

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)	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			
# contigs (>= 25000 bp)	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			
Total length (>= 5000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7		
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4764595	4764670	4763481	
Total length	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205		
GC (%)	44.80	44.80	44.80	44.80	44.79	44.79	44.77	44.77	44.80	44.80	44.80	44.79	44.77	44.80	44.80	44.80	44.79	44.78	44.77		
Reference GC (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69		
N50	4045600	4045625	4045591	4045593	4045204	4045287	4043049	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045340	4042483	
NG50	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765354	4764595	4764670	4763481	
N75	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845321	2843857	2845424	2845363	2845431	2845321	2845321	2843845			
NG75	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765354	4764595	4764670	4763481	
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	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	2719574	2717922	2719543	2719562	2720329	2720423	2718431	2719745	2717983	2719603	2719633	2720494	2720498	2718867	2719589	2717938	2719539	2719544	2720372	2720459	2718437
# local misassemblies	10	9	9	9	10	10	20	9	9	9	9	10	19	9	9	9	10	9	19		
# 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	6	6	6	6	6	6	4	6	6	6	6	6	5	6	6	6	6	6	5		
# unaligned contigs	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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part		
Unaligned length	21274658	21271555	21273233	21261883	21263760	21253836	21322606	21275861	21273678	21273285	21265050	21263380	21257264	21320082	21274857	21273023	21273407	21256346	21265173	21252622	21318452
Genome fraction (%)	99.537	99.537	99.537	99.537	99.537	99.537	99.538	99.537	99.537	99.537	99.537	99.537	99.537	99.537	99.537	99.537	99.537	99.537	99.538		
Duplication ratio	1.046	1.045	1.046	1.046	1.045	1.046	1.023	1.046	1.045	1.046	1.045	1.045	1.046	1.024	1.046	1.045	1.046	1.044	1.046	1.024	
# N's per 100 kbp	0.00	0.04	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	286.80	257.07	286.73	289.01	284.67	299.50	244.40	283.37	252.13	287.36	283.85	285.16	291.14	255.89	286.77						

Misassemblies report

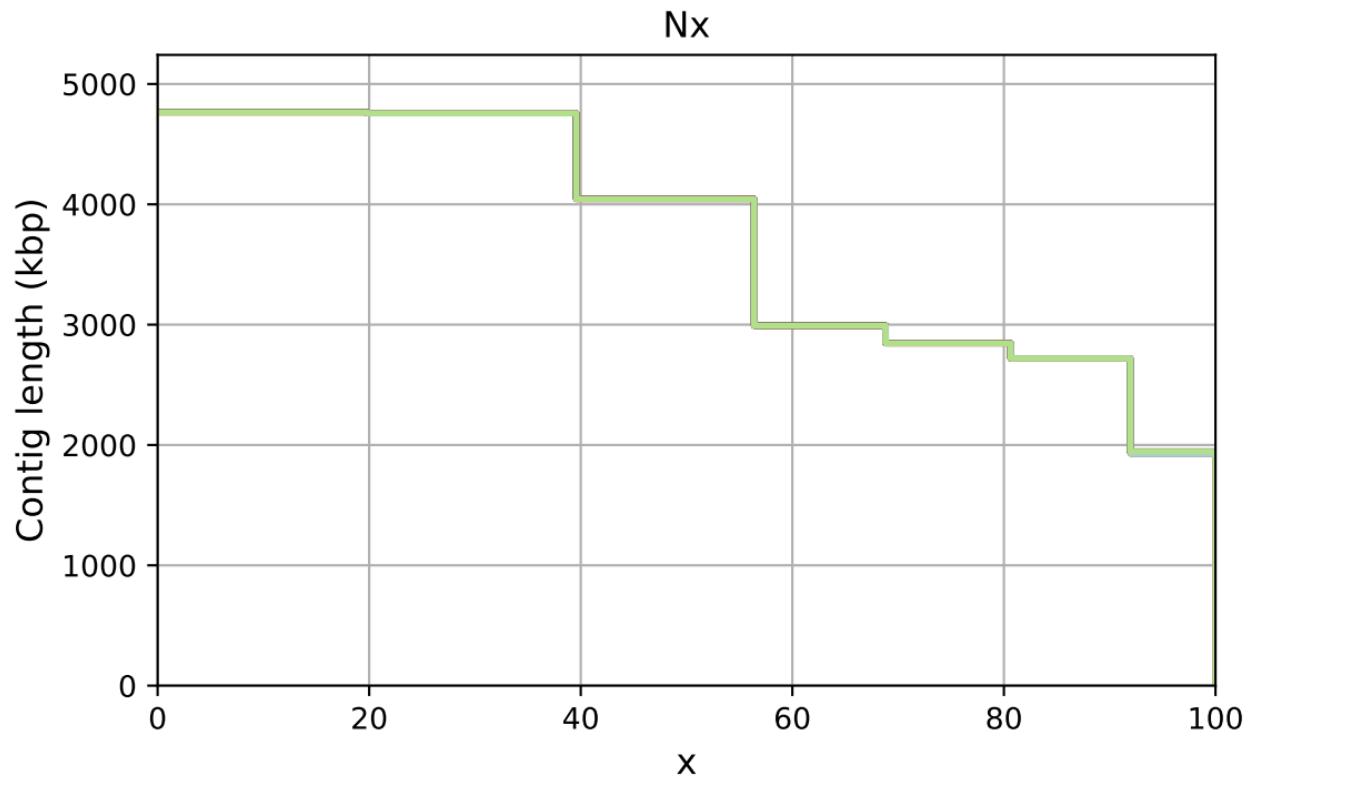
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# misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13			
# contig misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13			
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
# c. translocations	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13			
# 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	2719574	2717922	2719543	2719562	2720329	2720423	2718431	2719745	2717983	2719603	2719633	2720494	2720498	2718867	2717938	2719539	2719544	2720372	2720459	2718437	
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# possible misassemblies	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	16		
# local misassemblies	10	9	9	9	9	10	10	10	20	9	9	9	9	9	10	9	10	9	19		
# 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		
# misassemblies caused by fragmented reference	26	26	26	26	26	26	26	23	26	26	26	26	26	26	22	26	26	26	25		
# unaligned mis. contigs	6	6	6	6	6	6	6	4	6	6	6	6	6	5	6	6	6	6	5		
# mismatches	7677	6881	7675	7736	7620	8017	6542	7585	6749	7692	7598	7633	7793	6850	7676	6889	7661	7766	7472	7995	6711
# indels	2965	1176	2024	2051	2937	3009	4268	2978	1117	2058	2067	2940	4444	2964	1176	2015	2058	2921	3005	4262	
# indels (<= 5 bp)	2889	1110	1973	2000	2884	2955	4205	2911	1054	2007	2016	2906	2887	4389	2888	1110	1964	2006	2869	2953	4202
# indels (> 5 bp)	76	66	51	51	53	54	63	67	52	51	53	55	76	66	51	52	52	60	60		
Indels length	6931	4974	5351	5372	6680	6687	8388	6853	4886	5389	5399	6731	6659	8526	6929	4979	5341	5404	6672	6718	8364

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	7	
Partially unaligned length	21274658	21271555	21273233	21261883	21263760	21253836	21322606	21275861	21273678	21273285	21265050	21263380	21257264	21274857	21273023	21256346	21265173	21252622	21318452
# 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

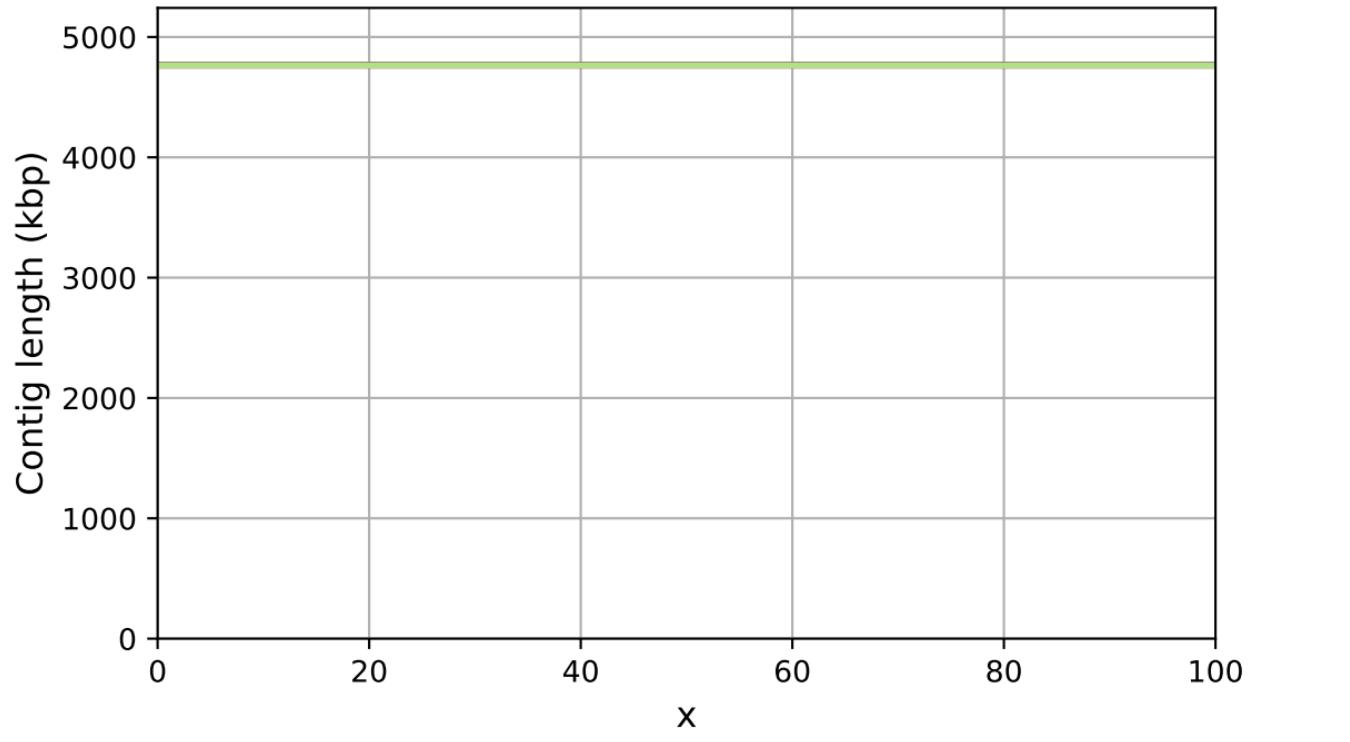
r10_2bins_v2_3_MP

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

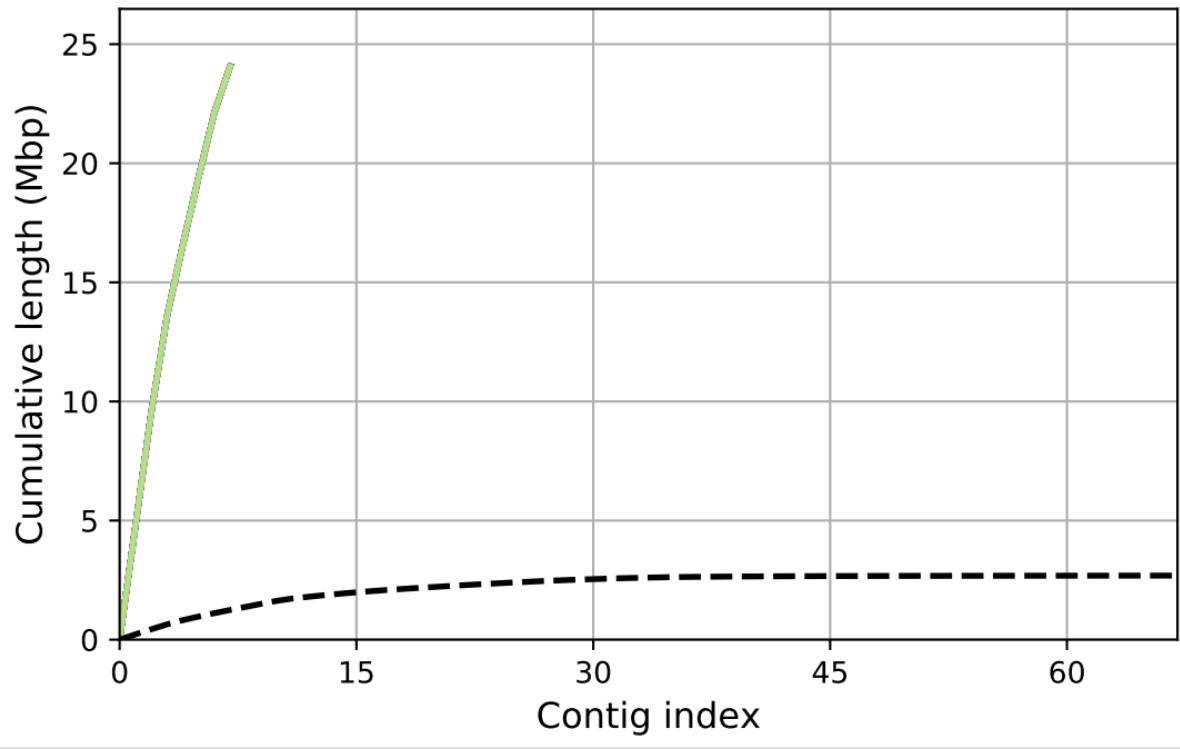
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r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_

