

Report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_racon_r1	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_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)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24052467	24060967	24075545	24072103	24075113	2406593	24065155	2406597	24062694	
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24052467	24060967	24075545	24072103	24075113	2406593	24065155	2406597	24062694	
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24052467	24060967	24075545	24072103	24075113	2406593	24065155	2406597	24062694	
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24052467	24060967	24075545	24072103	24075113	2406593	24065155	2406597	24062694	
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7			
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
Total length	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24052467	24060967	24075545	24072103	24075113	2406593	24065155	2406597	24062694	
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	44.78	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.77	44.80	44.81	44.80	44.80	44.79	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	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045608	4045229	4045315	4042940	4045596	4045614	4045593	4045228	4045344	4043027		
NG50	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4764481	4764622	4763482	4765372	4765362	4765559	476361	4764967	4764598	4763422	
N75	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845282	2845426	2843855	2845434	2845426	2845420	2845336	2843848			
NG75	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4764481	4764622	4763482	4765372	4765362	4765559	476361	4764967	4764598	4763422	
L50	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			
L75	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			
# misassemblies	14	14	14	14	14	14	14	13	14	14	14	14	14	14	14	14	14	14			
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
Misassembled contigs length	2719597	2717966	2719541	2719590	2720576	2720615	2718428	2719618	2717942	2719541	2719616	2720432	2720646	2718430	2719555	2717972	2719594	2719599	2720567	2720658	2718818
# local misassemblies	10	10	9	10	9	9	20	9	9	9	9	9	9	9	8	8	9	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	5	6	6	6	6	6	6	6	6	6	6	6			
# 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			
Unaligned length	21275184	21271369	21272515	21264526	21261875	21256848	21322161	21274830	21271766	21273207	21263246	21251966	21276777	21274939	21276207	21271604	21266299	21259924	21322355		
Genome fraction (%)	99.544	99.544	99.544	99.544	99.544	99.544	99.538	99.546	99.546	99.546	99.546	99.546	99.538	99.544	99.544	99.544	99.544	99.542			
Duplication ratio	1.046	1.045	1.046	1.046	1.045	1.046	1.023	1.046	1.045	1.045	1.046	1.045	1.046	1.045	1.046	1.045	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			
# mismatches per 100 kbp	285.92	254.62	291.08	290.00	293.81	295.64	239.47	286.85	257.08	286.29	291.04	285.43	301.68	247.05	282.23	249.35	286.00	281.93	295.86	300.87	253.91
# indels per 100 kbp	110.28	36.24	76.02	76.51	113.15	112.96	158.10	110.83	43.48	74.97	76.47										

Misassemblies report

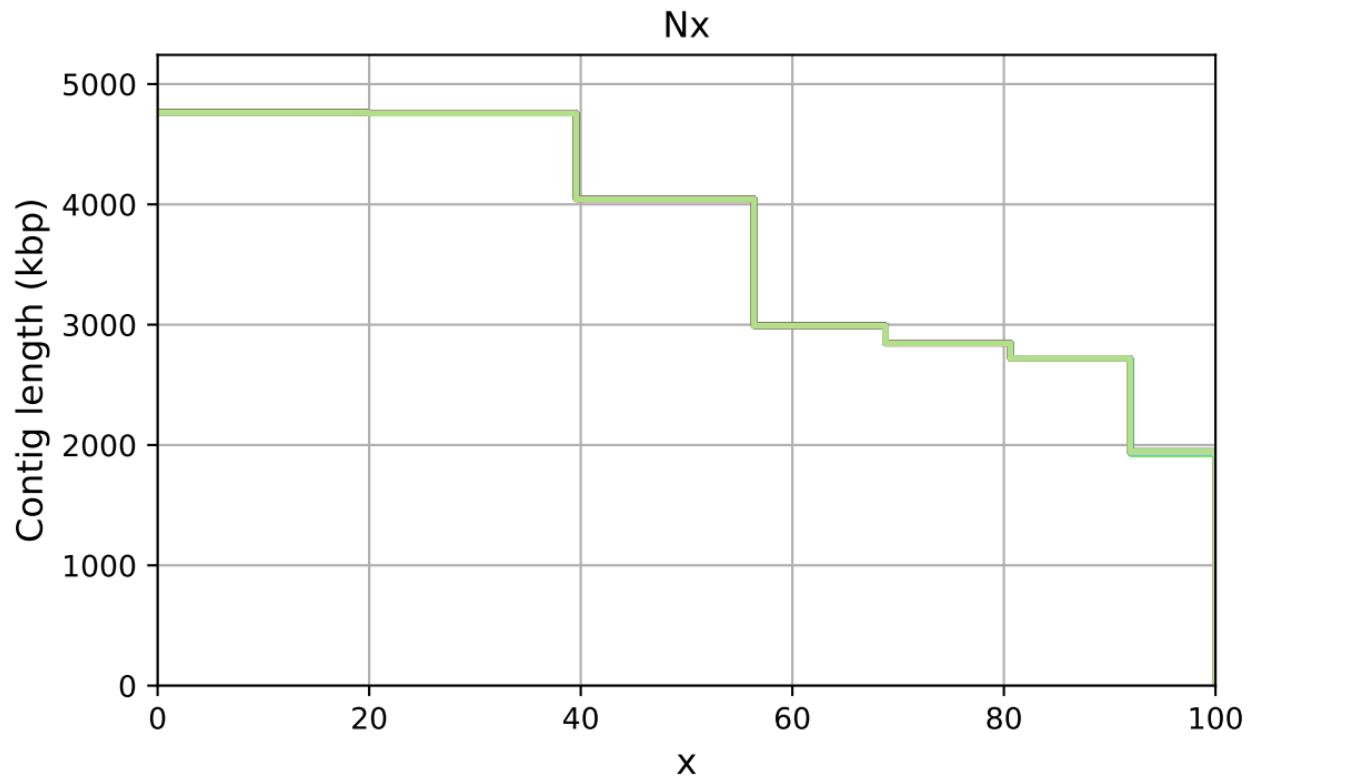
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# misassemblies	14	14	14	14	14	14	13	14	14	14	14	14	13	14	14	14	14	14	14		
# contig misassemblies	14	14	14	14	14	14	13	14	14	14	14	14	13	14	14	14	14	14	14		
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# c. translocations	14	14	14	14	14	14	13	14	14	14	14	14	13	14	14	14	14	14	14		
# c. inversions	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		
# s. relocations	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		
# s. inversions	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		
Misassembled contigs length	2719597	2717966	2719541	2719590	2720576	2720615	2718428	2719618	2717942	2719541	2719616	2720432	2720646	2718430	2719555	2717972	2719594	2719599	2720567	2720658	2718818
# 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	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	19	
# local misassemblies	10	10	9	10	9	9	9	20	9	9	9	9	9	9	9	8	8	9	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	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	26	26	26	26	26	26	24	26	26	26	26	26	26	26	26	26	26	26	26	22	
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	6	6	6	6	6	6	5	
# mismatches	7654	6816	7792	7763	7865	7914	6410	7679	6882	7664	7791	7641	8076	6613	7555	6675	7656	7547	7920	8054	6797
# indels	2952	970	2035	2048	3029	3024	4232	2967	1164	2007	2047	2994	3025	4241	2926	969	2108	2044	3117	3071	4462
# indels (<= 5 bp)	2885	904	1984	1997	2979	2973	4171	2893	1099	1956	1995	2943	2972	4181	2852	905	2056	1993	3062	3017	4406
# indels (> 5 bp)	67	66	51	51	50	51	61	74	65	51	52	51	53	60	74	64	52	51	55	54	56
Indels length	6848	4687	5388	5385	6828	6722	8352	6905	4943	5330	5393	6743	8348	4681	5461	5376	6887	6832	8548		

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_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw	
# fully unaligned contigs	0	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	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Partially unaligned length	21275184	21271369	21272515	21264526	21261875	21256848	21322161	21274830	21271766	21273207	21261392	21263246	21251966	21319606	21276777	21276207	21271604	21266299	21259924	21322355
# N's	0	10	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).

