

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	37	37	61	61
# contigs (>= 5000 bp)	22	22	29	29
# contigs (>= 10000 bp)	16	16	23	23
# contigs (>= 25000 bp)	13	13	20	20
# contigs (>= 50000 bp)	12	12	19	19
Total length (>= 1000 bp)	3957474	3957474	3914629	3914629
Total length (>= 5000 bp)	3915433	3915433	3844015	3844015
Total length (>= 10000 bp)	3869519	3869519	3802771	3802771
Total length (>= 25000 bp)	3814177	3814177	3742356	3742356
Total length (>= 50000 bp)	3767693	3767693	3696900	3696900
# contigs	40	37	90	61
Largest contig	803085	803085	534889	534889
Total length	3959278	3957474	3934558	3914629
Reference length	4033813	4033813	4033813	4033813
GC (%)	47.48	47.48	47.50	47.51
Reference GC (%)	47.64	47.64	47.64	47.64
N50	355673	355673	259127	259127
NG50	355673	355673	259127	259127
N75	283234	283234	156590	156590
NG75	283234	283234	121406	121406
L50	4	4	6	6
LG50	4	4	6	6
L75	7	7	11	11
LG75	7	7	12	12
# misassemblies	38	38	38	35
# misassembled contigs	14	14	24	21
Misassembled contigs length	3653660	3653660	3250507	3248301
# local misassemblies	42	41	50	50
# scaffold gap ext. mis.	2	2	1	1
# scaffold gap loc. mis.	4	4	0	0
# unaligned mis. contigs	12	11	19	17
# unaligned contigs	0 + 25 part	0 + 25 part	3 + 42 part	0 + 38 part
Unaligned length	286021	286021	264892	259701
Genome fraction (%)	90.865	90.853	90.704	90.478
Duplication ratio	1.002	1.002	1.003	1.001
# N's per 100 kbp	28.44	28.45	4.73	4.75
# mismatches per 100 kbp	1495.70	1494.58	1498.29	1496.89
# indels per 100 kbp	28.37	28.32	27.85	27.65
Largest alignment	418174	418174	373417	373417
Total aligned length	3665322	3663941	3663810	3651678
NA50	122386	122386	107194	107194
NGA50	122386	122386	107194	107194
NA75	67869	67869	57814	57814
NGA75	66191	66191	53828	53828
LA50	10	10	12	12
LGA50	10	10	12	12
LA75	21	21	24	24
LGA75	22	22	25	25

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

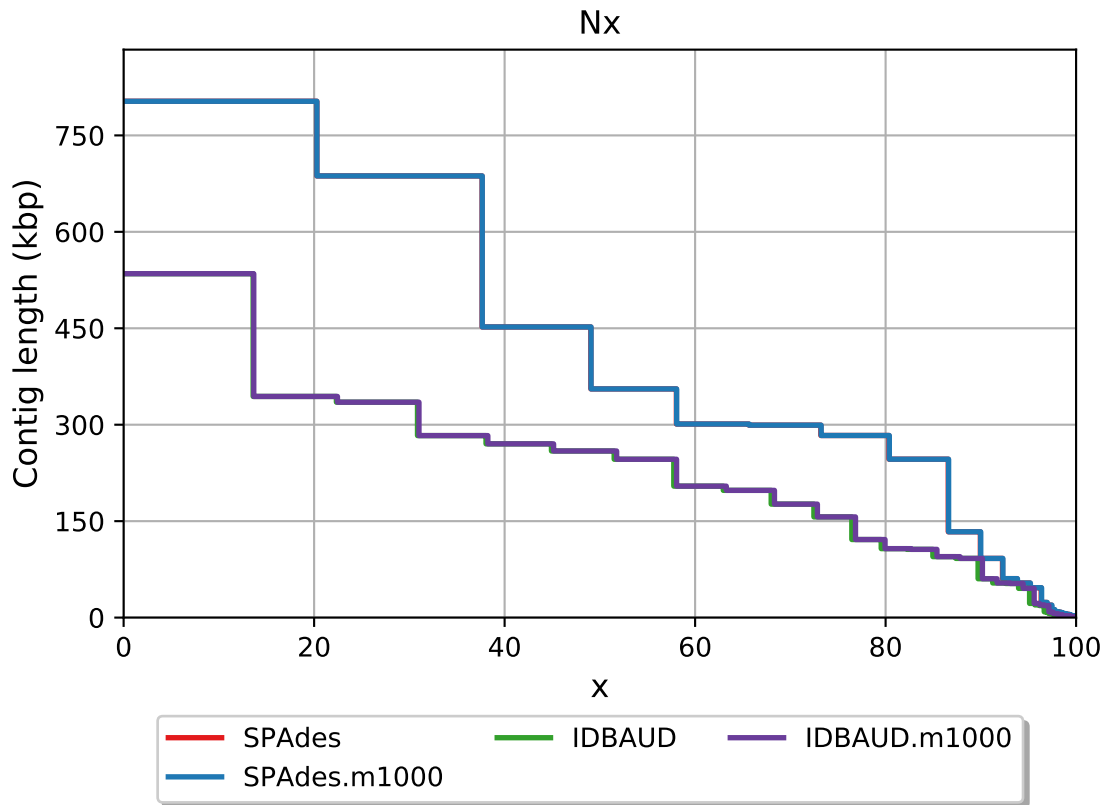
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	38	38	38	35
# contig misassemblies	36	36	38	35
# c. relocations	33	33	38	35
# c. translocations	3	3	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	2	2	0	0
# s. relocations	2	2	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	14	14	24	21
Misassembled contigs length	3653660	3653660	3250507	3248301
# possibly misassembled contigs	14	14	20	18
# possible misassemblies	82	82	74	72
# local misassemblies	42	41	50	50
# scaffold gap ext. mis.	2	2	1	1
# scaffold gap loc. mis.	4	4	0	0
# unaligned mis. contigs	12	11	19	17
# mismatches	54822	54774	54820	54632
# indels	1040	1038	1019	1009
# indels (<= 5 bp)	878	876	881	871
# indels (> 5 bp)	162	162	138	138
Indels length	4170	4164	3993	3982

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).

