

## Report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw	
# contigs (>= 0 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 1000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Total length (>= 0 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 1000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 5000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 10000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 25000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 50000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Largest contig	6792242	6792185	6792243	6792248	6791549	6791659	6788581	6792253	6792197	6792245	6792241	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
Total length	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	4756002
N75	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2991915	2991980	2990633	2992084	2992069	2992075	2991930	2991998	2990669		
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	
# misassemblies	170	168	169	171	169	173	173	167	168	168	172	169	172	171	168	168	169	172	173	173	175
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Misassembled contigs length	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
# local misassemblies	115	119	133	137	148	147	209	116	118	132	130	147	141	206	117	120	133	131	152	140	212
# 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	
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# 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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	
Unaligned length	78463	79346	81484	81562	77781	76859	137275	79154	78921	82258	78952	78197	77608	135612	79720	79969	81512	82511	77386	77494	137527
Genome fraction (%)	99.400	99.395	99.399	99.399	99.398	99.397	99.371	99.400	99.395	99.398	99.396	99.397	99.372	99.400	99.390	99.398	99.397	99.398	99.397	99.398	99.371
Duplication ratio	1.043	1.044	1.043	1.043	1.043	1.043	1.027	1.044	1.044	1.043	1.043	1.043	1.028	1.044	1.044	1.043	1.043	1.043	1.043	1.028	
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
# mismatches per 100 kbp	174.38	168.25	177.43	175.39	177.26	178.49	273.31	176.08	168.18	177.19	176.10	178.36	180.96	272.80	176.32	168.20	178.96	176.05	177.31	178.20	277.06
# indels per 100 kbp																					

## Misassemblies report

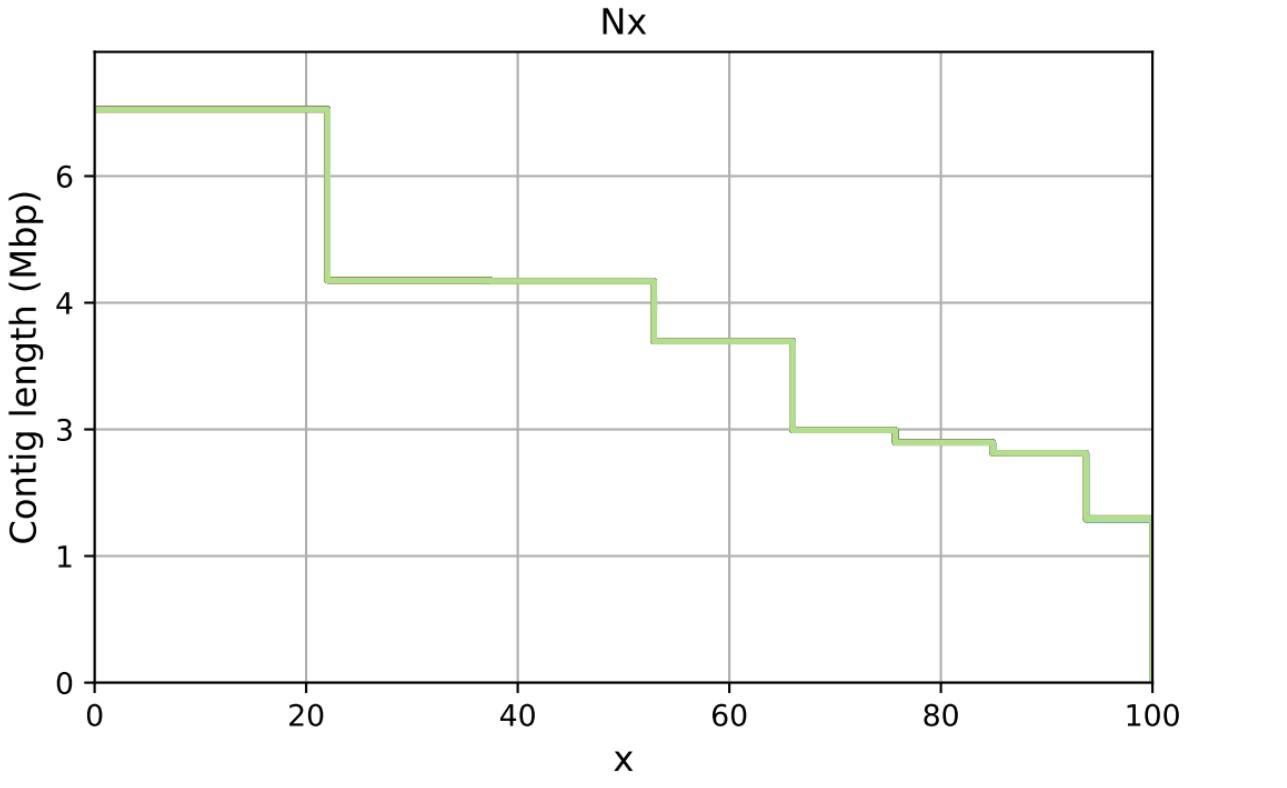
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# misassemblies	170	168	169	171	169	173	173	167	168	168	168	172	169	172	171	168	168	169	172	173	175
# contig misassemblies	170	168	169	171	169	173	173	167	168	168	168	172	169	172	171	168	168	169	172	173	175
# c. relocations	6	4	4	6	4	6	5	4	4	4	4	7	4	7	5	5	4	6	4	6	5
# c. translocations	162	162	163	163	163	165	164	161	162	162	163	163	162	161	162	163	164	167	165	166	
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# c. interspecies translocations	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	
# s. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Misassembled contigs length	30866736	30862385	30864454	30856532	30852547	30847337	30849498	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
# possibly misassembled contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	7	7	7	7	7	7	8	
# possible misassemblies	98	100	96	98	96	92	168	100	98	94	96	96	96	166	100	100	94	96	94	170	
# local misassemblies	115	119	133	137	148	147	209	116	118	132	130	147	141	206	117	120	133	131	152	140	212
# 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	1	0	0	0	0	0	0	0	0	0	0	
# misassemblies caused by fragmented reference	252	252	251	252	252	250	174	253	253	252	251	250	250	174	253	251	250	252	249	251	175
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# mismatches	52883	51020	53809	53190	53757	54127	82862	53400	51000	53734	53403	54087	54878	82708	53472	51004	54270	53389	53770	54039	83998
# indels	11557	7162	8065	7978	20066	18503	94305	11544	7216	8001	7886	20095	18406	93702	11655	7266	8113	8041	20144	19061	94925
# indels (<= 5 bp)	10904	6491	7469	7378	19413	17870	93076	10884	6560	7403	7286	19439	17764	92454	11005	6592	7522	7439	19490	18413	93689
# indels (> 5 bp)	653	671	596	600	653	633	1229	660	656	598	600	656	642	1248	650	674	591	602	654	648	1236
Indels length	45878	41359	40658	40732	57723	54293	158982	45985	41304	40613	58002	54332	158809	45839	41681	40727	40812	57709	56081	160267	

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

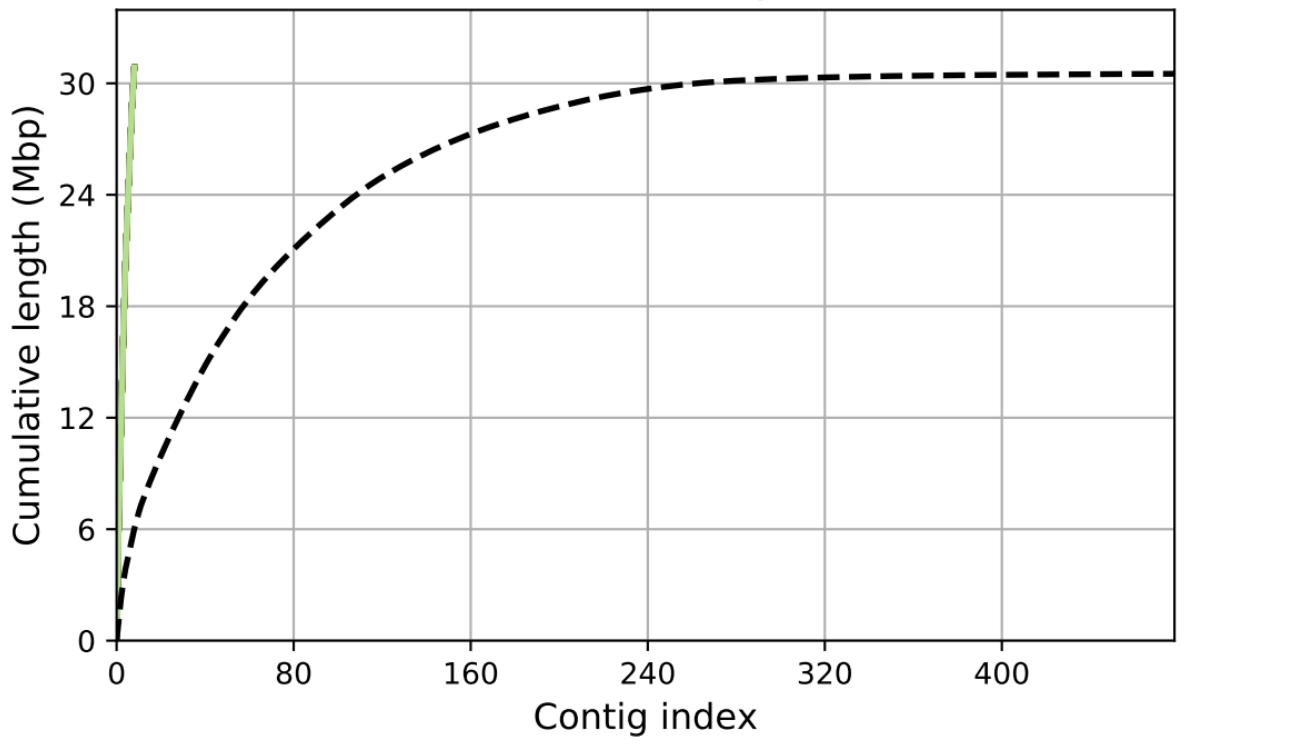
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	
Partially unaligned length	78463	79346	81484	81562	77781	76859	137275	79154	78921	82258	78952	78197	77608	135612	79720	79969	81512	82511	77386	77494	137527
# N's	0	0	0	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  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



