

## 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_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	8	7	7	7	7	8	7	7	7	7	7	8			
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	8	7	7	7	7	7	8			
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	8	7	7	7	7	7	8			
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	8	7	7	7	7	7	8			
Total length (>= 5000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667	
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667	
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667	
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667	
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	7	7	7	7	8			
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	30848193	24074490	24070611	24075114	24065831	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667	
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	49.48	44.80	44.80	44.79	44.79	44.78	49.48	44.80	44.81	44.80	44.79	44.79	44.79	49.48	
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	
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	2845564	2845301	2990628	2845422	2845572	2845563	2845260	2845299	2990626	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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2		
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
Misassembled contigs length	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992173	2991893	2991931	2990628	2992084	2992068	2992178	2992176	2991922	2991951	2990626
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	7	7	7	7	7	12		
# 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	7	6	6	6	6	6	6	6	6	6	6	6	7		
# 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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part		
Unaligned length	20956540	20949552	20952382	20945364	20942573	20937602	27788160	20956888	20950605	20957178	20948833	20942016	20936441	27792561	20960694	20950789	20961124	20955176	20945168	20939944	27795908
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.983	99.984	99.984	99.984	99.984	99.984	99.983		
Duplication ratio	1.054	1.055	1.055	1.054	1.054	1.054	1.035	1.054	1.055	1.054	1.054	1.055	1.033	1.054	1.055	1.054	1.054	1.055	1.033		
# 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	0.32		
# mismatches per 100 kbp	230.85	236.83	231.46	226.72	227.97	229.63	148.14	228.75	235.55	228.65	225.20	228.96	232.07	140.97	228.45	235.21	226.52	223.04	232.4		

## Misassemblies report

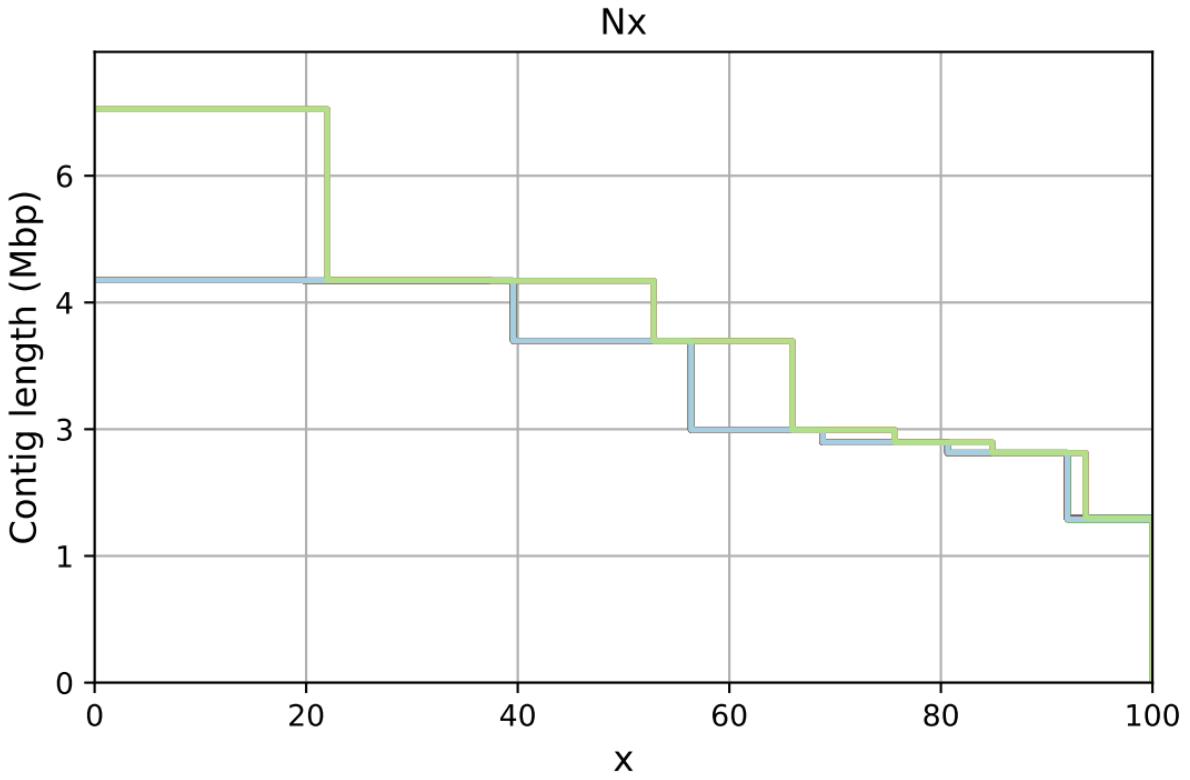
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# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# c. translocations	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# c. inversions	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	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992073	2991893	2991931	2990628	2992084	2992178	2992176	2991922	2991951	2990626	
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	
# possible misassemblies	8	8	8	8	8	8	8	9	8	8	8	8	8	8	8	8	8	8	8	9	
# local misassemblies	7	7	7	7	7	7	7	14	7	7	7	7	7	7	7	7	7	7	7	12	
# 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	16	16	16	16	16	16	16	10	16	16	16	16	16	16	16	16	16	16	16	11	
# unaligned mis. contigs	6	6	6	6	6	6	6	7	6	6	6	6	6	6	6	6	6	6	6	7	
# mismatches	6827	7004	6845	6705	6742	6791	4381	6765	6966	6762	6660	6771	6863	4169	6756	6956	6699	6596	6814	6861	4135
# indels	653	662	662	637	944	879	3432	630	642	777	757	943	876	3419	630	644	774	750	992	871	3424
# indels (<= 5 bp)	629	637	637	613	919	855	3405	607	618	918	752	732	851	3390	607	620	749	726	966	847	3395
# indels (> 5 bp)	24	25	25	24	25	24	25	27	23	25	25	25	25	29	23	24	25	24	26	24	29
Indels length	1955	1971	1978	1928	2356	2238	5280	1920	1937	2348	2232	5300	1920	2098	2073	2348	2094	2044	2231	5318	

All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

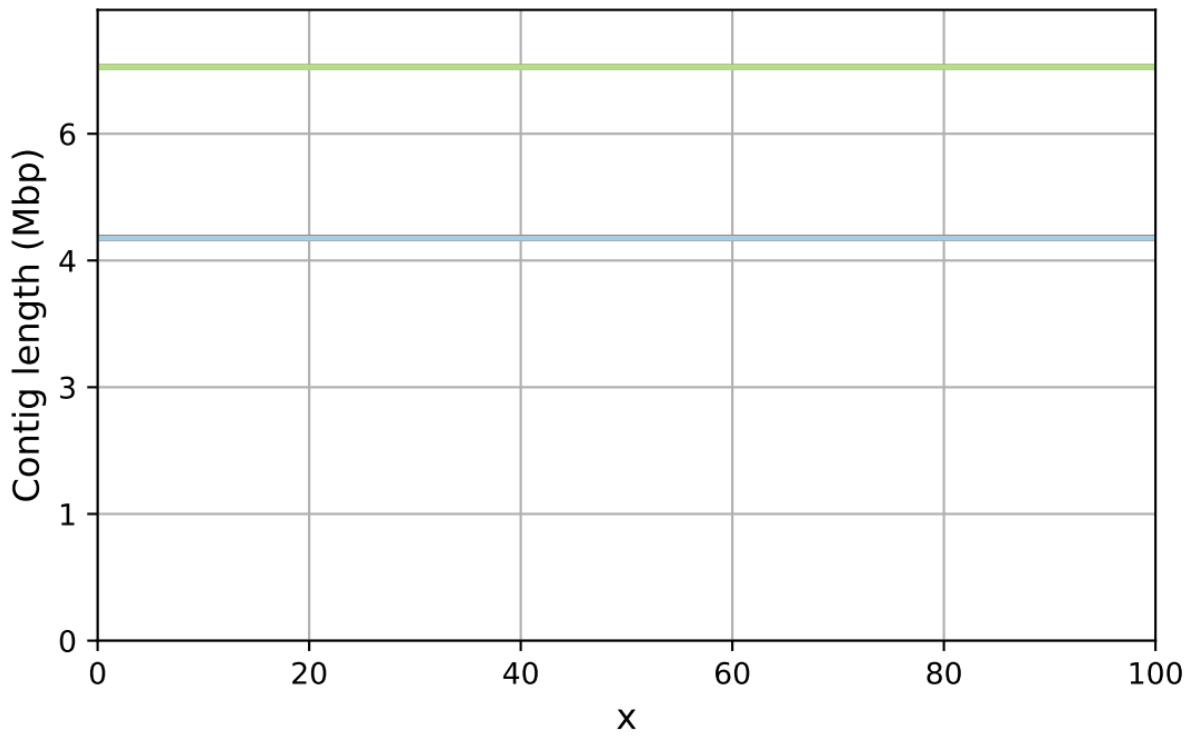
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8
Partially unaligned length	20956540	20949552	20952382	20945364	20942573	20937602	27788160	20956888	20950605	20957178	20948833	20942016	20936441	27792561	20960694	20955176	20945168	20939944	27795908
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100

All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



r10\_1bin\_v3\_1\_MP  
r10\_1bin\_v3\_1\_MP\_helen  
r10\_1bin\_v3\_1\_r1\_medaka  
r10\_1bin\_v3\_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

NGx

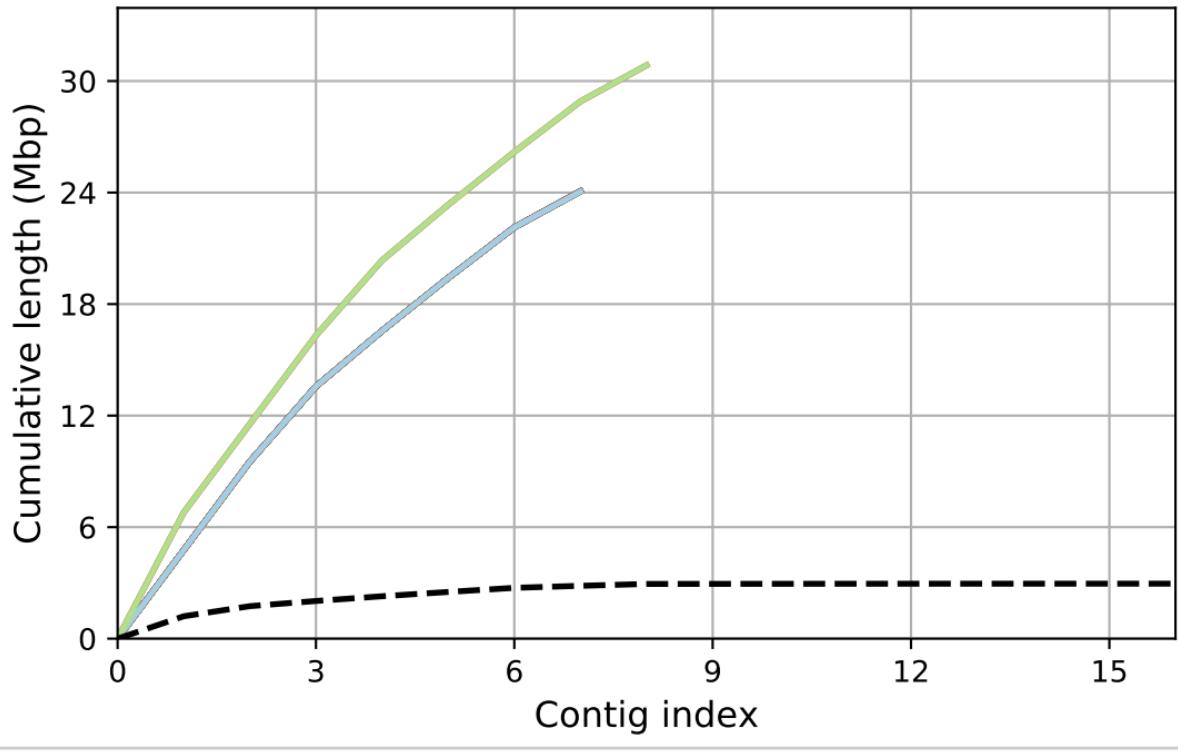


r10\_1bin\_v3\_1\_MP  
r10\_1bin\_v3\_1\_MP\_helen  
r10\_1bin\_v3\_1\_r1\_medaka  
r10\_1bin\_v3\_1\_r2\_medaka

