

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_r2_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 (>= 5000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
Total length	24074494	24070200	24072211	24064284	24060998	24055678	30849498	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	30849309
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	49.48	44.80	44.80	44.80	44.80	44.79	44.78	49.48	44.80	44.80	44.80	44.78	44.78	49.48	
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	
N50	4045598	4045621	4045594	4045589	4045227	4045309	4756088	4045598	4045629	4045591	4045590	4045220	4045285	4756101	4045598	4045626	4045592	4045592	4045212	4045306	4756002
NG50	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
N75	2845422	2845369	2845428	2845432	2845260	2845328	2990628	2845425	2845372	2845428	2845431	2845275	2845354	2990633	2845425	2845364	2845429	284527	2845324	2990669	
NG75	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
# 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	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2992073	2991915	2991980	2990633	2992084	2992069	2992075	2992075	2991930	2991998	2990669
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	14	7	7	7	7	7	7	14	
# 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	7	6	6	6	6	6	7	6	6	6	6	6	6	7	
# 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	20956939	20950528	20952220	20944866	20943406	20935724	27793486	20956187	20949732	20953225	20941031	20943020	20936986	27790293	20957524	20949878	20951732	20944712	20942887	20936401	27791828
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.984	99.981	
Duplication ratio	1.054	1.055	1.055	1.055	1.054	1.055	1.033	1.054	1.055	1.055	1.055	1.054	1.055	1.055	1.055	1.055	1.055	1.055	1.055	1.034	
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00								

Misassemblies report

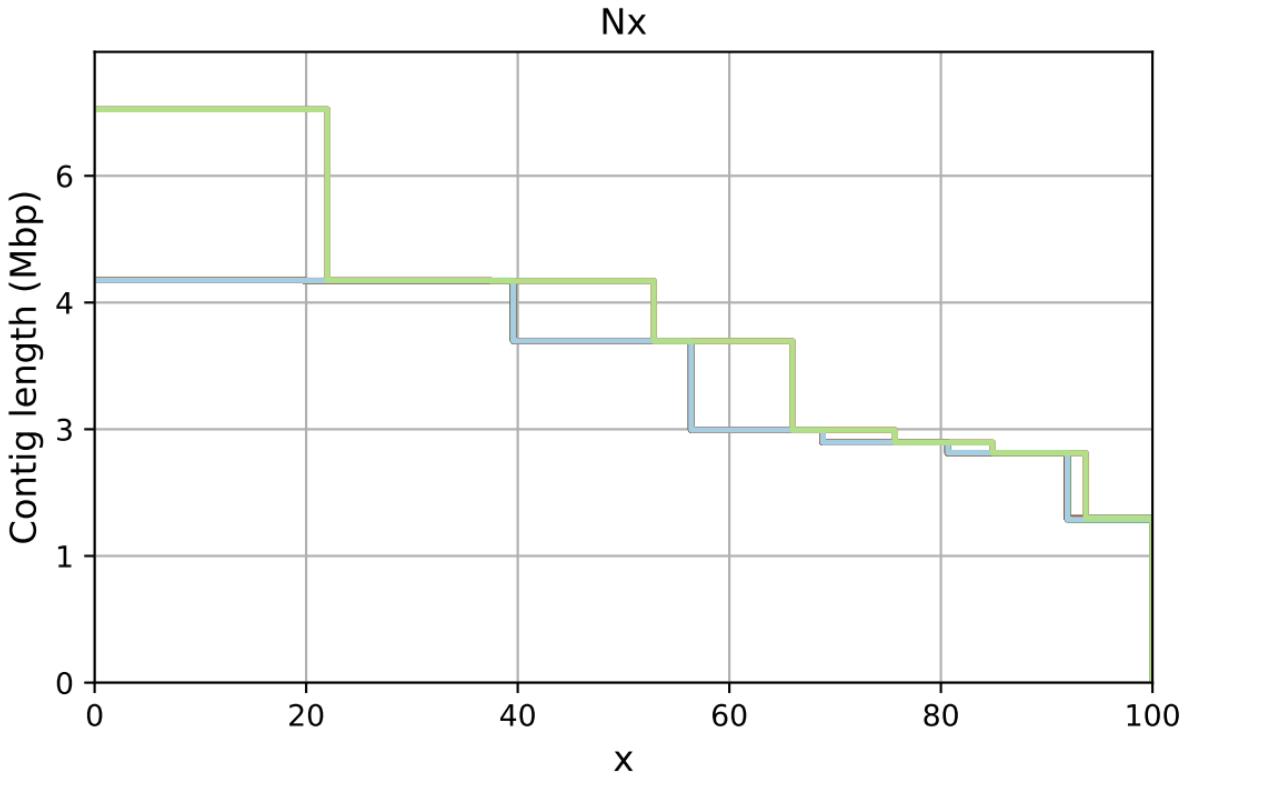
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# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# c. 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	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2992073	2991915	2991980	2990633	2992084	2992069	2992075	2991930	2991998	2990669	
# possibly misassembled contigs	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	2
# possible misassemblies	8	8	8	8	8	8	8	9	8	8	8	8	8	9	8	8	8	8	8	8	9
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	14	7	7	7	7	7	7	14
# 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	16	16	16	16	16	16	10	16	16	16	16	16	16	10	16	16	16	16	16	16	10
# unaligned mis. contigs	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6756	6931	6908	6879	6681	6970	4202	6804	7001	6874	6937	6621	6854	4340	6754	6896	6976	6943	6649	6925	4255
# indels	632	642	662	645	933	879	3453	651	661	656	641	927	862	3414	630	642	665	642	939	874	3453
# indels (<= 5 bp)	609	618	637	621	908	854	3425	627	636	631	617	902	838	3387	607	618	640	618	914	849	3425
# indels (> 5 bp)	23	24	25	24	25	25	28	24	25	25	24	27	23	24	25	24	25	25	25	28	
Indels length	1919	1935	1978	1947	2331	2253	5304	1958	1974	1971	1932	2338	2206	5251	1920	1937	1981	1933	2346	2243	5316

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

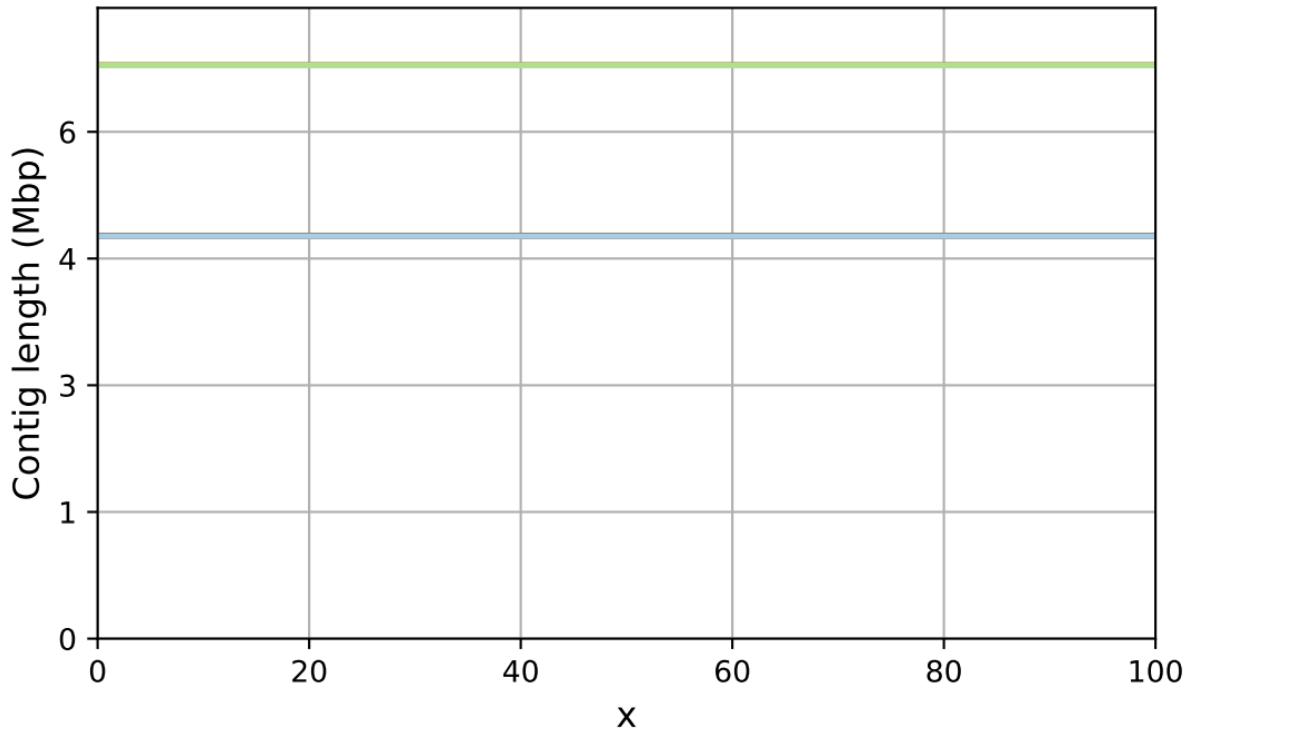
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	
Partially unaligned length	20956939	20950528	20952220	20944866	20943406	20935724	20941031	20943020	20936986	20949732	20953225	20941031	20944712	20942887	20936401	20956187	20949878	20951732	20944712	20942887	20936401	27791828
# 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 ≥ 5000 bp, unless otherwise noted
(e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— r10_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_2_MP
— 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

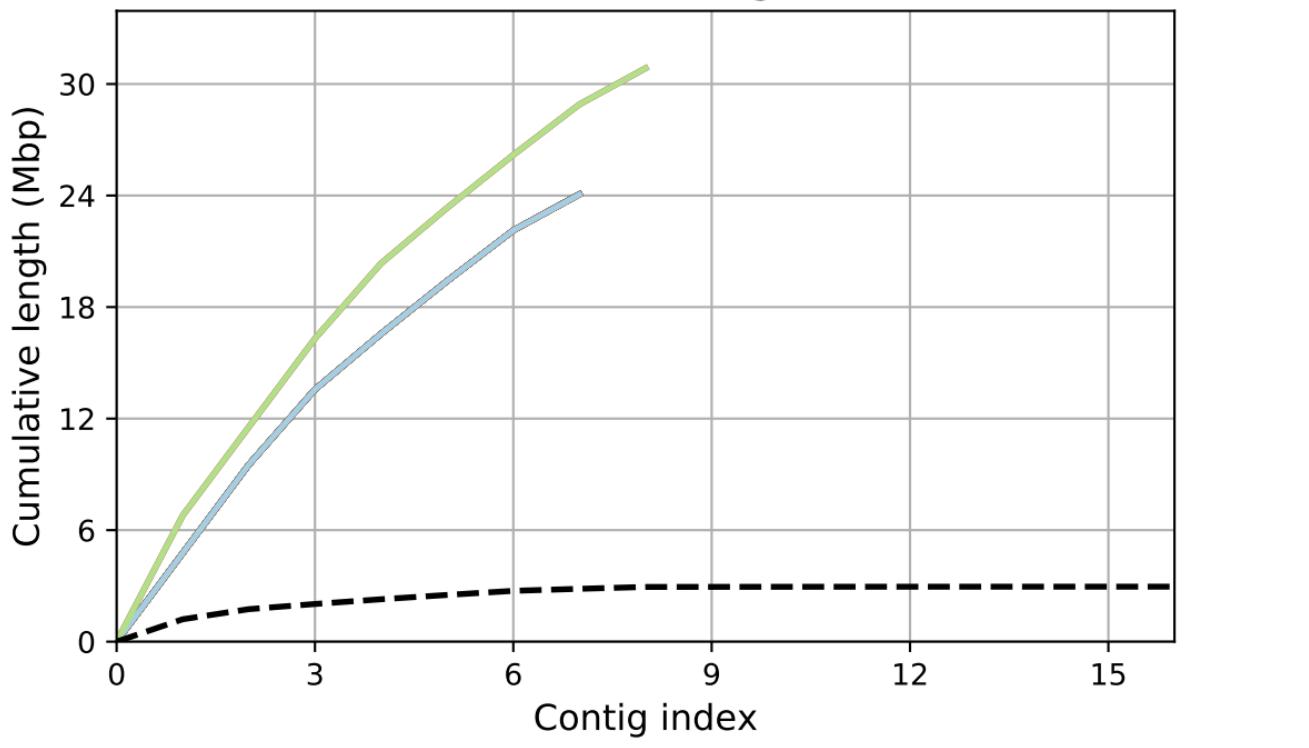
NGx



Legend:

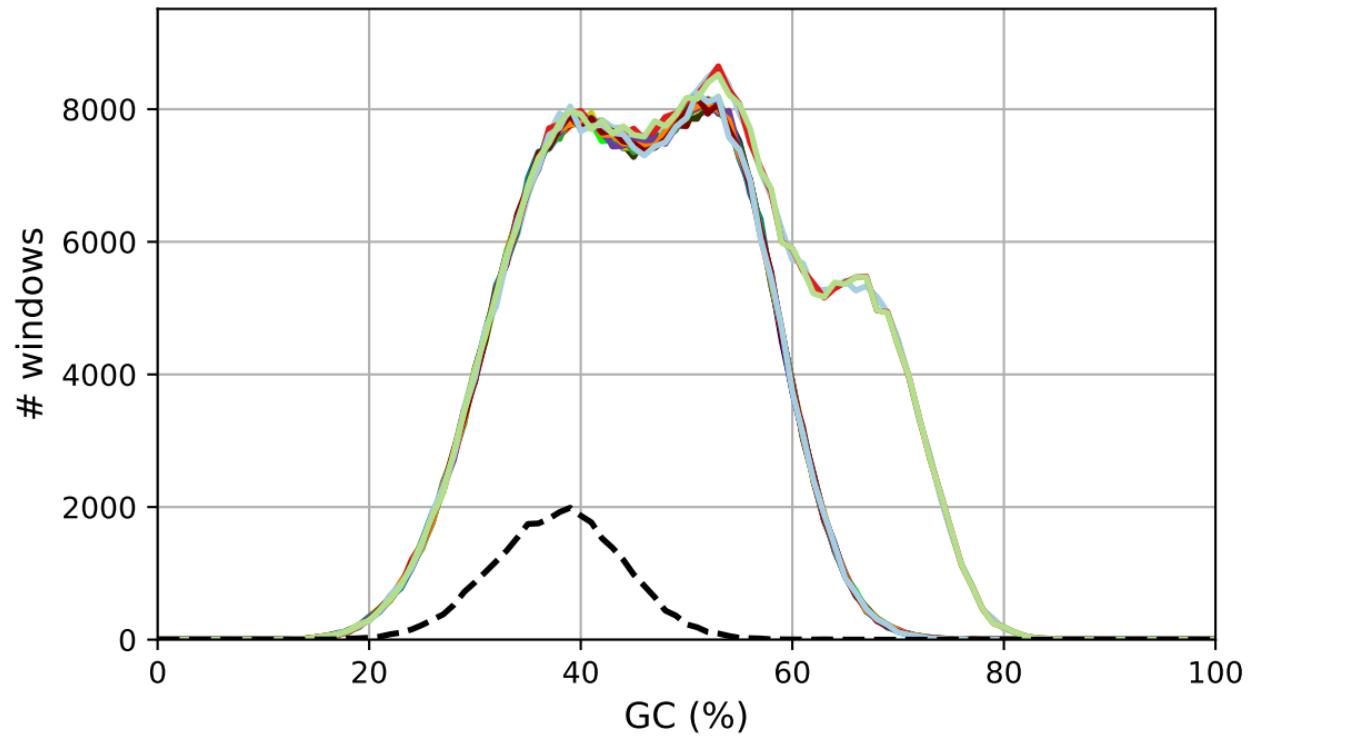
Series	Color	Line Style
r10_1bin_1_MP	Red	Solid
r10_1bin_1_MP_helen	Blue	Solid
r10_1bin_1_r1_medaka	Green	Solid
r10_1bin_1_r2_medaka	Purple	Solid
r10_1bin_2_MP	Light Green	Solid
r10_1bin_2_MP_helen	Black	Solid
r10_1bin_2_r1_medaka	Yellow	Solid
r10_1bin_2_r2_medaka	Dark Blue	Solid
r10_1bin_3_MP	Light Blue	Solid
r10_1bin_3_MP_helen	Dark Green	Solid
r10_1bin_3_r1_medaka	Purple	Solid
r10_1bin_3_r2_medaka	Orange	Solid

Cumulative length



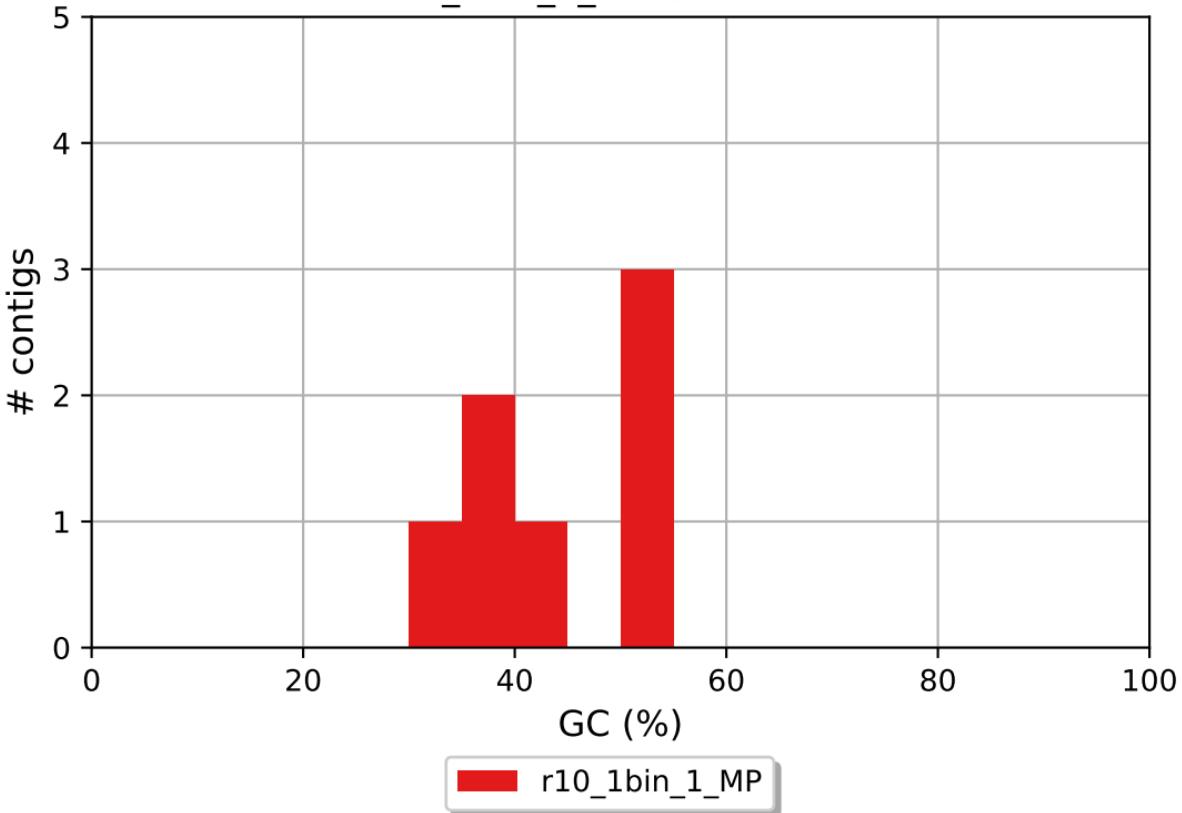
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— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_1_r2_medaka
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_2_r2_medaka
— r10_1bin_2_racoon_r1
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka
— r10_1bin_3_racoon_r1

GC content

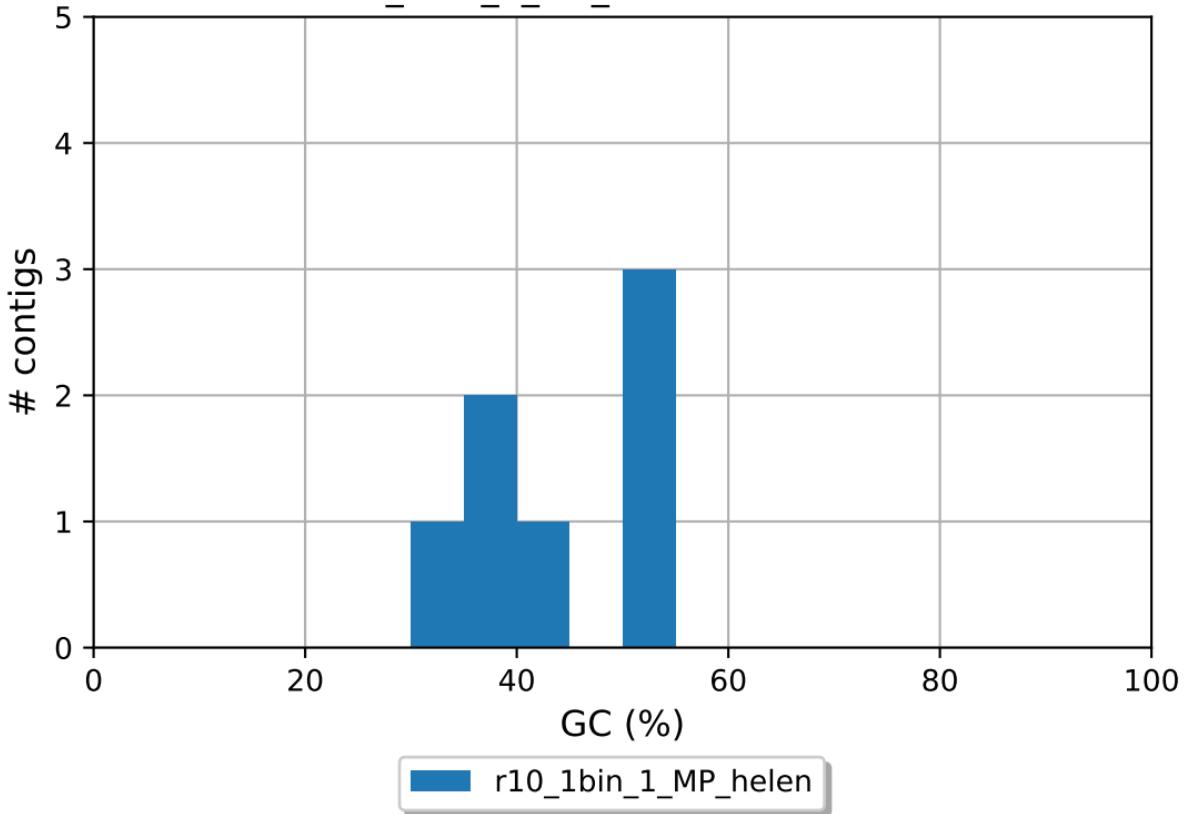


— r10_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_1_r2_medaka
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_2_r2_medaka
— r10_1bin_2_racop_r1
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka
— r10_1bin_3_racop_r1