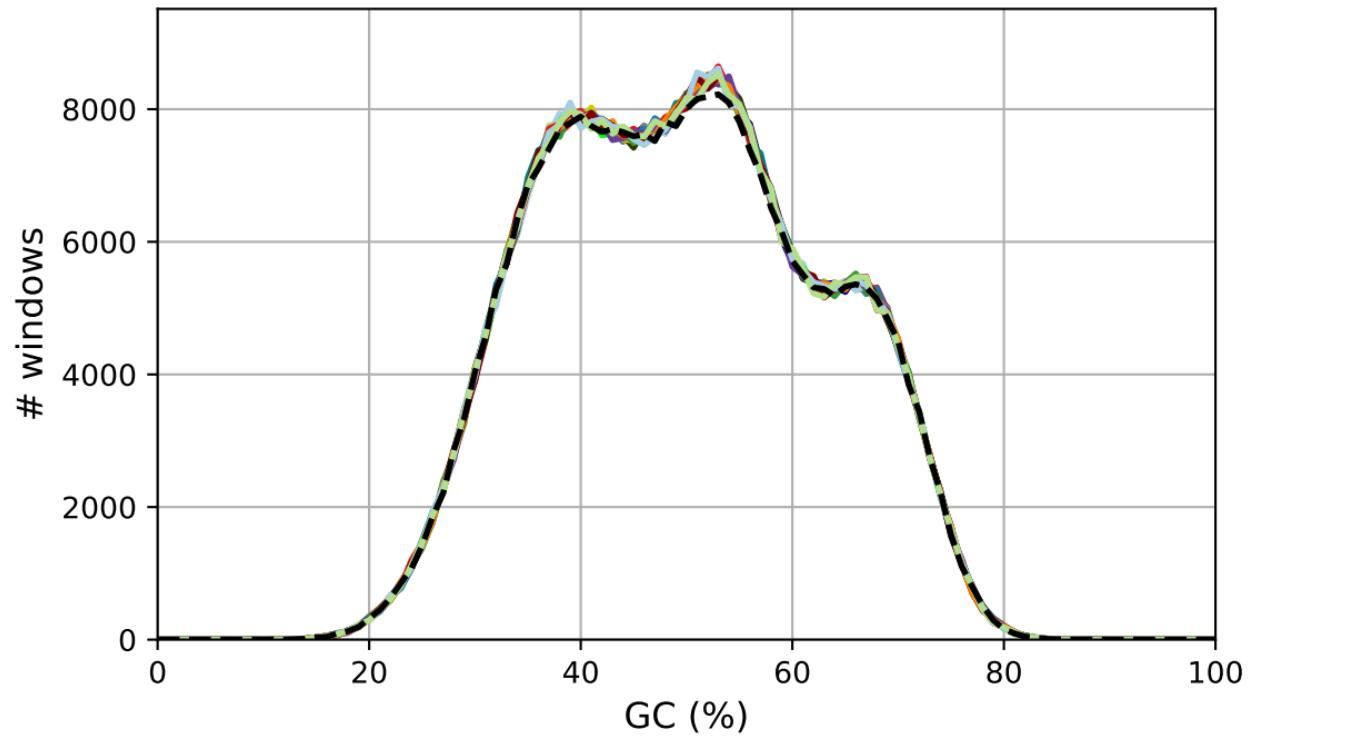
— r10\_1bin\_1\_MP  
— r10\_1bin\_1\_MP\_helen  
— r10\_1bin\_1\_r1\_medaka  
— r10\_1bin\_1\_r2\_medaka  
— r10\_1bin\_2\_MP  
— r10\_1bin\_2\_MP\_helen  
— r10\_1bin\_2\_r1\_medaka  
— r10\_1bin\_2\_r2\_medaka  
— r10\_1bin\_3\_MP\_helen  
— r10\_1bin\_3\_r1\_medaka  
— r10\_1bin\_3\_r2\_medaka

Cumulative length



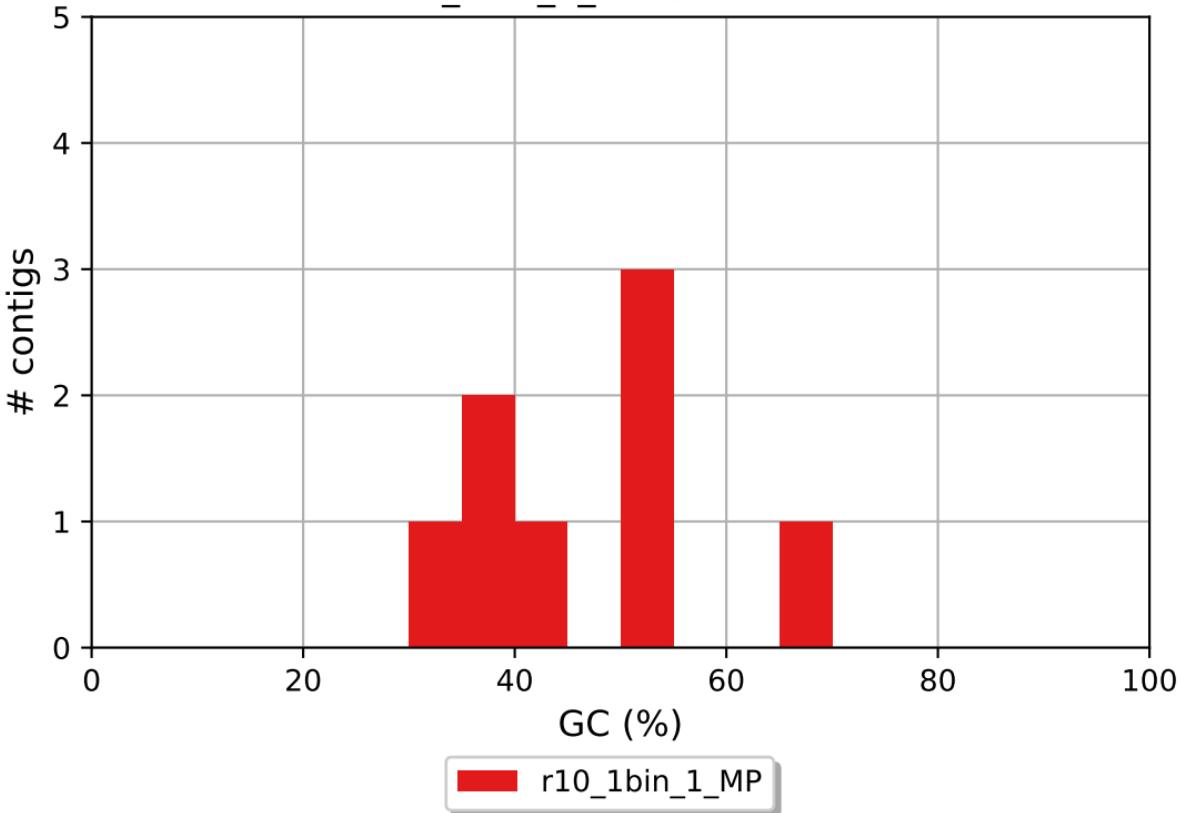
- r10\_1bin\_1\_MP
- r10\_1bin\_1\_MP\_helen
- r10\_1bin\_1\_r1\_medaka
- r10\_1bin\_1\_r2\_medaka
- r10\_1bin\_2\_MP\_helen
- r10\_1bin\_2\_r1\_medaka
- r10\_1bin\_2\_r2\_medaka
- r10\_1bin\_2\_racoon\_r1
- r10\_1bin\_3\_MP\_helen
- r10\_1bin\_3\_r1\_medaka
- r10\_1bin\_3\_r2\_medaka
- r10\_1bin\_3\_racoon\_r1

## GC content

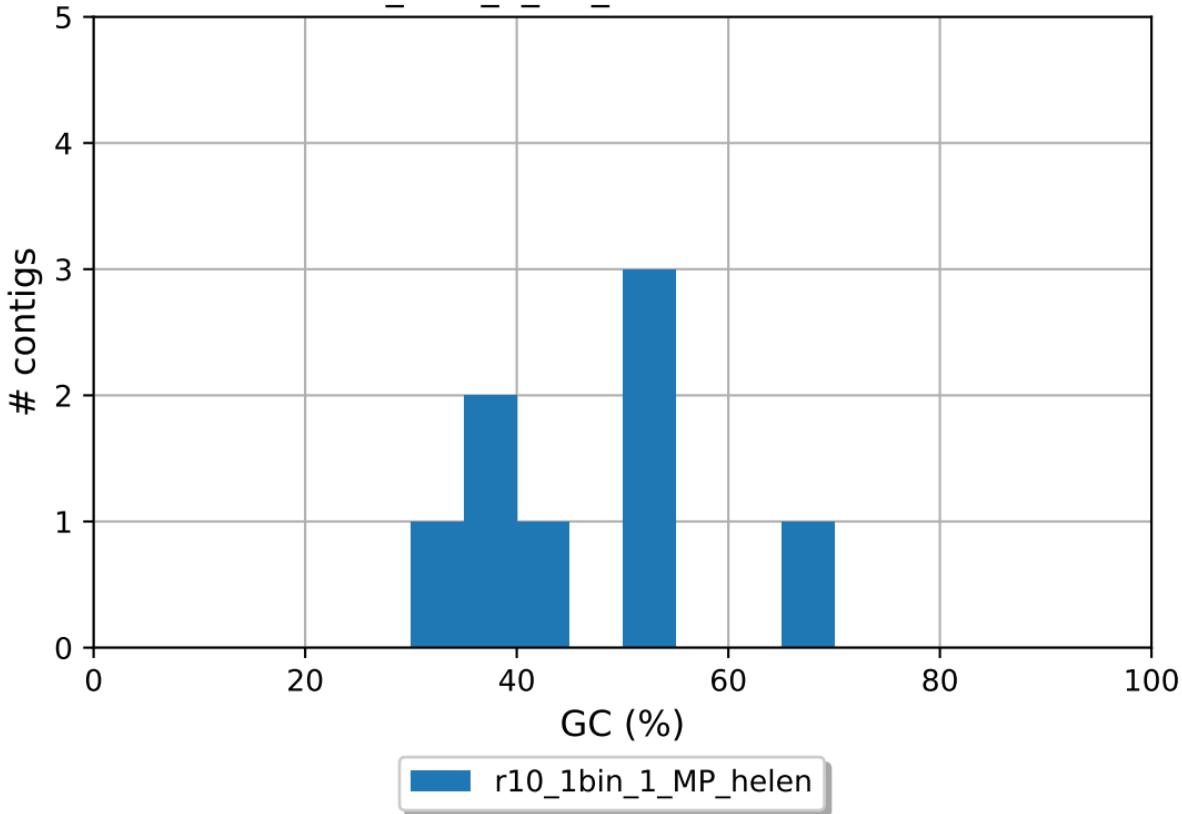


- r10\_1bin\_1\_MP
- r10\_1bin\_1\_MP\_helen
- r10\_1bin\_1\_r1\_medaka
- r10\_1bin\_1\_r2\_medaka
- r10\_1bin\_2\_MP\_helen
- r10\_1bin\_2\_r1\_medaka
- r10\_1bin\_2\_r2\_medaka
- r10\_1bin\_3\_MP\_helen
- r10\_1bin\_3\_r1\_medaka
- r10\_1bin\_3\_r2\_medaka
- r10\_1bin\_3\_racoon\_r1
- r10\_1bin\_3\_racoon\_r1

