

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

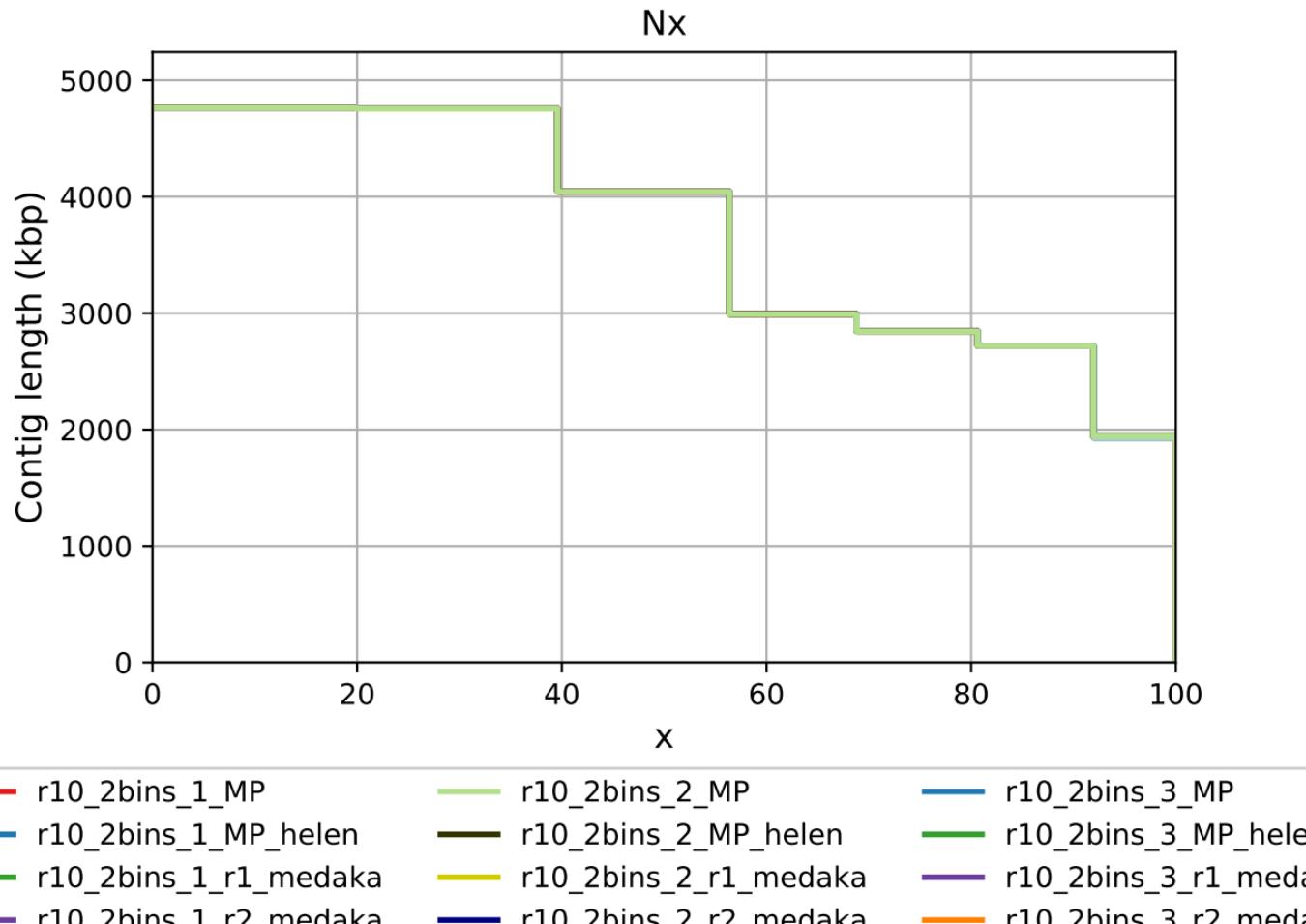
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw		
# misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	15	13	13	13	13	13	15		
# contig misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	15	13	13	13	13	13	15		
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# c. translocations	13	13	13	13	13	13	14	13	13	13	13	13	15	13	13	13	13	13	15		
# 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	2719957	2718112	2719591	2719604	2720370	2720447	2718870	2719959	2718085	2719577	2719610	2720473	2720445	2718867	2719961	2718084	2719576	2719620	2720476	2720441	2718867
# 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	10	10	10	10	10	10	10	18	10	10	10	10	20	10	10	10	10	10	10	20	
# local misassemblies	9	9	9	9	9	10	9	19	9	10	9	9	9	9	9	9	9	10	9	19	
# 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	26	26	26	26	26	26	26	22	26	26	26	26	26	26	26	26	26	26	26	21	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	4	
# mismatches	7726	6871	7795	7806	7435	7920	6776	7757	6892	7645	7688	7588	8038	6841	7752	6889	7634	7749	7727	8037	6828
# indels	2989	1115	2051	2065	2934	2942	4413	3012	1123	2061	2076	2989	2978	4444	3005	1113	2057	2067	3007	2948	4441
# indels (<= 5 bp)	2926	1057	2000	2014	2881	2890	4358	2949	1063	2010	2025	2937	2927	4389	2941	1052	2006	2015	2955	2895	4386
# indels (> 5 bp)	63	58	51	51	53	52	55	63	60	51	51	55	64	61	51	52	53	55	55	55	
Indels length	6767	4779	5365	5395	6654	6631	8482	6791	4812	5404	5425	6769	6670	8526	6787	4808	5400	5422	6789	6652	8523

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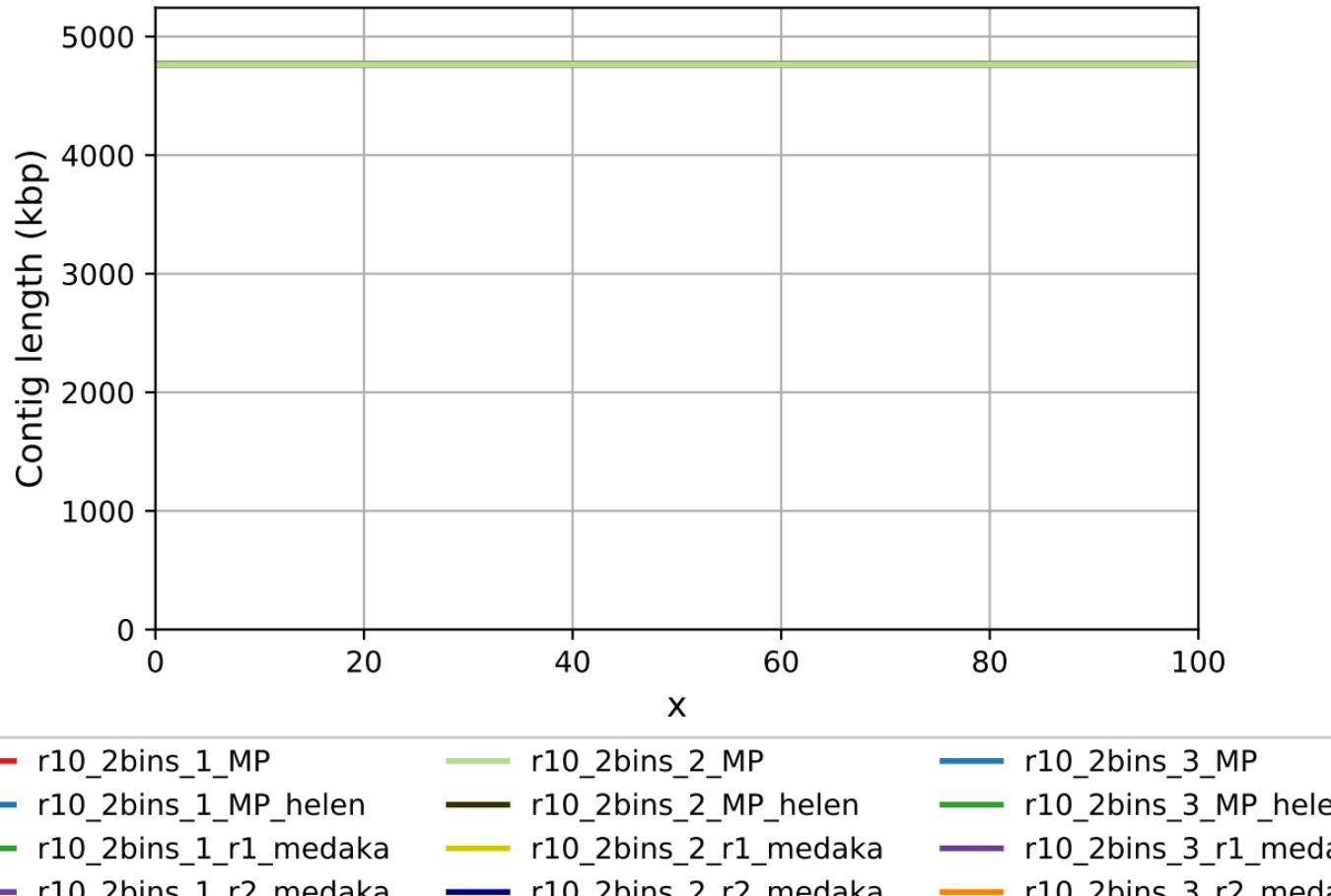
## Unaligned report

	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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21275494	21272822	21273068	21262531	21264862	21254585	21320528	21275005	21273170	21264831	21254957	21320663	21274902	21272670	21274358	21263748	21262681	21254198	21320562
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

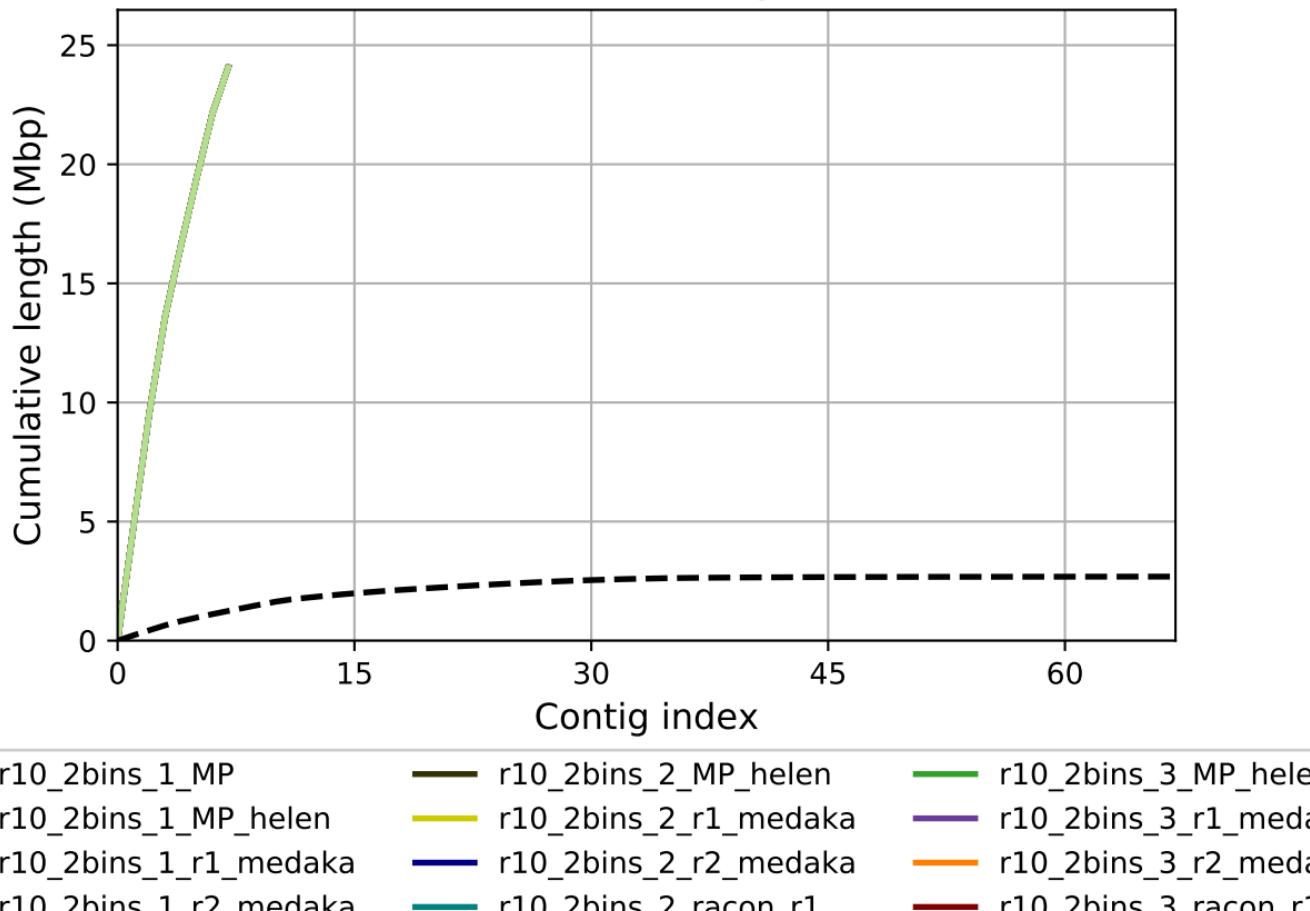
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted  
(e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



