

# Report

	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	0	11	4	1	11	6	3	1	1
# contigs (>= 5000 bp)	0	2	4	1	9	6	3	1	1
# contigs (>= 10000 bp)	0	2	4	1	9	6	3	1	1
# contigs (>= 25000 bp)	0	2	4	1	9	6	3	1	1
# contigs (>= 50000 bp)	0	2	4	1	9	6	3	1	1
Total length (>= 1000 bp)	0	159024	1233921	1861292	894881	2085856	560810	475637	568045
Total length (>= 5000 bp)	0	142244	1233921	1861292	891581	2085856	560810	475637	568045
Total length (>= 10000 bp)	0	142244	1233921	1861292	891581	2085856	560810	475637	568045
Total length (>= 25000 bp)	0	142244	1233921	1861292	891581	2085856	560810	475637	568045
Total length (>= 50000 bp)	0	142244	1233921	1861292	891581	2085856	560810	475637	568045
# contigs	1	11	4	1	11	6	3	1	1
Largest contig	647	71122	410716	1861292	208158	839617	211364	475637	568045
Total length	647	159024	1233921	1861292	894881	2085856	560810	475637	568045
Reference length	11017	11017	11017	11017	11017	11017	11017	11017	11017
GC (%)	43.28	42.27	41.84	42.74	42.13	42.14	41.79	41.89	41.80
Reference GC (%)	39.79	39.79	39.79	39.79	39.79	39.79	39.79	39.79	39.79
N50	647	71122	350668	1861292	114494	321201	174723	475637	568045
NG50	-	71122	410716	1861292	208158	839617	211364	475637	568045
N75	647	71122	311222	1861292	60816	220902	174723	475637	568045
NG75	-	71122	410716	1861292	208158	839617	211364	475637	568045
LS0	1	2	2	1	3	2	2	1	1
LG50	-	1	1	1	1	1	1	1	1
L75	1	2	3	1	6	4	3	1	1
LG75	-	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	1	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	1	0	0	0	1	1
# unaligned contigs	0 + 0 part	0 + 6 part	0 + 4 part	0 + 1 part	0 + 9 part	0 + 6 part	0 + 3 part	0 + 1 part	0 + 1 part
Unaligned length	0	144646	1211677	1850275	868993	2052805	554873	464619	556640
Genome fraction (%)	5.873	49.850	100.000	100.000	100.000	100.000	53.027	100.000	100.000
Duplication ratio	1.000	2.618	2.019	1.000	2.350	3.000	1.016	1.000	1.035
# N's per 100 kbp	0.00	881.63	17.02	0.00	0.00	0.00	0.00	0.21	68.30
# mismatches per 100 kbp	0.00	1256.37	0.00	0.00	1452.30	0.00	0.00	199.69	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	108.92	0.00	68.47	0.00	0.00
Largest alignment	647	2885	5747	5747	5747	5747	5747	5747	5747
Total aligned length	647	11395	22034	11017	25887	33051	5937	11017	11017
NA50	647	-	-	-	-	-	-	-	-
NGA50	-	988	5747	5747	5747	5747	5747	5747	5747
NA75	647	-	-	-	-	-	-	-	-
NGA75	-	798	5747	5270	5270	5747	-	5270	5270
LA50	1	-	-	-	-	-	-	-	-
LGA50	-	3	1	1	1	1	1	1	1
LA75	1	-	-	-	-	-	-	-	-
LGA75	-	6	2	2	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

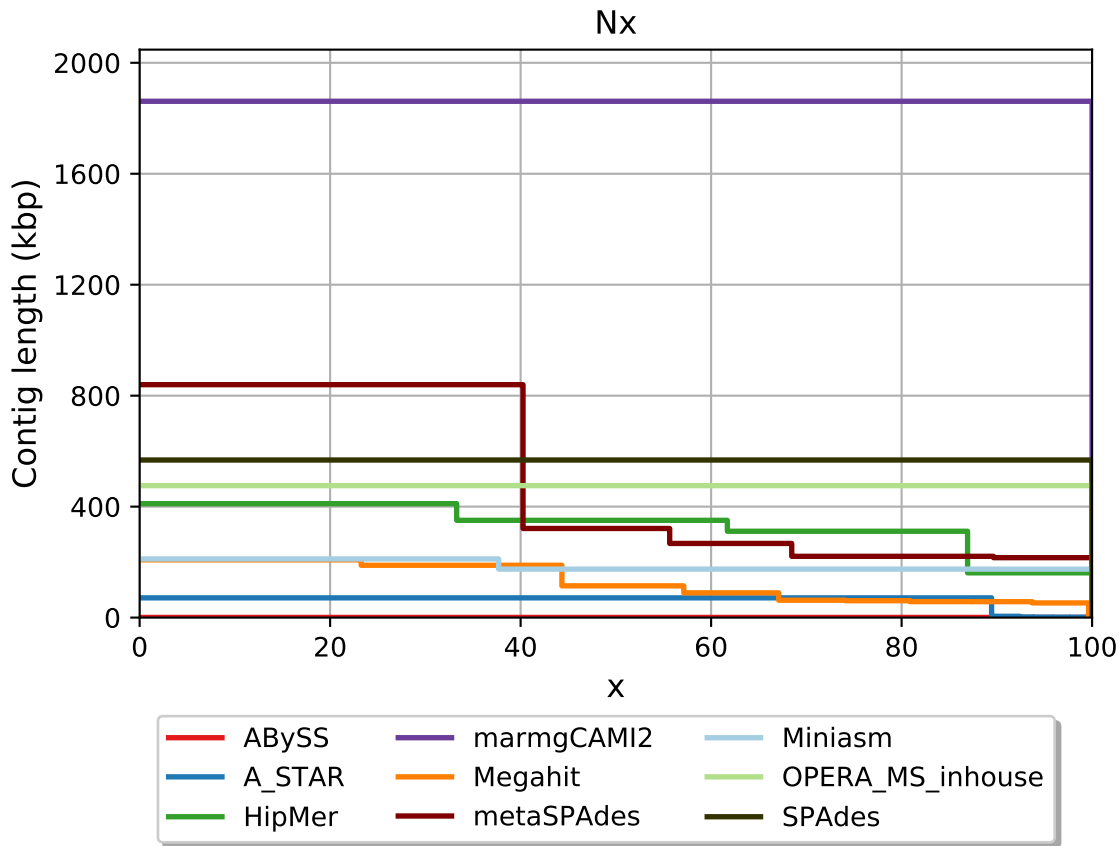
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0
# possibly misassembled contigs	0	6	4	0	9	6	3	0	0
# possible misassemblies	0	6	8	0	12	12	4	0	0
# local misassemblies	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	1	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	1	0	0	0	1	1
# mismatches	0	69	0	0	160	0	0	22	0
# indels	0	0	0	0	12	0	4	0	0
# indels (<= 5 bp)	0	0	0	0	10	0	4	0	0
# indels (> 5 bp)	0	0	0	0	2	0	0	0	0
Indels length	0	0	0	0	72	0	4	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).

