

# Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	15	21	1	33	22	10	5	9
# contigs (>= 5000 bp)	7	17	1	25	19	9	5	4
# contigs (>= 10000 bp)	2	17	1	25	19	9	5	2
# contigs (>= 25000 bp)	1	13	1	19	18	8	5	0
# contigs (>= 50000 bp)	1	8	1	11	14	4	5	0
Total length (>= 1000 bp)	121549	906314	4719539	1319775	1189252	525960	465206	57040
Total length (>= 5000 bp)	103166	893254	4719539	1298017	1178428	522054	465206	46097
Total length (>= 10000 bp)	68864	893254	4719539	1298017	1178428	522054	465206	31655
Total length (>= 25000 bp)	52937	806852	4719539	1183903	1156217	504334	465206	0
Total length (>= 50000 bp)	52937	606109	4719539	882960	1010566	338068	465206	0
# contigs	17	21	1	38	22	10	7	9
Largest contig	52937	114060	4719539	140059	106950	118567	145003	18741
Total length	123471	906314	4719539	1323094	1189252	525960	466444	57040
Reference length	13840	13840	13840	13840	13840	13840	13840	13840
GC (%)	53.73	54.17	54.17	54.13	53.98	54.11	54.01	54.17
Reference GC (%)	59.83	59.83	59.83	59.83	59.83	59.83	59.83	59.83
N50	15927	60189	4719539	63522	65124	63183	120652	12914
NG50	52937	114060	4719539	140059	106950	118567	145003	18741
N75	5973	45946	4719539	39908	51751	44522	67210	6909
NG75	52937	114060	4719539	140059	106950	118567	145003	18741
L50	2	6	1	8	7	3	2	2
LG50	1	1	1	1	1	1	1	1
L75	6	10	1	14	12	6	4	4
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	2	0	0	1	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	3	3	1	7	3	0	2	1
# unaligned contigs	2 + 13 part	0 + 17 part	0 + 1 part	0 + 28 part	0 + 22 part	0 + 10 part	0 + 5 part	0 + 8 part
Unaligned length	100574	881748	4705620	1294641	1153569	514352	455186	45862
Genome fraction (%)	26.965	89.928	100.000	95.419	90.116	81.481	79.415	78.699
Duplication ratio	6.135	1.974	1.006	2.155	2.861	1.029	1.024	1.026
# N's per 100 kbp	11921.02	17.32	0.00	0.00	8.41	0.00	0.00	0.00
# mismatches per 100 kbp	830.65	224.97	57.80	1582.61	489.10	124.15	409.43	321.34
# indels per 100 kbp	53.59	24.10	0.00	15.14	8.02	133.01	0.00	0.00
Largest alignment	896	4153	9260	4327	9260	9260	4759	5784
Total aligned length	7361	24400	14270	27963	35683	11608	11136	11168
NGA50	135	4153	9260	2919	9260	9260	4178	3043
NGA75	-	2352	1570	1745	9260	344	200	224
LGA50	17	2	1	2	1	1	2	2
LGA75	-	3	2	4	2	4	6	5

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

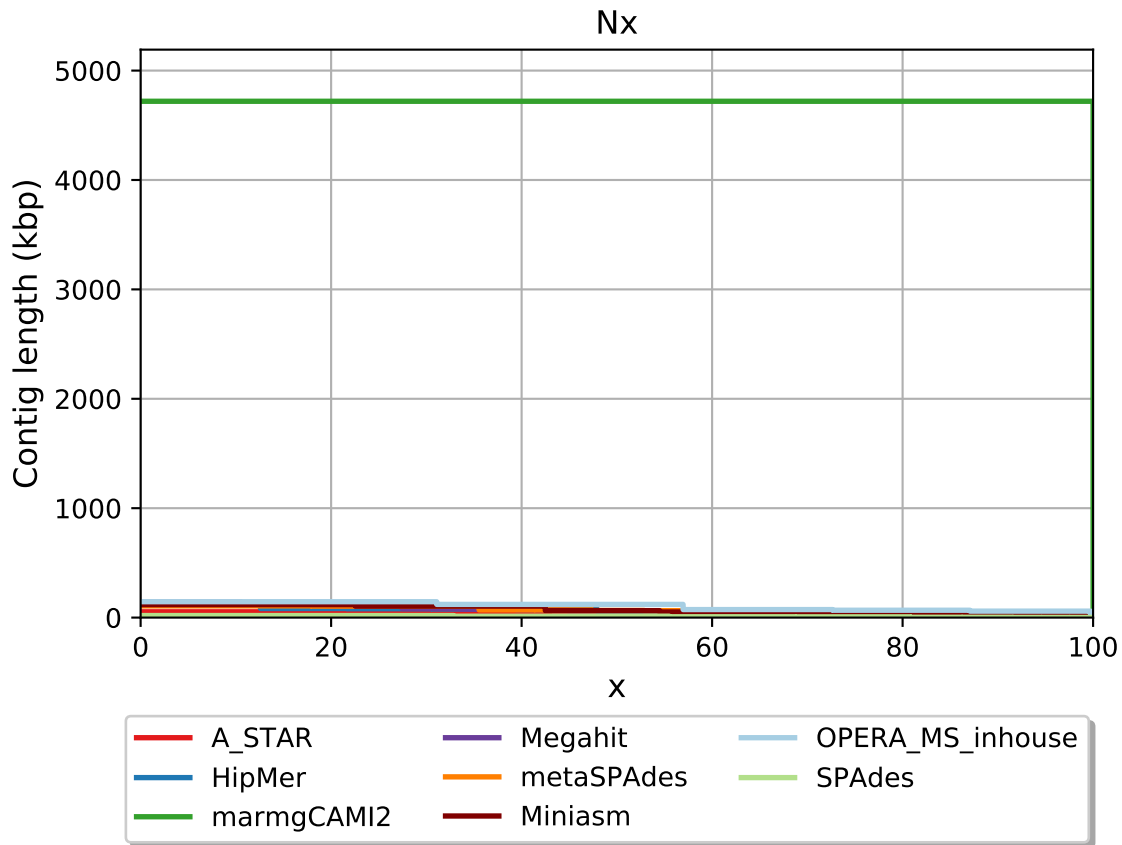
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	14	0	19	17	9	2	6
# possible misassemblies	12	14	0	20	21	12	2	6
# local misassemblies	0	0	0	2	0	0	1	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	3	3	1	7	3	0	2	1
# mismatches	31	28	8	209	61	14	45	35
# indels	2	3	0	2	1	15	0	0
# indels (<= 5 bp)	0	0	0	0	0	15	0	0
# indels (> 5 bp)	2	3	0	2	1	0	0	0
Indels length	28	114	0	99	21	17	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).

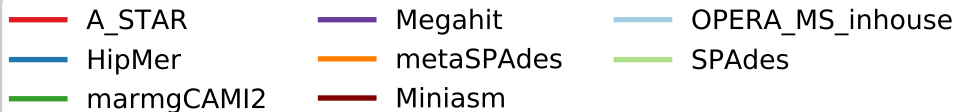
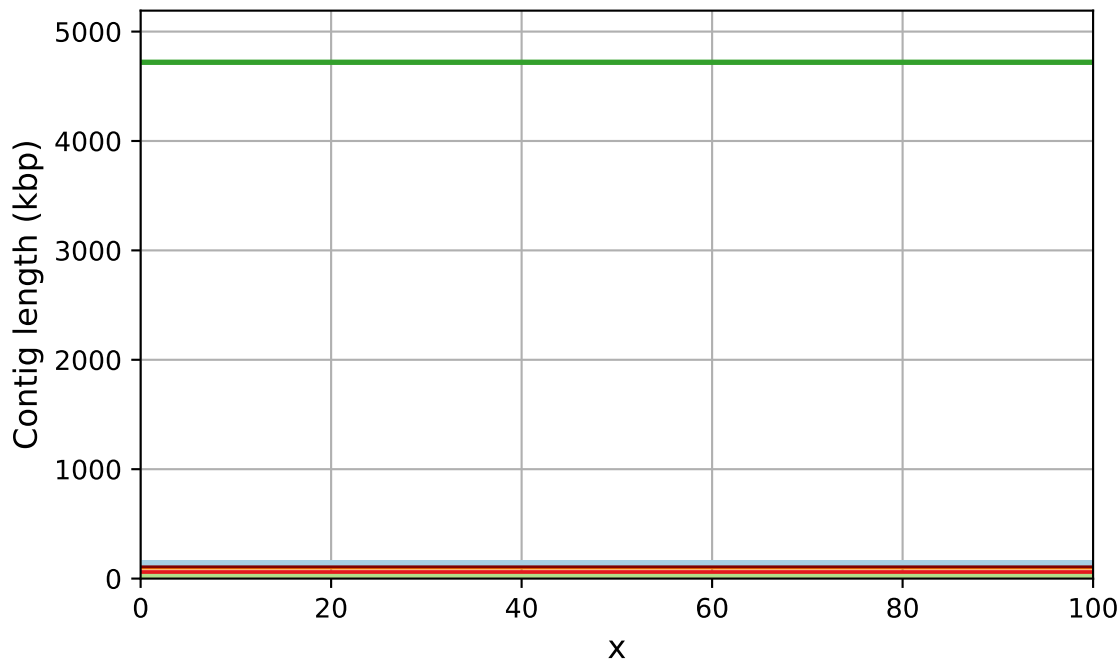
## Unaligned report

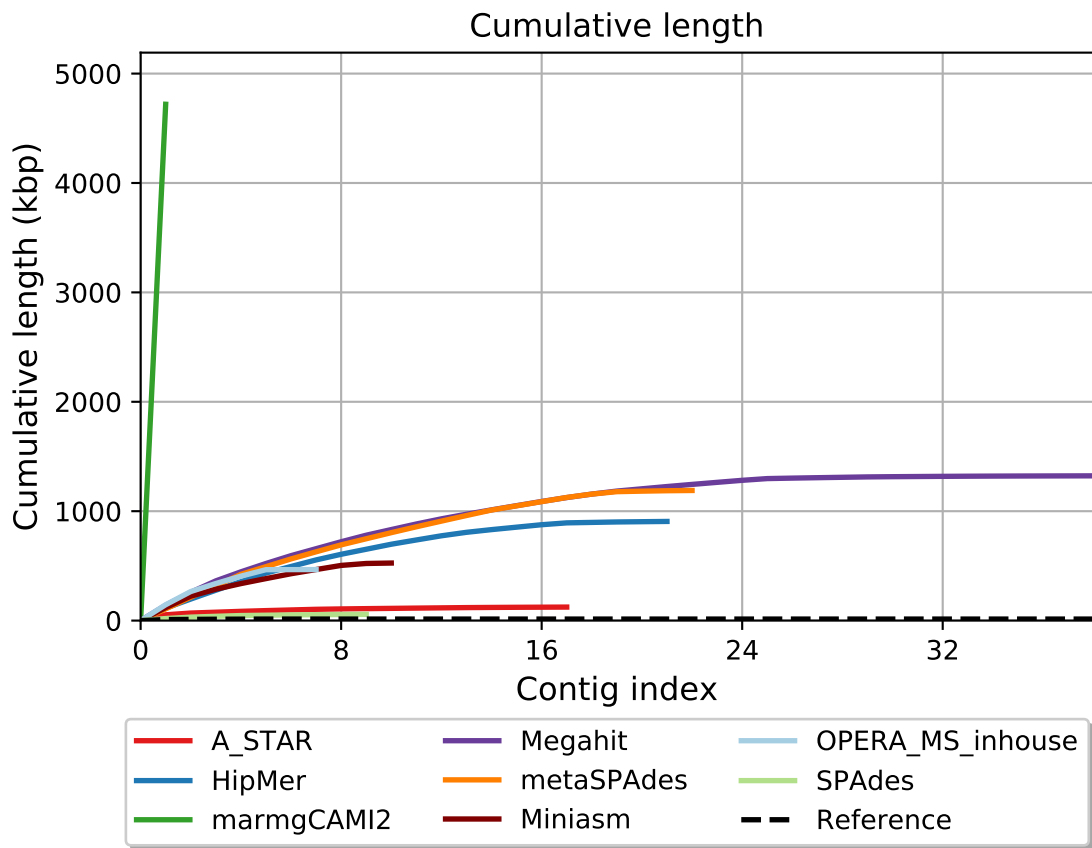
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# fully unaligned contigs	2	0	0	0	0	0	0	0
Fully unaligned length	17957	0	0	0	0	0	0	0
# partially unaligned contigs	13	17	1	28	22	10	5	8
Partially unaligned length	82617	881748	4705620	1294641	1153569	514352	455186	45862
# N's	14719	157	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).

