

## 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_helen	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_3_raw		
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Total length (>= 5000 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
Total length (>= 10000 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
Total length (>= 25000 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
Total length (>= 50000 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Largest contig	6792200	6792201	6792230	6792235	6791646	6791695	6788614	6792246	6792183	6792245	6792249	6791667	6791726	6788581	6792689	6792361	6792415	6791833	6791907	6788292	
Total length	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151		
GC (%)	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.48		
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21		
N50	4758957	4758026	4758581	4758584	4758019	4758050	4755933	4758981	4757842	4758589	4758101	4757934	4757912	4756088	4758992	4758031	4758588	4758092	4757964	4757944	4756065
NG50	6792200	6792201	6792230	6792235	6791646	6791695	6788614	6792246	6792183	6792245	6792249	6791667	6791726	6788581	6792689	6792361	6792415	6791833	6791907	6788292	
N75	2992094	2992072	2992073	2992074	2991951	2991999	2990636	2992084	2992066	2992073	2992074	2991957	2990626	2992095	2992076	2992073	2991935	2991970	2990261		
NG75	6792200	6792201	6792230	6792235	6791646	6791695	6788614	6792246	6792183	6792245	6792249	6791667	6791726	6788581	6792689	6792361	6792415	6791833	6791907	6788292	
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	8	6	6	6	6	6	6	10	8	6	6	6	6	10	8	6	6	6	10		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	6792200	6792201	6792230	6792235	6791646	6791695	6788614	6792246	6792183	6792245	6792249	6791667	6791726	6788581	6792689	6792361	6792415	6791833	6791907	6788292	
# local misassemblies	11	11	11	11	11	11	24	11	11	11	11	11	11	25	12	11	11	11	11	31	
# 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	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7		
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part		
Unaligned length	24047149	24043641	24044751	24036610	24033406	24026051	24077409	24047444	24042659	24044582	24035233	24034373	24028213	24077072	24048207	24043465	24045328	24033377	24028998	24075679	
Genome fraction (%)	99.894	99.894	99.894	99.894	99.894	99.894	99.875	99.893	99.893	99.893	99.893	99.893	99.878	99.895	99.894	99.894	99.894	99.894	99.863		
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.008		
# 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	59.19	56.23	56.51	56.93	59.50	59.65	65.44	58.64	55.86	56.18	55.77	58.12	57.82	64.79	58.10	55.35	55.74	55.69	58.03	58.16	66.83
# indels per 100 kbp	5																				

## Misassemblies report

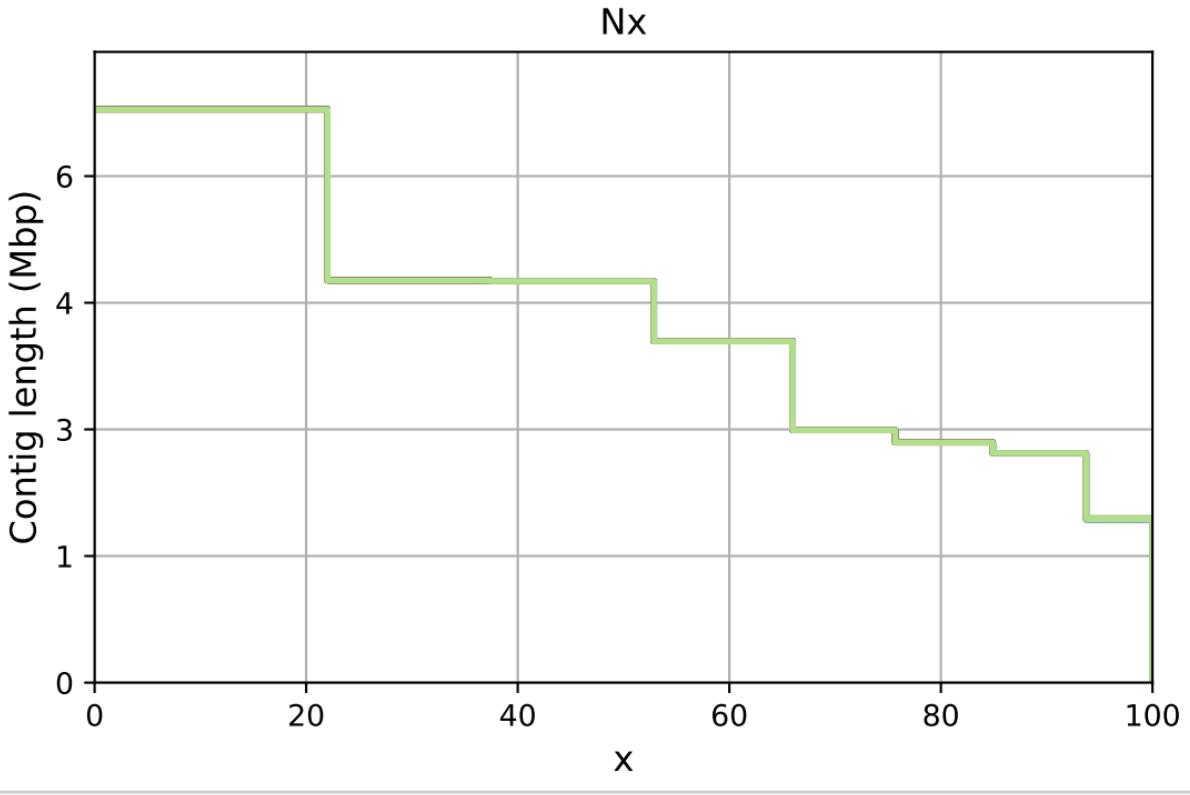
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# misassemblies	8	6	6	6	6	6	10	8	6	6	6	6	6	10	8	6	6	6	6	10	
# contig misassemblies	8	6	6	6	6	6	10	8	6	6	6	6	6	10	8	6	6	6	6	10	
# c. relocations	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	
# c. translocations	7	6	6	6	6	6	10	7	6	6	6	6	6	10	7	6	6	6	6	10	
# c. inversions	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	
# s. relocations	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	
# s. inversions	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	
Misassembled contigs length	6792200	6792201	6792230	6792235	6791646	6791695	6788614	6792246	6792183	6792245	6792249	6791667	6791726	6788581	6792689	6792361	6792415	6792413	6791833	6791907	6788292
# 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	16	18	18	18	18	18	34	16	18	18	18	18	34	16	18	18	18	18	18	34	
# local misassemblies	11	11	11	11	11	11	24	11	11	11	11	11	25	12	11	11	11	11	11	31	
# 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	20	21	21	21	21	21	16	20	21	21	21	21	16	20	21	21	21	21	21	16	
# unaligned mis. contigs	7	7	7	7	7	7	6	7	7	7	7	7	7	7	7	7	7	7	7	7	
# mismatches	3978	3779	3798	3826	3999	4009	4397	3941	3754	3776	3748	3906	3886	4354	3905	3720	3746	3743	3900	3909	4490
# indels	383	254	244	248	890	826	6545	365	339	244	244	897	832	6528	381	347	250	244	932	830	6506
# indels (<= 5 bp)	288	159	151	155	796	732	6421	270	242	150	150	802	738	6405	285	249	156	150	834	736	6386
# indels (> 5 bp)	95	95	93	93	94	94	124	95	97	94	94	98	94	94	98	94	94	98	94	120	
Indels length	5428	5291	5244	5247	6019	5920	12976	5398	5399	5261	5261	6030	5935	12917	5434	5268	5259	6078	5927	12810	

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).

## Unaligned report

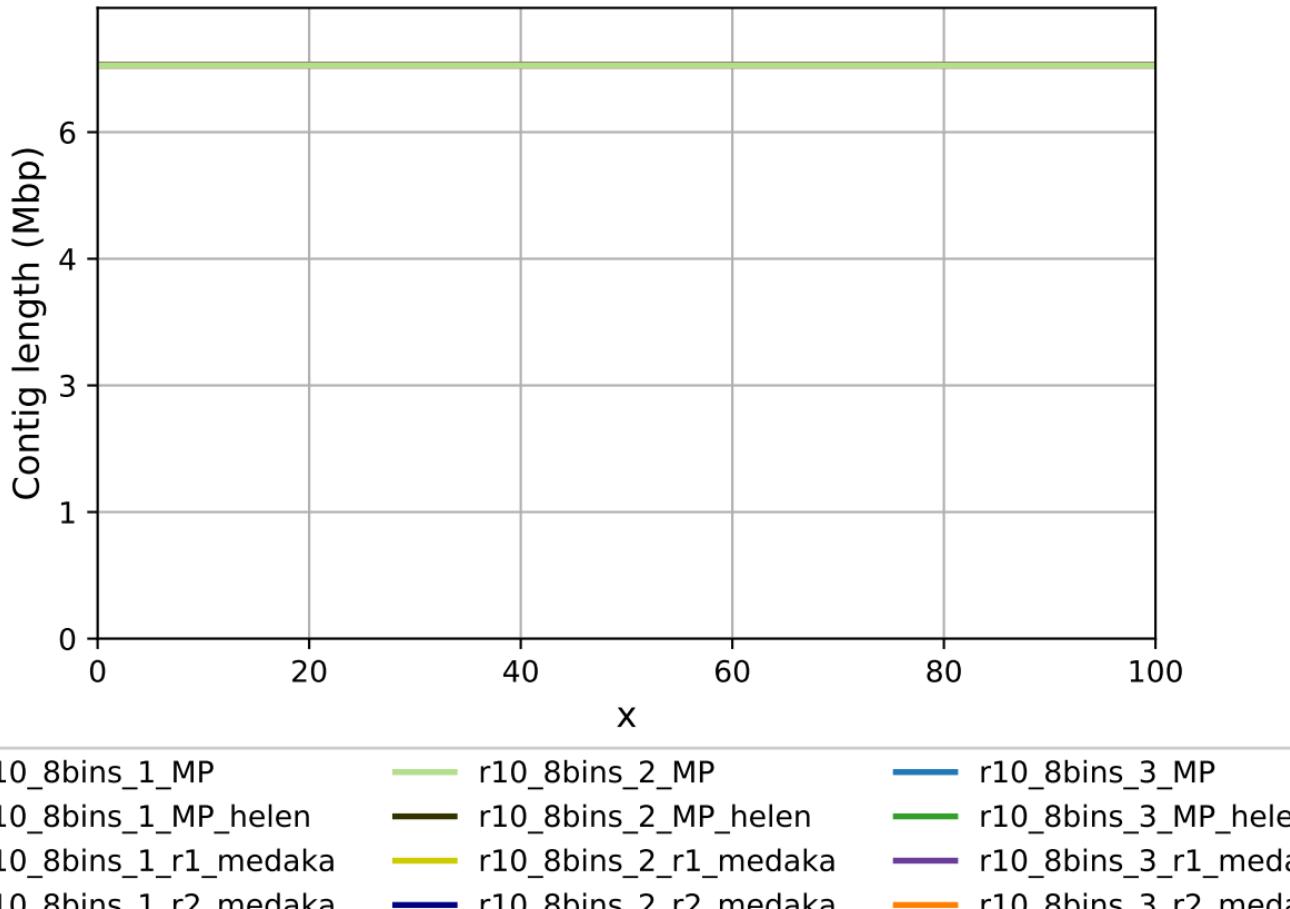
	r10_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_racon_r1	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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Partially unaligned length	24047149	24043641	24044751	24036610	24033406	24026051	24077409	24047444	24042659	24035233	24034373	24028213	24077072	24048207	24043465	24037932	24033377	24028998	24075679
# 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).

