

Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	
# contigs (>= 10000 bp)	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	
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Total length (>= 5000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
Total length	24074828	24070090	24071888	24063470	24060900	24056048	24060486	24074490	24070611	24075114	24065831	24060635	24055783	24060933	24078180	24070683	24078524	24071188	24064158	24059056	24063949
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	44.81	44.80	44.79	44.79	44.79	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	4045594	4045616	4045591	4045596	4045200	4045302	4042945	4045598	4045623	4045846	4045845	4045161	4045304	4043043	4045599	4045602	4045842	4045840	4045210	4045276	4043035
NG50	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
N75	2845421	2845364	2845429	2845429	2845295	2845304	2843358	2845423	2845360	2845571	2845301	2845564	2845301	2843368	2845422	2845361	2845572	2845563	2845260	2845299	2843358
NG75	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
L50	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	
L75	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	
# misassemblies	73	74	76	78	75	81	75	74	73	76	77	75	78	75	76	76	76	78	78	80	77
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Misassembled contigs length	1947311	1945172	1945343	1936940	1935218	1930341	1945501	1947346	1946452	1945713	1937018	1935181	1930119	1945498	1951039	1946515	1949116	1942386	1938651	1933401	1948659
# local misassemblies	12	12	26	25	43	33	29	11	12	28	26	44	31	30	11	15	23	33	40	41	81
# scaffold gap ext. mis.	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	1	0	0	0	0	0	0	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	
# 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	
Unaligned length	22081849	22080589	22083857	22083004	22078751	22079208	22105818	22081986	22078925	22087757	22086216	22079638	22078846	22110721	22082572	22082851	22086862	22087029	22079596	22077757	22161154
Genome fraction (%)	99.943	99.820	99.935	99.907	99.922	99.847	99.861	99.943	99.943	99.925	99.917	99.918	99.906	99.871	99.940	99.563	99.931	99.904	99.898	99.887	97.222
Duplication ratio	1.105	1.104	1.102	1.098	1.099	1.097	1.084	1.104	1.104	1.102	1.097	1.098	1.096	1.082	1.106	1.106	1.104	1.100	1.100	1.099	1.084
# N's per 100 kbp	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	0.00	0.00	0.00	0.00	0.00	0.42	
# mismatches per 100 kbp	270.08	265.81	302.64	287.64	275.85	268.23	371.64	268.64	267.86	306.11	283.01	270.92	271.51	353.64	266.21	265.05	314.68	287.76	272.09	272.50	430.73
# indels per 100 kbp	11.20	10.99	15.96	13.81	58.54	52.15	353.56	12.25	12.30	24.22	23.78	57.71	53.67	348.87	13.19	18.42	25.28	22.68	61.55	55.79	386.63
Largest alignment	177203	177206	173114	177197	173007	176953	177003	177207	177205	176692	177223	176539	176977	176989	177207	177205	176690	177221	176516	177081	177003
Total aligned length	1986954	1983466	1982055	1974626	1975300	1970998	1951247	1986418	1985600	1983720	1973807	1974649	1971207	1944429	1989466	1981684	1985611	1977829	1978762	1975038	1899177
NGA50	89791	69719	89789	81643	89762	81544	69730	89789	89686	89796	81639	89773	81573	69730	81648	81650	82129	81623	82063	81556	69730
NGA75	35033	35032	34852	35032	34818	35027	34946	35032	35032	35034	35034	34888	34991	34946	35504	35503	35510	34844	35453	34812	34788
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
LGA75	17	18	17	17	17	17	18	17	17	17	17	17	17	18	17	17	17	17	17	17	

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

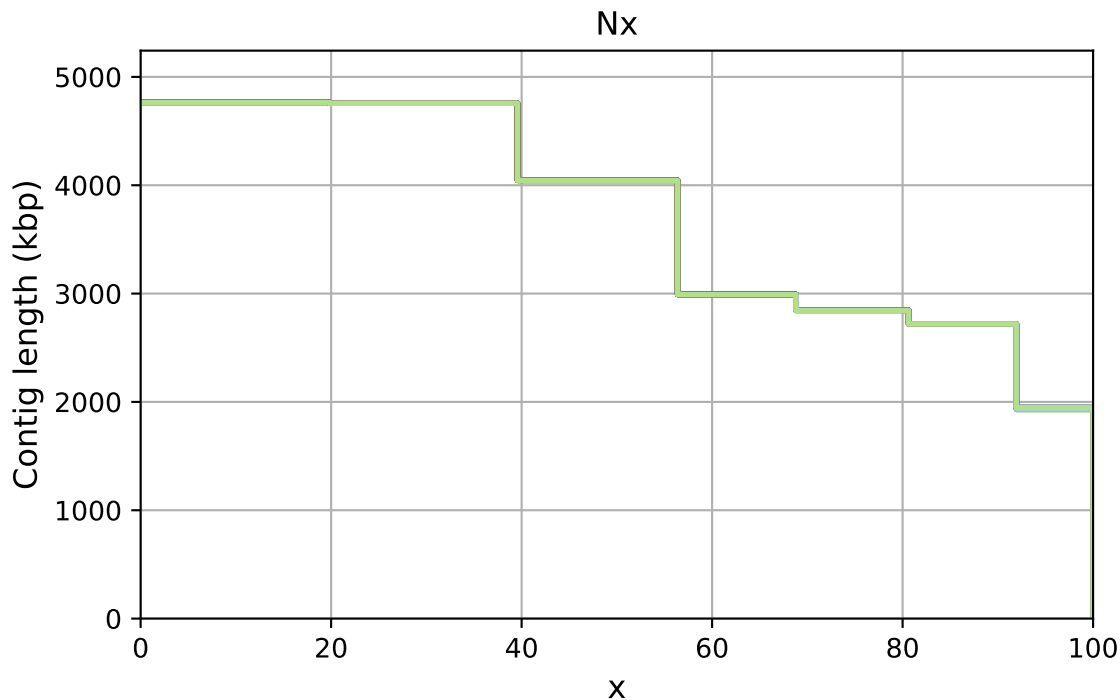
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# misassemblies	73	74	76	78	75	81	75	74	73	76	77	75	78	75	76	76	76	78	78	80	77
# contig misassemblies	73	74	76	78	75	81	75	74	73	76	77	75	78	75	76	76	76	78	78	80	76
# c. relocations	3	4	3	6	3	6	4	4	3	3	6	3	6	4	5	5	4	5	4	6	5
# c. translocations	70	70	73	72	72	75	71	70	70	73	71	72	72	71	71	71	71	72	73	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	1
# 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	1
# 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	1947311	1945172	1945343	1936940	1935218	1930341	1945501	1947346	1946452	1945713	1937018	1935181	1930119	1945498	1951039	1946515	1949116	1942386	1938651	1933401	1948659
# 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	36	34	36	36	34	42	36	36	34	34	36	34	42	36	38	34	32	38	28	102
# local misassemblies	12	12	26	25	43	33	29	11	12	28	26	44	31	30	11	15	23	33	40	41	81
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassemblies caused by fragmented reference	66	66	64	65	64	64	41	66	66	63	66	63	65	40	67	67	63	62	60	60	43
# 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	4873	4790	5460	5188	4976	4835	6700	4847	4833	5522	5105	4887	4897	6376	4803	4764	5677	5190	4907	4914	7560
# indels	202	198	288	249	1056	940	6374	221	222	437	429	1041	968	6290	238	331	456	409	1110	1006	6786
# indels (<= 5 bp)	154	144	239	196	976	869	6272	172	169	388	376	968	901	6191	187	273	407	360	1031	922	6692
# indels (> 5 bp)	48	54	49	53	80	71	102	49	53	49	53	73	67	99	51	58	49	49	79	84	94
Indels length	2684	2746	2786	3054	5146	4648	11319	2712	2773	2846	2963	5106	4511	11281	2775	3007	3011	2960	5596	5128	11631

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_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	22081849	22080589	22083857	22083004	22078751	22079208	22105818	22081986	22078925	22087757	22086216	22079638	22078846	22110721	22082572	22082851	22086862	22087029	22079596	22077757	22161154
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	100

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_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

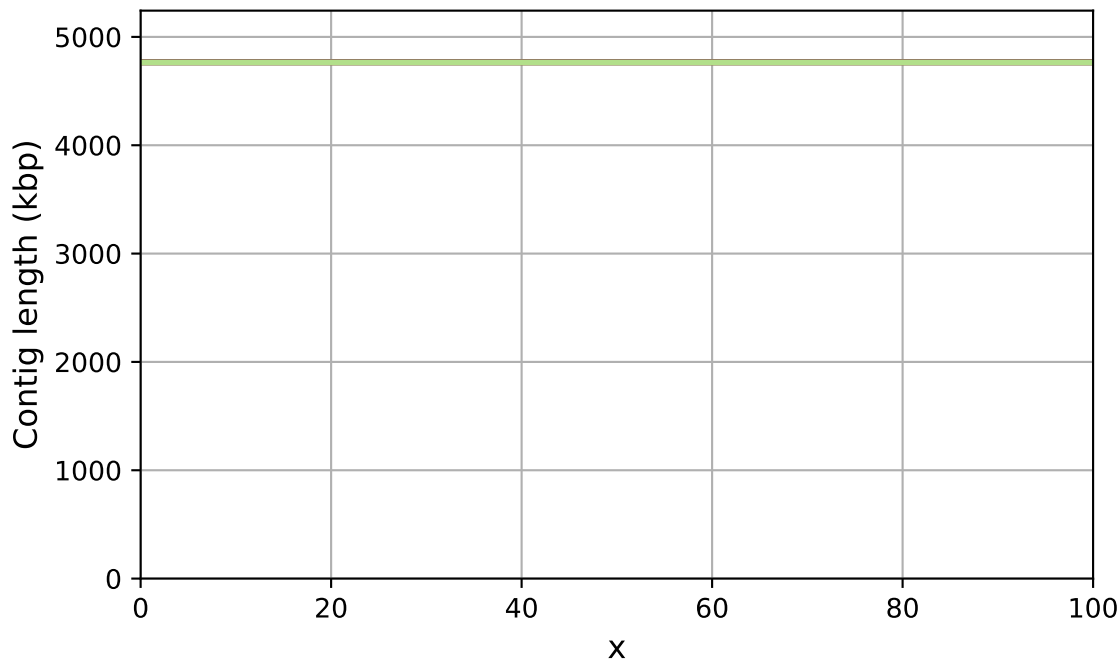
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

