

Report

	ref	sig	hifiasm
# contigs (>= 0 bp)	96	150	110
# contigs (>= 1000 bp)	96	150	110
# contigs (>= 5000 bp)	96	150	110
# contigs (>= 10000 bp)	96	148	110
# contigs (>= 25000 bp)	95	128	104
# contigs (>= 50000 bp)	45	71	56
Total length (>= 0 bp)	59489377	140868786	139274762
Total length (>= 1000 bp)	59489377	140868786	139274762
Total length (>= 5000 bp)	59489377	140868786	139274762
Total length (>= 10000 bp)	59489377	140853622	139274762
Total length (>= 25000 bp)	59471039	140490422	139158198
Total length (>= 50000 bp)	57530124	138346059	137451656
# contigs	123	150	110
Largest contig	27949910	27949603	24514243
Total length	140684339	140868786	139274762
Reference length	140687039	140687039	140687039
GC (%)	41.93	41.93	41.96
Reference GC (%)	41.93	41.93	41.93
N50	22407379	14873452	15937274
NG50	22407379	14873452	15937274
N75	21354878	6495835	8496362
NG75	21354878	6495835	8496362
L50	3	4	4
LG50	3	4	4
L75	5	7	7
LG75	5	7	7
# misassemblies	0	3	13
# misassembled contigs	0	2	11
Misassembled contigs length	0	479038	1570095
# local misassemblies	1	6	11
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# possible TEs	0	0	0
# unaligned mis. contigs	1	0	0
# unaligned contigs	0 + 2 part	0 + 4 part	0 + 12 part
Unaligned length	47452	44721	399105
Genome fraction (%)	99.966	99.847	98.606
Duplication ratio	1.000	1.003	1.001
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.02	0.32
# indels per 100 kbp	0.00	0.04	0.47
Largest alignment	27949910	27949603	24514243
Total aligned length	140636887	140806010	138861287
NA50	22407379	14857353	15937274
NGA50	22407379	14857353	15937274
NA75	21354878	6495835	8215069
NGA75	21354878	6495835	8215069
LA50	3	4	4
LGA50	3	4	4
LA75	5	7	7
LGA75	5	7	7

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

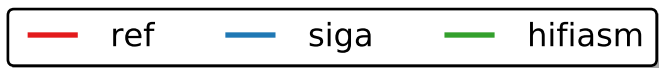
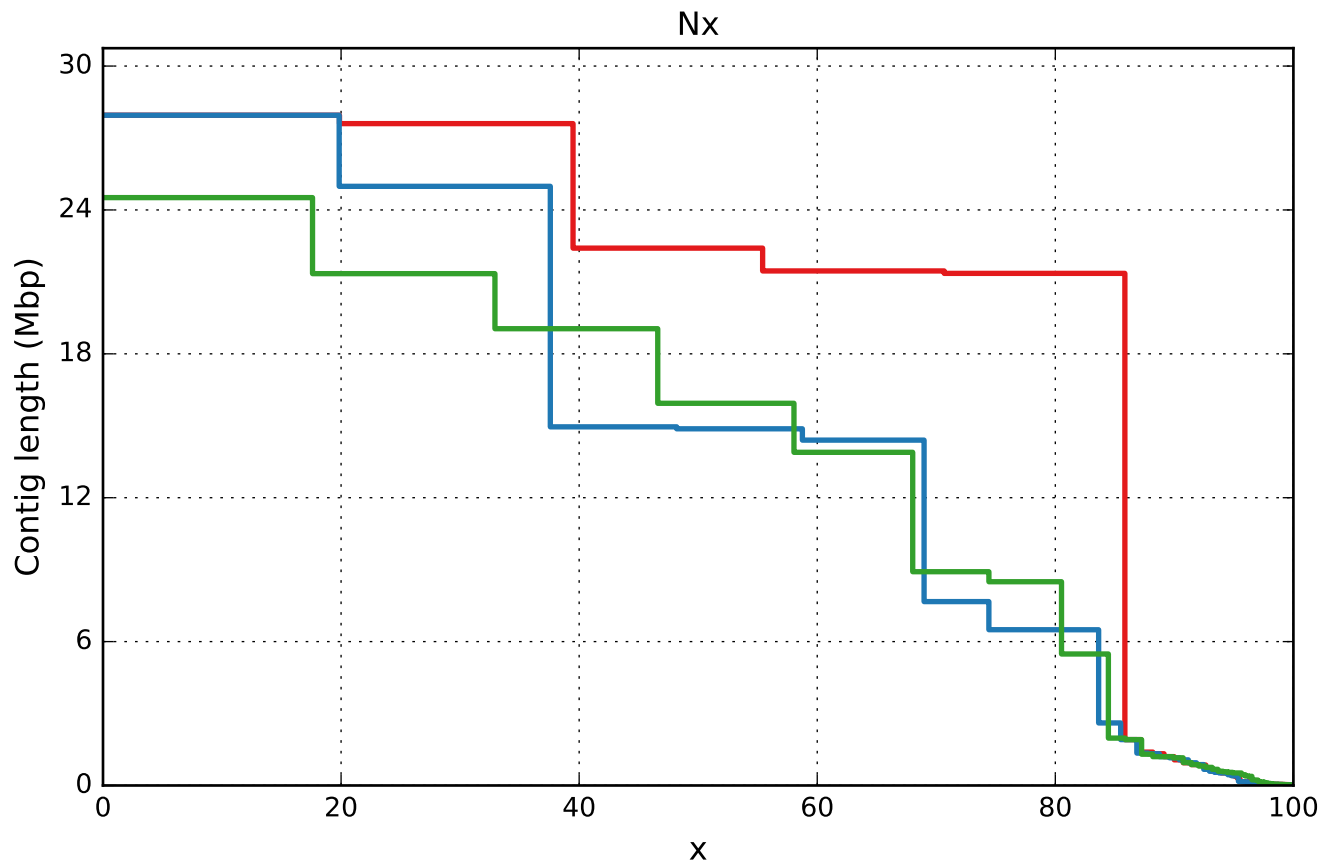
	ref	sig	hifi asm
# misassemblies	0	3	13
# contig misassemblies	0	3	13
# c. relocations	0	0	2
# c. translocations	0	3	10
# c. inversions	0	0	1
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	2	11
Misassembled contigs length	0	479038	1570095
# local misassemblies	1	6	11
# 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	1	0	0
# mismatches	0	23	446
# indels	0	54	658
# indels (<= 5 bp)	0	51	614
# indels (> 5 bp)	0	3	44
Indels length	0	5245	67099

