

Report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Total length (>= 5000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 10000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 25000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 50000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Largest contig	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
Total length	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21
N50	4758965	4757933	4758577	4758103	4757936	4757875	4756113	4758986	4758029	4758599	4758140	4757918	4757909	4756067	4758962	4757806	4758586	4758100	4757923	4757852	4756051
NG50	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
N75	2992084	2992068	2992075	2992072	2991900	2991958	2990676	2992084	2992066	2992074	2992072	2991919	2991966	2990627	2992084	2992066	2992074	2992073	2991919	2991966	2990627
NG75	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LG50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassemblies	6	6	6	6	6	6	10	8	6	6	6	6	6	10	8	6	6	6	6	6	10
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Misassembled contigs length	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
# local misassemblies	11	11	11	11	11	11	29	11	11	11	11	11	11	25	11	11	11	11	11	11	25
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	7	7	7	7	7	7	6	7	7	7	7	7	7	6	7	7	7	7	7	7	6
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24048558	24044027	24045318	24035007	24033709	24027509	24078621	24047337	24044395	24045165	24034572	24034525	24027052	24079193	24047396	24043859	24045122	24035509	24033005	24025704	24077872
Genome fraction (%)	99.894	99.894	99.894	99.894	99.894	99.894	99.864	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.893	99.893	99.893	99.893	99.893	99.893	99.878
Duplication ratio	1.015	1.015	1.015	1.015	1.014	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008
# 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	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	58.70	56.20	56.44	56.08	57.73	58.34	64.88	59.25	56.23	56.62	56.53	58.59	59.86	64.38	59.03	56.17	56.62	56.56	59.74	60.31	65.08
# indels per 100 kbp	5.46	5.09	3.66	3.63	14.57	13.39	96.71	5.37	5.03	3.53	3.53	14.86	13.47	97.06	5.37	5.03	3.54	3.63	14.88	13.54	97.24
Largest alignment	1643841	1643830	1643846	1643846	1643660	1643672	2098268	1643839	2052184	2052214	2052214	2052072	2052098	2098630	1643839	2052184	2052213	2052214	2052072	2052059	2098630
Total aligned length	6815349	6815307	6815923	6815686	6814362	6814608	6768630	6816075	6815379	6816198	6816108	6814892	6816238	6768894	6815915	6815286	6816197	6816213	6815474	6816362	6769853
NGA50	1274469	1274461	1274469	1274469	1274323	1274352	1471391	1274459	1643839	1643848	1643848	1643664	1643668	1471418	1274459	1643839	1643848	1643849	1643664	1643656	1471418
NGA75	1070338	1070324	1070329	1070332	1070244	1070249	610115	1070335	1070324	1070329	1070331	1070258	1070257	610213	1070335	1070324	1070329	1070331	1070260	1070261	610213
LGA50	3	3	3	3	3	3	2	3	2	2	2	2	2	2	3	2	2	2	2	2	2
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4

All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# misassemblies	6	6	6	6	6	6	10	8	6	6	6	6	6	10	8	6	6	6	6	6	10
# contig misassemblies	6	6	6	6	6	6	10	8	6	6	6	6	6	10	8	6	6	6	6	6	10
# c. relocations	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
# c. translocations	6	6	6	6	6	6	10	7	6	6	6	6	6	10	7	6	6	6	6	6	10
# c. inversions	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Misassembled contigs length	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# possible misassemblies	18	18	18	18	18	18	34	16	18	18	18	18	18	34	16	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	29	11	11	11	11	11	11	25	11	11	11	11	11	11	25
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0
# misassemblies caused by fragmented reference	21	21	21	21	21	21	16	20	21	21	21	21	21	16	20	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	6	7	7	7	7	7	7	6	7	7	7	7	7	7	6
# mismatches	3945	3777	3793	3769	3880	3921	4359	3982	3779	3805	3799	3938	4023	4326	3967	3775	3805	3801	4015	4053	4373
# indels	367	342	246	244	979	900	6498	361	338	237	237	999	905	6522	361	338	238	244	1000	910	6534
# indels (<= 5 bp)	271	244	152	150	883	806	6377	266	241	143	143	904	810	6399	266	241	144	150	905	816	6411
# indels (> 5 bp)	96	98	94	94	96	94	121	95	97	94	94	95	95	123	95	97	94	94	95	94	123
Indels length	5411	5408	5265	5261	6096	6012	12810	5393	5398	5253	5252	6126	6000	12909	5393	5398	5254	5260	6128	6002	12929

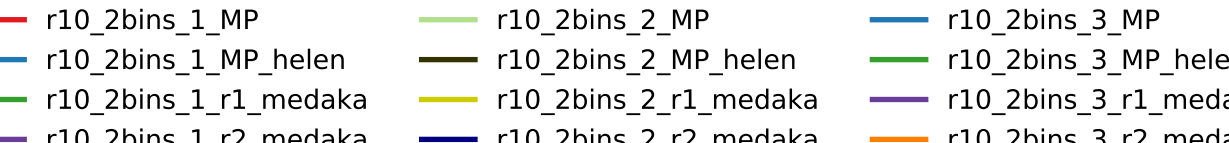
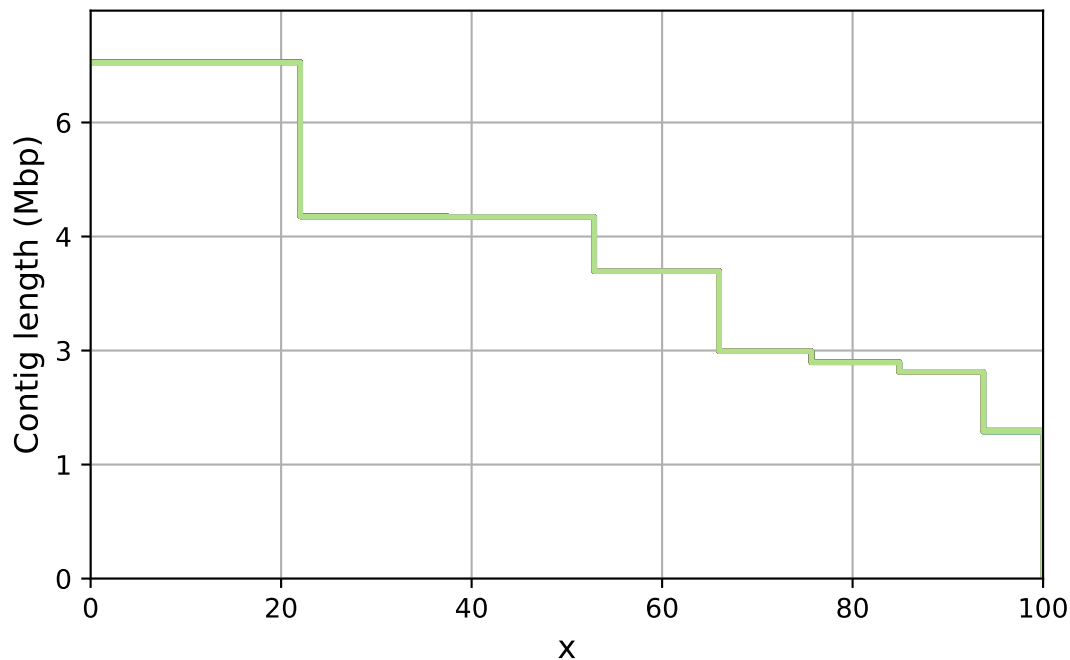
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

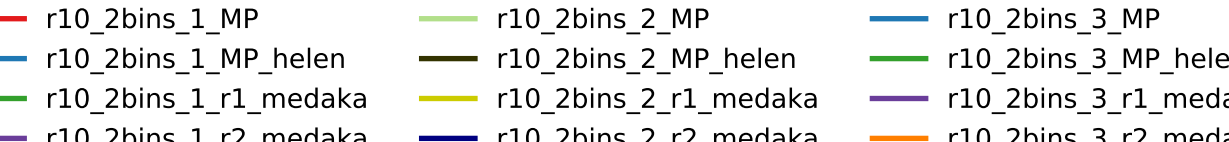
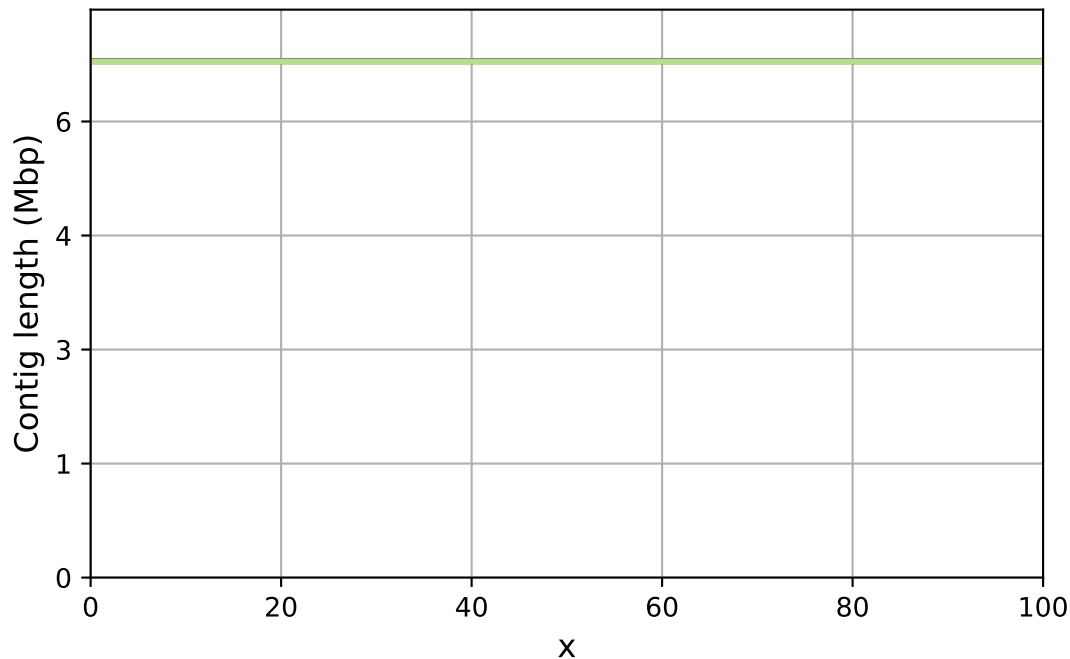
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24048558	24044027	24045318	24035007	24033709	24027509	24078621	24047337	24044395	24045165	24034572	24034525	24027052	24079193	24047396	24043859	24045122	24035509	24033005	24025704	24077872
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