NGx



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP

r10_1bin_v3_3_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r1_medaka

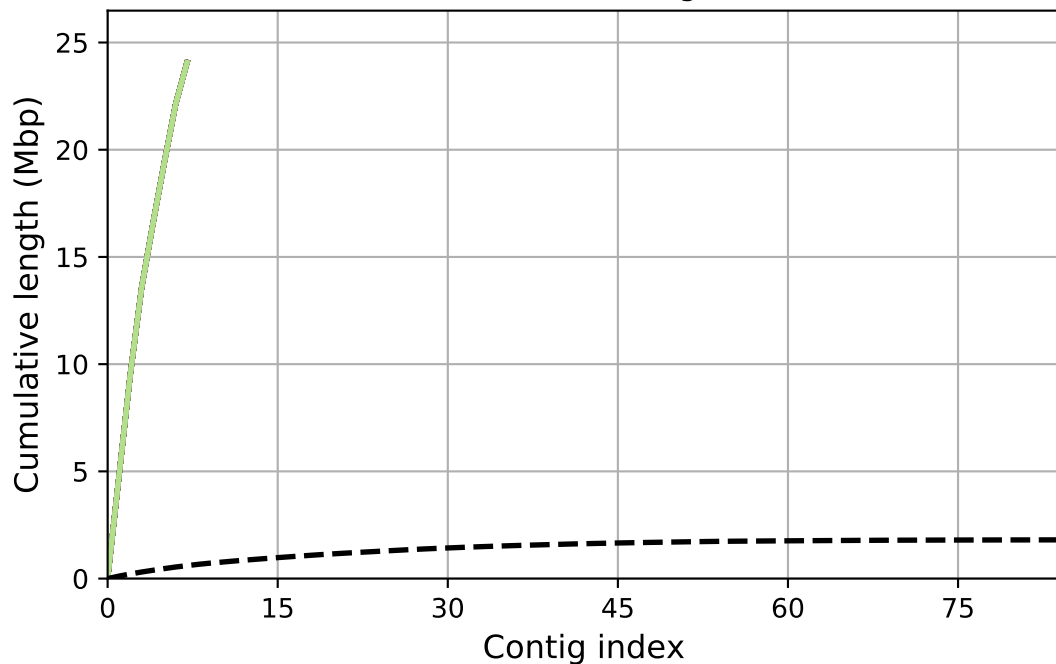
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_helen

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r2_medaka

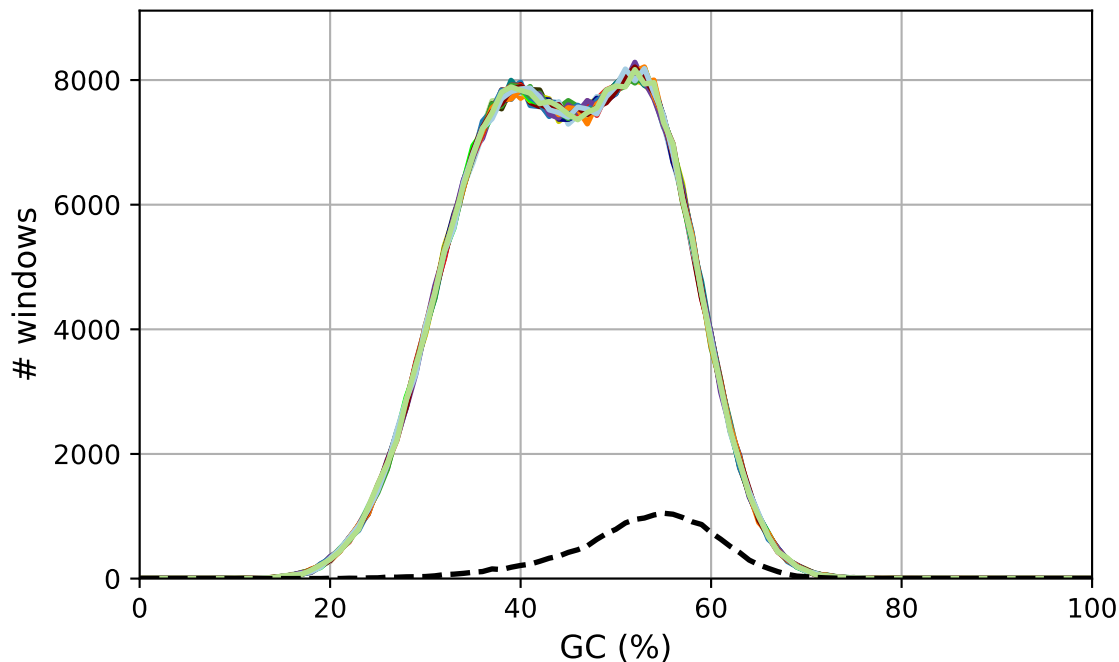
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_racon_r1