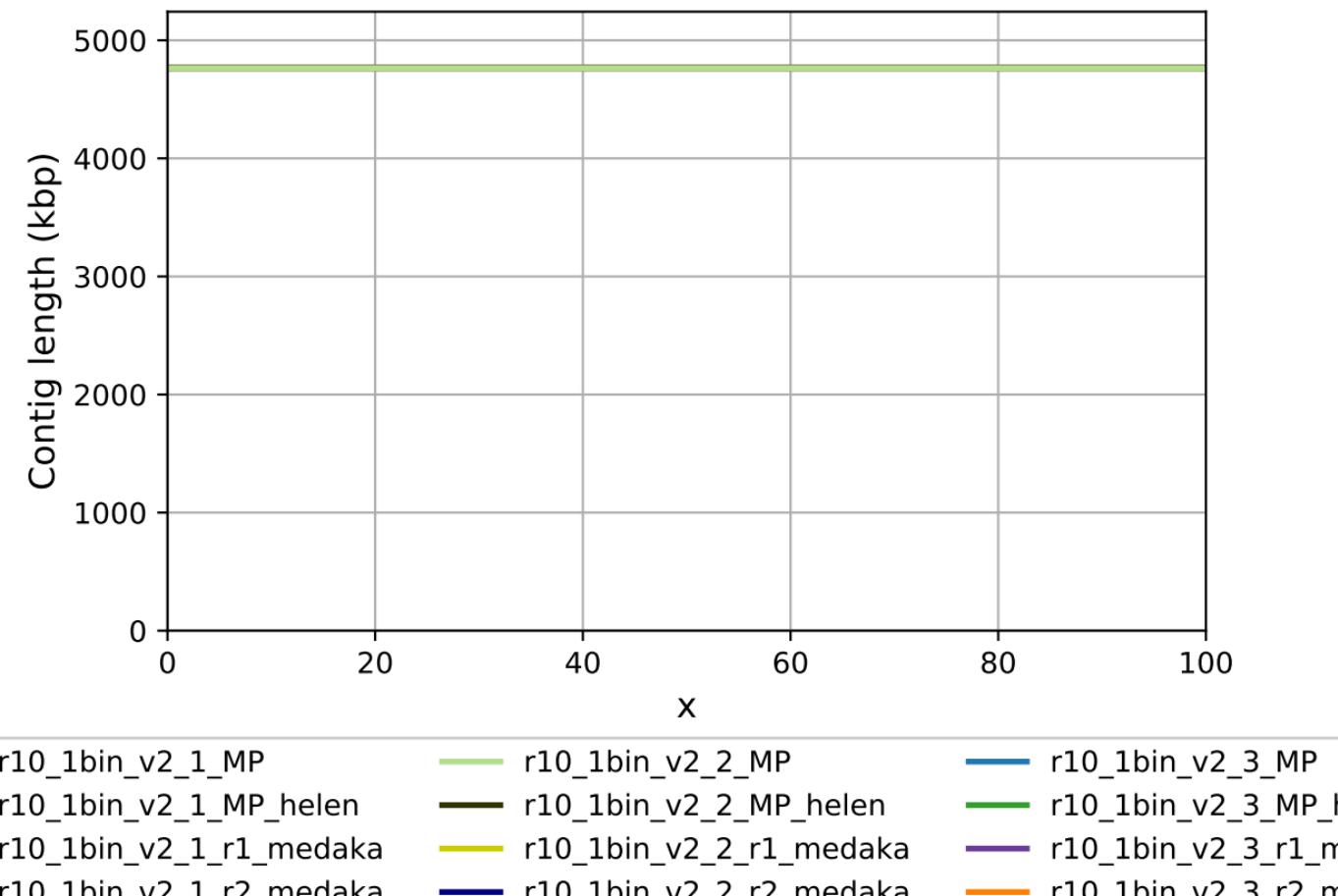


r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_1_r2_medaka

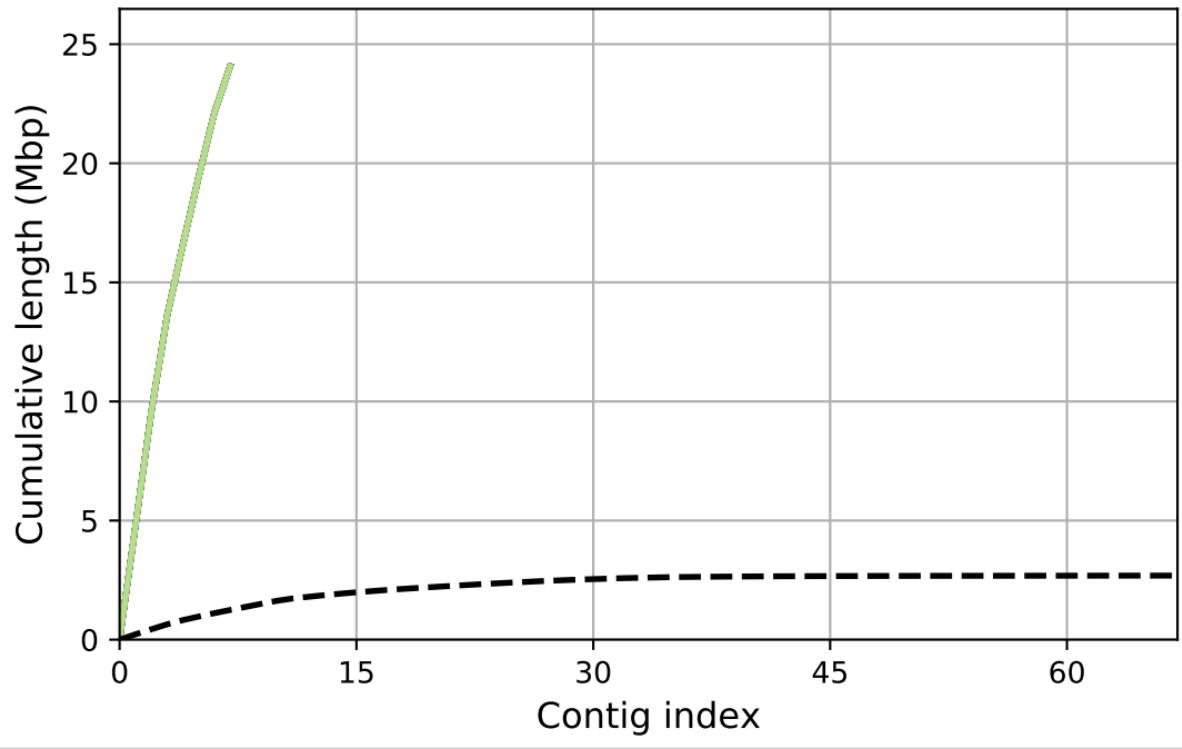
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r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_helen
r10_1bin_v2_3_r1_medaka
r10_1bin_v2_3_r2_medaka

NGx



Cumulative length



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

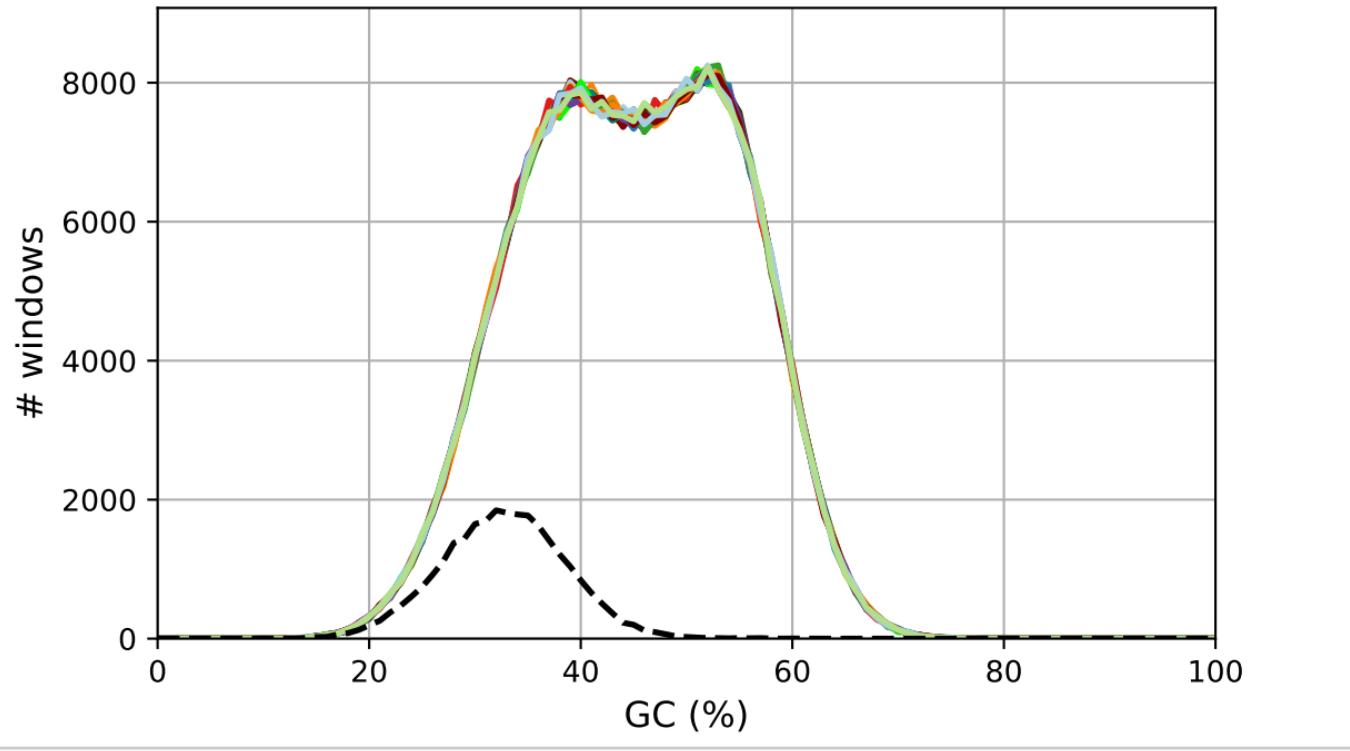
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r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racoon_r1

GC content

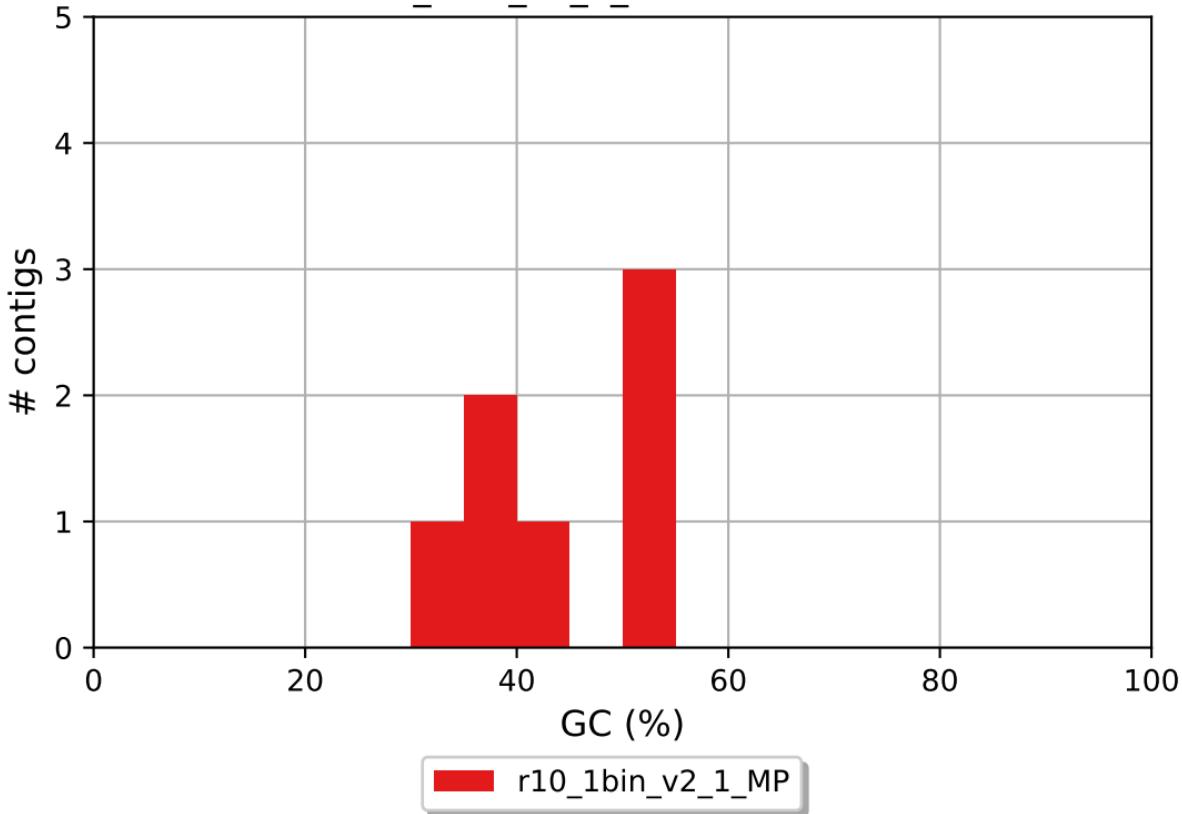


r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_1_r2_medaka

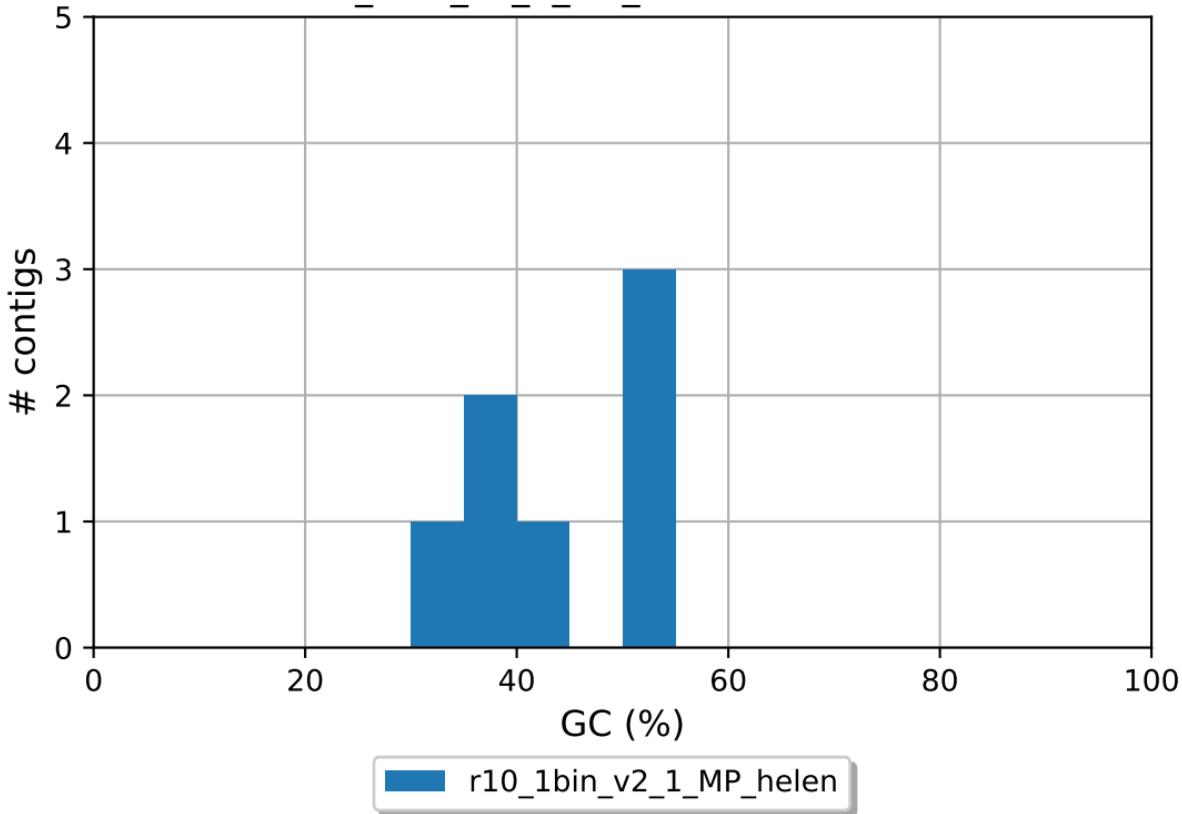
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— r10_1bin_v2_2_racon_r1

