

Report

	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	0	16	14	1	21	15	8	5	6
# contigs (>= 5000 bp)	0	14	14	1	21	15	8	5	5
# contigs (>= 10000 bp)	0	12	13	1	18	15	8	5	5
# contigs (>= 25000 bp)	0	10	12	1	13	12	8	5	3
# contigs (>= 50000 bp)	0	2	8	1	9	8	5	5	1
Total length (>= 1000 bp)	0	453904	820465	2269117	1025321	940149	596167	987916	147314
Total length (>= 5000 bp)	0	449134	820465	2269117	1025321	940149	596167	987916	143268
Total length (>= 10000 bp)	0	435360	812028	2269117	1005048	940149	596167	987916	143268
Total length (>= 25000 bp)	0	400554	791274	2269117	899041	887697	596167	987916	105319
Total length (>= 50000 bp)	0	119776	670193	2269117	739111	715382	481843	987916	52820
# contigs	1	18	14	1	23	15	8	5	6
Largest contig	511	59888	127595	2269117	108229	126490	126603	362693	52820
Total length	511	455710	820465	2269117	1026867	940149	596167	987916	147314
Reference length	10774	10774	10774	10774	10774	10774	10774	10774	10774
GC (%)	50.68	67.47	67.63	68.08	67.64	67.39	67.23	67.61	67.50
Reference GC (%)	60.19	60.19	60.19	60.19	60.19	60.19	60.19	60.19	60.19
N50	511	35027	71182	2269117	71995	69690	94061	185526	26258
NG50	-	59888	127595	2269117	108229	126490	126603	362693	52820
N75	511	30716	57027	2269117	47996	57105	69341	153643	22334
NG75	-	59888	127595	2269117	108229	126490	126603	362693	52820
L50	1	5	4	1	6	5	3	2	2
LG50	-	1	1	1	1	1	1	1	1
L75	1	8	8	1	10	8	5	4	4
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 + 18 part	0 + 14 part	0 + 1 part	0 + 21 part	0 + 15 part	0 + 8 part	0 + 5 part	0 + 6 part
Unaligned length	0	444982	798906	2258534	1000026	907896	585117	977302	136380
Genome fraction (%)	4.743	48.803	99.722	98.227	100.000	100.000	100.000	97.587	100.000
Duplication ratio	1.000	2.040	2.007	1.000	2.491	2.994	1.026	1.010	1.015
# N's per 100 kbp	0.00	2.19	0.00	0.00	0.00	0.00	0.00	0.20	0.00
# mismatches per 100 kbp	0.00	190.19	0.00	0.00	1095.23	0.00	9.28	275.82	55.69
# indels per 100 kbp	0.00	38.04	0.00	0.00	9.28	9.28	18.56	0.00	0.00
Largest alignment	511	1779	3455	3455	3455	3455	3455	3446	3455
Total aligned length	511	10718	21559	10583	26791	32253	11050	10612	10934
NA50	511	-	-	-	-	-	-	-	-
NGA50	-	585	3446	3446	2789	3455	3446	2201	2658
NA75	511	-	-	-	-	-	-	-	-
NGA75	-	389	3198	1848	1933	3455	1848	1490	1834
LA50	1	-	-	-	-	-	-	-	-
LGA50	-	5	2	2	2	2	2	2	2
LA75	1	-	-	-	-	-	-	-	-
LGA75	-	10	3	3	3	3	3	4	4

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

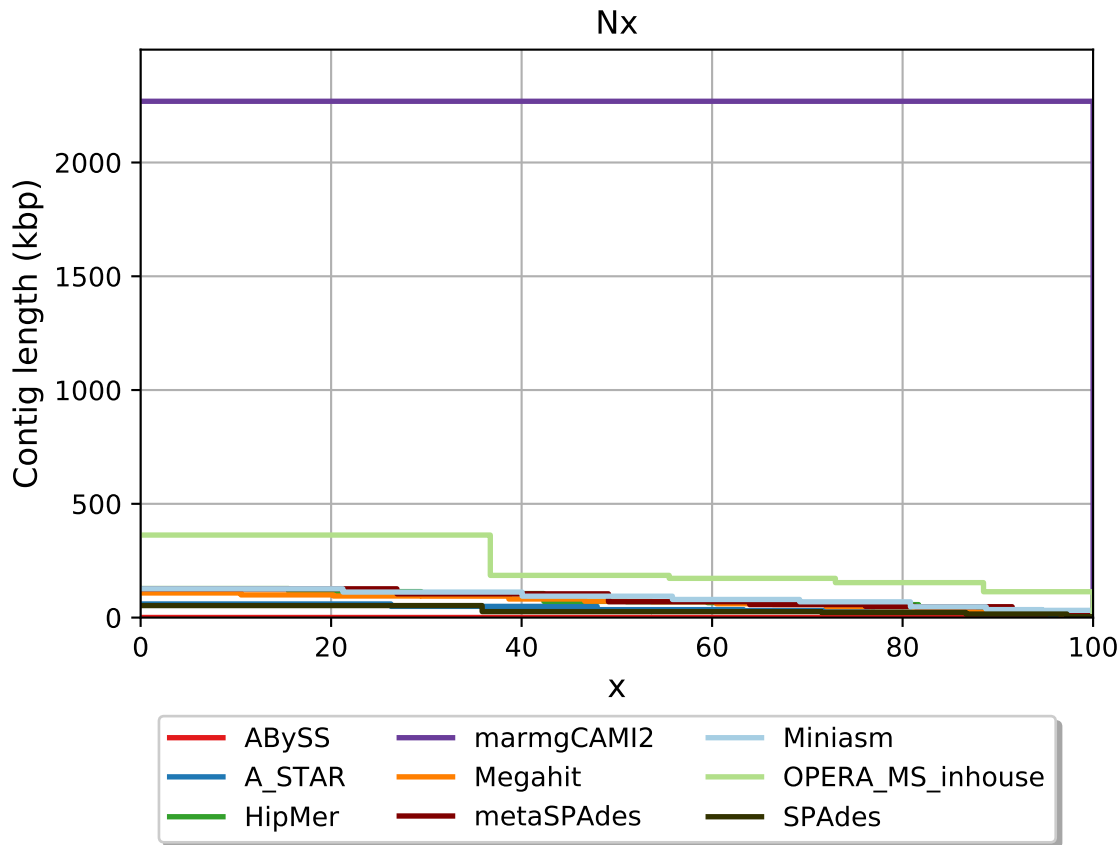
	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	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	16	14	0	20	15	8	3	6
# possible misassemblies	0	20	19	0	27	30	16	5	9
# 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	10	0	0	118	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 ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

