

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_r
# contigs (>= 5000 bp)	7	7	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	7	7	
# contigs (>= 25000 bp)	7	7	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	7	7	
Total length (>= 5000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061	
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763
Total length	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	24061
Reference length	2820294	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	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.79	44.78	
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	37.44	
N50	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	4043
NG50	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763
N75	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843
NG75	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763
L50	3	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	1	
L75	5	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	1	
# misassemblies	1	1	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	1	1	
Misassembled contigs length	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	
# 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	6	6	6	6	6	6	6	5	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 + 6 part	0 + 7 p		
Unaligned length	21097930	21092901	21094423	21083316	21087603	21079114	21153360	21098146	21093152	21094312	21083055	21088330	21081943	21152966	21098045	21092443	21094294	21086667	21087551	21080142	21152
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	
Duplication ratio	1.056	1.057	1.057	1.057	1.057	1.055	1.056	1.032	1.056	1.057	1.057	1.057	1.055	1.055	1.032	1.056	1.057	1.057	1.055	1.055	
# N's per 100 kbp	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	0.00	0.00	0.00	
# mismatches per 100 kbp	249.68	251.10	251.31	254.15	232.51	241.59	146.68	247.87	251.98	252.23	254.79	234.74	234.60	148.81	247.87	252.05	251.95	245.95	2		

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).

## Misassemblies report

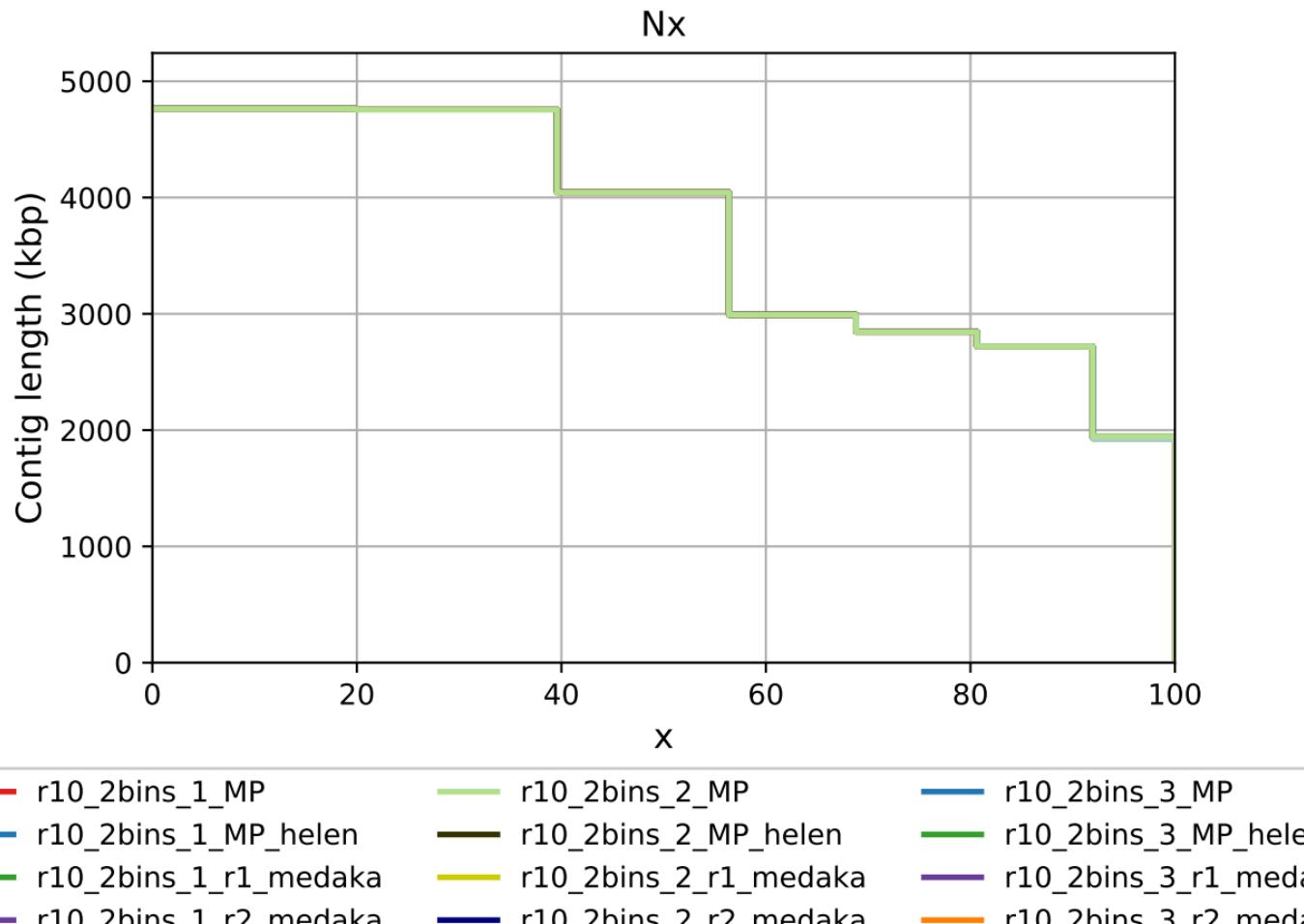
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw		
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
# contig misassemblies	1	1	1	1	1	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	0		
# c. translocations	1	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	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	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	0	6	0	0	0	0	0	0	6	
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	20	16	16	16	16	16	16	20	
# 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	19	19	19	19	19	19	11	19	19	19	19	19	11	19	19	19	19	19	19	11	
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	6	6	6	6	6	6	6	
# mismatches	7037	7077	7083	7163	6553	6809	4134	6986	7102	7109	7181	6616	6612	4194	6986	7104	7101	6932	6614	6719	4195
# indels	438	443	400	415	582	591	3549	437	443	399	403	616	570	3566	437	444	403	386	609	564	3566
# indels (<= 5 bp)	397	401	359	374	543	554	3513	396	401	360	363	578	533	3530	396	402	364	346	570	528	3530
# indels (> 5 bp)	41	42	41	41	39	37	36	41	42	39	40	38	37	36	41	42	39	40	39	36	36
Indels length	2456	2473	2370	2425	2566	2592	6143	2455	2473	2359	2393	2605	2547	6163	2455	2474	2366	2346	2608	2519	6163

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).

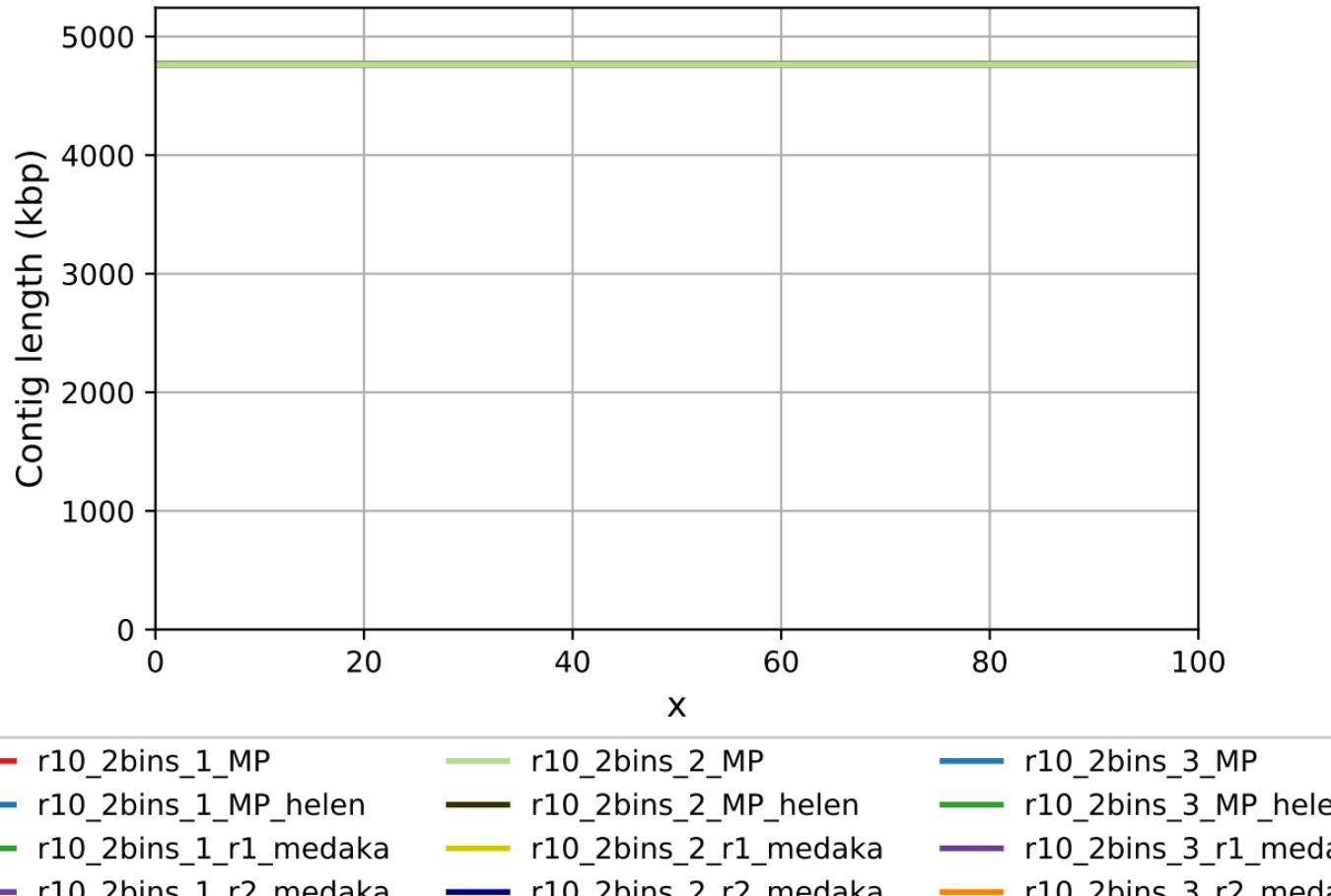
## Unaligned report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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	21097930	21092901	21094423	21083316	21087603	21079114	21153360	21098146	21093152	21083055	21088330	21081943	21152966	21094294	21086667	21087551	21080142	21152518	
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

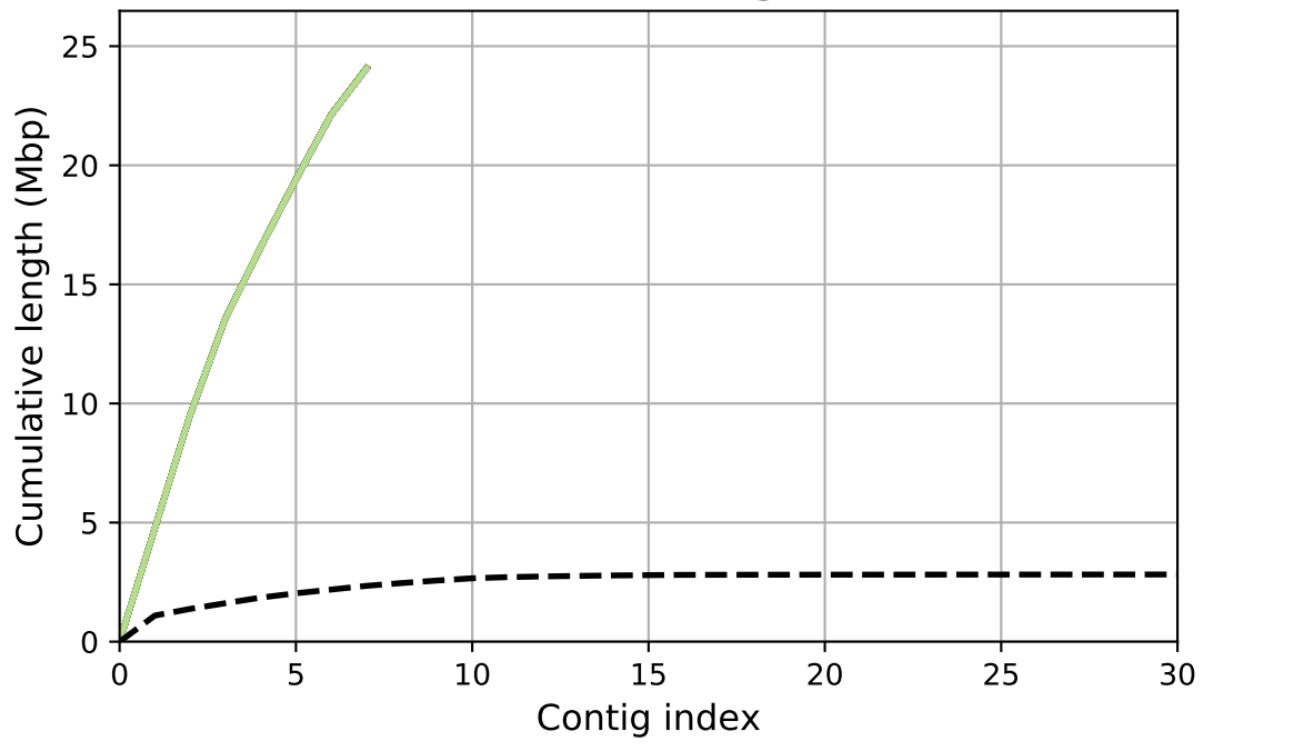
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



# NGx

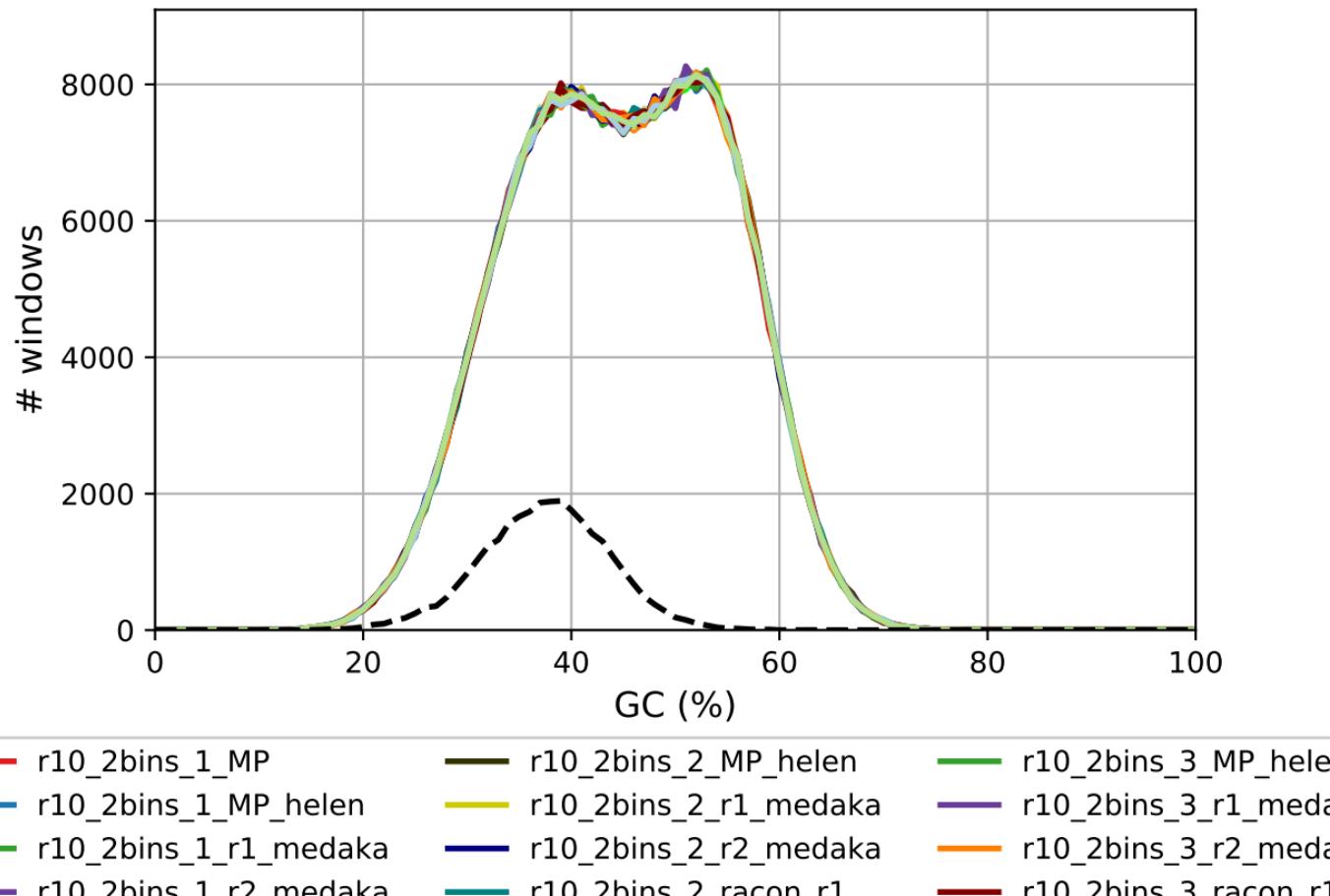


Cumulative length

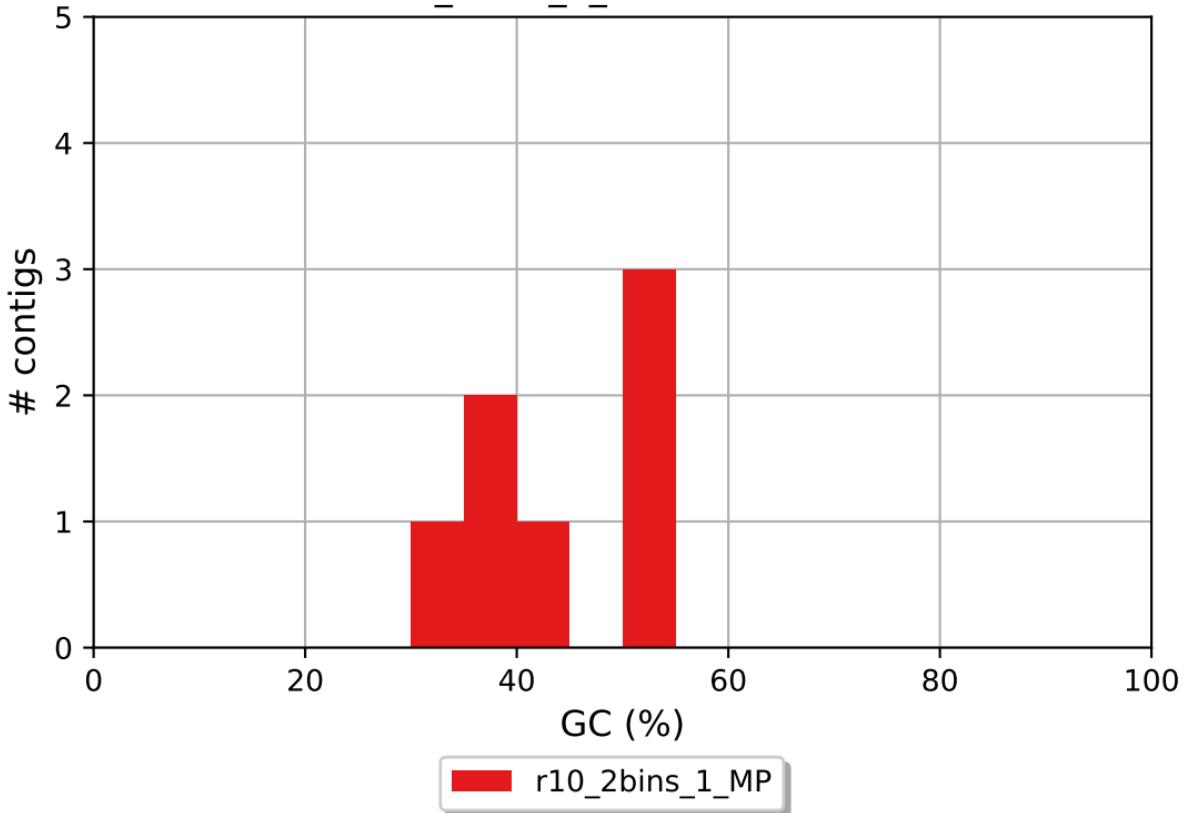


- r10\_2bins\_1\_MP
- r10\_2bins\_1\_MP\_helen
- r10\_2bins\_1\_r1\_medaka
- r10\_2bins\_1\_r2\_medaka
- r10\_2bins\_2\_MP\_helen
- r10\_2bins\_2\_r1\_medaka
- r10\_2bins\_2\_r2\_medaka
- r10\_2bins\_3\_MP\_helen
- r10\_2bins\_3\_r1\_medaka
- r10\_2bins\_3\_r2\_medaka
- r10\_2bins\_3\_racoon\_r1
- r10\_2bins\_3\_racoon\_r2

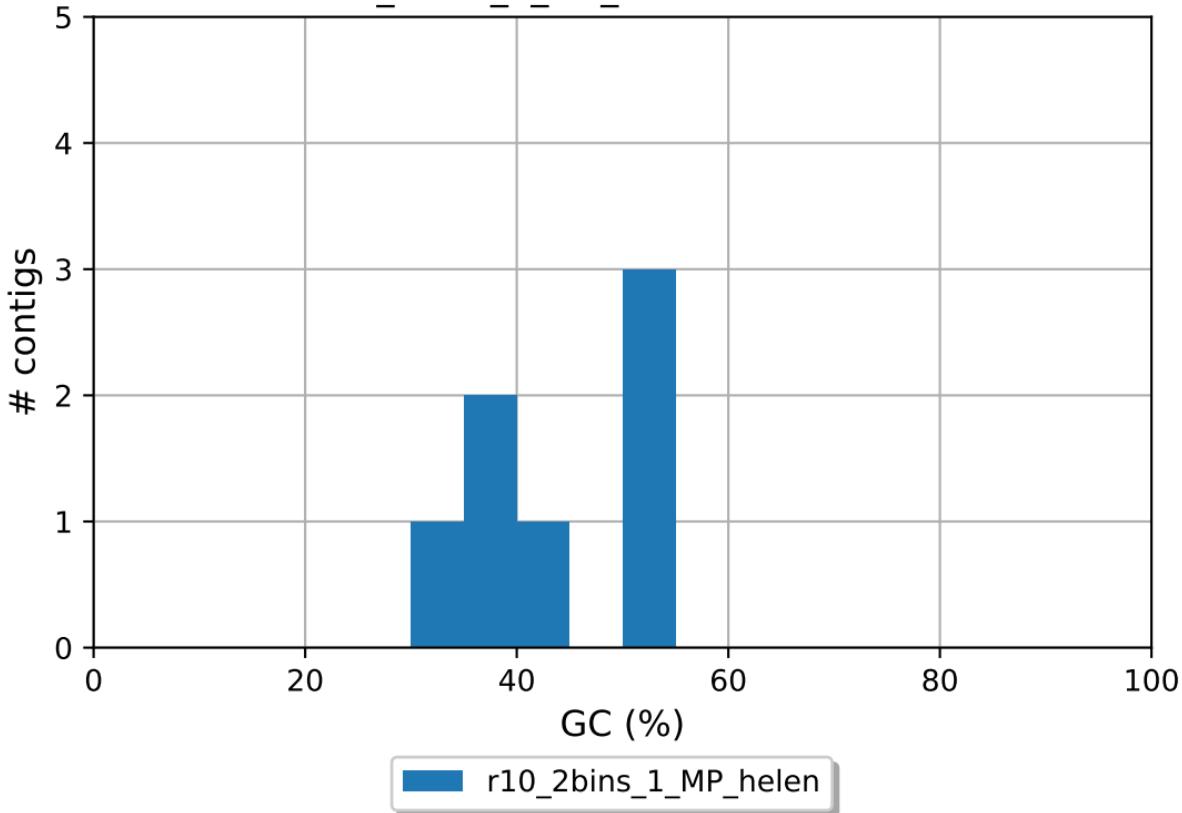
## GC content



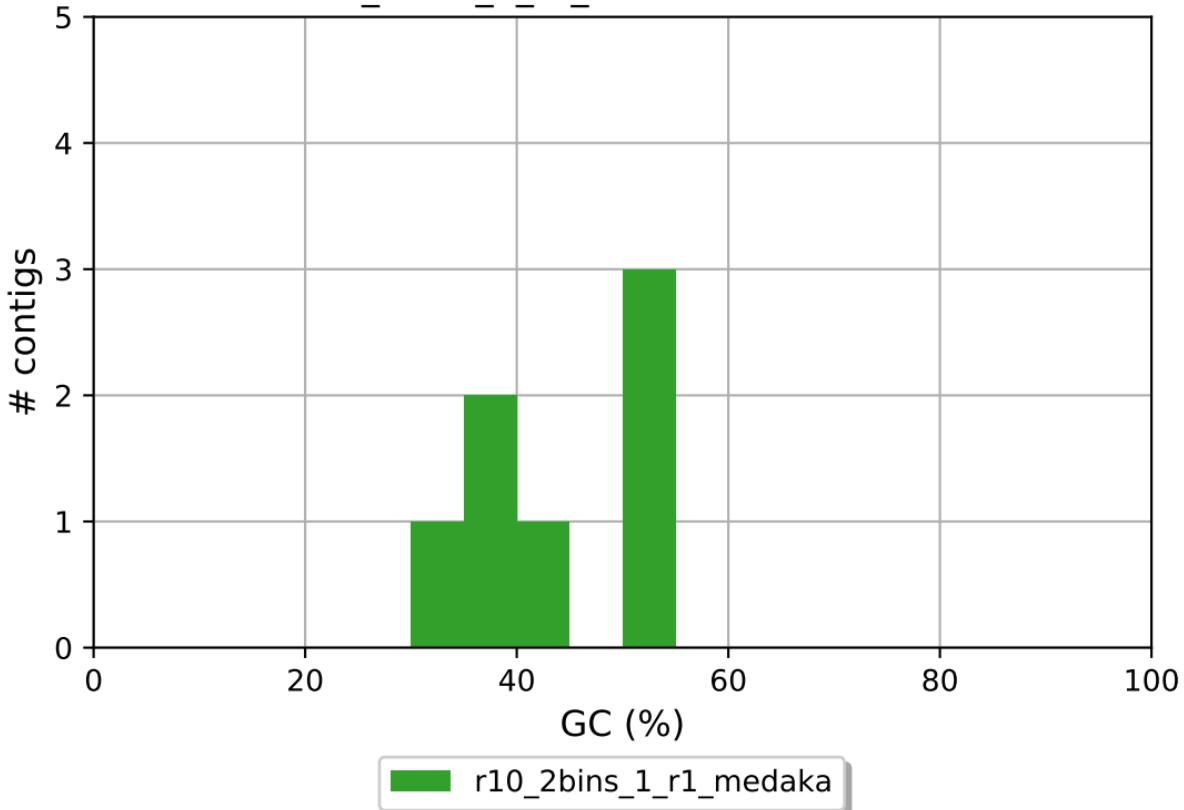
r10\_2bins\_1\_MP GC content



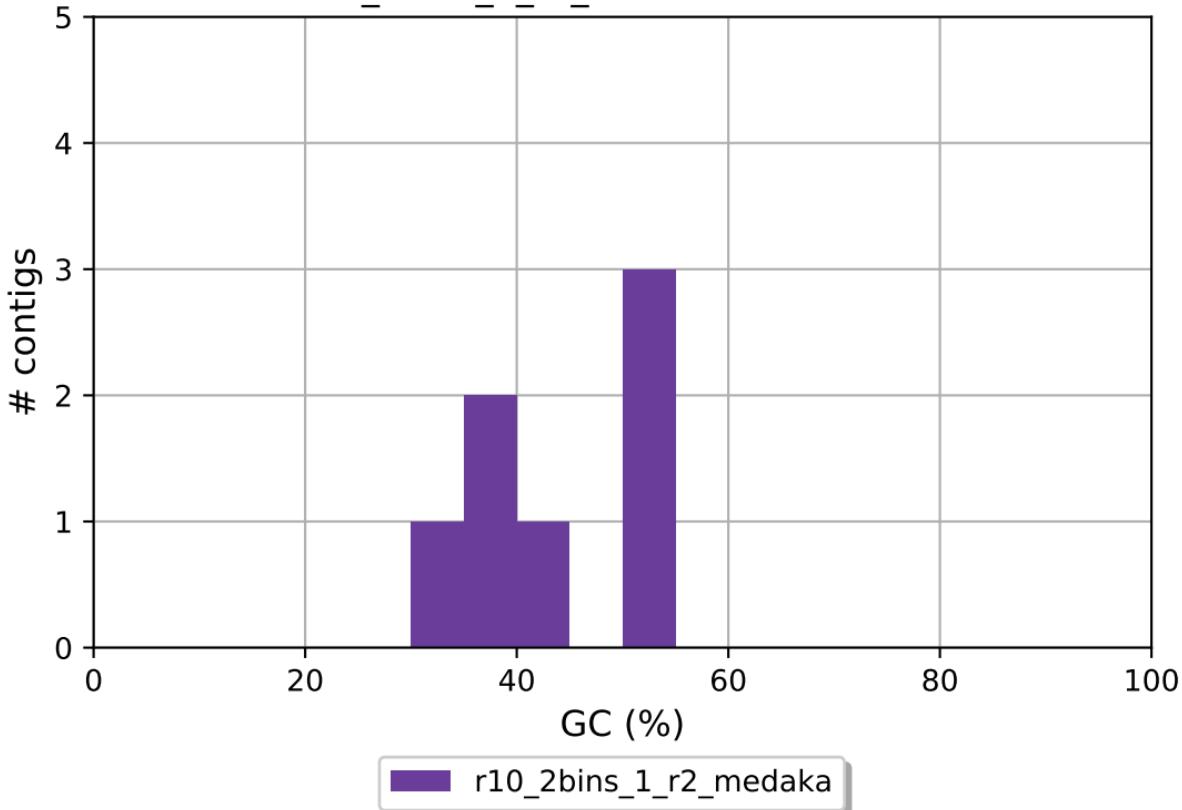
r10\_2bins\_1\_MP\_helen GC content



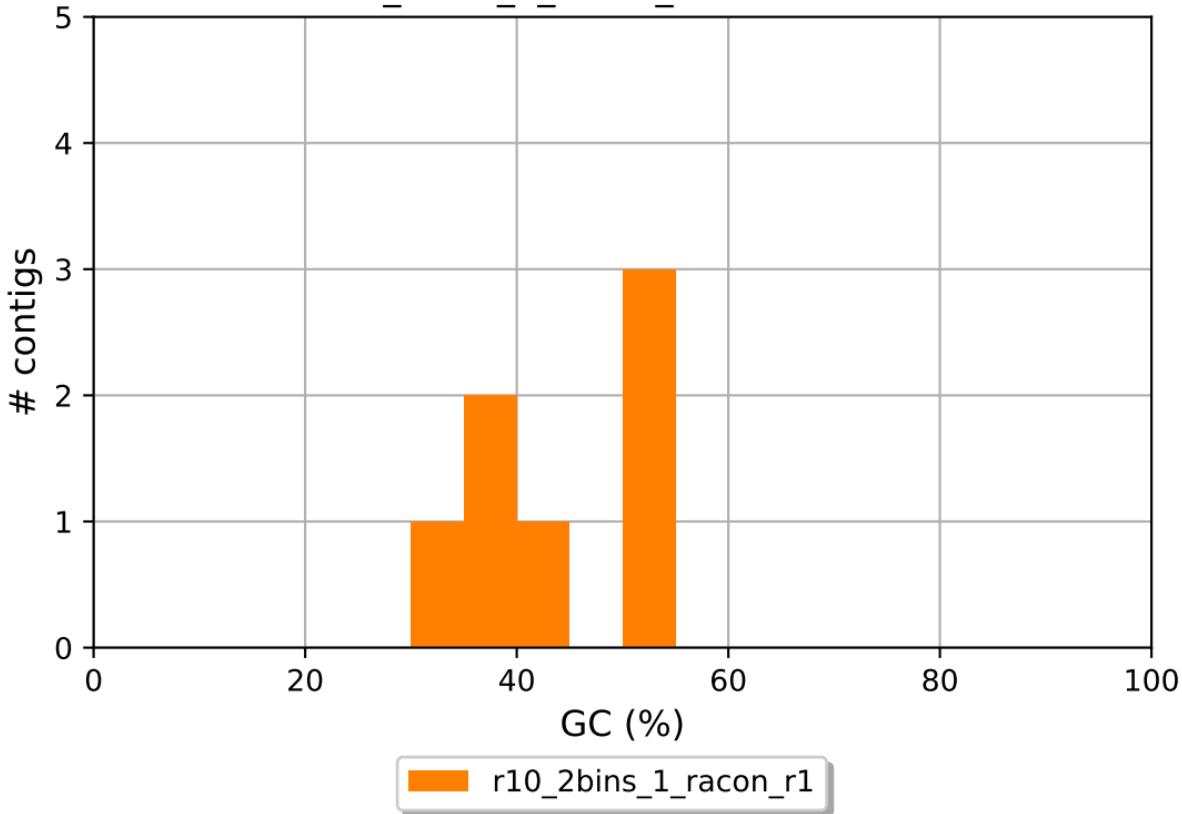
r10\_2bins\_1\_r1\_medaka GC content



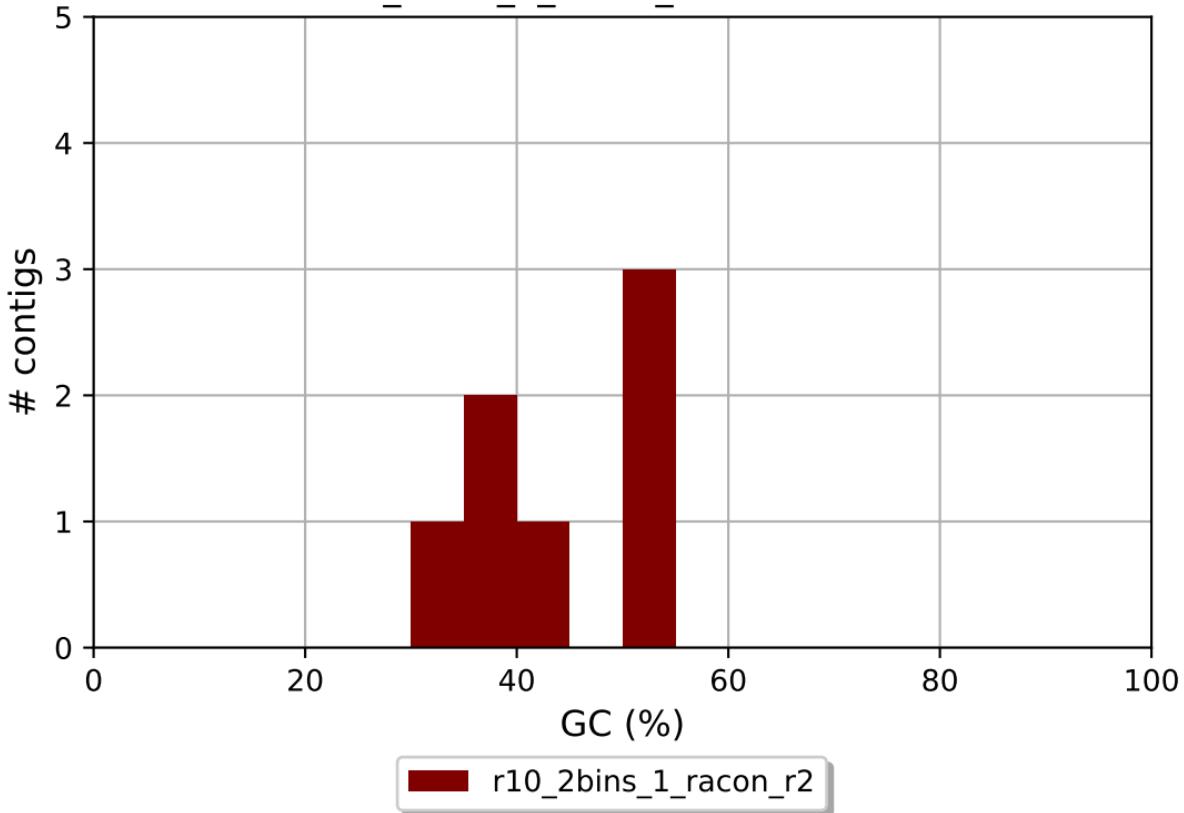
