

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_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw			
# contigs (>= 5000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8			
# contigs (>= 10000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8			
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8			
# contigs (>= 50000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8			
Total length (>= 5000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 10000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 25000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 50000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# contigs	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8		
Largest contig	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718	
Total length	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
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	49.50	50.69	49.50	49.51	49.50	49.49	49.48	49.50	49.51	49.50	49.50	49.49	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	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758065	4757922	4757649	4756088	4758954	4757856	4758593	4758140	4757950	4757852	4756101	
NG50	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792243	6791577	6791686	6787718	6792252	6792243	6791577	6791686	6787718			
N75	2992083	2992068	2992071	2992074	2991989	2991964	2990667	2992084	2992066	2992071	2991914	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633		
NG75	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792243	6791577	6791686	6787718	6792252	6792243	6791577	6791686	6787718			
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	10	6	6	6	6	6	6	6	6	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	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6791577	6791686	6787718	6792252	6792198	6792243	6791577	6791686	6787718		
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	29	11	11	11	11	11	29		
# 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	6	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 + 7 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	24046874	24042487	24044291	24033589	24032131	24026773	21233862	24047726	24043803	24044012	24035756	24032504	24029144	24078261	24047588	24044416	24028070	24033065	24024838	24076495	
Genome fraction (%)	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.864		
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	1.015	1.015	1.015	1.015	1.015	1.015	1.008		
# 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	58.73	56.18	56.60	56.66	59.56	58.80	64.65	58.40	56.18	57.18	56.51	59.43	58.33	64.73	58.41	56.24	56.56	56.51	58.71	58.89	65.49
# indels per 100 kbp	5.42	5.06	3.60																		

Misassemblies report

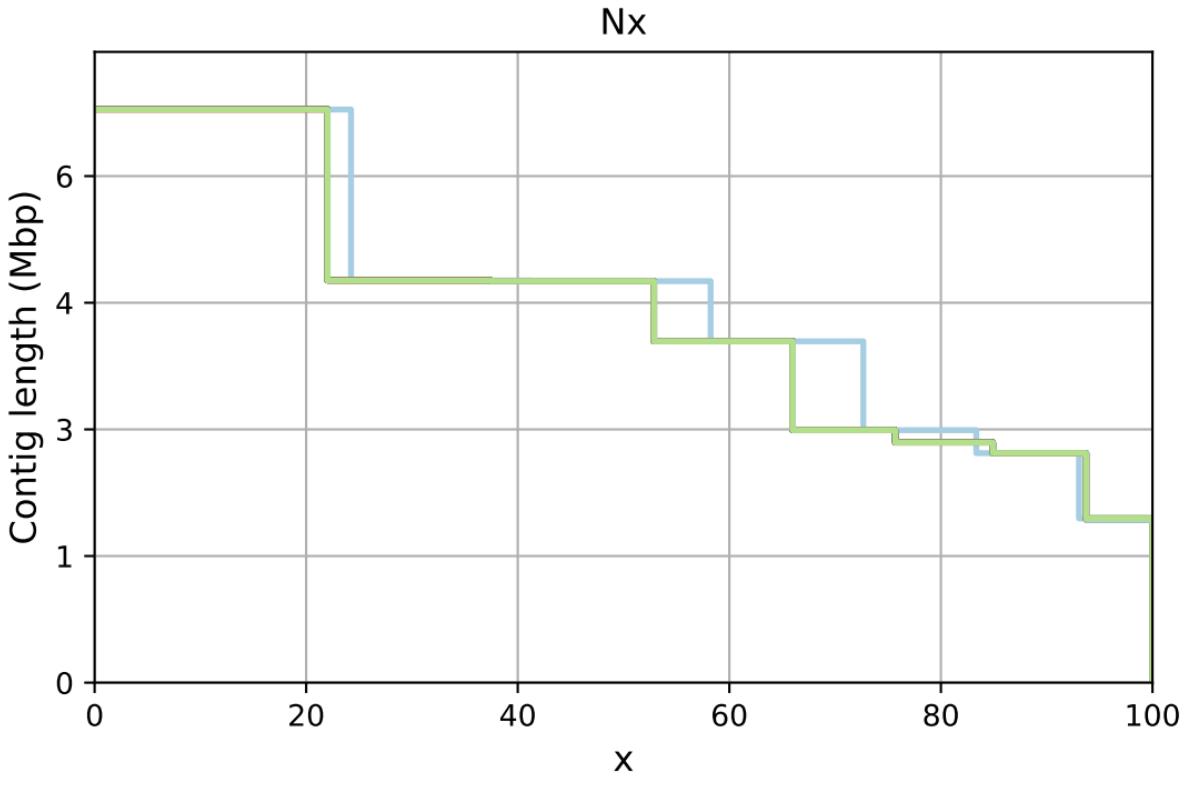
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# misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	6	6	6	6	10			
# contig misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	6	6	6	6	10			
# c. relocations	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
# c. translocations	7	6	6	6	6	6	10	6	6	6	6	6	6	6	6	6	6	10			
# c. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
# 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			
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
Misassembled contigs length	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6791577	6791686	6787718		
# possibly misassembled contigs	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	18	18	18	18	18	18	18	18	18	18	34			
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	11	11	11	11	11	29			
# scaffold gap ext. mis.	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			
# misassemblies caused by fragmented reference	20	21	21	21	21	21	16	21	21	21	21	21	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			
# mismatches	3947	3776	3804	3808	4003	3952	4344	3925	3776	3843	3798	3994	3920	4349	3926	3780	3801	3798	3946	3958	4400
# indels	364	340	242	241	980	904	6534	369	346	243	242	959	907	6504	368	346	244	243	961	909	6498
# indels (<= 5 bp)	269	243	148	147	886	808	6411	273	248	149	148	864	812	6383	272	248	150	149	866	814	6377
# indels (> 5 bp)	95	97	94	94	94	96	123	96	98	94	94	95	121	96	98	94	95	95	121		
Indels length	5394	5400	5259	5258	6103	6027	12929	5412	5261	5258	6021	12818	5411	5262	5259	6023	12810				

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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24046874	24042487	24044291	24033589	24032131	24047726	24043803	24044012	24035756	24032504	24029144	24078261	24044048	24044016	24028070	24033065	24024838	24076495
# 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

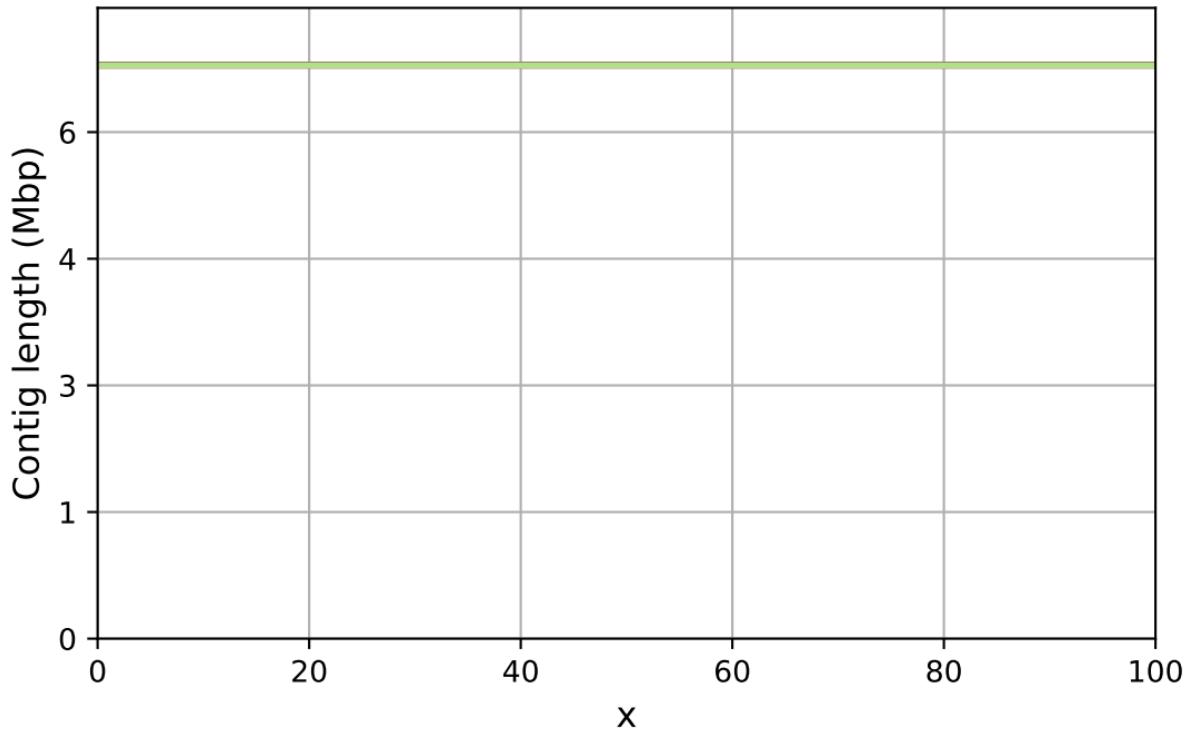
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

NGx



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

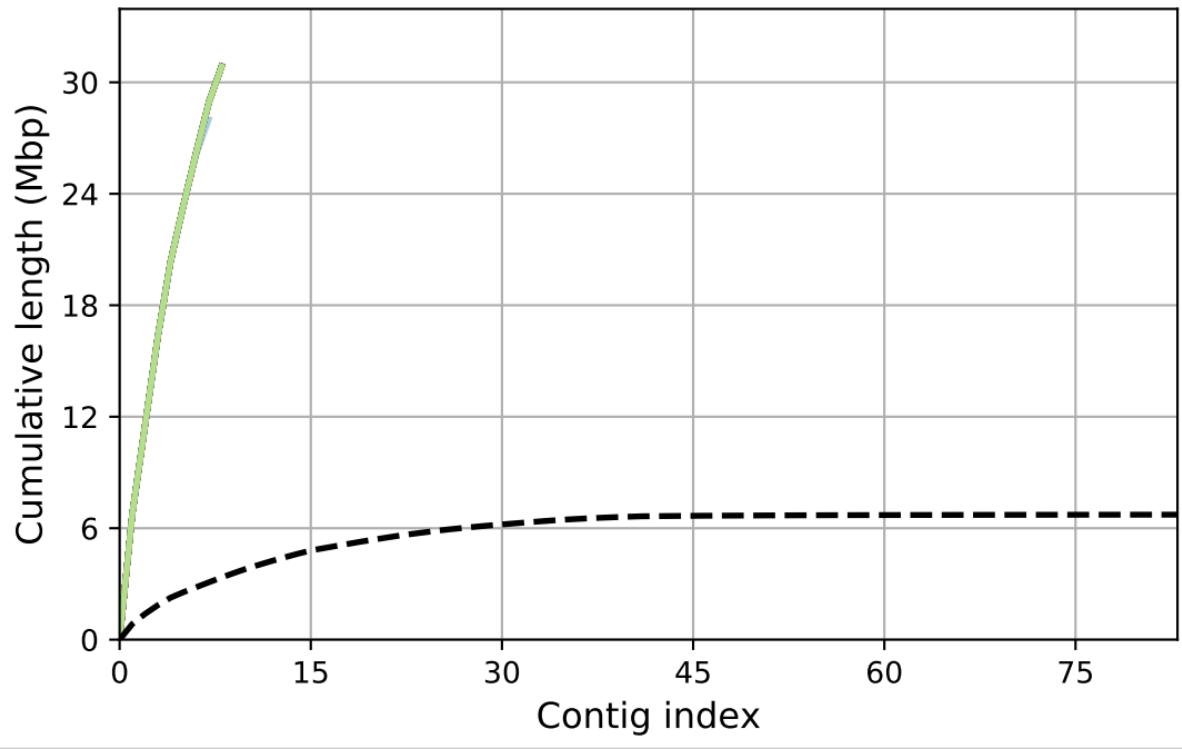
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r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length