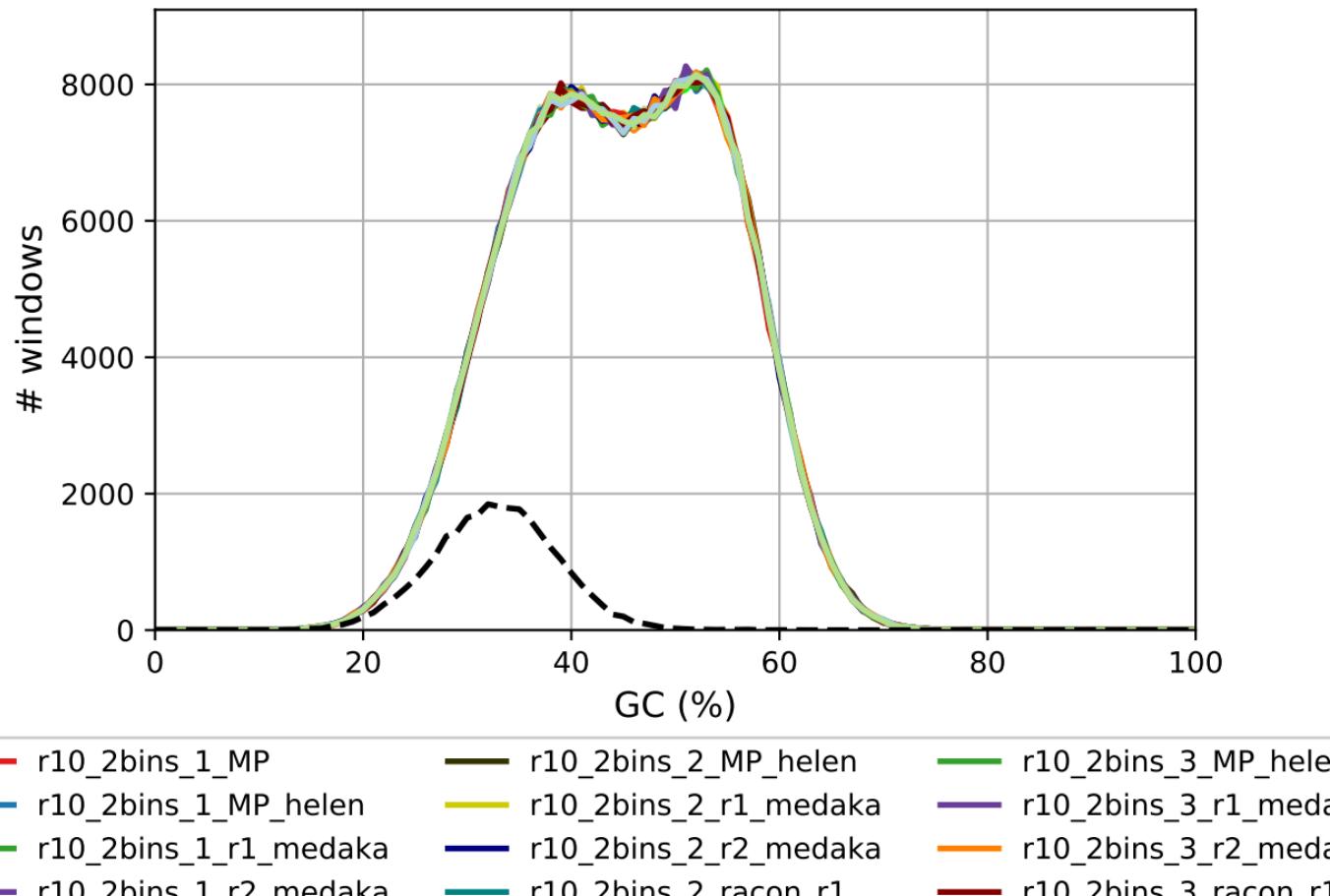
# NGx



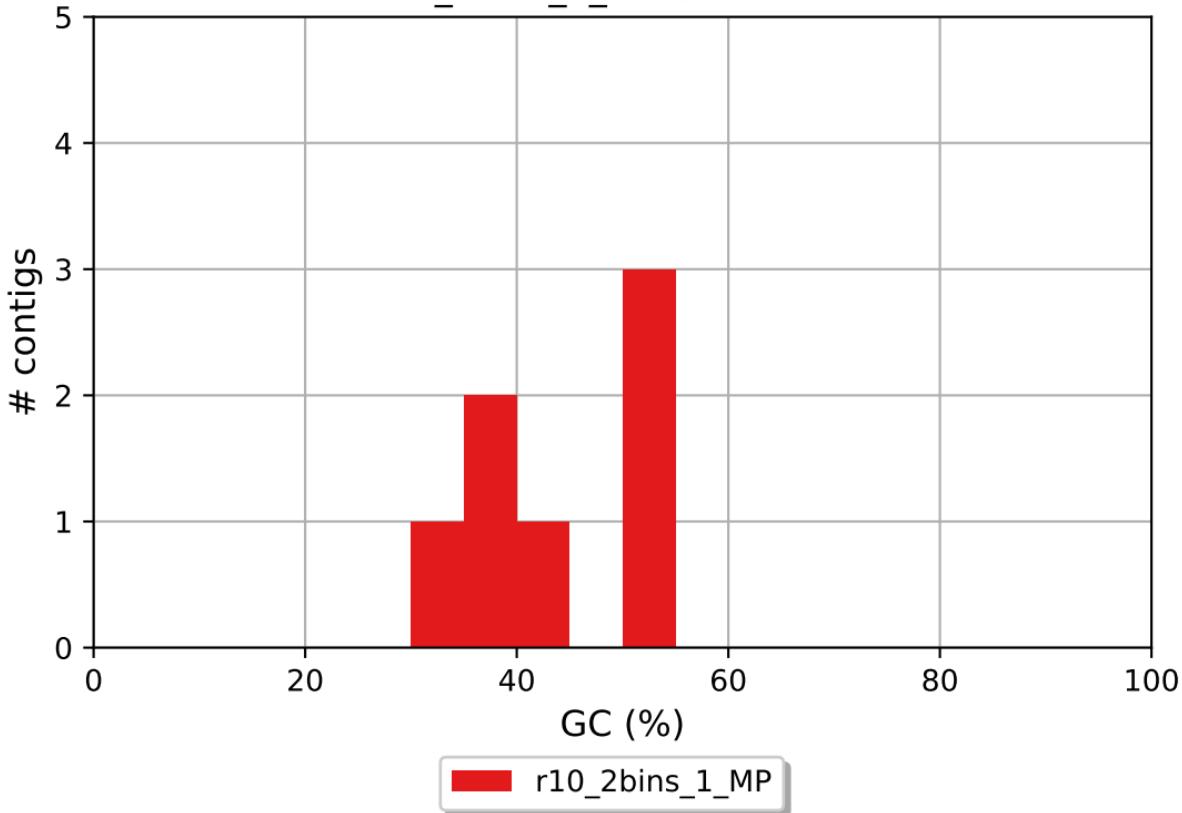
### Cumulative length



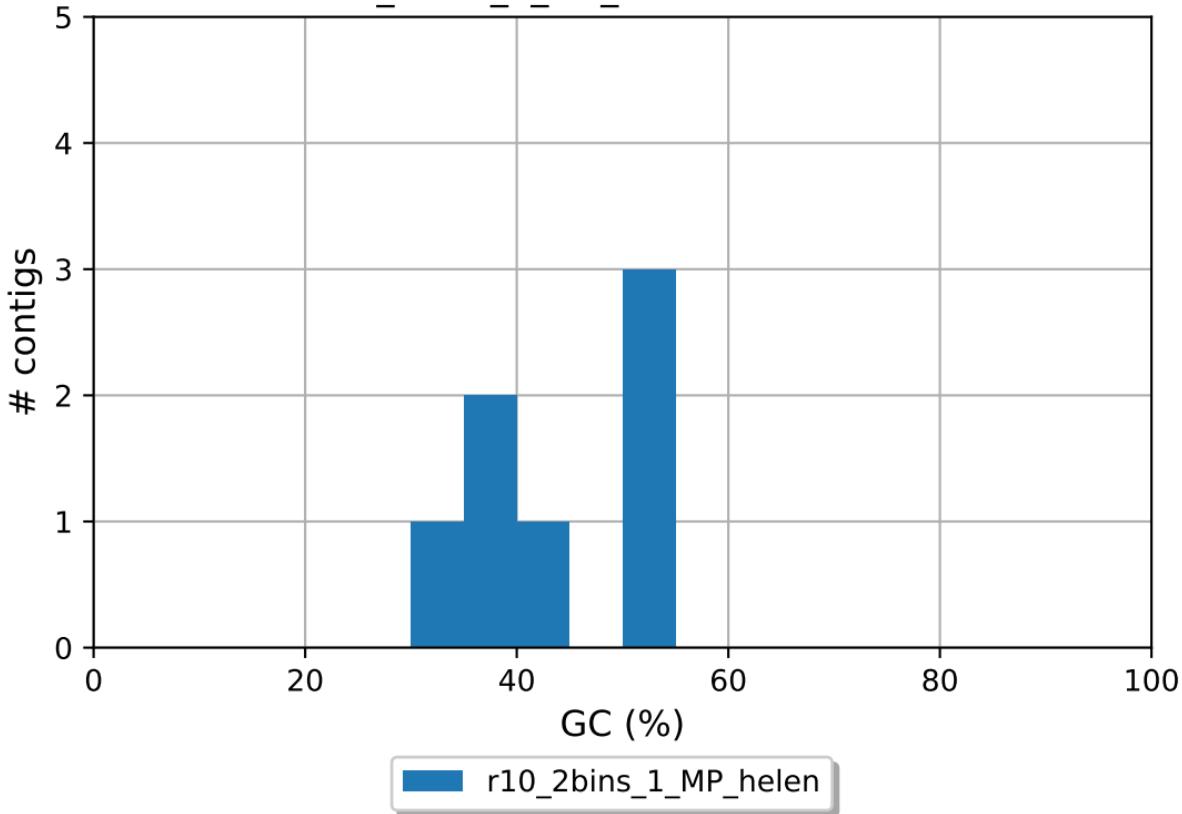
## GC content



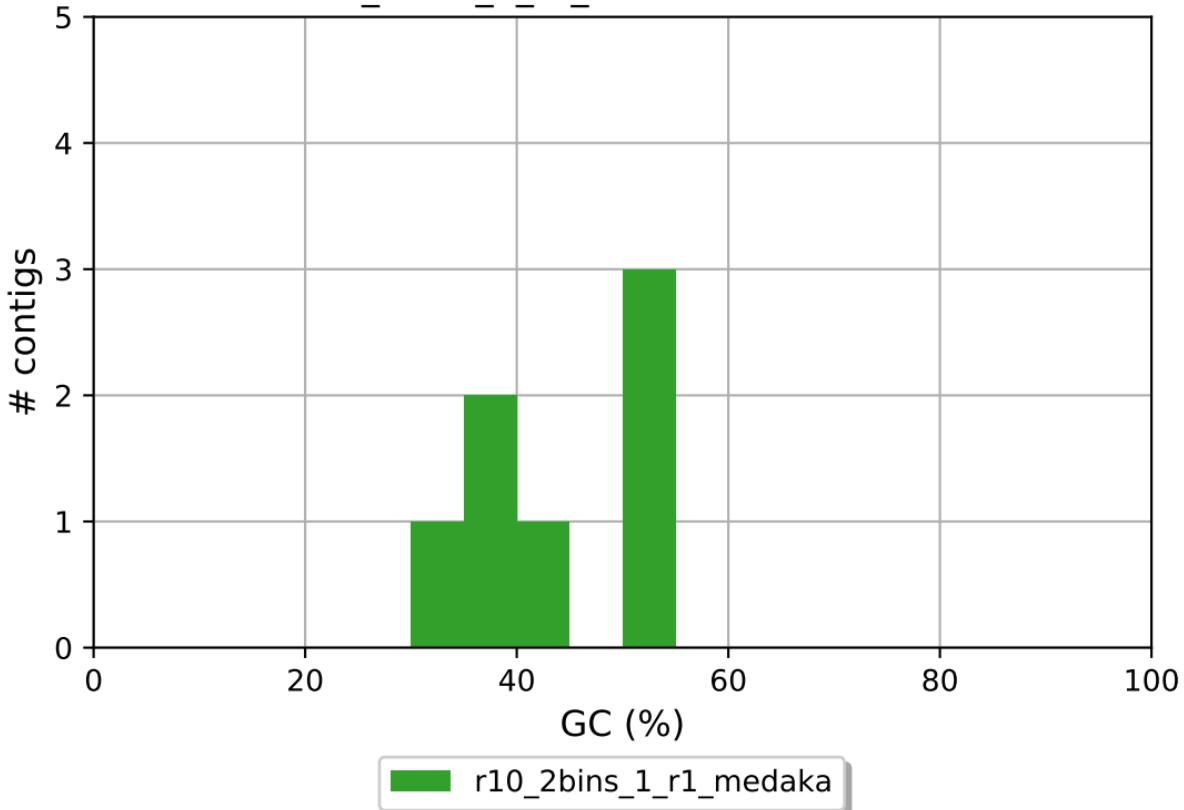
r10\_2bins\_1\_MP GC content



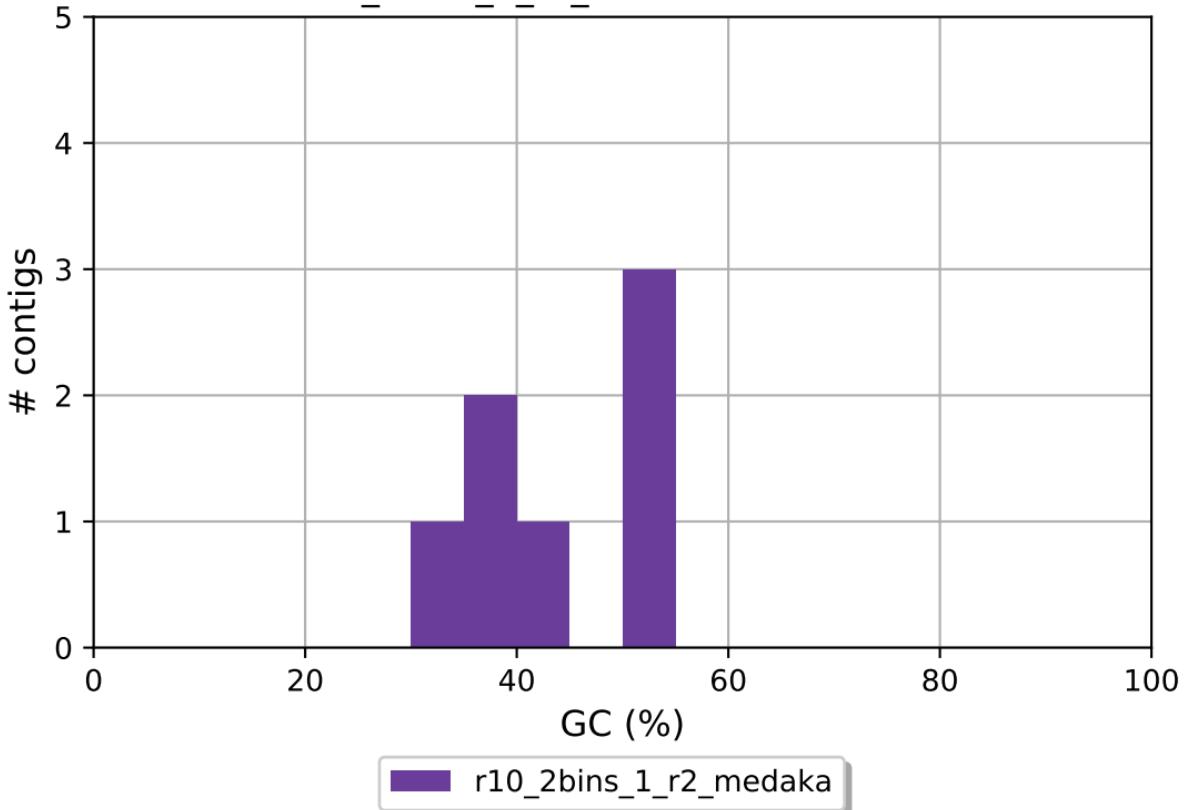
