

Report

	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	0	9	8	1	13	10	1	2	2
# contigs (>= 5000 bp)	0	0	6	1	10	9	1	2	2
# contigs (>= 10000 bp)	0	0	6	1	10	9	1	2	2
# contigs (>= 25000 bp)	0	0	6	1	9	9	0	2	2
# contigs (>= 50000 bp)	0	0	4	1	5	6	0	2	2
Total length (>= 1000 bp)	0	25830	1246491	5051673	1229681	1400939	13654	989129	2581202
Total length (>= 5000 bp)	0	0	1244332	5051673	1225303	1399918	13654	989129	2581202
Total length (>= 10000 bp)	0	0	1244332	5051673	1225303	1399918	13654	989129	2581202
Total length (>= 25000 bp)	0	0	1244332	5051673	1211204	1399918	0	989129	2581202
Total length (>= 50000 bp)	0	0	1163172	5051673	1059974	1282040	0	989129	2581202
# contigs	3	14	8	1	15	12	1	2	2
Largest contig	614	4903	408855	5051673	407761	407606	13654	881144	1327807
Total length	1651	29570	1246491	5051673	1231326	1402893	13654	989129	2581202
Reference length	6584	6584	6584	6584	6584	6584	6584	6584	6584
GC (%)	54.51	54.57	51.87	51.31	51.62	51.78	52.39	51.95	51.54
Reference GC (%)	59.98	59.98	59.98	59.98	59.98	59.98	59.98	59.98	59.98
N50	519	3317	407637	5051673	305360	407606	13654	881144	1327807
NG50	-	4903	408855	5051673	407761	407606	13654	881144	1327807
N75	518	1372	218544	5051673	126107	128106	13654	881144	1253395
NG75	-	4903	408855	5051673	407761	407606	13654	881144	1327807
L50	2	4	2	1	2	2	1	1	1
LG50	-	1	1	1	1	1	1	1	1
L75	3	6	3	1	4	4	1	1	2
LG75	-	2	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	1	1
# unaligned contigs	0 + 0 part	0 + 9 part	0 + 6 part	0 + 1 part	0 + 10 part	0 + 9 part	0 + 1 part	0 + 2 part	0 + 2 part
Unaligned length	0	21390	1232762	5045089	1213389	1382797	13235	982605	2562427
Genome fraction (%)	20.033	45.930	100.000	100.000	100.000	100.000	6.364	100.000	100.000
Duplication ratio	1.252	2.705	2.085	1.000	2.724	3.052	1.000	0.991	2.852
# N's per 100 kbp	0.00	1159.96	13.24	0.00	0.00	0.00	0.00	0.00	472.30
# mismatches per 100 kbp	0.00	925.93	0.00	0.00	622.72	0.00	0.00	106.32	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15.19	0.00
Largest alignment	614	877	4288	4288	4288	4288	419	4228	4288
Total aligned length	1319	6930	13168	6584	17149	19752	419	6524	6584
NA50	519	-	-	-	-	-	-	-	-
NGA50	-	626	4288	4288	4288	4288	-	4228	4288
NA75	186	-	-	-	-	-	-	-	-
NGA75	-	389	4288	1000	2099	4288	-	1000	1000
LA50	2	-	-	-	-	-	-	-	-
LGA50	-	5	1	1	1	1	-	1	1
LA75	3	-	-	-	-	-	-	-	-
LGA75	-	8	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	7	6	0	9	9	1	1	1
# possible misassemblies	0	7	9	0	10	12	1	2	2
# 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	1	1
# mismatches	0	28	0	0	41	0	0	7	0
# indels	0	0	0	0	0	0	0	1	0
# indels (<= 5 bp)	0	0	0	0	0	0	0	0	0
# indels (> 5 bp)	0	0	0	0	0	0	0	1	0
Indels length	0	0	0	0	0	0	0	60	0

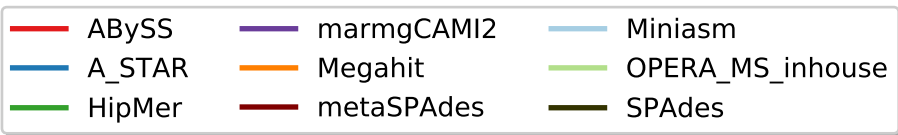
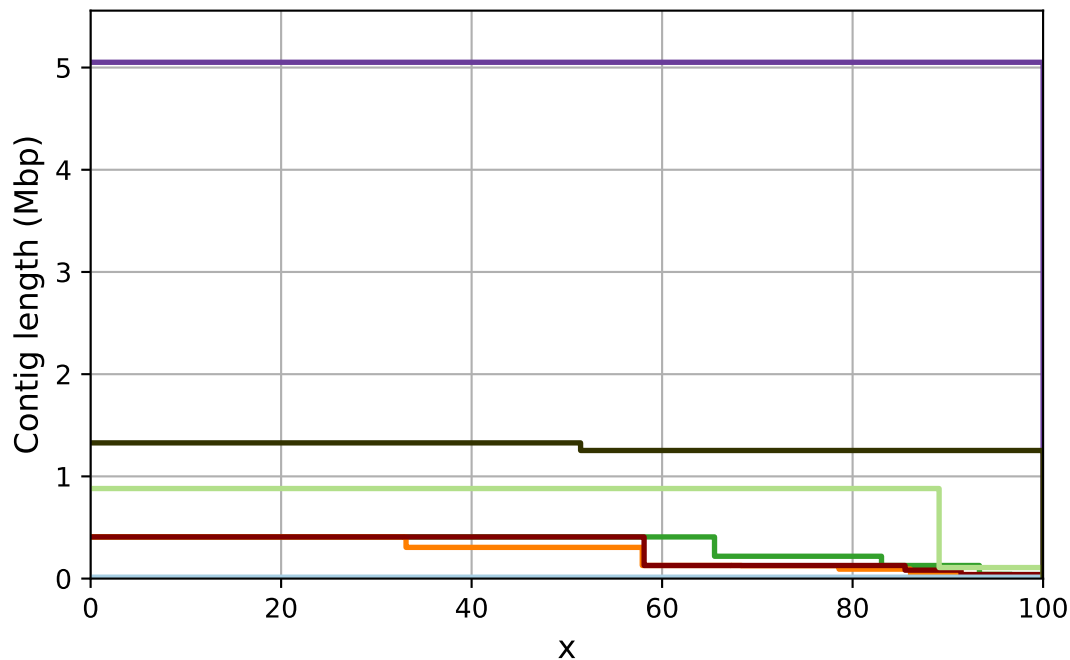
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

