

## Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	6	6	8	8
# contigs (>= 5000 bp)	6	6	5	5
# contigs (>= 10000 bp)	6	6	5	5
# contigs (>= 25000 bp)	6	6	5	5
# contigs (>= 50000 bp)	5	5	4	4
Total length (>= 1000 bp)	1660853	1660853	1657323	1657323
Total length (>= 5000 bp)	1660853	1660853	1650474	1650474
Total length (>= 10000 bp)	1660853	1660853	1650474	1650474
Total length (>= 25000 bp)	1660853	1660853	1650474	1650474
Total length (>= 50000 bp)	1623310	1623310	1612967	1612967
# contigs	6	6	11	8
Largest contig	871377	871377	866948	866948
Total length	1660853	1660853	1659285	1657323
Reference length	1676444	1676444	1676444	1676444
GC (%)	33.32	33.32	33.32	33.31
Reference GC (%)	33.51	33.51	33.51	33.51
N50	871377	871377	866948	866948
NG50	871377	871377	866948	866948
N75	245352	245352	496441	496441
NG75	245352	245352	496441	496441
L50	1	1	1	1
LG50	1	1	1	1
L75	3	3	2	2
LG75	3	3	2	2
# misassemblies	2	2	0	0
# misassembled contigs	1	1	0	0
Misassembled contigs length	871377	871377	0	0
# local misassemblies	1	1	7	7
# 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 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	99.054	99.054	98.958	98.846
Duplication ratio	1.000	1.000	1.000	1.000
# N's per 100 kbp	0.60	0.60	0.00	0.00
# mismatches per 100 kbp	0.30	0.30	1.99	1.99
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	868954	868954	866915	866915
Total aligned length	1660482	1660482	1659251	1657289
NA50	868954	868954	866915	866915
NGA50	868954	868954	866915	866915
NA75	245352	245352	496440	496440
NGA75	245352	245352	496440	496440
LA50	1	1	1	1
LGA50	1	1	1	1
LA75	3	3	2	2
LGA75	3	3	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

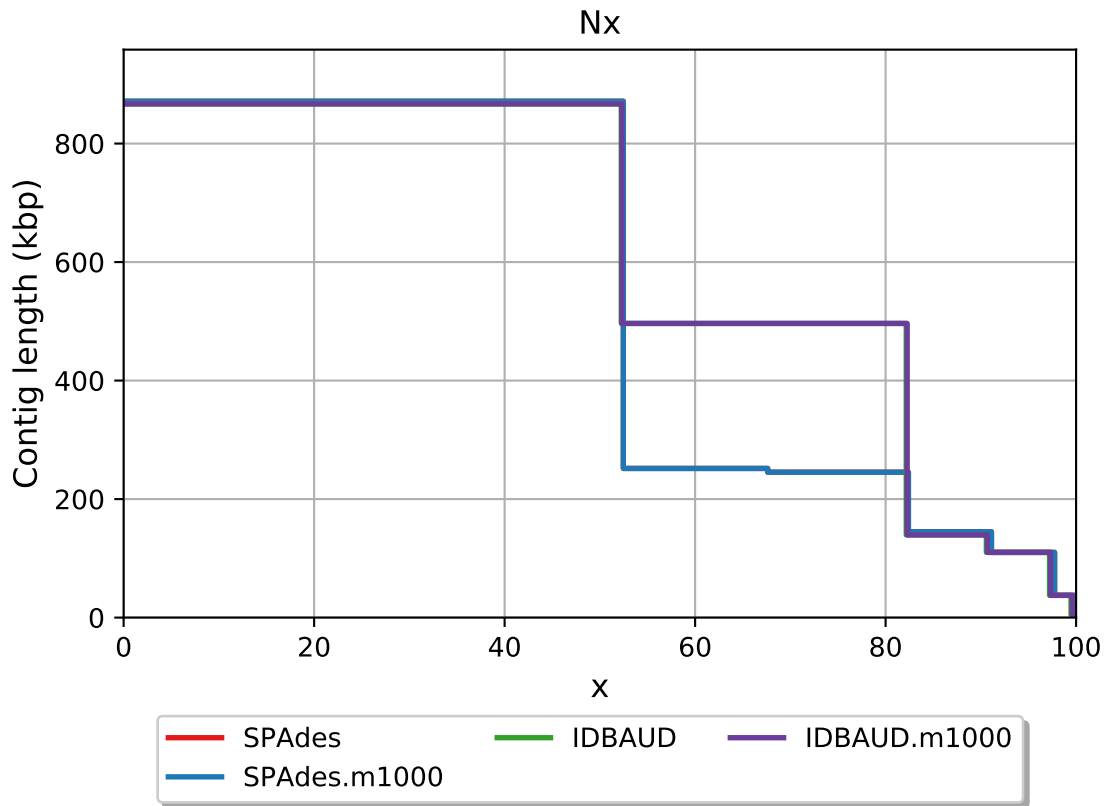
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	2	2	0	0
# contig misassemblies	1	1	0	0
# c. relocations	1	1	0	0
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	1	1	0	0
# s. relocations	1	1	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	1	1	0	0
Misassembled contigs length	871377	871377	0	0
# possibly misassembled contigs	0	0	0	0
# possible misassemblies	0	0	0	0
# local misassemblies	1	1	7	7
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	5	5	33	33
# indels	0	0	0	0
# indels (<= 5 bp)	0	0	0	0
# indels (> 5 bp)	0	0	0	0
Indels length	0	0	0	0

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).

