Report

	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	1	4	5	1	7	7	1	2	2
# contigs (>= 5000 bp)	1	4	5	1	7	7	1	2	2
# contigs (>= 10000 bp)	0	4	5	1	7	7	1	2	2
# contigs (>= 25000 bp)	0	4	5	1	6	7	1	2	2
# contigs (>= 50000 bp)	0	2	5	1	6	7	1	2	2
Total length (>= 1000 bp)	8996	289134	657555	4830178	549260	1907490	240219	626167	1730957
Total length (>= 5000 bp)	8996	289134	657555	4830178	549260	1907490	240219	626167	1730957
Total length (>= 10000 bp)	0	289134	657555	4830178	549260	1907490	240219	626167	1730957
Total length (>= 25000 bp)	0	289134	657555	4830178	535080	1907490	240219	626167	1730957
Total length (>= 50000 bp)	0	208600	657555	4830178	535080	1907490	240219	626167	1730957
# contigs	2	6	5	1	7	7	1	2	2
Largest contig	8996	104300	242212	4830178	138431	610486	240219	510819	1120427
Total length	9587	291058	657555	4830178	549260	1907490	240219	626167	1730957
Reference length	1020	1020	1020	1020	1020	1020	1020	1020	1020
GC (%)	67.79	67.66	67.17	67.29	67.39	67.45	67.25	67.13	67.29
Reference GC (%)	70.88	70.88	70.88	70.88	70.88	70.88	70.88	70.88	70.88
N50	8996	104300	143056	4830178	105284	610486	240219	510819	1120427
NG50	8996	104300	242212	4830178	138431	610486	240219	510819	1120427
N75	8996	40267	137926	4830178	64728	153475	240219	510819	610530
NG75	8996	104300	242212	4830178	138431	610486	240219	510819	1120427
L50	1	2	2	1	3	2	1	1	1
LG50	1	1	1	1	1	1	1	1	1
L75	1	3	3	1	4	4	1	1	2
LG75	1	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	2	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	2	1	1	0	3	1	0	1
# unaligned contigs	0 + 1 part	0 + 4 part	0 + 5 part	0 + 1 part	0 + 7 part	0 + 7 part	0 + 1 part	0 + 2 part	0 + 2 part
Unaligned length	8807	288206	655975	4829084	547716	1904442	239125	625345	1729336
Genome fraction (%)	49.510	71.275	80.588	84.314	80.588	86.863	84.314	80.588	100.000
Duplication ratio	1.545	3.923	1.922	1.272	1.878	3.440	1.272	1.000	1.589
# N's per 100 kbp	302.49	0.00	13.38	0.00	0.00	0.00	0.00	0.00	23.98
# mismatches per 100 kbp	0.00	3301.24	729.93	1511.63	973.24	2370.20	1511.63	364.96	1666.67
# indels per 100 kbp	0.00	550.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Largest alignment	345	527	662	860	662	726	860	662	860
Total aligned length	505	1982	1492	1627	1544	3498	1627	822	1589
NGA50	-	527	662	860	662	726	860	662	860
NGA75	-	527	265	860	183	659	860	160	860
LGA50	-	1	1	1	1	1	1	1	1
LGA75	-	2	2	1	2	2	1	2	1

