

## Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	55	55	112	112
# contigs (>= 5000 bp)	52	52	89	89
# contigs (>= 10000 bp)	50	50	81	81
# contigs (>= 25000 bp)	43	43	65	65
# contigs (>= 50000 bp)	35	35	47	47
Total length (>= 1000 bp)	6480405	6480405	6288981	6288981
Total length (>= 5000 bp)	6471498	6471498	6239999	6239999
Total length (>= 10000 bp)	6460616	6460616	6184058	6184058
Total length (>= 25000 bp)	6331186	6331186	5910809	5910809
Total length (>= 50000 bp)	6045228	6045228	5265791	5265791
# contigs	58	55	134	112
Largest contig	415966	415966	330349	330349
Total length	6482632	6480405	6304282	6288981
Reference length	6275467	6275467	6275467	6275467
GC (%)	65.47	65.48	65.69	65.69
Reference GC (%)	66.54	66.54	66.54	66.54
N50	221817	221817	109642	109642
NG50	221817	221817	109642	109642
N75	117316	117316	63091	63091
NG75	130463	130463	63091	63091
L50	11	11	19	19
LG50	11	11	19	19
L75	22	22	38	38
LG75	20	20	38	38
# misassemblies	58	58	53	51
# misassembled contigs	22	22	30	28
Misassembled contigs length	3991669	3991669	2742430	2741198
# local misassemblies	62	61	203	201
# scaffold gap ext. mis.	2	2	0	0
# scaffold gap loc. mis.	60	60	9	9
# unaligned mis. contigs	2	1	1	0
# unaligned contigs	0 + 31 part	0 + 31 part	0 + 39 part	0 + 39 part
Unaligned length	628675	628675	478268	478268
Genome fraction (%)	93.099	93.082	92.528	92.325
Duplication ratio	1.002	1.002	1.003	1.003
# N's per 100 kbp	70.62	70.64	12.88	12.91
# mismatches per 100 kbp	507.48	507.30	503.09	502.24
# indels per 100 kbp	43.10	43.04	39.30	38.90
Largest alignment	363140	363140	199909	199909
Total aligned length	5845118	5843376	5810094	5796025
NA50	102354	102354	78801	78801
NGA50	106283	106283	78801	78801
NA75	38136	38136	31339	31339
NGA75	41381	41381	31413	31413
LA50	20	20	27	27
LGA50	19	19	27	27
LA75	45	45	57	57
LGA75	41	41	56	56

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

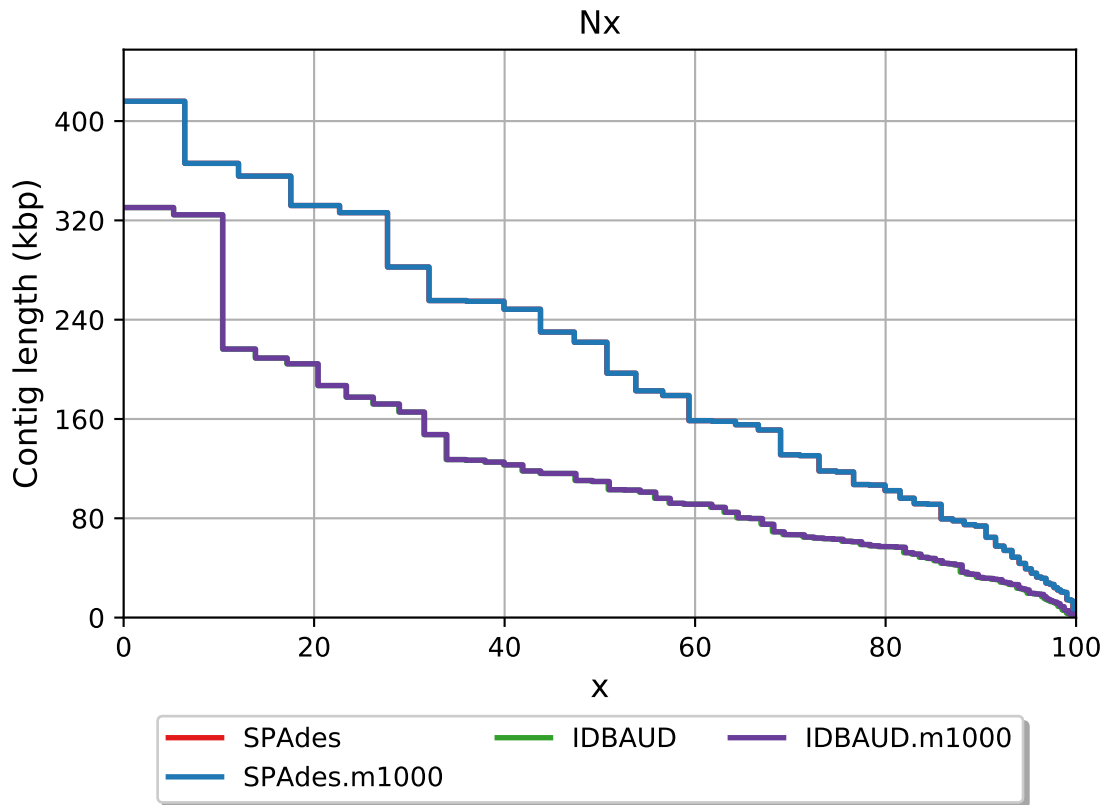
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	58	58	53	51
# contig misassemblies	57	57	53	51
# c. relocations	57	57	51	51
# c. translocations	0	0	0	0
# c. inversions	0	0	2	0
# scaffold misassemblies	1	1	0	0
# s. relocations	1	1	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	22	22	30	28
Misassembled contigs length	3991669	3991669	2742430	2741198
# possibly misassembled contigs	29	29	39	39
# possible misassemblies	105	105	106	106
# local misassemblies	62	61	203	201
# scaffold gap ext. mis.	2	2	0	0
# scaffold gap loc. mis.	60	60	9	9
# unaligned mis. contigs	2	1	1	0
# mismatches	29649	29633	29212	29099
# indels	2518	2514	2282	2254
# indels (<= 5 bp)	2342	2338	2169	2141
# indels (> 5 bp)	176	176	113	113
Indels length	6154	6148	5189	5157

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).