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\_racon\_r1

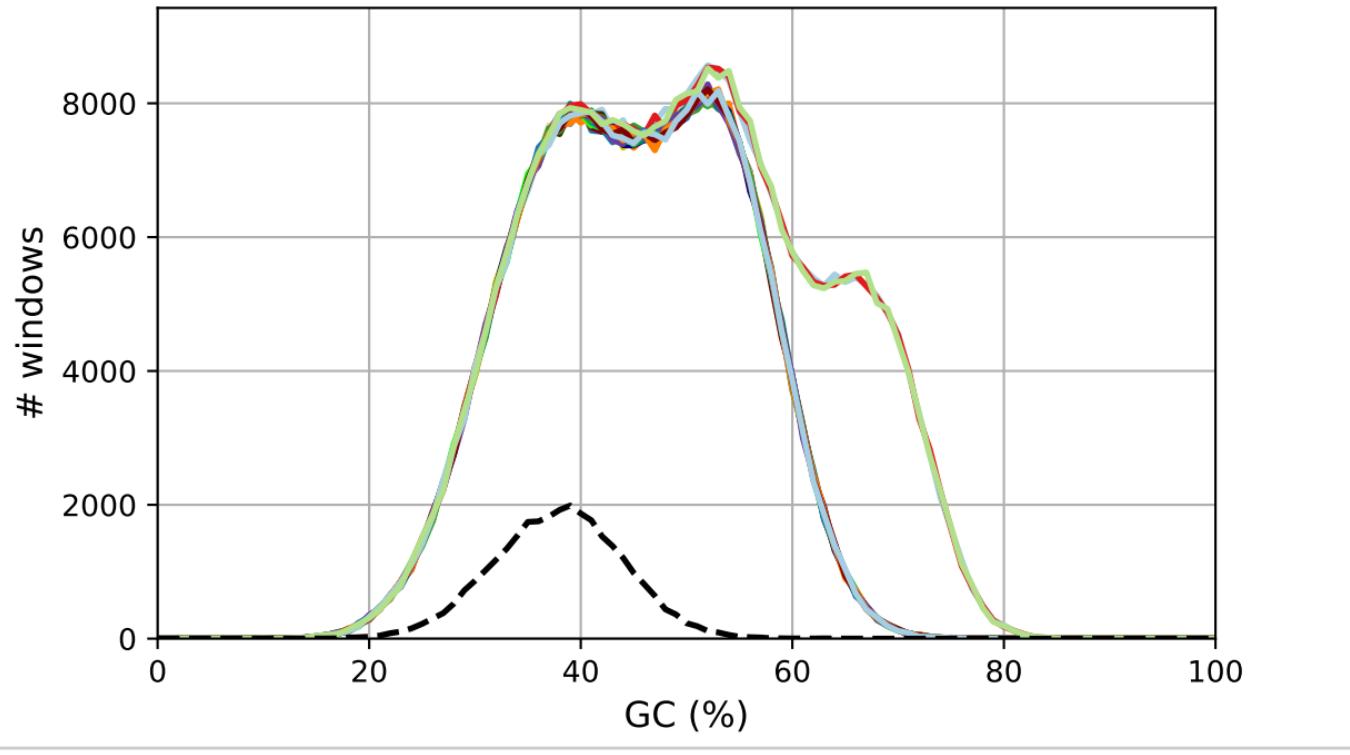
r10\_1bin\_v3\_3\_MP\_helen

r10\_1bin\_v3\_3\_r1\_medaka

r10\_1bin\_v3\_3\_r2\_medaka

r10\_1bin\_v3\_3\_racon\_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

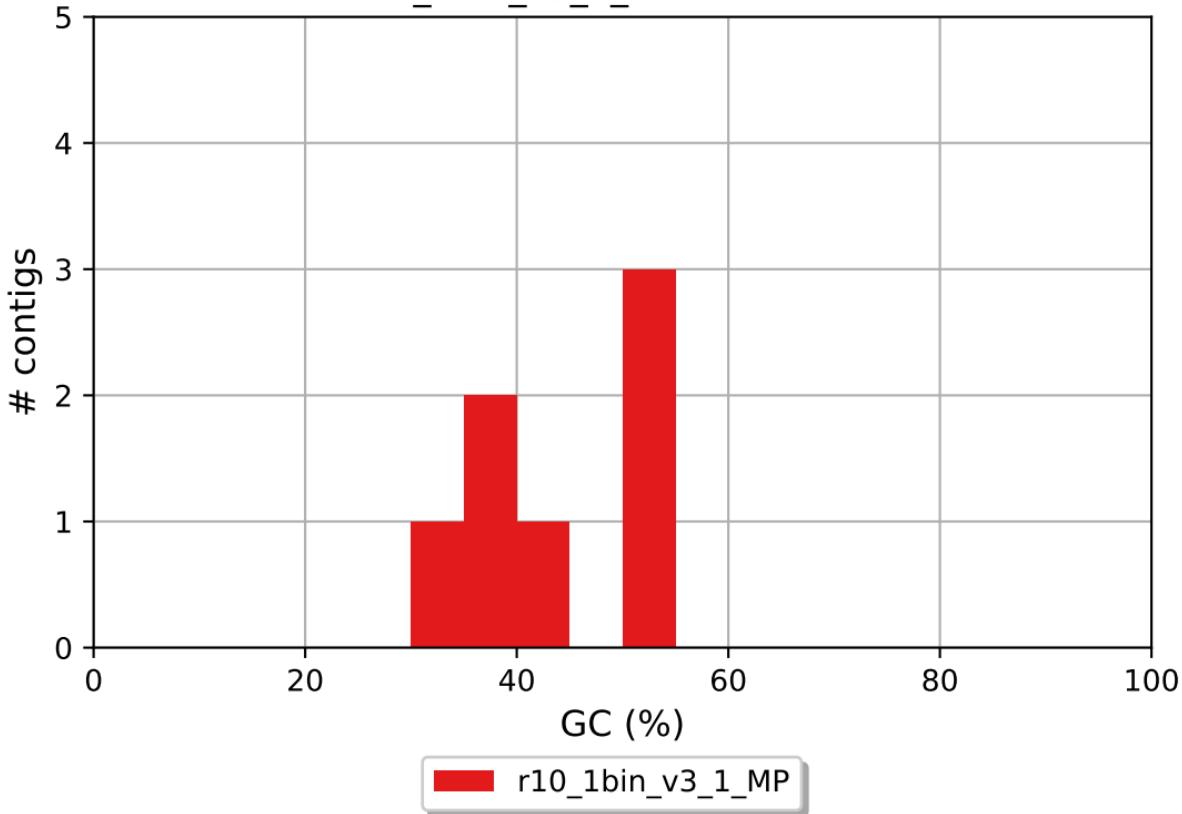
r10\_1bin\_v3\_3\_MP\_h

r10\_1bin\_v3\_3\_r1\_m

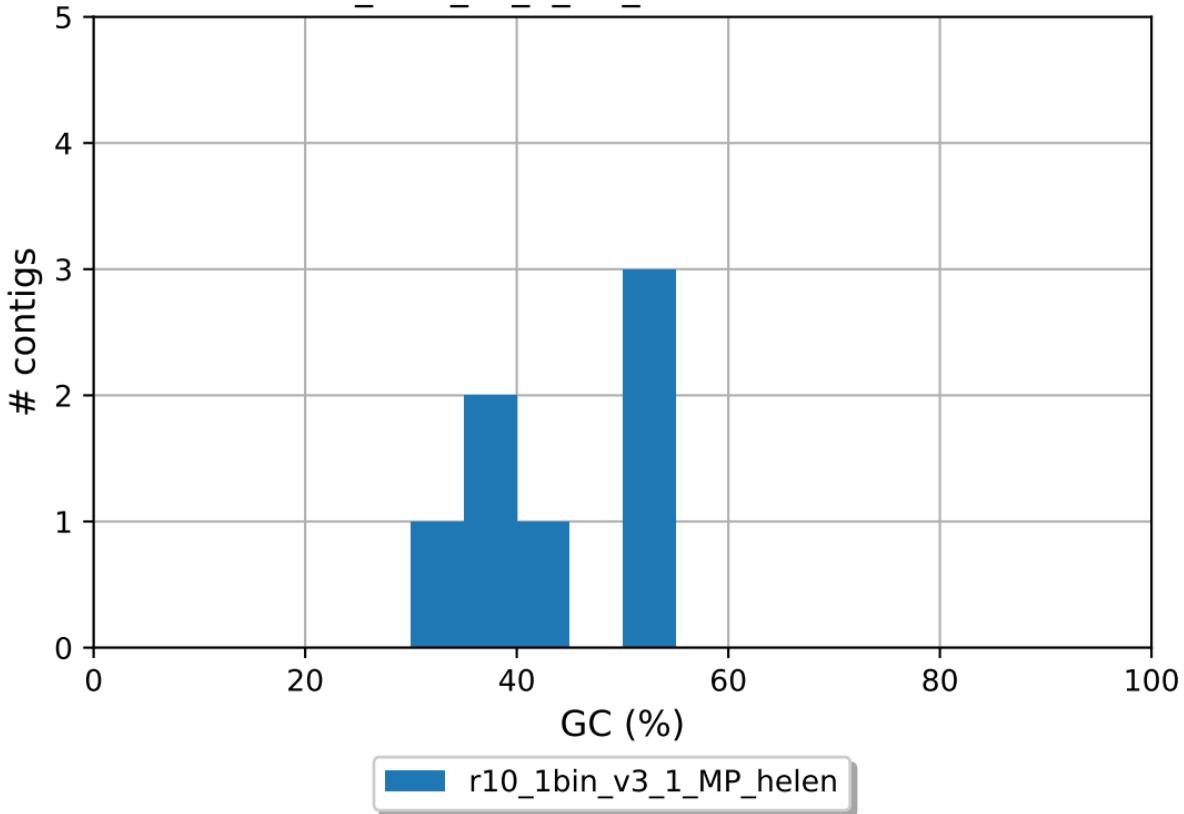
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r10\_1bin\_v3\_3\_racoon\_r1

