

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	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	
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 (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	
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	2845307	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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	2845436	2845374	2845428	2845430	2845286	2845307	2843860	2845427	2845364	2845435	284533	2845287	2845362	2843855	2845427	2845365	2845437	2845434	2845286	2845324	2843844
# local misassemblies	16	16	16	16	16	16	19	16	16	16	16	16	20	16	16	16	16	16	16	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		
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	5	6	6	6	6	6	6		
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part		
Unaligned length	21097894	21092211	21094007	21085751	21086456	21077999	21153624	21098121	21090238	21095079	21084838	21086483	21080326	21149376	21097603	21091560	21093542	21087873	21087452	21081144	21153872
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.953	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.954	99.948	
Duplication ratio	1.056	1.057	1.057	1.057	1.055	1.056	1.032	1.056	1.057	1.056	1.055	1.055	1.033	1.056	1.057	1.057	1.056	1.055	1.055	1.032	
# 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	
# mismatches per 100 kbp	247.87	252.98	250.92	252.69	239.18	244.43	147.96	246.66	253.97	246.87	248.54	240.42</									

Misassemblies report

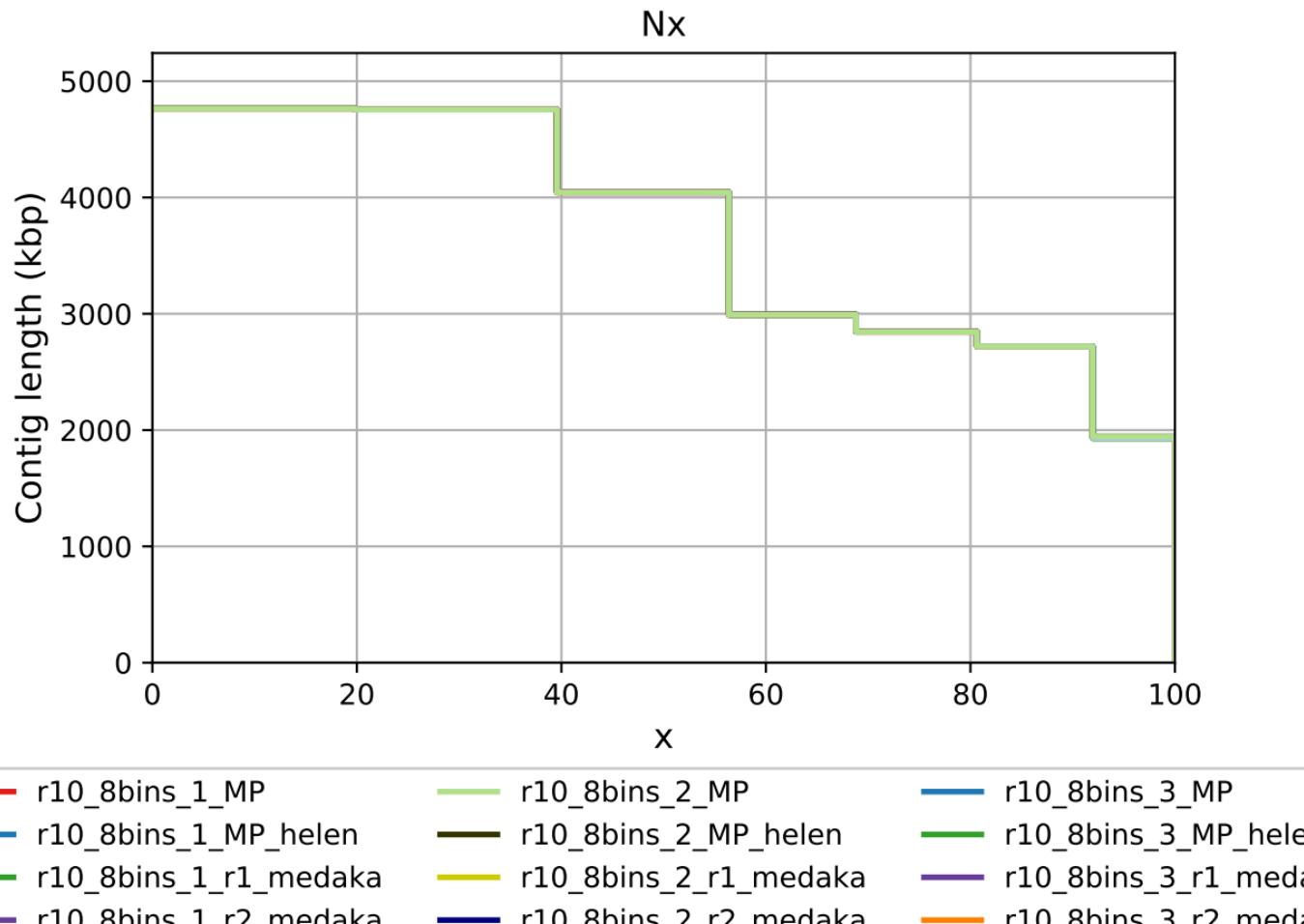
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# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# c. inversions	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	2845436	2845374	2845428	2845430	2845286	2845307	2843860	2845427	2845364	2845435	2845433	2845287	2845362	2843855	2845427	2845365	2845437	2845434	2845286	2845324	2843844
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	6	0	0	0	0	0	0	0	6	
# local misassemblies	16	16	16	16	16	16	19	16	16	16	16	16	20	16	16	16	16	16	16	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	19	19	19	19	19	19	11	19	19	19	19	19	11	19	19	19	19	19	19	10	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	
# mismatches	6986	7130	7072	7122	6741	6889	4170	6952	7158	6958	7005	6776	6773	4306	7007	7071	7076	6962	6536	6765	4098
# indels	446	438	406	399	633	612	3604	440	443	396	398	645	622	3532	439	447	407	391	595	597	3571
# indels (<= 5 bp)	405	395	365	359	594	573	3568	400	402	356	358	604	585	3497	399	405	367	351	560	561	3535
# indels (> 5 bp)	41	43	41	40	39	39	36	40	41	40	40	41	37	35	40	42	40	35	36	36	
Indels length	2464	2465	2389	2381	2667	2638	6209	2404	2416	2302	2319	2646	2591	6066	2400	2429	2337	2303	2541	2521	6209

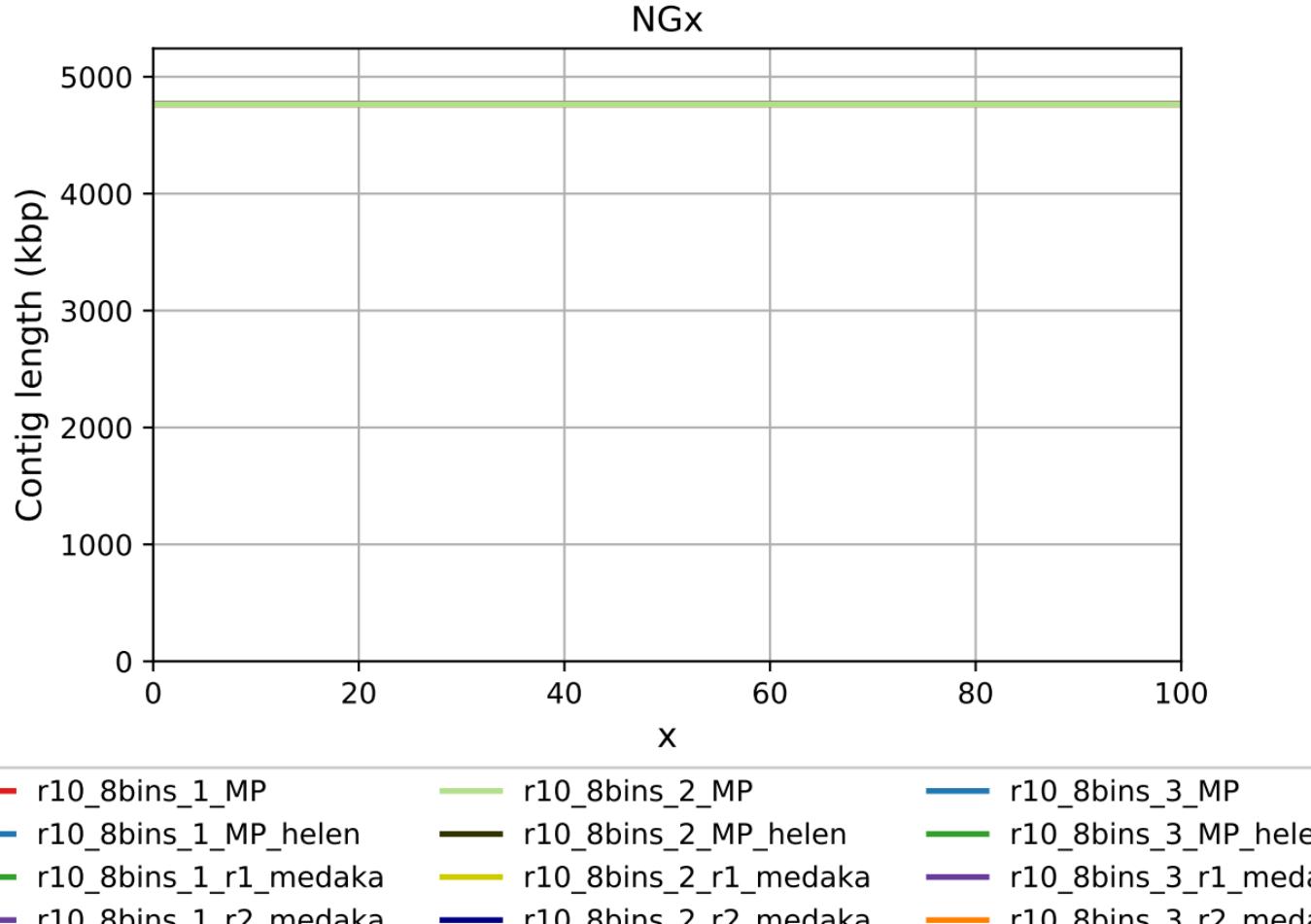
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted
(e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

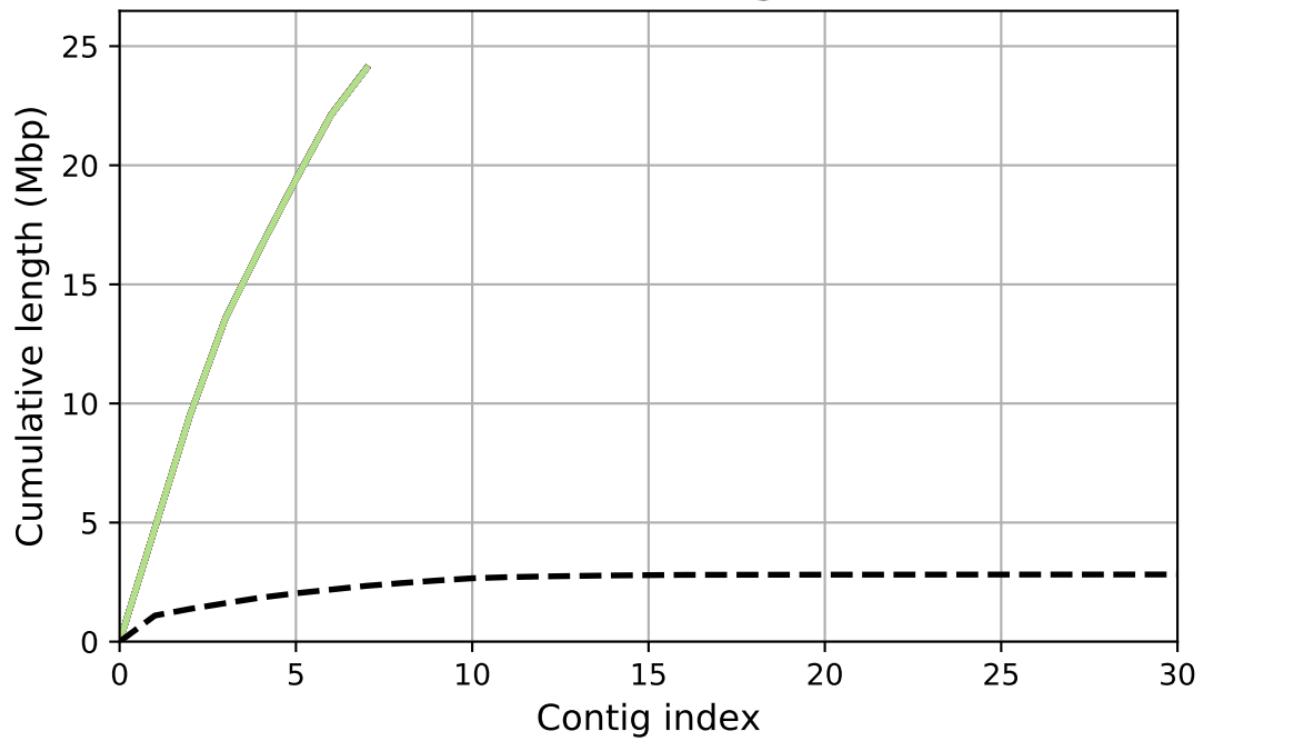
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	
Partially unaligned length	21097894	21092211	21094007	21085751	21086456	21077999	21153624	21098121	21090238	21084838	21086483	21080326	21149376	21097603	21093542	21087873	21087452	21081144	21153872
# 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 \geq 5000 bp, unless otherwise noted
(e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).



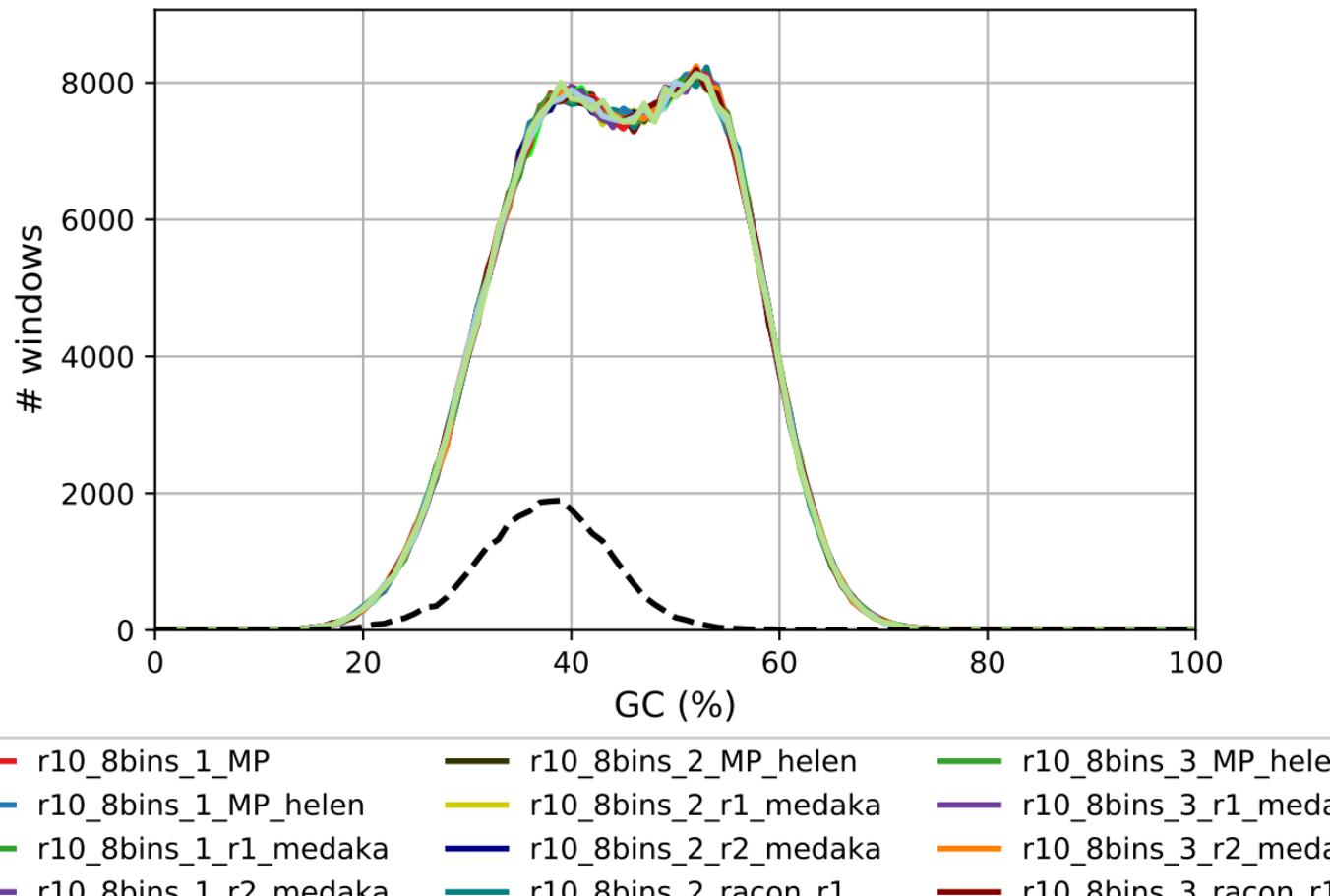


Cumulative length

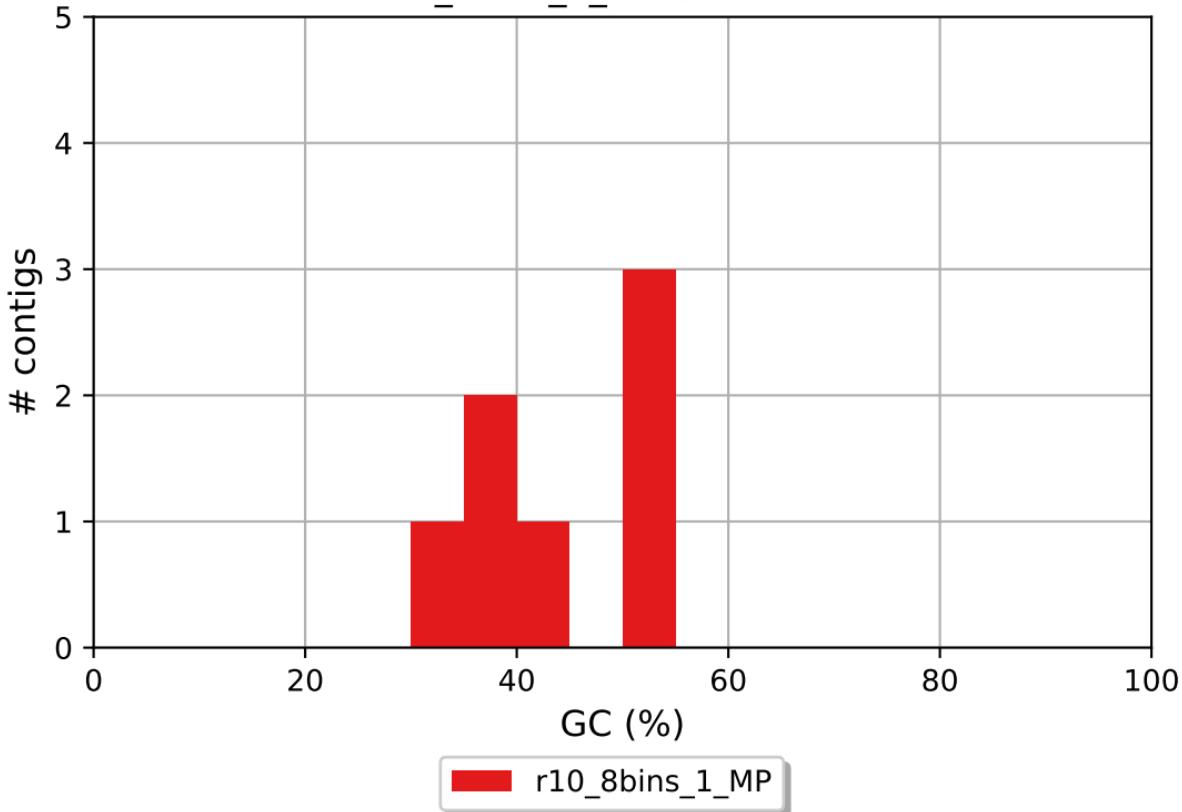


- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP_helen
- r10_8bins_3_r1_medaka
- r10_8bins_3_r2_medaka
- r10_8bins_3_racoon_r1
- r10_8bins_3_racoon_r2

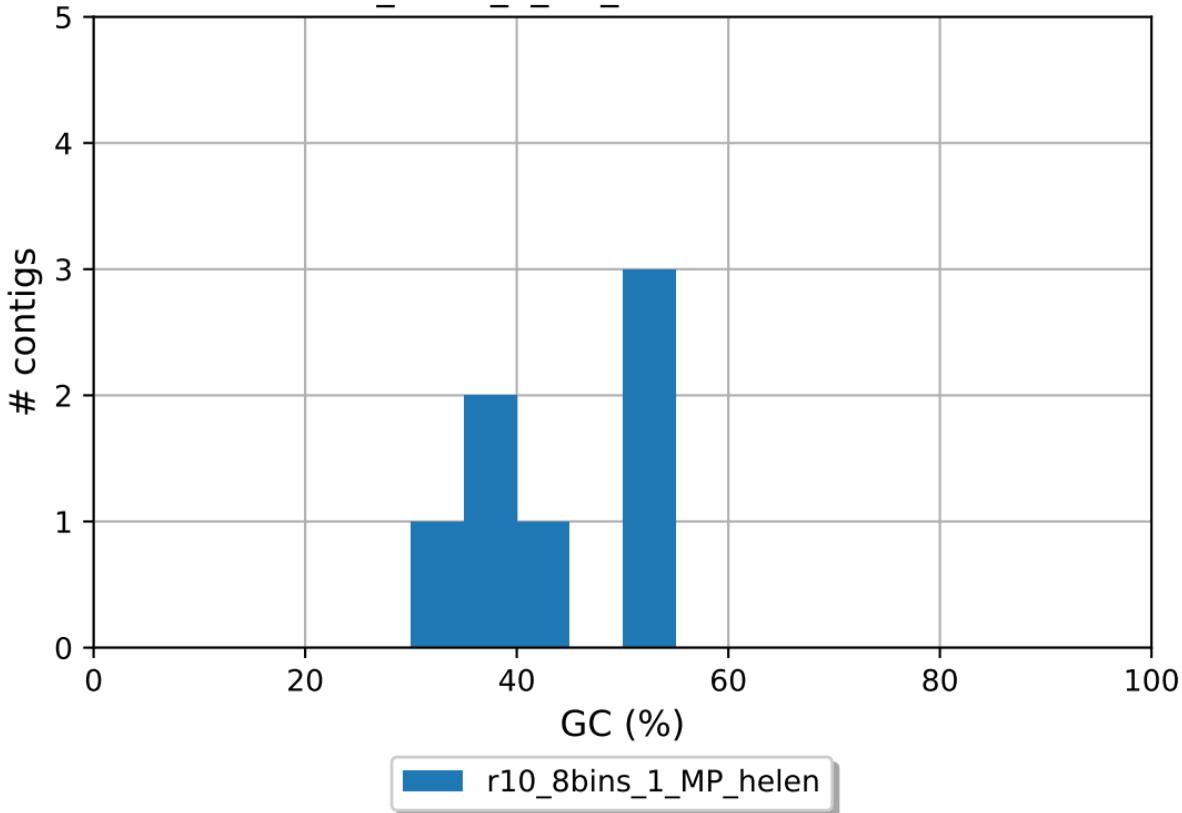
GC content



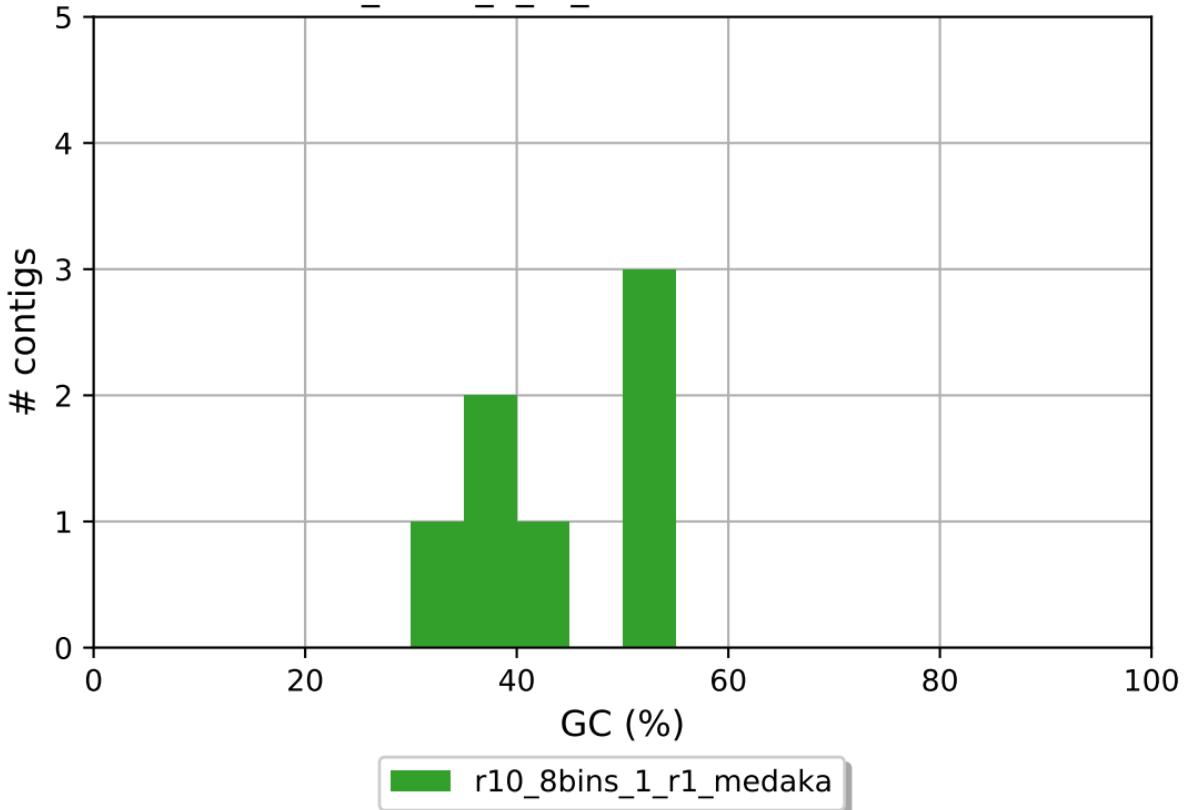
r10_8bins_1_MP GC content



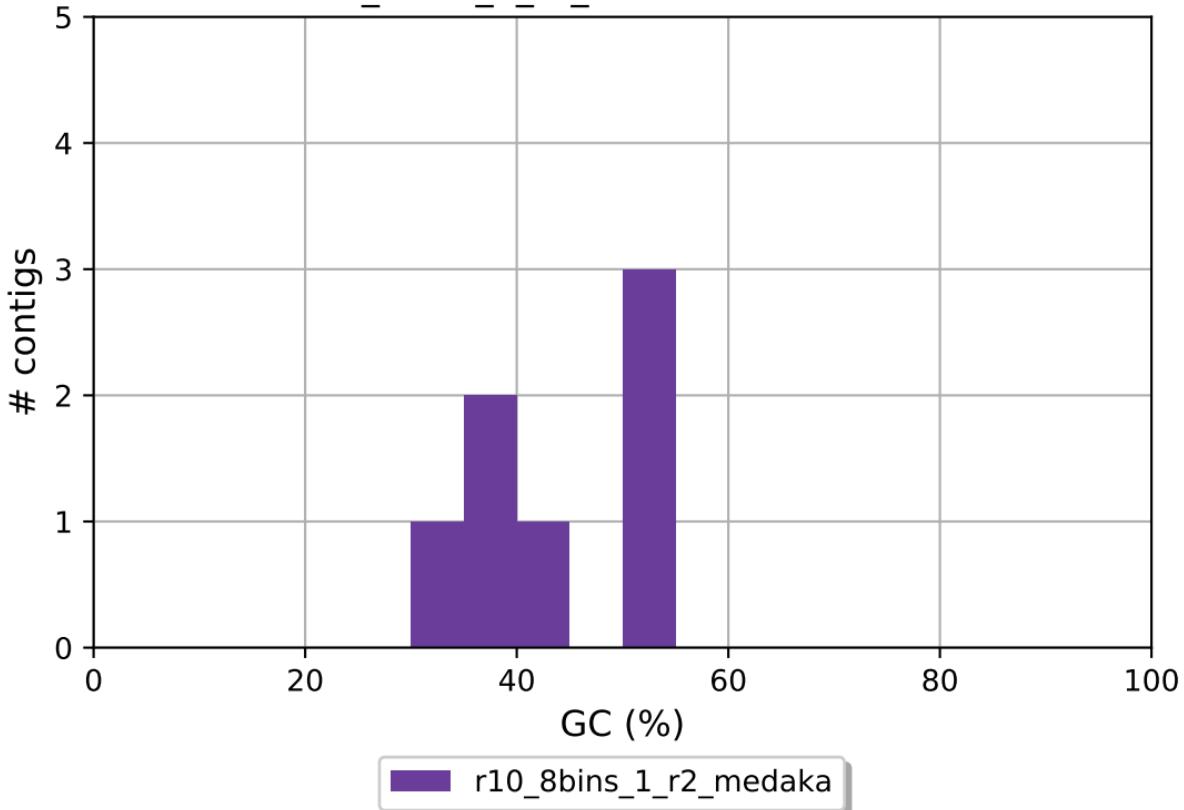
r10_8bins_1_MP_helen GC content



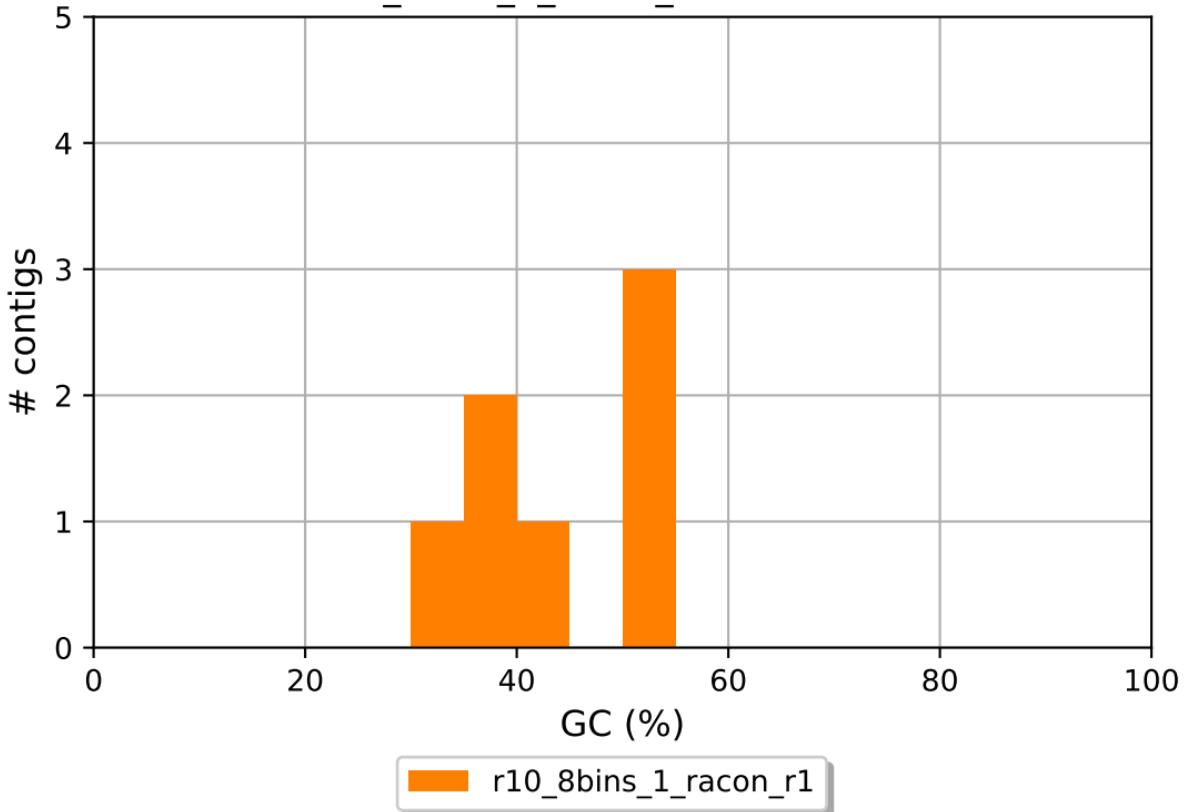
r10_8bins_1_r1_medaka GC content



