

## 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_r2_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	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294		
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	44.79	44.79	44.77		
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44		
N50	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	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	2845426	2845436	2845434	2845426	2845420	2845336	2845428	2845240	2845336	2845428	
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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
Misassembled contigs length	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2845434	2845416	2845426	2845429	2845336	2845428		
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	16	16	16	16	16	19		
# scaffold gap ext. mis.	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			
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6			
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part			
Unaligned length	21097387	21091591	21094767	21088130	21085780	21081270	21152205	21097440	21090841	21094417	21082959	21086085	21076942	21149560	21098067	21094339	21092427	21091093	21084544	21154983	
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.948	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.953			
Duplication ratio	1.056	1.057	1.056	1.056	1.055	1.055	1.032	1.056	1.057	1.056	1.057	1.055	1.056	1.057	1.056	1.057	1.056	1.056	1.032		
# 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		
# mismatches per 100 kbp	249.57	251.66	247.94	244.71	238.39	240.24	146.97	248.47	254.01	247.62	251.17	234.88	241.98	154.38	249.43	249.86	251.95	248.29	238.22	244.60	146.54
# indels per 100 kbp	15.29	15.75	14.58	13.84	22.74	21.11	126.82	15.58	15.75	13.23											

## Misassemblies report

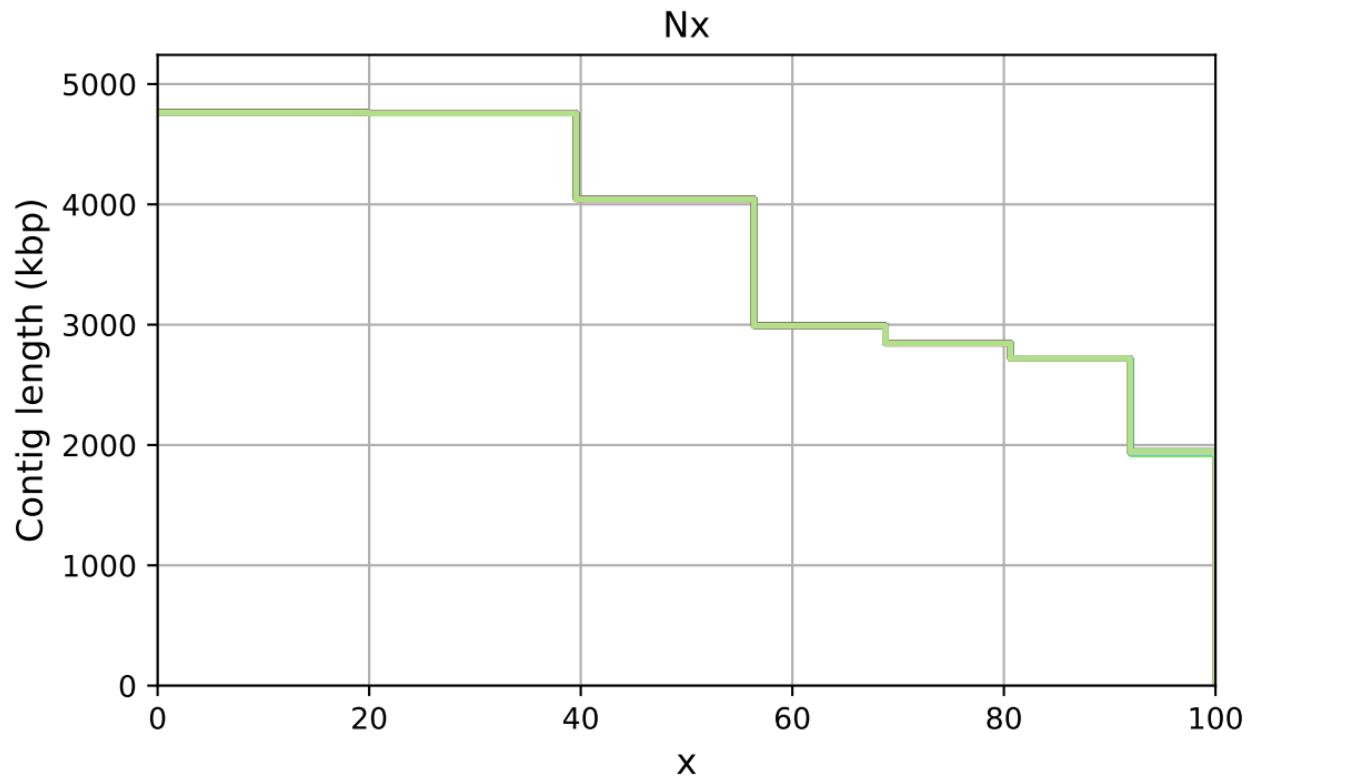
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw			
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
# contig misassemblies	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
# 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	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845429	2845336	2843848	
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1		
# possible misassemblies	0	0	0	0	0	0	0	6	0	0	0	0	6	0	0	0	0	0	6		
# local misassemblies	16	16	16	16	16	16	16	20	16	16	16	16	16	16	16	16	16	16	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	19	19	19	19	19	19	19	10	19	19	19	19	19	11	19	19	19	19	11		
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6		
# mismatches	7034	7093	6988	6897	6719	6771	4142	7003	7159	6979	7079	6620	6820	4351	7030	7042	7101	6998	6714	6894	4130
# indels	431	444	411	390	641	595	3574	439	444	373	394	592	571	3533	433	408	401	390	619	616	3601
# indels (<= 5 bp)	390	400	370	349	600	558	3537	399	552	334	354	535	3498	393	368	362	351	580	579	3567	
# indels (> 5 bp)	41	44	41	41	41	37	37	40	39	40	36	40	40	35	40	39	39	37	34		
Indels length	2440	2481	2395	2351	2709	2577	6266	2400	2417	2269	2316	2543	2490	6066	2388	2323	2304	2592	2545	6140	

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

	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_racon_r1	r10_1bin_v2_2_racon_r2	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_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	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7
Partially unaligned length	21097387	21091591	21094767	21088130	21085780	21081270	21152205	21097440	21090841	21094417	21082959	21086085	21076942	21149560	21094339	21092427	21091093	21084544	21154983
# 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  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

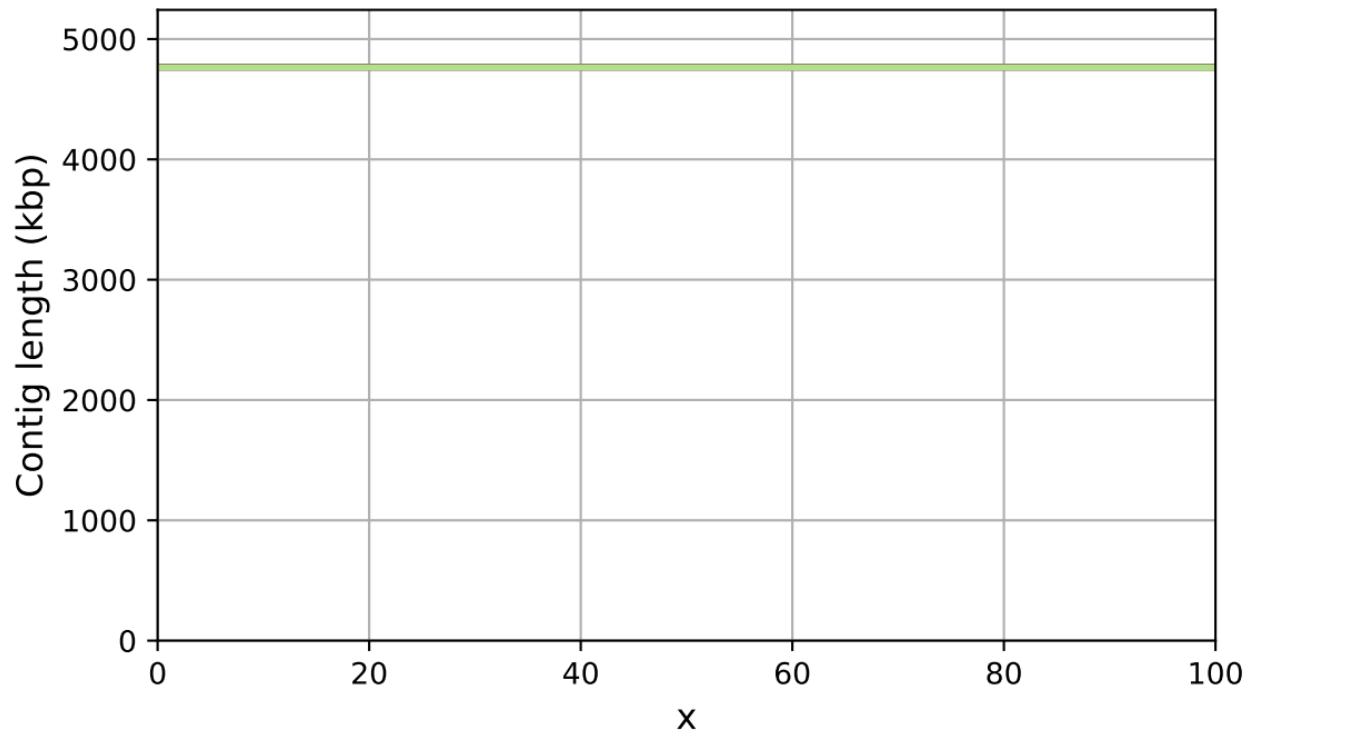


r10\_1bin\_v2\_1\_MP  
r10\_1bin\_v2\_1\_MP\_helen  
r10\_1bin\_v2\_1\_r1\_medaka  
r10\_1bin\_v2\_1\_r2\_medaka

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

# NGx

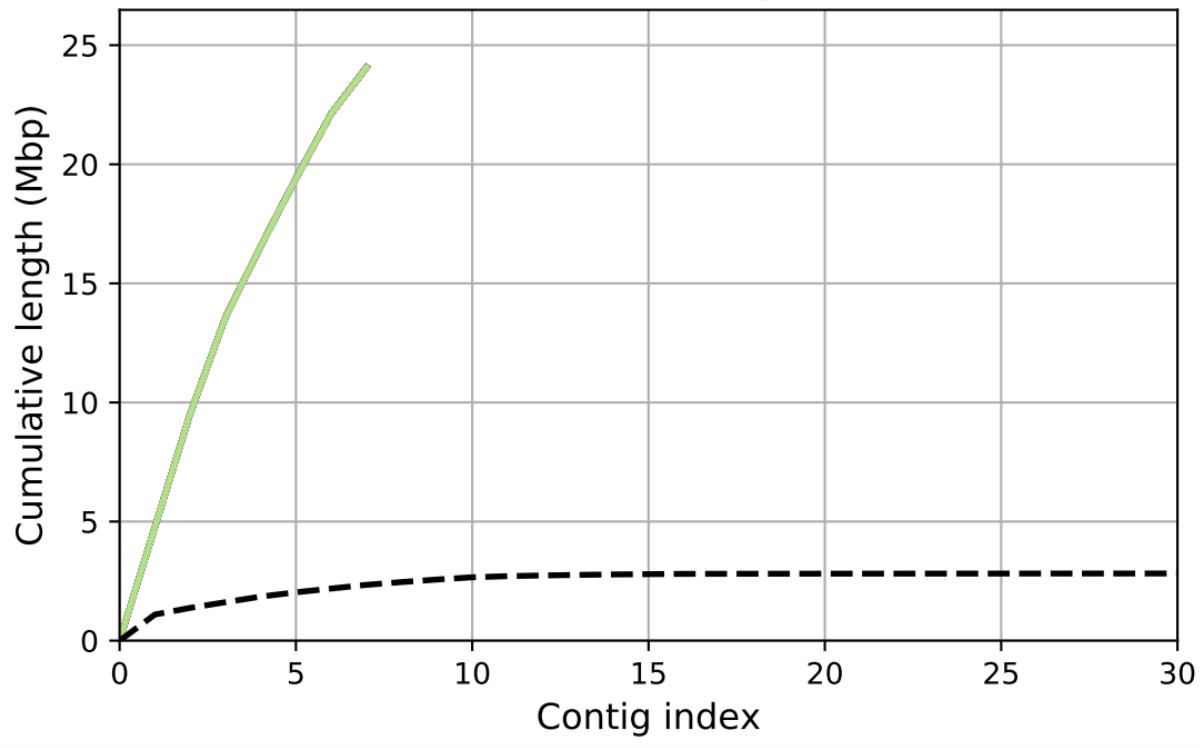


r10\_1bin\_v2\_1\_MP  
r10\_1bin\_v2\_1\_MP\_helen  
r10\_1bin\_v2\_1\_r1\_medaka  
r10\_1bin\_v2\_1\_r2\_medaka

