

Report

	ref	sig	hifi
# contigs (>= 0 bp)	61	694	291
# contigs (>= 1000 bp)	61	689	291
# contigs (>= 5000 bp)	50	670	289
# contigs (>= 10000 bp)	46	637	283
# contigs (>= 25000 bp)	40	530	257
# contigs (>= 50000 bp)	36	399	216
Total length (>= 0 bp)	674918548	2651746496	2632363436
Total length (>= 1000 bp)	674918548	2651743738	2632363436
Total length (>= 5000 bp)	674891566	2651685207	2632354218
Total length (>= 10000 bp)	674858128	2651431469	2632305397
Total length (>= 25000 bp)	674758534	2649282870	2631843951
Total length (>= 50000 bp)	674623615	2644761160	2630379358
# contigs	338	694	291
Largest contig	152907495	120702425	120702424
Total length	2654621305	2651746496	2632363436
Reference length	2728222451	2728222451	2728222451
GC (%)	41.67	41.67	41.68
Reference GC (%)	41.67	41.67	41.67
N50	46334773	44613395	52637589
NG50	46334773	42491999	46334307
N75	21983050	20705697	25290655
NG75	21153448	18421565	22303466
L50	19	21	17
LG50	19	22	18
L75	39	45	36
LG75	41	48	40
# misassemblies	0	10	104
# misassembled contigs	0	9	28
Misassembled contigs length	0	26612572	659793886
# local misassemblies	0	9	180
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# possible TEs	0	2	2
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	2 + 6 part	0 + 20 part
Unaligned length	0	473637	2757781
Genome fraction (%)	100.000	99.640	98.774
Duplication ratio	1.000	1.002	1.003
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.12	3.69
# indels per 100 kbp	0.00	0.04	0.32
Largest alignment	152907495	120702425	120702424
Total aligned length	2654621305	2651149192	2627741661
NA50	46334773	44613395	46065667
NGA50	46334773	42491999	45910920
NA75	21983050	19903223	20707047
NGA75	21153448	18421565	19731320
LA50	19	21	20
LGA50	19	22	21
LA75	39	45	42
LGA75	41	48	45

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

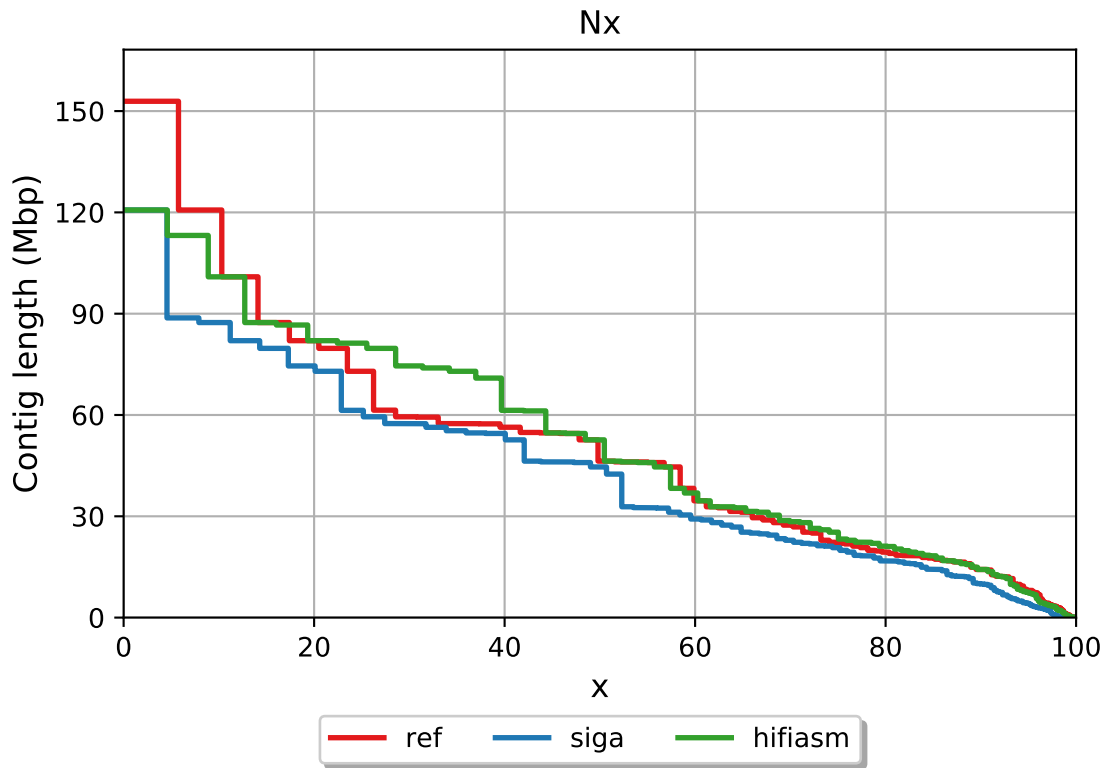
	ref	siga	hifiasm
# misassemblies	0	10	104
# contig misassemblies	0	10	104
# c. relocations	0	9	103
# c. translocations	0	1	1
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	9	28
Misassembled contigs length	0	26612572	659793886
# local misassemblies	0	9	180
# 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	2	2
# unaligned mis. contigs	0	0	0
# mismatches	0	3304	96870
# indels	0	967	8418
# indels (<= 5 bp)	0	760	6294
# indels (> 5 bp)	0	207	2124
Indels length	0	110968	979527