r10_2bins_v2_3_r2_

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_racoon_r1

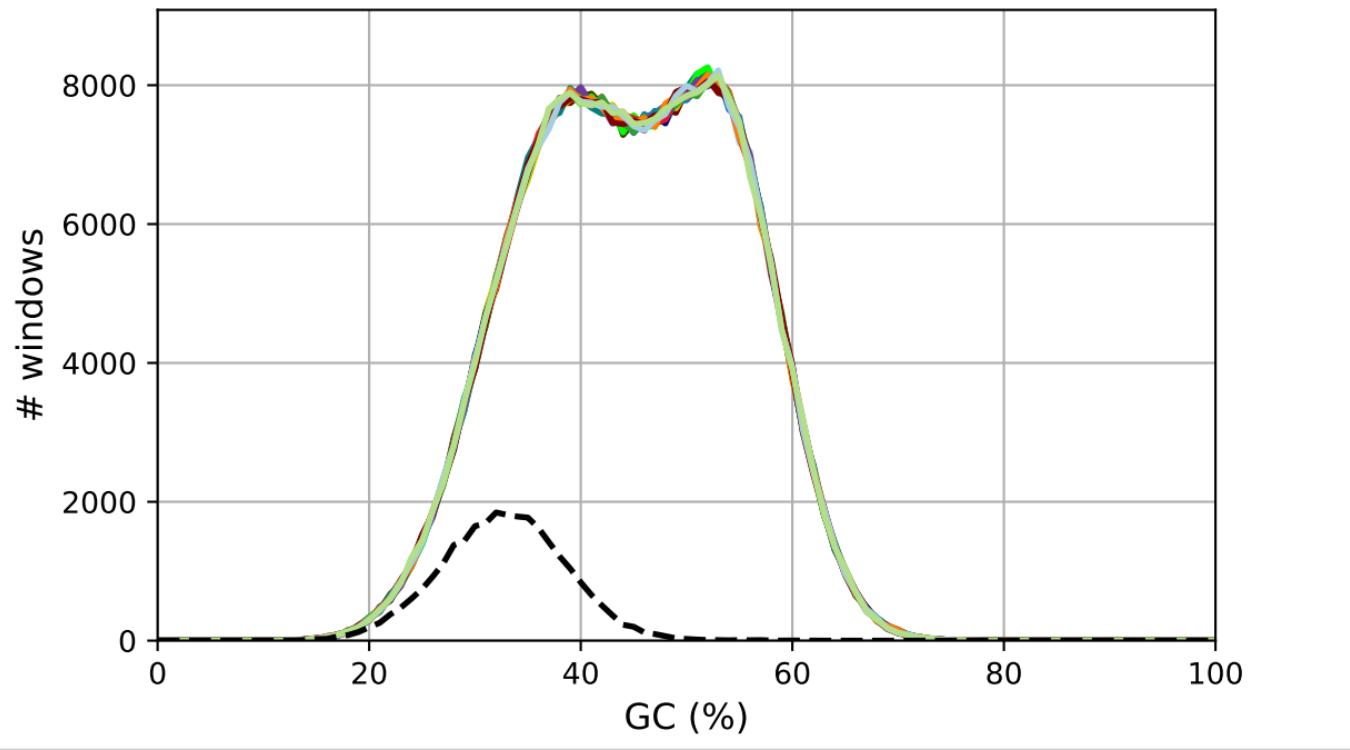
r10_2bins_v2_3_MP

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

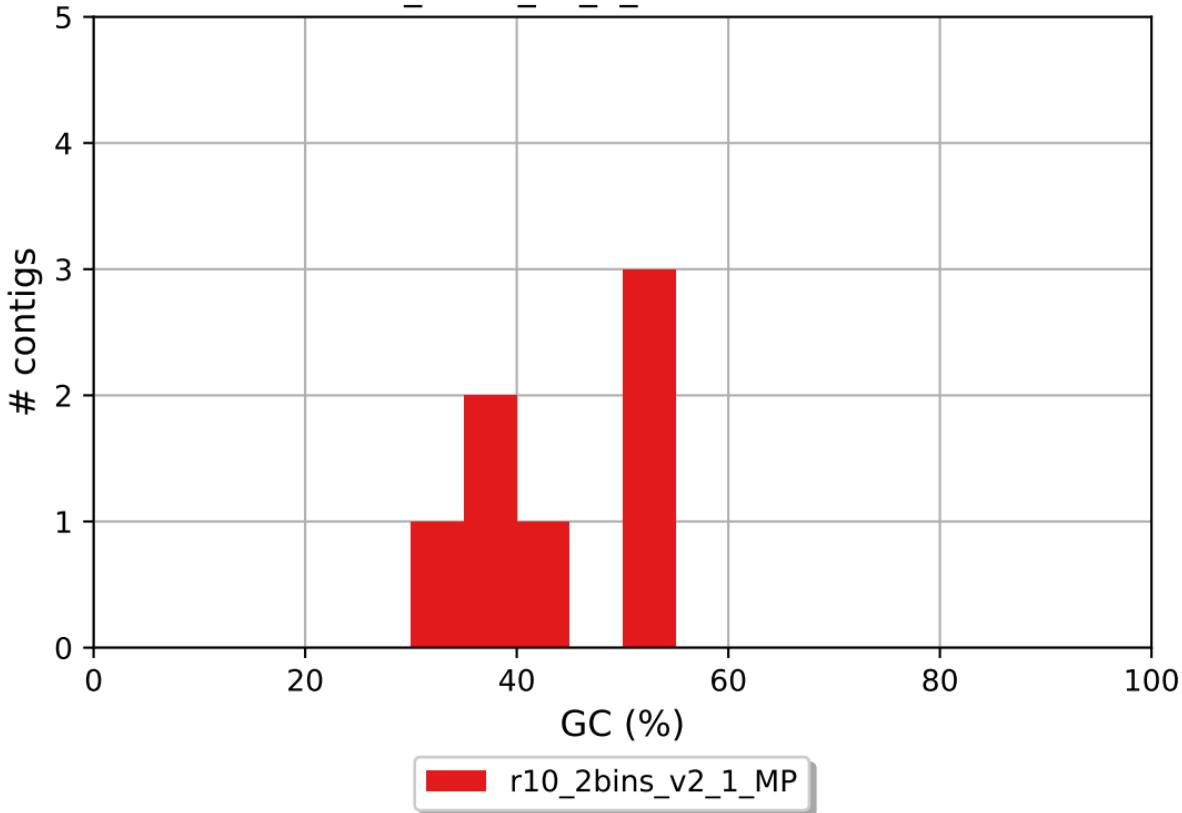
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r10_2bins_v2_3_MP_helen

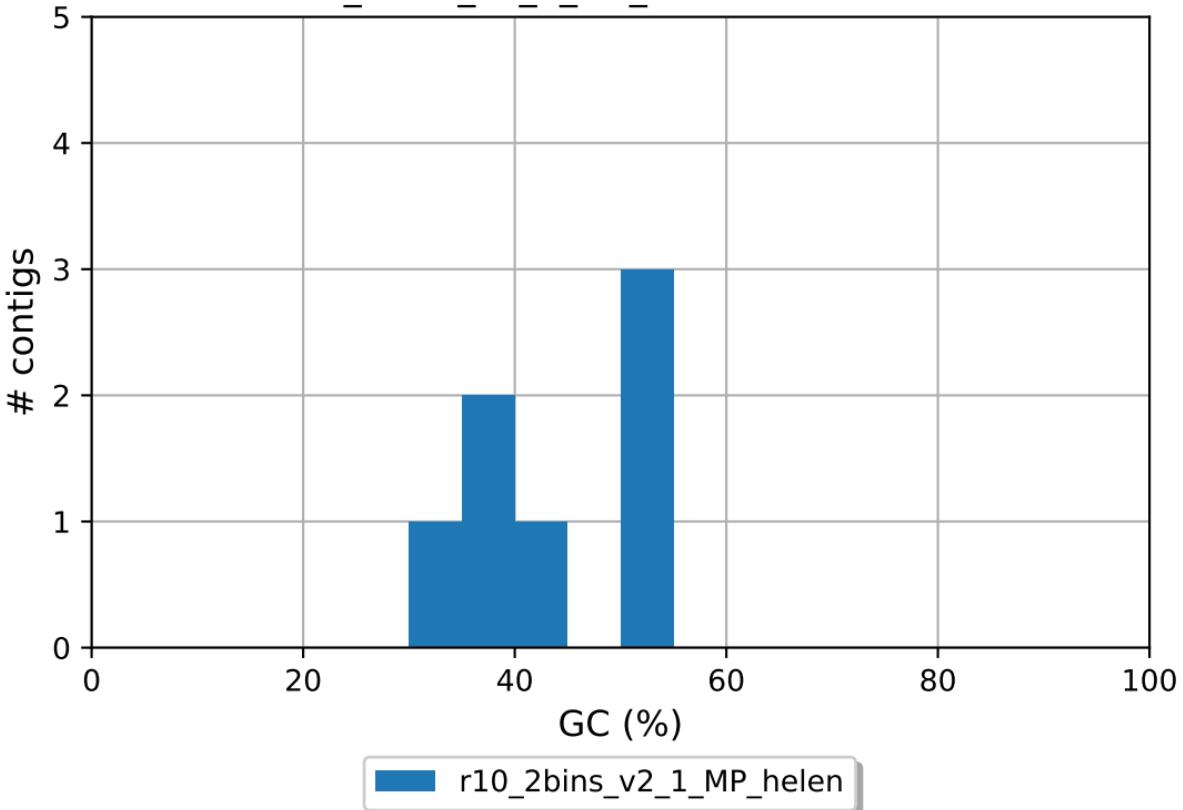
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r10_2bins_v2_3_r2_racoon_r1

