Report	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
Total length	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Reference length	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77
Reference GC (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
N50	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	4043032
NG50	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765360	4765353	4764528	4764900	4763766
N75	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
NG75	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
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	74	73	75	77	75	79	75	73	73	74	78	75	78	75	74	73	75	78	79	79	75
# 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	1947367	1945999	1945572	1938095	1935544	1929697	1945498	1947264	1945994	1946130	1935173	1934812	1930121	1945704	1947347	1944592	1945545	1938875	1934569	1930417	1945410
# local misassemblies	12	14	27	32	43	41	30	12	13	28	26	42	34	29	11	15	28	26	47	33	29
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	22082019	22079949	22084683	22084293	22078625	22077932	22111532	22082100	22079474	22085545	22081744	22080696	22079677	22110170	22082504	22080180	22084959	22085857	22078815	22079748	22111334
Genome fraction (%)	99.936	99.870	99.927	99.931	99.912	99.901	99.862	99.943	99.879	99.863	99.919	99.849	99.906	99.881	99.943	99.794	99.879	99.890	99.869	99.873	99.863
Duplication ratio	1.104	1.104	1.102	1.098	1.098	1.099	1.097	1.081	1.104	1.104	1.102	1.097	1.098	1.096	1.082	1.104	1.104	1.098	1.099	1.096	1.082
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	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	267.38	266.45	299.34	286.46	274.38	272.08	350.56	267.03	266.98	294.37	285.67	268.11	269.46	361.70	268.64	268.21	305.58	285.14	272.17	267.33	352.78
# indels per 100 kbp	11.70	11.65	15.19	12.92	57.99	51.73	350.45	12.36	10.81	14.64	11.81	60.19	54.45	350.38	11.75	12.32	14.86	14.09	56.96	56.52	351.73
Largest alignment	177208	177205	176662	177195	176544	176771	176989	177205	177204	177197	177110	176879	176985	177110	176985	177205	177206	177198	177102	177003	177197
Total aligned length	1988775	1984219	1981606	1974020	1978403	1973897	1945915	1986078	1984632	1983573	1975881	1976205	1967892	1945252	1986419	1982430	1981309	1973257	1975490	1970859	1946815
NGA50	89791	88351	89897	89503	89759	88942	69730	89791	88582	79489	83605	69716	83544	69730	89790	87200	79490	69610	79431	69513	69730
NGA75	35503	35032	34836	34818	34819	34946	35032	35502	35032	35032	35016	35022	34945	35032	35032	35032	35032	34818	35008	34946	35032
LGA50	8	8	8	8	8	8	8	8	8	8	8	9	8	8	8	8	8	9	8	9	8
LGA75	16	17	17	17	17	18	17	17	17	17	17	18	17	18	17	17	18	18	18	18	18