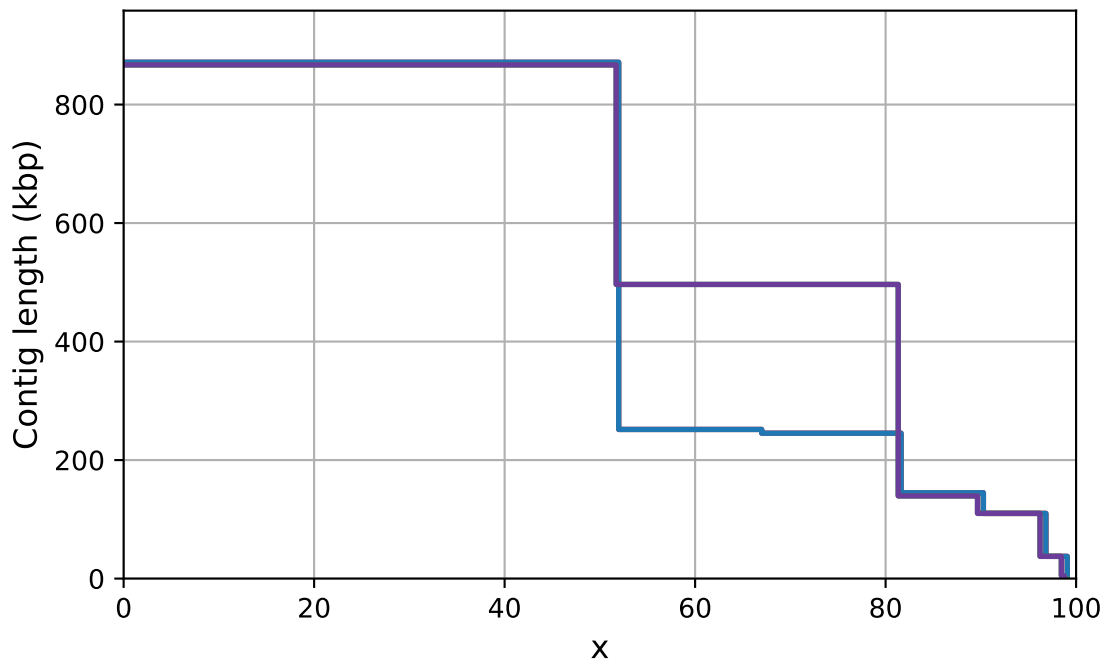
## Unaligned report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	10	10	0	0

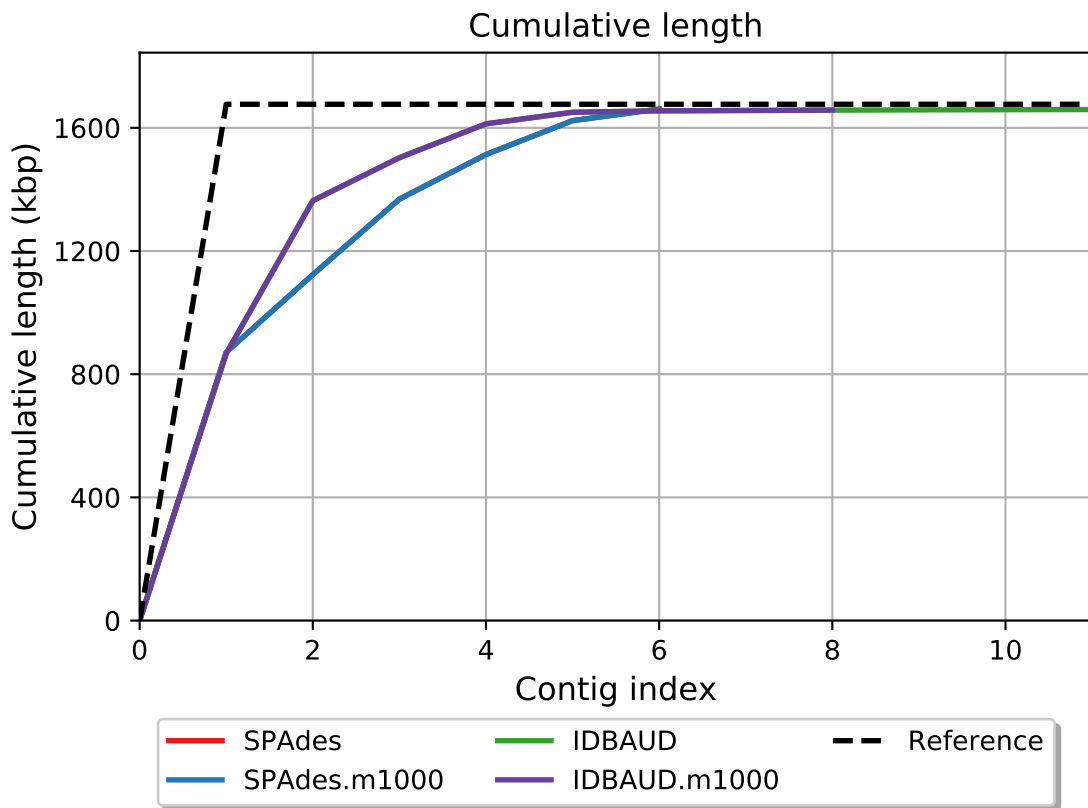
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



