

Report

	r10_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_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)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
Total length	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
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	44.79	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	44.79	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	4045595	4045615	4045602	4045598	4045293	4045319	4043044	4045596	4045616	4045587	4045593	4045258	4045323	4042479	4045596	4045613	4045582	4045587	4045248	4045358	4043002
NG50	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
N75	2845436	2845374	2845428	2845430	2845286	2845307	2843860	2845427	2845364	2845435	2845433	2845287	2845362	2843855	2845427	2845365	2845437	2845434	2845286	2845324	2843844
NG75	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
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	15	13	13	13	13	13	13	13	14	14	14	14	14	14	13
# 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	2719941	2718121	2719506	2719603	2720301	2720317	2718868	2719784	2717999	2719522	2719572	2720345	2720410	2718437	2719778	2718019	2719548	2719556	2720274	2720341	2718429
# local misassemblies	9	10	10	10	9	10	19	9	9	9	9	9	9	9	9	10	9	9	10	10	20
# 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	5	6	6	6	6	6	6	5	6	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	0 + 7 part
Unaligned length	21276230	21273903	21274145	21266469	21266438	21255182	21321559	21274894	21271384	21273185	21262585	21264875	21254555	21318447	21276104	21272622	21273511	21266251	21263756	21256890	21323181
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	99.538	99.546	99.546	99.546	99.546	99.546	99.546	99.538
Duplication ratio	1.045	1.045	1.045	1.045	1.044	1.046	1.024	1.046	1.045	1.046	1.046	1.045	1.046	1.024	1.045	1.045	1.045	1.045	1.045	1.046	1.023
# 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	282.21	250.98	283.96	282.17	276.72	293.83	252.85	287.25	256.62	286.65	291.77	284.41	302.42	250.71	281.51	250.80	284.16	283.90	283.75	294.77	239.24
# indels per 100 kbp	110.62	40.72	75.69	75.54	108.08	109.65	165.84	111.74	42.59	75.39	75.91	110.32	110.02	159.30	110.46	41.43	75.91	74.52	108.26	108.41	158.06
Largest alignment	948830	948257	948756	948808	948910	949051	948393	948731	948068	948643	948667	948937	948964	948372	948926	948399	948848	948865	949260	949283	1350628
Total aligned length	2796602	2794907	2796099	2795973	2792836	2796941	2738106	2797815	2796036	2796826	2797747	2794242	2798361	2740114	2796643	2794884	2796555	2796429	2794386	2796952	2735856
NGA50	480570	480279	480469	480494	480596	480583	480378	480577	480279	480494	480488	480641	480625	480398	480559	480279	480498	480485	480584	480602	1350628
NGA75	381494	381244	381433	381442	381535	381561	381350	381479	381236	381407	381433	381498	381584	381299	381478	381237	381420	381419	381541	381538	381299
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3

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

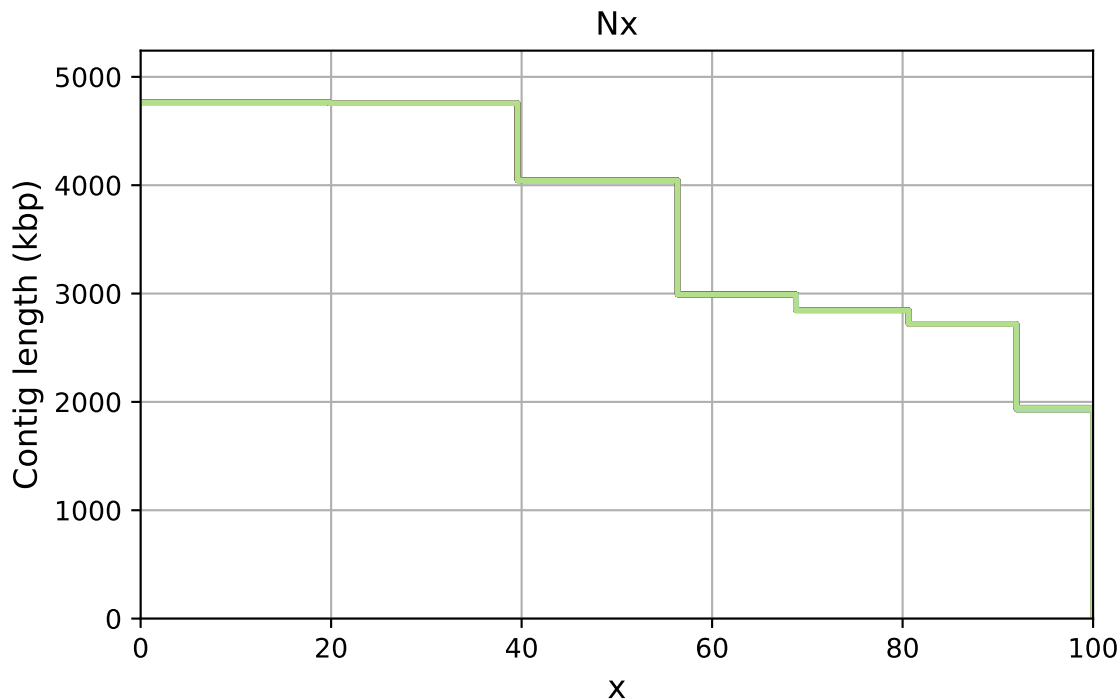
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# misassemblies	13	13	13	13	13	13	15	13	13	13	13	13	13	13	14	14	14	14	14	14	13
# contig misassemblies	13	13	13	13	13	13	15	13	13	13	13	13	13	13	14	14	14	14	14	14	13
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	13	13	13	13	13	13	15	13	13	13	13	13	13	13	14	14	14	14	14	14	13
# 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	2719941	2718121	2719506	2719603	2720301	2720317	2718868	2719784	2717999	2719522	2719572	2720345	2720410	2718437	2719778	2718019	2719548	2719556	2720274	2720341	2718429
# 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	20	10	10	10	10	10	10	16	10	10	10	10	10	10	16
# local misassemblies	9	10	10	10	9	10	19	9	9	9	9	9	9	19	9	10	9	9	10	10	20
# 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	21	26	26	26	26	26	26	25	26	26	26	26	26	26	24
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# mismatches	7554	6718	7601	7553	7407	7865	6768	7689	6869	7673	7810	7613	8095	6711	7536	6714	7607	7600	7596	7891	6404
# indels	2961	1090	2026	2022	2893	2935	4439	2991	1140	2018	2032	2953	2945	4264	2957	1109	2032	1995	2898	2902	4231
# indels (<= 5 bp)	2897	1030	1975	1970	2842	2883	4384	2923	1078	1967	1981	2900	2894	4204	2889	1047	1981	1944	2846	2850	4170
# indels (> 5 bp)	64	60	51	52	51	52	55	68	62	51	51	53	51	60	68	62	51	51	52	52	61
Indels length	6745	4763	5357	5353	6635	6604	8522	6858	4878	5362	5367	6743	6654	8366	6818	4826	5382	5315	6633	6553	8352

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

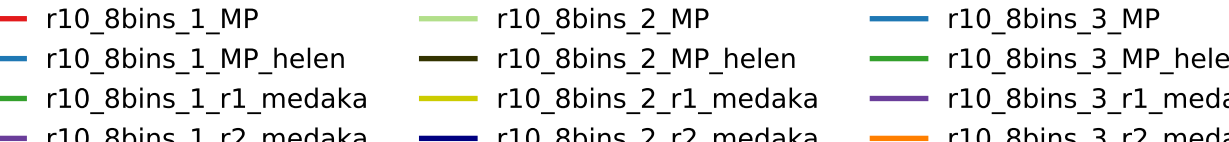
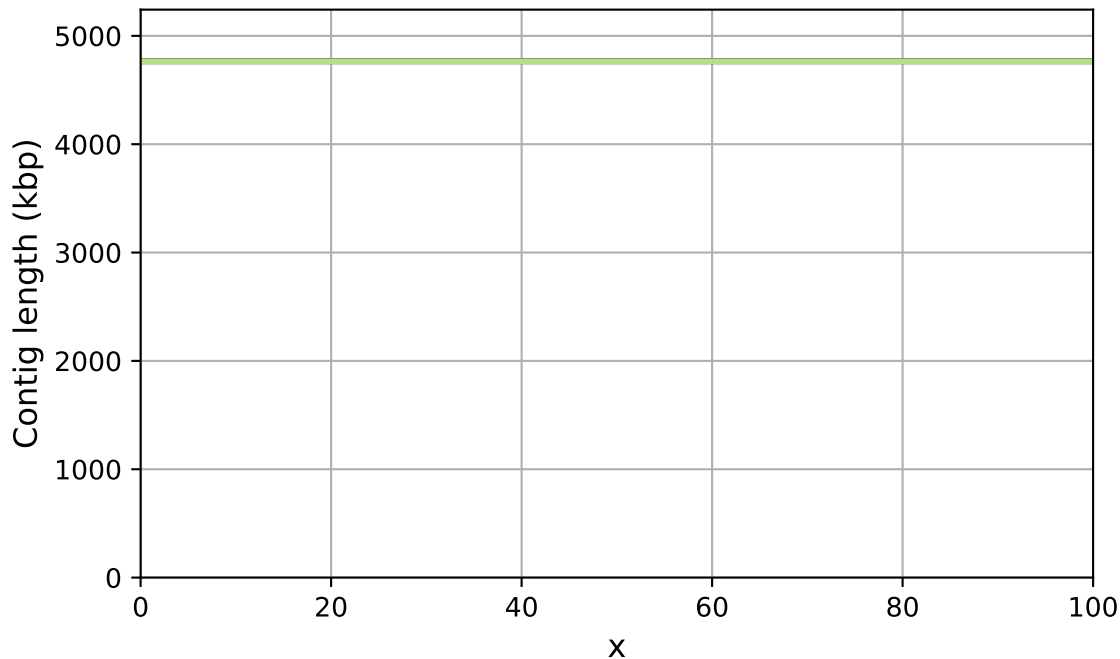
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21276230	21273903	21274145	21266469	21266438	21255182	21321559	21274894	21271384	21273185	21262585	21264875	21254555	21318447	21276104	21272622	21273511	21266251	21263756	21256890	21323181
# 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).

