

Report

	ABySS	A_STAR	Flye	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	SPAdes
# contigs (>= 1000 bp)	0	8	4	3	1	4	3	3	1
# contigs (>= 5000 bp)	0	4	4	2	1	4	3	3	1
# contigs (>= 10000 bp)	0	4	4	2	1	4	3	3	1
# contigs (>= 25000 bp)	0	4	2	2	1	4	3	3	1
# contigs (>= 50000 bp)	0	4	0	2	1	4	3	3	1
Total length (>= 1000 bp)	0	2436774	86436	779035	1667163	266645	3736443	7286997	1667163
Total length (>= 5000 bp)	0	2432046	86436	776721	1667163	266645	3736443	7286997	1667163
Total length (>= 10000 bp)	0	2432046	86436	776721	1667163	266645	3736443	7286997	1667163
Total length (>= 25000 bp)	0	2432046	56760	776721	1667163	266645	3736443	7286997	1667163
Total length (>= 50000 bp)	0	2432046	0	776721	1667163	266645	3736443	7286997	1667163
# contigs	4	8	4	3	1	10	3	3	1
Largest contig	847	1147365	28380	705729	1667163	73247	1667163	2428999	1667163
Total length	2941	2436774	86436	779035	1667163	270098	3736443	7286997	1667163
Reference length	6488	6488	6488	6488	6488	6488	6488	6488	6488
GC (%)	45.66	54.19	55.39	54.31	53.74	55.24	53.59	50.45	53.74
Reference GC (%)	45.75	45.75	45.75	45.75	45.75	45.75	45.75	45.75	45.75
N50	813	1147365	28380	705729	1667163	73227	1034640	2428999	1667163
NG50	-	1147365	28380	705729	1667163	73247	1667163	2428999	1667163
N75	704	1147365	14838	705729	1667163	68001	1034640	2428999	1667163
NG75	-	1147365	28380	705729	1667163	73247	1667163	2428999	1667163
L50	2	2	2	1	1	2	2	2	1
LG50	-	1	1	1	1	1	1	1	1
L75	3	2	3	1	1	3	3	3	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	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	4	0	2	1	3	3	3	1
# unaligned contigs	0 + 0 part	0 + 4 part	0 + 4 part	0 + 2 part	0 + 1 part	0 + 5 part	0 + 3 part	0 + 3 part	0 + 1 part
Unaligned length	0	2414786	75268	766011	1660675	252359	3716979	7267536	1660675
Genome fraction (%)	42.602	99.615	86.020	100.000	100.000	100.000	100.000	100.000	100.000
Duplication ratio	1.064	3.402	2.001	2.007	1.000	2.734	3.000	3.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	2.82	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	495.13	0.00	15.41	0.00	339.09	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	107.51	30.83	0.00	30.83	0.00	46.24	0.00
Largest alignment	805	2094	3184	3306	3306	3306	3306	3305	3306
Total aligned length	2764	20982	11168	12907	6488	17461	19464	19461	6488
NA50	704	-	-	-	-	-	-	-	-
NGA50	-	2094	3184	3306	3306	3306	3306	3305	3306
NA75	577	-	-	-	-	-	-	-	-
NGA75	-	1915	3184	3306	3182	3306	3306	3305	3182
LA50	2	-	-	-	-	-	-	-	-
LGA50	-	2	2	1	1	1	1	1	1
LA75	4	-	-	-	-	-	-	-	-
LGA75	-	3	2	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

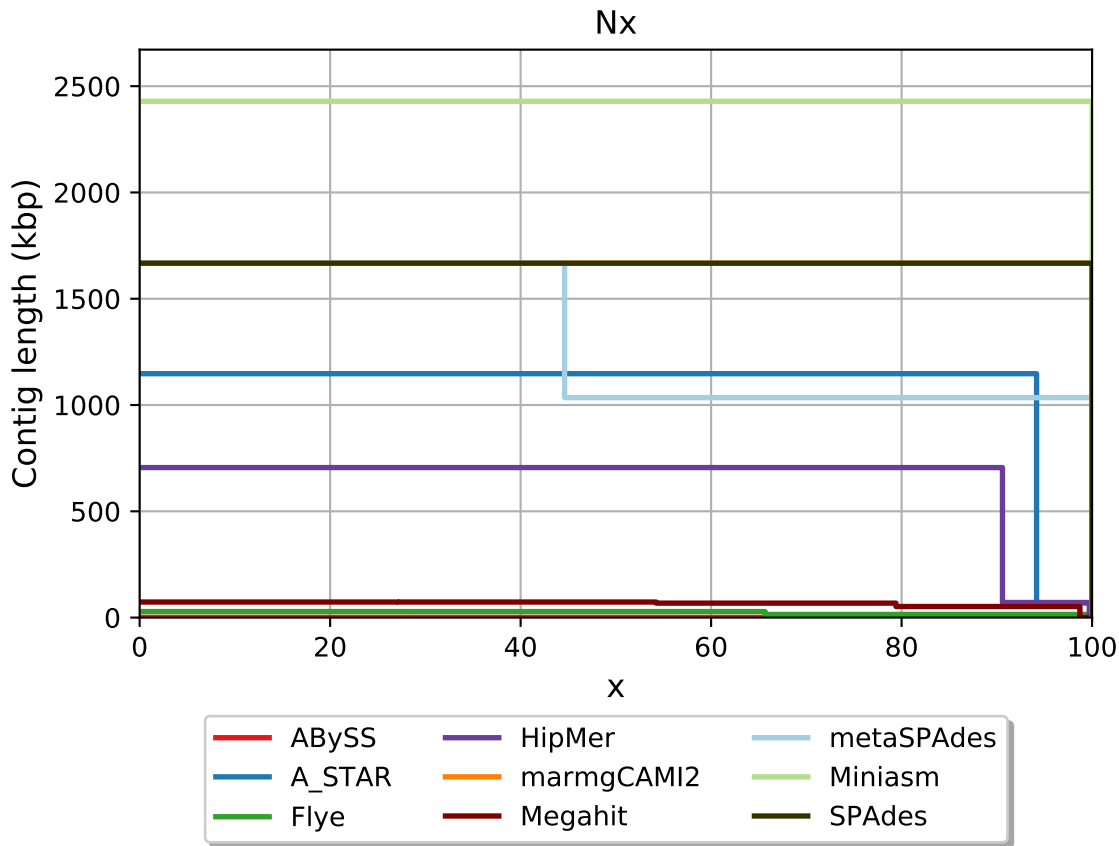
	ABYSS	A_STAR	Flye	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	SPAdes
# misassemblies	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0
# s. relocations	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	0	4	0	0	2	0	0	0
# possible misassemblies	0	0	6	0	0	2	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	4	0	2	1	3	3	3	1
# mismatches	0	32	0	1	0	22	0	0	0
# indels	0	0	6	2	0	2	0	3	0
# indels (<= 5 bp)	0	0	6	0	0	0	0	3	0
# indels (> 5 bp)	0	0	0	2	0	2	0	0	0
Indels length	0	0	6	182	0	270	0	3	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).