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

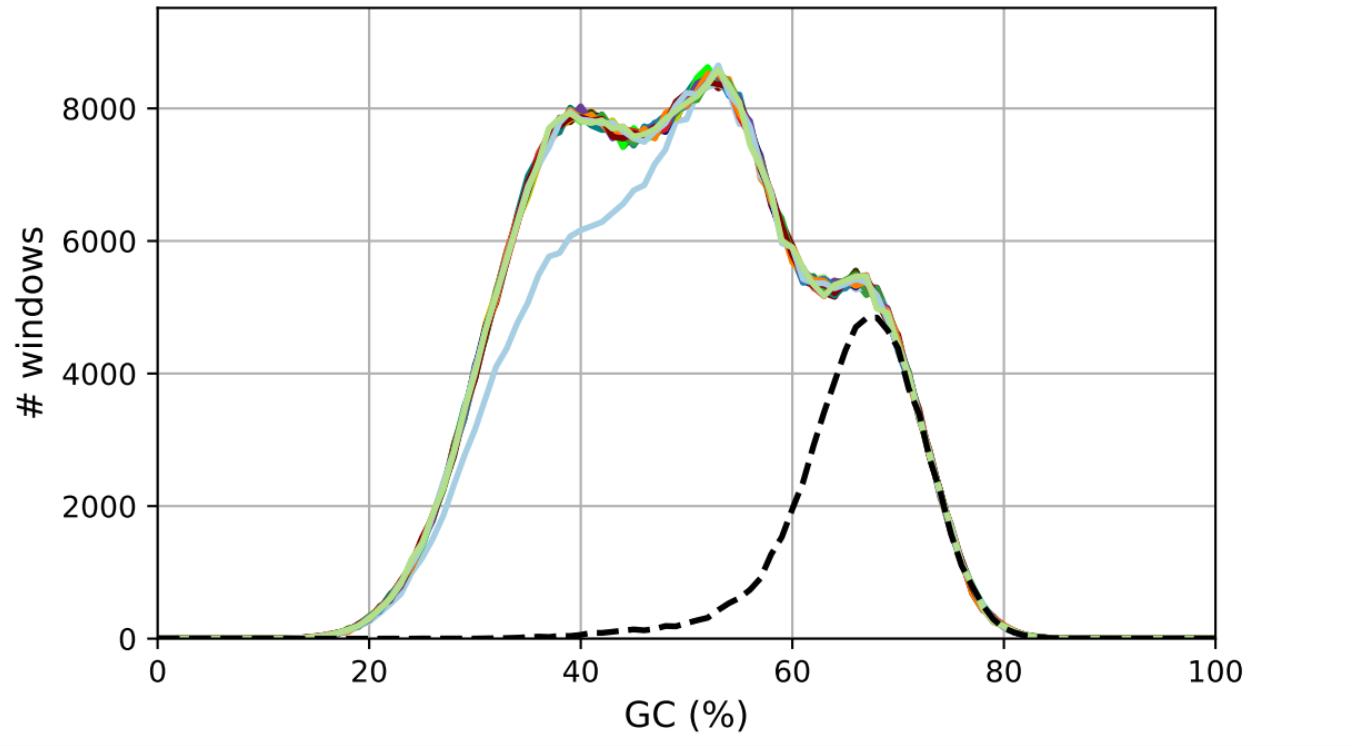
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_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

— r10_2bins_v2_2_r2_medaka

— r10_2bins_v2_2_racon_r1

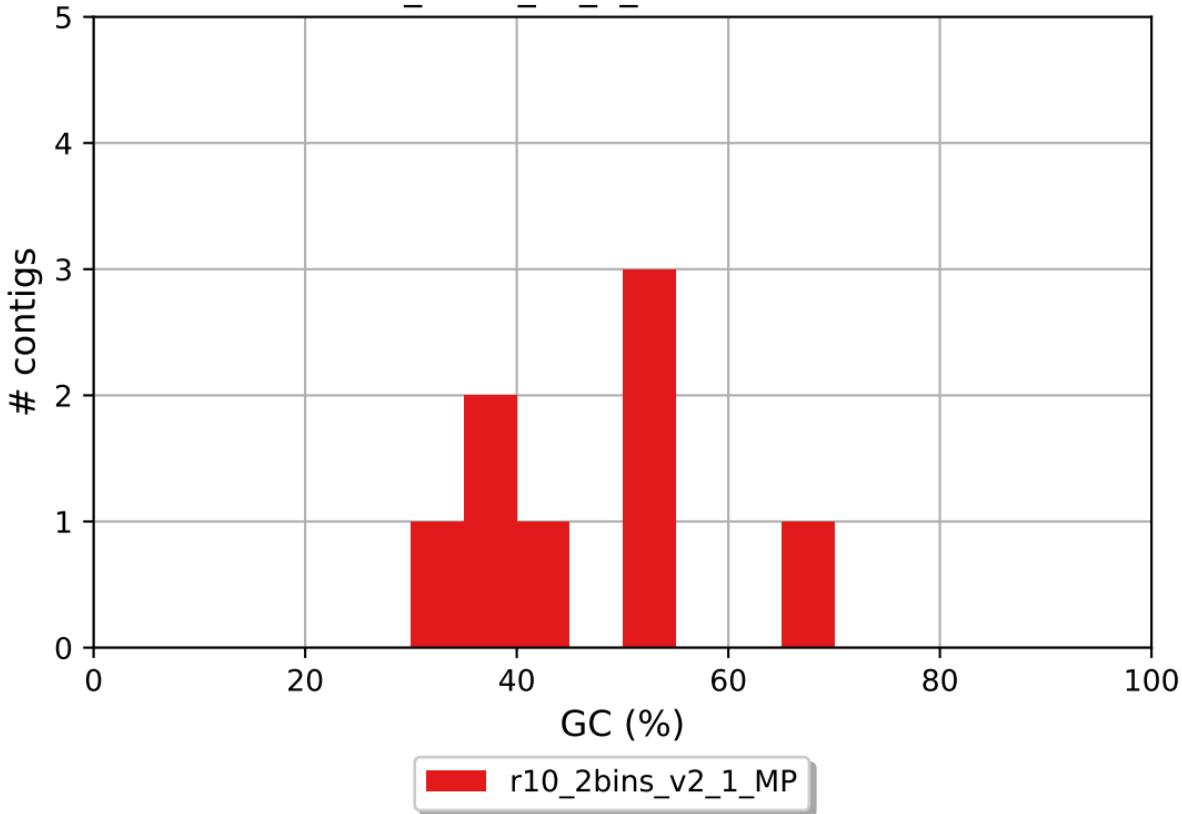
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— r10_2bins_v2_3_r1

