

Report

	dbg_no_error_ont_hq_50x.fastq_45	dbg_no_error_reads_hiseq_5k.fastq_45	dbg_ont_hq_50x.fastq_45	dbg_reads_hiseq_5k.fastq_45	rem_min_no_error_ont_hq_50x.fastq_45	rem_min_ont_hq_50x.fastq_45	rem_min_reads_hiseq_5k.fastq_45	uni_no_error_ont_hq_50x.fastq_45	uni_no_error_reads_hiseq_5k.fastq_45	uni_ont_hq_50x.fastq_45	uni_reads_hiseq_5k.fastq_45
# contigs (>= 0 bp)	1	1	1	1	1	1	1	1	3	20027	1184
# contigs (>= 1000 bp)	1	1	1	1	1	1	0	1	3	23	0
# contigs (>= 5000 bp)	1	0	1	1	1	1	0	1	3	0	0
# contigs (>= 10000 bp)	1	0	1	1	1	1	0	1	1	0	0
# contigs (>= 25000 bp)	1	0	1	0	1	0	0	1	0	0	0
# contigs (>= 50000 bp)	1	0	1	0	0	0	0	0	0	0	0
Total length (>= 0 bp)	459901	3498	625434	22279	29400	14328	731	29748	29553	1646469	97088
Total length (>= 1000 bp)	459901	3498	625434	22279	29400	14328	0	29748	29553	43999	0
Total length (>= 5000 bp)	459901	0	625434	22279	29400	14328	0	29748	29553	0	0
Total length (>= 10000 bp)	459901	0	625434	22279	29400	14328	0	29748	12290	0	0
Total length (>= 25000 bp)	459901	0	625434	0	29400	0	0	29748	0	0	0
Total length (>= 50000 bp)	459901	0	625434	0	0	0	0	0	0	0	0
# contigs	1	1	1	1	1	1	1	1	3	108	1
Largest contig	459901	3498	625434	22279	29400	14328	731	29748	12290	4280	642
Total length	459901	3498	625434	22279	29400	14328	731	29748	29553	100764	642
Reference length	30119	30119	30119	30119	30119	30119	30119	30119	30119	30119	30119
GC (%)	39.89	46.60	40.70	43.09	41.16	40.92	41.59	41.27	41.27	41.06	48.75
Reference GC (%)	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24
N50	459901	3498	625434	22279	29400	14328	731	29748	8725	933	642
NG50	459901	-	625434	22279	29400	-	-	29748	8725	3342	-
N90	459901	3498	625434	22279	29400	14328	731	29748	8538	529	642
NG90	459901	-	625434	-	29400	-	-	29748	8538	1612	-
auN	459901.0	3498.0	625434.0	22279.0	29400.0	14328.0	731.0	29748.0	10153.5	1427.5	642.0
auNG	7022442.0	406.3	12987406.2	16479.8	28698.2	6816.0	17.7	29381.6	9962.7	4775.7	13.7
L50	1	1	1	1	1	1	1	1	2	30	1
LG50	1	-	1	1	1	-	-	1	2	4	-
L90	1	1	1	1	1	1	1	1	3	89	1
LG90	1	-	1	-	1	-	-	1	3	11	-
# misassemblies	-	-	0	-	0	0	0	0	0	0	0
# misassembled contigs	-	-	0	-	0	0	0	0	0	0	0
Misassembled contigs length	-	-	0	-	0	0	0	0	0	0	0
# local misassemblies	-	-	0	-	0	0	0	0	0	0	0
# scaffold gap ext. mis.	-	-	0	-	0	0	0	0	0	0	0
# scaffold gap loc. mis.	-	-	0	-	0	0	0	0	0	0	0
# unaligned mis. contigs	-	-	1	-	0	0	0	0	0	0	0
# unaligned contigs	1 + 0 part	1 + 0 part	0 + 1 part	1 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	107 + 0 part	0 + 0 part
Unaligned length	459901	3498	608223	22279	0	0	0	0	0	100054	0
Genome fraction (%)	-	-	29.251	-	97.613	45.011	2.427	98.768	97.885	2.334	2.132
Duplication ratio	-	-	1.954	-	1.000	1.035	1.000	1.000	1.002	1.010	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	-	-	784.38	-	0.00	0.00	136.80	0.00	0.00	845.07	0.00
# indels per 100 kbp	-	-	3172.39	-	0.00	135.42	0.00	0.00	0.00	985.92	0.00
Largest alignment	-	-	728	-	29400	14030	731	29748	12290	710	642
Total aligned length	-	-	17211	-	29400	14030	731	29748	29553	710	642
NA50	-	-	-	-	29400	14030	731	29748	8725	-	642
NGA50	-	-	85	-	29400	-	-	29748	8725	-	-
NA90	-	-	-	-	29400	14030	731	29748	8538	-	642
NGA90	-	-	-	-	29400	-	-	29748	8538	-	-
auNA	-	-	5.0	-	29400.0	13738.2	731.0	29748.0	10153.5	5.0	642.0
auNGA	-	-	103.4	-	28698.2	6535.4	17.7	29381.6	9962.7	16.7	13.7
LA50	-	-	-	-	1	1	1	1	2	-	1
LGA50	-	-	99	-	1	-	-	1	2	-	-
LA90	-	-	-	-	1	1	1	1	3	-	1
LGA90	-	-	-	-	1	-	-	1	3	-	-

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

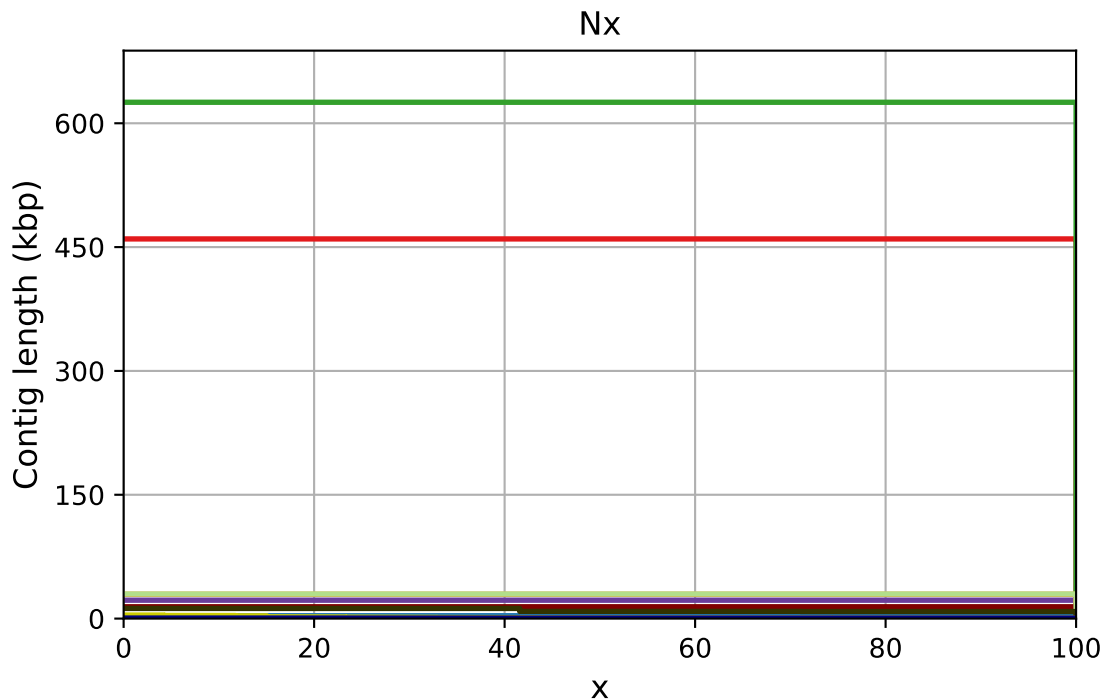
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# misassemblies	-	-	0	-	0	0	0	0	0	0	0
# contig misassemblies	-	-	0	-	0	0	0	0	0	0	0
# c. relocations	-	-	0	-	0	0	0	0	0	0	0
# c. translocations	-	-	0	-	0	0	0	0	0	0	0
# c. inversions	-	-	0	-	0	0	0	0	0	0	0
# scaffold misassemblies	-	-	0	-	0	0	0	0	0	0	0
# s. relocations	-	-	0	-	0	0	0	0	0	0	0
# s. translocations	-	-	0	-	0	0	0	0	0	0	0
# s. inversions	-	-	0	-	0	0	0	0	0	0	0
# misassembled contigs	-	-	0	-	0	0	0	0	0	0	0
Misassembled contigs length	-	-	0	-	0	0	0	0	0	0	0
# local misassemblies	-	-	0	-	0	0	0	0	0	0	0
# scaffold gap ext. mis.	-	-	0	-	0	0	0	0	0	0	0
# scaffold gap loc. mis.	-	-	0	-	0	0	0	0	0	0	0
# unaligned mis. contigs	-	-	1	-	0	0	0	0	0	0	0
# mismatches	-	-	135	-	0	0	1	0	0	6	0
# indels	-	-	546	-	0	19	0	0	0	7	0
# indels (<= 5 bp)	-	-	546	-	0	4	0	0	0	7	0
# indels (> 5 bp)	-	-	0	-	0	15	0	0	0	0	0
Indels length	-	-	621	-	0	473	0	0	0	9	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).

