

## Report

	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# contigs (>= 1000 bp)	3	3	6	6
# contigs (>= 5000 bp)	3	3	6	6
# contigs (>= 10000 bp)	3	3	5	5
# contigs (>= 25000 bp)	3	3	5	5
# contigs (>= 50000 bp)	3	3	5	5
Total length (>= 1000 bp)	1734139	1734139	1017807	1017807
Total length (>= 5000 bp)	1734139	1734139	1017807	1017807
Total length (>= 10000 bp)	1734139	1734139	1011630	1011630
Total length (>= 25000 bp)	1734139	1734139	1011630	1011630
Total length (>= 50000 bp)	1734139	1734139	1011630	1011630
# contigs	3	3	6	6
Largest contig	1221431	1221431	484747	484747
Total length	1734139	1734139	1017807	1017807
Reference length	1697959	1697959	1697959	1697959
GC (%)	49.82	49.82	51.21	51.21
Reference GC (%)	31.13	31.13	31.13	31.13
NS0	1221431	1221431	193275	193275
NG50	1221431	1221431	83319	83319
N75	327269	327269	170794	170794
NG75	327269	327269	-	-
LS0	1	1	2	2
LG50	1	1	4	4
L75	2	2	3	3
LG75	2	2	-	-
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	3	3
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1	1	1	1
# unaligned contigs	0 + 3 part	0 + 3 part	0 + 6 part	0 + 6 part
Unaligned length	1729880	1729880	1013207	1013207
Genome fraction (%)	0.250	0.250	0.267	0.267
Duplication ratio	1.005	1.005	1.013	1.013
# N's per 100 kbp	1.15	1.15	5.70	5.70
# mismatches per 100 kbp	3491.39	3491.39	3676.79	3676.79
# indels per 100 kbp	0.00	0.00	66.05	66.05
Largest alignment	1500	1500	4083	4083
Total aligned length	4239	4239	4542	4542
NGA50	-	-	-	-

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

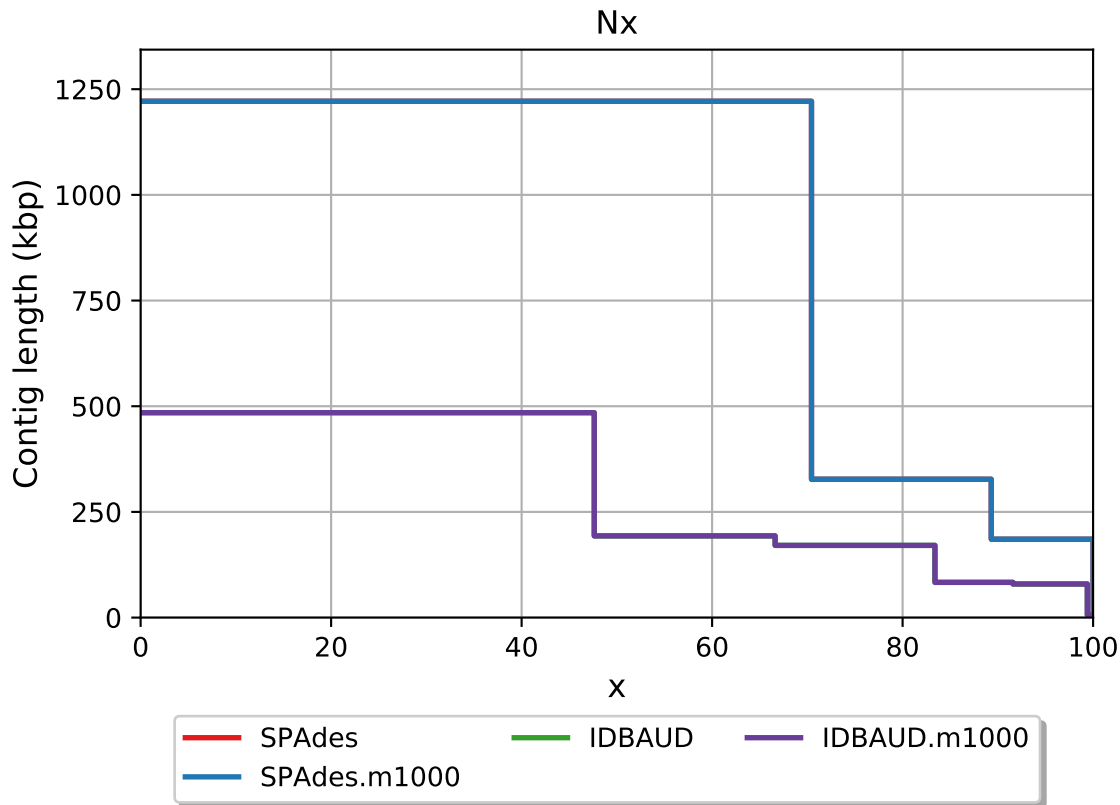
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# misassemblies	0	0	0	0
# contig misassemblies	0	0	0	0
# c. relocations	0	0	0	0
# c. translocations	0	0	0	0
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# possibly misassembled contigs	2	2	5	5
# possible misassemblies	4	4	11	11
# local misassemblies	0	0	3	3
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1	1	1	1
# mismatches	148	148	167	167
# indels	0	0	3	3
# indels (<= 5 bp)	0	0	3	3
# indels (> 5 bp)	0	0	0	0
Indels length	0	0	6	6

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).