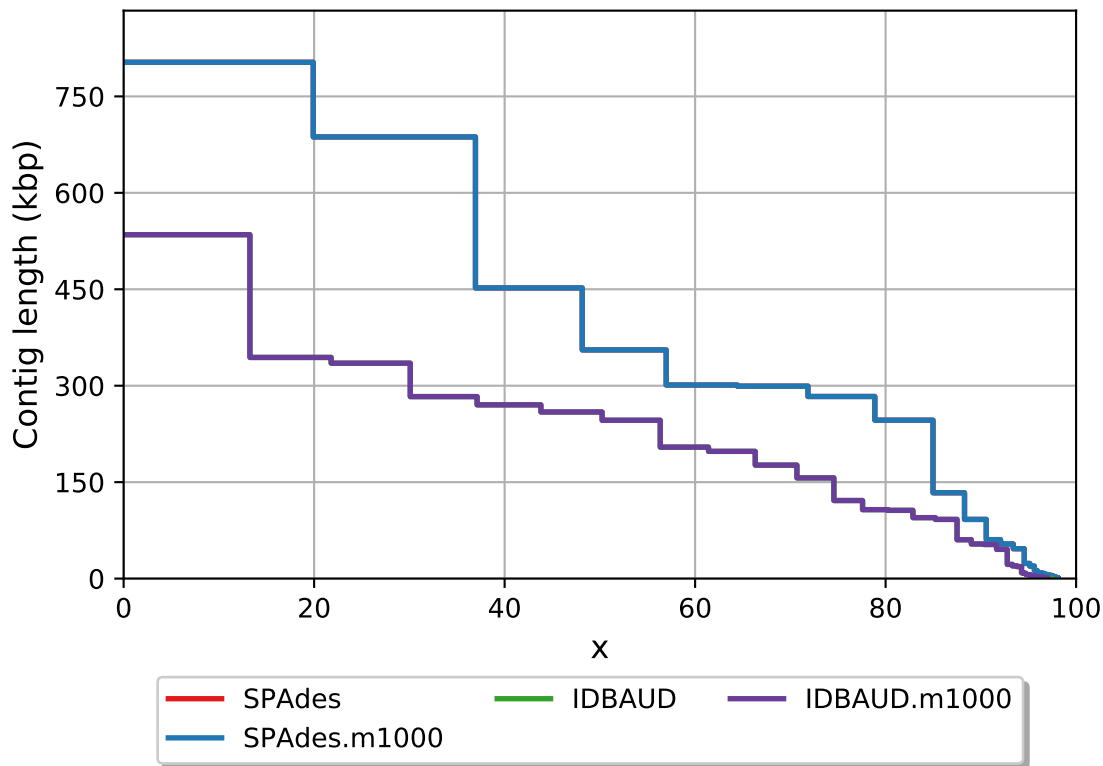
Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	3	0
Fully unaligned length	0	0	2456	0
# partially unaligned contigs	25	25	42	38
Partially unaligned length	286021	286021	262436	259701
# N's	1126	1126	186	186

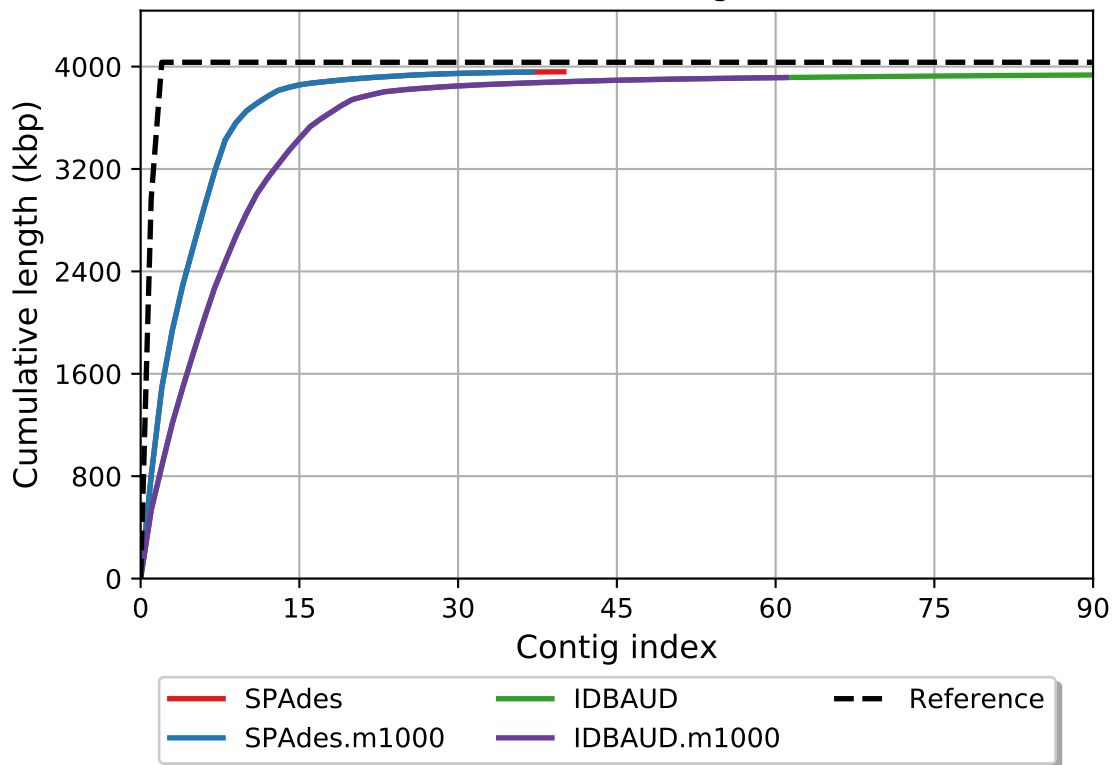
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



