

Report

	draft_assembly	illumina_contigs	hybrid_contigs
# contigs (>= 0 bp)	6	168	7
# contigs (>= 1000 bp)	6	87	1
# contigs (>= 5000 bp)	6	62	1
# contigs (>= 10000 bp)	6	57	1
# contigs (>= 25000 bp)	1	47	1
# contigs (>= 50000 bp)	1	31	1
Total length (>= 0 bp)	4865333	4567292	4642799
Total length (>= 1000 bp)	4865333	4548539	4641722
Total length (>= 5000 bp)	4865333	4493976	4641722
Total length (>= 10000 bp)	4865333	4458325	4641722
Total length (>= 25000 bp)	4764783	4312386	4641722
Total length (>= 50000 bp)	4764783	3762852	4641722
# contigs	6	97	2
Largest contig	4764783	221601	4641722
Total length	4865333	4555330	4642264
Reference length	4639675	4639675	4639675
GC (%)	50.64	50.74	50.79
Reference GC (%)	50.79	50.79	50.79
N50	4764783	129054	4641722
NG50	4764783	129054	4641722
N75	4764783	60768	4641722
NG75	4764783	59669	4641722
L50	1	14	1
LG50	1	14	1
L75	1	26	1
LG75	1	27	1
# misassemblies	0	0	6
# misassembled contigs	0	0	1
Misassembled contigs length	0	0	4641722
# local misassemblies	0	4	5
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	6	0	0
# unaligned contigs	0 + 6 part	1 + 0 part	1 + 0 part
Unaligned length	4733675	542	542
Genome fraction (%)	2.834	98.142	99.983
Duplication ratio	1.001	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	1226.09	1.03	8.32
# indels per 100 kbp	3.80	0.33	0.86
Largest alignment	170	221546	3023578
Total aligned length	131658	4554465	4638936
NA50	-	129054	3023578
NGA50	-	129054	3023578
NA75	-	60768	572346
NGA75	-	59669	572346
LA50	-	14	1
LGA50	-	14	1
LA75	-	26	2
LGA75	-	27	2

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

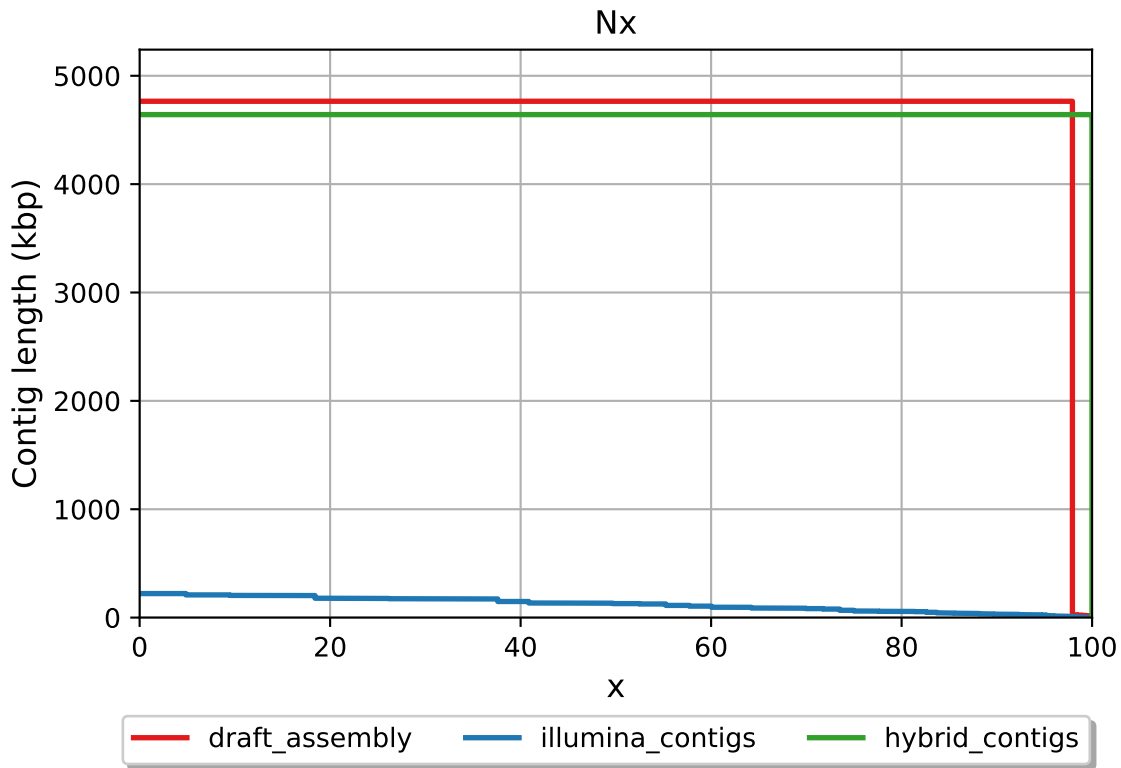
	draft_assembly	illumina_contigs	hybrid_contigs
# misassemblies	0	0	6
# contig misassemblies	0	0	6
# c. relocations	0	0	6
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	0	1
Misassembled contigs length	0	0	4641722
# local misassemblies	0	4	5
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	6	0	0
# mismatches	1612	47	386
# indels	5	15	40
# indels (<= 5 bp)	5	12	37
# indels (> 5 bp)	0	3	3
Indels length	5	77	183

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).

