

Report

	hybrid10x_contigs	hybrid20x_contigs	hybrid40x_contigs	hybrid80x_contigs	illumina100x_contigs	pacbio10x.contigs	pacbio20x.contigs	pacbio40x.contigs	pacbio80x.contigs
# contigs (>= 0 bp)	77	29	14	6	182	132	24	3	1
# contigs (>= 1000 bp)	24	6	4	1	72	132	24	3	1
# contigs (>= 5000 bp)	22	6	4	1	55	118	24	3	1
# contigs (>= 10000 bp)	21	6	4	1	50	96	22	1	1
# contigs (>= 25000 bp)	20	6	4	1	45	55	20	1	1
# contigs (>= 50000 bp)	18	6	4	1	32	24	18	1	1
Total length (>= 0 bp)	4616659	4622136	4632342	4643106	4581324	3817958	4606872	4656608	4652982
Total length (>= 1000 bp)	4598895	4618736	4630770	4642160	4555857	3817958	4606872	4656608	4652982
Total length (>= 5000 bp)	4593245	4618736	4630770	4642160	4521561	3776647	4606872	4656608	4652982
Total length (>= 10000 bp)	4585190	4618736	4630770	4642160	4486505	3605179	4589829	4640800	4652982
Total length (>= 25000 bp)	4568867	4618736	4630770	4642160	4411989	2956461	4561599	4640800	4652982
Total length (>= 50000 bp)	4503280	4618736	4630770	4642160	3958065	1795449	4492379	4640800	4652982
# contigs	42	7	5	2	80	132	24	3	1
Largest contig	586206	2076249	2774924	4642160	315011	180610	749388	4640800	4652982
Total length	4611325	4619278	4631312	4642702	4561438	3817958	4606872	4656608	4652982
Reference length	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675	4639675
GC (%)	50.76	50.78	50.78	50.79	50.74	50.50	50.76	50.76	50.79
Reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
N50	292022	737360	2774924	4642160	133059	47884	273158	4640800	4652982
NG50	292022	737360	2774924	4642160	133059	42731	273158	4640800	4652982
N75	176460	693225	1035676	4642160	67374	26677	199297	4640800	4652982
NG75	176460	693225	1035676	4642160	66204	12082	199297	4640800	4652982
L50	6	2	1	1	12	27	5	1	1
LG50	6	2	1	1	12	36	5	1	1
L75	11	3	2	1	23	52	10	1	1
LG75	11	3	2	1	24	85	10	1	1
# misassemblies	5	6	6	6	1	11	8	8	8
# misassembled contigs	3	1	1	1	1	7	3	1	1
Misassembled contigs length	1220159	2076249	2774924	4642160	201176	345889	1187160	4640800	4652982
# local misassemblies	6	6	5	5	9	1	2	2	2
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# unaligned contigs	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	1 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	542	542	542	542	542	0	0	0	0
Genome fraction (%)	99.070	99.485	99.745	99.988	98.274	82.135	98.615	99.994	99.998
Duplication ratio	1.003	1.001	1.001	1.001	1.000	1.002	1.007	1.004	1.003
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	6.46	7.34	7.02	8.36	1.40	48.81	6.05	1.23	0.41
# indels per 100 kbp	10.03	0.67	0.67	0.73	0.44	677.23	151.42	34.19	11.38
Largest alignment	572344	1040112	1040379	2594619	315011	149583	514798	3022594	3026086
Total aligned length	4609153	4618120	4630328	4641984	4560177	3817753	4606854	4653328	4652980
NA50	241223	693225	727539	2594619	133059	46336	243578	3022594	3026086
NGA50	241223	693225	727539	2594619	133059	41896	243578	3022594	3026086
NA75	172303	572346	431487	1040647	66204	25885	174362	938540	824431
NGA75	172303	572346	431487	1040647	64244	11459	142485	938540	824431
LA50	7	3	3	1	12	28	6	1	1
LGA50	7	3	3	1	12	37	6	1	1
LA75	12	5	5	2	24	54	11	2	2
LGA75	12	5	5	2	25	90	12	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

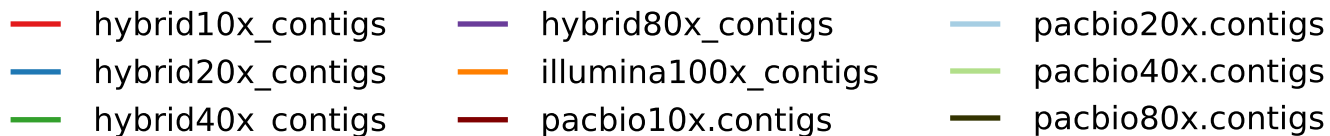
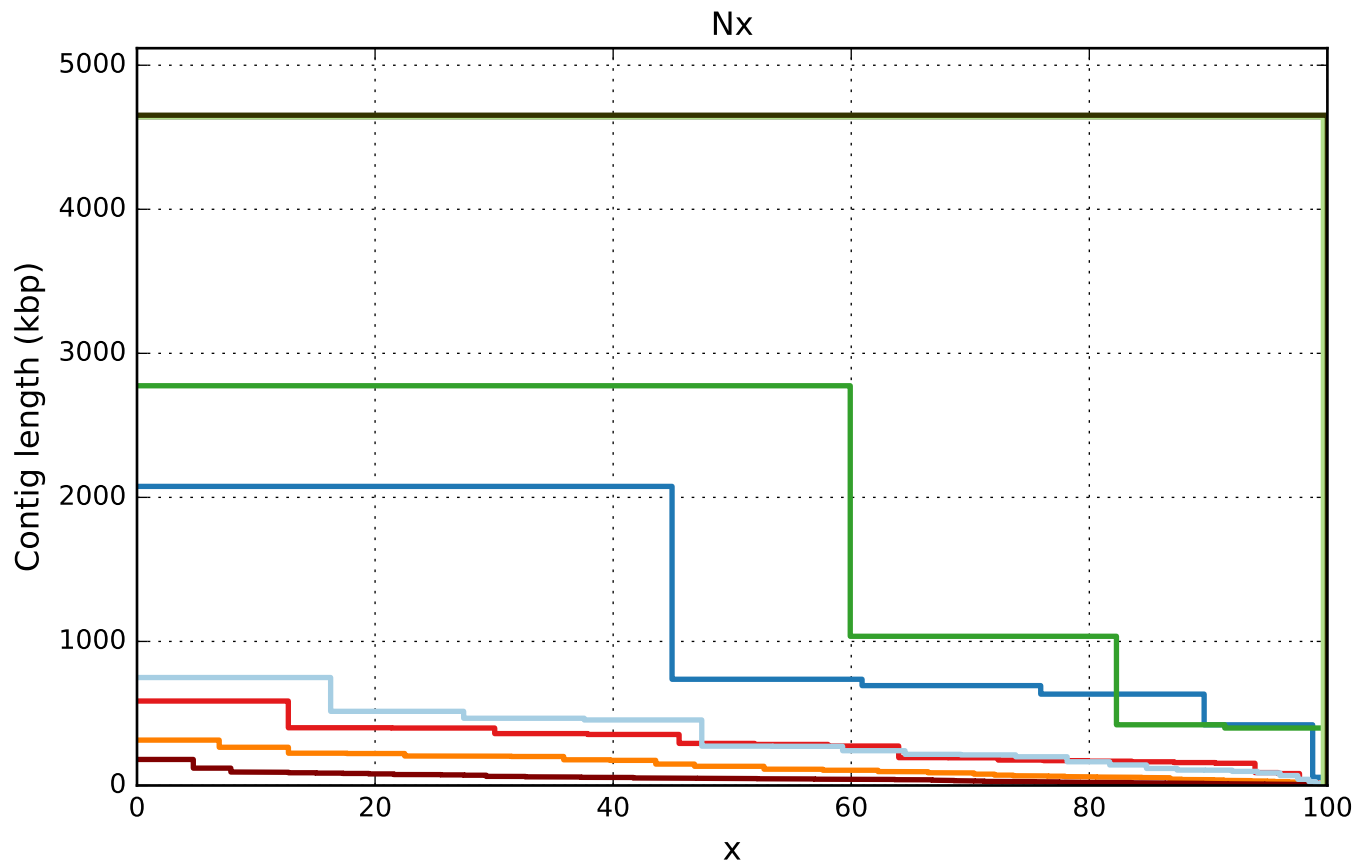
	hybrid10x_contigs	hybrid20x_contigs	hybrid40x_contigs	hybrid80x_contigs	illumina100x_contigs	pacbio10x.contigs	pacbio20x.contigs	pacbio40x.contigs	pacbio80x.contigs
# misassemblies	5	6	6	6	1	11	8	8	8
# contig misassemblies	5	6	6	6	1	11	8	8	8
# c. relocations	5	6	6	6	1	7	6	6	6
# c. translocations	0	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	4	2	2	2
# 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	3	1	1	1	1	7	3	1	1
Misassembled contigs length	1220159	2076249	2774924	4642160	201176	345889	1187160	4640800	4652982
# local misassemblies	6	6	5	5	9	1	2	2	2
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# mismatches	297	339	325	388	64	1860	277	57	19
# indels	461	31	31	34	20	25808	6928	1586	528
# indels (<= 5 bp)	457	29	29	32	16	25785	6926	1586	528
# indels (> 5 bp)	4	2	2	2	4	23	2	0	0
Indels length	586	84	84	87	252	27524	7166	1633	537

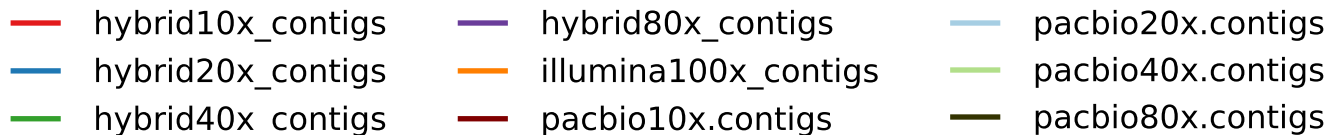
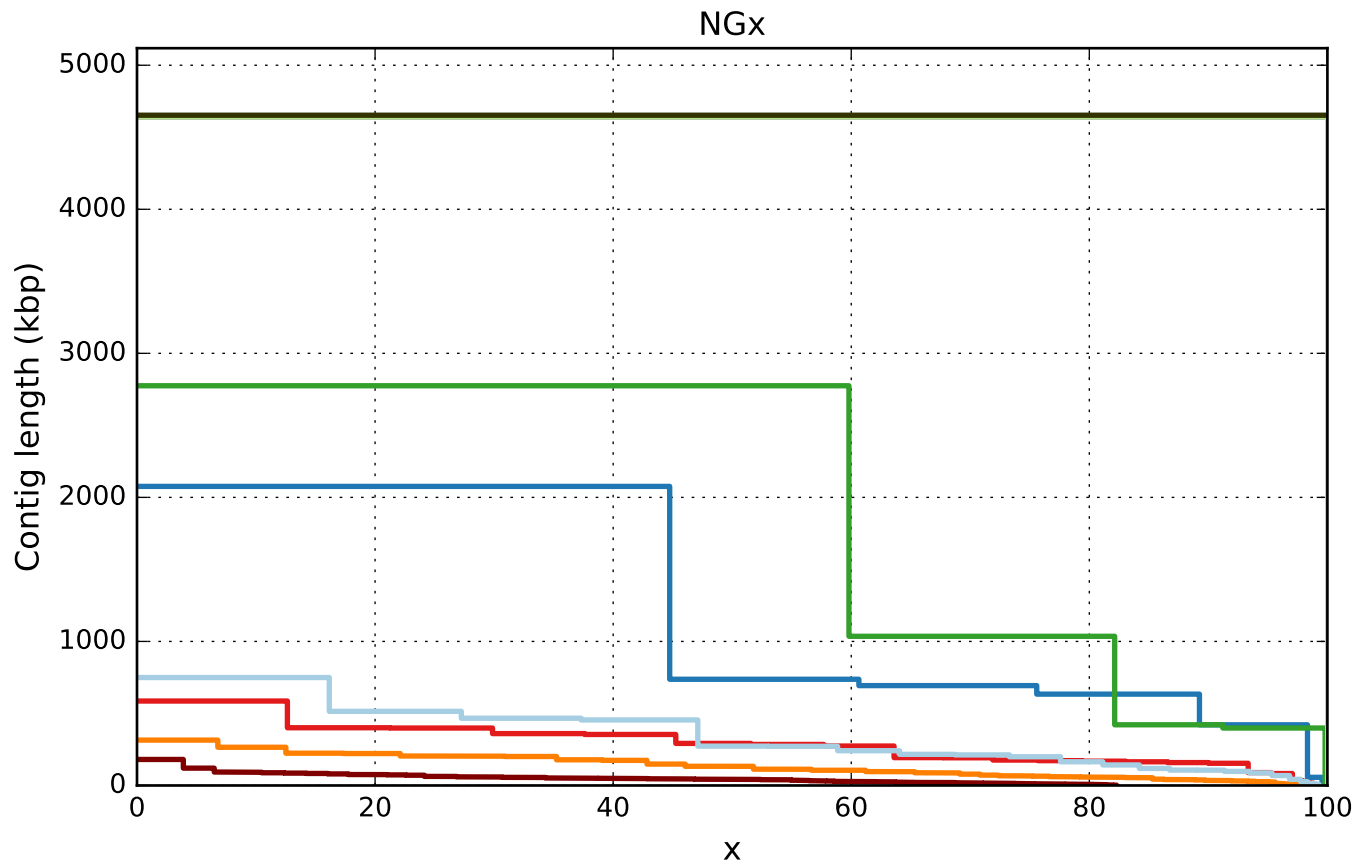
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