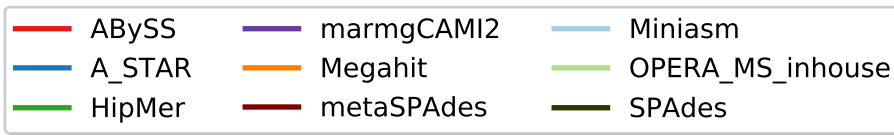
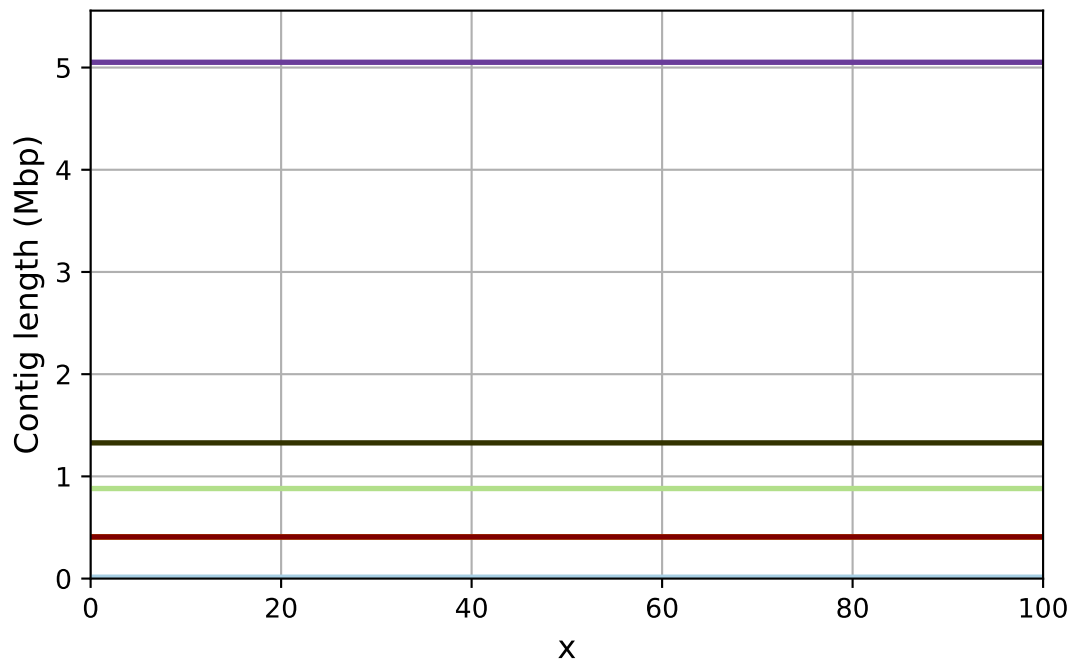
	ABYSS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	0	9	6	1	10	9	1	2	2
Partially unaligned length	0	21390	1232762	5045089	1213389	1382797	13235	982605	2562427
# N's	0	343	165	0	0	0	0	0	12191

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).

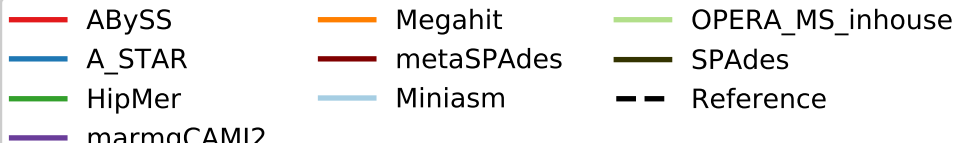
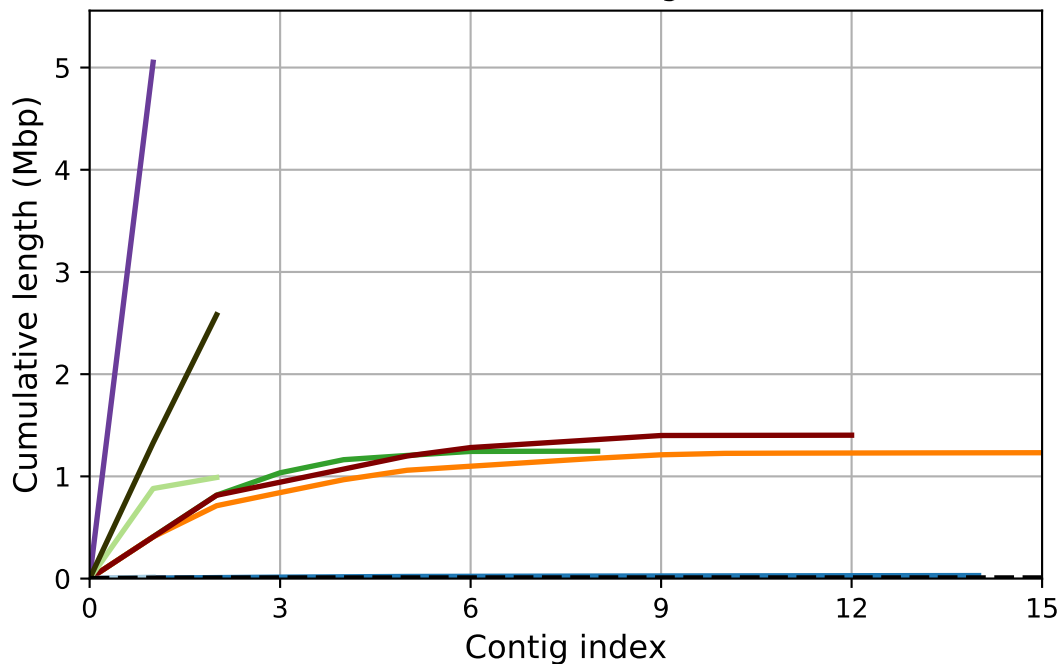
Nx