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

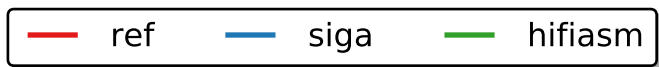
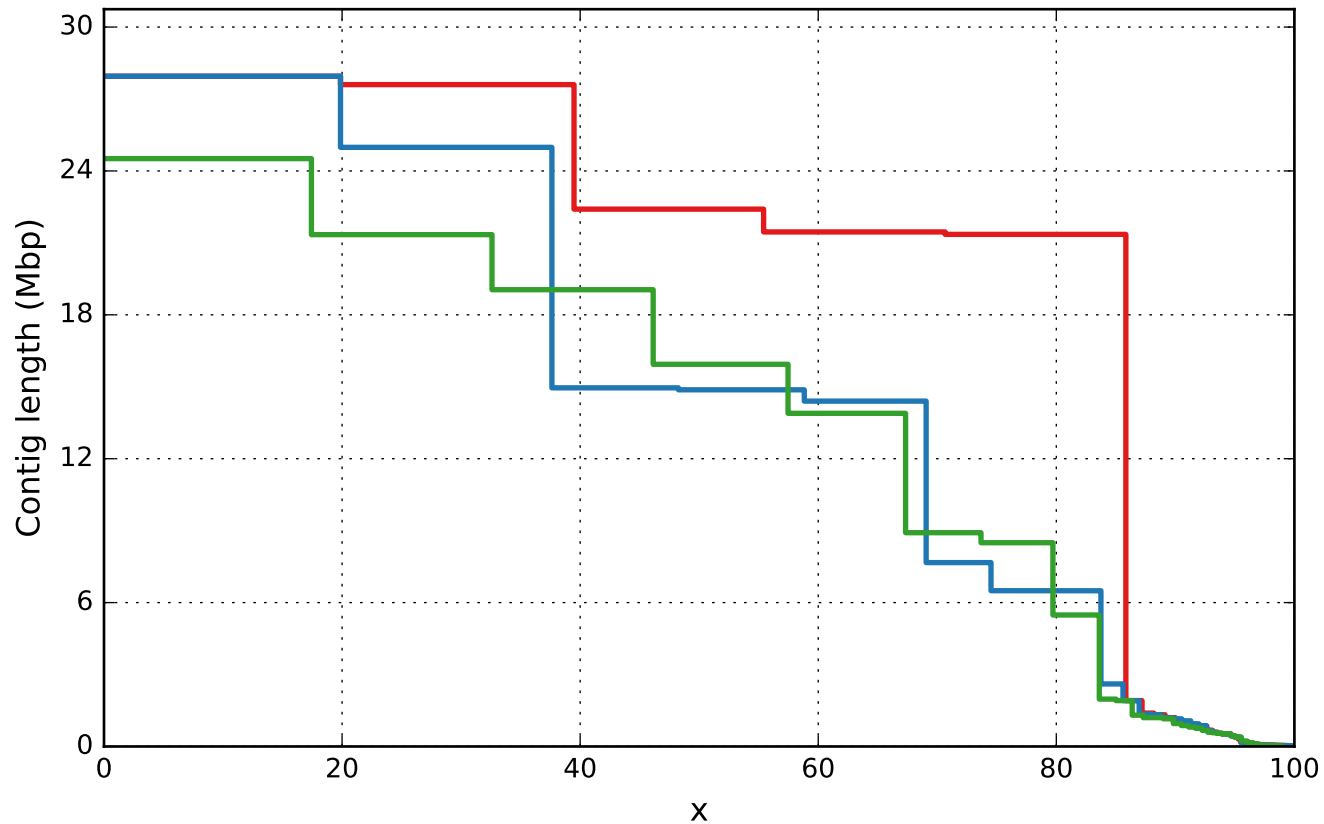
## Unaligned report

	ref	sig	hifiasm
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	2	4	12
Partially unaligned length	47452	44721	399105
# N's	0	0	0