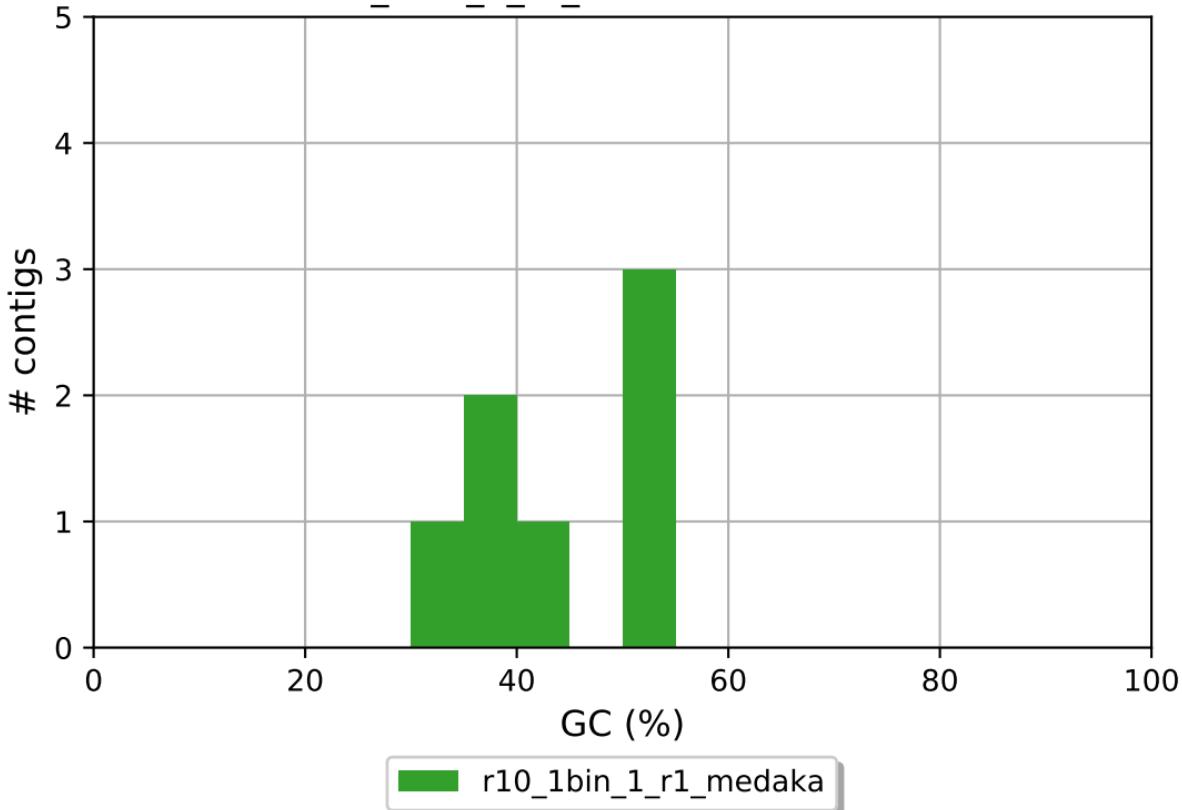
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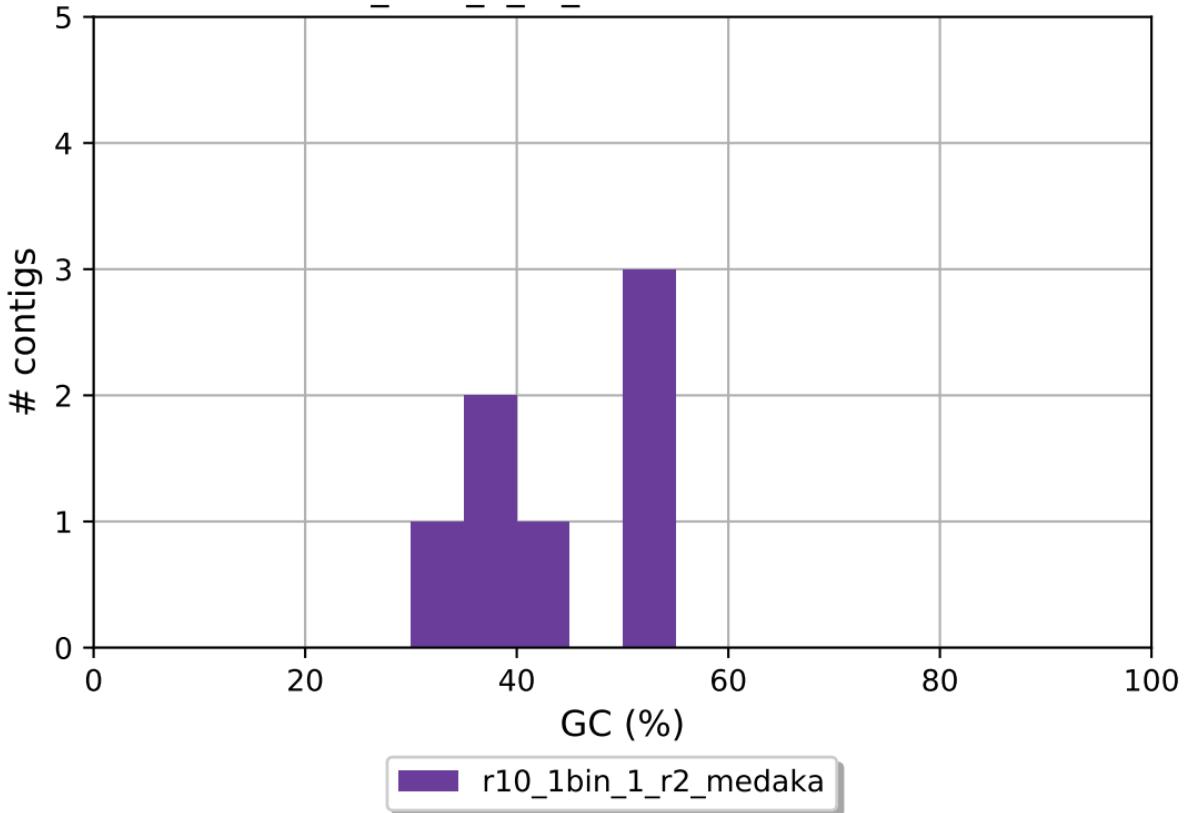
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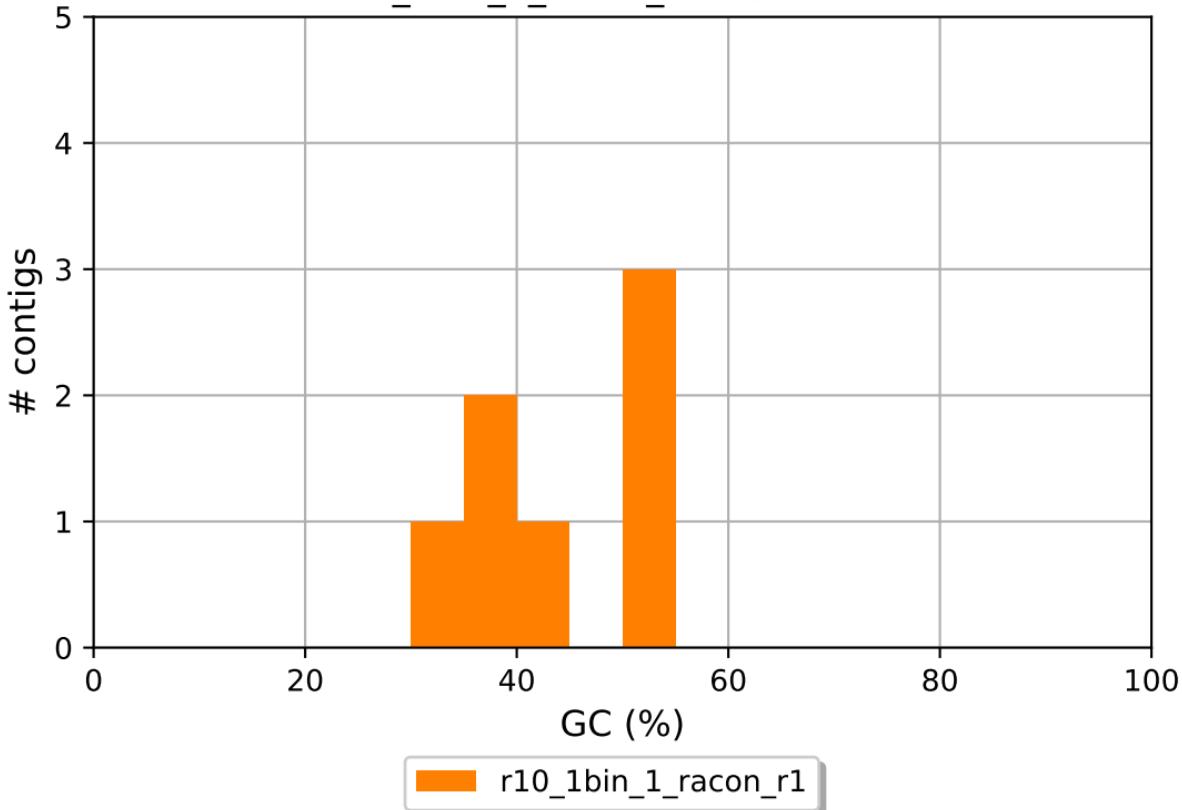
r10_1bin_1_r1_medaka GC content



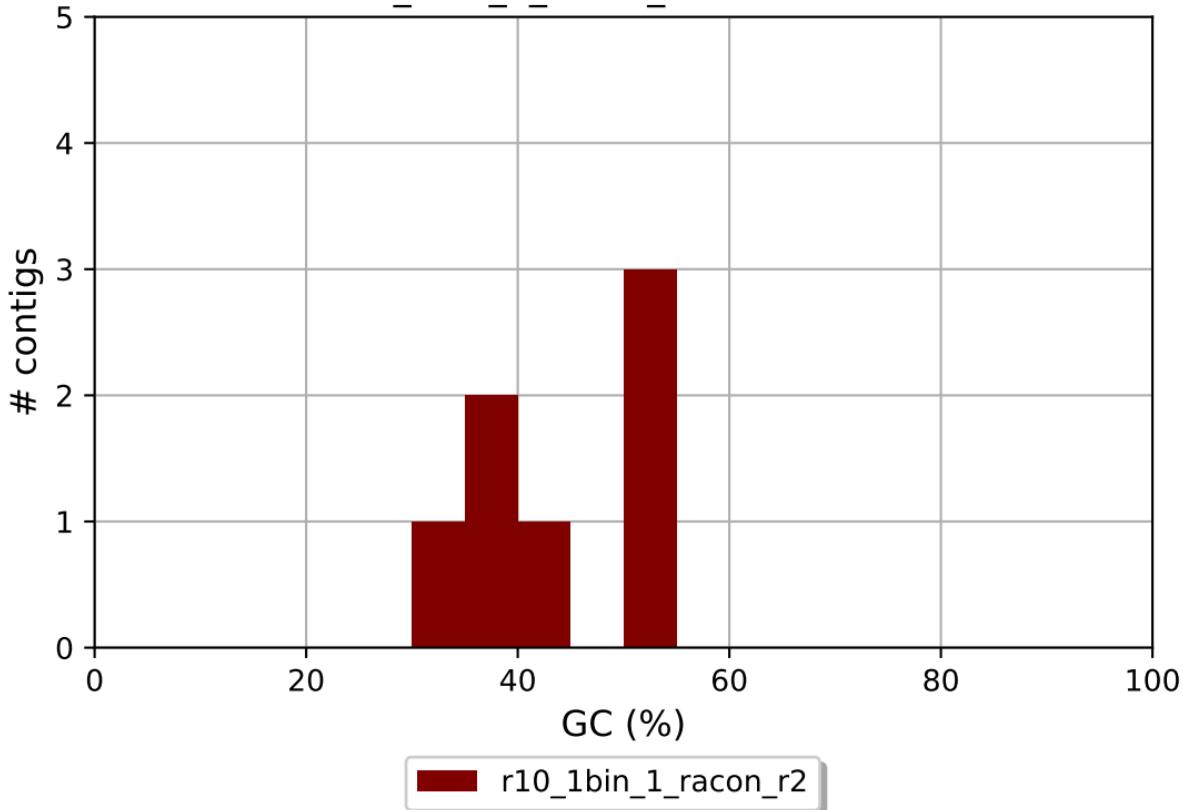
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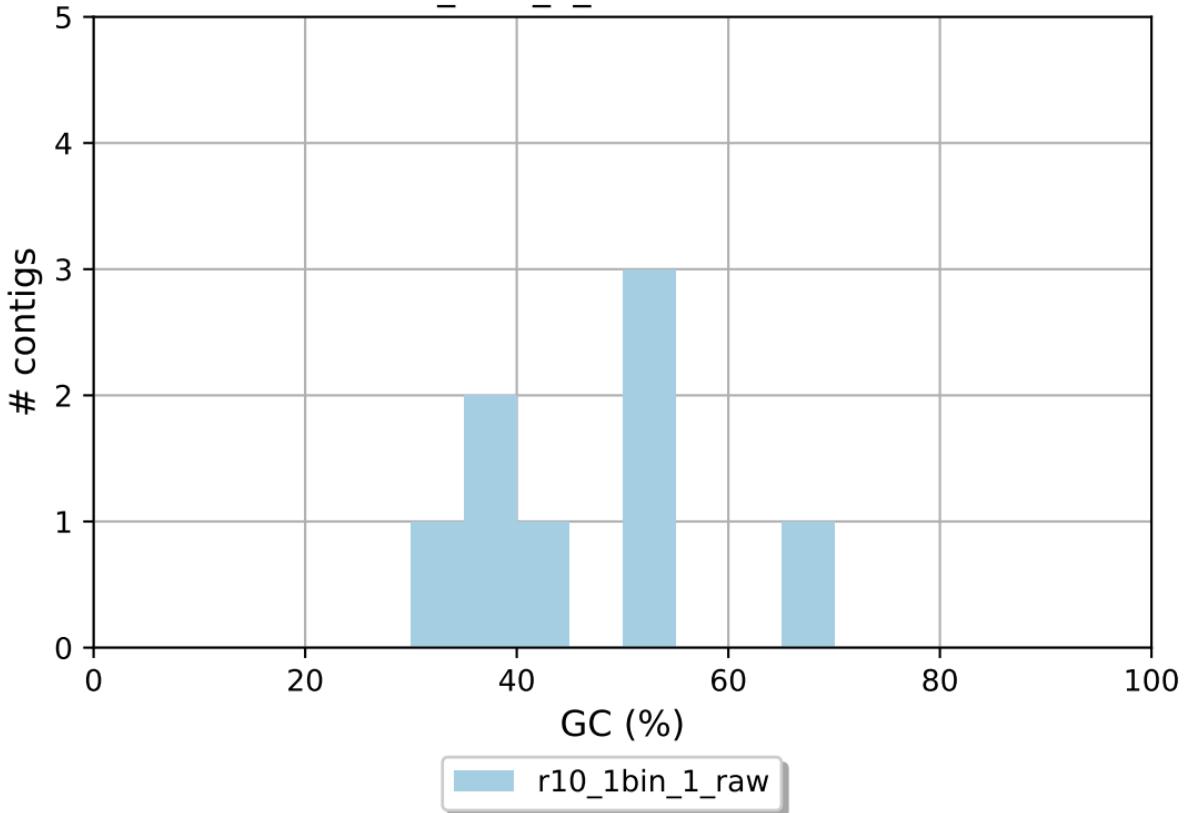
r10_1bin_1_racon_r1 GC content