— r10_1bin_v2_3_MP_helen
— r10_1bin_v2_3_r1_medaka
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— r10_1bin_v2_3_racon_r1

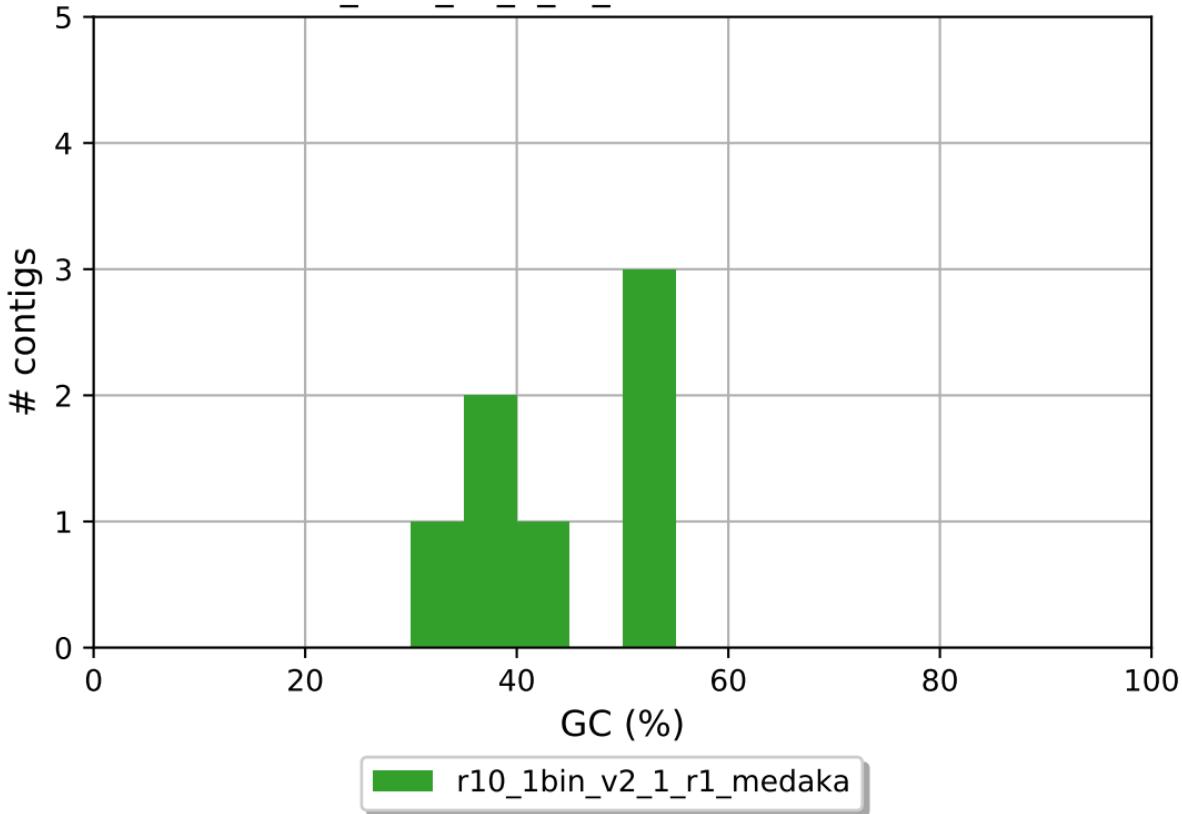
r10_1bin_v2_1_MP GC content



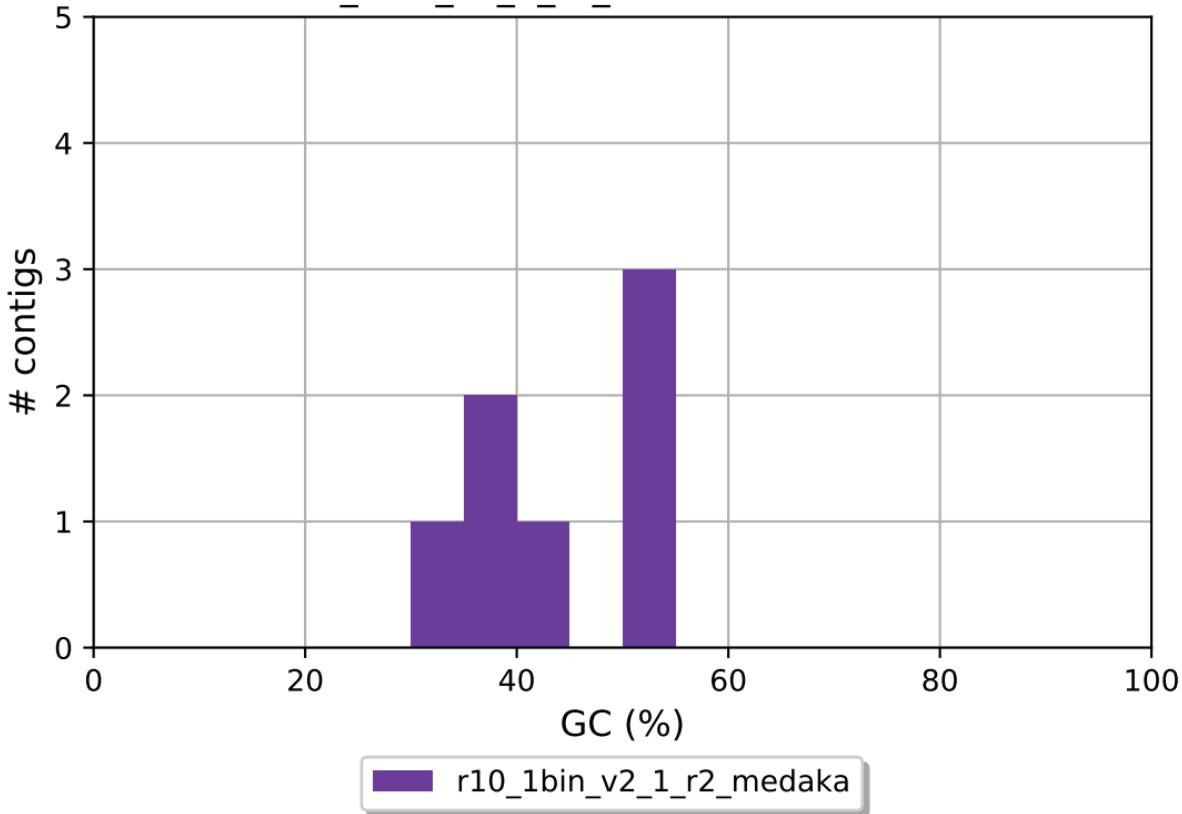
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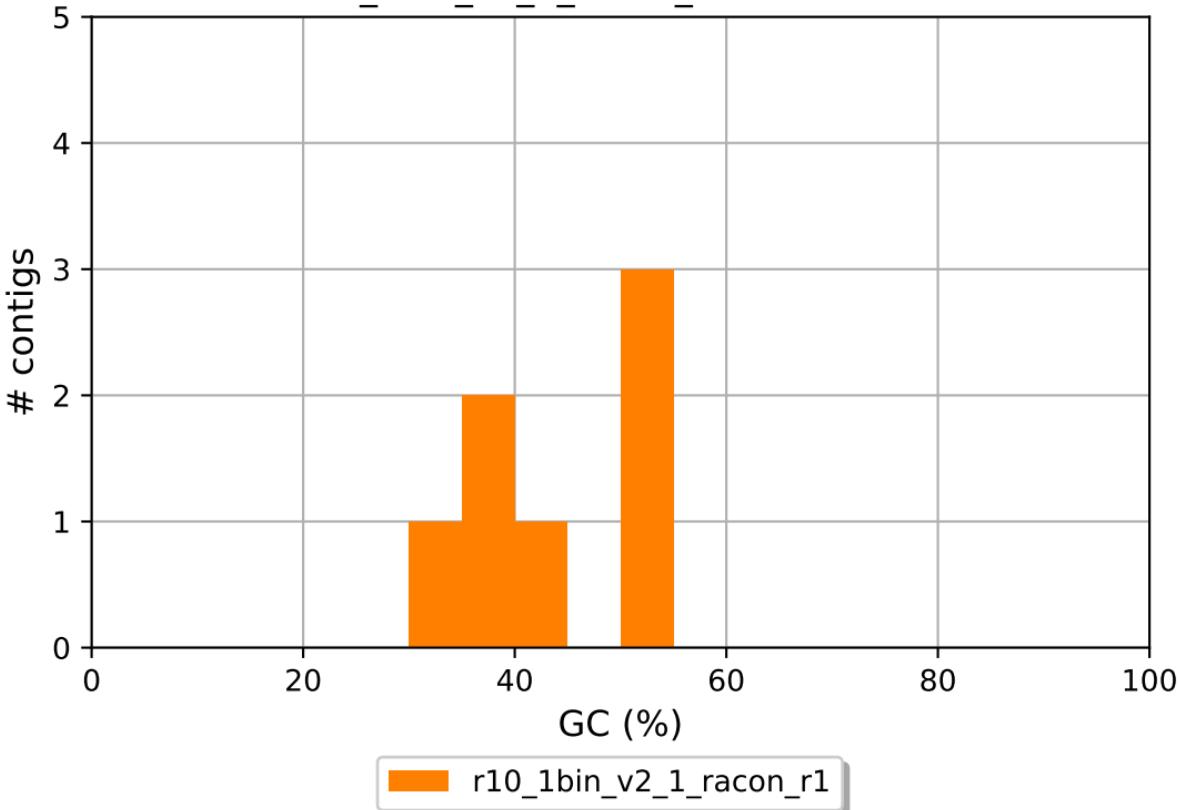
r10_1bin_v2_1_r1_medaka GC content



