

Report

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw		
# contigs (>= 0 bp)	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			
# contigs (>= 5000 bp)	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			
# contigs (>= 25000 bp)	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			
Total length (>= 0 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 1000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 5000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 10000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 25000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 50000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8			
Largest contig	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792245	6791577	6791686	6787718		
Total length	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	
N50	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758065	4757922	4757649	4758088	4758954	4757856	4758593	4758140	4757950	4757852	4756101	
N75	2992083	2992068	2992071	2992074	2991898	2991964	2990667	2992084	2992066	2992071	2992072	2991914	2991953	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633
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	169	169	169	174	169	169	178	172	168	169	171	169	172	176	168	169	177	168	175	172	
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Misassembled contigs length	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	3086651	30863115	30864187	30847828	30851884	30843598	30848199
# local misassemblies	118	117	138	131	149	139	208	115	116	132	133	149	135	211	115	117	134	130	150	145	204
# 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	1	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 + 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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part		
Unaligned length	78429	78867	82596	81033	78571	78067	141701	79248	78734	81756	80845	78355	77917	136441	79252	78804	81829	80999	78252	77033	134441
Genome fraction (%)	99.400	99.393	99.398	99.397	99.398	99.396	99.370	99.400	99.397	99.399	99.398	99.399	99.371	99.400	99.399	99.398	99.398	99.396	99.370		
Duplication ratio	1.044	1.044	1.043	1.043	1.043	1.043	1.027	1.044	1.044	1.043	1.043	1.043	1.043	1.044	1.044	1.043	1.043	1.043	1.028		
# N's per 100 kbp	0.00	0.03	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	176.22	168.20	176.25	175.31	179.29	179.06	270.98	175.53	167.54	178.27	174.58	176.13	176.89	274.19	175.99	168.64	175.32	173.93	176.43	176.69	274.68
# indels per 100 kbp	38.29	24.09	26.35	26.63	63.57	59.60	309.19	38.10	23.02	27.10	26.36	62.95	59.92								

Misassemblies report

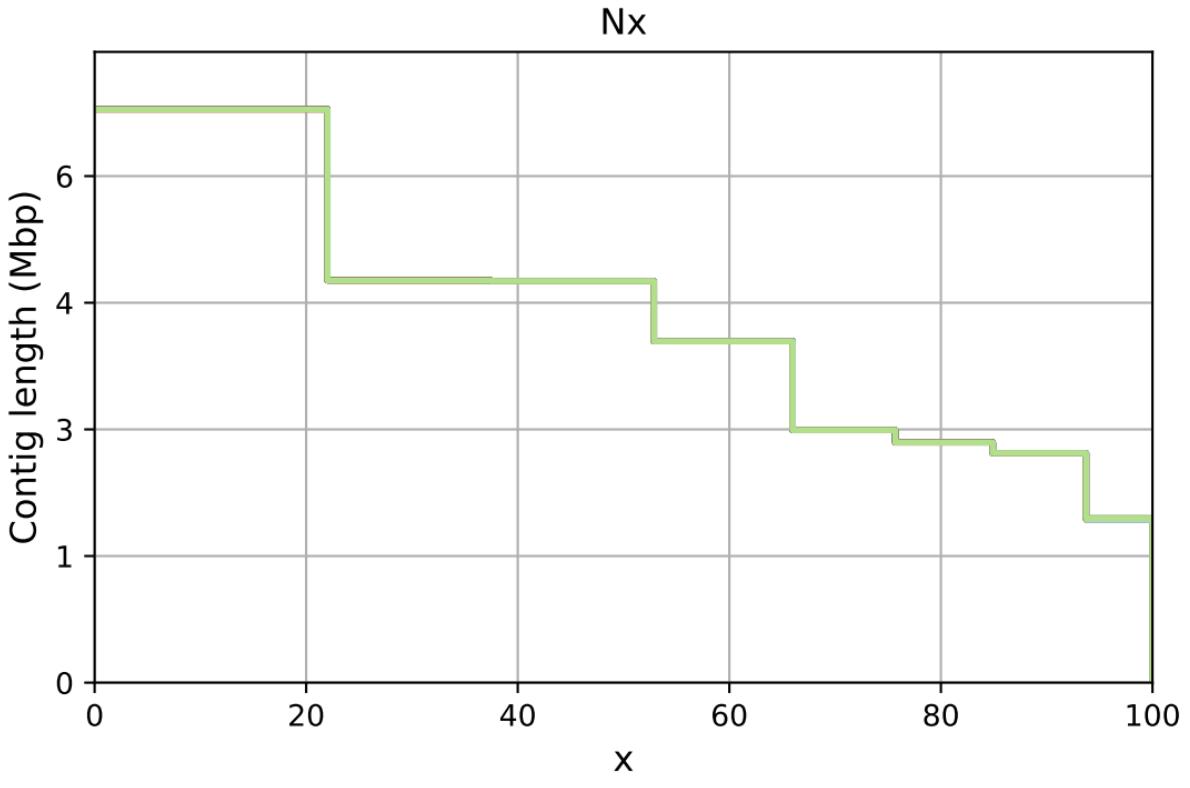
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw			
# misassemblies	169	169	169	174	169	178	172	168	168	169	171	169	172	168	169	177	168	175	172		
# contig misassemblies	169	169	169	169	174	169	178	172	168	168	171	169	172	168	169	177	168	175	172		
# c. relocations	5	5	4	9	4	9	5	5	4	6	5	4	4	4	10	4	7	5			
# c. translocations	162	162	163	163	163	167	163	161	162	163	164	167	161	163	165	162	166	163			
# c. inversions	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	2			
# scaffold misassemblies	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			
# s. translocations	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			
# s. interspecies translocations	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			
Misassembled contigs length	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# possibly misassembled contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	7	7	7	7	7	8		
# possible misassemblies	98	98	96	98	98	96	96	100	98	96	96	96	100	98	96	96	98	94	164		
# local misassemblies	118	117	138	131	149	139	208	115	116	132	133	149	135	211	115	117	134	130	150	145	204
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# misassemblies caused by fragmented reference	252	253	250	252	249	249	172	253	253	250	251	250	173	253	250	251	251	248	181		
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# mismatches	53441	51005	53448	53163	54372	54301	82153	53232	50808	54062	52943	53413	53645	83129	53370	51141	53166	52746	53505	53583	83275
# indels	11611	7304	7990	8075	19279	18073	93739	11555	6980	8217	7994	19089	18171	94105	11578	7241	8043	8004	19128	18068	93530
# indels (<= 5 bp)	10951	6630	7393	7474	18618	17440	92494	10903	6320	7613	7391	18438	17513	92885	10910	6575	7452	7411	18475	17433	92300
# indels (> 5 bp)	660	674	597	601	661	633	1245	652	660	604	651	658	1220	668	666	591	593	653	635	1230	
Indels length	45792	41705	40616	41121	56997	54561	158364	45916	41322	40634	40565	45914	57107	55122	158766	46106	41387	40634	56803	55379	158210

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_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_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	8
Partially unaligned length	78429	78867	82596	81033	78571	78067	141701	79248	78734	81756	80845	78355	77917	136441	79252	78804	81829	80999
# N's	0	10	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).



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

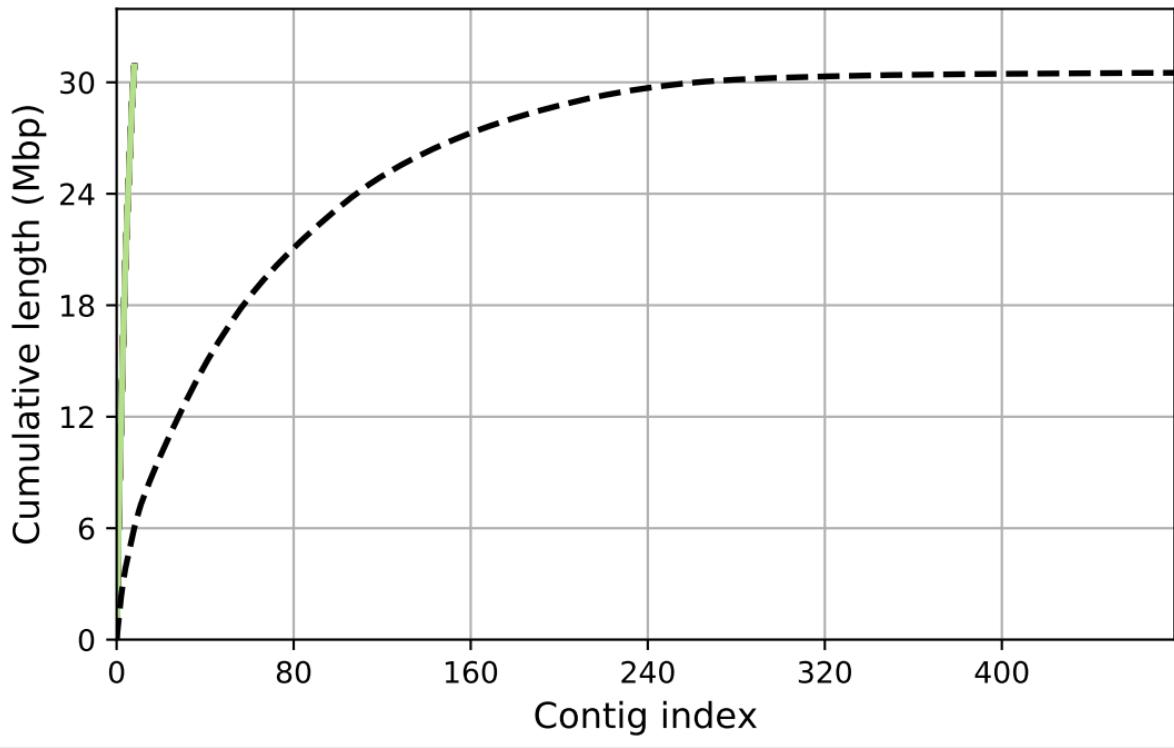
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length



r0_2bins_v2_1_MP

r0_2bins_v2_1_MP_helen

r0_2bins_v2_1_r1_medaka

r0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

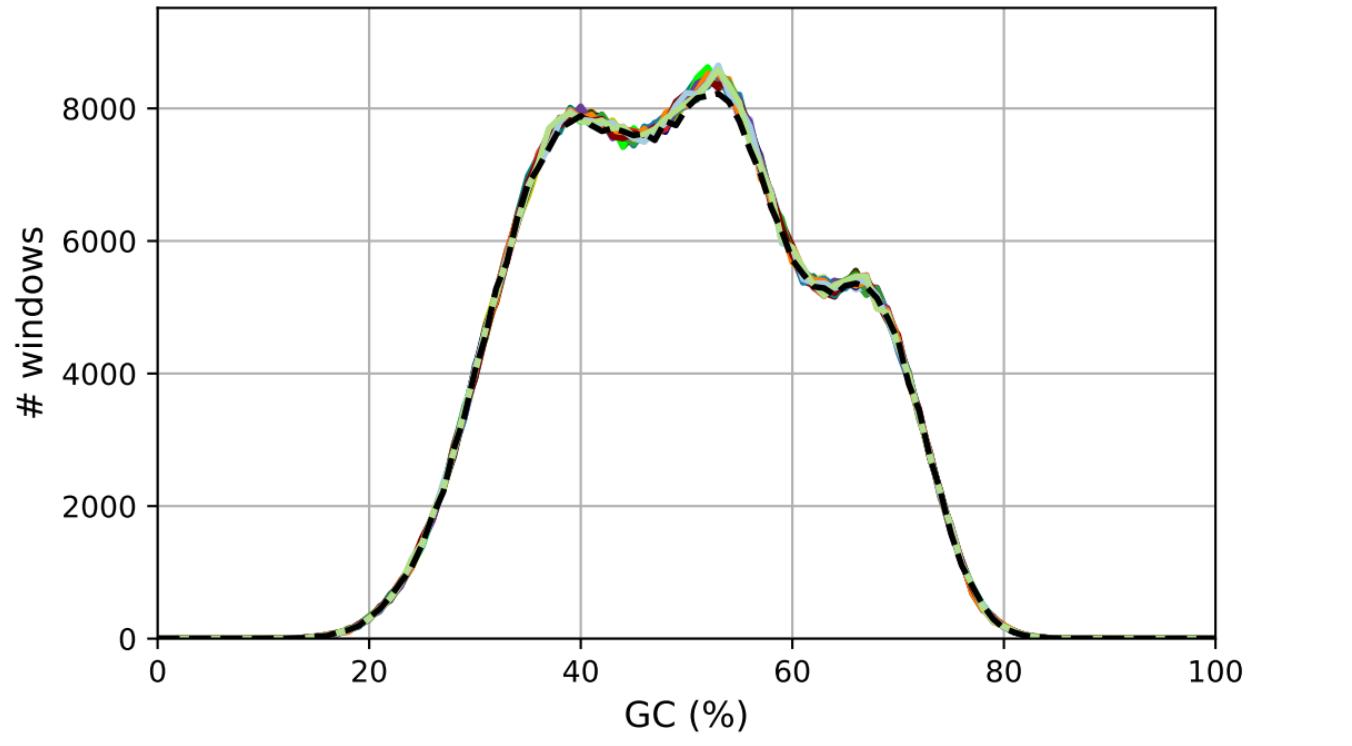
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racoon_r1

GC content



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

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r10_2bins_v2_2_racon_r1

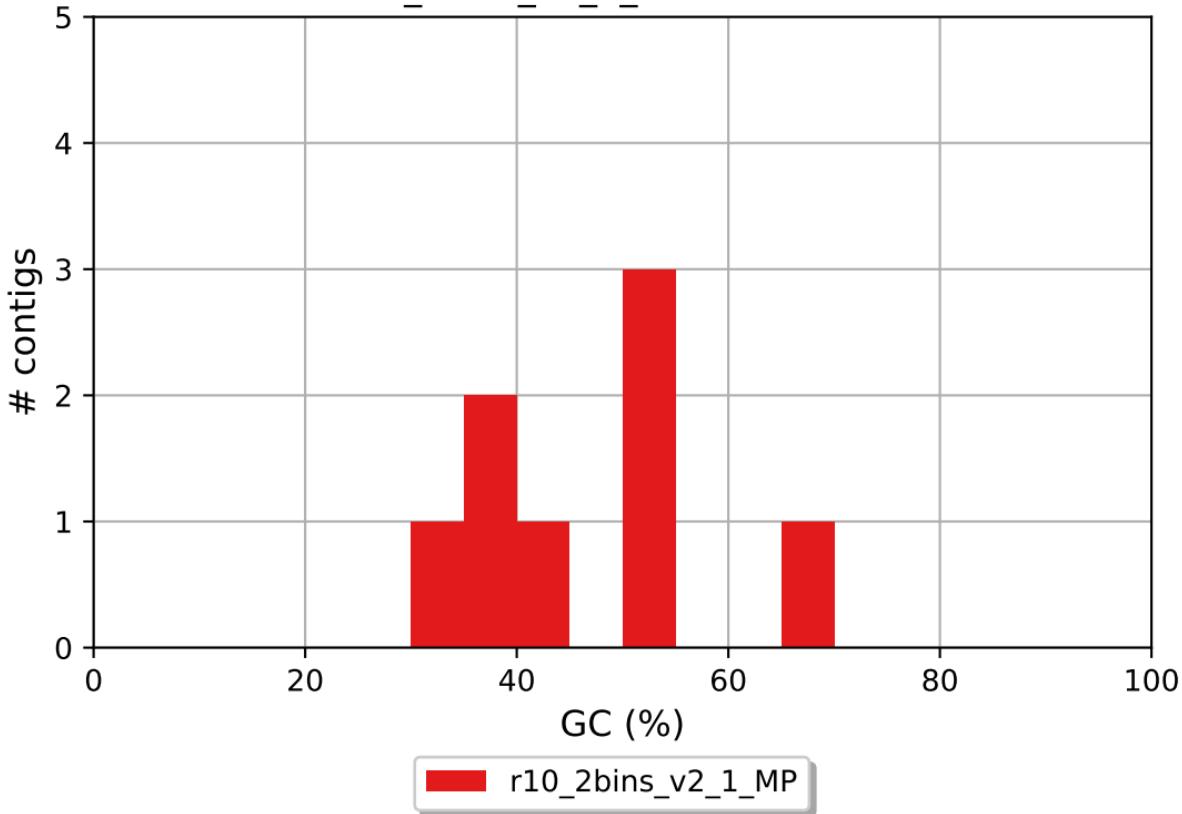
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r10_2bins_v2_3_r1

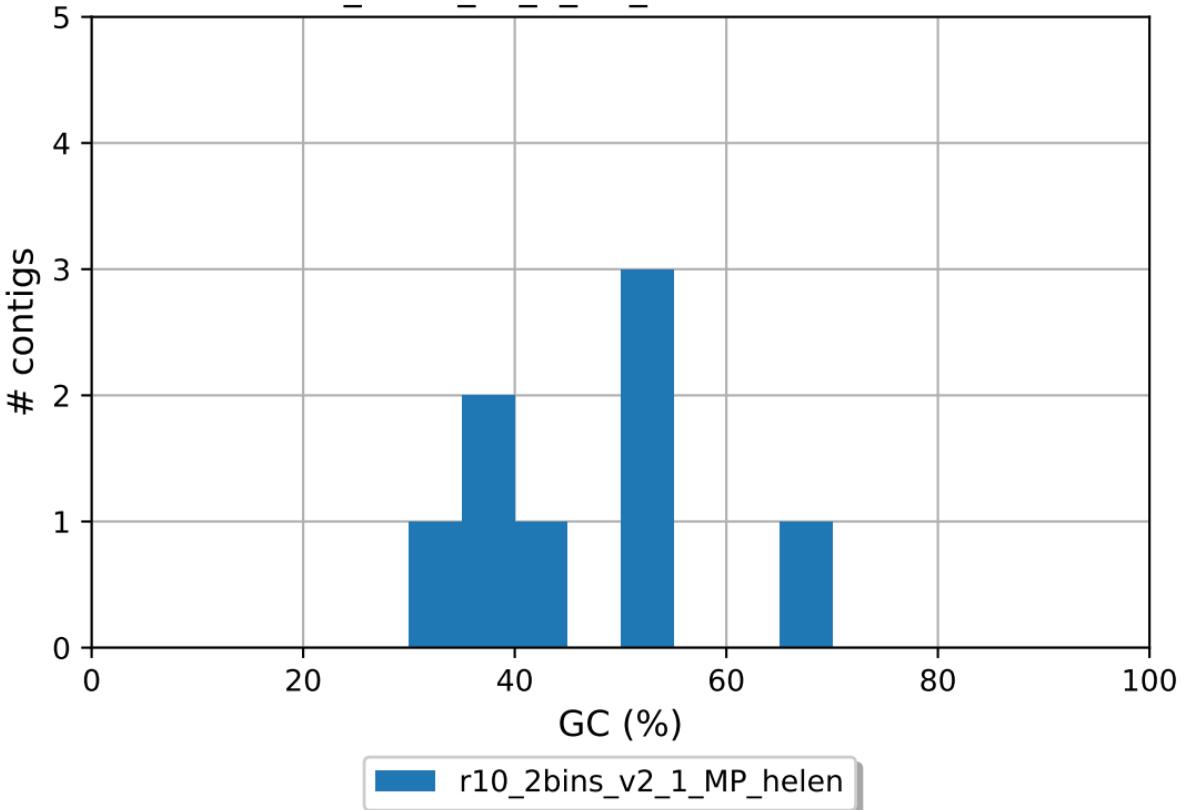
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r10_2bins_v2_3_r3

