

Report

	out_pacbio_10x_assembly	out_pacbio_20x_assembly	out_pacbio_40x_assembly	out_illumina_pacbio_10x_contigs	out_illumina_pacbio_20x_contigs	out_illumina_pacbio_40x_contigs	out_illumina_pacbio_80x_contigs	out_illumina_contigs
# contigs (>= 0 bp)	93	24	1	22	8	6	6	167
# contigs (>= 1000 bp)	93	24	1	7	2	1	1	87
# contigs (>= 5000 bp)	92	23	1	7	1	1	1	62
# contigs (>= 10000 bp)	91	23	1	7	1	1	1	57
# contigs (>= 25000 bp)	69	22	1	7	1	1	1	47
# contigs (>= 50000 bp)	36	19	1	7	1	1	1	31
Total length (>= 0 bp)	4333634	4681275	4642048	4634402	4642146	4642668	4642668	4567161
Total length (>= 1000 bp)	4333634	4681275	4642048	4630978	4641094	4641722	4641722	4548539
Total length (>= 5000 bp)	4329652	4676868	4642048	4630978	4636416	4641722	4641722	4493976
Total length (>= 10000 bp)	4321011	4676868	4642048	4630978	4636416	4641722	4641722	4458325
Total length (>= 25000 bp)	3898840	4659549	4642048	4630978	4636416	4641722	4641722	4312386
Total length (>= 50000 bp)	2810496	4548725	4642048	4630978	4636416	4641722	4641722	3762852
# contigs	93	24	1	10	3	2	2	97
Largest contig	155648	589942	4642048	1460522	4636416	4641722	4641722	221601
Total length	4333634	4681275	4642048	4633017	4641636	4642264	4642264	4555330
Reference length	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675
GC (%)	50.62	50.77	50.79	50.78	50.79	50.79	50.79	50.74
Reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
N50	61597	303960	4642048	1034546	4636416	4641722	4641722	129054
NG50	60121	303960	4642048	1034546	4636416	4641722	4641722	129054
N75	34871	187937	4642048	538524	4636416	4641722	4641722	60768
NG75	30767	187937	4642048	538524	4636416	4641722	4641722	59669
L50	25	6	1	2	1	1	1	14
LG50	28	6	1	2	1	1	1	14
L75	47	11	1	4	1	1	1	26
LG75	54	11	1	4	1	1	1	27
# misassemblies	16	9	8	6	6	6	6	0
# misassembled contigs	10	5	1	2	1	1	1	0
Misassembled contigs length	586450	1365787	4642048	1963782	4636416	4641722	4641722	0
# local misassemblies	8	4	2	6	5	5	5	4
# 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	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 47 part	0 + 10 part	0 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	143387	32261	0	542	542	542	542	542
Genome fraction (%)	88.312	99.334	99.998	99.779	99.969	99.983	99.983	98.142
Duplication ratio	1.023	1.009	1.001	1.001	1.001	1.001	1.001	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	39.85	7.12	1.10	7.09	8.19	8.32	8.32	1.03
# indels per 100 kbp	552.43	82.73	10.48	0.71	0.78	0.86	0.86	0.33
Largest alignment	154705	589942	2167286	1034546	3023576	3023578	3023578	221546
Total aligned length	4186218	4646823	4641120	4632300	4638308	4638936	4638936	4554465
NA50	56579	302625	948762	572346	3023576	3023578	3023578	129054
NGA50	55056	302625	948762	572346	3023576	3023578	3023578	129054
NA75	30502	152003	858344	538524	572346	572346	572346	60768
NGA75	27296	152003	858344	538524	572346	572346	572346	59669
LA50	26	6	2	3	1	1	1	14
LGA50	29	6	2	3	1	1	1	14
LA75	53	12	3	5	2	2	2	26
LGA75	61	12	3	5	2	2	2	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

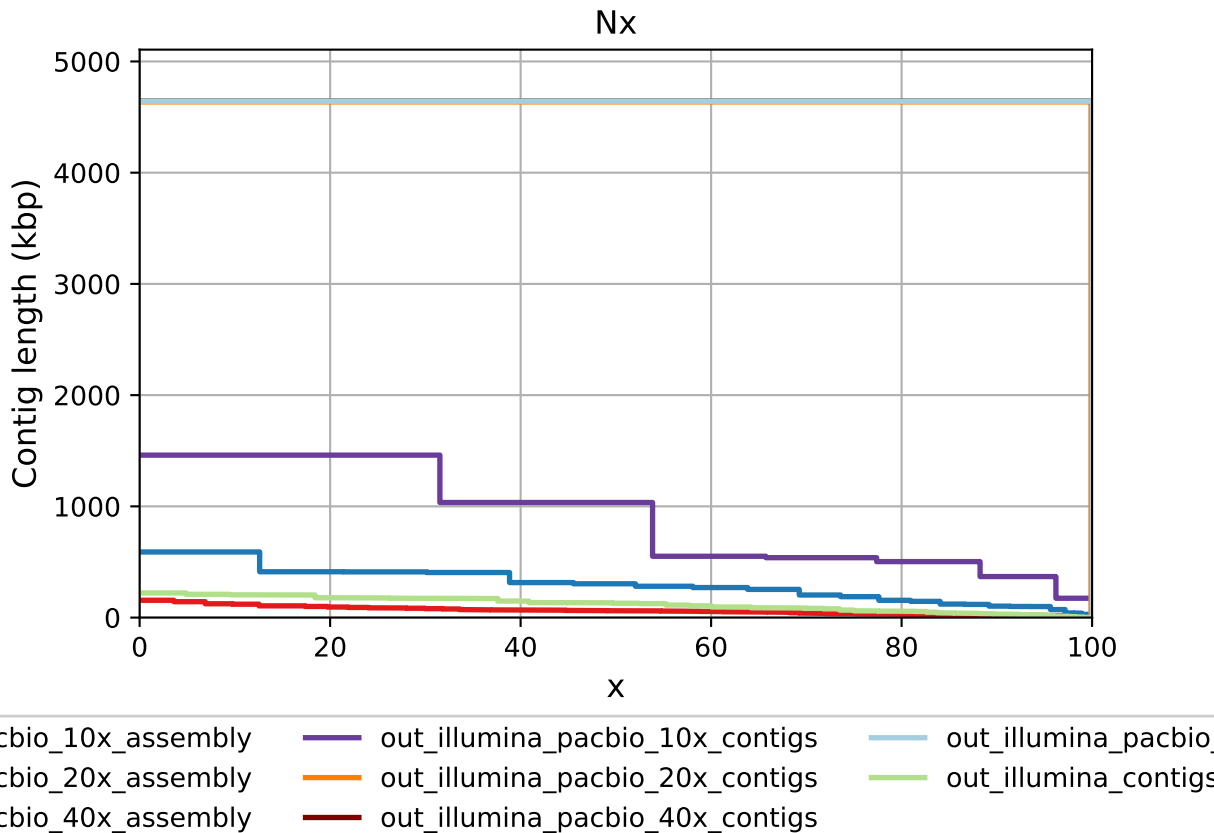
	out_pacbio_10x_assembly	out_pacbio_20x_assembly	out_pacbio_40x_assembly	out_illumina_pacbio_10x_contigs	out_illumina_pacbio_20x_contigs	out_illumina_pacbio_40x_contigs	out_illumina_pacbio_80x_contigs	out_illumina_contigs
# misassemblies	16	9	8	6	6	6	6	0
# contig misassemblies	16	9	8	6	6	6	6	0
# c. relocations	13	7	6	6	6	6	6	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	3	2	2	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	10	5	1	2	1	1	1	0
Misassembled contigs length	586450	1365787	4642048	1963782	4636416	4641722	4641722	0
# local misassemblies	8	4	2	6	5	5	5	4
# 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	0	0	0	0	0	0	0	0
# mismatches	1633	328	51	328	380	386	386	47
# indels	22635	3813	486	33	36	40	40	15
# indels (<= 5 bp)	22617	3806	486	31	33	37	37	12
# indels (> 5 bp)	18	7	0	2	3	3	3	3
Indels length	24116	4071	503	82	179	183	183	77

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).

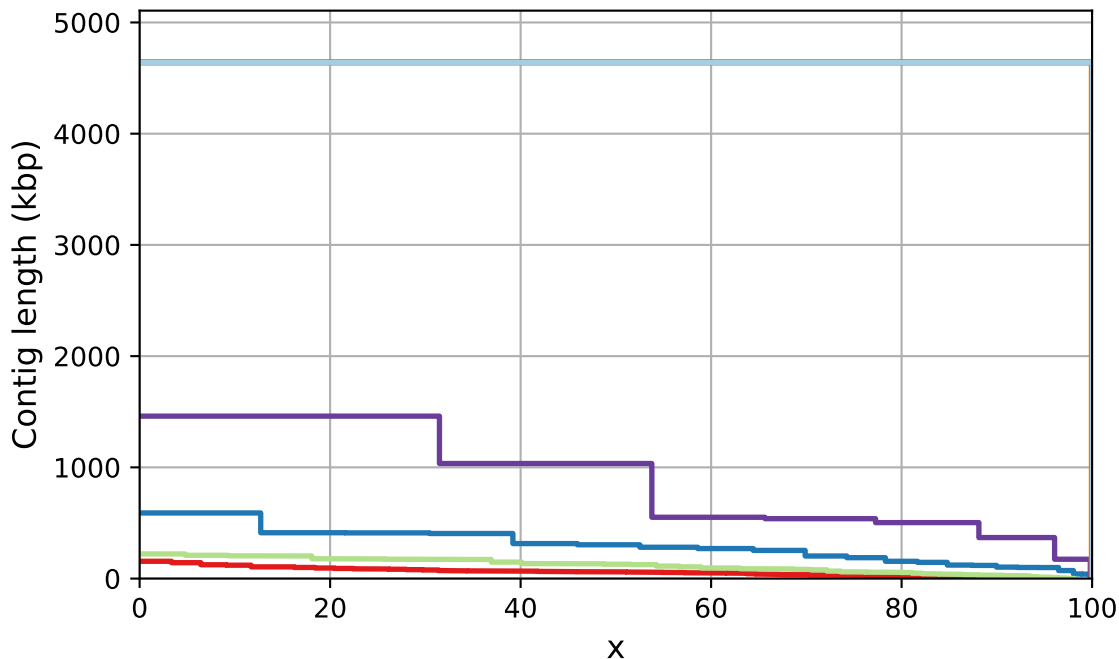
Unaligned report

	out_pacbio_10x_assembly	out_pacbio_20x_assembly	out_pacbio_40x_assembly	out_illumina_pacbio_10x_contigs	out_illumina_pacbio_20x_contigs	out_illumina_pacbio_40x_contigs	out_illumina_pacbio_80x_contigs	out_illumina_contigs
# fully unaligned contigs	0	0	0	1	1	1	1	1
Fully unaligned length	0	0	0	542	542	542	542	542
# partially unaligned contigs	47	10	0	0	0	0	0	0
Partially unaligned length	143387	32261	0	0	0	0	0	0
# N's	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).

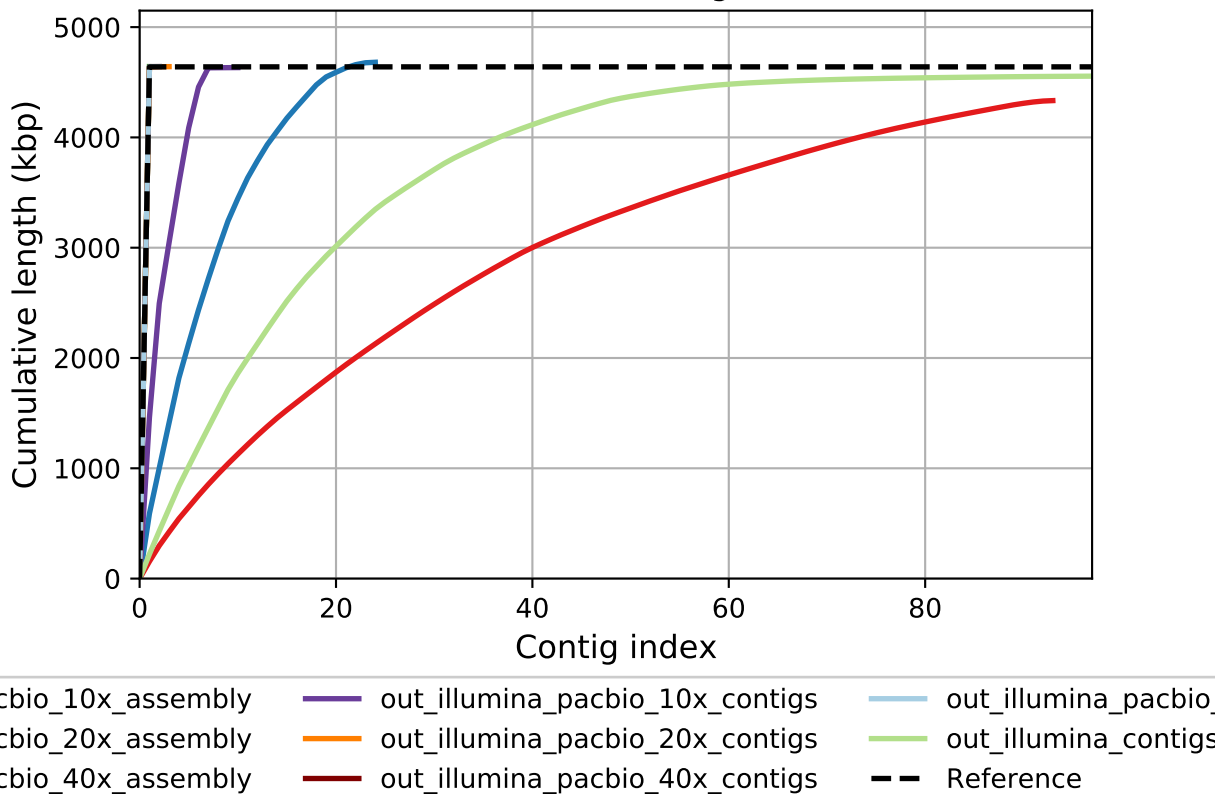


NGx

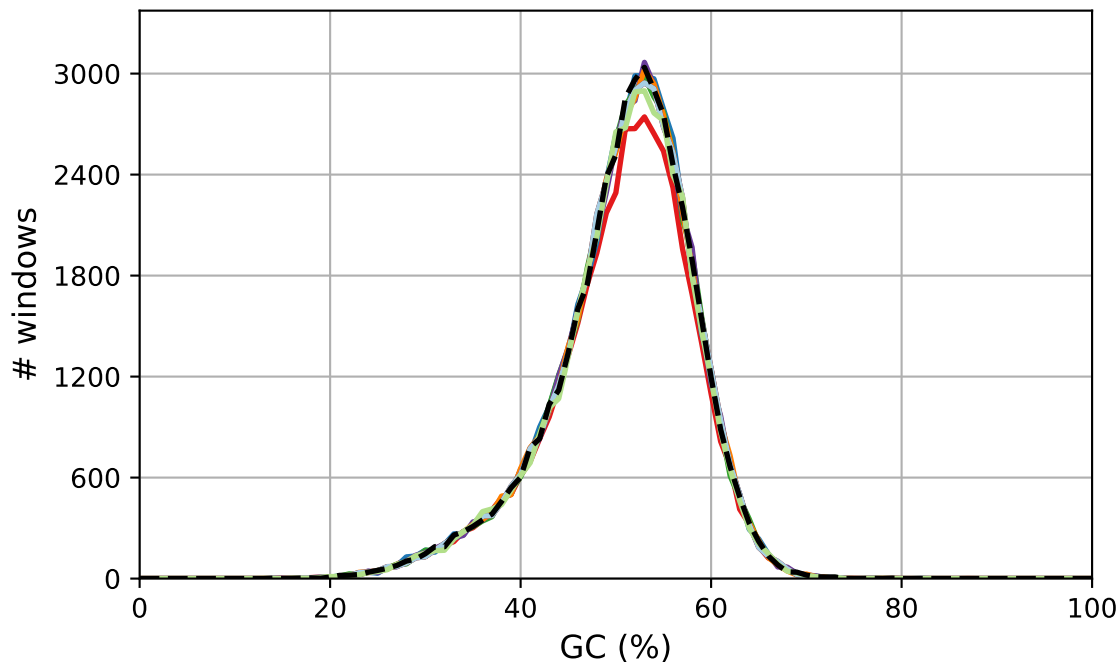


pacbio_10x_assembly out_illumina_pacbio_10x_contigs out_illumina_pacbio_10x_contigs
 pacbio_20x_assembly out_illumina_pacbio_20x_contigs out_illumina_pacbio_20x_contigs
 pacbio_40x_assembly out_illumina_pacbio_40x_contigs out_illumina_pacbio_40x_contigs

Cumulative length



GC content

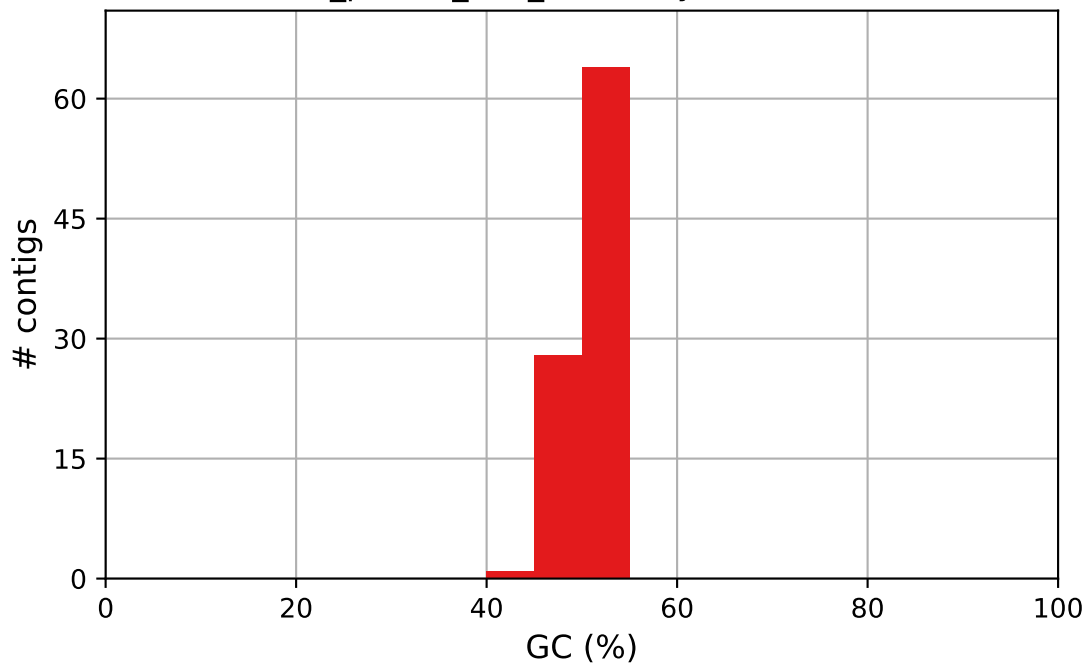


pacbio_10x_assembly
pacbio_20x_assembly
pacbio_40x_assembly

out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs

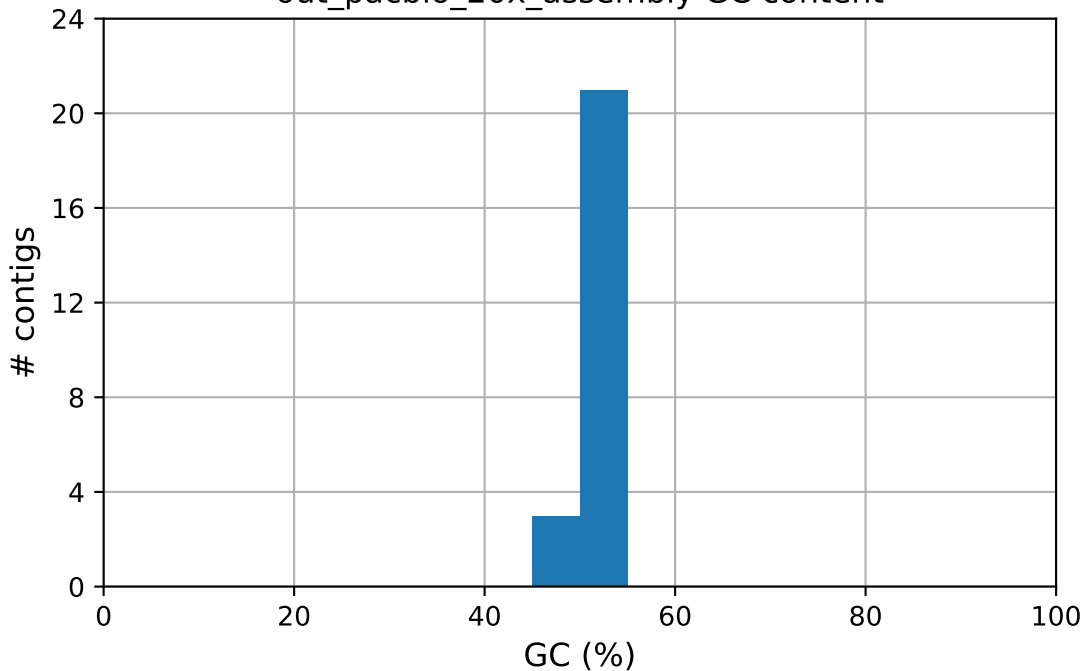
out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs
Reference

out_pacbio_10x_assembly GC content



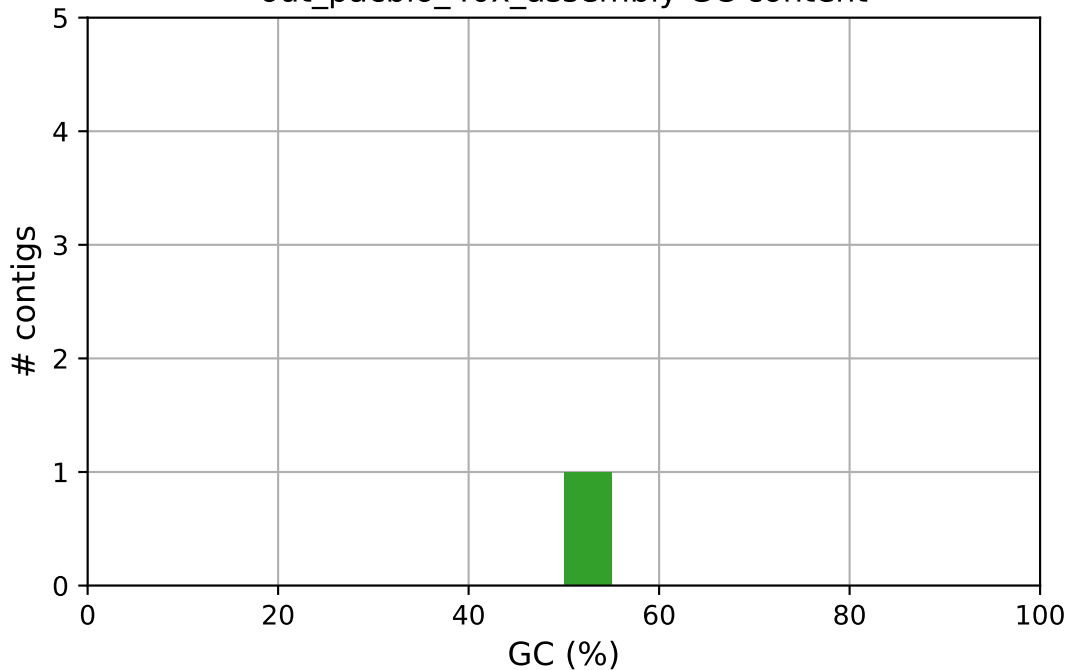
out_pacbio_10x_assembly

out_pacbio_20x_assembly GC content



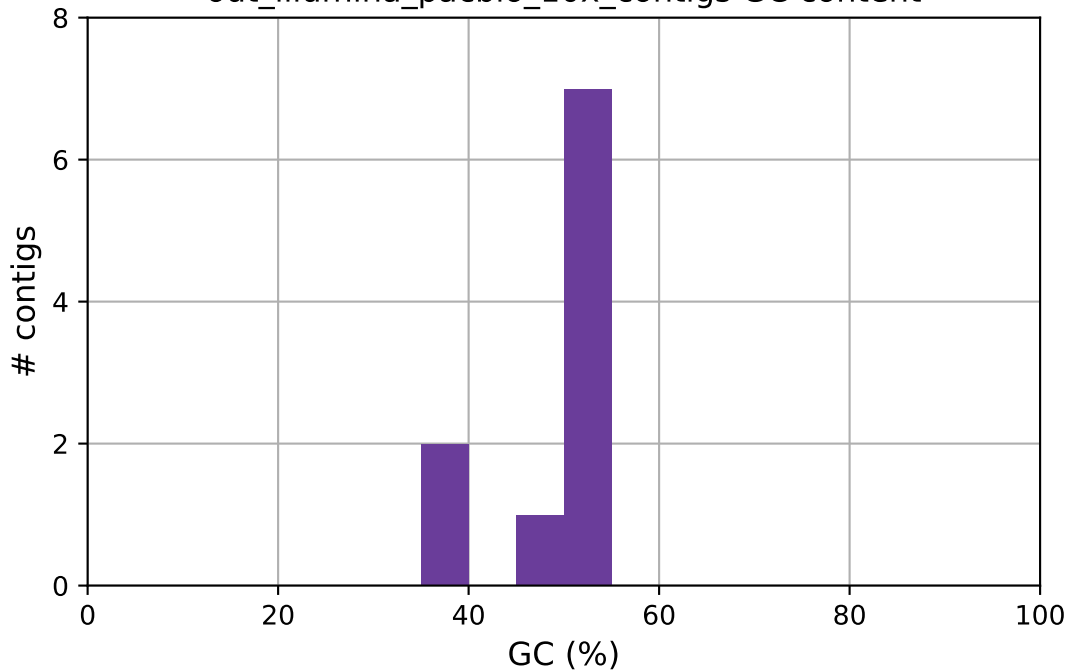
out_pacbio_20x_assembly

out_pacbio_40x_assembly GC content



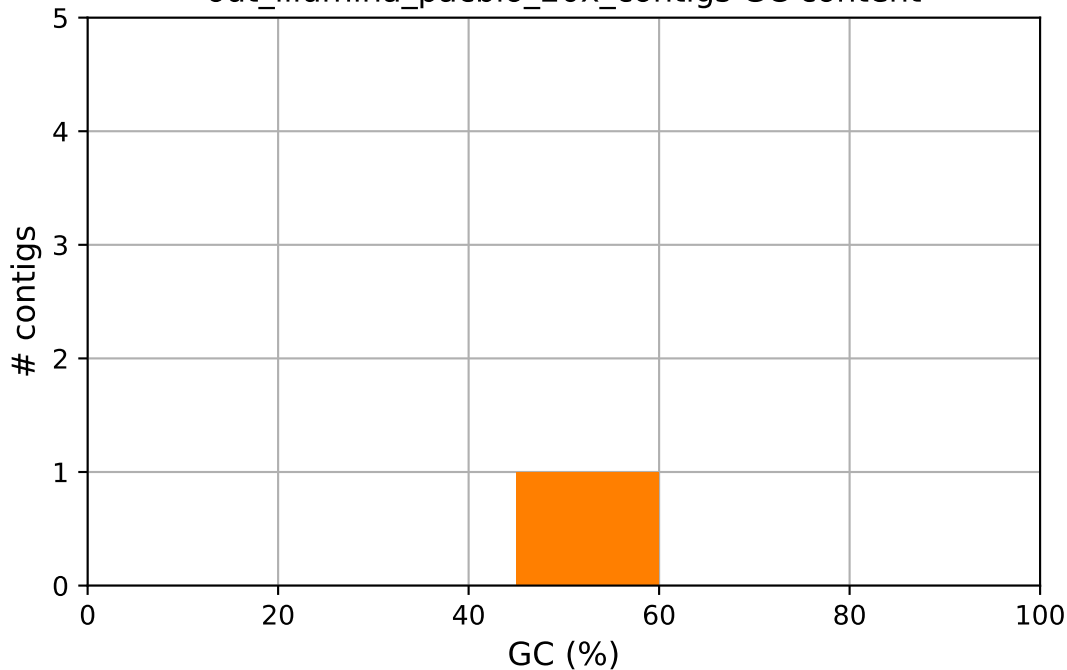
out_pacbio_40x_assembly

out_illumina_pacbio_10x_contigs GC content



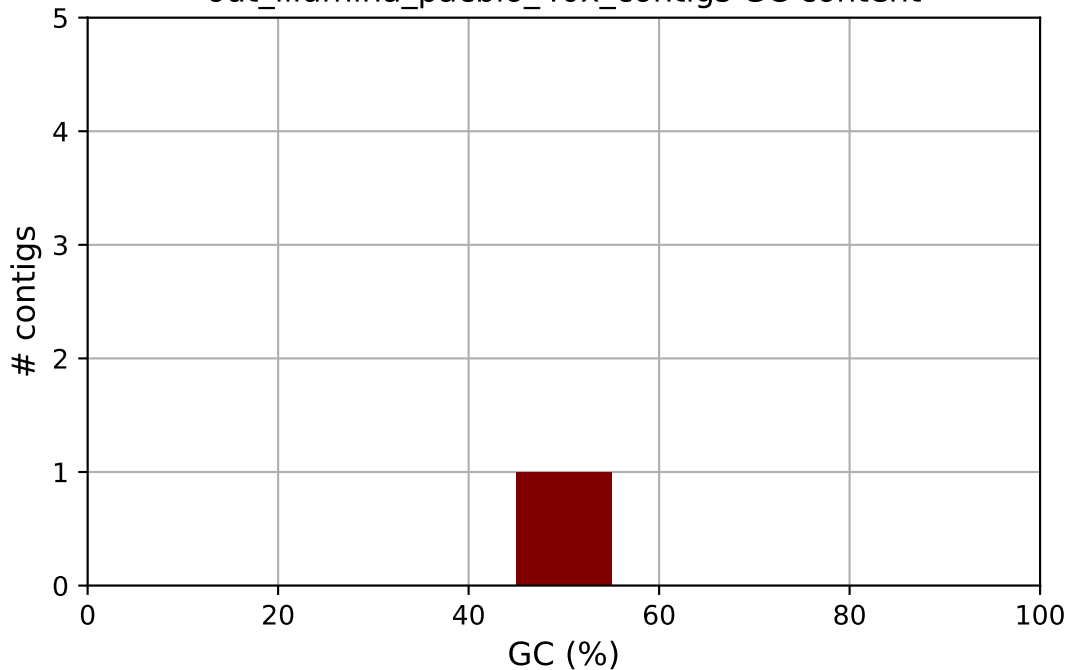
out_illumina_pacbio_10x_contigs

out_illumina_pacbio_20x_contigs GC content



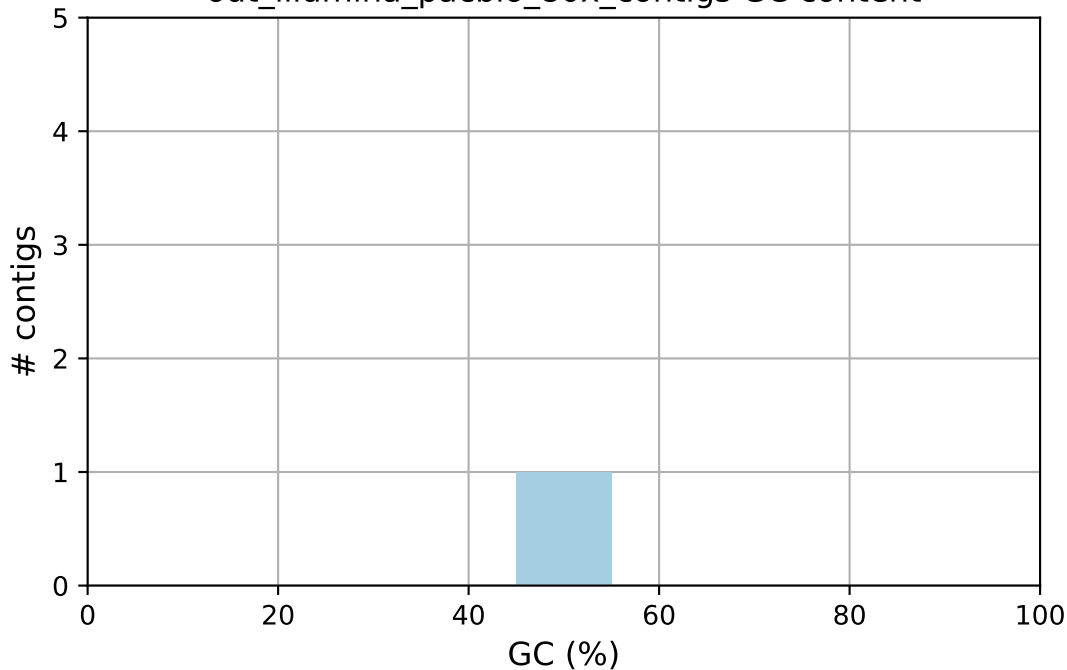
out_illumina_pacbio_20x_contigs

out_illumina_pacbio_40x_contigs GC content



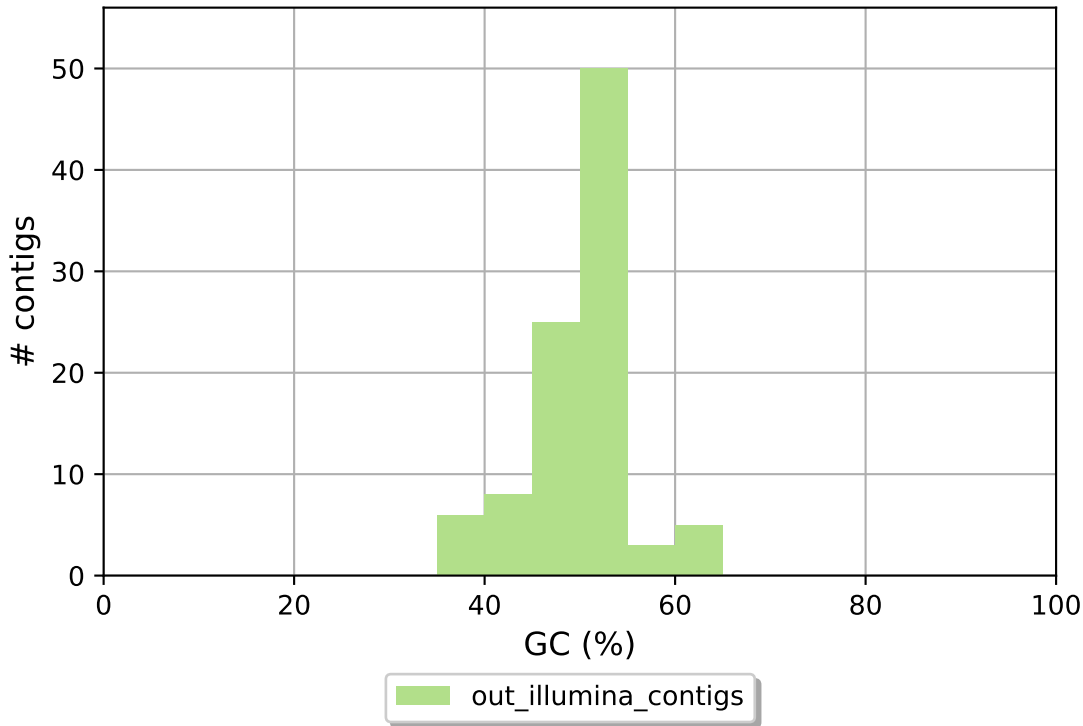
out_illumina_pacbio_40x_contigs

out_illumina_pacbio_80x_contigs GC content

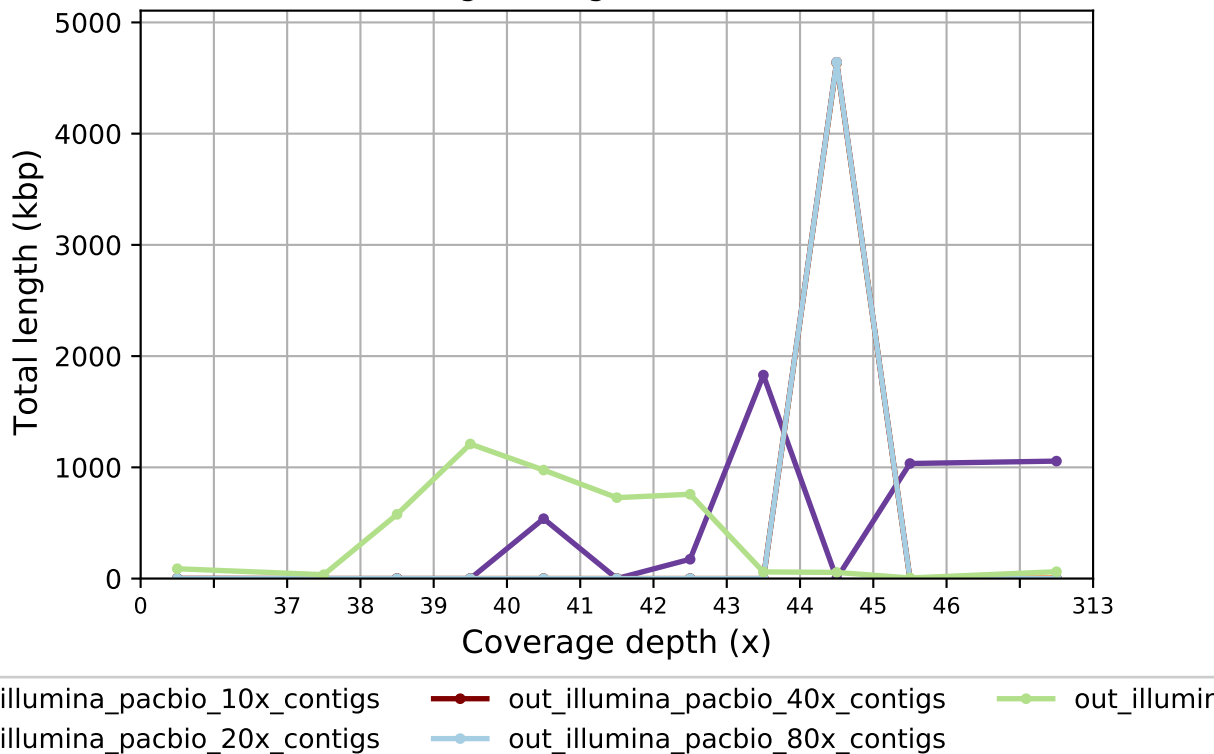


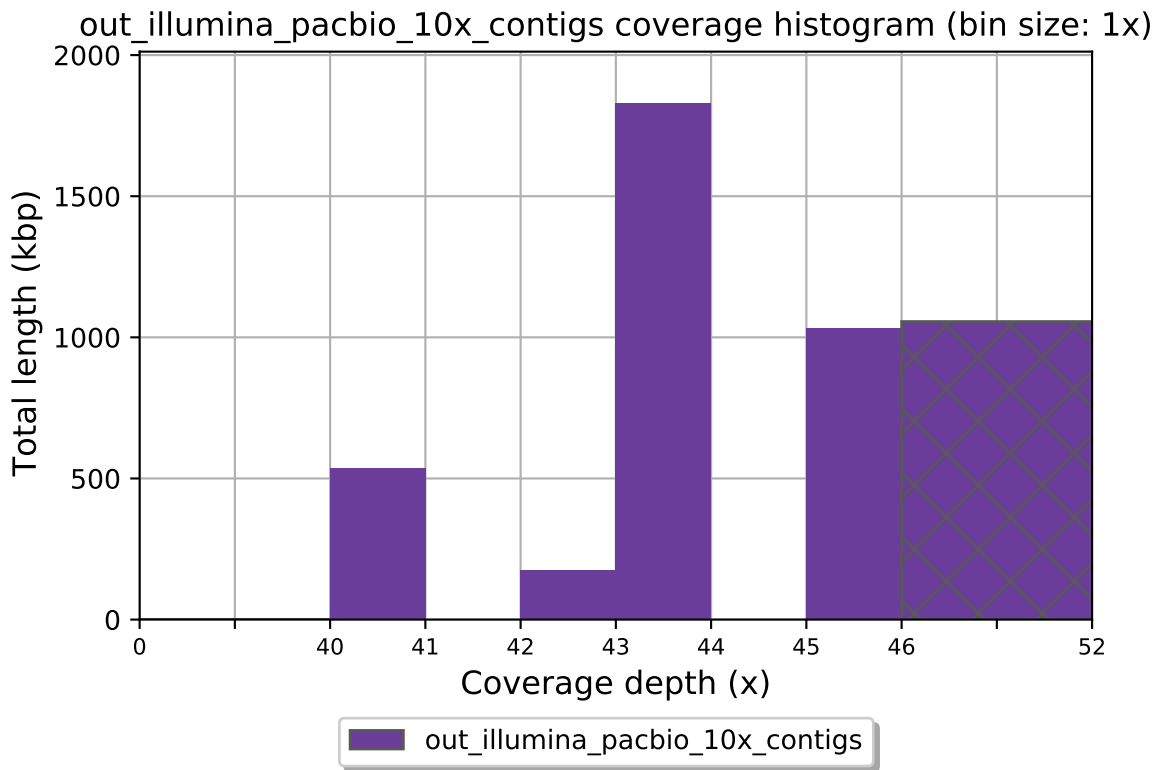
out_illumina_pacbio_80x_contigs

out_illumina_contigs GC content

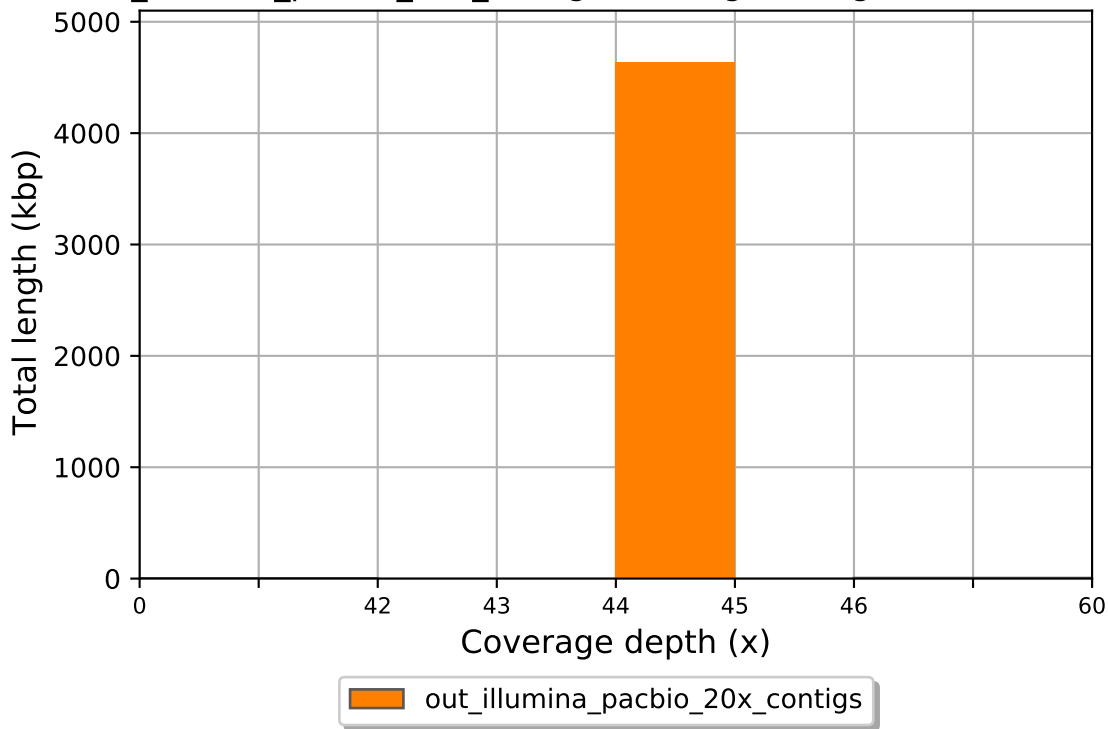


Coverage histogram (bin size: 1x)

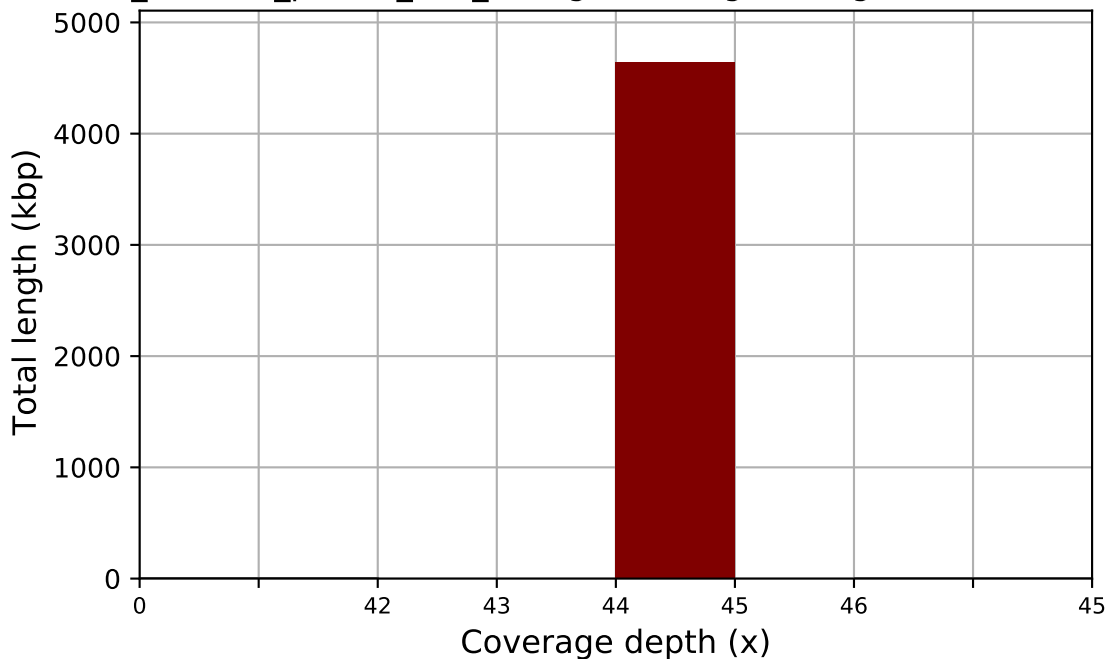




out_illumina_pacbio_20x_contigs coverage histogram (bin size: 1x)

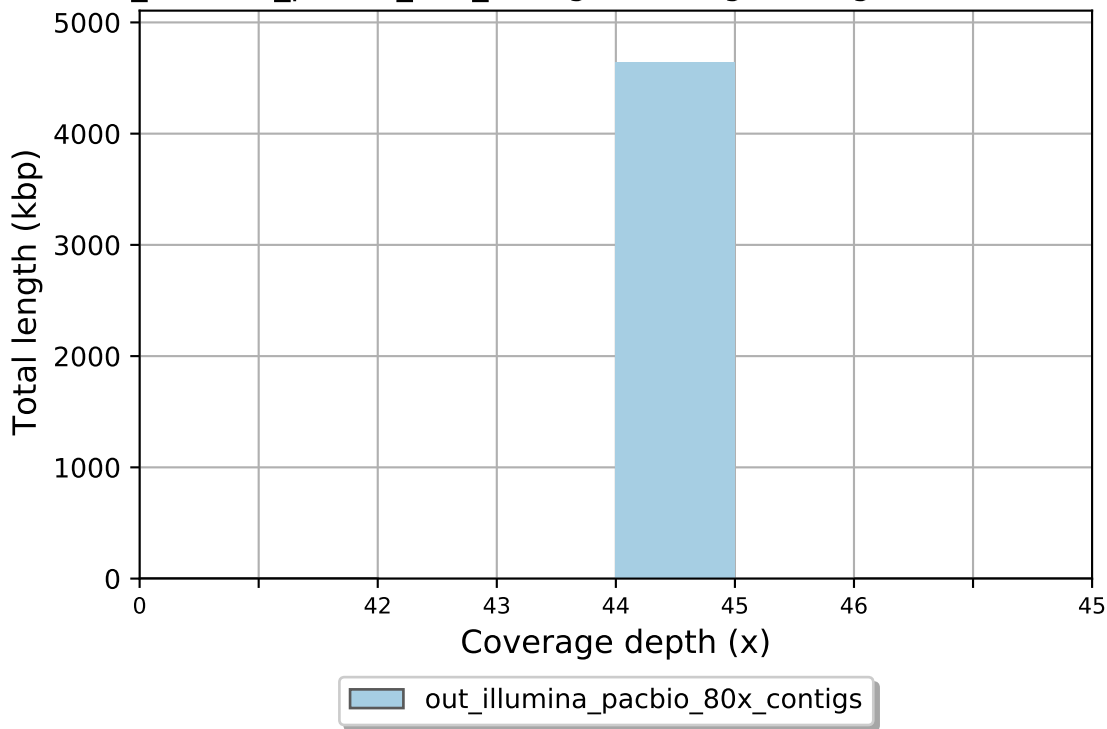


out_illumina_pacbio_40x_contigs coverage histogram (bin size: 1x)

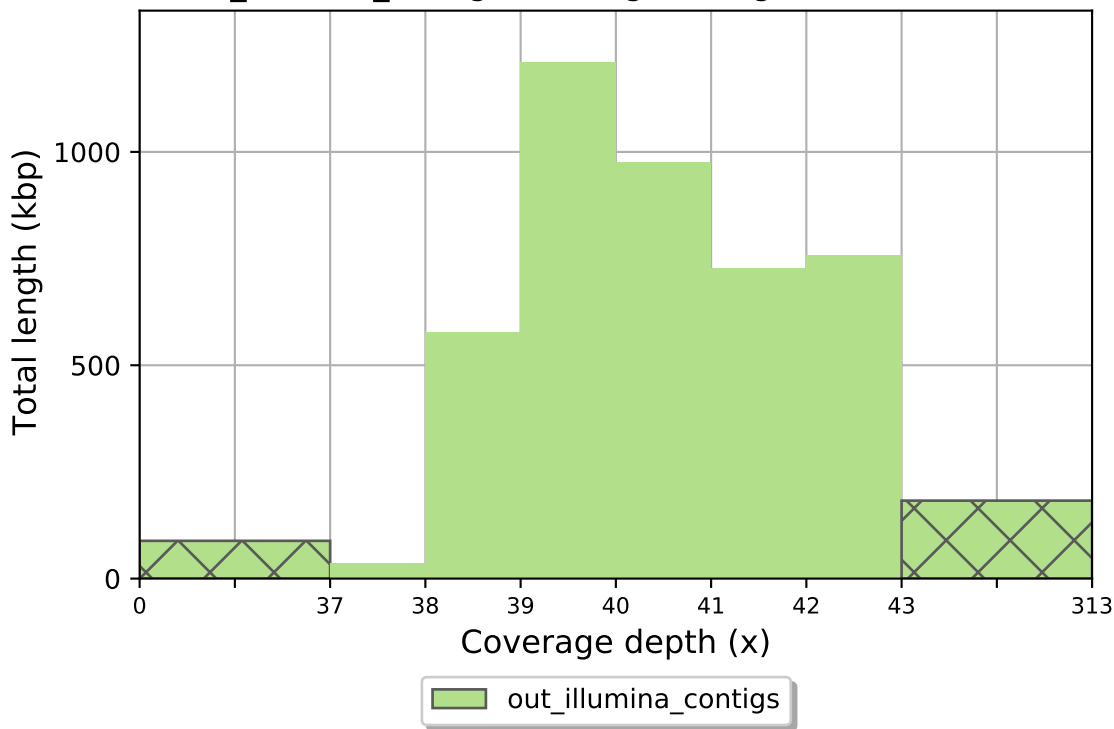


out_illumina_pacbio_40x_contigs

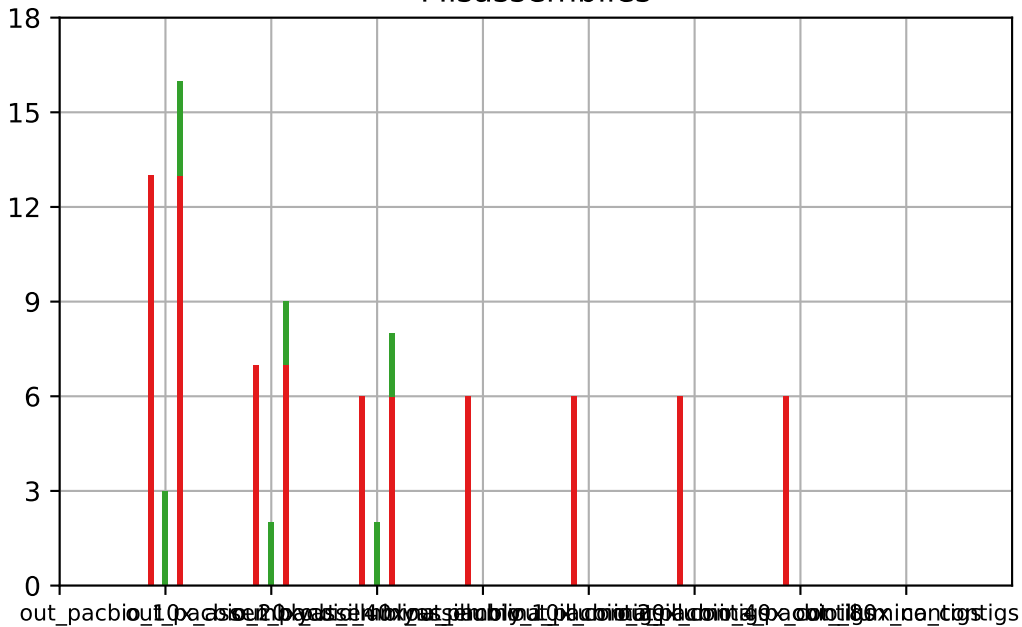
out_illumina_pacbio_80x_contigs coverage histogram (bin size: 1x)



out_illumina_contigs coverage histogram (bin size: 1x)



Misassemblies

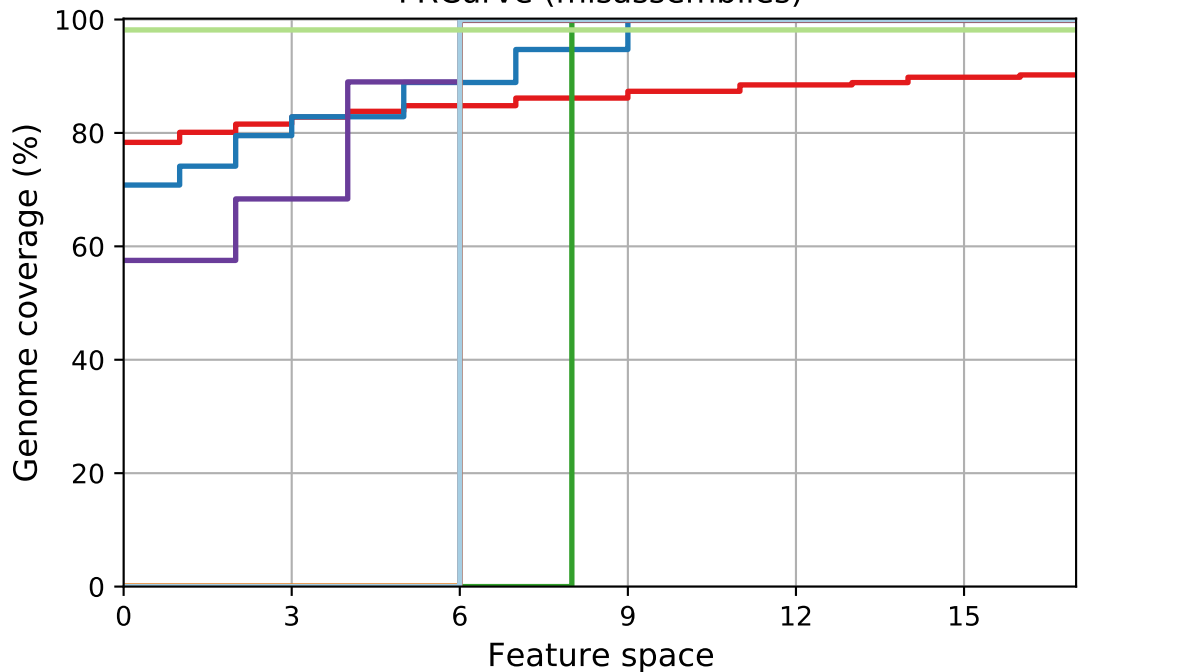


```
# relocations
```

8

```
# inversions
```

FRCurve (misassemblies)

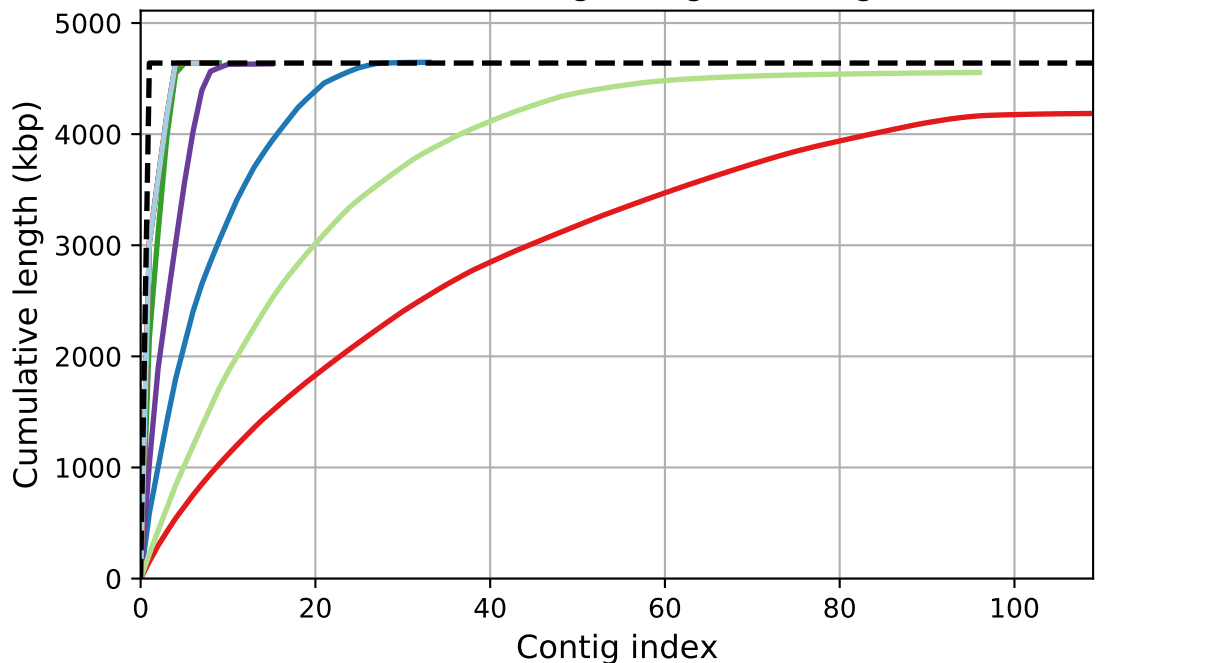


pacbio_10x_assembly
pacbio_20x_assembly
pacbio_40x_assembly

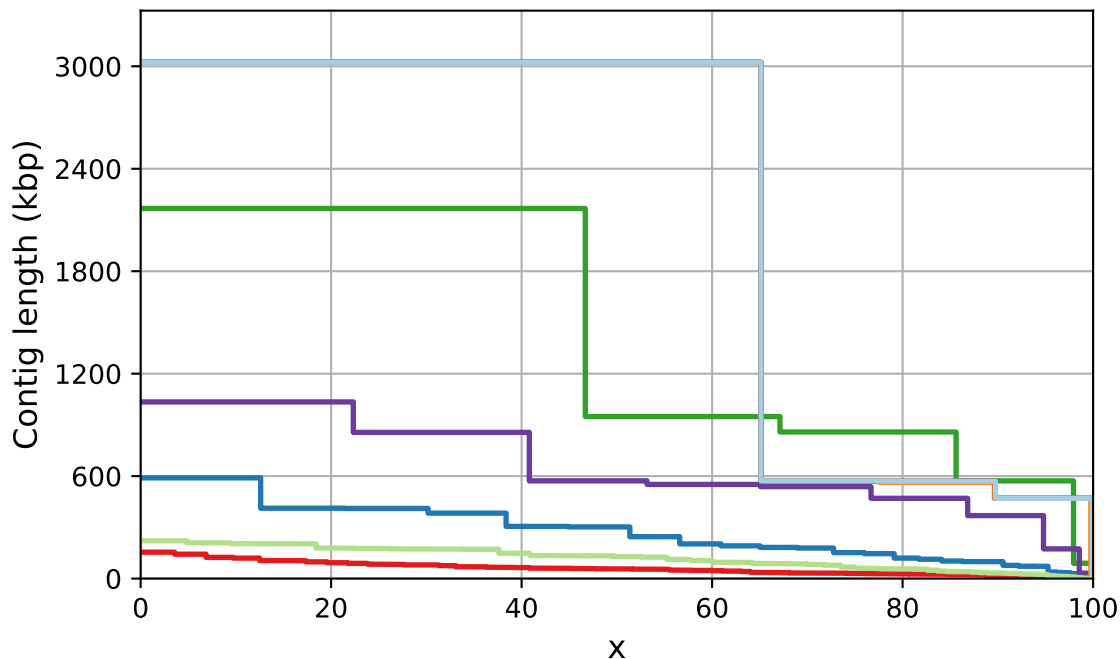
out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs

out_illumina_pacbio_10x_assembly
out_illumina_pacbio_20x_assembly
out_illumina_pacbio_40x_assembly

Cumulative length (aligned contigs)



NAx

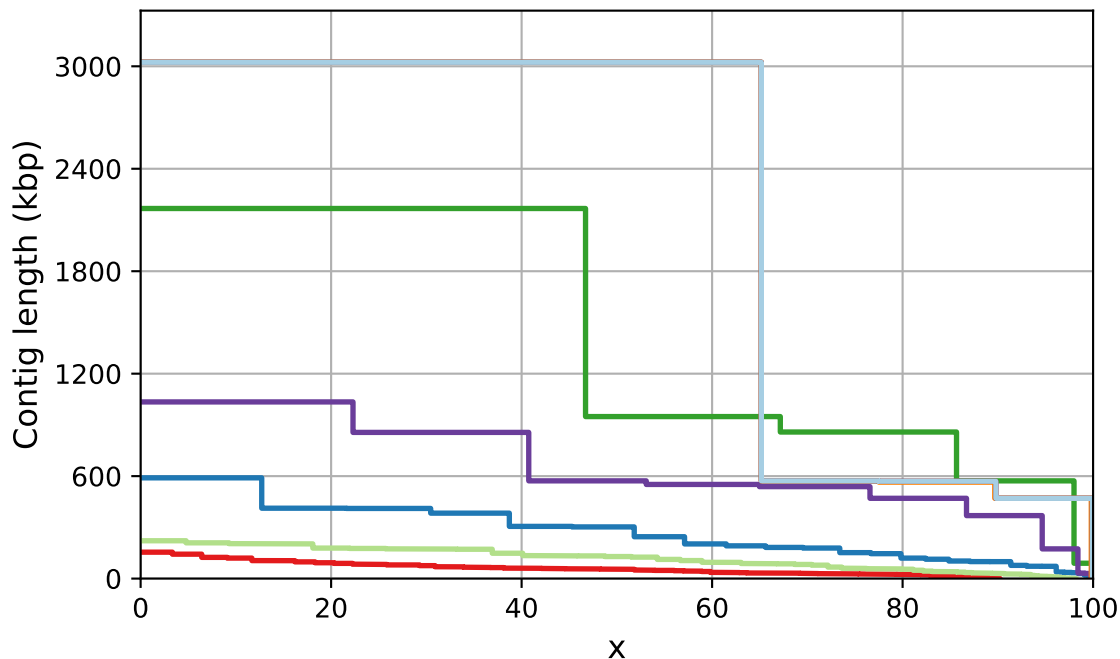


pacbio_10x_assembly
pacbio_20x_assembly
pacbio_40x_assembly

out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs

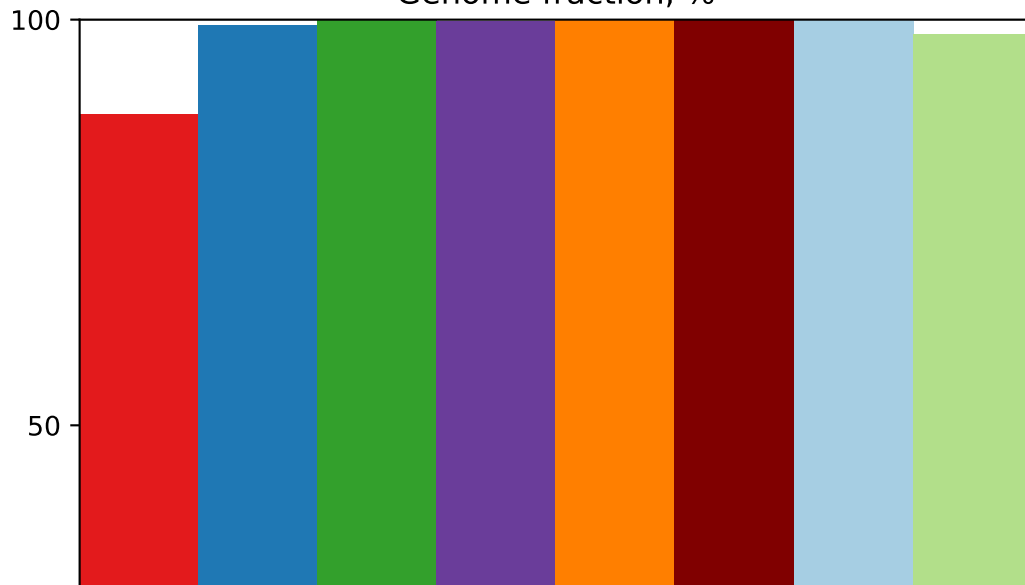
out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs

NGAx



pacbio_10x_assembly out_illumina_pacbio_10x_contigs out_illumina_pacbio_20x_contigs
 pacbio_20x_assembly out_illumina_pacbio_20x_contigs out_illumina_pacbio_40x_contigs
 pacbio_40x_assembly out_illumina_pacbio_40x_contigs out_illumina_contigs

Genome fraction, %



pacbio_10x_assembly
pacbio_20x_assembly
pacbio_40x_assembly

out_illumina_pacbio_10x_contigs
out_illumina_pacbio_20x_contigs
out_illumina_pacbio_40x_contigs

out_illumina_pacbio_10x_contigs
out_illumina_contigs