Report

	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# contigs (>= 1000 bp)	2	2	1	3	3	1	1	1
# contigs (>= 5000 bp)	1	0	1	3	0	1	1	0
# contigs (>= 10000 bp)	1	0	1	3	0	0	1	0
# contigs (>= 25000 bp)	1	0	1	0	0	0	1	0
# contigs (>= 50000 bp)	0	0	1	0	0	0	0	0
Total length (>= 1000 bp)	28890	4566	3975877	43970	11925	7719	40410	1539
Total length (>= 5000 bp)	26194	0	3975877	43970	0	7719	40410	0
Total length (>= 10000 bp)	26194	0	3975877	43970	0	0	40410	0
Total length (>= 25000 bp)	26194	0	3975877	0	0	0	40410	0
Total length (>= 50000 bp)	0	0	3975877	0	0	0	0	0
# contigs	2	2	1	3	3	1	1	1
Largest contig	26194	2731	3975877	20836	4061	7719	40410	1539
Total length	28890	4566	3975877	43970	11925	7719	40410	1539
Reference length	580	580	580	580	580	580	580	580
GC (%)	59.03	61.98	57.60	58.72	60.12	58.98	57.96	61.99
Reference GC (%)	62.76	62.76	62.76	62.76	62.76	62.76	62.76	62.76
N50	26194	2731	3975877	12404	4061	7719	40410	1539
NG50	26194	2731	3975877	20836	4061	7719	40410	1539
N75	26194	1835	3975877	12404	3803	7719	40410	1539
NG75	26194	2731	3975877	20836	4061	7719	40410	1539
L50	1	1	1	2	2	1	1	1
LG50	1	1	1	1	1	1	1	1
L75	1	2	1	2	3	1	1	1
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	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 2 part	0 + 2 part	0 + 1 part	0 + 3 part	0 + 3 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	27380	3406	3975297	42230	10185	7139	39828	957
Genome fraction (%)	100.000	100.000	100.000	100.000	100.000	100.000	100.000	99.828
Duplication ratio	2.603	2.000	1.000	3.000	3.000	1.000	1.003	1.005
# N's per 100 kbp	1211.49	0.00	0.00	0.00	0.00	0.00	4.95	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	689.66	0.00	0.00	0.00	2590.67
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1899.83
Largest alignment	580	580	580	580	580	580	580	582
Total aligned length	1160	1160	580	1740	1740	580	580	582
NGA50	580	580	580	580	580	580	580	582
NGA75	580	580	580	580	580	580	580	582
LGA50	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	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).
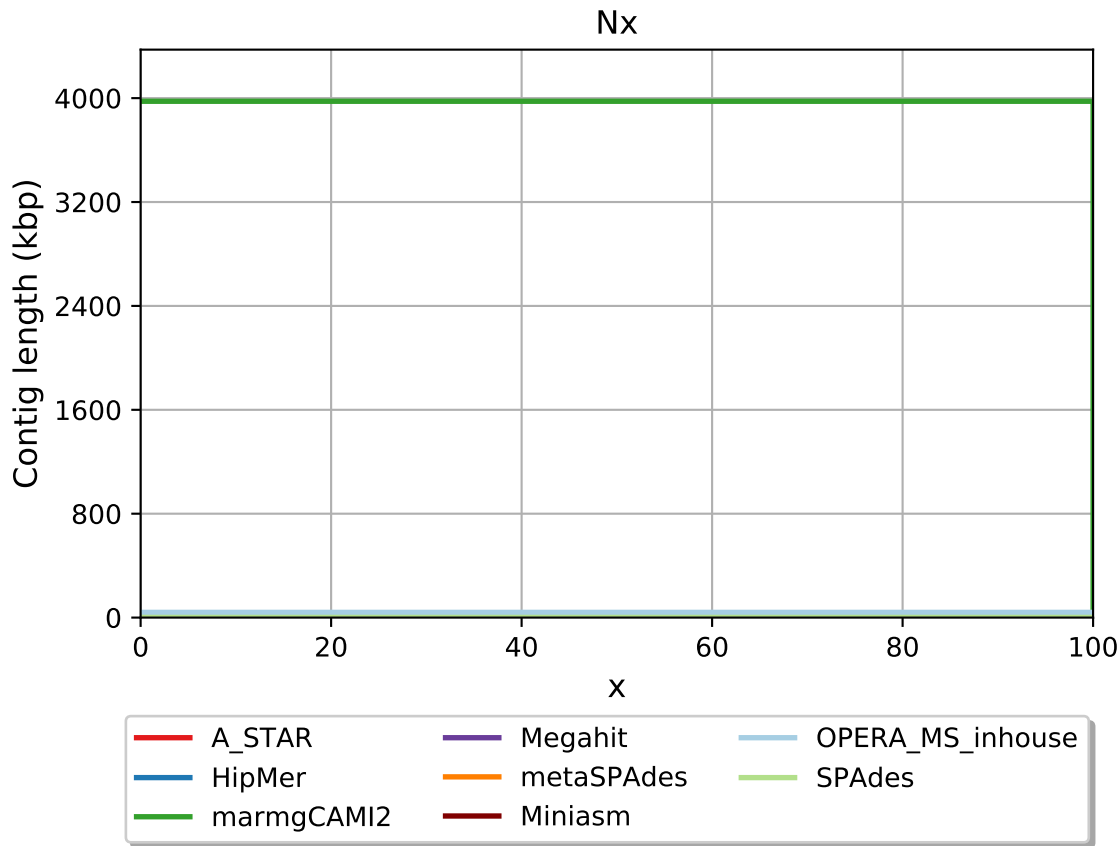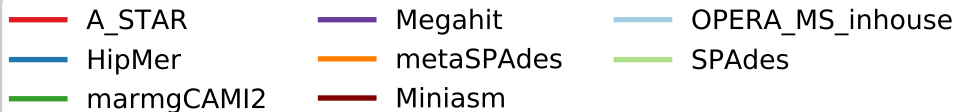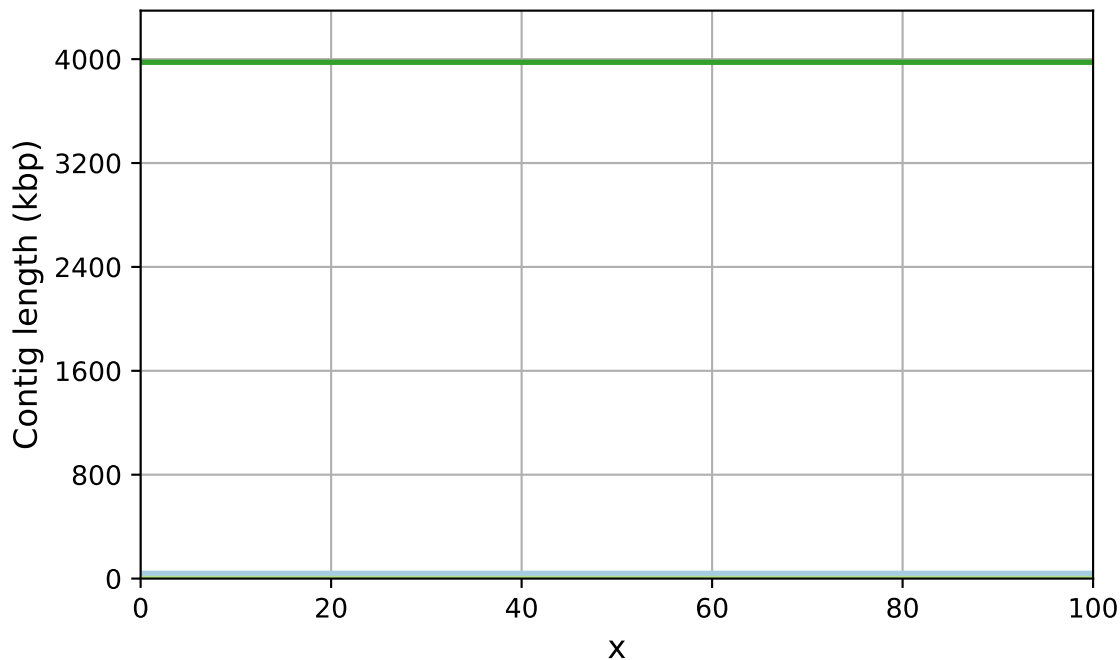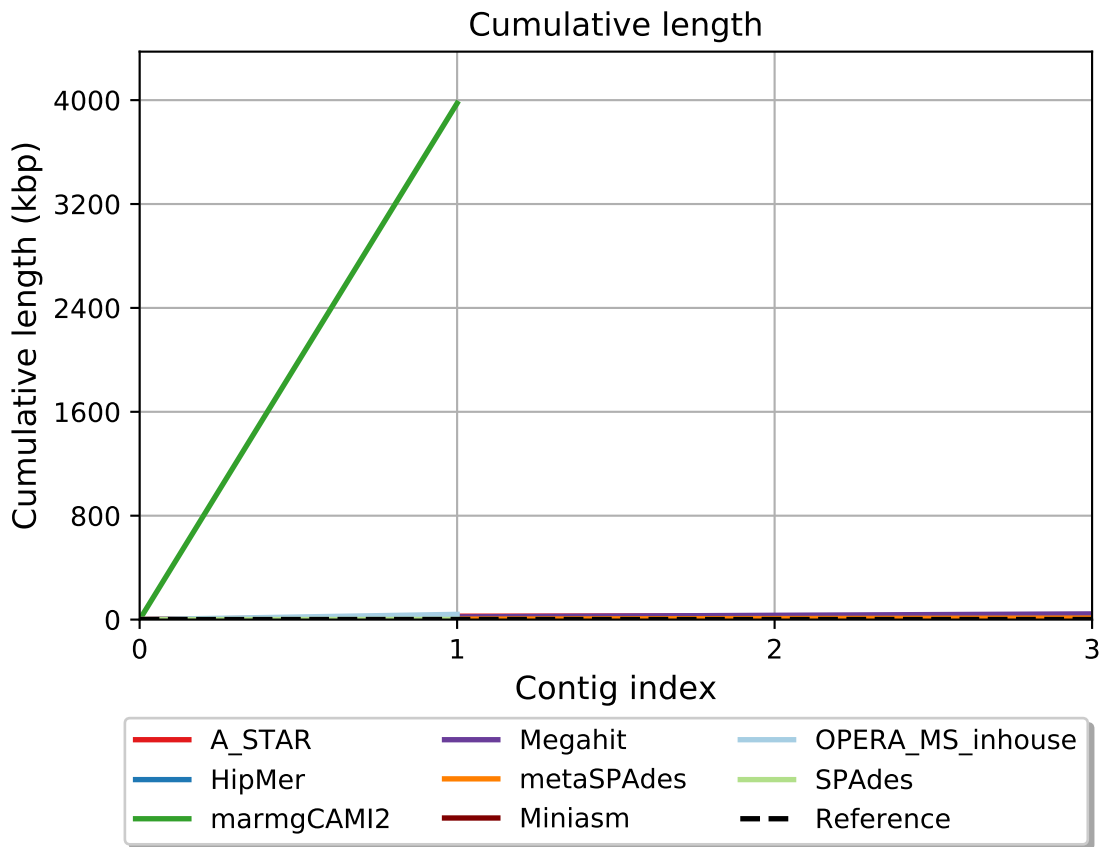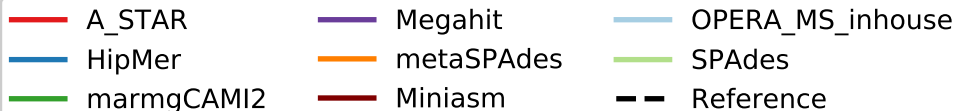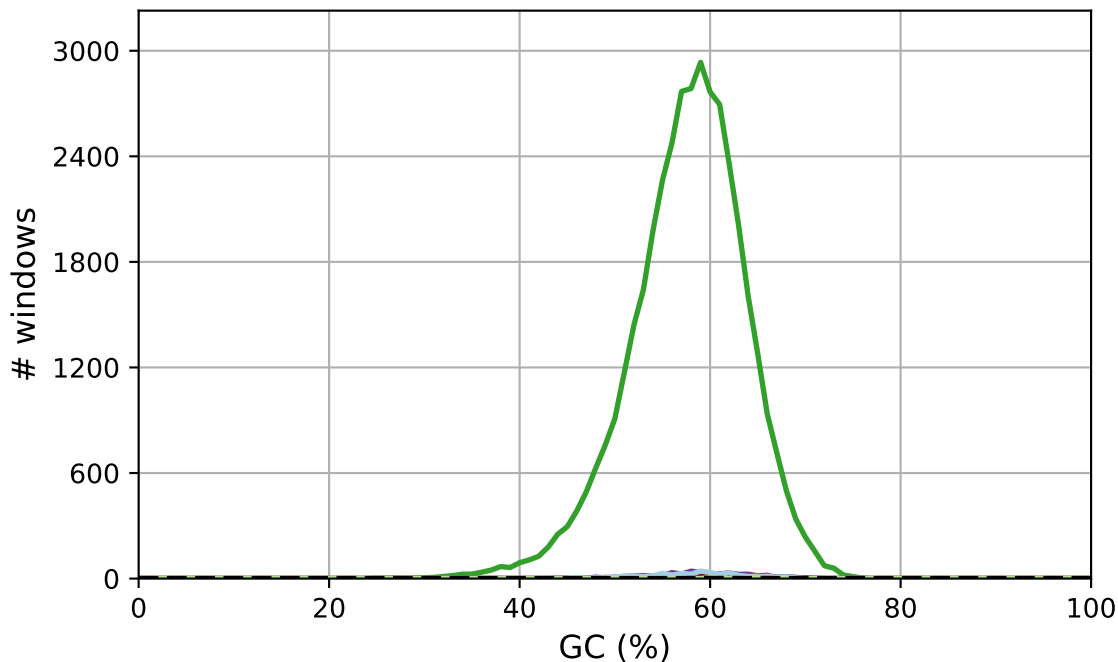
Misassemblies report
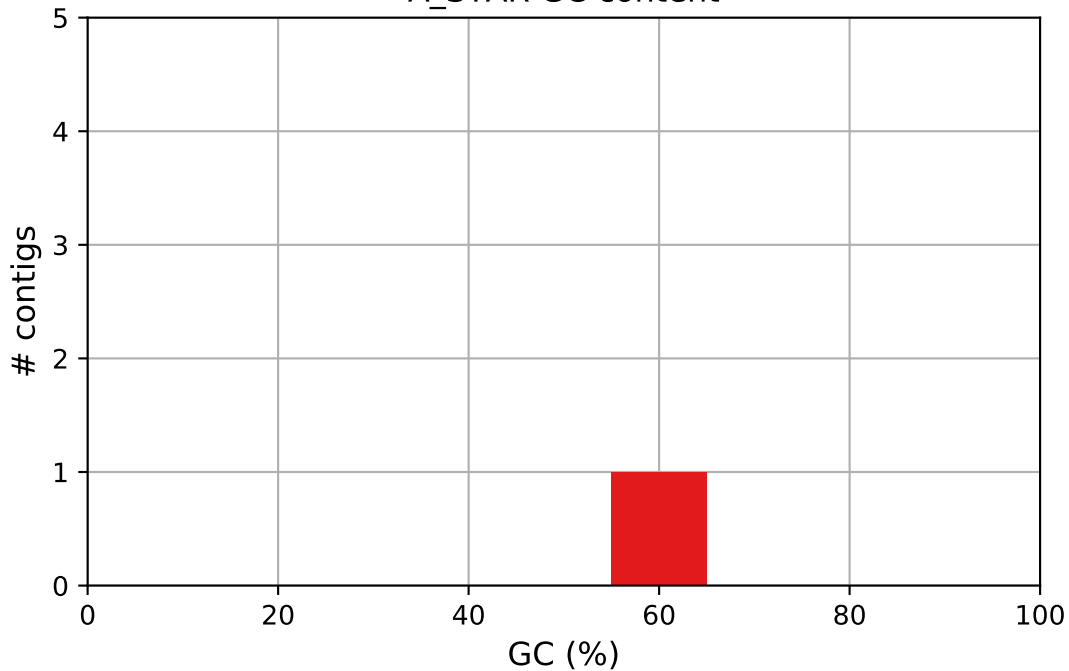
	A_STAR	HipMer	marmgCAMI2	Megahit	metaSPAdes	Miniasm	OPERA_MS_inhouse	SPAdes
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	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	2	2	1	3	3	1	1	1
# possible misassemblies	3	3	2	6	6	2	2	1
# 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	0	0	0	0	0	0	0	0
# mismatches	0	0	0	4	0	0	0	15
# indels	0	0	0	0	0	0	0	11
# indels (<= 5 bp)	0	0	0	0	0	0	0	11
# indels (> 5 bp)	0	0	0	0	0	0	0	0
Indels length	0	0	0	0	0	0	0	11

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	2	2	1	3	3	1	1	1
Partially unaligned length	27380	3406	3975297	42230	10185	7139	39828	957
# N's	350	0	0	0	0	0	2	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

Legend: A_STAR, HipMer, marmgCAMI2, Megahit, metaSPAdes, Miniasm, OPERA_MS_inhouse, SPAdes, Reference

A_STAR GC content

HipMer GC content
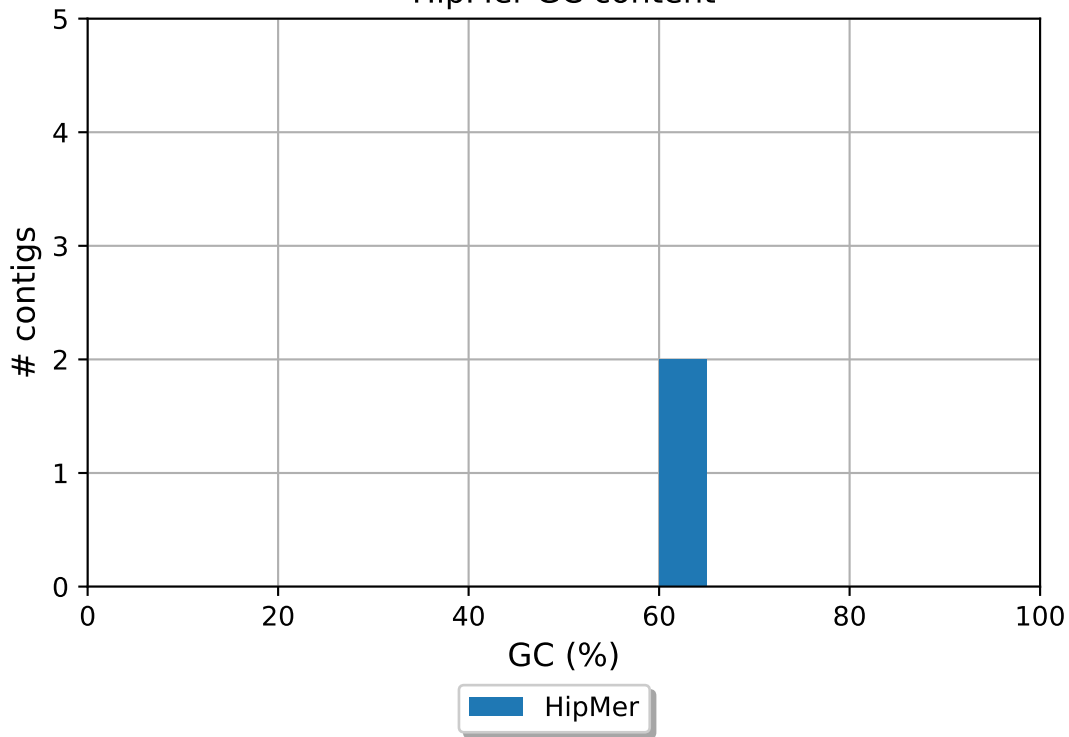
marmgCAMI2 GC content
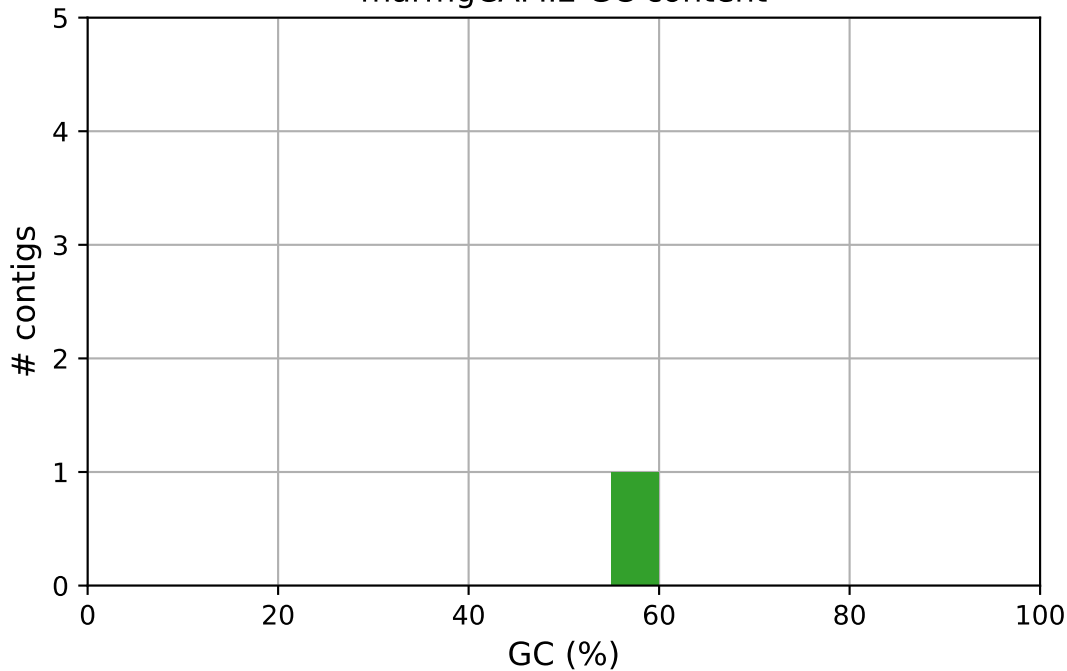
Megahit GC content
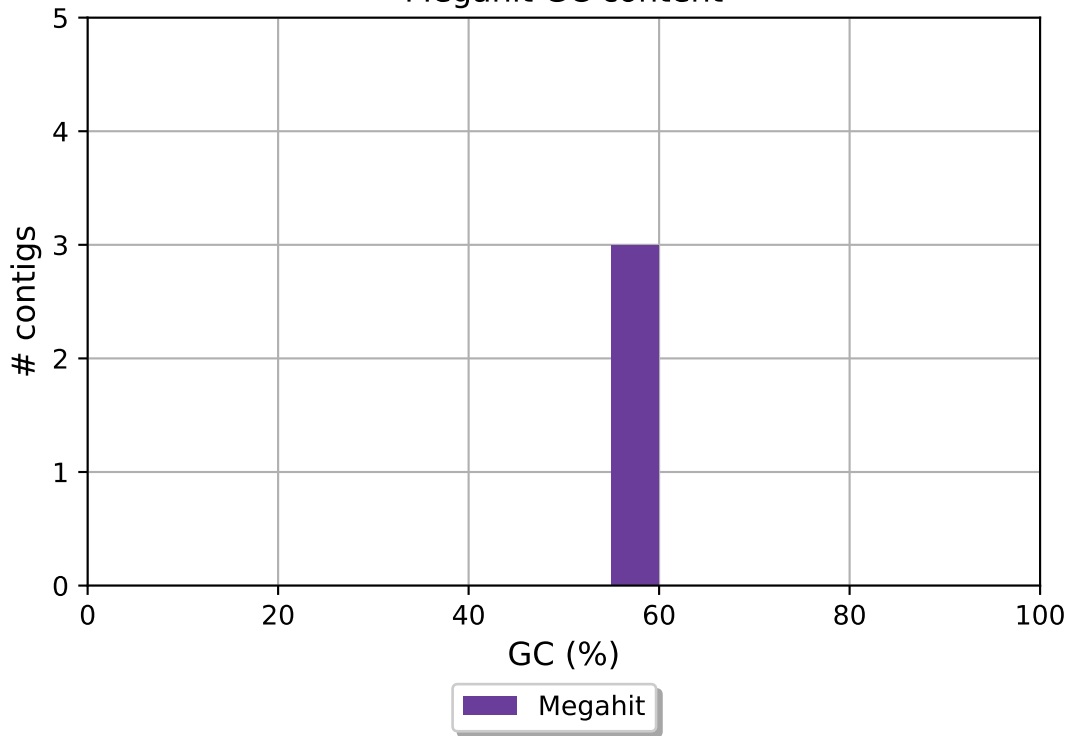
metaSPAdes GC content
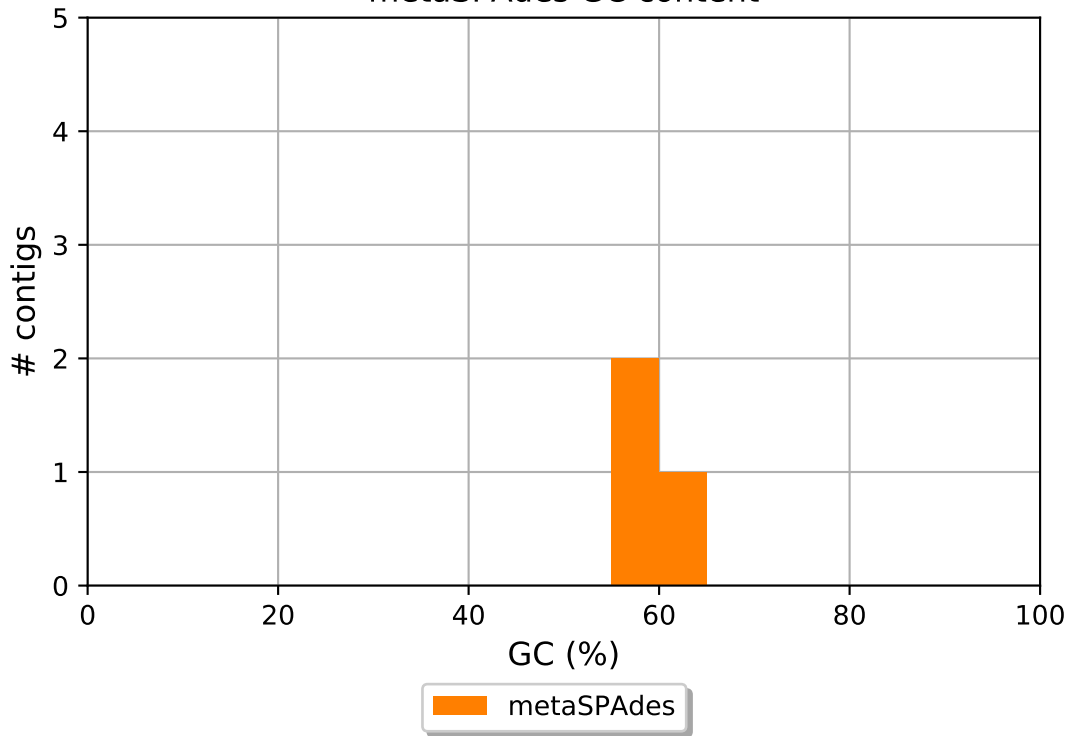
Miniasm GC content
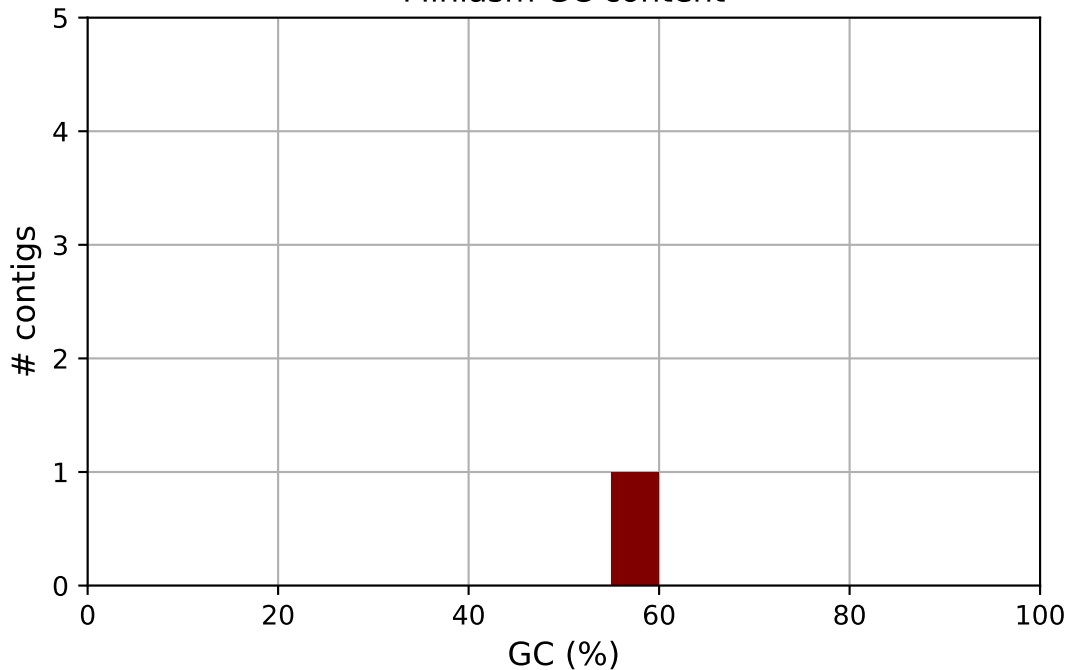
OPERA_MS_inhouse GC content
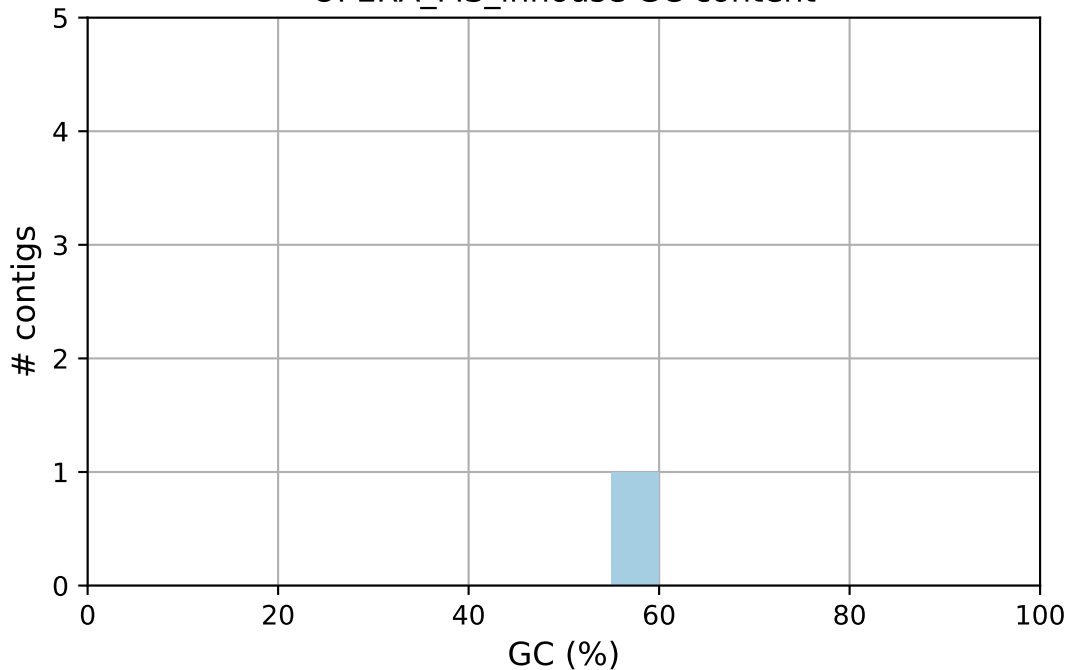
SPAdes GC content
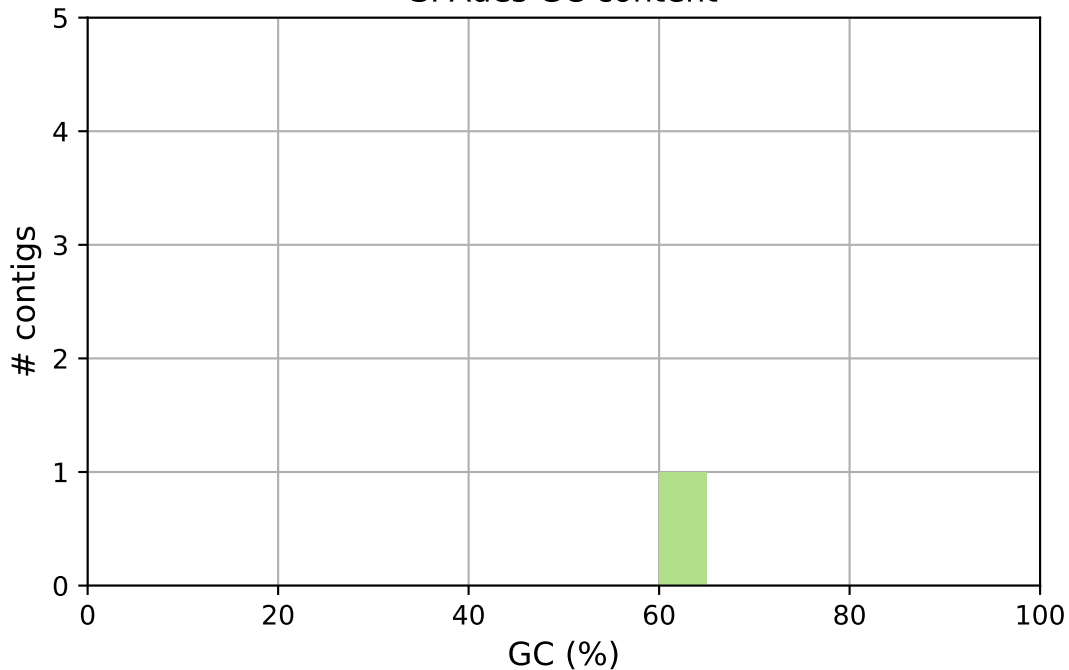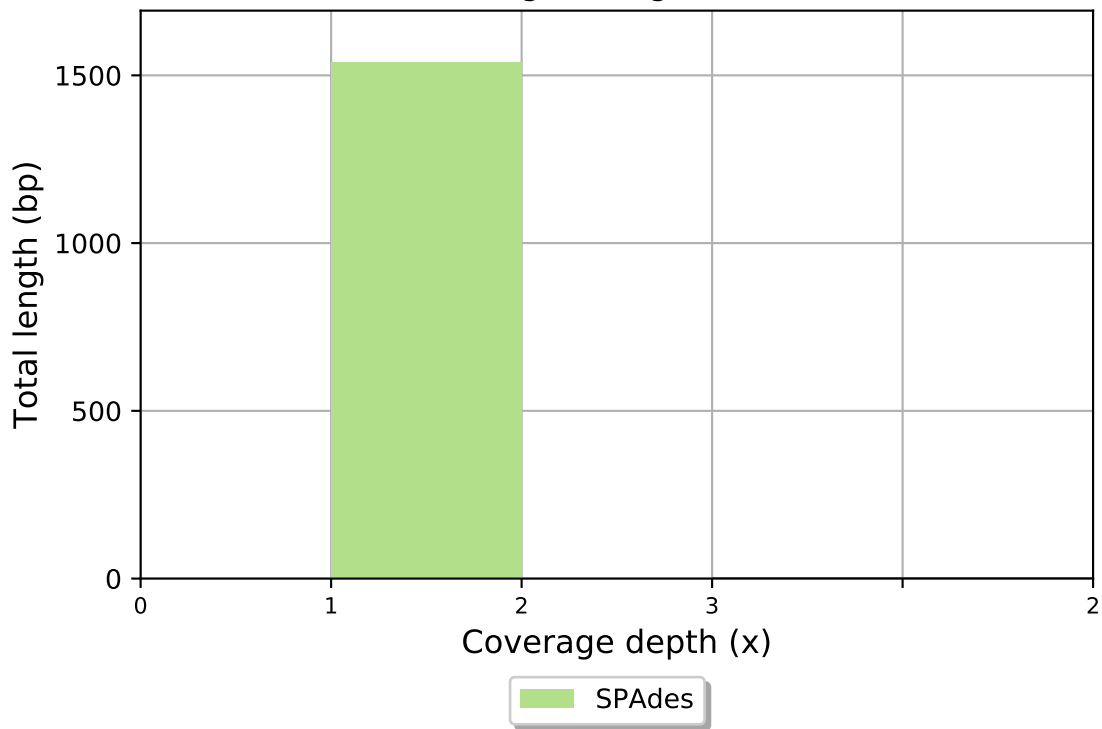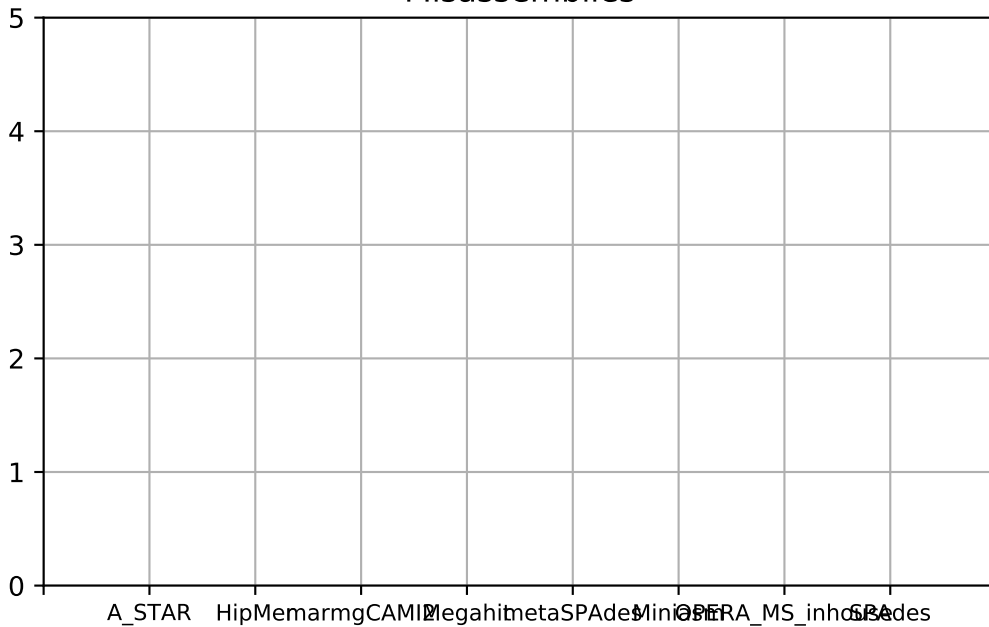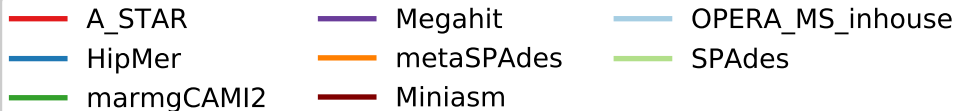
Coverage histogram (bin size: 1x)
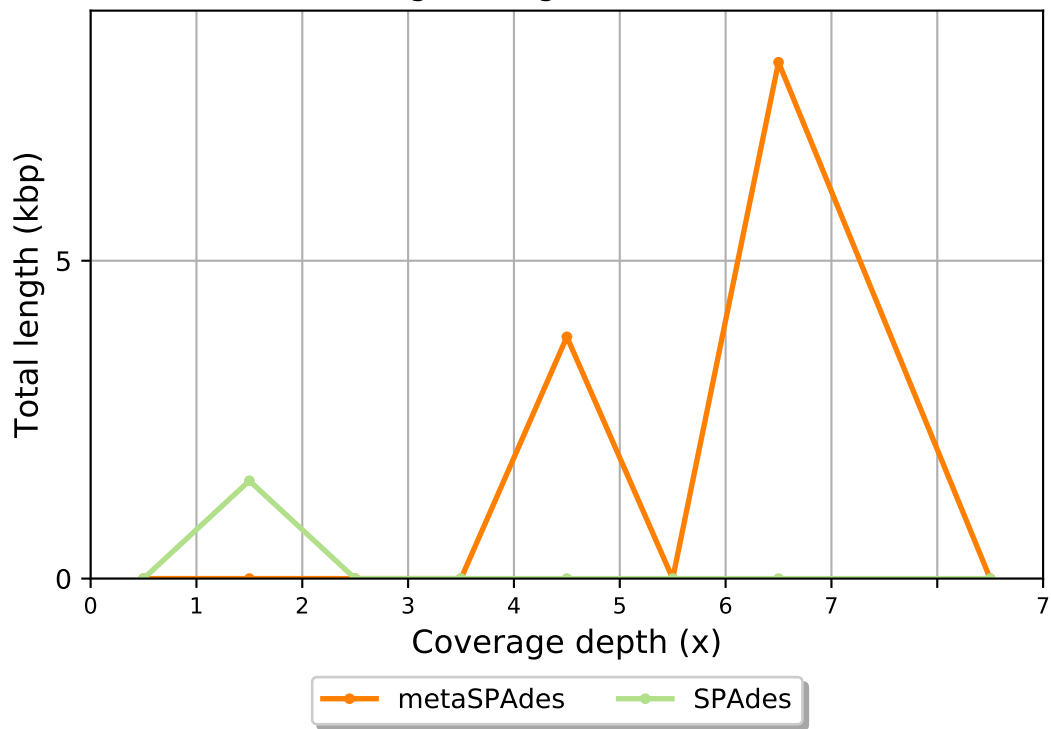
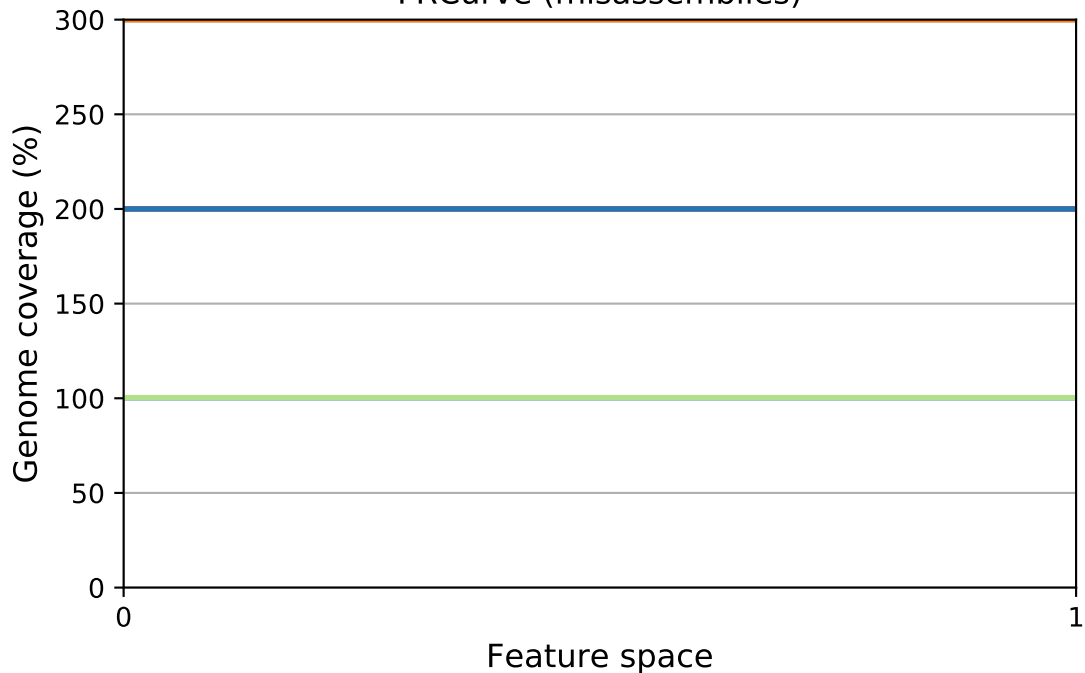metaSPAdes coverage histogram (bin size: 1x)
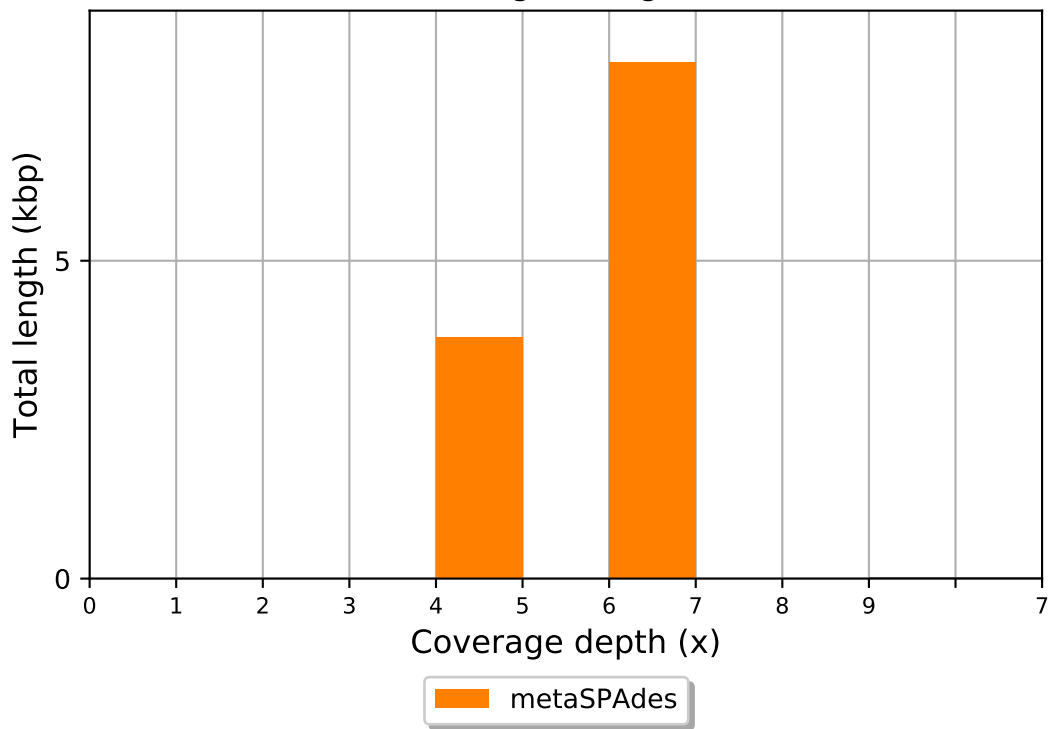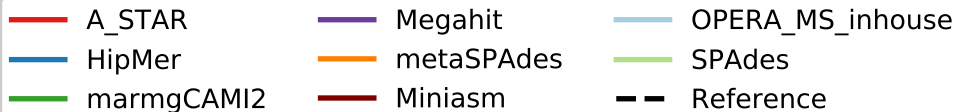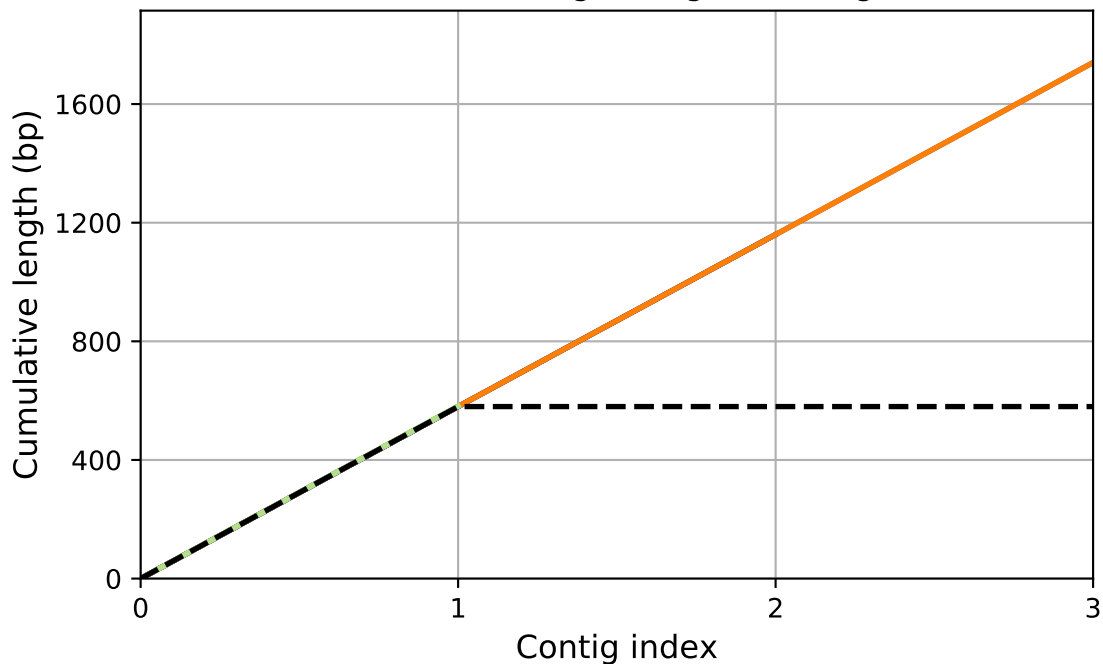
SPAdes coverage histogram (bin size: 1x)

Misassemblies

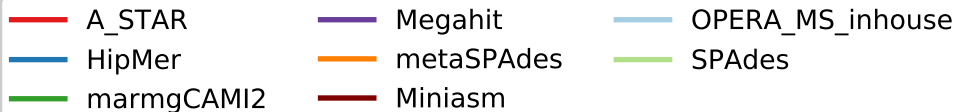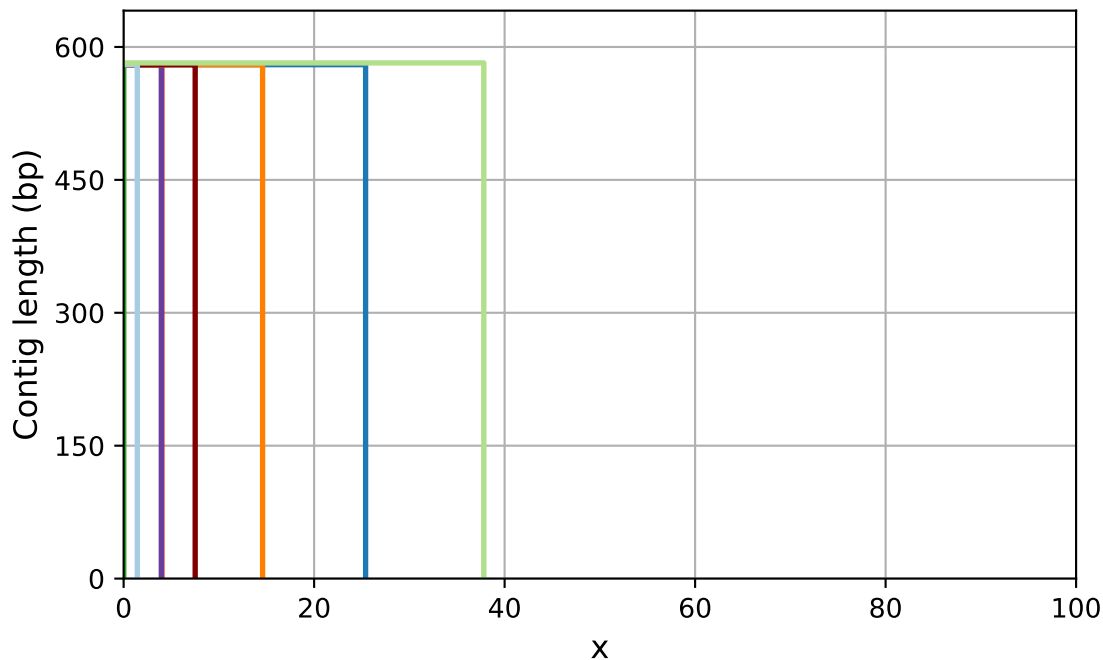A_STAR   HipMemarmgCAMIMegahitmetaSPAdesMiniaSPERA_MS_inhoSPAdes
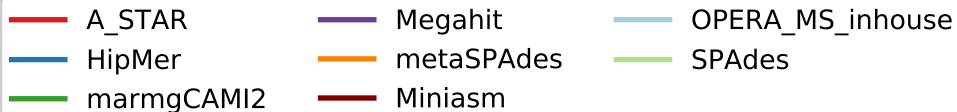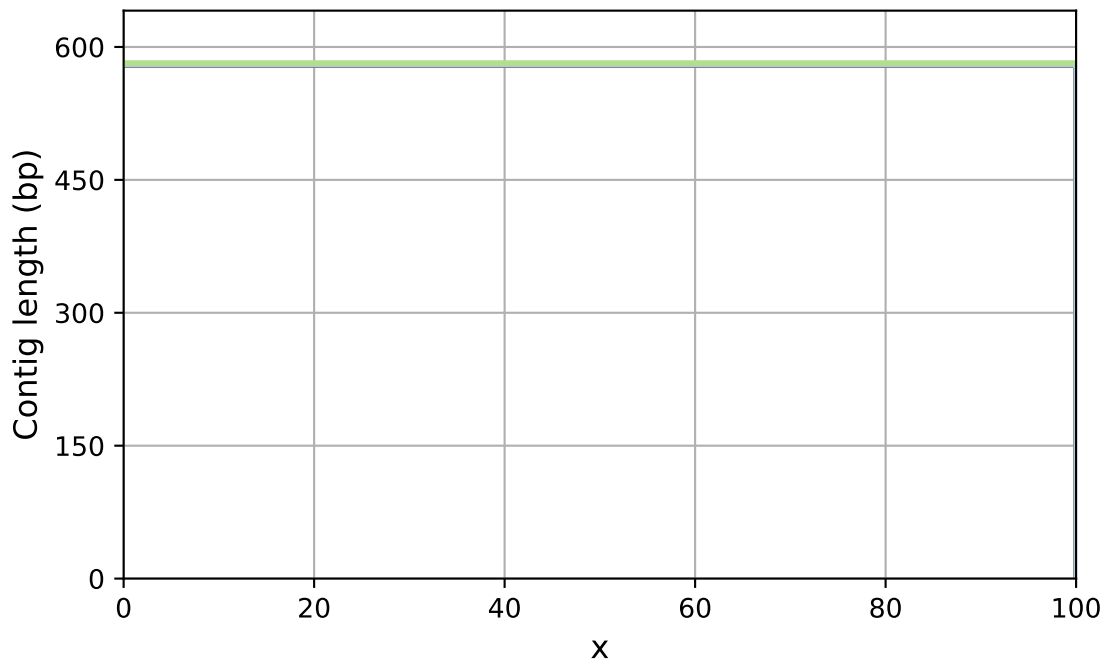
FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx

Genome fraction, %

A_STAR	Megahit	OPERA_MS_inhouse
HipMer	metaSPAdes	SPAdes
marmgCAMI2	Miniasm	