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).

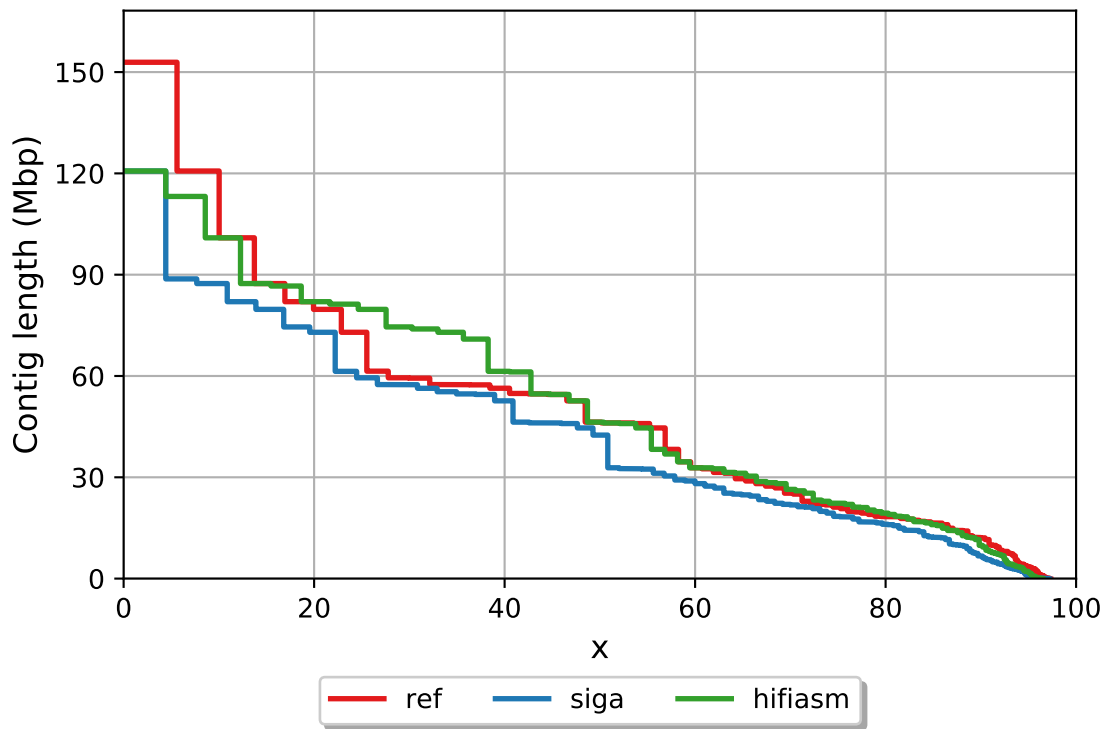
Unaligned report

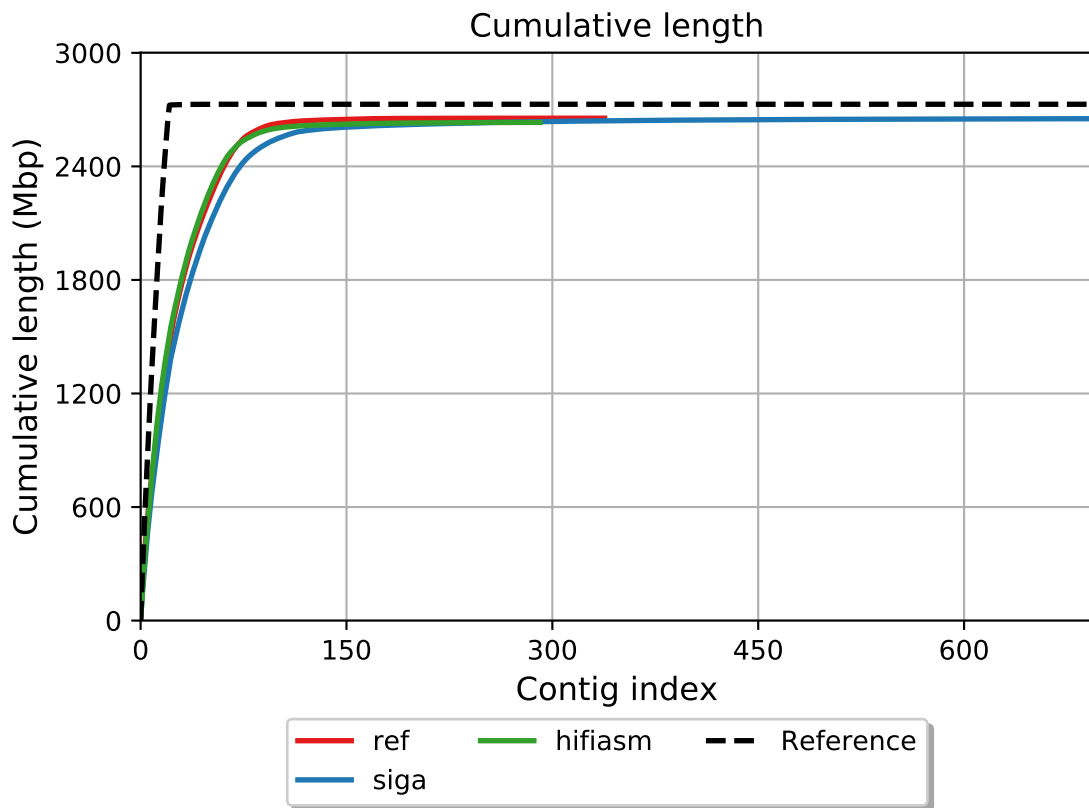
	ref	sig	hifiasm
# fully unaligned contigs	0	2	0
Fully unaligned length	0	800	0
# partially unaligned contigs	0	6	20
Partially unaligned length	0	472837	2757781
# N's	0	0	0

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).

