

Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1
# contigs (>= 50000 bp)	1	1	1	1
Total length (>= 1000 bp)	158289	158289	158289	158289
Total length (>= 5000 bp)	158289	158289	158289	158289
Total length (>= 10000 bp)	158289	158289	158289	158289
Total length (>= 25000 bp)	158289	158289	158289	158289
Total length (>= 50000 bp)	158289	158289	158289	158289
# contigs	1	1	1	1
Largest contig	158289	158289	158289	158289
Total length	158289	158289	158289	158289
Reference length	159145	159145	159145	159145
GC (%)	38.75	38.75	38.75	38.75
Reference GC (%)	38.77	38.77	38.77	38.77
N50	158289	158289	158289	158289
NG50	158289	158289	158289	158289
N75	158289	158289	158289	158289
NG75	158289	158289	158289	158289
L50	1	1	1	1
LG50	1	1	1	1
L75	1	1	1	1
LG75	1	1	1	1
# misassemblies	2	2	2	2
# misassembled contigs	1	1	1	1
Misassembled contigs length	158289	158289	158289	158289
# local misassemblies	12	12	12	12
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	8290	8290	8290	8290
Genome fraction (%)	94.244	94.244	94.244	94.244
Duplication ratio	1.000	1.000	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	993.43	993.43	993.43	993.43
# indels per 100 kbp	42.67	42.67	42.67	42.67
Largest alignment	102680	102680	102678	102678
Total aligned length	149999	149999	149997	149997
NA50	102680	102680	102678	102678
NGA50	102680	102680	102678	102678
NA75	45738	45738	45738	45738
NGA75	45738	45738	45738	45738
LA50	1	1	1	1
LGA50	1	1	1	1
LA75	2	2	2	2
LGA75	2	2	2	2

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

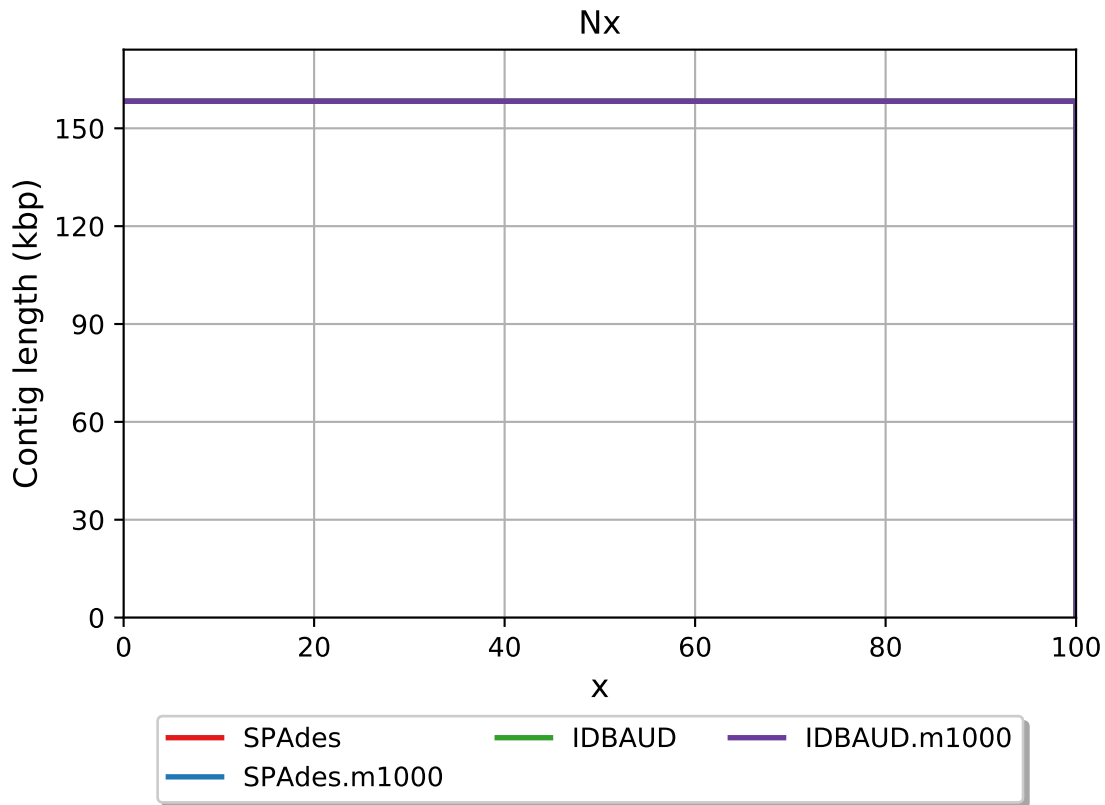
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	2	2	2	2
# contig misassemblies	2	2	2	2
# c. relocations	0	0	0	0
# c. translocations	0	0	0	0
# c. inversions	2	2	2	2
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	1	1	1	1
Misassembled contigs length	158289	158289	158289	158289
# possibly misassembled contigs	1	1	1	1
# possible misassemblies	10	10	10	10
# local misassemblies	12	12	12	12
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	1490	1490	1490	1490
# indels	64	64	64	64
# indels (<= 5 bp)	57	57	57	57
# indels (> 5 bp)	7	7	7	7
Indels length	148	148	148	148

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).