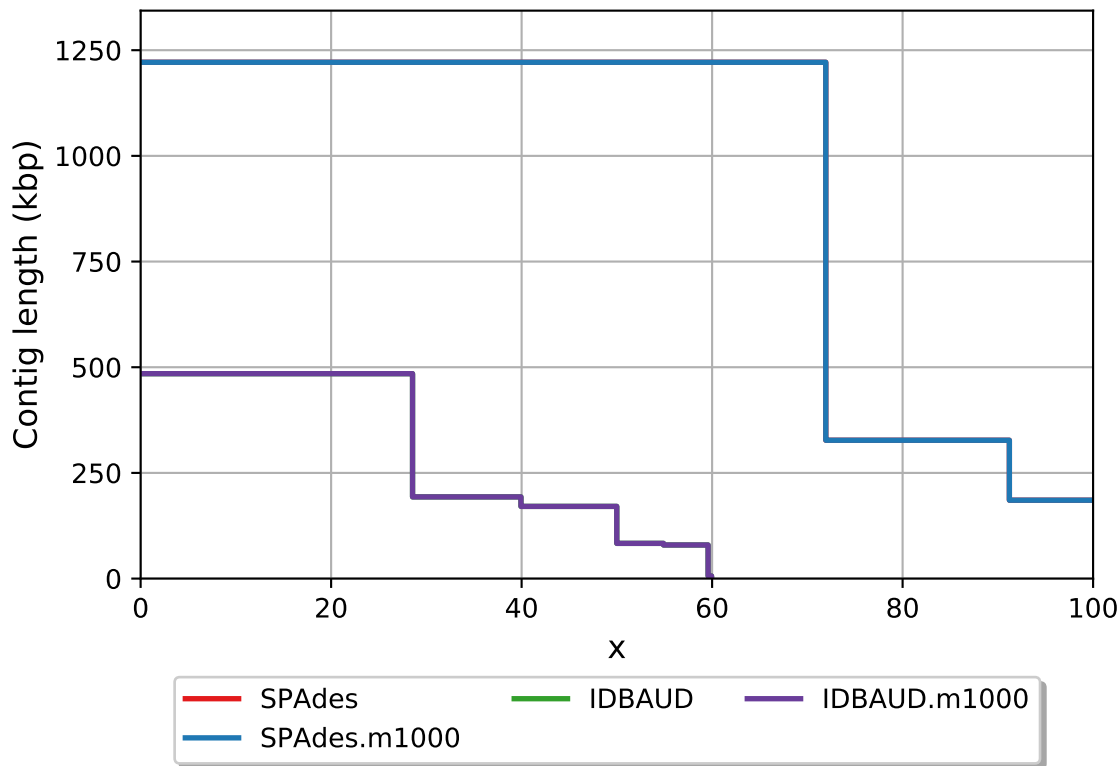
## Unaligned report

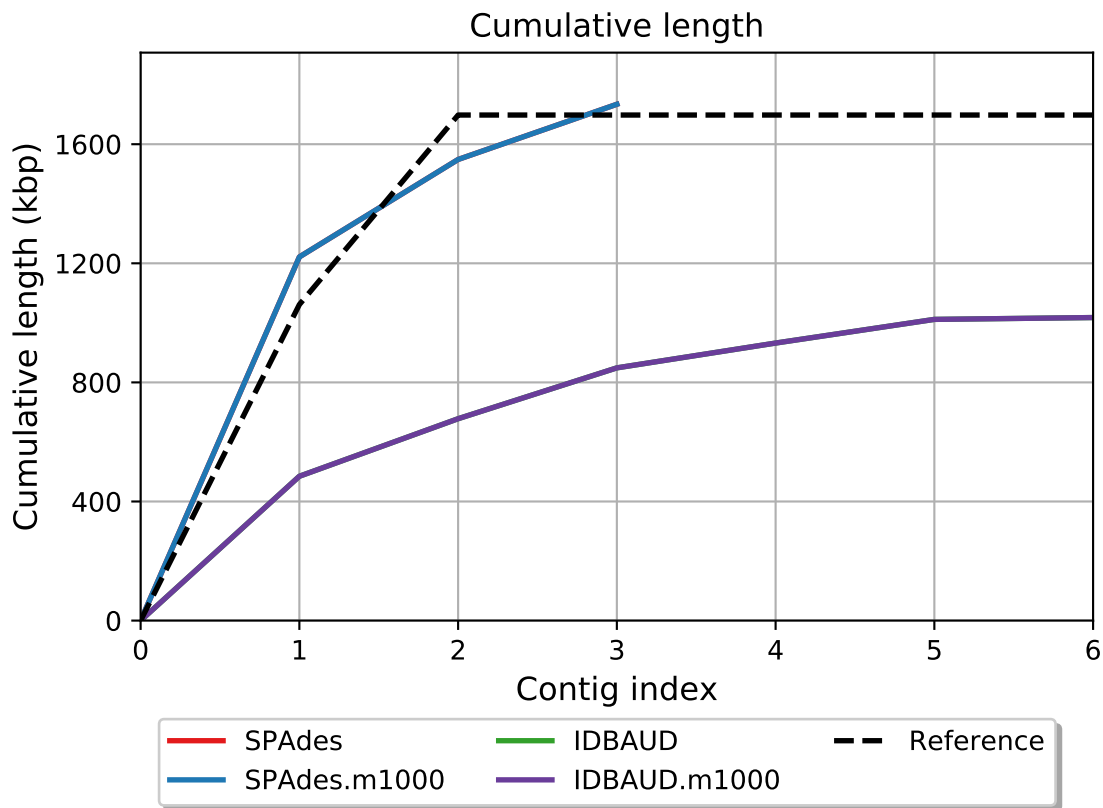
	SPAdes	SPAdes.m1000	IDBAUD	IDBAUD.m1000
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	3	3	6	6
Partially unaligned length	1729880	1729880	1013207	1013207
# N's	20	20	58	58

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).

