

# Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	12	9	1	14	11	3	4	4
# contigs (>= 5000 bp)	10	8	1	14	11	3	4	4
# contigs (>= 10000 bp)	6	8	1	13	11	3	4	4
# contigs (>= 25000 bp)	4	7	1	8	11	3	4	0
# contigs (>= 50000 bp)	4	5	1	6	7	3	4	0
Total length (>= 1000 bp)	321620	807750	4684311	1021397	894208	396596	371708	83540
Total length (>= 5000 bp)	315960	806333	4684311	1021397	894208	396596	371708	83540
Total length (>= 10000 bp)	292442	806333	4684311	1013935	894208	396596	371708	83540
Total length (>= 25000 bp)	271428	782639	4684311	926879	894208	396596	371708	0
Total length (>= 50000 bp)	271428	715096	4684311	834489	743381	396596	371708	0
# contigs	12	10	1	15	11	3	4	5
Largest contig	74413	333744	4684311	231064	132475	229334	201639	24754
Total length	321620	808566	4684311	1022080	894208	396596	371708	84053
Reference length	10252	10252	10252	10252	10252	10252	10252	10252
GC (%)	44.65	44.21	44.13	44.09	44.32	44.03	43.66	45.10
Reference GC (%)	49.68	49.68	49.68	49.68	49.68	49.68	49.68	49.68
N50	61301	139945	4684311	122131	124560	229334	201639	23209
NG50	74413	333744	4684311	231064	132475	229334	201639	24754
N75	61301	67441	4684311	76024	78851	111769	52360	19019
NG75	74413	333744	4684311	231064	132475	229334	201639	24754
L50	3	2	1	3	4	1	1	2
LG50	1	1	1	1	1	1	1	1
L75	4	4	1	5	6	2	3	3
LG75	1	1	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	2	2	1	2	3	1	1	0
# unaligned contigs	0 + 12 part	0 + 8 part	0 + 1 part	0 + 14 part	0 + 11 part	0 + 3 part	0 + 4 part	0 + 4 part
Unaligned length	312118	788696	4674165	996138	863775	392044	361753	73392
Genome fraction (%)	43.835	98.673	98.966	98.966	98.966	42.041	93.396	98.966
Duplication ratio	2.114	1.964	1.000	2.557	3.000	1.056	1.040	1.051
# N's per 100 kbp	159.82	6.18	0.00	0.00	11.18	0.00	0.00	0.00
# mismatches per 100 kbp	222.52	0.00	0.00	995.47	19.71	23.20	229.77	59.14
# indels per 100 kbp	0.00	9.89	0.00	108.42	29.57	0.00	0.00	19.71
Largest alignment	929	3088	4153	3614	4153	3148	3148	4155
Total aligned length	8988	19827	10146	25942	30433	4552	9957	10523
NGA50	739	2247	3148	3148	4152	-	2247	3148
NGA75	598	2168	2247	3148	4152	-	785	2247
LGA50	6	2	2	2	2	-	2	2
LGA75	10	4	3	3	2	-	5	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

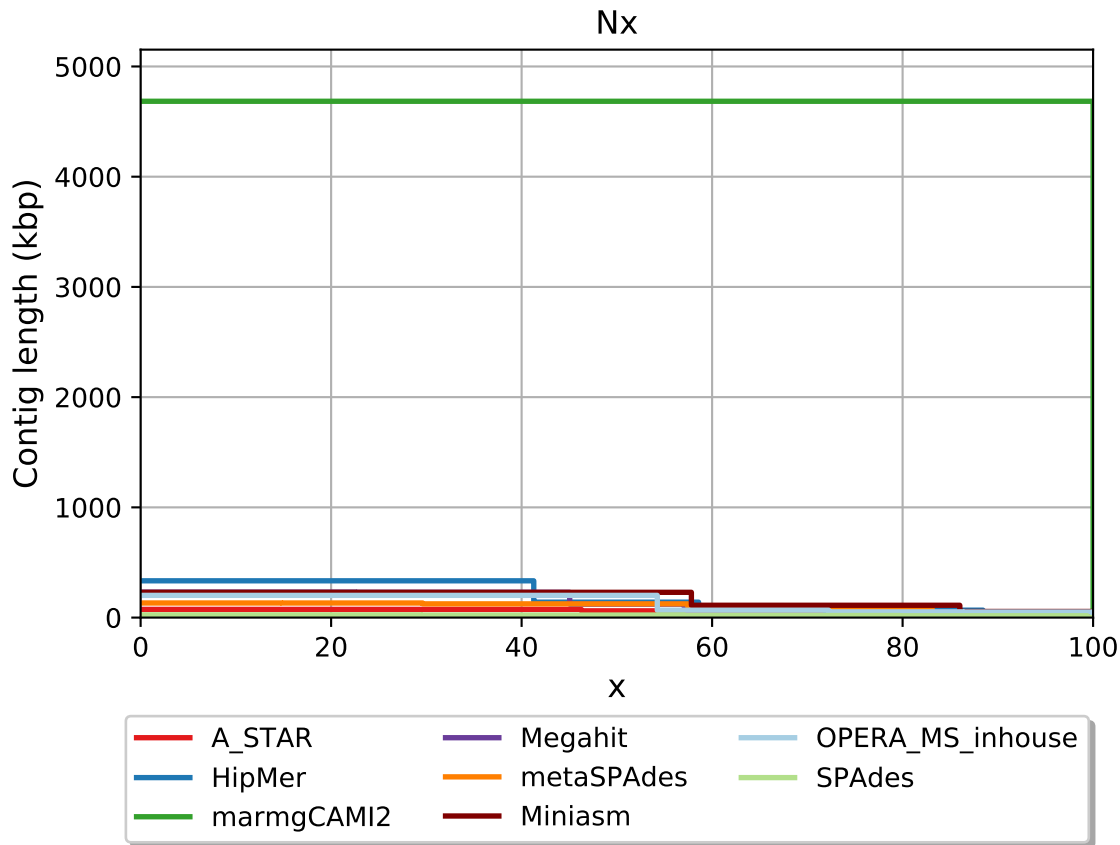
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# possibly misassembled contigs	10	6	0	12	8	2	3	4
# possible misassemblies	12	9	0	16	12	4	5	8
# local misassemblies	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	2	2	1	2	3	1	1	0
# mismatches	10	0	0	101	2	1	22	6
# indels	0	1	0	11	3	0	0	2
# indels (<= 5 bp)	0	0	0	9	1	0	0	2
# indels (> 5 bp)	0	1	0	2	2	0	0	0
Indels length	0	60	0	159	245	0	0	2

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).

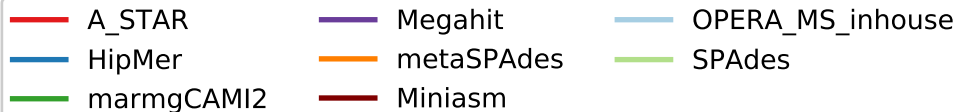
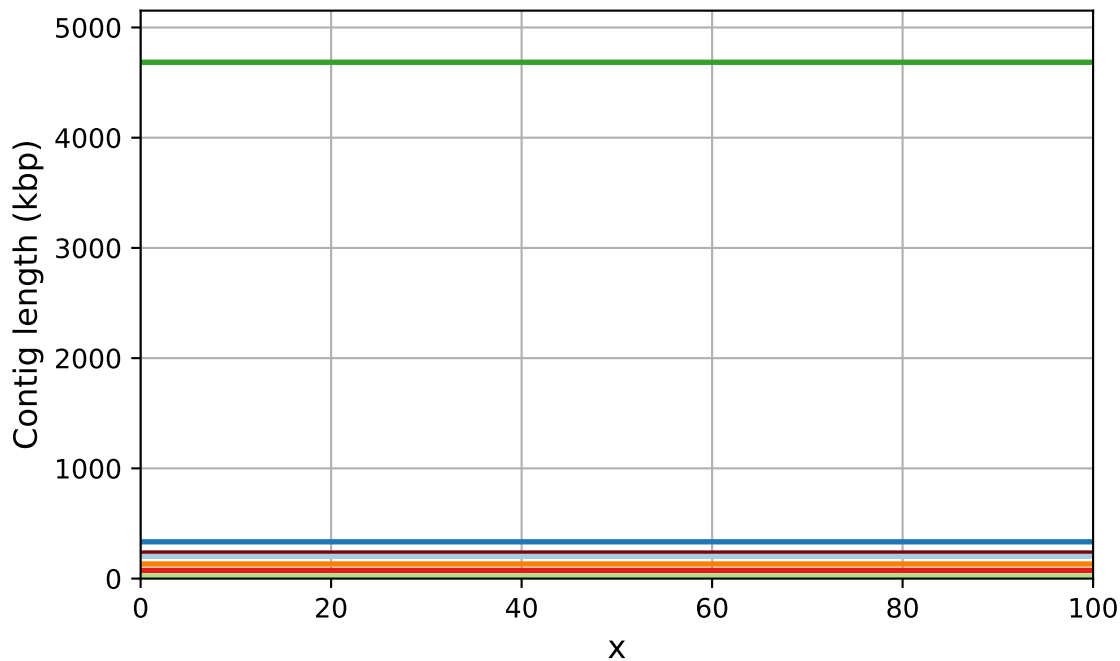
## Unaligned report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	12	8	1	14	11	3	4	4
Partially unaligned length	312118	788696	4674165	996138	863775	392044	361753	73392
# N's	514	50	0	0	100	0	0	0

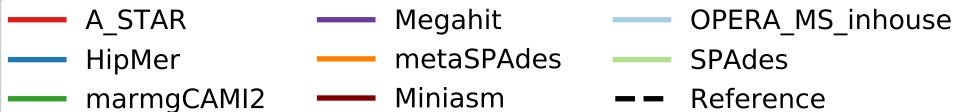
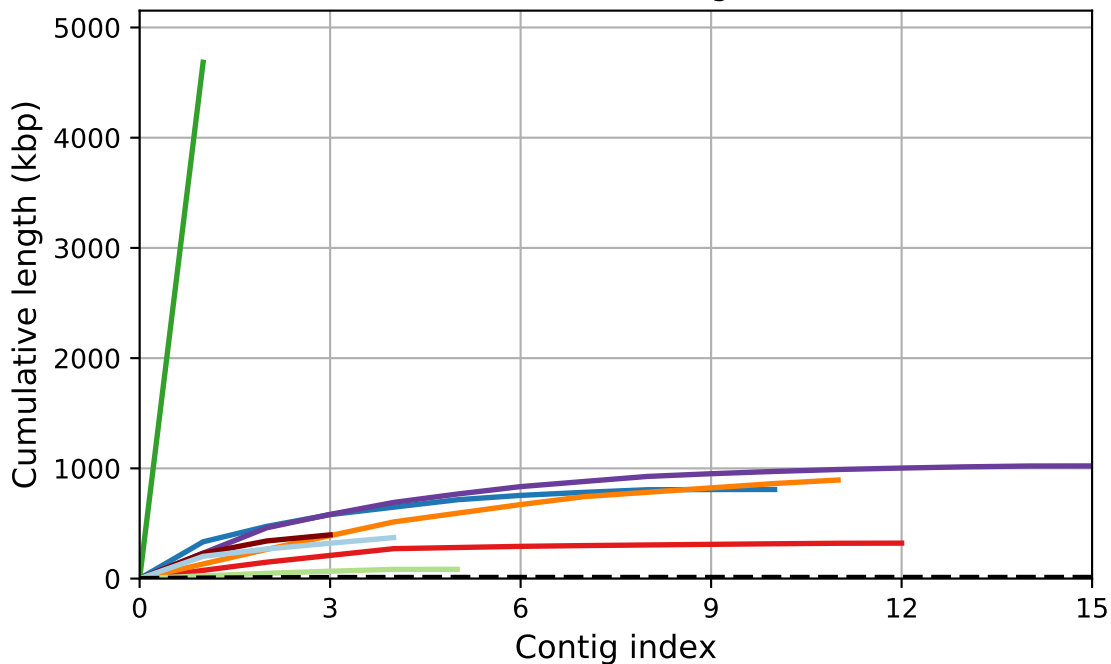
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



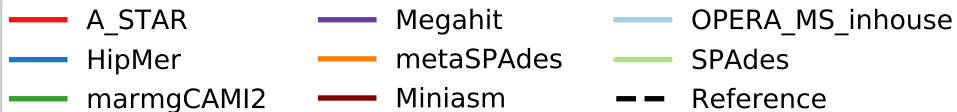
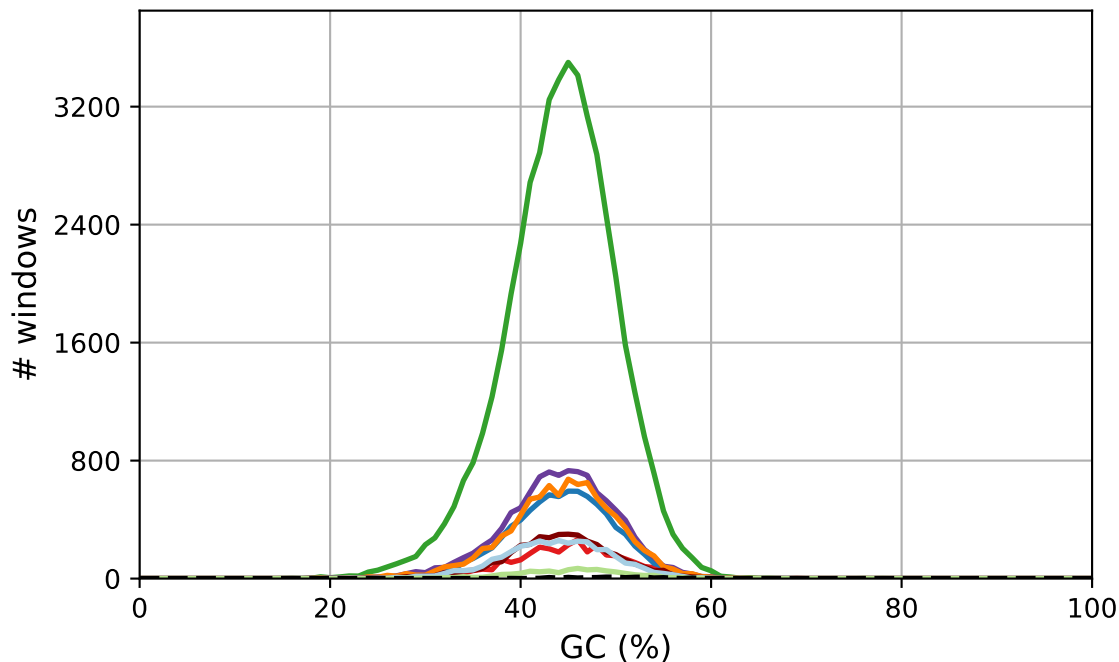
# NGx



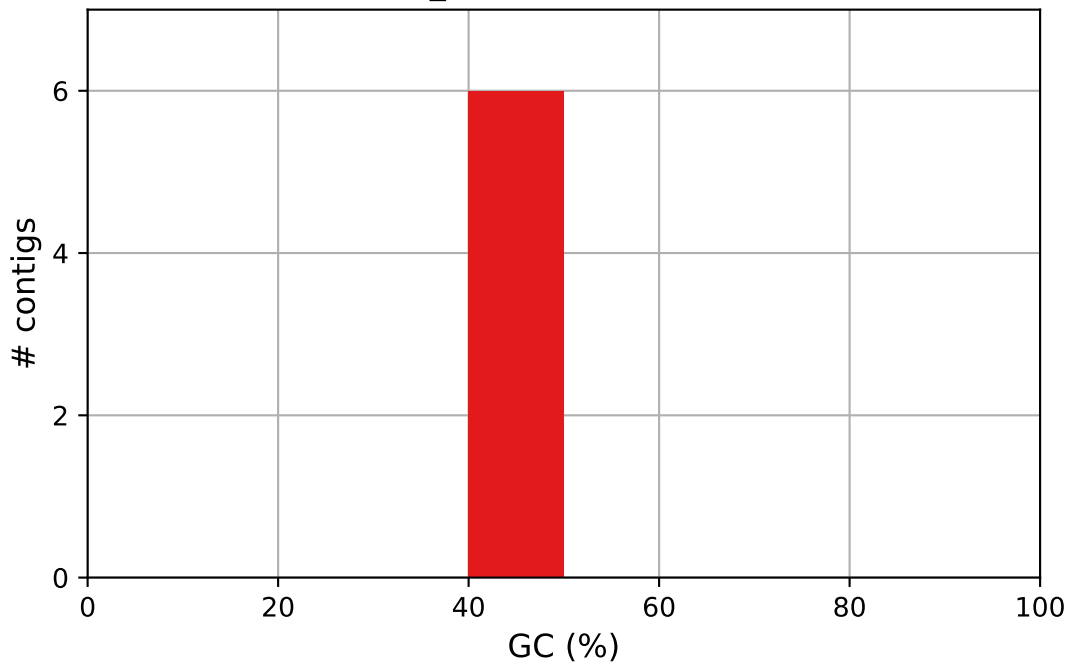
# Cumulative length



## GC content



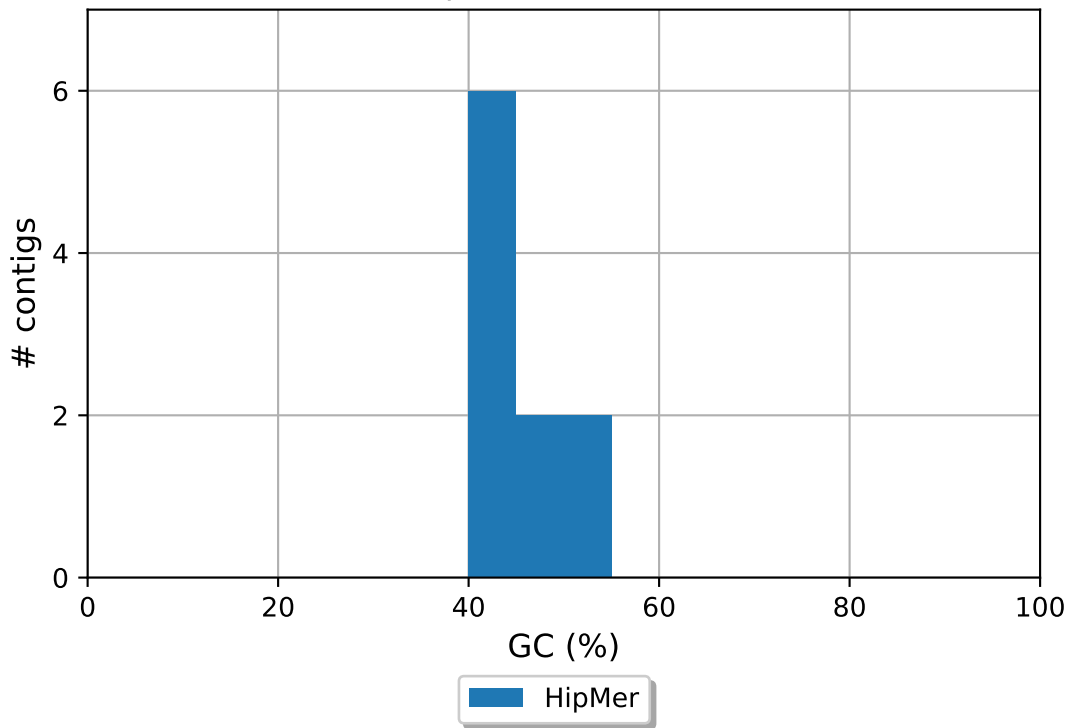
# A\_STAR GC content



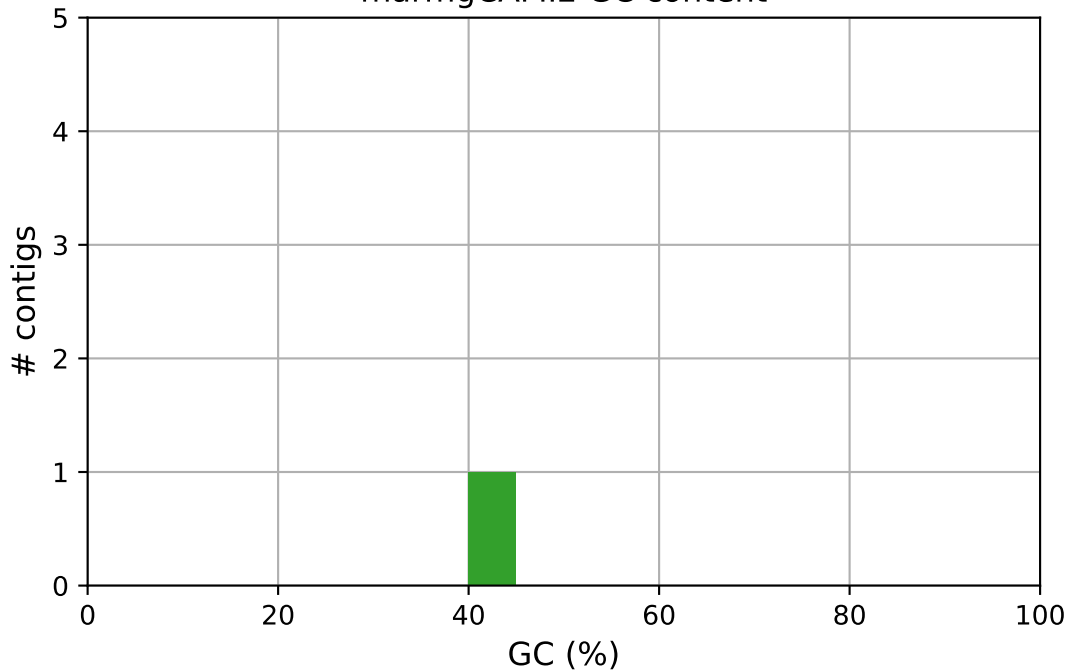
A\_STAR



# HipMer GC content

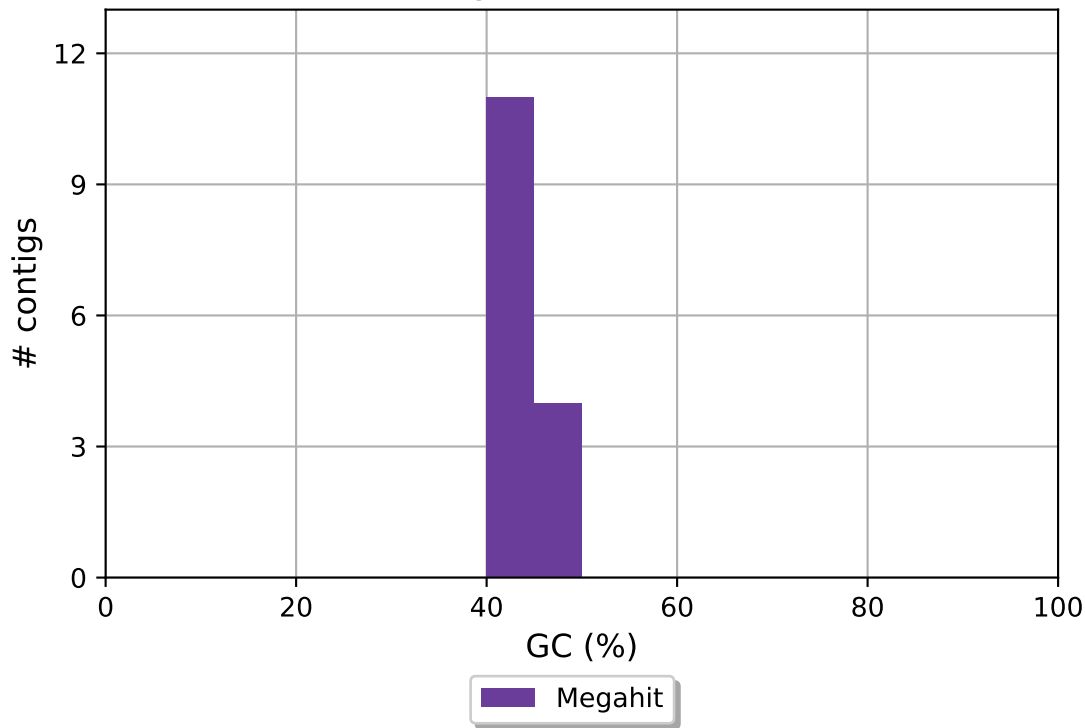