r10\_2bins\_1\_MP\_helen GC content



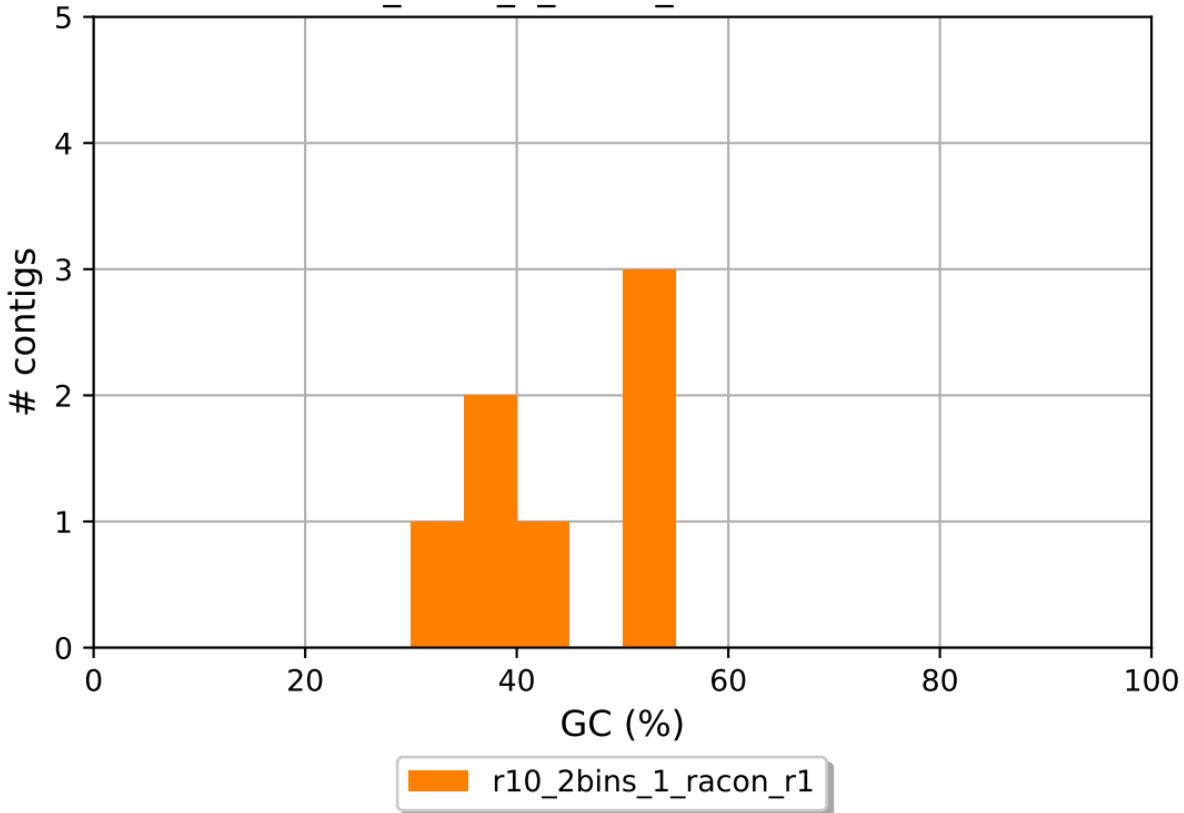
r10\_2bins\_1\_r1\_medaka GC content



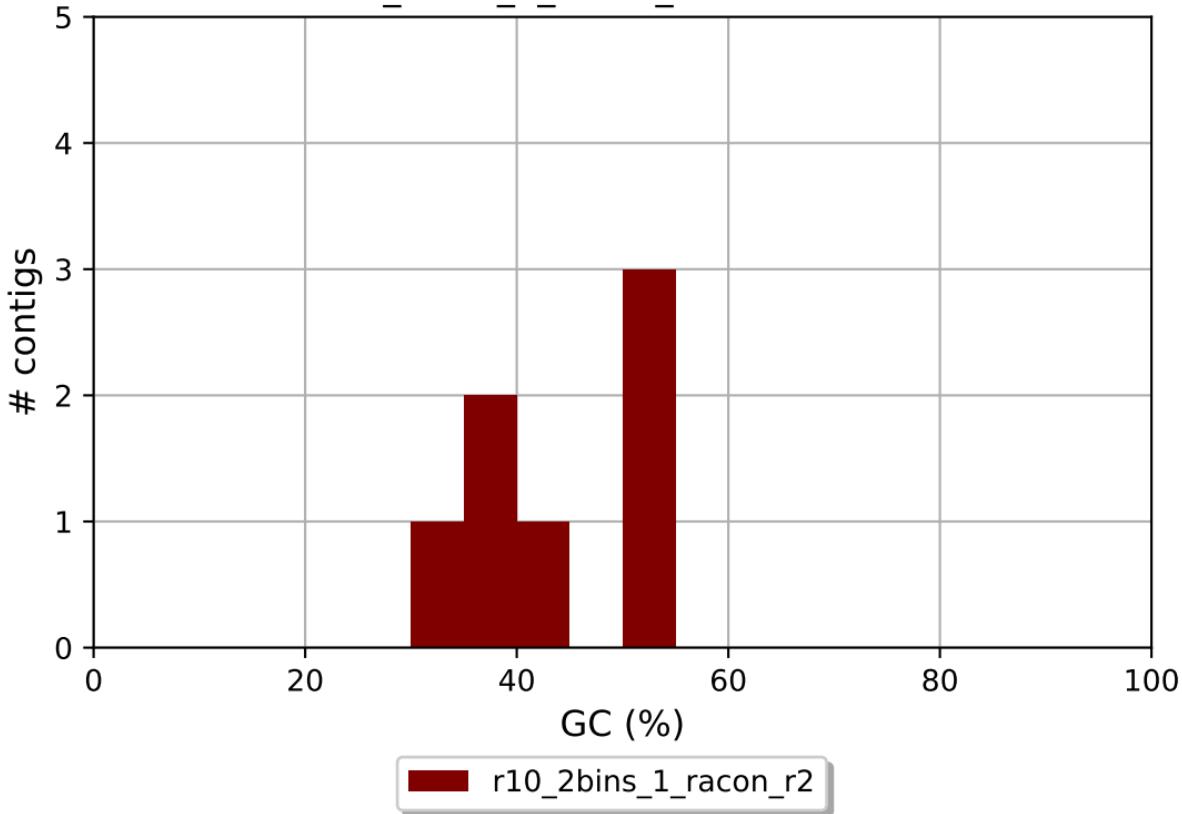
r10\_2bins\_1\_r2\_medaka GC content



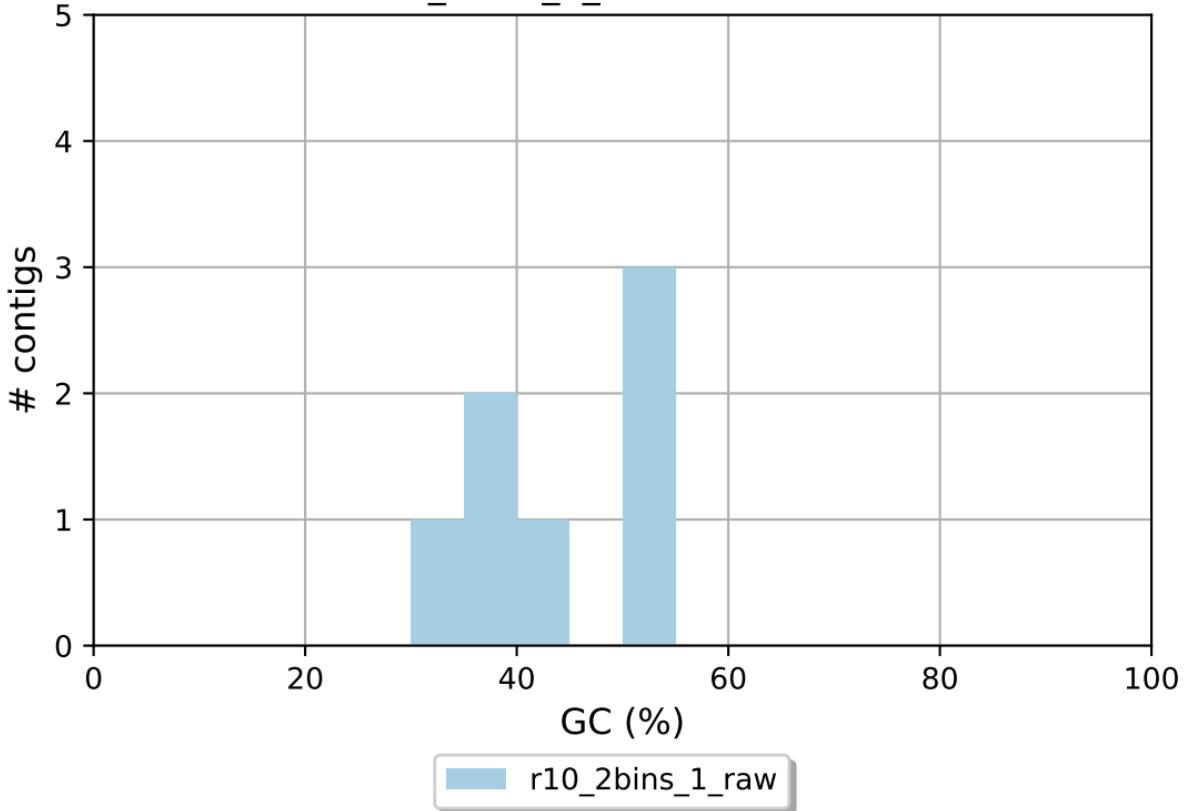
r10\_2bins\_1\_racon\_r1 GC content



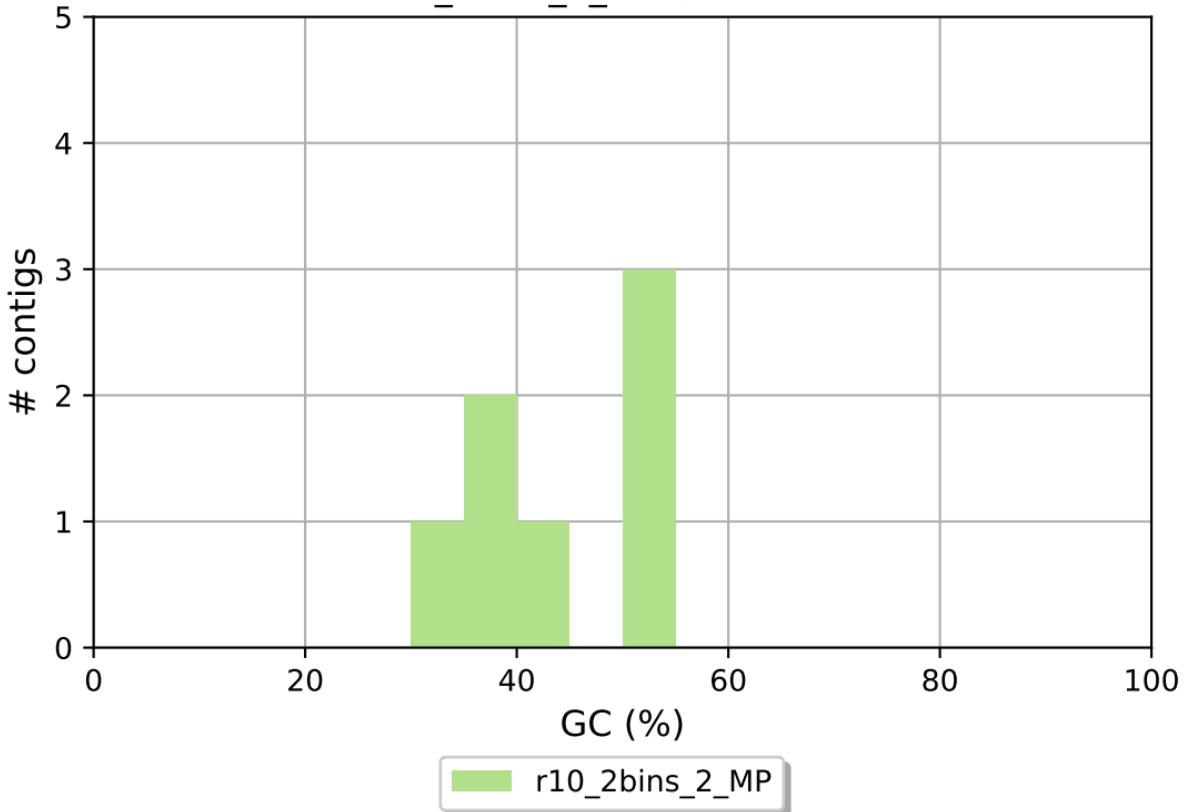
r10\_2bins\_1\_racon\_r2 GC content



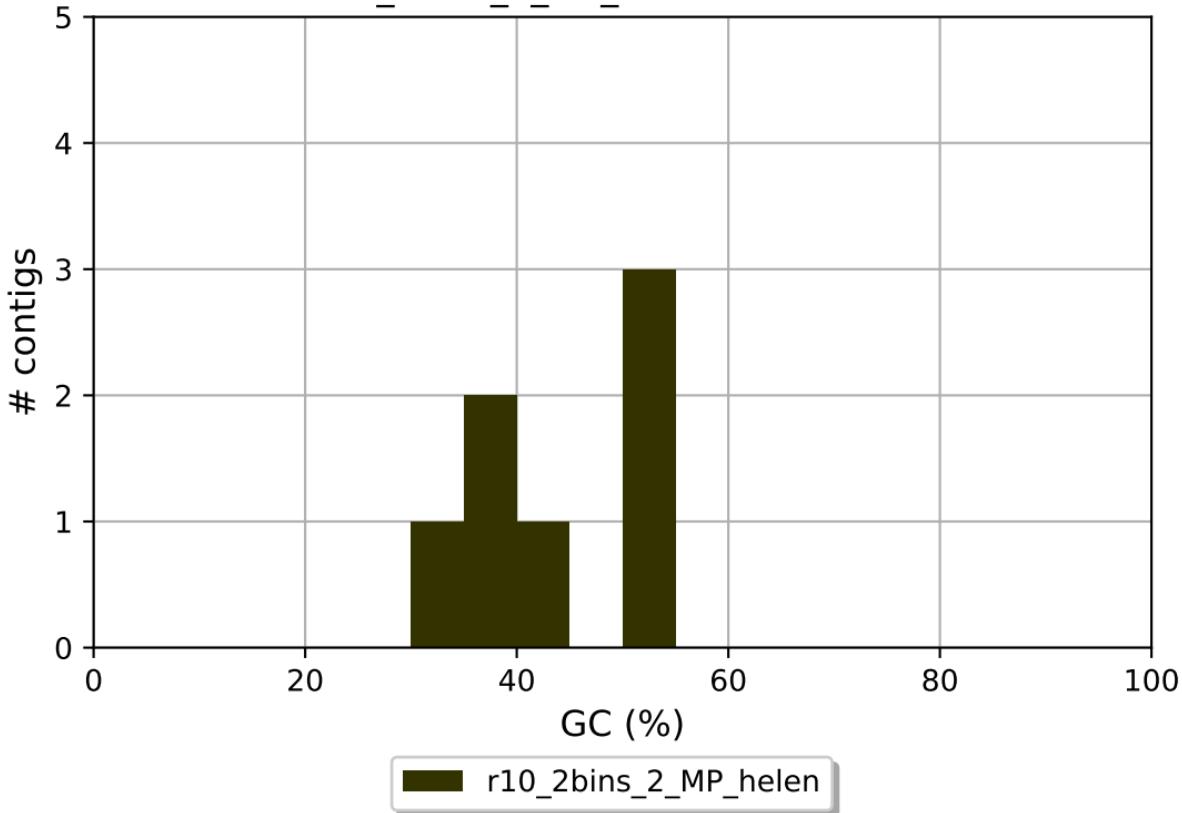
r10\_2bins\_1\_raw GC content



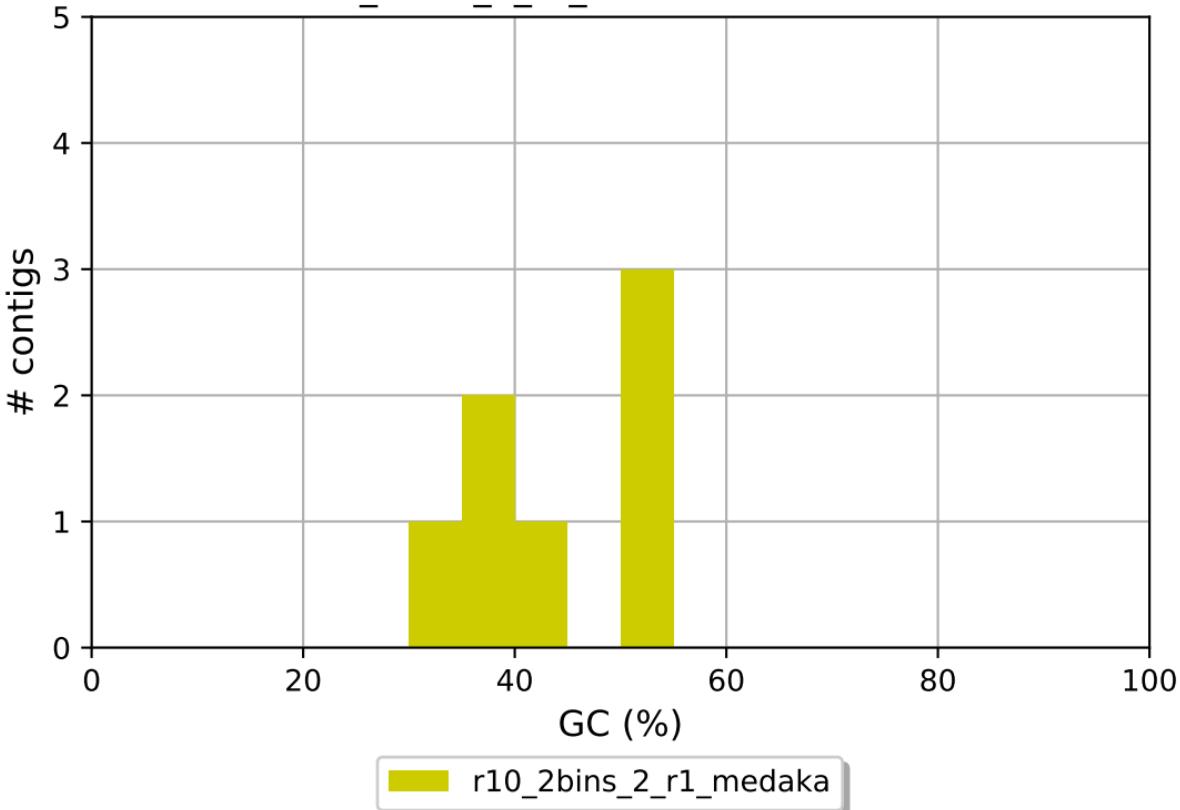
r10\_2bins\_2\_MP GC content



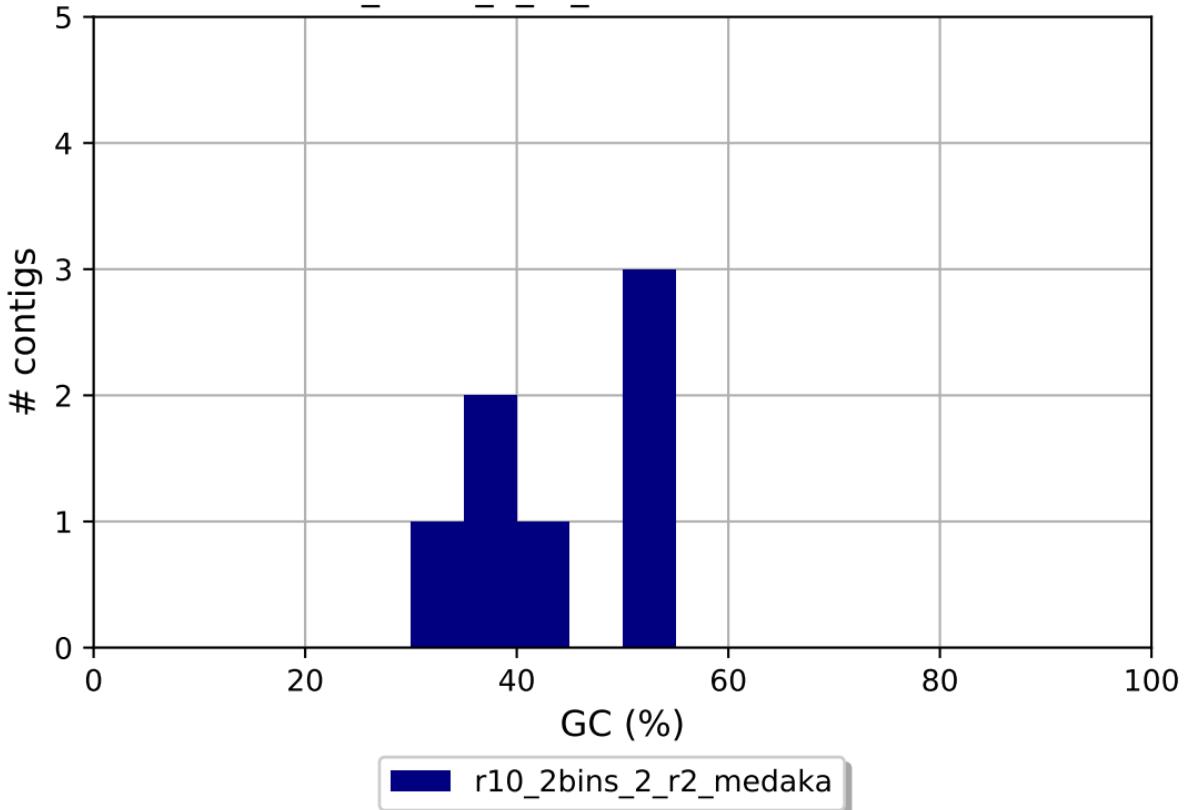
r10\_2bins\_2\_MP\_helen GC content



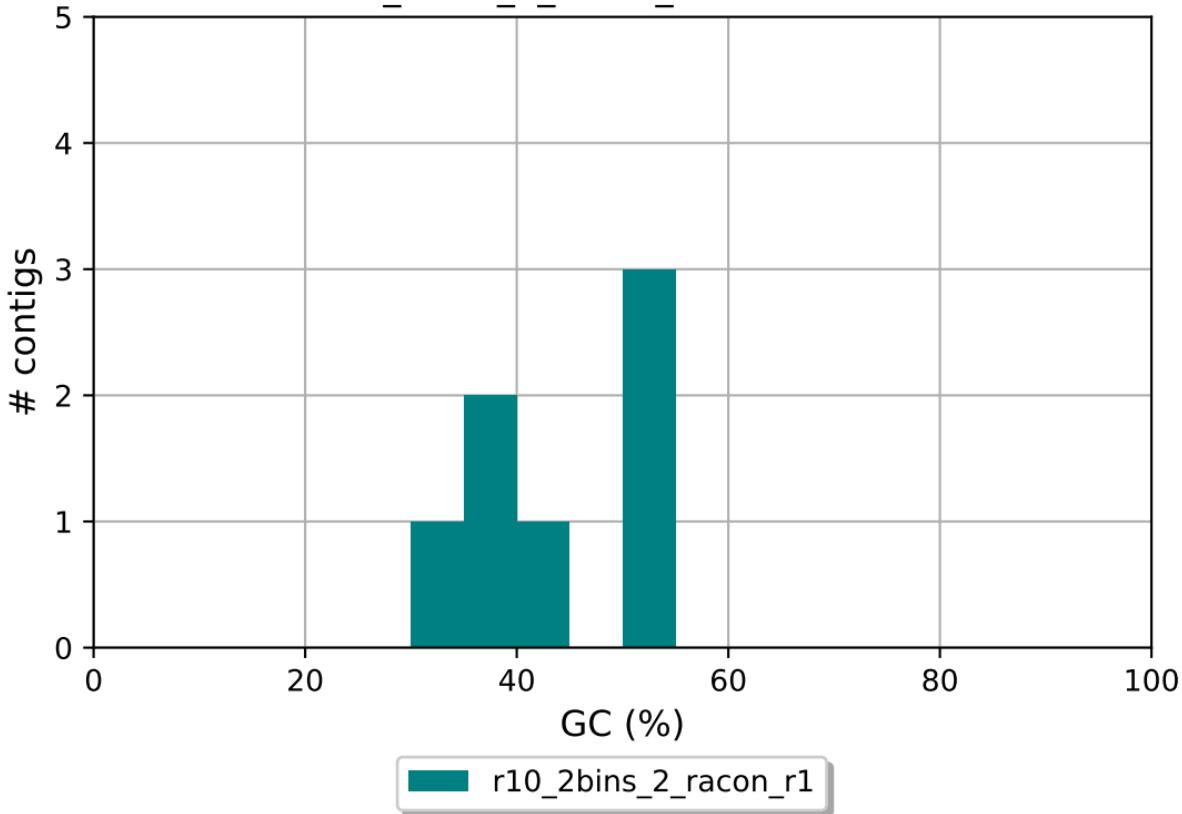