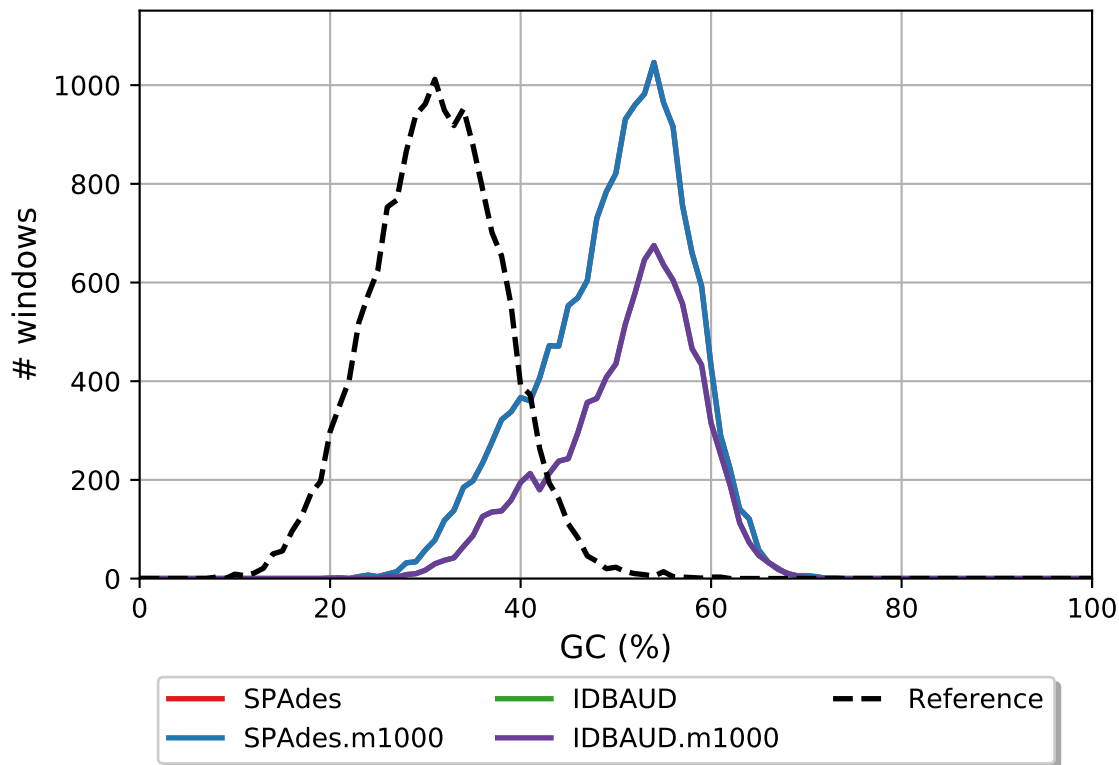


# NGx

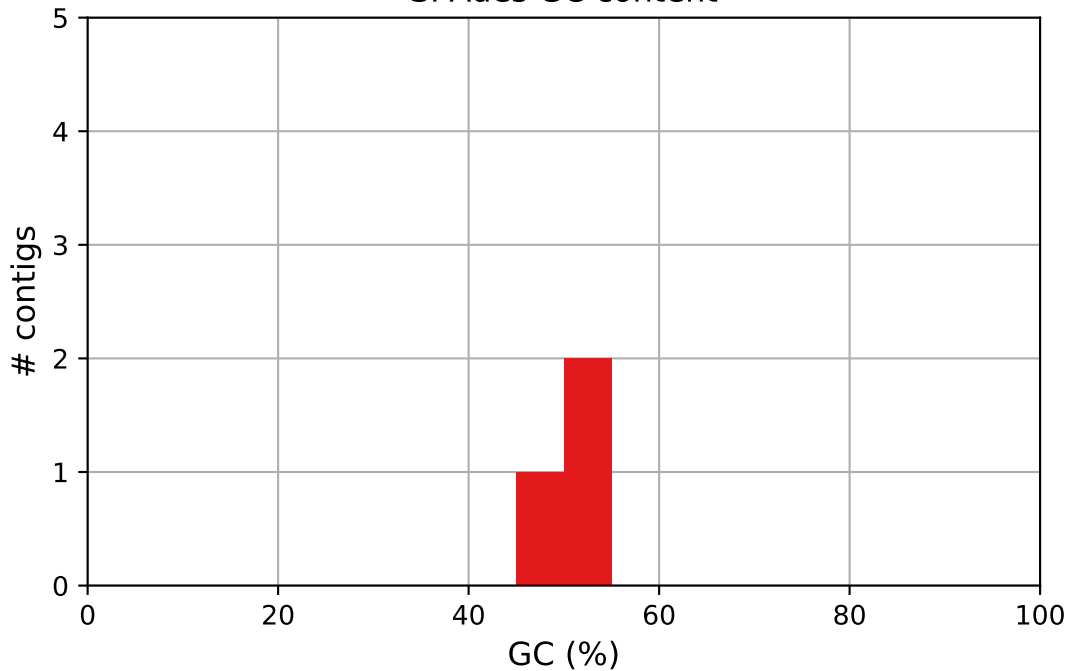




GC content



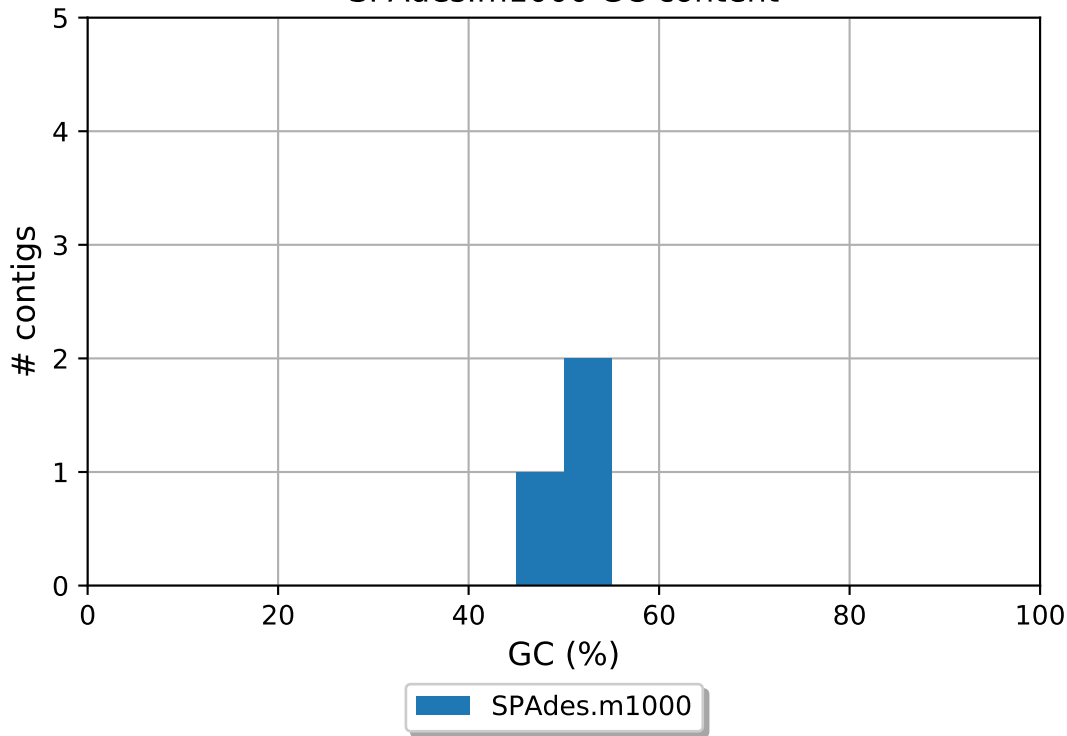