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

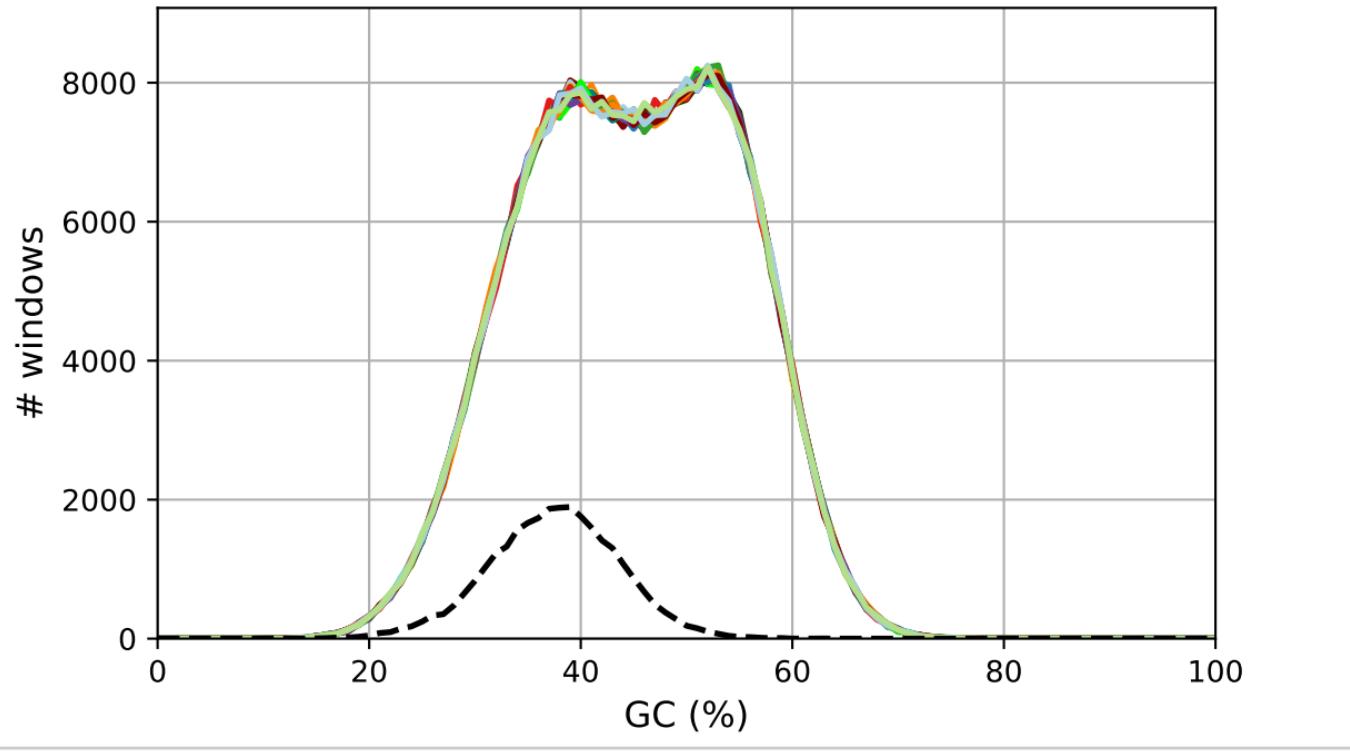


r10\_1bin\_v2\_1\_MP  
r10\_1bin\_v2\_1\_MP\_helen  
r10\_1bin\_v2\_1\_r1\_medaka  
r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_2\_MP\_helen  
r10\_1bin\_v2\_2\_r1\_medaka  
r10\_1bin\_v2\_2\_r2\_medaka  
r10\_1bin\_v2\_3\_MP\_helen  
r10\_1bin\_v2\_3\_r1\_medaka  
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_MP\_helen  
r10\_1bin\_v2\_3\_r1\_medaka  
r10\_1bin\_v2\_3\_r2\_medaka  
r10\_1bin\_v2\_3\_racoon\_r1  
r10\_1bin\_v2\_3\_racoon\_r2

## 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

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_2\_racoon\_r1

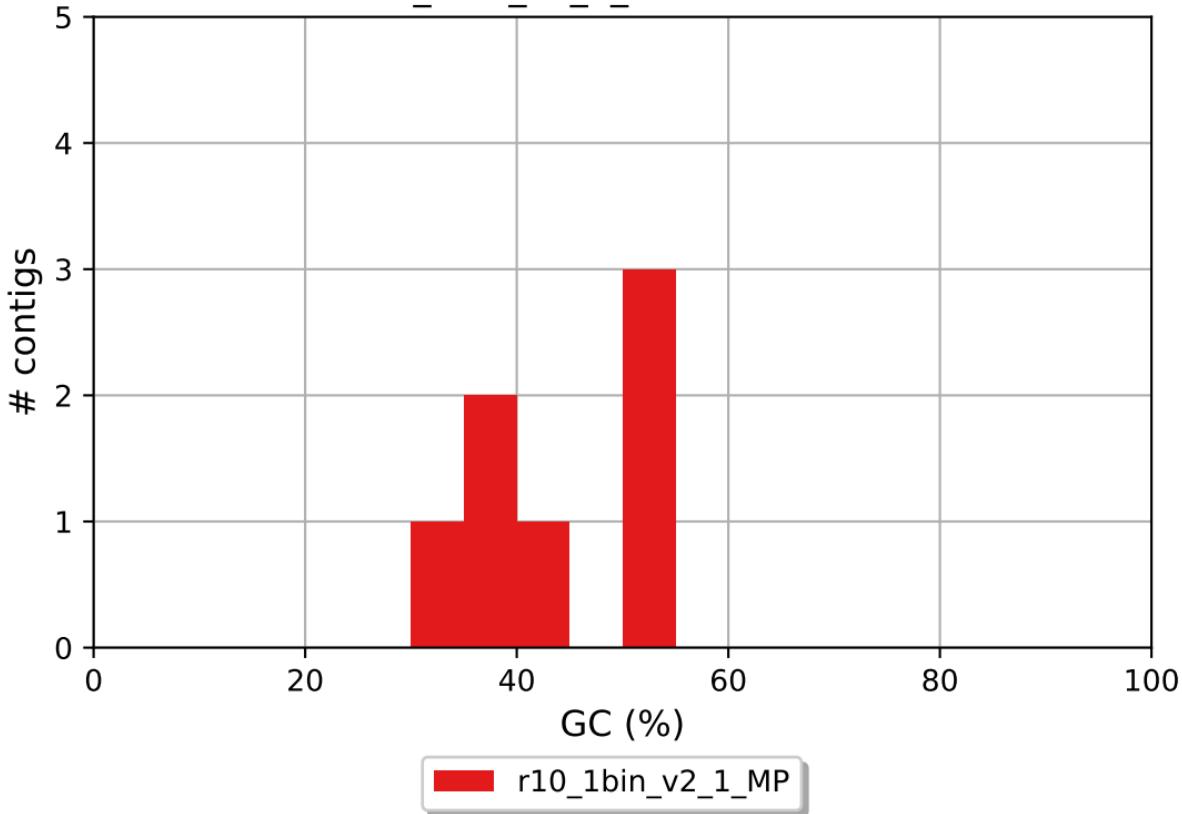
r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

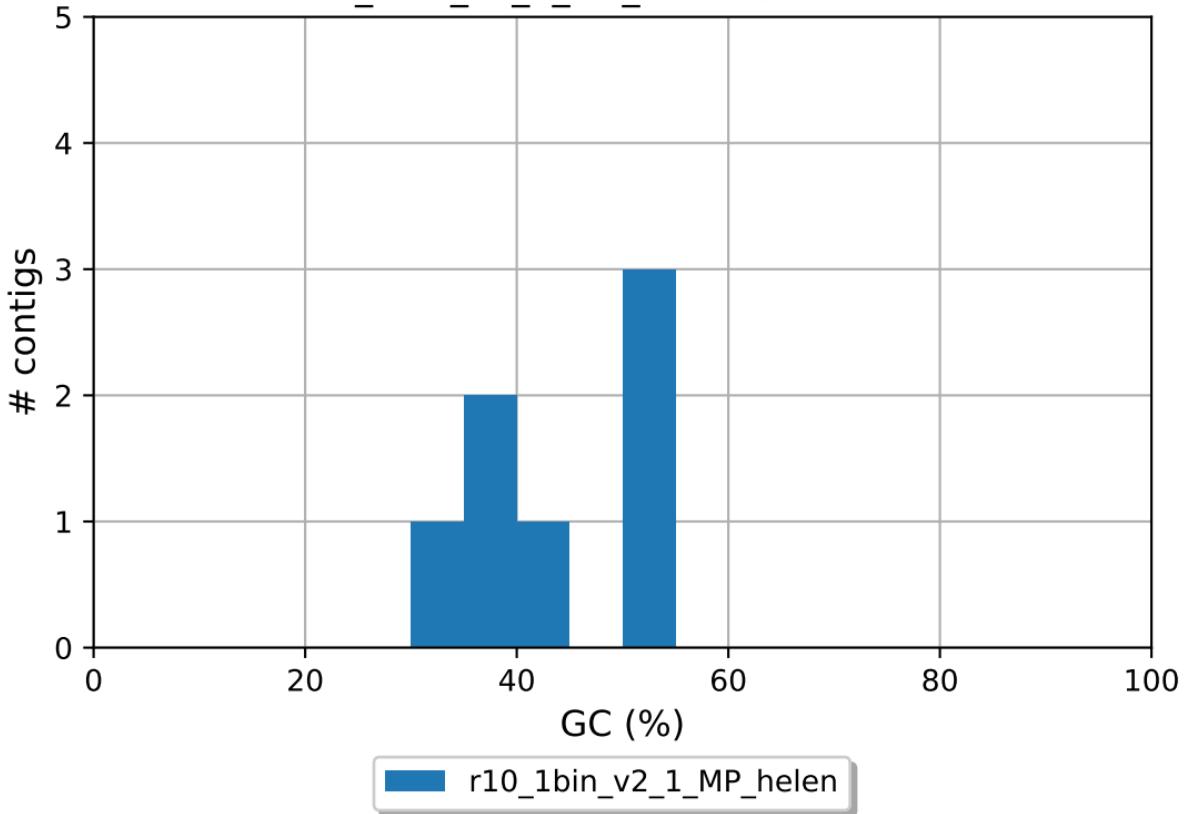
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racoon\_r1