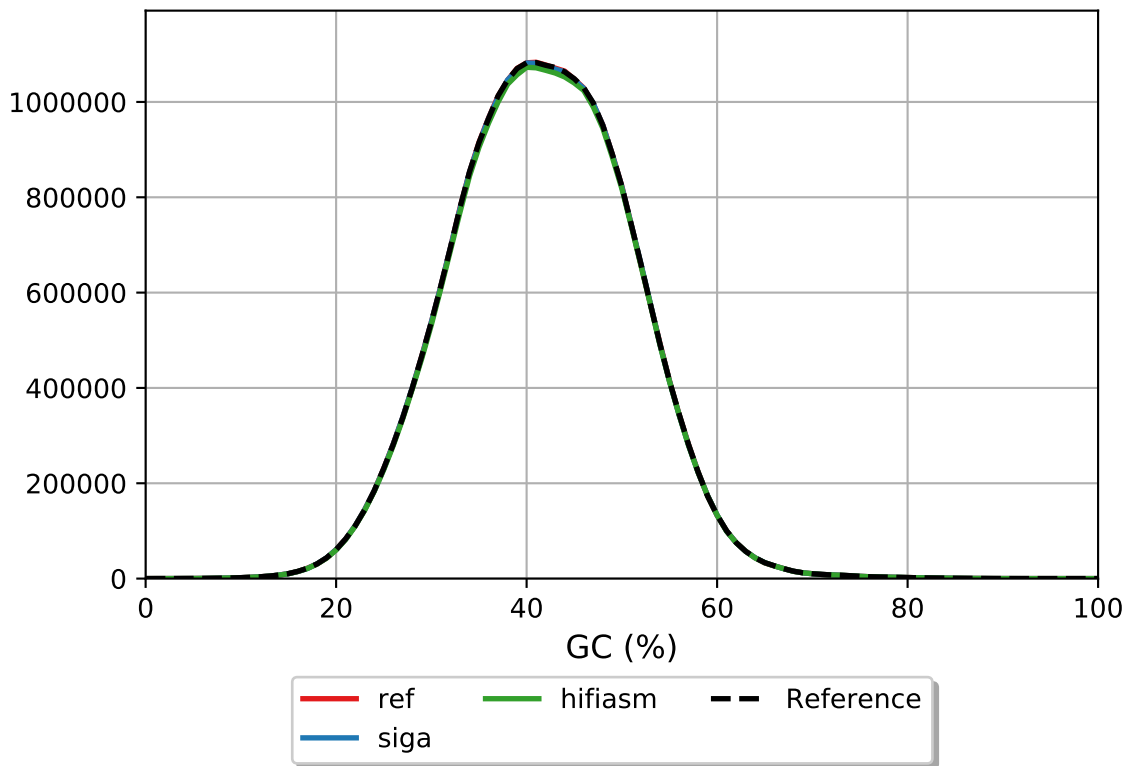


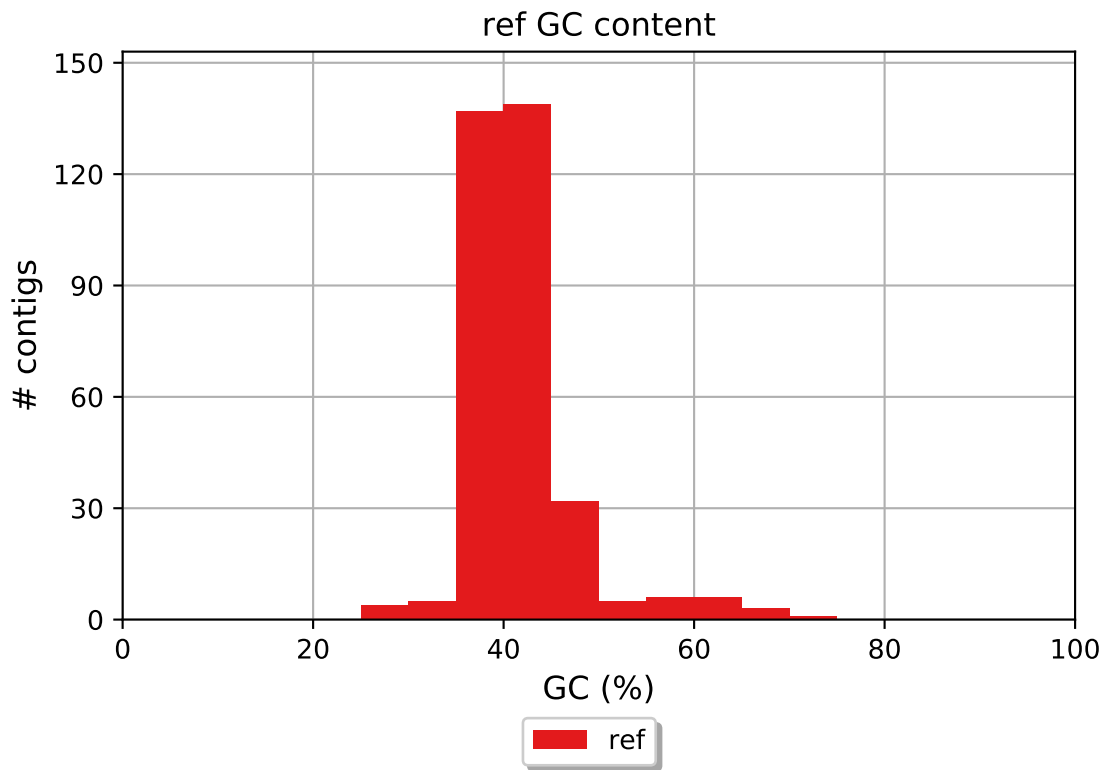
NGx