Unaligned report

	dbg_no_error_ont_hq_50x.fastq_45	dbg_no_error_reads_hiseq_5k.fastq_45	dbg_ont_hq_50x.fastq_45	dbg_reads_hiseq_5k.fastq_45	rem_min_no_error_ont_hq_50x.fastq_45	rem_min_ont_hq_50x.fastq_45	rem_min_reads_hiseq_5k.fastq_45	uni_no_error_ont_hq_50x.fastq_45	uni_no_error_reads_hiseq_5k.fastq_45	uni_ont_hq_50x.fastq_45	uni_reads_hiseq_5k.fastq_45
# fully unaligned contigs	1	1	0	1	0	0	0	0	0	107	0
Fully unaligned length	459901	3498	0	22279	0	0	0	0	0	100054	0
# partially unaligned contigs	-	-	1	-	0	0	0	0	0	0	0
Partially unaligned length	-	-	608223	-	0	0	0	0	0	0	0
# N's	0	0	0	0	0	0	0	0	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).

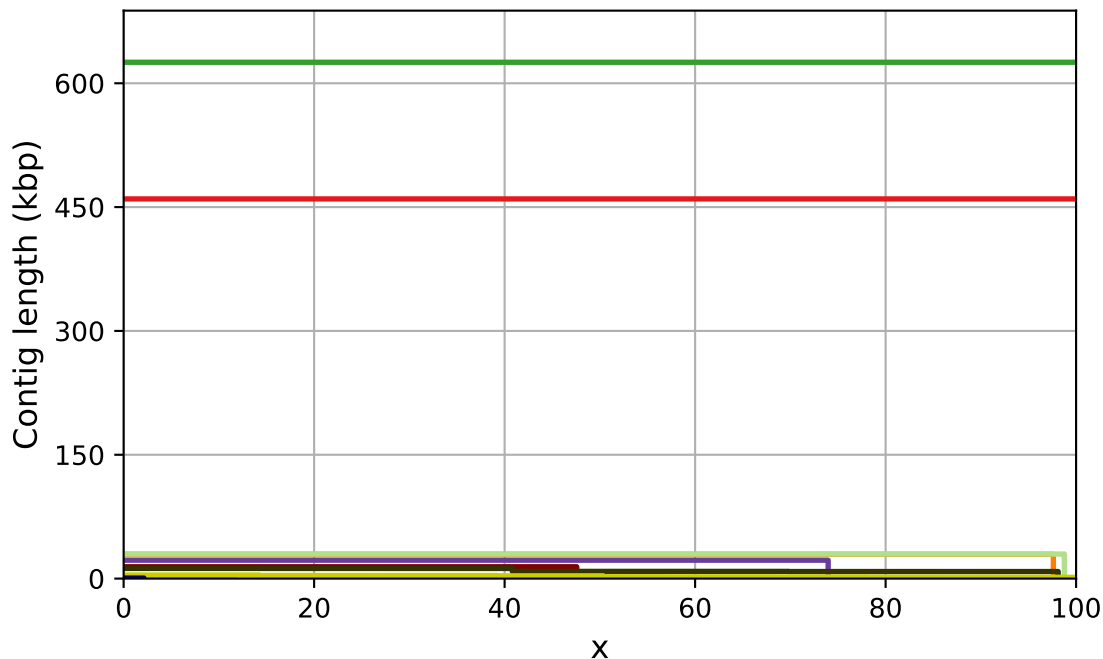


hq_50x.fastq_45
 s_hiseq_5k.fastq_45
 fastq_45
 5k fastq_45

rem_min_no_error_ont_hq_50x.fastq_45
 rem_min_ont_hq_50x.fastq_45
 rem_min_reads_hiseq_5k.fastq_45
 uni_no_error_ont_hq_50x.fastq_45

uni_no_error_ont_hq_50x.fastq_45
 uni_ont_hq_50x.fastq_45
 uni_reads_hiseq_5k.fastq_45

NGx

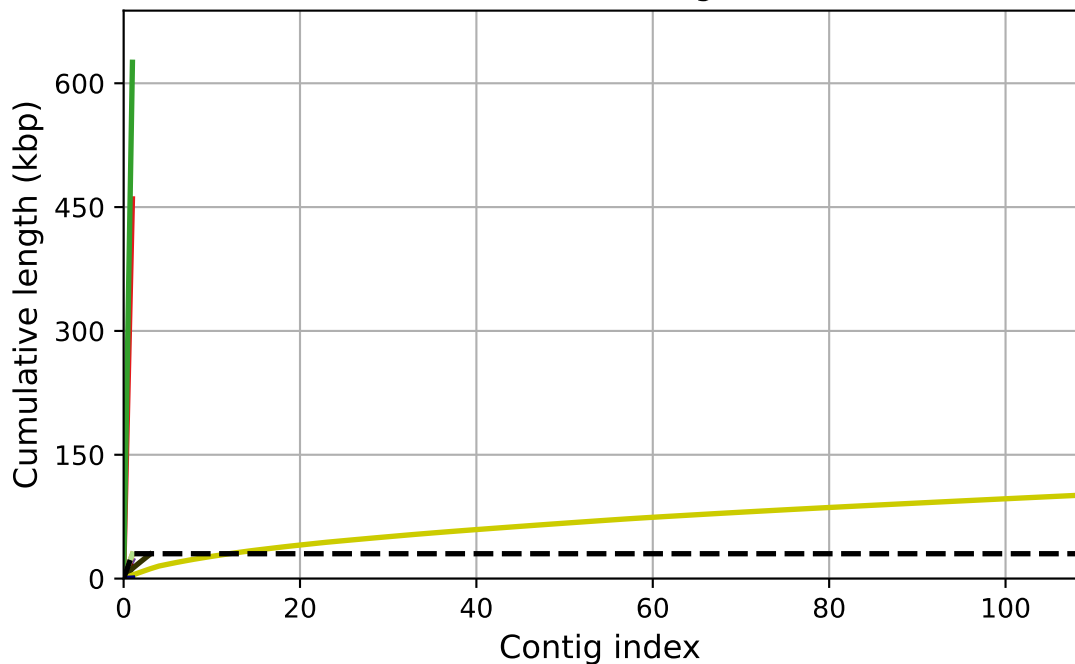


hq_50x.fastq_45
 s_hiseq_5k.fastq_45
 fastq_45
 5k fastq_45

rem_min_no_error_ont_hq_50x.fastq_45
 rem_min_ont_hq_50x.fastq_45
 rem_min_reads_hiseq_5k.fastq_45
 uni_no_error_ont_hq_50x.fastq_45

uni_no_error_reads_hiseq_5k.fastq_45
 uni_ont_hq_50x.fastq_45
 uni_reads_hiseq_5k.fastq_45

Cumulative length



rem_min_no_error_ont_hq_50x.fastq_45

rem_min_ont_hq_50x.fastq_45

rem_min_reads_hiseq_5k.fastq_45

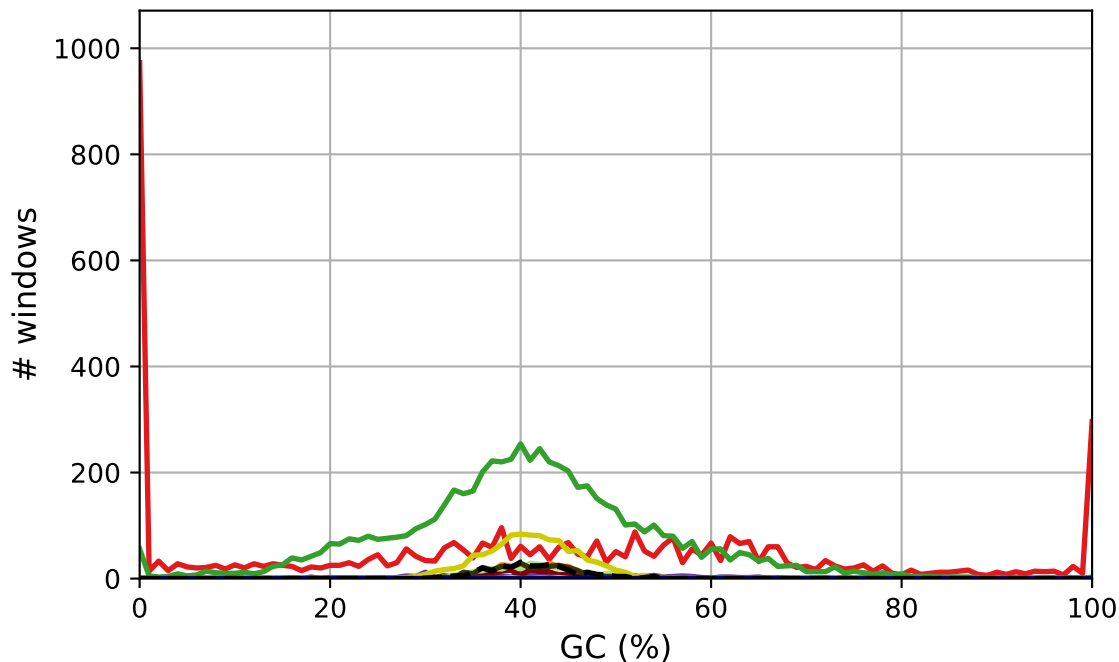
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uni_ont_hq_50x.fastq_45

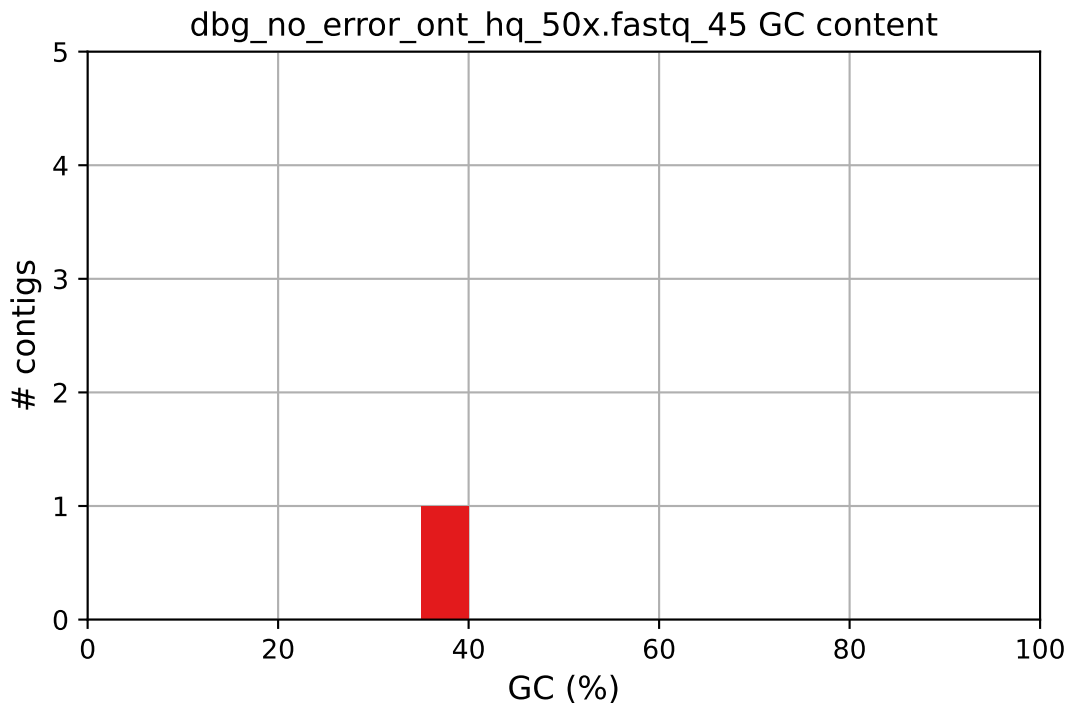
uni_reads_hiseq_5k.fastq_45

Reference

GC content

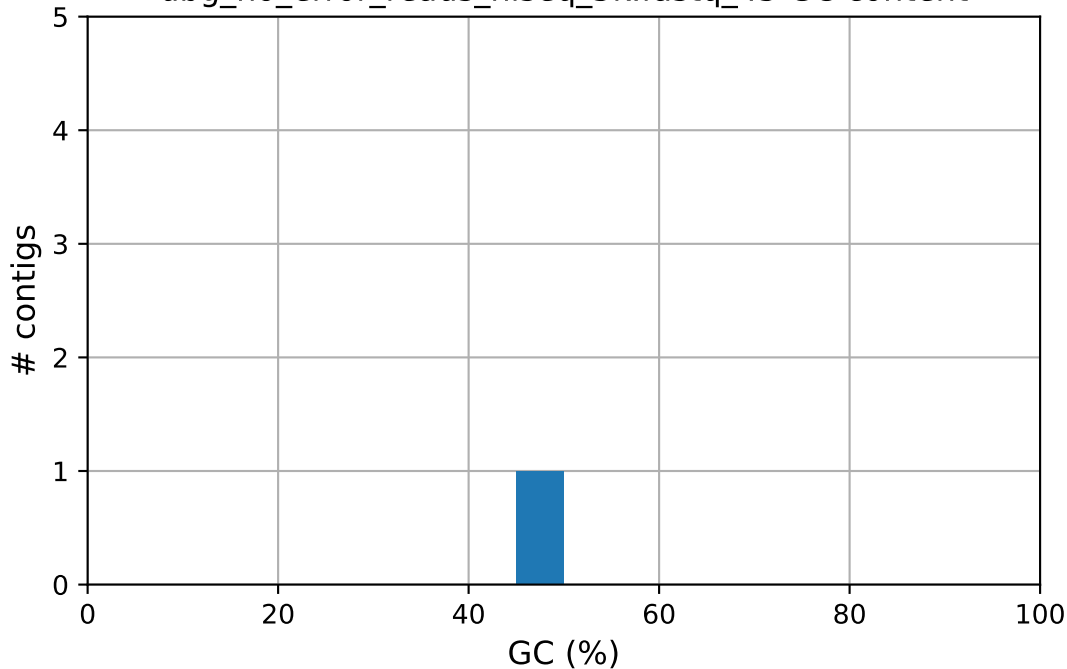


hseq_50x.fastq_45	rem_min_no_error_ont_hq_50x.fastq_45	uni_no_error_ont_hq_50x.fastq_45
s_hiseq_5k.fastq_45	rem_min_ont_hq_50x.fastq_45	uni_ont_hq_50x.fastq_45
fastq_45	rem_min_reads_hiseq_5k.fastq_45	uni_reads_hiseq_5k.fastq_45
5k fastq_45	uni_no_error_ont_hq_50x.fastq_45	Reference



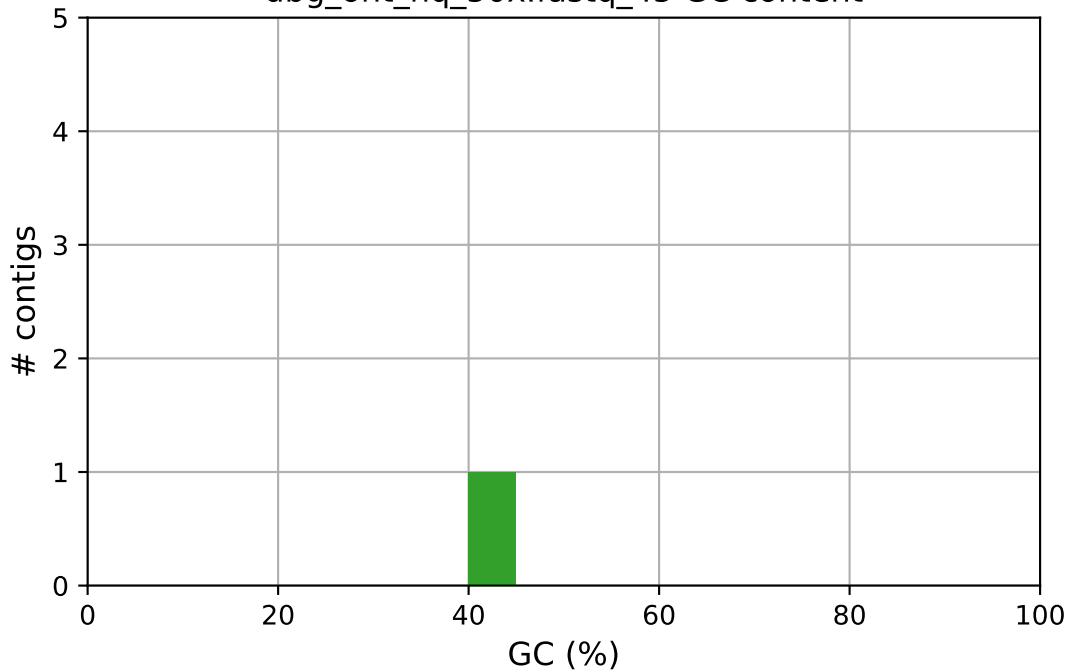
dbg_no_error_ont_hq_50x.fastq_45

dbg_no_error_reads_hiseq_5k.fastq_45 GC content



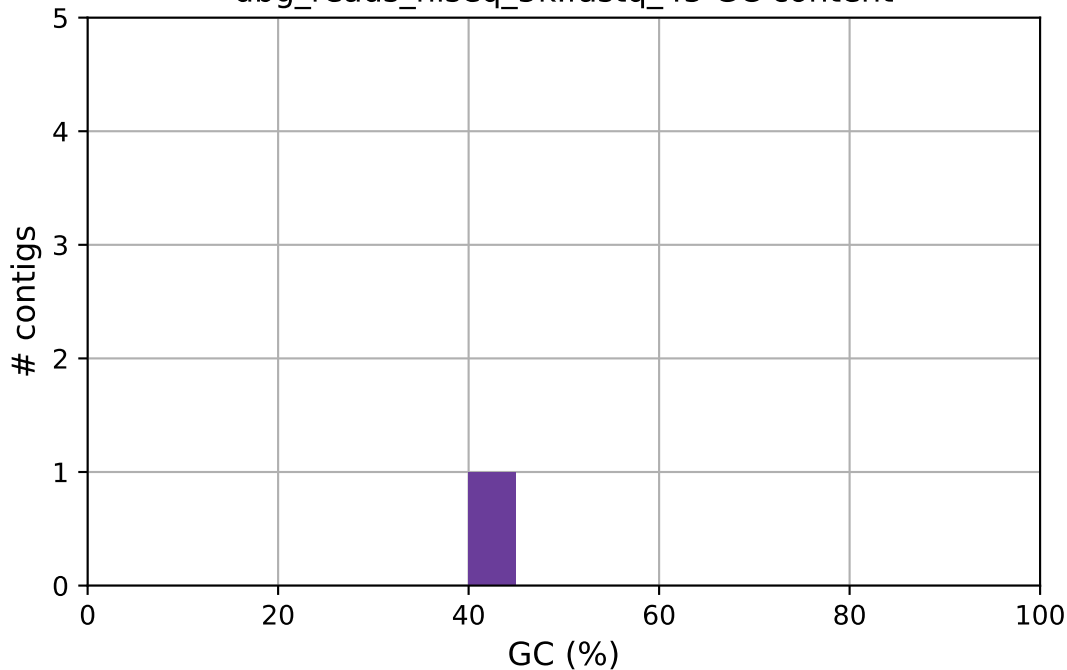
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dbg_ont_hq_50x.fastq_45 GC content



