

Report

	dbg_mers_error_illumina	dbg_mers_error_ont	dbg_mers_errorless_illumina	dbg_mers_errorless_ont	olc_mers_error_illumina	olc_mers_error_ont	olc_mers_errorless_illumina	olc_mers_errorless_ont	spades_mers_errorless_illumina_contigs	spades_mers_error_illumina_contigs	spades_mers_errorless_ont_contigs	spades_mers_error_ont_contigs
# contigs (>= 0 bp)	202	3966	3	1	351	8	351	408	1	1	1	1
# contigs (>= 1000 bp)	0	23	3	1	2	8	2	408	1	1	1	1
# contigs (>= 5000 bp)	0	0	3	1	0	8	0	408	1	1	1	1
# contigs (>= 10000 bp)	0	0	1	1	0	8	0	169	1	1	1	1
# contigs (>= 25000 bp)	0	0	0	1	0	0	0	0	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0	0	0	0	0	0	0	0	0
Total length (>= 0 bp)	30143	736737	29553	29748	76363	139308	76363	4019081	29482	29482	29748	29754
Total length (>= 1000 bp)	0	43999	29553	29748	2514	139308	2514	4019081	29482	29482	29748	29754
Total length (>= 5000 bp)	0	0	29553	29748	0	139308	0	4019081	29482	29482	29748	29754
Total length (>= 10000 bp)	0	0	12290	29748	0	139308	0	1831308	29482	29482	29748	29754
Total length (>= 25000 bp)	0	0	0	29748	0	0	0	0	29482	29482	29748	29754
Total length (>= 50000 bp)	0	0	0	0	0	0	0	0	0	0	0	0
# contigs	1	108	3	1	23	8	23	408	1	1	1	1
Largest contig	642	4280	12290	29748	1476	19916	1476	13554	29482	29482	29748	29754
Total length	642	100764	29553	29748	16791	139308	16791	4019081	29482	29482	29748	29754
Reference length	30119	30119	30119	30119	30119	30119	30119	30119	30119	30119	30119	30119
GC (%)	48.75	41.06	41.27	41.27	41.48	40.66	41.46	40.65	41.26	41.26	41.27	41.27
Reference GC (%)	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24	41.24
N50	642	933	8725	29748	725	18607	725	29482	29482	29482	29748	29754
NG50	-	3342	8725	29748	545	19916	545	13057	29482	29482	29748	29754
N90	642	529	8538	29748	545	14300	545	8748	29482	29482	29748	29754
NG90	-	1612	8538	29748	-	19067	-	13006	29482	29482	29748	29754
auN	642.0	1427.5	10153.5	29748.0	786.9	17649.5	786.9	9958.4	29482.0	29482.0	29748.0	29754.0
auNG	13.7	4775.7	9962.7	29381.6	438.7	81633.3	438.7	1328855.2	28858.5	28858.5	29381.6	29393.4
L50	1	30	2	1	10	4	10	187	1	1	1	1
LG50	-	4	2	1	20	1	20	2	1	1	1	1
L90	1	89	3	1	20	8	20	360	1	1	1	1
LG90	-	11	3	1	-	2	-	3	1	1	1	1
# misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 0 part	107 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	100054	0	0	0	0	0	0	0	0	0	0
Genome fraction (%)	2.132	2.334	97.885	98.768	53.883	93.439	53.883	98.768	97.885	97.885	98.768	98.738
Duplication ratio	1.000	1.010	1.002	1.000	1.035	4.947	1.035	135.104	1.000	1.000	1.000	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	0.00
# mismatches per 100 kbp	0.00	845.07	0.00	0.00	17.87	253.53	0.00	0.00	0.00	0.00	0.00	26.90
# indels per 100 kbp	0.00	985.92	0.00	0.00	0.00	836.01	0.00	0.00	0.00	0.00	0.00	73.96
Largest alignment	642	710	12290	29748	1476	19902	1476	13554	29482	29482	29748	29744
Total aligned length	642	710	29553	29748	16791	139233	16791	4019081	29482	29482	29748	29744
NA50	642	-	8725	29748	725	18604	725	9870	29482	29482	29748	29744
NGA50	-	-	8725	29748	545	19902	545	13057	29482	29482	29748	29744
NA90	642	-	8538	29748	545	14286	545	8748	29482	29482	29748	29744
NGA90	-	-	8538	29748	-	19067	-	13006	29482	29482	29748	29744
auNA	642.0	5.0	10153.5	29748.0	786.9	17631.3	786.9	9958.4	29482.0	29482.0	29748.0	29734.0
auNGA	13.7	16.7	9962.7	29381.6	438.7	81549.4	438.7	1328855.2	28858.5	28858.5	29381.6	29373.7
LA50	1	-	2	1	10	4	10	187	1	1	1	1
LGA50	-	-	2	1	20	1	20	2	1	1	1	1
LA90	1	-	3	1	20	8	20	360	1	1	1	1
LGA90	-	-	3	1	-	2	-	3	1	1	1	1

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

	dbg_mers_error_illumina	dbg_mers_error_ont	dbg_mers_errorless_illumina	dbg_mers_errorless_ont	olc_mers_error_illumina	olc_mers_error_ont	olc_mers_errorless_illumina	olc_mers_errorless_ont	spades_mers_errorless_illumina_contigs	spades_mers_error_illumina_contigs	spades_mers_errorless_ont_contigs	spades_mers_error_ont_contigs
# misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0
# mismatches	0	6	0	0	3	353	0	0	0	0	0	8
# indels	0	7	0	0	0	1164	0	0	0	0	0	22
# indels (<= 5 bp)	0	7	0	0	0	1162	0	0	0	0	0	22
# indels (> 5 bp)	0	0	0	0	0	2	0	0	0	0	0	0
Indels length	0	9	0	0	0	1393	0	0	0	0	0	31

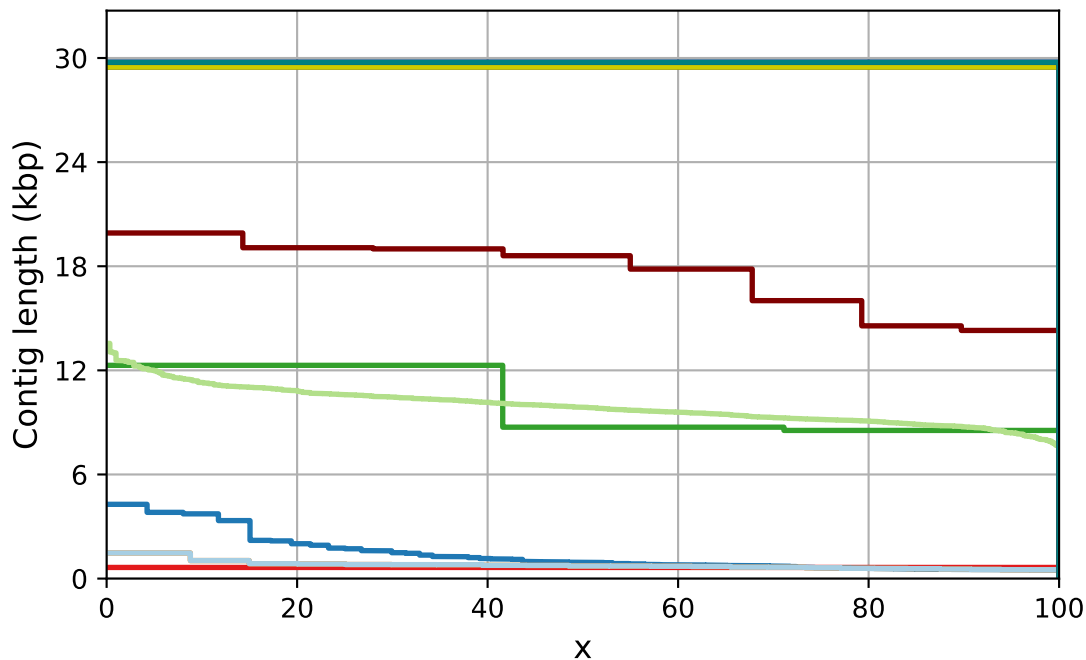
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	dbg_mers_error_illumina	dbg_mers_error_ont	dbg_mers_errorless_illumina	dbg_mers_errorless_ont	olc_mers_error_illumina	olc_mers_error_ont	olc_mers_errorless_illumina	olc_mers_errorless_ont	spades_mers_errorless_illumina_contigs	spades_mers_error_illumina_contigs	spades_mers_errorless_ont_contigs	spades_mers_error_ont_contigs
# fully unaligned contigs	0	107	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	100054	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0	0	0	0
# N's	0	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).