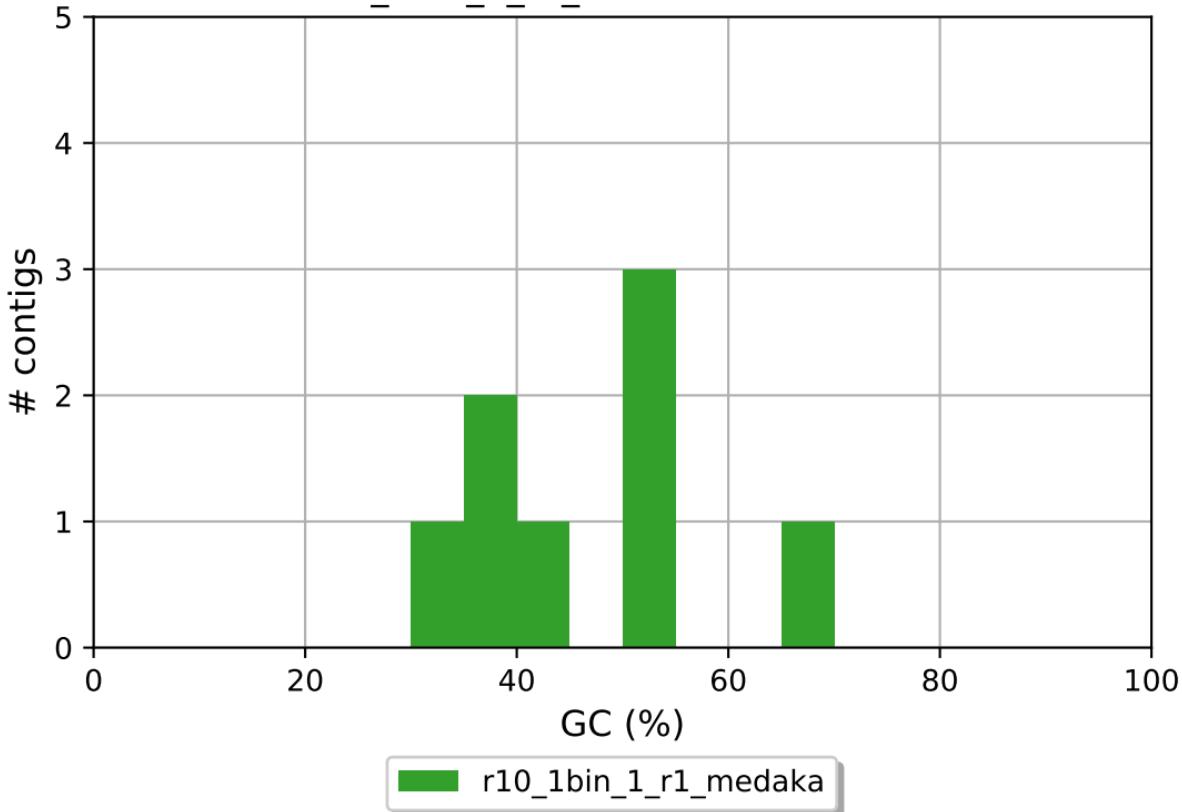
r10\_1bin\_1\_MP GC content



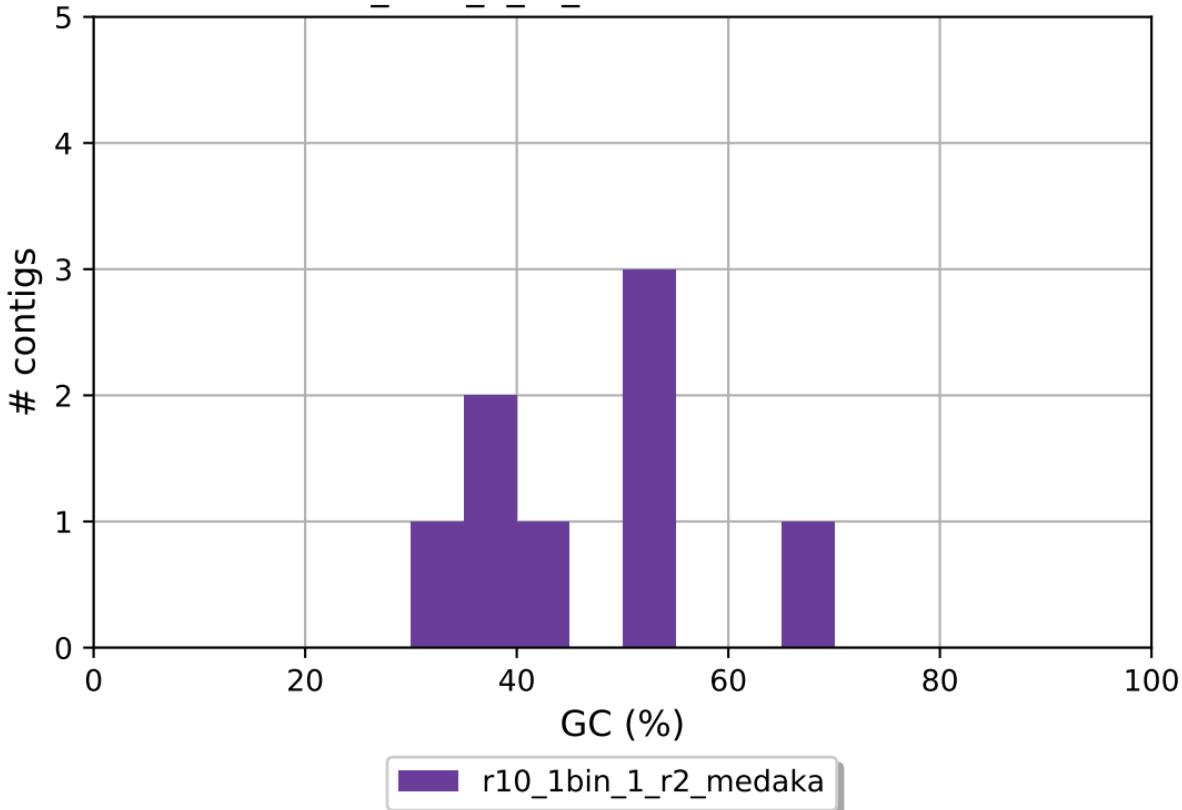
r10\_1bin\_1\_MP\_helen GC content



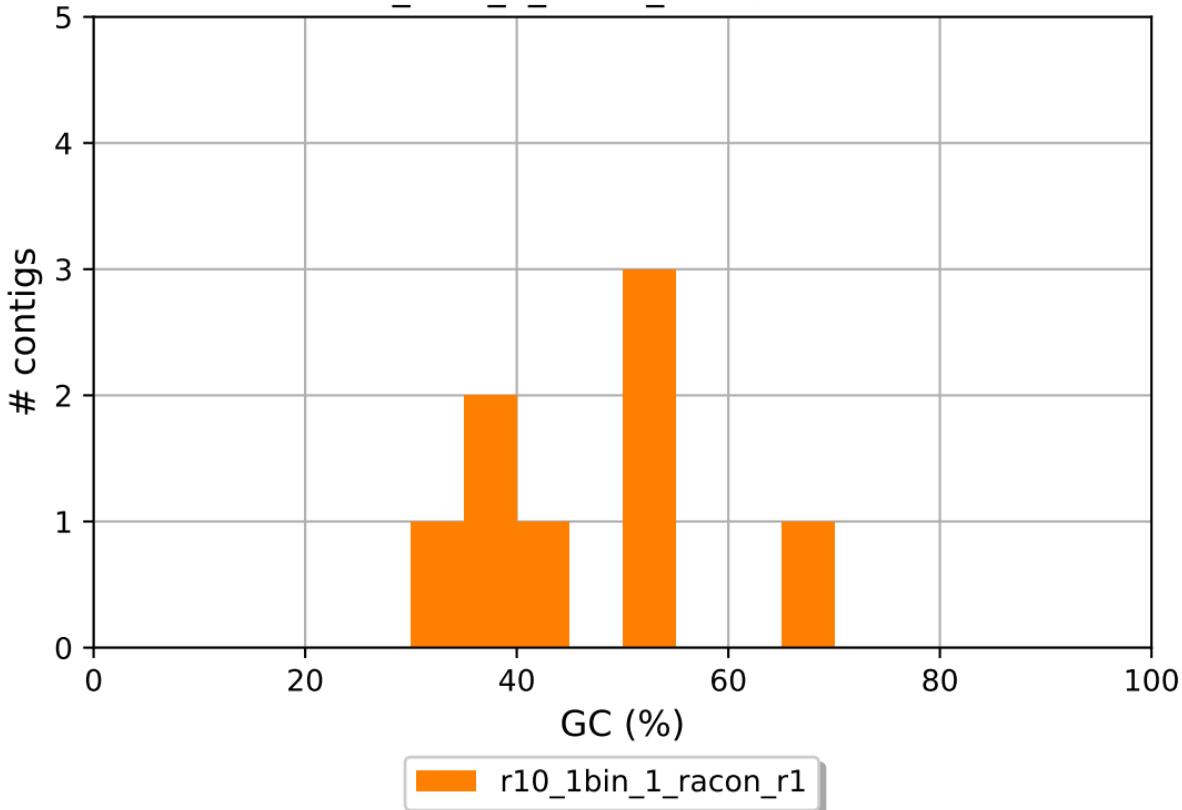
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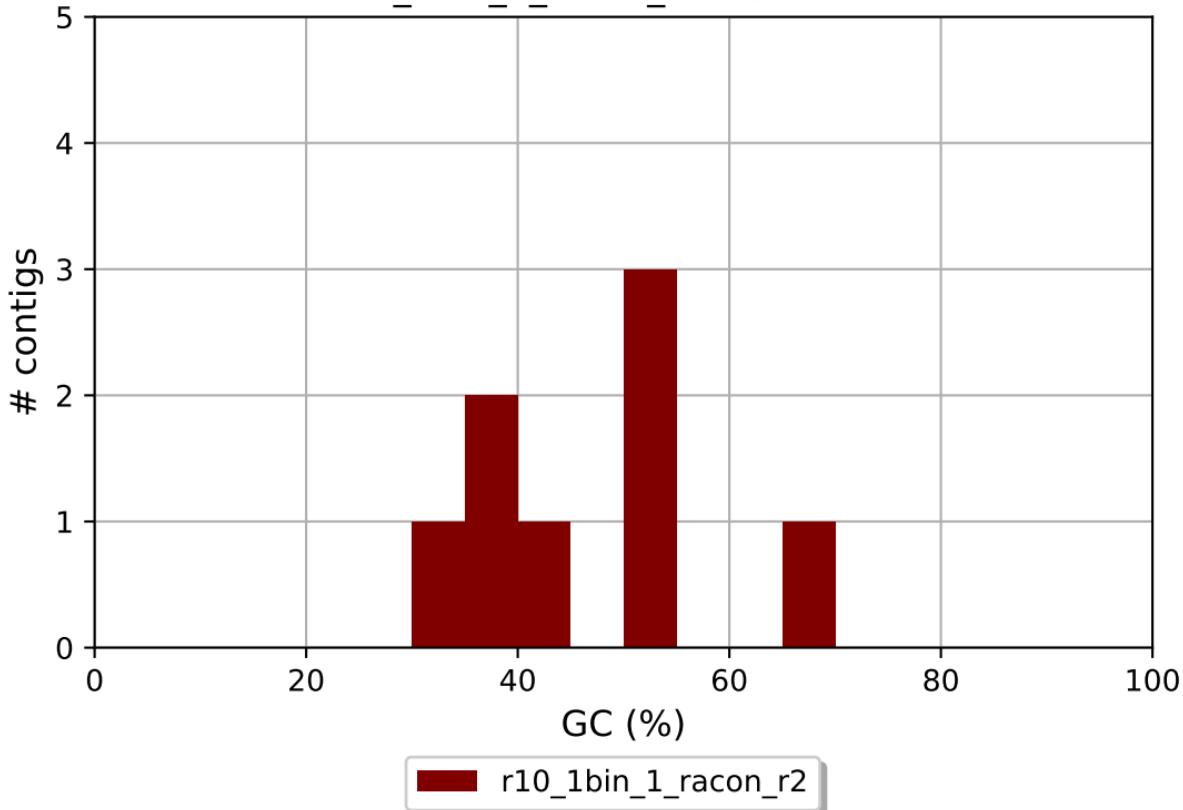
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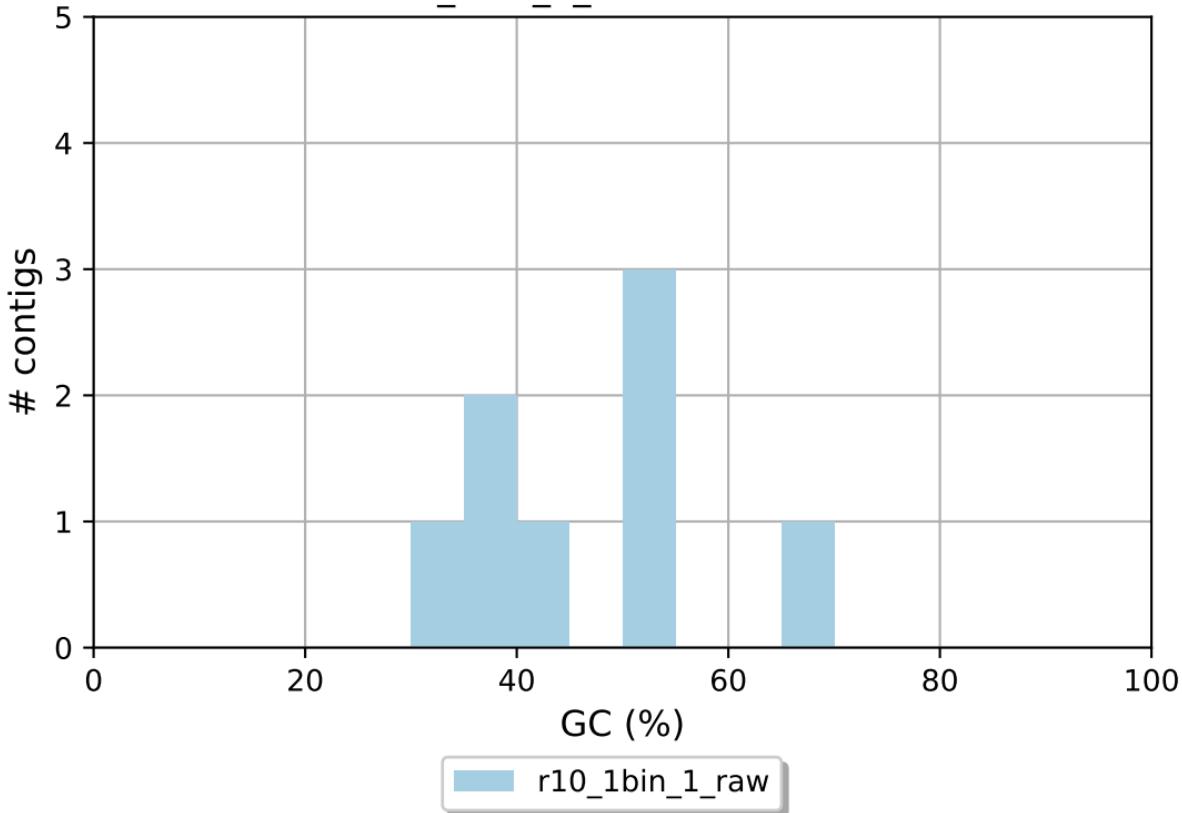
r10\_1bin\_1\_racon\_r1 GC content



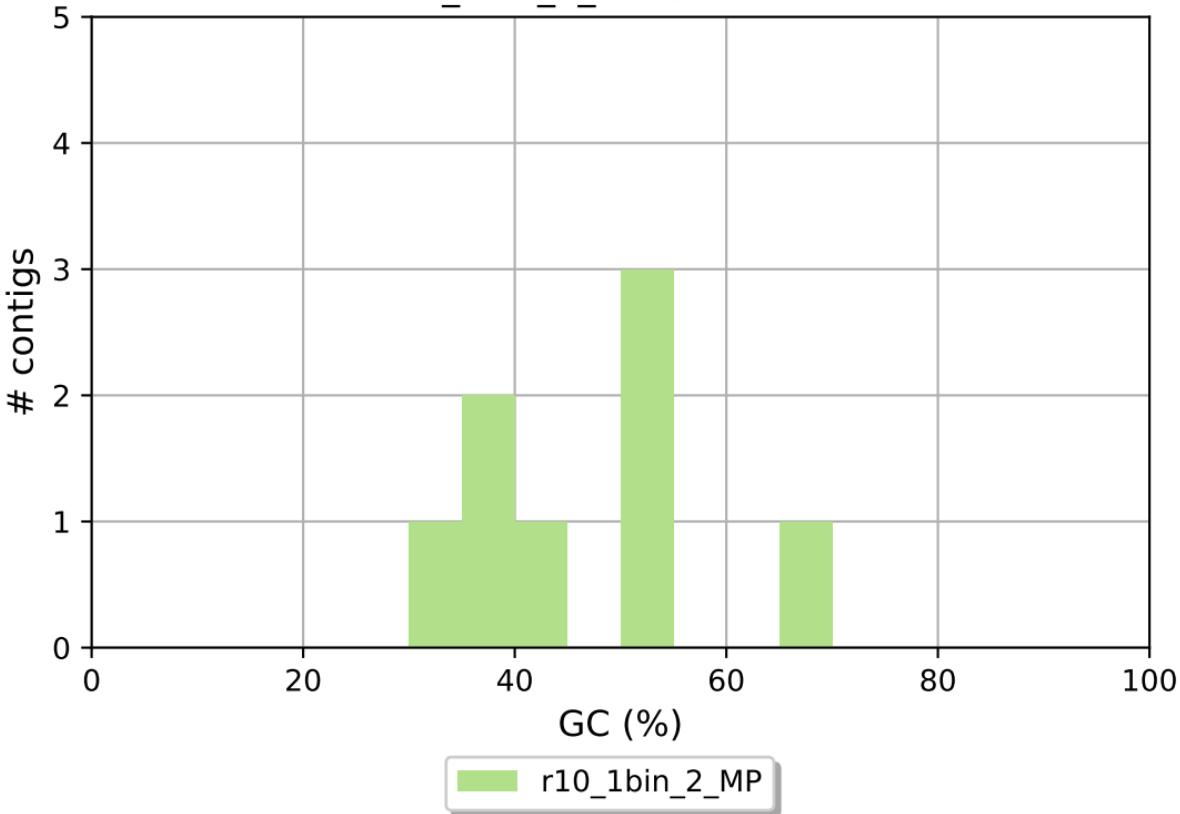
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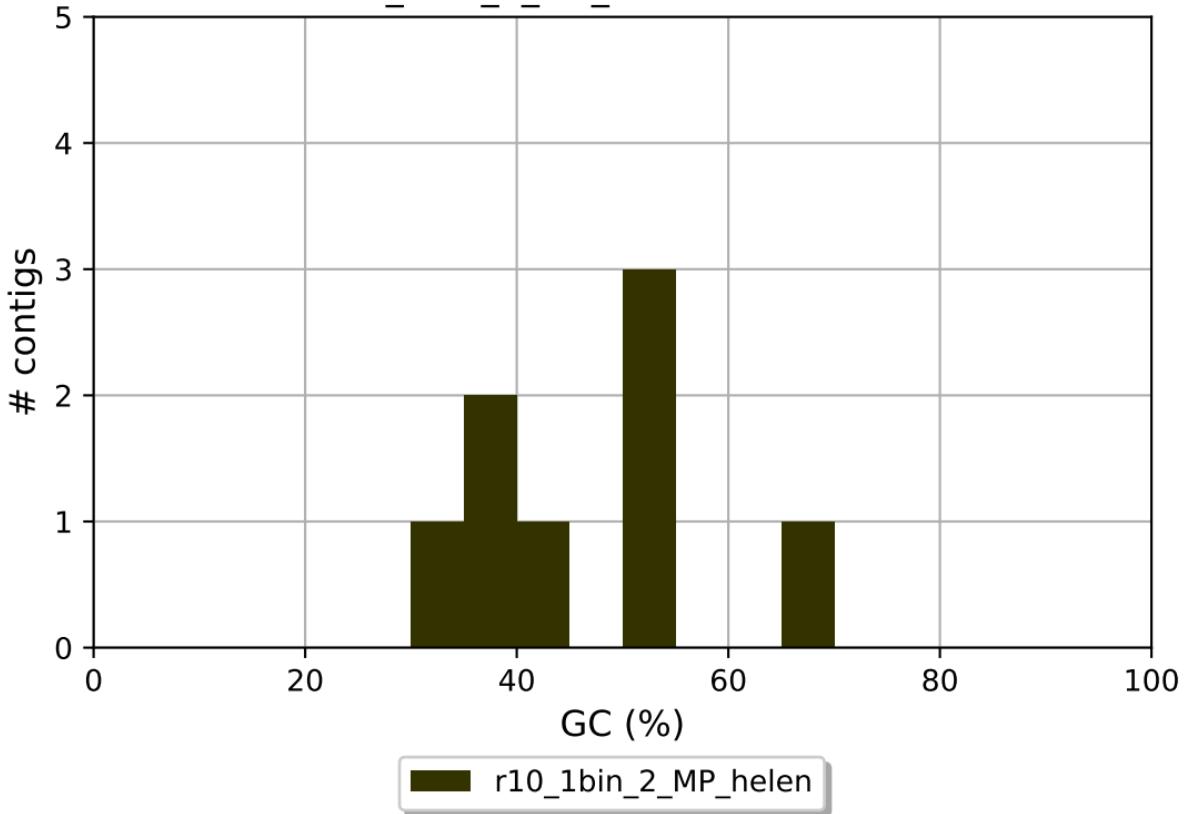
r10\_1bin\_1\_raw GC content



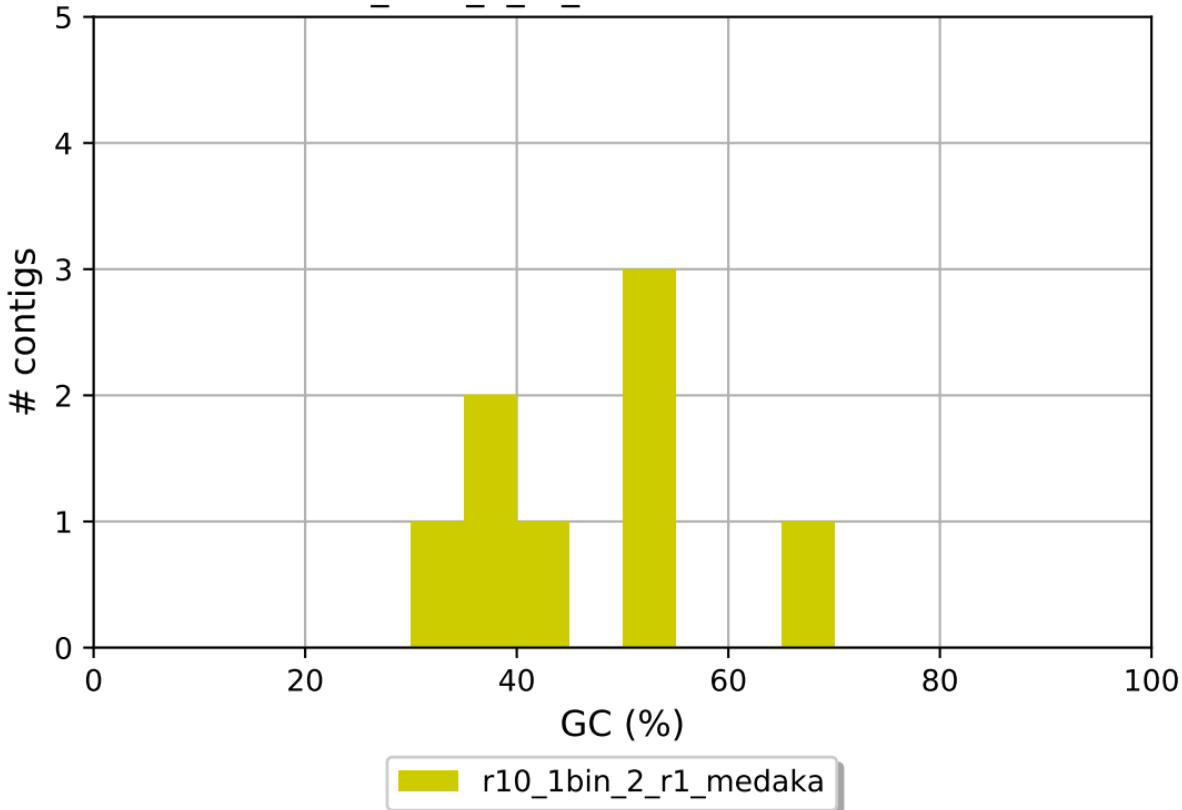
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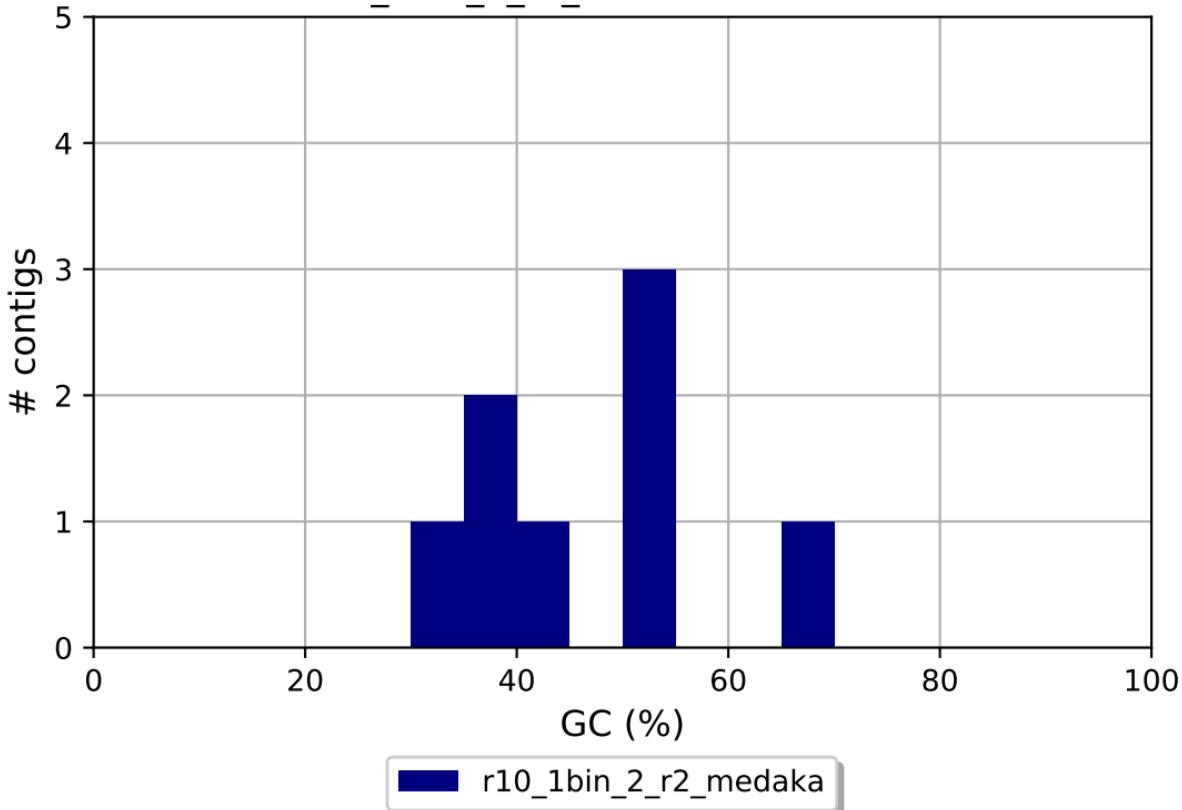
r10\_1bin\_2\_MP\_helen GC content