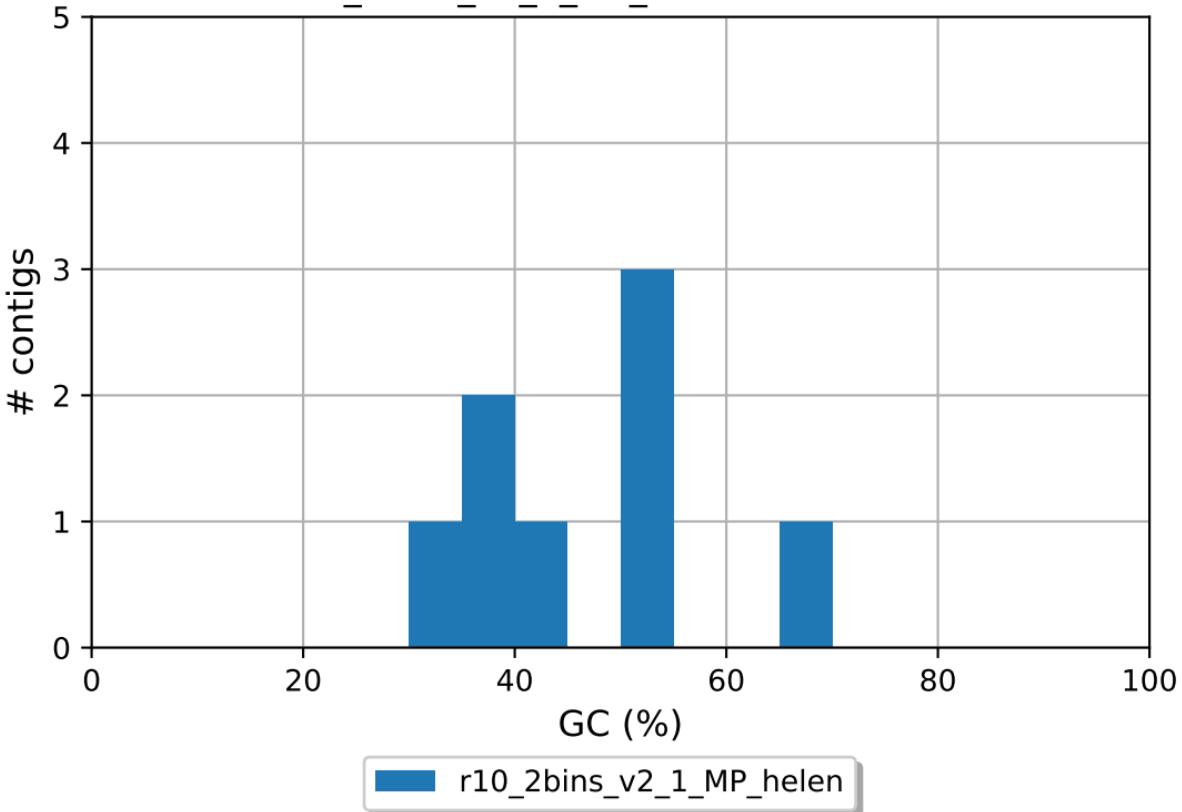
— r10_2bins_v2_3_r2

— r10_2bins_v2_3_racoon

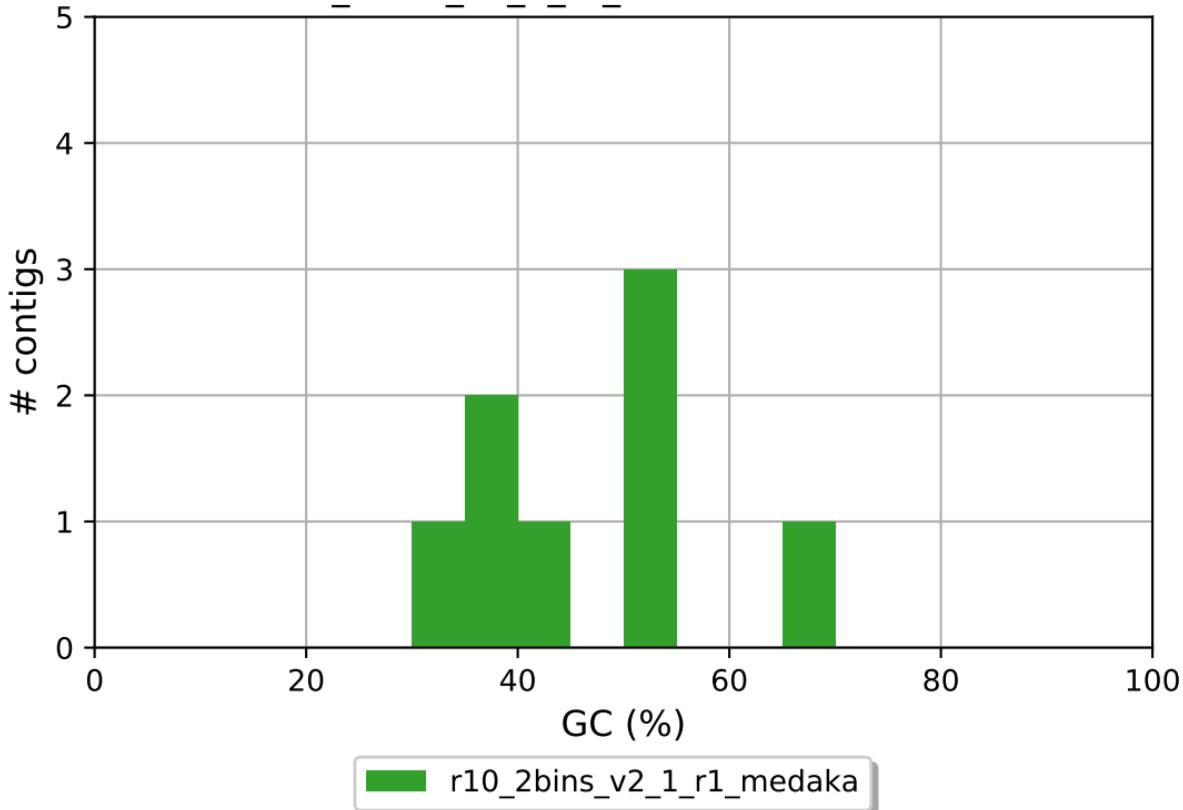
r10_2bins_v2_1_MP GC content



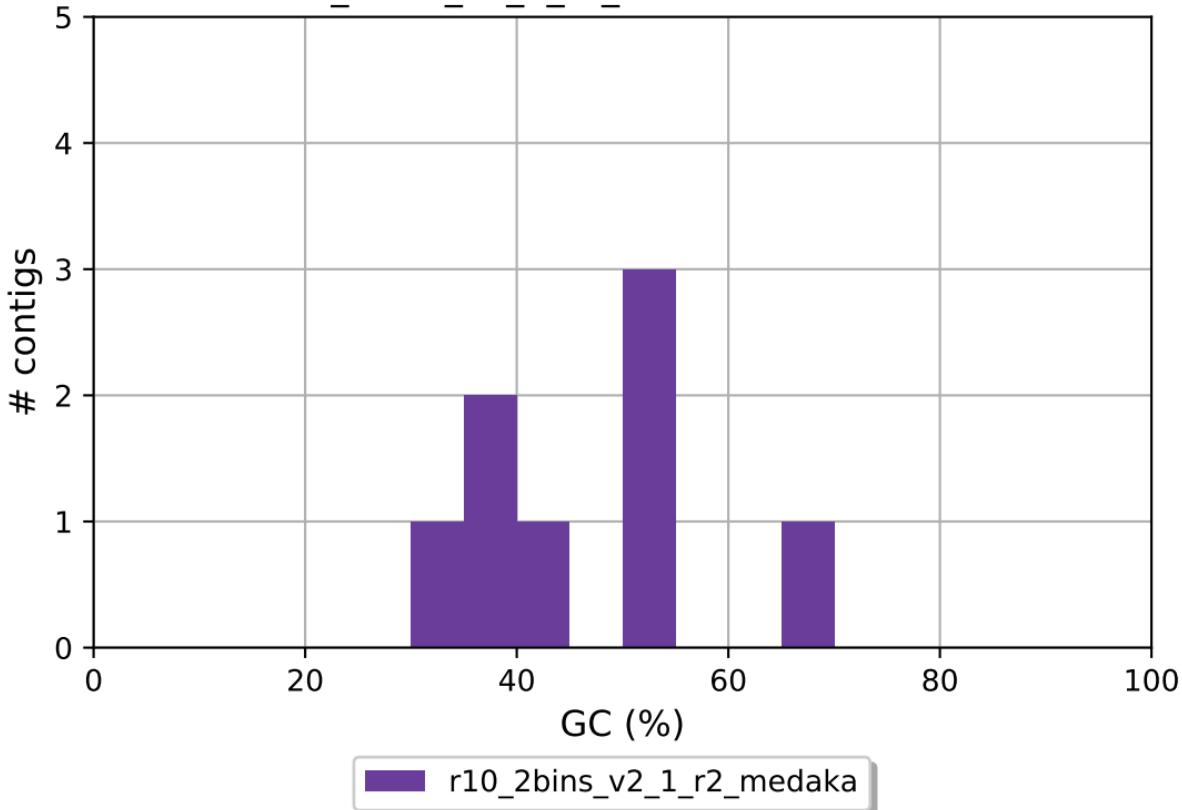
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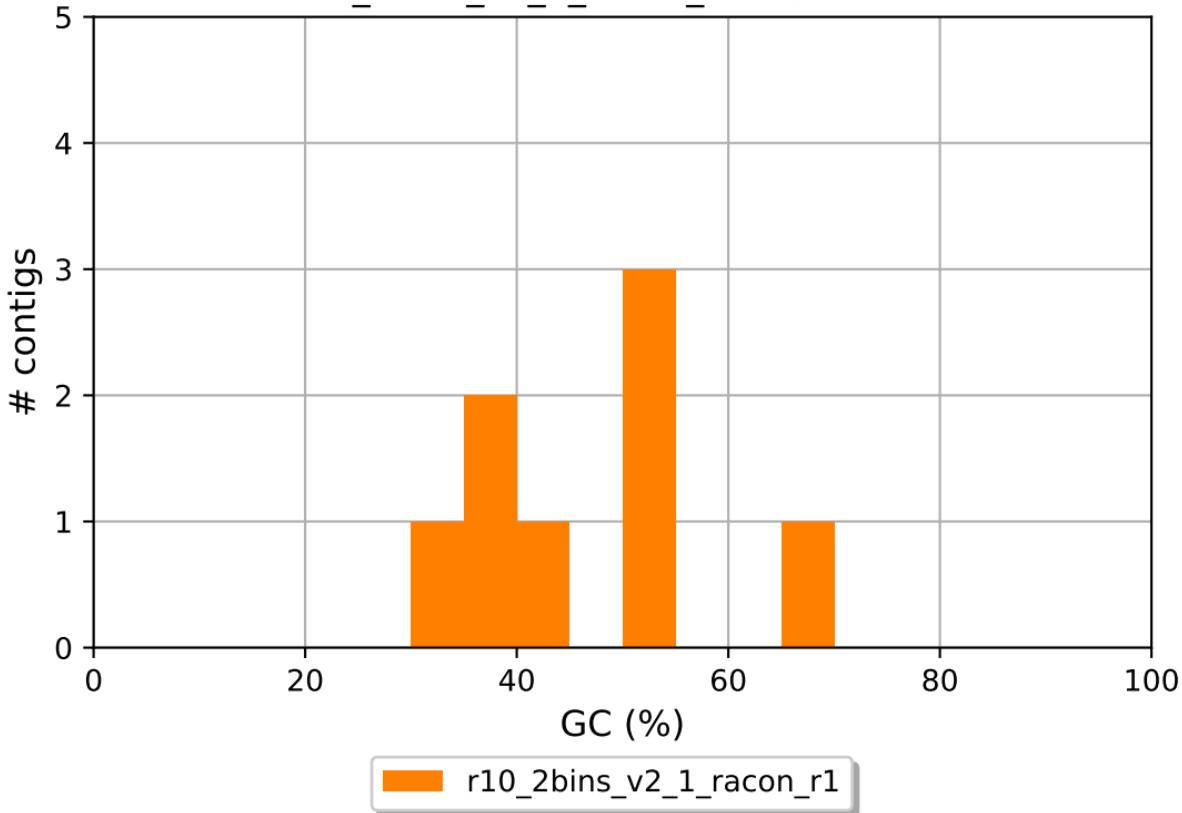
r10_2bins_v2_1_r1_medaka GC content



