

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 0 bp)	1318	933	5057	1996
# contigs (>= 1000 bp)	933	933	1996	1996
# contigs (>= 5000 bp)	579	579	602	602
# contigs (>= 10000 bp)	396	396	397	397
# contigs (>= 25000 bp)	237	237	248	248
# contigs (>= 50000 bp)	151	151	162	162
Total length (>= 0 bp)	34469539	34299647	34437403	33155263
Total length (>= 1000 bp)	34299647	34299647	33155263	33155263
Total length (>= 5000 bp)	33383109	33383109	30082348	30082348
Total length (>= 10000 bp)	32059731	32059731	28613902	28613902
Total length (>= 25000 bp)	29559828	29559828	26330093	26330093
Total length (>= 50000 bp)	26330017	26330017	23178226	23178226
# contigs	1031	933	3088	1996
Largest contig	1221431	1221431	866948	866948
Total length	34369970	34299647	33933237	33155263
Reference length	30132142	30132142	30132142	30132142
N50	158395	158668	109642	112474
N75	57571	57604	31778	37507
L50	53	52	80	76
L75	141	140	217	200
# misassemblies	200	199	159	148
# misassembled contigs	93	92	98	87
Misassembled contigs length	14331191	14330216	8884790	8876787
# local misassemblies	356	354	716	714
# scaffold gap ext. mis.	11	11	1	1
# scaffold gap loc. mis.	134	134	29	29
# unaligned mis. contigs	23	21	37	30
# unaligned contigs	644 + 109 part	561 + 109 part	2133 + 164 part	1229 + 155 part
Unaligned length	7883859	7824485	7640352	6989689
Genome fraction (%)	87.806	87.788	87.940	87.391
Duplication ratio	1.015	1.015	1.006	1.005
# N's per 100 kbp	186.17	186.43	23.09	23.63
# mismatches per 100 kbp	1417.85	1417.83	1275.51	1280.22
# indels per 100 kbp	55.02	55.00	43.84	43.77
Largest alignment	868954	868954	866915	866915
Total aligned length	26391906	26382211	26254019	26131800
NA50	73706	73706	58055	60839
NA75	9781	10141	4961	7769
LA50	114	114	136	129
LA75	380	375	582	490

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

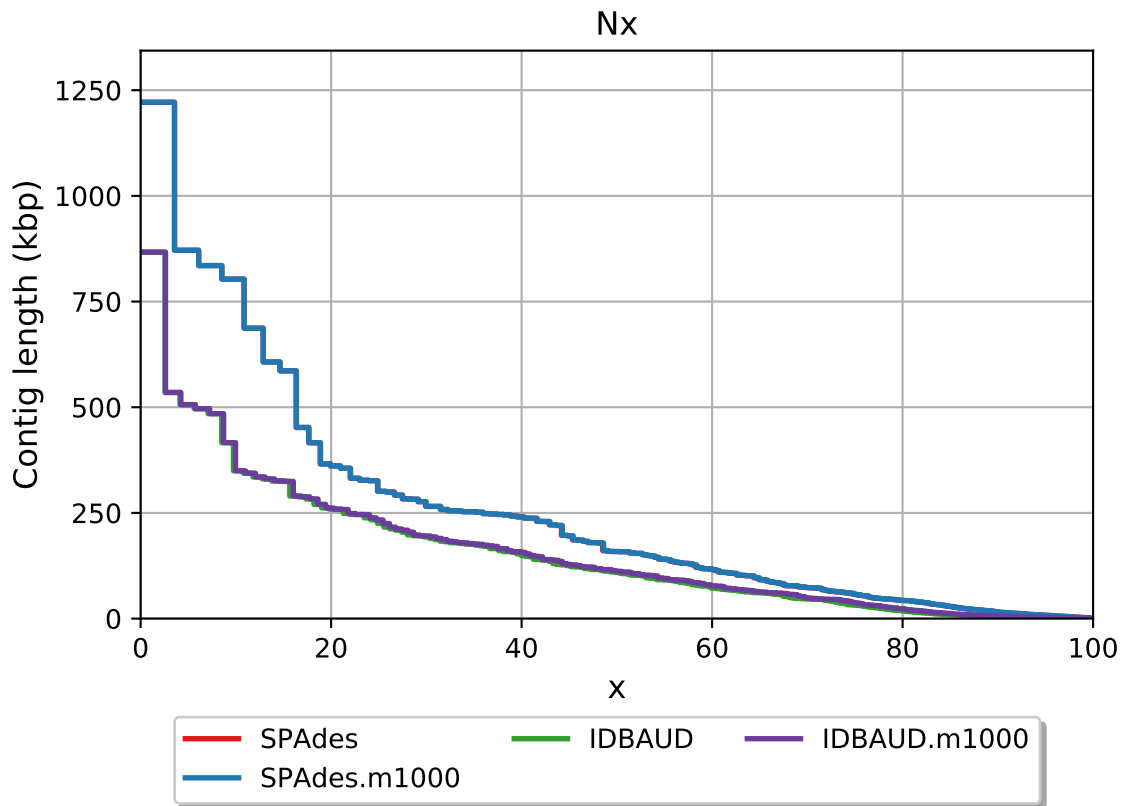
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	200	199	159	148
# contig misassemblies	189	188	159	148
# c. relocations	183	182	153	145
# c. translocations	4	4	0	0
# c. inversions	2	2	6	3
# c. interspecies translocations	0	0	0	0
# scaffold misassemblies	11	11	0	0
# s. relocations	10	10	0	0
# s. translocations	1	1	0	0
# s. inversions	0	0	0	0
# s. interspecies translocations	0	0	0	0
# misassembled contigs	93	92	98	87
Misassembled contigs length	14331191	14330216	8884790	8876787
# possibly misassembled contigs	89	89	131	126
# possible misassemblies	530	530	530	525
# local misassemblies	356	354	716	714
# scaffold gap ext. mis.	11	11	1	1
# scaffold gap loc. mis.	134	134	29	29
# unaligned mis. contigs	23	21	37	30
# mismatches	375133	375048	337990	337118
# indels	14557	14550	11616	11525
# indels (<= 5 bp)	13031	13025	10694	10603
# indels (> 5 bp)	1526	1525	922	922
Indels length	49975	49943	35323	35225