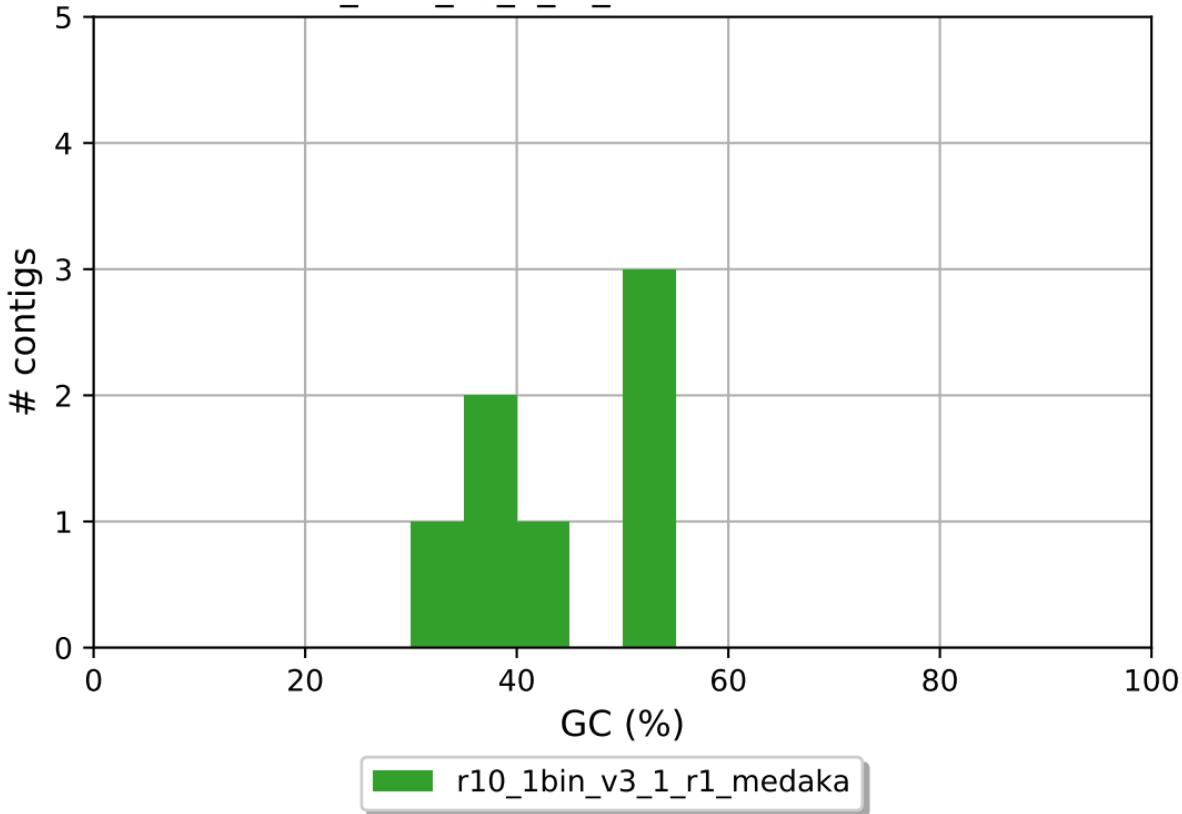
r10\_1bin\_v3\_1\_MP GC content



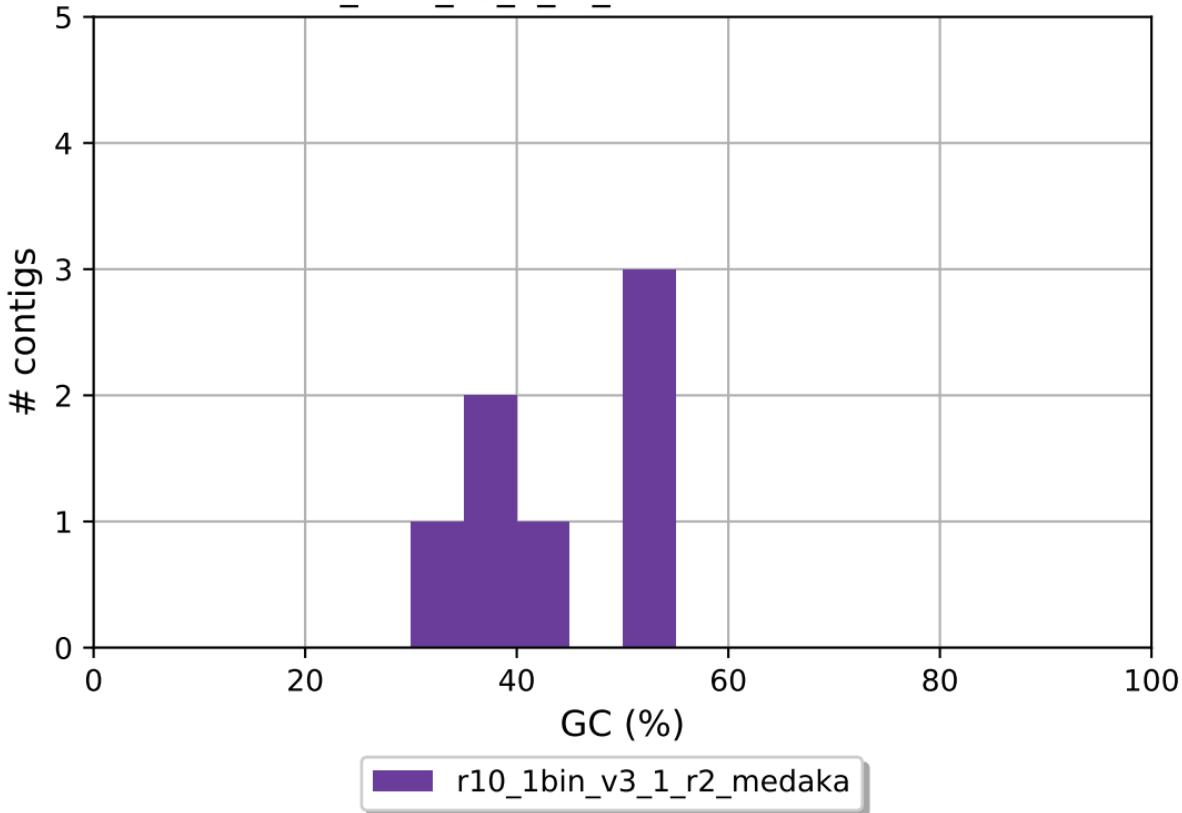
r10\_1bin\_v3\_1\_MP\_helen GC content



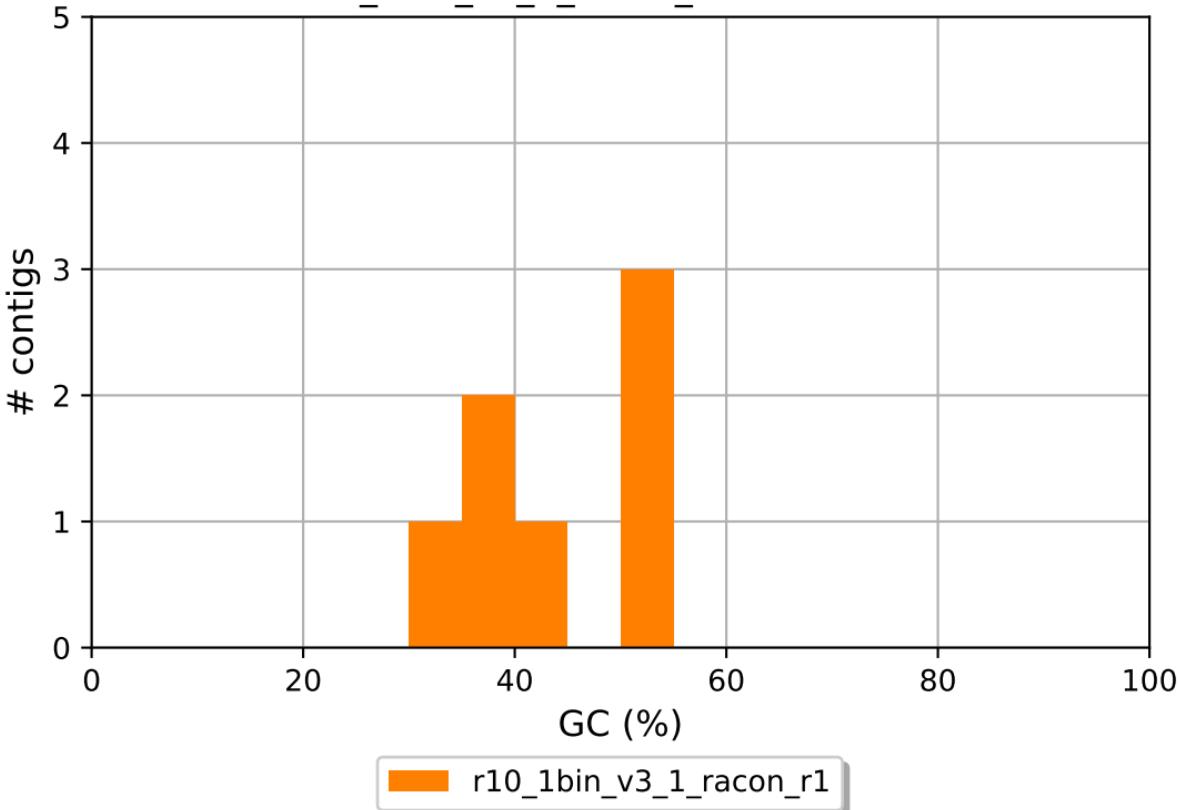
r10\_1bin\_v3\_1\_r1\_medaka GC content



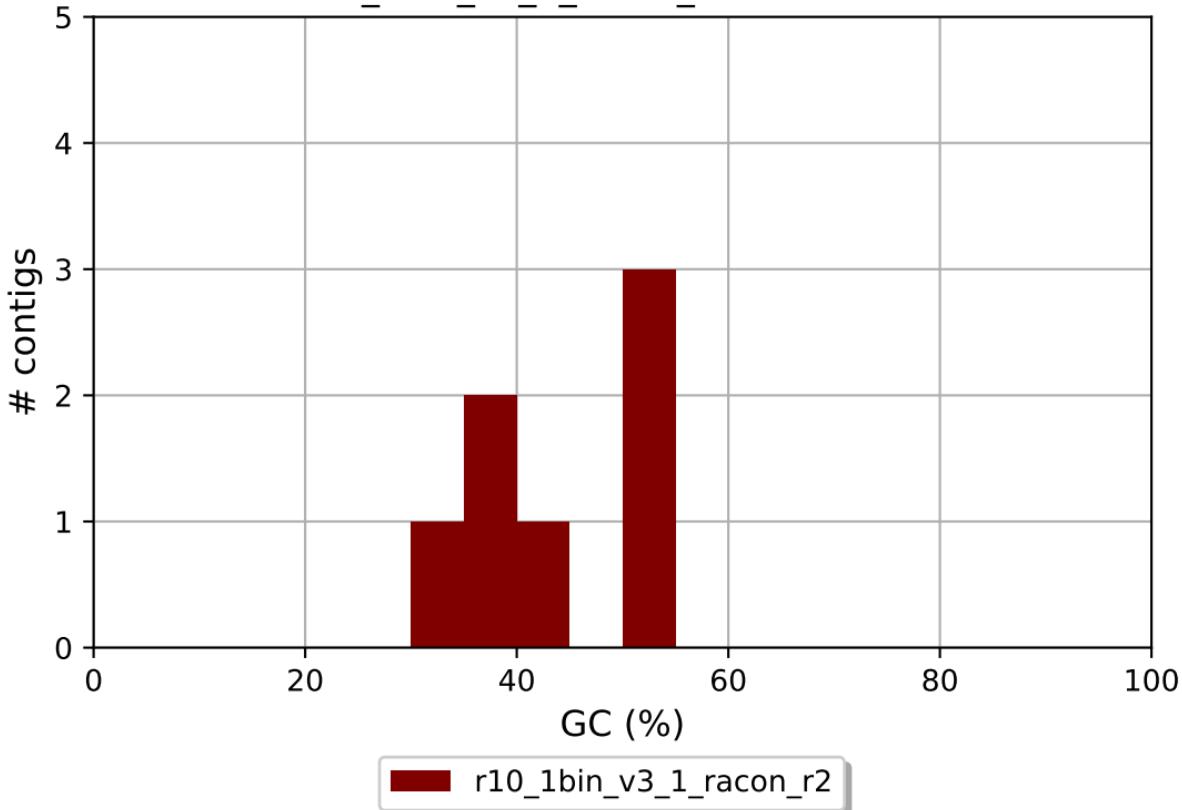
r10\_1bin\_v3\_1\_r2\_medaka GC content



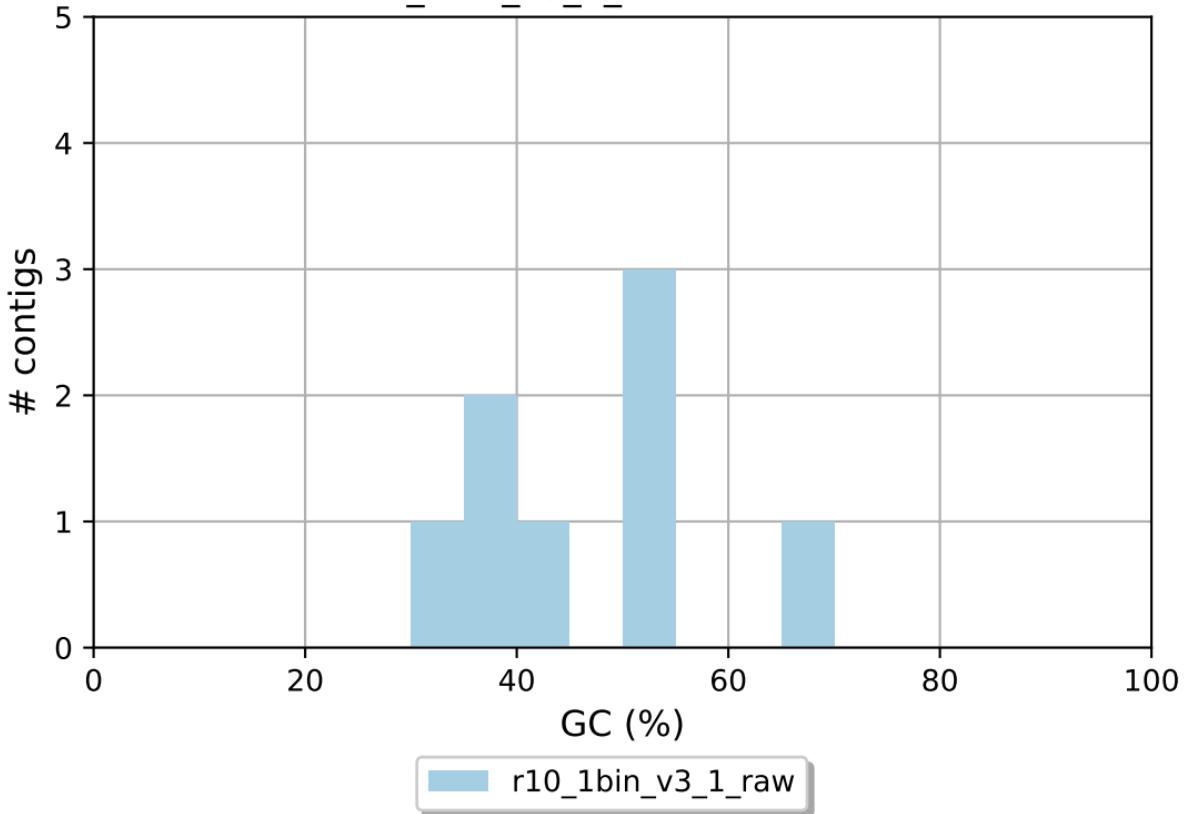
r10\_1bin\_v3\_1\_racon\_r1 GC content



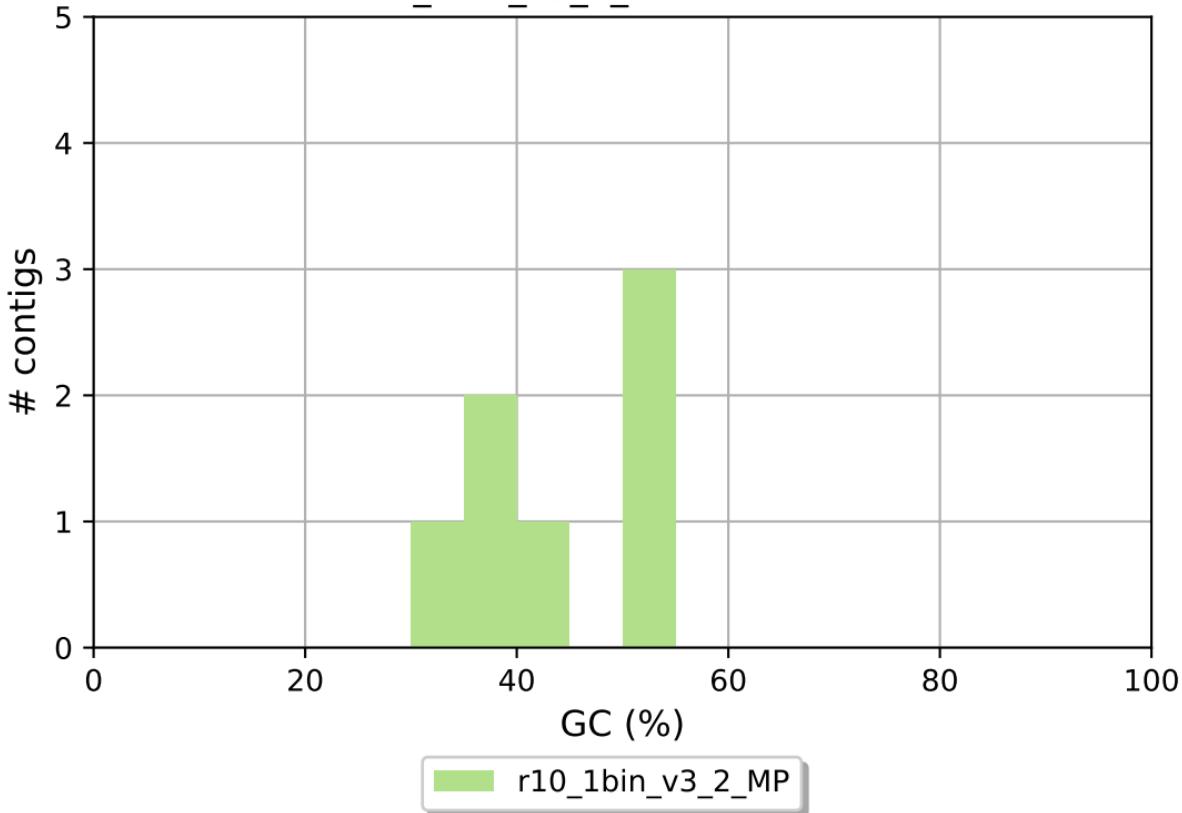
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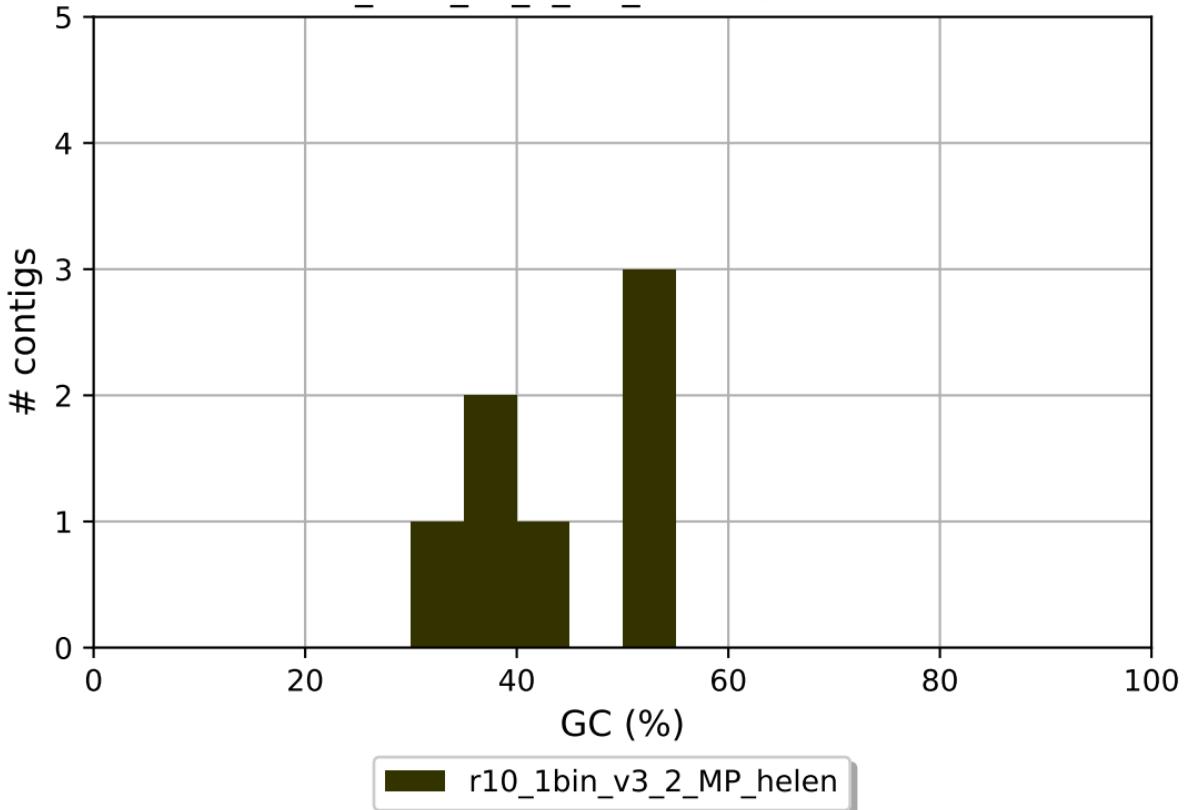
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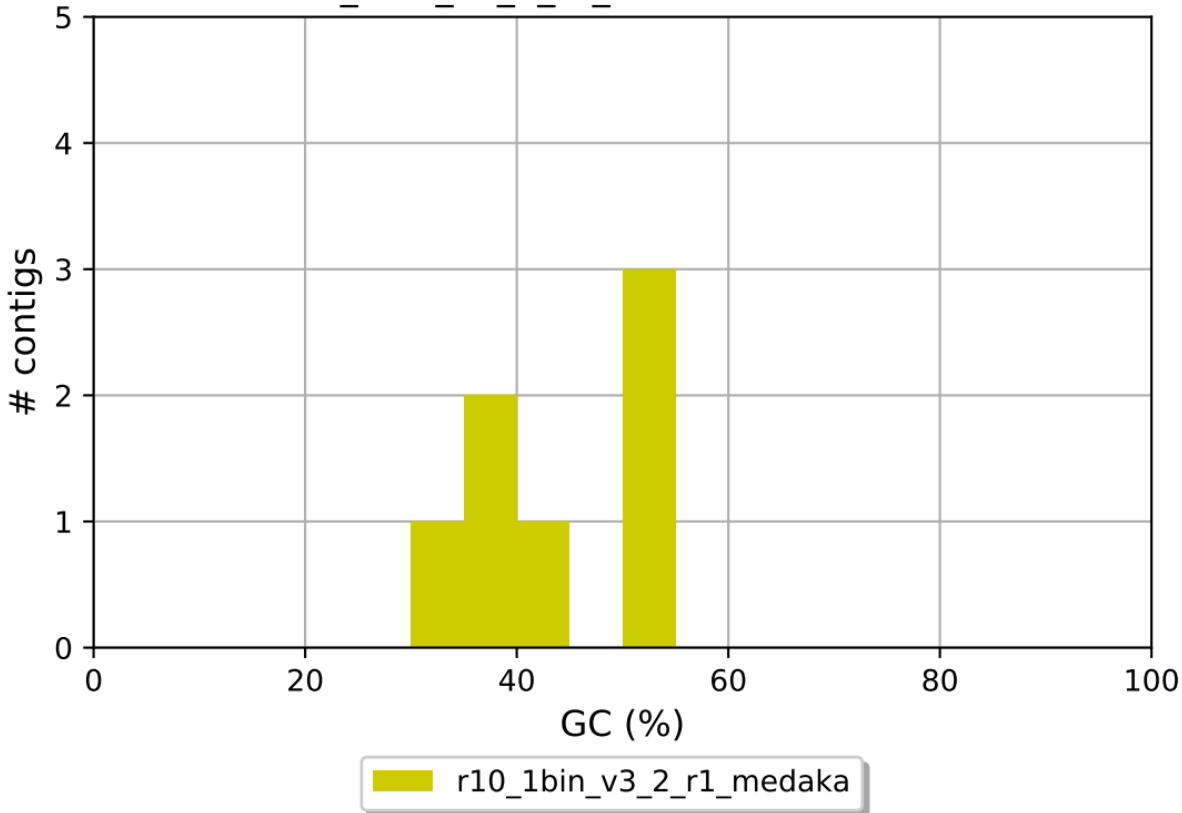
r10\_1bin\_v3\_2\_MP GC content



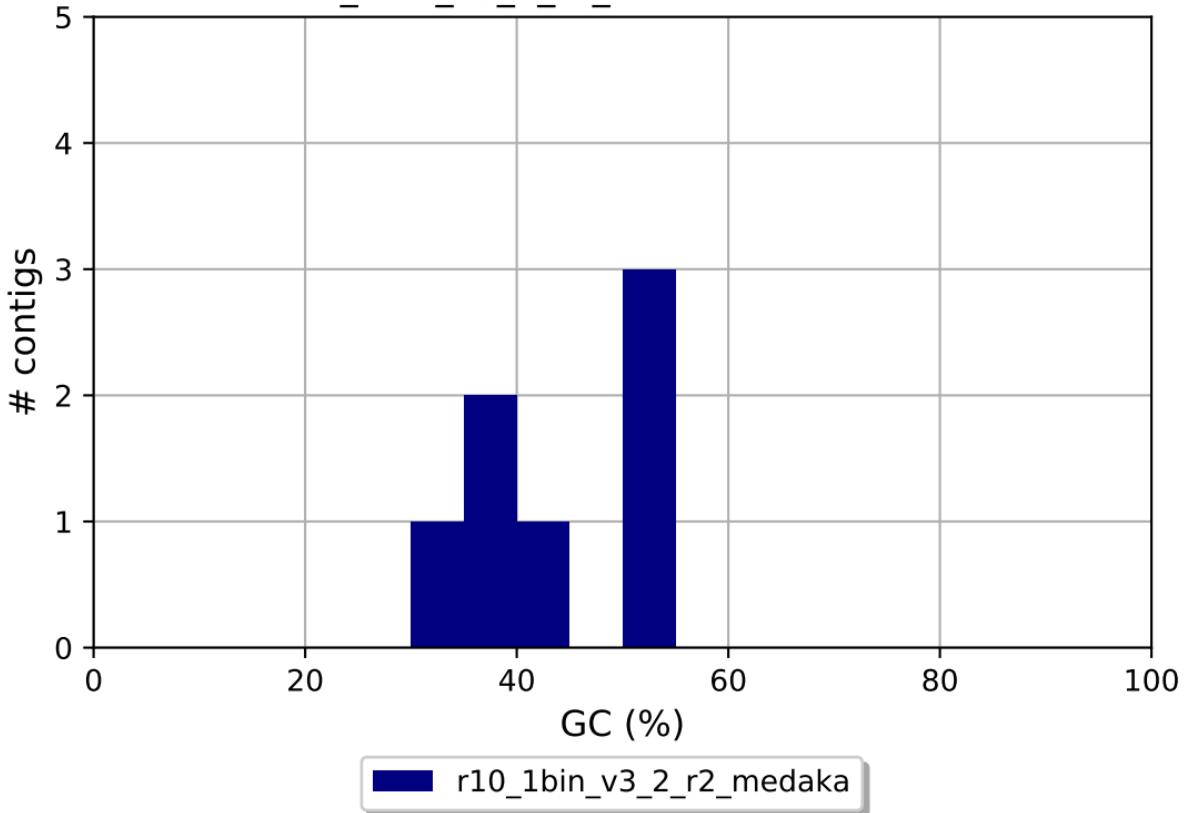
r10\_1bin\_v3\_2\_MP\_helen GC content



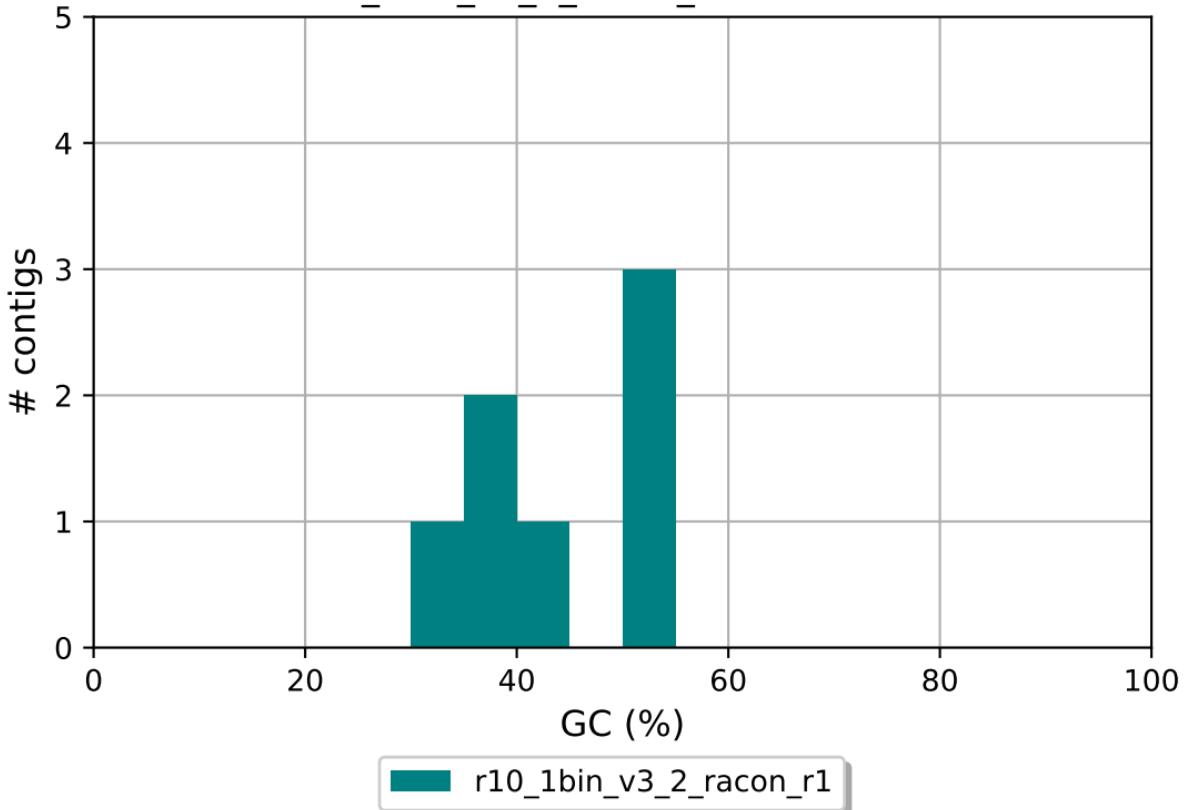
r10\_1bin\_v3\_2\_r1\_medaka GC content



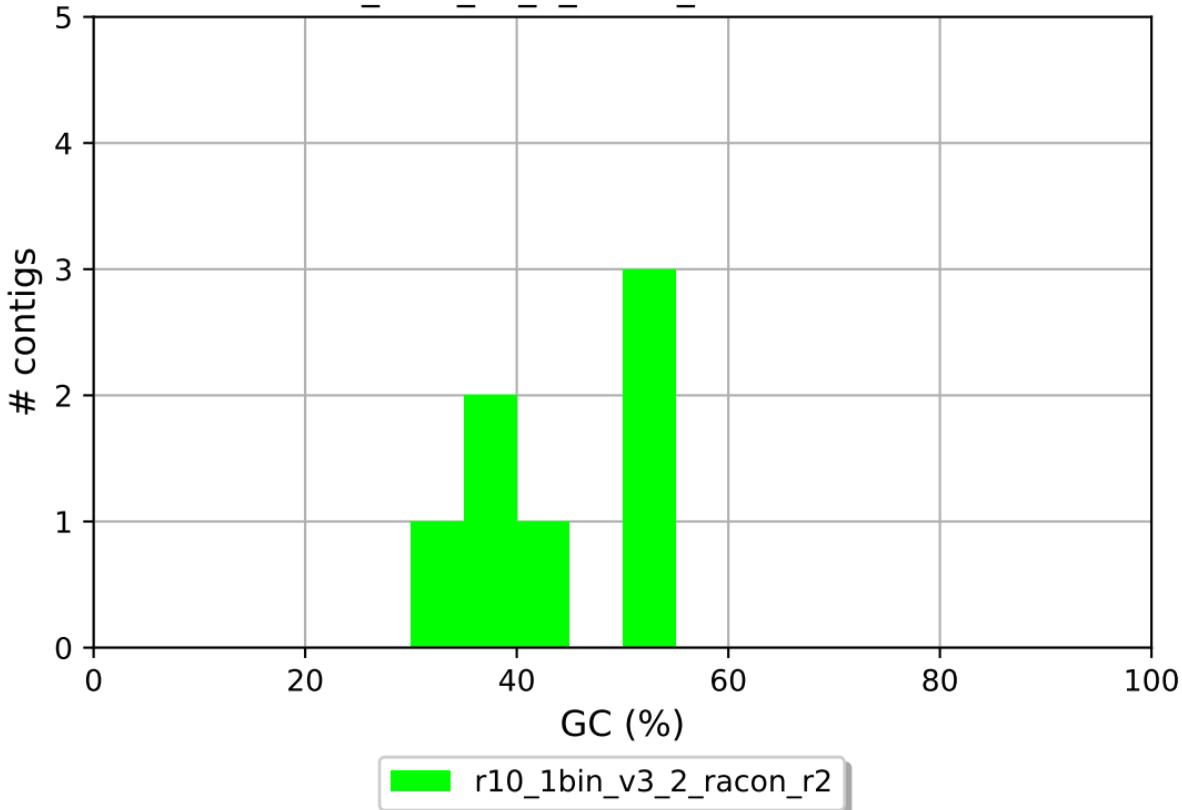
r10\_1bin\_v3\_2\_r2\_medaka GC content



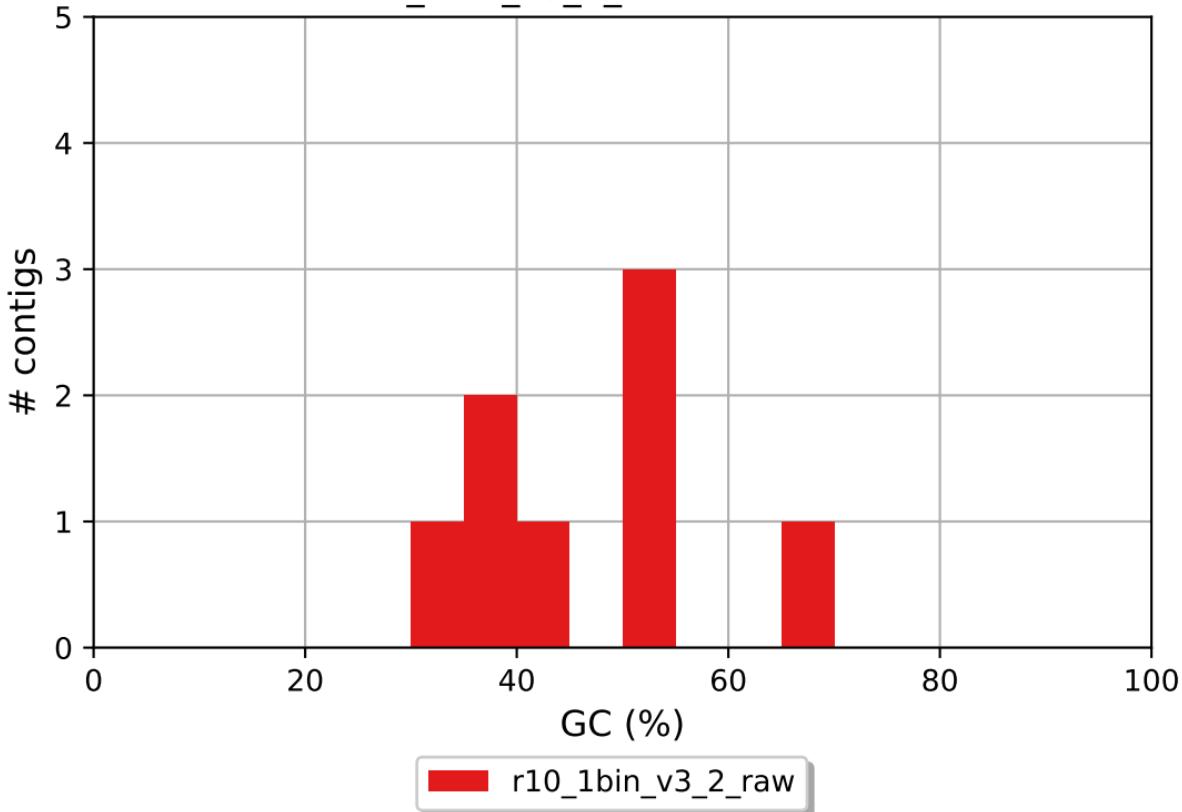
r10\_1bin\_v3\_2\_racon\_r1 GC content



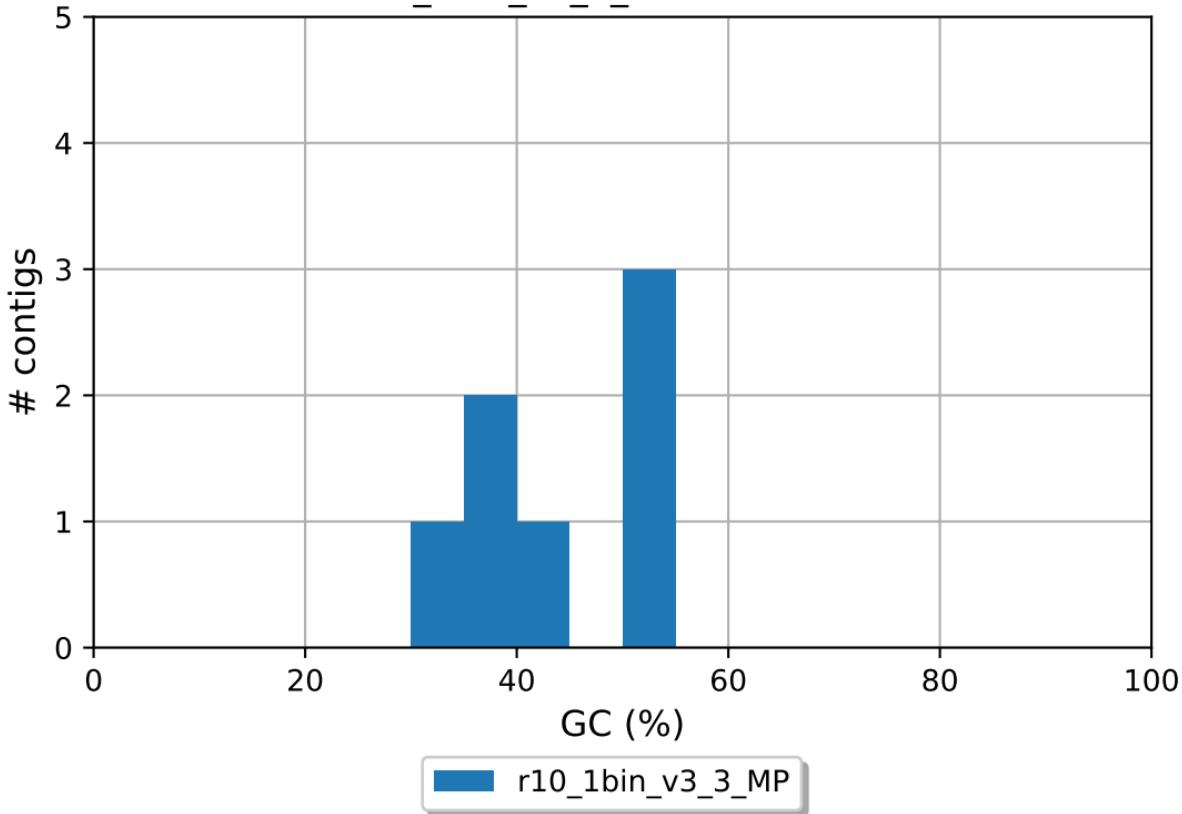
r10\_1bin\_v3\_2\_racon\_r2 GC content



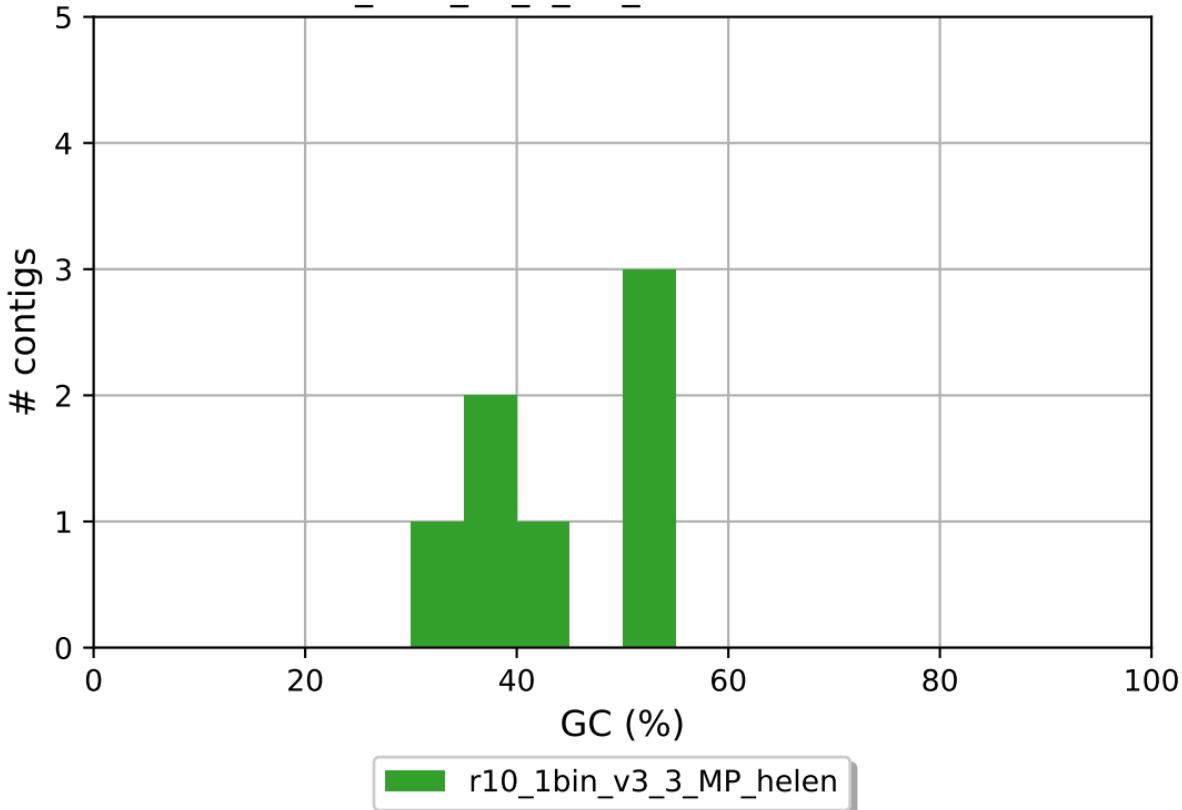
r10\_1bin\_v3\_2\_raw GC content



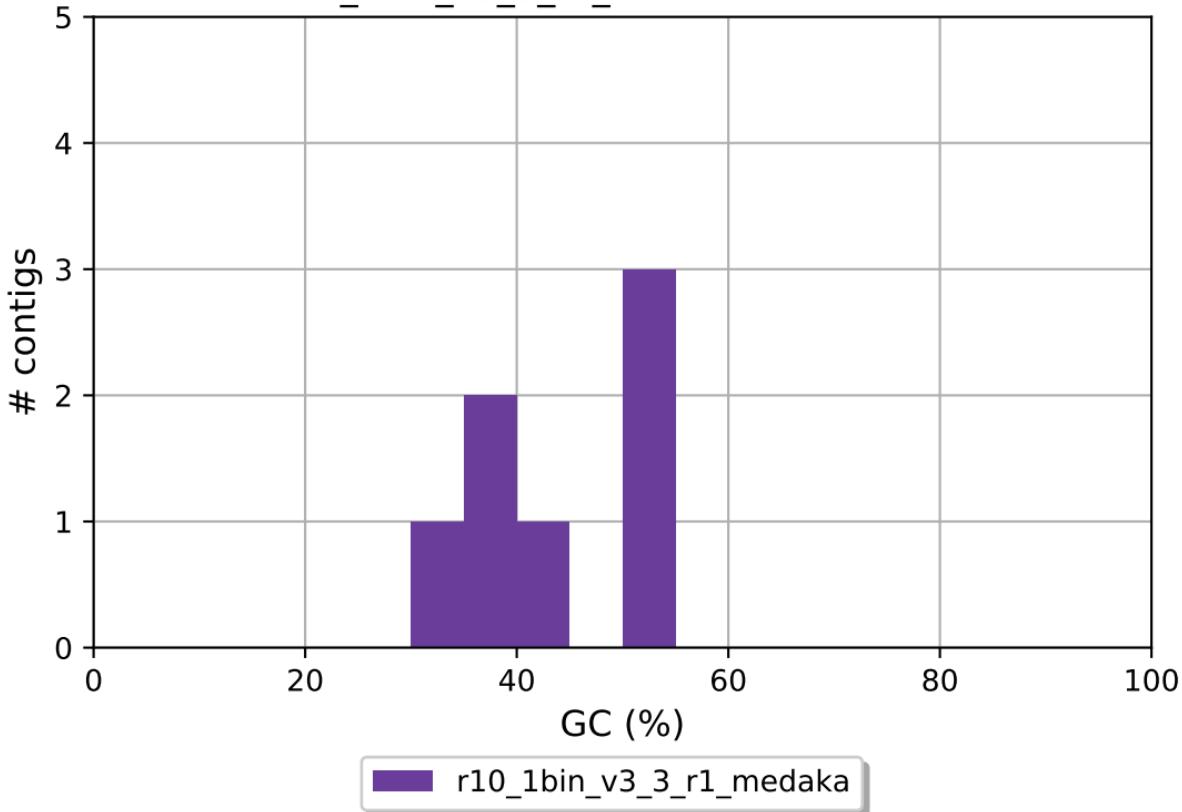
r10\_1bin\_v3\_3\_MP GC content



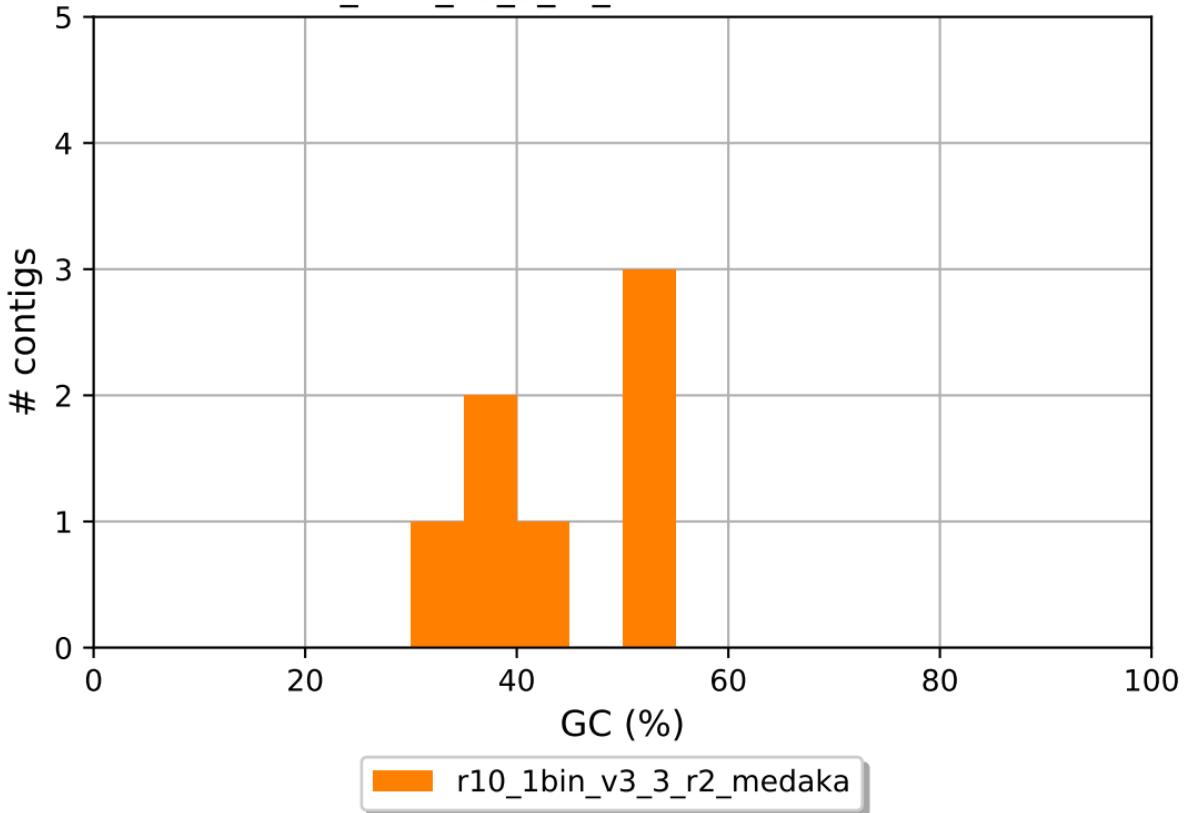
r10\_1bin\_v3\_3\_MP\_helen GC content



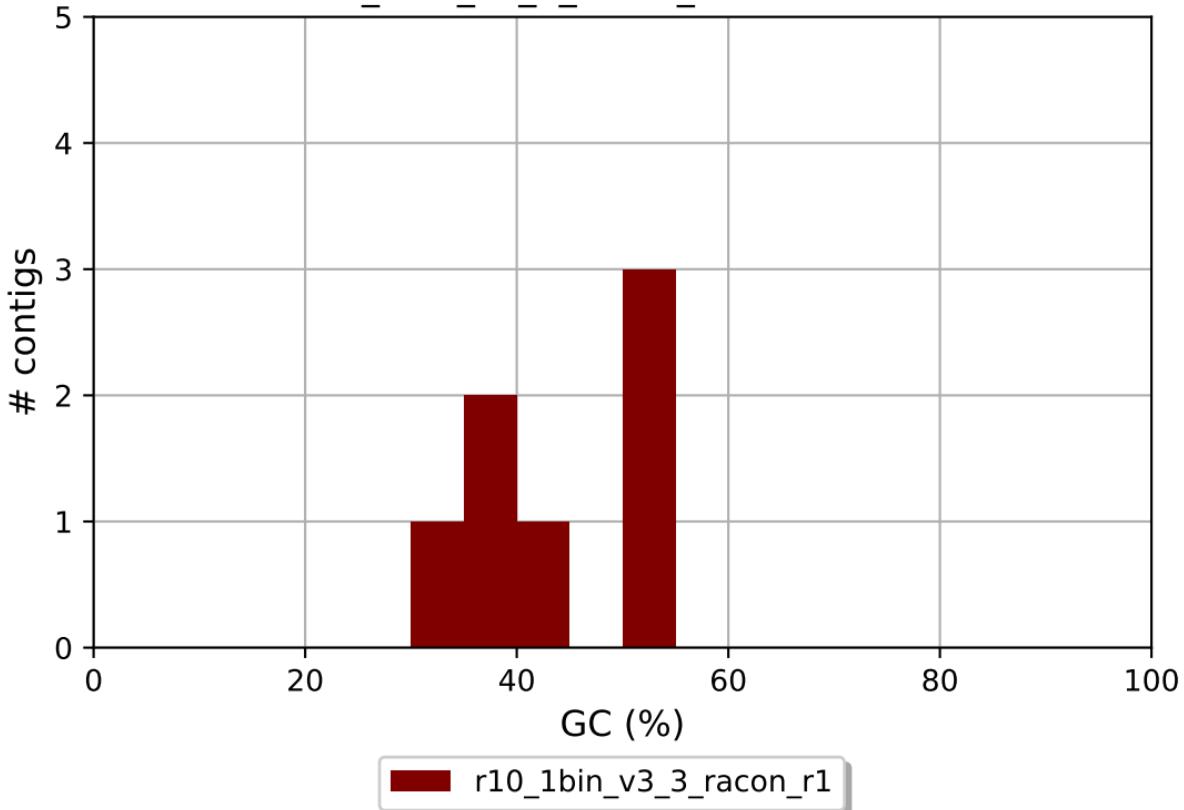
r10\_1bin\_v3\_3\_r1\_medaka GC content



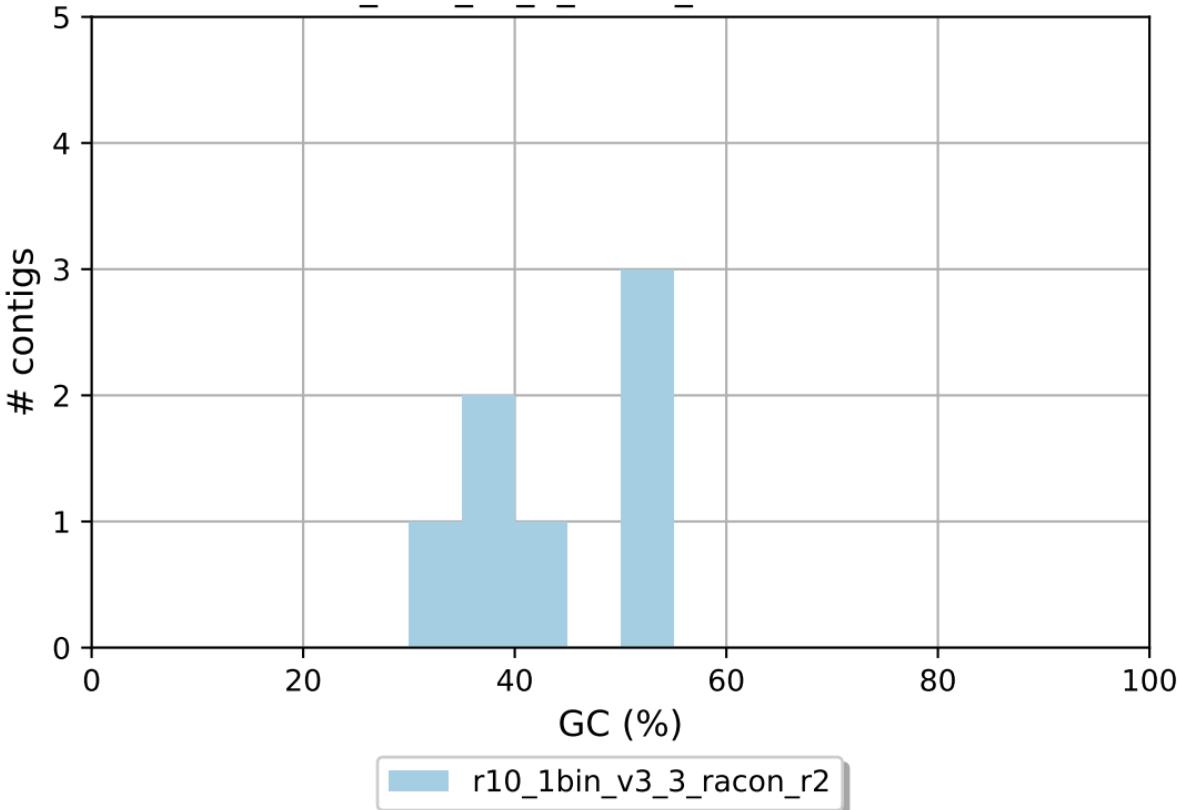
r10\_1bin\_v3\_3\_r2\_medaka GC content



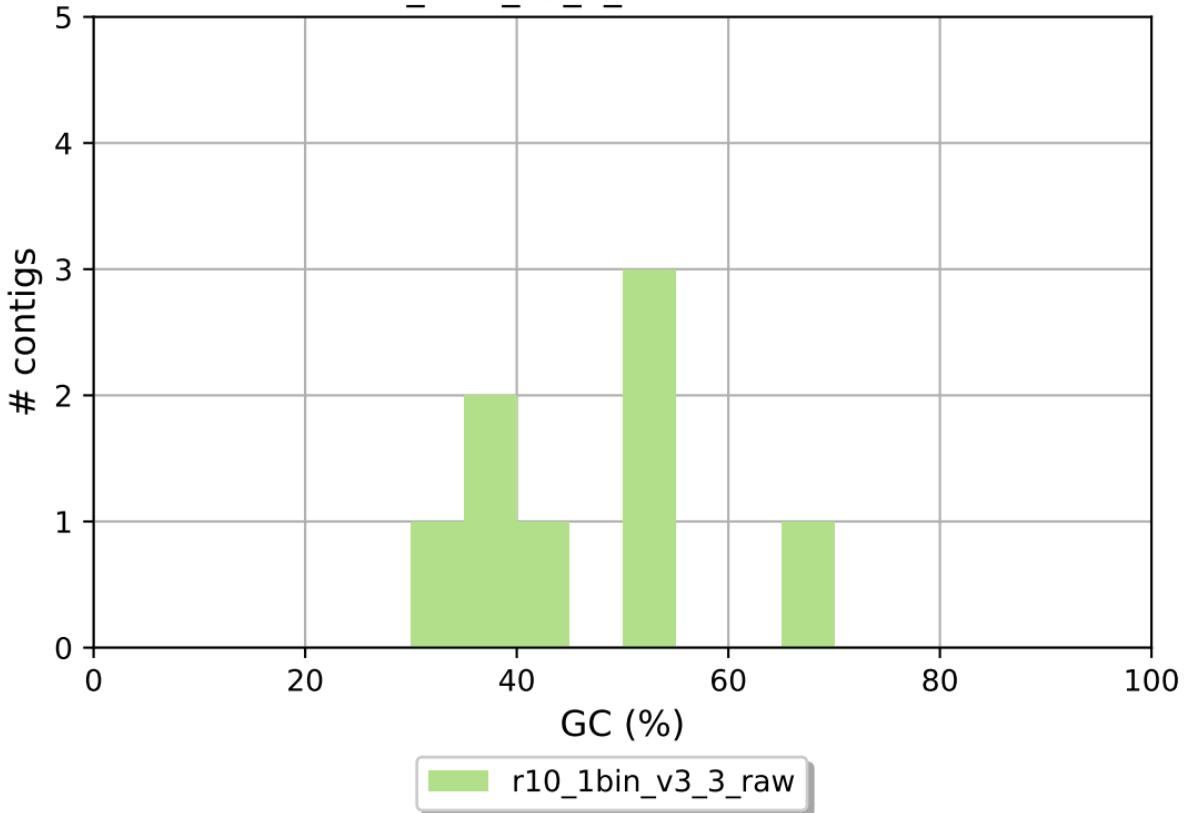
r10\_1bin\_v3\_3\_racon\_r1 GC content



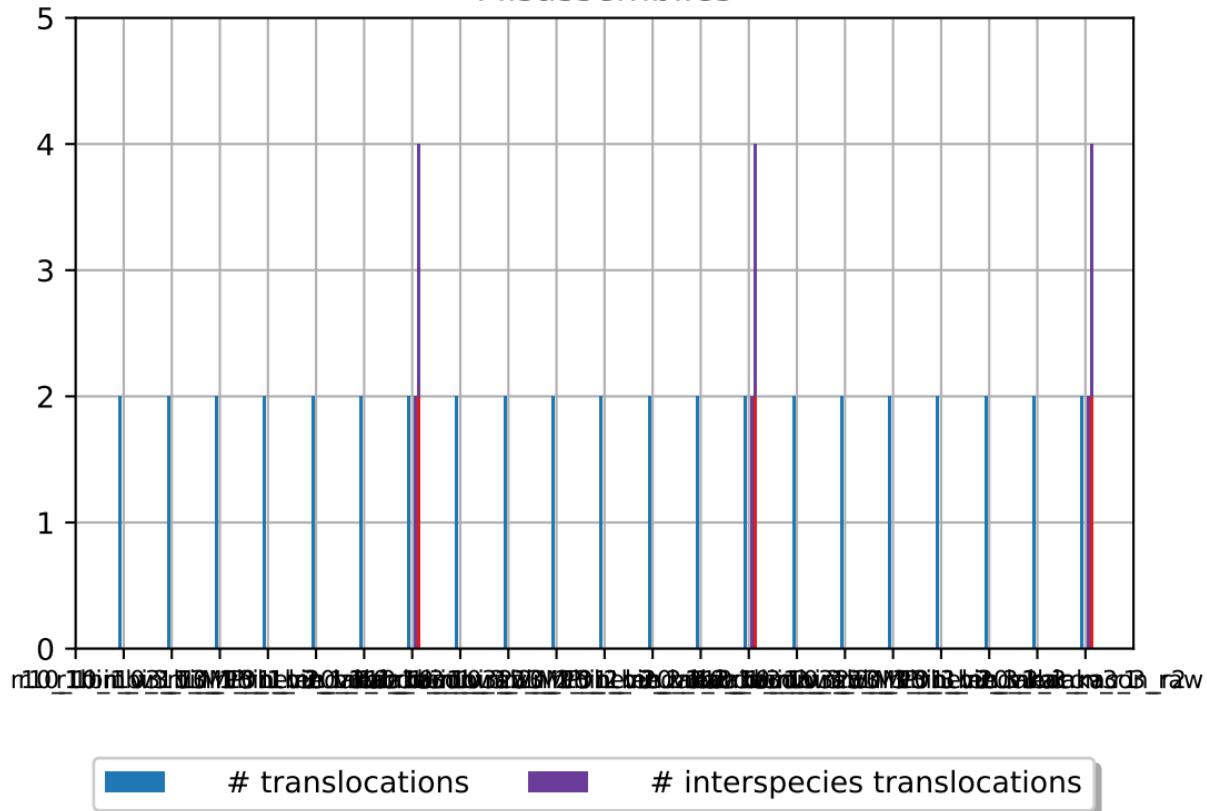
r10\_1bin\_v3\_3\_racon\_r2 GC content



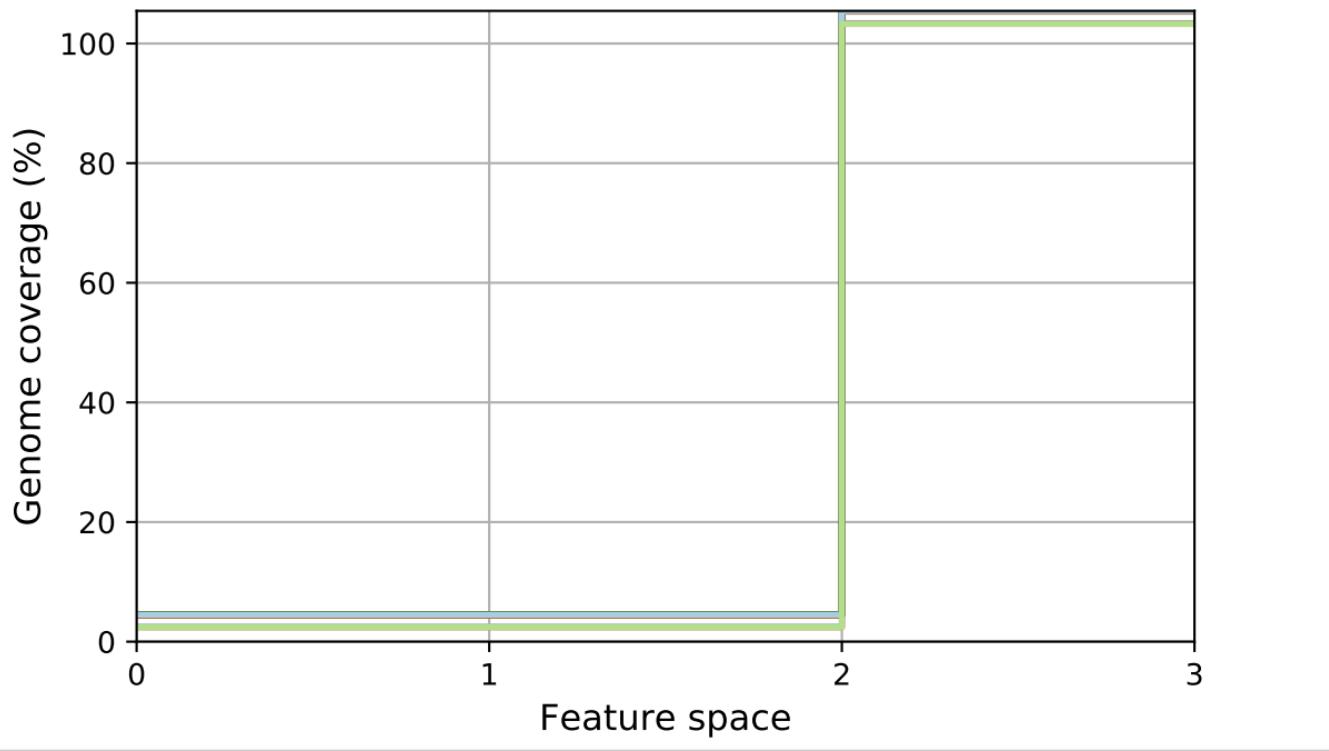
r10\_1bin\_v3\_3\_raw GC content



## Misassemblies



### FRCurve (misassemblies)

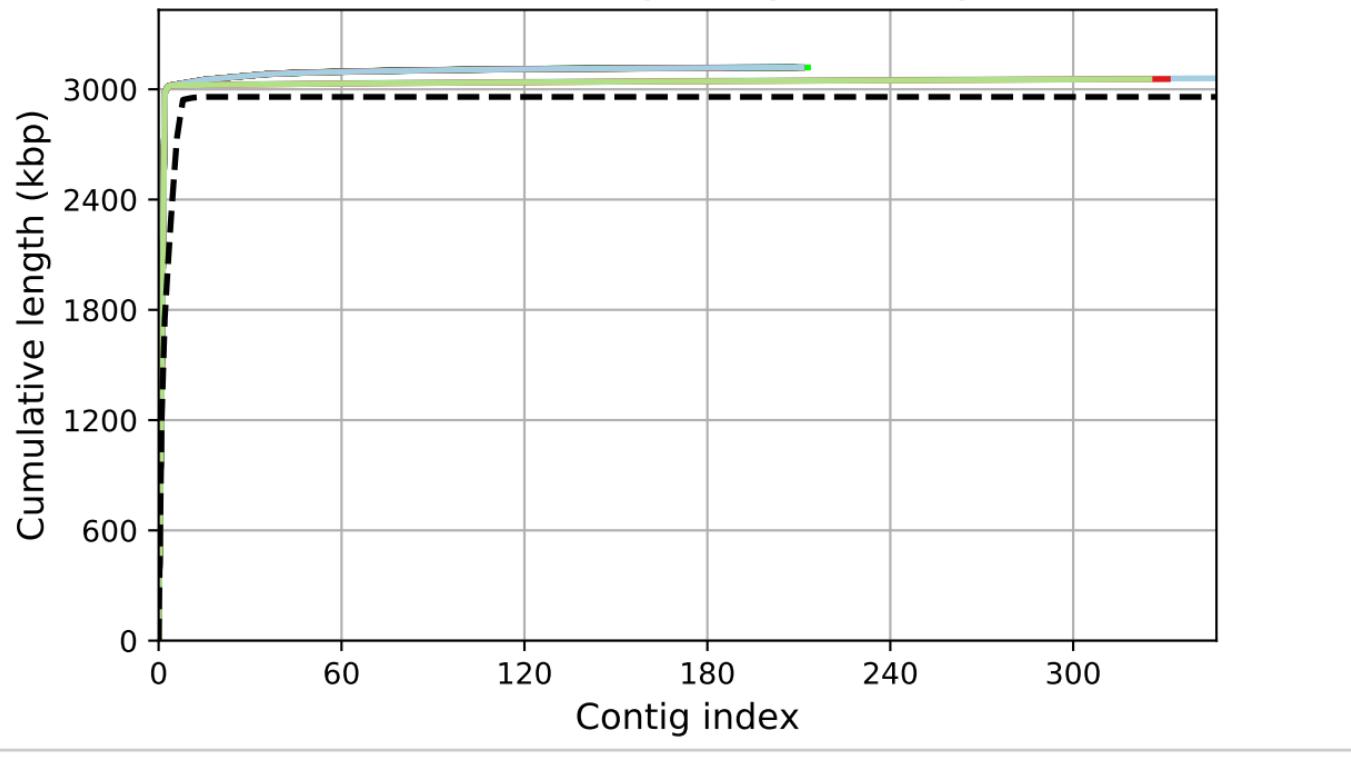


r10\_1bin\_v3\_1\_MP  
r10\_1bin\_v3\_1\_MP\_helen  
r10\_1bin\_v3\_1\_r1\_medaka  
r10\_1bin\_v3\_1\_r2\_medaka

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

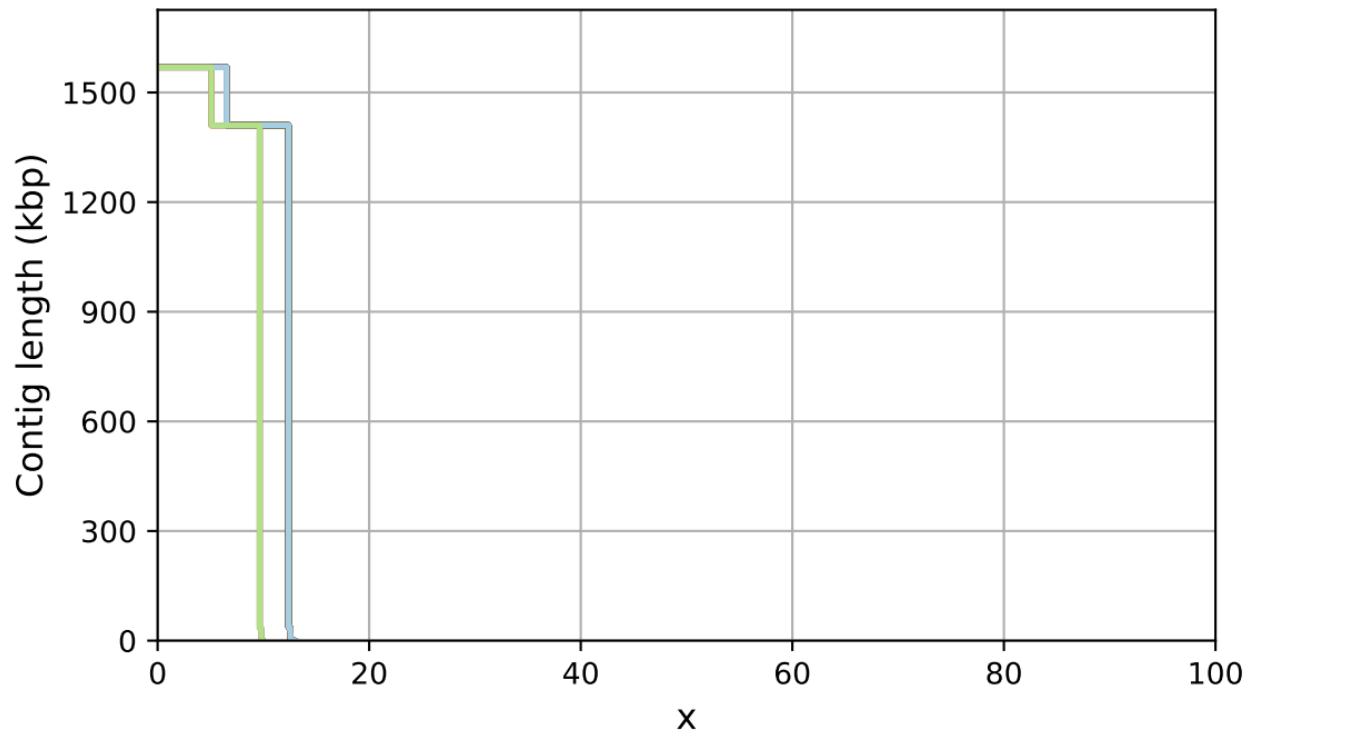
### Cumulative length (aligned contigs)



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\_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

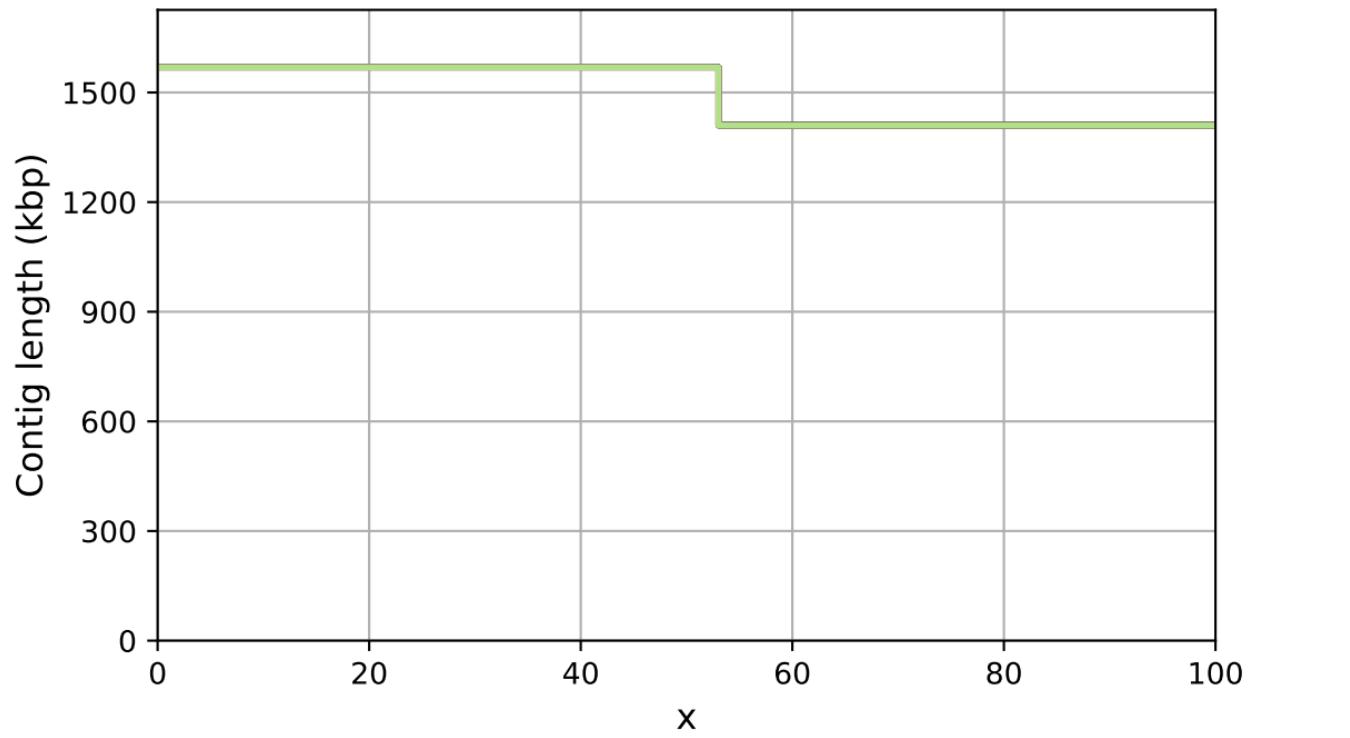


r10\_1bin\_v3\_1\_MP  
r10\_1bin\_v3\_1\_MP\_helen  
r10\_1bin\_v3\_1\_r1\_medaka  
r10\_1bin\_v3\_1\_r2\_medaka

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

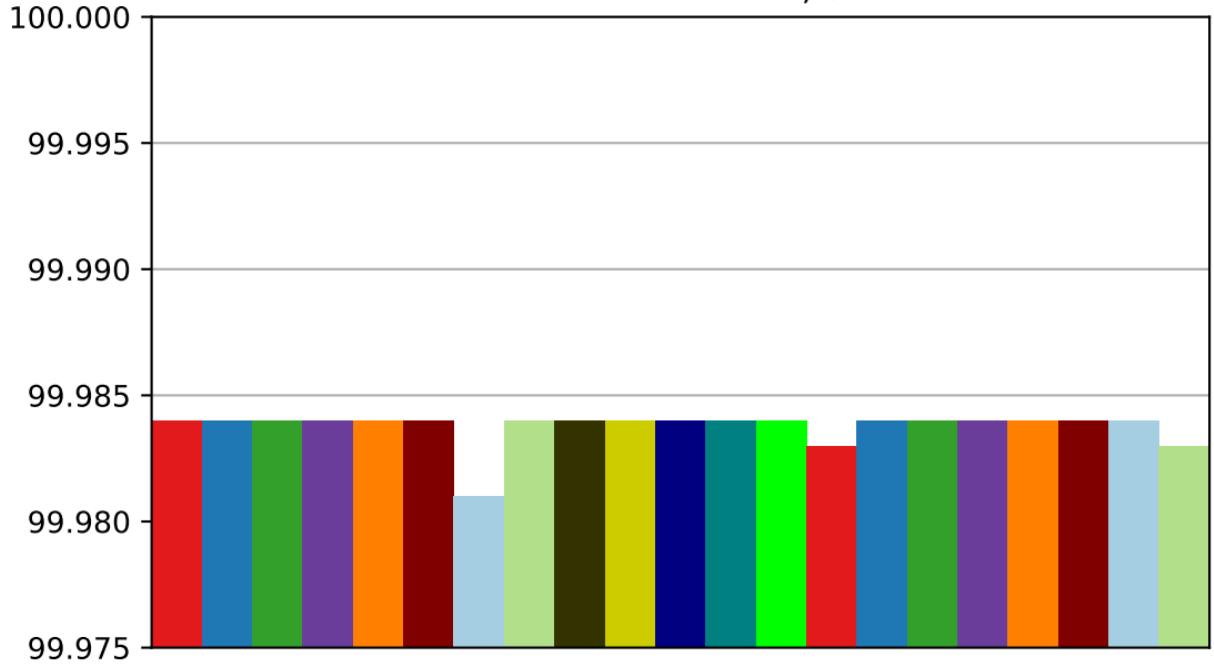
# NGAx



Legend:

Contig ID	Color
r10_1bin_v3_1_MP	Light Green
r10_1bin_v3_1_MP_helen	Dark Green
r10_1bin_v3_1_r1_medaka	Yellow
r10_1bin_v3_1_r2_medaka	Blue
r10_1bin_v3_2_MP	Light Green
r10_1bin_v3_2_MP_helen	Dark Green
r10_1bin_v3_2_r1_medaka	Yellow
r10_1bin_v3_2_r2_medaka	Blue
r10_1bin_v3_3_MP	Light Green
r10_1bin_v3_3_MP_helen	Dark Green
r10_1bin_v3_3_r1_medaka	Yellow
r10_1bin_v3_3_r2_medaka	Blue

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