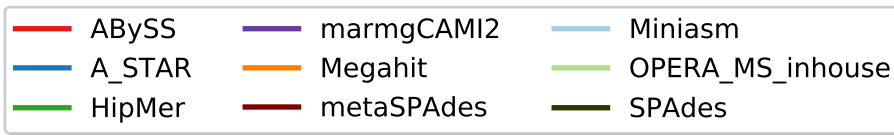
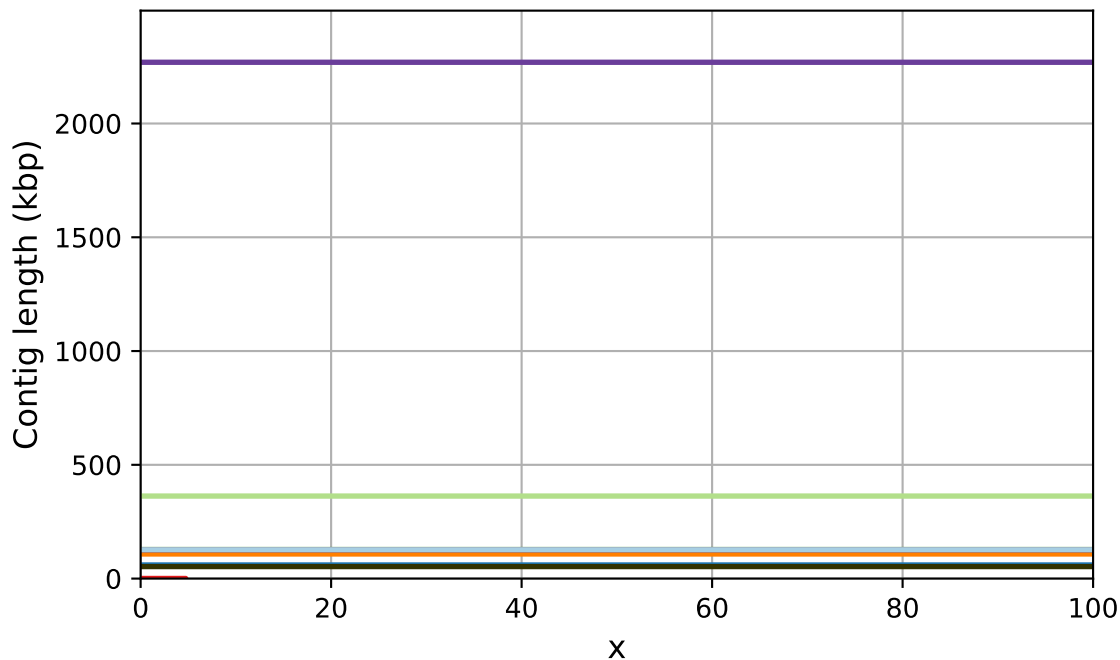
Unaligned report

	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	18	14	1	21	15	8	5	6
Partially unaligned length	0	444982	798906	2258534	1000026	907896	585117	977302	136380
# N's	0	10	0	0	0	0	0	2	0

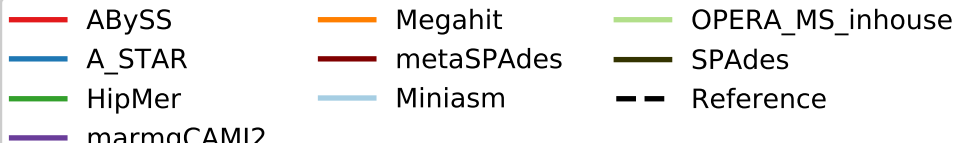
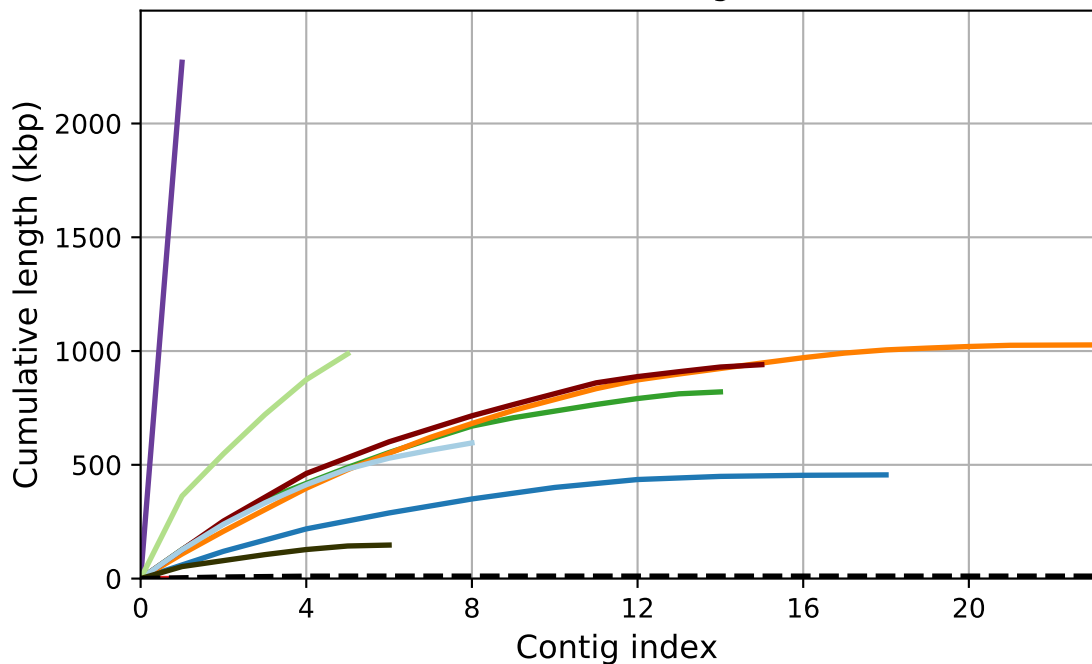
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



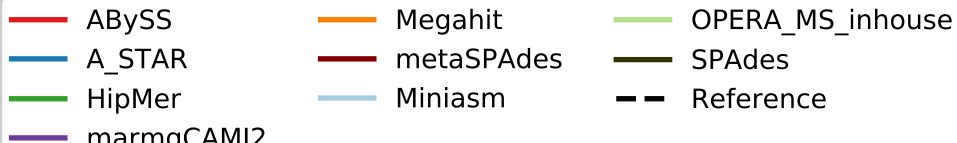
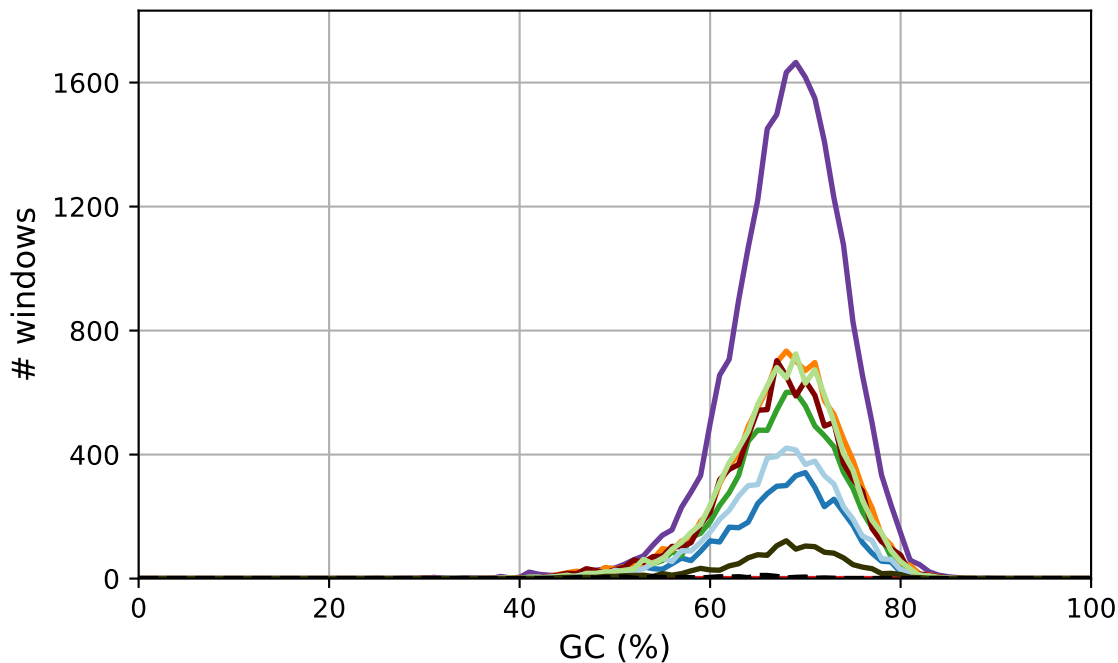
NGx