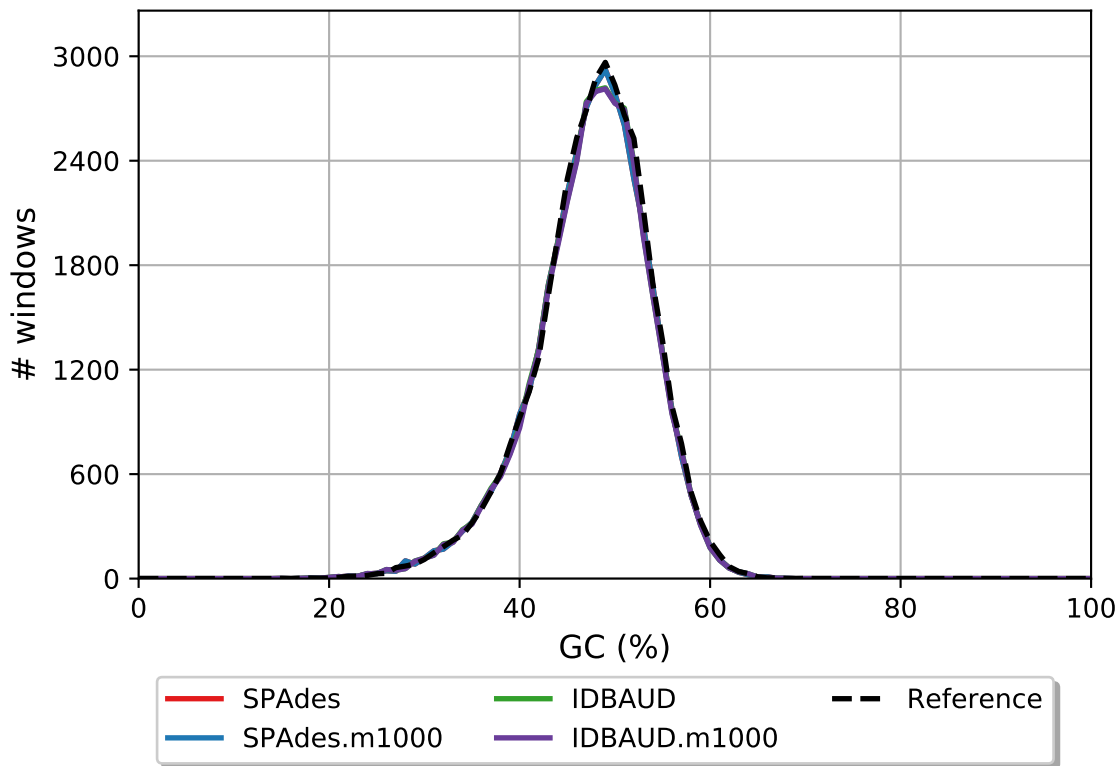
NGx



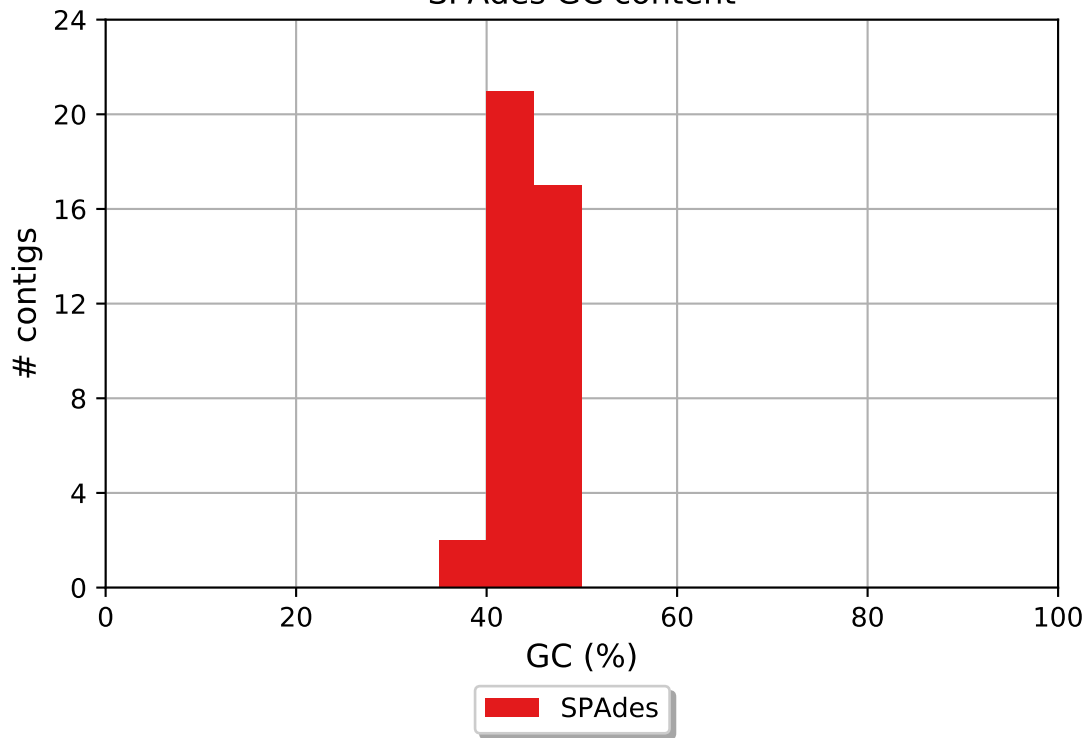
Cumulative length



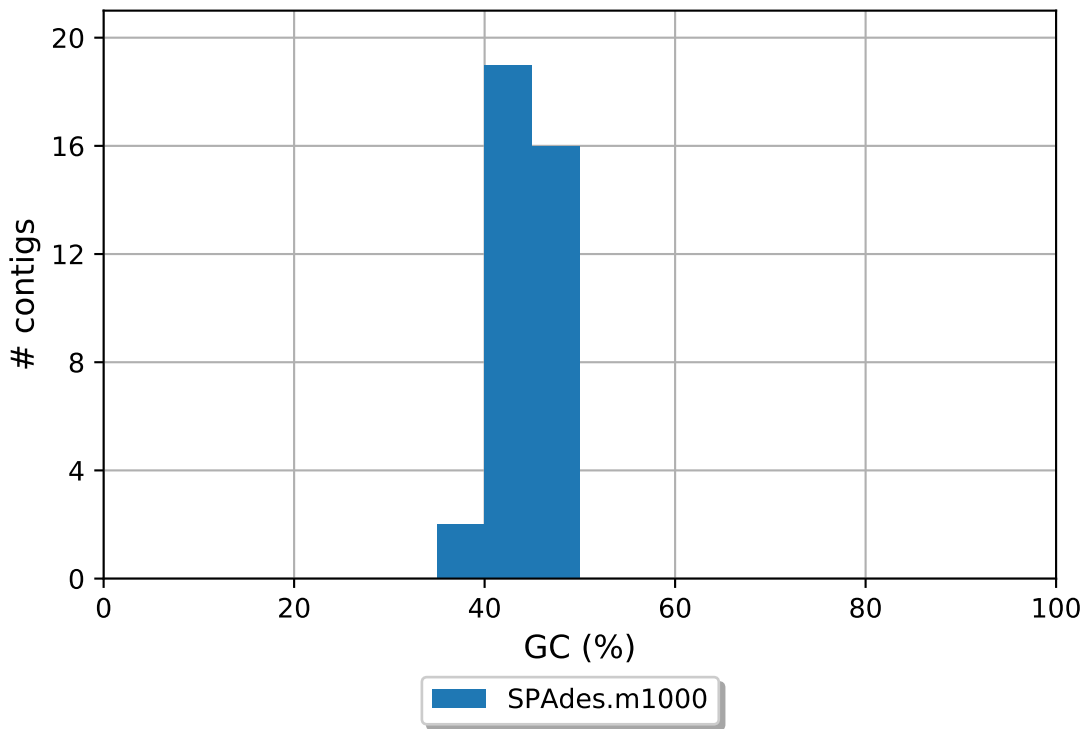
GC content



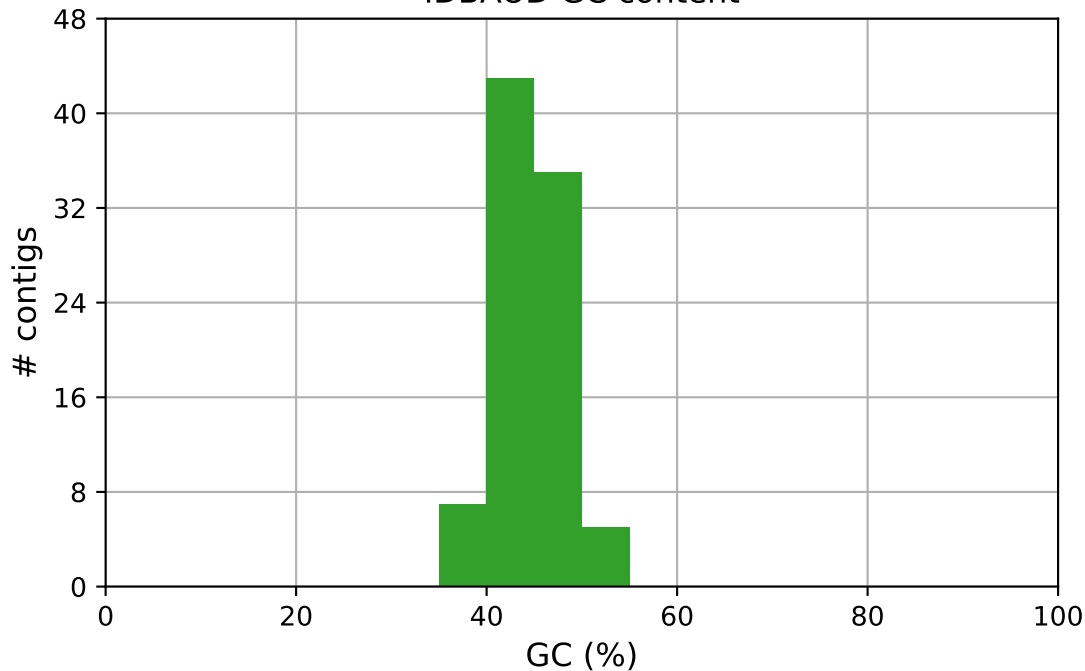
SPAdes GC content



SPAdes.m1000 GC content

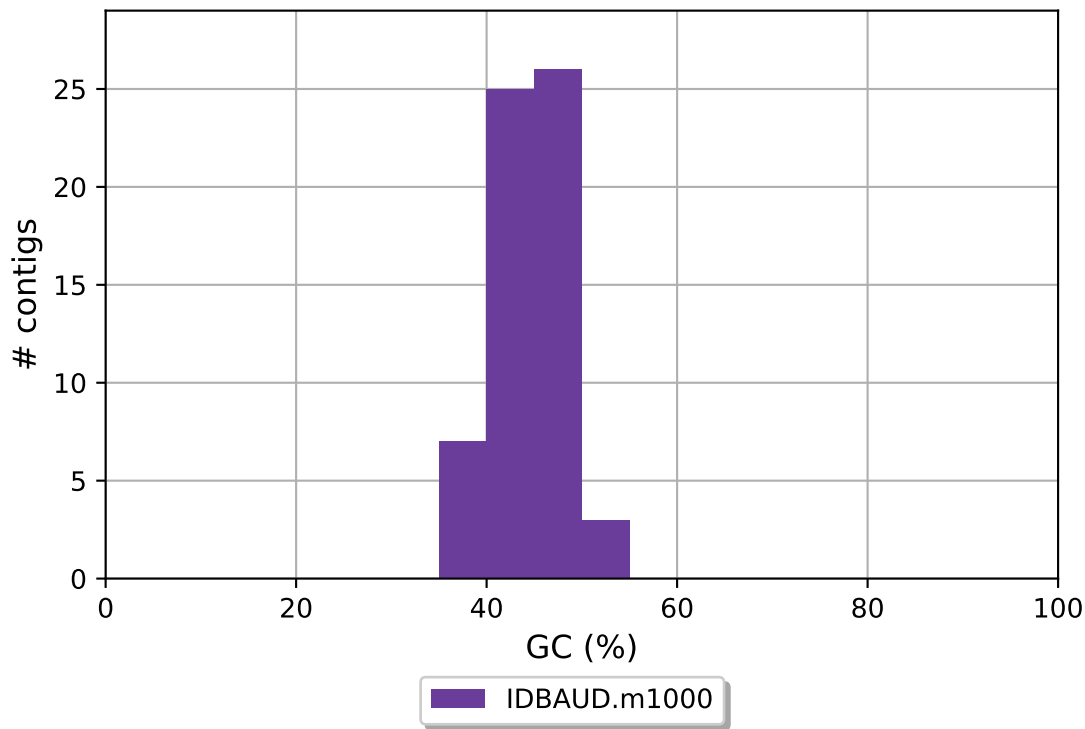


IDBAUD GC content

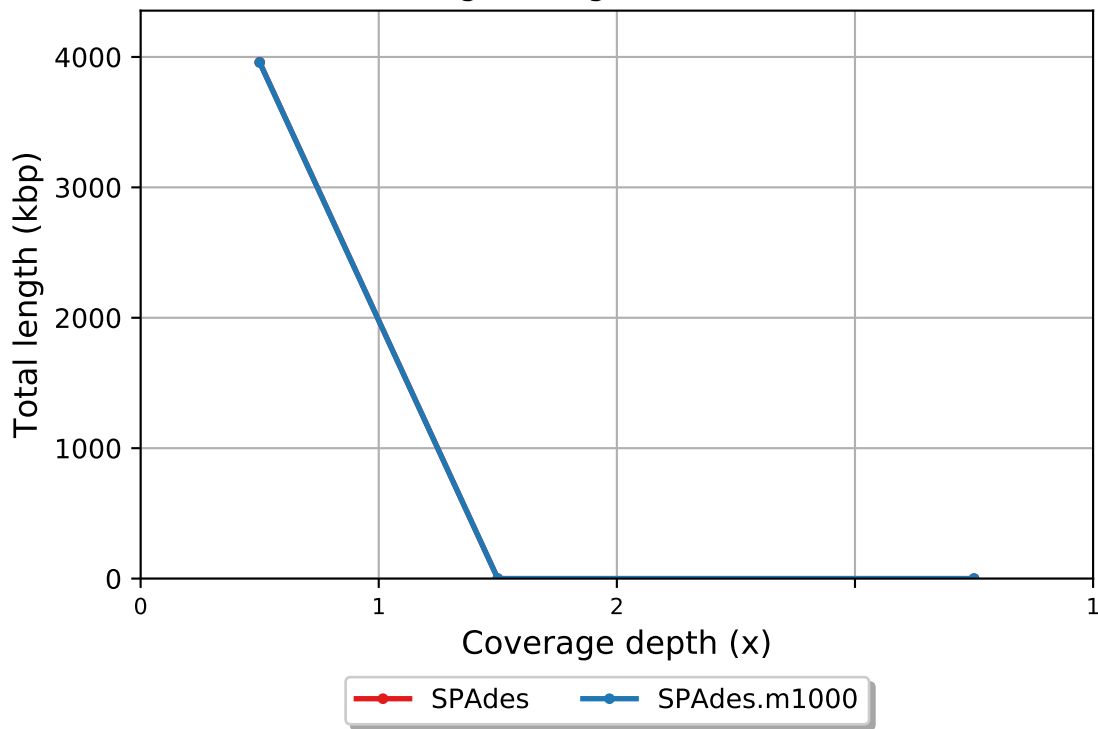


IDBAUD

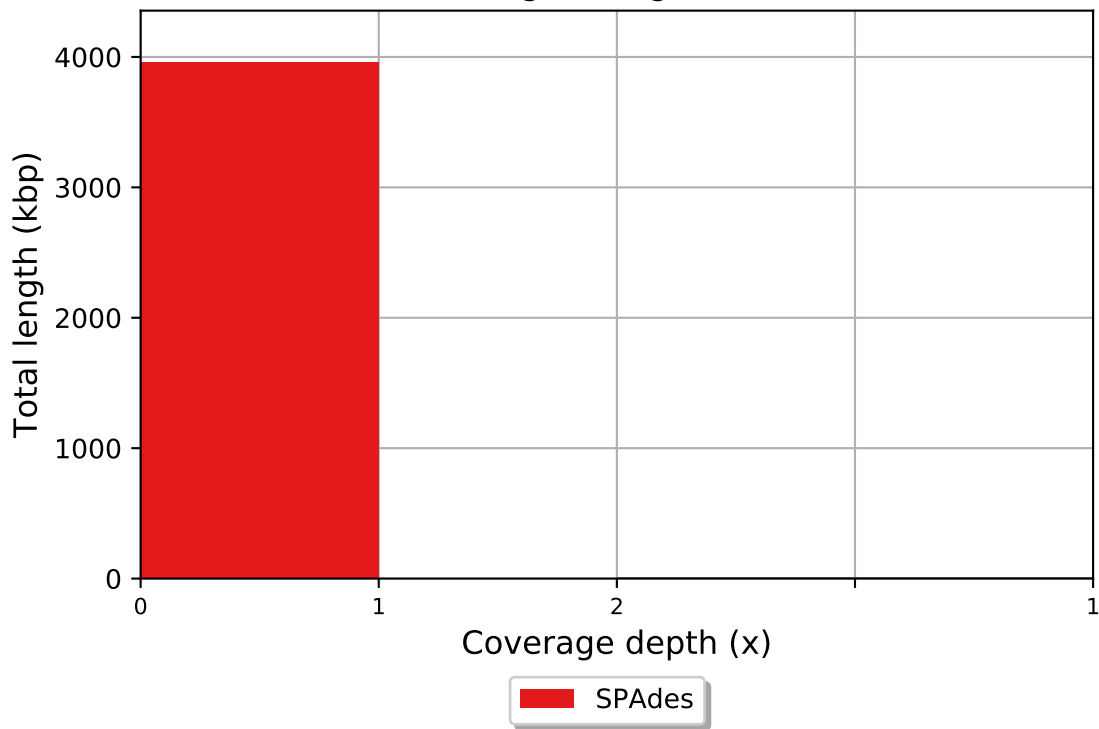
IDBAUD.m1000 GC content



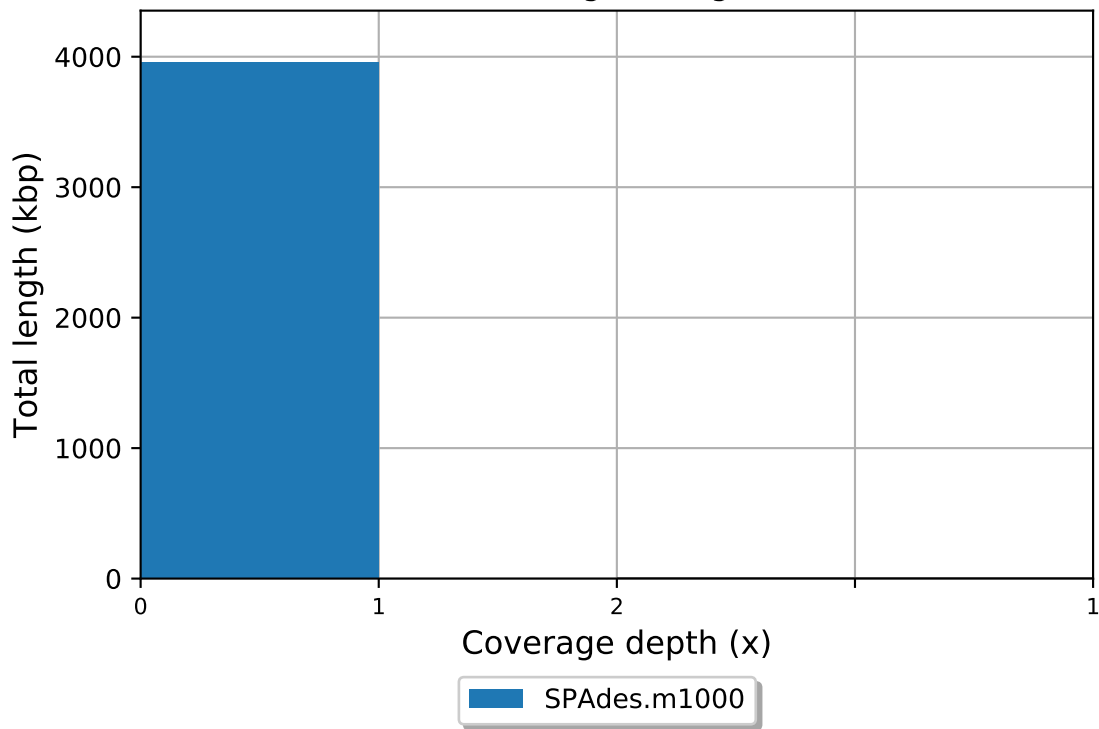
Coverage histogram (bin size: 1x)



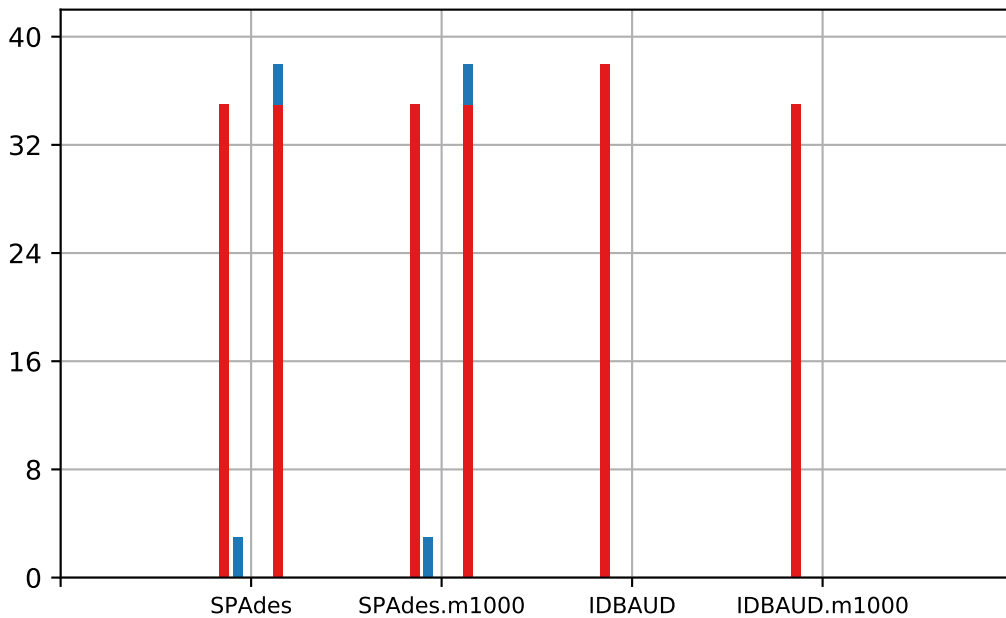
SPAdes coverage histogram (bin size: 1x)