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).

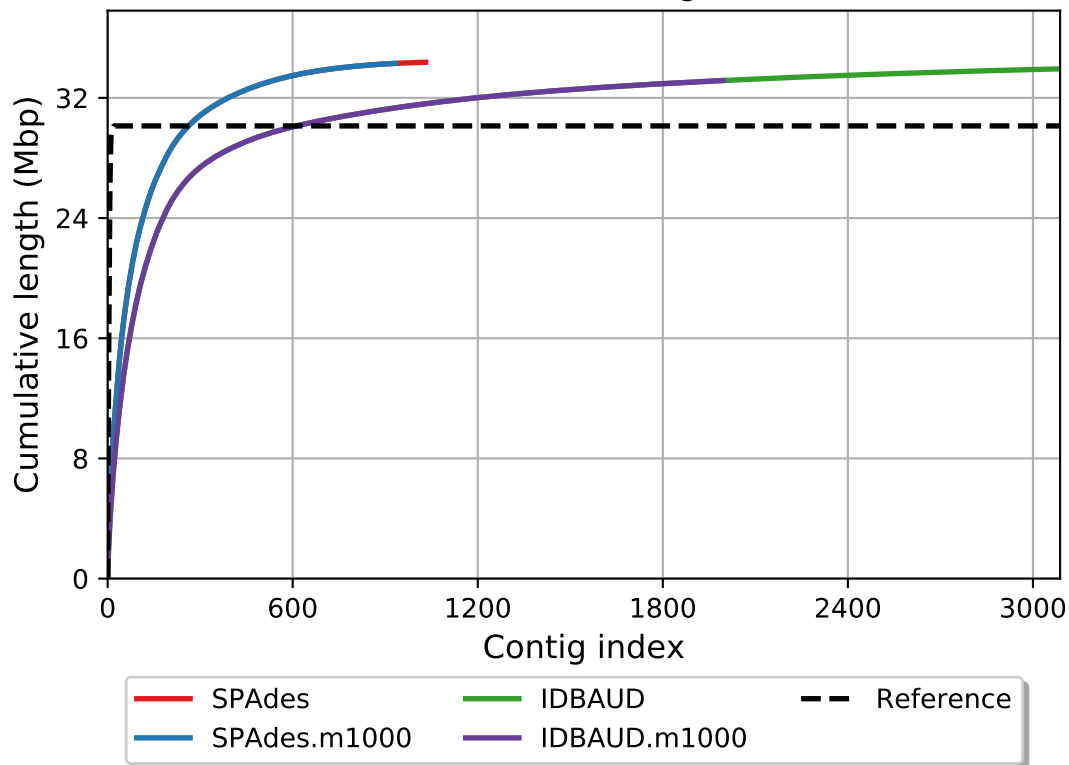
Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	644	561	2133	1229
Fully unaligned length	4666599	4607225	5208700	4563854
# partially unaligned contigs	109	109	164	155
Partially unaligned length	3217260	3217260	2431652	2425835
# N's	63985	63945	7835	7835

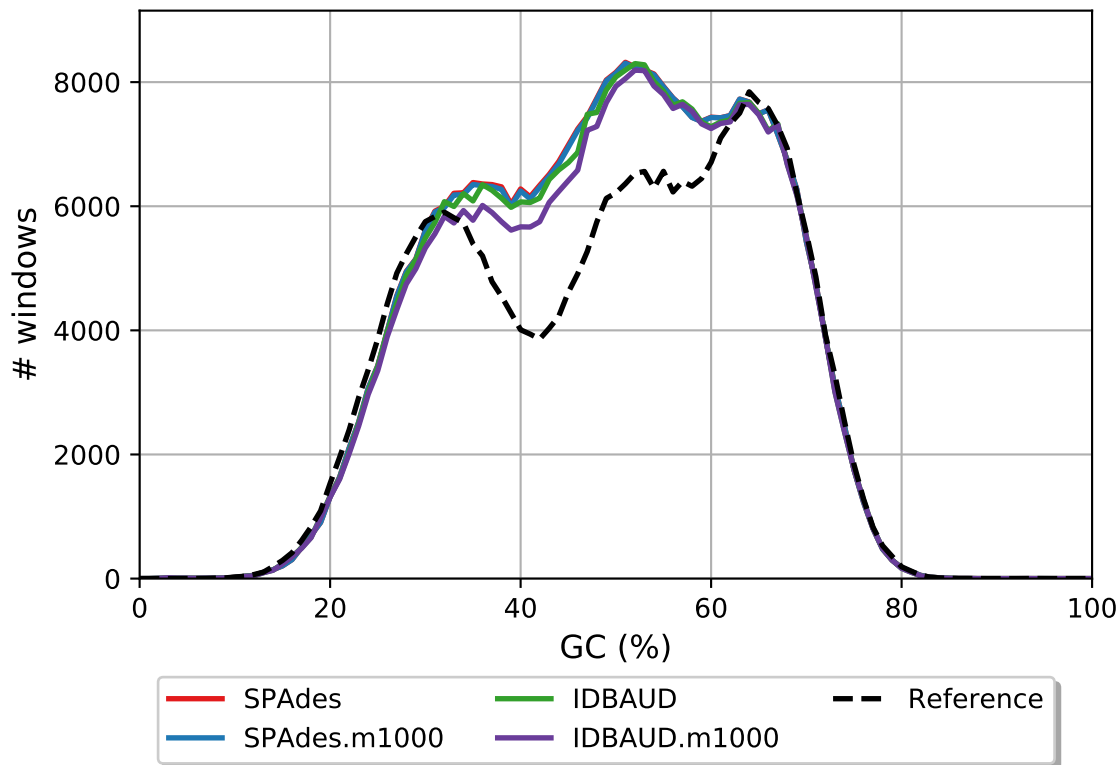
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



