

Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_racon_r1	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24064158	24059056	28132800	
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24064158	24059056	28132800	
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24064158	24059056	28132800	
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24064158	24059056	28132800	
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7			
Largest contig	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	6787718
Total length	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	51.10	44.80	44.80	44.79	44.79	44.78	51.10	44.80	44.79	44.79	44.79	44.79	44.79	51.10	
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	
N50	4045594	4045616	4045591	4045596	4045200	4045302	4756098	4045598	4045623	4045846	4045845	4045161	4045304	4756089	4045599	4045602	4045842	4045840	4045210	4045276	4756074
NG50	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	6787718
N75	2845421	2845364	2845429	2845429	2845295	2845304	2990633	2845423	2845360	2845571	2845301	2990628	2845422	2845361	2845563	2845260	2845299	2990626			
NG75	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	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	21	21	21	21	21	21	19	21	21	21	21	21	21	21	21	21	21	21	19		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	4765884	4765881	4765833	4765837	4765031	4765076	4763514	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
# local misassemblies	36	36	36	36	36	36	58	36	36	37	37	36	36	37	37	36	36	36	62		
# 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	6	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	19039678	19035435	19036101	19028114	19024190	19018053	23181250	19039066	19035399	19036973	19030194	19027567	19018512	23182729	19043407	19036231	19042055	19035604	19029052	19018318	23185362
Genome fraction (%)	97.703	97.703	97.703	97.703	97.703	97.703	97.666	97.703	97.703	97.701	97.701	97.703	97.703	97.701	97.701	97.701	97.703	97.703	97.661		
Duplication ratio	1.077	1.077	1.077	1.077	1.077	1.077	1.059	1.077	1.077	1.077	1.076	1.077	1.077	1.077	1.077	1.077	1.077	1.078	1.058		
# 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	0.36		
# mismatches per 100 kbp	441.48	437.35	440.58	439.96	447.02	451.49	487.28	443.42	439.68	446.90	442.49	438.96	450.01	484.40	442.36	438.25	44				

Misassemblies report

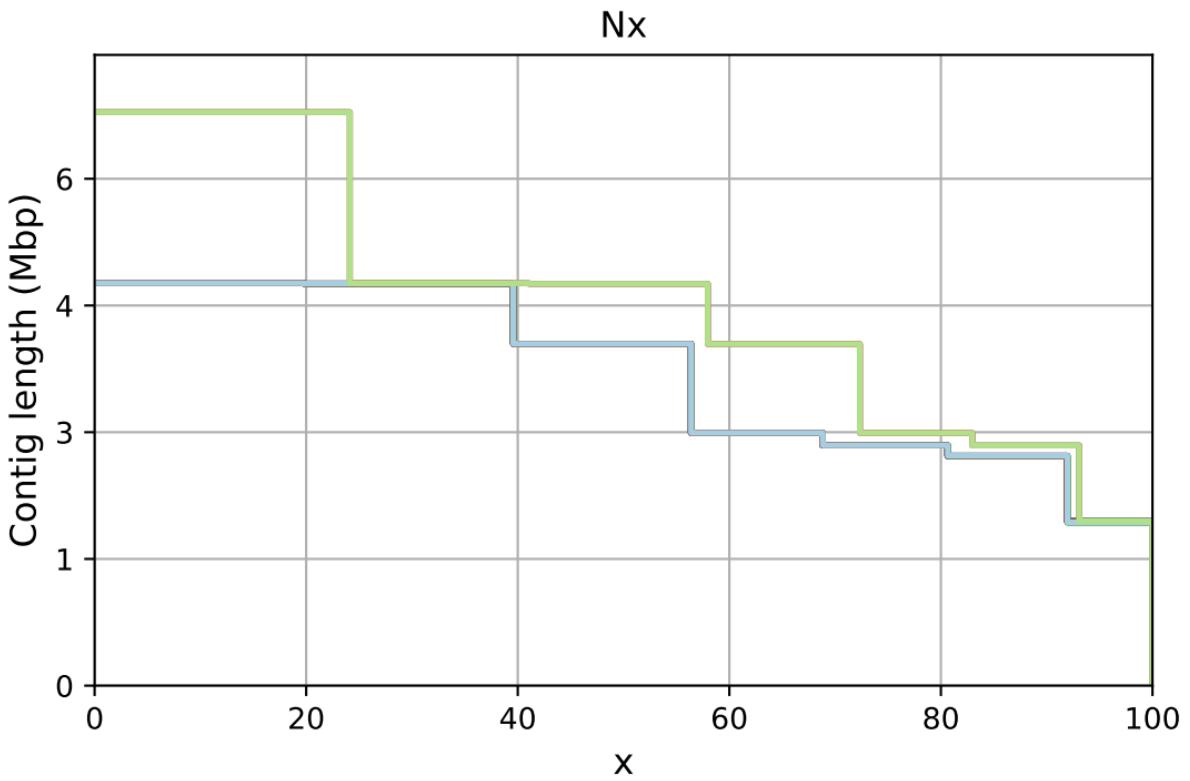
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# misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	19	
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	19	
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	18	20	20	20	20	20	18	
# c. inversions	0	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	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	
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Misassembled contigs length	4765884	4765881	4765833	4765837	4765031	4765076	4765314	4765366	4765332	4765684	4765663	4764521	4764646	4763440	4765358	4765330	4765688	4765655	4764491	4764636	4763330
# 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	12	12	12	12	12	12	33	12	12	12	12	12	12	34	12	12	12	12	12	34	
# local misassemblies	36	36	36	36	36	36	58	36	36	36	36	36	36	60	36	36	36	36	36	62	
# 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	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	35	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	
# mismatches	20646	20453	20604	20575	20905	21114	22779	20737	20562	20899	20693	20528	21045	22644	20687	20495	20745	20691	20792	21389	22660
# indels	961	787	738	712	1885	1724	11172	965	860	998	977	1841	1714	11063	953	841	1015	979	1863	1698	11070
# indels (<= 5 bp)	858	687	640	614	1788	1626	10964	866	759	902	881	1744	1616	10860	854	741	919	883	1764	1601	10866
# indels (> 5 bp)	103	100	98	98	97	98	208	99	101	96	96	97	98	203	99	100	96	96	97	204	
Indels length	6264	6067	5970	5943	7308	7092	20575	6247	6122	7087	20443	6217	7224	6140	6173	6125	7255	7052	20402		

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_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	19039678	19035435	19036101	19028114	19024190	19018053	23181250	19039066	19035399	19036973	19030194	19027567	19018512	23182729	19043407	19036231	19042055	19029052	19018318	23185362
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	100	

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).

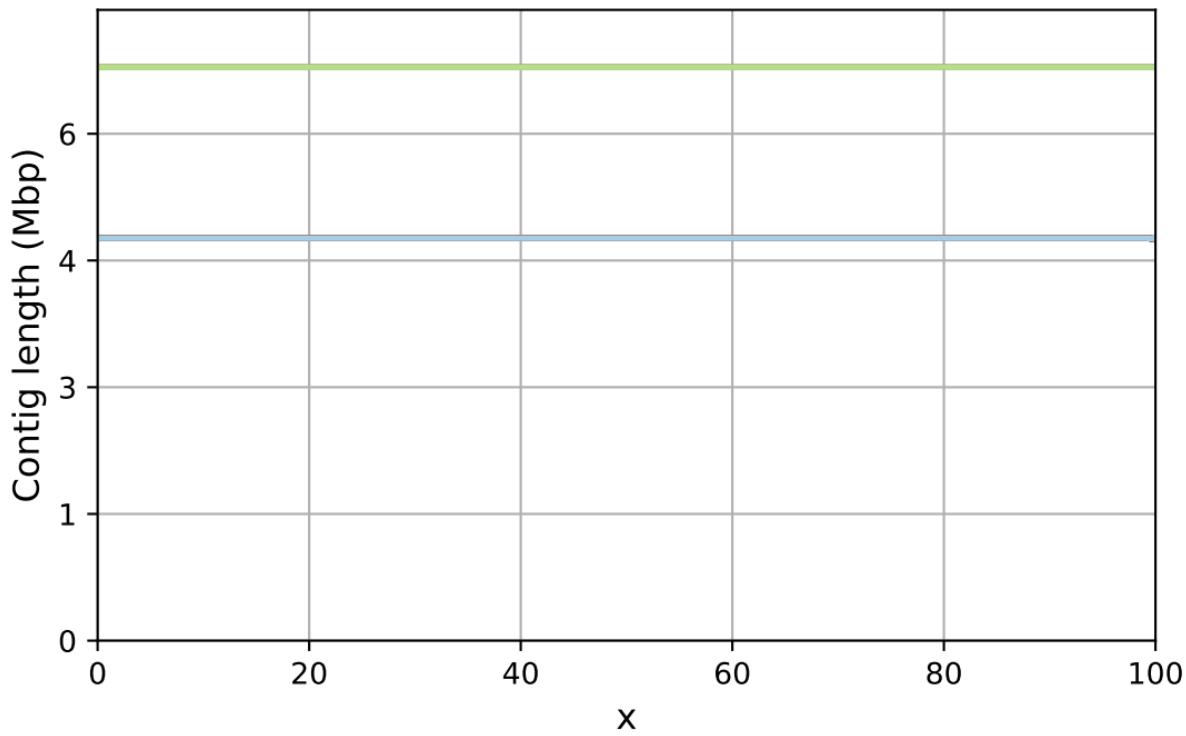


r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP_H
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

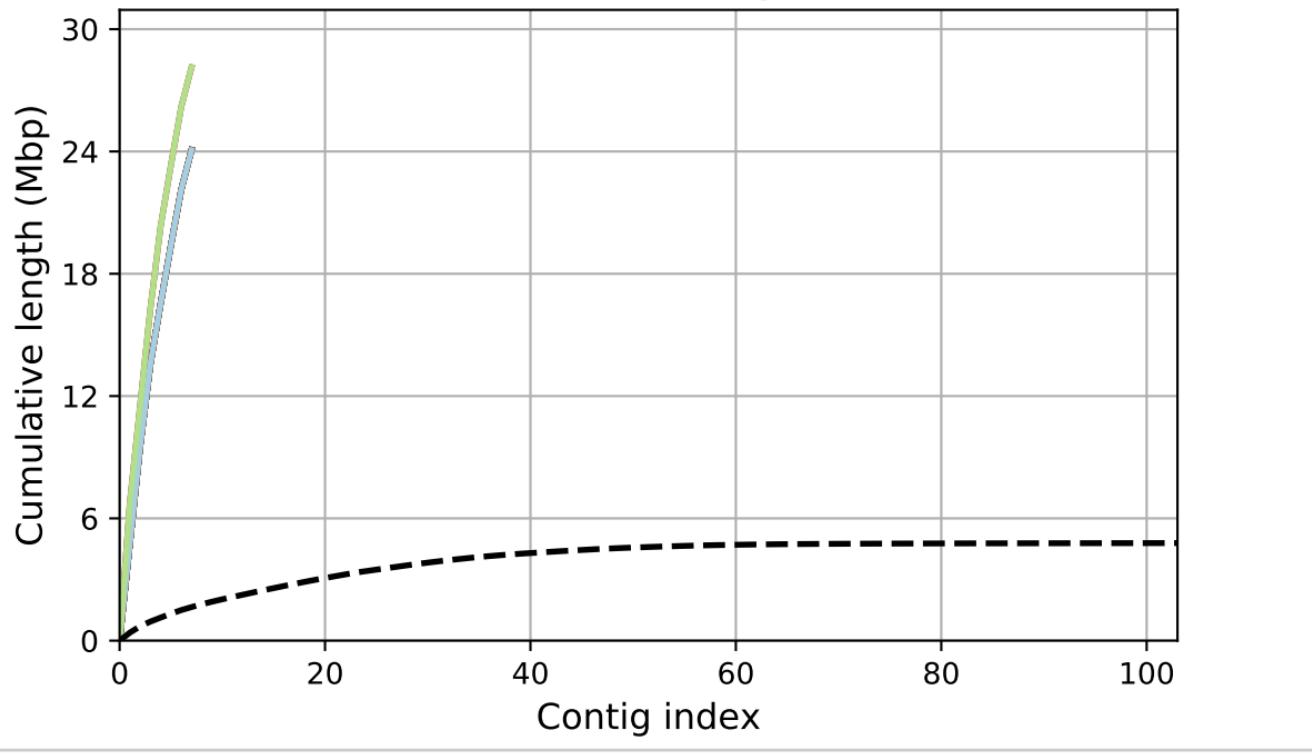
NGx



Legend:

- r10_1bin_v3_1_MP
- r10_1bin_v3_1_MP_helen
- r10_1bin_v3_1_r1_medaka
- r10_1bin_v3_1_r2_medaka
- r10_1bin_v3_2_MP
- r10_1bin_v3_2_MP_helen
- r10_1bin_v3_2_r1_medaka
- r10_1bin_v3_2_r2_medaka
- r10_1bin_v3_3_MP
- r10_1bin_v3_3_MP_helen
- r10_1bin_v3_3_r1_medaka
- r10_1bin_v3_3_r2_medaka

Cumulative length



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racoon_r1

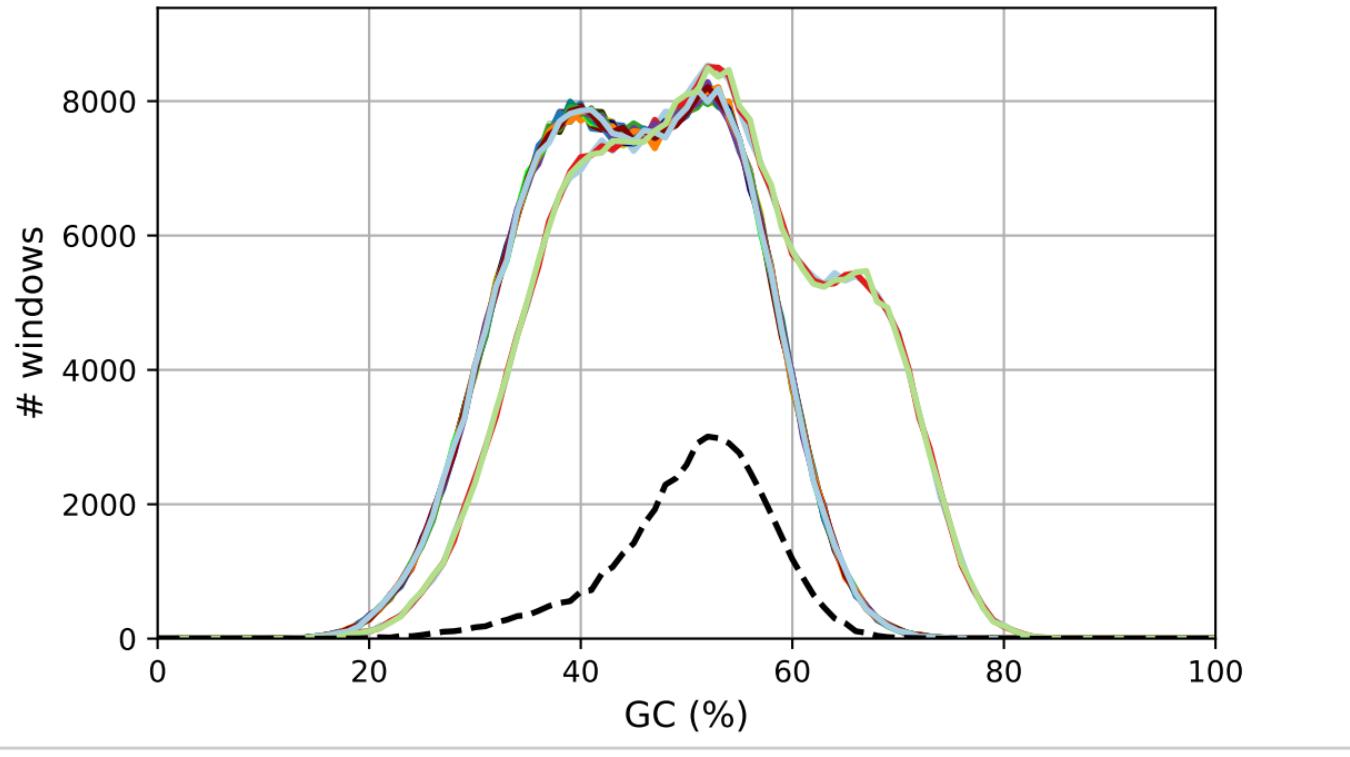
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r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racoon_r1

GC content



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racoon_r1

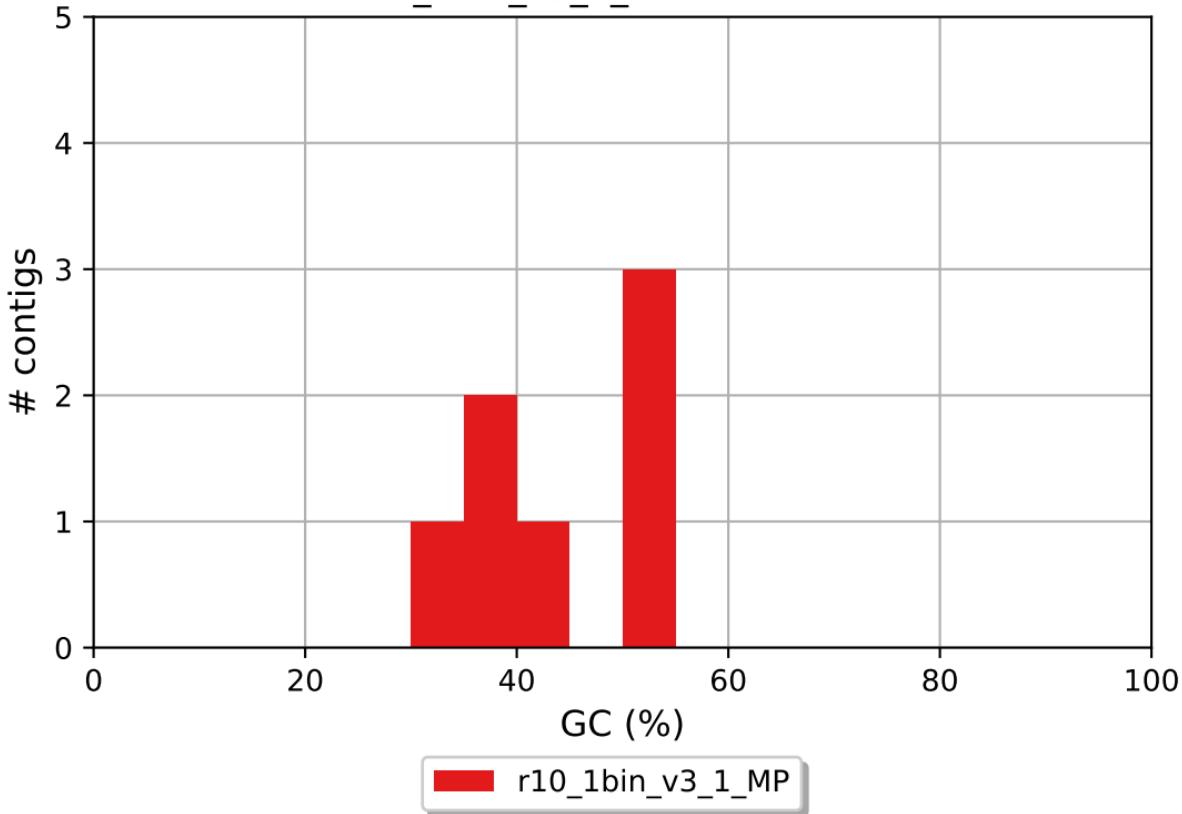
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r10_1bin_v3_3_r1_medaka

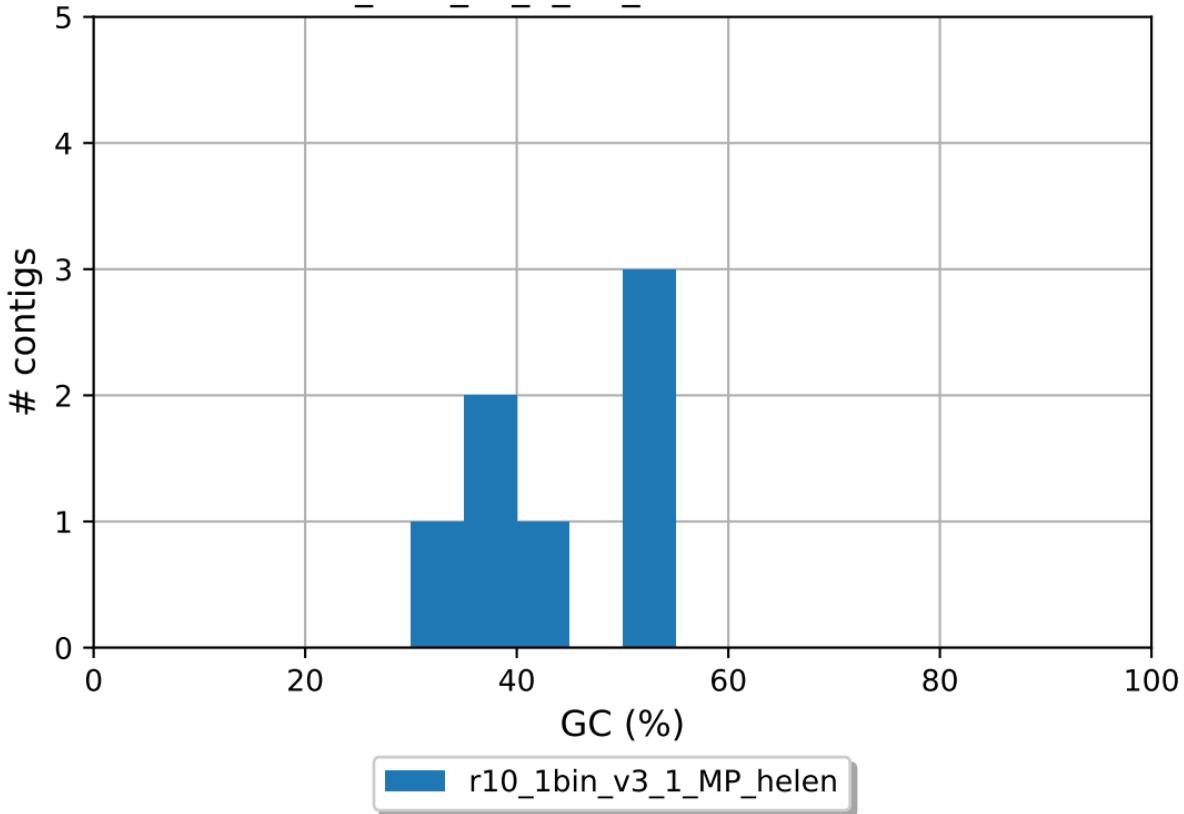
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r10_1bin_v3_3_racoon_r1