Nx



rs\_error\_illumina

olc\_mers\_error\_illumina

spades\_mers\_errorless\_ill

rs\_error\_ont

olc\_mers\_error\_ont

spades\_mers\_error\_illumi

rs\_errorless\_illumina

olc\_mers\_errorless\_illumina

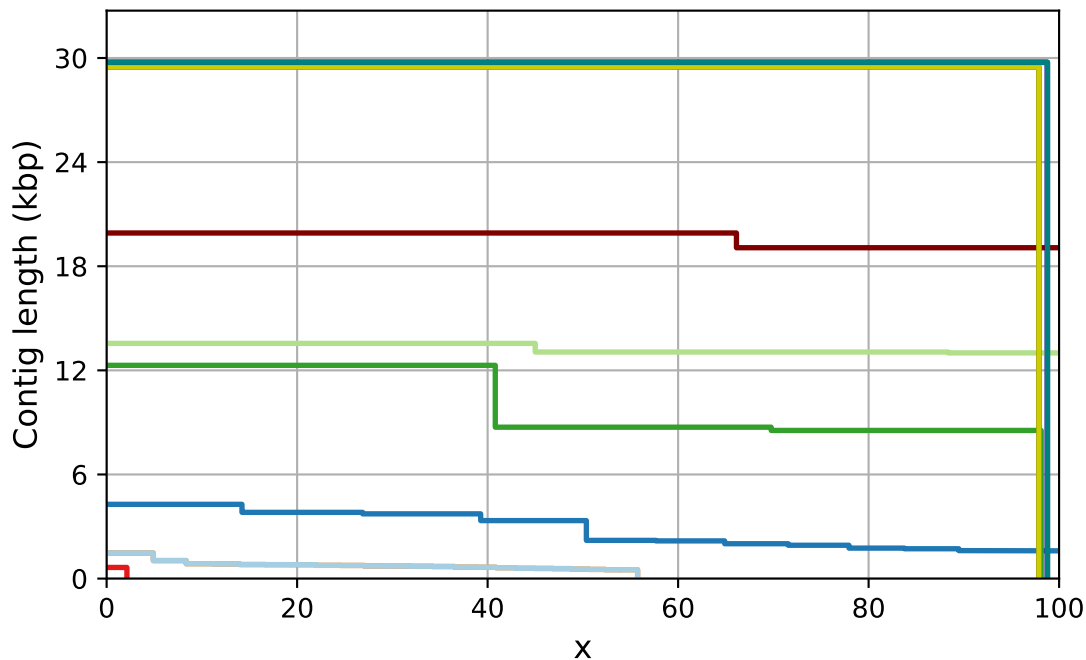
spades\_mers\_errorless\_o

rs\_errorless\_ont

olc\_mers\_errorless\_ont

spades\_mers\_error\_ont

# NGx



rs\_error\_illumina

olc\_mers\_error\_illumina

spades\_mers\_errorless\_ill

rs\_error\_ont

olc\_mers\_error\_ont

spades\_mers\_error\_illumi