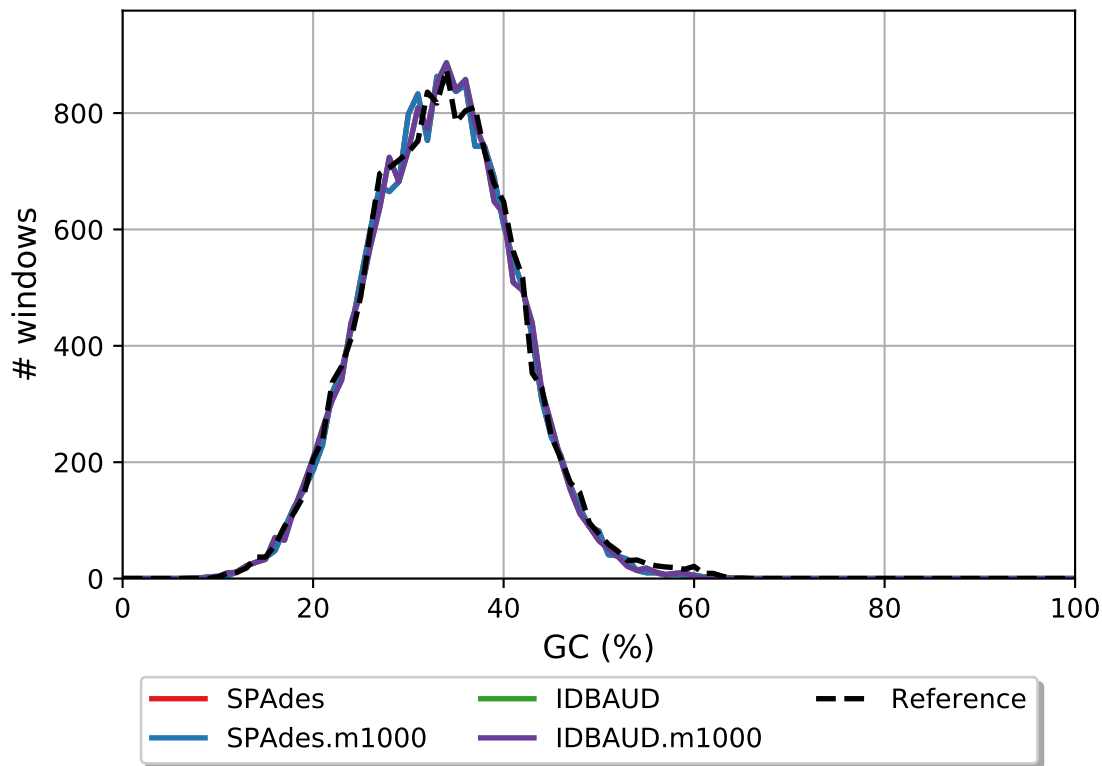
NGx



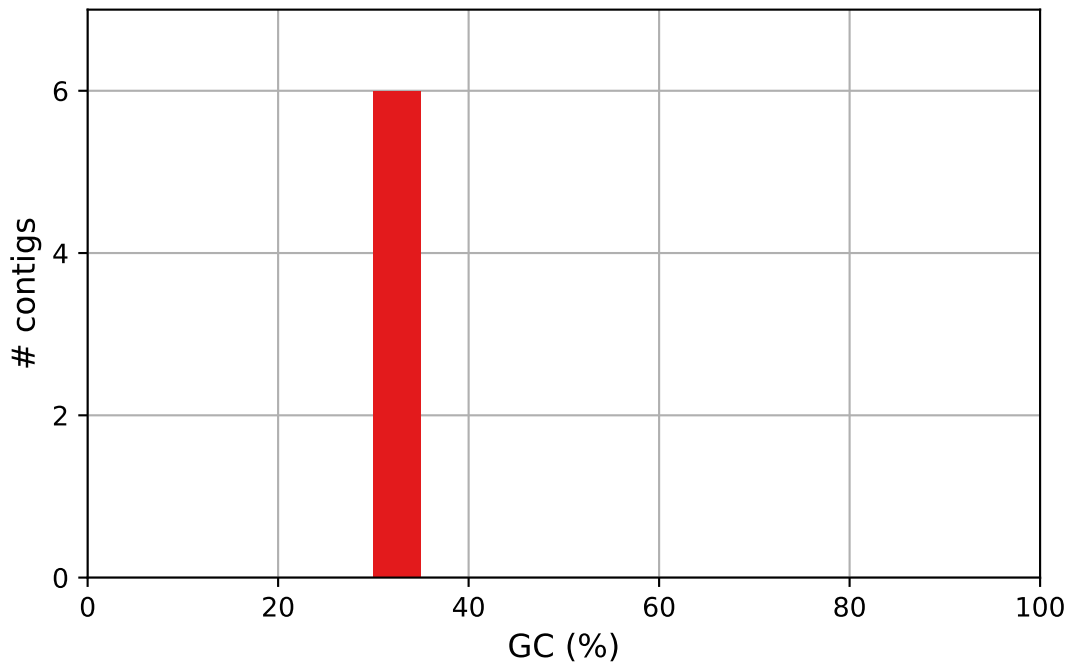
— SPAdes — IDBAUD — IDBAUD.m1000  
— SPAdes.m1000