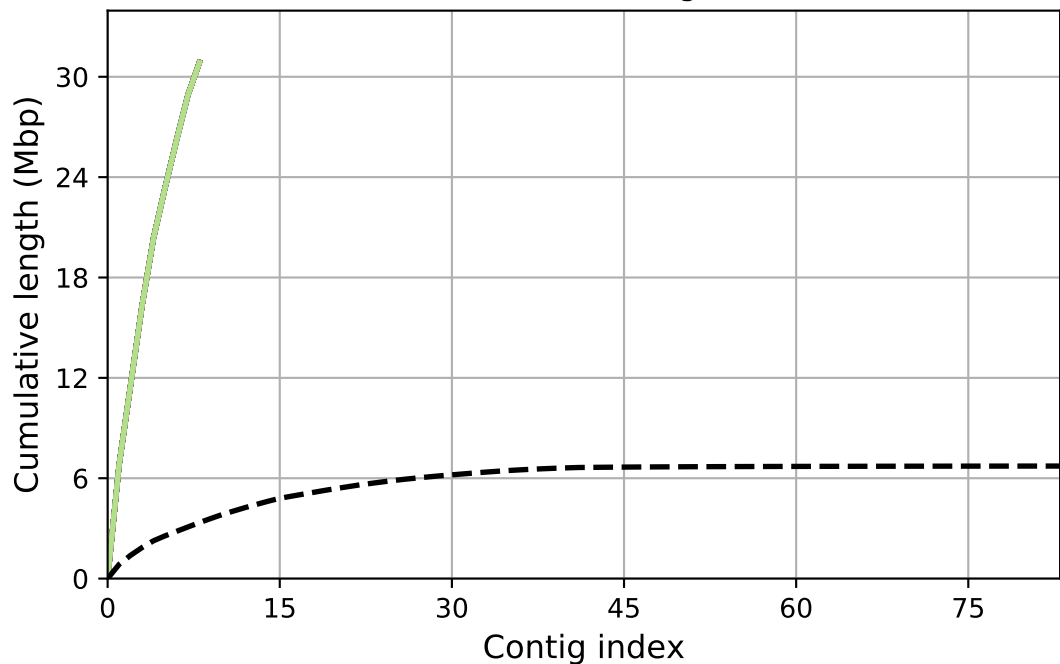
Nx



NGx

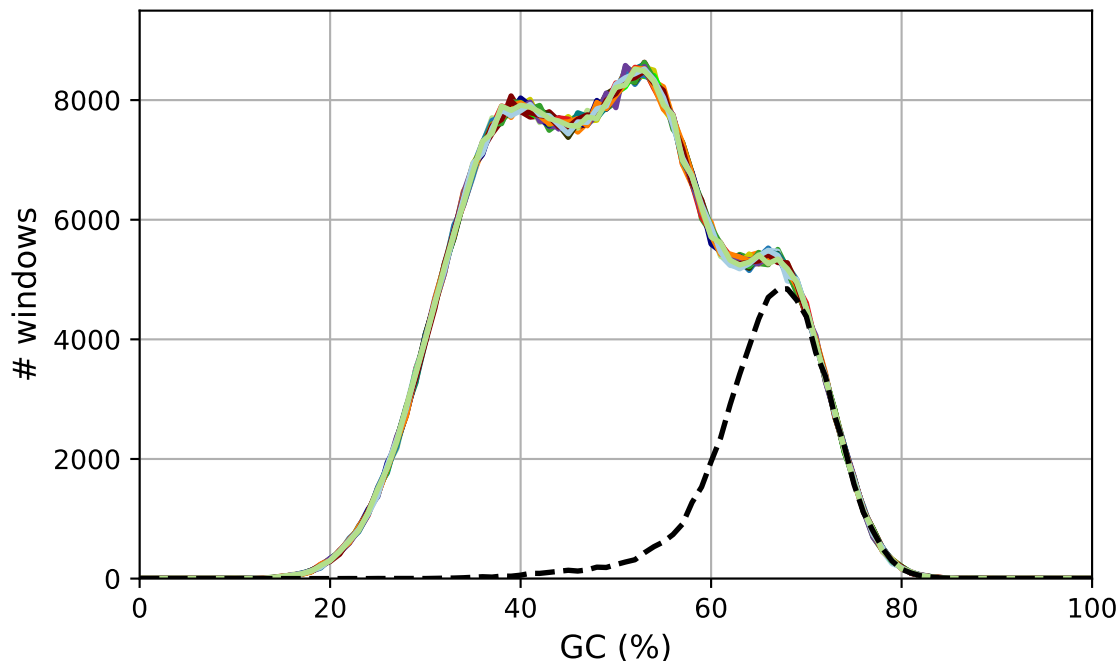


Cumulative length



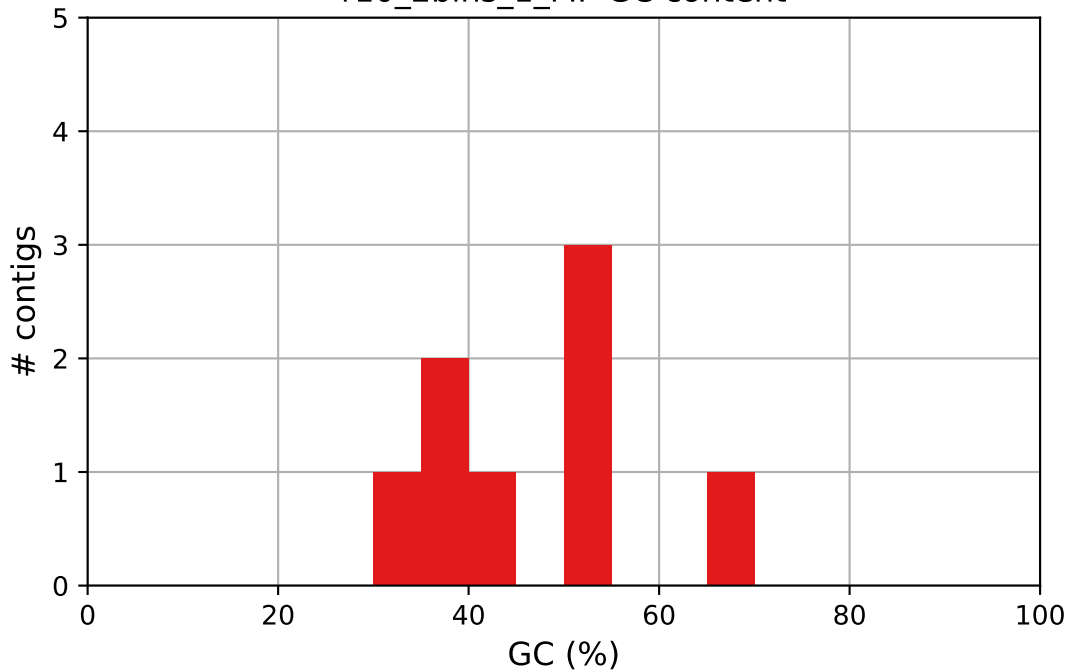
r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

GC content



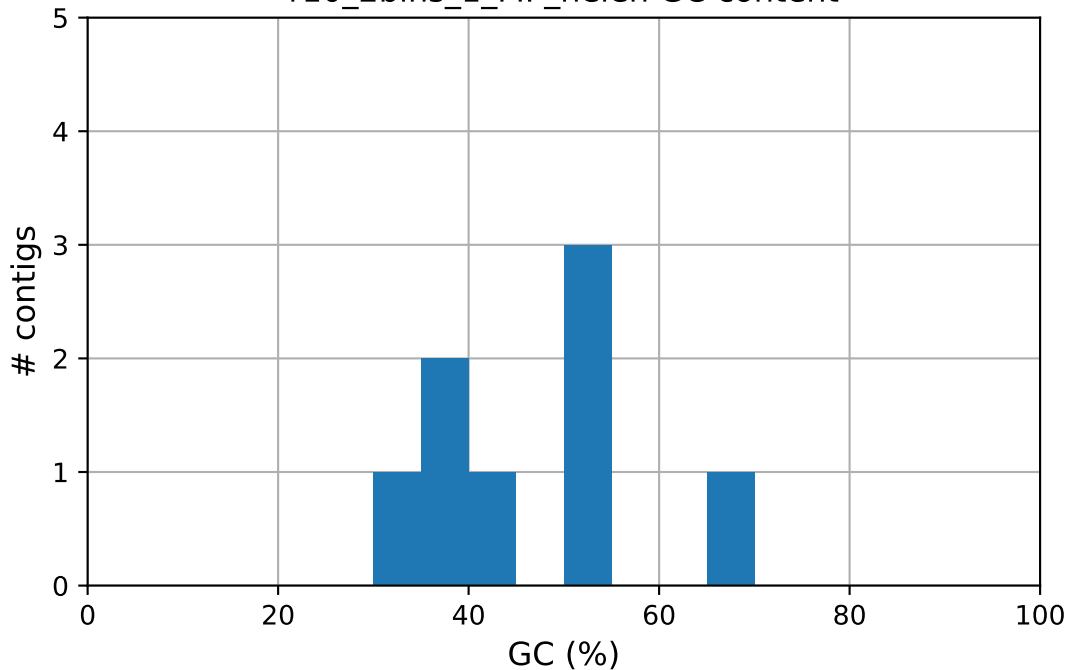
— r10_2bins_1_MP — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_MP_helen — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r1_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_racon_r1 — r10_2bins_3_racon_r1

