

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_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_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Total length (>= 5000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	19305568
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	19305568
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	19305568
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	19305568
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
Total length	24075406	24070890	24072753	24062203	24060263	24054195	24062019	24074923	24071344	24072870	24062184	24061558	24055354	24061981	24074822	24070715	24072827	24063225	24060618	24054198	19305568
Reference length	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	44.78	42.96
Reference GC (%)	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82
N50	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	2990627
NG50	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
N75	2845426	2845369	2845429	2845431	2845288	2845343	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857	2845426	2845369	2845430	2845431	2845286	2845339	2843857
NG75	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
L50	3	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	1
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	4
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	34	31	34	34	34	34	34	31
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Misassembled contigs length	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	4043031
# local misassemblies	13	13	13	13	12	13	19	13	13	13	13	13	13	17	13	13	13	13	13	13	17
# scaffold gap ext. mis.	0	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	0
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# unaligned contigs	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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 6 part
Unaligned length	19977236	19974311	19976337	19965355	19963337	19955619	20001036	19977273	19974993	19975687	19965651	19964065	19958342	20002728	19977172	19974359	19975646	19966290	19962787	19956918	15246376
Genome fraction (%)	99.999	99.999	99.999	99.999	99.999	99.999	99.994	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.999	99.999	99.999	99.999	99.999	99.999	99.993
Duplication ratio	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.028	1.028	1.028	1.028	1.028	1.018
# 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	0.00
# mismatches per 100 kbp	98.53	96.09	95.87	96.49	98.38	100.88	87.59	97.70	95.72	97.22	96.32	98.30	97.67	85.91	97.70	95.72	97.12	96.77	98.10	96.71	85.71
# indels per 100 kbp	11.24	11.24	10.26	10.51	21.68	20.12	104.50	10.94	11.04	10.44	10.66	22.81	19.75	104.70	10.94	11.01	10.66	10.39	22.40	20.32	104.63
Largest alignment	788681	788688	788690	788689	788618	788636	788158	788689	788691	788690	788690	788631	788626	788122	788689	788691	788691	788691	788603	788629	788119
Total aligned length	4097672	4096081	4095918	4096350	4096483	4098132	4060046	4097152	4095853	4096685	4096035	4096993	4096514	4058267	4097152	4095858	4096683	4096437	4097385	4096836	4058206
NGA50	329482	329468	329466	329465	329431	329441	329372	329480	329467	329466	329466	329435	329449	329353	329480	329467	329466	329466	329439	329443	329354
NGA75	257049	257052	257051	257051	257029	257030	256893	257049	257050	257051	257051	257024	257028	256904	257049	257052	257051	257051	257024	257031	256906
LGA50	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
LGA75	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8

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).

# Misassemblies report

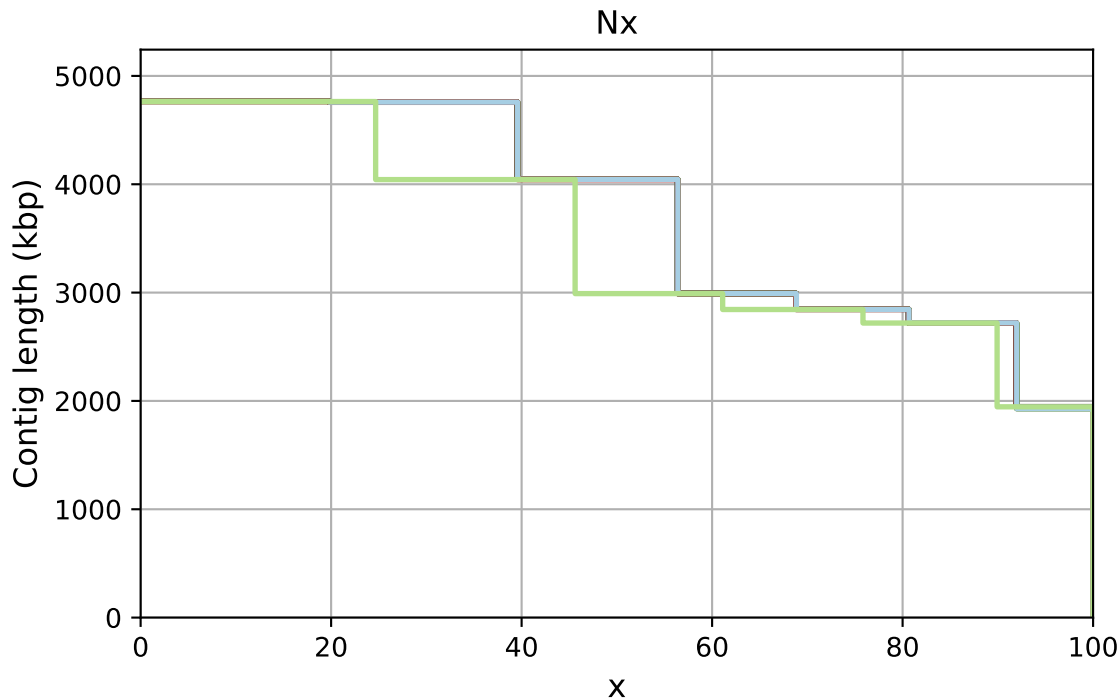
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# misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# contig misassemblies	34	34	34	34	33	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	34	34	34	34	33	34	31	34	34	34	34	34	34	31	34	34	34	34	34	34	31
# c. inversions	0	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	0
# s. relocations	0	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	0
# s. inversions	0	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	1
Misassembled contigs length	4045595	4045617	4045595	4045588	4045225	4045305	4042957	4045604	4045620	4045593	4045591	4045221	4045309	4043006	4045604	4045624	4045591	4045594	4045221	4045286	4043031
# possibly misassembled contigs	1	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	11	10	10	10	10	10	10	11	10	10	10	10	10	10	11
# local misassemblies	13	13	13	13	12	13	19	13	13	13	13	13	13	17	13	13	13	13	13	13	17
# scaffold gap ext. mis.	0	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	0
# misassemblies caused by fragmented reference	49	49	49	49	50	49	30	49	49	49	49	49	49	30	49	49	49	49	49	49	30
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# mismatches	3927	3830	3821	3846	3921	4021	3491	3894	3815	3875	3839	3918	3893	3424	3894	3815	3871	3857	3972	3910	3416
# indels	448	448	409	419	864	802	4165	436	440	416	425	909	787	4173	436	439	425	414	893	810	4170
# indels (<= 5 bp)	397	398	361	370	815	753	4109	386	391	367	376	859	737	4110	386	390	376	366	845	762	4106
# indels (> 5 bp)	51	50	48	49	49	49	56	50	49	49	49	50	50	63	50	49	49	48	48	48	64
Indels length	2608	2601	2529	2556	3043	3014	7179	2577	2580	2555	2561	3163	3023	7354	2577	2579	2563	2537	3149	3012	7350

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

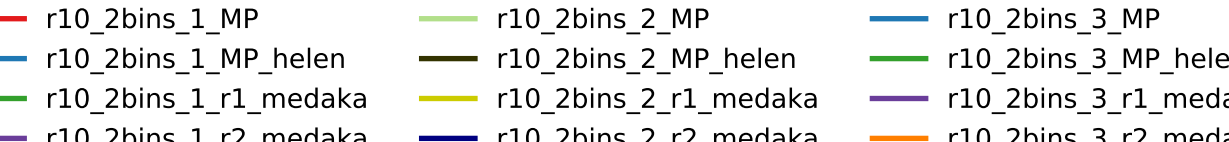
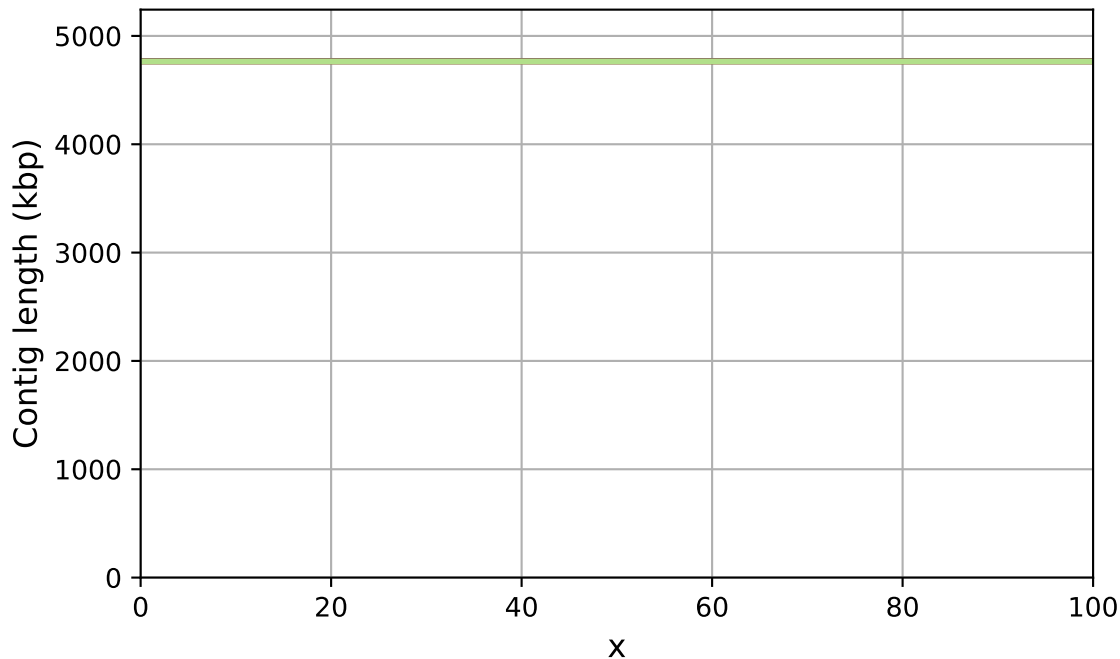
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# fully unaligned contigs	0	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	0
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	6
Partially unaligned length	19977236	19974311	19976337	19965355	19963337	19955619	20001036	19977273	19974993	19975687	19965651	19964065	19958342	20002728	19977172	19974359	19975646	19966290	19962787	19956918	15246376
# N's	0	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).