r10\_2bins\_2\_r1\_medaka GC content



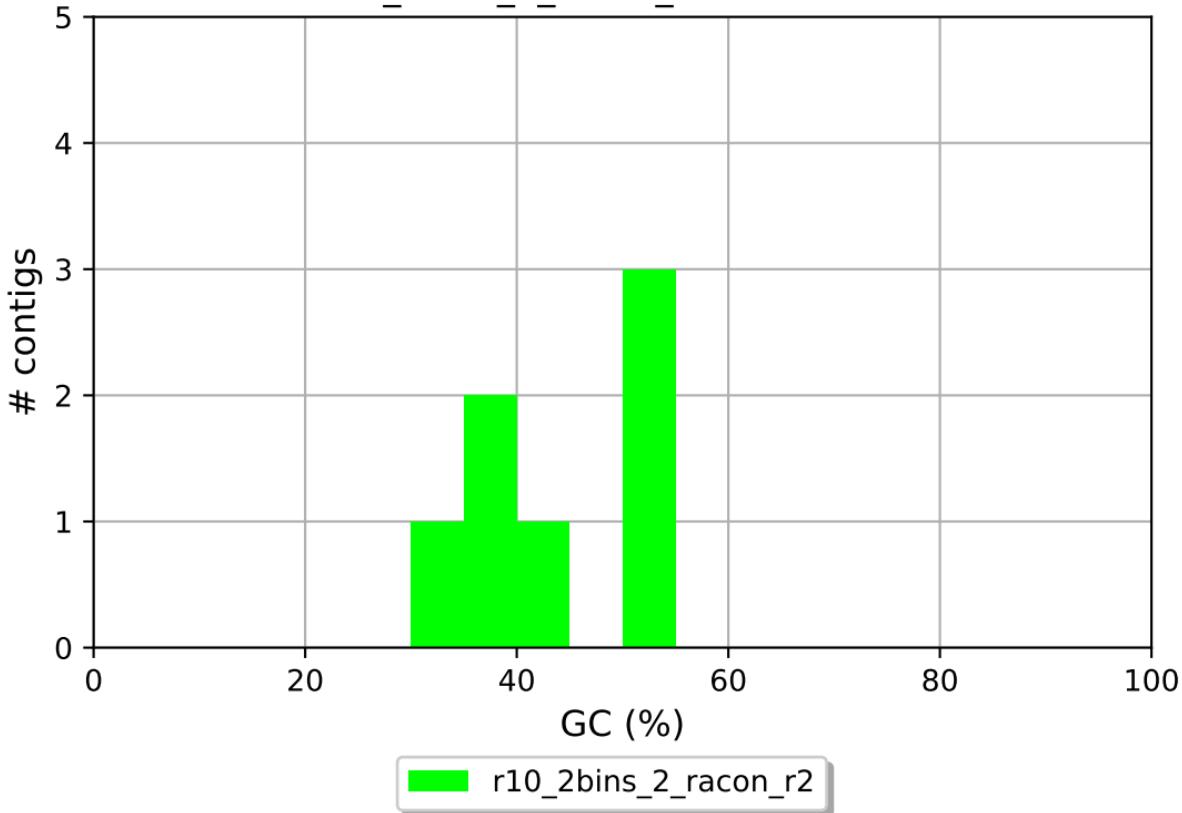
r10\_2bins\_2\_r2\_medaka GC content



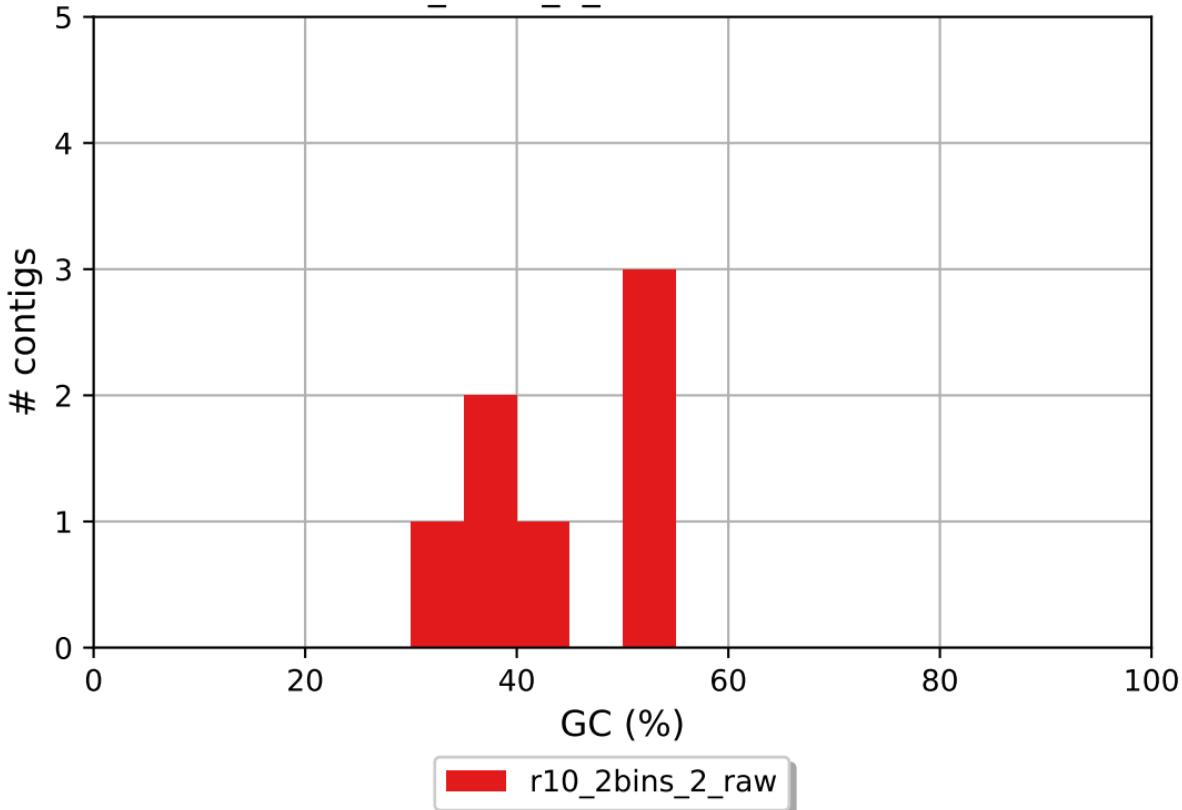
r10\_2bins\_2\_racon\_r1 GC content



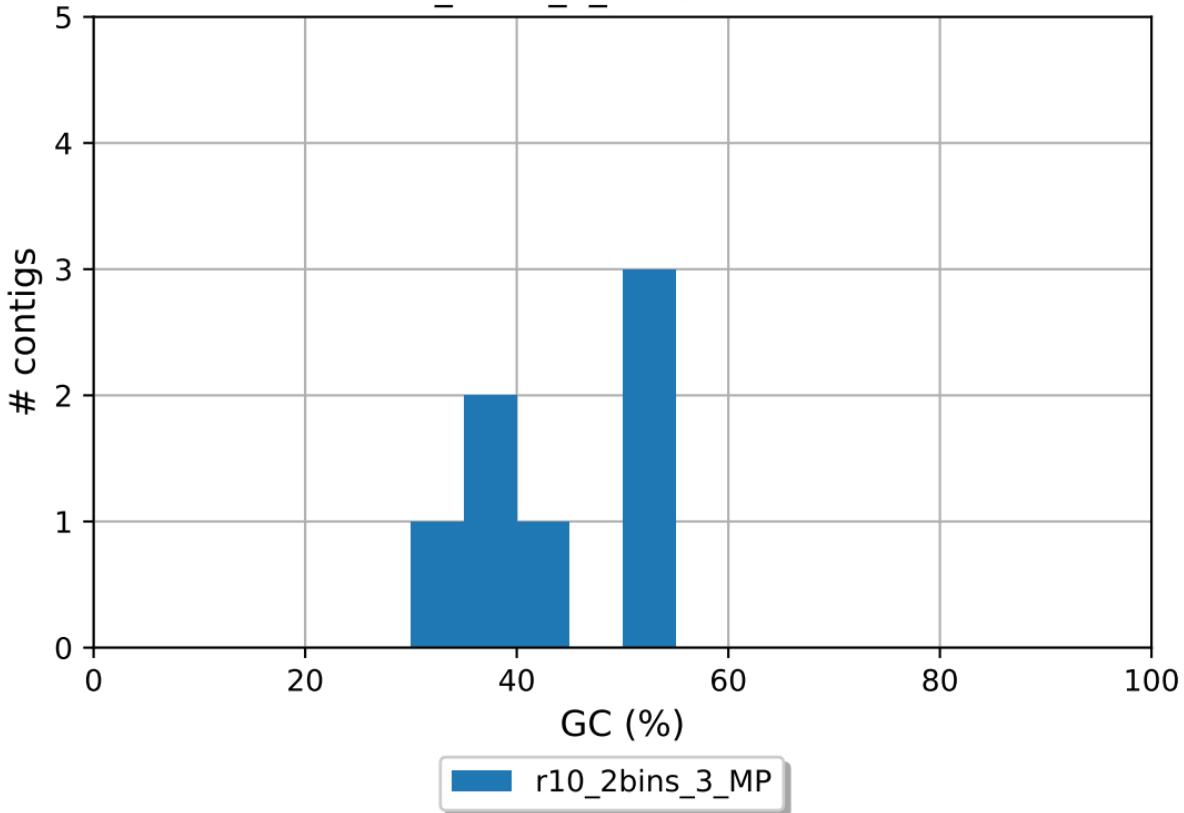
r10\_2bins\_2\_racon\_r2 GC content