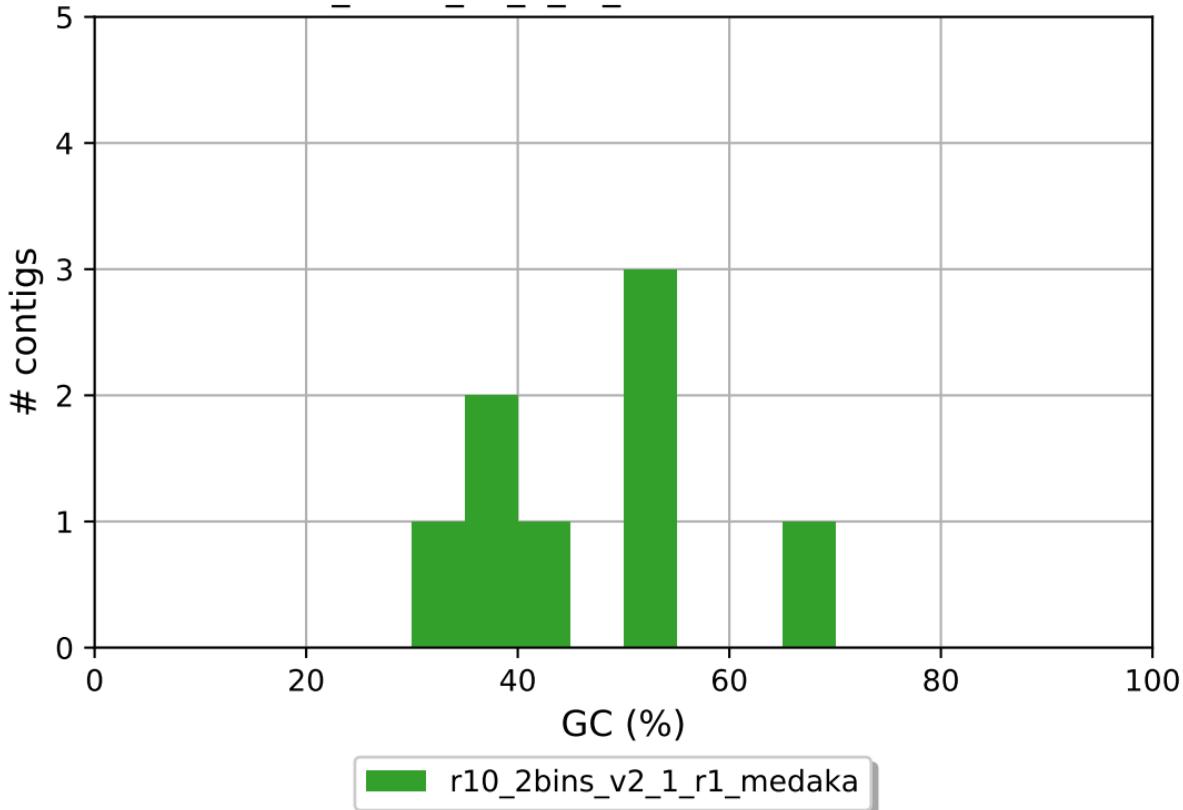
r10_2bins_v2_1_MP GC content



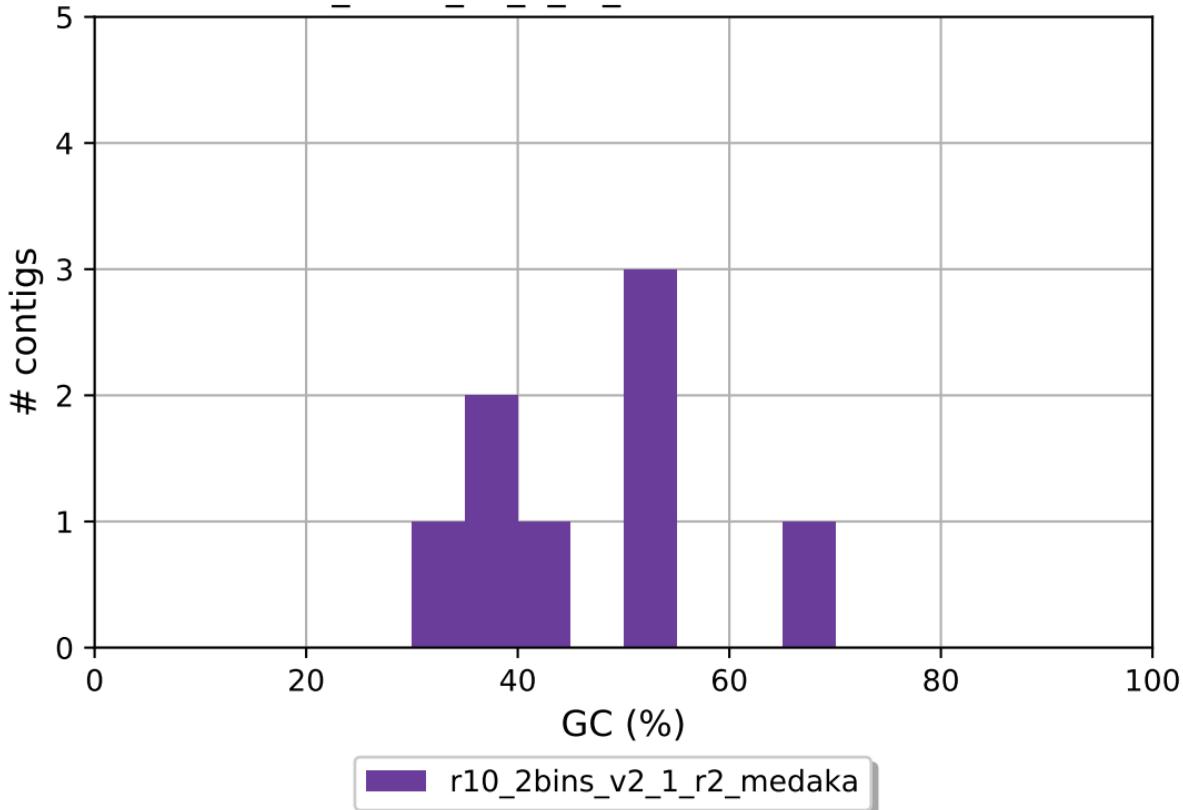
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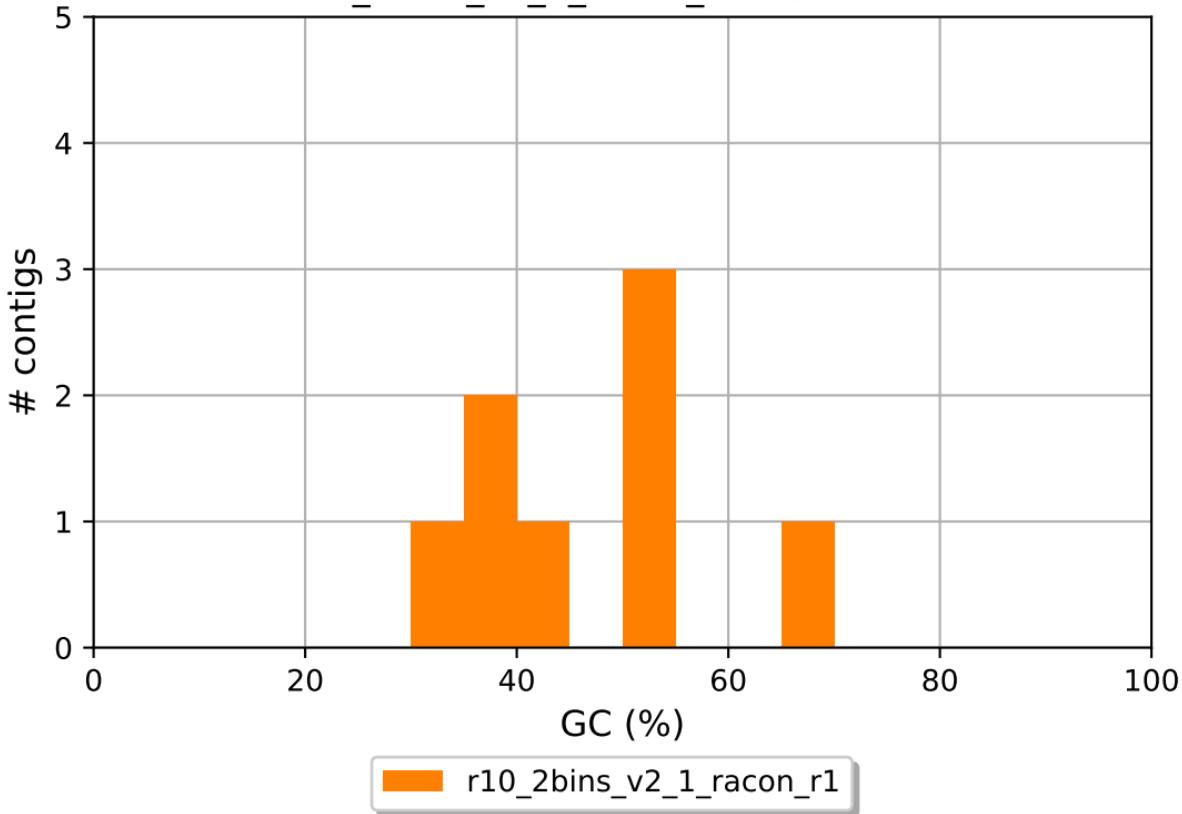
r10_2bins_v2_1_r1_medaka GC content



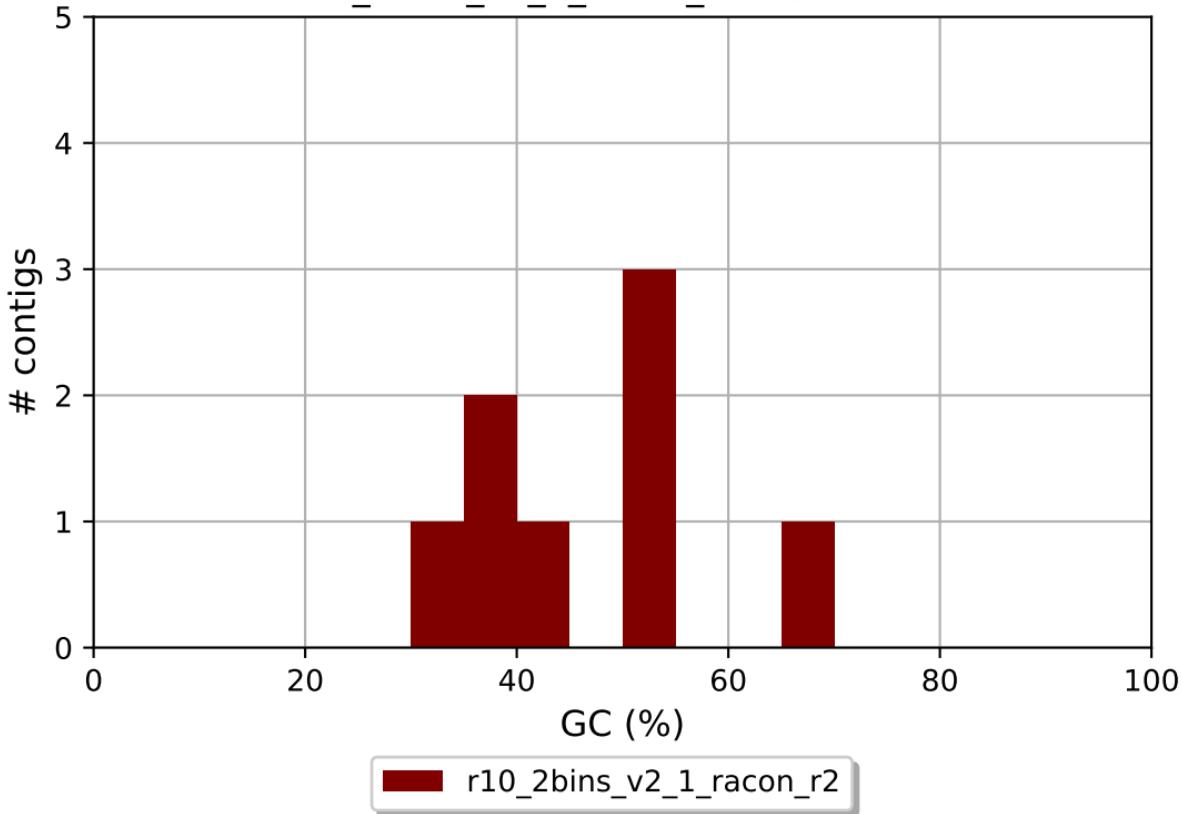
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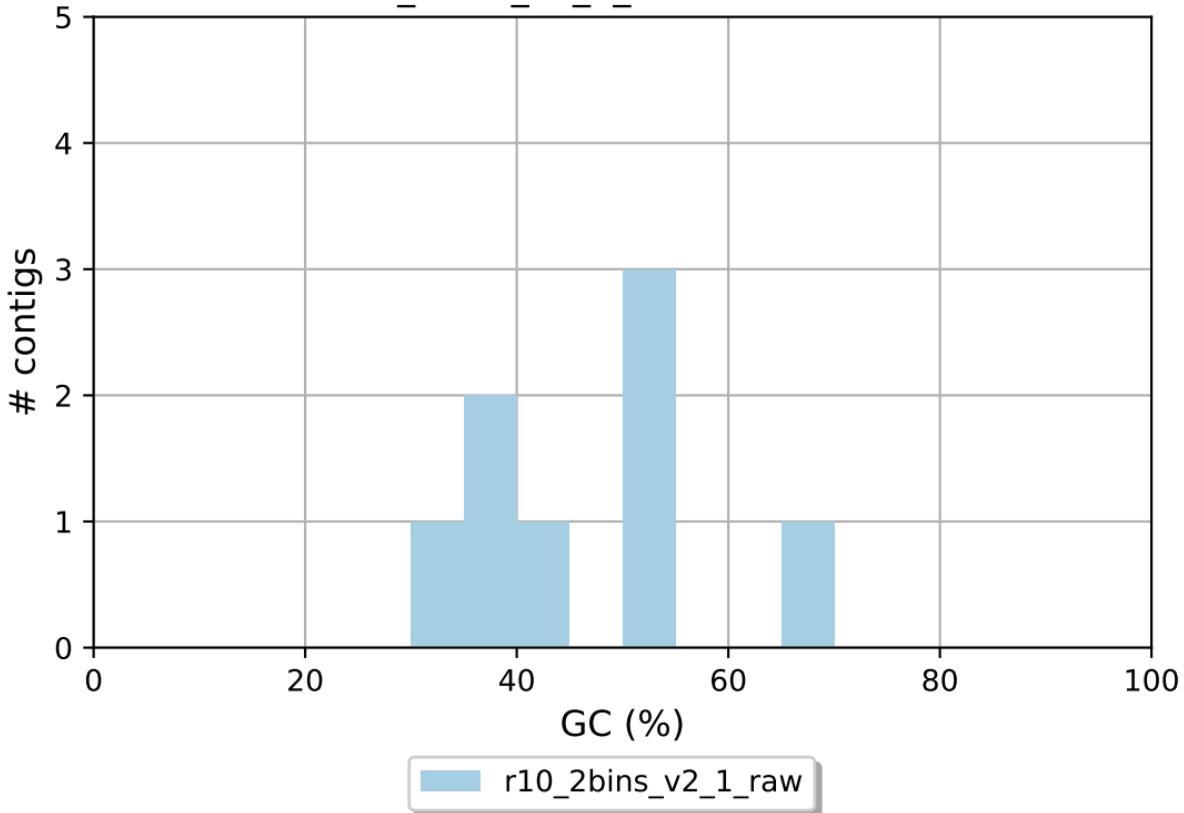
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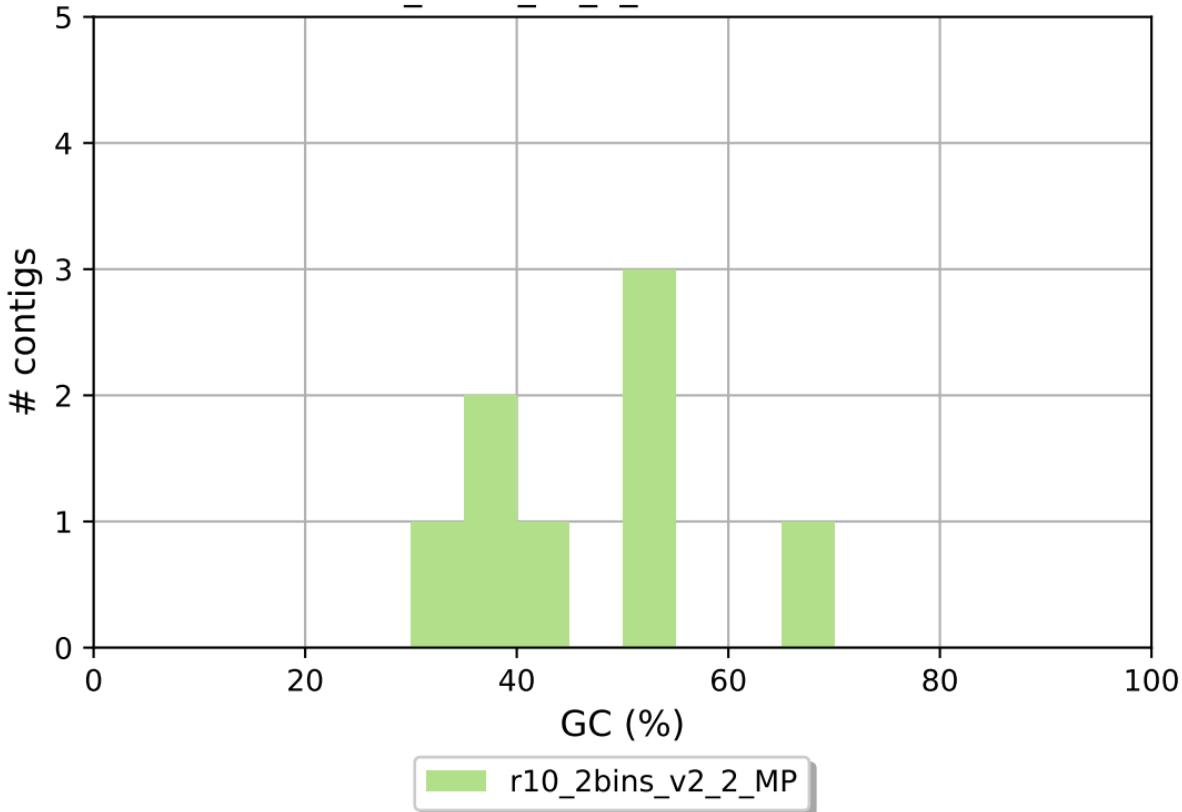
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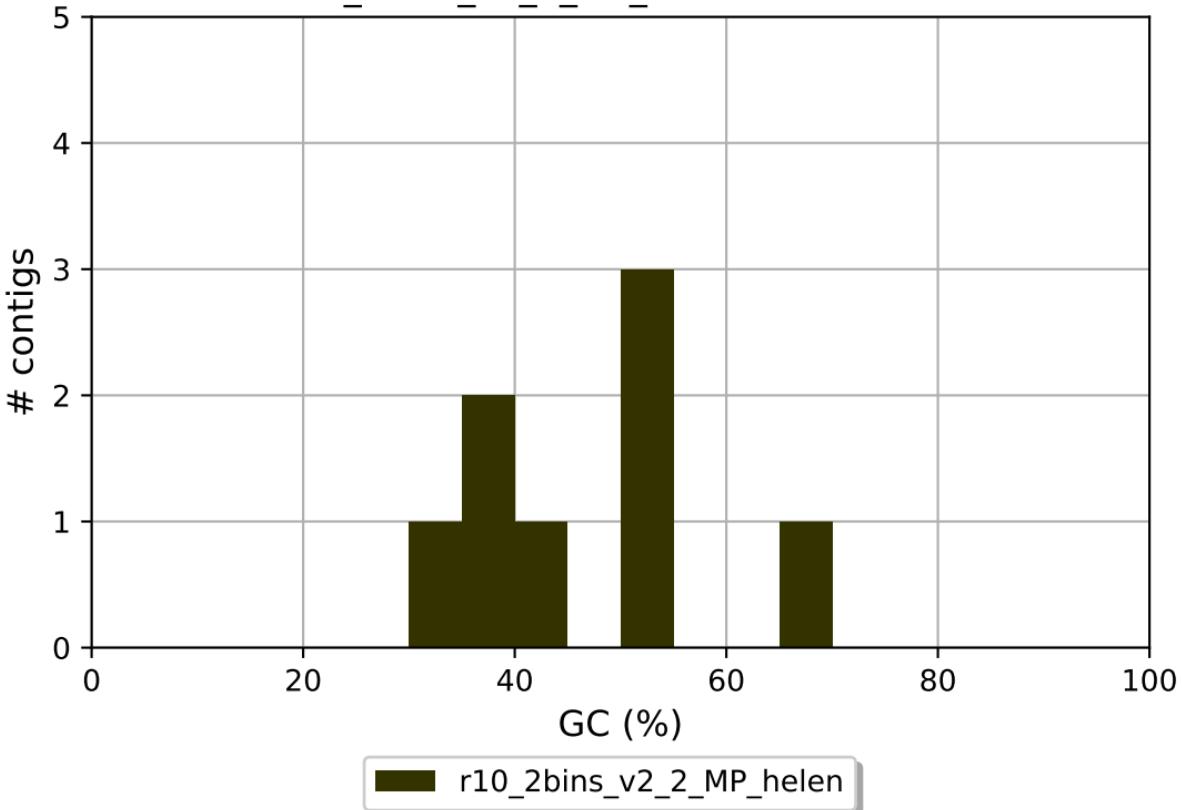
r10_2bins_v2_1_raw GC content



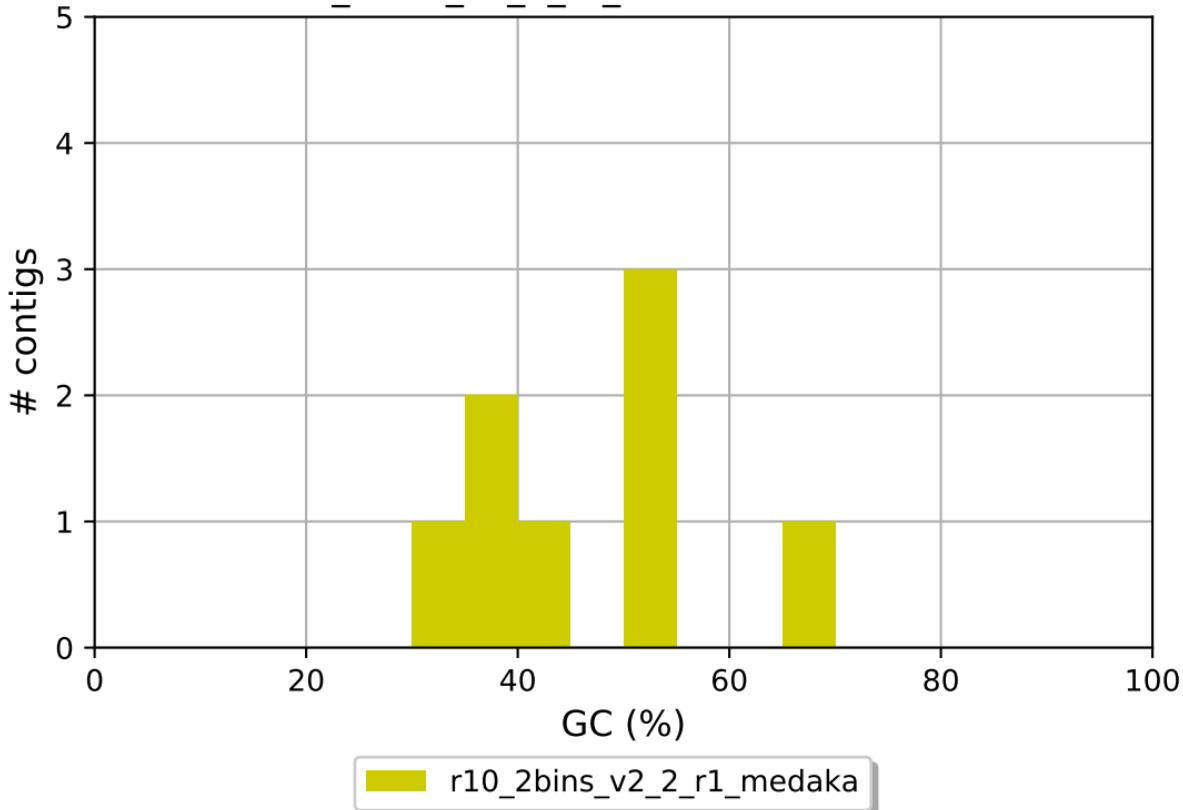
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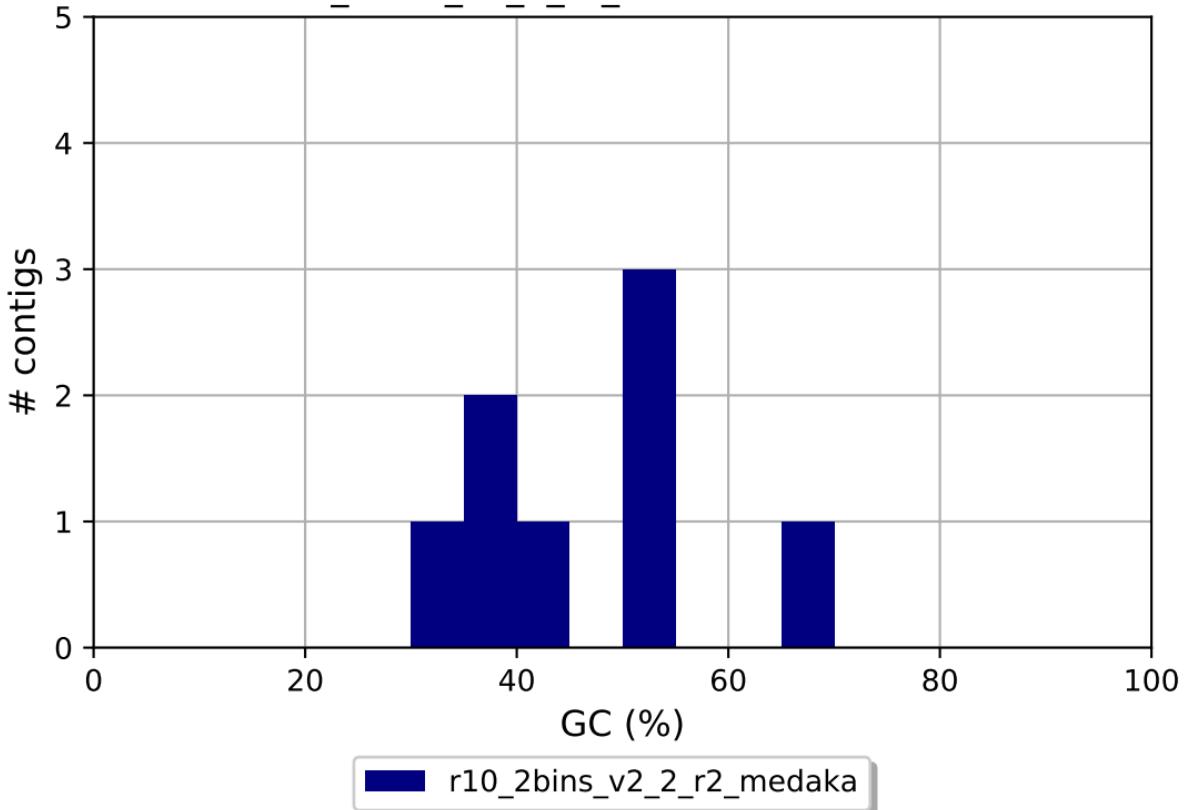
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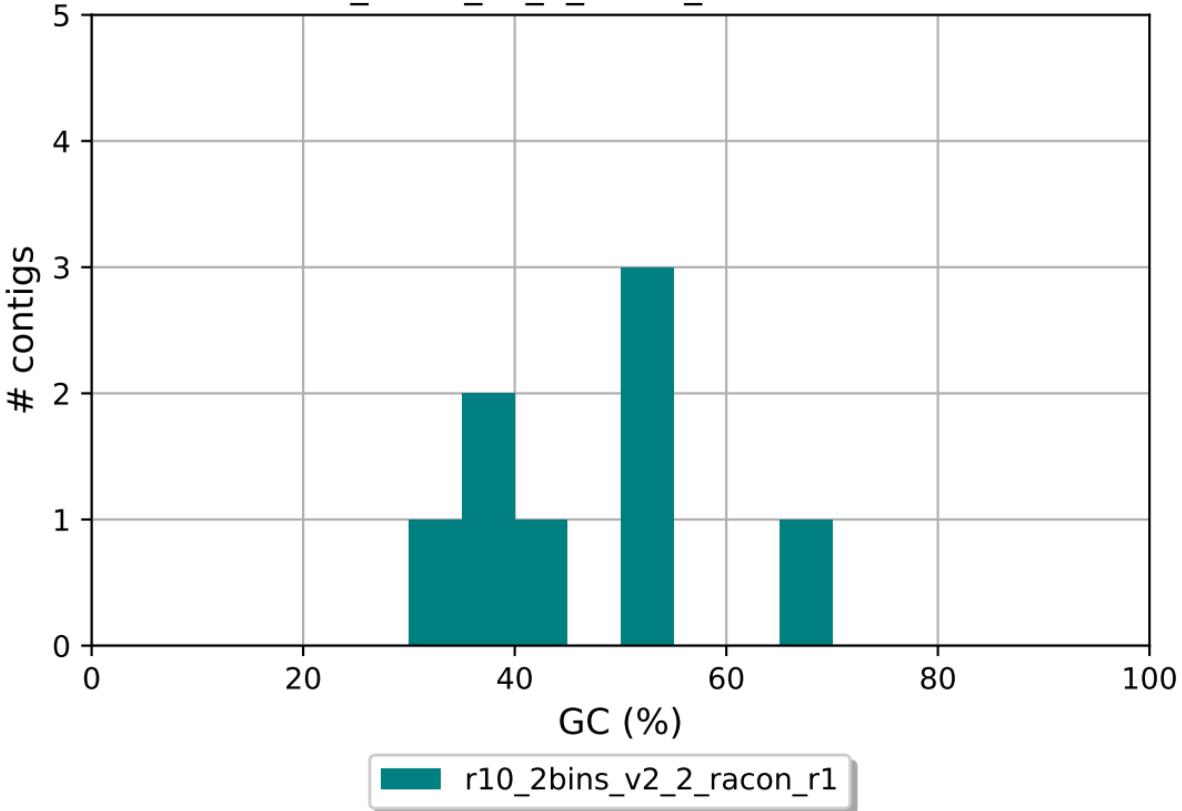
r10_2bins_v2_2_r1_medaka GC content



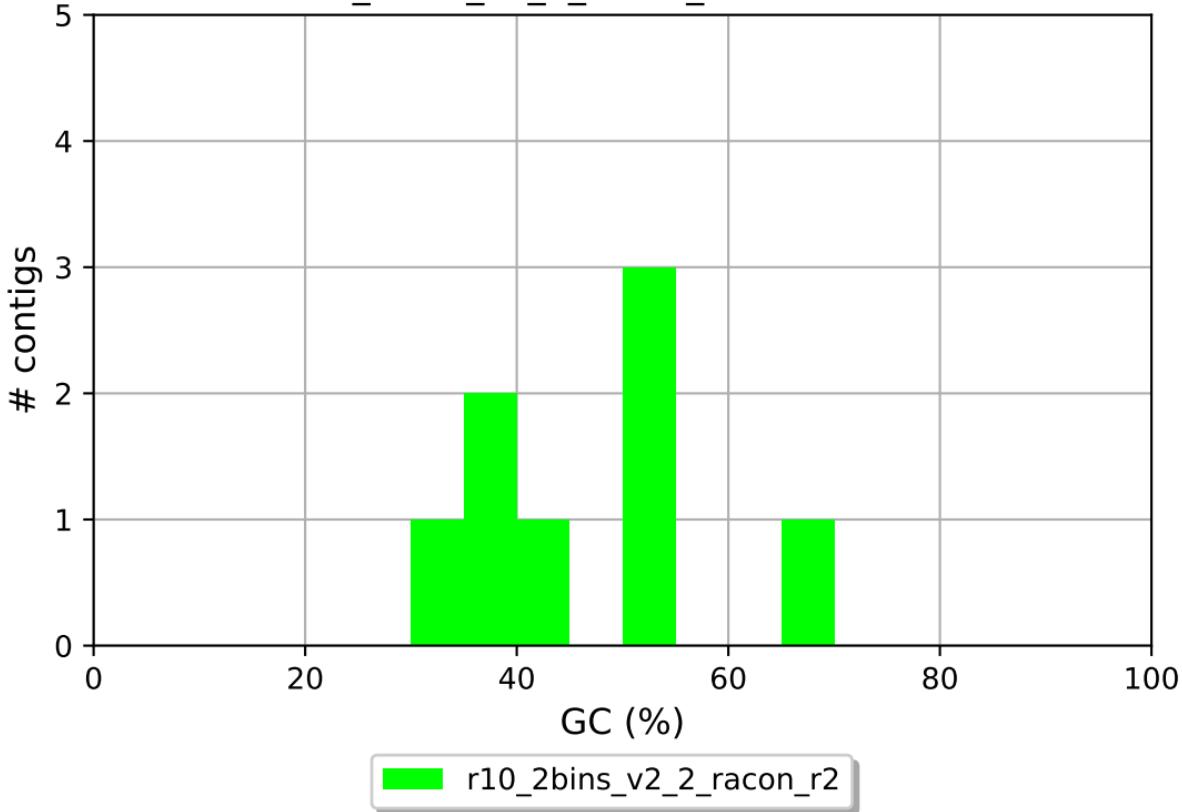
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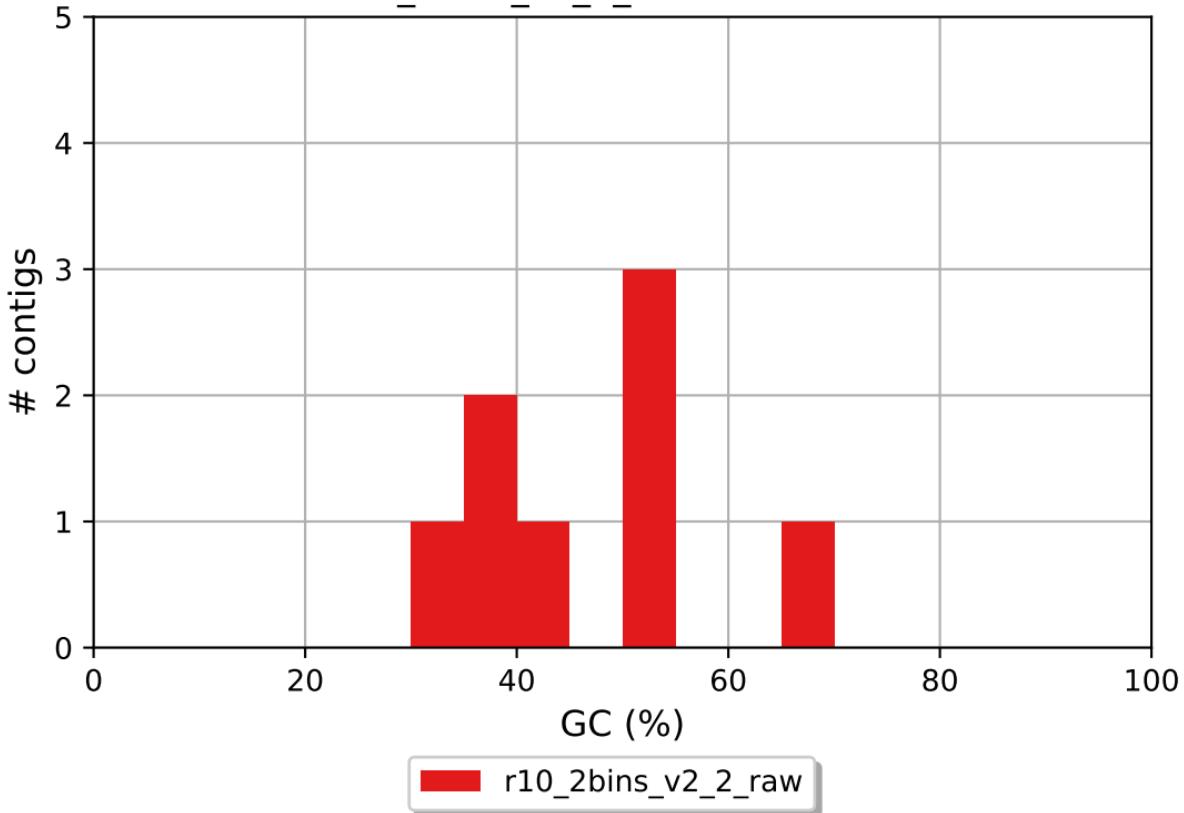
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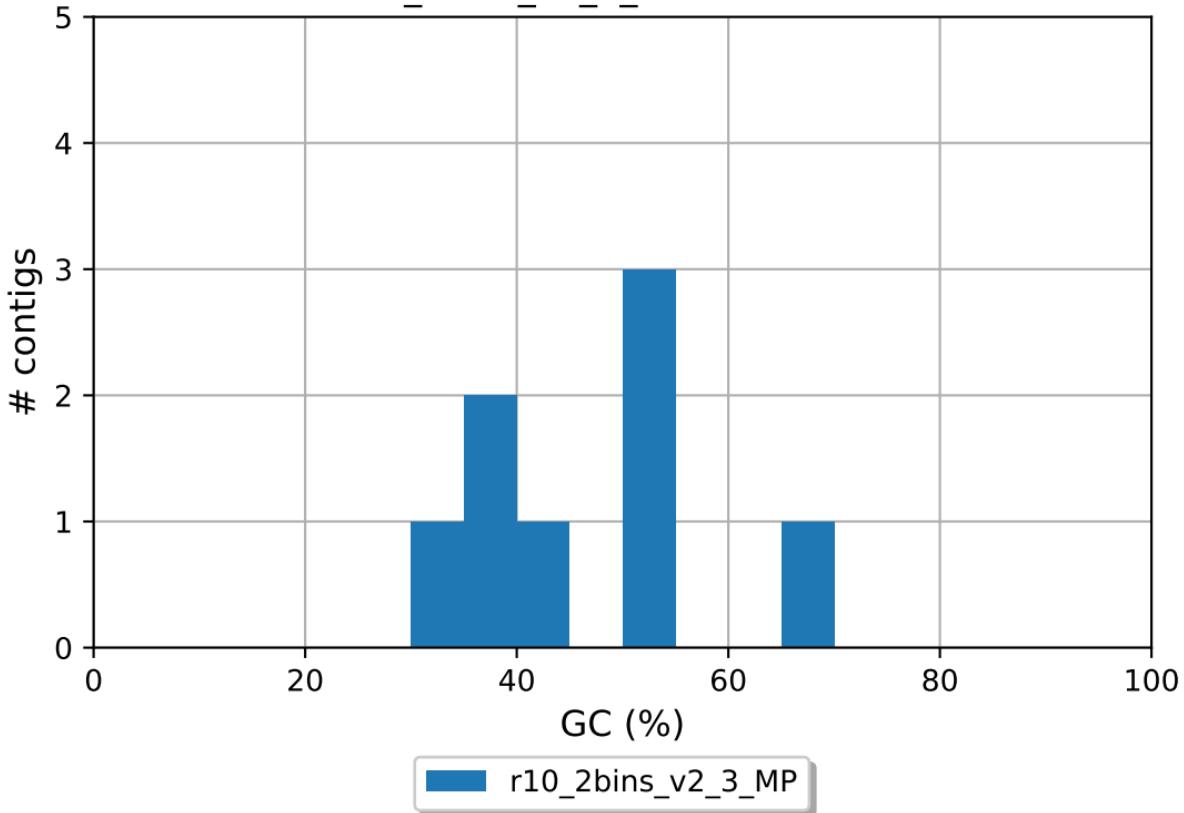
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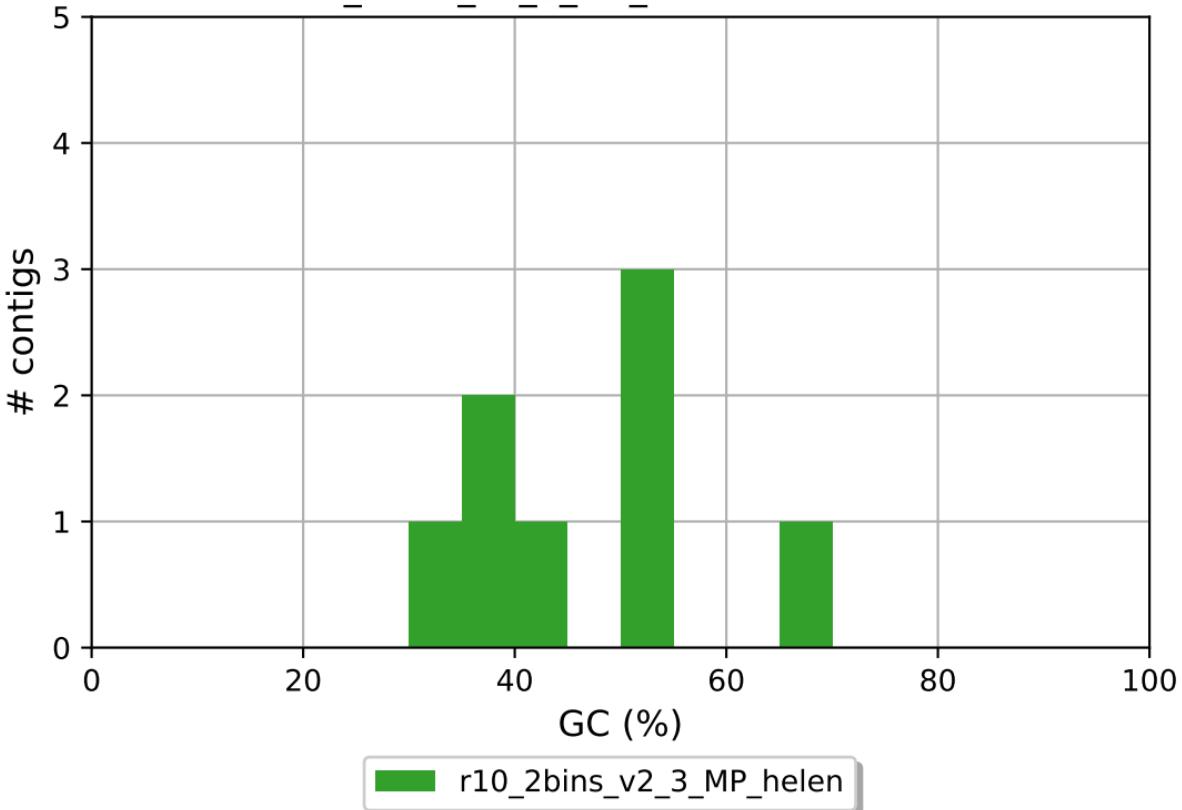
r10_2bins_v2_2_raw GC content



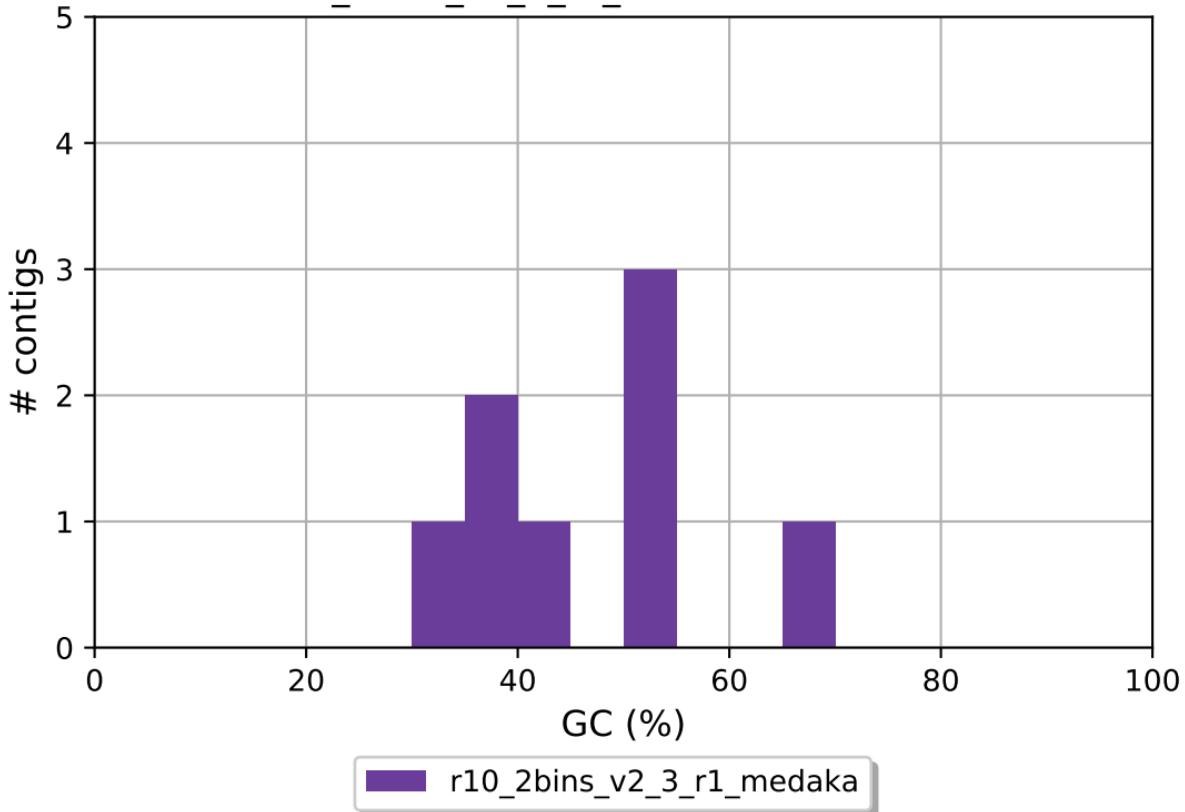
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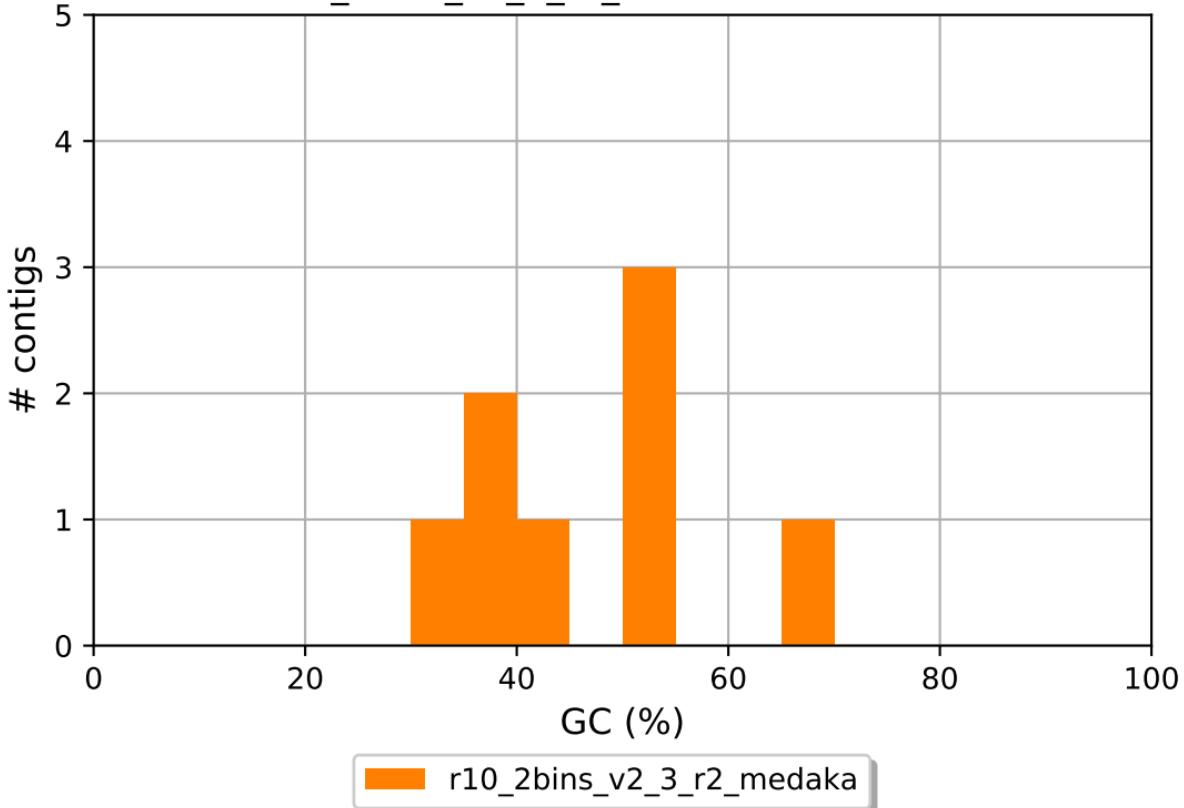
r10_2bins_v2_3_MP_helen GC content



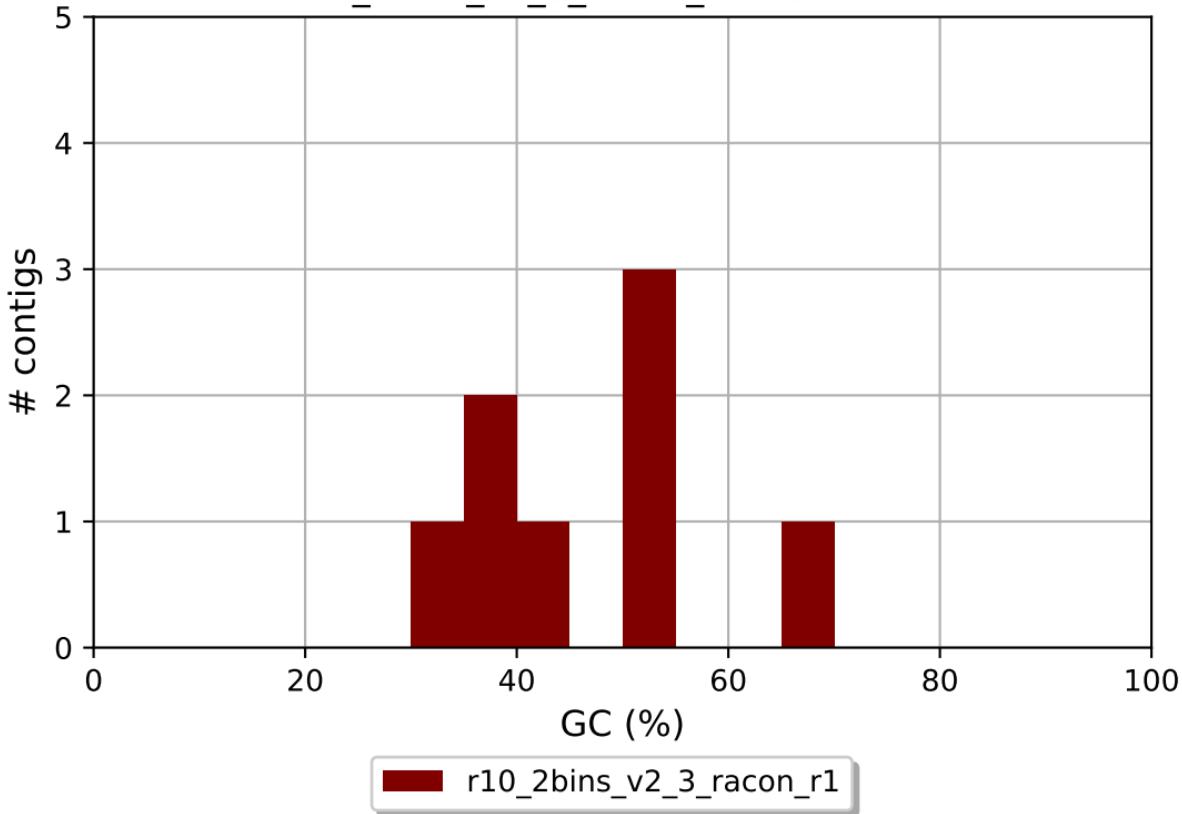
r10_2bins_v2_3_r1_medaka GC content



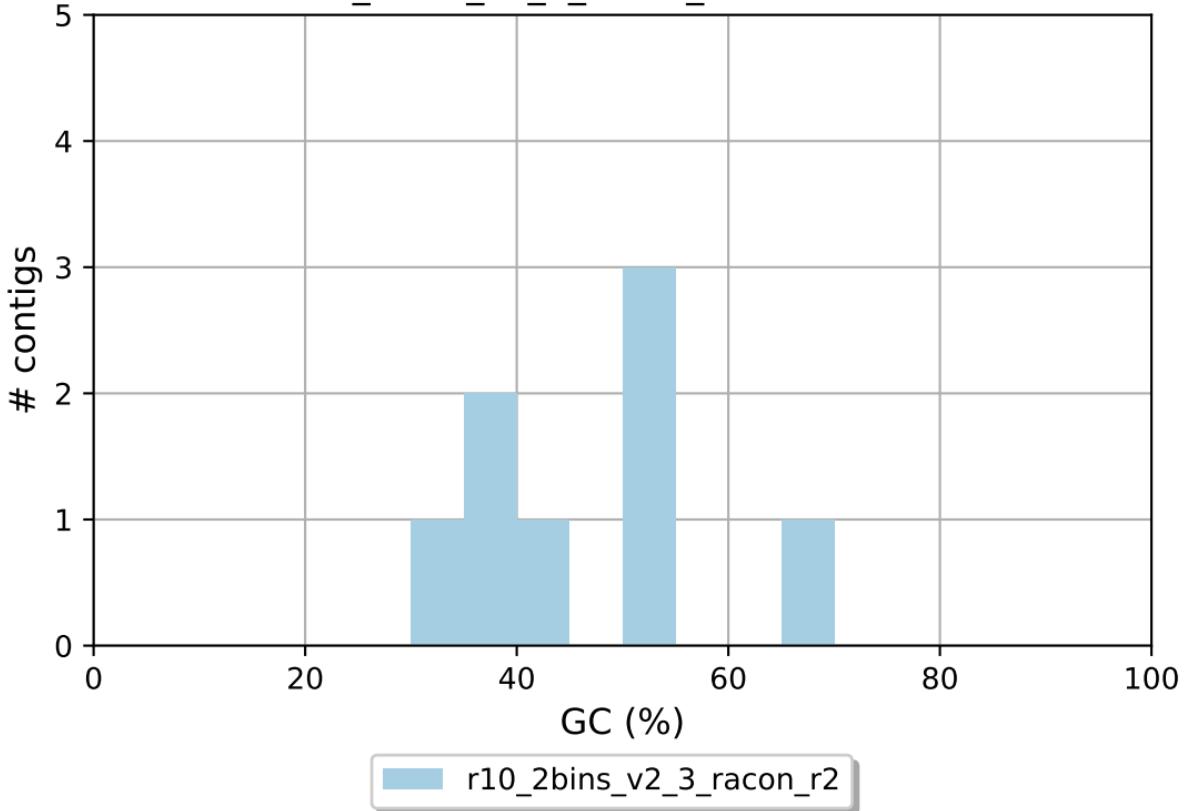
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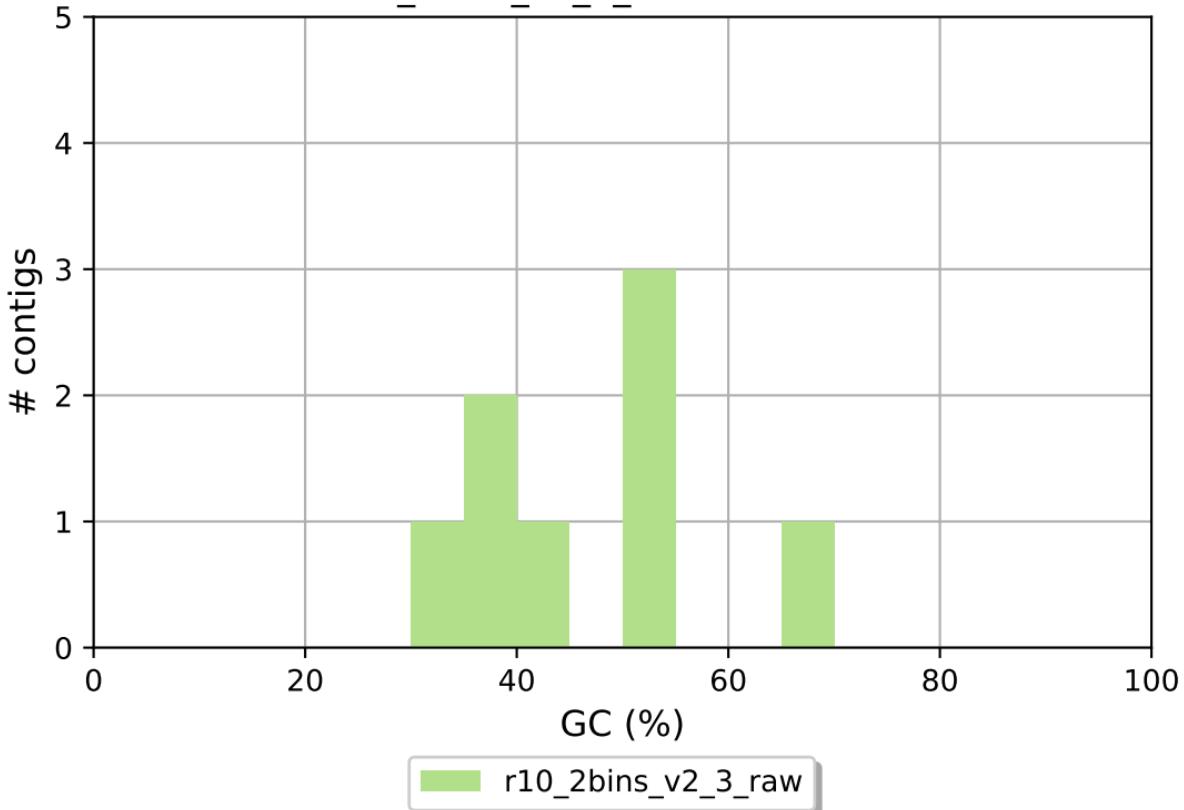
r10_2bins_v2_3_racon_r1 GC content



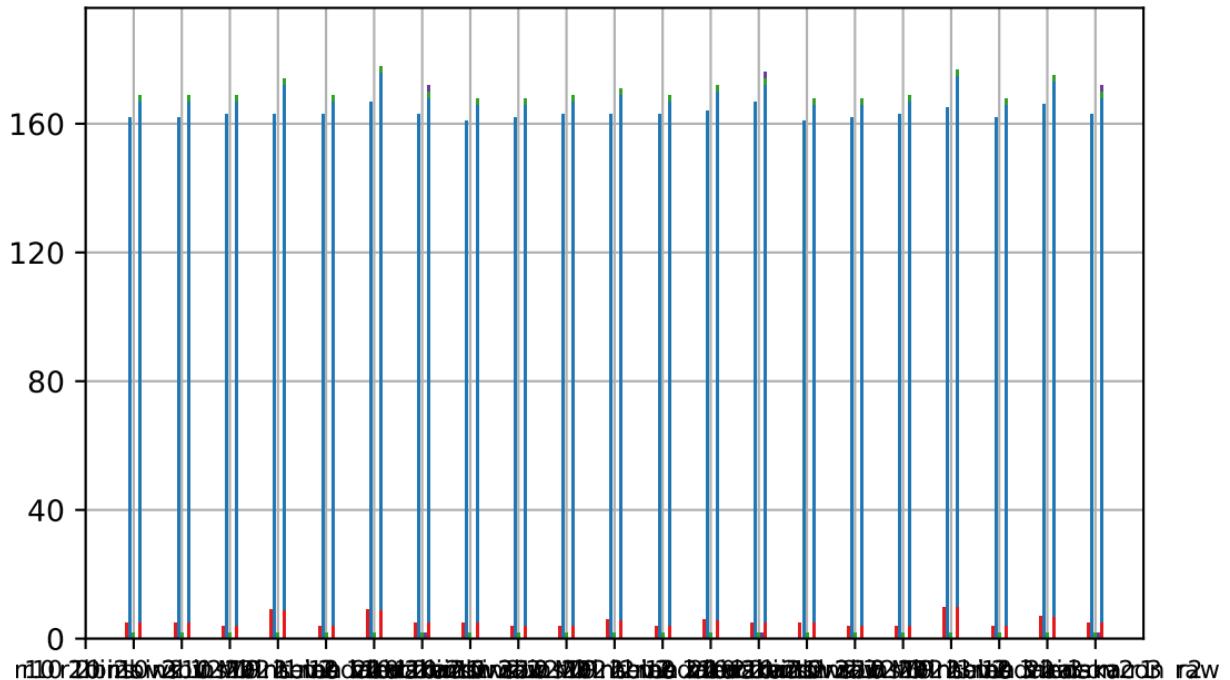
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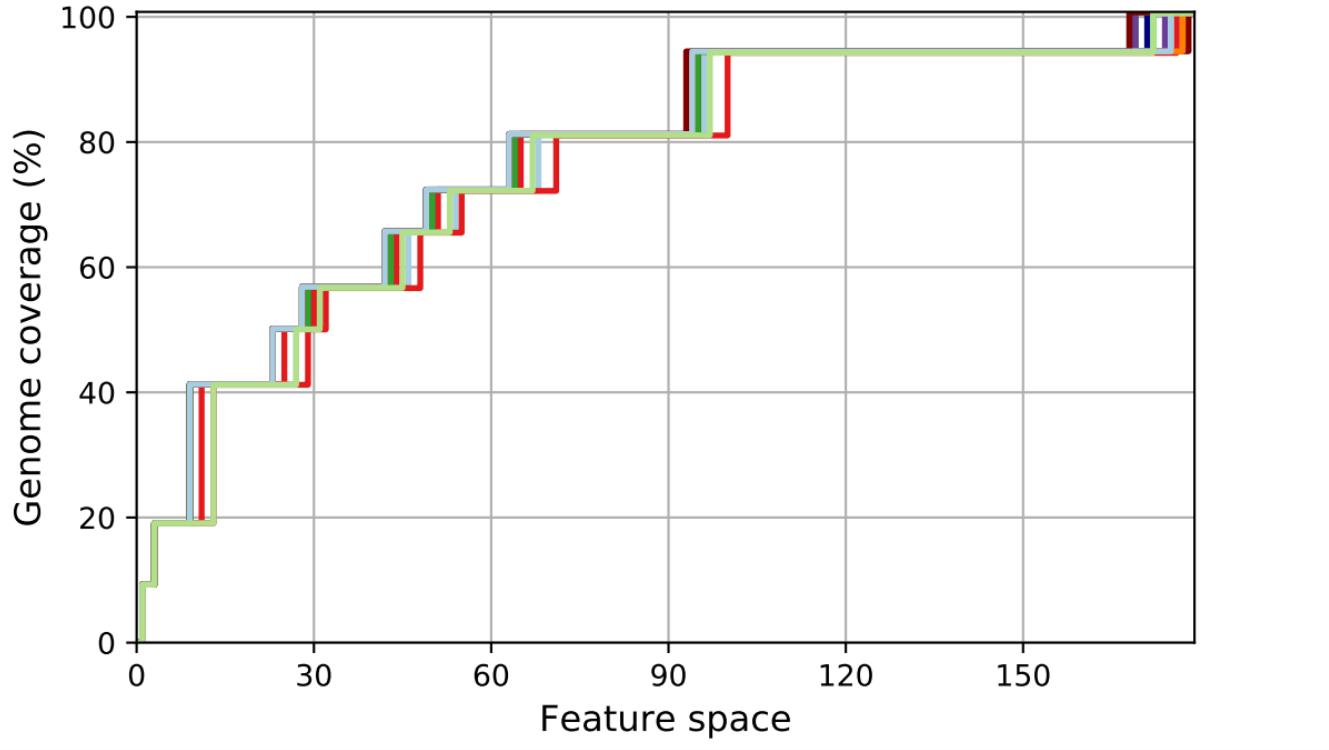
r10_2bins_v2_3_raw GC content



Misassemblies



FRCurve (misassemblies)



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

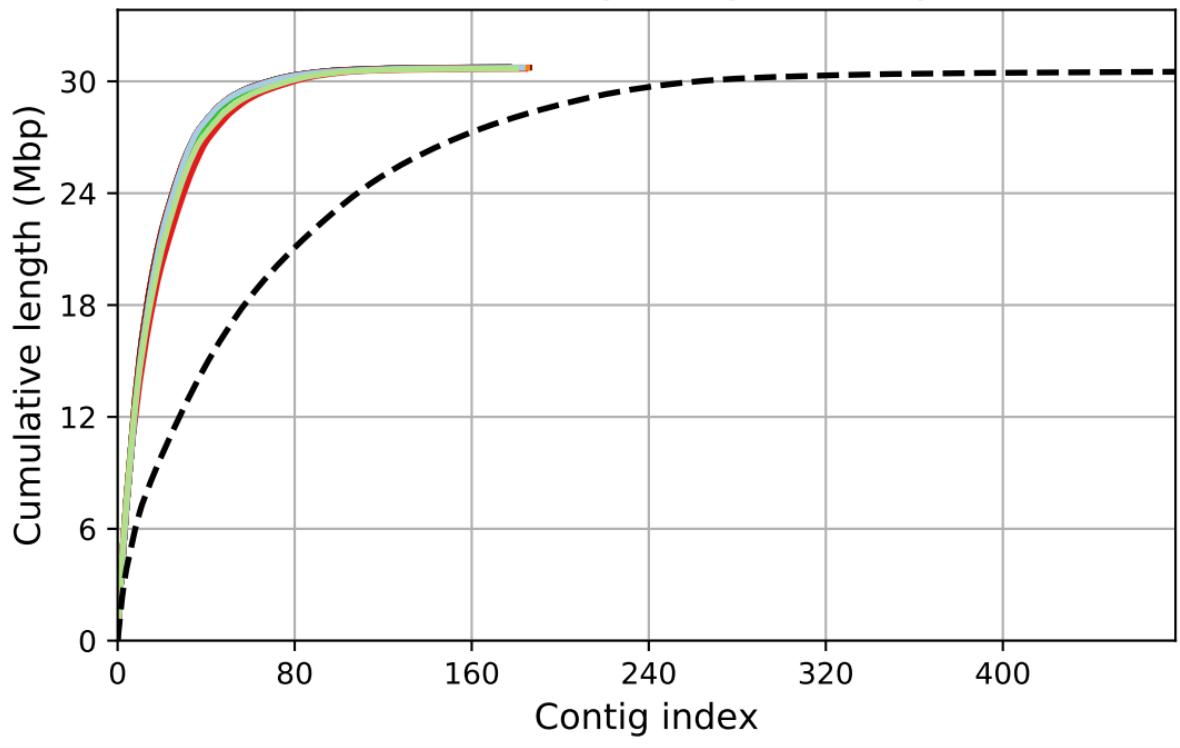
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

Cumulative length (aligned contigs)



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

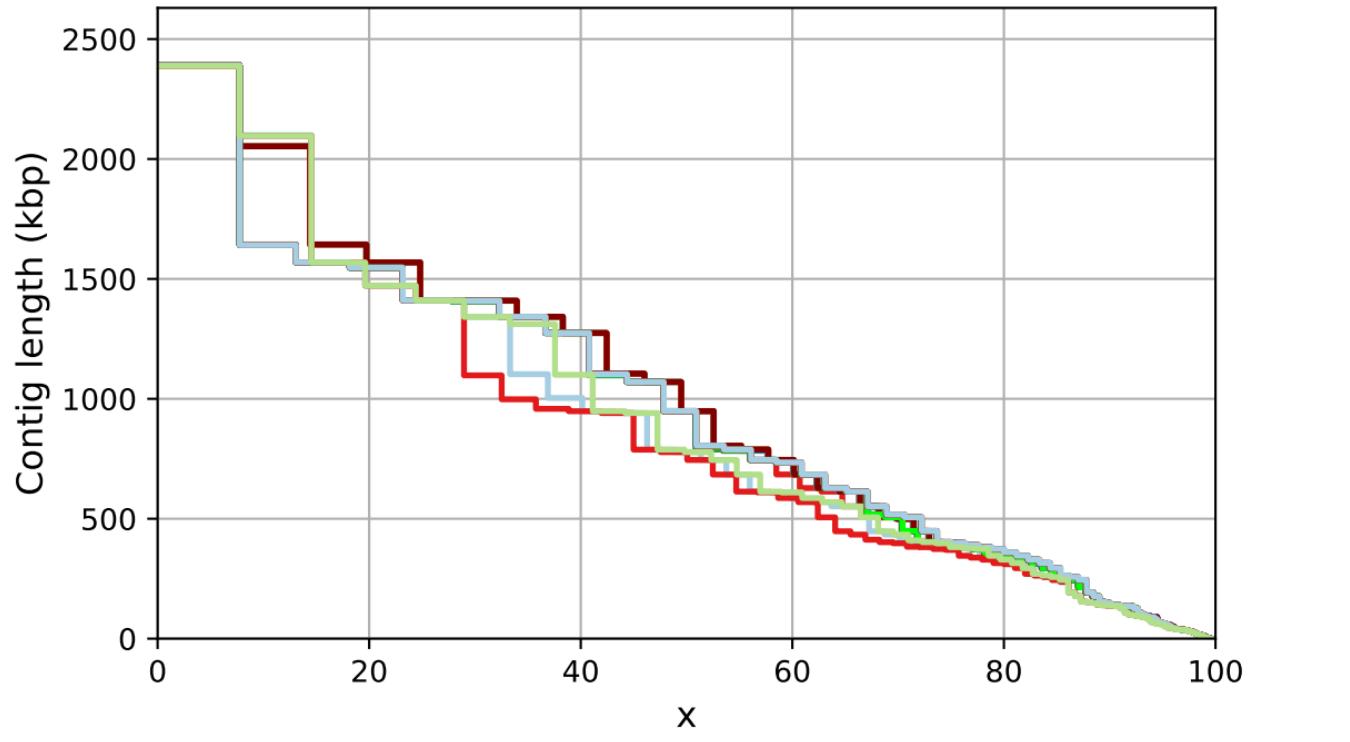
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

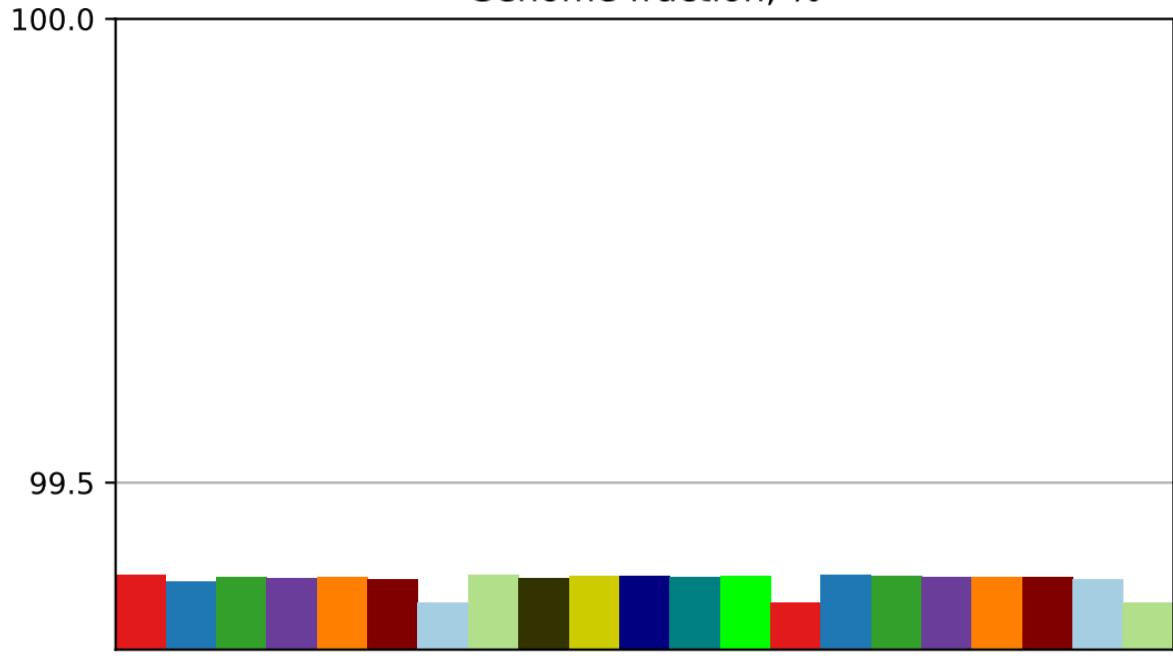
r10_2bins_v2_3_r3

NAx



0_2bins_v2_1_MP
0_2bins_v2_1_MP_helen
0_2bins_v2_1_r1_medaka
0_2bins_v2_1_r2_medaka
r10_2bins_v2_2_MP
r10_2bins_v2_2_MP_helen
r10_2bins_v2_2_r1_medaka
r10_2bins_v2_2_r2_medaka
r10_2bins_v2_3_MP
r10_2bins_v2_3_MP_helen
r10_2bins_v2_3_r1_medaka
r10_2bins_v2_3_r2_medaka

Genome fraction, %



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_

r10_2bins_v2_3_r2_