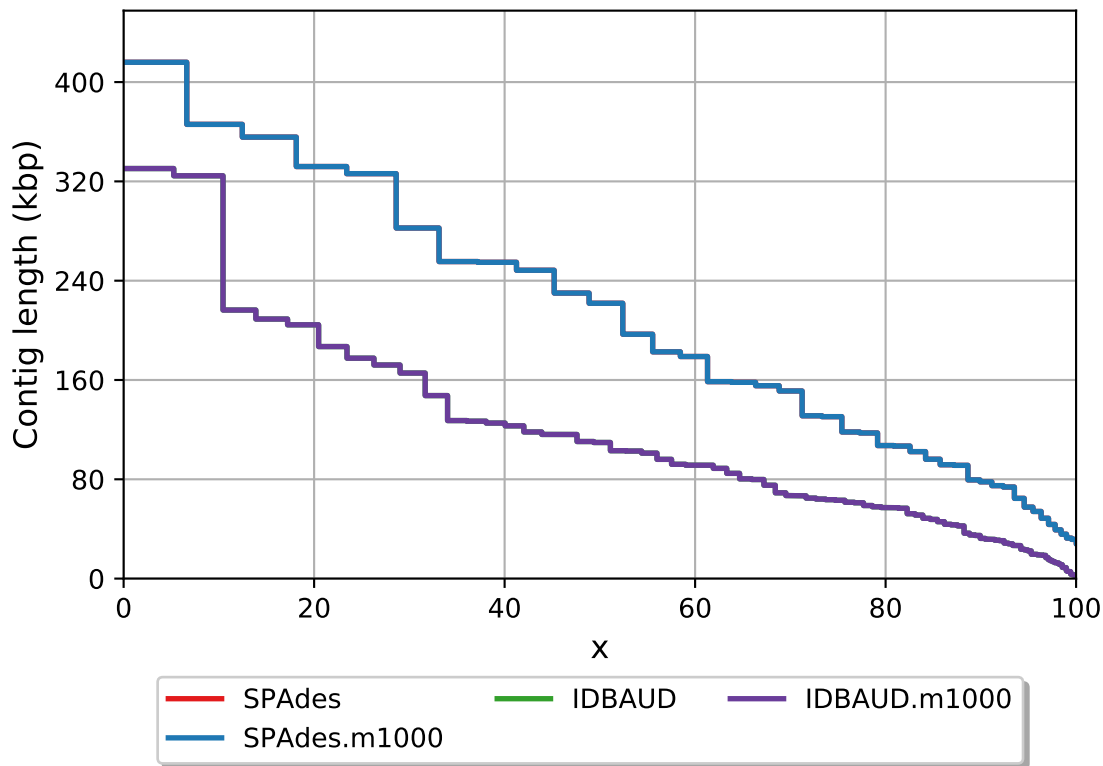
## Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	31	31	39	39
Partially unaligned length	628675	628675	478268	478268
# N's	4578	4578	812	812

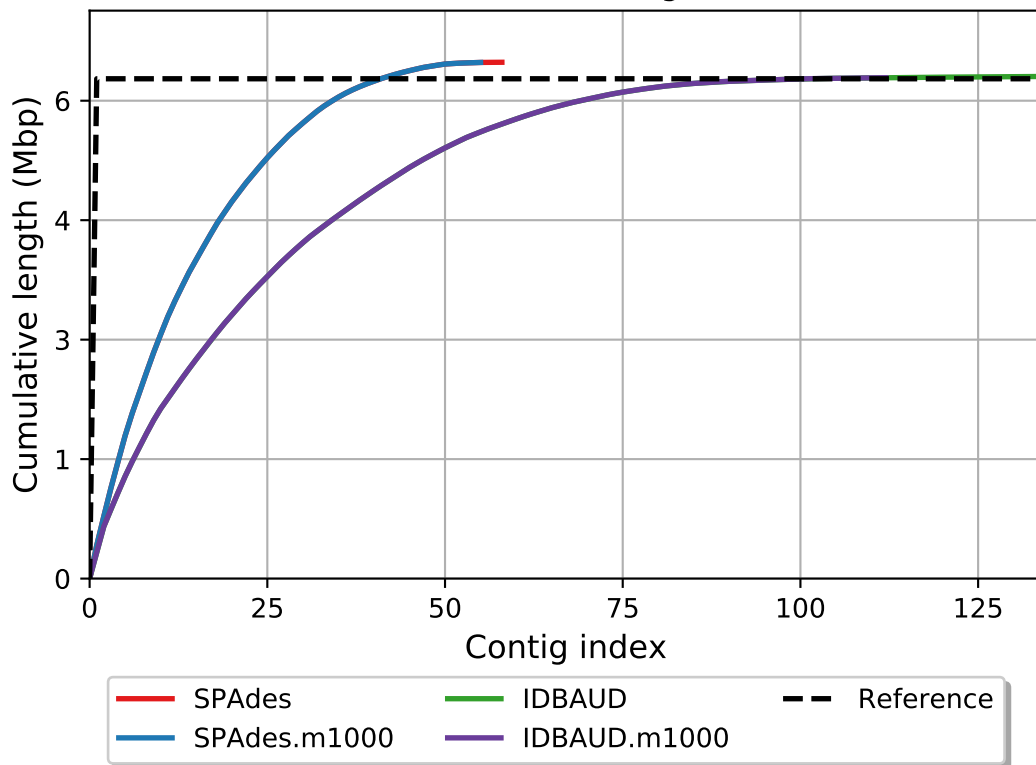
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