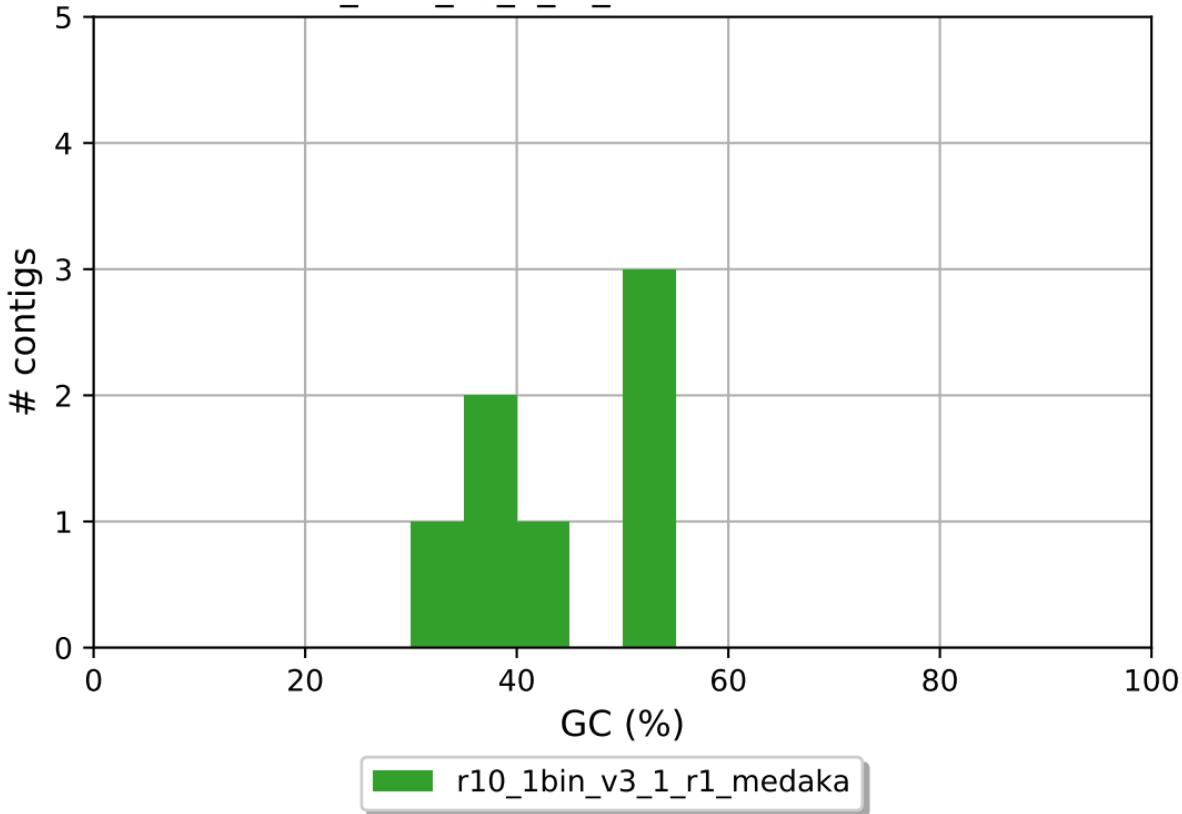
r10_1bin_v3_1_MP GC content



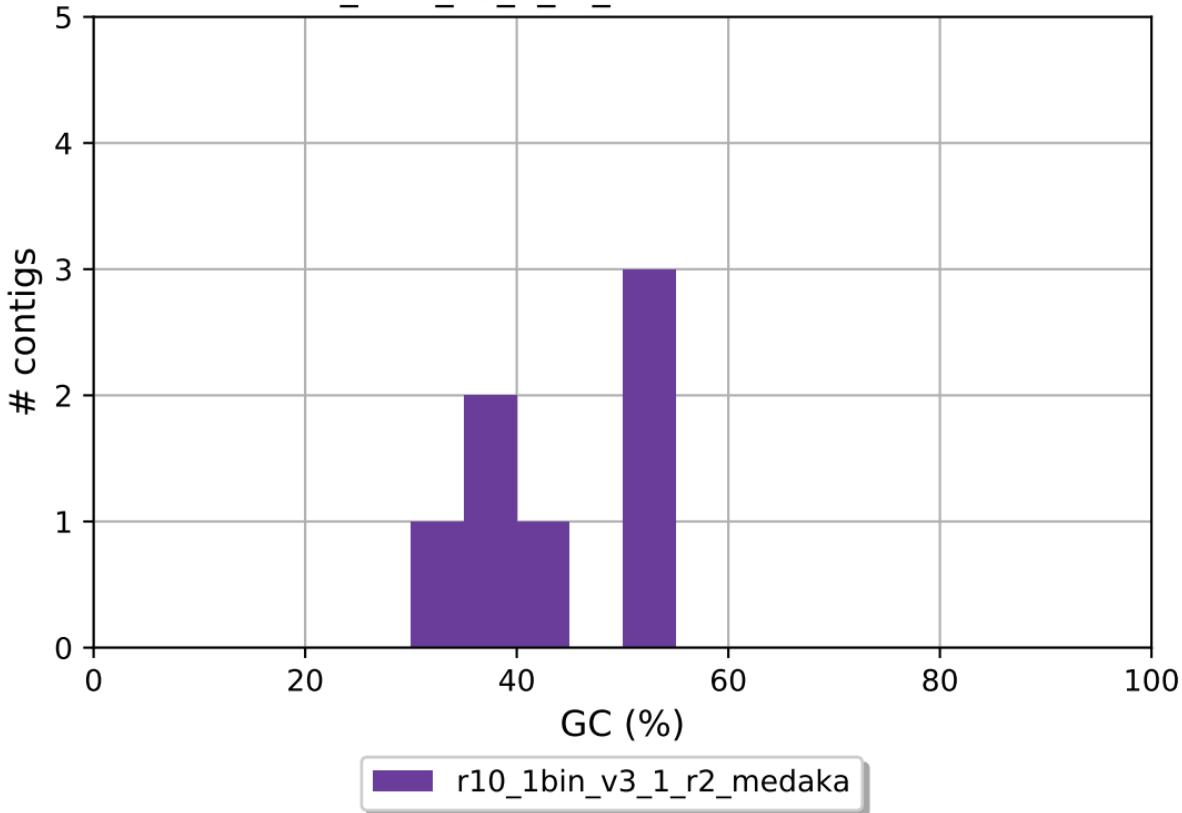
r10_1bin_v3_1_MP_helen GC content



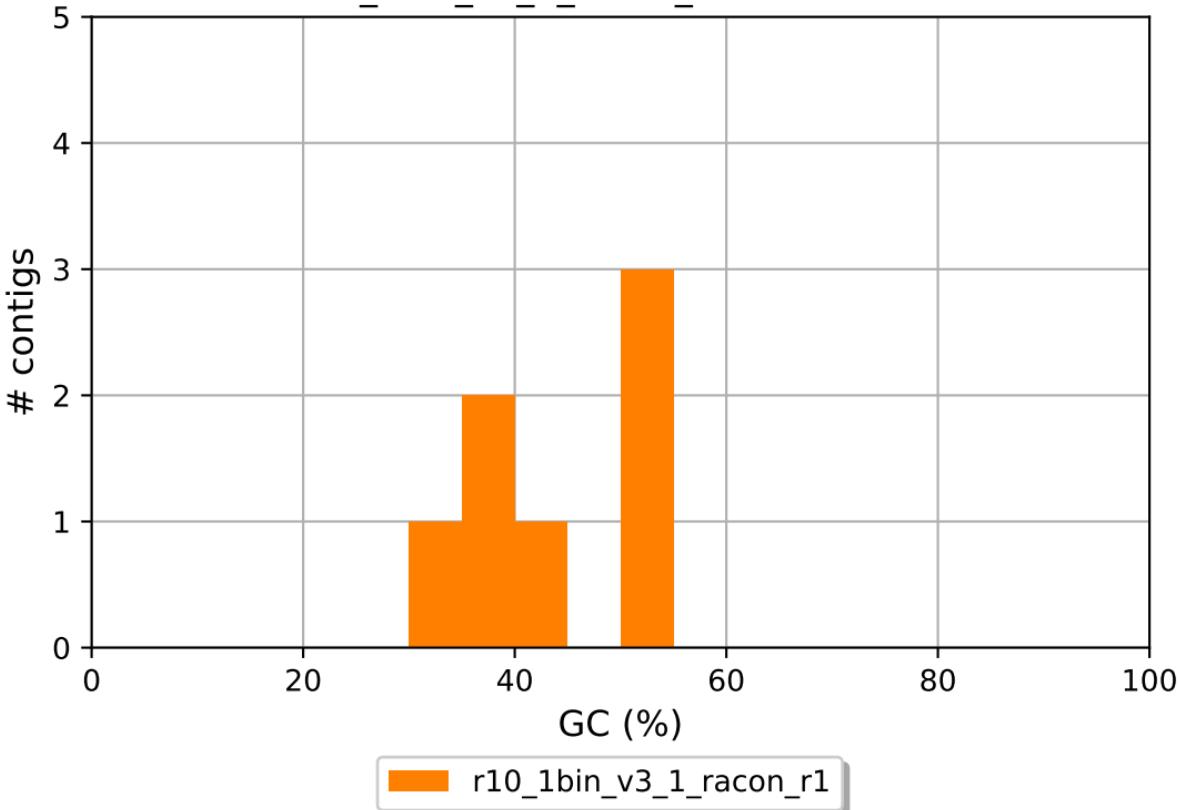
r10_1bin_v3_1_r1_medaka GC content



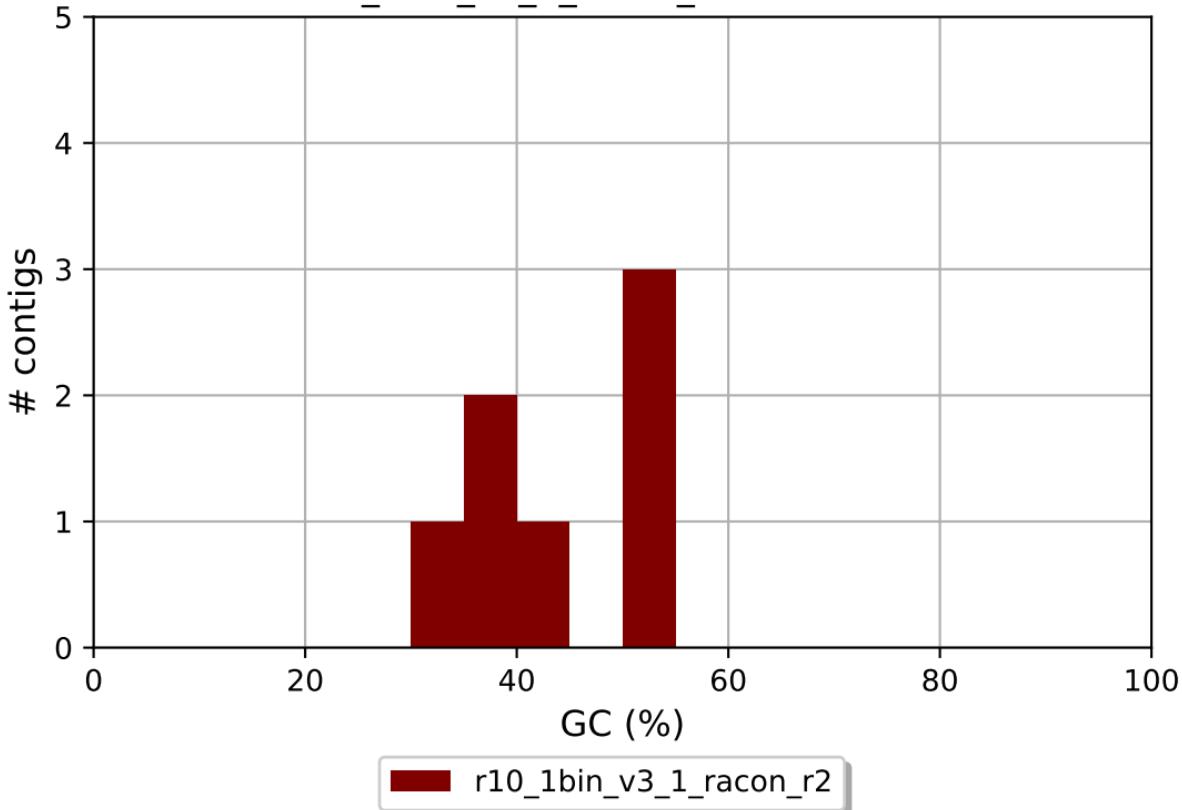
r10_1bin_v3_1_r2_medaka GC content