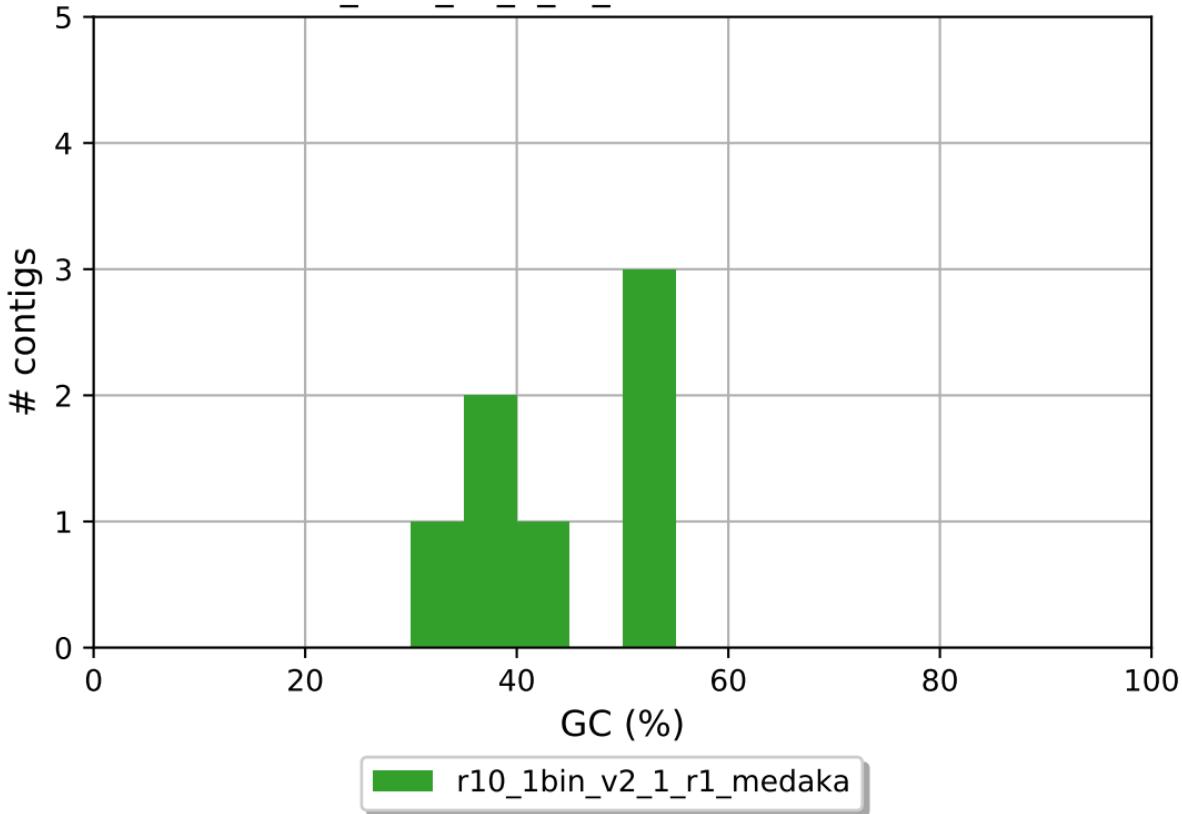
r10\_1bin\_v2\_1\_MP GC content



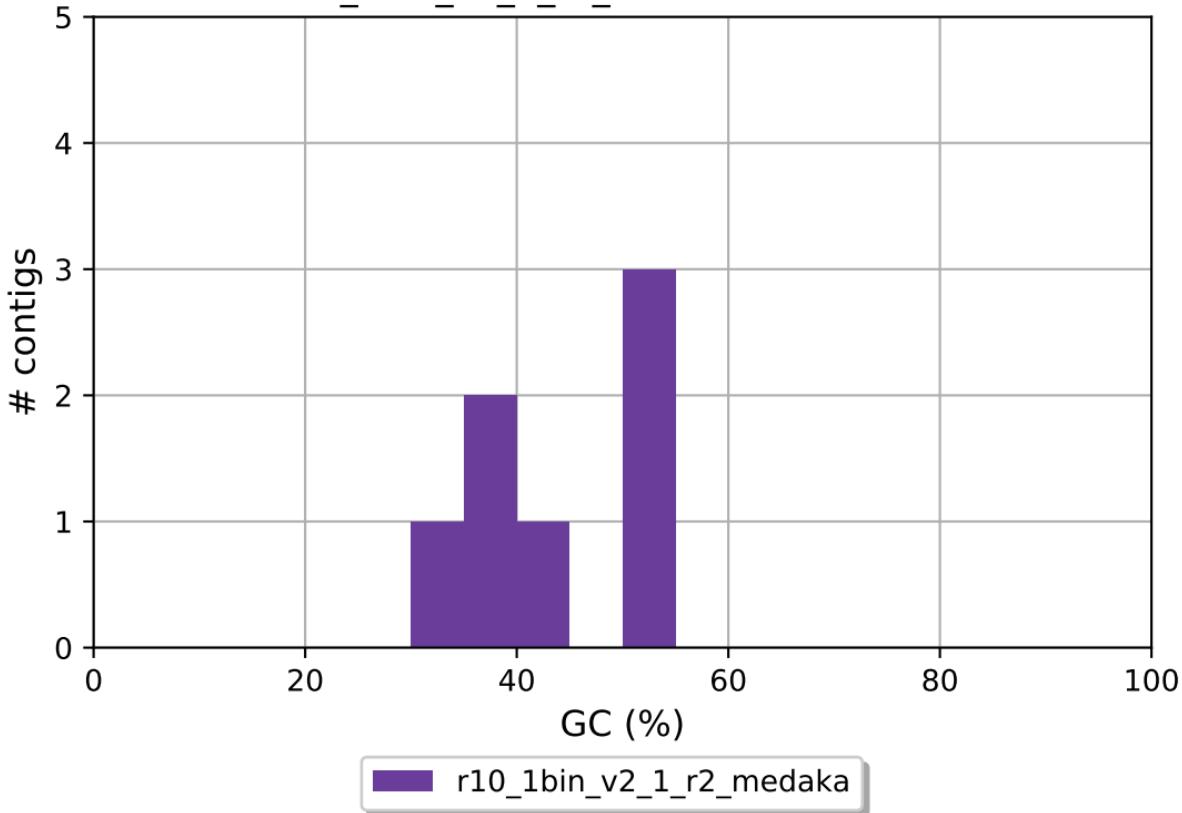
r10\_1bin\_v2\_1\_MP\_helen GC content



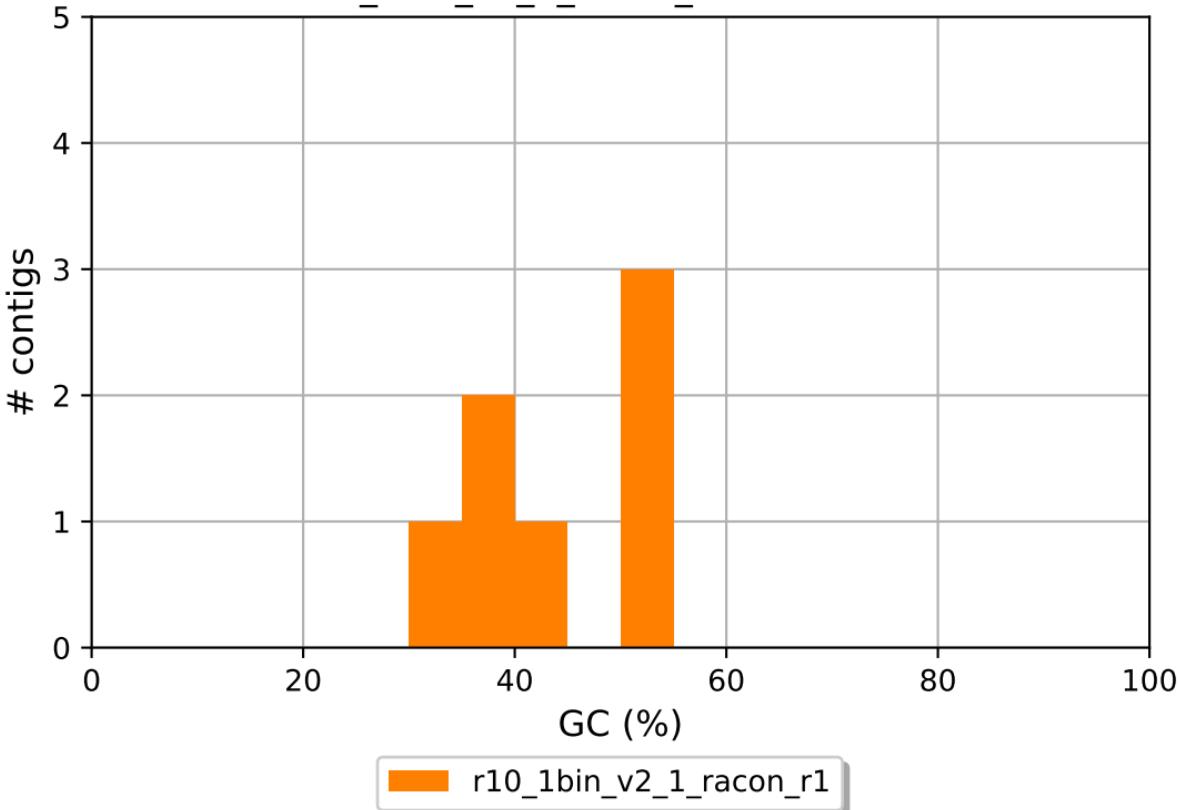
r10\_1bin\_v2\_1\_r1\_medaka GC content



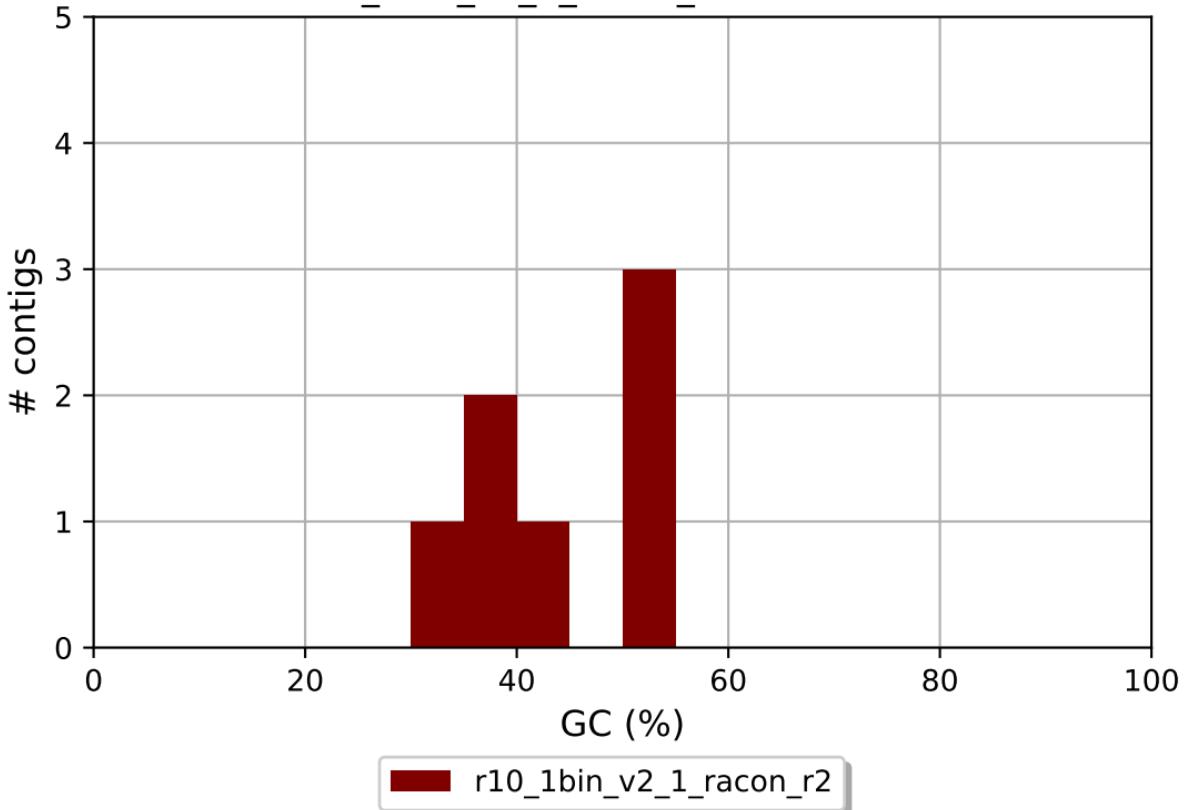
r10\_1bin\_v2\_1\_r2\_medaka GC content



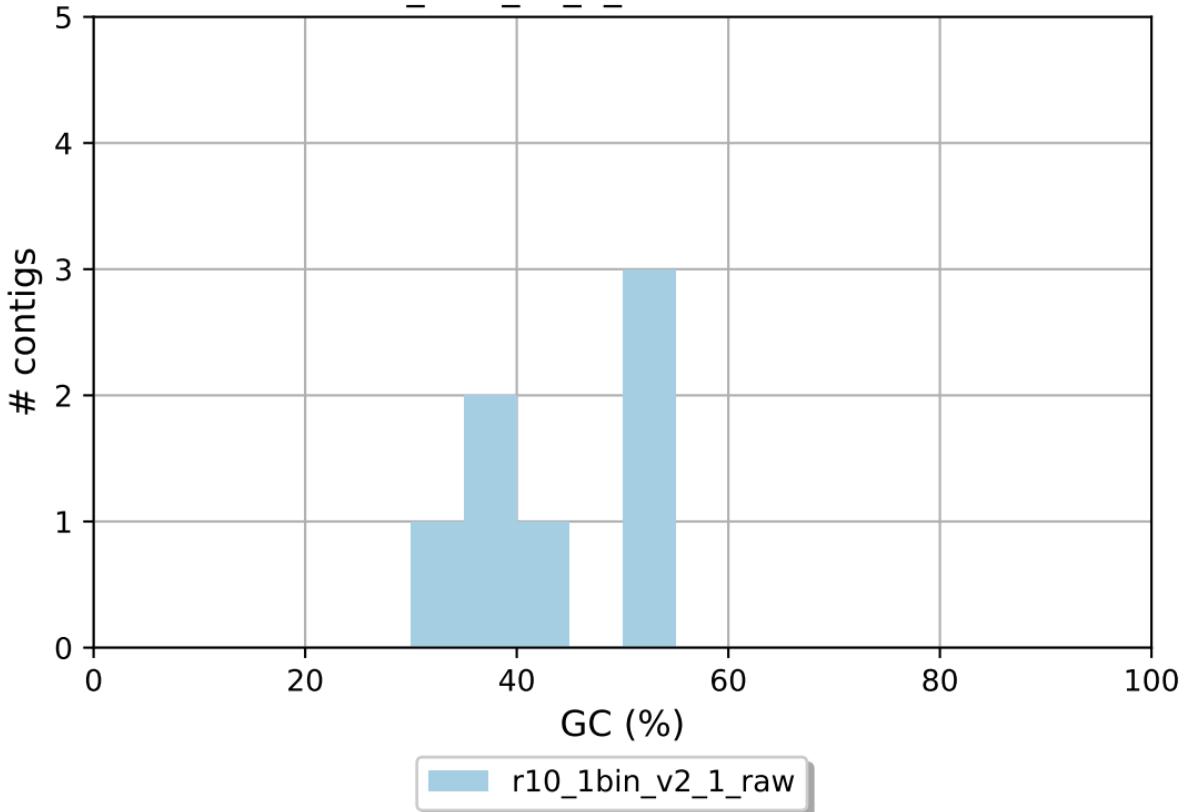
r10\_1bin\_v2\_1\_racon\_r1 GC content



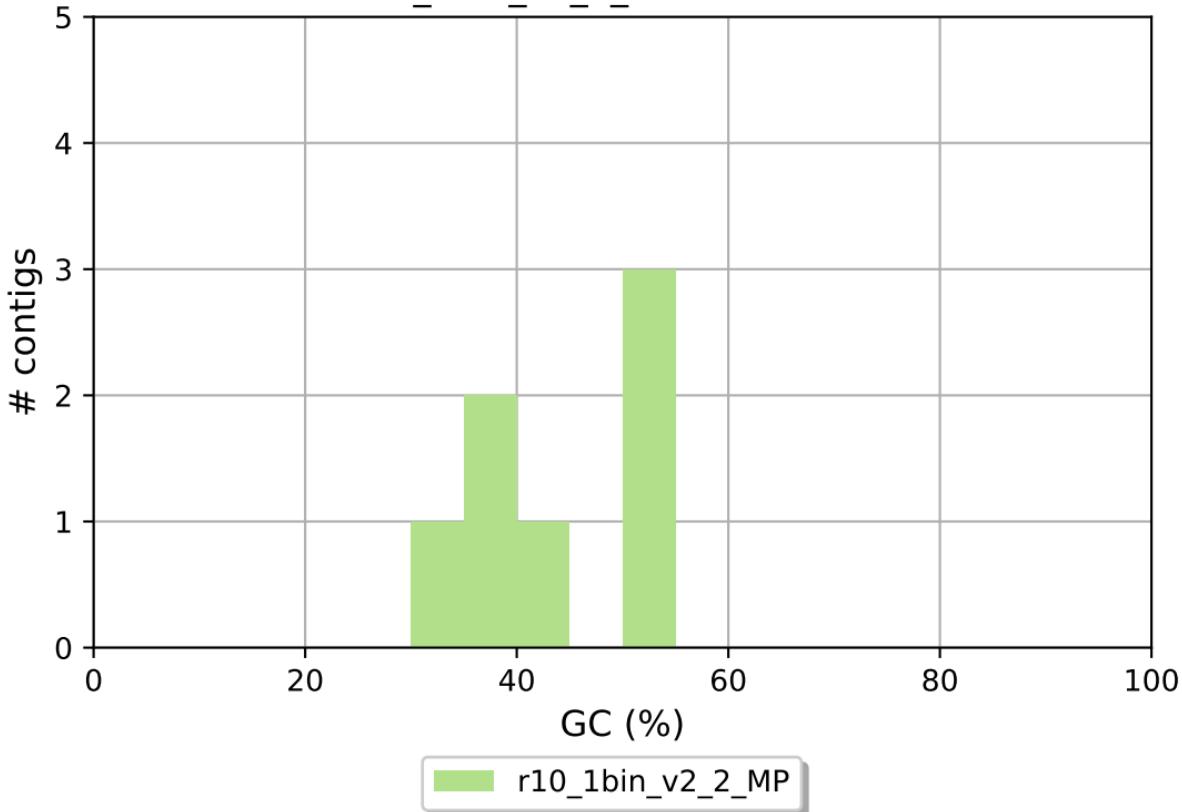
