

Report

	hifiasm.asm.bp.p_ctg	canu.contigs	assembly
# contigs (>= 0 bp)	49	96	25
# contigs (>= 1000 bp)	49	96	25
# contigs (>= 5000 bp)	49	96	24
# contigs (>= 10000 bp)	49	85	23
# contigs (>= 25000 bp)	21	18	16
# contigs (>= 50000 bp)	17	17	16
Total length (>= 0 bp)	12730920	13150776	12090146
Total length (>= 1000 bp)	12730920	13150776	12090146
Total length (>= 5000 bp)	12730920	13150776	12085358
Total length (>= 10000 bp)	12730920	13047603	12079771
Total length (>= 25000 bp)	12243602	12111163	11962685
Total length (>= 50000 bp)	12121907	12083485	11962685
# contigs	49	96	25
Largest contig	1506376	1506339	1497679
Total length	12730920	13150776	12090146
Reference length	12157105	12157105	12157105
GC (%)	38.44	37.83	38.29
Reference GC (%)	38.15	38.15	38.15
N50	809047	778969	902771
NG50	809047	808829	902771
N75	579659	564190	681019
NG75	609882	610214	681019
L50	6	7	6
LG50	6	6	6
L75	11	12	10
LG75	10	10	10
# misassemblies	124	114	87
# misassembled contigs	41	38	19
Misassembled contigs length	12606913	12407888	12015914
# local misassemblies	68	356	79
# scaffold gap ext. mis.	0	0	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	1 + 17 part	6 + 21 part	0 + 16 part
Unaligned length	100841	172442	73594
Genome fraction (%)	97.496	97.560	97.063
Duplication ratio	1.066	1.094	1.018
# N's per 100 kbp	0.00	0.00	1.65
# mismatches per 100 kbp	226.72	247.17	221.80
# indels per 100 kbp	27.17	32.28	20.09
Largest alignment	843303	843303	843303
Total aligned length	12617941	12959506	12002412
NA50	273893	247983	284119
NGA50	284119	284116	284119
NA75	137797	127396	165509
NGA75	168184	168185	162182
LA50	13	14	12
LGA50	12	12	12
LA75	29	32	26
LGA75	26	26	27

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

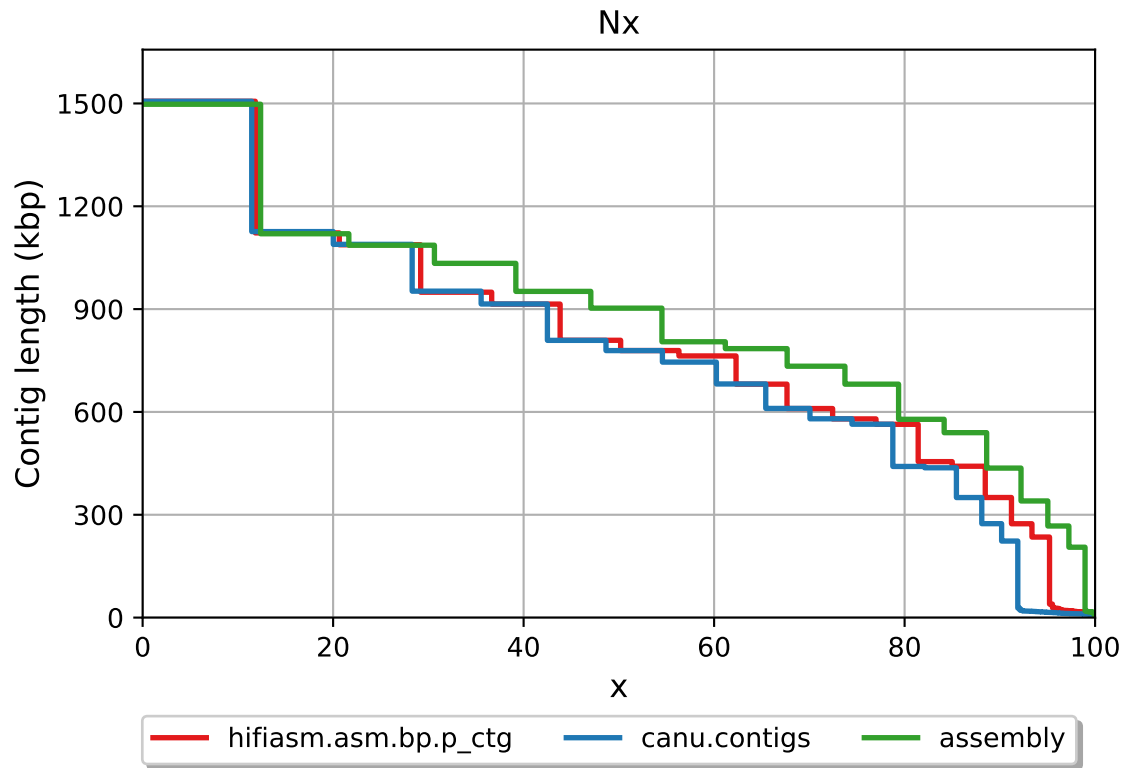
	hifiasm.asm.bp.p_ctg	canu.contigs	assembly
# misassemblies	124	114	87
# contig misassemblies	124	114	87
# c. relocations	59	39	28
# c. translocations	65	72	59
# c. inversions	0	3	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	41	38	19
Misassembled contigs length	12606913	12407888	12015914
# local misassemblies	68	356	79
# scaffold gap ext. mis.	0	0	2
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	26873	29315	26173
# indels	3220	3829	2371
# indels (<= 5 bp)	2728	3092	1998
# indels (> 5 bp)	492	737	373
Indels length	15578	21248	11642