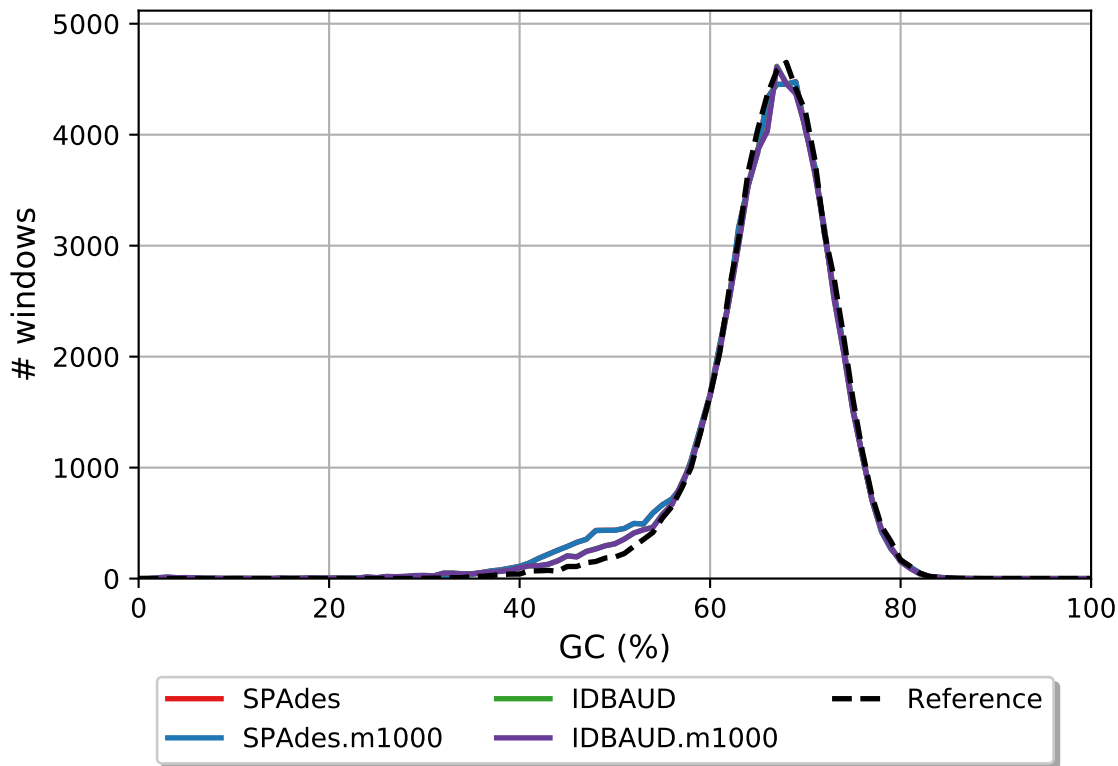
# NGx



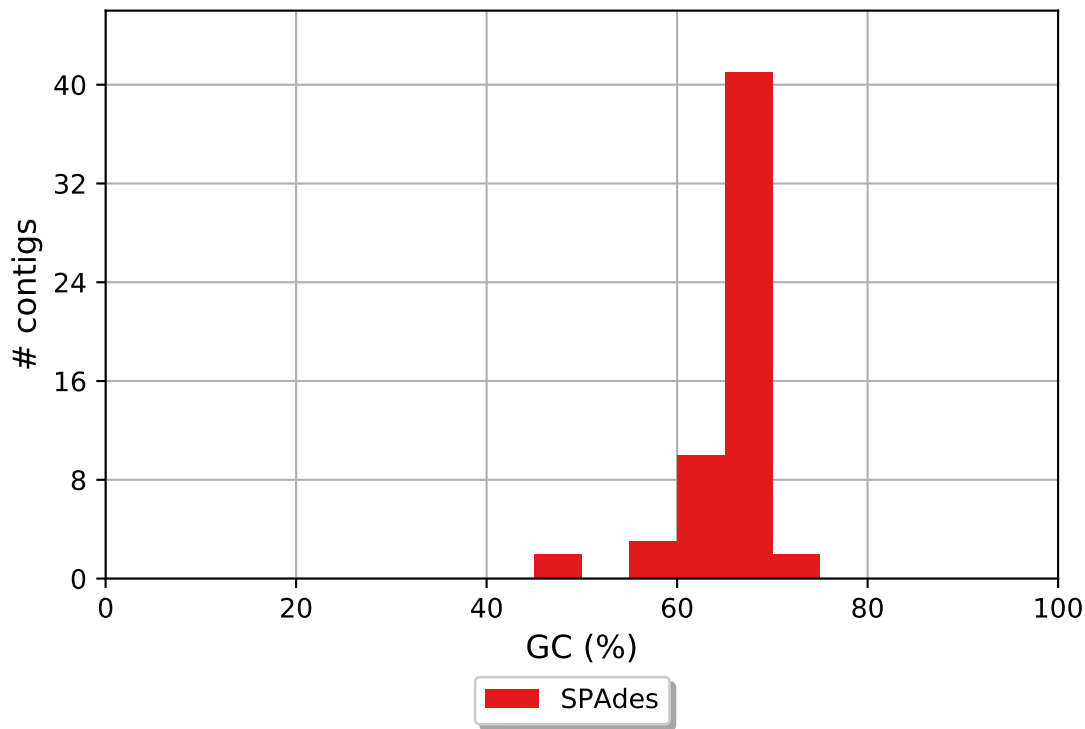
Cumulative length



GC content

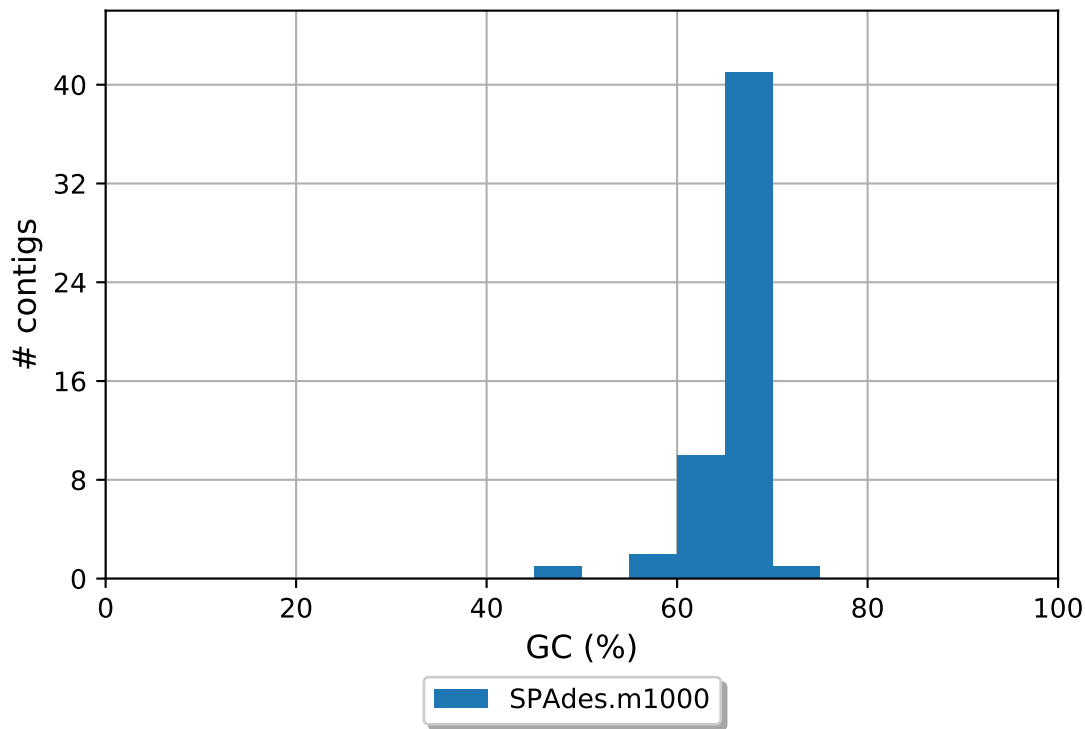