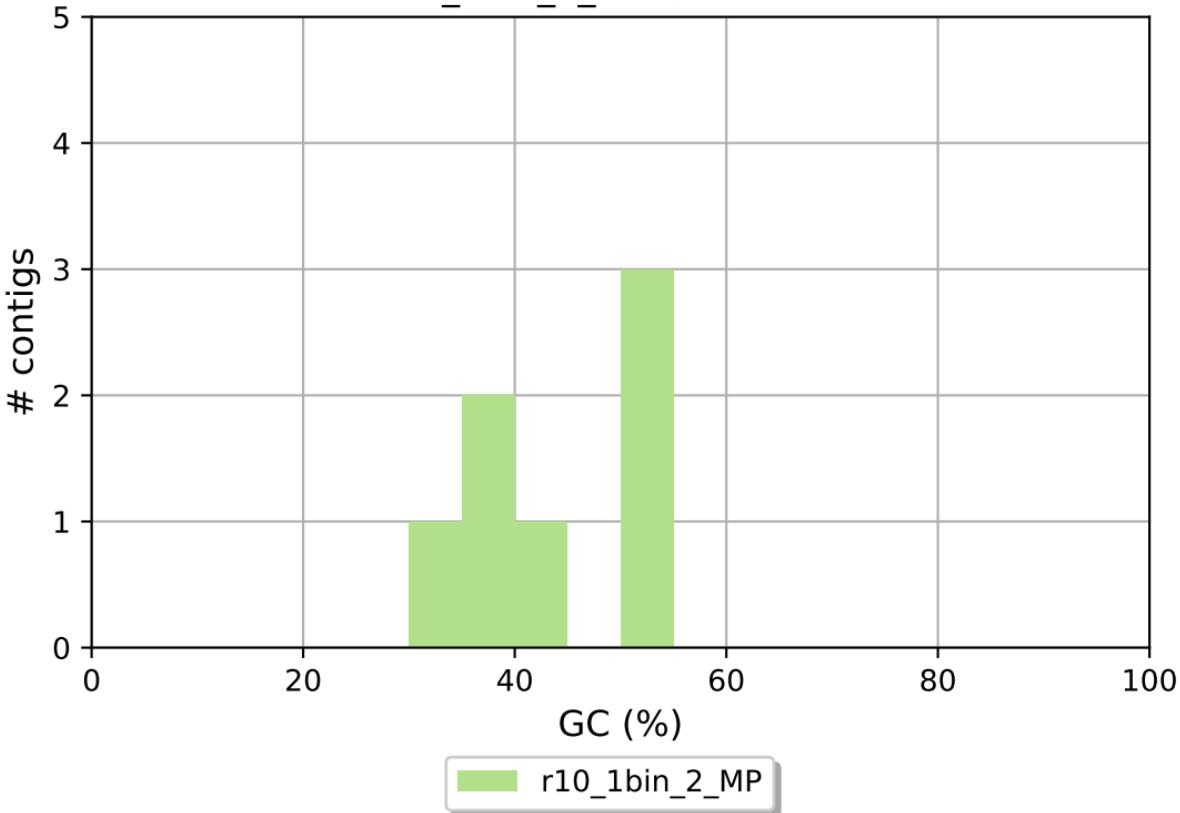
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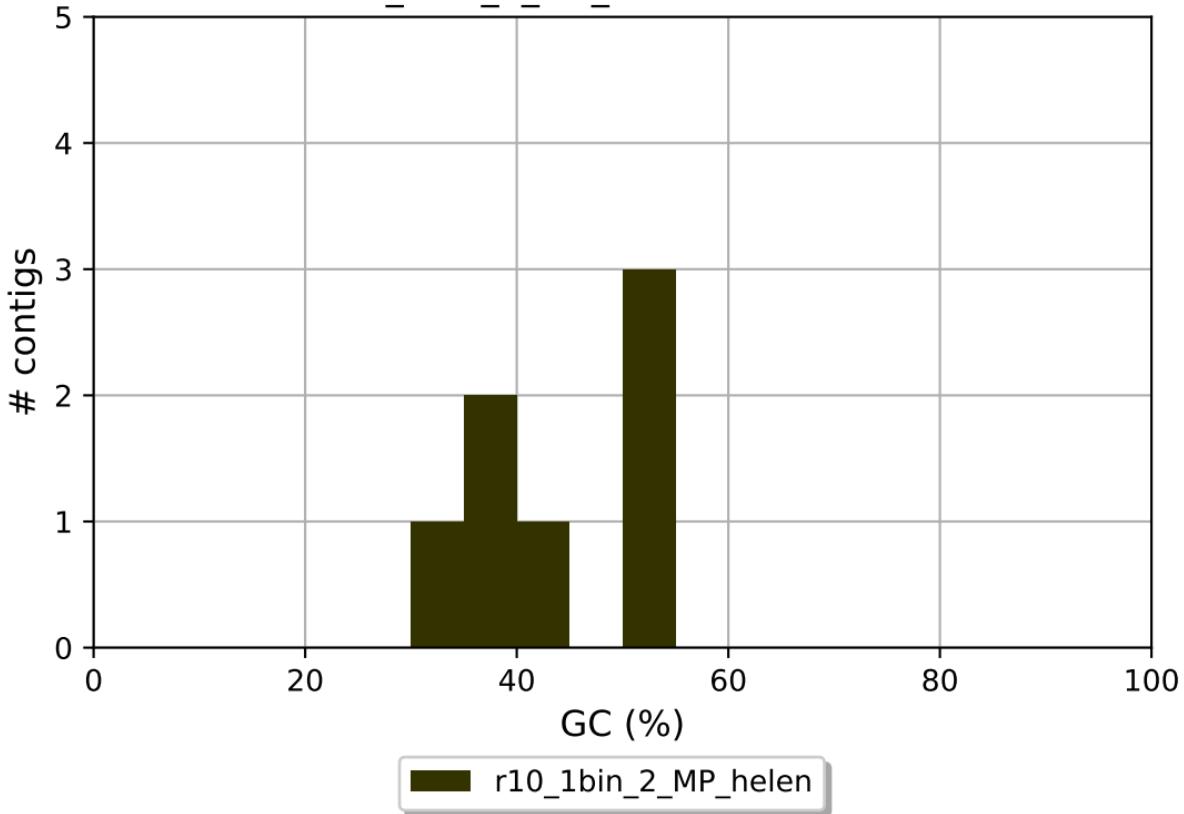
r10_1bin_1_raw GC content