r10\_1bin\_v2\_1\_racon\_r2 GC content



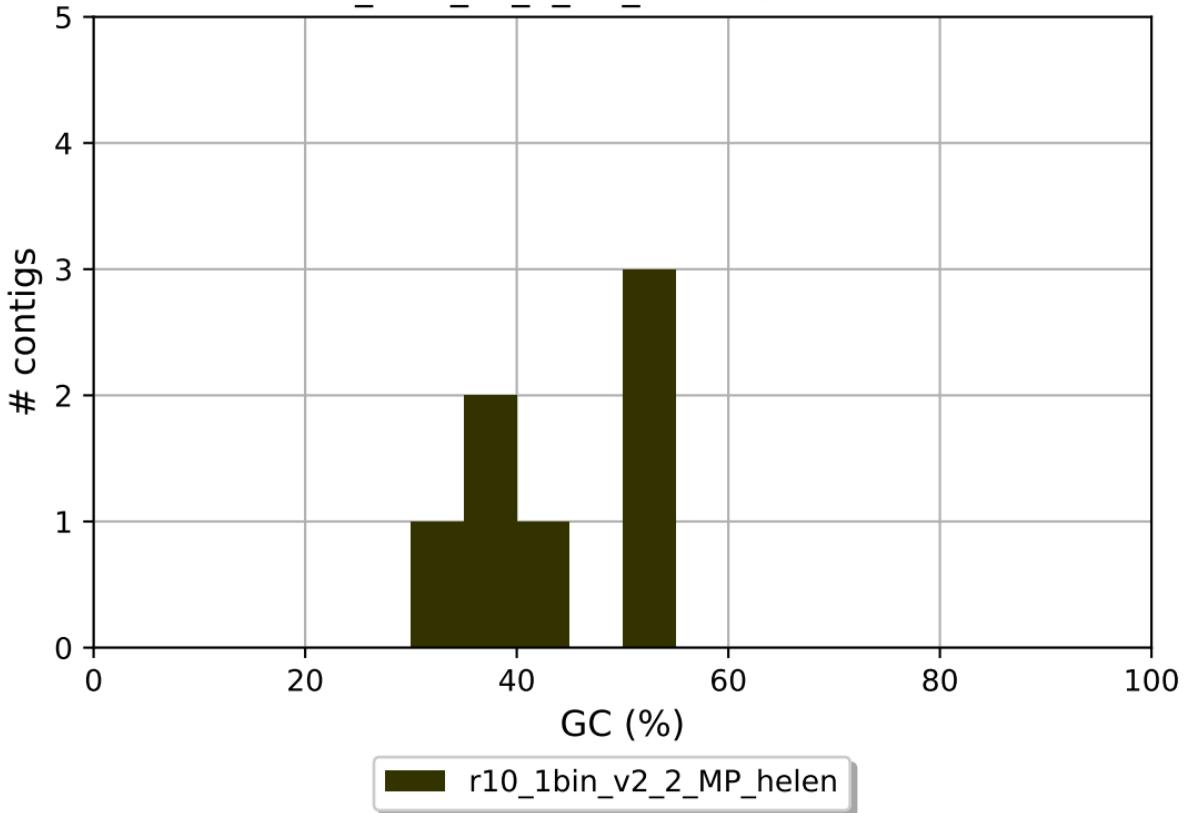
r10\_1bin\_v2\_1\_raw GC content



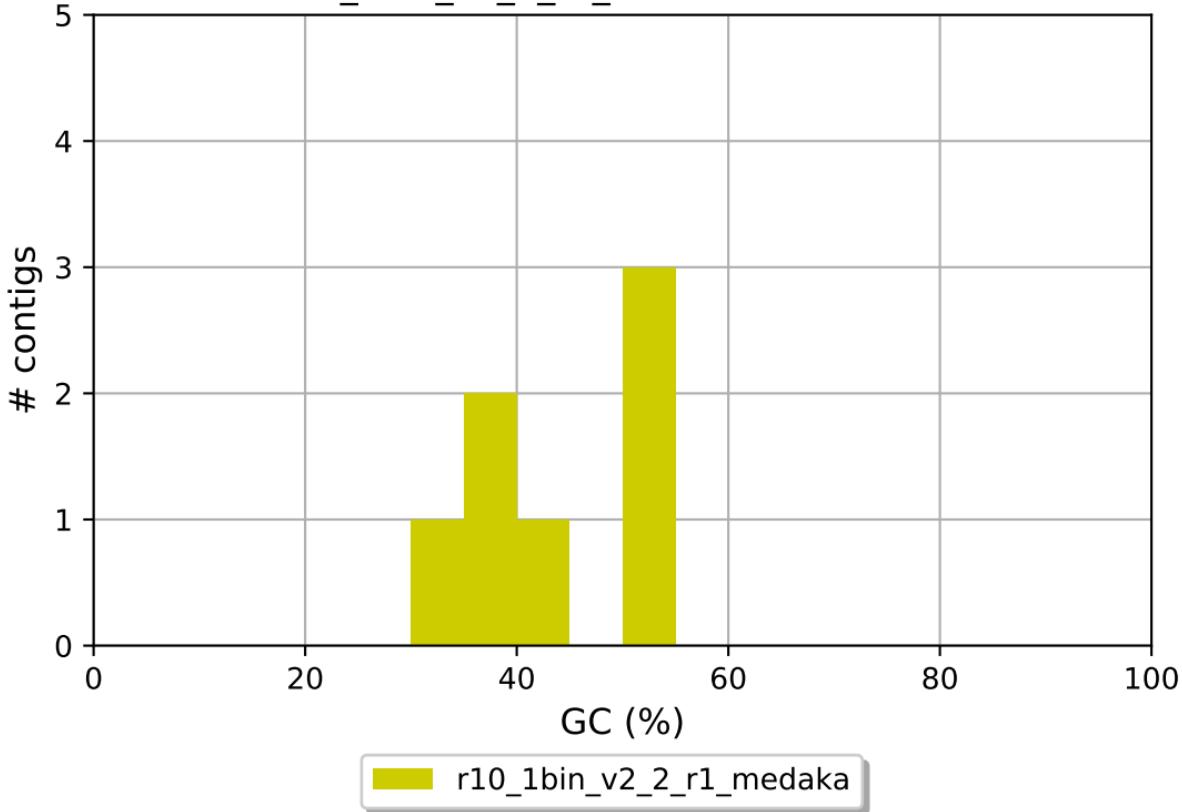
r10\_1bin\_v2\_2\_MP GC content



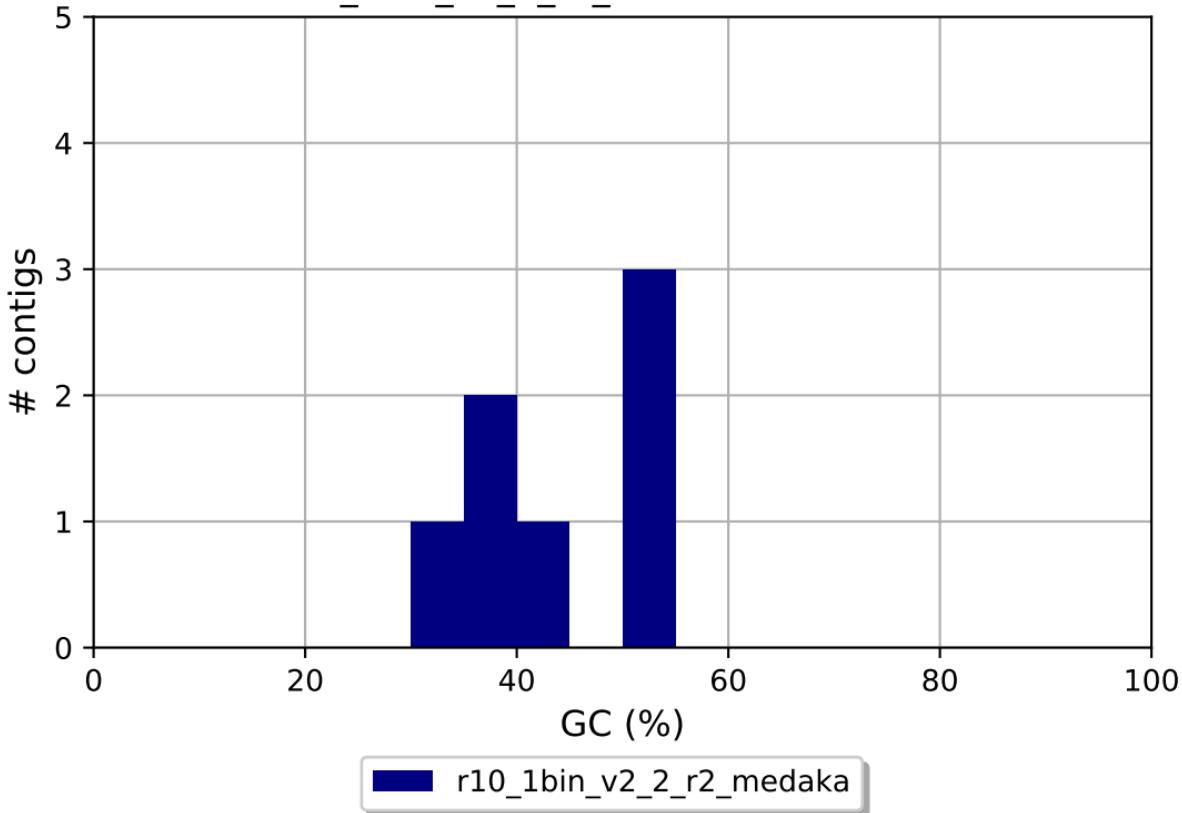
r10\_1bin\_v2\_2\_MP\_helen GC content



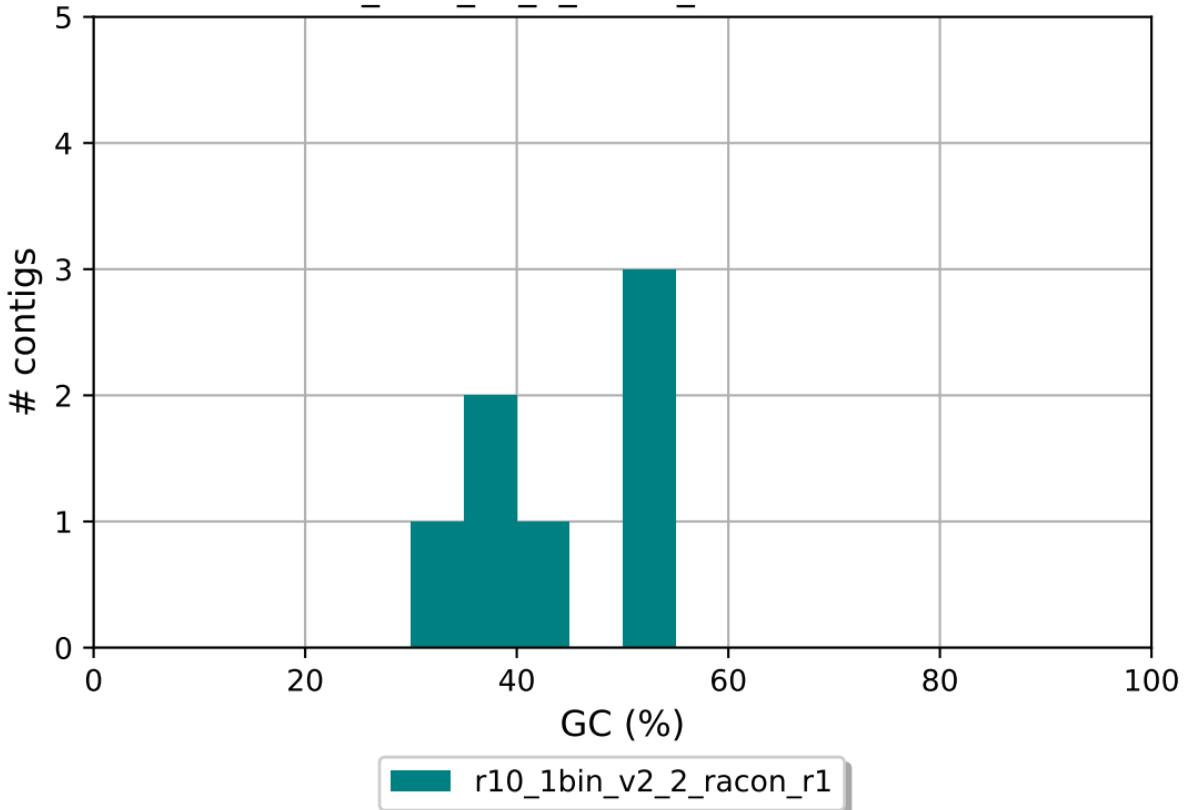
r10\_1bin\_v2\_2\_r1\_medaka GC content



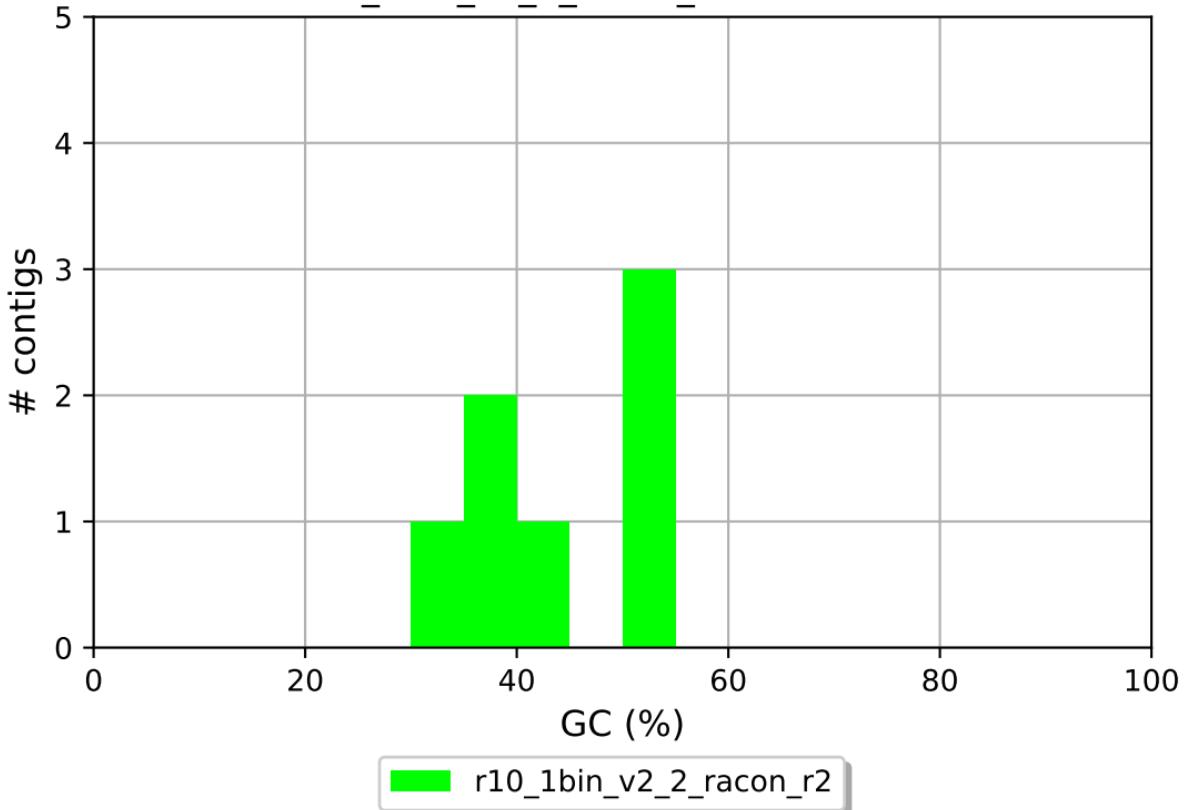
r10\_1bin\_v2\_2\_r2\_medaka GC content



