Report

	assembling_cov10_assembly	assembling_cov20_assembly	assembling_cov40_assembly	assembling_cov80_assembly	illumina_assembling_contigs	hybrid_assembling_cov10_contigs	hybrid_assembling_cov20_contigs	hybrid_assembling_cov40_contigs
# contigs (>= 0 bp)	97	26	1	2	167	22	8	6
# contigs (>= 1000 bp)	97	26	1	2	87	7	2	1
# contigs (>= 5000 bp)	95	26	1	1	62	7	1	1
# contigs (>= 10000 bp)	94	24	1	1	57	7	1	1
# contigs (>= 25000 bp)	68	19	1	1	47	7	1	1
# contigs (>= 50000 bp)	33	18	1	1	31	7	1	1
Total length (>= 0 bp)	4336541	4683515	4642057	4642314	4567161	4634402	4642146	4642668
Total length (>= 1000 bp)	4336541	4683515	4642057	4642314	4548539	4630978	4641094	4641722
Total length (>= 5000 bp)	4328867	4683515	4642057	4640510	4493976	4630978	4636416	4641722
Total length (>= 10000 bp)	4320107	4671505	4642057	4640510	4458325	4630978	4636416	4641722
Total length (>= 25000 bp)	3815663	4583851	4642057	4640510	4312386	4630978	4636416	4641722
Total length (>= 50000 bp)	2588123	4542209	4642057	4640510	3762852	4630978	4636416	4641722
# contigs	97	26	1	2	97	10	3	2
Largest contig	155636	718724	4642057	4640510	221601	1460522	4636416	4641722
Total length	4336541	4683515	4642057	4642314	4555330	4633017	4641636	4642264
Reference length	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675
GC (%)	50.60	50.76	50.78	50.79	50.74	50.78	50.79	50.79
Reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
N50	60526	314698	4642057	4640510	129054	1034546	4636416	4641722
NG50	54797	314698	4642057	4640510	129054	1034546	4636416	4641722
N75	34860	187936	4642057	4640510	60768	538524	4636416	4641722
NG75	30774	187936	4642057	4640510	59669	538524	4636416	4641722
L50	26	5	1	1	14	2	1	1
LG50	28	5	1	1	14	2	1	1
L75	49	10	1	1	26	4	1	1
LG75	56	10	1	1	27	4	1	1
# misassemblies	18	9	8	6	0	6	6	6
# misassembled contigs	12	5	1	1	0	2	1	1
Misassembled contigs length	712234	1366070	4642057	4640510	0	1963782	4636416	4641722
# local misassemblies	7	8	4	3	4	6	5	5
# 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 + 41 part	0 + 10 part	0 + 1 part	0 + 1 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	155101	34324	2228	914	542	542	542	542
Genome fraction (%)	88.417	99.318	99.950	99.979	98.142	99.779	99.969	99.983
Duplication ratio	1.019	1.009	1.001	1.001	1.000	1.001	1.001	1.001
# 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	39.39	7.42	1.21	0.56	1.03	7.09	8.19	8.32
# indels per 100 kbp	547.16	84.70	10.46	5.17	0.33	0.71	0.78	0.86
Largest alignment	154693	718723	2167286	3025410	221546	1034546	3023576	3023578
Total aligned length	4177492	4647959	4638901	4641398	4554465	4632300	4638308	4638936
NA50	50155	305719	948761	3025410	129054	572346	3023576	3023578
NGA50	47920	305719	948761	3025410	129054	572346	3023576	3023578
NA75	29930	151864	857478	949247	60768	538524	572346	572346
NGA75	26918	151864	857478	949247	59669	538524	572346	572346
LA50	28	5	2	1	14	3	1	1
LGA50	31	5	2	1	14	3	1	1
LA75	56	11	3	2	26	5	2	2
LGA75	64	11	3	2	27	5	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).
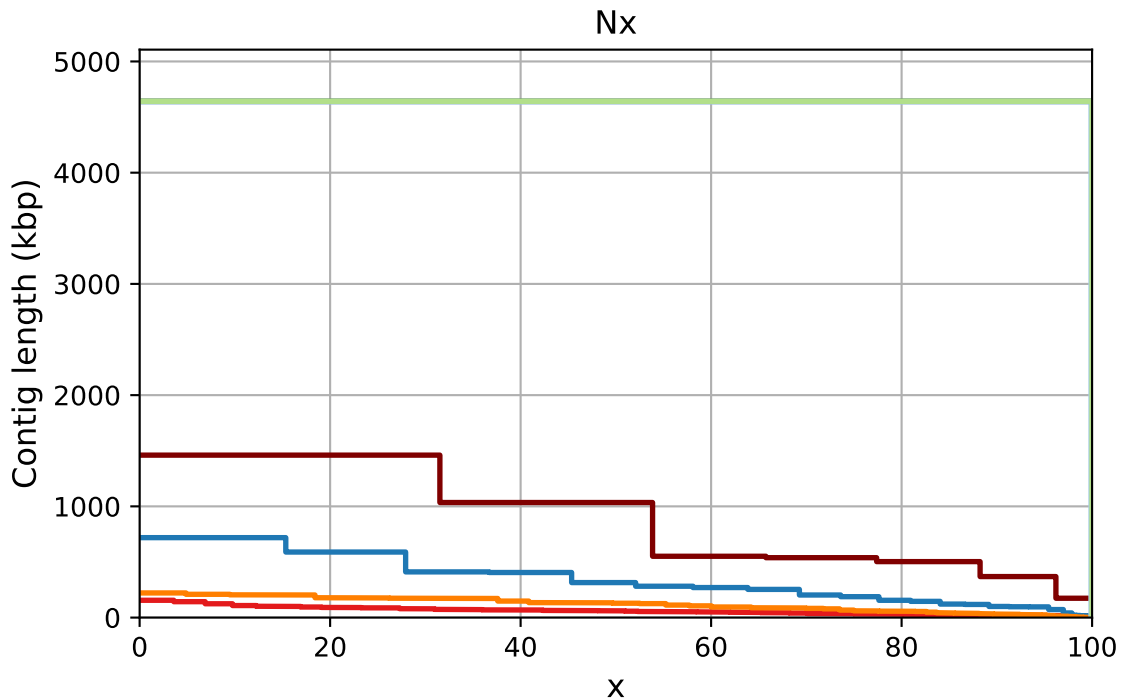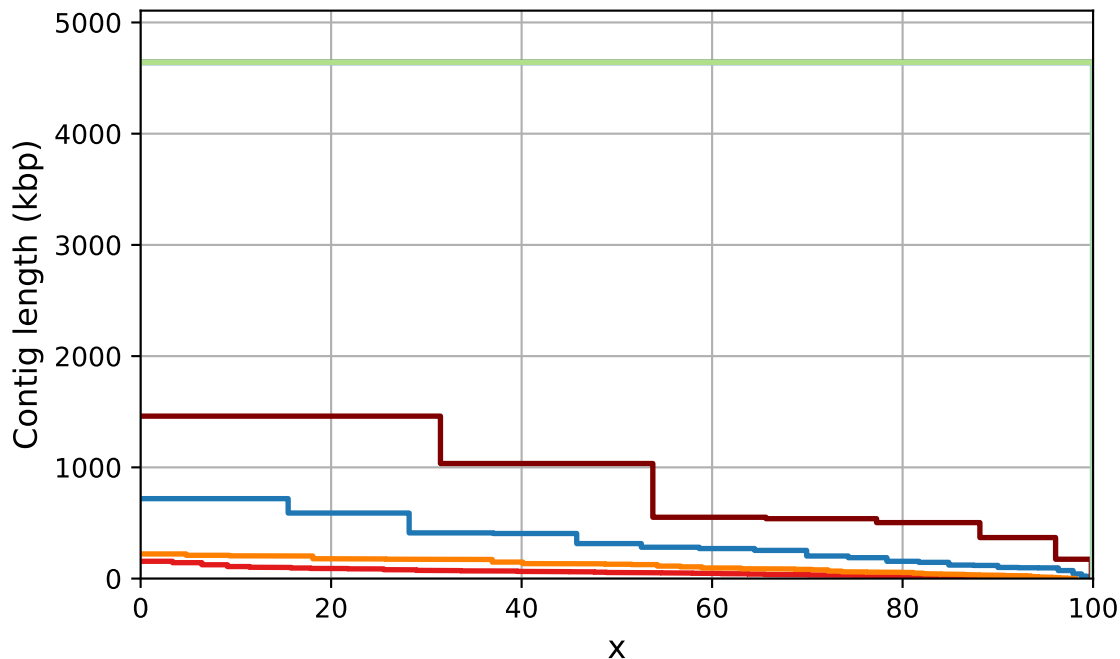
Misassemblies report

