

# Report

	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	0	14	12	1	18	12	7	5	5
# contigs (>= 5000 bp)	0	12	12	1	18	12	7	5	4
# contigs (>= 10000 bp)	0	10	11	1	15	12	7	5	4
# contigs (>= 25000 bp)	0	8	10	1	11	9	7	5	2
# contigs (>= 50000 bp)	0	2	6	1	7	6	4	5	1
Total length (>= 1000 bp)	0	383850	635843	2269117	811083	637696	469564	987916	121056
Total length (>= 5000 bp)	0	379080	635843	2269117	811083	637696	469564	987916	117010
Total length (>= 10000 bp)	0	365306	627406	2269117	790810	637696	469564	987916	117010
Total length (>= 25000 bp)	0	330500	606652	2269117	709074	585244	469564	987916	79061
Total length (>= 50000 bp)	0	119776	485571	2269117	549144	462402	355240	987916	52820
# contigs	1	14	12	1	20	12	7	5	5
Largest contig	511	59888	114138	2269117	99683	104406	112186	362693	52820
Total length	511	383850	635843	2269117	812629	637696	469564	987916	121056
Reference length	10583	10583	10583	10583	10583	10583	10583	10583	10583
GC (%)	50.68	67.09	67.15	68.08	67.26	66.64	66.71	67.61	67.13
Reference GC (%)	60.27	60.27	60.27	60.27	60.27	60.27	60.27	60.27	60.27
N50	511	49327	69915	2269117	70106	69690	79652	185526	26241
NG50	-	59888	114138	2269117	99683	104406	112186	362693	52820
N75	511	25319	59096	2269117	47554	47723	69341	153643	22334
NG75	-	59888	114138	2269117	99683	104406	112186	362693	52820
L50	1	4	4	1	5	4	3	2	2
LG50	-	1	1	1	1	1	1	1	1
L75	1	7	6	1	9	7	4	4	3
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	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	2	0	1	1	0	0	2	0
# unaligned contigs	0 + 0 part	0 + 14 part	0 + 12 part	0 + 1 part	0 + 18 part	0 + 12 part	0 + 7 part	0 + 5 part	0 + 5 part
Unaligned length	0	373850	614666	2258534	786339	606016	458705	977302	110313
Genome fraction (%)	4.828	47.879	99.717	100.000	100.000	100.000	100.000	99.348	100.000
Duplication ratio	1.000	1.974	2.007	1.000	2.484	2.993	1.026	1.010	1.015
# N's per 100 kbp	0.00	1.04	0.00	0.00	0.00	0.00	0.00	0.20	0.00
# mismatches per 100 kbp	0.00	78.94	0.00	0.00	1096.10	0.00	9.45	275.82	56.69
# indels per 100 kbp	0.00	39.47	0.00	0.00	9.45	9.45	18.90	0.00	0.00
Largest alignment	511	1779	3455	3455	3455	3455	3455	3446	3455
Total aligned length	511	9996	21177	10583	26240	31680	10859	10612	10743
NA50	511	-	-	-	-	-	-	-	-
NGA50	-	585	3446	3446	2789	3455	3446	2201	2658
NA75	511	-	-	-	-	-	-	-	-
NGA75	-	389	3198	1848	1933	3455	1848	1490	1848
LA50	1	-	-	-	-	-	-	-	-
LGA50	-	5	2	2	2	2	2	2	2
LA75	1	-	-	-	-	-	-	-	-
LGA75	-	9	3	3	3	3	3	4	3

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

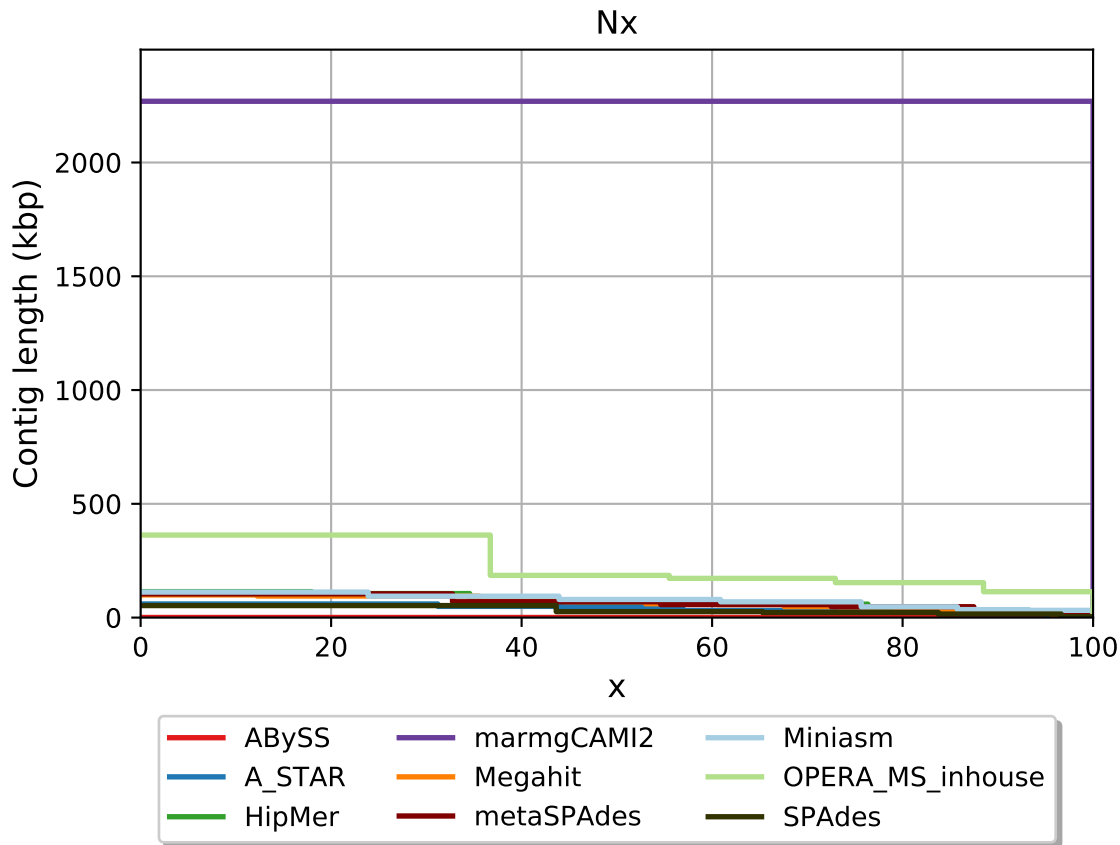
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	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	12	12	0	17	12	7	3	5
# possible misassemblies	0	14	16	0	22	24	14	5	7
# 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	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	2	0	1	1	0	0	2	0
# mismatches	0	4	0	0	116	0	1	29	6
# indels	0	2	0	0	1	1	2	0	0
# indels (<= 5 bp)	0	0	0	0	0	0	2	0	0
# indels (> 5 bp)	0	2	0	0	1	1	0	0	0
Indels length	0	138	0	0	69	69	2	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).

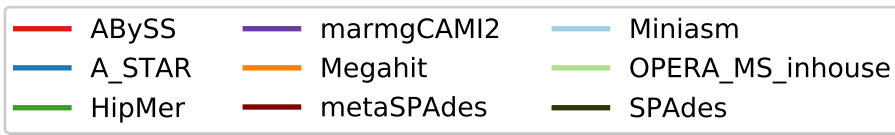
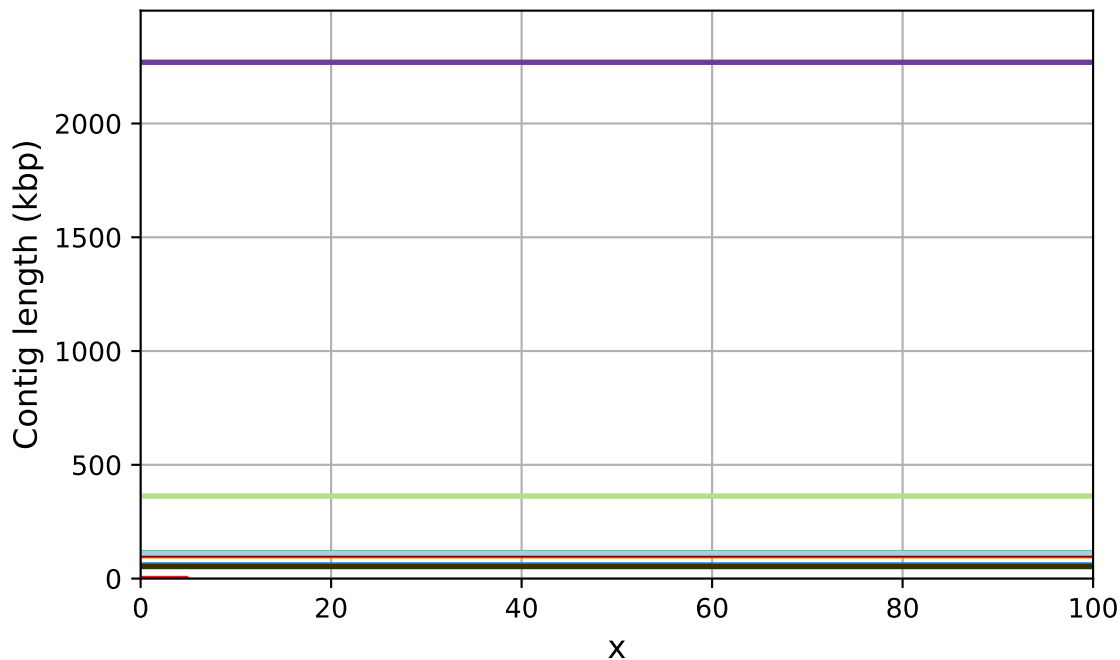
## Unaligned report

	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	14	12	1	18	12	7	5	5
Partially unaligned length	0	373850	614666	2258534	786339	606016	458705	977302	110313
# N's	0	4	0	0	0	0	0	2	0

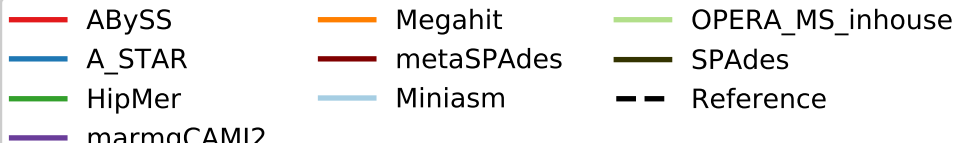
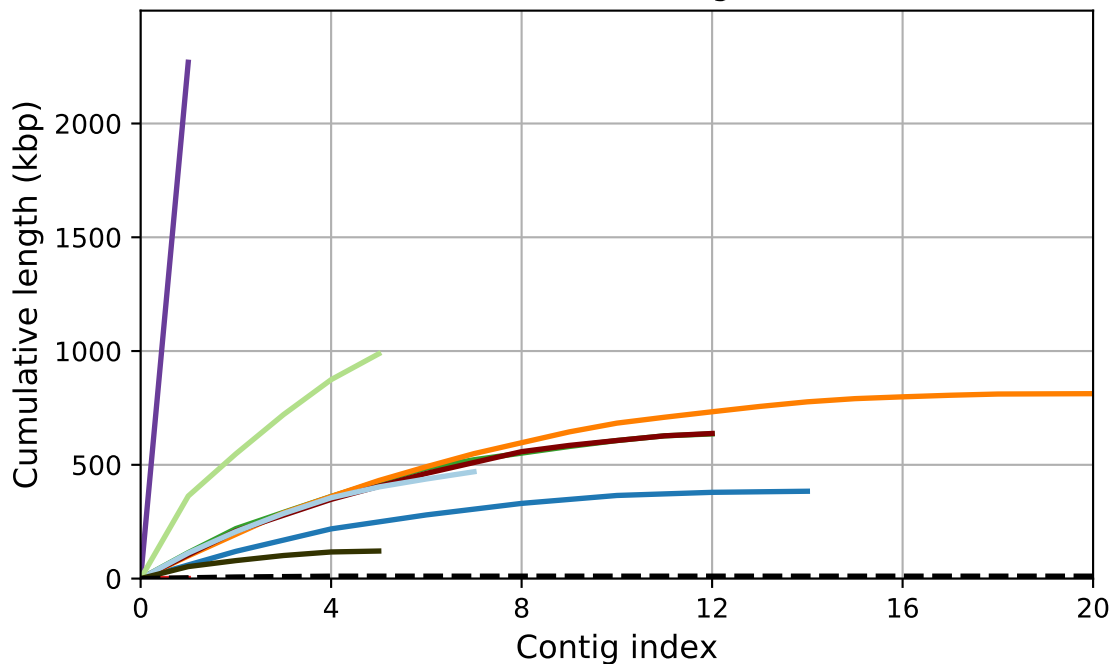
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



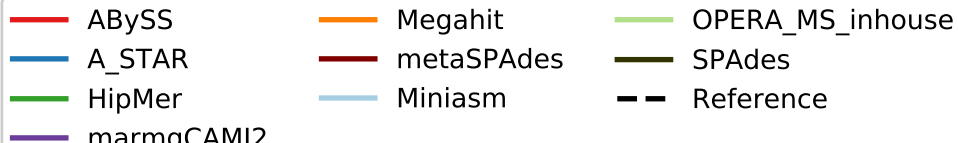
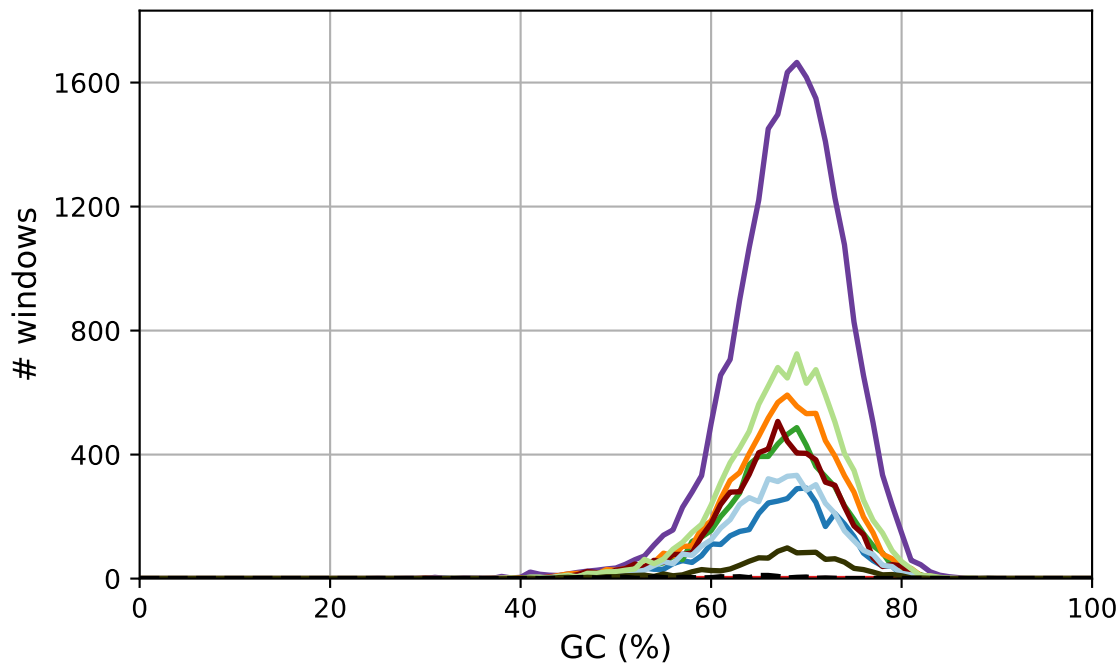
# NGx



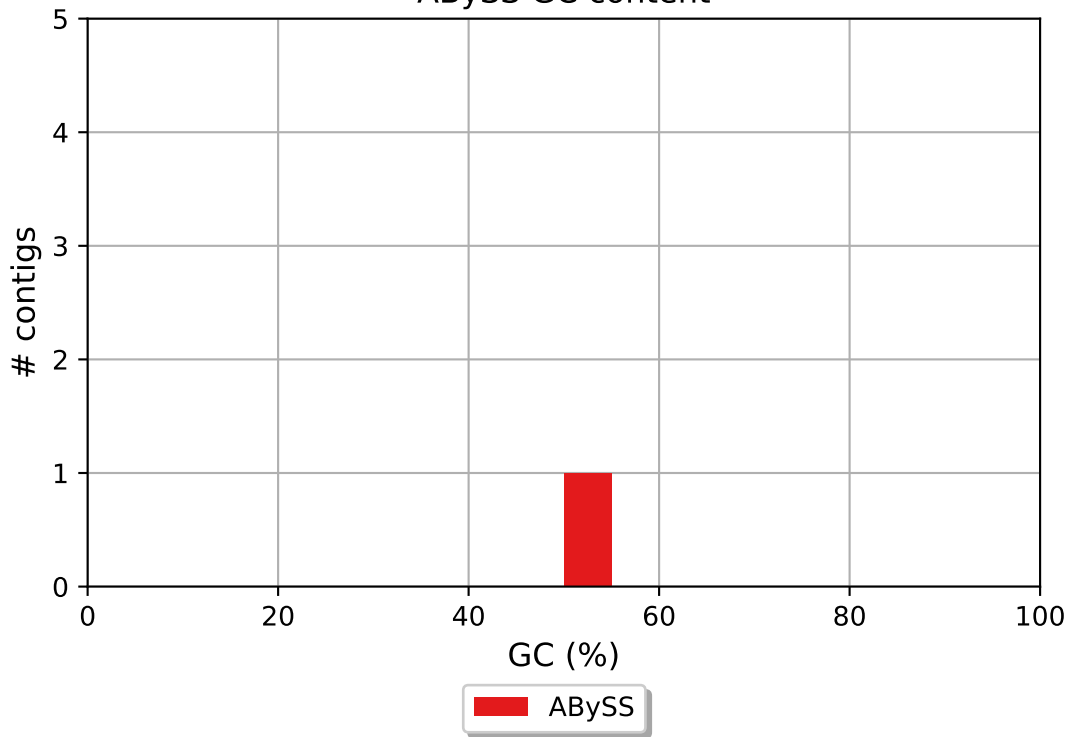
# Cumulative length



GC content

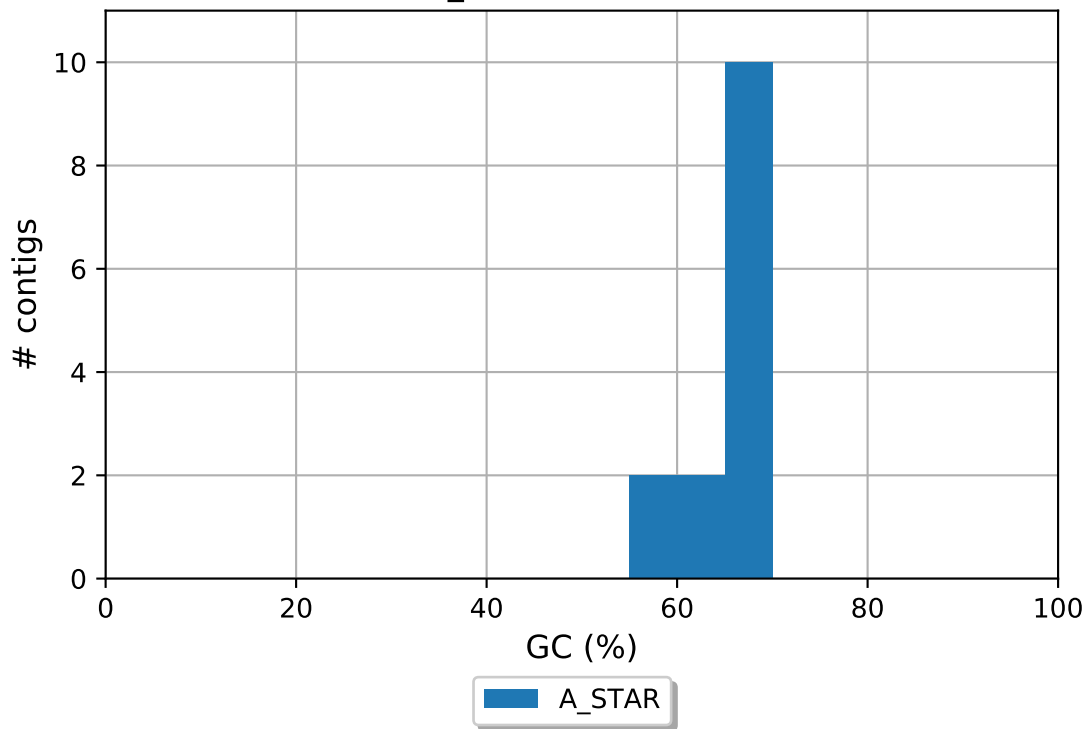


# ABySS GC content

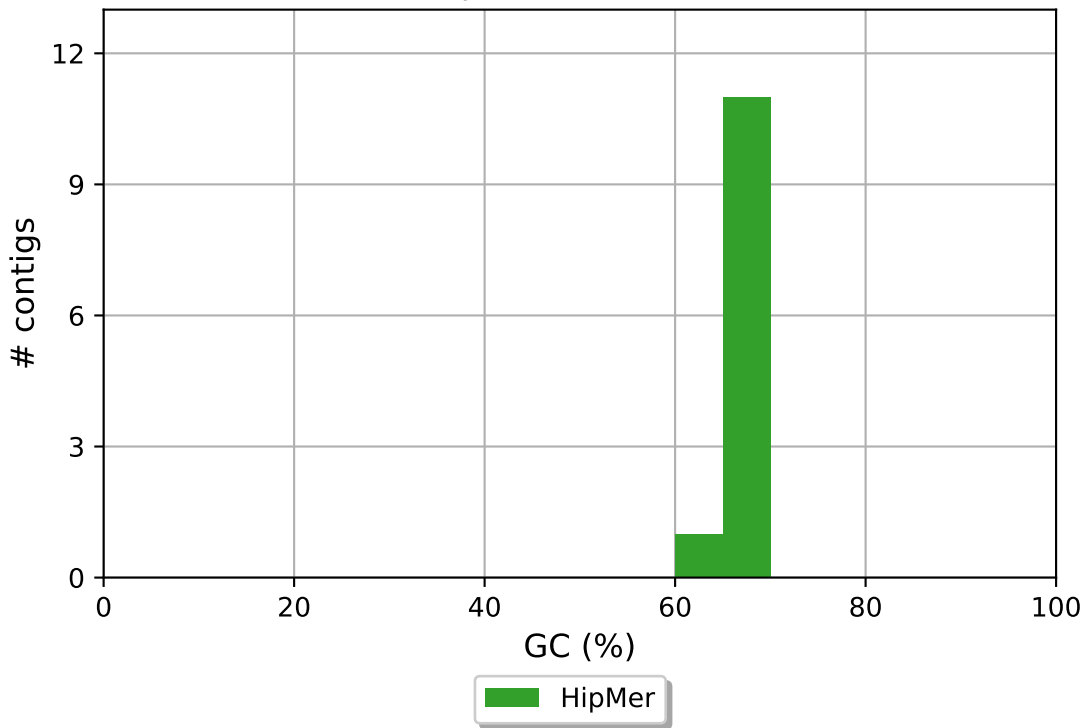




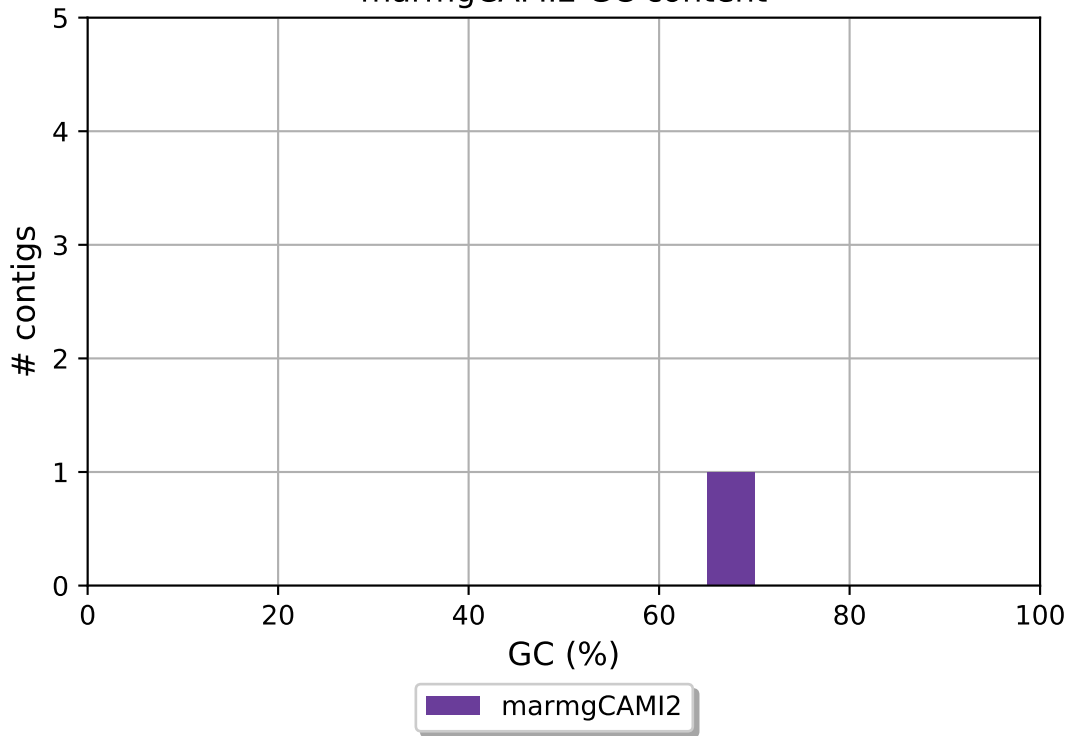
A\_STAR GC content



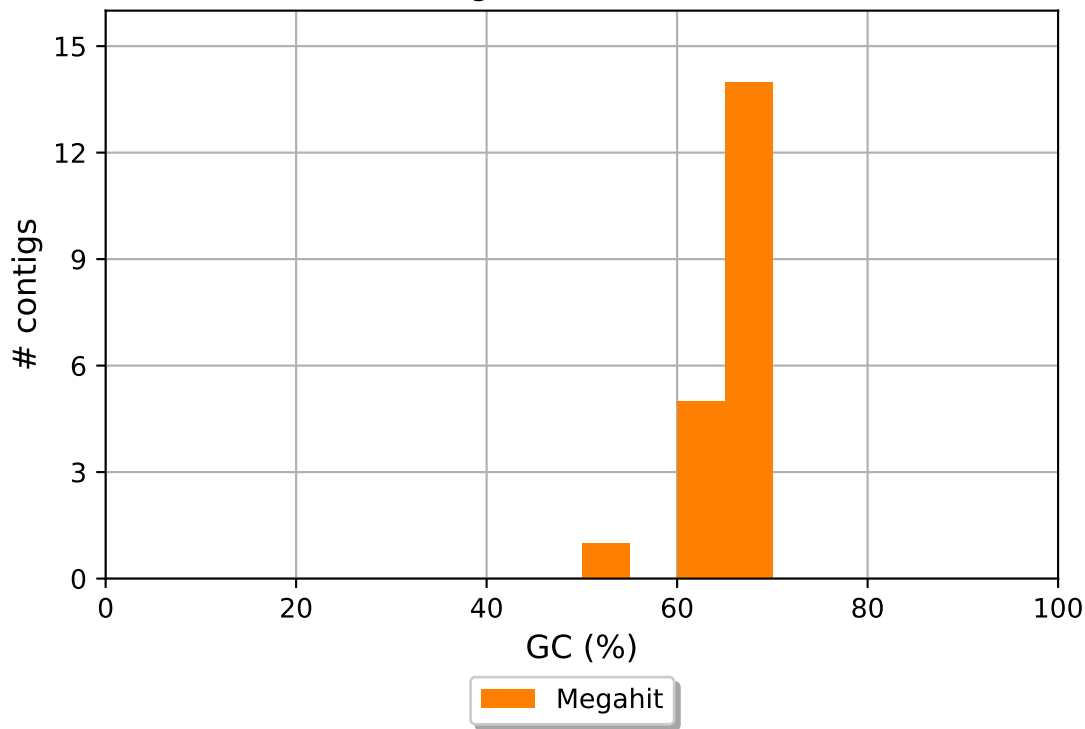
# HipMer GC content



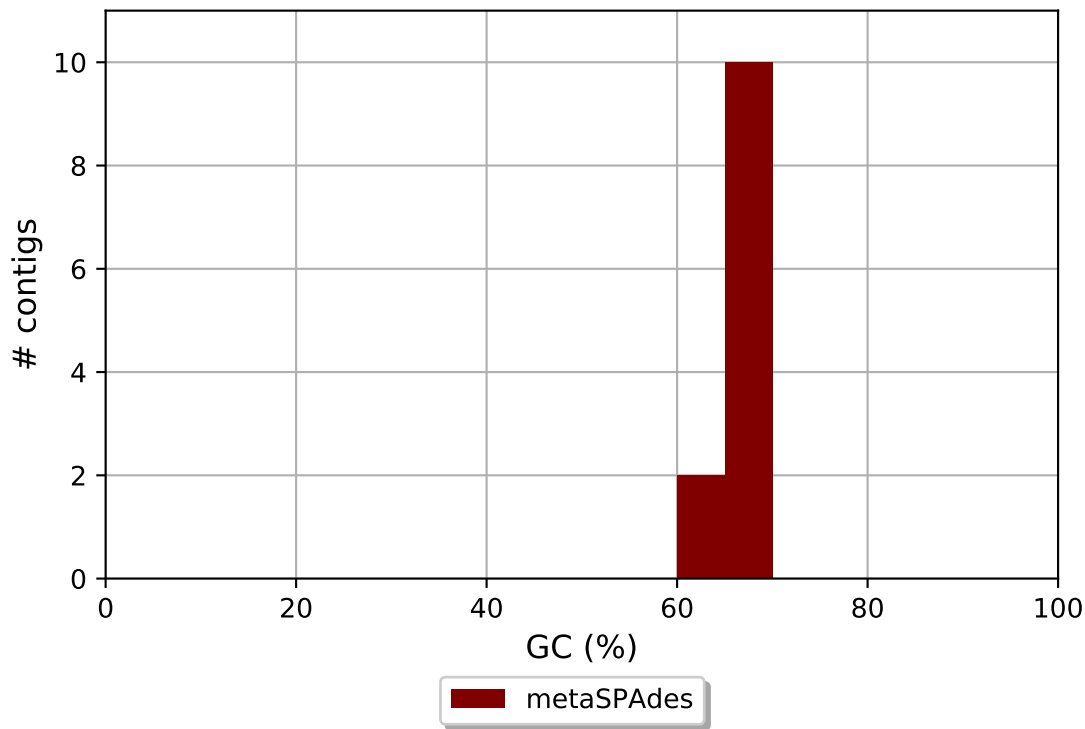
marmgCAMI2 GC content



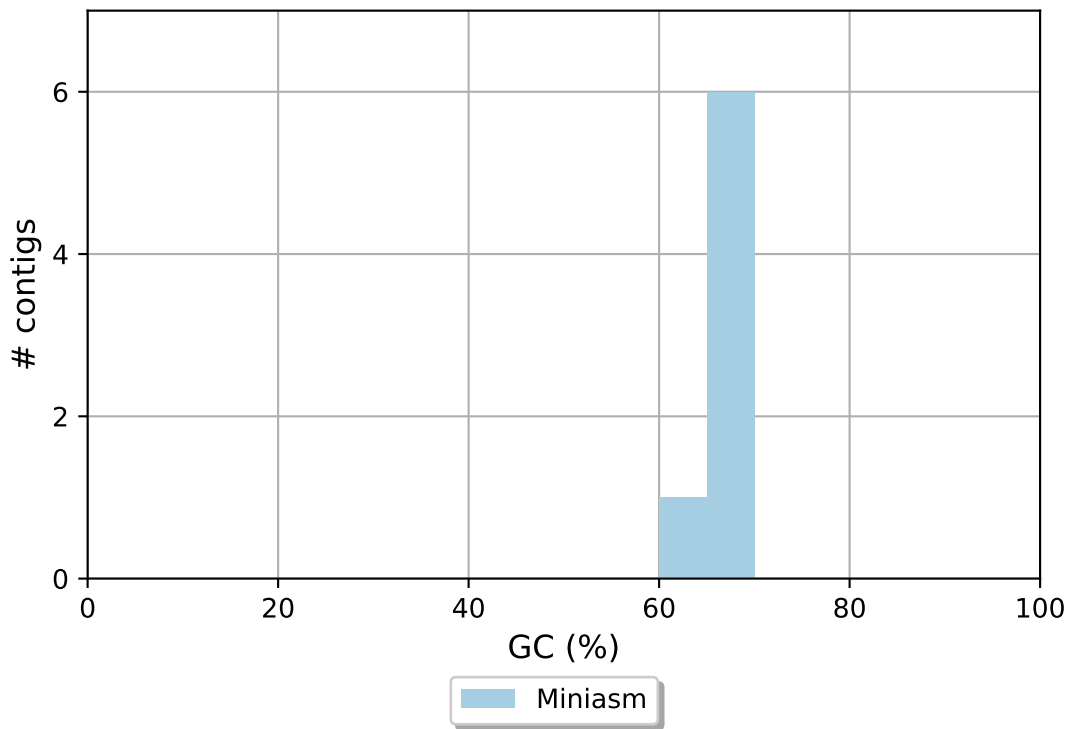
Megahit GC content



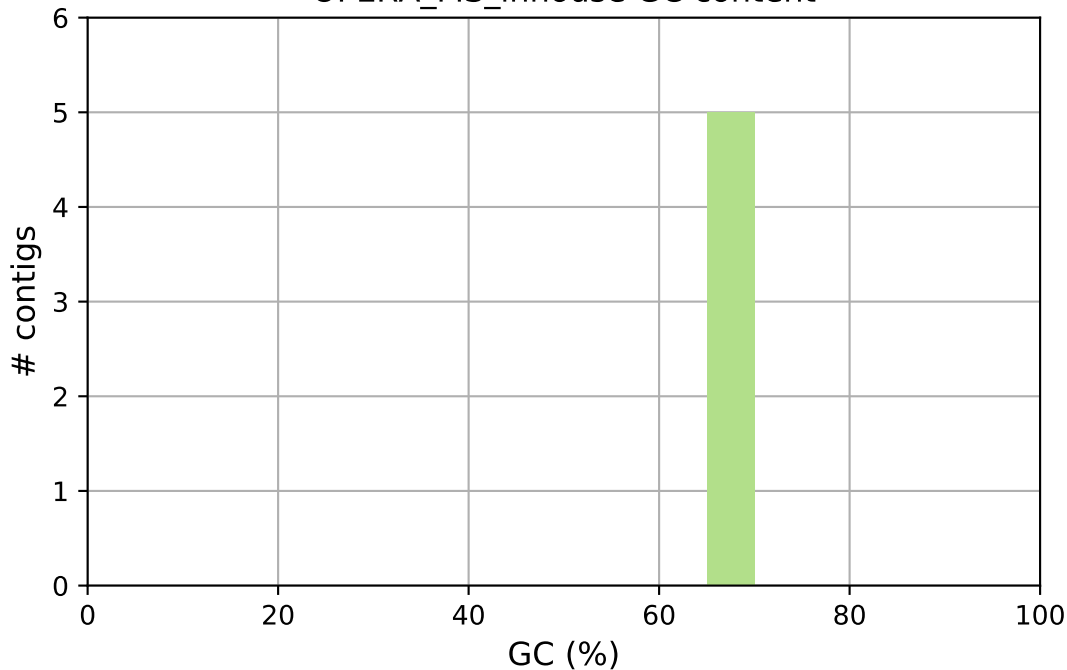
metaSPAdes GC content



# Miniasm GC content