## GC content



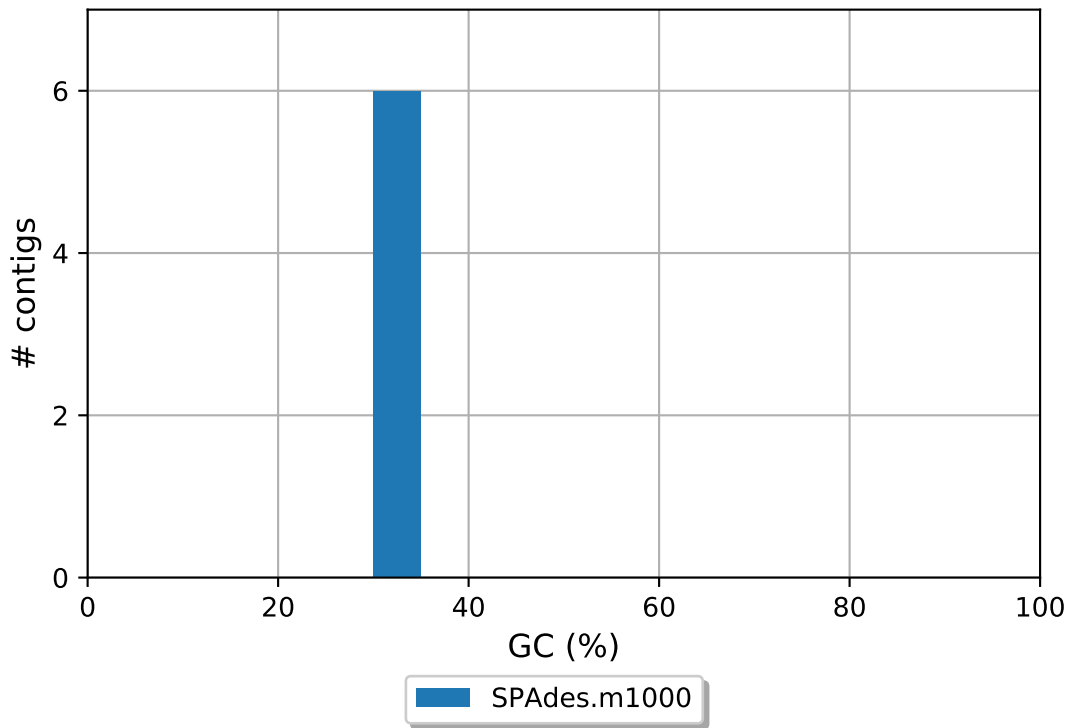
# SPAdes GC content



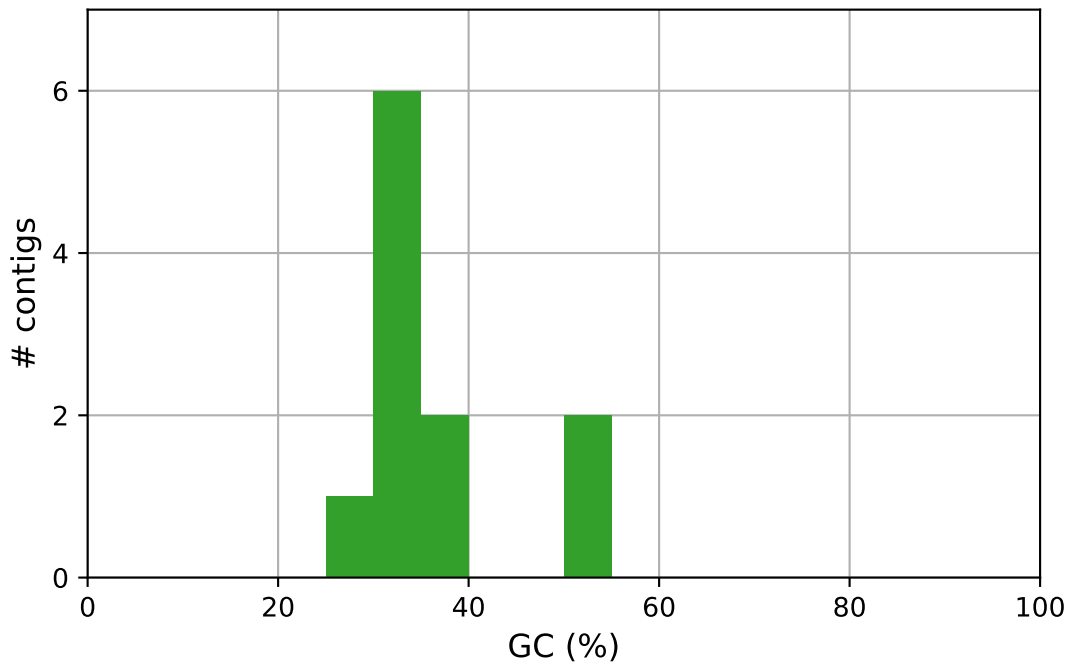
SPAdes



SPAdes.m1000 GC content