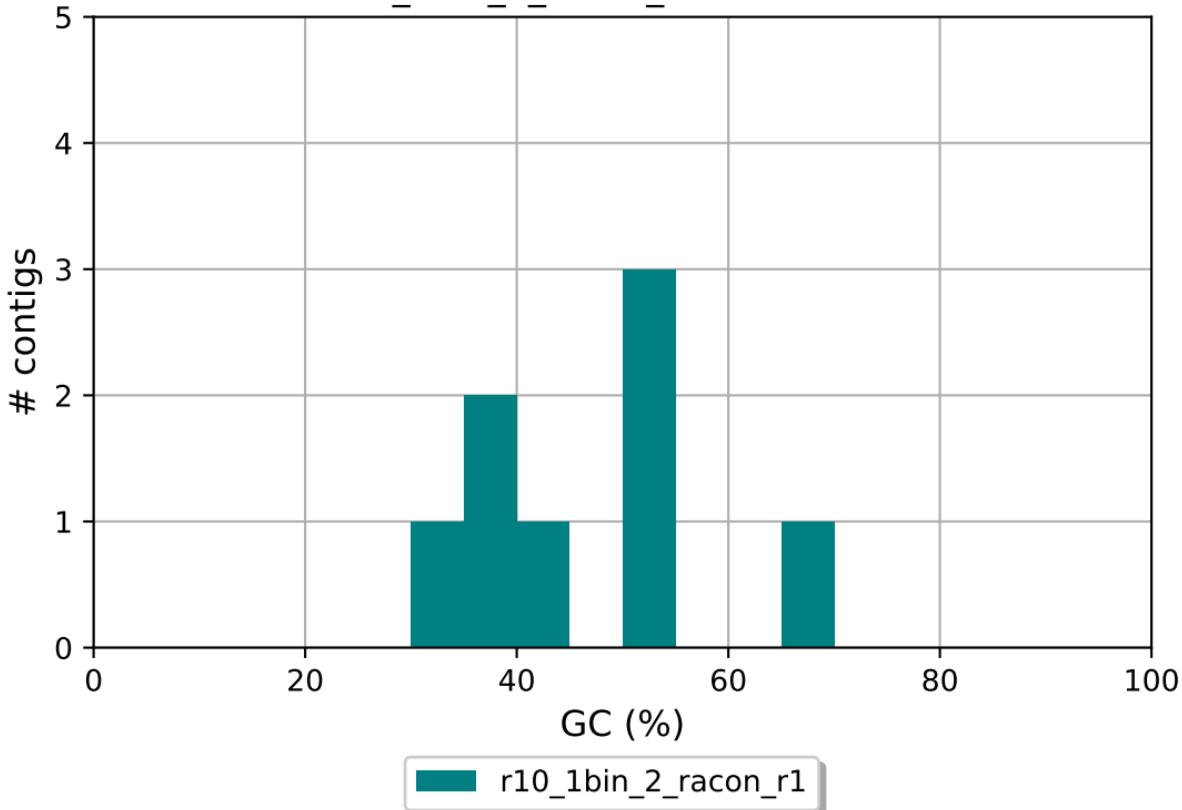
r10\_1bin\_2\_r1\_medaka GC content



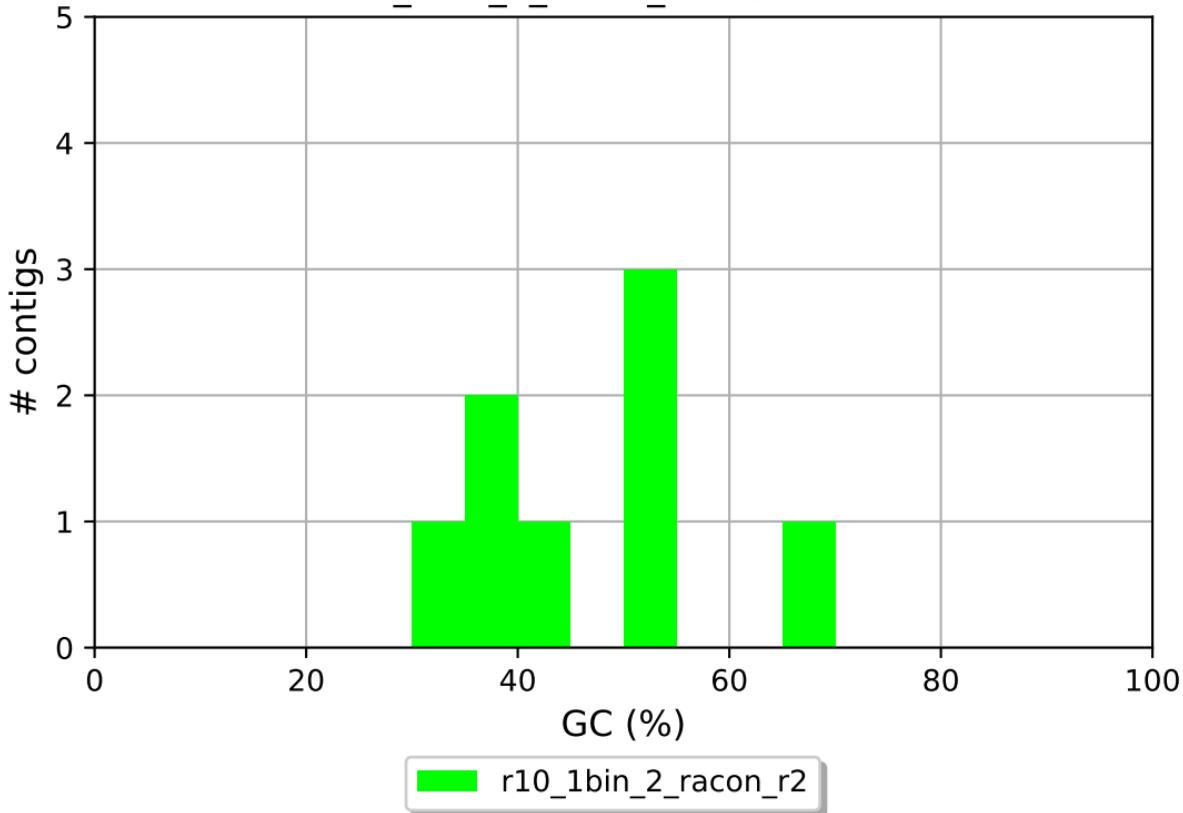
r10\_1bin\_2\_r2\_medaka GC content



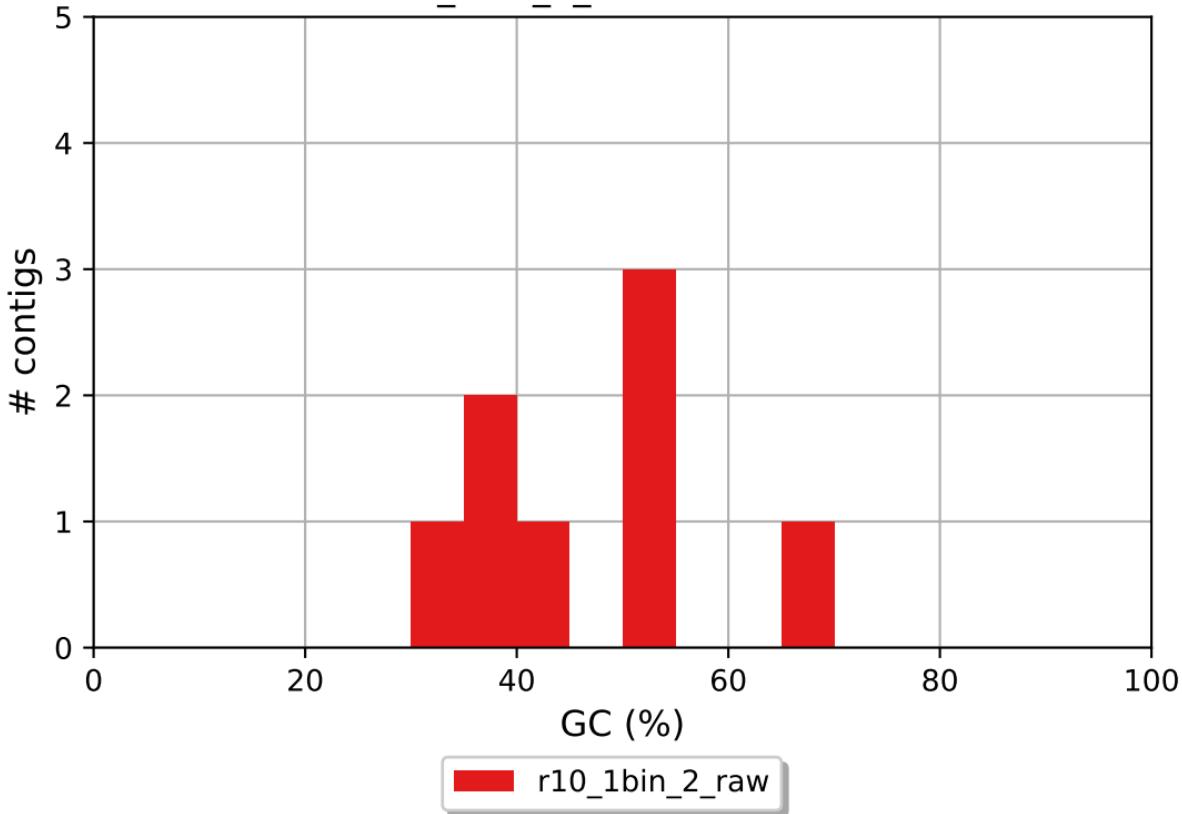
r10\_1bin\_2\_racon\_r1 GC content



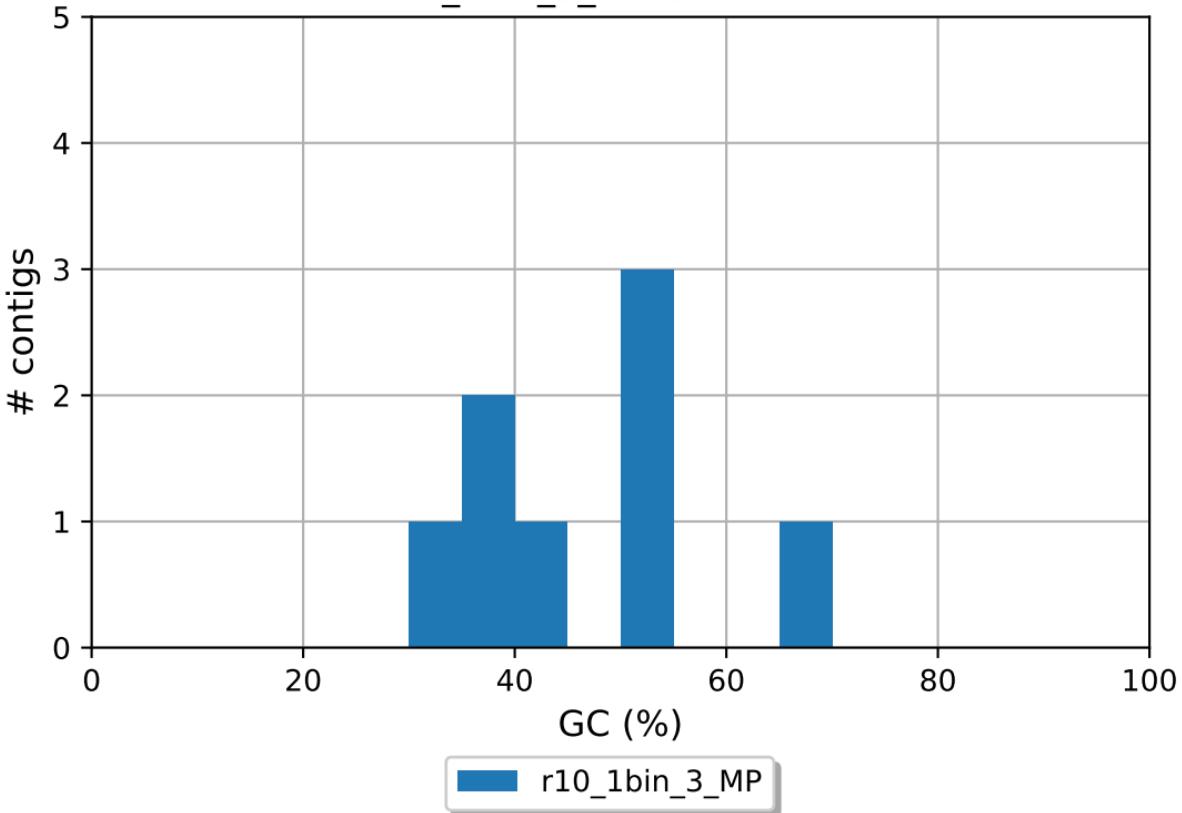
r10\_1bin\_2\_racon\_r2 GC content



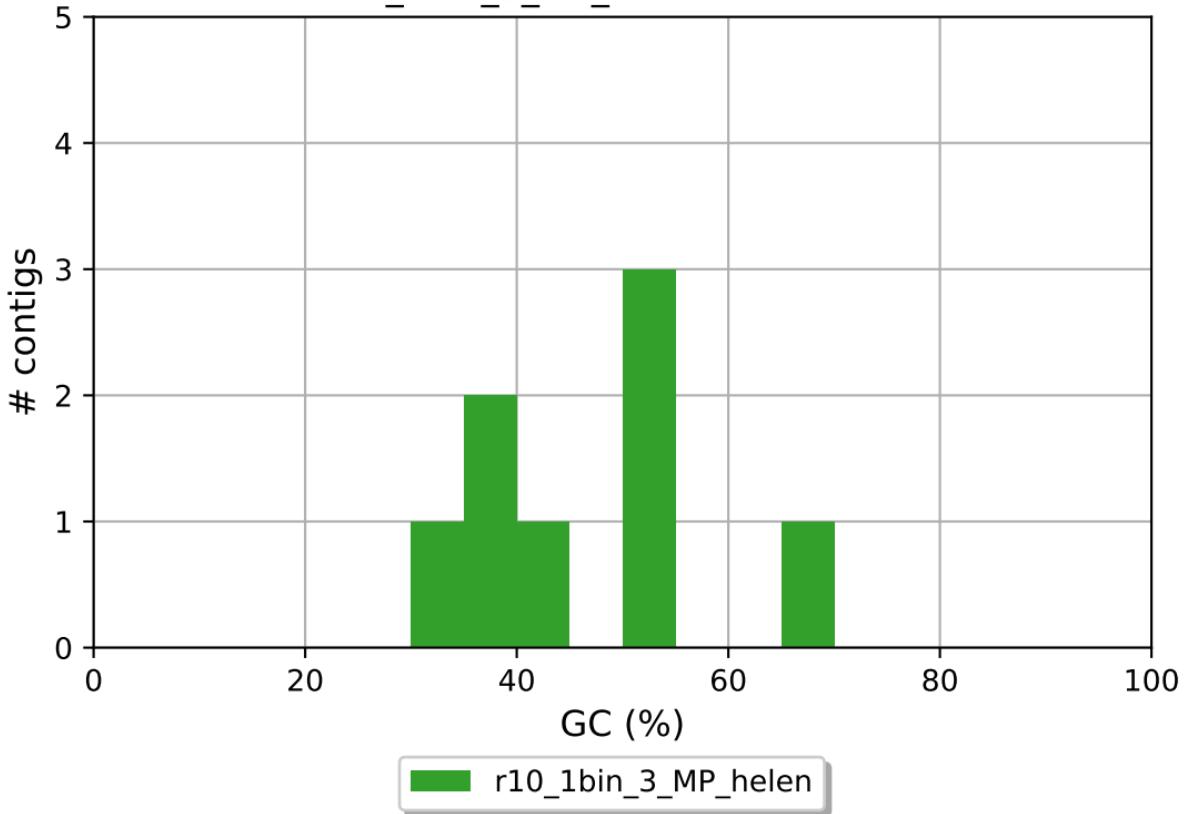
r10\_1bin\_2\_raw GC content



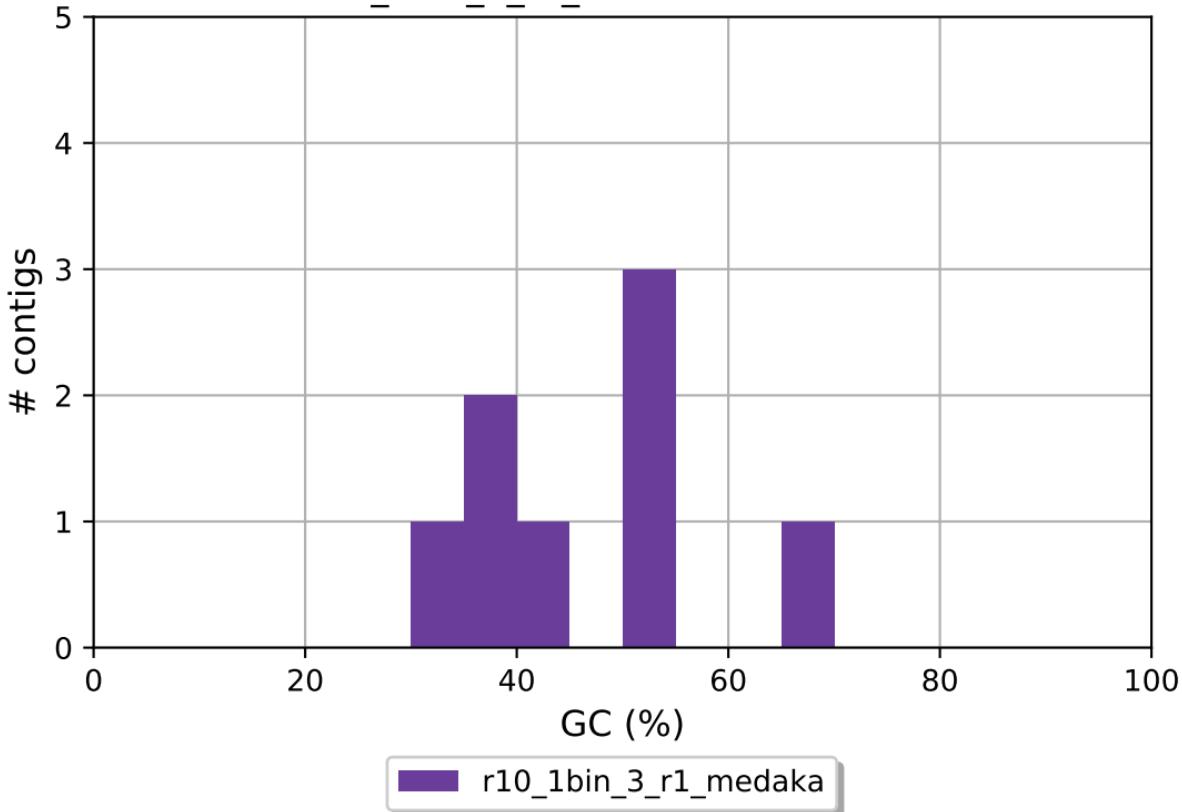