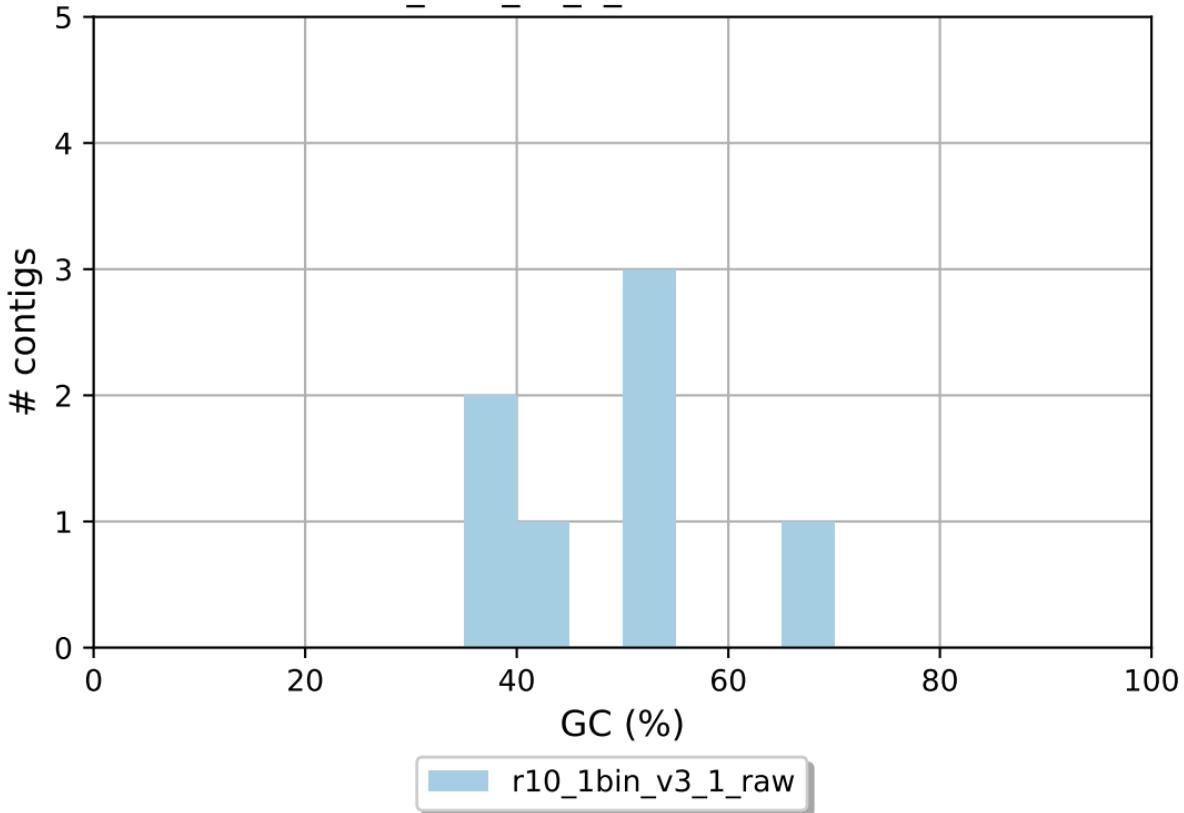
r10_1bin_v3_1_racon_r1 GC content



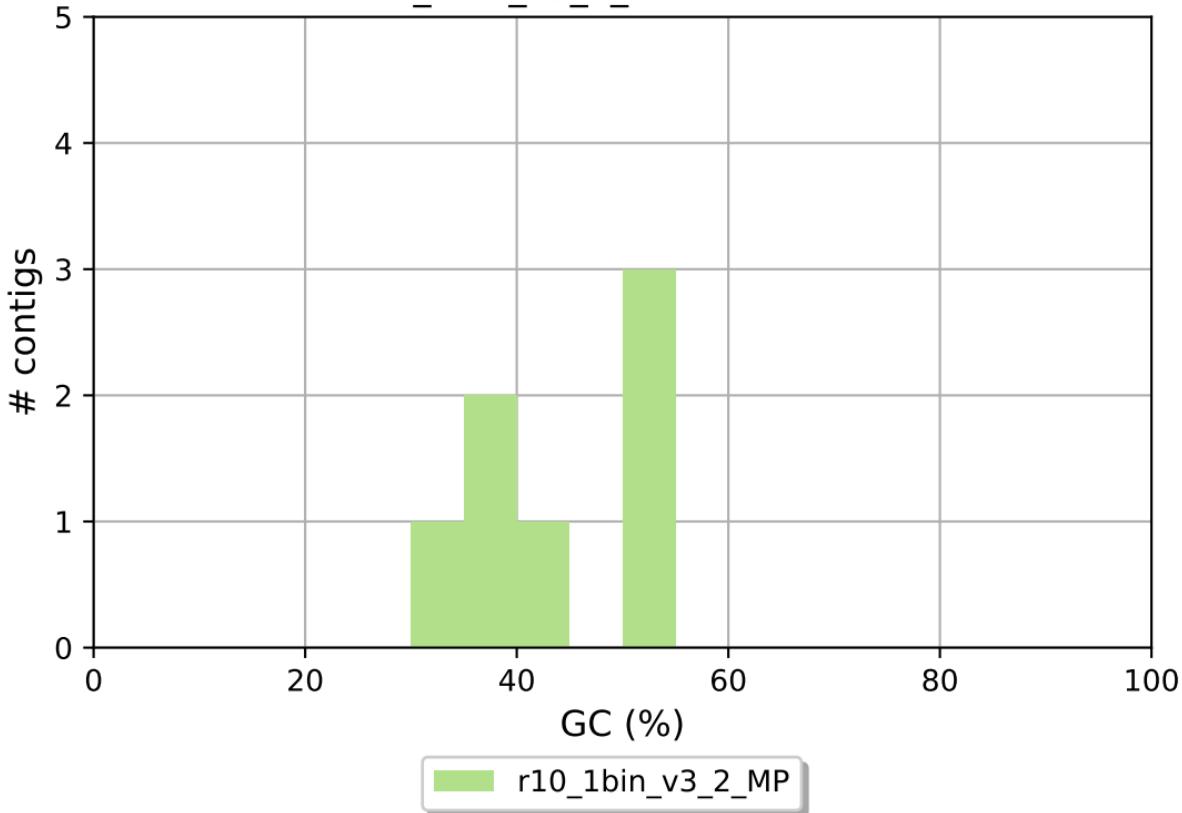
r10_1bin_v3_1_racon_r2 GC content



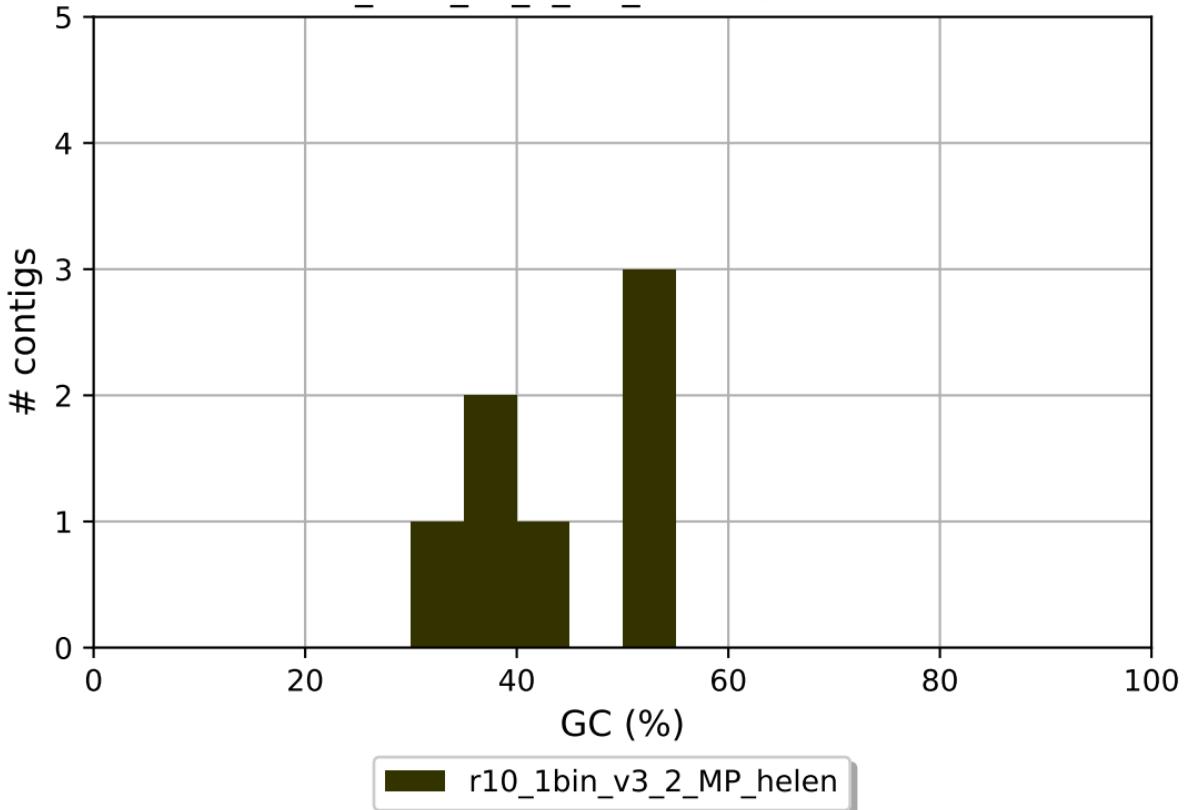
r10_1bin_v3_1_raw GC content



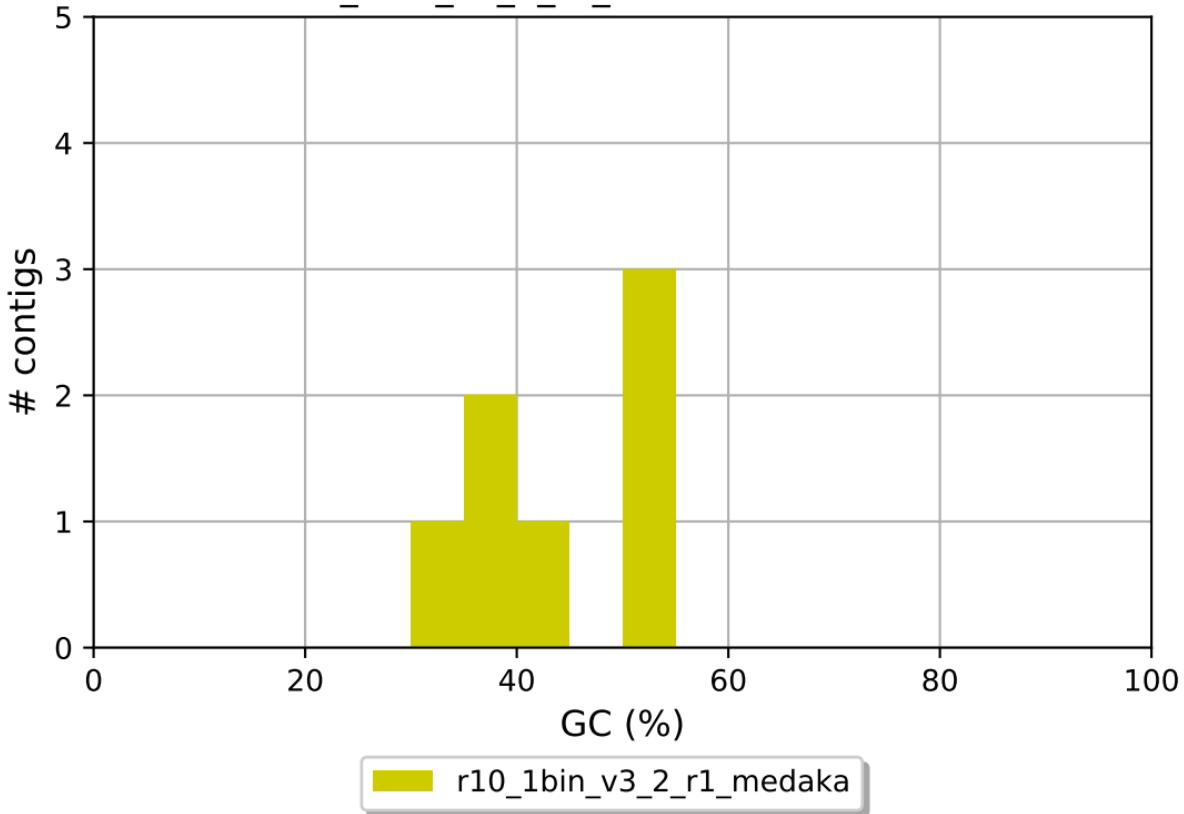
r10_1bin_v3_2_MP GC content