rs\_errorless\_illumina

olc\_mers\_errorless\_illumina

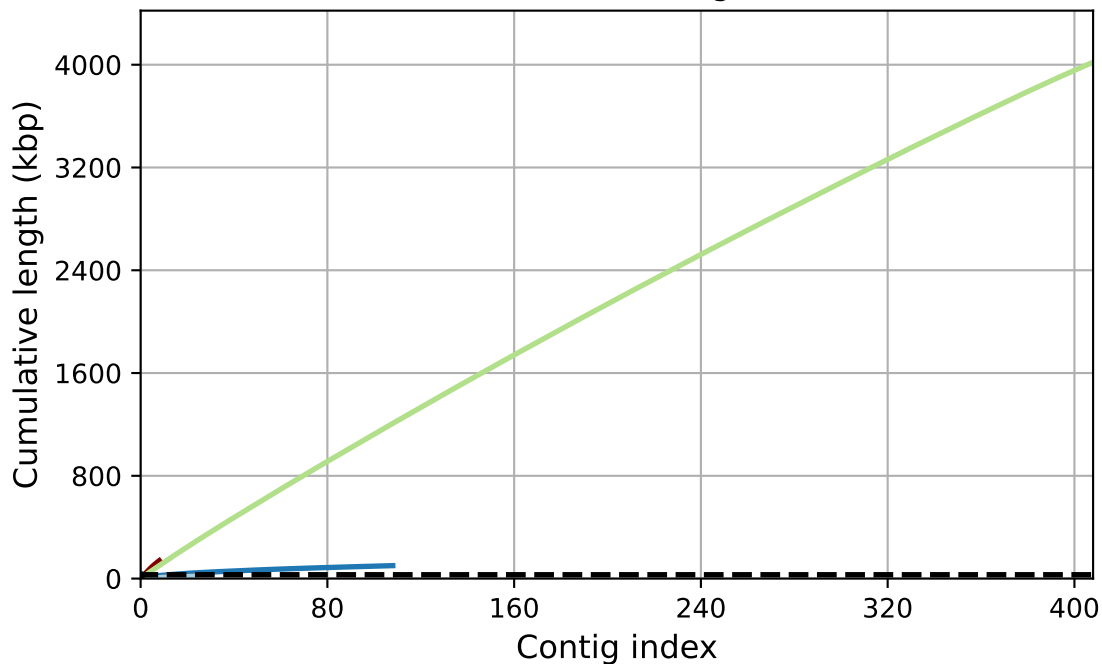
spades\_mers\_errorless\_o

rs\_errorless\_ont

olc\_mers\_errorless\_ont

spades\_mers\_error\_ont

# Cumulative length



error\_illumina

olc\_mers\_error\_ont

spades\_mers\_err

error\_ont

olc\_mers\_errorless\_illumina

spades\_mers\_err

errorless\_illumina

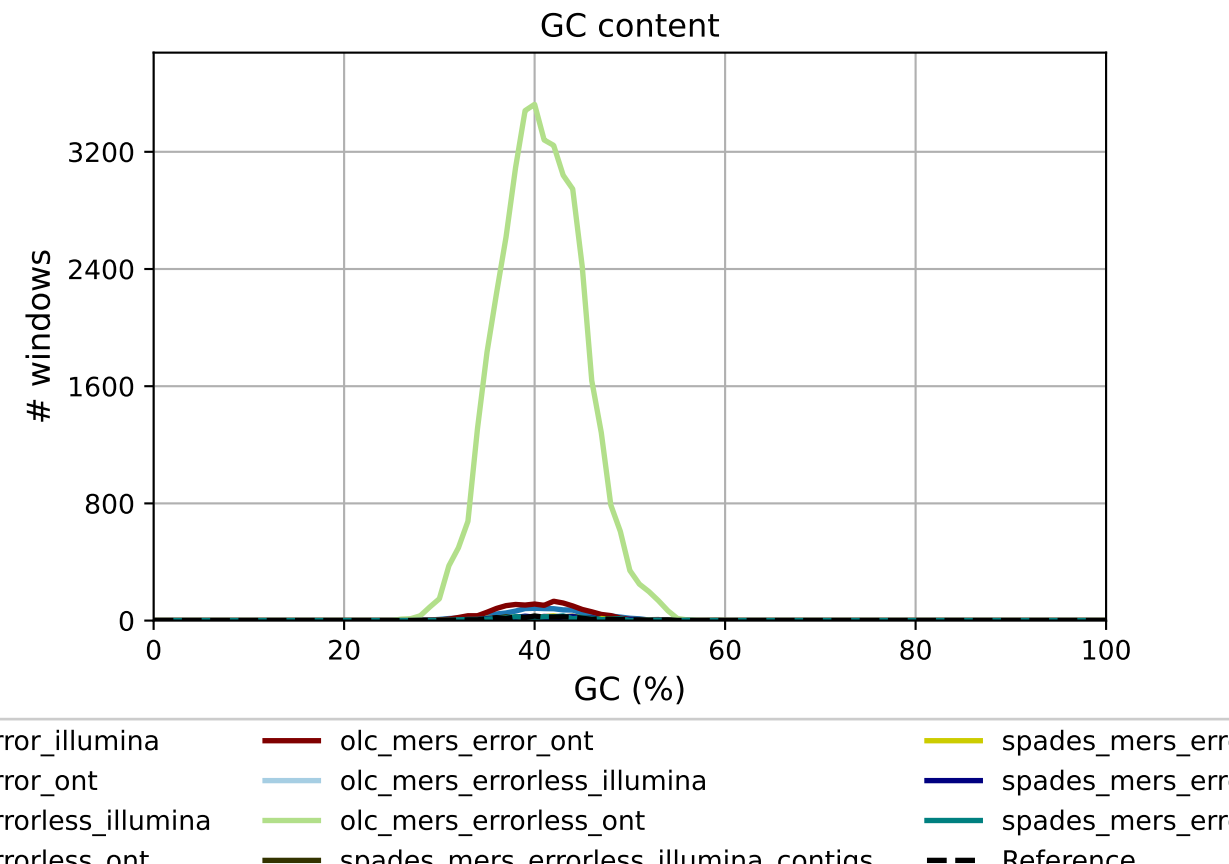
olc\_mers\_errorless\_ont

spades\_mers\_err

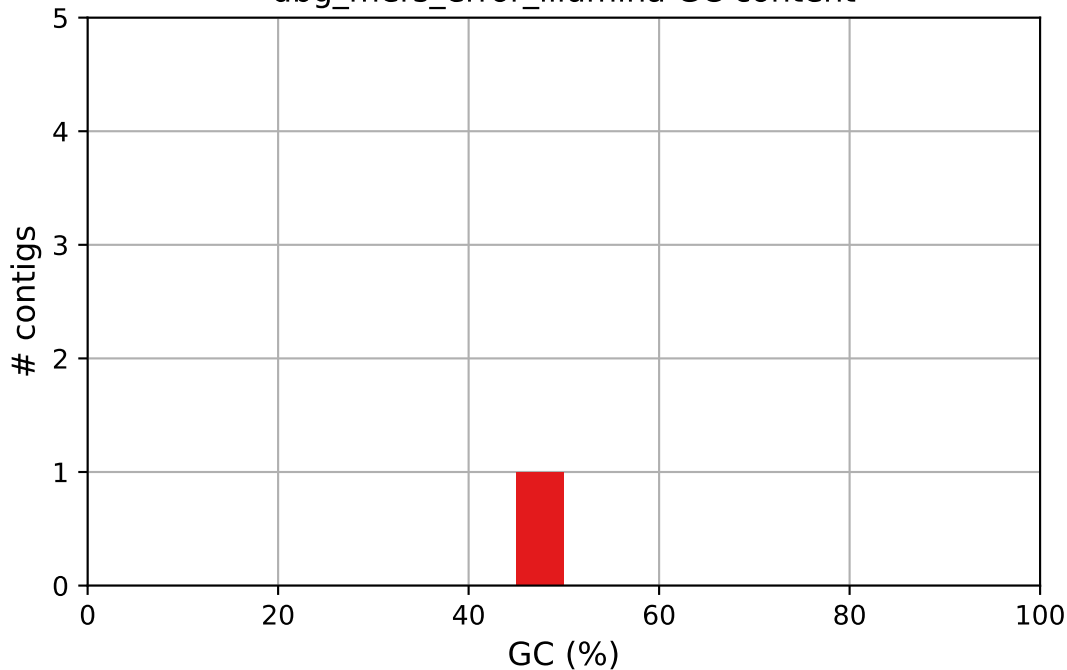