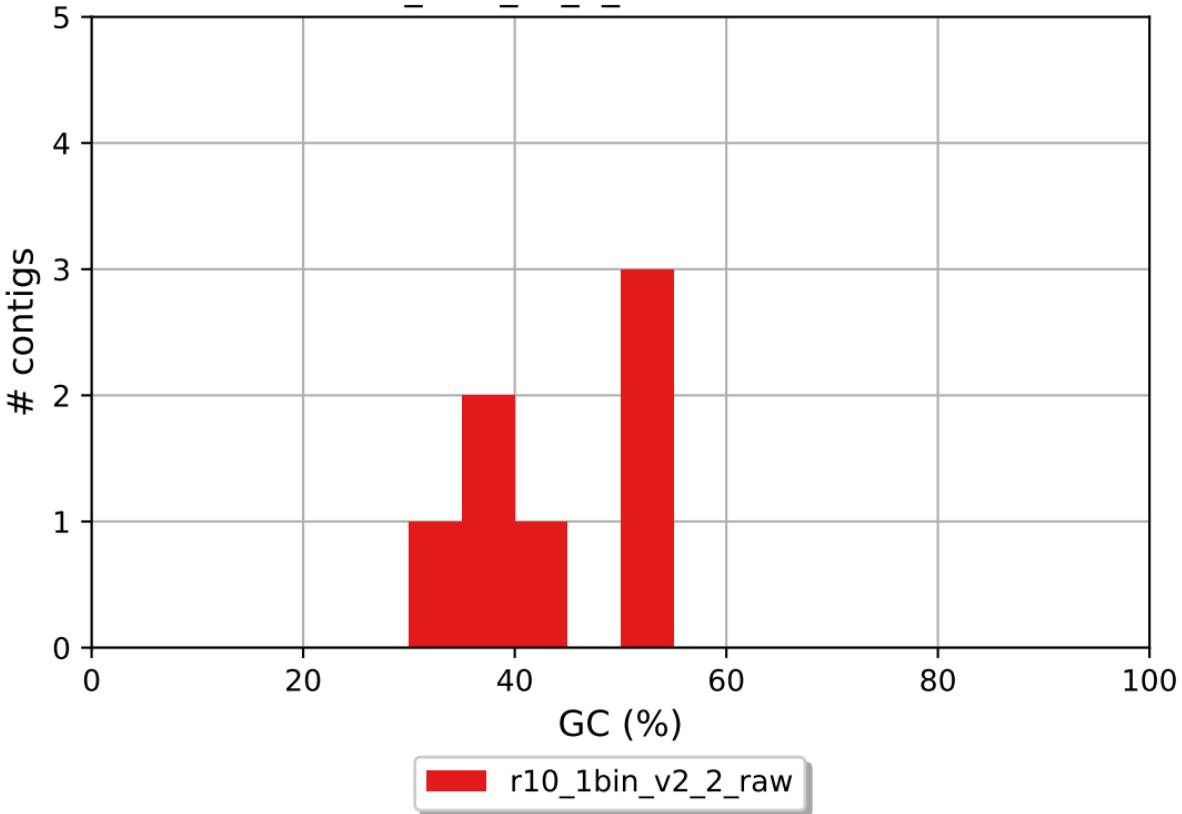
r10\_1bin\_v2\_2\_racon\_r1 GC content



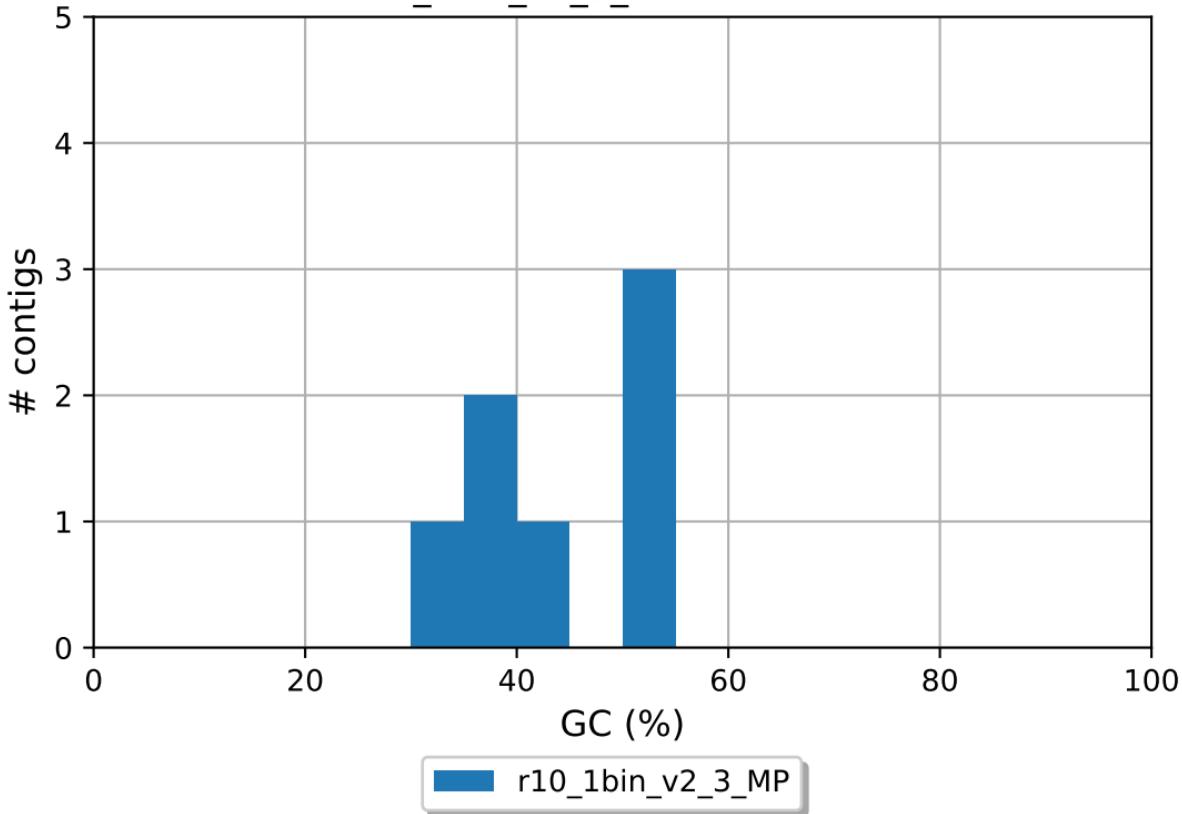
r10\_1bin\_v2\_2\_racon\_r2 GC content



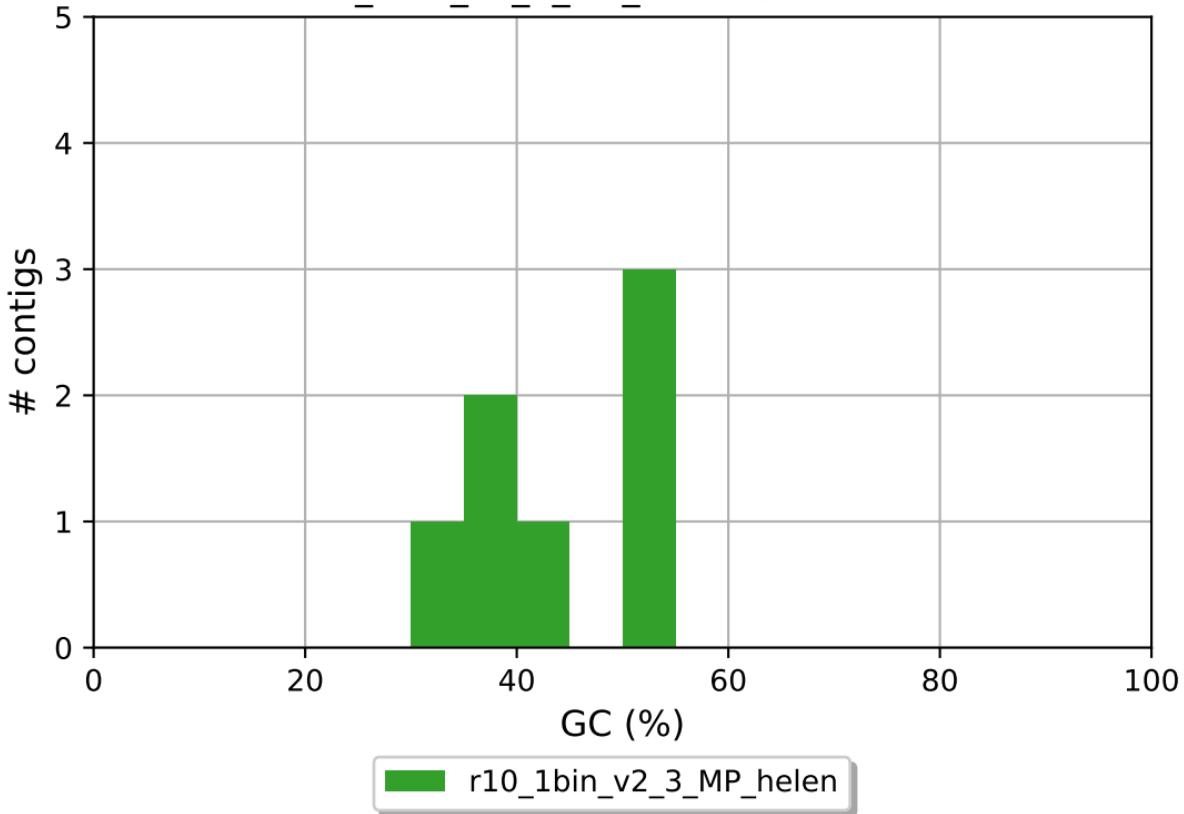
r10\_1bin\_v2\_2\_raw GC content



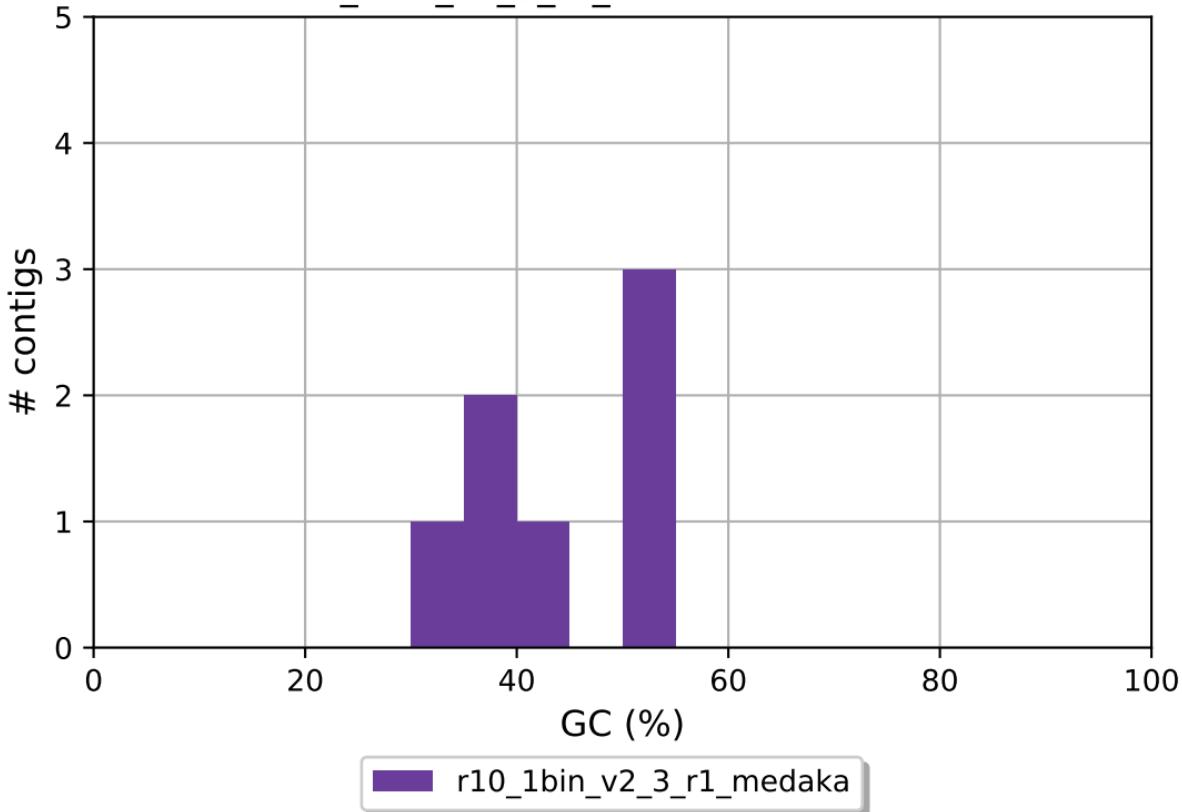
r10\_1bin\_v2\_3\_MP GC content



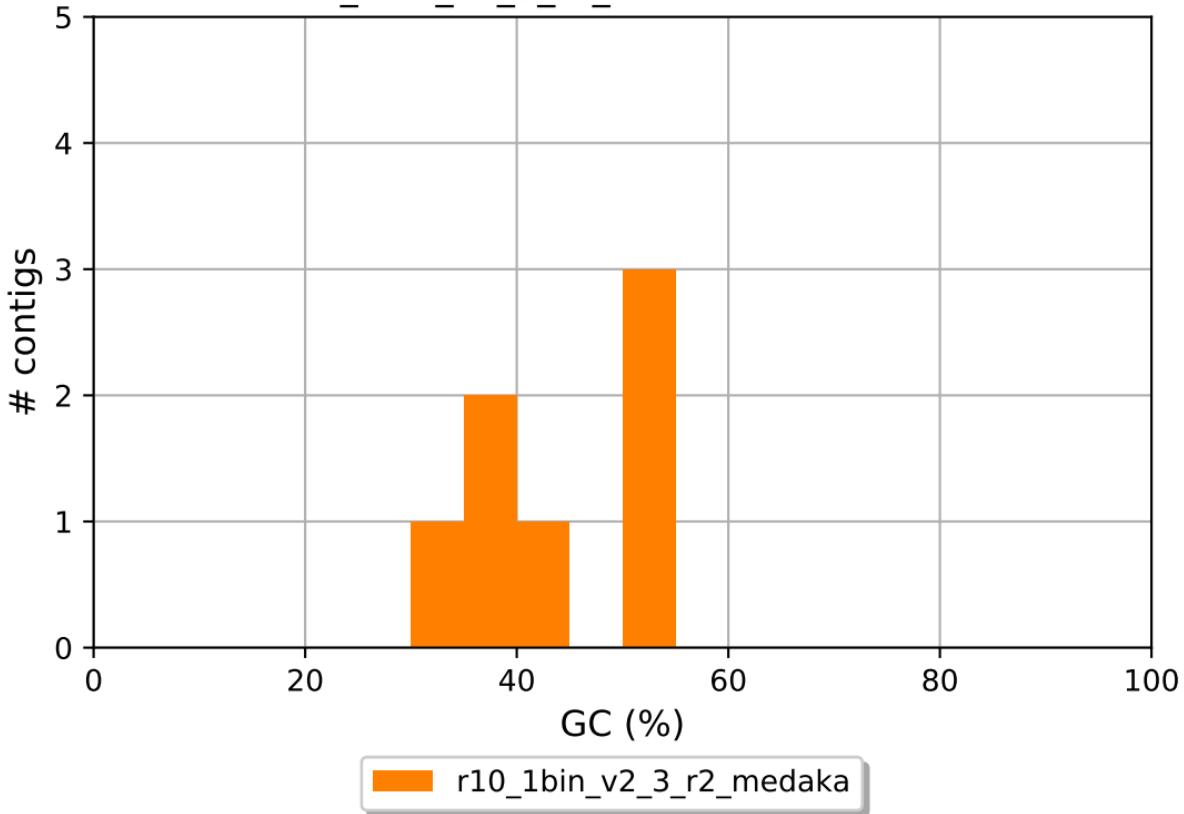
r10\_1bin\_v2\_3\_MP\_helen GC content



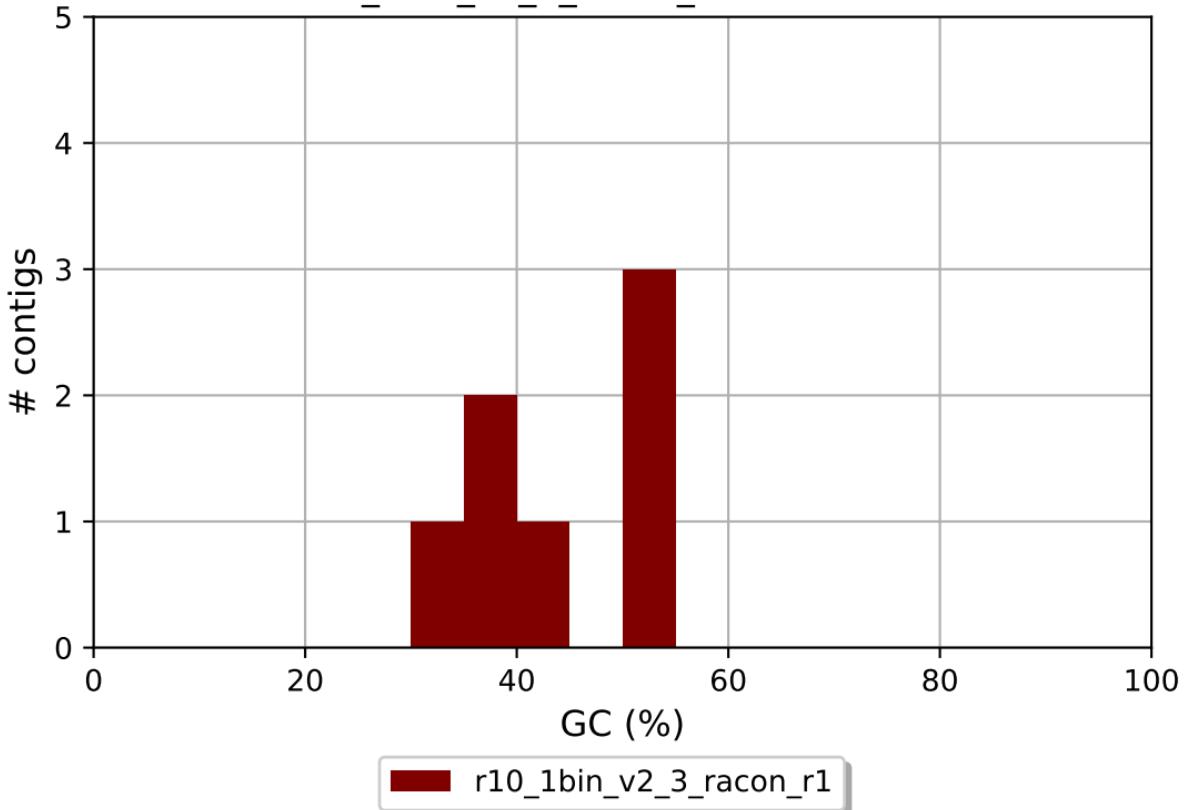
r10\_1bin\_v2\_3\_r1\_medaka GC content



