

# Report

	pacbio_10x	pacbio_20x	pacbio_40x	pacbio_80x	illumina	illumina_pacbio_10x	illumina_pacbio_20x	illumina_pacbio_40x	illumina_pacbio_80x
# contigs (>= 0 bp)	188	27	2	1	156	20	20	17	17
# contigs (>= 1000 bp)	188	27	2	1	77	1	2	1	1
# contigs (>= 5000 bp)	164	27	2	1	54	1	1	1	1
# contigs (>= 10000 bp)	127	27	1	1	50	1	1	1	1
# contigs (>= 25000 bp)	48	26	1	1	43	1	1	1	1
# contigs (>= 50000 bp)	13	22	1	1	30	1	1	1	1
Total length (>= 0 bp)	3711522	4599531	4660281	4653172	4568145	4644141	4642746	4644499	4644499
Total length (>= 1000 bp)	3711522	4599531	4660281	4653172	4549457	4640301	4639608	4641733	4641733
Total length (>= 5000 bp)	3626288	4599531	4660281	4653172	4497628	4640301	4636213	4641733	4641733
Total length (>= 10000 bp)	3347194	4599531	4651851	4653172	4468021	4640301	4636213	4641733	4641733
Total length (>= 25000 bp)	2079447	4584084	4651851	4653172	4365494	4640301	4636213	4641733	4641733
Total length (>= 50000 bp)	876571	4436814	4651851	4653172	3922327	4640301	4636213	4641733	4641733
# contigs	188	27	2	1	87	3	3	2	2
Largest contig	87550	751505	4651851	4653172	285426	4640301	4636213	4641733	4641733
Total length	3711522	4599531	4660281	4653172	4556248	4641646	4640150	4642275	4642275
Reference length	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675
GC (%)	50.55	50.75	50.77	50.79	50.74	50.78	50.78	50.79	50.79
Reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
N50	27922	272518	4651851	4653172	134691	4640301	4636213	4641733	4641733
NG50	20713	272518	4651851	4653172	134691	4640301	4636213	4641733	4641733
N75	16500	120357	4651851	4653172	78605	4640301	4636213	4641733	4641733
NG75	8087	120357	4651851	4653172	67330	4640301	4636213	4641733	4641733
L50	40	5	1	1	12	1	1	1	1
LG50	59	5	1	1	12	1	1	1	1
L75	84	13	1	1	22	1	1	1	1
LG75	142	13	1	1	23	1	1	1	1
# misassemblies	9	9	8	8	0	6	6	6	6
# misassembled contigs	5	4	1	1	0	1	1	1	1
Misassembled contigs length	125937	1108020	4651851	4653172	0	4640301	4636213	4641733	4641733
# local misassemblies	1	2	2	2	6	6	5	5	5
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	6	4	1	1	1
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	0	0	0	0	542	542	542	542	542
Genome fraction (%)	79.785	98.967	99.998	99.998	98.110	99.904	99.916	99.962	99.962
Duplication ratio	1.003	1.002	1.004	1.003	1.001	1.001	1.001	1.001	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	21.95	63.94	21.25	21.24	21.24
# mismatches per 100 kbp	31.71	4.33	1.12	0.32	1.08	10.20	9.15	9.62	9.66
# indels per 100 kbp	548.58	140.51	29.38	9.85	0.40	1.40	0.73	0.88	0.88
Largest alignment	87550	484372	2161944	2981897	285326	3023180	3023576	3023577	3023577
Total aligned length	3711381	4599517	4659840	4653170	4552795	4637945	4635836	4637961	4637961
NA50	26796	200681	948576	2981897	134691	3023180	3023576	3023577	3023577
NGA50	20241	200681	948576	2981897	134691	3023180	3023576	3023577	3023577
NA75	15933	107489	874273	949202	78605	572345	572345	572345	572345
NGA75	7871	107489	874273	949202	67330	572345	572345	572345	572345
LA50	41	7	2	1	12	1	1	1	1
LGA50	60	7	2	1	12	1	1	1	1
LA75	86	15	3	2	22	2	2	2	2
LGA75	146	15	3	2	23	2	2	2	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

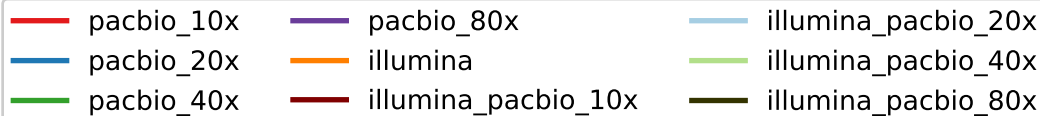
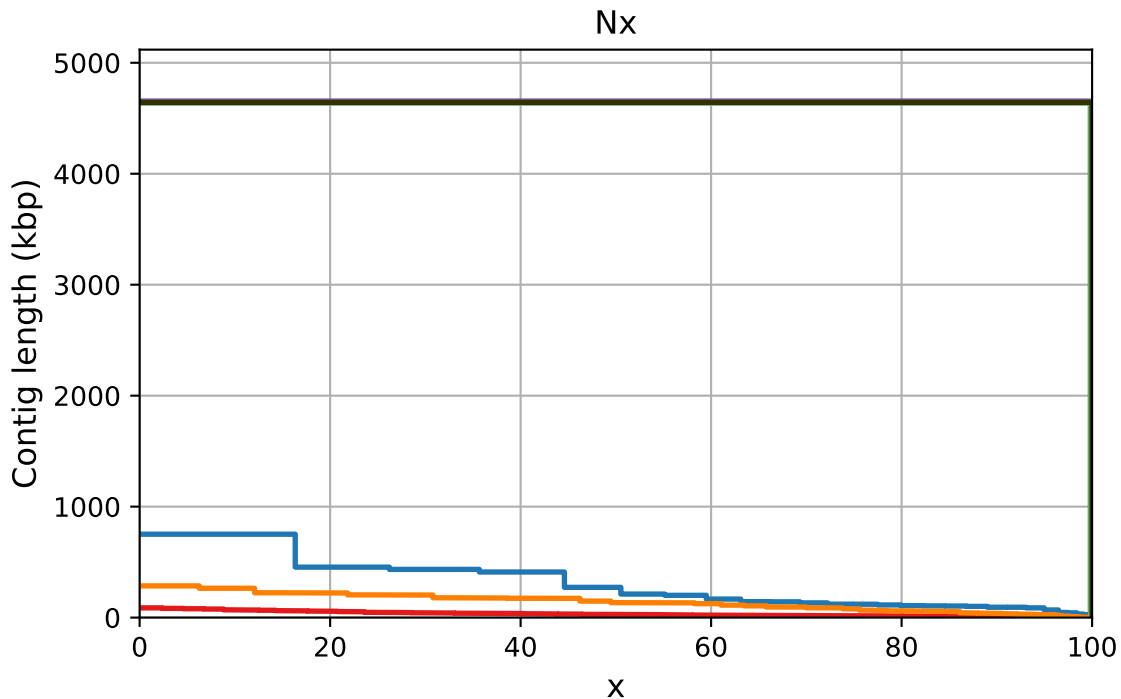
	pacbio_10x	pacbio_20x	pacbio_40x	pacbio_80x	illumina	illumina_pacbio_10x	illumina_pacbio_20x	illumina_pacbio_40x	illumina_pacbio_80x
# misassemblies	9	9	8	8	0	6	6	6	6
# contig misassemblies	9	9	8	8	0	6	6	6	6
# c. relocations	6	7	6	6	0	6	6	6	6
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	3	2	2	2	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0
# misassembled contigs	5	4	1	1	0	1	1	1	1
Misassembled contigs length	125937	1108020	4651851	4653172	0	4640301	4636213	4641733	4641733
# local misassemblies	1	2	2	2	6	6	5	5	5
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	6	4	1	1	1
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# mismatches	1174	199	52	15	49	473	424	446	448
# indels	20307	6452	1363	457	18	65	34	41	41
# indels (<= 5 bp)	20303	6448	1360	457	14	58	31	38	38
# indels (> 5 bp)	4	4	3	0	4	7	3	3	3
Indels length	21196	6677	1404	465	96	298	172	183	183