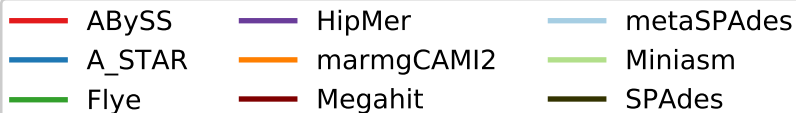
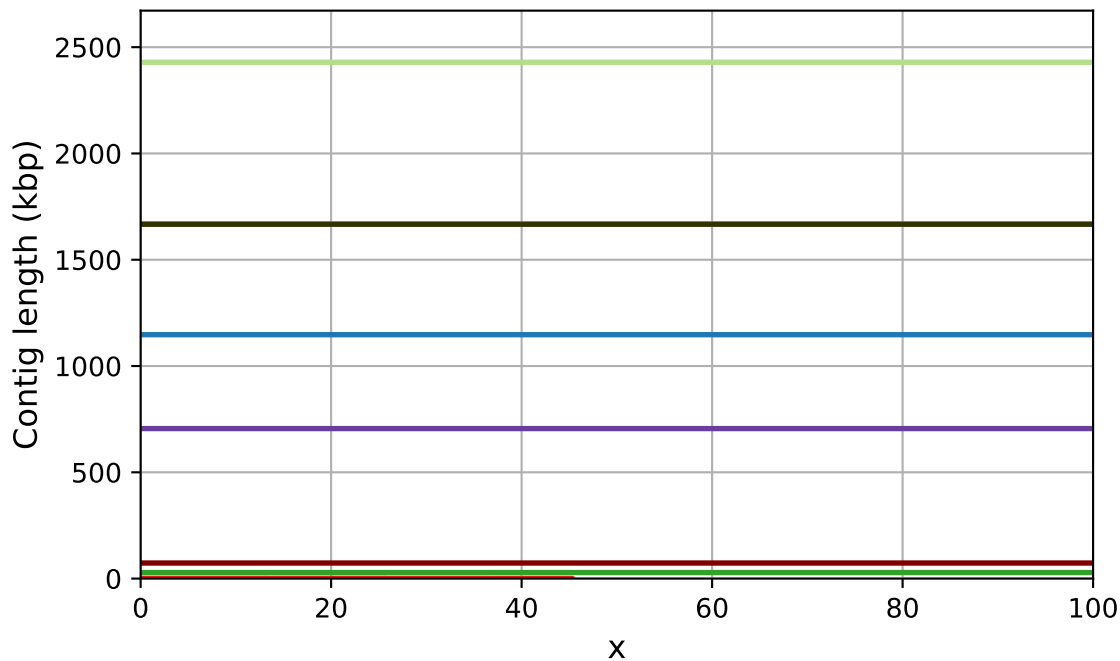
Unaligned report

	ABYSS	A_STAR	Flye	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	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	4	4	2	1	5	3	3	1
Partially unaligned length	0	2414786	75268	766011	1660675	252359	3716979	7267536	1660675
# N's	0	0	0	22	0	0	0	0	0

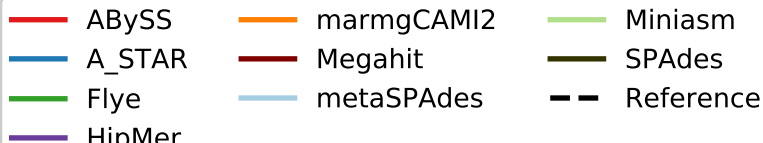
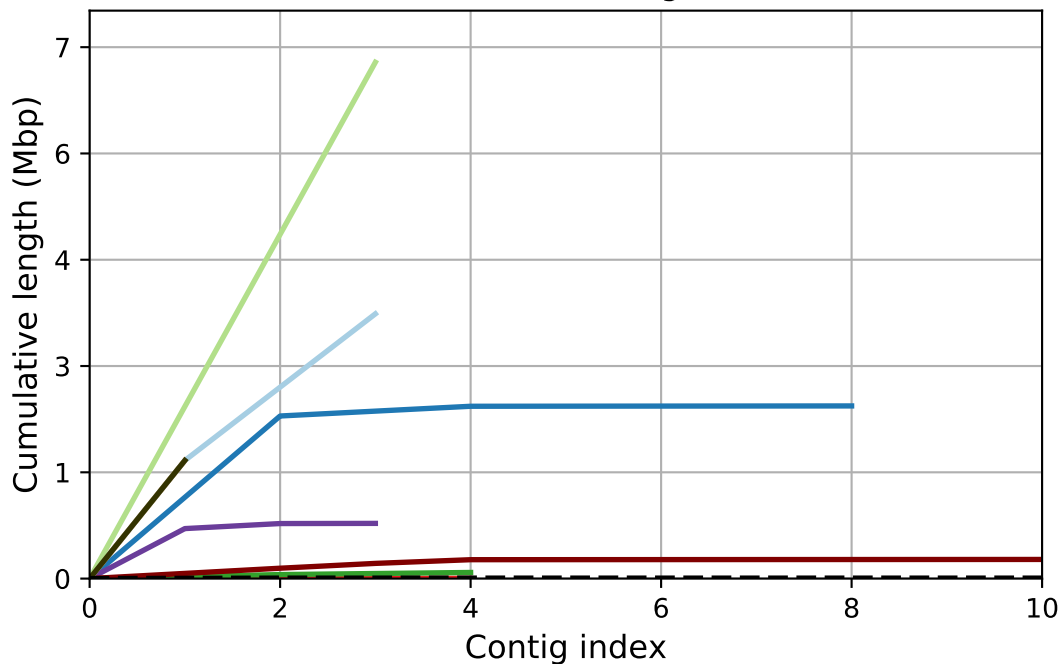
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