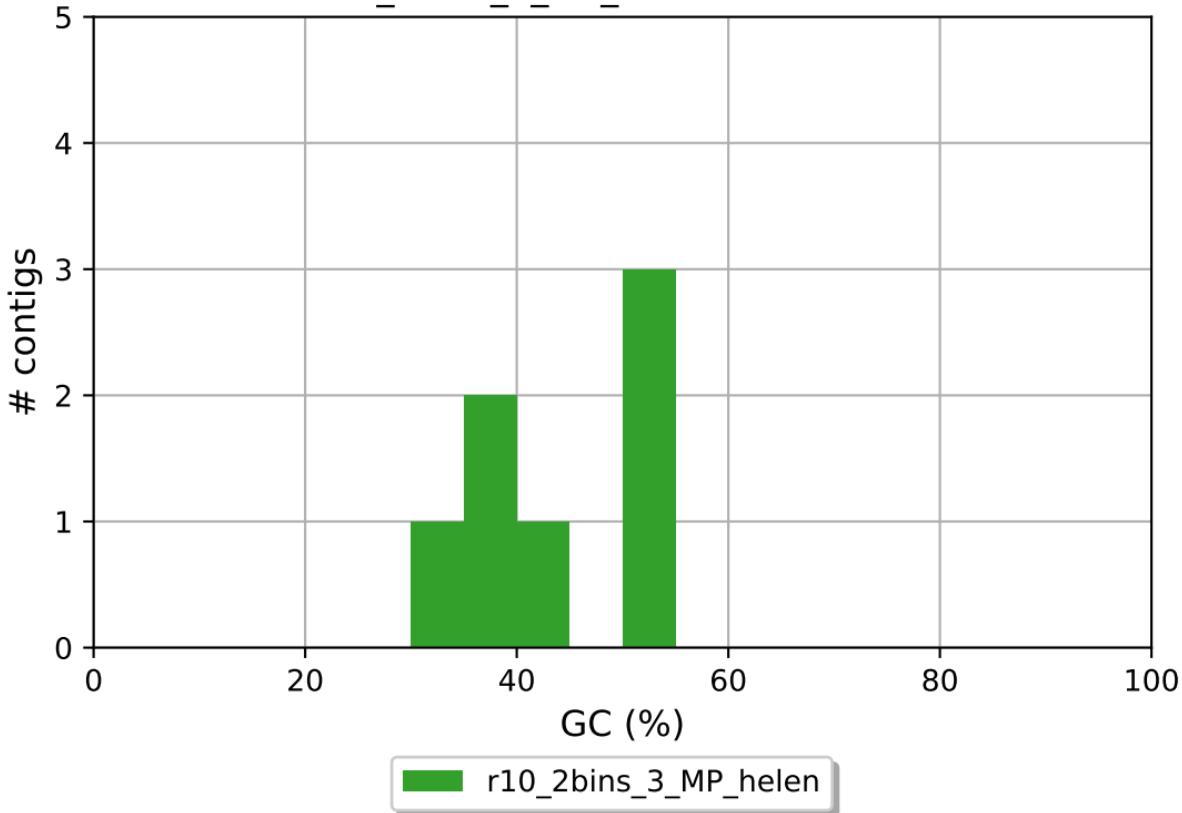
r10\_2bins\_2\_raw GC content



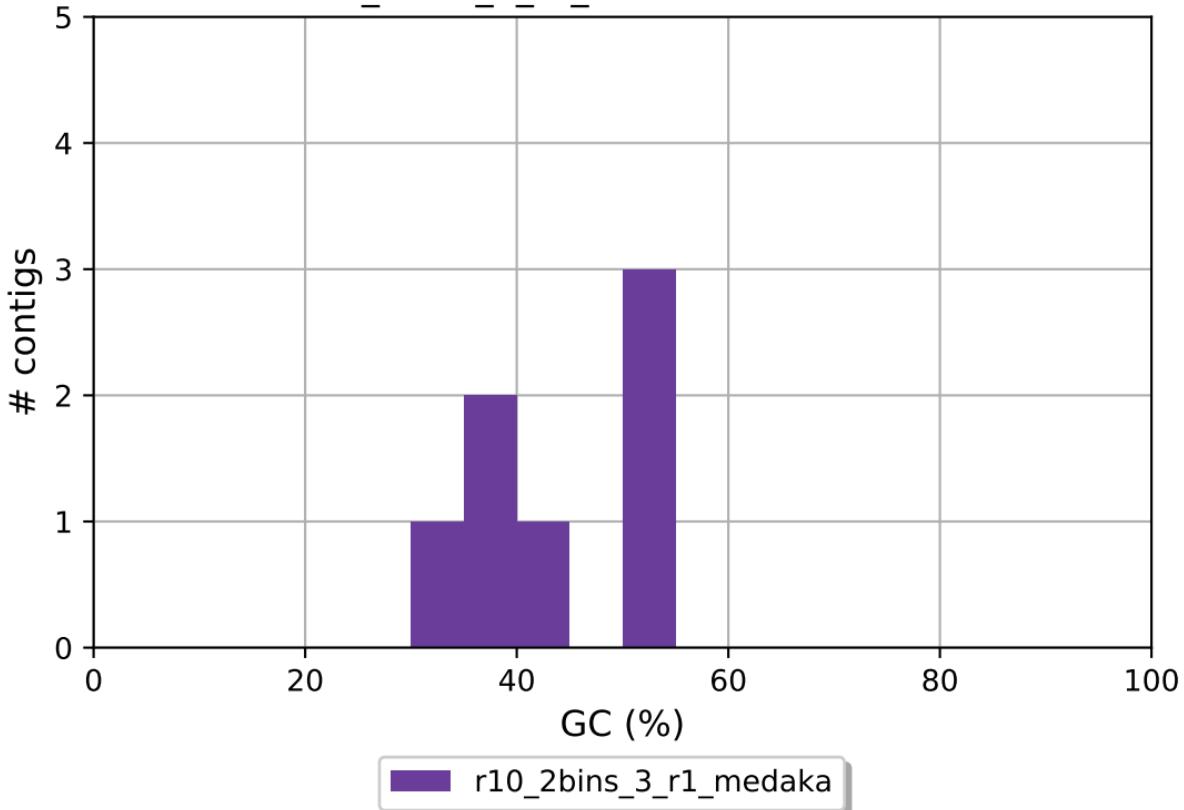
r10\_2bins\_3\_MP GC content



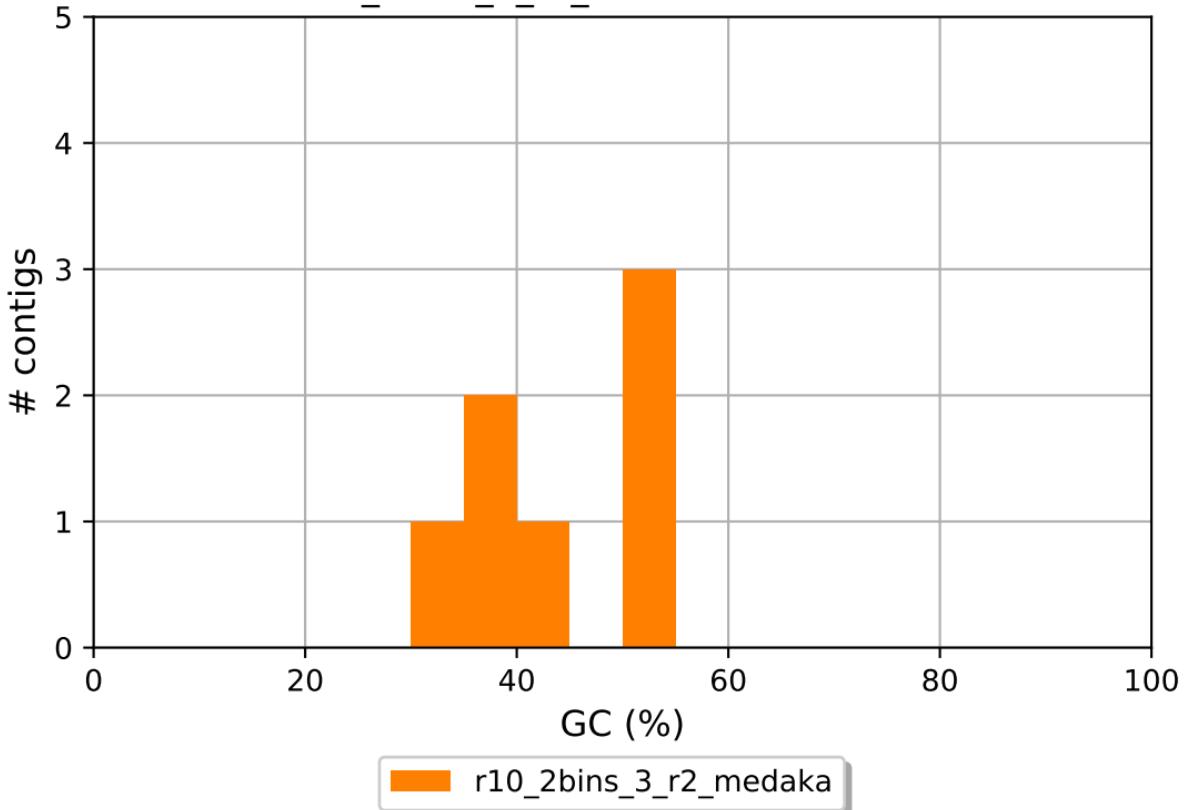
r10\_2bins\_3\_MP\_helen GC content



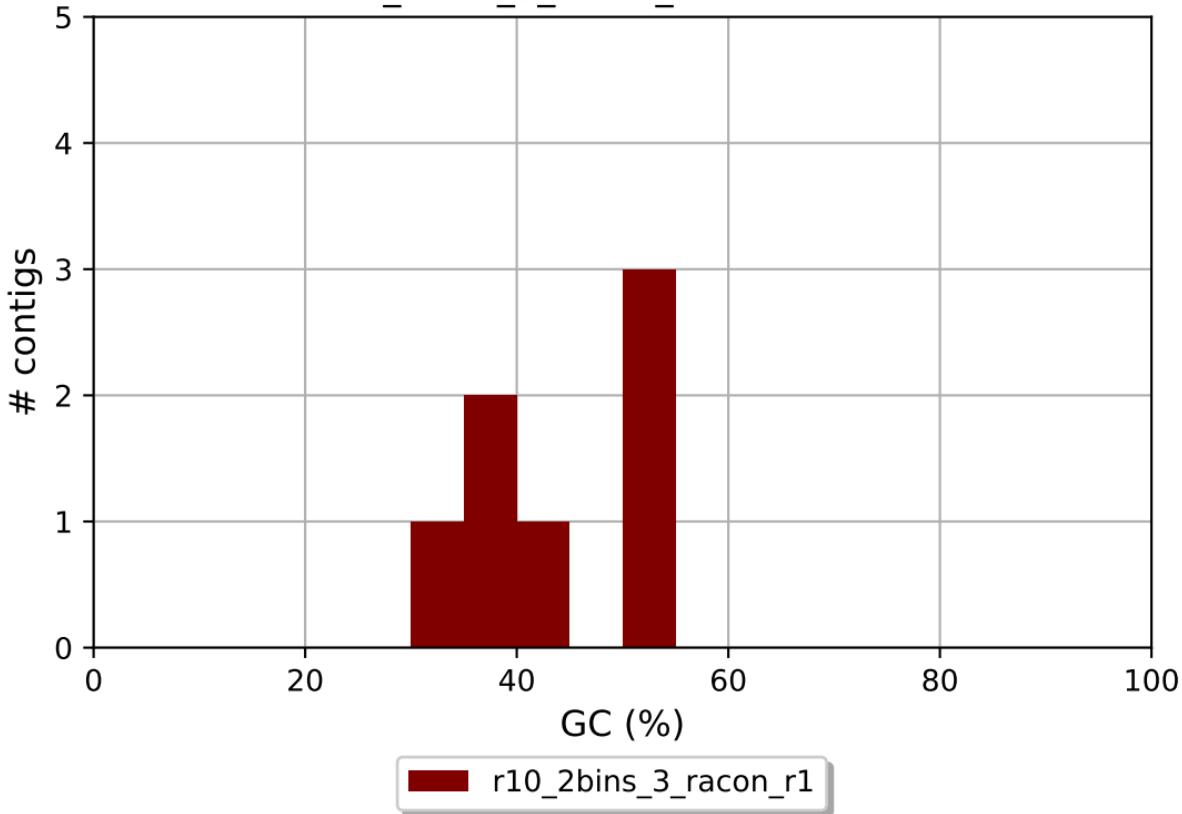
r10\_2bins\_3\_r1\_medaka GC content



