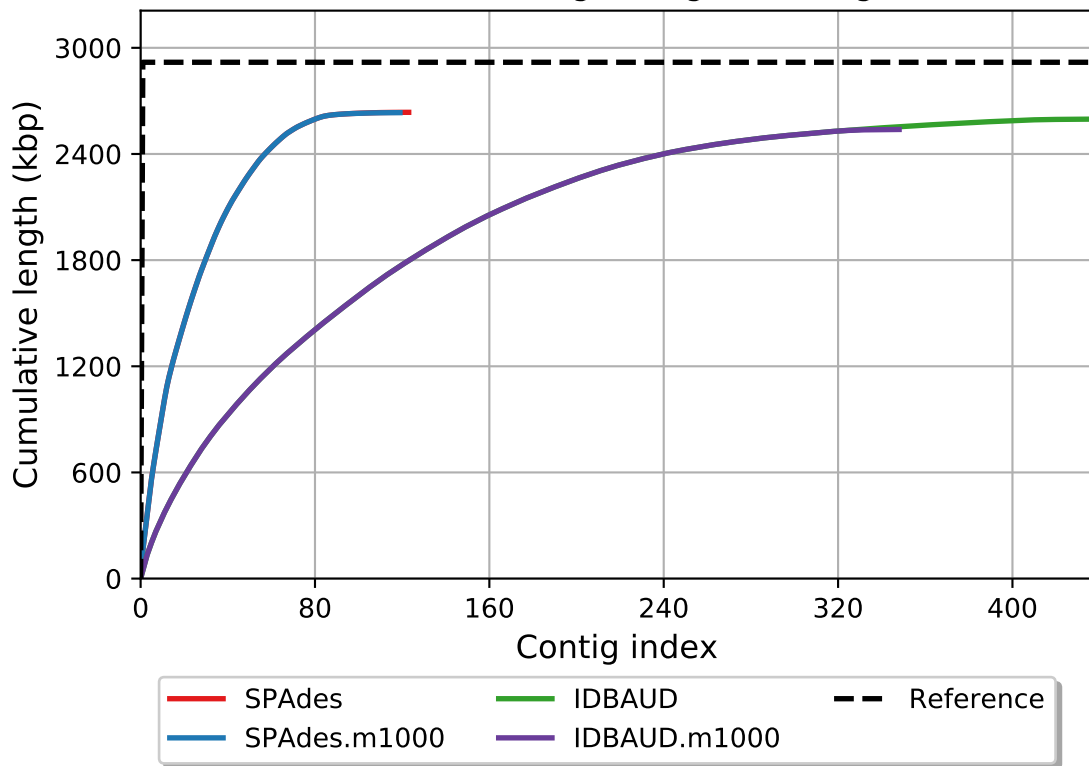


# inversions

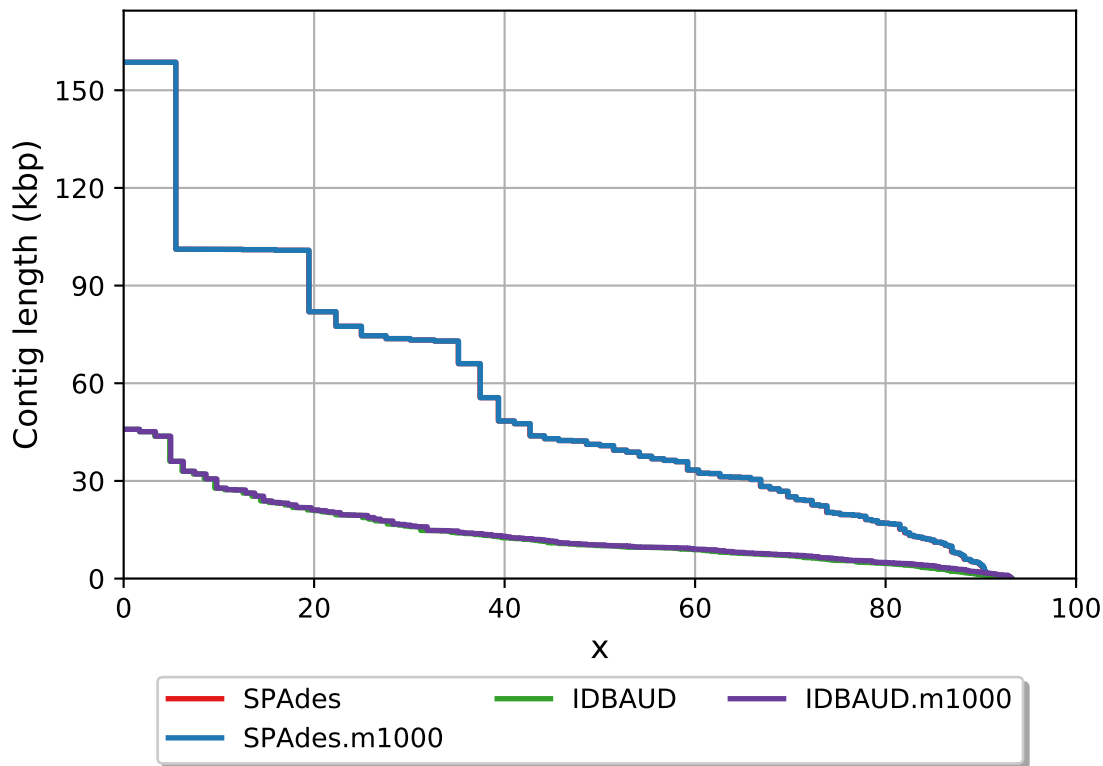
FRCurve (misassemblies)