r10_1bin_v3_3_racon_r1

GC content



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_h

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_3_r1_m

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r2_medaka

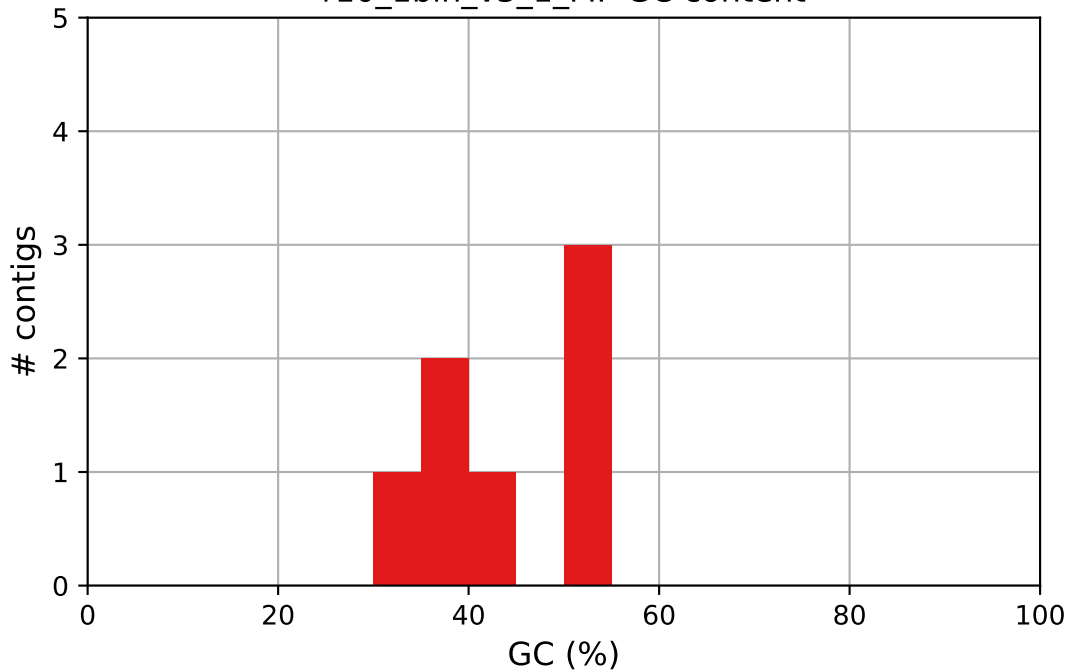
r10_1bin_v3_3_r2_m

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_racon_r1

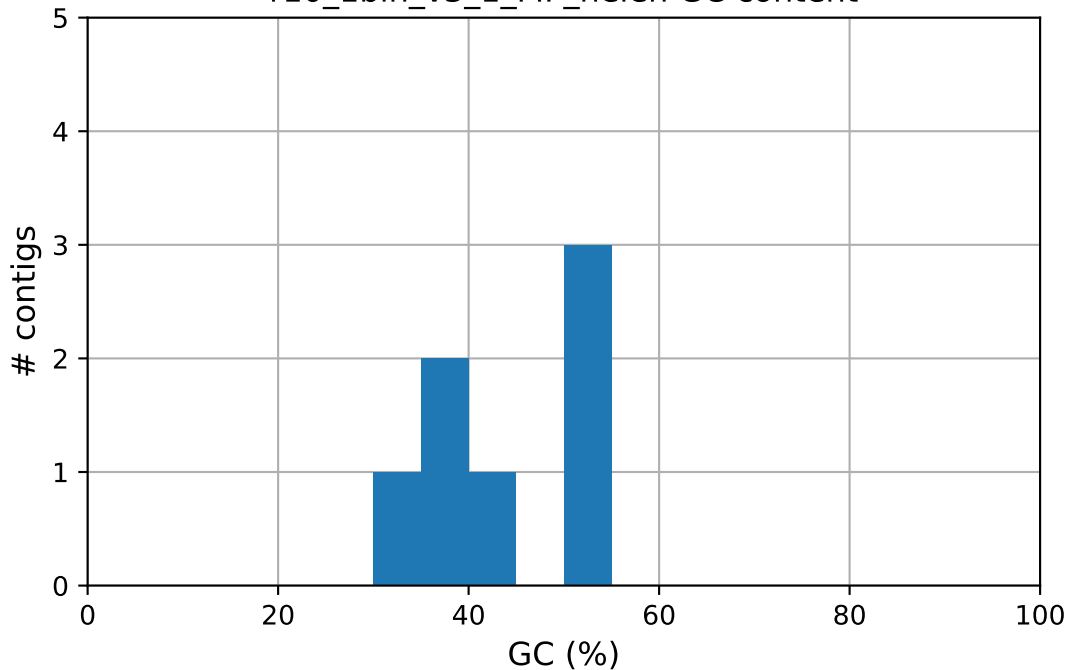
r10_1bin_v3_3_racon_r1

r10_1bin_v3_1_MP GC content



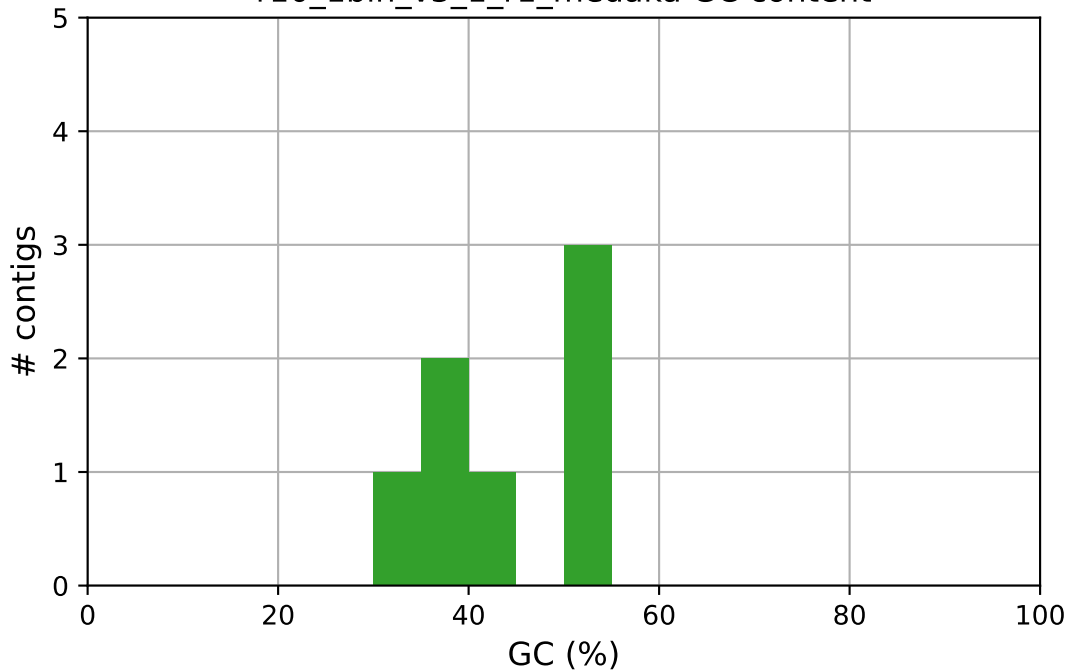
r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen GC content



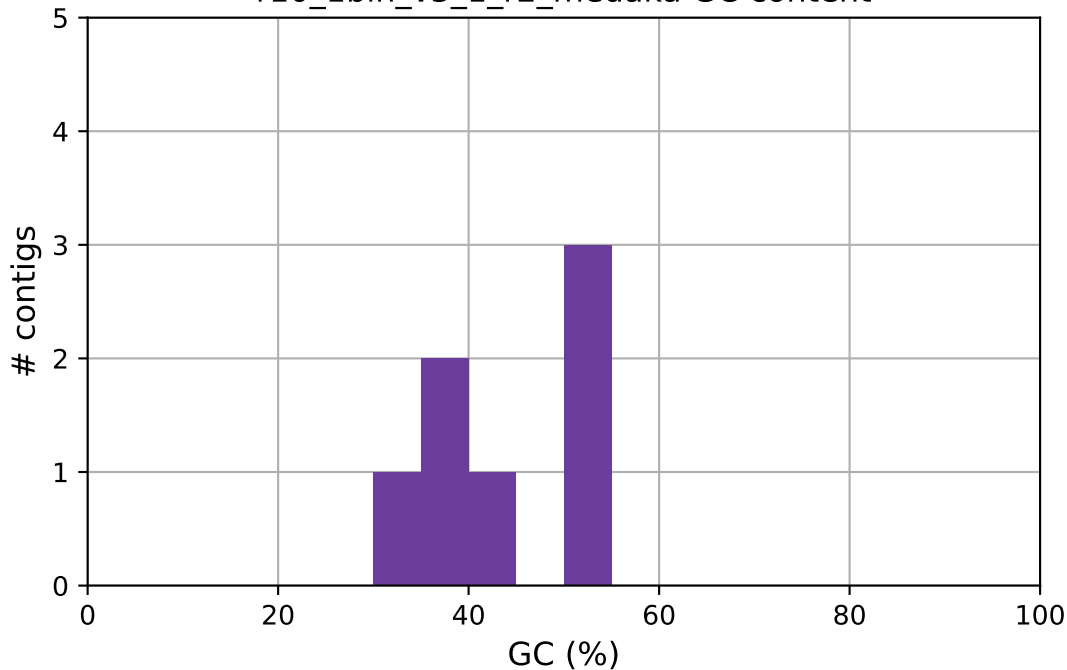
r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka GC content



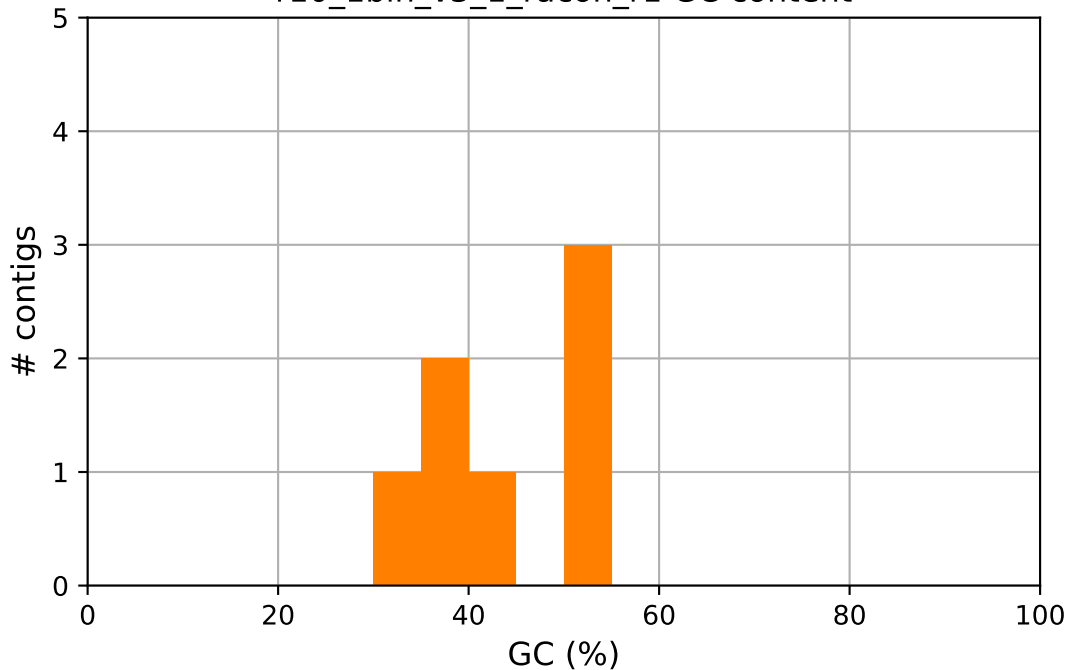
r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka GC content



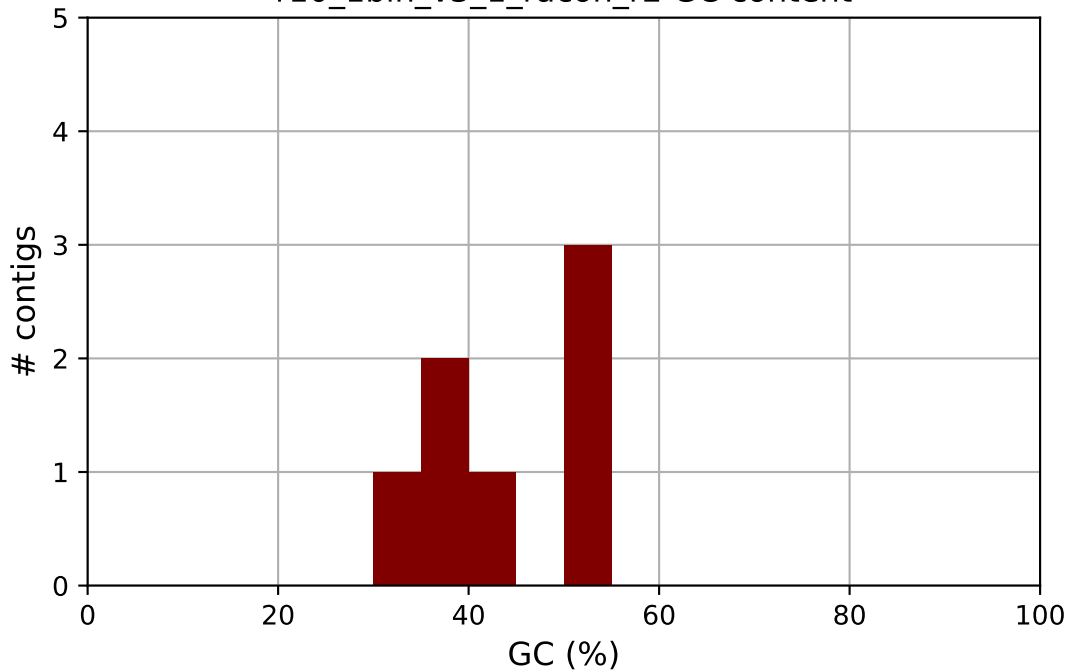
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_1_racon_r1 GC content