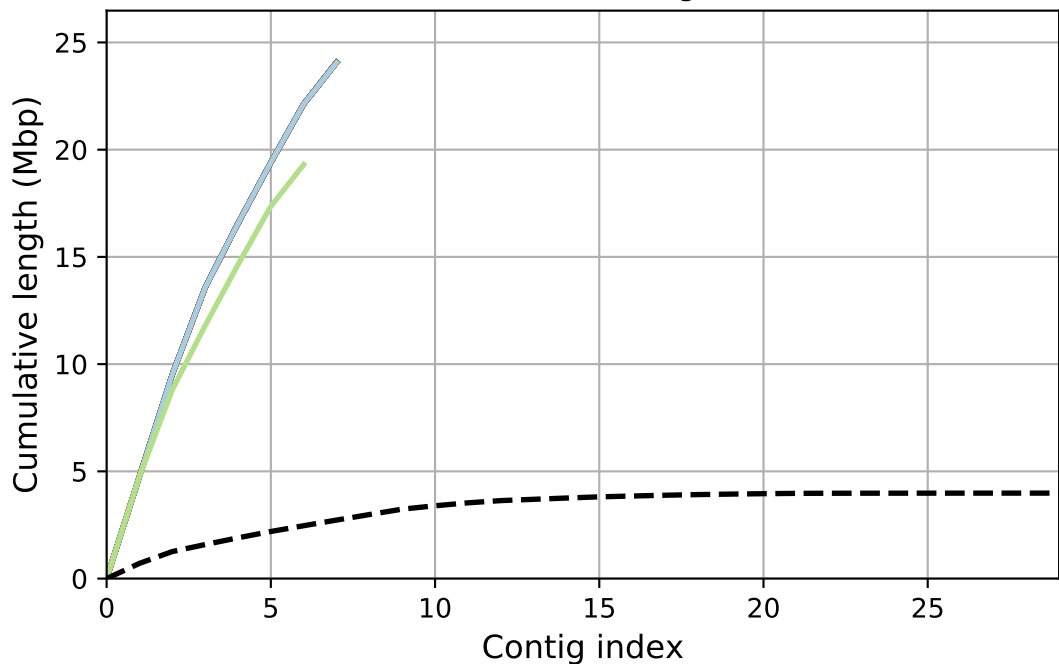


r10_2bins_1_MP	r10_2bins_2_MP	r10_2bins_3_MP
r10_2bins_1_MP_helen	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_r1_medaka	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka

# NGx

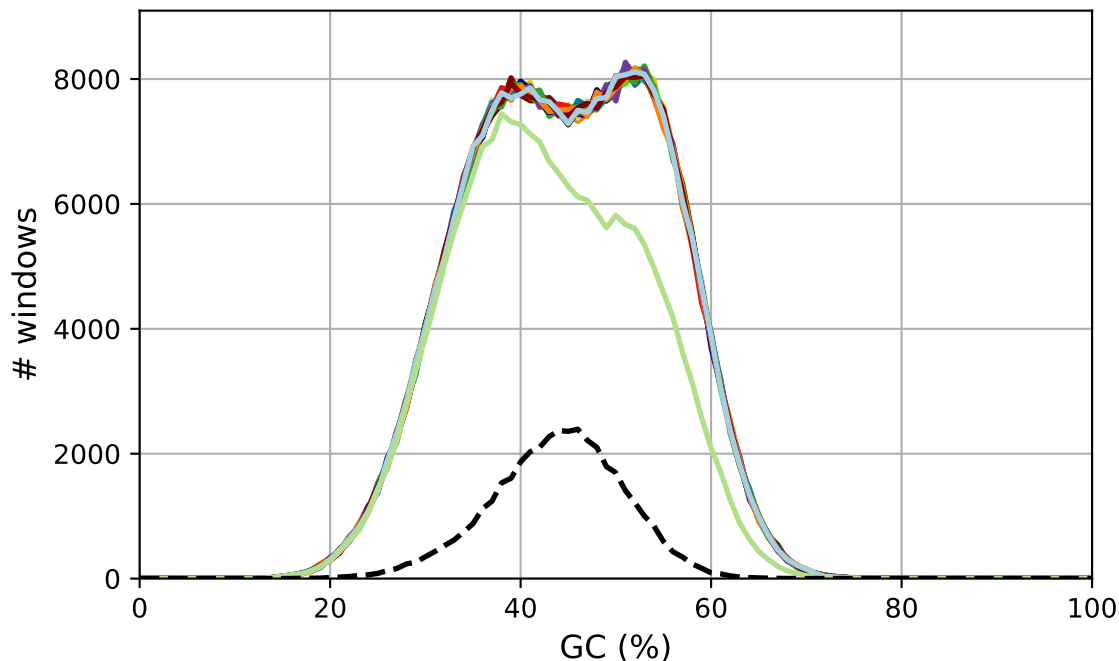


Cumulative length



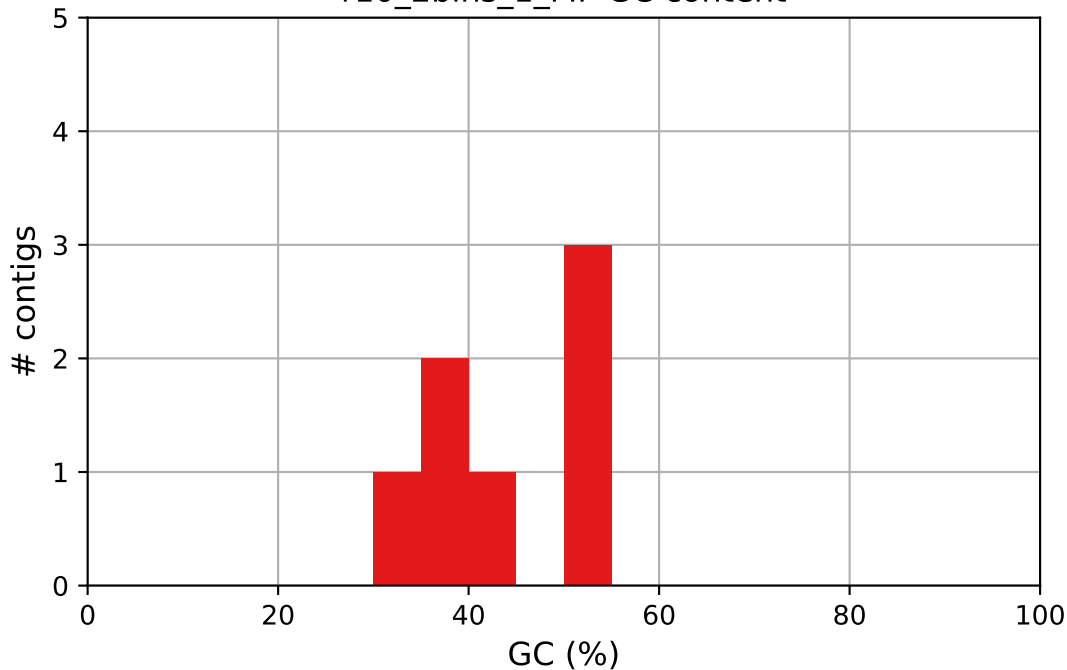
r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

GC content



— r10\_2bins\_1\_MP      — r10\_2bins\_2\_MP\_helen      — r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_1\_MP\_helen      — r10\_2bins\_2\_r1\_medaka      — r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_1\_r1\_medaka      — r10\_2bins\_2\_r2\_medaka      — r10\_2bins\_3\_r2\_medaka  
— r10\_2bins\_1\_r2\_medaka      — r10\_2bins\_2\_racon\_r1      — r10\_2bins\_3\_racon\_r1

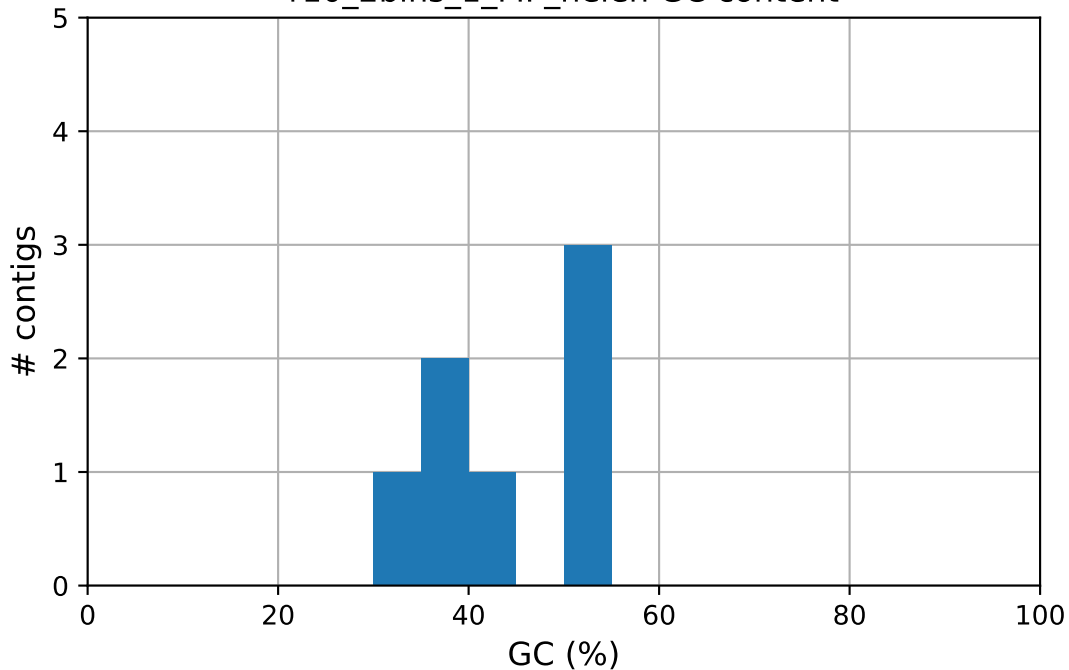
r10\_2bins\_1\_MP GC content



r10\_2bins\_1\_MP

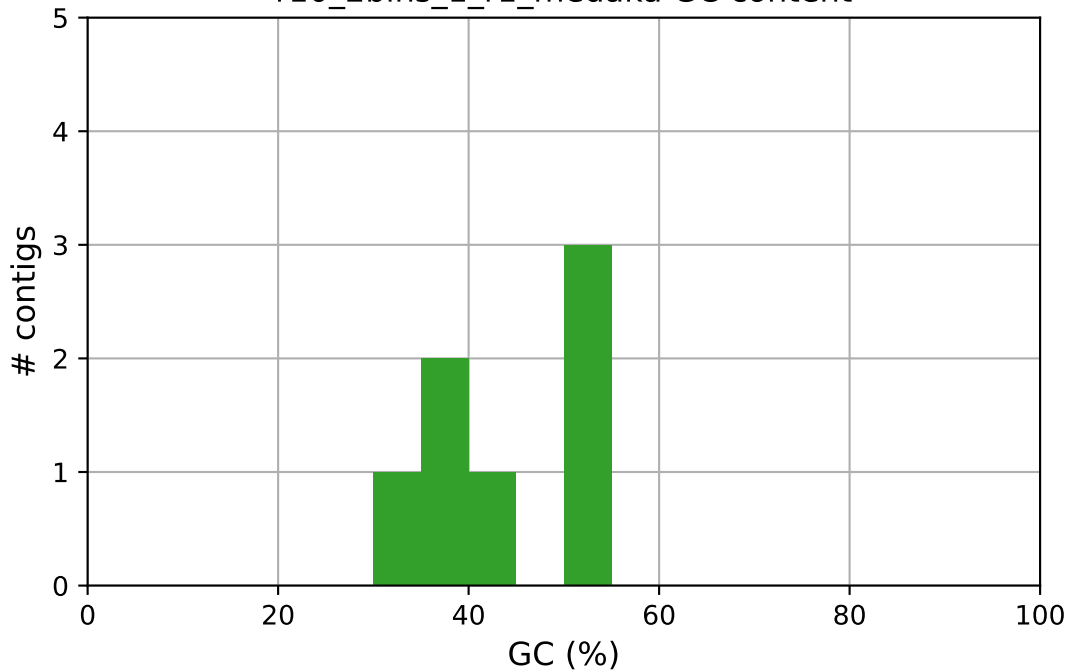


r10\_2bins\_1\_MP\_helen GC content



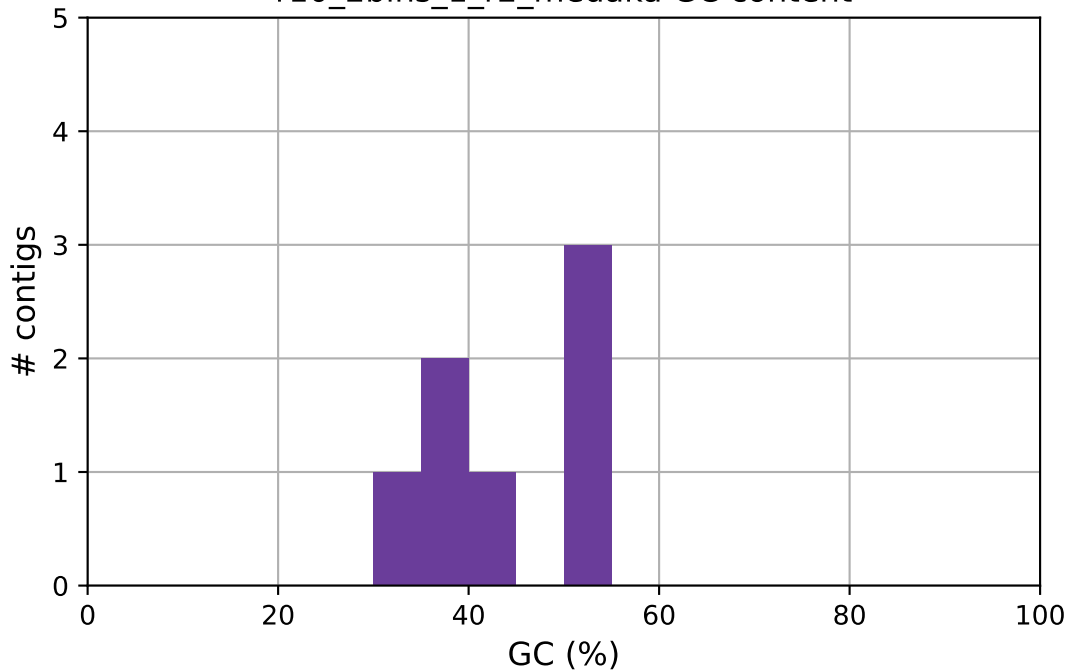
r10\_2bins\_1\_MP\_helen

r10\_2bins\_1\_r1\_medaka GC content



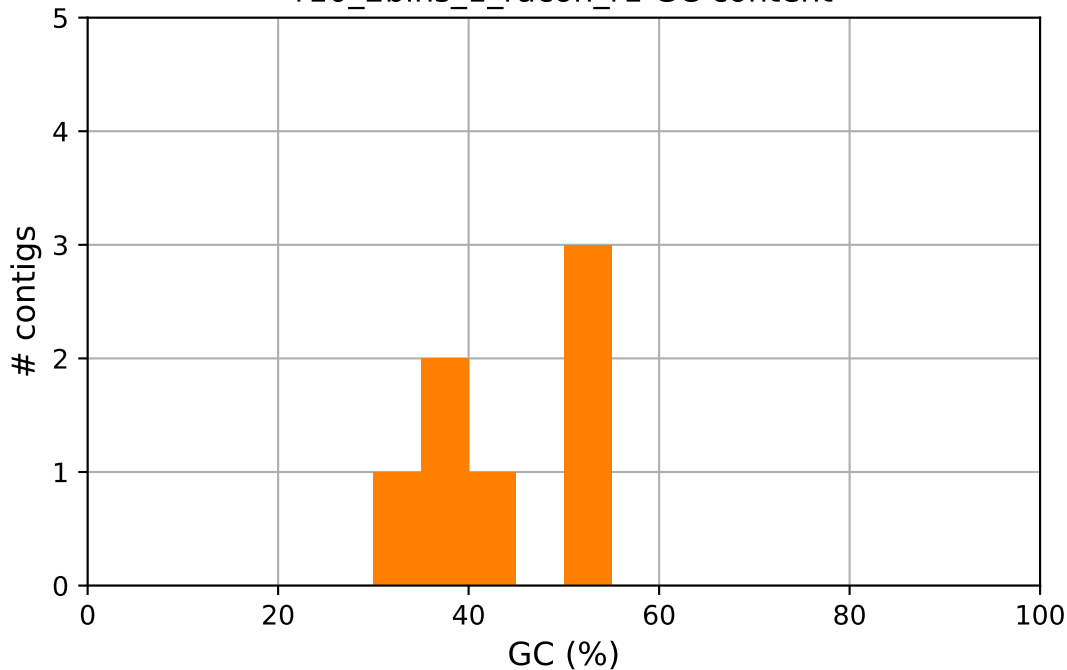
r10\_2bins\_1\_r1\_medaka

r10\_2bins\_1\_r2\_medaka GC content



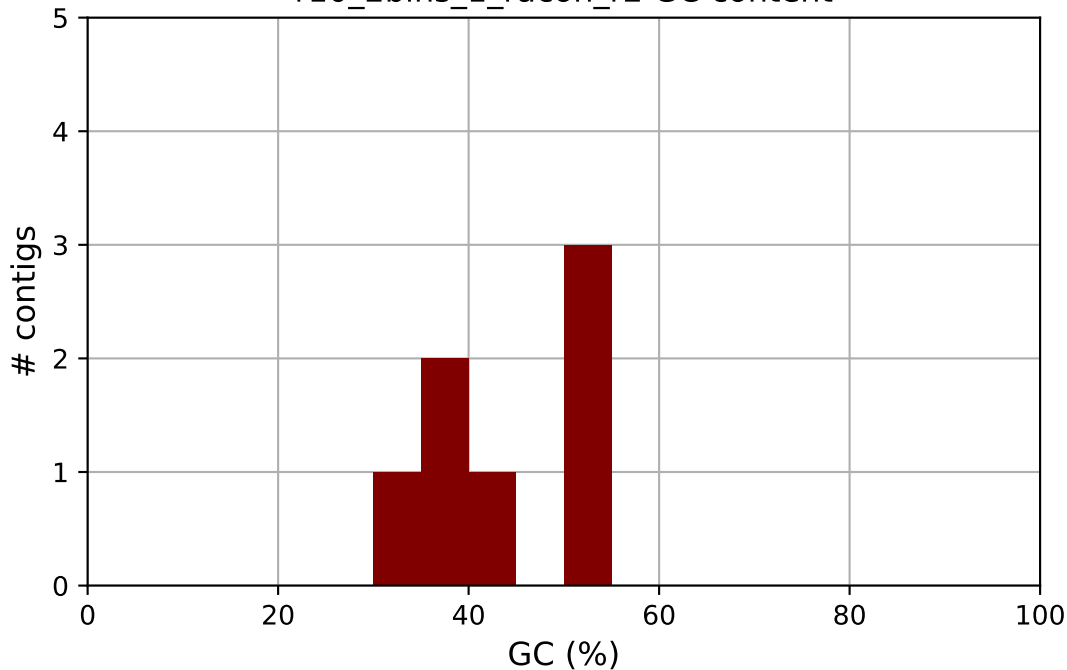
r10\_2bins\_1\_r2\_medaka

r10\_2bins\_1\_racon\_r1 GC content



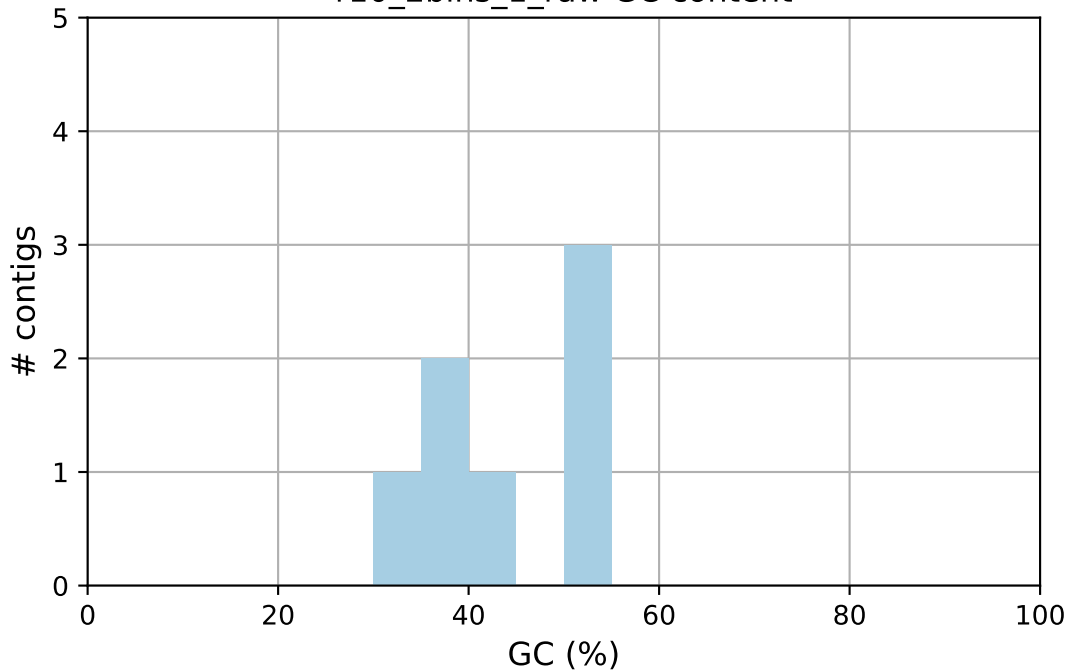
r10\_2bins\_1\_racon\_r1