r10_2bins_1_MP GC content



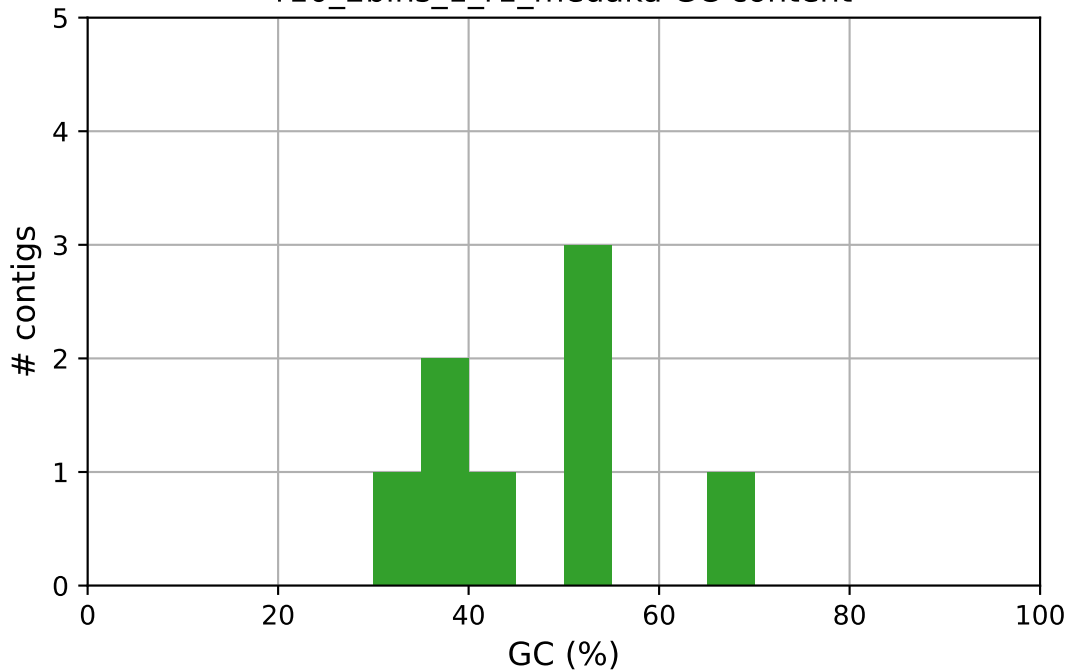
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



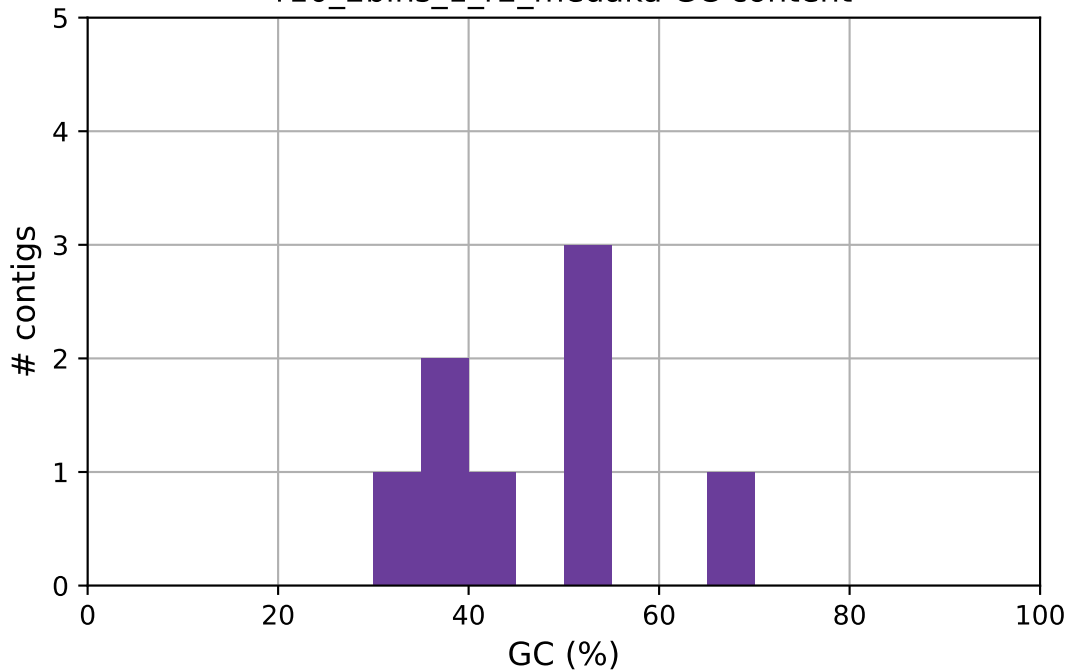
r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka GC content



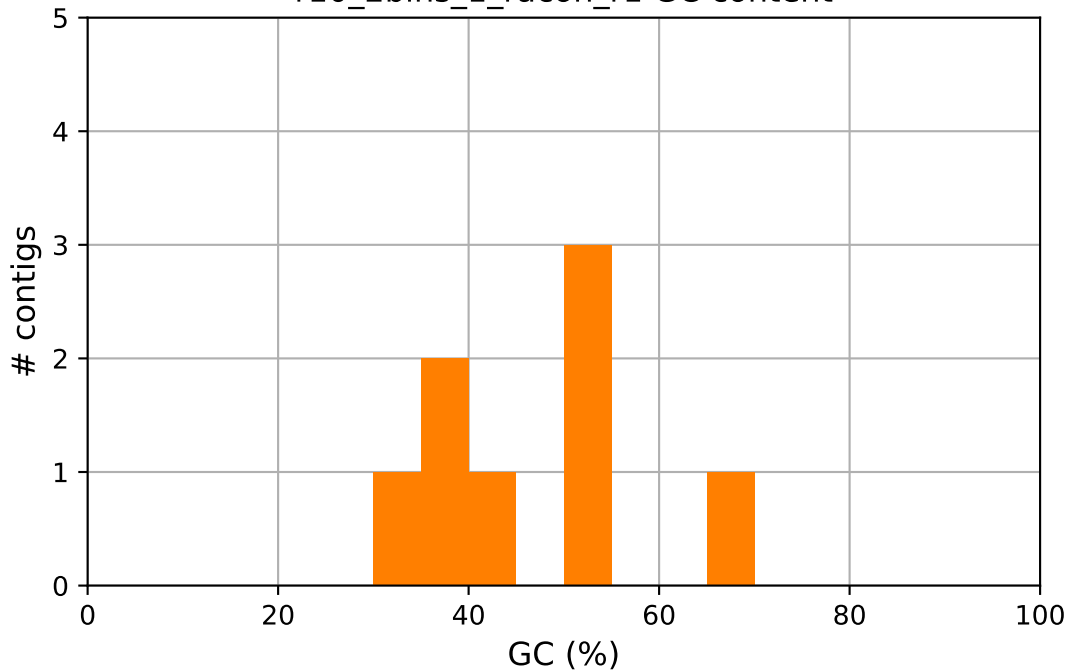
r10_2bins_1_r1_medaka

r10_2bins_1_r2_medaka GC content



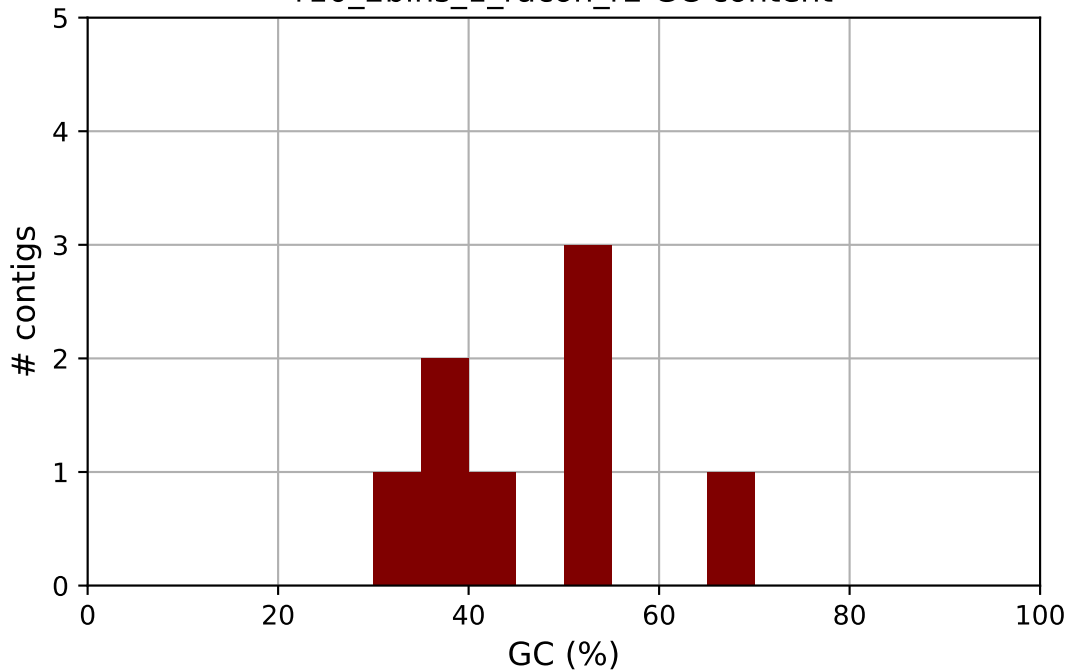
r10_2bins_1_r2_medaka

r10_2bins_1_racon_r1 GC content



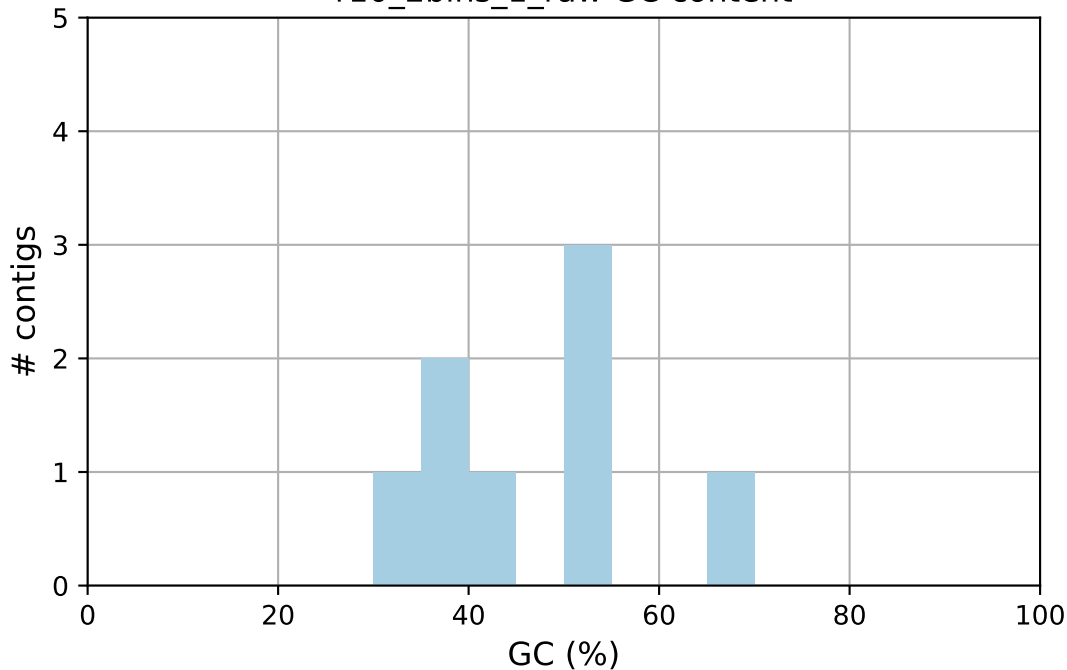
r10_2bins_1_racon_r1

r10_2bins_1_racon_r2 GC content



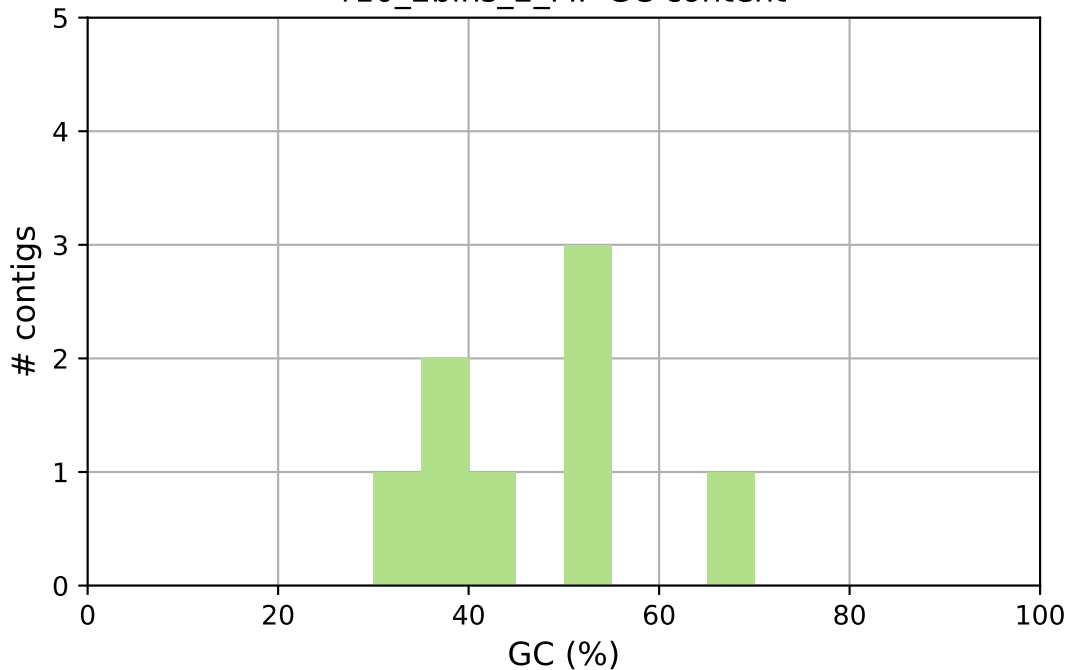
r10_2bins_1_racon_r2

r10_2bins_1_raw GC content



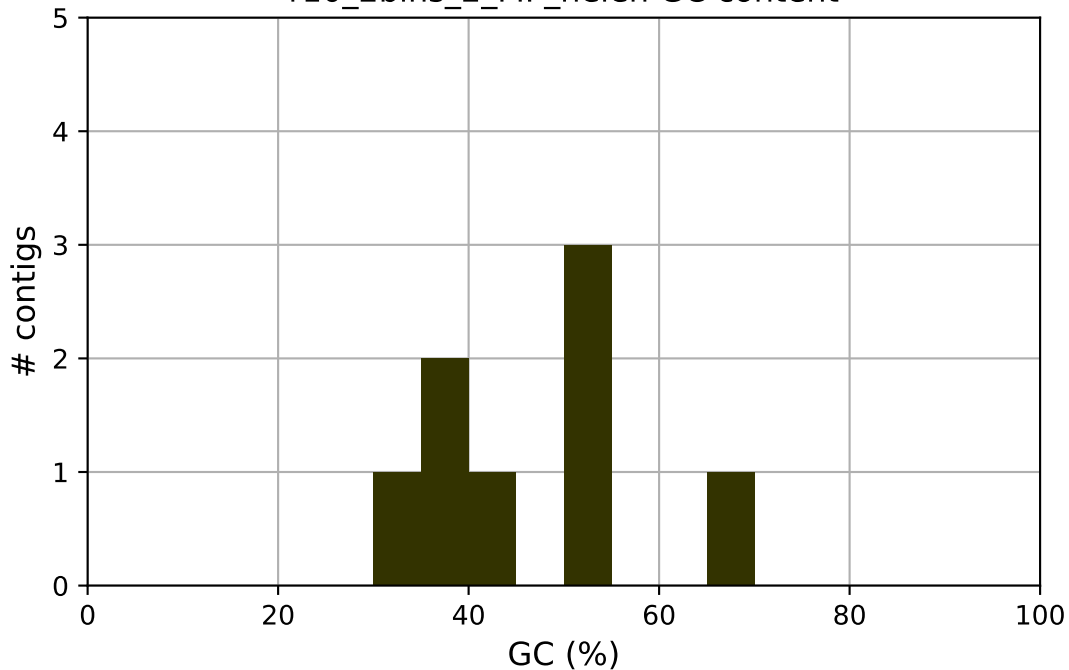
r10_2bins_1_raw

r10_2bins_2_MP GC content



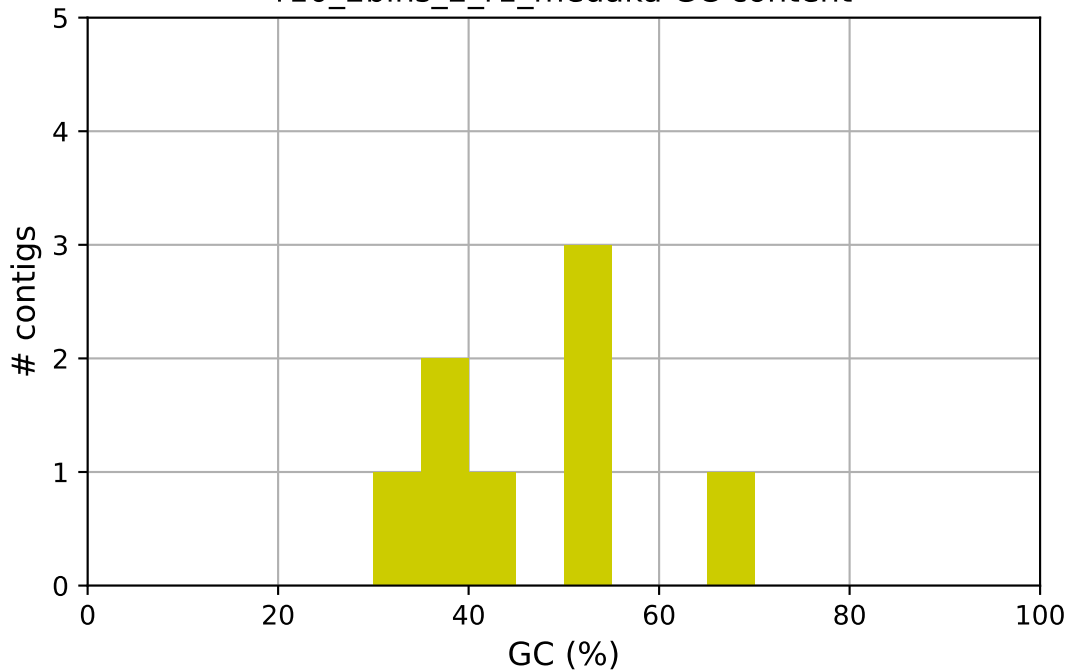
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



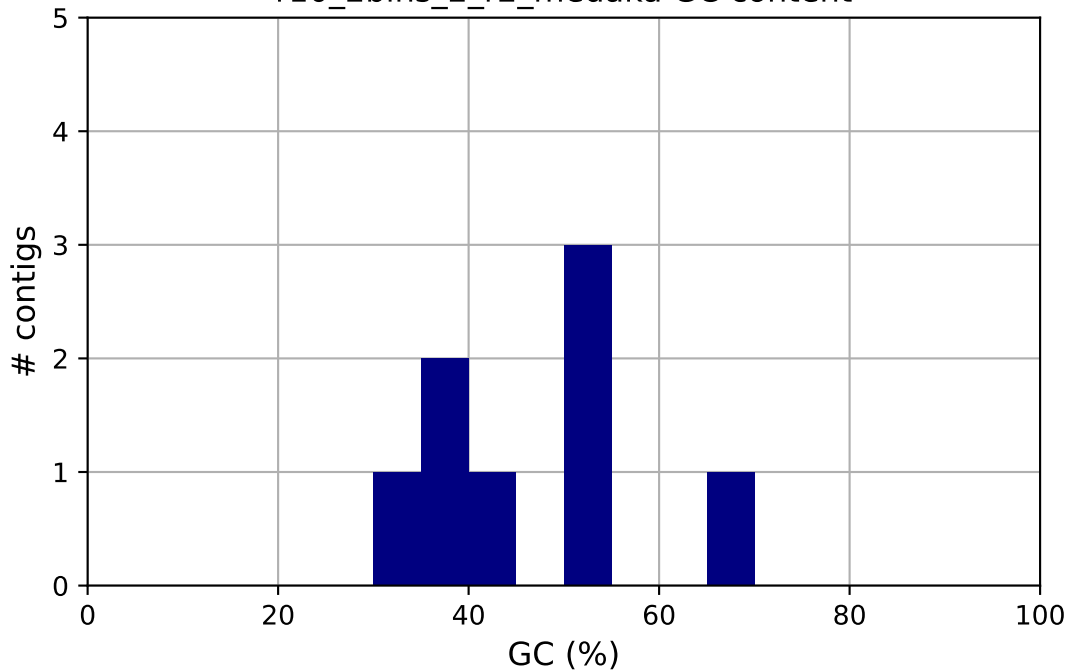
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