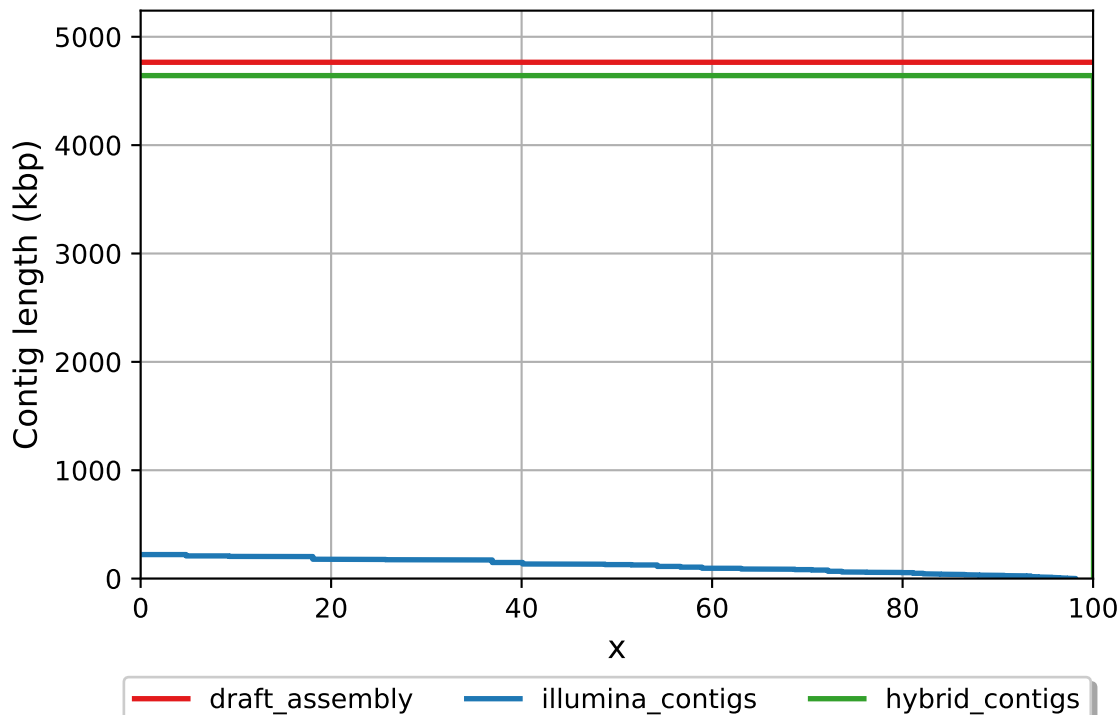
Unaligned report

	draft_assembly	illumina_contigs	hybrid_contigs
# fully unaligned contigs	0	1	1
Fully unaligned length	0	542	542
# partially unaligned contigs	6	0	0
Partially unaligned length	4733675	0	0
# N's	0	0	0

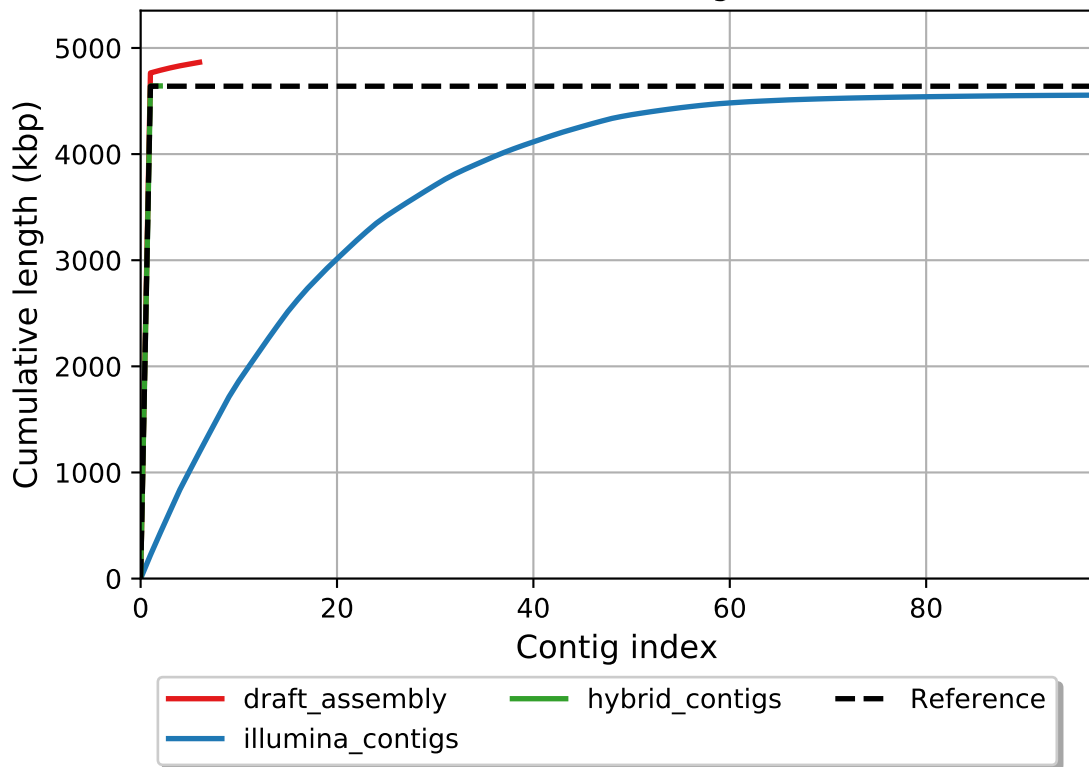
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