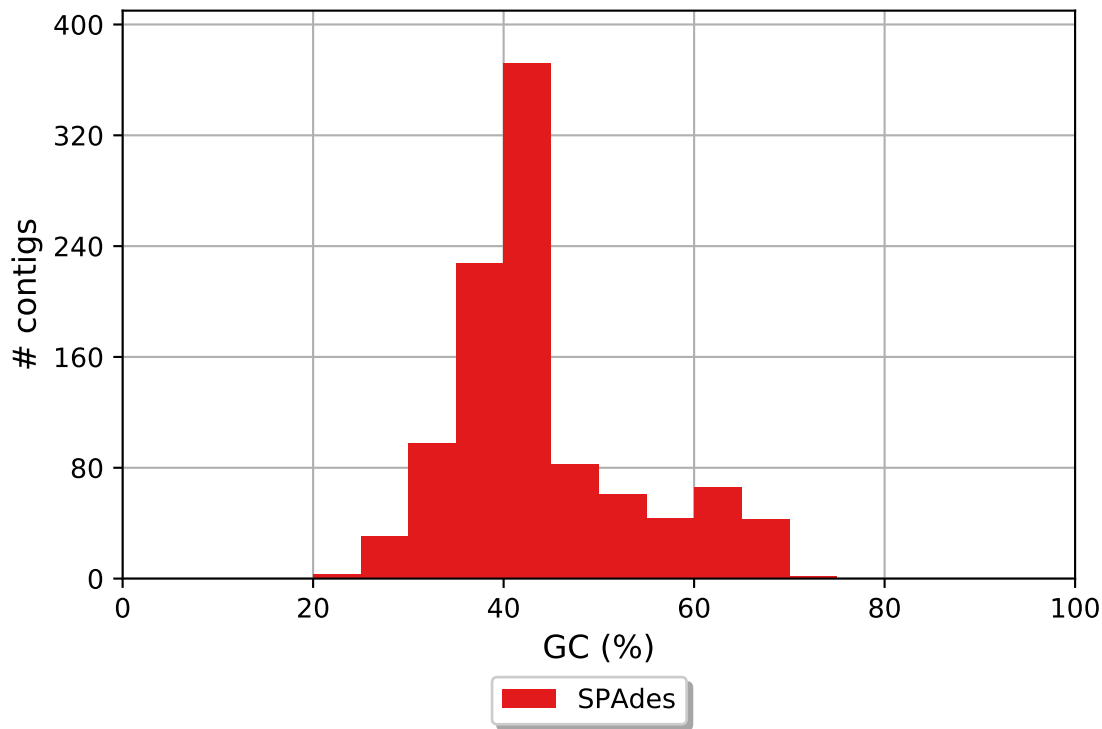
Cumulative length



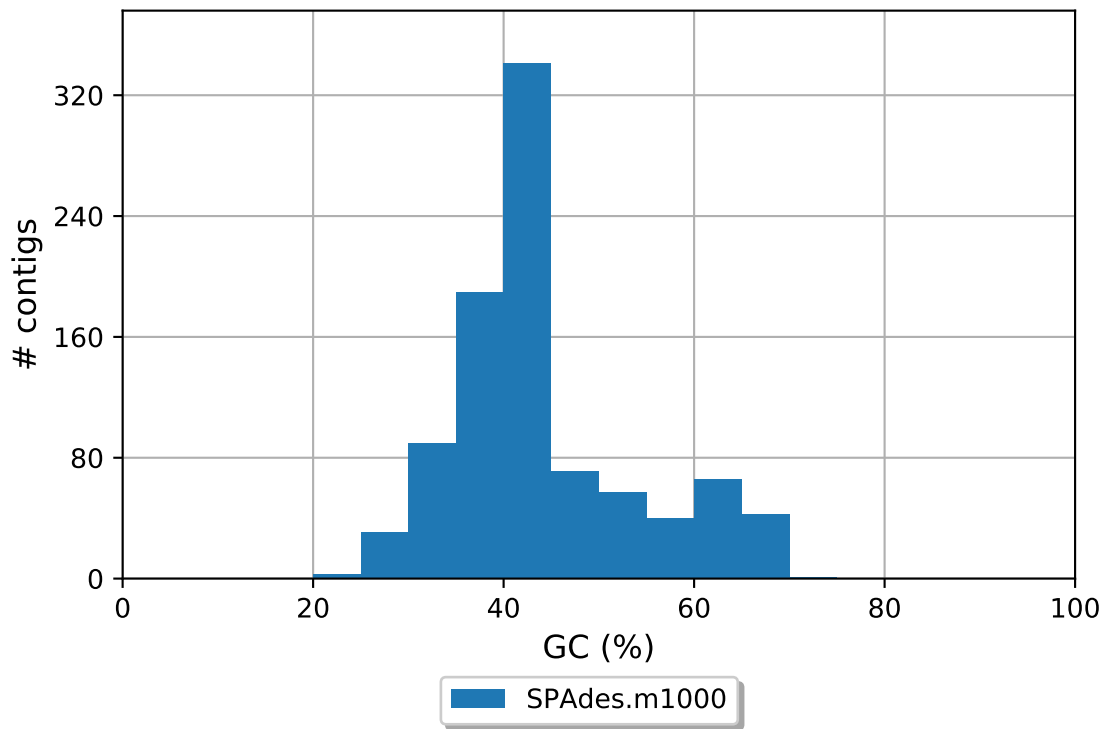
GC content



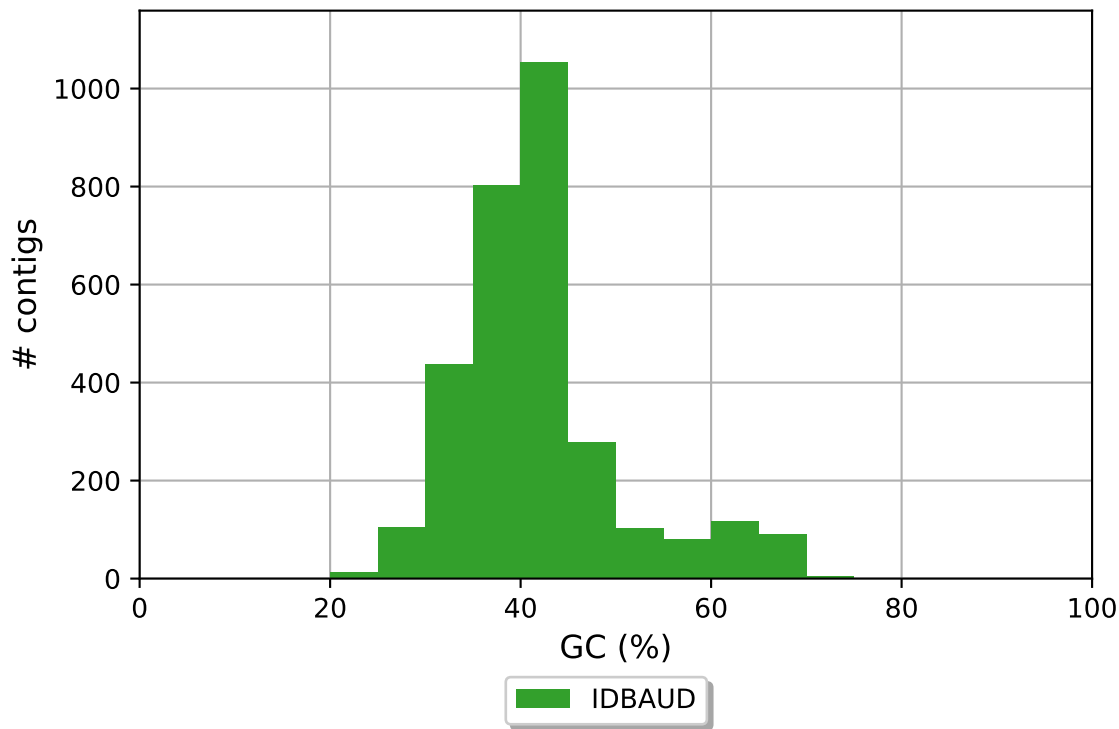
SPAdes GC content



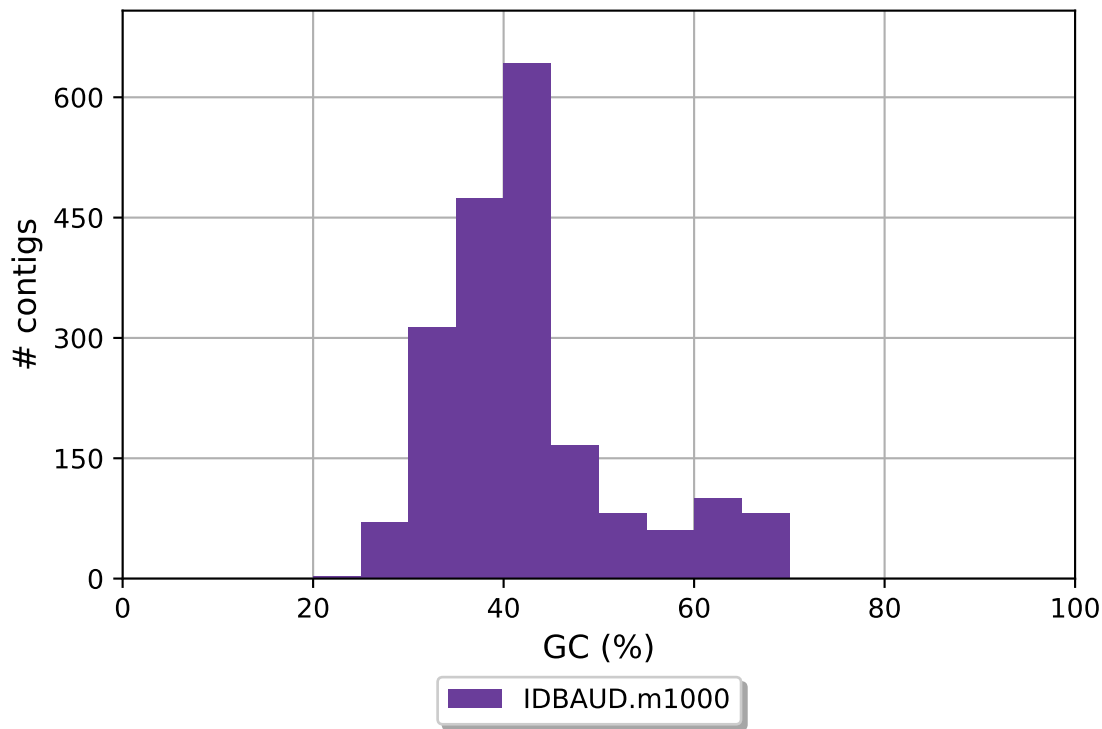
SPAdes.m1000 GC content



