

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	12	16	1	25	16	6	5	8
# contigs (>= 5000 bp)	9	10	1	14	12	6	5	4
# contigs (>= 10000 bp)	7	5	1	11	10	6	5	1
# contigs (>= 25000 bp)	6	0	1	3	0	2	3	0
# contigs (>= 50000 bp)	4	0	1	1	0	1	1	0
Total length (>= 1000 bp)	317602	155178	5183322	362772	204955	144290	158136	47200
Total length (>= 5000 bp)	311771	136912	5183322	334316	198587	144290	158136	36573
Total length (>= 10000 bp)	296838	99636	5183322	314890	184137	144290	158136	15693
Total length (>= 25000 bp)	278914	0	5183322	175306	0	78212	133747	0
Total length (>= 50000 bp)	220870	0	5183322	107331	0	52601	57927	0
# contigs	14	16	1	27	20	7	6	8
Largest contig	55632	23069	5183322	107331	22718	52601	57927	15693
Total length	318832	155178	5183322	364042	207105	144804	158797	47200
Reference length	5107	5107	5107	5107	5107	5107	5107	5107
GC (%)	67.69	66.76	69.46	67.77	67.22	66.64	67.73	66.42
Reference GC (%)	70.24	70.24	70.24	70.24	70.24	70.24	70.24	70.24
N50	54803	17938	5183322	24357	19596	25611	42573	9414
NG50	55632	23069	5183322	107331	22718	52601	57927	15693
N75	29022	8700	5183322	19325	13991	17134	33247	5454
NG75	55632	23069	5183322	107331	22718	52601	57927	15693
L50	3	4	1	4	5	2	2	2
LG50	1	1	1	1	1	1	1	1
L75	5	7	1	8	8	4	3	4
LG75	1	1	1	1	1	1	1	1
# misassemblies	2	0	0	0	0	0	0	0
# misassembled contigs	2	0	0	0	0	0	0	0
Misassembled contigs length	3622	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	8	3	1	2	3	3	2	2
# unaligned contigs	0 + 12 part	0 + 16 part	0 + 1 part	0 + 24 part	0 + 16 part	0 + 6 part	0 + 5 part	0 + 8 part
Unaligned length	308820	147629	5178366	352390	194336	140826	154247	42692
Genome fraction (%)	56.883	74.995	95.516	88.623	80.419	64.578	76.914	83.160
Duplication ratio	3.446	1.971	1.016	2.574	3.109	1.206	1.158	1.061
# N's per 100 kbp	772.19	0.00	0.00	0.00	0.00	0.00	0.00	211.86
# mismatches per 100 kbp	895.01	52.22	0.00	1568.71	486.97	121.29	483.71	306.10
# indels per 100 kbp	0.00	0.00	0.00	0.00	24.35	30.32	0.00	23.55
Largest alignment	556	1624	1624	943	1624	957	1624	877
Total aligned length	7242	7549	5106	11465	11565	3857	4327	4593
NGA50	461	1624	988	708	1624	516	438	516
NGA75	332	452	860	516	1624	67	289	294
LGA50	6	2	2	4	2	4	3	4
LGA75	9	4	4	6	3	12	7	7

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

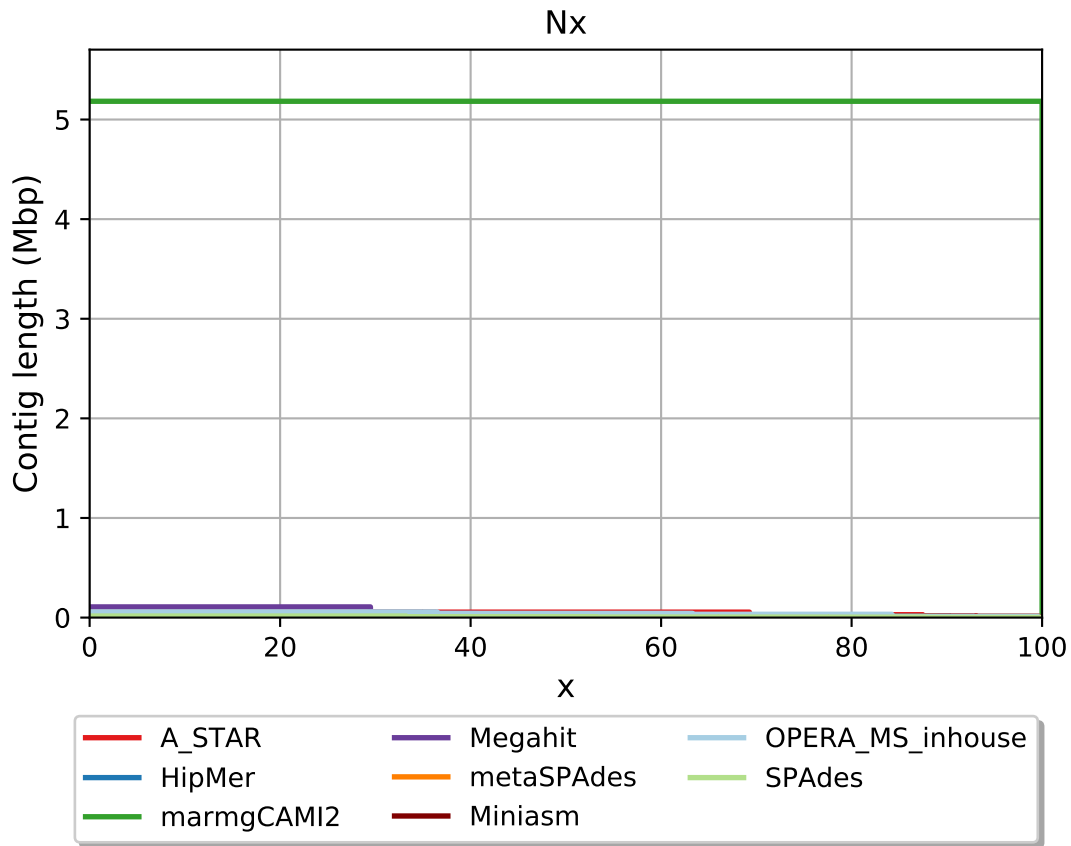
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	2	0	0	0	0	0	0	0
# contig misassemblies	2	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	2	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	2	0	0	0	0	0	0	0
Misassembled contigs length	3622	0	0	0	0	0	0	0
# possibly misassembled contigs	4	13	0	22	12	3	3	6
# possible misassemblies	6	17	0	27	21	4	5	7
# 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	8	3	1	2	3	3	2	2
# mismatches	26	2	0	71	20	4	19	13
# indels	0	0	0	0	1	1	0	1
# indels (<= 5 bp)	0	0	0	0	0	1	0	0
# indels (> 5 bp)	0	0	0	0	1	0	0	1
Indels length	0	0	0	0	18	1	0	18

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).