# SPAdes GC content



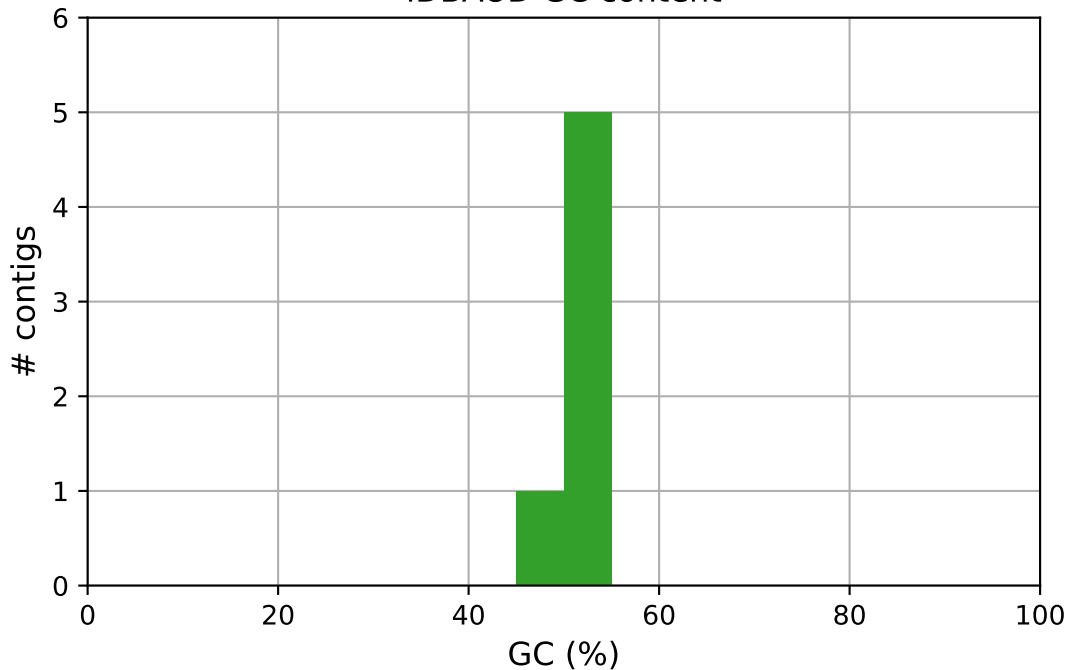
SPAdes



SPAdes.m1000 GC content

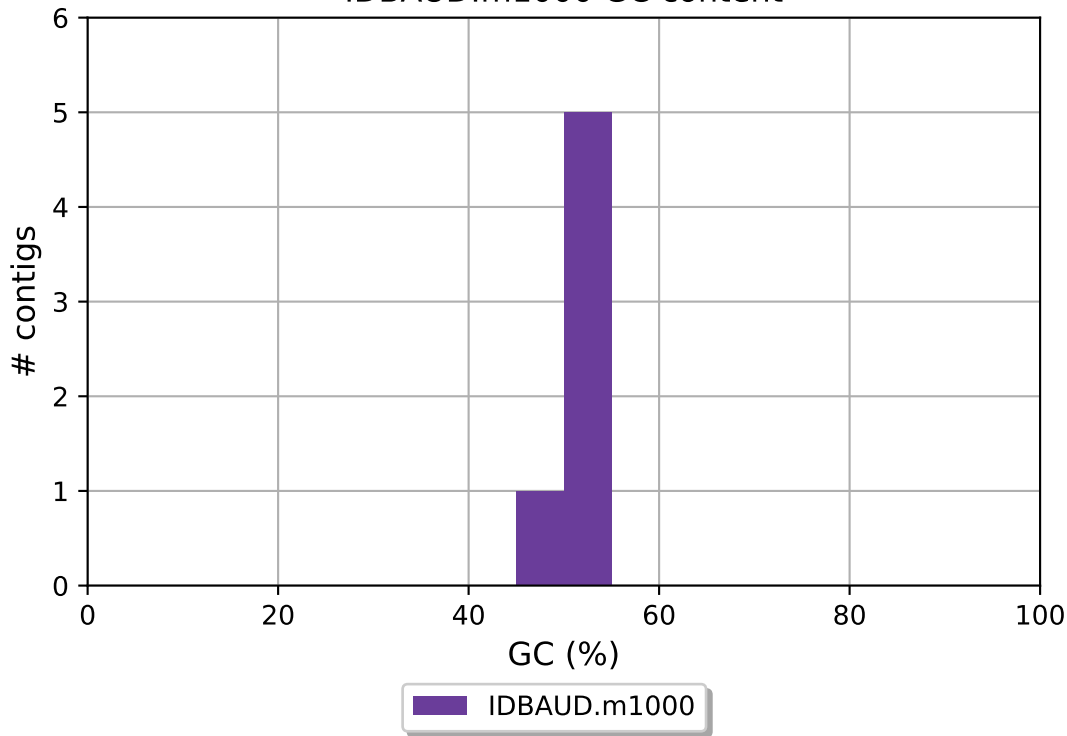