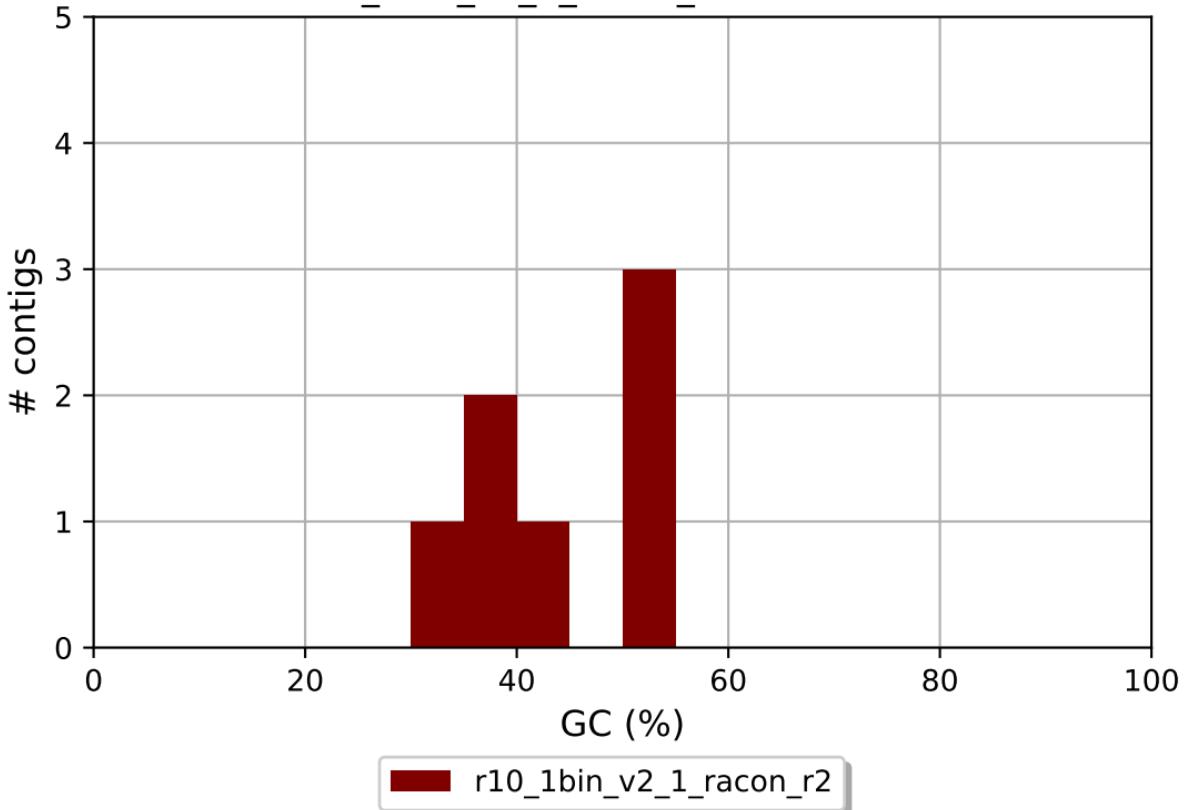
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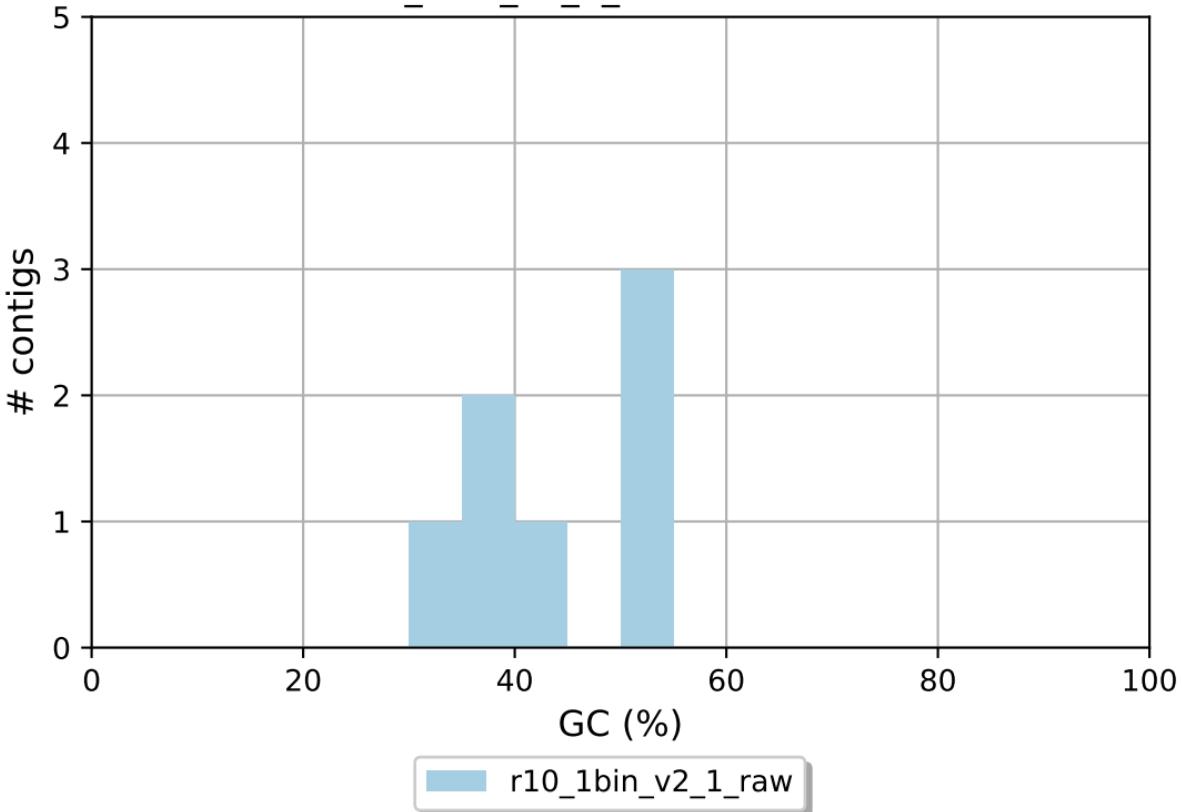
r10_1bin_v2_1_racon_r1 GC content



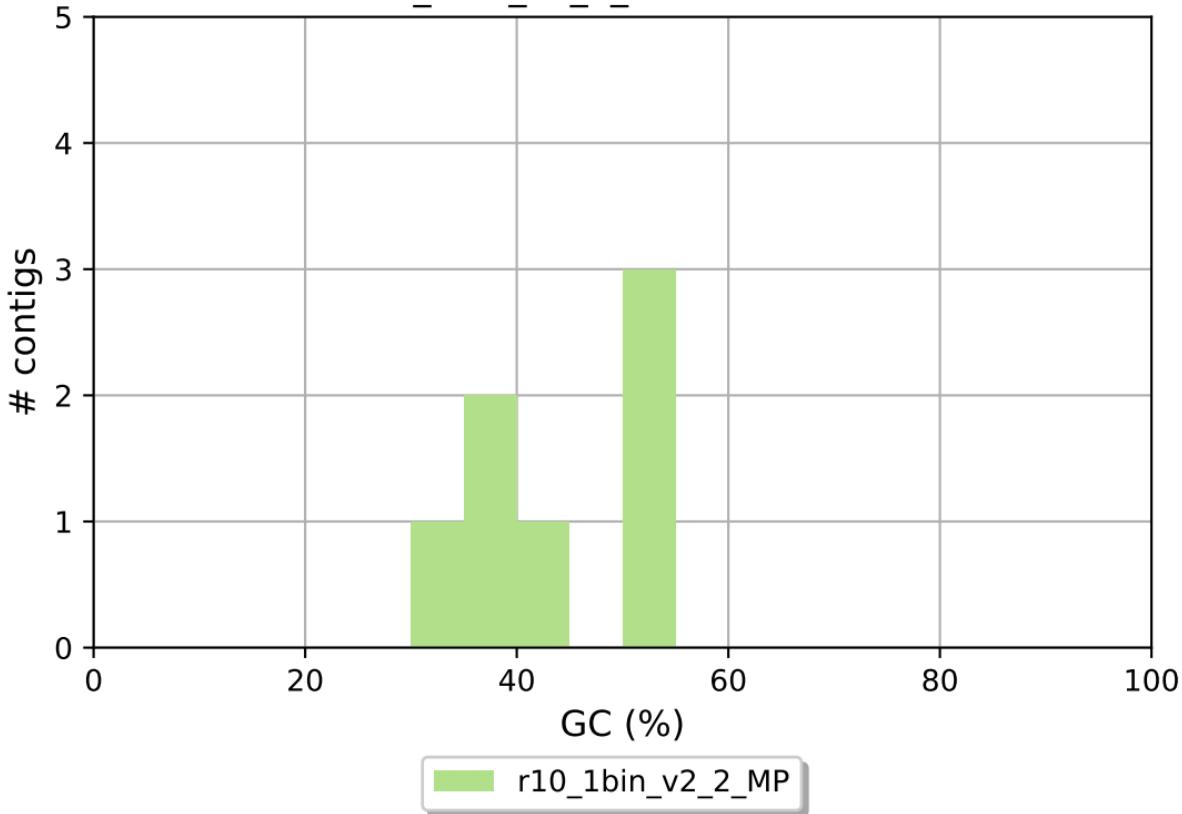
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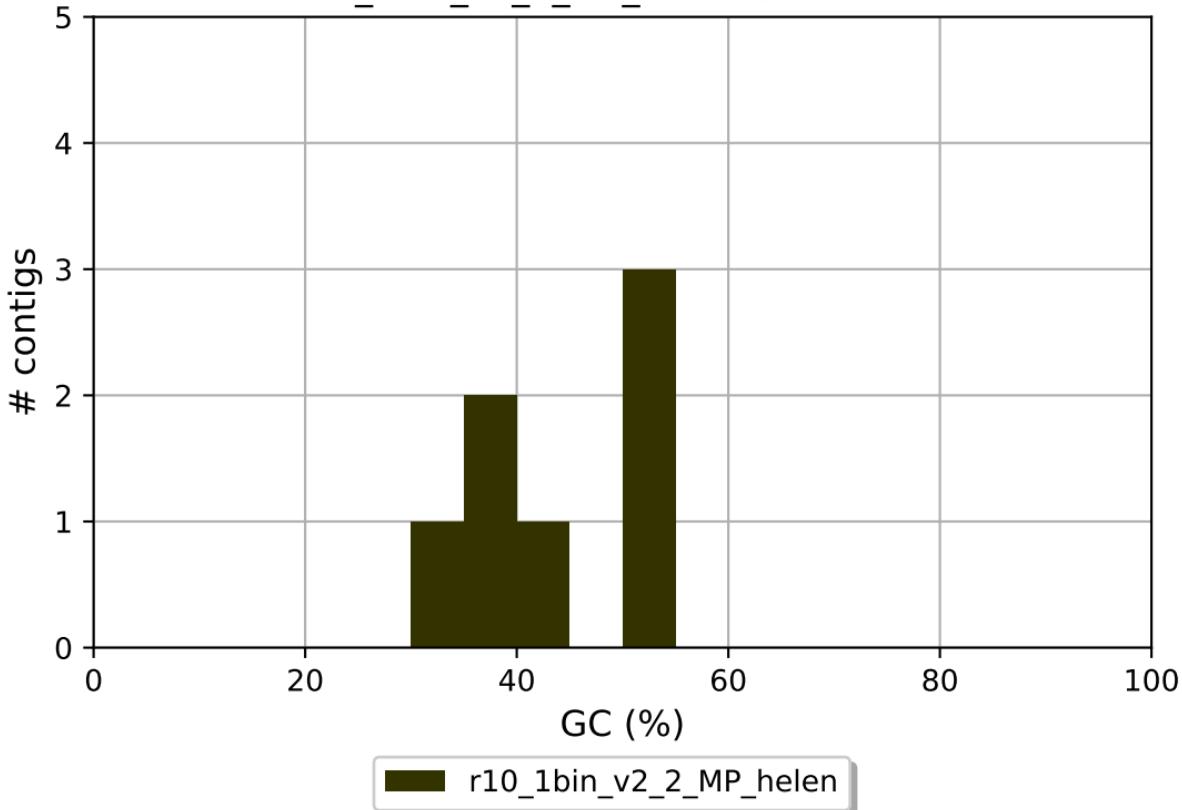
r10_1bin_v2_1_raw GC content