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).
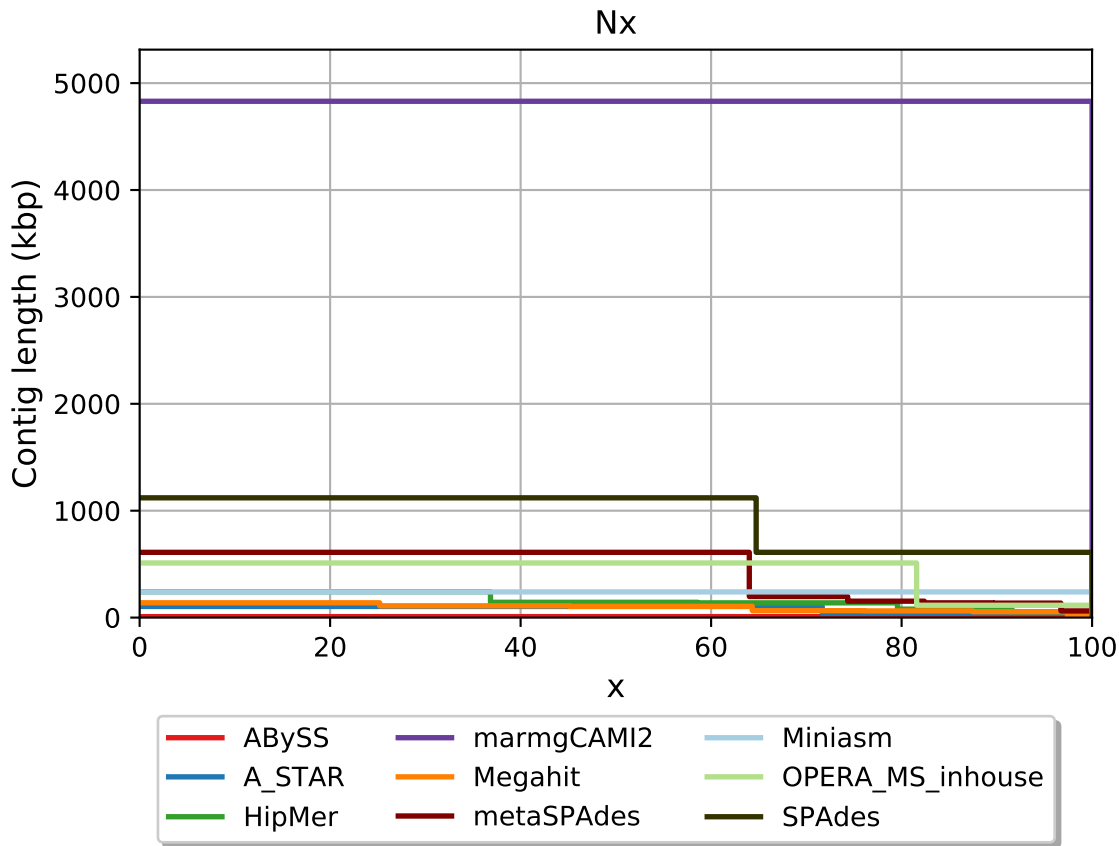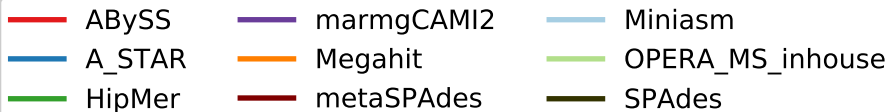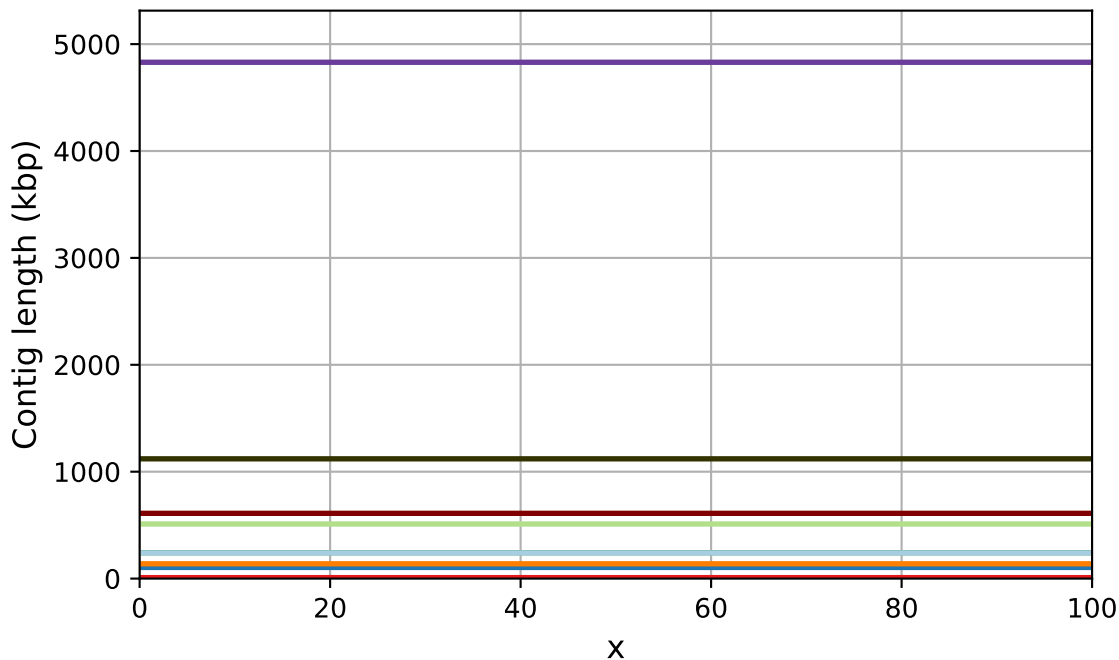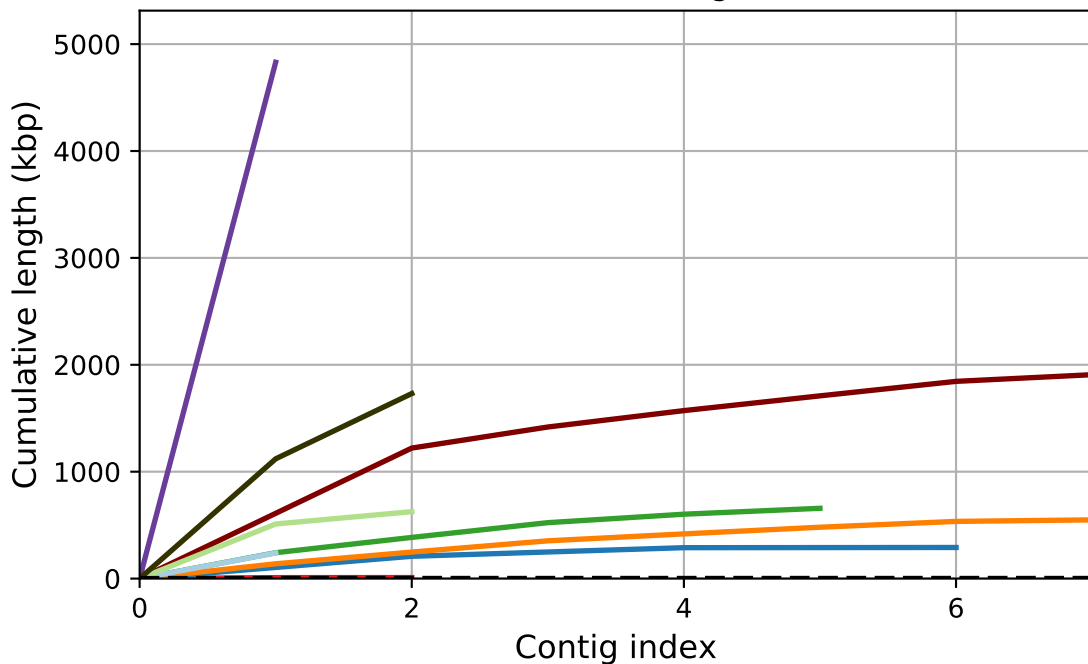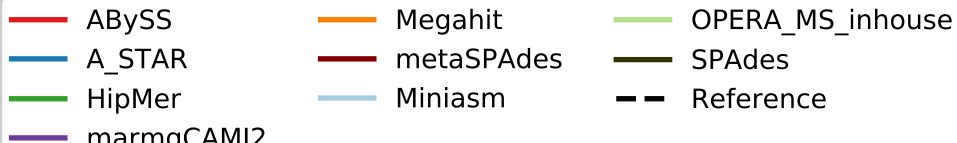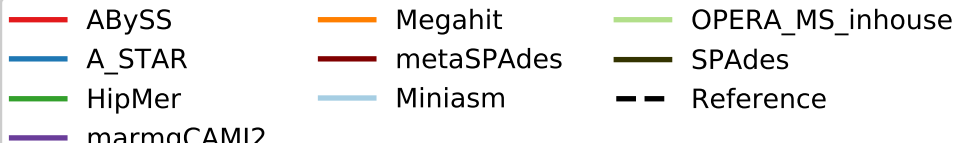
Misassemblies report

	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	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	1	2	4	0	7	4	0	2	1
# possible misassemblies	2	4	7	0	10	7	0	4	2
# local misassemblies	0	2	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	2	1	1	0	3	1	0	1
# mismatches	0	24	6	13	8	21	13	3	17
# indels	0	4	0	0	0	0	0	0	0
# indels (<= 5 bp)	0	4	0	0	0	0	0	0	0
# indels (> 5 bp)	0	0	0	0	0	0	0	0	0
Indels length	0	6	0	0	0	0	0	0	0

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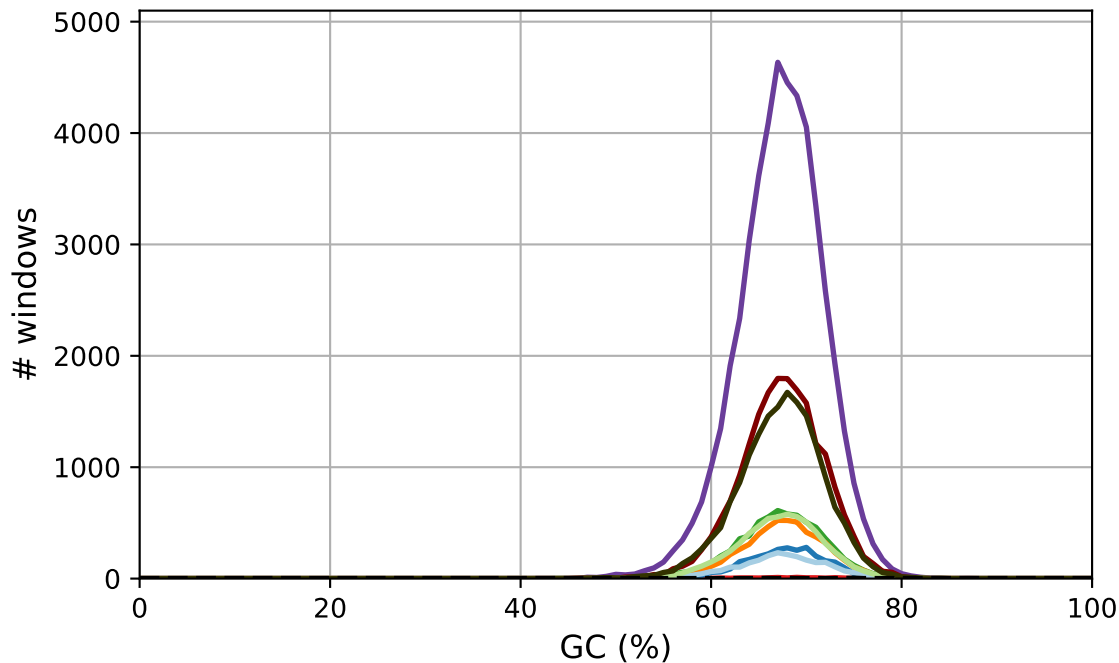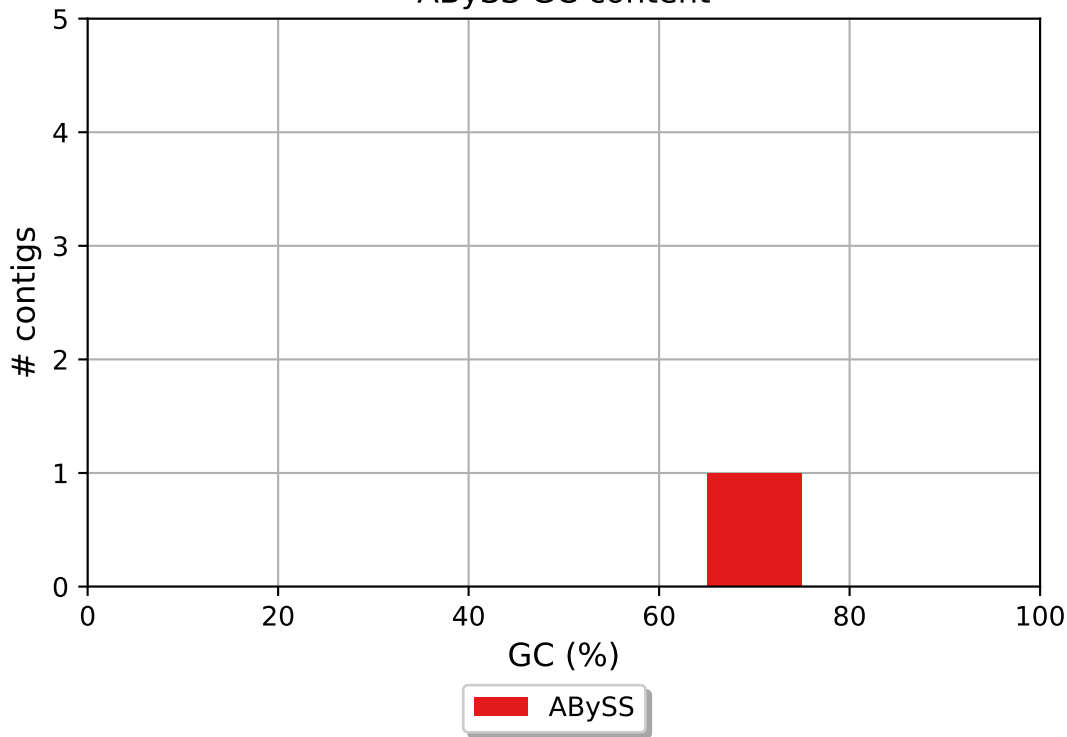(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	ABySS	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	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	1	4	5	1	7	7	1	2	2
Partially unaligned length	8807	288206	655975	4829084	547716	1904442	239125	625345	1729336
# N's	29	0	88	0	0	0	0	0	415

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

Legend		
ABySS	marmgCAMI2	Miniasm
A_STAR	Megahit	OPERA_MS_inhouse
HipMer	metaSPAdes	SPAdes

NGx

Legend:
- ABySS
- A_STAR
- HipMer
- marmgCAMI2
- Megahit
- metaSPAdes
- Miniasm
- OPERA_MS_inhouse
- SPAdes

x-axis: x

y-axis: Contig length (kbp)

Cumulative length

GC content

ABySS GC content
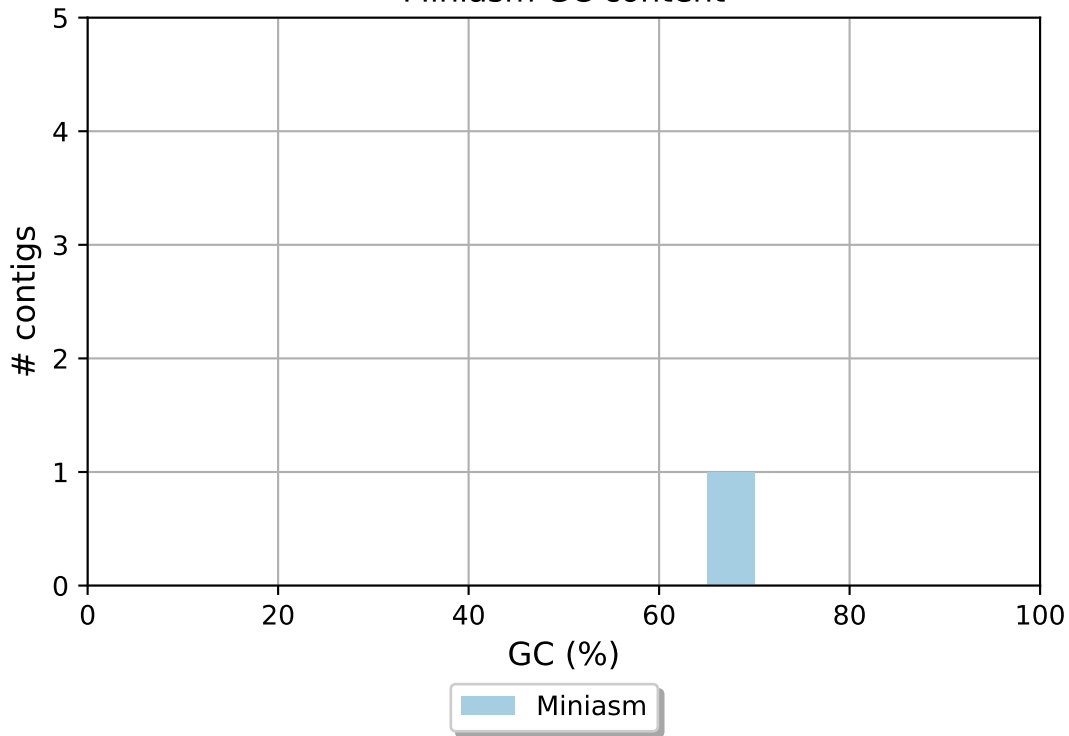
A_STAR GC content
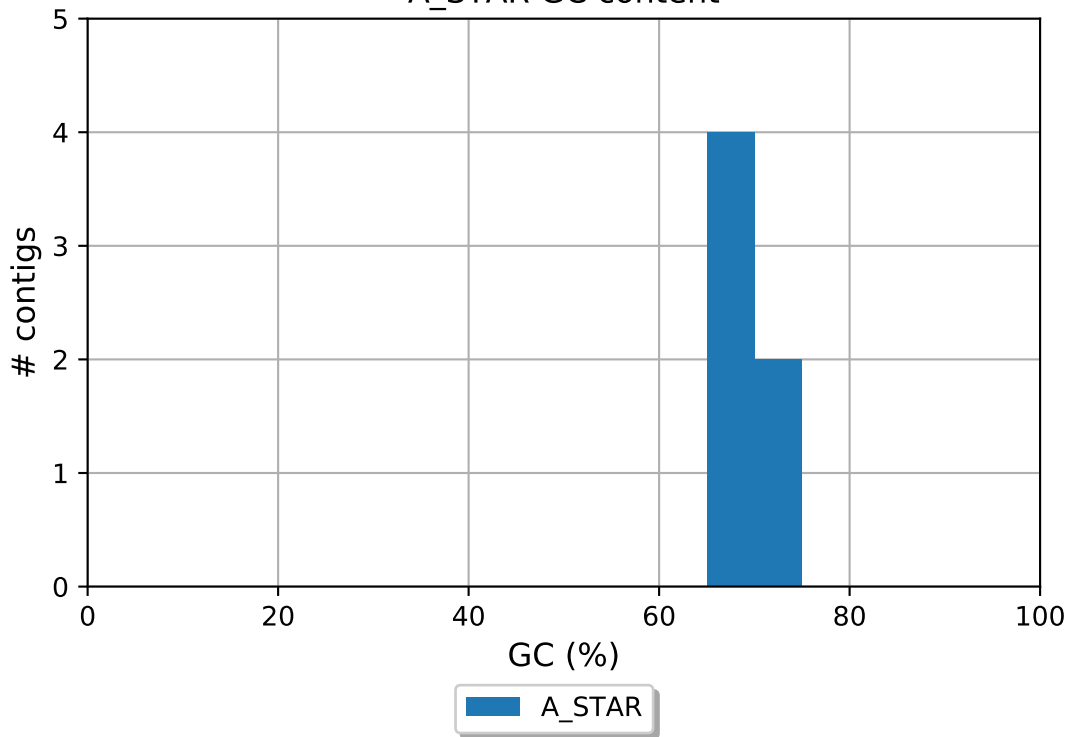
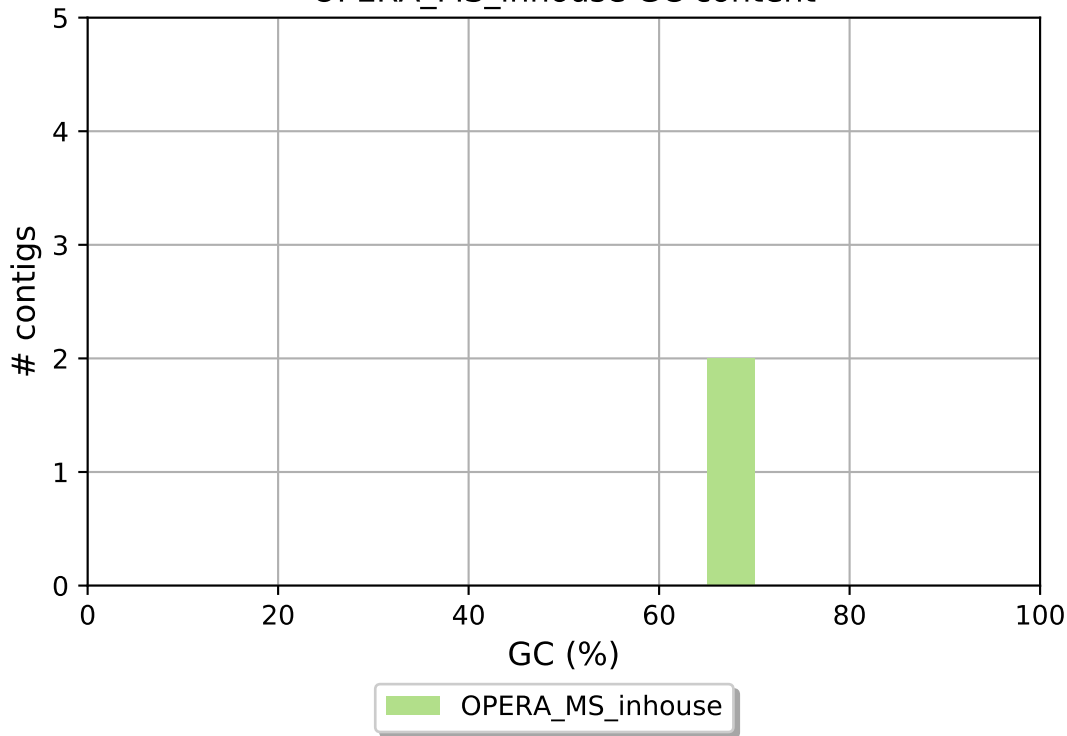HipMer GC content
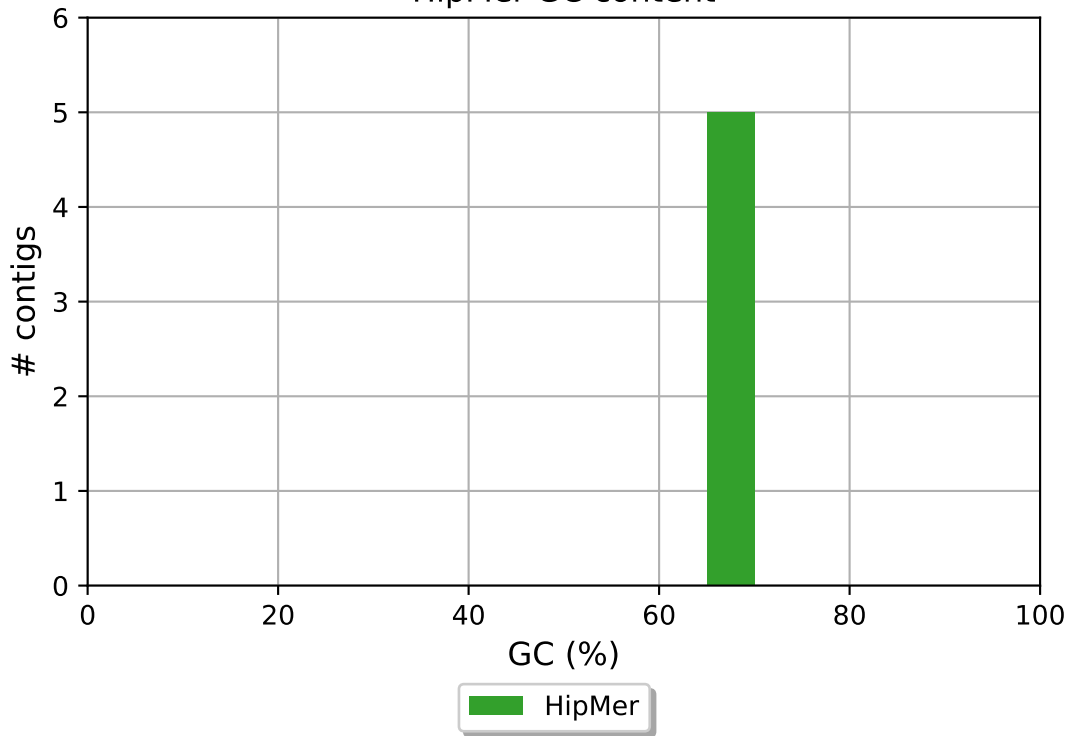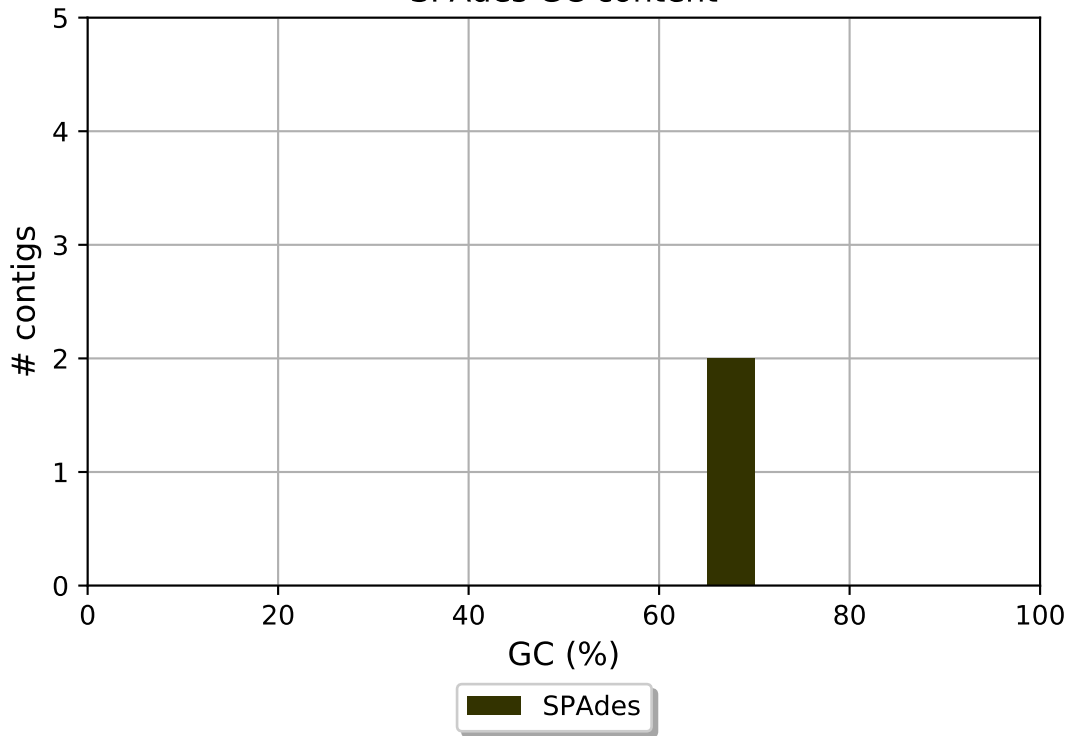
marmgCAMI2 GC content
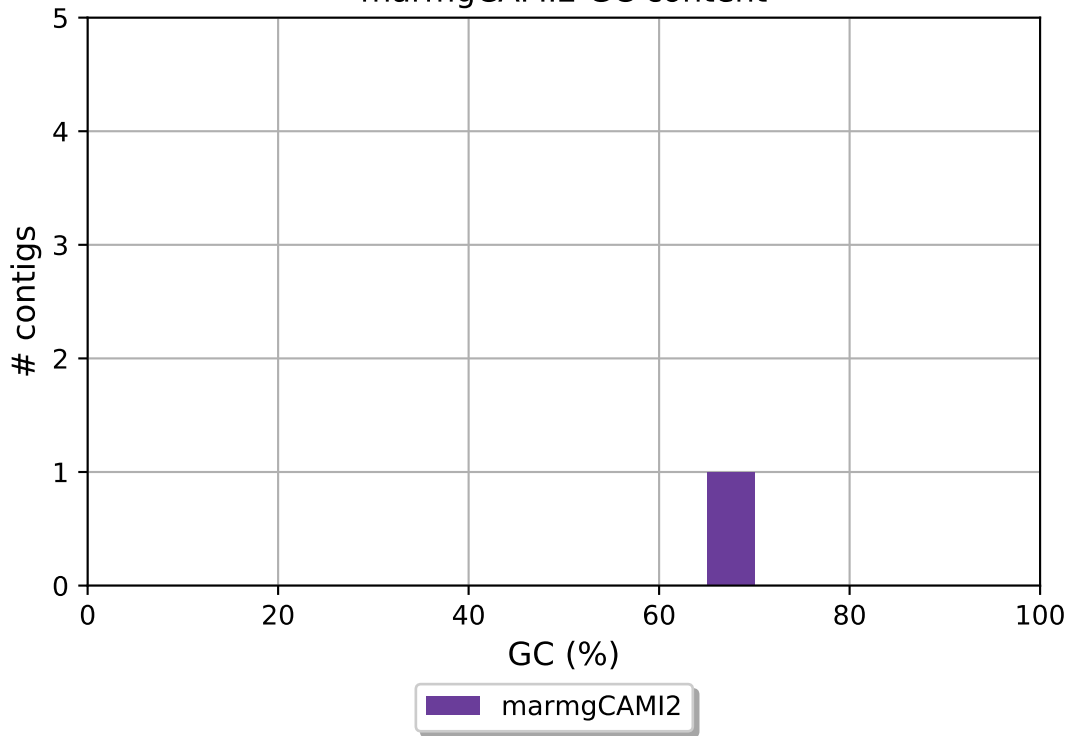
Megahit GC content
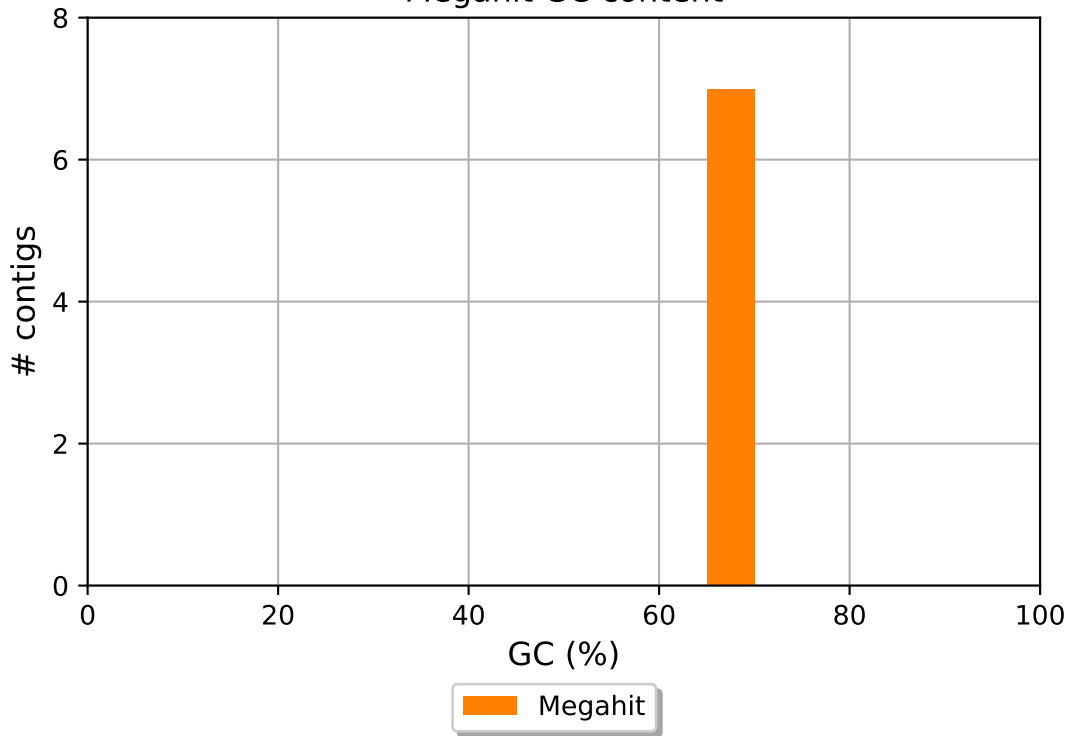
metaSPAdes GC content
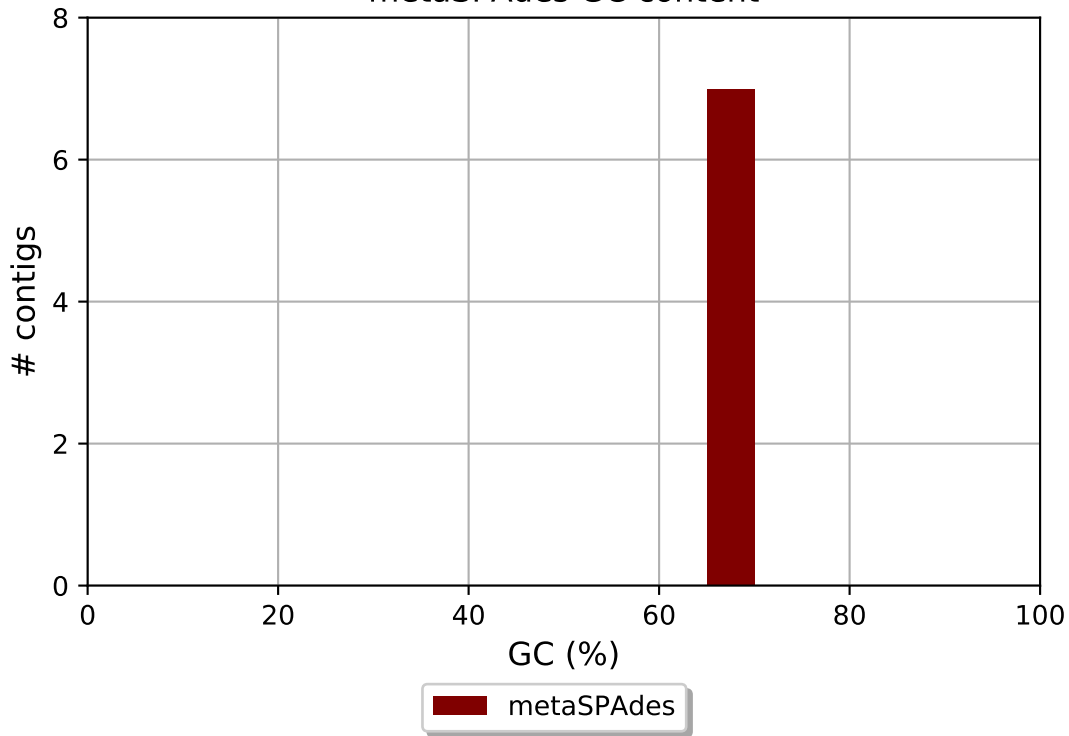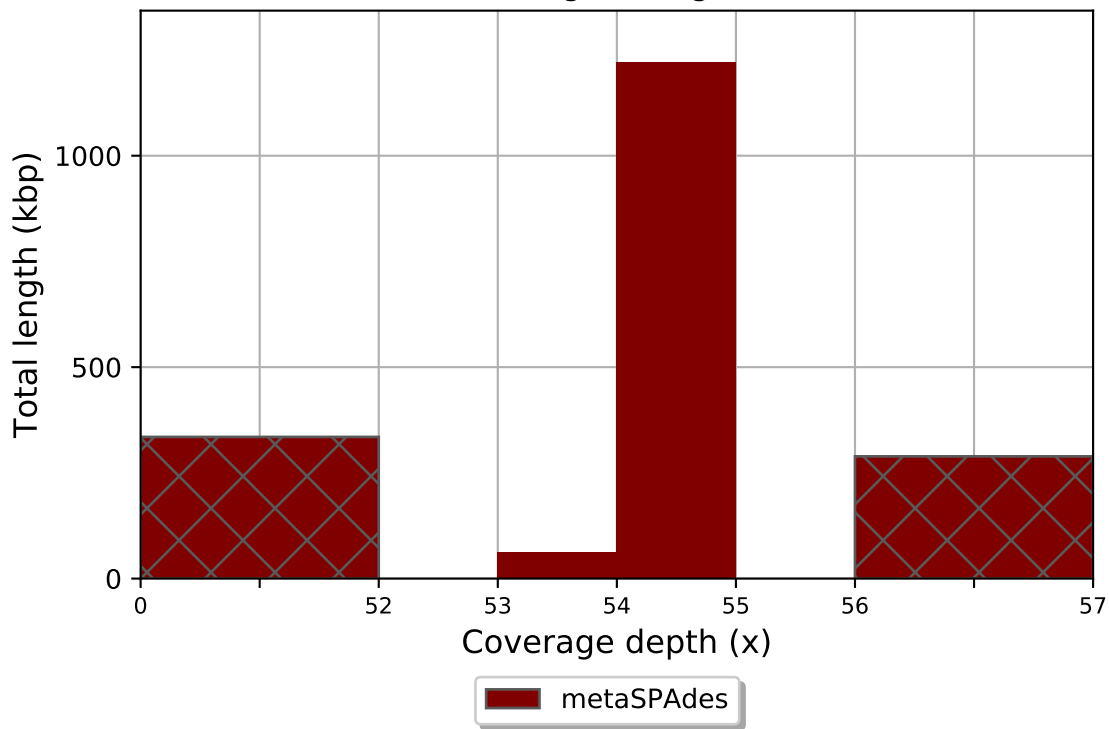
Miniasm GC content
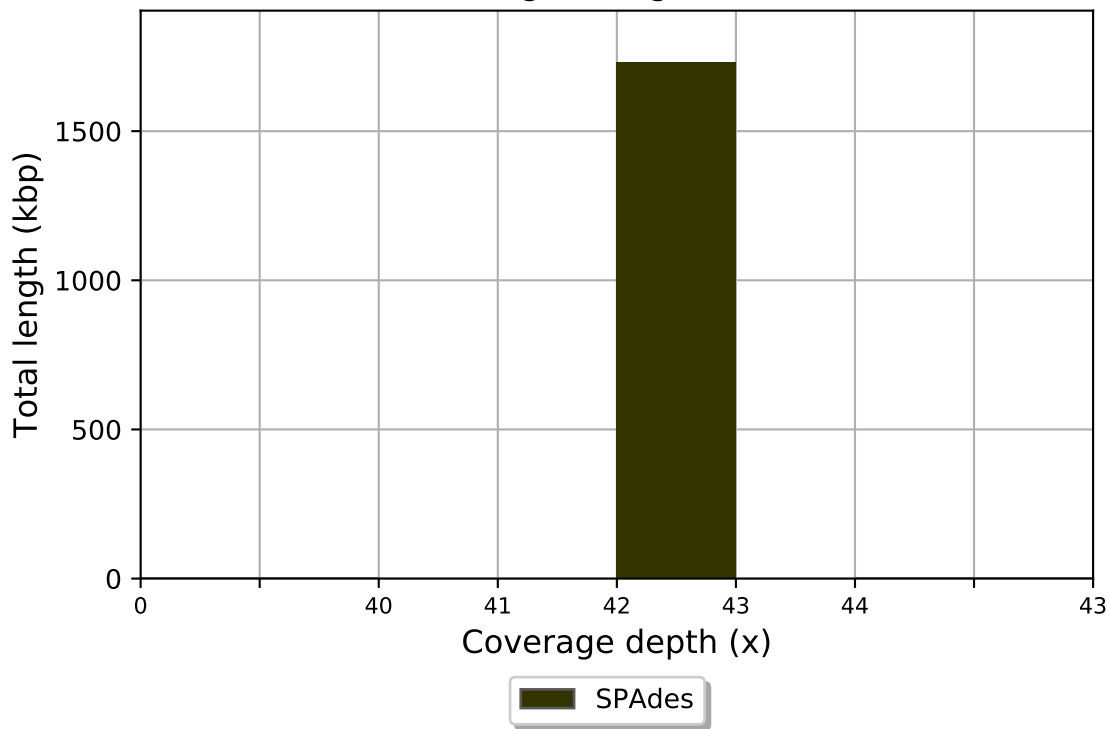
OPERA_MS_inhouse GC content
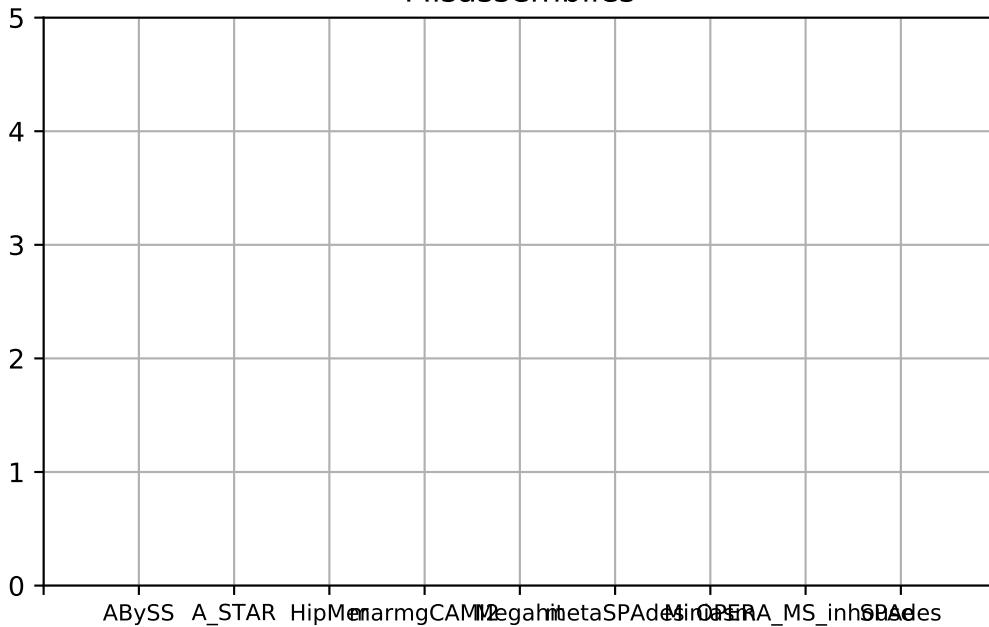
SPAdes GC content

Coverage histogram (bin size: 1x)
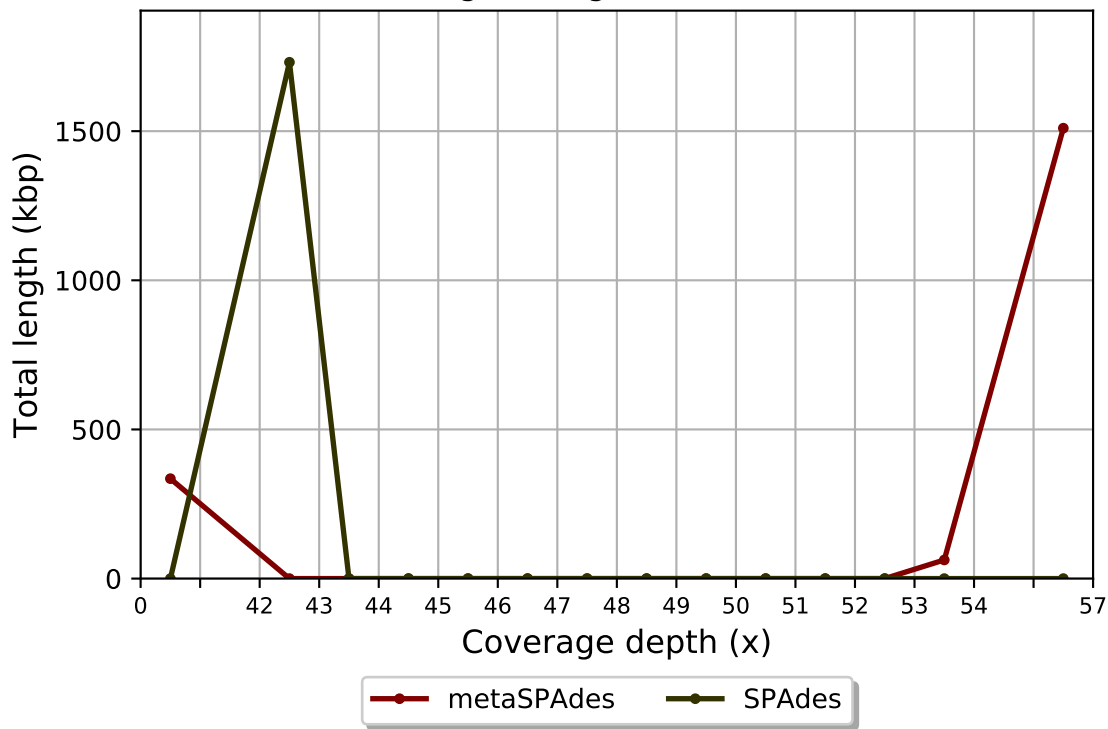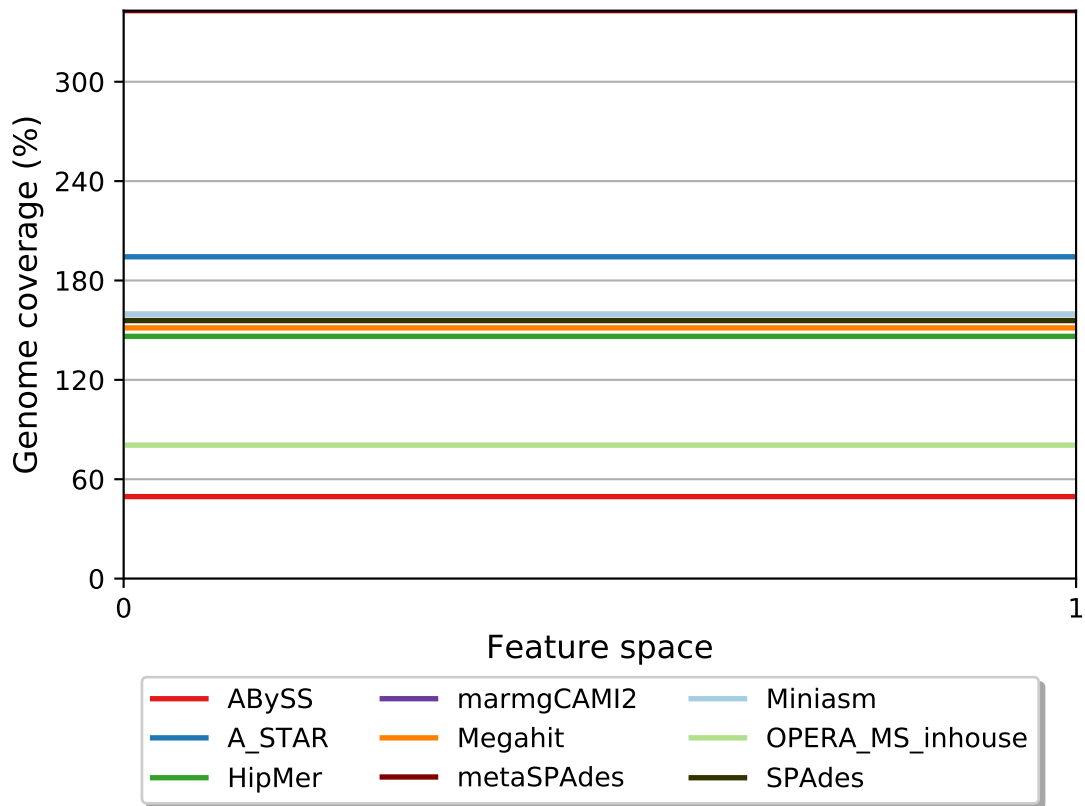
metaSPAdes coverage histogram (bin size: 1x)
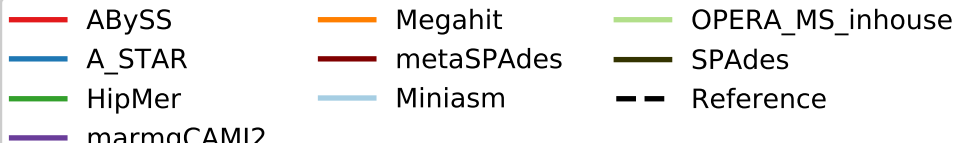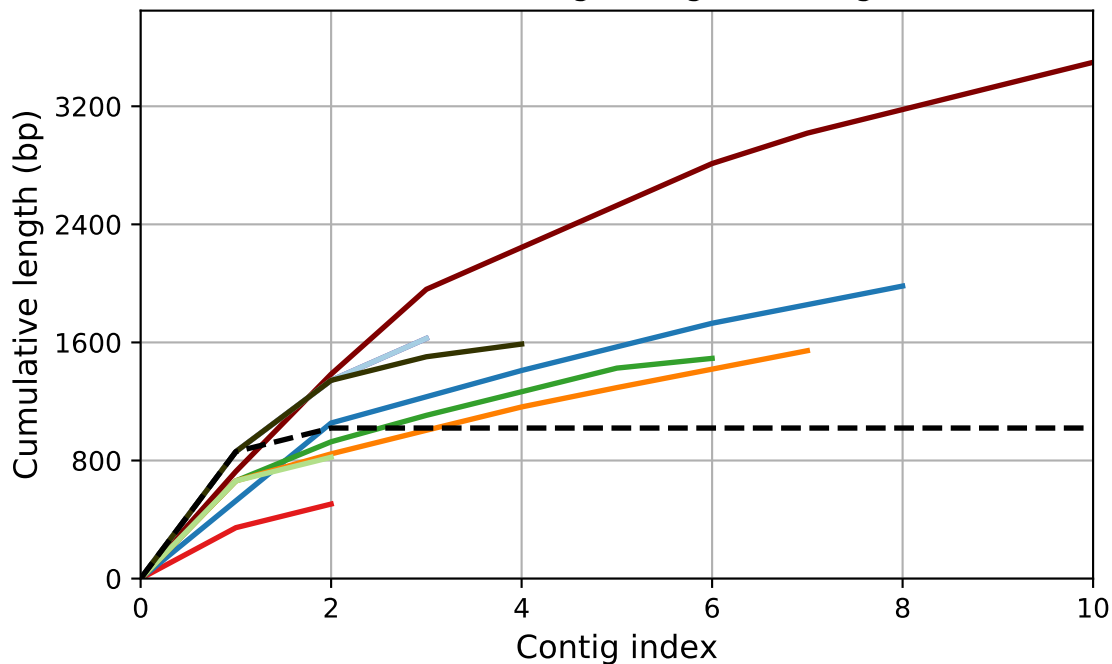
SPAdes coverage histogram (bin size: 1x)
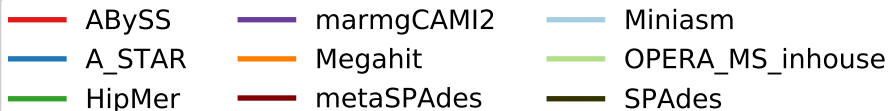
Misassemblies

FRCurve (misassemblies)

Legend:
- ABySS
- A_STAR
- HipMer
- marmgCAMI2
- Megahit
- metaSPAdes
- Miniasm
- OPERA_MS_inhouse
- SPAdes

Cumulative length (aligned contigs)

ABySS	Megahit	OPERA_MS_inhouse
A_STAR	metaSPAdes	SPAdes
HipMer	Miniasm	Reference
marmgCAMI2		

NAx

ABySS	marmgCAMI2	Miniasm
A_STAR	Megahit	OPERA_MS_inhouse
HipMer	metaSPAdes	SPAdes

NGAx

Genome fraction, %

Color	Legend
Red	ABySS
Blue	A_STAR
Green	HipMer
Purple	marmgCAMI2
Orange	Megahit
Dark red	metaSPAdes
Light blue	Miniasm
Light green	OPERA_MS_inhouse
Dark	SPAdes