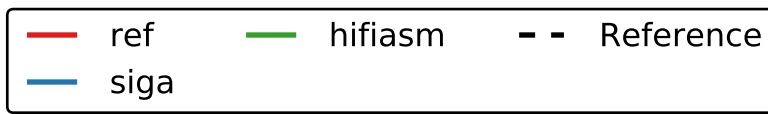
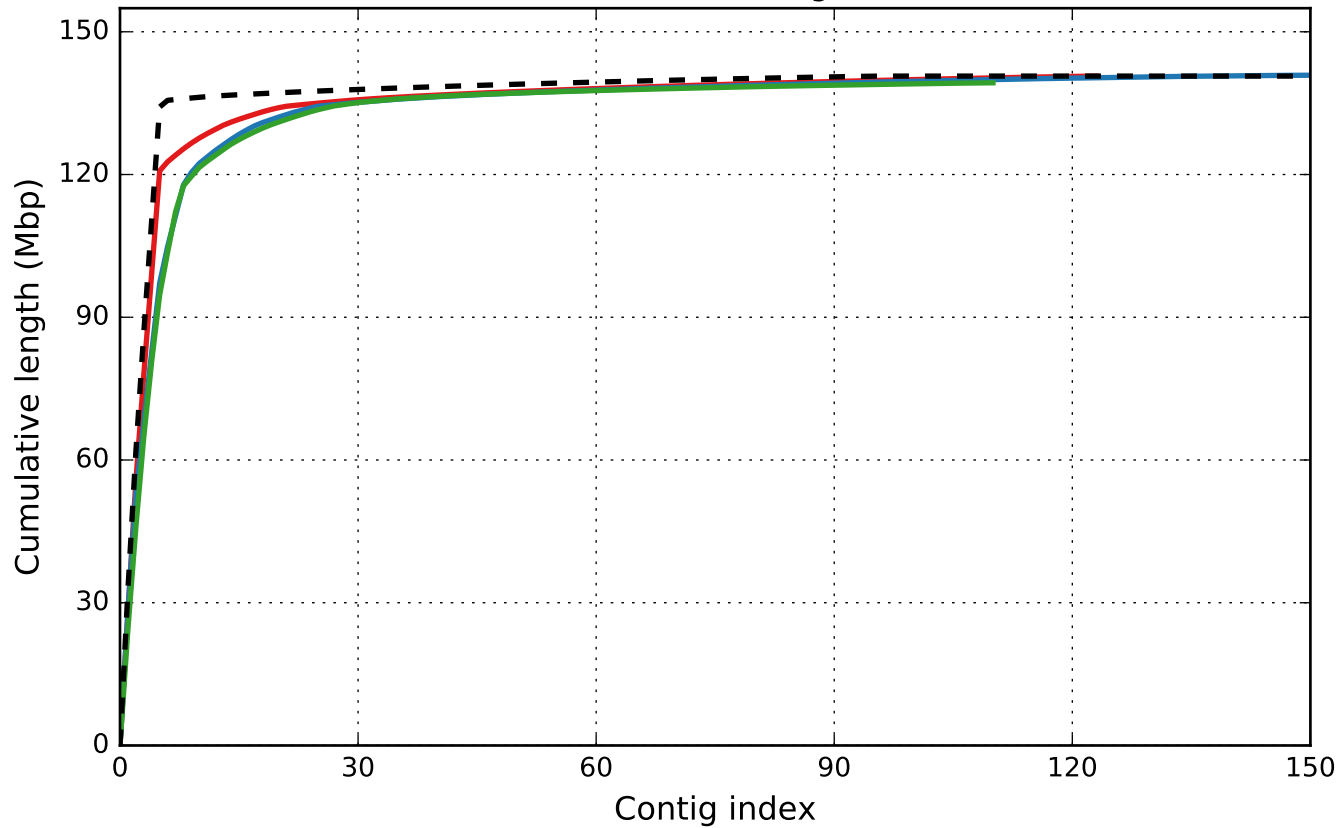
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

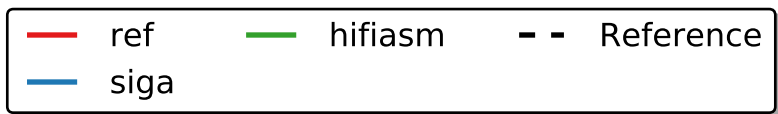
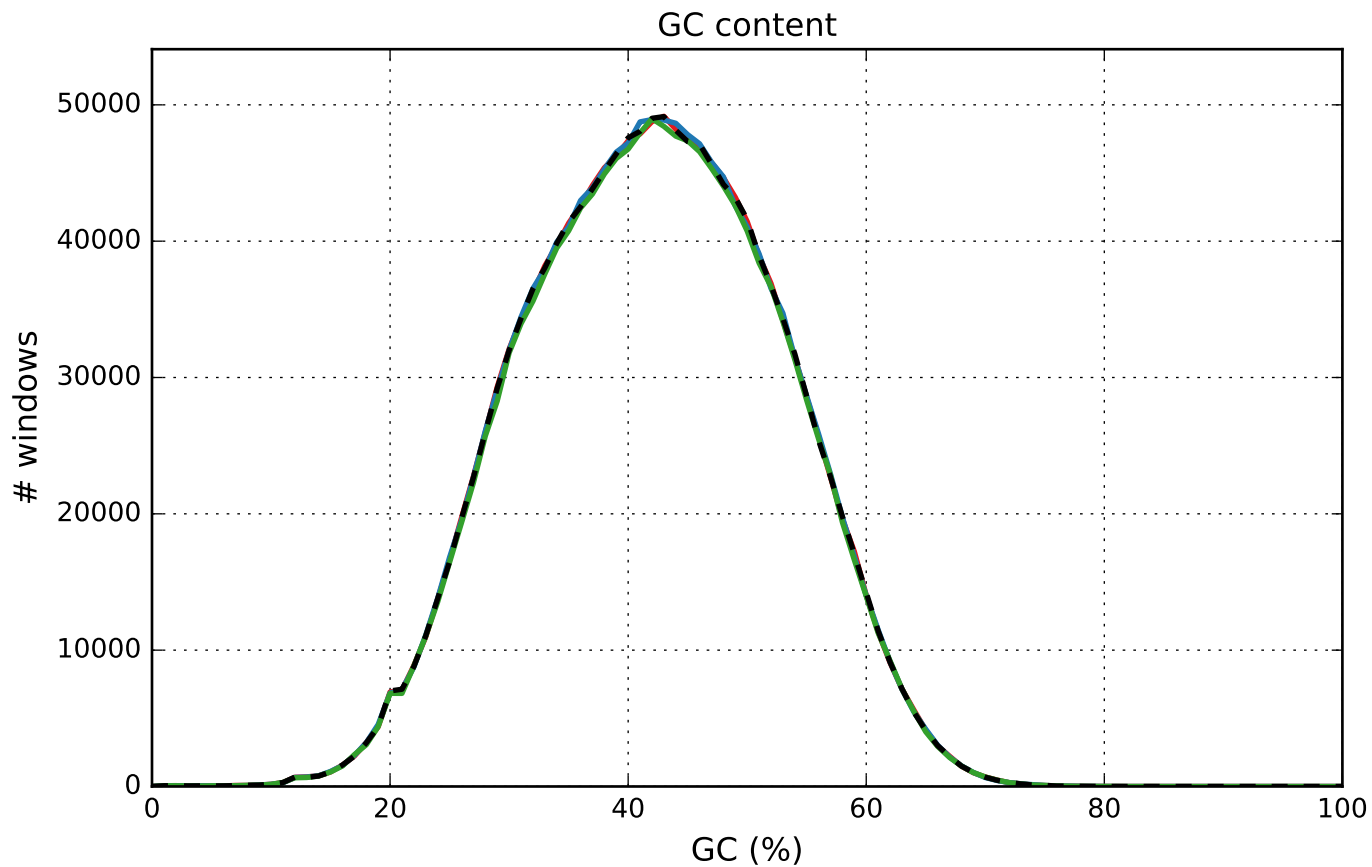


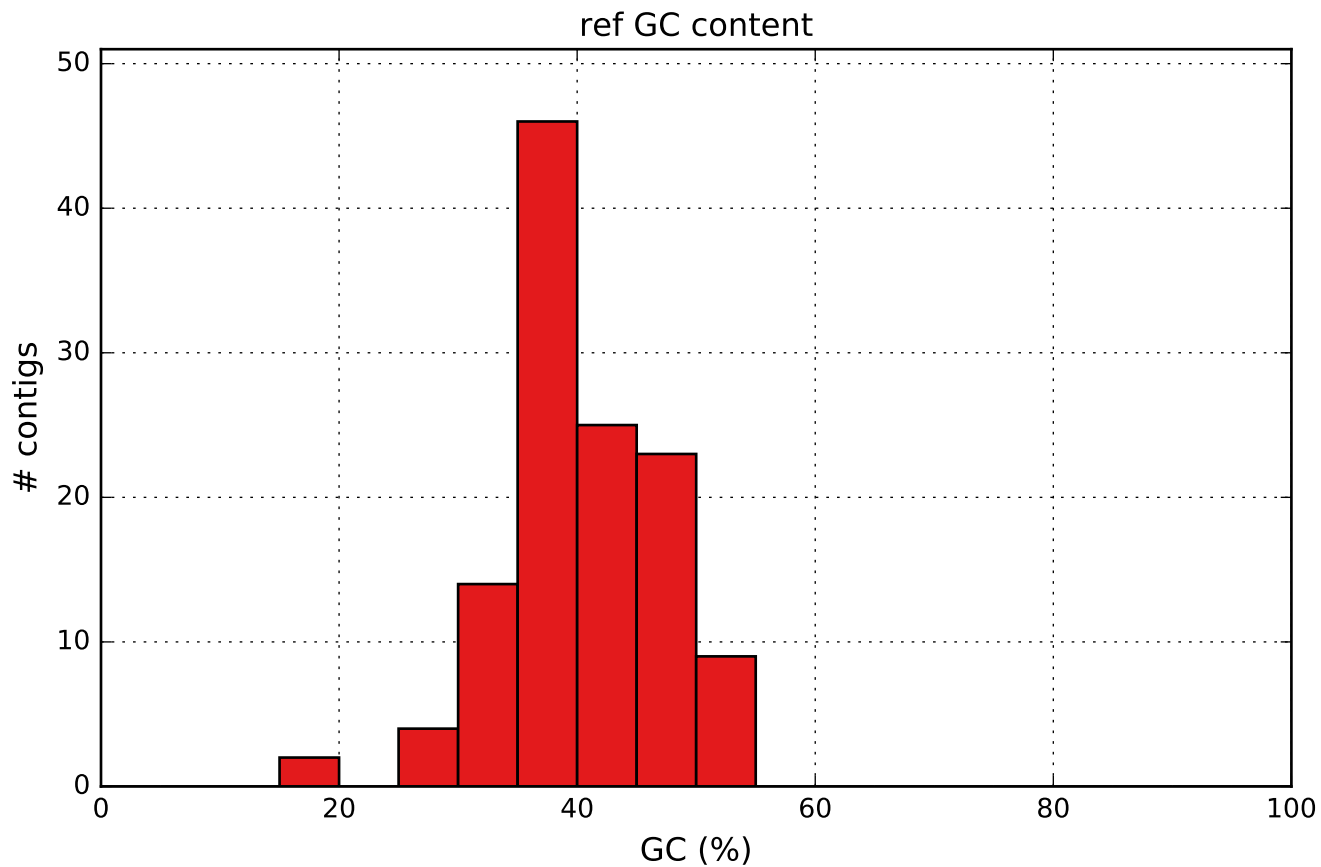
NGx



Cumulative length

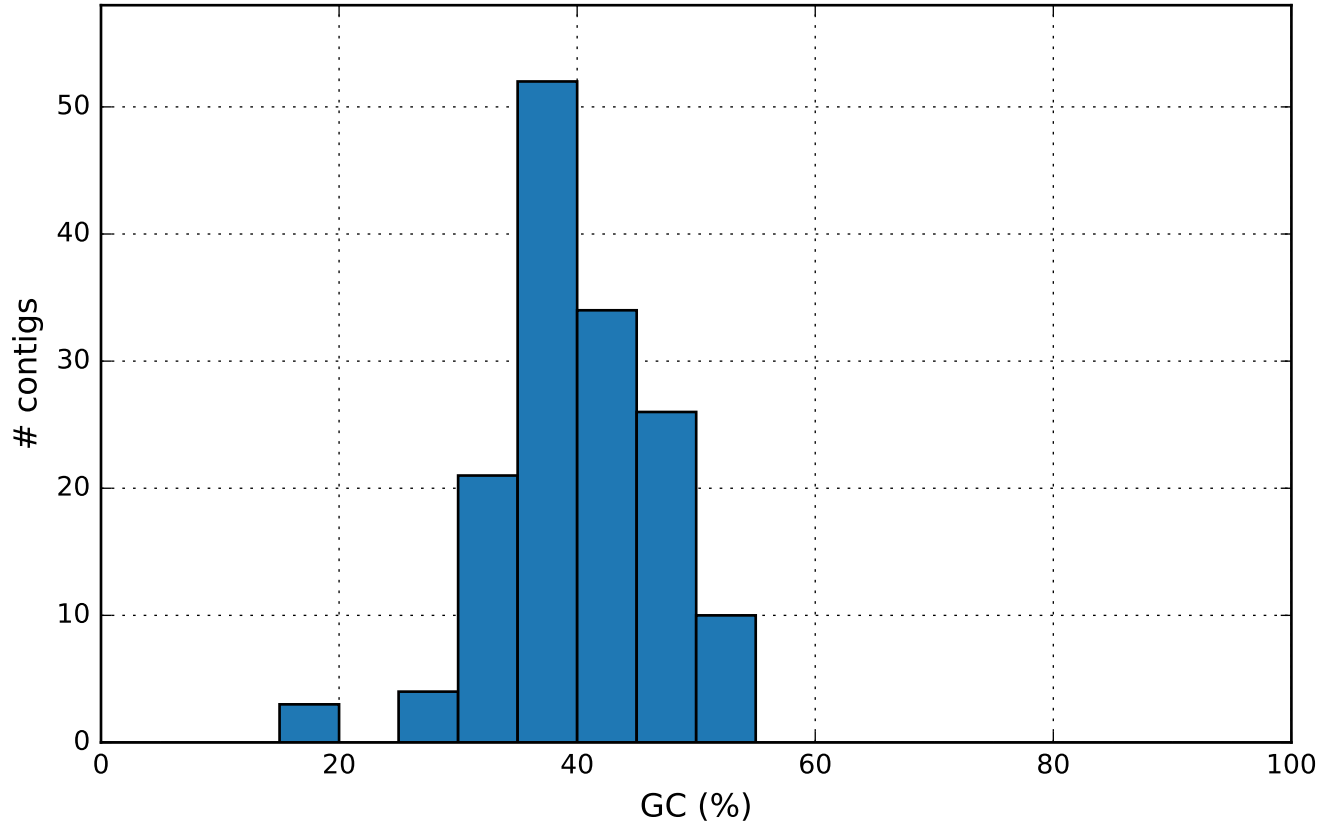






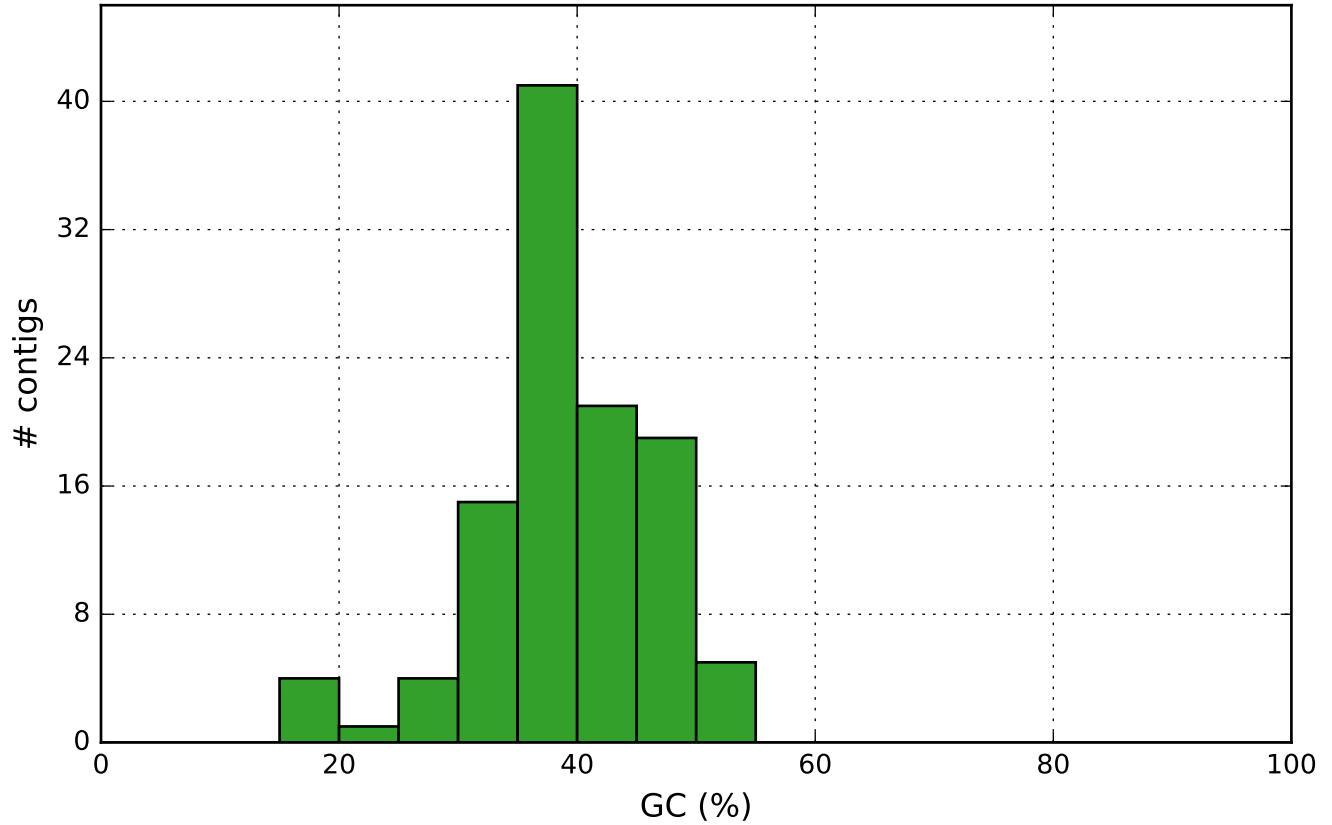


sigA GC content