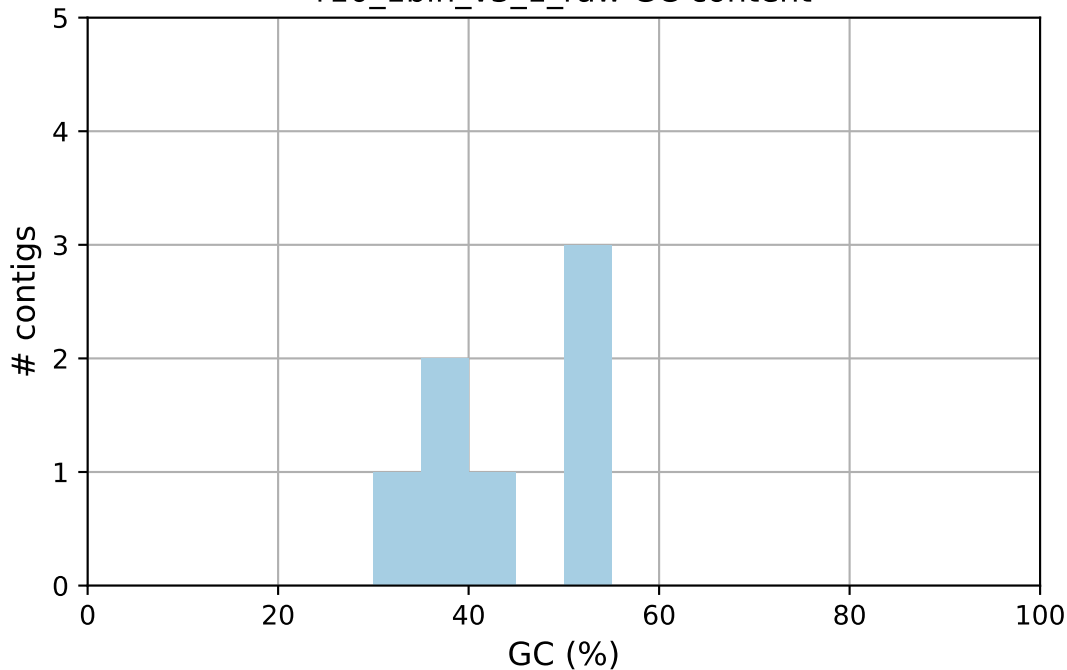
r10_1bin_v3_1_racon_r1

r10_1bin_v3_1_racon_r2 GC content



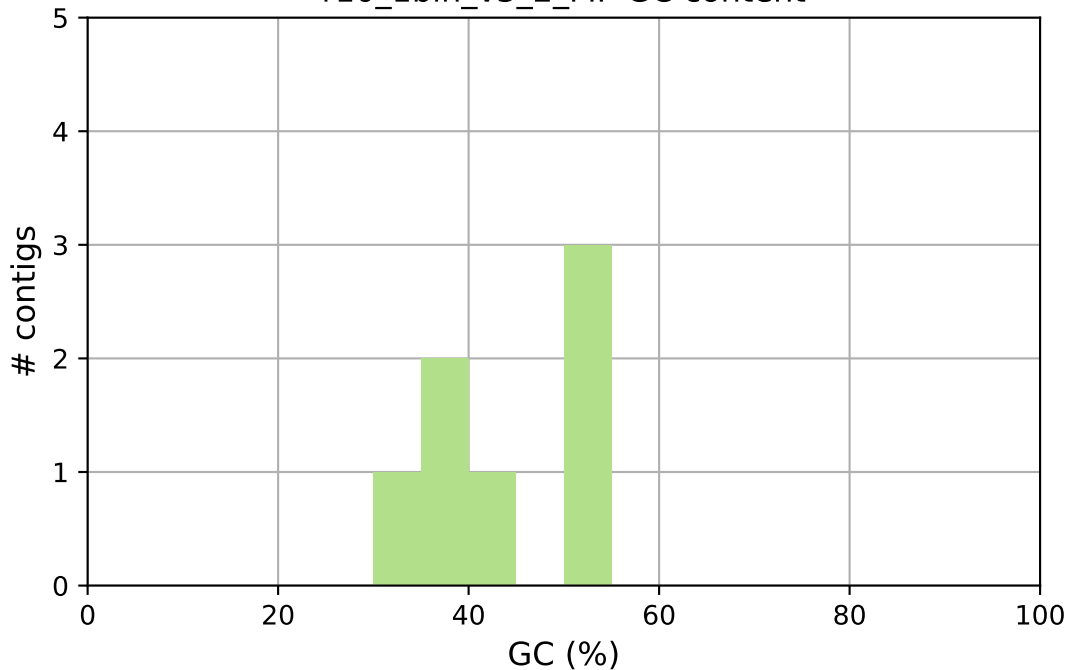
r10_1bin_v3_1_racon_r2

r10_1bin_v3_1_raw GC content



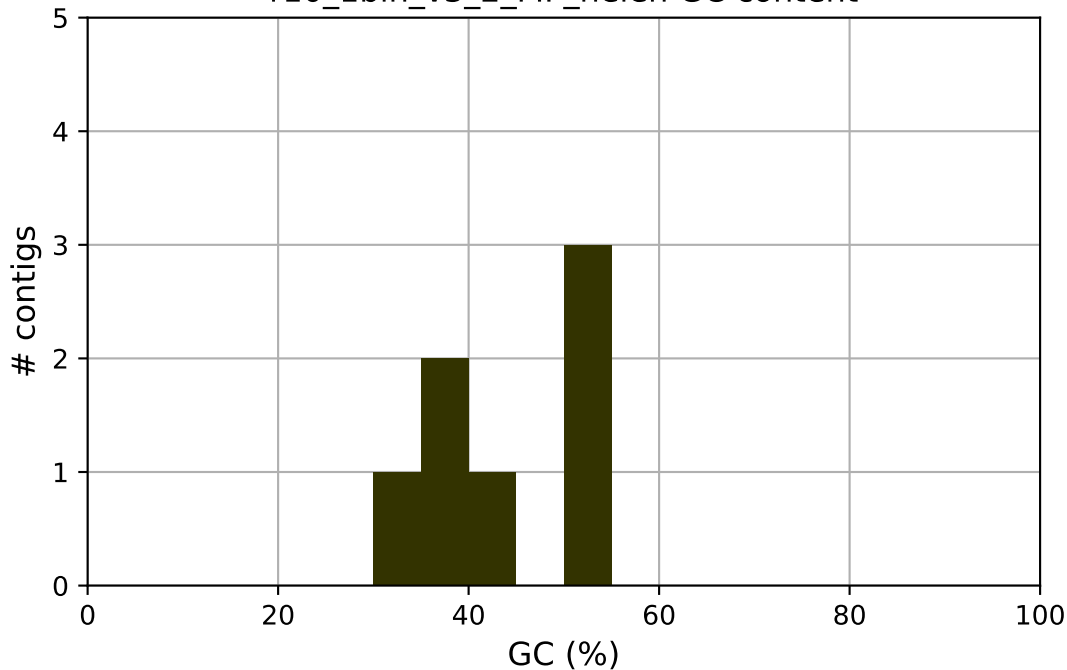
r10_1bin_v3_1_raw

r10_1bin_v3_2_MP GC content



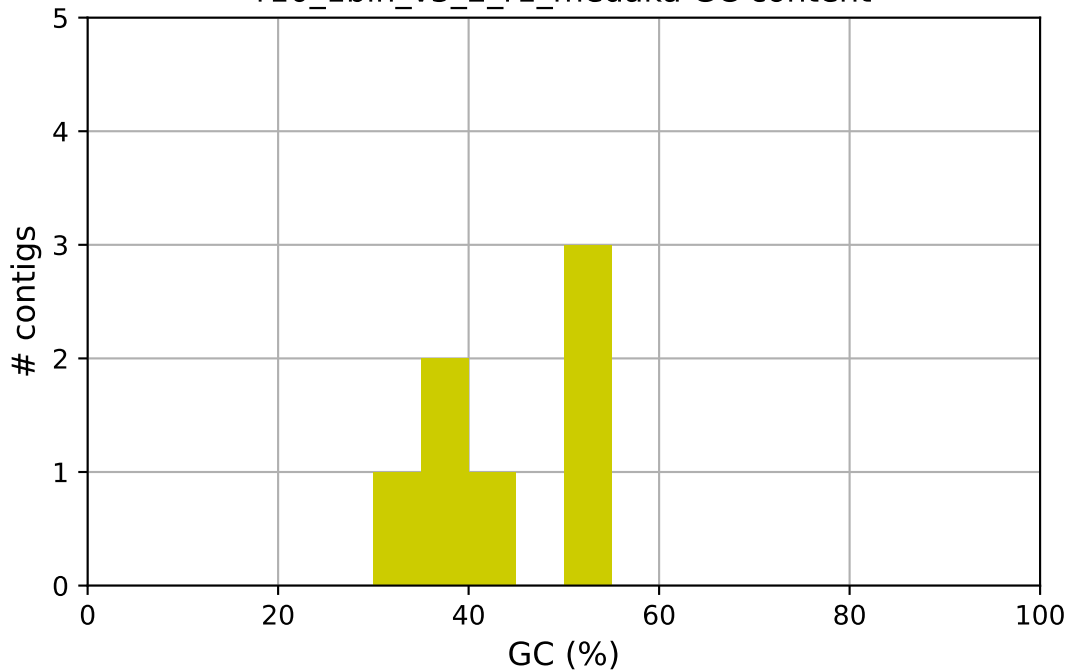
r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen GC content



