

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_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 (>= 0 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 1000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# 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(>= 0 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
Total length(>= 1000 bp)	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
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	6792413	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	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	
N50	4758957	4758026	4758581	4758584	4758019	4758050	4755933	4758981	4757842	4758589	4758101	4757934	4757912	4756088	4758992	4758031	4758588	4758092	4757964	4757944	4756065
N75	2992094	2992072	2992073	2992074	2991951	2991999	2990636	2992084	2992066	2992073	2992074	2991957	2991981	2990626	2992095	2992076	2992073	2991935	2991970	2990261	
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3		
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5		
# misassemblies	170	167	167	171	167	174	177	170	168	170	173	169	176	173	170	168	170	172	173	174	
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Misassembled contigs length	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
# local misassemblies	118	121	134	137	150	146	212	116	119	130	133	146	139	206	116	120	124	133	151	136	208
# 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	
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part		
Unaligned length	78700	78796	81721	82202	78296	77725	141489	78433	79128	80804	80526	77783	75888	136427	78646	79823	80228	83038	77250	76289	137042
Genome fraction (%)	99.399	99.396	99.398	99.396	99.397	99.395	99.374	99.400	99.392	99.399	99.399	99.398	99.398	99.371	99.400	99.393	99.398	99.399	99.397	99.398	
Duplication ratio	1.044	1.044	1.043	1.043	1.043	1.043	1.028	1.044	1.044	1.043	1.043	1.043	1.043	1.028	1.044	1.044	1.043	1.043	1.028		
# 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	176.02	168.03	176.25	176.24	176.51	180.05	272.23	176.28	168.46	175.49	175.78	178.88	180.43	274.79	175.53	167.26	179.13	173.63	178.18	177.56	270.09
# indels per 100 kbp	38.36	23.02	26.55	26.27	61.00	58.36	306.53	38.54	23.63	26.75	26.22	61.45									

Misassemblies report

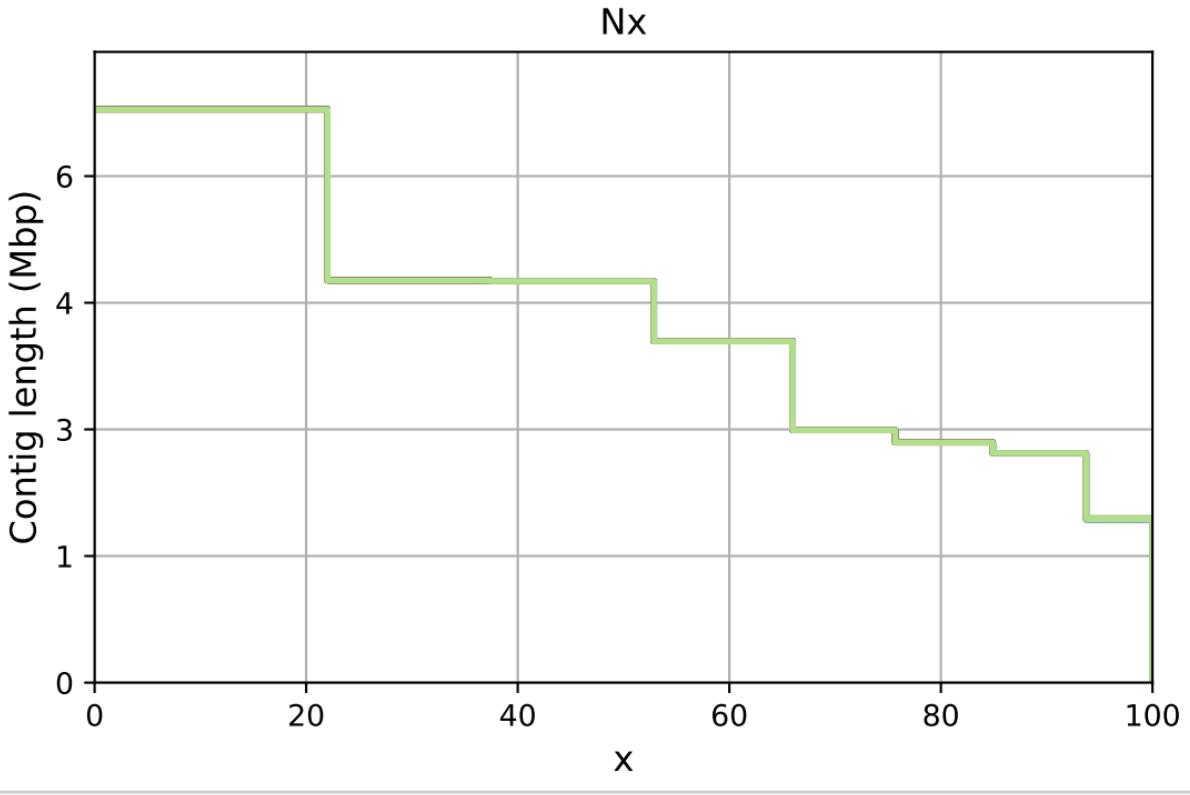
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# misassemblies	170	167	167	171	167	174	177	170	168	170	173	169	176	173	170	168	172	173	177	174	
# contig misassemblies	170	167	167	171	167	174	177	170	168	170	173	169	176	173	170	168	172	173	177	174	
# c. relocations	6	4	4	6	4	7	5	6	4	4	8	4	7	5	6	4	6	4	6	5	
# c. translocations	162	161	161	163	161	165	168	162	163	164	163	163	167	164	162	164	164	167	169	165	
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# c. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	
# 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	
# s. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Misassembled contigs length	30866945	30862930	30864385	30856589	30852831	30845731	30850202	30866877	30861522	30864168	30854493	30852705	30846555	30849057	30867413	30861841	30864447	30857058	30851941	30847715	30849244
# possibly misassembled contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	7	7	7	7	7	7	8	
# possible misassemblies	98	98	96	98	98	96	176	98	100	94	98	96	90	166	98	100	94	98	90	164	
# local misassemblies	118	121	134	137	150	146	212	116	119	130	133	146	139	206	116	120	124	133	151	136	208
# 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	252	253	252	253	250	250	167	252	253	252	250	252	249	180	252	252	252	249	248	179	
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# mismatches	53380	50955	53449	53444	53526	54601	82537	53460	51084	53219	53307	54247	54717	83311	53232	50720	54322	52656	54034	53847	81885
# indels	11634	6982	8051	7965	18500	17699	92934	11689	7167	8112	7952	18635	17676	93558	11659	7114	8308	7898	18633	17704	93337
# indels (<= 5 bp)	11006	6350	7459	7369	17838	17061	91725	11039	6510	7524	7340	17979	17028	92326	11000	6450	7711	7293	17991	17070	92118
# indels (> 5 bp)	628	632	592	596	662	638	1209	650	657	588	612	648	659	597	605	642	634	6219			
Indels length	45124	40531	40402	40439	56495	54236	156187	45757	41214	40747	41243	56720	55192	157955	46144	41574	41371	40982	56314	54059	158411

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

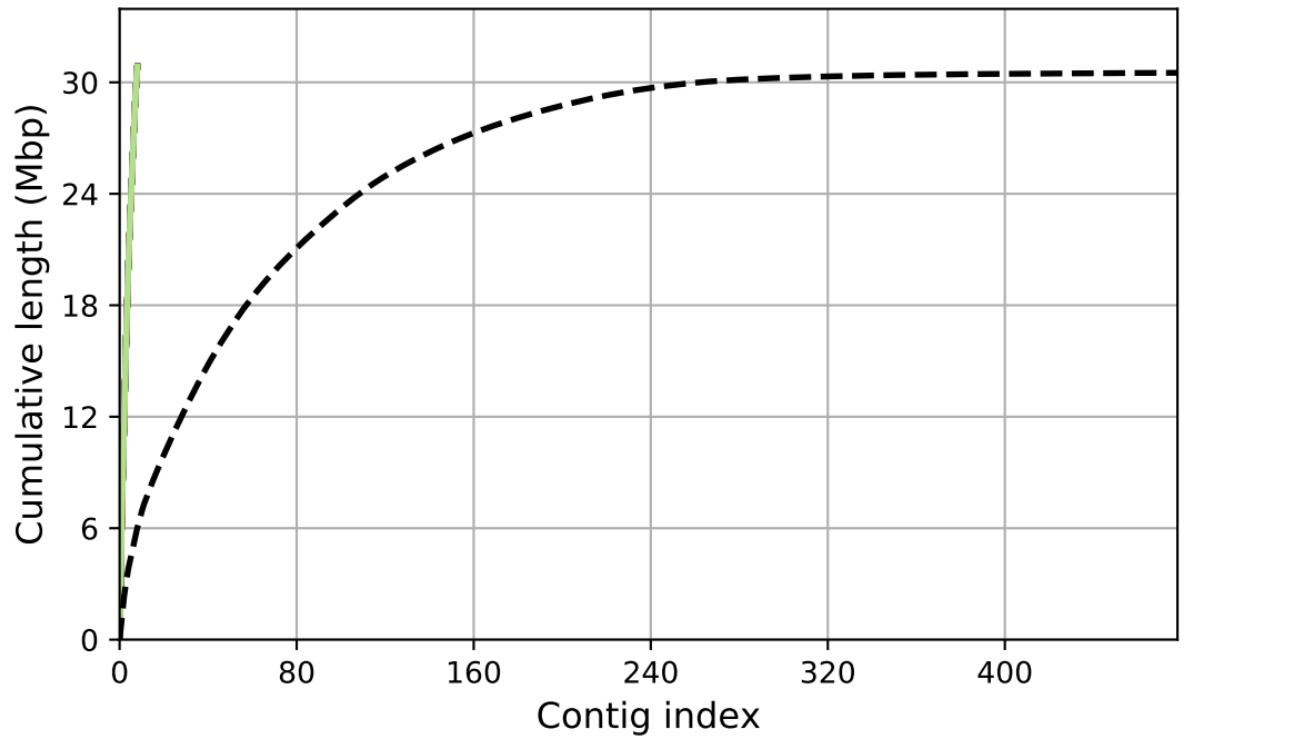
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	
Partially unaligned length	78700	78796	81721	82202	78296	77725	141489	78433	79128	80804	80526	77783	75888	136427	78646	79823	80228	83038	77250
# 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).



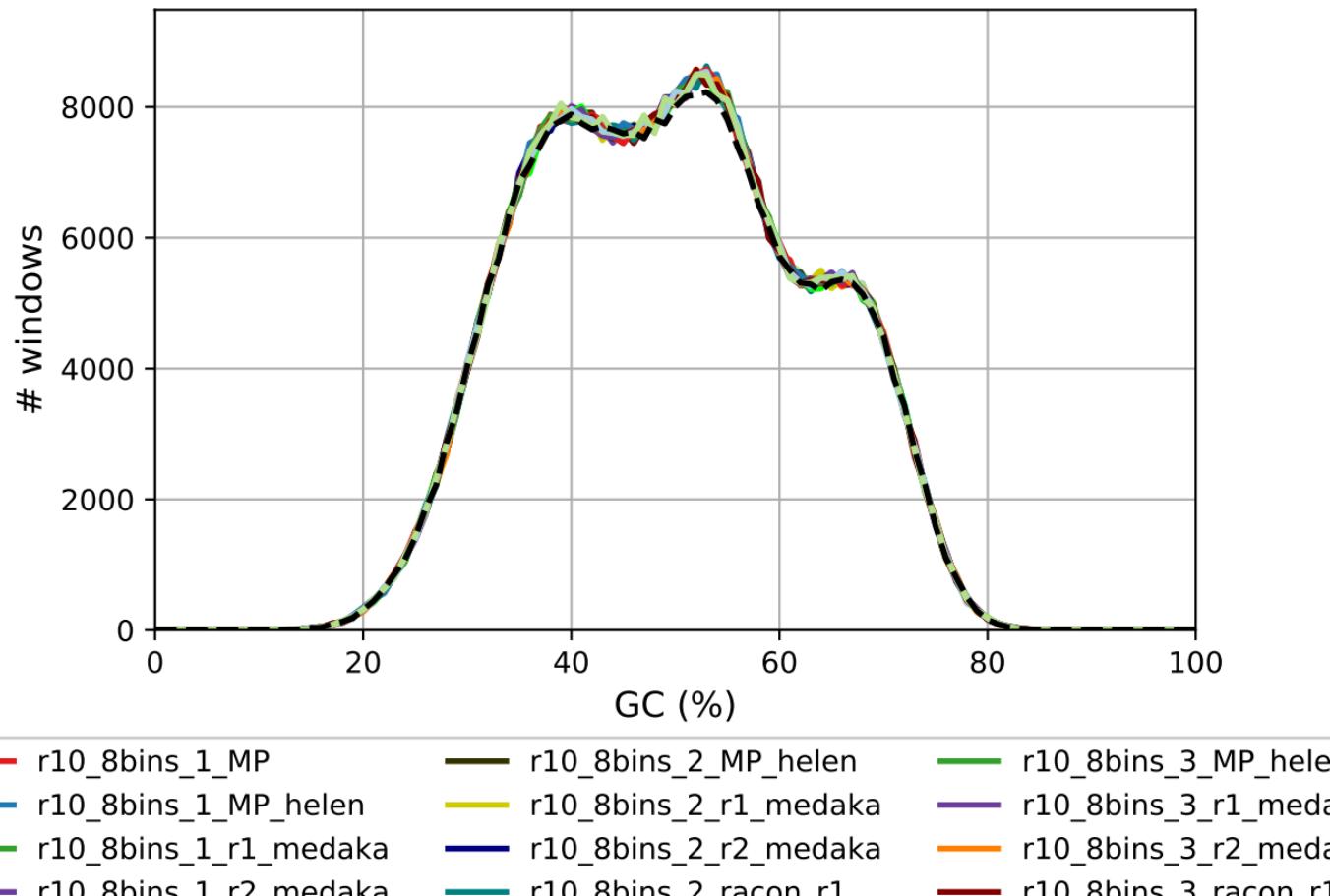
— r10_8bins_1_MP
— r10_8bins_1_MP_helen
— r10_8bins_1_r1_medaka
— r10_8bins_1_r2_medaka
— r10_8bins_2_MP_helen
— r10_8bins_2_r1_medaka
— r10_8bins_2_r2_medaka
— r10_8bins_3_MP_helen
— r10_8bins_3_r1_medaka
— r10_8bins_3_r2_medaka