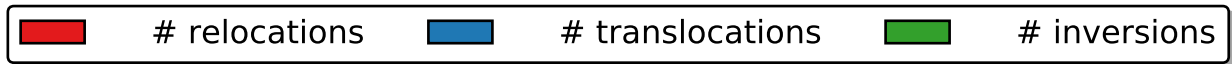
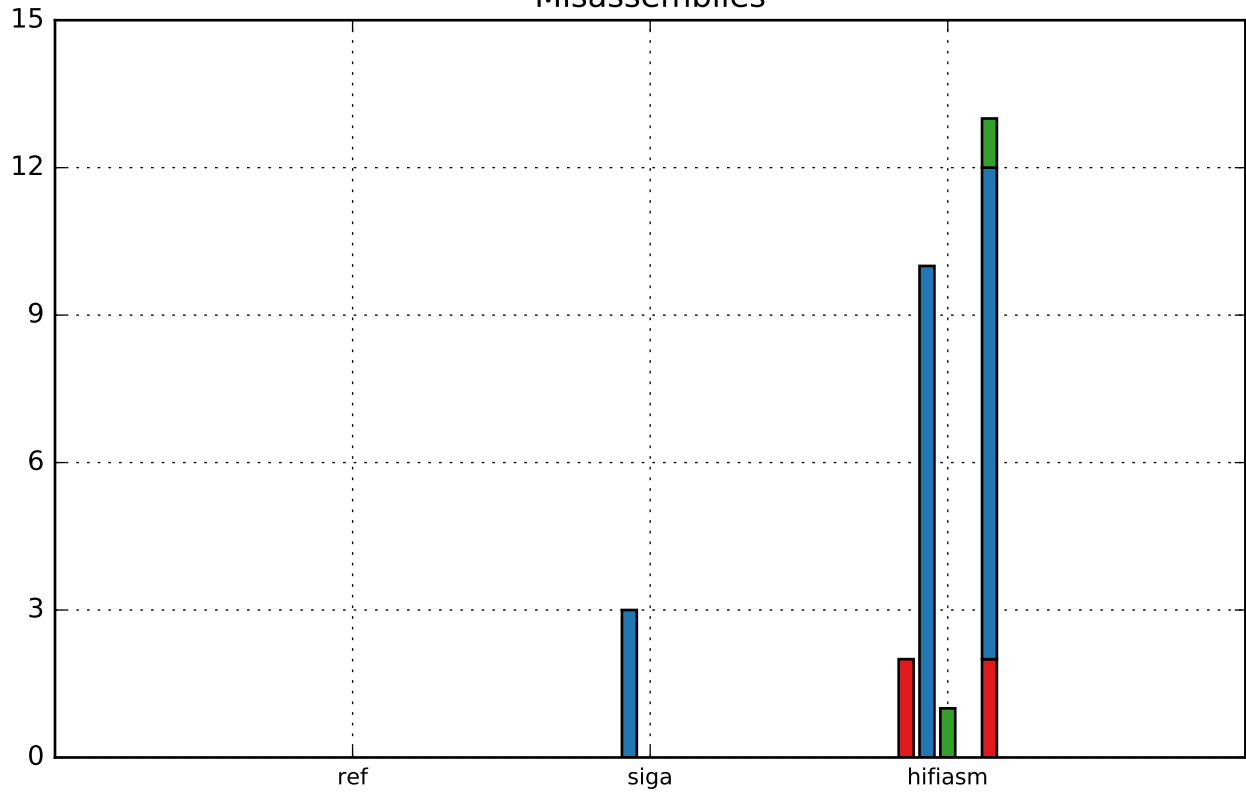
sigA

hifiasm GC content

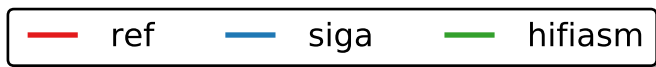
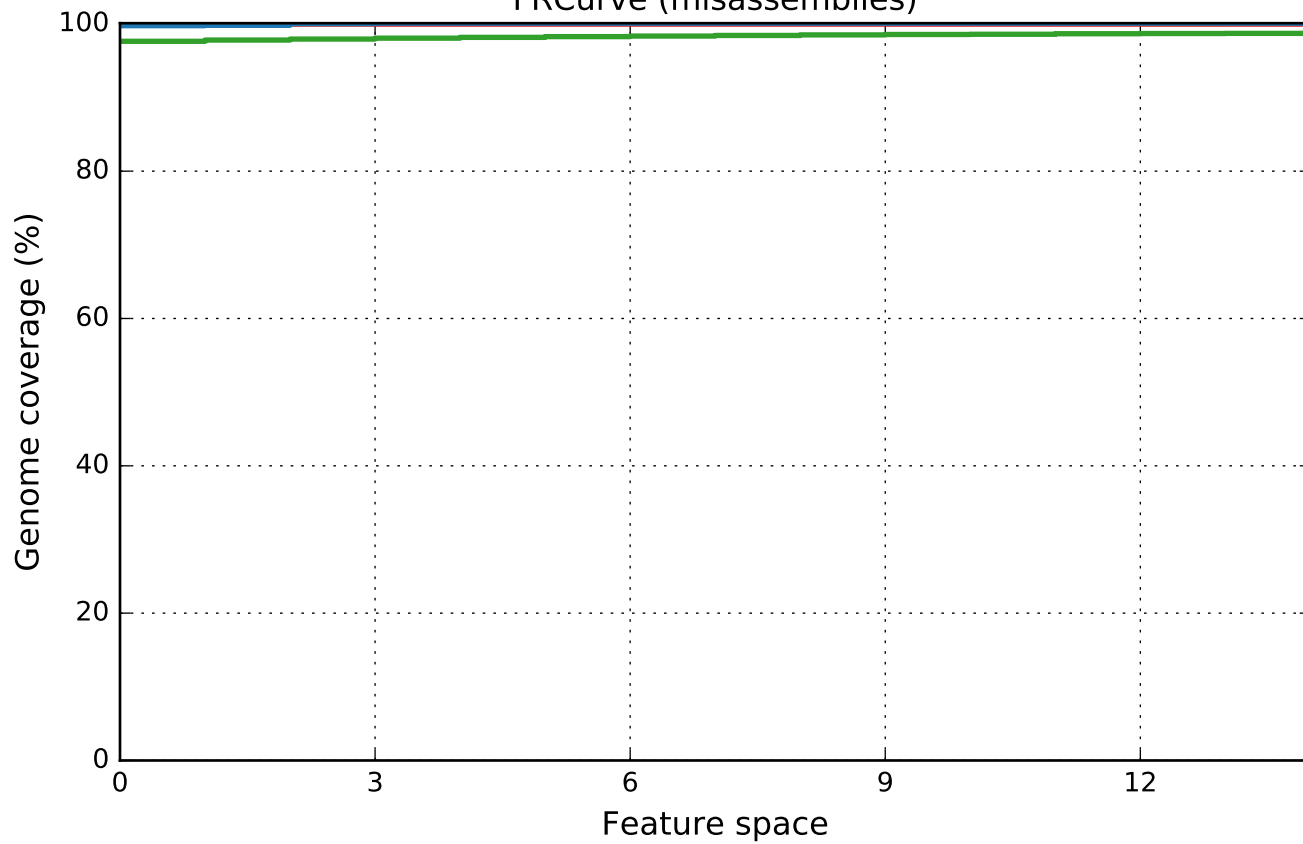


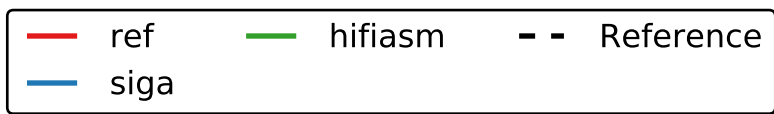
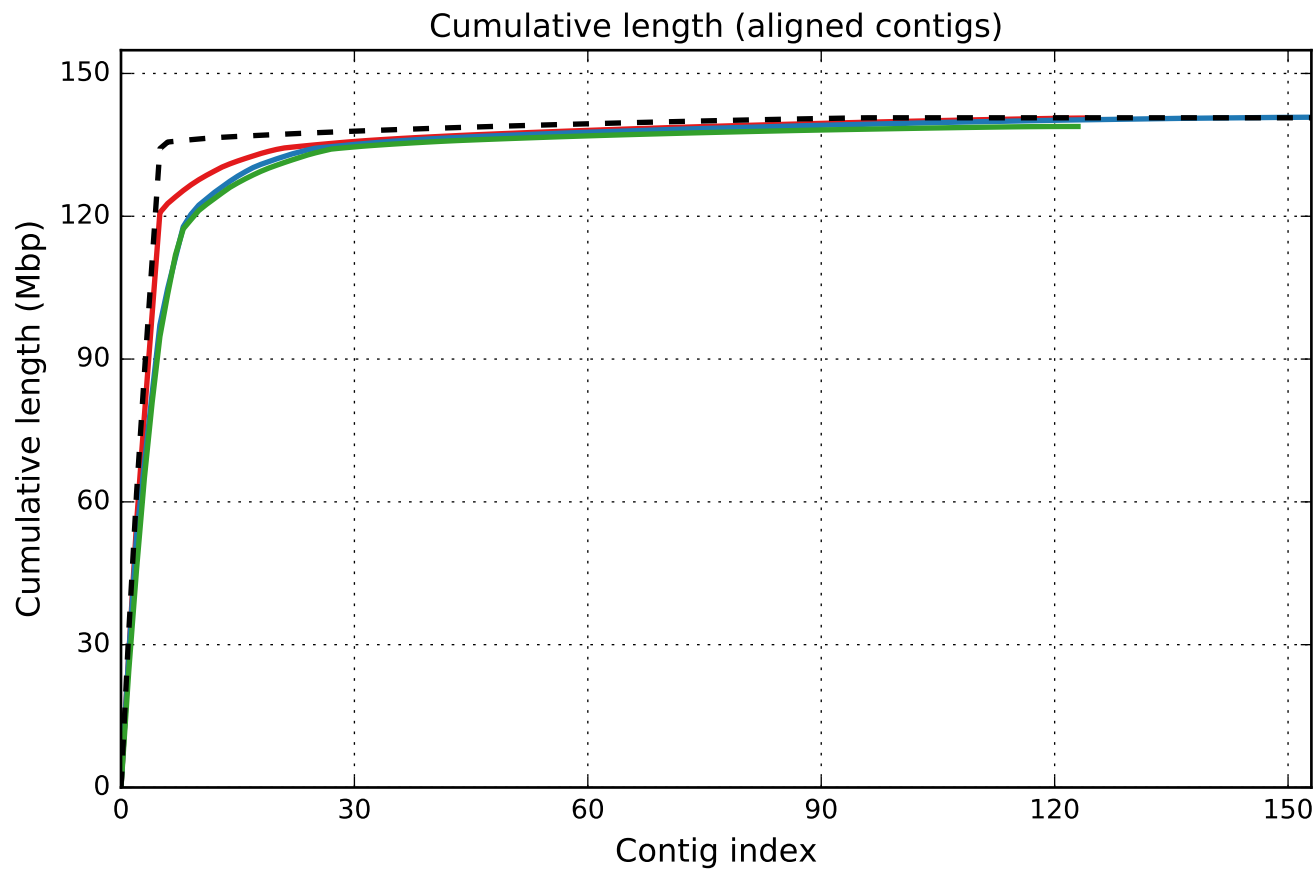
hifiasm

Misassemblies

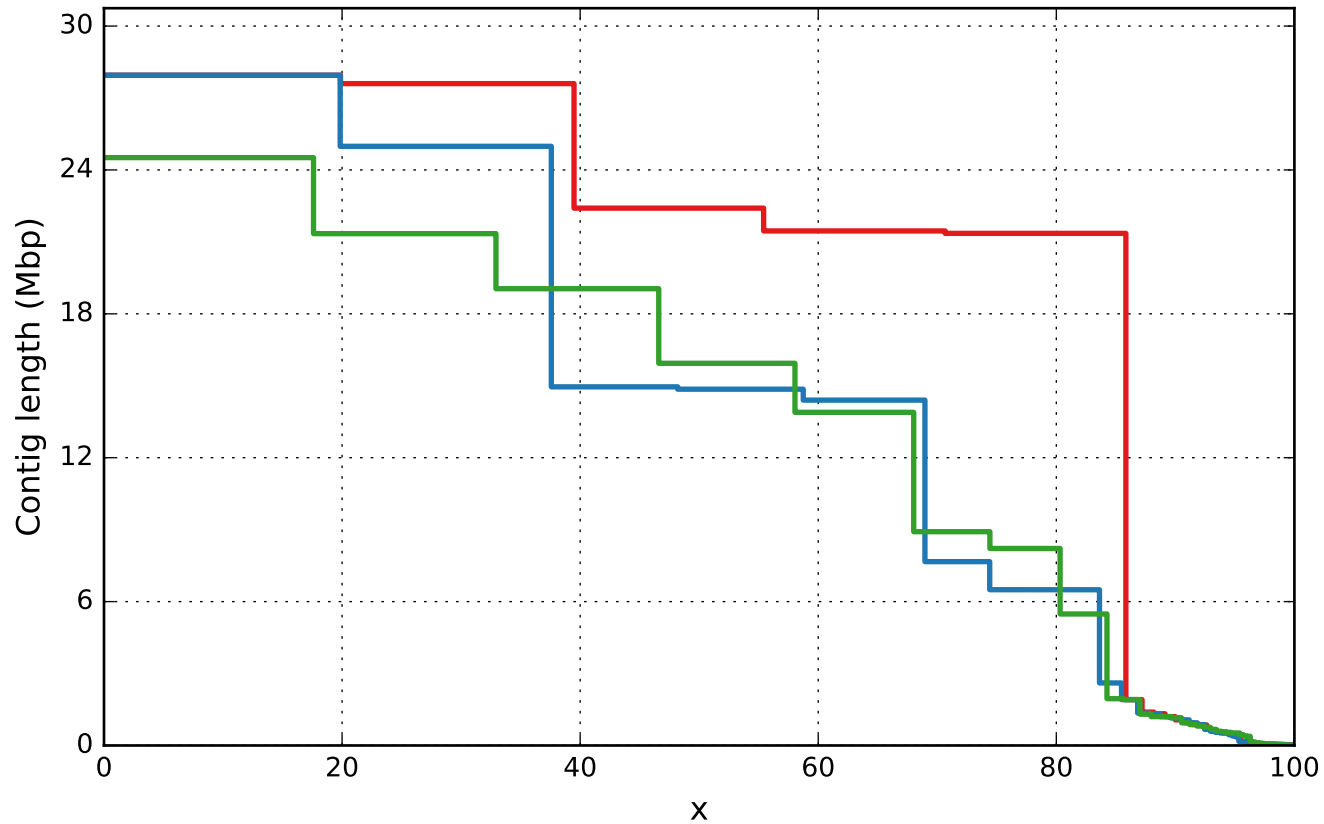


FRCurve (misassemblies)





NAx



# NGAx