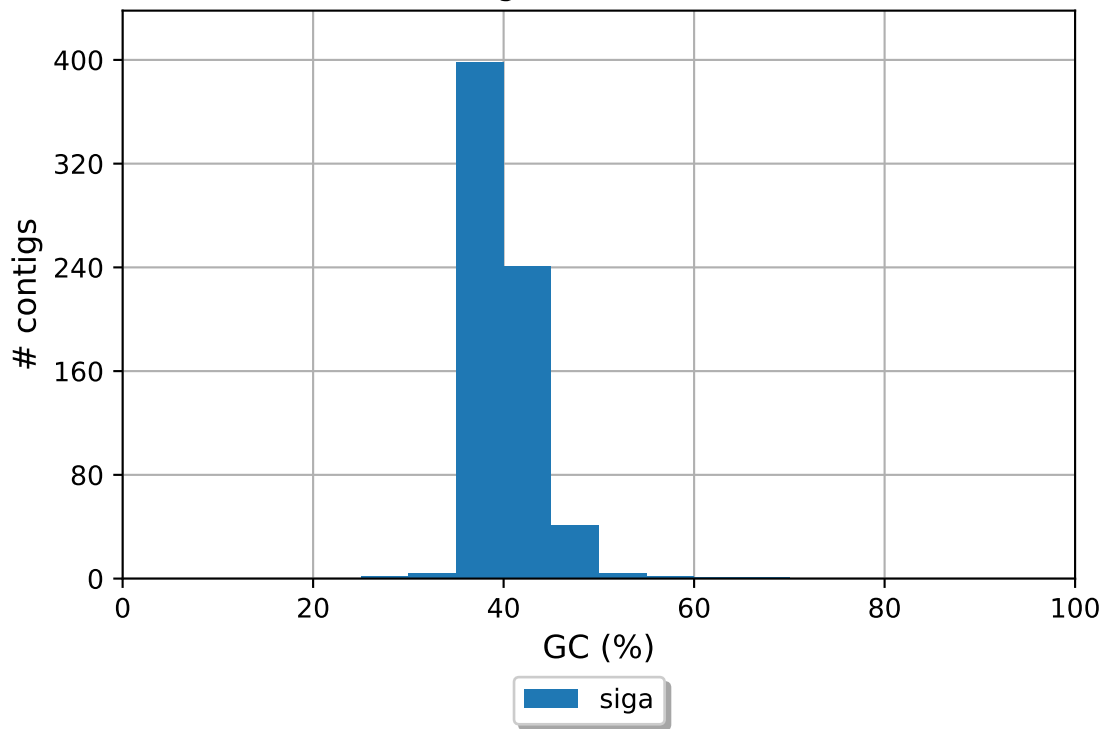


GC content

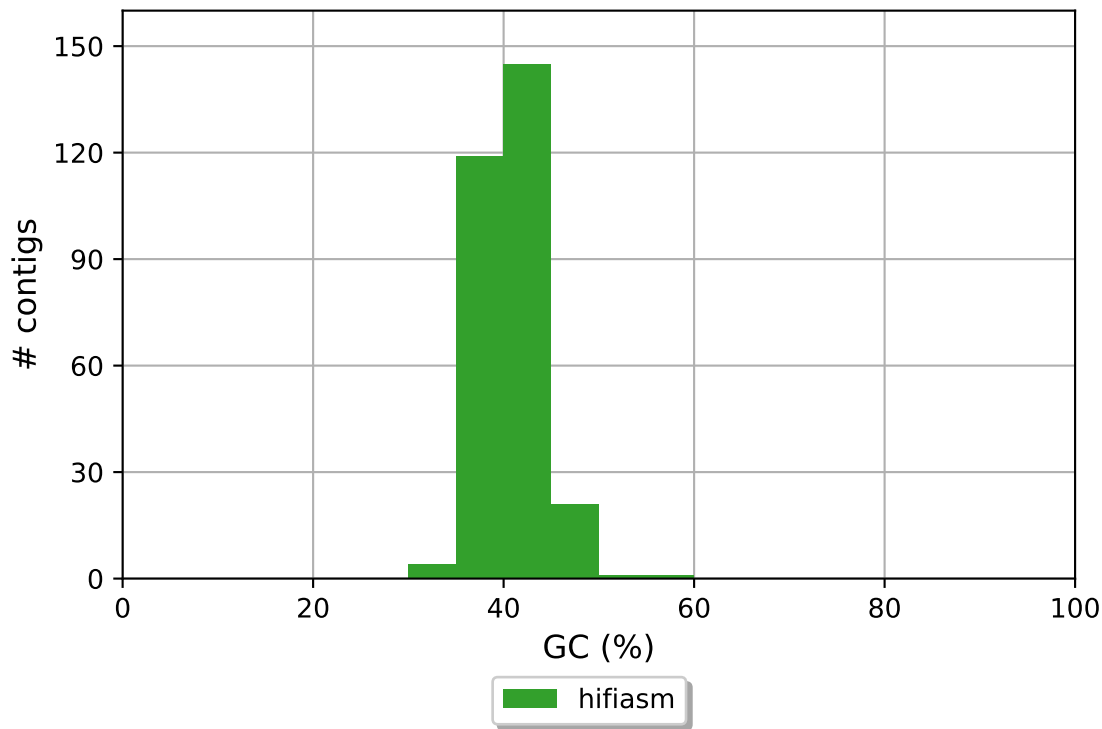