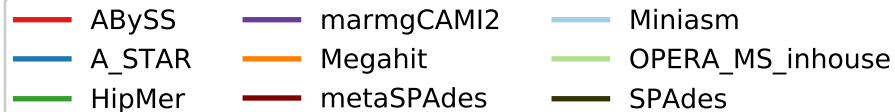
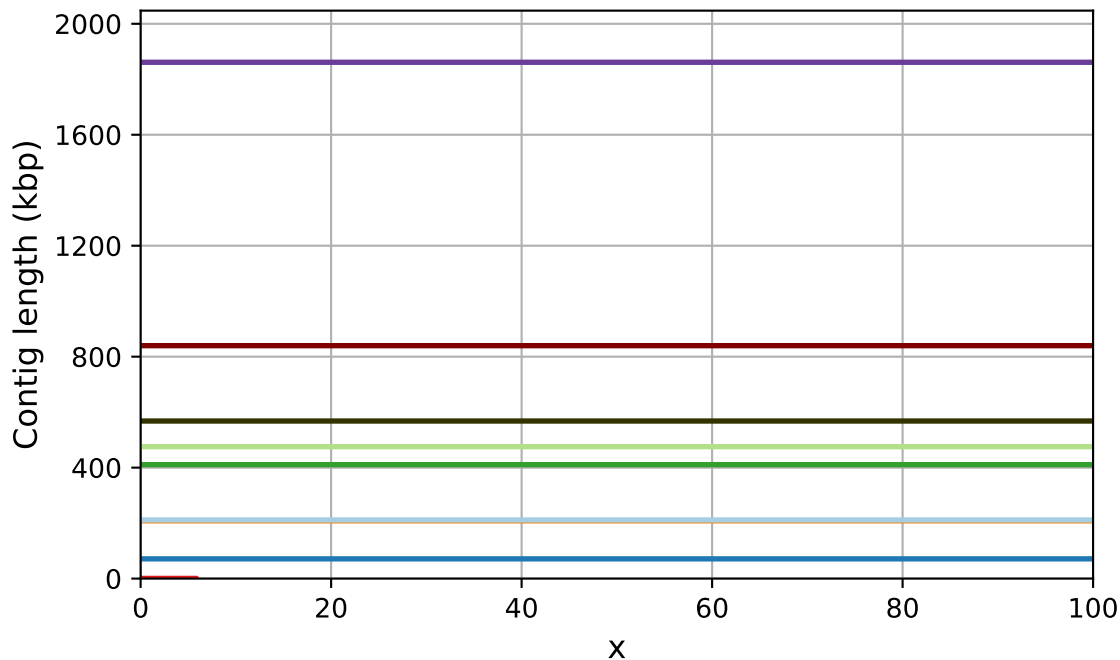
## Unaligned report

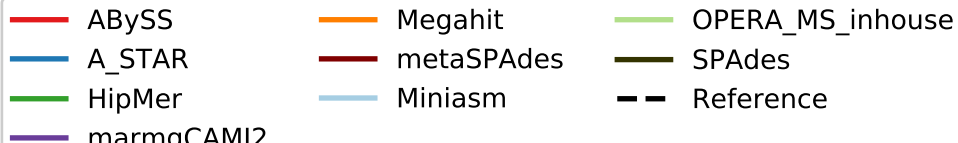
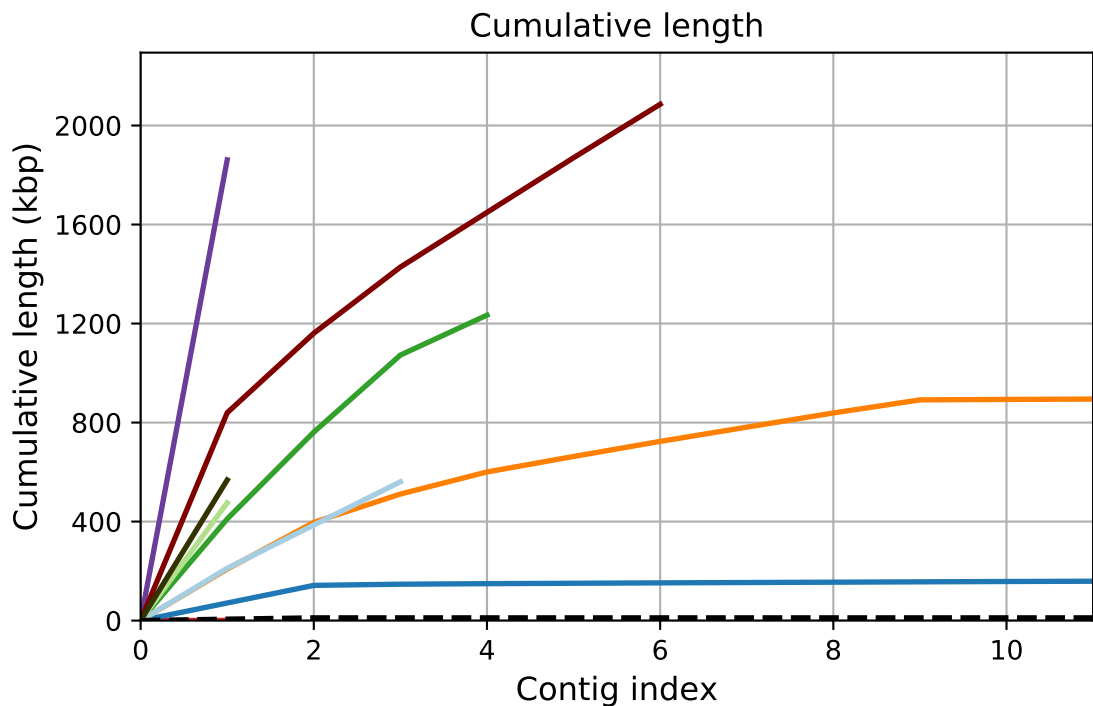
	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	0	6	4	1	9	6	3	1	1
Partially unaligned length	0	144646	1211677	1850275	868993	2052805	554873	464619	556640
# N's	0	1402	210	0	0	0	0	1	388

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).