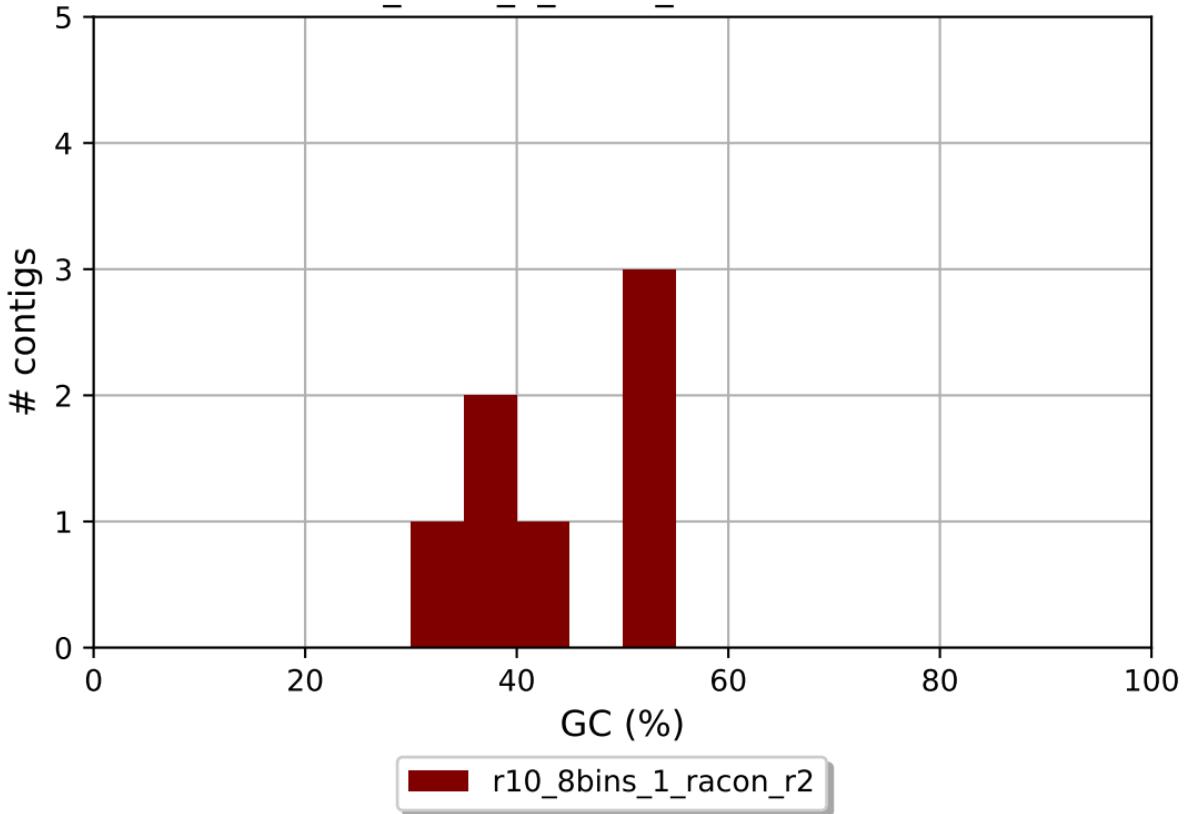
r10_8bins_1_r2_medaka GC content



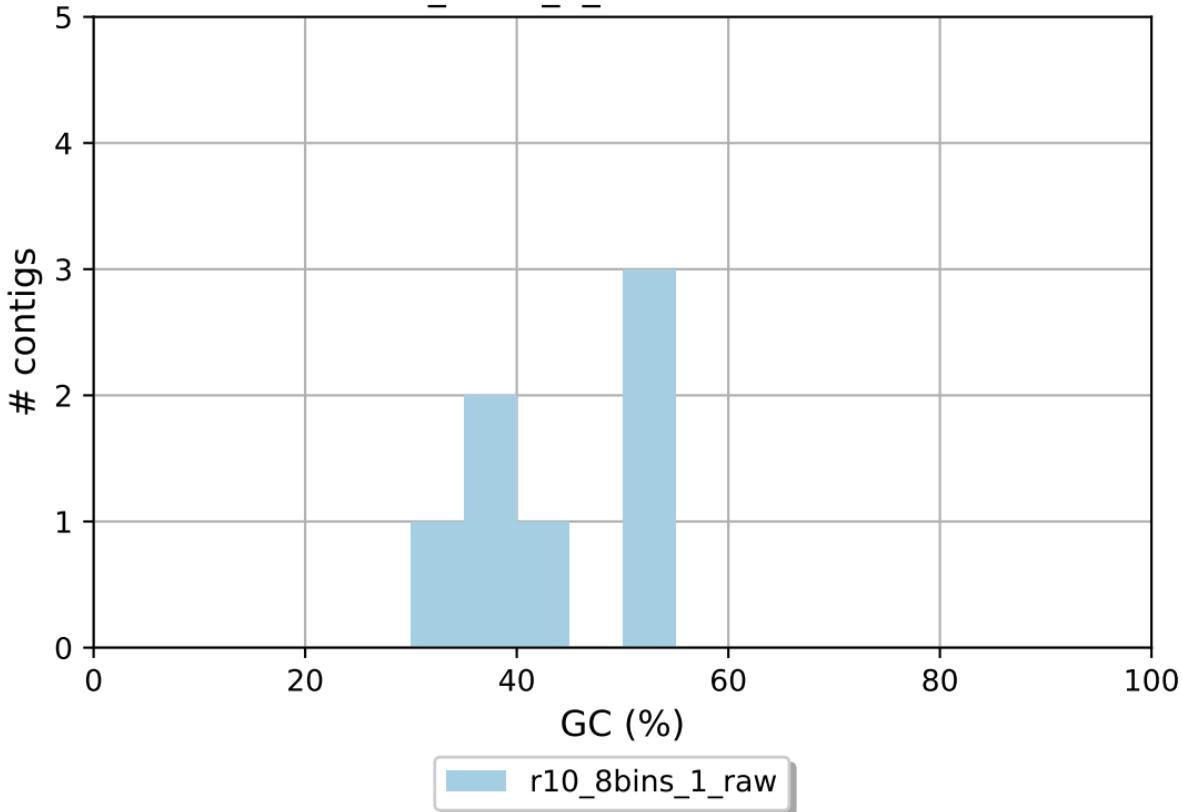
r10_8bins_1_racon_r1 GC content



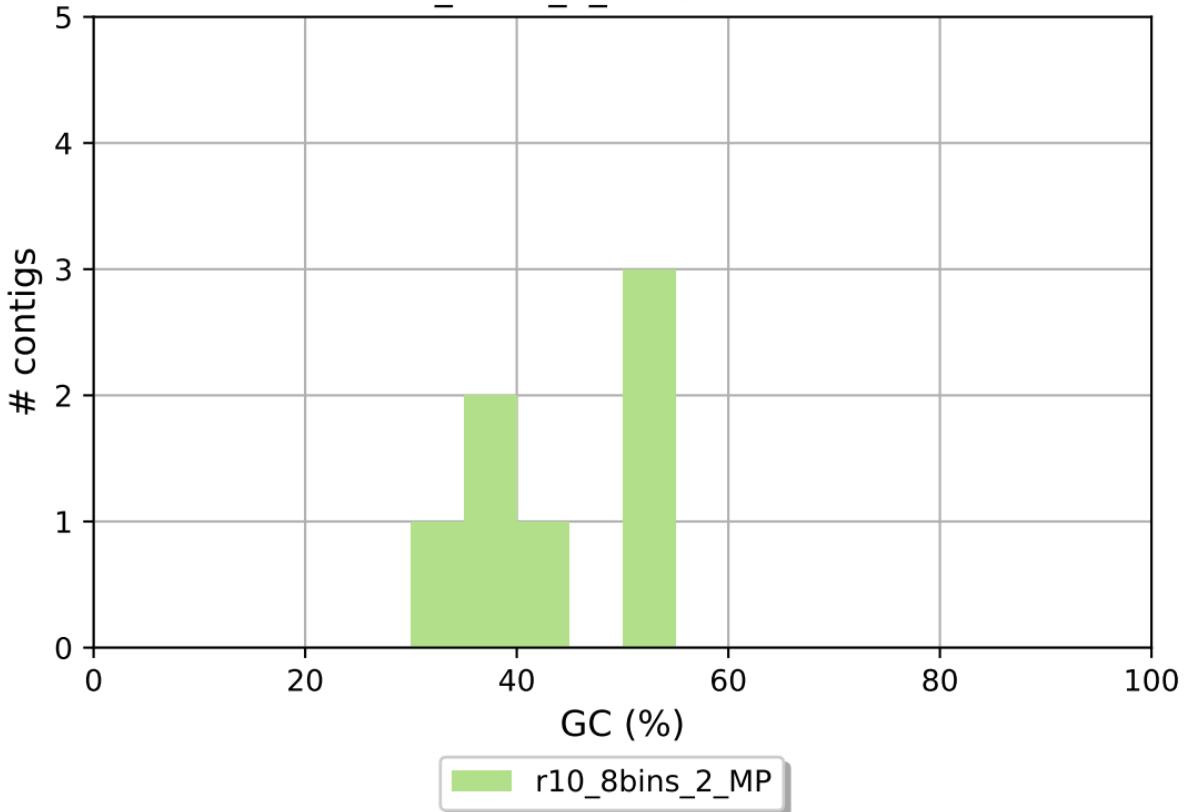
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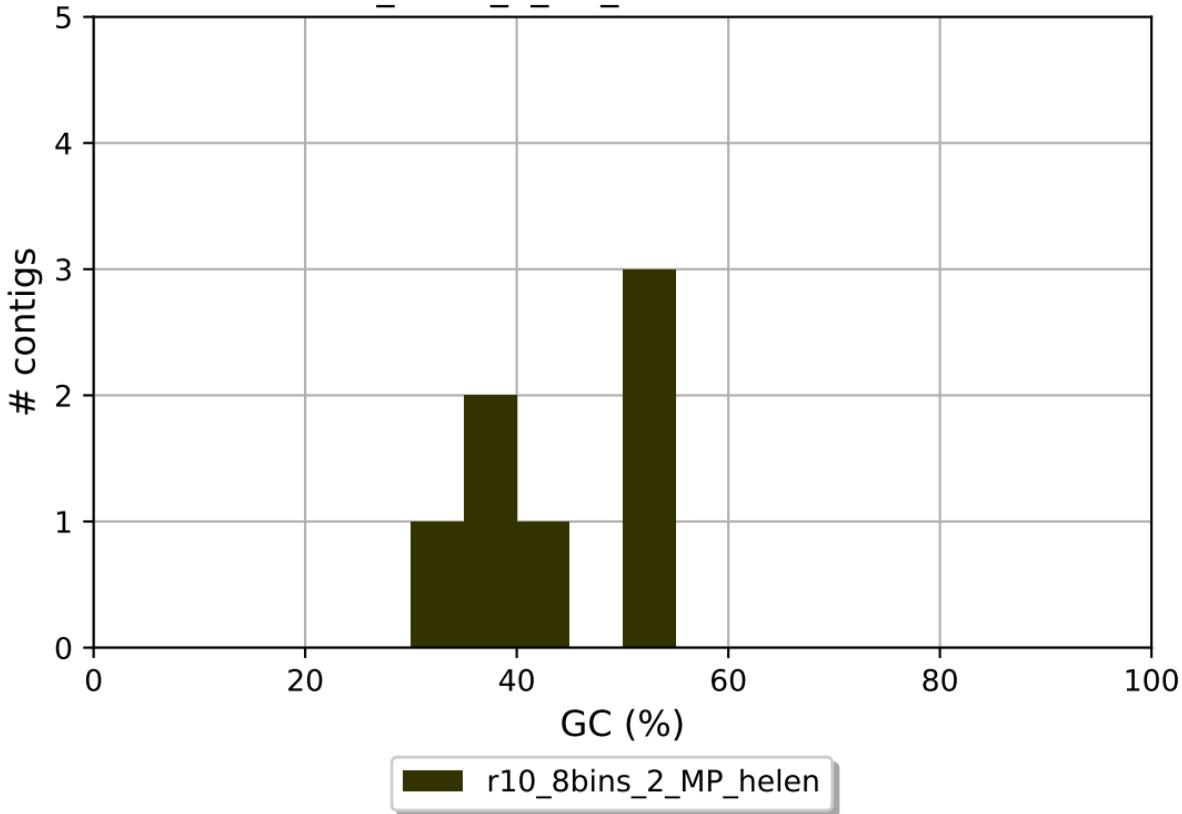
r10_8bins_1_raw GC content



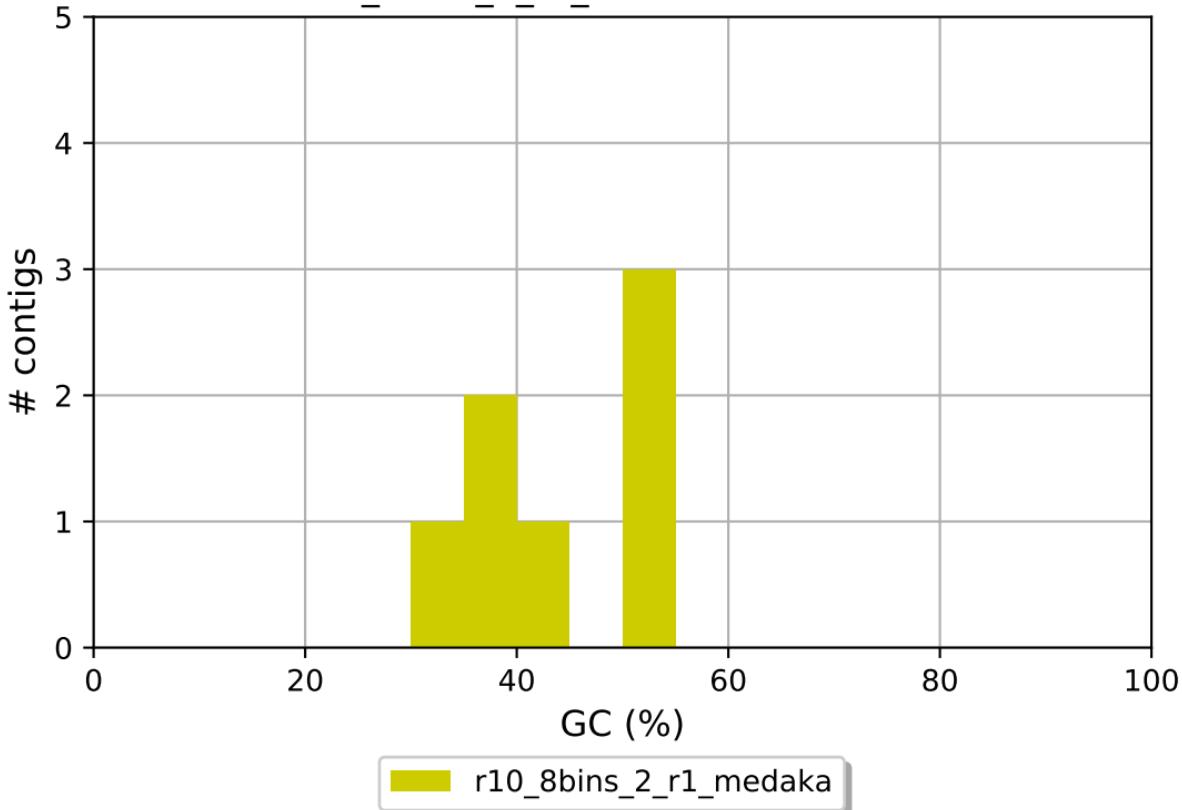
r10_8bins_2_MP GC content



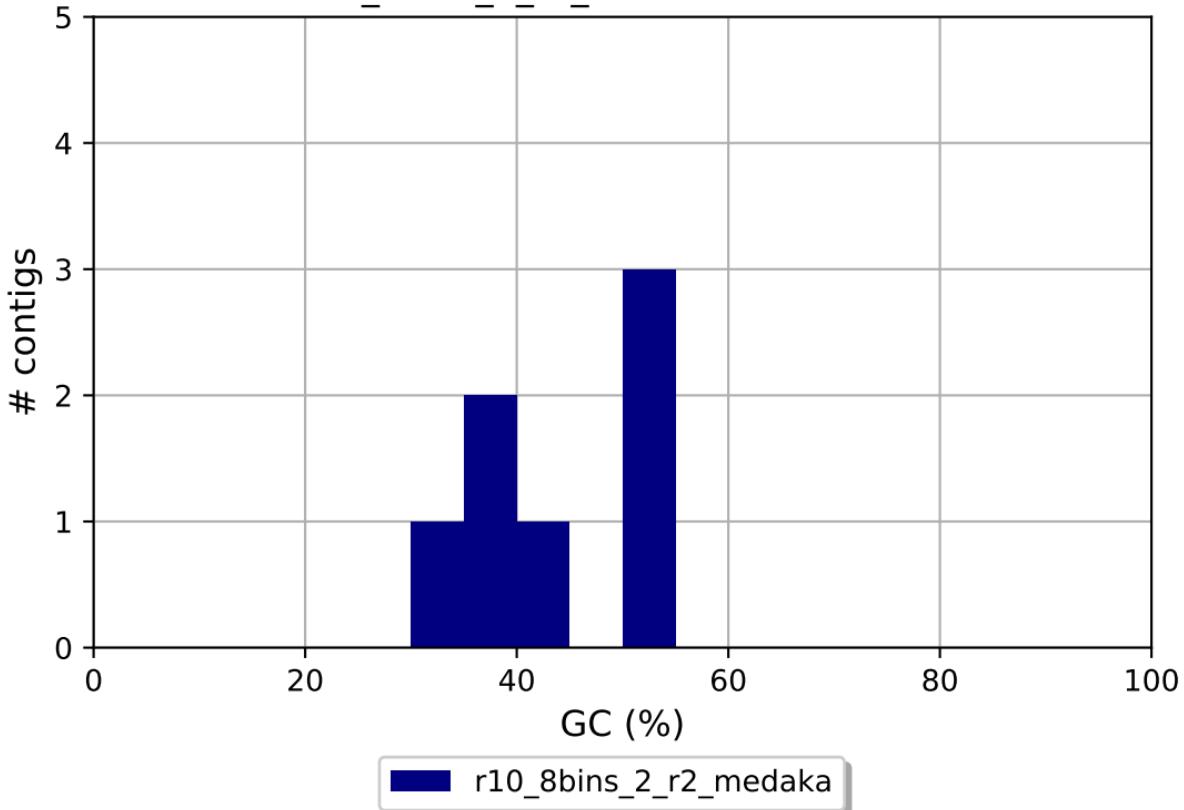
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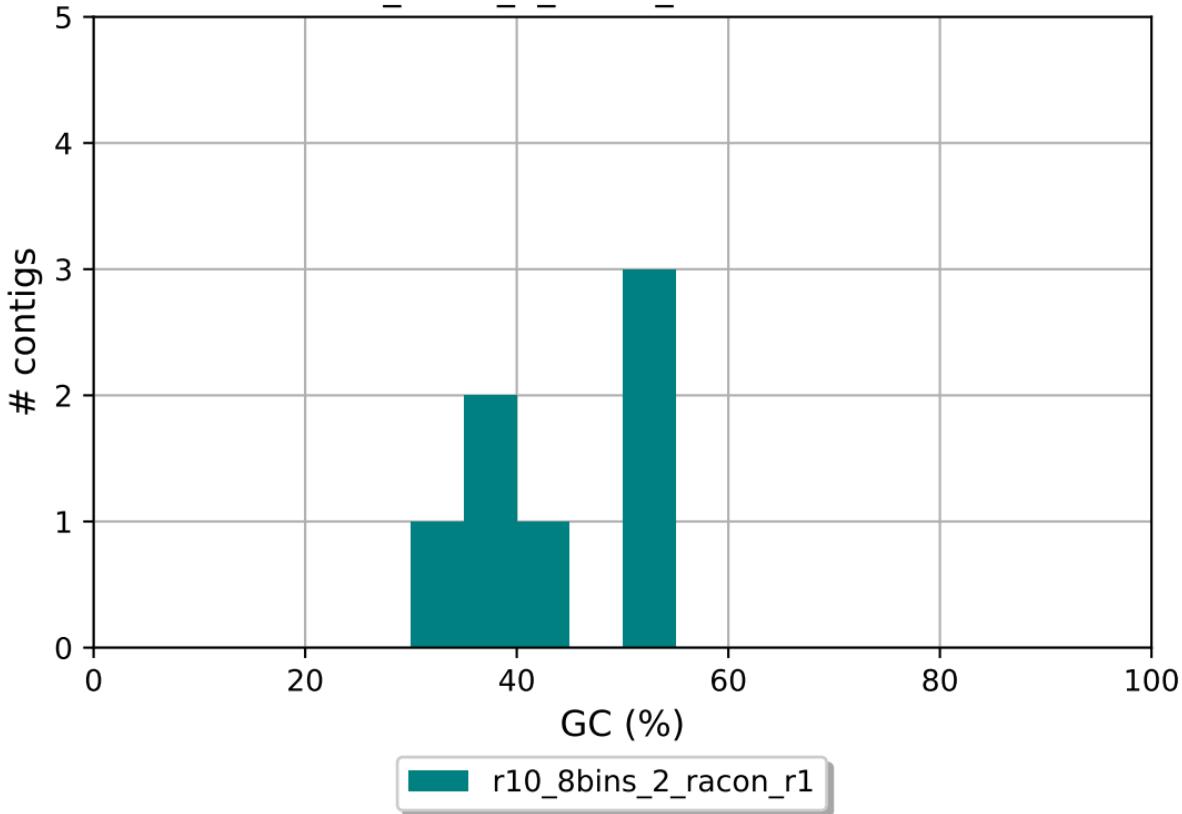
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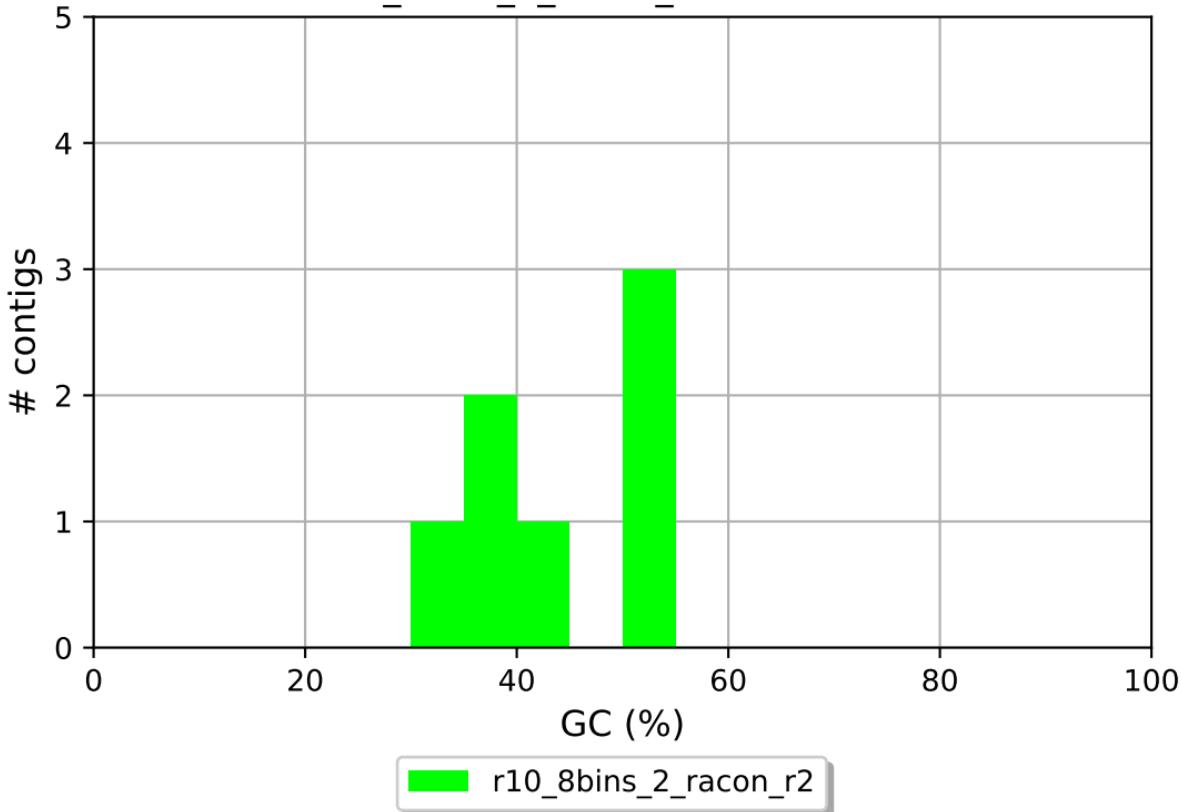
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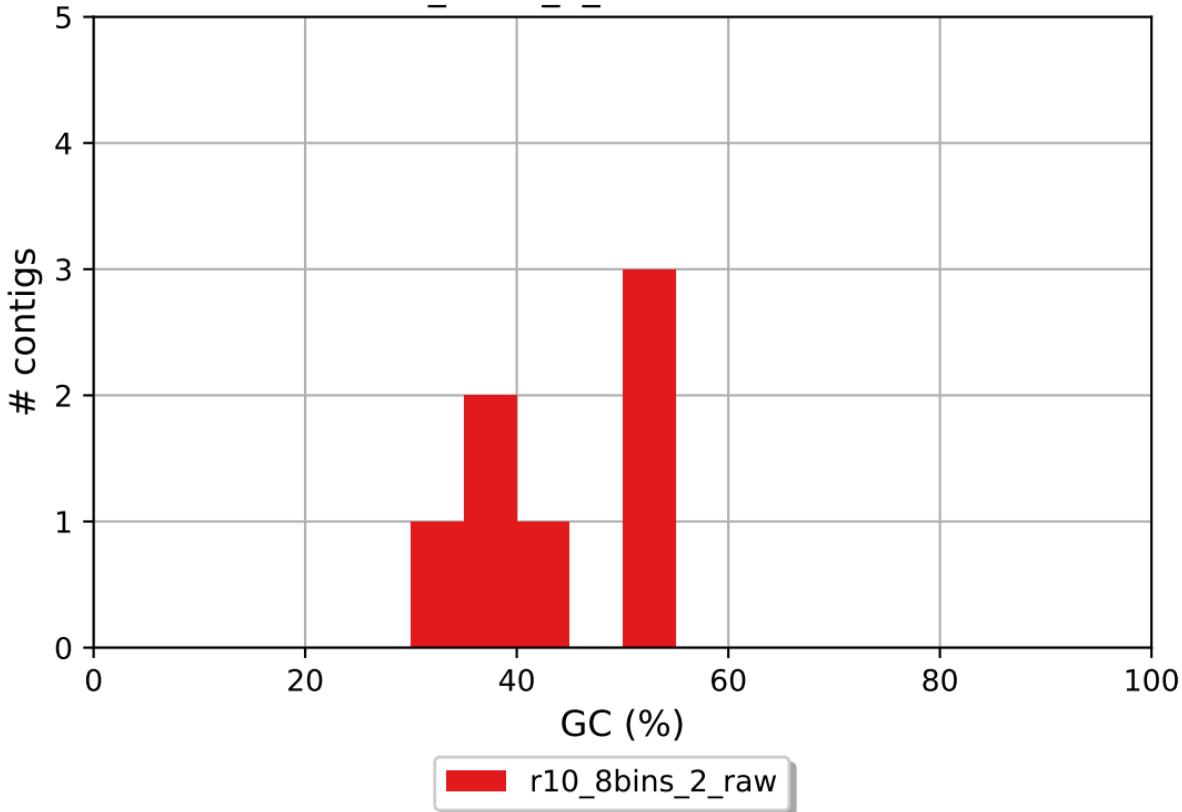
r10_8bins_2_racon_r1 GC content