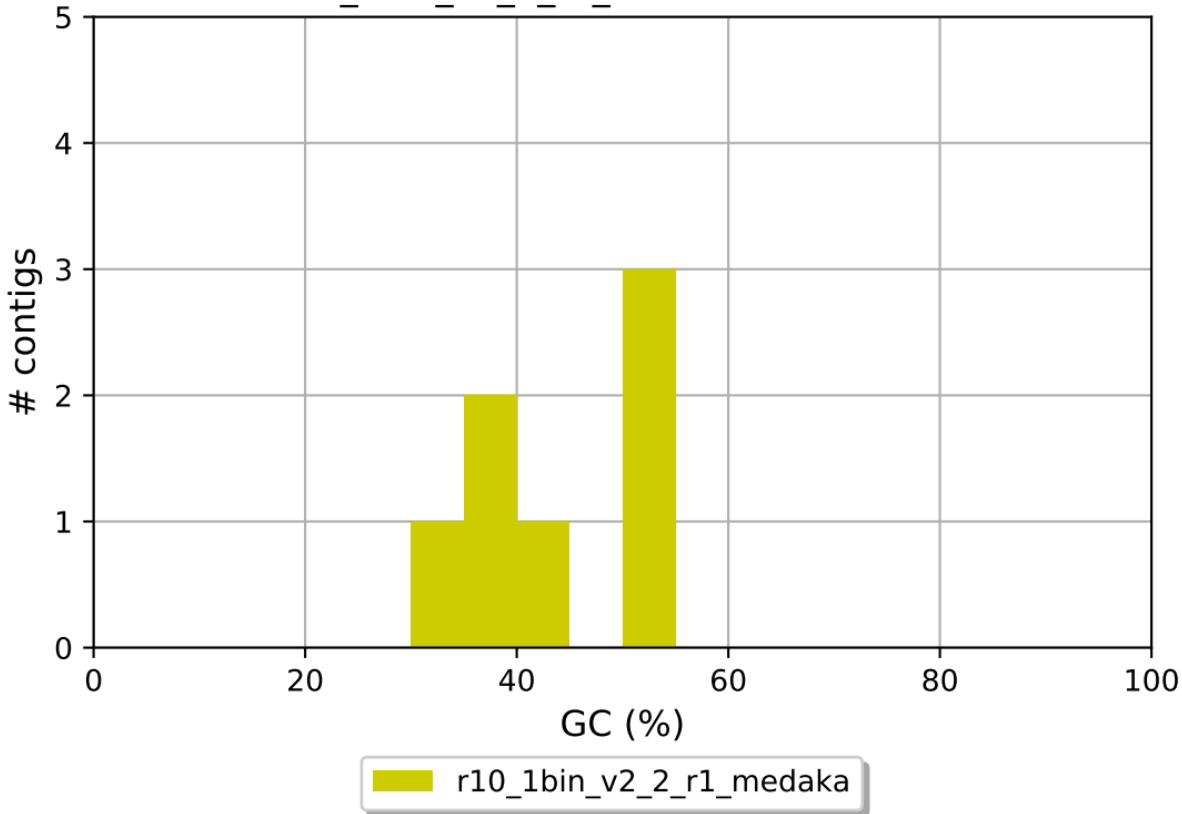
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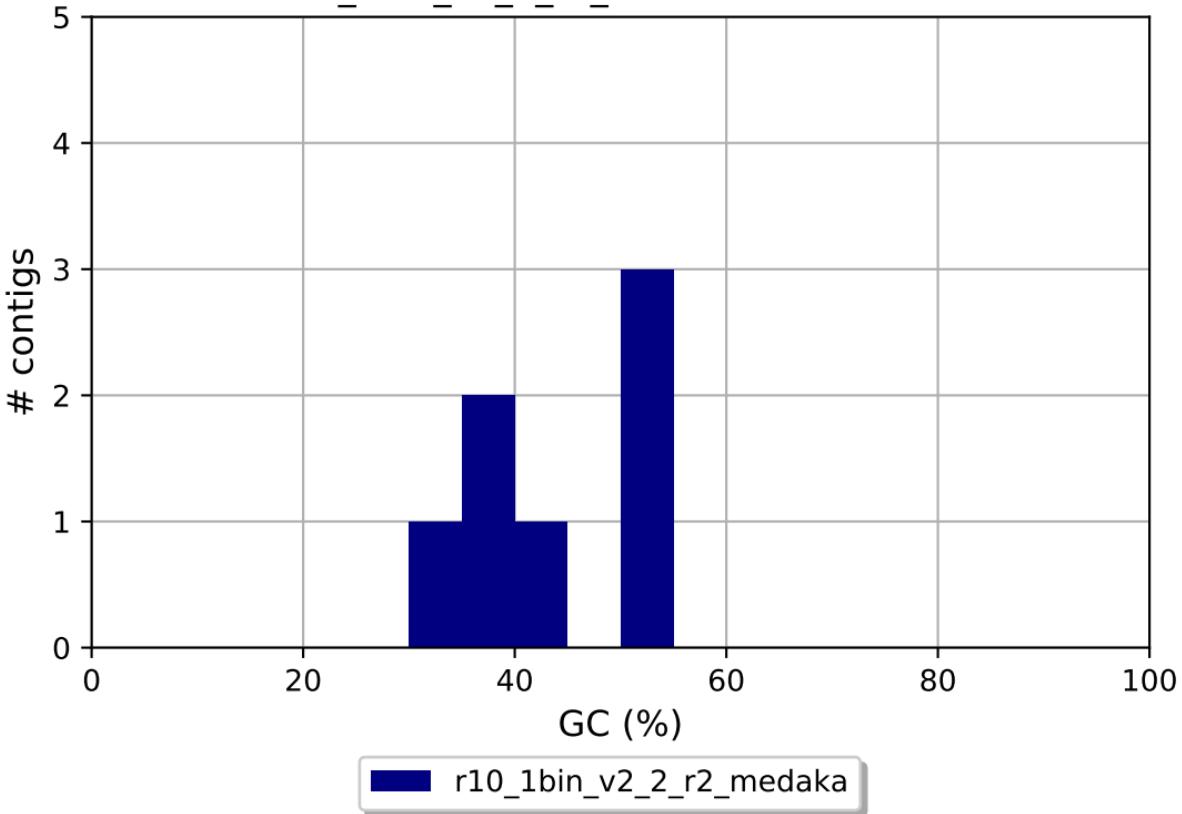
r10_1bin_v2_2_MP_helen GC content



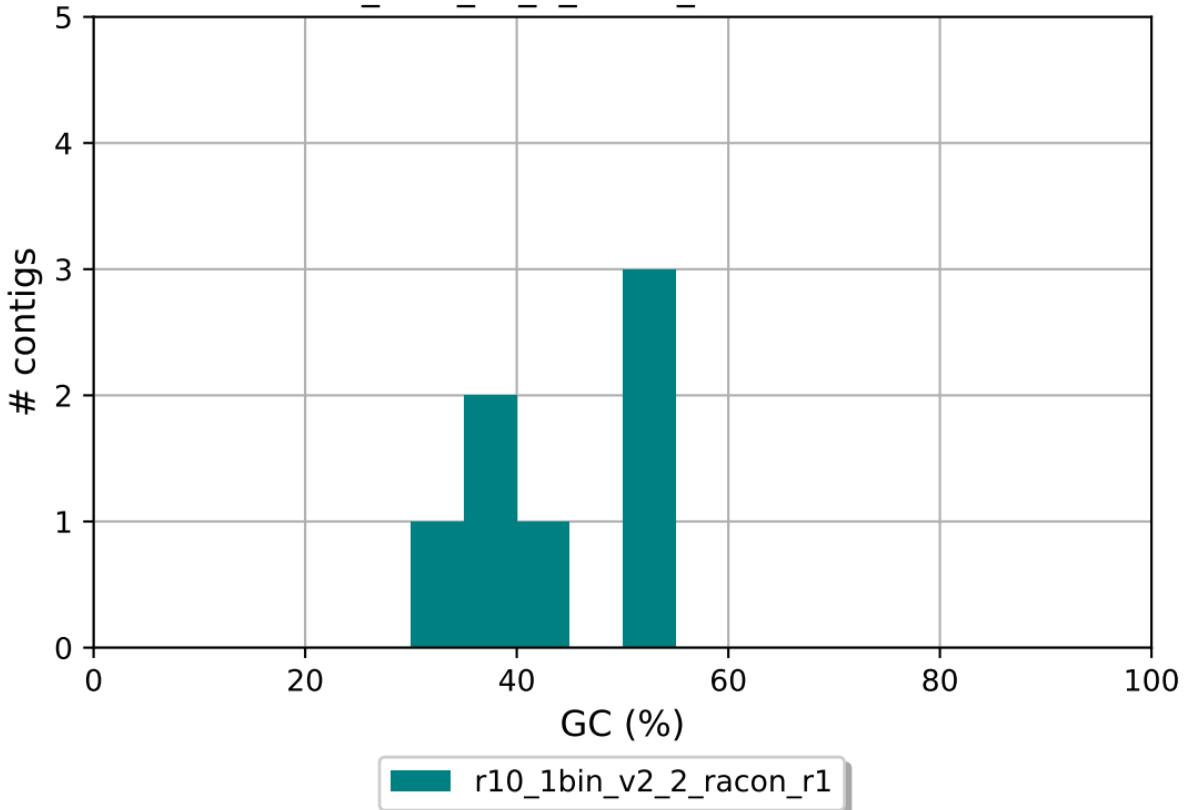
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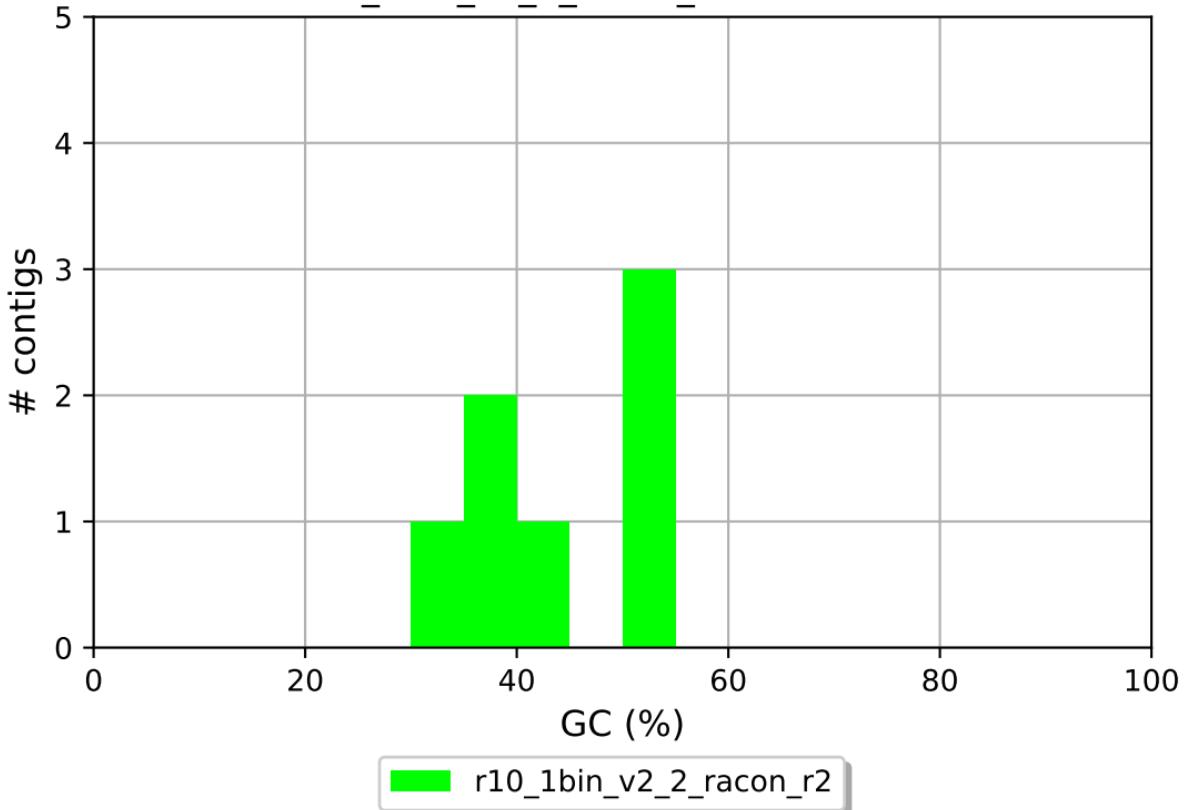
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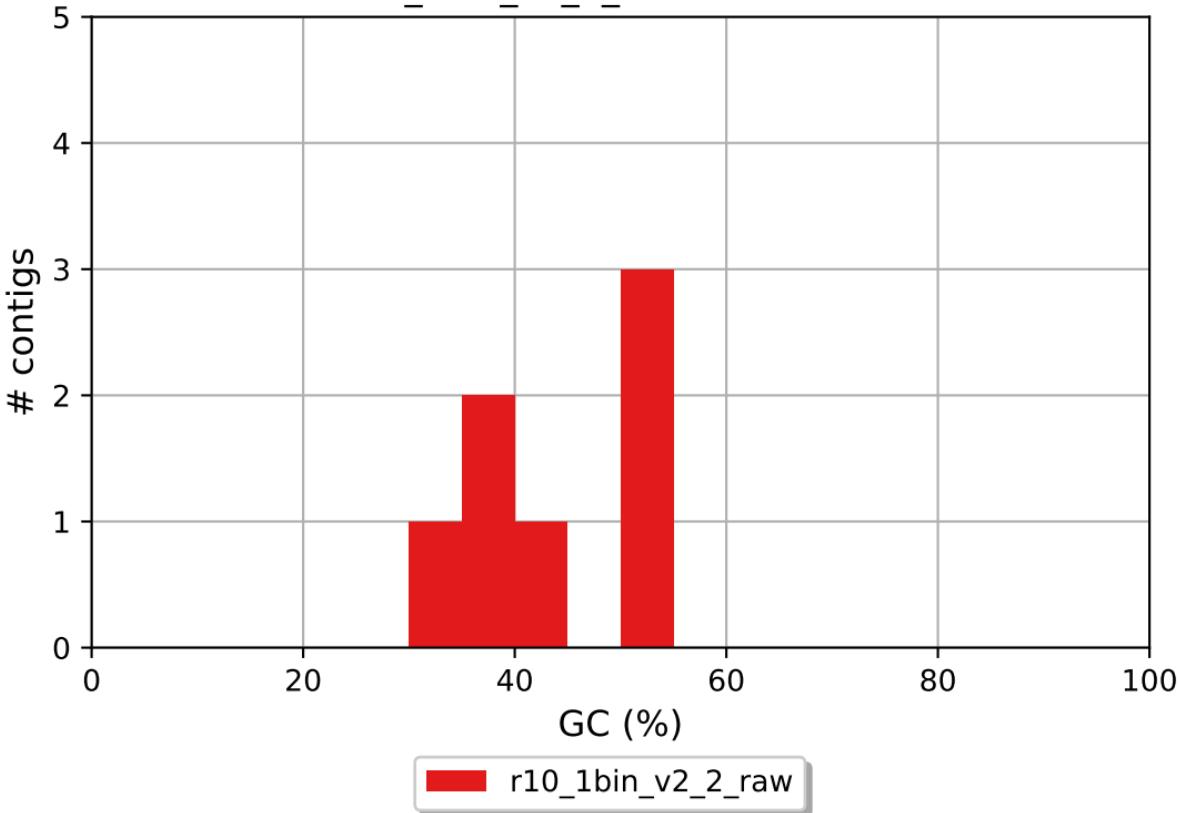
r10_1bin_v2_2_racon_r1 GC content