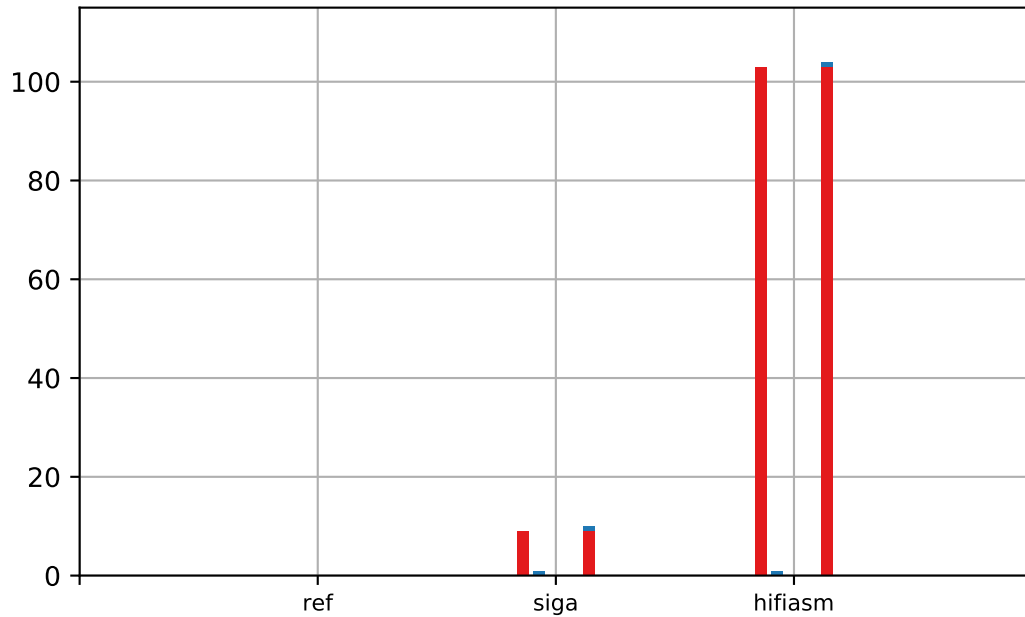
siga GC content



hifiasm GC content



Misassemblies

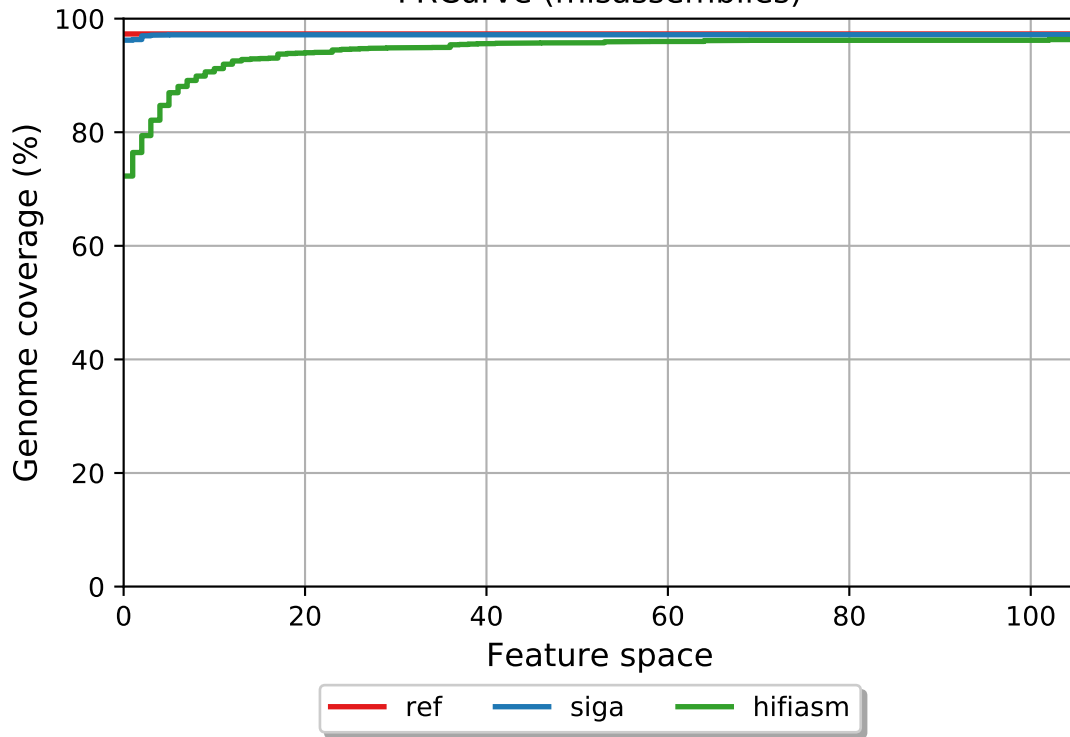


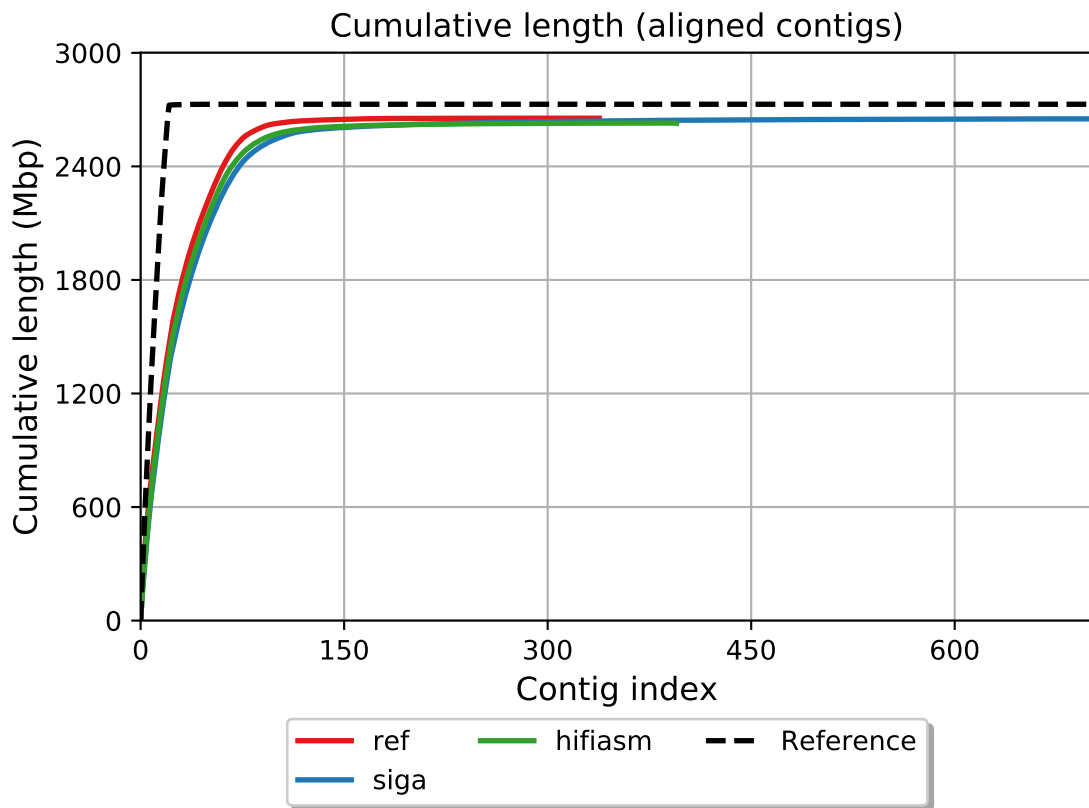
