

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)	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)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
Total length	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061619
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	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	44.78	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	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	4043031
NG50	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
N75	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857
NG75	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
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	13	13	13	13	13	13	14	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# 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	2719957	2718112	2719591	2719604	2720370	2720447	2718870	2719959	2718085	2719577	2719610	2720473	2720445	2718867	2719961	2718084	2719576	2719620	2720476	2720441	2718867
# local misassemblies	9	9	9	9	10	9	19	9	10	10	9	9	9	19	9	9	9	9	10	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
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	4
# 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	21275494	21272822	21273068	21262531	21264862	21254585	21320528	21275005	21273170	21274232	21263132	21264831	21254957	21320663	21274902	21272670	21274358	21263748	21262681	21254198	21320562
Genome fraction (%)	99.537	99.537	99.537	99.537	99.537	99.537	99.535	99.537	99.537	99.537	99.537	99.537	99.537	99.542	99.537	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	1.046	1.045	1.046	1.045	1.045	1.046	1.045	1.024
# 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	288.63	256.69	291.21	291.62	277.76	295.88	253.15	289.79	257.48	285.61	287.21	283.48	300.29	255.56	289.60	257.36	285.20	289.49	288.67	300.25	255.09
# indels per 100 kbp	111.67	41.65	76.62	77.15	109.61	109.91	164.87	112.52	41.95	77.00	77.56	111.67	111.25	166.01	112.26	41.58	76.85	77.22	112.34	110.13	165.91
Largest alignment	948835	948132	948683	948668	949071	948990	948394	948834	948258	948799	948659	948996	948996	948394	948836	948131	948671	948663	949124	948985	948394
Total aligned length	2797990	2796149	2797764	2797760	2793471	2797697	2739551	2798005	2796255	2796726	2797140	2794814	2798484	2739395	2798007	2796126	2796557	2797565	2796024	2798087	2739134
NGA50	480571	480265	480496	480503	480646	480631	480377	480571	480269	480494	480494	480646	480604	480377	480564	480259	480494	480503	480646	480612	480377
NGA75	381480	381241	381438	381432	381547	381568	381359	381488	381239	381431	381442	381560	381561	381350	381498	381244	381432	381444	381560	381565	381350
LGA50	2	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	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

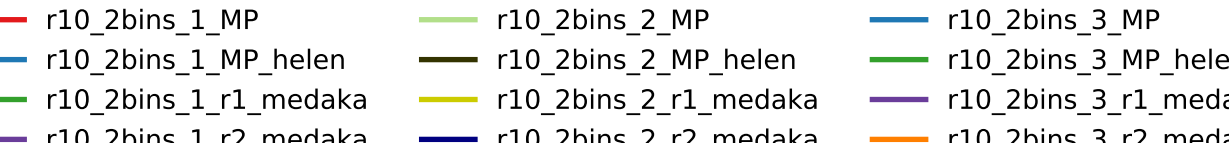
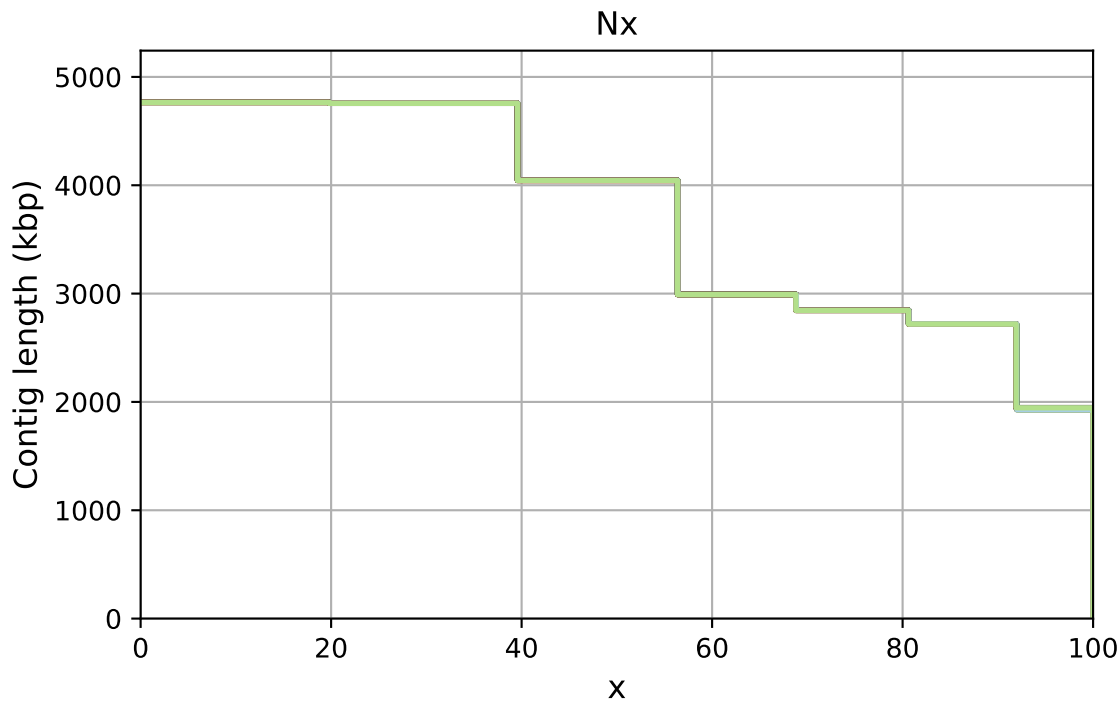
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# misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# contig misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	13	15	13	13	13	13	13	13	15
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	13	13	13	13	13	13	14	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	2719957	2718112	2719591	2719604	2720370	2720447	2718870	2719959	2718085	2719577	2719610	2720473	2720445	2718867	2719961	2718084	2719576	2719620	2720476	2720441	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	18	10	10	10	10	10	10	20	10	10	10	10	10	10	20
# local misassemblies	9	9	9	9	10	9	19	9	10	10	9	9	9	19	9	9	9	9	10	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	22	26	26	26	26	26	26	22	26	26	26	26	26	26	21
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	4
# mismatches	7726	6871	7795	7806	7435	7920	6776	7757	6892	7645	7688	7588	8038	6841	7752	6889	7634	7749	7727	8037	6828
# indels	2989	1115	2051	2065	2934	2942	4413	3012	1123	2061	2076	2989	2978	4444	3005	1113	2057	2067	3007	2948	4441
# indels (<= 5 bp)	2926	1057	2000	2014	2881	2890	4358	2949	1063	2010	2025	2937	2927	4389	2941	1052	2006	2015	2955	2895	4386
# indels (> 5 bp)	63	58	51	51	53	52	55	63	60	51	51	52	51	55	64	61	51	52	52	53	55
Indels length	6767	4779	5365	5395	6654	6631	8482	6791	4812	5404	5425	6769	6670	8526	6787	4808	5400	5422	6789	6652	8523

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).

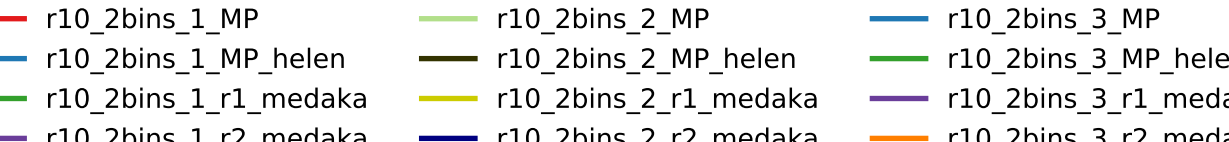
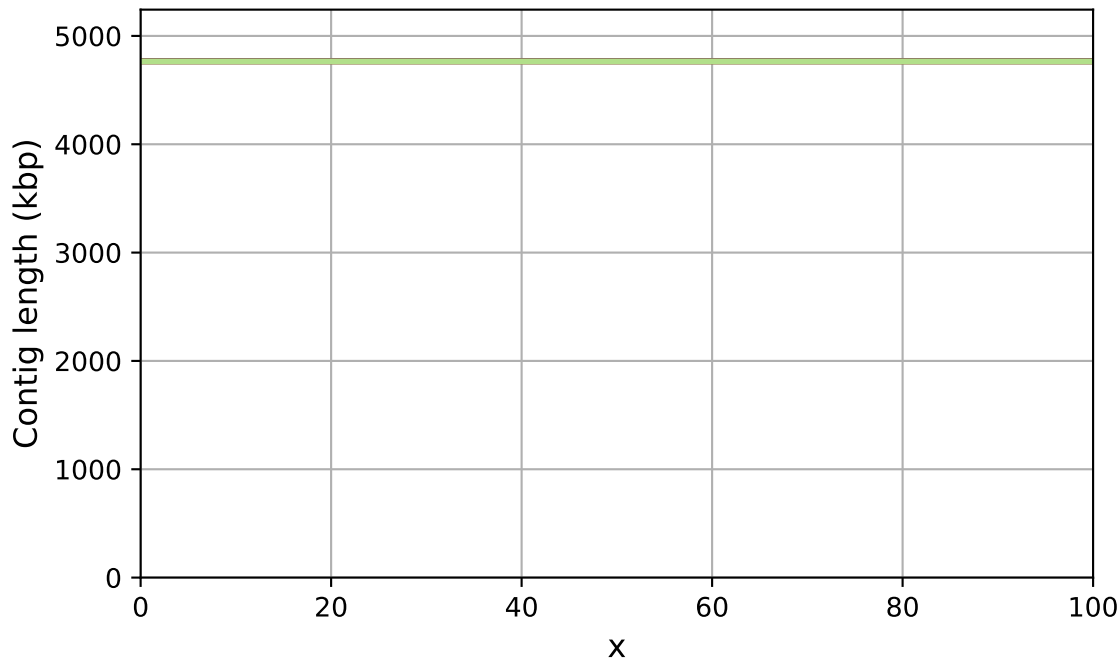
Unaligned report

	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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21275494	21272822	21273068	21262531	21264862	21254585	21320528	21275005	21273170	21274232	21263132	21264831	21254957	21320663	21274902	21272670	21274358	21263748	21262681	21254198	21320562
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

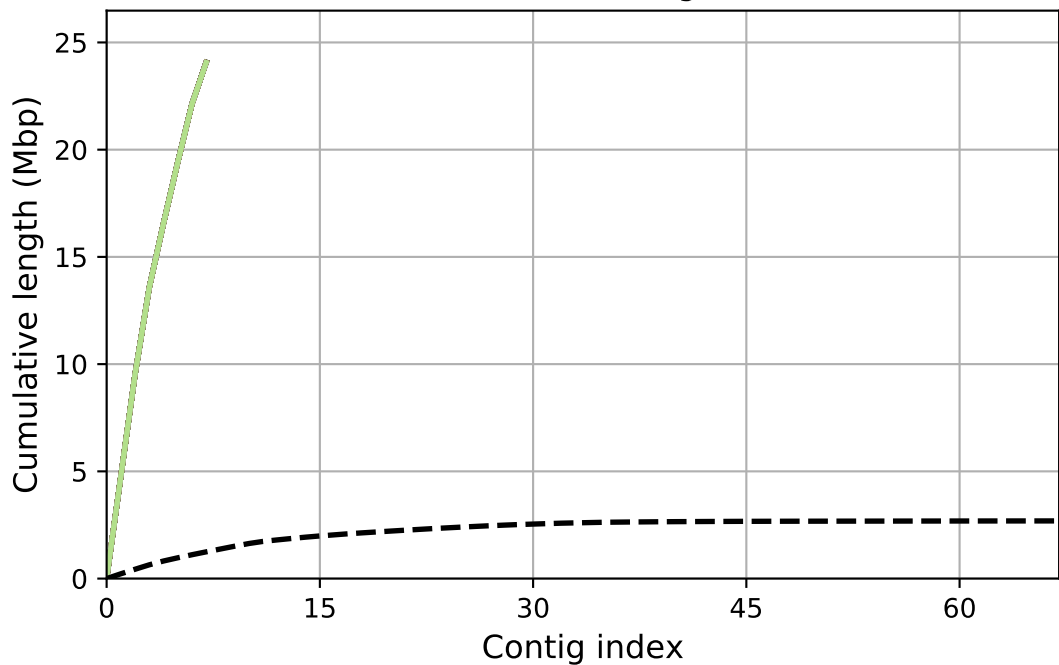
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

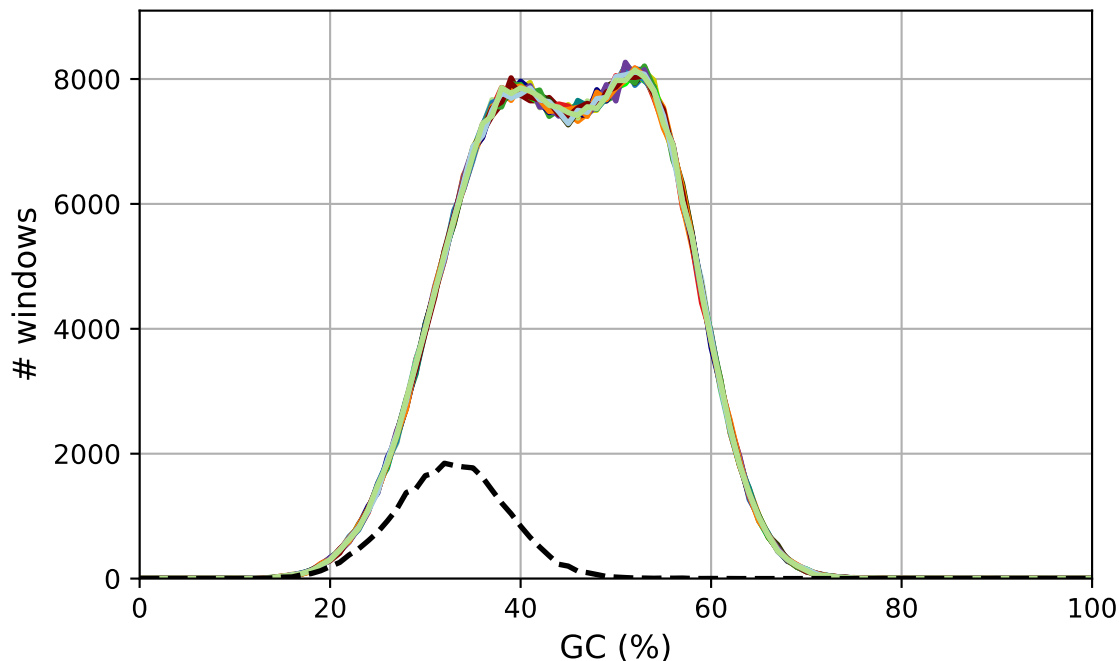


Cumulative length



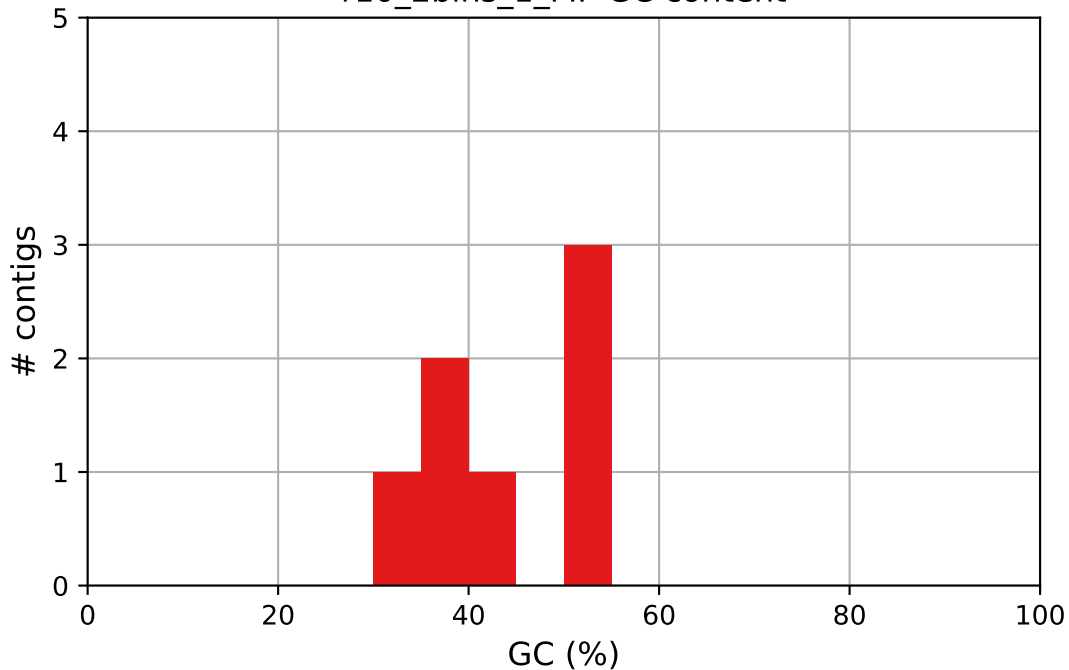
— r10_2bins_1_MP
— r10_2bins_1_MP_helen
— r10_2bins_1_r1_medaka
— r10_2bins_1_r2_medaka
— r10_2bins_2_MP_helen
— r10_2bins_2_r1_medaka
— r10_2bins_2_r2_medaka
— r10_2bins_2_racon_r1
— r10_2bins_3_MP_helen
— r10_2bins_3_r1_medaka
— r10_2bins_3_r2_medaka
— r10_2bins_3_racon_r1

GC content



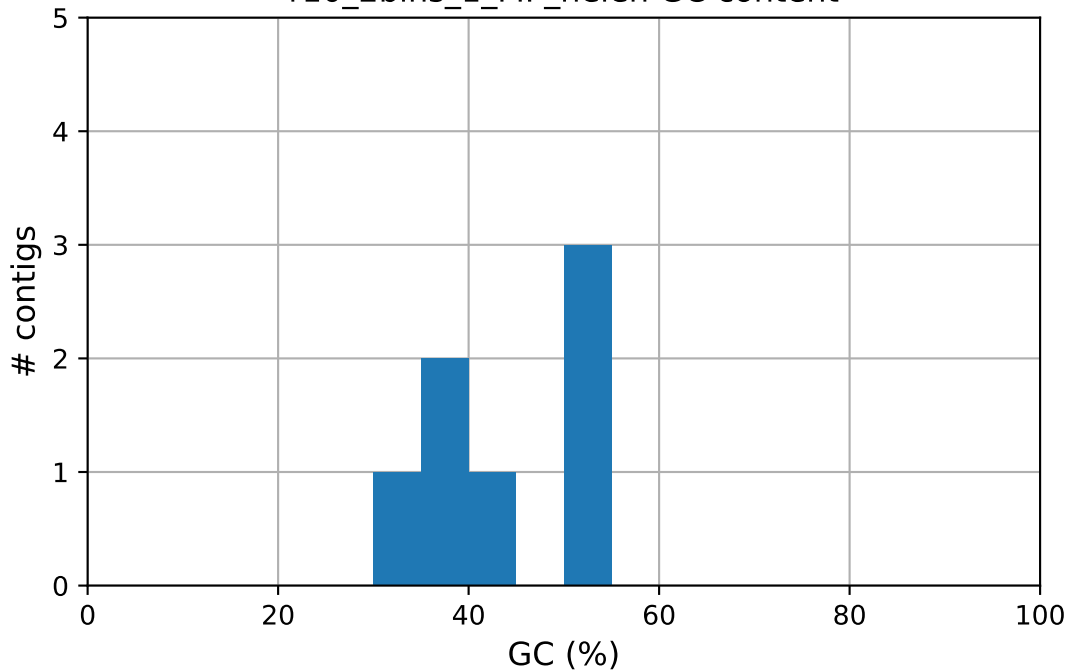
— r10_2bins_1_MP — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_MP_helen — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r1_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_racon_r1 — r10_2bins_3_racon_r1

r10_2bins_1_MP GC content



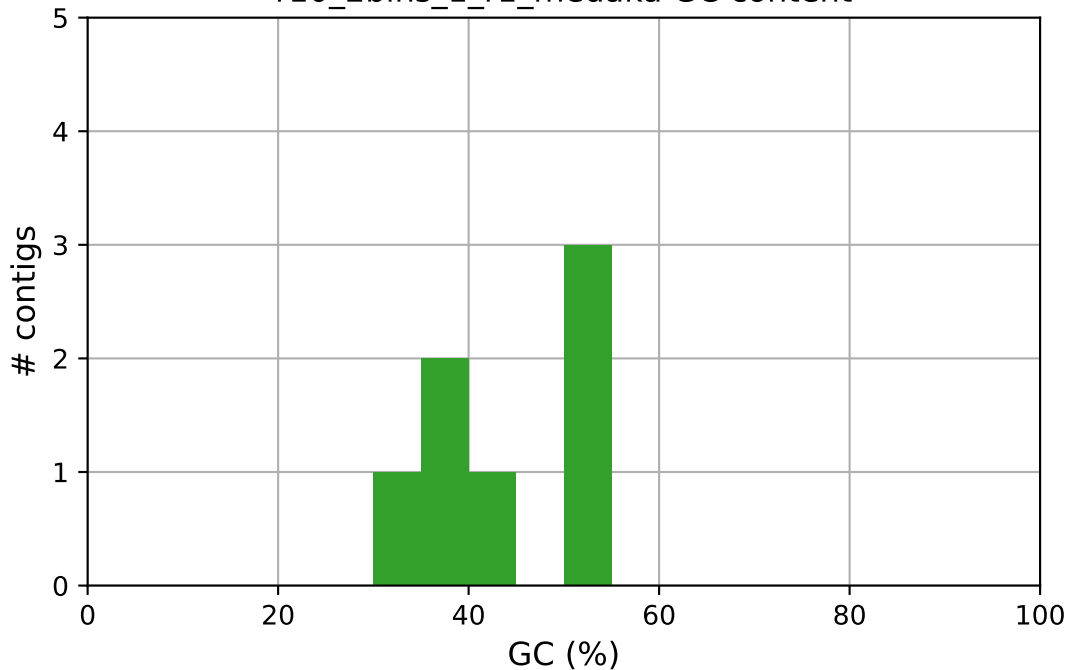
r10_2bins_1_MP

r10_2bins_1_MP_helen GC content



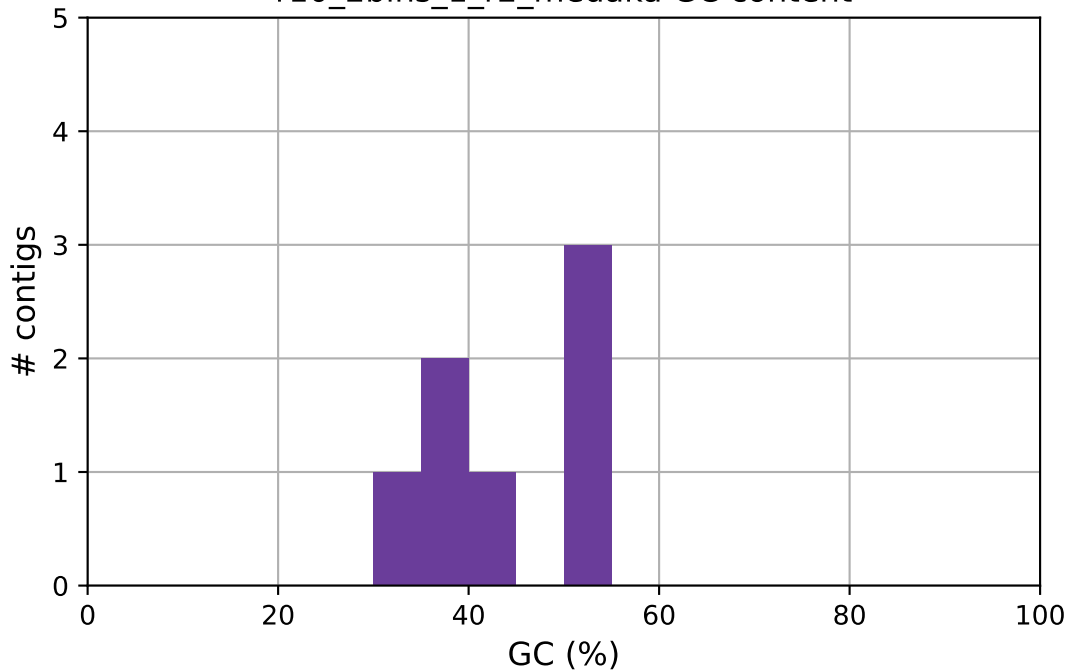
r10_2bins_1_MP_helen

r10_2bins_1_r1_medaka GC content



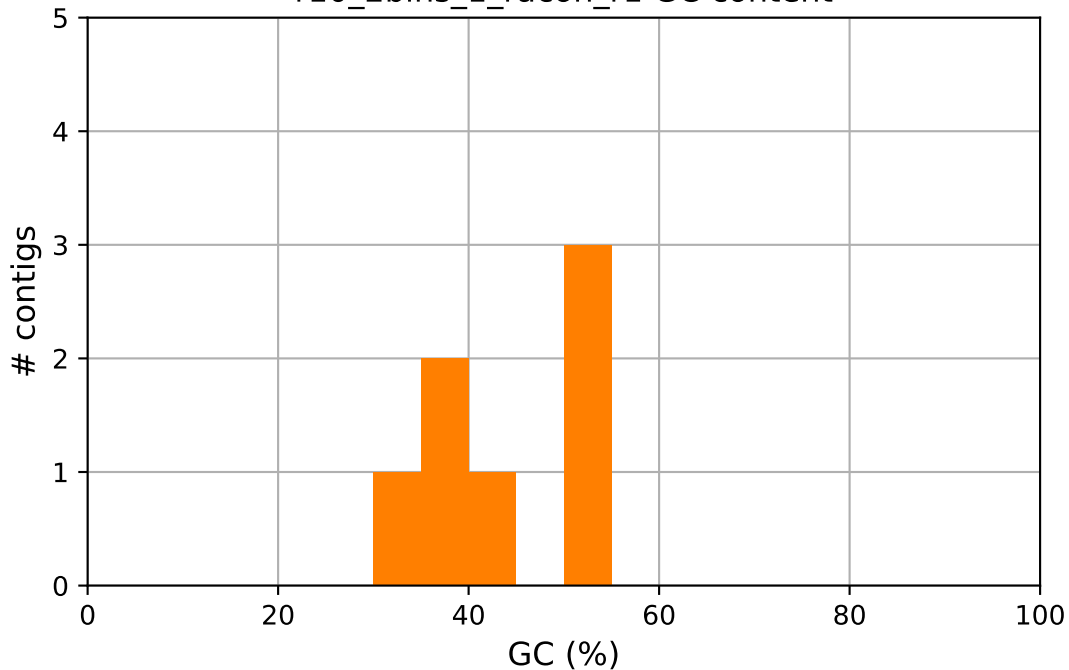
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r10_2bins_1_r2_medaka GC content



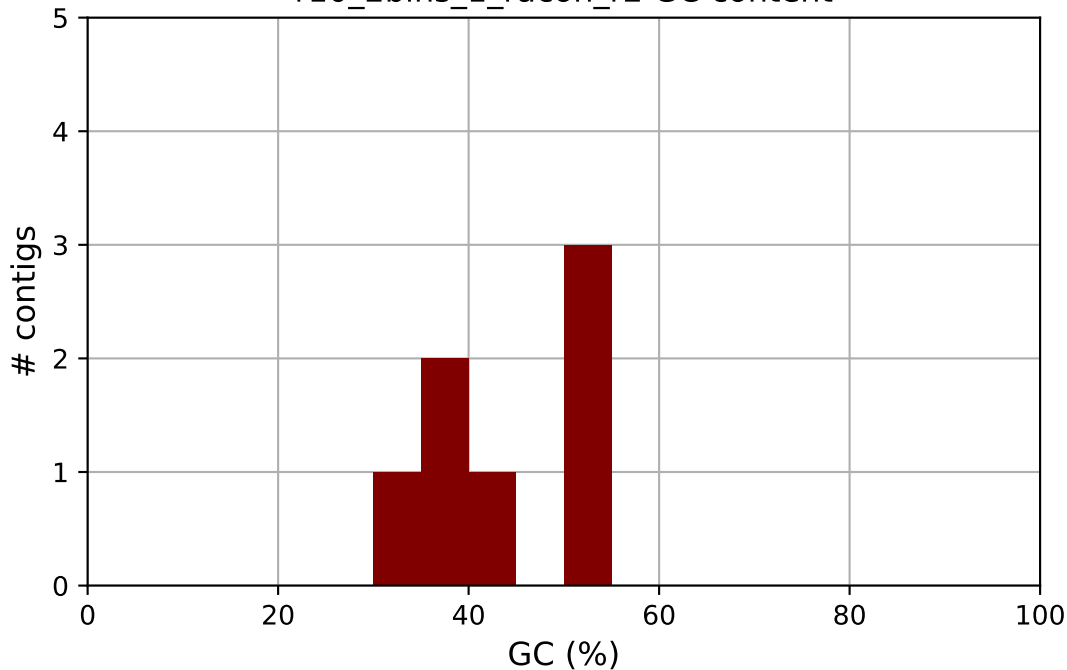
r10_2bins_1_r2_medaka

r10_2bins_1_racon_r1 GC content



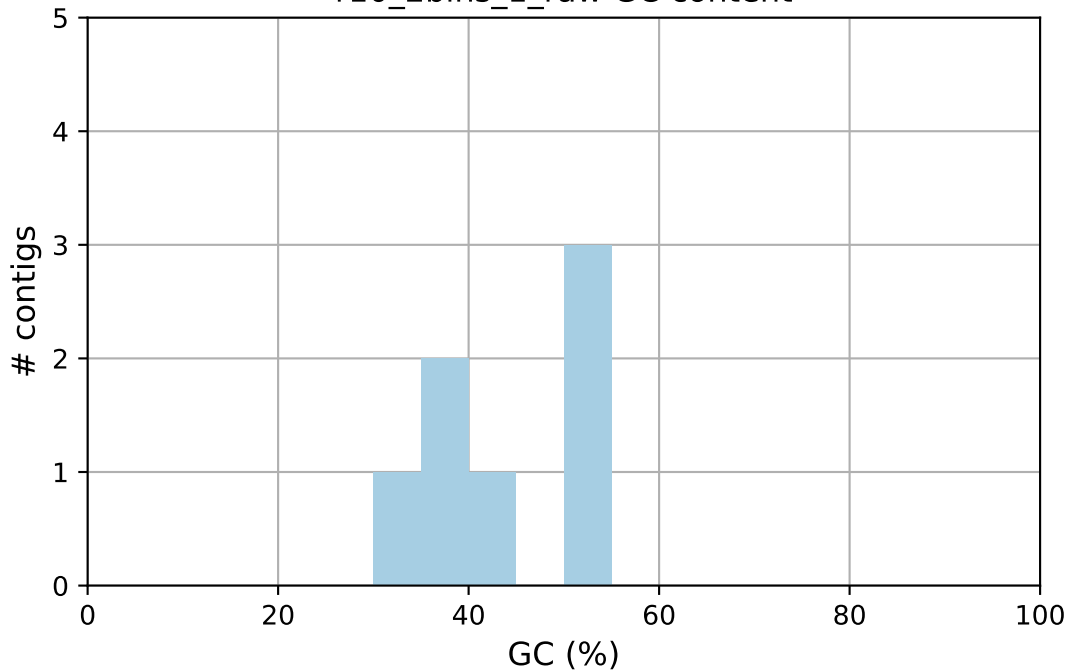
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r10_2bins_1_racon_r2 GC content



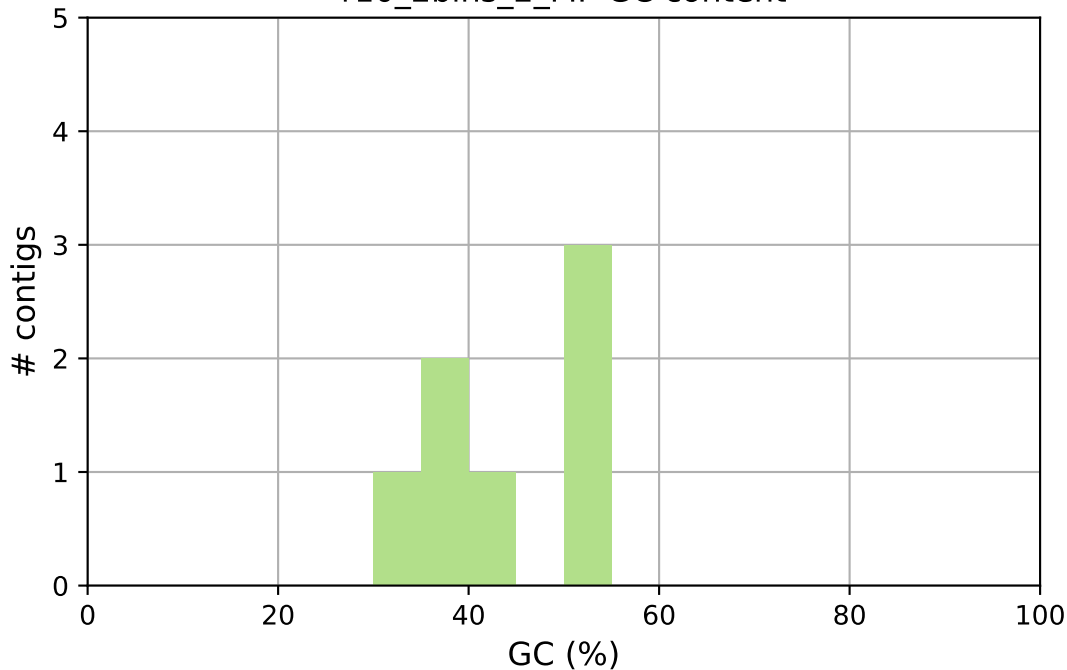
r10_2bins_1_racon_r2

r10_2bins_1_raw GC content



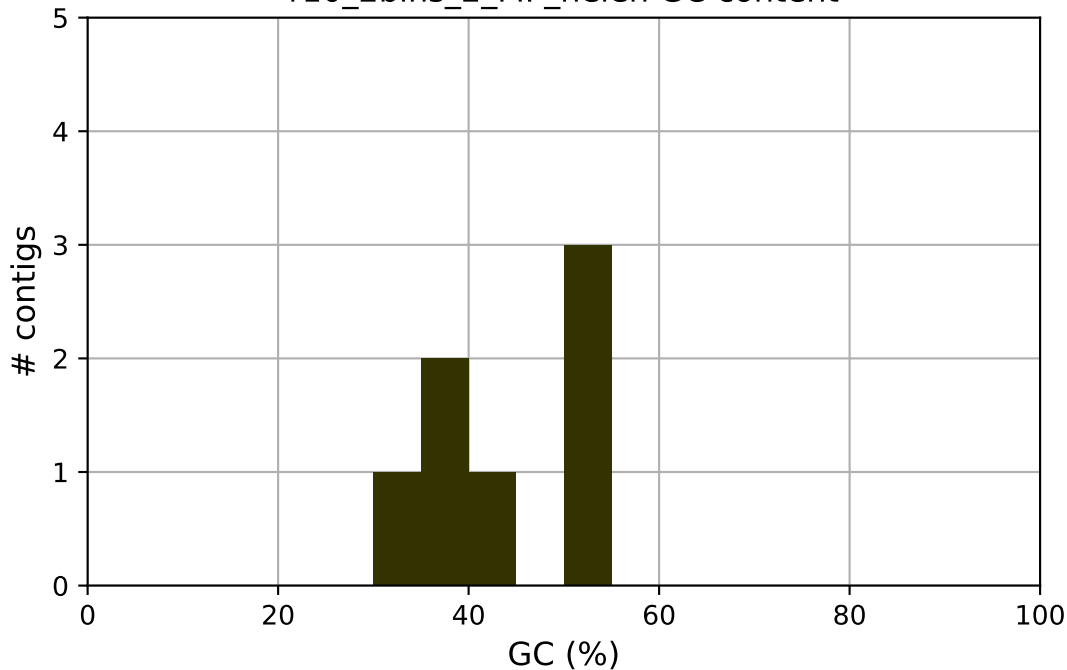
r10_2bins_1_raw

r10_2bins_2_MP GC content



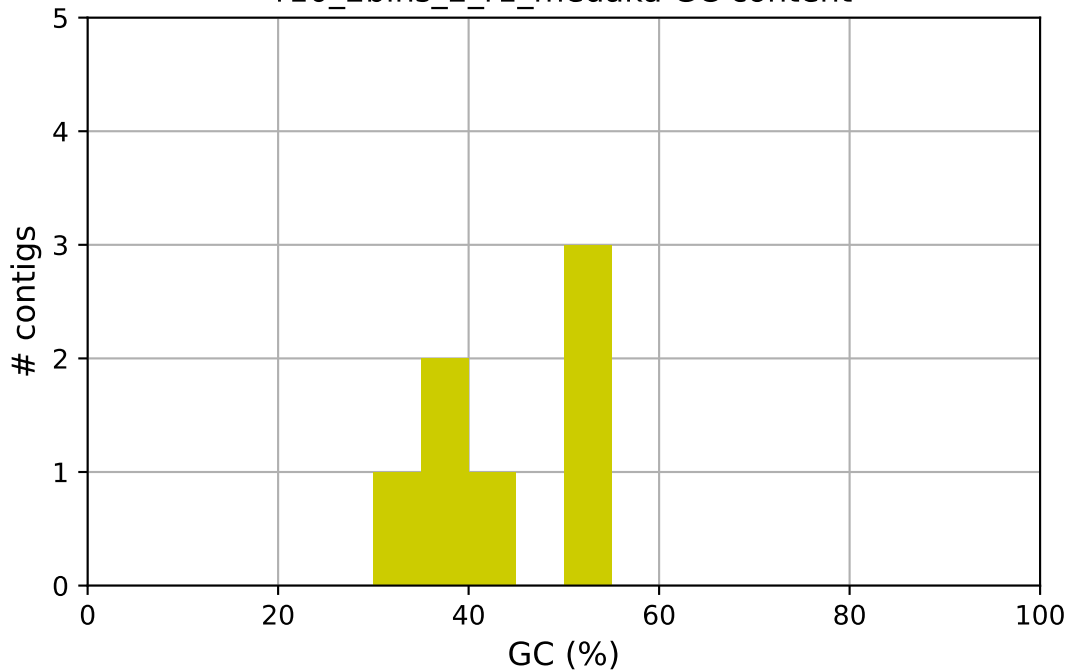
r10_2bins_2_MP

r10_2bins_2_MP_helen GC content



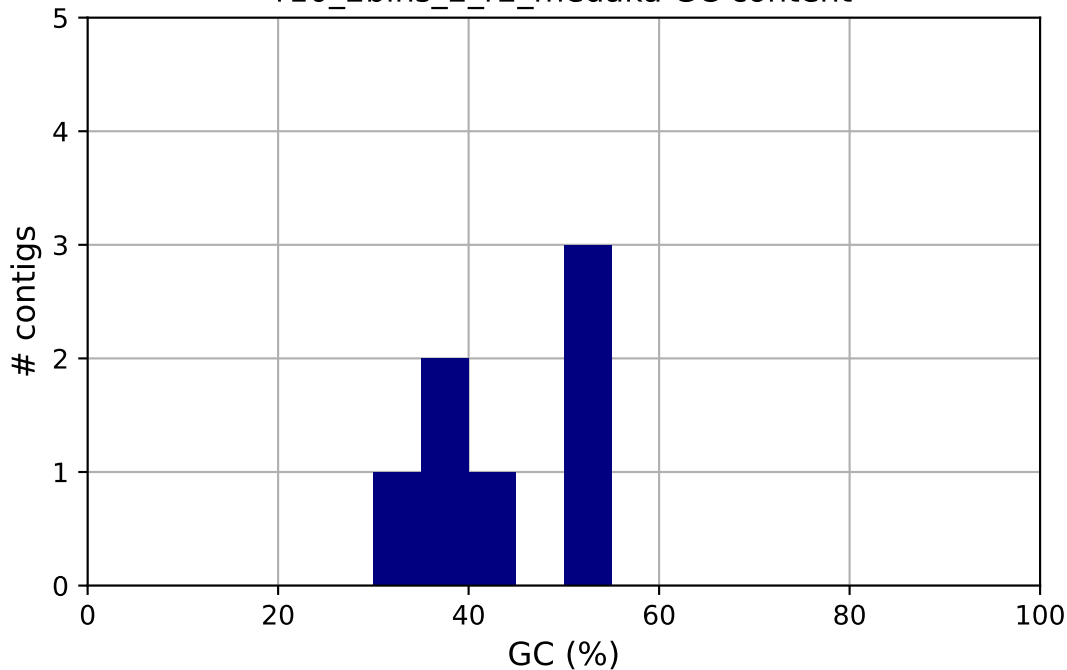
r10_2bins_2_MP_helen

r10_2bins_2_r1_medaka GC content



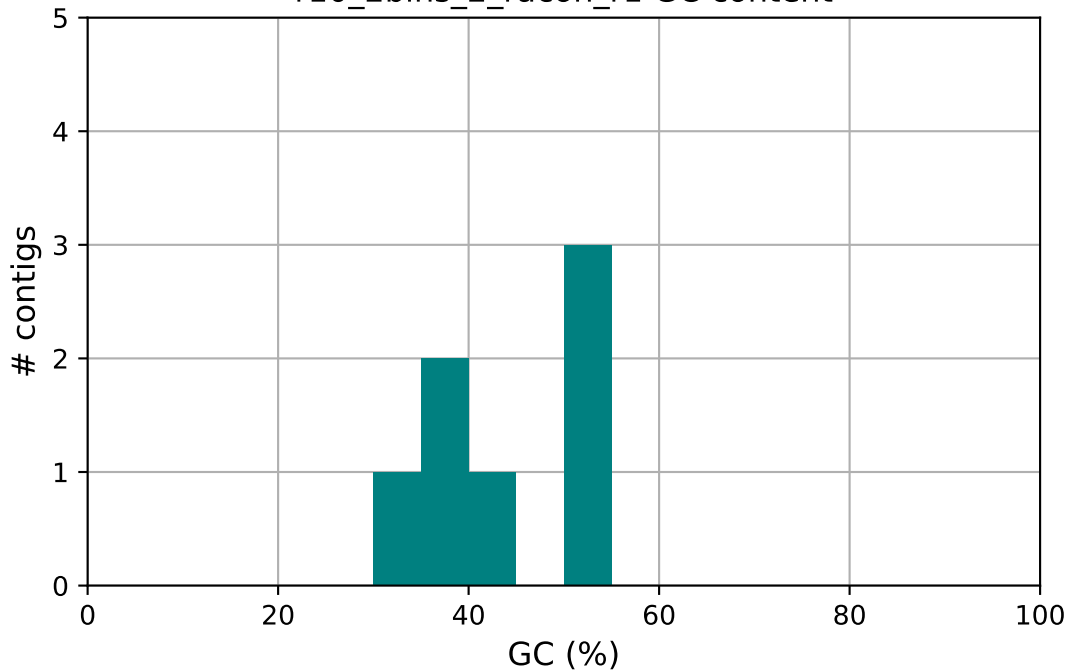
r10_2bins_2_r1_medaka

r10_2bins_2_r2_medaka GC content



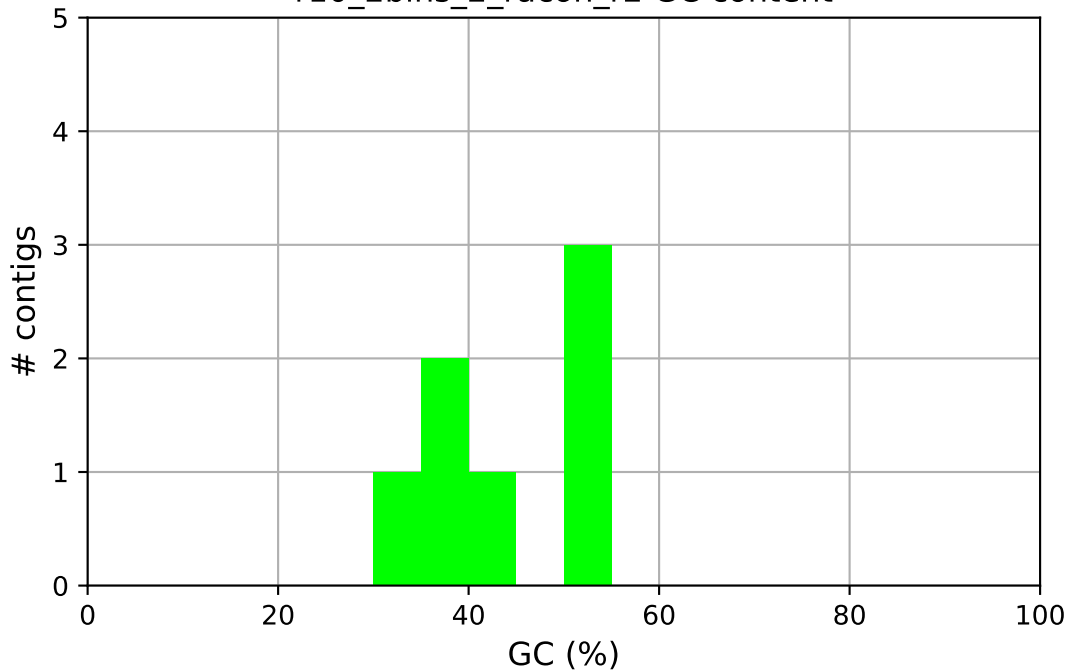
r10_2bins_2_r2_medaka

r10_2bins_2_racon_r1 GC content



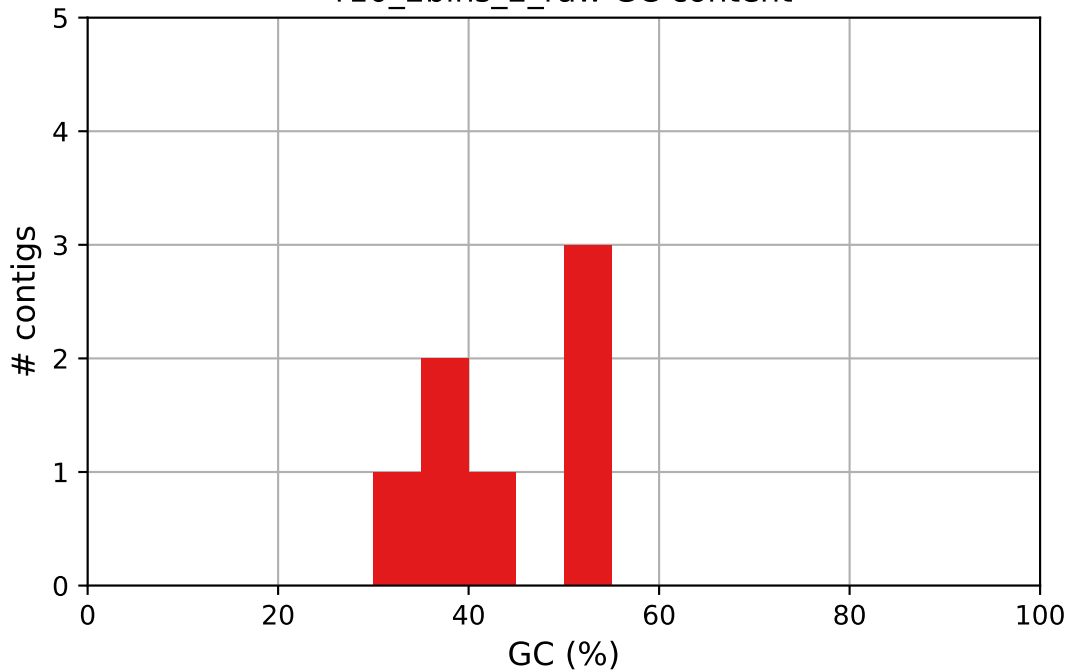
r10_2bins_2_racon_r1

r10_2bins_2_racon_r2 GC content



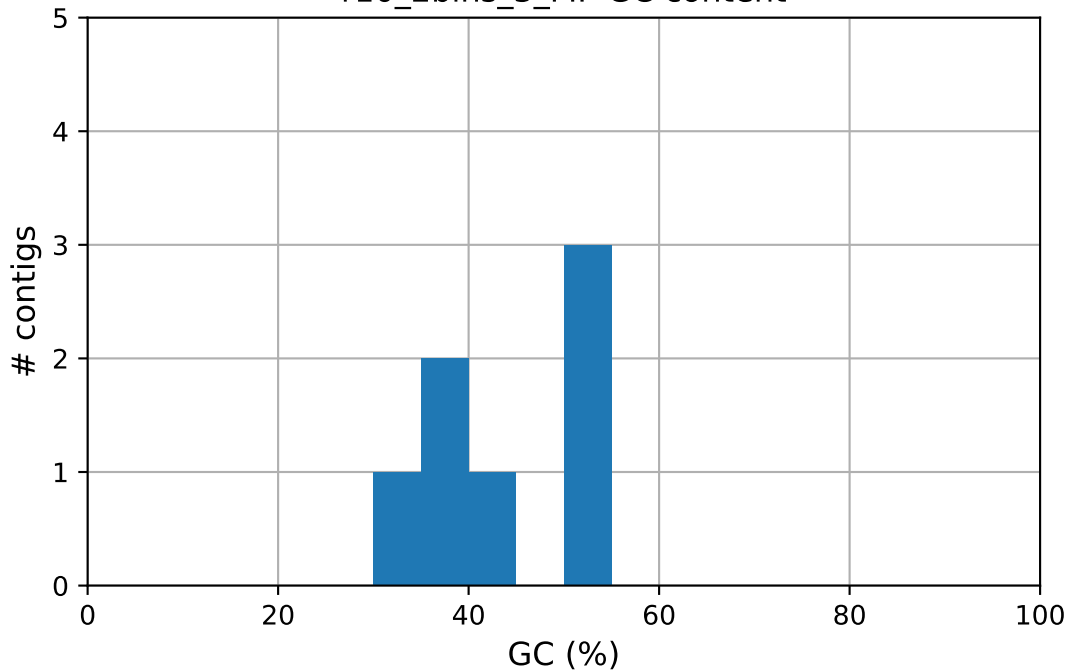
r10_2bins_2_racon_r2

r10_2bins_2_raw GC content



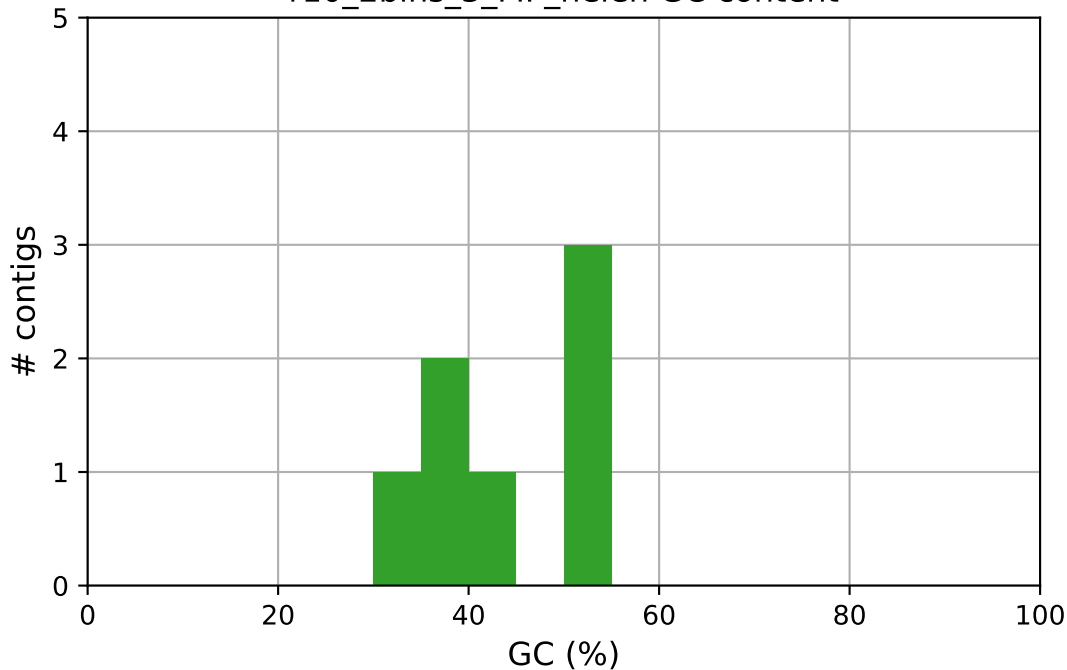
r10_2bins_2_raw

r10_2bins_3_MP GC content



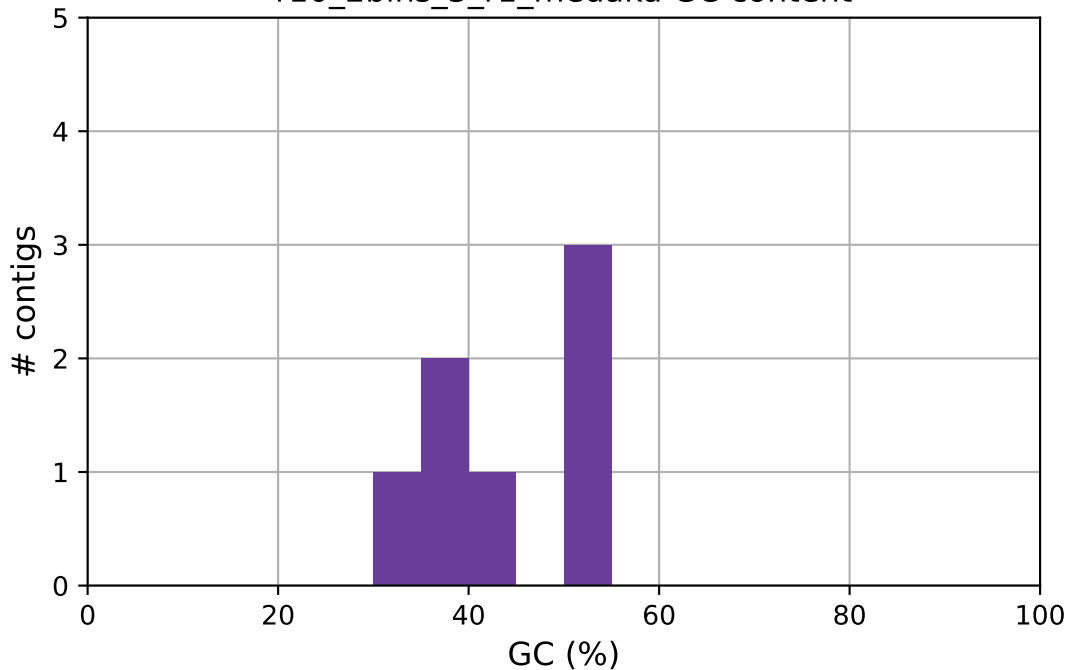
r10_2bins_3_MP

r10_2bins_3_MP_helen GC content



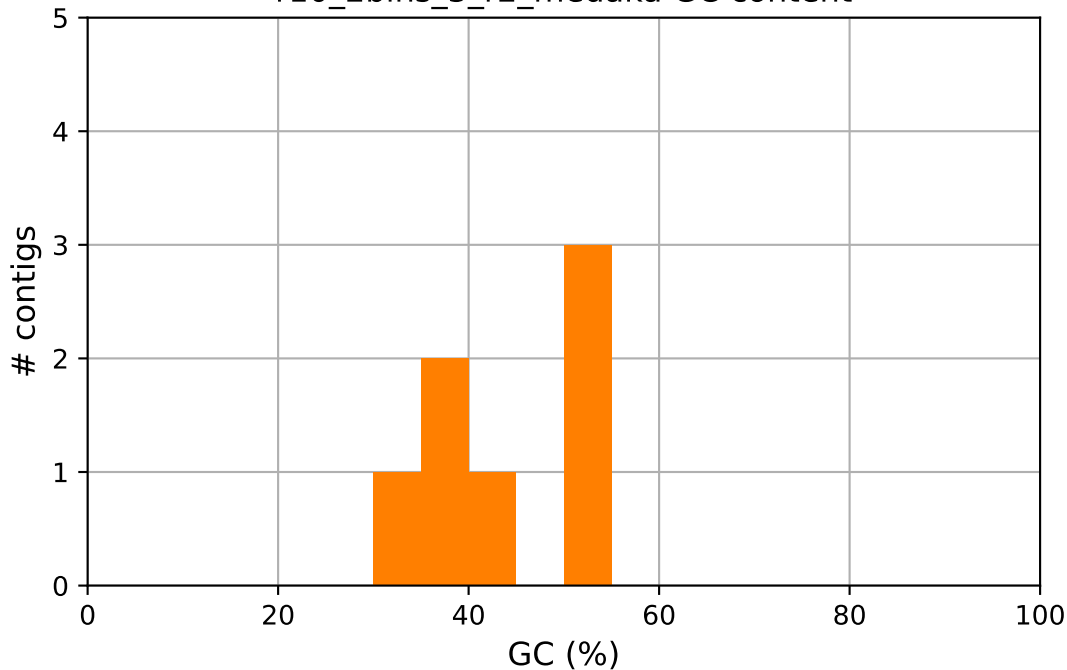
r10_2bins_3_MP_helen

r10_2bins_3_r1_medaka GC content



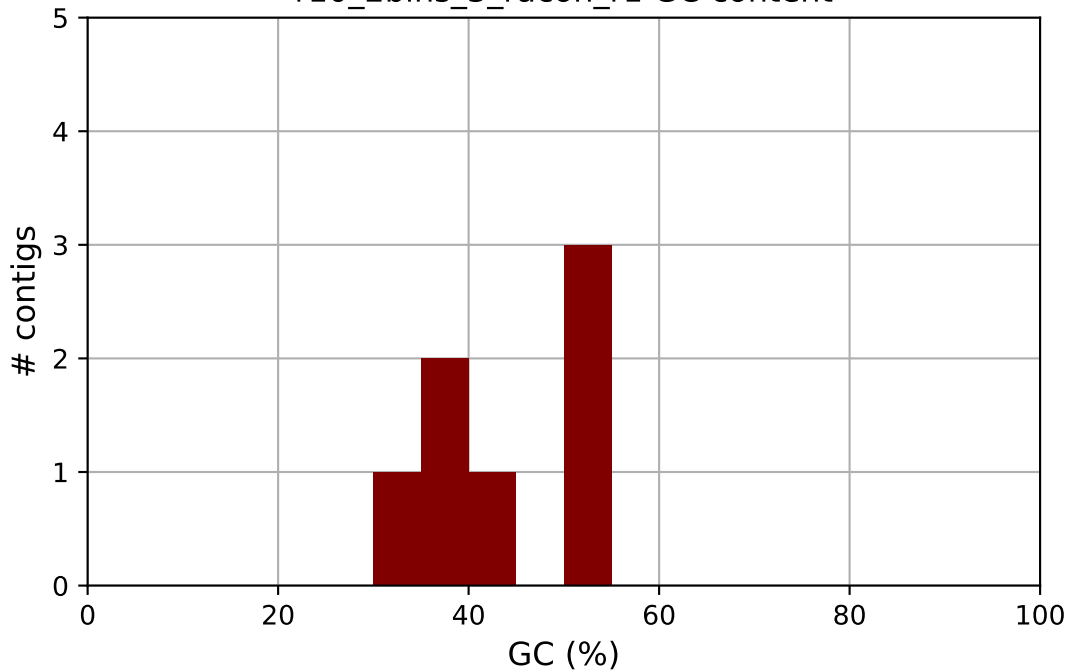
r10_2bins_3_r1_medaka

r10_2bins_3_r2_medaka GC content



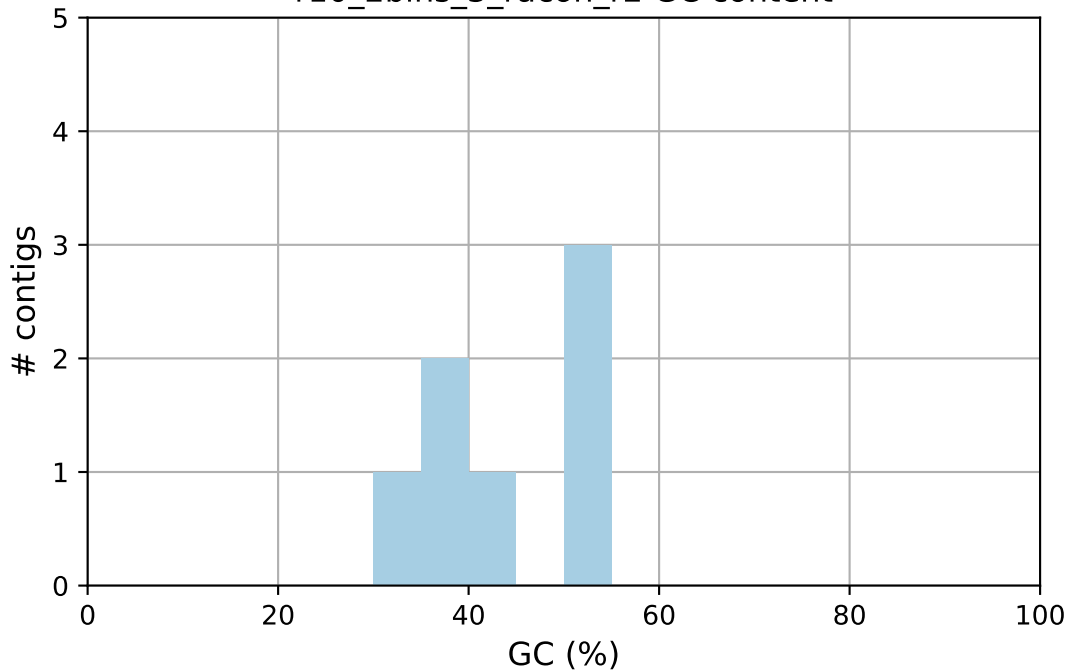
r10_2bins_3_r2_medaka

r10_2bins_3_racon_r1 GC content



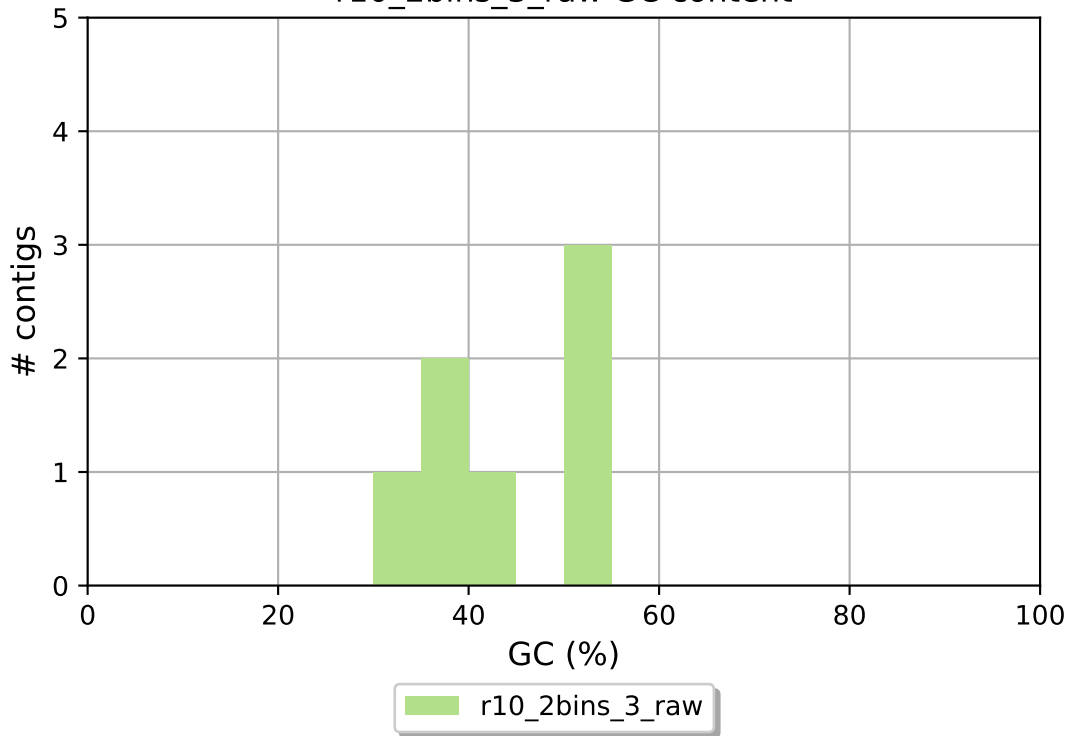
r10_2bins_3_racon_r1

r10_2bins_3_racon_r2 GC content

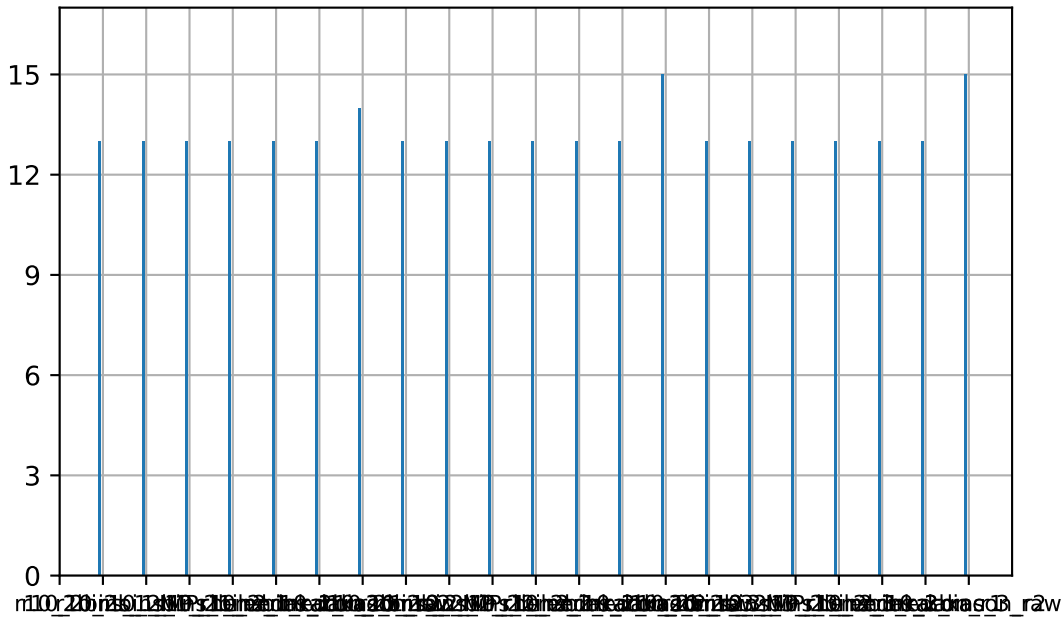


r10_2bins_3_racon_r2

r10_2bins_3_raw GC content

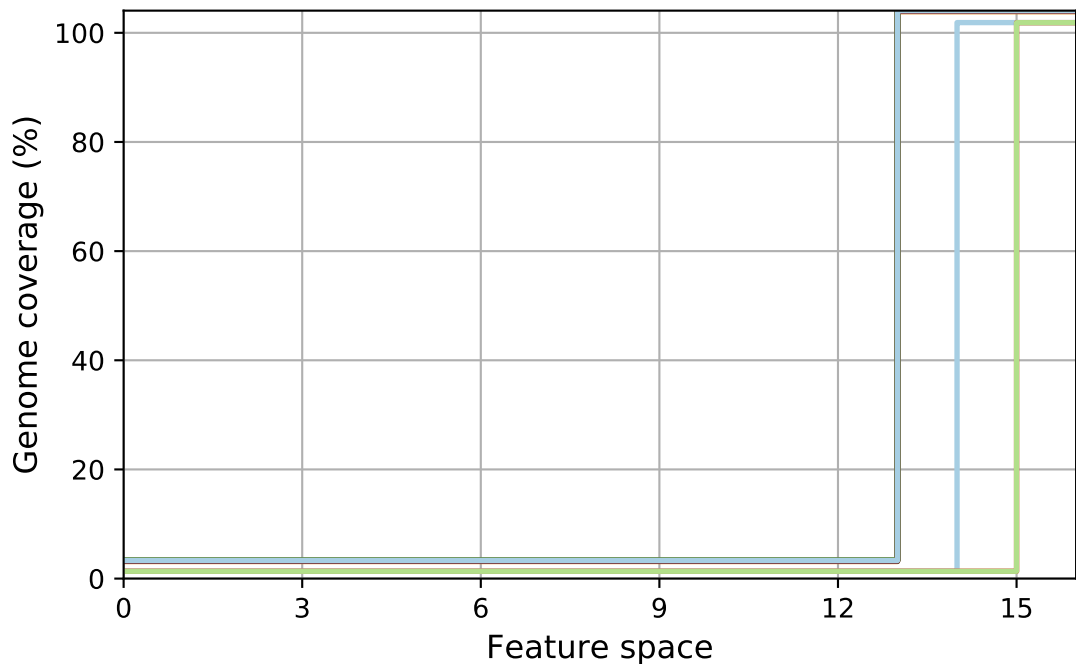


Misassemblies



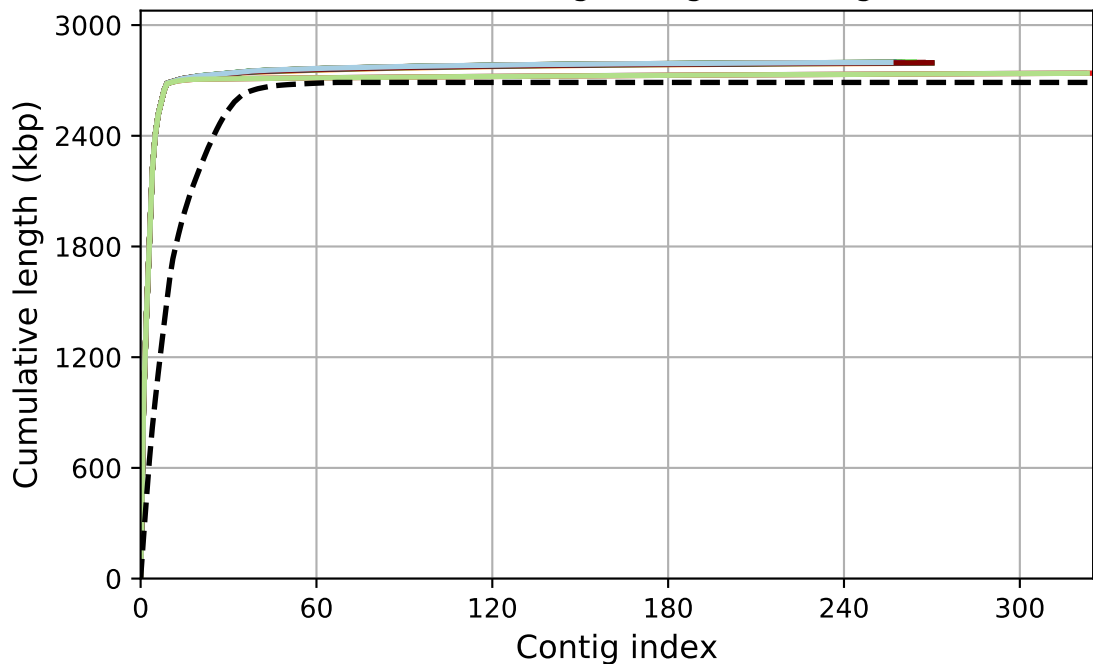
translocations

FRCurve (misassemblies)

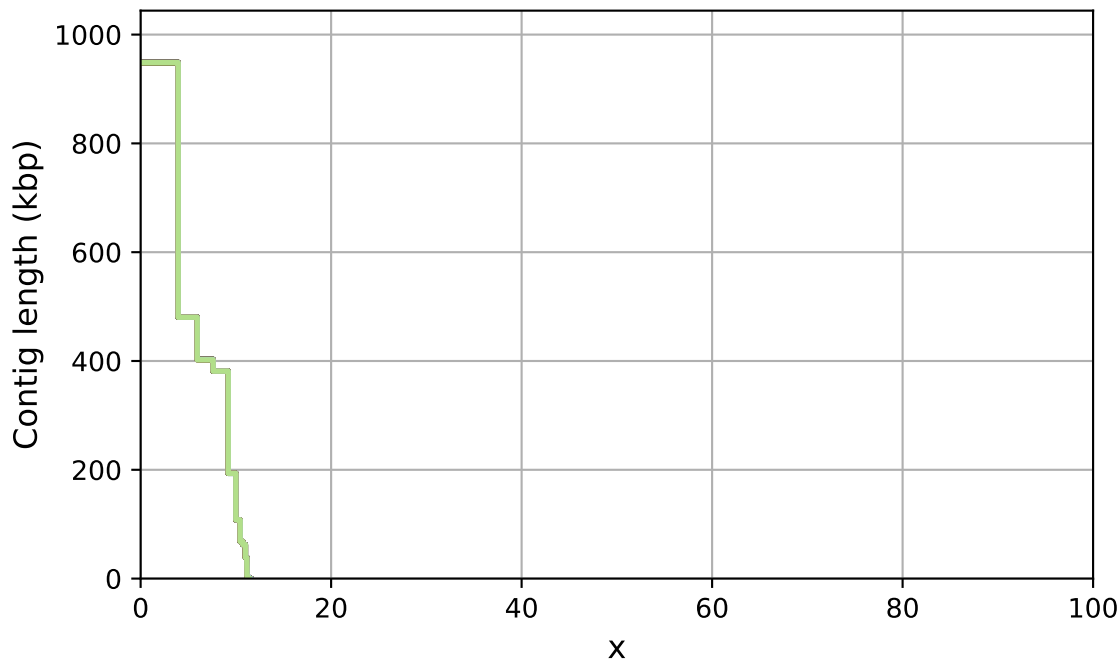


— r10_2bins_1_MP — r10_2bins_2_MP — r10_2bins_3_MP
— r10_2bins_1_MP_helen — r10_2bins_2_MP_helen — r10_2bins_3_MP_helen
— r10_2bins_1_r1_medaka — r10_2bins_2_r1_medaka — r10_2bins_3_r1_medaka
— r10_2bins_1_r2_medaka — r10_2bins_2_r2_medaka — r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)

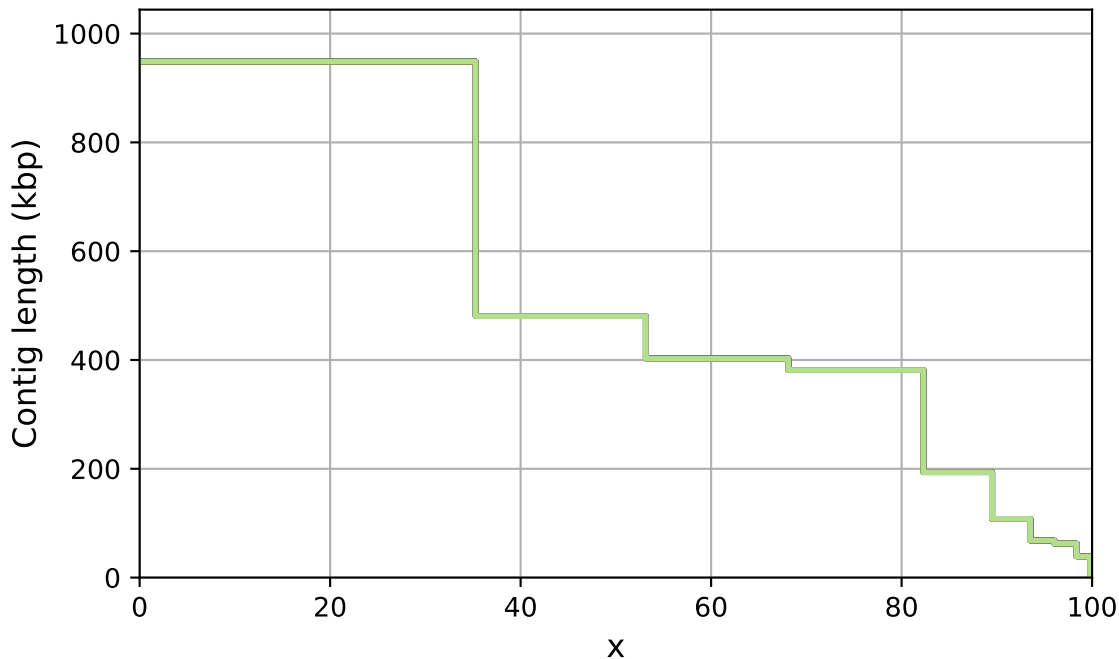


NAx



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

NGAx



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

Genome fraction, %