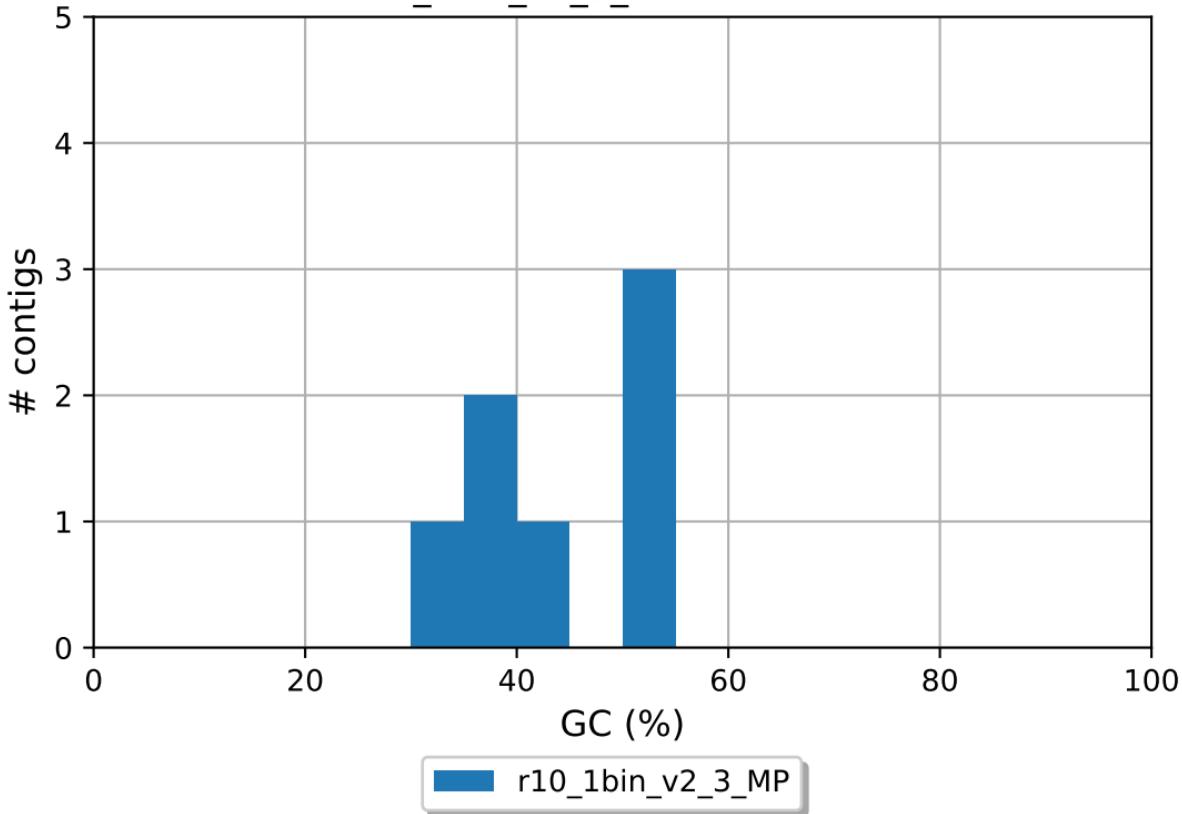
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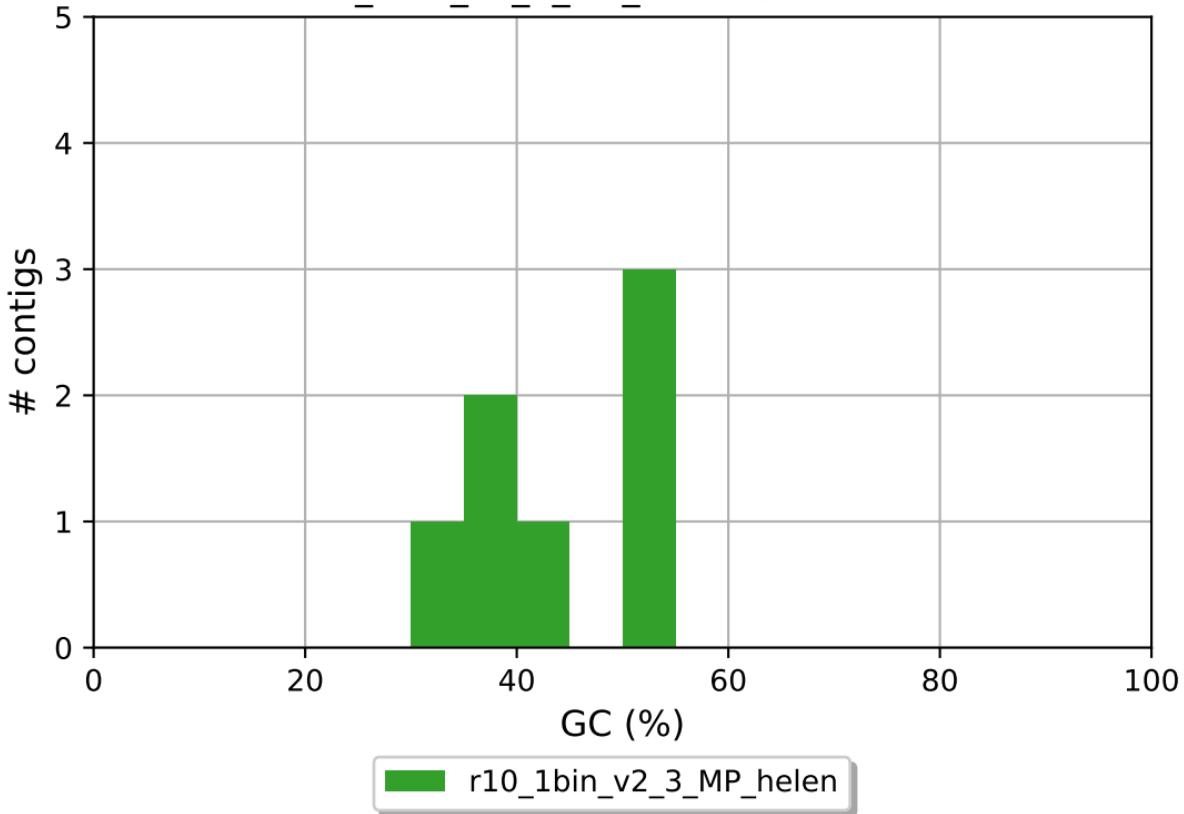
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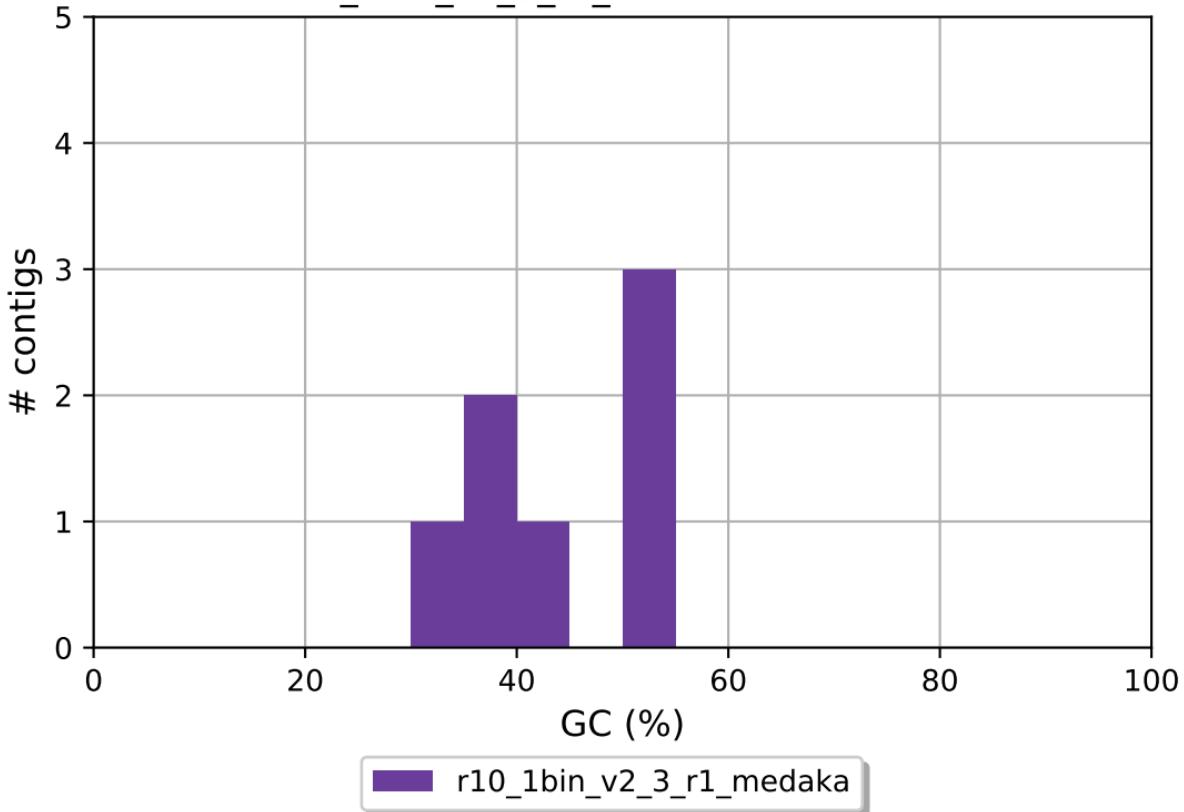
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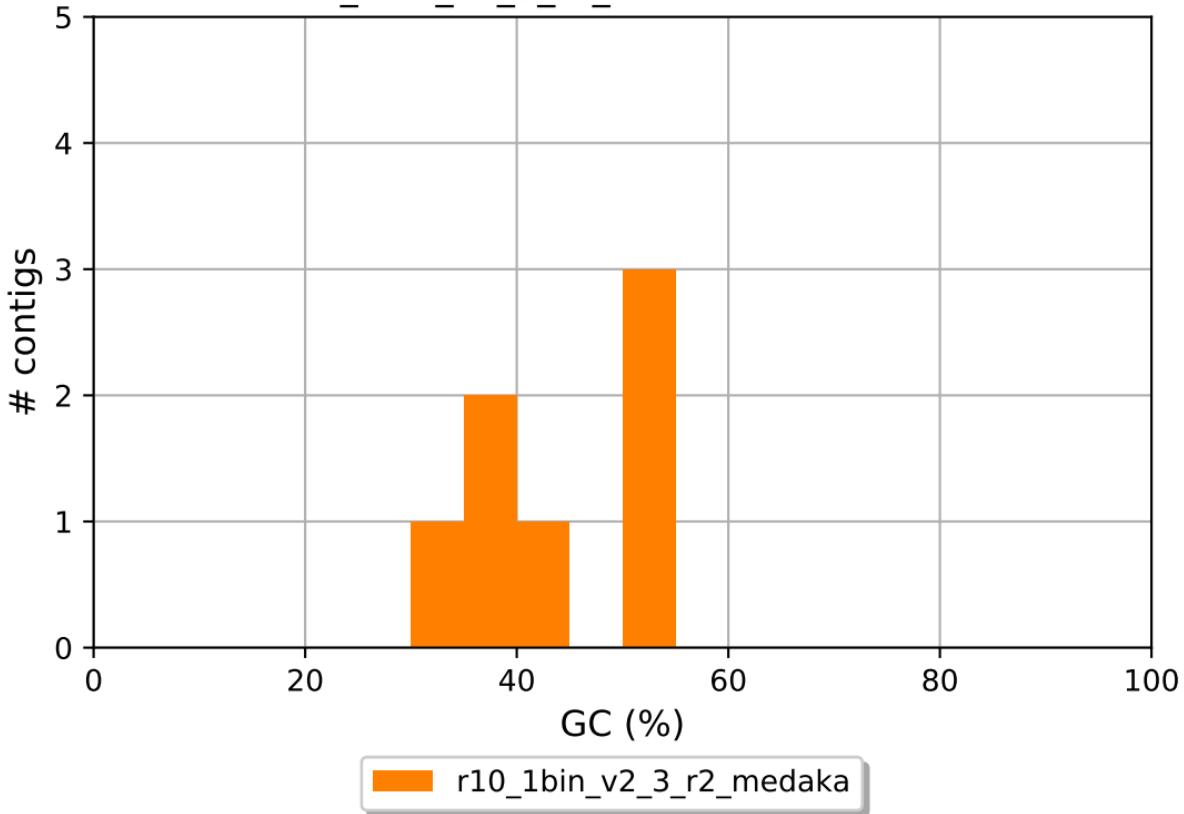
r10_1bin_v2_3_MP_helen GC content