IDBAUD GC content

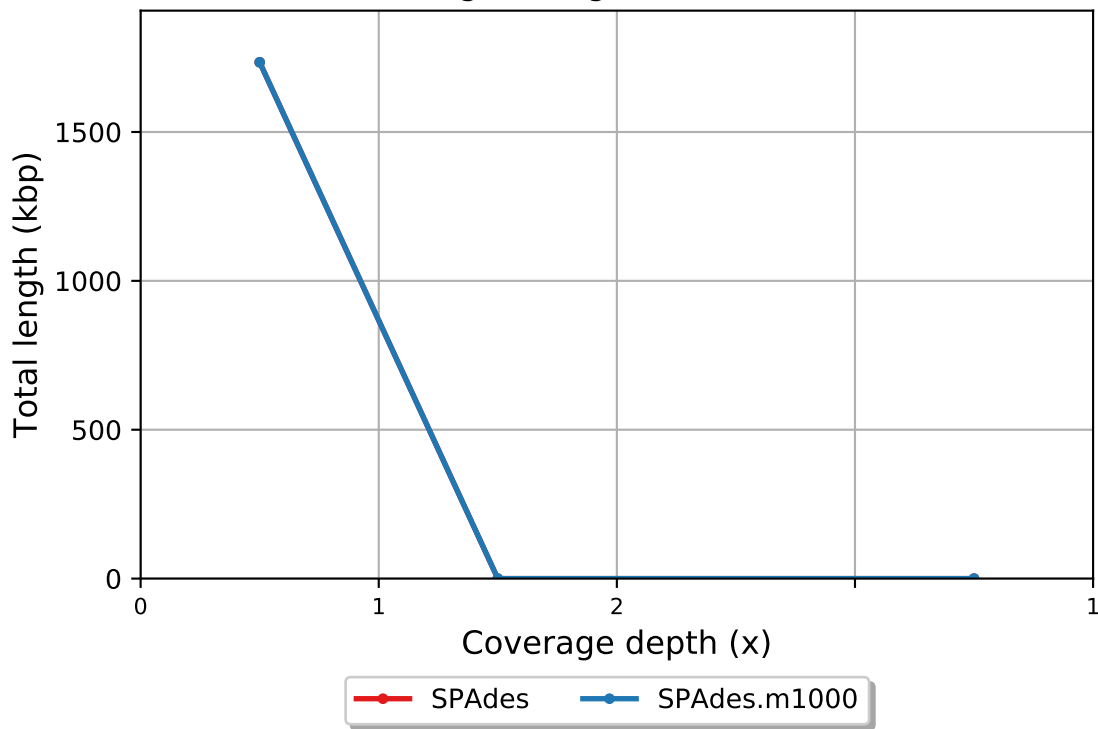


IDBAUD

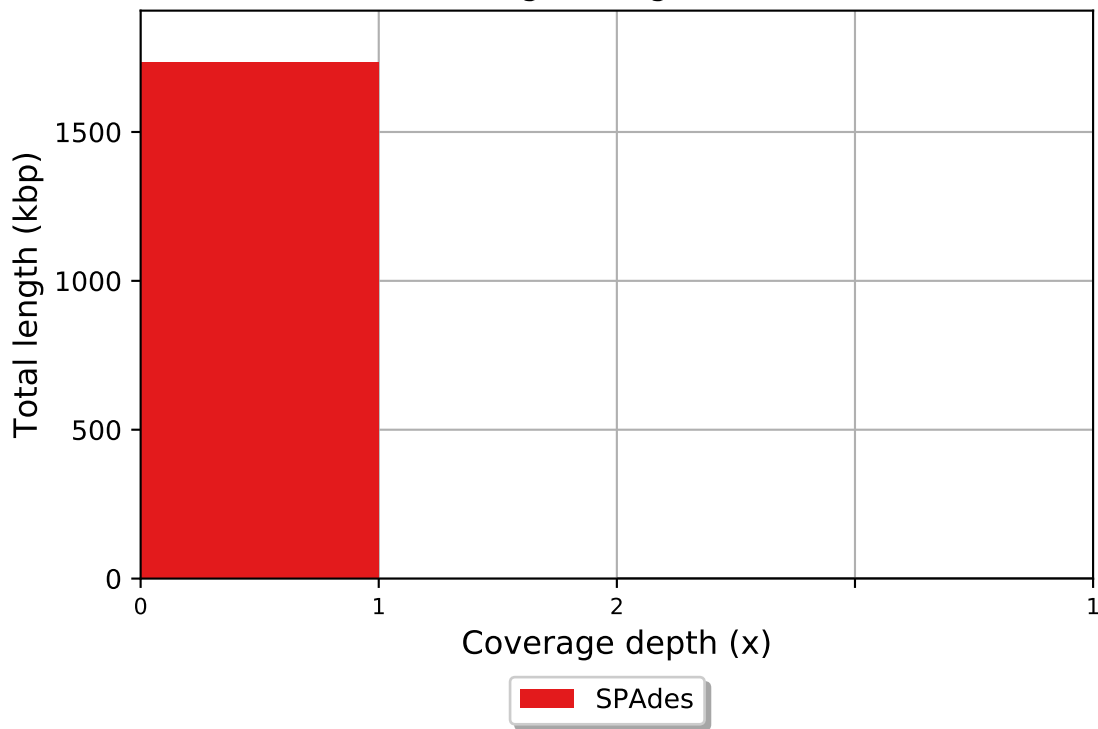
IDBAUD.m1000 GC content



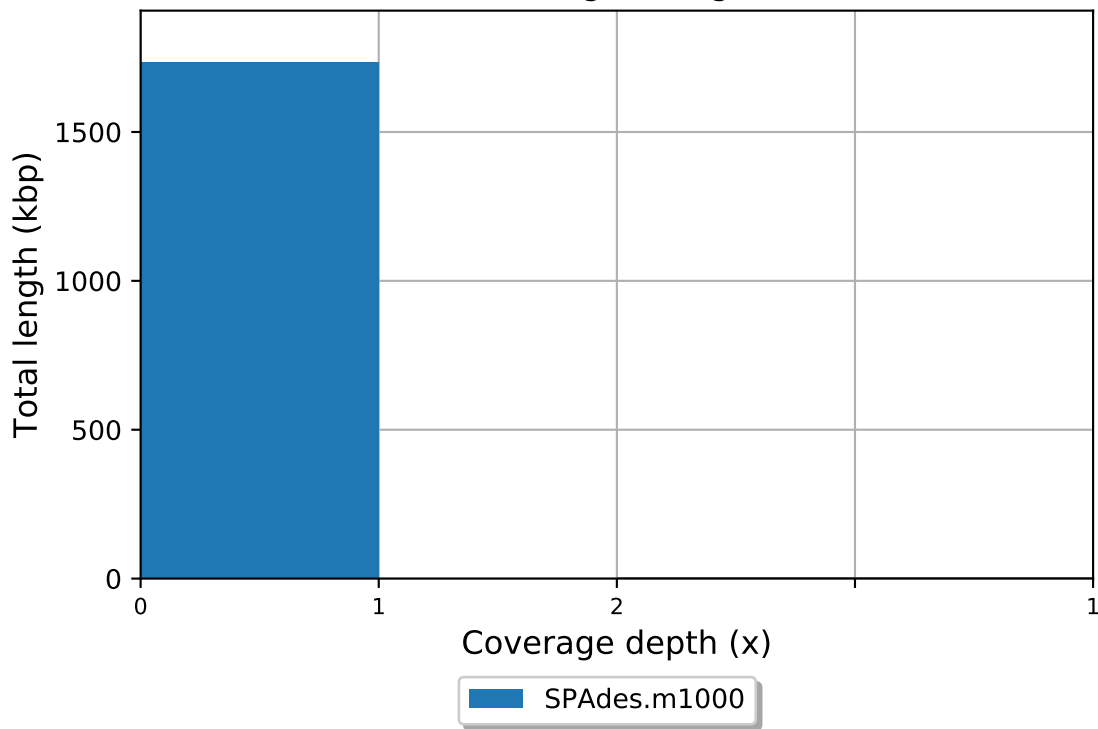
Coverage histogram (bin size: 1x)



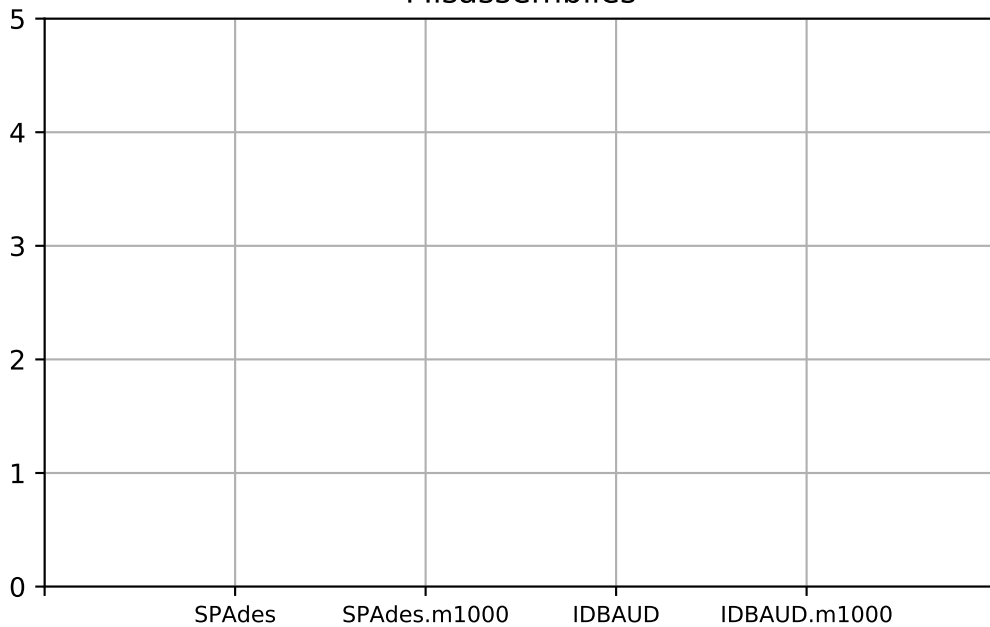
SPAdes coverage histogram (bin size: 1x)