r10\_2bins\_1\_r2\_medaka GC content



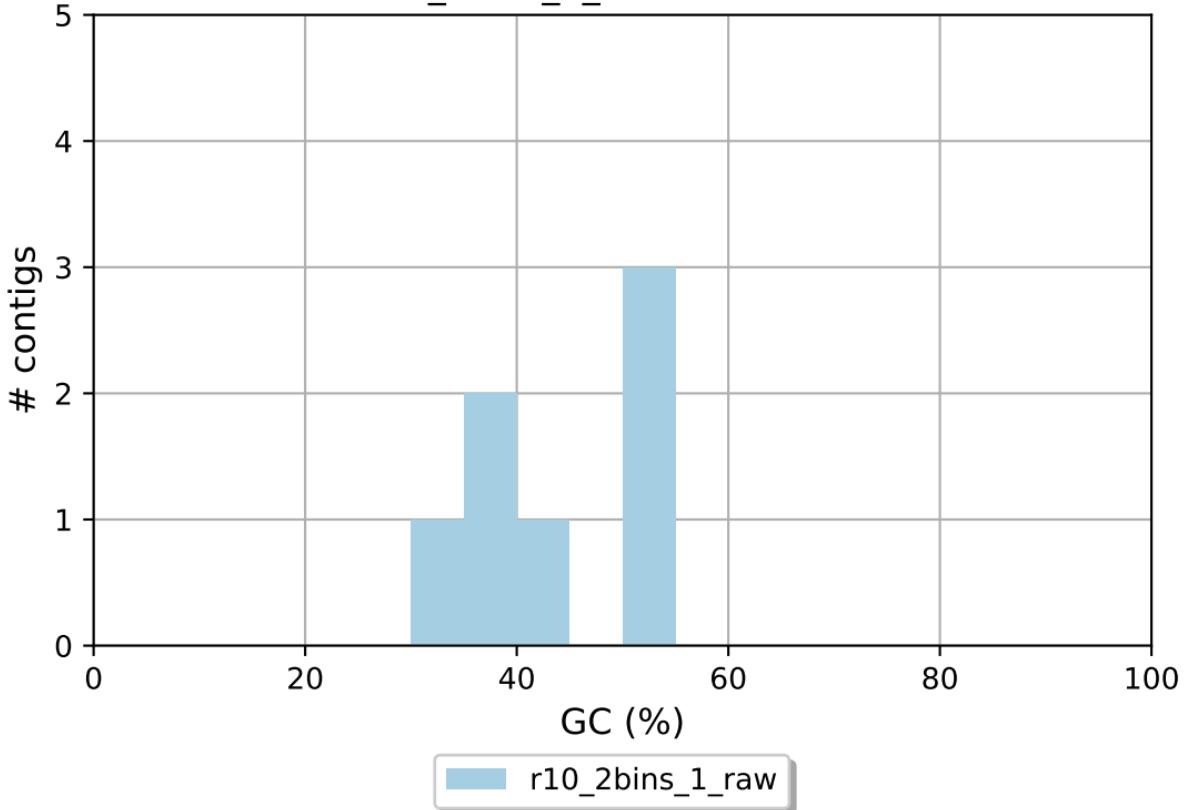
r10\_2bins\_1\_racon\_r1 GC content



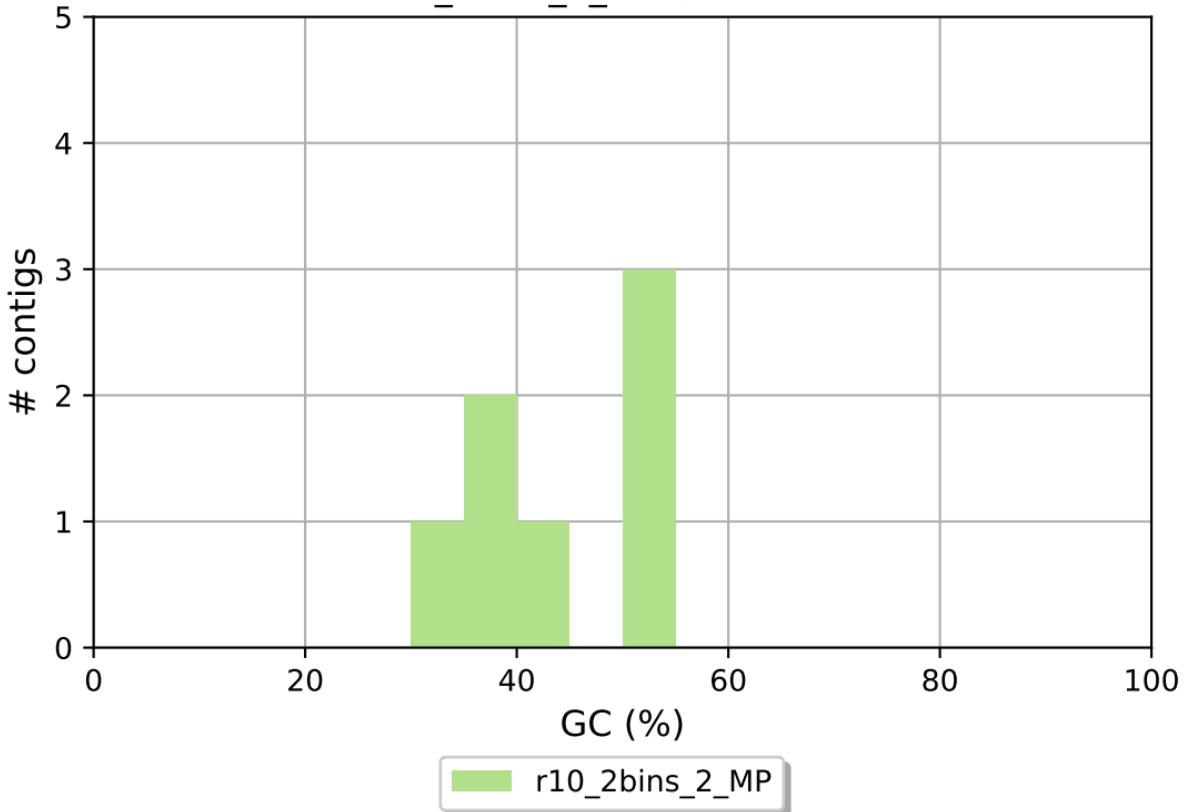
r10\_2bins\_1\_racon\_r2 GC content



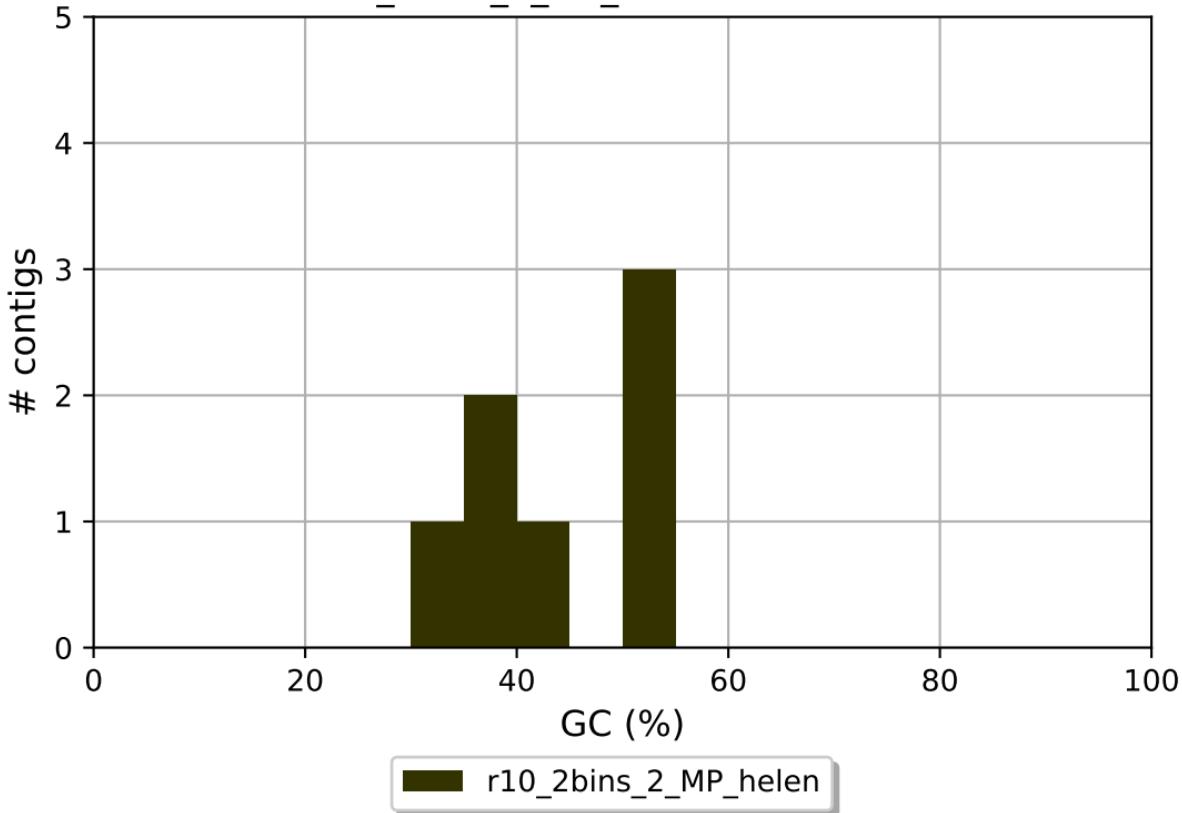
r10\_2bins\_1\_raw GC content



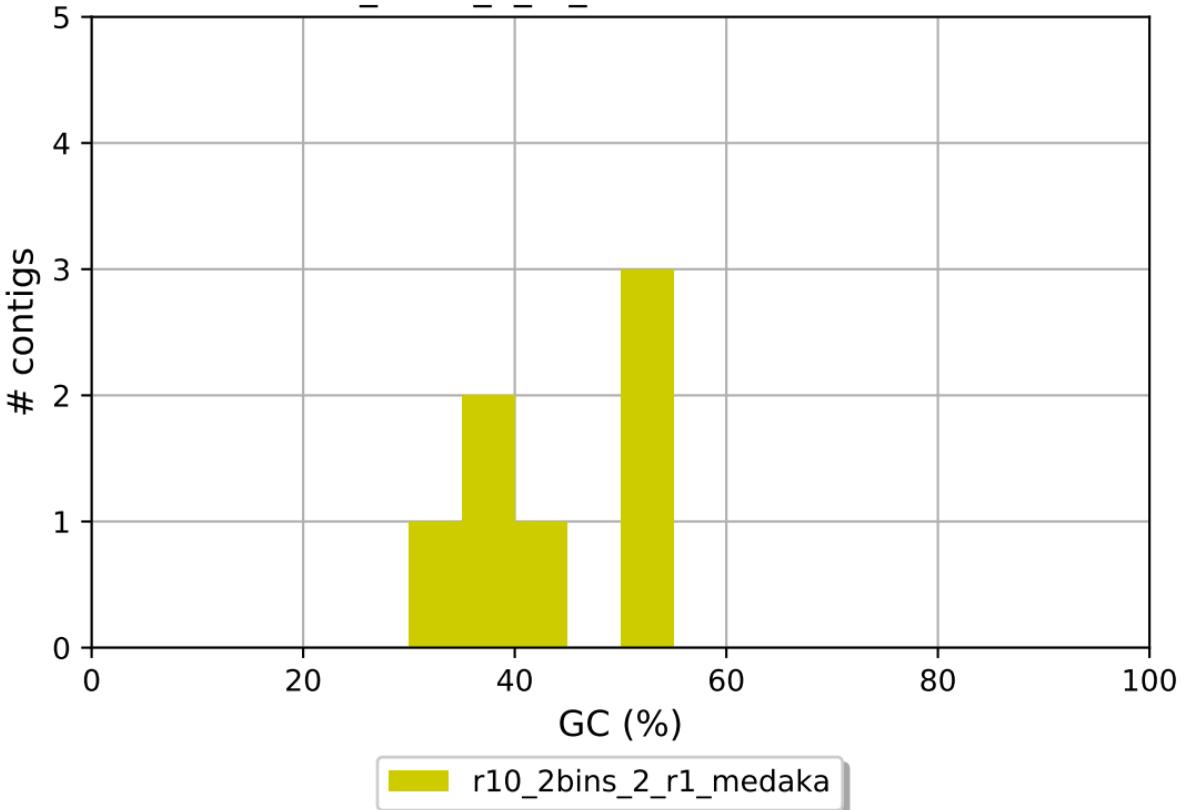