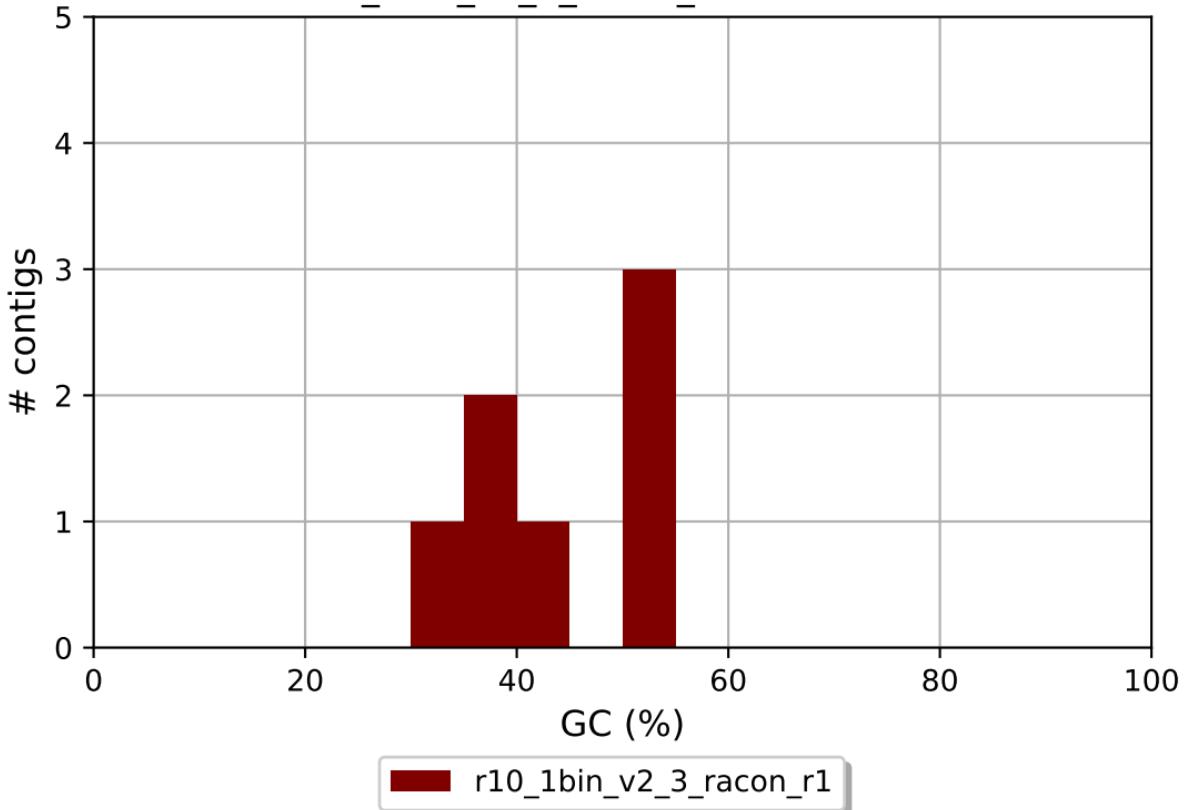
r10_1bin_v2_3_r1_medaka GC content



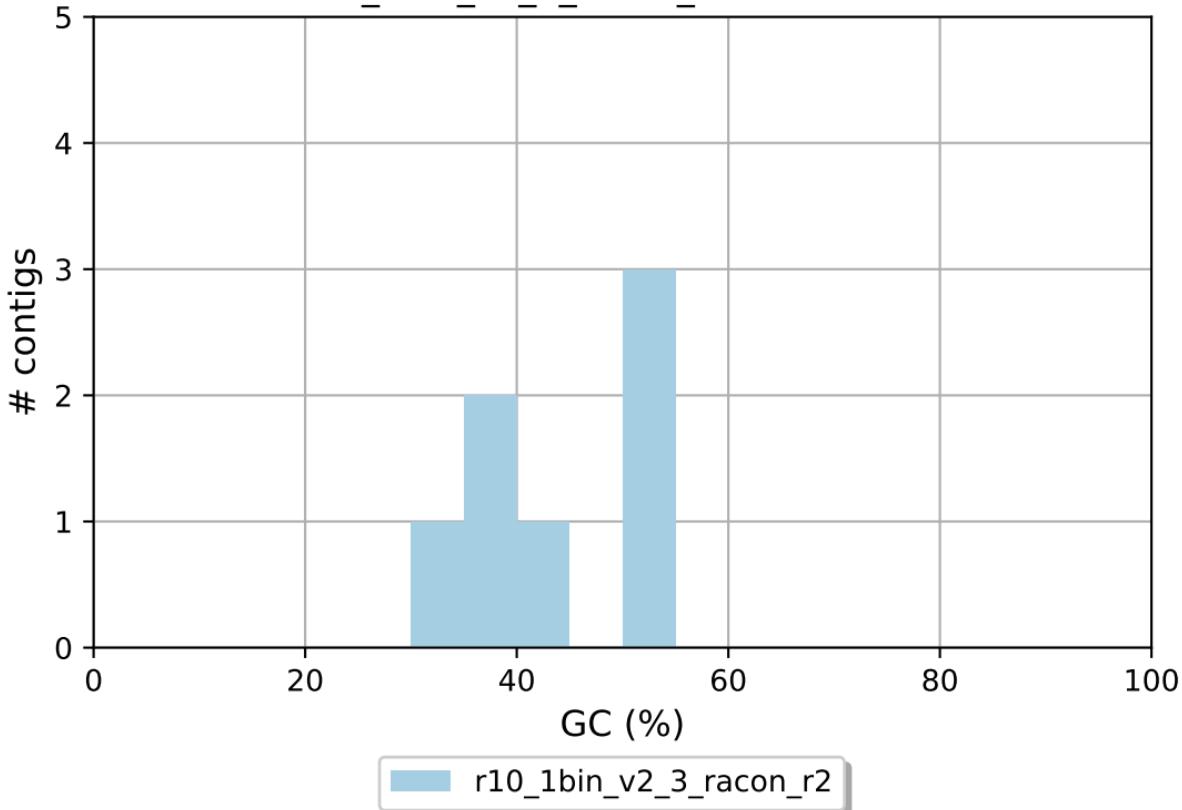
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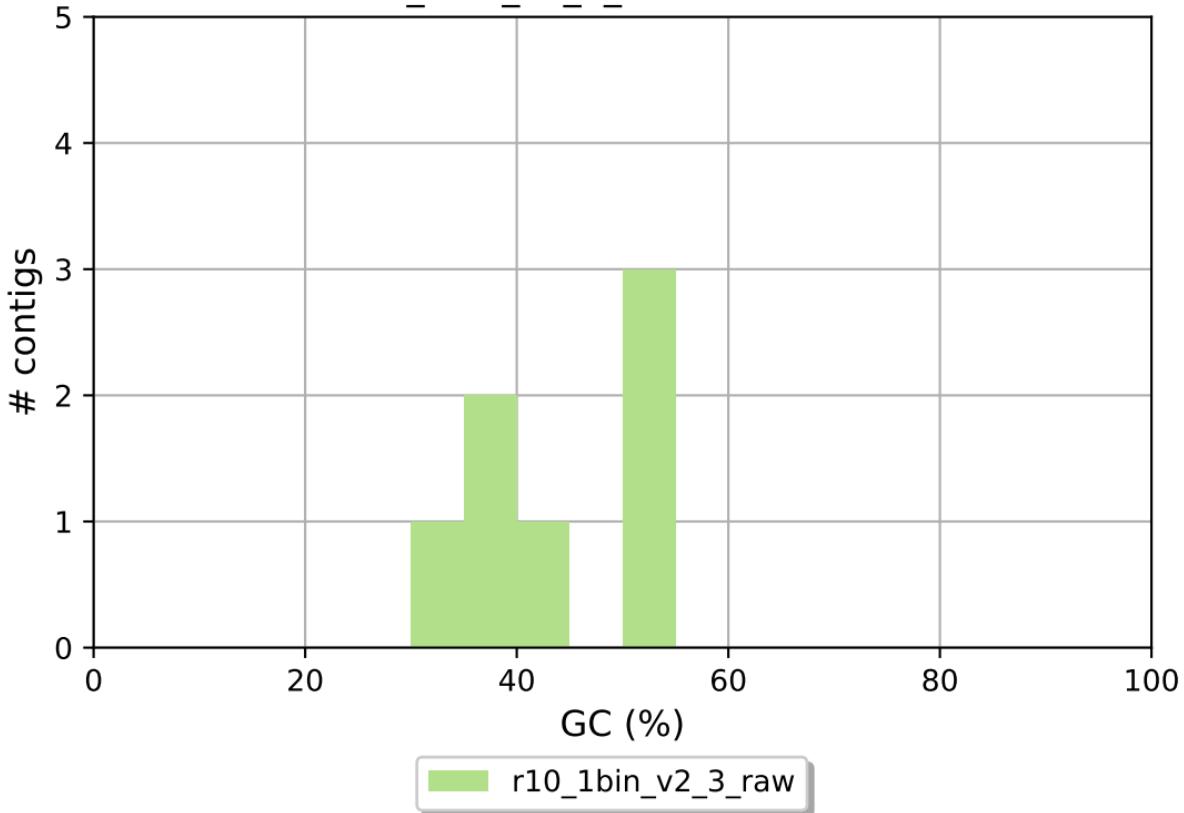
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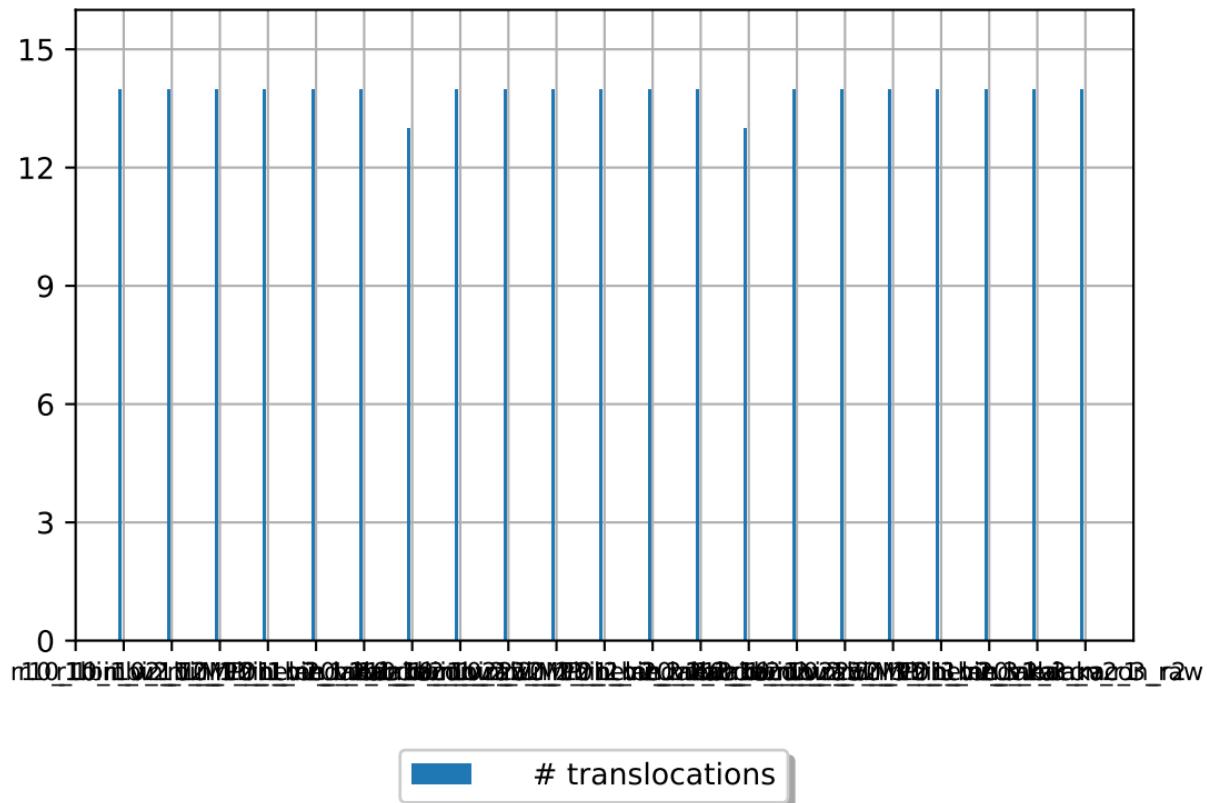
r10_1bin_v2_3_racon_r2 GC content



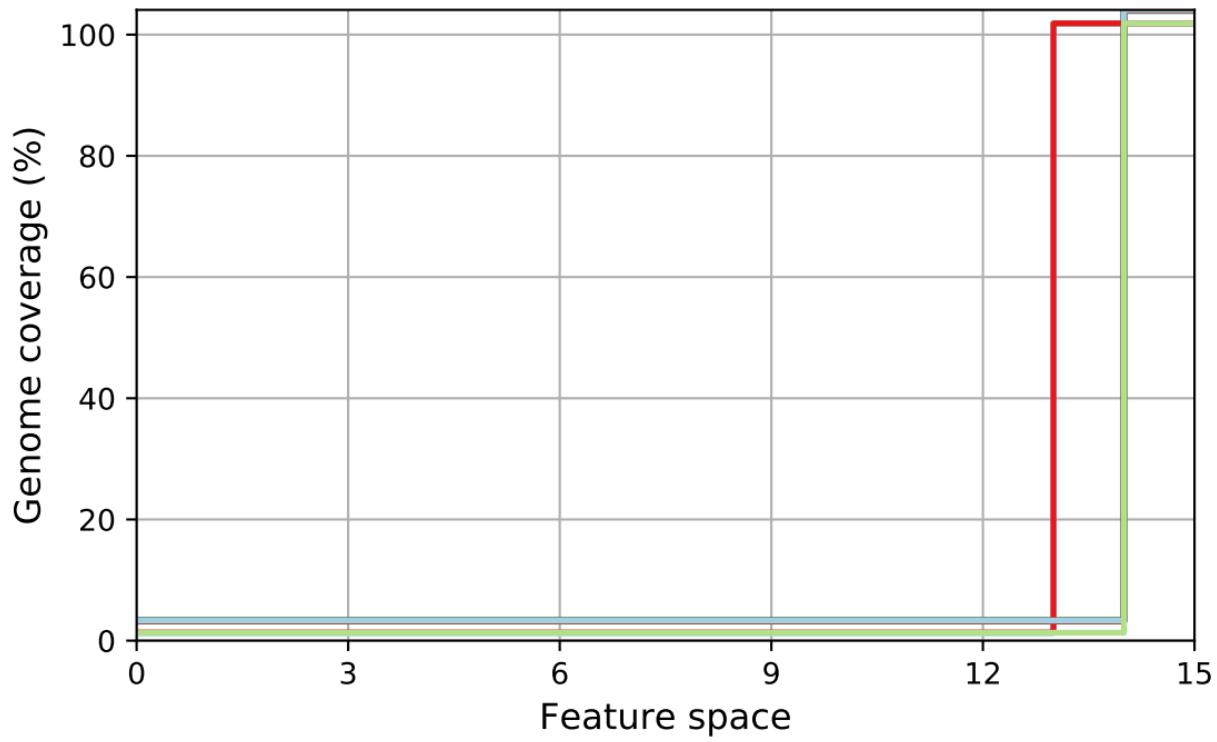
r10_1bin_v2_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

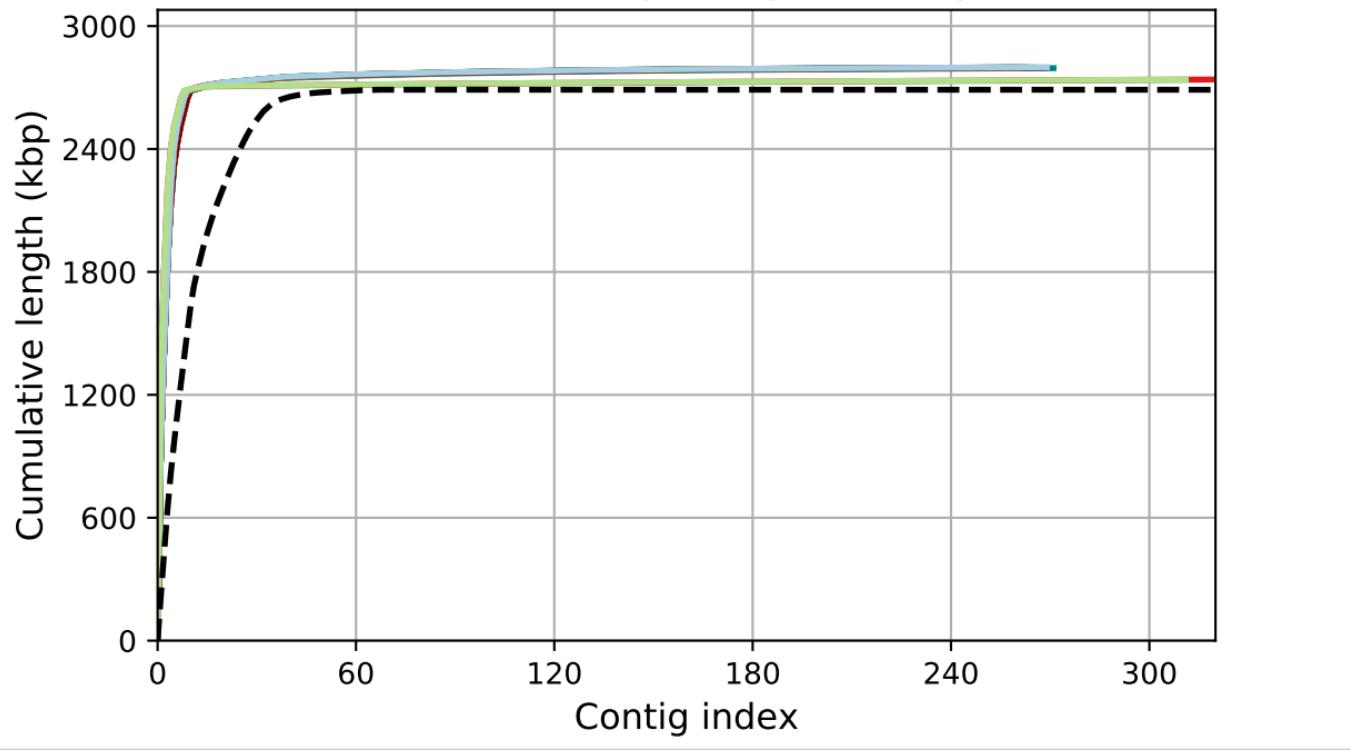
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racoon_r1

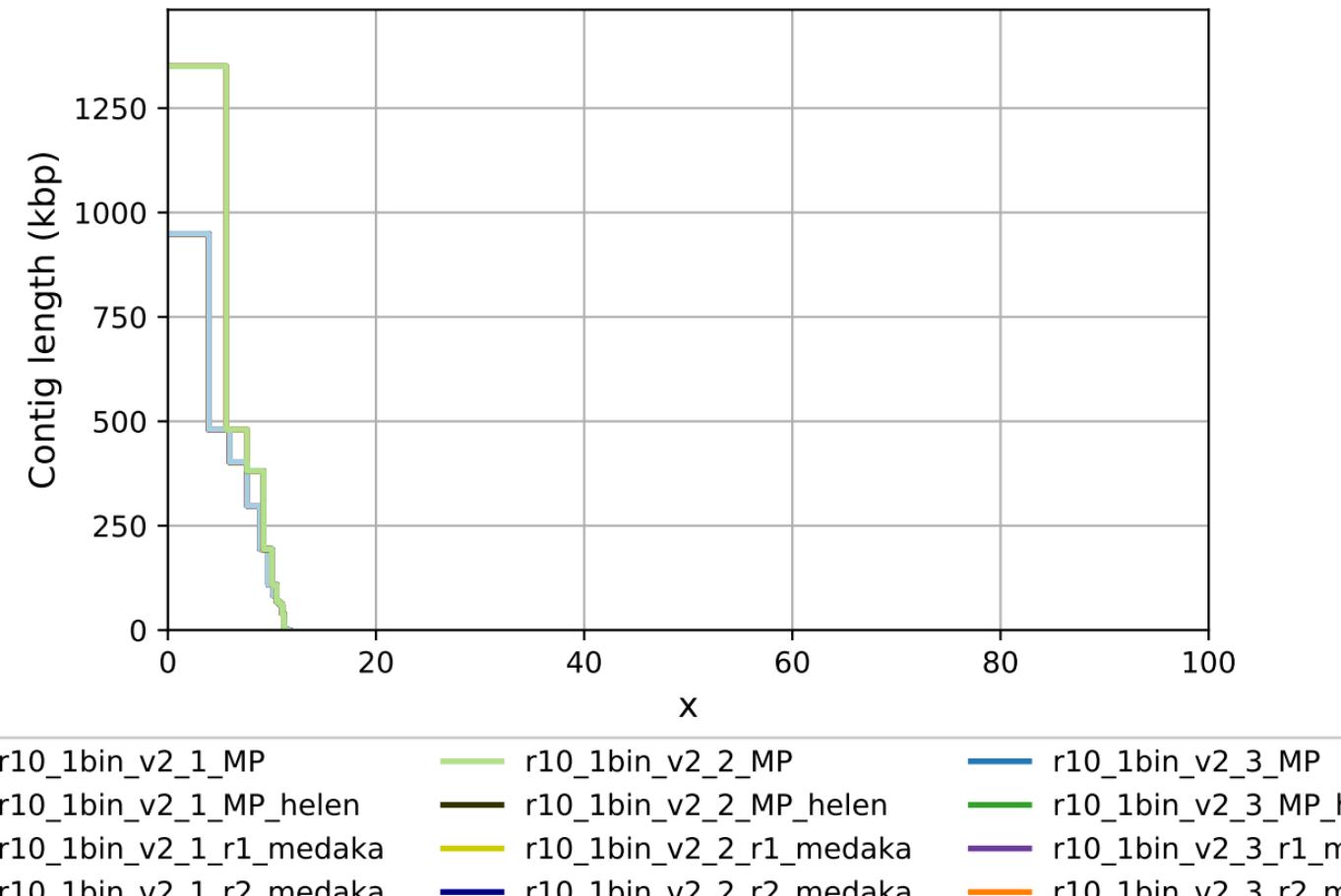
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racoon_r1

NAx



NGAx