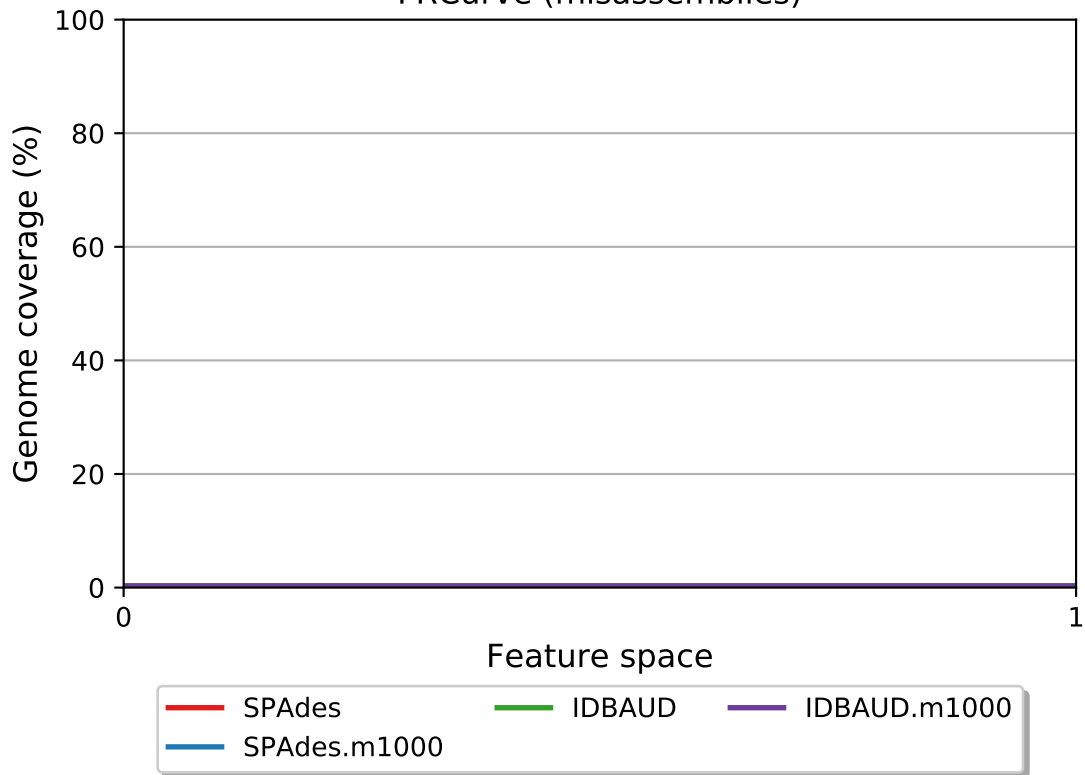
SPAdes.m1000 coverage histogram (bin size: 1x)



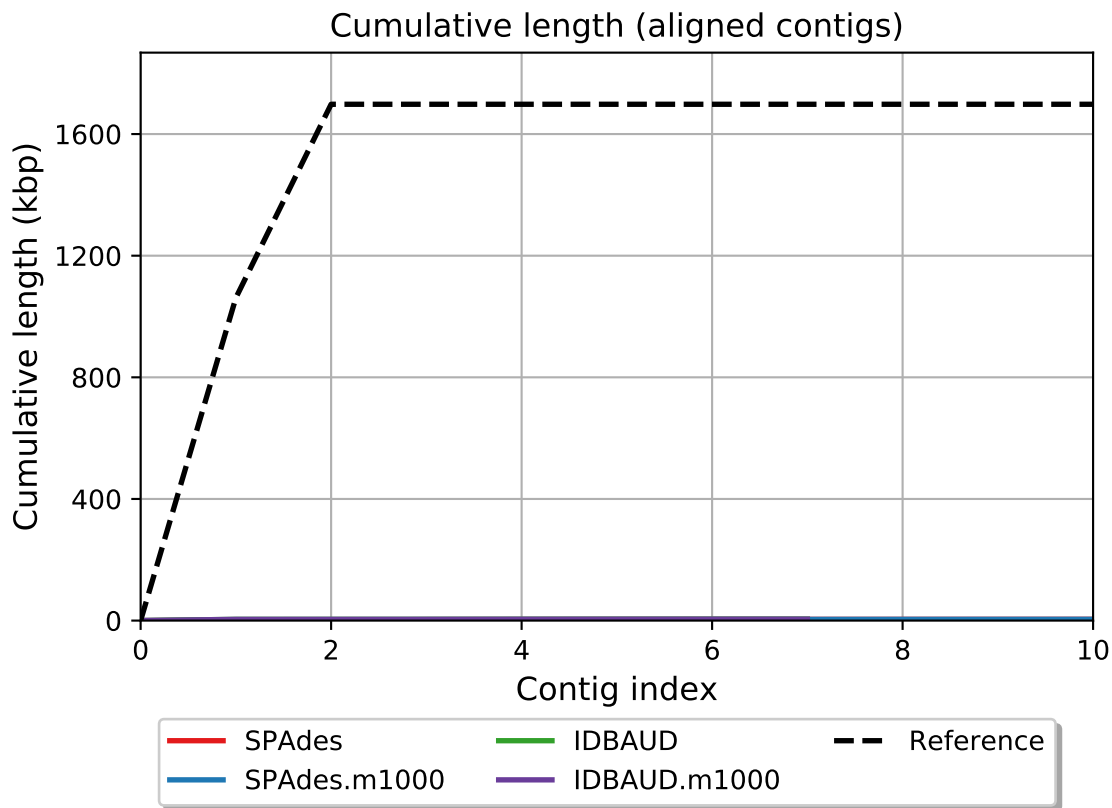
## Misassemblies



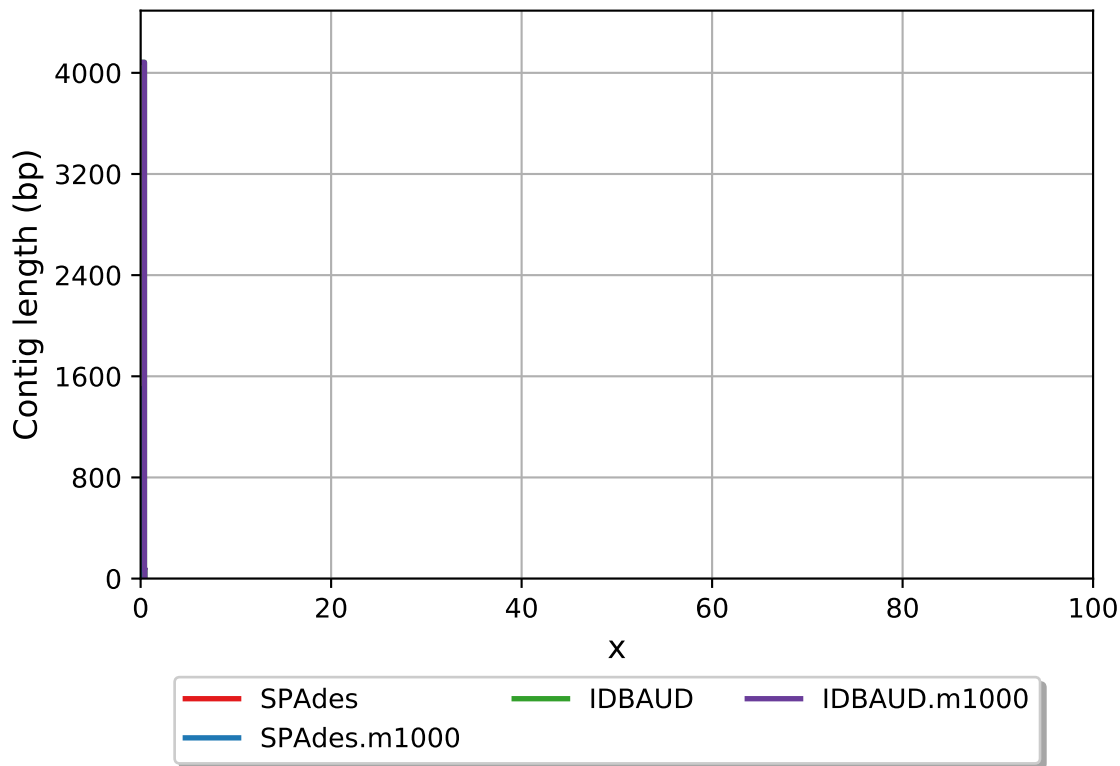
FRCurve (misassemblies)



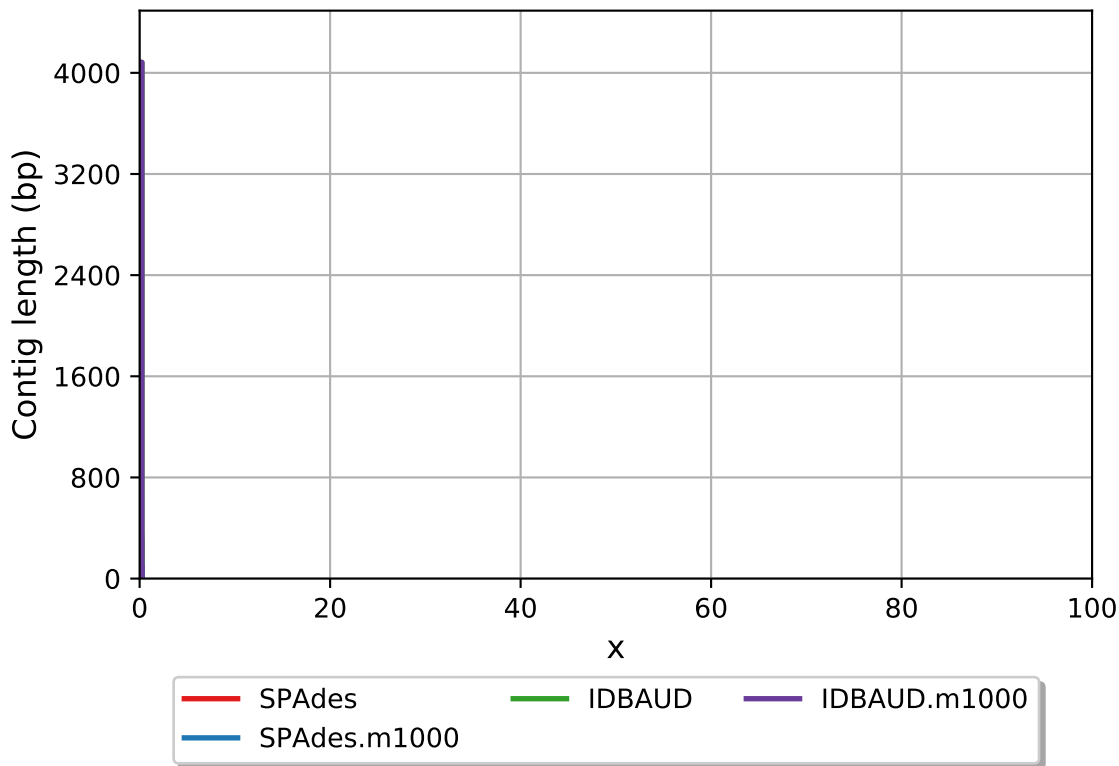




# NAx



# NGAx



# Genome fraction, %