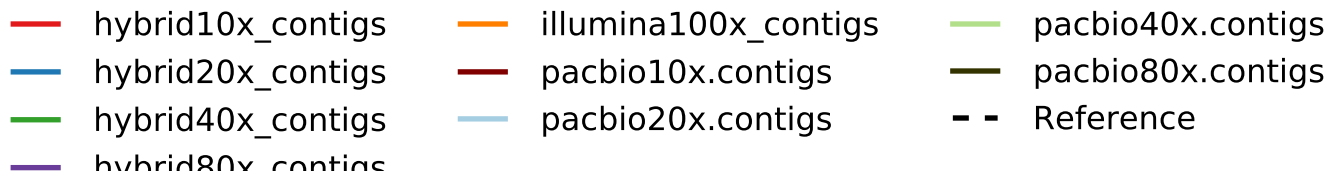
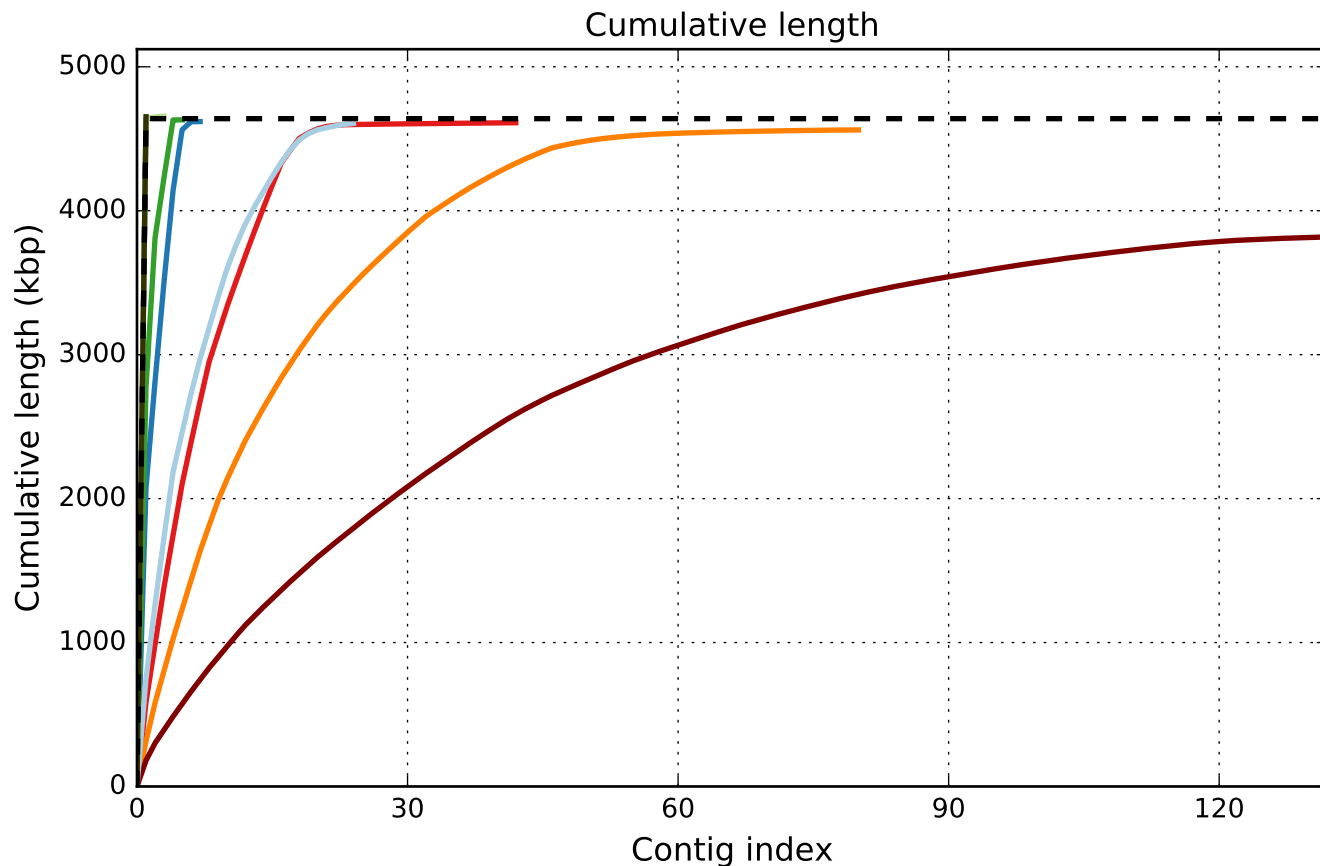
Unaligned report

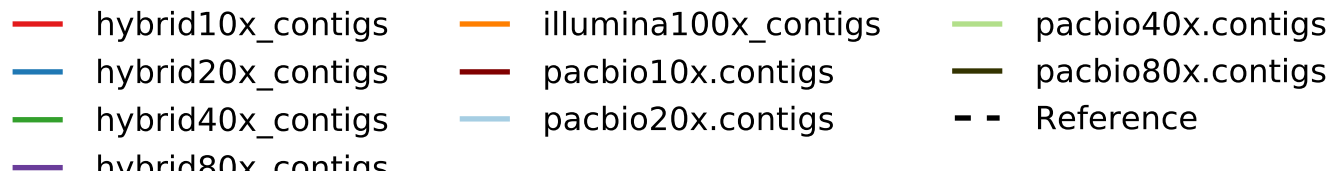
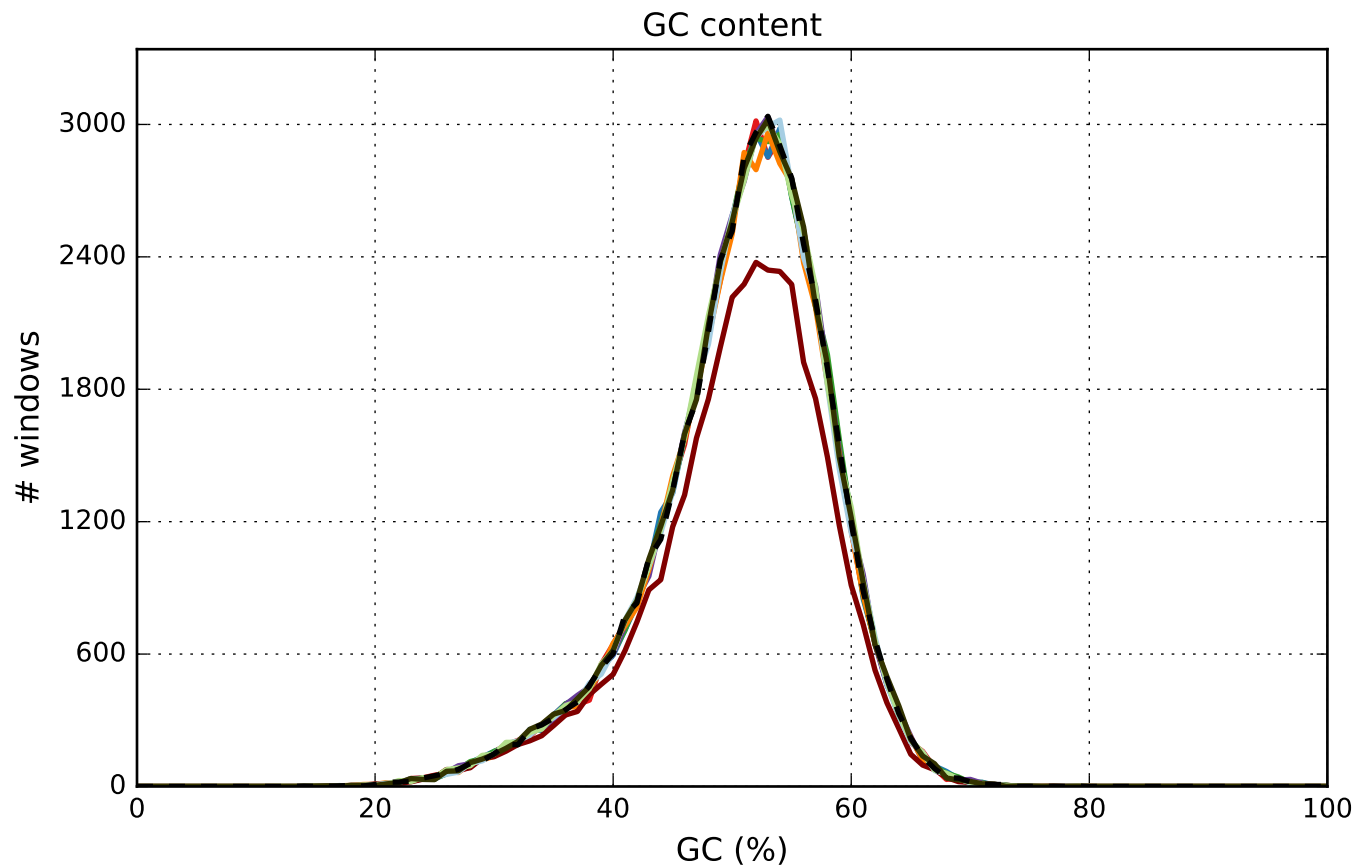
	hybrid10x_contigs	hybrid20x_contigs	hybrid40x_contigs	hybrid80x_contigs	illumina100x_contigs	pacbio10x.contigs	pacbio20x.contigs	pacbio40x.contigs	pacbio80x.contigs
# fully unaligned contigs	1	1	1	1	1	0	0	0	0
Fully unaligned length	542	542	542	542	542	0	0	0	0
# partially unaligned contigs	0	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0
# N's	0	0	0	0	0	0	0	0	0