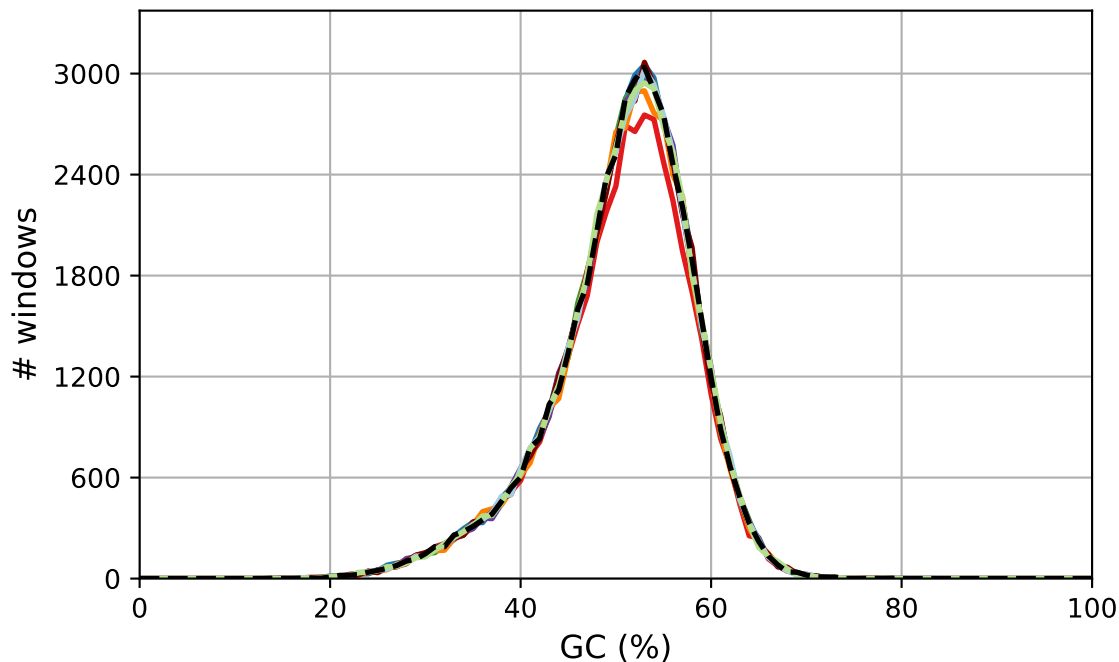|	assembling_cov10_assembly	assembling_cov20_assembly	assembling_cov40_assembly	assembling_cov80_assembly	illumina_assembling_contigs	hybrid_assembling_cov10_contigs	hybrid_assembling_cov20_contigs	hybrid_assembling_cov40_contigs
# misassemblies	18	9	8	6	0	6	6	6
# contig misassemblies	18	9	8	6	0	6	6	6
# c. relocations	15	7	6	6	0	6	6	6
# 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	12	5	1	1	0	2	1	1
Misassembled contigs length	712234	1366070	4642057	4640510	0	1963782	4636416	4641722
# local misassemblies	7	8	4	3	4	6	5	5
# 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	1616	342	56	26	47	328	380	386
# indels	22446	3903	485	240	15	33	36	40
# indels (<= 5 bp)	22427	3894	485	240	12	31	33	37
# indels (> 5 bp)	19	9	0	0	3	2	3	3
Indels length	23957	4187	501	244	77	82	179	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