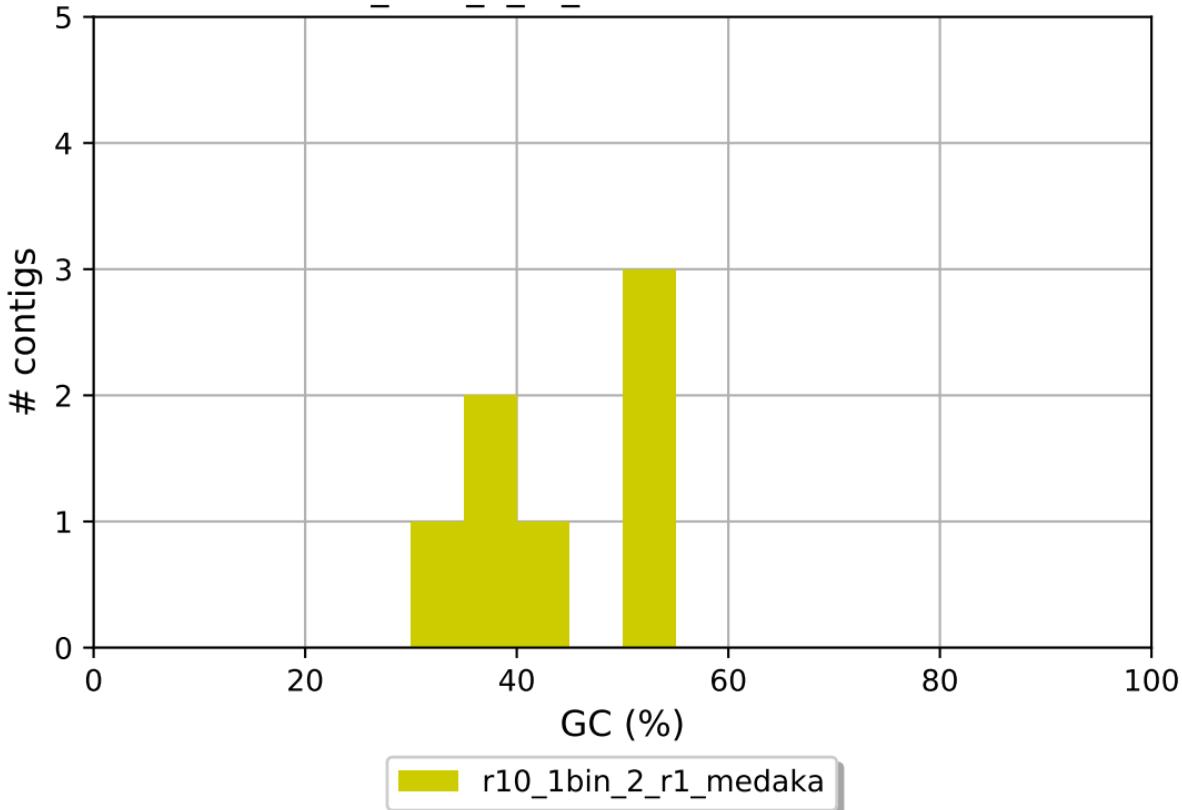
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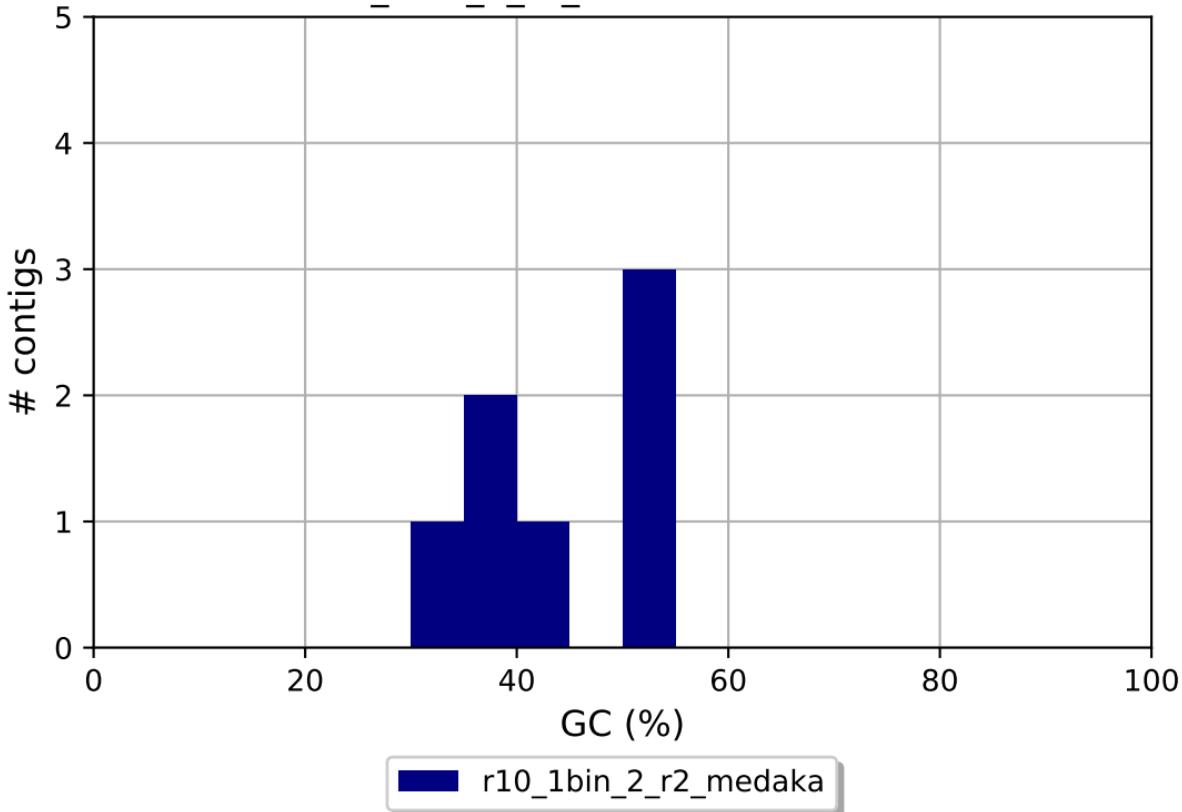
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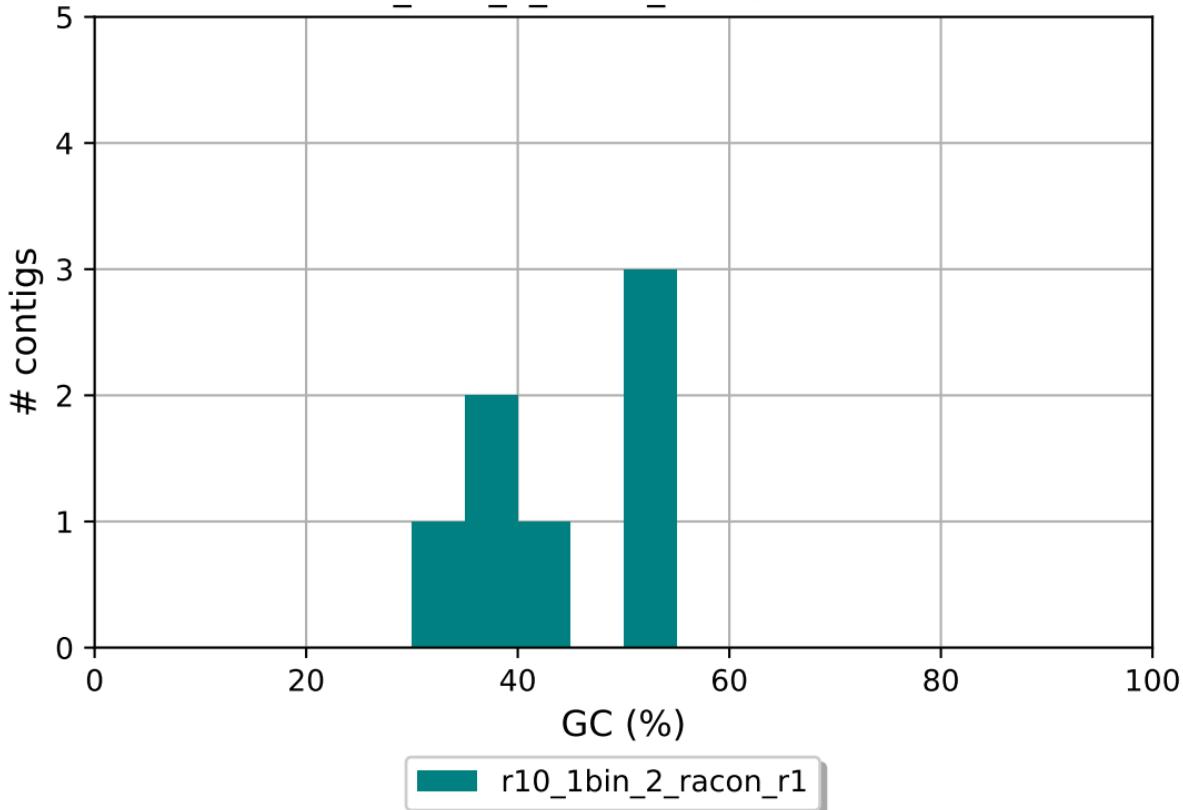
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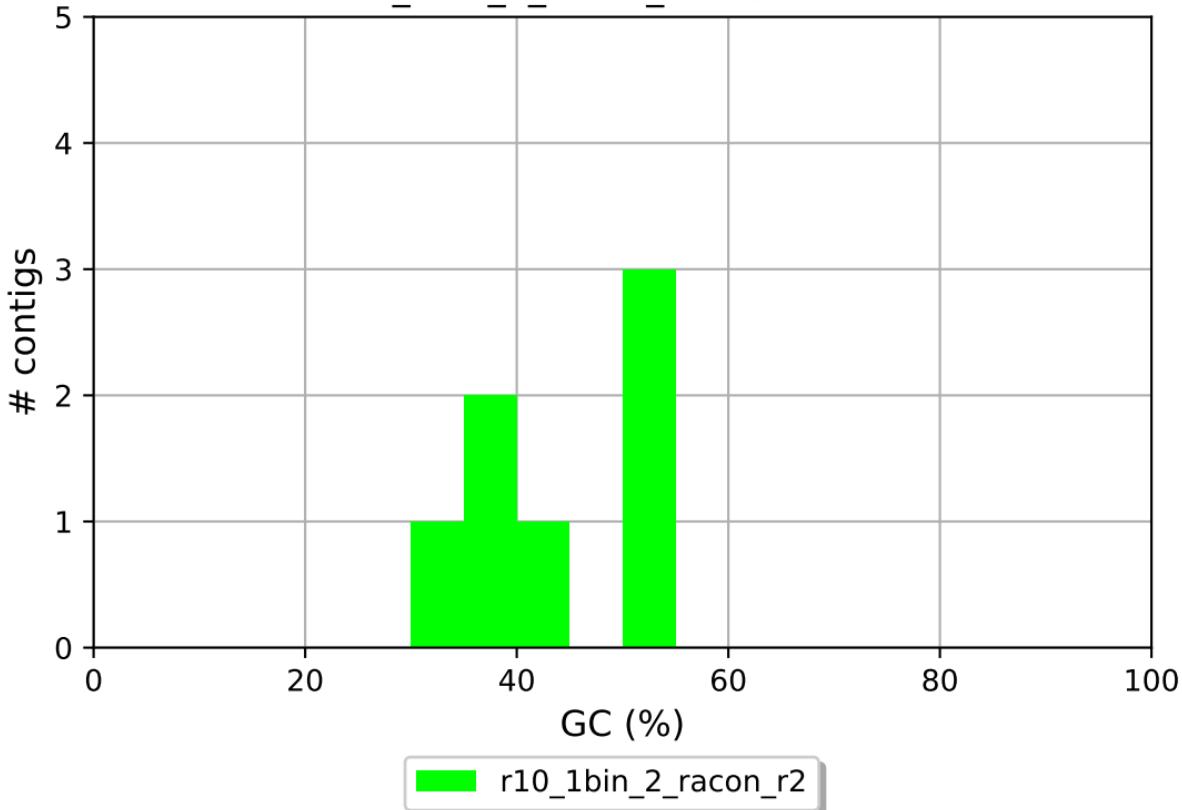
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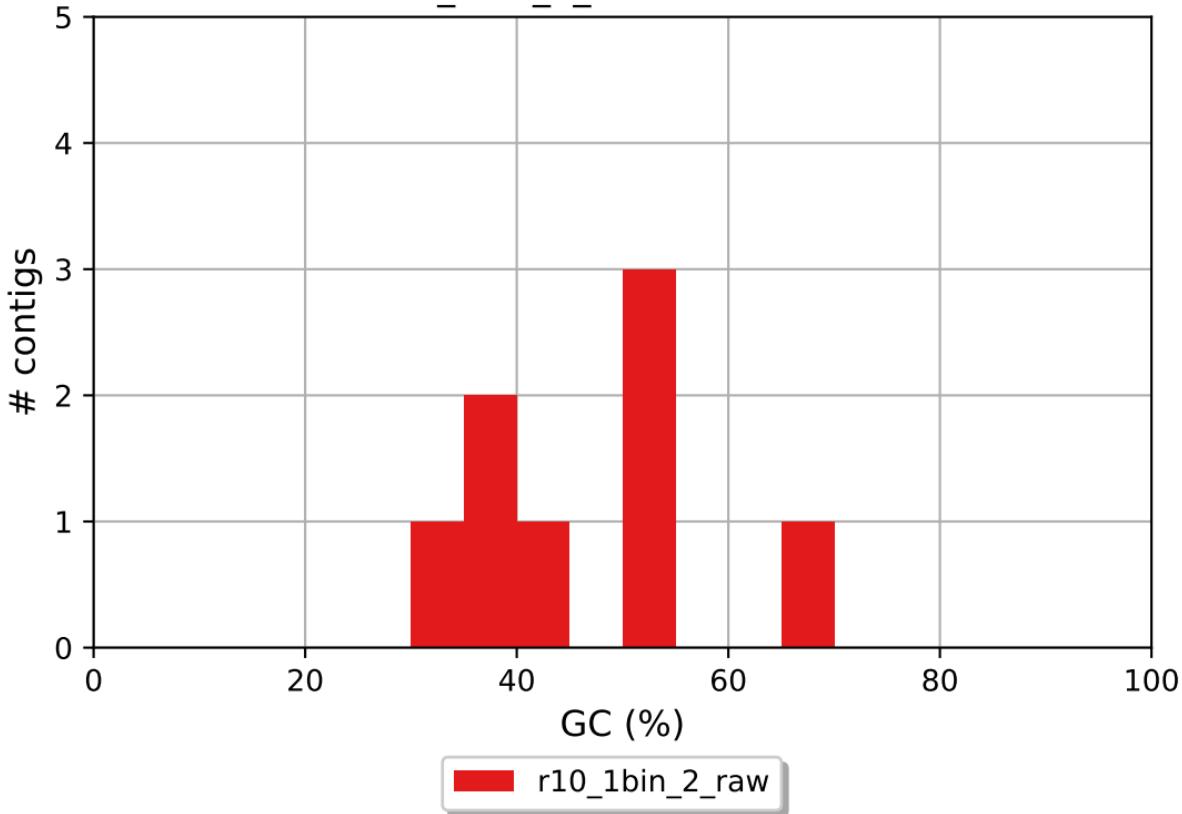
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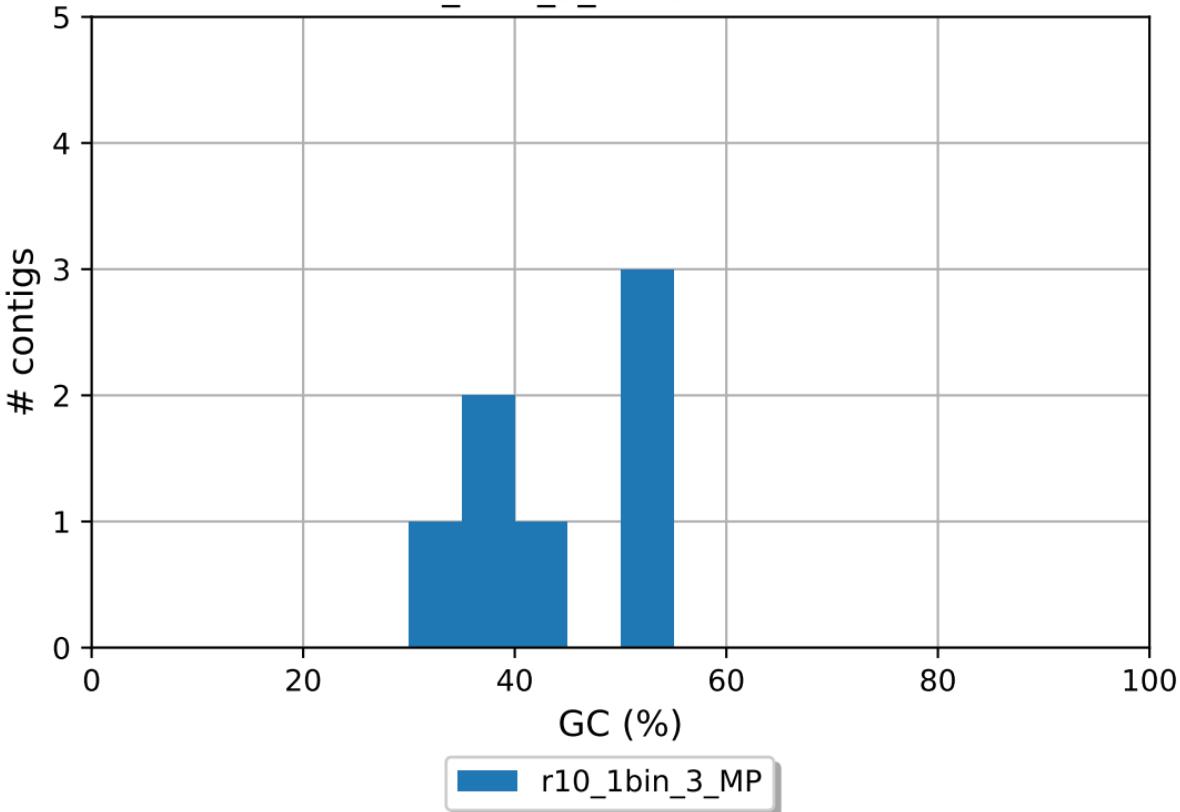
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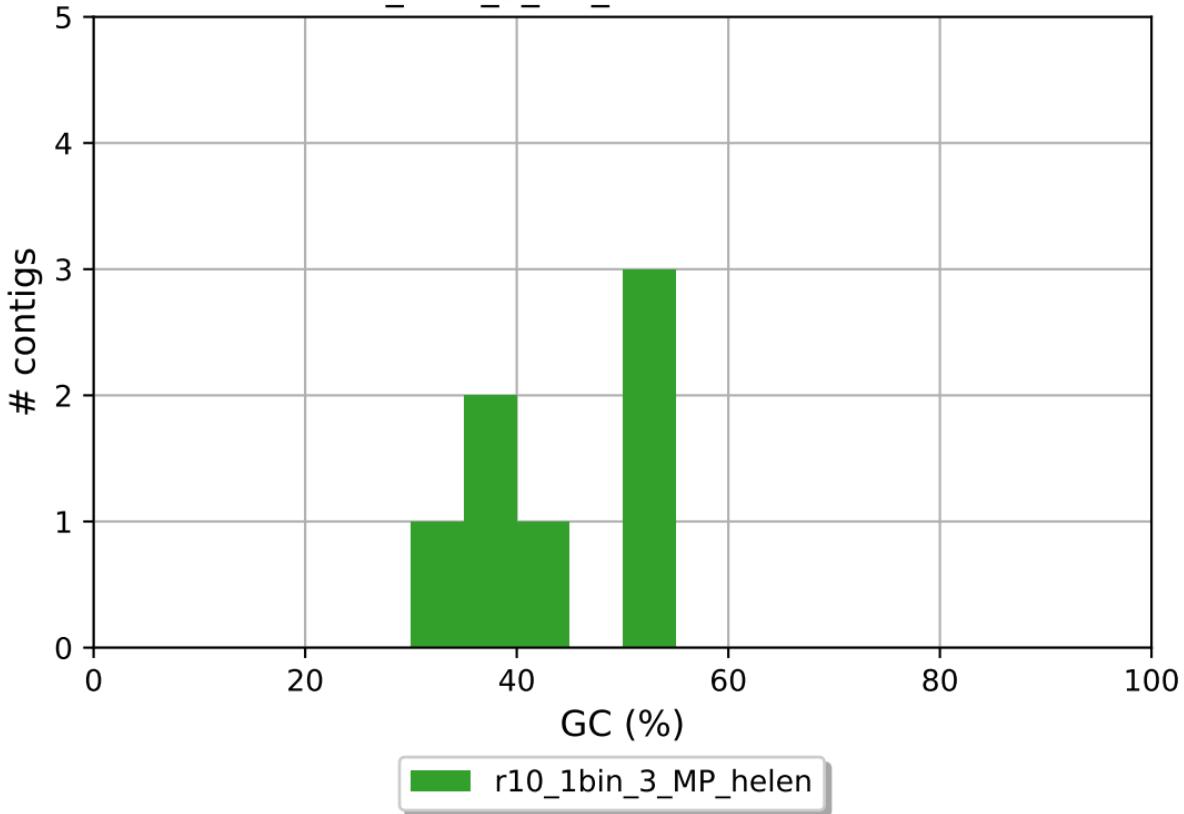
r10_1bin_2_raw GC content



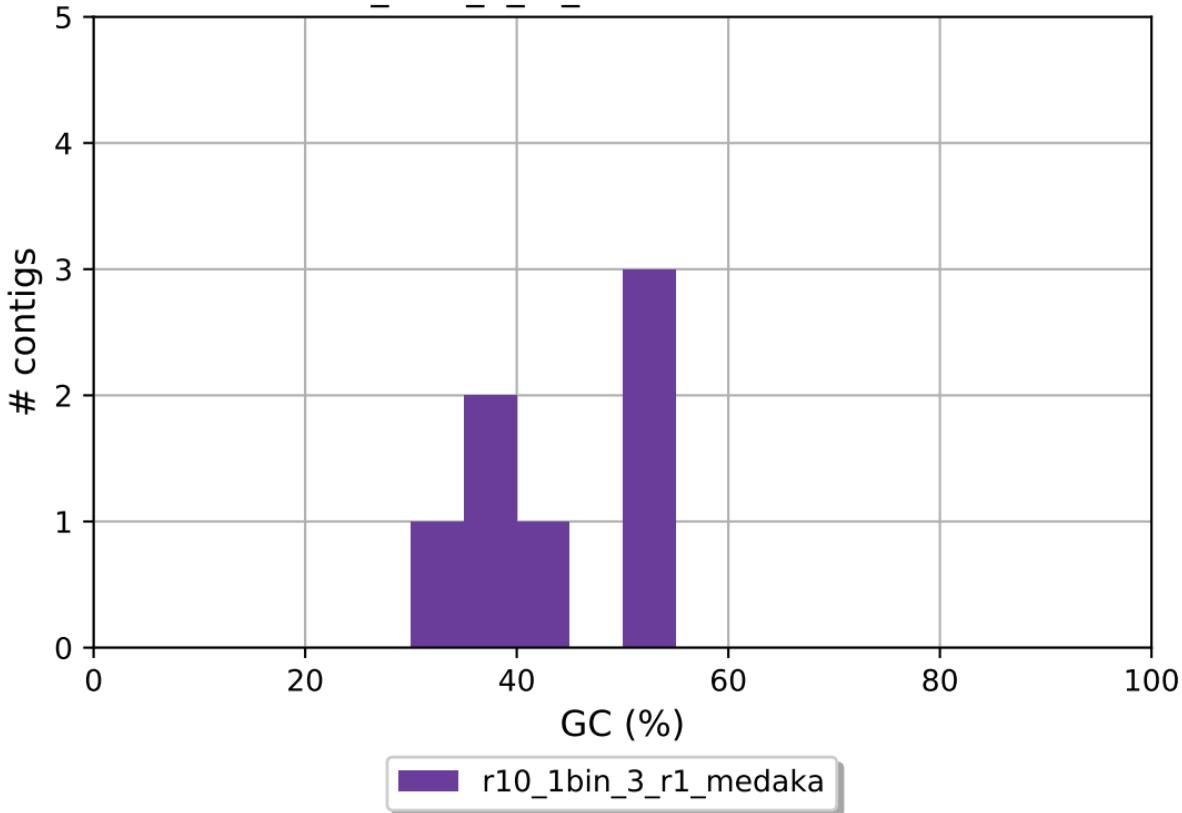
r10_1bin_3_MP GC content



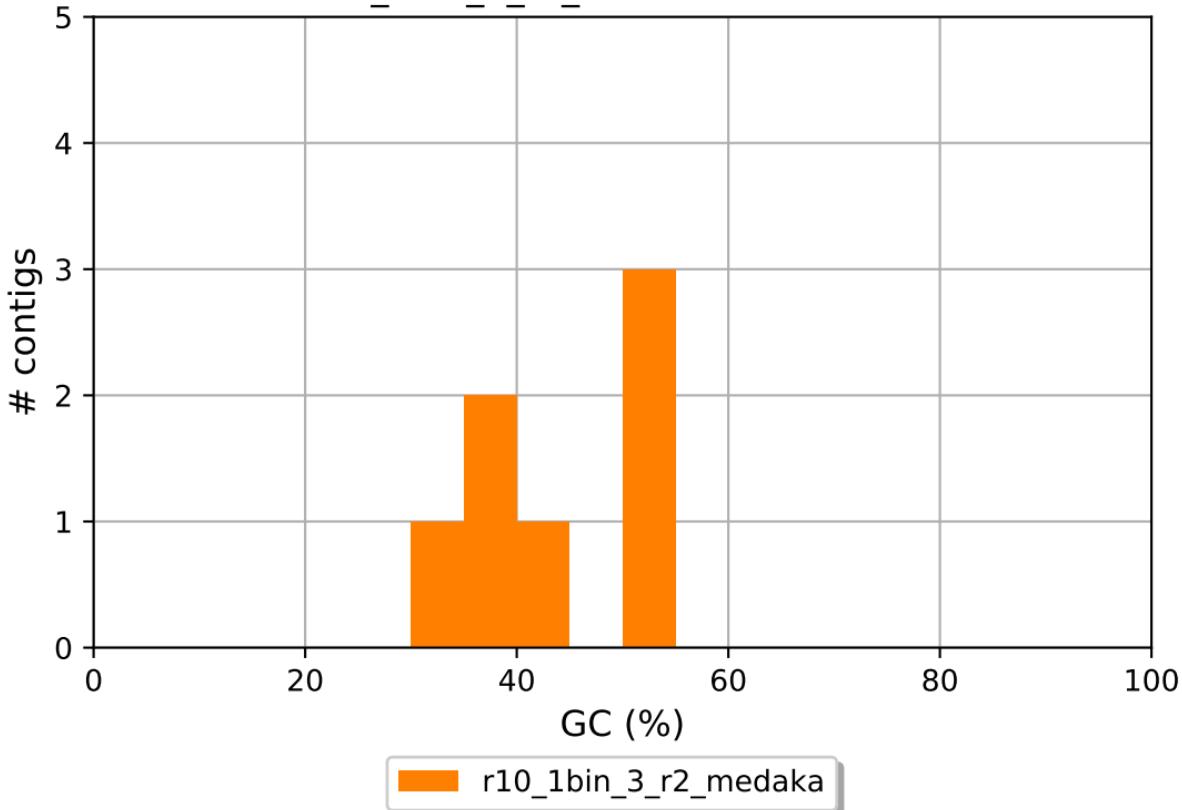
r10_1bin_3_MP_helen GC content



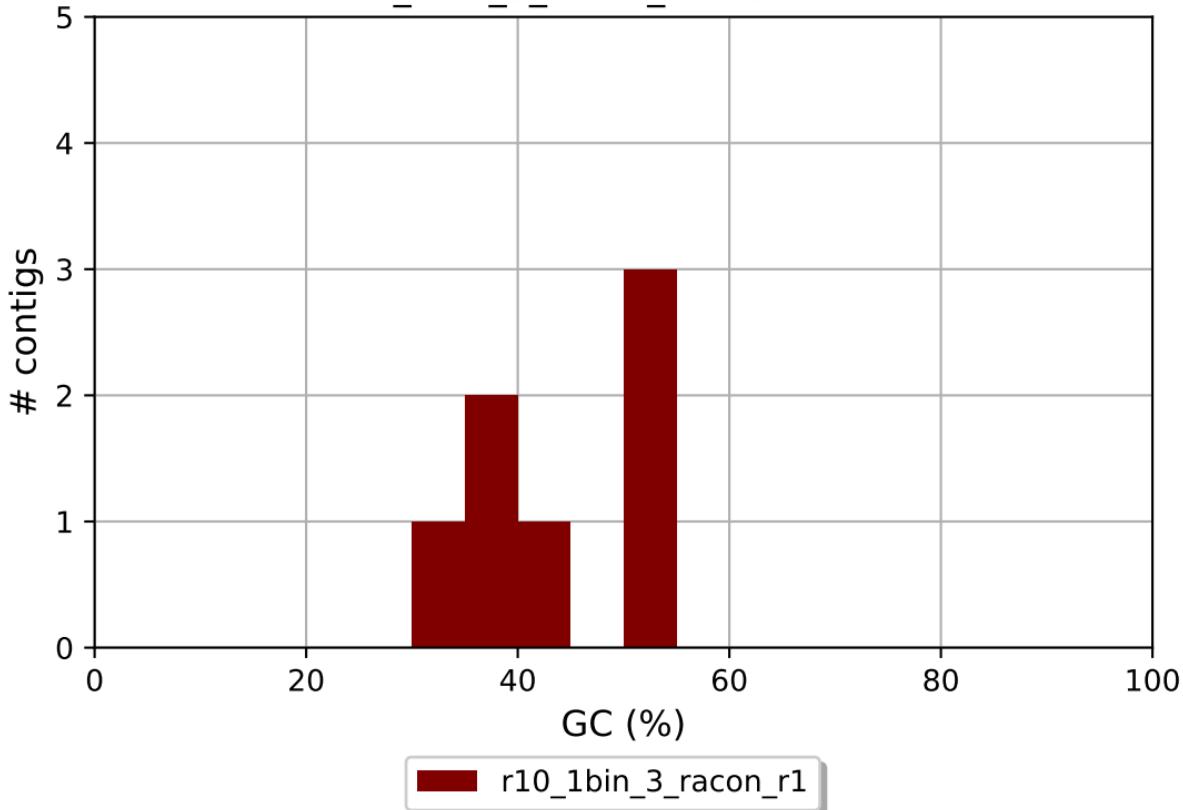
r10_1bin_3_r1_medaka GC content



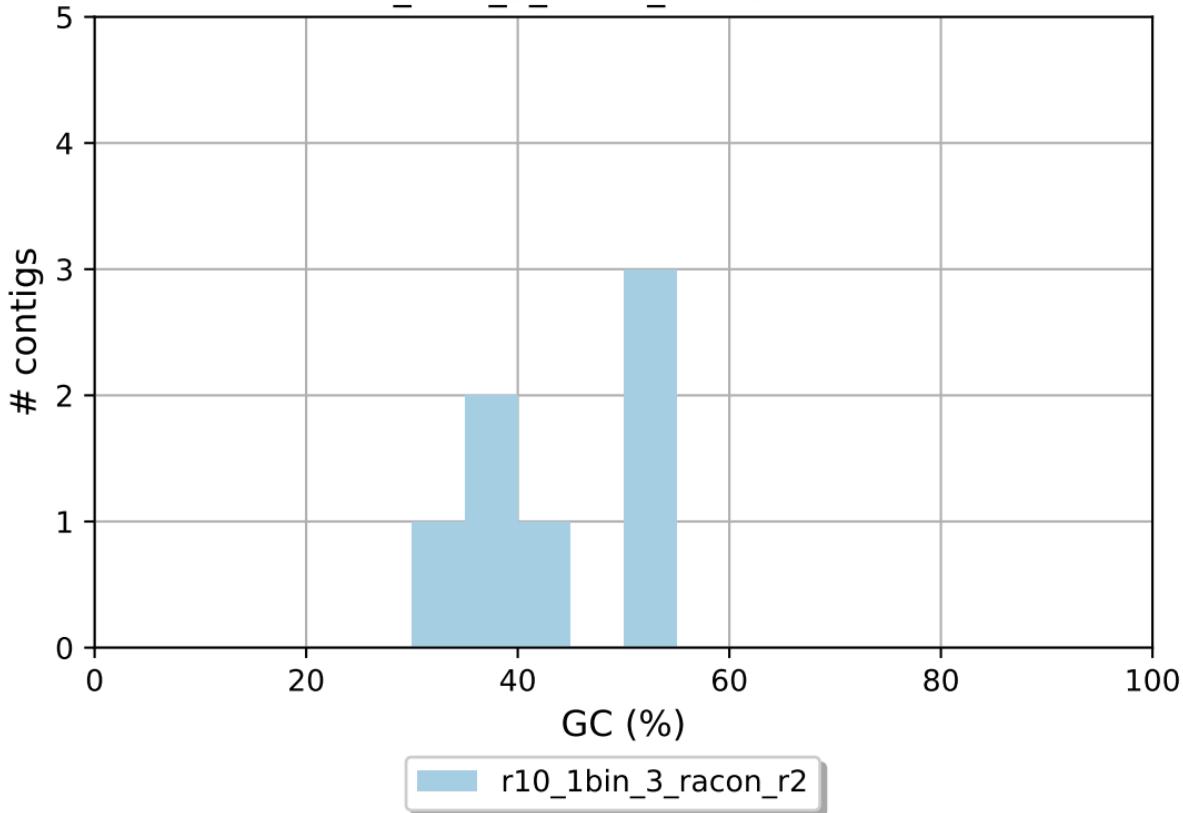
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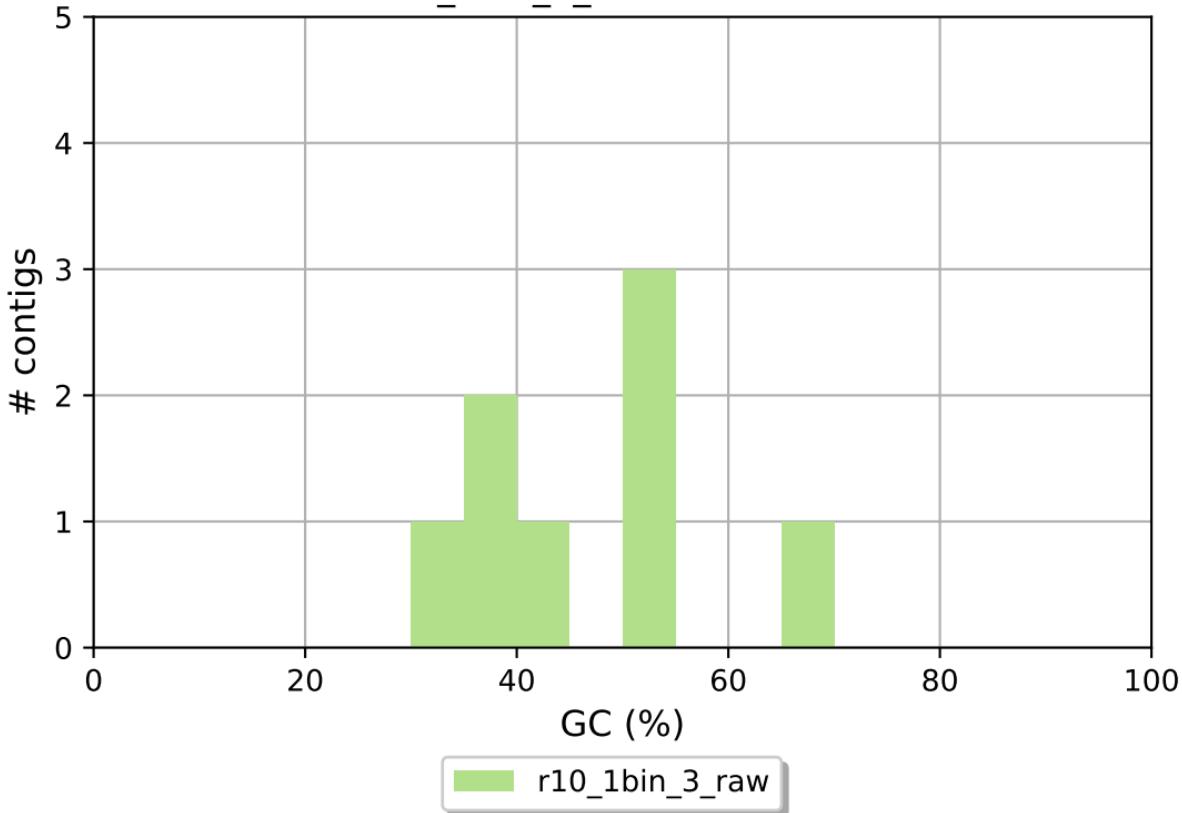
r10_1bin_3_racon_r1 GC content



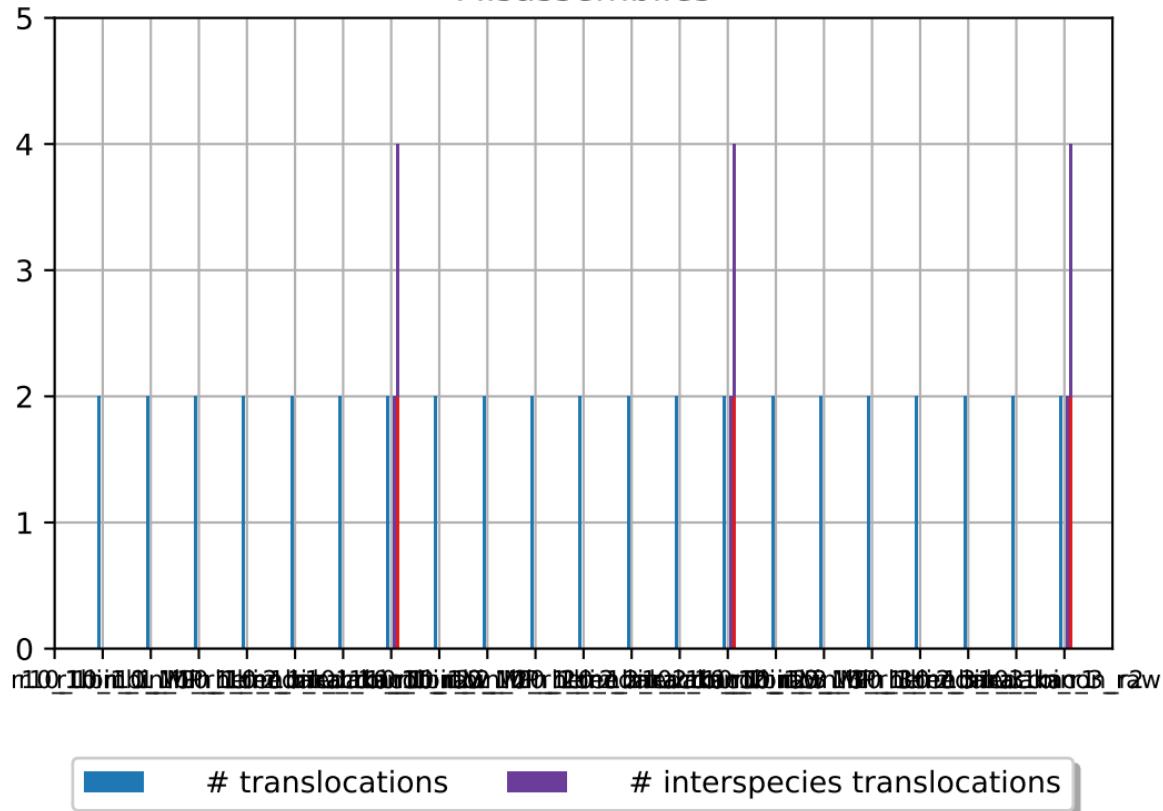
r10_1bin_3_racon_r2 GC content



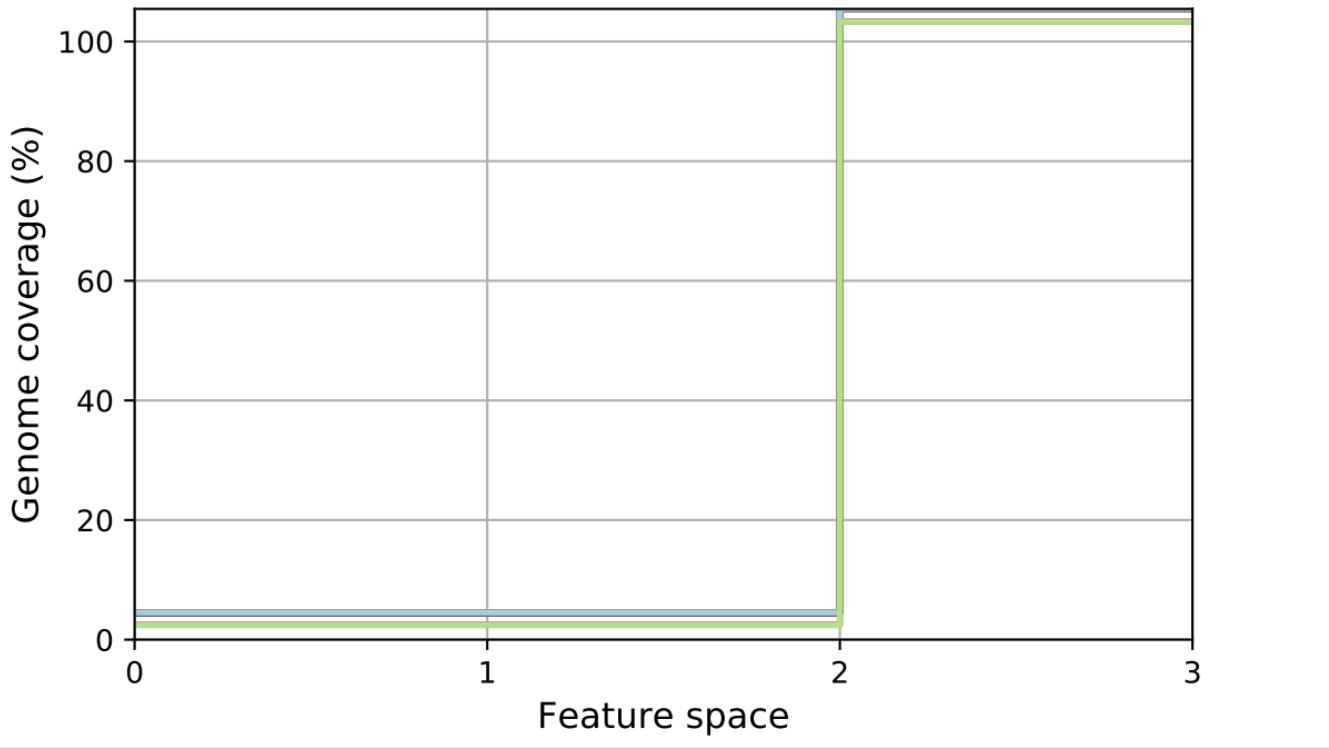
r10_1bin_3_raw GC content



Misassemblies

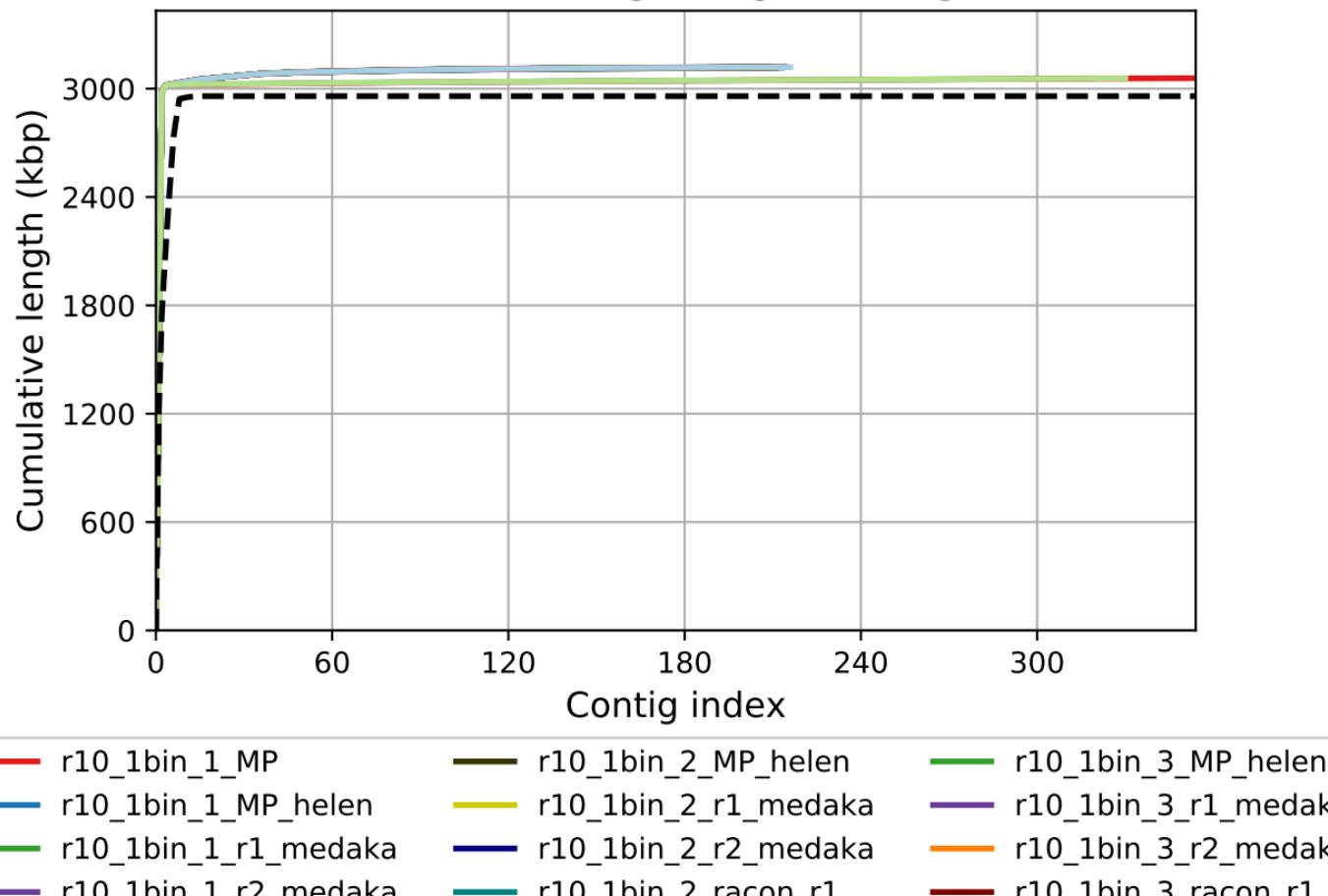


FRCurve (misassemblies)

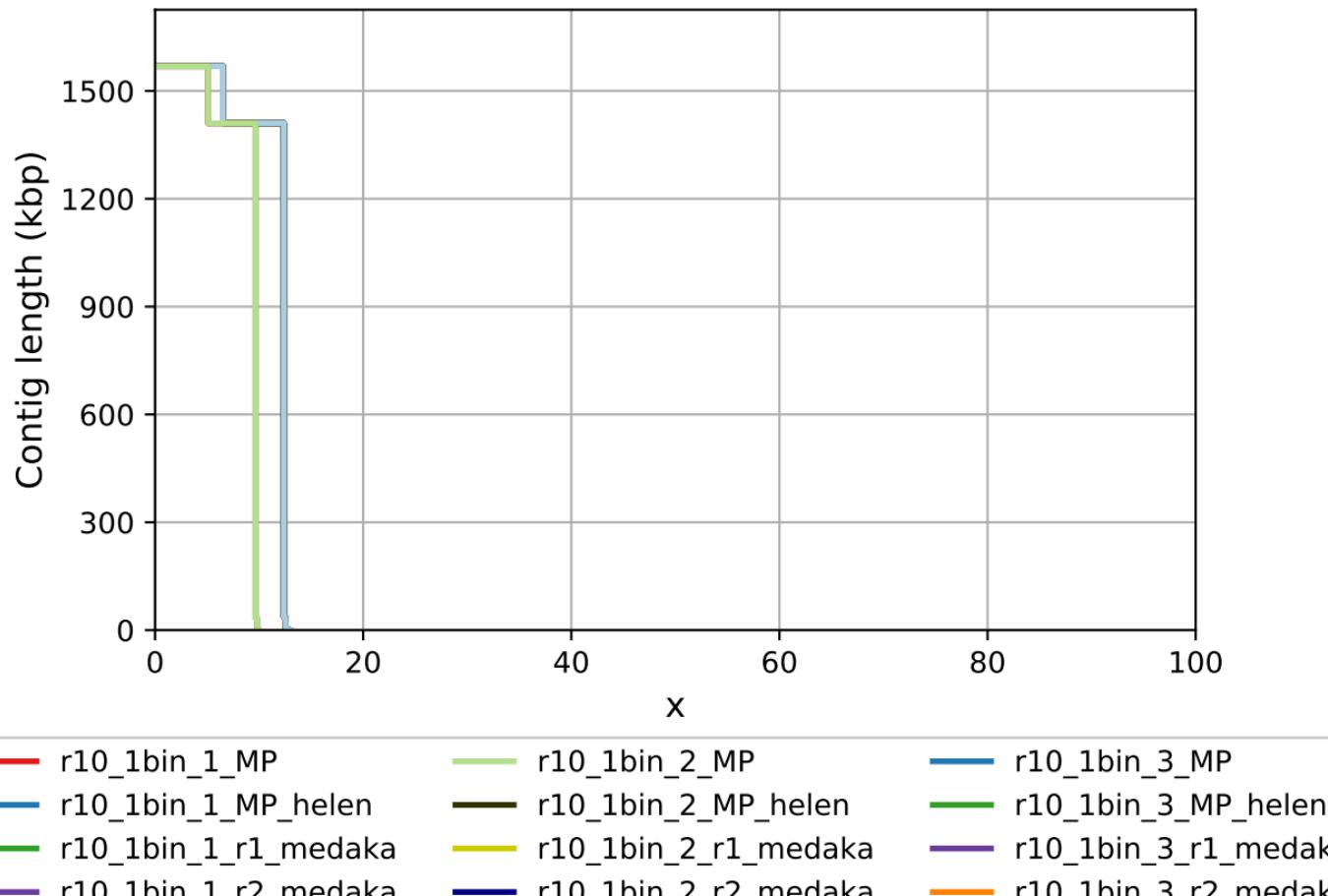


— r10_1bin_1_MP
— r10_1bin_1_MP_helen
— r10_1bin_1_r1_medaka
— r10_1bin_2_MP
— r10_1bin_2_MP_helen
— r10_1bin_2_r1_medaka
— r10_1bin_3_MP
— r10_1bin_3_MP_helen
— r10_1bin_3_r1_medaka
— r10_1bin_3_r2_medaka

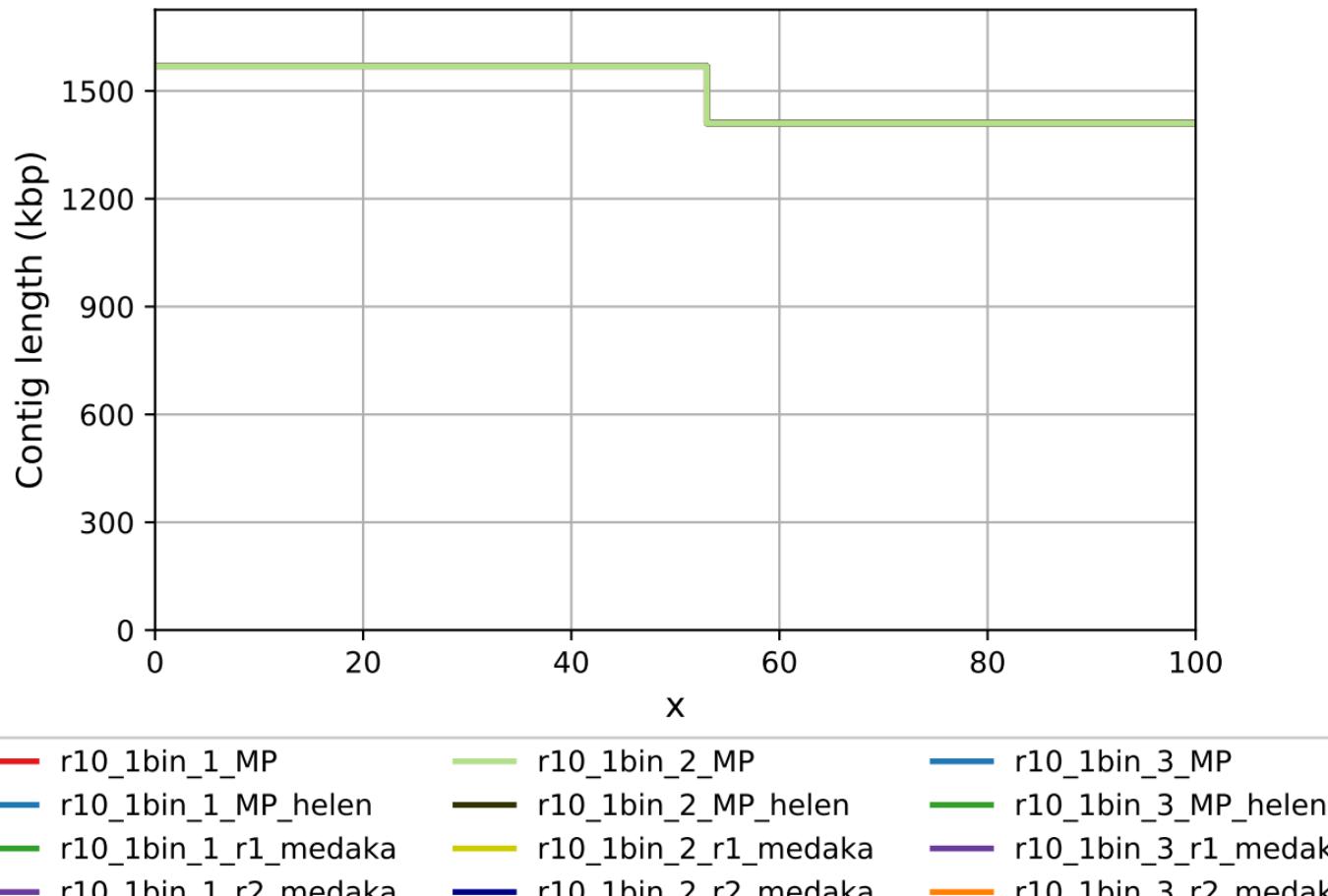
Cumulative length (aligned contigs)



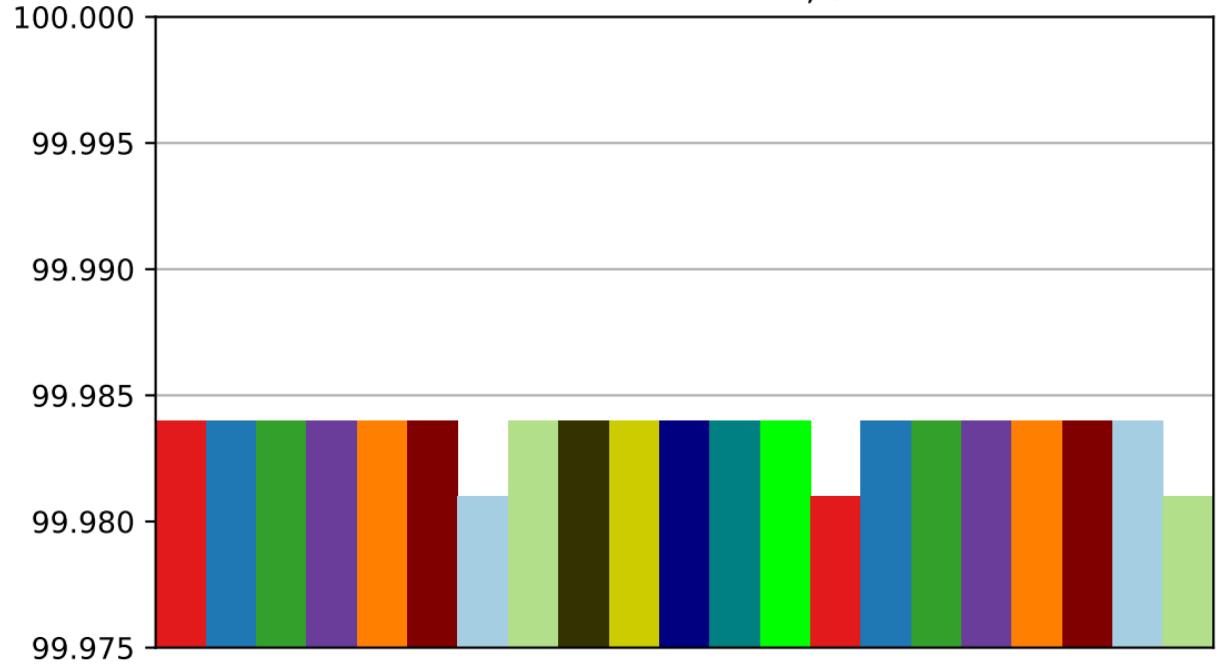
NAx



NGAx



Genome fraction, %



- 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
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medak
- r10_1bin_3_r2_medak