r10\_1bin\_3\_MP GC content



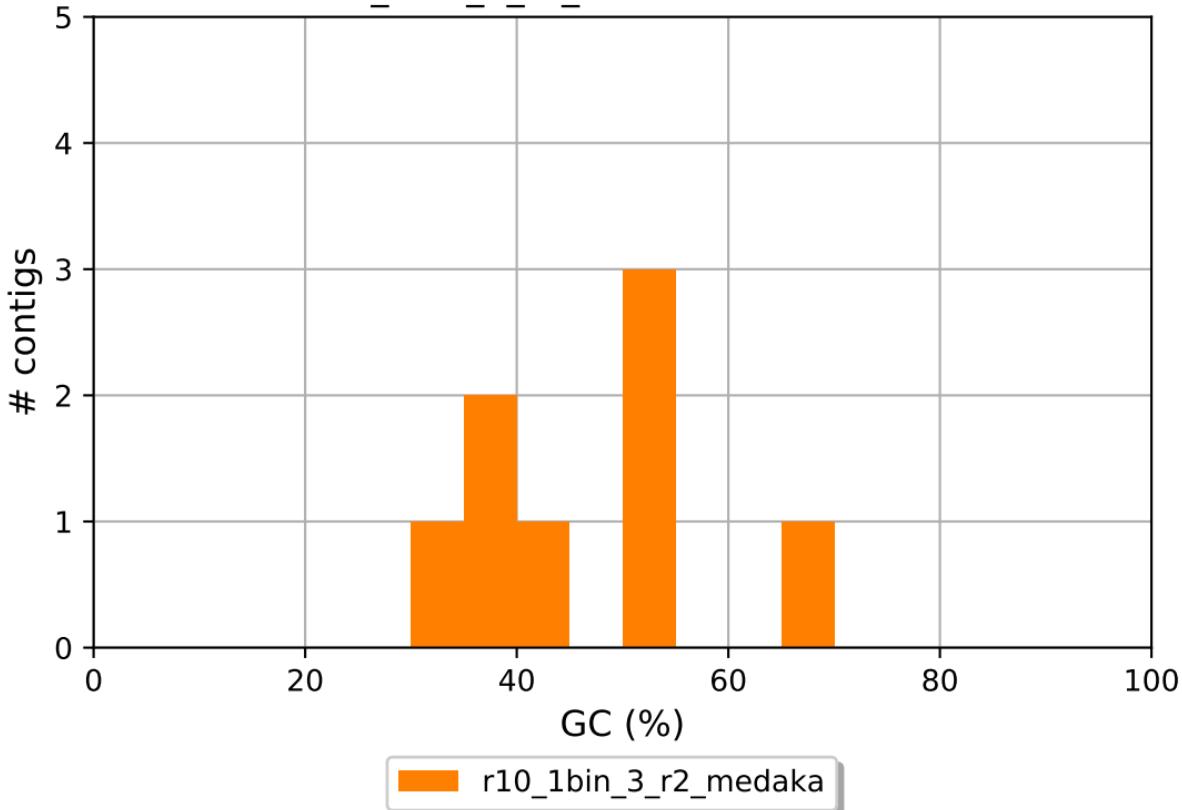
r10\_1bin\_3\_MP\_helen GC content



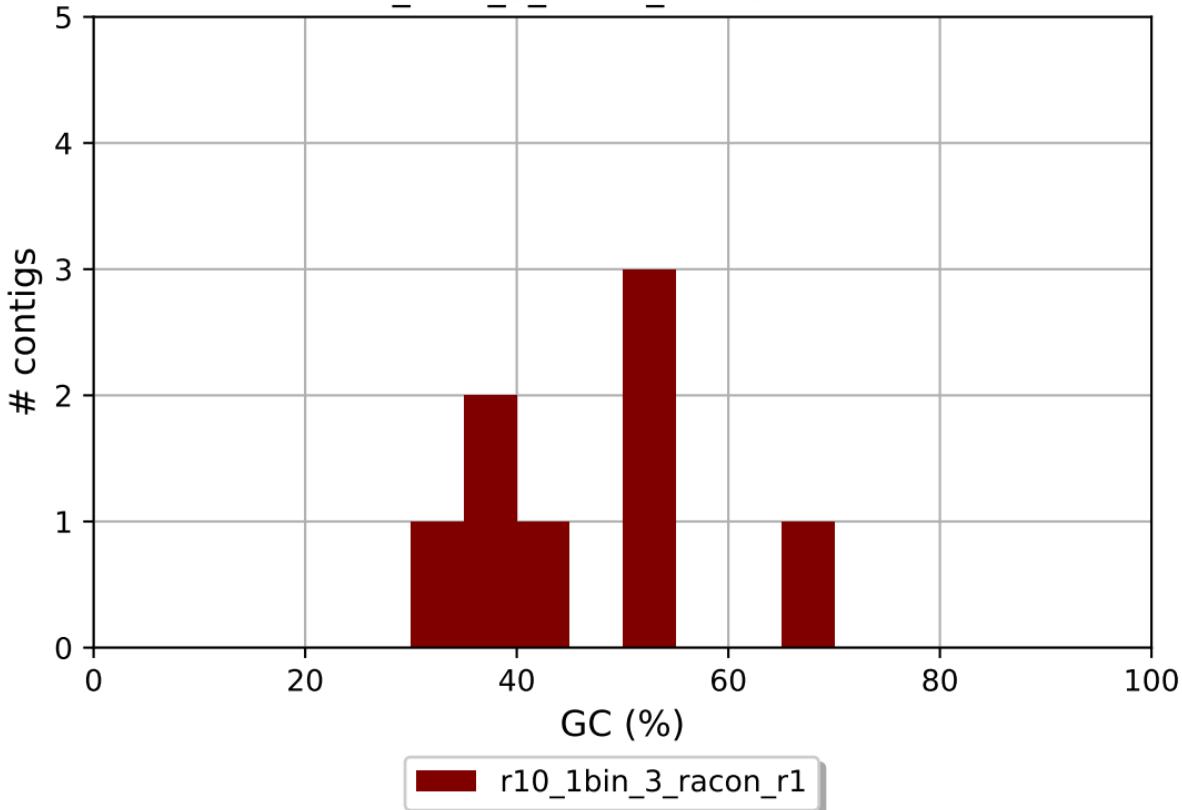
r10\_1bin\_3\_r1\_medaka GC content



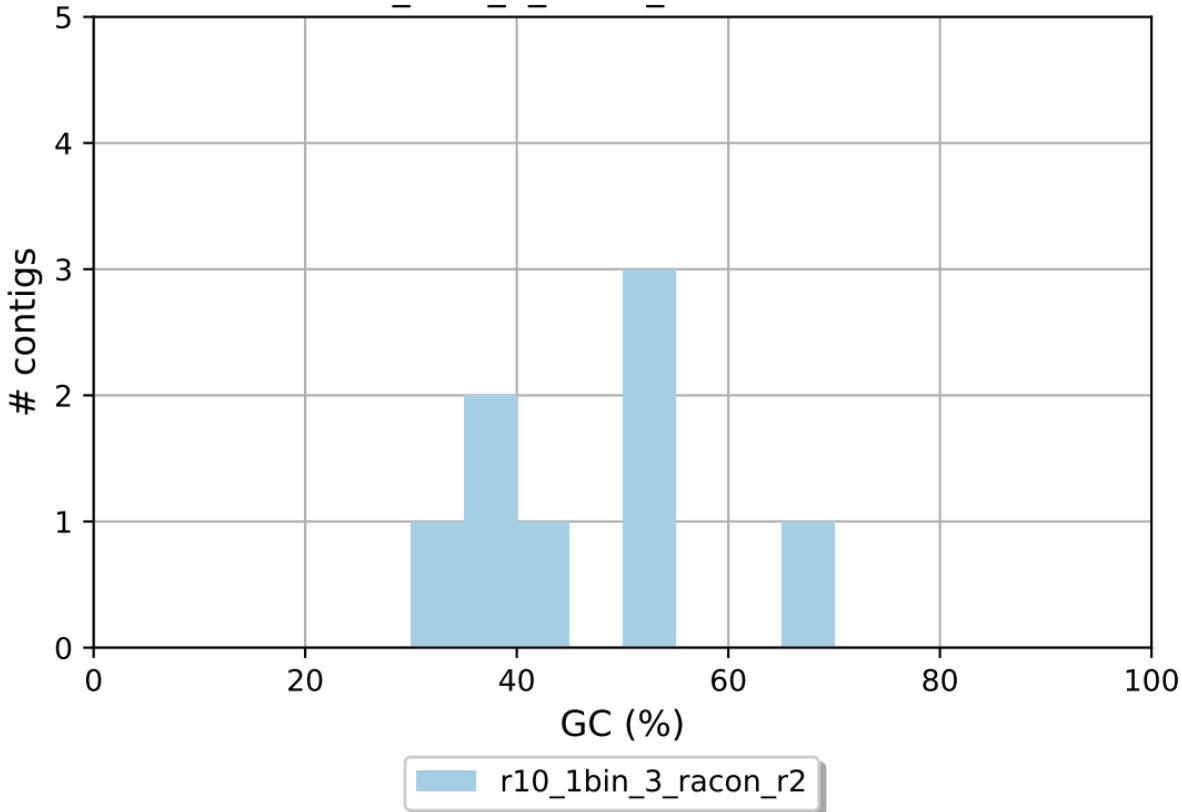
r10\_1bin\_3\_r2\_medaka GC content



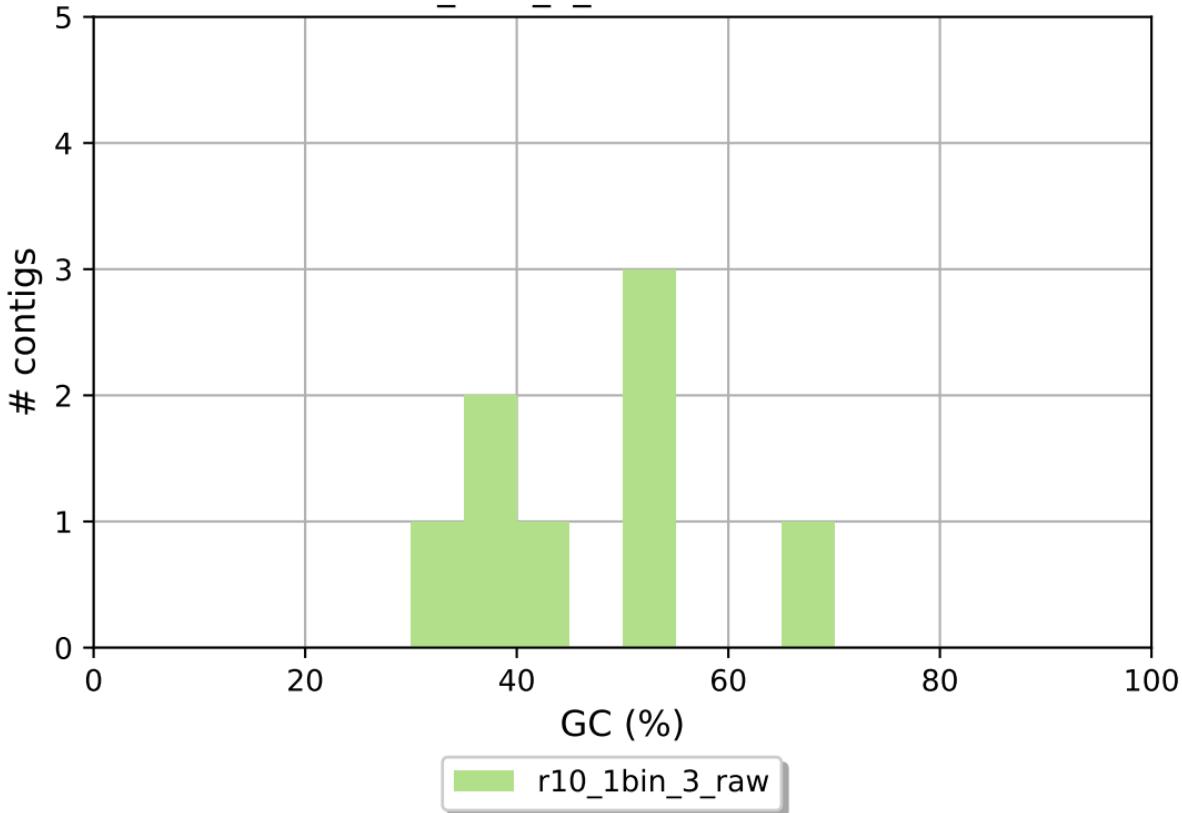
r10\_1bin\_3\_racon\_r1 GC content



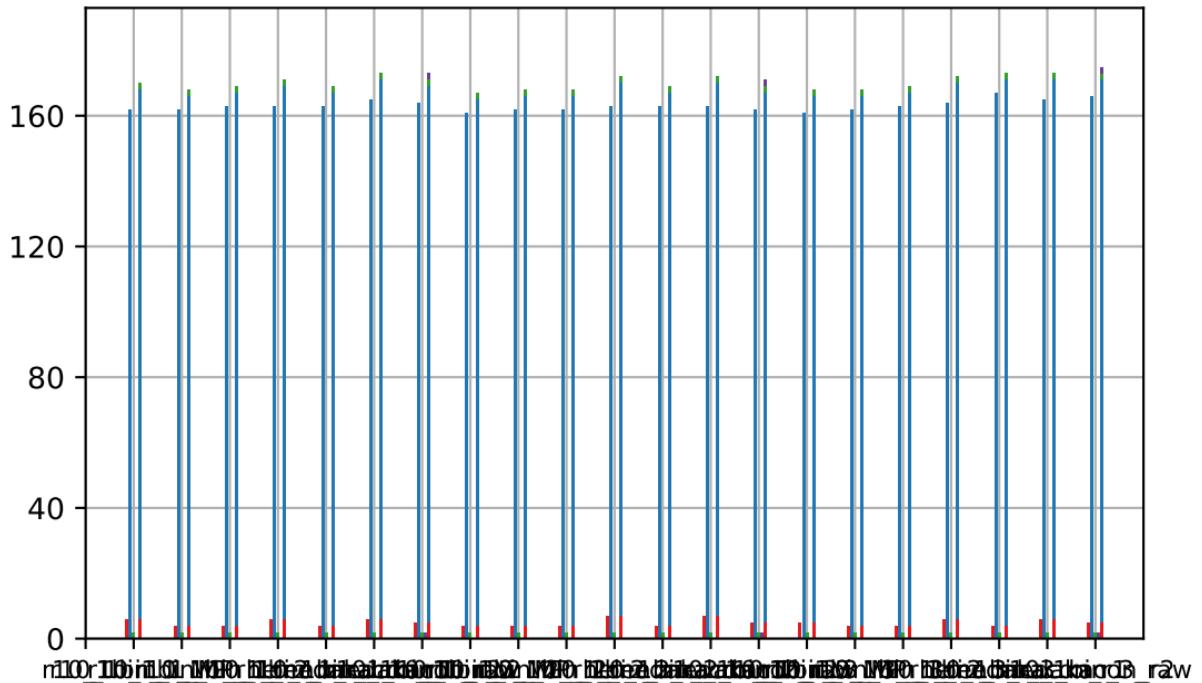
r10\_1bin\_3\_racon\_r2 GC content



r10\_1bin\_3\_raw GC content

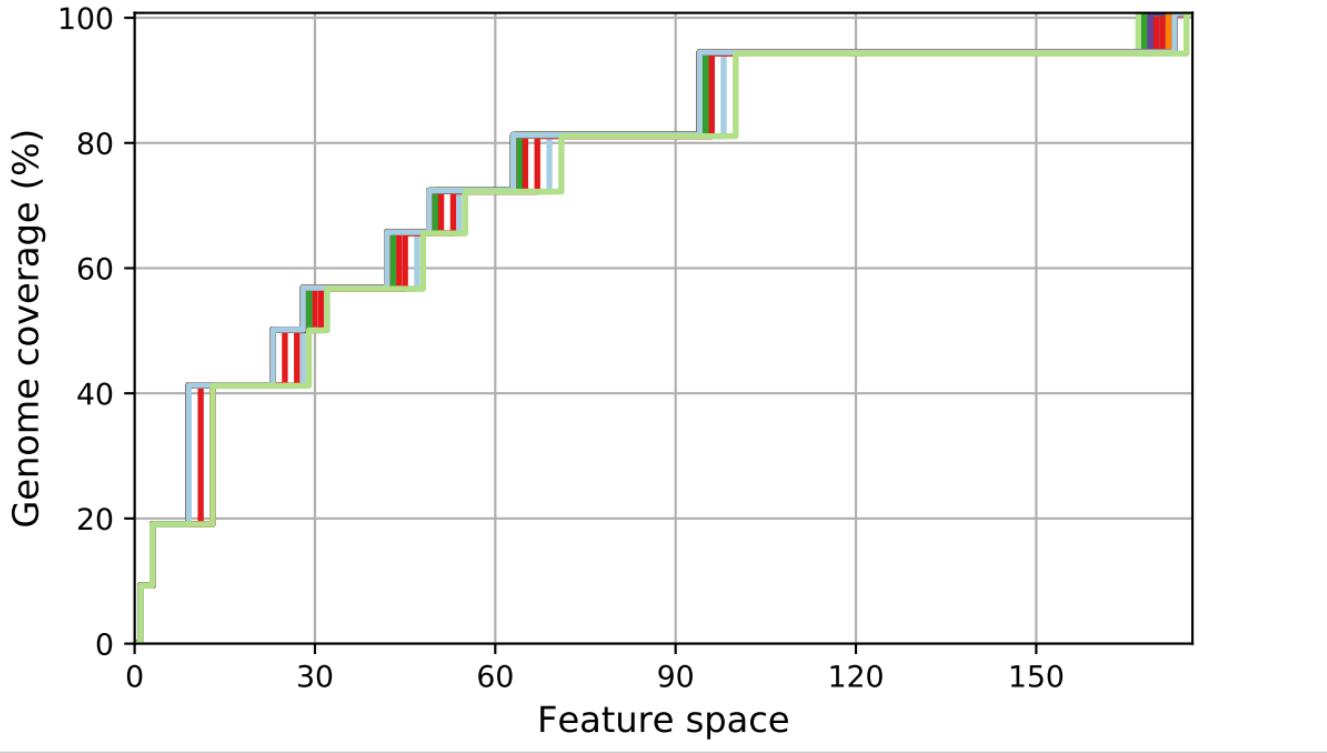


## Misassemblies



█ # relocations      █ # inversions      █ # interspecies translocations  
█ # translocations

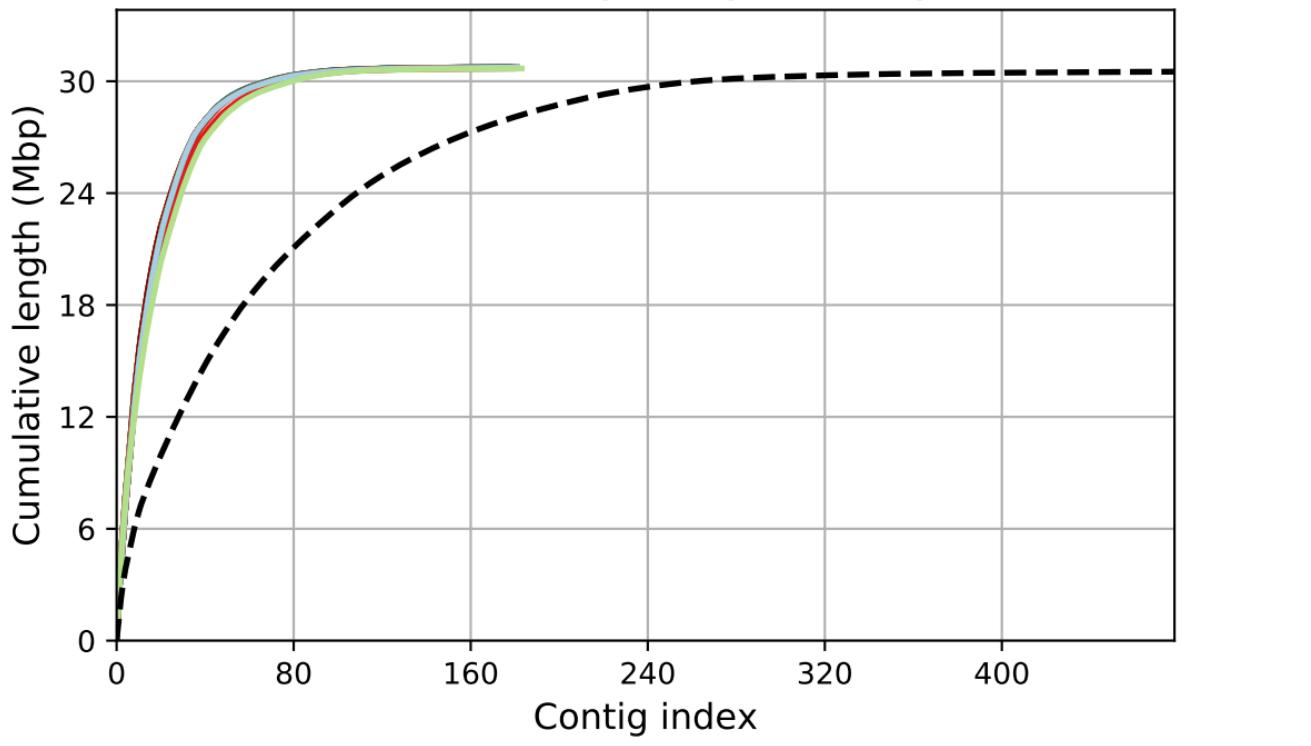
### FRCurve (misassemblies)



Legend:

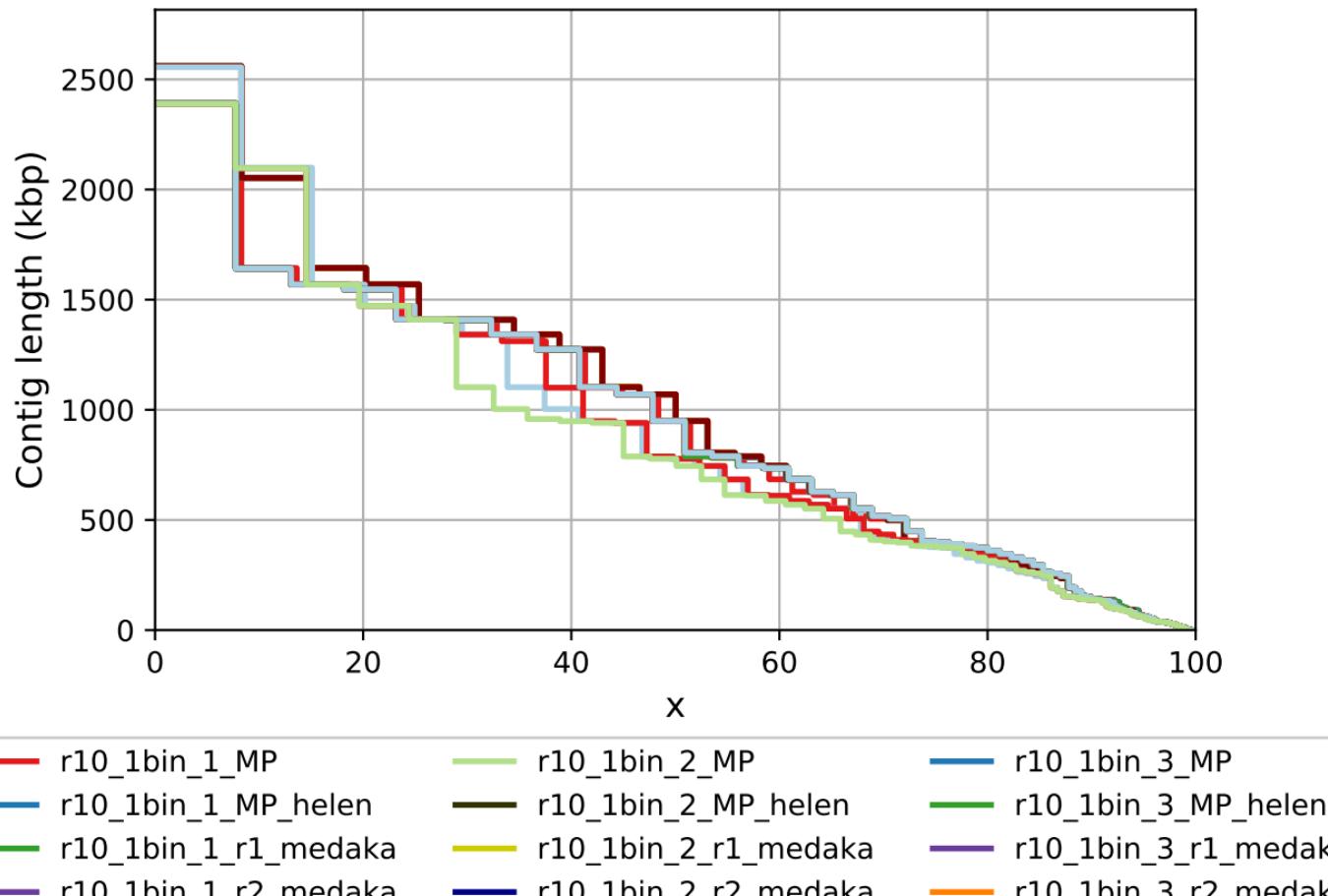
- r10\_1bin\_1\_MP
- r10\_1bin\_1\_MP\_helen
- r10\_1bin\_1\_r1\_medaka
- r10\_1bin\_2\_MP\_helen
- r10\_1bin\_2\_r1\_medaka
- r10\_1bin\_3\_MP\_helen
- r10\_1bin\_3\_r1\_medaka
- r10\_1bin\_3\_r2\_medaka

### Cumulative length (aligned contigs)



- r10\_1bin\_1\_MP
- r10\_1bin\_1\_MP\_helen
- r10\_1bin\_1\_r1\_medaka
- r10\_1bin\_2\_MP\_helen
- r10\_1bin\_2\_r1\_medaka
- r10\_1bin\_3\_MP\_helen
- r10\_1bin\_3\_r1\_medaka
- r10\_1bin\_3\_r2\_medaka
- r10\_1bin\_2\_raccon\_r1
- r10\_1bin\_3\_raccon\_r1

# NAx



Genome fraction, %