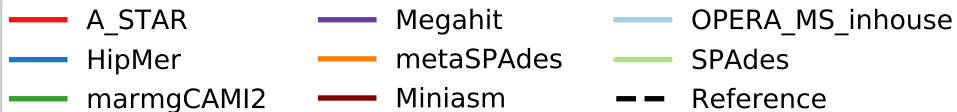
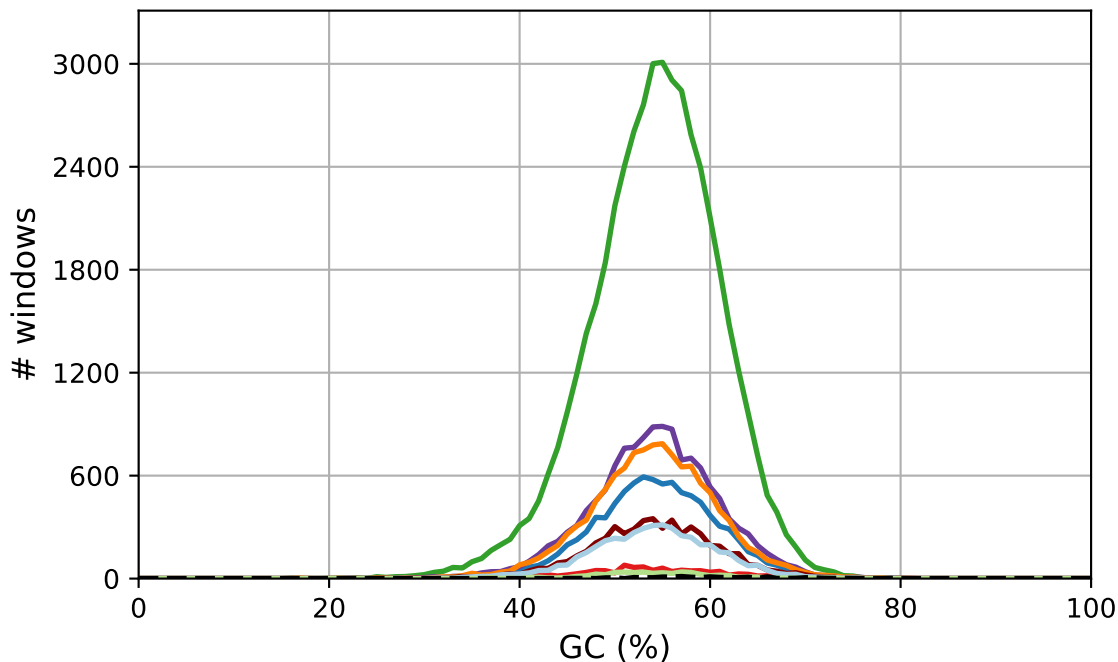


# NGx

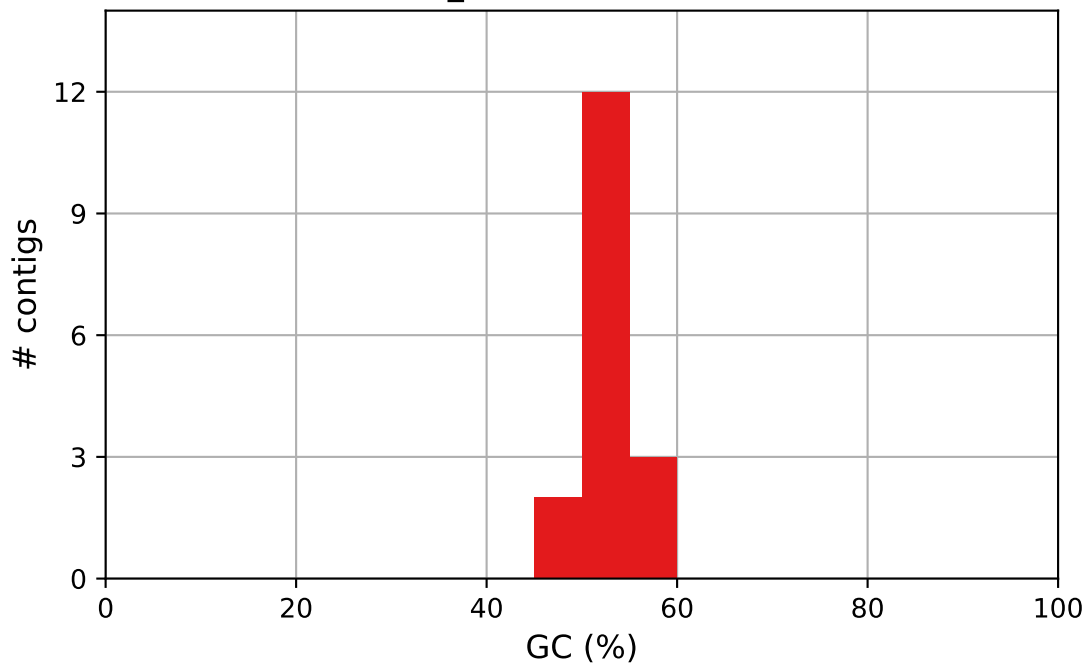




## GC content



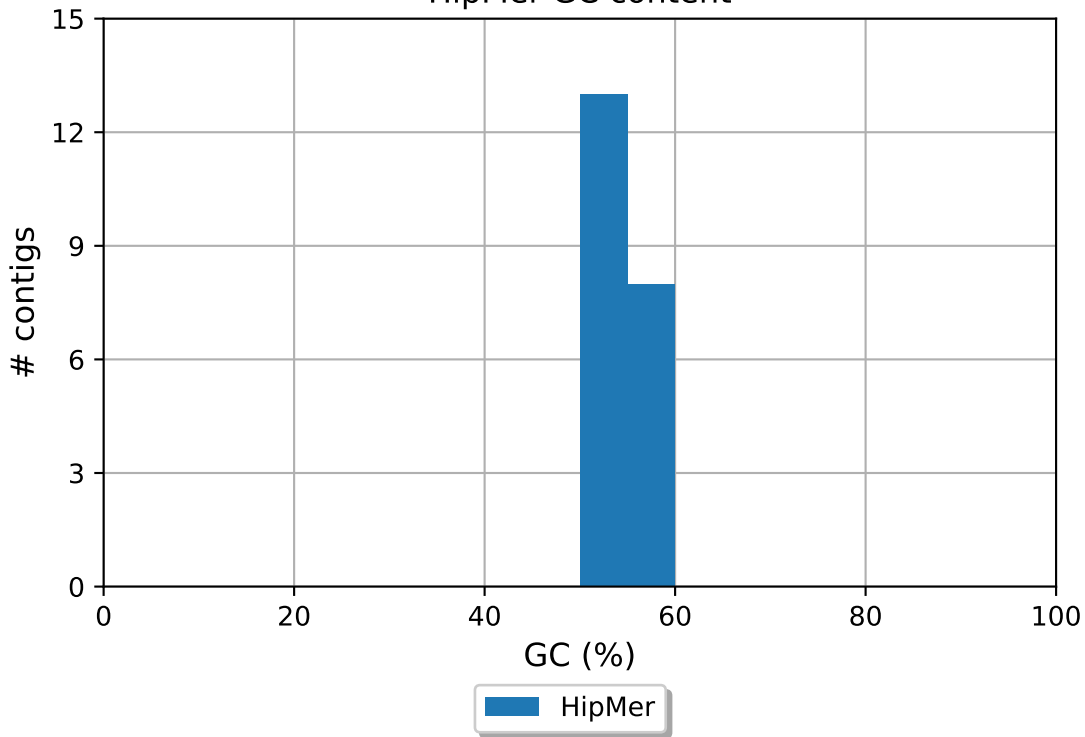
A\_STAR GC content



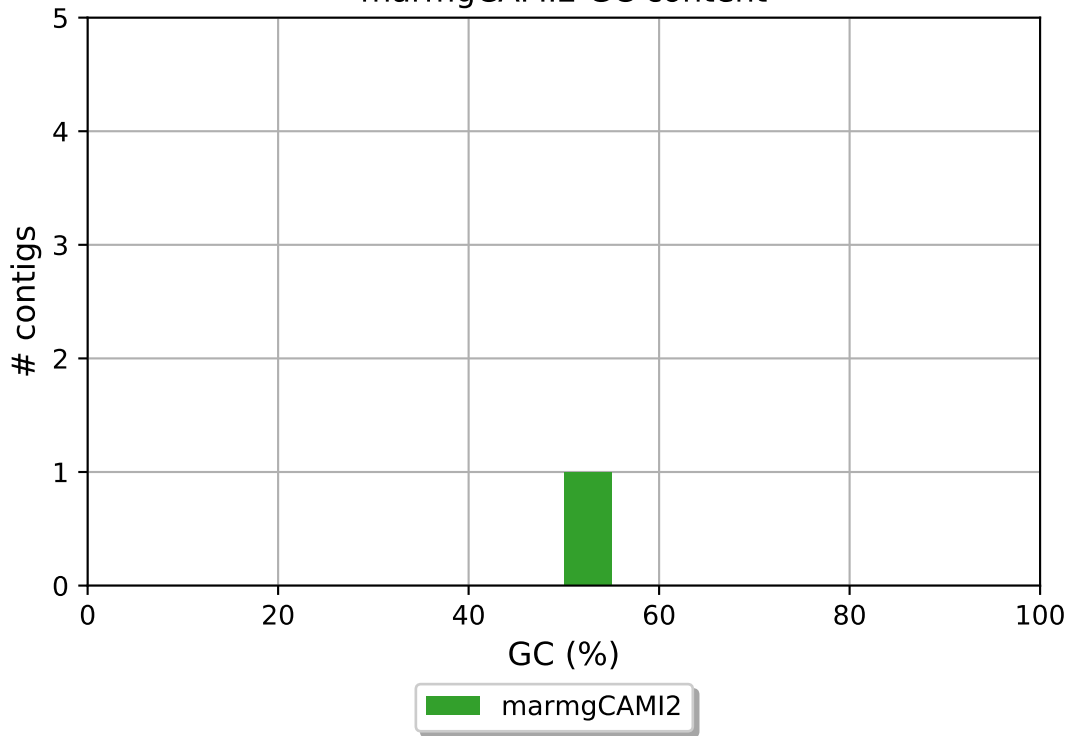
A\_STAR



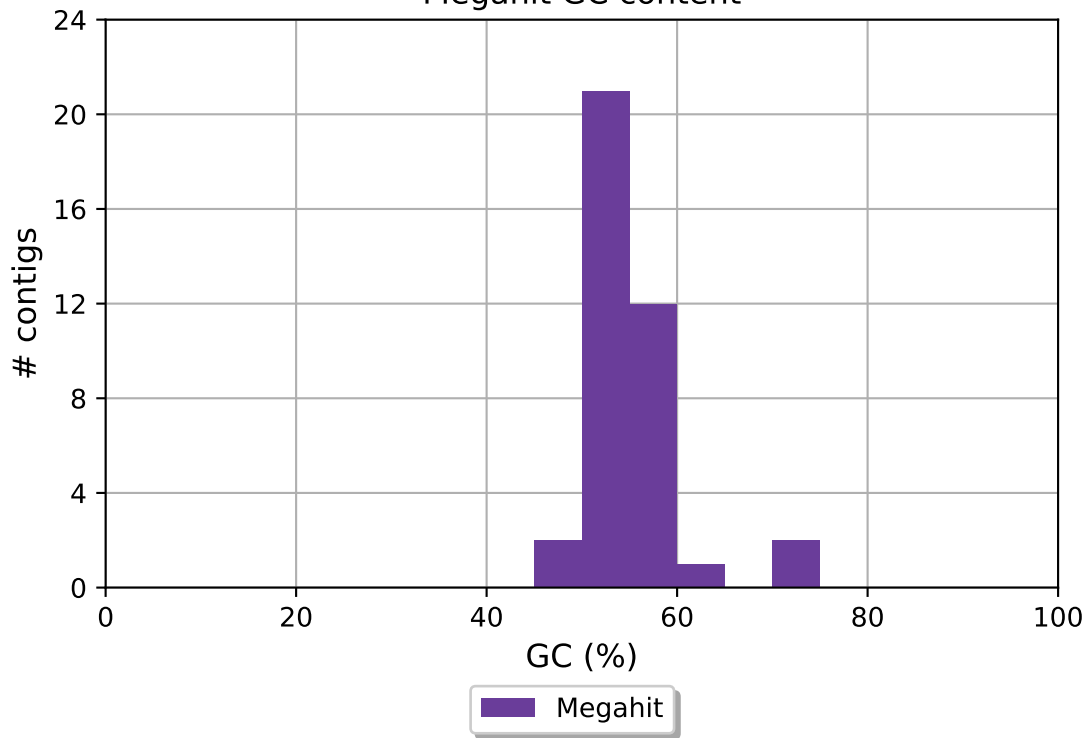
HipMer GC content



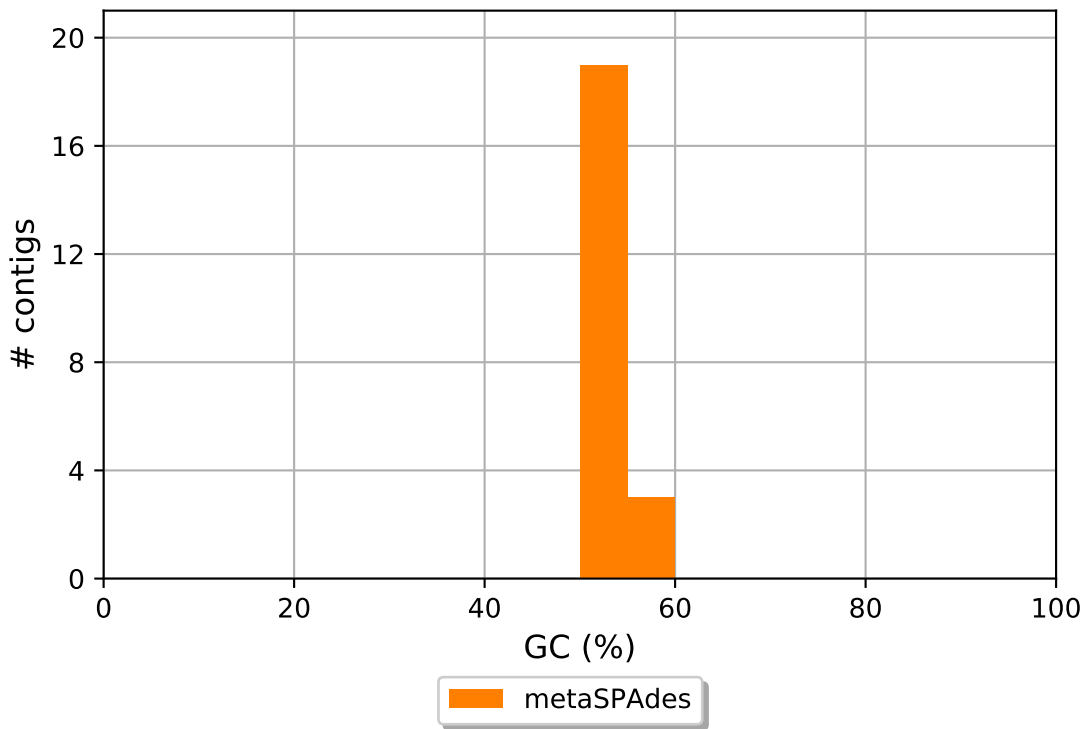
marmgCAMI2 GC content



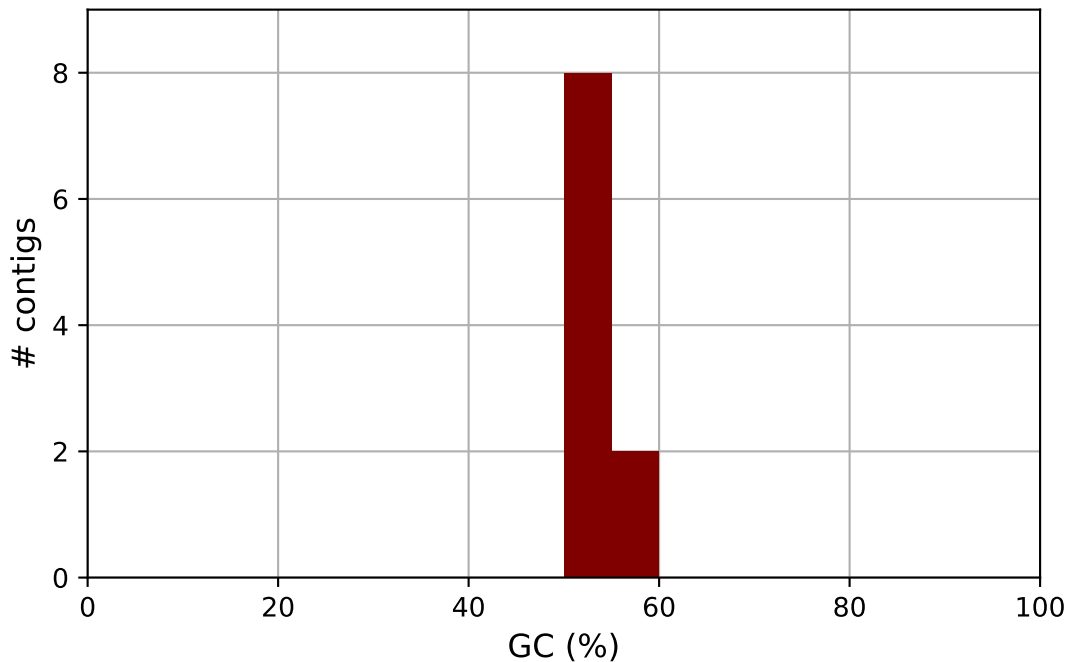
Megahit GC content



metaSPAdes GC content

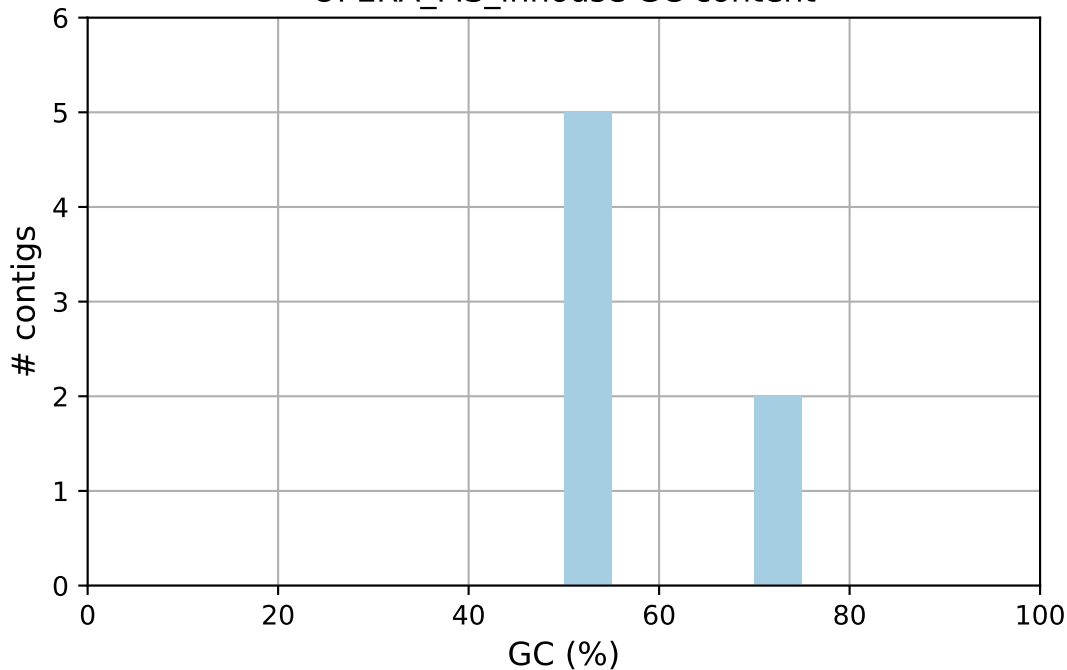


Miniasm GC content



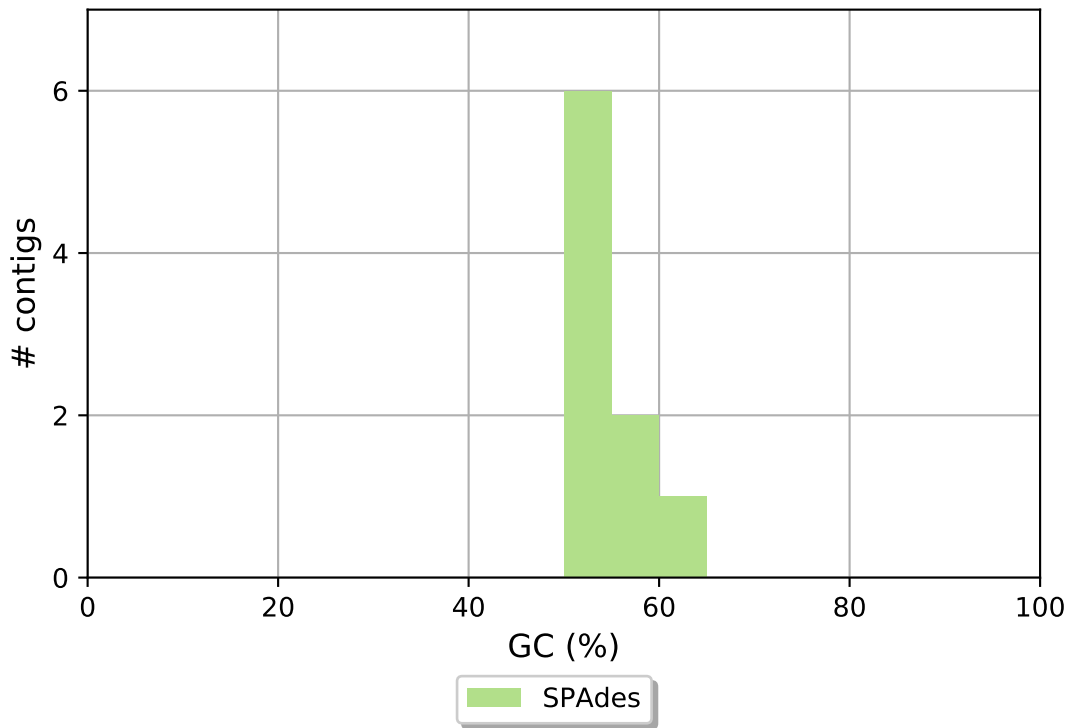
Miniasm

OPERA\_MS\_inhouse GC content

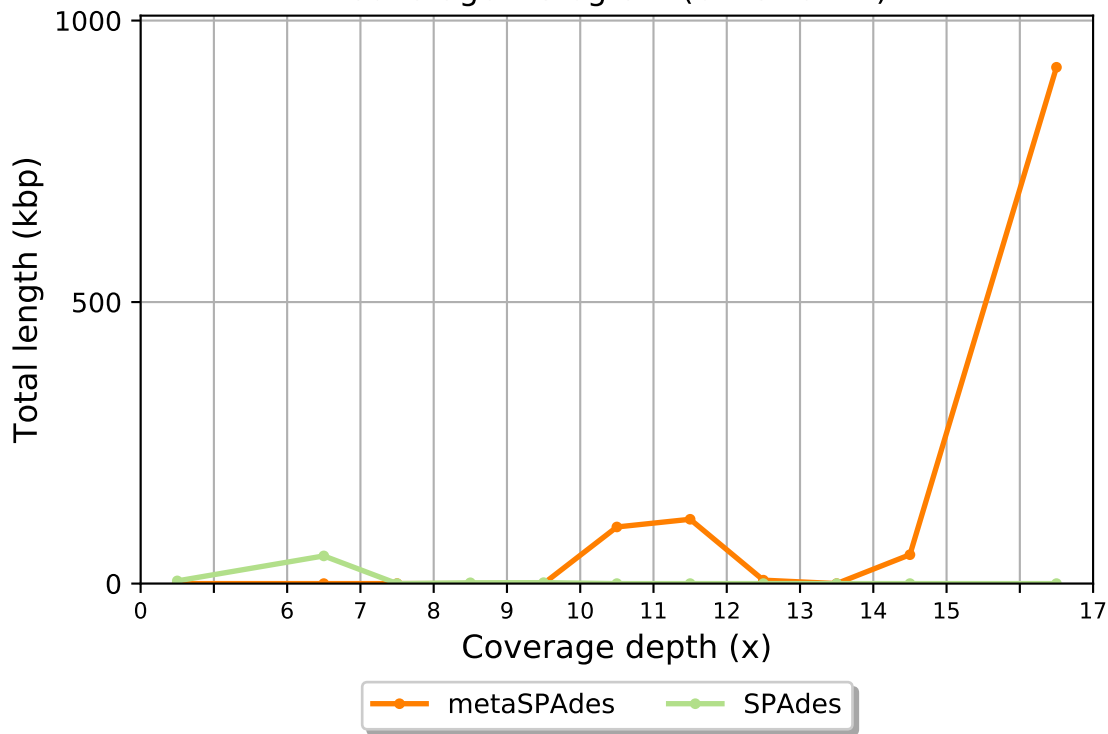


OPERA\_MS\_inhouse

## SPAdes GC content

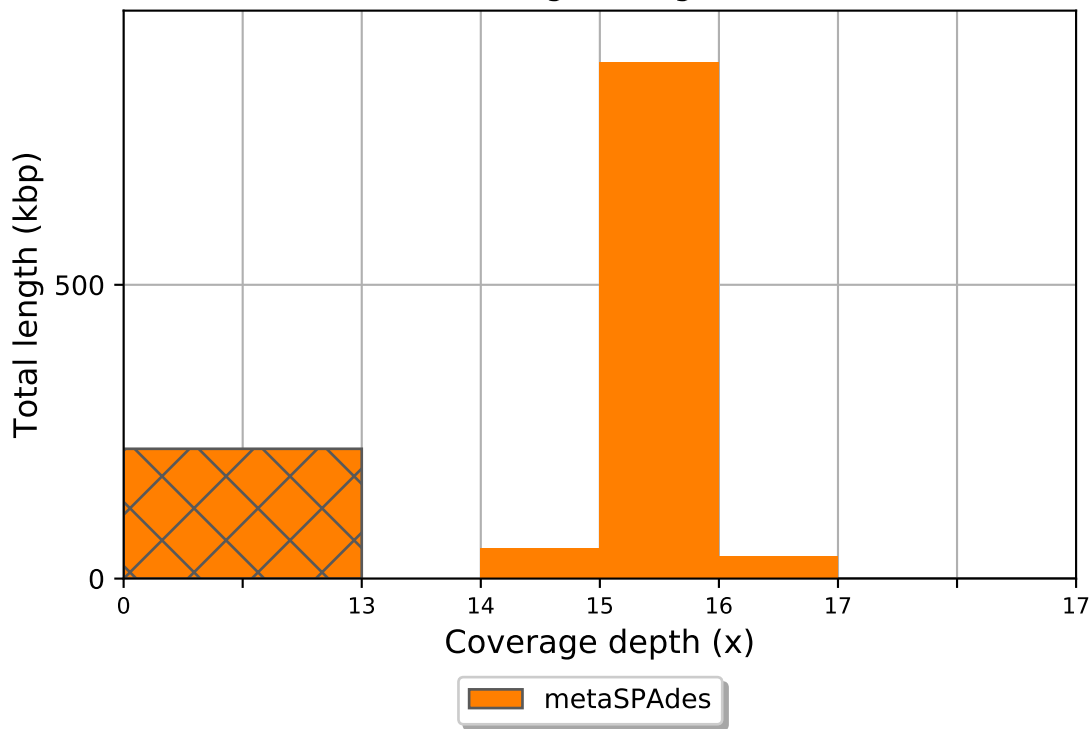


Coverage histogram (bin size: 1x)

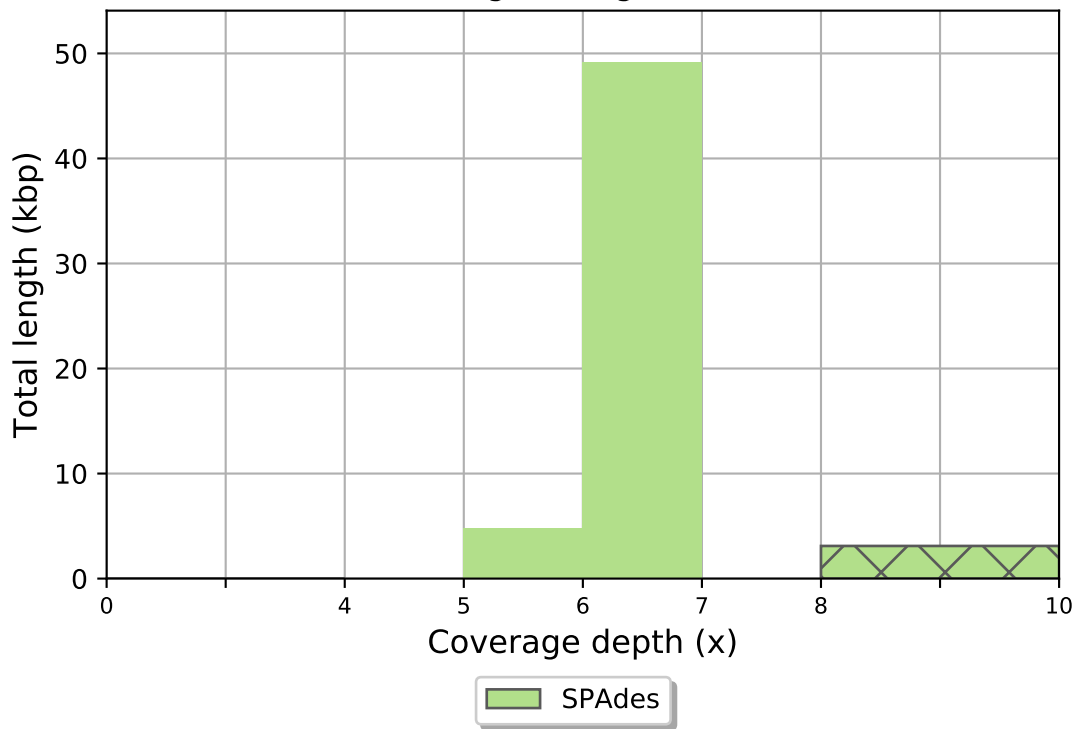




metaSPAdes coverage histogram (bin size: 1x)



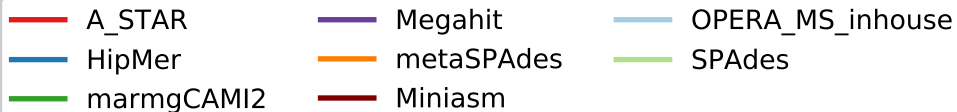
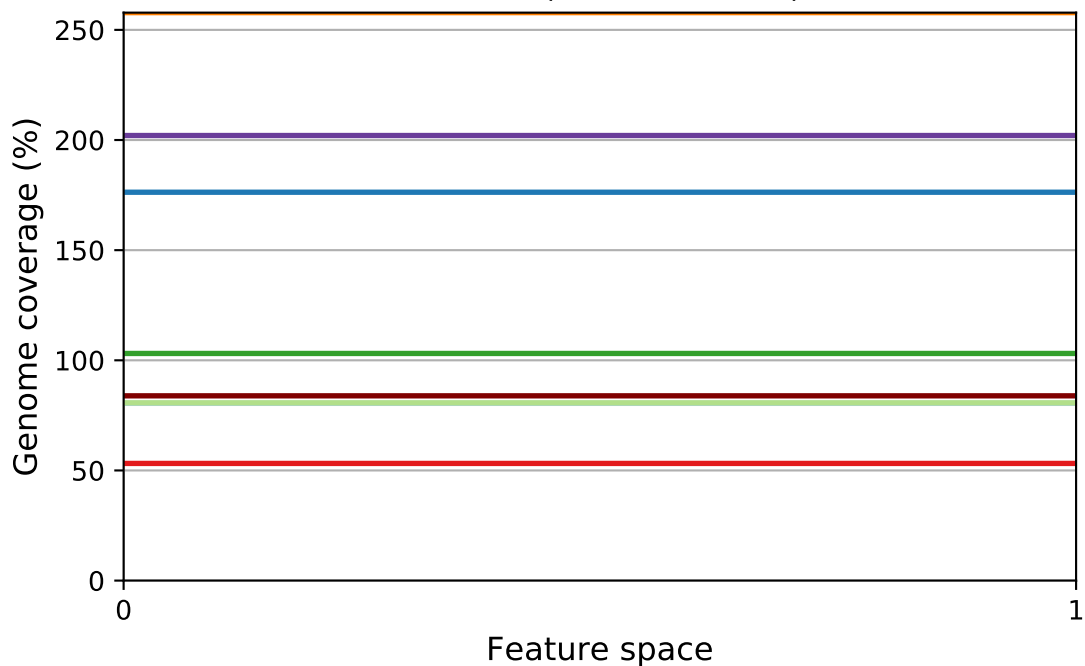
SPAdes coverage histogram (bin size: 1x)



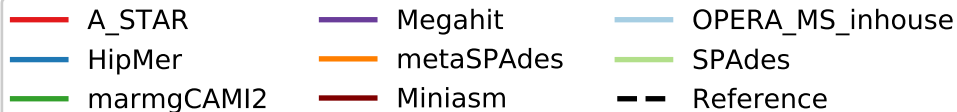
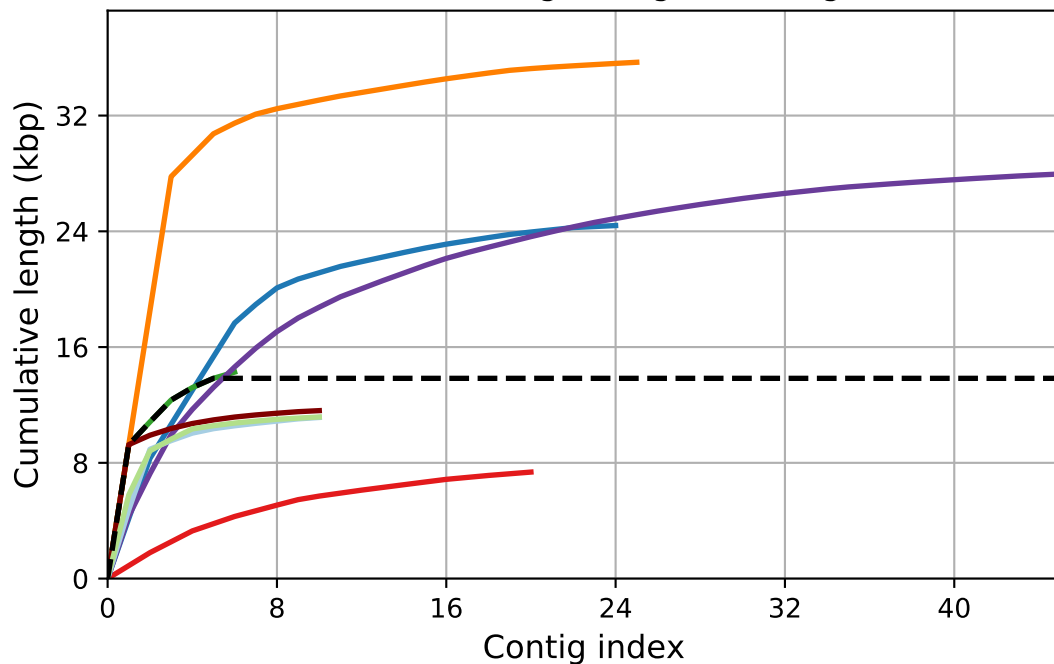
## Misassemblies



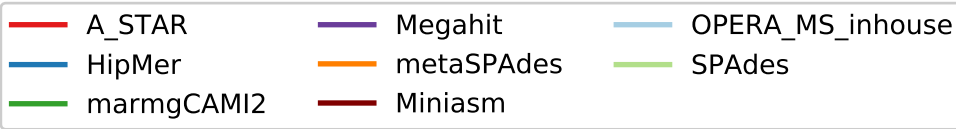
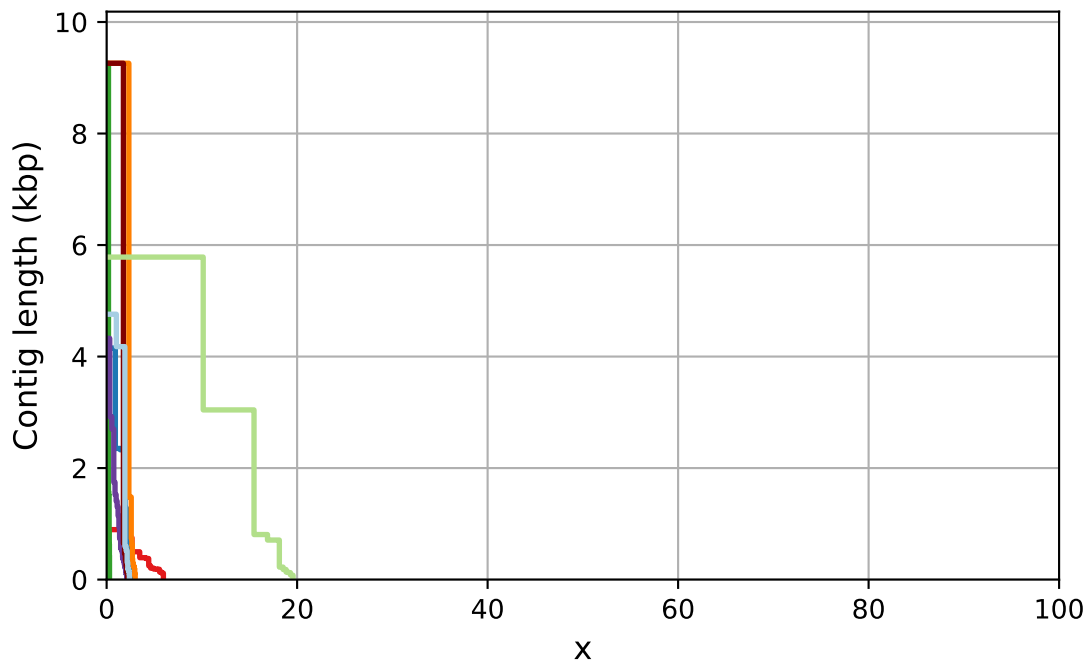
FRCurve (misassemblies)



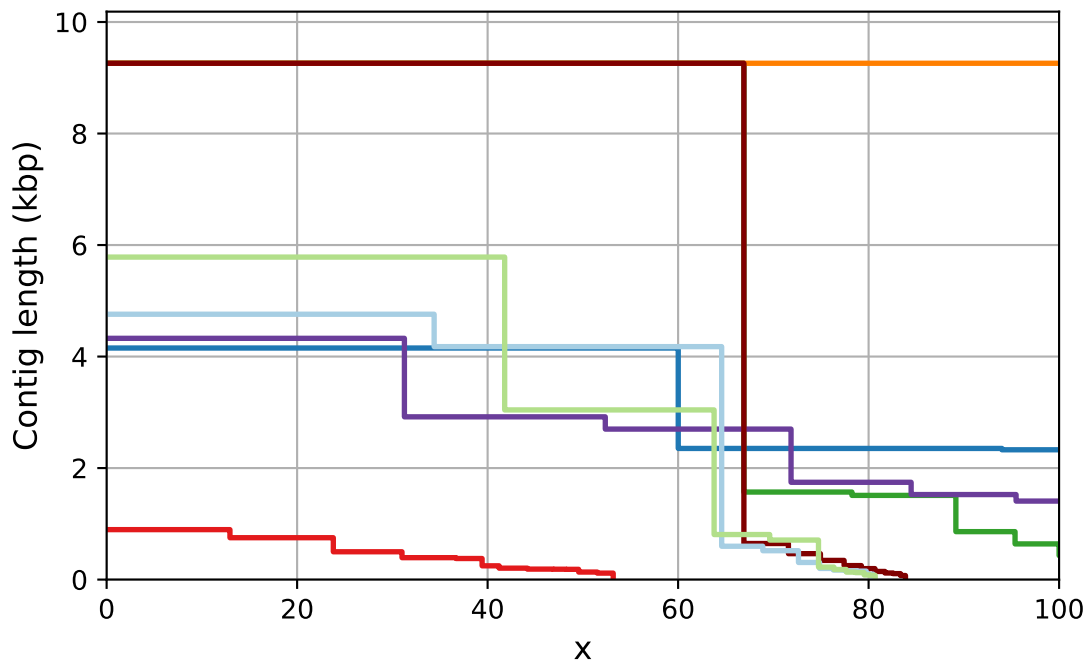
Cumulative length (aligned contigs)



# NAx



# NGAx



- A\_STAR
- HipMer
- marmgCAMI2
- Megahit
- metaSPAdes
- Miniasm
- OPERA\_MS\_inhouse
- SPAdes