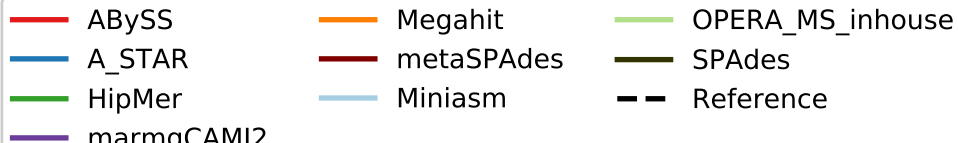
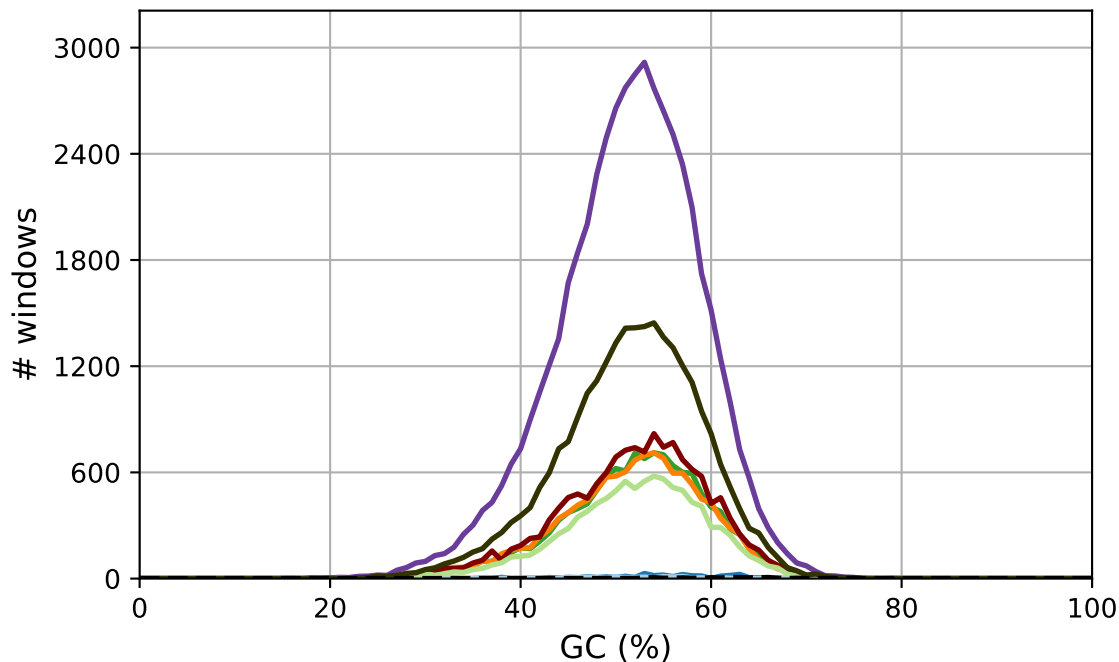
NGx