## SPAdes GC content

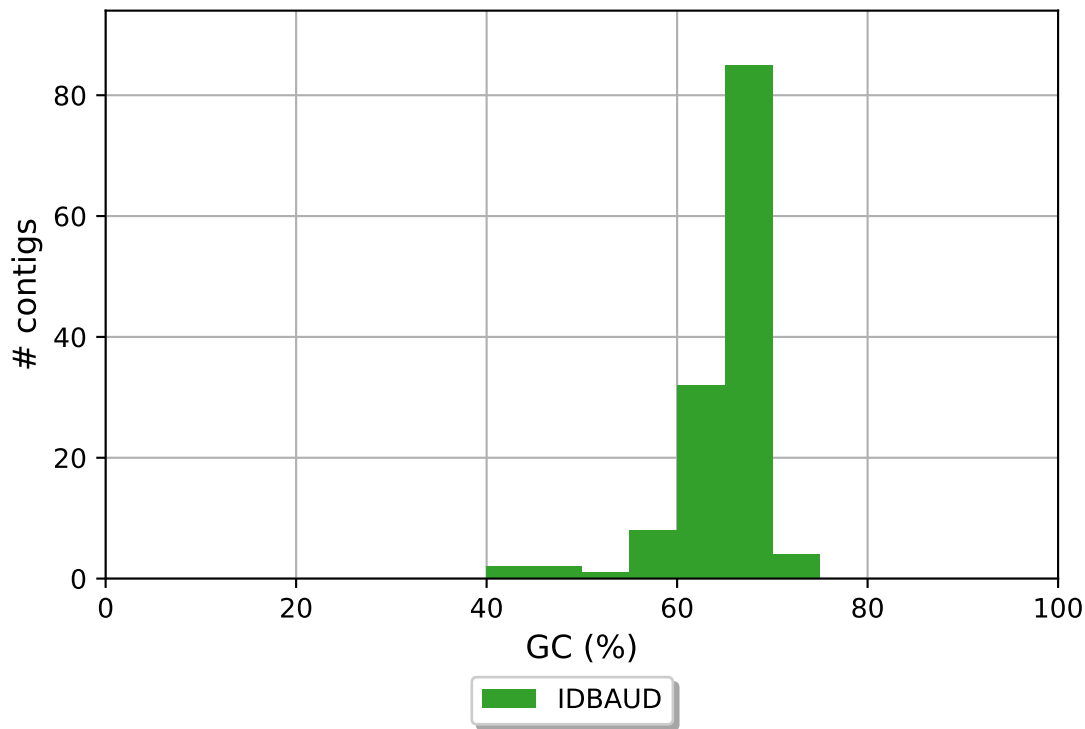




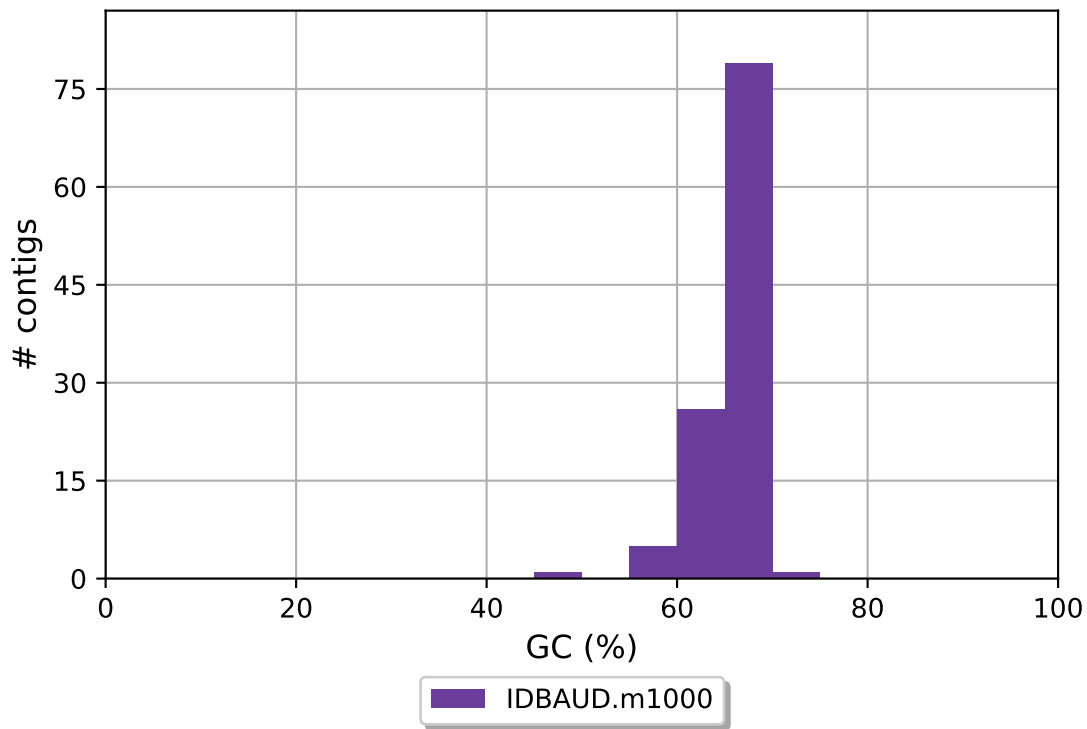
SPAdes.m1000 GC content



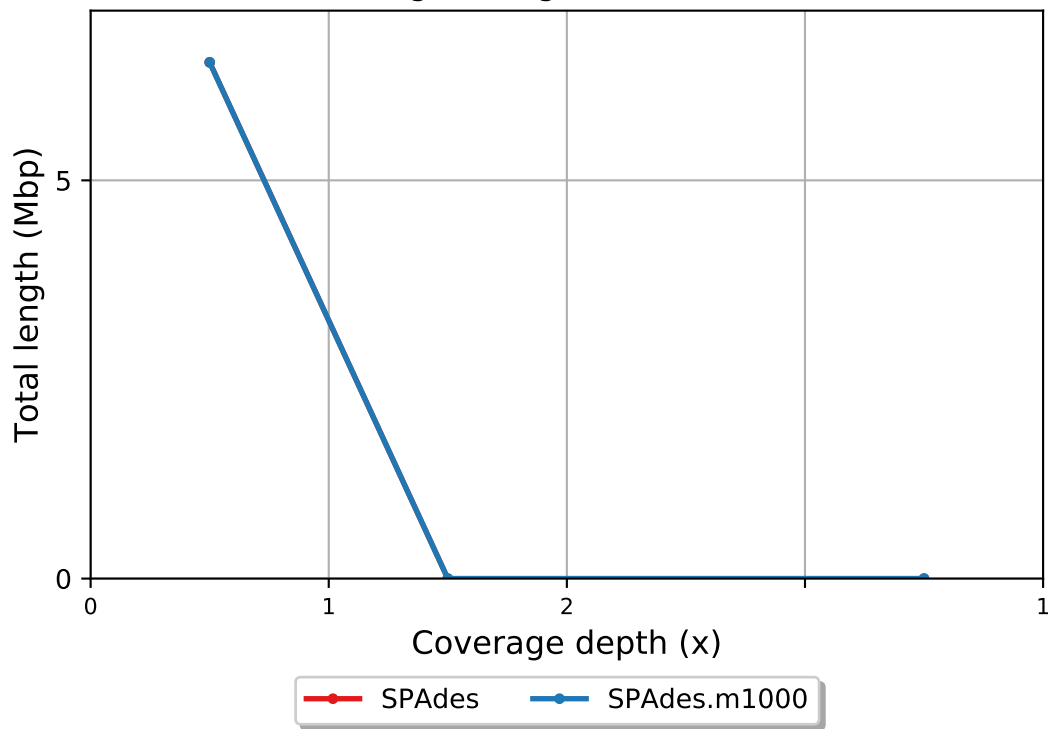
IDBAUD GC content



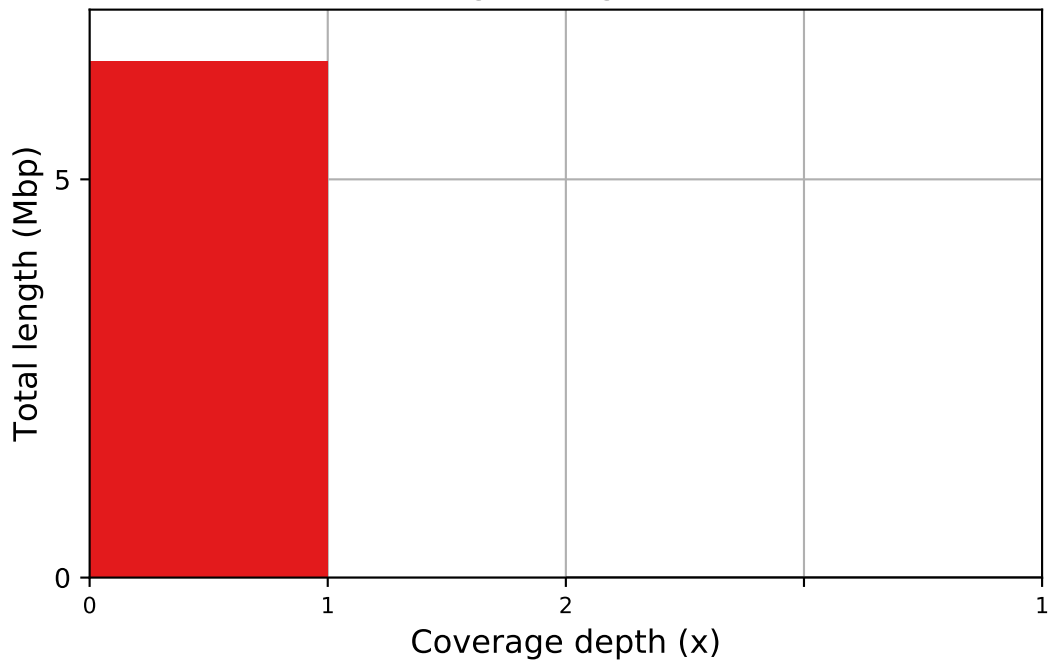
IDBAUD.m1000 GC content



Coverage histogram (bin size: 1x)