marmgCAMI2 GC content

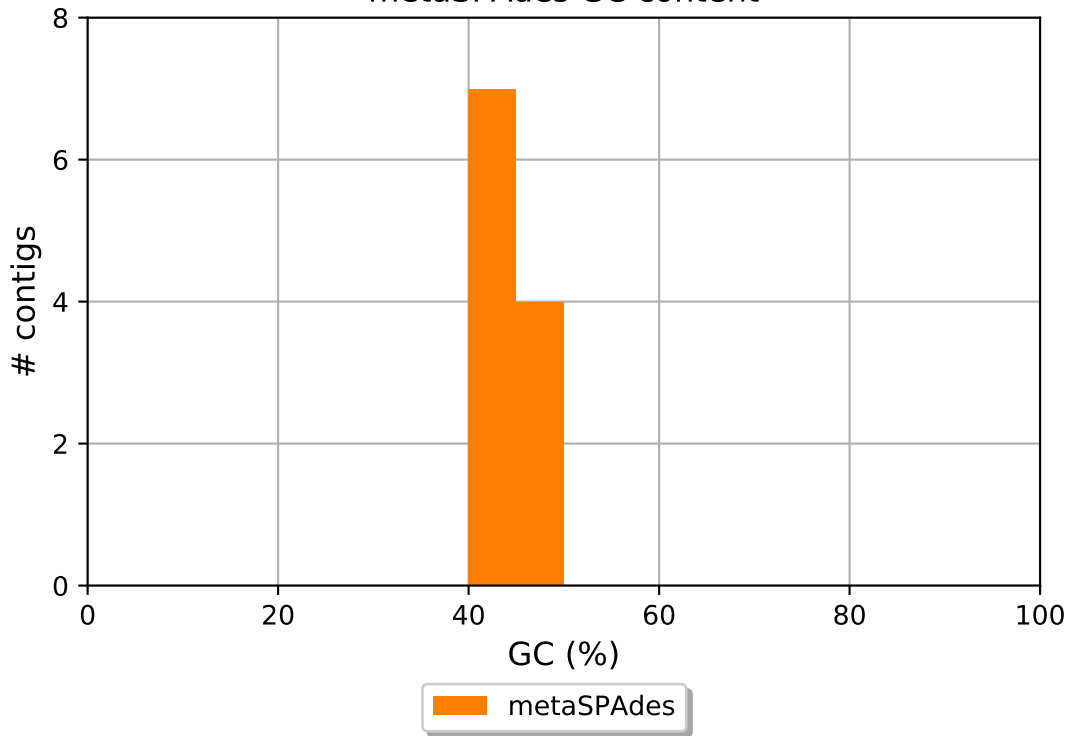


marmgCAMI2

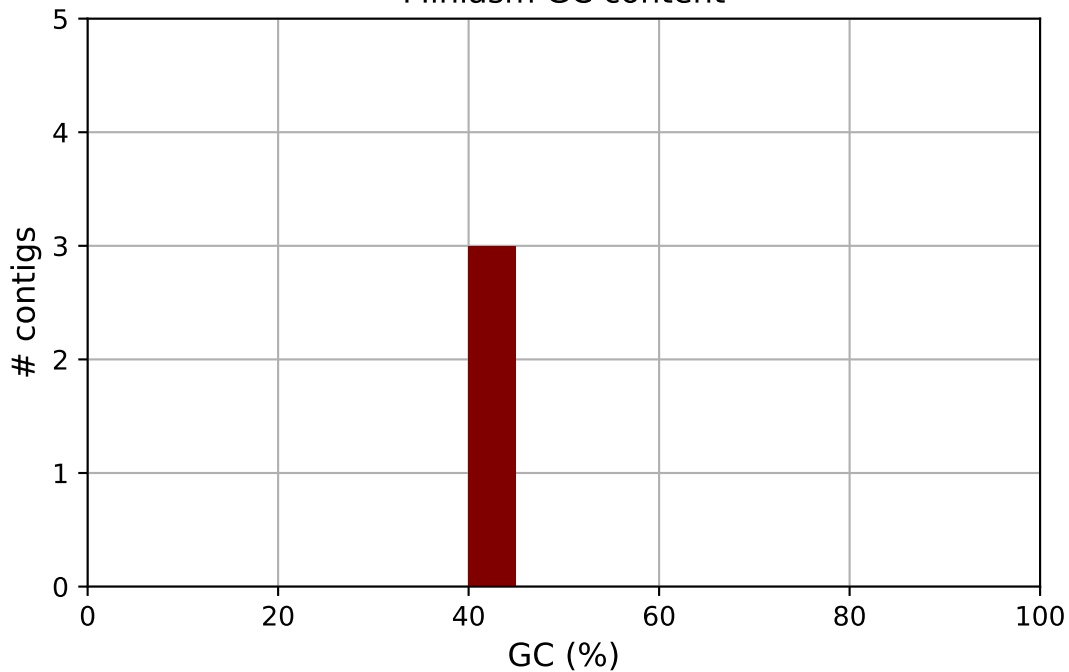
Megahit GC content



metaSPAdes GC content

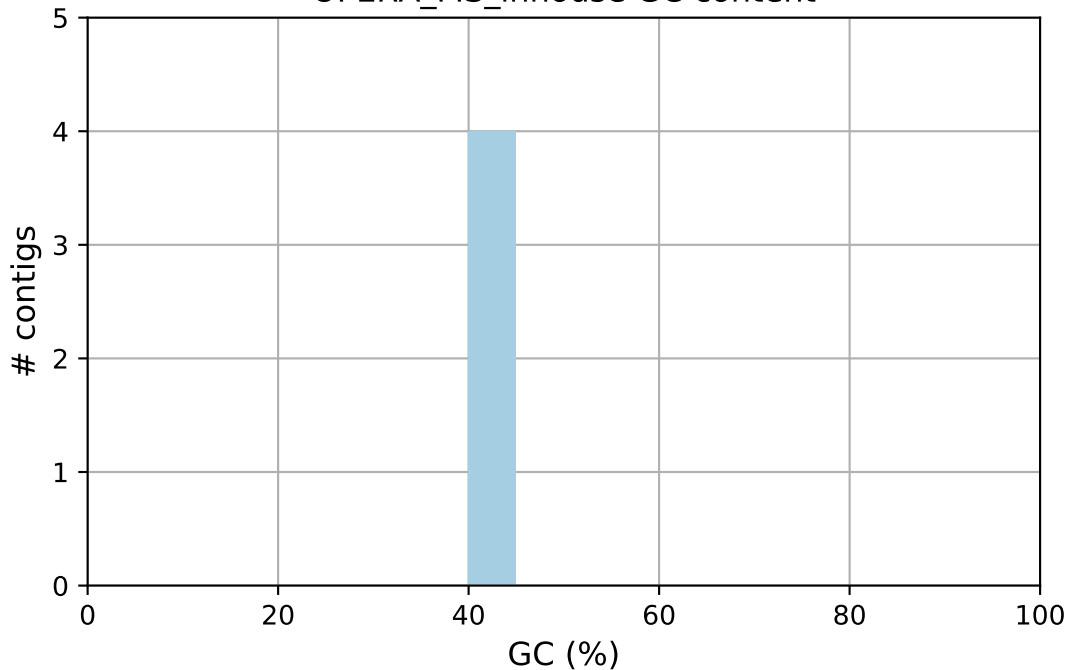


Miniasm GC content