errorless\_ont

spades\_mers\_errorless\_illumina\_contigs

Reference



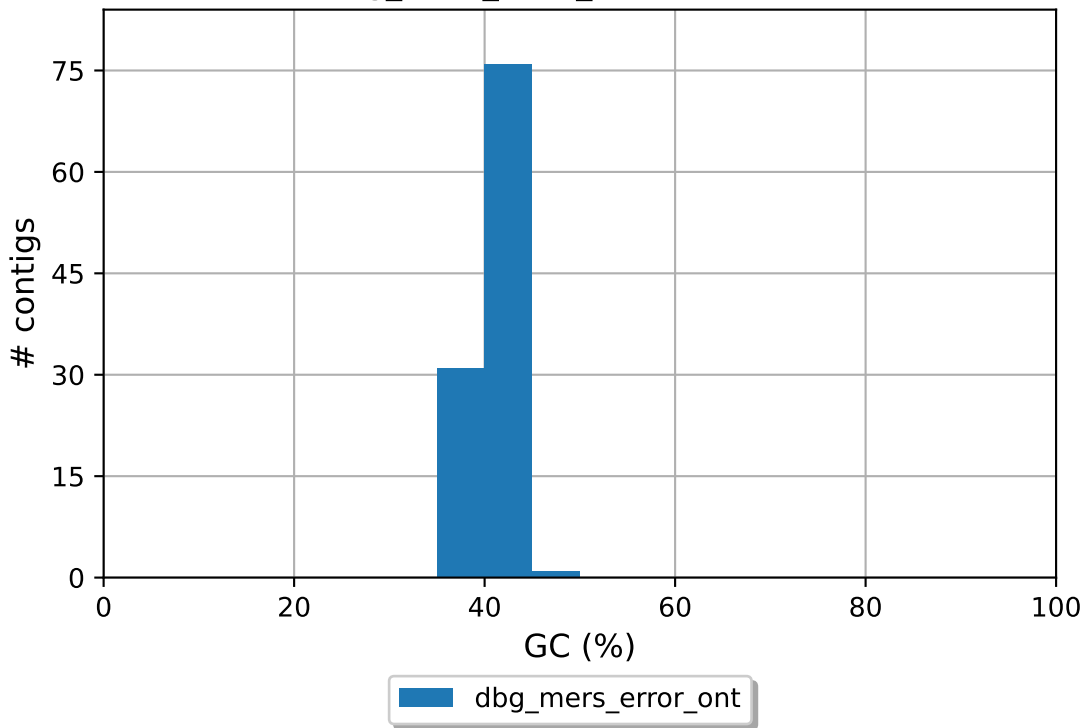
dbg\_mers\_error\_illumina GC content



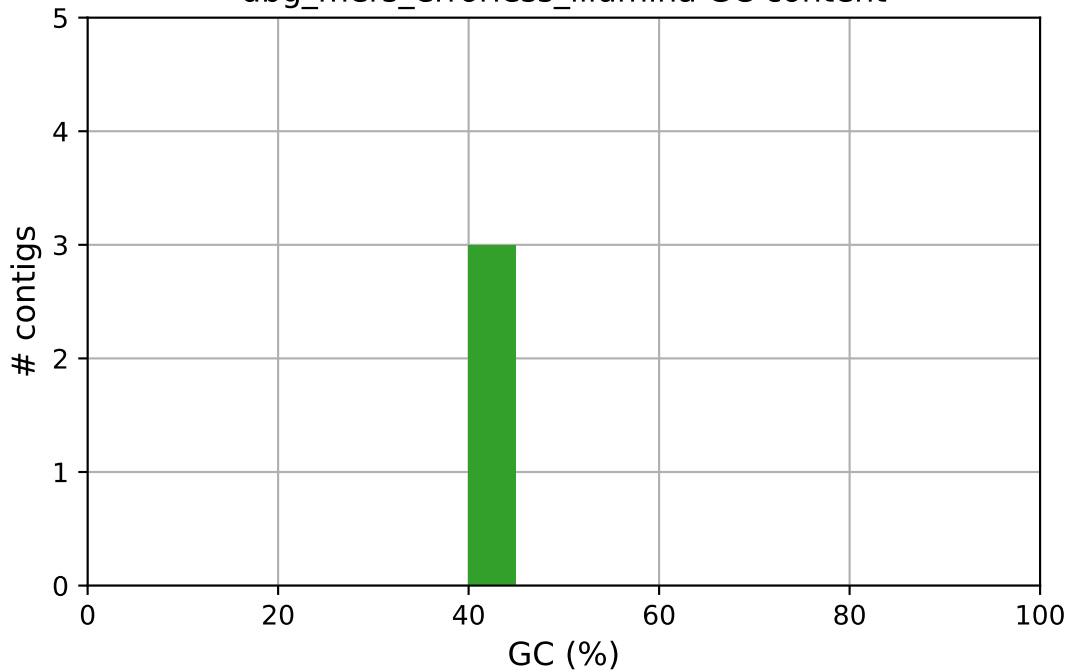
dbg\_mers\_error\_illumina



dbg\_mers\_error\_ont GC content

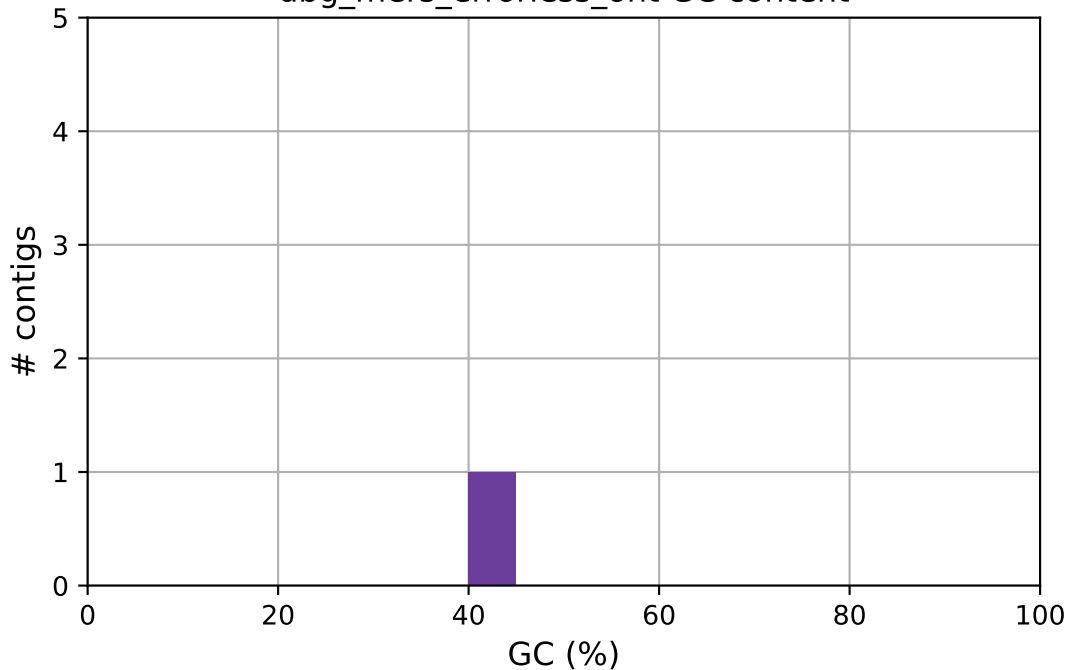


dbg\_mers\_errorless\_illumina GC content



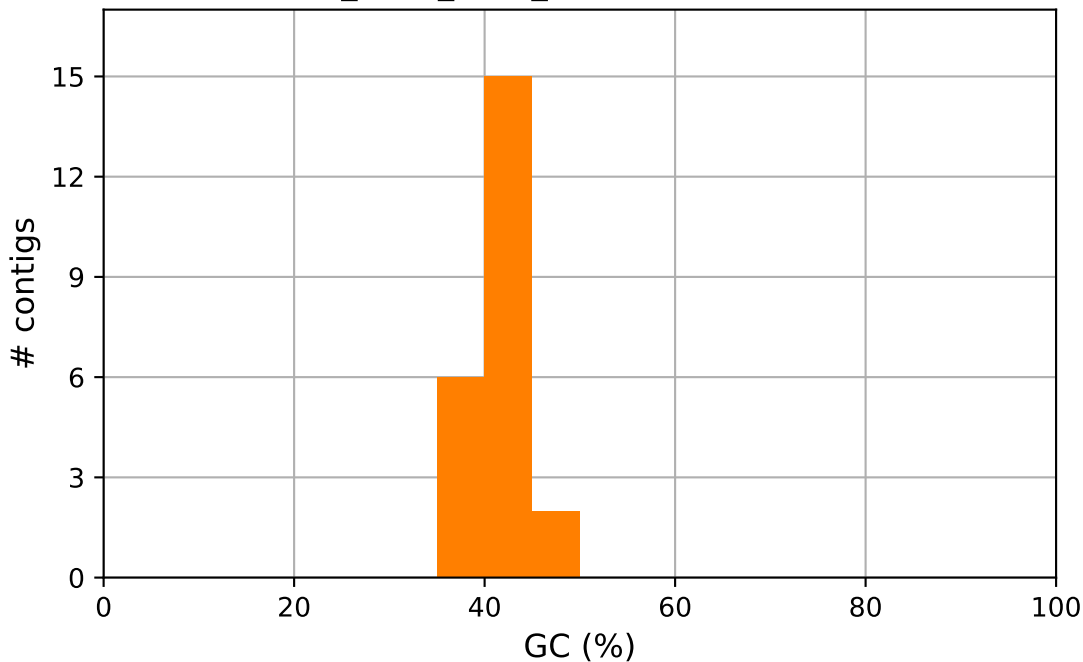
dbg\_mers\_errorless\_illumina

dbg\_mers\_errorless\_ont GC content



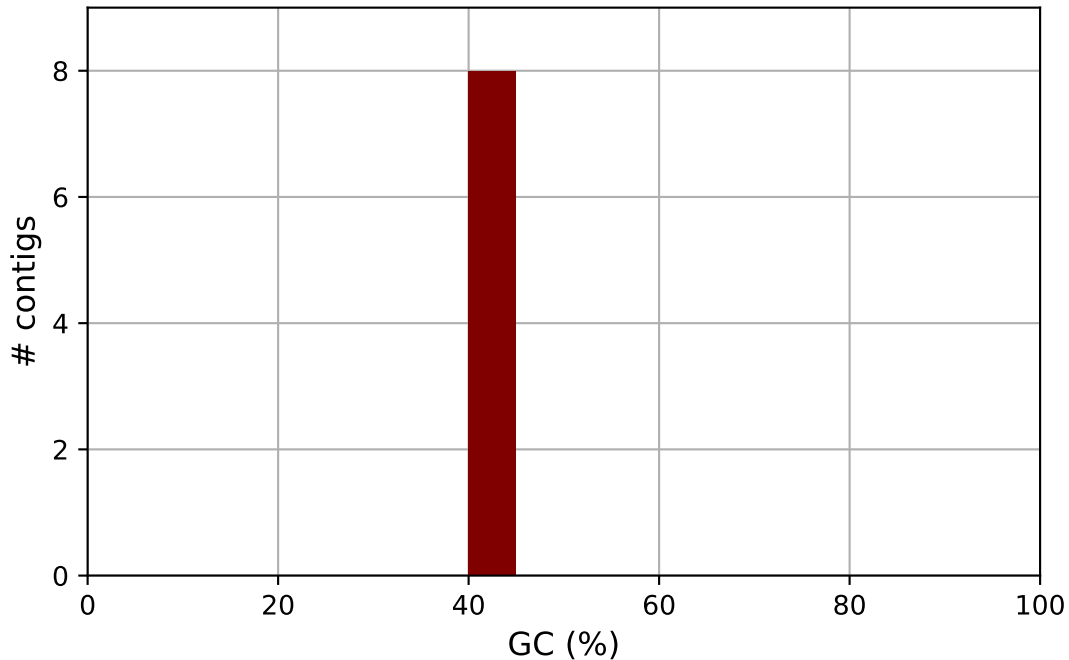