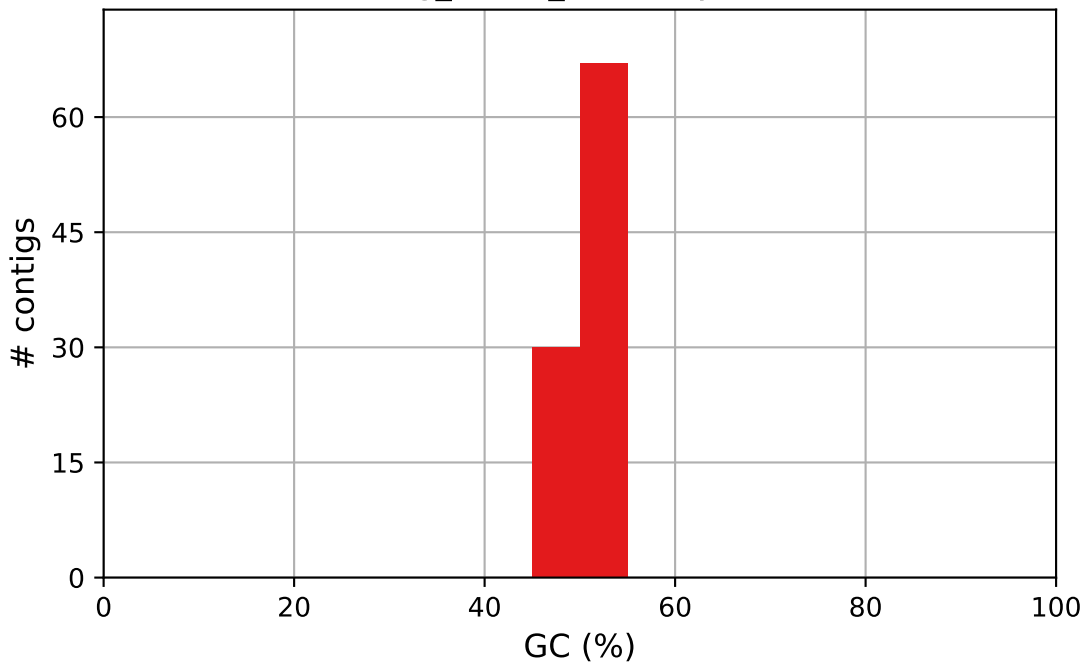
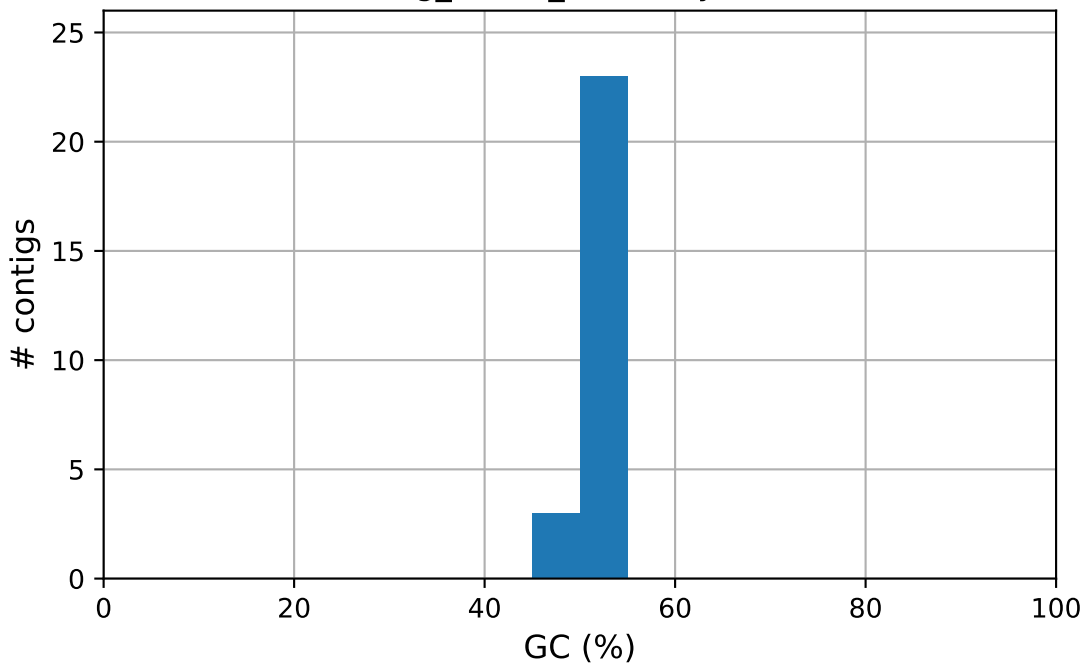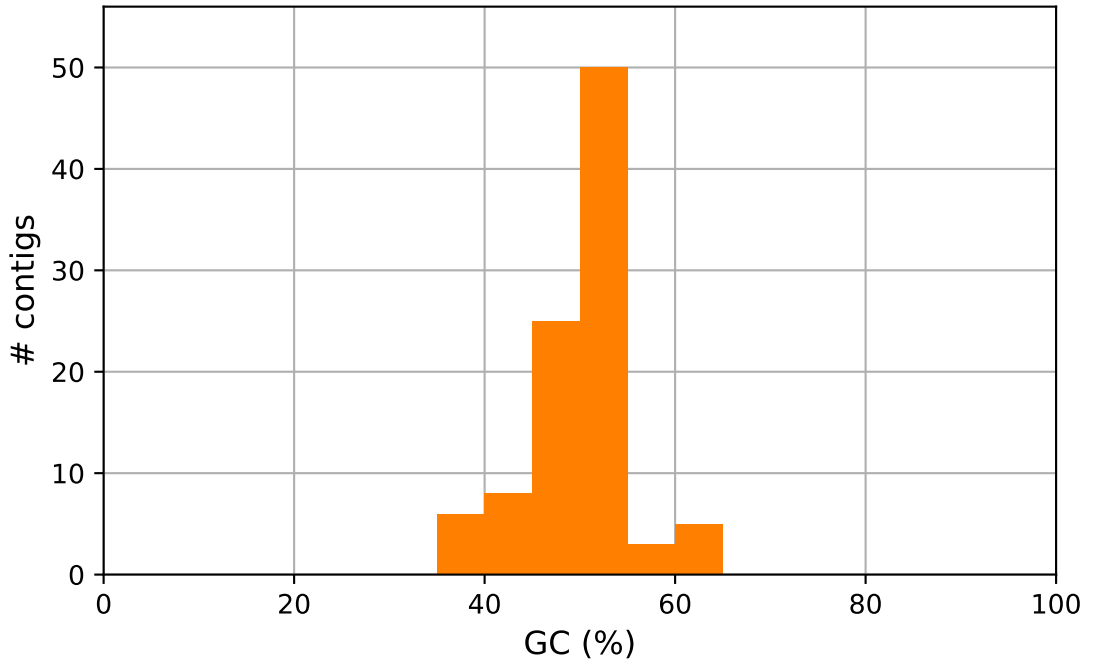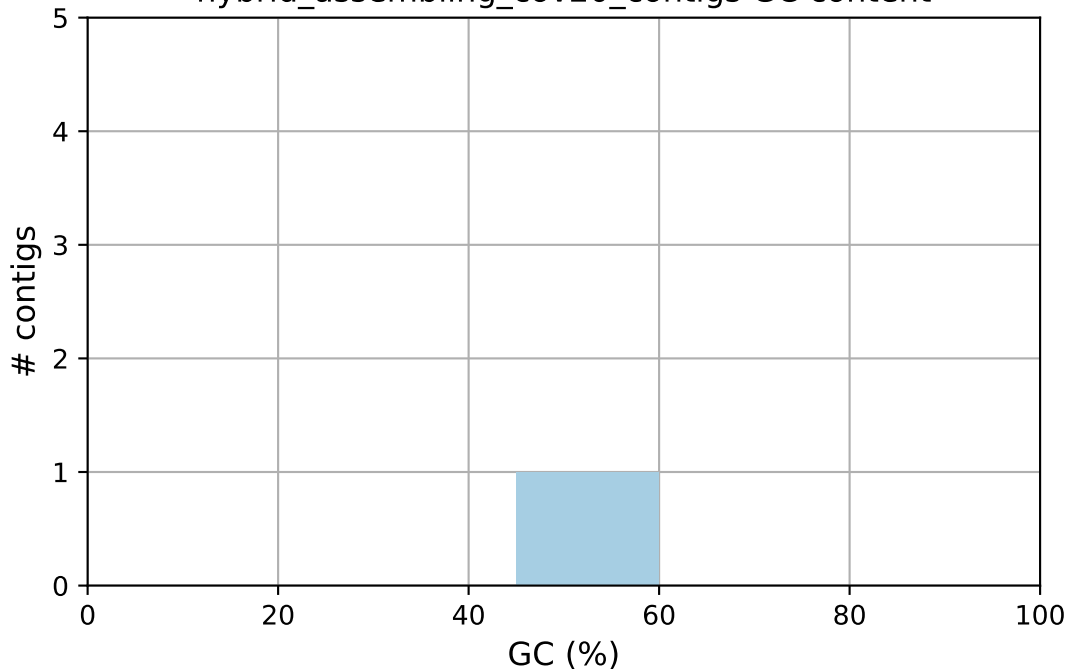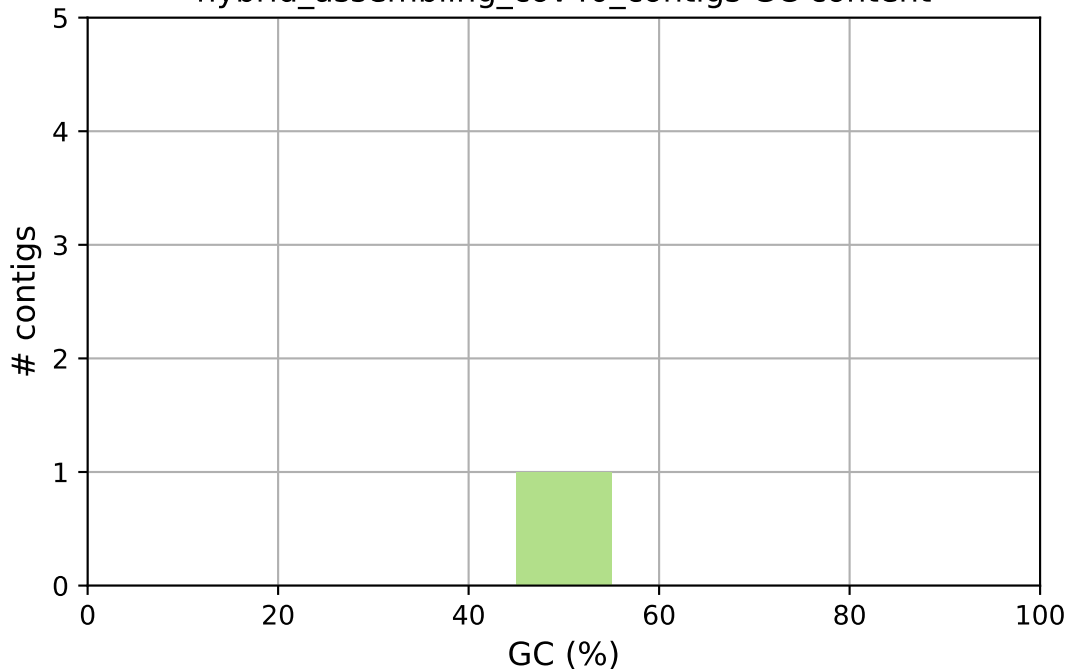|	assembling_cov10_assembly	assembling_cov20_assembly	assembling_cov40_assembly	assembling_cov80_assembly	illumina_assembling_contigs	hybrid_assembling_cov10_contigs	hybrid_assembling_cov20_contigs	hybrid_assembling_cov40_contigs
# fully unaligned contigs	0	0	0	0	1	1	1	1
Fully unaligned length	0	0	0	0	542	542	542	542
# partially unaligned contigs	41	10	1	1	0	0	0	0
Partially unaligned length	155101	34324	2228	914	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).