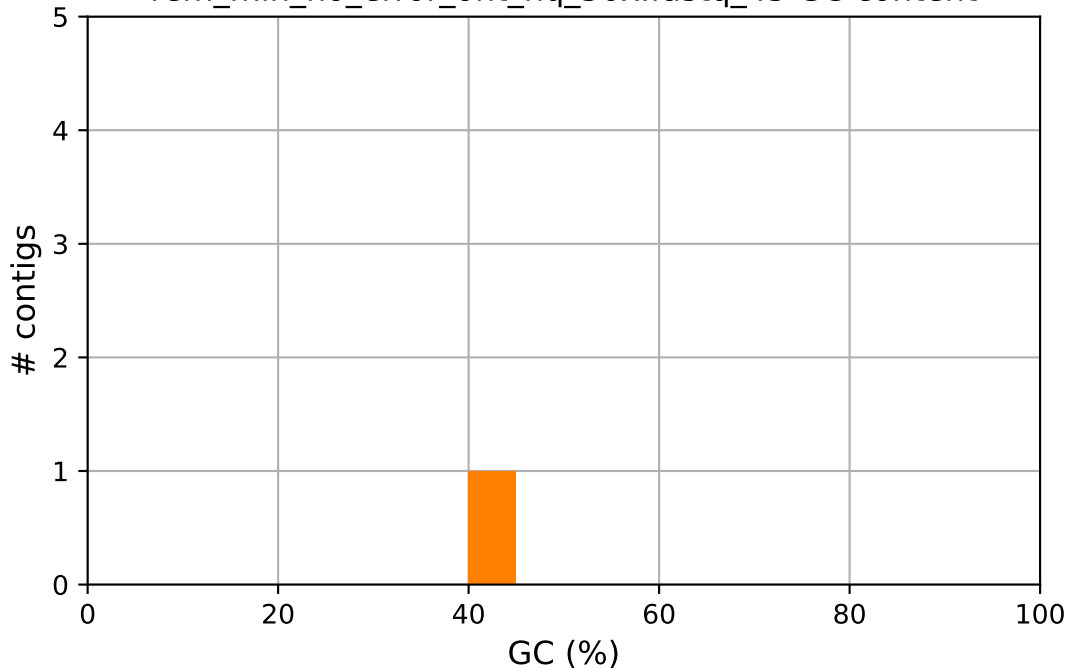
dbg_ont_hq_50x.fastq_45

dbg_reads_hiseq_5k.fastq_45 GC content



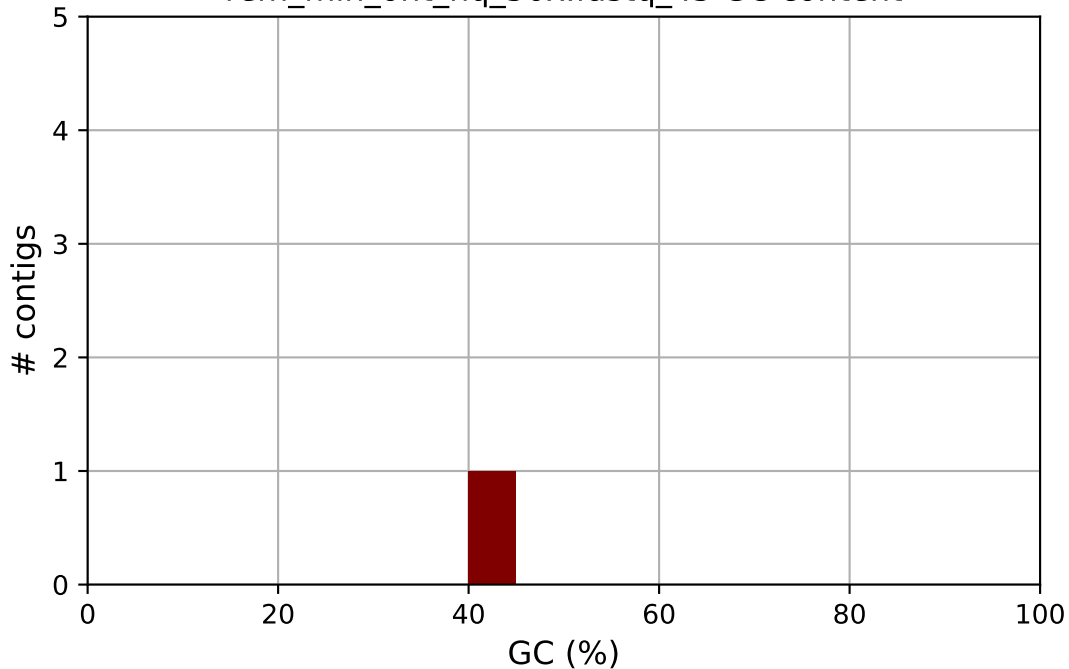
dbg_reads_hiseq_5k.fastq_45

rem_min_no_error_ont_hq_50x.fastq_45 GC content

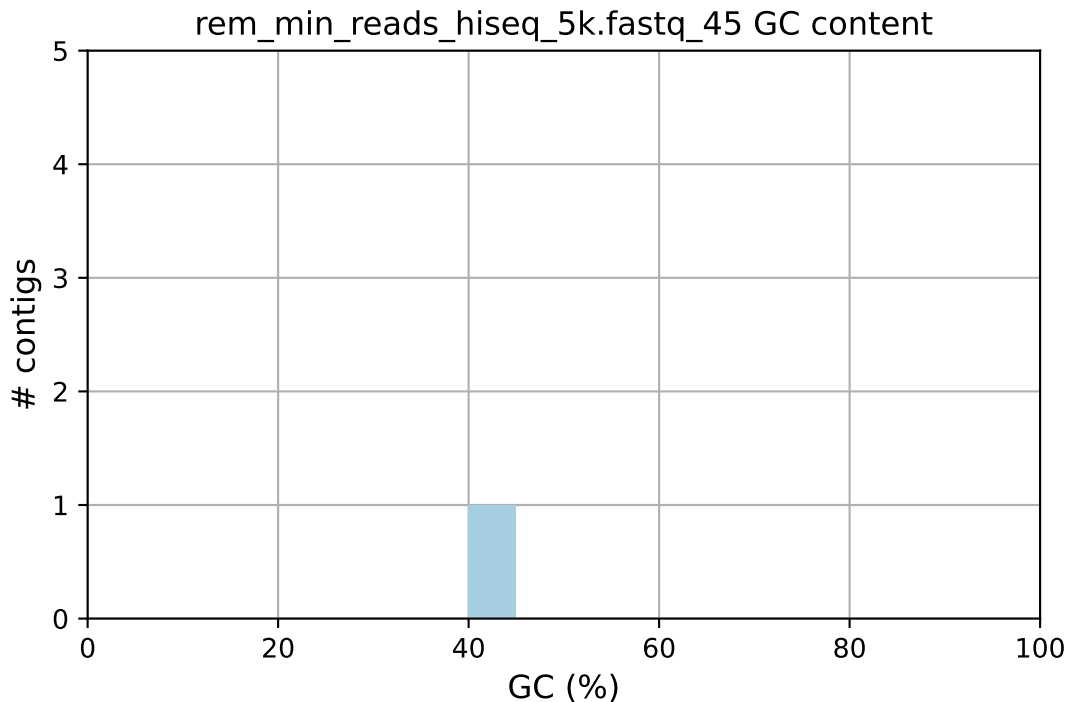


rem_min_no_error_ont_hq_50x.fastq_45

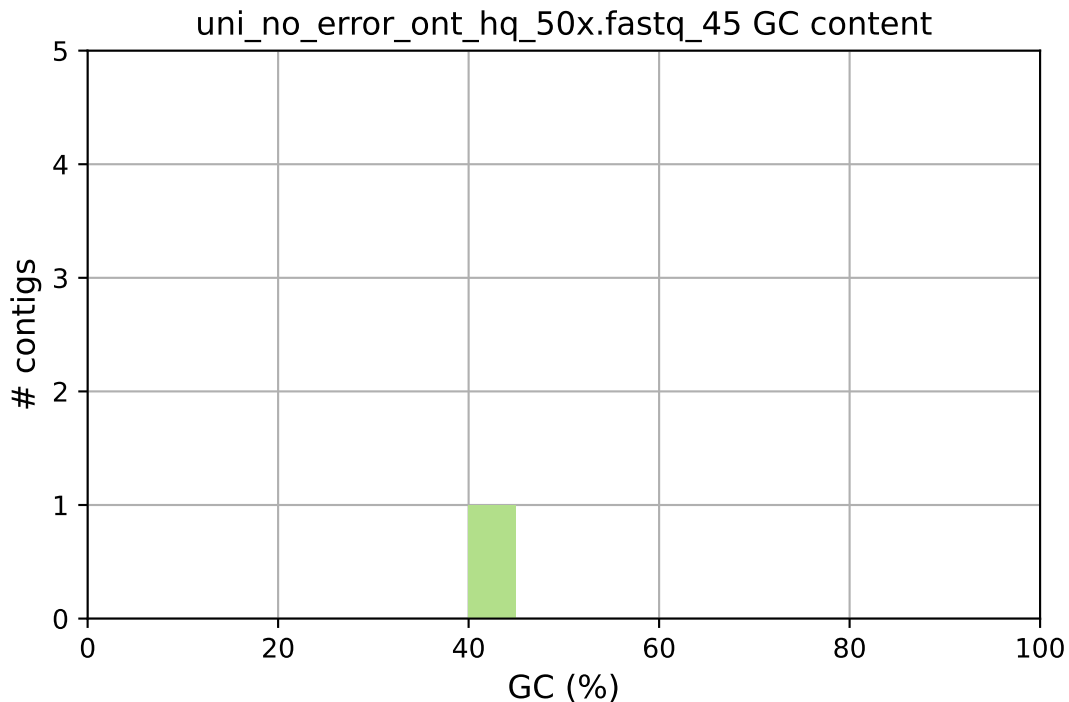
rem_min_ont_hq_50x.fastq_45 GC content



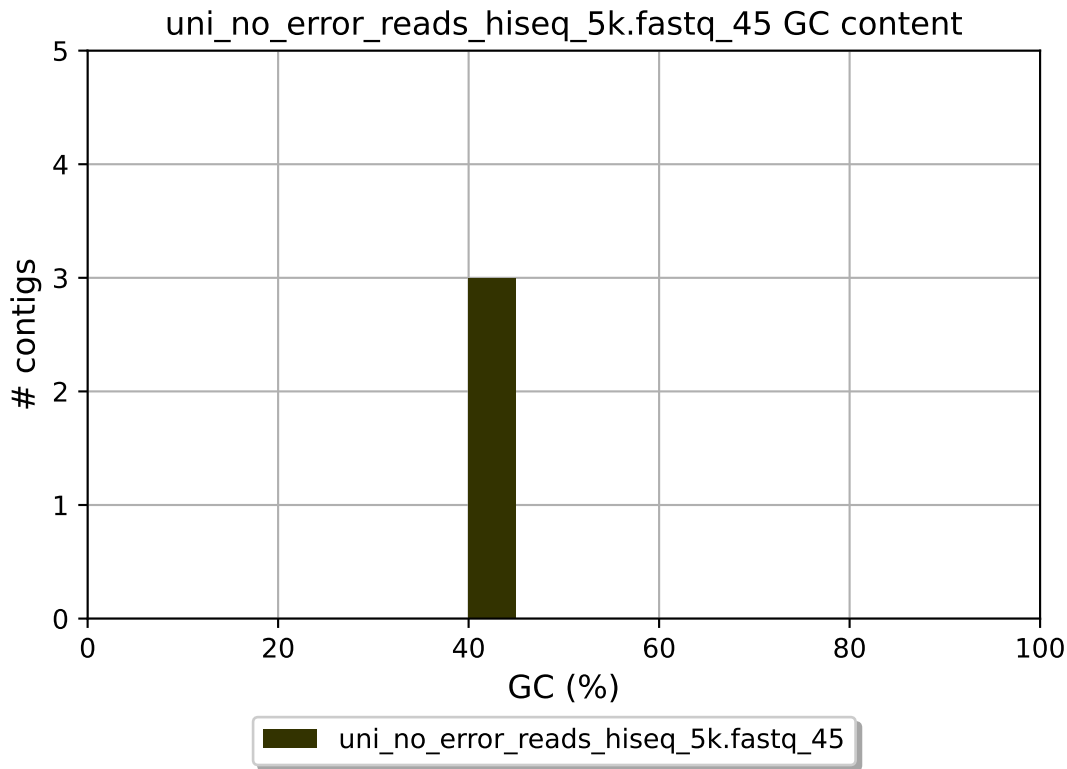
rem_min_ont_hq_50x.fastq_45



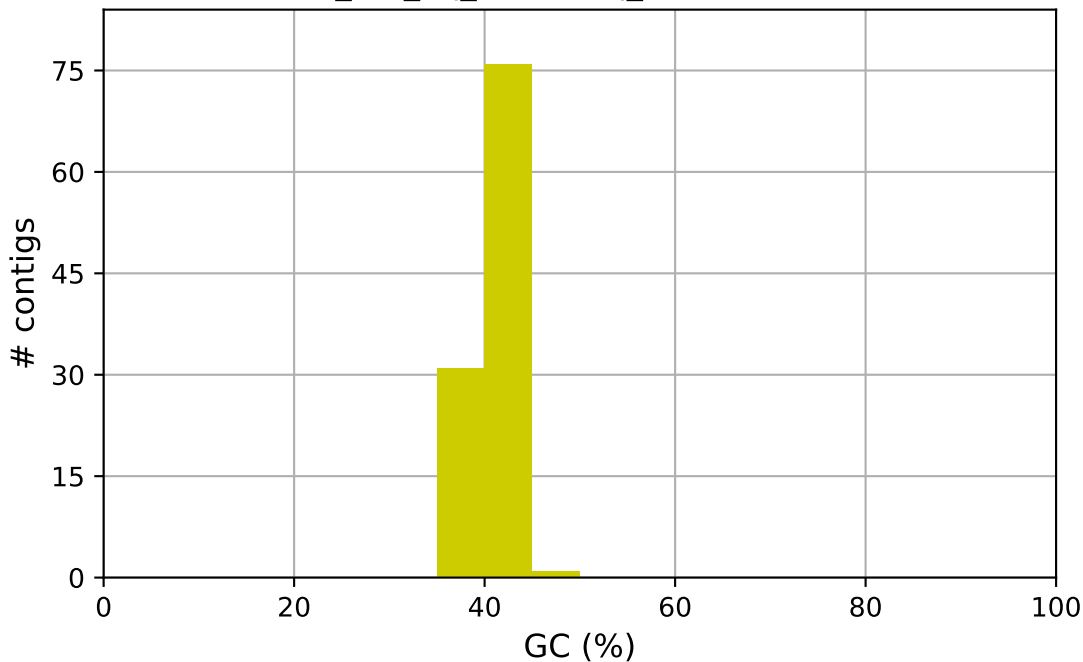
rem_min_reads_hiseq_5k.fastq_45



uni_no_error_ont_hq_50x.fastq_45

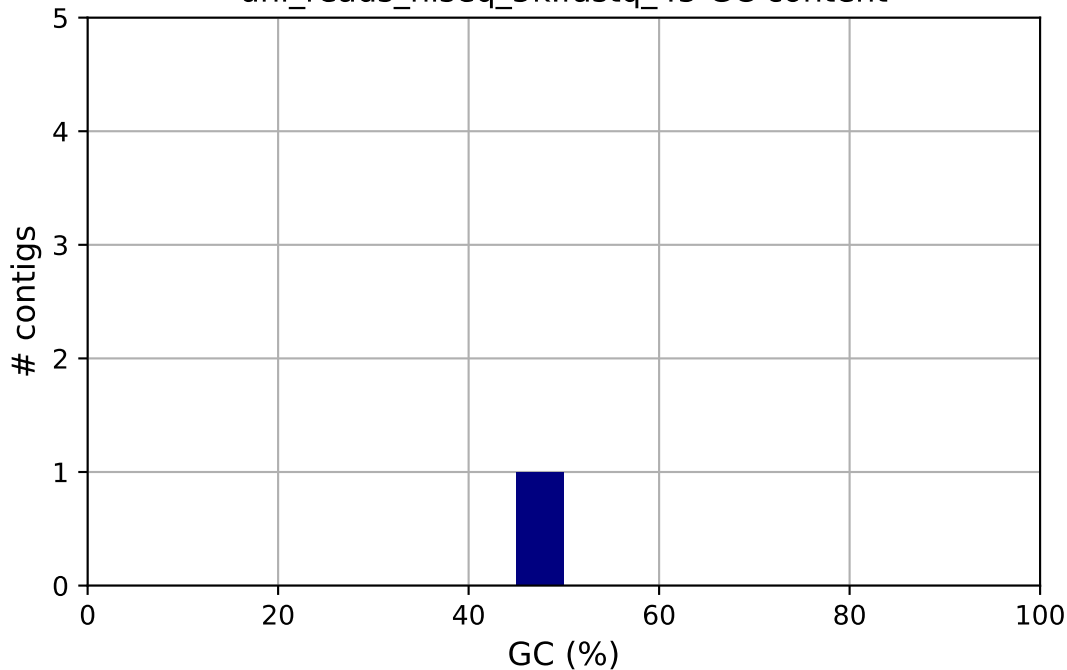


uni_ont_hq_50x.fastq_45 GC content



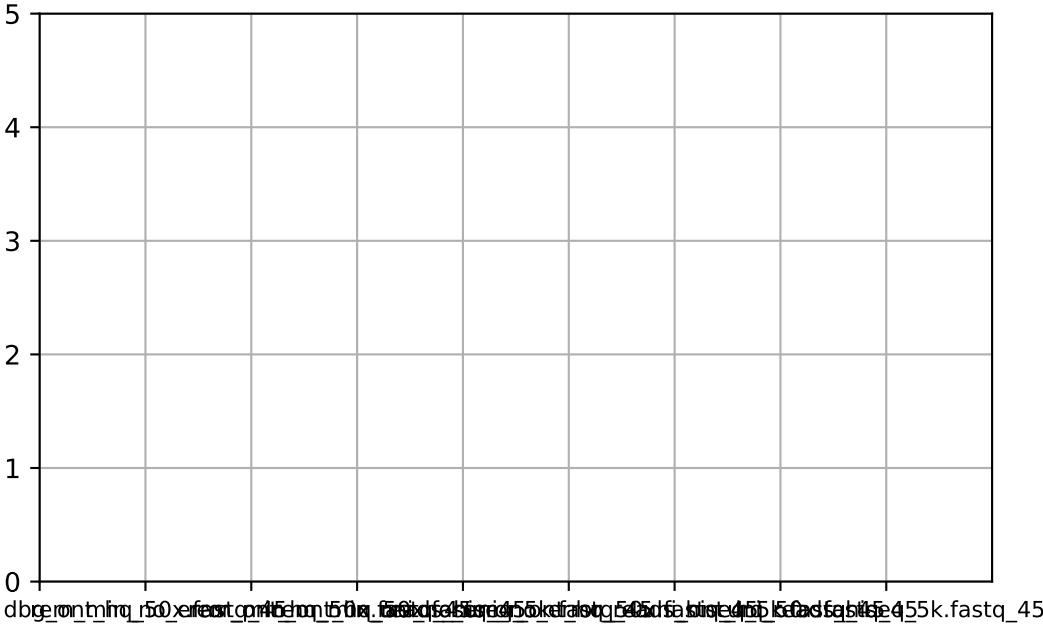
uni_ont_hq_50x.fastq_45

uni_reads_hiseq_5k.fastq_45 GC content

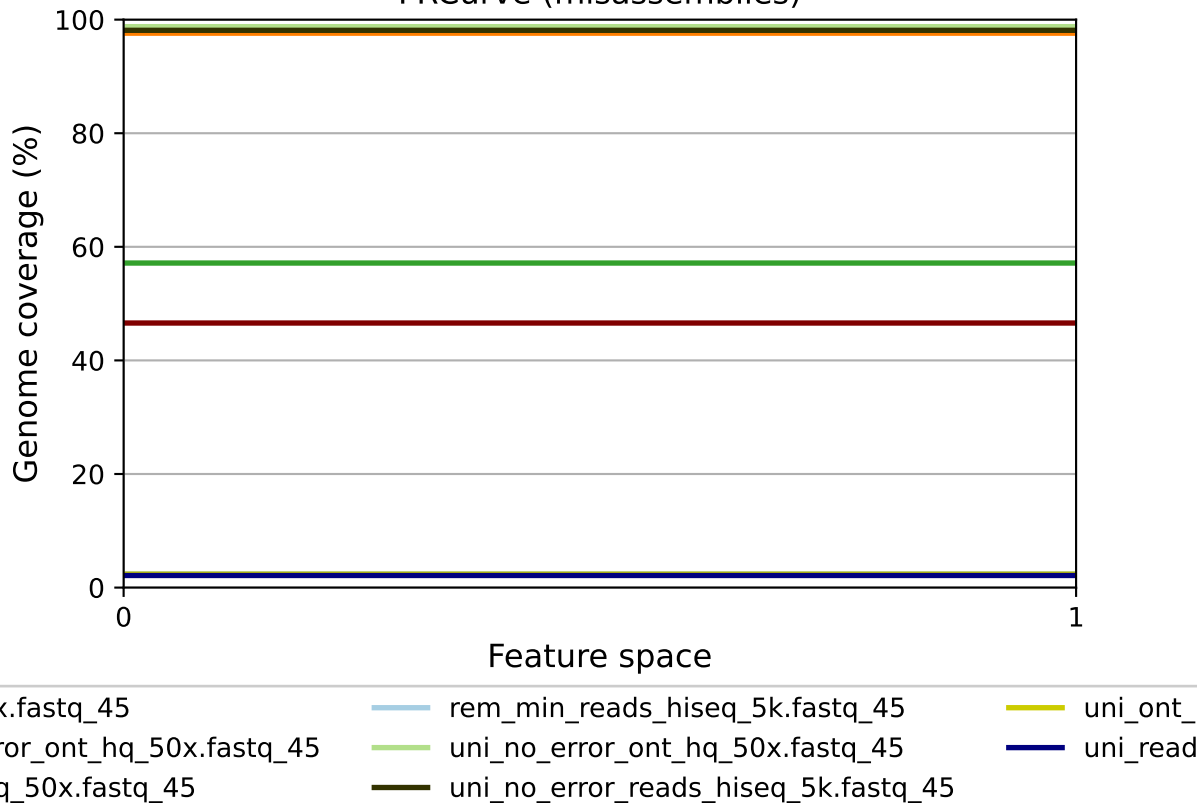


uni_reads_hiseq_5k.fastq_45

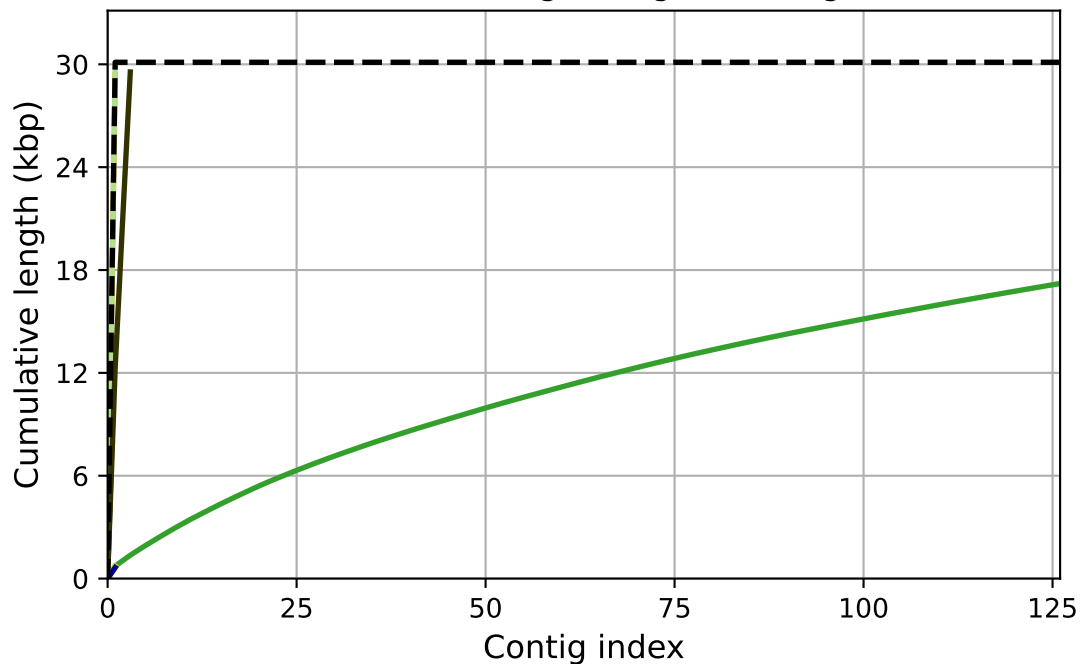
Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)