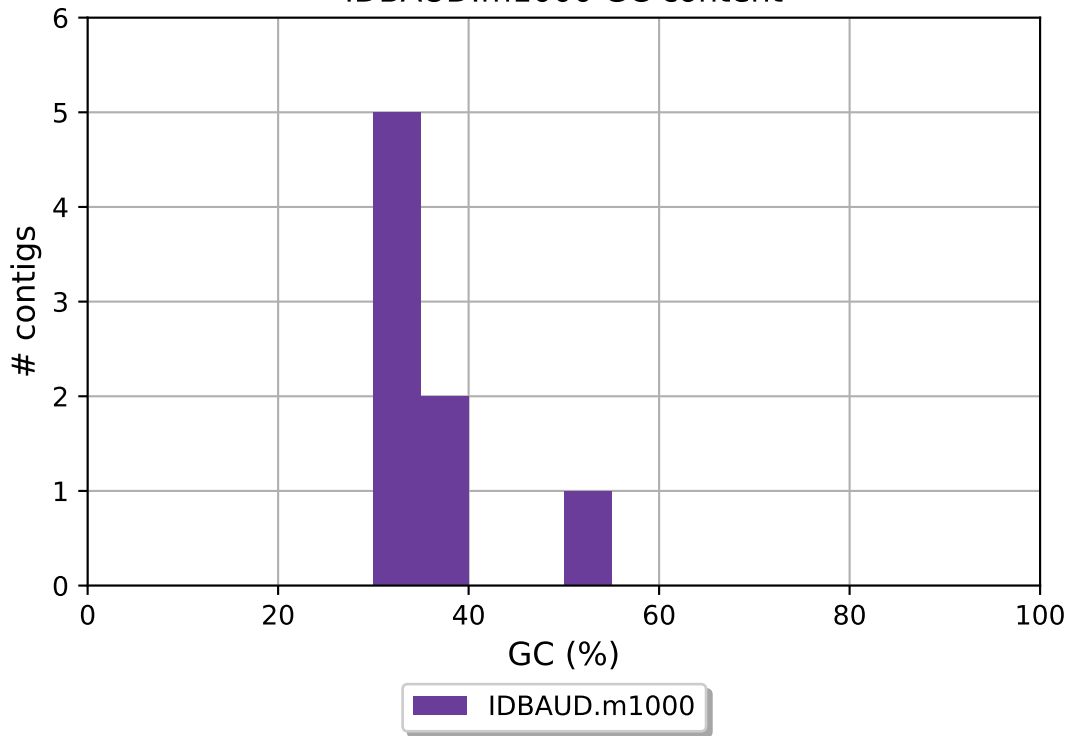


IDBAUD GC content

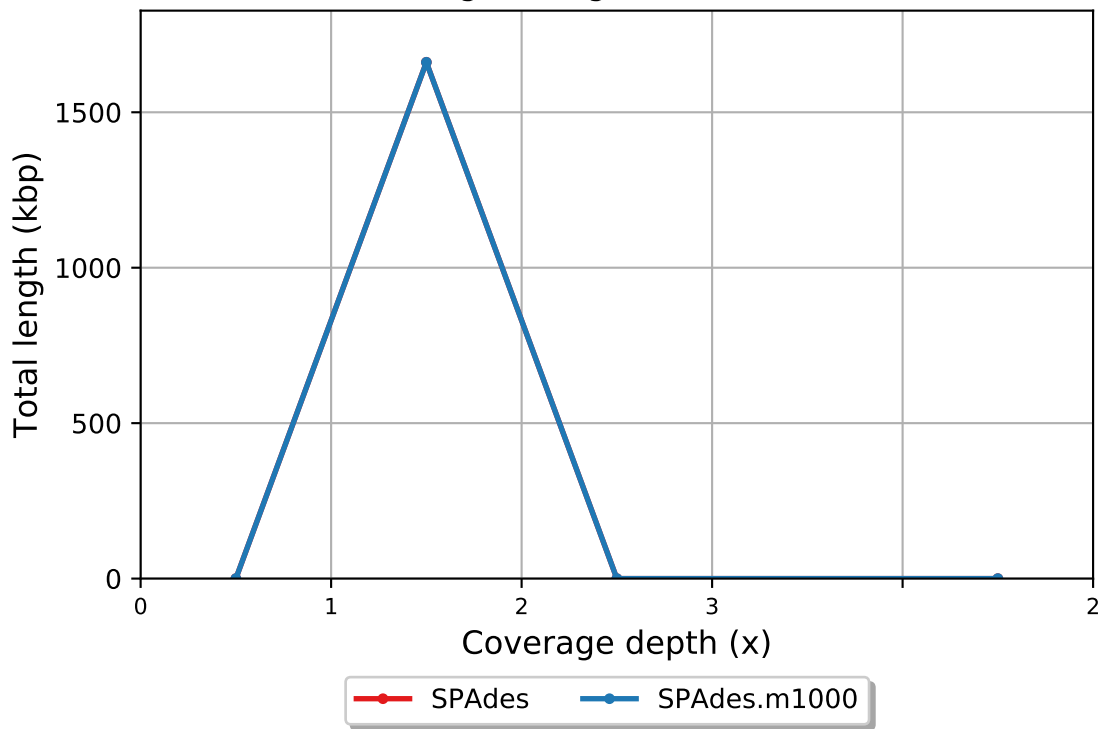


IDBAUD

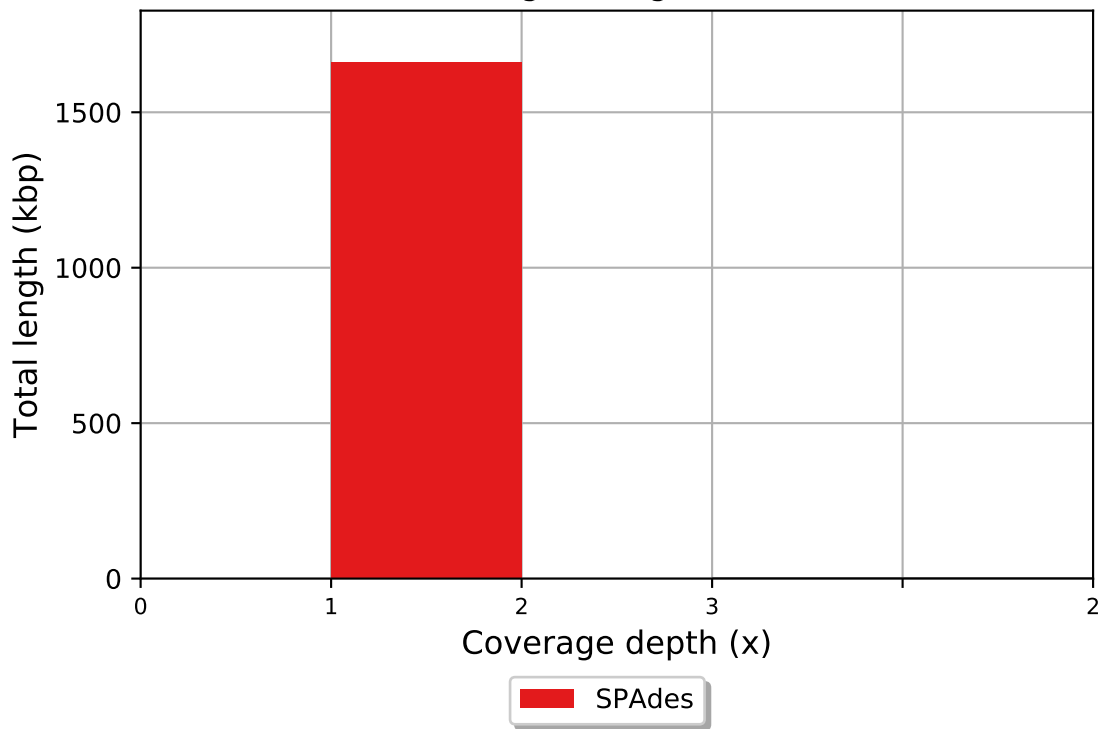
IDBAUD.m1000 GC content



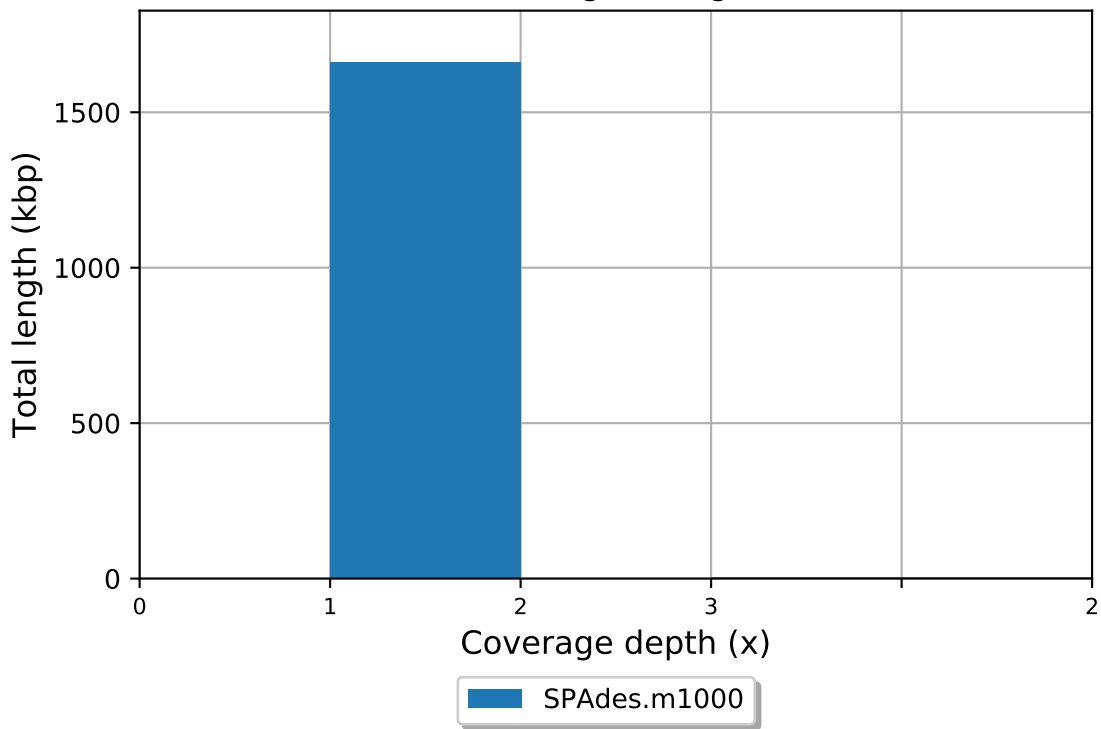
Coverage histogram (bin size: 1x)



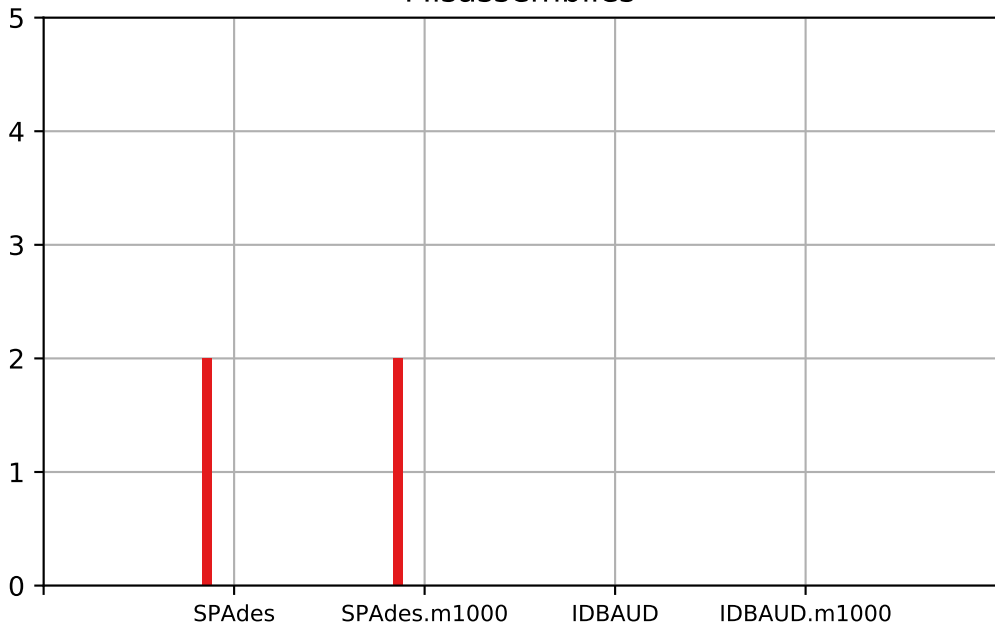
SPAdes coverage histogram (bin size: 1x)



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

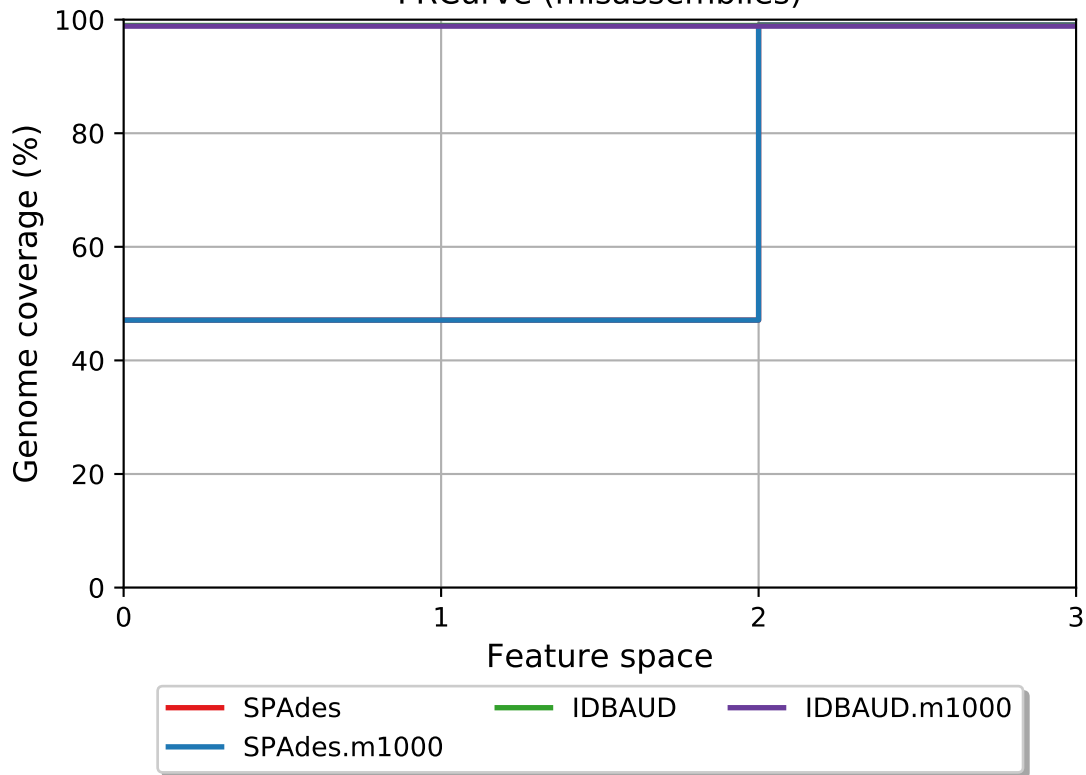


## Misassemblies



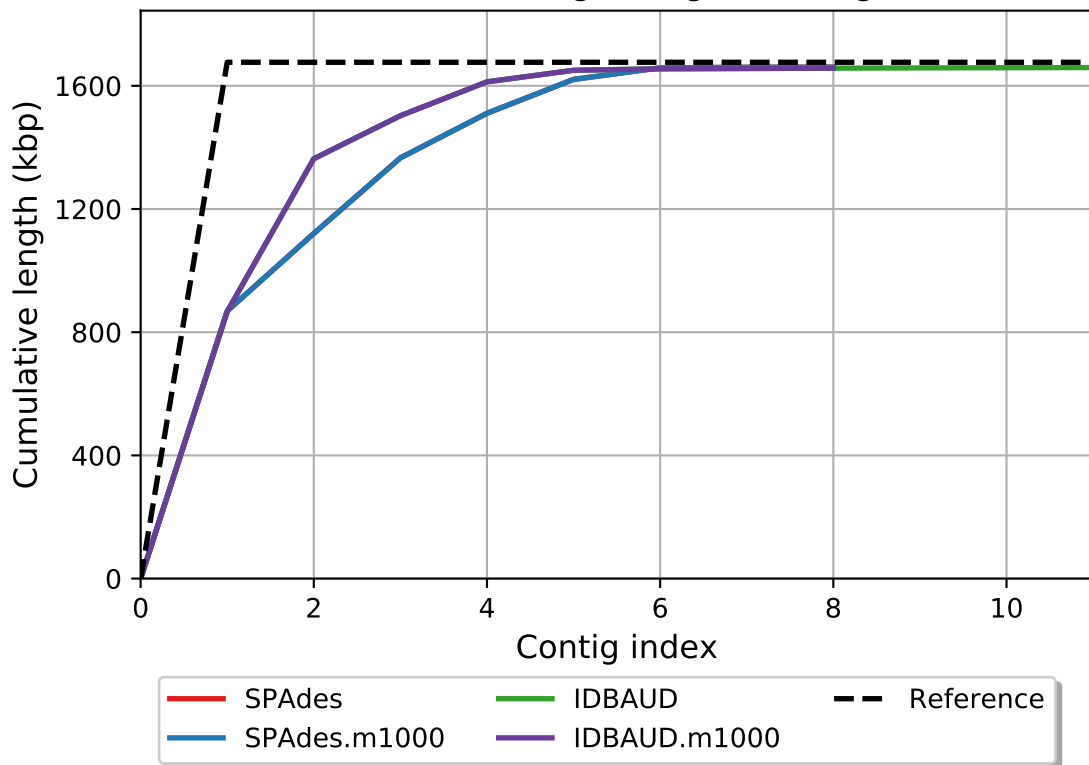
 # relocations

FRCurve (misassemblies)

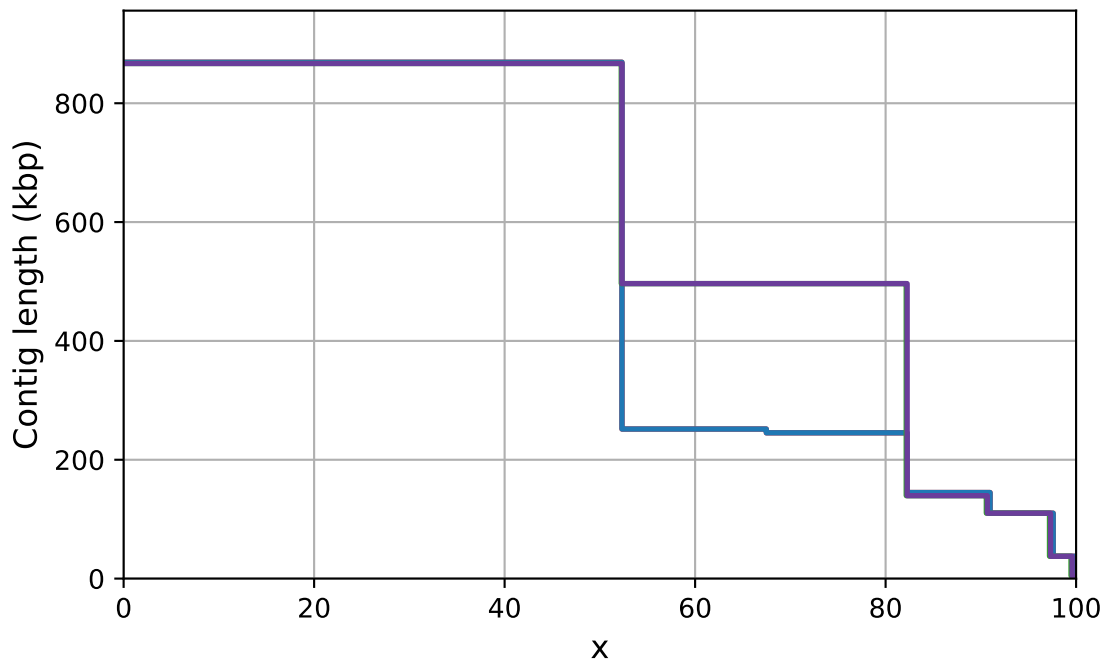




Cumulative length (aligned contigs)

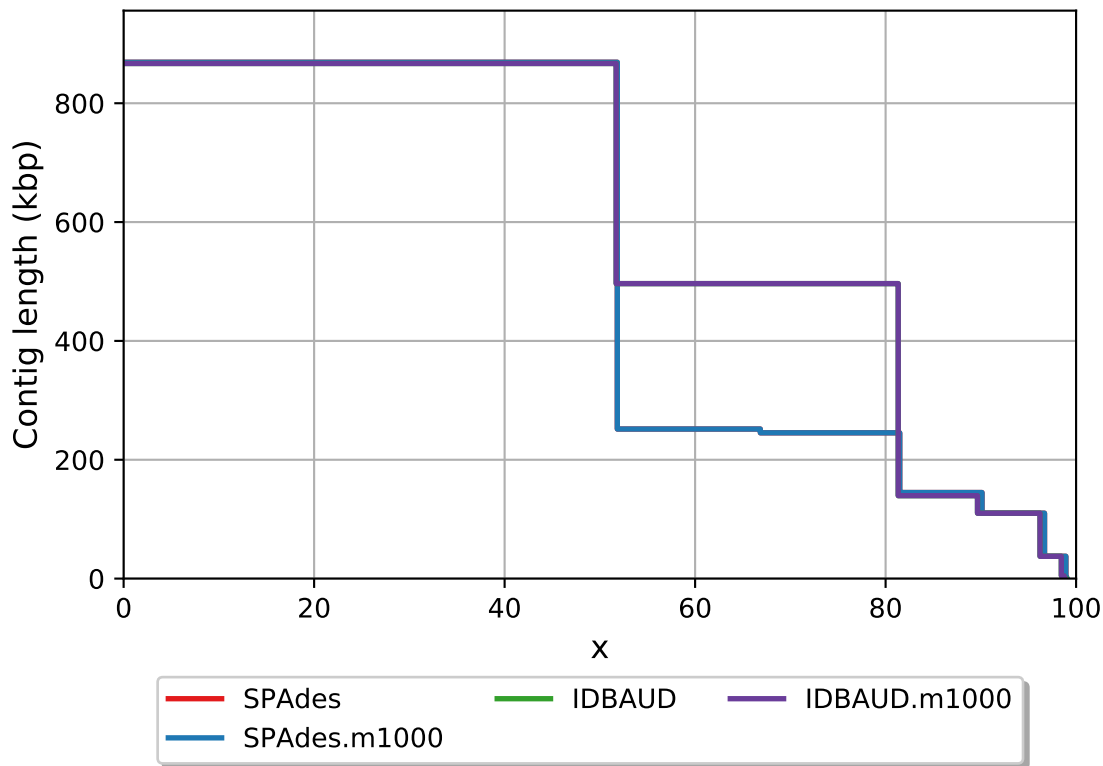


NAx

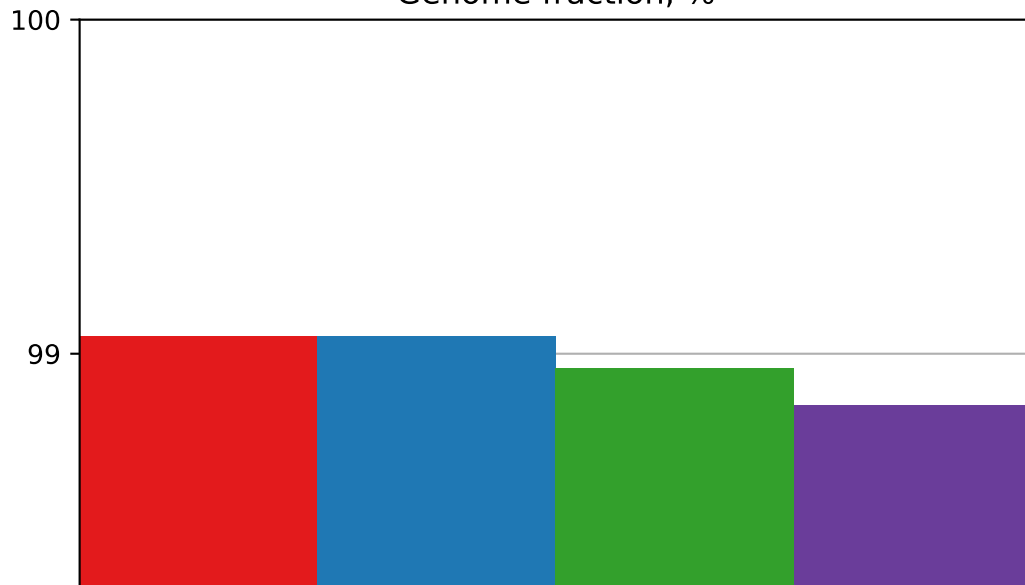


SPAdes IDBAUD IDBAUD.m1000  
SPAdes.m1000

# NGAx



Genome fraction, %



SPAdes

IDBAUD

IDBAUD.m1000

SPAdes.m1000