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).
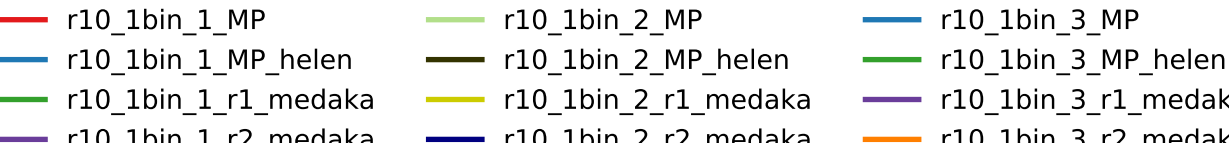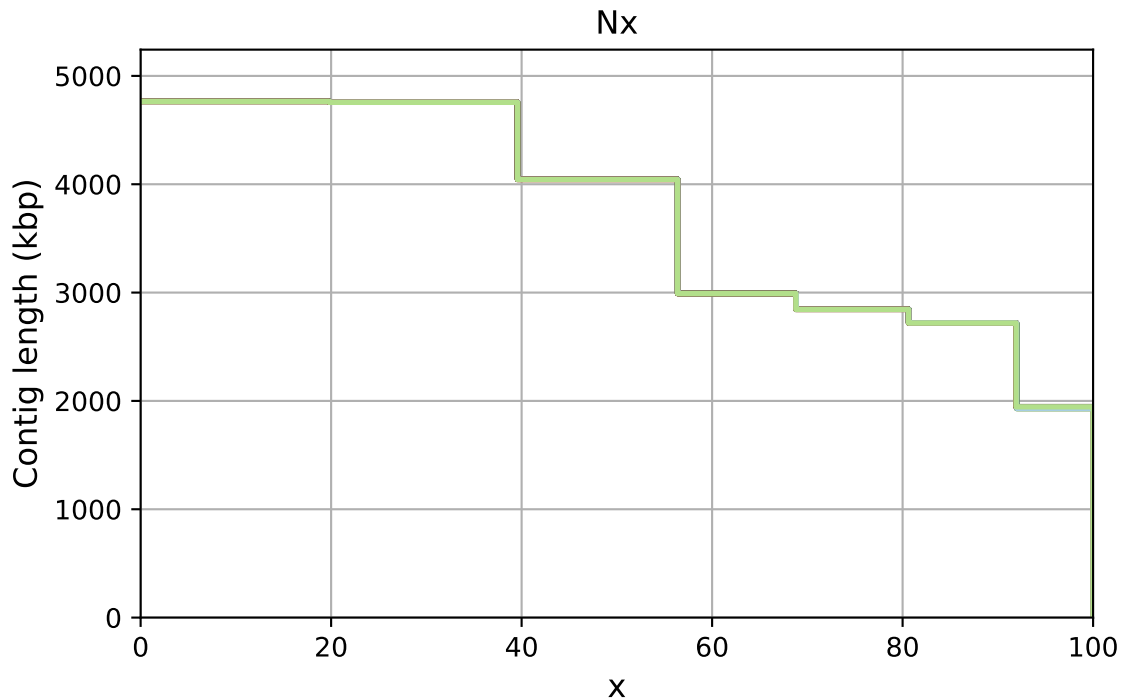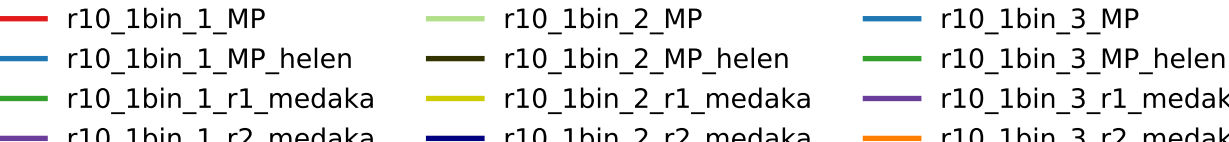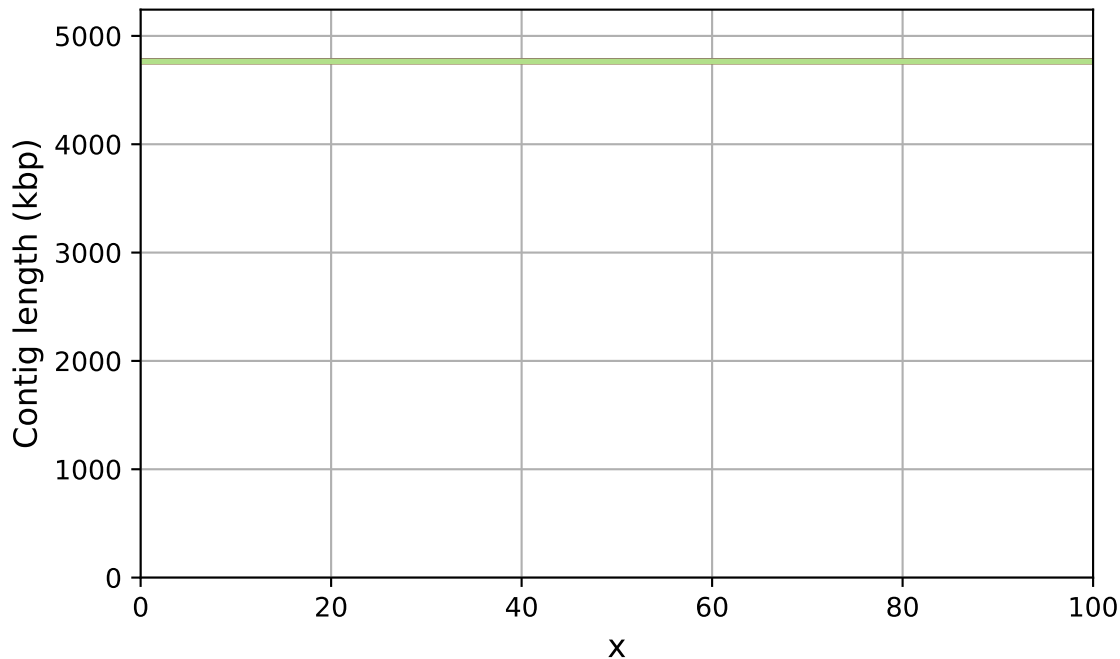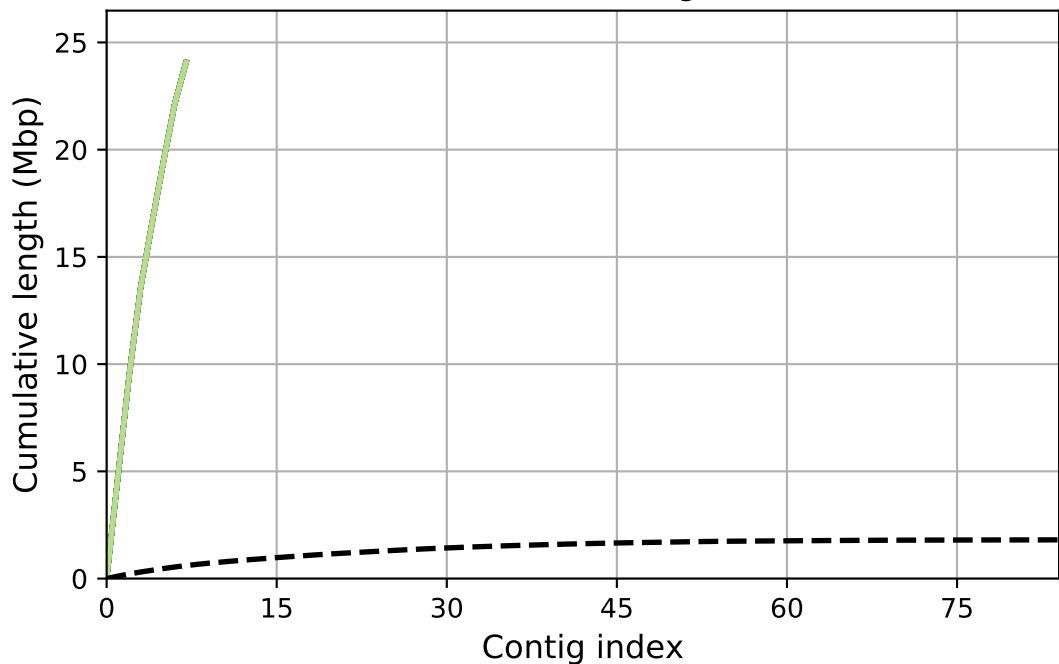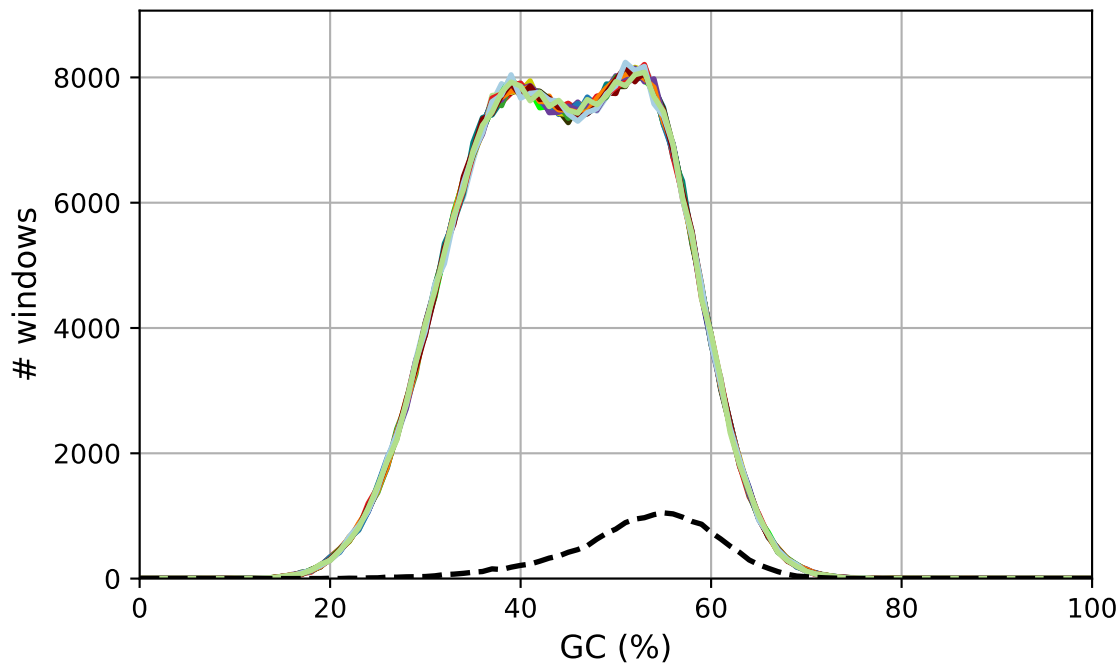
Misassemblies report
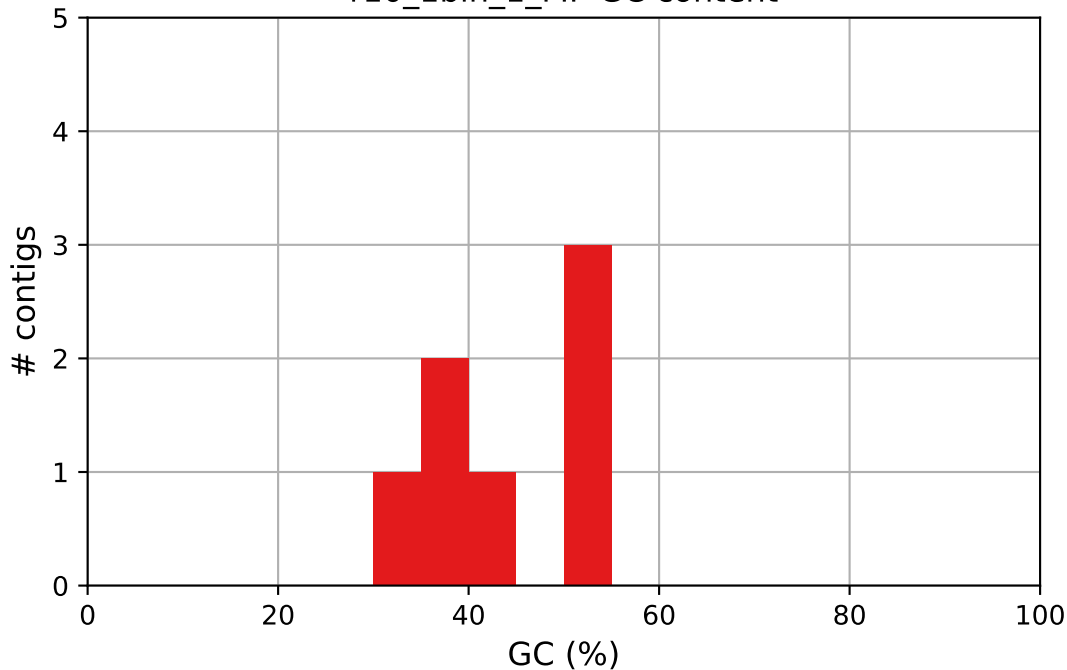
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	74	73	75	77	75	79	75	73	73	74	78	75	78	75	74	73	75	78	79	79	75
# contig misassemblies	74	73	75	77	75	79	75	73	73	74	78	75	78	75	74	73	75	78	79	79	75
# c. relocations	4	3	3	5	3	5	4	3	3	3	6	3	6	4	4	3	3	5	3	5	4
# c. translocations	70	70	72	72	72	74	71	70	70	71	72	72	72	71	70	70	72	73	76	74	71
# 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	1947367	1945999	1945572	1938095	1935544	1929697	1945498	1947264	1945994	1946130	1935173	1934812	1930121	1945704	1947347	1944592	1945545	1938875	1934569	1930417	1945410
# 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	36	38	34	36	34	30	42	36	36	32	34	34	34	44	36	38	32	34	32	32	42
# local misassemblies	12	14	27	32	43	41	30	12	13	28	26	42	34	29	11	15	28	26	47	33	29
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0
# misassemblies caused by fragmented reference	66	66	64	65	65	63	41	66	66	65	64	63	63	38	66	64	63	65	62	64	42
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	4824	4804	5400	5168	4949	4907	6320	4818	4814	5307	5153	4833	4860	6522	4847	4832	5510	5142	4907	4820	6360
# indels	211	210	274	233	1046	933	6318	223	195	264	213	1085	982	6318	212	222	268	254	1027	1019	6341
# indels (<= 5 bp)	162	153	223	180	973	866	6220	174	146	213	162	1011	913	6214	161	167	220	203	955	948	6240
# indels (> 5 bp)	49	57	51	53	73	67	98	49	49	51	51	74	69	104	51	55	48	51	72	71	101
Indels length	2607	2777	2820	2832	4904	4460	11218	2711	2704	2749	2643	5045	4607	11321	2737	2867	2771	2824	4764	4824	11278

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).