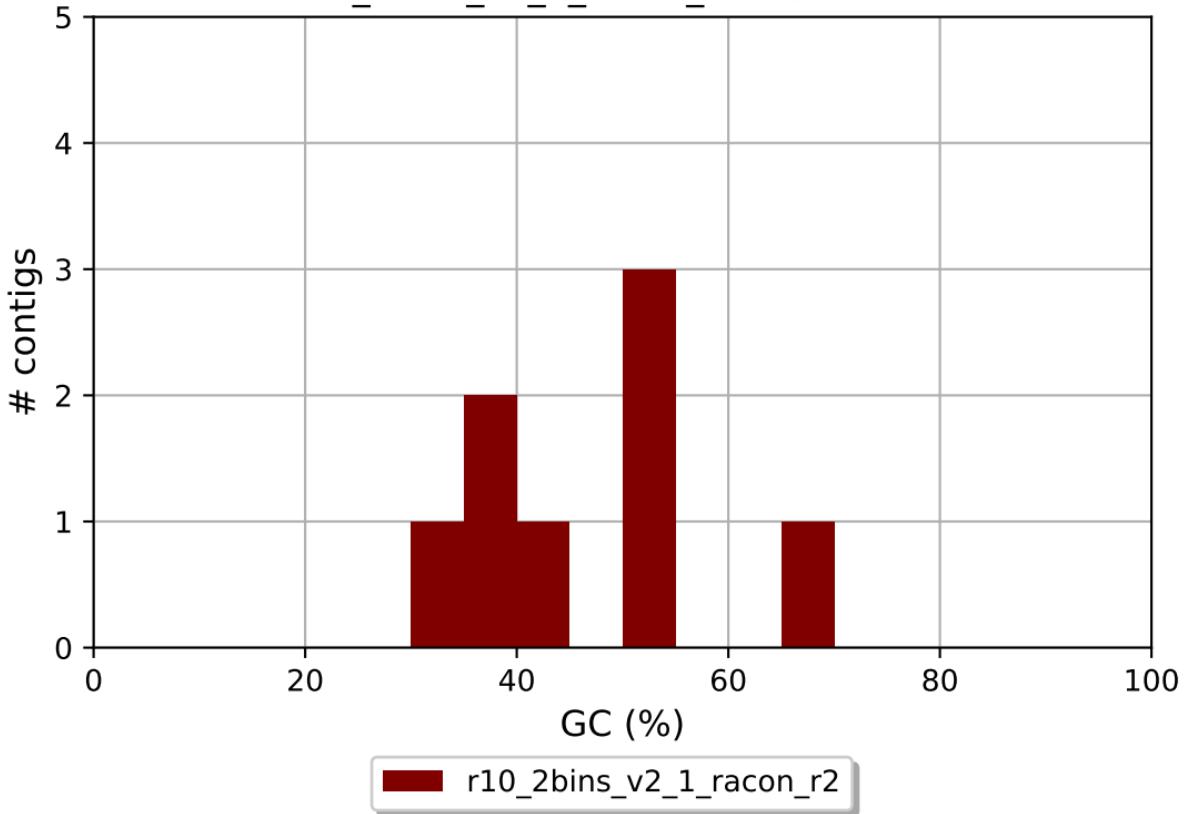
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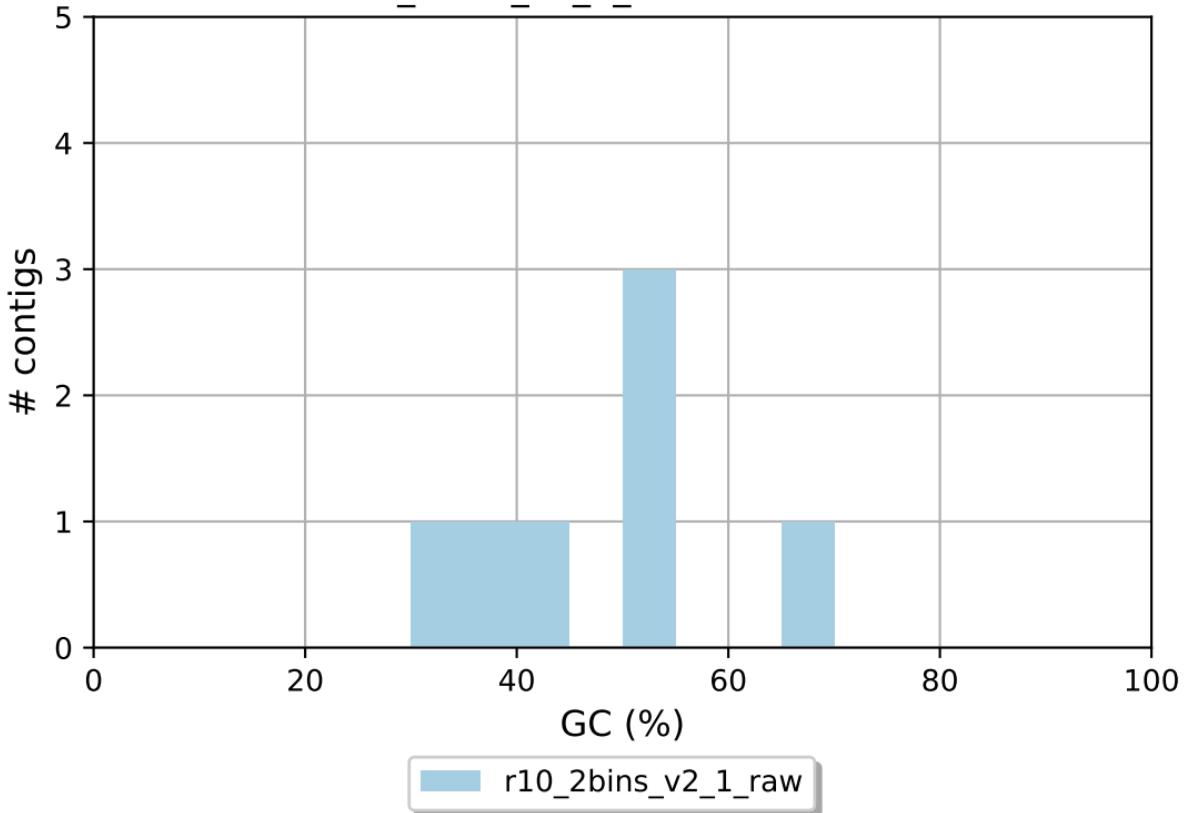
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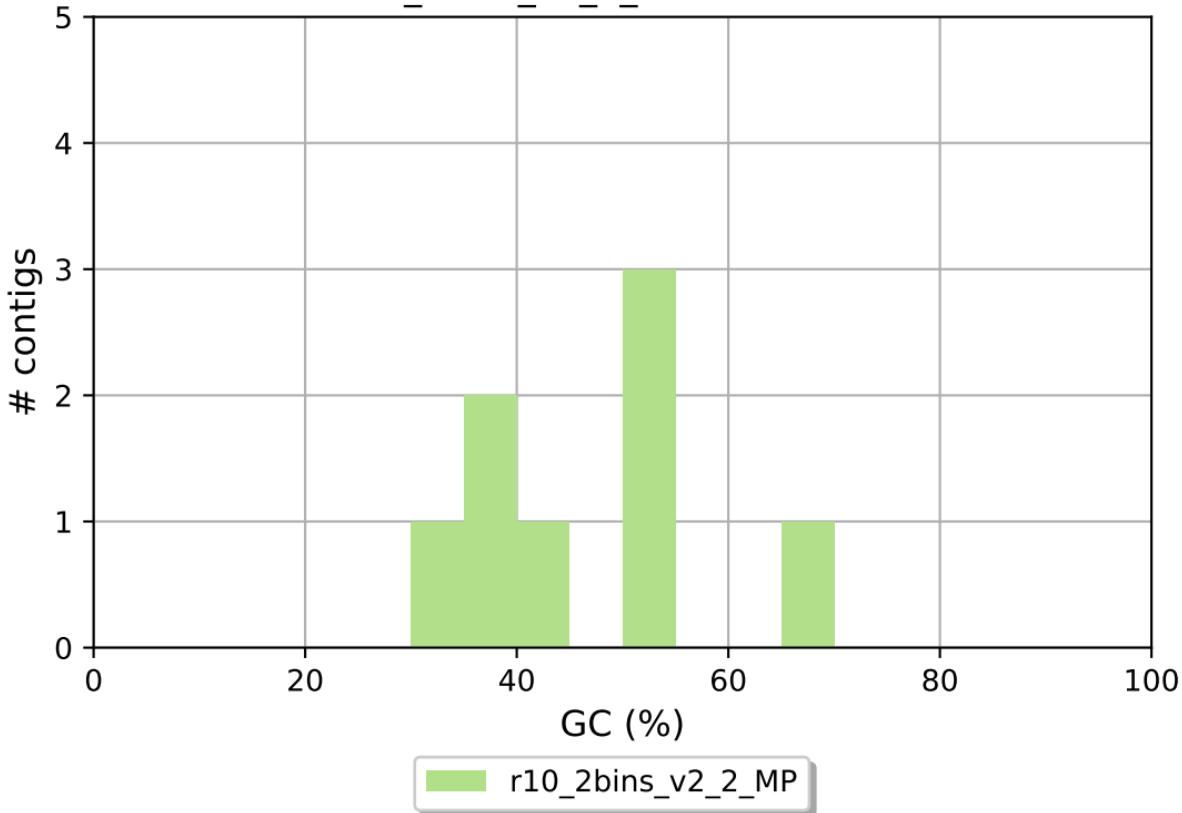
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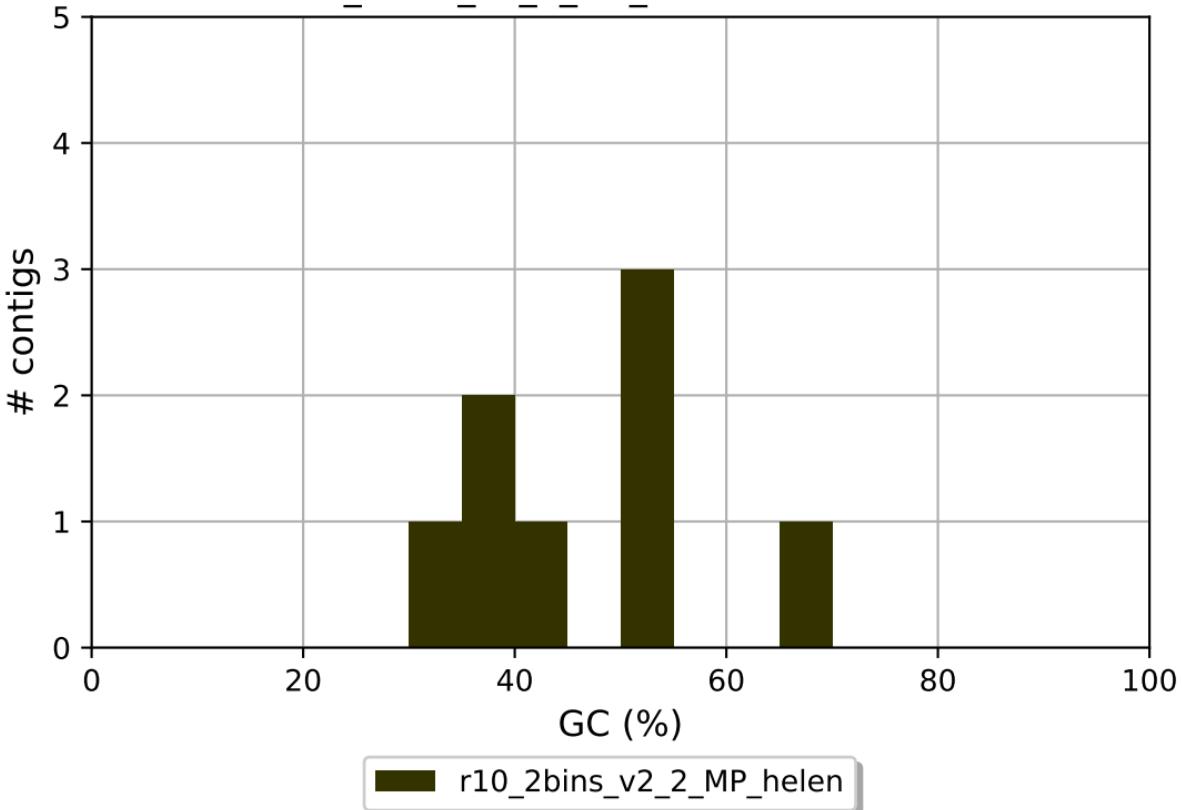
r10_2bins_v2_1_raw GC content



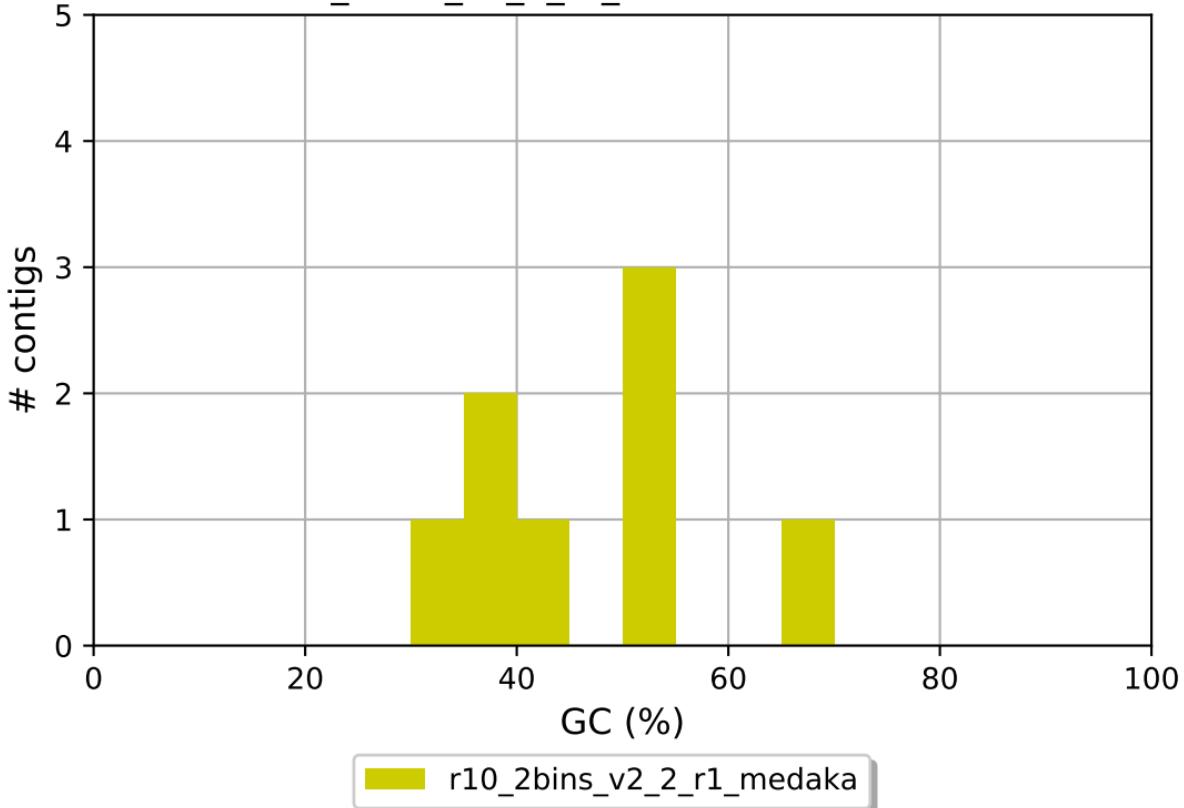
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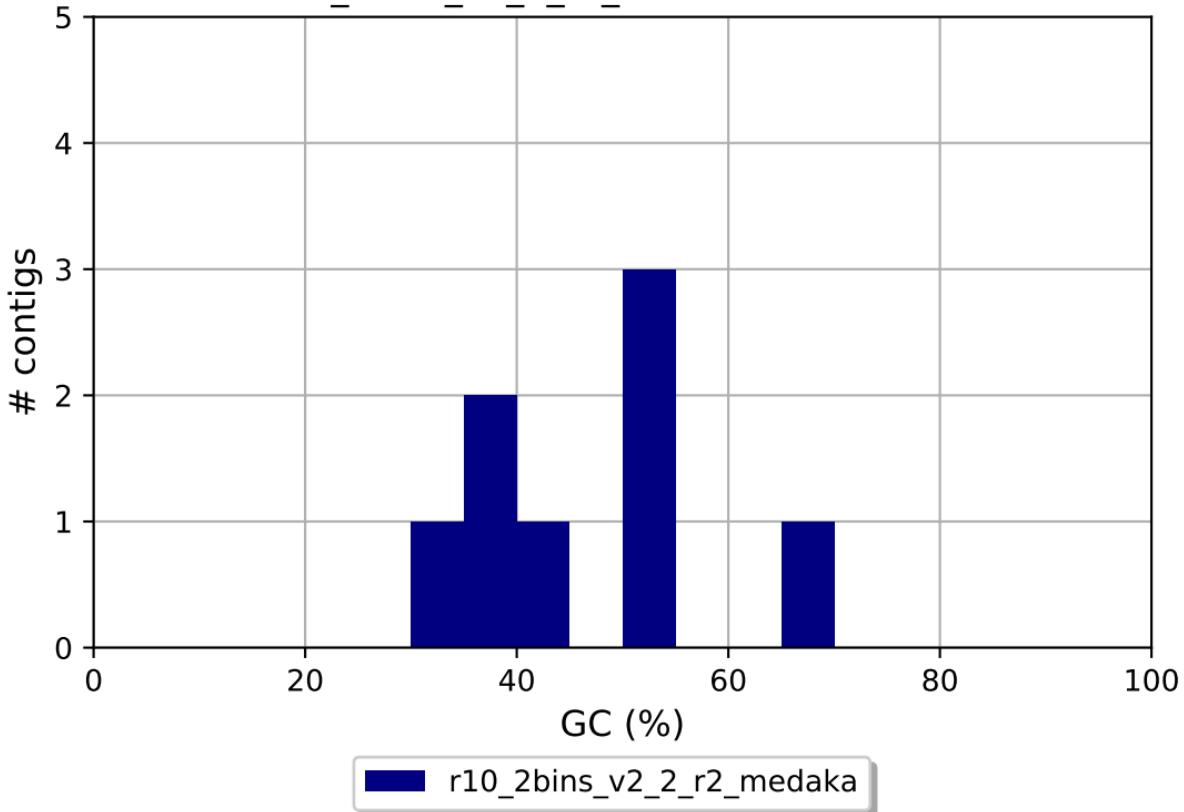
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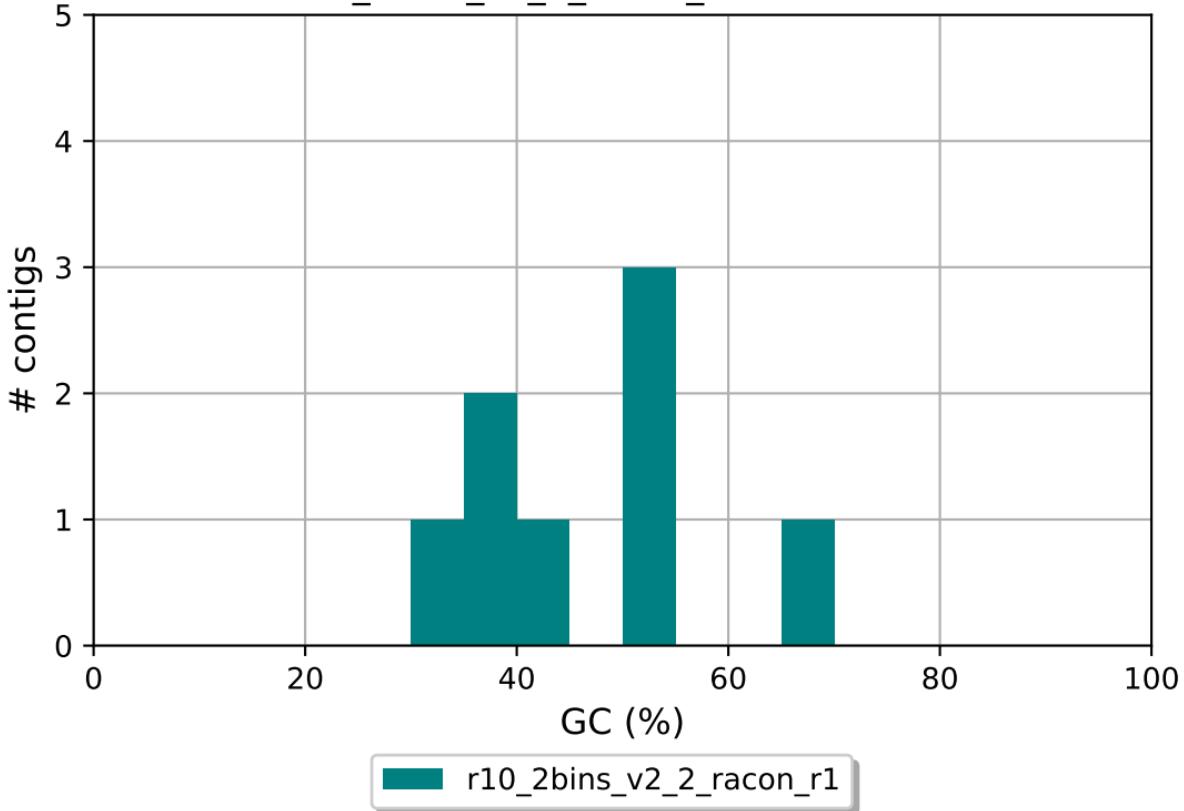
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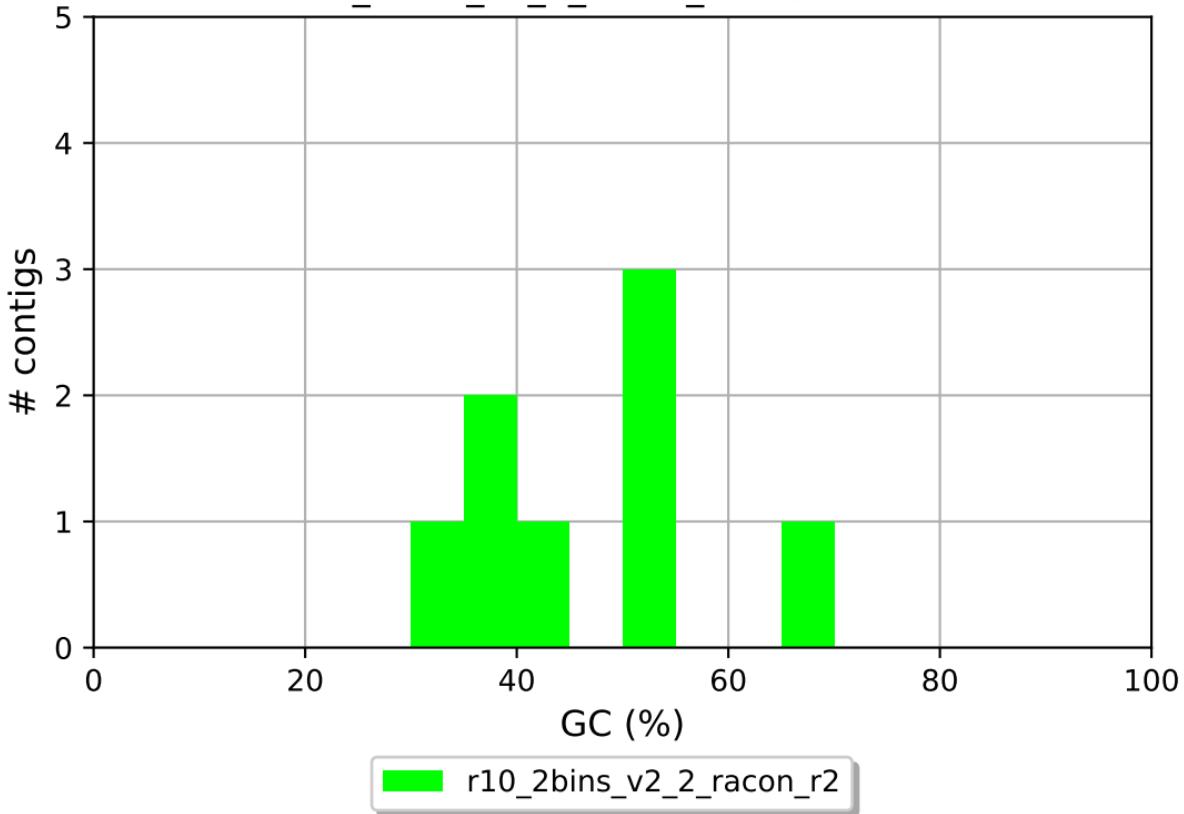
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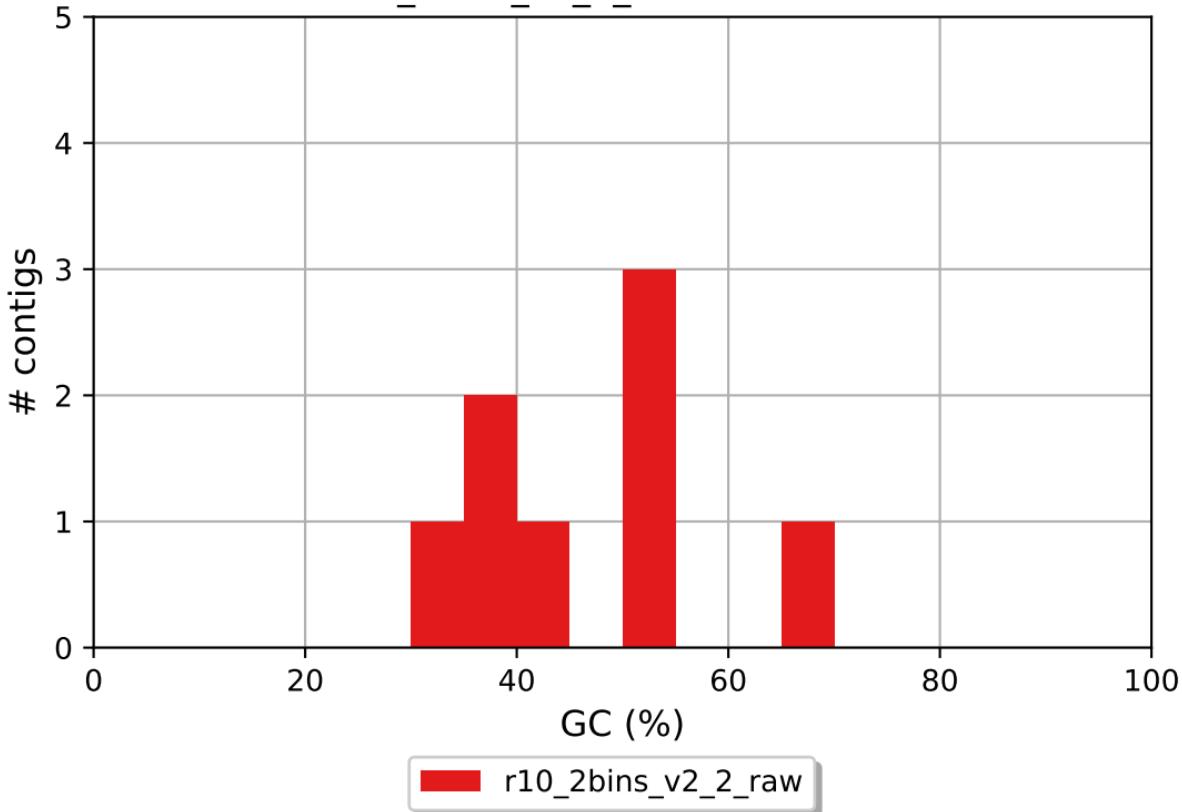
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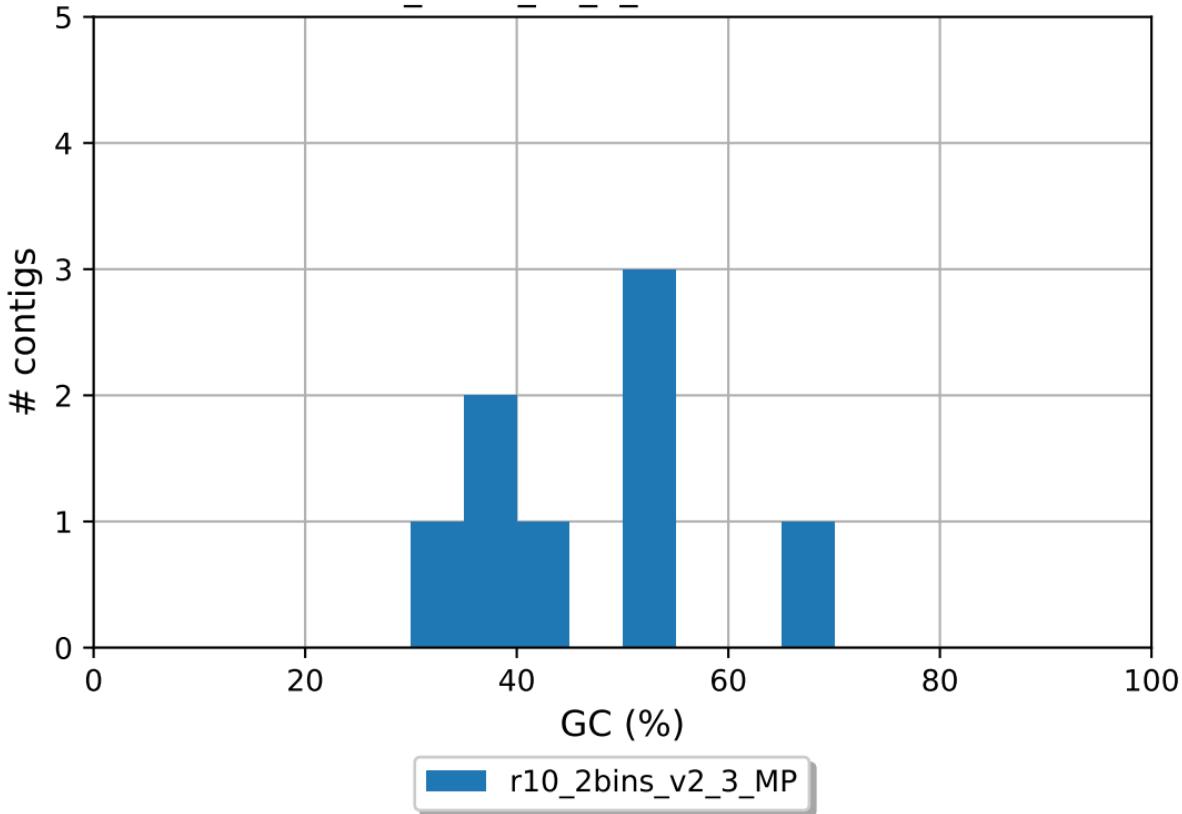
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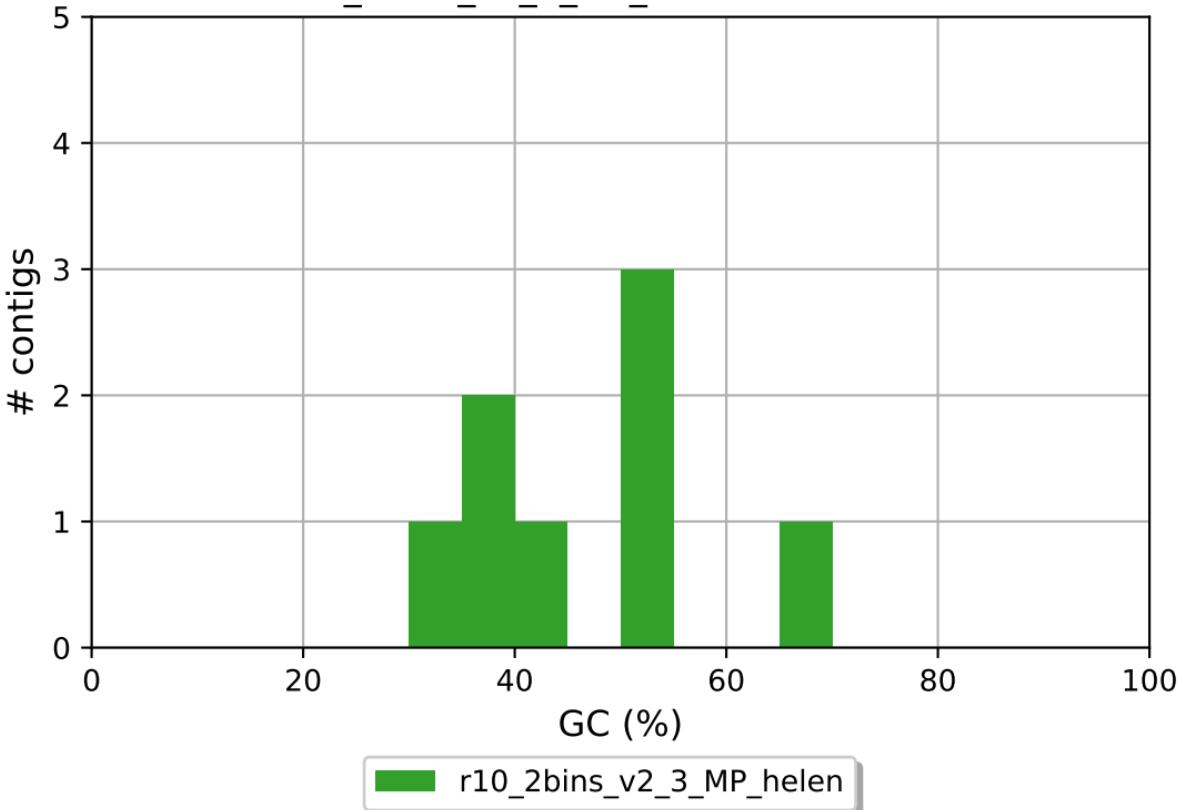
r10_2bins_v2_2_raw GC content



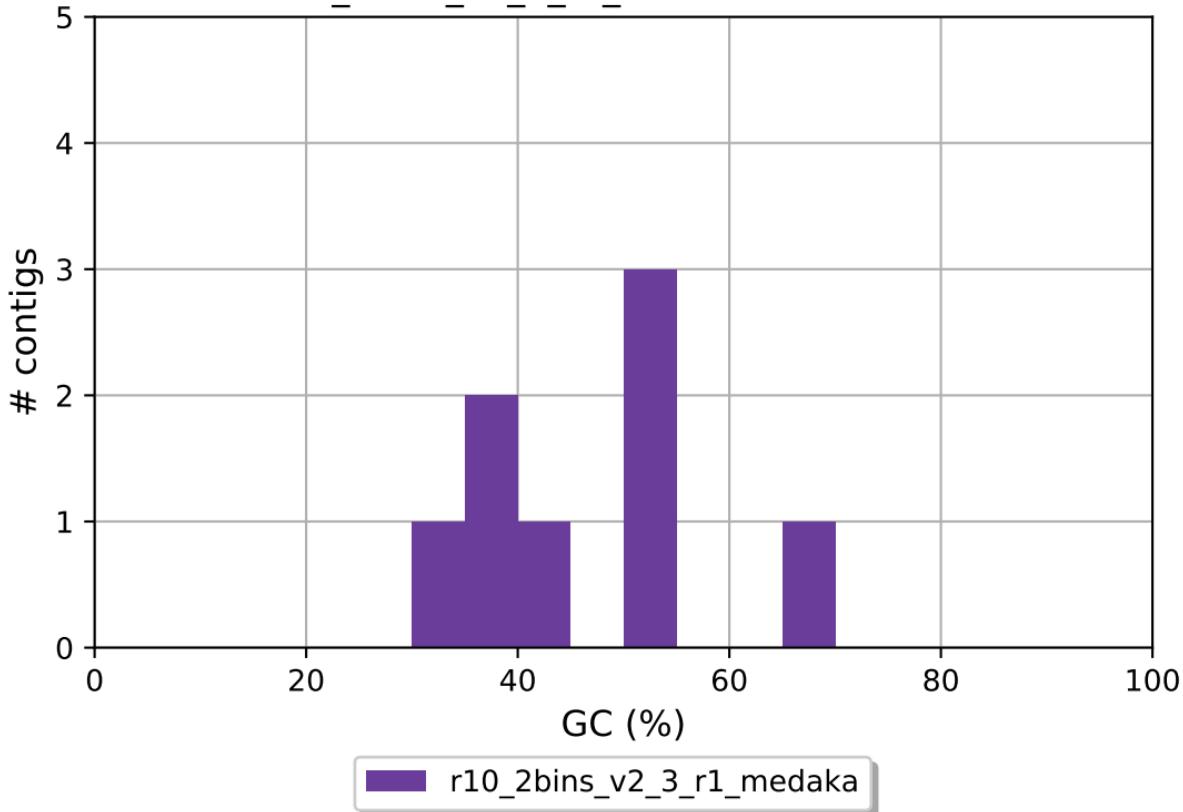
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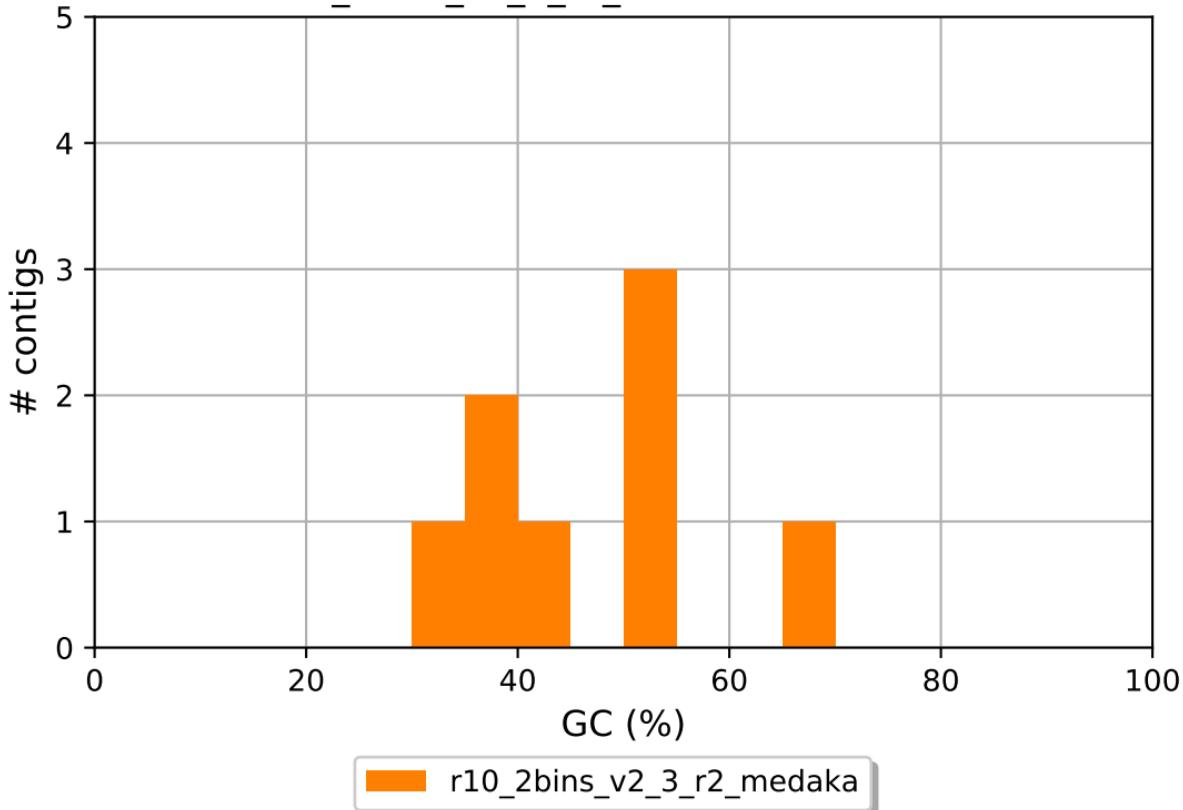
r10_2bins_v2_3_MP_helen GC content



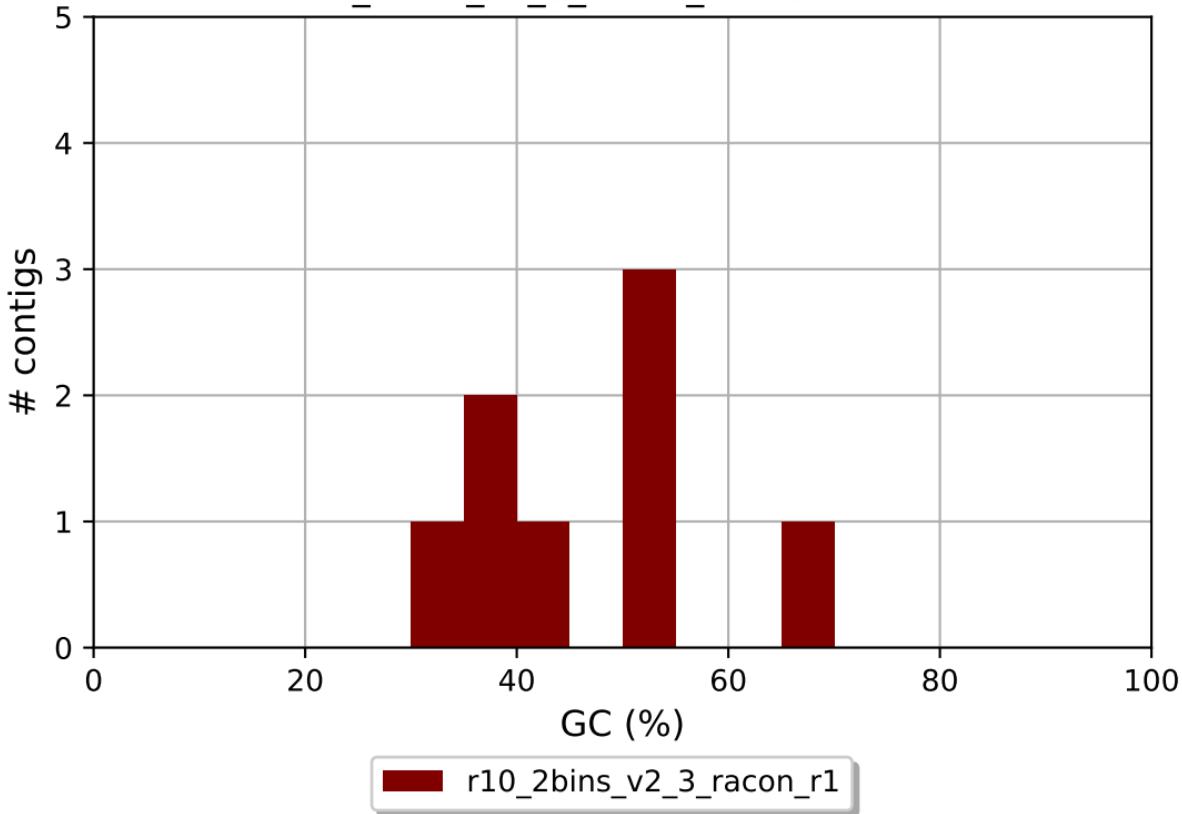
r10_2bins_v2_3_r1_medaka GC content



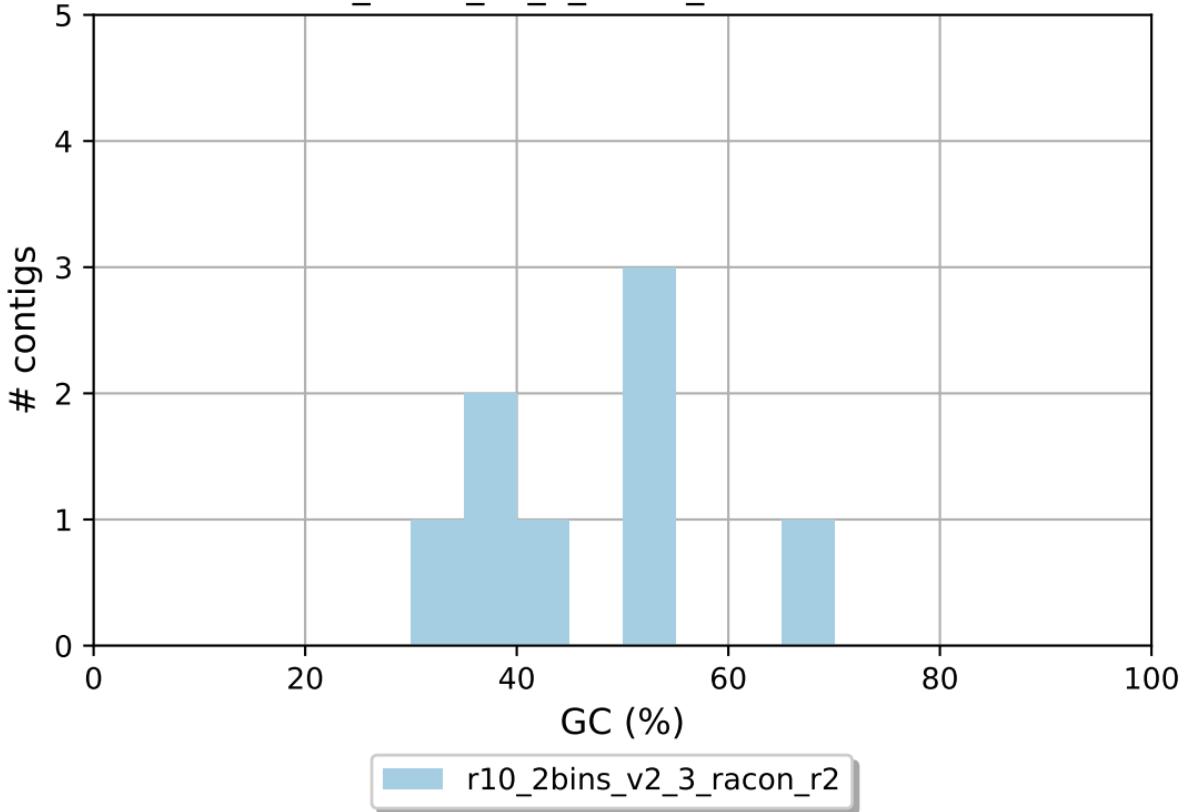
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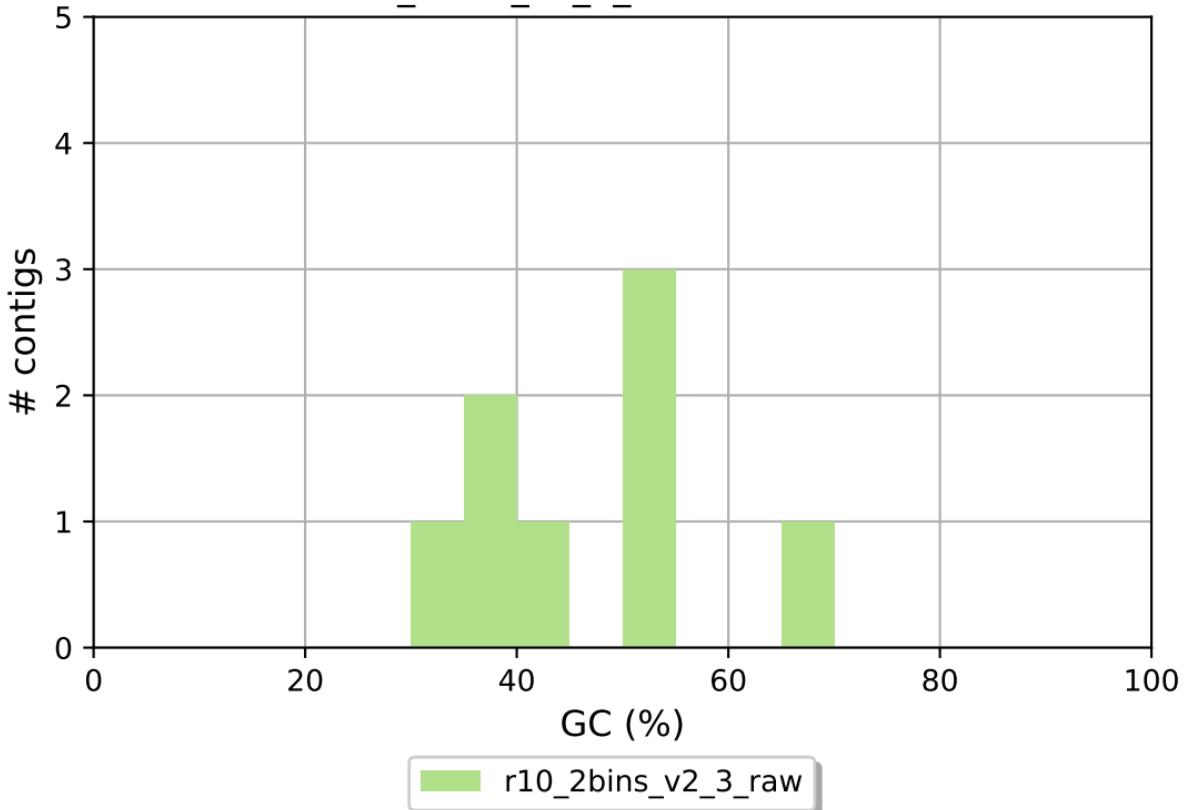
r10_2bins_v2_3_racon_r1 GC content



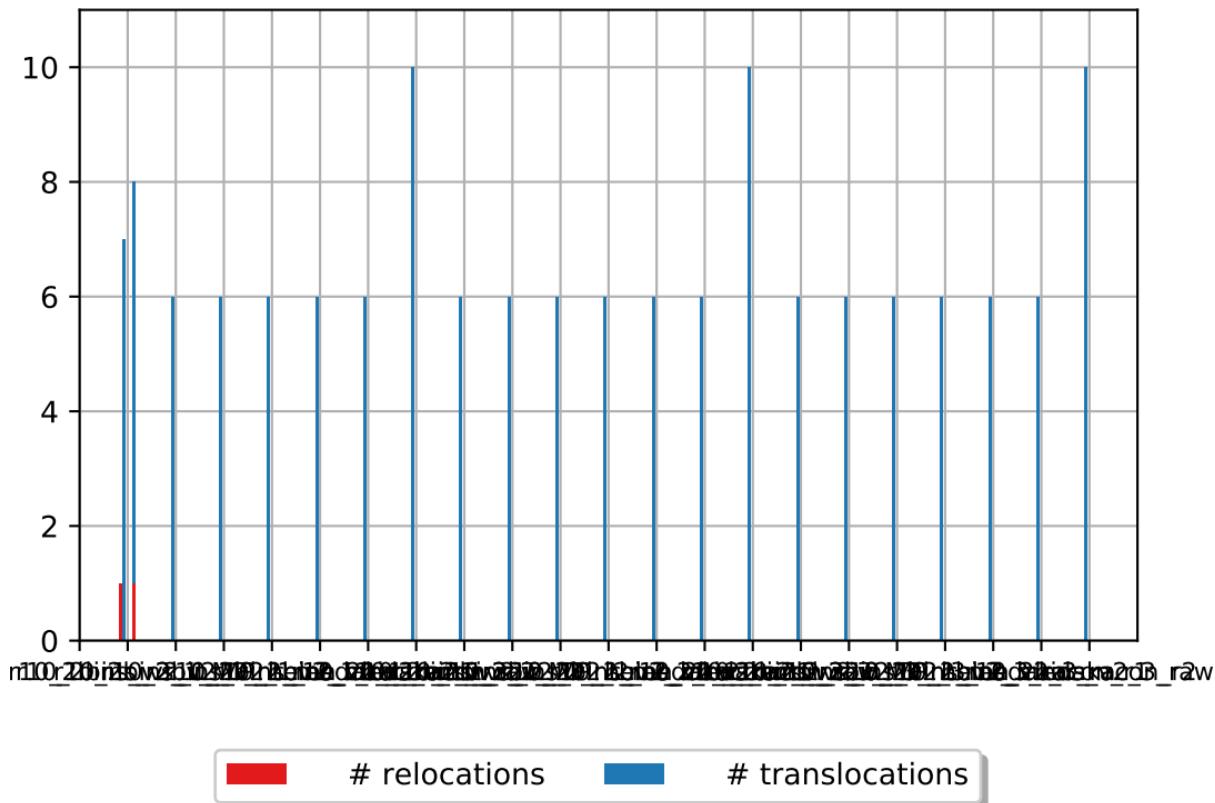
r10_2bins_v2_3_racon_r2 GC content



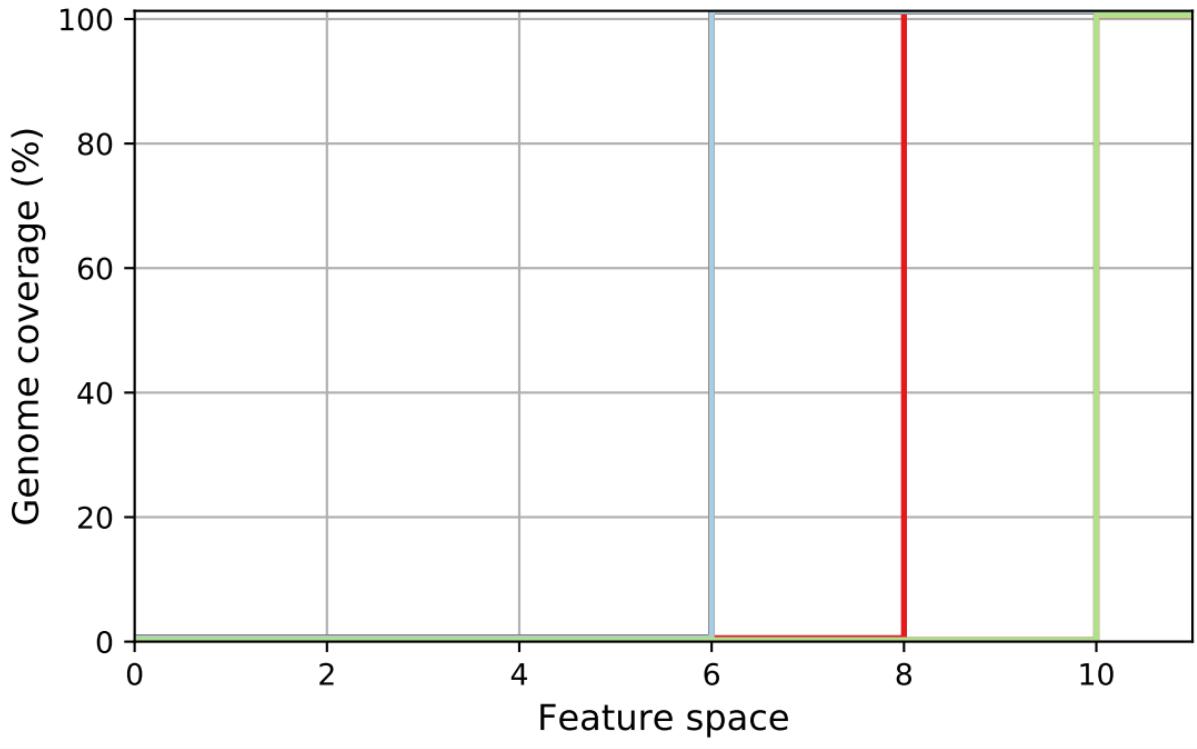
r10_2bins_v2_3_raw GC content



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

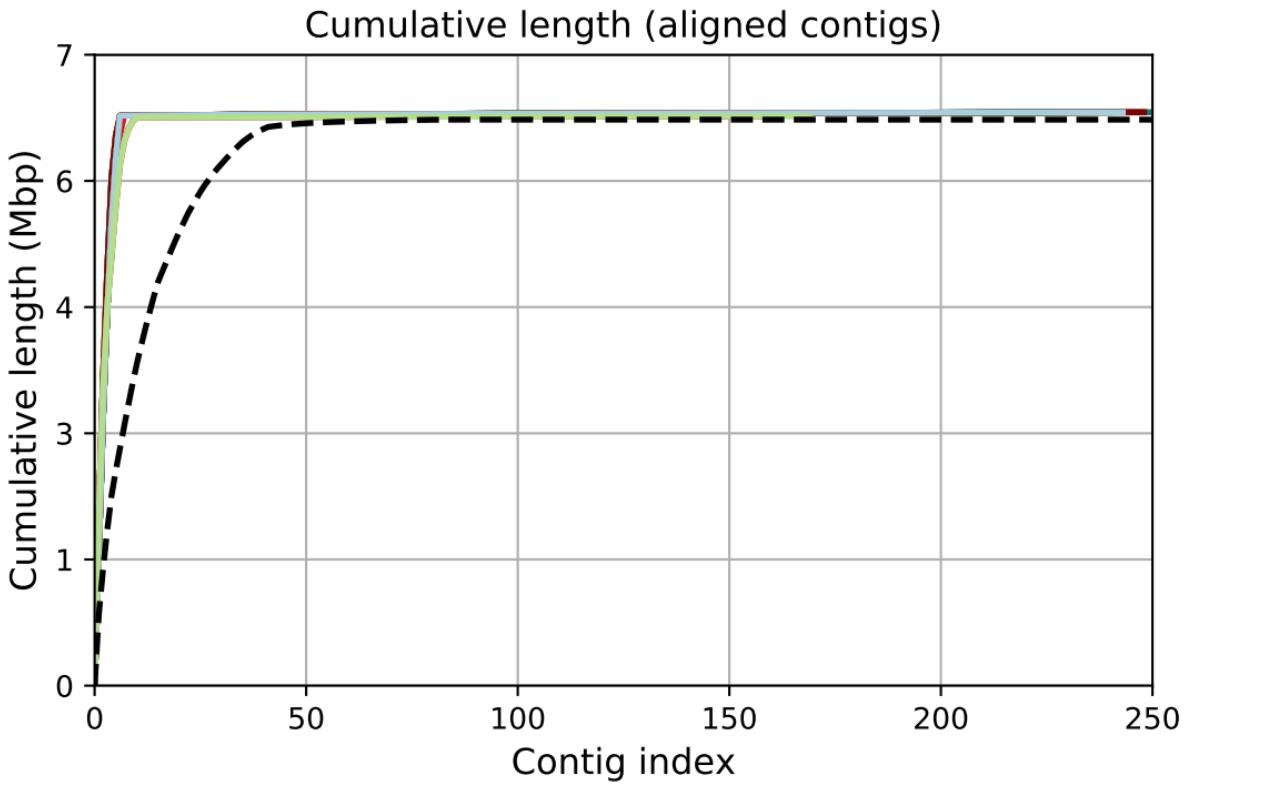
r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2



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

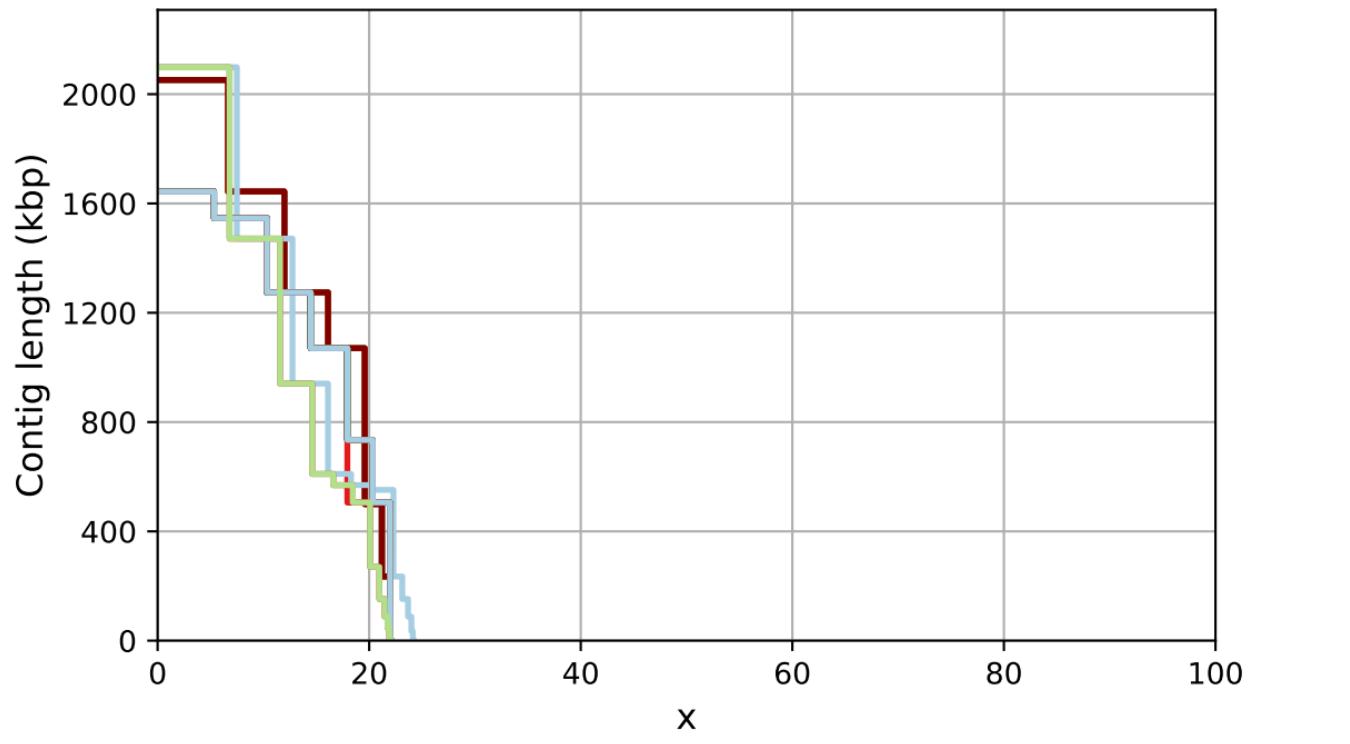
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_rac

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

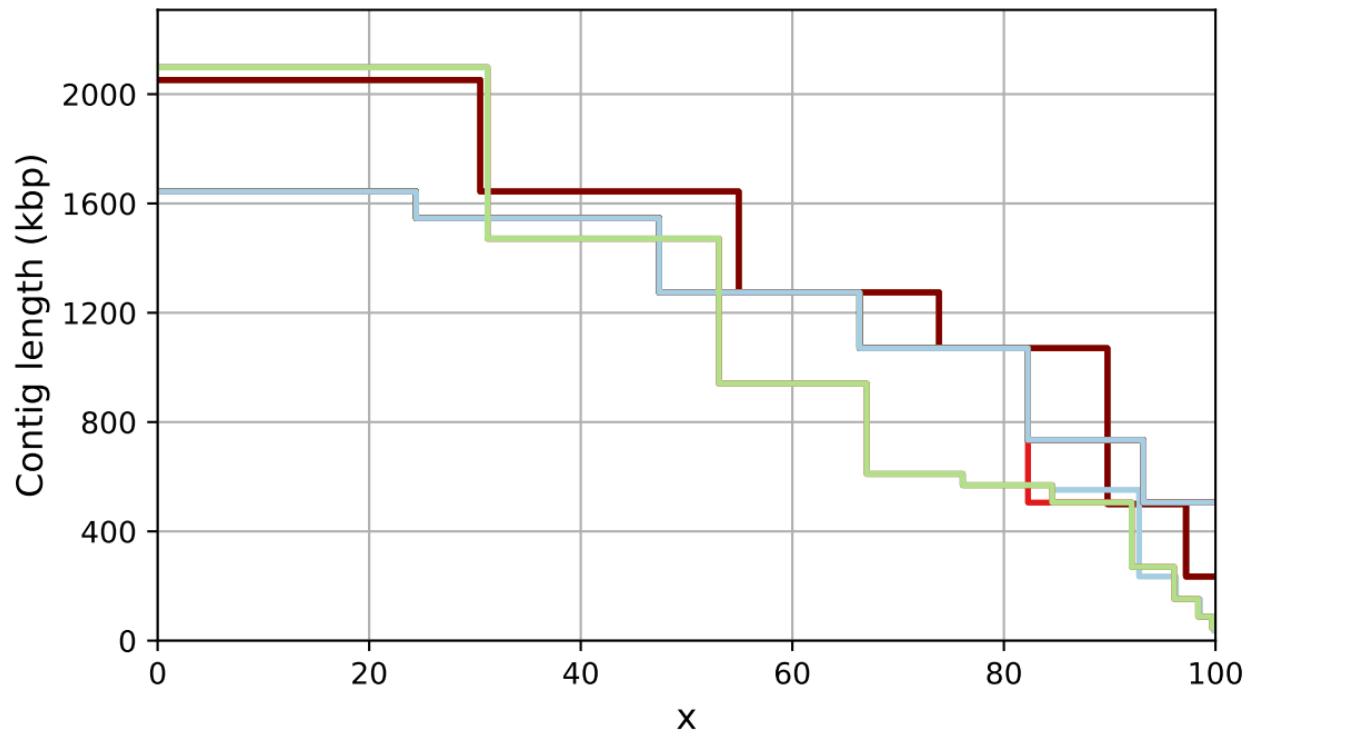
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

NGAx



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

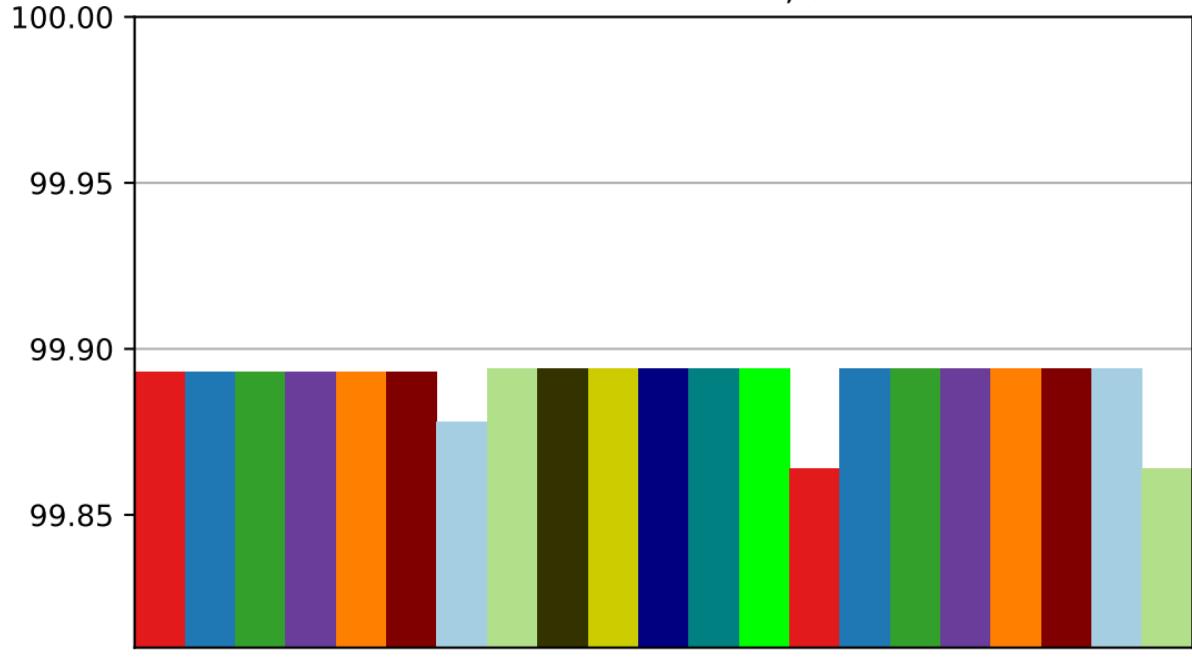
r10_2bins_v2_3_MP

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