Cumulative length

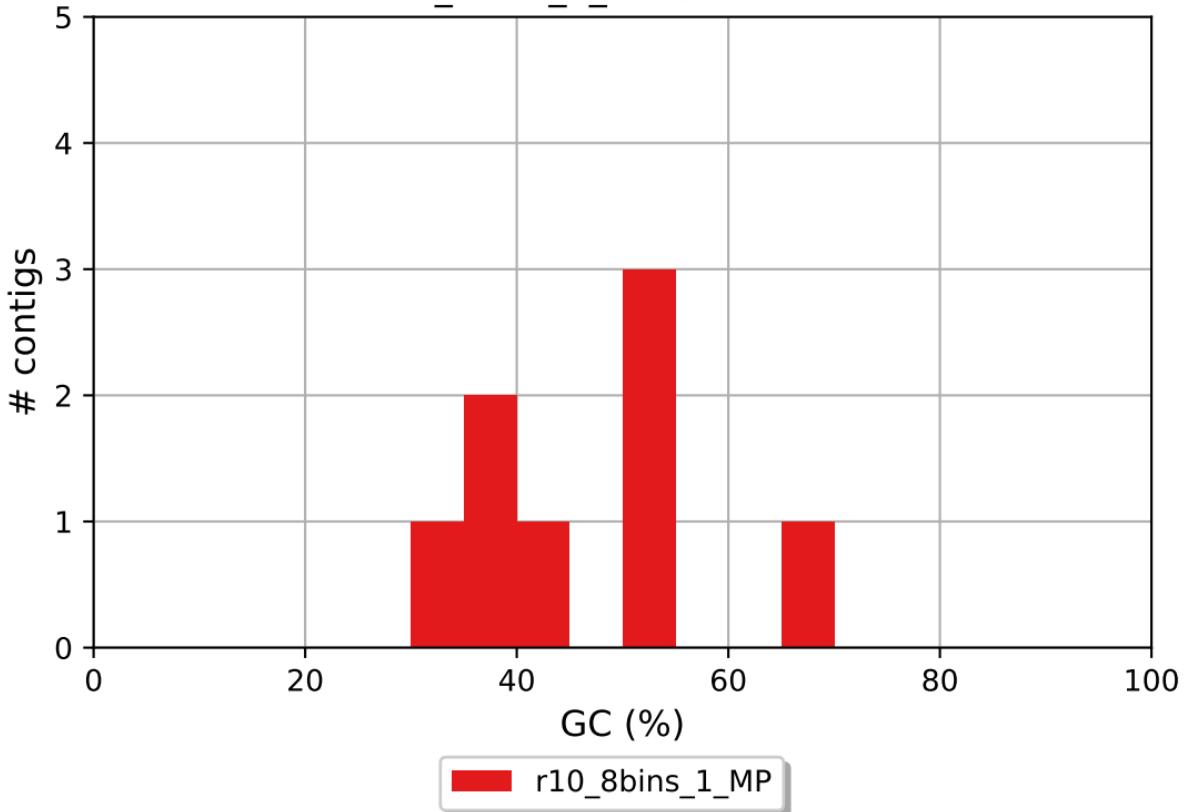


- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_1_r2_medaka

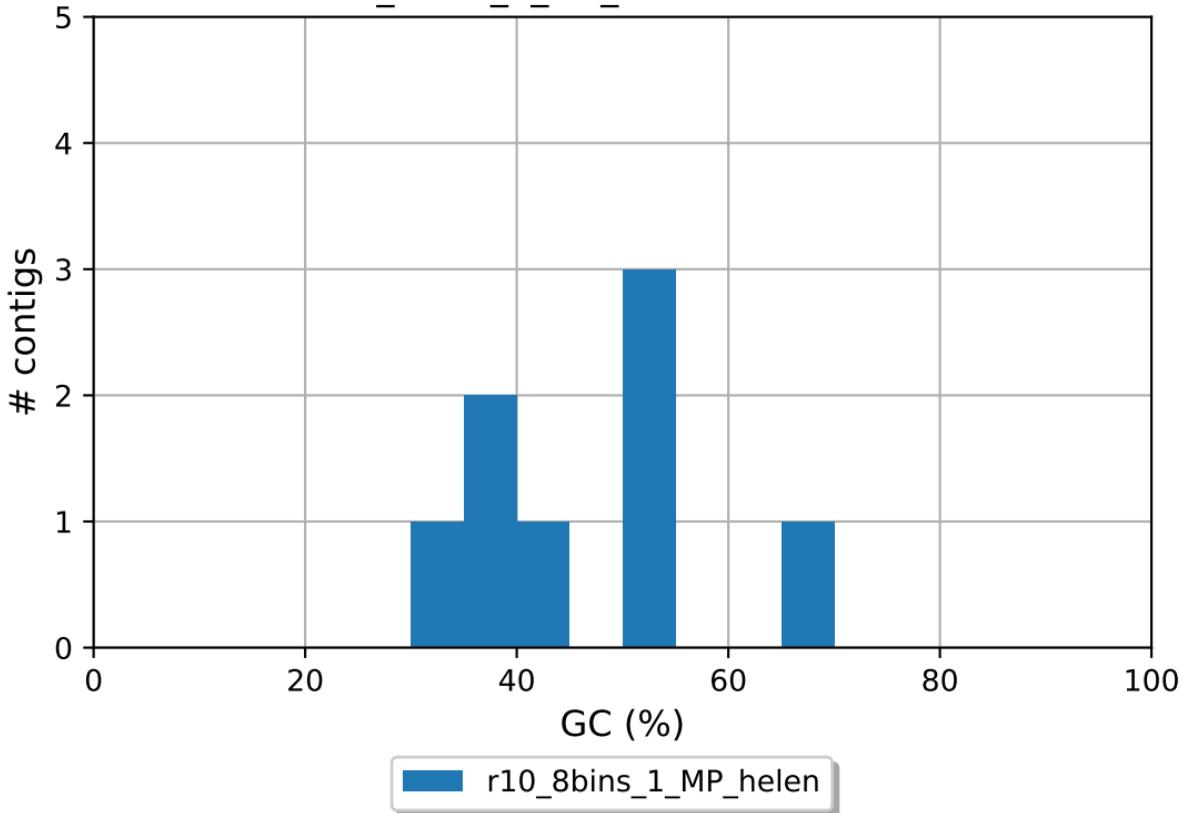
GC content



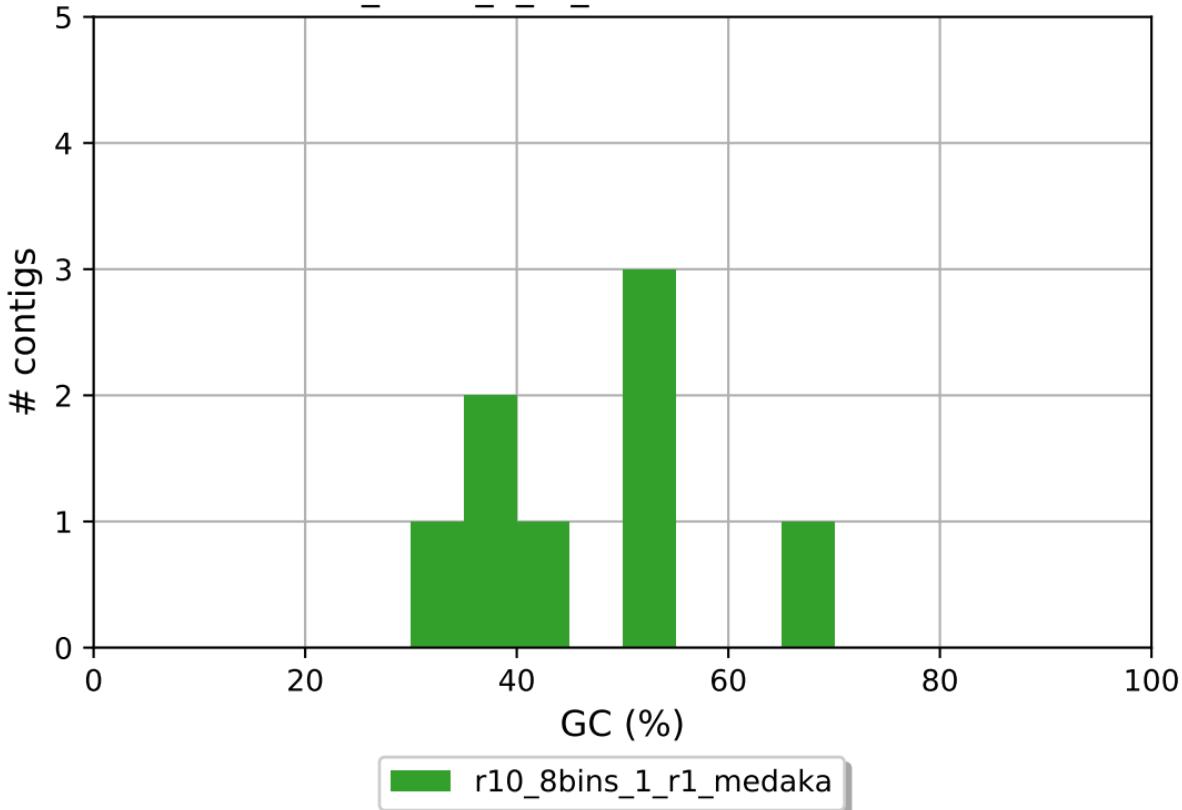
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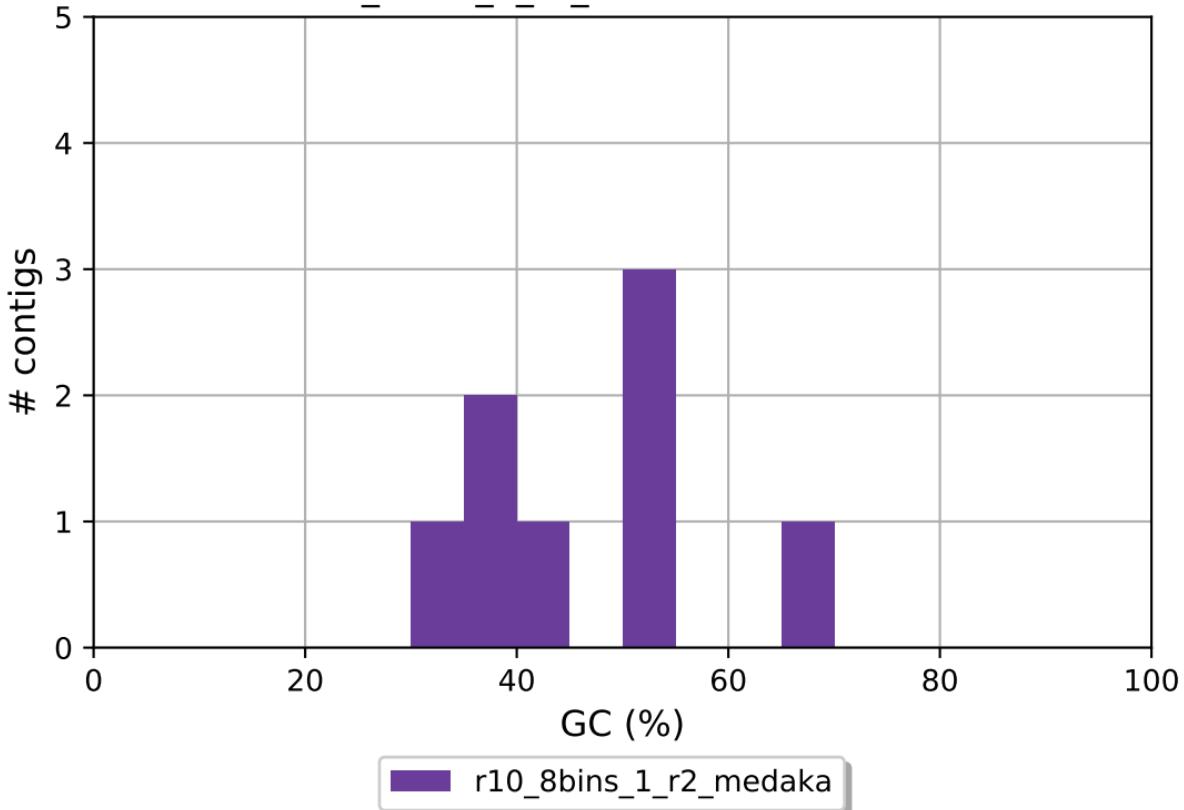
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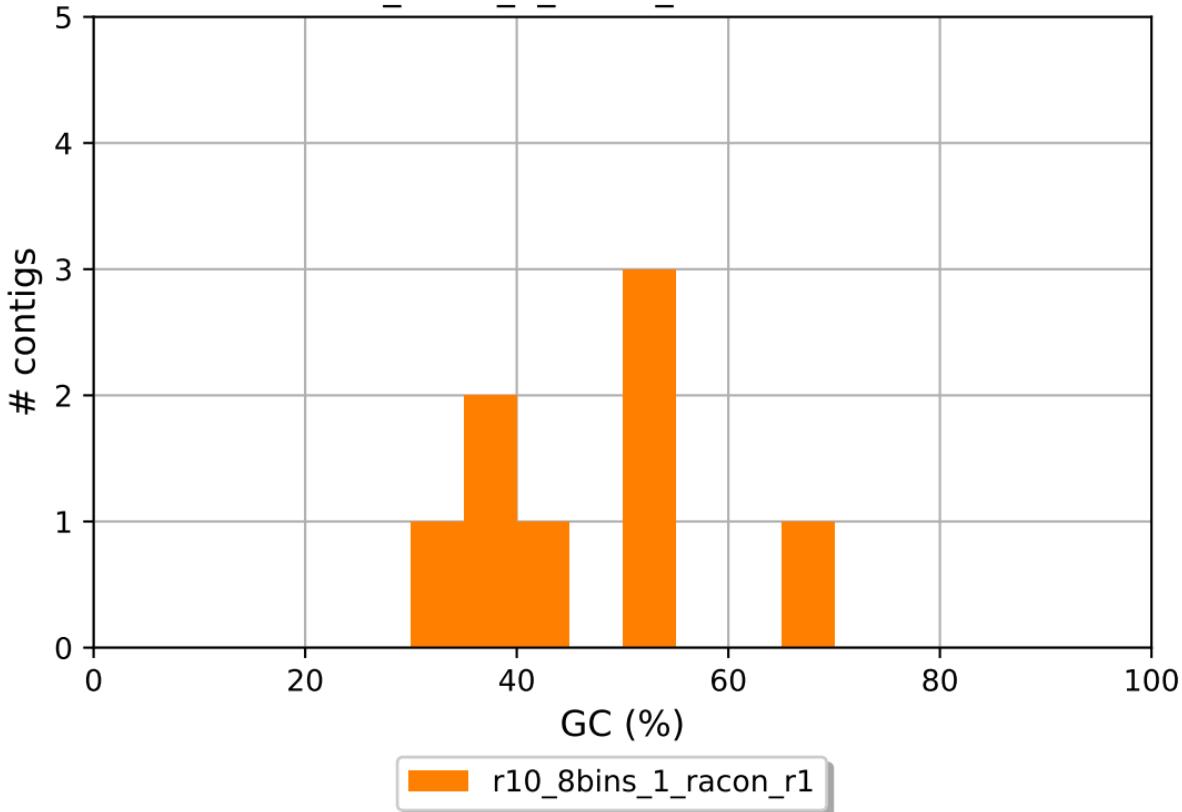
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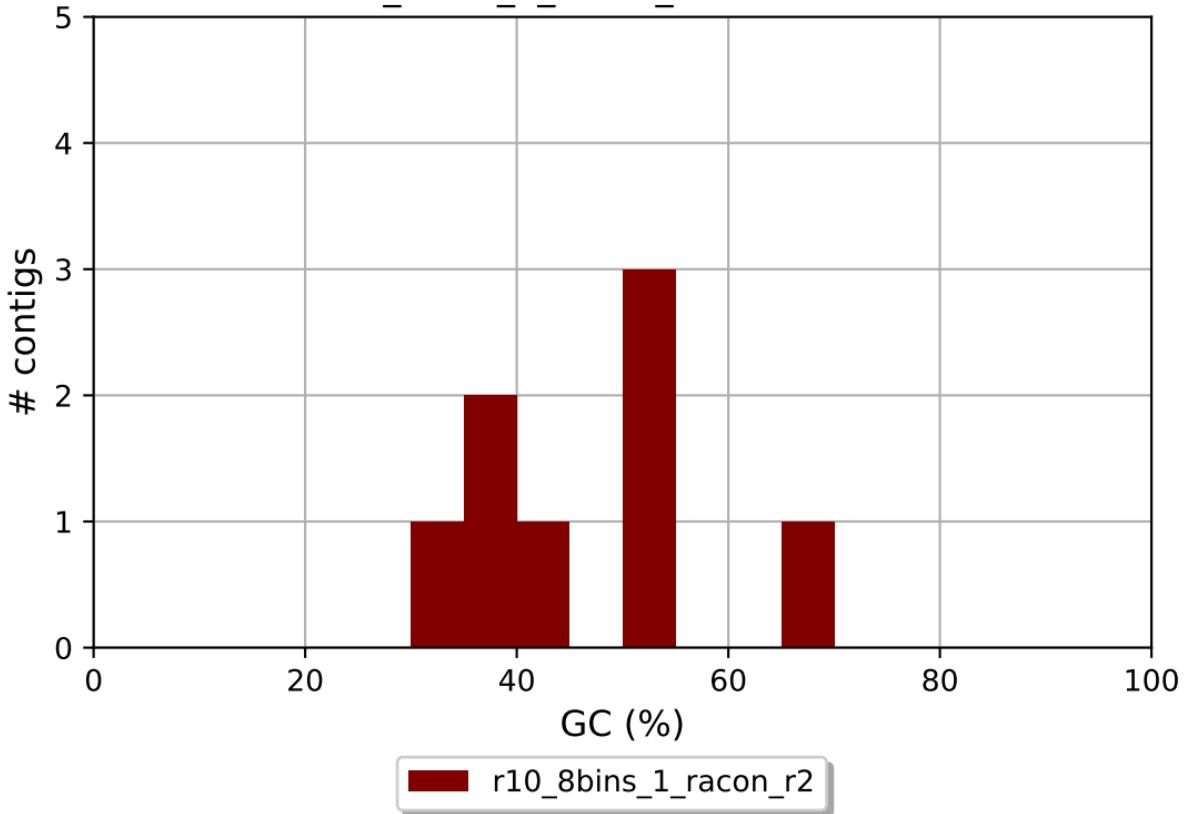
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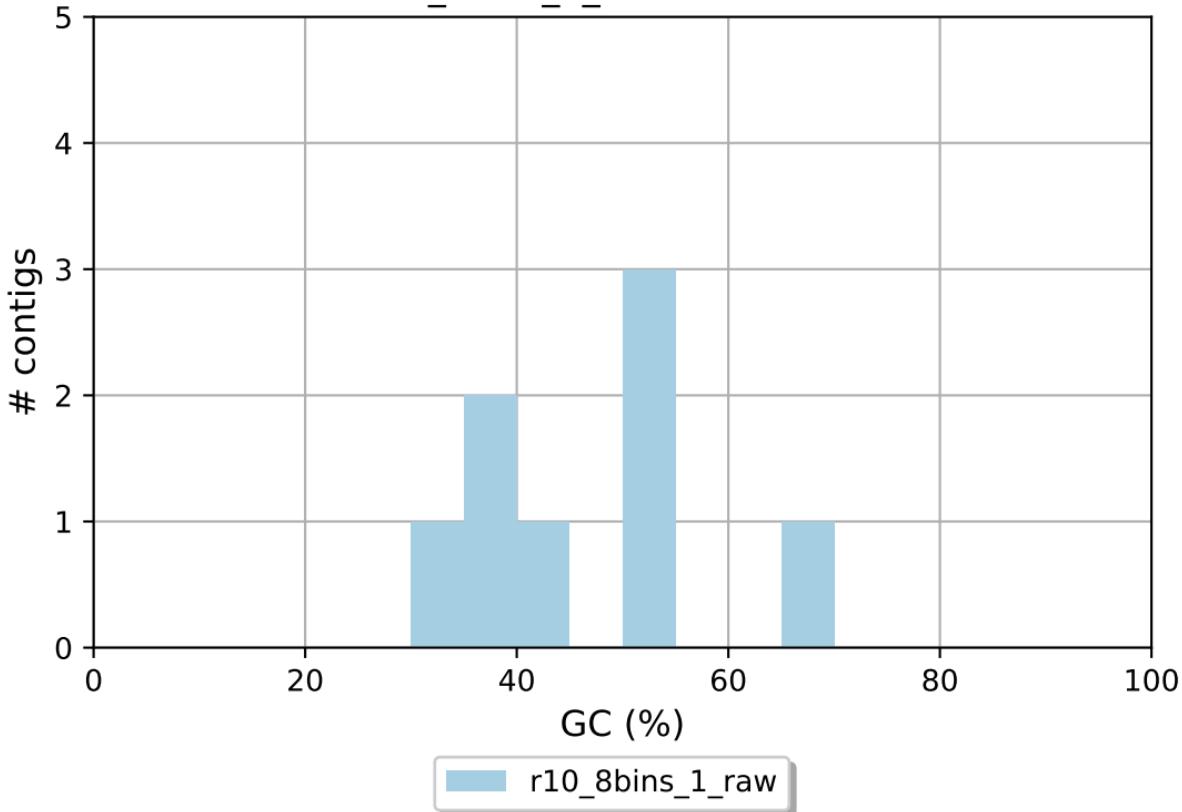
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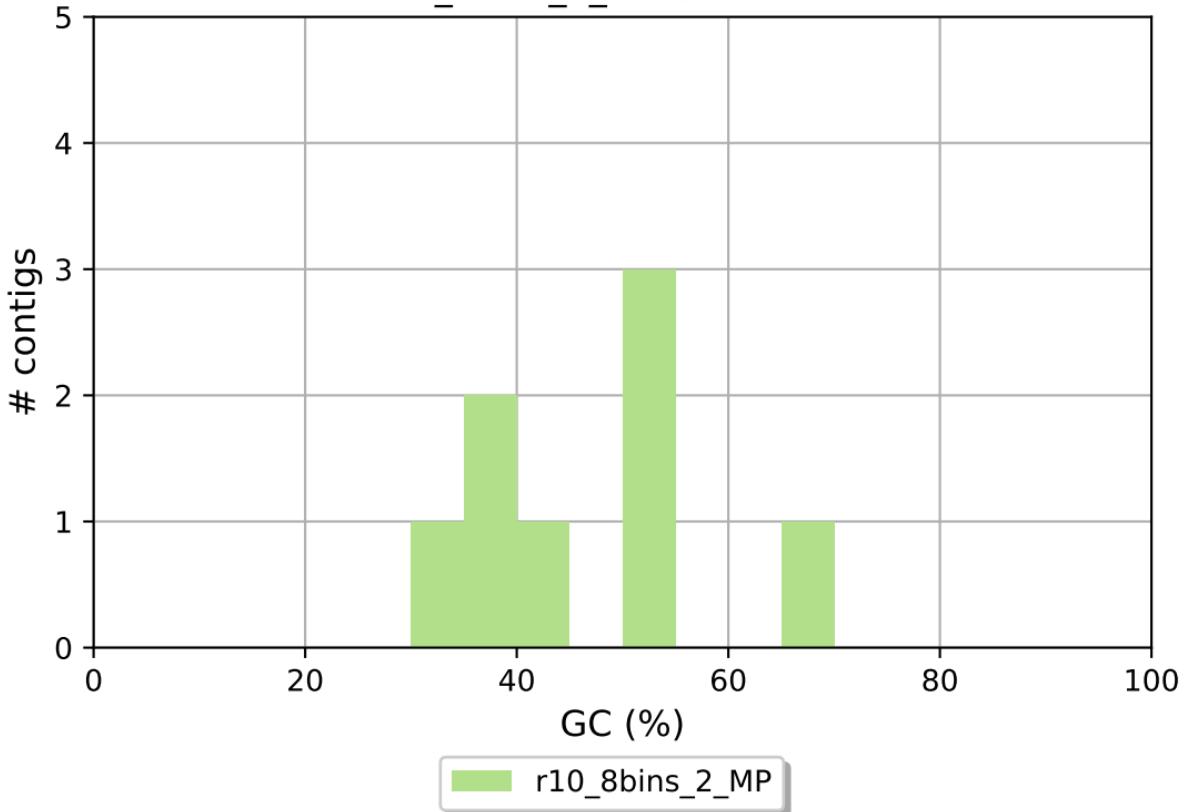
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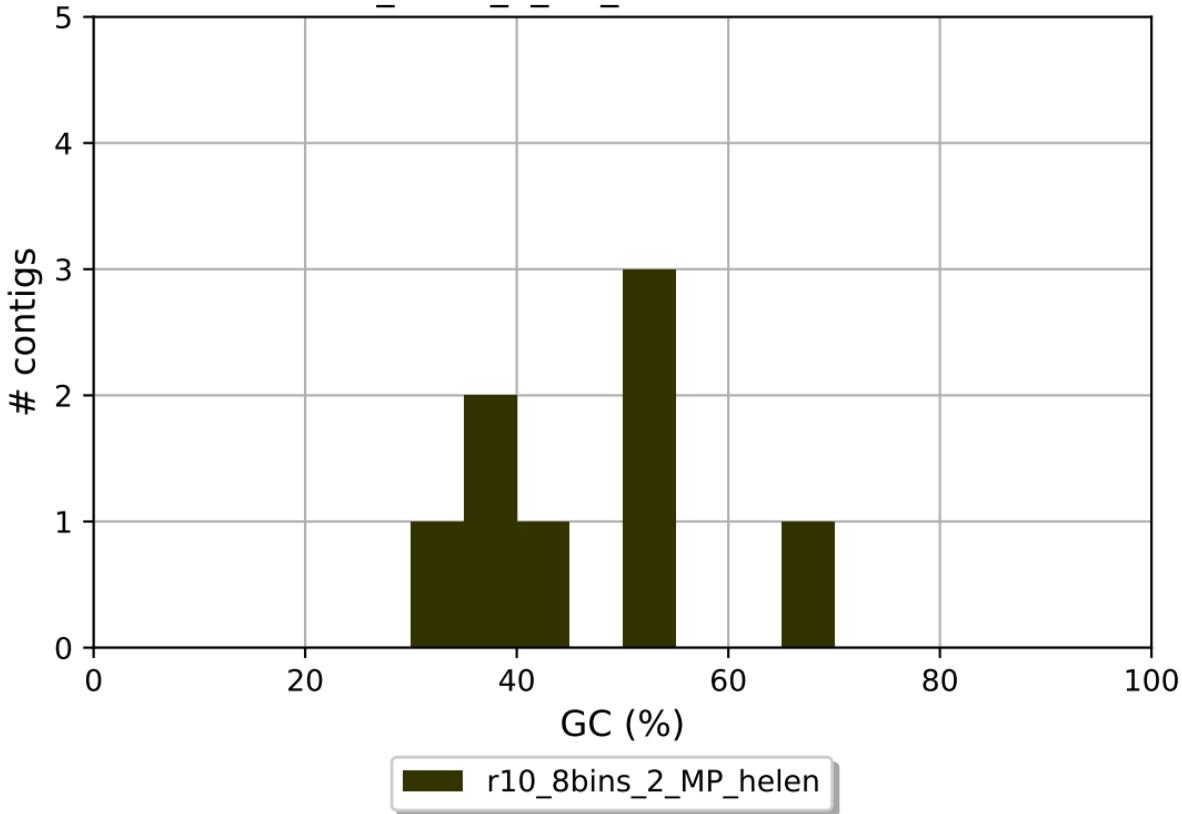
r10_8bins_1_raw GC content



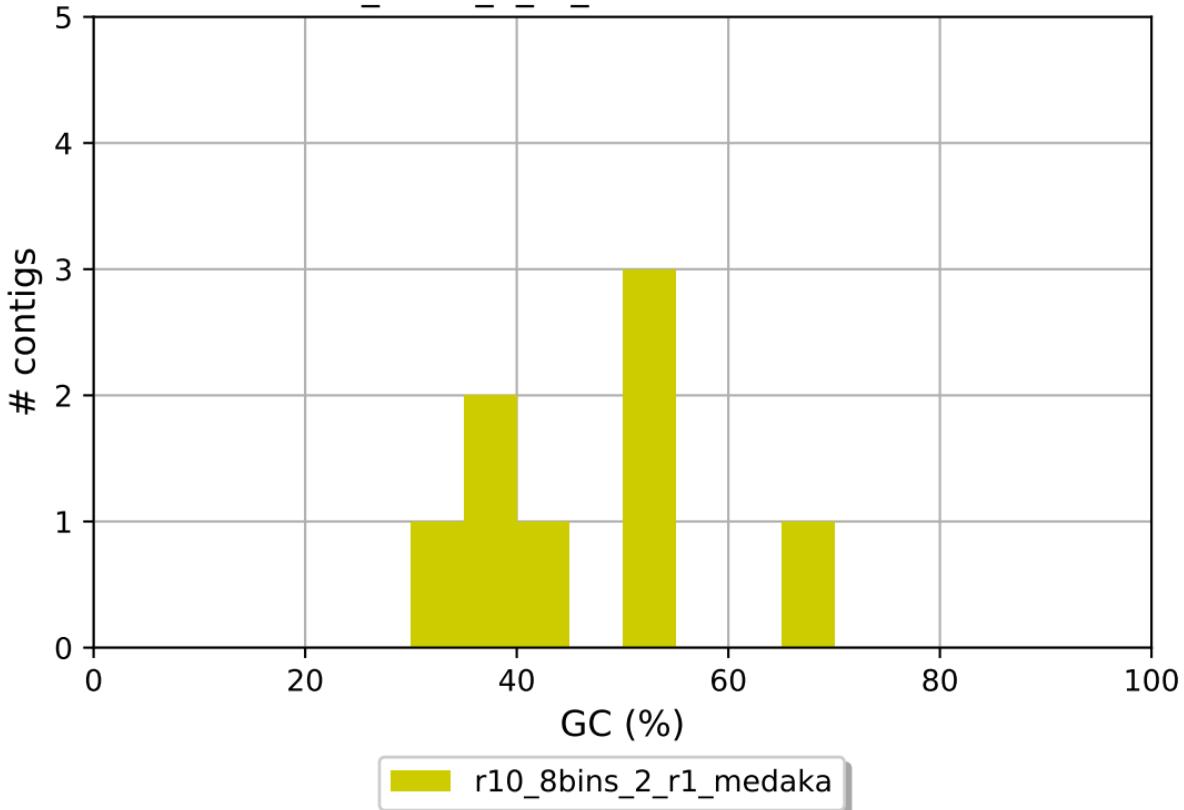
r10_8bins_2_MP GC content



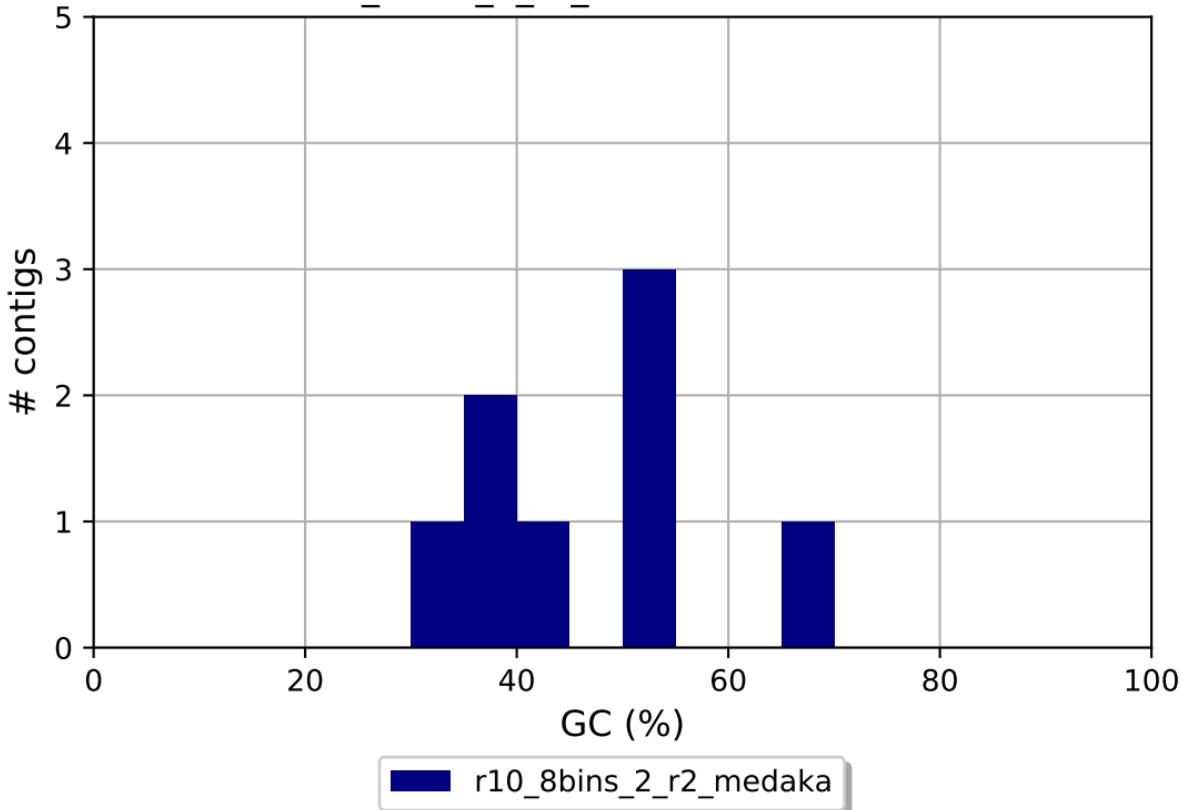
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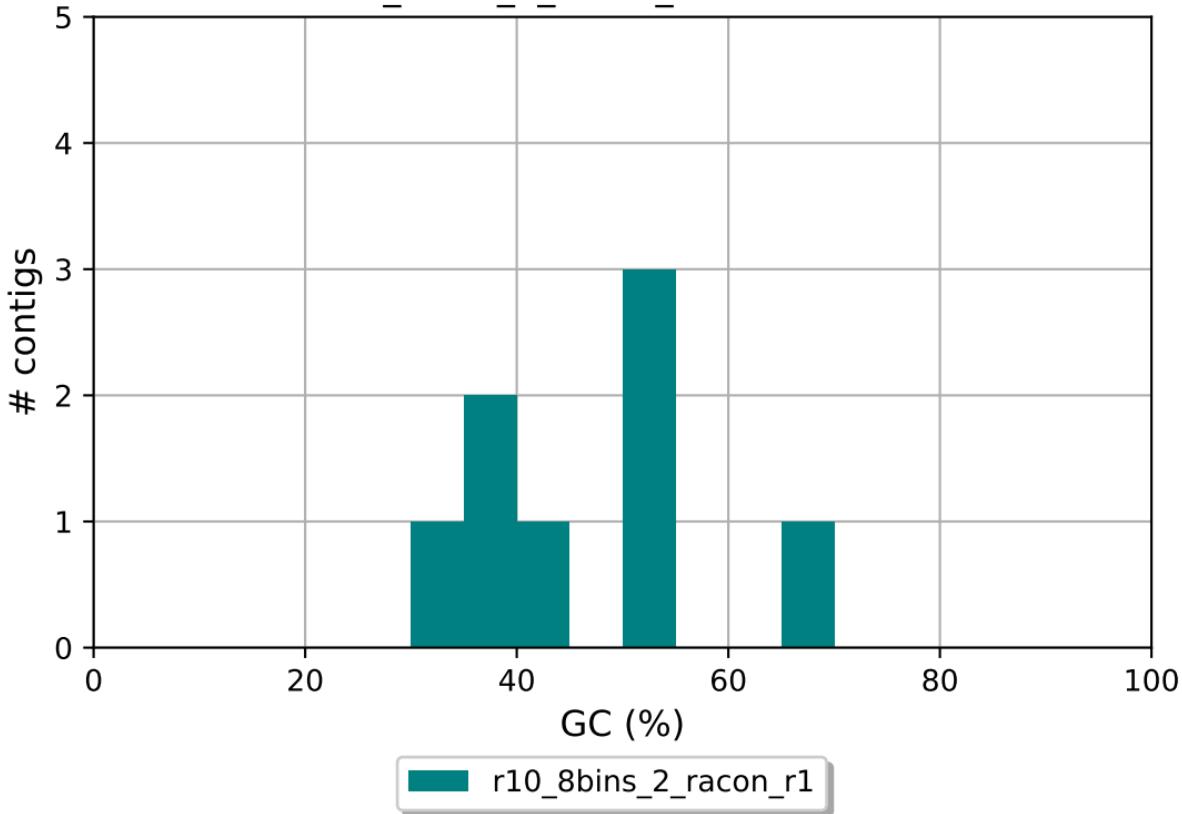
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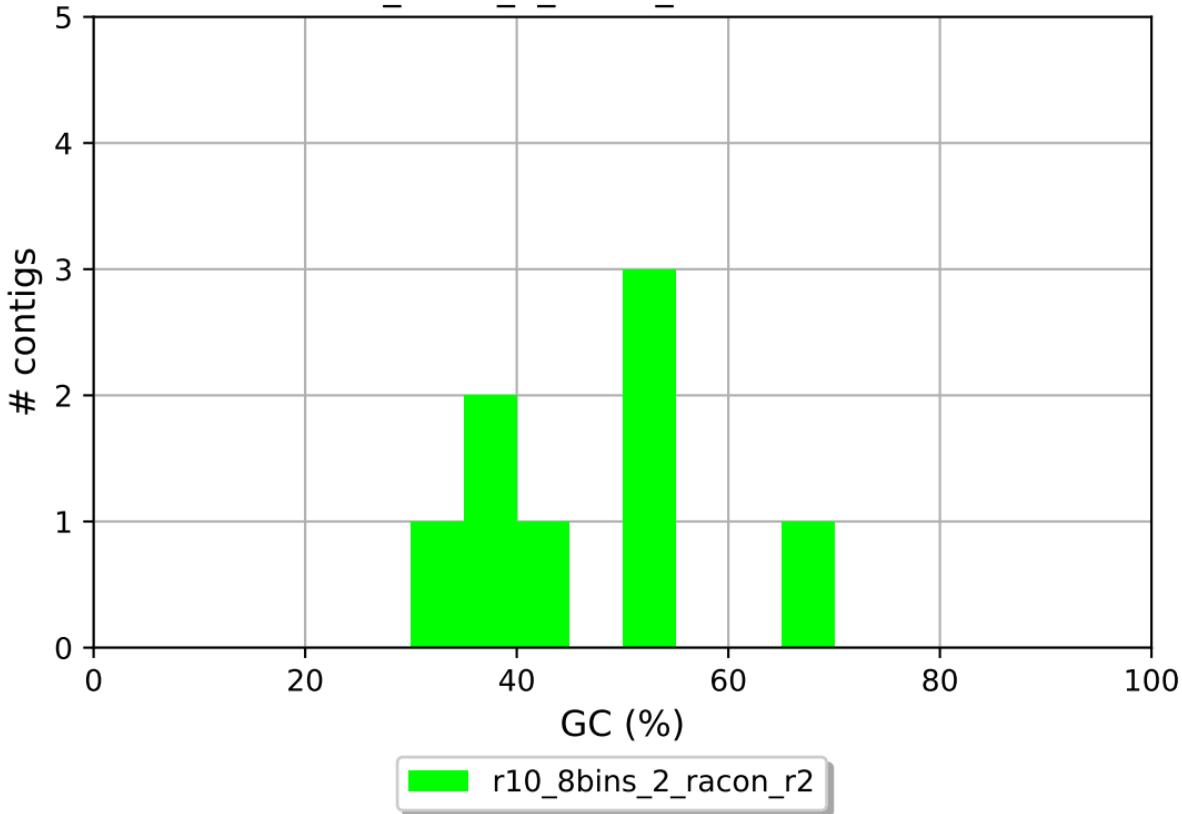