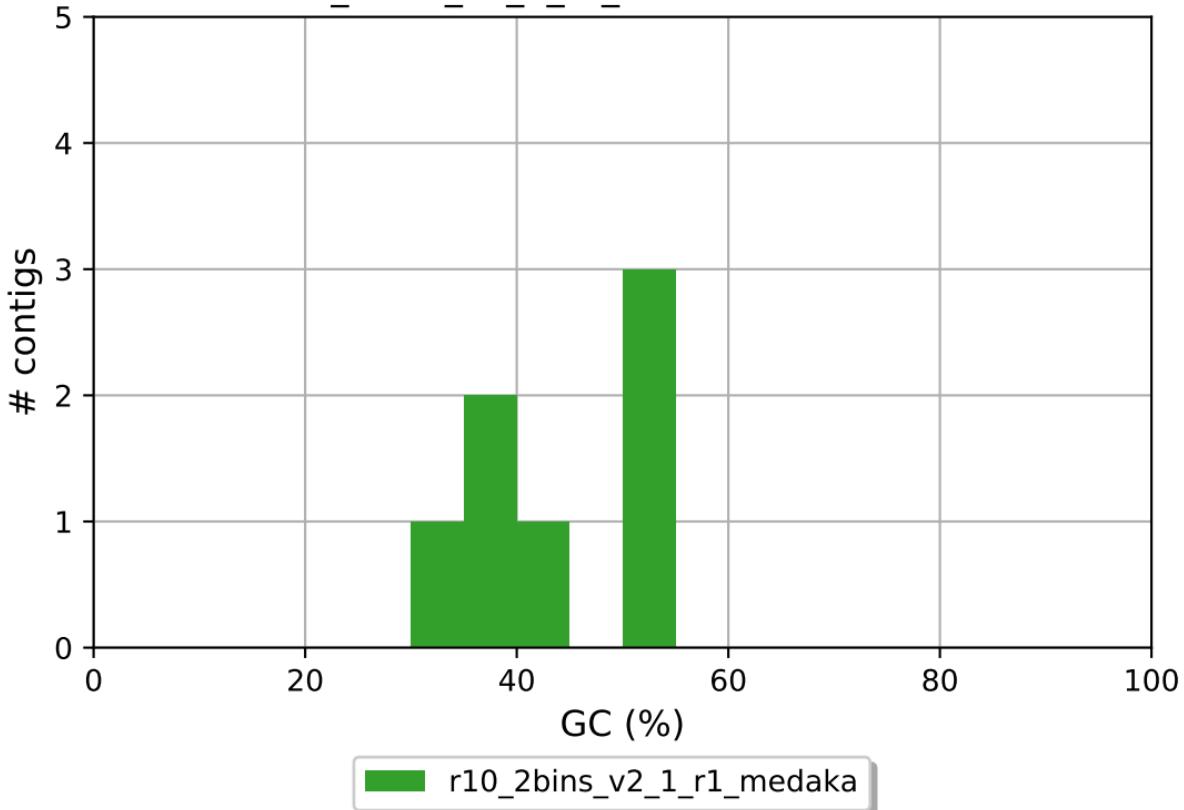
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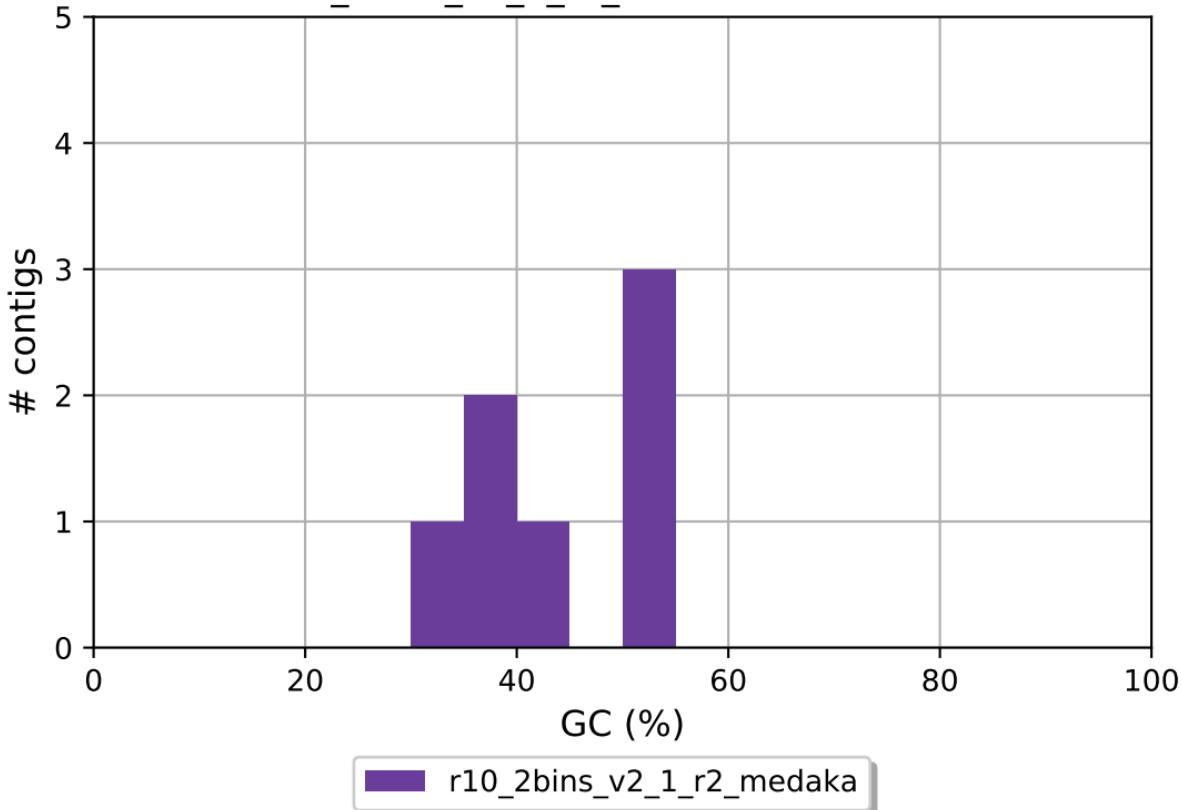
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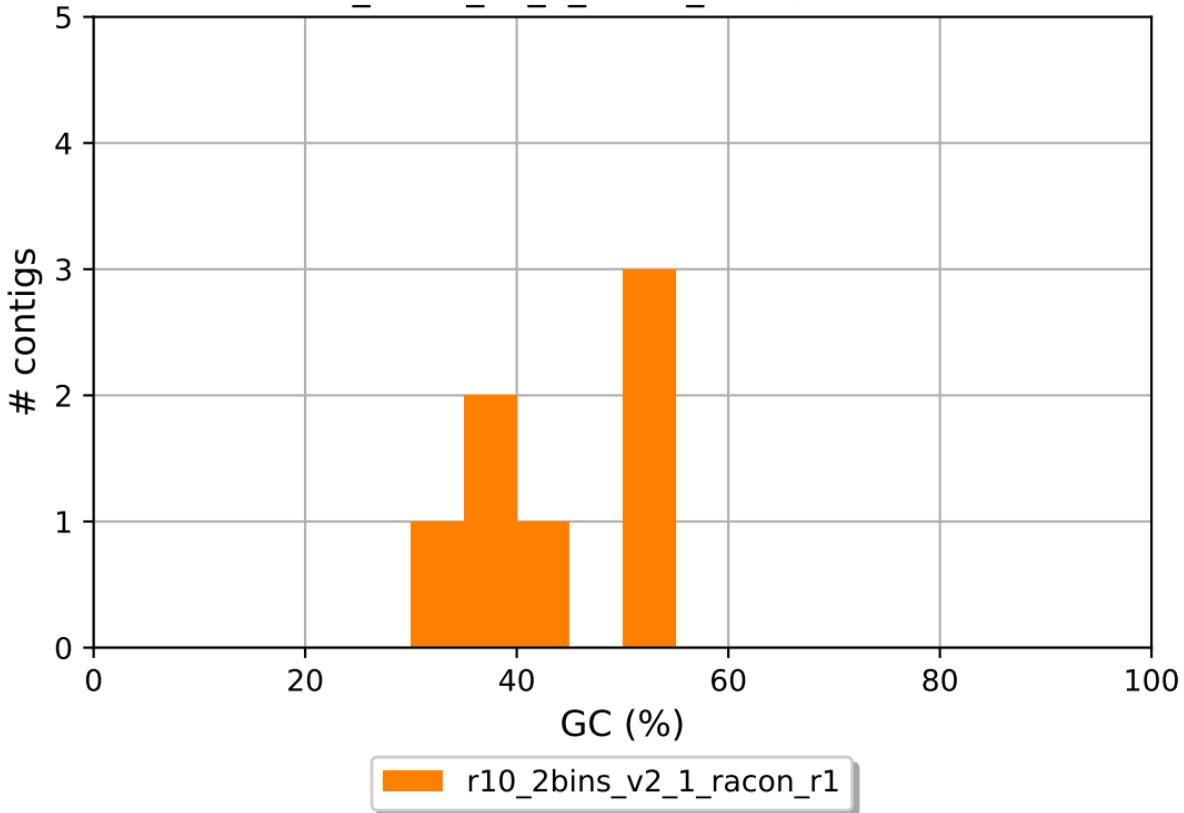
r10_2bins_v2_1_r1_medaka GC content



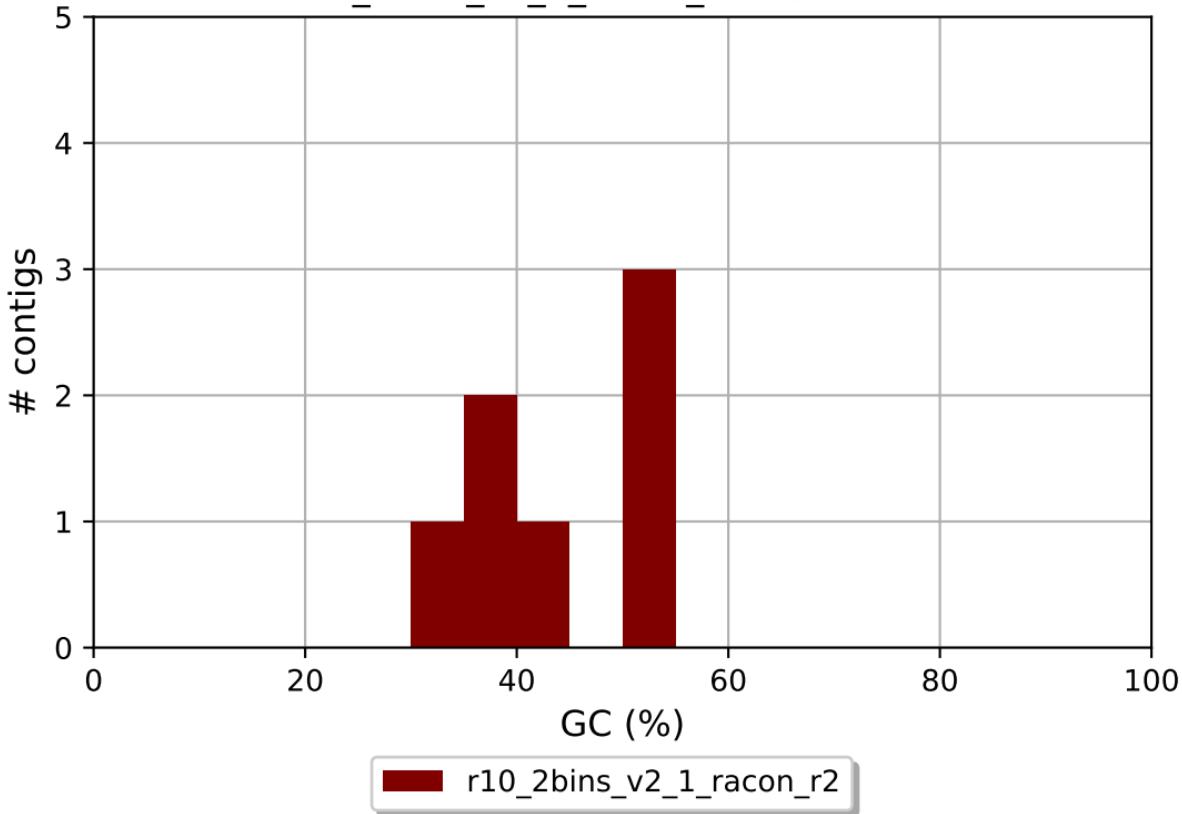
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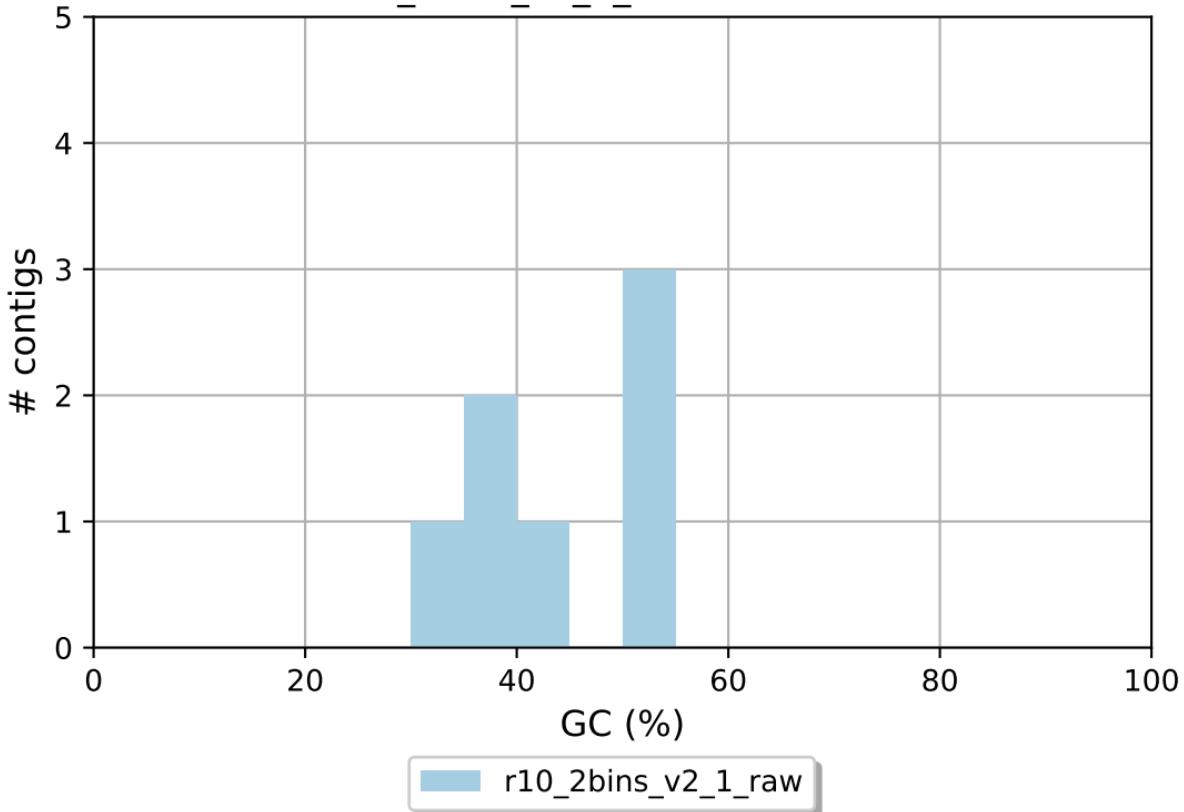
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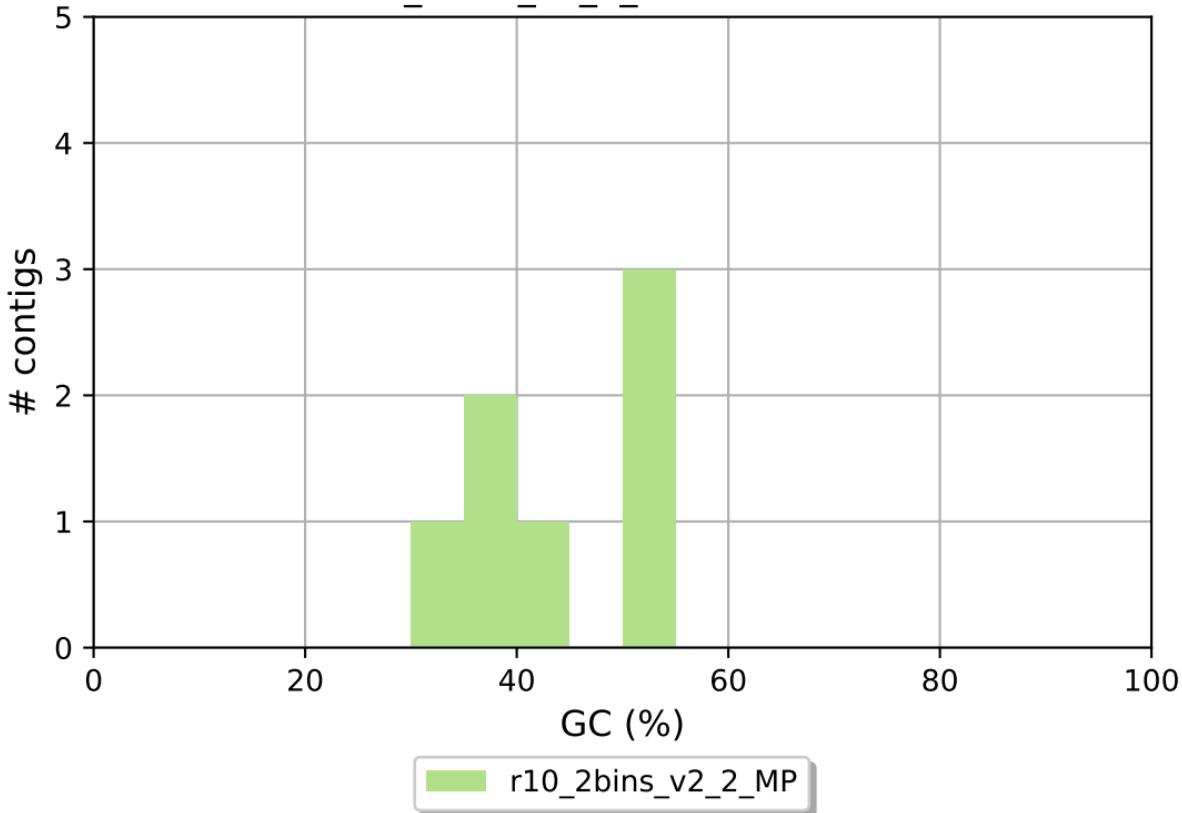
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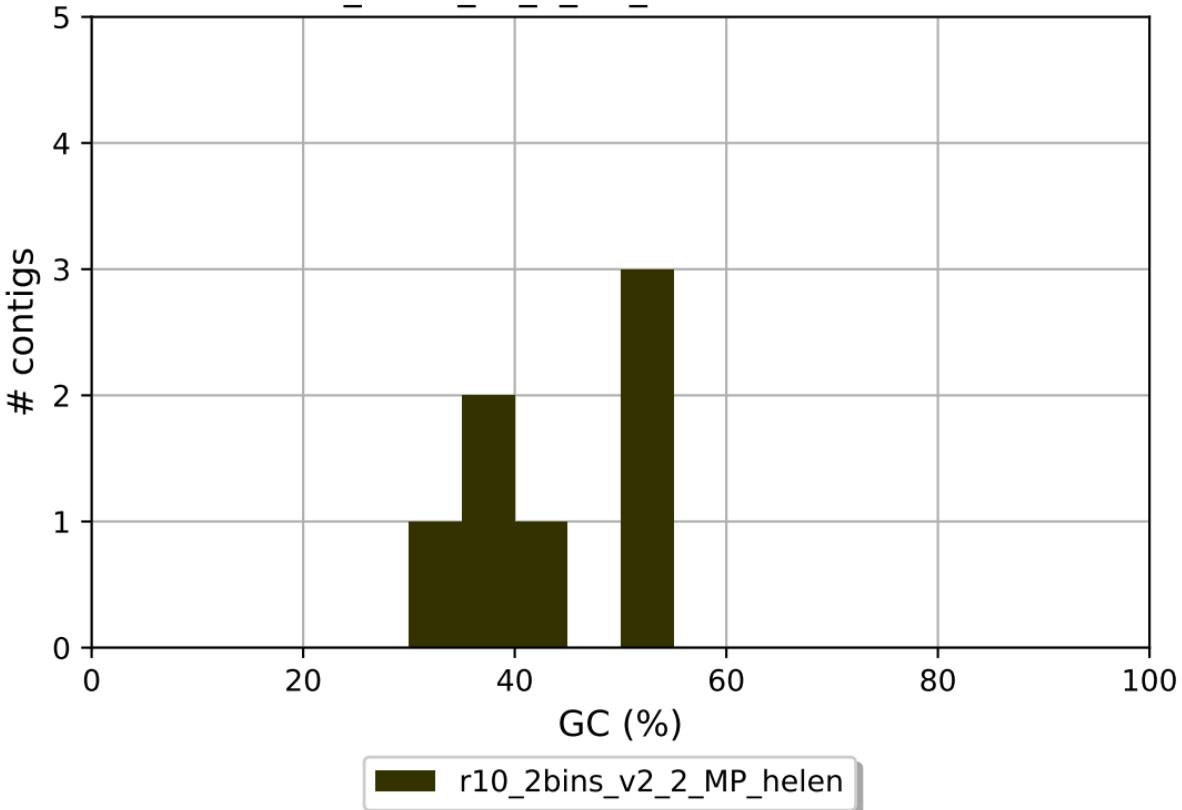
r10_2bins_v2_1_raw GC content



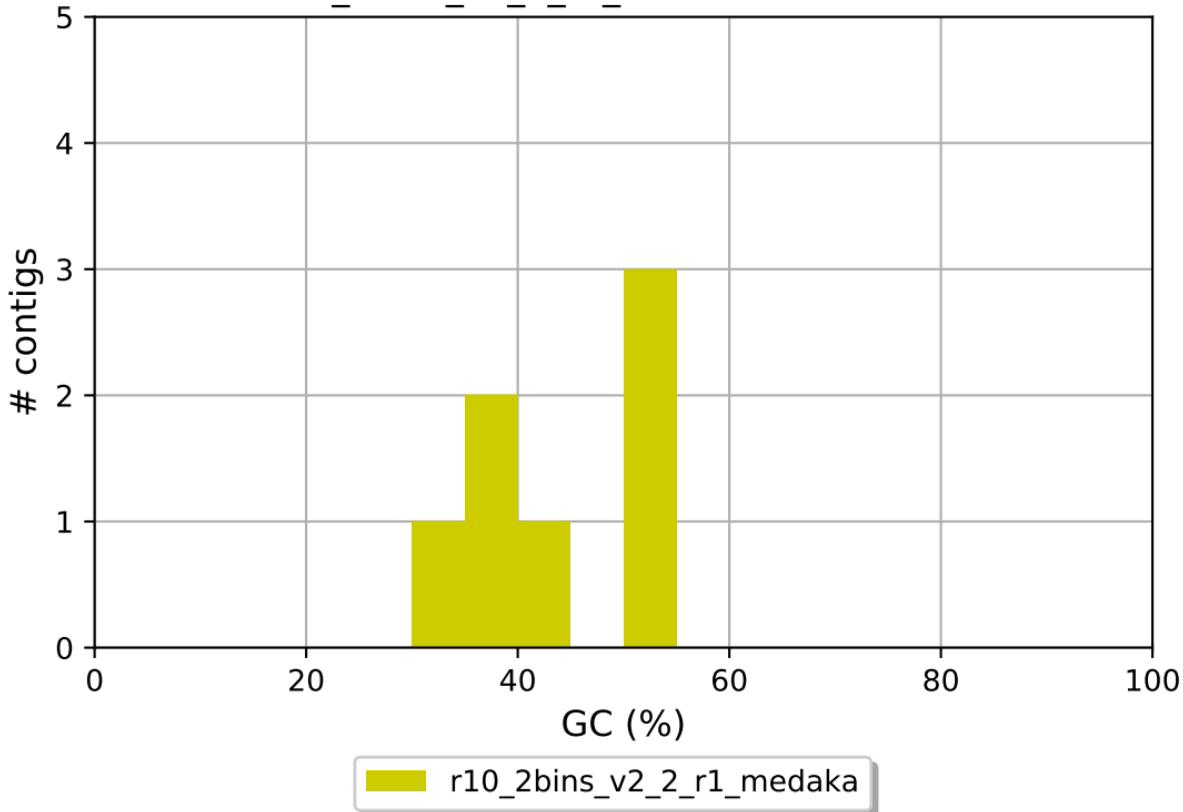
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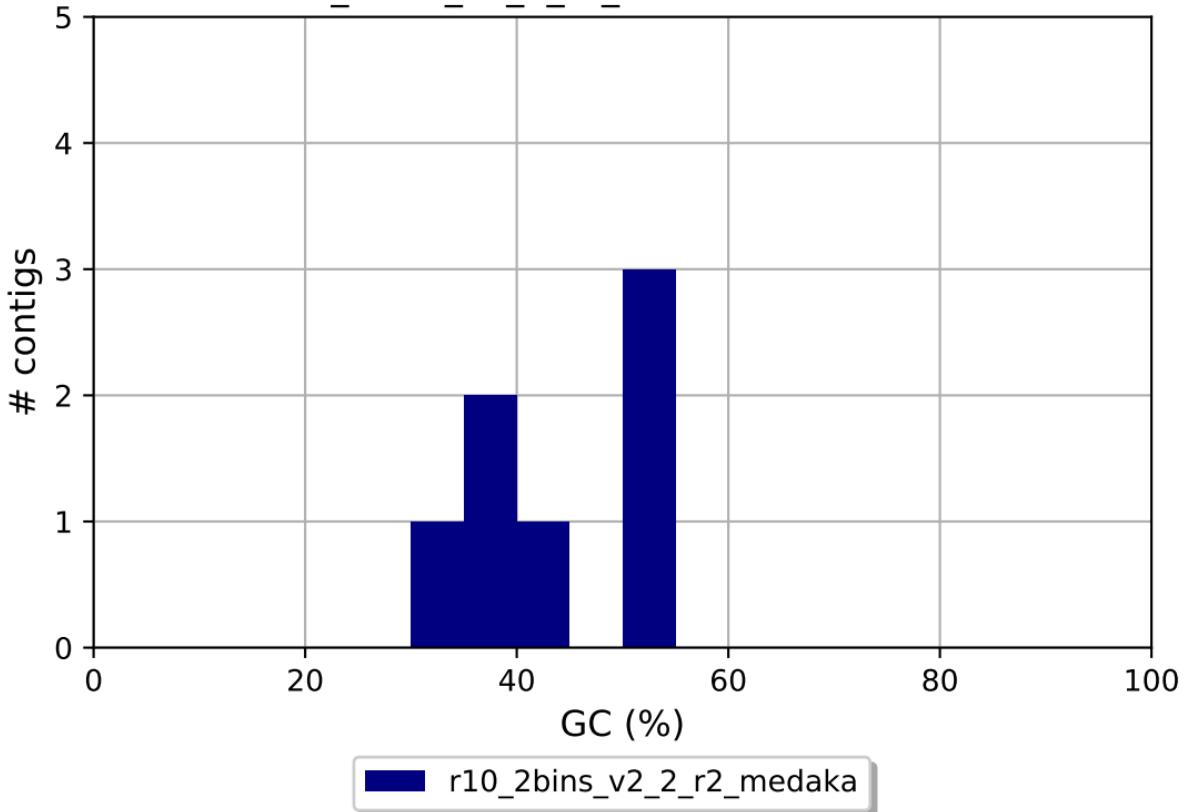
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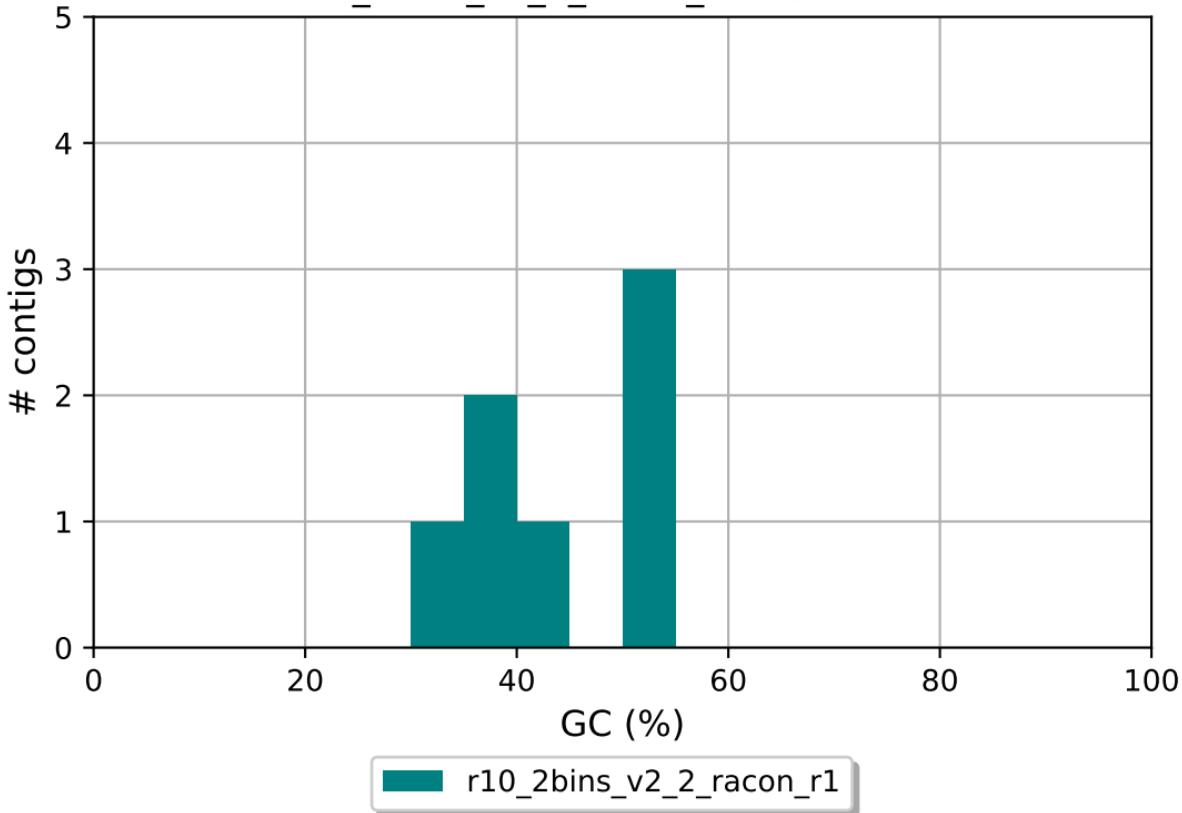
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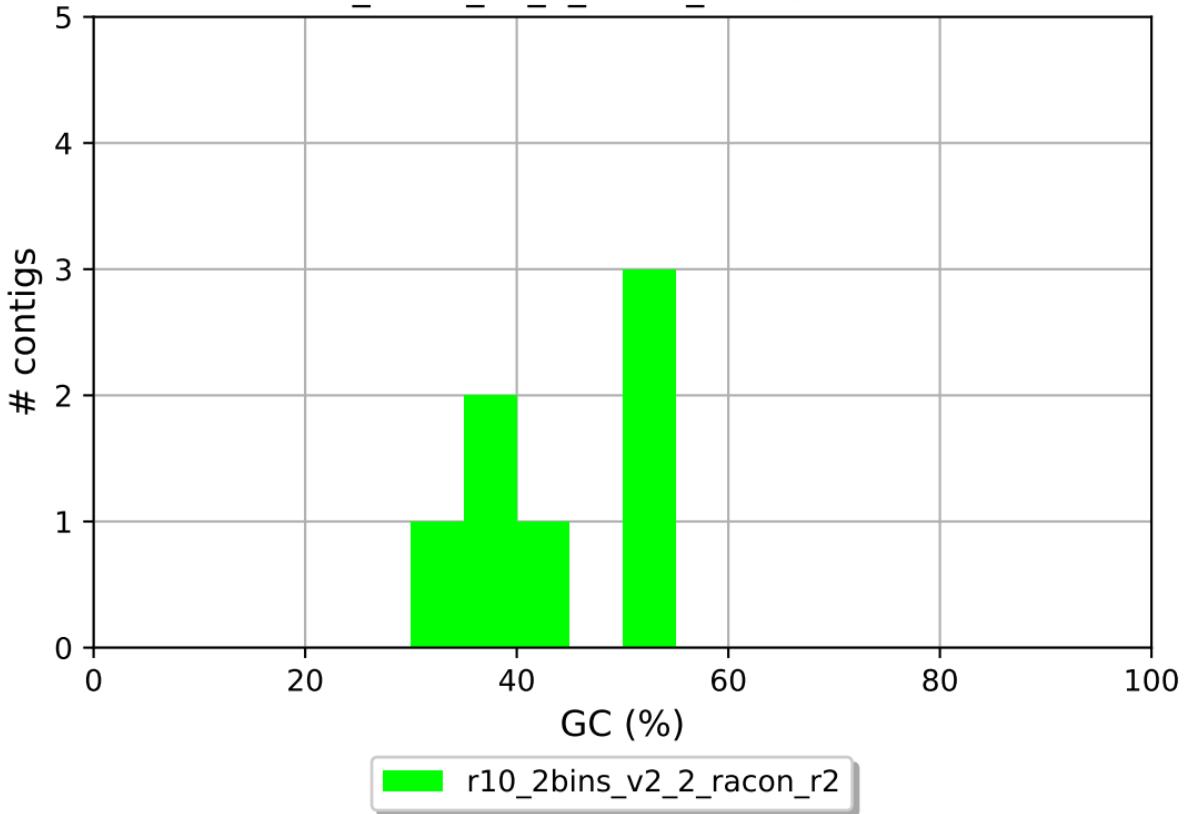
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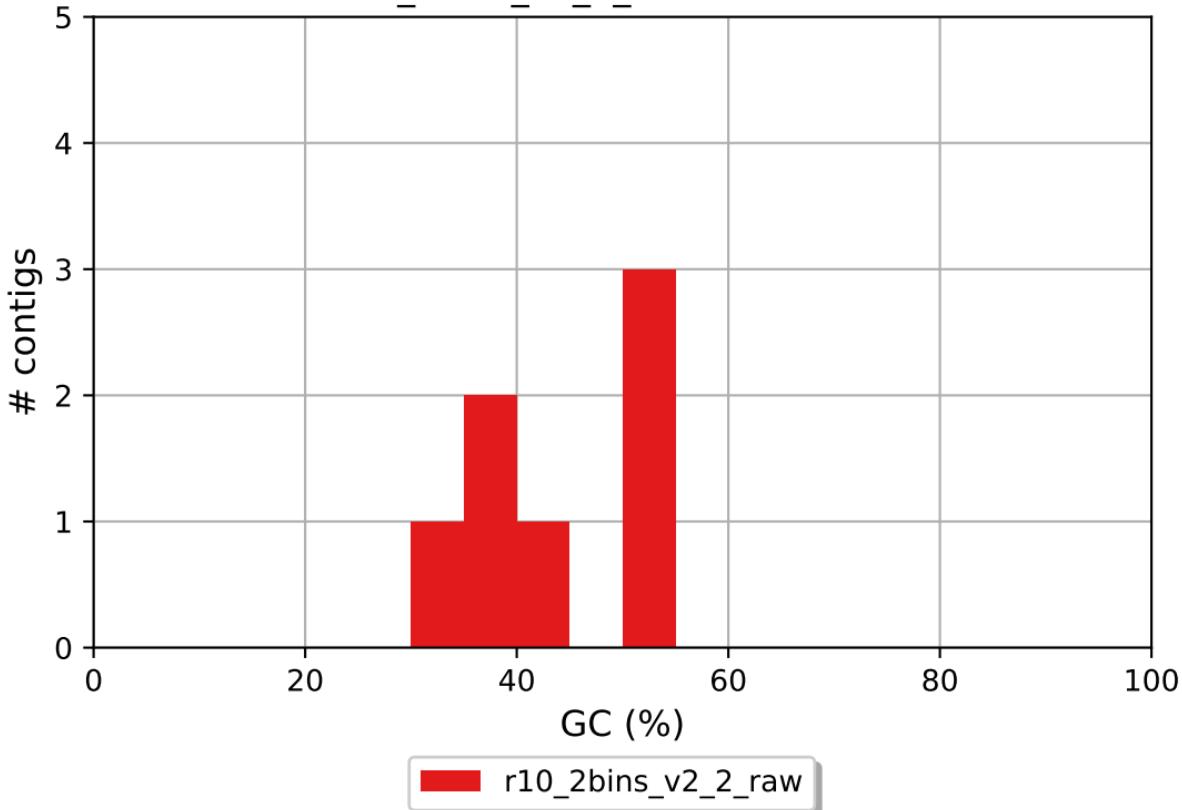
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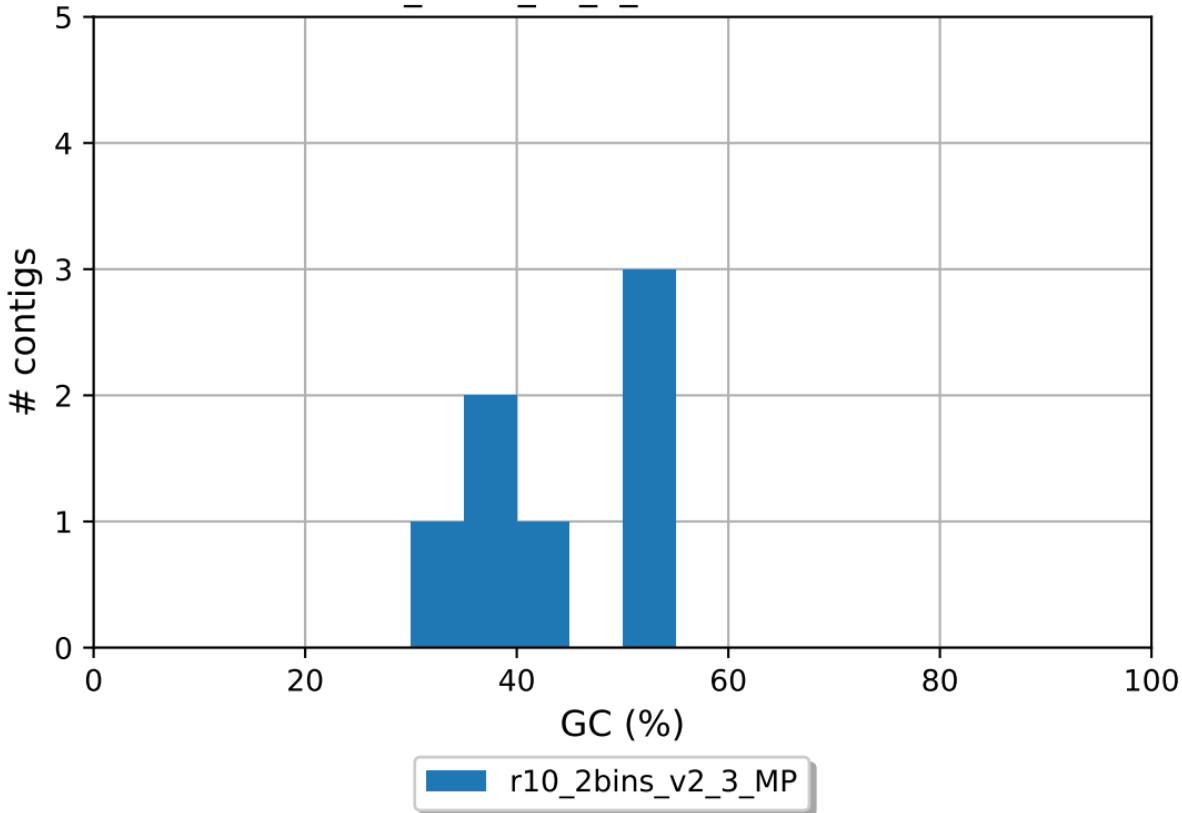
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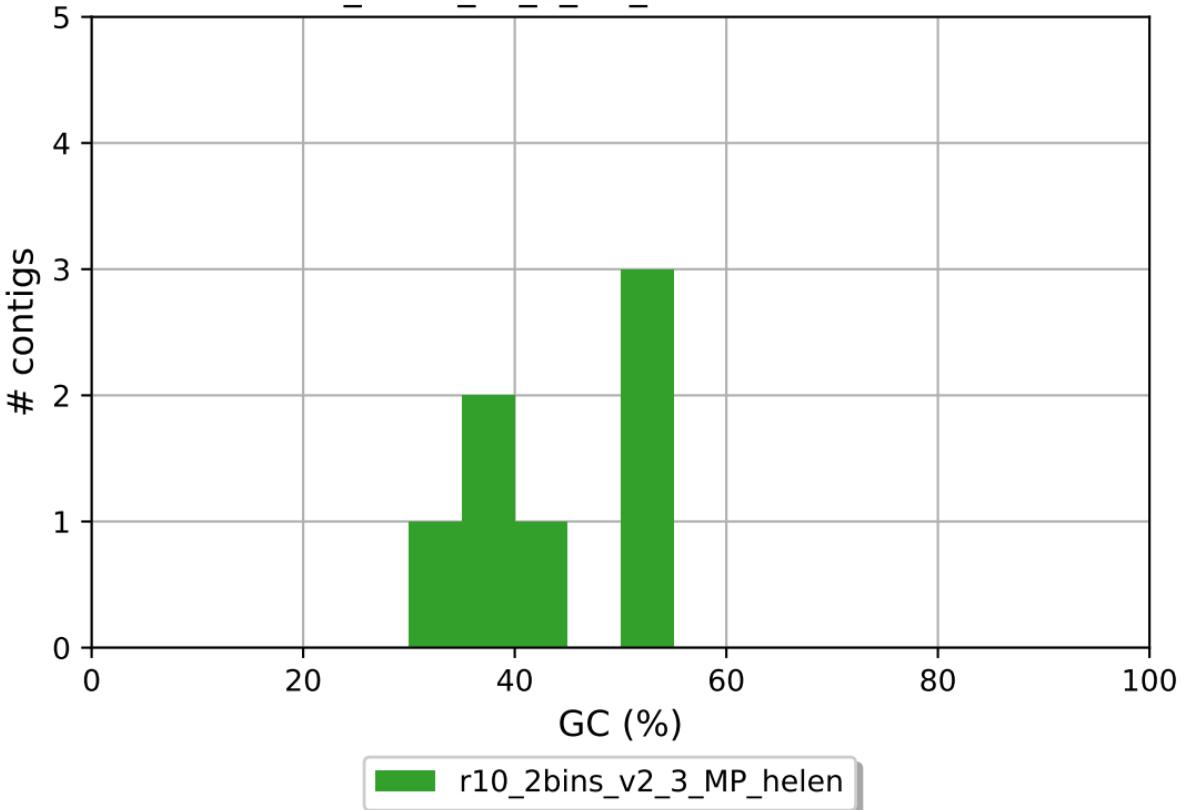
r10_2bins_v2_2_raw GC content



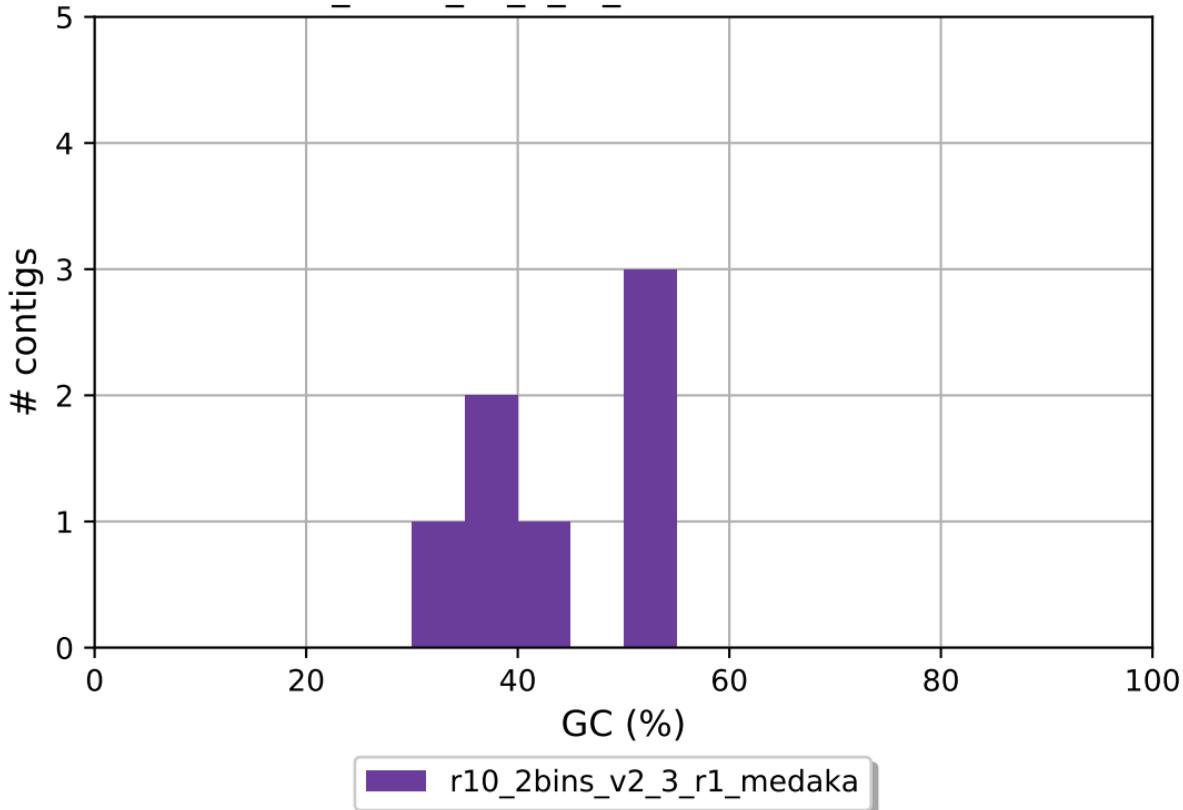
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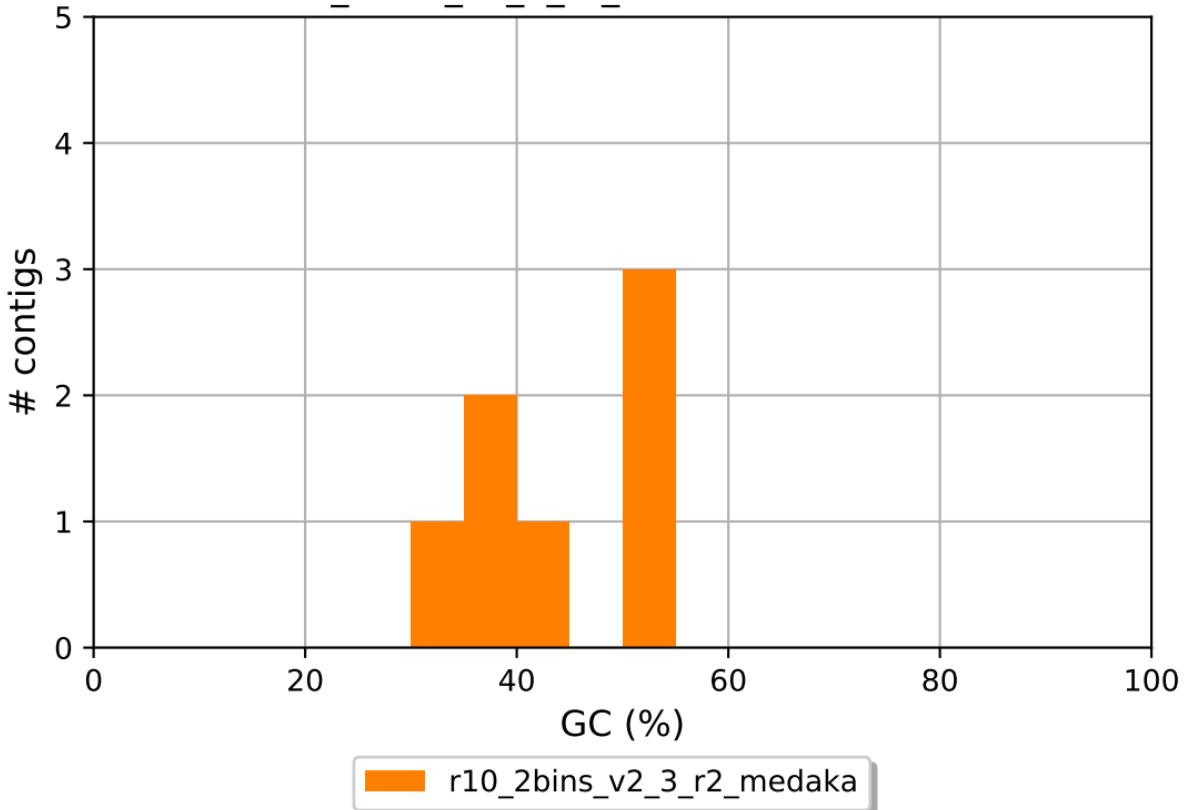
r10_2bins_v2_3_MP_helen GC content



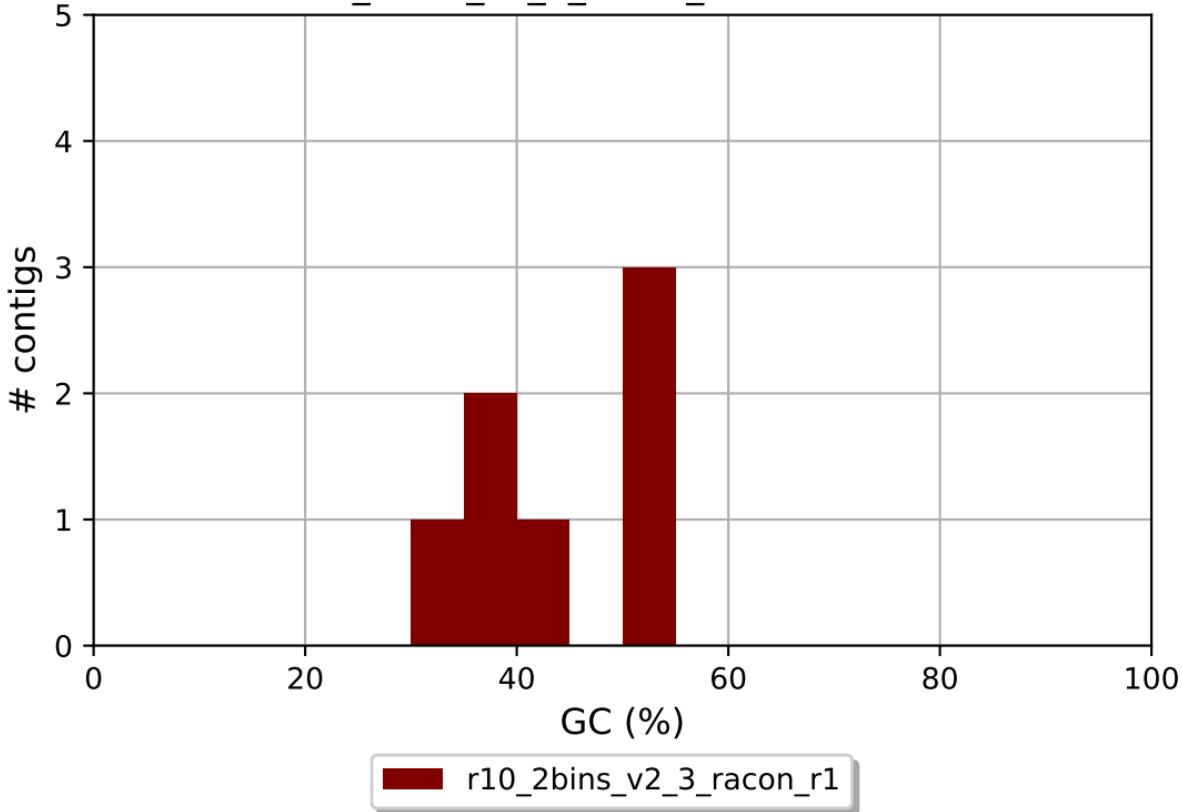
r10_2bins_v2_3_r1_medaka GC content



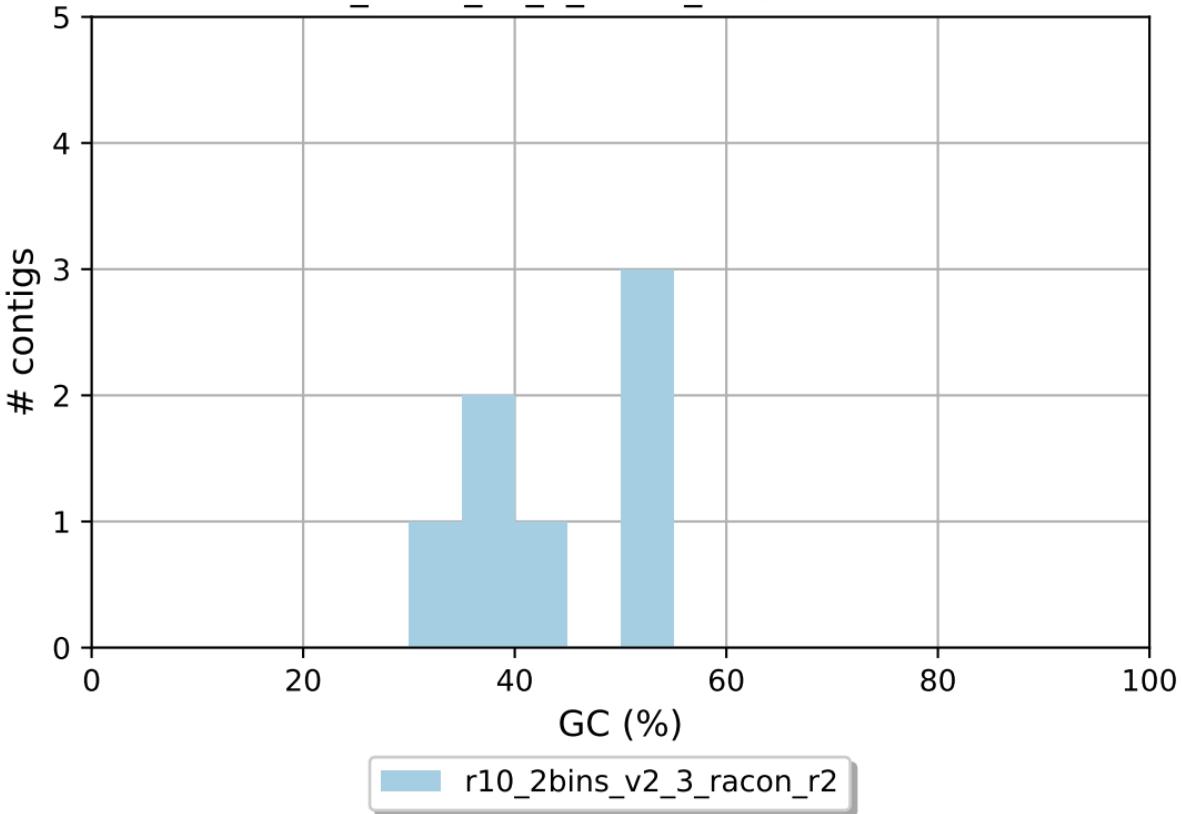
r10_2bins_v2_3_r2_medaka GC content



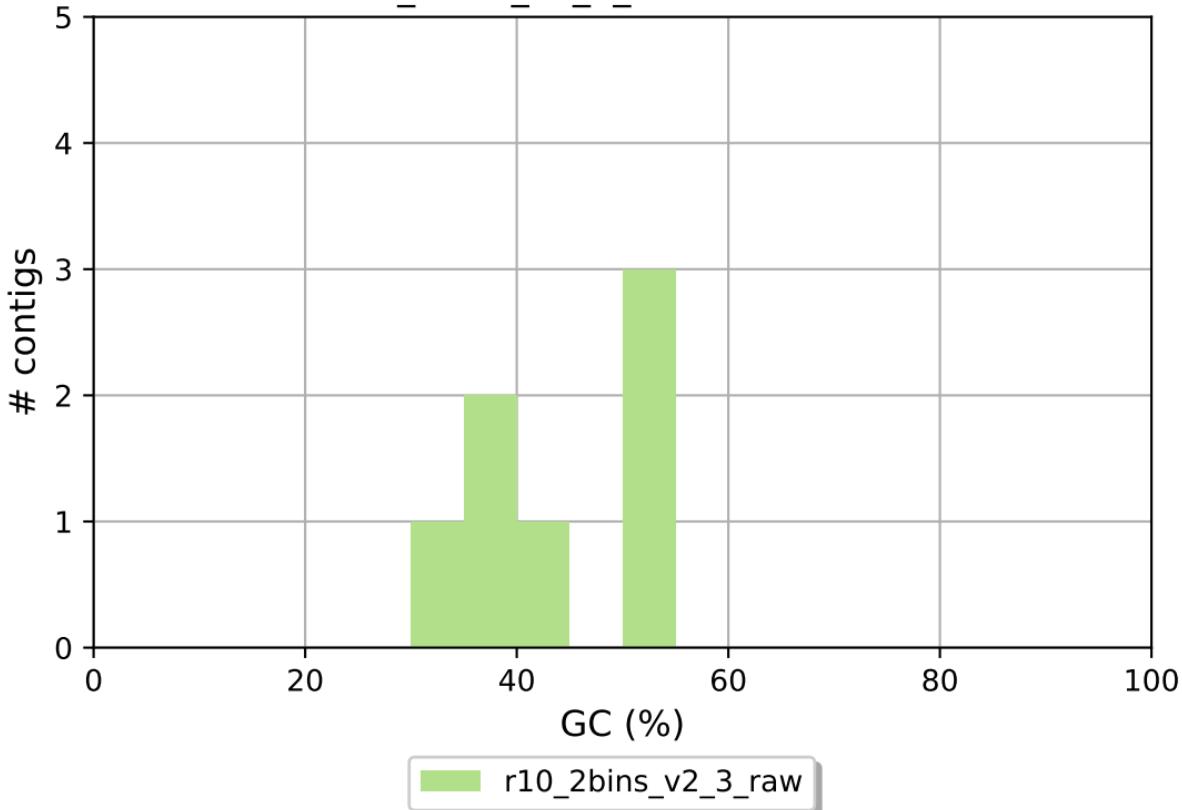
r10_2bins_v2_3_racon_r1 GC content



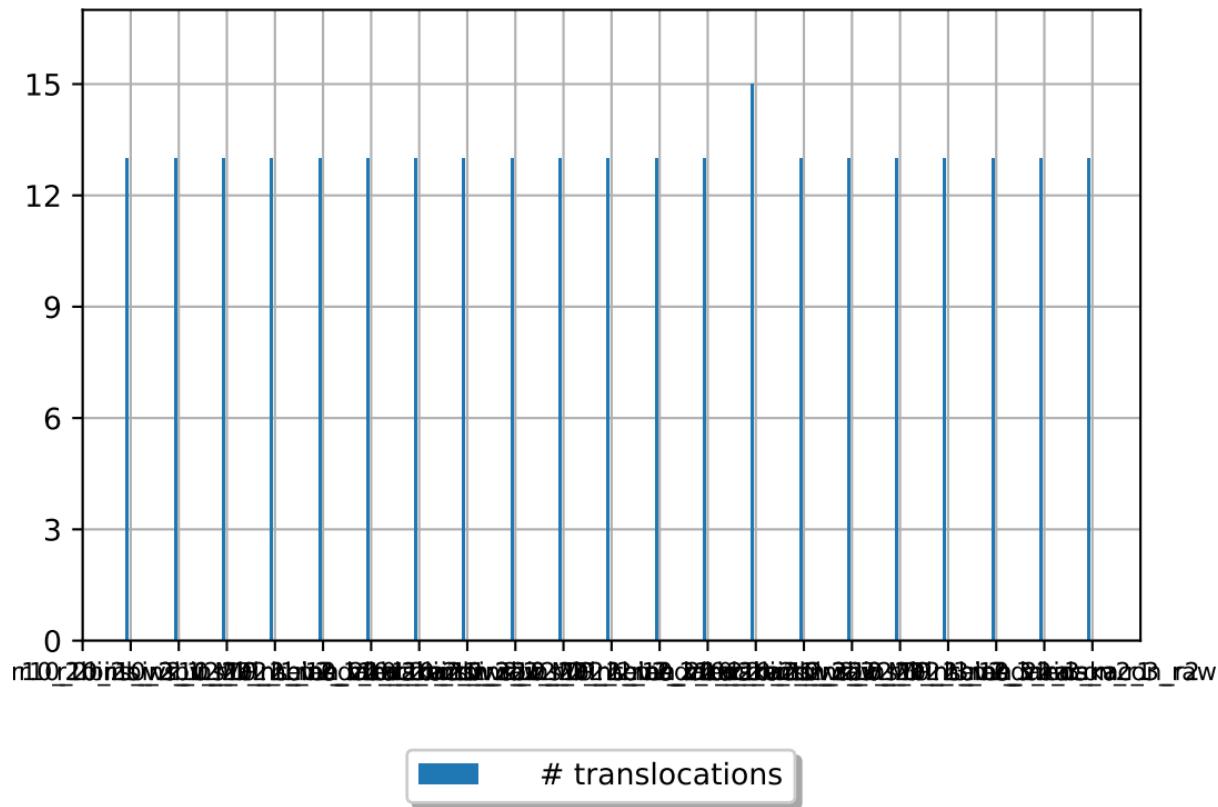
r10_2bins_v2_3_racon_r2 GC content



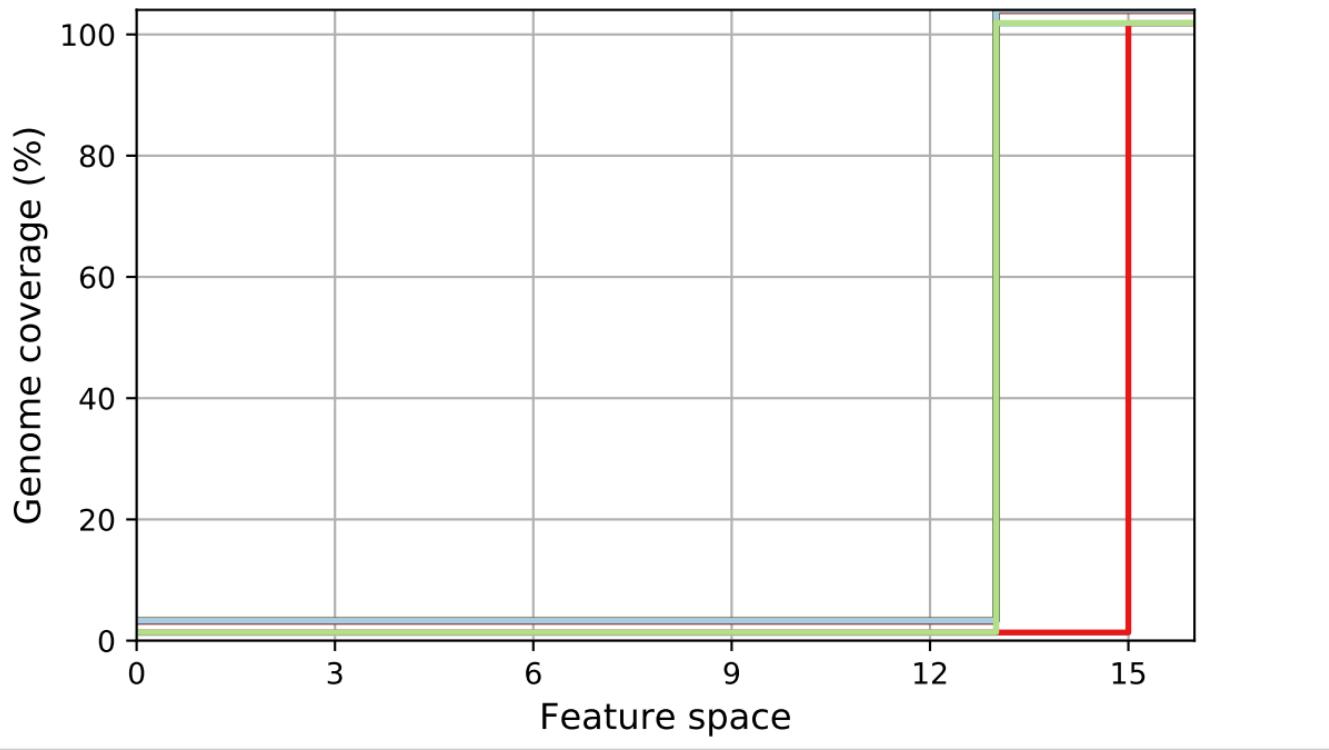
r10_2bins_v2_3_raw GC content



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

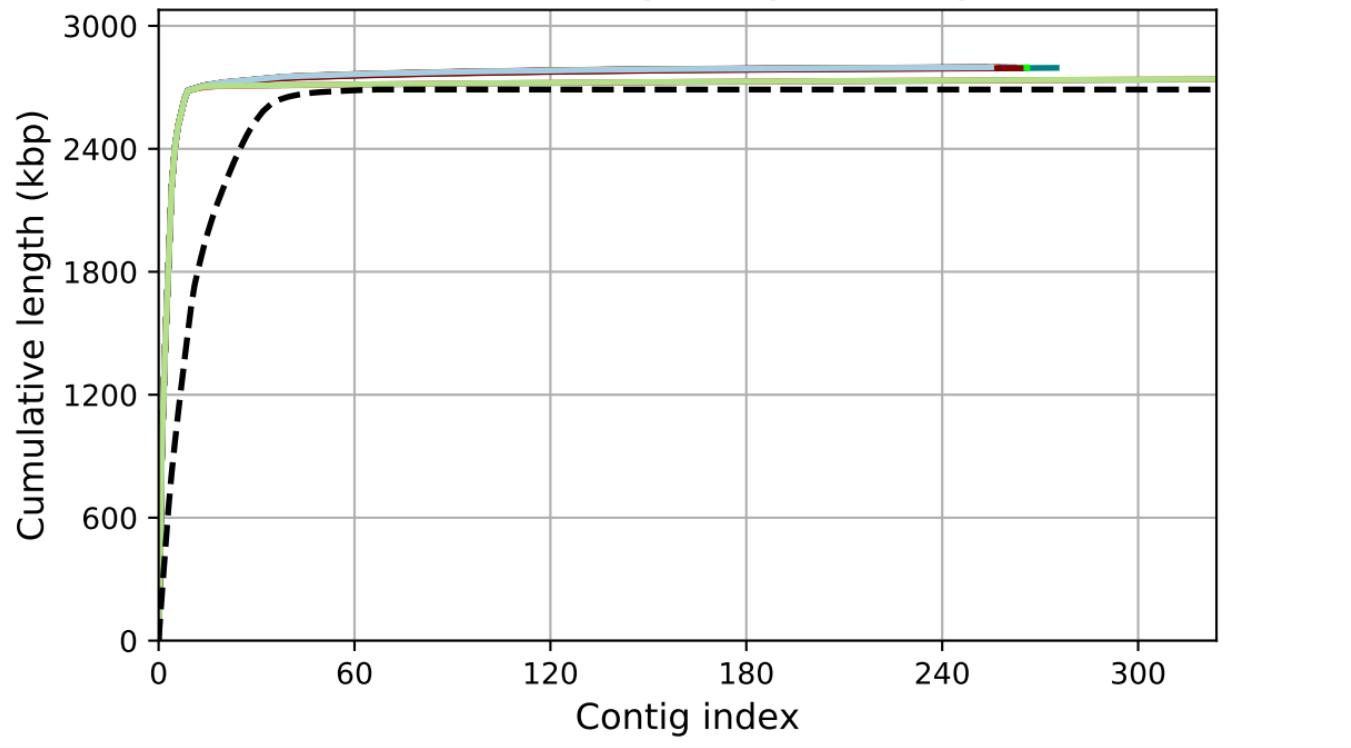
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1

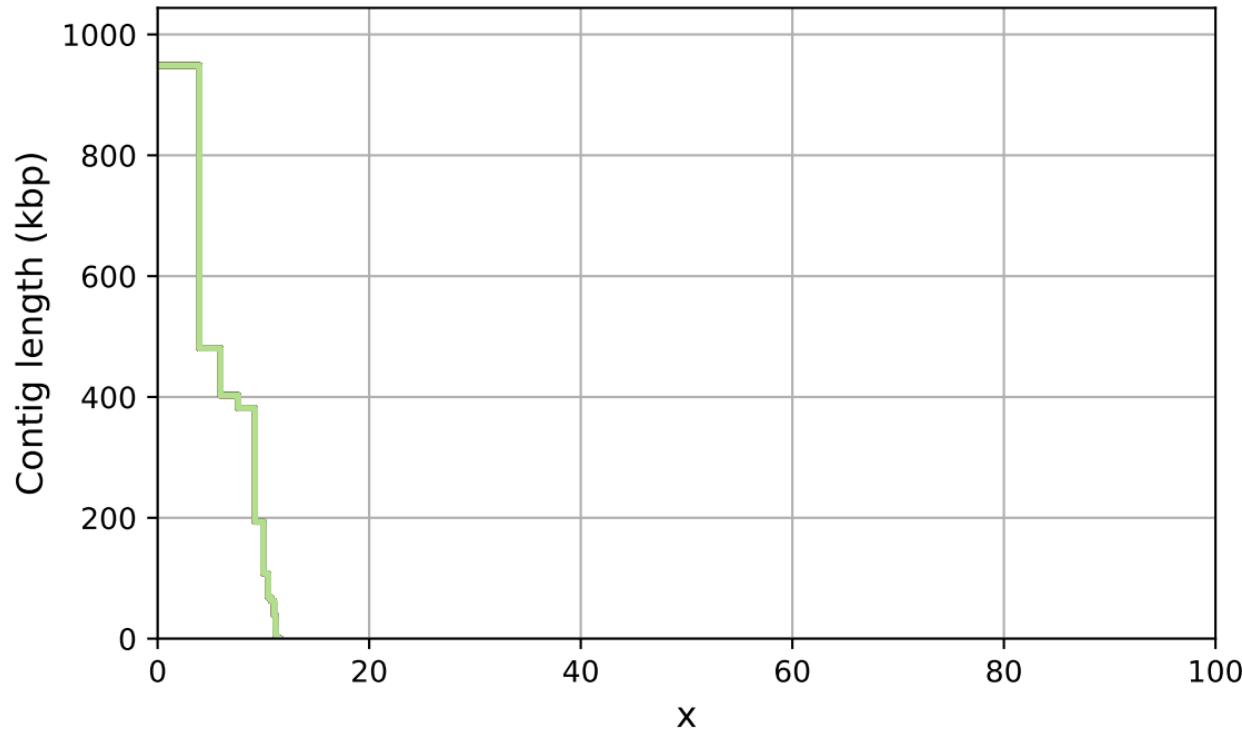
r10_2bins_v2_3_r2

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
0_2bins_v2_2_r1_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_helen
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

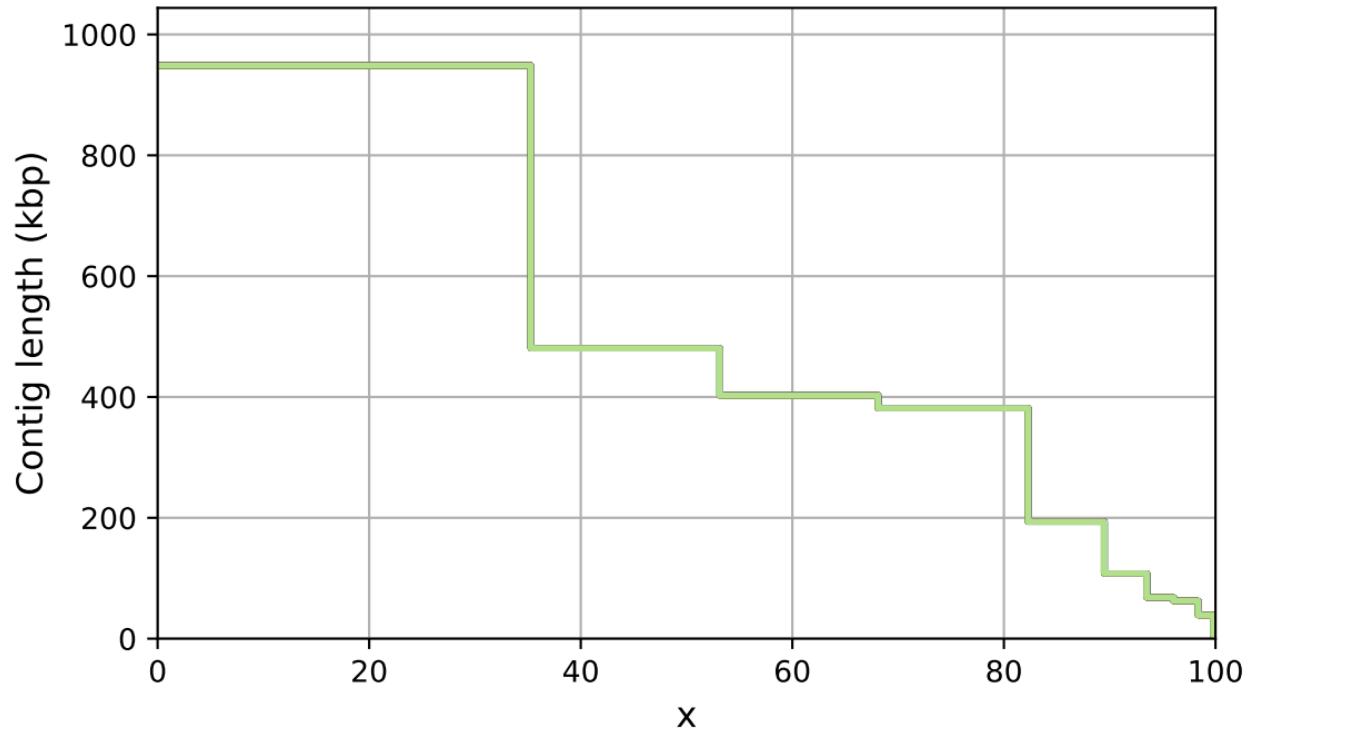
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_

r10_2bins_v2_3_r2_

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

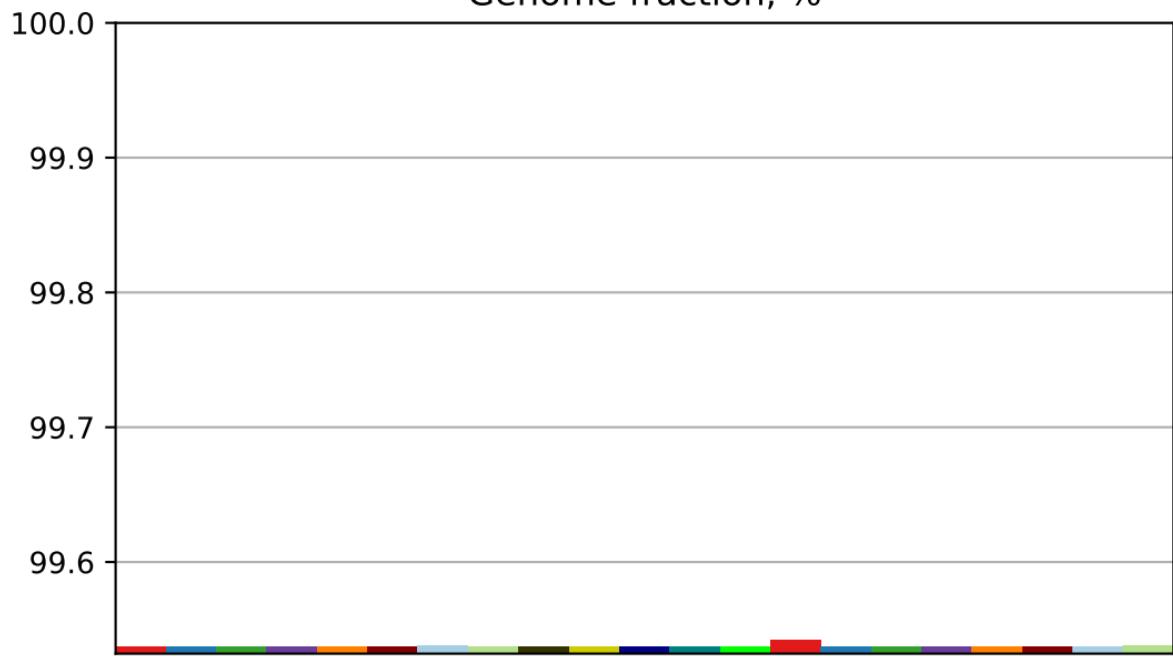
r10_2bins_v2_3_MP

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_