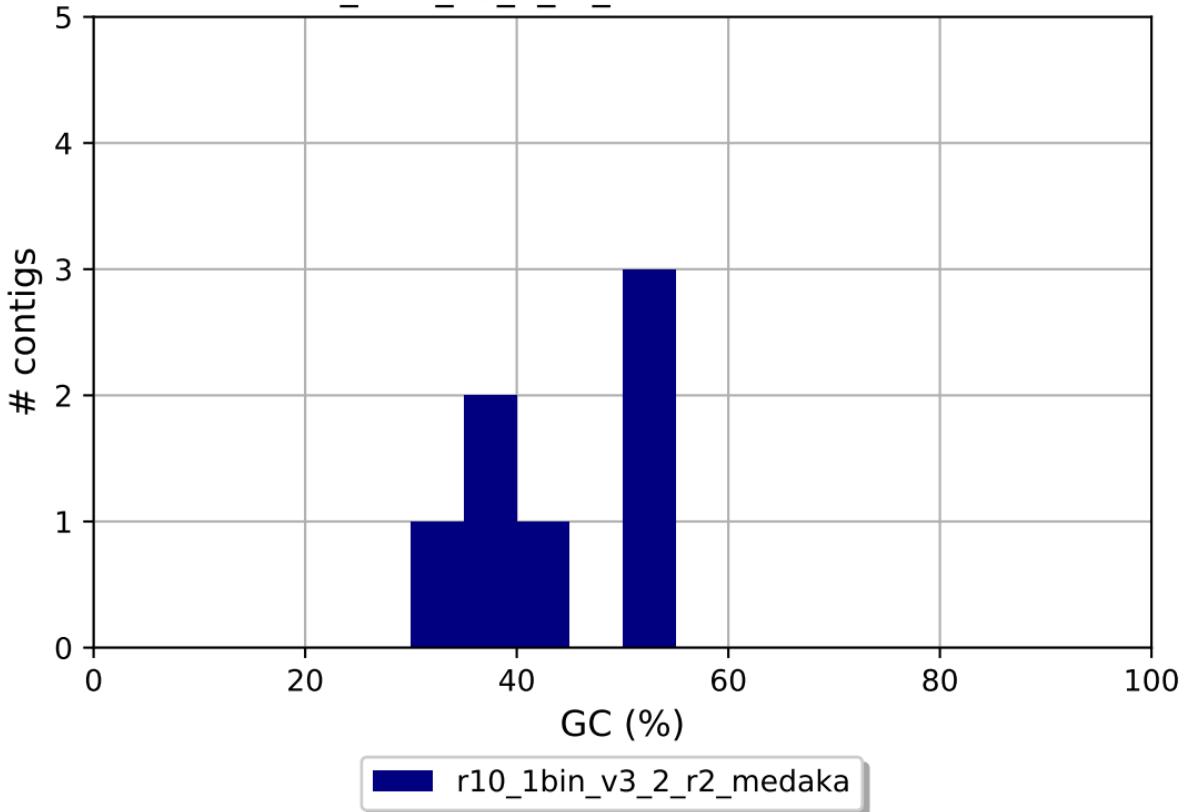
r10_1bin_v3_2_MP_helen GC content



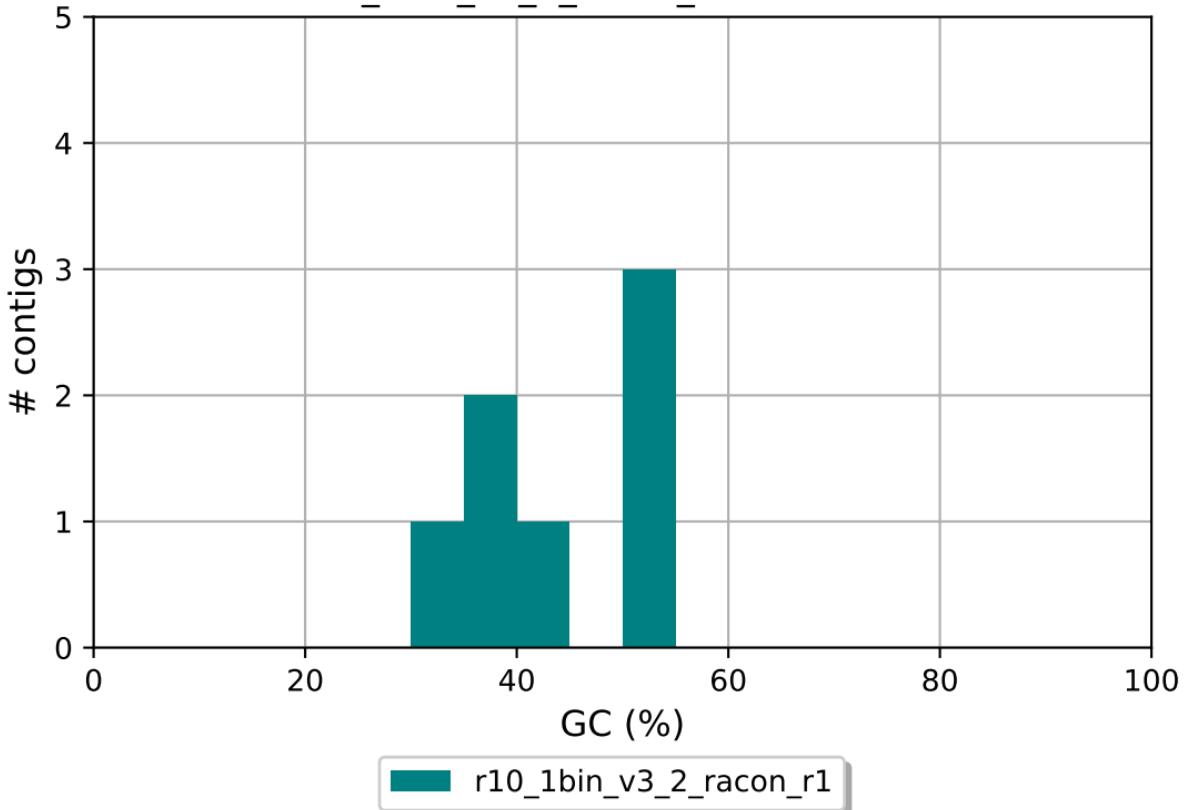
r10_1bin_v3_2_r1_medaka GC content



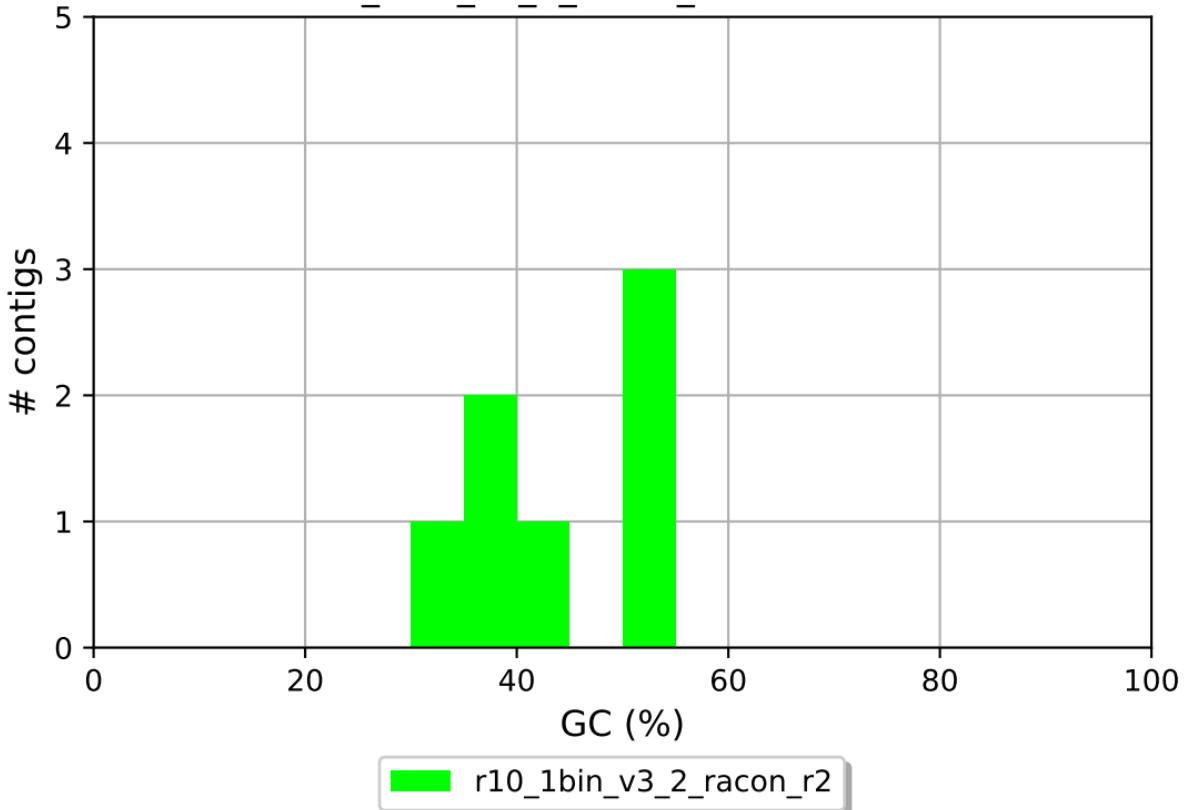
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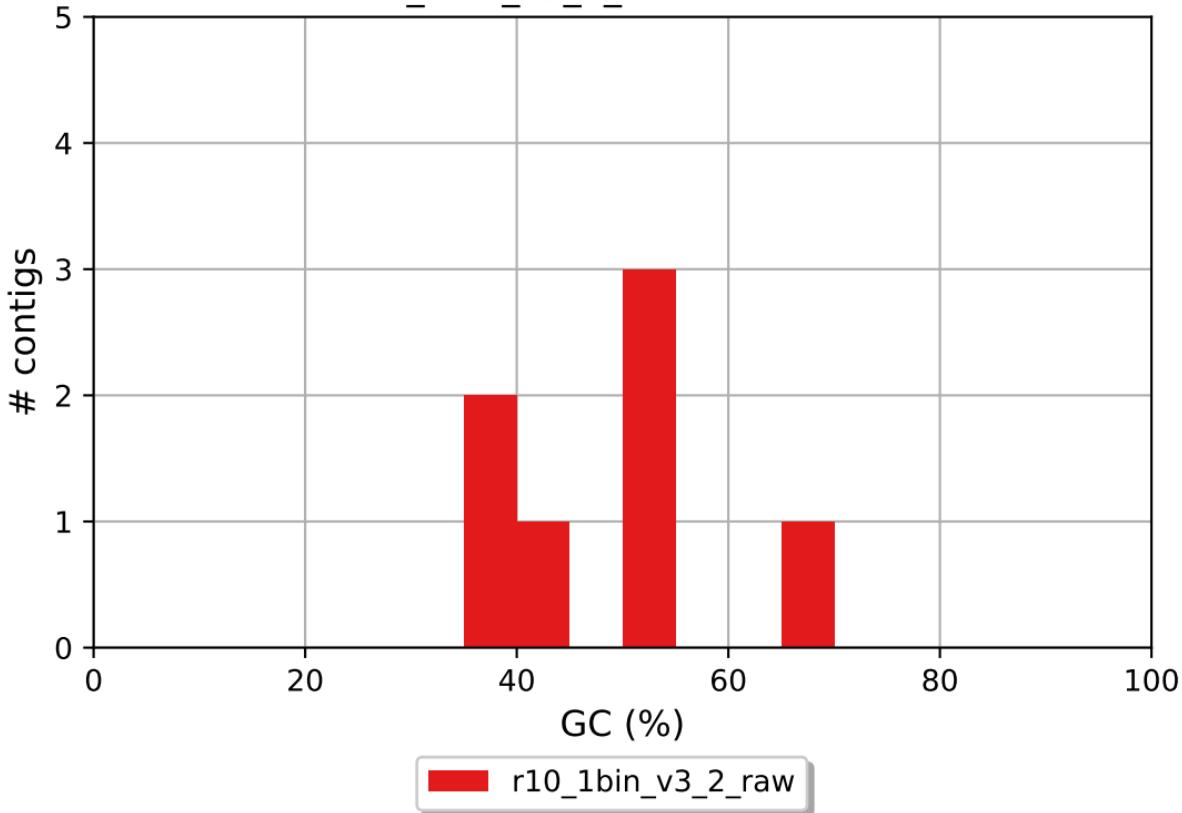
r10_1bin_v3_2_racon_r1 GC content