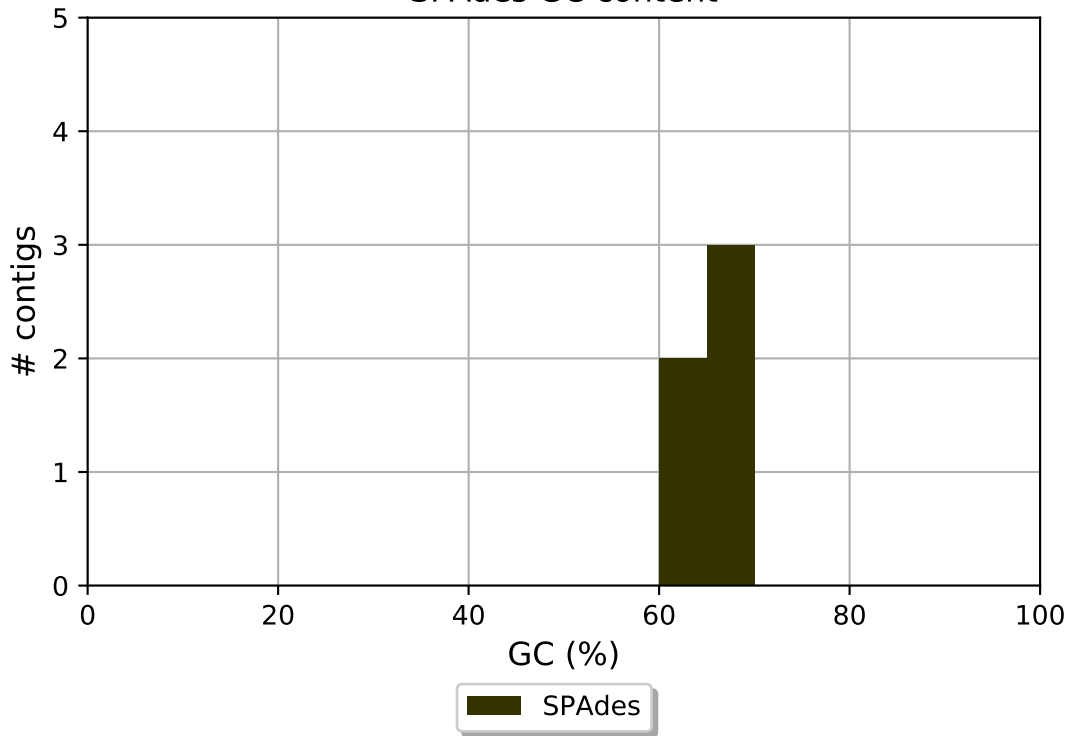


OPERA\_MS\_inhouse GC content



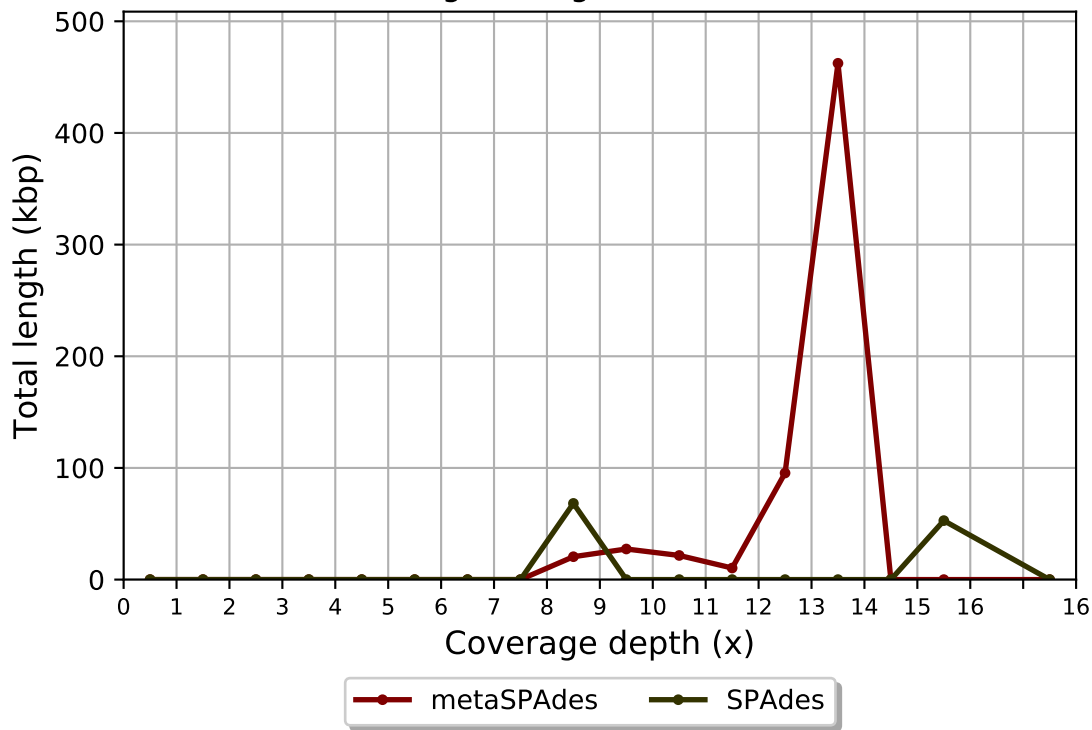
OPERA\_MS\_inhouse

# SPAdes GC content

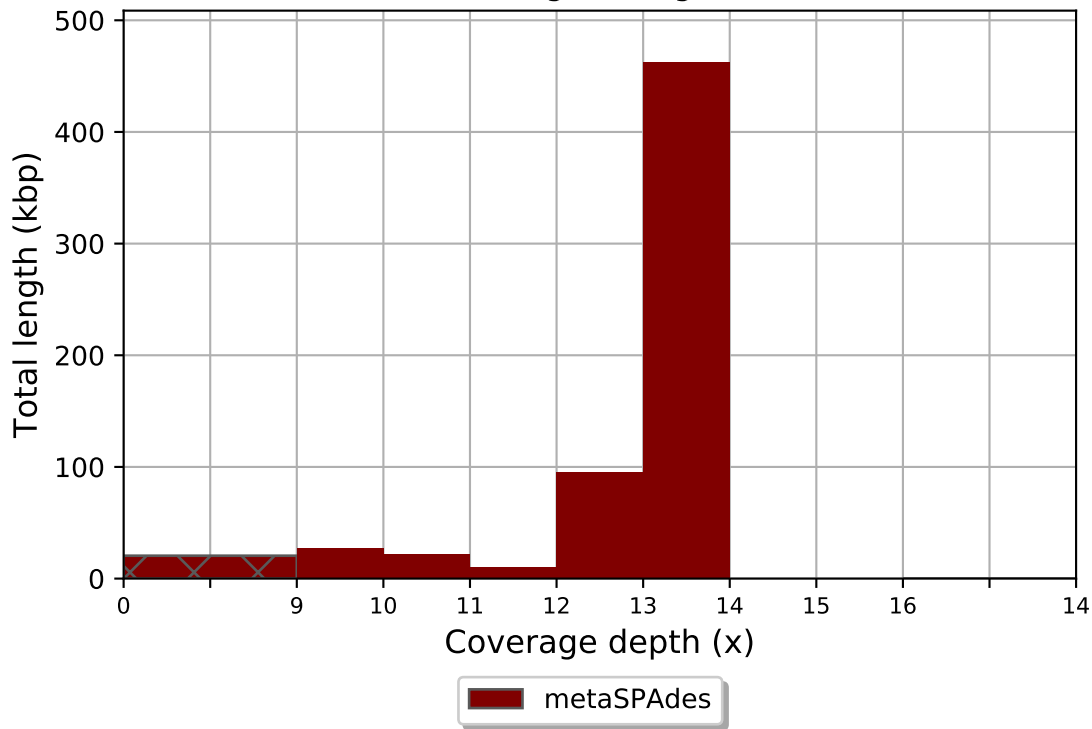




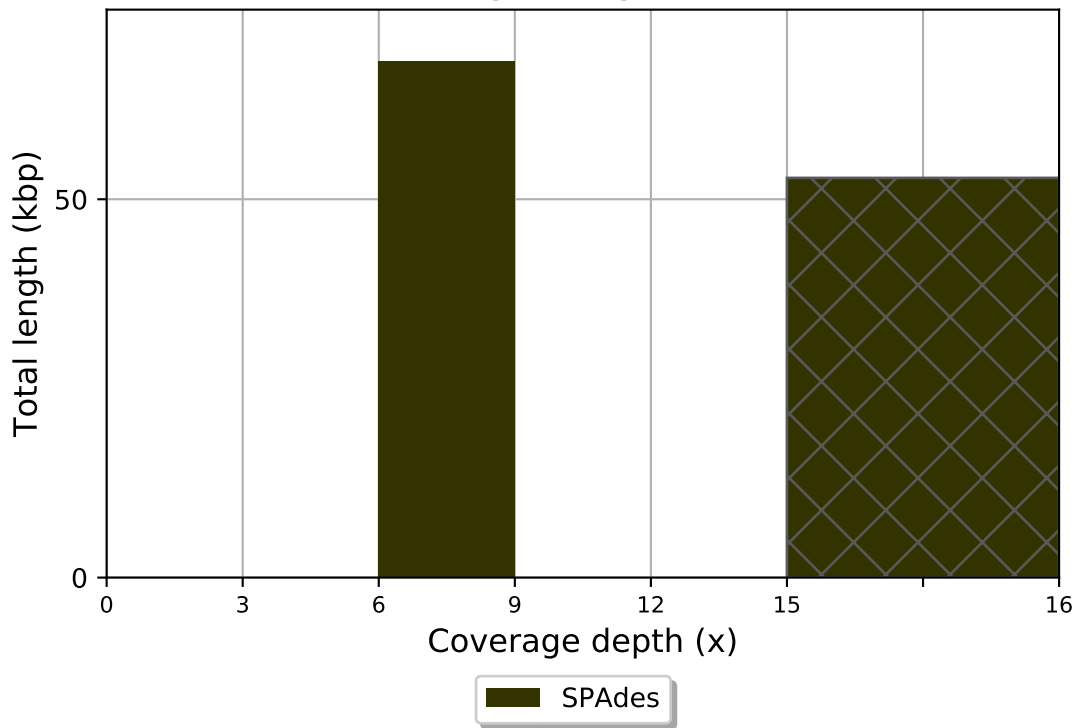
Coverage histogram (bin size: 1x)



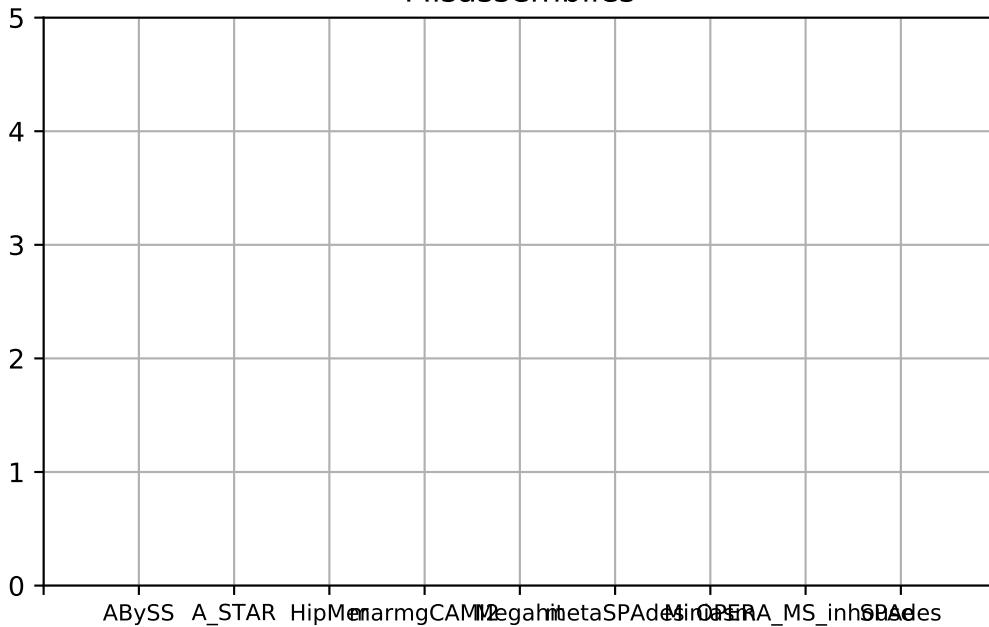
metaSPAdes coverage histogram (bin size: 1x)



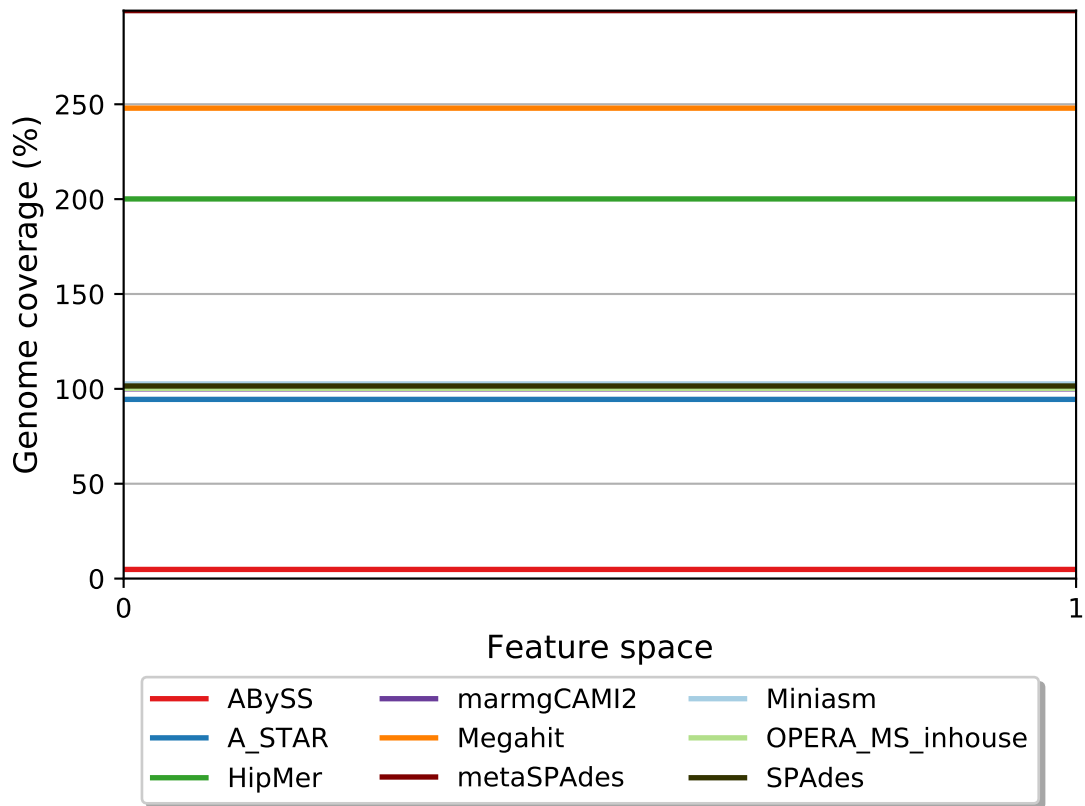
SPAdes coverage histogram (bin size: 3x)



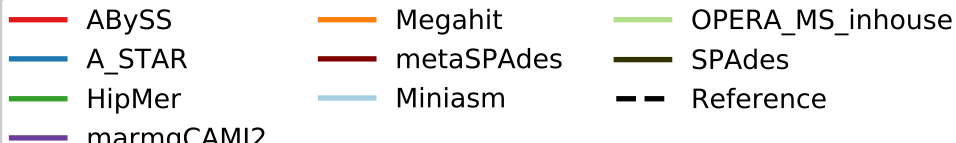
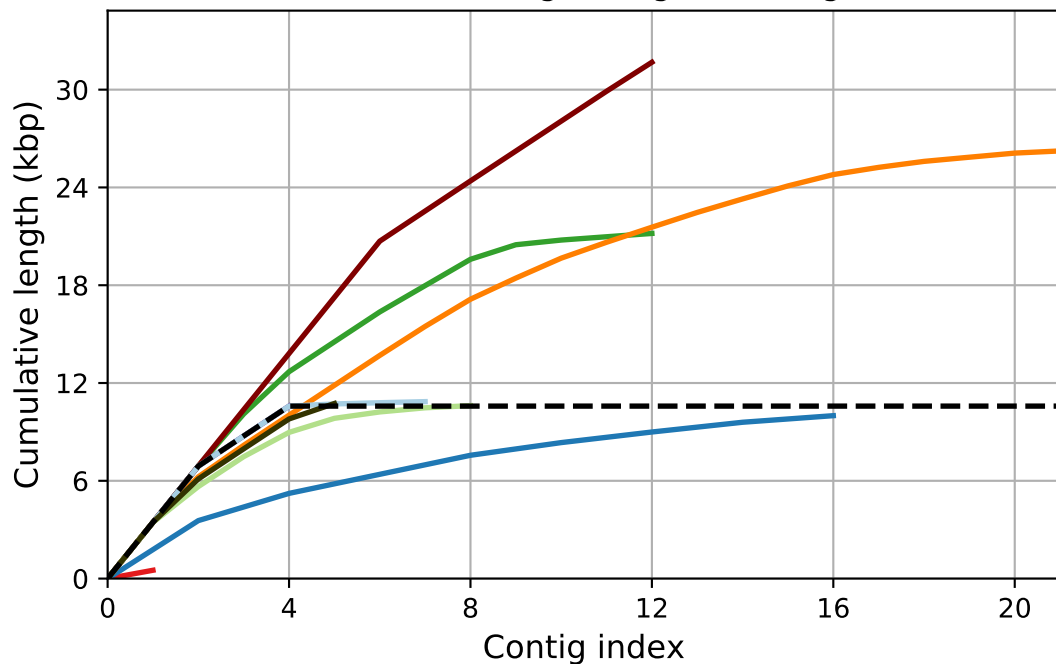
# Misassemblies



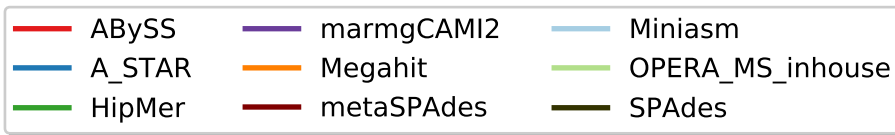
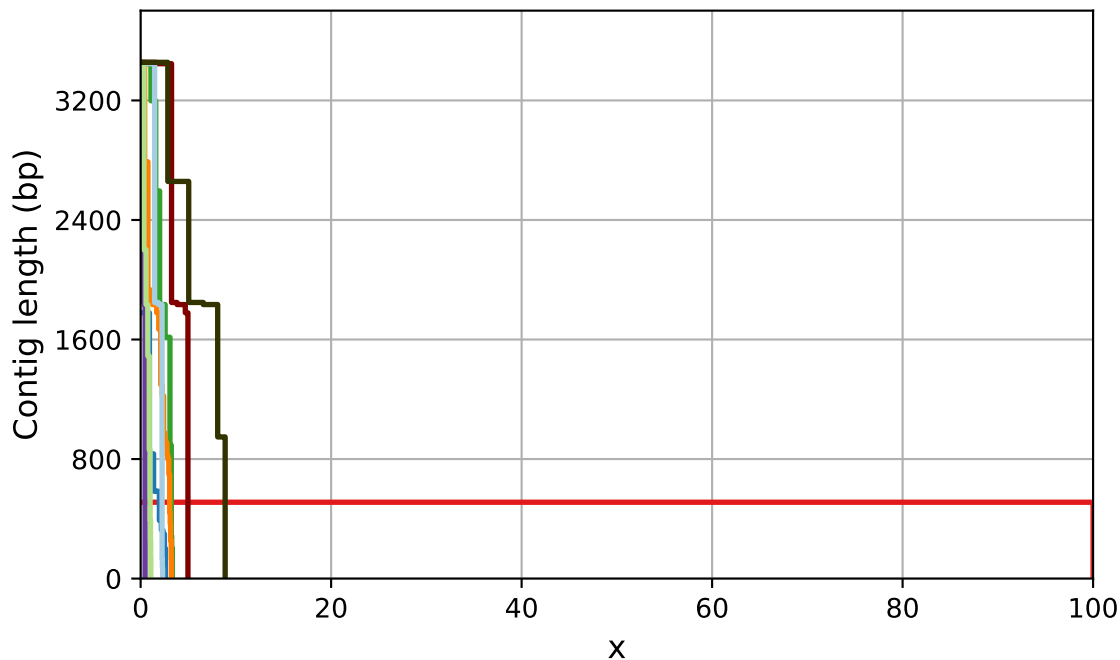
# FRCurve (misassemblies)



# Cumulative length (aligned contigs)



# NAX



# NGAx