r10\_2bins\_1\_racon\_r2 GC content



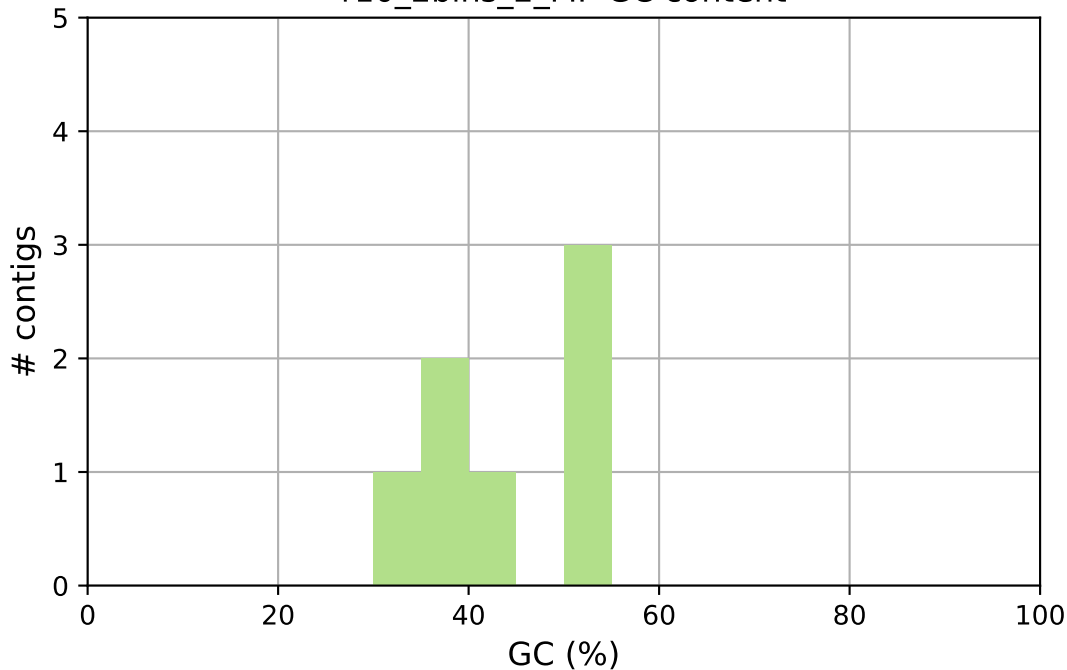
r10\_2bins\_1\_racon\_r2

r10\_2bins\_1\_raw GC content



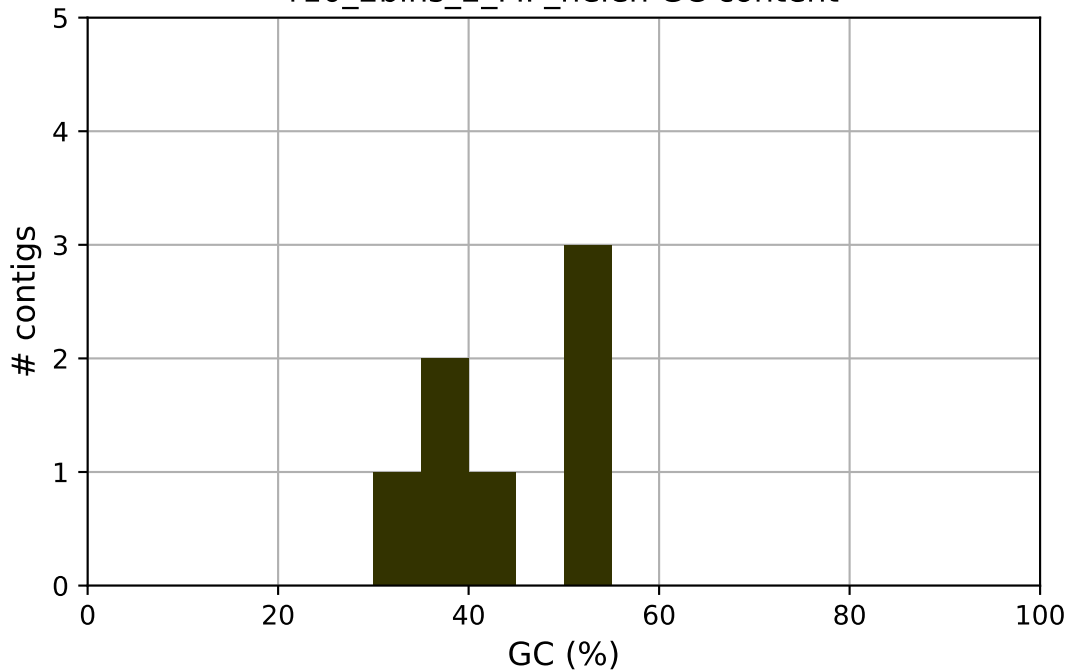
r10\_2bins\_1\_raw

r10\_2bins\_2\_MP GC content



r10\_2bins\_2\_MP

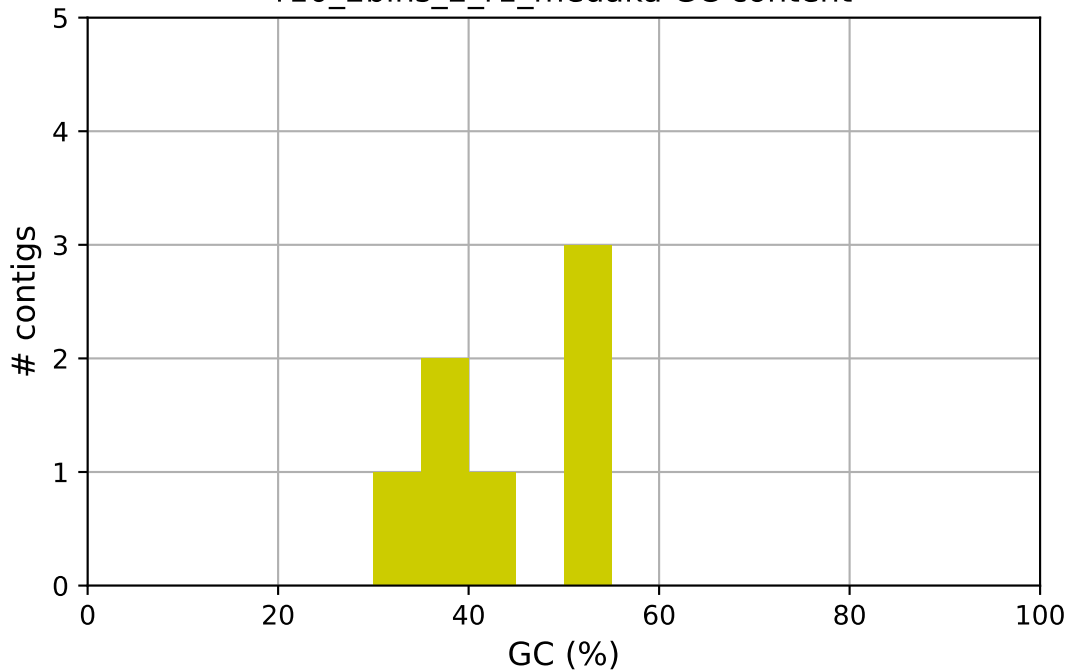
r10\_2bins\_2\_MP\_helen GC content



r10\_2bins\_2\_MP\_helen

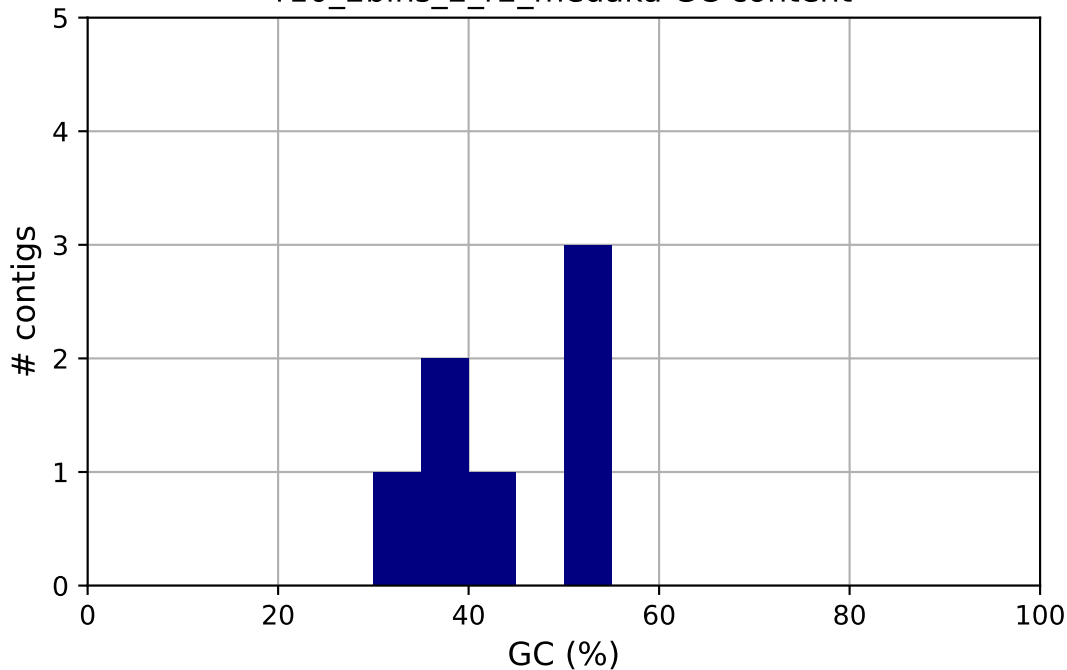


r10\_2bins\_2\_r1\_medaka GC content



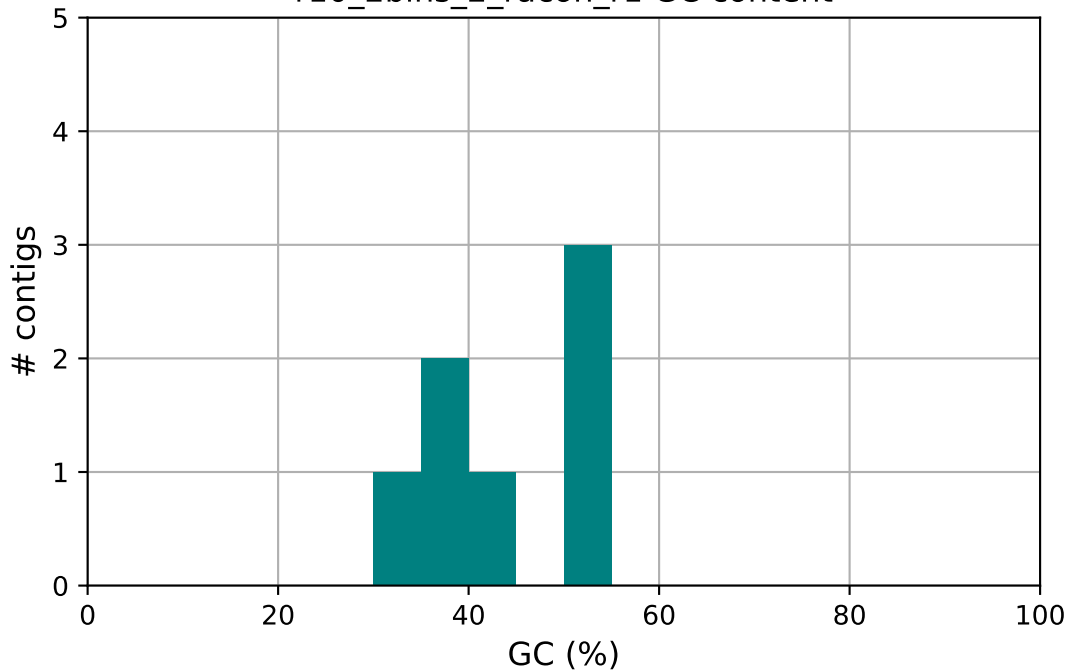
r10\_2bins\_2\_r1\_medaka

r10\_2bins\_2\_r2\_medaka GC content



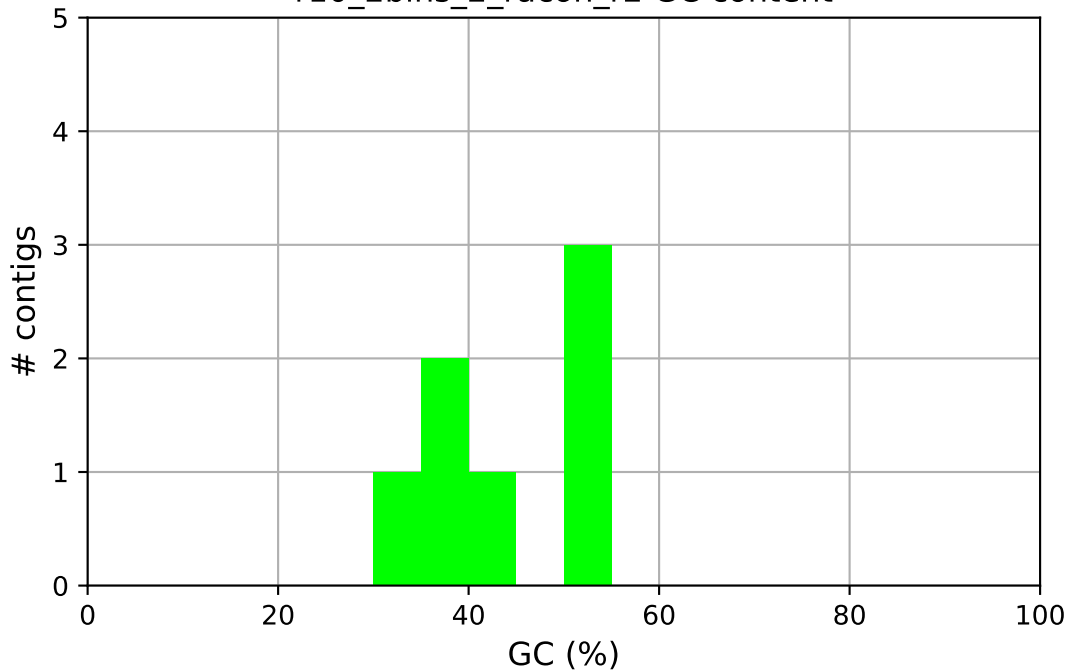