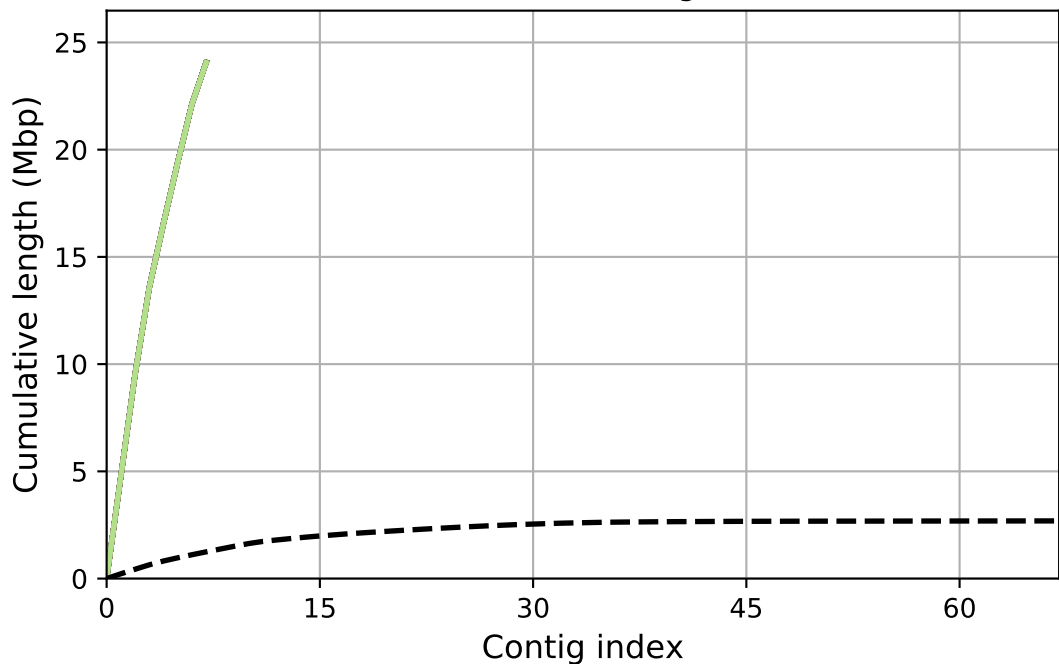


r10_8bins_1_MP	r10_8bins_2_MP	r10_8bins_3_MP
r10_8bins_1_MP_helen	r10_8bins_2_MP_helen	r10_8bins_3_MP_helen
r10_8bins_1_r1_medaka	r10_8bins_2_r1_medaka	r10_8bins_3_r1_medaka
r10_8bins_1_r2_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_medaka

NGx

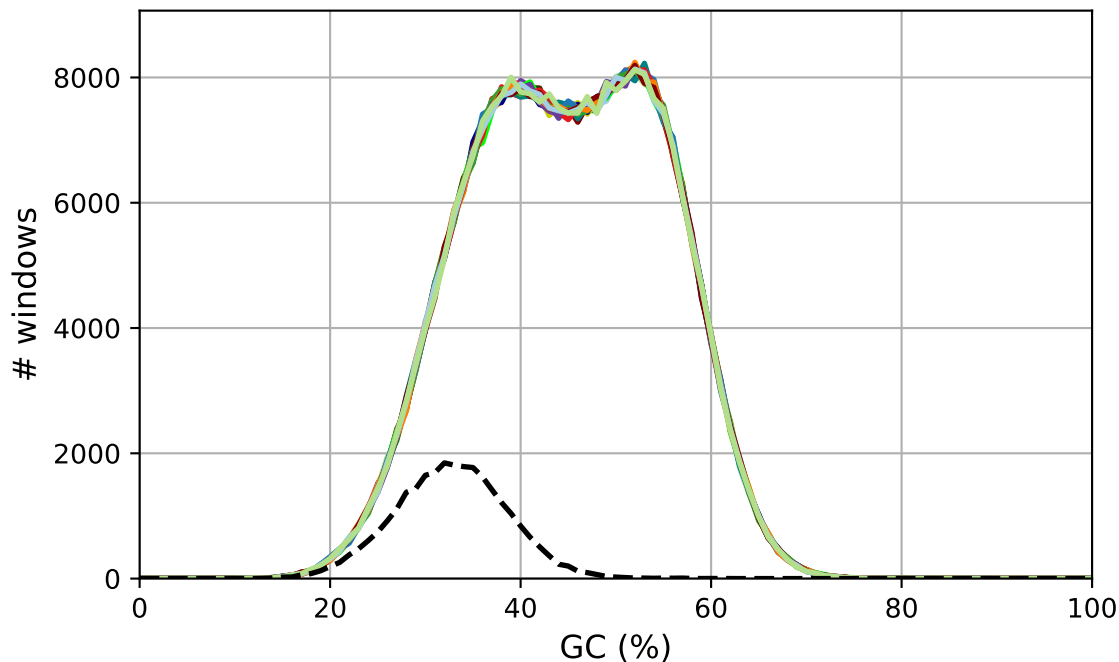


Cumulative length



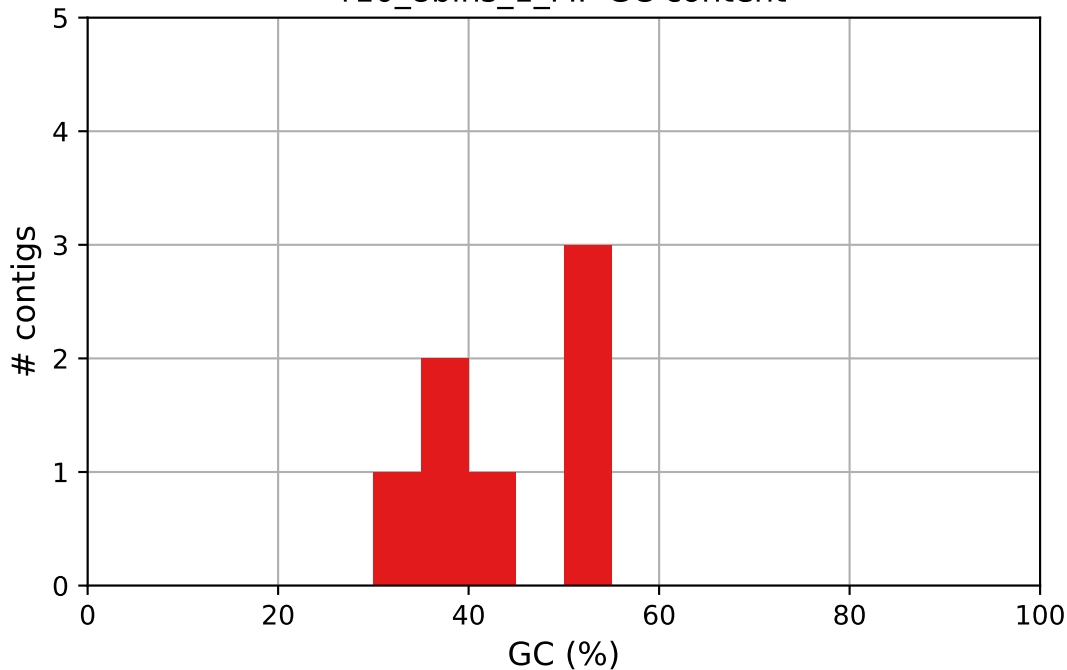
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r10_8bins_1_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_3_r1_medaka
r10_8bins_1_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_medaka
r10_8bins_1_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_3_racon_r1

GC content



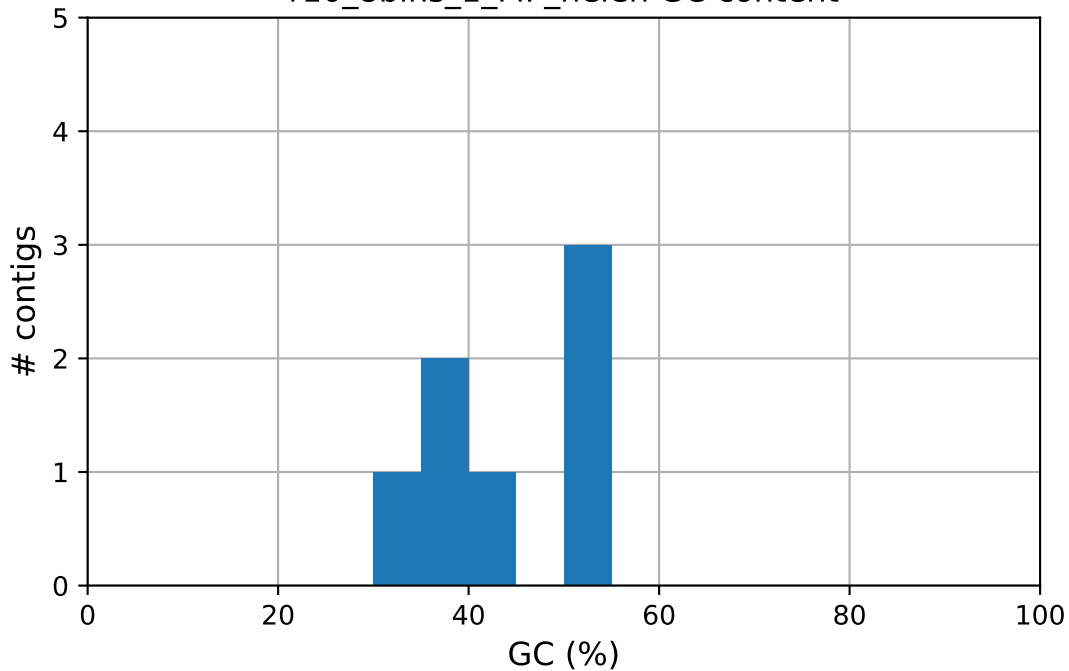
— r10_8bins_1_MP — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_MP_helen — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r1_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_racon_r1 — r10_8bins_3_racon_r1

r10_8bins_1_MP GC content



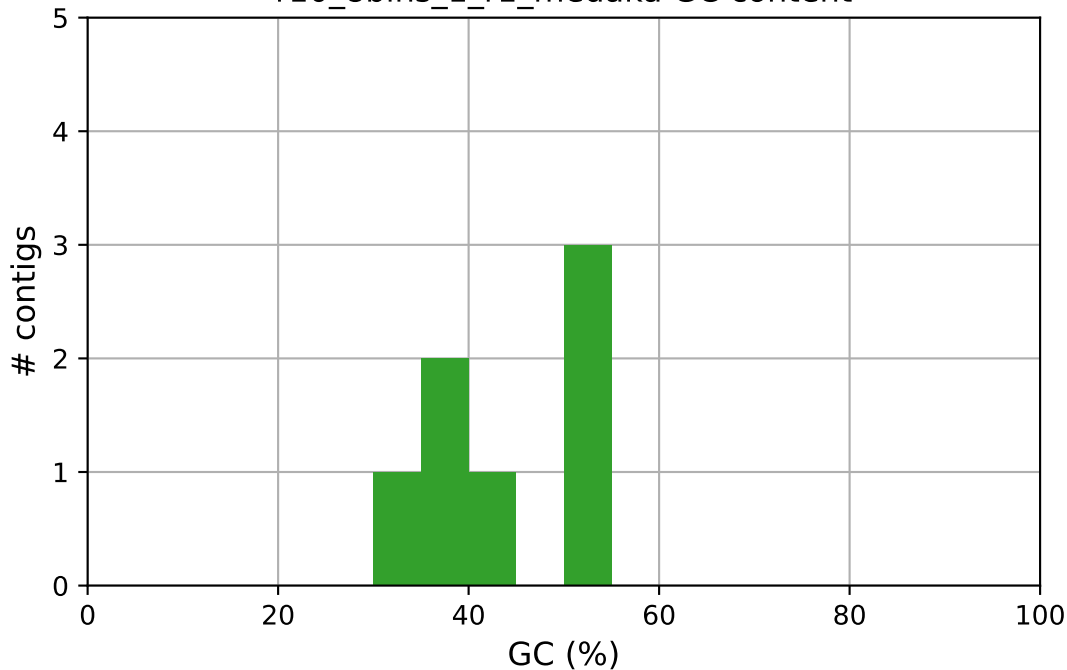
r10_8bins_1_MP

r10_8bins_1_MP_helen GC content



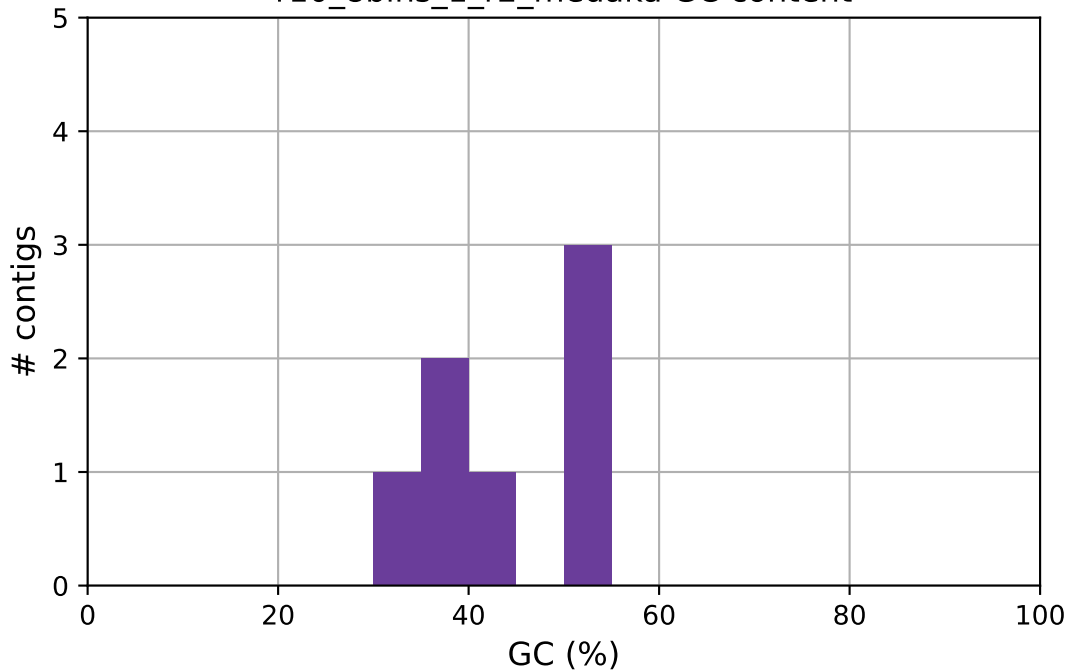
r10_8bins_1_MP_helen

r10_8bins_1_r1_medaka GC content



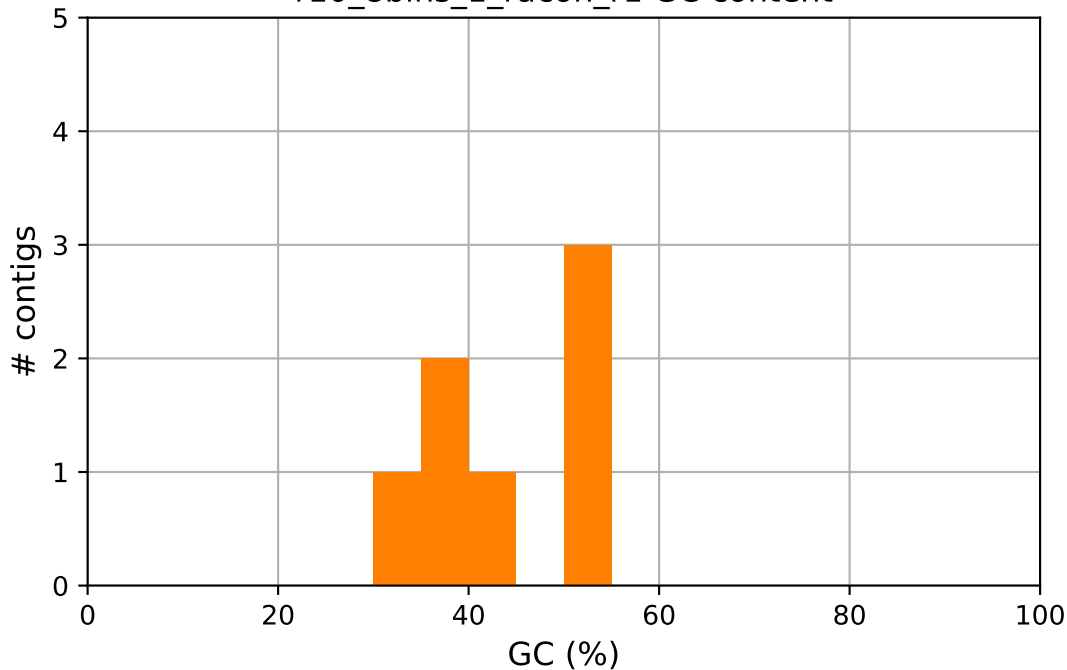
r10_8bins_1_r1_medaka

r10_8bins_1_r2_medaka GC content



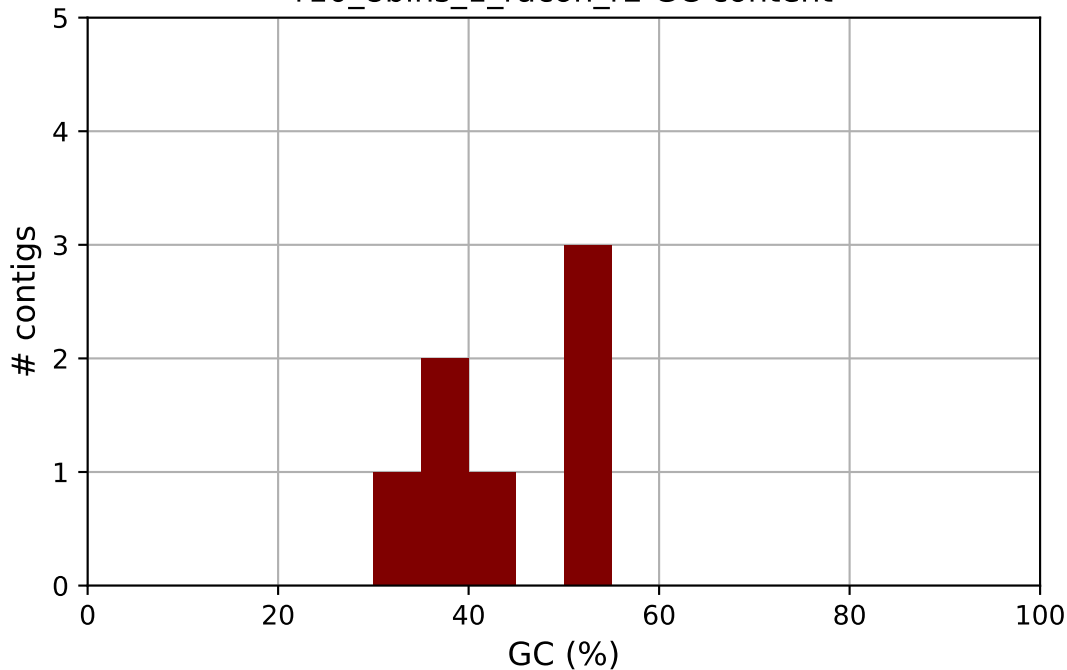
r10_8bins_1_r2_medaka

r10_8bins_1_racon_r1 GC content



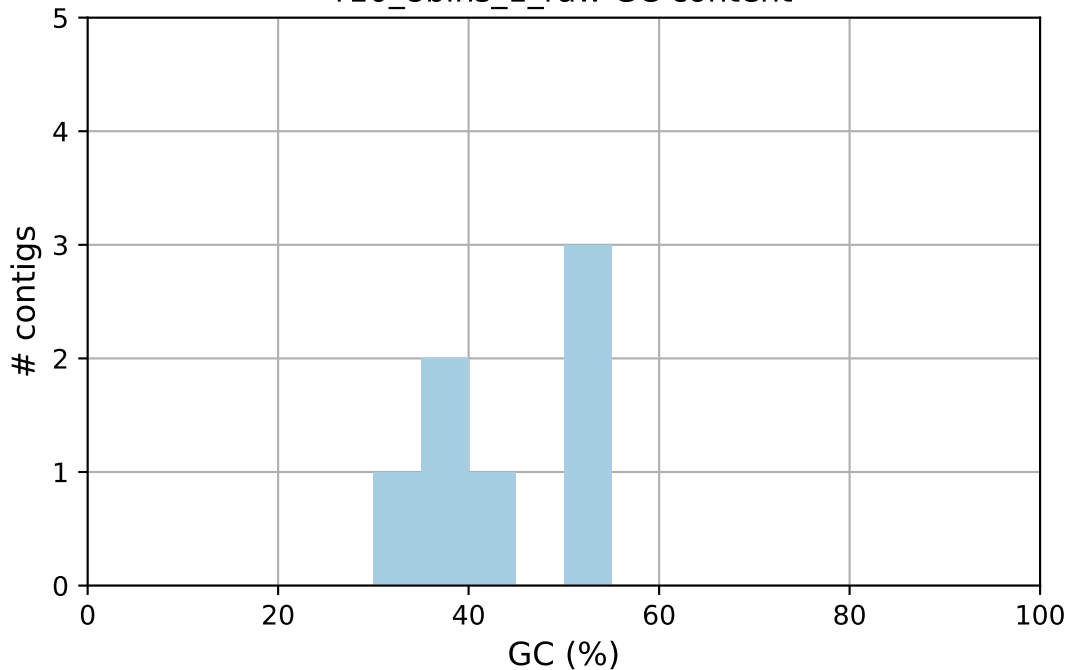
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r10_8bins_1_racon_r2 GC content



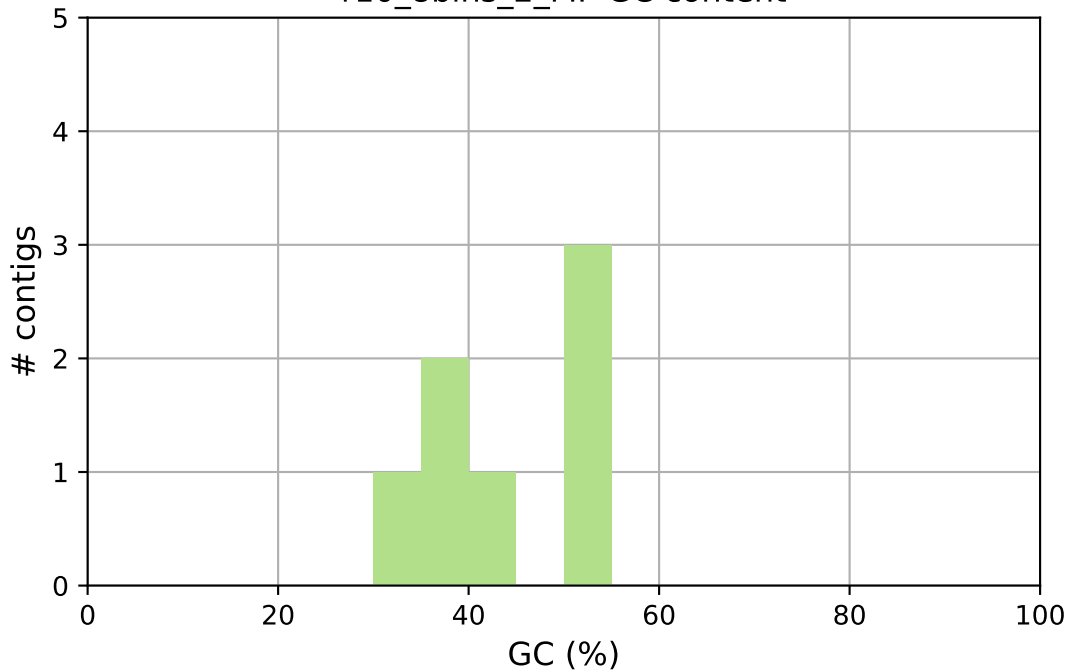
r10_8bins_1_racon_r2

r10_8bins_1_raw GC content



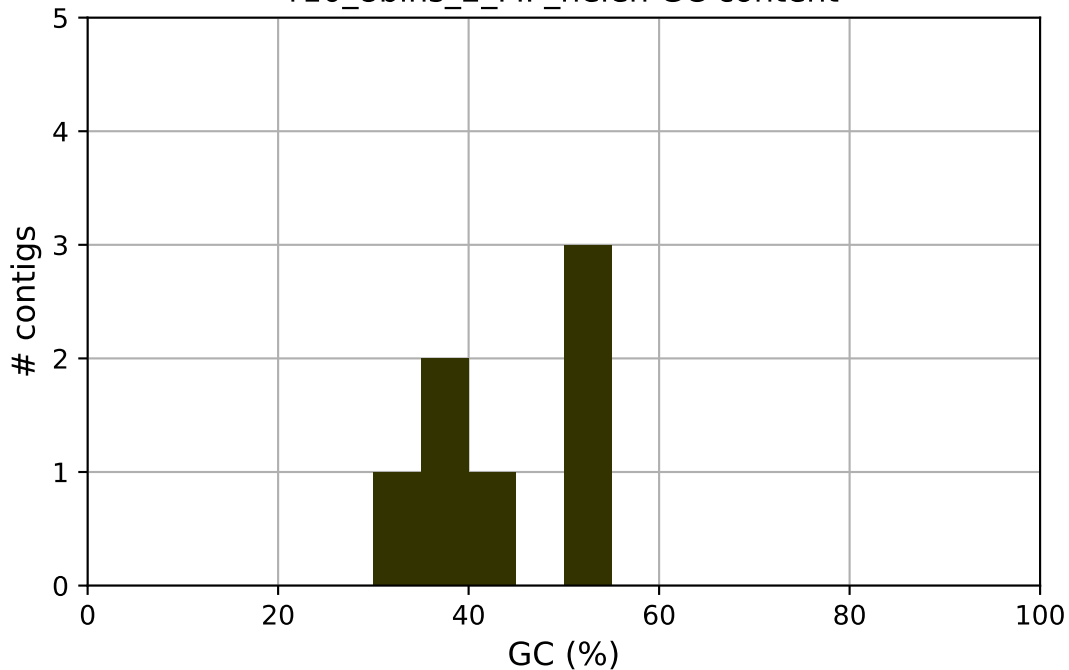
r10_8bins_1_raw

r10_8bins_2_MP GC content



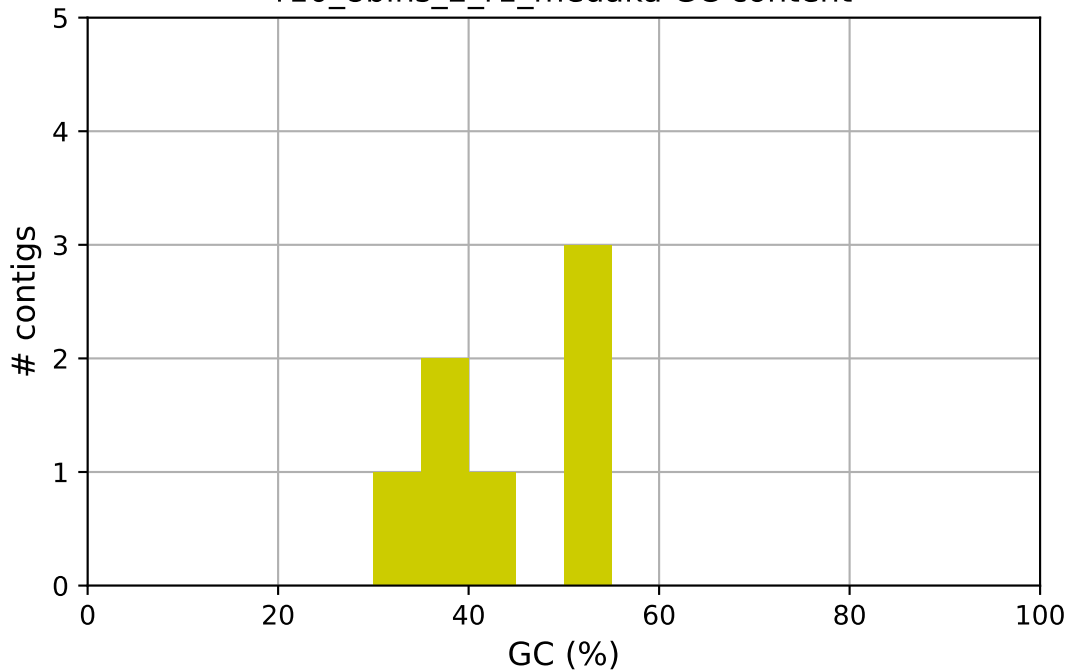
r10_8bins_2_MP

r10_8bins_2_MP_helen GC content



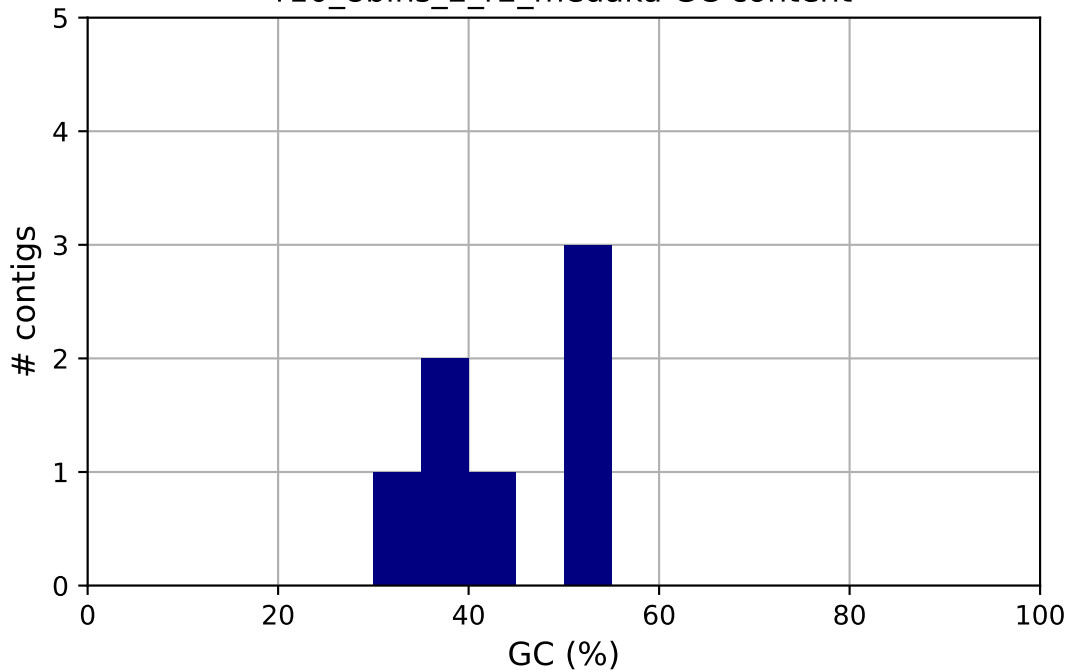
r10_8bins_2_MP_helen

r10_8bins_2_r1_medaka GC content



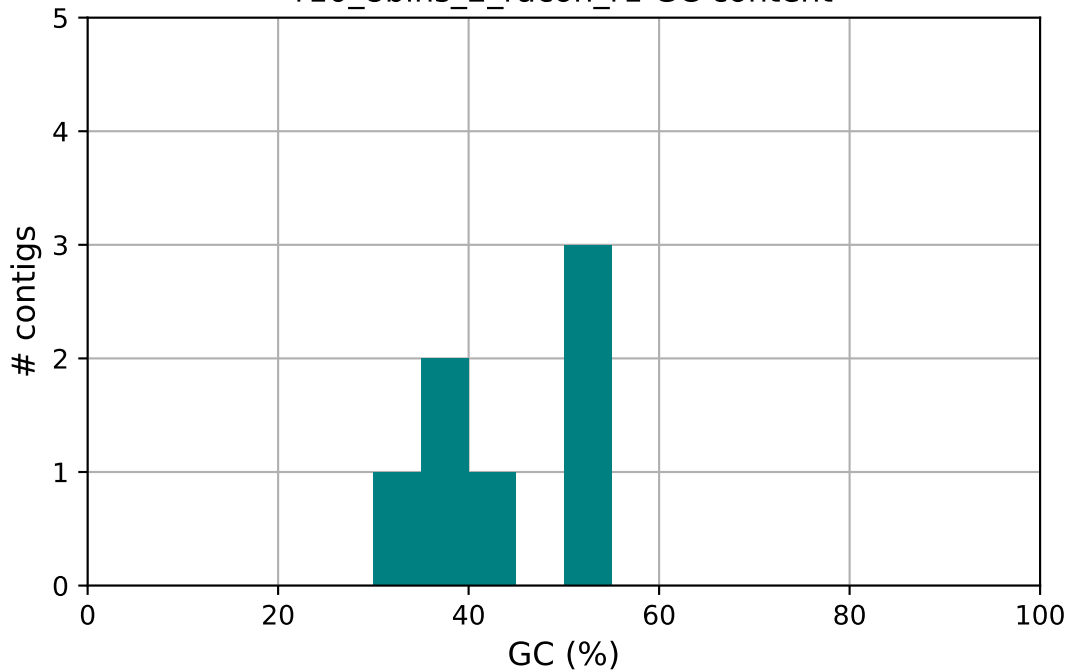
r10_8bins_2_r1_medaka

r10_8bins_2_r2_medaka GC content



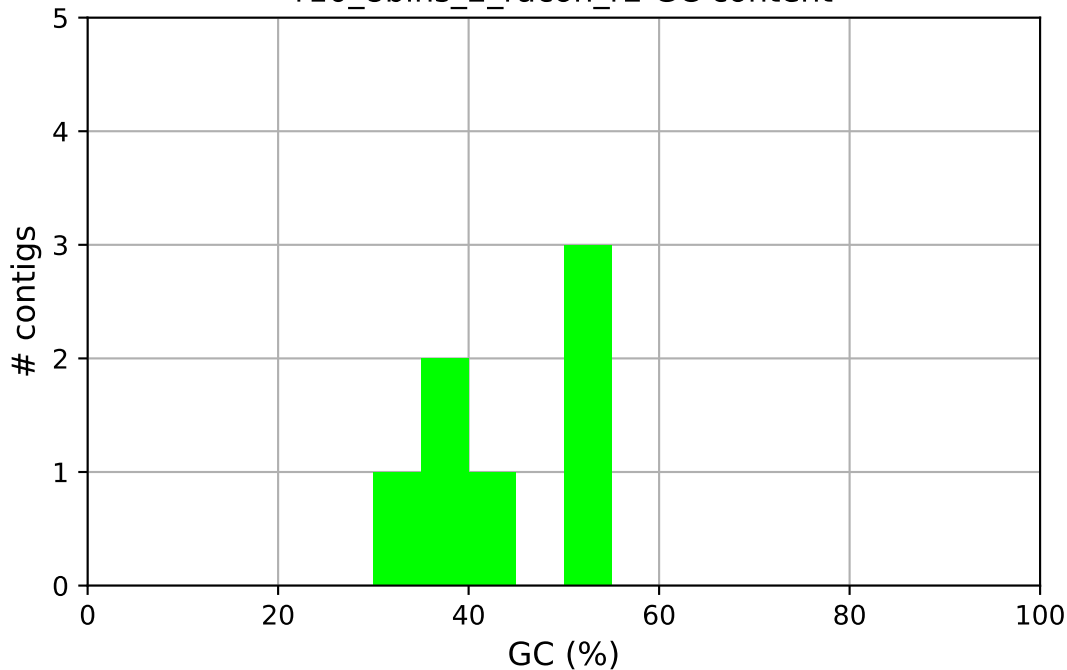
r10_8bins_2_r2_medaka

r10_8bins_2_racon_r1 GC content



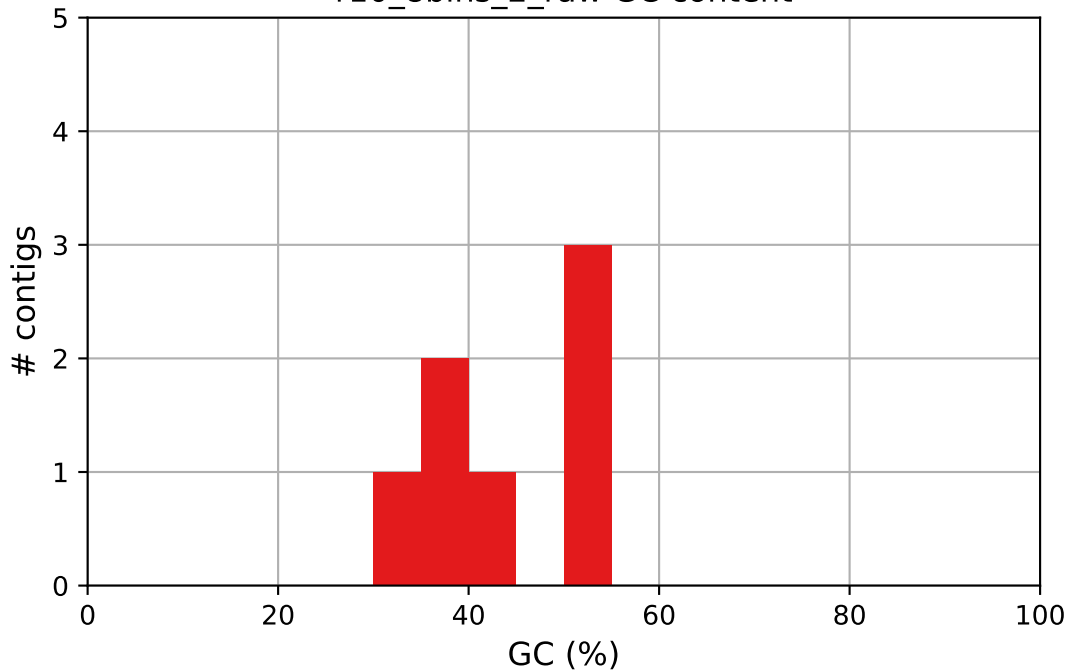
r10_8bins_2_racon_r1

r10_8bins_2_racon_r2 GC content



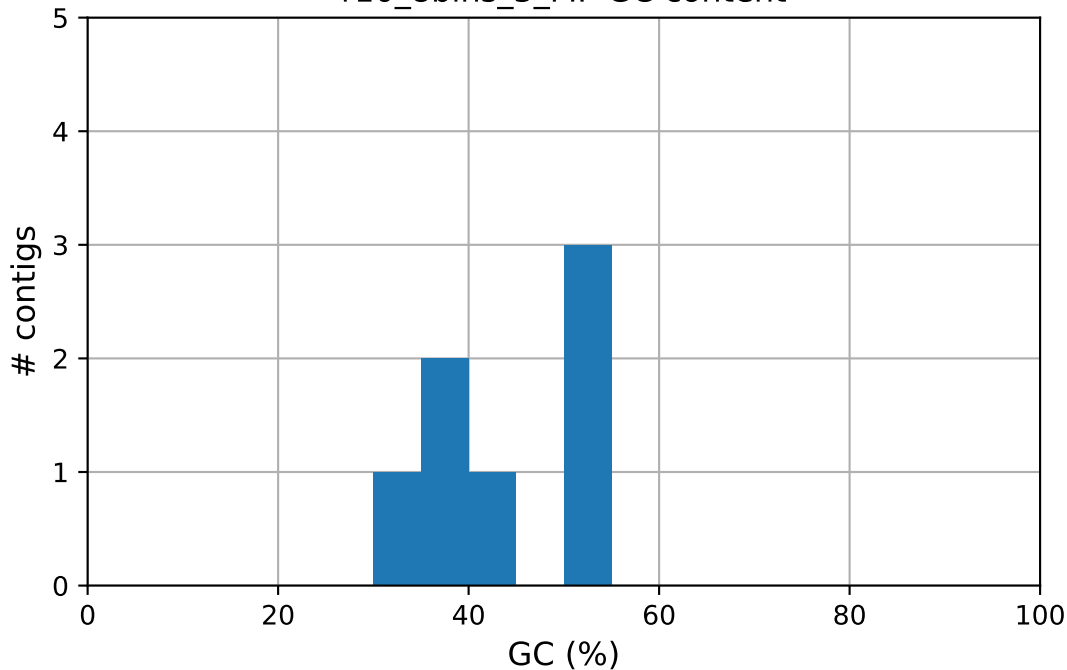
■ r10_8bins_2_racon_r2

r10_8bins_2_raw GC content



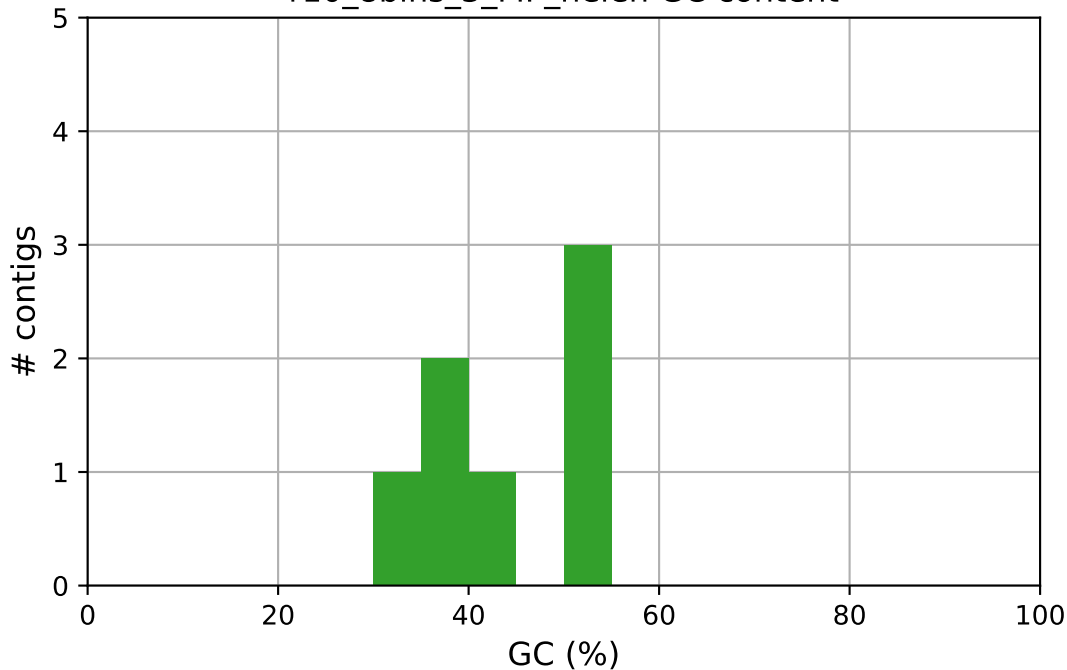
r10_8bins_2_raw

r10_8bins_3_MP GC content



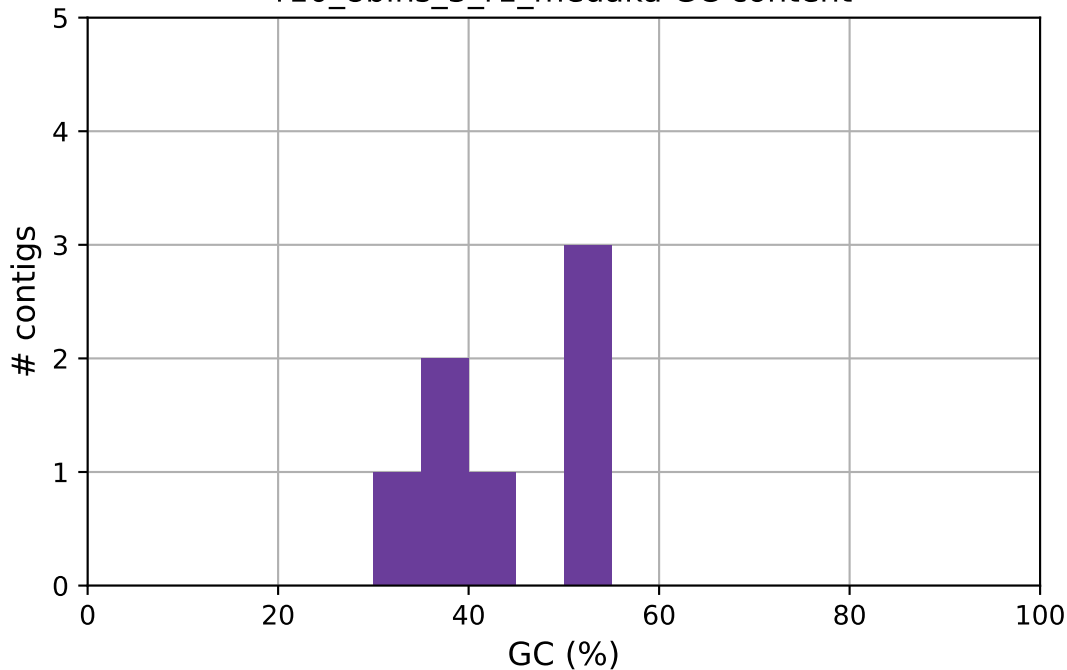
r10_8bins_3_MP

r10_8bins_3_MP_helen GC content



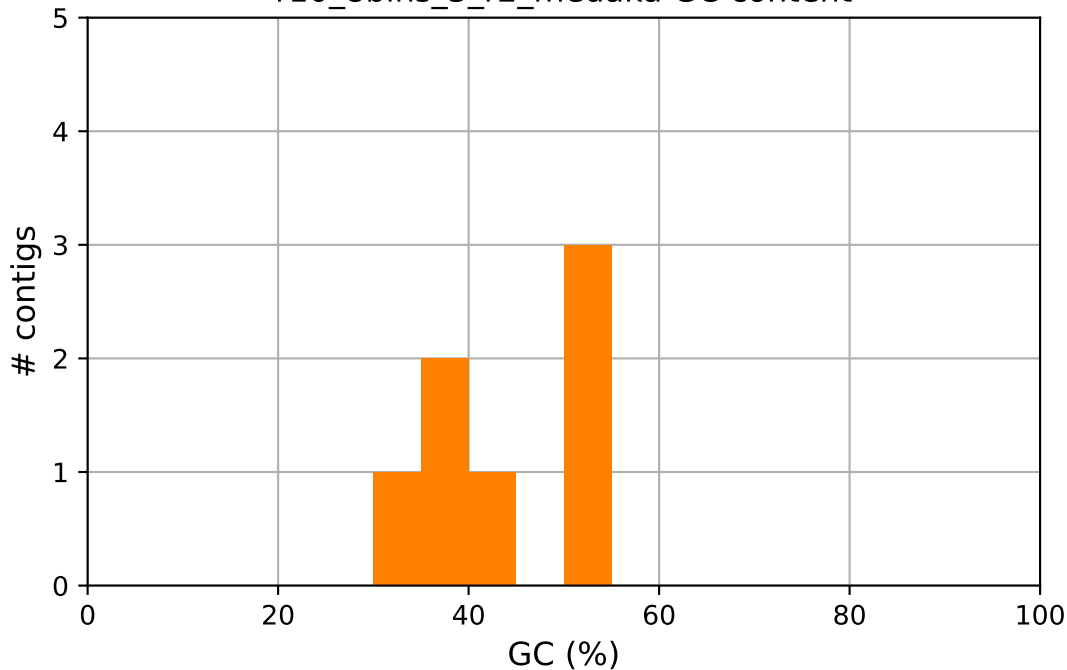
r10_8bins_3_MP_helen

r10_8bins_3_r1_medaka GC content



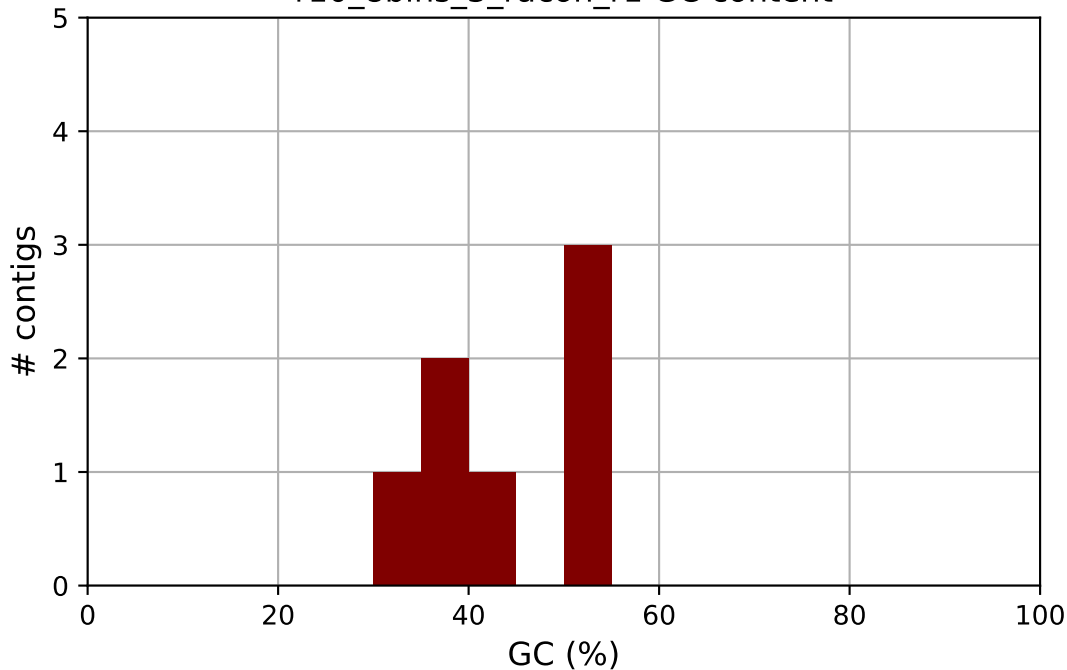
r10_8bins_3_r1_medaka

r10_8bins_3_r2_medaka GC content



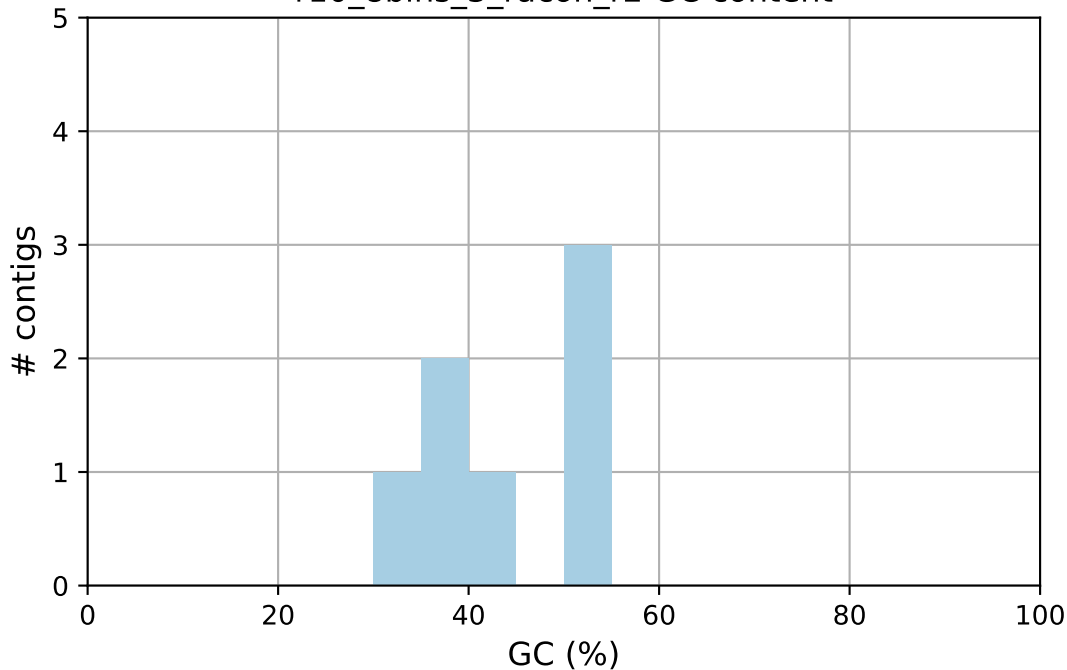
r10_8bins_3_r2_medaka

r10_8bins_3_racon_r1 GC content



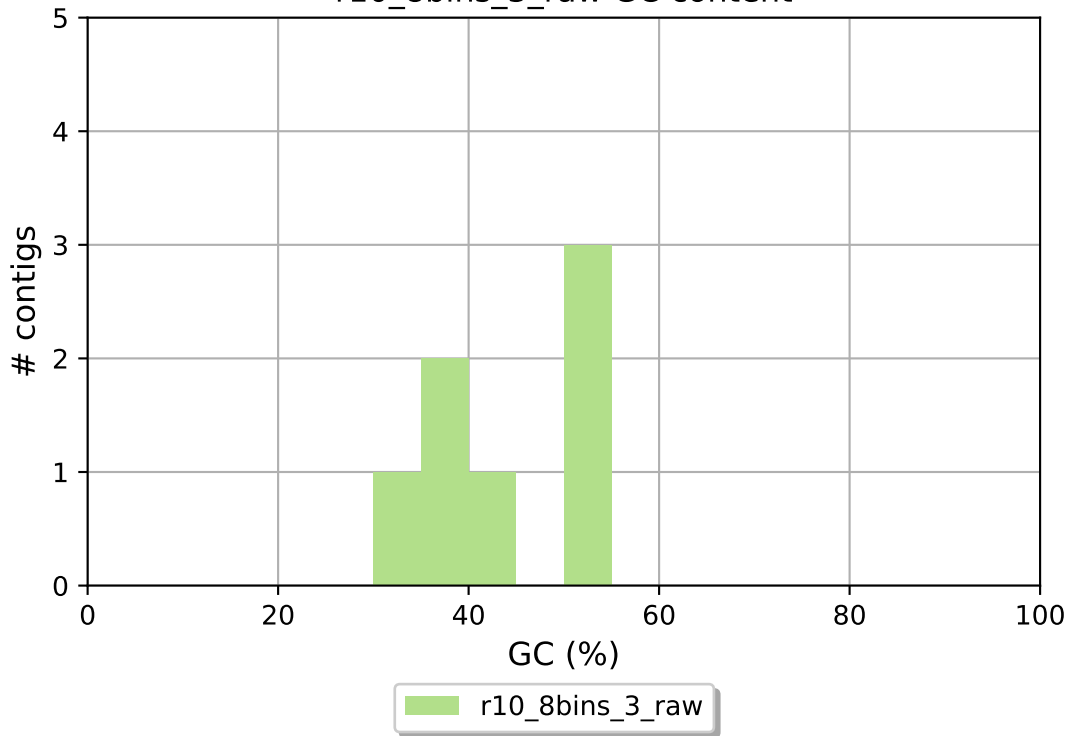
r10_8bins_3_racon_r1

r10_8bins_3_racon_r2 GC content

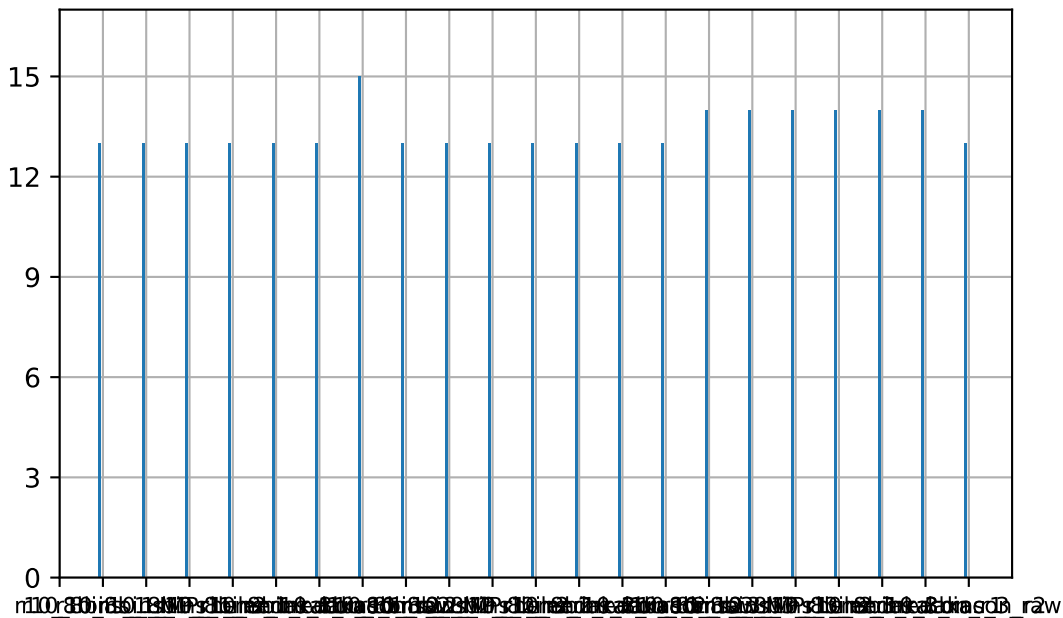


r10_8bins_3_racon_r2

r10_8bins_3_raw GC content

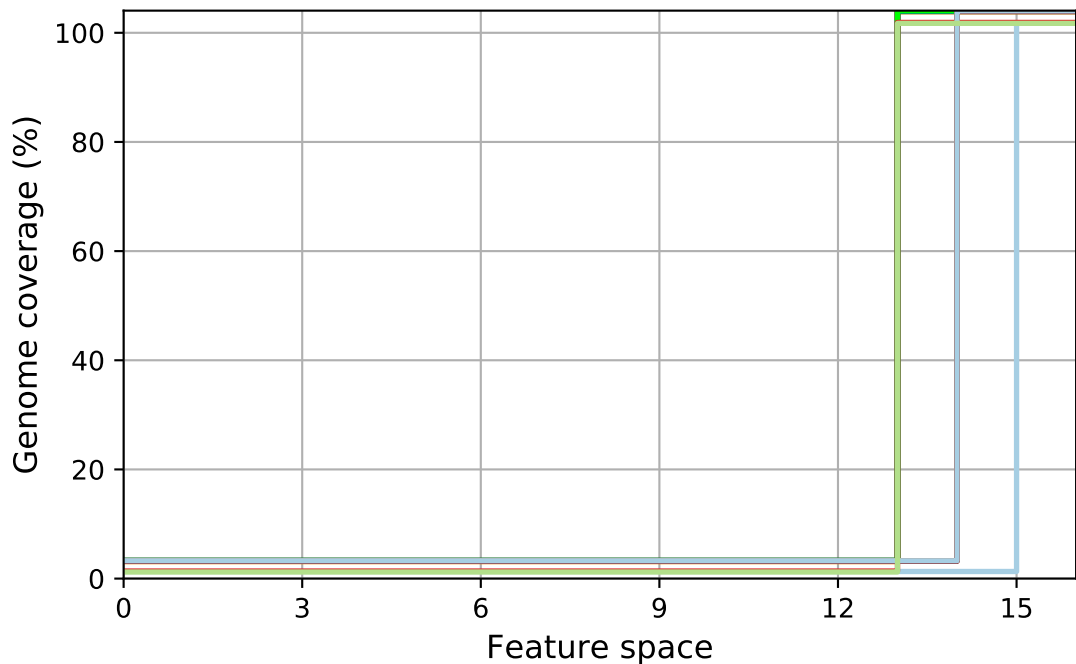


Misassemblies



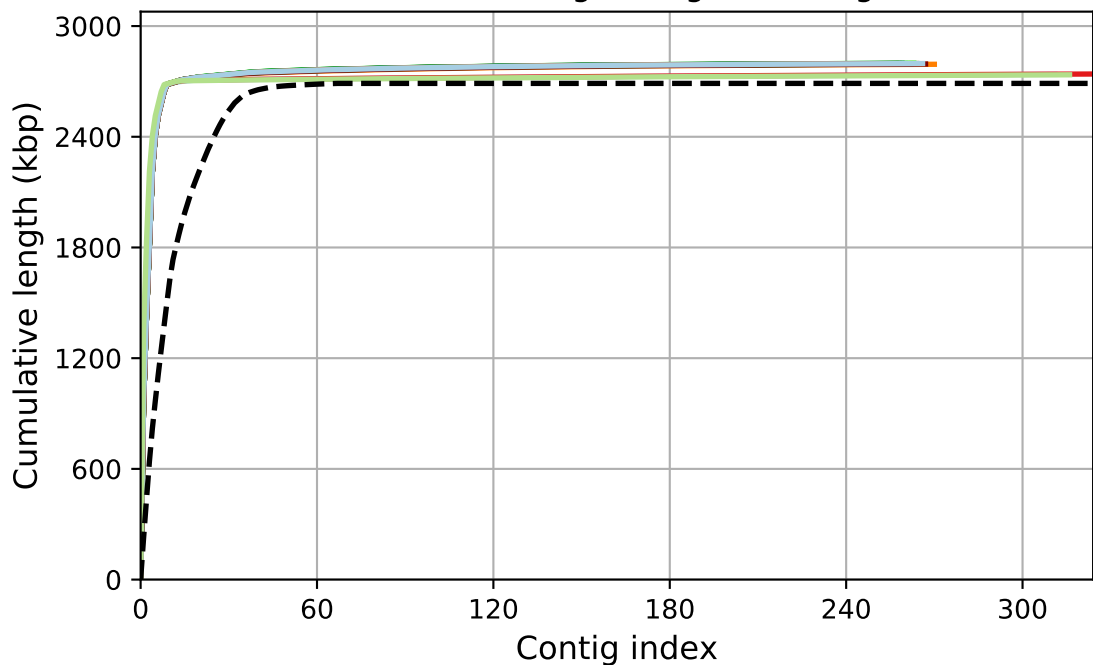
translocations

FRCurve (misassemblies)



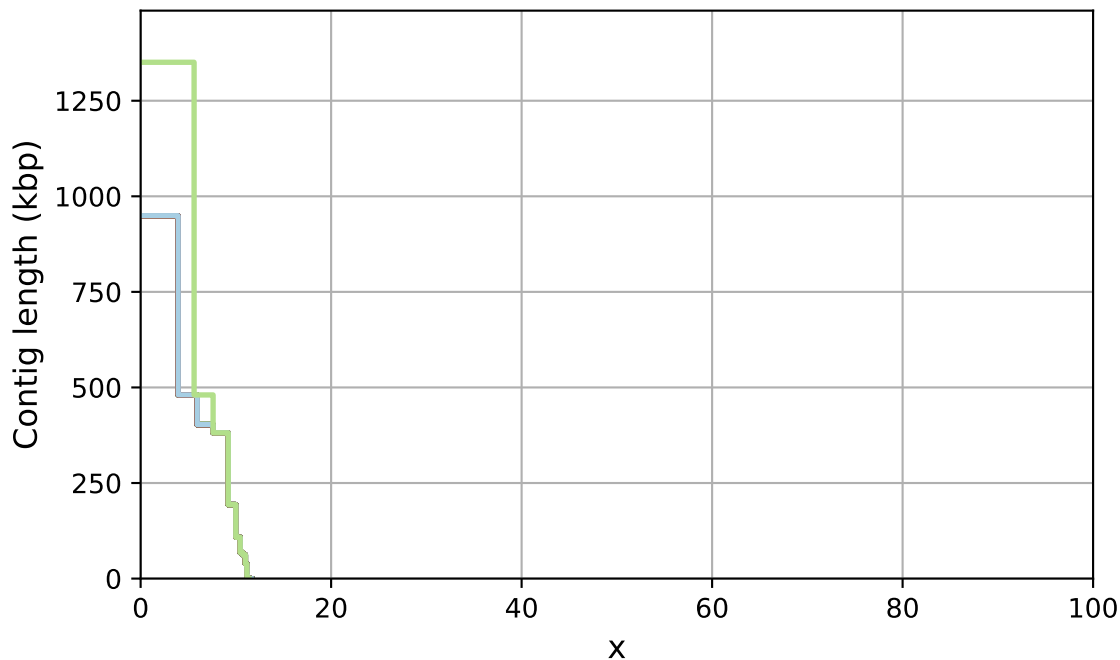
r10_8bins_1_MP	r10_8bins_2_MP	r10_8bins_3_MP
r10_8bins_1_MP_helen	r10_8bins_2_MP_helen	r10_8bins_3_MP_helen
r10_8bins_1_r1_medaka	r10_8bins_2_r1_medaka	r10_8bins_3_r1_medaka
r10_8bins_1_r2_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_medaka

Cumulative length (aligned contigs)



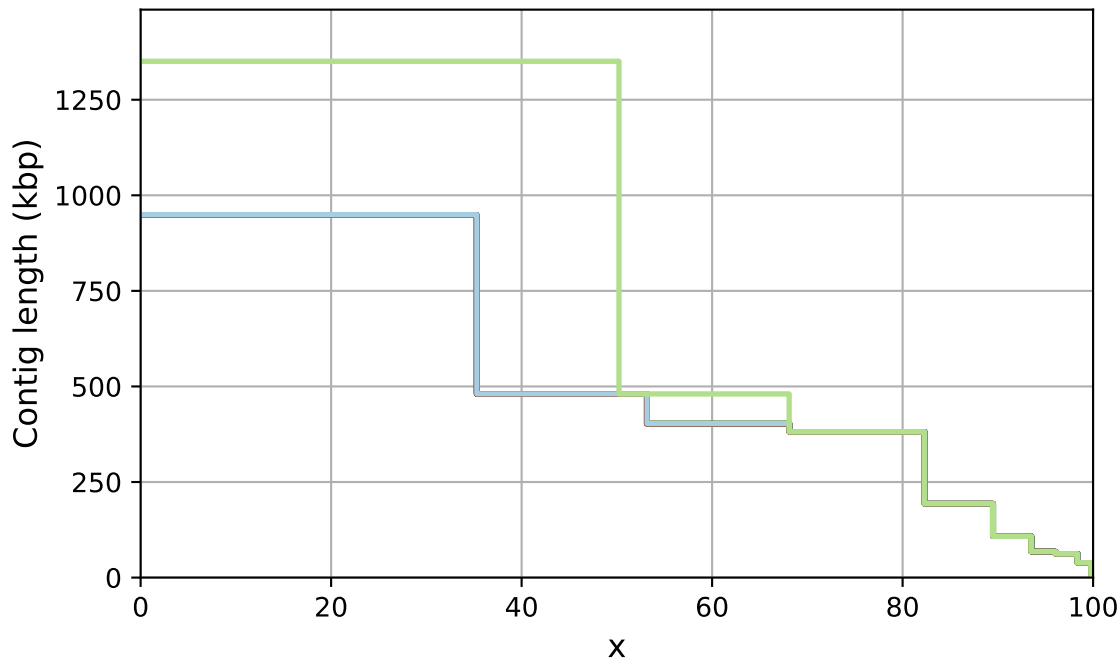
— r10_8bins_1_MP — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_MP_helen — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r1_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_racon_r1 — r10_8bins_3_racon_r1

NAX



r10_8bins_1_MP	r10_8bins_2_MP	r10_8bins_3_MP
r10_8bins_1_MP_helen	r10_8bins_2_MP_helen	r10_8bins_3_MP_helen
r10_8bins_1_r1_medaka	r10_8bins_2_r1_medaka	r10_8bins_3_r1_medaka
r10_8bins_1_r2_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_medaka

NGAx



— r10_8bins_1_MP — r10_8bins_2_MP — r10_8bins_3_MP
— r10_8bins_1_MP_helen — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_r1_medaka — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka

Genome fraction, %