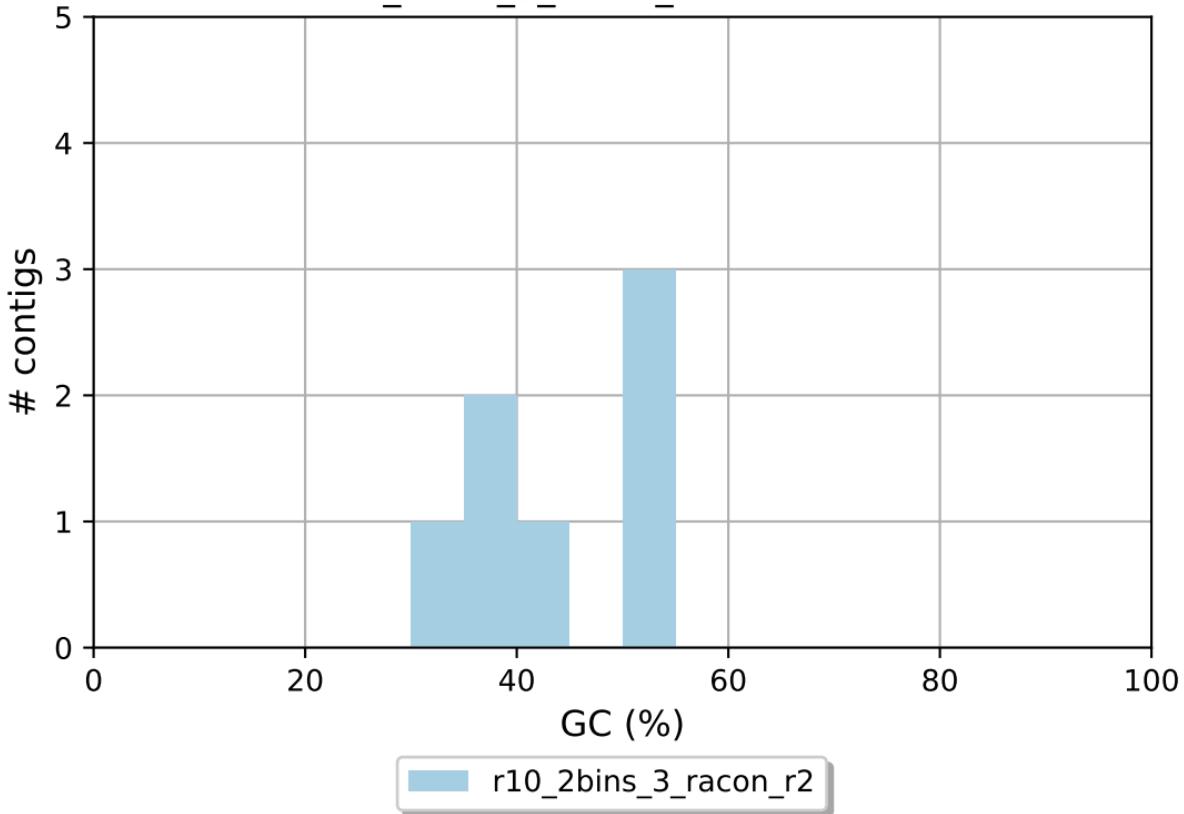
r10\_2bins\_3\_r2\_medaka GC content



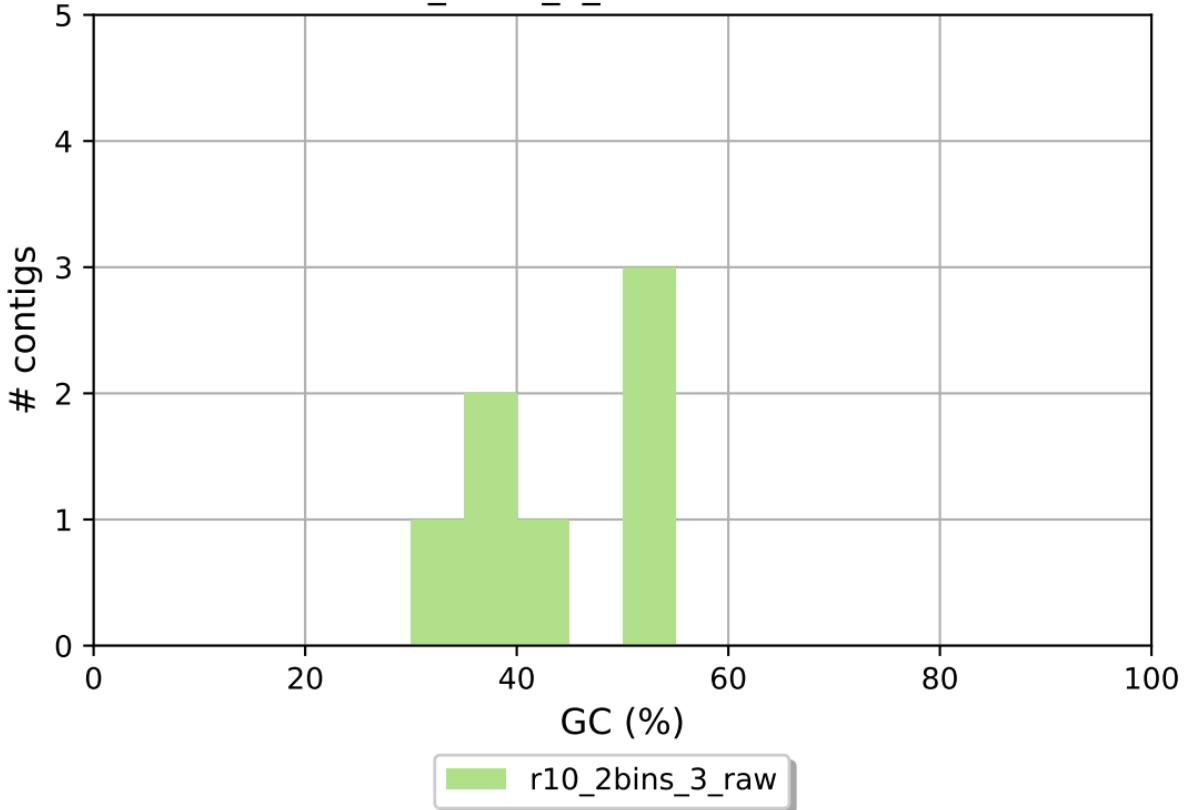
r10\_2bins\_3\_racon\_r1 GC content



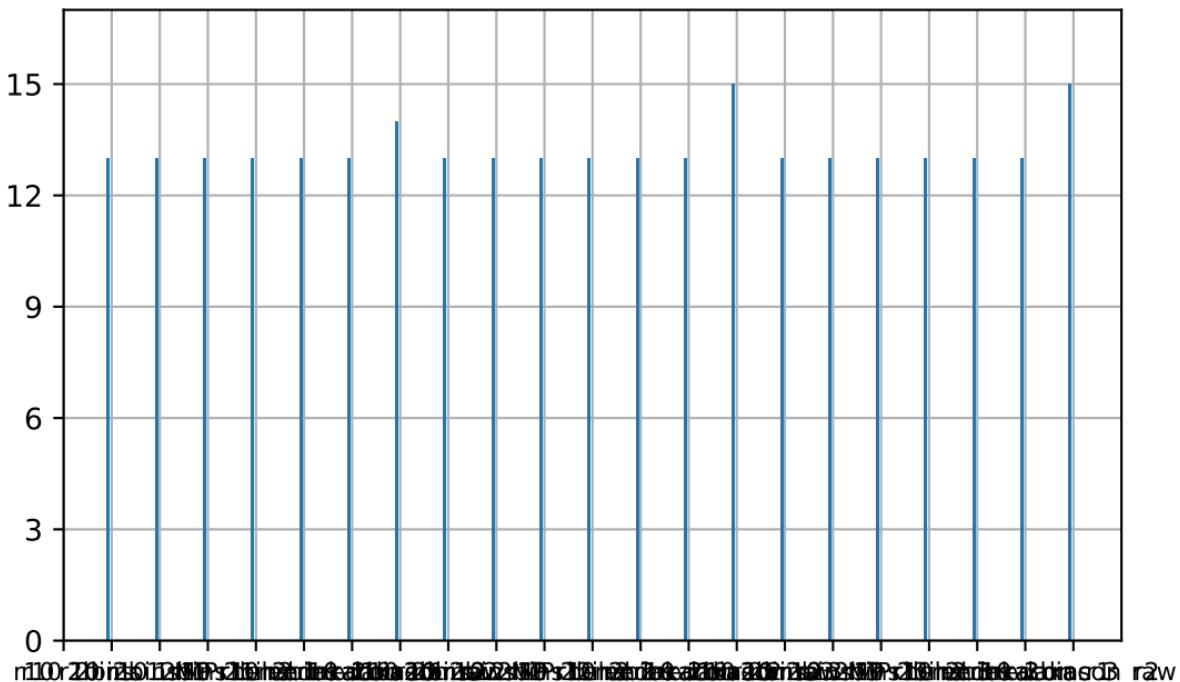
r10\_2bins\_3\_racon\_r2 GC content



r10\_2bins\_3\_raw GC content

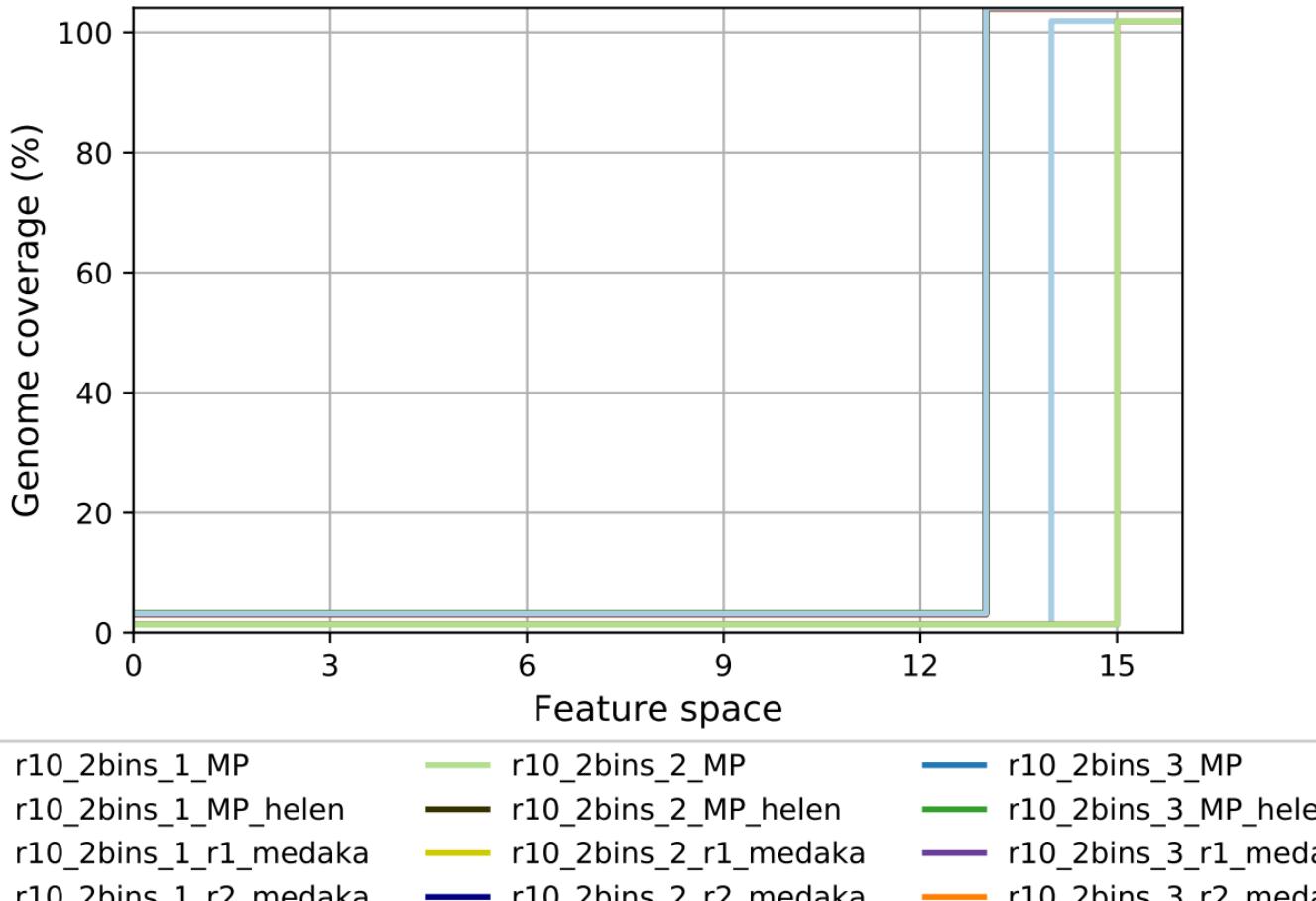


## Misassemblies

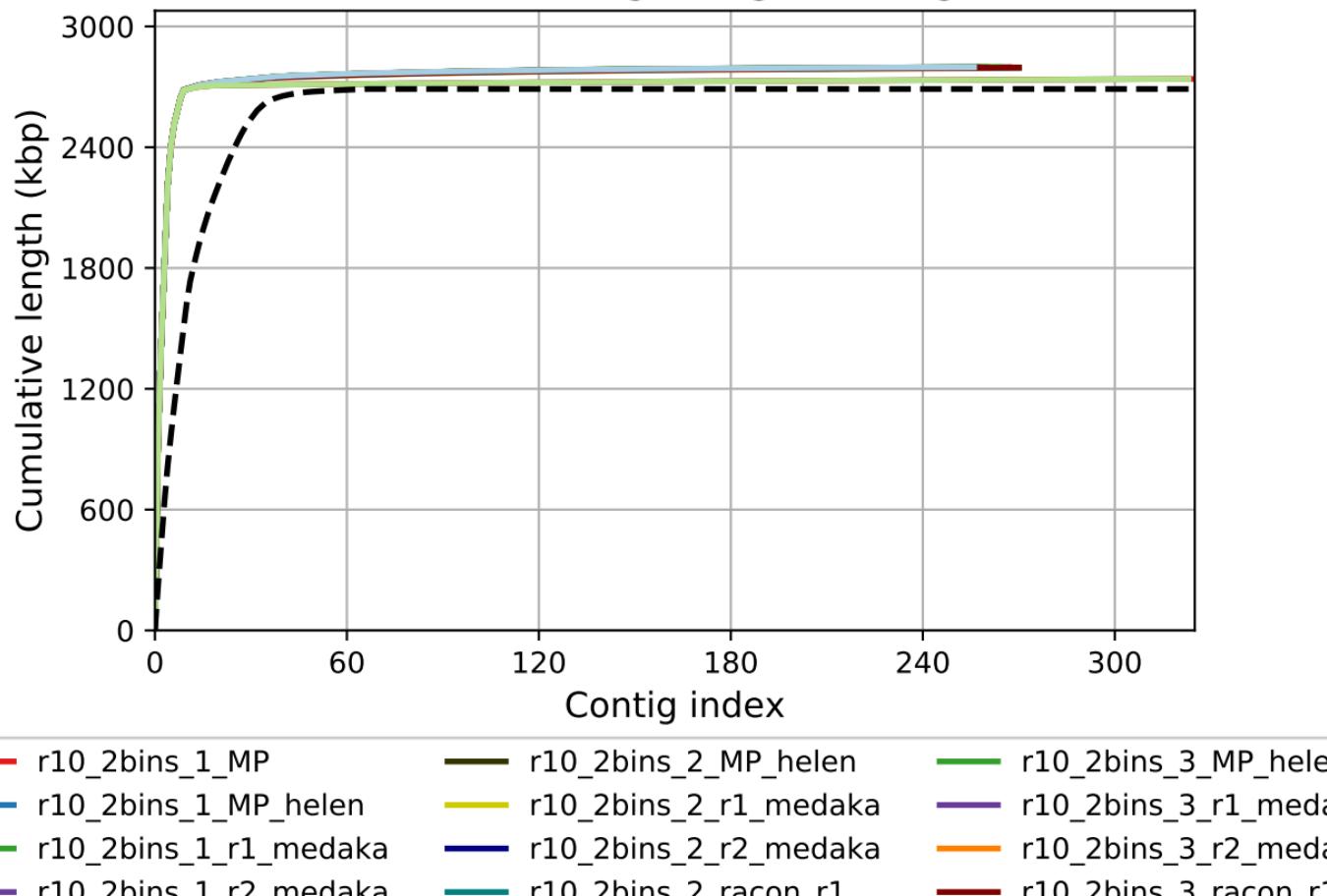


# translocations

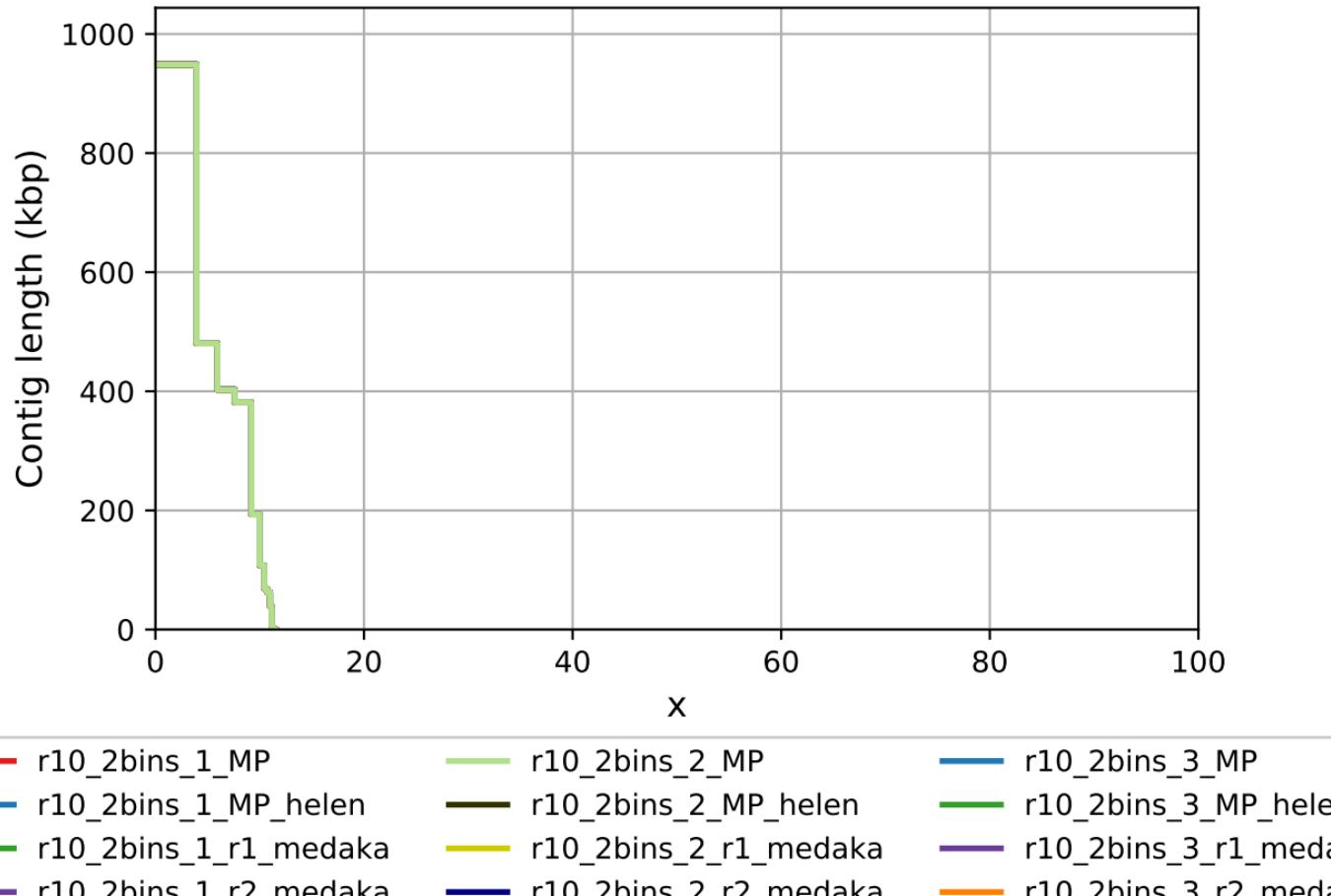
## FRCurve (misassemblies)



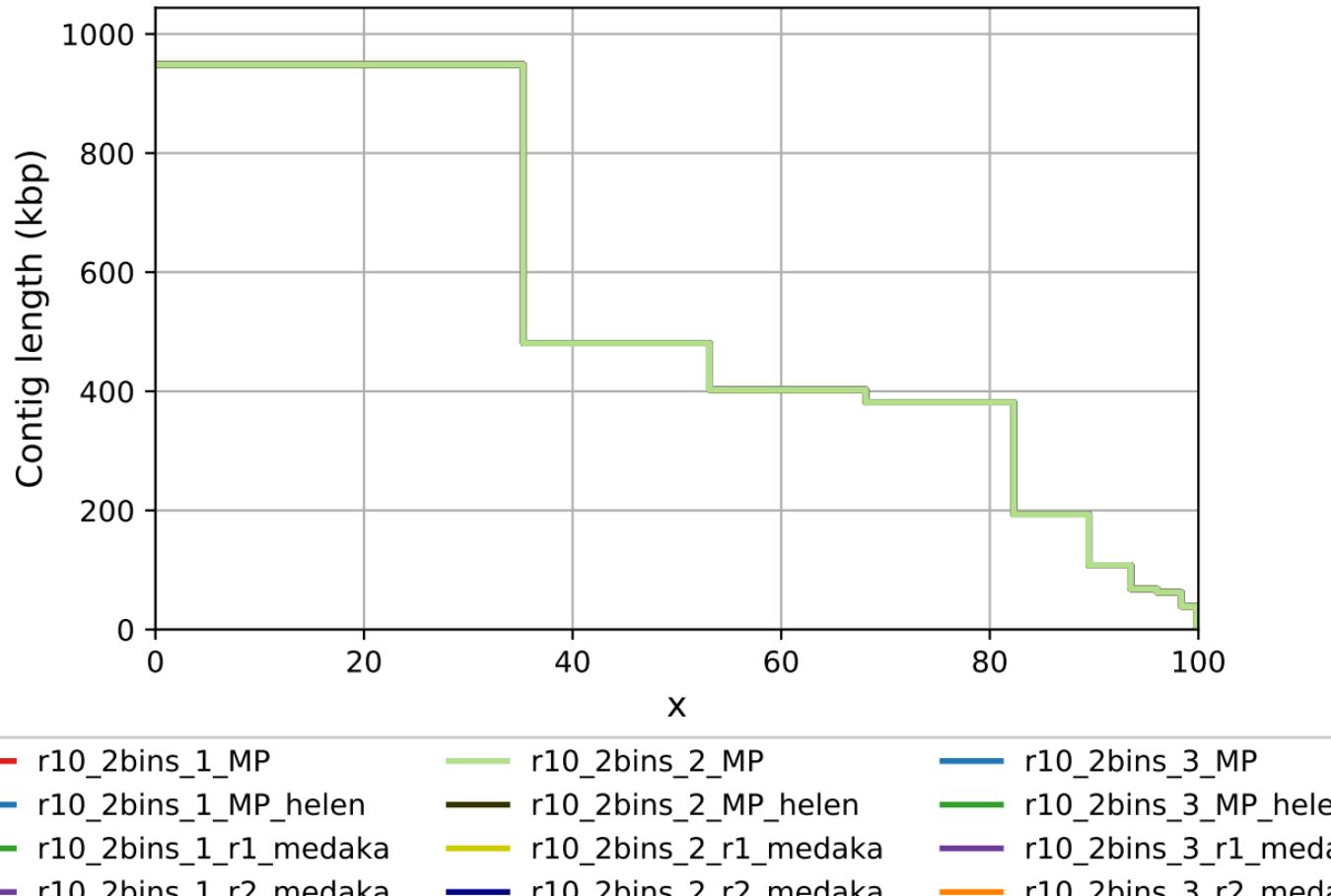
### Cumulative length (aligned contigs)



NAx



# NGAx



### Genome fraction, %