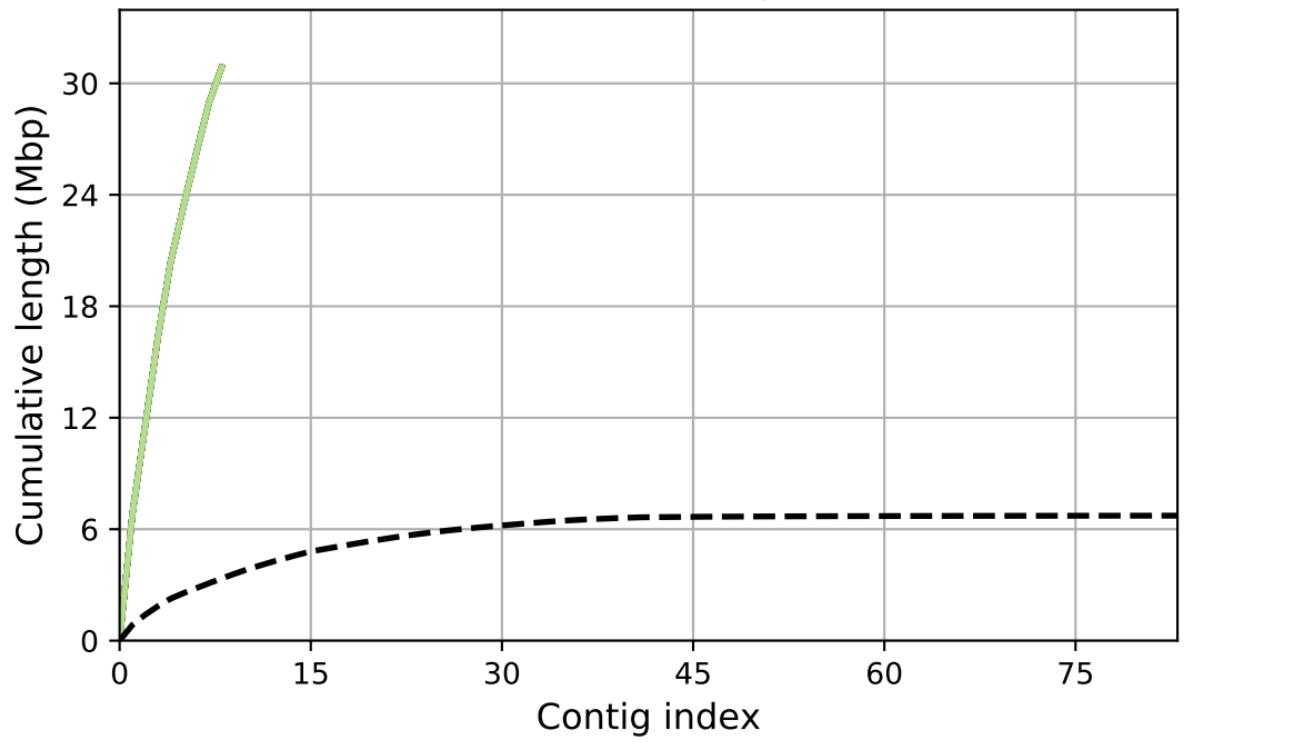


- r10\_8bins\_1\_MP
- r10\_8bins\_1\_MP\_helen
- r10\_8bins\_1\_r1\_medaka
- r10\_8bins\_1\_r2\_medaka
- r10\_8bins\_2\_MP
- r10\_8bins\_2\_MP\_helen
- r10\_8bins\_2\_r1\_medaka
- r10\_8bins\_2\_r2\_medaka
- r10\_8bins\_3\_MP
- r10\_8bins\_3\_MP\_helen
- r10\_8bins\_3\_r1\_medaka
- r10\_8bins\_3\_r2\_medaka

NGx

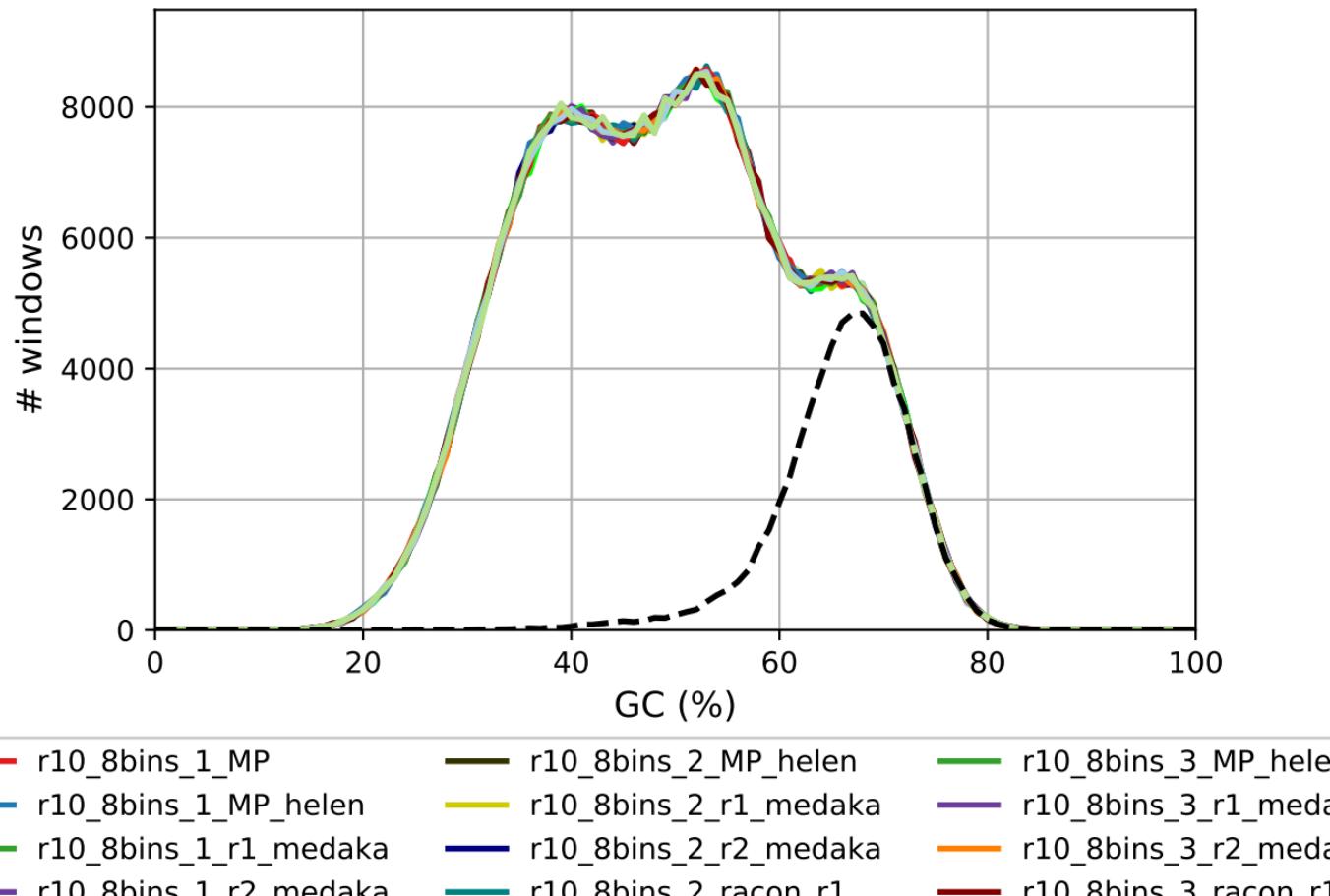


Cumulative length

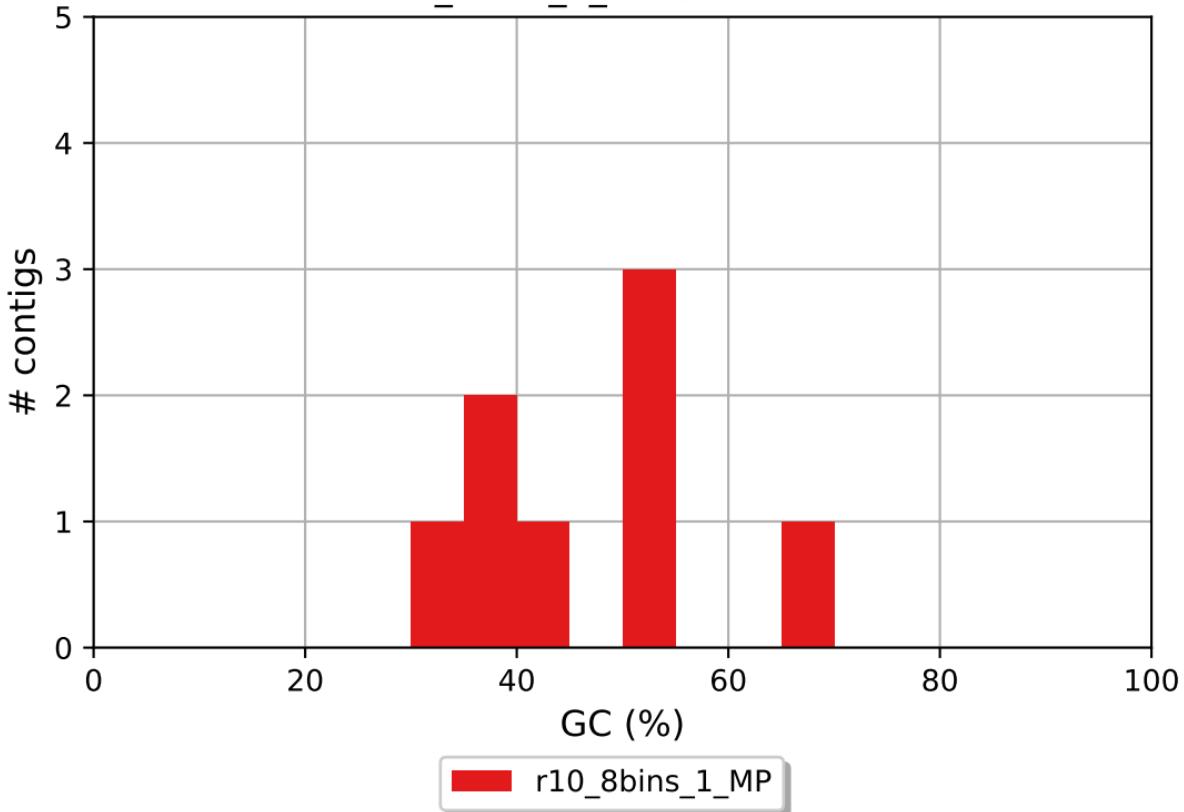


— r10\_8bins\_1\_MP  
- - - r10\_8bins\_1\_MP\_helen  
— r10\_8bins\_1\_r1\_medaka  
— r10\_8bins\_1\_r2\_medaka  
— r10\_8bins\_2\_MP\_helen  
— r10\_8bins\_2\_r1\_medaka  
— r10\_8bins\_2\_r2\_medaka  
— r10\_8bins\_2\_racon\_r1  
— r10\_8bins\_3\_MP\_helen  
— r10\_8bins\_3\_r1\_medaka  
— r10\_8bins\_3\_r2\_medaka  
— r10\_8bins\_3\_racon\_r1

