

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	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
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 (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
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	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	
# 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	2719591	2717945	2719536	2719598	2720563	2720641	2718437	2719739	2717966	2721106	2721103	2720628	2720631	2718867	2719745	2717968	2721103	2721099	2720626	2720626	2718867
# local misassemblies	10	9	9	9	9	10	20	10	9	9	9	9	10	19	10	10	9	9	9	19	
# 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	0	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	5	6	6	6	6	6	6	4	6	6	6	6	6	5	
# 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	21275928	21272950	21273045	21264910	21266025	21257050	21319060	21274781	21272685	21274378	21265358	21264194	21256210	21320909	21278349	21272626	21277562	21270977	21266489	21258997	21323737
Genome fraction (%)	99.537	99.537	99.537	99.537	99.537	99.537	99.538	99.537	99.537	99.537	99.537	99.537	99.537	99.535	99.537	99.537	99.537	99.537	99.537	99.535	
Duplication ratio	1.046	1.045	1.046	1.046	1.044	1.046	1.024	1.046	1.045	1.046	1.046	1.045	1.046	1.024	1.046	1.045	1.046	1.046	1.045	1.024	
# 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	284.52	255.31	290.05	287.44	280.45	293.86	248.66	288.26	257.55	289.90	288.90	283.03	296.14	251.24	288.75	257.48	290.99	289.34	286.84	300.10	251.43
# indels per 100 kbp	110.54	43.60	76.44	77.74	110.36	115.03	160.01	112.30	42.51	107.63	106.77	113.05	112.26	164.98	112.38	42.66	107.74	107.18	113.31	113.23	164.94
Largest alignment	948792	948048	948662	948676	949040	949160	948372	948895	948103	949204	949208	949045	949146	948394	948893	948229	949204	949201	949045	949041	948394
Total aligned length	2796978	2795211	2796923	2796639	2792946	2797265	2739511	2797796	2796007	2798816	2798552	2794521	2797651	2738101	2797917	2796138	2799042	2798290	2795749	2798137	2738189
NGA50	480532	480263	480493	480504	480705	480678	480398	480548	480250	480736	480755	480648	480677	480377	480545	480253	480734	480738	480648	480670	480377
NGA75	381466	381231	381425	381443	381547	381611	381299	381468	381232	381656	381656	381577	381605	381350	381465	381231	381657	381659	381577	381586	381350
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	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	

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

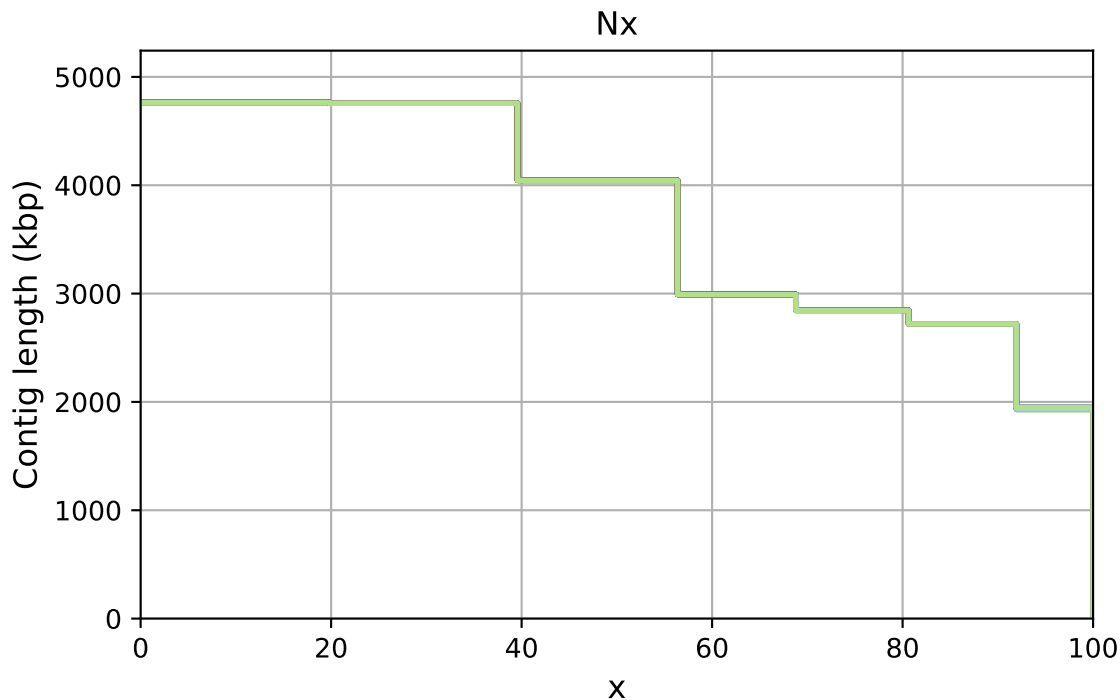
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	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	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# contig misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# 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	2719591	2717945	2719536	2719598	2720563	2720641	2718437	2719739	2717966	2721106	2721103	2720628	2720631	2718867	2719745	2717968	2721103	2721099	2720626	2720626	2718867
# 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	10	10	10	10	10	10	16	10	10	10	10	10	10	20	10	10	10	10	10	10	20
# local misassemblies	10	9	9	9	9	10	20	10	9	9	9	9	10	19	10	10	9	9	9	19	
# 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	26	26	26	26	26	26	24	26	26	26	26	26	26	21	26	26	26	26	26	26	21
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	4	6	6	6	6	6	6	5
# mismatches	7616	6834	7764	7694	7507	7866	6656	7716	6894	7760	7733	7576	7927	6725	7729	6892	7789	7745	7678	8033	6730
# indels	2959	1167	2046	2081	2954	3079	4283	3006	1138	2881	2858	3026	3005	4416	3008	1142	2884	2869	3033	3031	4415
# indels (<= 5 bp)	2885	1102	1995	2030	2901	3026	4223	2938	1075	2829	2807	2972	2953	4361	2940	1079	2831	2818	2978	2979	4360
# indels (> 5 bp)	74	65	51	51	53	53	60	68	63	52	51	54	52	55	68	63	53	51	55	52	55
Indels length	6902	4947	5387	5435	6737	6814	8400	6894	4917	6501	6447	6796	6711	8492	6892	4915	6512	6454	6810	6740	8491

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	21275928	21272950	21273045	21264910	21266025	21257050	21319060	21274781	21272685	21274378	21265358	21264194	21256210	21320909	21278349	21272626	21277562	21270977	21266489	21258997	21323737
# 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

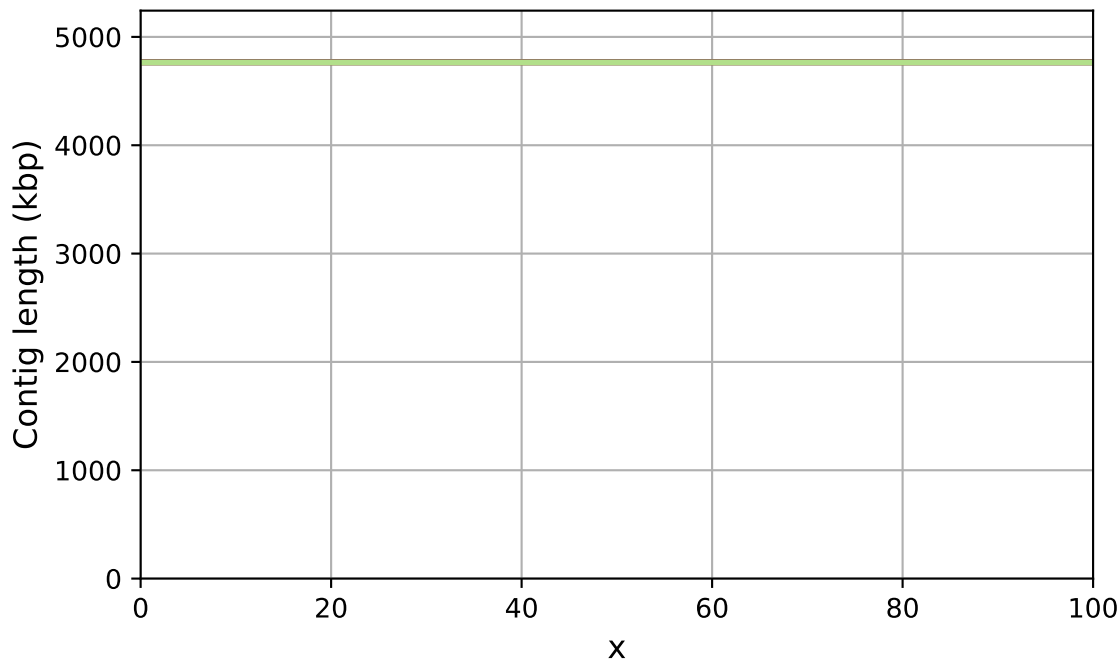
r10_1bin_v3_3_MP

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

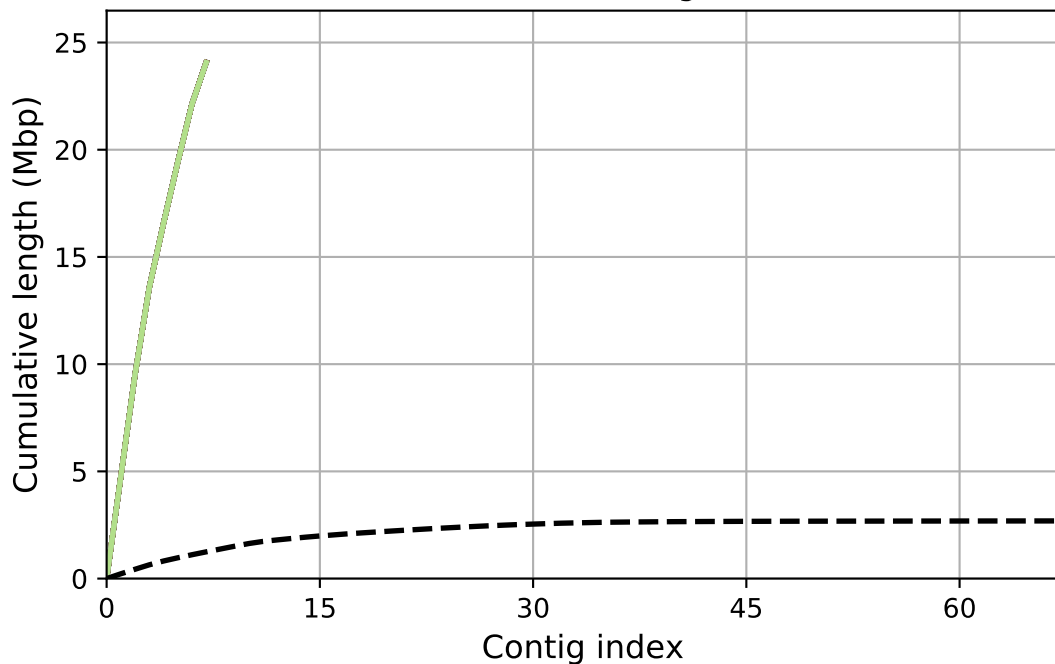
r10_1bin_v3_3_r1_medaka

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_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

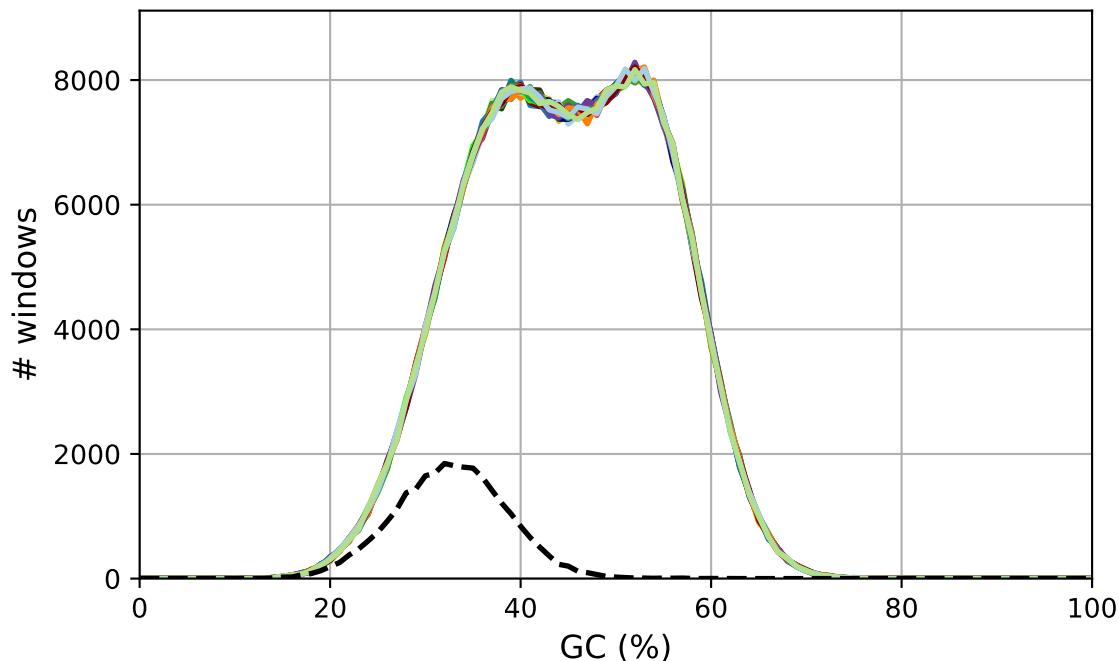
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1

GC content



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

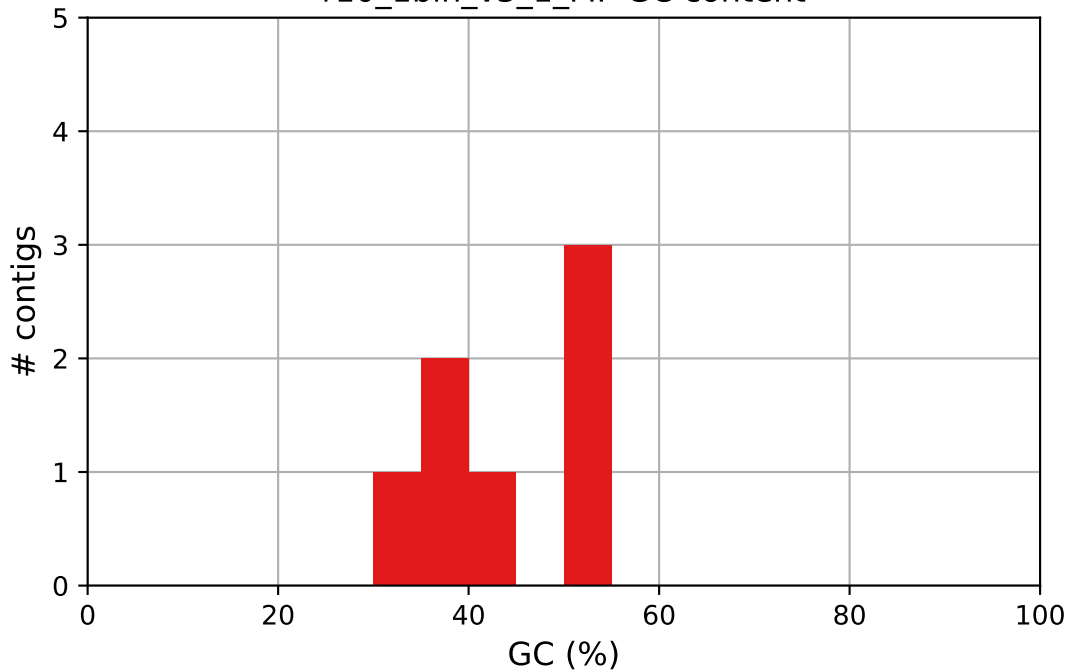
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

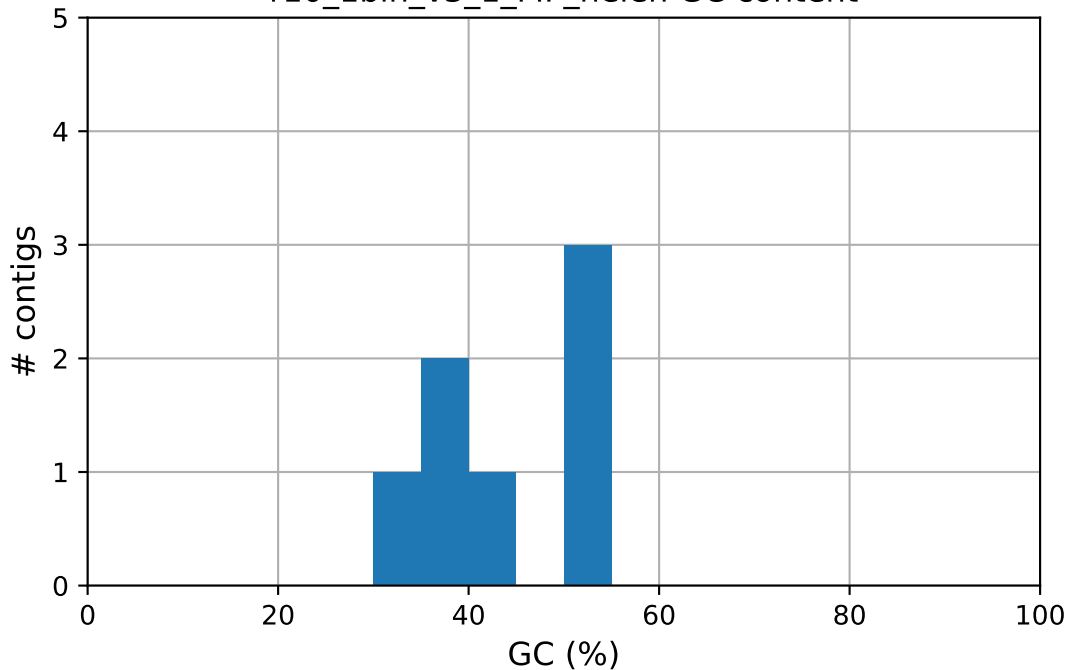
r10_1bin_v3_3_racon_r1

r10_1bin_v3_1_MP GC content



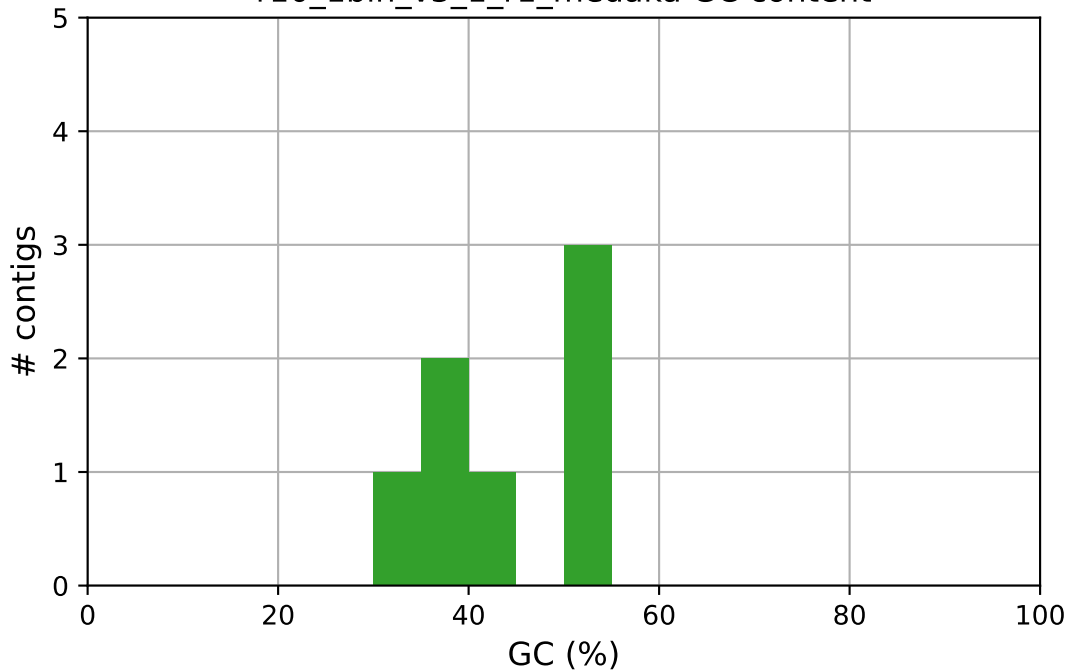
r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen GC content



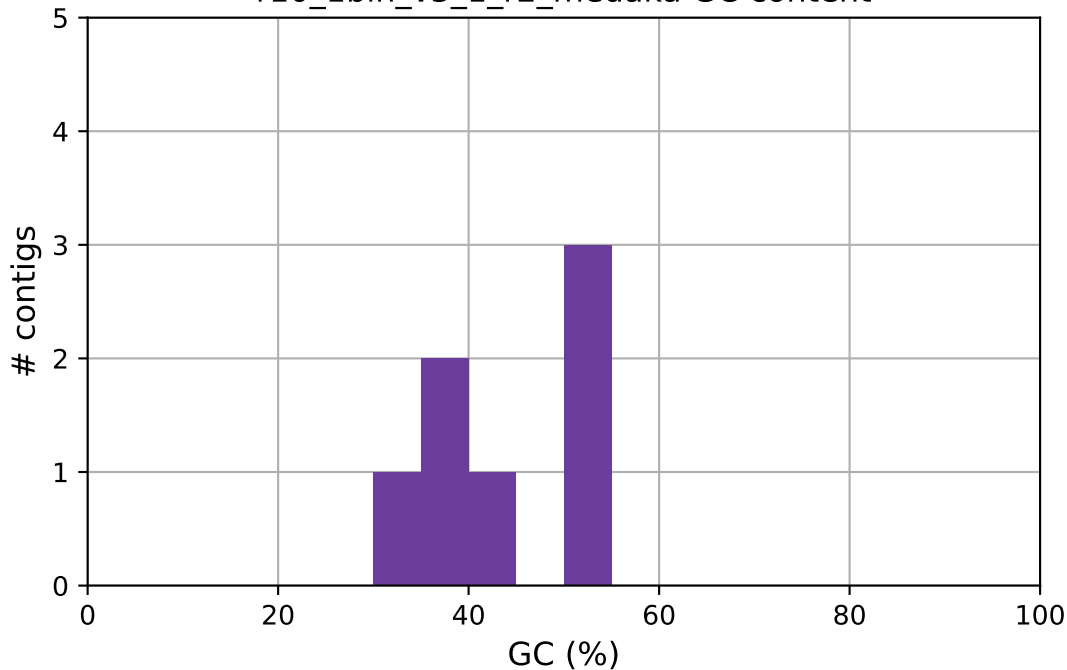
r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka GC content



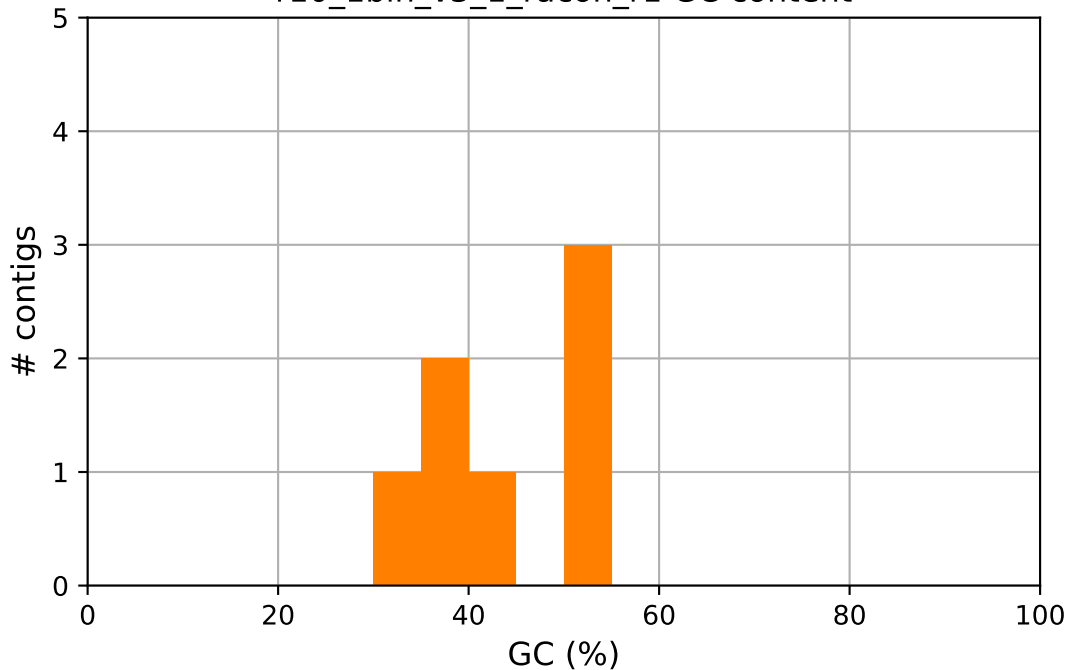
r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka GC content



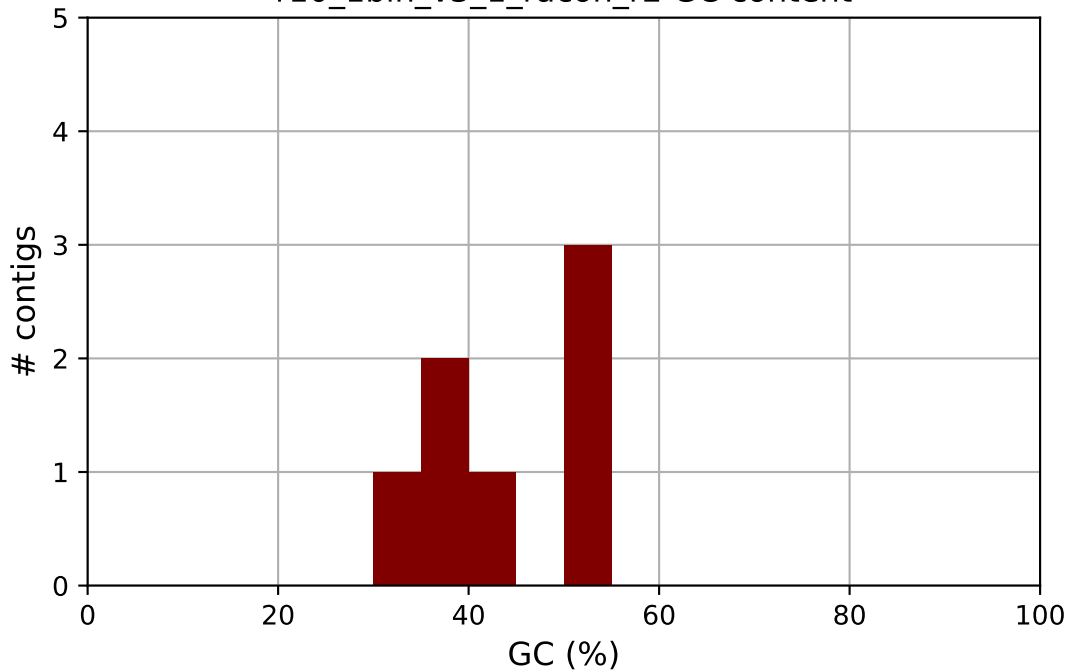
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_1_racon_r1 GC content



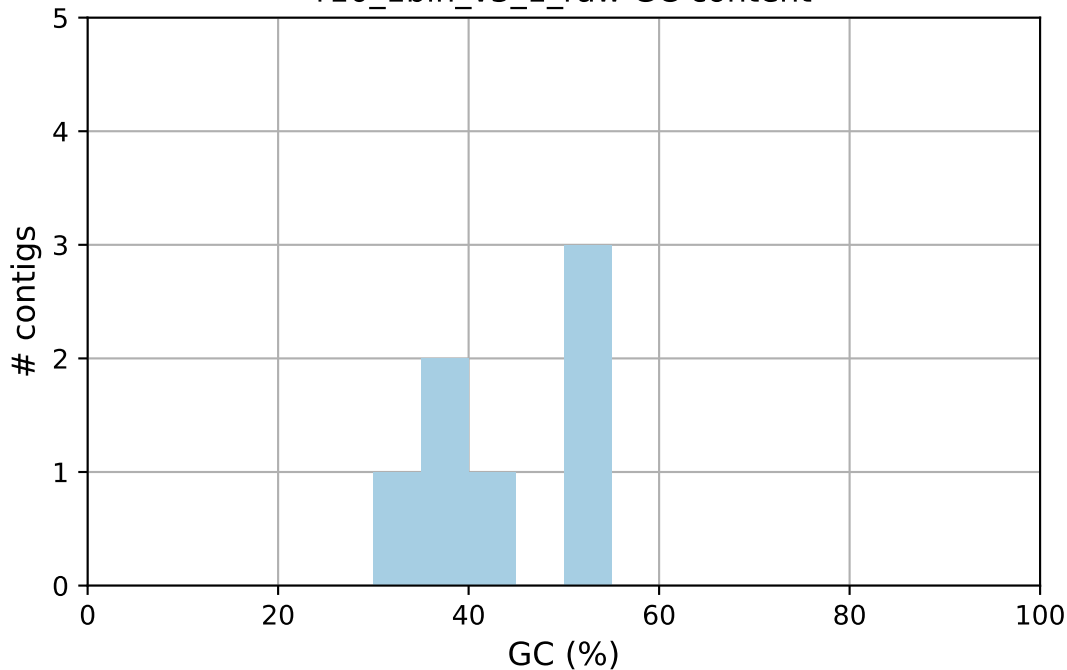
r10_1bin_v3_1_racon_r1

r10_1bin_v3_1_racon_r2 GC content



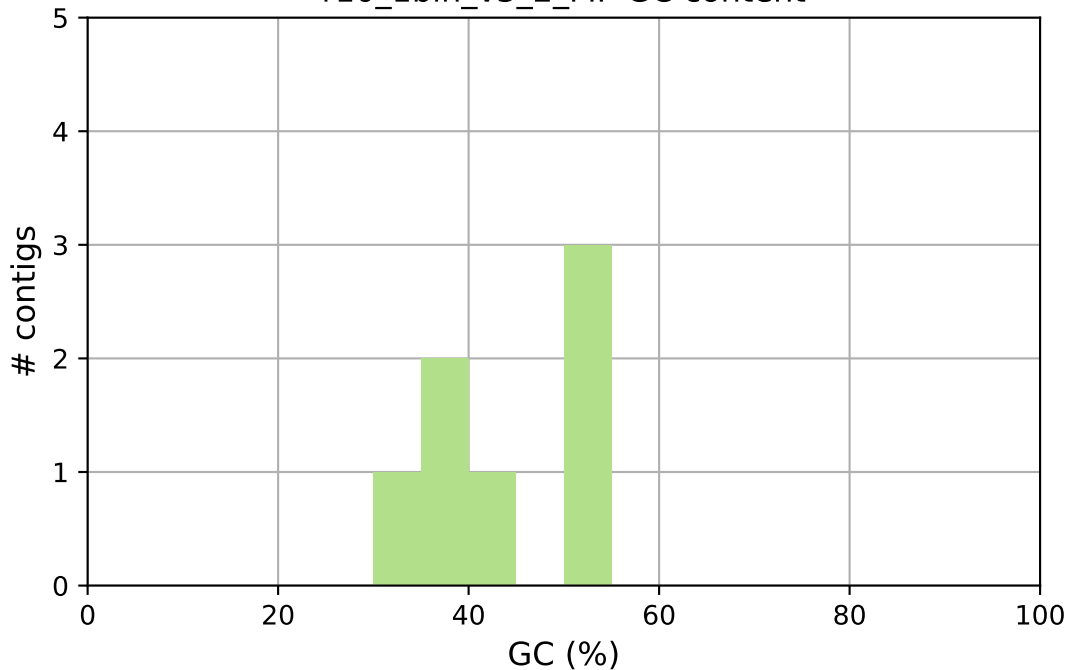
r10_1bin_v3_1_racon_r2

r10_1bin_v3_1_raw GC content



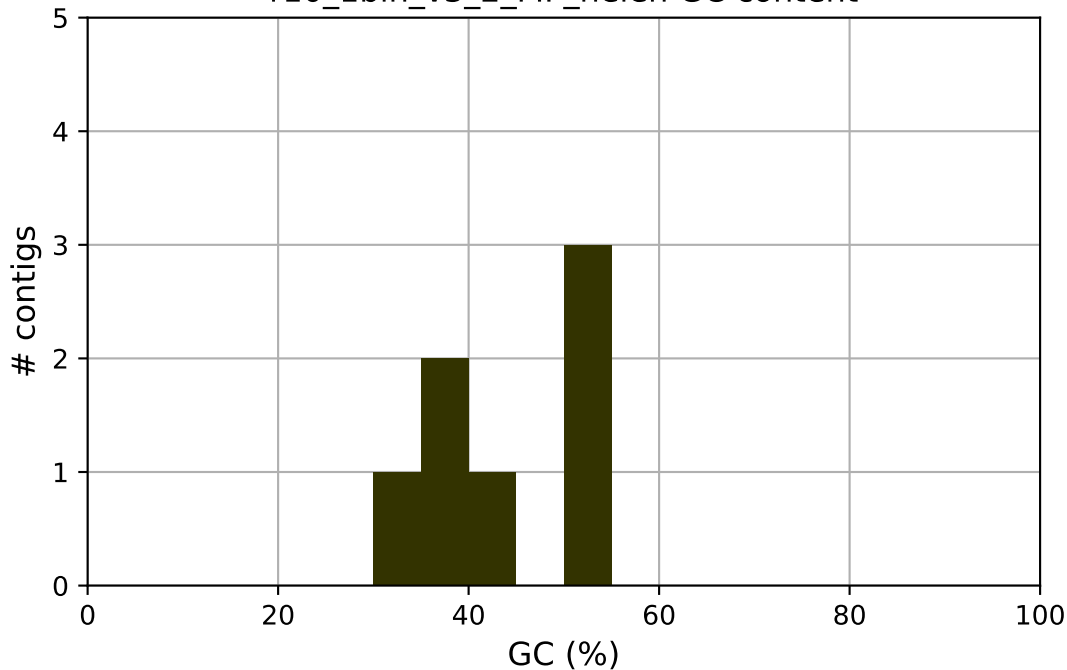
r10_1bin_v3_1_raw

r10_1bin_v3_2_MP GC content



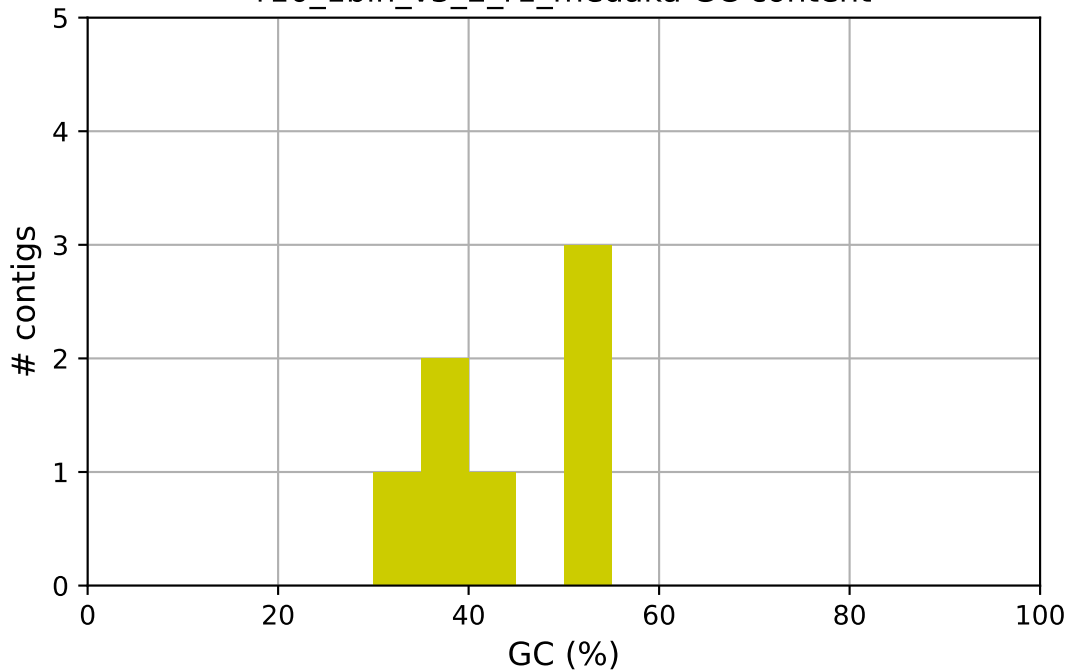
r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen GC content



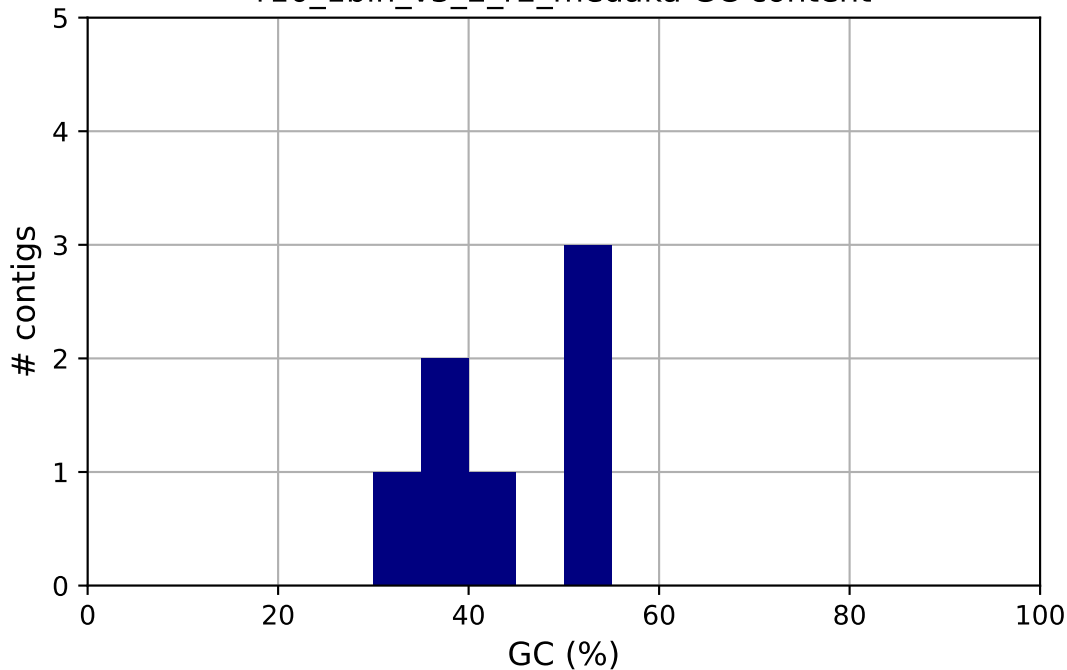
r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka GC content



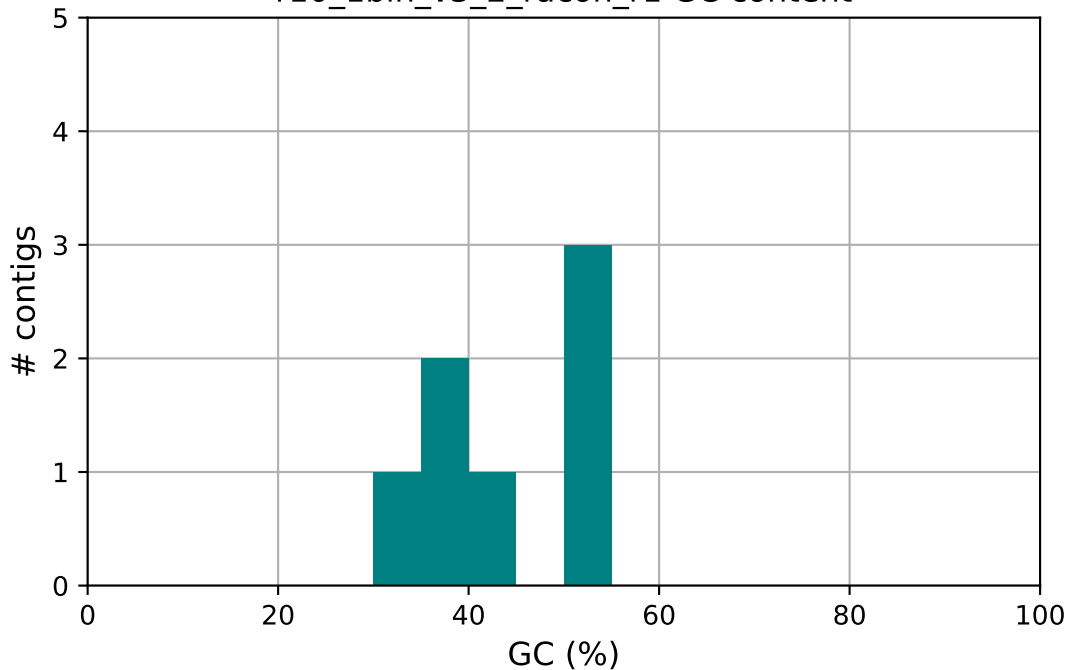
r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka GC content



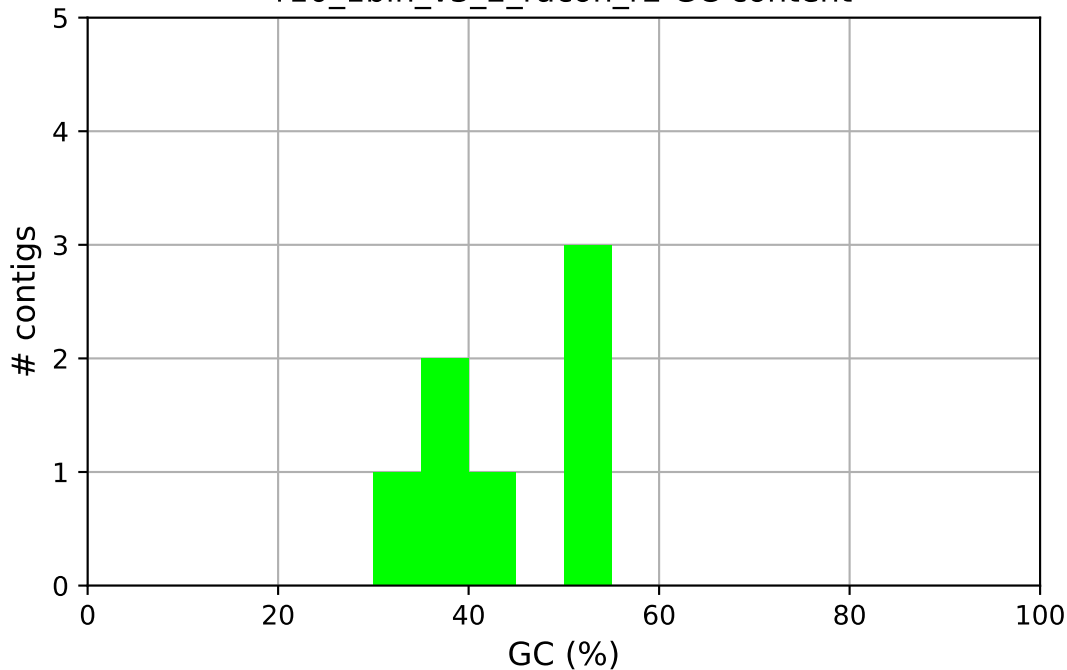
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1 GC content



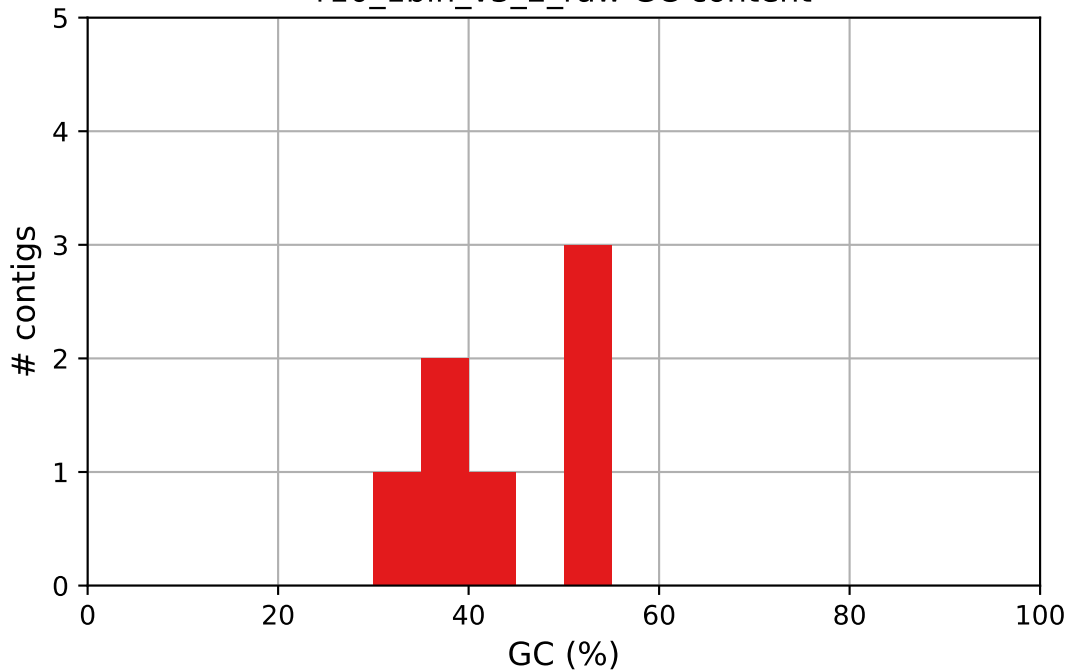
r10_1bin_v3_2_racon_r1

r10_1bin_v3_2_racon_r2 GC content



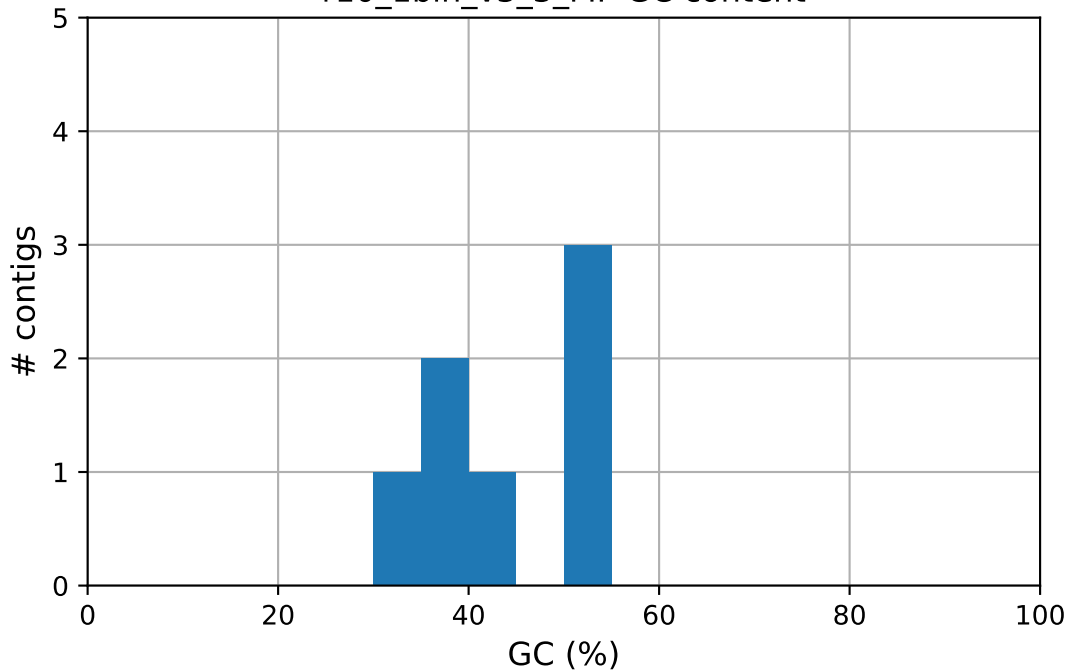
r10_1bin_v3_2_racon_r2

r10_1bin_v3_2_raw GC content



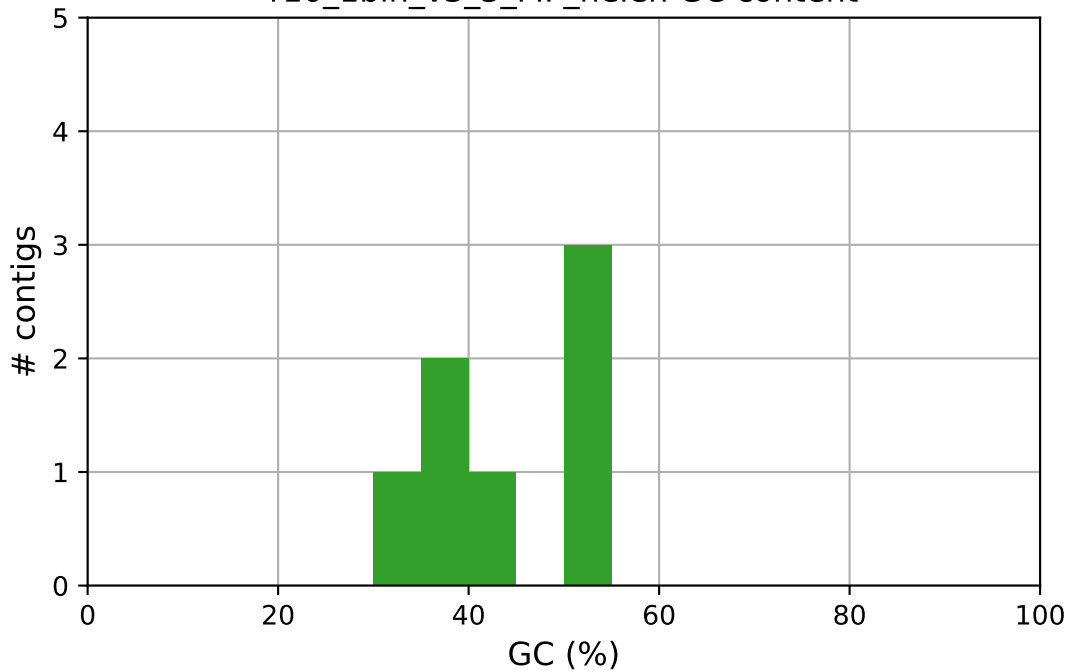
r10_1bin_v3_2_raw

r10_1bin_v3_3_MP GC content



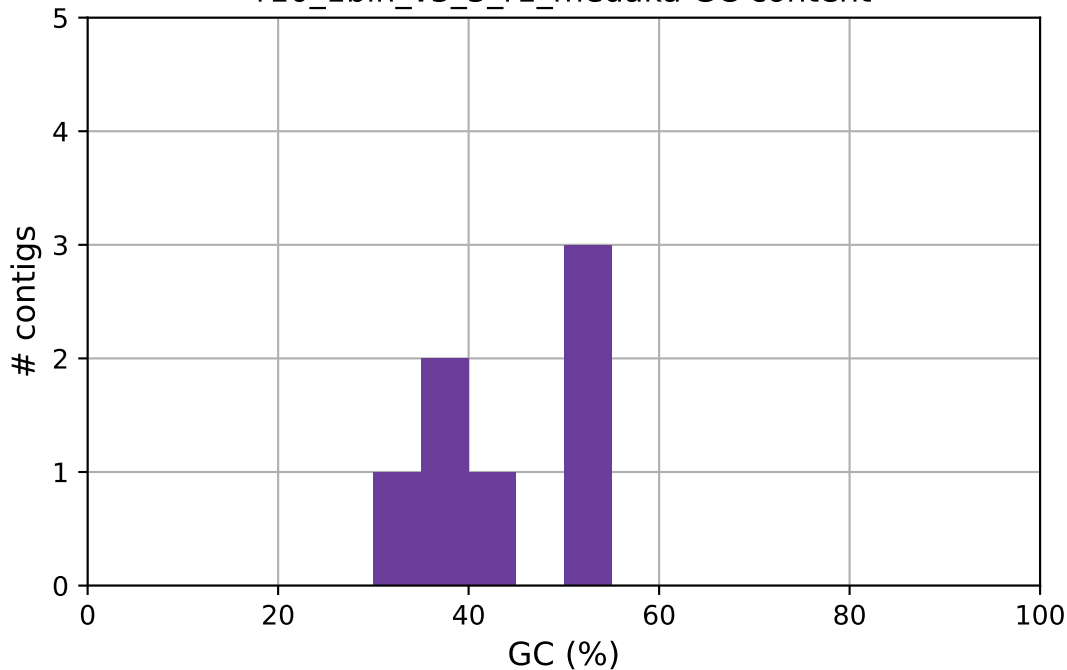
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen GC content



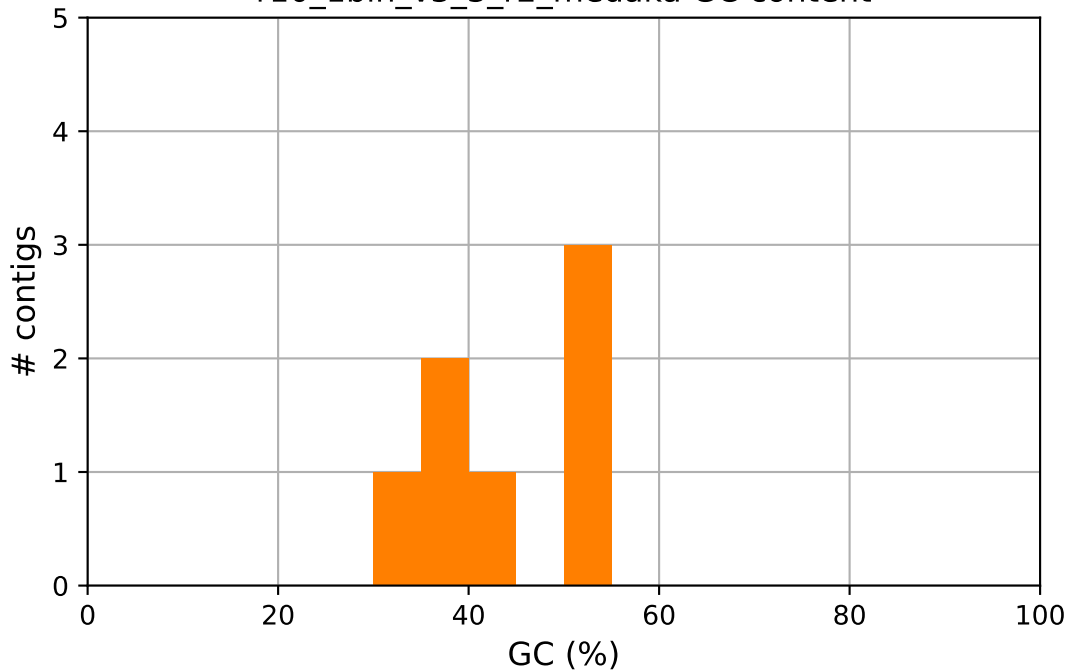
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka GC content



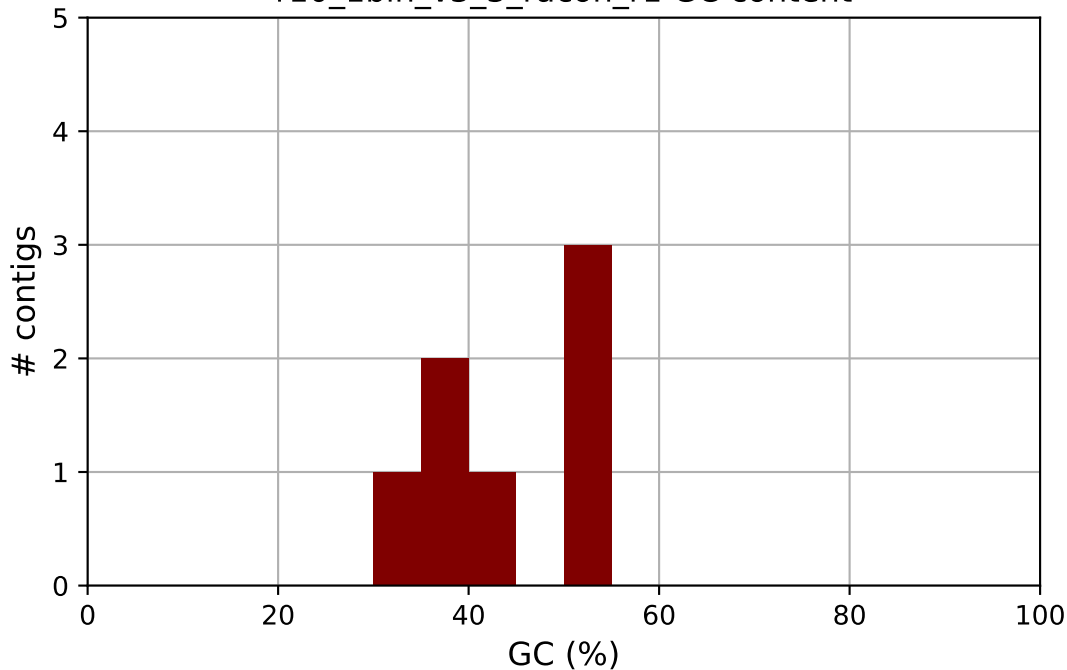
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka GC content



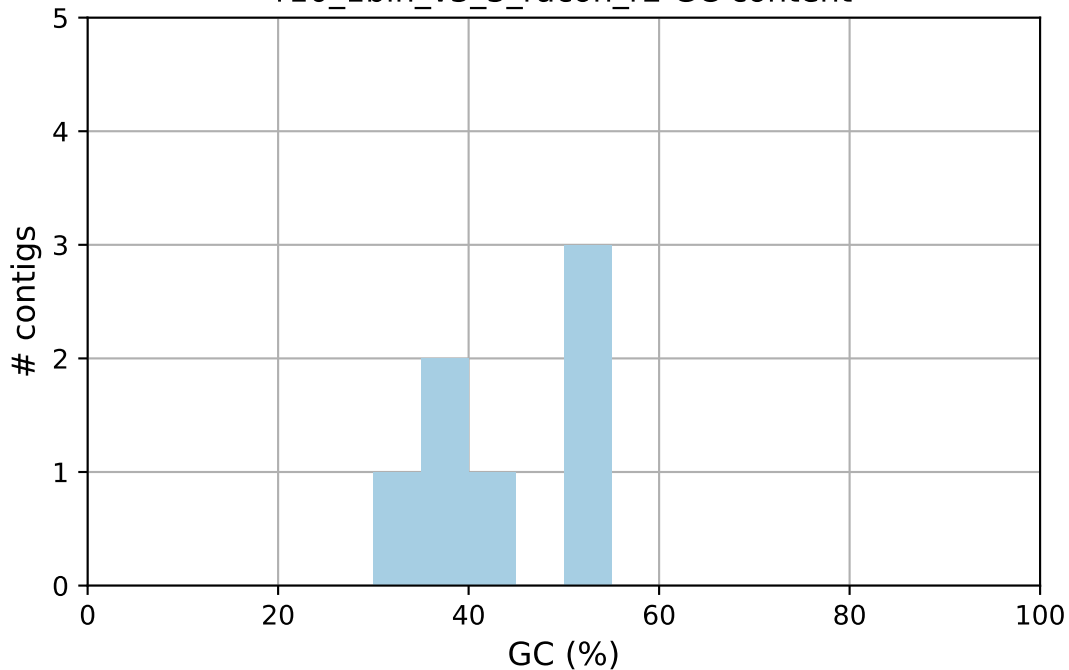
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1 GC content



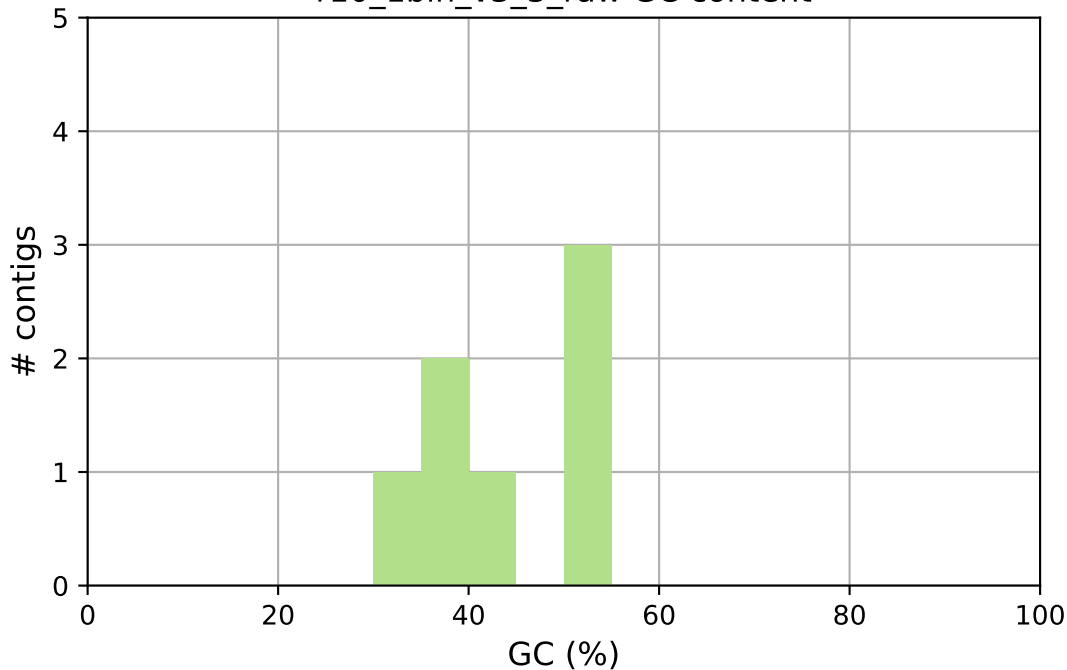
r10_1bin_v3_3_racon_r1

r10_1bin_v3_3_racon_r2 GC content



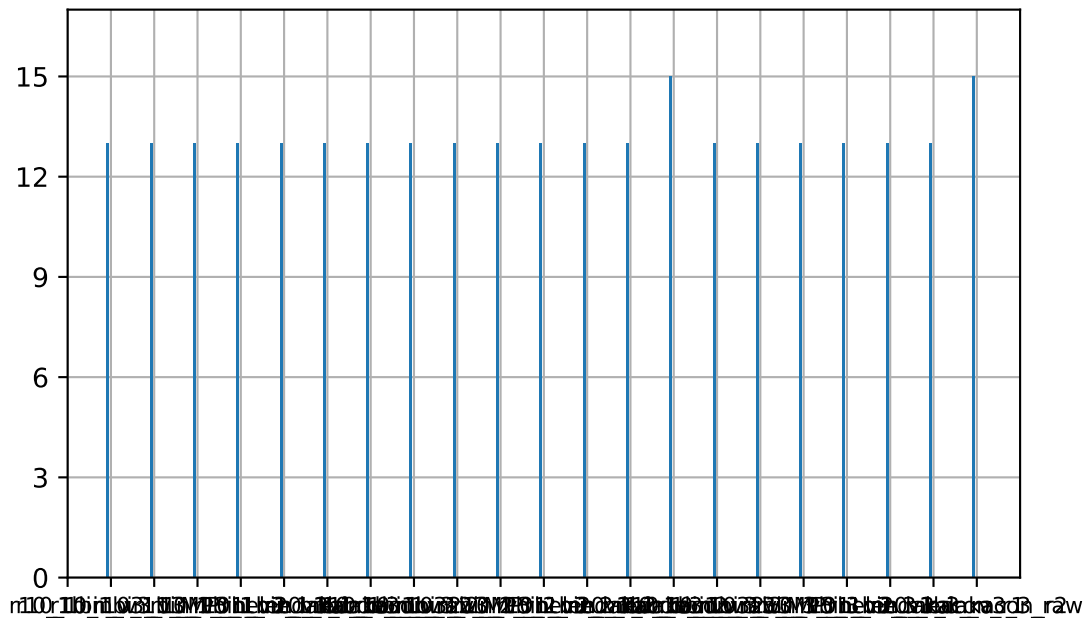
r10_1bin_v3_3_racon_r2

r10_1bin_v3_3_raw GC content



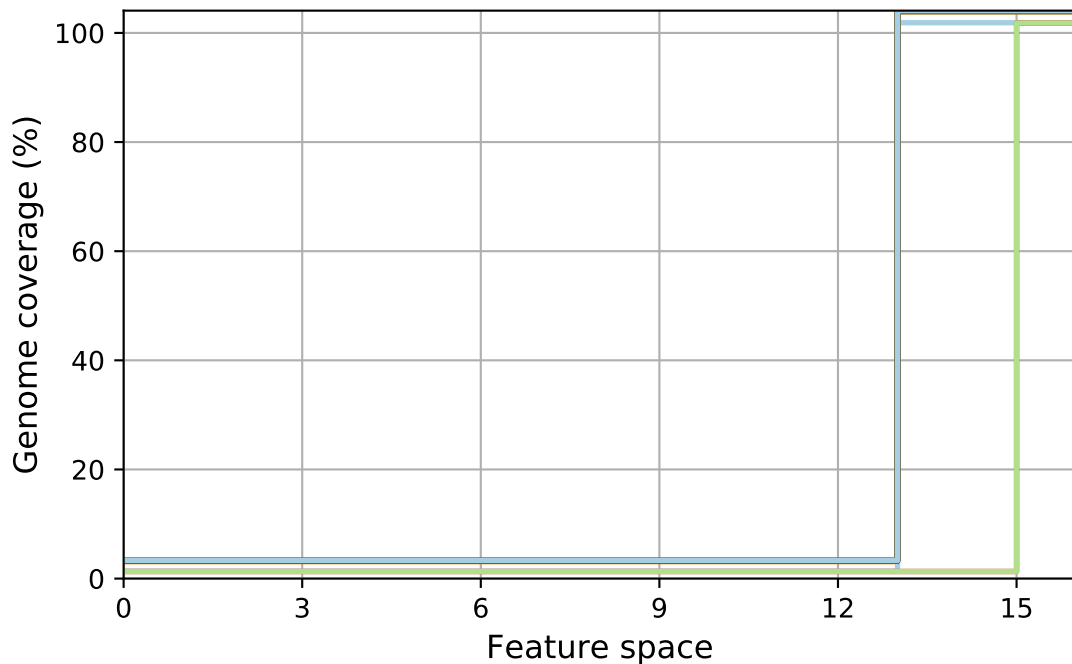
r10_1bin_v3_3_raw

Misassemblies



translocations

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

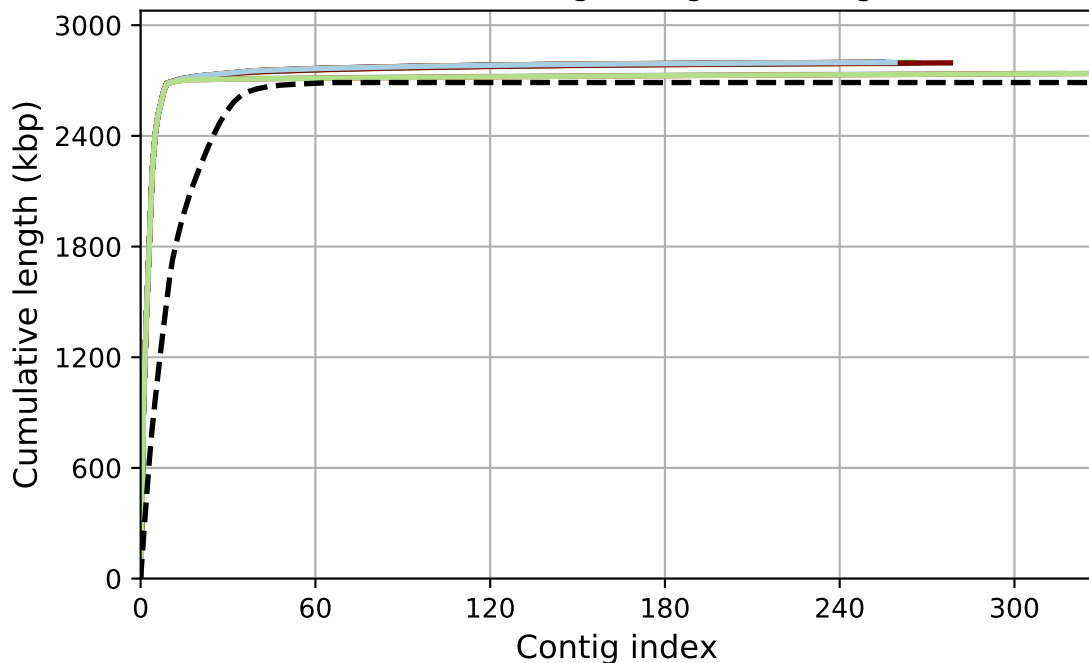
r10_1bin_v3_3_MP

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_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

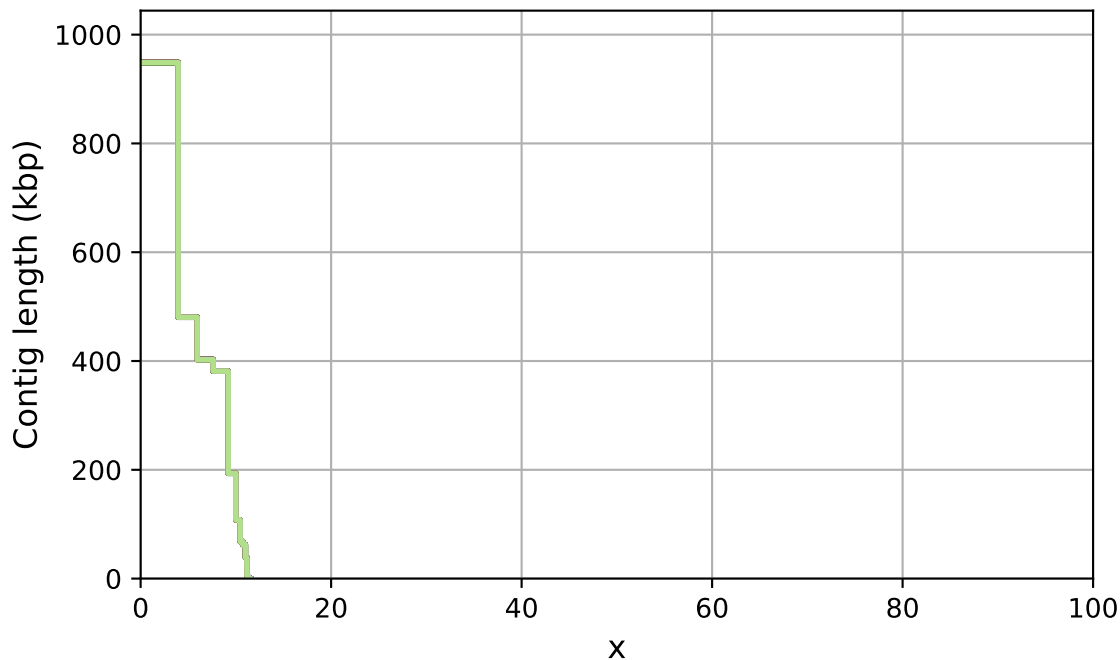
r10_1bin_v3_3_r2_m

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_racon_r1

r10_1bin_v3_3_rac

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

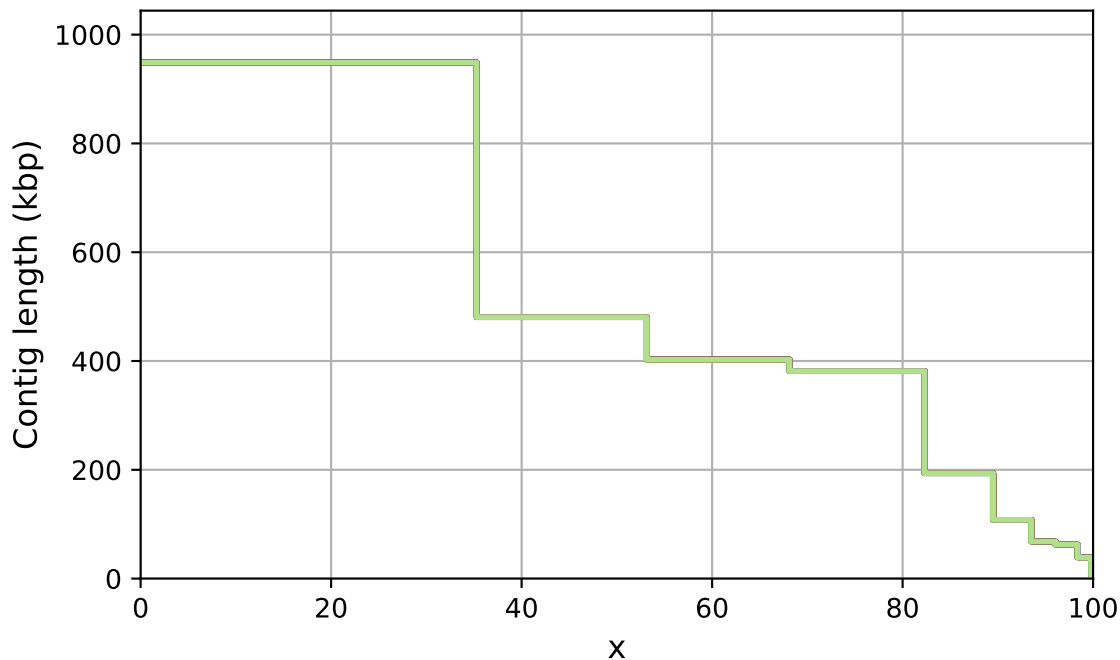
r10_1bin_v3_3_MP

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

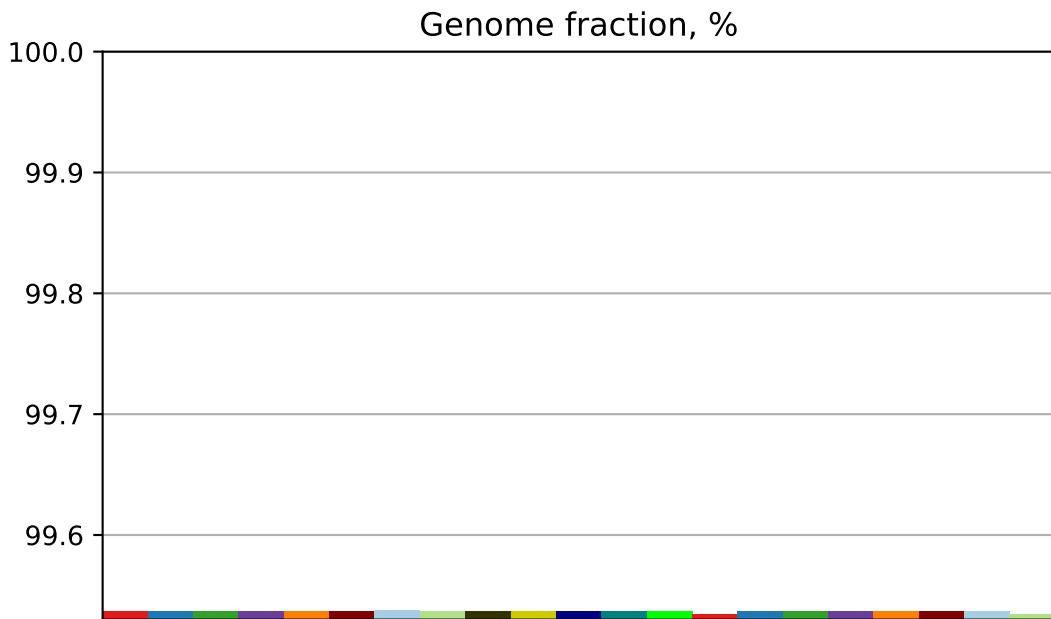
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka



r10_1bin_v3_1_MP

r10 1bin v3 1 MP helen

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r10 1bin v3 1 r1 medaka
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■ r10_1bin_v3_2_MP

■ r10 1bin v3 2 MP helen

■ r10 1bin v3 2 r1 medaka

■ r10_1bin_v3_3_MP

■ r10 1bin v3 3 MP

■ r10 1bin v3 3 r1