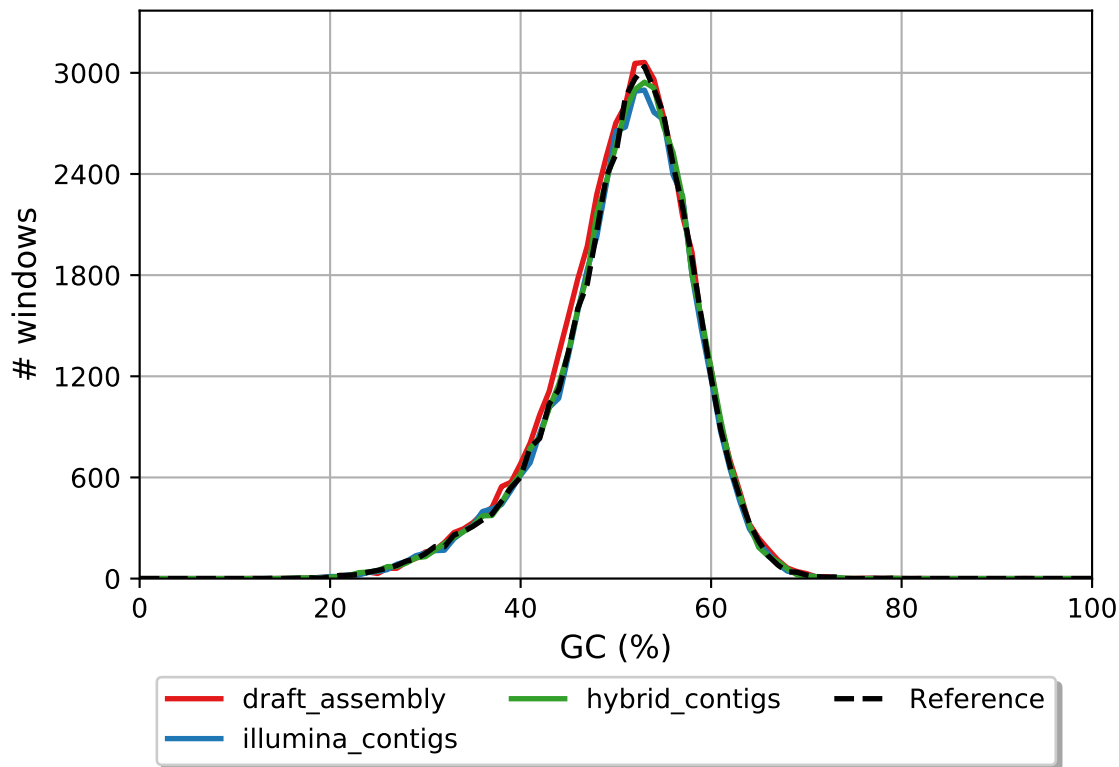
NGx



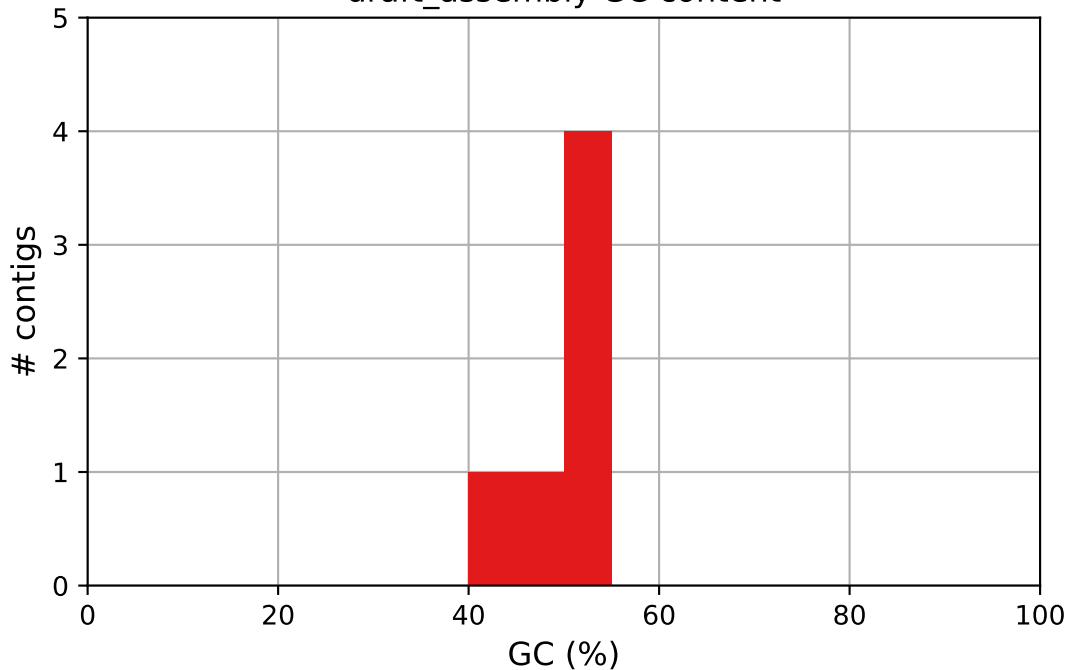
Cumulative length



GC content

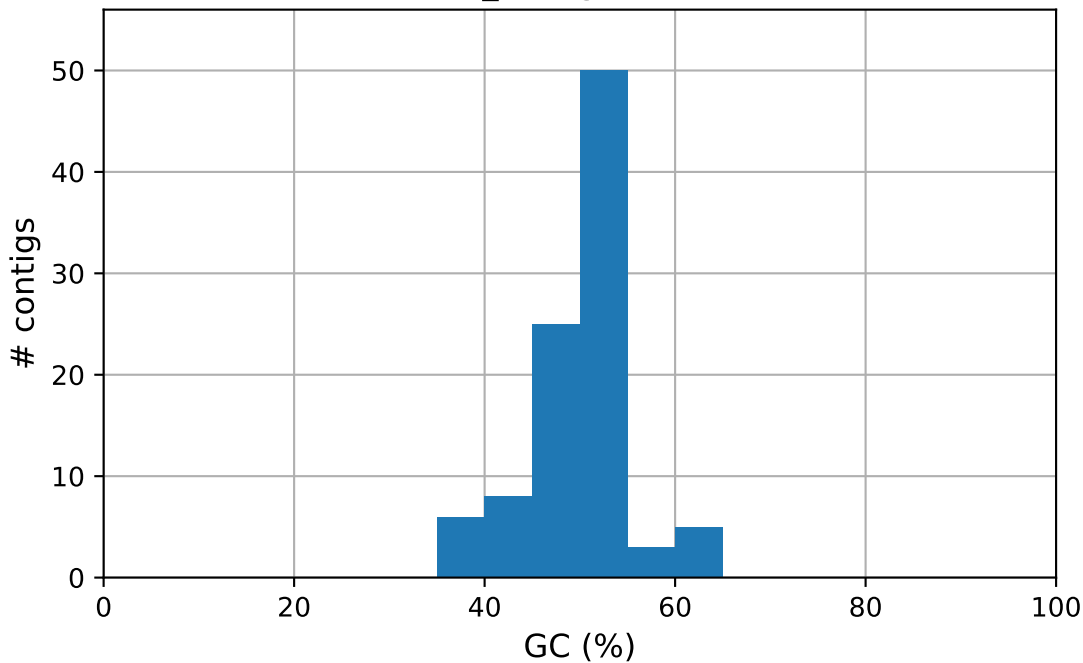


draft_assembly GC content



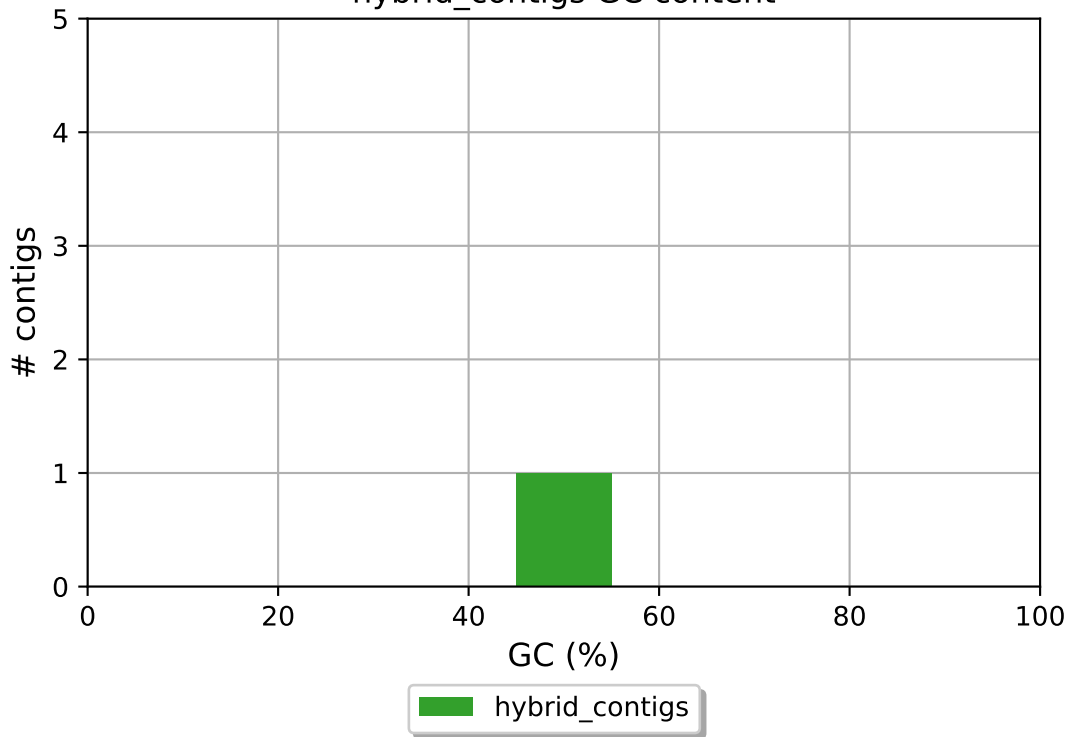
draft_assembly