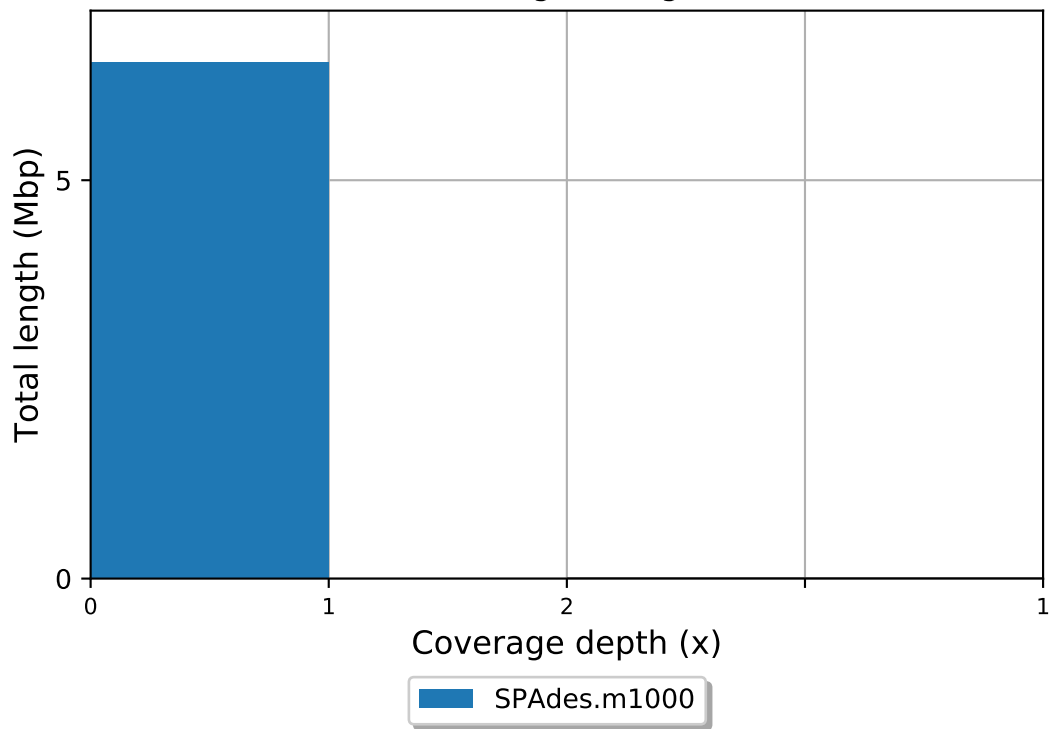


SPAdes coverage histogram (bin size: 1x)

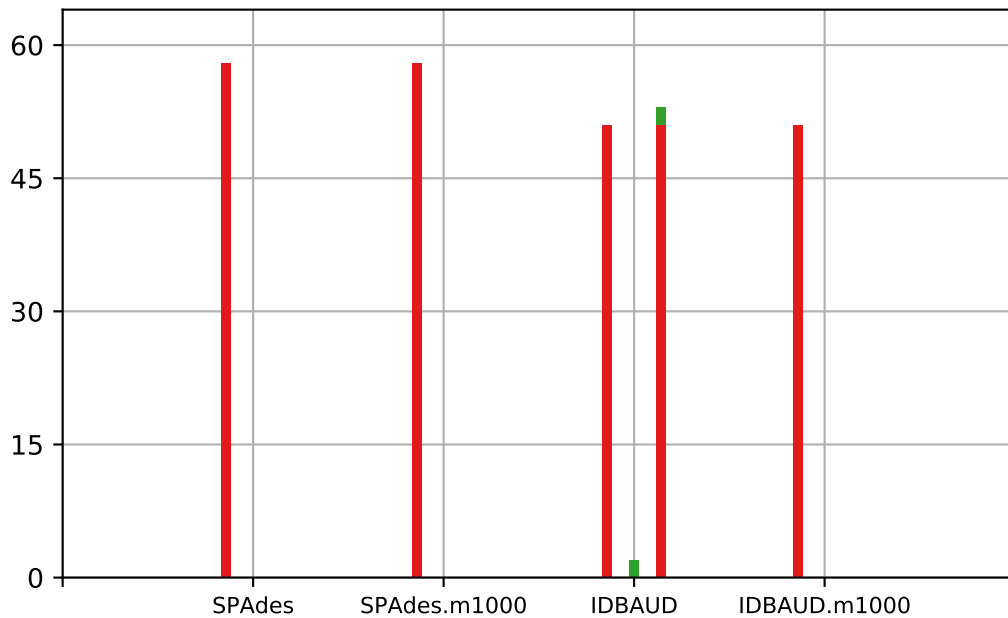


SPAdes

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



## Misassemblies

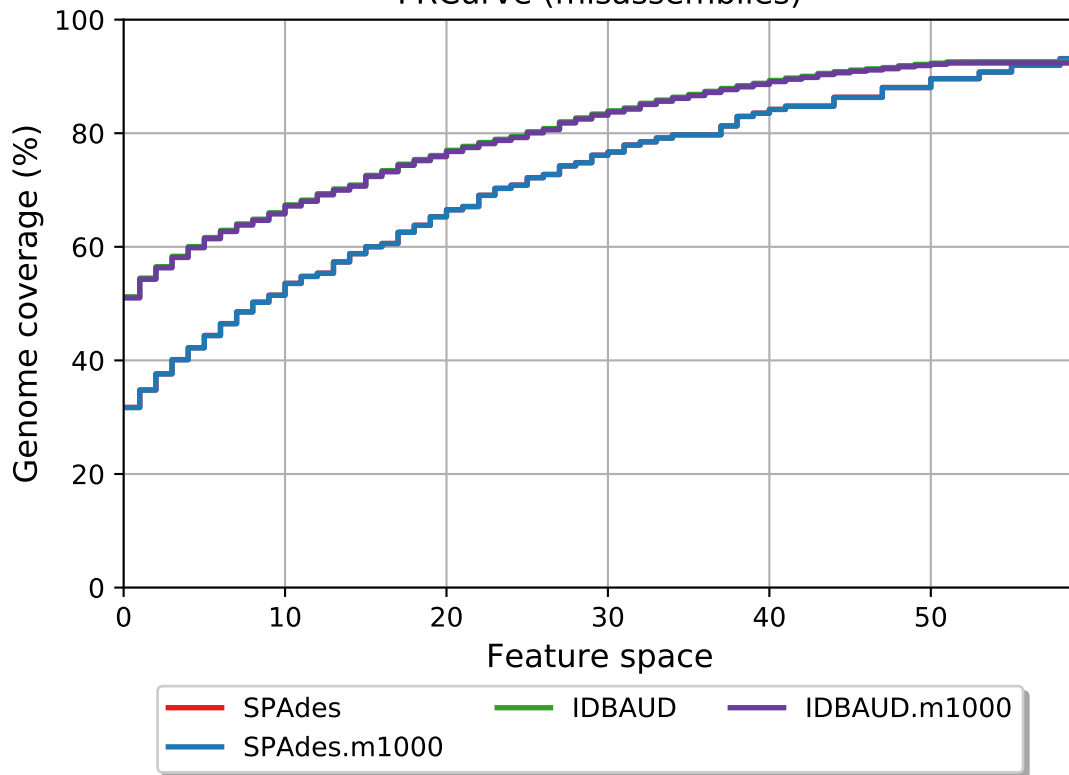


# relocations



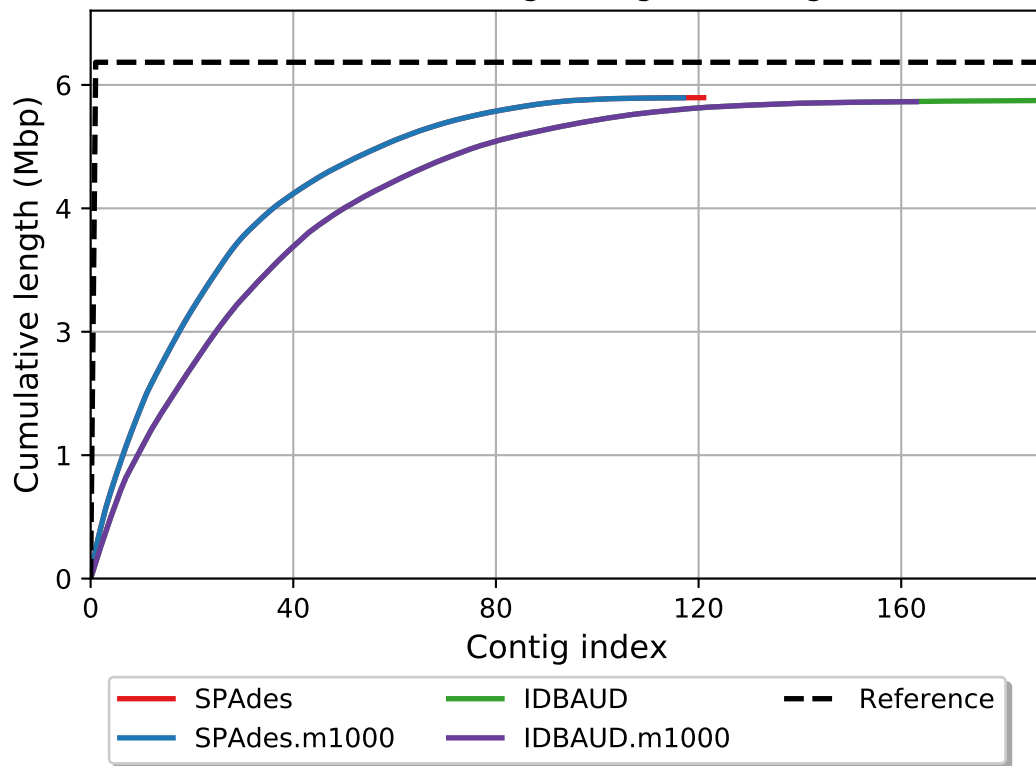
# inversions

FRCurve (misassemblies)

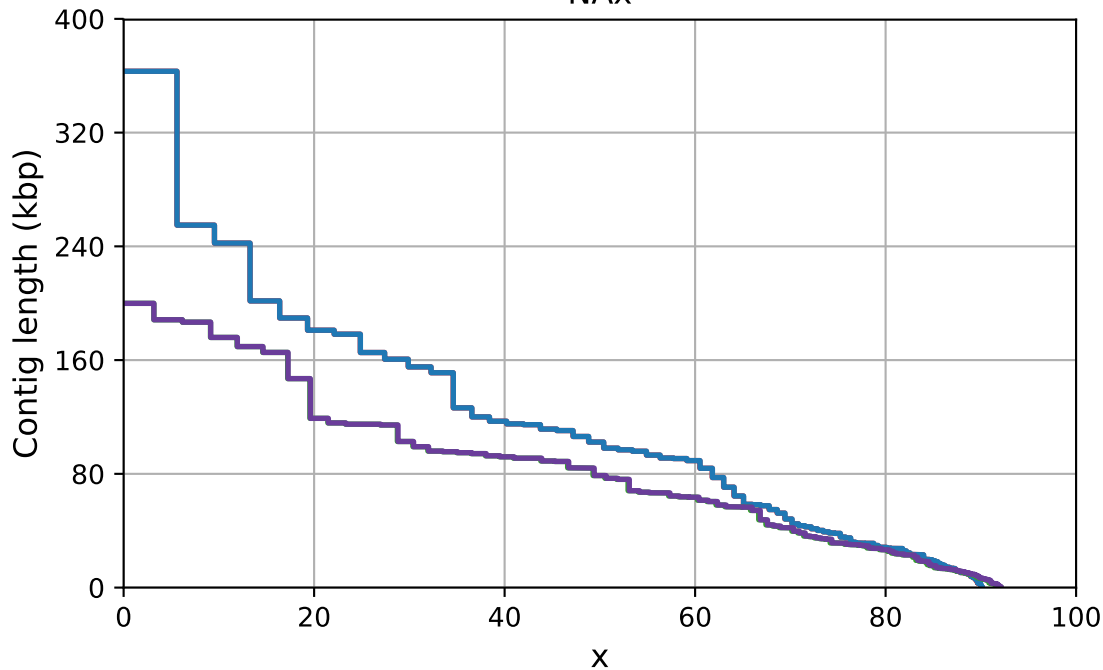




Cumulative length (aligned contigs)

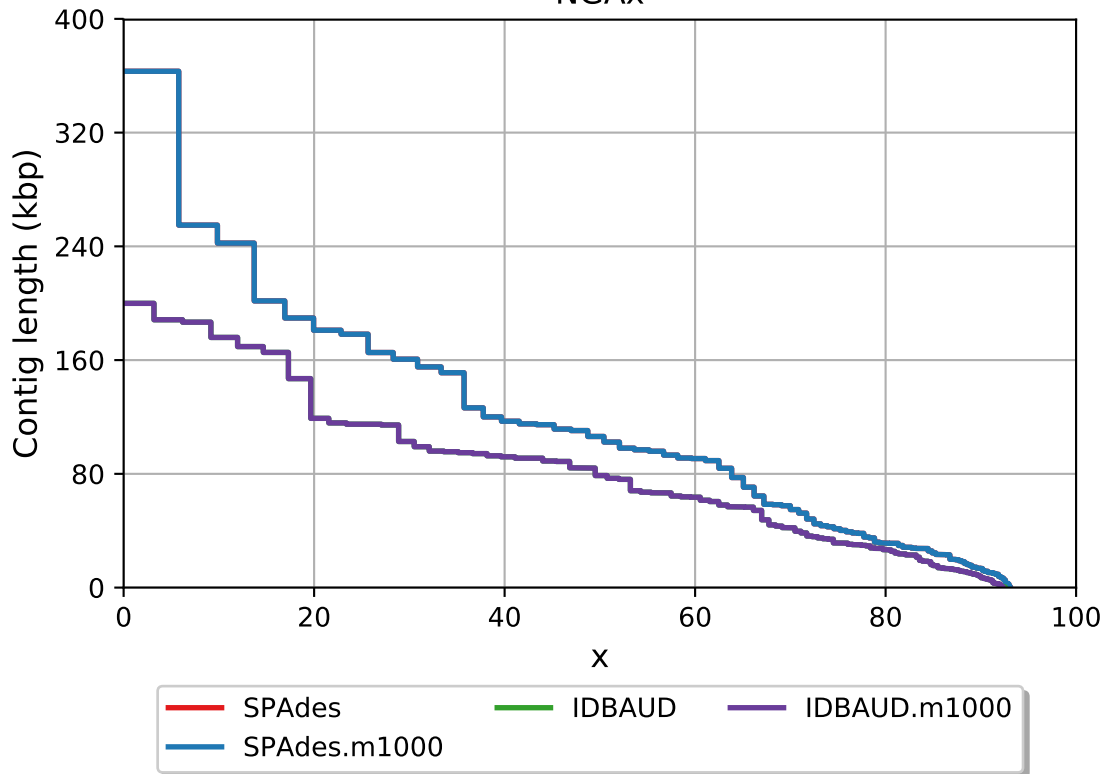


NAx

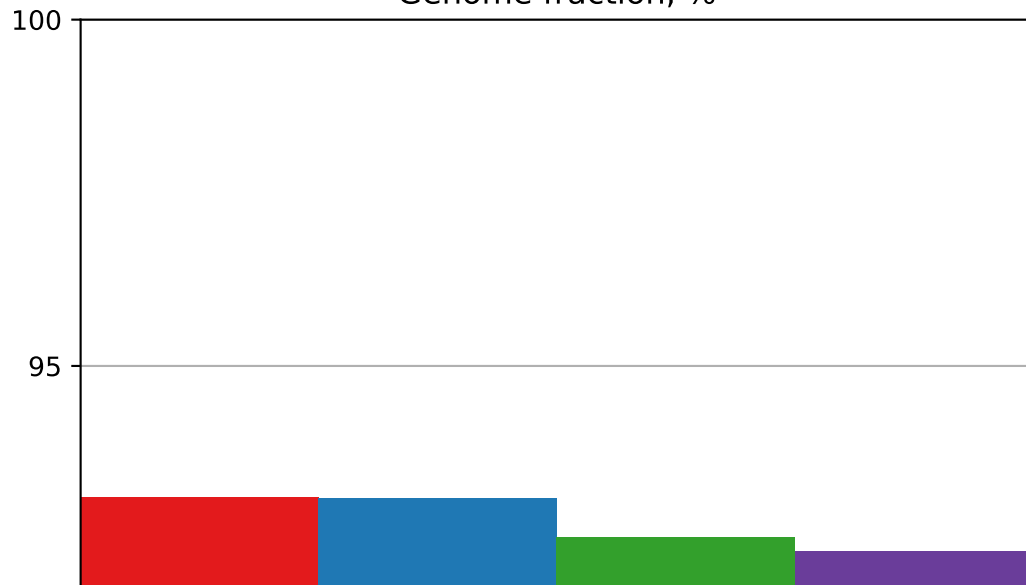


SPAdes IDBAUD IDBAUD.m1000  
SPAdes.m1000

# NGAx



Genome fraction, %



SPAdes  
SPAdes.m1000

IDBAUD

IDBAUD.m1000