

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_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	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		
# contigs (>= 10000 bp)	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		
# contigs (>= 50000 bp)	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	24061018	24055808	24060952
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24061018	24055808	24060952
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24061018	24055808	24060952
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24061018	24055808	24060952
# contigs	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	24061018	24055808	24060952
Reference length	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	44.77	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	
N50	4045595	4045615	4045602	4045598	4045293	4045319	4043044	4045596	4045616	4045587	4045593	4045258	4045323	4042479	4045596	4045613	4045582	4045248	4045358	4043002	
NG50	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	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	2845434	2845286	2845324	2843844	
NG75	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	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		
LG50	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		
LG75	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	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		
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	19	9	10	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		
# scaffold gap loc. mis.	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	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		
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	99.538		
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	1.023		
# 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		
# 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							

Misassemblies report

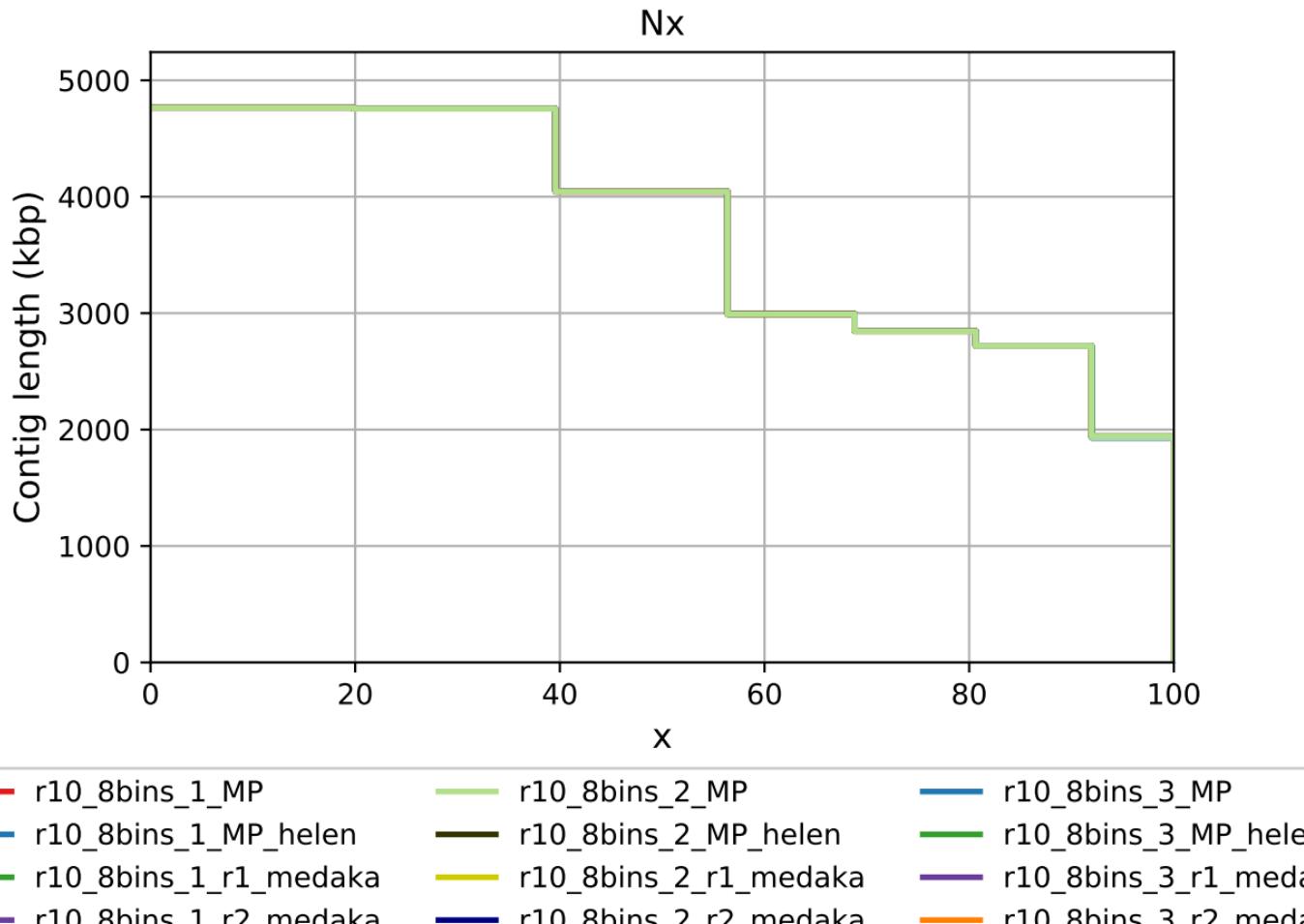
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# misassemblies	13	13	13	13	13	13	15	13	13	13	13	13	14	14	14	14	14	14	13		
# contig misassemblies	13	13	13	13	13	13	15	13	13	13	13	13	14	14	14	14	14	14	13		
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# c. translocations	13	13	13	13	13	13	15	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		
# scaffold misassemblies	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		
# s. translocations	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		
# misassembled contigs	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	
# possible misassemblies	10	10	10	10	10	10	10	20	10	10	10	10	10	10	10	10	10	10	10	16	
# local misassemblies	9	10	10	10	10	9	10	19	9	9	9	9	9	9	9	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	
# scaffold gap loc. mis.	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	26	21	26	26	26	26	25	26	26	26	26	26	26	24	
# unaligned mis. contigs	6	6	6	6	6	6	6	5	6	6	6	6	5	6	6	6	6	6	5	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	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).

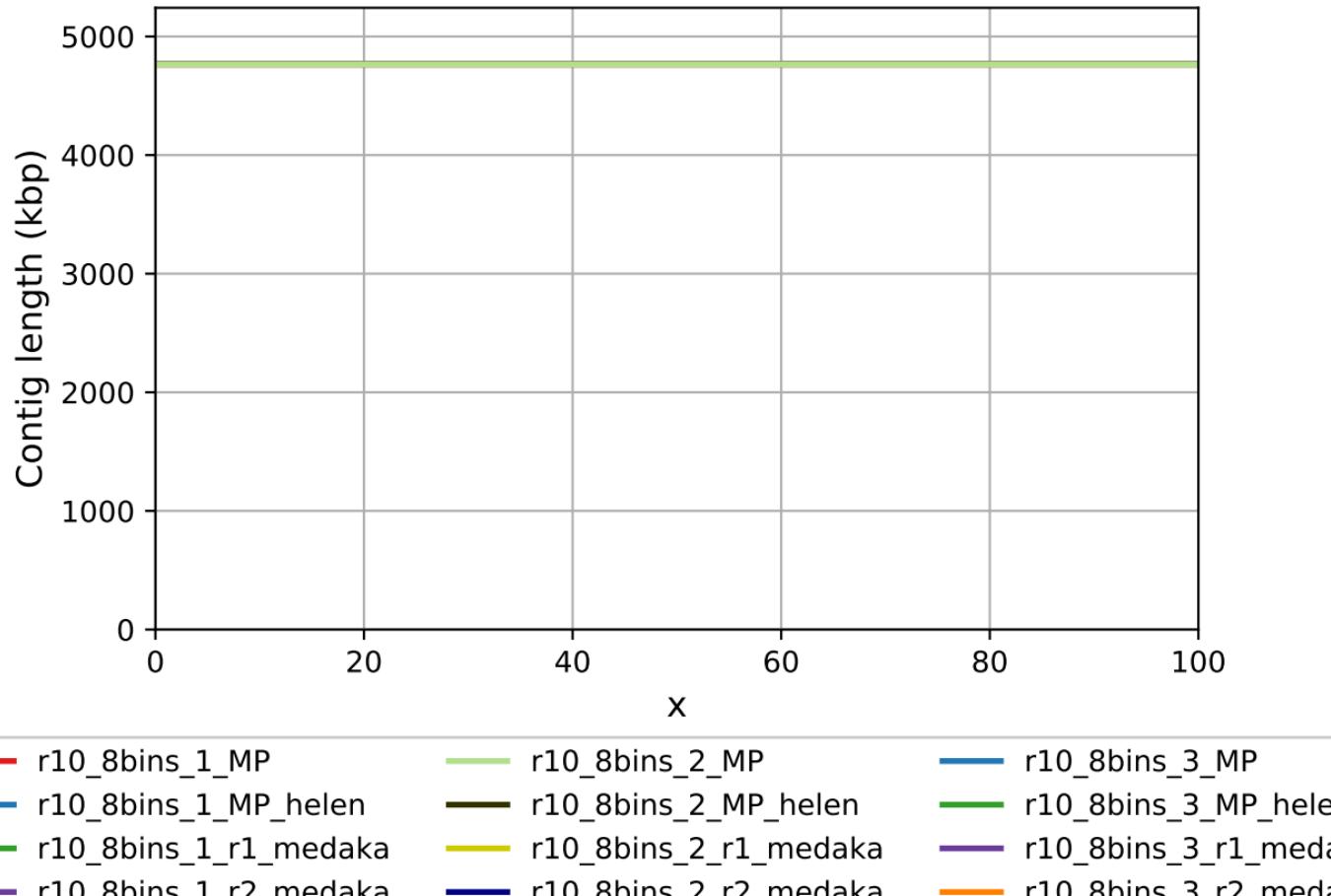
Unaligned report

	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_racon_r1	r10_8bins_2_racon_r2	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_3_raw	
# fully unaligned contigs	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	
# partially unaligned contigs	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	21262585	21264875	21254555	21318447	21272622	212763511	21266251	21263756	21256890	21323181
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

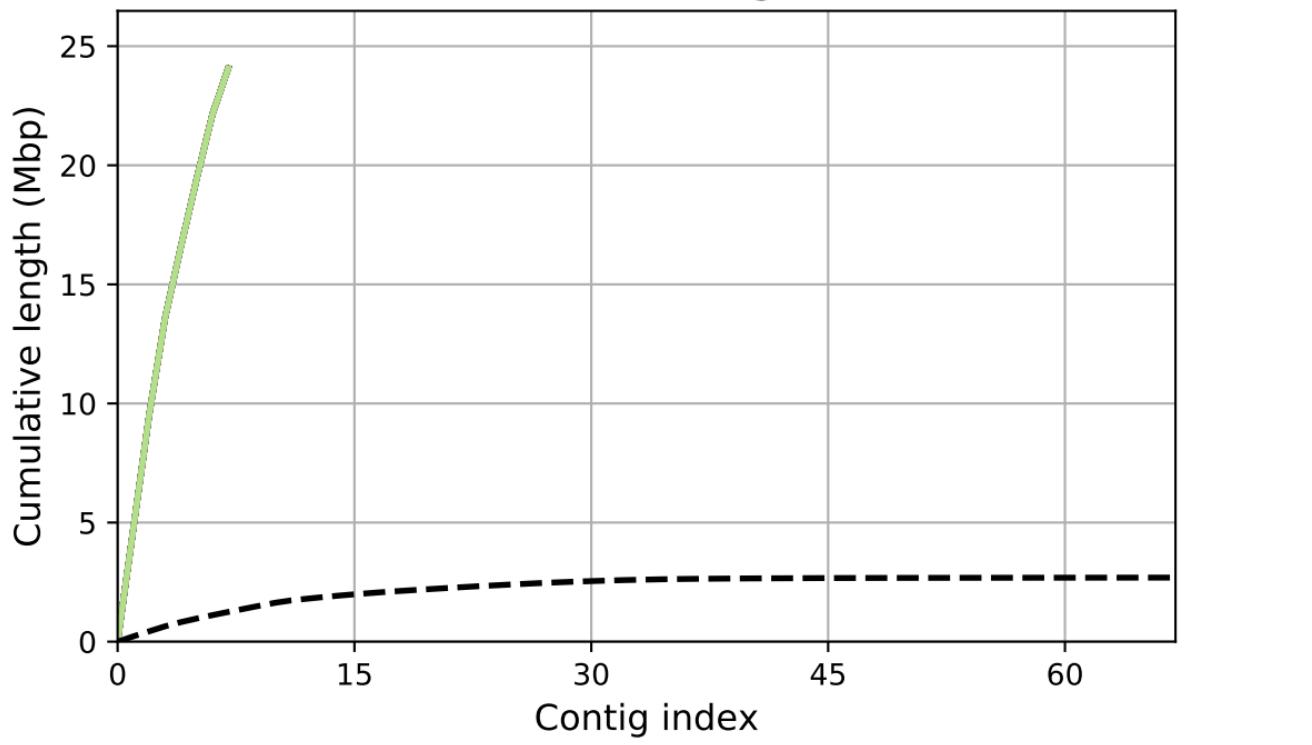
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted
(e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

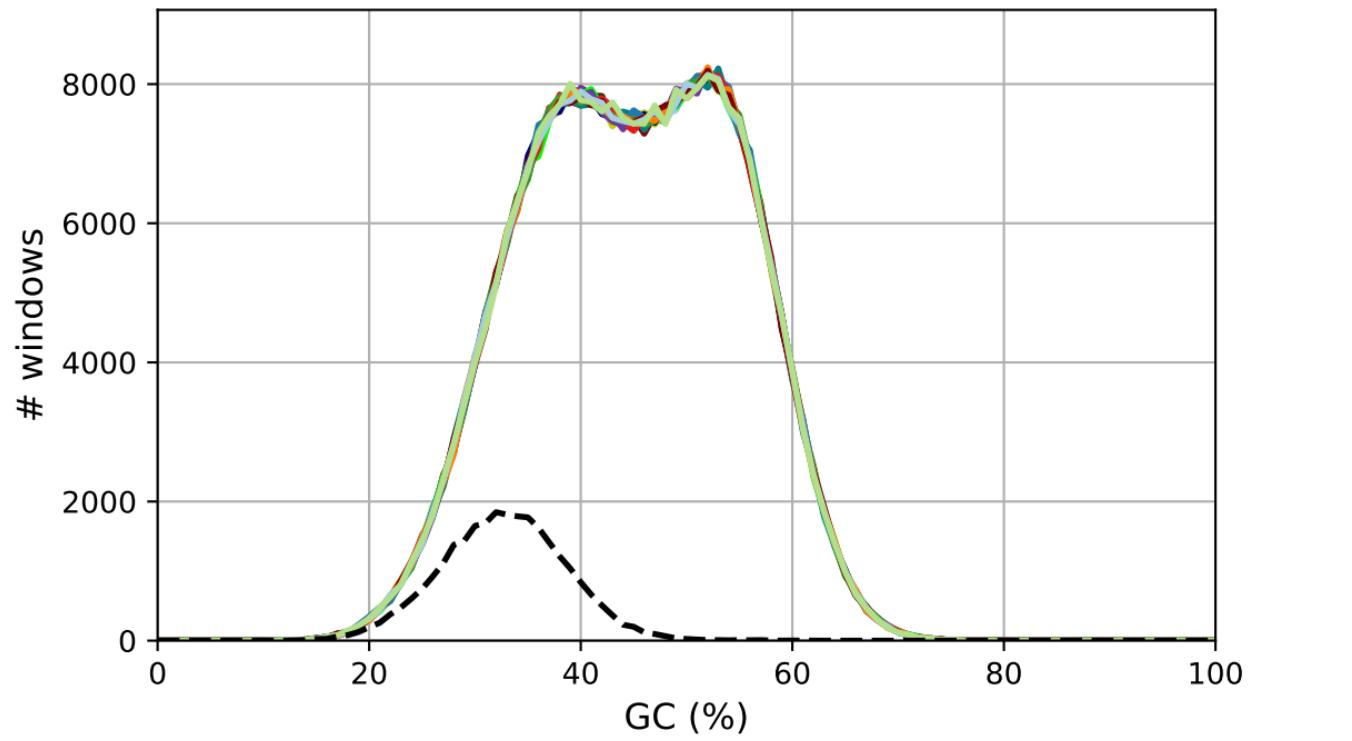


Cumulative length



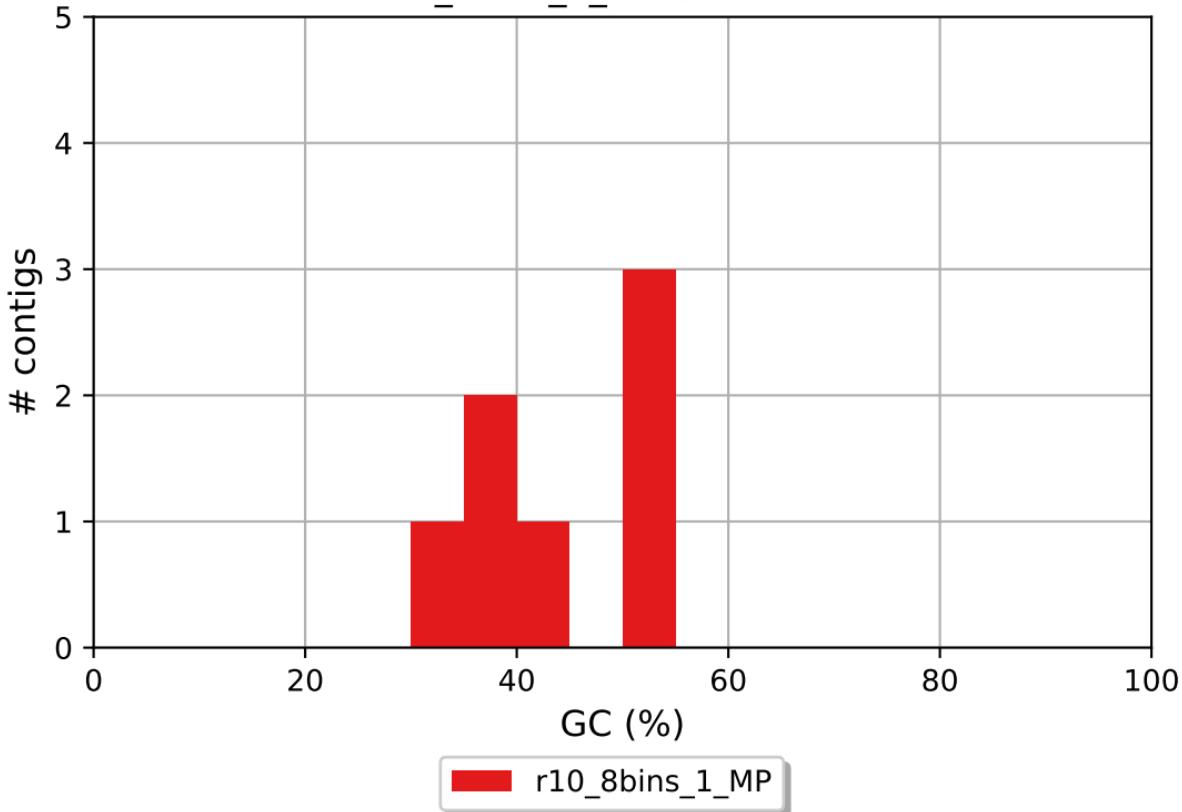
- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP_helen
- r10_8bins_3_r1_medaka
- r10_8bins_3_r2_medaka
- r10_8bins_3_racoon_r1
- r10_8bins_3_racoon_r2

GC content

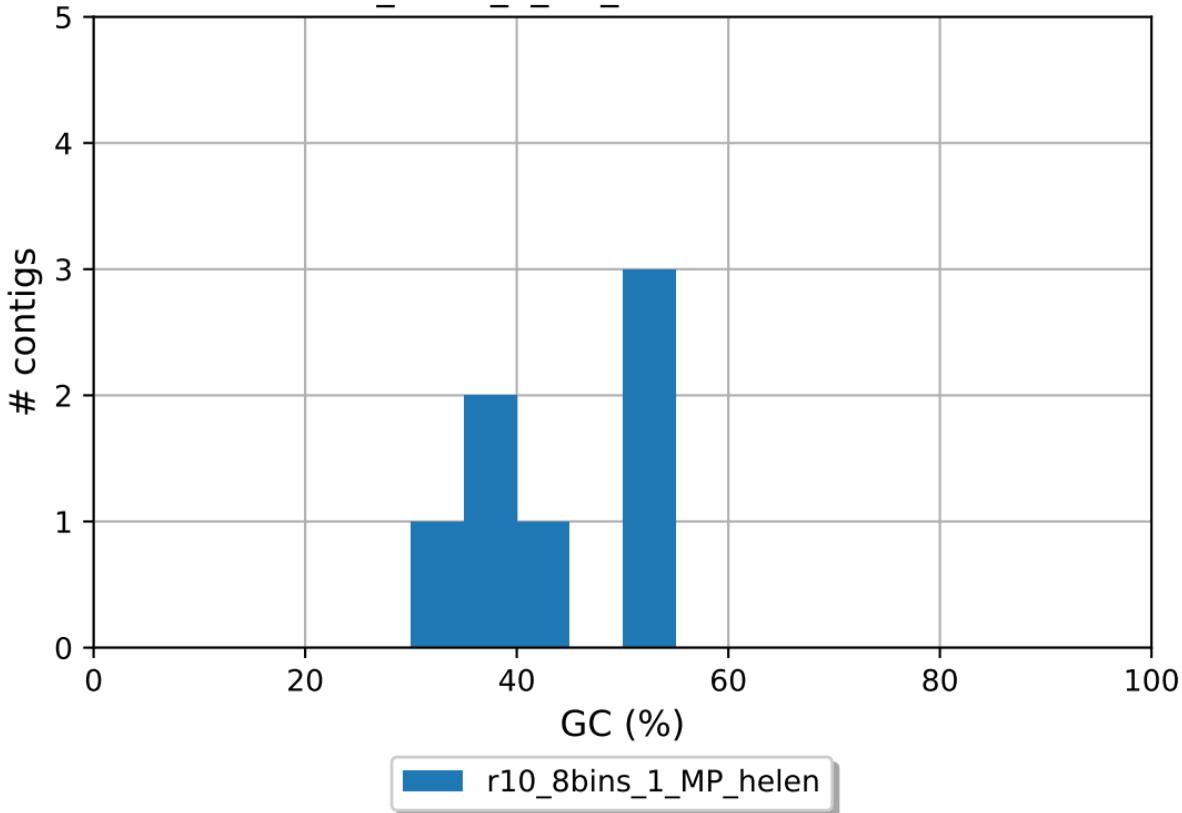


A horizontal legend bar consisting of nine colored segments and their corresponding labels. The colors are red, blue, green, purple, black, yellow, dark blue, orange, and brown. The labels are: r10_8bins_1_MP, r10_8bins_1_MP_helen, r10_8bins_1_r1_medaka, r10_8bins_1_r2_medaka, r10_8bins_2_MP_helen, r10_8bins_2_r1_medaka, r10_8bins_2_r2_medaka, r10_8bins_2_racon_r1, and r10_8bins_3_MP_helen.

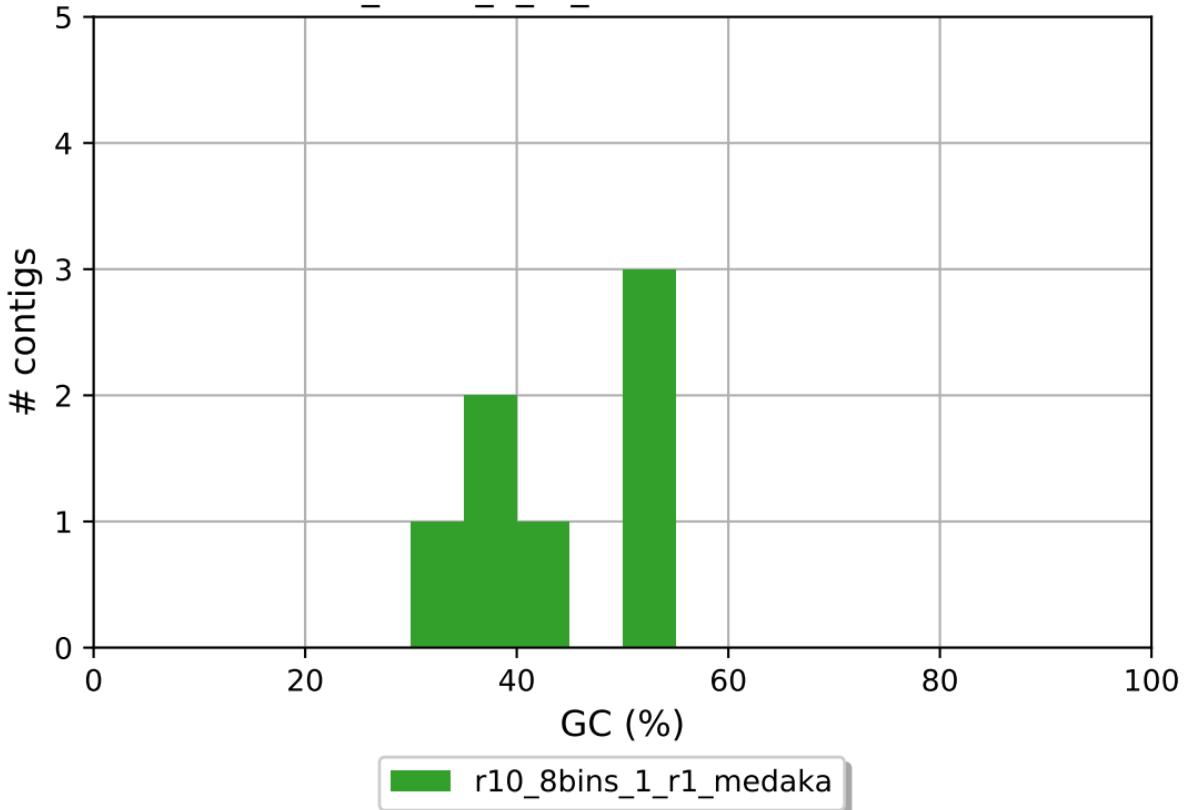
r10_8bins_1_MP GC content



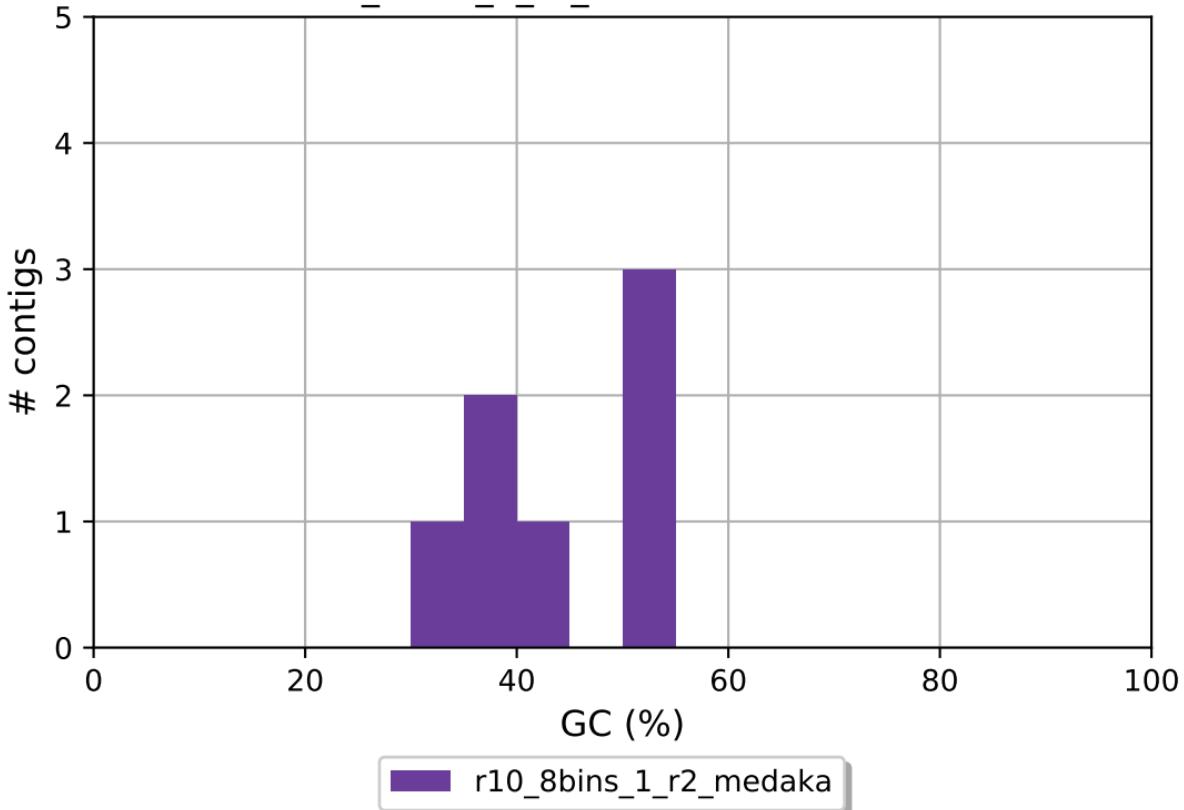
r10_8bins_1_MP_helen GC content



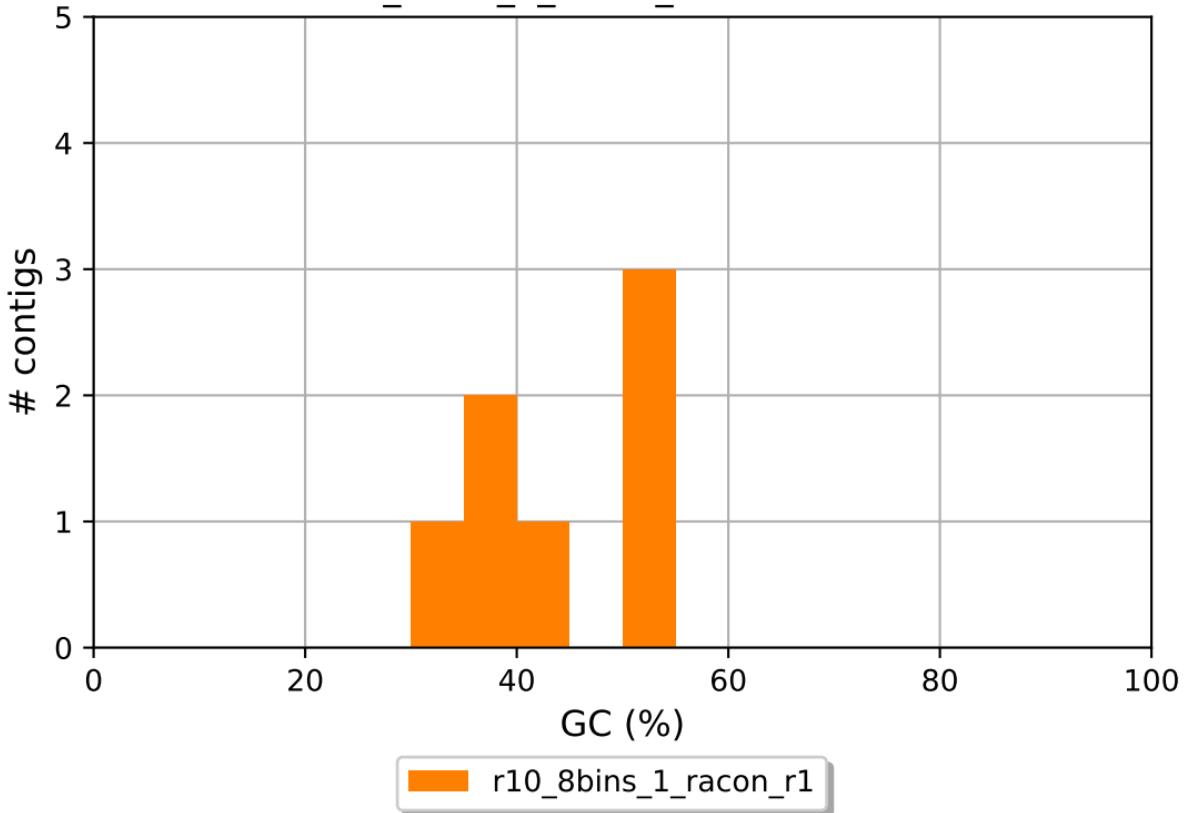
r10_8bins_1_r1_medaka GC content



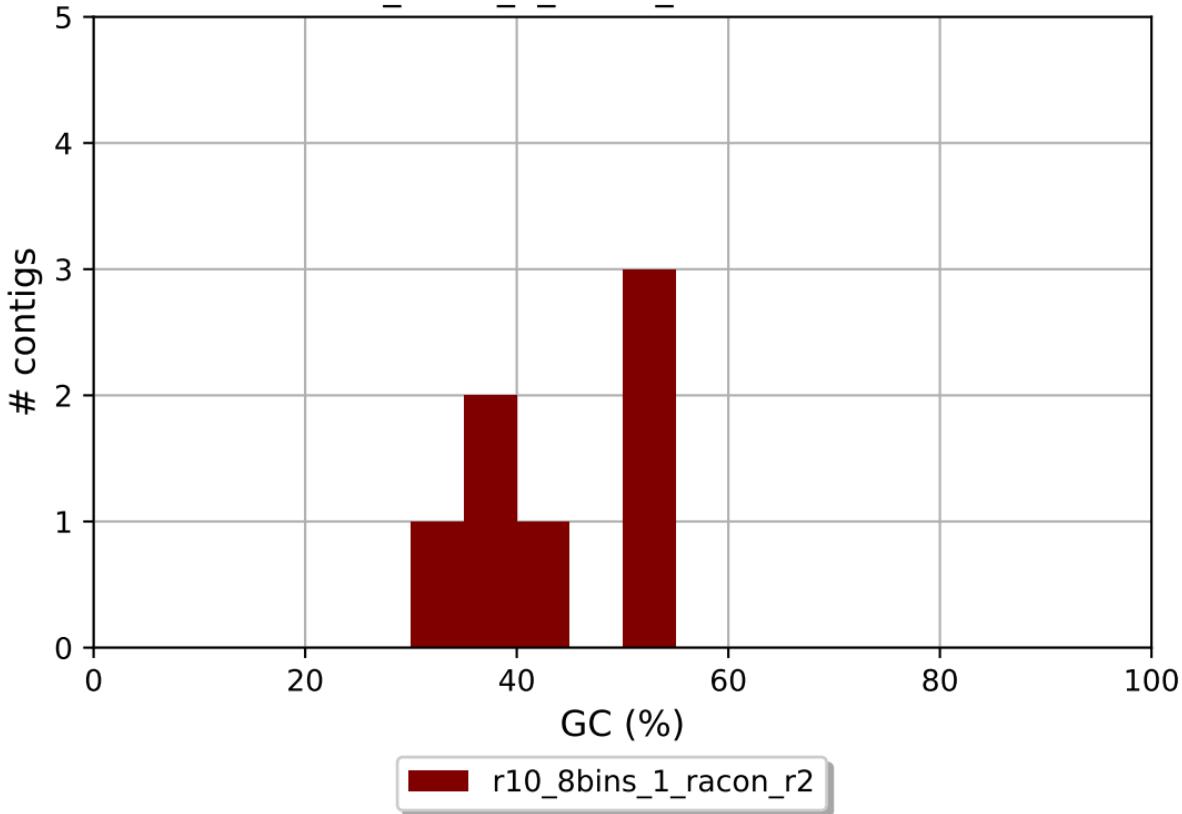
r10_8bins_1_r2_medaka GC content



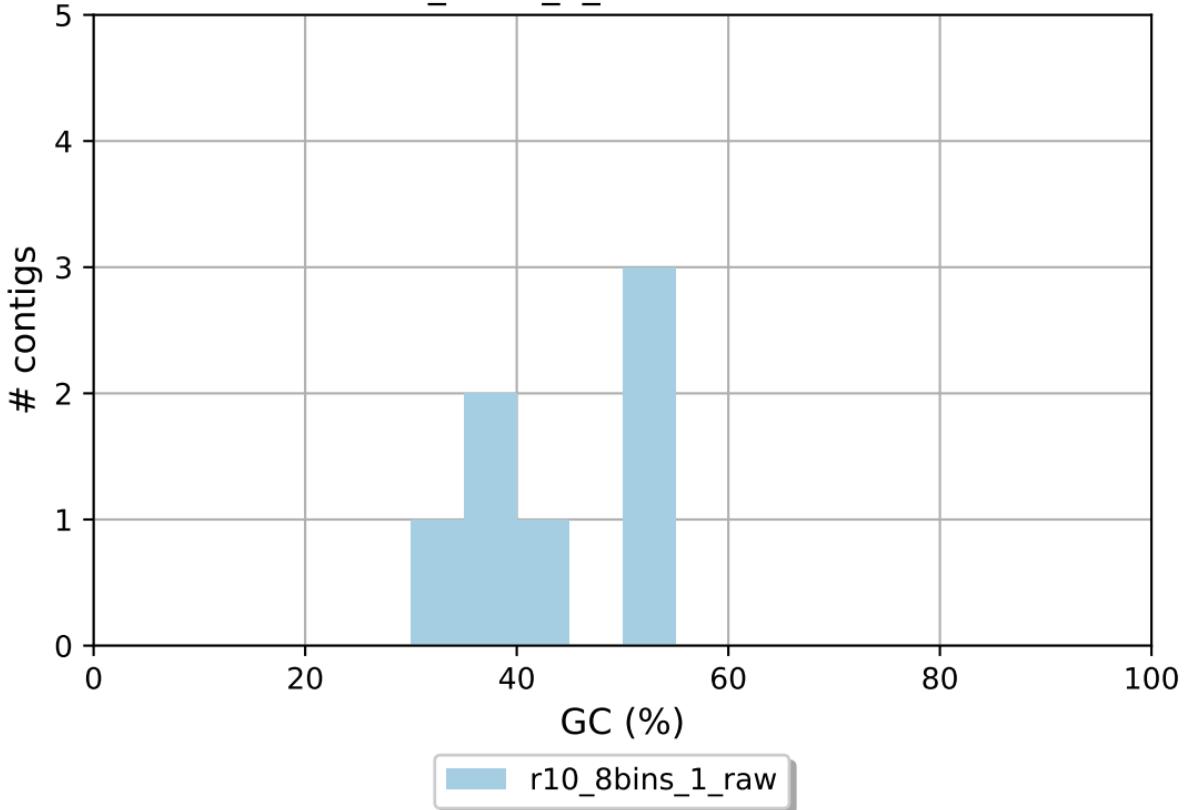
r10_8bins_1_racon_r1 GC content



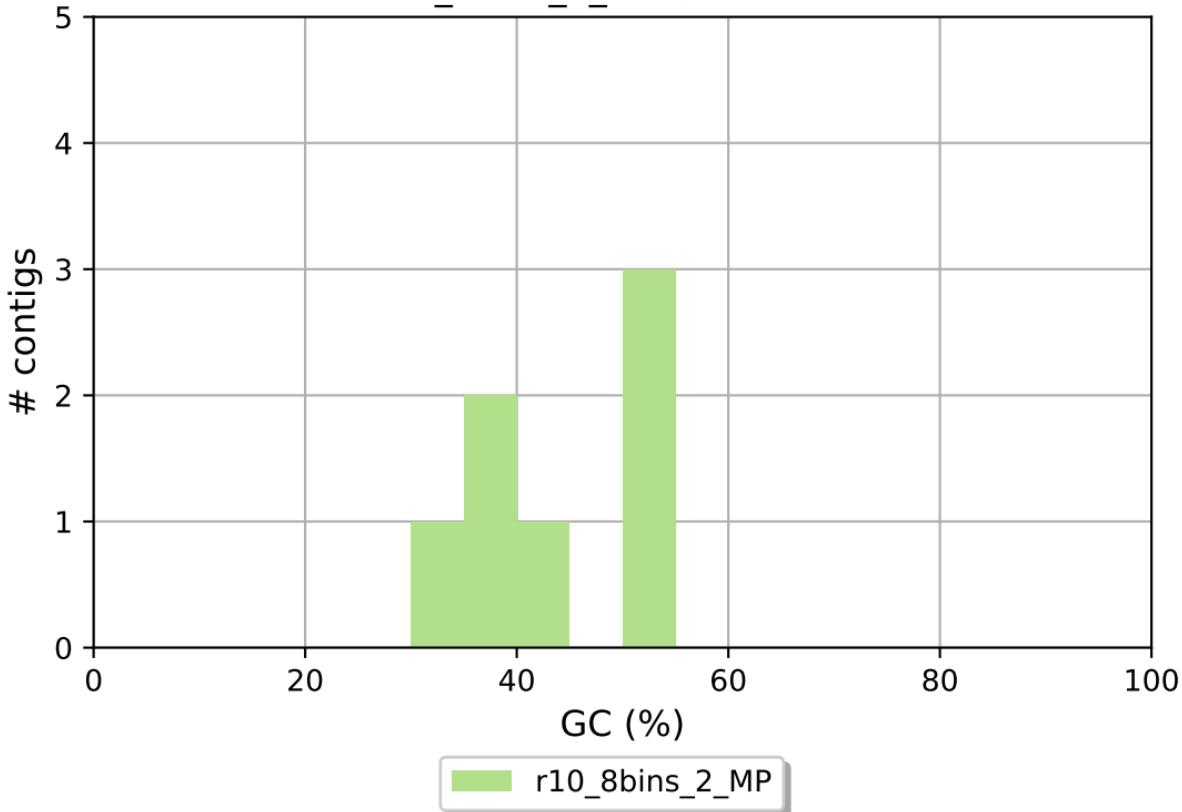
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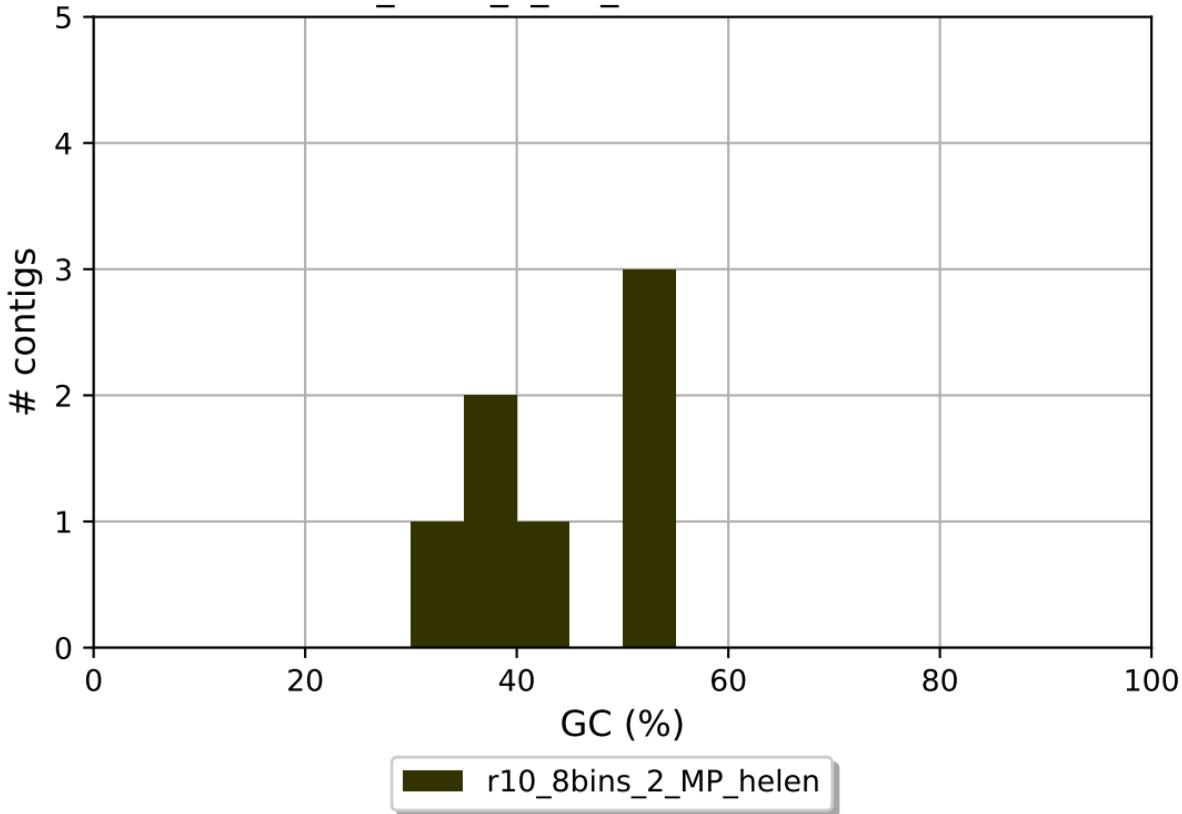
r10_8bins_1_raw GC content



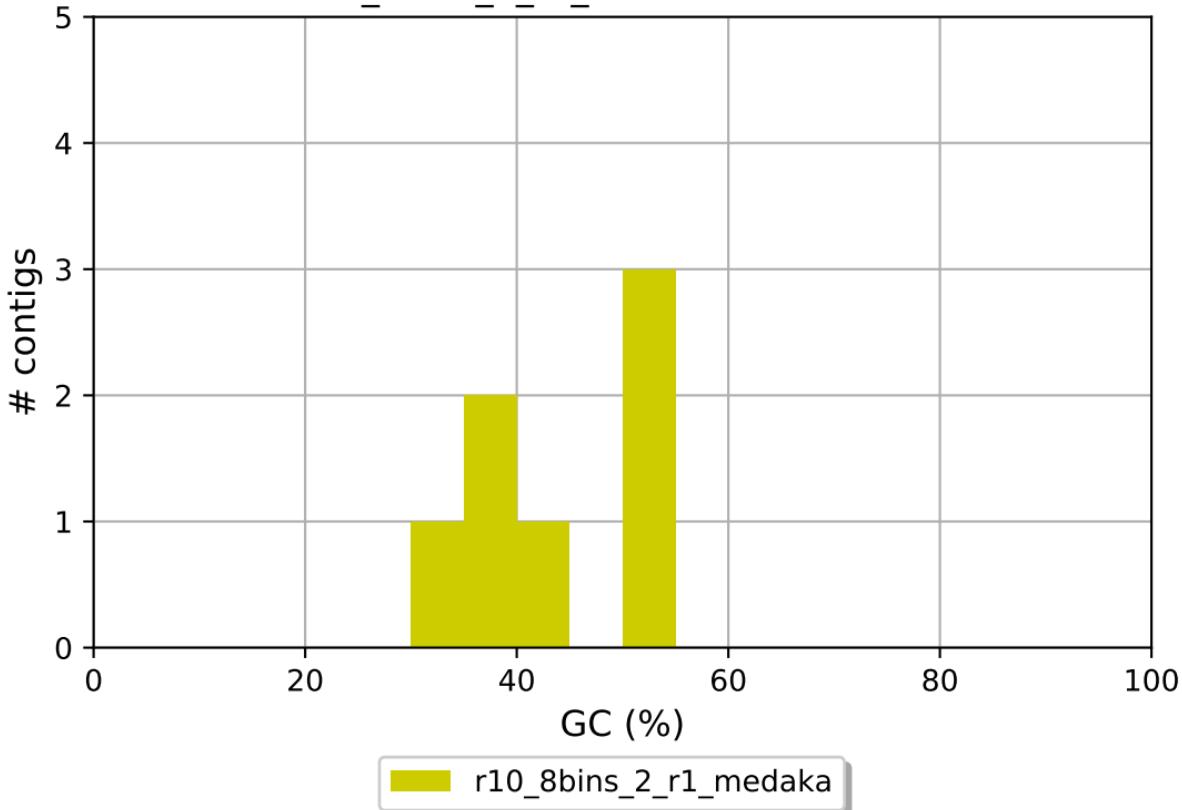
r10_8bins_2_MP GC content



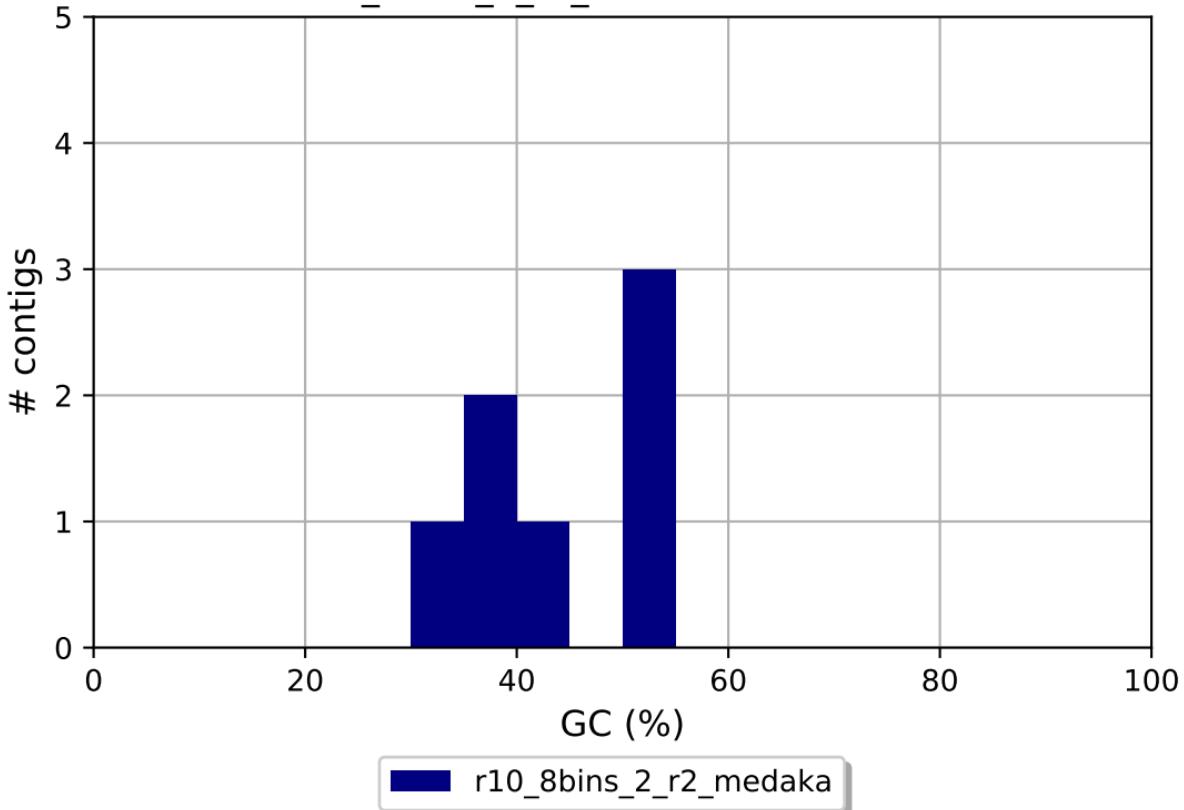
r10_8bins_2_MP_helen GC content



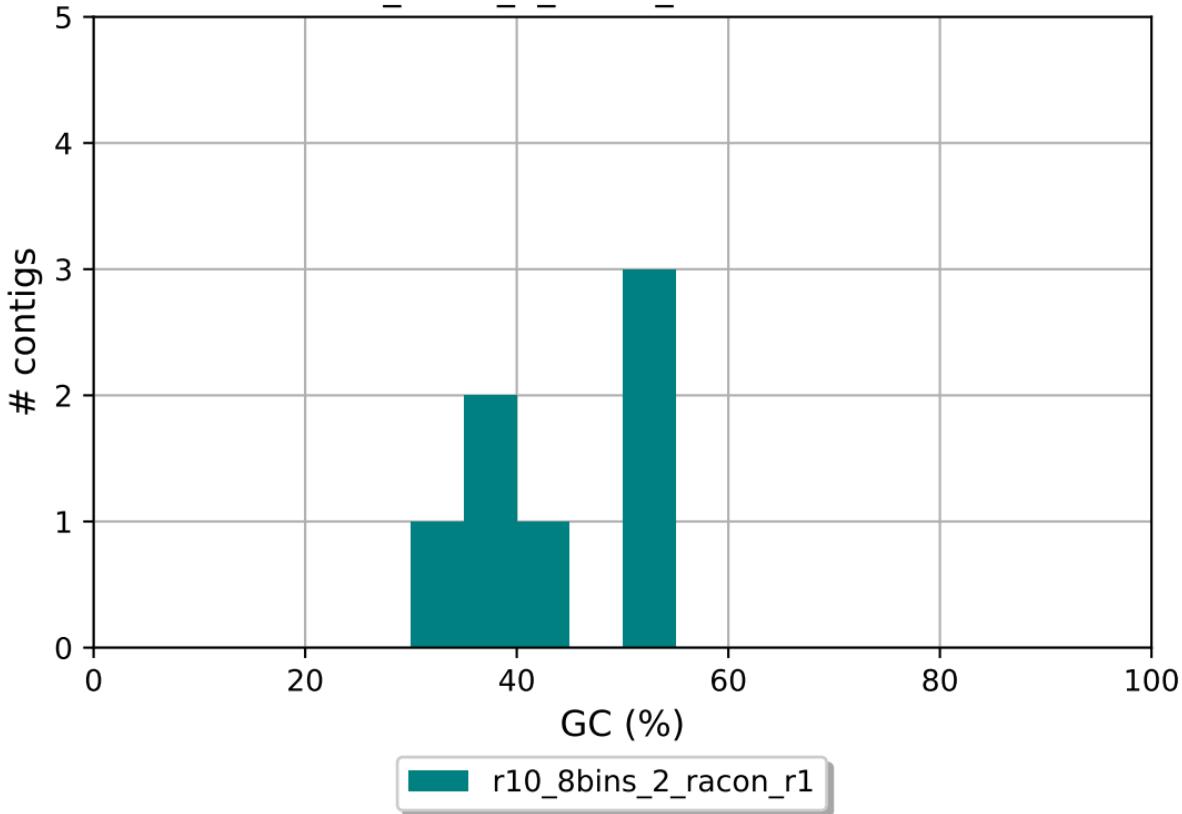
r10_8bins_2_r1_medaka GC content



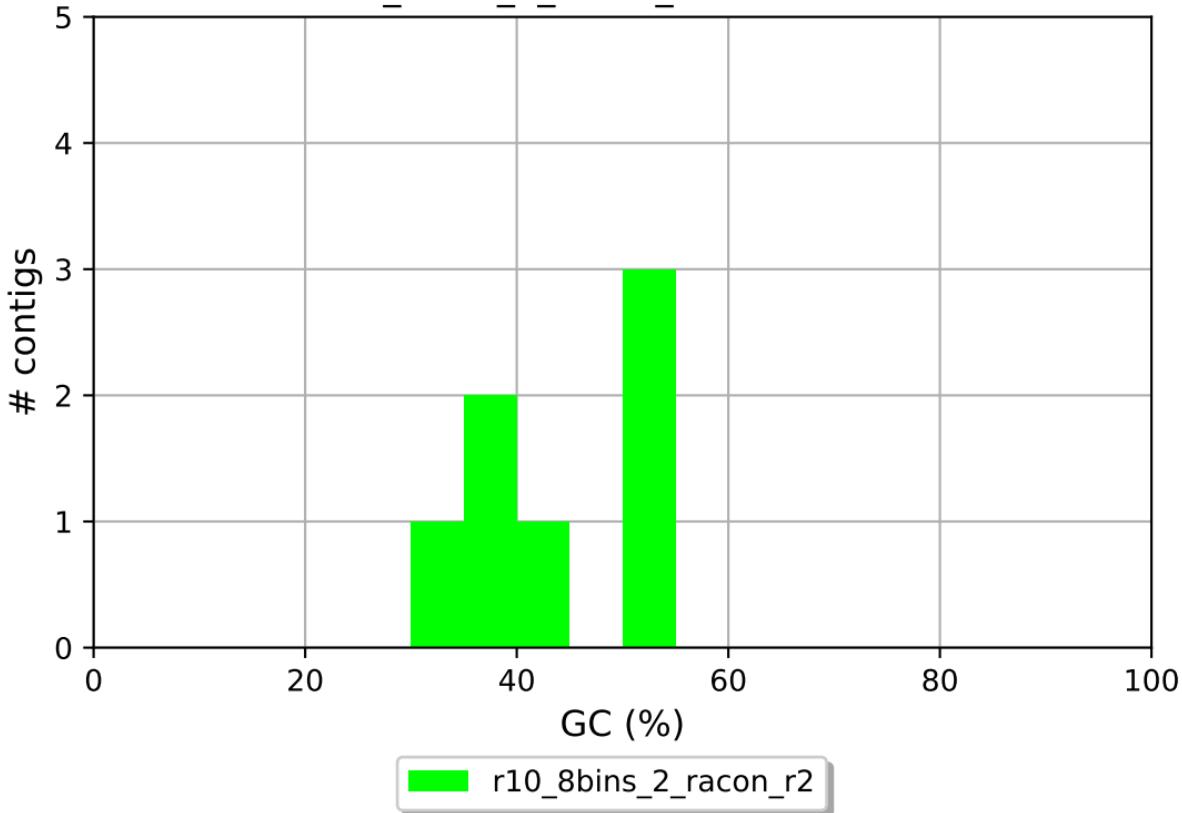
r10_8bins_2_r2_medaka GC content



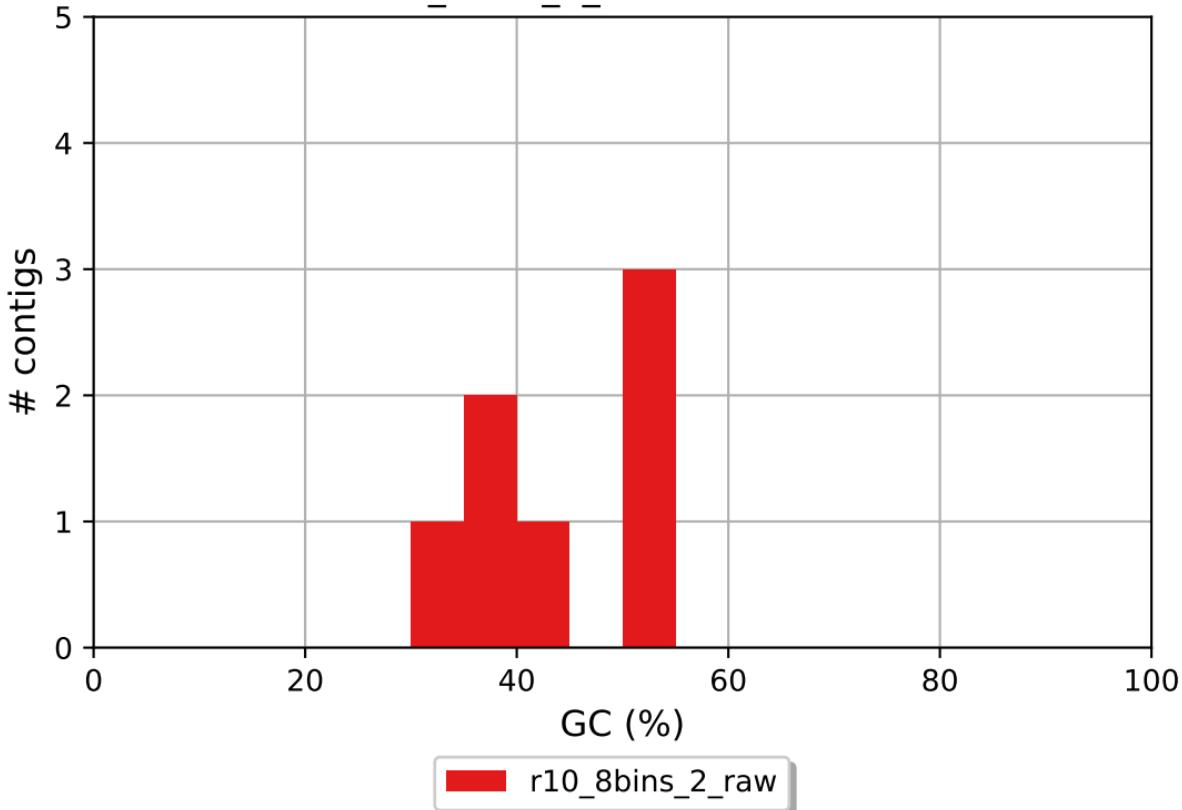
r10_8bins_2_racon_r1 GC content



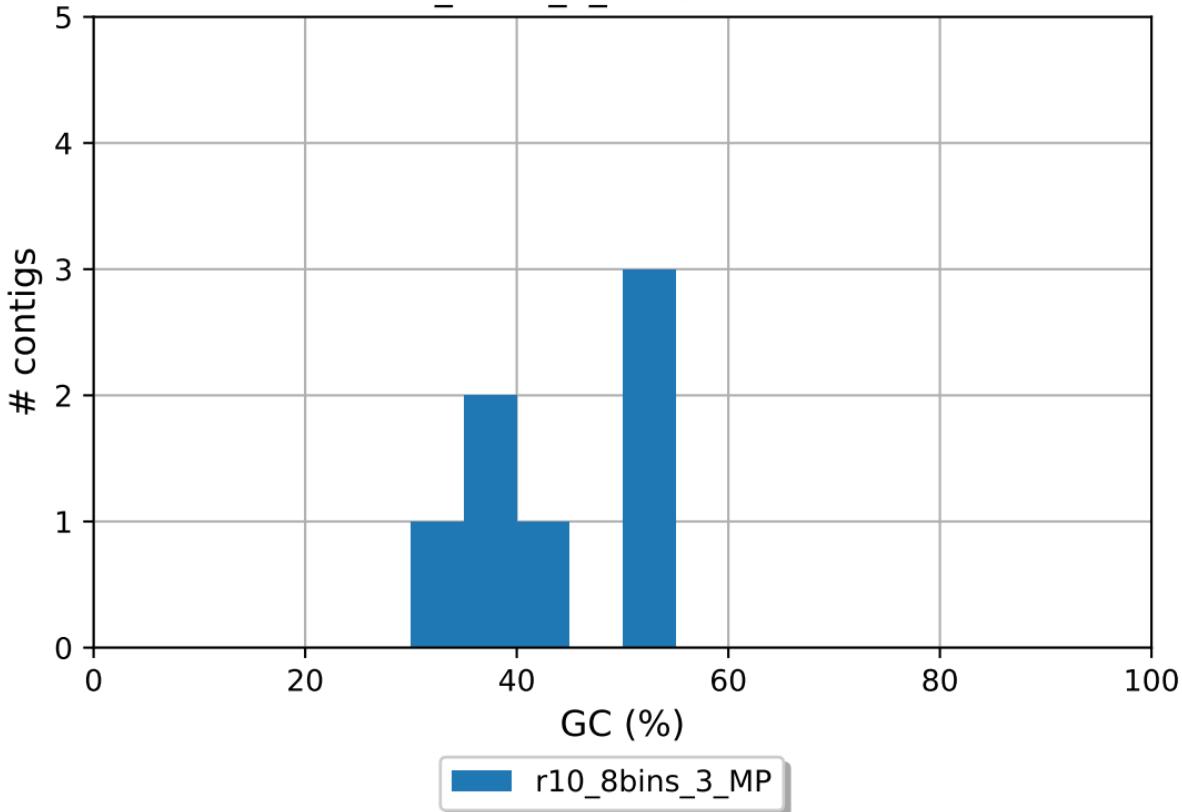
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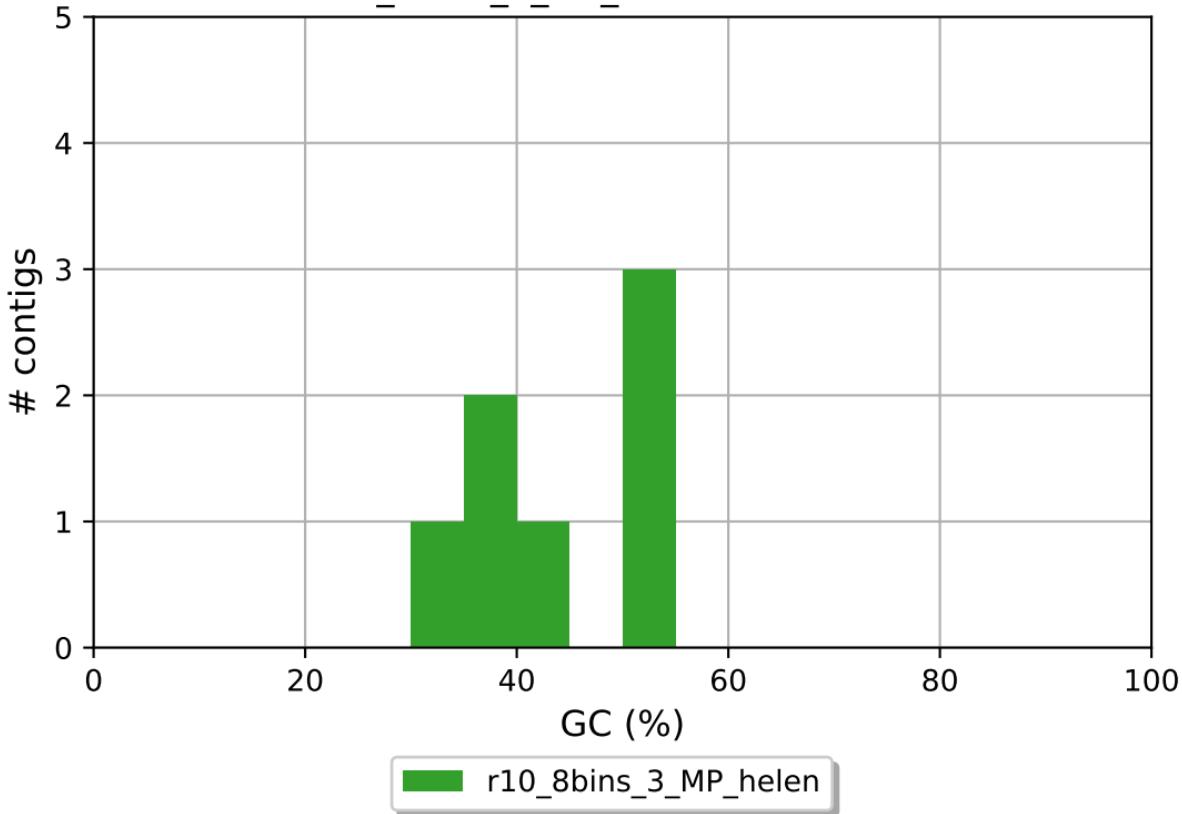
r10_8bins_2_raw GC content



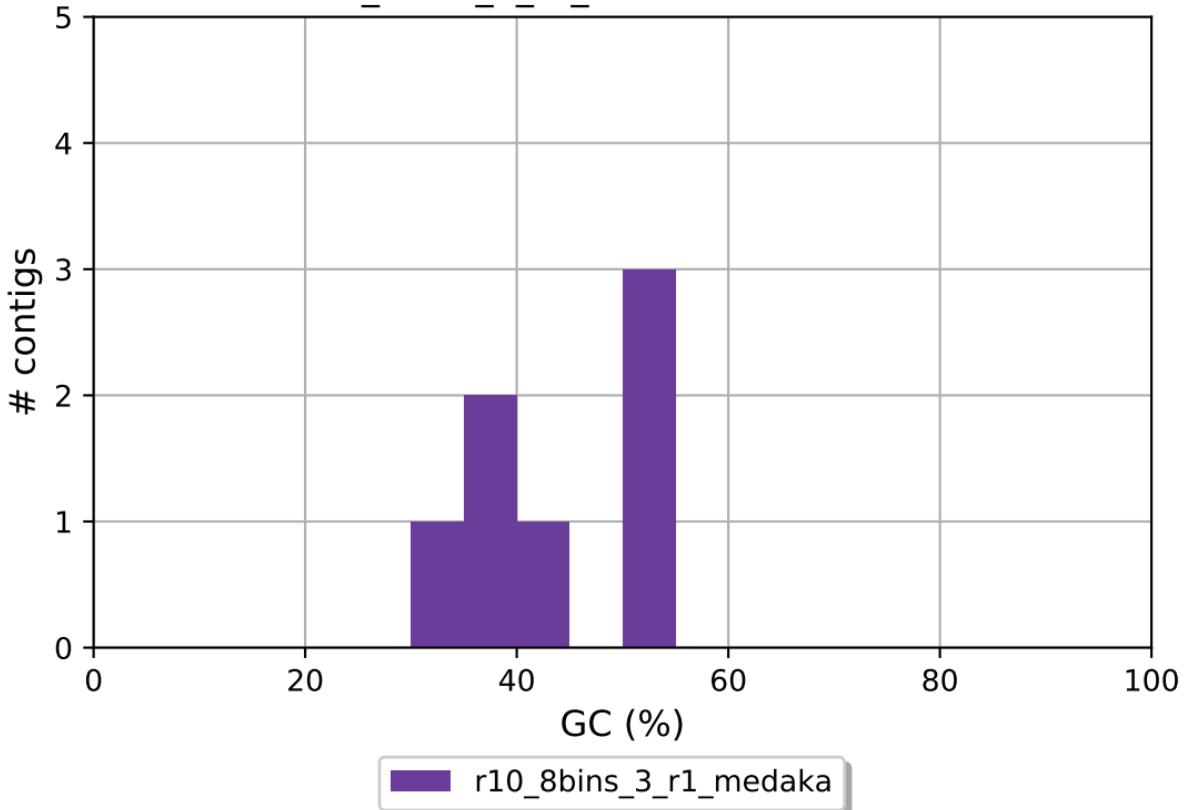
r10_8bins_3_MP GC content



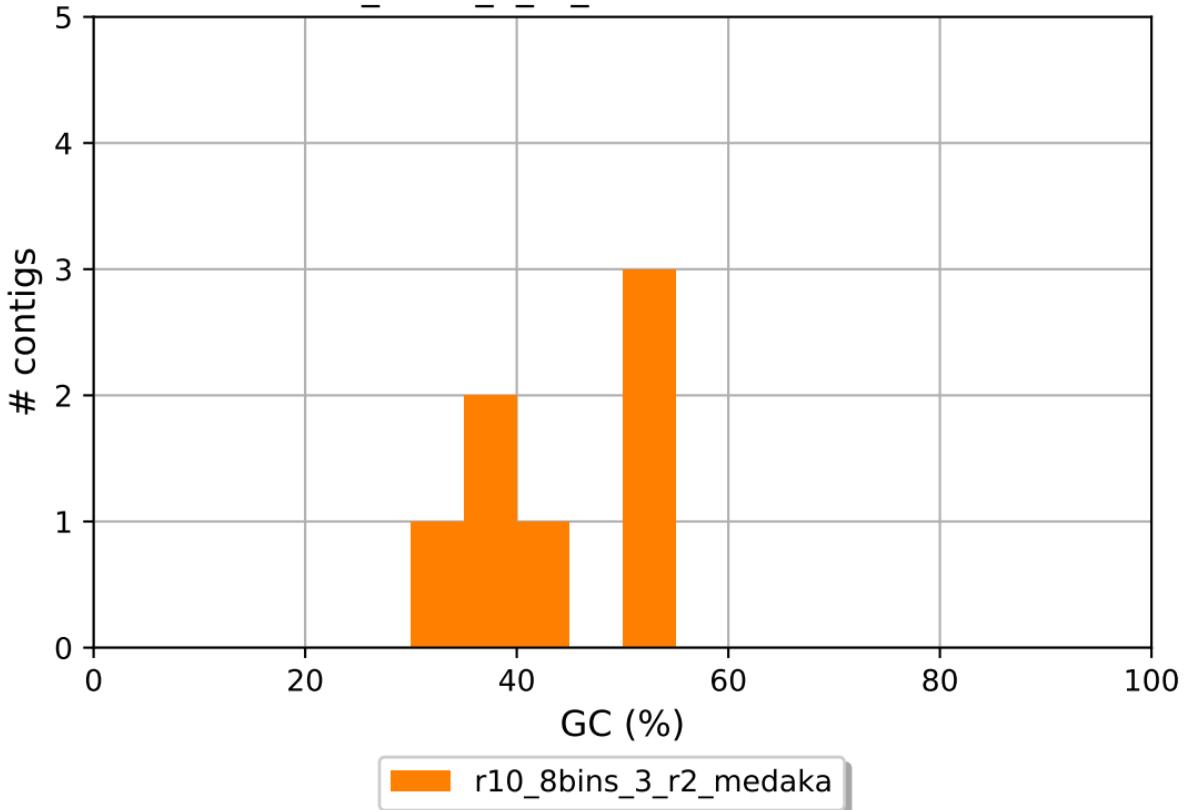
r10_8bins_3_MP_helen GC content



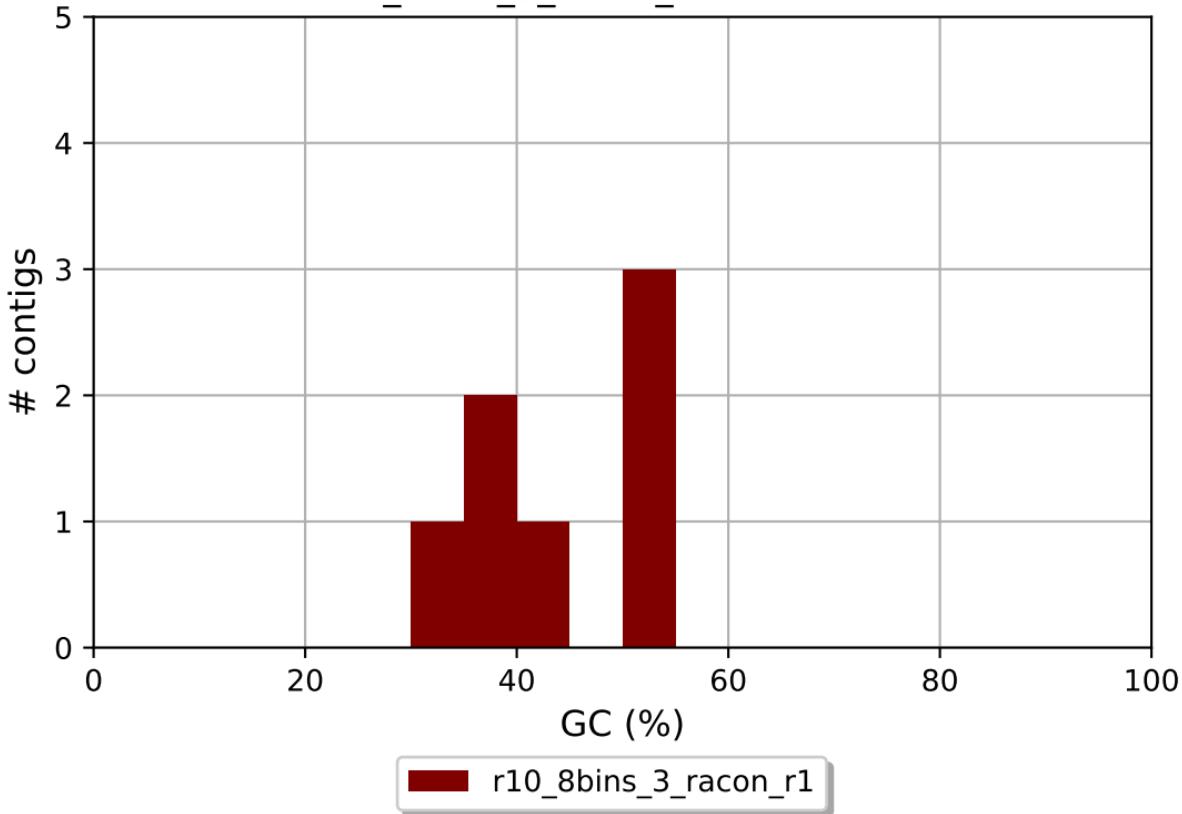
r10_8bins_3_r1_medaka GC content



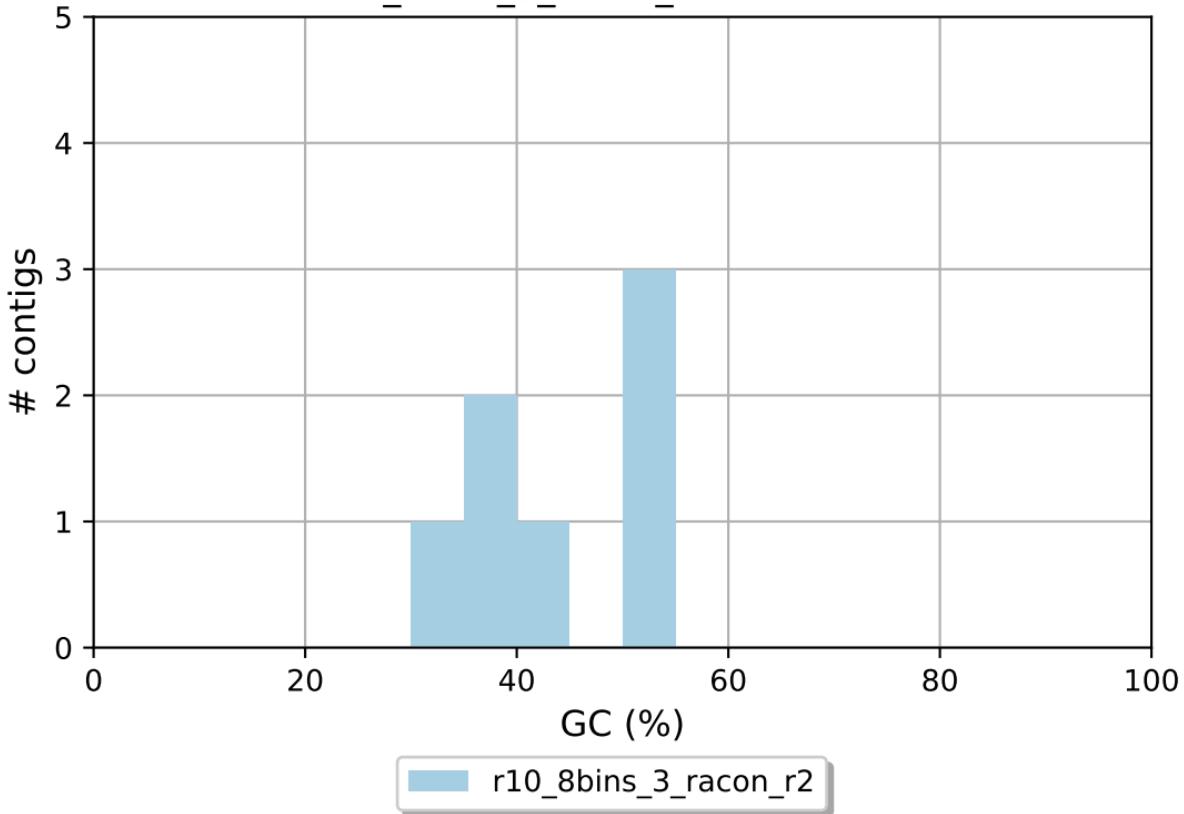
r10_8bins_3_r2_medaka GC content



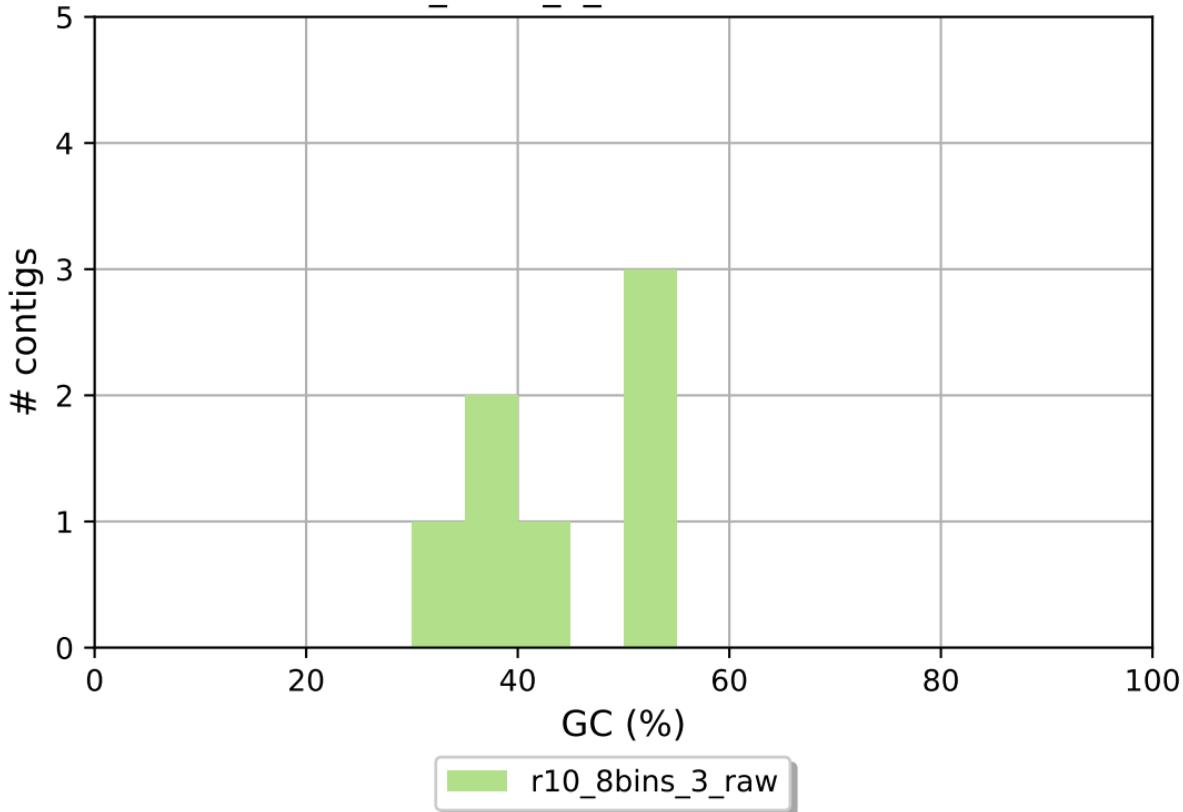
r10_8bins_3_racon_r1 GC content



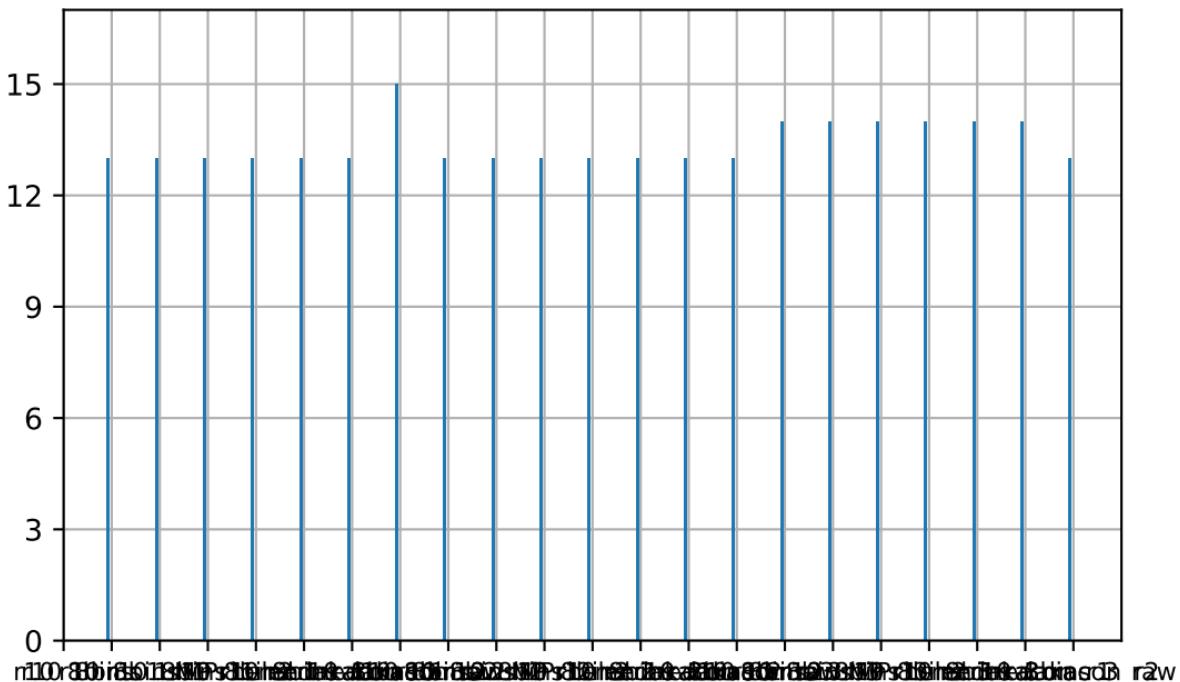
r10_8bins_3_racon_r2 GC content



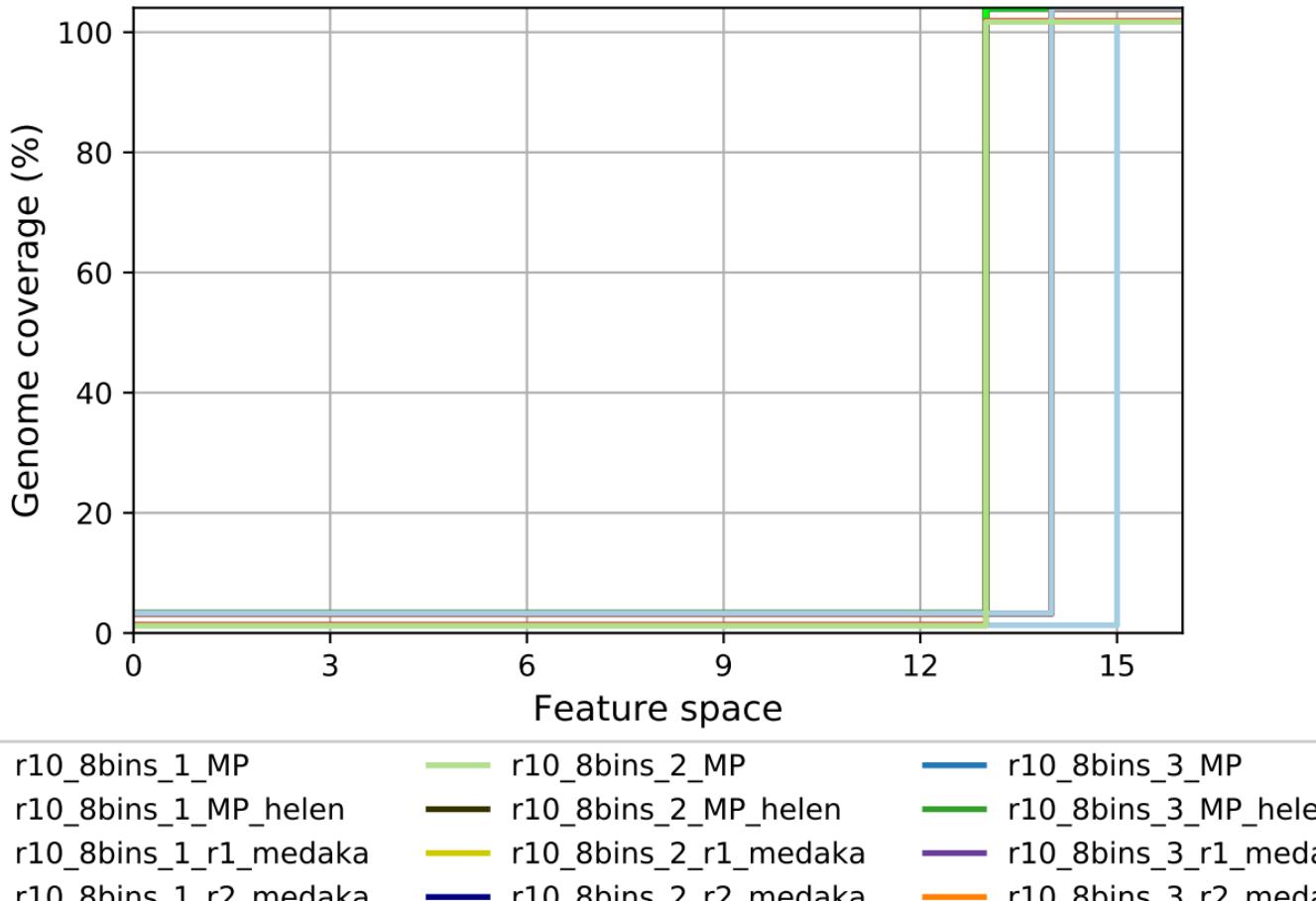
r10_8bins_3_raw GC content



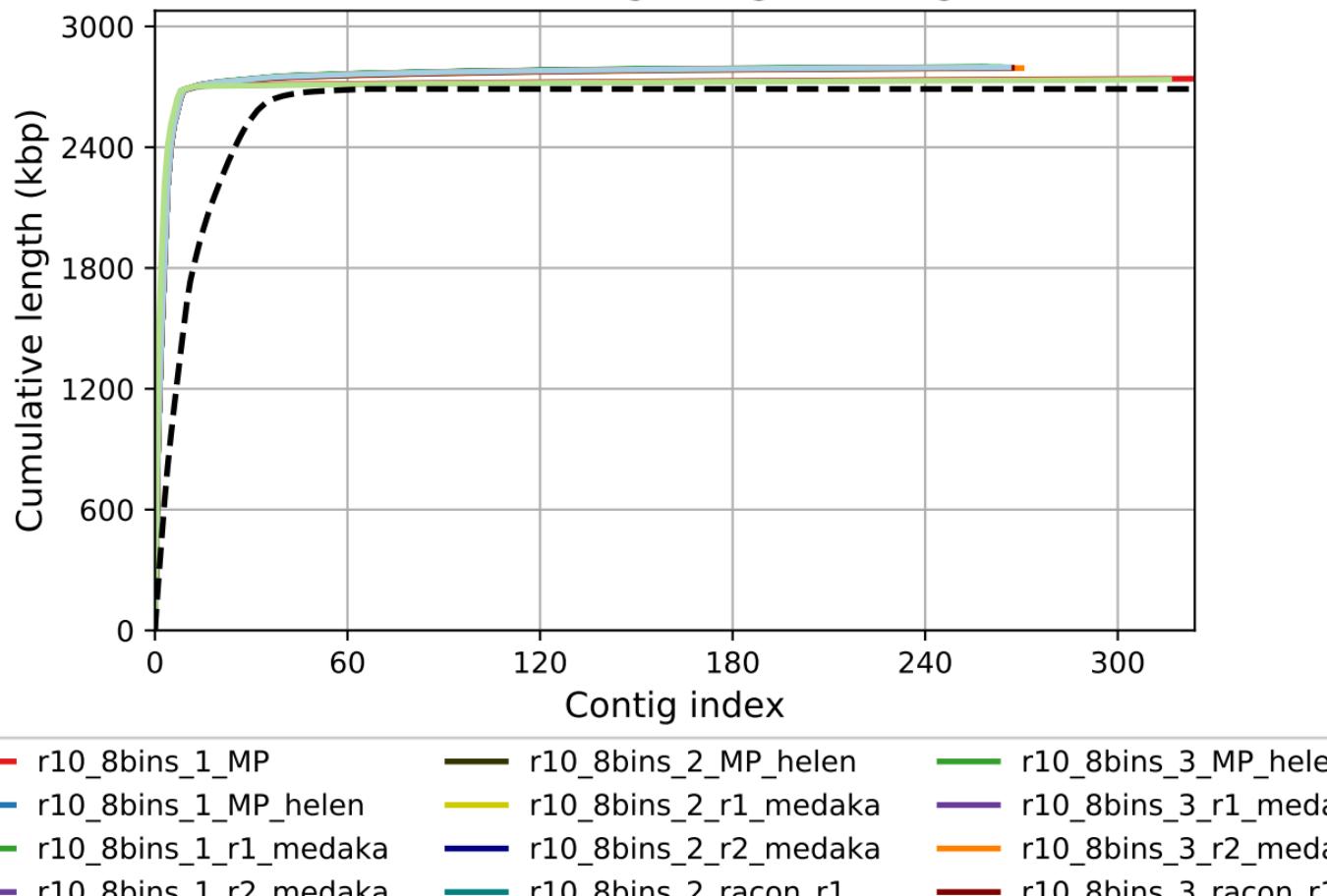
Misassemblies



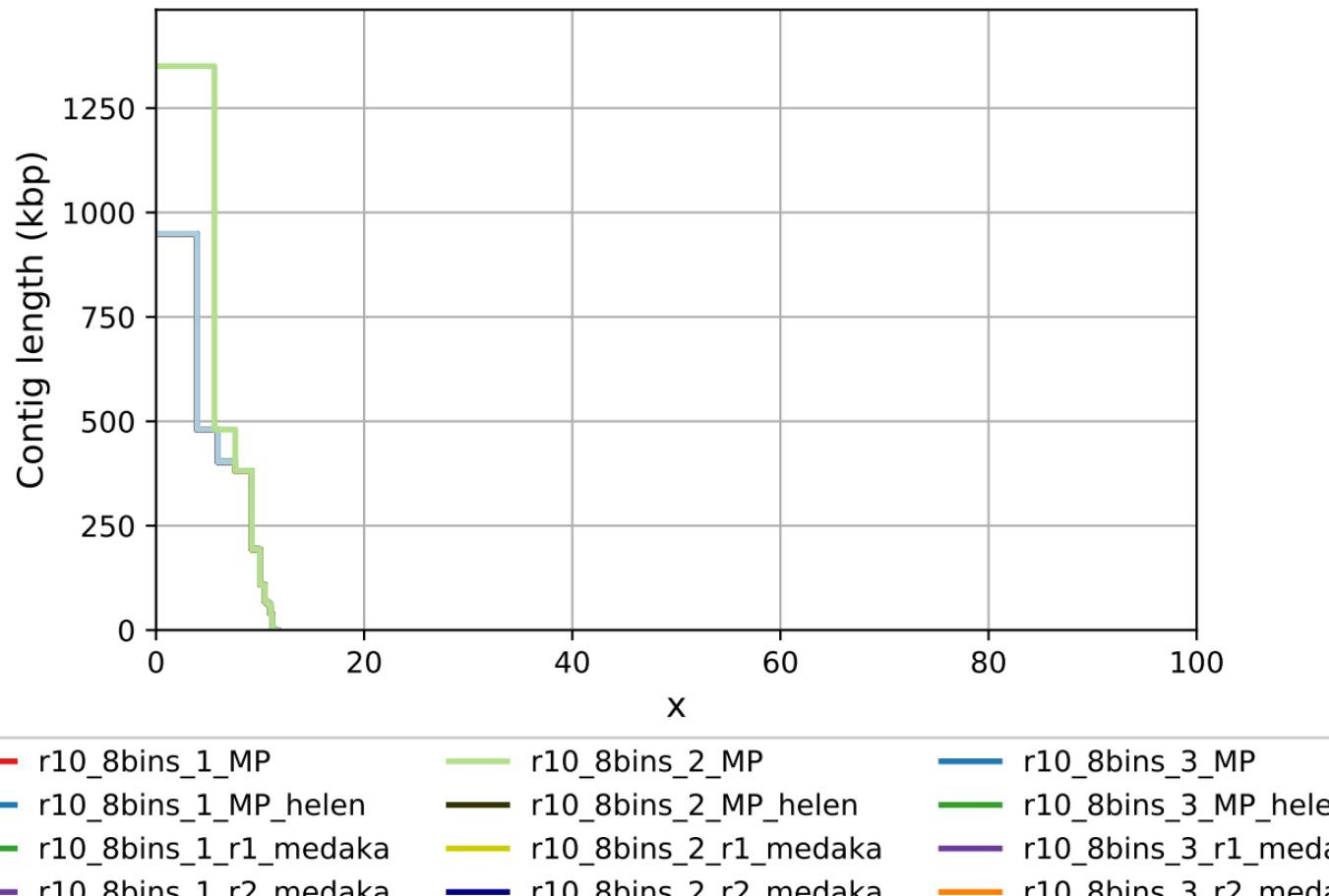
FRCurve (misassemblies)



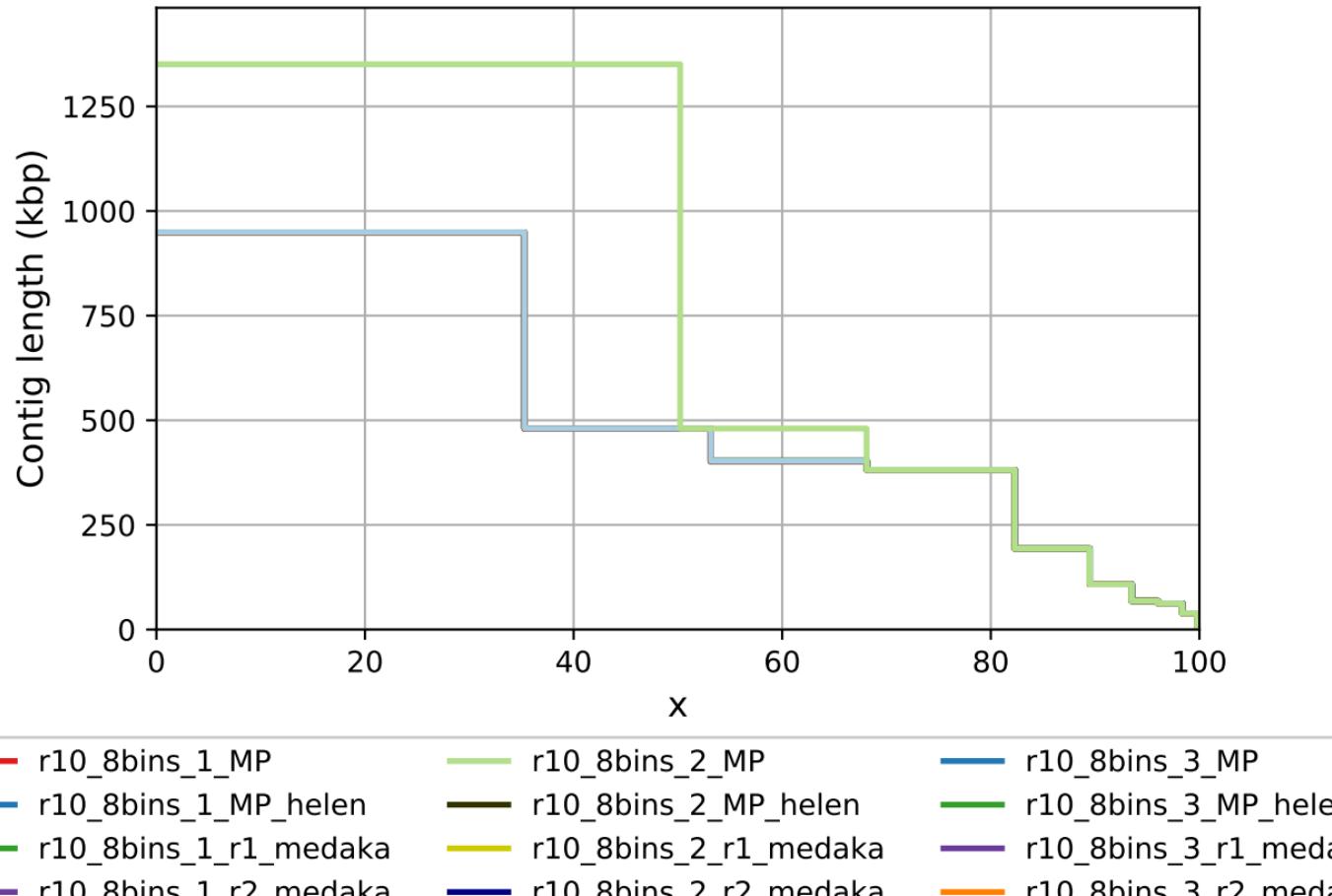
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