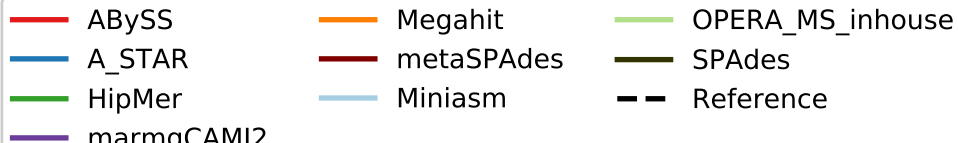
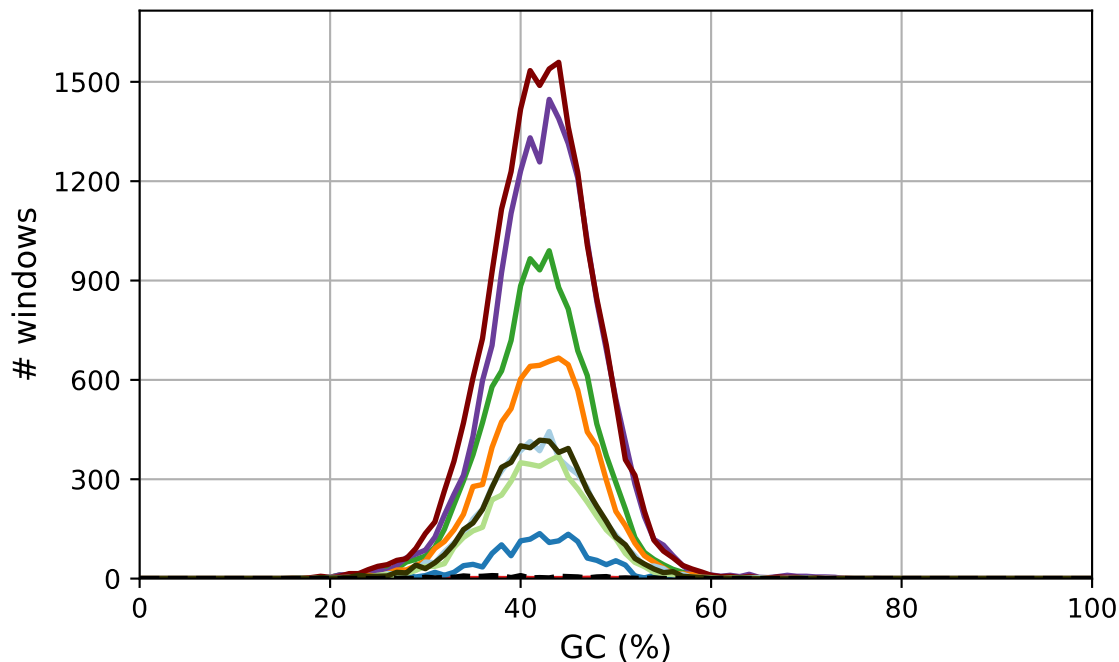


# NGx

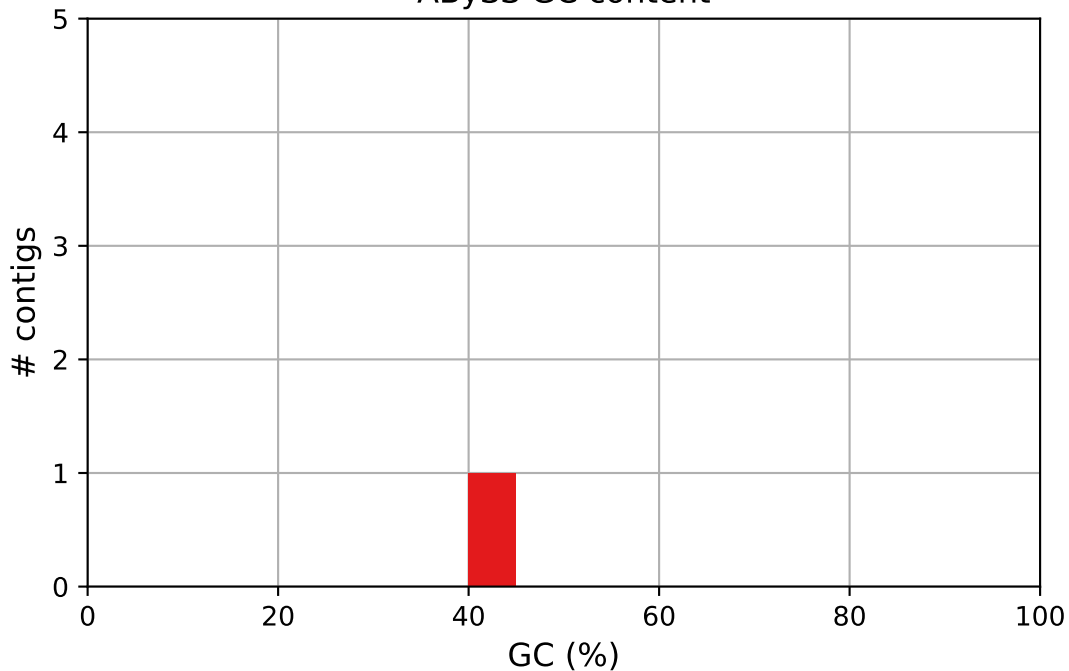




# GC content



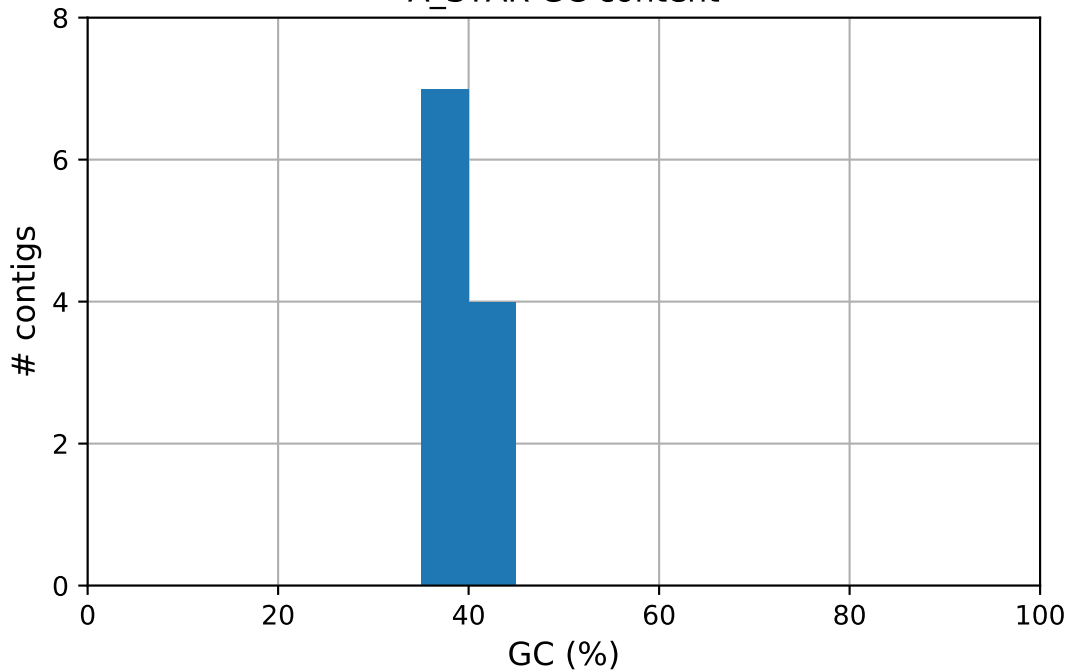
# ABySS GC content



ABySS

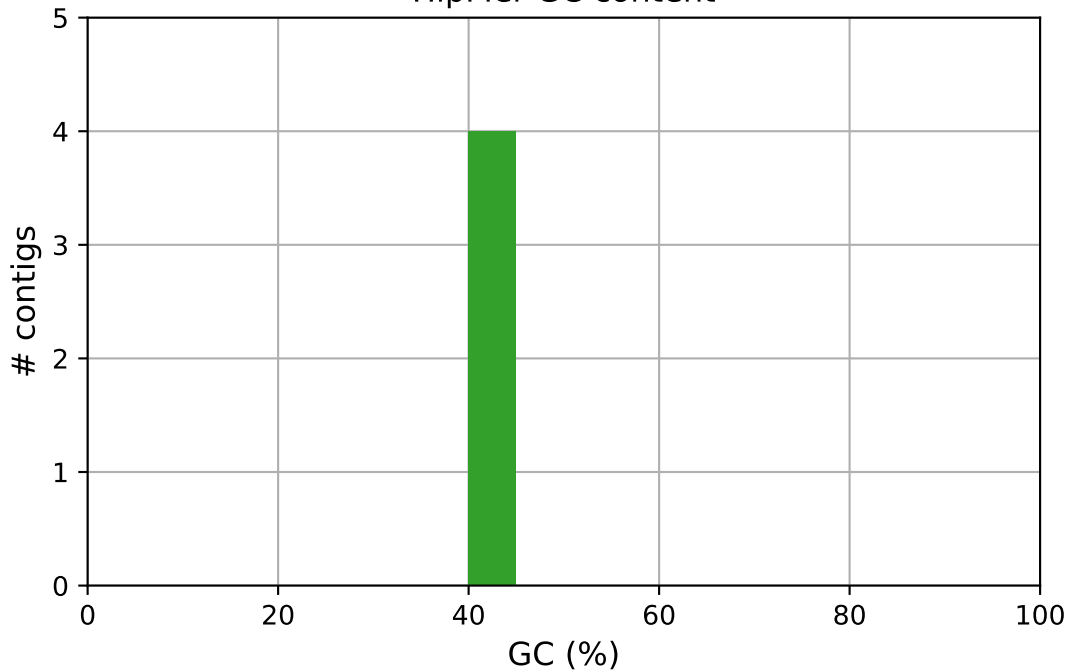


A\_STAR GC content



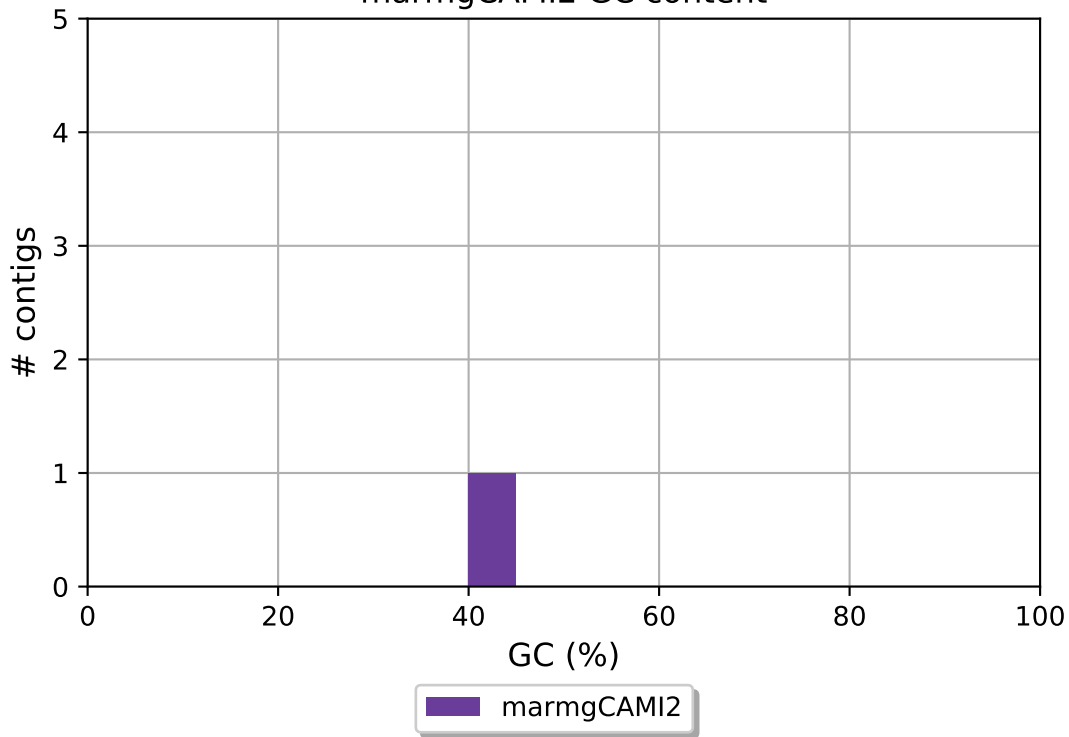
A\_STAR

HipMer GC content

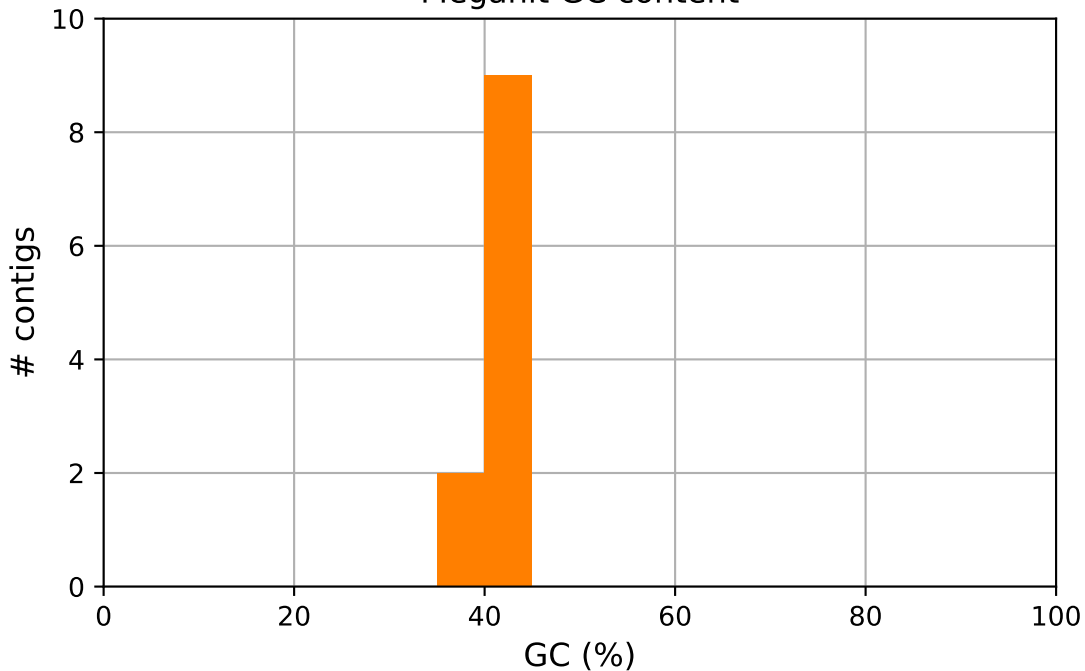


HipMer

marmgCAMI2 GC content

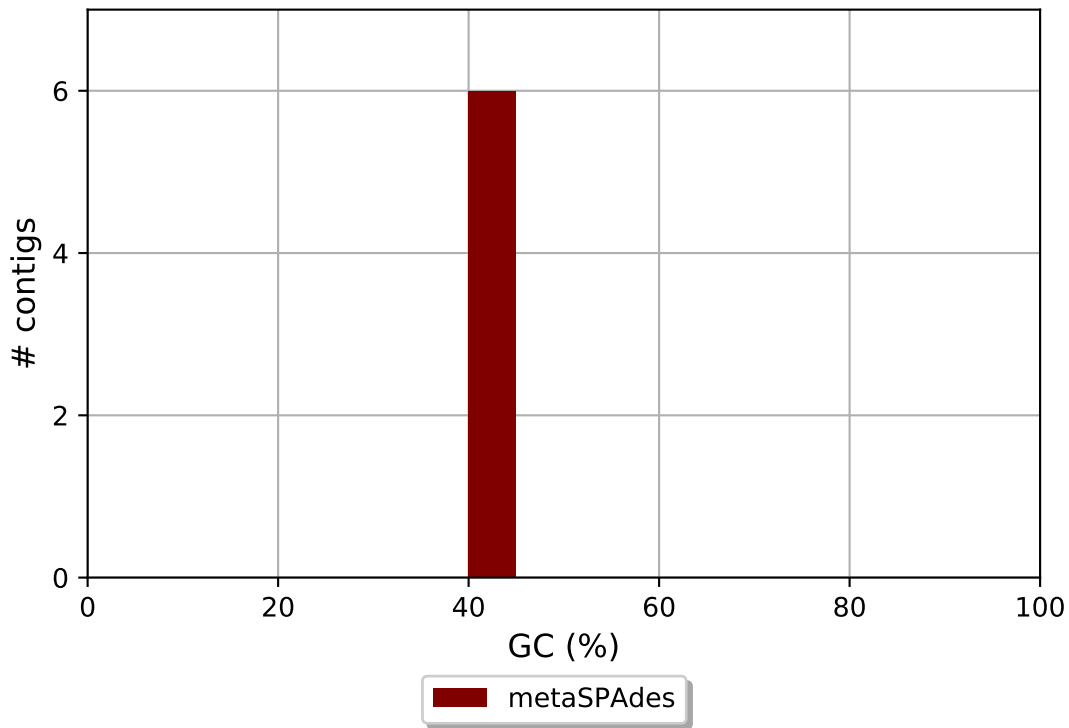


Megahit GC content

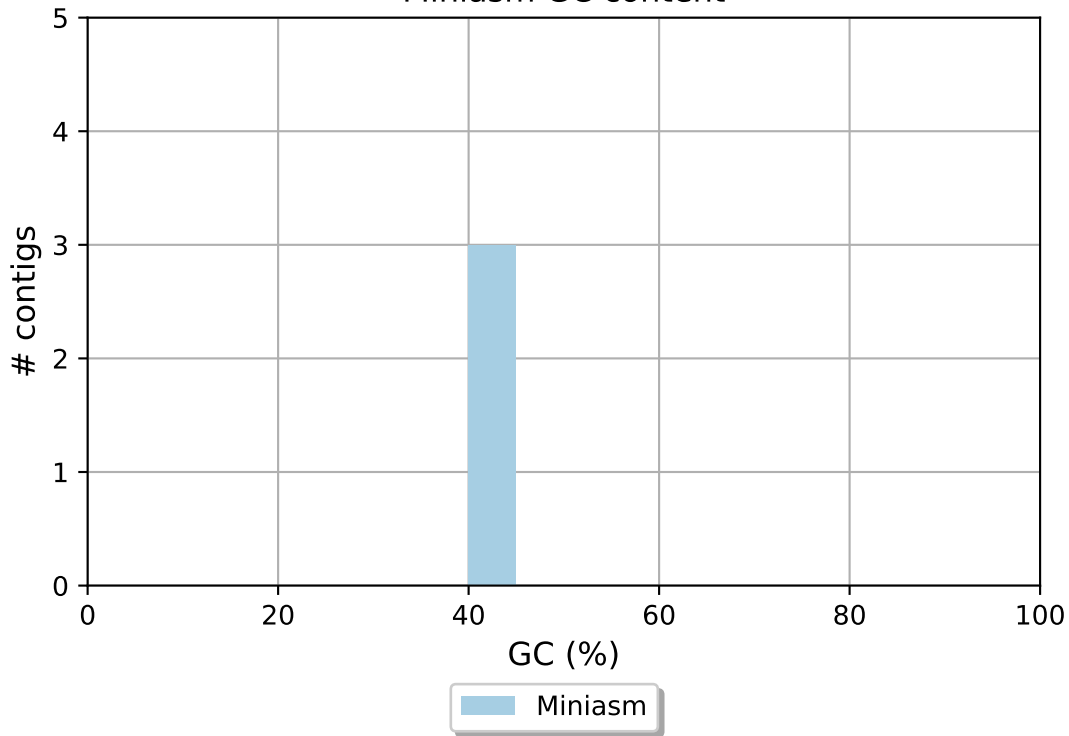


Megahit