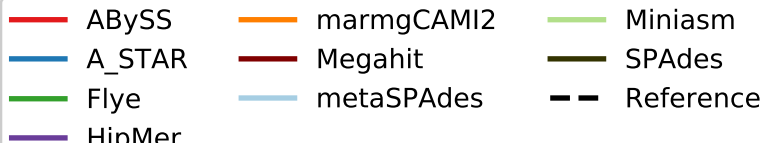
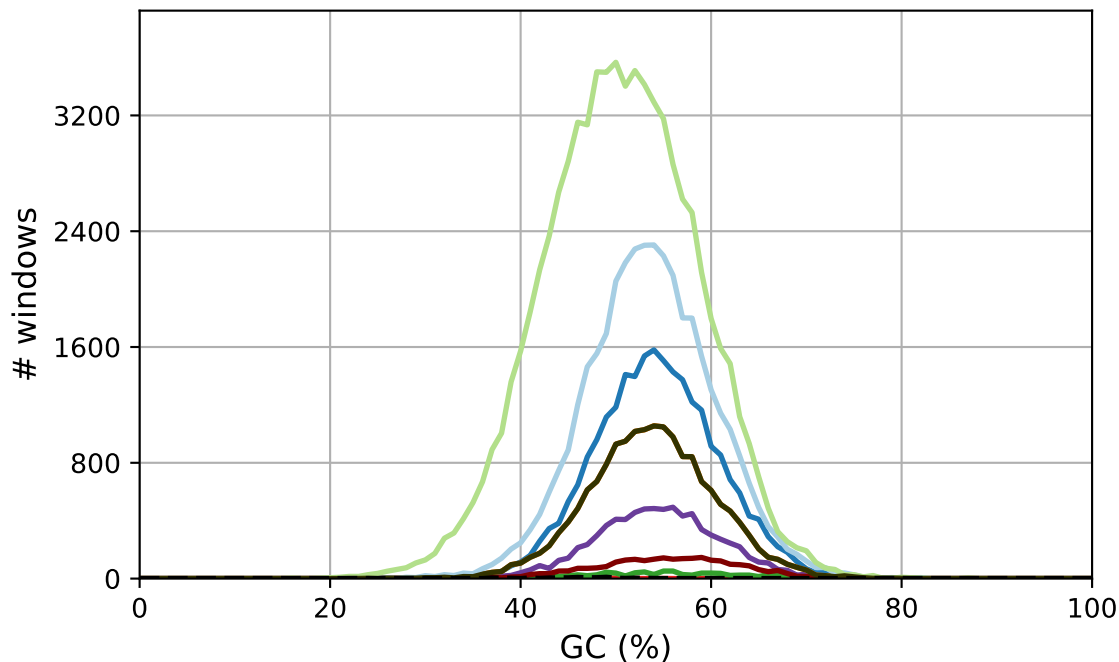
NGx



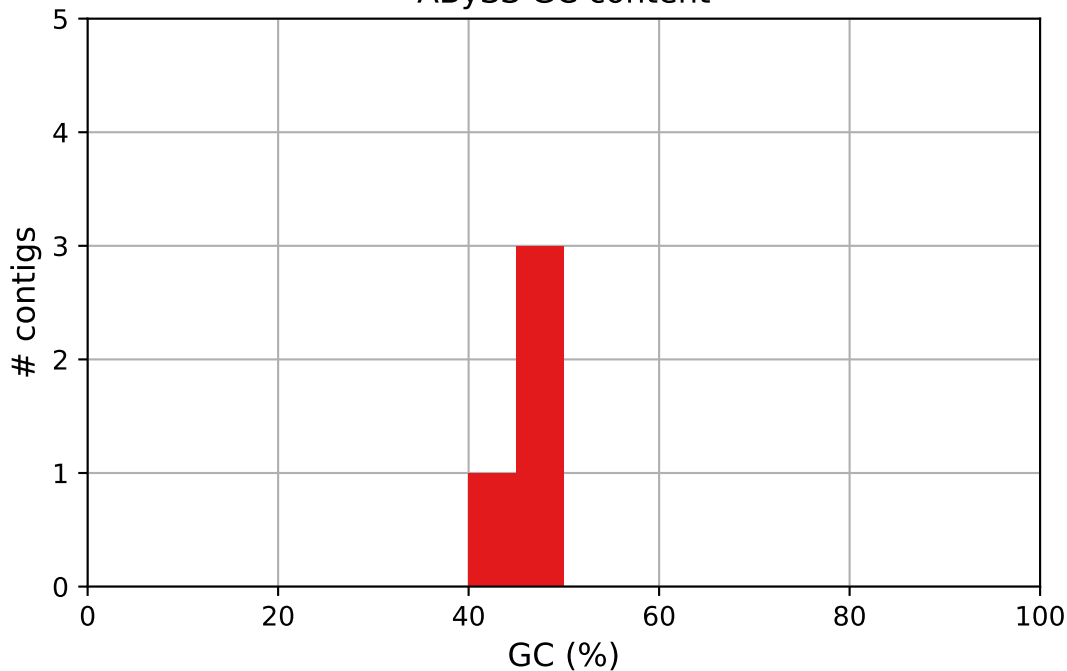
Cumulative length



GC content

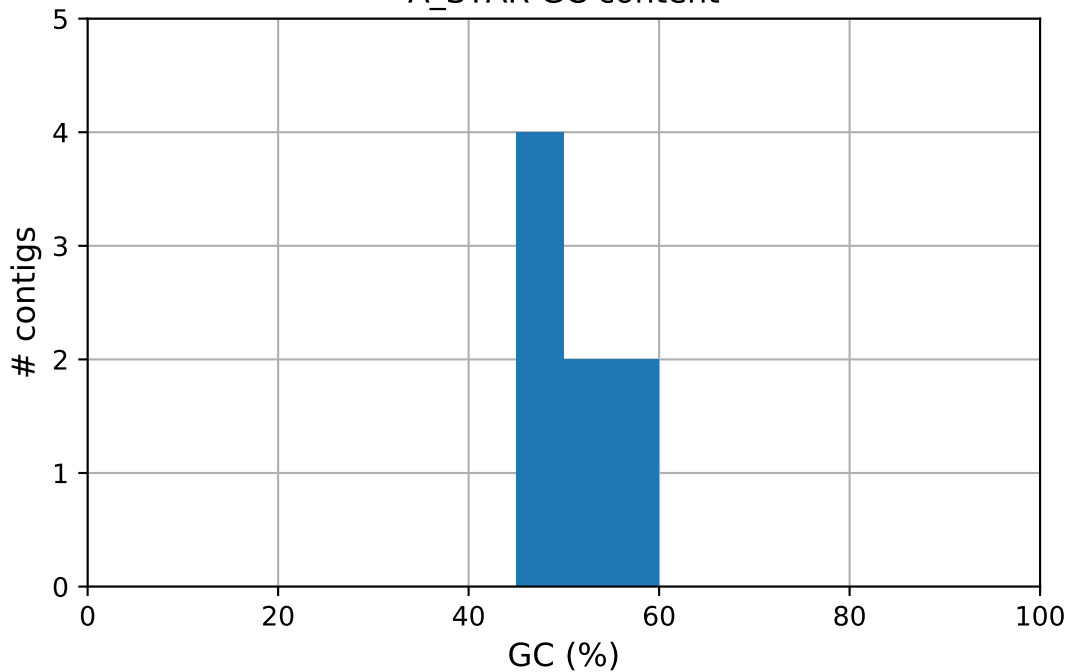


ABySS GC content



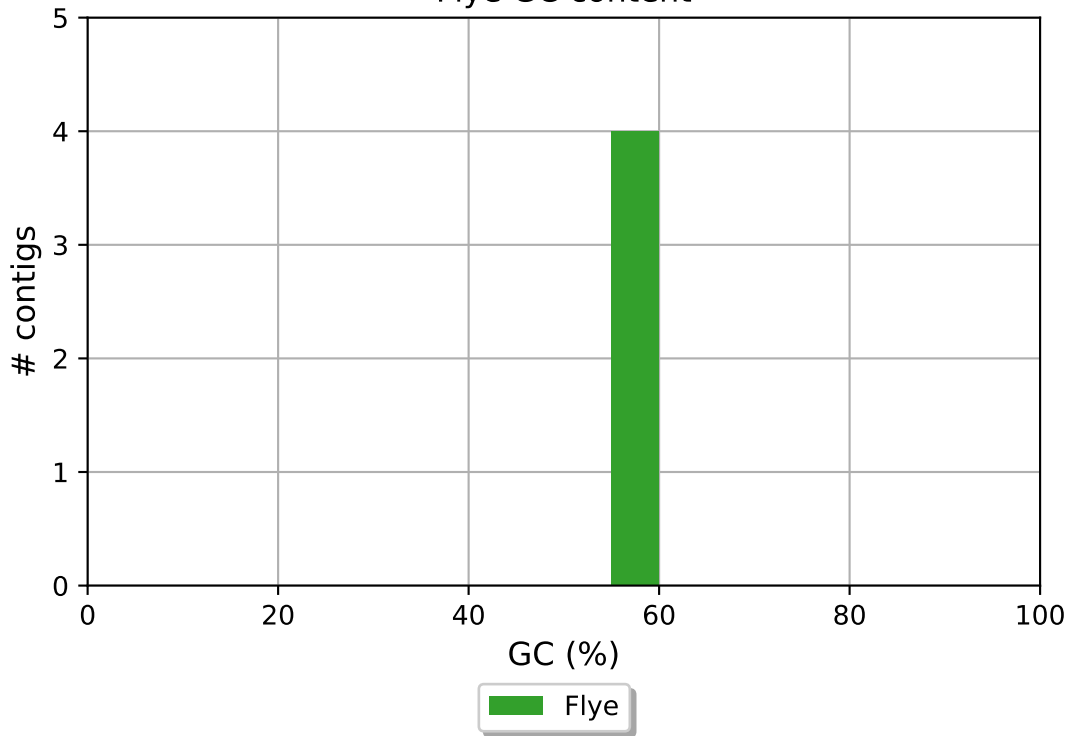
■ ABySS

A_STAR GC content