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).

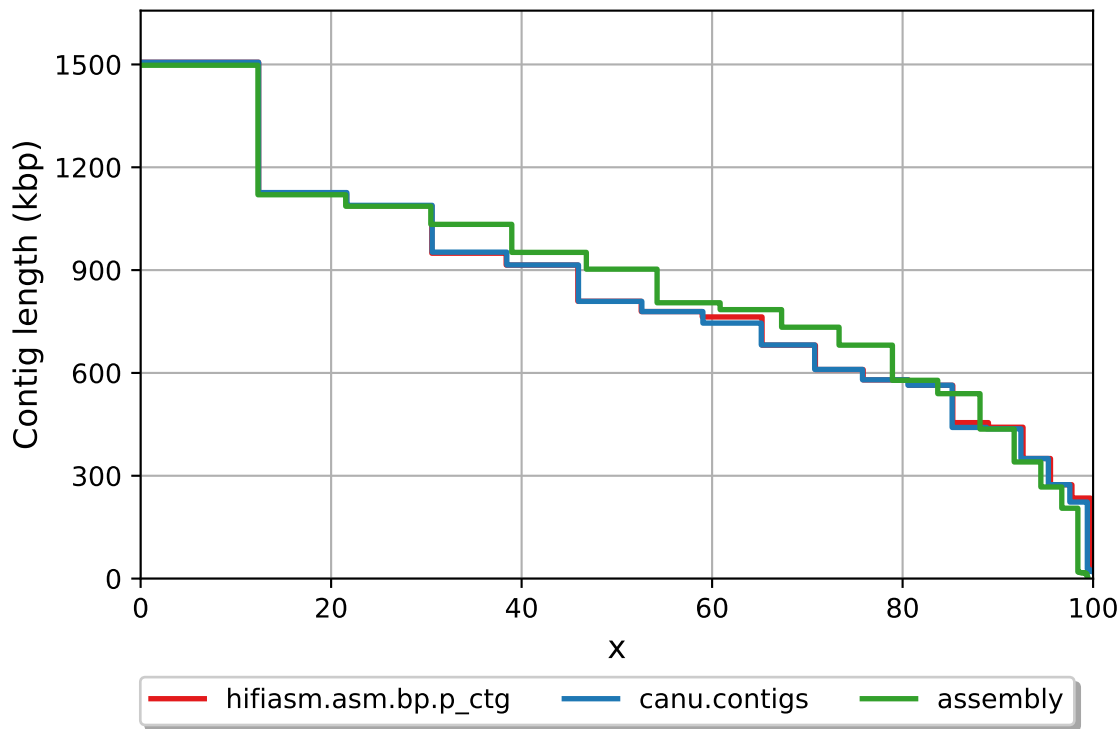
Unaligned report

	hifiasm.asm.bp.p_ctg	canu.contigs	assembly
# fully unaligned contigs	1	6	0
Fully unaligned length	16066	73393	0
# partially unaligned contigs	17	21	16
Partially unaligned length	84775	99049	73594
# N's	0	0	200