r10\_2bins\_2\_MP GC content



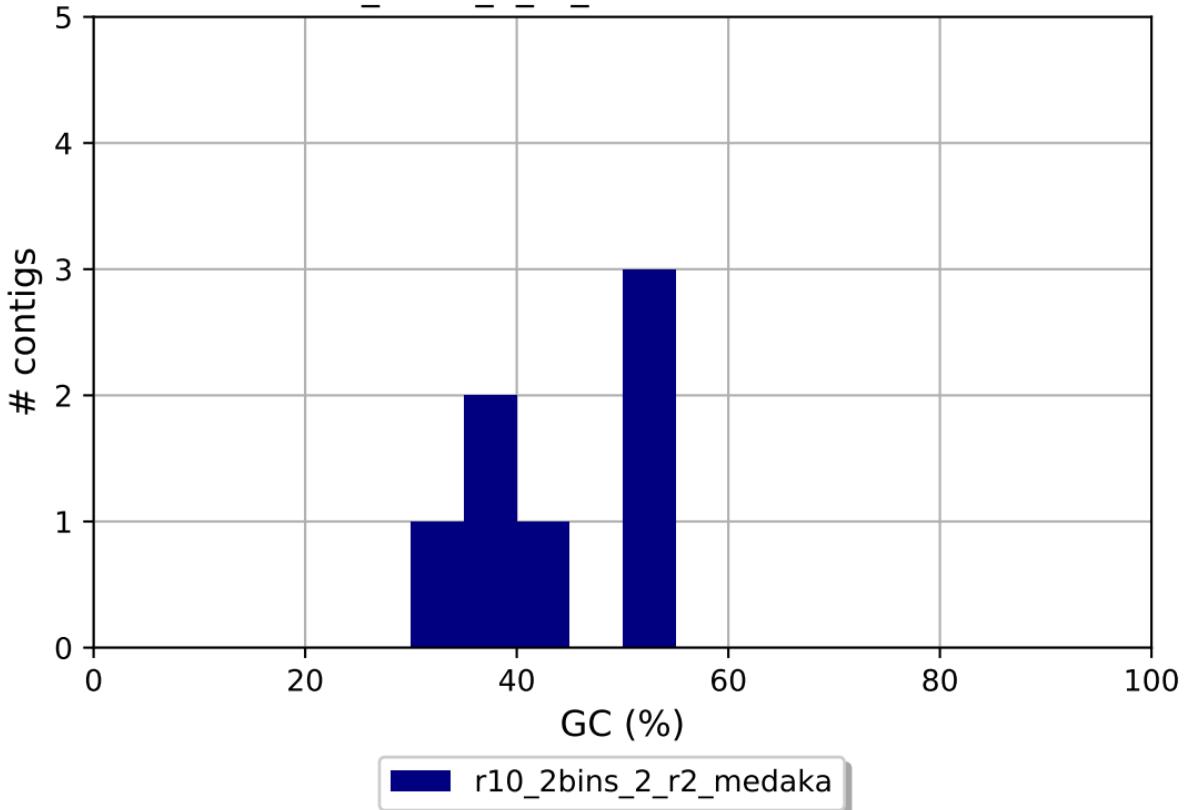
r10\_2bins\_2\_MP\_helen GC content



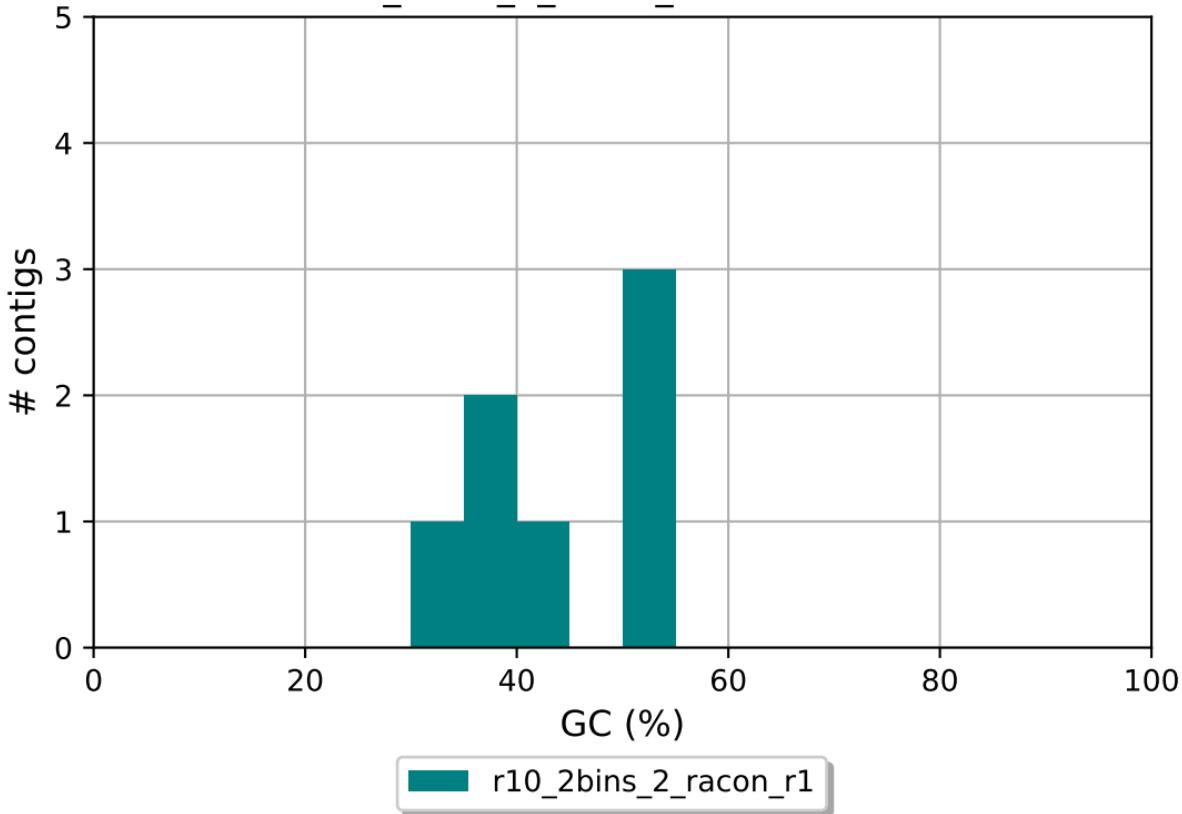
r10\_2bins\_2\_r1\_medaka GC content



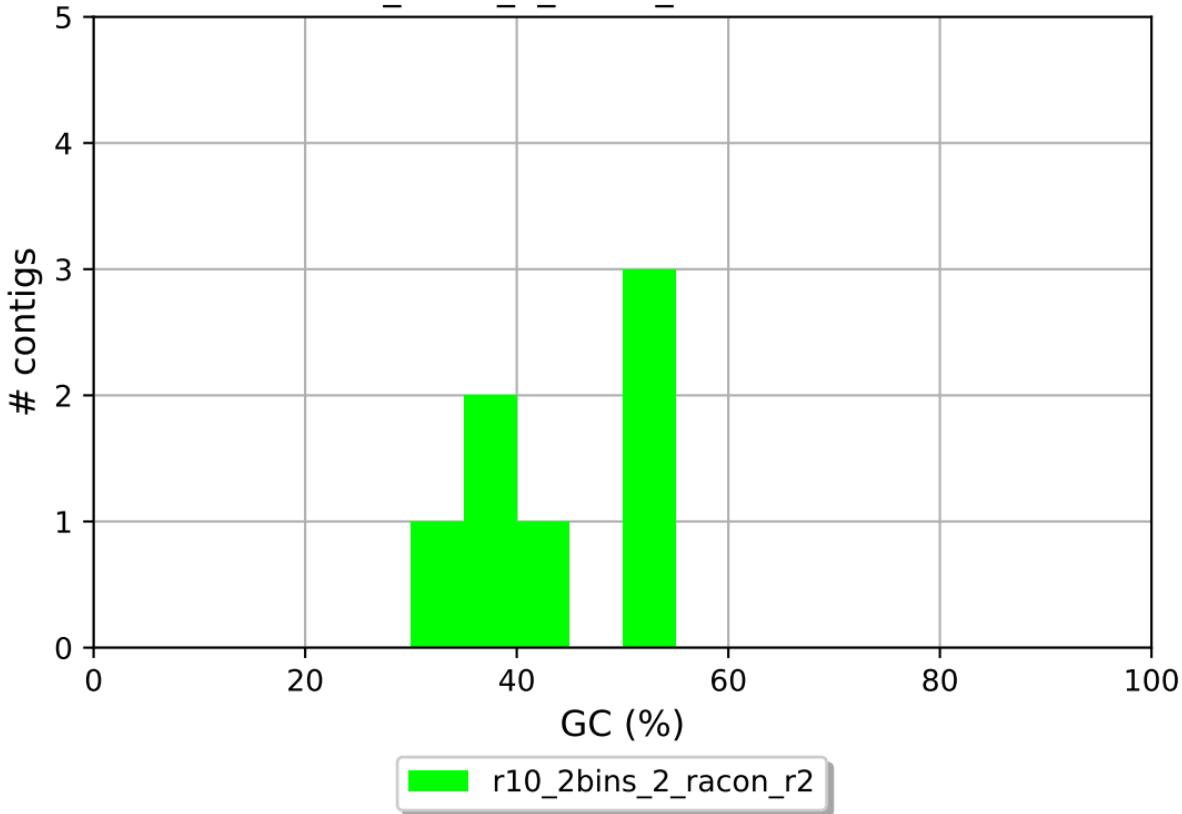
r10\_2bins\_2\_r2\_medaka GC content



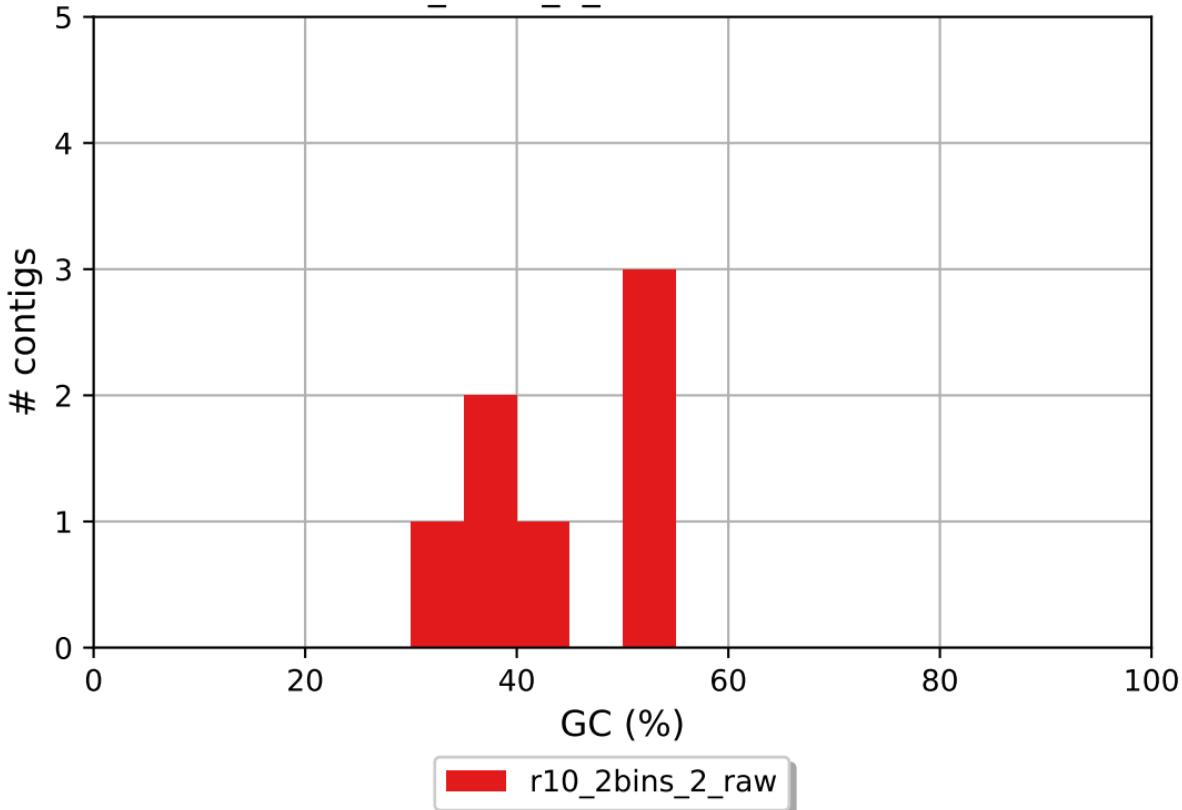
r10\_2bins\_2\_racon\_r1 GC content



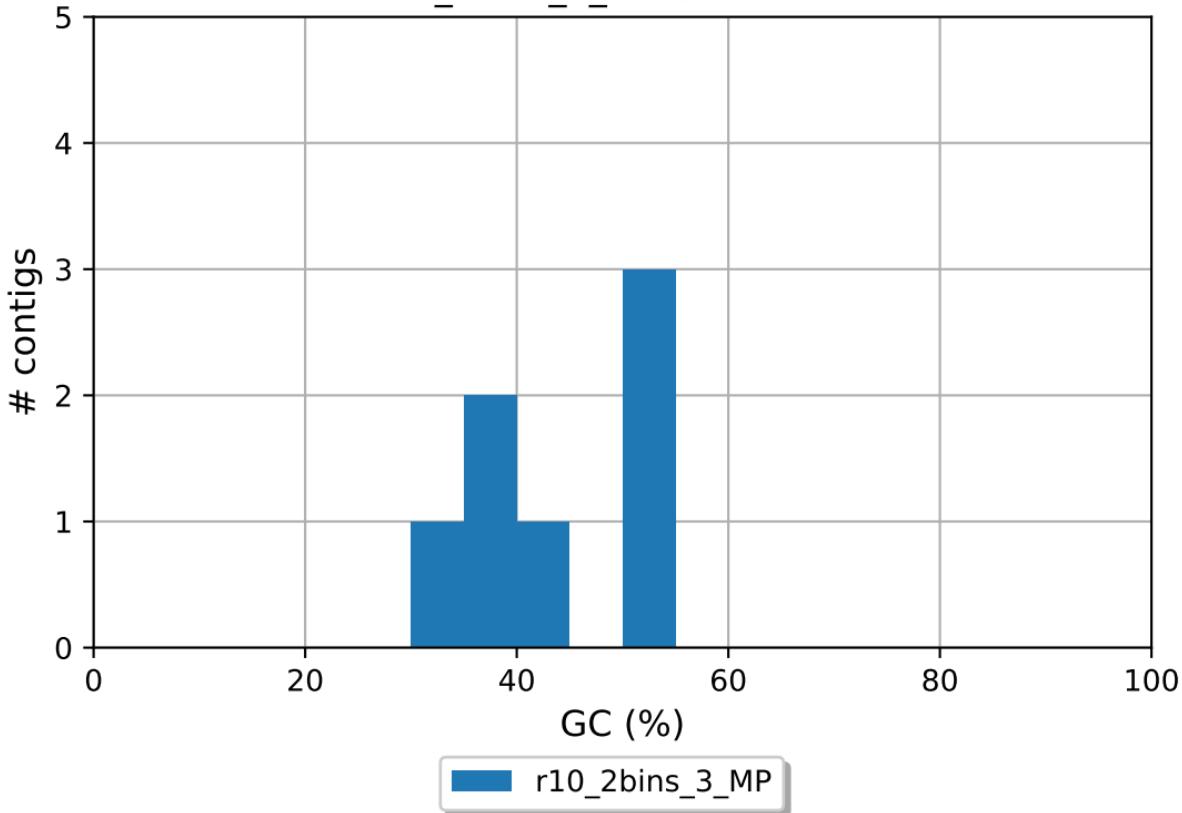
r10\_2bins\_2\_racon\_r2 GC content



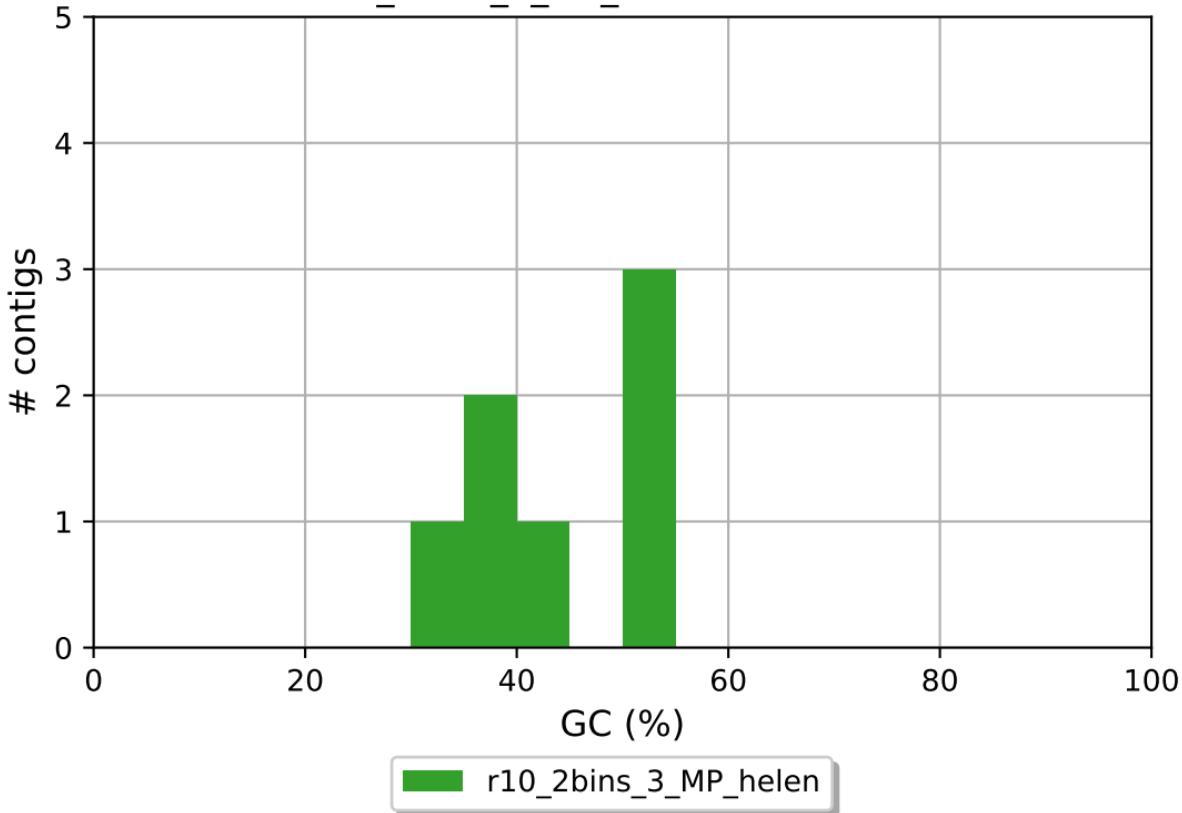
r10\_2bins\_2\_raw GC content



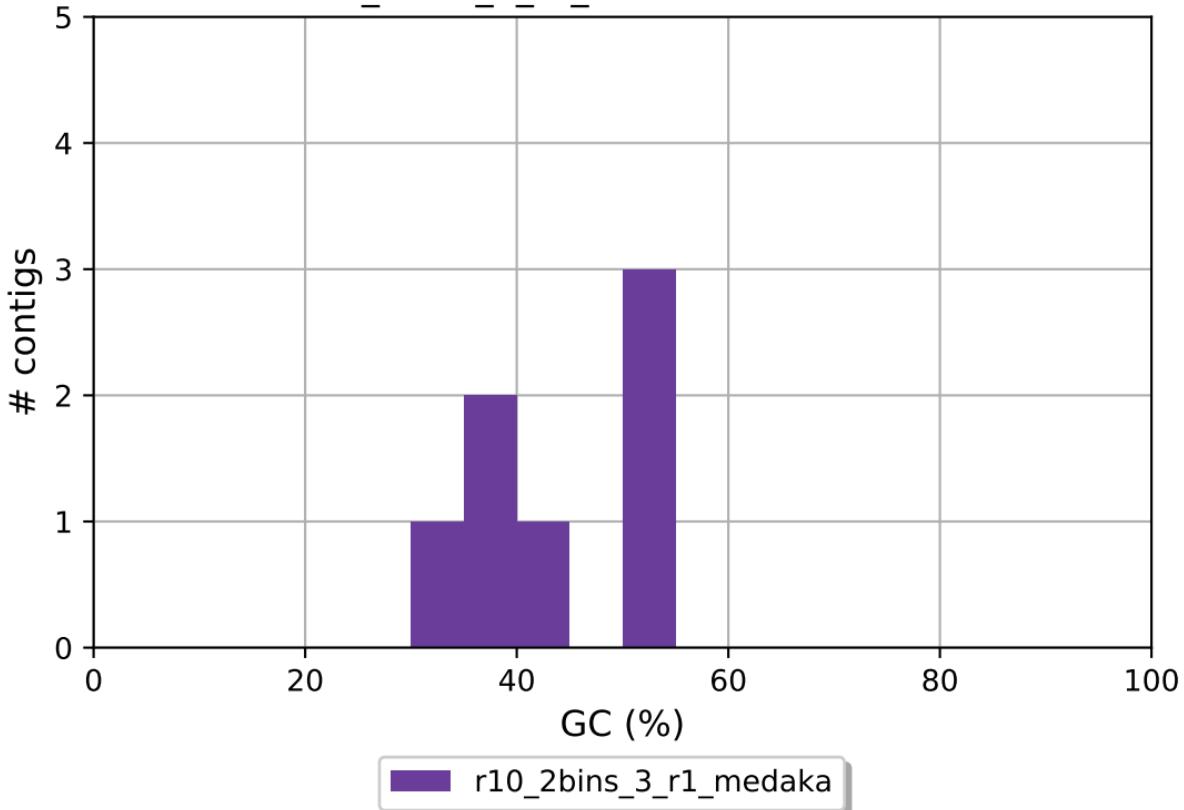
r10\_2bins\_3\_MP GC content



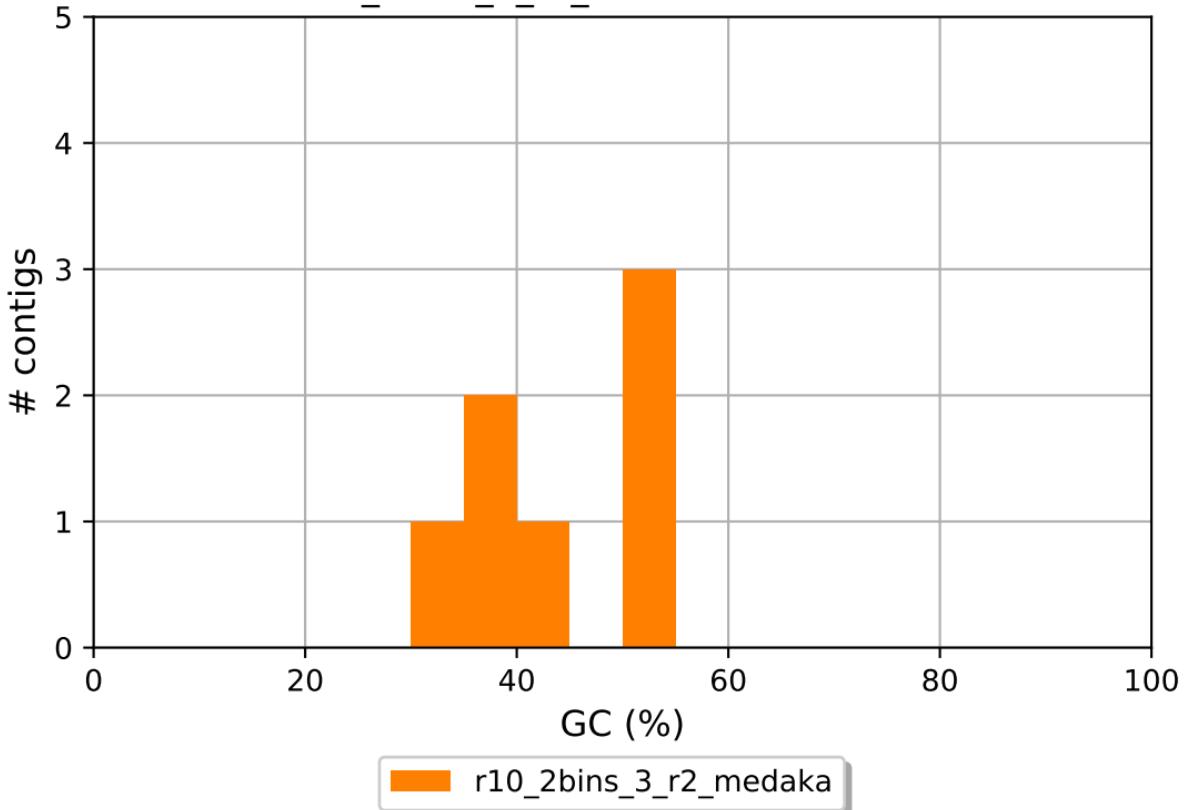
r10\_2bins\_3\_MP\_helen GC content



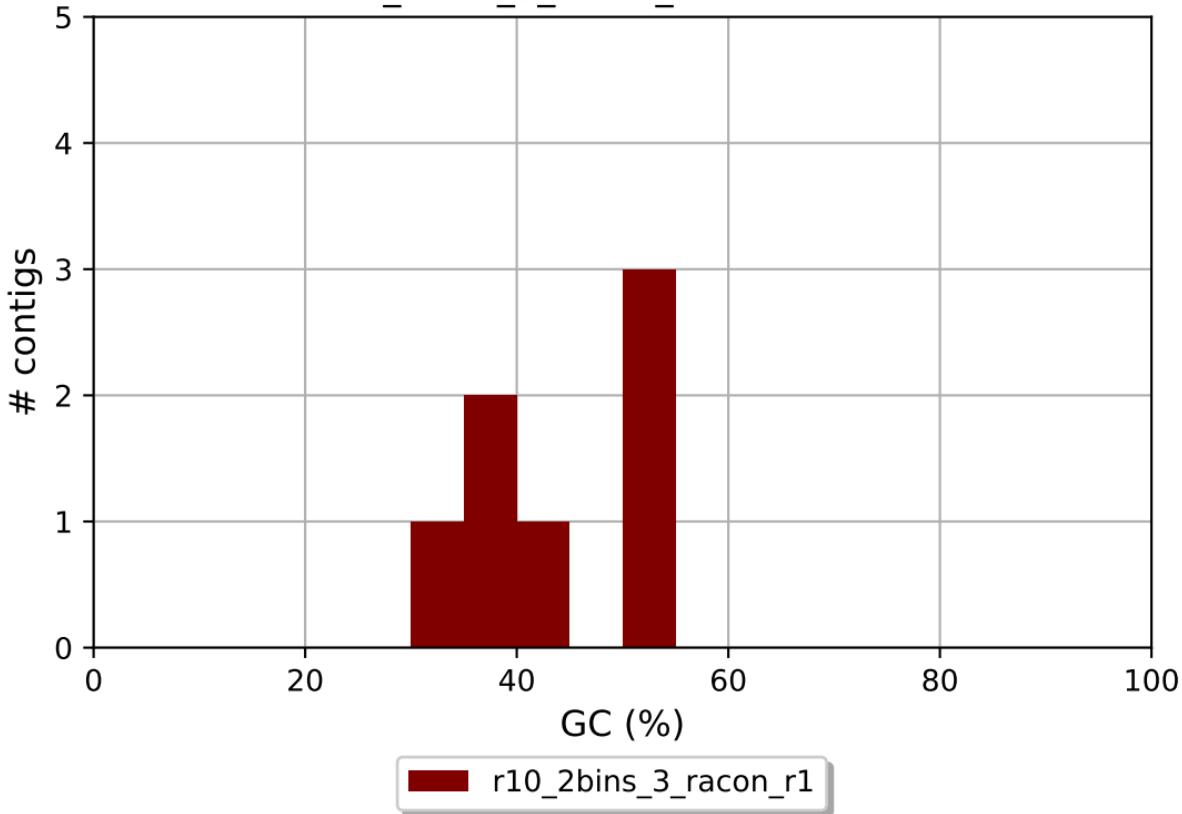
r10\_2bins\_3\_r1\_medaka GC content



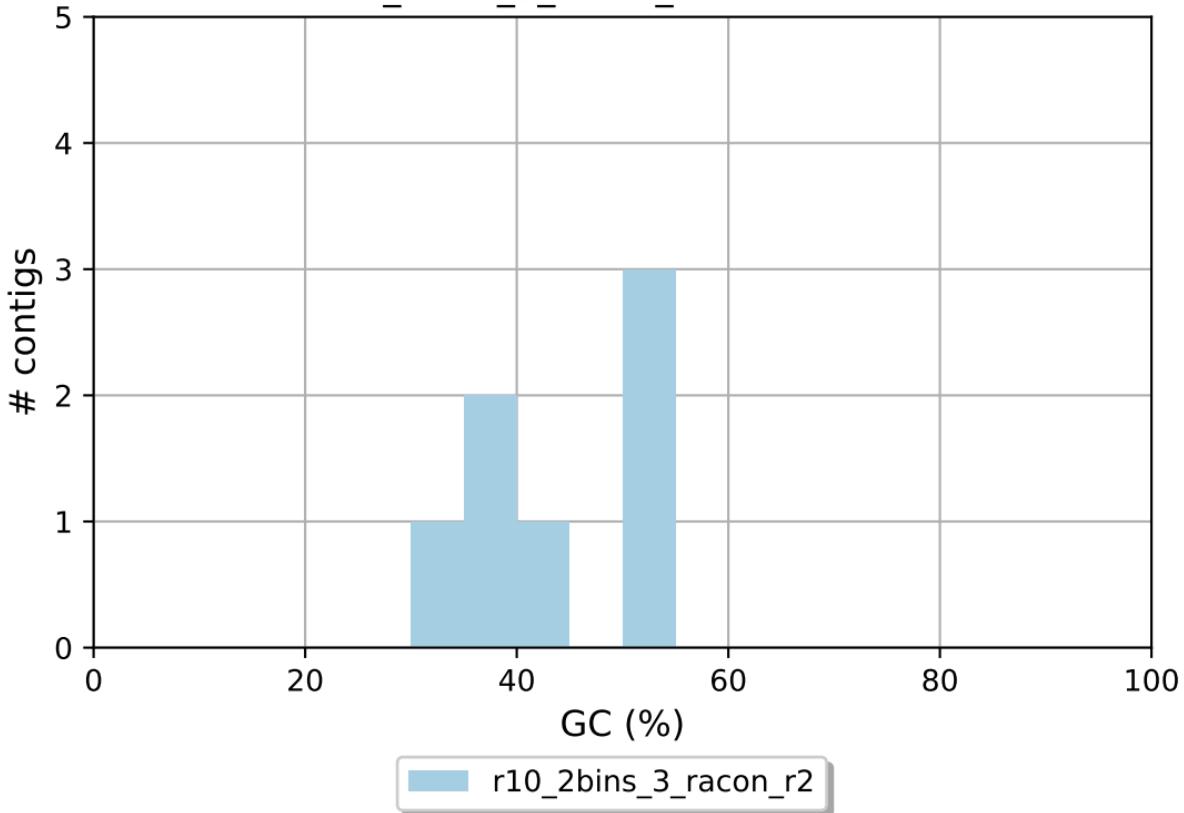
r10\_2bins\_3\_r2\_medaka GC content



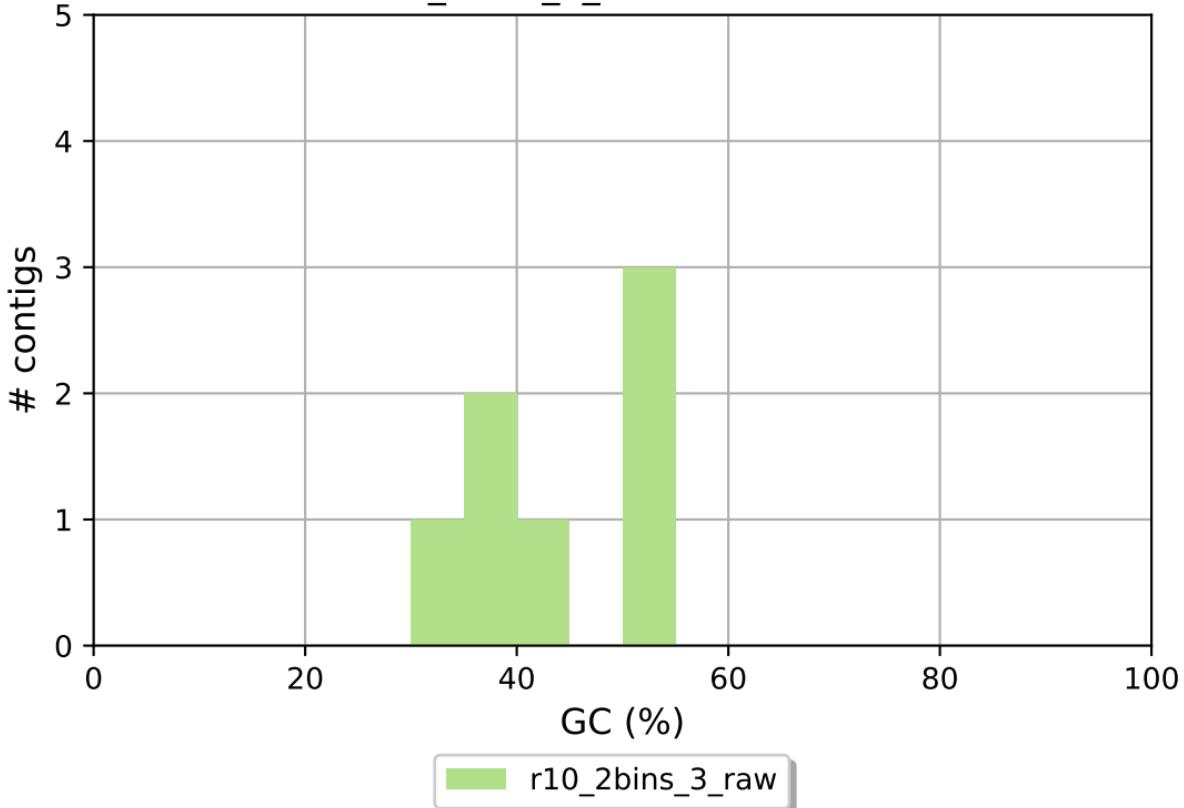
r10\_2bins\_3\_racon\_r1 GC content



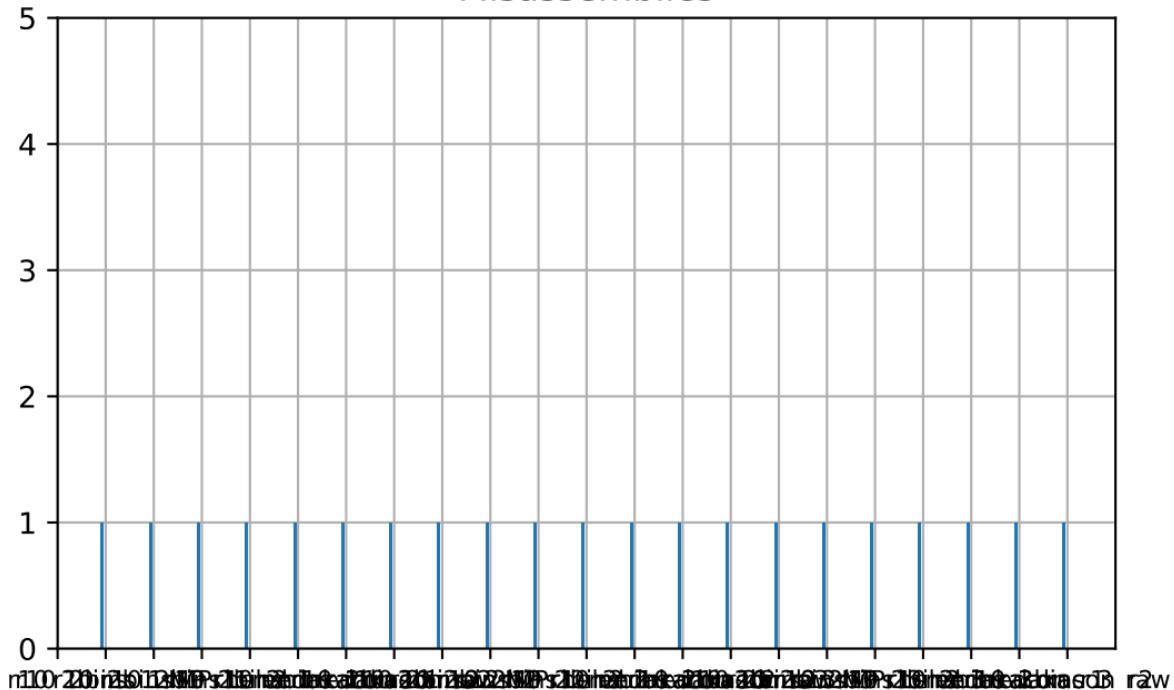
r10\_2bins\_3\_racon\_r2 GC content



r10\_2bins\_3\_raw GC content

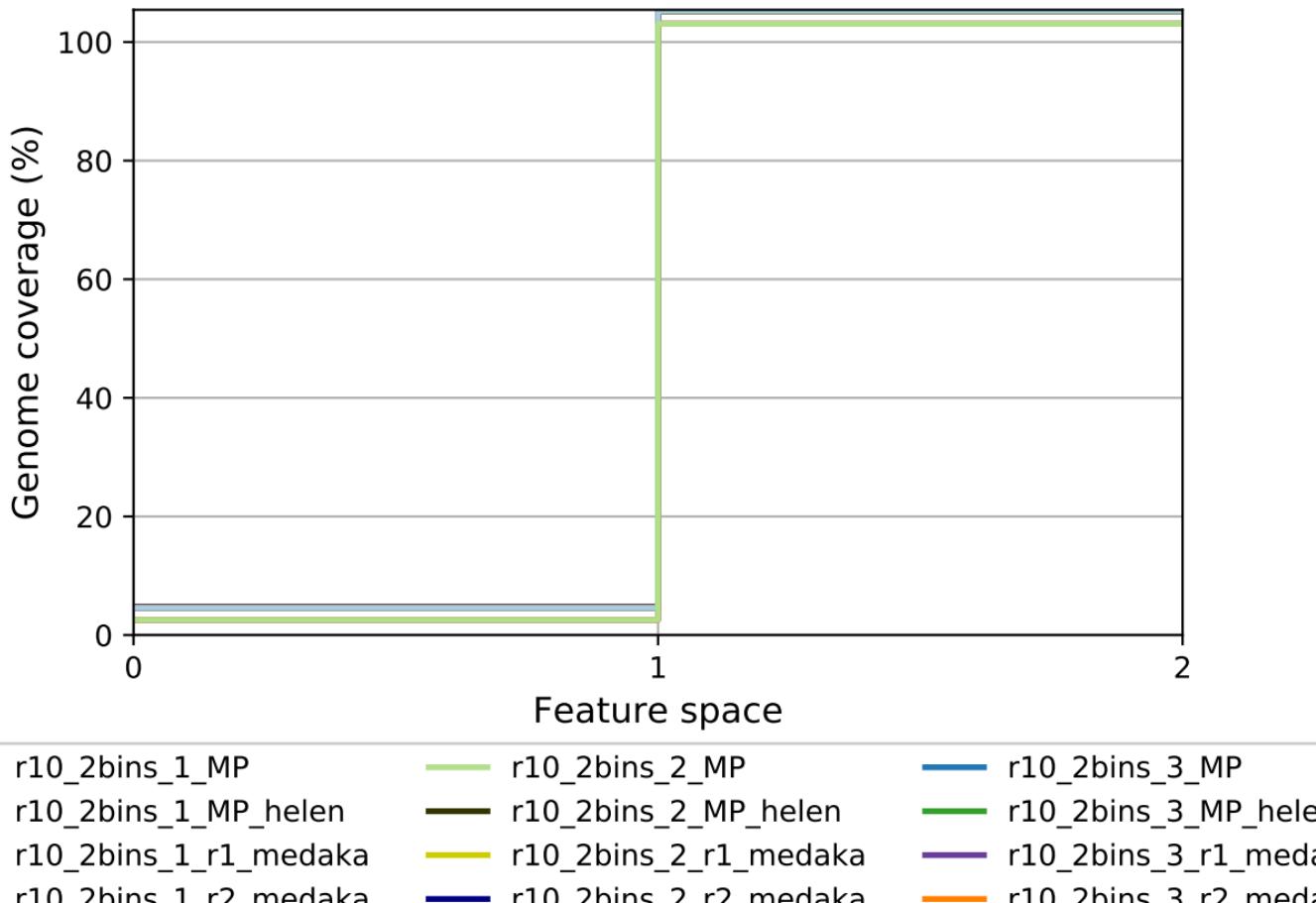


## Misassemblies

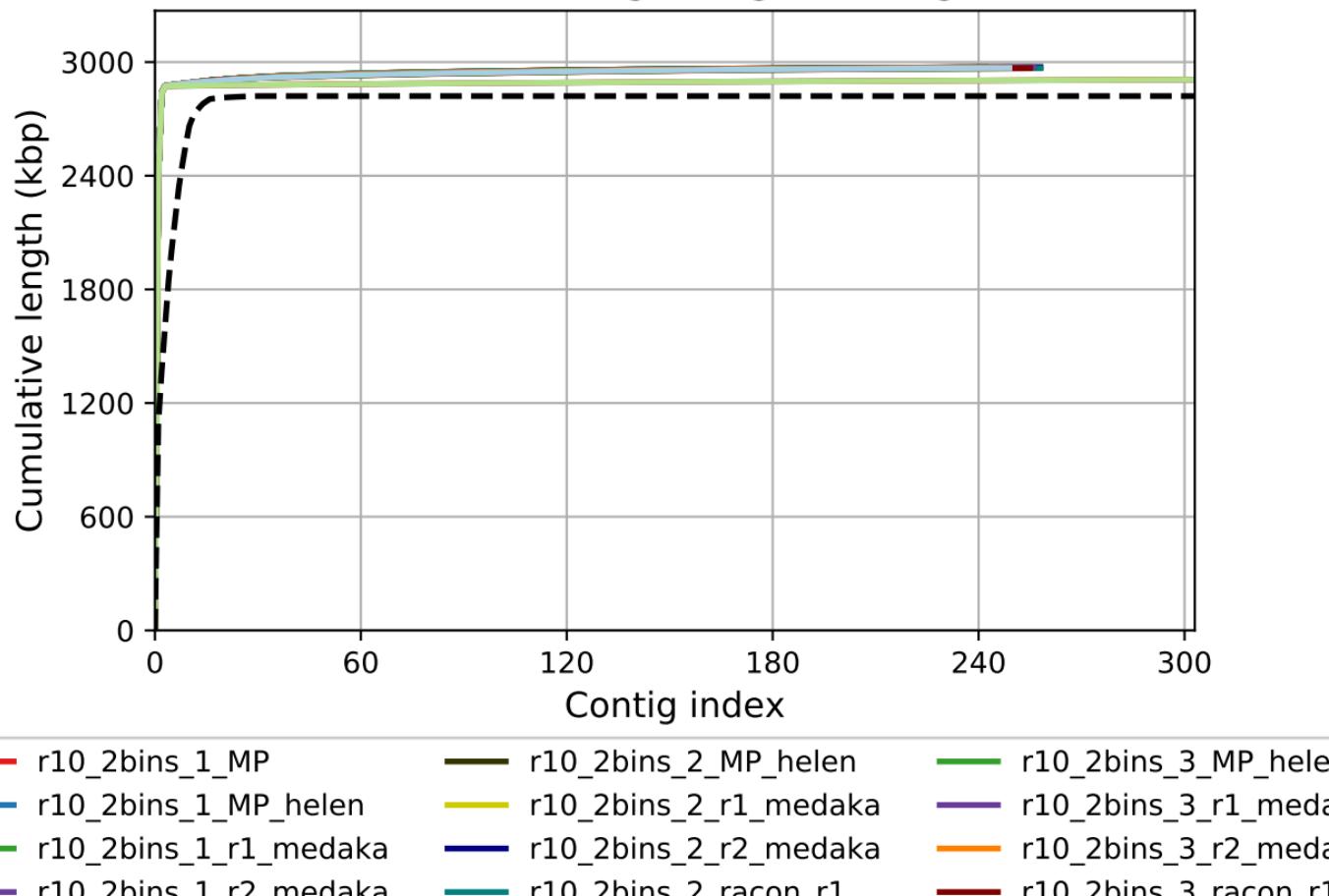


# translocations

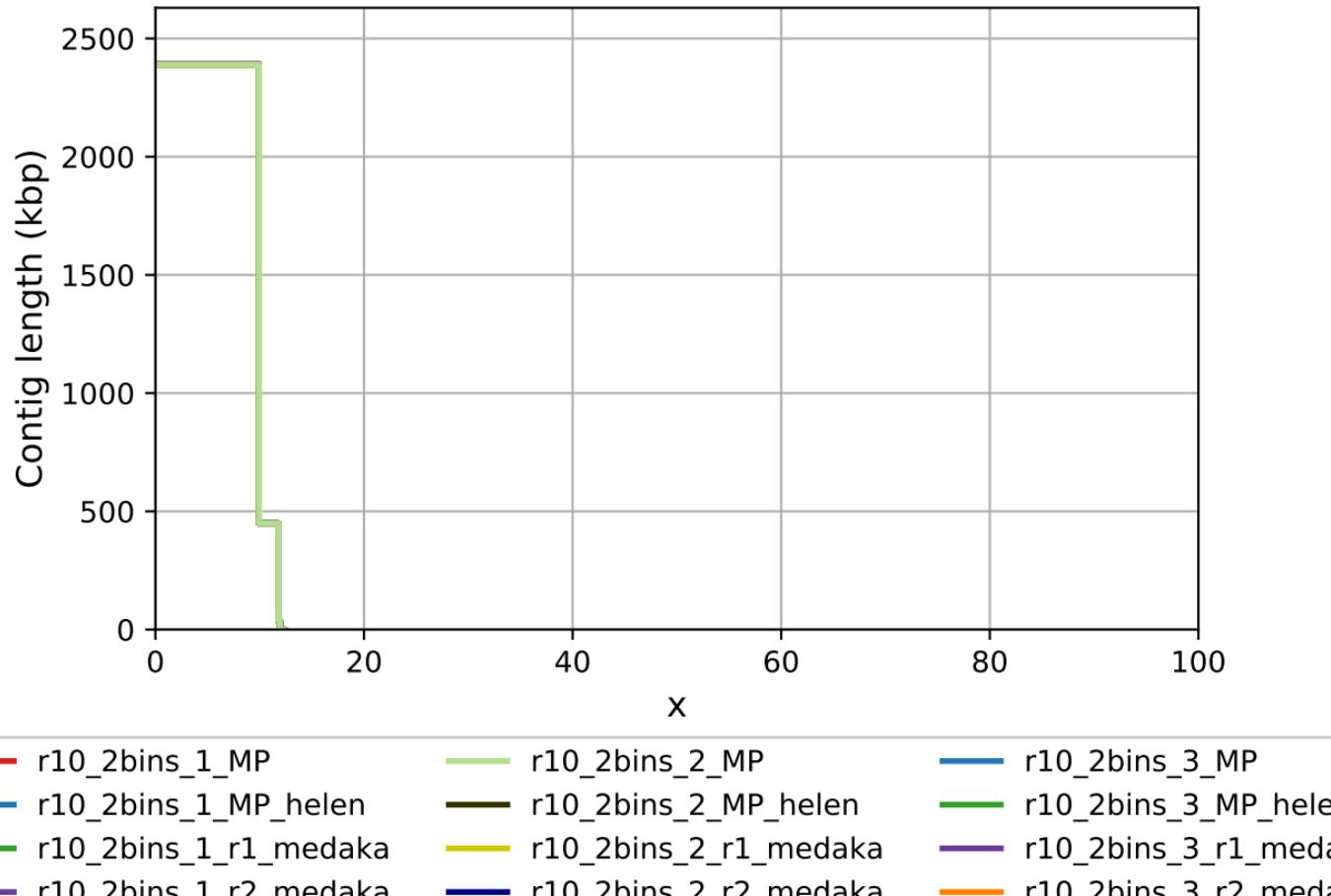
### FRCurve (misassemblies)



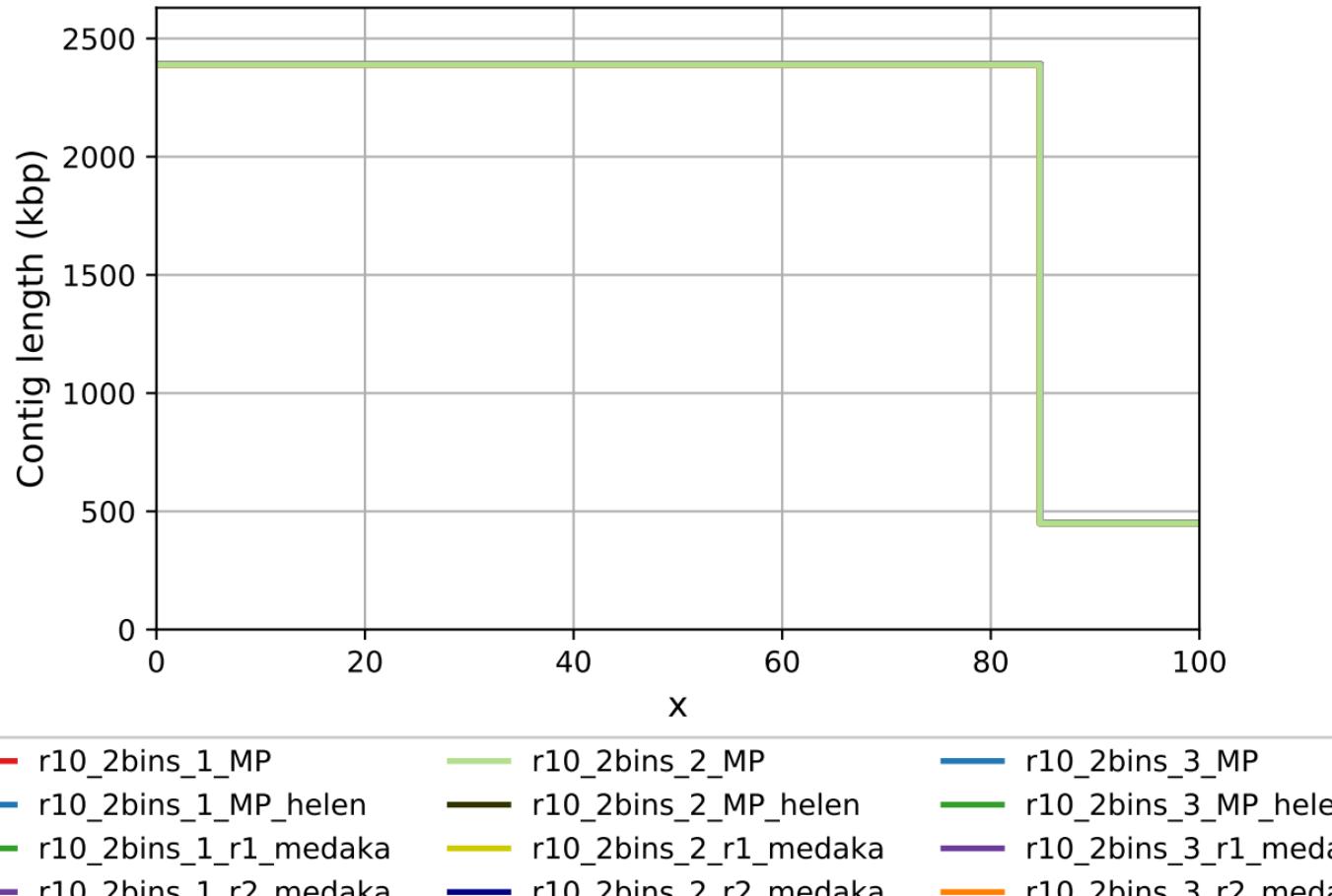
### Cumulative length (aligned contigs)



NAx



# NGAx



### Genome fraction, %