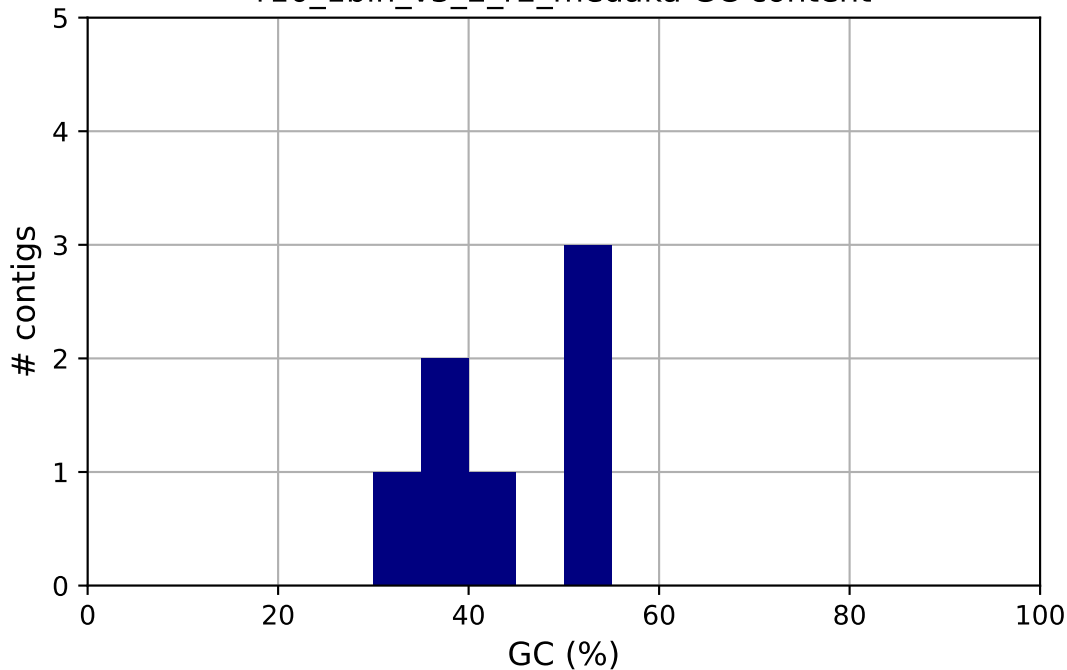
r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka GC content



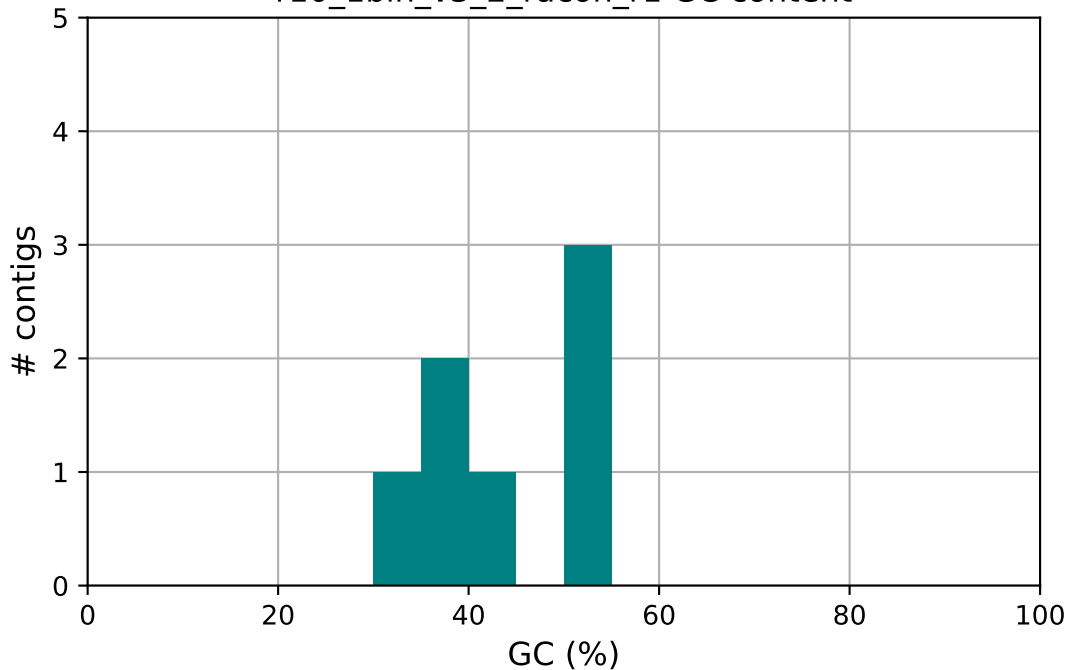
r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka GC content



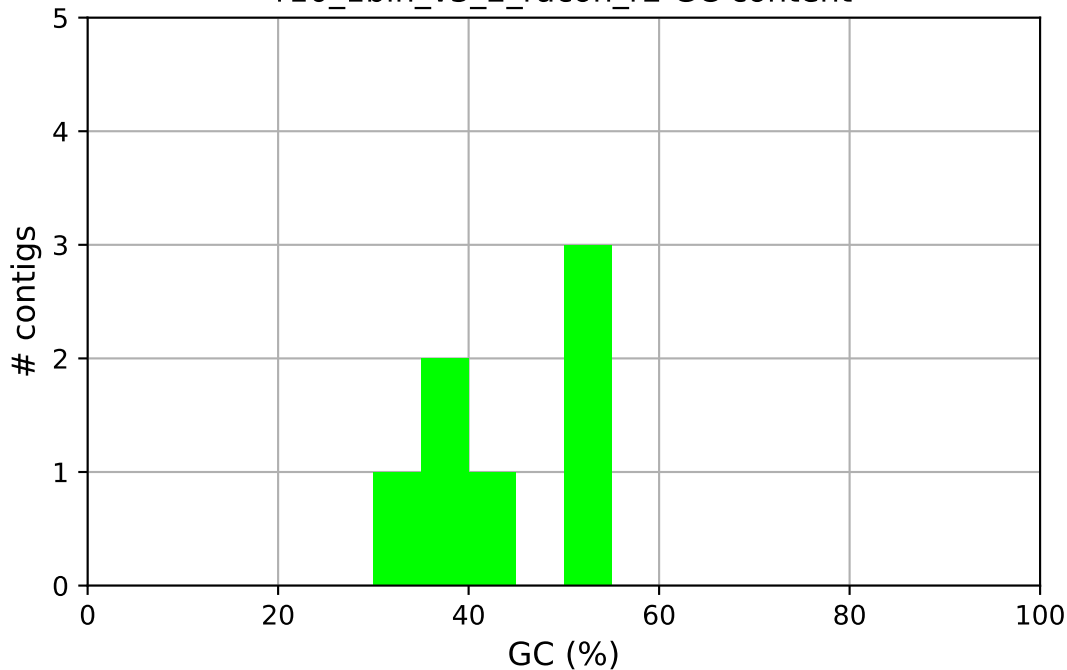
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1 GC content



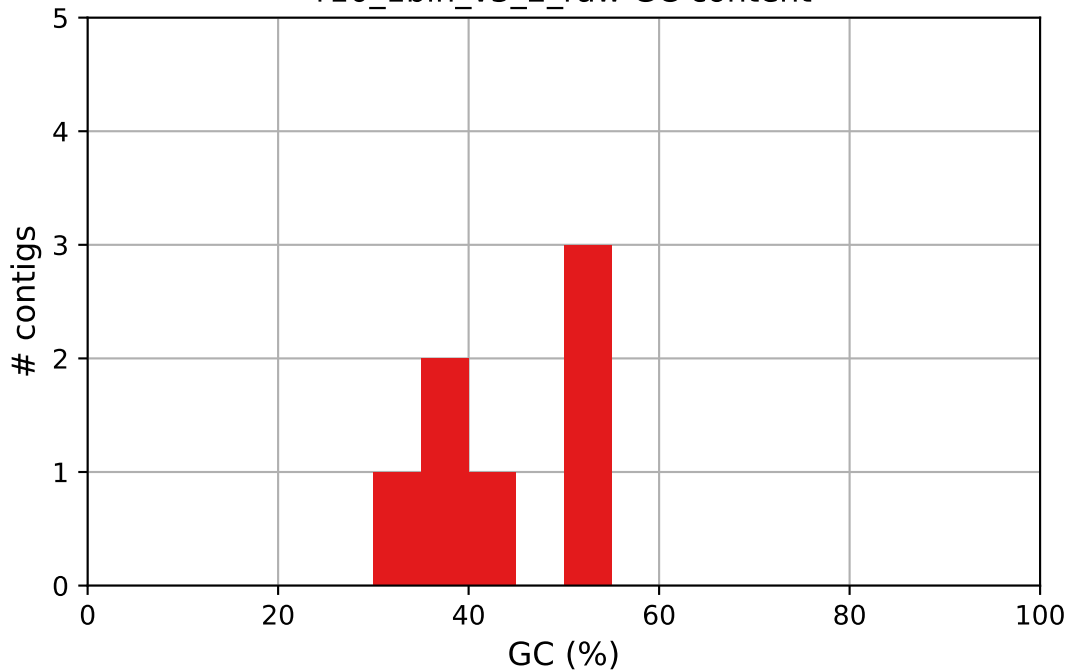
r10_1bin_v3_2_racon_r1

r10_1bin_v3_2_racon_r2 GC content



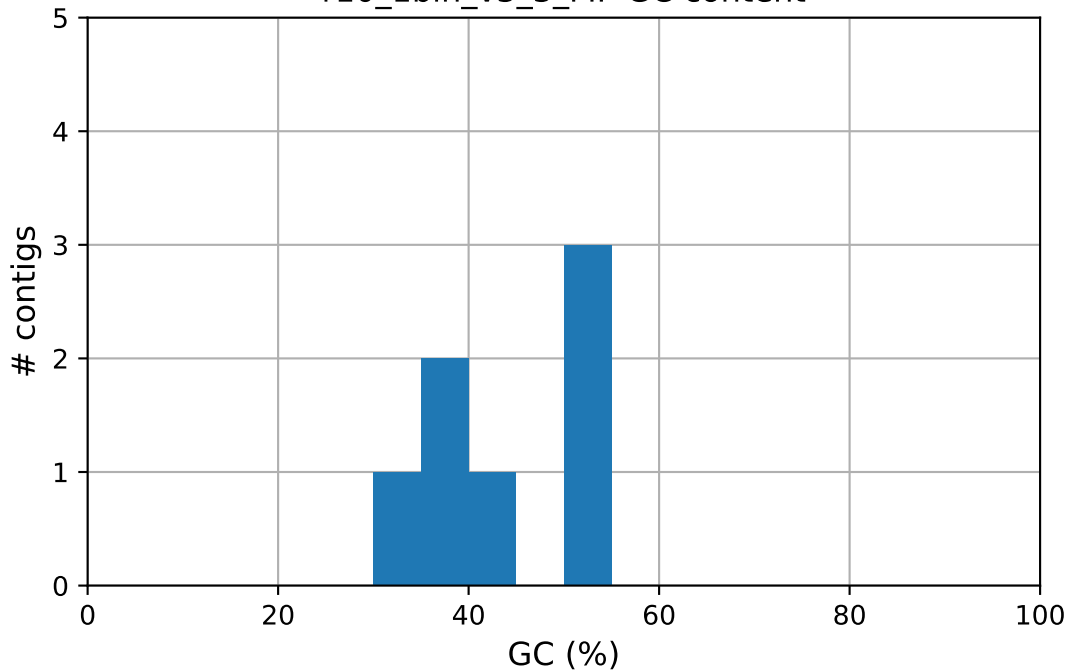
r10_1bin_v3_2_racon_r2

r10_1bin_v3_2_raw GC content



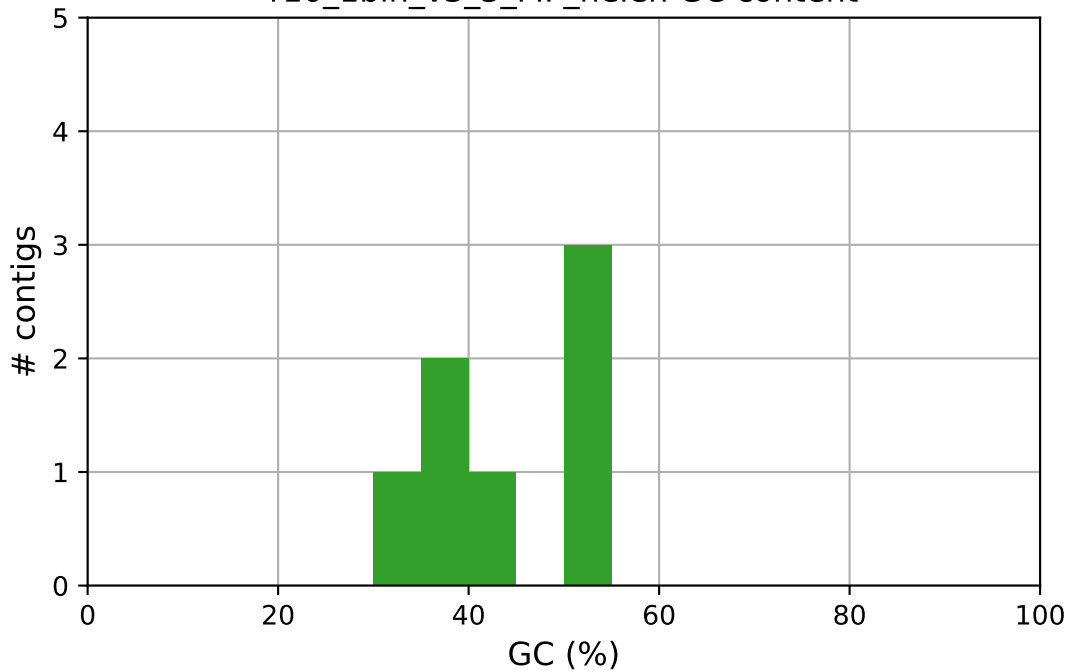
r10_1bin_v3_2_raw

r10_1bin_v3_3_MP GC content



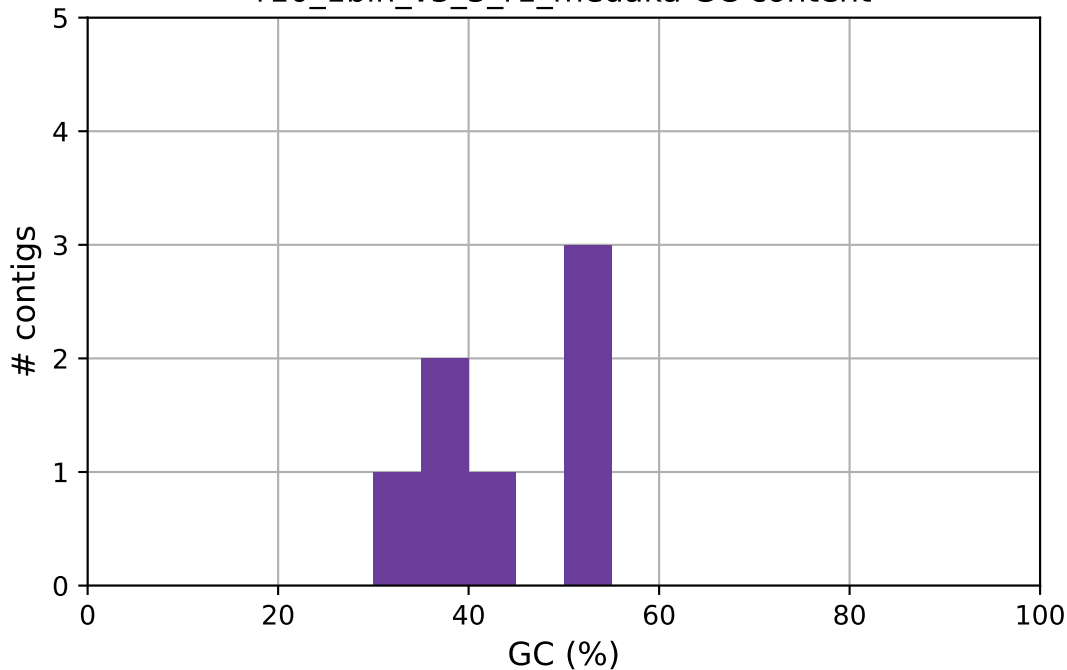
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen GC content



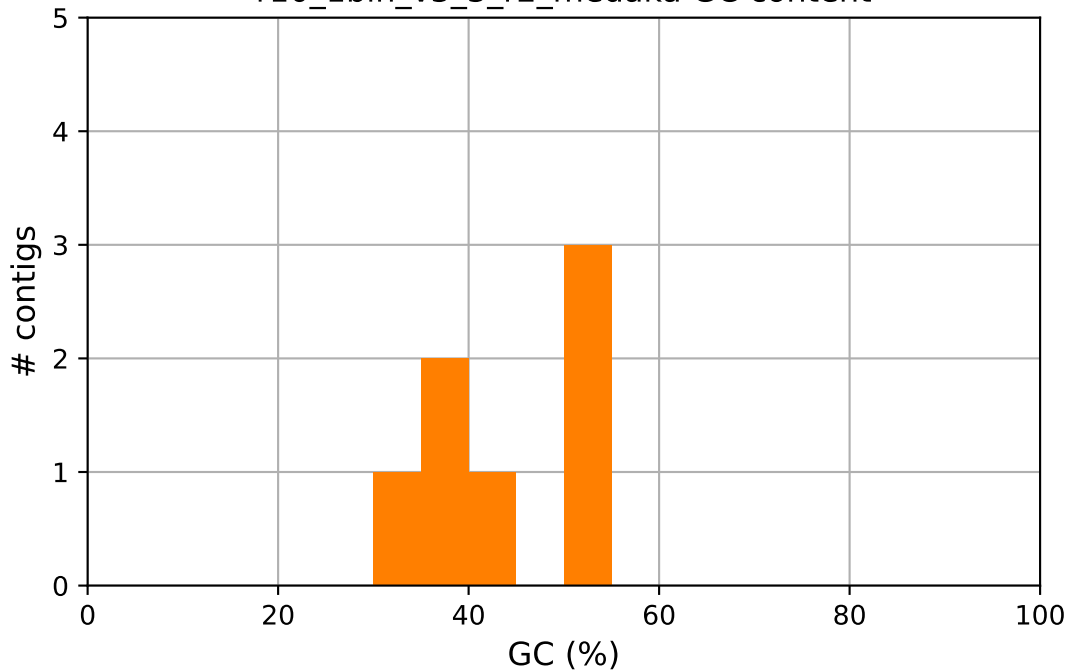
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka GC content



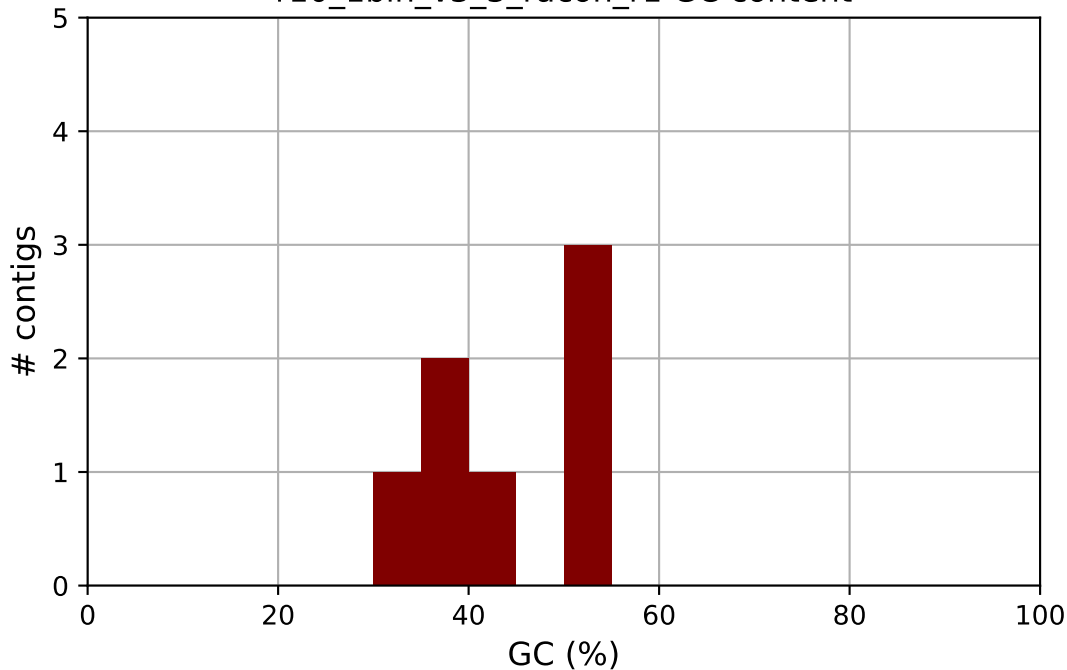
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka GC content



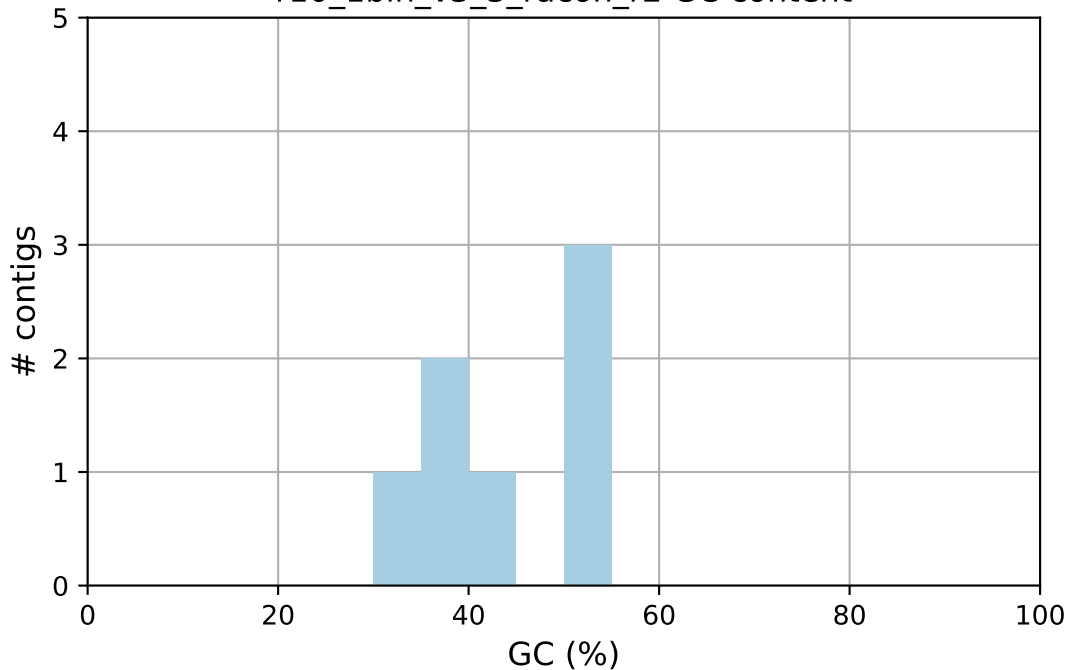
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1 GC content



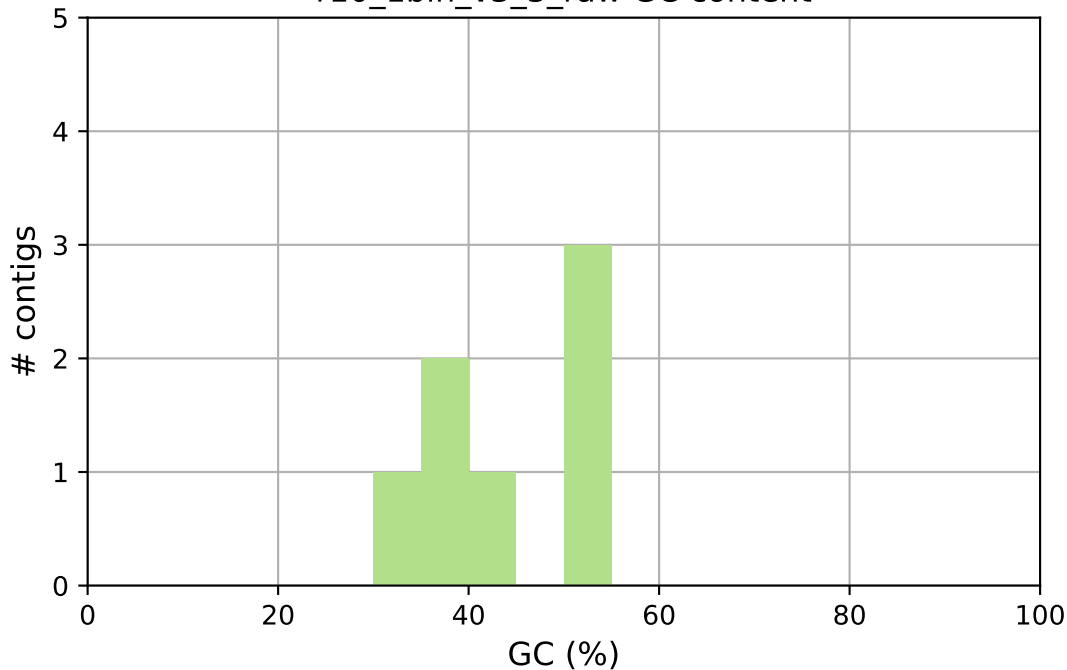
r10_1bin_v3_3_racon_r1

r10_1bin_v3_3_racon_r2 GC content



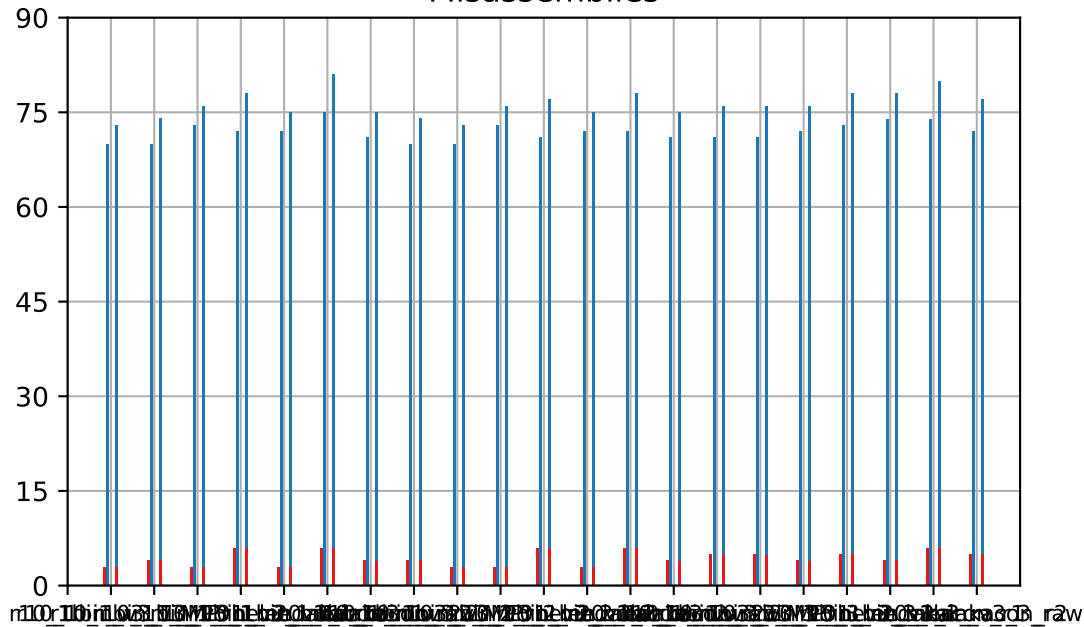
r10_1bin_v3_3_racon_r2

r10_1bin_v3_3_raw GC content

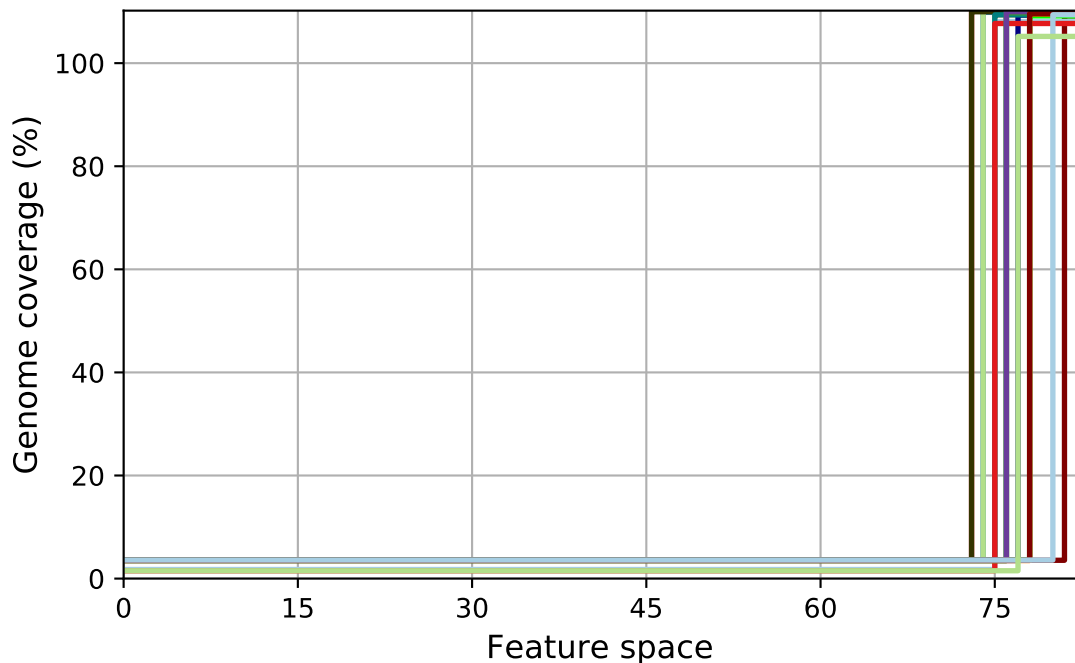


r10_1bin_v3_3_raw

Misassemblies



FRCurve (misassemblies)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

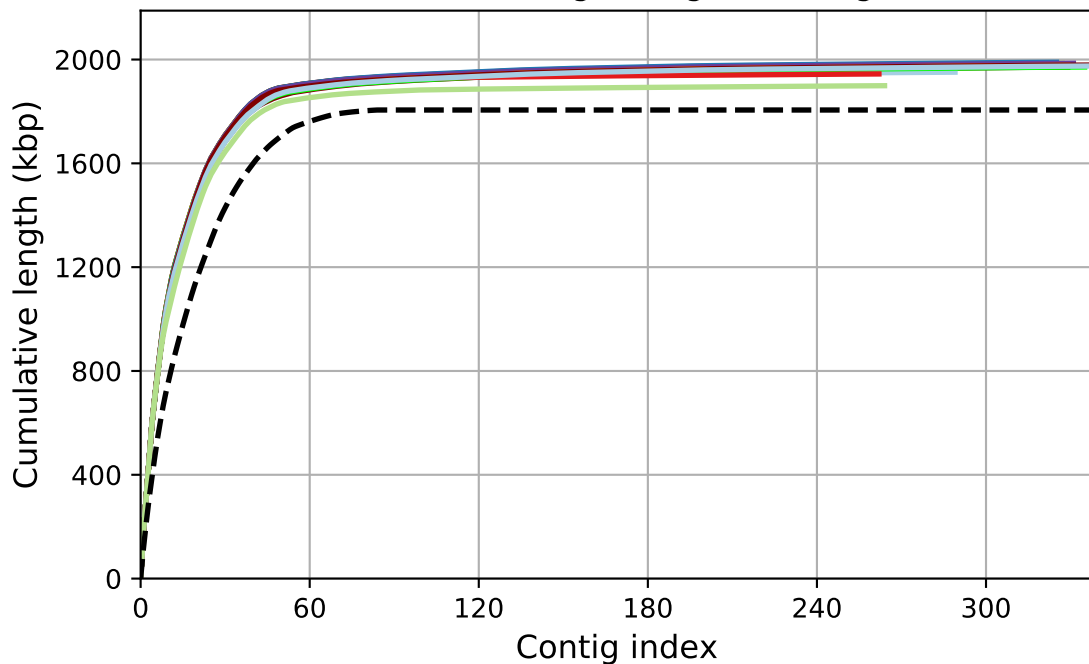
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1

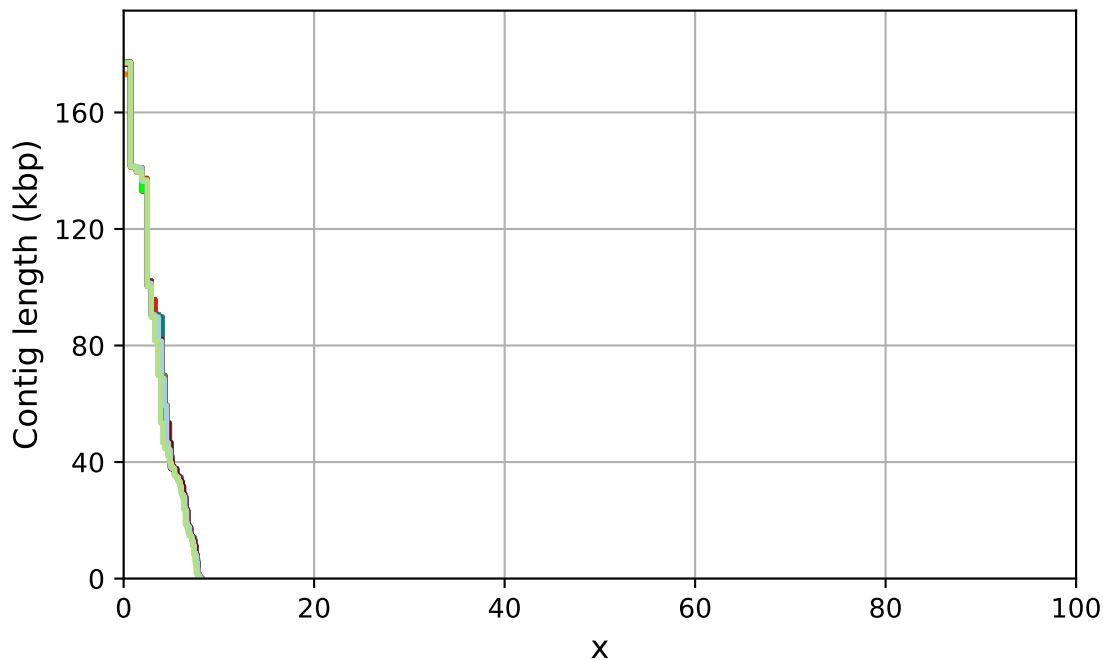
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1

NAx



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

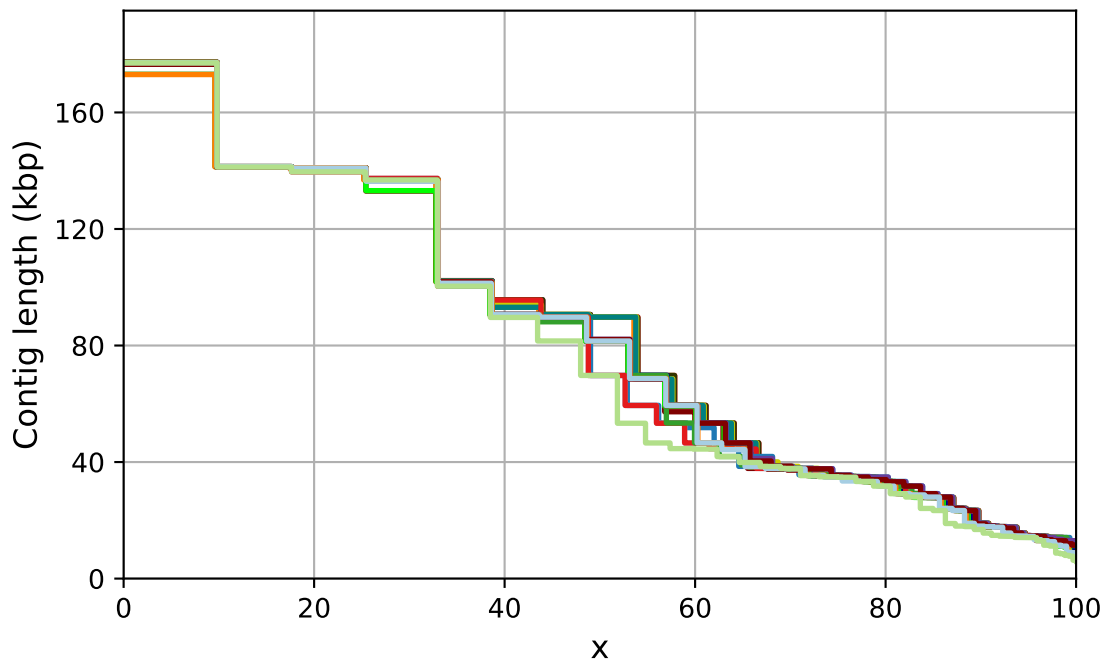
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

NGAx



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

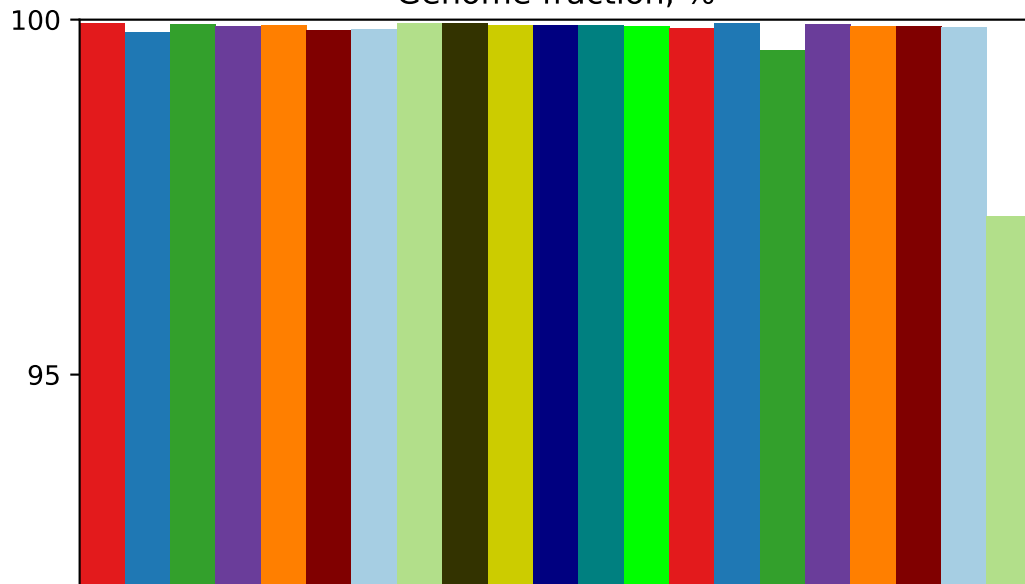
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Genome fraction, %



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka