Report

	ref	siga	hifiasm
# contigs (>= 0 bp)	687	991	302
# contigs (>= 1000 bp)	687	988	302
# contigs (>= 5000 bp)	687	983	301
# contigs (>= 10000 bp)	687	971	298
# contigs (>= 25000 bp)	687	861	258
# contigs (>= 50000 bp)	486	572	215
Total length (>= 0 bp)	313628516	2176400468	2143853045
Total length (>= 1000 bp)	313628516	2176398956	2143853045
Total length (>= 5000 bp)	313628516	2176383399	2143848428
Total length (>= 10000 bp)	313628516	2176294607	2143827229
Total length (>= 25000 bp)	313628516	2174252095	2143071830
Total length (>= 50000 bp)	305303197	2163315678	2141533709
# contigs	838	991	302
Largest contig	128929007	128978556	160459971
Total length	2178974780	2176400468	2143853045
Reference length	2182786008	2182786008	2182786008
GC (%)	46.77	46.77	46.79
Reference GC (%)	46.77	46.77	46.77
N50	47037903	39073285	63673969
NG50	47037903	39073285	63673969
N75	20099827	17652537	32553861
NG75	20099827	17652537	30949767
L50	16	17	12
LG50	16	17	12
L75	32	38	23
LG75	32	38	24
# misassemblies	0	8	157
# misassembled contigs	0	8	93
Misassembled contigs length	0	853186	905390237
# local misassemblies	2	18	78
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# possible TEs	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 2 part	2 + 4 part	0 + 38 part
Unaligned length	19317	97412	1235063
Genome fraction (%)	99.997	99.808	98.285
Duplication ratio	1.000	1.001	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.03	0.59
# indels per 100 kbp	0.00	0.06	0.34
Largest alignment	128929007	128978556	128858610
Total aligned length	2178903808	2176200349	2141466821
NA50	47037903	39073285	56635102
NGA50	47037903	39073285	56635102
NA75	20099827	17652537	24244347
NGA75	20099827	17652537	24008378
LA50	16	17	14
LGA50	16	17	14
LA75	32	38	28
LGA75	32	38	29