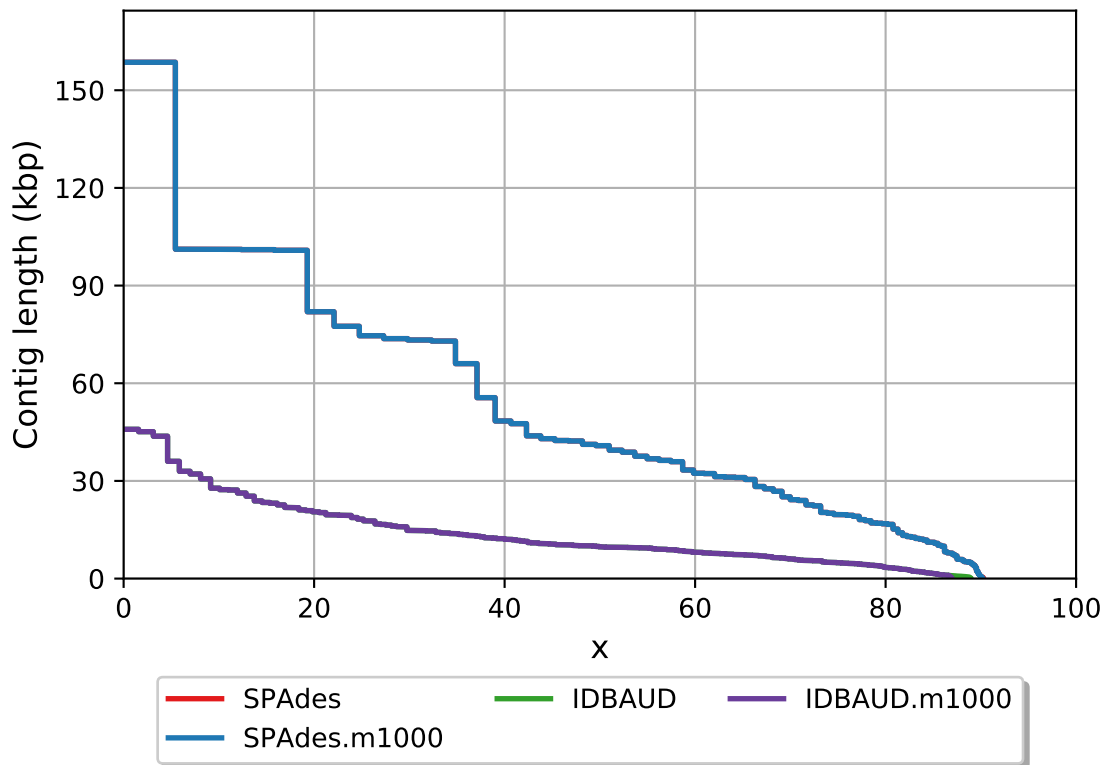
Cumulative length (aligned contigs)



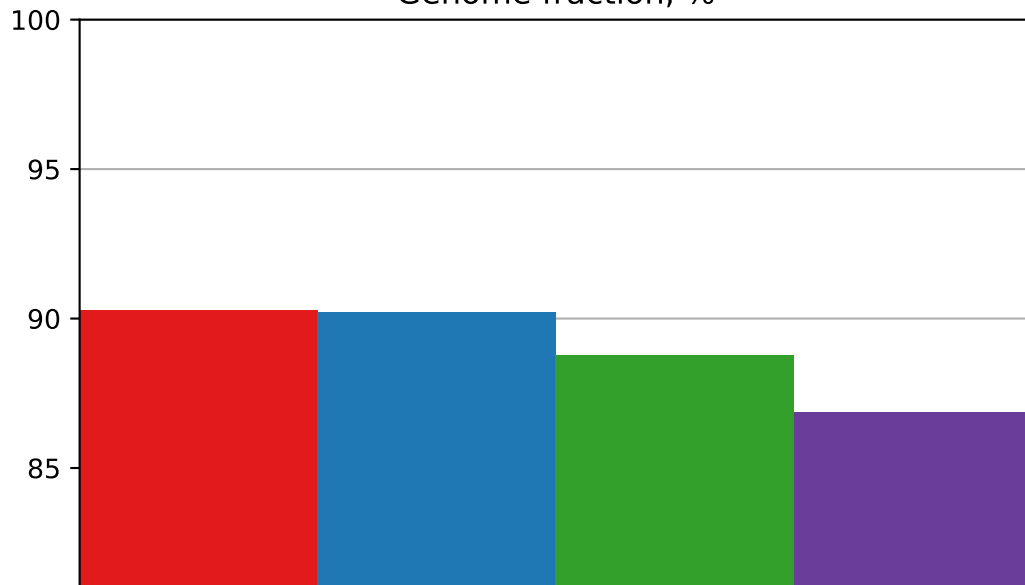
NAx



## NGAx



Genome fraction, %



SPAdes  
SPAdes.m1000

IDBAUD

IDBAUD.m1000