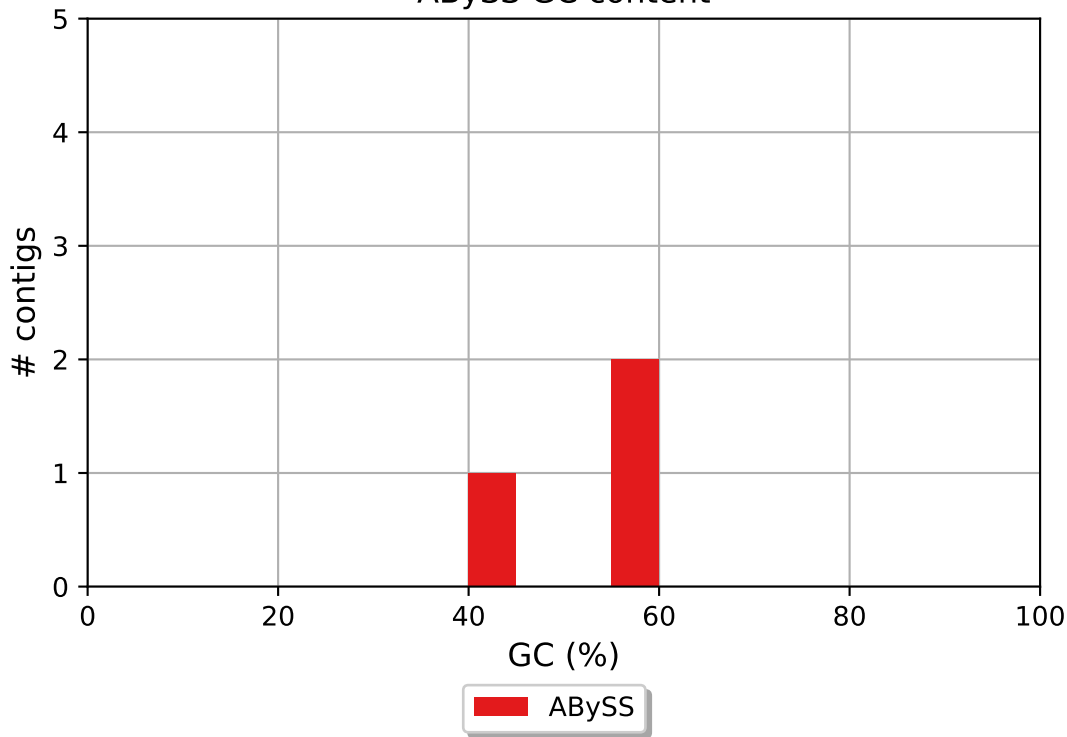
Cumulative length



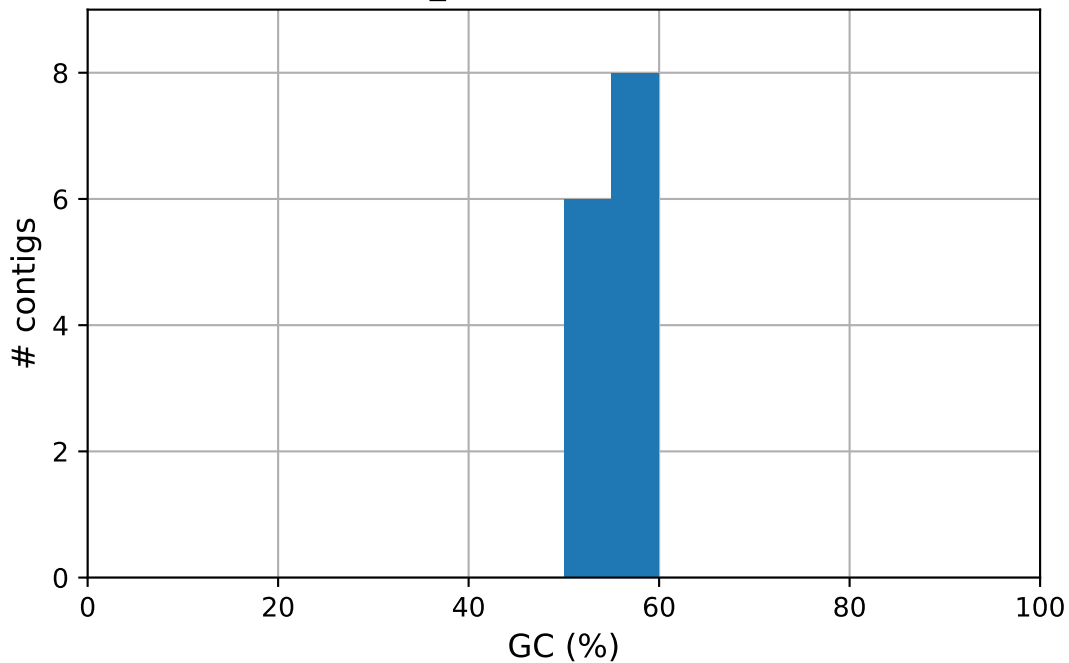
GC content



ABySS GC content

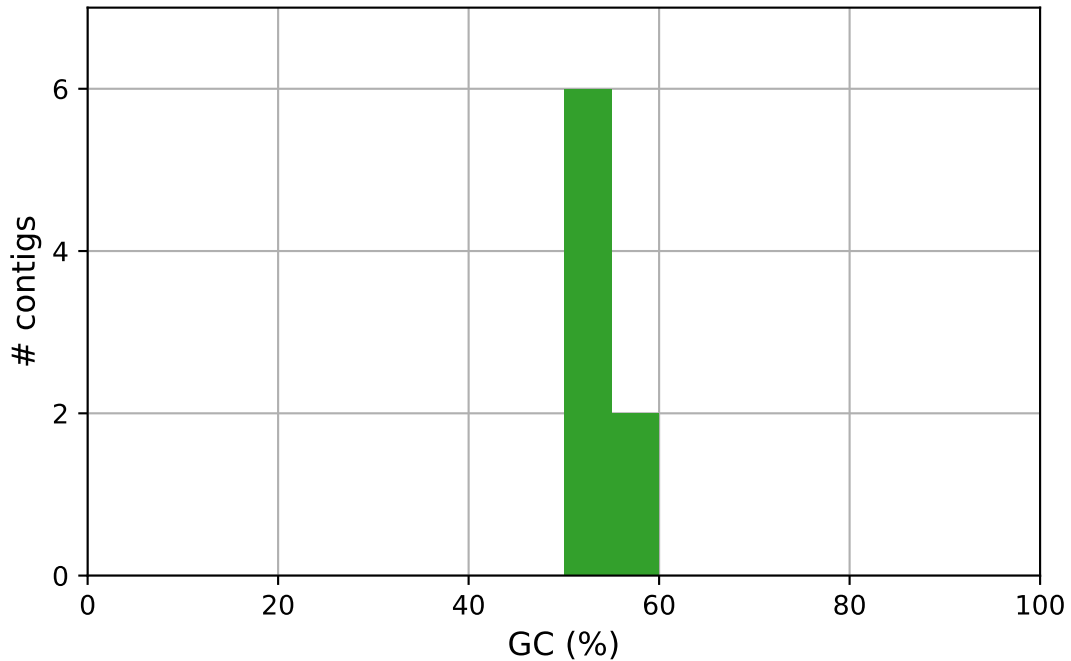


A_STAR GC content



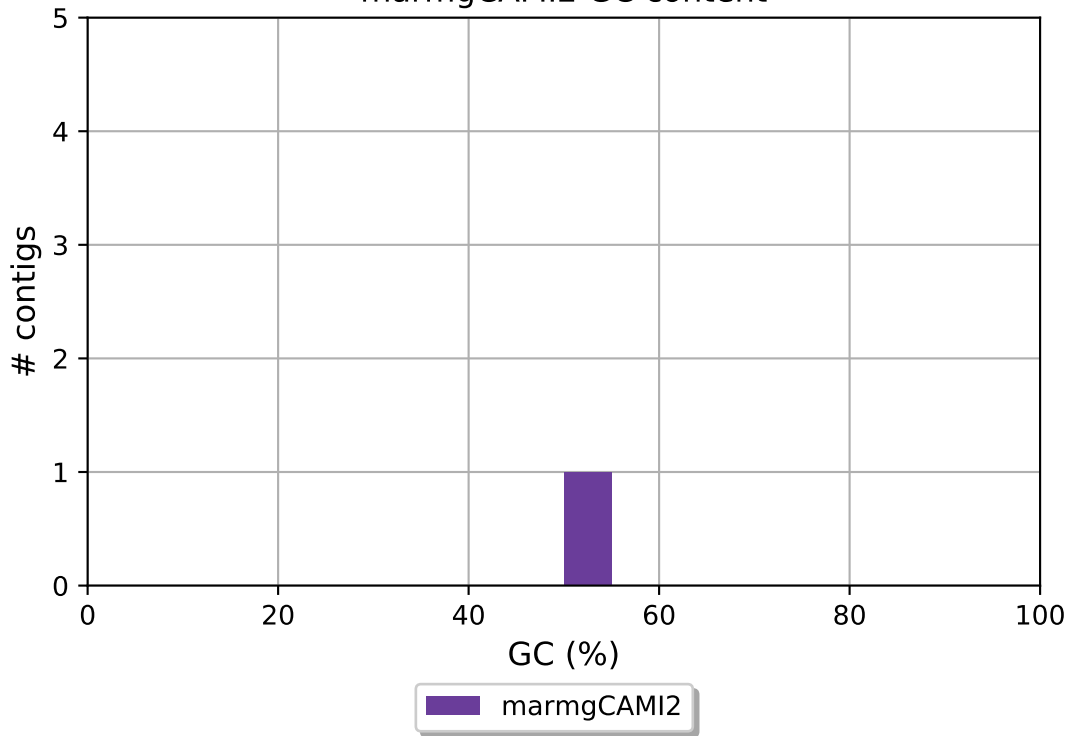
A_STAR

HipMer GC content

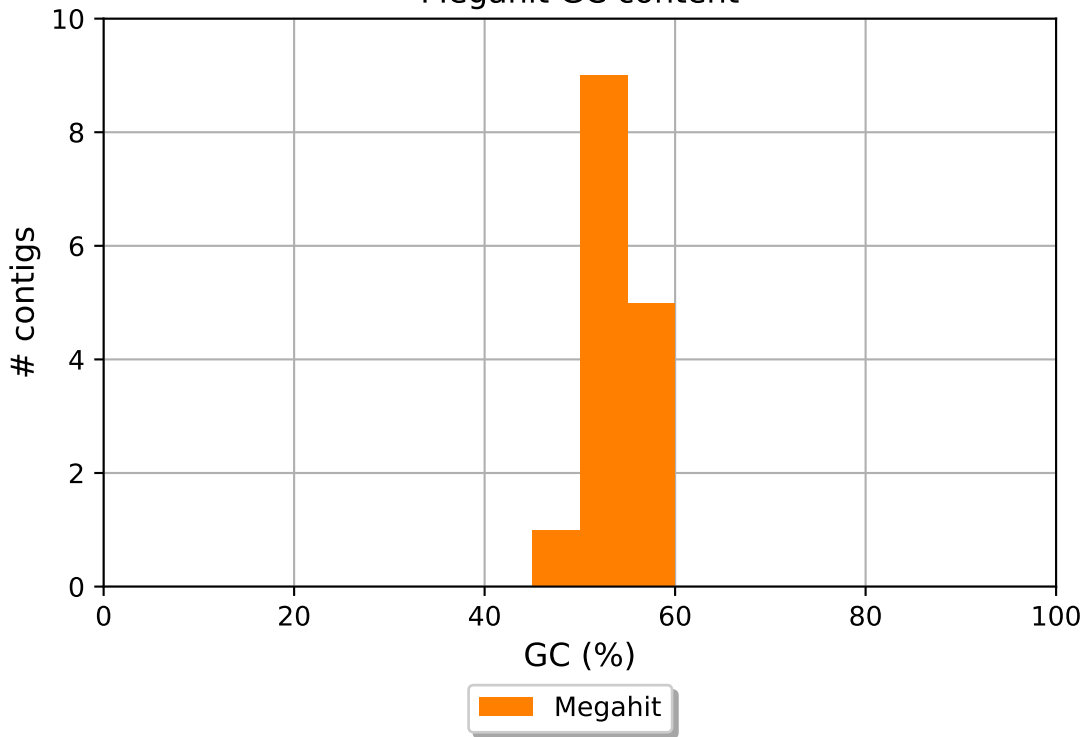


HipMer

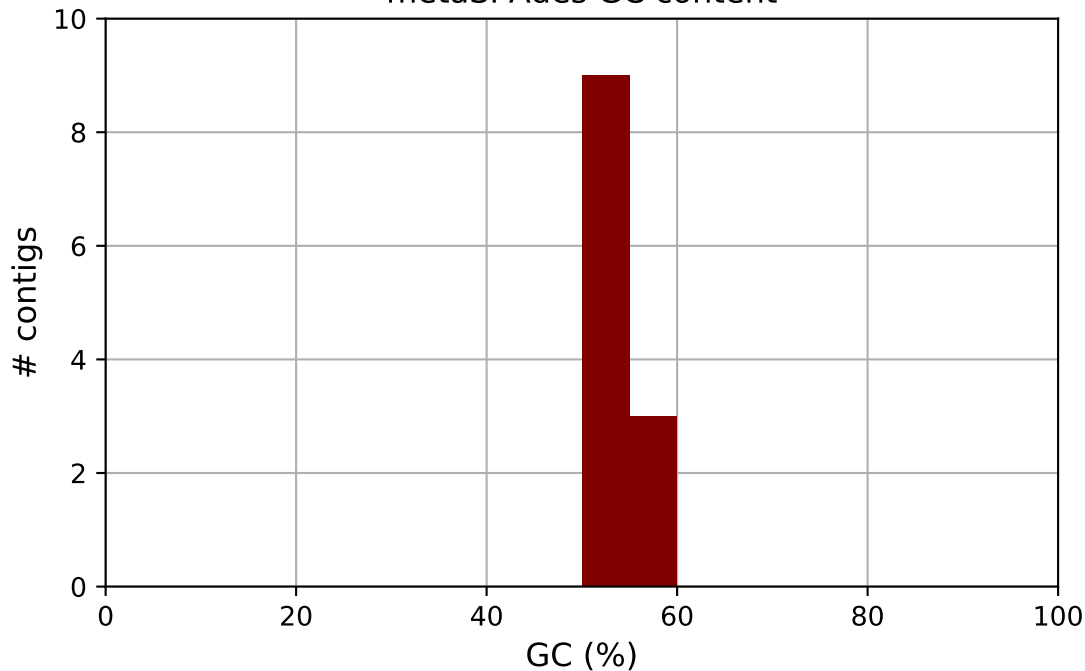
marmgCAMI2 GC content



Megahit GC content

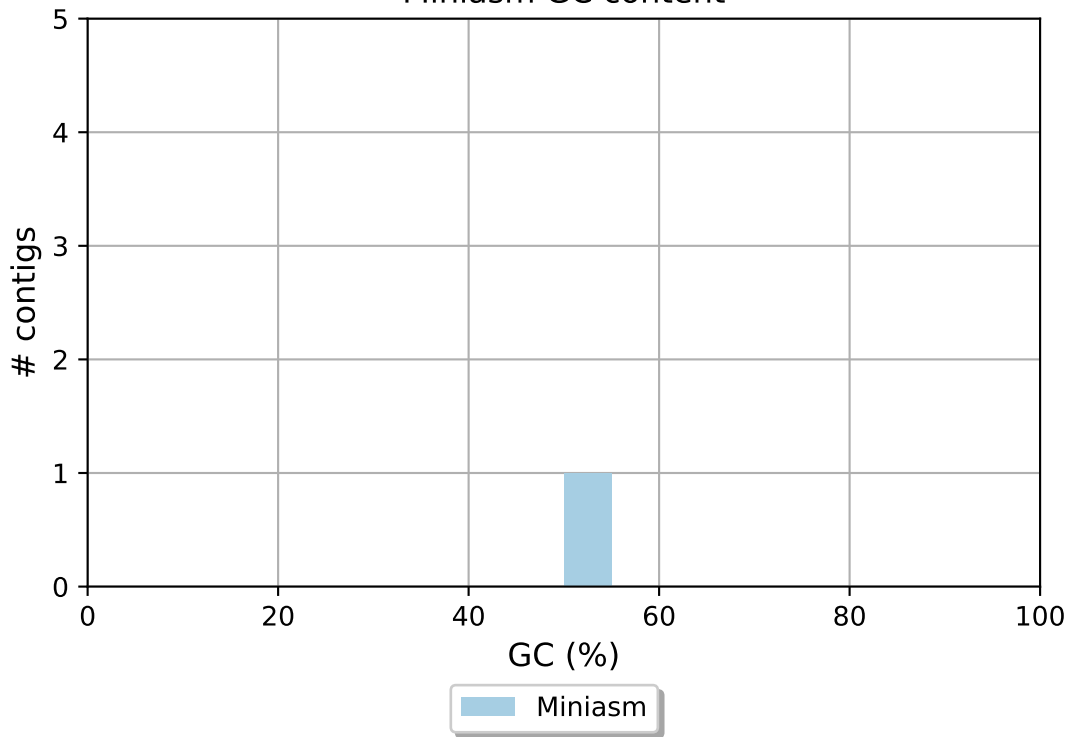


metaSPAdes GC content

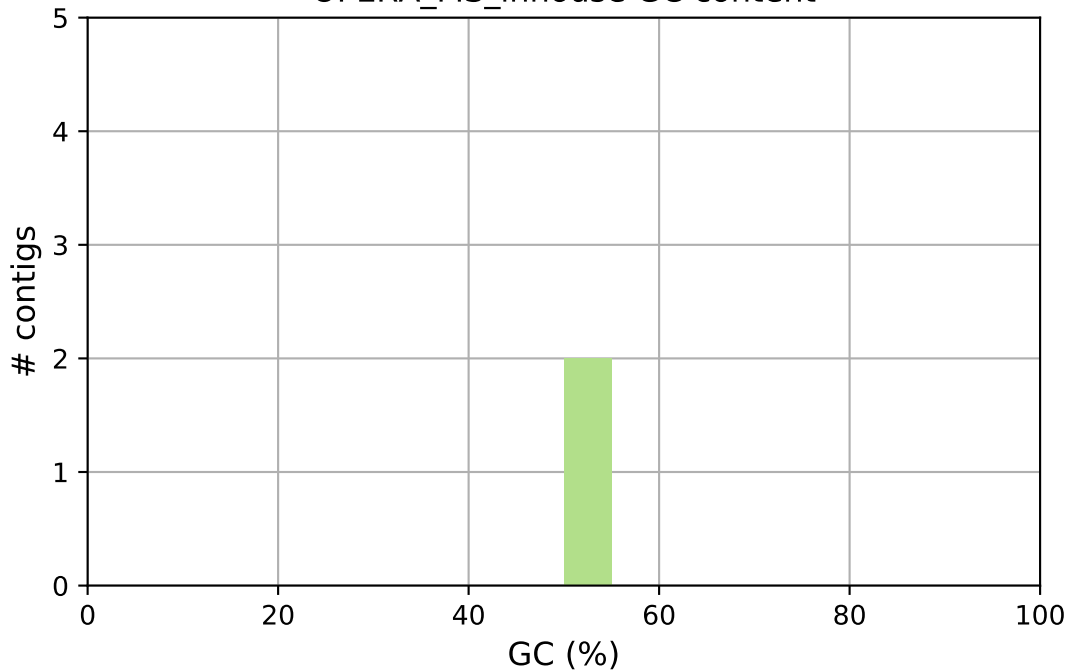


metaSPAdes

Miniasm GC content

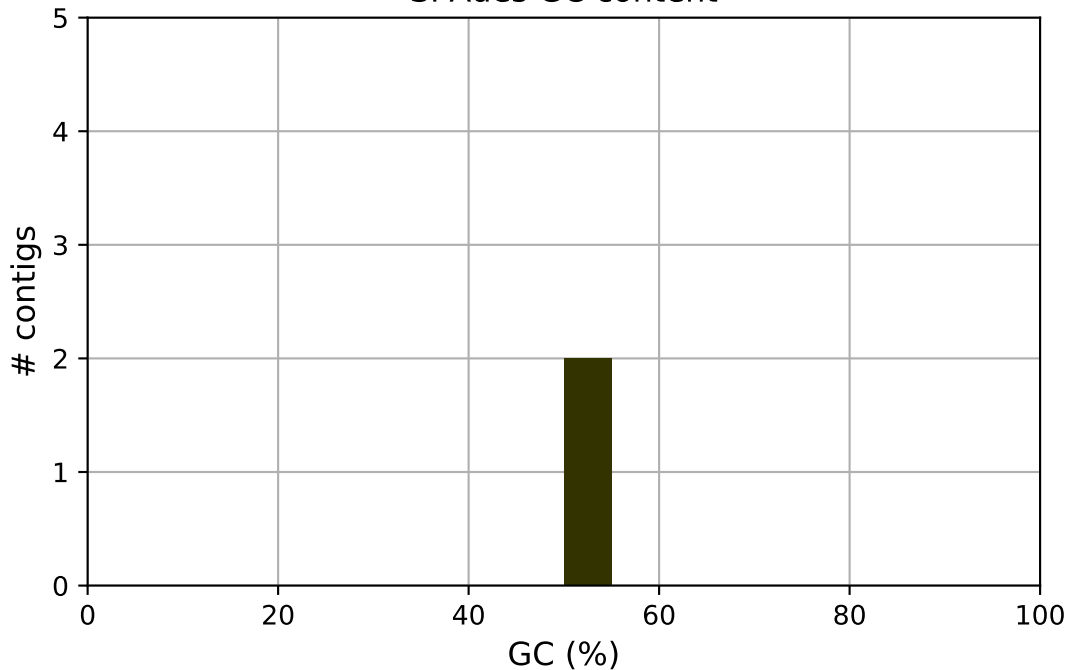


OPERA_MS_inhouse GC content



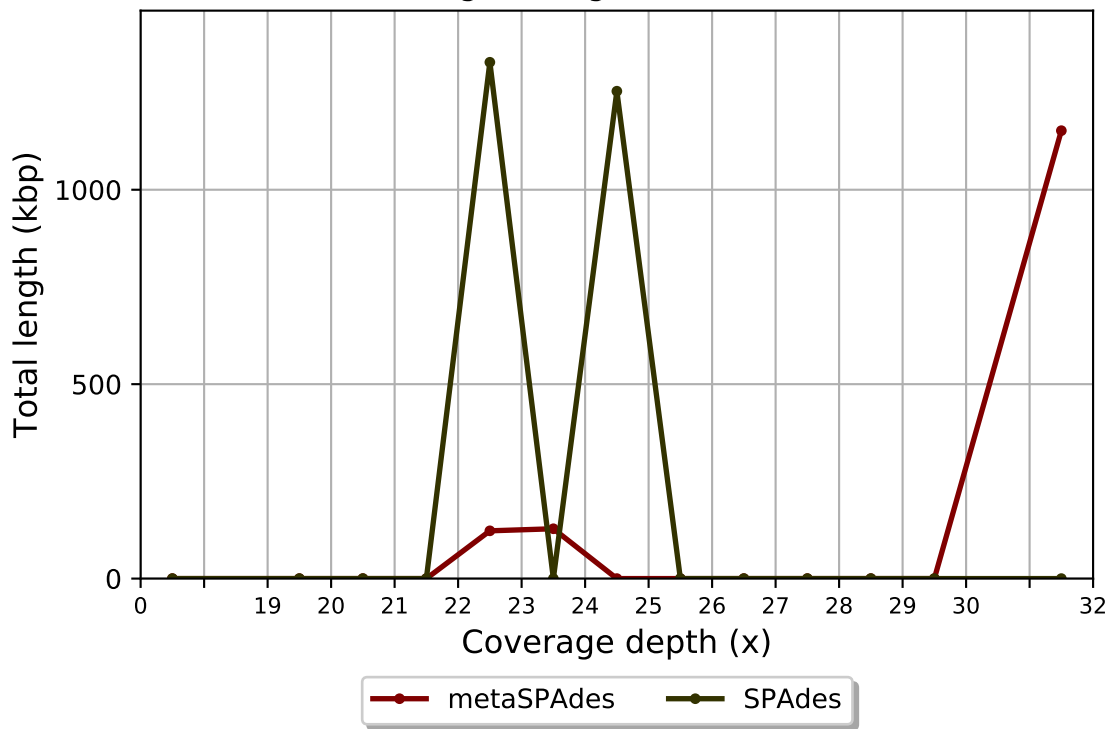
OPERA_MS_inhouse

SPAdes GC content

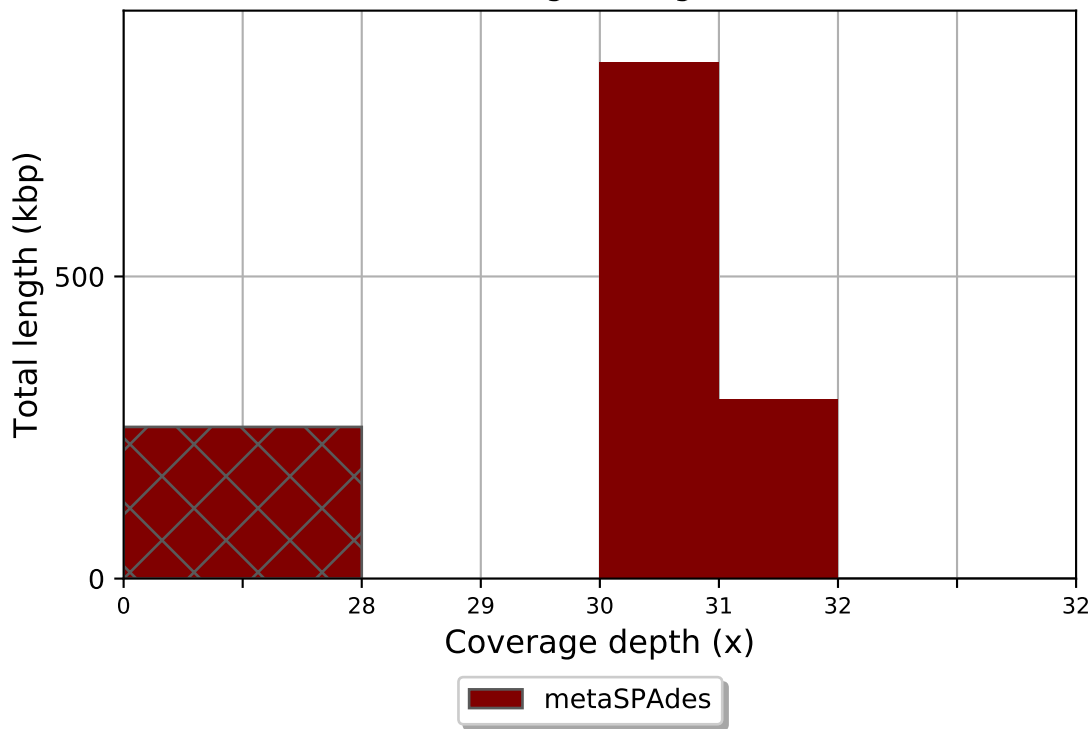


SPAdes

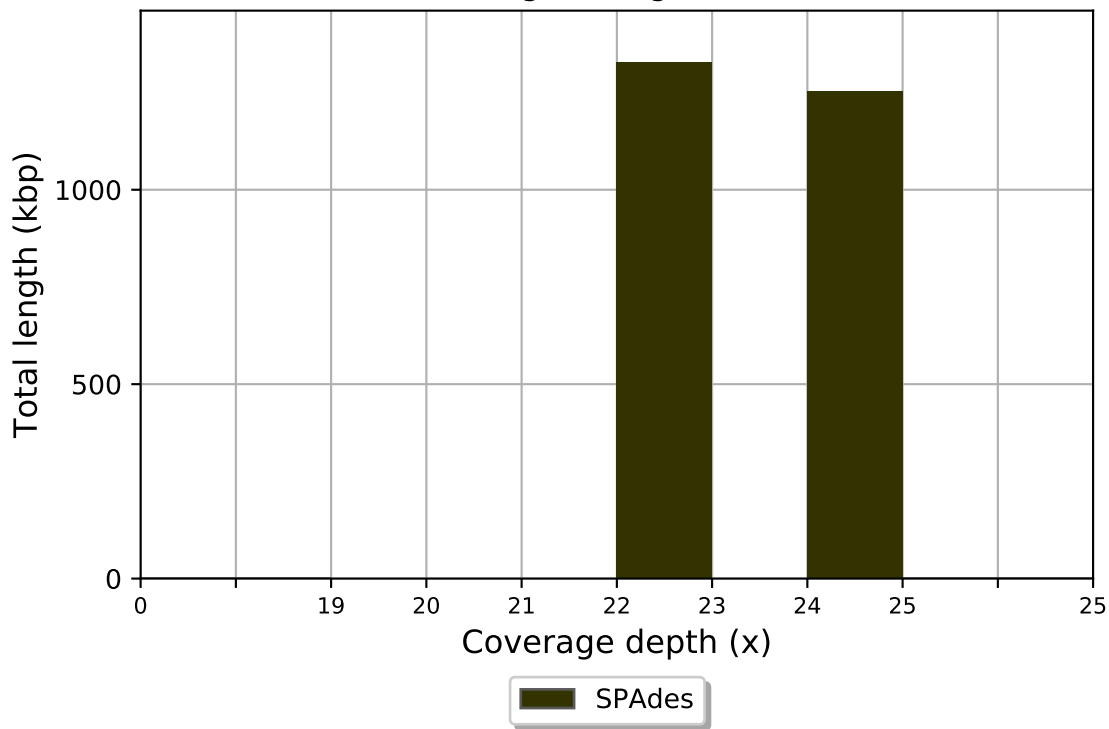
Coverage histogram (bin size: 1x)



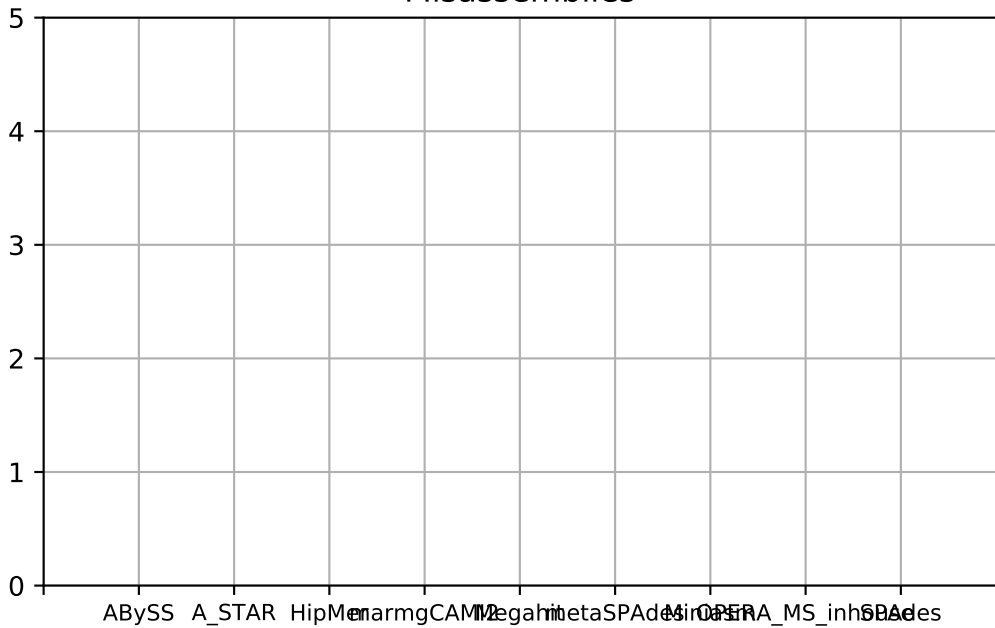
metaSPAdes coverage histogram (bin size: 1x)



SPAdes coverage histogram (bin size: 1x)



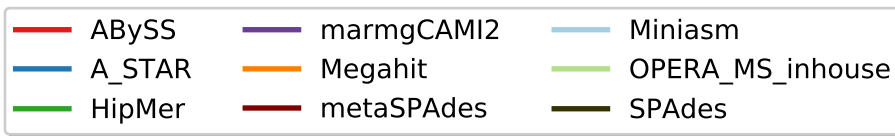
Misassemblies



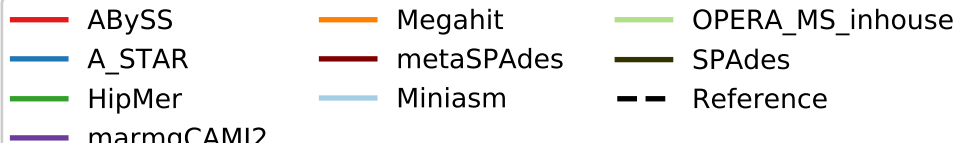
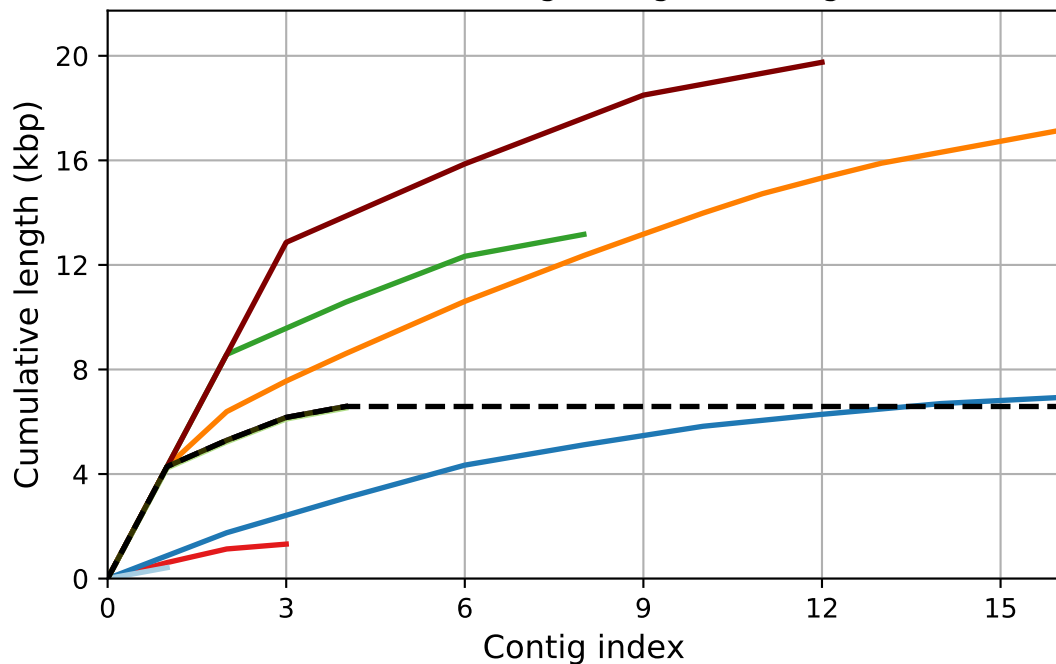
FRCurve (misassemblies)



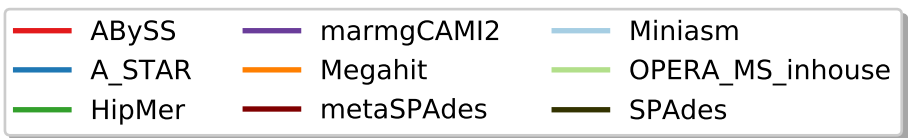
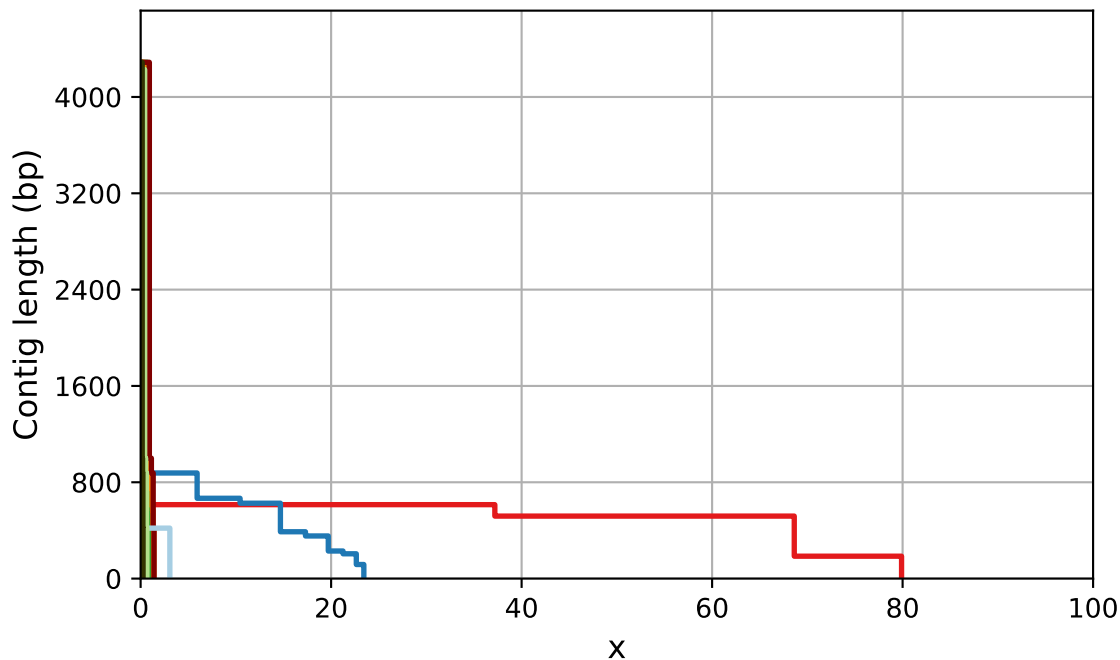
Feature space



Cumulative length (aligned contigs)



NAx



NGAx