Nx

ng_cov10_assembly	assembling_cov80_assembly	hybrid_assembling
ng_cov20_assembly	illumina_assembling_contigs	hybrid_assembling
ng_cov40_assembly	hybrid_assembling_cov10_contigs	

NGx

Cumulative length

ng_cov10_assembly	assembling_cov80_assembly	hybrid_assembling
ng_cov20_assembly	illumina_assembling_contigs	hybrid_assembling
ng_cov40_assembly	hybrid_assembling_cov10_contigs	- - - Reference

GC content

Legend		
ng_cov10_assembly	assembling_cov80_assembly	hybrid_assembling
ng_cov20_assembly	illumina_assembling_contigs	hybrid_assembling
ng_cov40_assembly	hybrid_assembling_cov10_contigs	Reference

assembling_cov10_assembly GC content

assembling_cov20_assembly GC content

assembling_cov40_assembly GC content
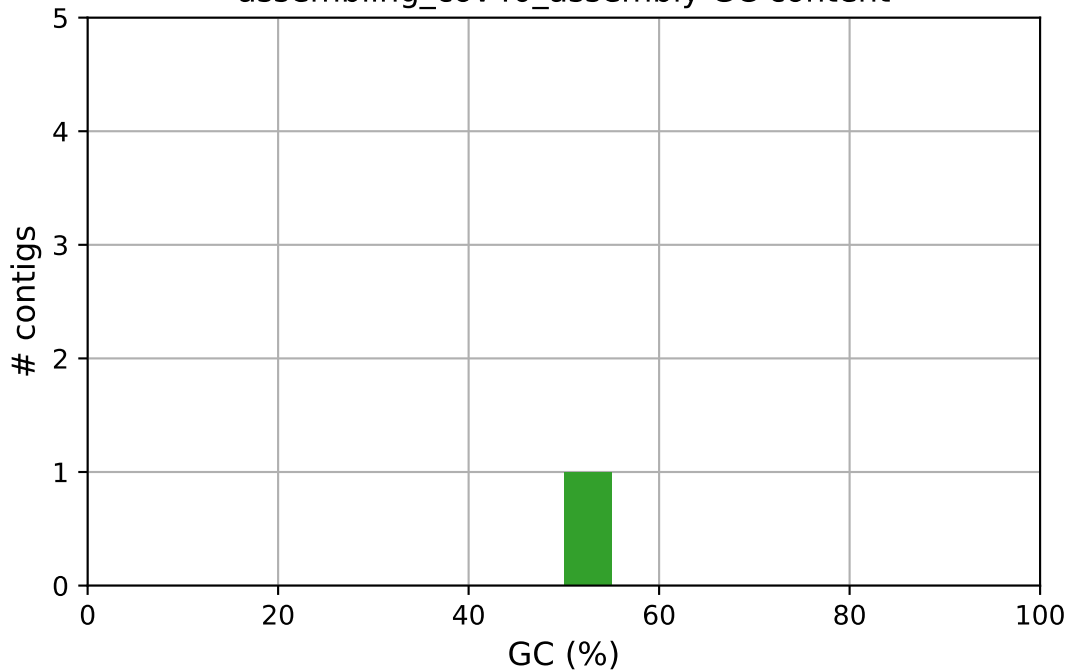
assembling_cov80_assembly GC content
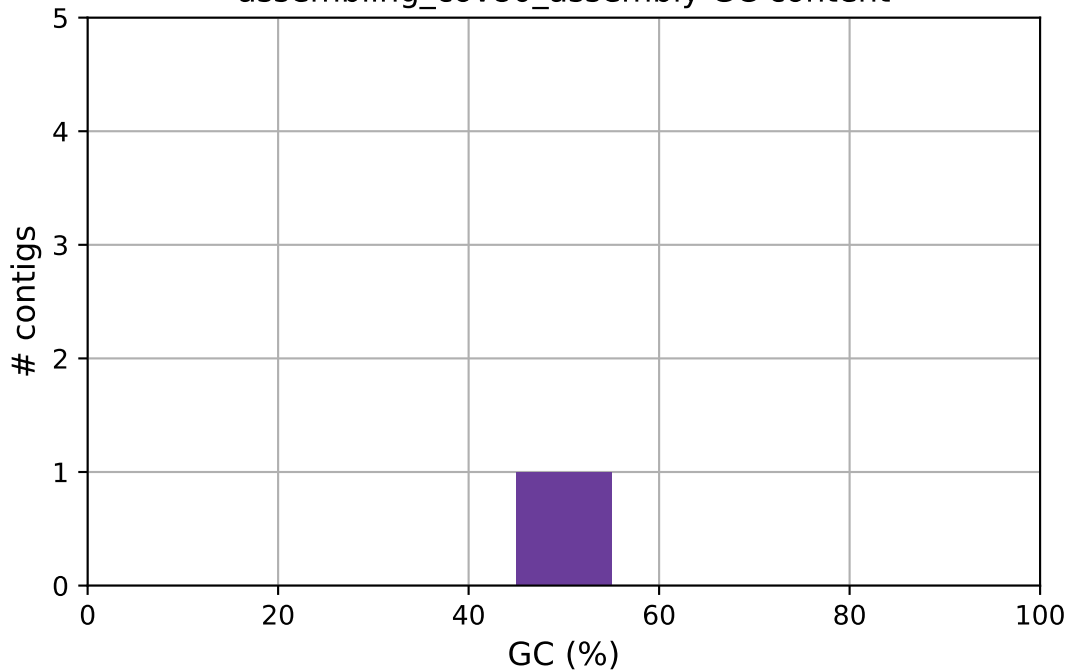
hybrid_assembling_cov10_contigs GC content
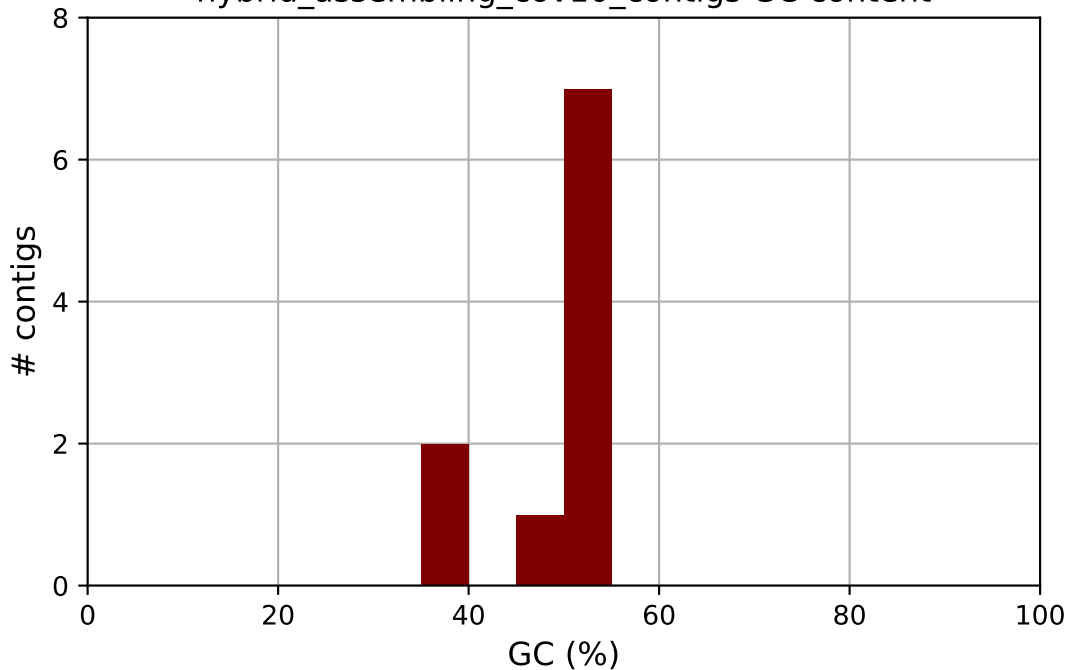
hybrid_assembling_cov20_contigs GC content

hybrid_assembling_cov40_contigs GC content
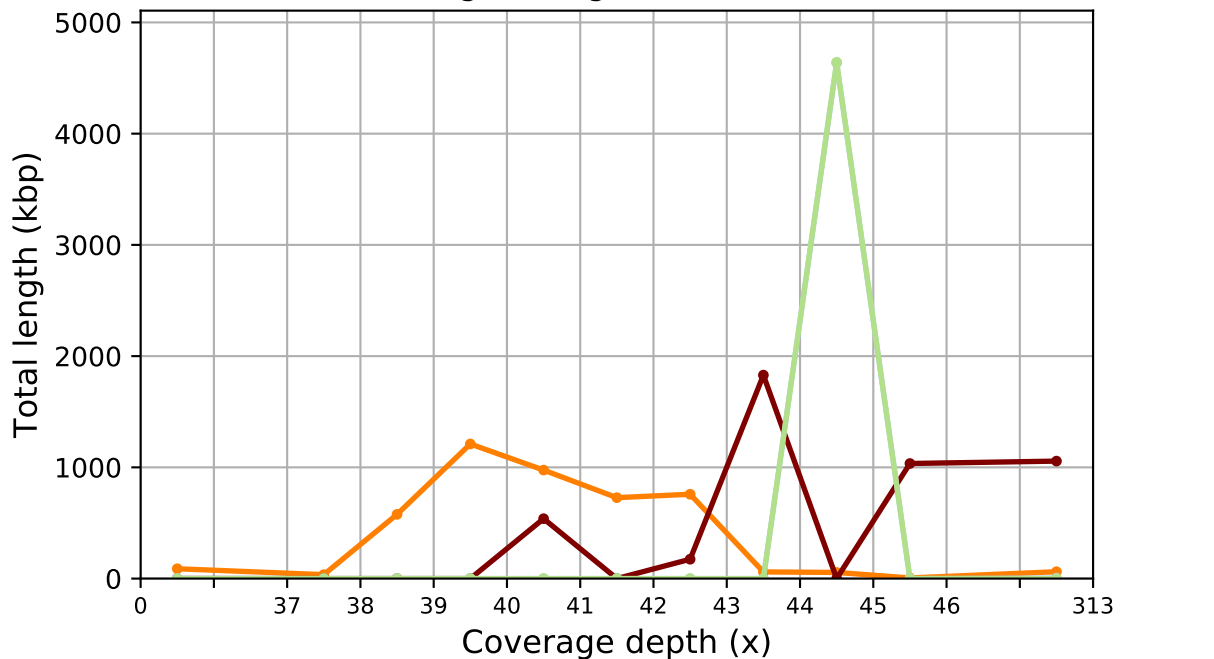
Coverage histogram (bin size: 1x)

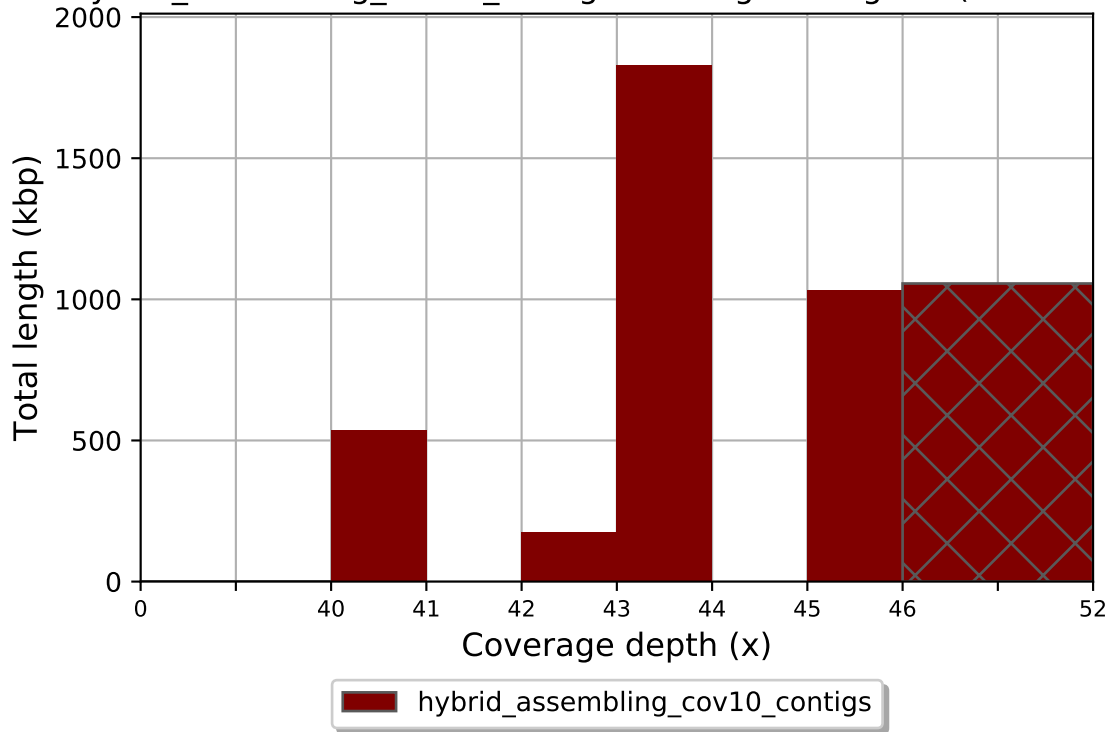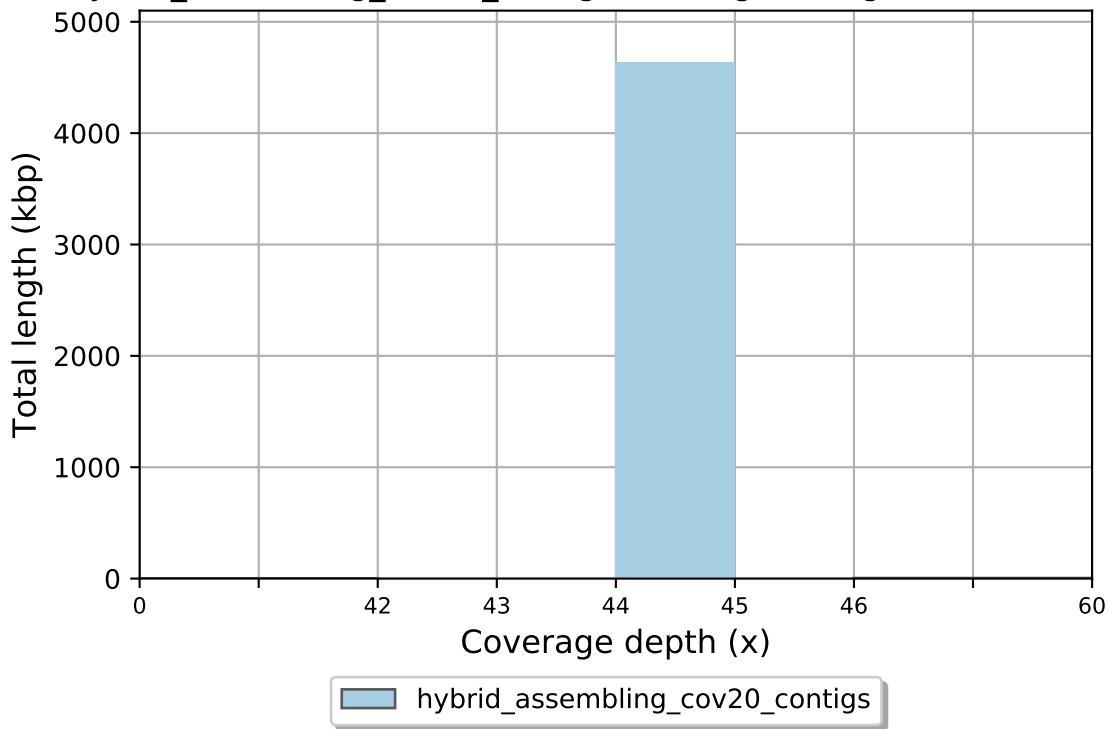Legend: sembling_contigs, hybrid_assembling_cov20_contigs, hybrid_assembli, embling_cov10_contigs