50x.fastq_45

error_ont_hq_50x.fastq_45

_hq_50x.fastq_45

rem_min_reads_hiseq_5k.fastq_45

uni_no_error_ont_hq_50x.fastq_45

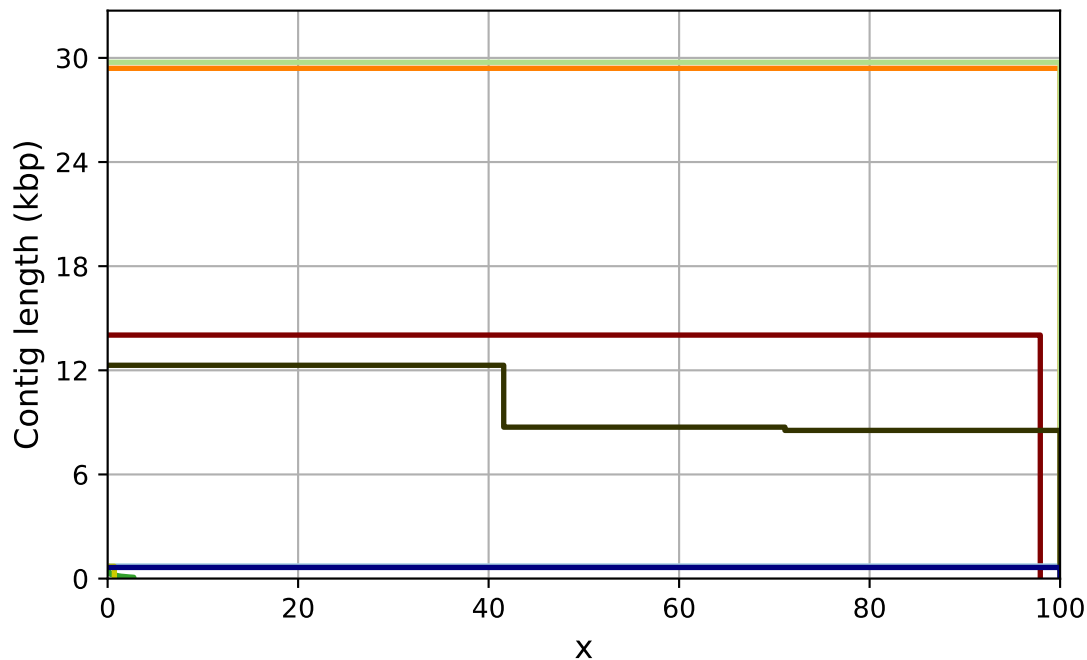
uni_no_error_reads_hiseq_5k.fastq_45

uni_ont_hq_50x.fastq_45

uni_read

Reference

NAX



50x.fastq_45

error_ont_hq_50x.fastq_45

_hq_50x.fastq_45

rem_min_reads_hiseq_5k.fastq_45

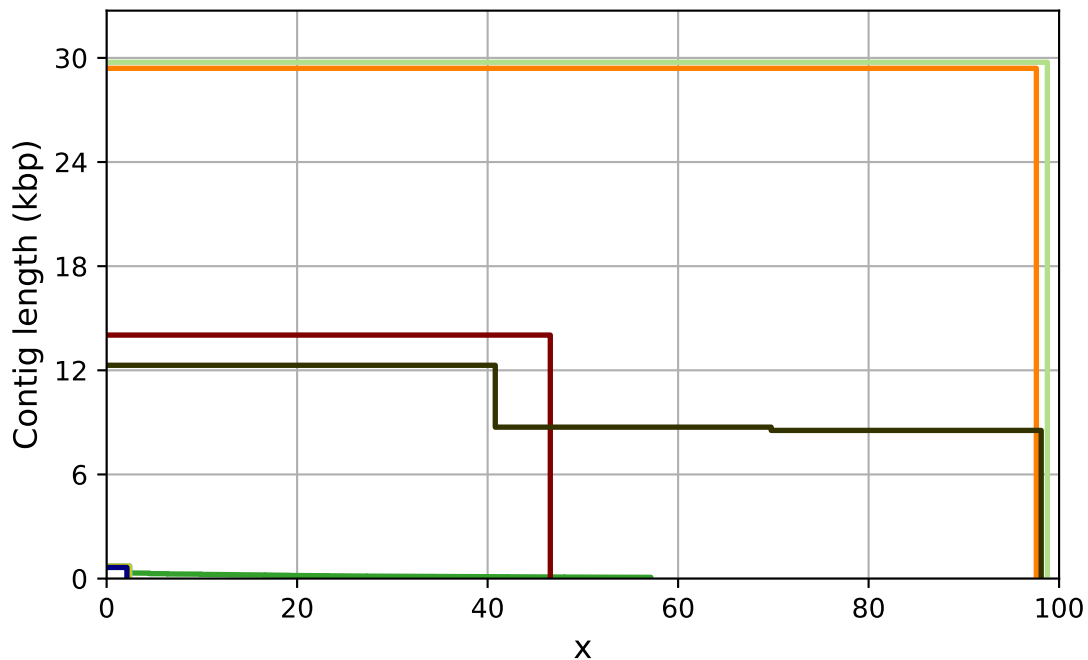
uni_no_error_ont_hq_50x.fastq_45

uni_no_error_reads_hiseq_5k.fastq_45

uni_ont_hq_50x.fastq_45

uni_read

NGAx



50x.fastq_45

error_ont_hq_50x.fastq_45

_hq_50x.fastq_45

rem_min_reads_hiseq_5k.fastq_45

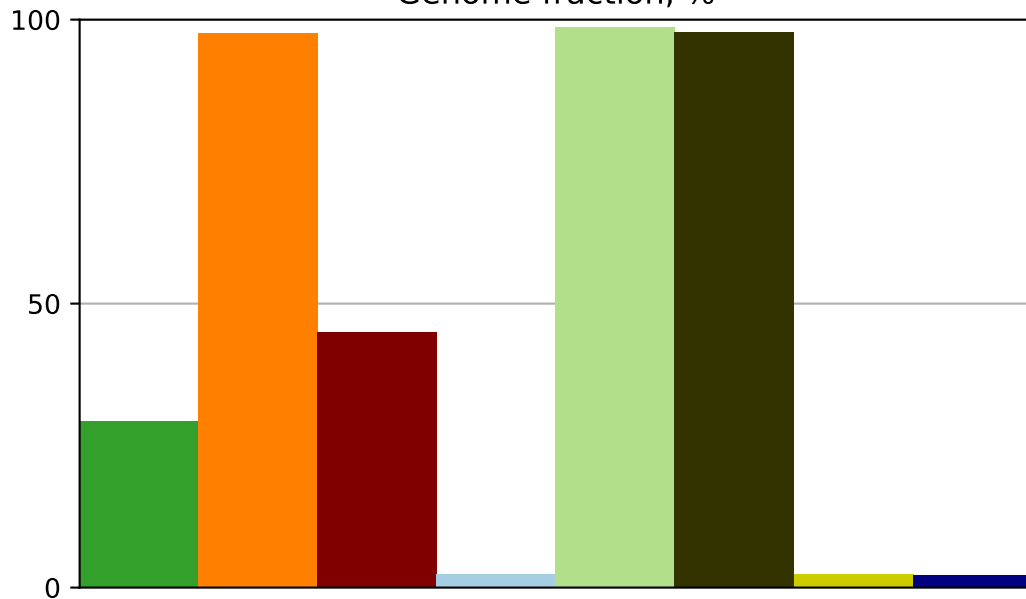
uni_no_error_ont_hq_50x.fastq_45

uni_no_error_reads_hiseq_5k.fastq_45

uni_ont_hq_50x.fastq_45

uni_read

Genome fraction, %



50x.fastq_45

error_ont_hq_50x.fastq_45

_hq_50x.fastq_45

rem_min_reads_hiseq_5k.fastq_45

uni_no_error_ont_hq_50x.fastq_45

uni_no_error_reads_hiseq_5k.fastq_45

uni_ont_l

uni_read