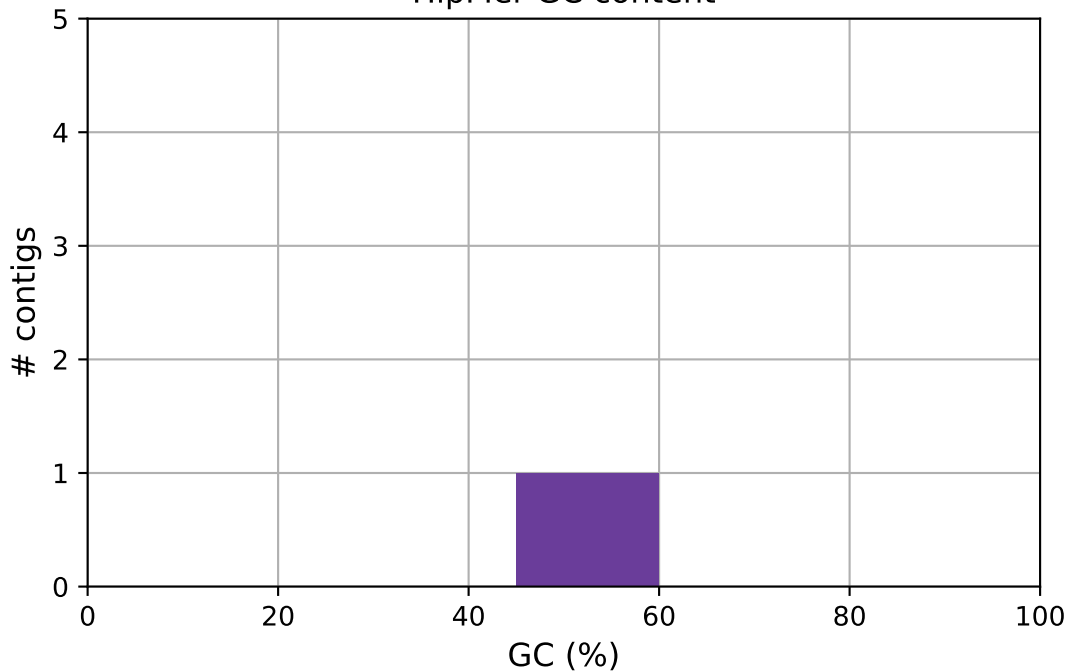


A_STAR

Flye GC content

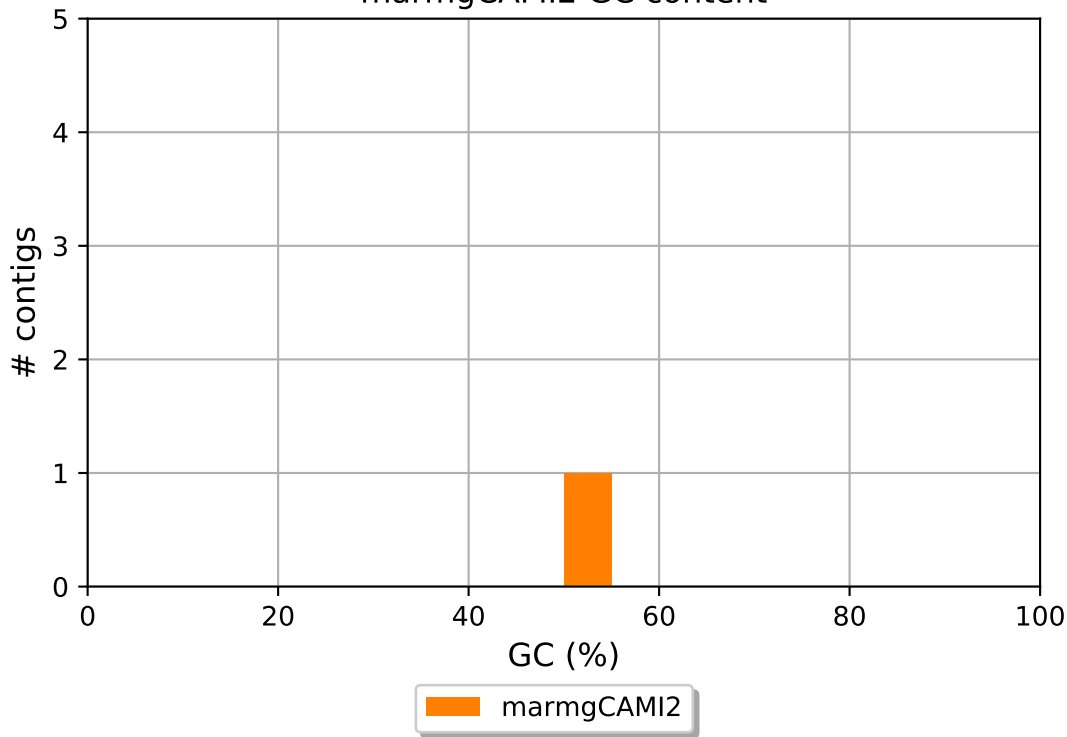


HipMer GC content

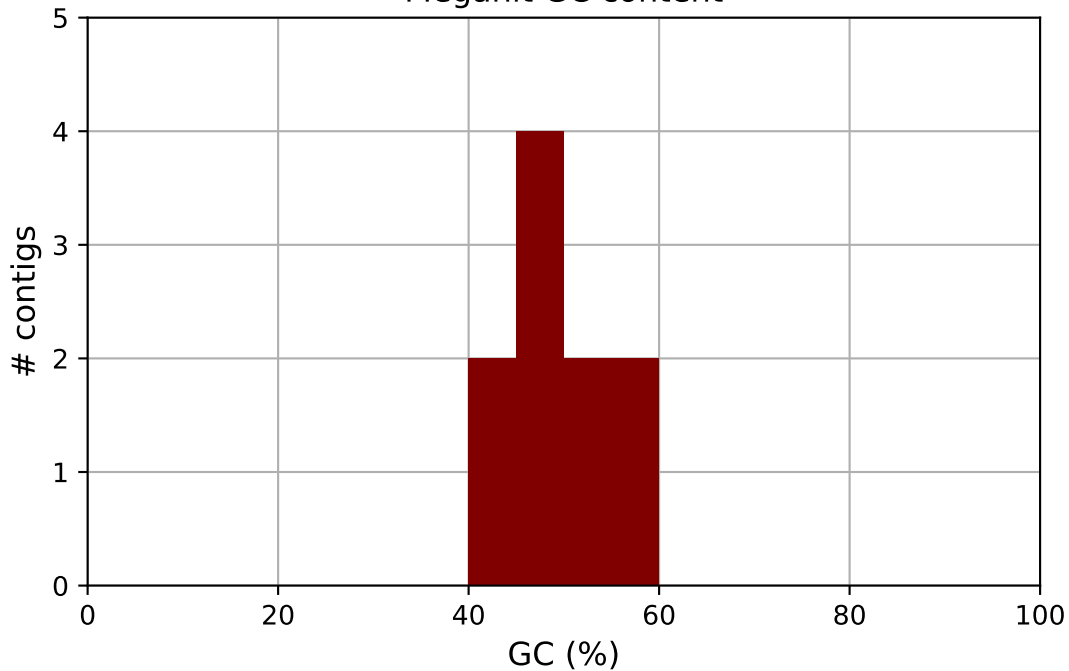


 HipMer

marmgCAMI2 GC content

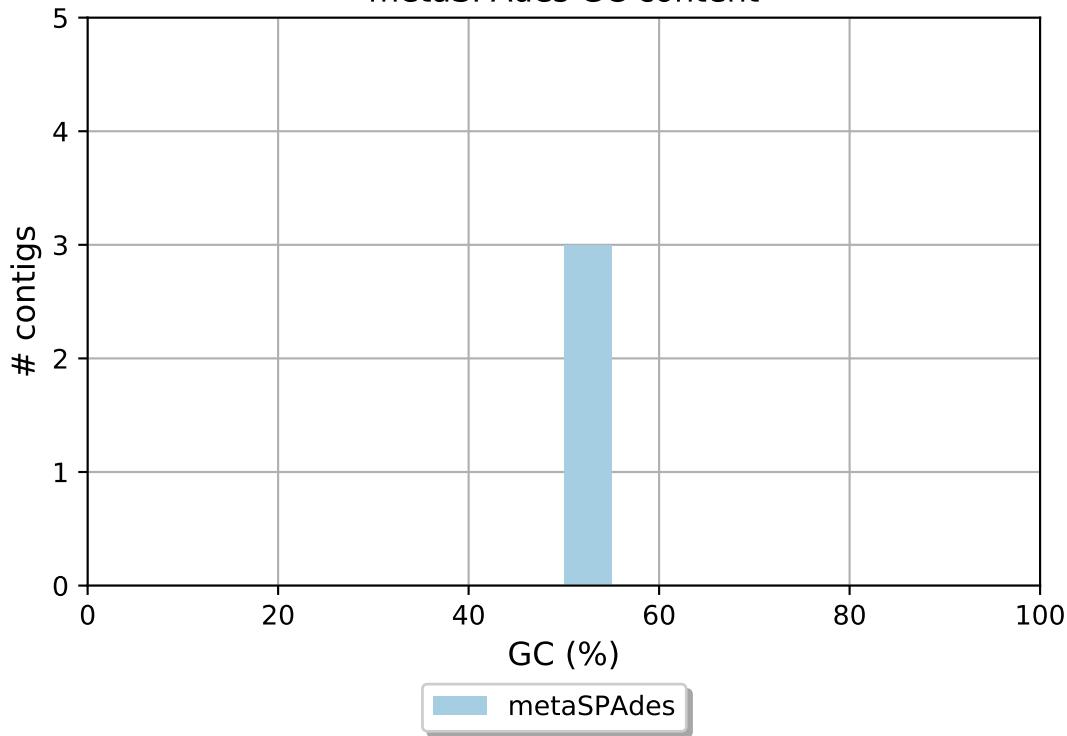


Megahit GC content

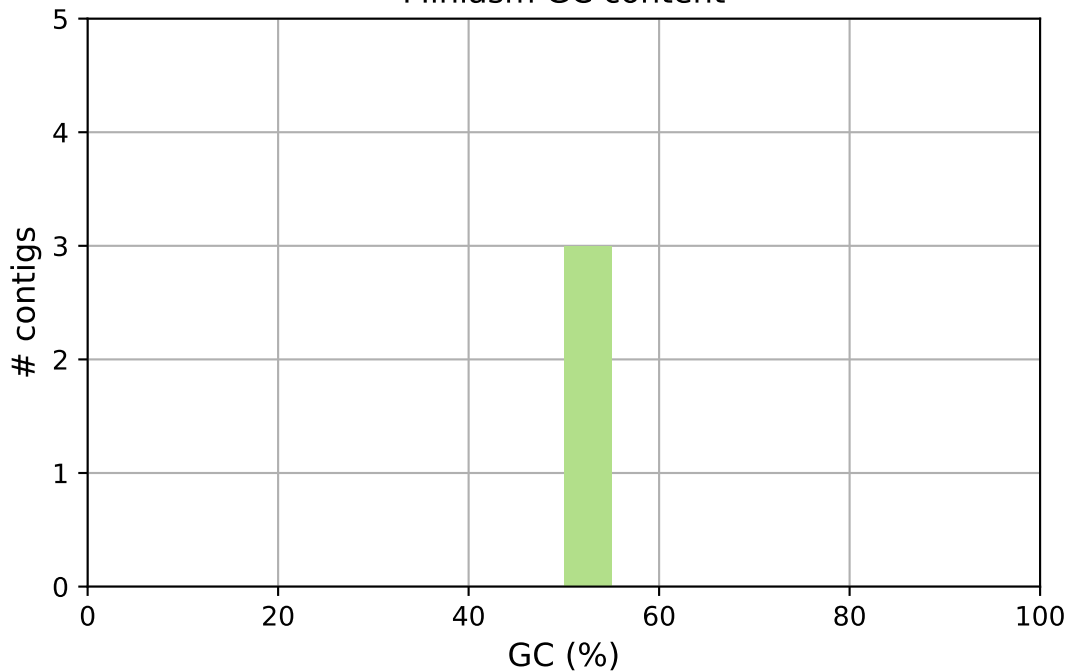


Megahit

metaSPAdes GC content

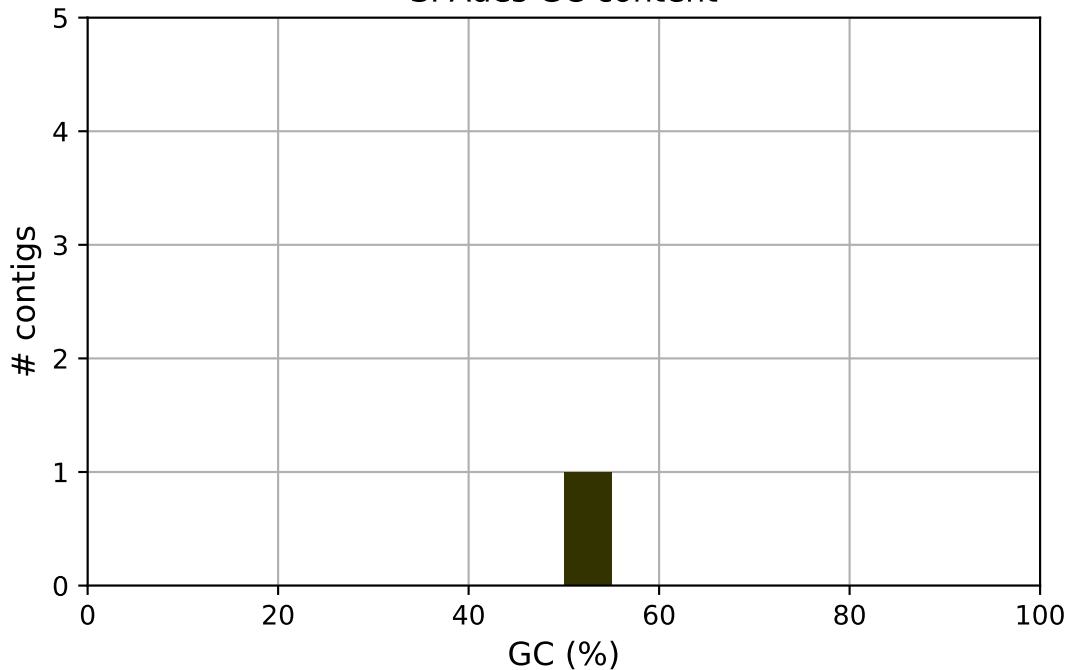


Miniasm GC content



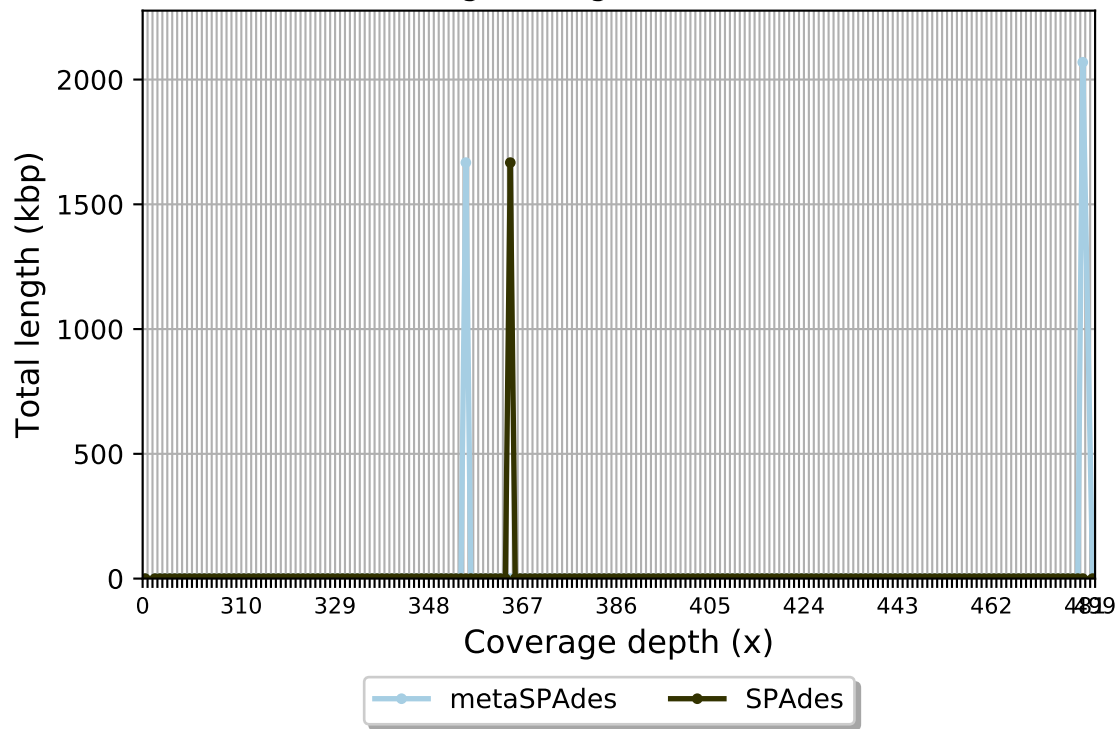
Miniasm

SPAdes GC content