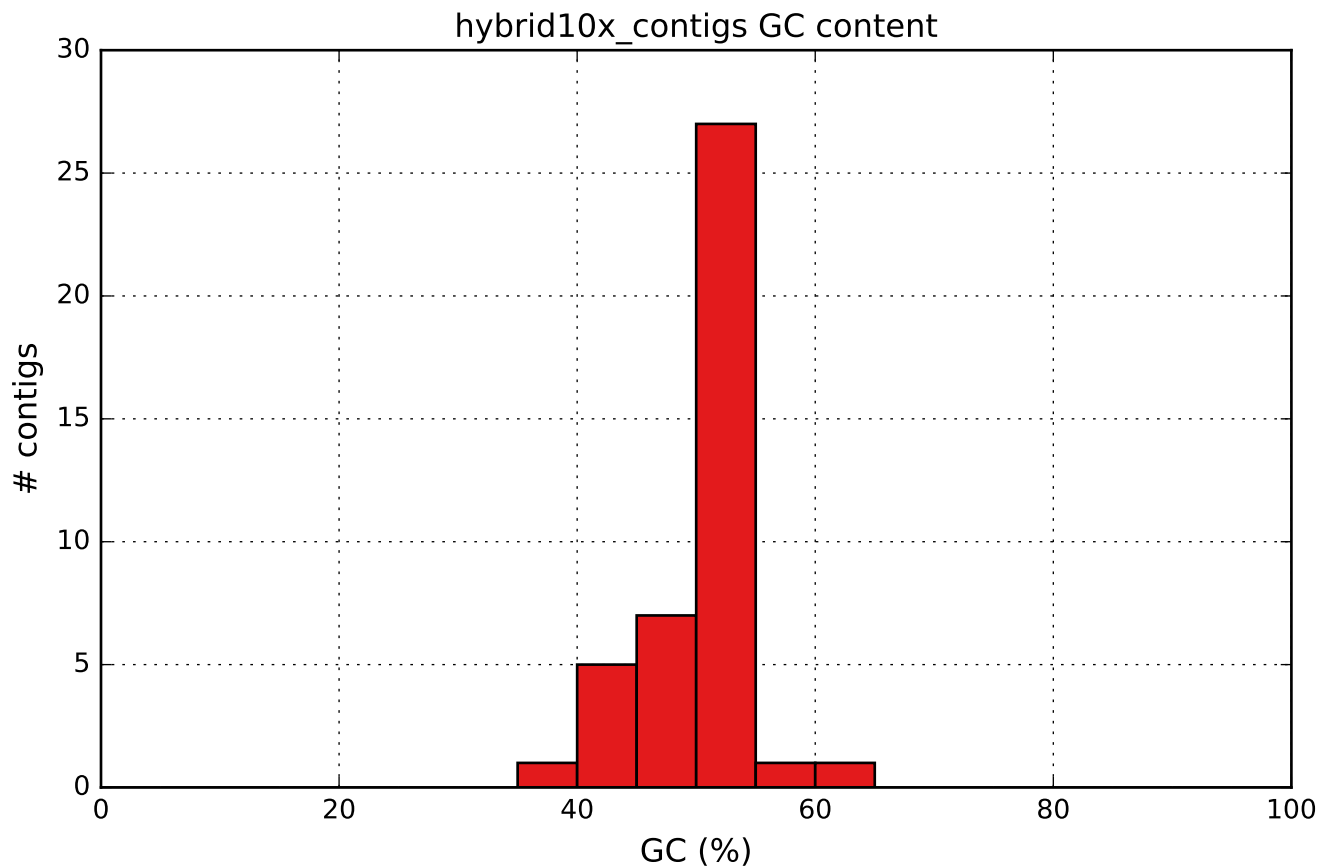
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





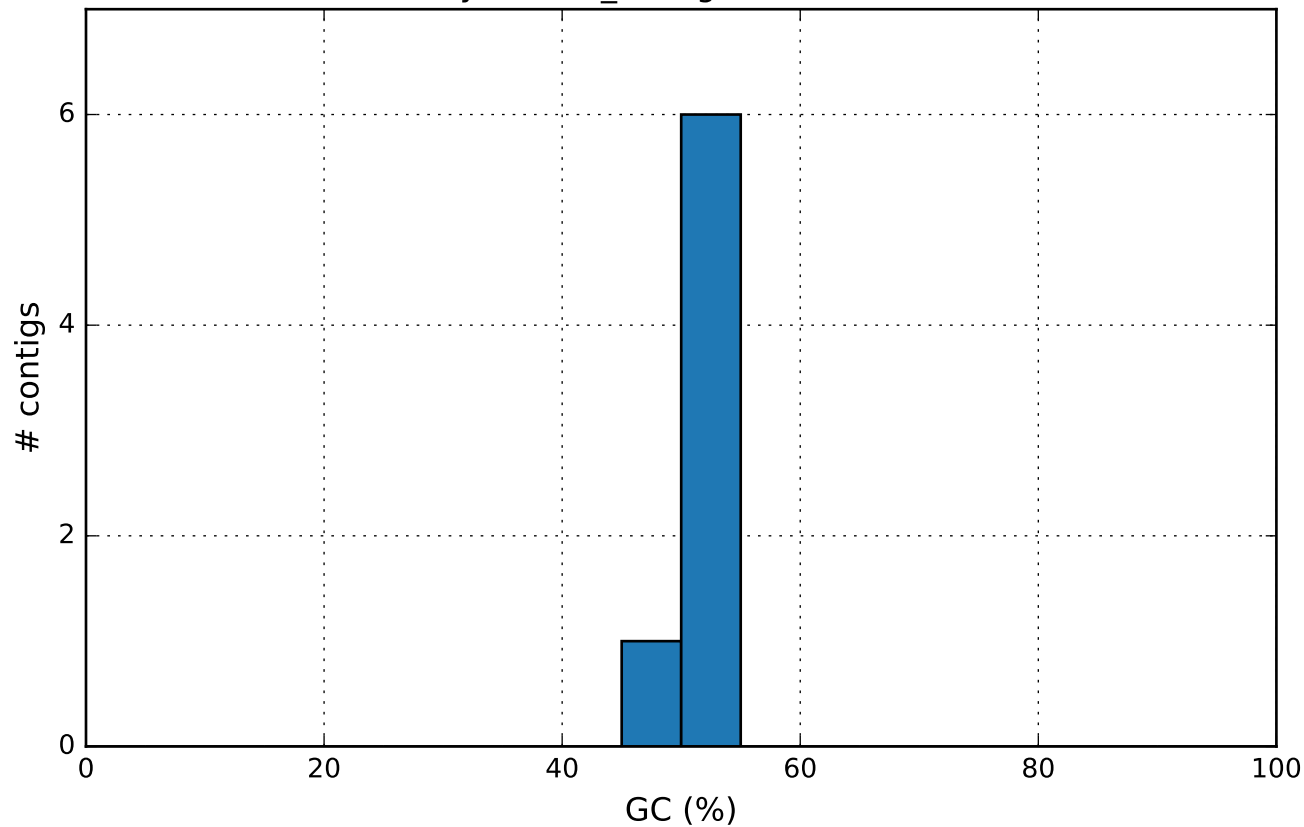






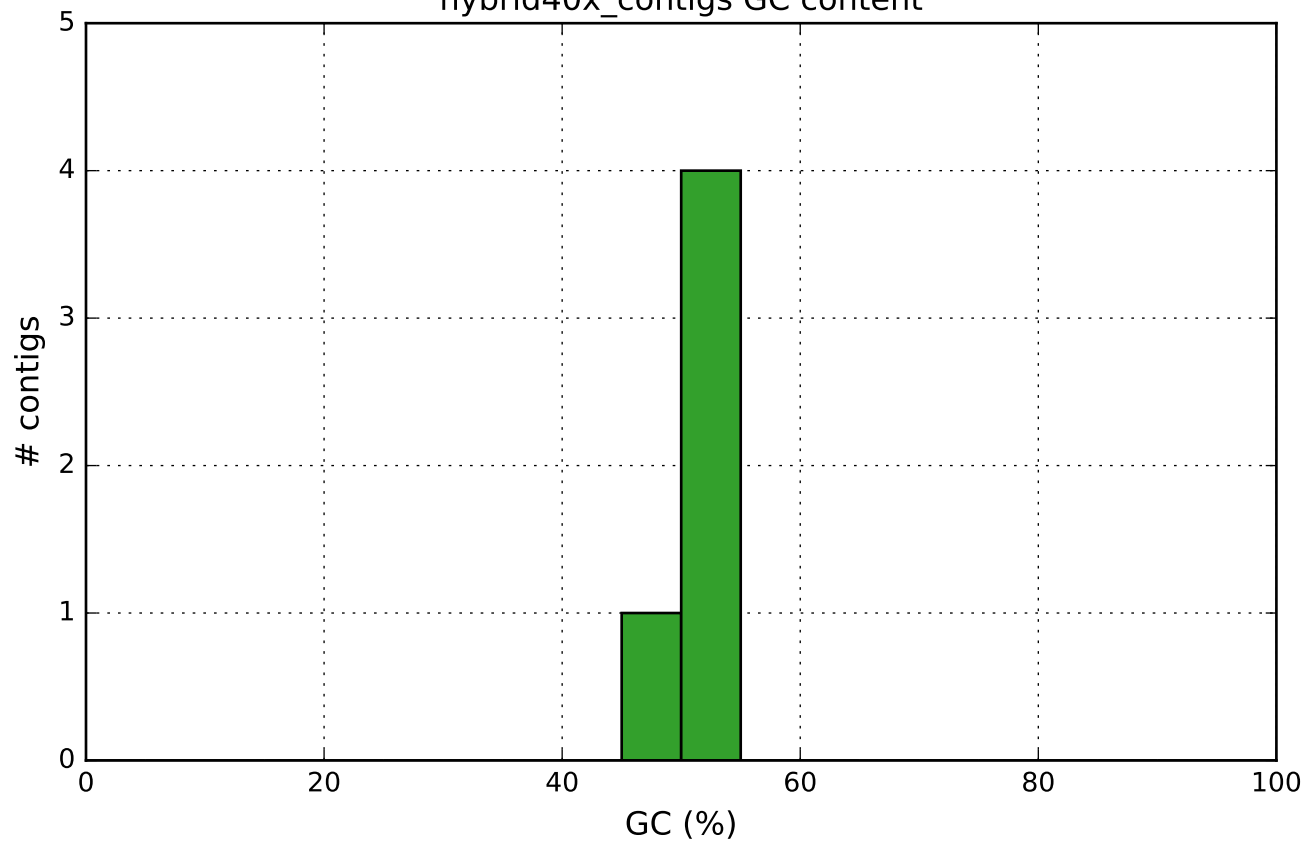
hybrid10x_contigs

hybrid20x_contigs GC content

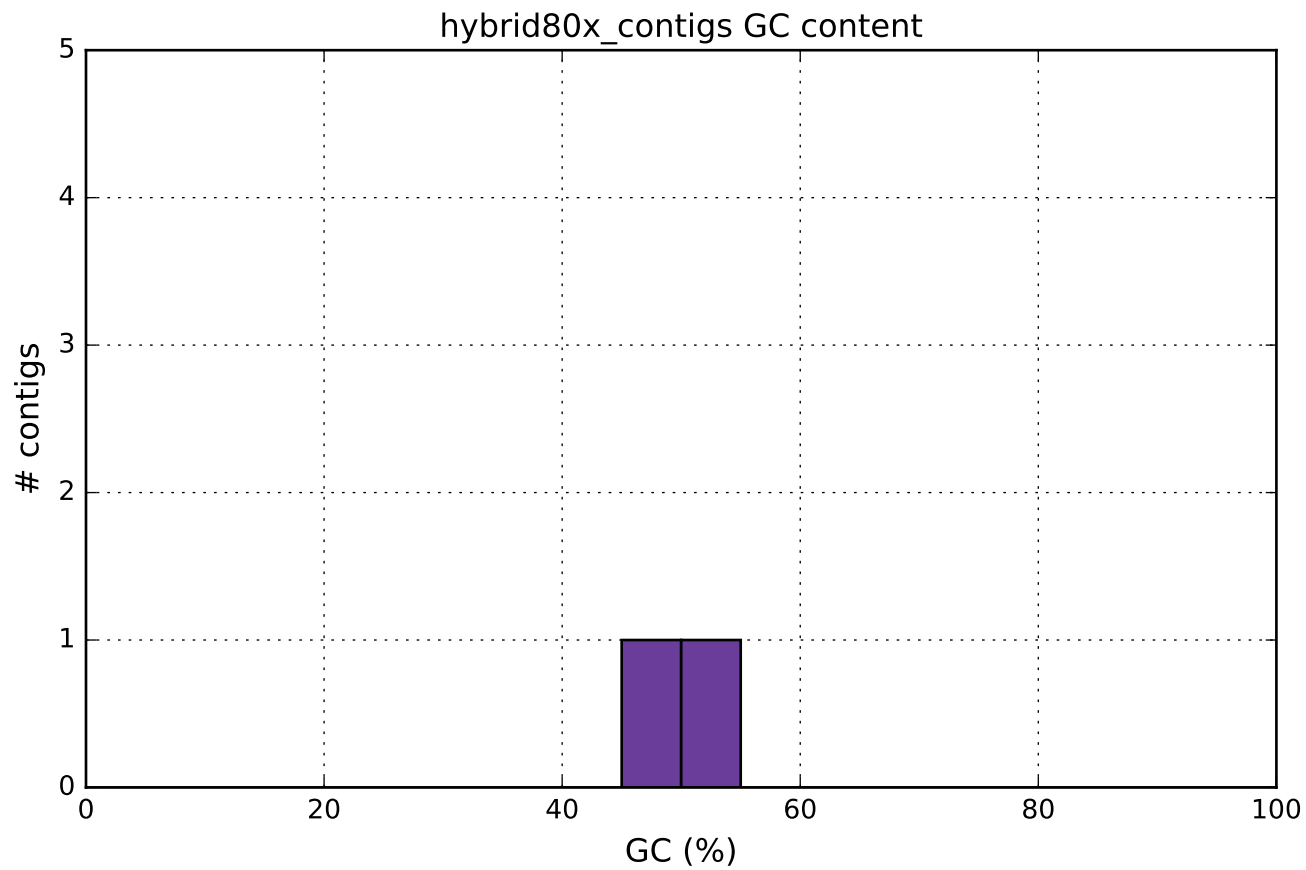


hybrid20x_contigs

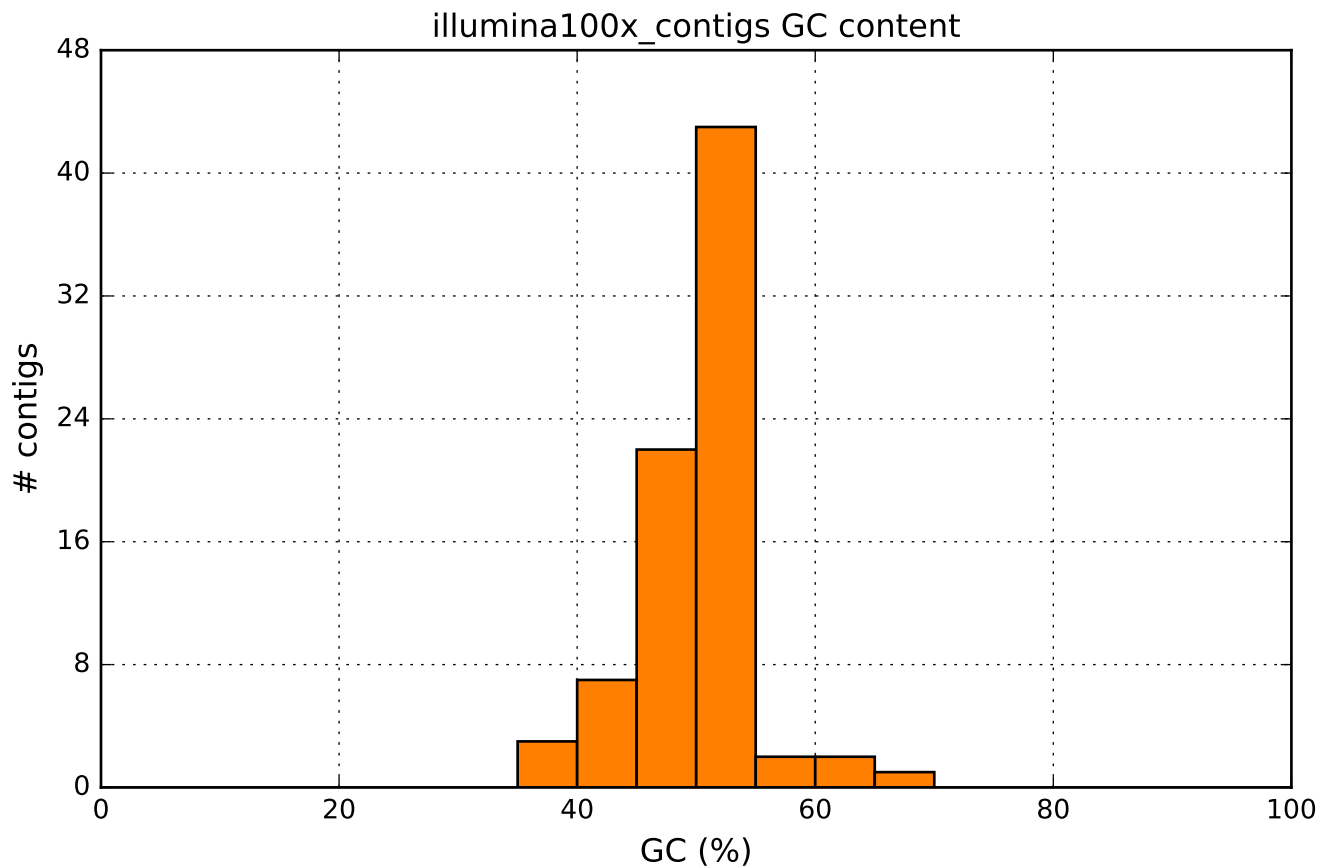
hybrid40x_contigs GC content



hybrid40x_contigs

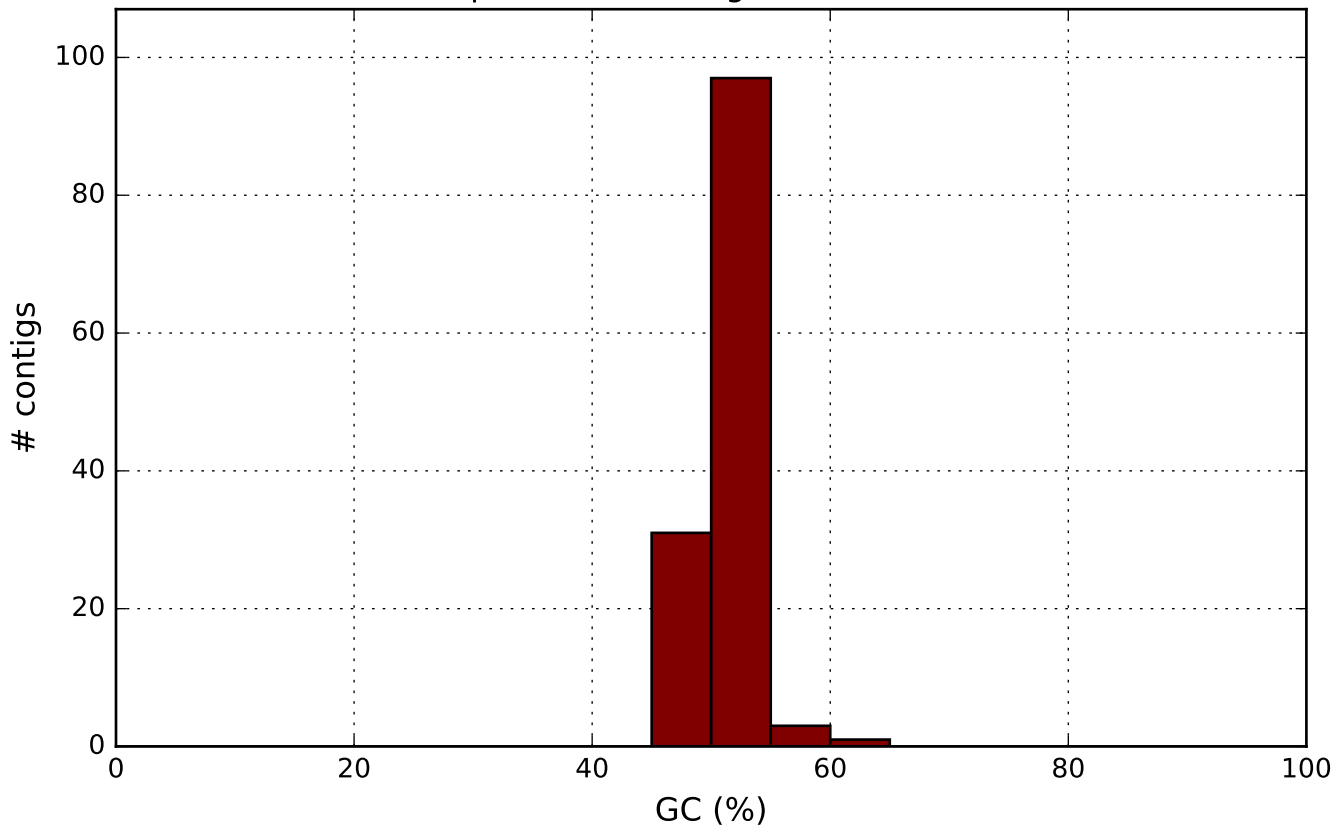


hybrid80x_contigs

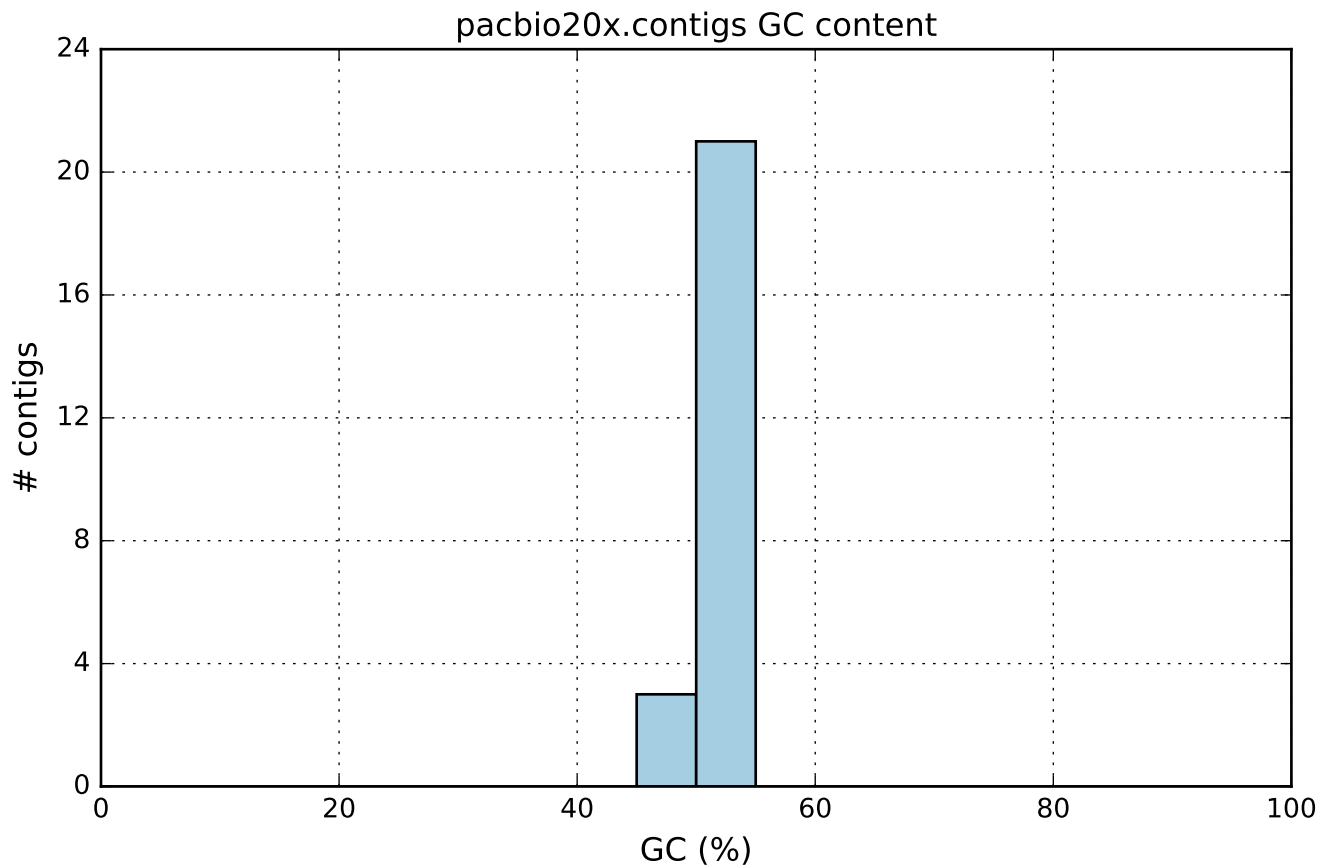


illumina100x_contigs

pacbio10x.contigs GC content

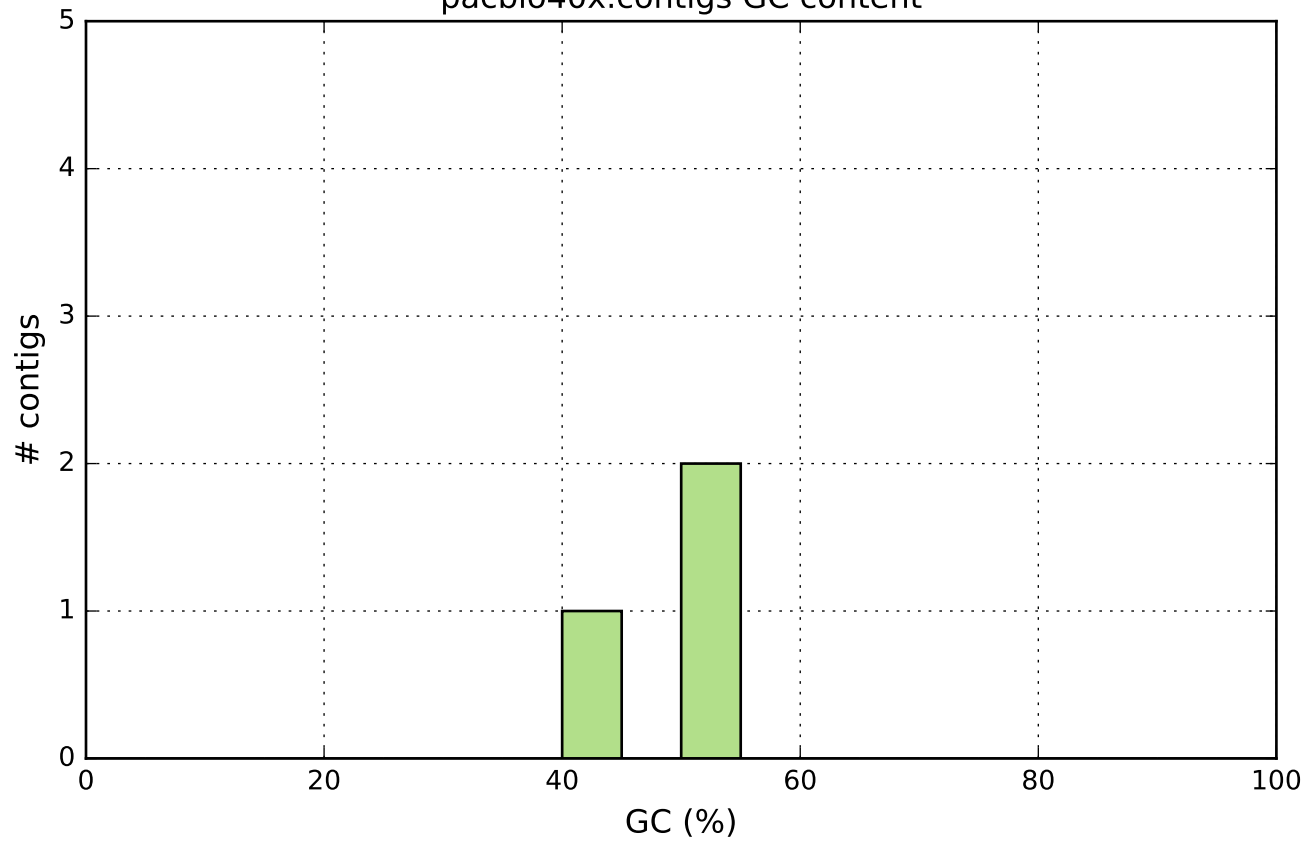


pacbio10x.contigs



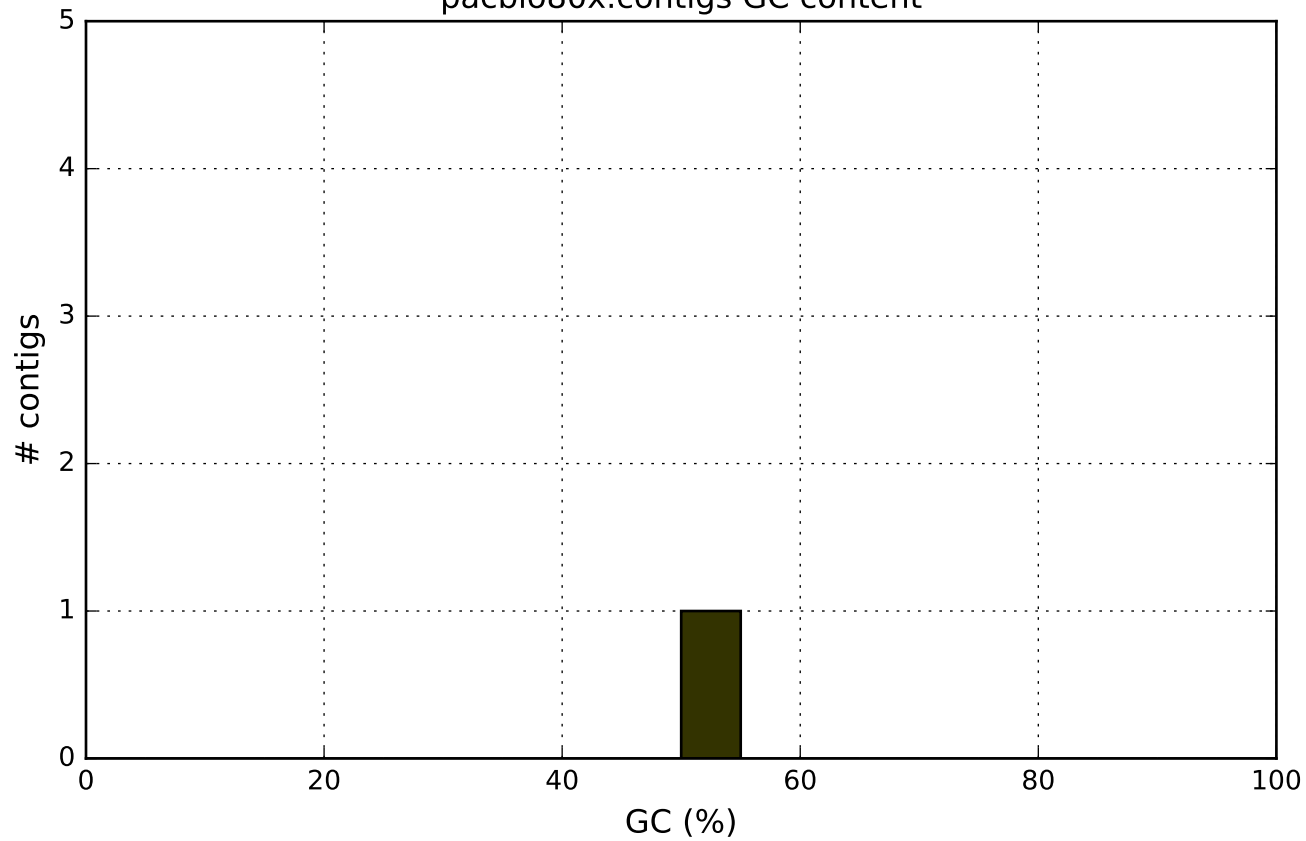
pacbio20x.contigs

pacbio40x.contigs GC content



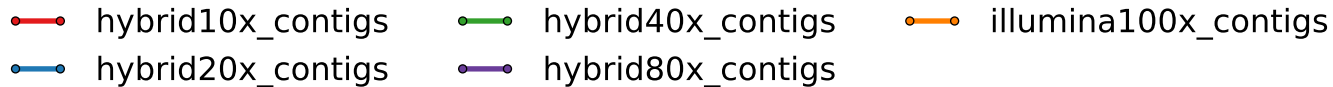
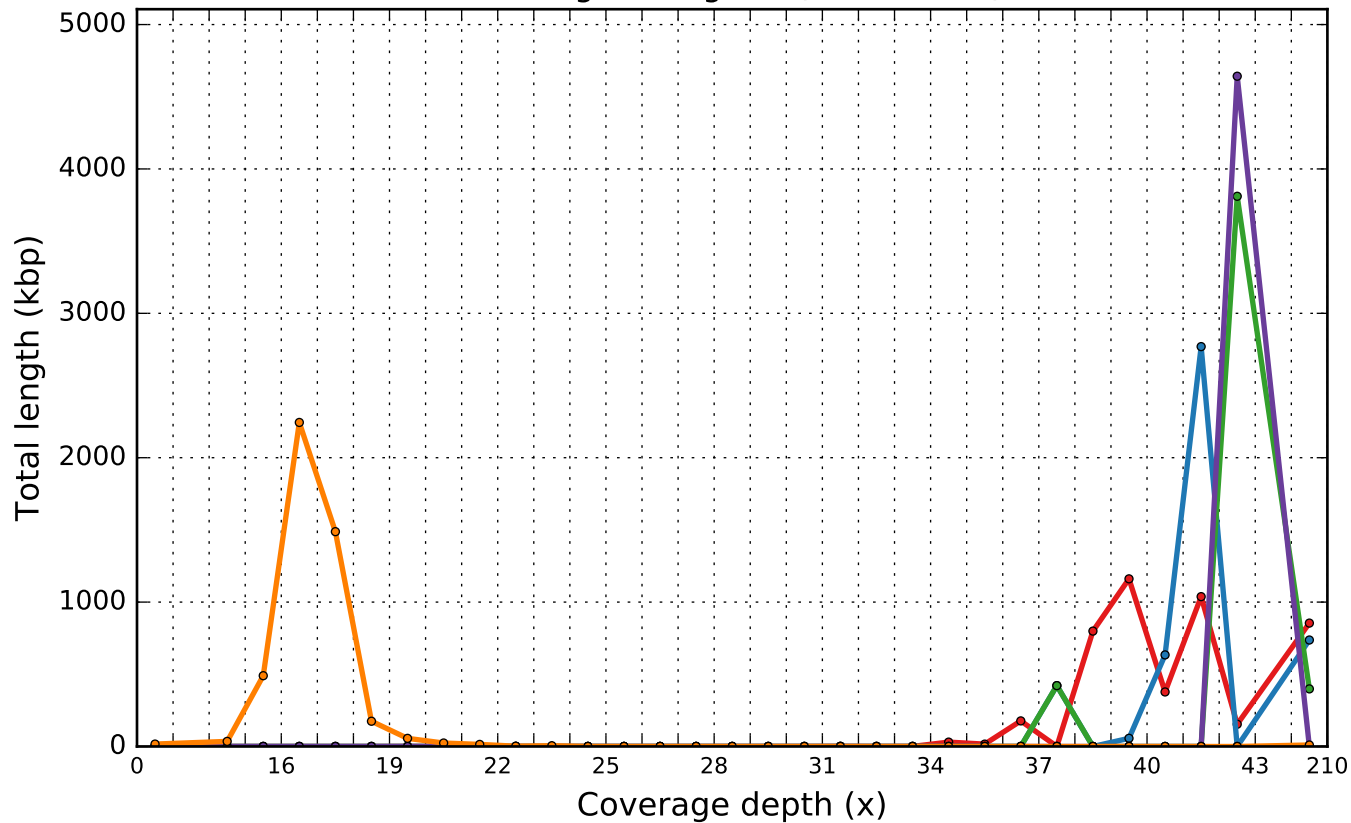
pacbio40x.contigs

pacbio80x.contigs GC content

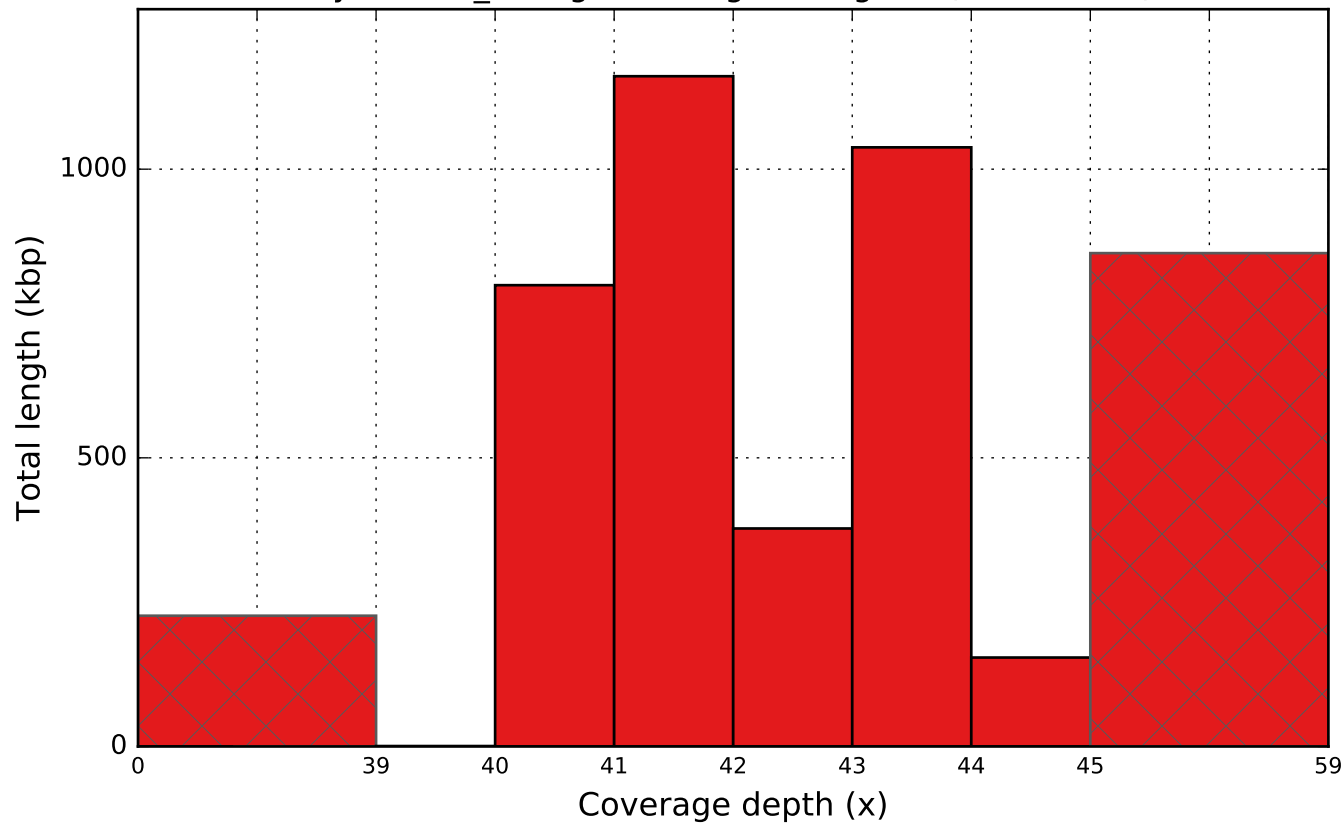


pacbio80x.contigs

Coverage histogram (bin size: 1x)

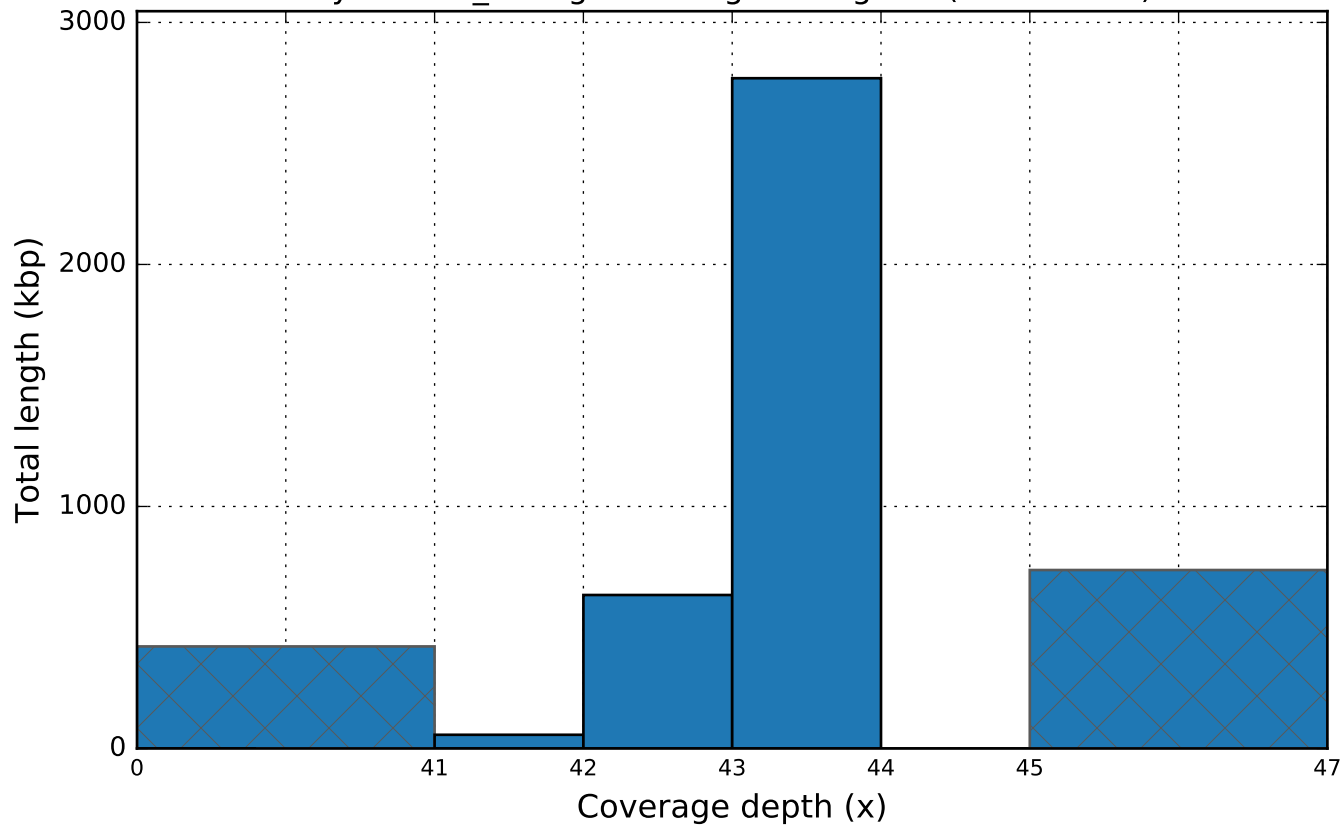


hybrid10x_contigs coverage histogram (bin size: 1x)



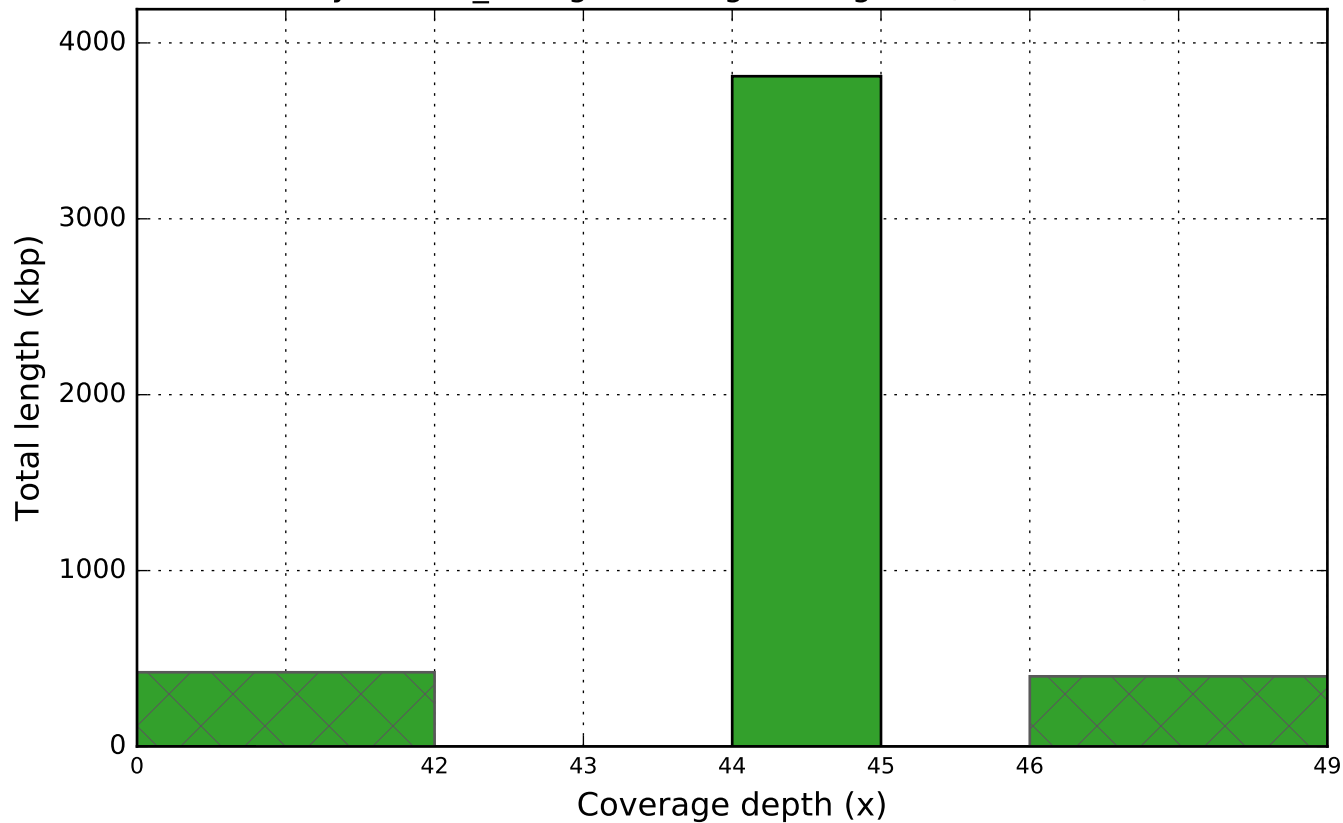
hybrid10x_contigs

hybrid20x_contigs coverage histogram (bin size: 1x)



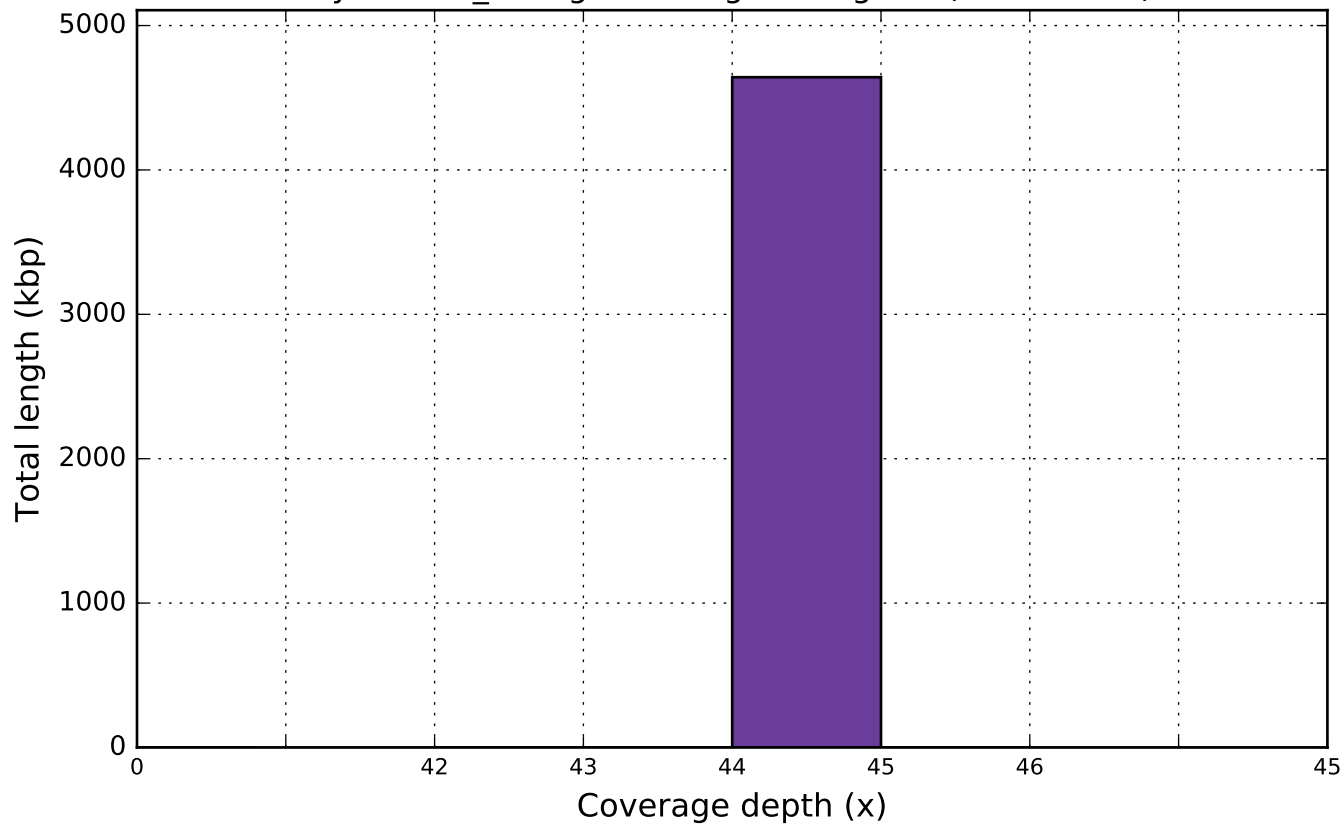
hybrid20x_contigs

hybrid40x_contigs coverage histogram (bin size: 1x)



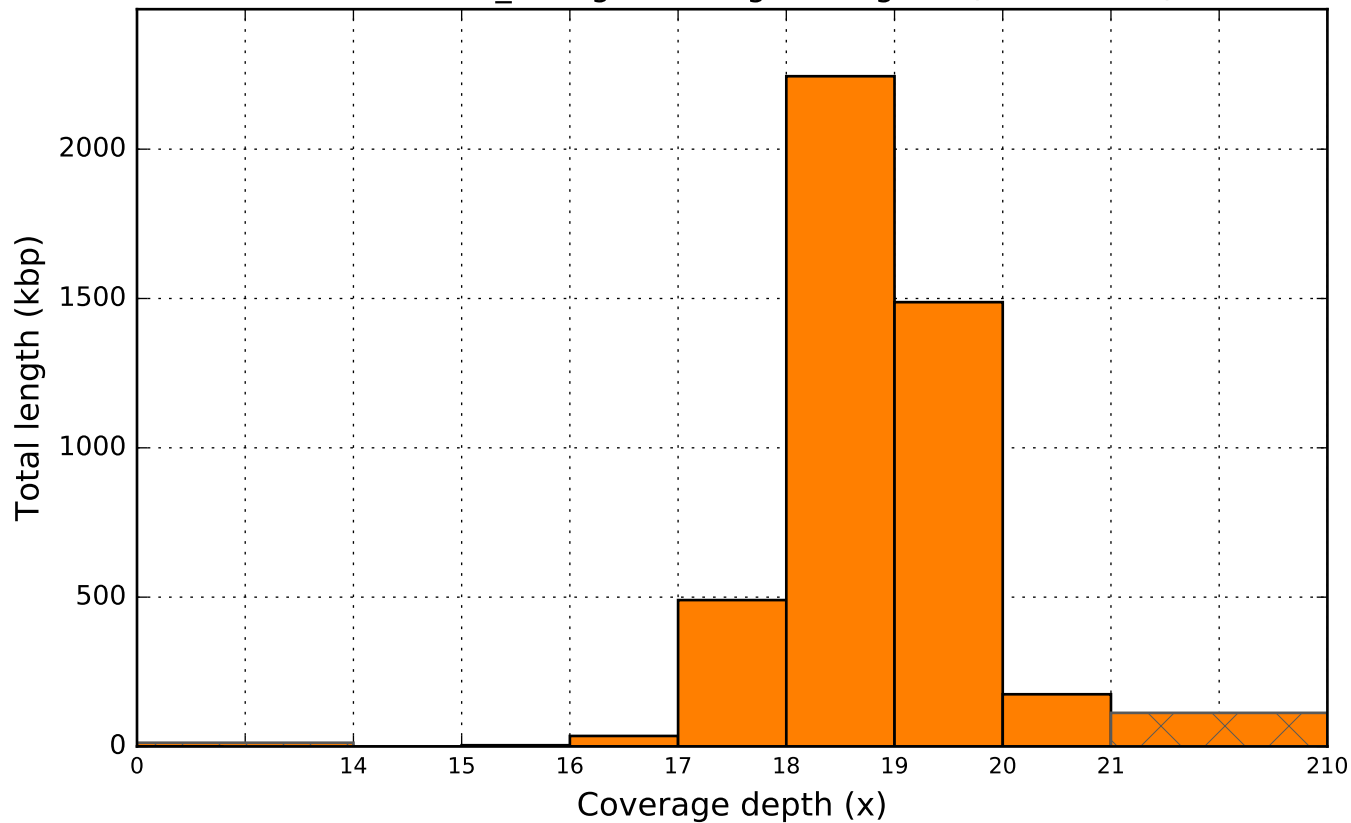
hybrid40x_contigs

hybrid80x_contigs coverage histogram (bin size: 1x)



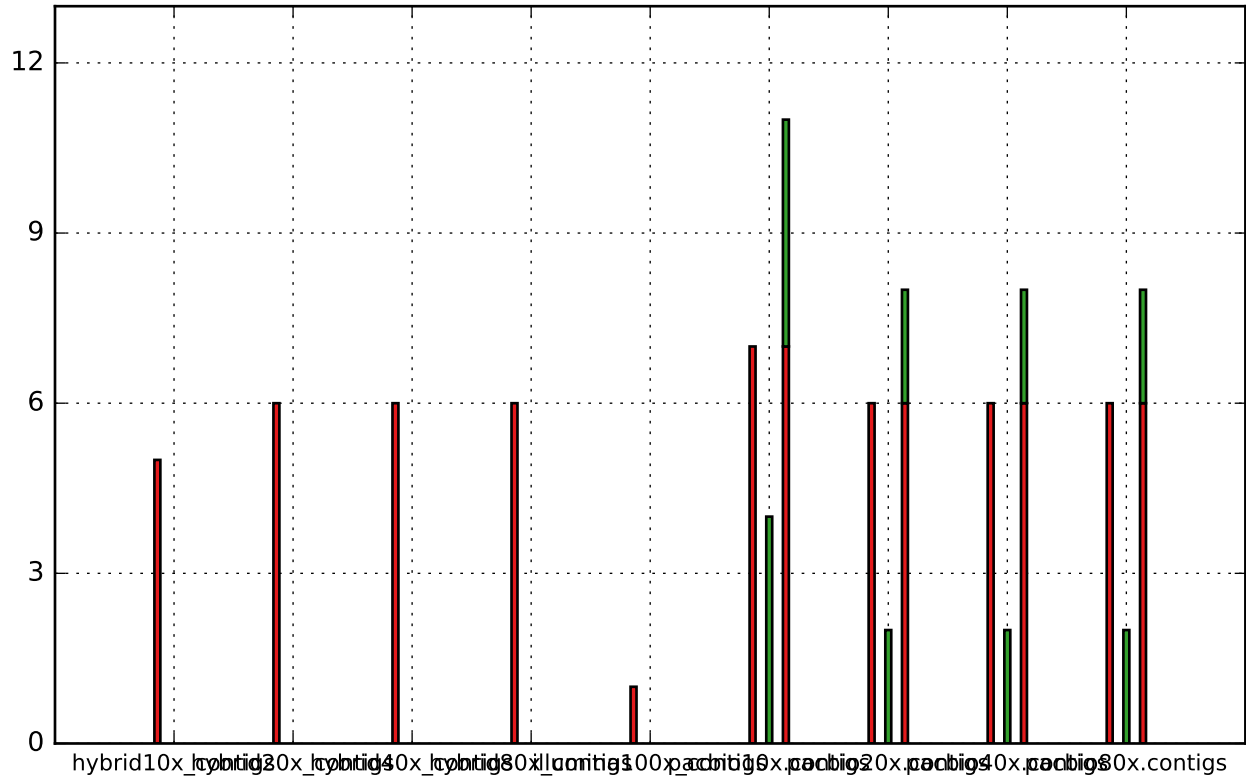
hybrid80x_contigs

illumina100x_contigs coverage histogram (bin size: 1x)

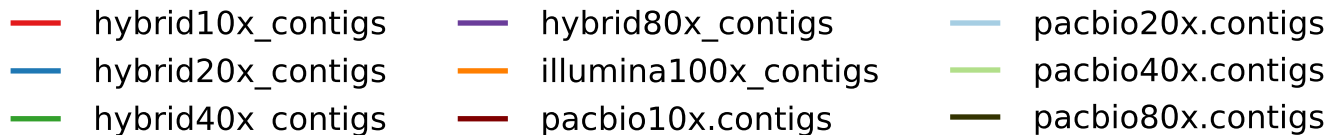
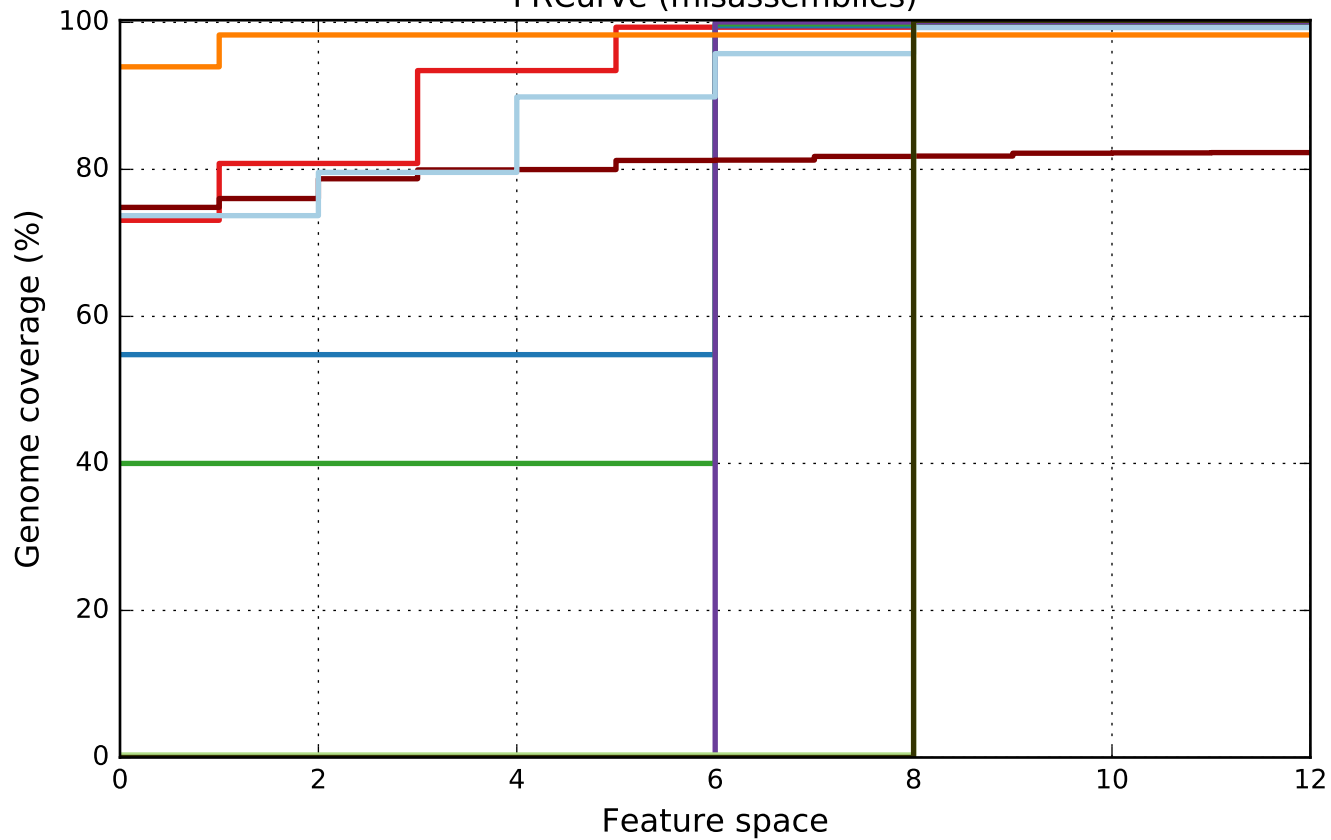


illumina100x_contigs

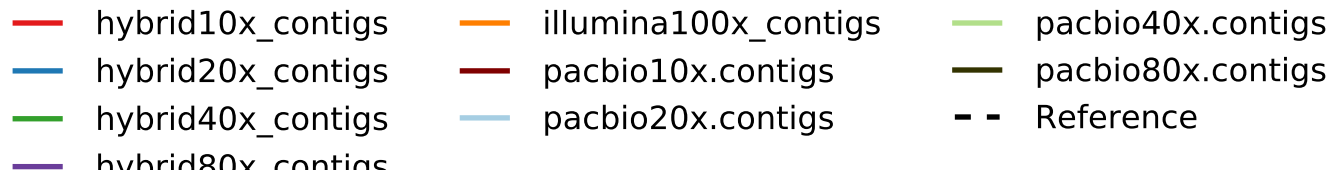
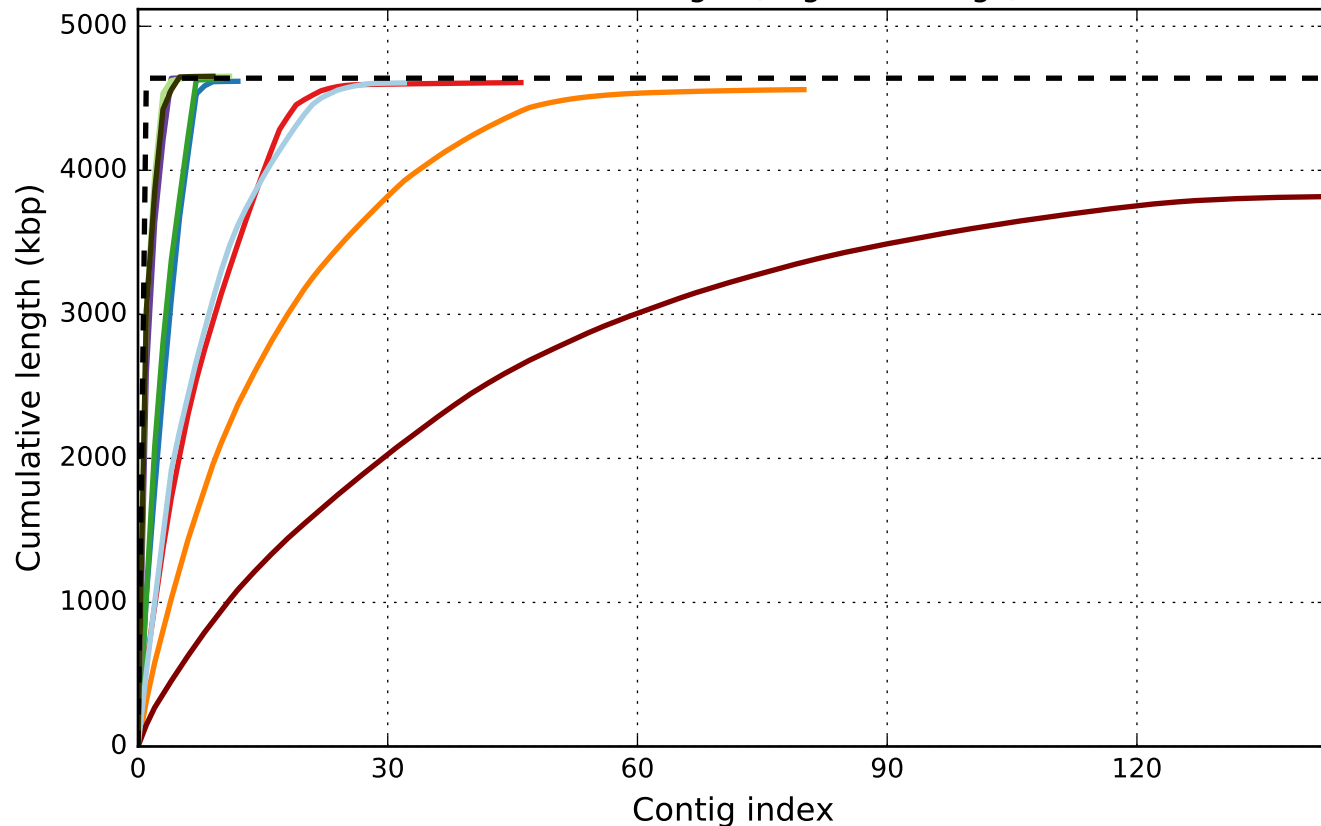
Misassemblies

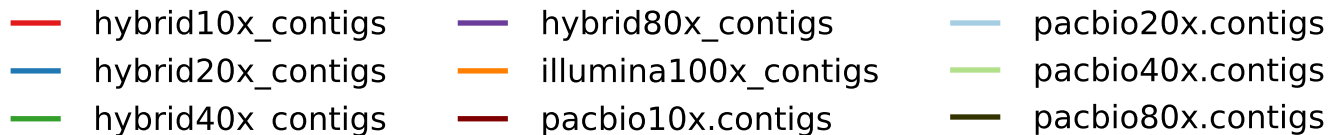
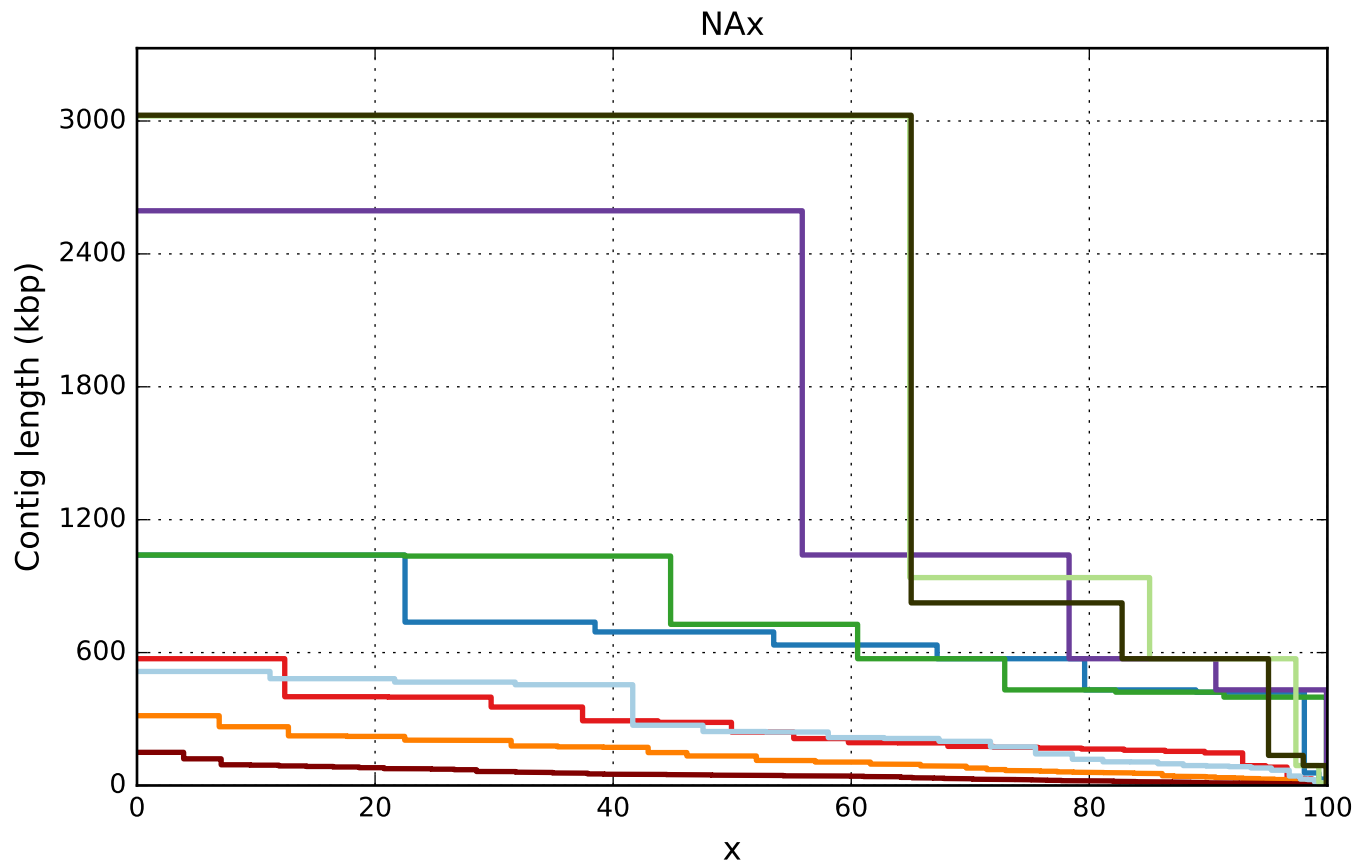


FRCurve (misassemblies)

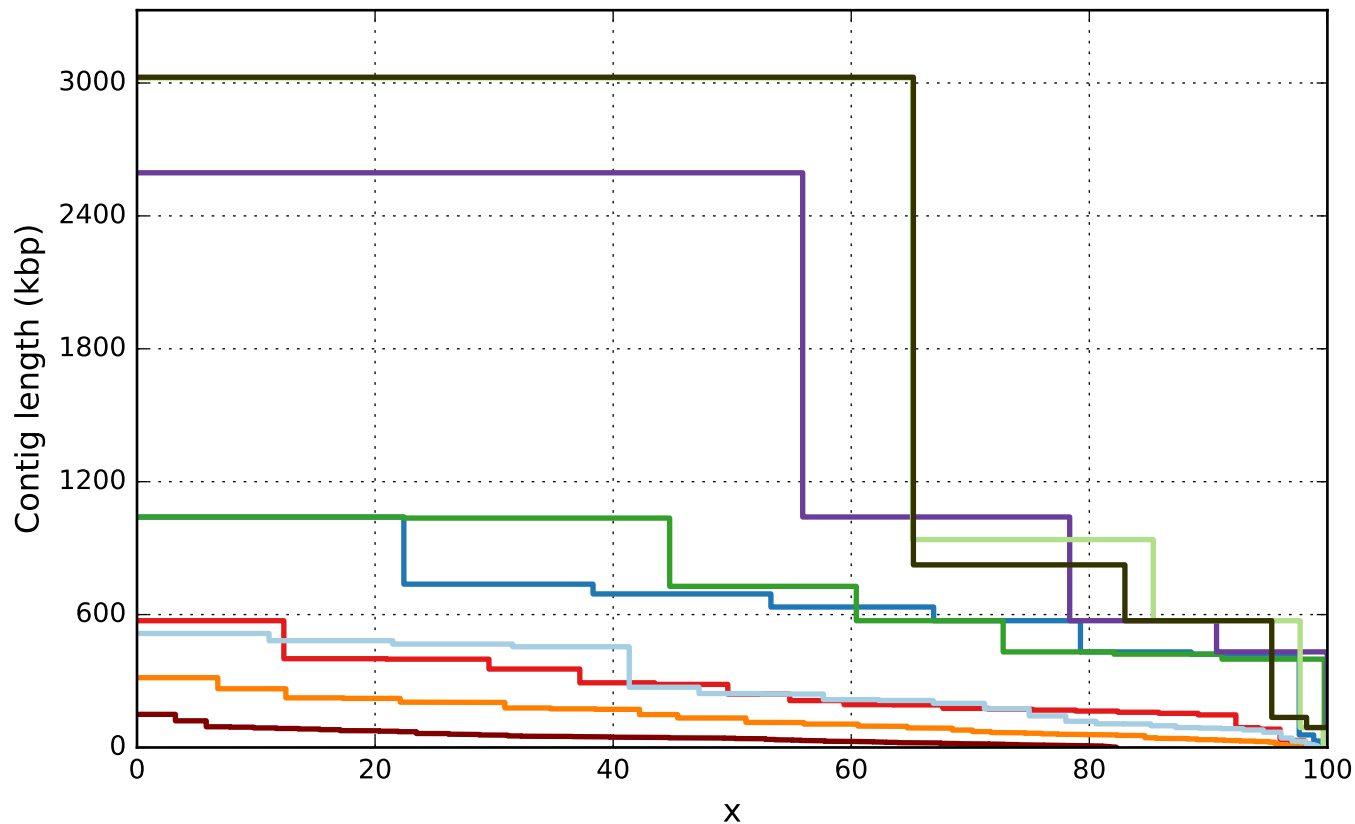


Cumulative length (aligned contigs)





NGAx



- | | | |
|-------------------|----------------------|-------------------|
| hybrid10x_contigs | hybrid80x_contigs | pacbio20x.contigs |
| hybrid20x_contigs | illumina100x_contigs | pacbio40x.contigs |
| hybrid40x_contigs | pacbio10x.contigs | pacbio80x.contigs |