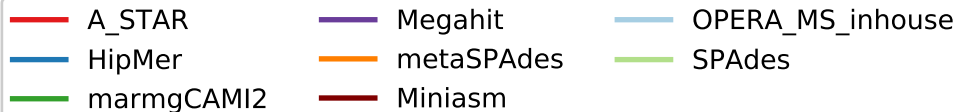
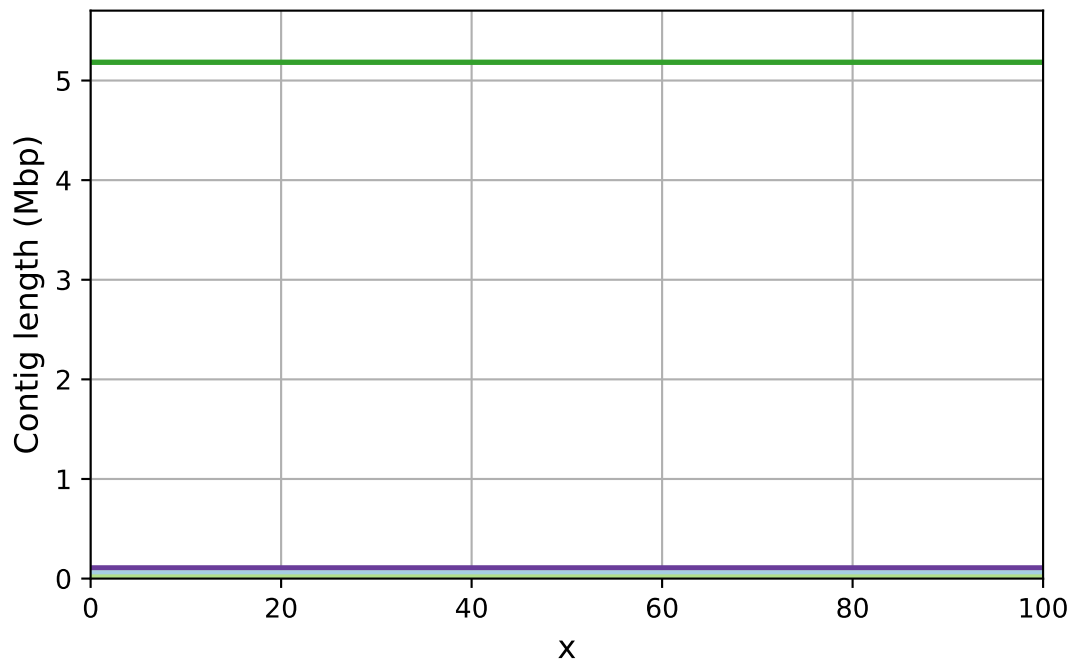
Unaligned report

	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	16	1	24	16	6	5	8
Partially unaligned length	308820	147629	5178366	352390	194336	140826	154247	42692
# N's	2462	0	0	0	0	0	0	100

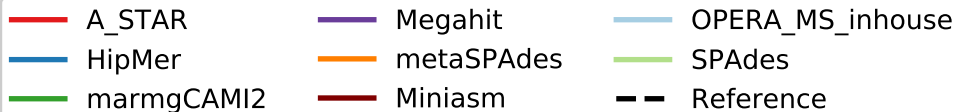
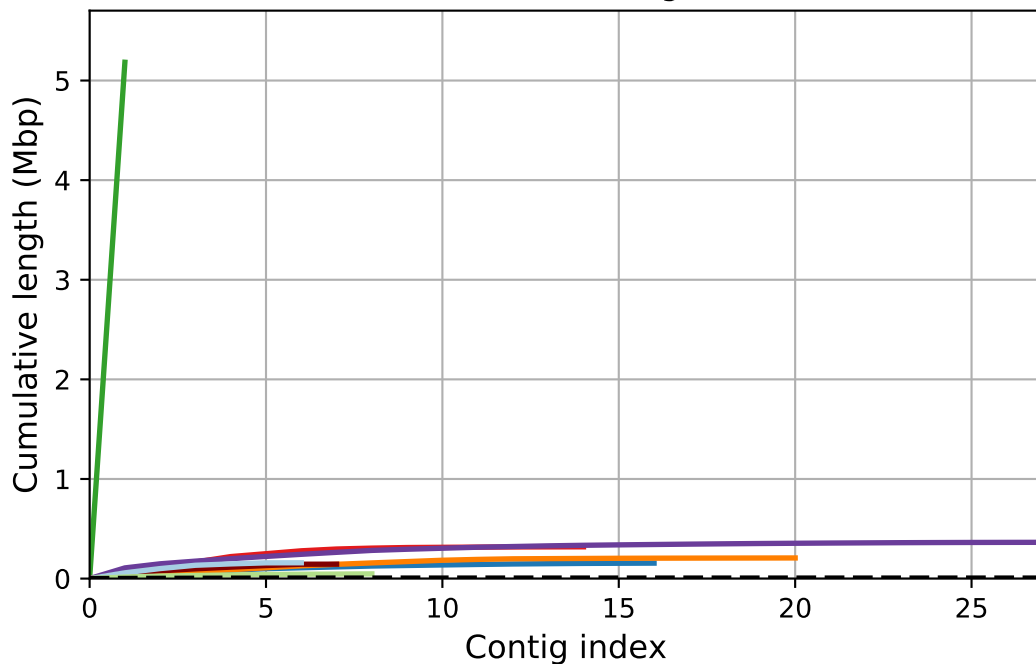
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



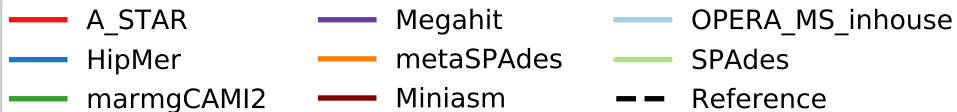
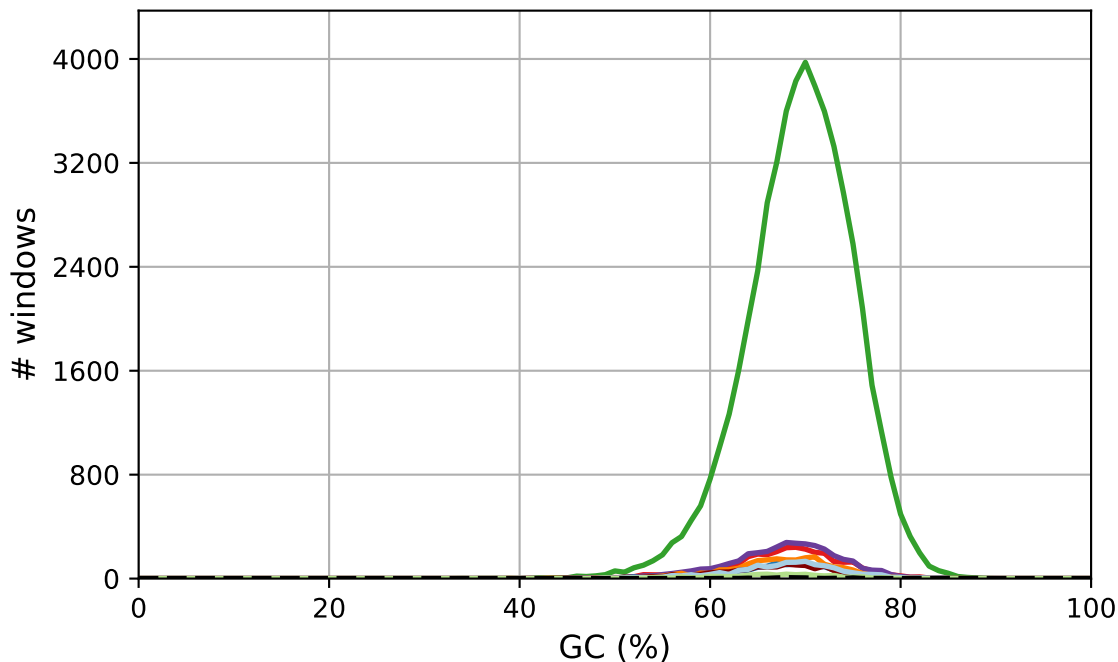
NGx