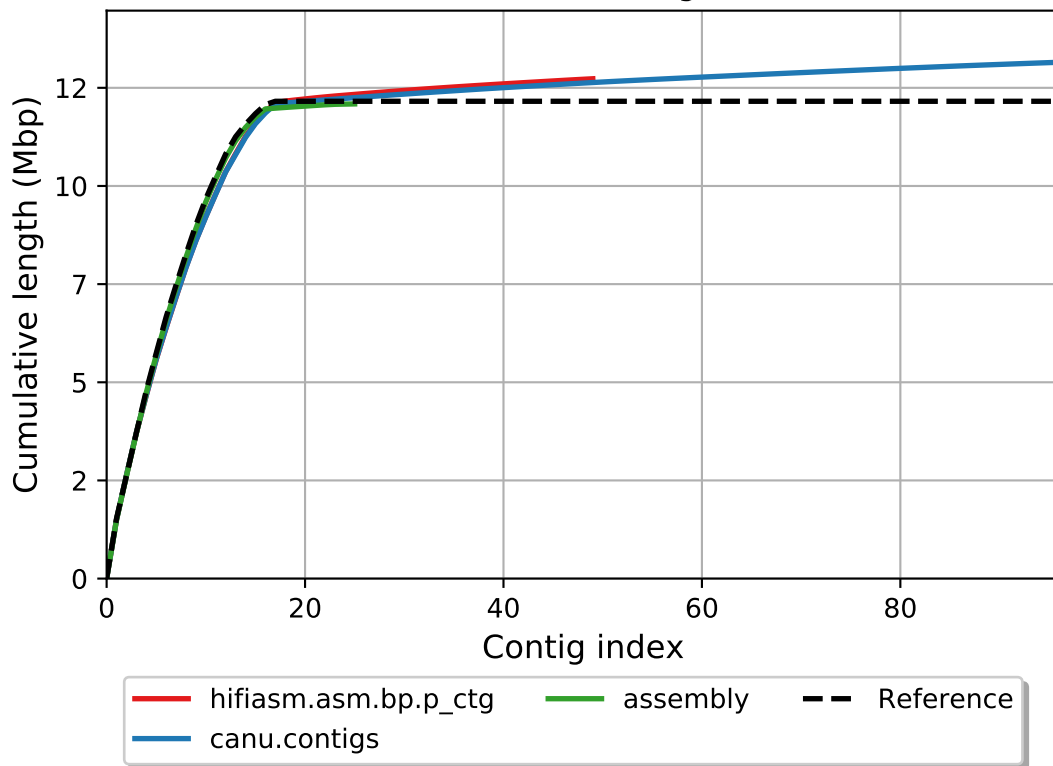
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



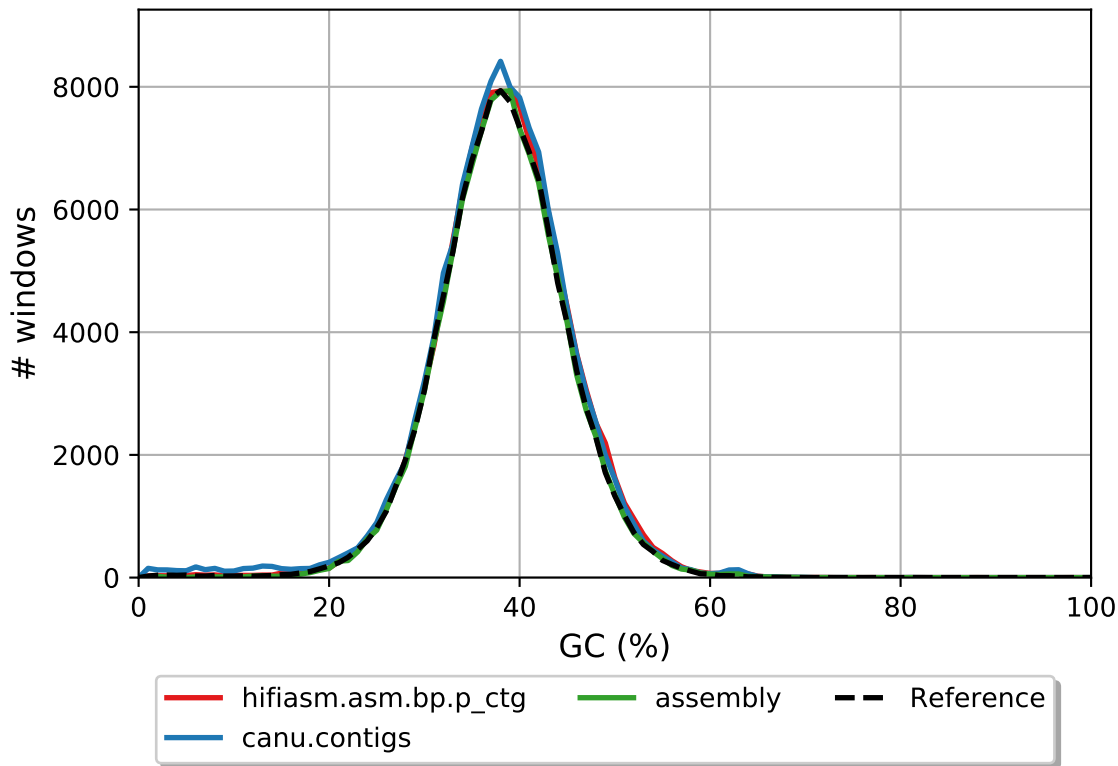
NGx



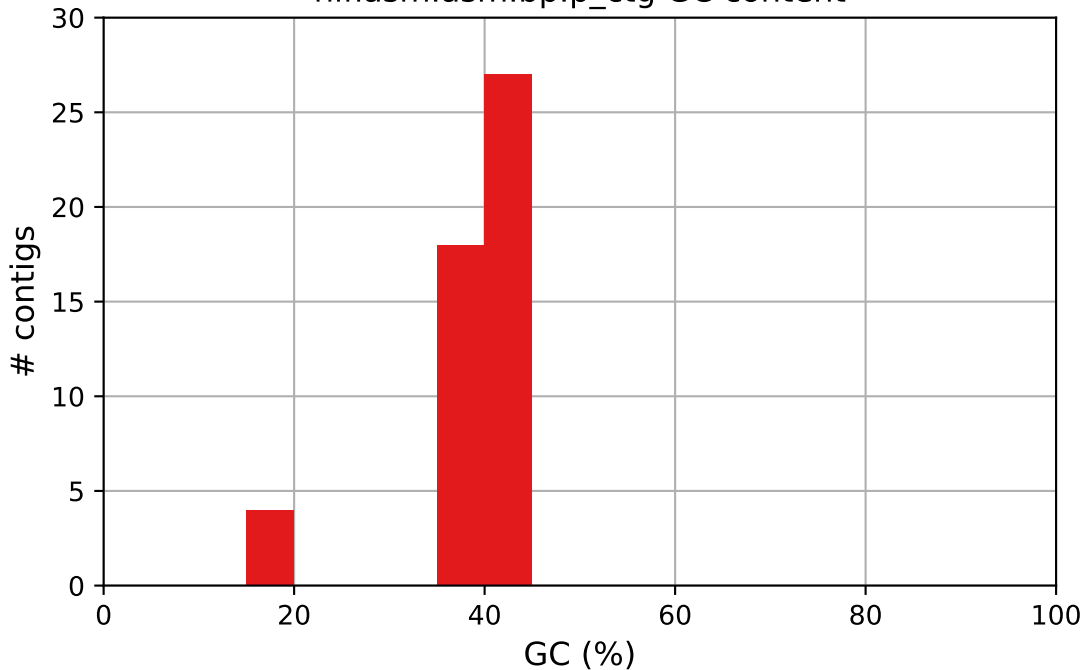
Cumulative length



GC content

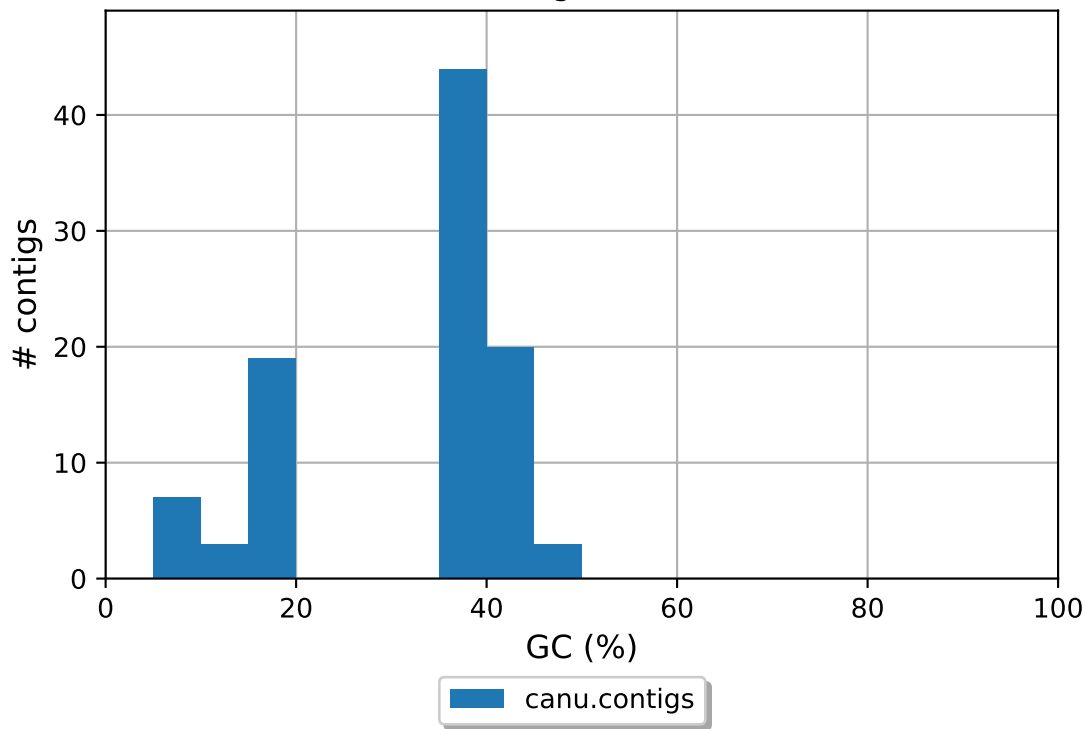


hifi.asm.bp.p_ctg GC content

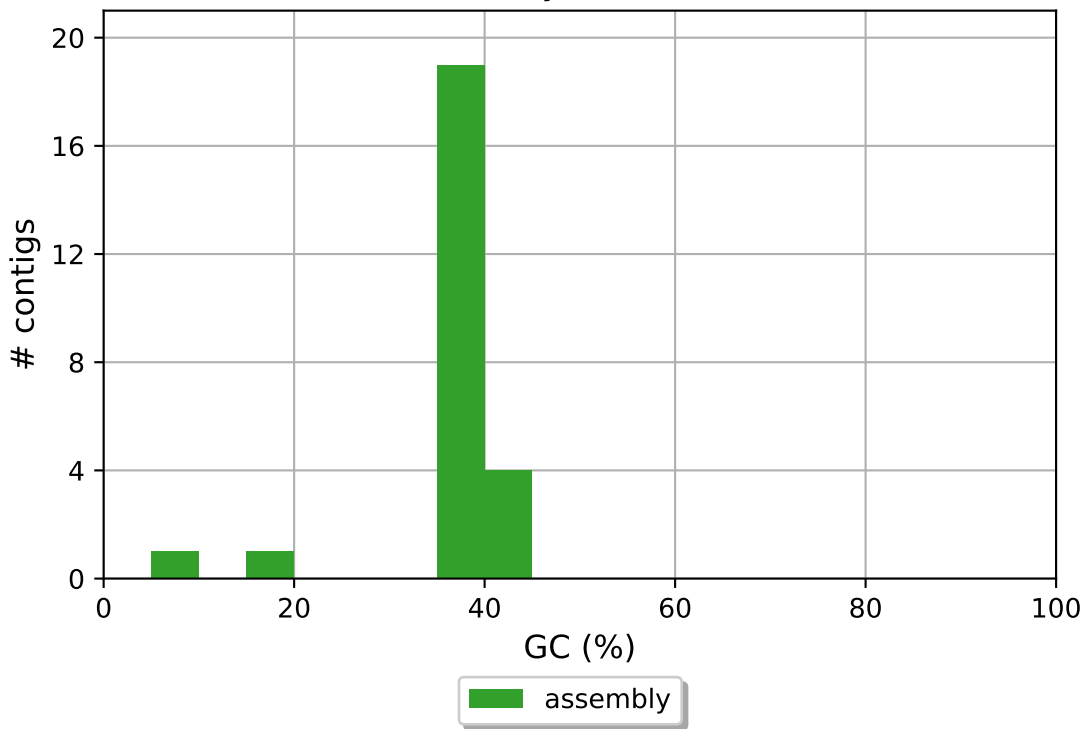


hifi.asm.bp.p_ctg

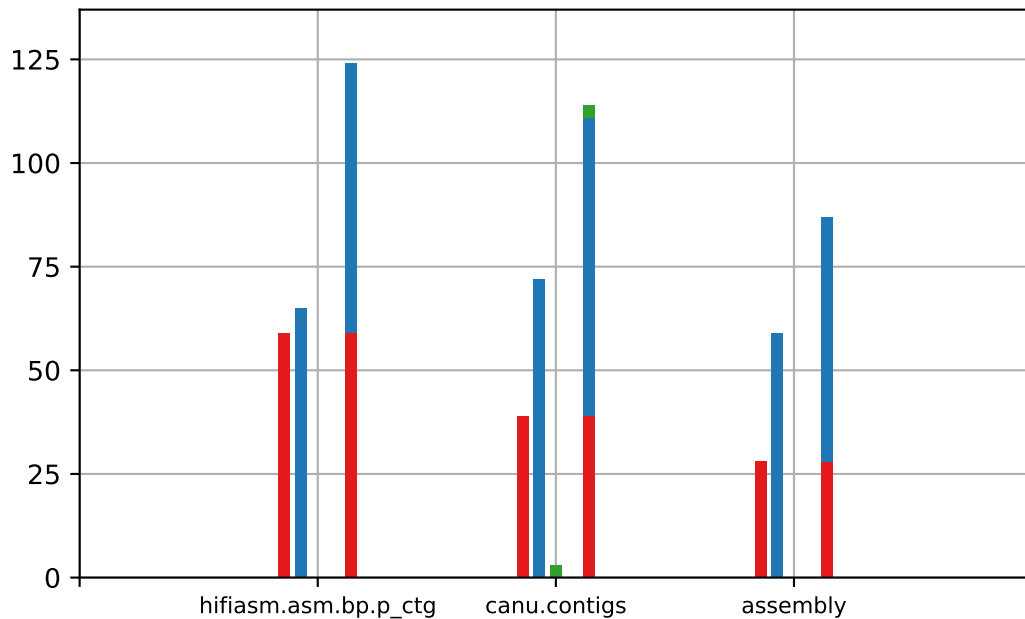