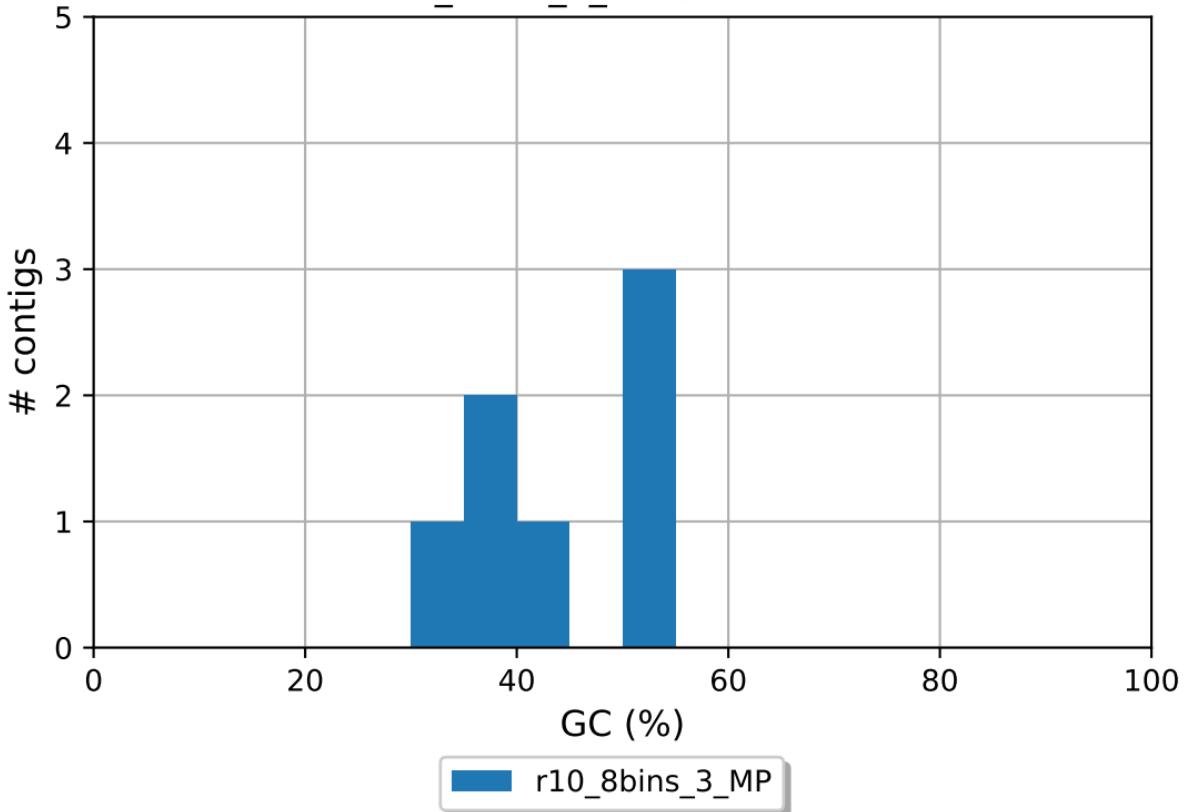
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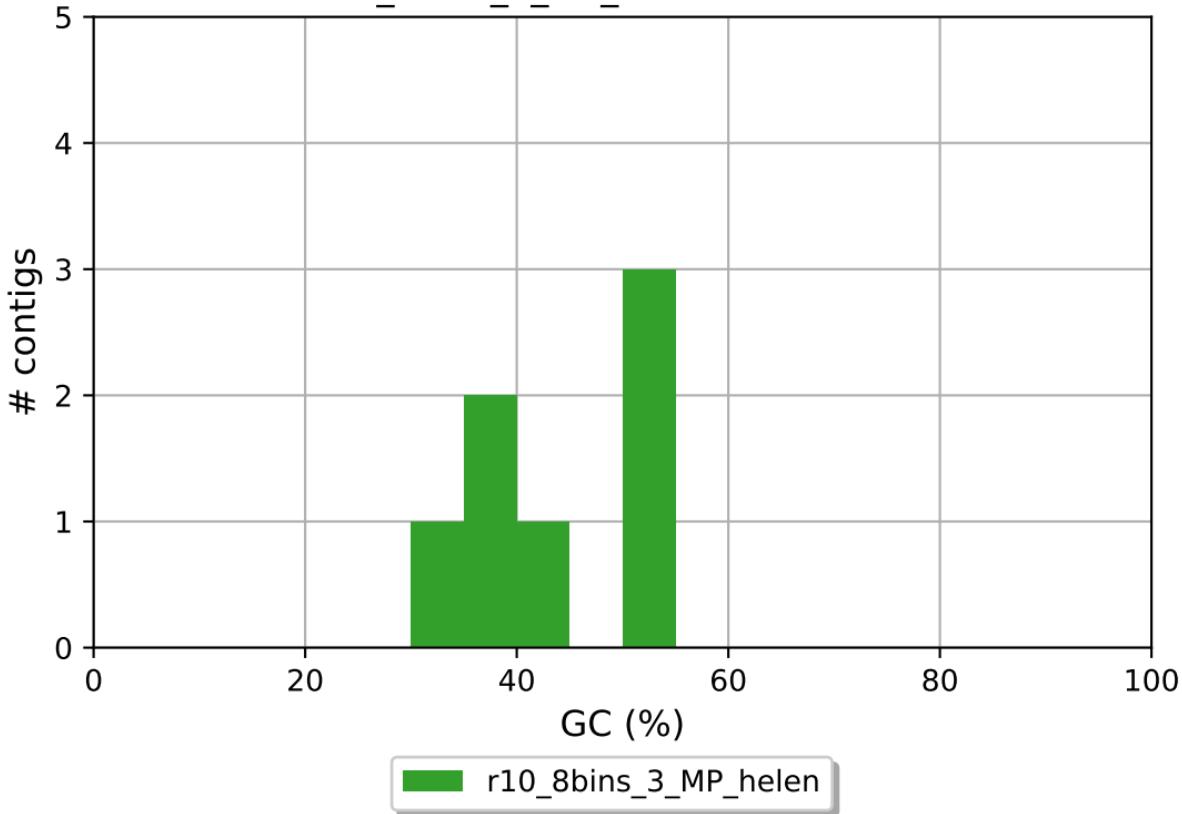
r10_8bins_2_raw GC content



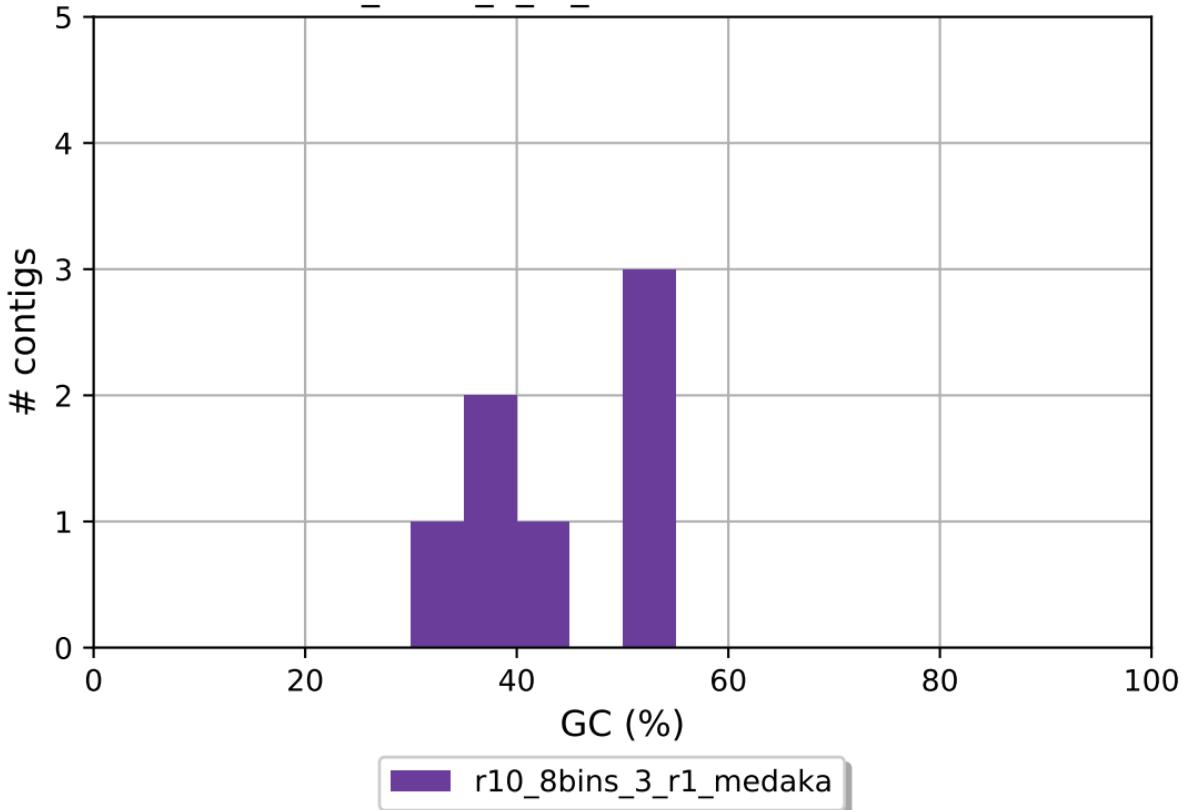
r10_8bins_3_MP GC content



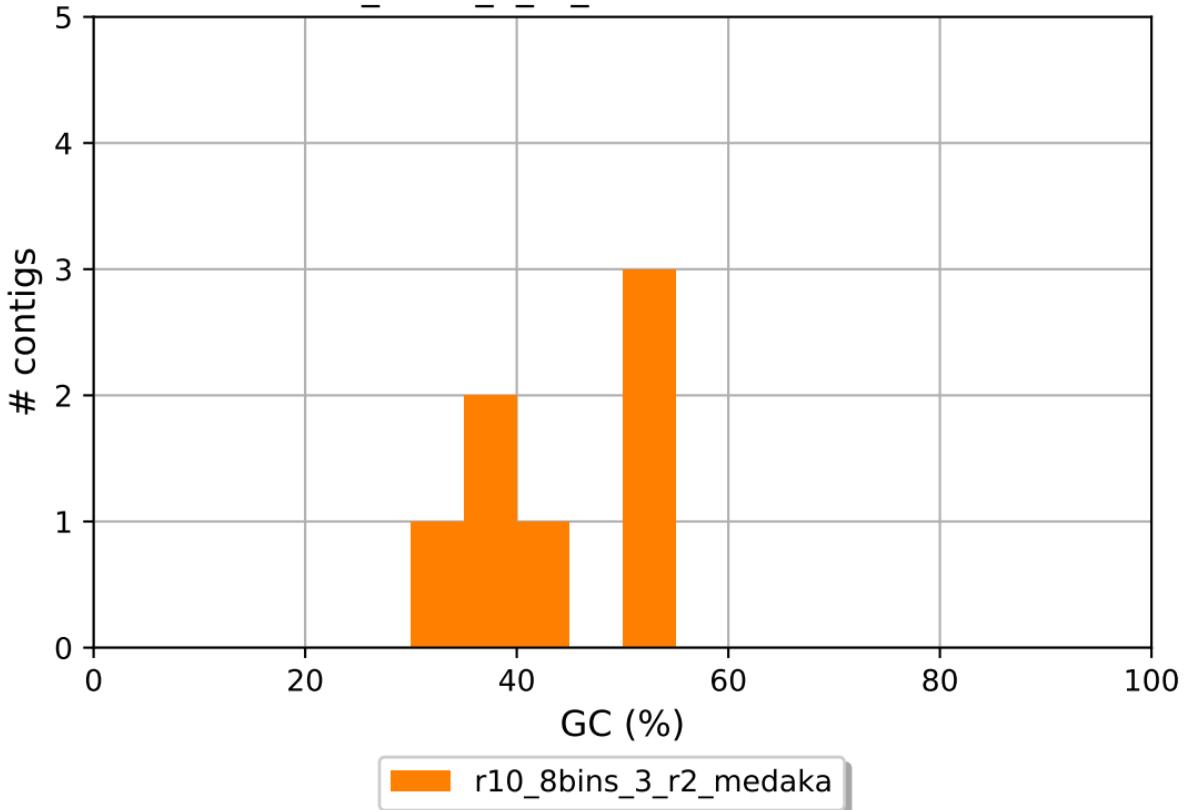
r10_8bins_3_MP_helen GC content



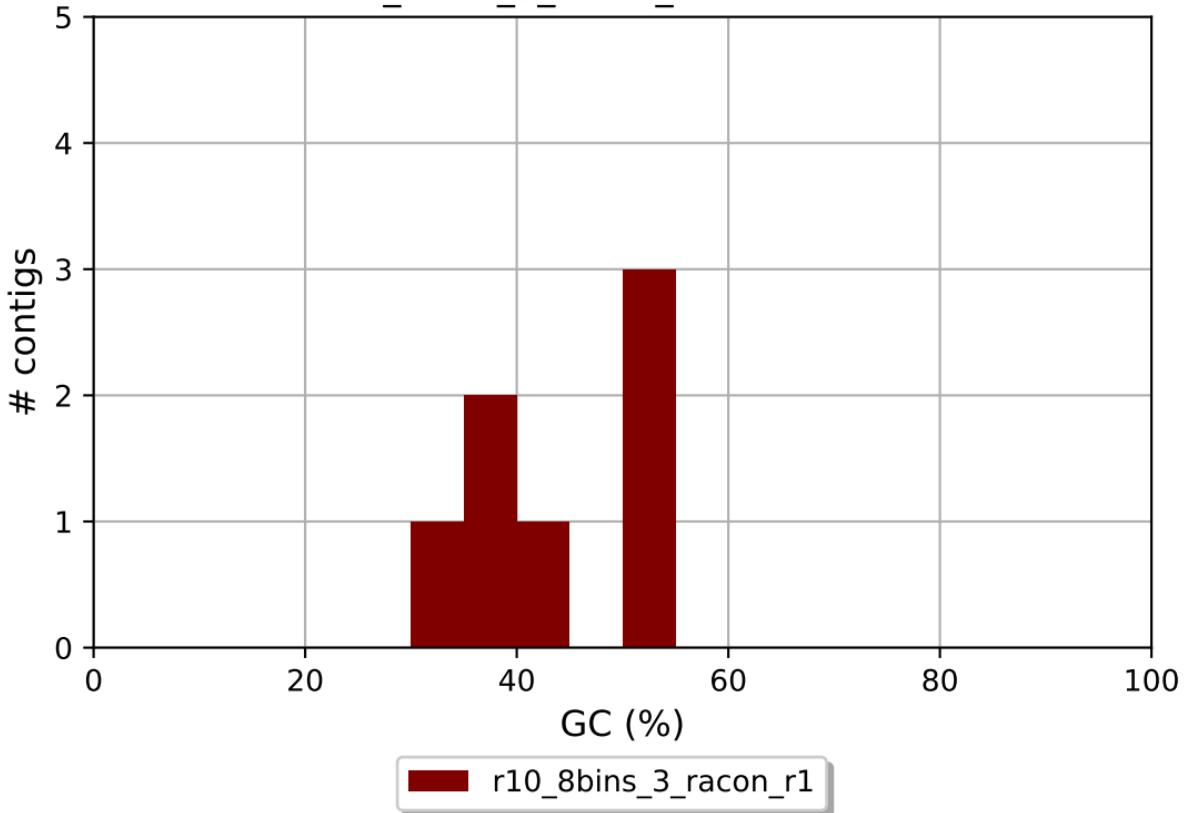
r10_8bins_3_r1_medaka GC content



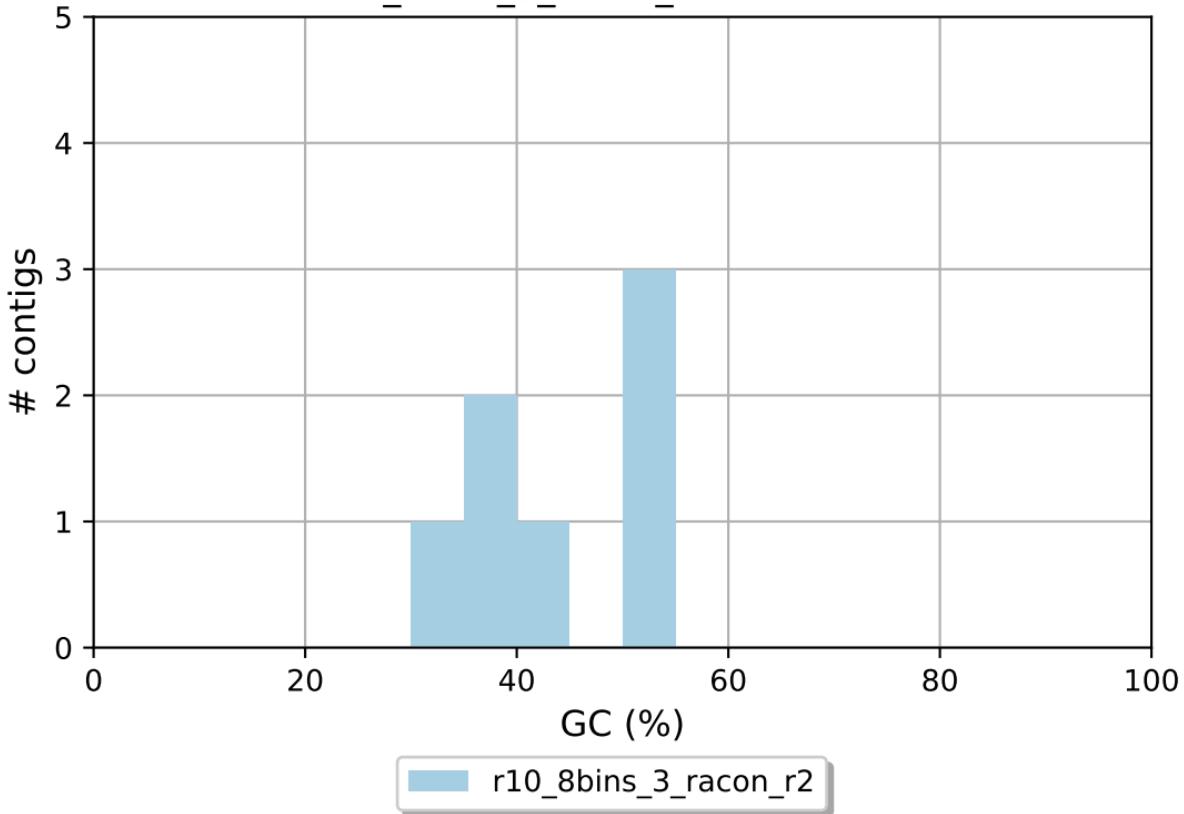
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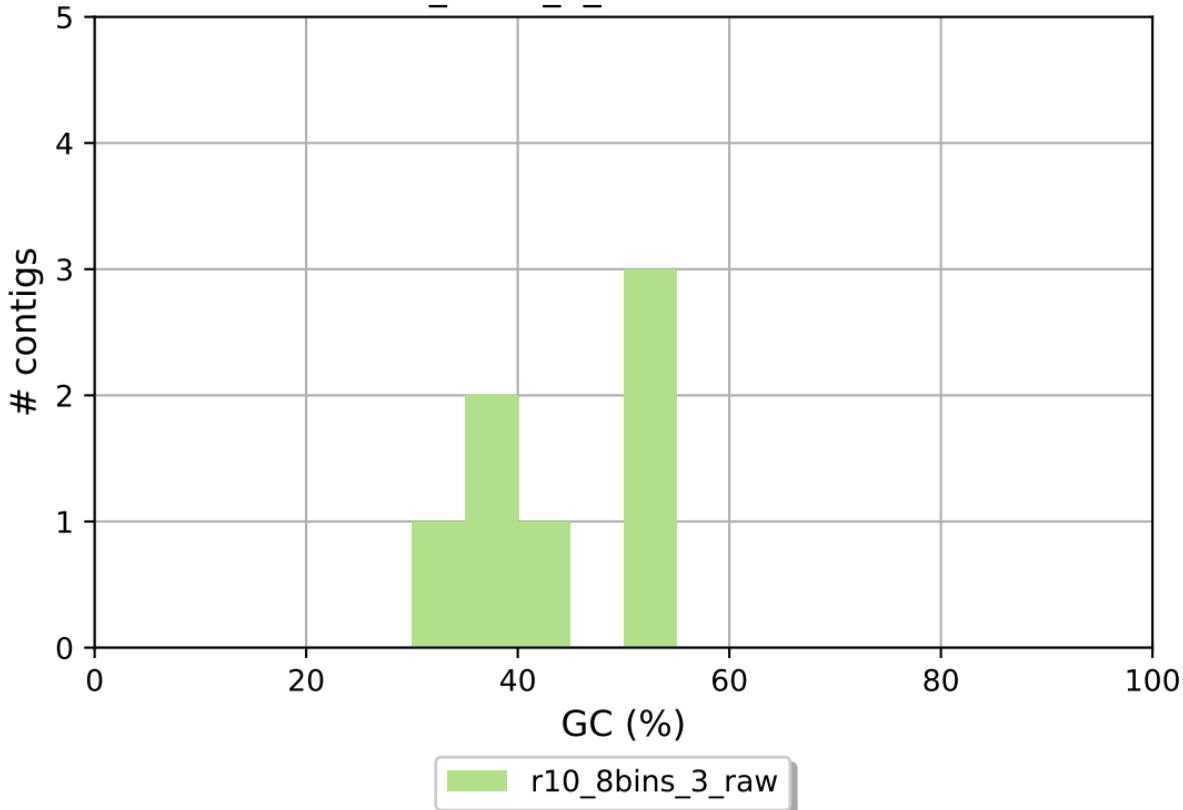
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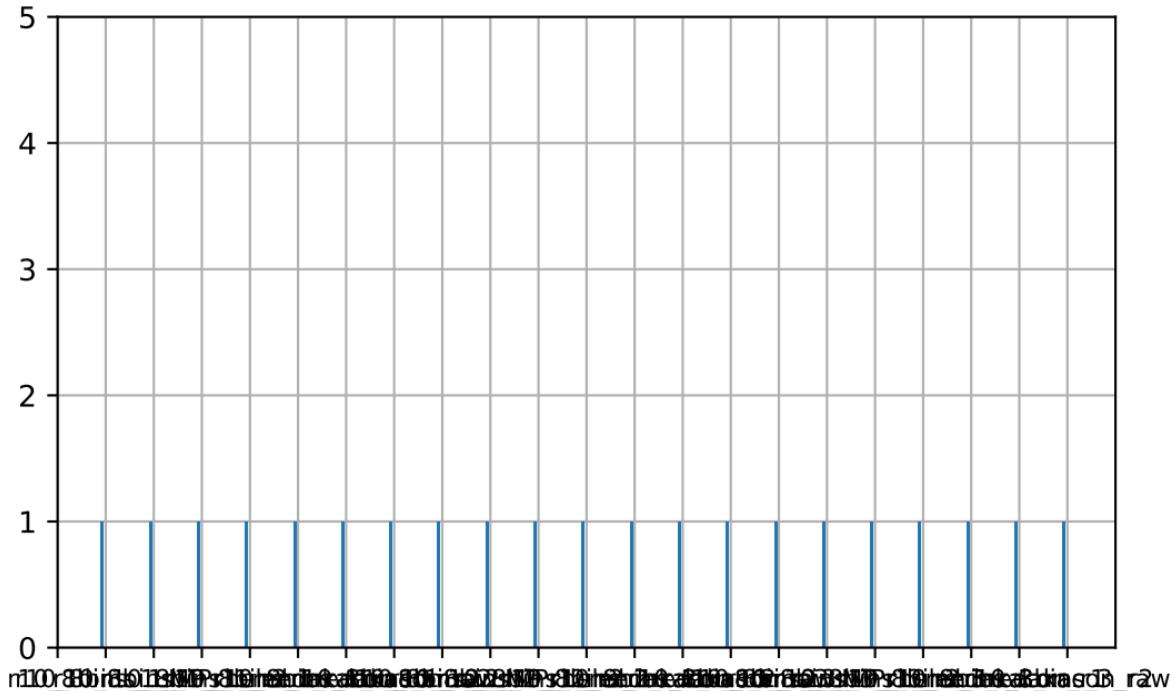
r10_8bins_3_racon_r2 GC content



r10_8bins_3_raw GC content

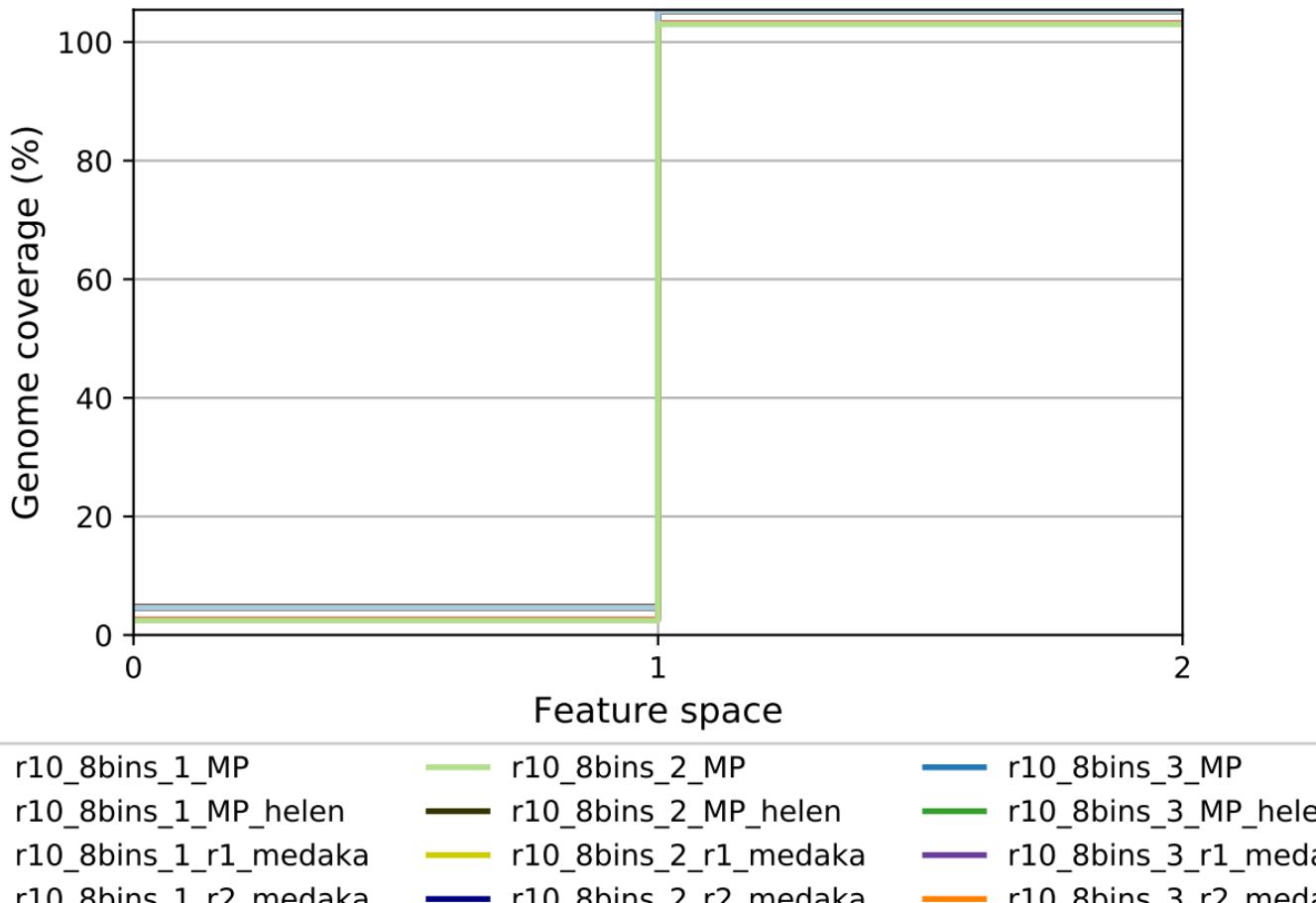


Misassemblies

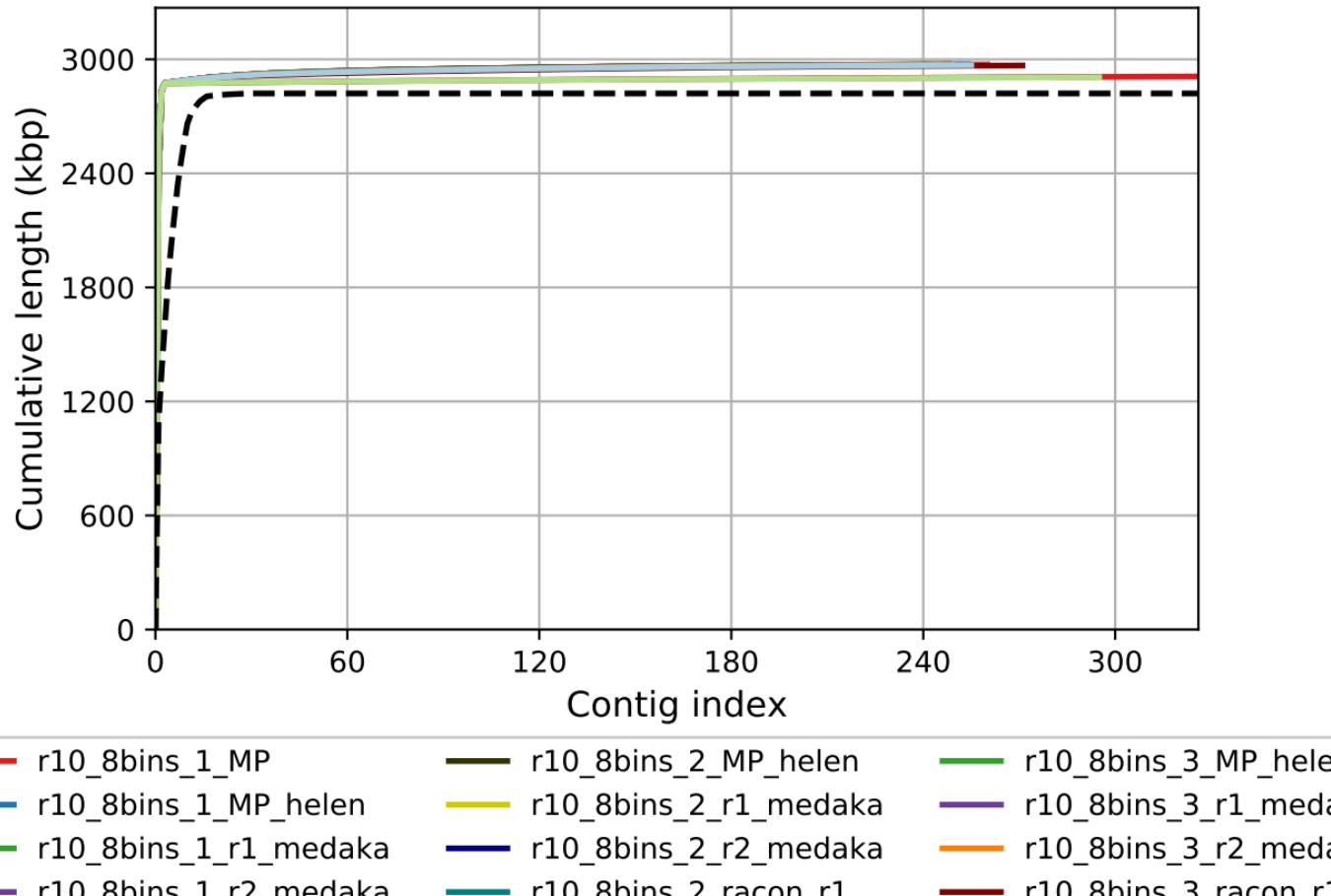


translocations

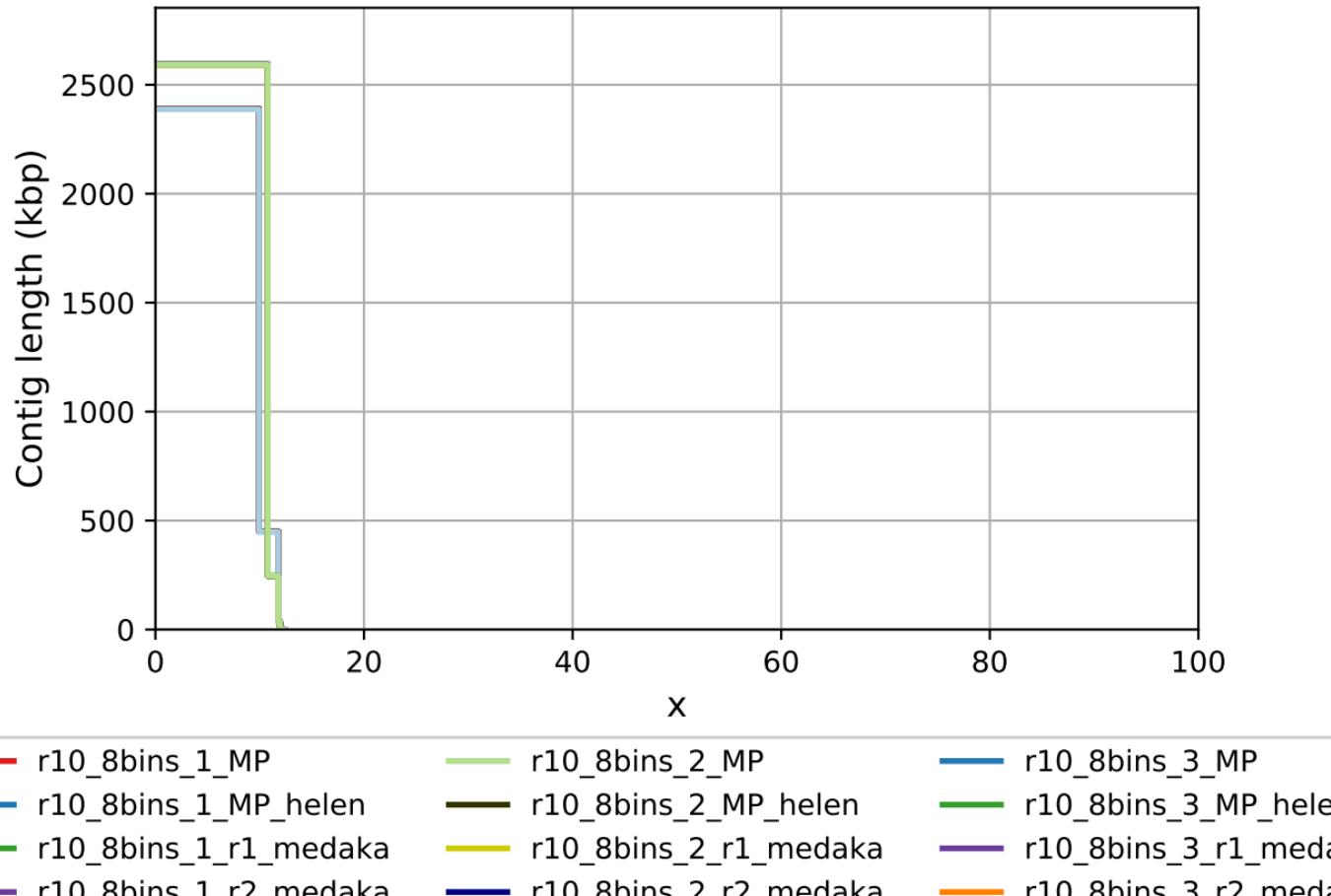
FRCurve (misassemblies)



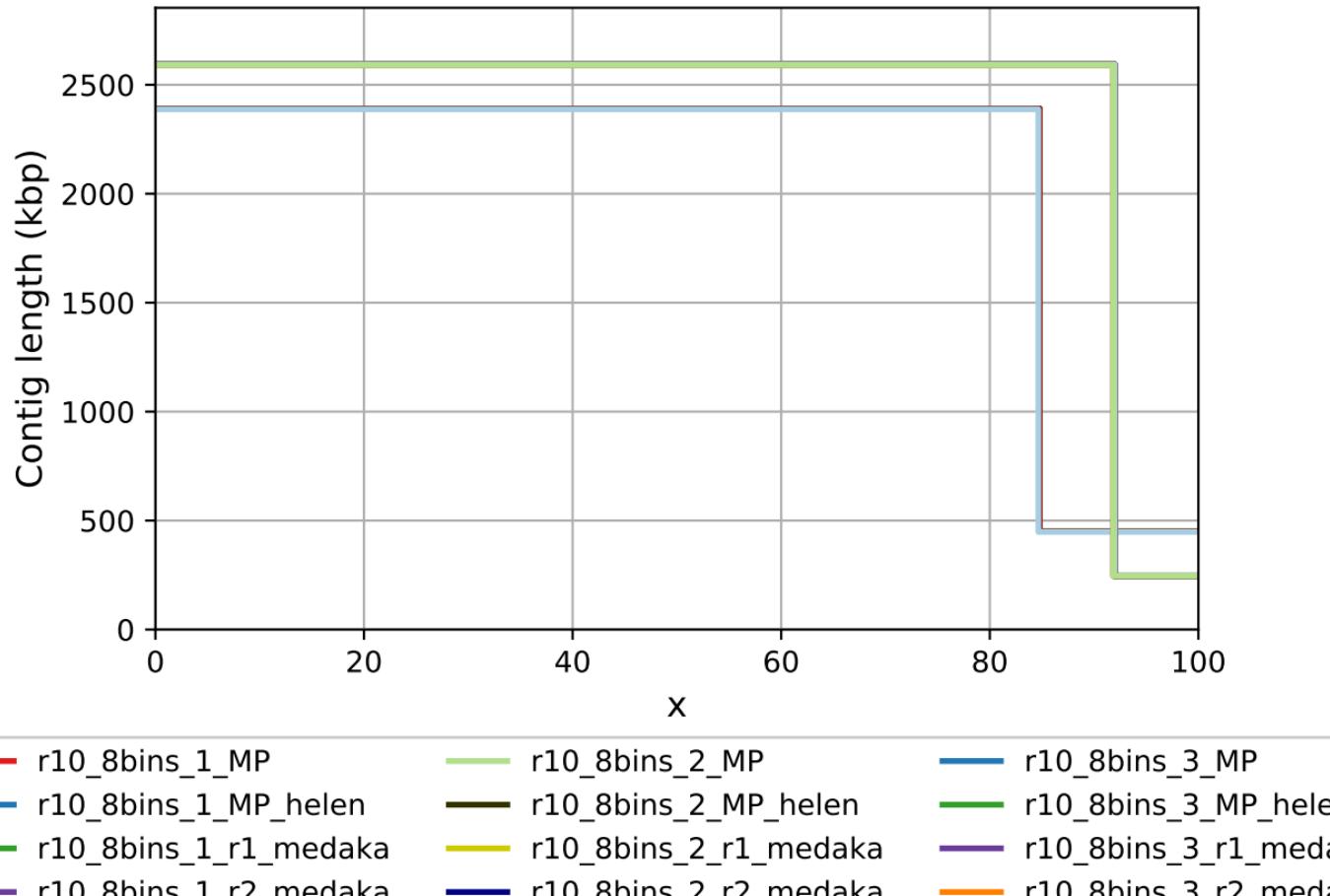
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