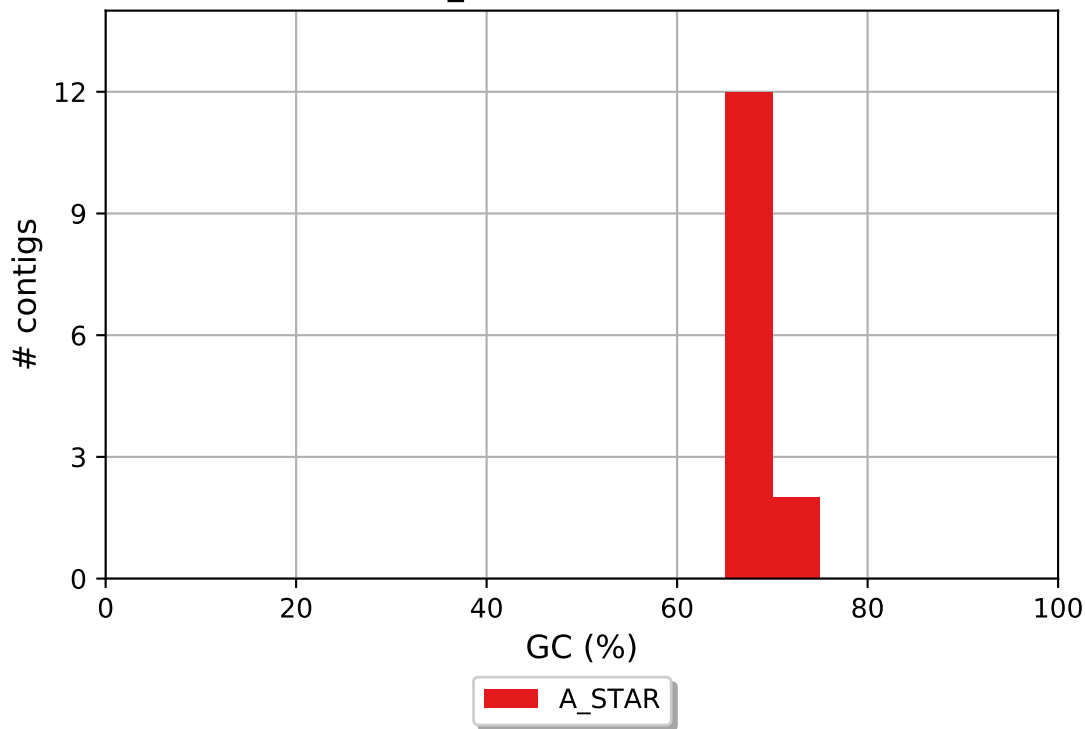
Cumulative length



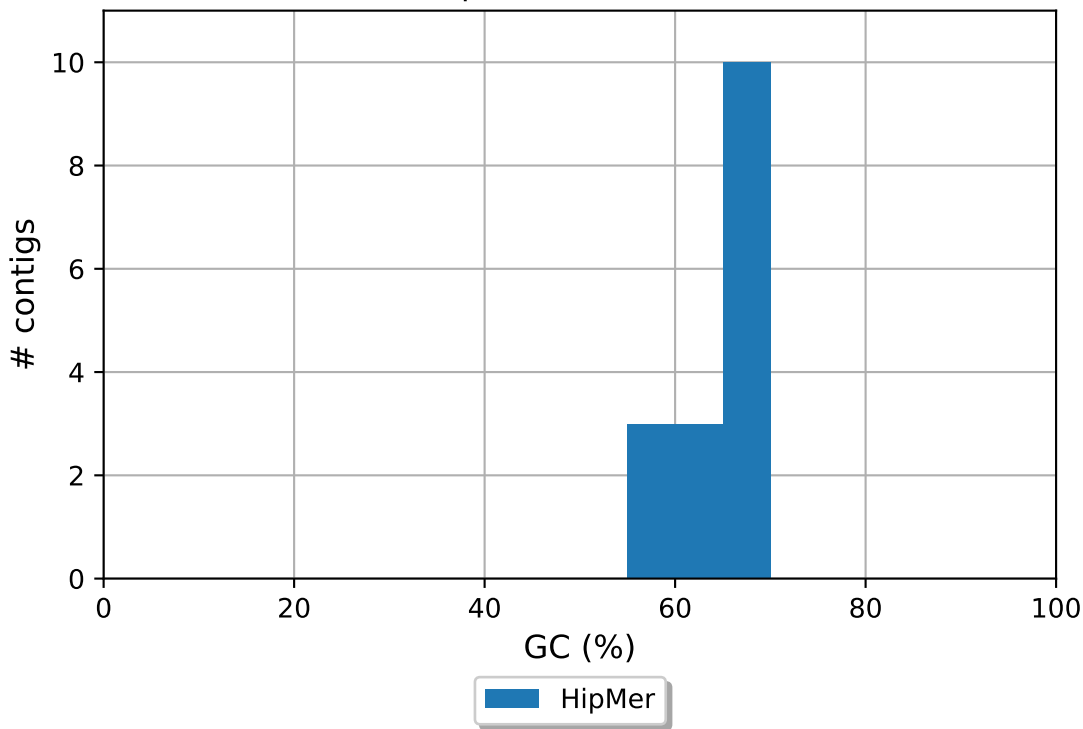
GC content



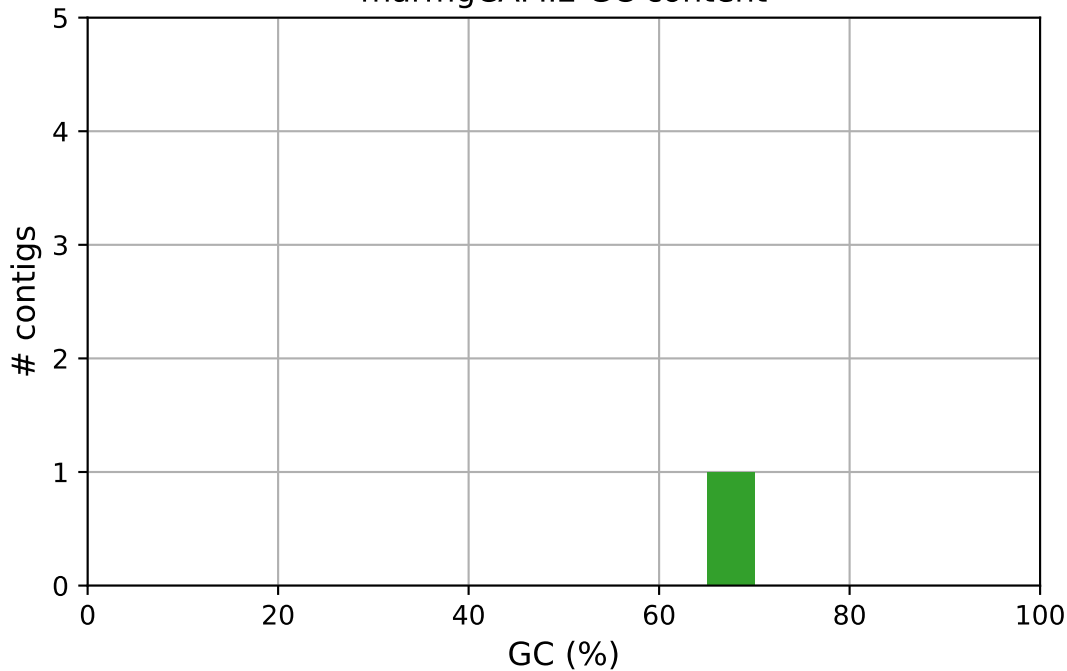
A_STAR GC content



HipMer GC content

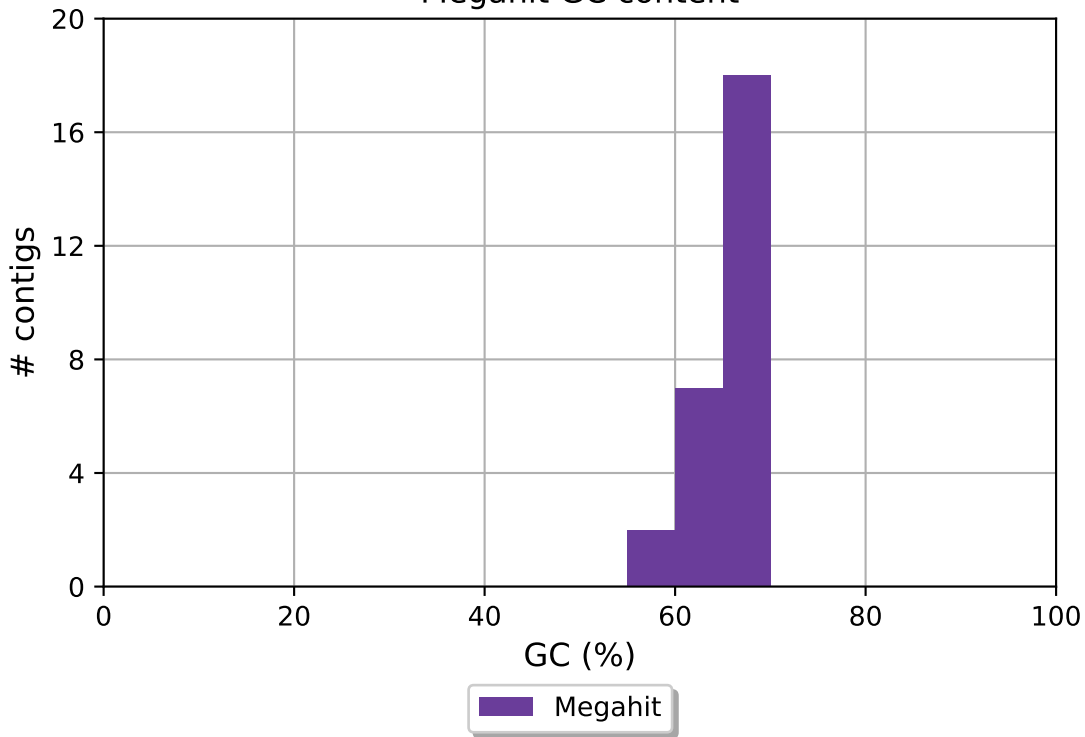


marmgCAMI2 GC content

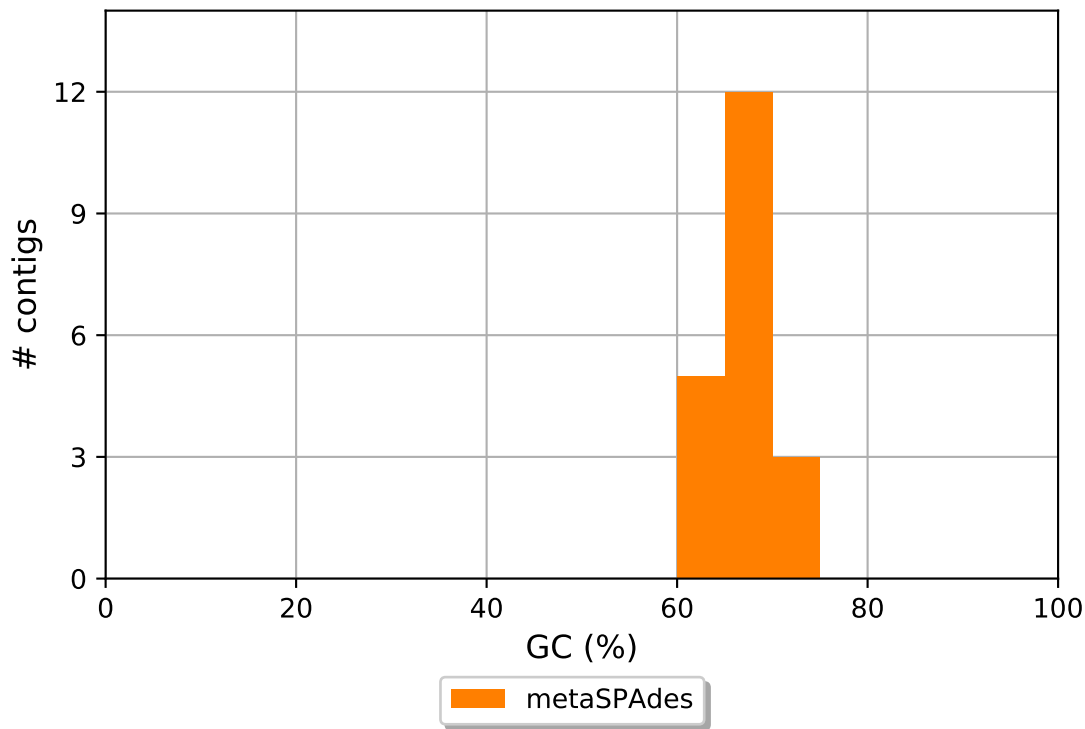


marmgCAMI2

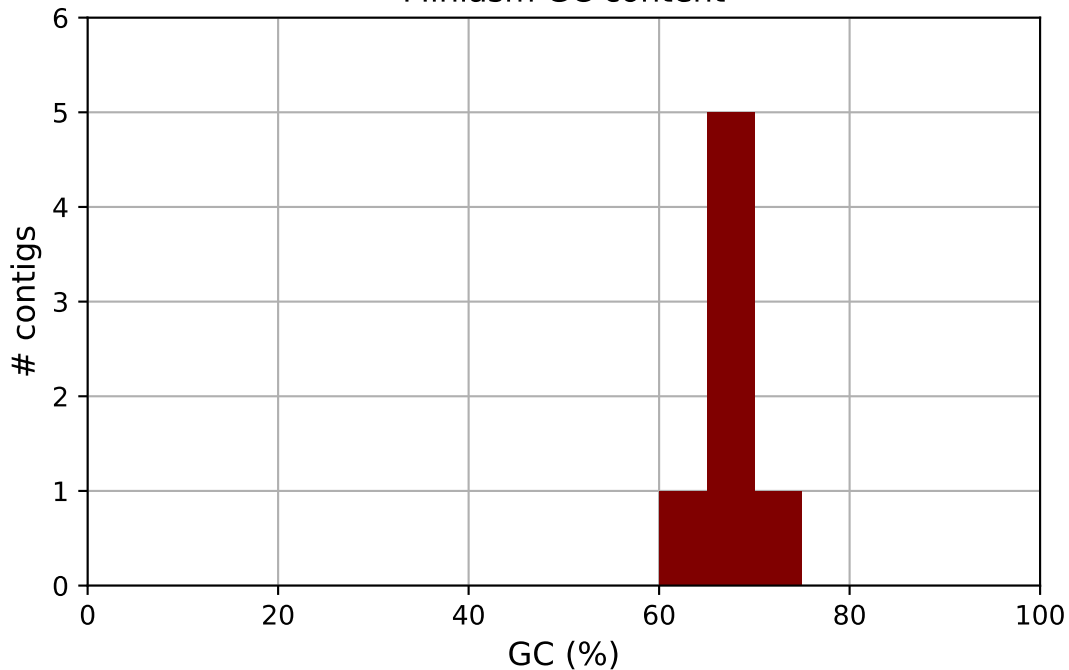
Megahit GC content



metaSPAdes GC content

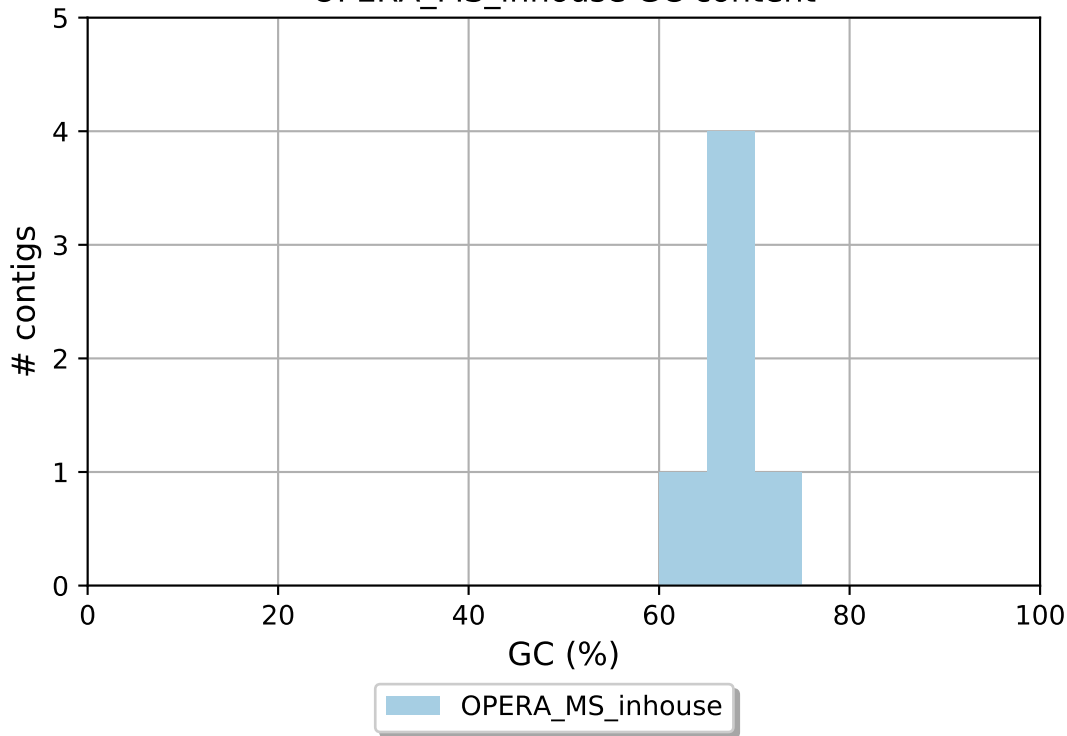


Miniasm GC content

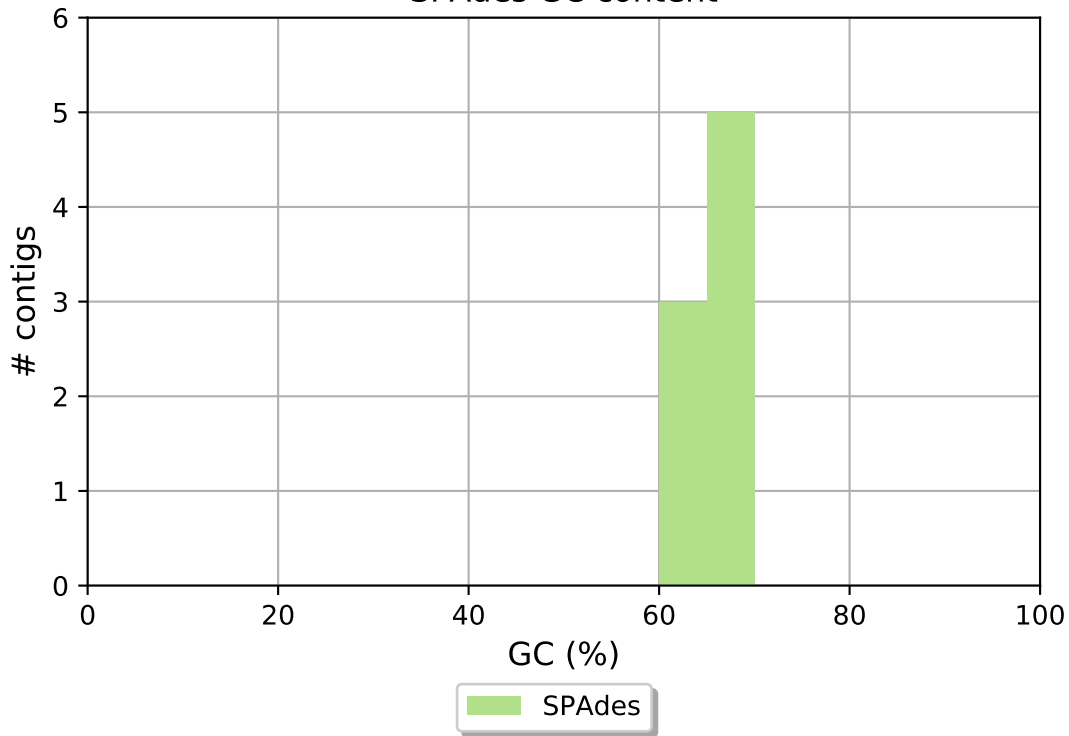


Miniasm

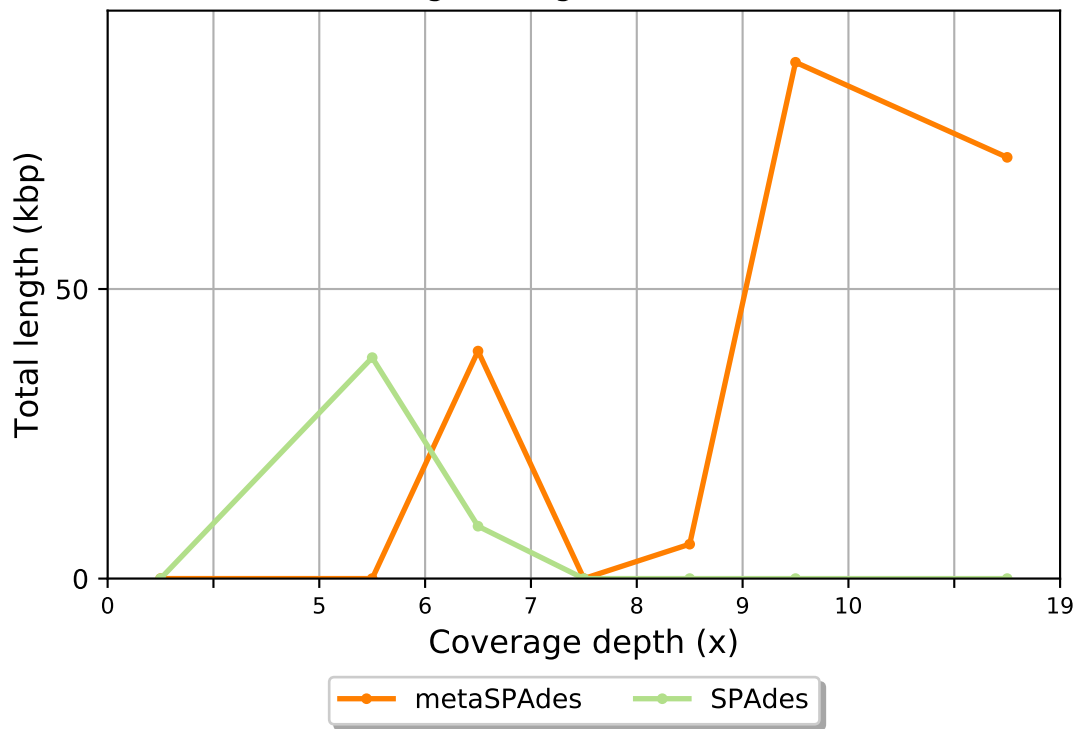
OPERA_MS_inhouse GC content



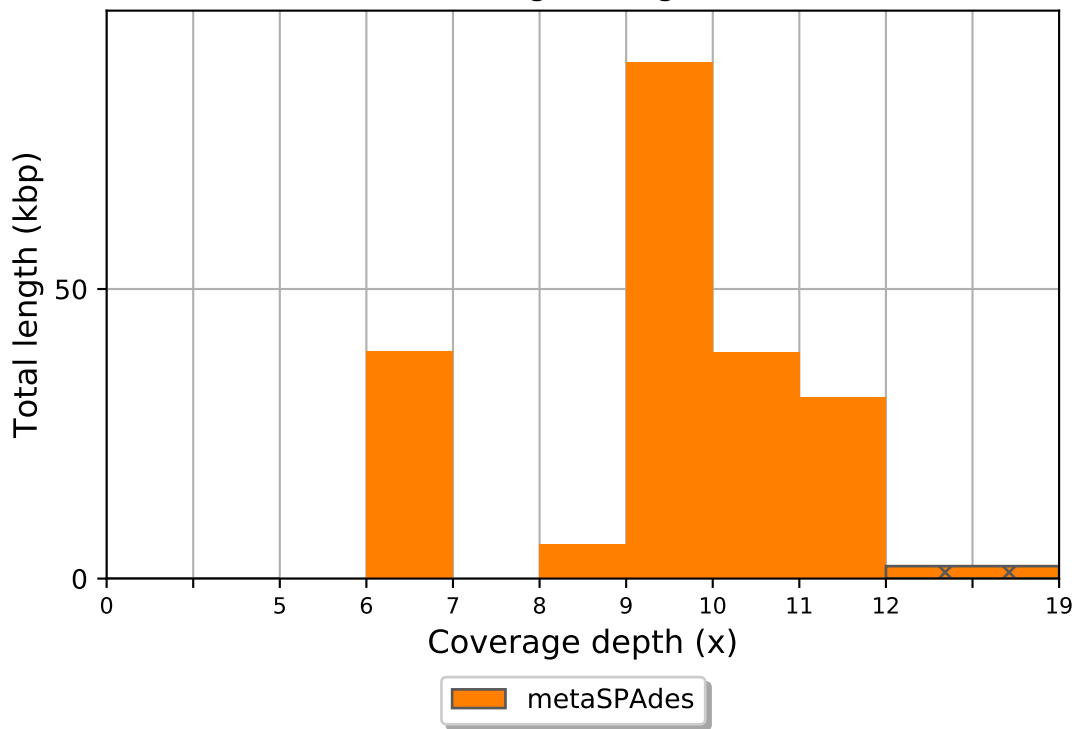
SPAdes GC content



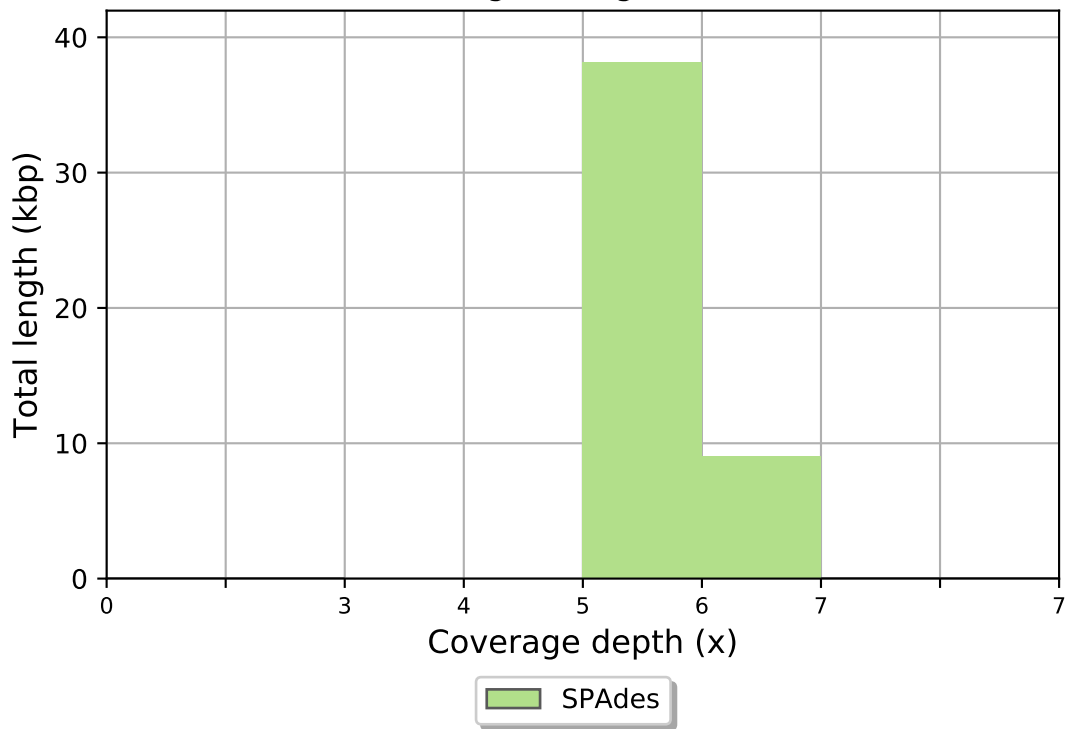
Coverage histogram (bin size: 1x)



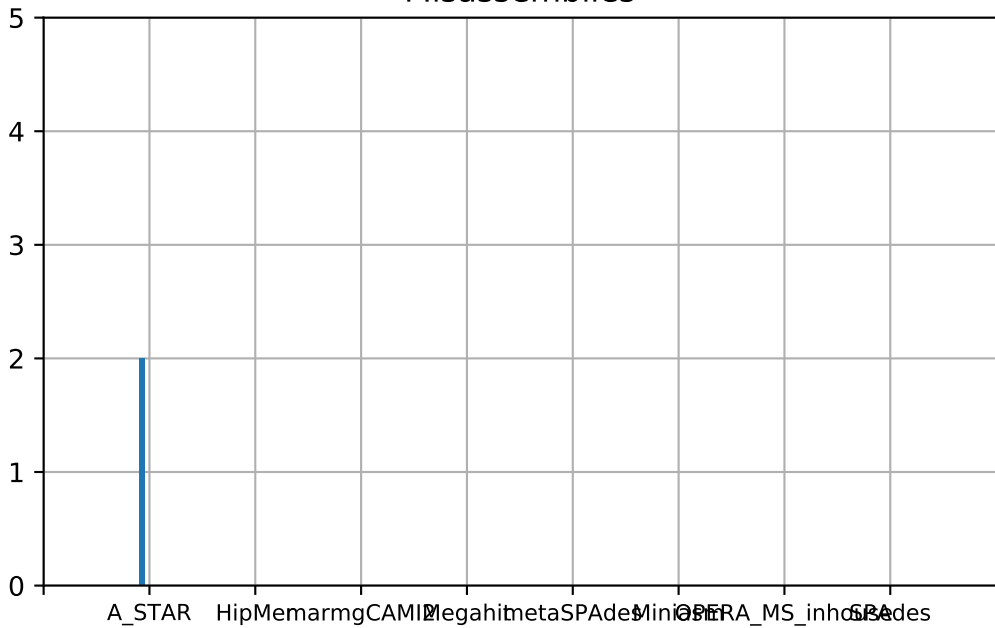
metaSPAdes coverage histogram (bin size: 1x)



SPAdes coverage histogram (bin size: 1x)

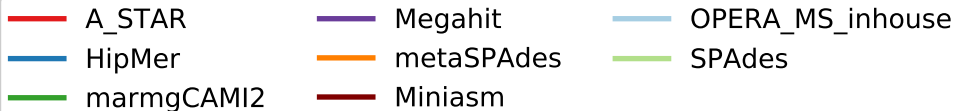
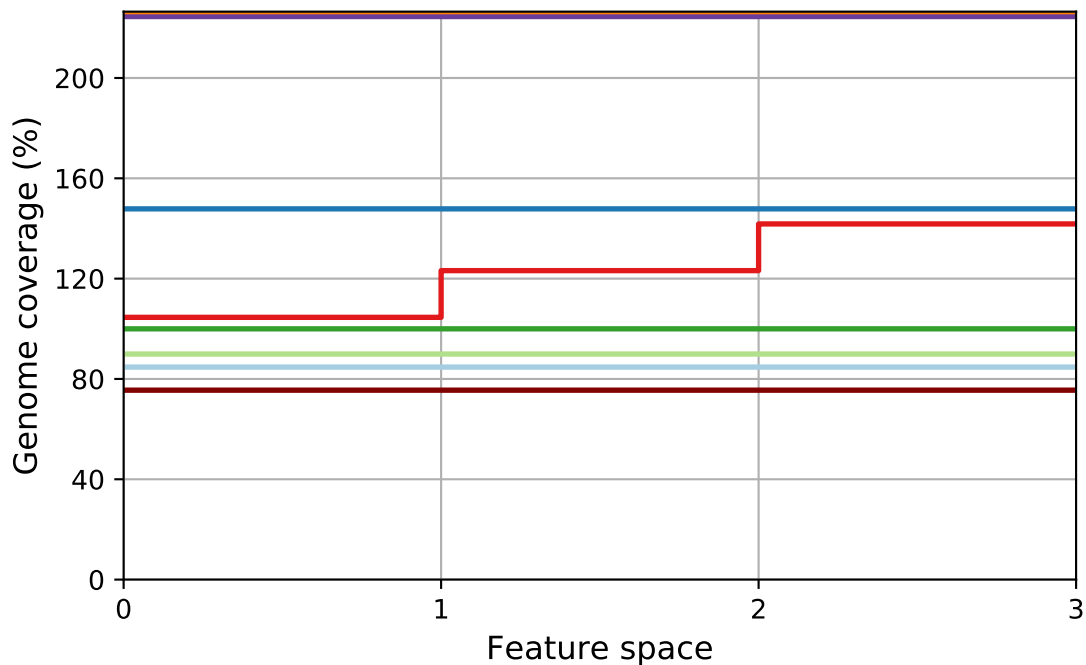


Misassemblies

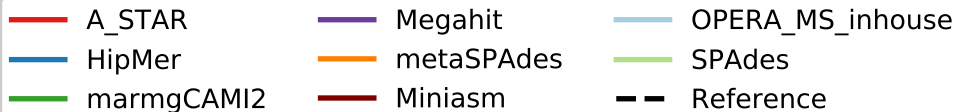
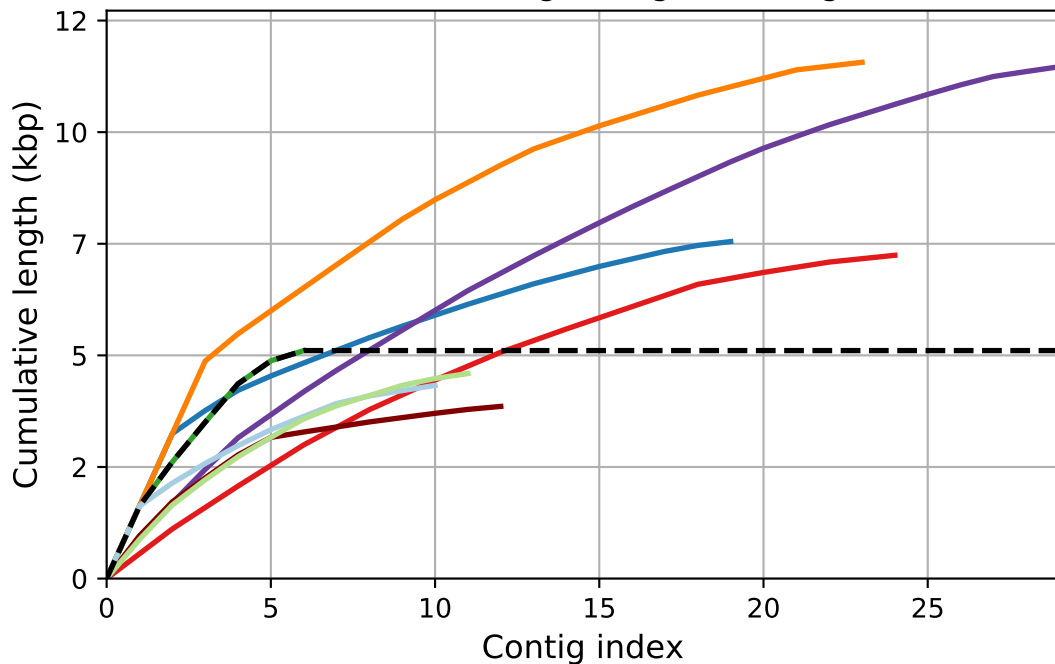