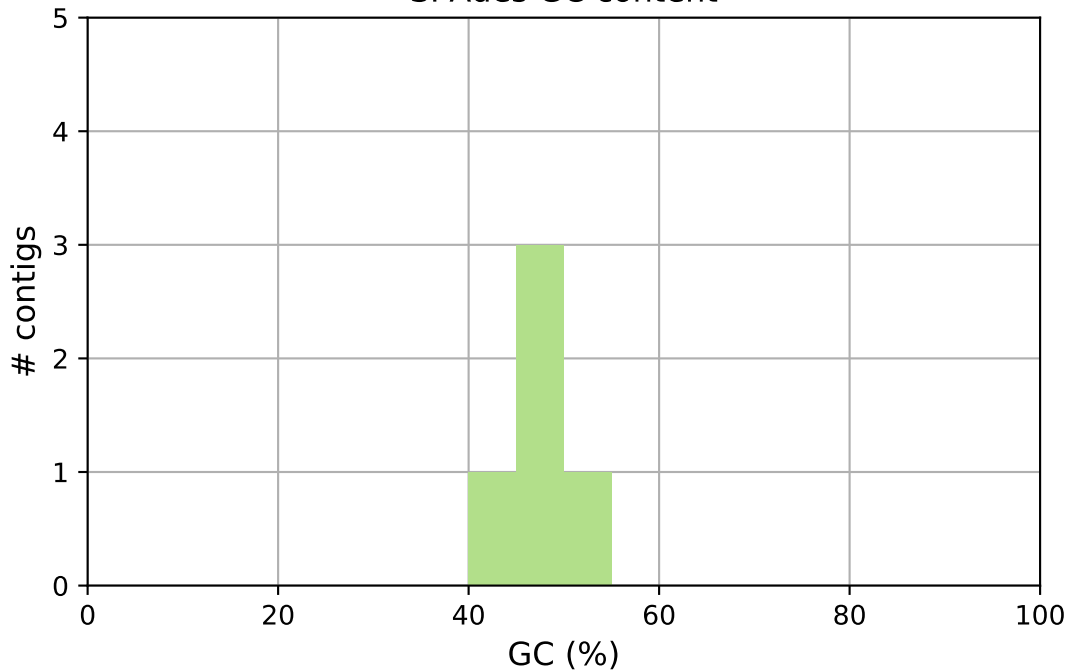
Miniasm

OPERA\_MS\_inhouse GC content



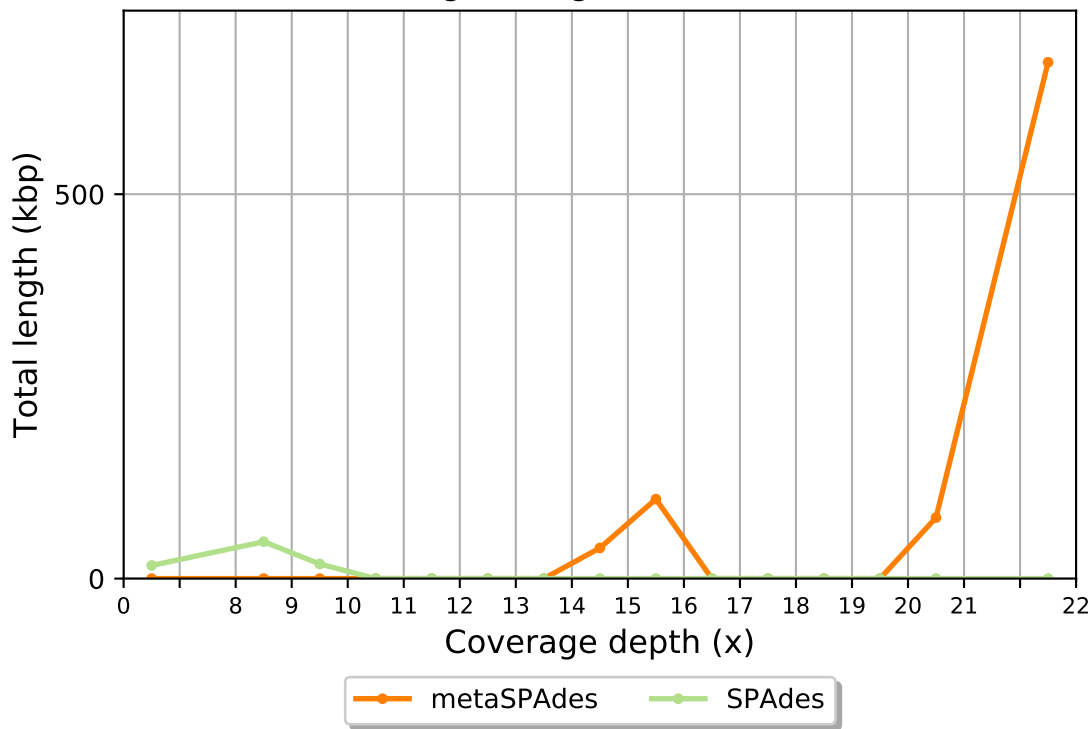
OPERA\_MS\_inhouse

SPAdes GC content



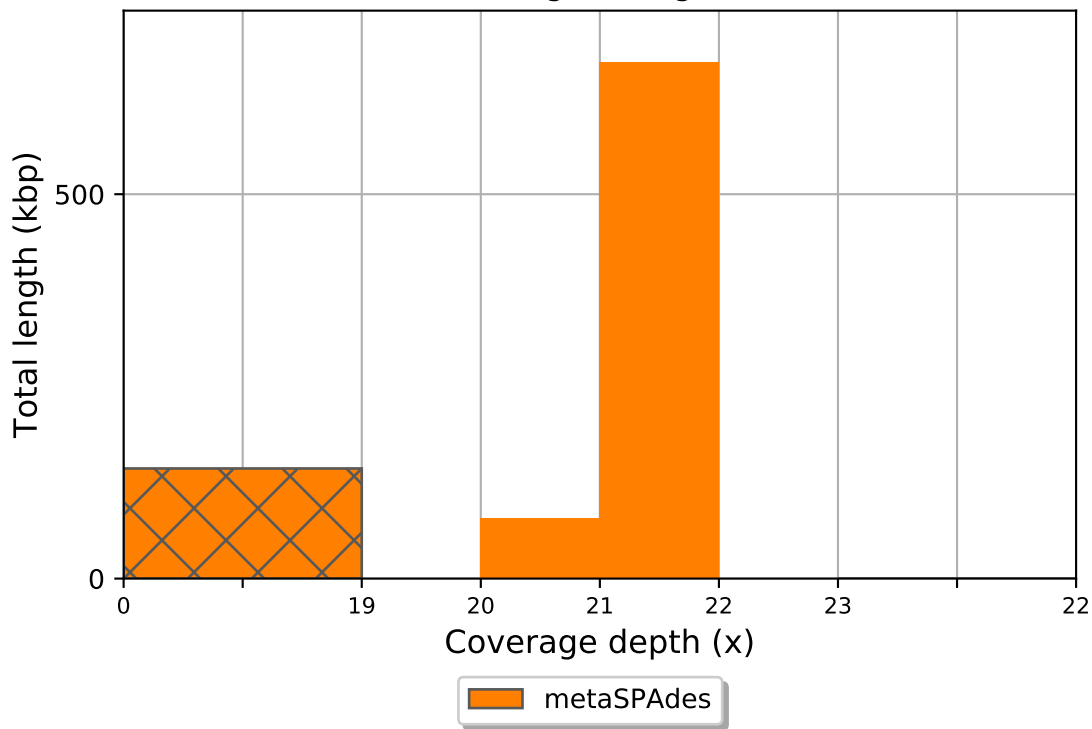
SPAdes

Coverage histogram (bin size: 1x)

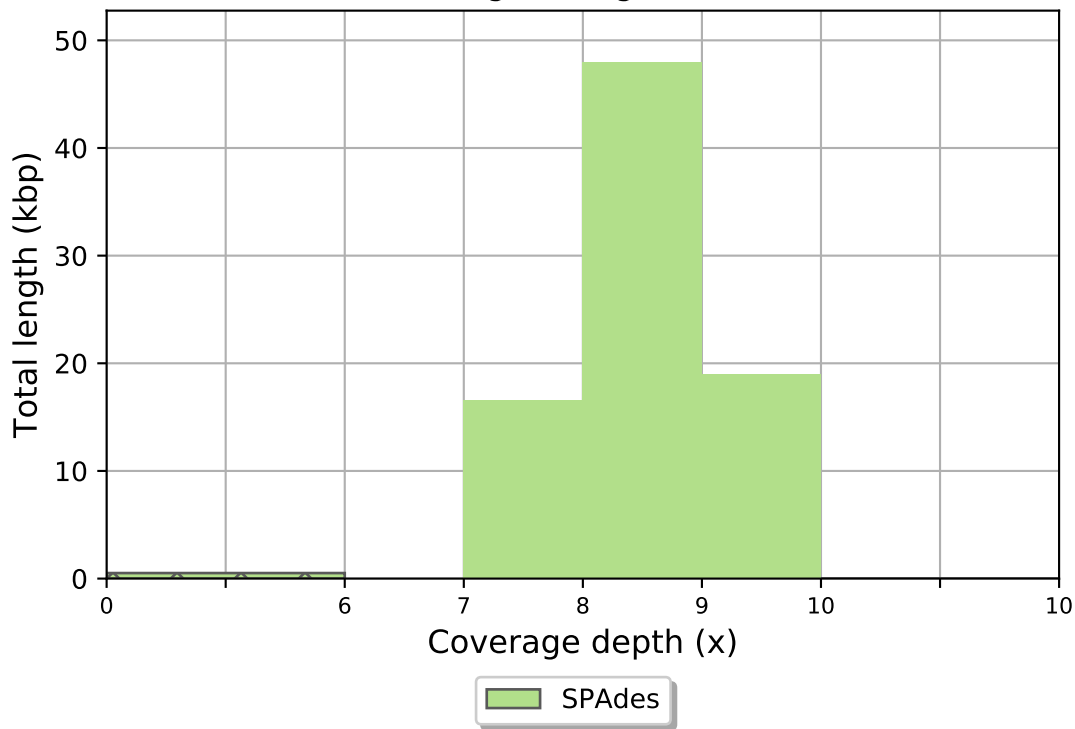




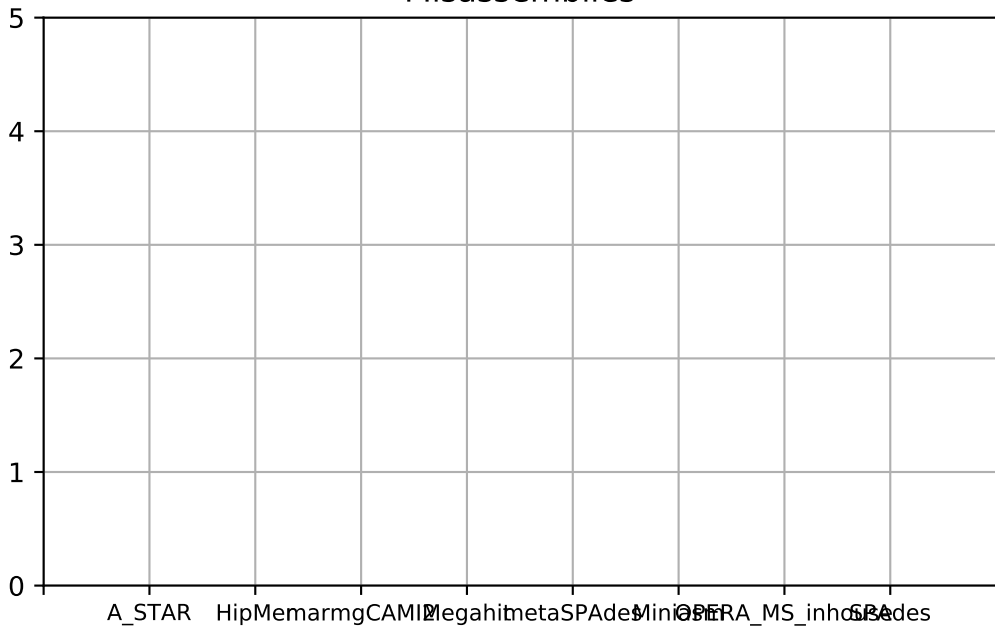
metaSPAdes coverage histogram (bin size: 1x)



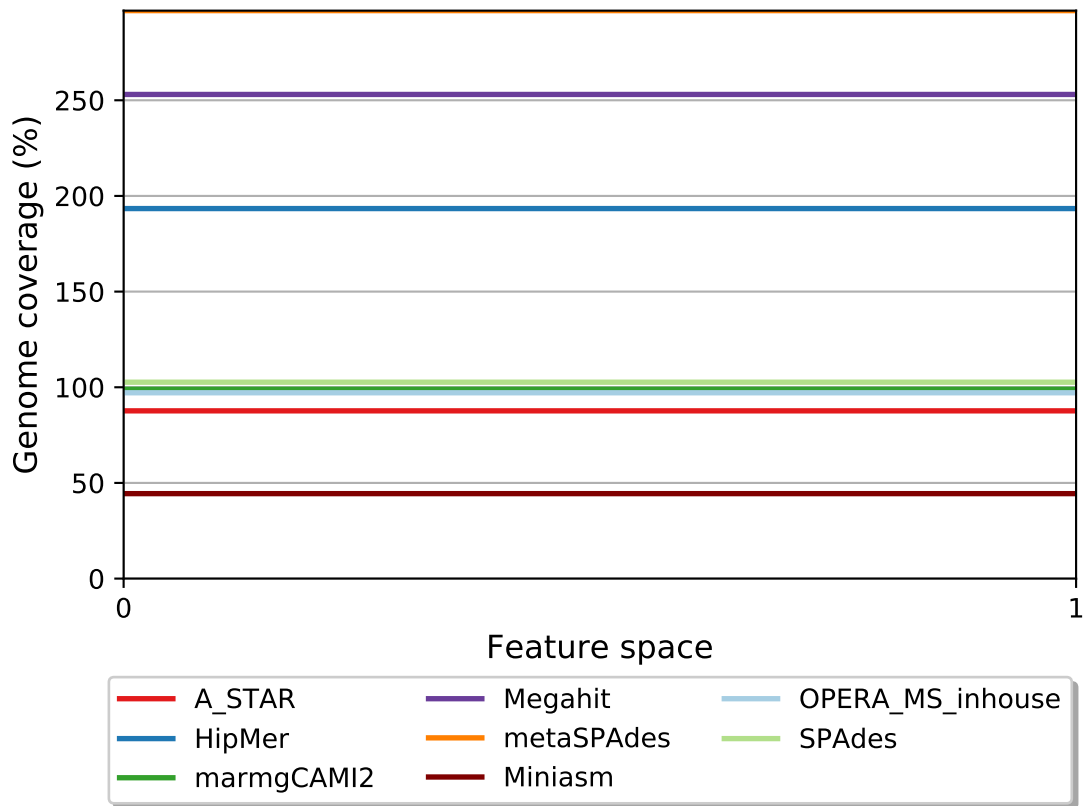
SPAdes coverage histogram (bin size: 1x)



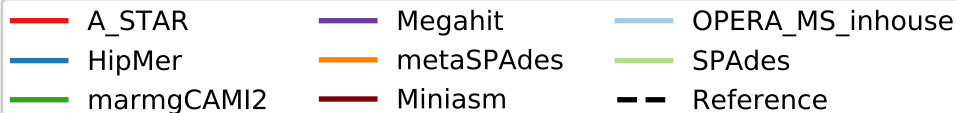
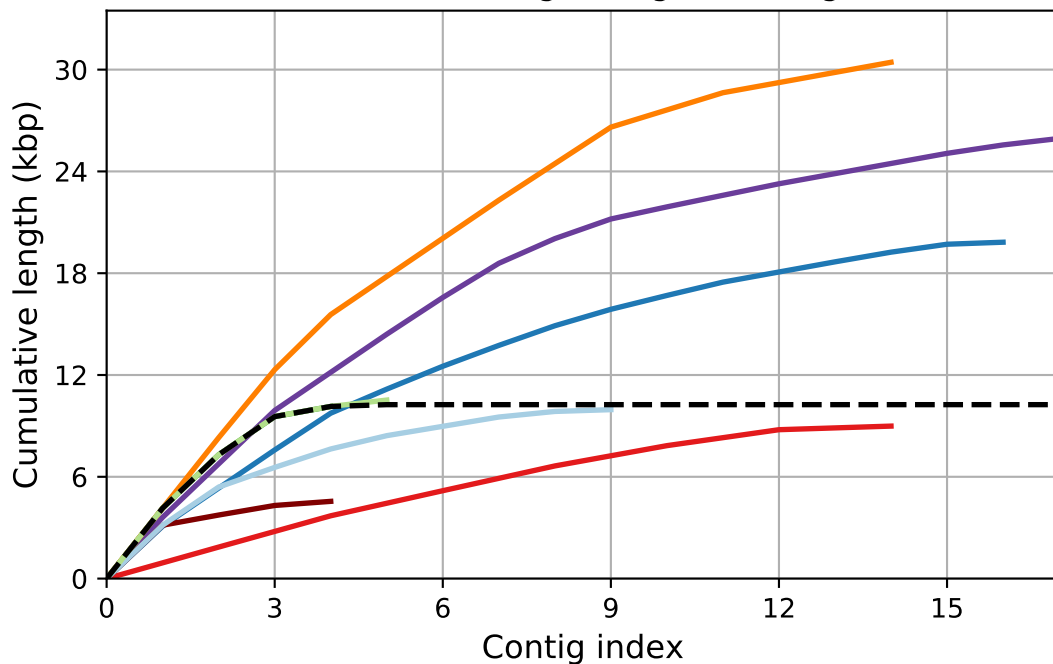
## Misassemblies



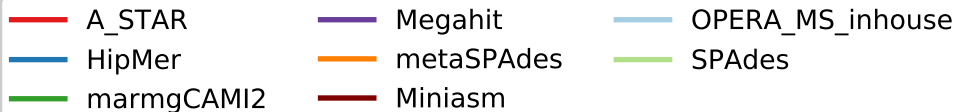
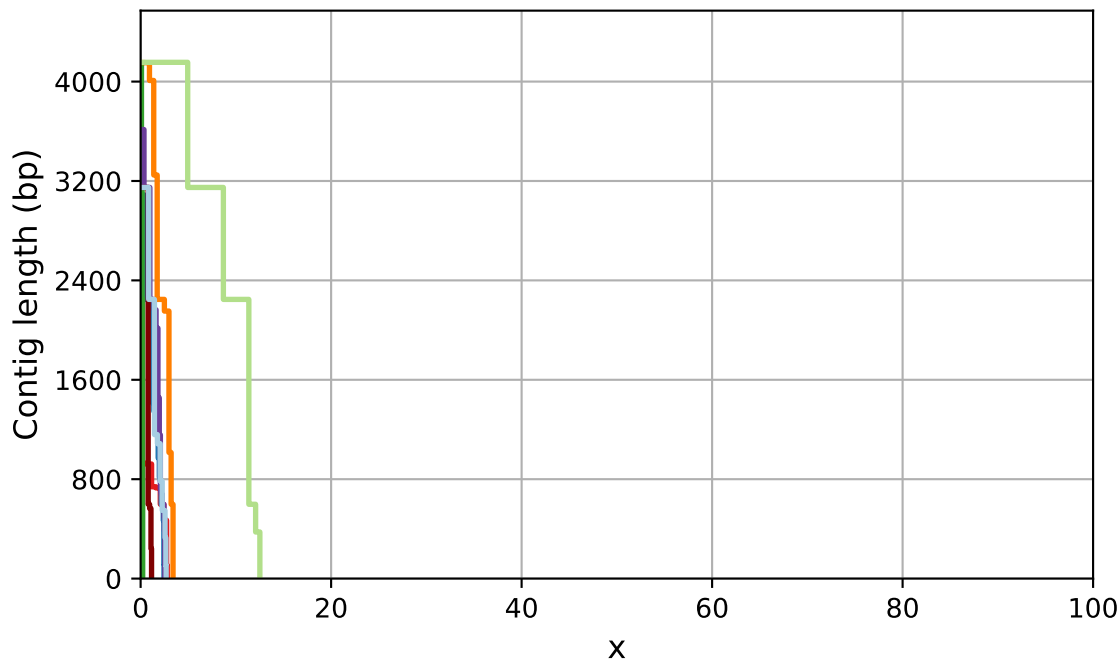
FRCurve (misassemblies)



# Cumulative length (aligned contigs)



# NAx



# NGAx