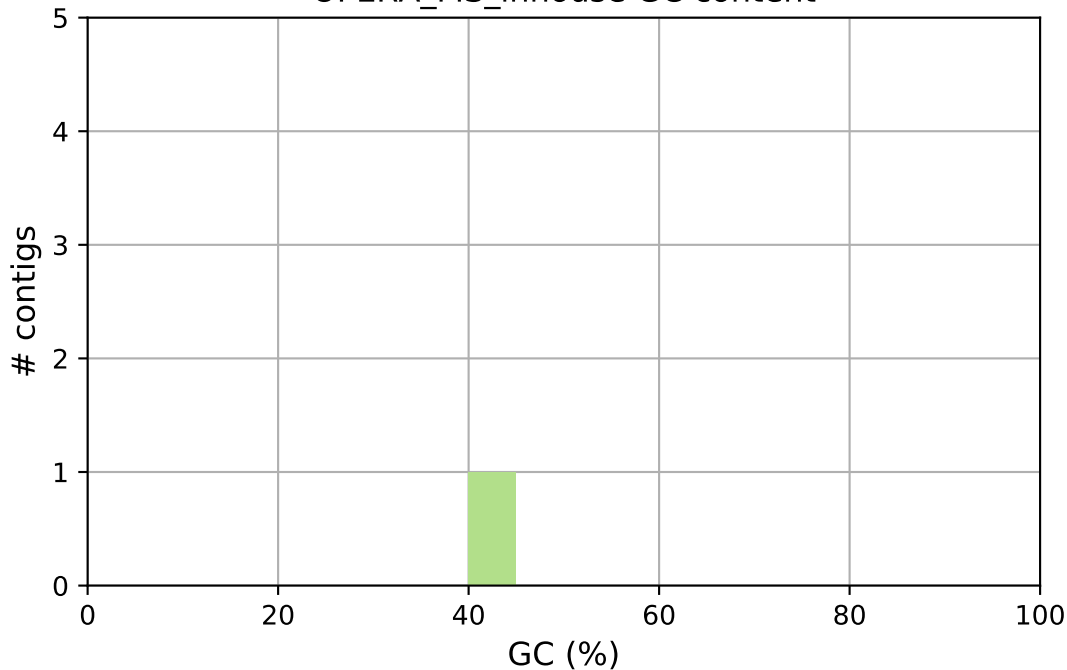
metaSPAdes GC content



Miniasm GC content

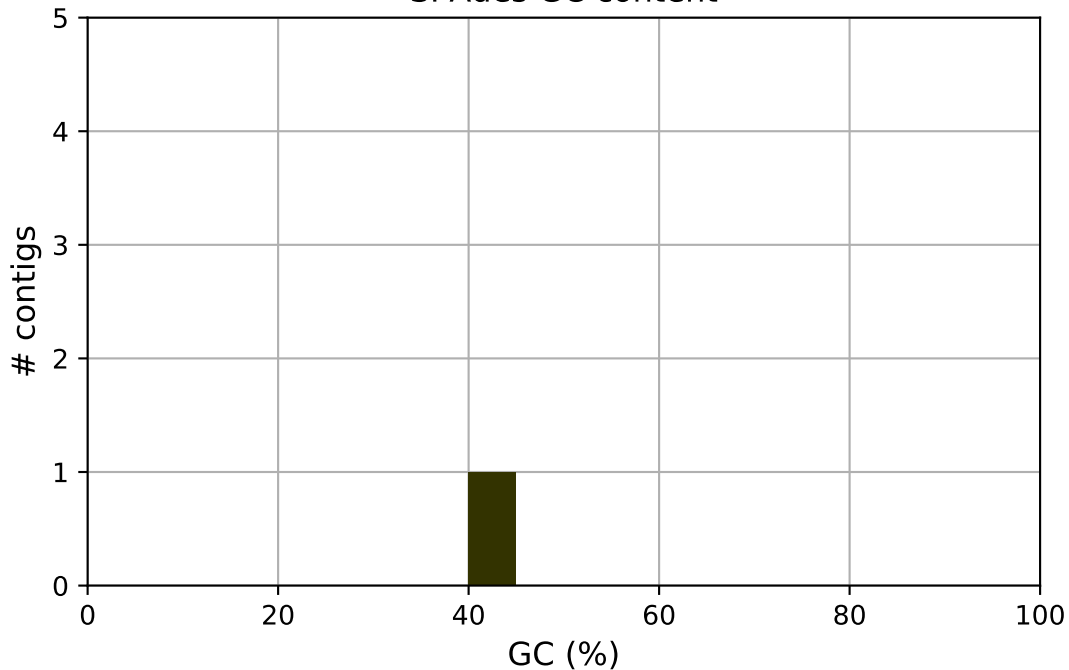


OPERA\_MS\_inhouse GC content



OPERA\_MS\_inhouse

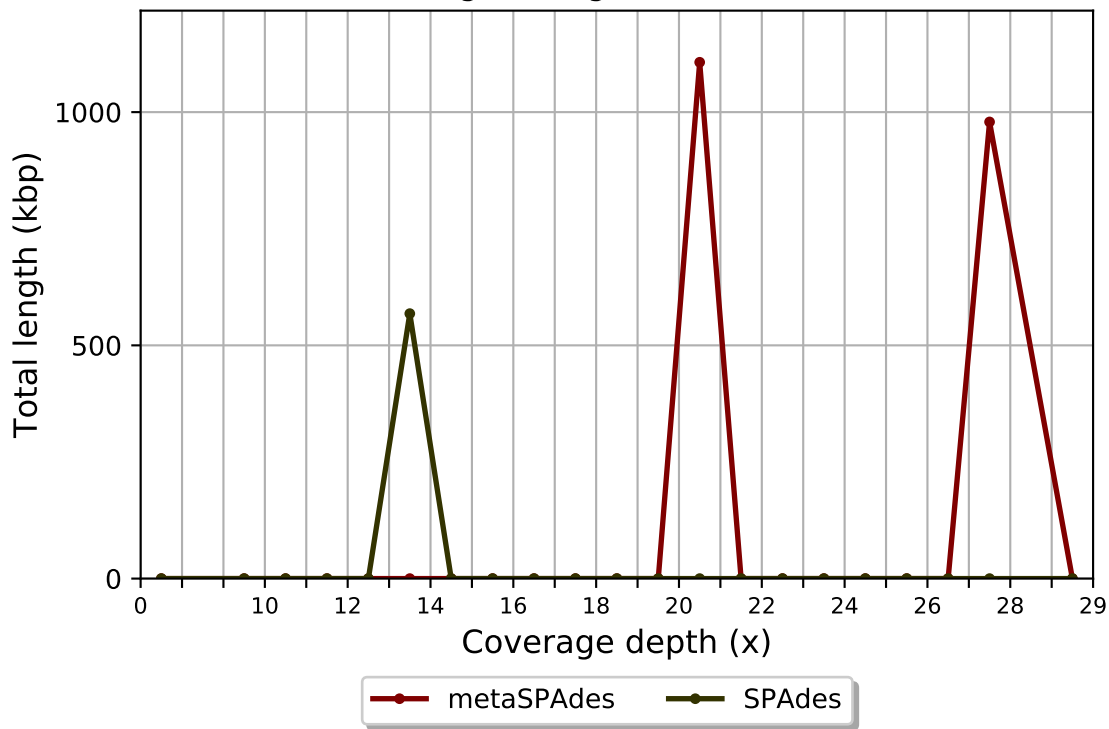