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	22082019	22079949	22084683	22084293	22078625	22077932	22111532	22082100	22079474	22085545	22081744	22080696	22079677	22110170	22082504	22080180	22084959	22085857	22078815	22079748	22111334
# N's	0	0	0	0	0	0	10	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

r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak

NGx

r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak

Cumulative length

GC content

r10_1bin_1_MP   r10_1bin_2_MP_helen   r10_1bin_3_MP_helen

r10_1bin_1_MP_helen   r10_1bin_2_r1_medaka   r10_1bin_3_r1_medak

r10_1bin_1_r1_medaka   r10_1bin_2_r2_medaka   r10_1bin_3_r2_medak

r10_1bin_1_r2_medaka   r10_1bin_2_racon_r1   r10_1bin_3_racon_r1

r10_1bin_1_MP GC content

r10_1bin_1_MP_helen GC content
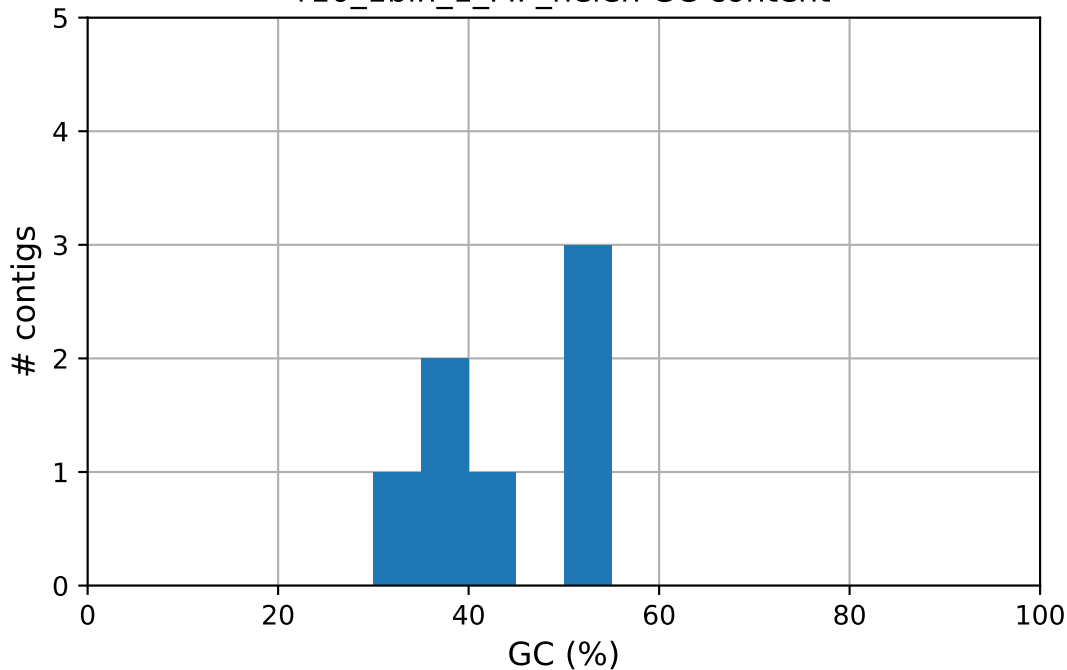
r10_1bin_1_r1_medaka GC content
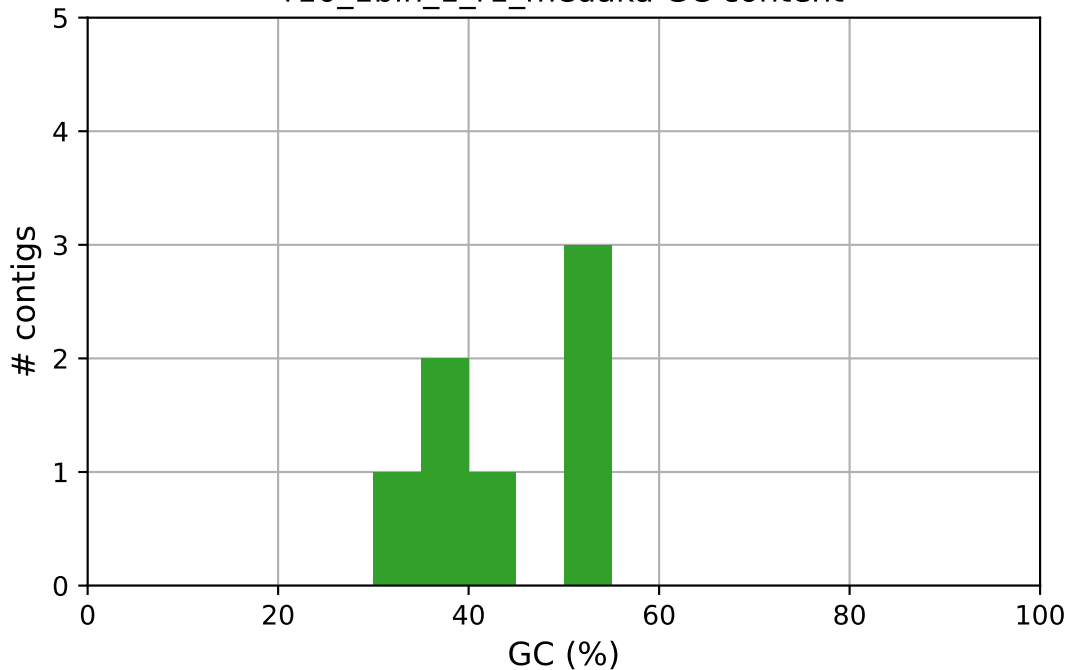
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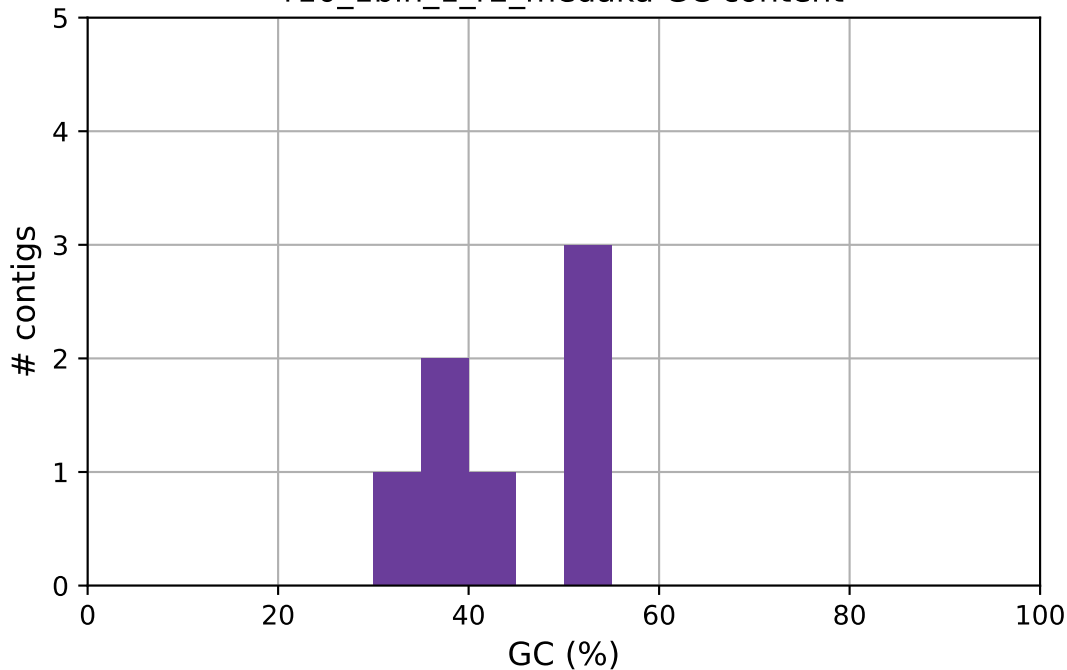
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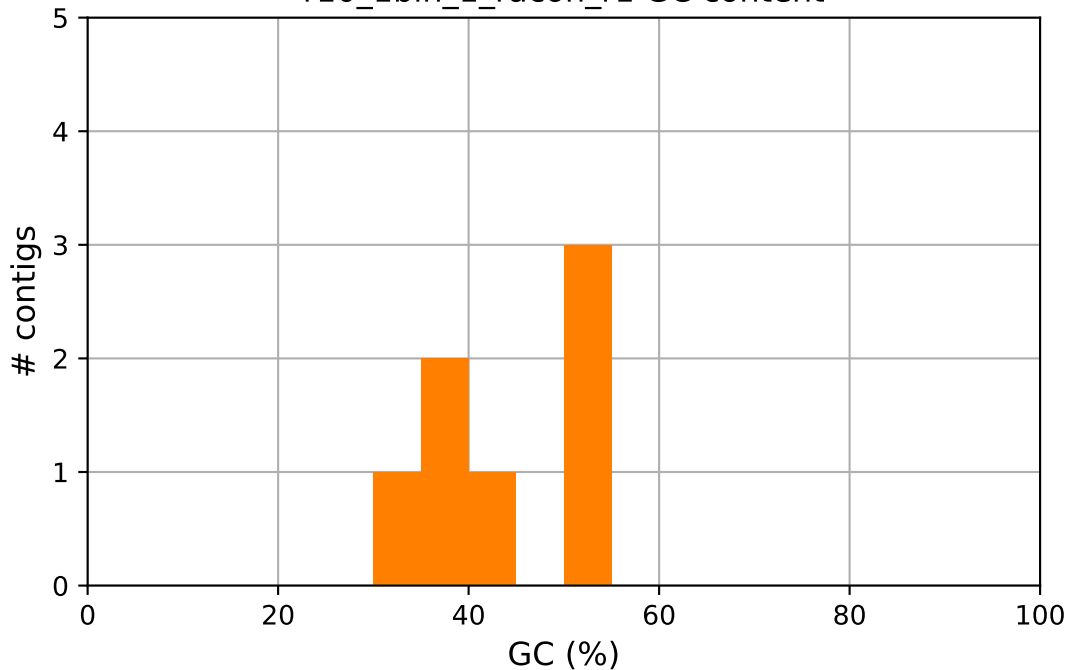
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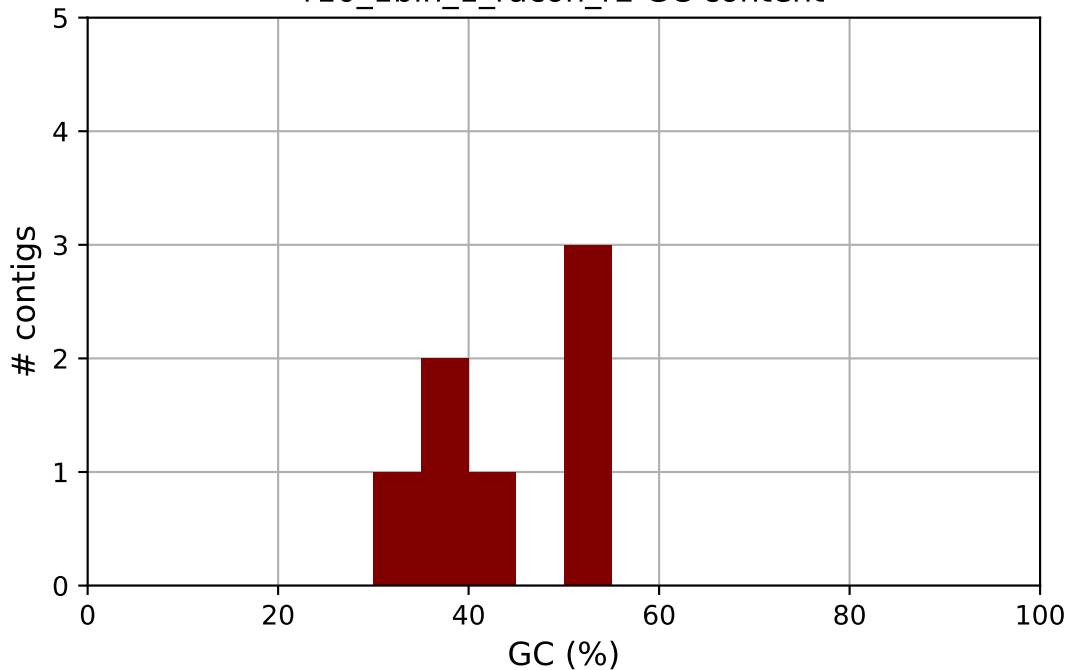
r10_1bin_1_raw GC content
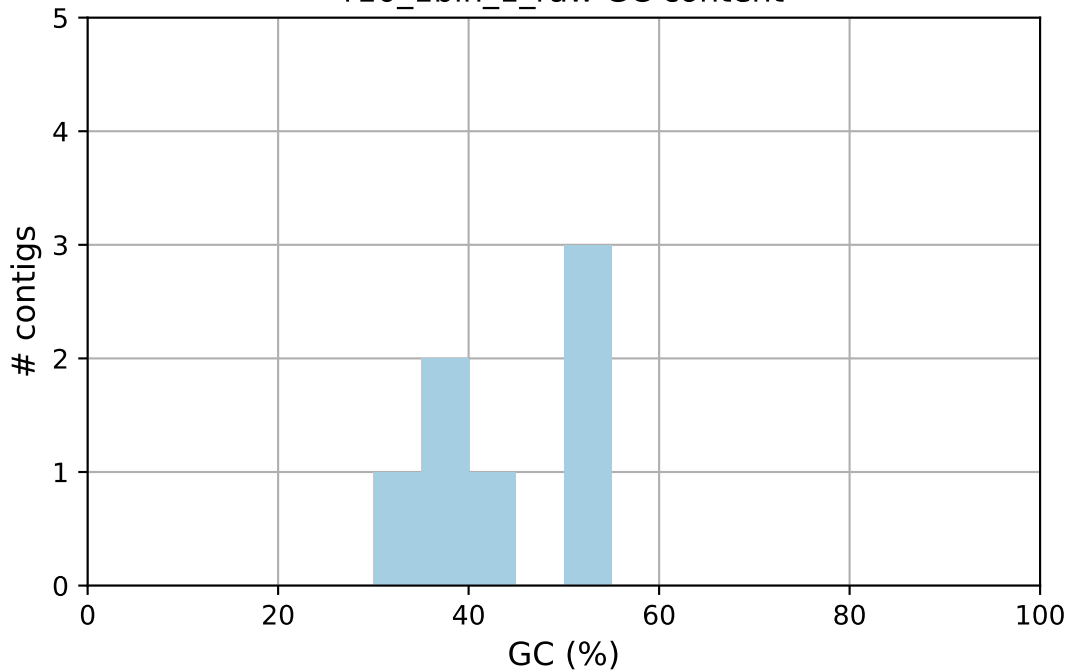
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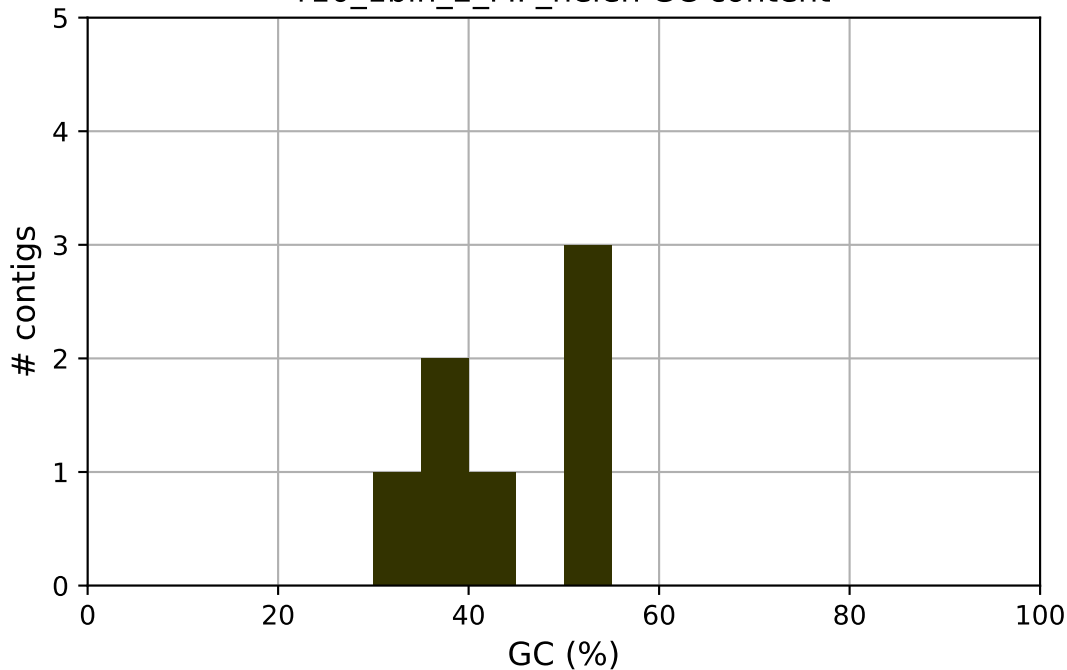
r10_1bin_2_r1_medaka GC content
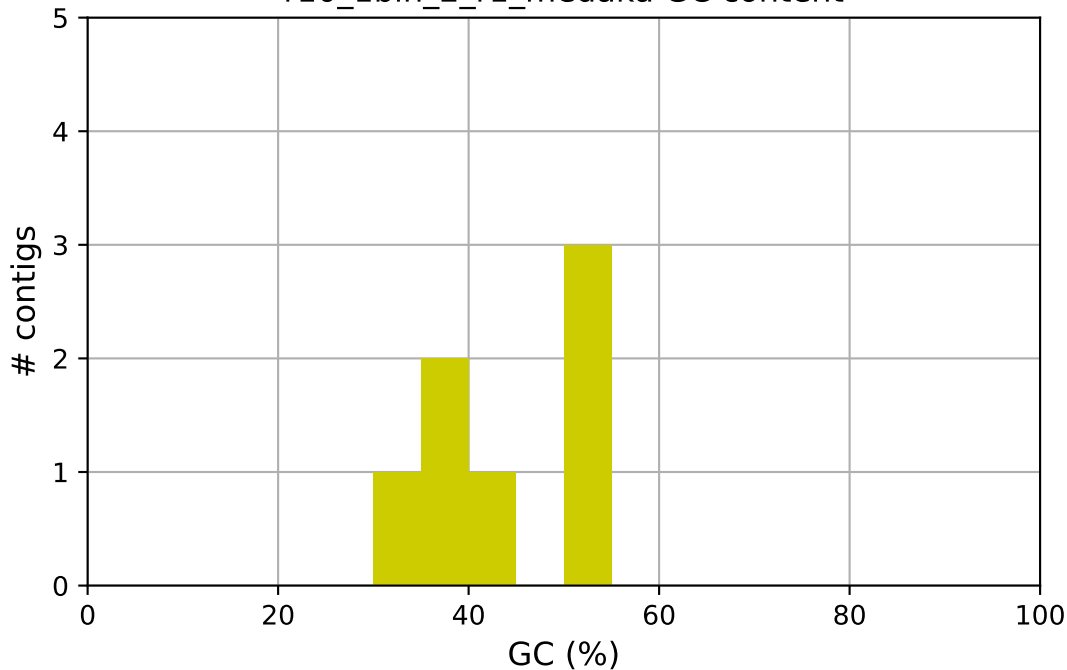
r10_1bin_2_r2_medaka GC content
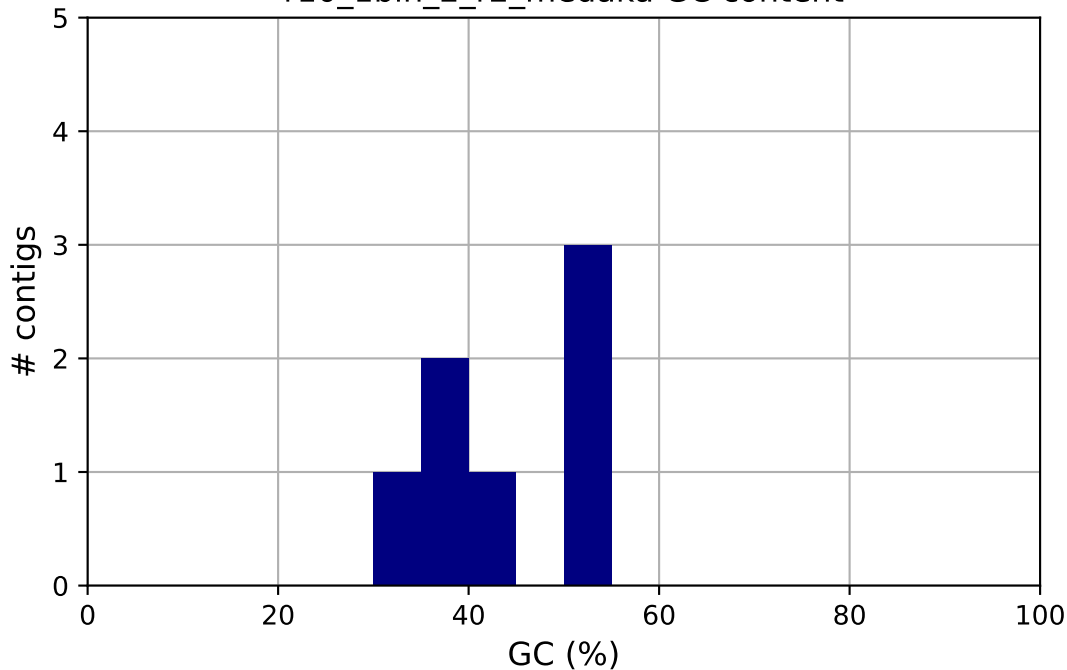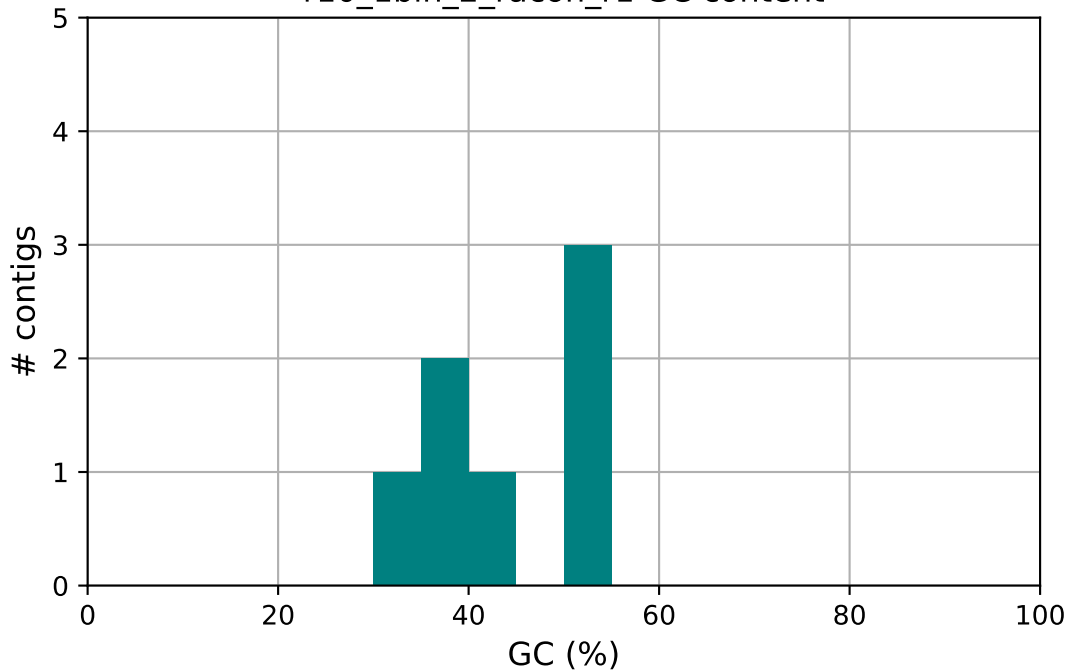
r10_1bin_2_racon_r2 GC content
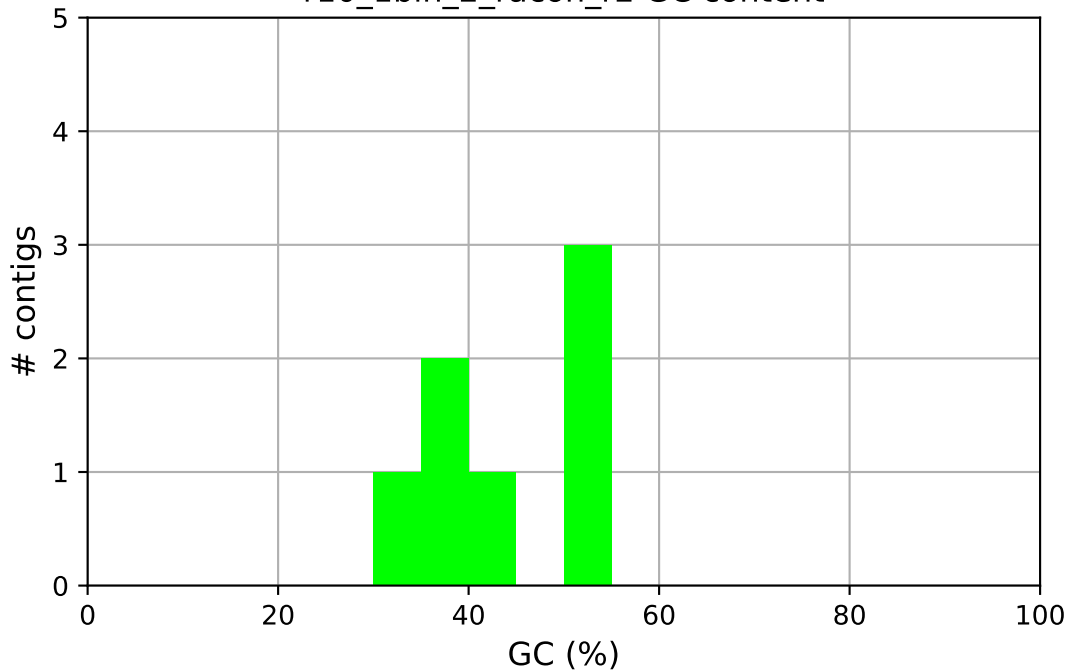
r10_1bin_2_raw GC content
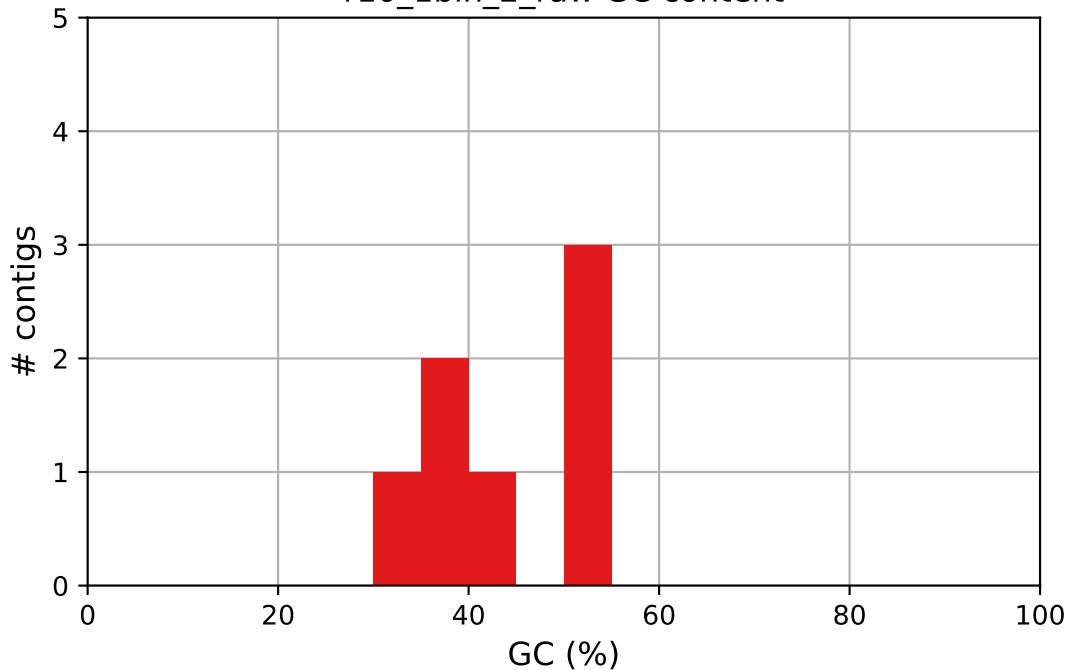
r10_1bin_3_MP GC content
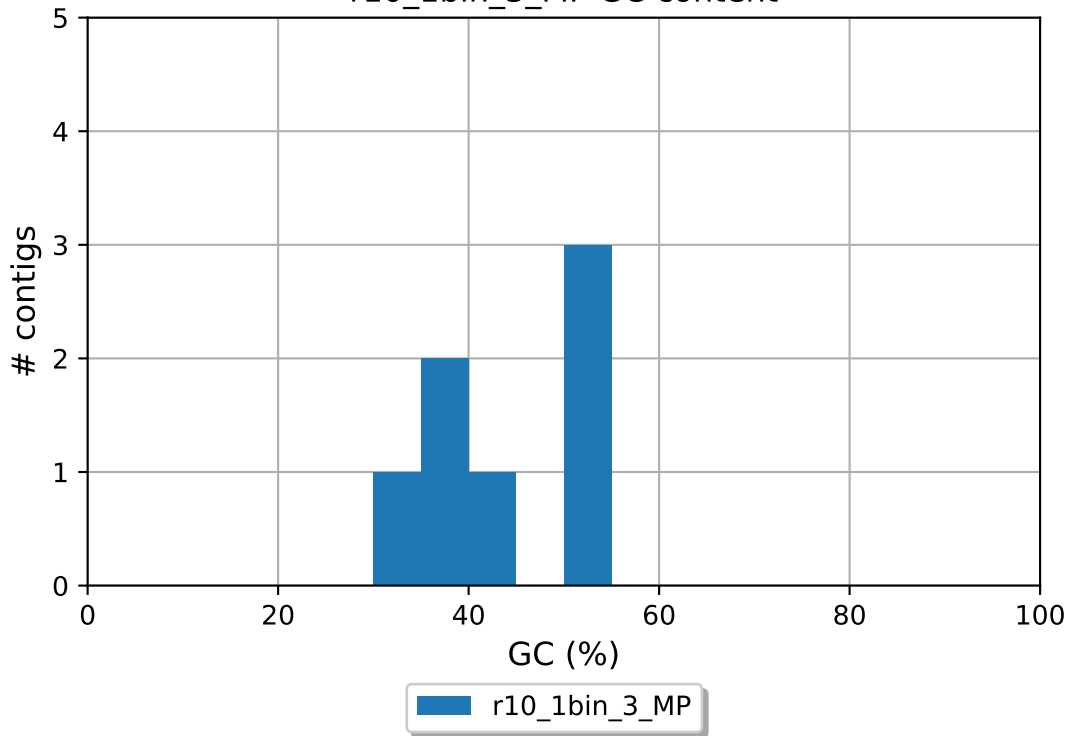
r10_1bin_3_MP_helen GC content
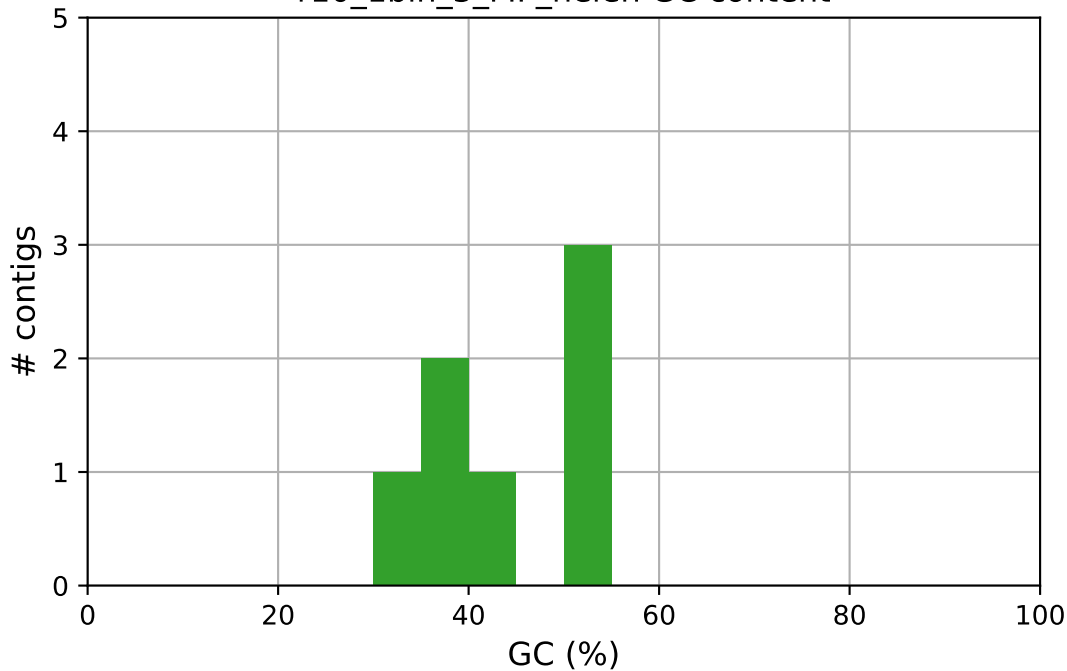
r10_1bin_3_r1_medaka GC content
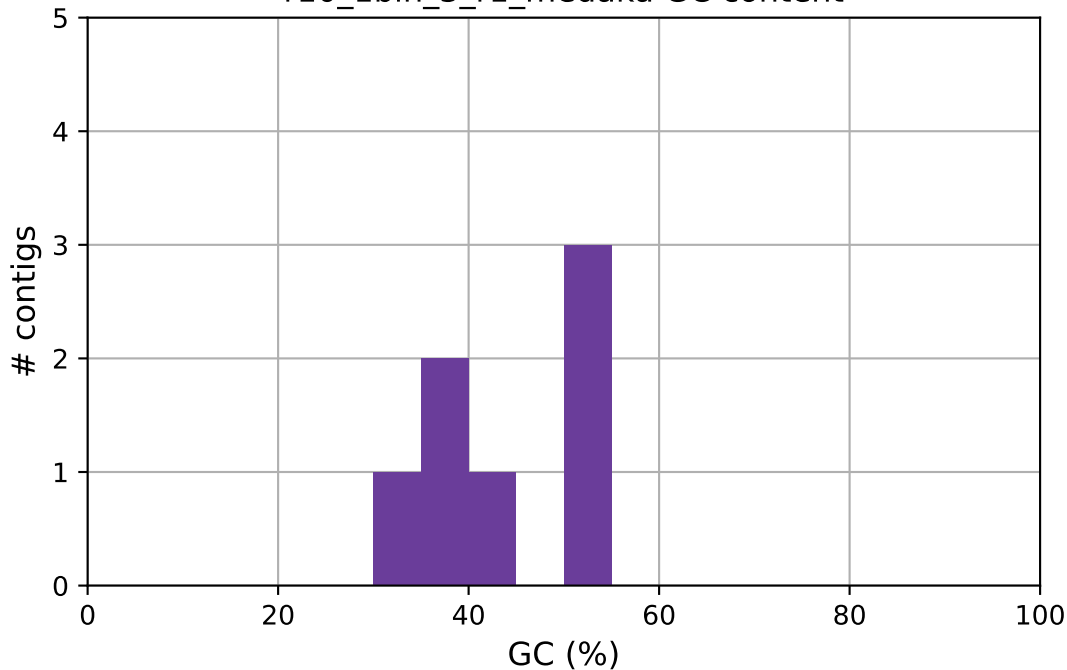
r10_1bin_3_r2_medaka GC content
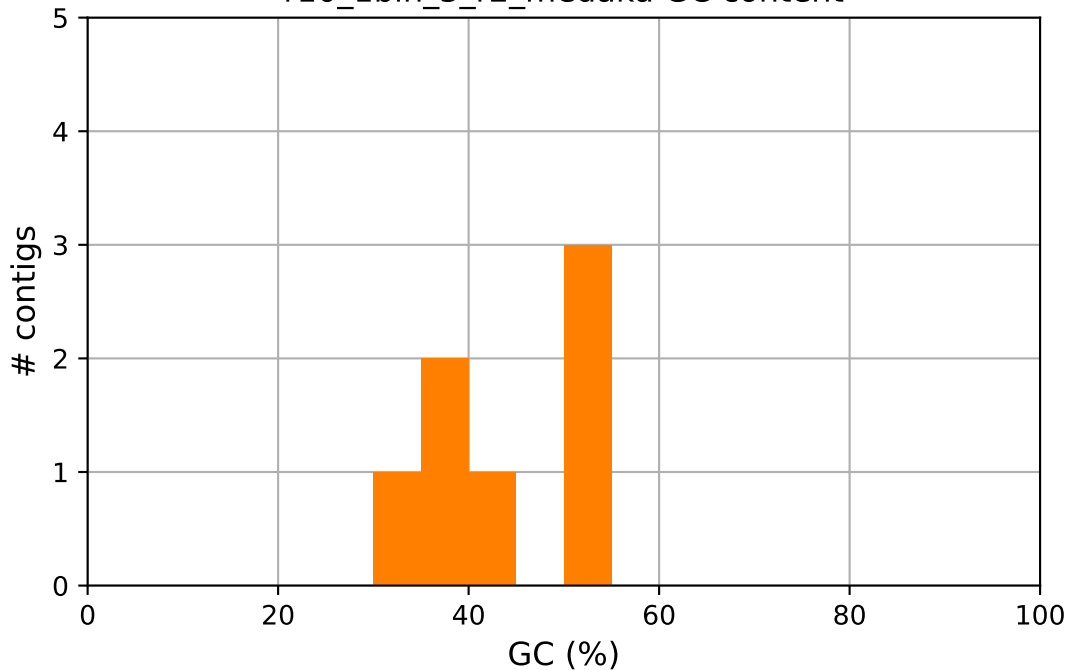
r10_1bin_3_racon_r1 GC content
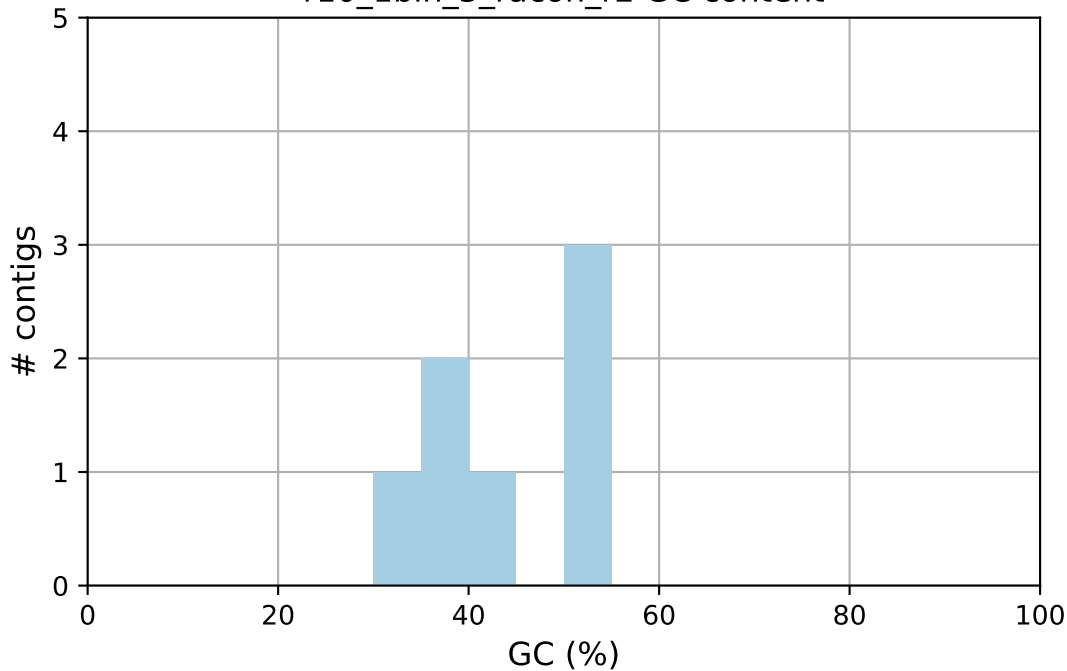
r10_1bin_3_raw GC content
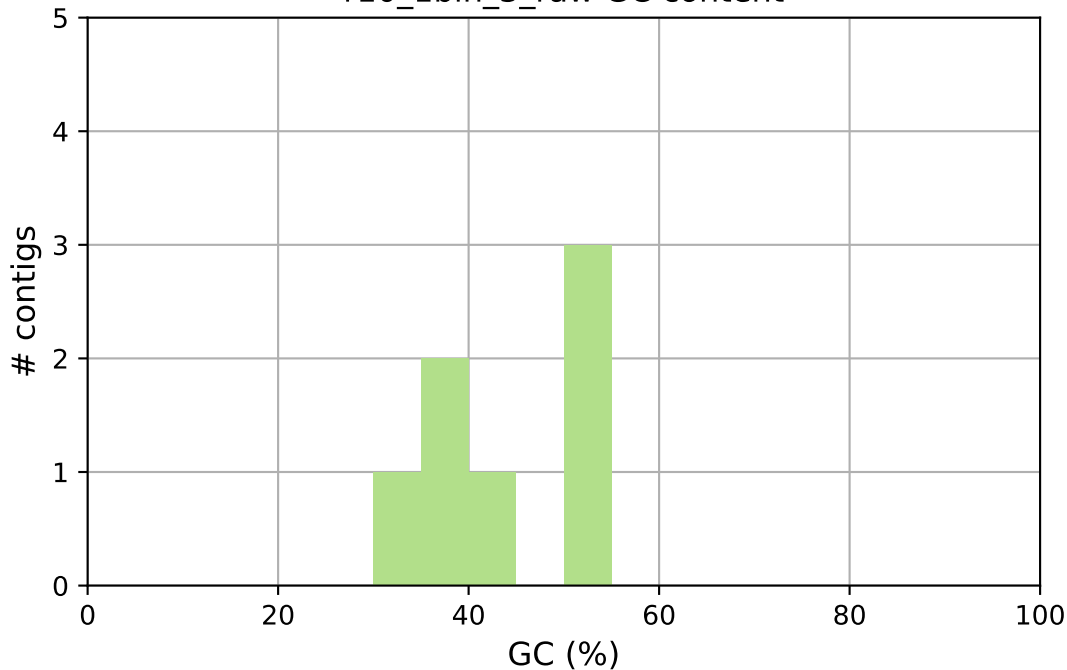
Misassemblies
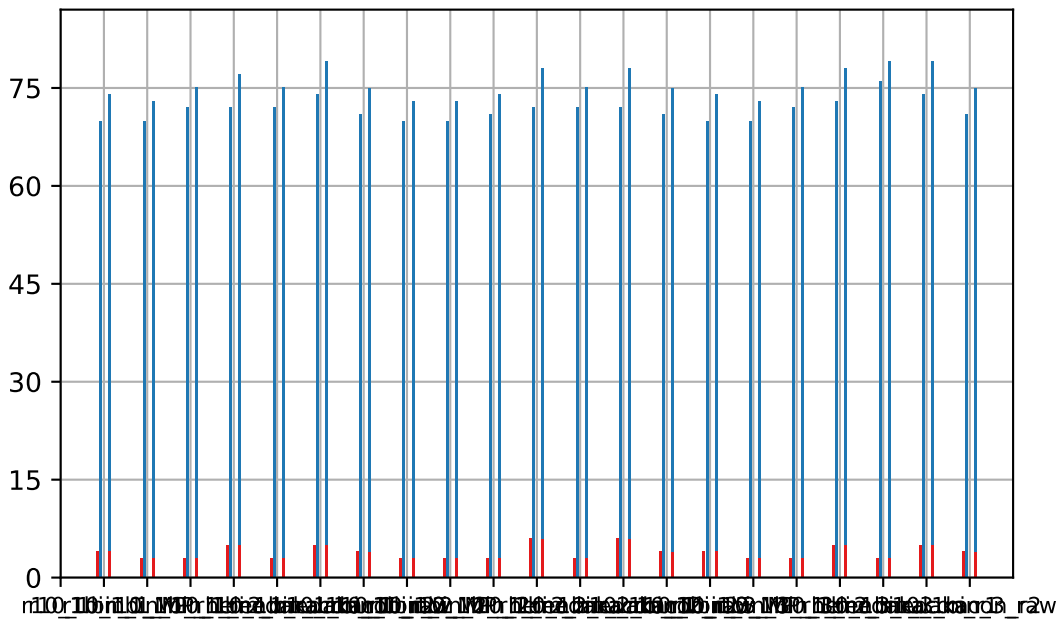
Legend:
- # relocations
- # translocations

FRCurve (misassemblies)

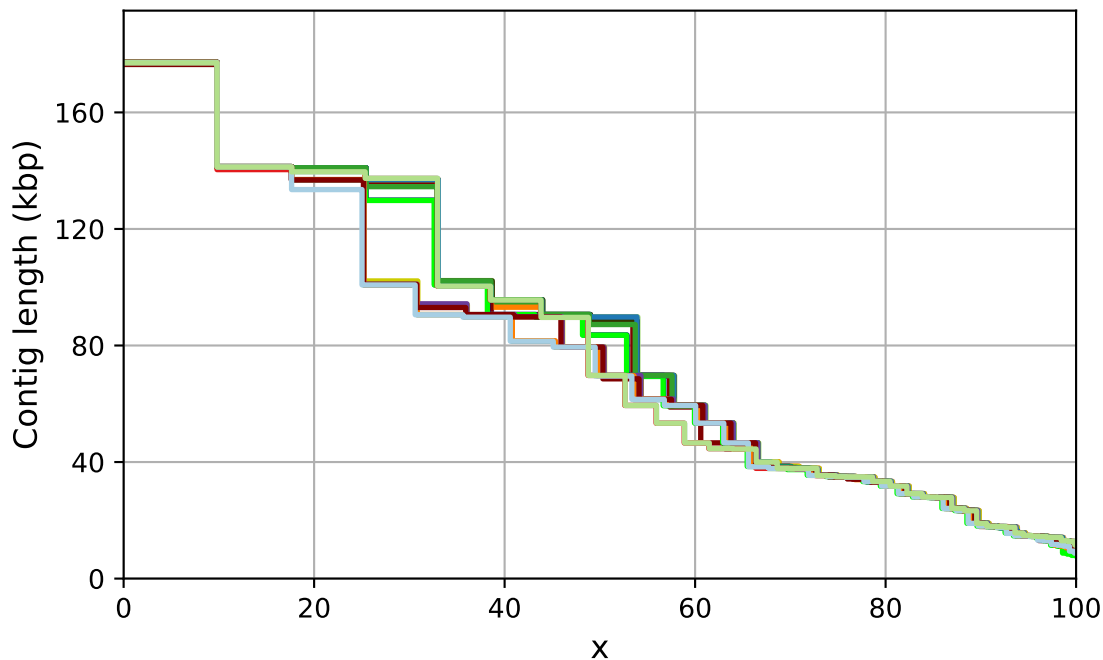| Legend		
r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak
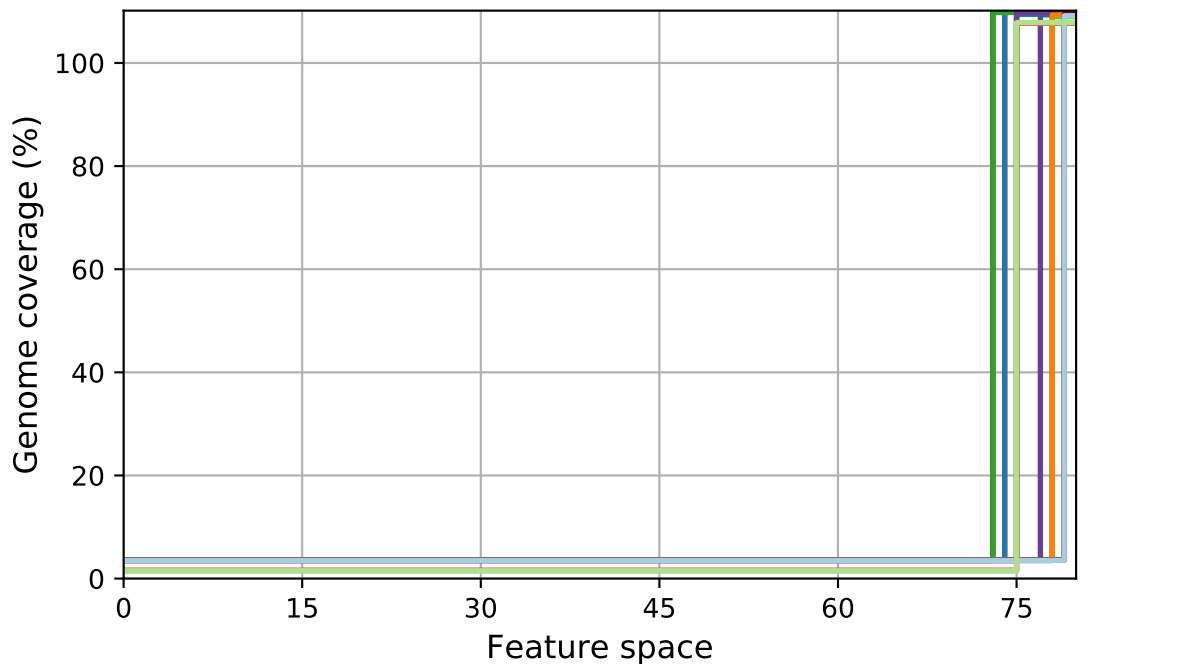
Cumulative length (aligned contigs)