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

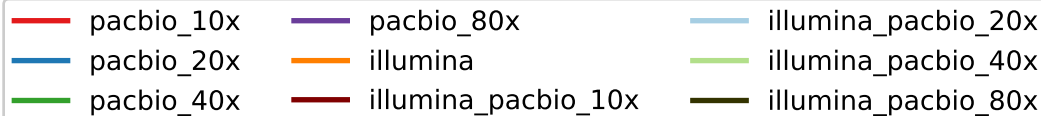
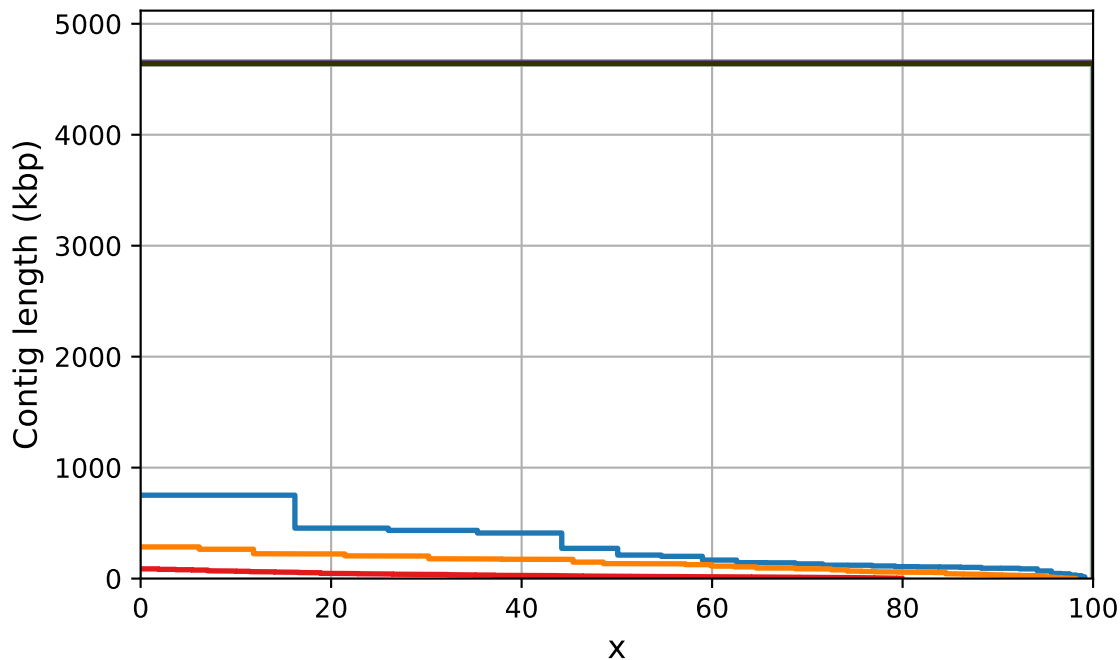
## Unaligned report

	pacbio_10x	pacbio_20x	pacbio_40x	pacbio_80x	illumina	illumina_pacbio_10x	illumina_pacbio_20x	illumina_pacbio_40x	illumina_pacbio_80x
# fully unaligned contigs	0	0	0	0	1	1	1	1	1
Fully unaligned length	0	0	0	0	542	542	542	542	542
# partially unaligned contigs	0	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0
# N's	0	0	0	0	1000	2968	986	986	986

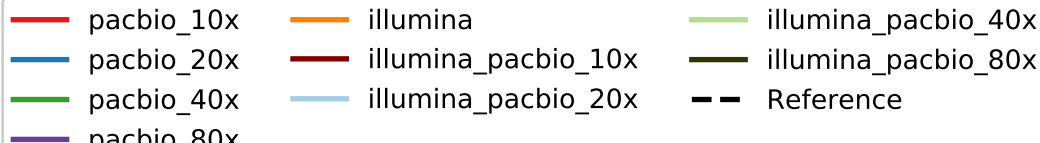
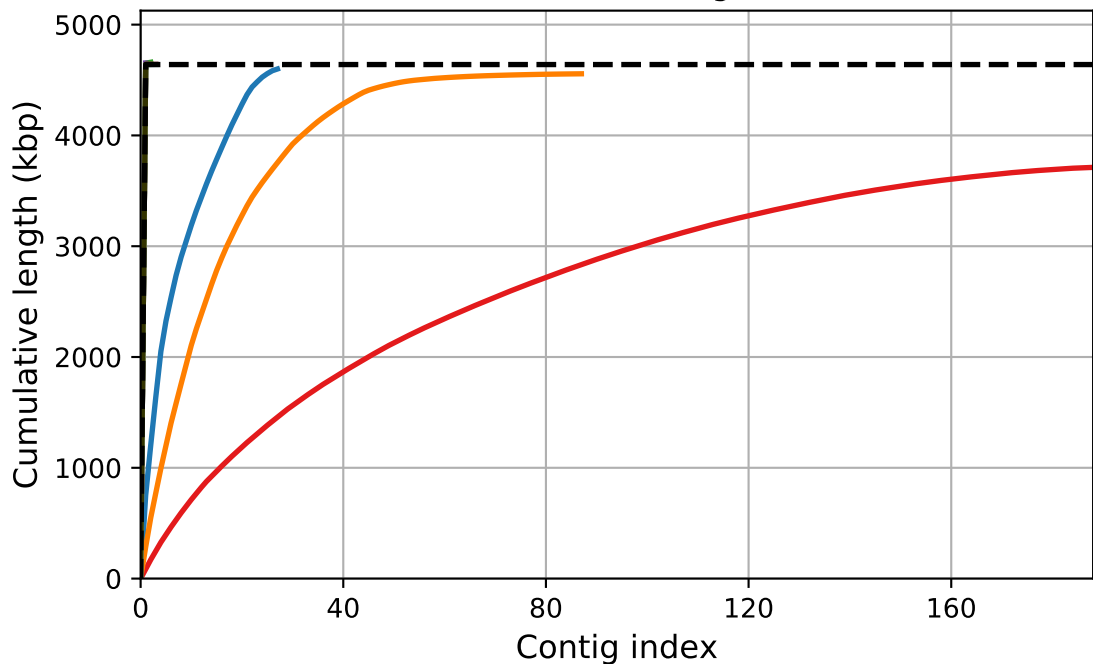
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



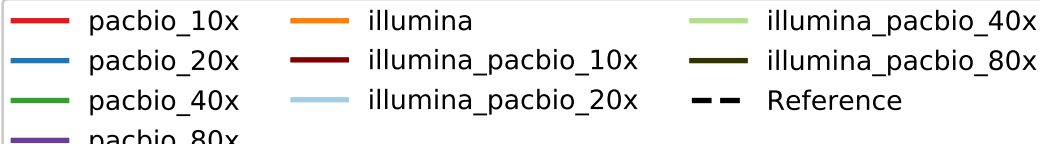
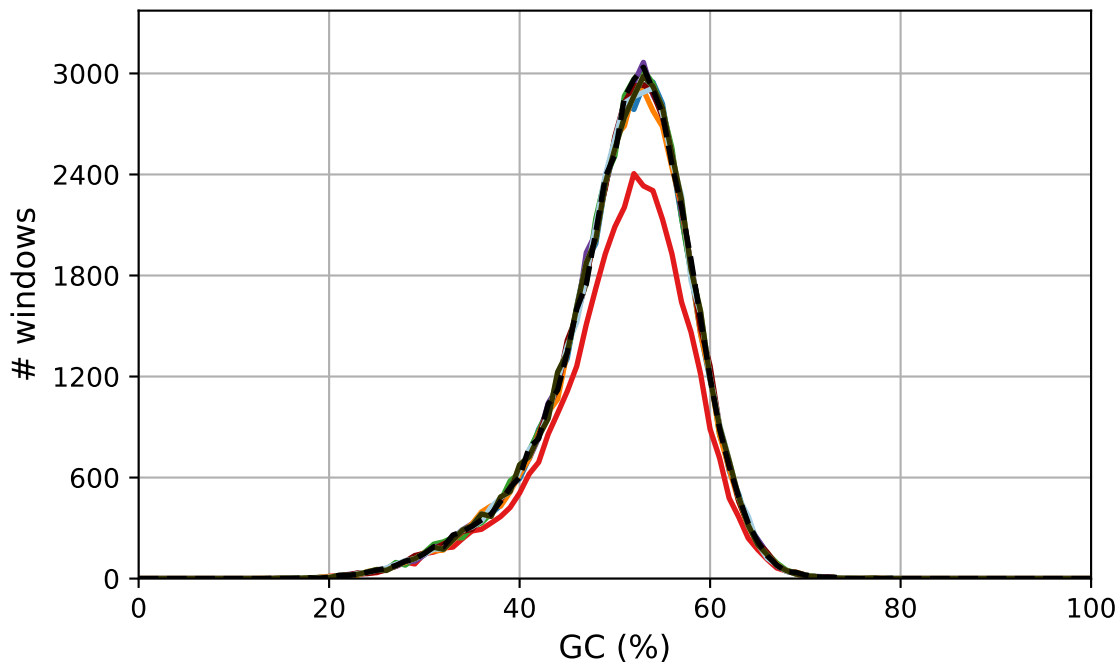
# NGx



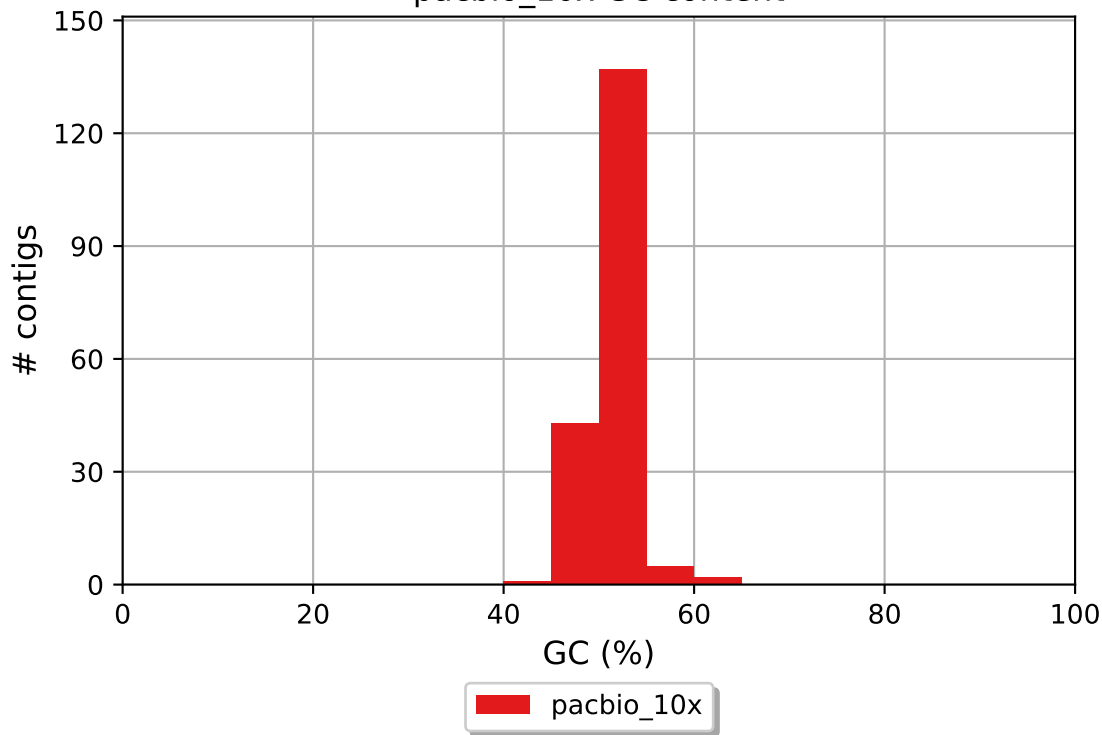
# Cumulative length



# GC content

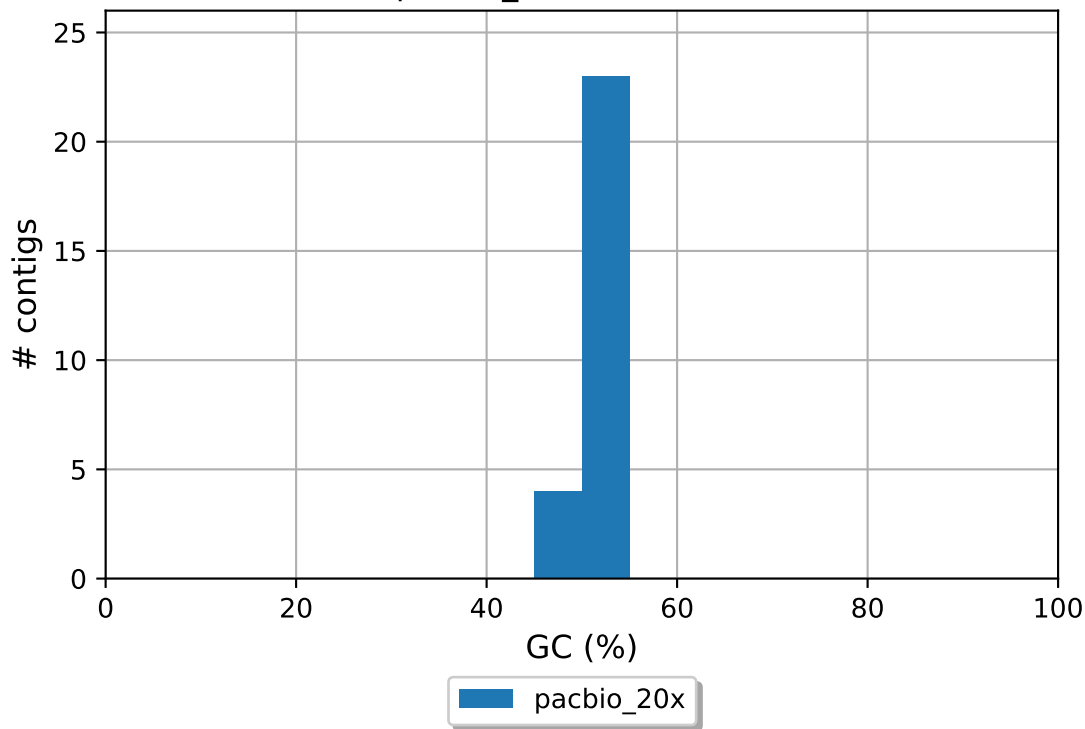


pacbio\_10x GC content

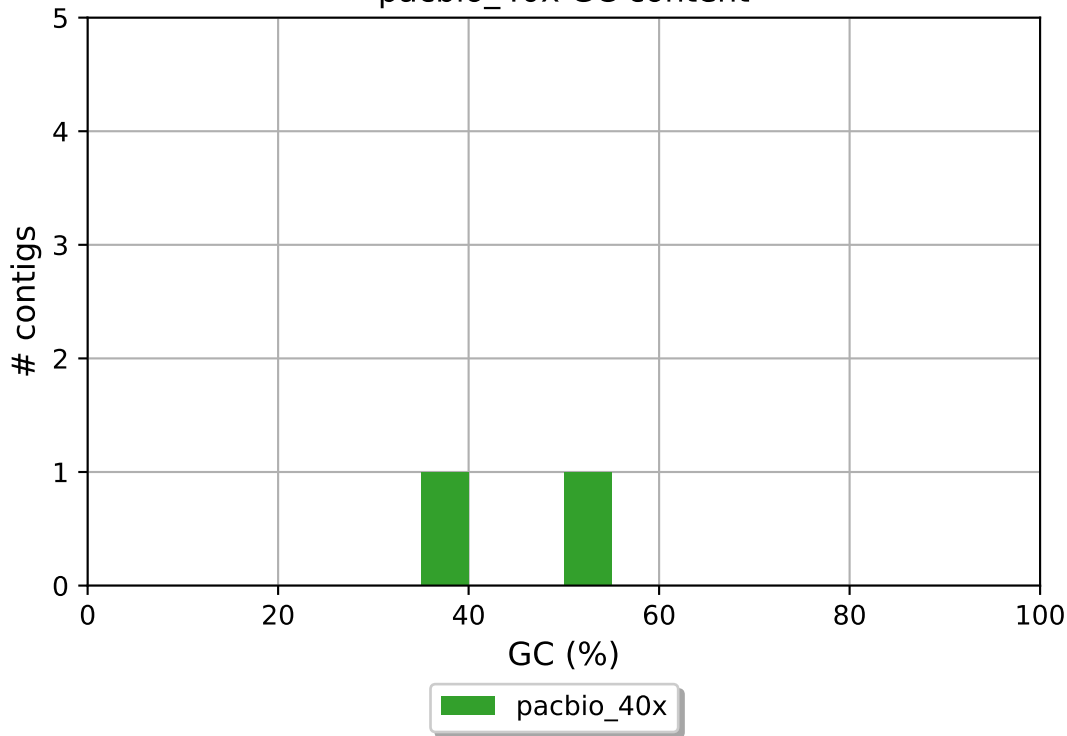




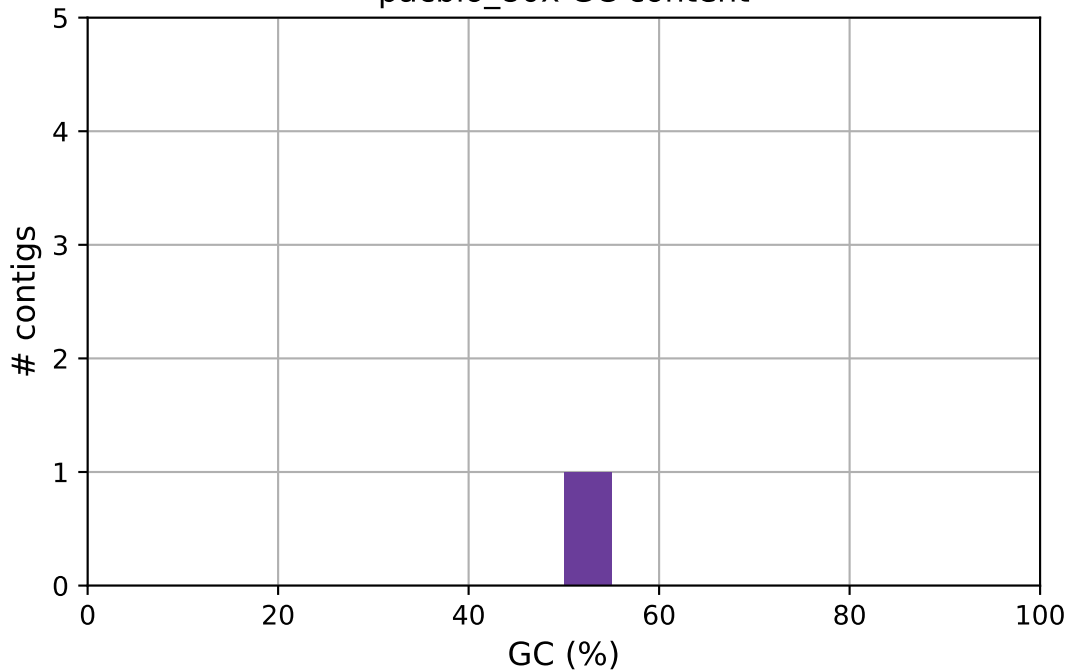
pacbio\_20x GC content



pacbio\_40x GC content

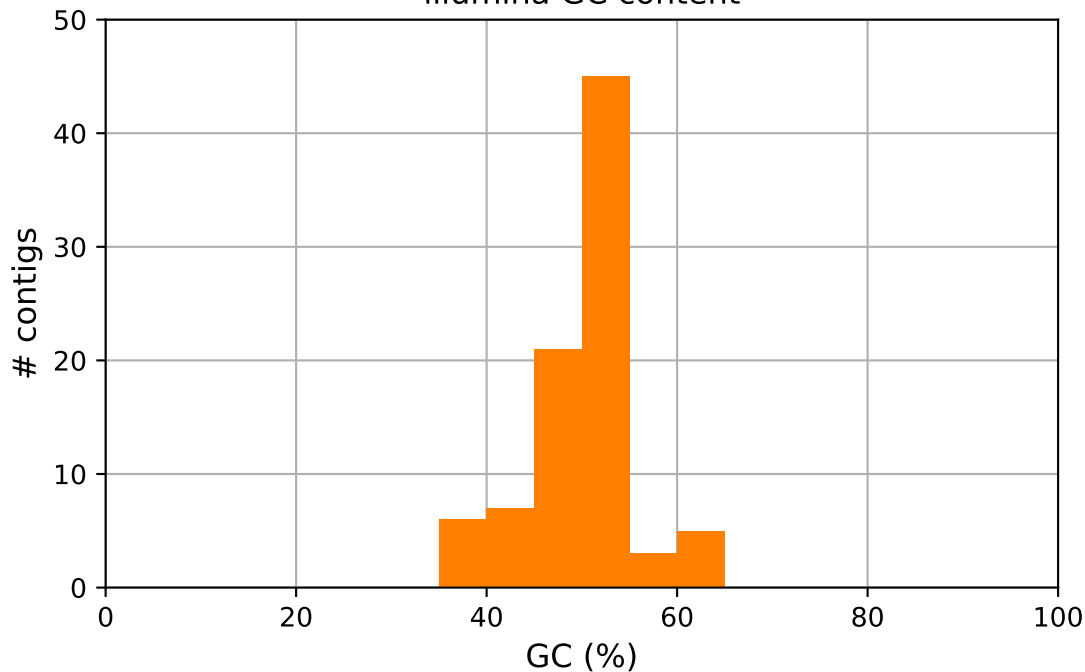


pacbio\_80x GC content



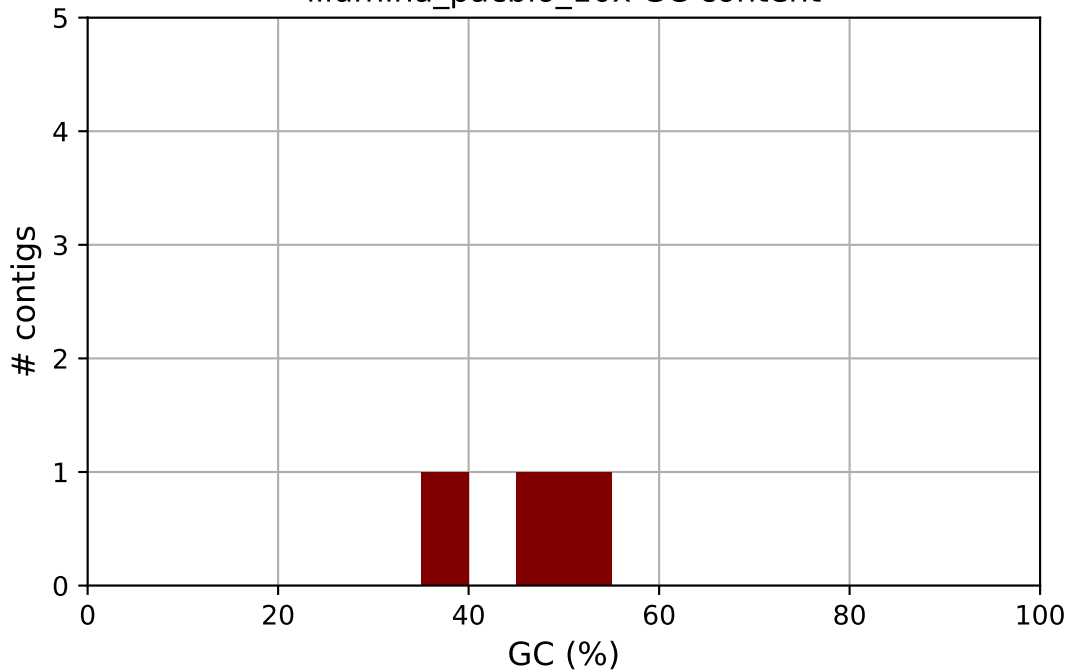
pacbio\_80x

illumina GC content



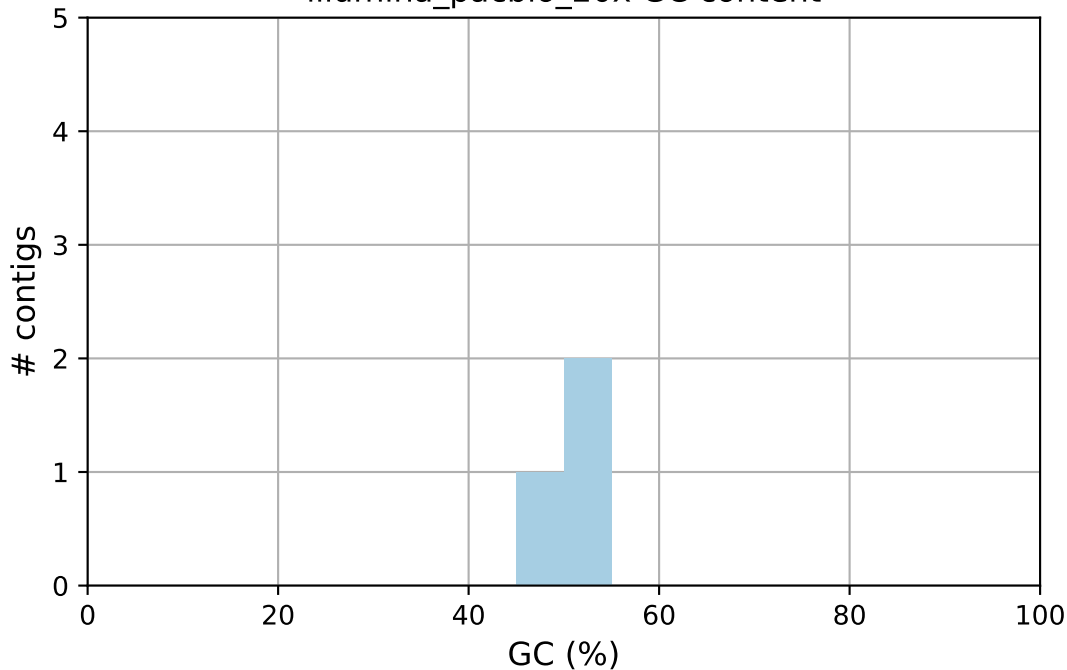
illumina

illumina\_pacbio\_10x GC content



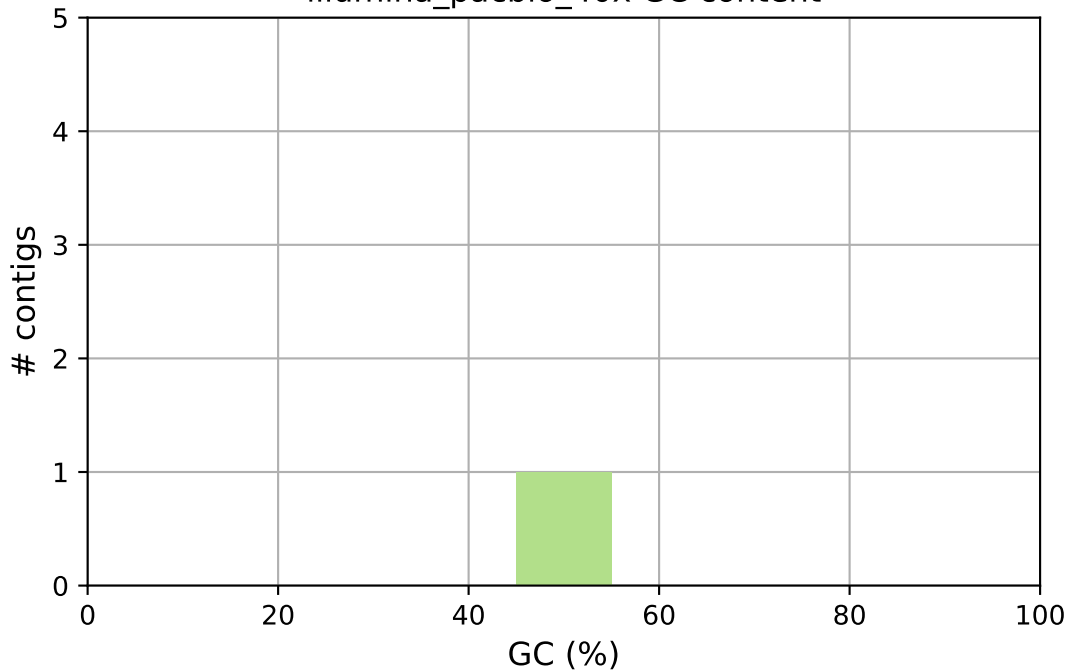
illumina\_pacbio\_10x

illumina\_pacbio\_20x GC content



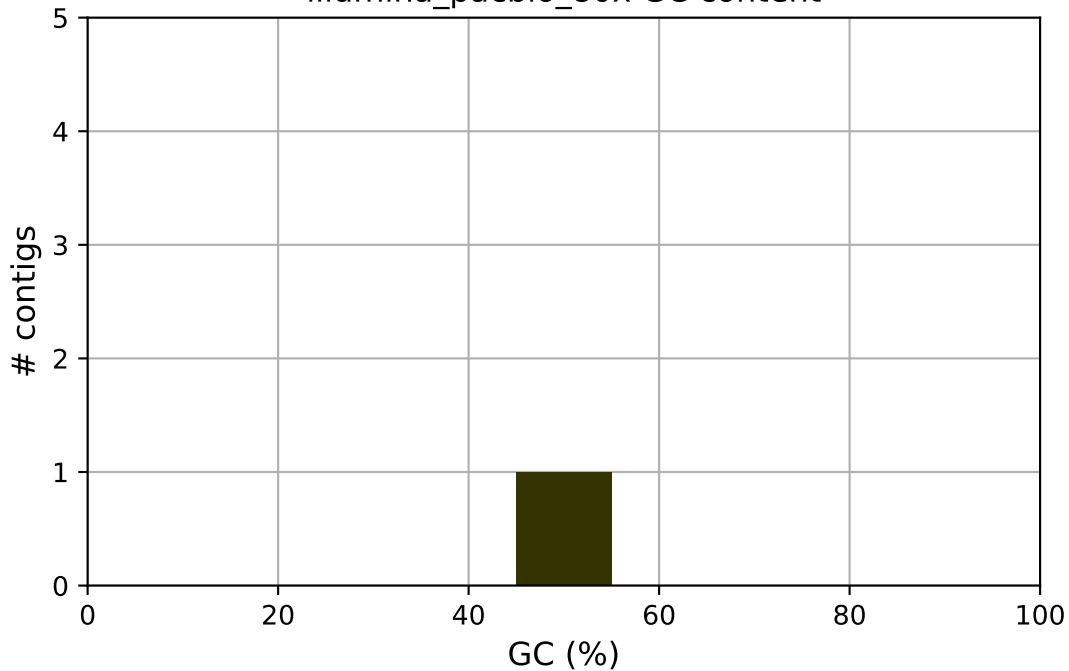
illumina\_pacbio\_20x

illumina\_pacbio\_40x GC content



illumina\_pacbio\_40x

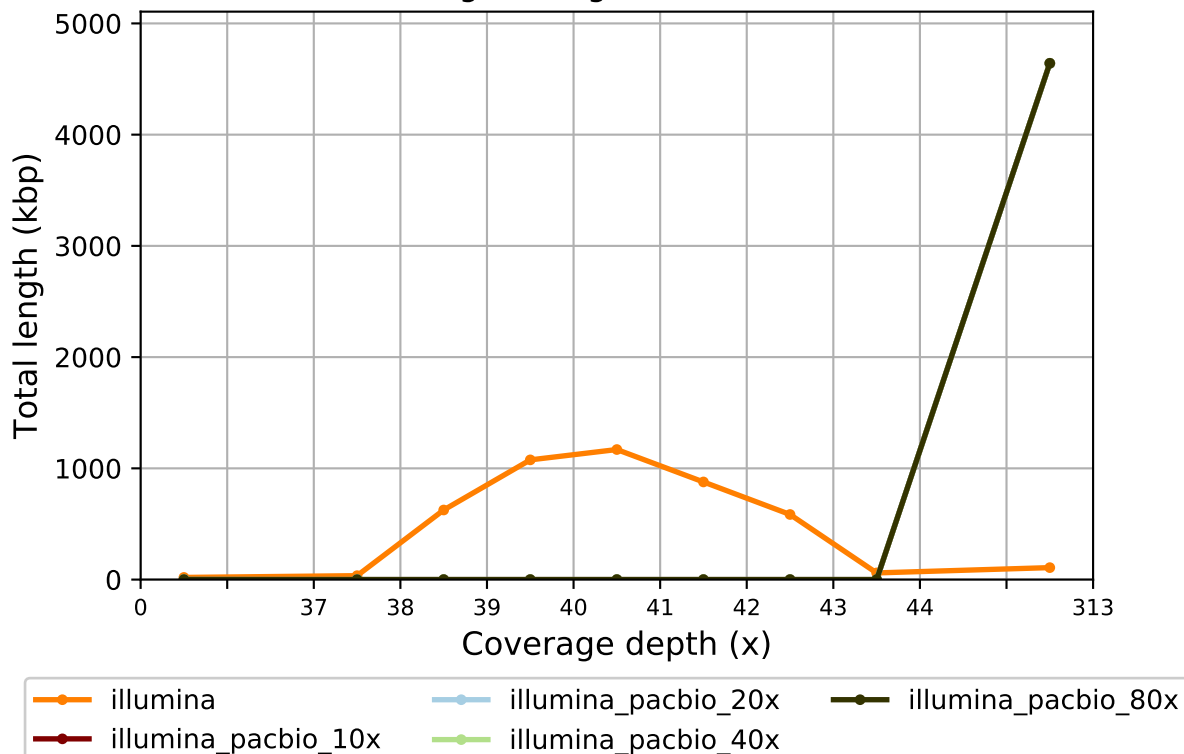
illumina\_pacbio\_80x GC content



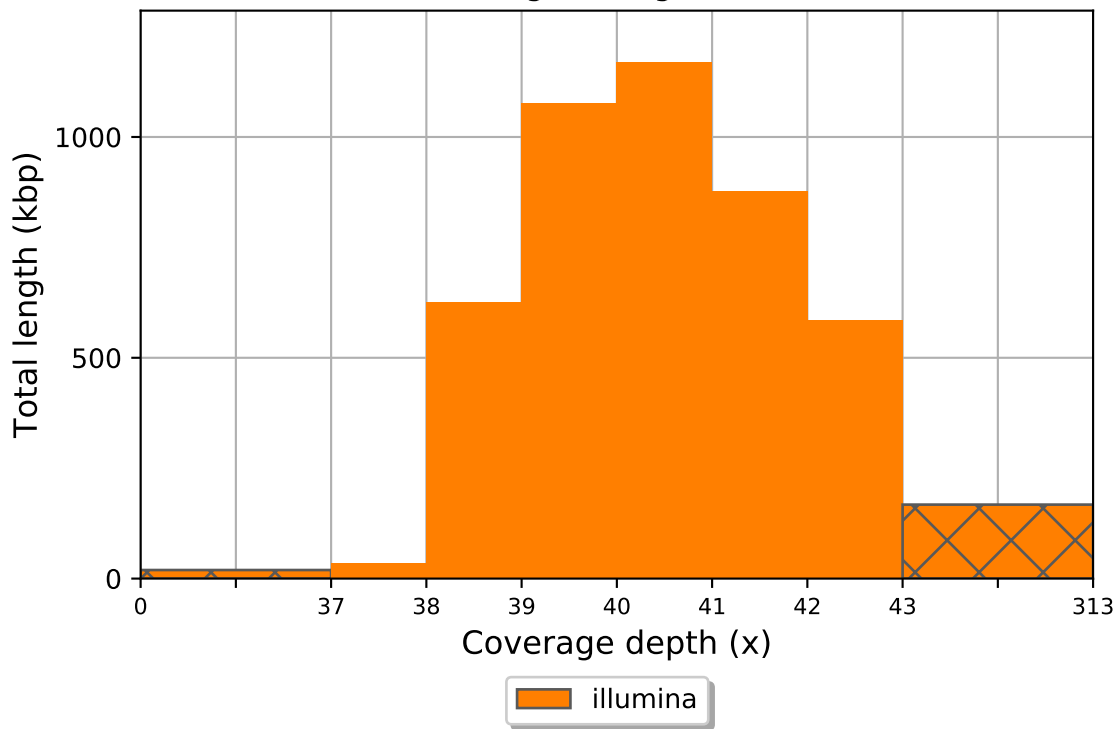
illumina\_pacbio\_80x



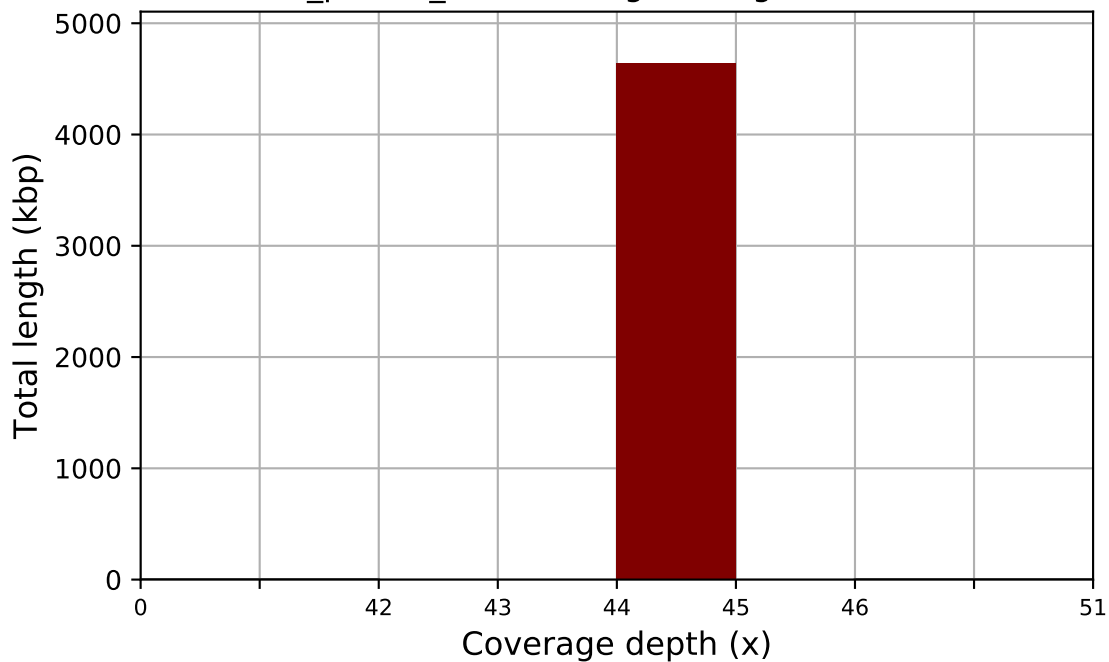
Coverage histogram (bin size: 1x)



illumina coverage histogram (bin size: 1x)

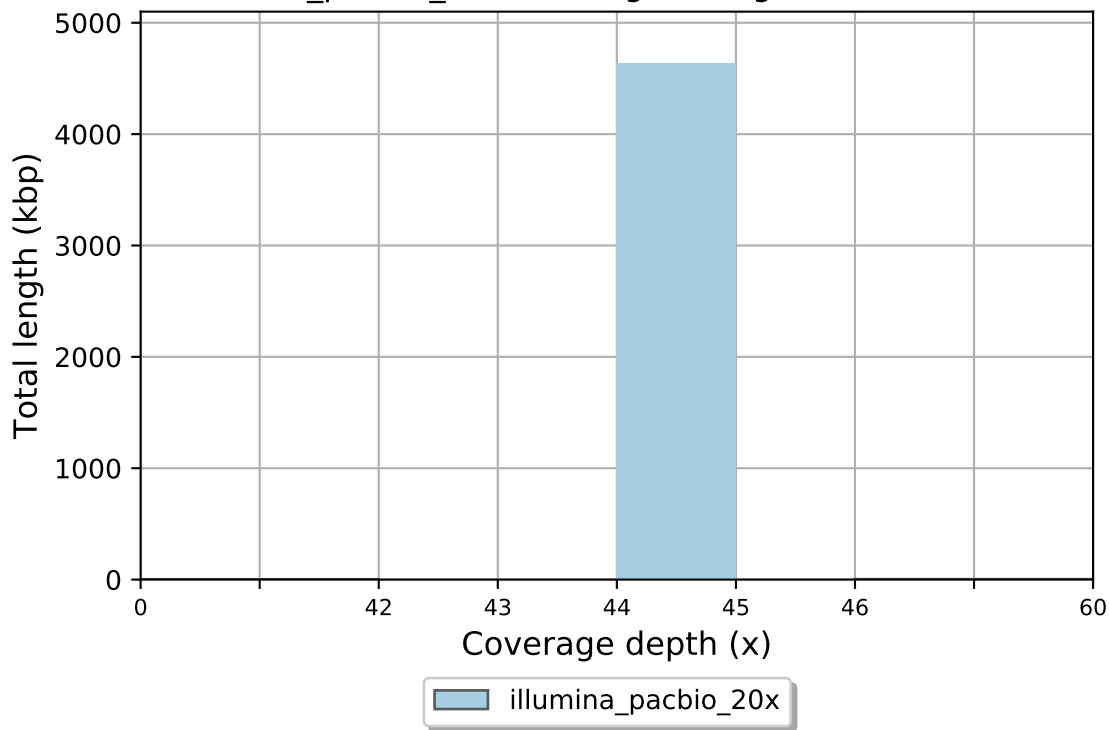


illumina\_pacbio\_10x coverage histogram (bin size: 1x)

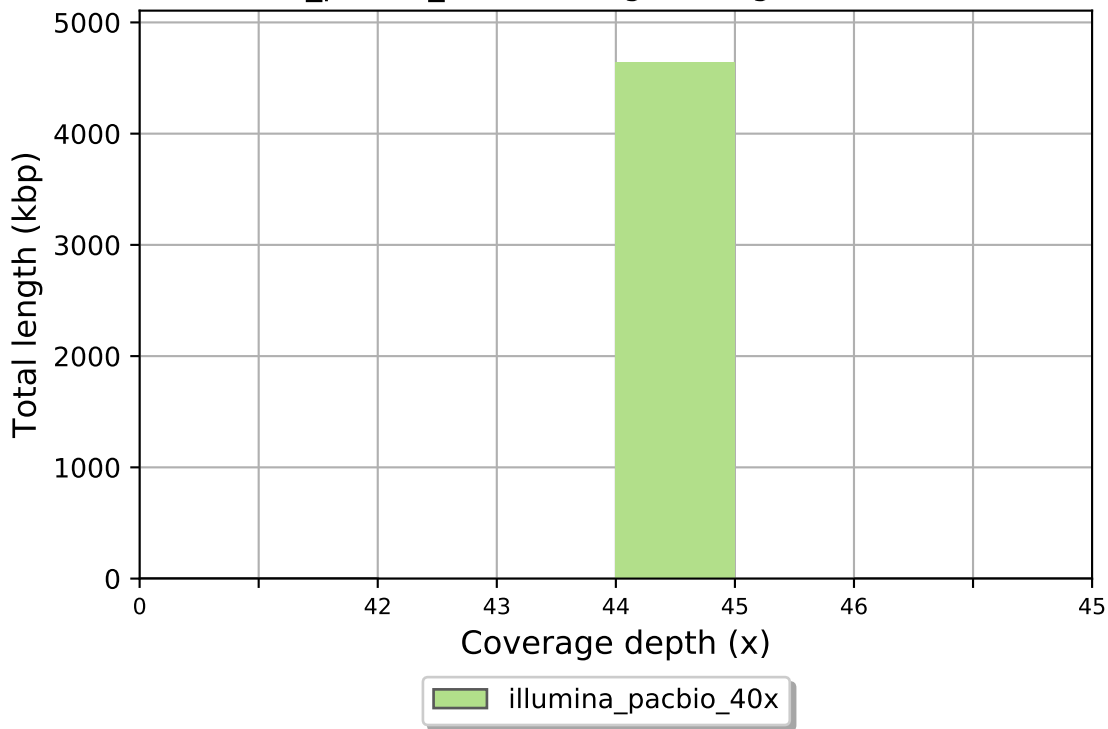


illumina\_pacbio\_10x

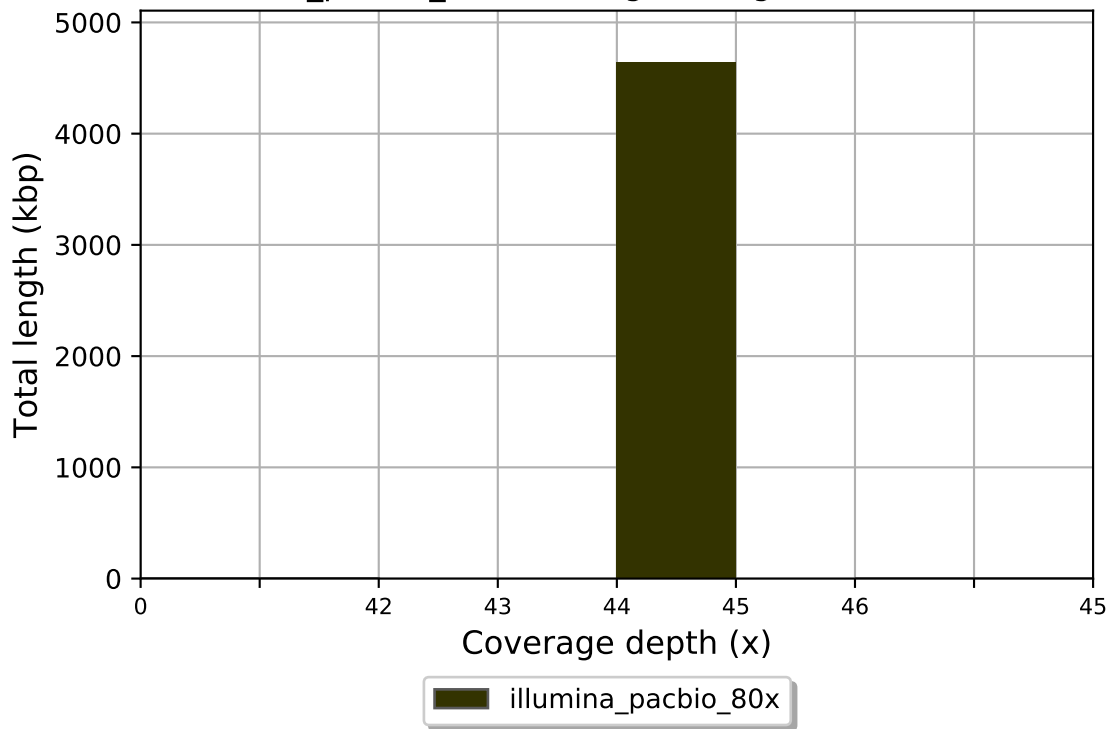
illumina\_pacbio\_20x coverage histogram (bin size: 1x)



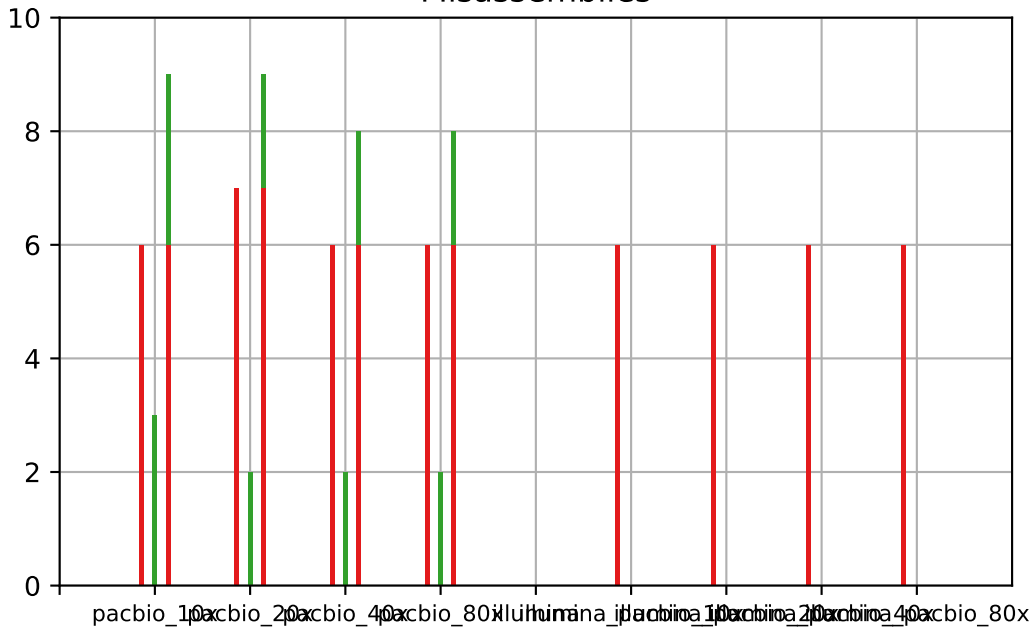
illumina\_pacbio\_40x coverage histogram (bin size: 1x)



illumina\_pacbio\_80x coverage histogram (bin size: 1x)



## Misassemblies

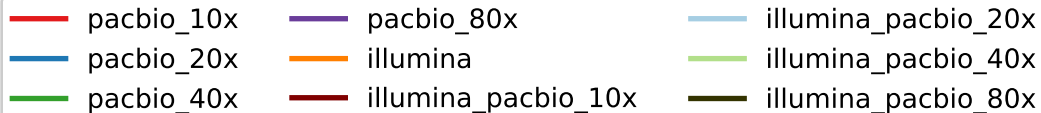
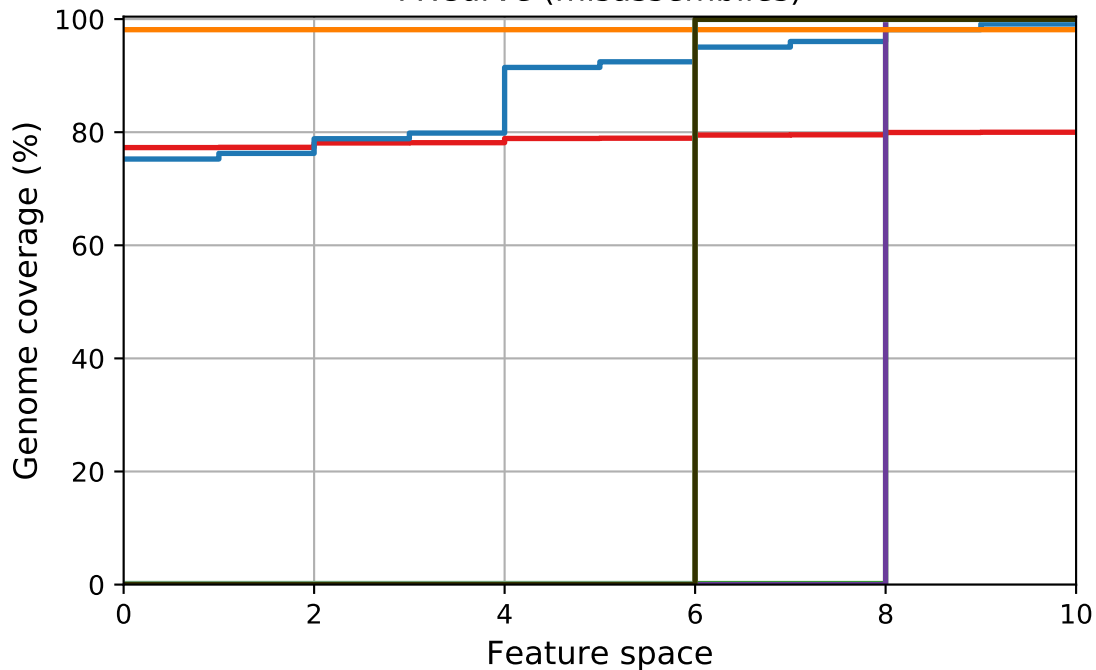


# relocations



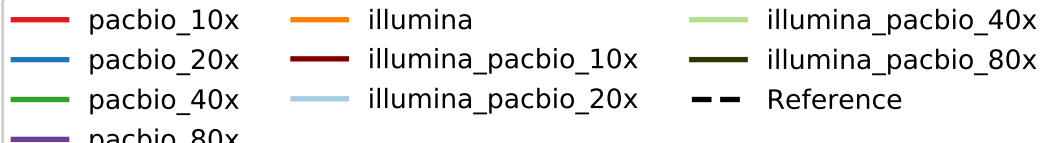
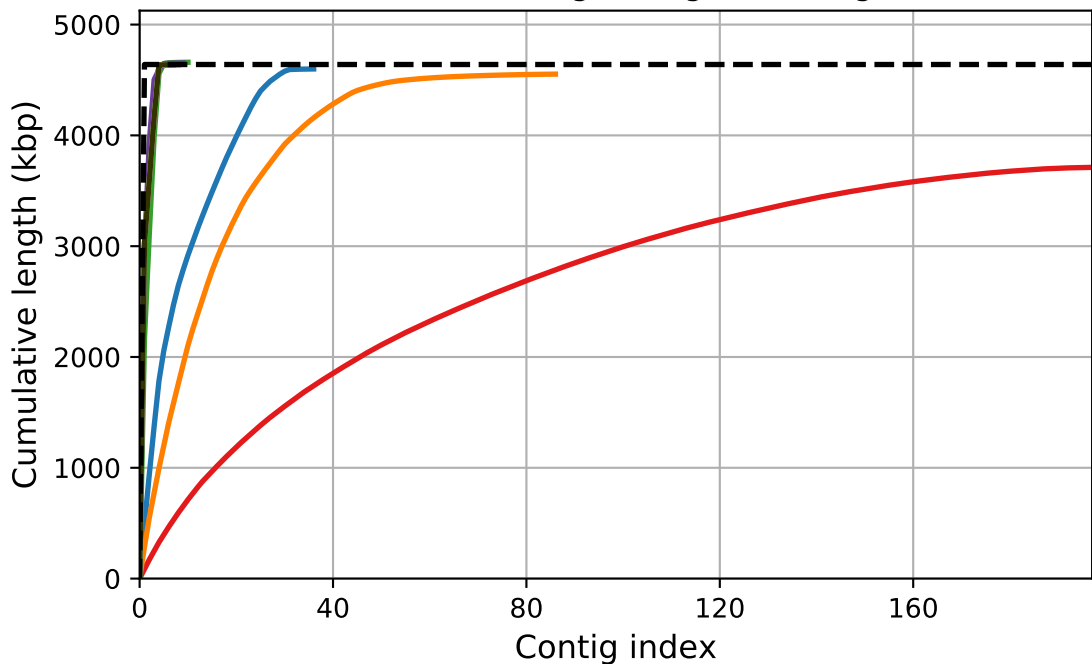
# inversions

# FRCurve (misassemblies)

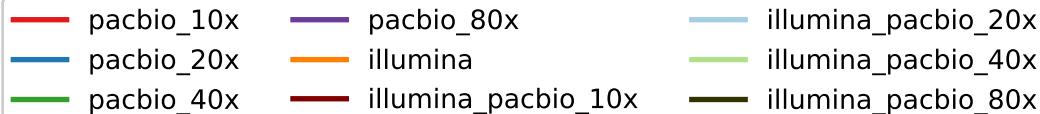
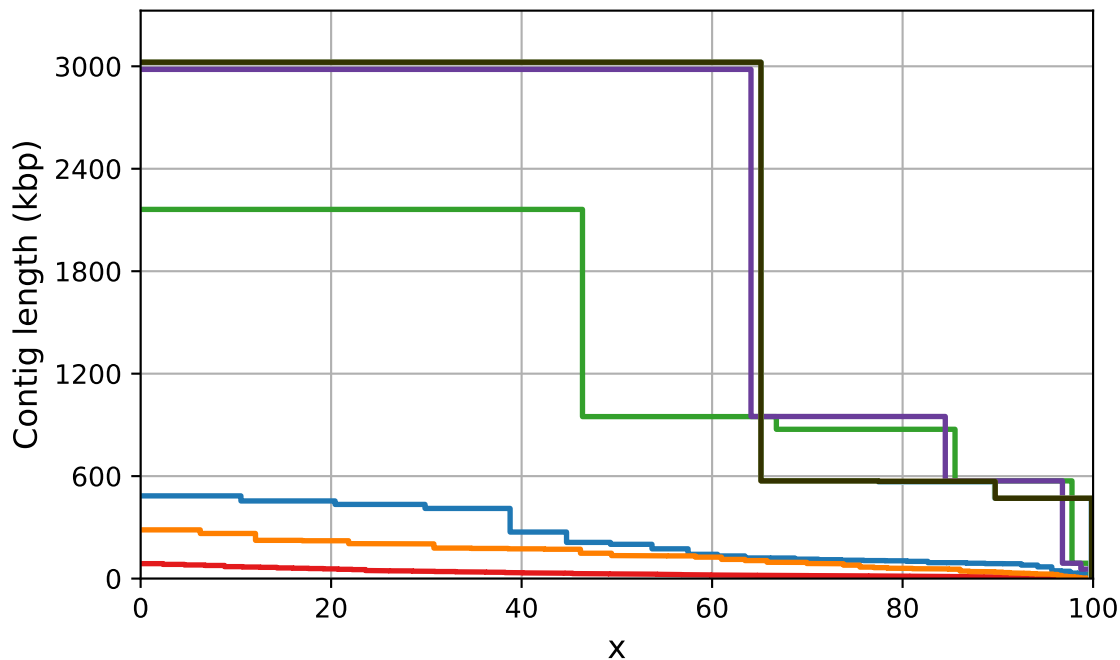




# Cumulative length (aligned contigs)



NAx



# NGAx