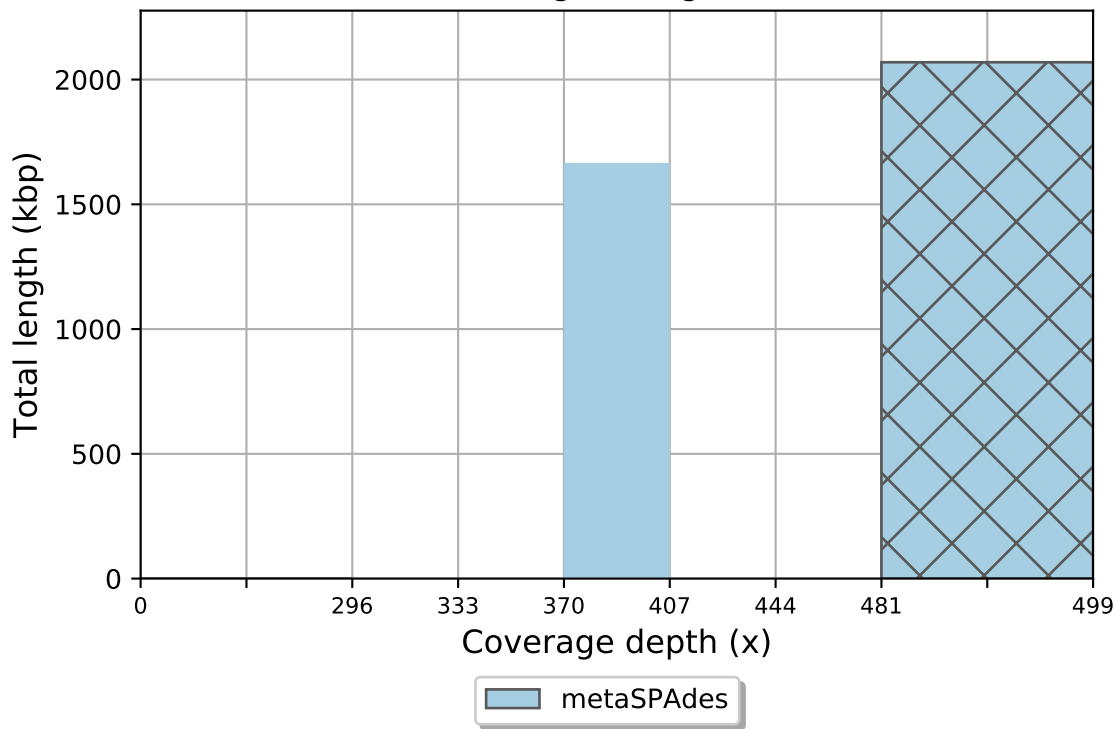


SPAdes

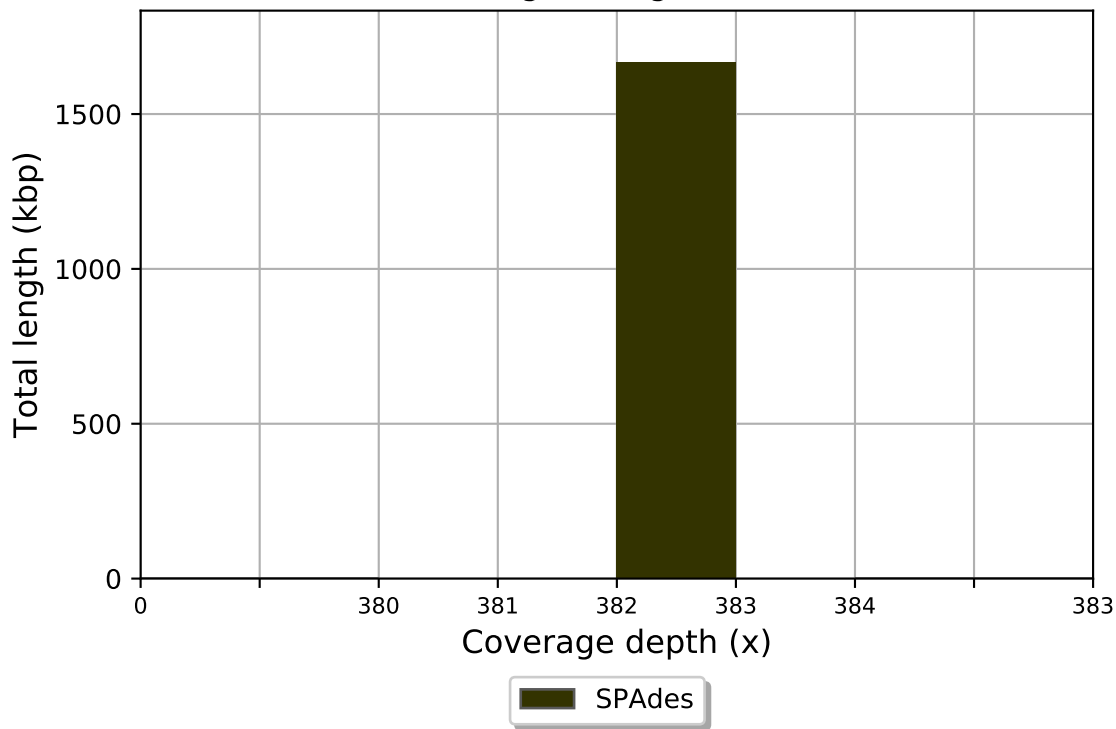
Coverage histogram (bin size: 1x)



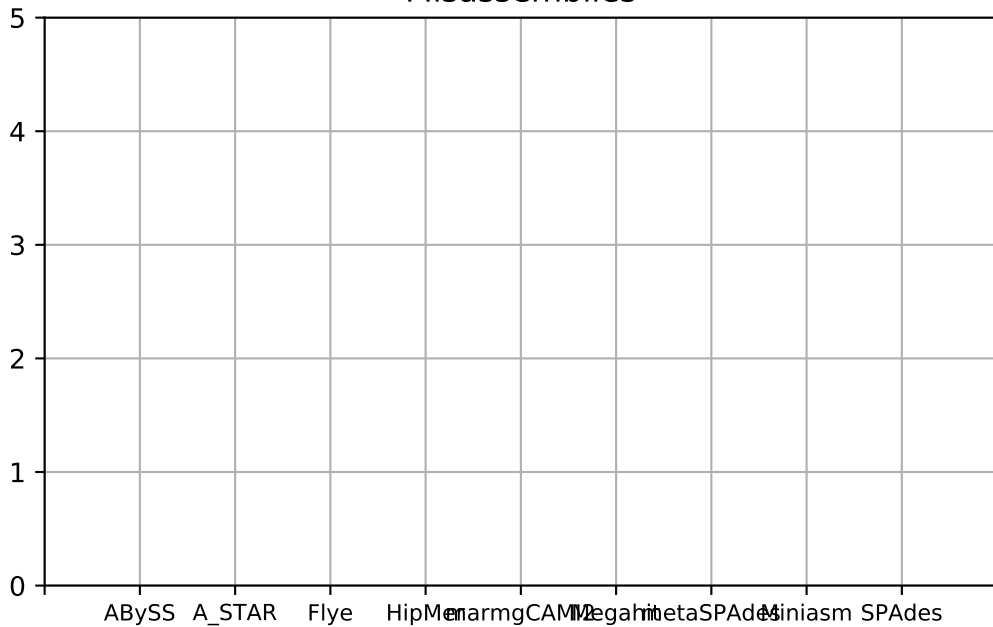
metaSPAdes coverage histogram (bin size: 37x)



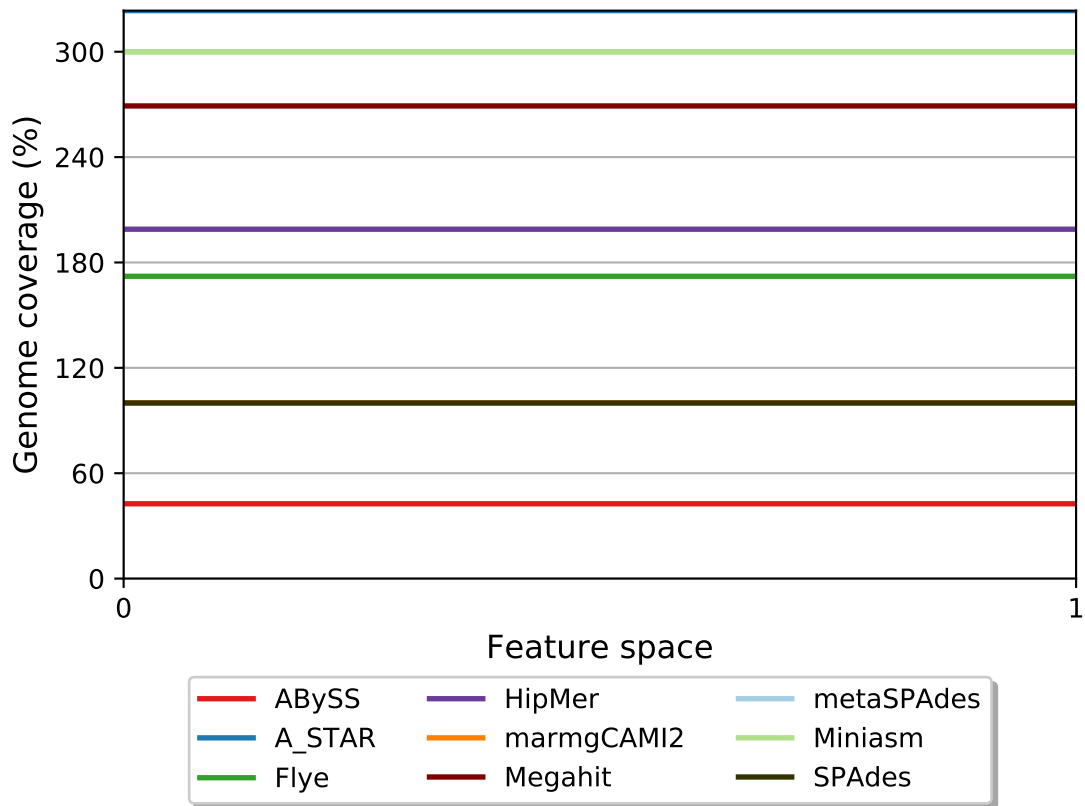
SPAdes coverage histogram (bin size: 1x)



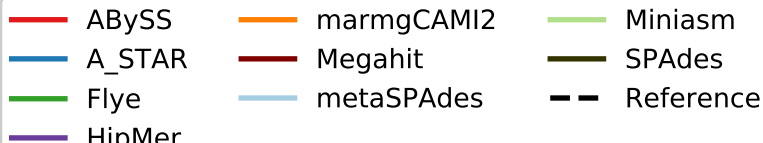
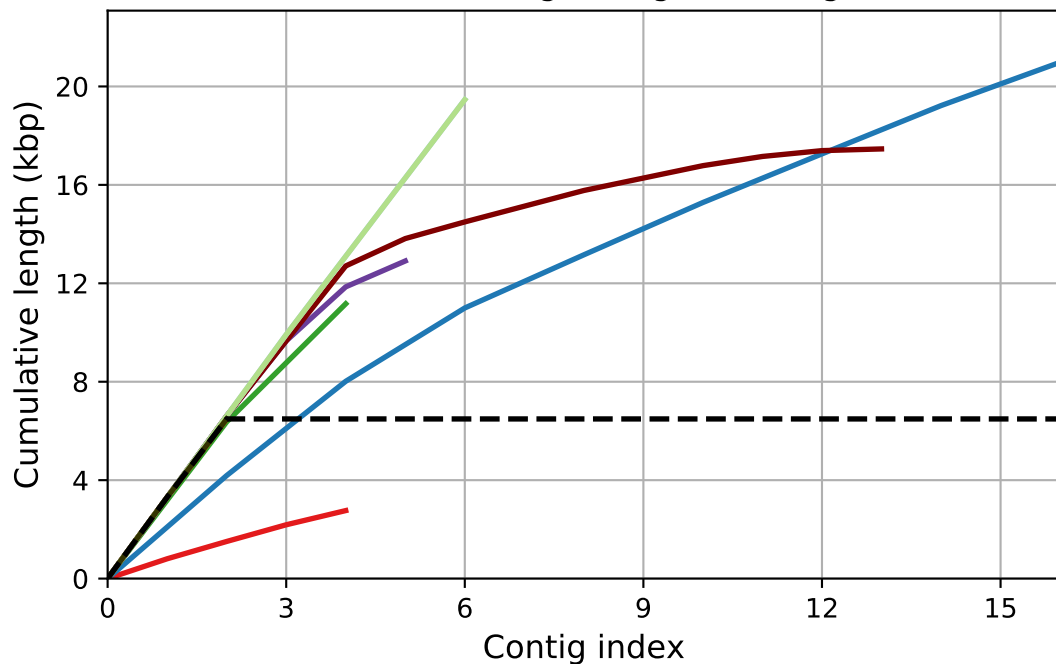
Misassemblies



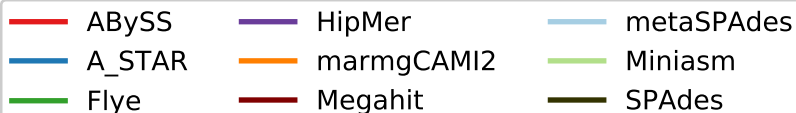
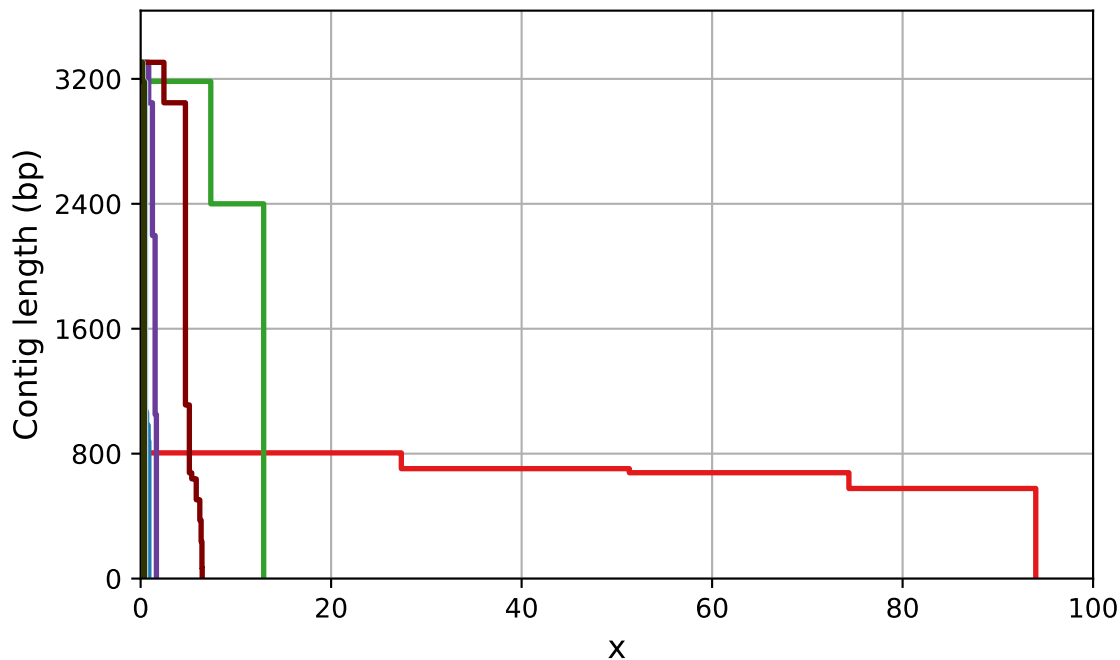
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