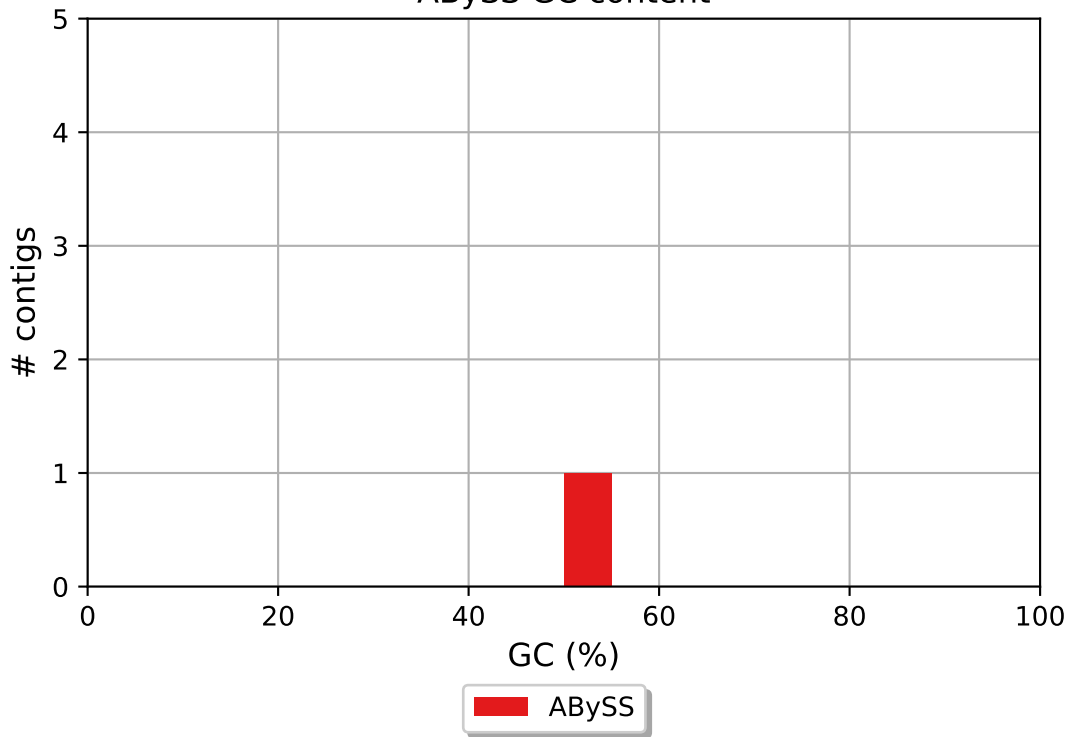
Cumulative length



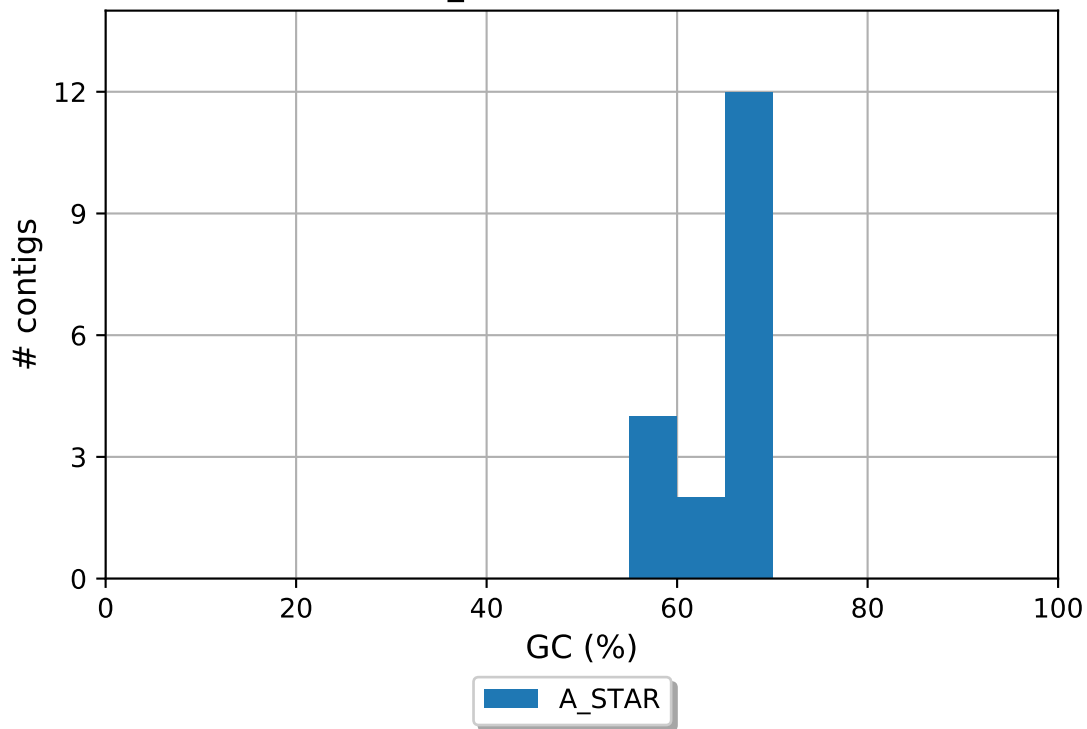
GC content



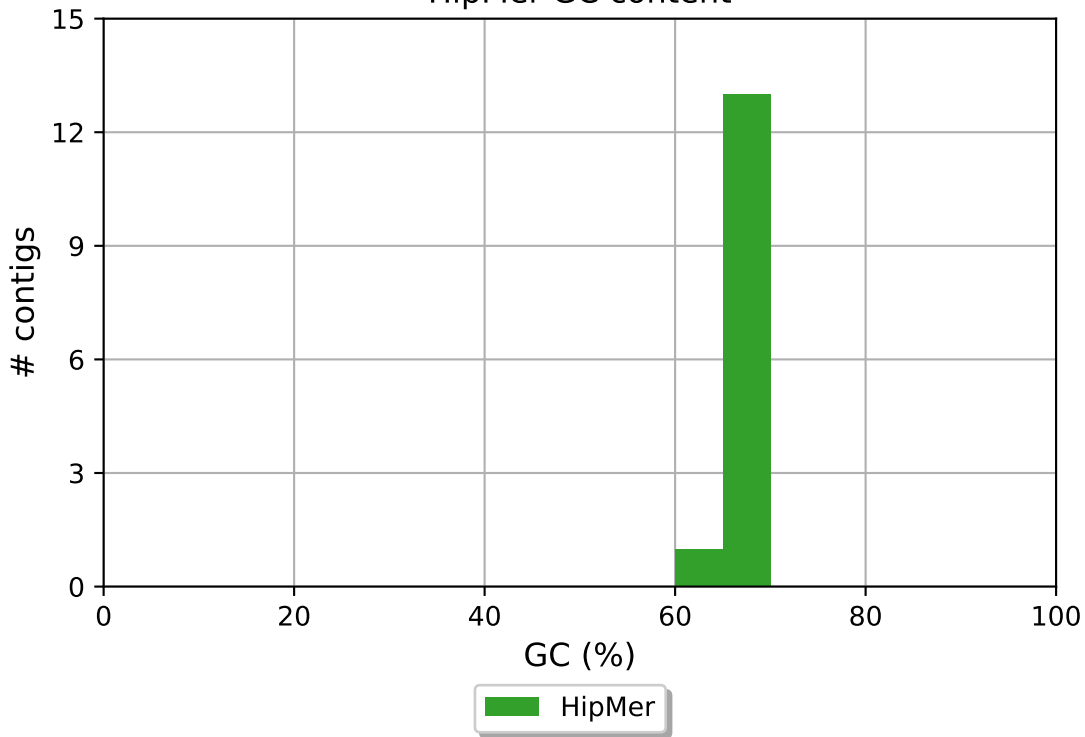
ABySS GC content



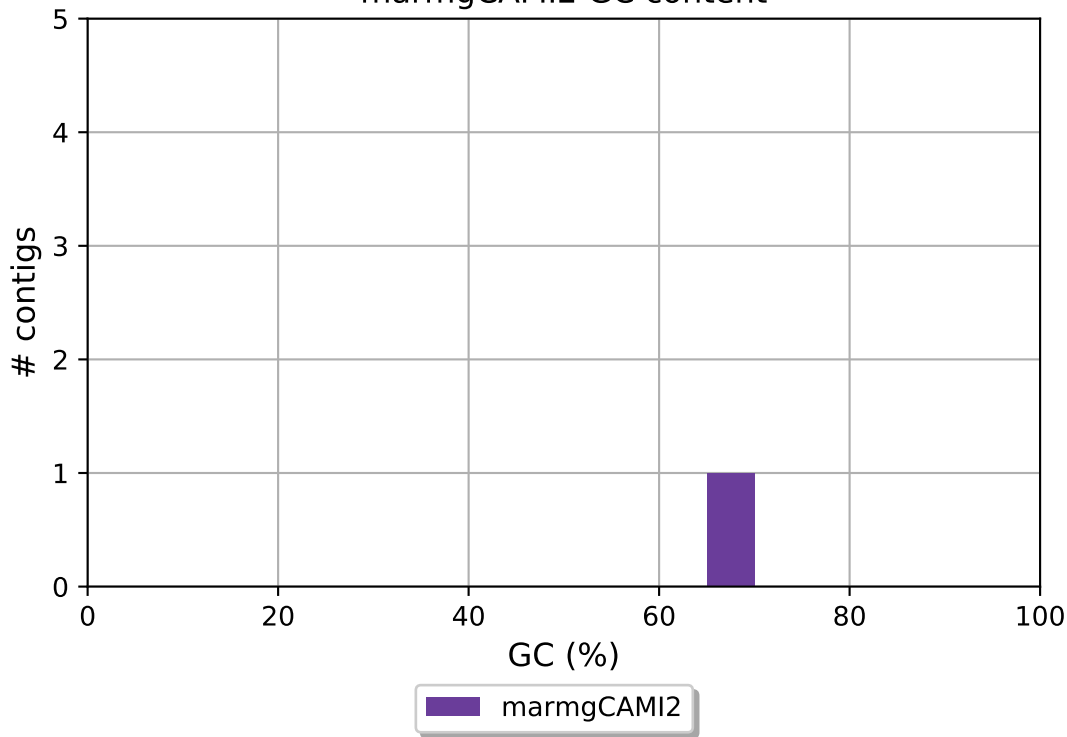
A_STAR GC content



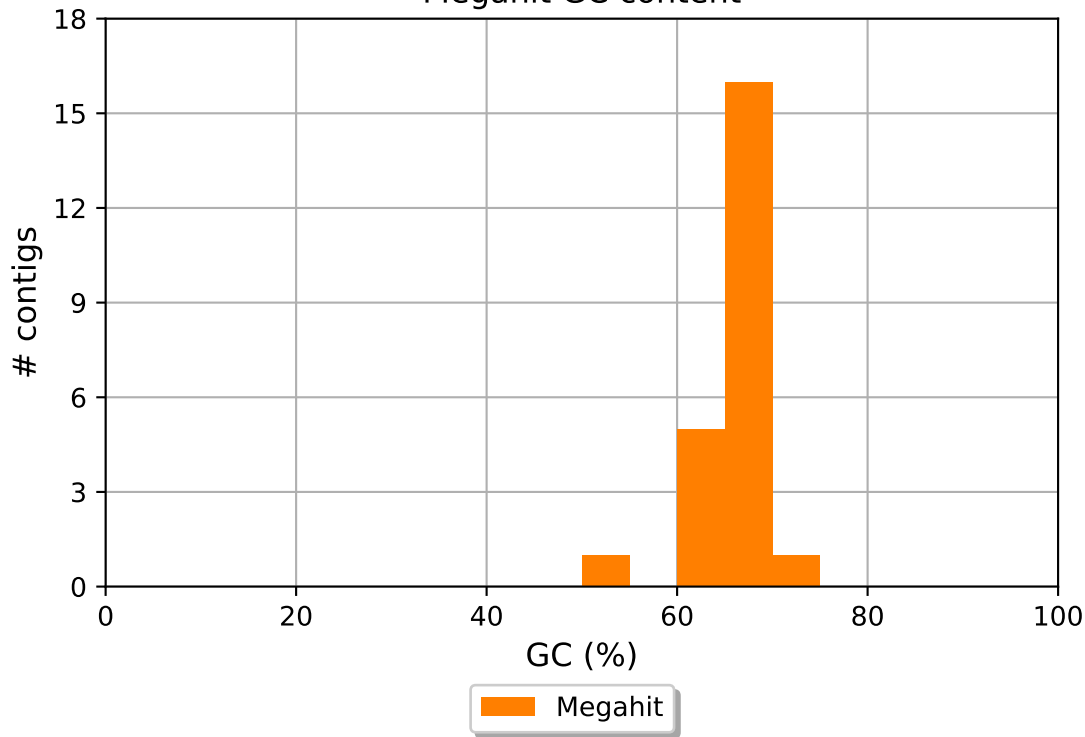
HipMer GC content



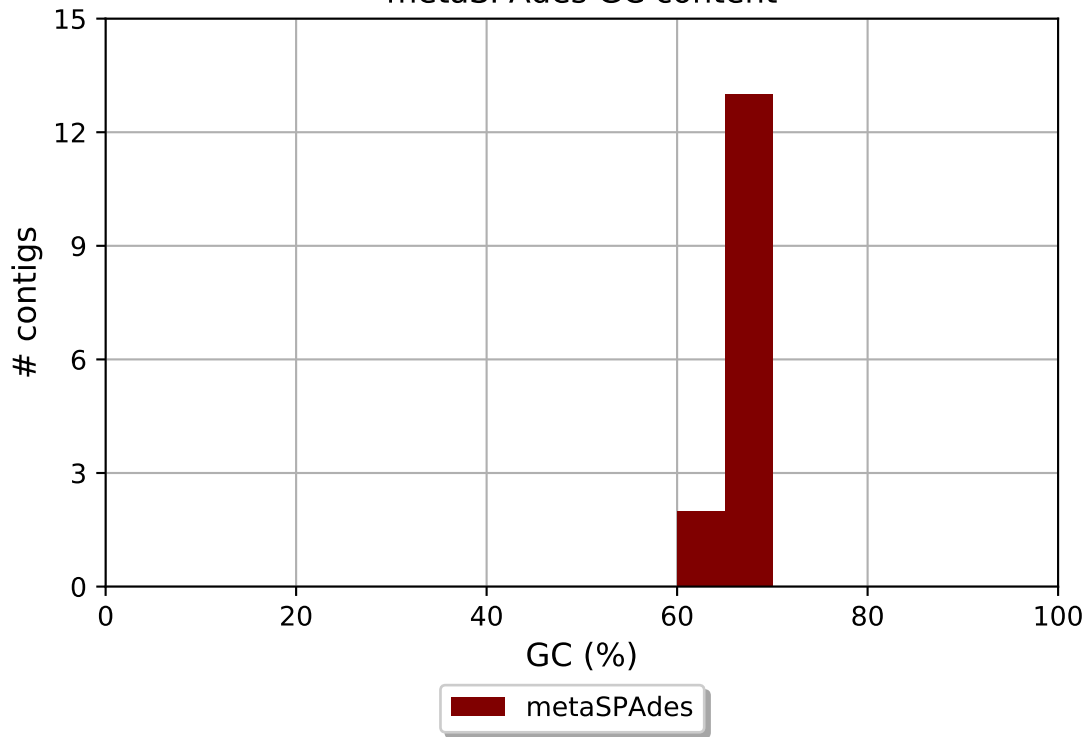