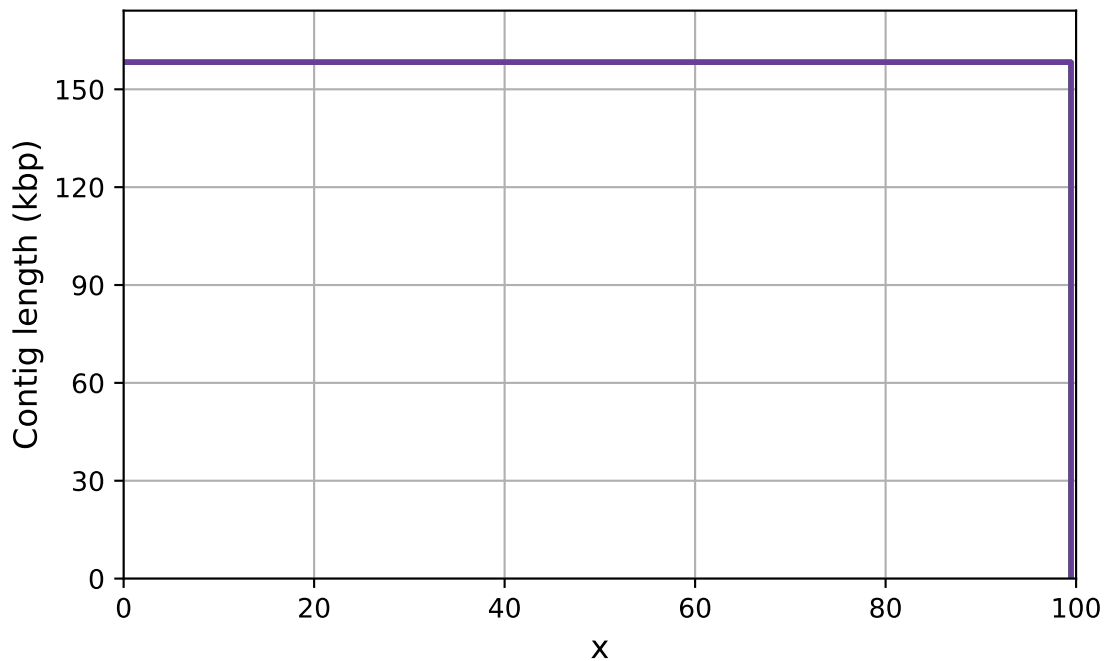
Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	1	1	1	1
Partially unaligned length	8290	8290	8290	8290
# N's	0	0	0	0

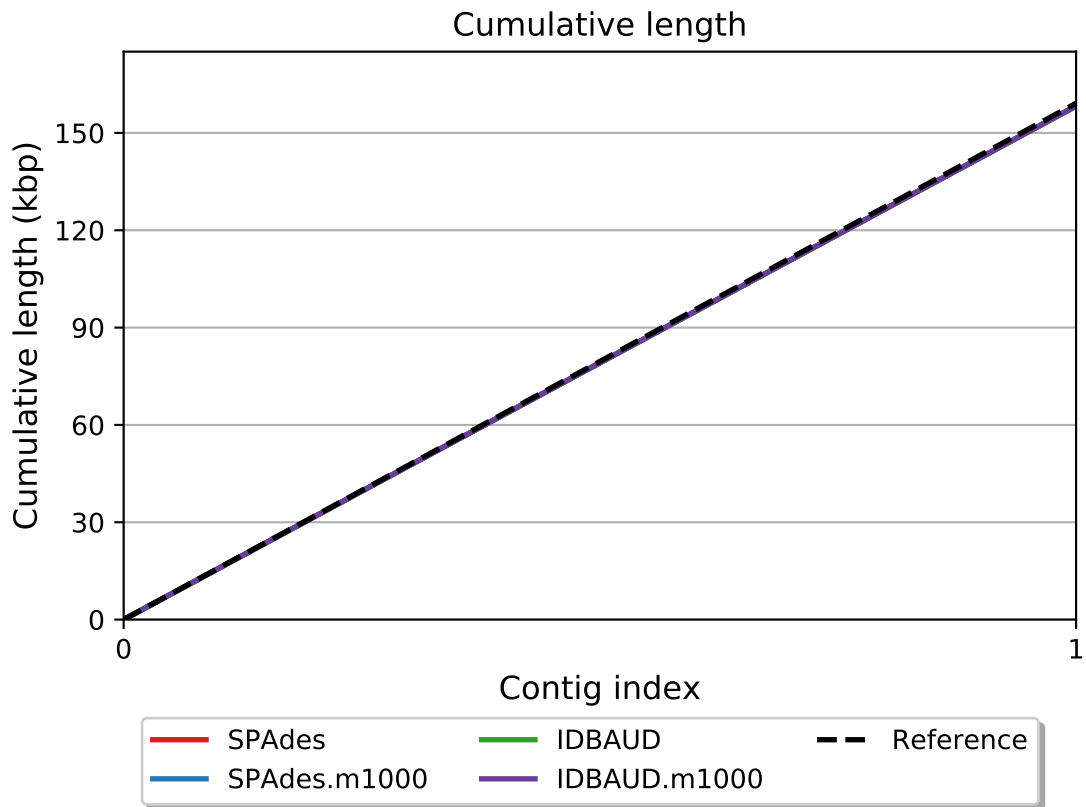
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