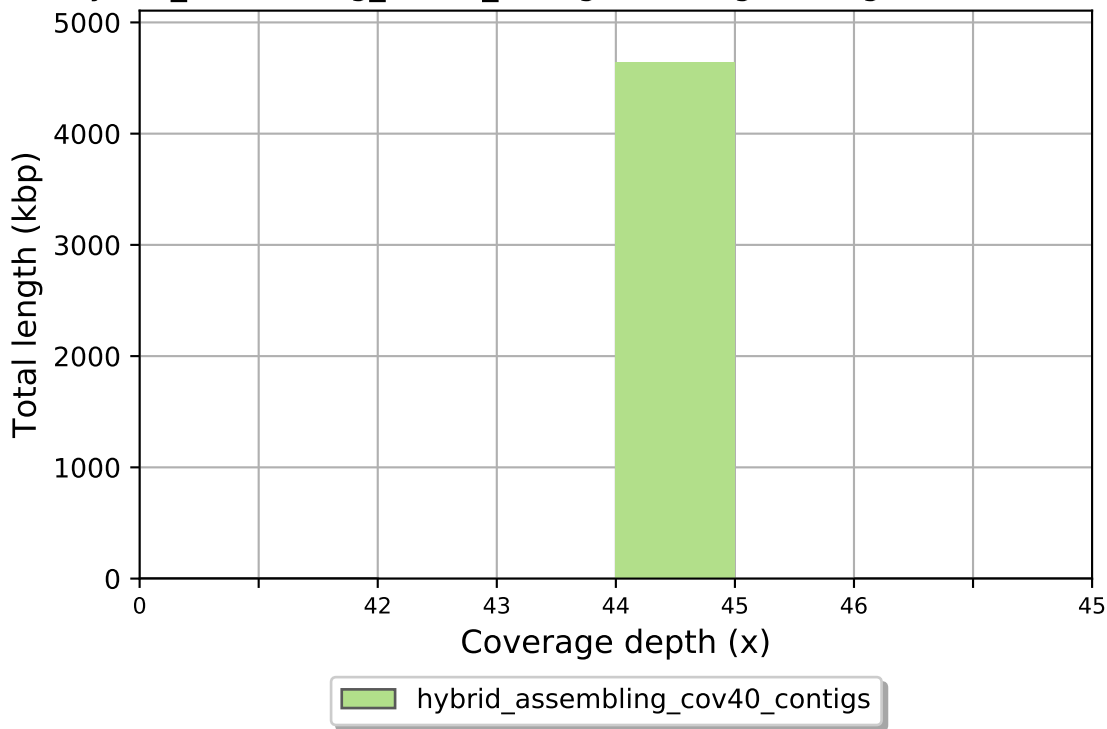illumina_assembling_contigs coverage histogram (bin size: 1x)
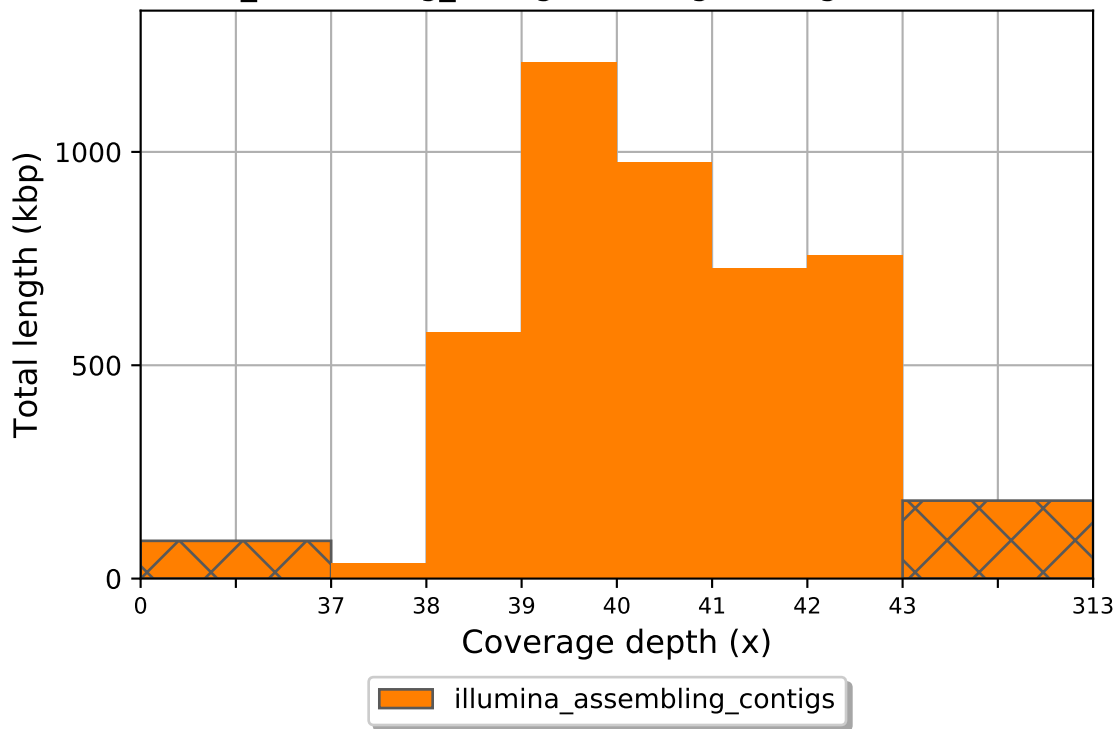
hybrid_assembling_cov10_contigs coverage histogram (bin size: 1x)
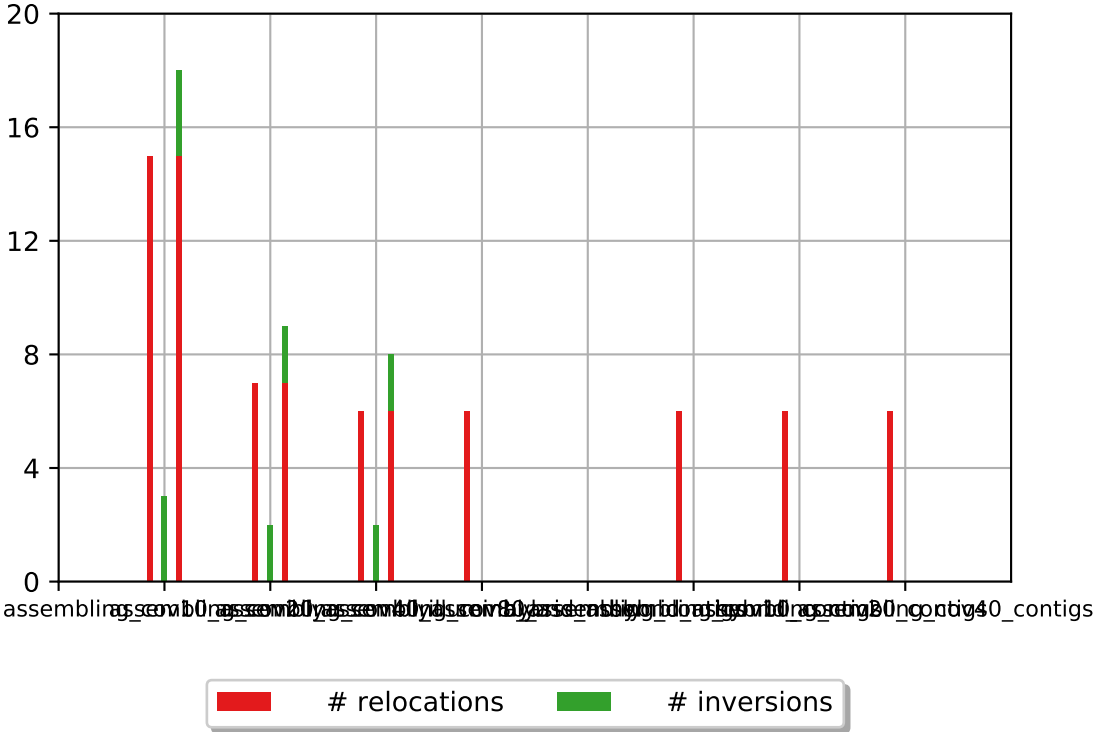
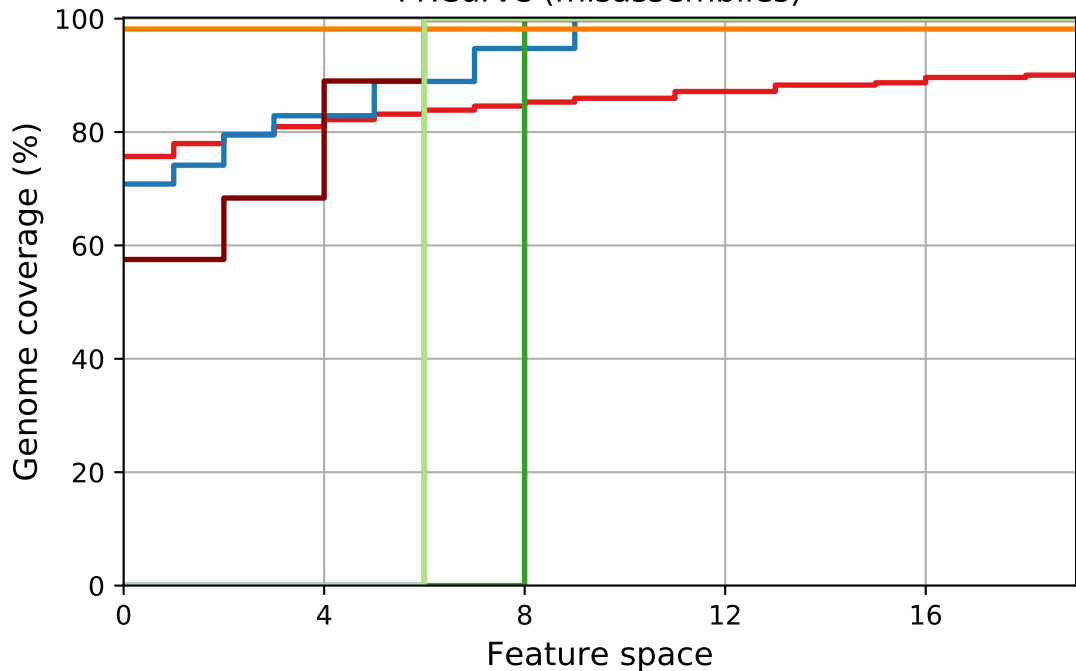hybrid_assembling_cov20_contigs coverage histogram (bin size: 1x)

hybrid_assembling_cov40_contigs coverage histogram (bin size: 1x)

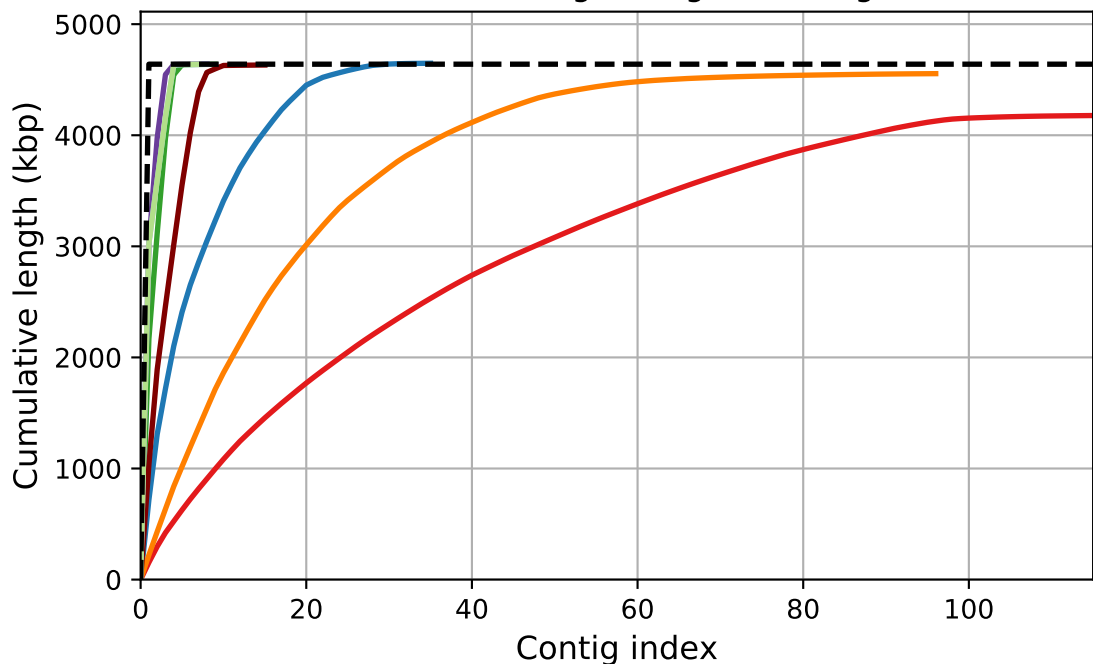Misassemblies

FRCurve (misassemblies)

Legend:
- ng_cov10_assembly
- ng_cov20_assembly
- ng_cov40_assembly
- assembling_cov80_assembly
- illumina_assembling_contigs
- hybrid_assembling_cov10_contigs
- hybrid_assembling
- hybrid_assembling

Cumulative length (aligned contigs)

Legend:
- ng_cov10_assembly
- ng_cov20_assembly
- ng_cov40_assembly
- assembling_cov80_assembly
- illumina_assembling_contigs
- hybrid_assembling_cov10_contigs
- hybrid_assembling
- hybrid_assembling
- Reference

NAx

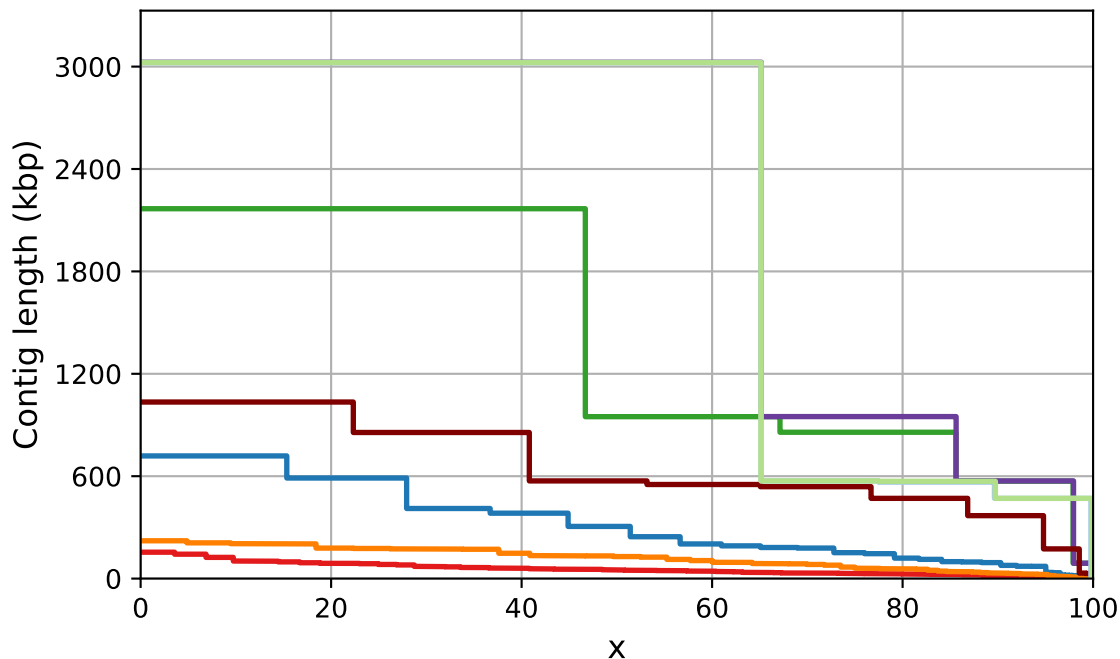Contig length (kbp) vs x

Legend:
- ng_cov10_assembly
- ng_cov20_assembly
- ng_cov40_assembly
- assembling_cov80_assembly
- illumina_assembling_contigs
- hybrid_assembling_cov10_contigs
- hybrid_assembling
- hybrid_assembling

NGAx

ng_cov10_assembly	assembling_cov80_assembly	hybrid_assembling
ng_cov20_assembly	illumina_assembling_contigs	hybrid_assembling
ng_cov40_assembly	hybrid_assembling_cov10_contigs	

Genome fraction, %

ng_cov10_assembly	assembling_cov80_assembly	hybrid_assembling
ng_cov20_assembly	illumina_assembling_contigs	hybrid_assembling
ng_cov40_assembly	hybrid_assembling_cov10_contigs	