# SPAdes GC content



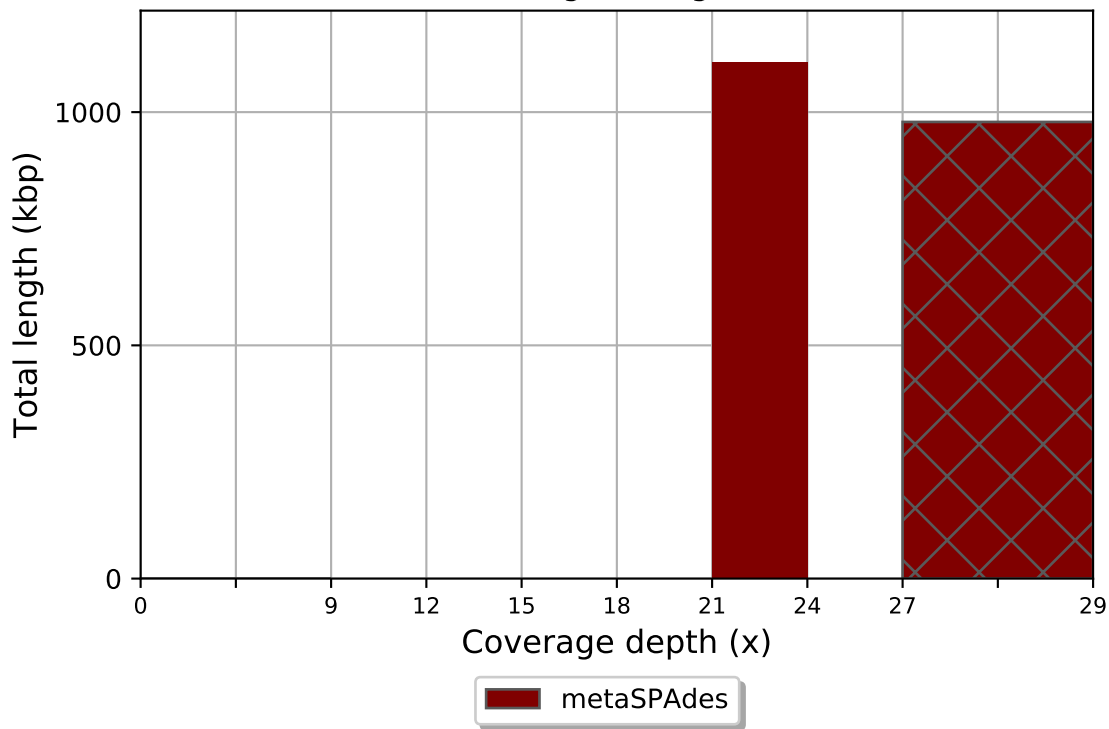
SPAdes



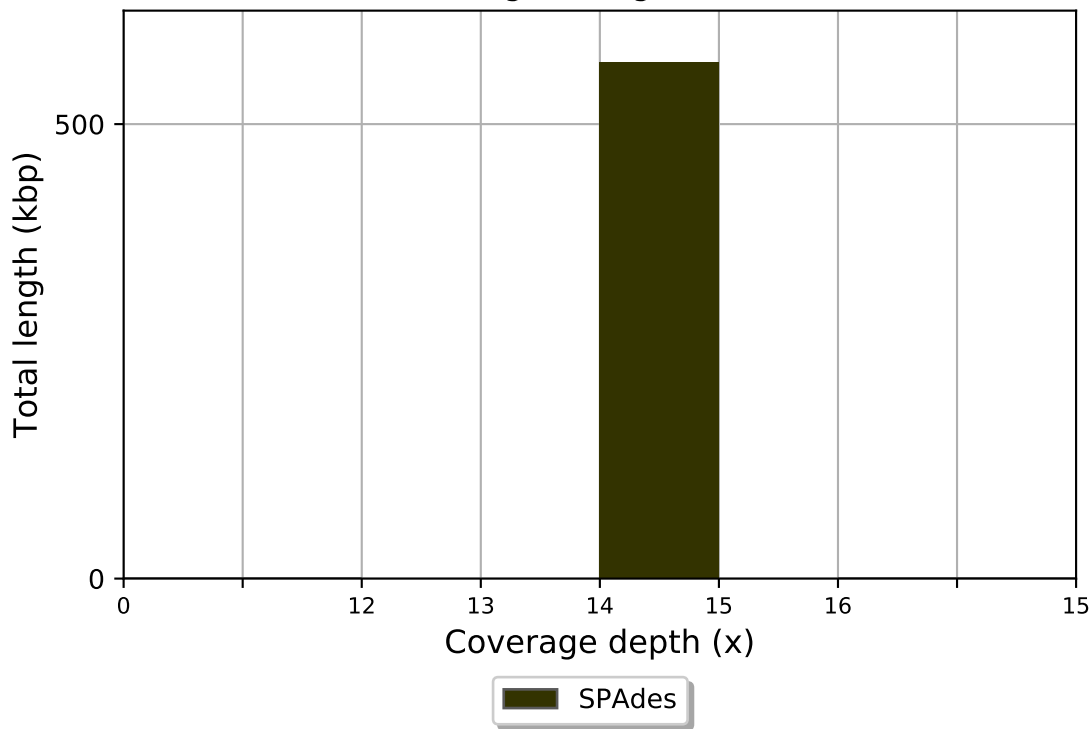
Coverage histogram (bin size: 1x)



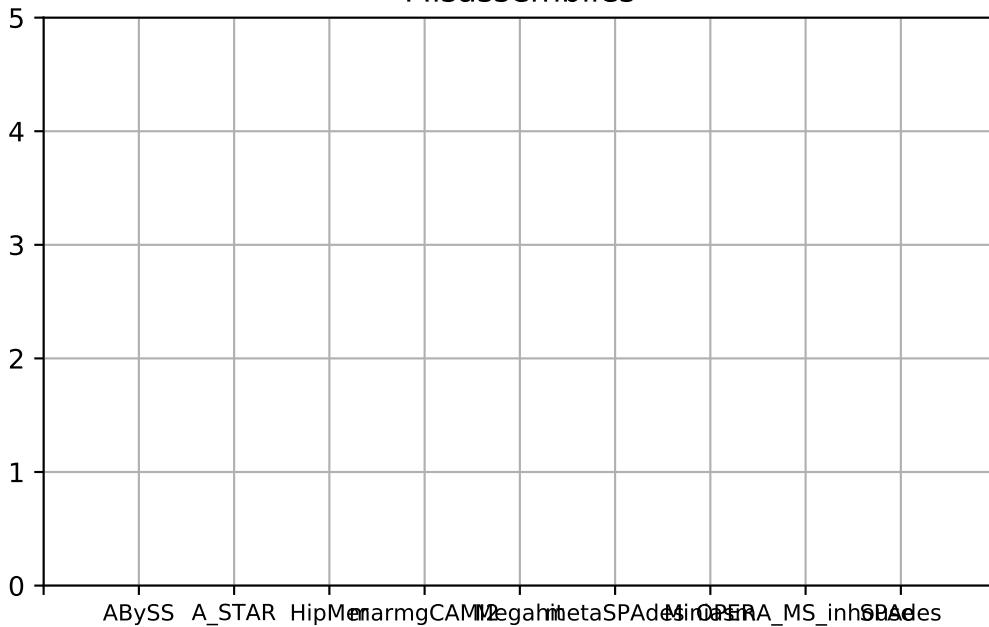
metaSPAdes coverage histogram (bin size: 3x)