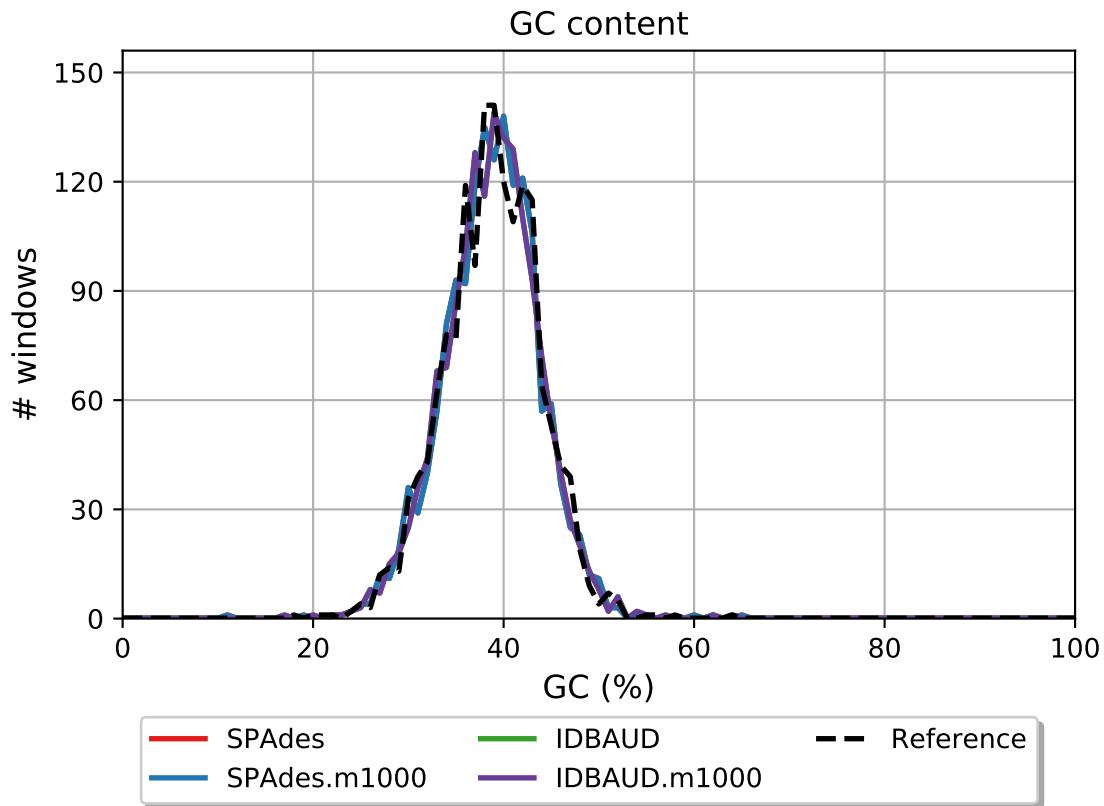


NGx

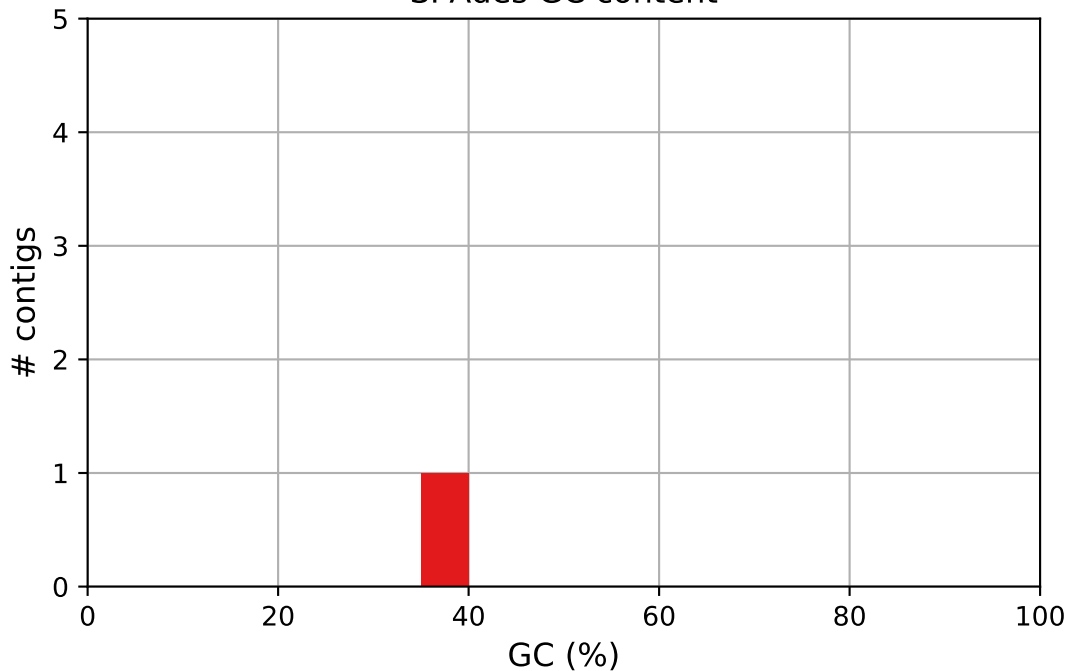


— SPAdes — IDBAUD — IDBAUD.m1000
— SPAdes.m1000



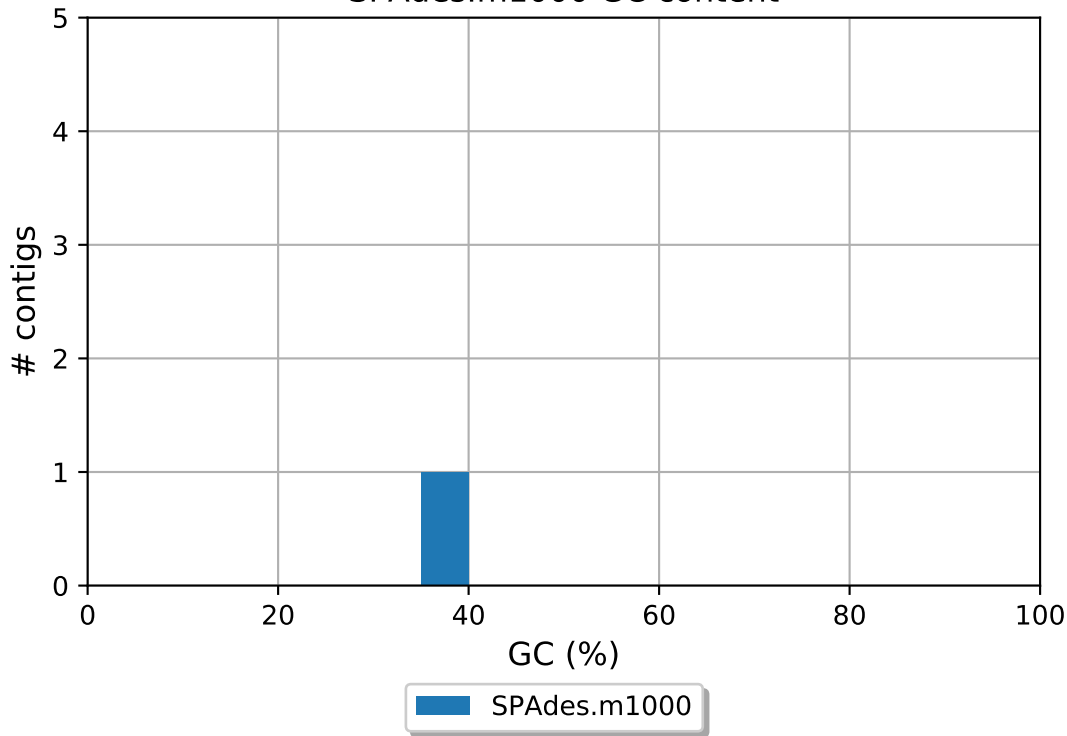


SPAdes GC content

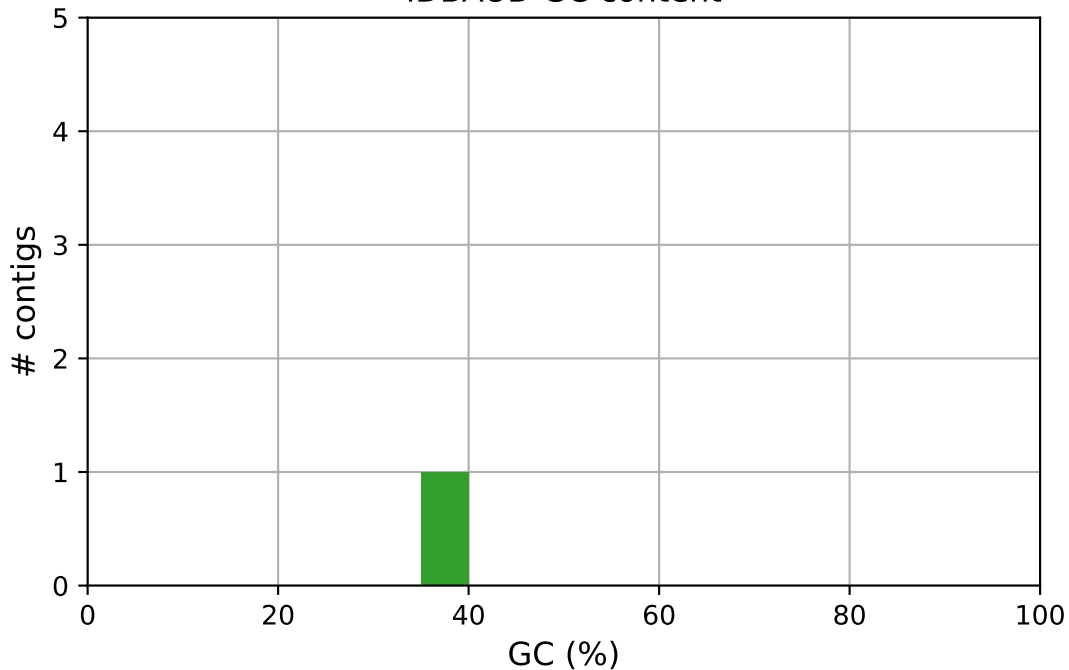


SPAdes

SPAdes.m1000 GC content

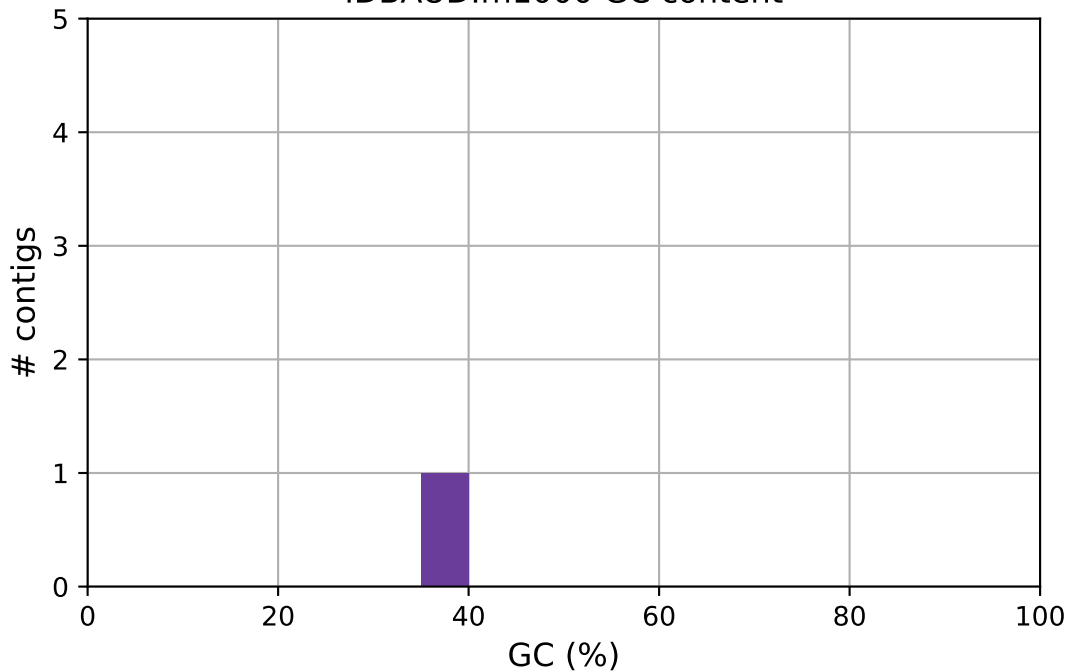


IDBAUD GC content