r10\_2bins\_2\_r2\_medaka

r10\_2bins\_2\_racon\_r1 GC content



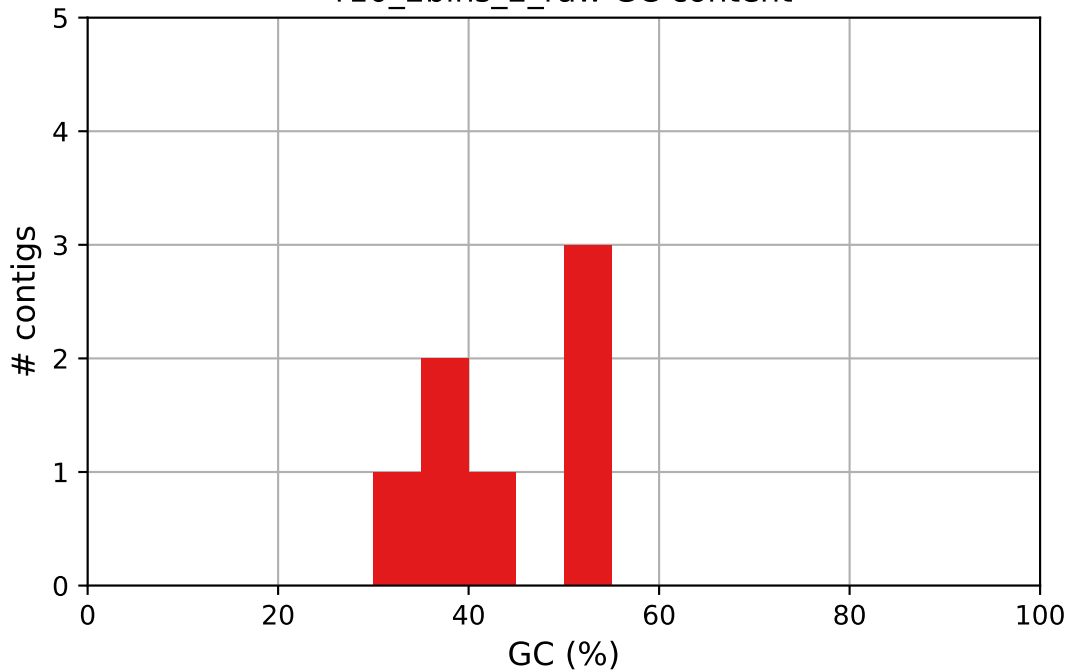
r10\_2bins\_2\_racon\_r1

r10\_2bins\_2\_racon\_r2 GC content



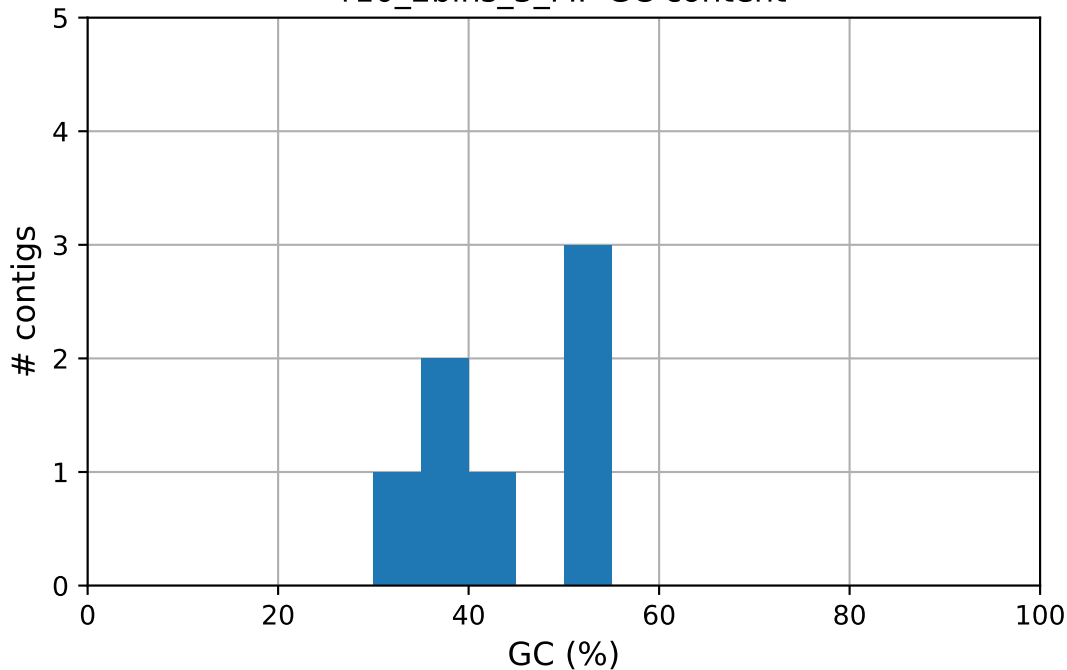
r10\_2bins\_2\_racon\_r2

r10\_2bins\_2\_raw GC content



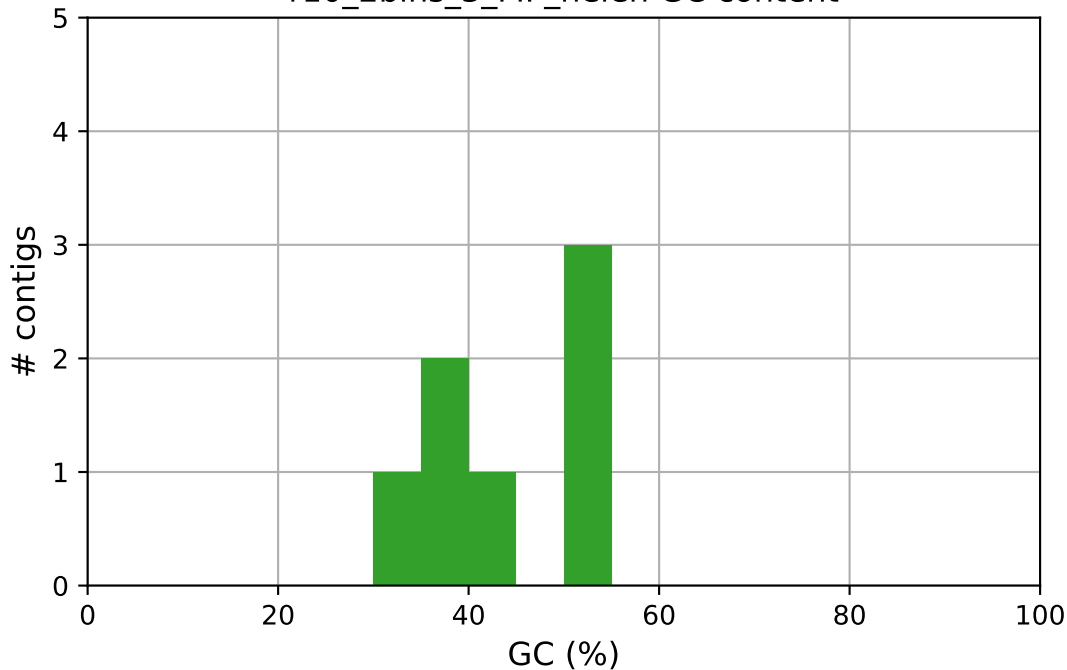
r10\_2bins\_2\_raw

r10\_2bins\_3\_MP GC content



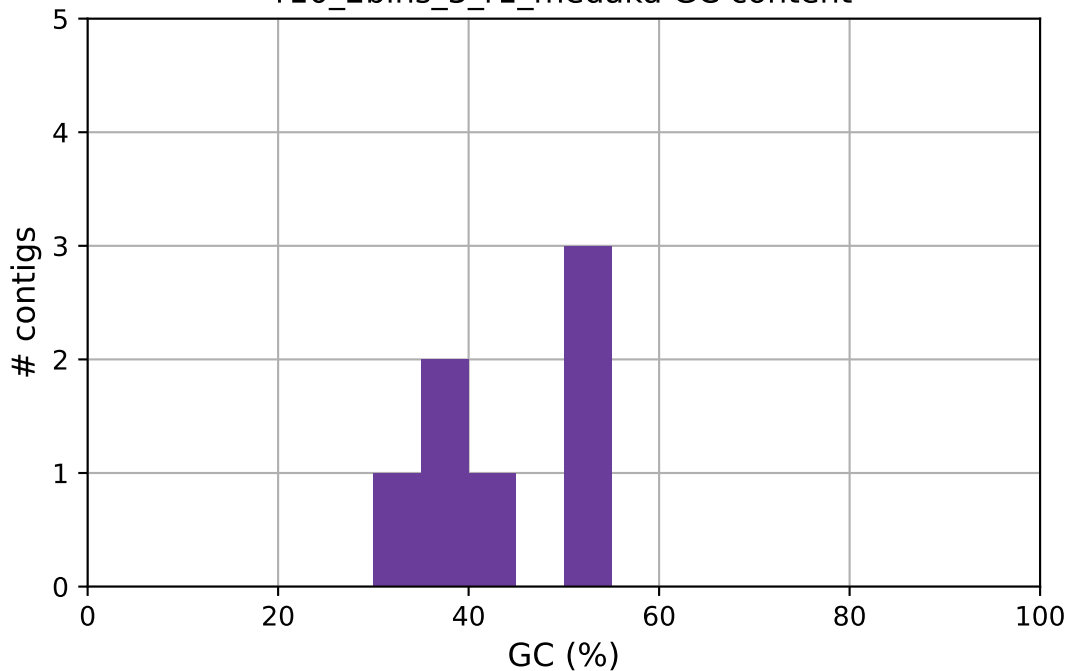
r10\_2bins\_3\_MP

r10\_2bins\_3\_MP\_helen GC content



r10\_2bins\_3\_MP\_helen

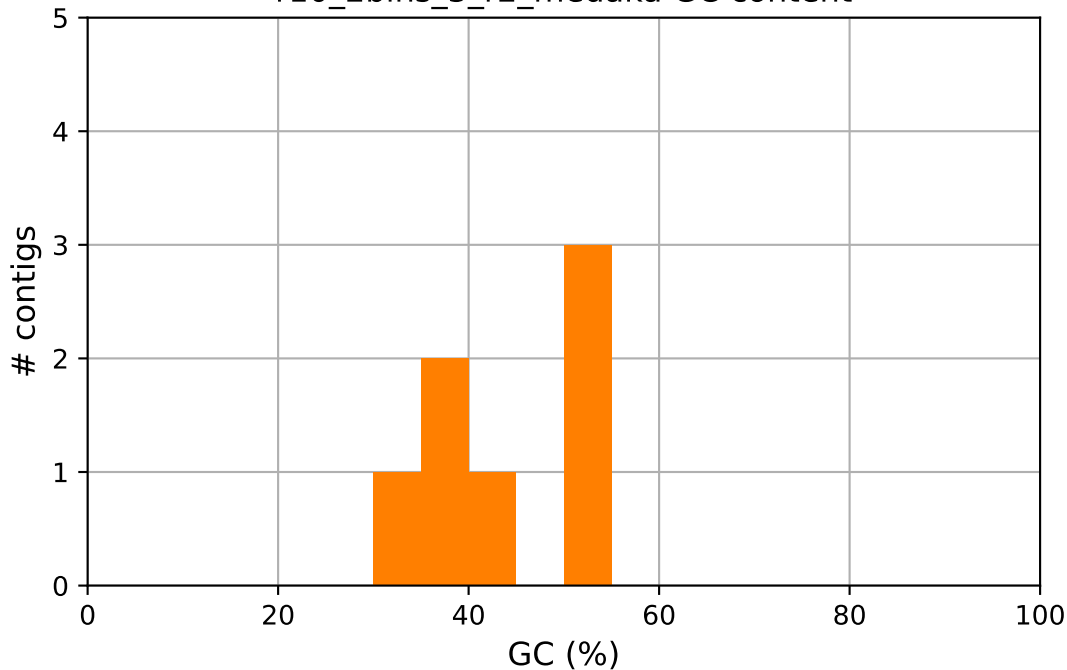
r10\_2bins\_3\_r1\_medaka GC content



r10\_2bins\_3\_r1\_medaka

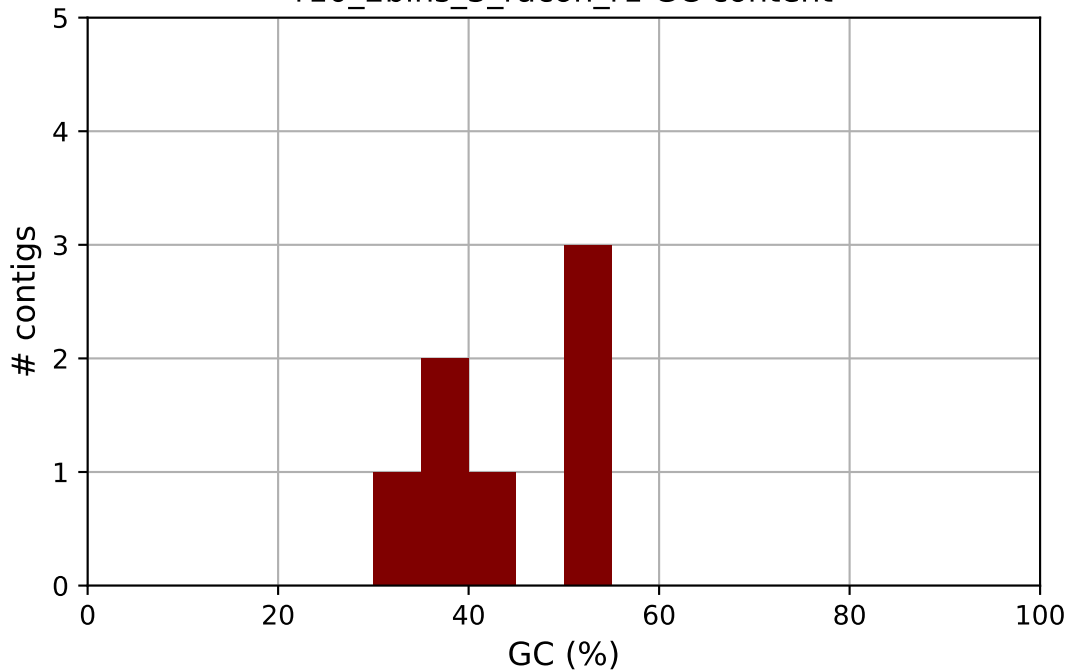


r10\_2bins\_3\_r2\_medaka GC content



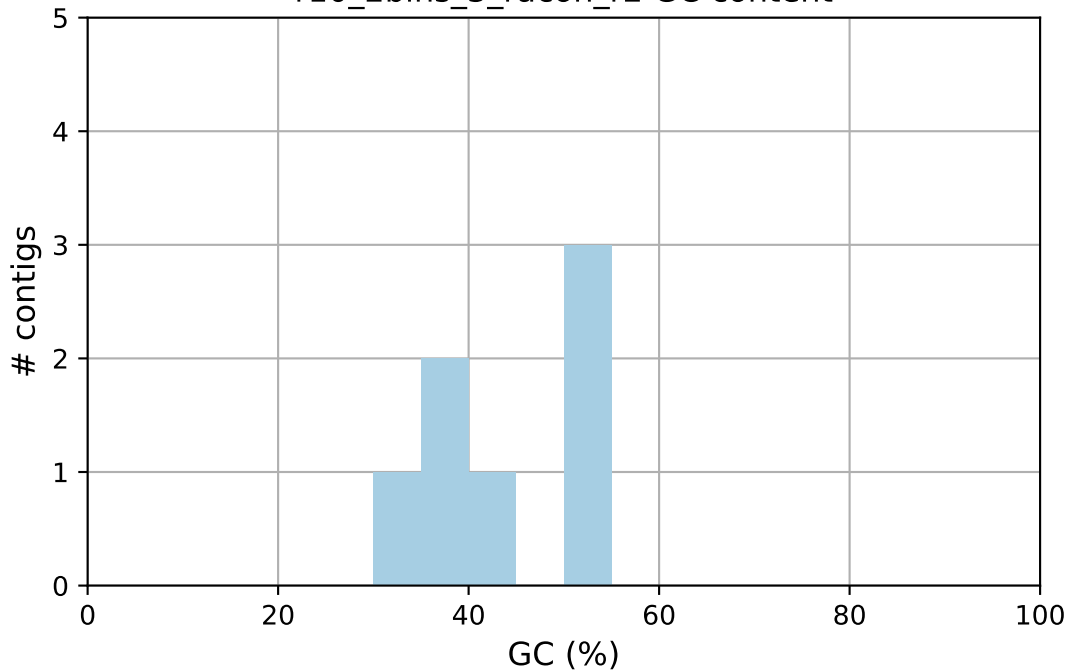
r10\_2bins\_3\_r2\_medaka

r10\_2bins\_3\_racon\_r1 GC content



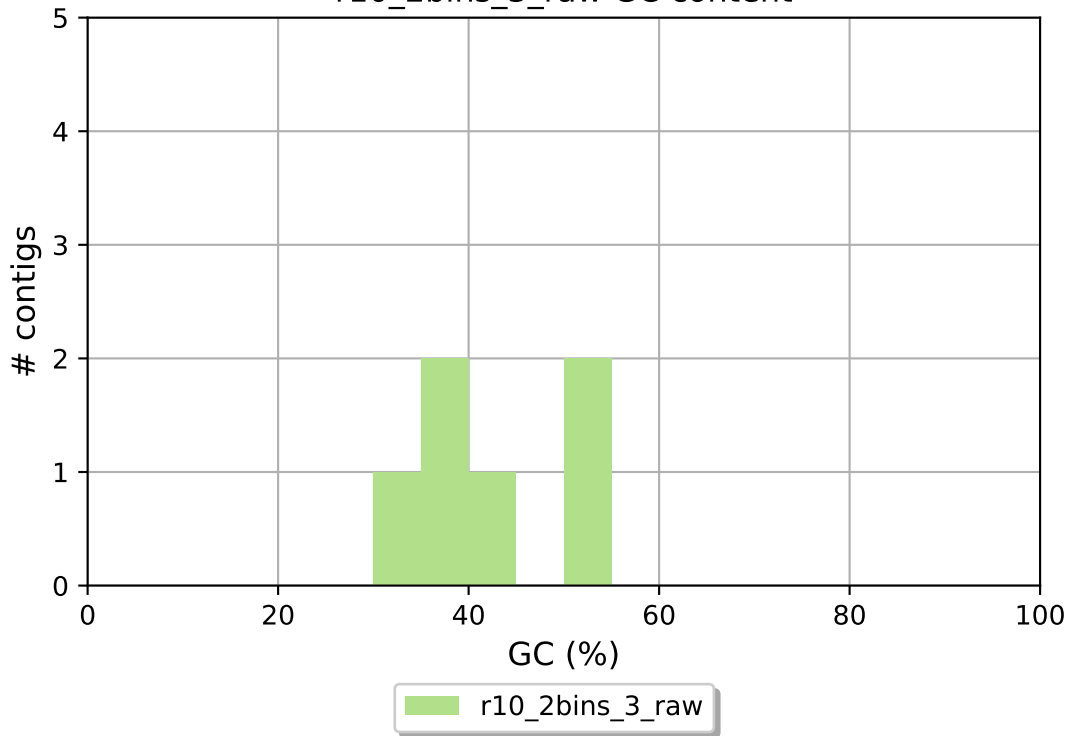
r10\_2bins\_3\_racon\_r1

r10\_2bins\_3\_racon\_r2 GC content

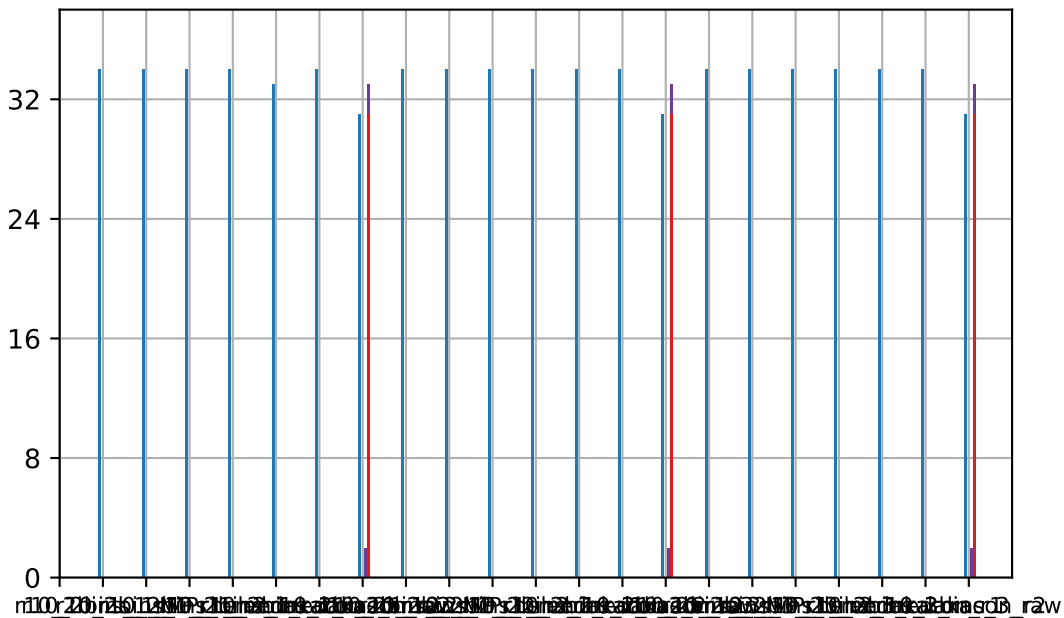


r10\_2bins\_3\_racon\_r2

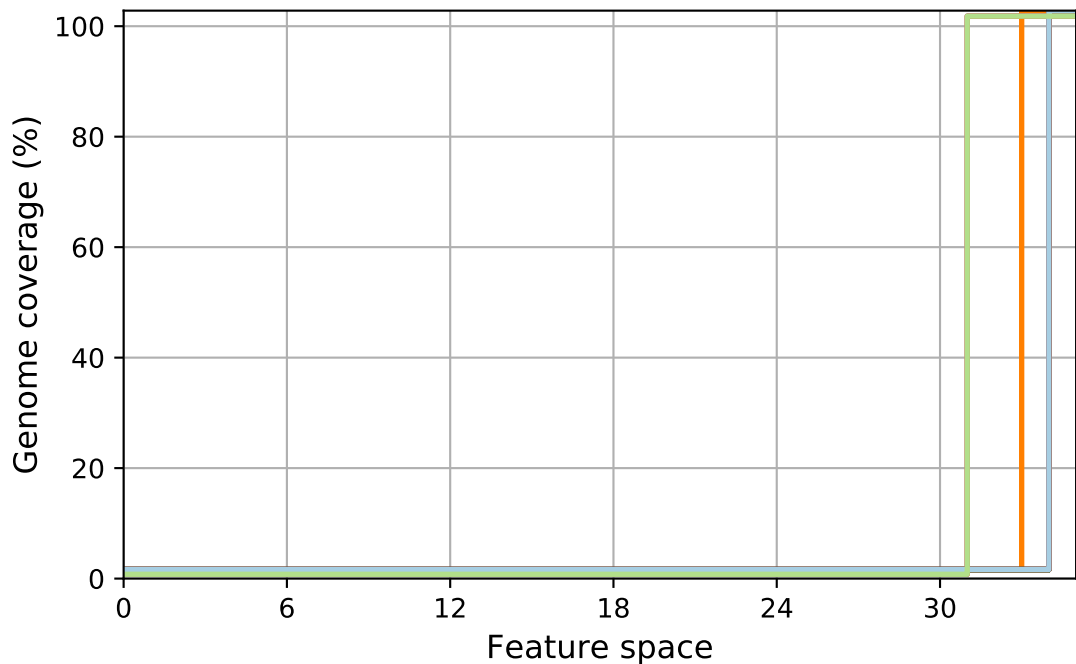
r10\_2bins\_3\_raw GC content



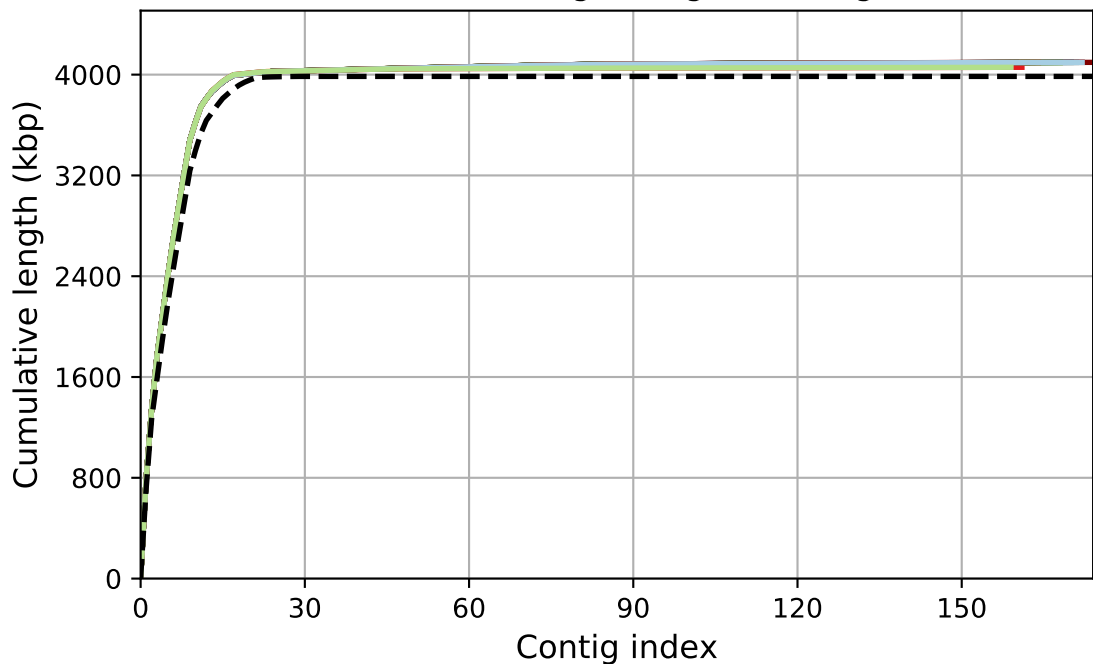
# Misassemblies



# FRCurve (misassemblies)

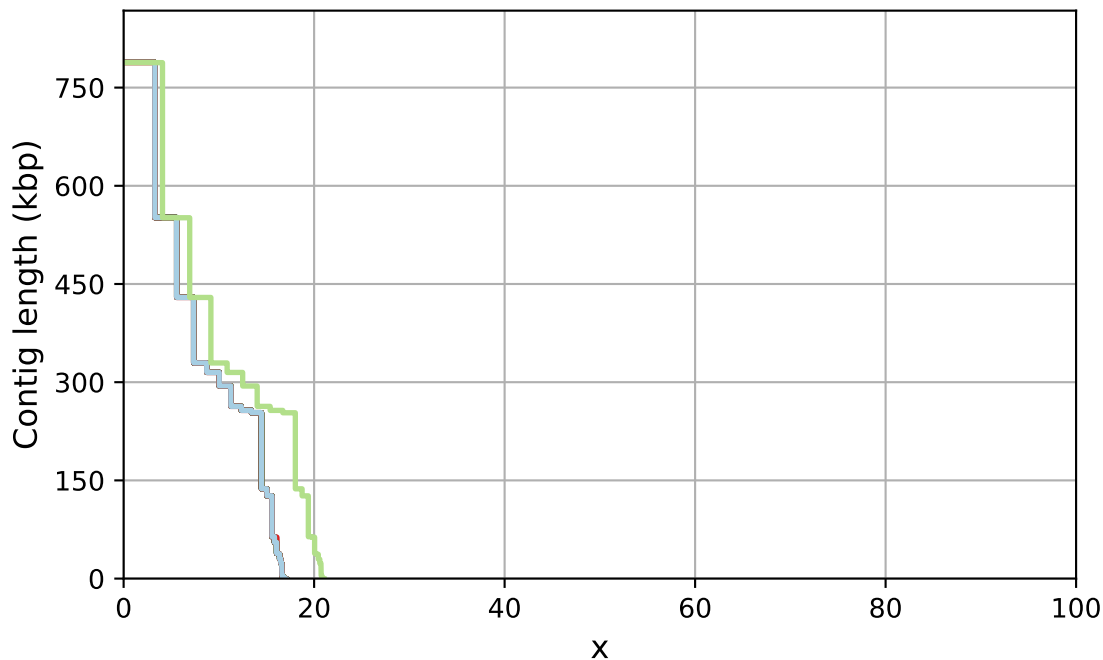


# Cumulative length (aligned contigs)



— 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\_2\_racon\_r1  
— r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_3\_r2\_medaka  
— r10\_2bins\_3\_racon\_r1

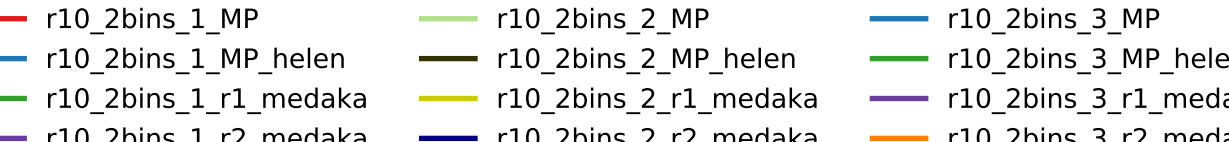
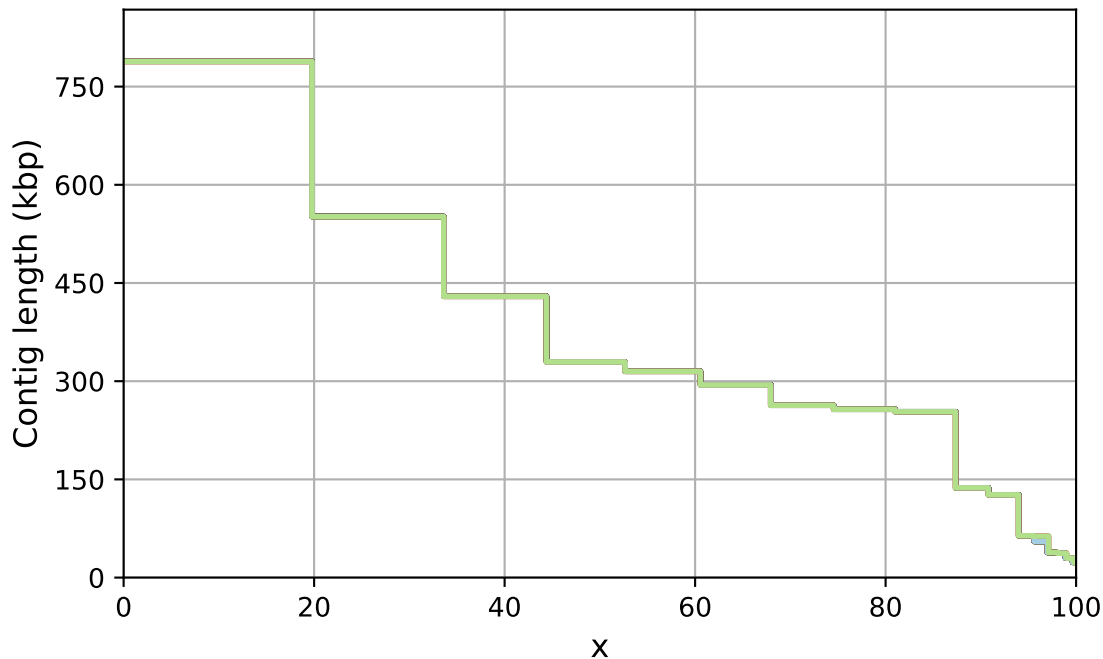
# NAx



— r10\_2bins\_1\_MP      — r10\_2bins\_2\_MP      — r10\_2bins\_3\_MP  
— r10\_2bins\_1\_MP\_helen      — r10\_2bins\_2\_MP\_helen      — r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_1\_r1\_medaka      — r10\_2bins\_2\_r1\_medaka      — r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_1\_r2\_medaka      — r10\_2bins\_2\_r2\_medaka      — r10\_2bins\_3\_r2\_medaka



# NGAx



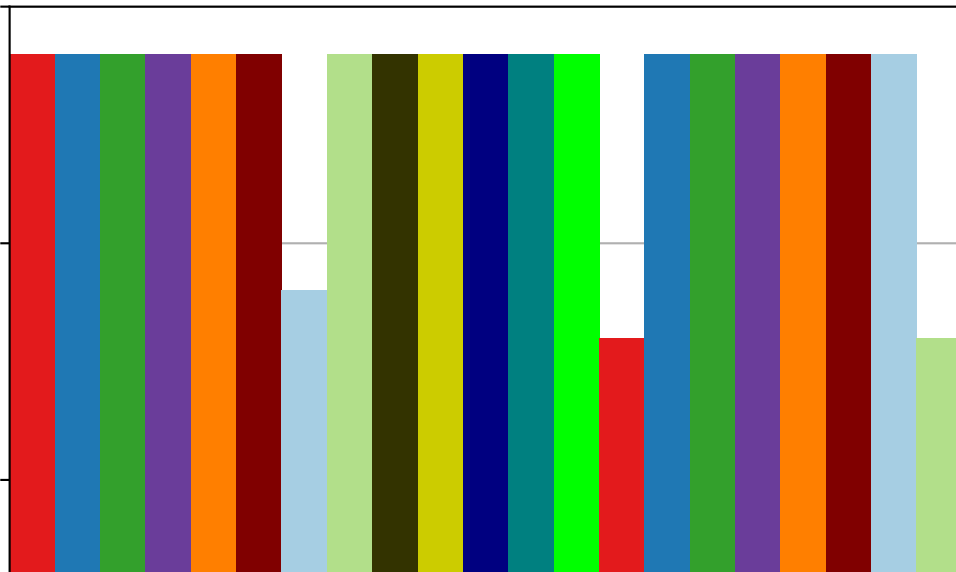
Genome fraction, %

+9.999e1

0.010

0.005

0.000



r10\_2bins\_1\_MP

r10\_2bins\_1\_MP\_helen

r10\_2bins\_1\_r1\_medaka

r10\_2bins\_1\_r2\_medaka

r10\_2bins\_2\_MP

r10\_2bins\_2\_MP\_helen

r10\_2bins\_2\_r1\_medaka

r10\_2bins\_2\_r2\_medaka

r10\_2bins\_3\_MP

r10\_2bins\_3\_MP\_helen

r10\_2bins\_3\_r1\_medaka

r10\_2bins\_3\_r2\_medaka