SPAdes coverage histogram (bin size: 1x)



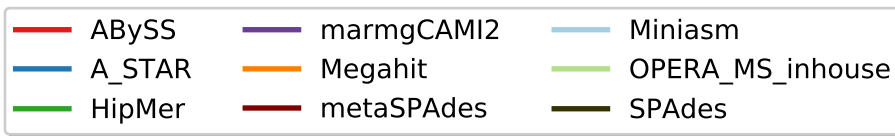
# Misassemblies



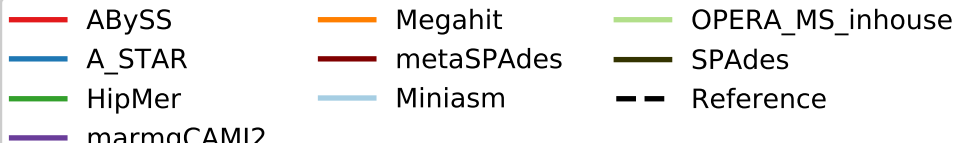
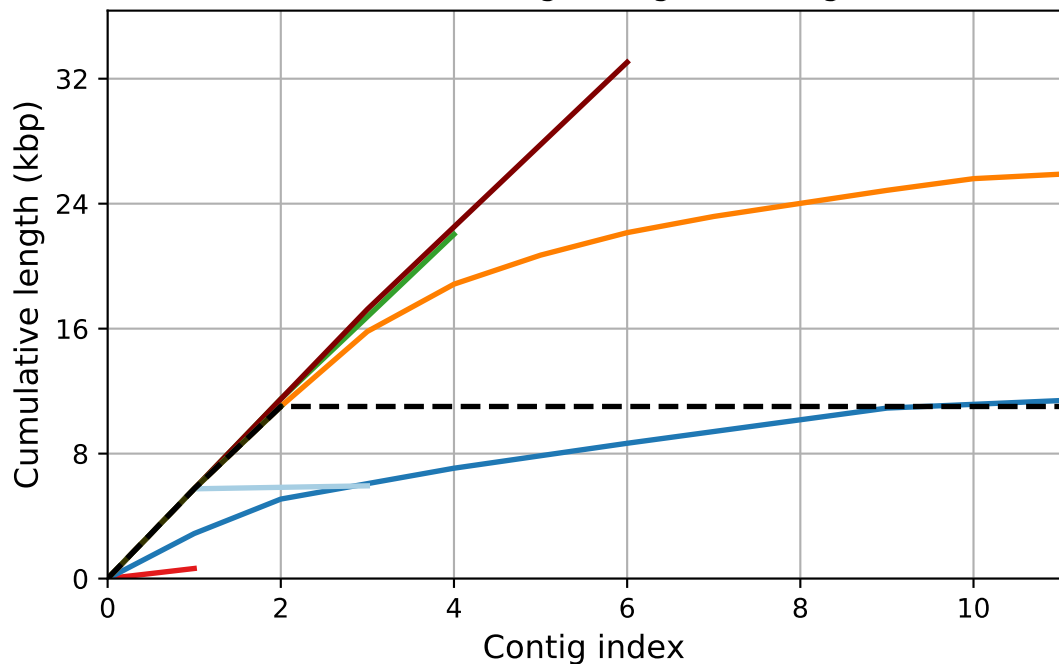
# FRCurve (misassemblies)



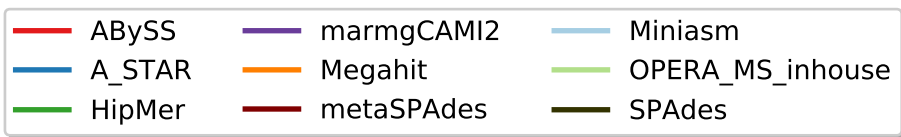
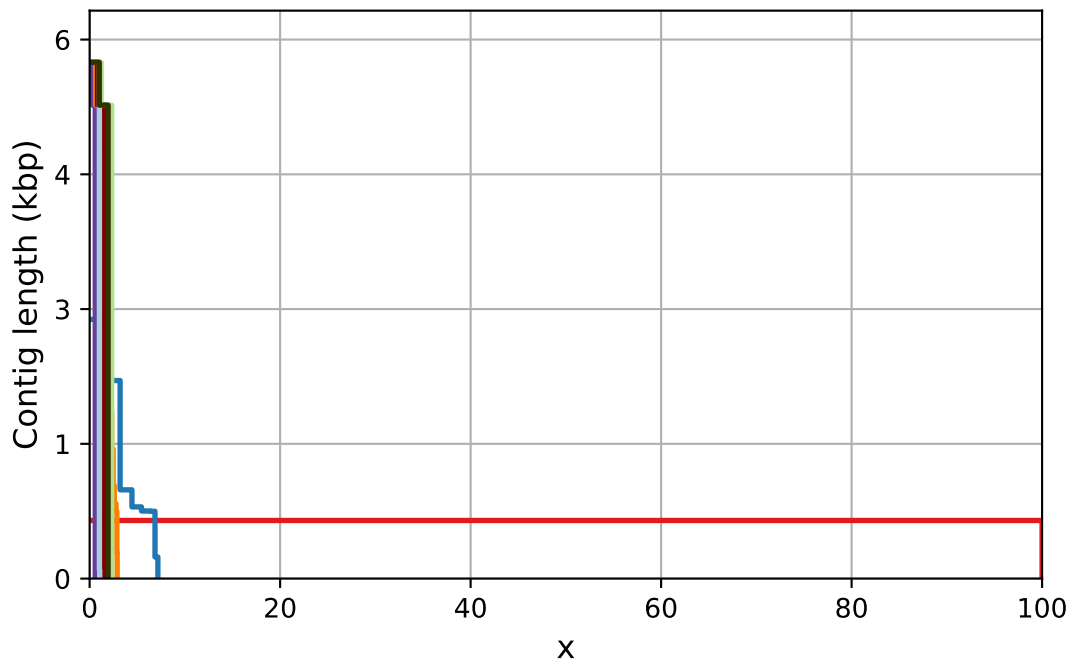
Feature space



Cumulative length (aligned contigs)



# NAX



# NGAx