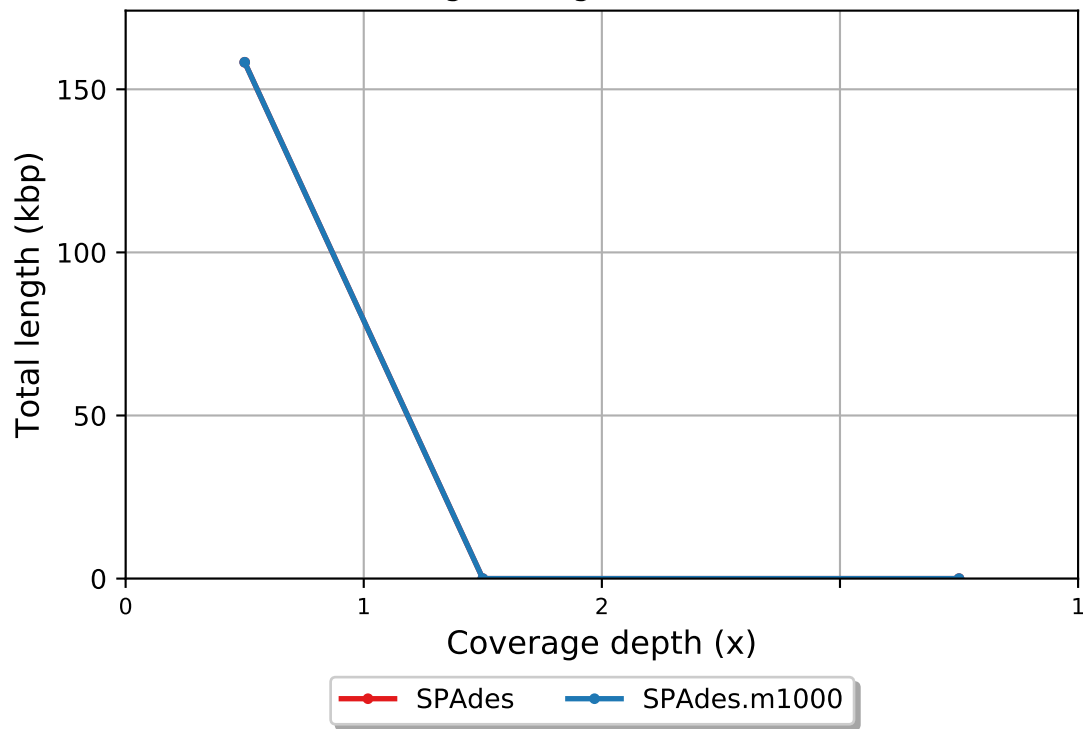
IDBAUD

IDBAUD.m1000 GC content

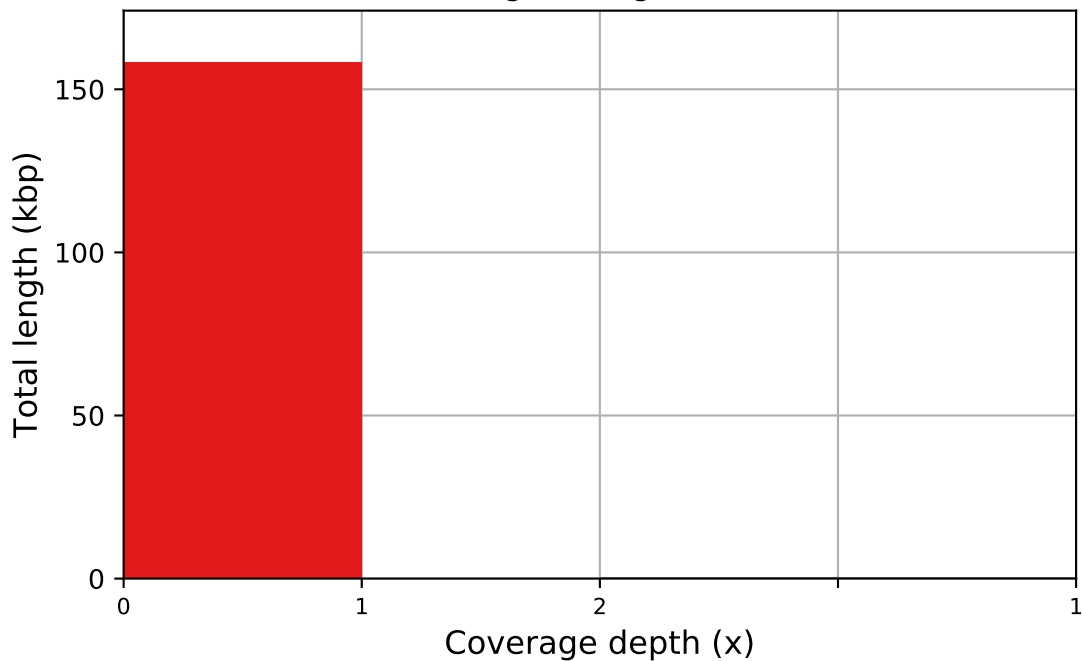


IDBAUD.m1000

Coverage histogram (bin size: 1x)

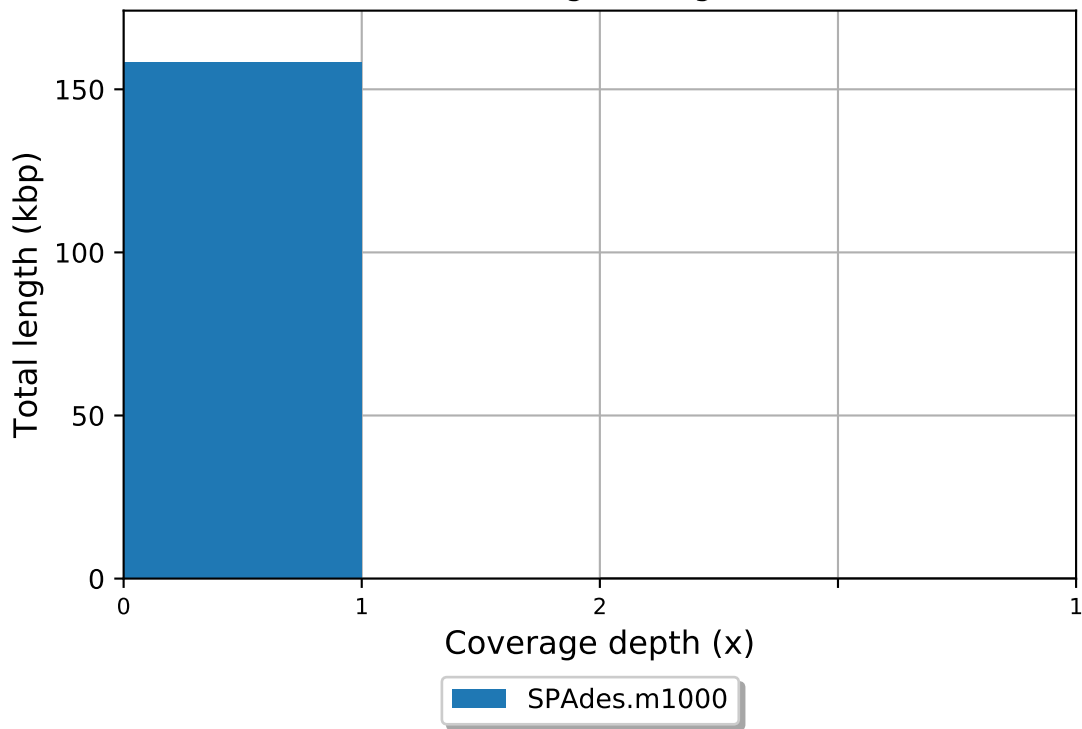


SPAdes coverage histogram (bin size: 1x)

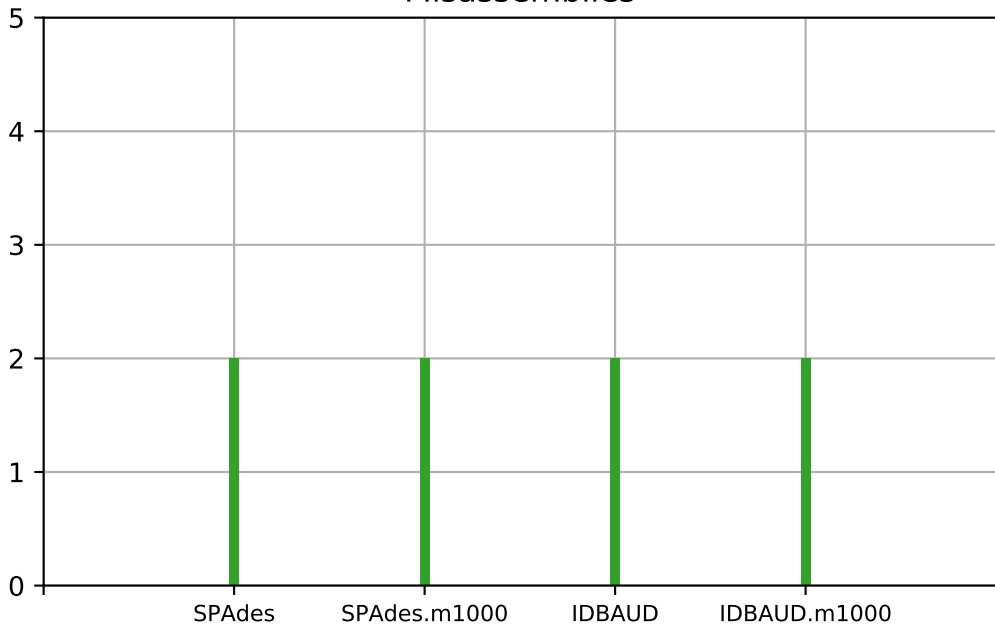


SPAdes

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

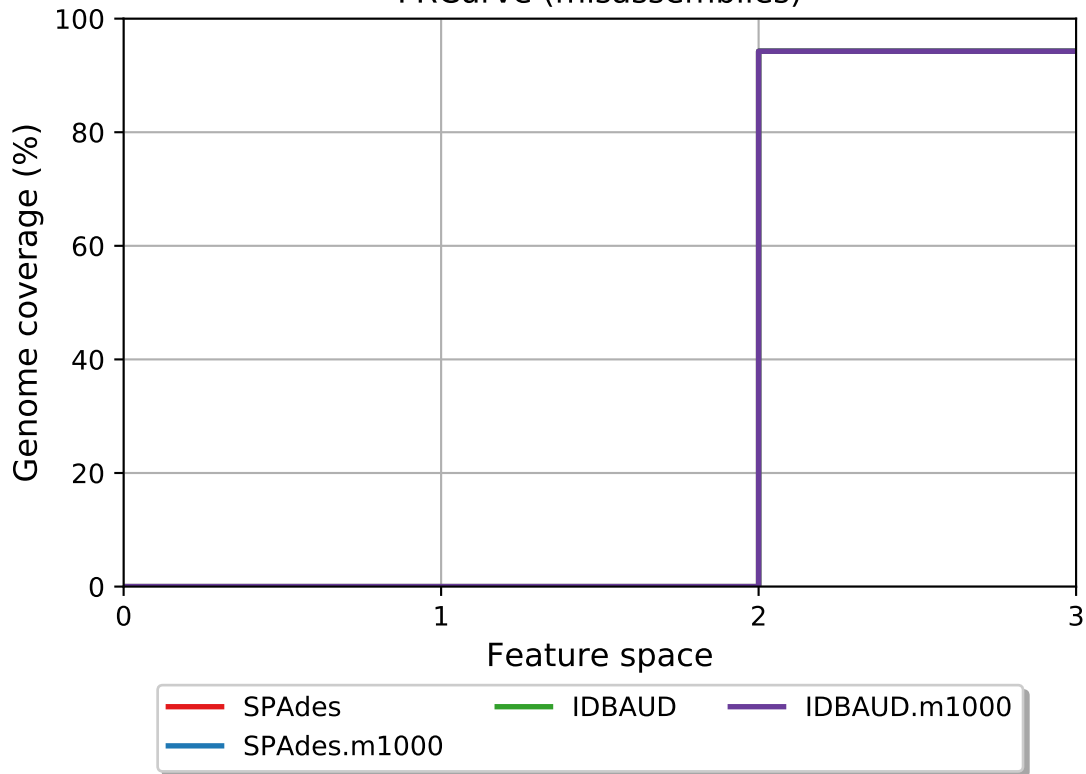


Misassemblies

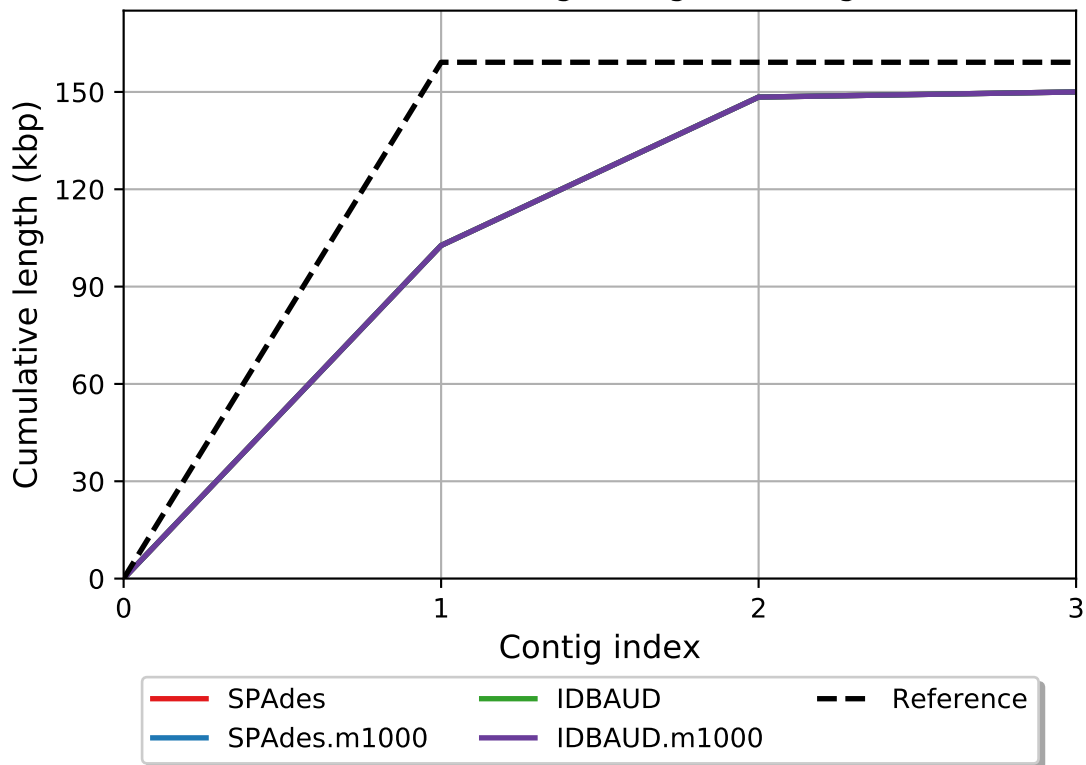


inversions

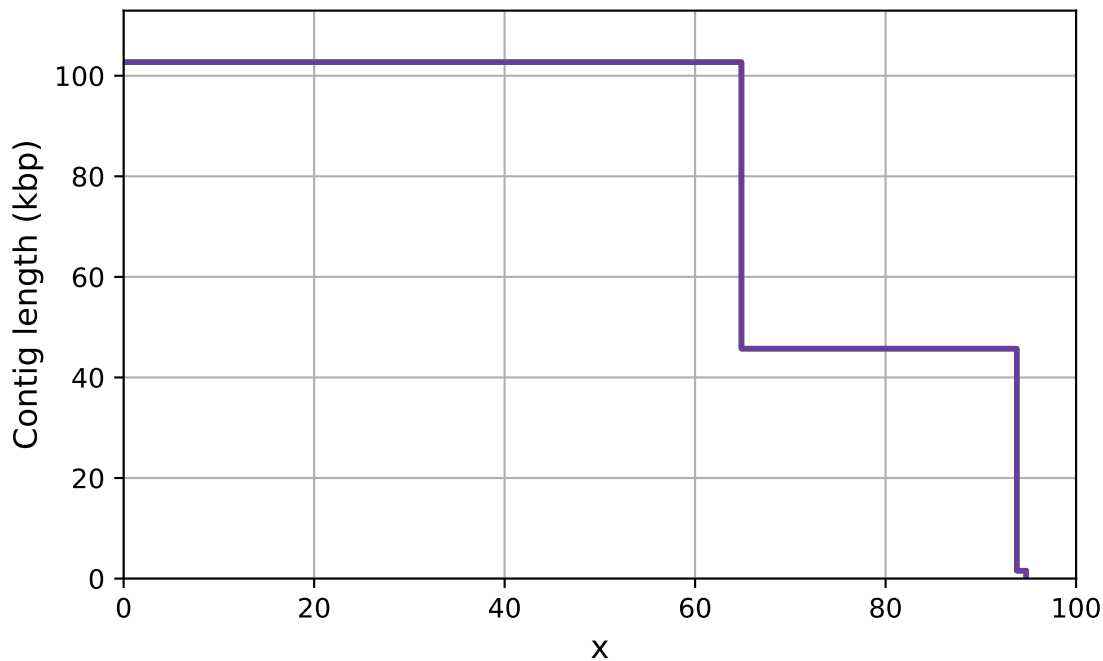
FRCurve (misassemblies)



Cumulative length (aligned contigs)

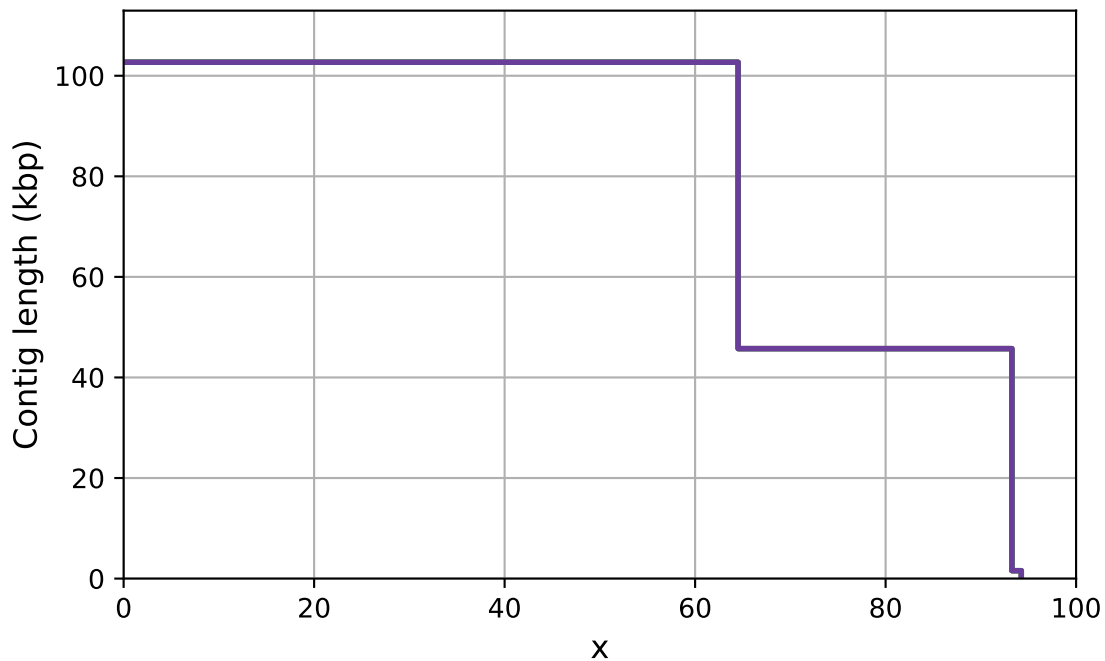


NAx



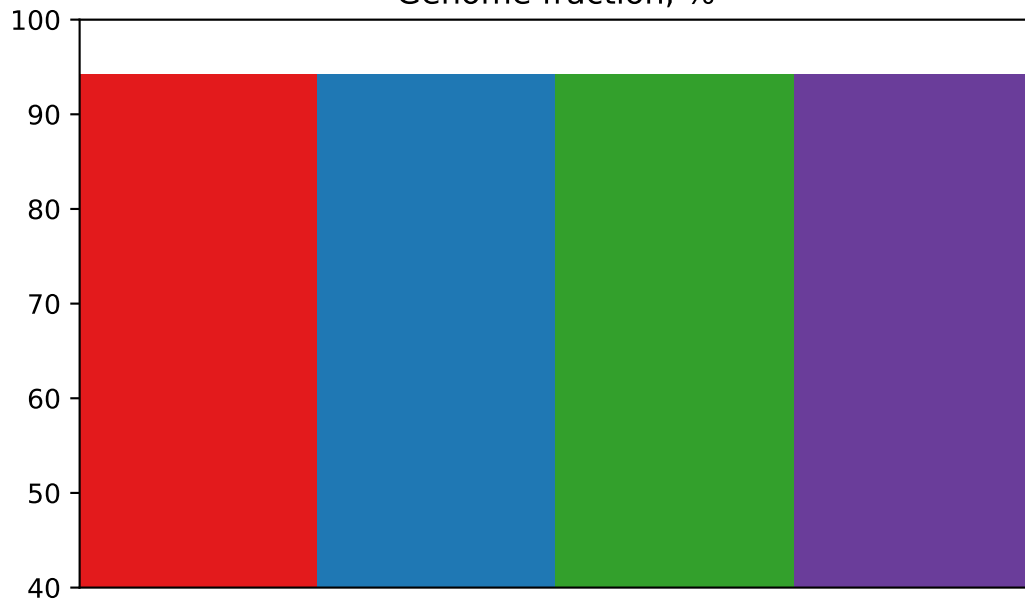
SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

NGAx



SPAdes IDBAUD IDBAUD.m1000
SPAdes.m1000

Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000