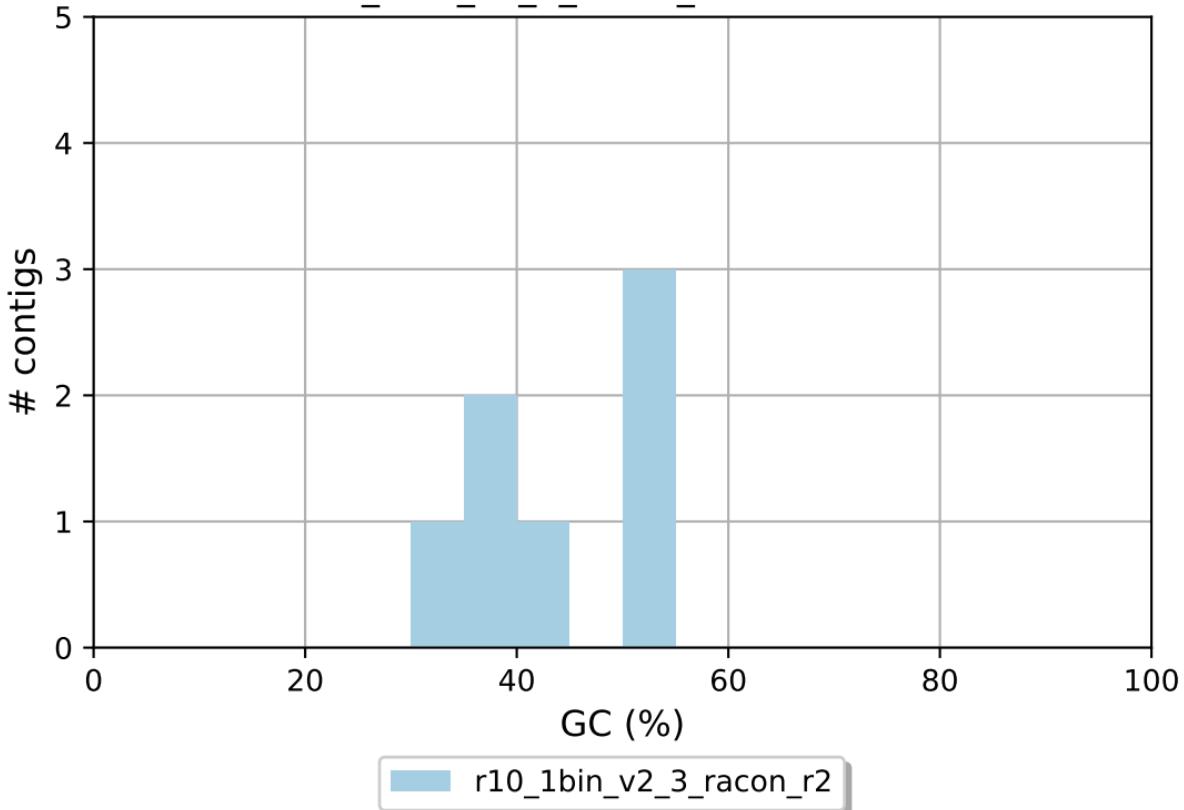
r10\_1bin\_v2\_3\_r2\_medaka GC content



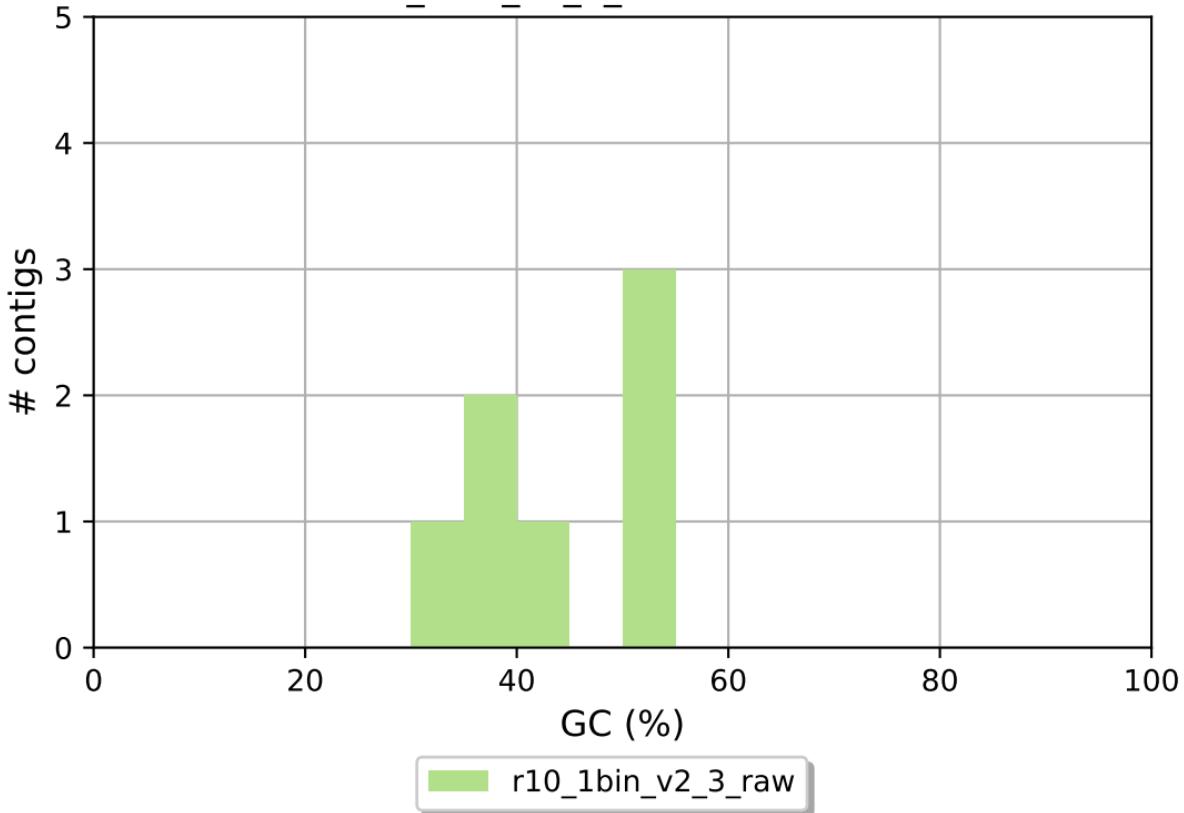
r10\_1bin\_v2\_3\_racon\_r1 GC content



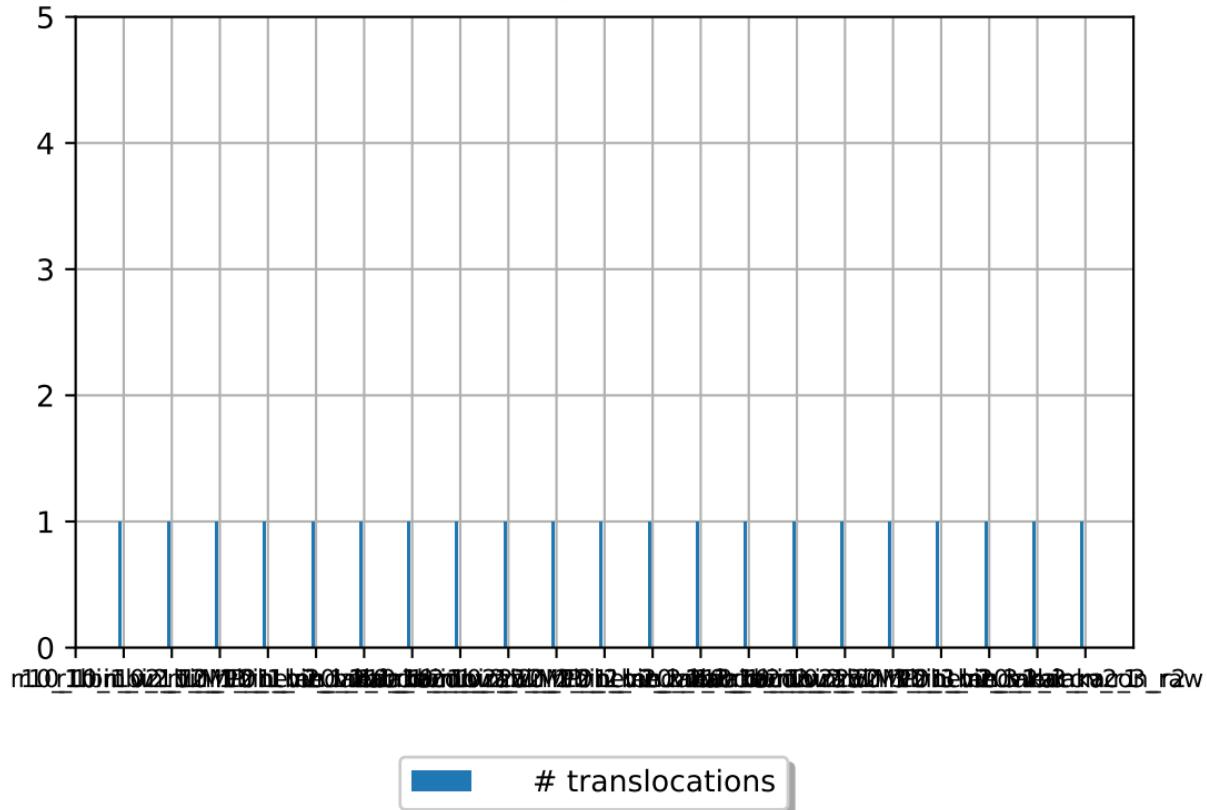
r10\_1bin\_v2\_3\_racon\_r2 GC content



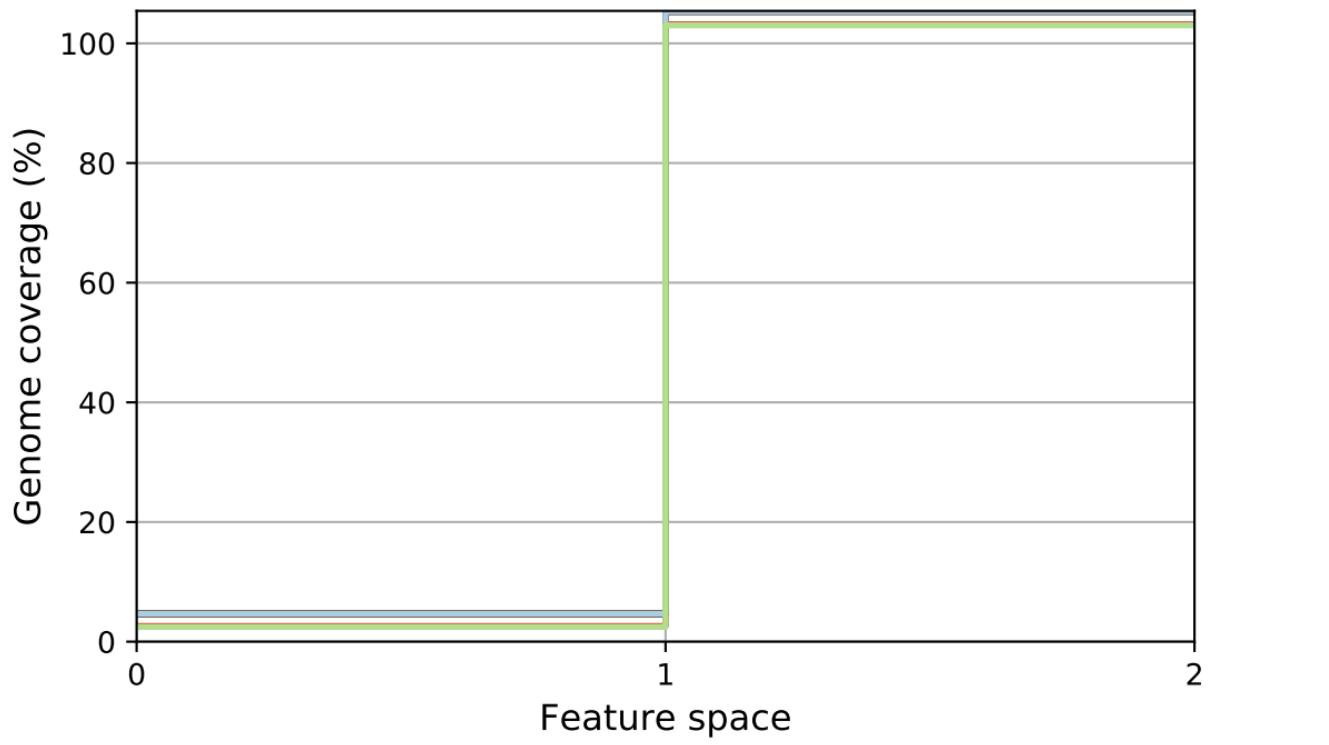
r10\_1bin\_v2\_3\_raw GC content



## Misassemblies



### FRCurve (misassemblies)

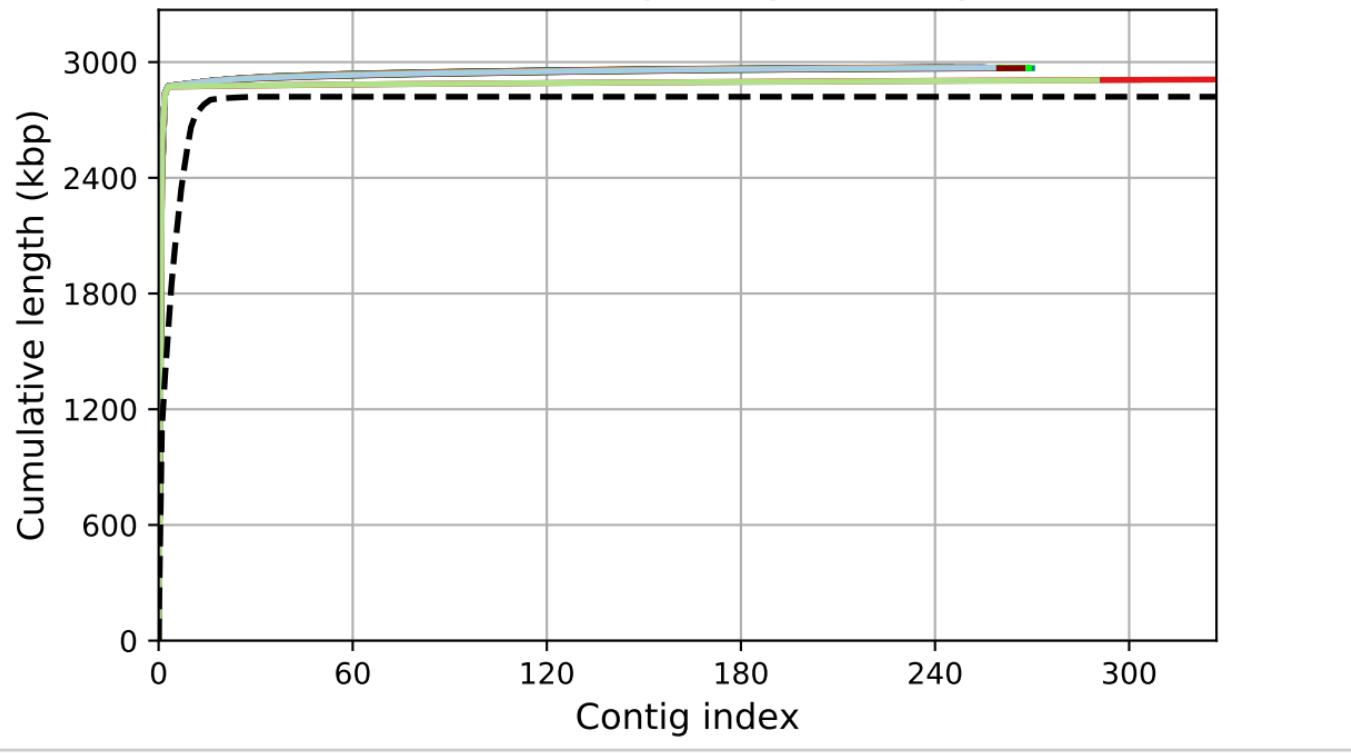


r10\_1bin\_v2\_1\_MP  