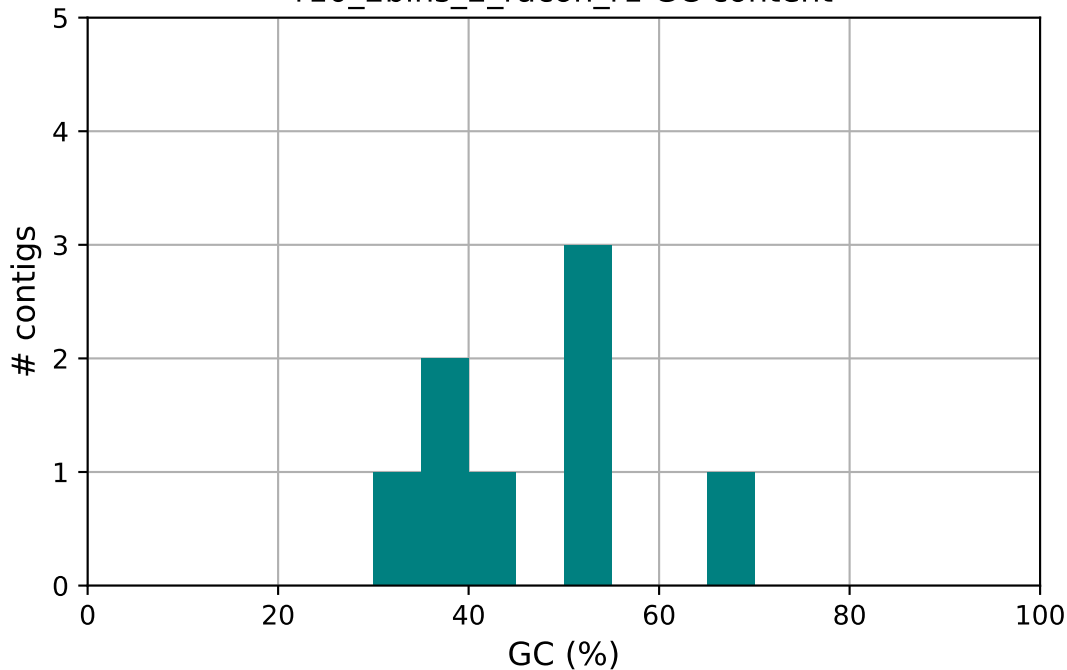
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



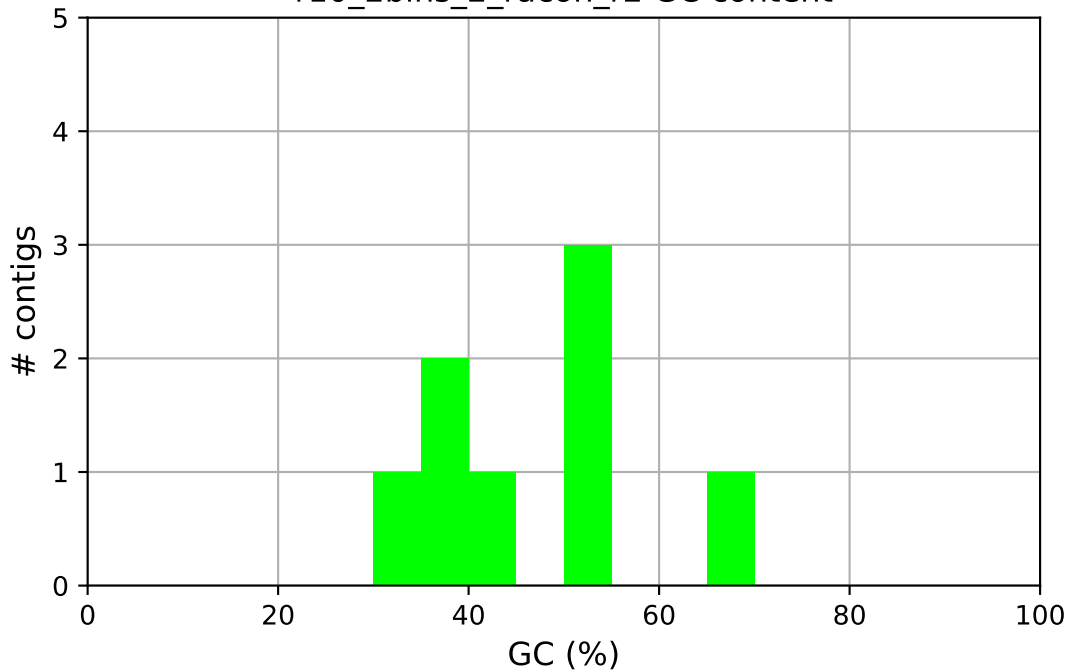
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



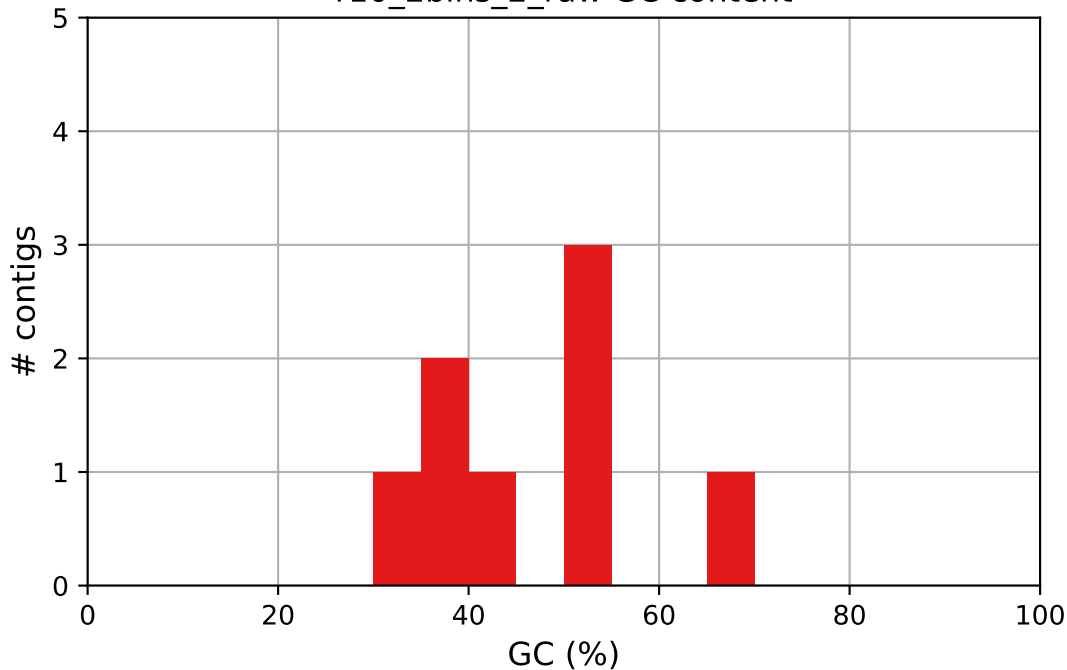
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



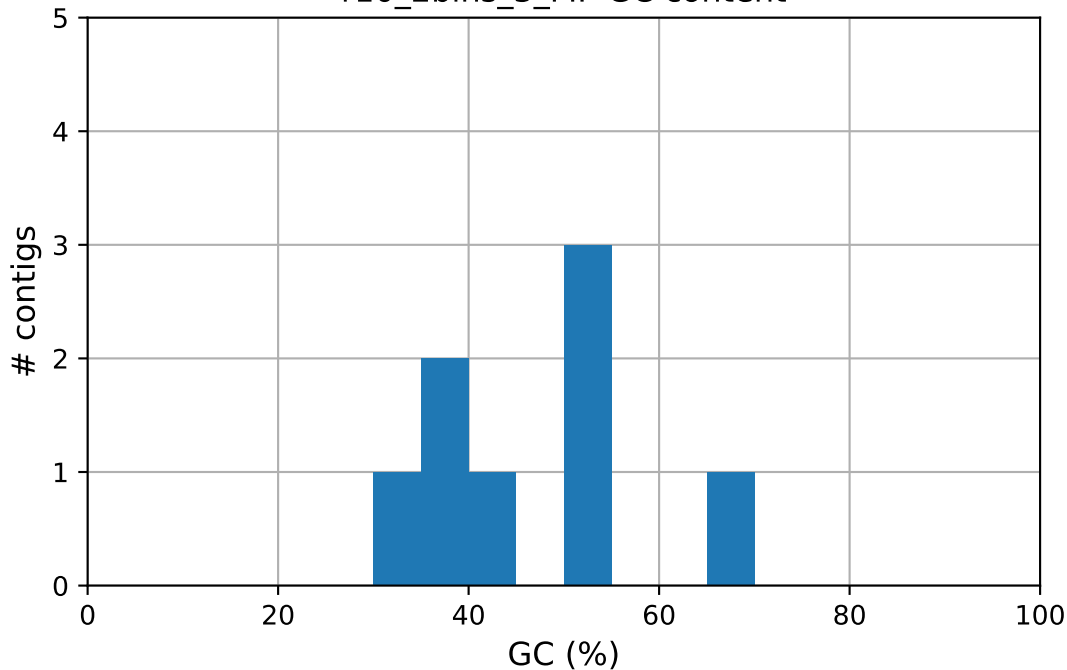
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



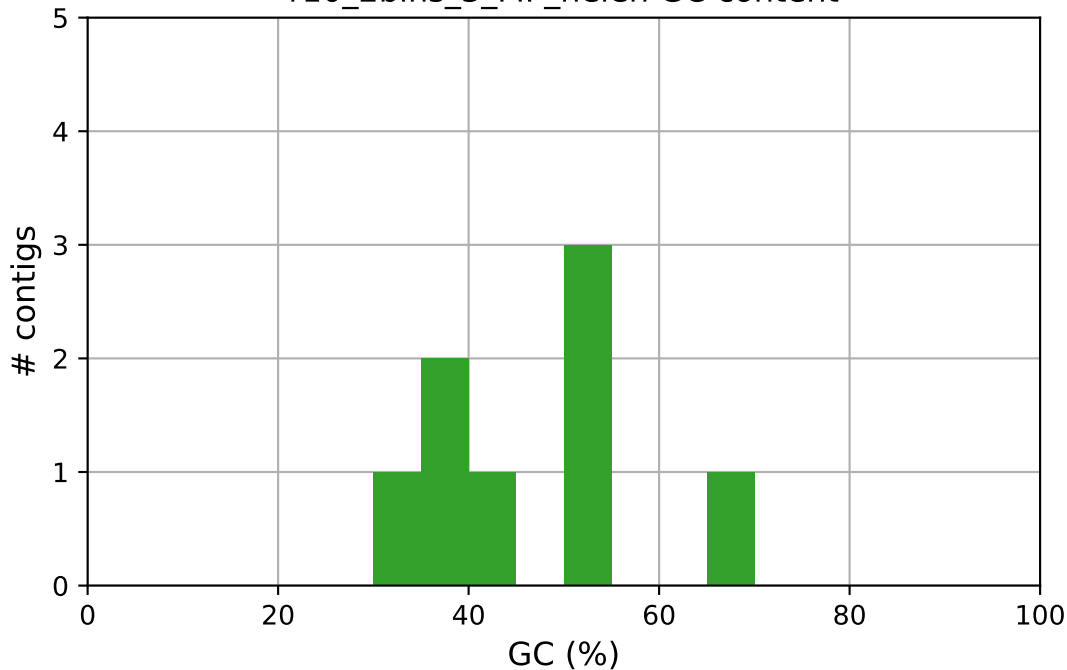
r10_2bins_2_raw

r10_2bins_3_MP GC content



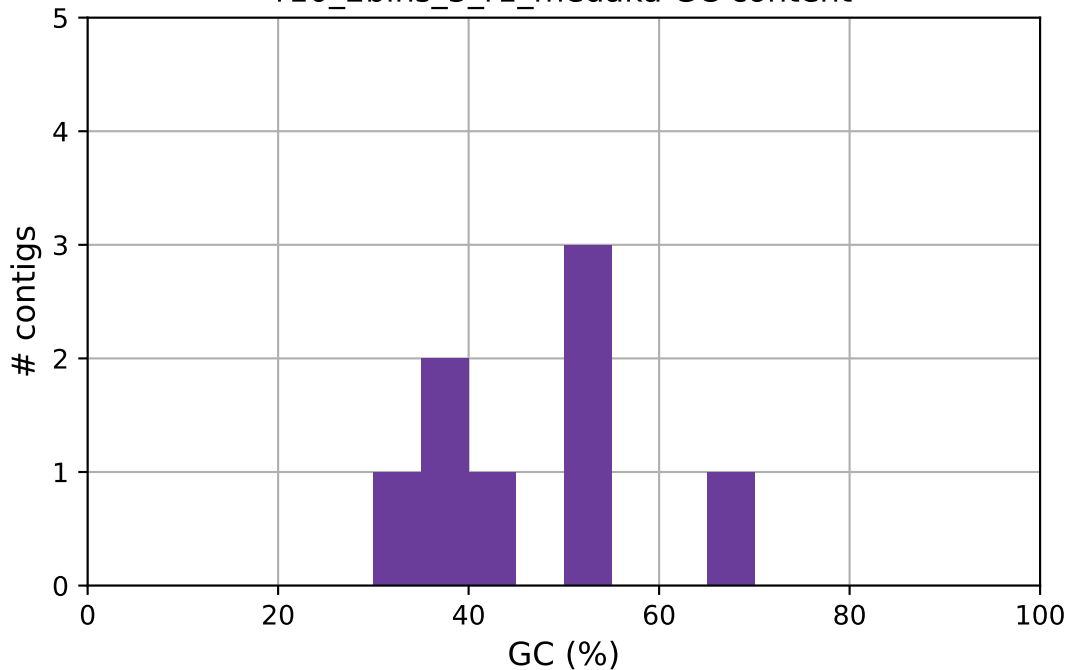
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



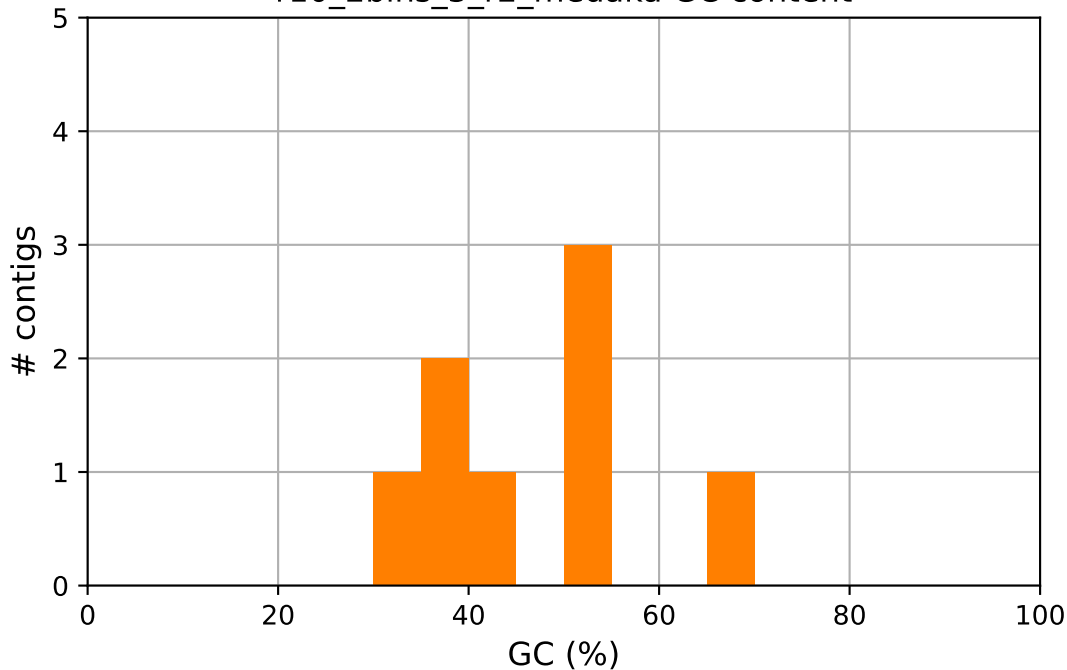
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



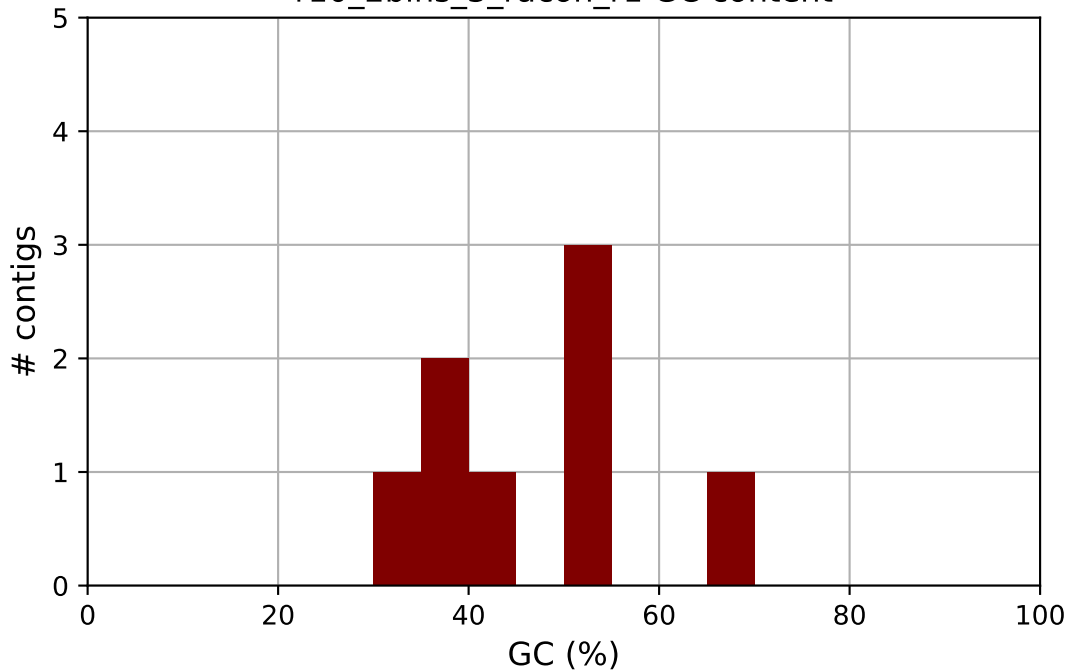
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



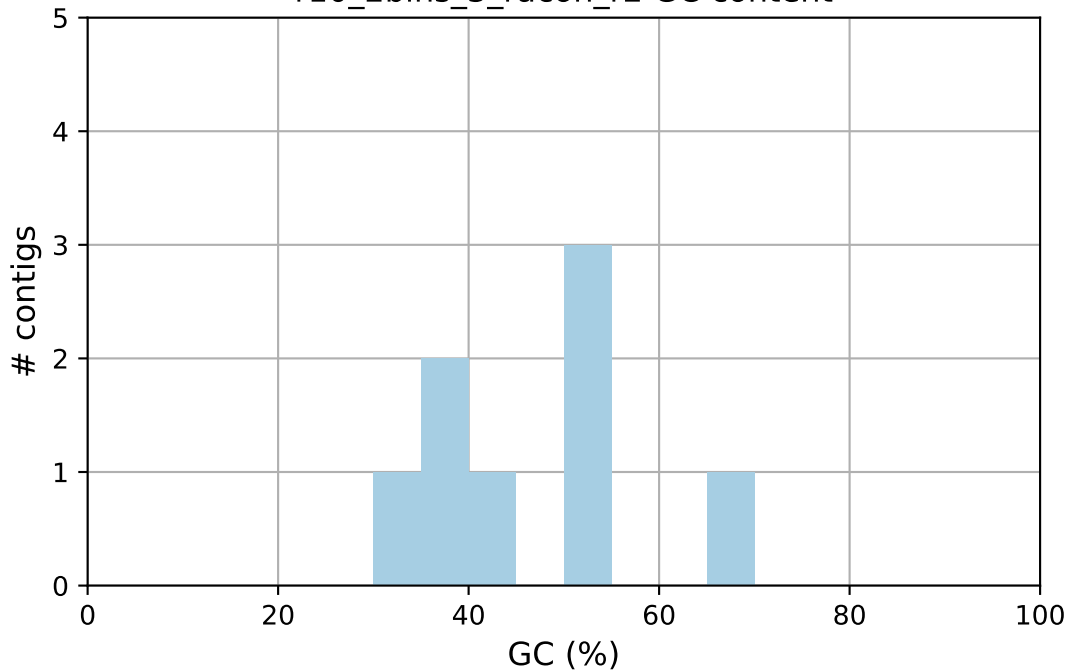
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



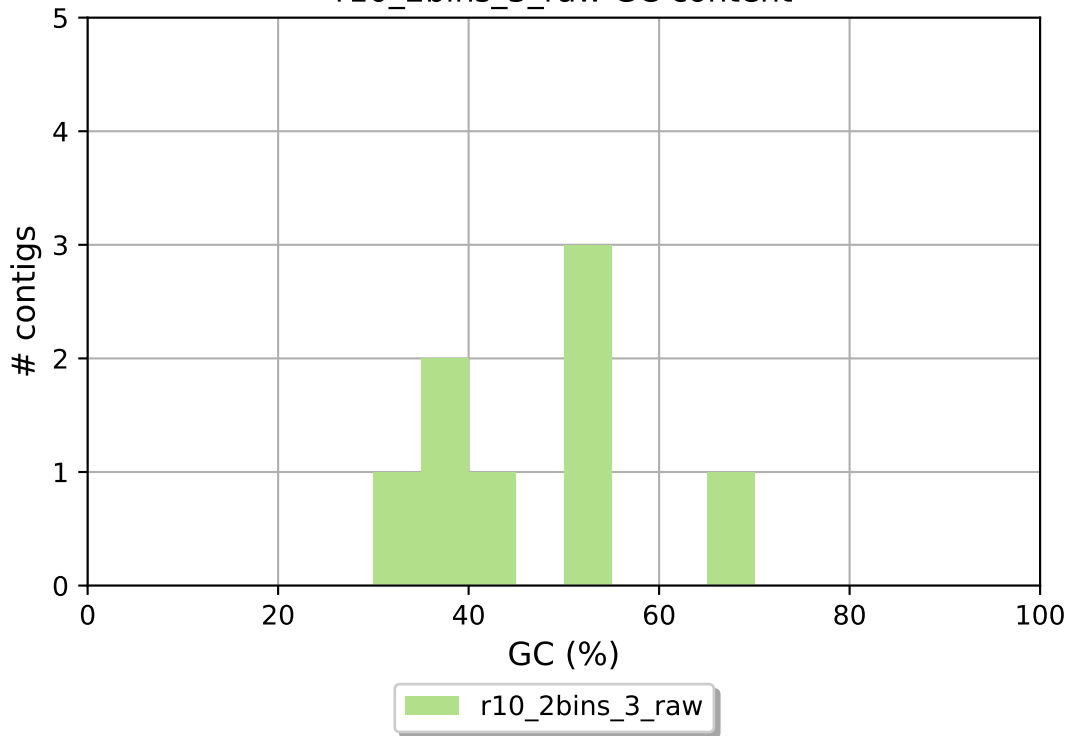
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

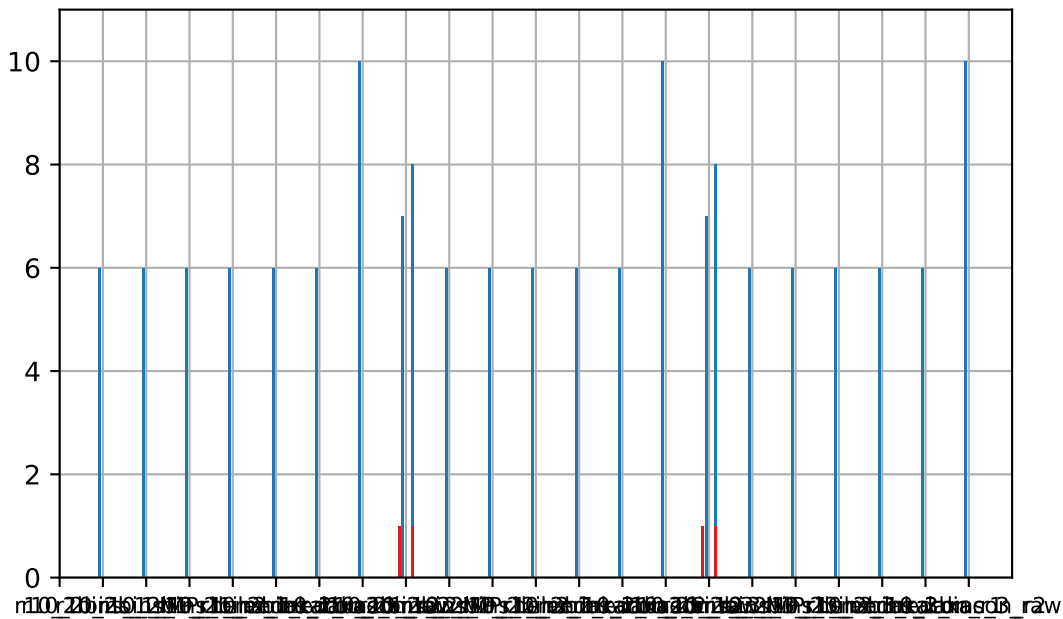


r10_2bins_3_racon_r2

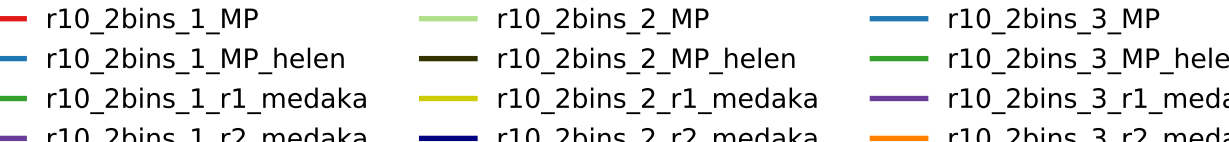
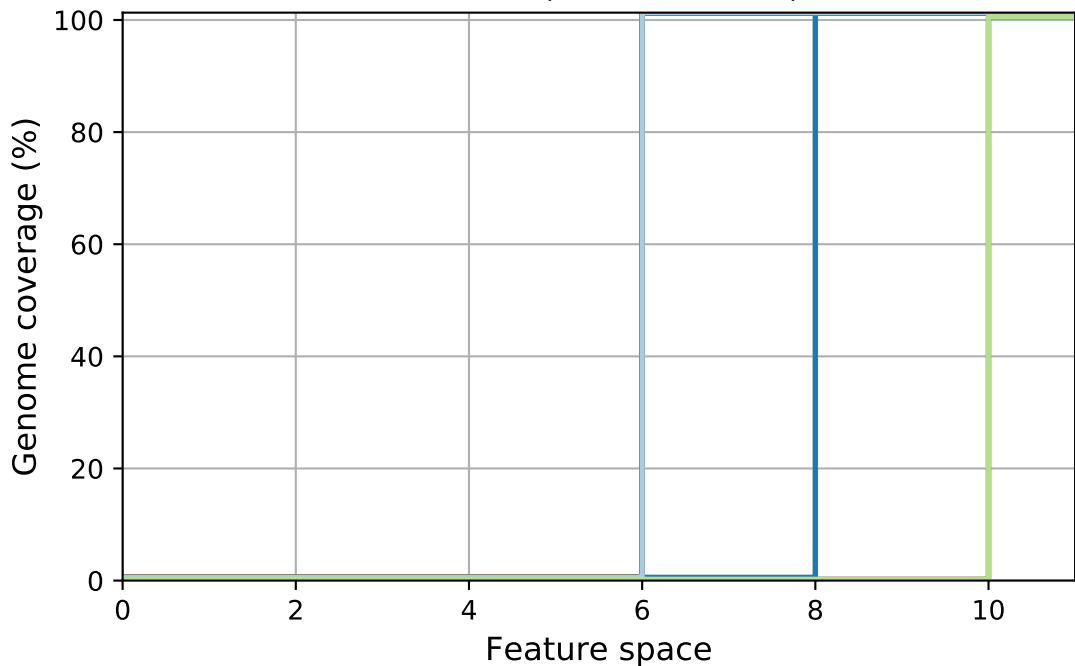
r10_2bins_3_raw GC content