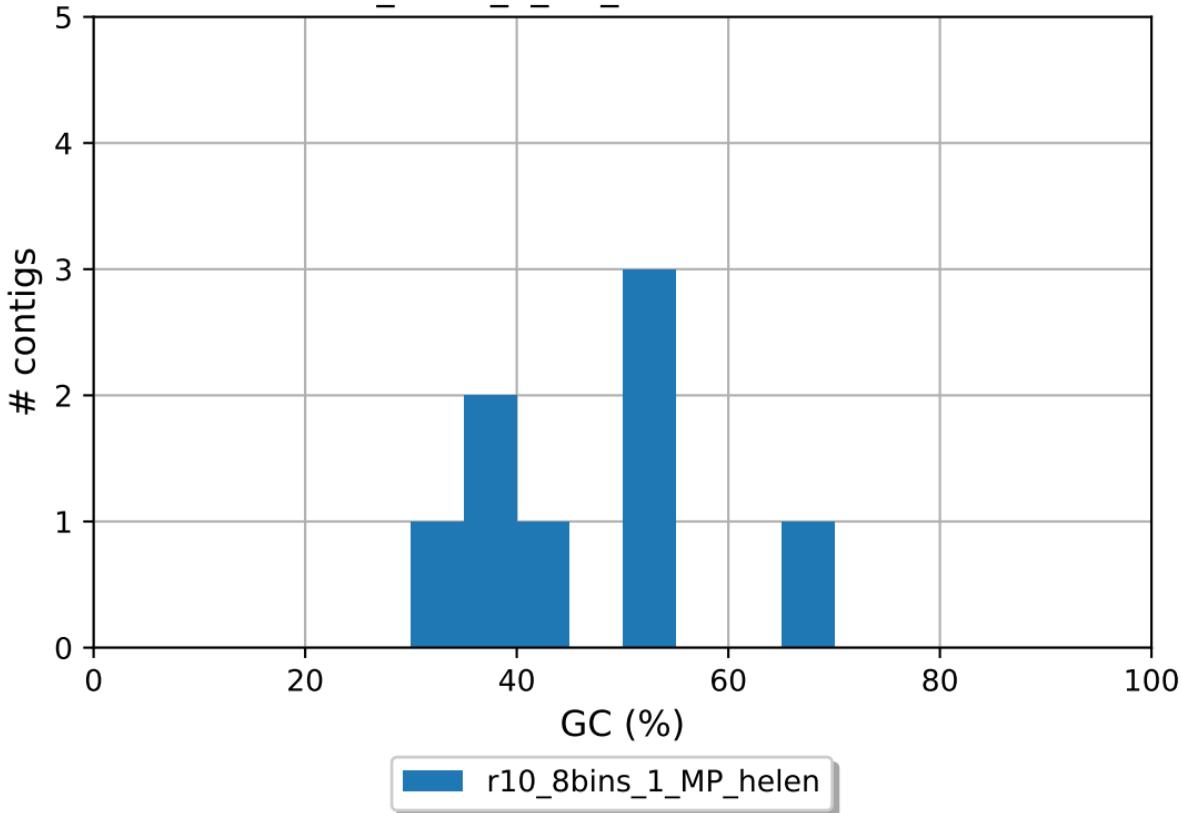
## GC content



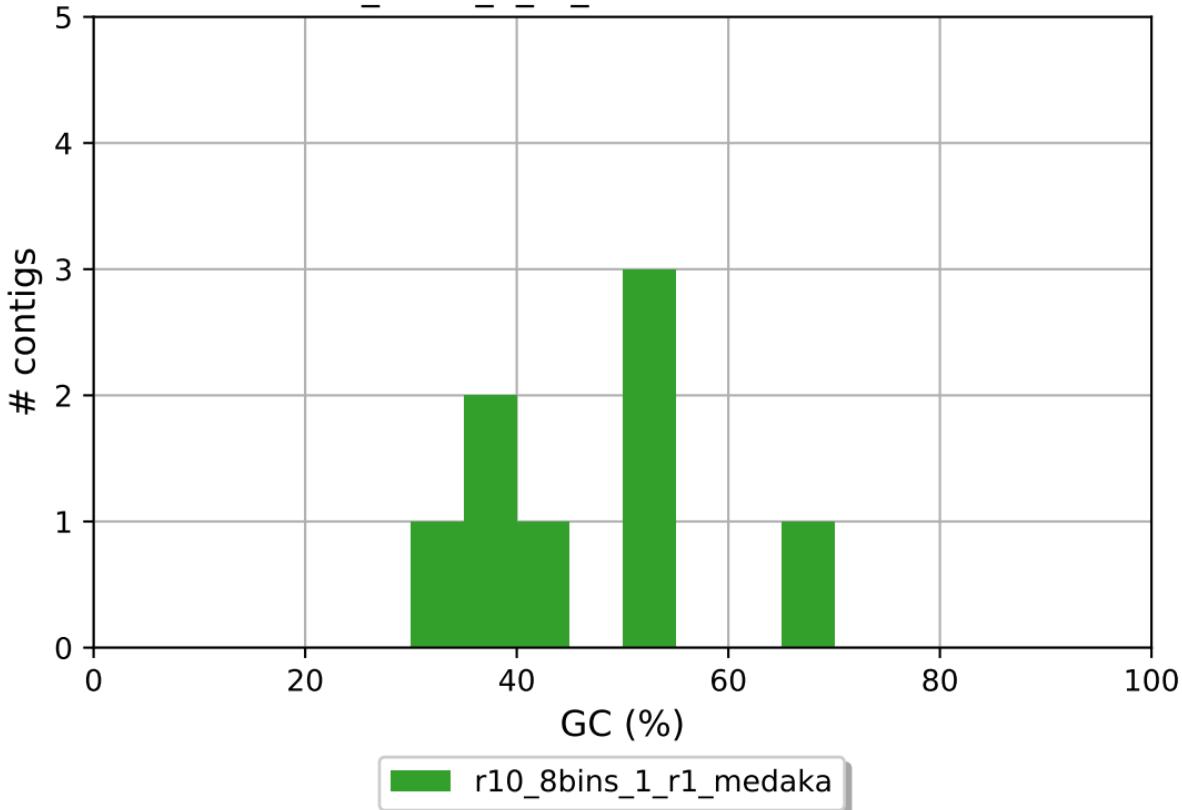
r10\_8bins\_1\_MP GC content



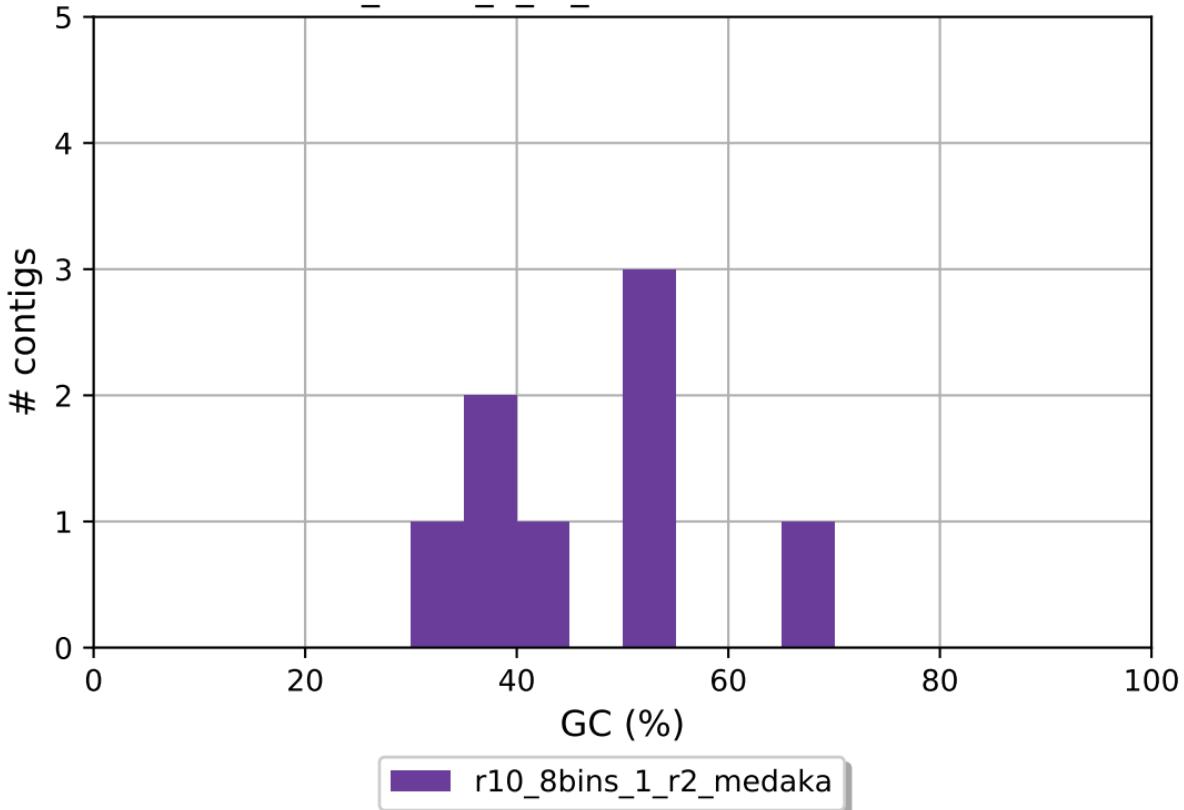
r10\_8bins\_1\_MP\_helen GC content



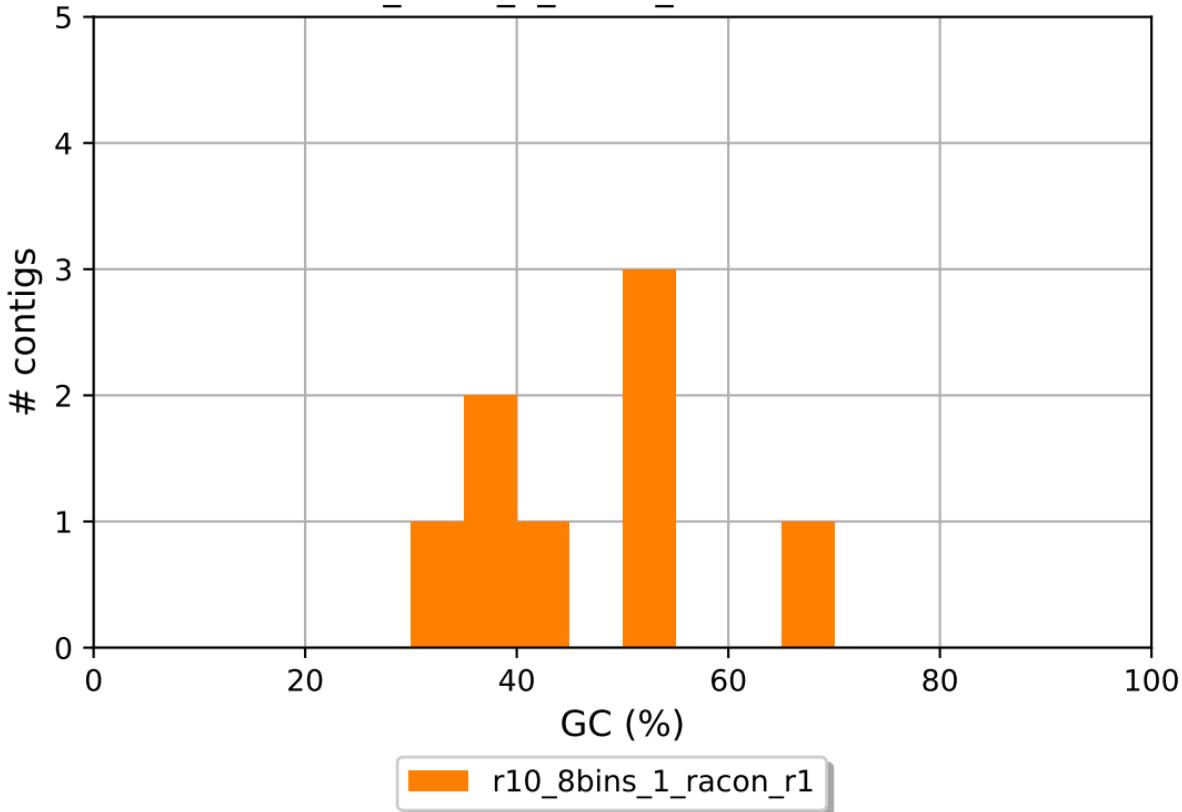
r10\_8bins\_1\_r1\_medaka GC content



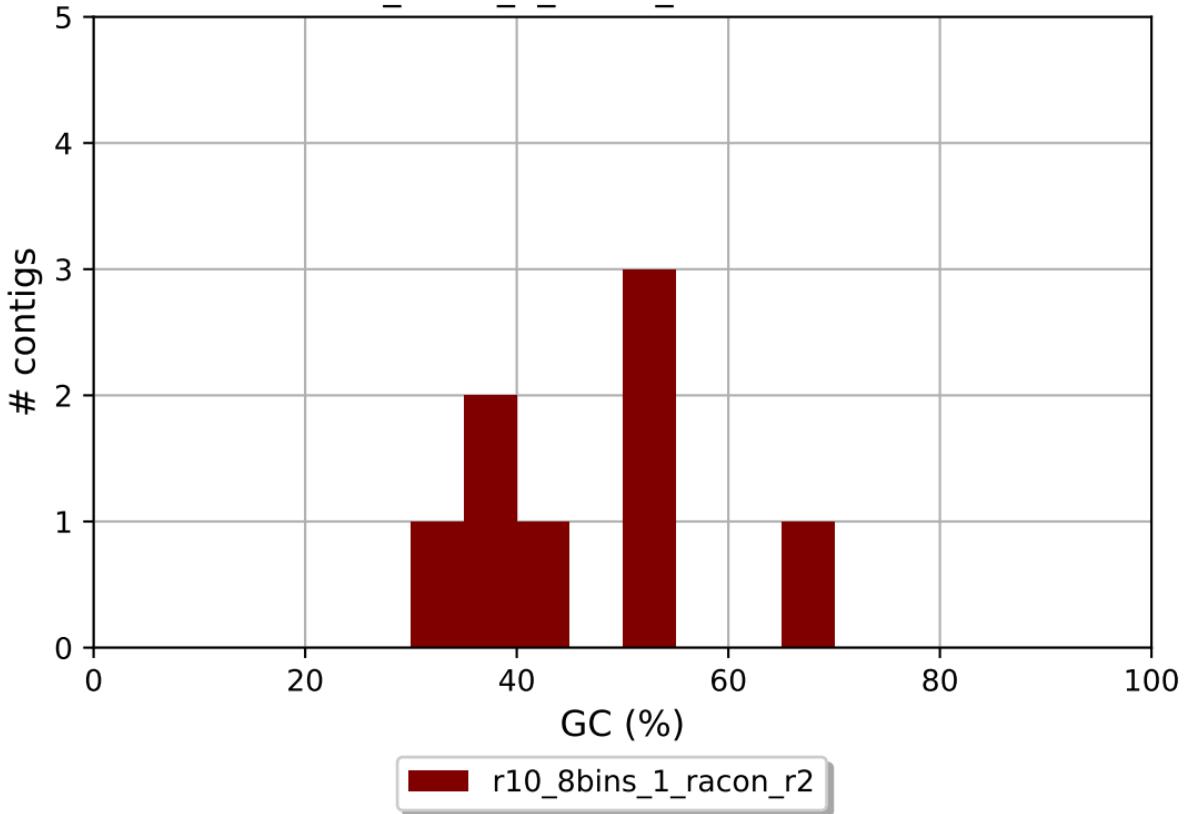
r10\_8bins\_1\_r2\_medaka GC content



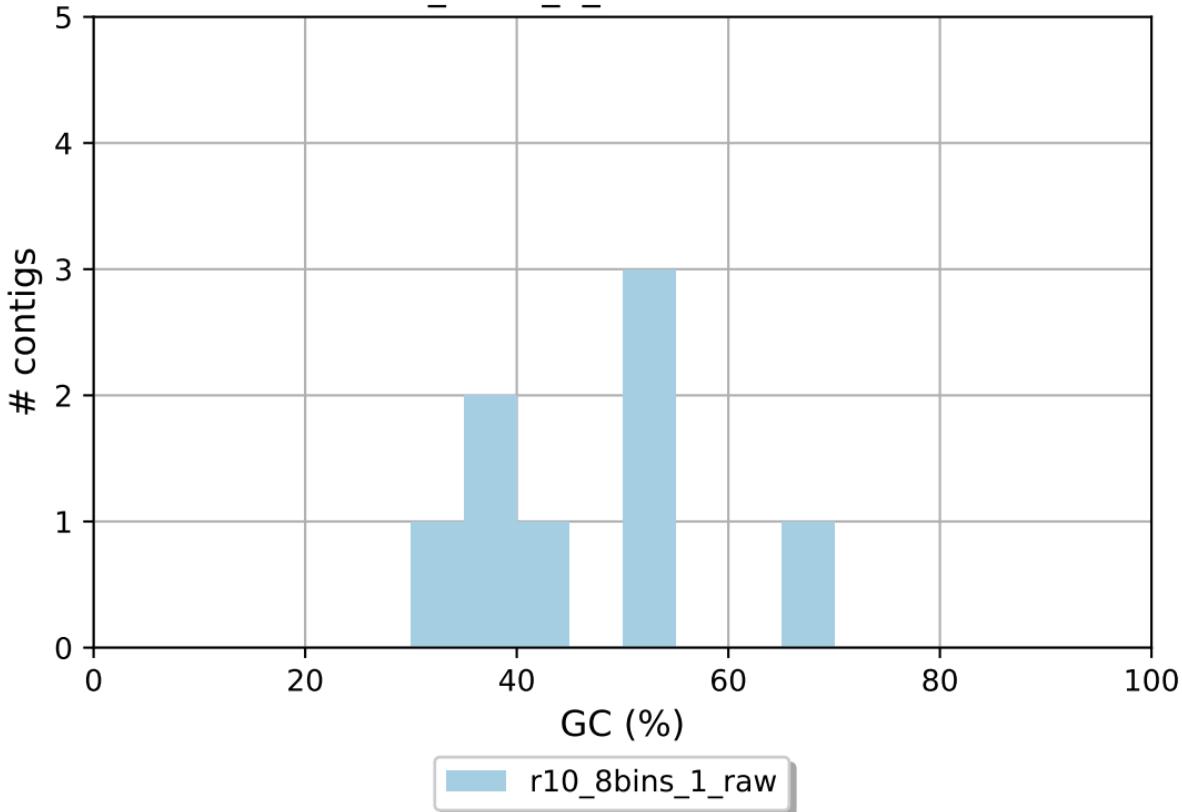
r10\_8bins\_1\_racon\_r1 GC content



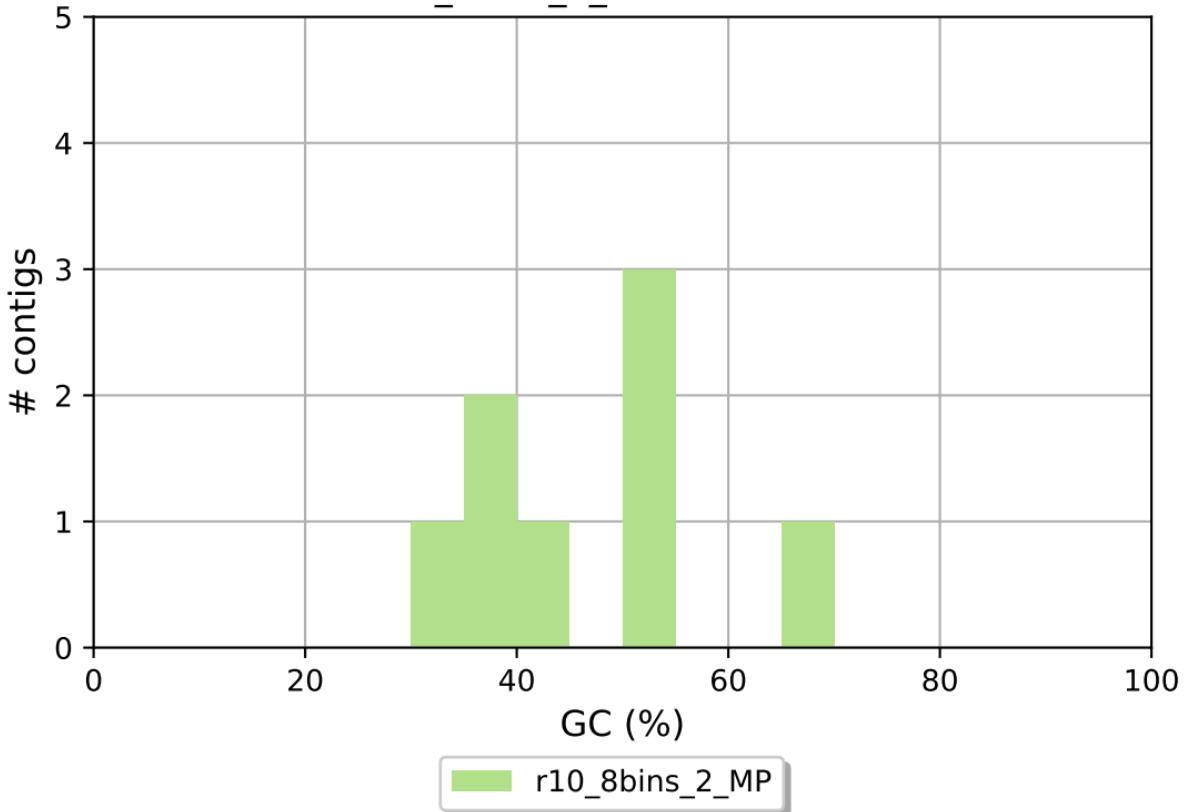
r10\_8bins\_1\_racon\_r2 GC content



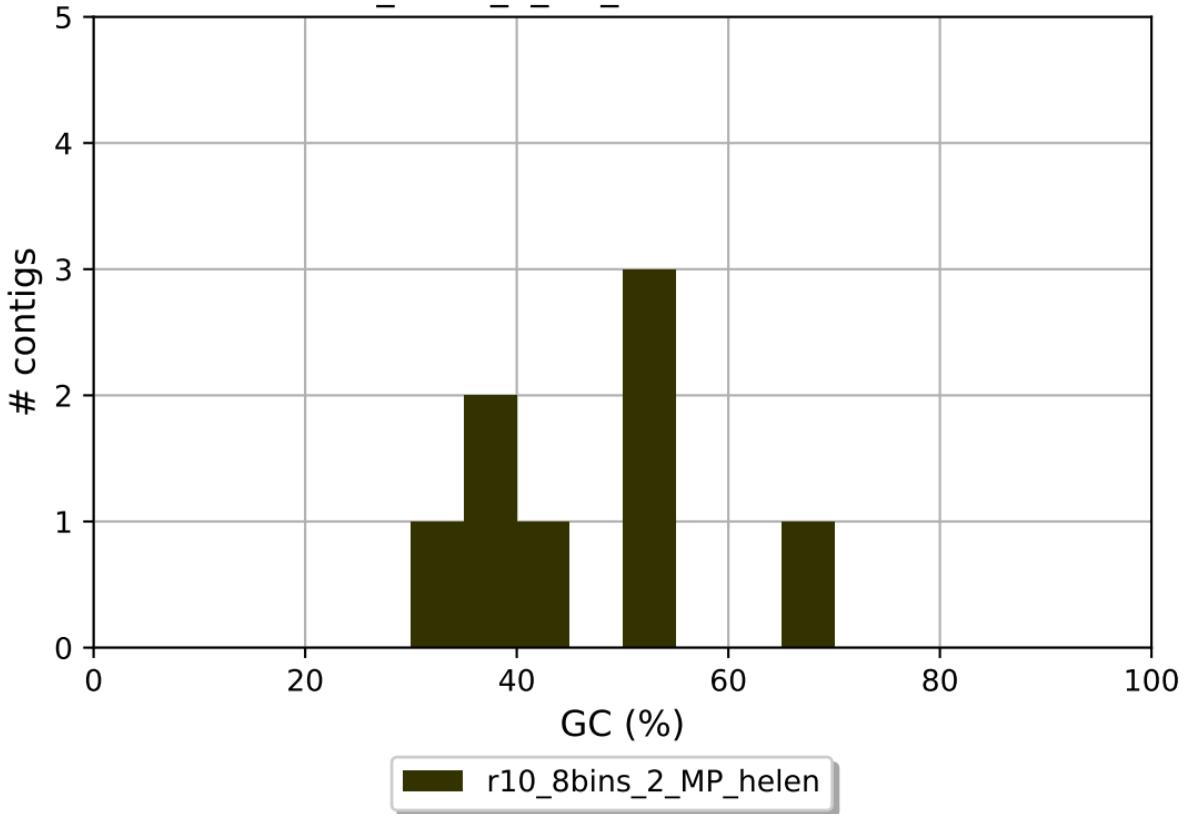
r10\_8bins\_1\_raw GC content



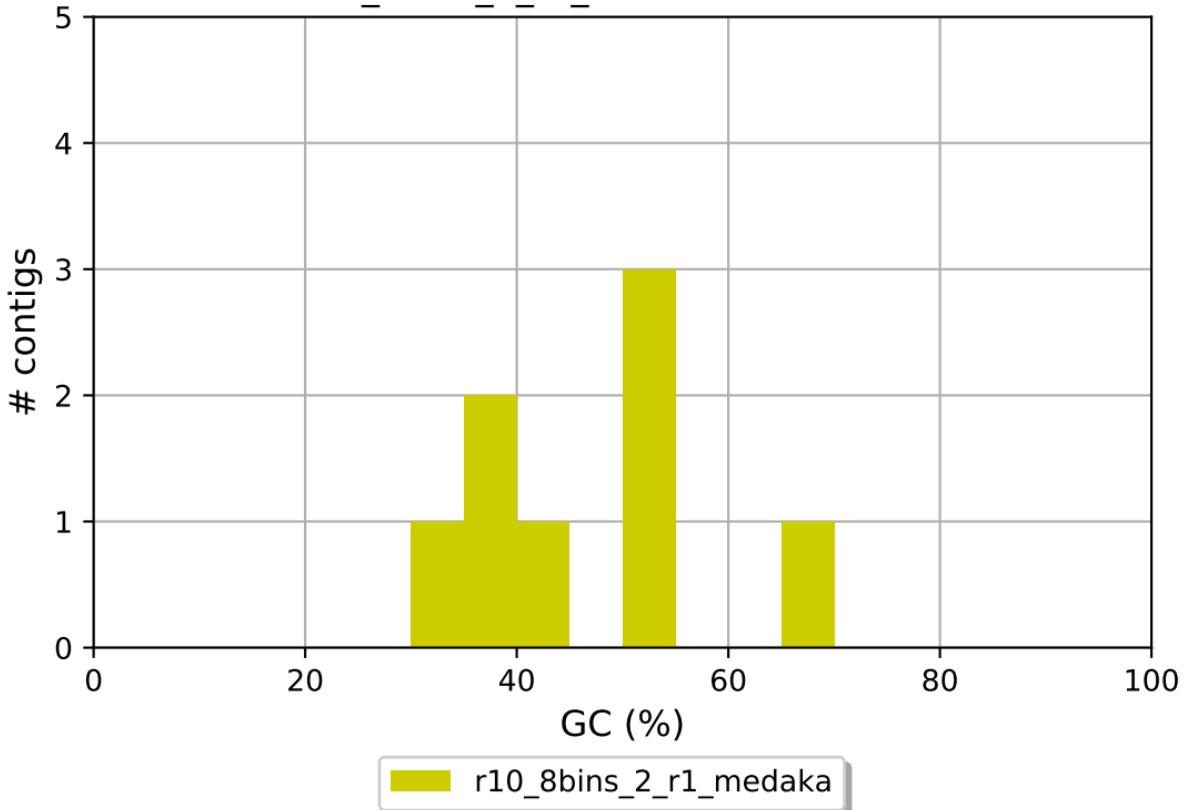
r10\_8bins\_2\_MP GC content



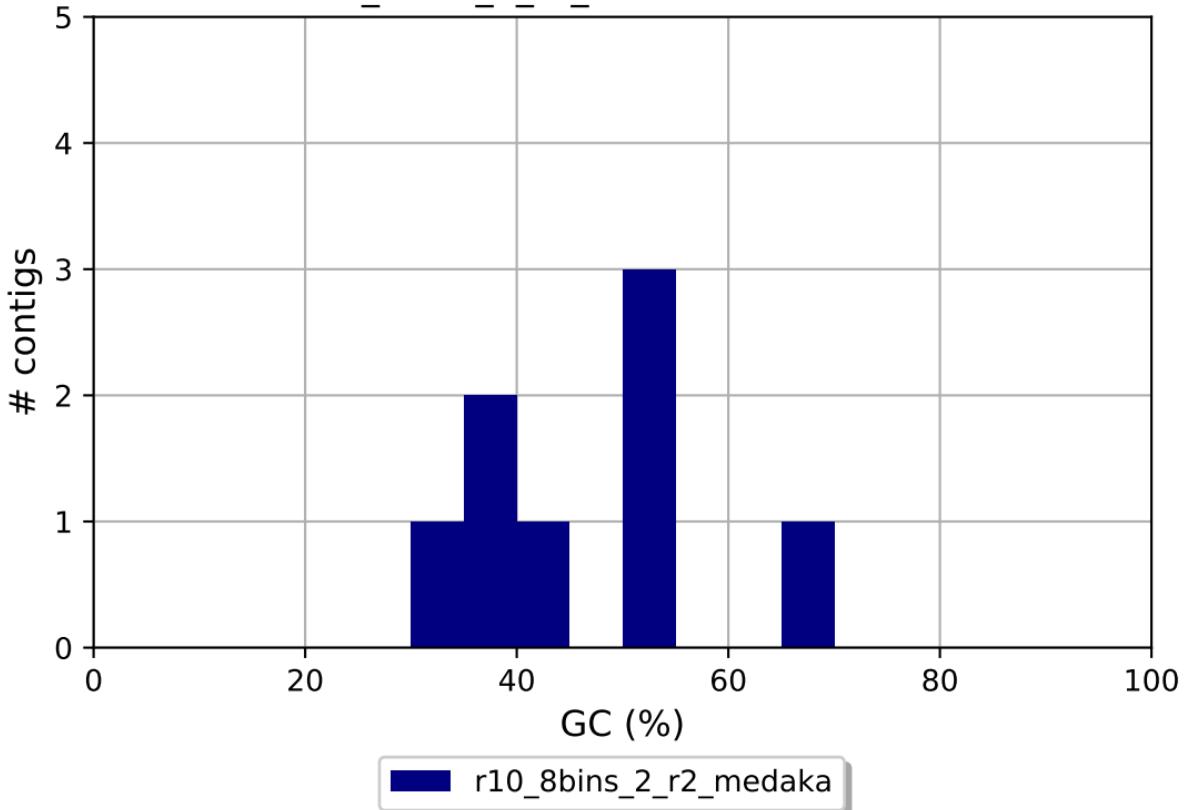
r10\_8bins\_2\_MP\_helen GC content



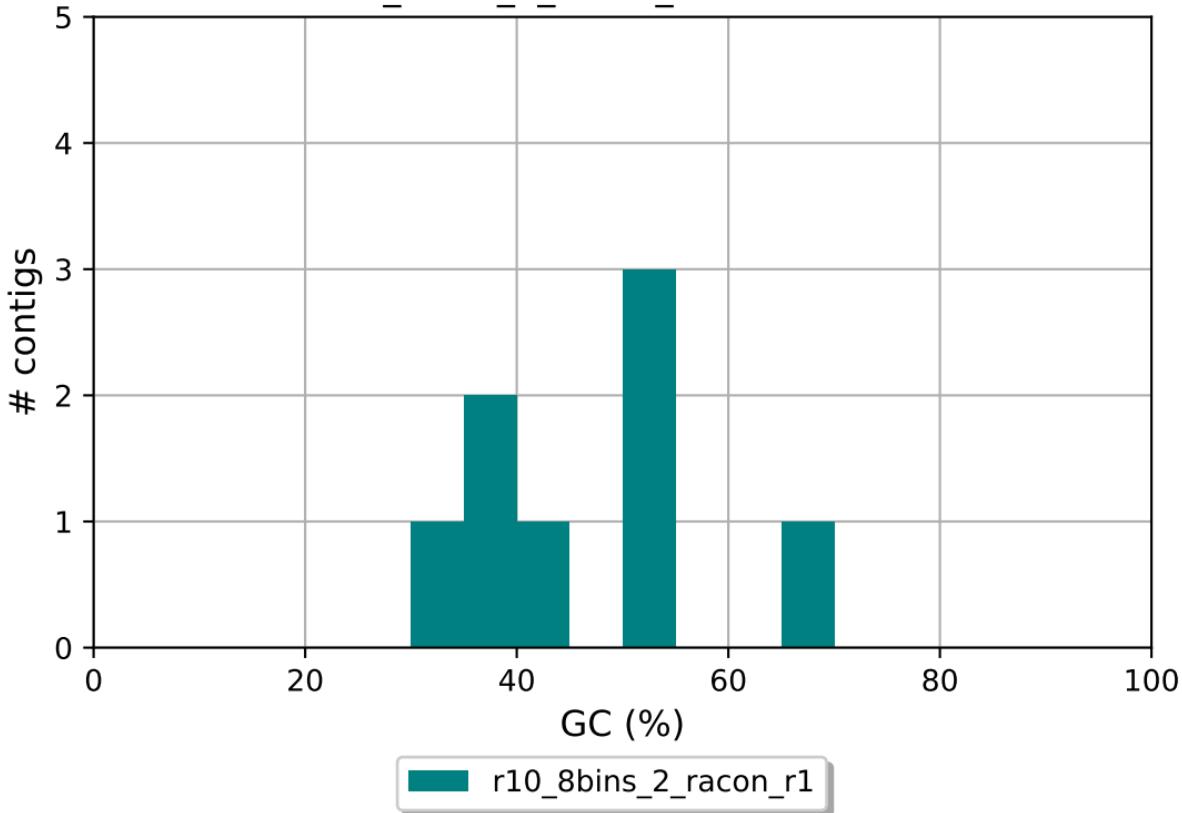
r10\_8bins\_2\_r1\_medaka GC content



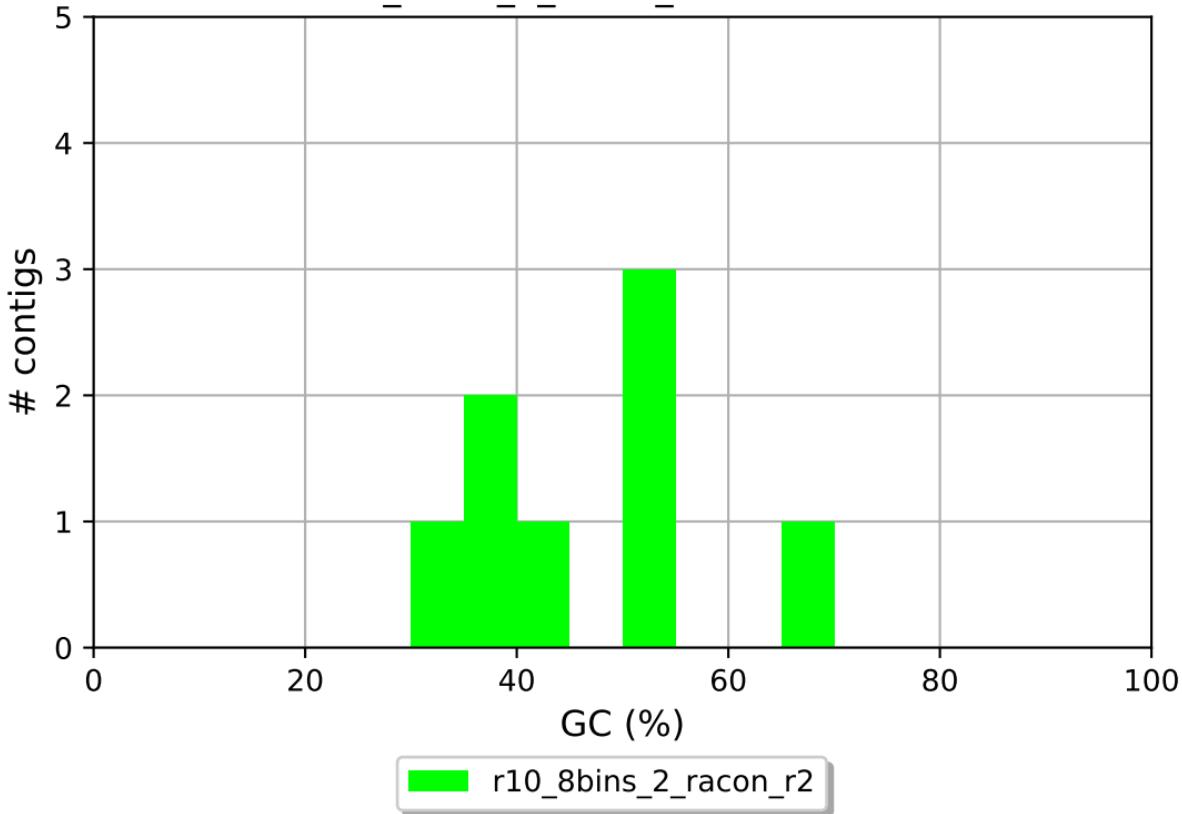
r10\_8bins\_2\_r2\_medaka GC content



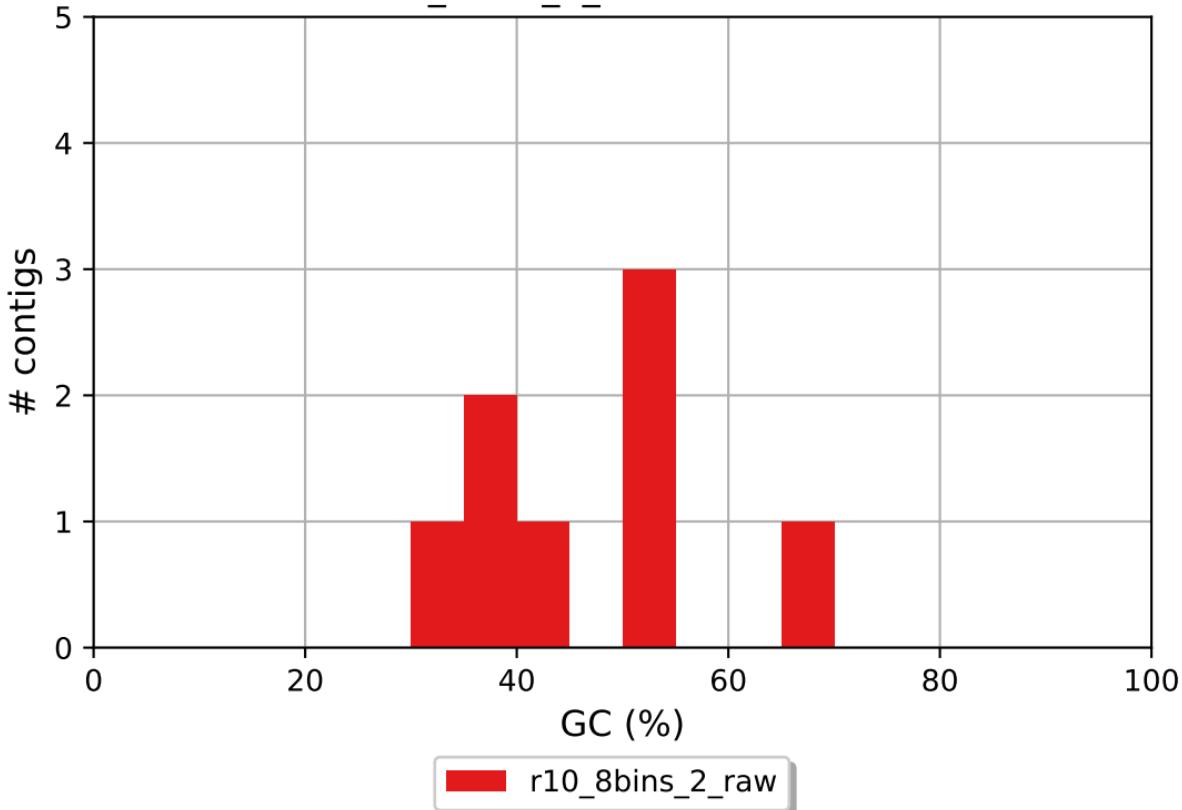
r10\_8bins\_2\_racon\_r1 GC content



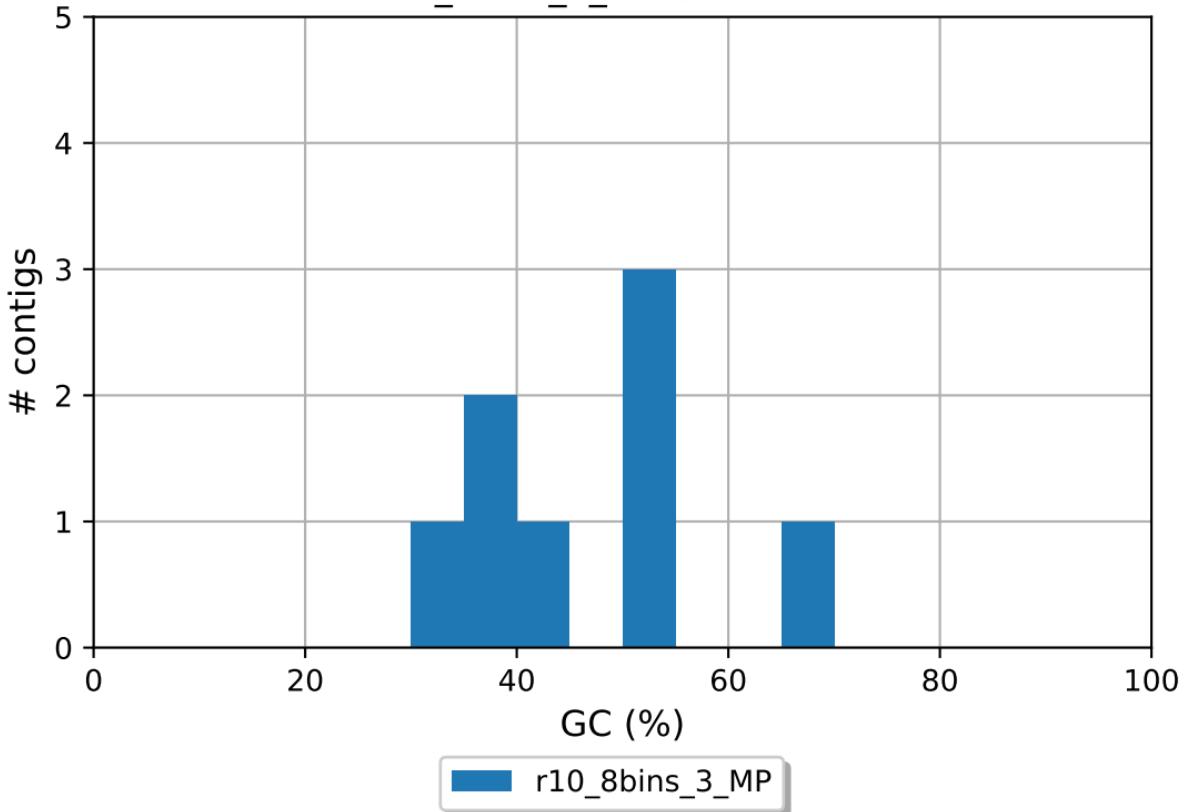
r10\_8bins\_2\_racon\_r2 GC content



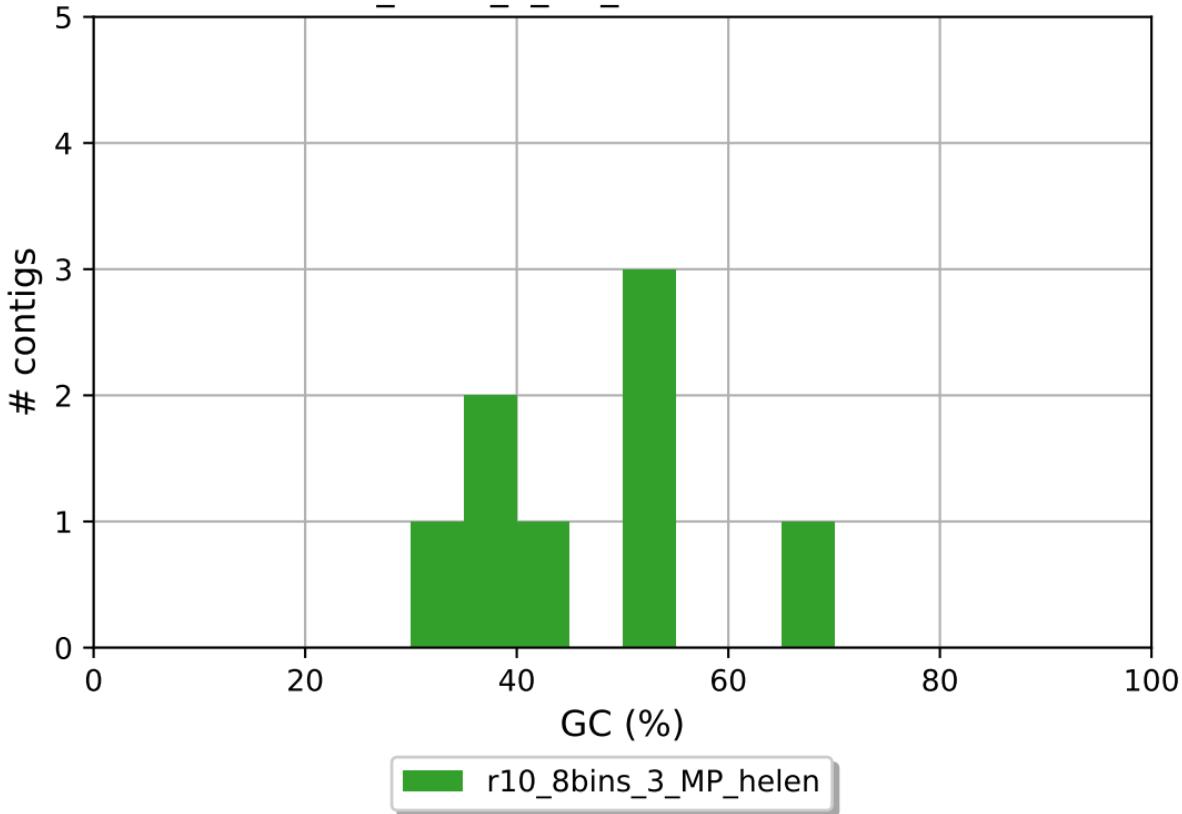
r10\_8bins\_2\_raw GC content



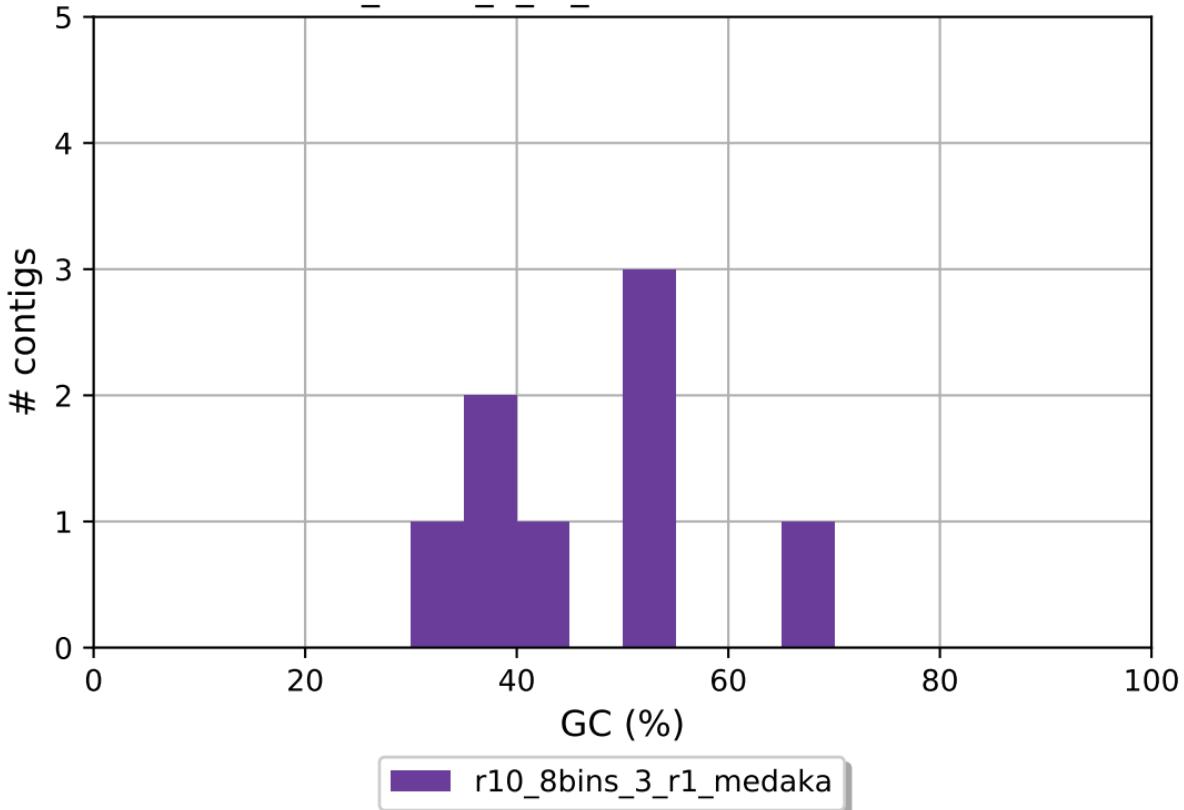
r10\_8bins\_3\_MP GC content



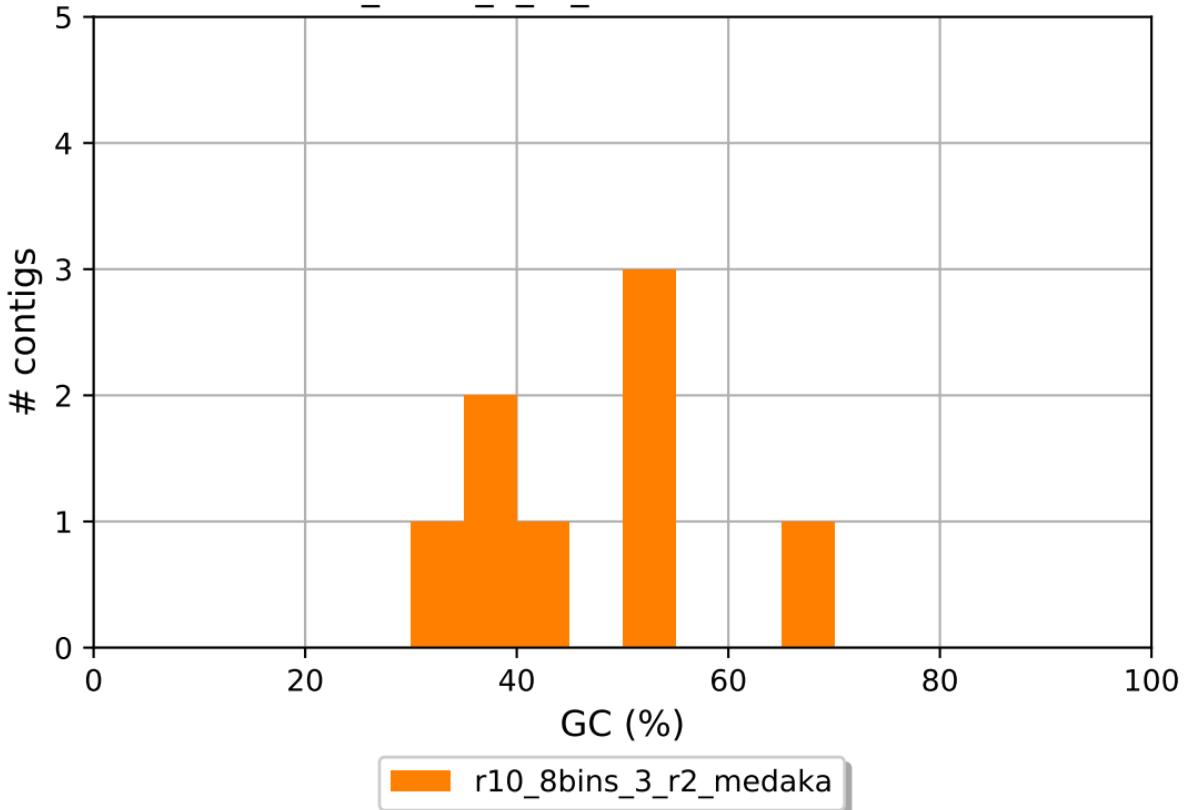
r10\_8bins\_3\_MP\_helen GC content



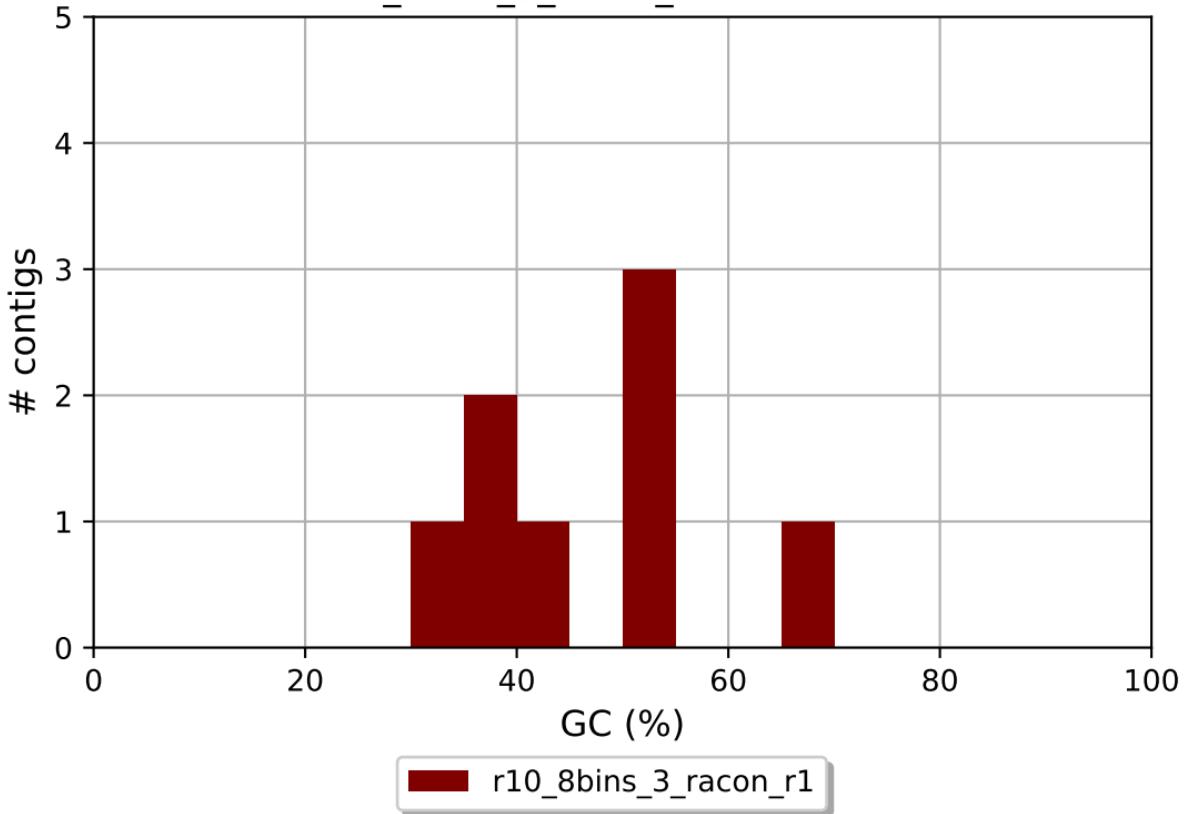
r10\_8bins\_3\_r1\_medaka GC content



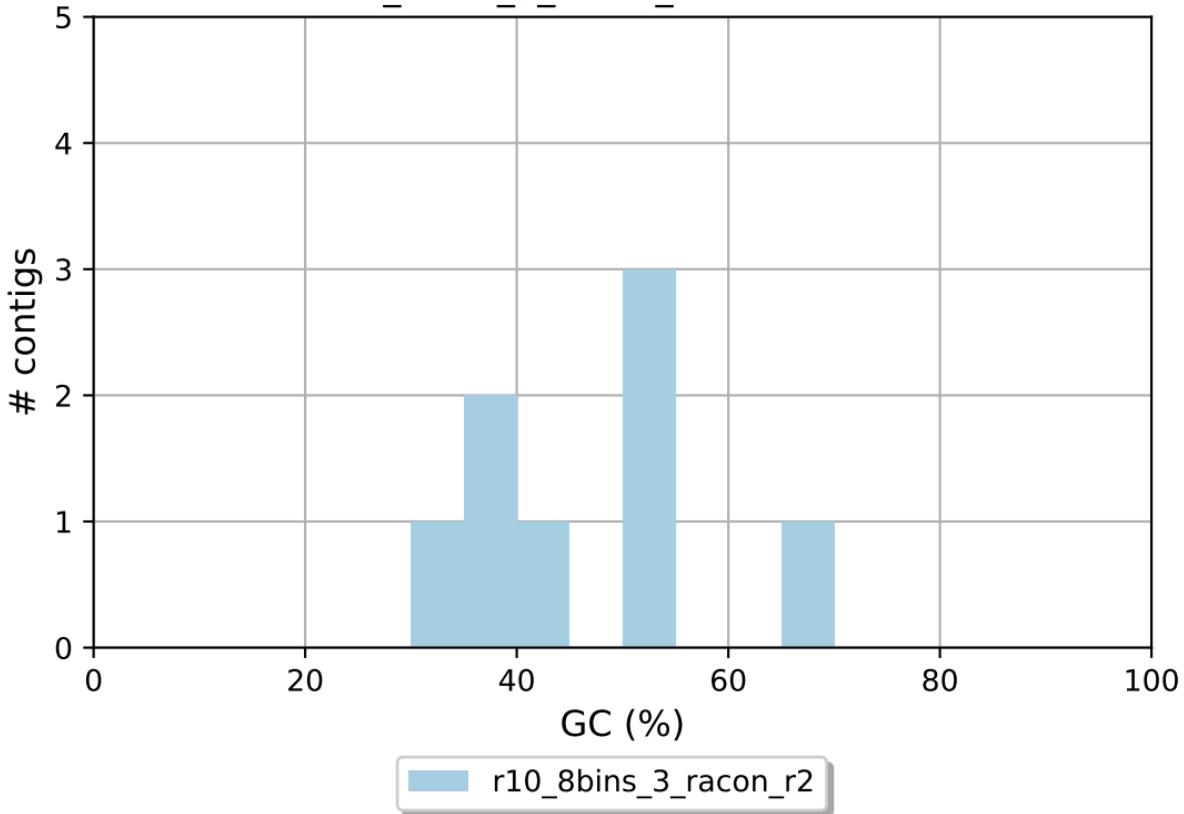
r10\_8bins\_3\_r2\_medaka GC content



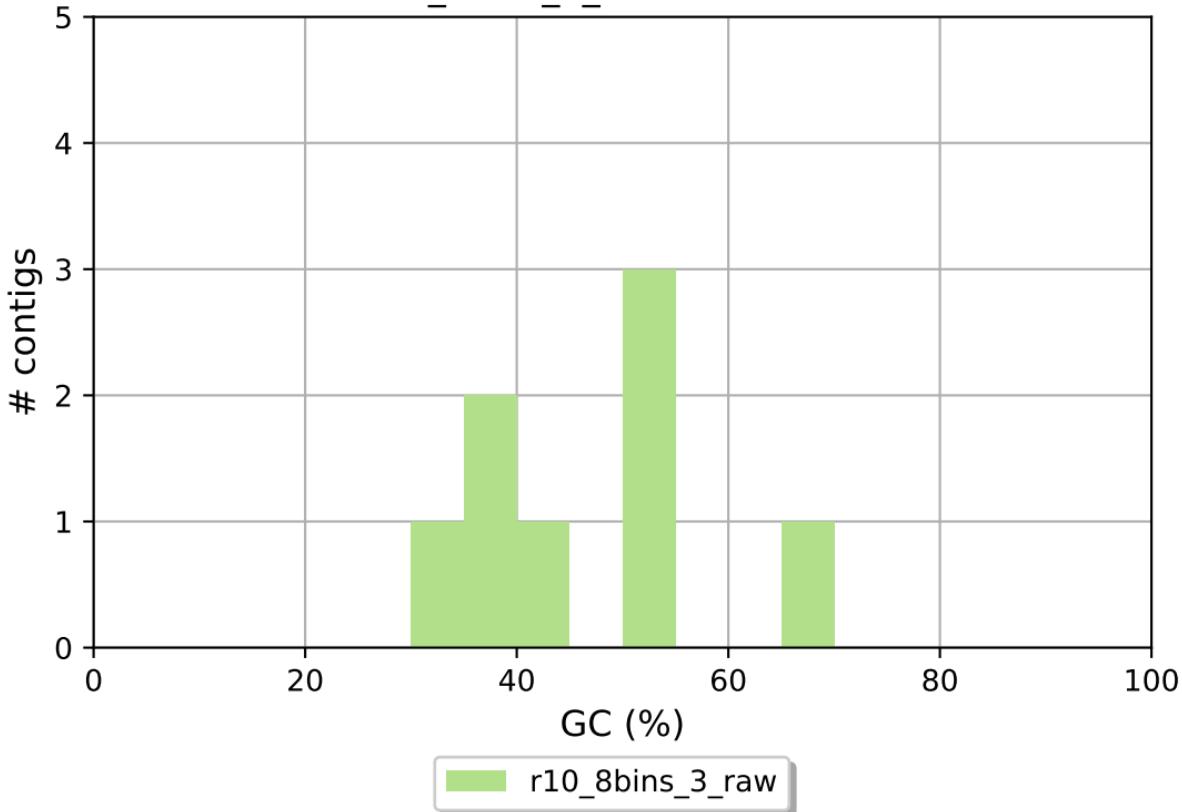
r10\_8bins\_3\_racon\_r1 GC content



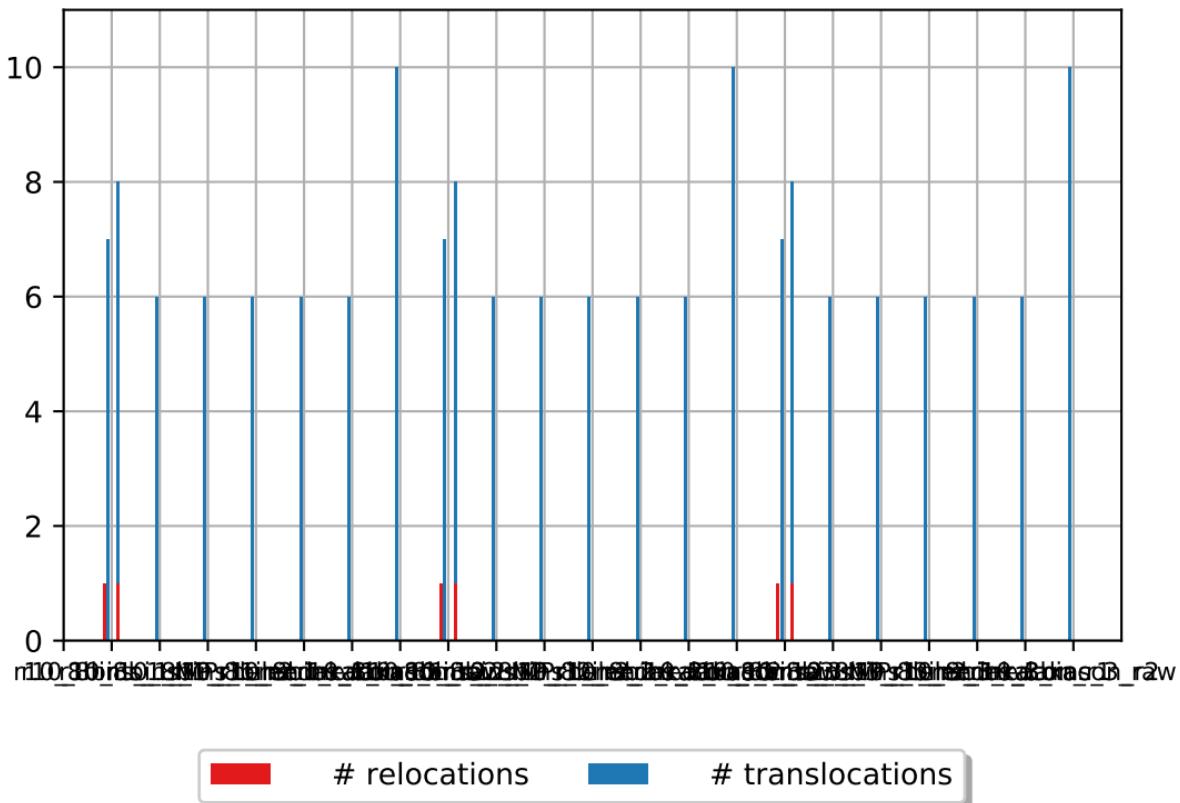
r10\_8bins\_3\_racon\_r2 GC content



r10\_8bins\_3\_raw GC content

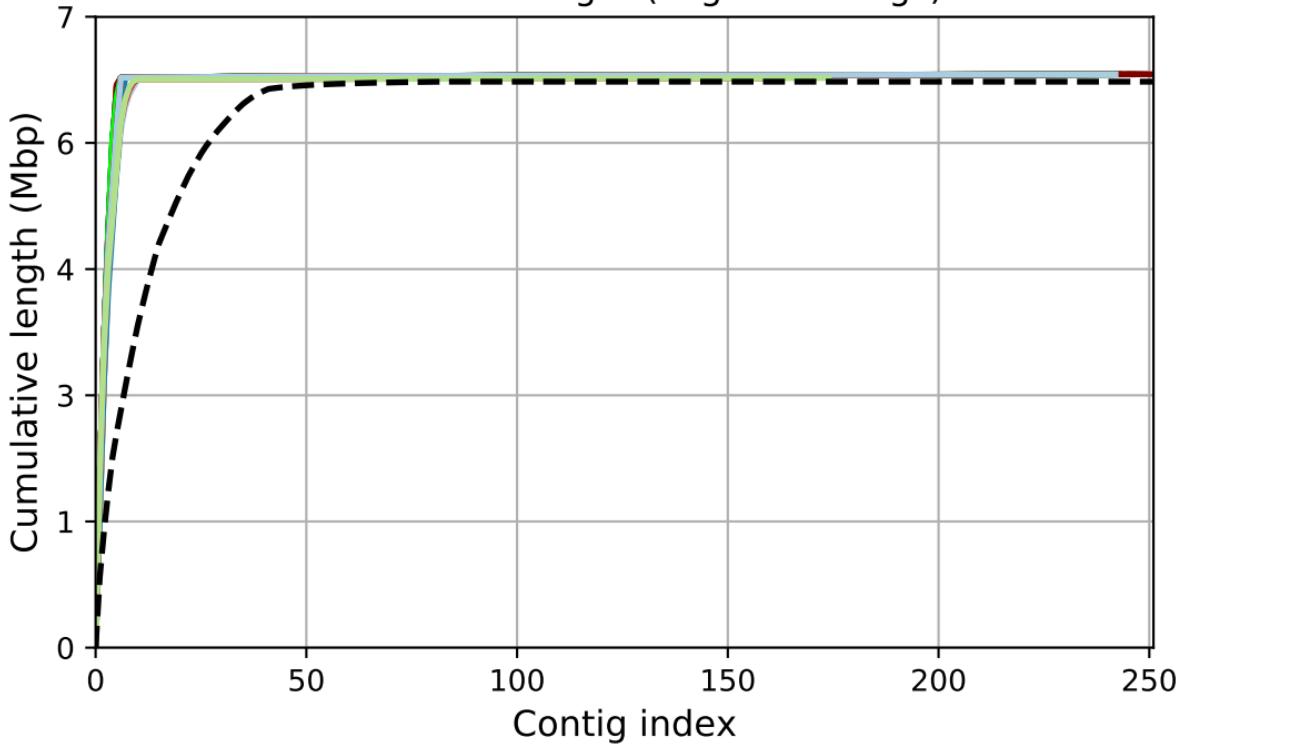


## Misassemblies





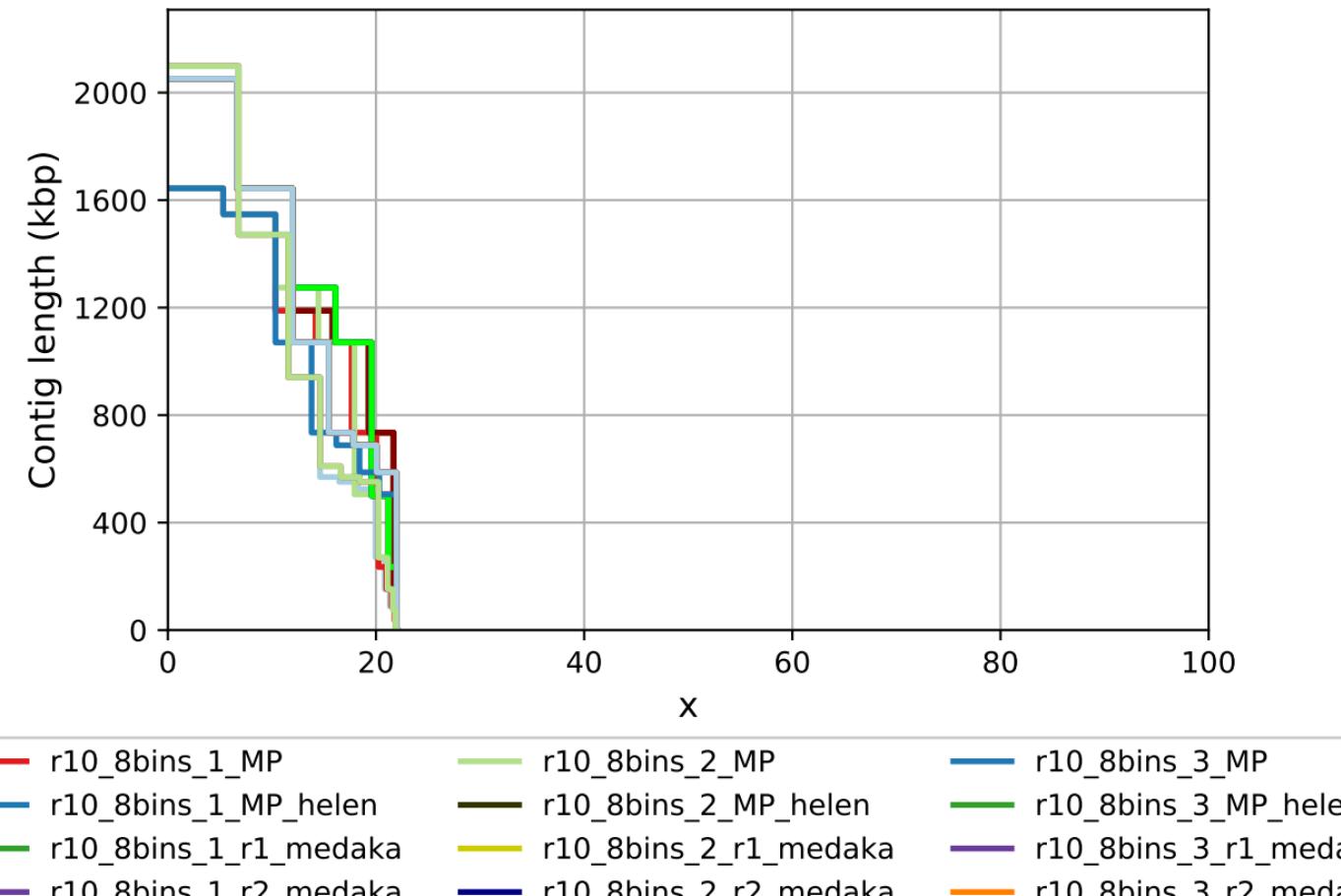
### Cumulative length (aligned contigs)



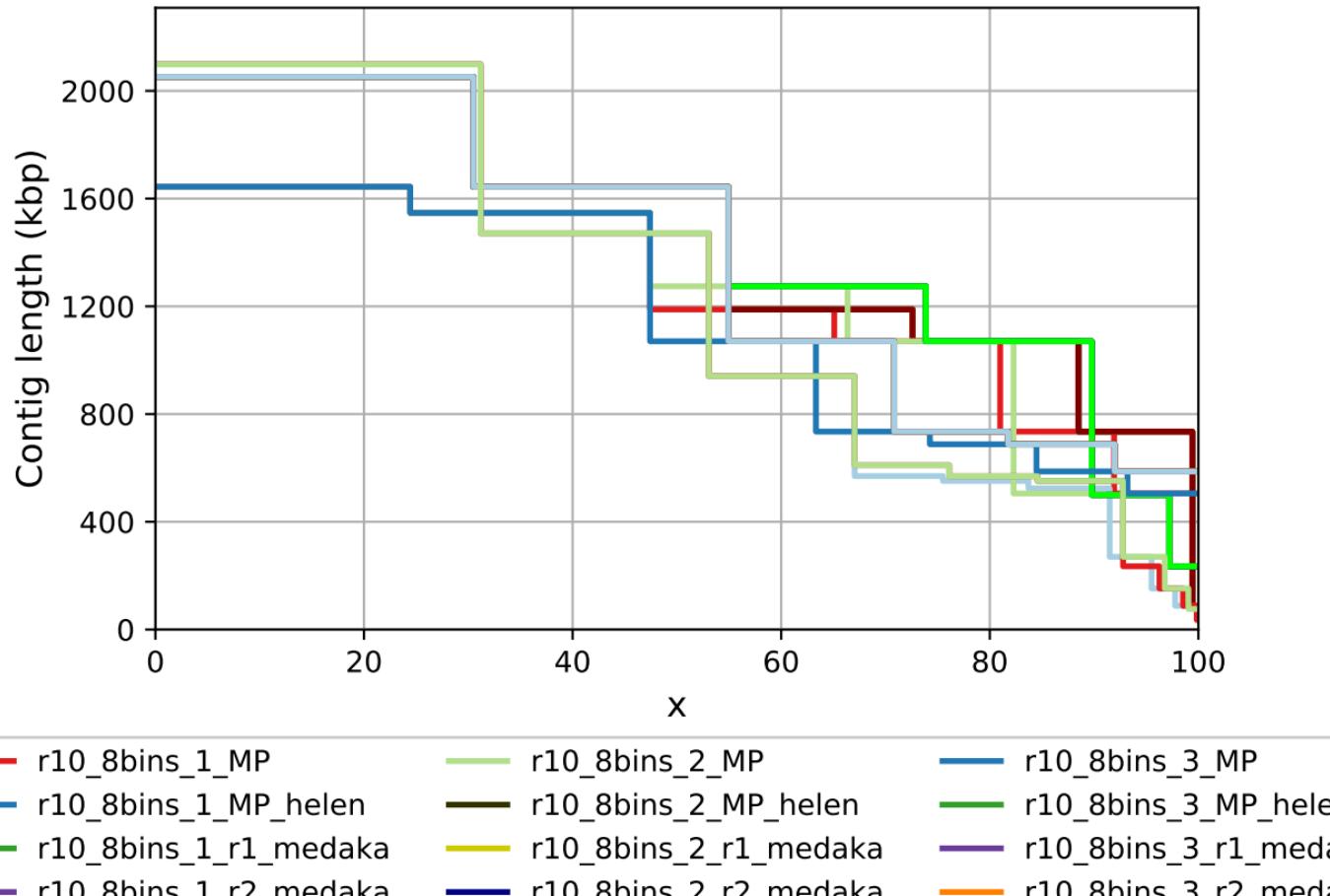
Legend:

- 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\_racon\_r1
- r10\_8bins\_3\_racon\_r2

NAX



NGAx



Genome fraction, %