NAx

Contig length (kbp)		

r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka

r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka

r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak

NGAx

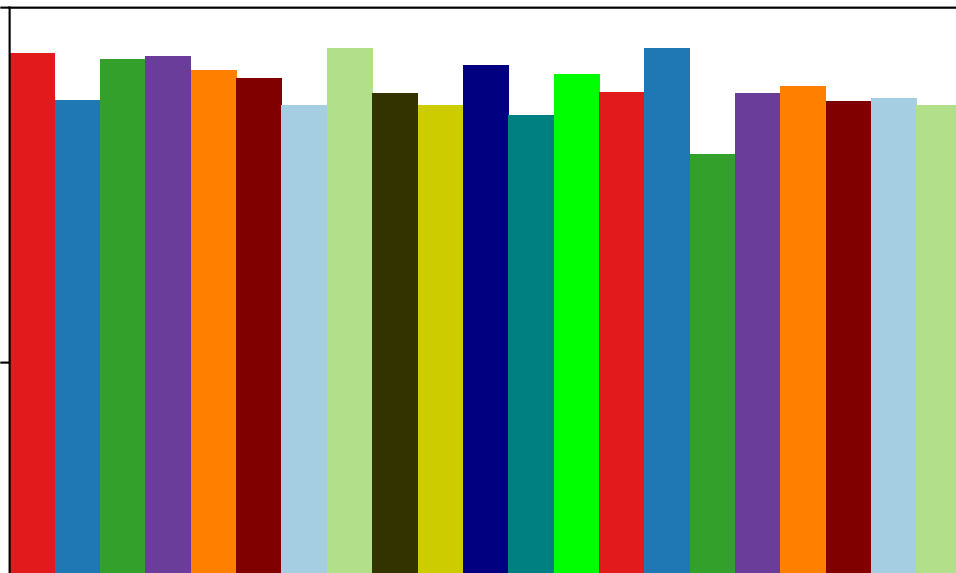| Legend		
r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak

Genome fraction, %