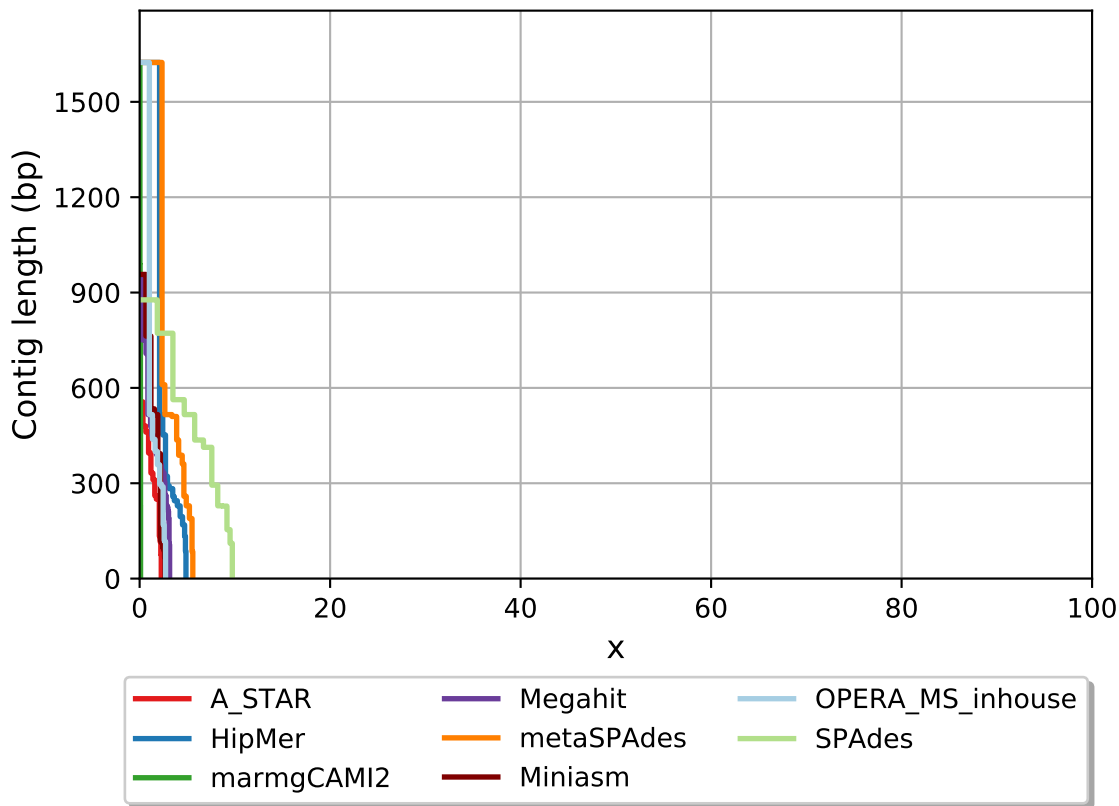
translocations

FRCurve (misassemblies)

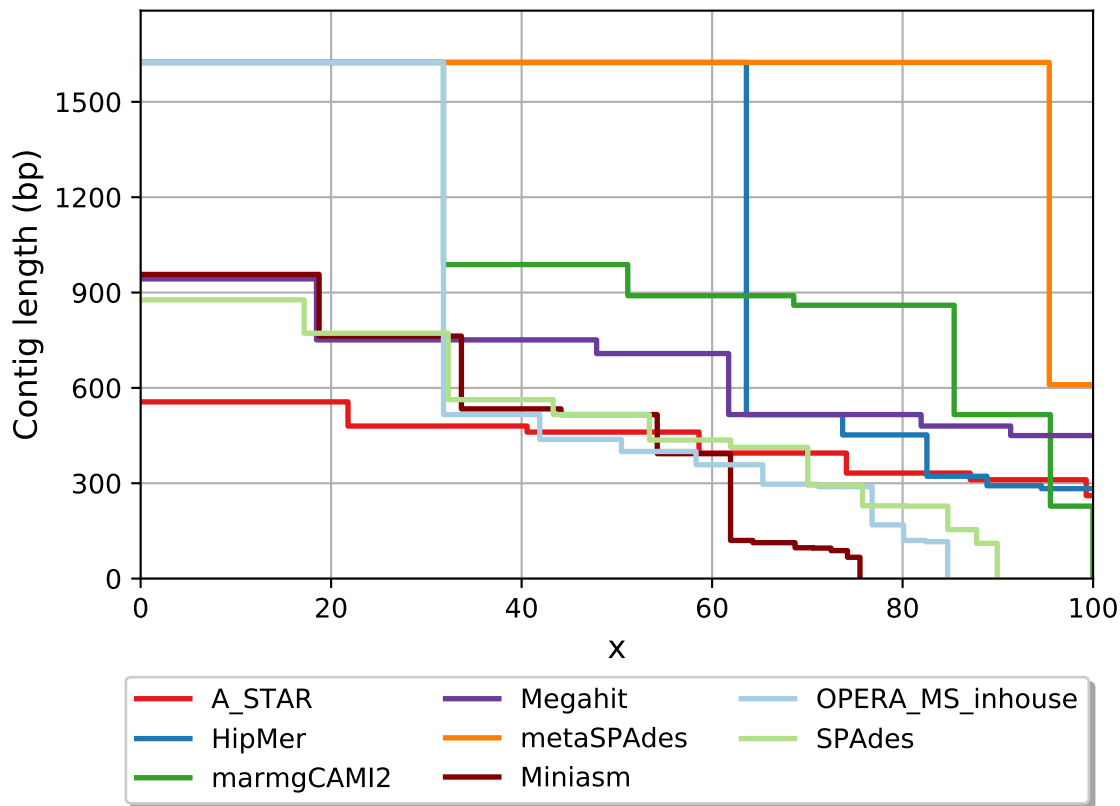


Cumulative length (aligned contigs)



Na^x 

NGAx



Genome fraction, %