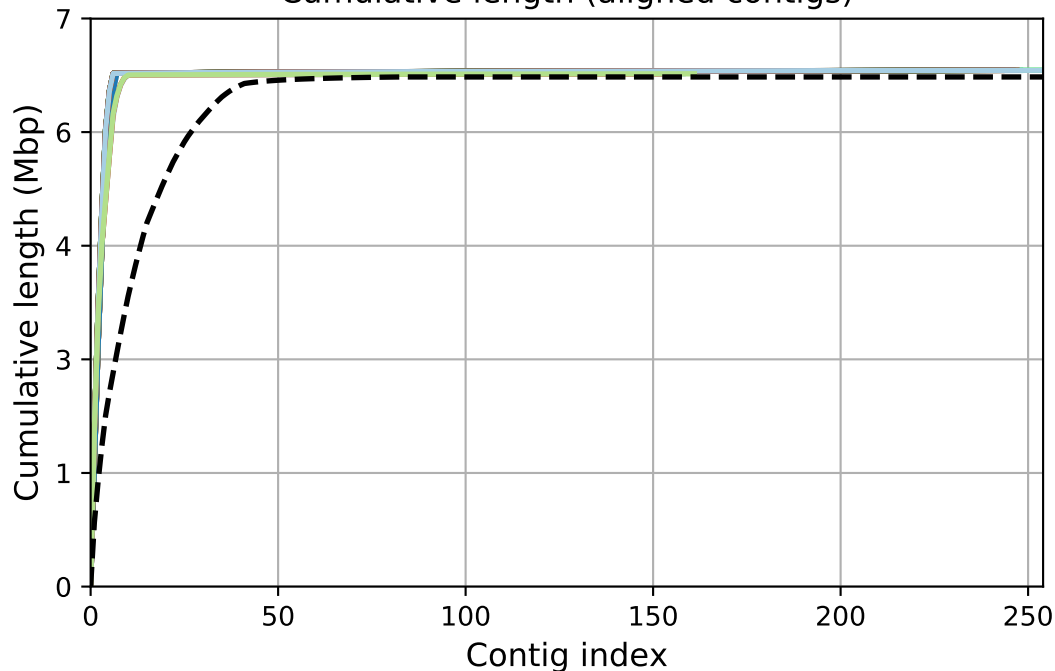
Misassemblies



FRCurve (misassemblies)

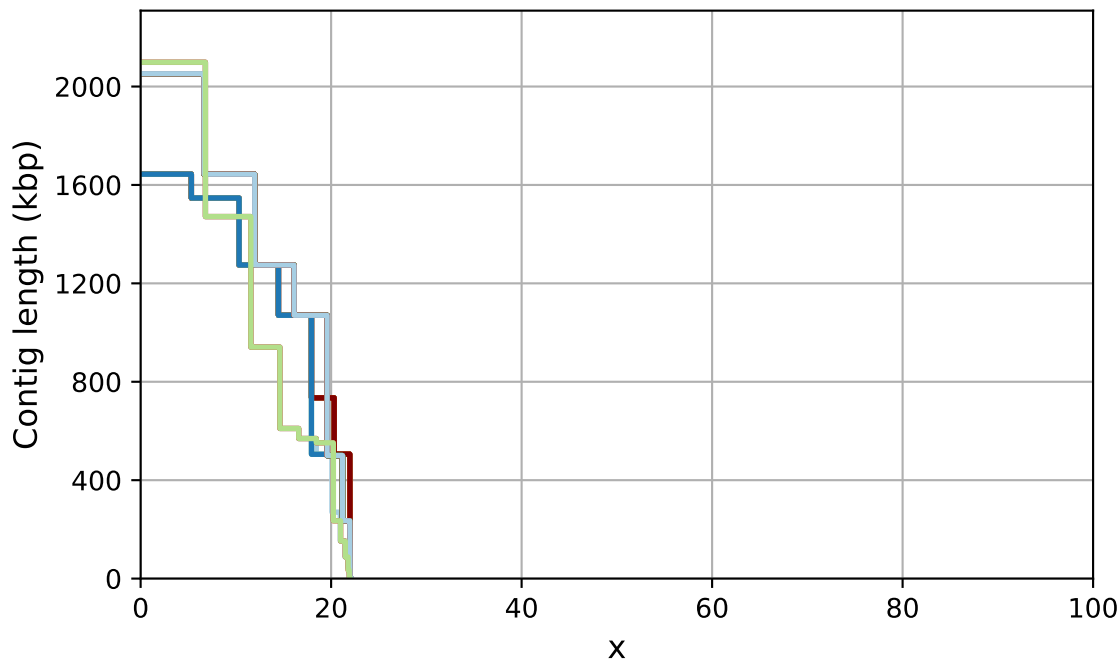


Cumulative length (aligned contigs)



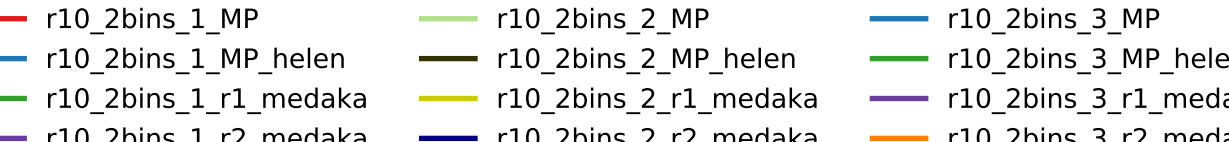
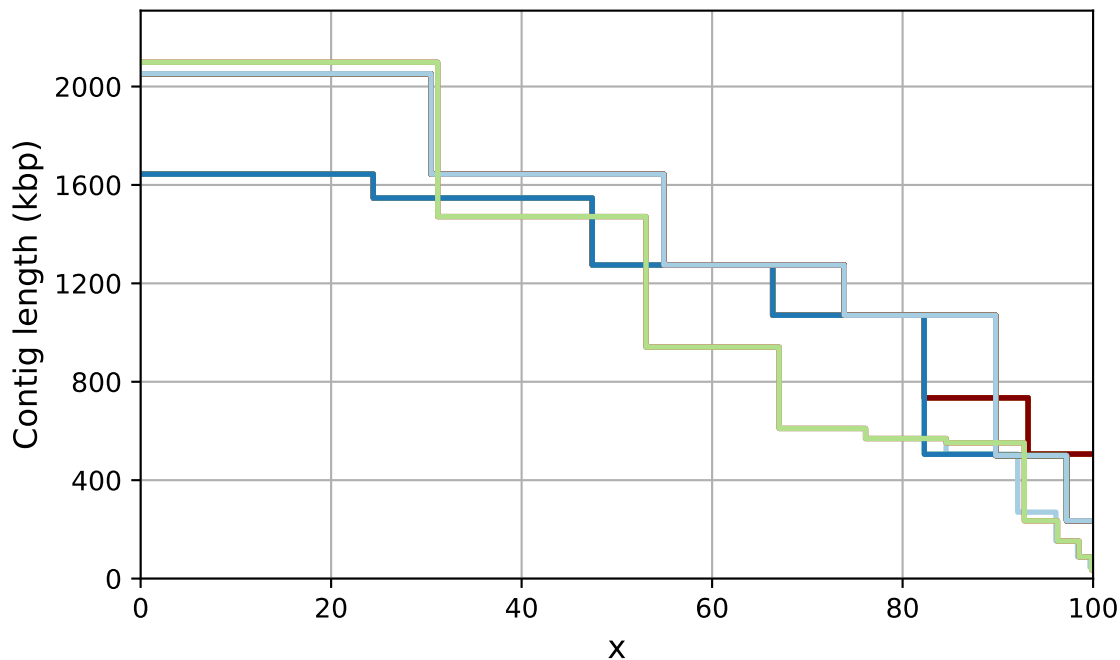
— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_2_racon_r1
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1

NAX



r10_2bins_1_MP
 r10_2bins_1_MP_helen
 r10_2bins_1_r1_medaka
 r10_2bins_1_r2_medaka
 r10_2bins_2_MP
 r10_2bins_2_MP_helen
 r10_2bins_2_r1_medaka
 r10_2bins_2_r2_medaka
 r10_2bins_3_MP
 r10_2bins_3_MP_helen
 r10_2bins_3_r1_medaka
 r10_2bins_3_r2_medaka

NGAx



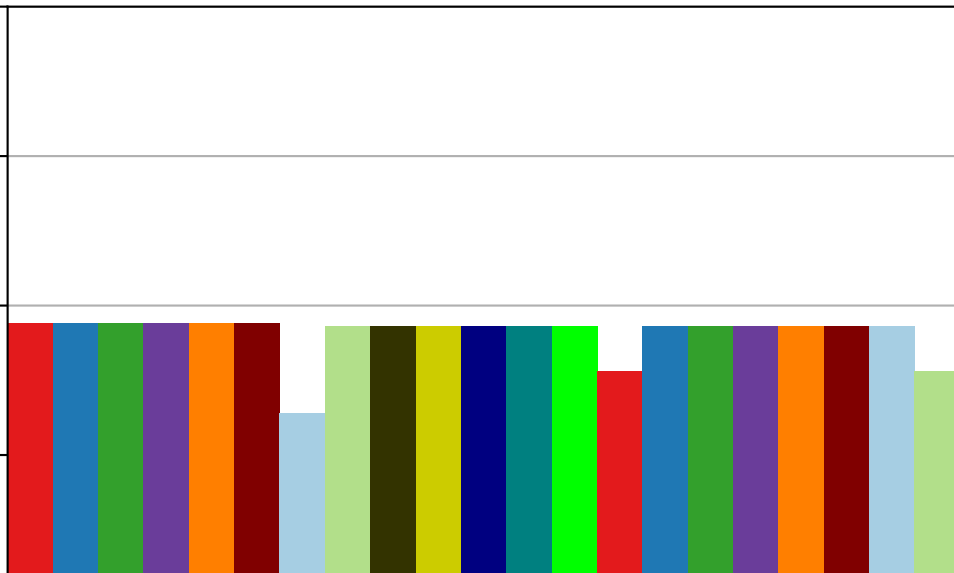
Genome fraction, %

100.00

99.95

99.90

99.85



r10_2bins_1_MP

r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka

r10_2bins_1_r2_medaka

r10_2bins_2_MP

r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka

r10_2bins_3_MP

r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka