

Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	12	13	1	17	14	6	5	4
# contigs (>= 5000 bp)	5	10	1	14	11	5	5	2
# contigs (>= 10000 bp)	3	9	1	12	10	4	5	2
# contigs (>= 25000 bp)	2	3	1	4	4	2	3	0
# contigs (>= 50000 bp)	0	0	1	3	4	1	3	0
Total length (>= 1000 bp)	104778	224951	5017042	373553	389813	141235	413836	31448
Total length (>= 5000 bp)	94479	221016	5017042	368140	382619	139819	413836	25925
Total length (>= 10000 bp)	80797	212281	5017042	352171	375416	132481	413836	25925
Total length (>= 25000 bp)	57192	88897	5017042	235558	257712	102728	380564	0
Total length (>= 50000 bp)	0	0	5017042	204776	257712	54612	380564	0
# contigs	14	13	1	22	15	6	5	5
Largest contig	30525	31845	5017042	87878	74338	54612	178489	13038
Total length	106303	224951	5017042	377426	390483	141235	413836	32121
Reference length	5818	5818	5818	5818	5818	5818	5818	5818
GC (%)	61.58	62.38	62.61	62.72	62.88	62.76	62.81	61.50
Reference GC (%)	64.58	64.58	64.58	64.58	64.58	64.58	64.58	64.58
N50	26667	22180	5017042	57776	54518	48116	128370	12887
NG50	30525	31845	5017042	87878	74338	54612	178489	13038
N75	23605	20300	5017042	14287	20718	16317	73705	12887
NG75	30525	31845	5017042	87878	74338	54612	178489	13038
L50	2	5	1	3	3	2	2	2
LG50	1	1	1	1	1	1	1	1
L75	3	7	1	7	6	3	3	2
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	0	1	1	0	0	2	0
# unaligned contigs	0 + 10 part	0 + 11 part	0 + 1 part	0 + 16 part	0 + 12 part	0 + 5 part	0 + 5 part	0 + 4 part
Unaligned length	70063	213704	5011224	359695	372527	134805	407885	27209
Genome fraction (%)	93.520	94.981	100.000	100.000	100.000	100.000	98.195	83.654
Duplication ratio	6.661	2.035	1.000	3.048	3.086	1.105	1.042	1.009
# N's per 100 kbp	23181.85	1.33	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	845.43	90.48	0.00	1512.55	51.56	0.00	490.11	349.29
# indels per 100 kbp	36.76	18.10	0.00	0.00	0.00	17.19	17.50	82.19
Largest alignment	2037	2716	2716	2716	2716	2716	2782	2716
Total aligned length	10880	10485	5818	16290	17163	5930	5951	4863
NGA50	1307	2716	1186	2128	2716	1186	1186	1186
NGA75	1218	2716	916	2128	2716	916	540	624
LGA50	2	2	2	2	2	2	2	2
LGA75	3	2	3	2	2	3	3	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	8	11	0	14	12	5	3	3
# possible misassemblies	10	15	0	16	20	8	5	5
# 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	0	1	1	0	0	2	0
# mismatches	46	5	0	88	3	0	28	17
# indels	2	1	0	0	0	1	1	4
# indels (<= 5 bp)	0	0	0	0	0	1	0	4
# indels (> 5 bp)	2	1	0	0	0	0	1	0
Indels length	47	18	0	0	0	3	66	6

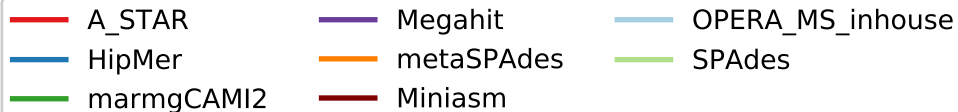
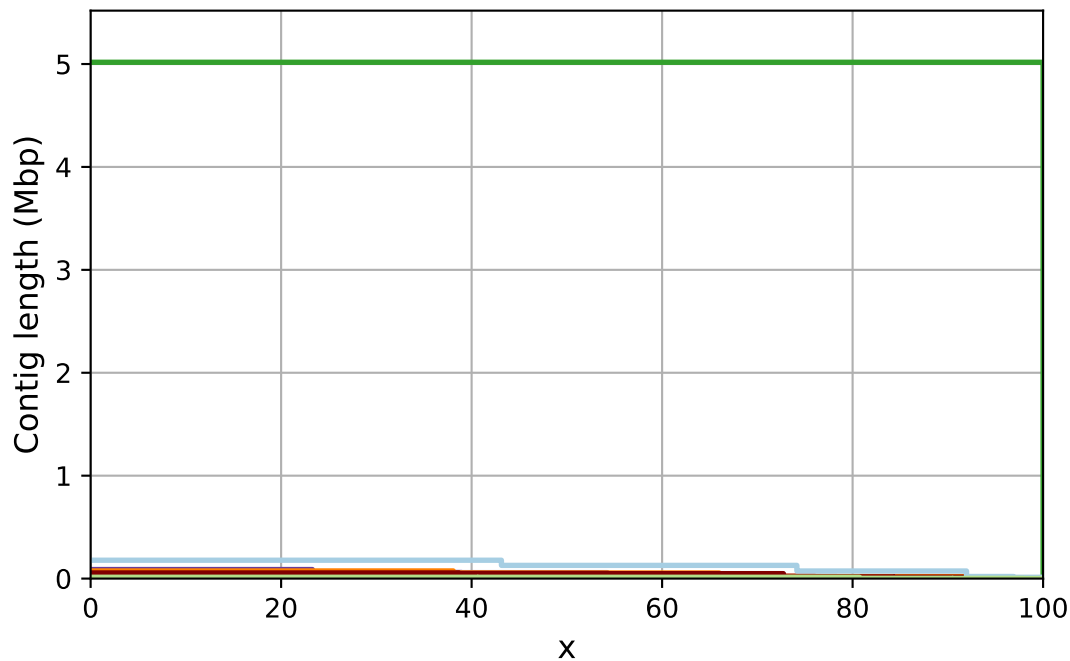
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