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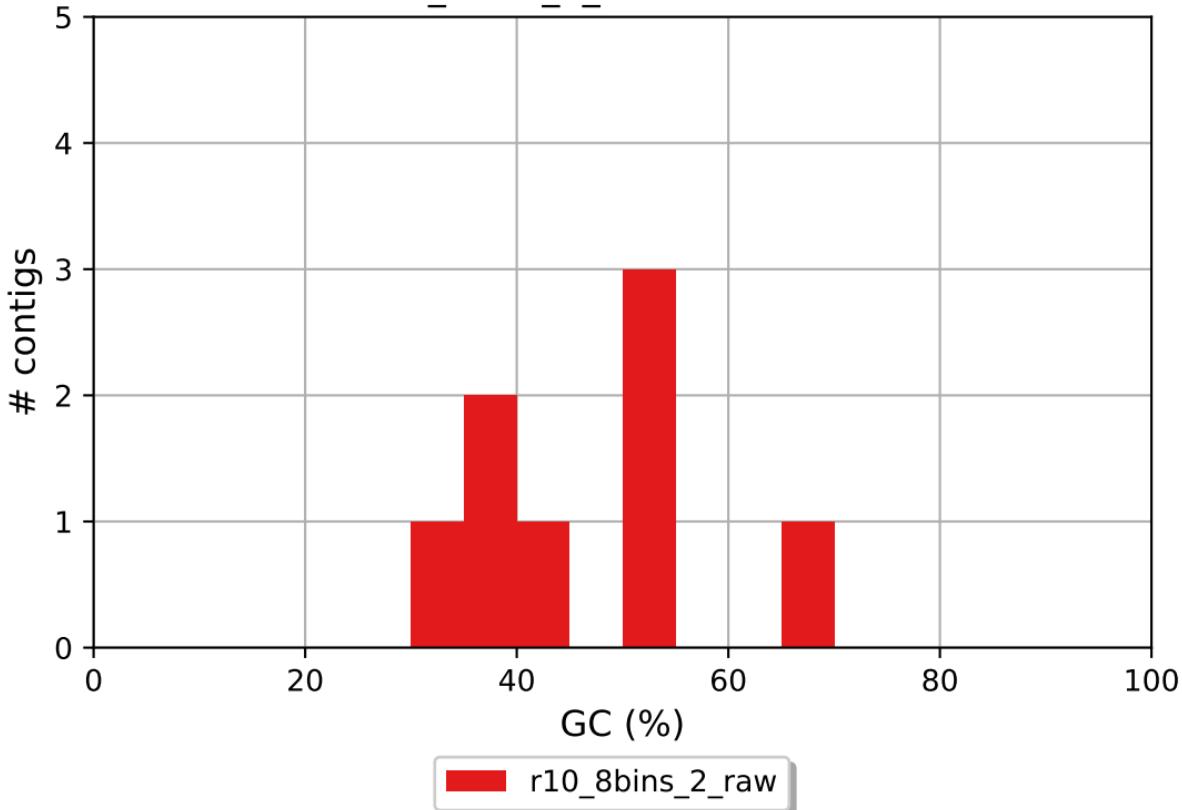
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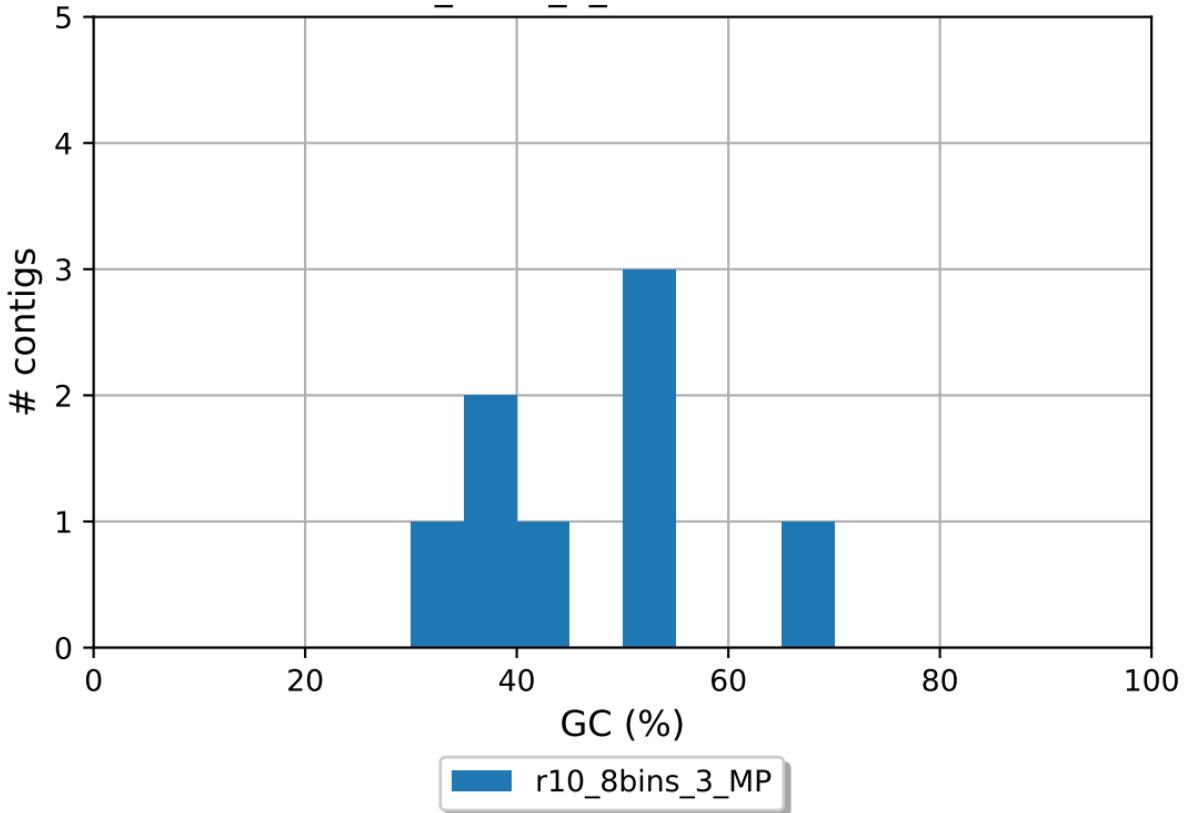
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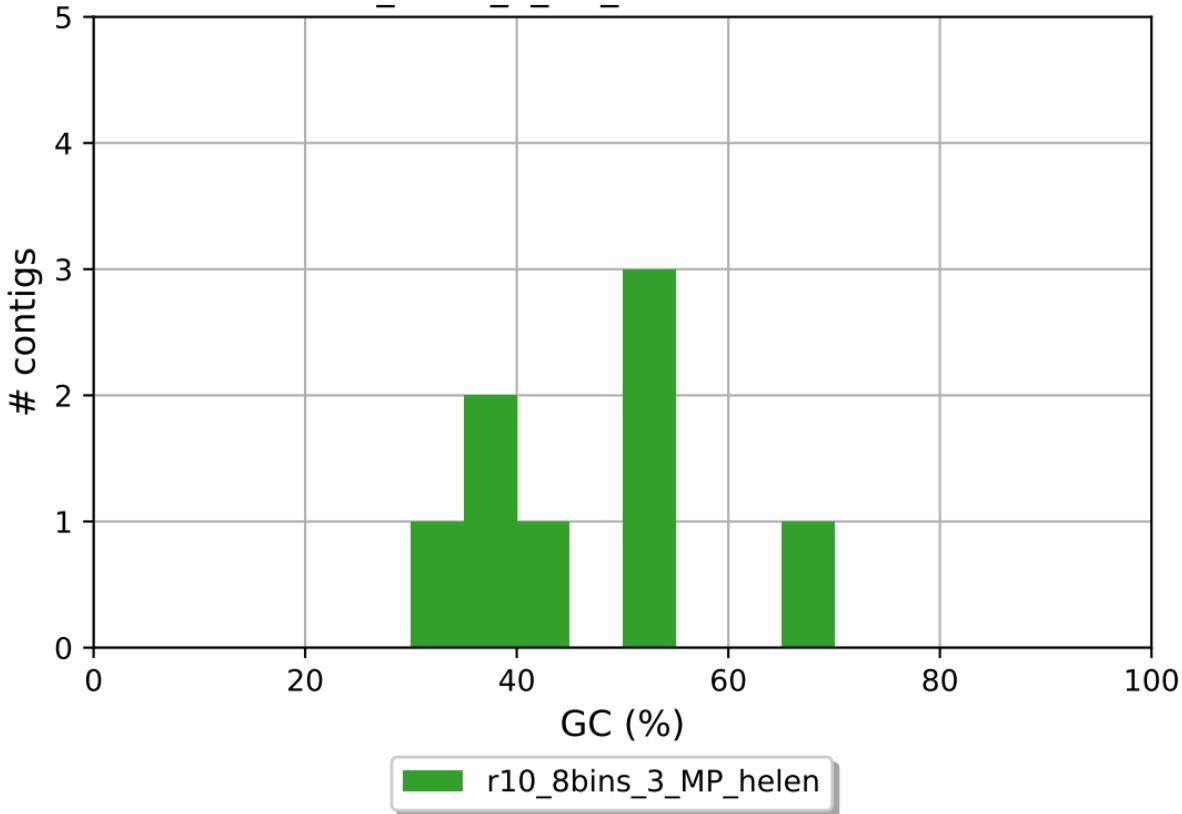
r10_8bins_2_raw GC content



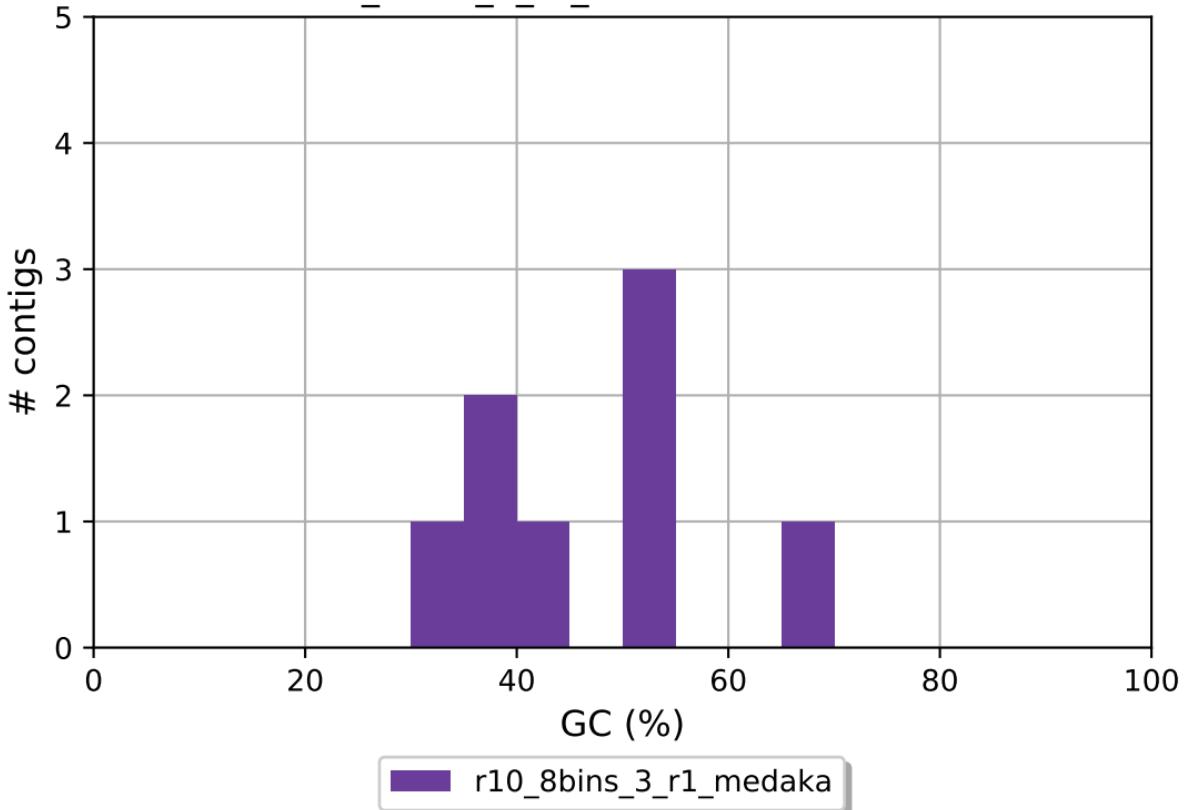
r10_8bins_3_MP GC content



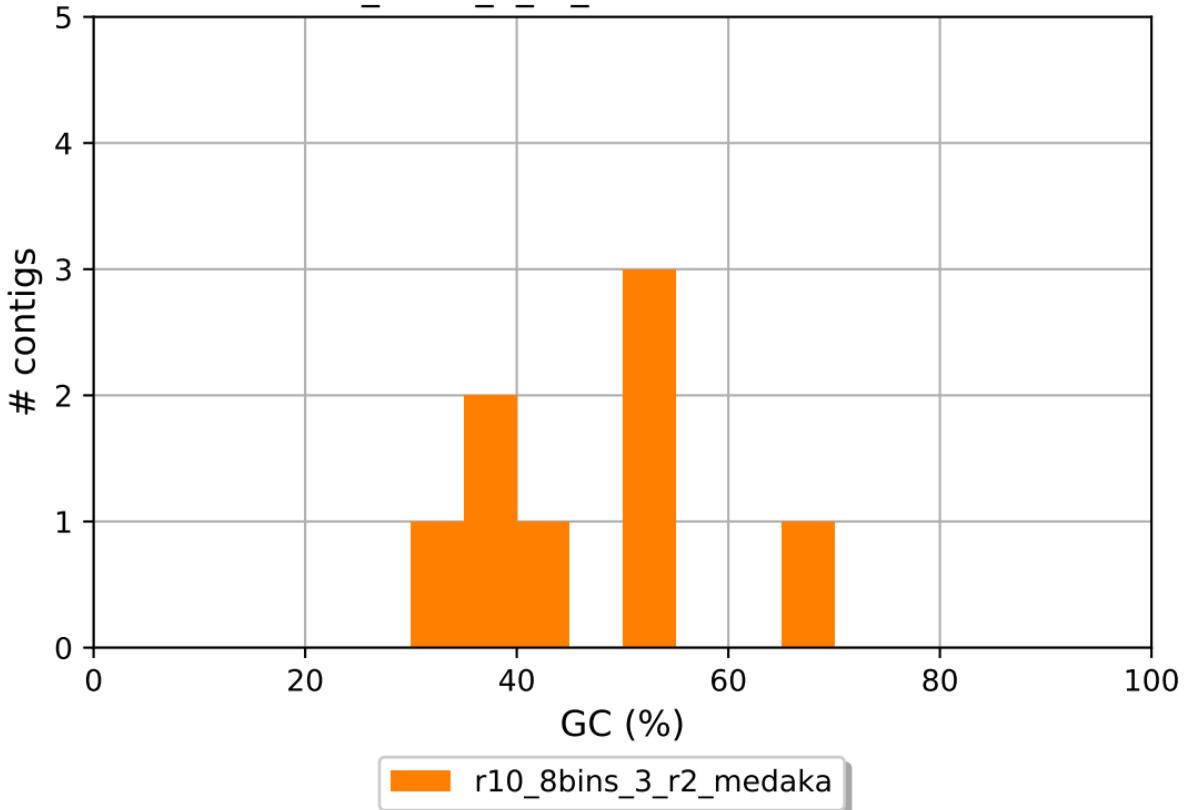
r10_8bins_3_MP_helen GC content



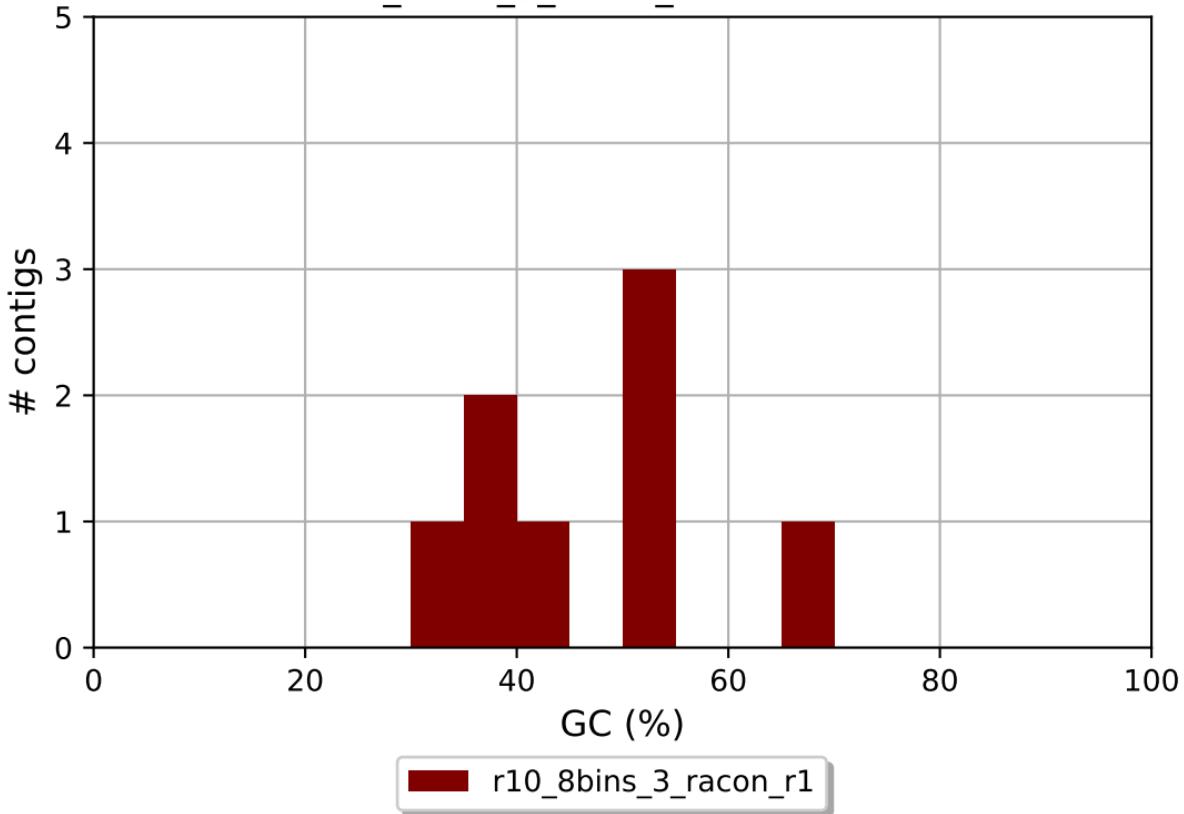
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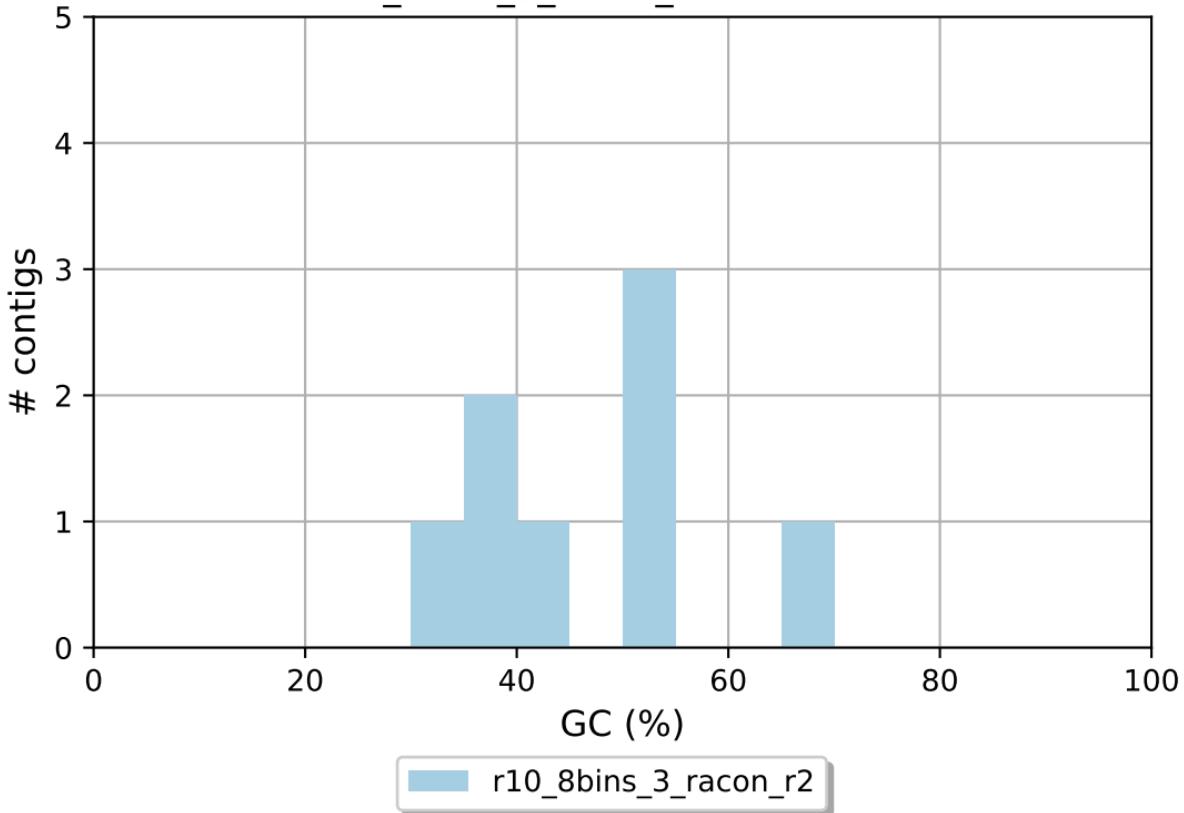
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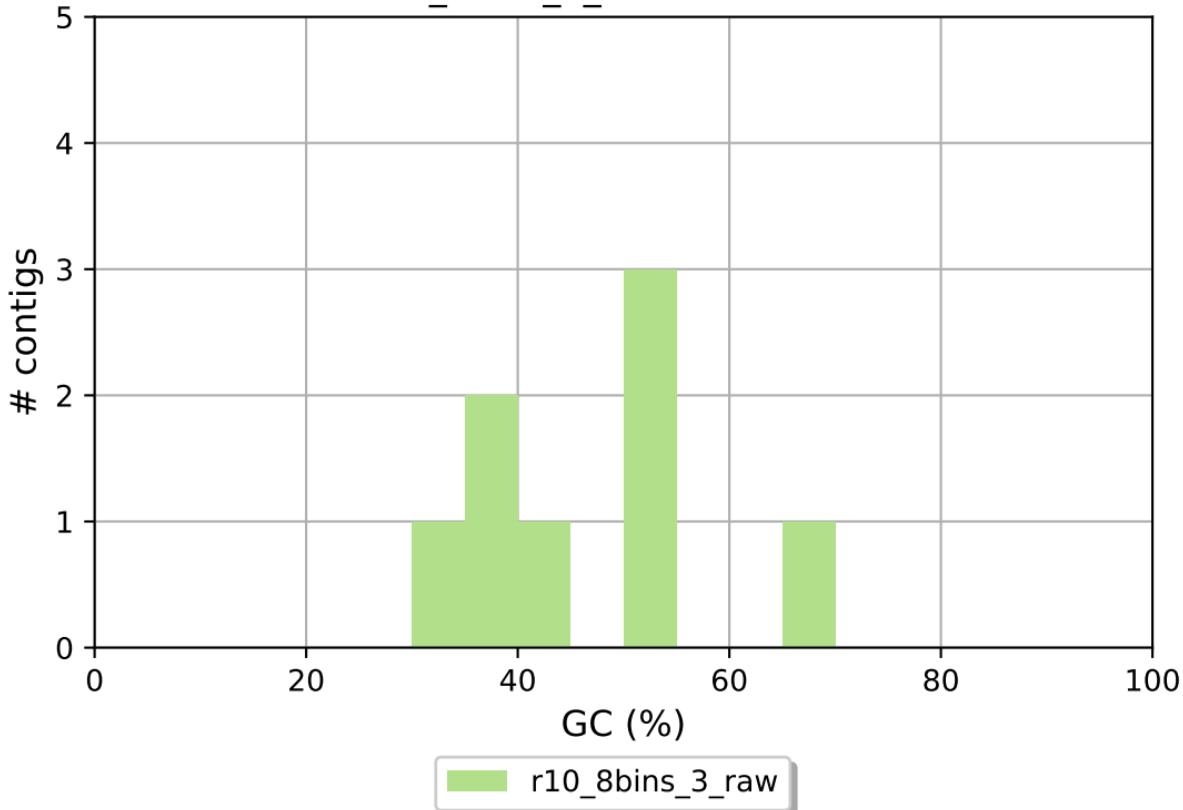
r10_8bins_3_racon_r1 GC content



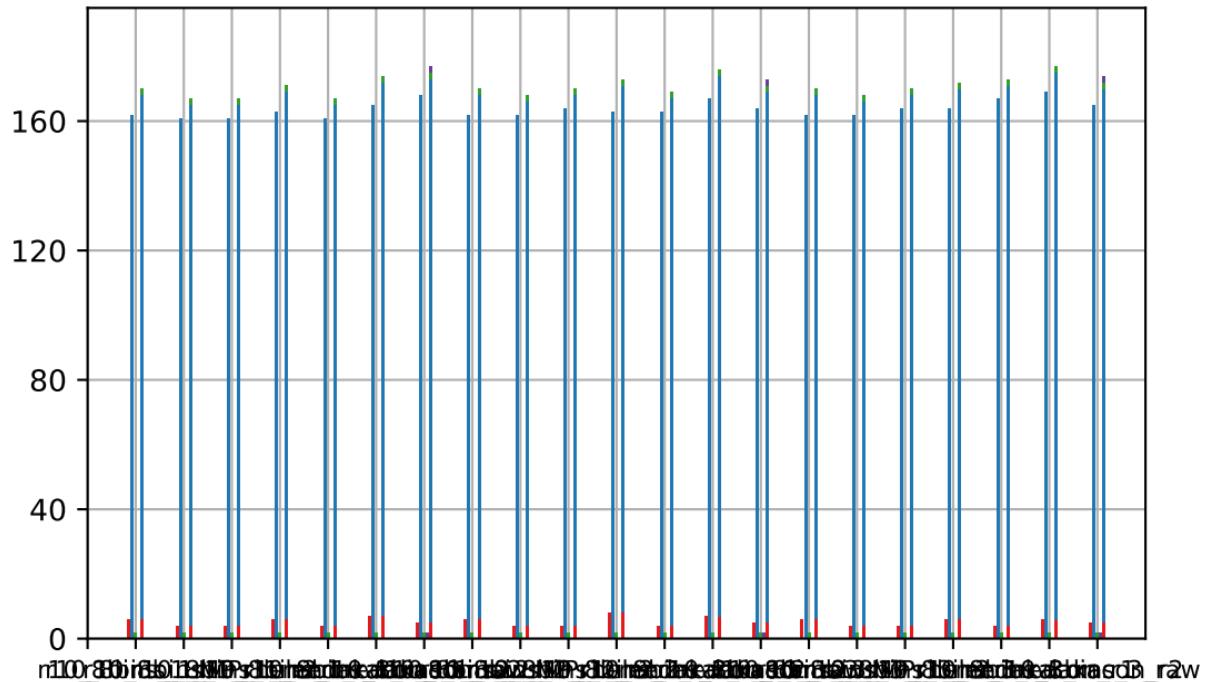
r10_8bins_3_racon_r2 GC content



r10_8bins_3_raw GC content

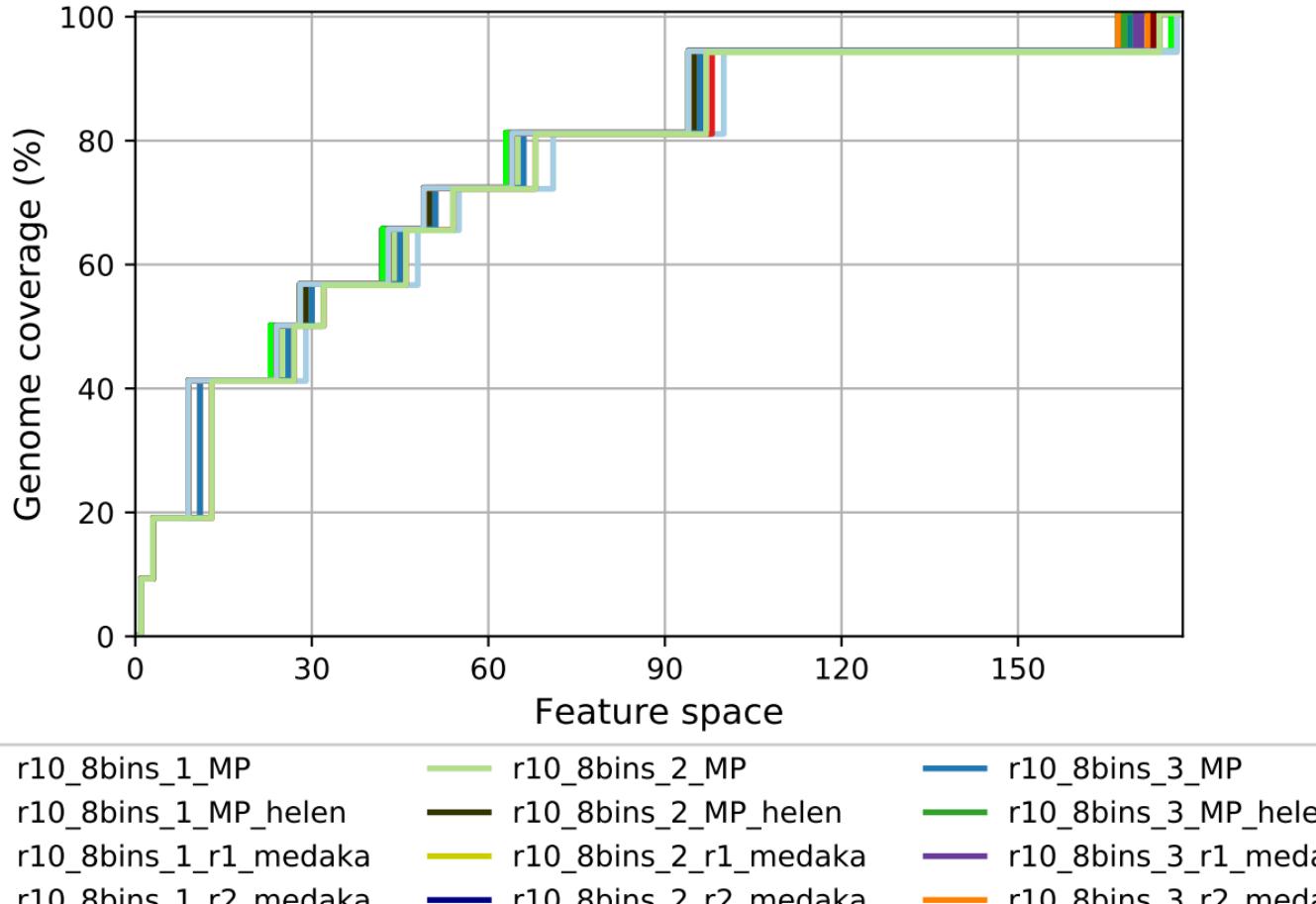


Misassemblies

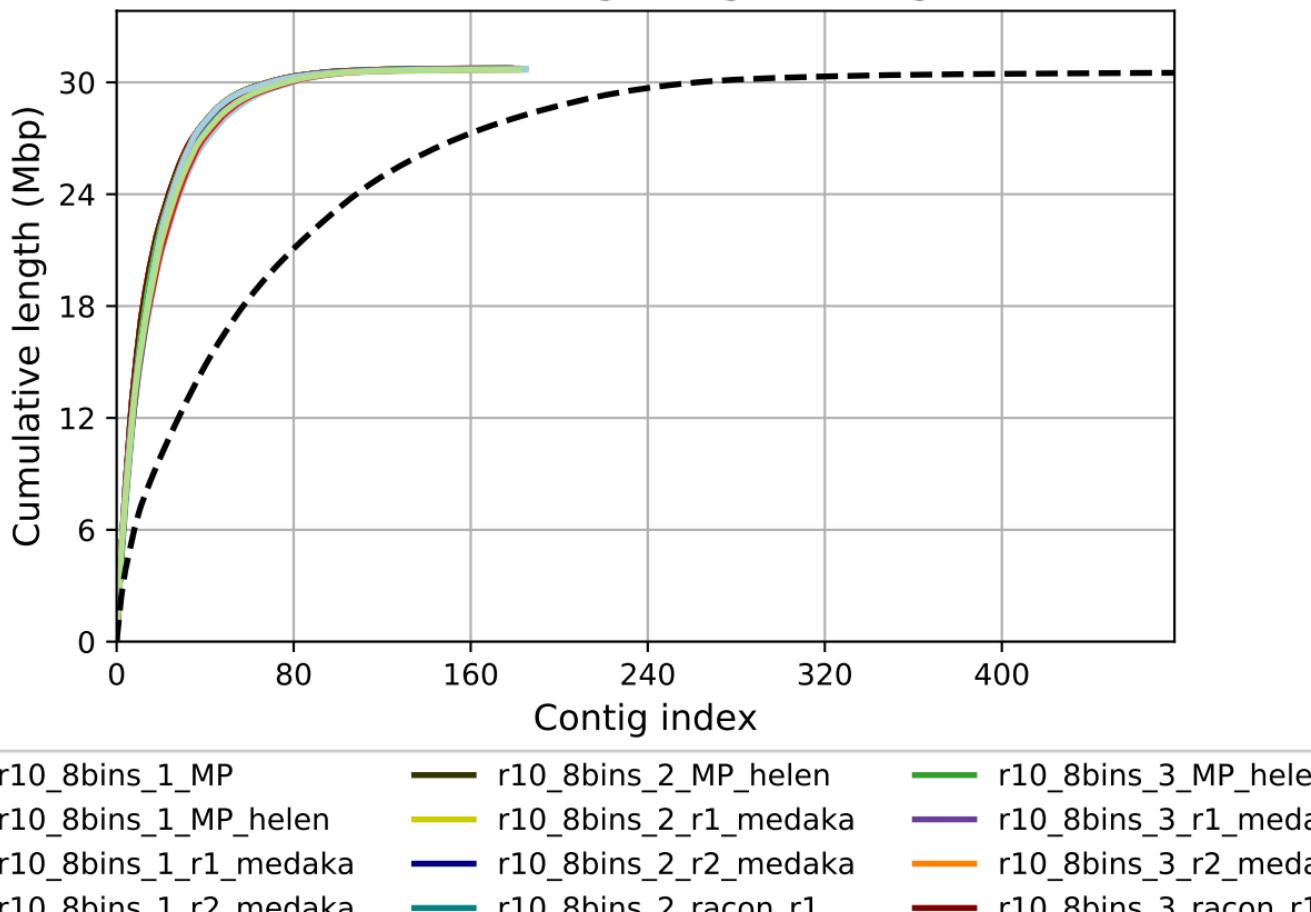


- # relocations
- # inversions
- # interspecies translocations
- # translocations

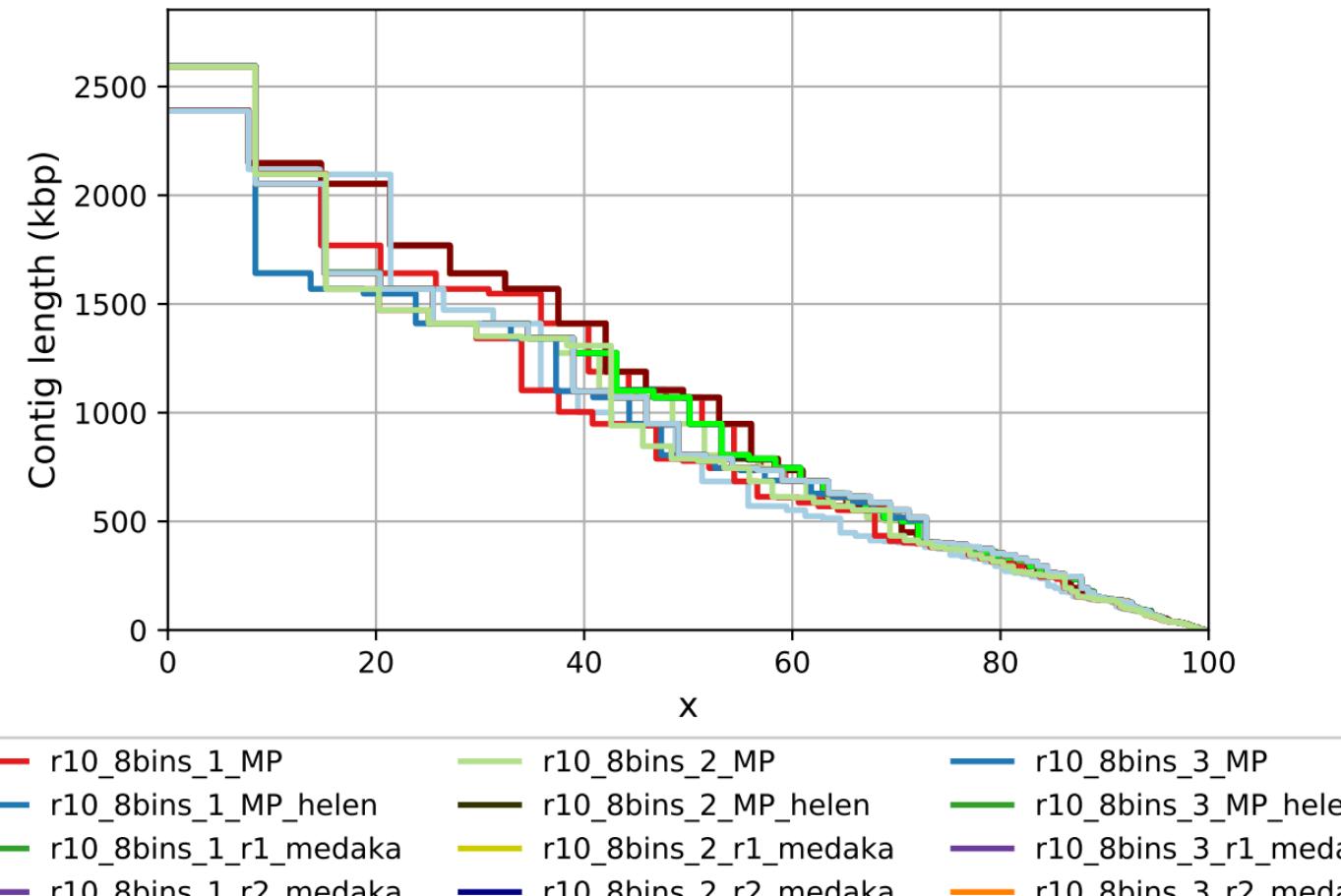
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



Genome fraction, %