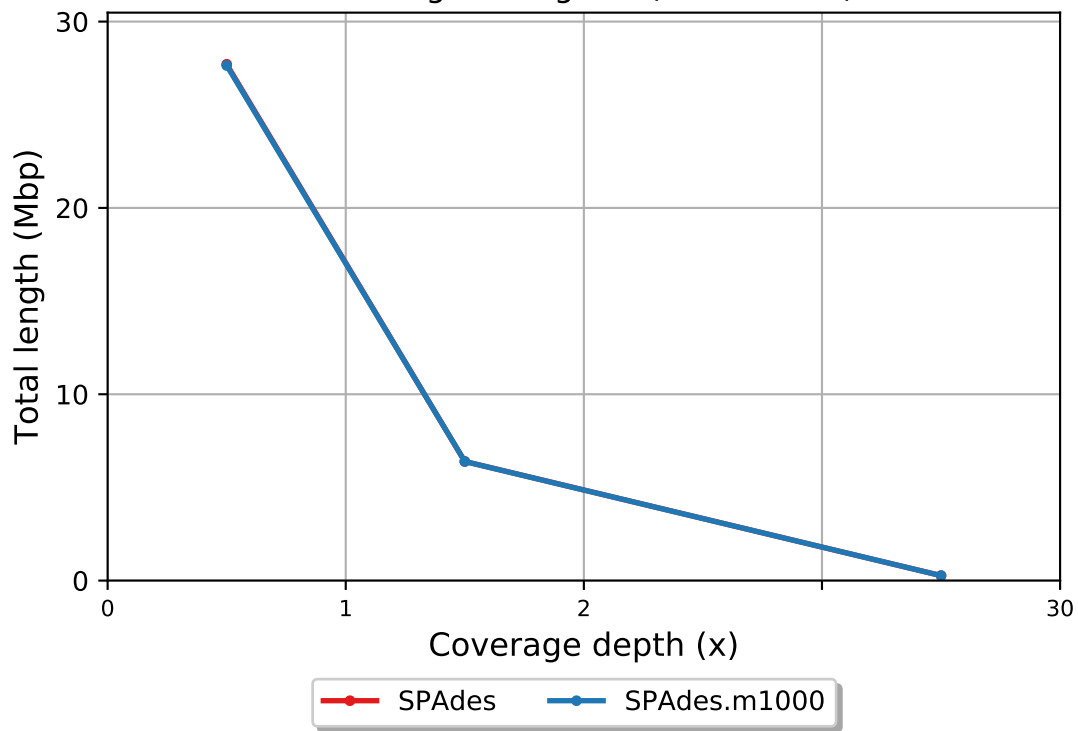
IDBAUD GC content



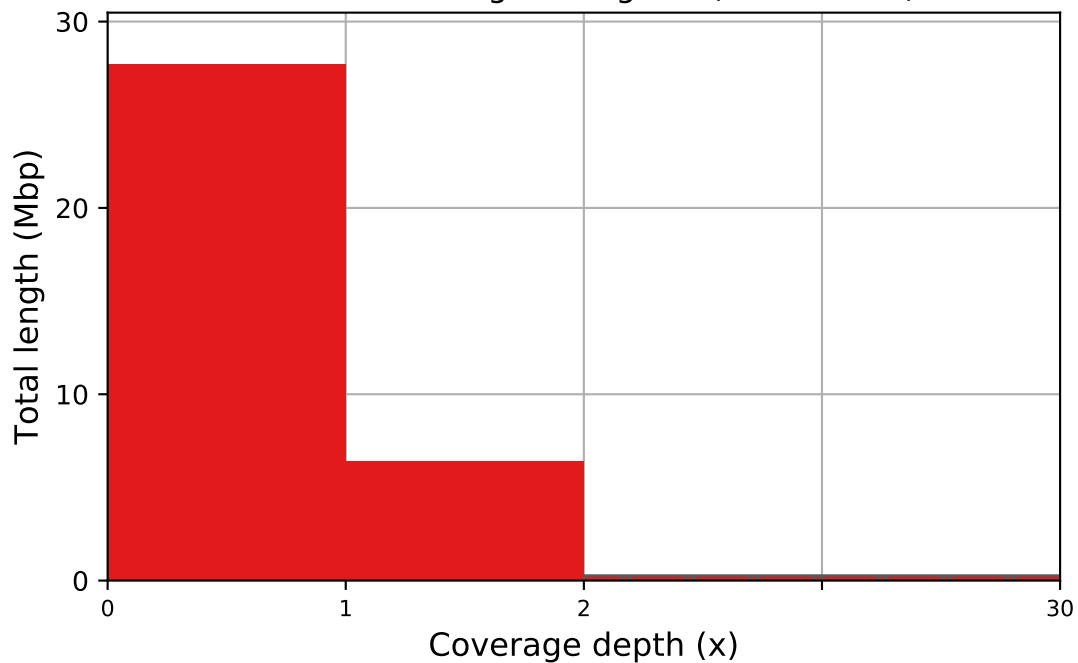
IDBAUD.m1000 GC content



Coverage histogram (bin size: 1x)

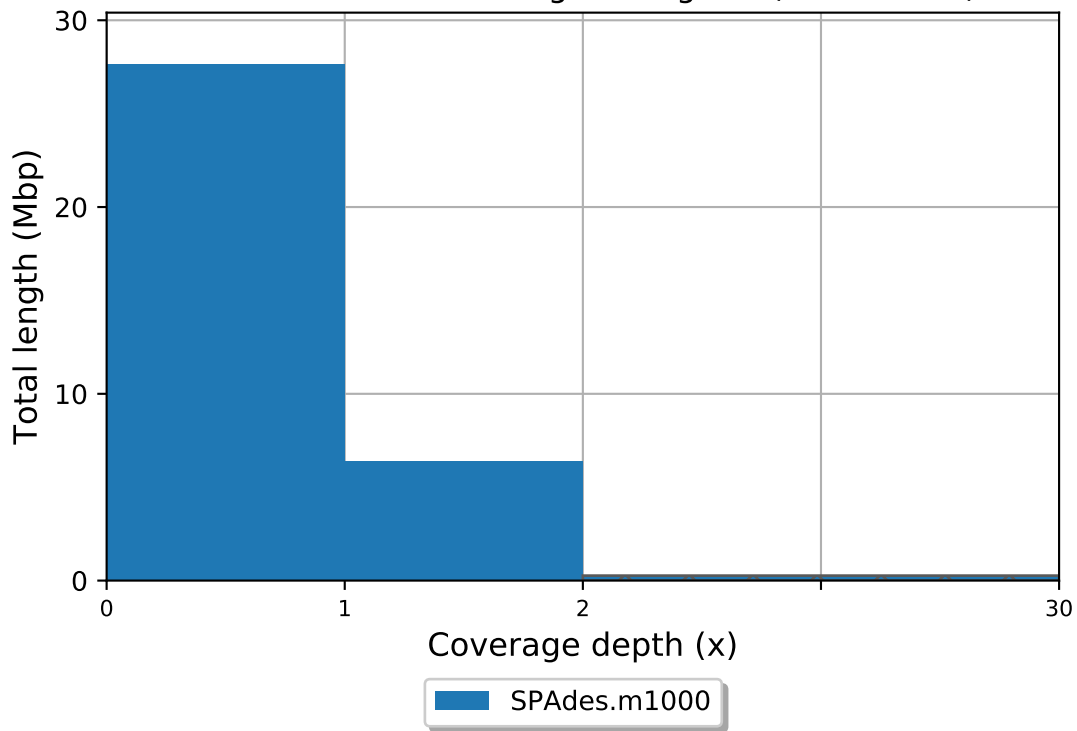


SPAdes coverage histogram (bin size: 1x)

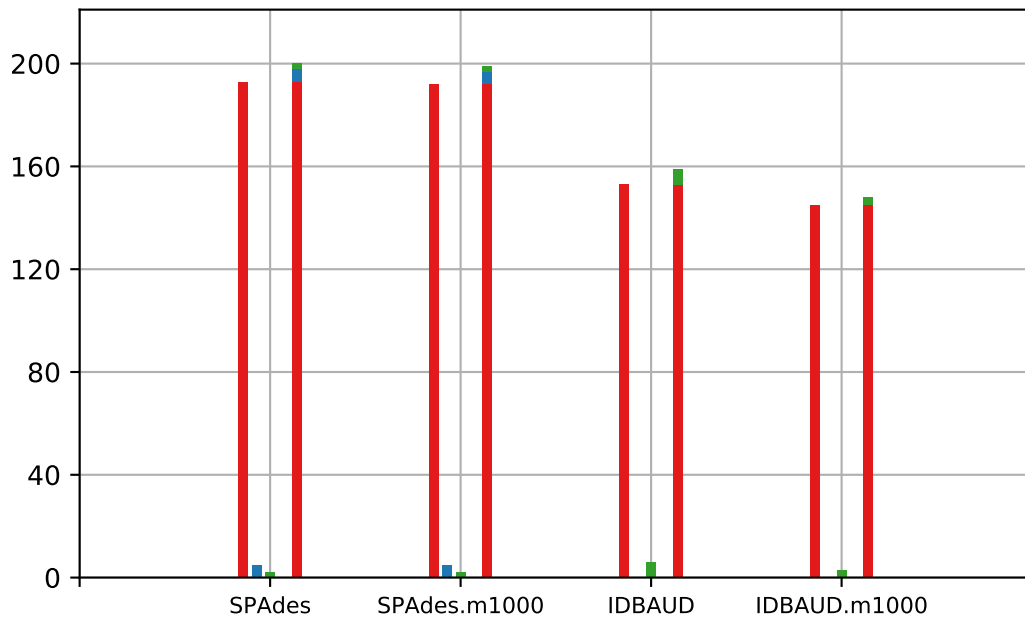


SPAdes

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

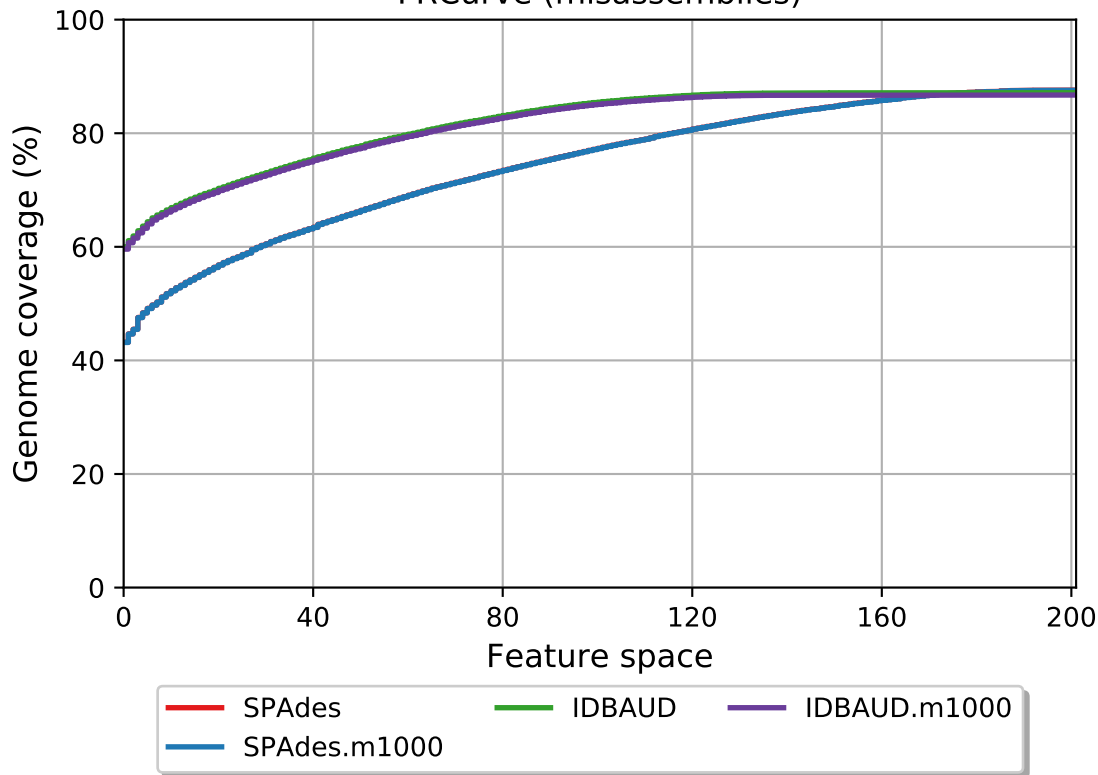


Misassemblies

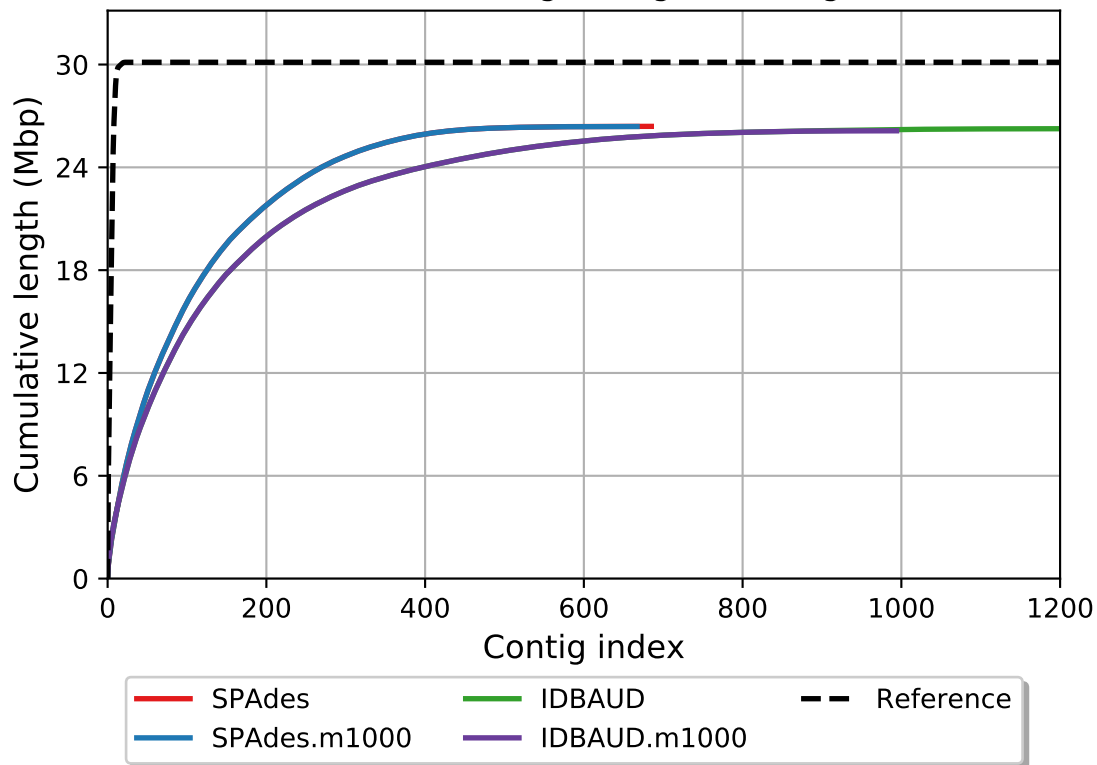


■ # relocations ■ # translocations ■ # inversions

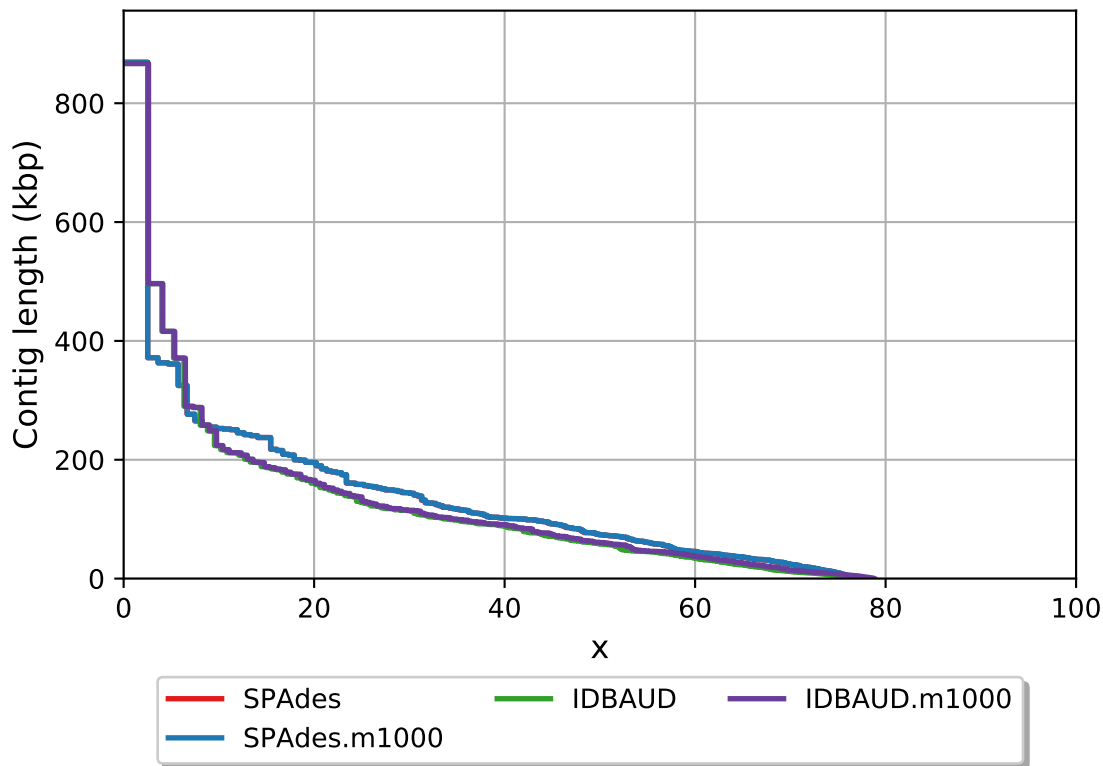
FRCurve (misassemblies)



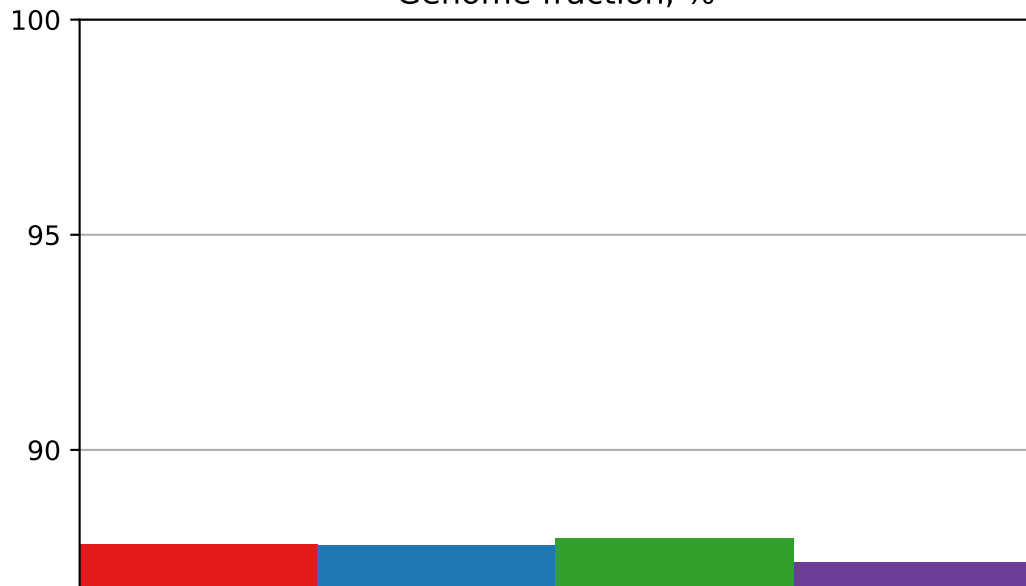
Cumulative length (aligned contigs)



NAX



Genome fraction, %



SPAdes

IDBAUD

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