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



Misassemblies

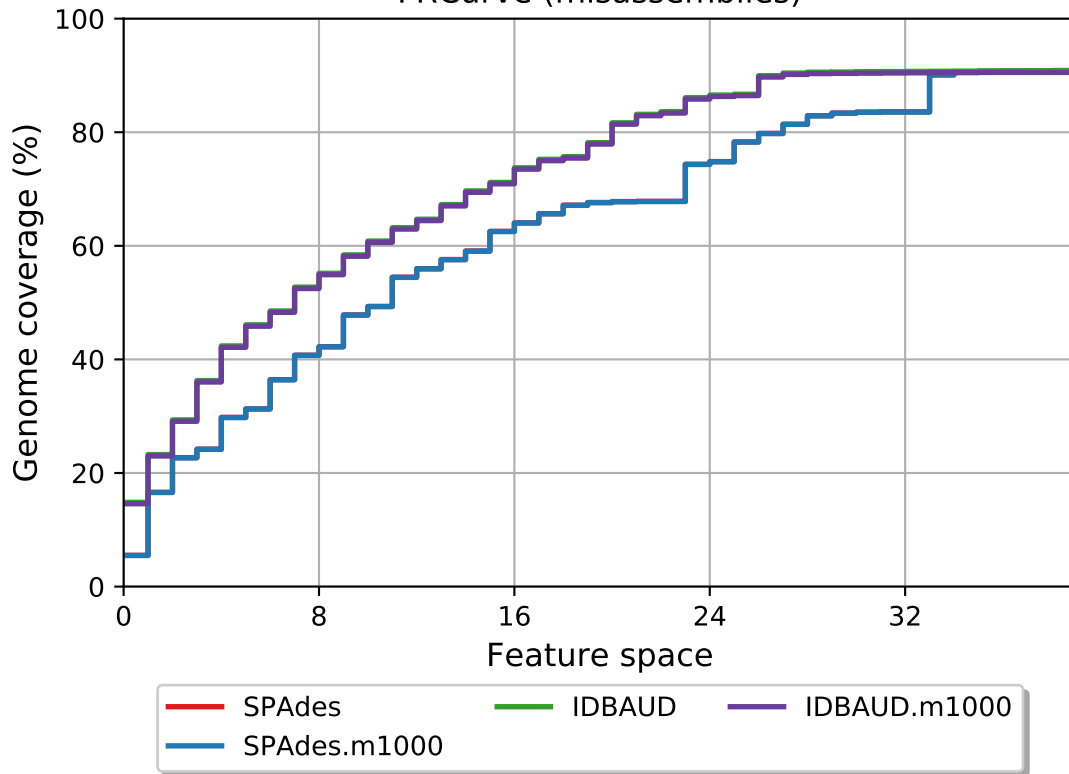


relocations

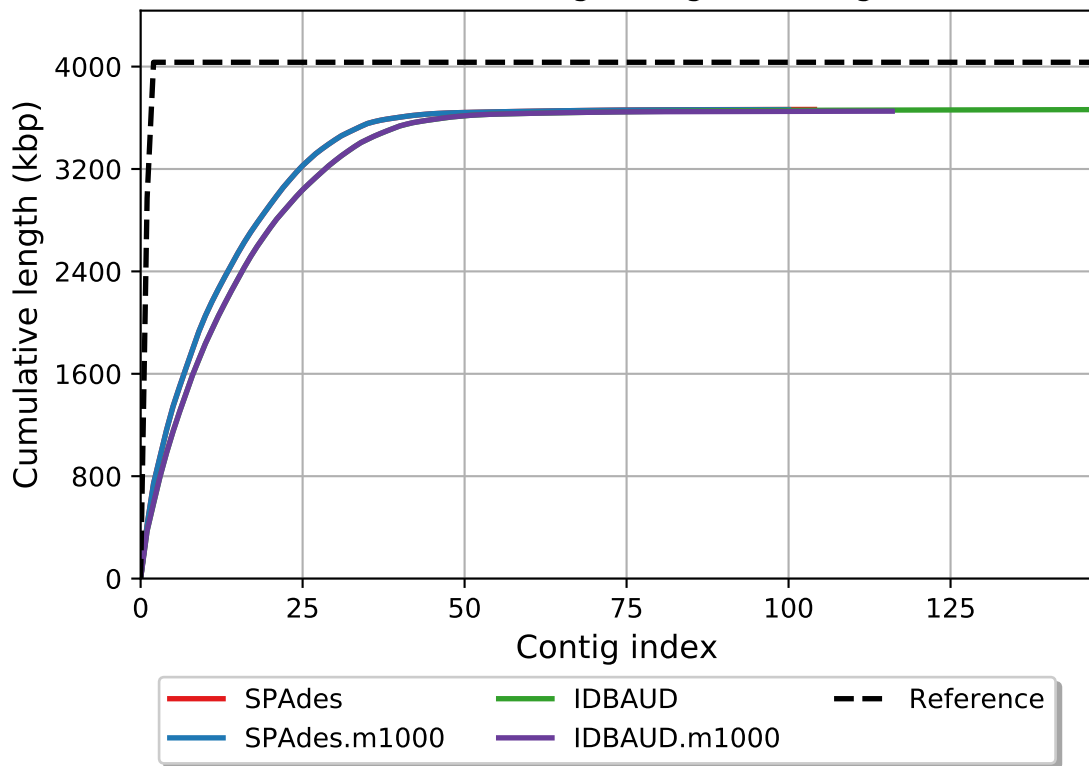


translocations

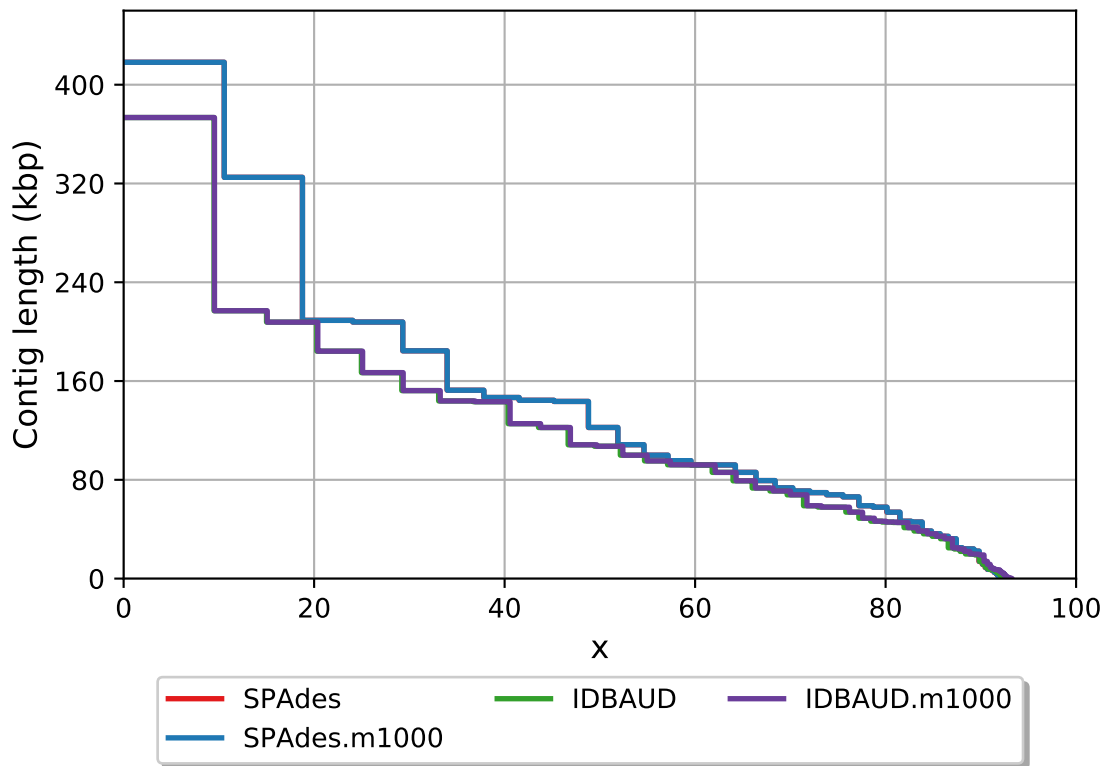
FRCurve (misassemblies)