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
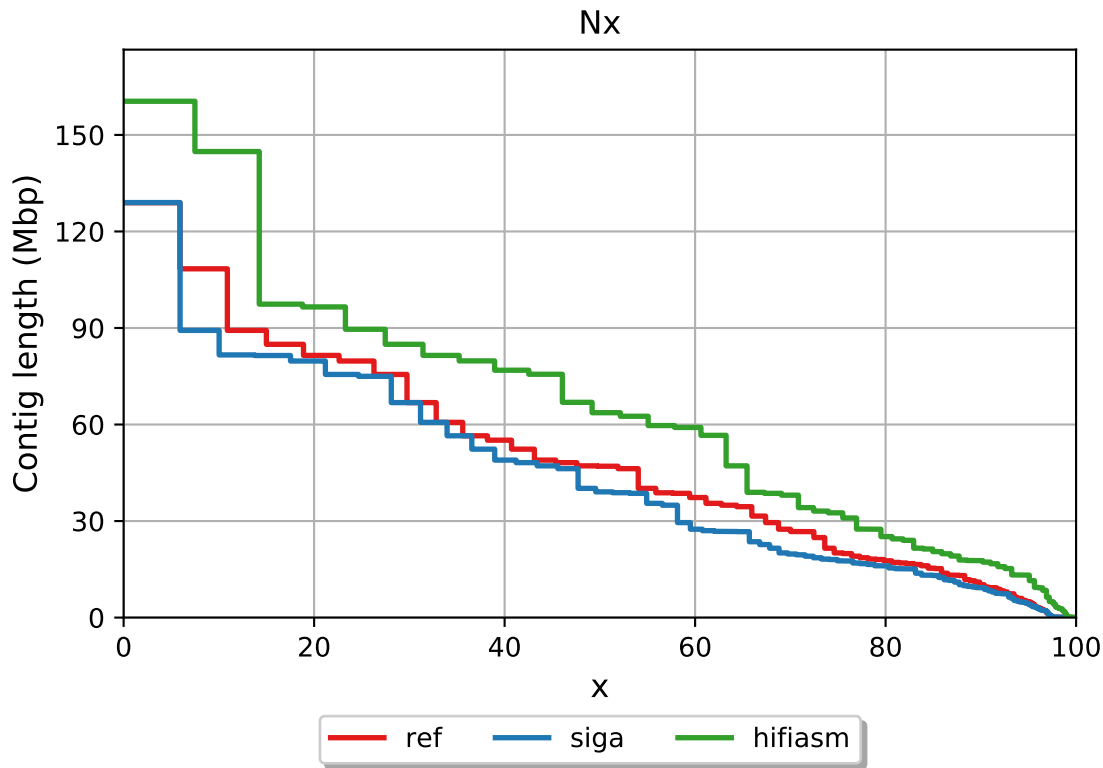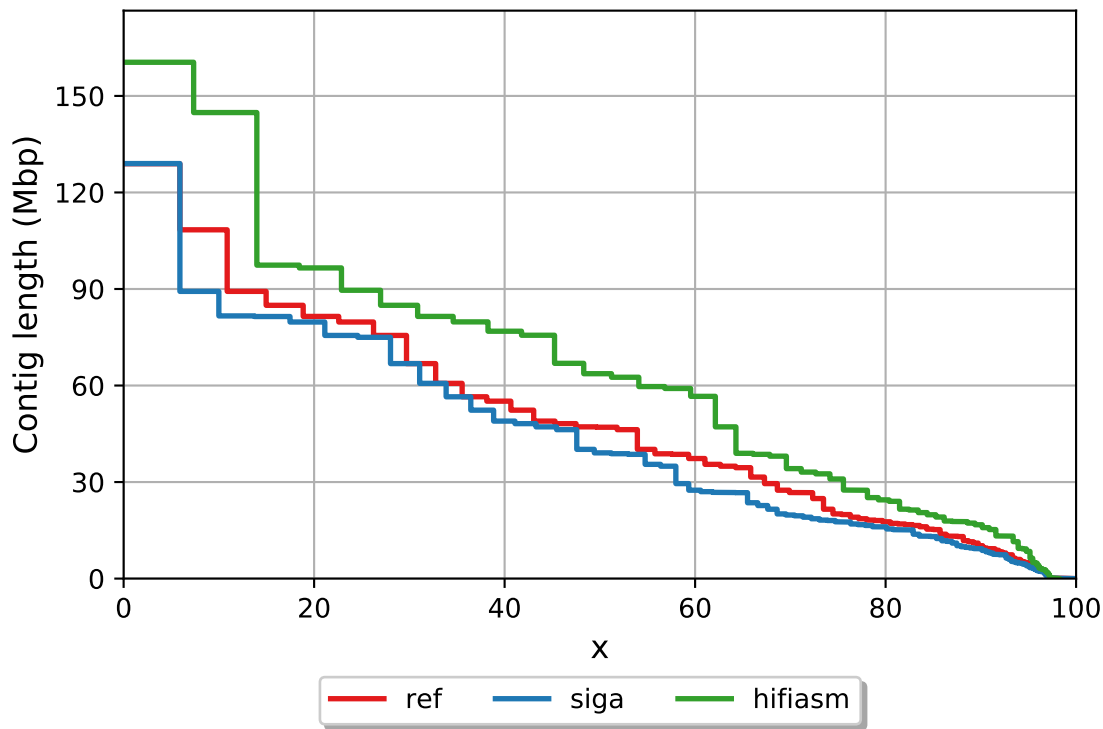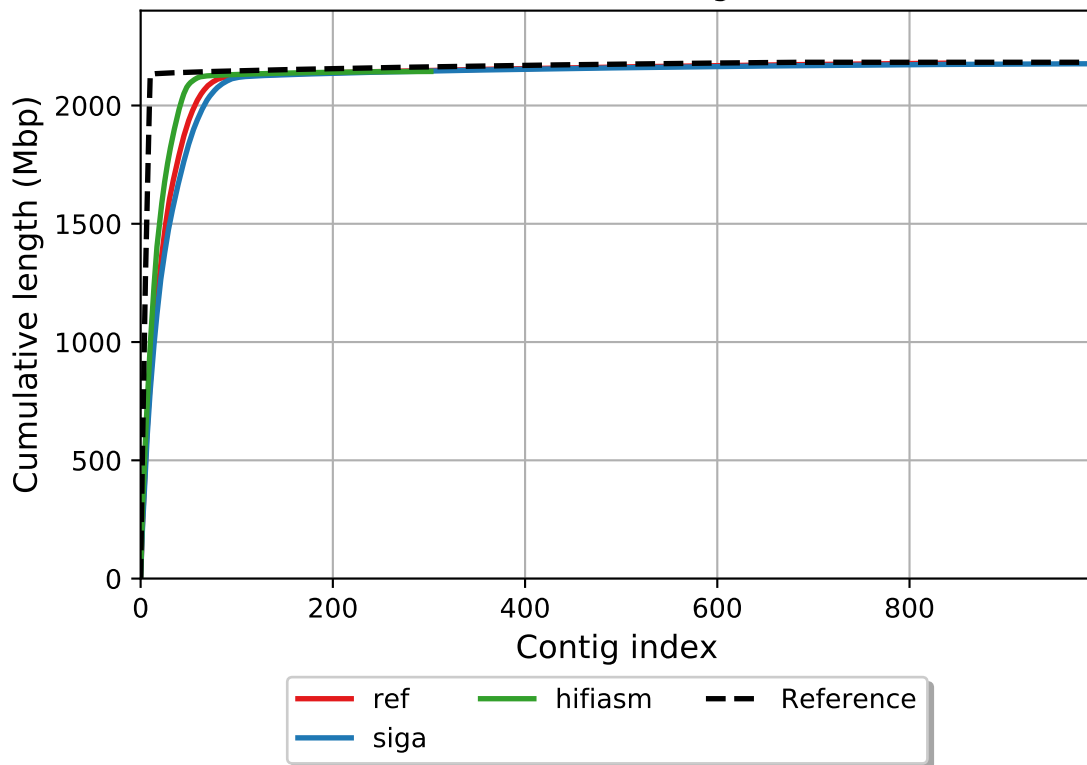
Misassemblies report

	ref	siga	hifiasm
# misassemblies	0	8	157
# contig misassemblies	0	8	157
# c. relocations	0	1	36
# c. translocations	0	7	121
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	8	93
Misassembled contigs length	0	853186	905390237
# local misassemblies	2	18	78
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# misassemblies caused by fragmented reference	0	0	0
# possible TEs	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	0	633	12558
# indels	0	1214	7205
# indels (<= 5 bp)	0	1192	6902
# indels (> 5 bp)	0	22	303
Indels length	0	100198	1044739

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	ref	siga	hifiasm
# fully unaligned contigs	0	2	0
Fully unaligned length	0	800	0
# partially unaligned contigs	2	4	38
Partially unaligned length	19317	96612	1235063
# N's	0	0	0

All statistics are based on contigs of size >= 400 bp, unless otherwise noted
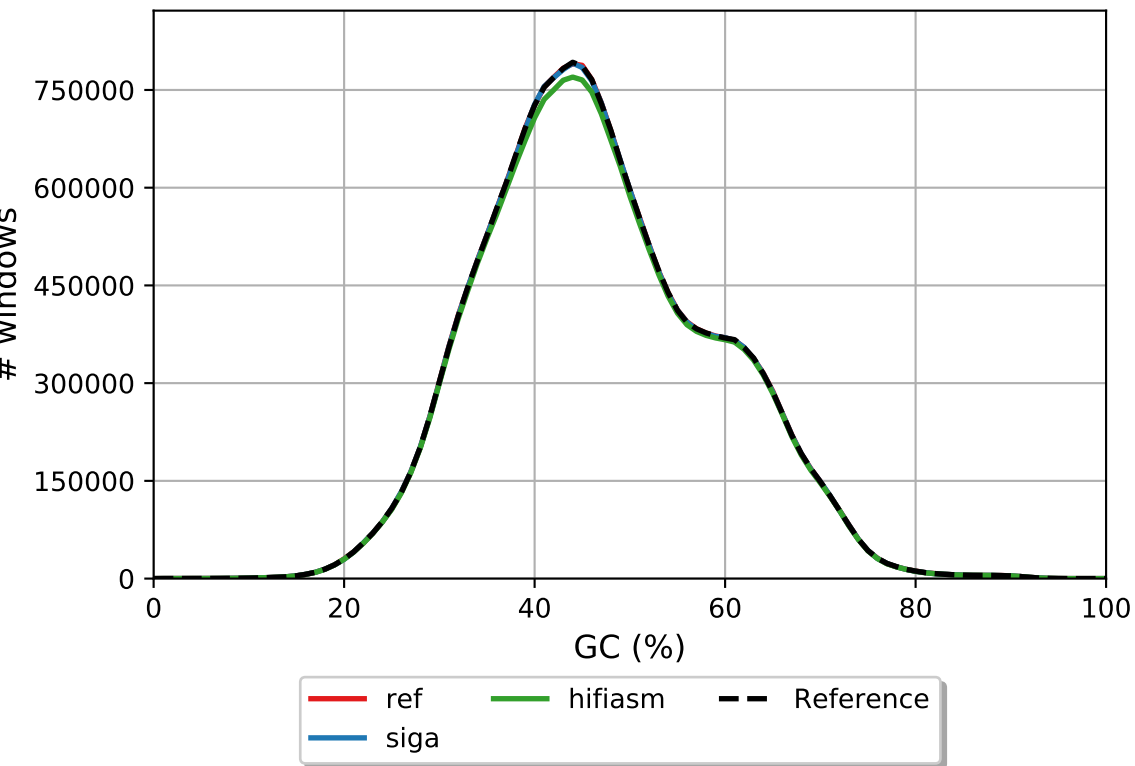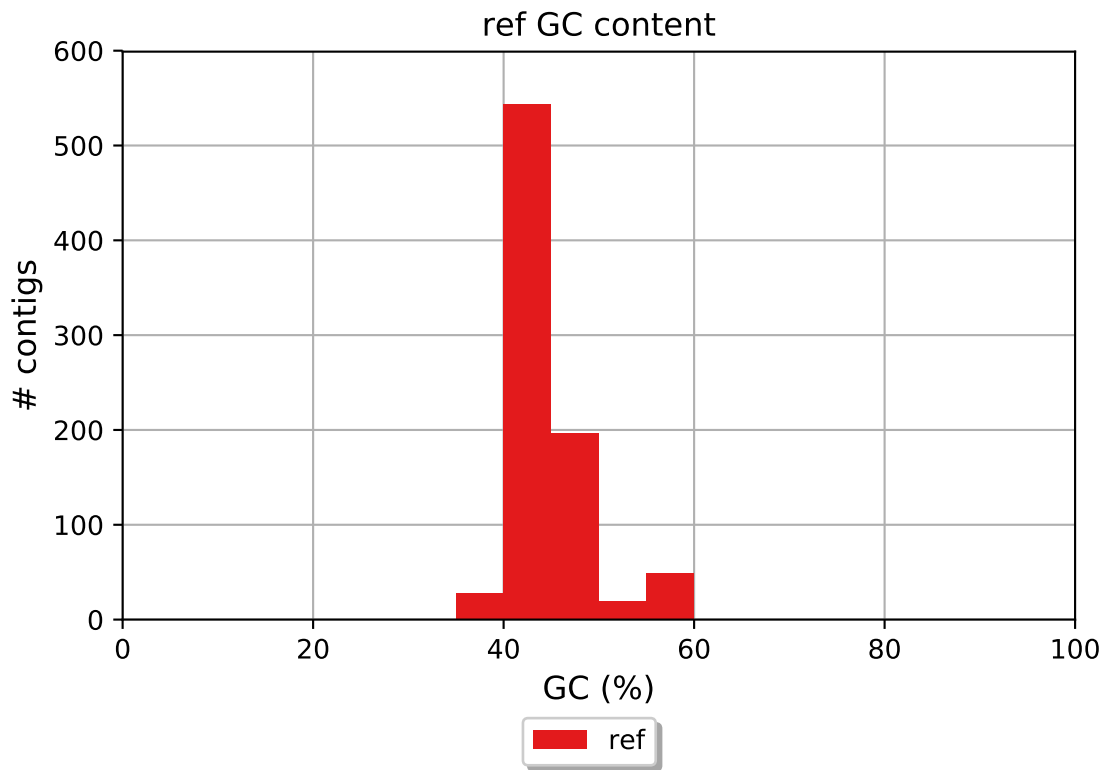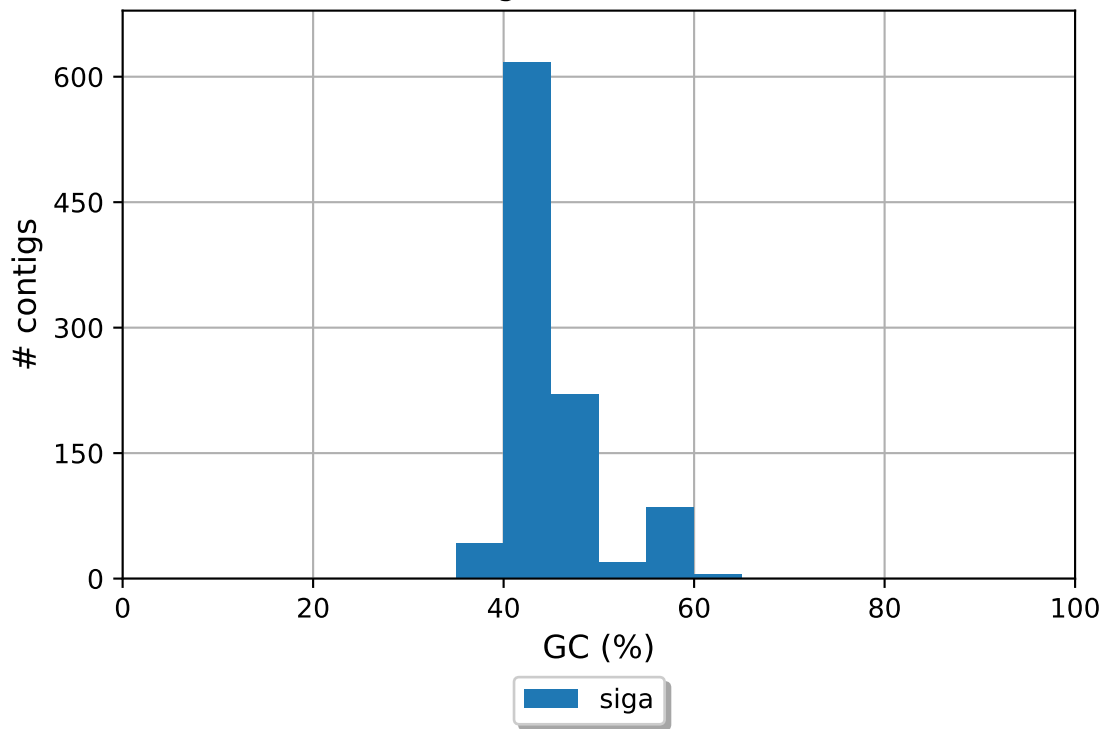(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
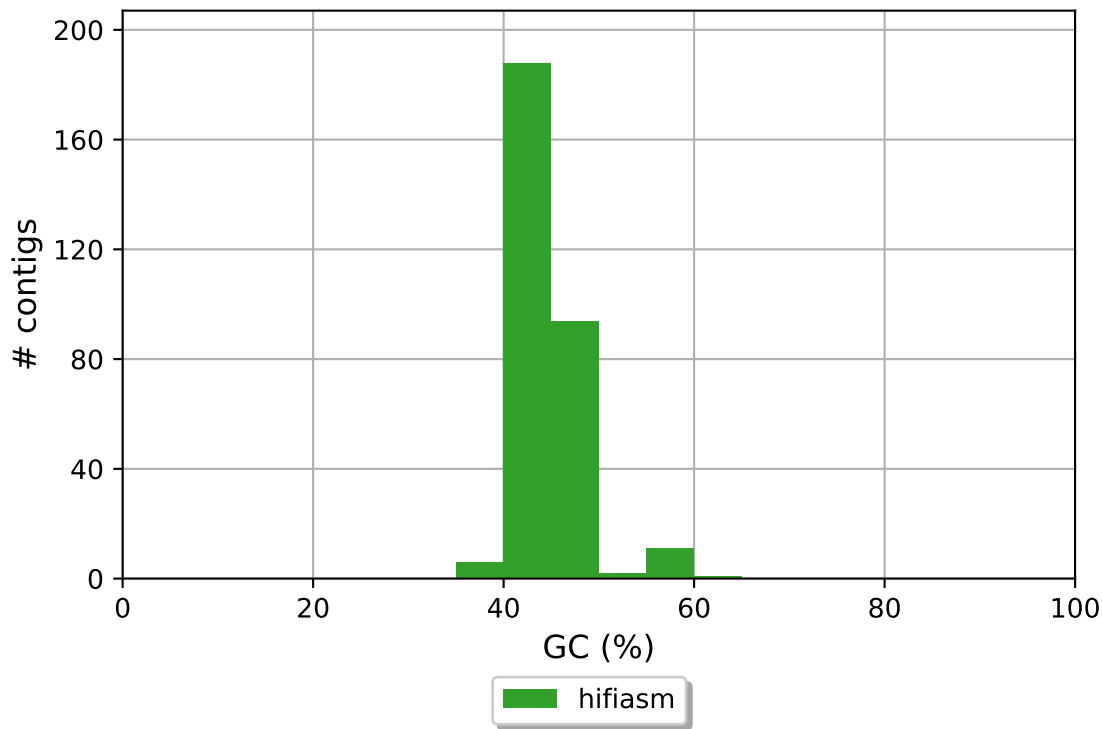
NGx

Cumulative length

GC content

ref GC content

siga GC content

hifiasm GC content
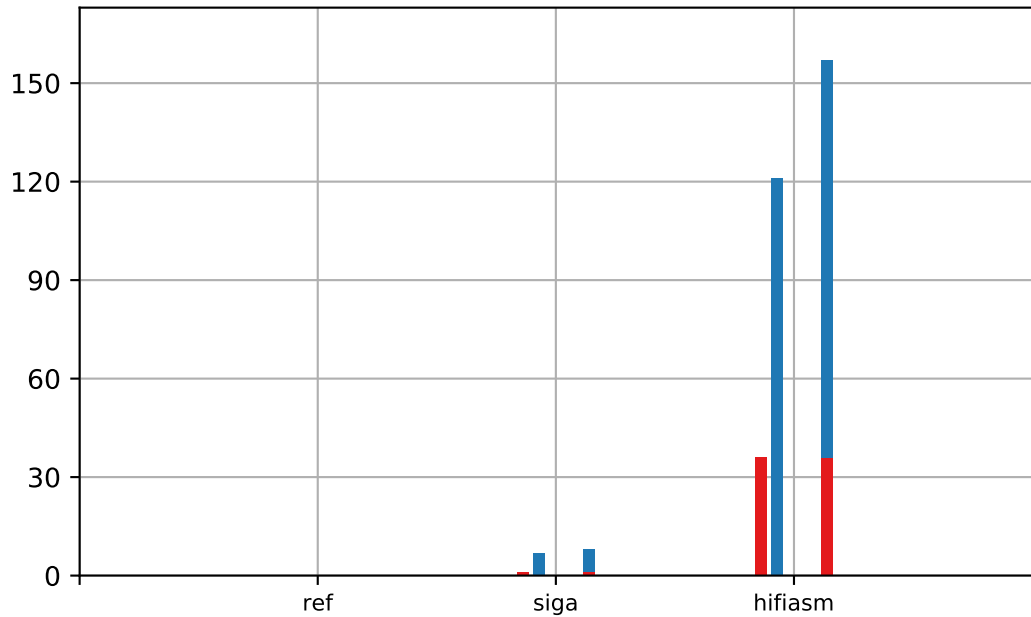
Misassemblies

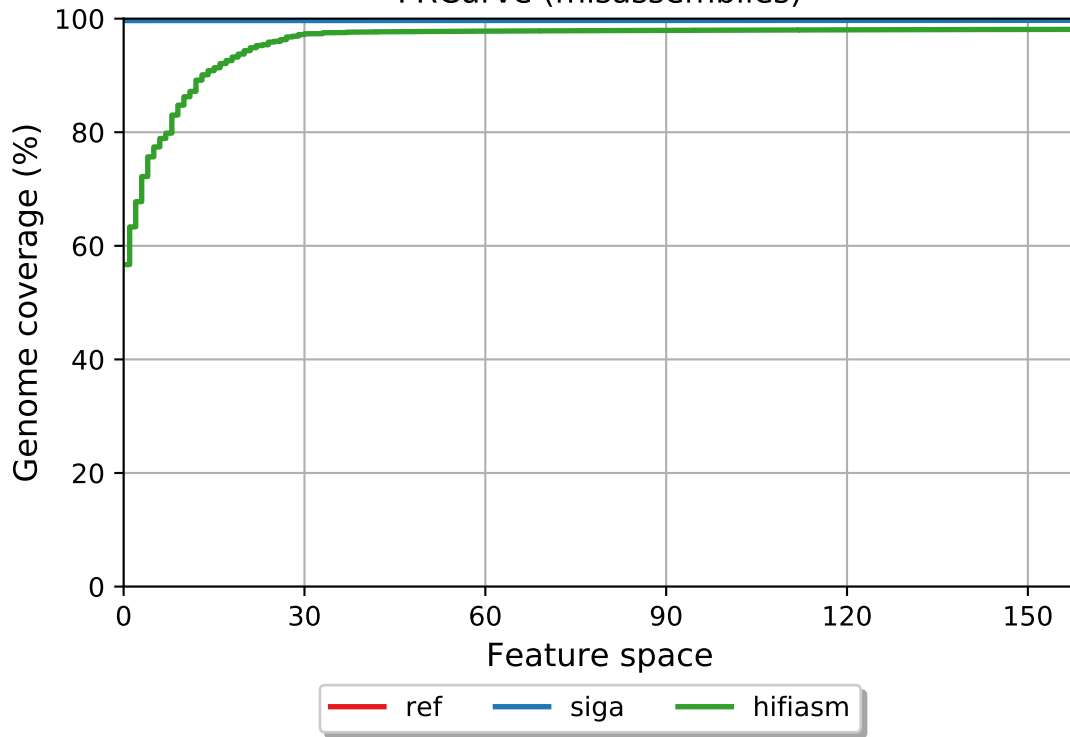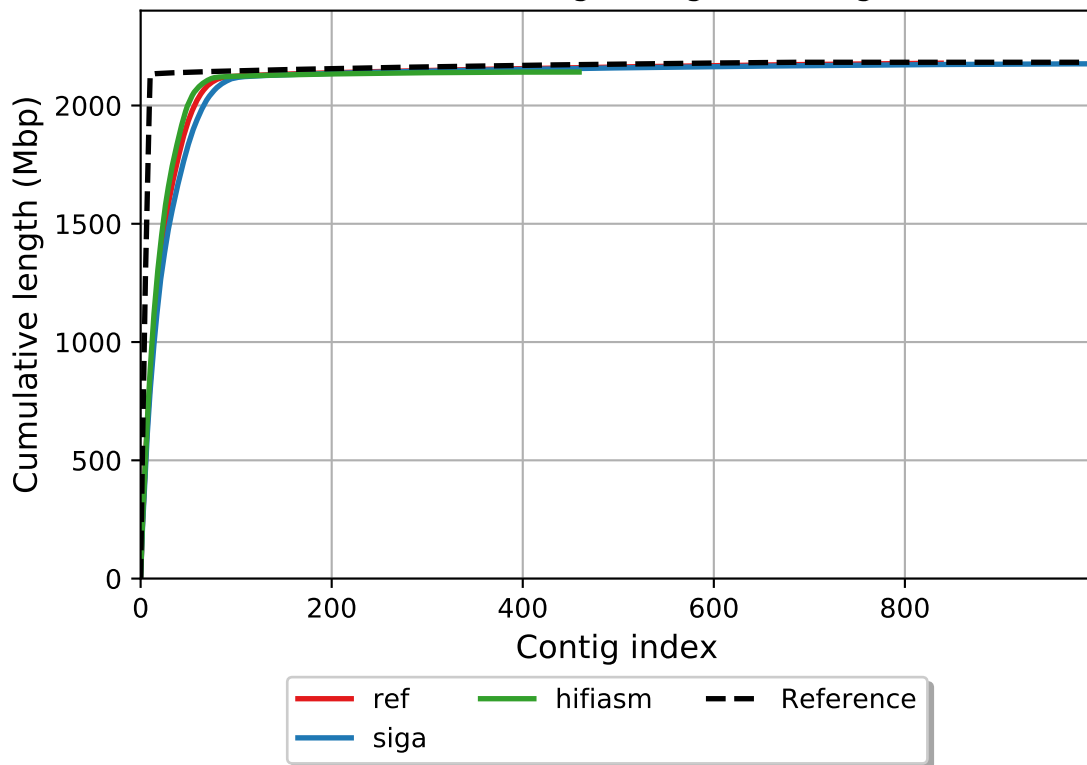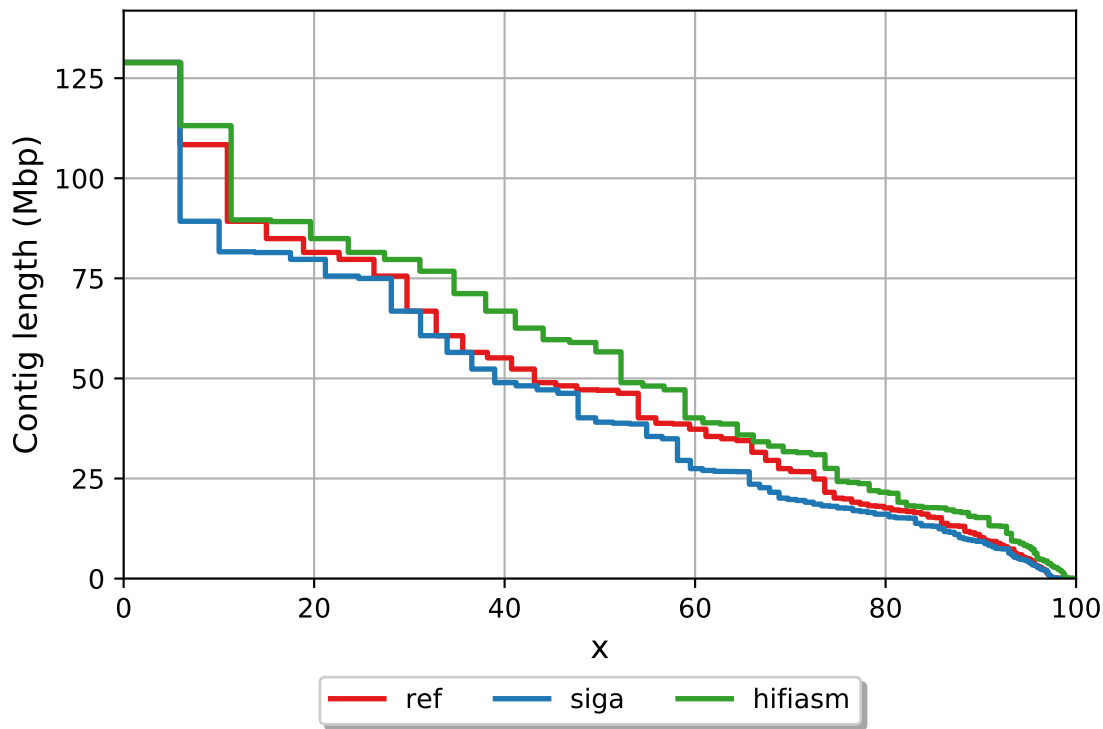FRCurve (misassemblies)

Cumulative length (aligned contigs)

Legend: ref, siga, hifiasm, Reference

NAx

Contig length (Mbp) vs x

ref — siga — hifiasm

NGAx

Genome fraction, %