dbg\_mers\_errorless\_ont

olc\_mers\_error\_illumina GC content



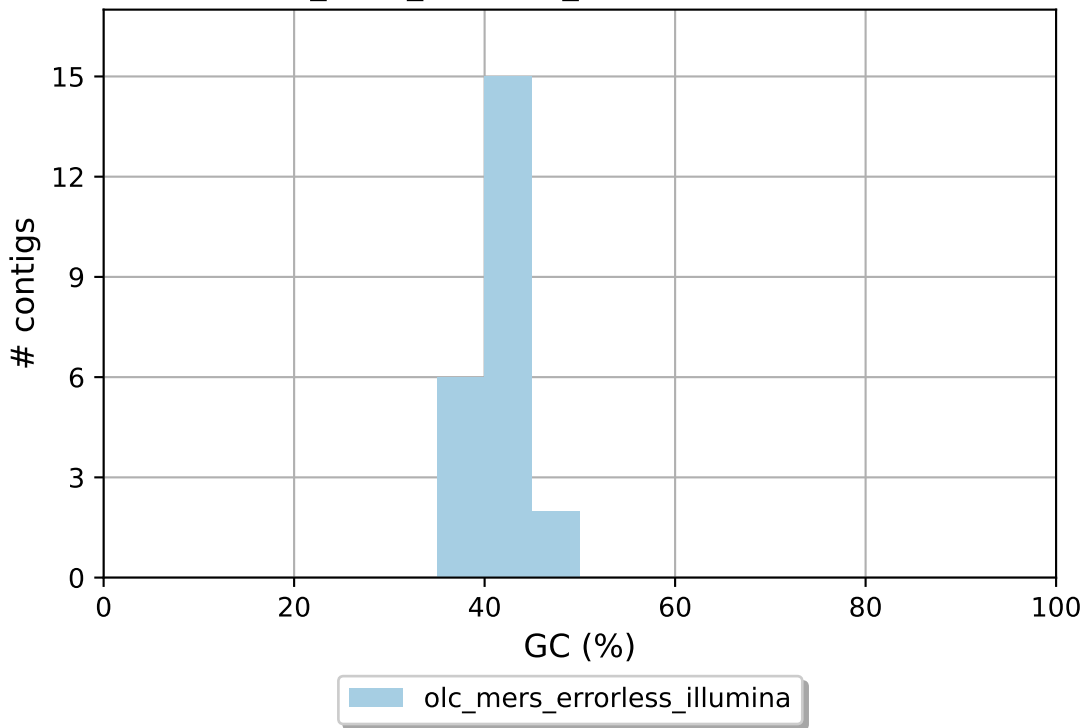
olc\_mers\_error\_illumina

olc\_mers\_error\_ont GC content

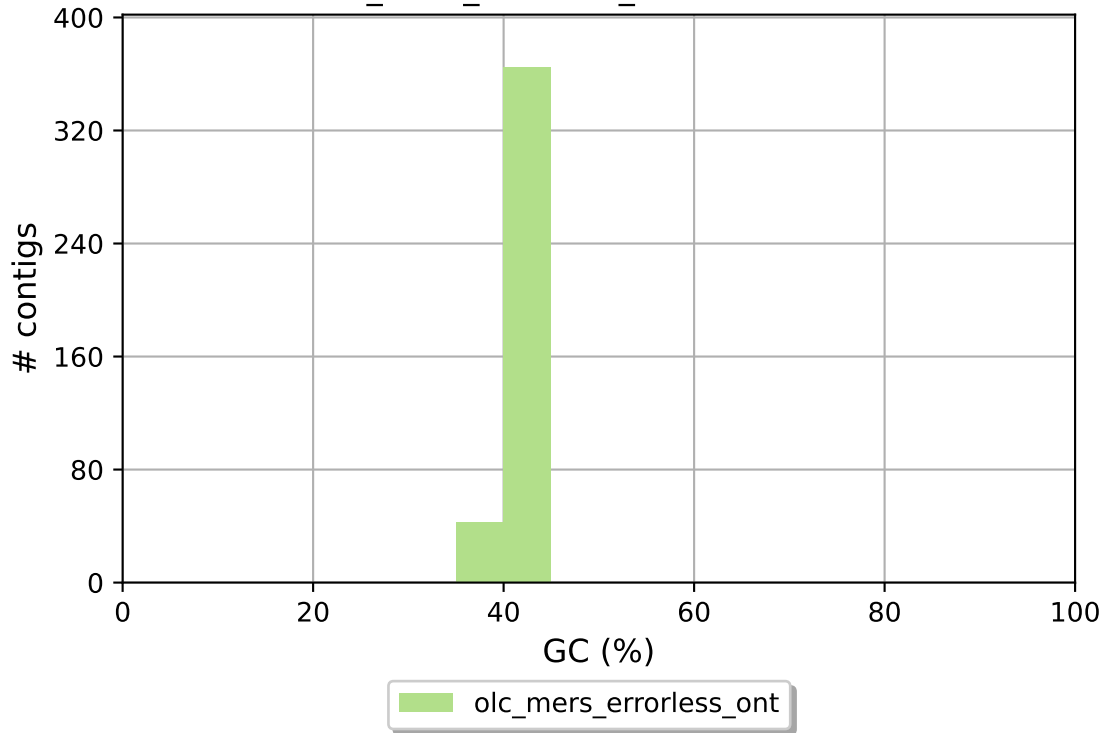


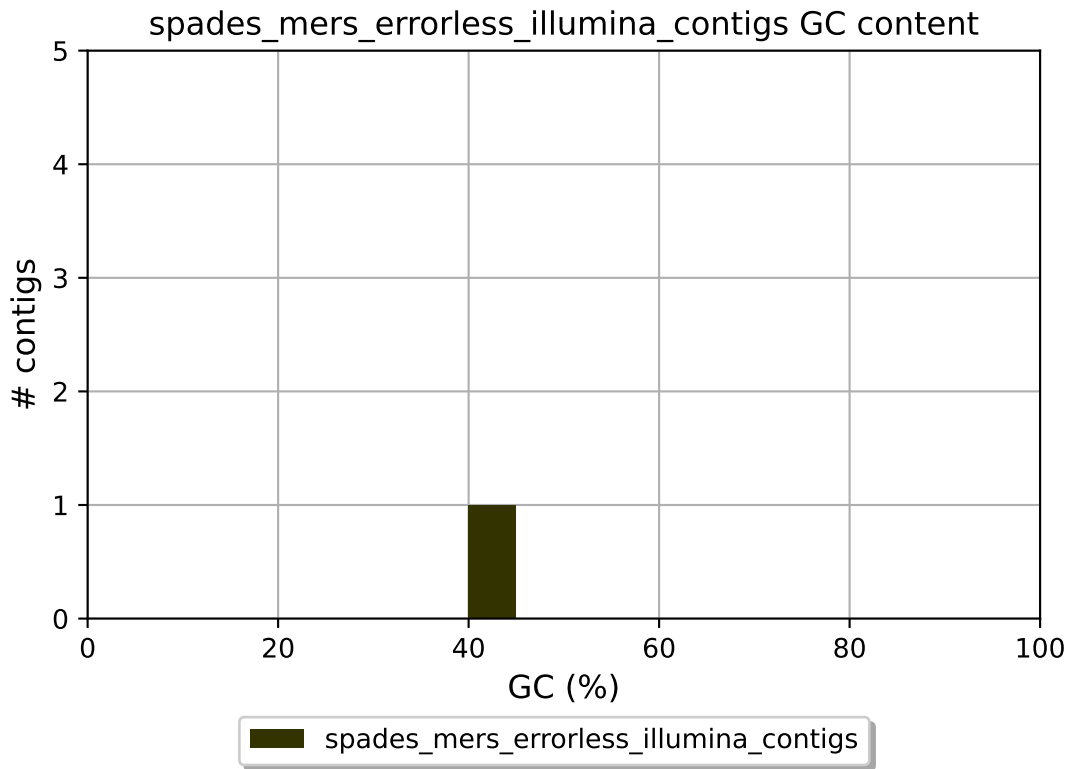
olc\_mers\_error\_ont

olc\_mers\_errorless\_illumina GC content

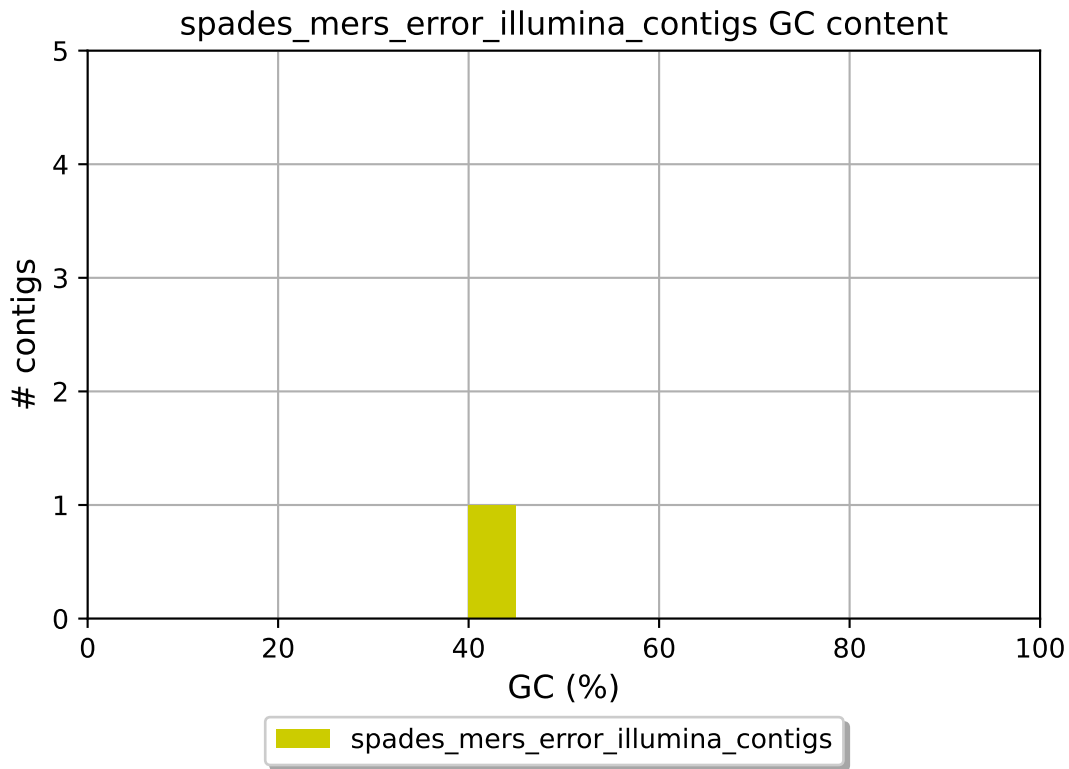


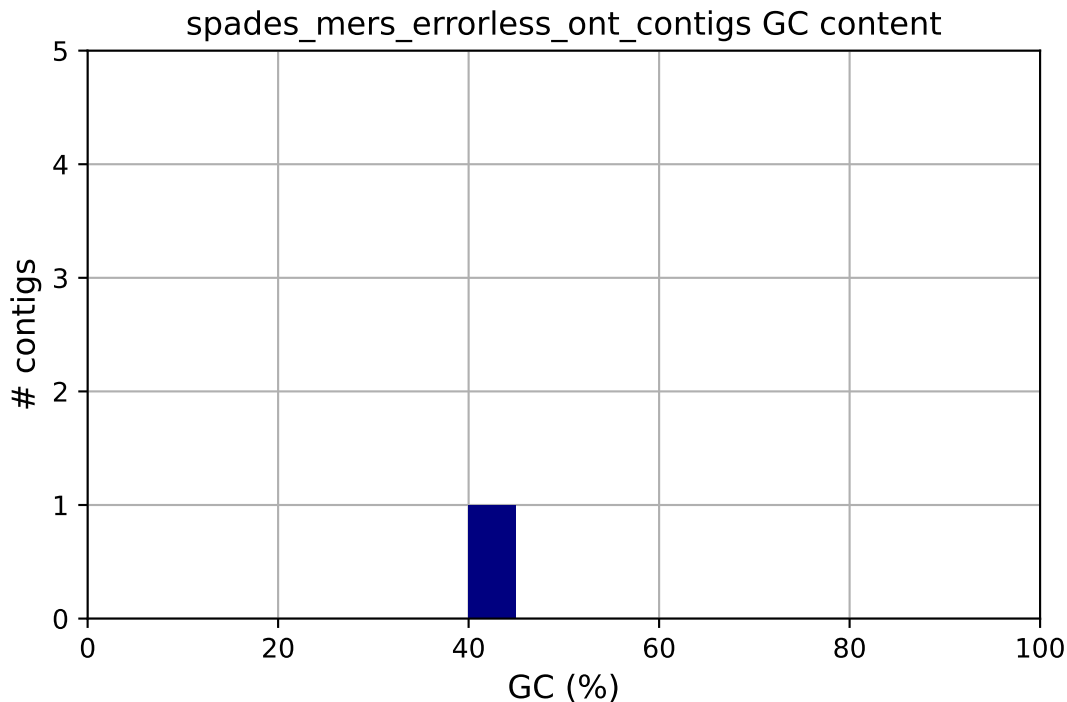
olc\_mers\_errorless\_ont GC content





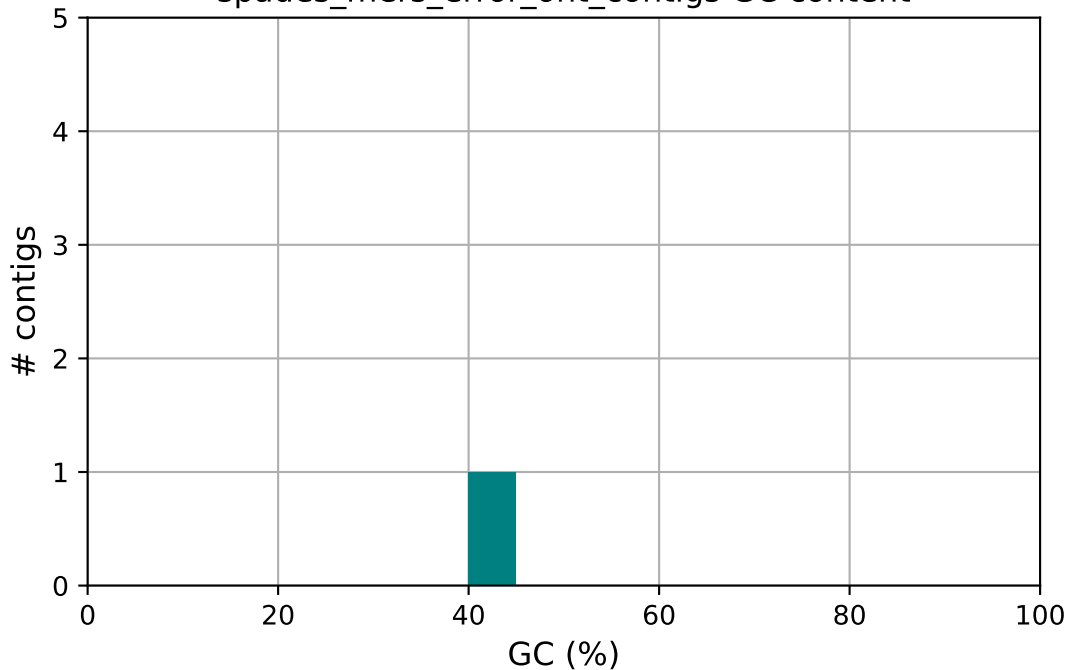