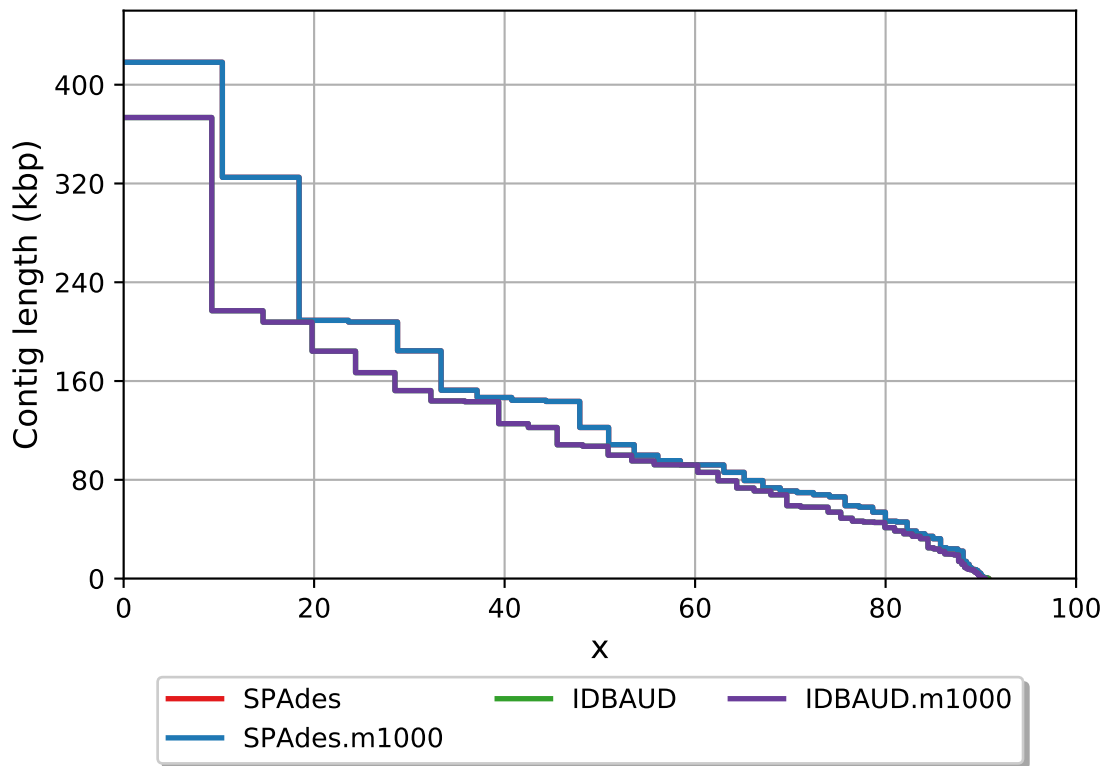
Cumulative length (aligned contigs)



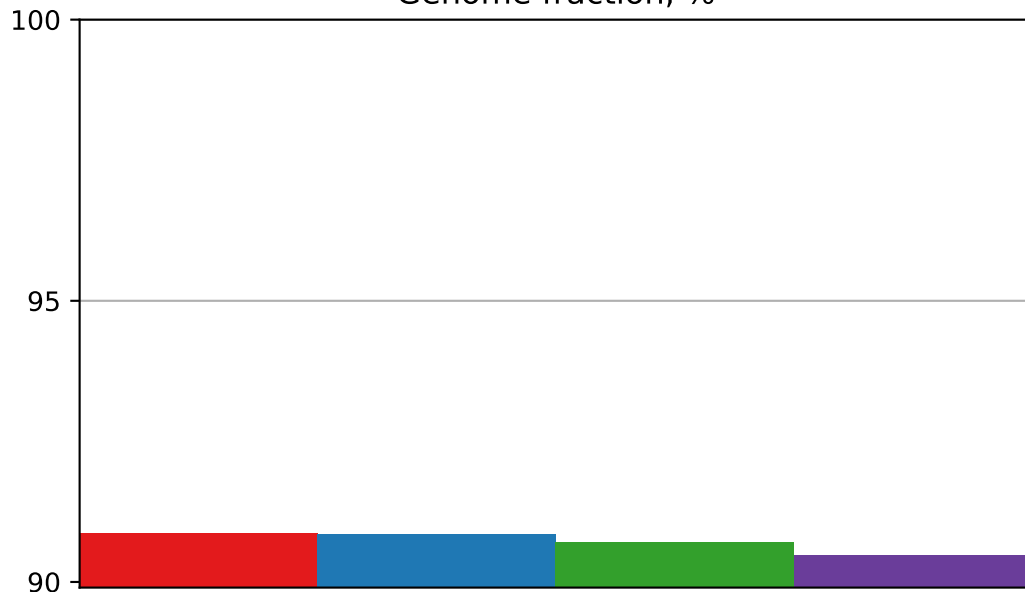
NAx



NGAx



Genome fraction, %



SPAdes
SPAdes.m1000

IDBAUD

IDBAUD.m1000