marmgCAMI2 GC content



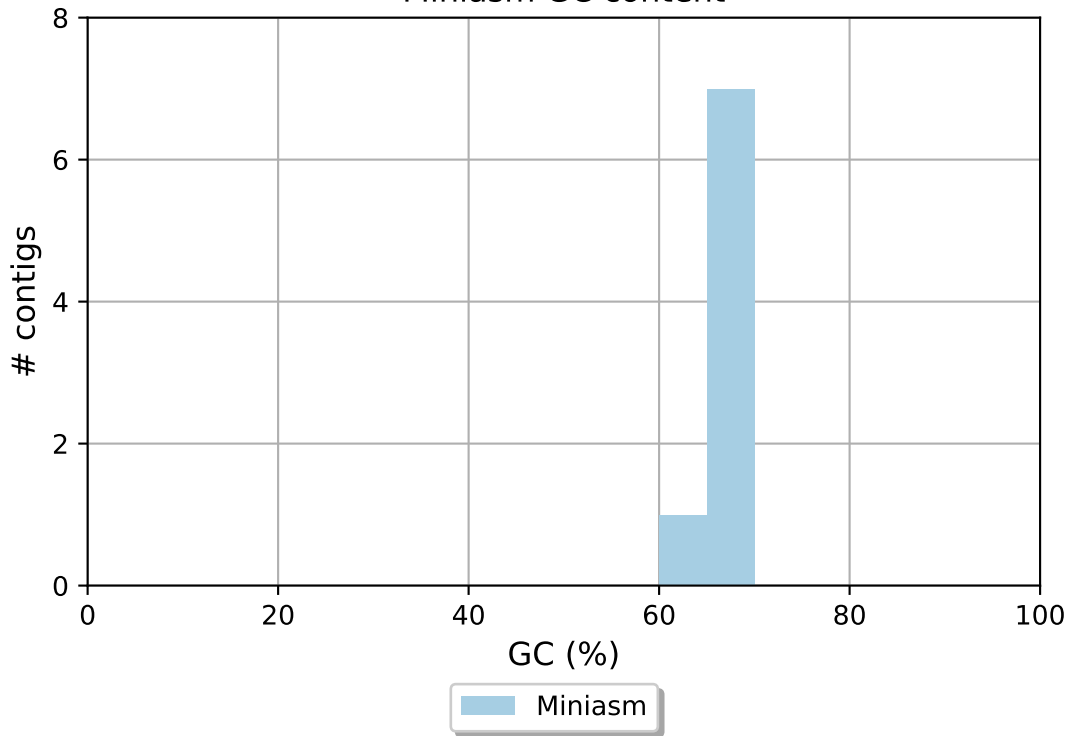
Megahit GC content



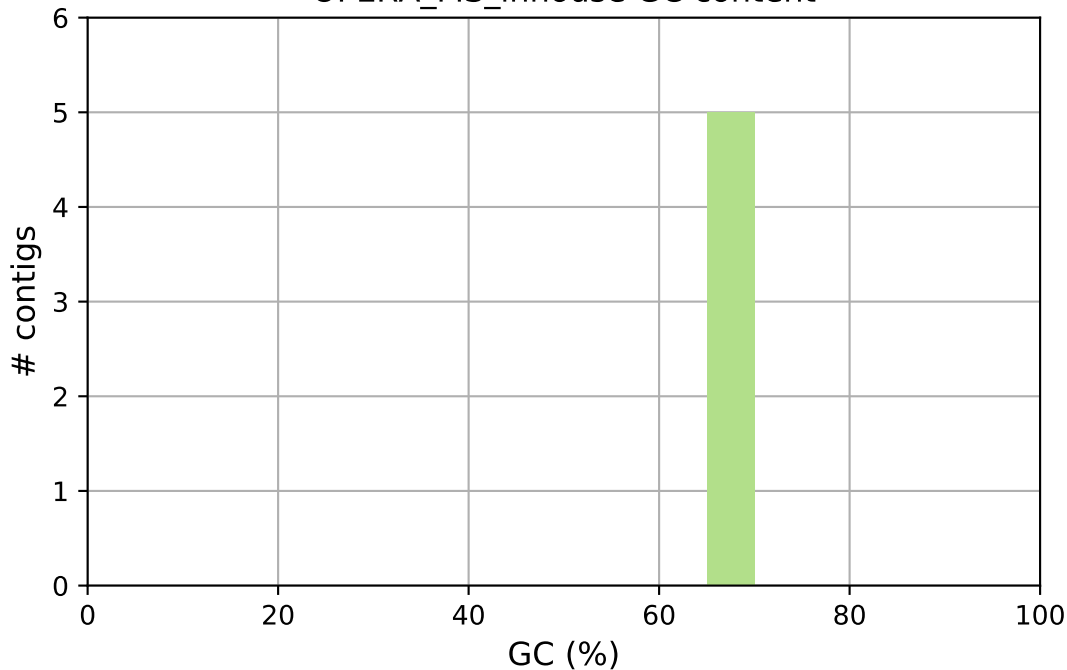
metaSPAdes GC content



Miniasm GC content

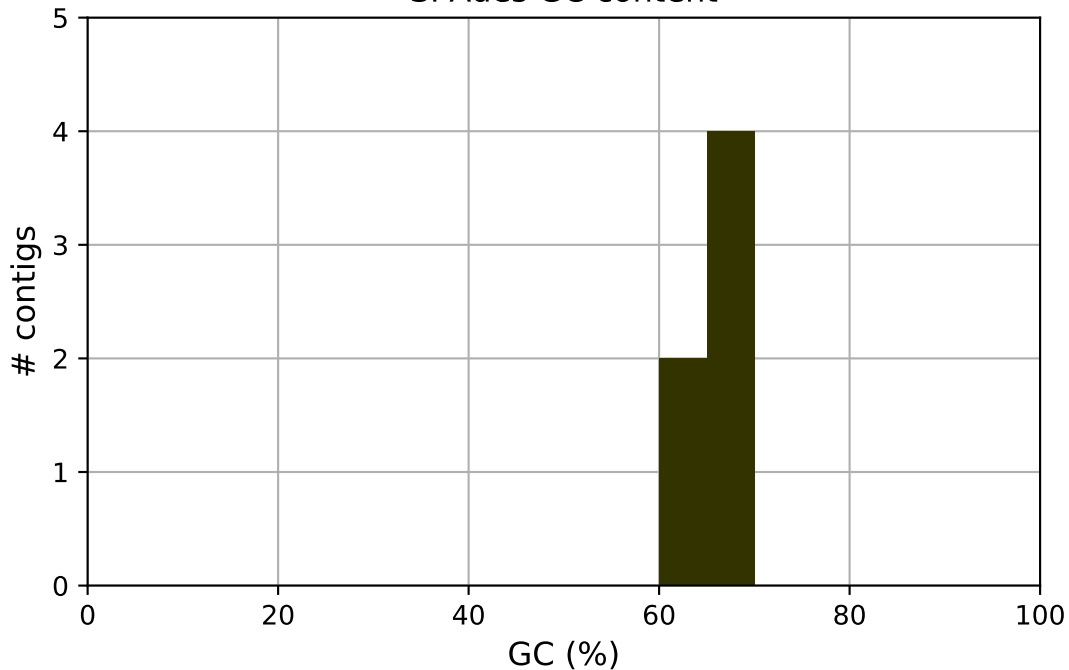


OPERA_MS_inhouse GC content



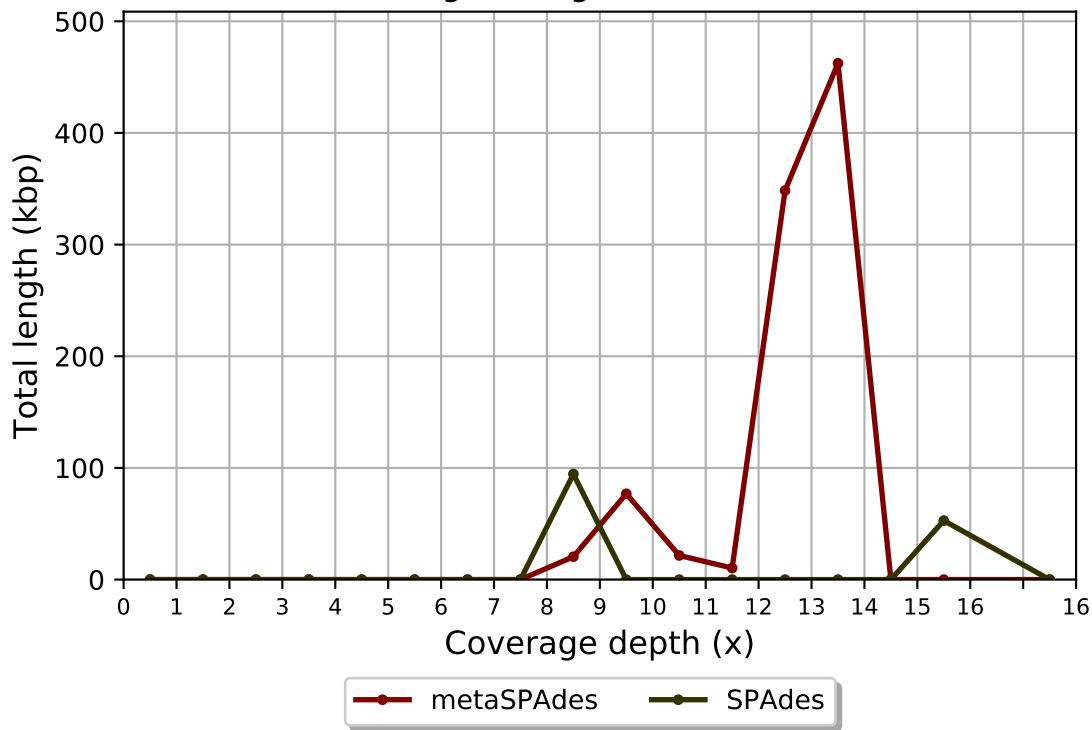
OPERA_MS_inhouse

SPAdes GC content

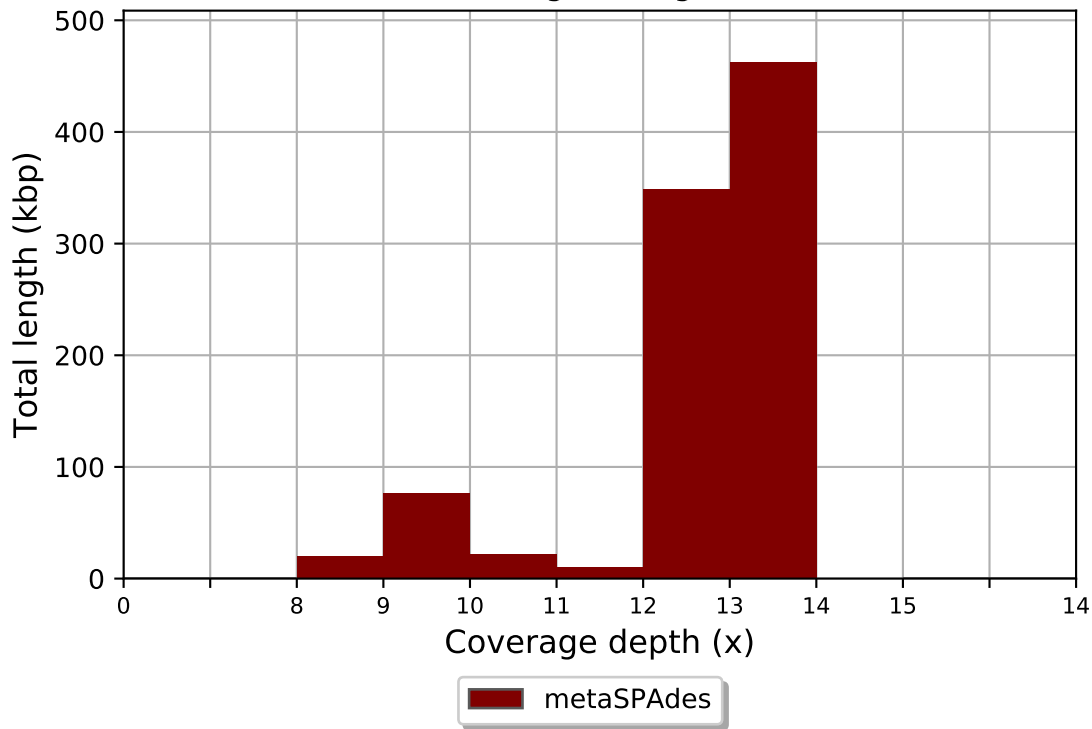


SPAdes

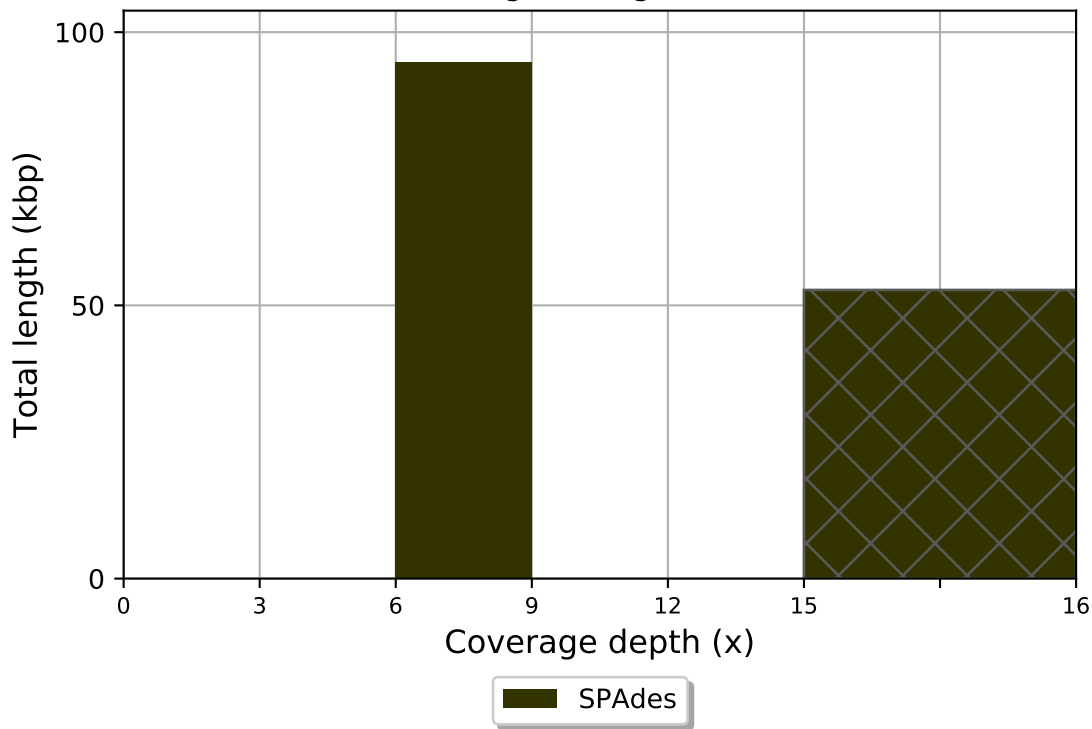
Coverage histogram (bin size: 1x)



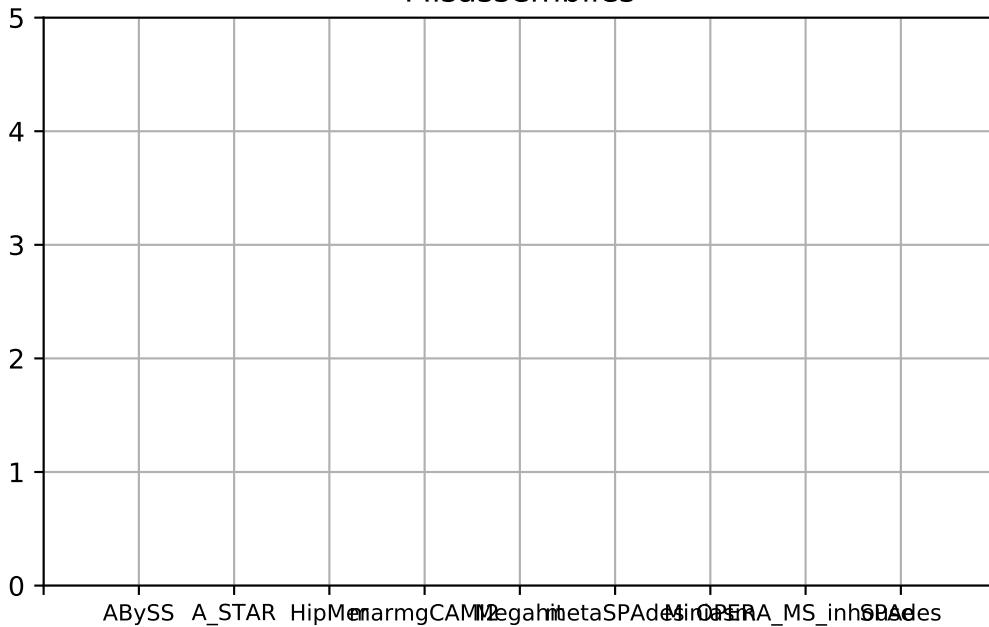
metaSPAdes coverage histogram (bin size: 1x)



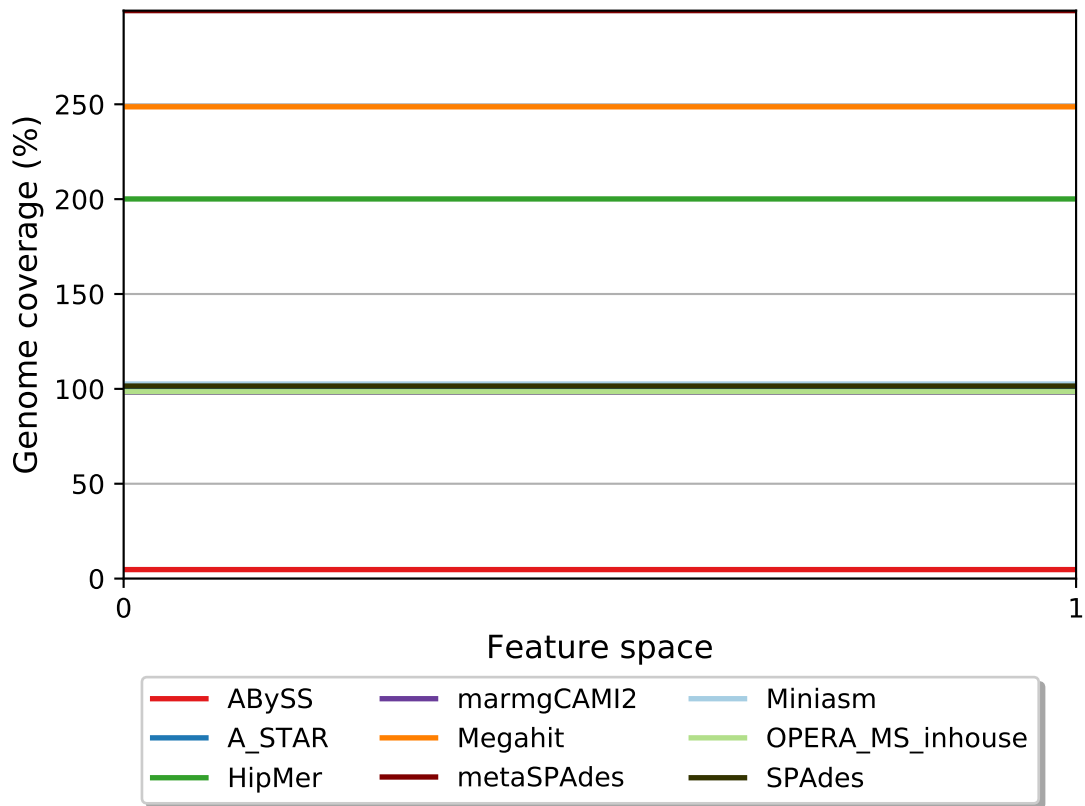
SPAdes coverage histogram (bin size: 3x)



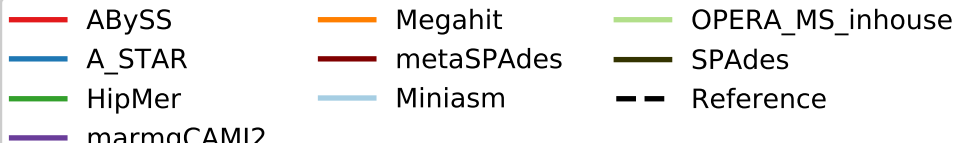
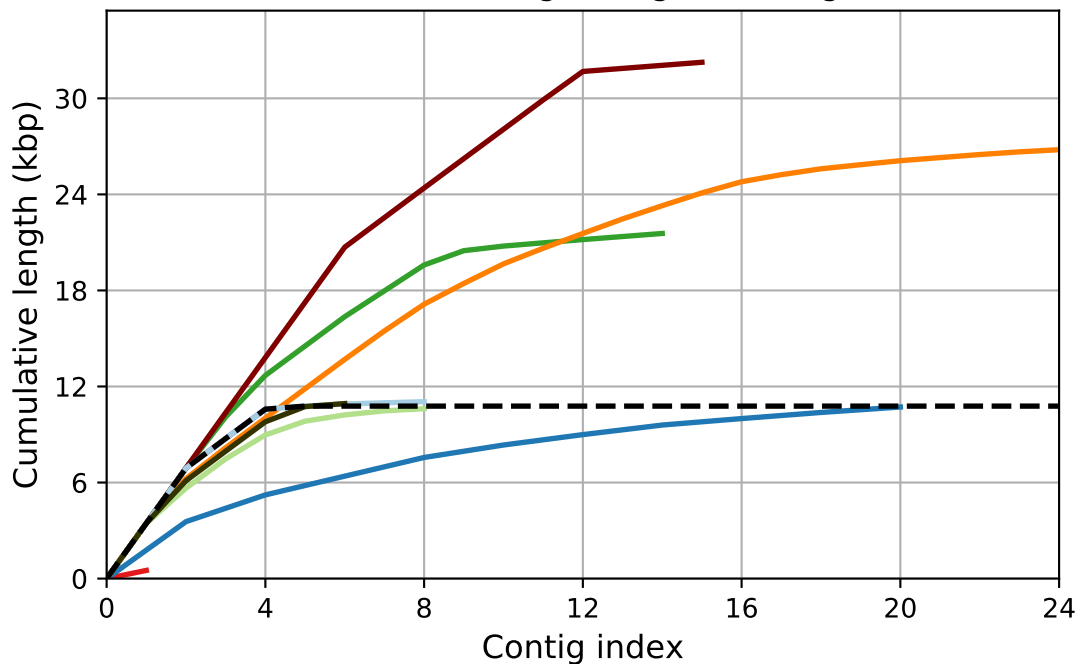
Misassemblies



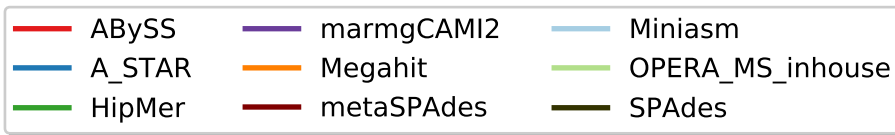
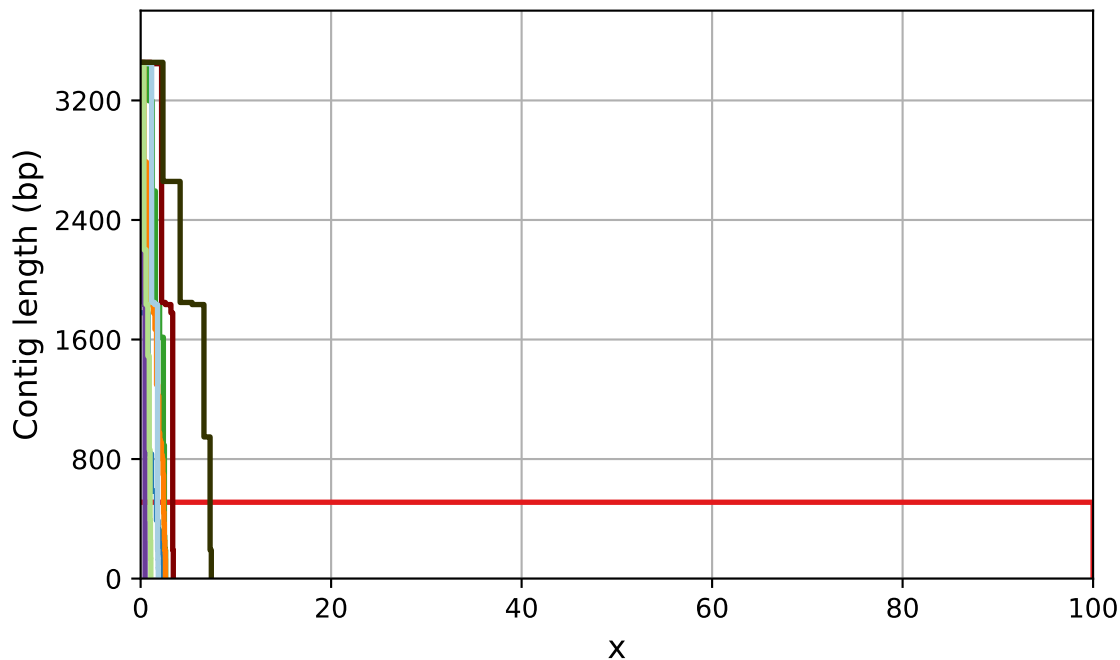
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