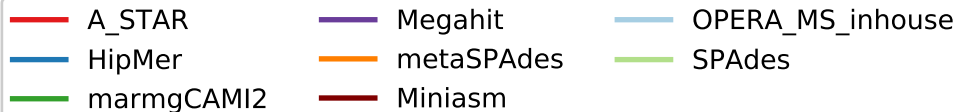
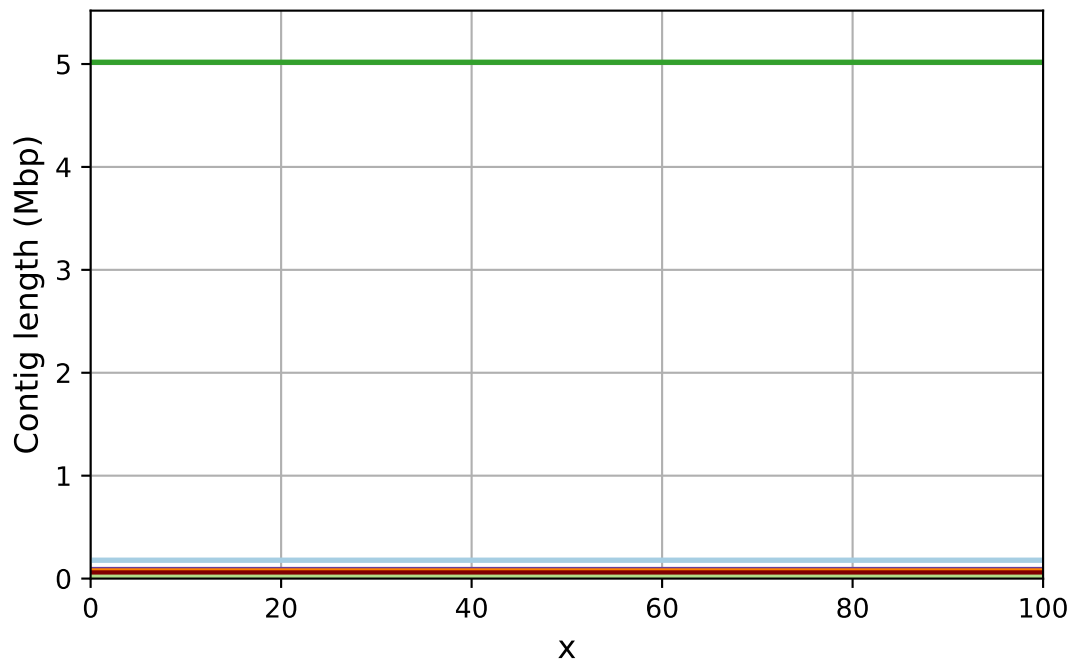
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0
# partially unaligned contigs	10	11	1	16	12	5	5	4
Partially unaligned length	70063	213704	5011224	359695	372527	134805	407885	27209
# N's	24643	3	0	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).

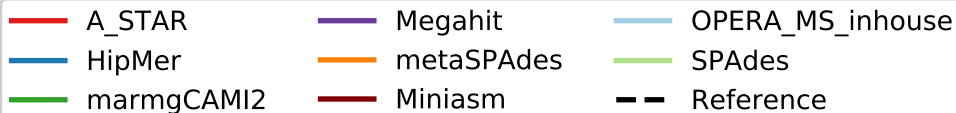
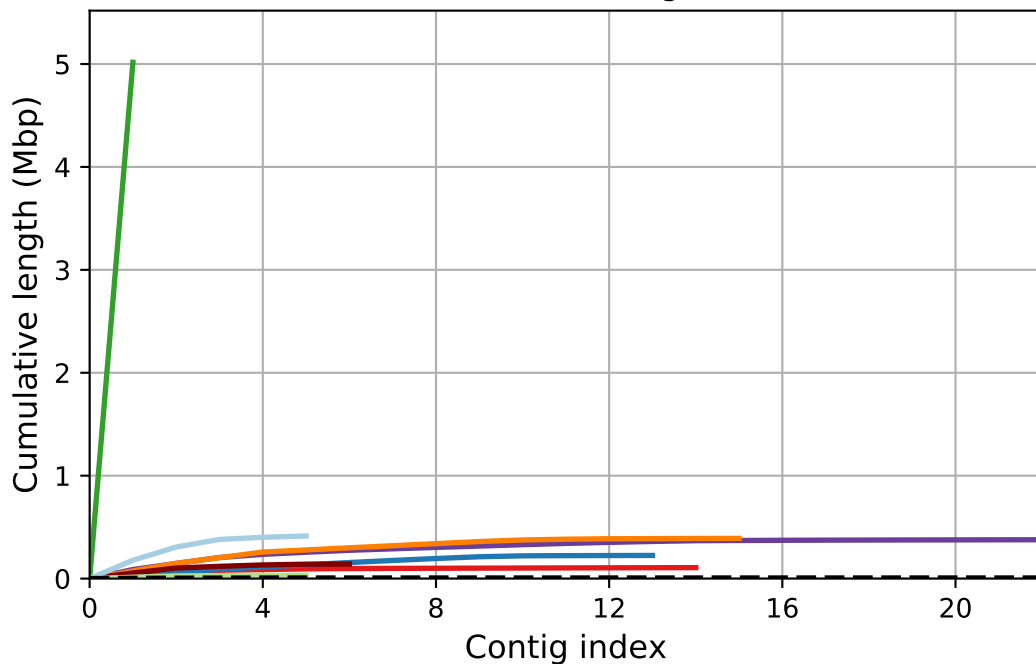
Nx



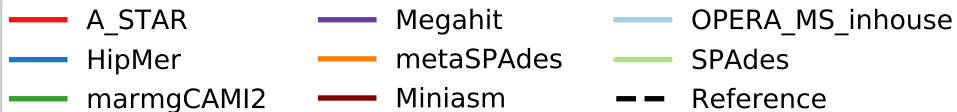
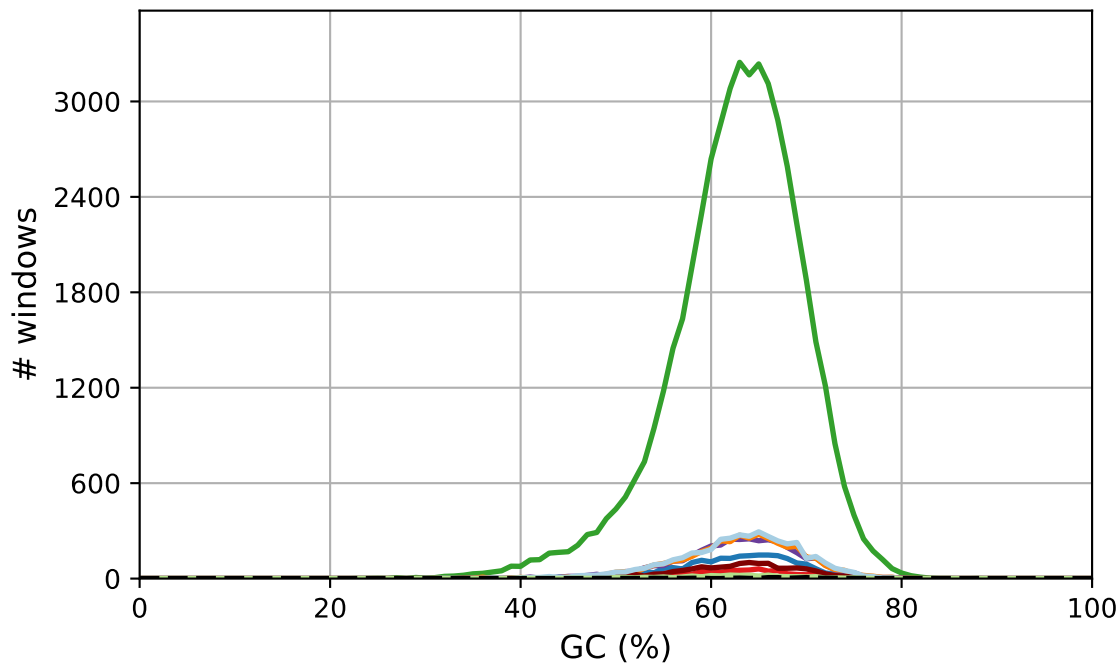
NGx



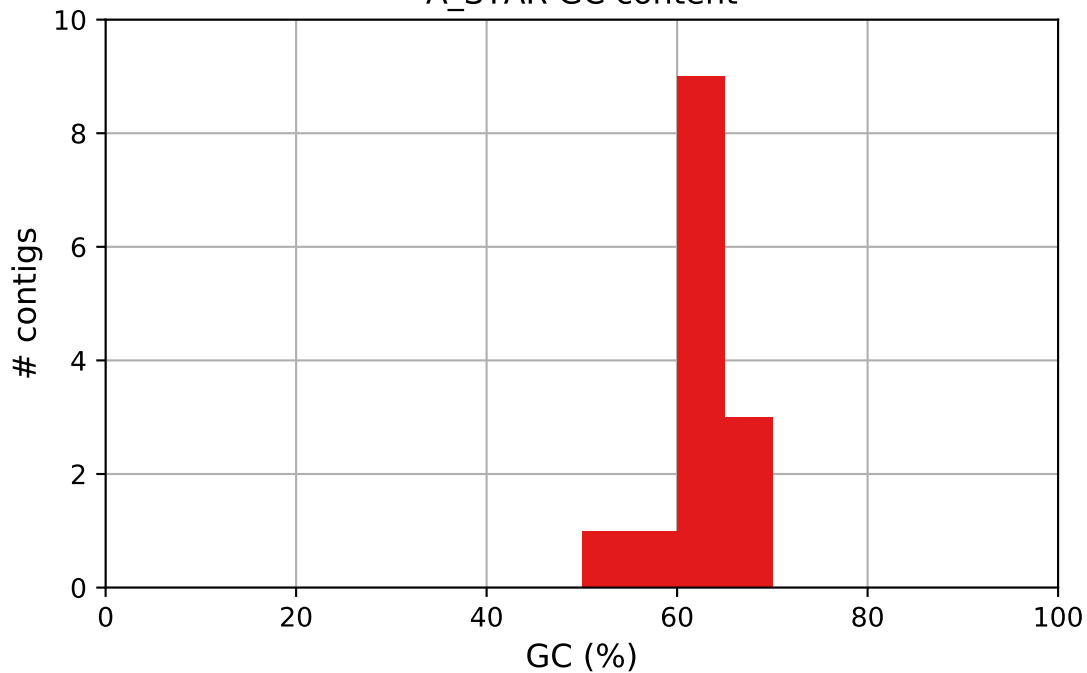
Cumulative length



GC content

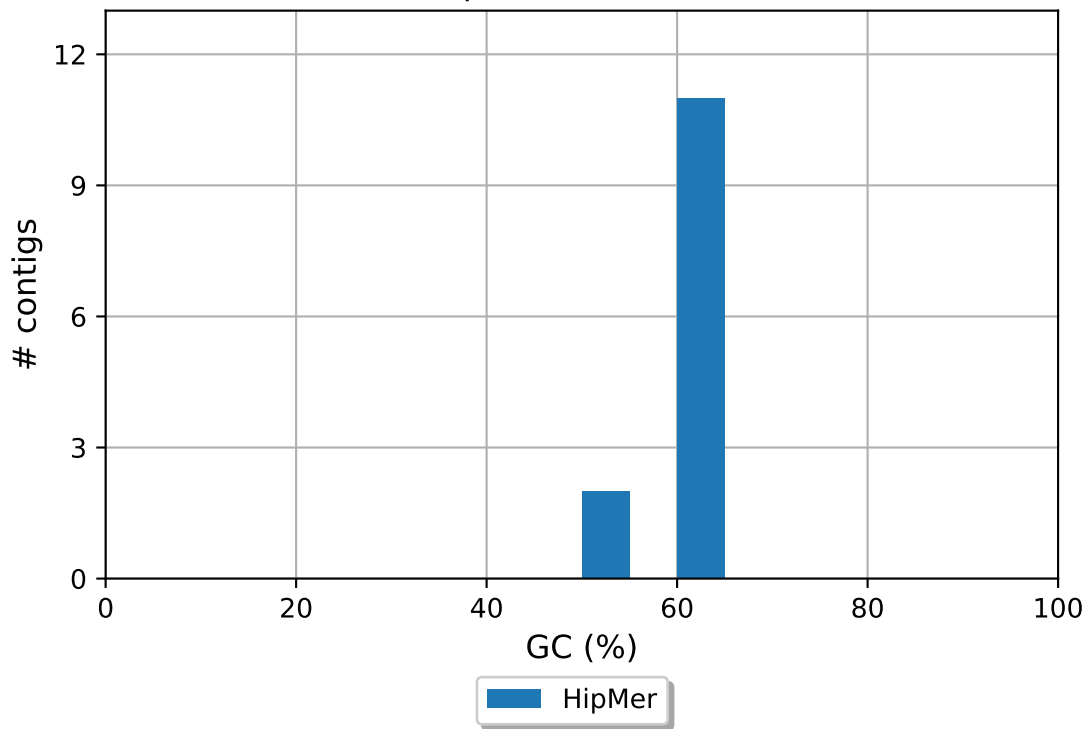


A_STAR GC content

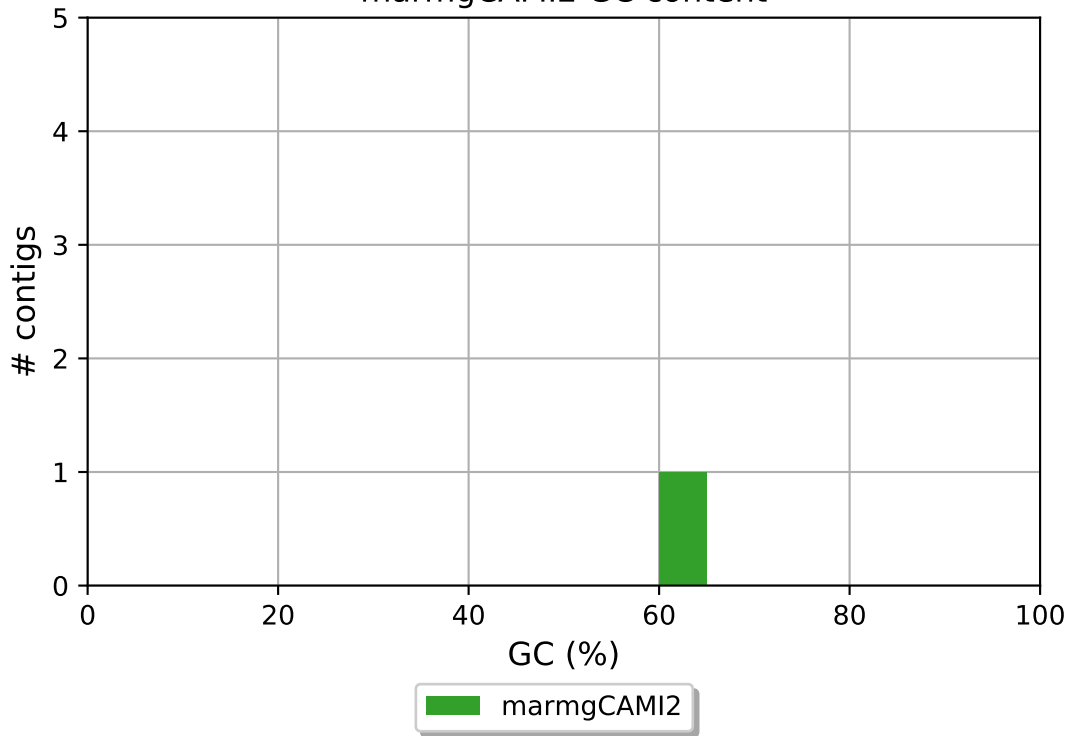


A_STAR

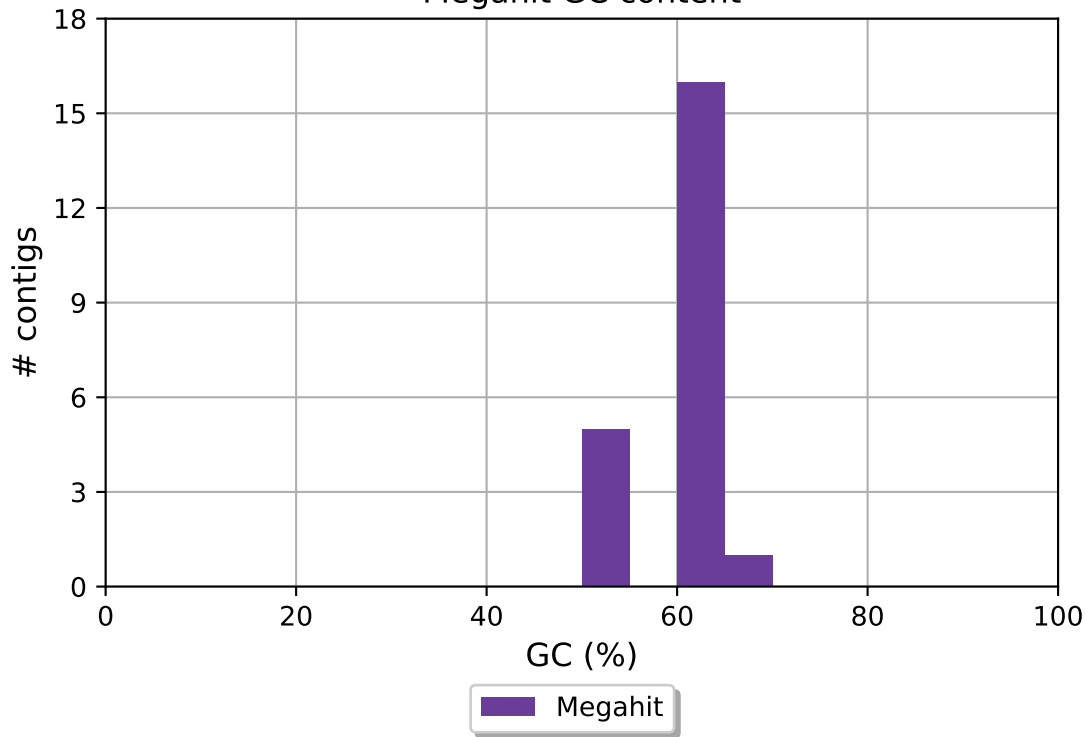
HipMer GC content



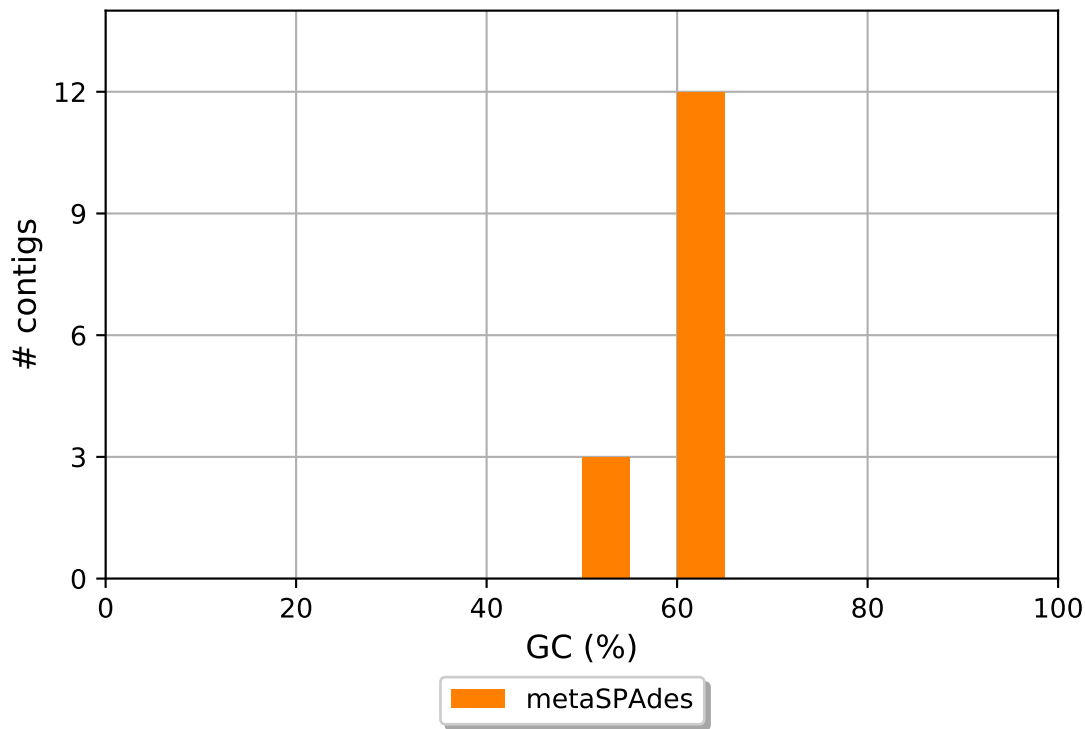
marmgCAMI2 GC content



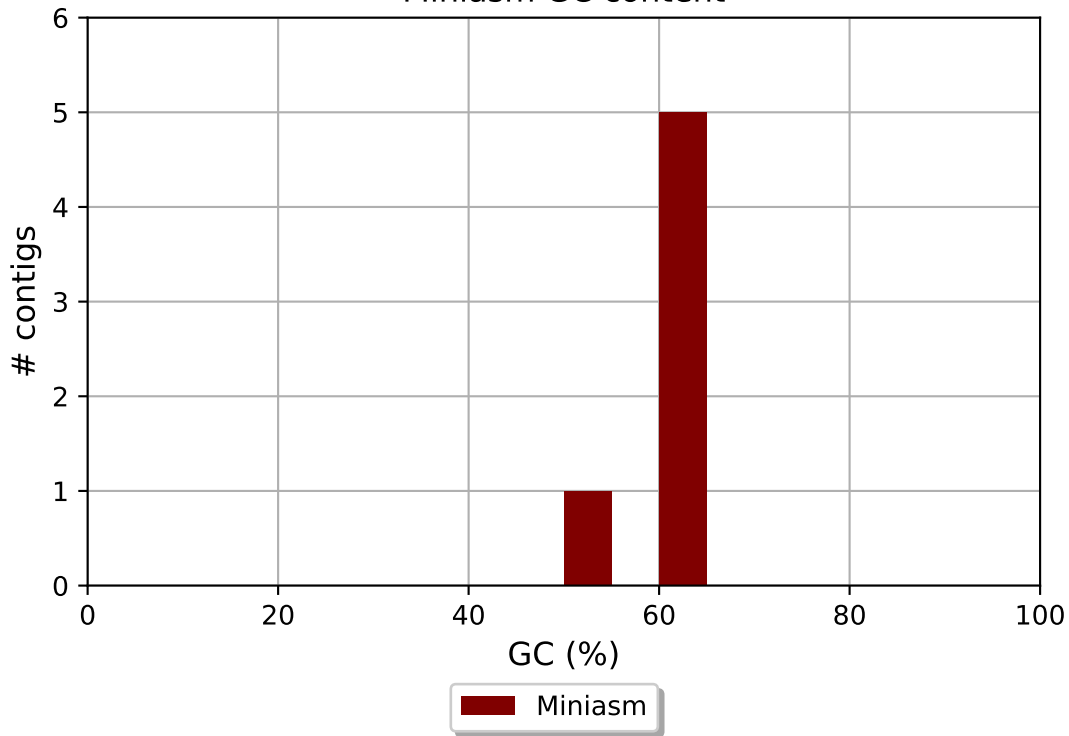
Megahit GC content



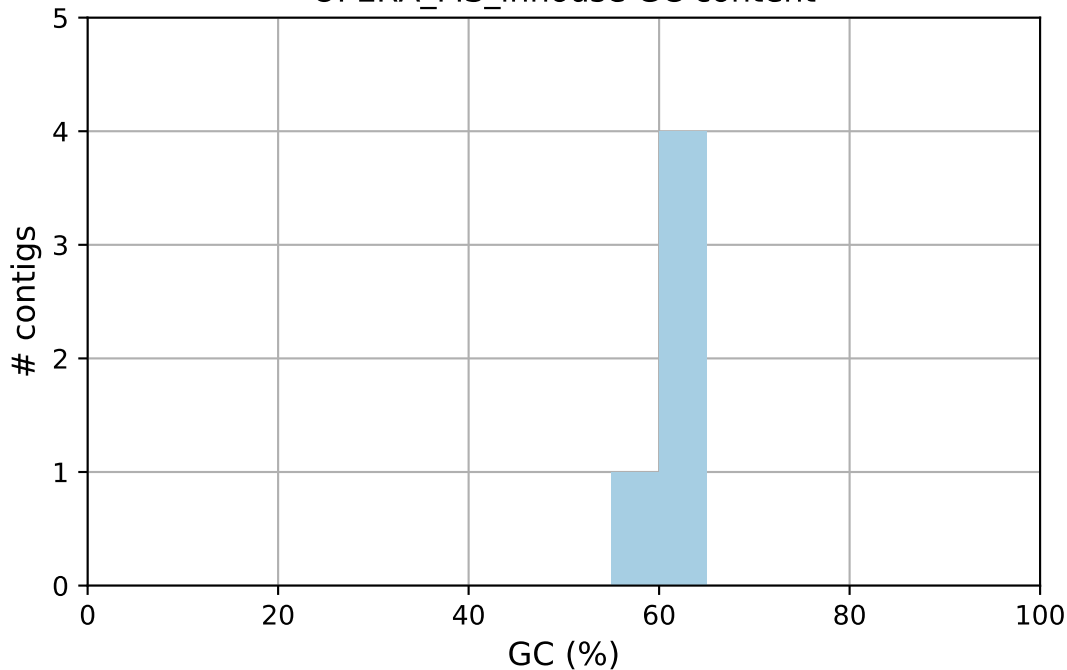
metaSPAdes GC content



Miniasm GC content

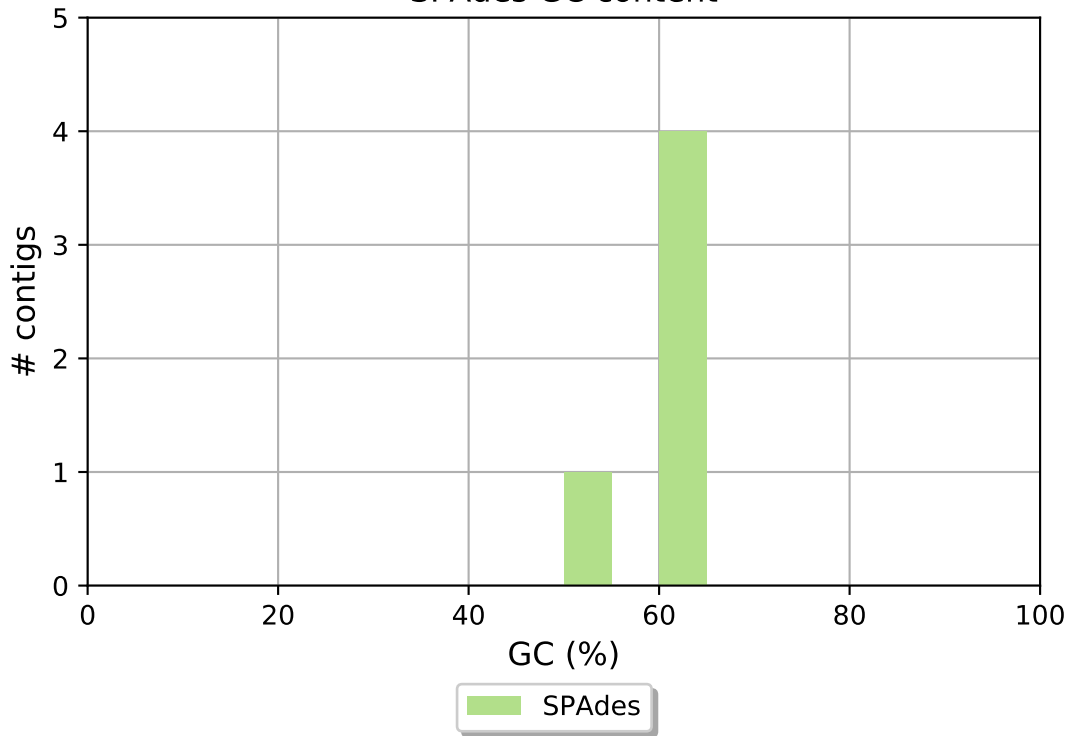


OPERA_MS_inhouse GC content

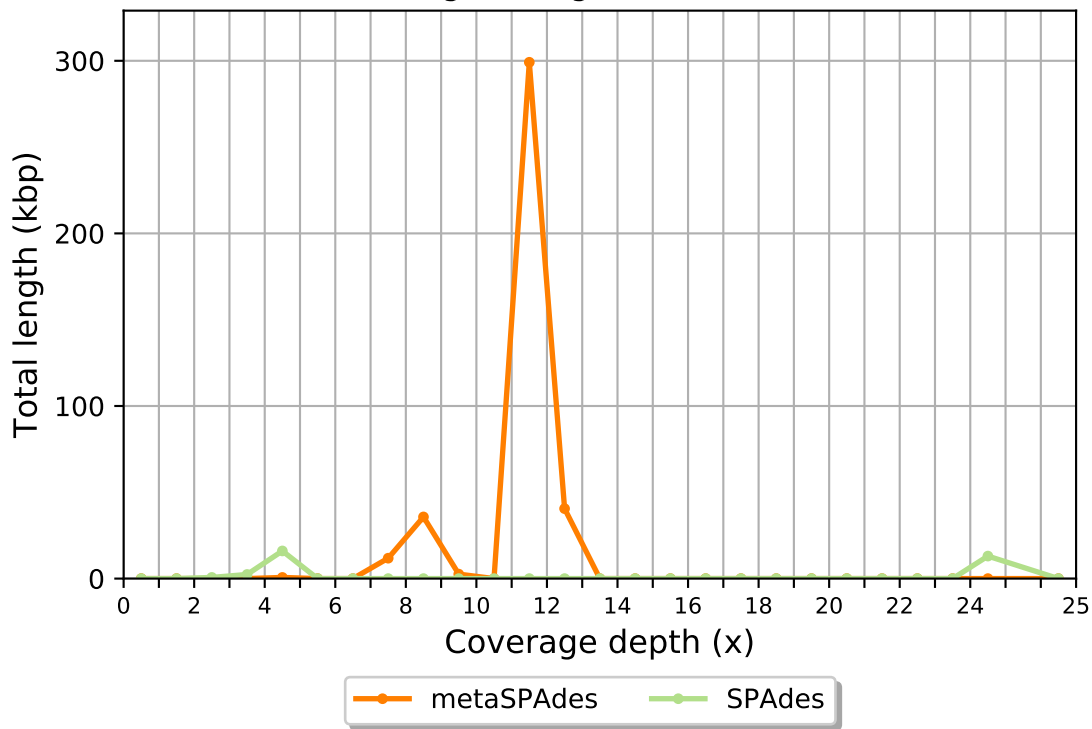


OPERA_MS_inhouse

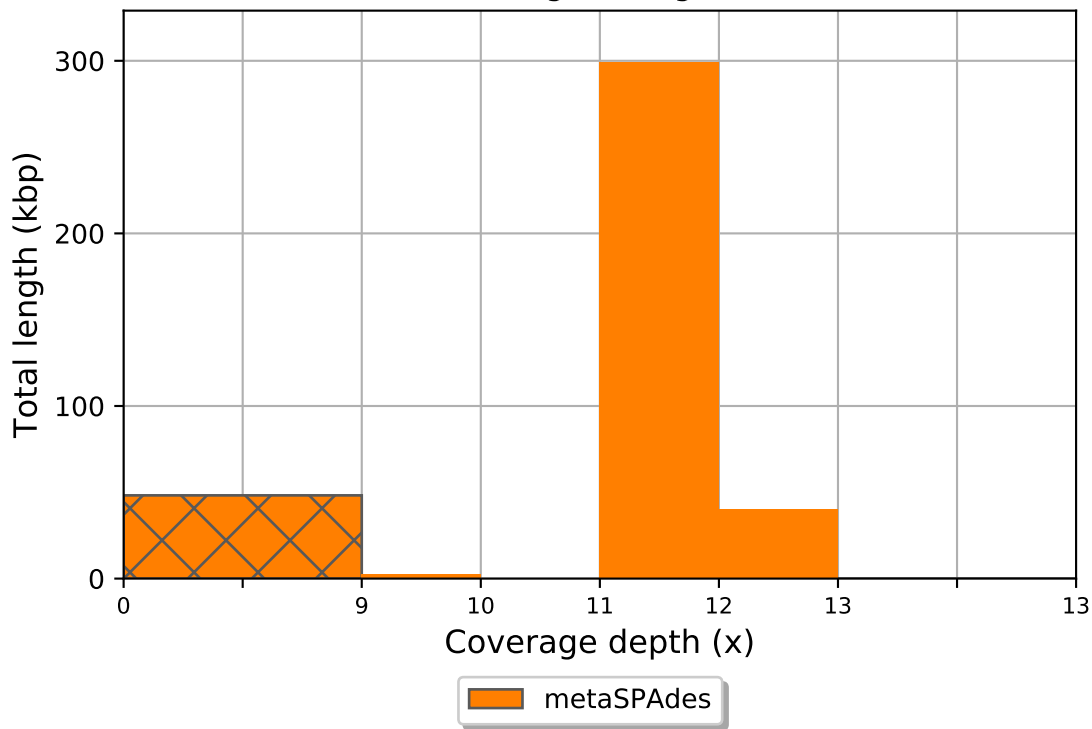
SPAdes GC content



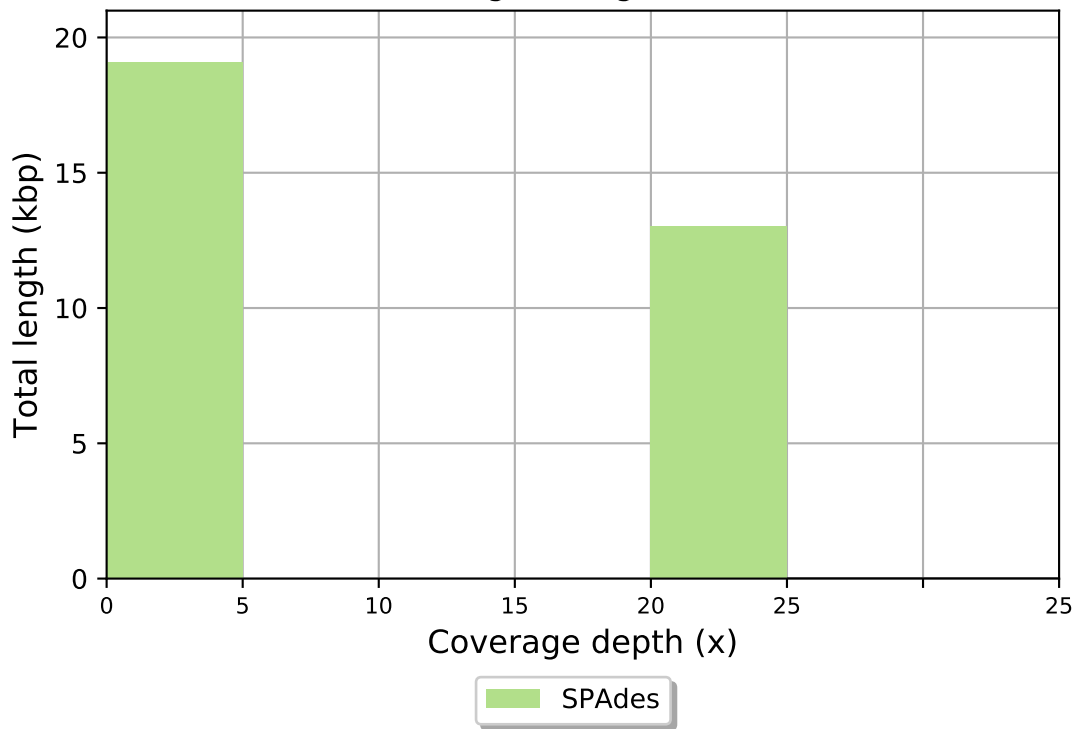
Coverage histogram (bin size: 1x)



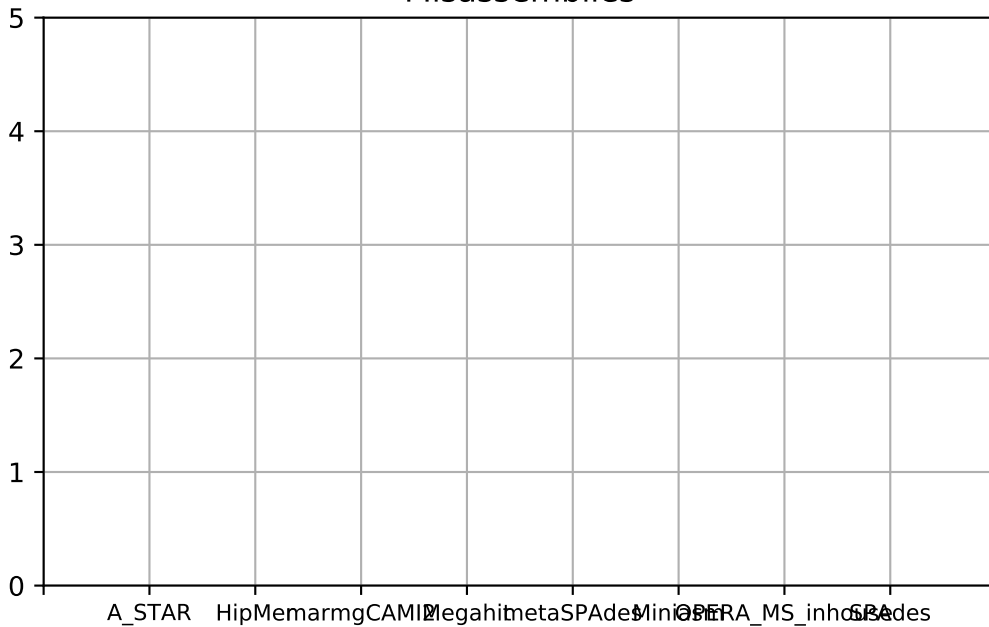
metaSPAdes coverage histogram (bin size: 1x)



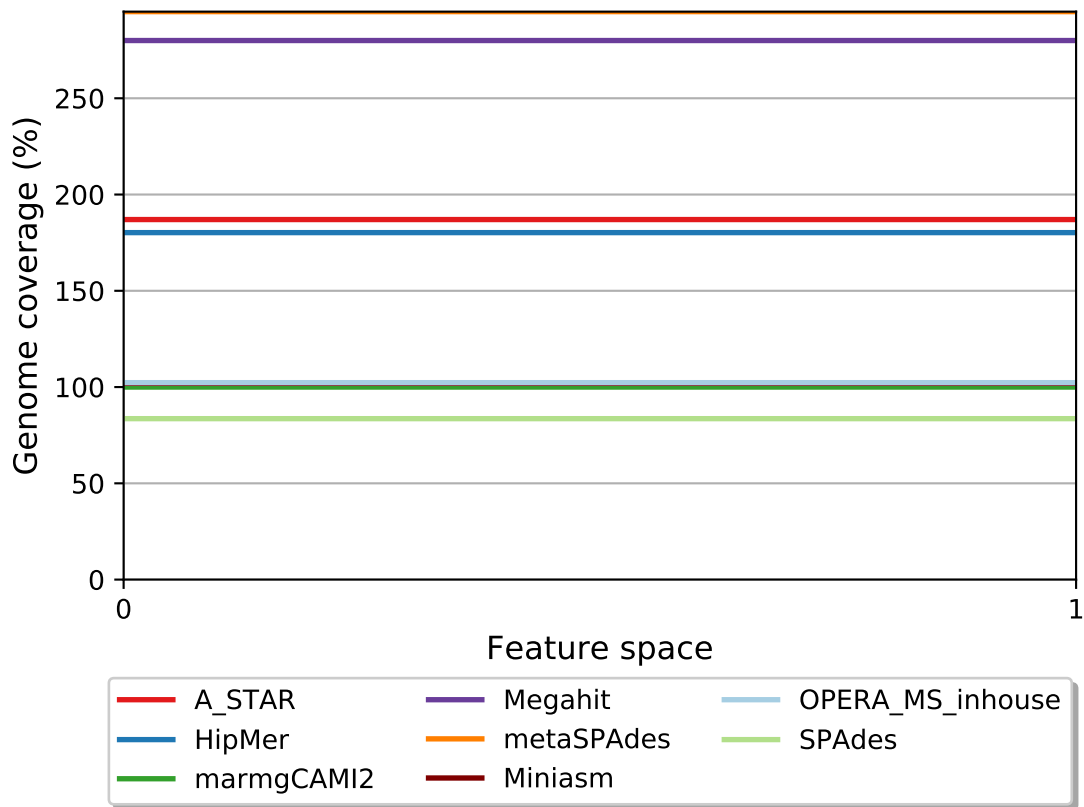
SPAdes coverage histogram (bin size: 5x)



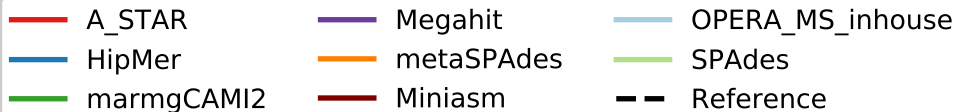
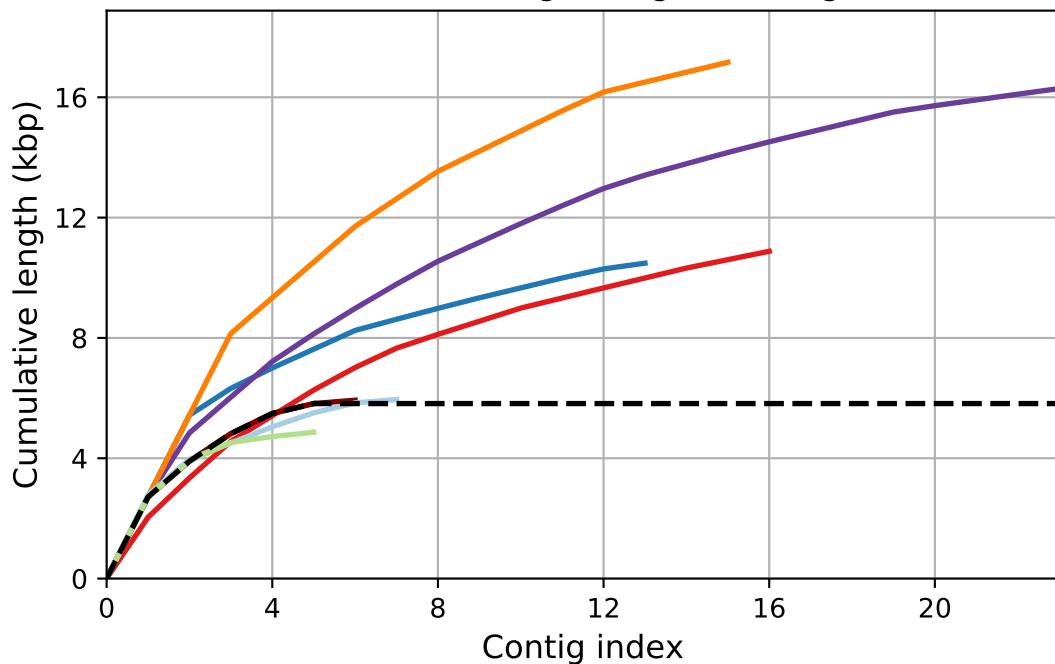
Misassemblies



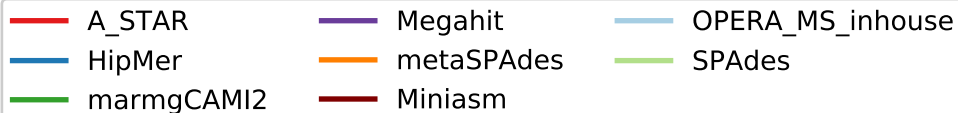
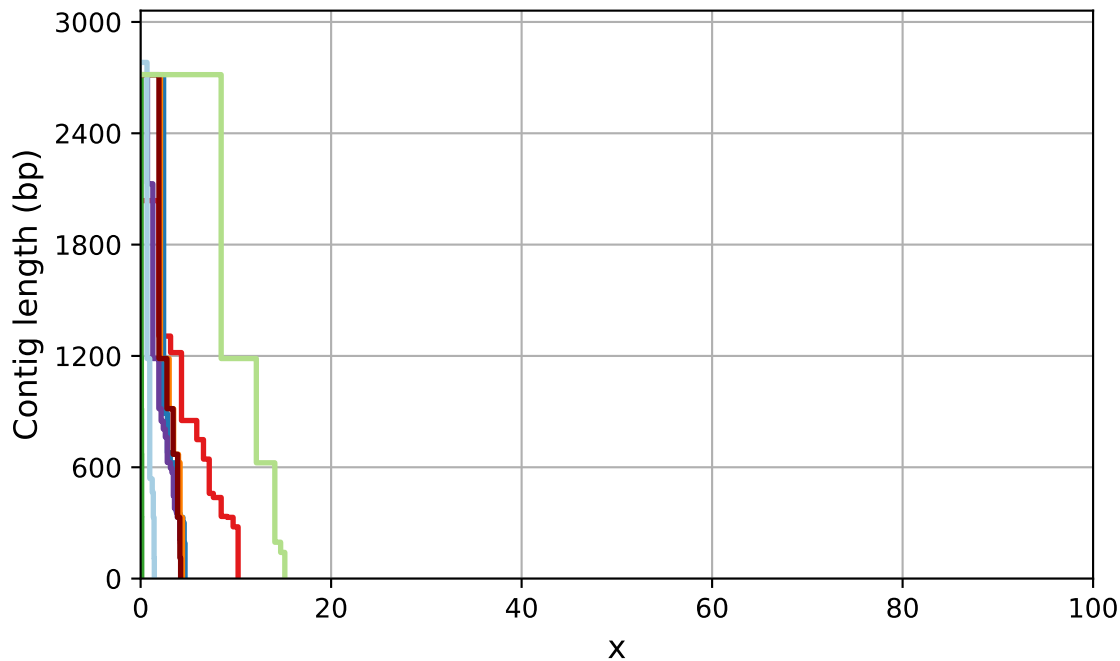
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