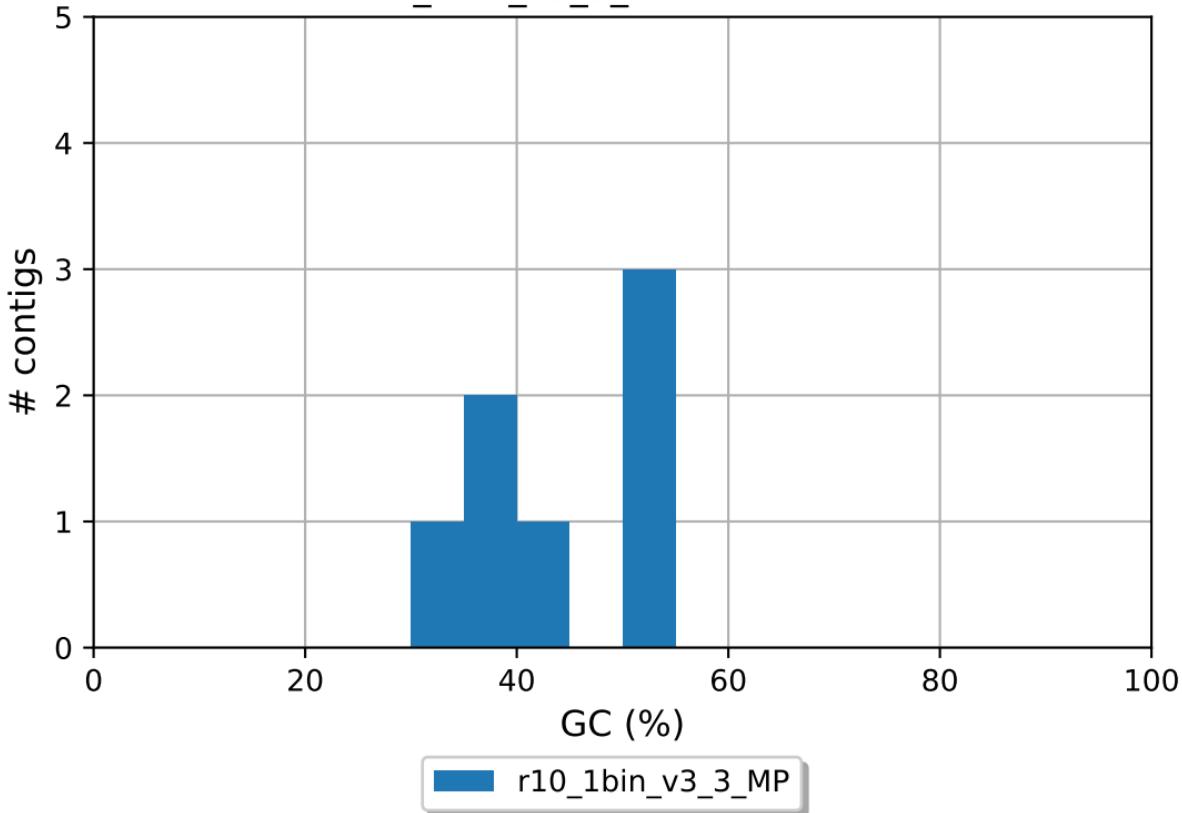
r10_1bin_v3_2_racon_r2 GC content



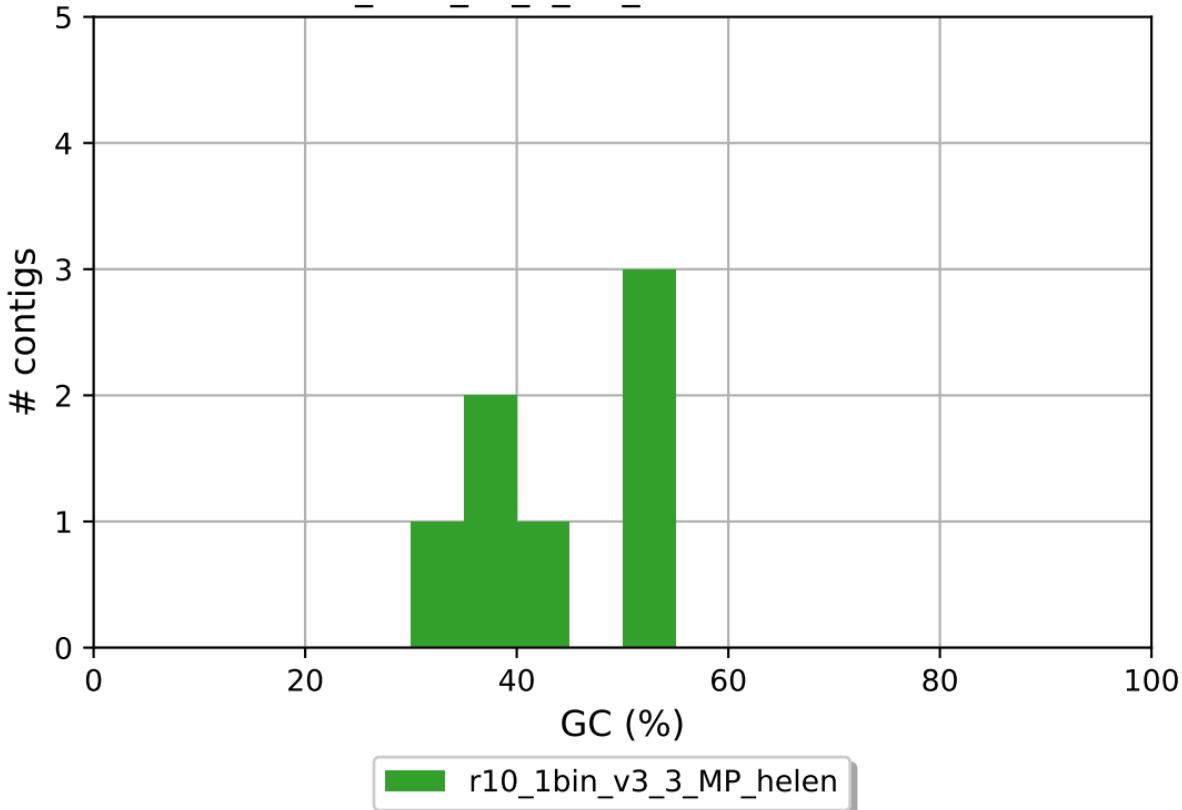
r10_1bin_v3_2_raw GC content



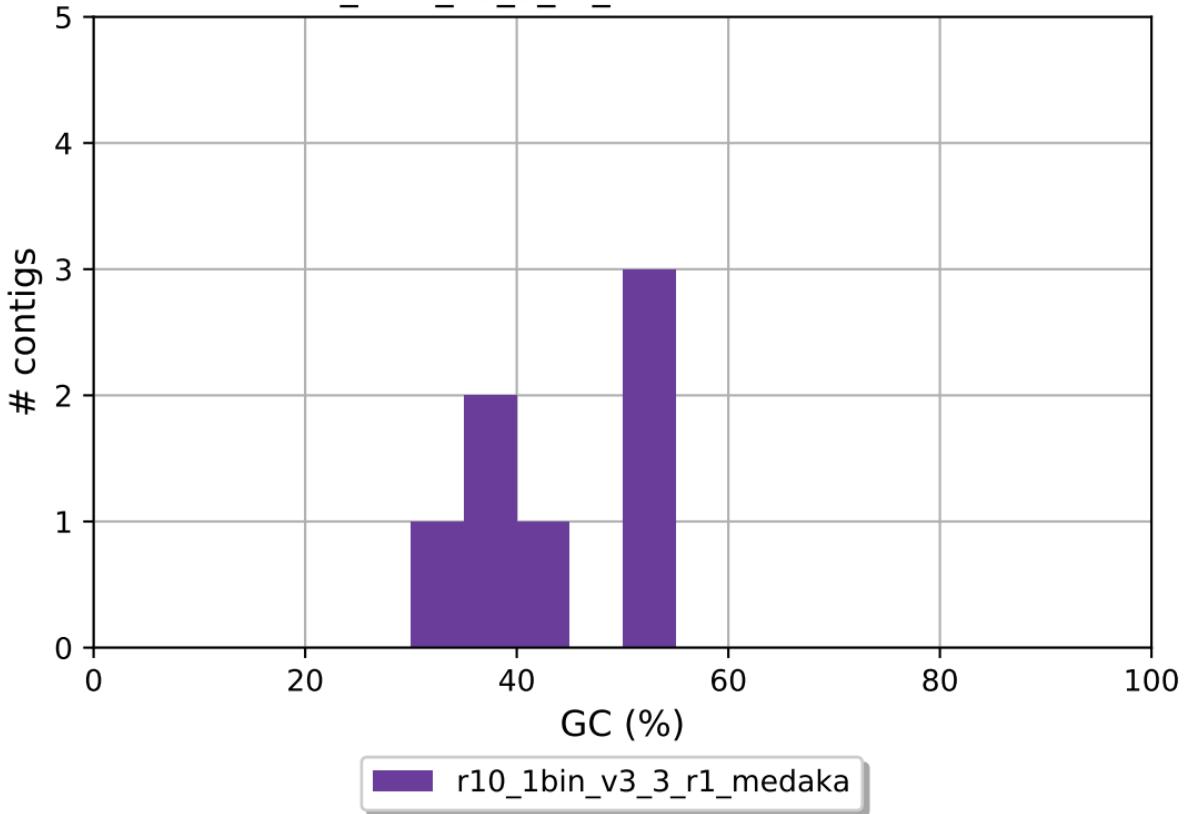
r10_1bin_v3_3_MP GC content



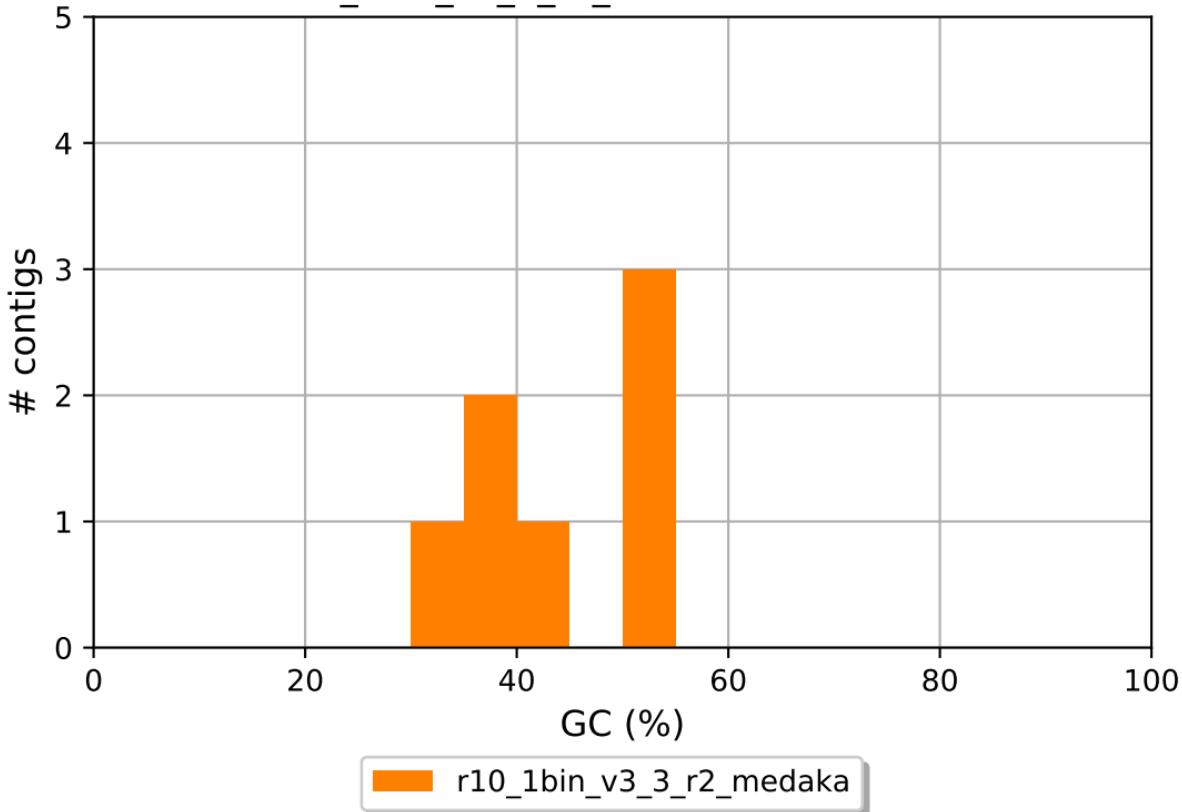
r10_1bin_v3_3_MP_helen GC content



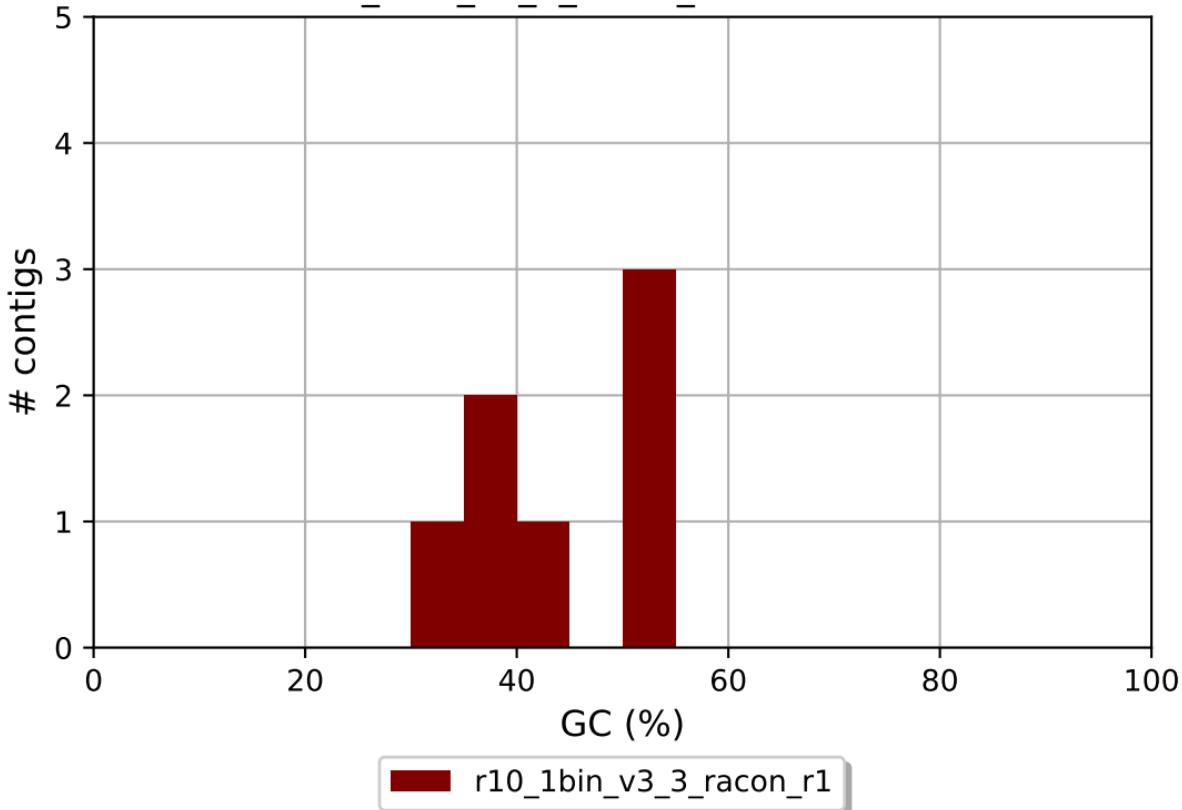
r10_1bin_v3_3_r1_medaka GC content



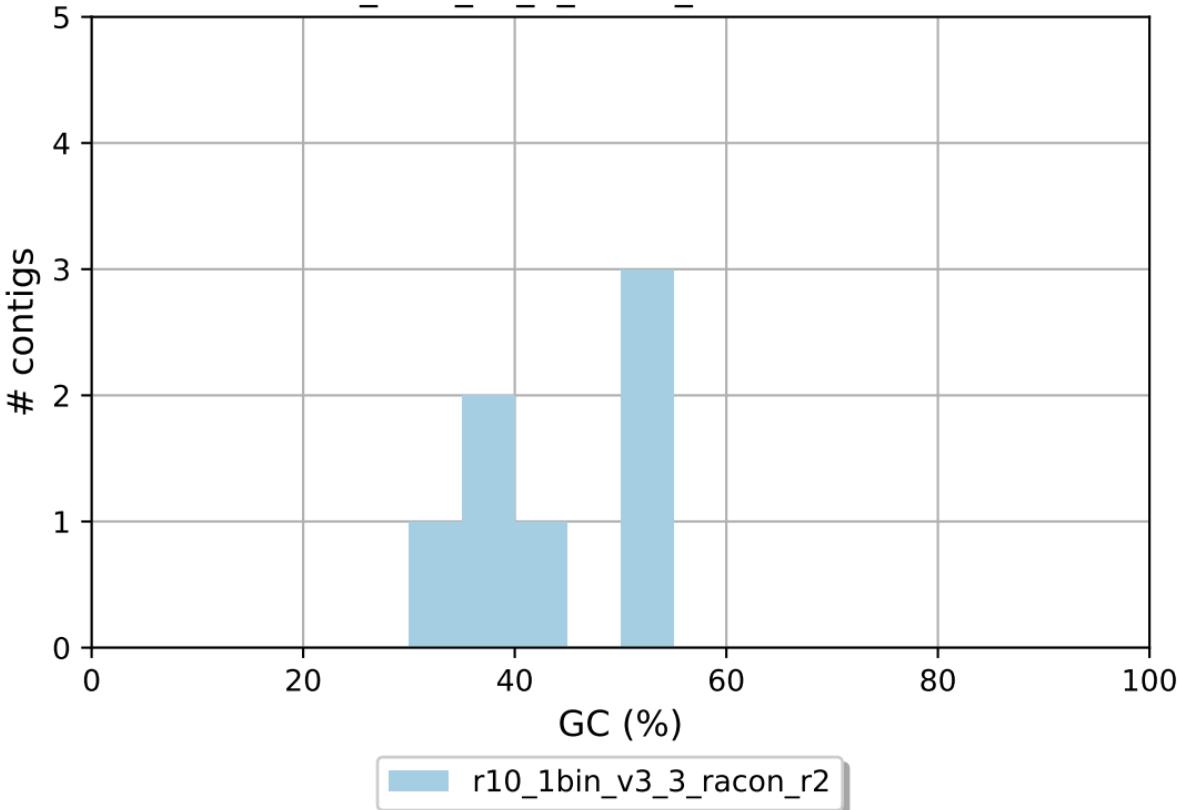
r10_1bin_v3_3_r2_medaka GC content