relocations



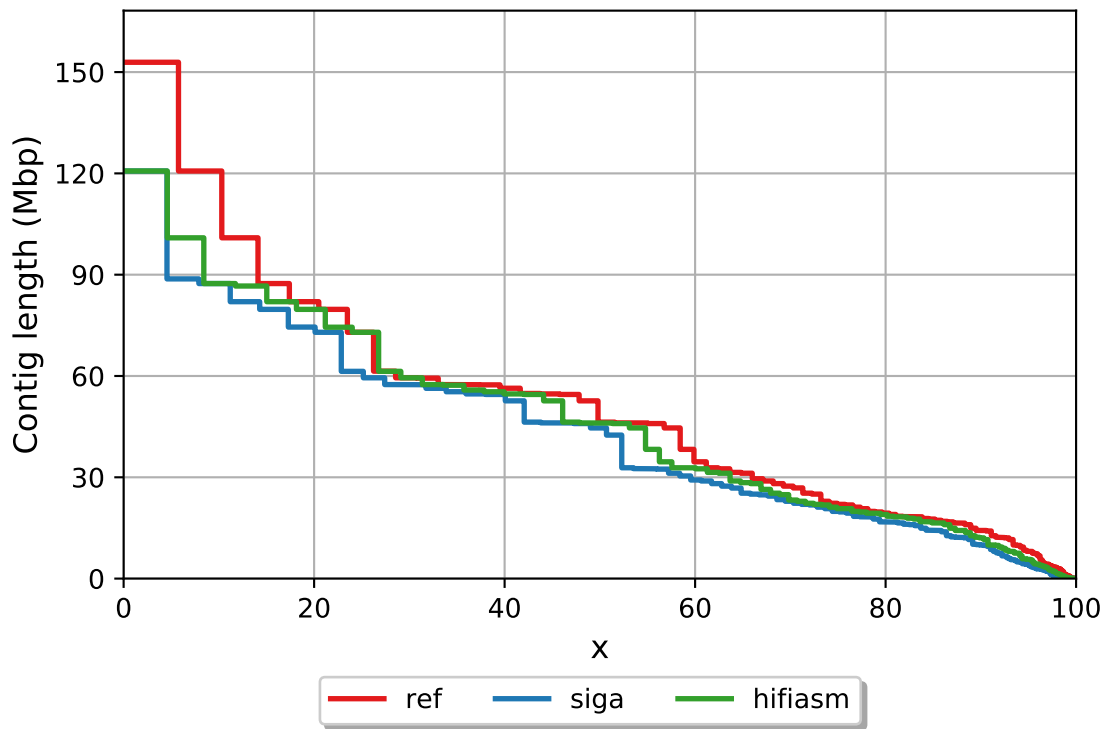
translocations

FRCurve (misassemblies)

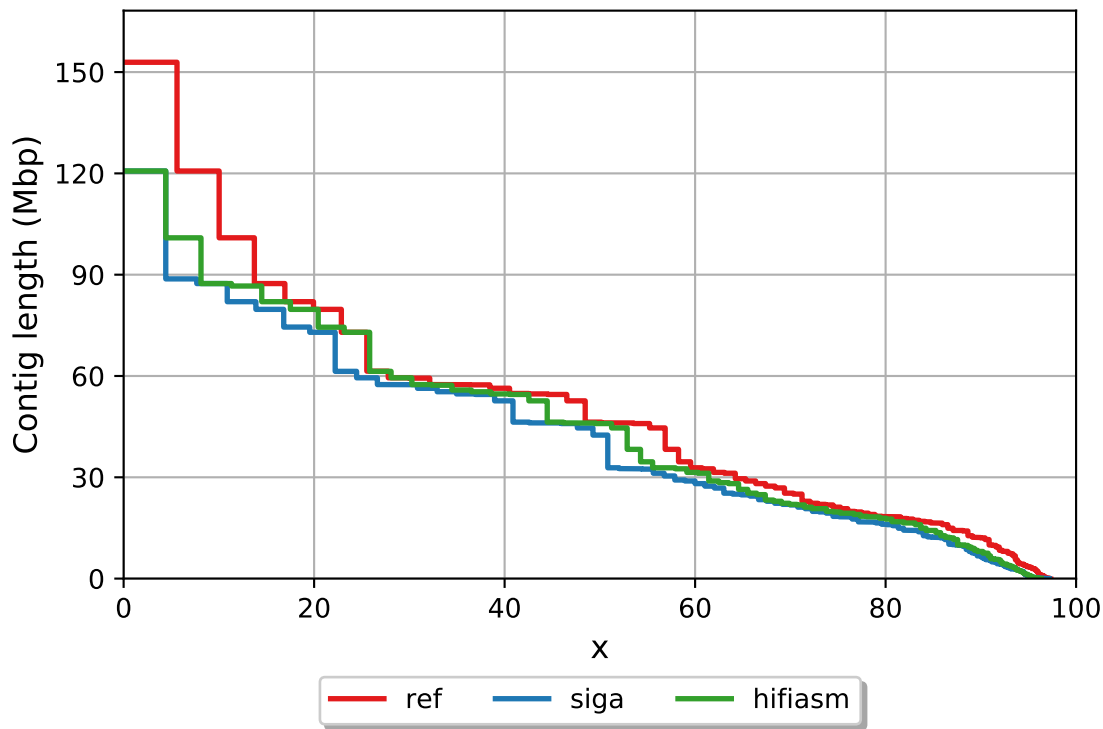


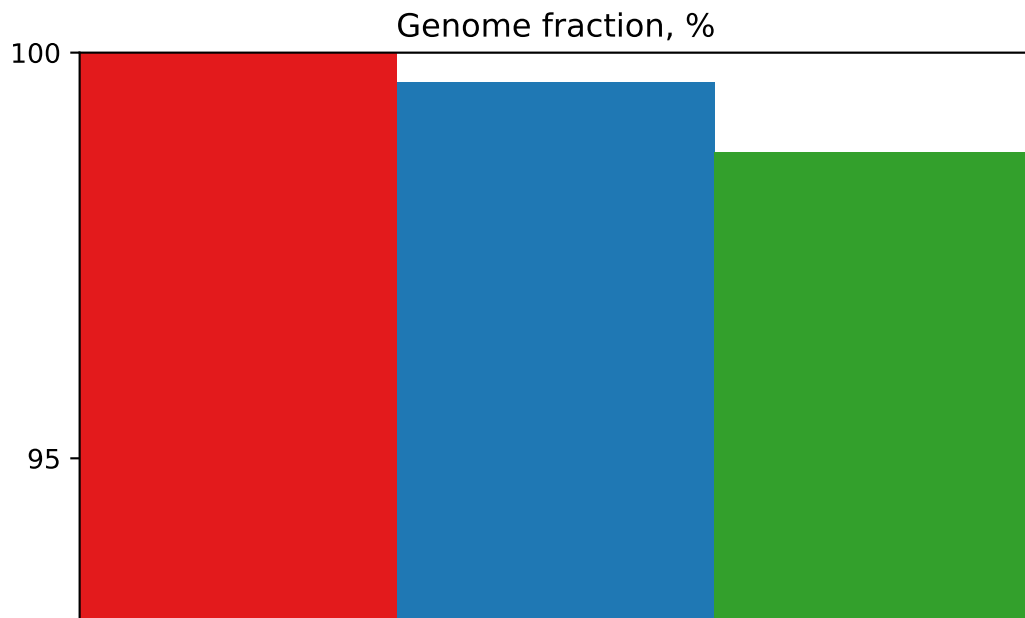


NAx



NGAx





ref



siga



hifiasm