illumina_contigs GC content

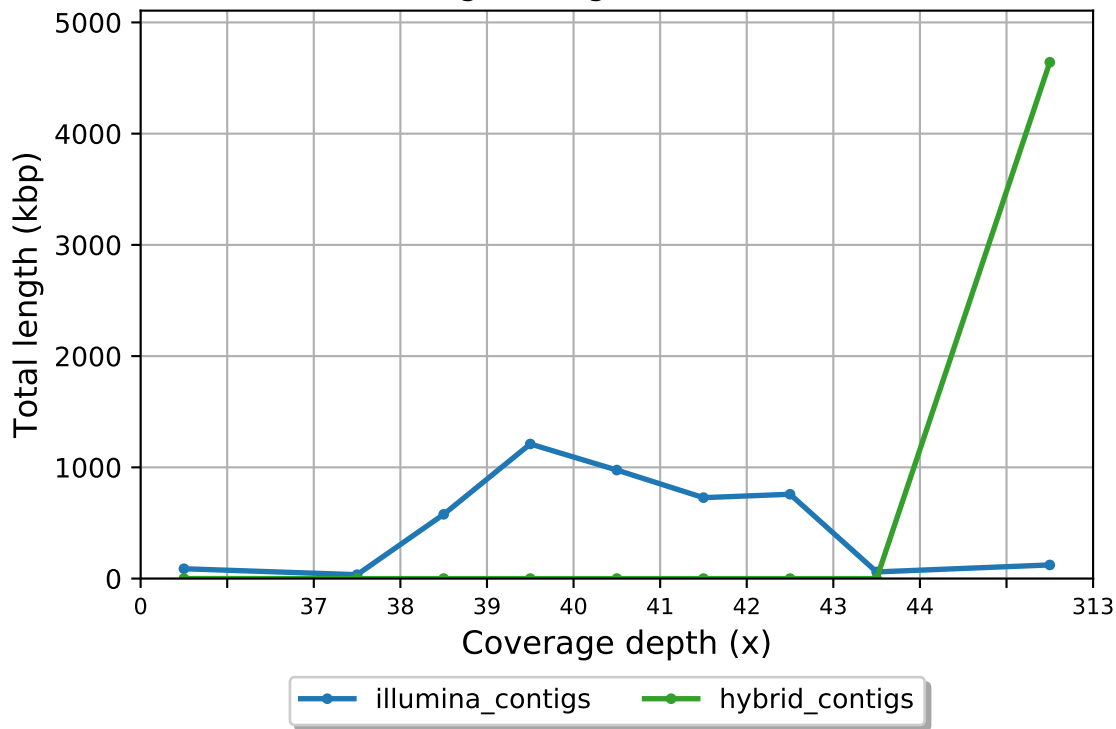


illumina_contigs

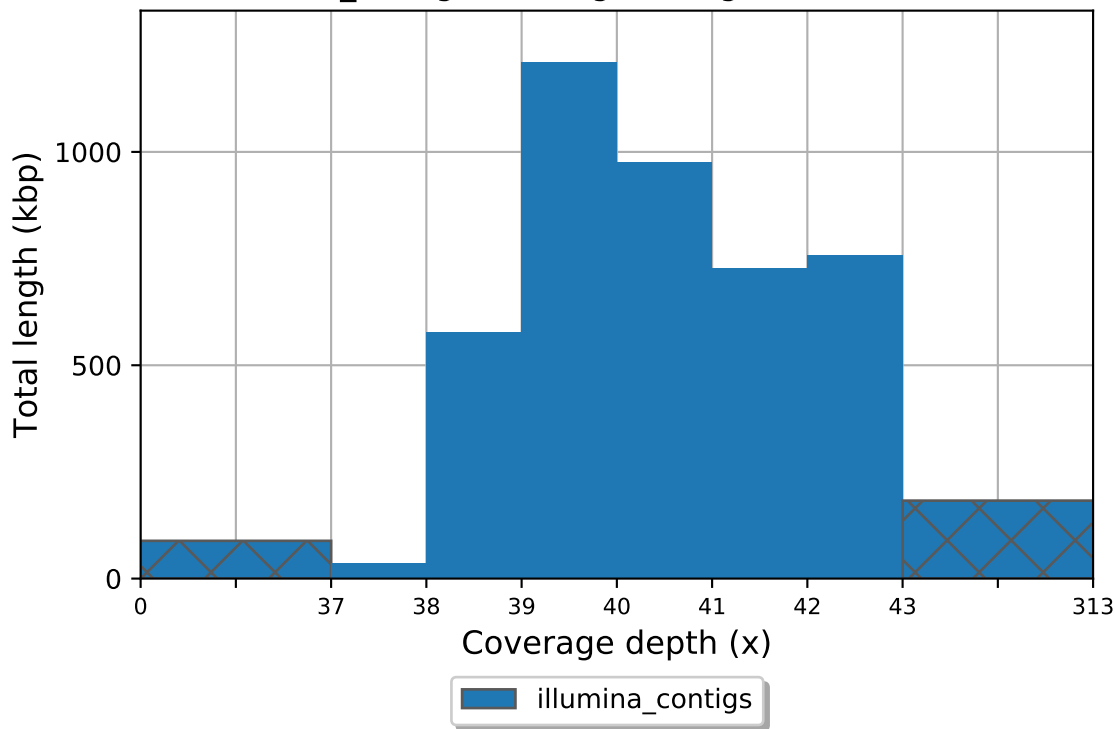
hybrid_contigs GC content



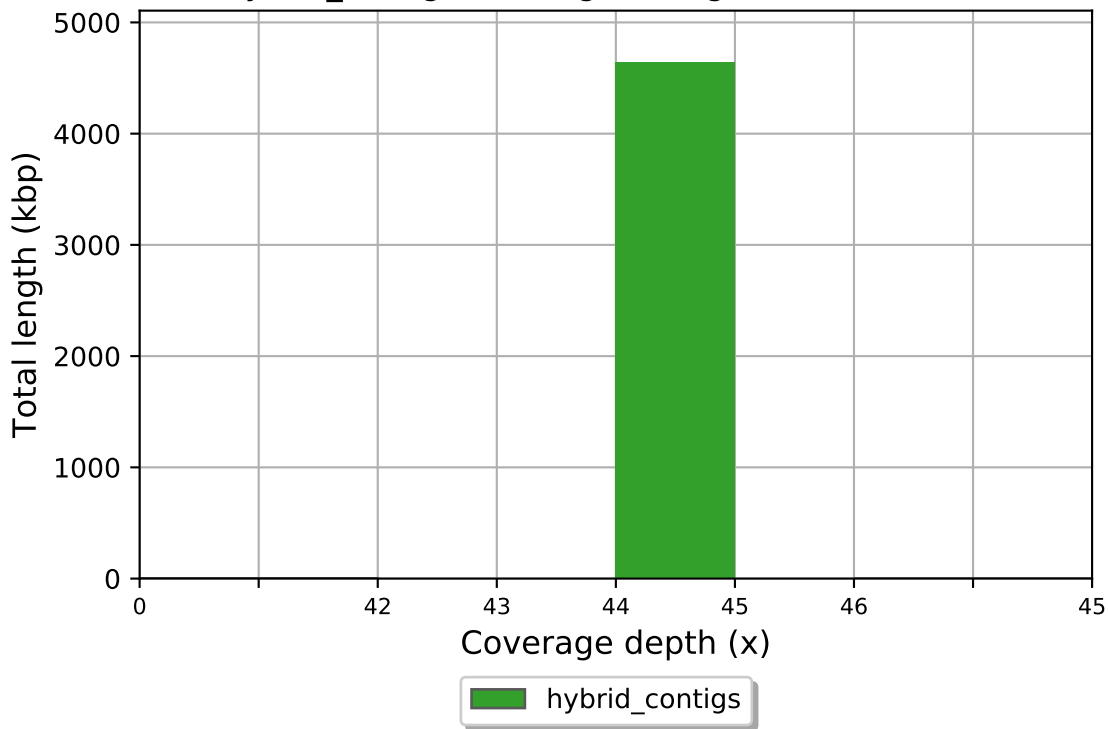
Coverage histogram (bin size: 1x)



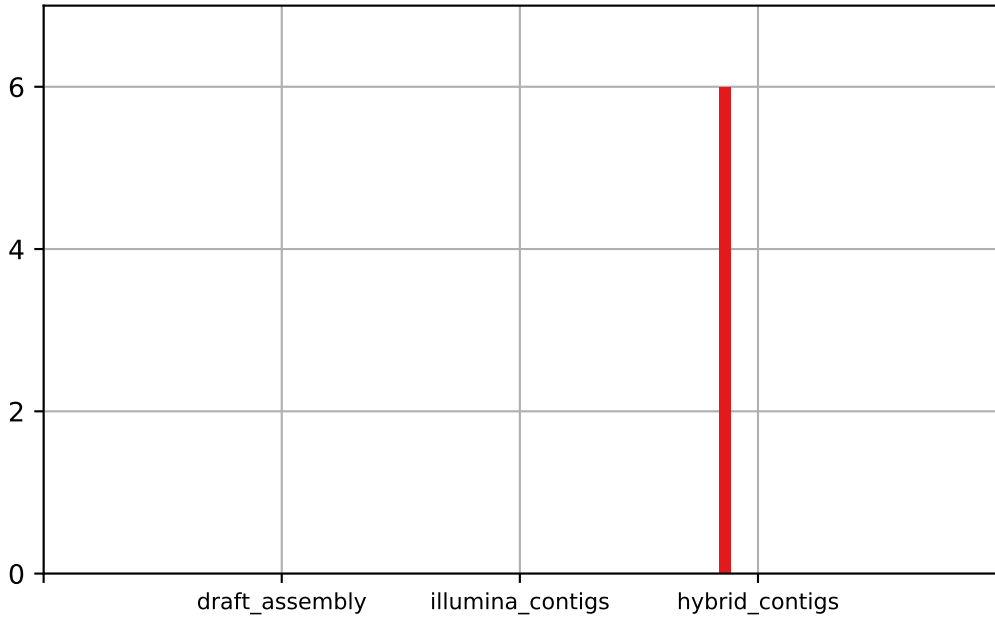
illumina_contigs coverage histogram (bin size: 1x)



hybrid_contigs coverage histogram (bin size: 1x)

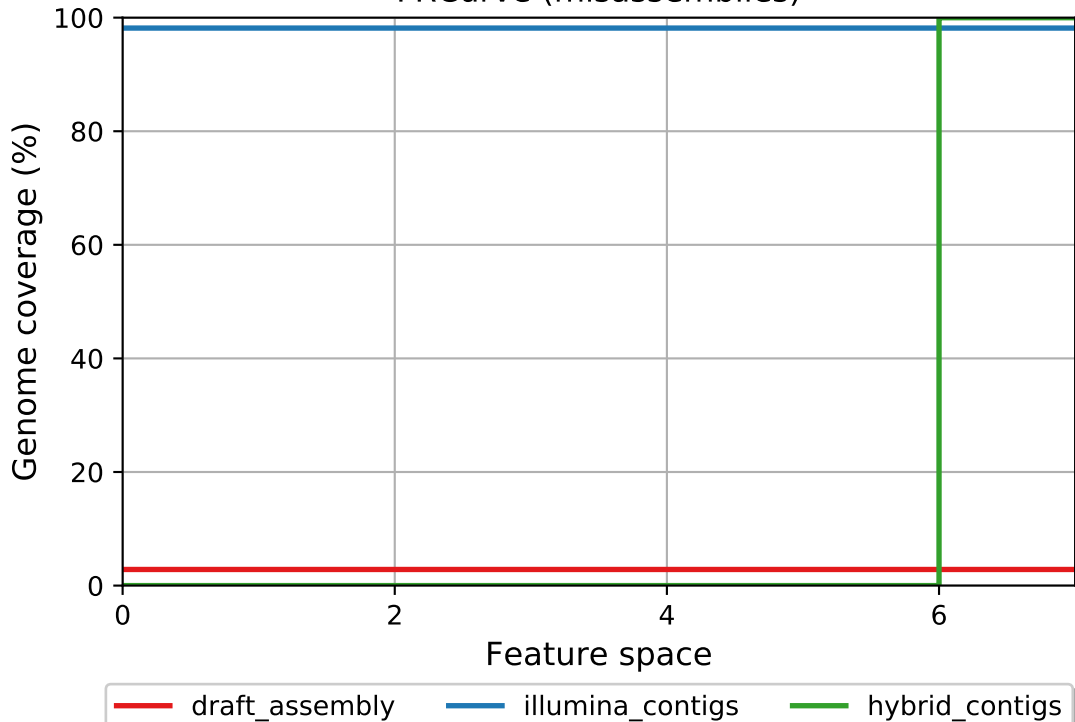


Misassemblies

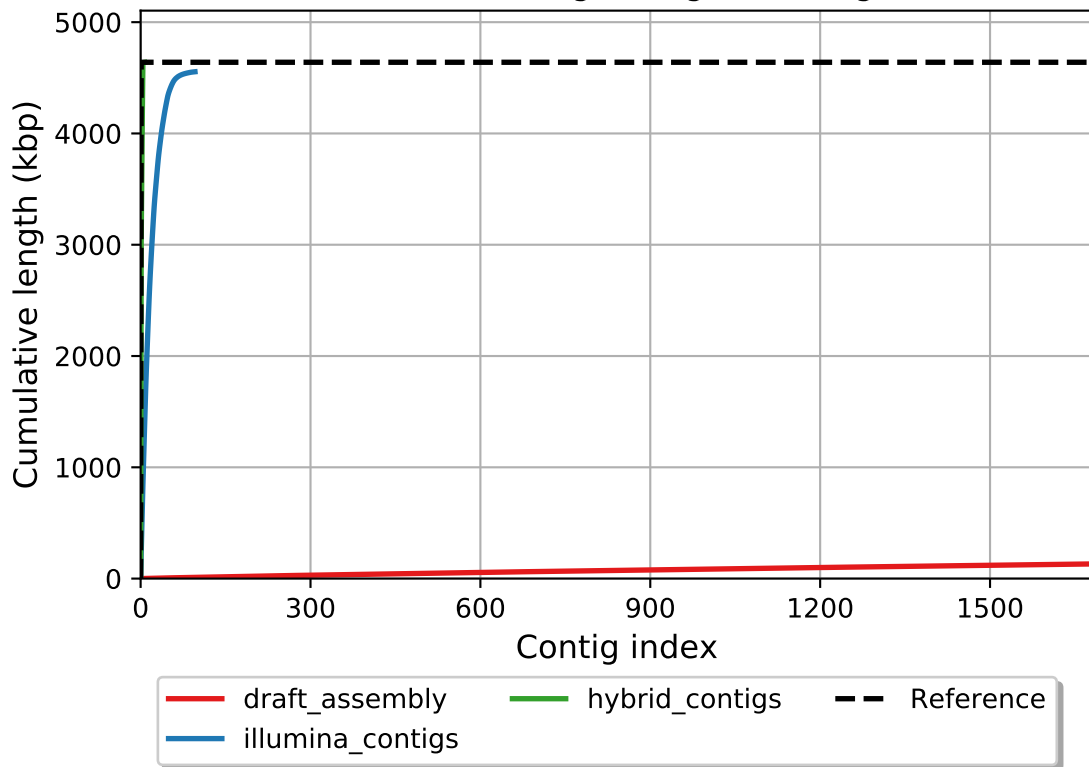


 # relocations

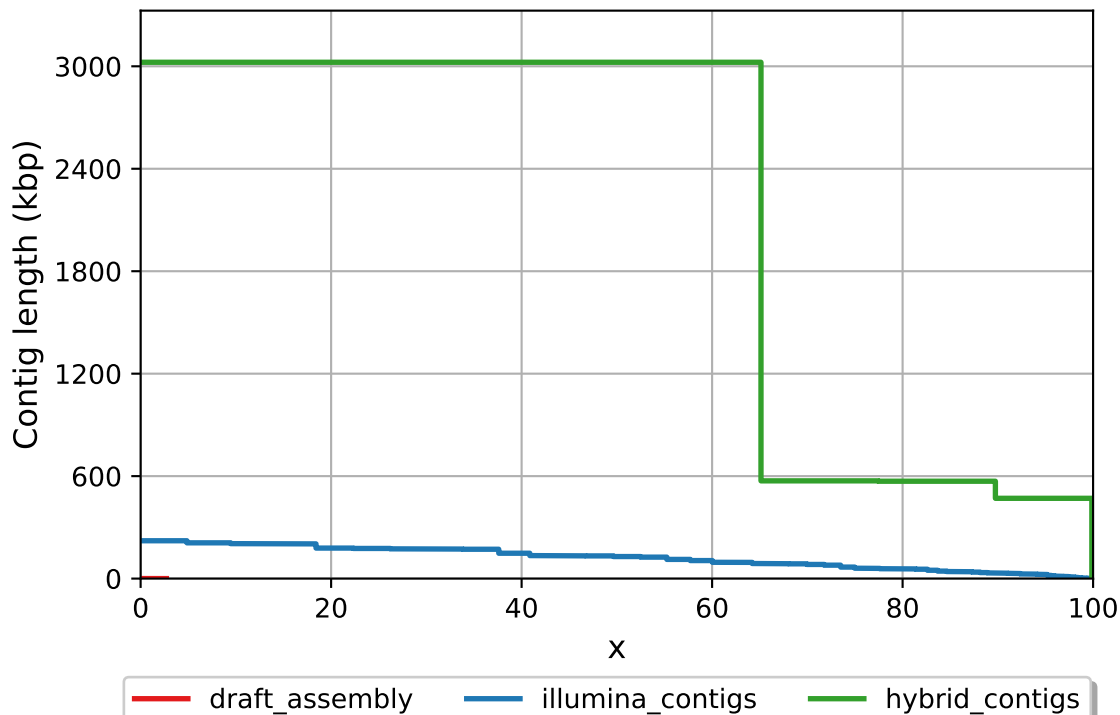
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