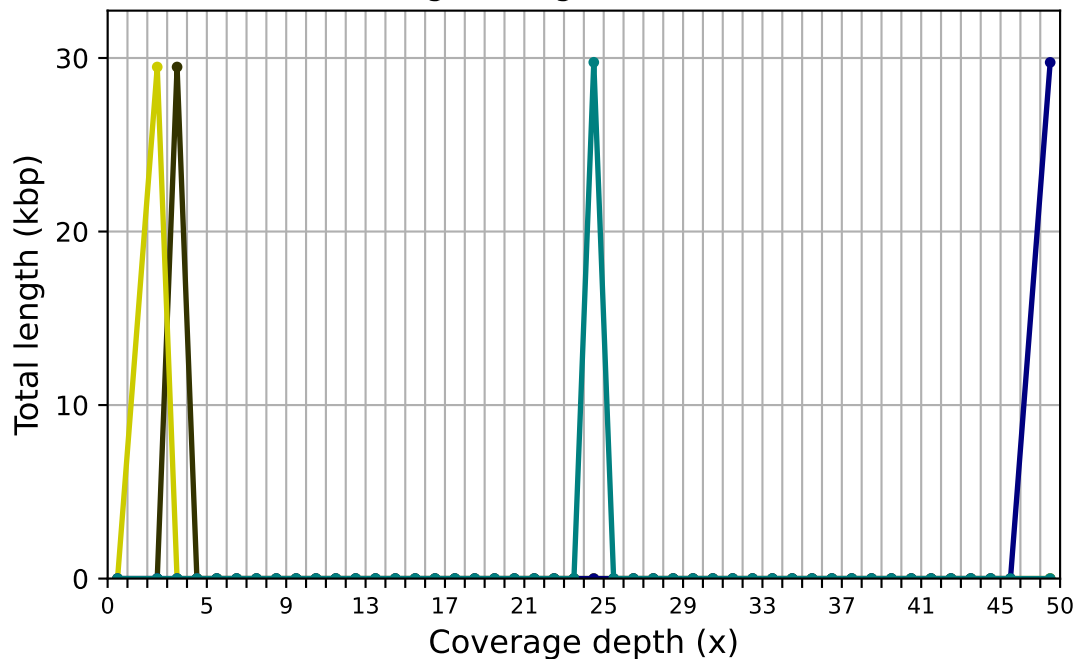
spades\_mers\_errorless\_ont\_contigs

spades\_mers\_error\_ont\_contigs GC content



spades\_mers\_error\_ont\_contigs

Coverage histogram (bin size: 1x)

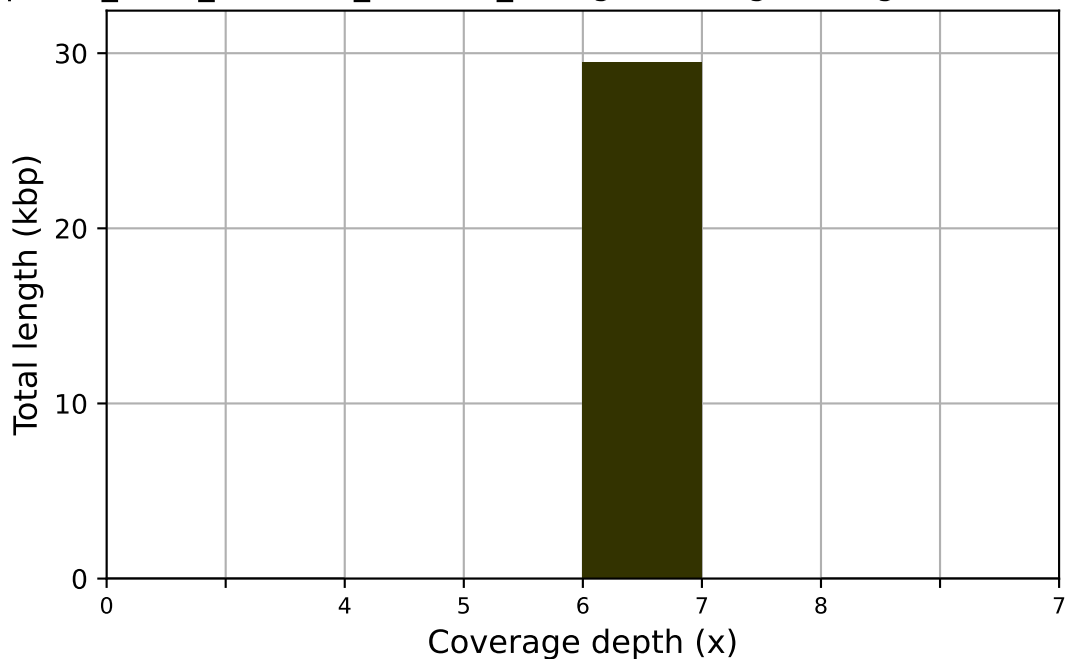


\_errorless\_illumina\_contigs  
\_error\_illumina\_contigs

—●— spades\_mers\_errorless\_ont\_contigs

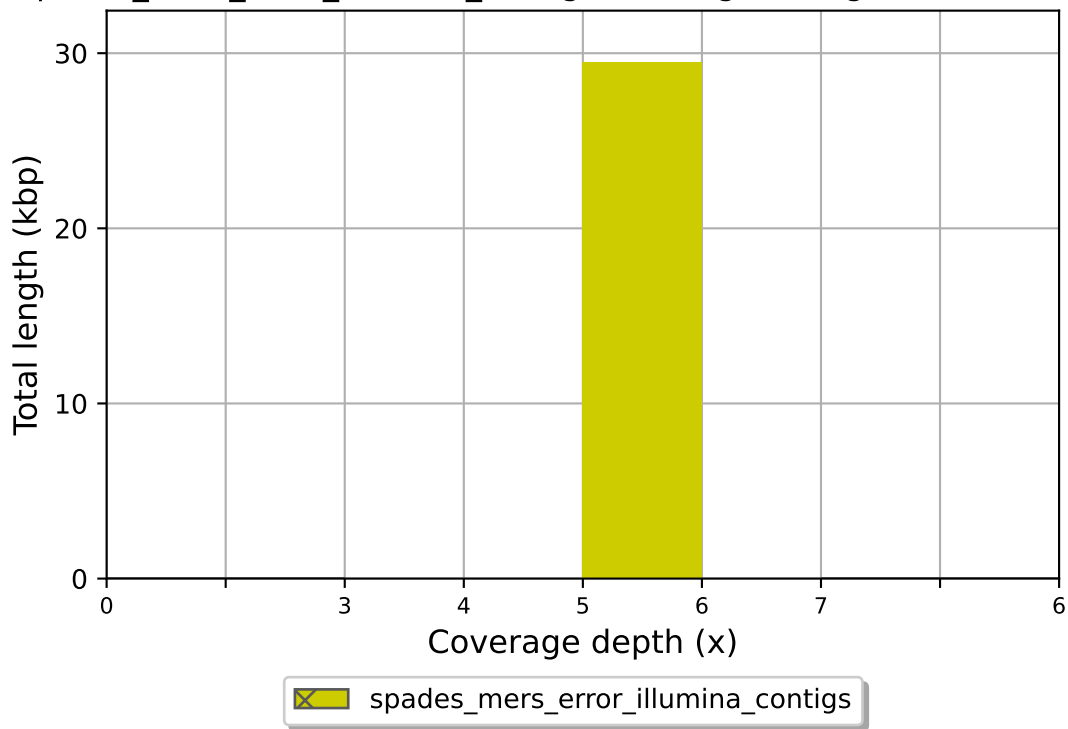
—●— spades\_me

spades\_mers\_errorless\_illumina\_contigs coverage histogram (bin size: 1x)

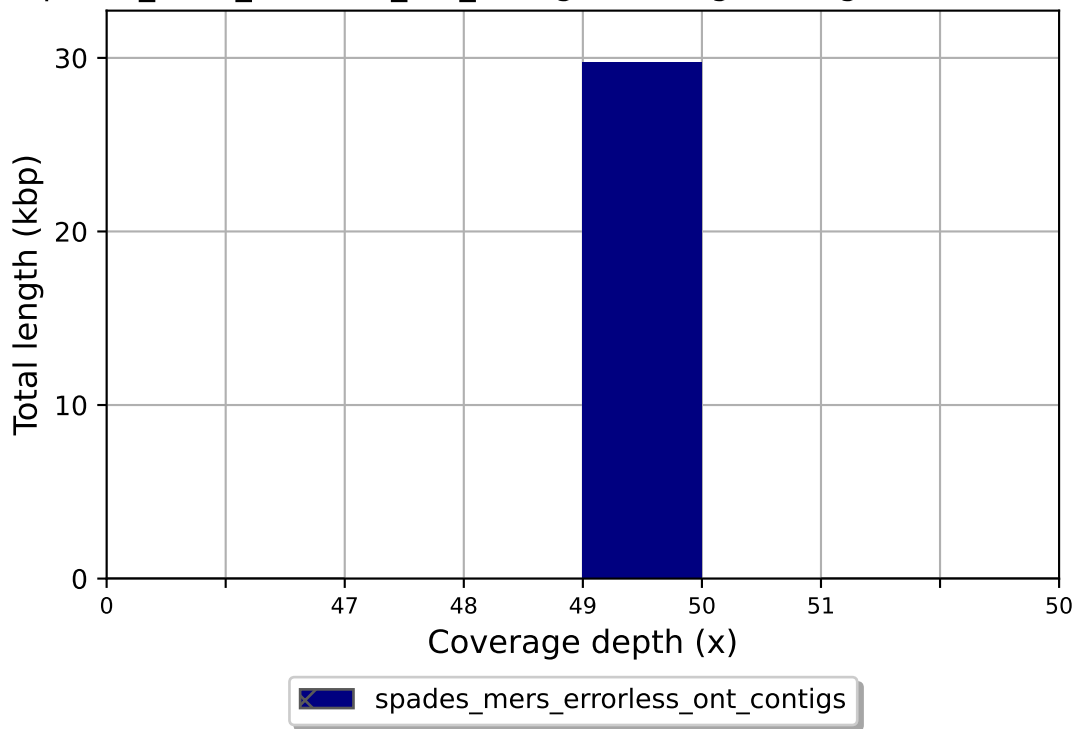


spades\_mers\_errorless\_illumina\_contigs

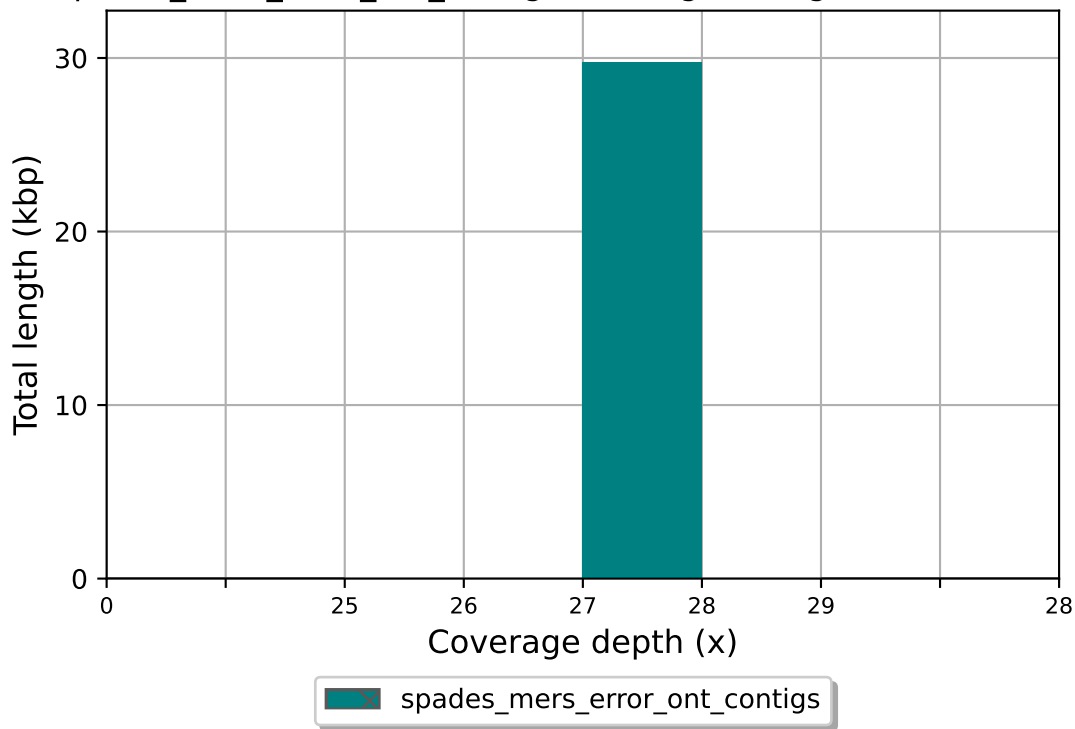
spades\_mers\_error\_illumina\_contigs coverage histogram (bin size: 1x)



spades\_mers\_errorless\_ont\_contigs coverage histogram (bin size: 1x)

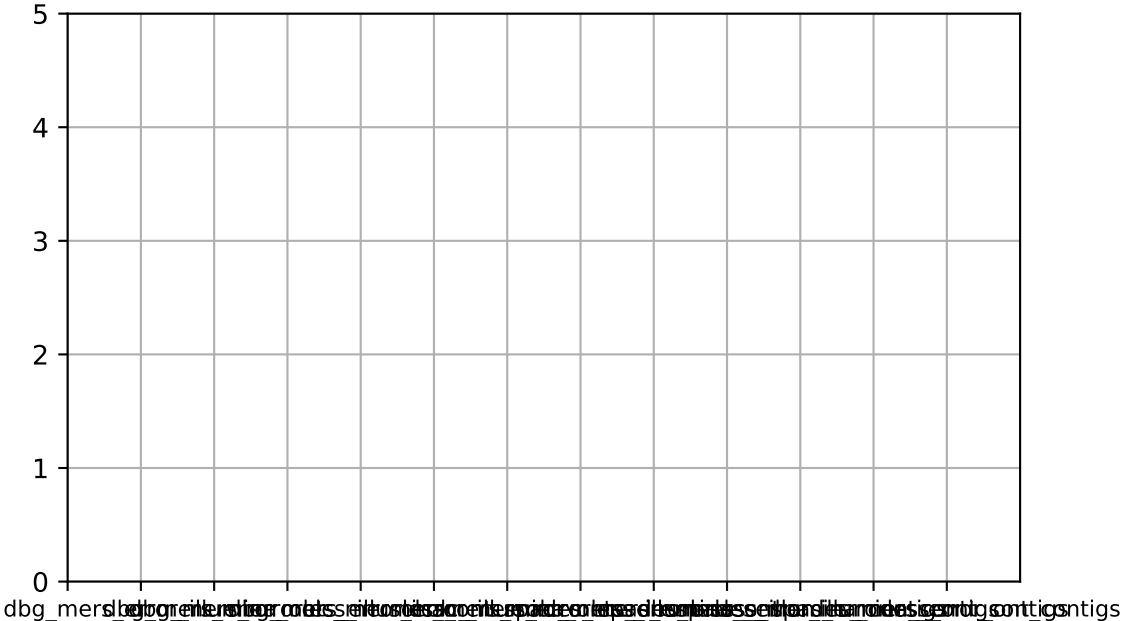


spades\_mers\_error\_ont\_contigs coverage histogram (bin size: 1x)

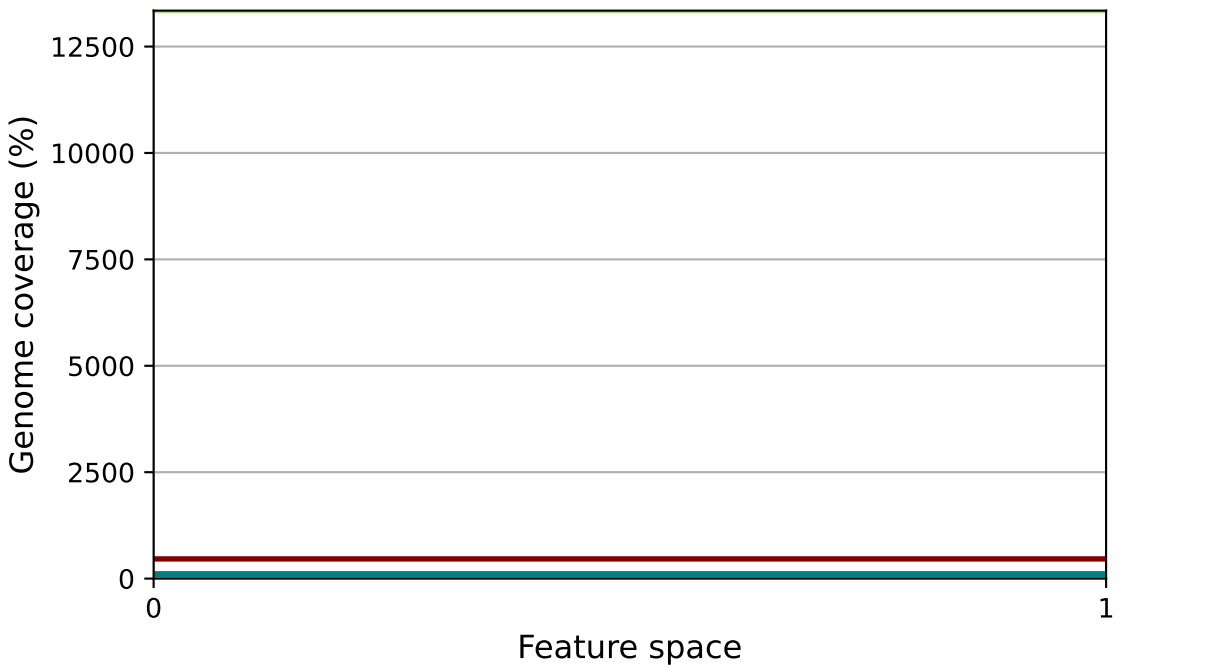




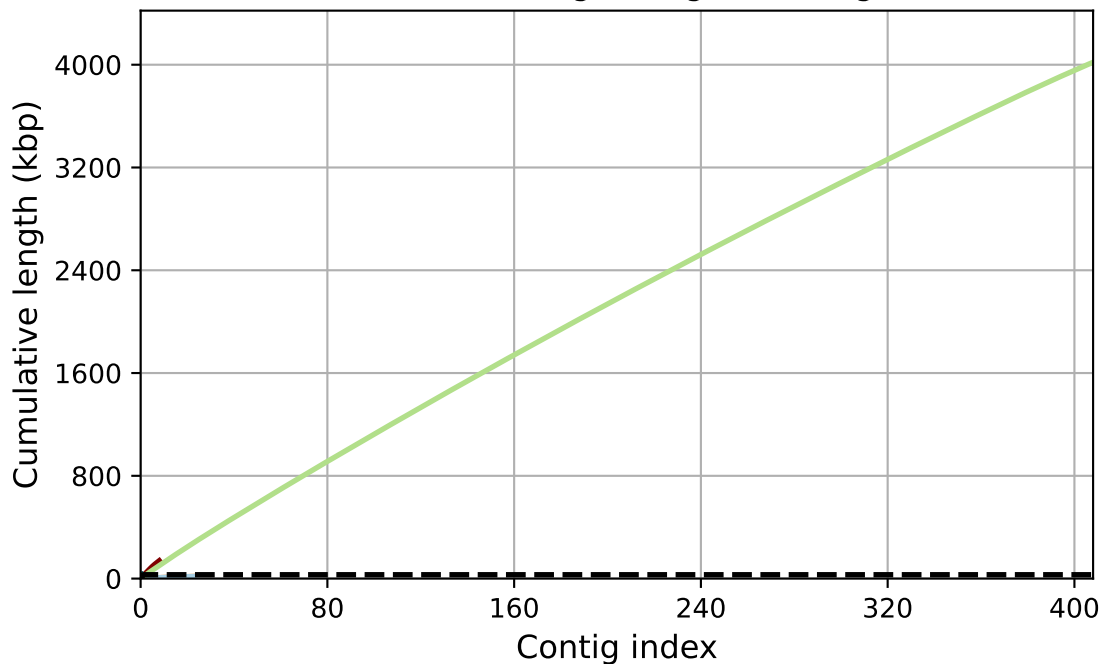
# Misassemblies



# FRCurve (misassemblies)



# Cumulative length (aligned contigs)



error\_illumina

error\_ont

errorless\_illumina

errorless\_ont

olc\_mers\_error\_ont

olc\_mers\_errorless\_illumina

olc\_mers\_errorless\_ont

spades\_mers\_errorless\_illumina\_contigs

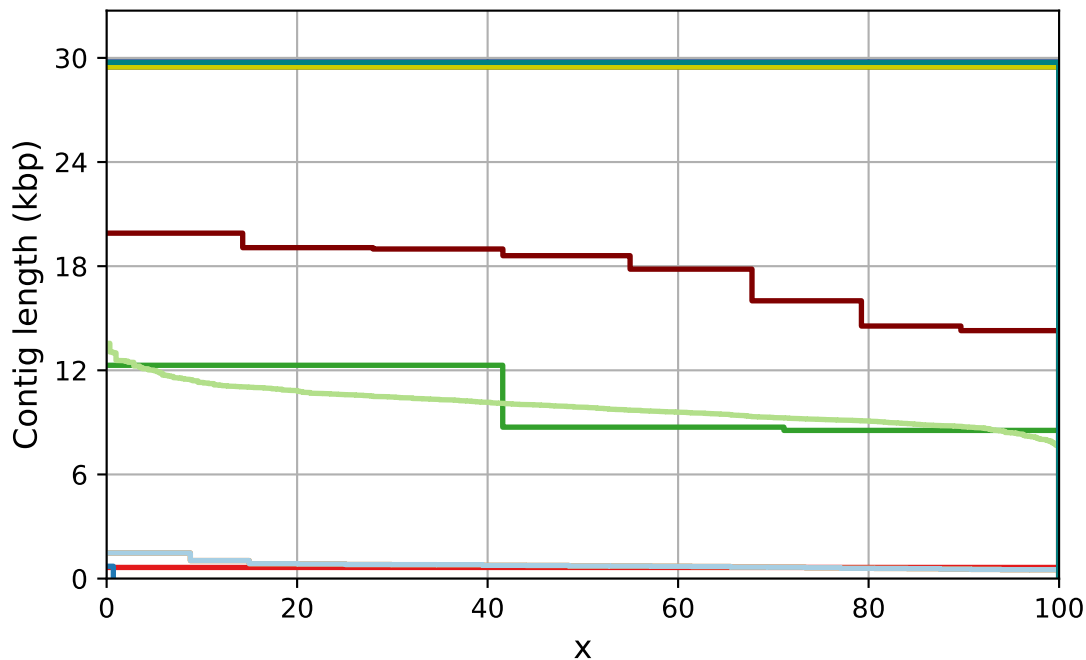
spades\_mers\_error\_ont

spades\_mers\_errorless\_illumina

spades\_mers\_errorless\_ont

Reference

# NAx

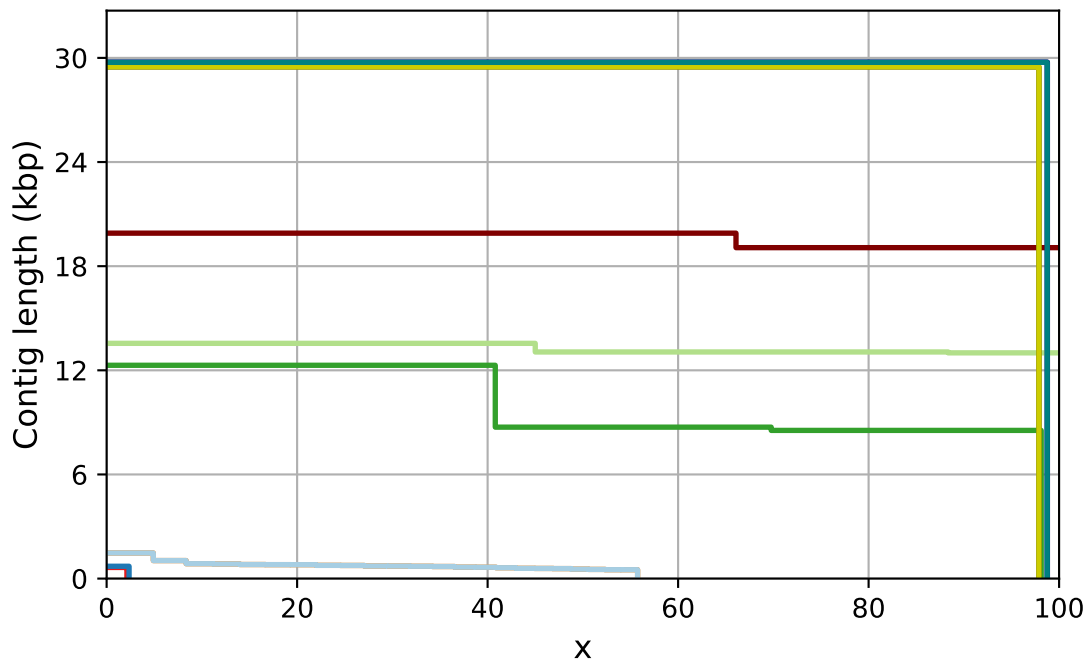


rs\_error\_illumina  
rs\_error\_ont  
rs\_errorless\_illumina  
rs\_errorless\_ont

olc\_mers\_error\_illumina  
olc\_mers\_error\_ont  
olc\_mers\_errorless\_illumina  
olc\_mers\_errorless\_ont

spades\_mers\_errorless\_illumina  
spades\_mers\_error\_illumina  
spades\_mers\_errorless\_ont  
spades\_mers\_error\_ont

# NGAx



rs\_error\_illumina

rs\_error\_ont

rs\_errorless\_illumina

rs\_errorless\_ont

olc\_mers\_error\_illumina

olc\_mers\_error\_ont

olc\_mers\_errorless\_illumina

olc\_mers\_errorless\_ont

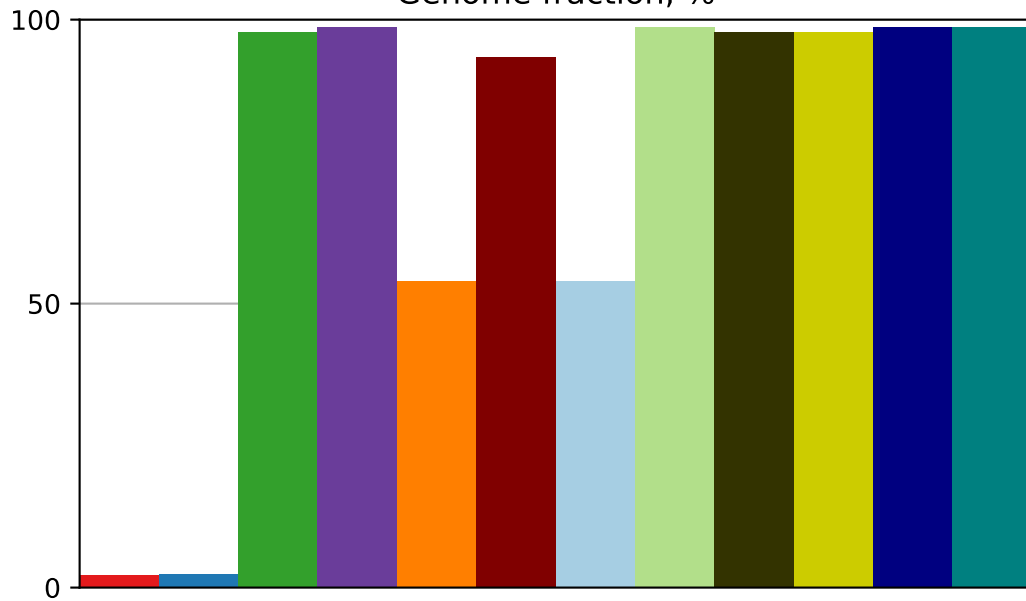
spades\_mers\_errorless\_illumina

spades\_mers\_error\_illumina

spades\_mers\_errorless\_ont

spades\_mers\_error\_ont

Genome fraction, %



rs\_error\_illumina

rs\_error\_ont

rs\_errorless\_illumina

rs\_errorless\_ont

olc\_mers\_error\_illumina

olc\_mers\_error\_ont

olc\_mers\_errorless\_illumina

olc\_mers\_errorless\_ont

spades\_mers\_errorless\_illumina

spades\_mers\_error\_illumina

spades\_mers\_errorless\_ont

spades\_mers\_error\_ont