canu.contigs GC content



assembly GC content



Misassemblies



relocations

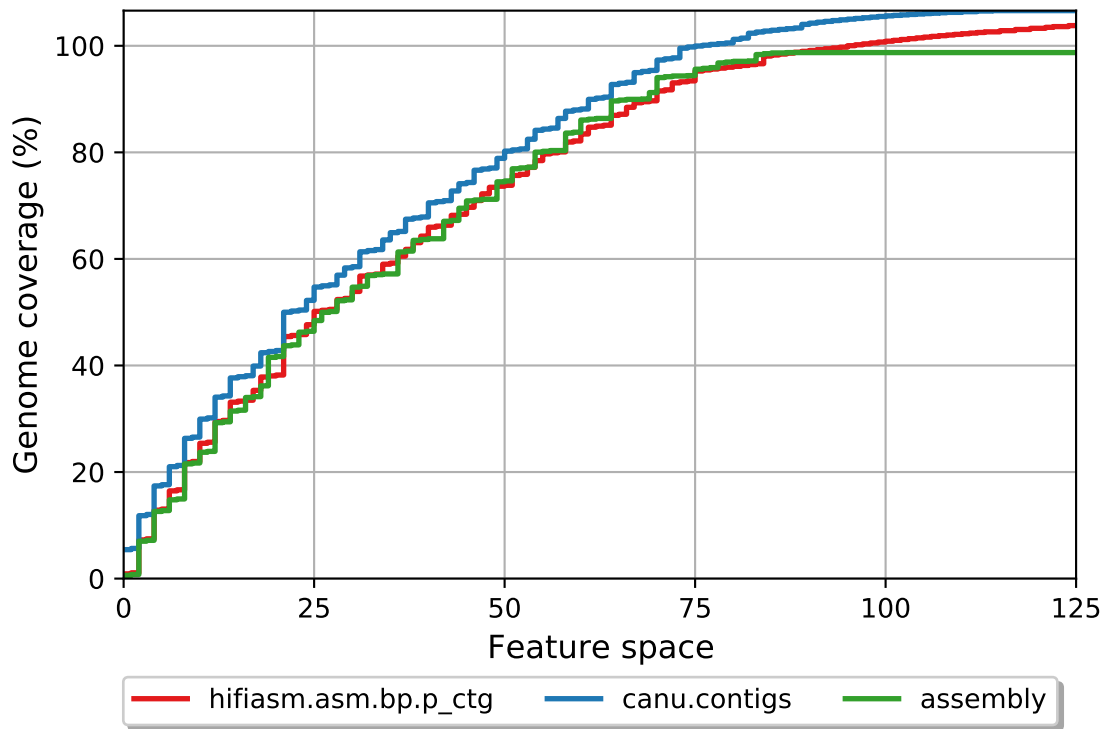


translocations

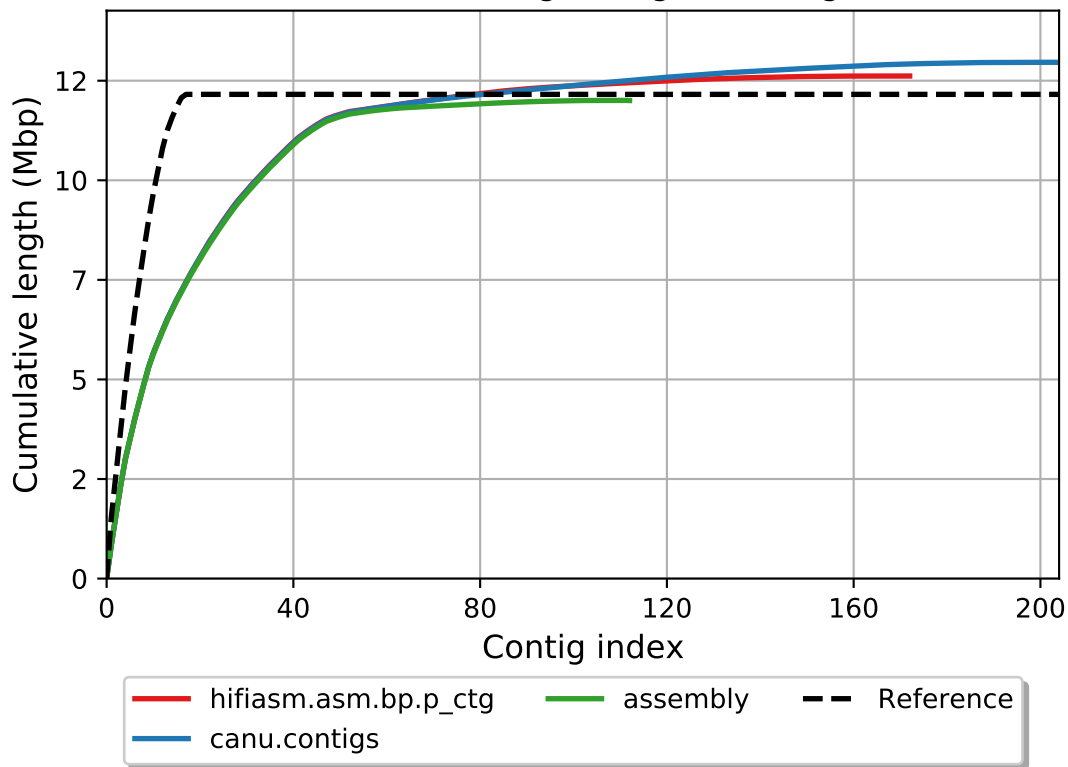


inversions

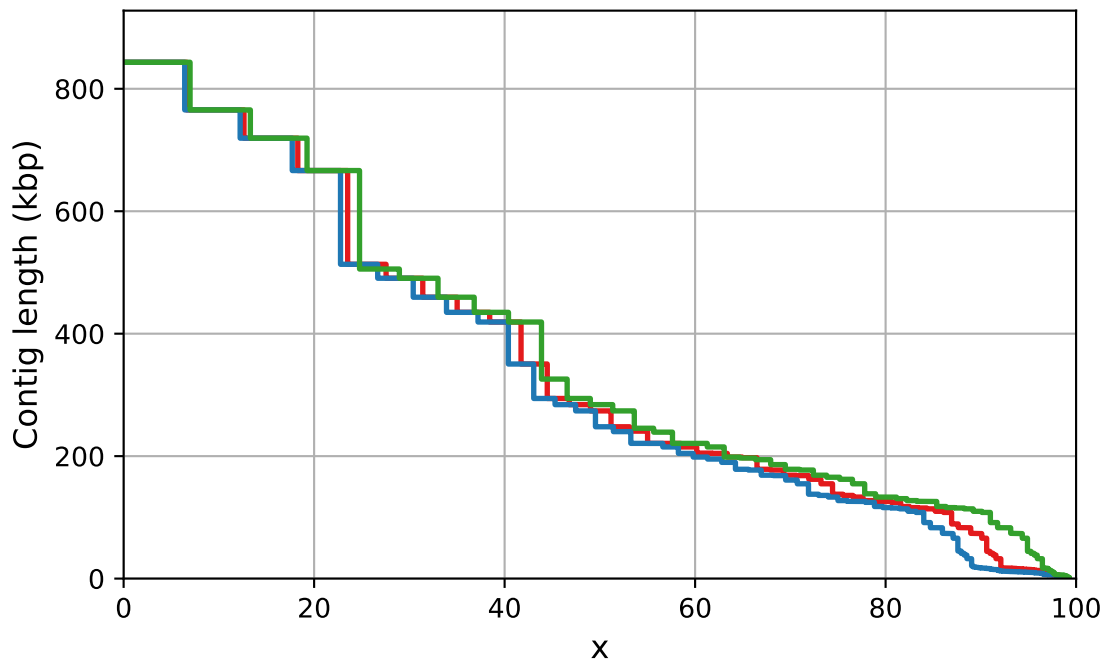
FRCurve (misassemblies)



Cumulative length (aligned contigs)

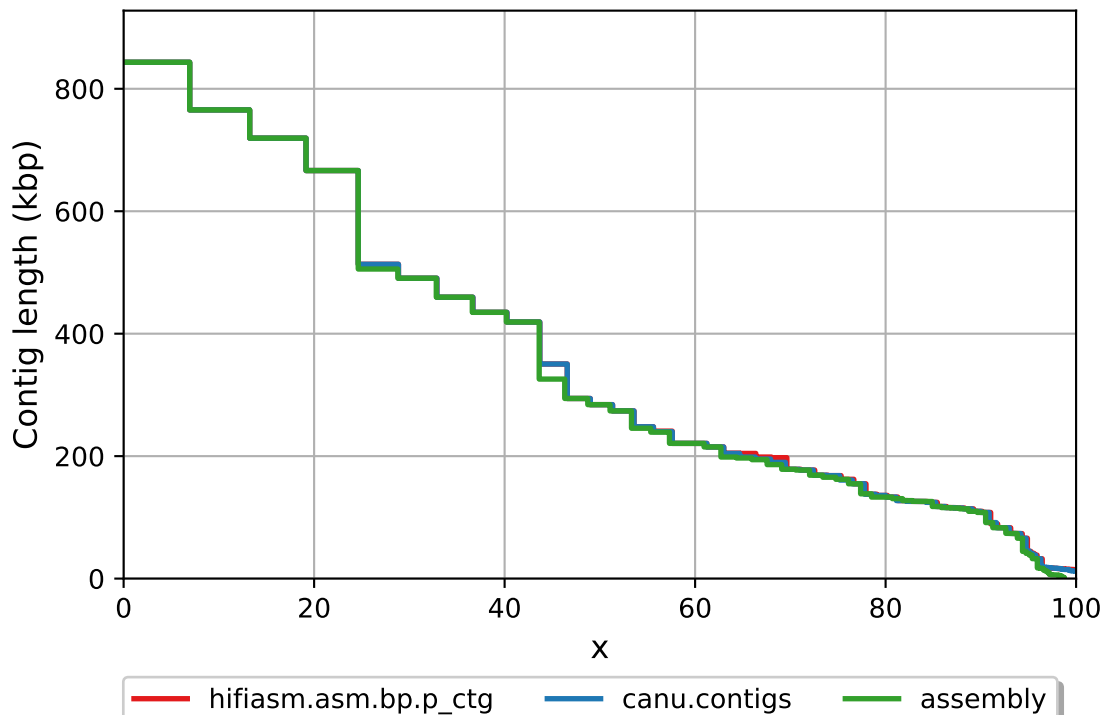


NAx

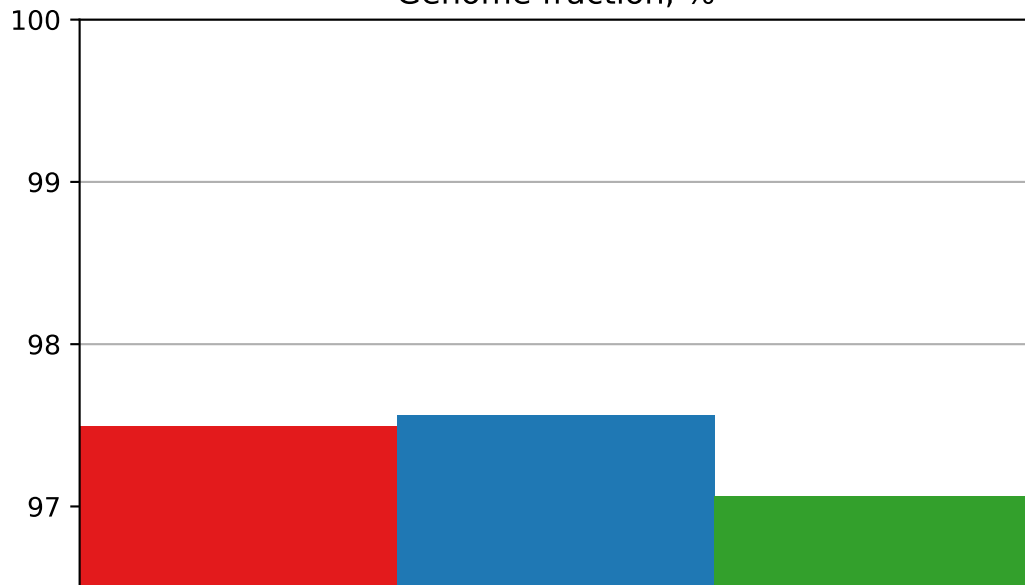


hifiasm.asm.bp.p_ctg canu.contigs assembly

NGAx



Genome fraction, %



hifiasm.asm.bp.p_ctg



canu.contigs



assembly