r10\_1bin\_v2\_1\_MP\_helen  
r10\_1bin\_v2\_1\_r1\_medaka  
r10\_1bin\_v2\_1\_r2\_medaka

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)

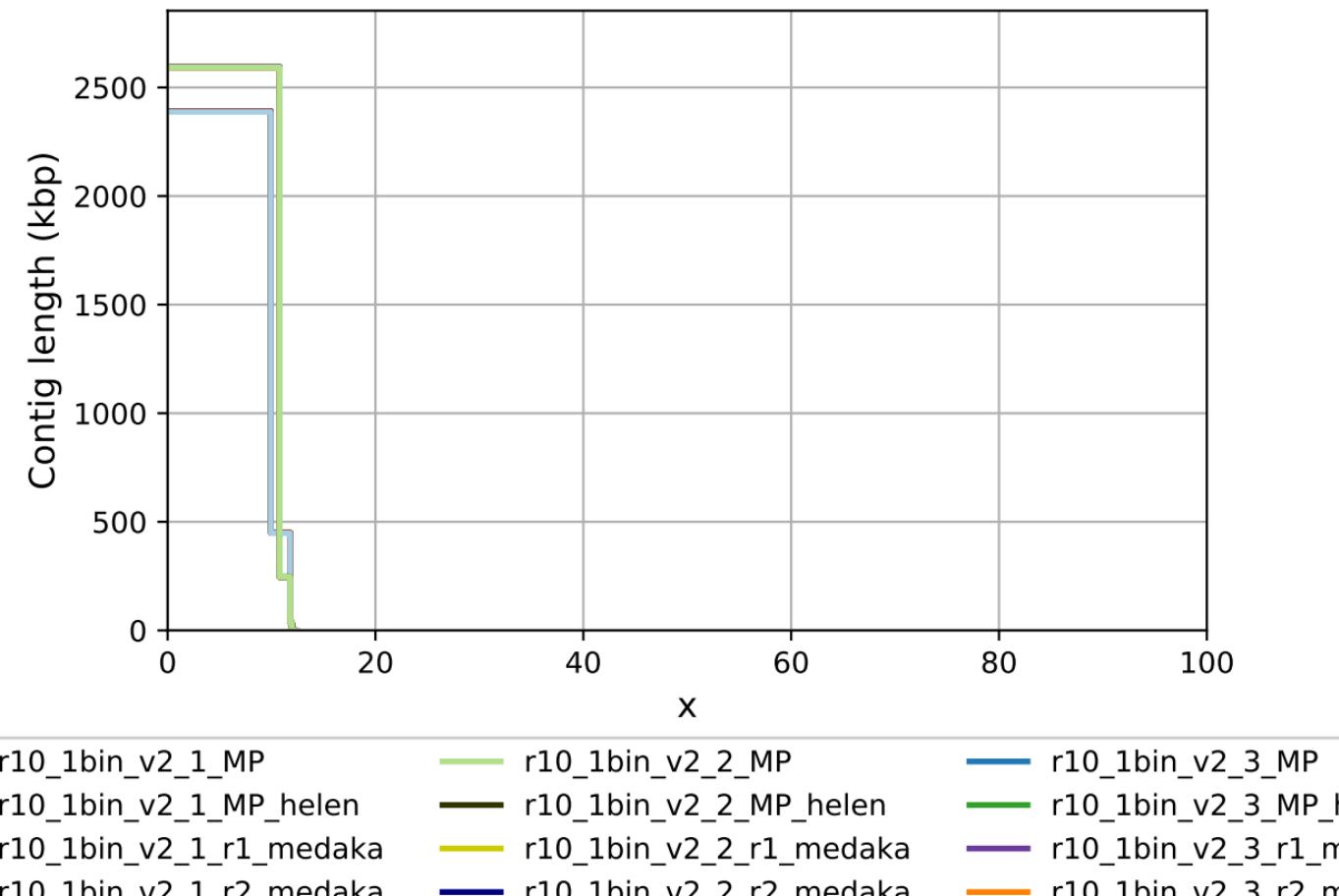


r10\_1bin\_v2\_1\_MP  
r10\_1bin\_v2\_1\_MP\_helen  
r10\_1bin\_v2\_1\_r1\_medaka  
r10\_1bin\_v2\_1\_r2\_medaka

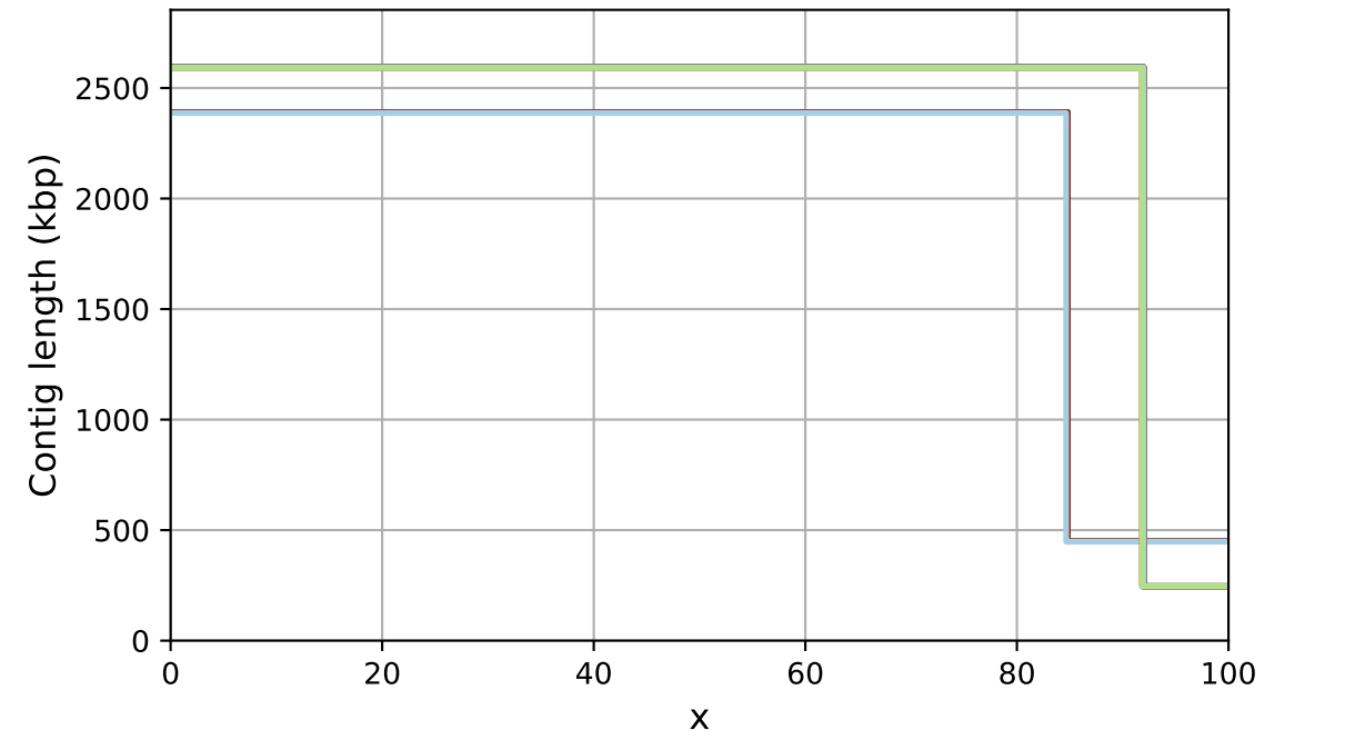
r10\_1bin\_v2\_2\_MP\_helen  
r10\_1bin\_v2\_2\_r1\_medaka  
r10\_1bin\_v2\_2\_r2\_medaka  
r10\_1bin\_v2\_3\_MP\_helen  
r10\_1bin\_v2\_3\_r1\_medaka  
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_MP\_helen  
r10\_1bin\_v2\_3\_r1\_medaka  
r10\_1bin\_v2\_3\_r2\_medaka

NAx



# NGAx



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

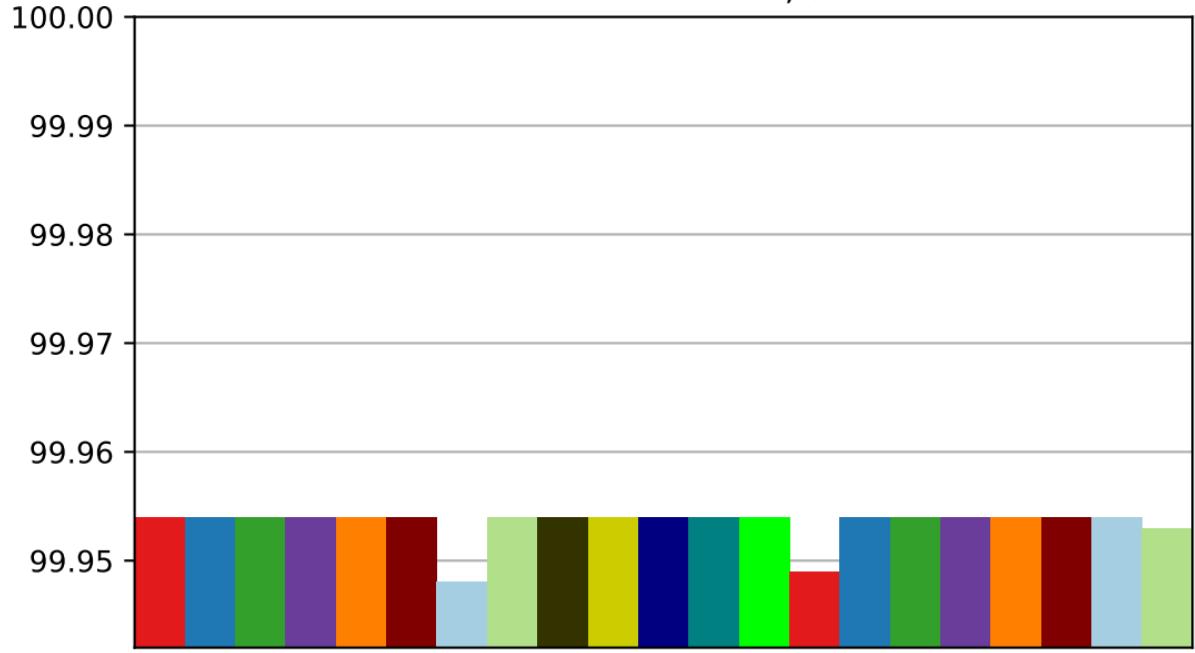
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_h

r10\_1bin\_v2\_3\_r1\_m

r10\_1bin\_v2\_3\_r2\_m

Genome fraction, %



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