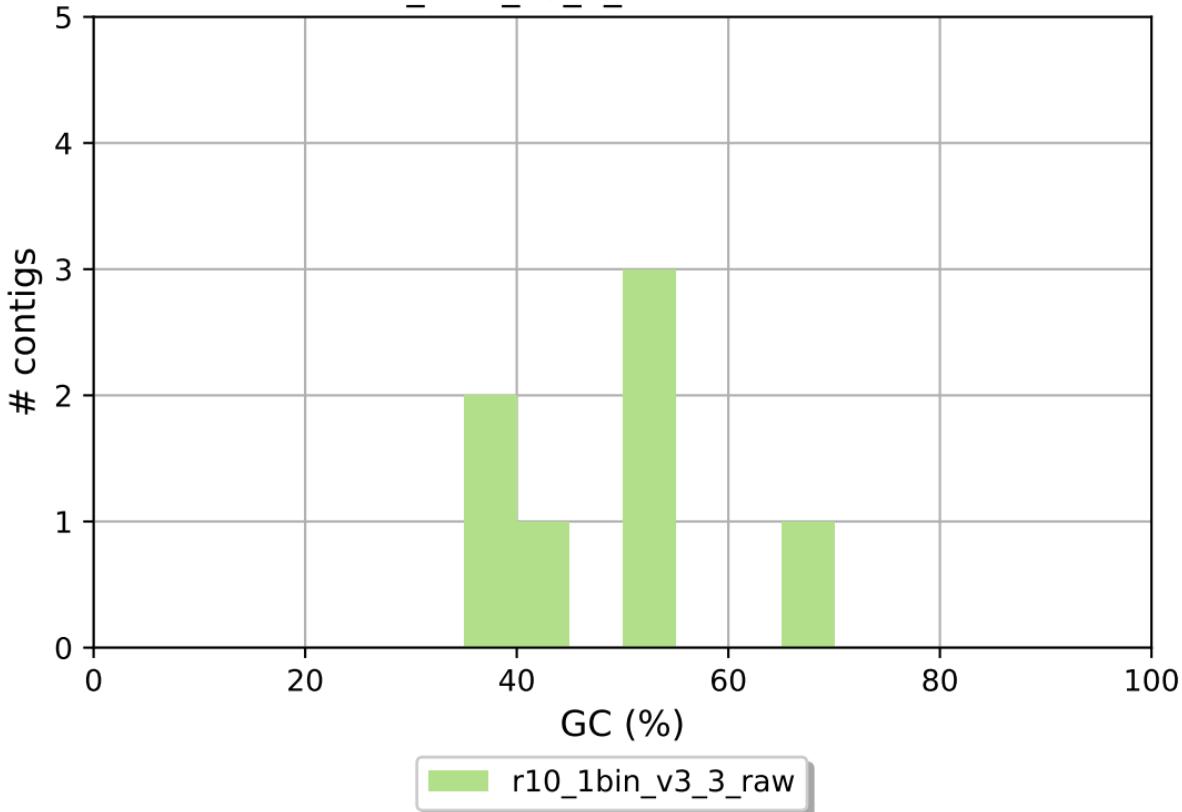
r10_1bin_v3_3_racon_r1 GC content



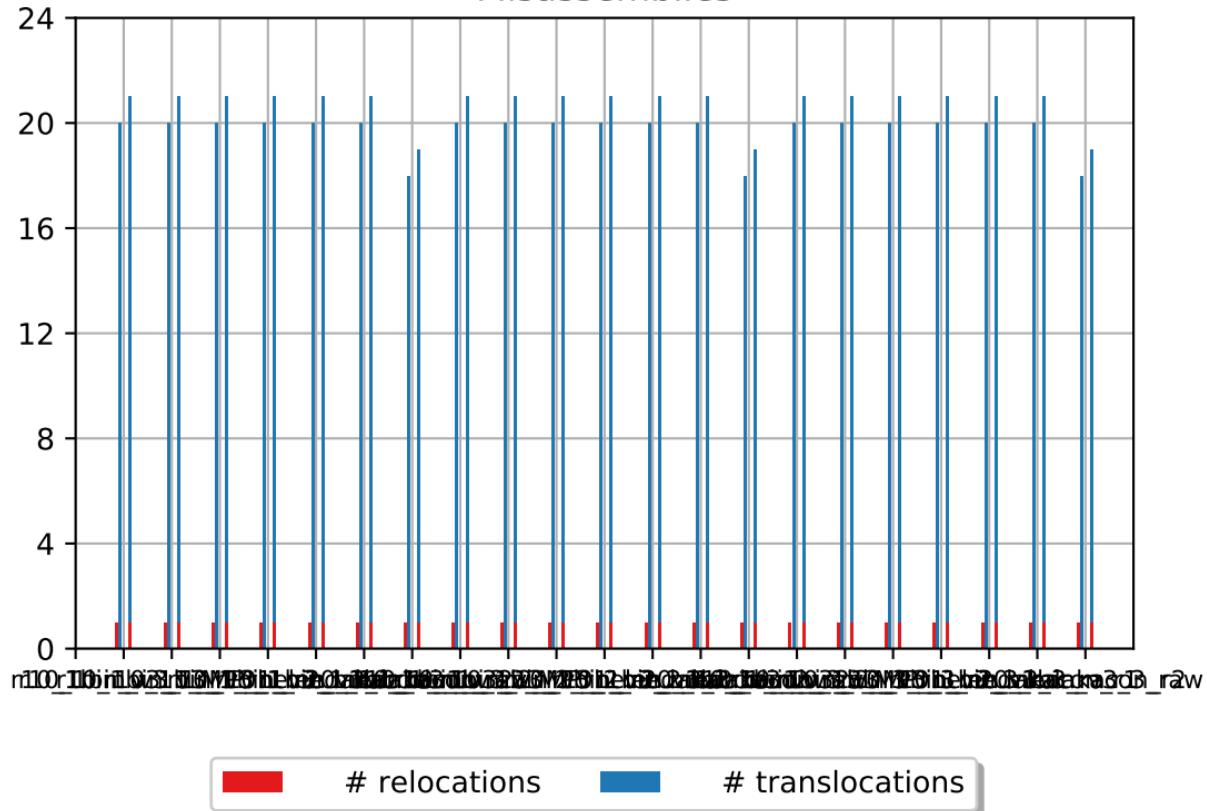
r10_1bin_v3_3_racon_r2 GC content



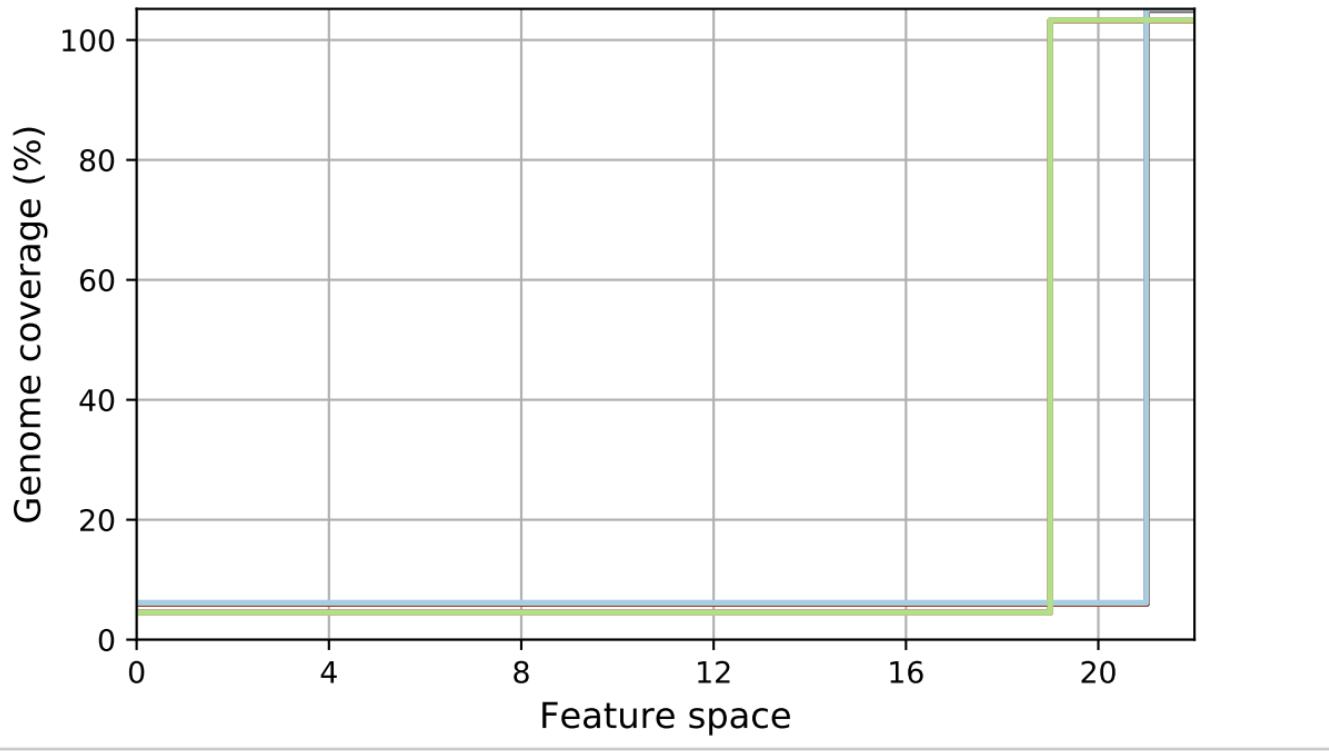
r10_1bin_v3_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

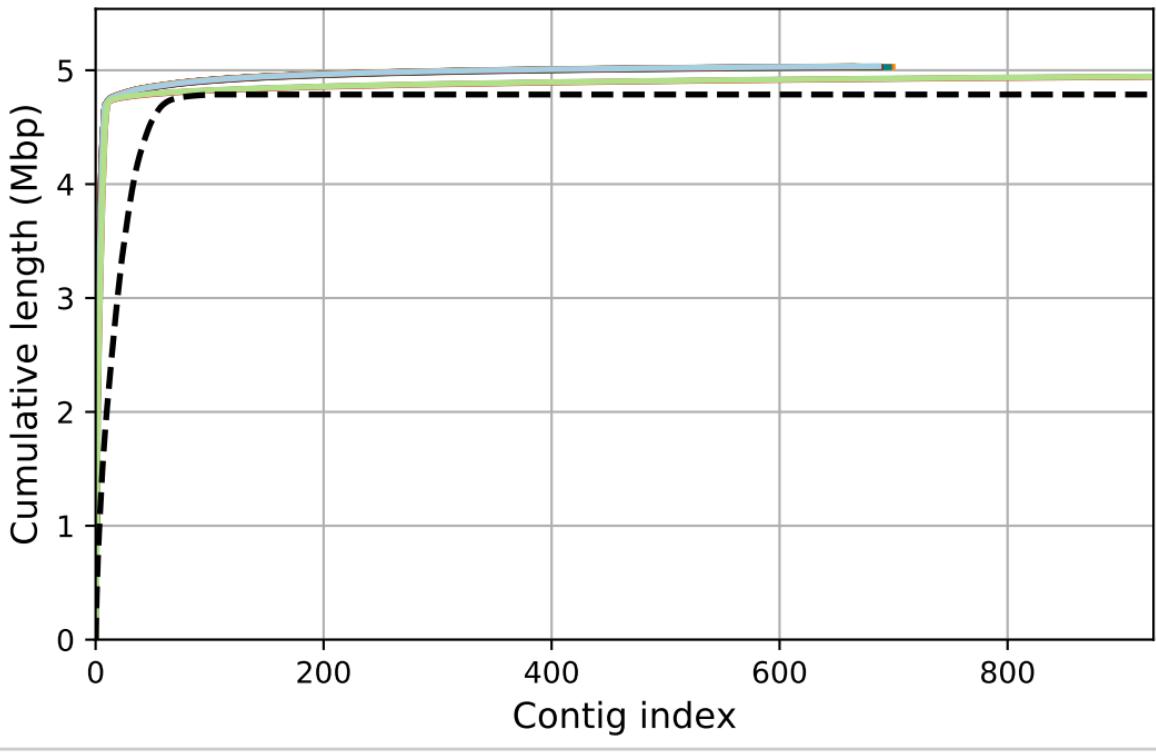
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racoon_r1

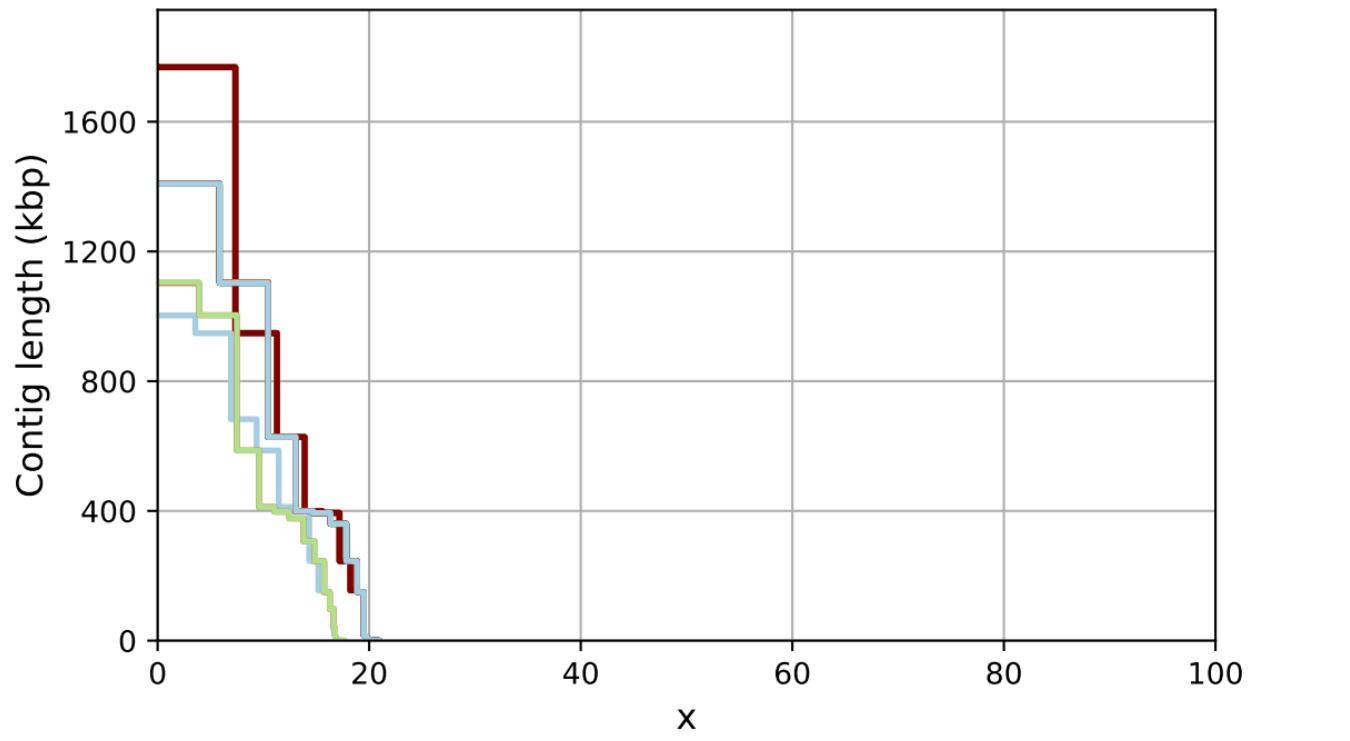
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racoon_r1

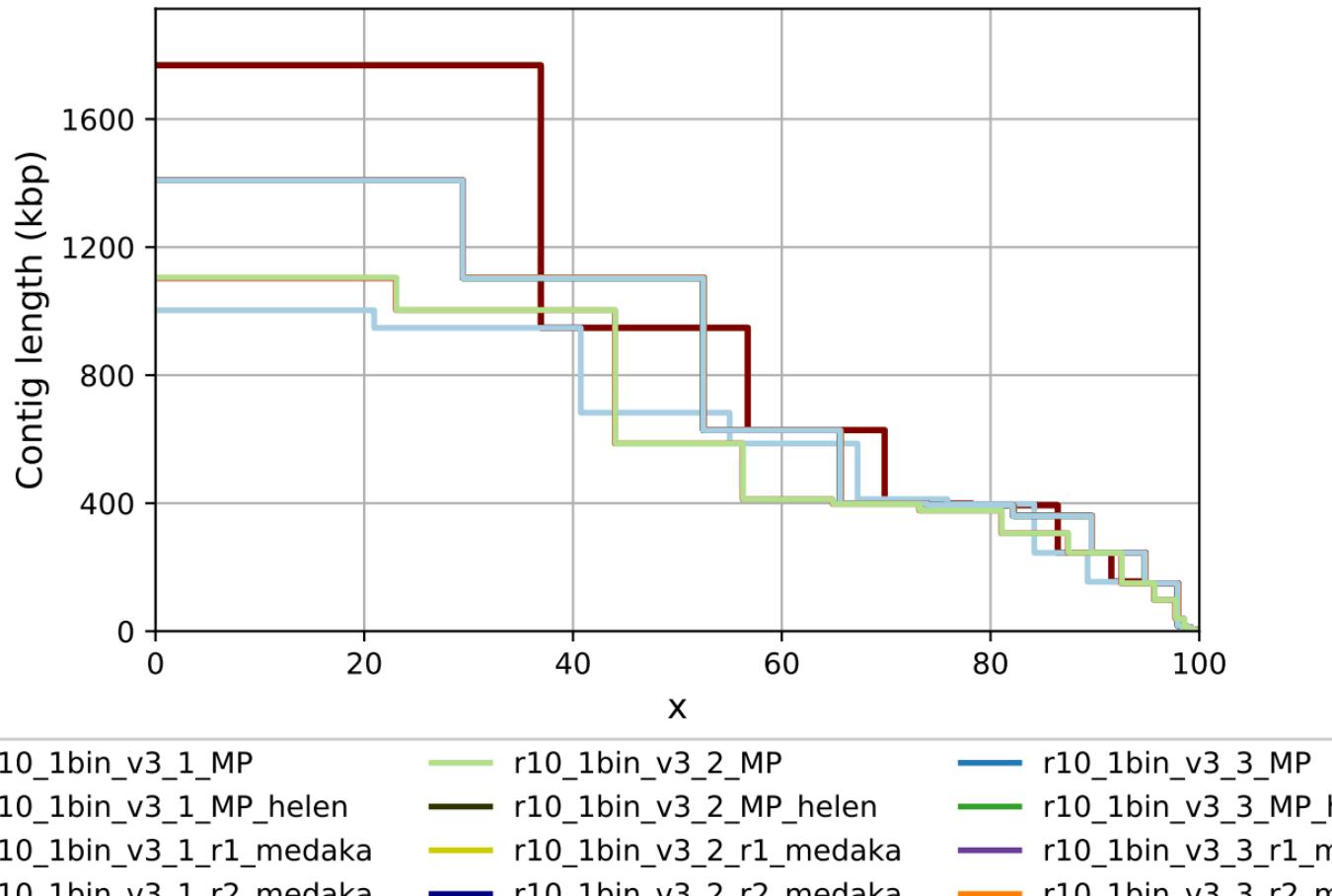
NAX



Legend:

- r10_1bin_v3_1_MP
- r10_1bin_v3_1_MP_helen
- r10_1bin_v3_1_r1_medaka
- r10_1bin_v3_2_MP
- r10_1bin_v3_2_MP_helen
- r10_1bin_v3_2_r1_medaka
- r10_1bin_v3_3_MP
- r10_1bin_v3_3_MP_helen
- r10_1bin_v3_3_r1_medaka
- r10_1bin_v3_3_r2_medaka
- r10_1bin_v3_3_r2_mp_helen

NGAx



Genome fraction, %



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka