

Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw	
# contigs (>= 0 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 1000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Total length (>= 0 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Total length (>= 1000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Total length (>= 5000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Total length (>= 10000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Total length (>= 25000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Total length (>= 50000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Largest contig	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792395	6791556	6791638	6787718	
Total length	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959		
N50	4758942	4758045	4758082	4757996	4757676	4757433	4756098	4758934	4757811	4759010	4758465	4757950	4757851	4756089	4758933	4757839	4759025	4758469	4757998	4757867	4756074
N75	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992173	2991893	2991931	2990628	2992084	2992068	2992176	2991922	2991951	2990626	
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3		
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5		
# misassemblies	169	168	170	171	168	174	173	170	168	170	171	169	172	175	170	171	172	171	174	176	
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Misassembled contigs length	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30863583	30855714	30850694	30851667	
# local misassemblies	117	117	130	129	147	136	207	115	116	131	129	150	139	213	117	120	127	136	146	261	
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# unaligned contigs	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 + 8 part	0 + 8 part		
Unaligned length	78638	79438	81428	80407	78587	77441	136848	78652	80368	81775	78110	77641	138584	79262	81659	80873	81101	78367	76681	189211	
Genome fraction (%)	99.400	99.392	99.399	99.397	99.398	99.395	99.370	99.400	99.399	99.398	99.398	99.397	99.370	99.399	99.399	99.397	99.397	99.396	99.211		
Duplication ratio	1.044	1.044	1.044	1.043	1.043	1.043	1.028	1.044	1.044	1.043	1.043	1.043	1.027	1.044	1.044	1.043	1.043	1.043	1.028		
# N's per 100 kbp	0.00	0.03	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	0.32		
# mismatches per 100 kbp	176.16	168.04	177.89	175.27	178.44	175.71	273.54	176.40	168.25	177.61	175.37	177.38	178.28	273.80	176.13	168.17	181.02	176.01	179.04	178.79	281.55
# indels per 100 kbp	38.14	22.42	26.90	26.56	66.12	62.58	309.41	38.45	23.87	43.40	42.62	66.34	62.35	309.83	38.42	23.62	43.55	42.69	65.27	62	

Misassemblies report

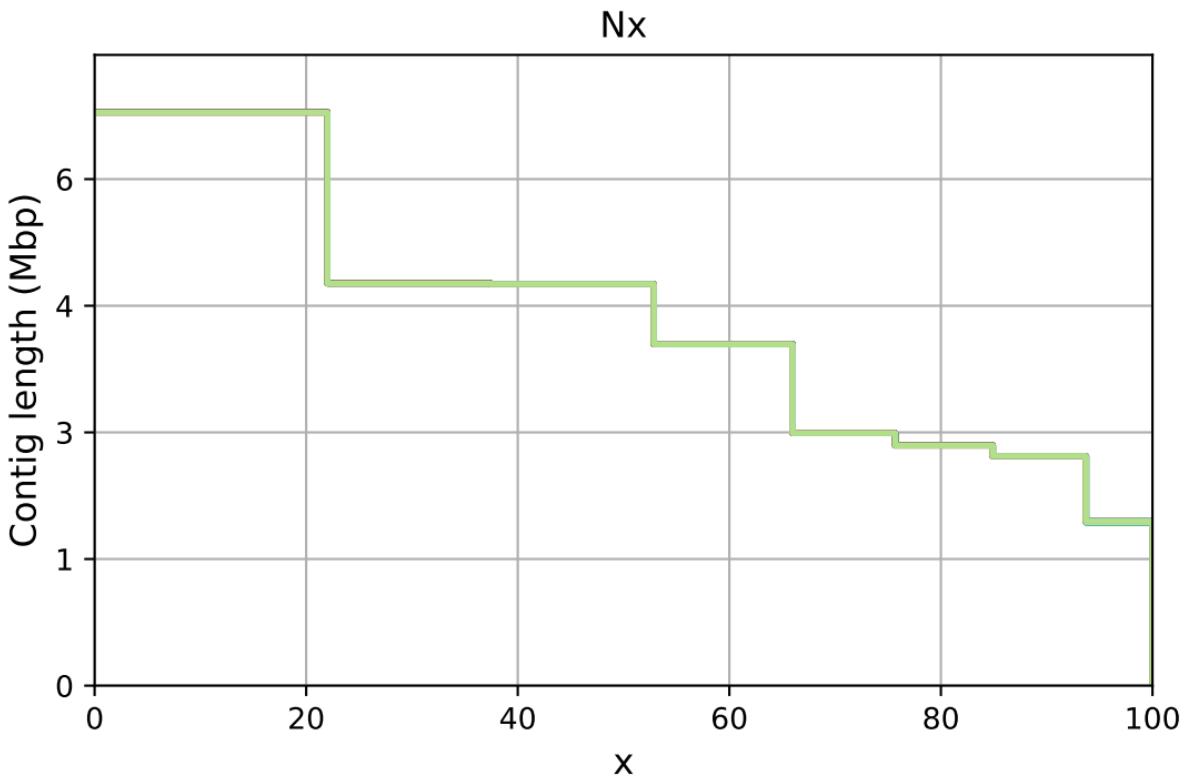
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# misassemblies	169	168	170	171	168	174	173	170	168	170	171	169	172	175	170	172	171	174	176		
# contig misassemblies	169	168	170	171	168	174	173	170	168	170	171	169	172	175	170	172	171	174	175		
# c. relocations	5	5	4	7	4	7	5	6	4	7	5	6	5	6	5	6	5	7	6		
# c. translocations	162	161	164	162	162	165	164	162	163	162	163	166	162	163	164	162	164	165	165		
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2		
# c. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2		
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1		
# 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	1		
# s. inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# s. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8		
Misassembled contigs length	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
# possibly misassembled contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	7	7	7	7	7	8		
# possible misassemblies	98	98	96	98	98	96	165	98	98	96	98	96	98	96	98	96	94	100	90	232	
# local misassemblies	117	117	130	129	147	136	207	115	116	131	129	150	139	213	117	120	127	136	146	145	261
# 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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# misassemblies caused by fragmented reference	252	253	251	253	252	252	181	252	253	250	251	173	254	250	249	247	247	247	179		
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
# mismatches	53422	50956	53947	53151	54113	53283	82928	53496	51023	53862	53182	53791	54064	83008	53415	50987	54896	53376	54296	54219	85224
# indels	11565	6799	8159	8053	20051	18978	93804	11660	7238	13161	12926	20118	18907	93931	11650	7161	13208	12947	19794	19048	94972
# indels (<= 5 bp)	10897	6143	7559	7448	19386	18329	92550	11014	6576	12564	12320	19465	18271	92705	11003	6486	12610	12352	19120	18383	93741
# indels (> 5 bp)	668	656	600	605	665	649	1254	646	662	597	606	653	636	1226	647	675	598	595	674	665	1231
Indels length	45931	40873	41062	41412	58395	56336	158948	45924	41423	46688	46470	57921	55235	158543	45656	46825	41353	46525	58181	56940	160047

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

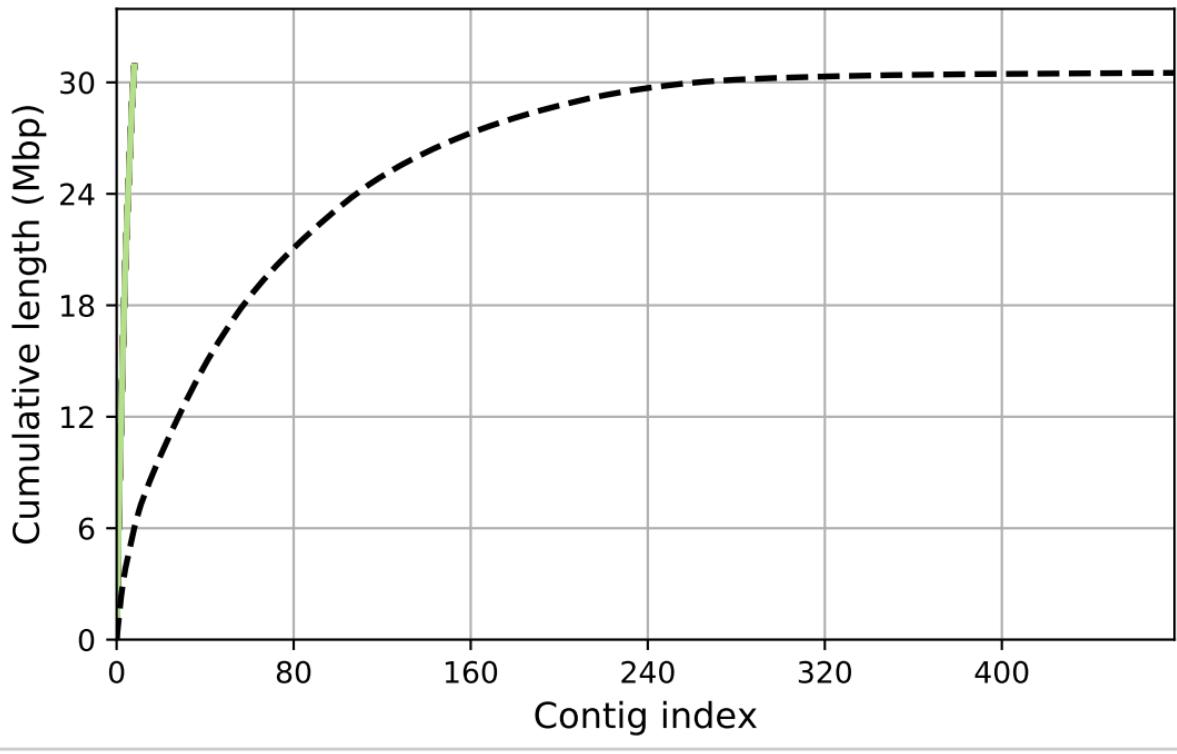
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# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# partially unaligned contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	
Partially unaligned length	78638	79438	81428	80407	78587	77441	136848	78652	78658	80368	78110	77641	138584	79262	81659	80873	81101	78367	76681	189211
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	100	

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_v3_1_MP	r10_1bin_v3_2_MP	r10_1bin_v3_3_MP
r10_1bin_v3_1_MP_helen	r10_1bin_v3_2_MP_helen	r10_1bin_v3_3_MP_helen
r10_1bin_v3_1_r1_medaka	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_3_r1_medaka
r10_1bin_v3_1_r2_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_3_r2_medaka

Cumulative length



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1

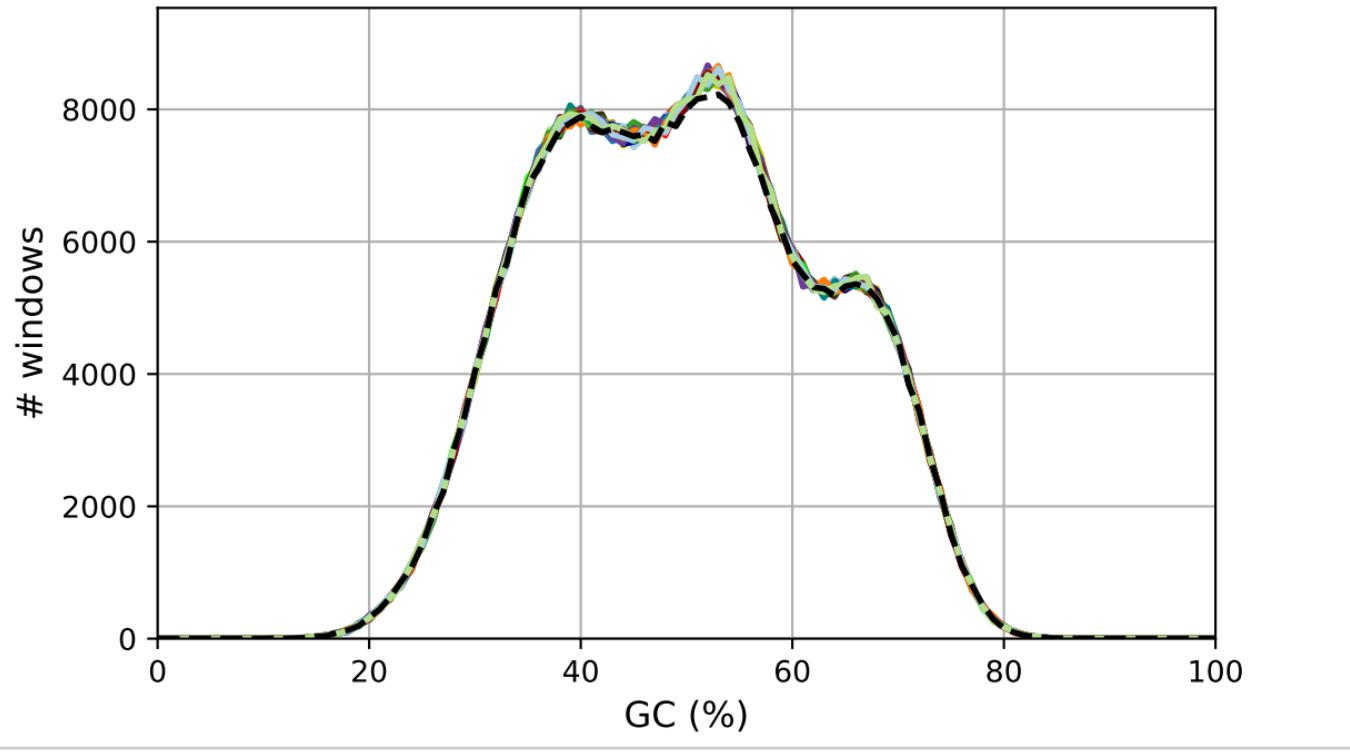
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r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

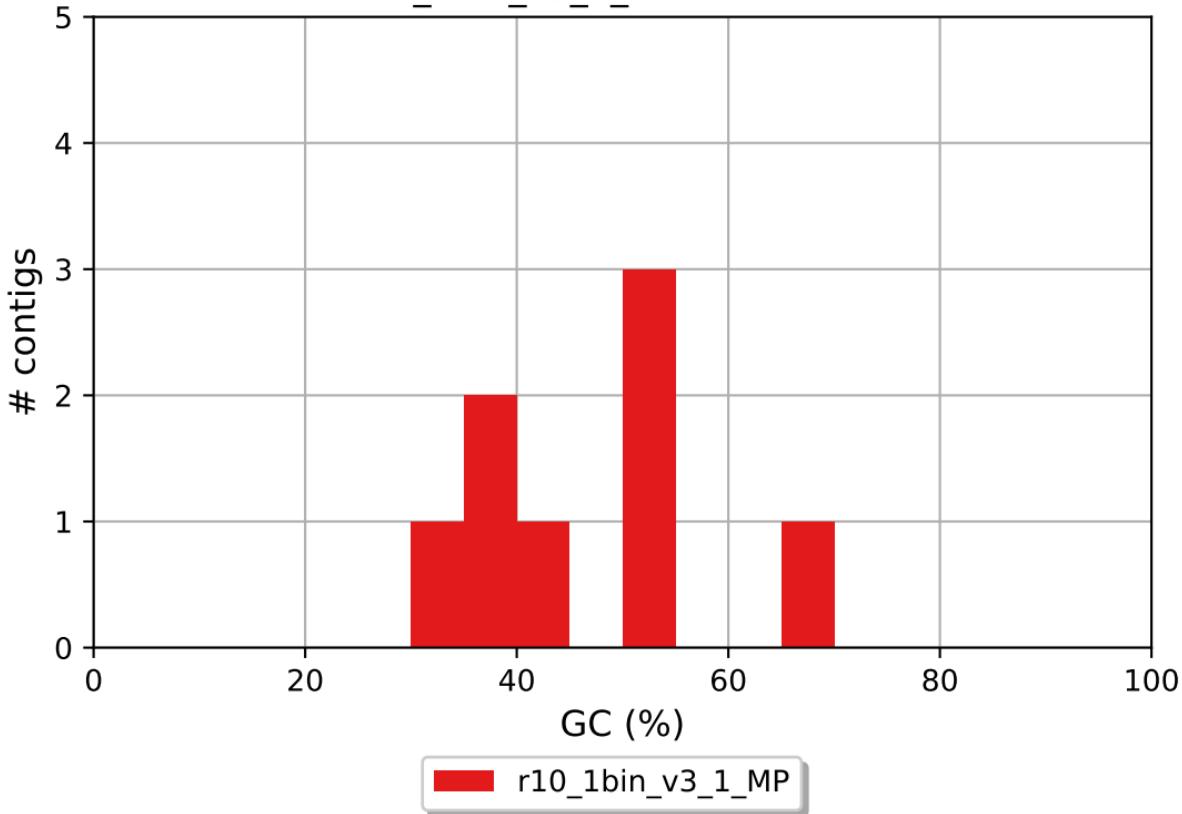
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GC content

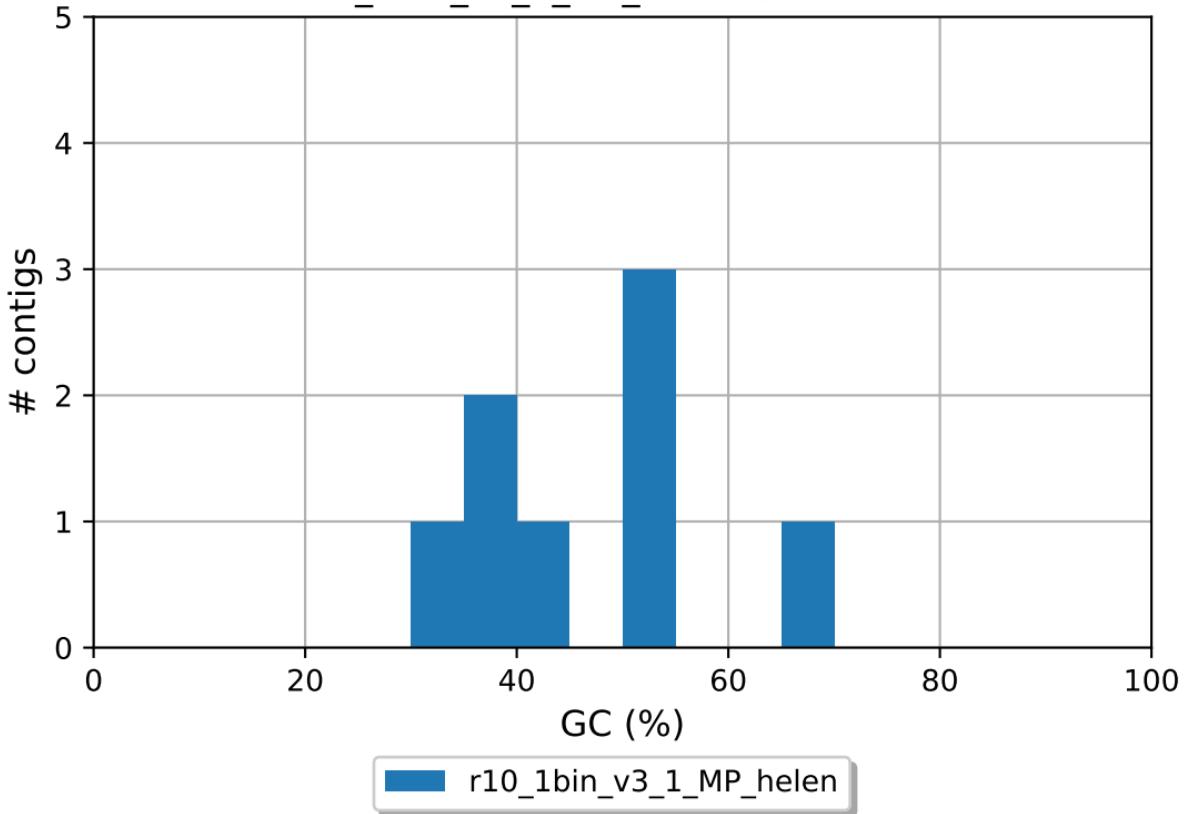


r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_1_r2_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_2_racoon_r1
r10_1bin_v3_3_MP_helen
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r10_1bin_v3_3_racoon_r1

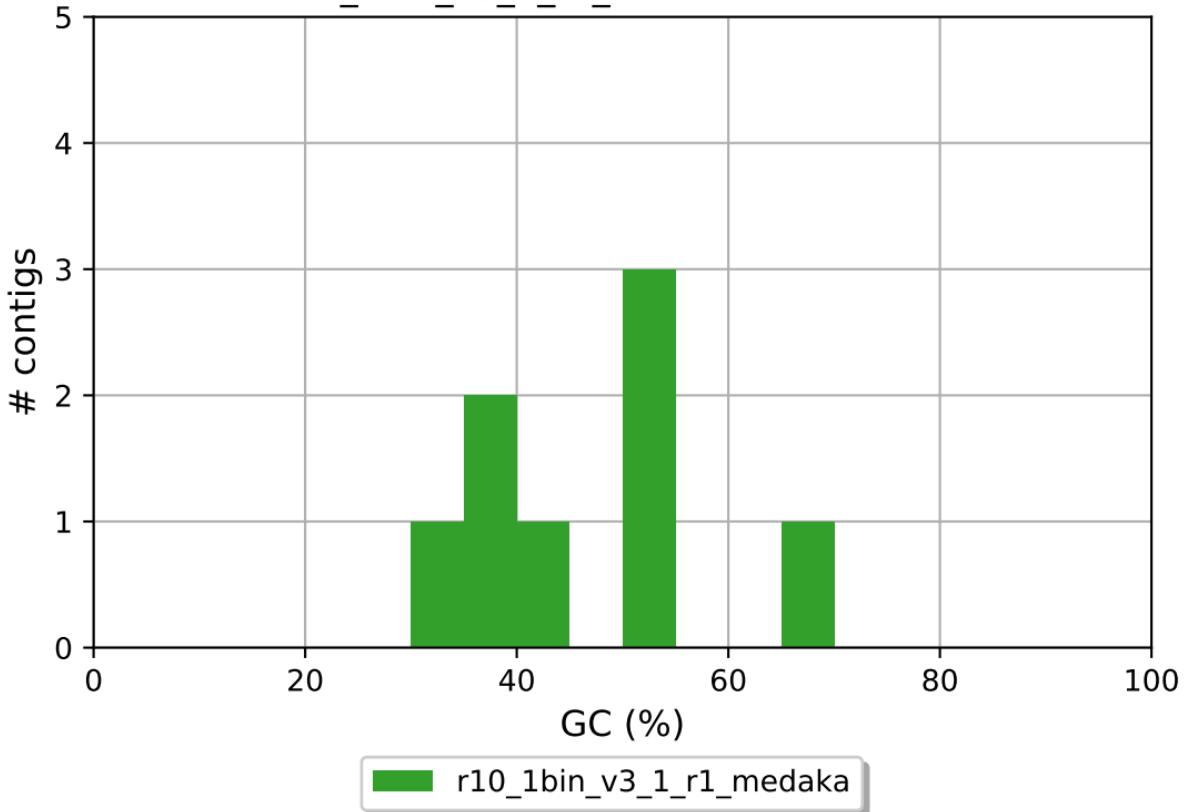
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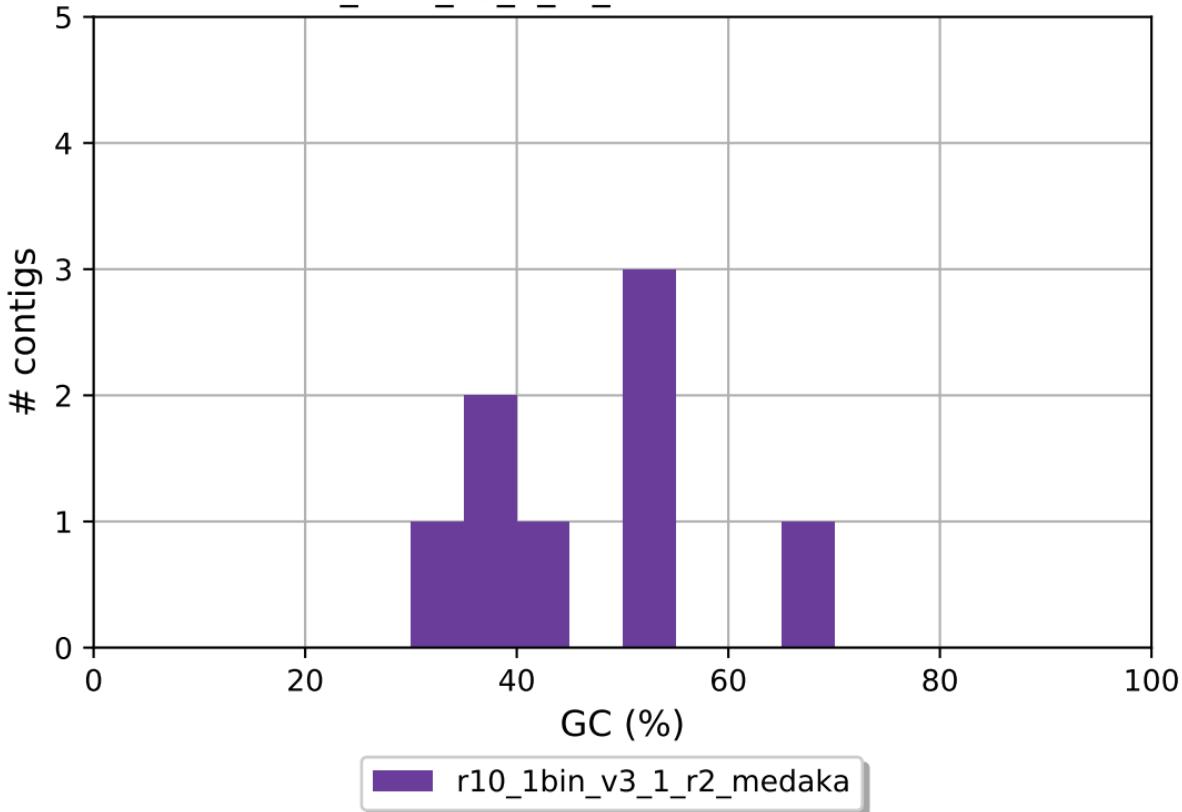
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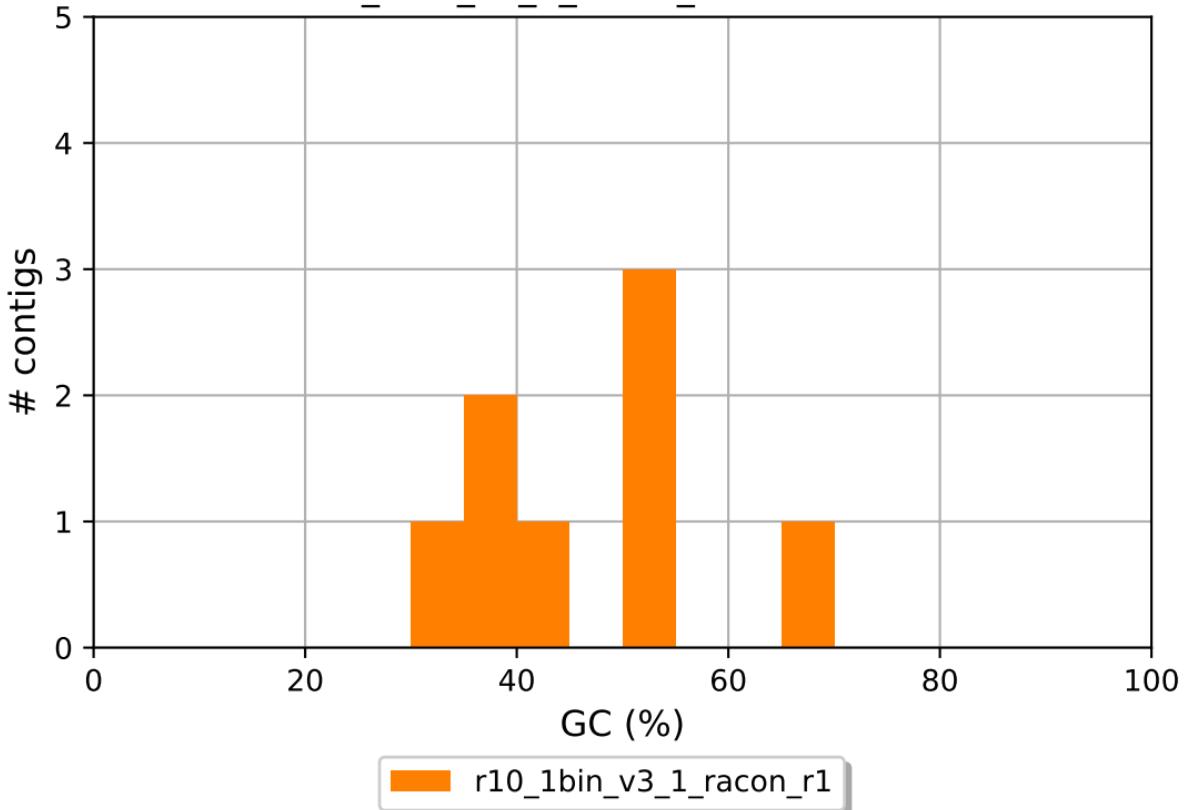
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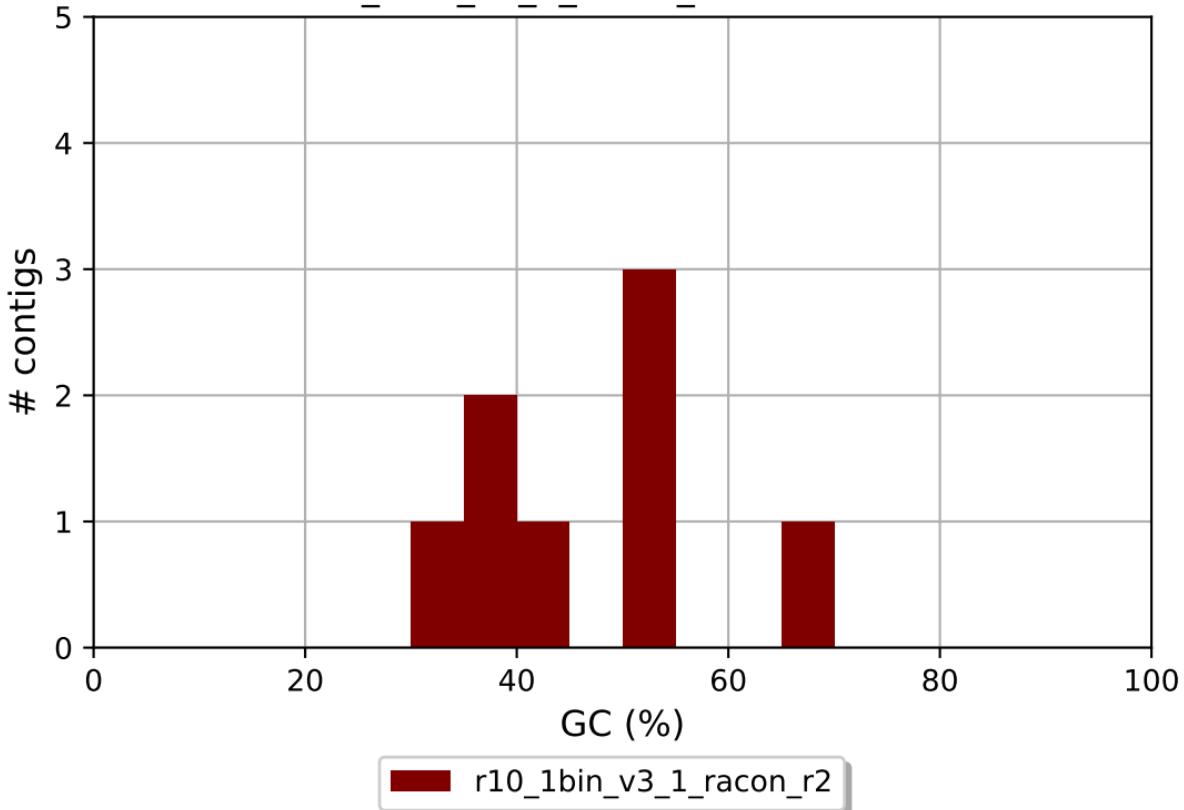
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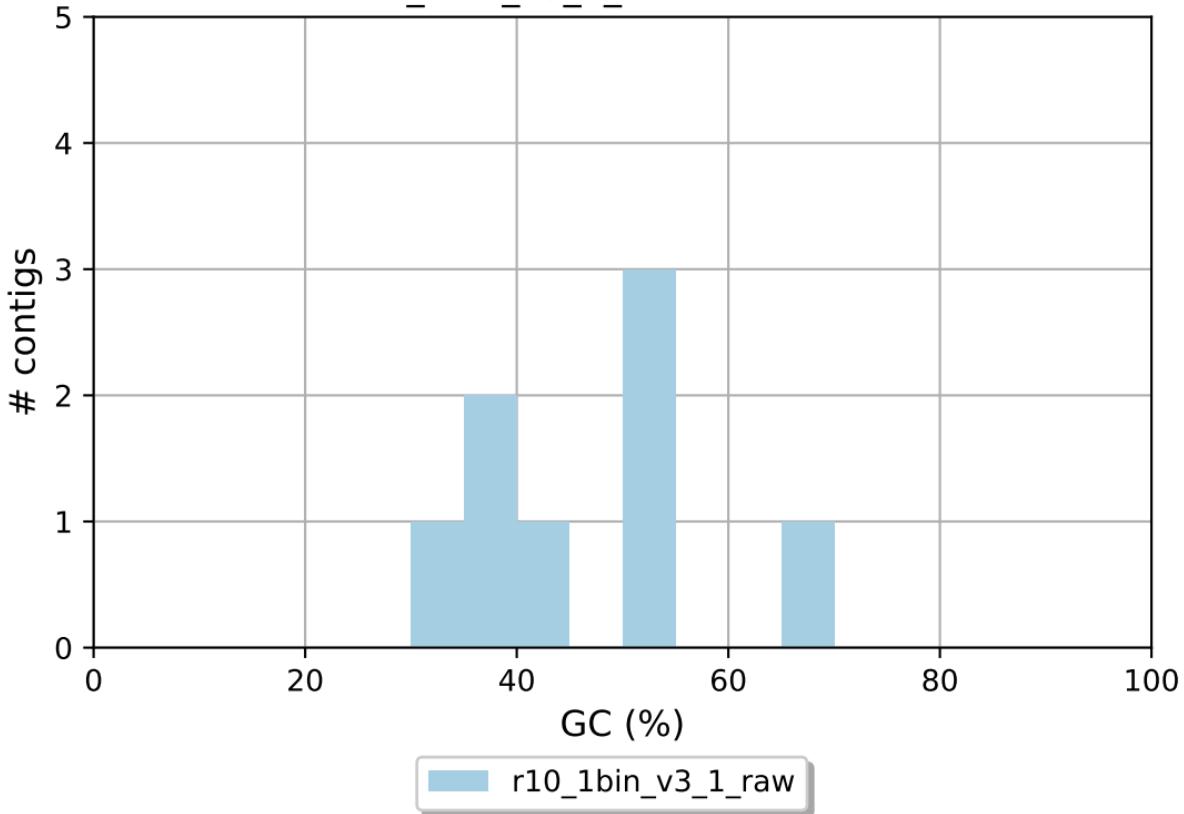
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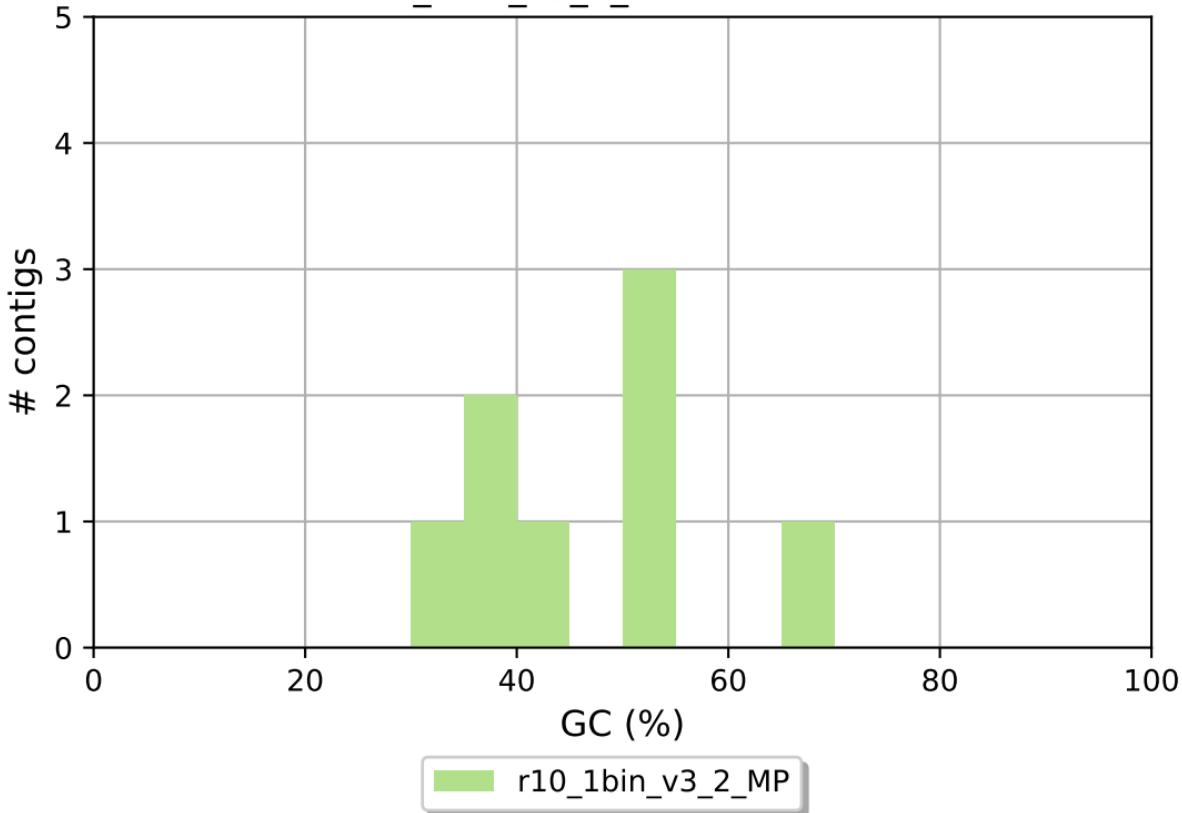
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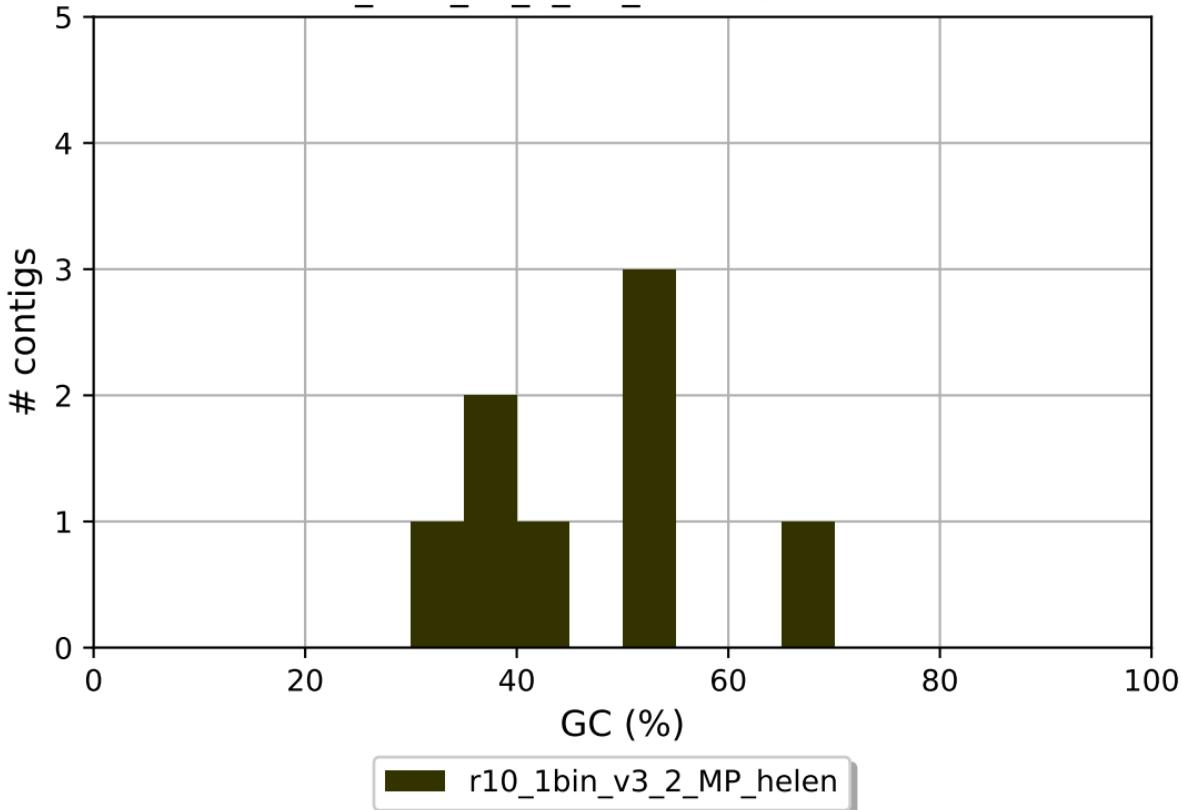
r10_1bin_v3_1_raw GC content



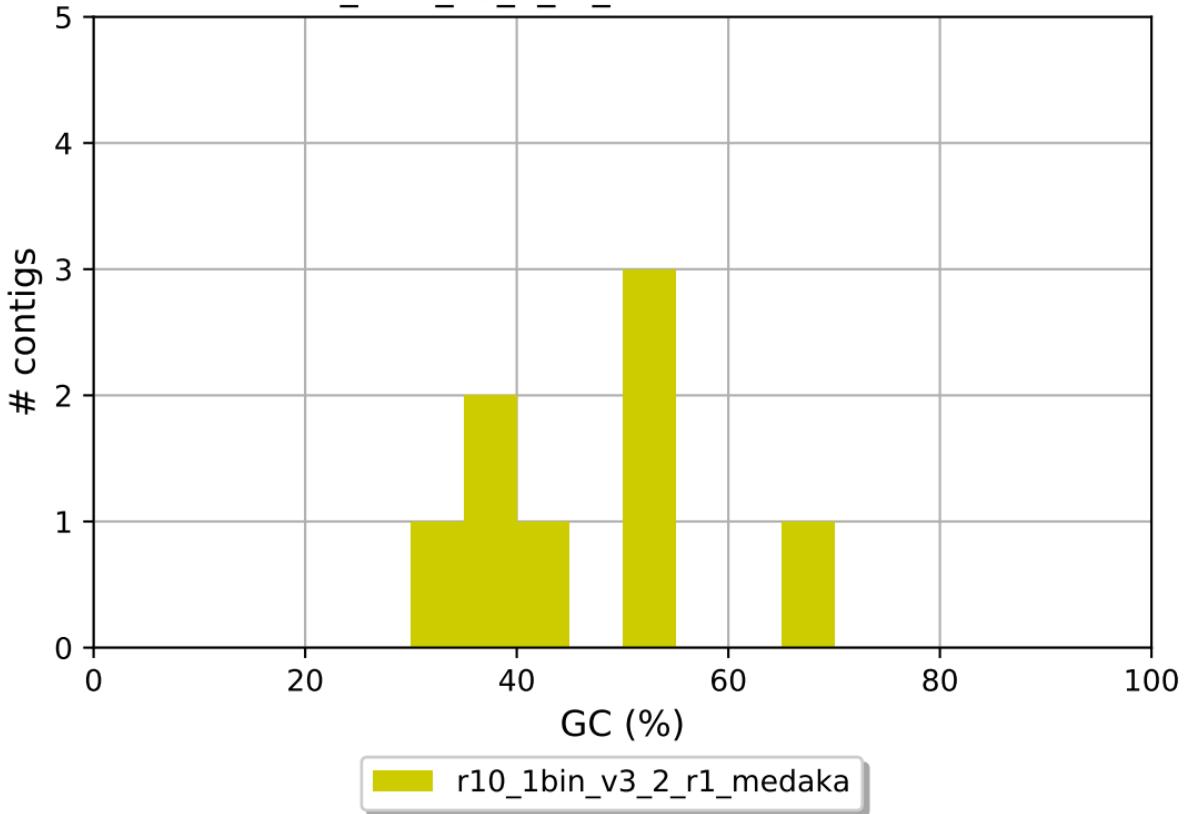
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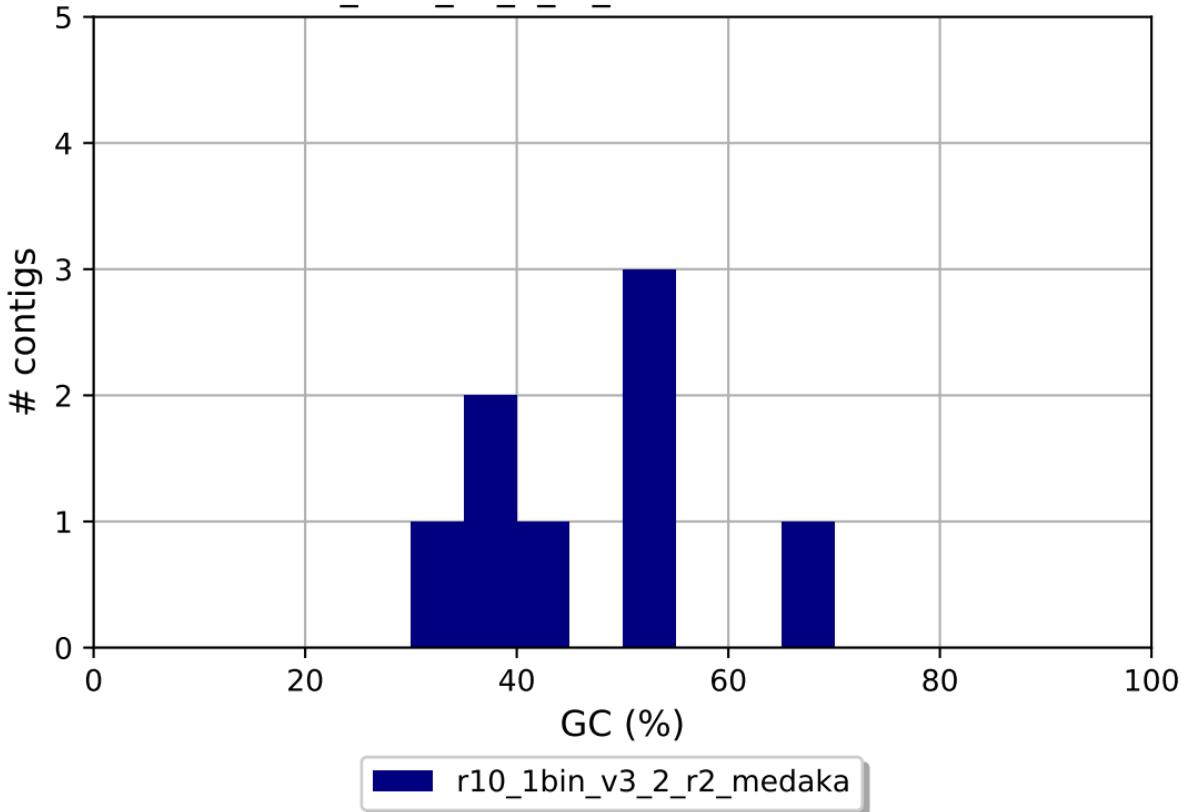
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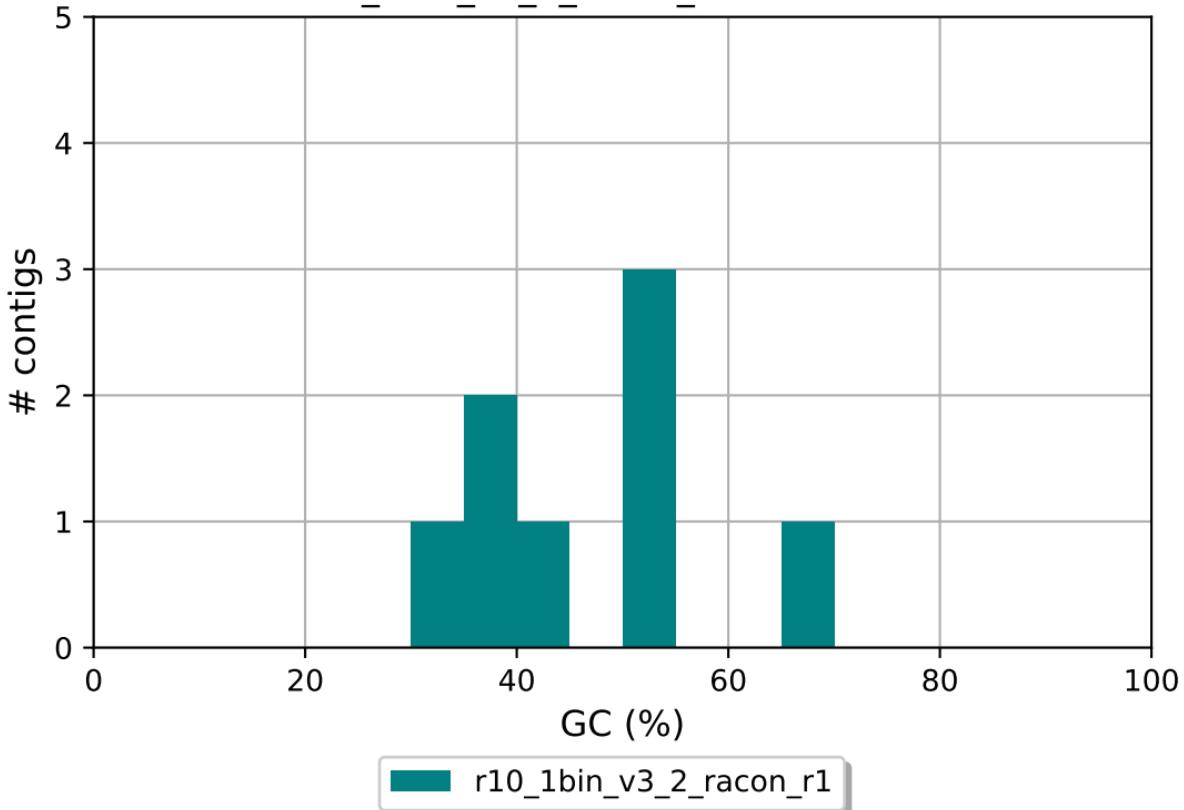
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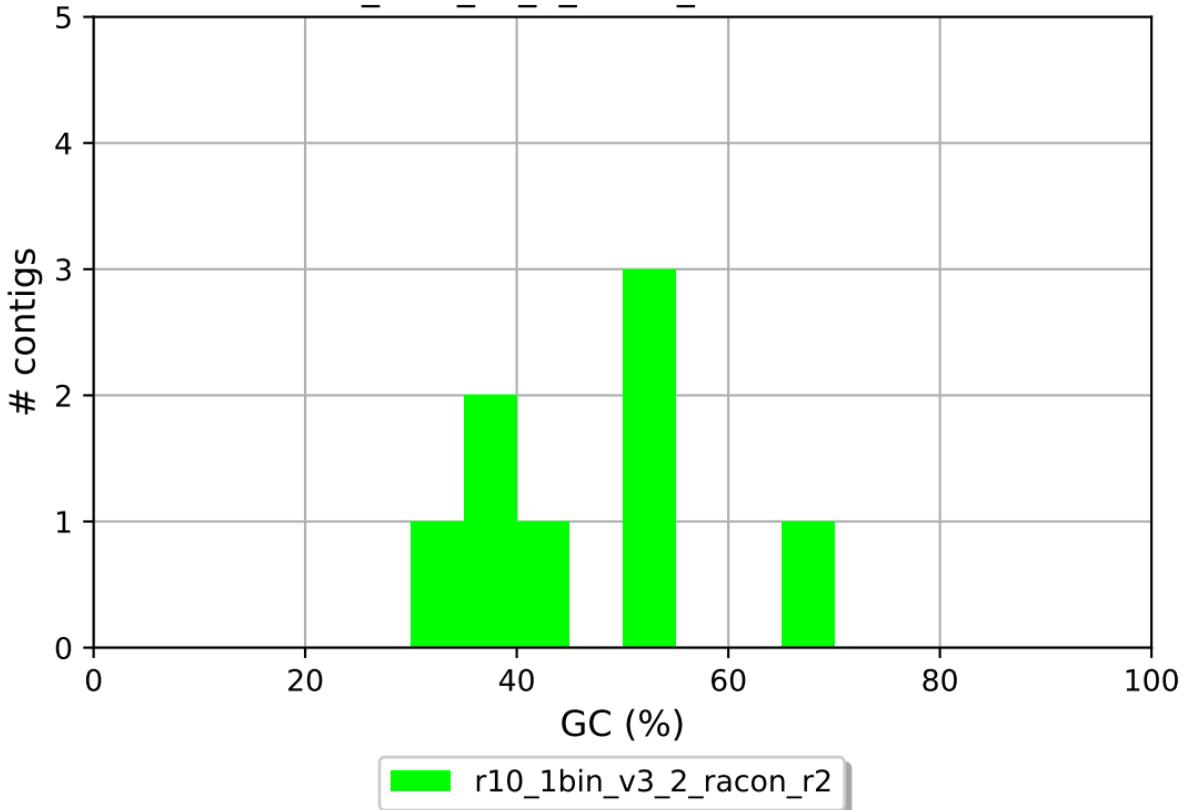
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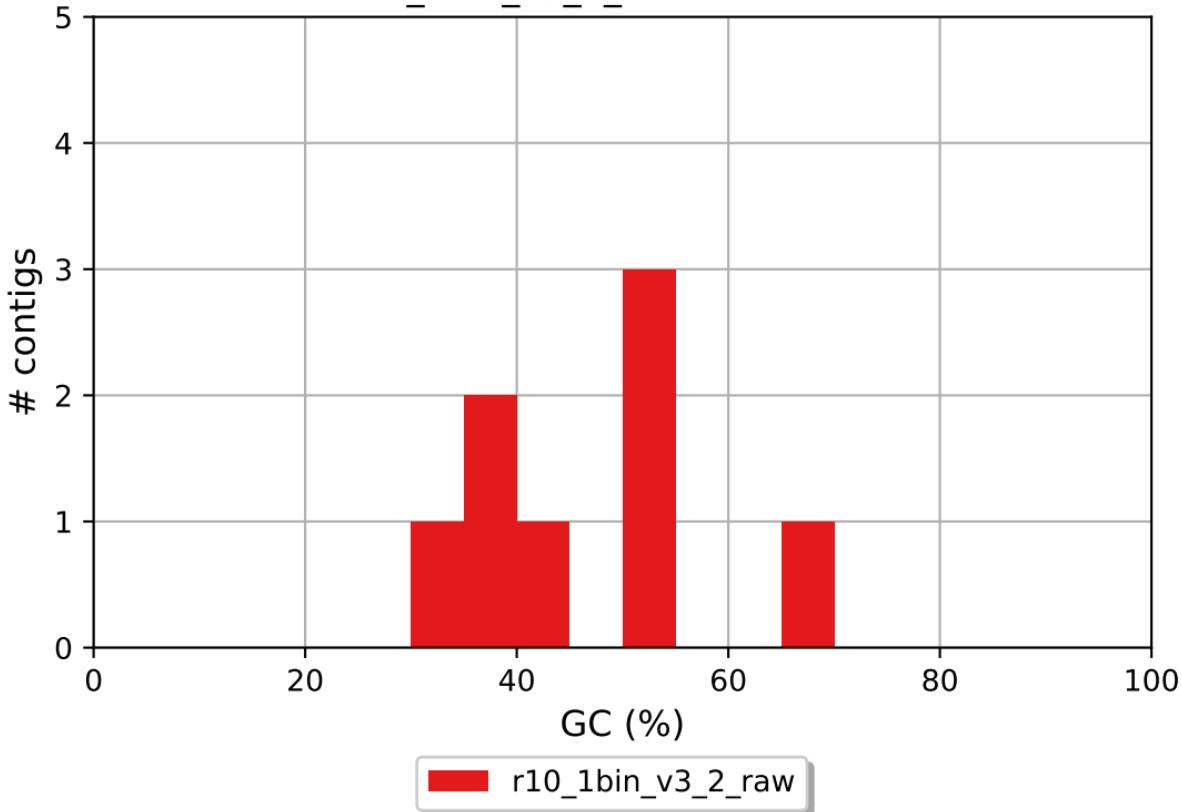
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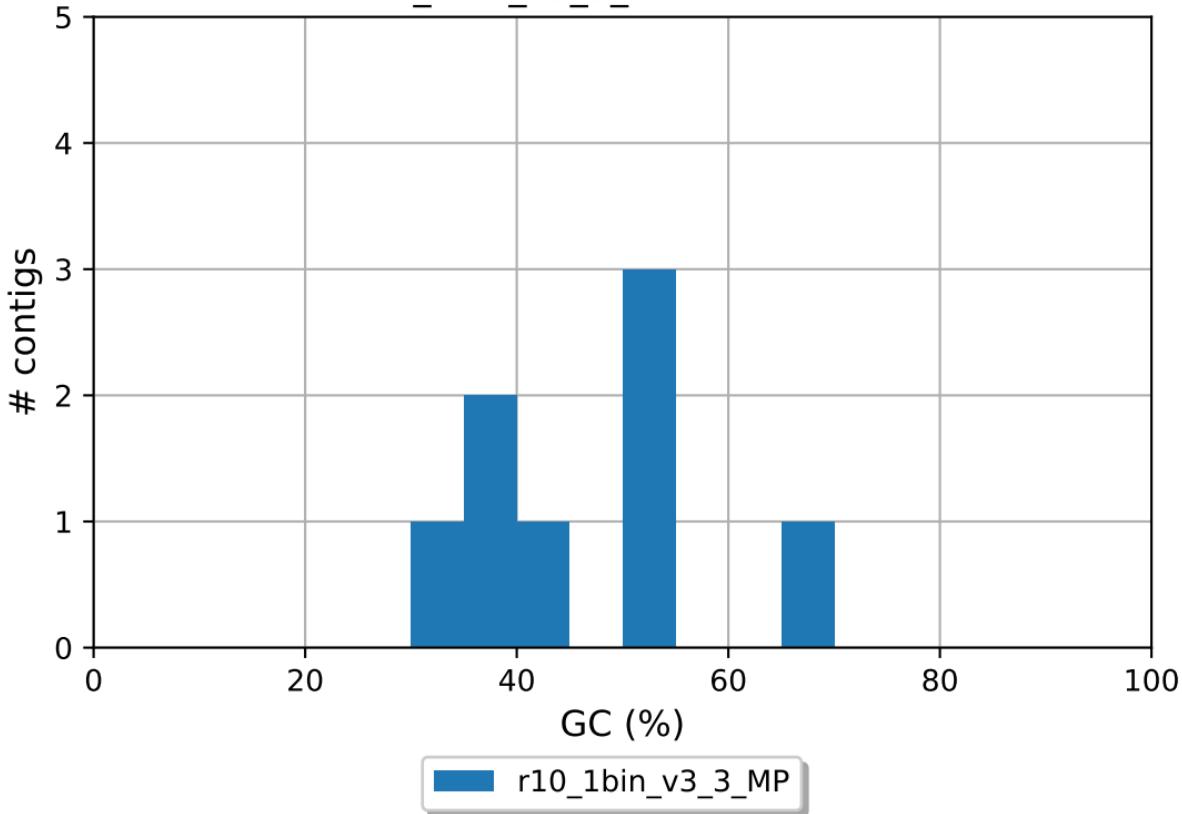
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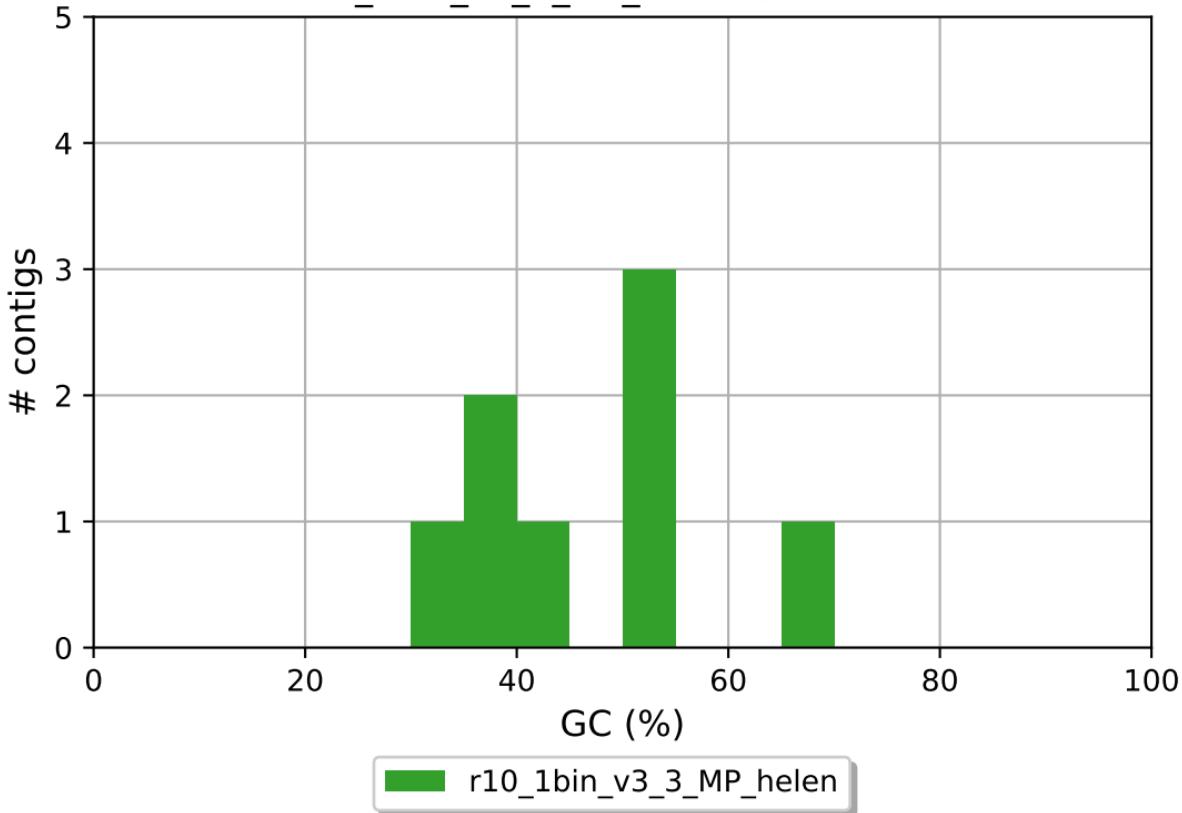
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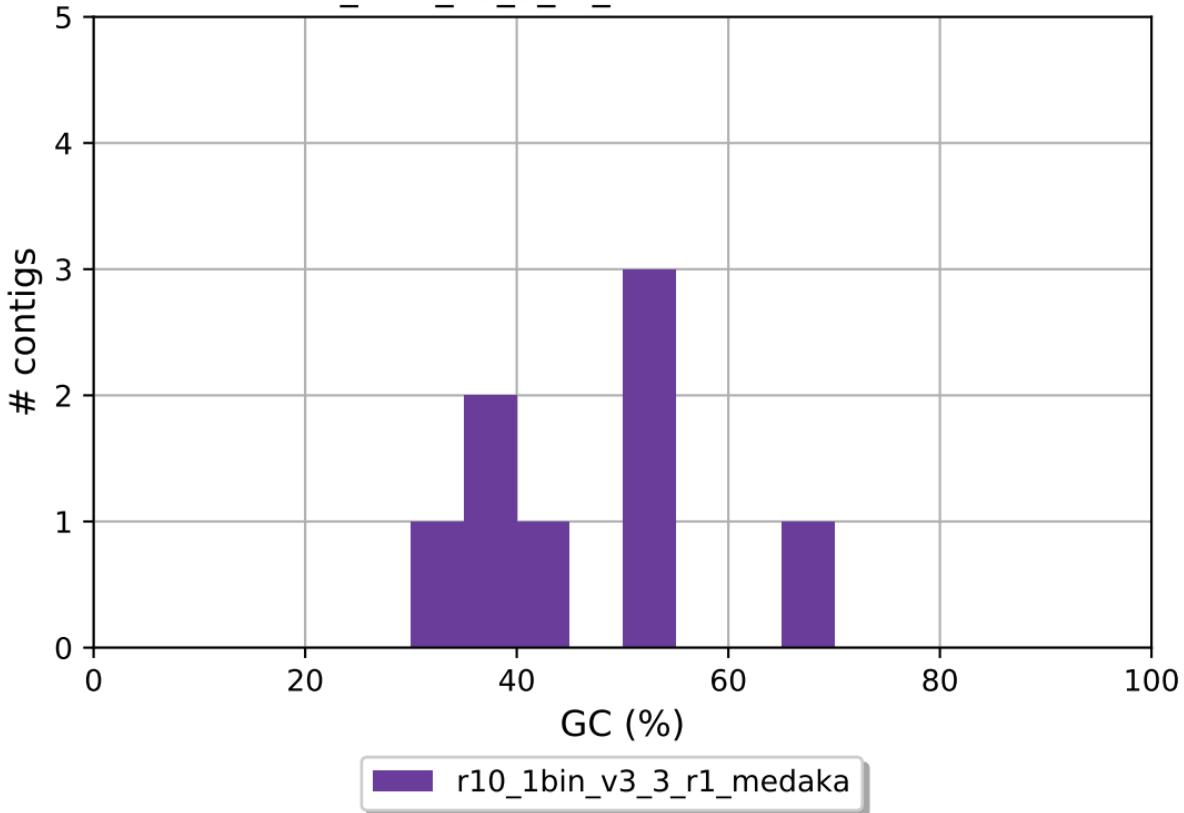
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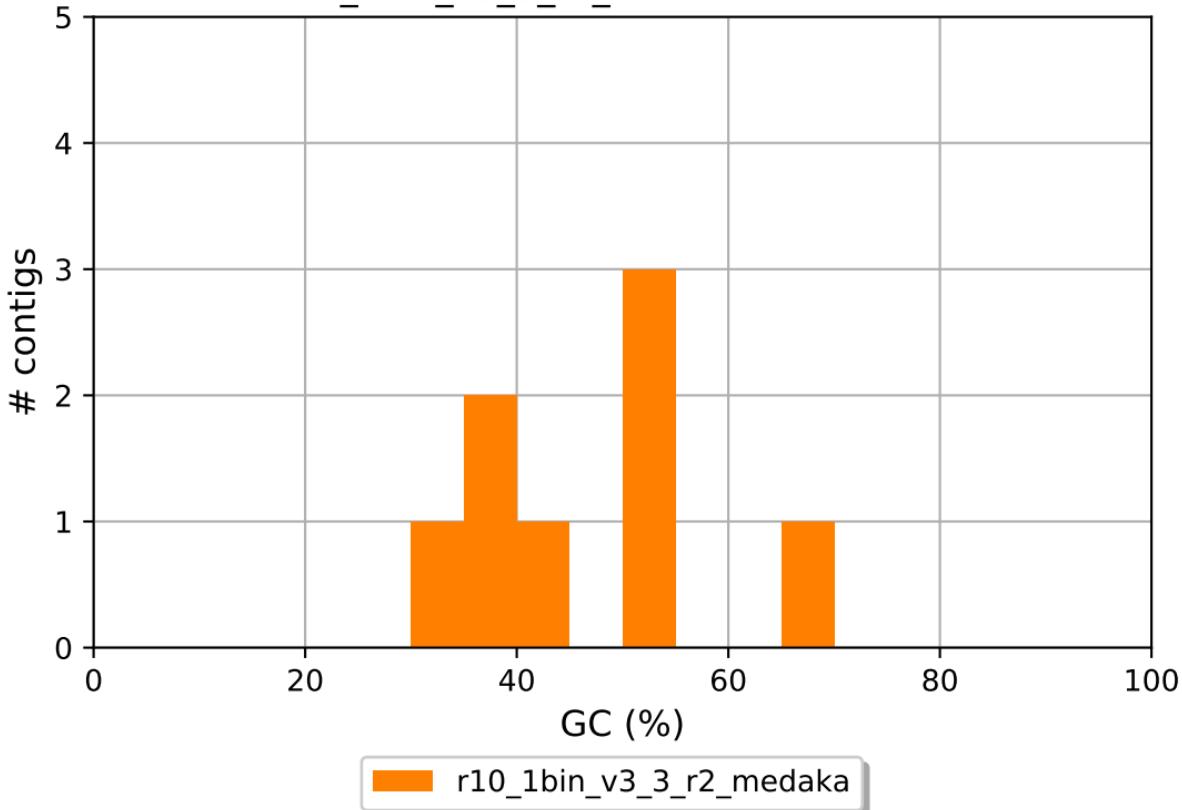
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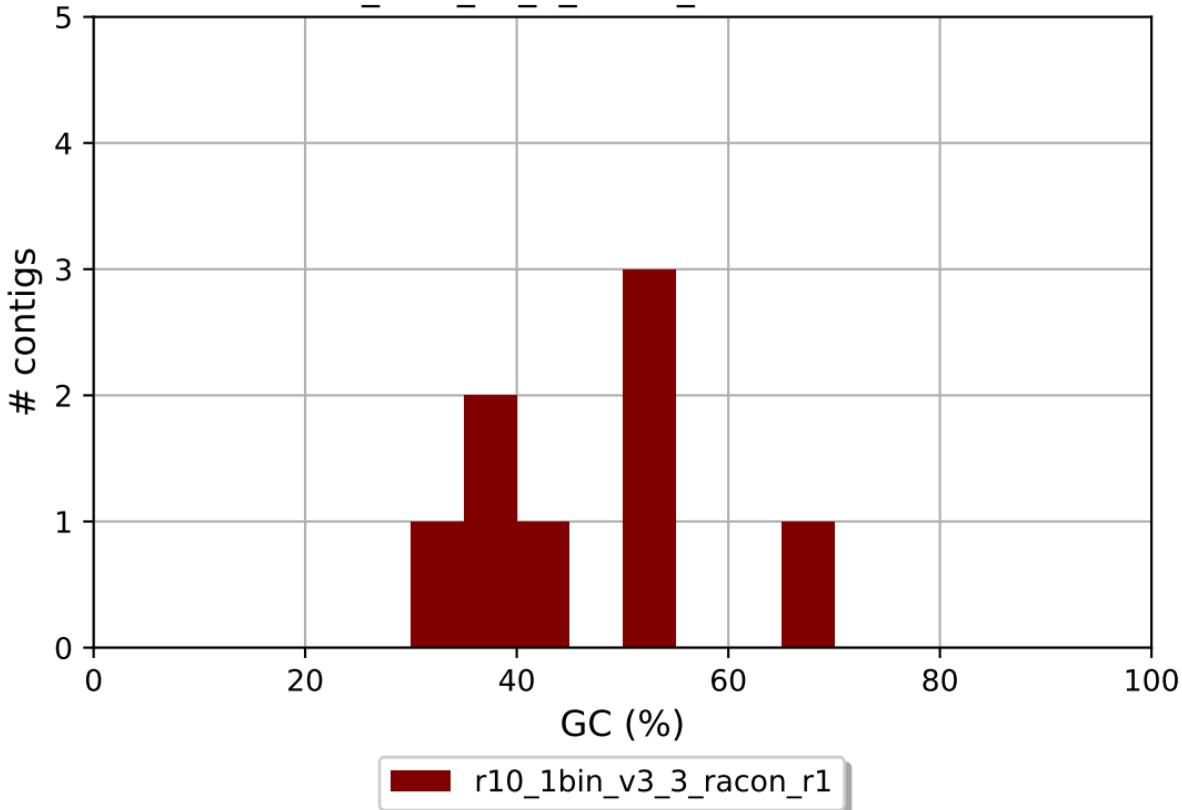
r10_1bin_v3_3_r1_medaka GC content



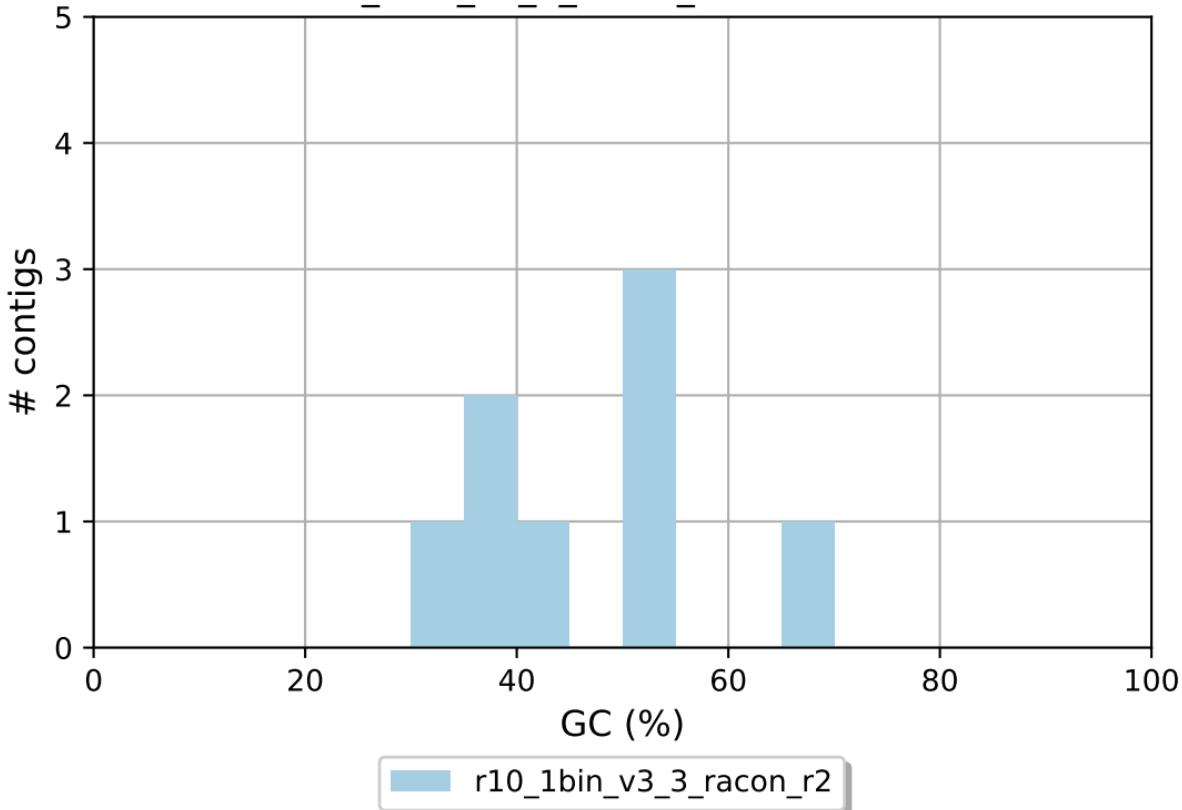
r10_1bin_v3_3_r2_medaka GC content



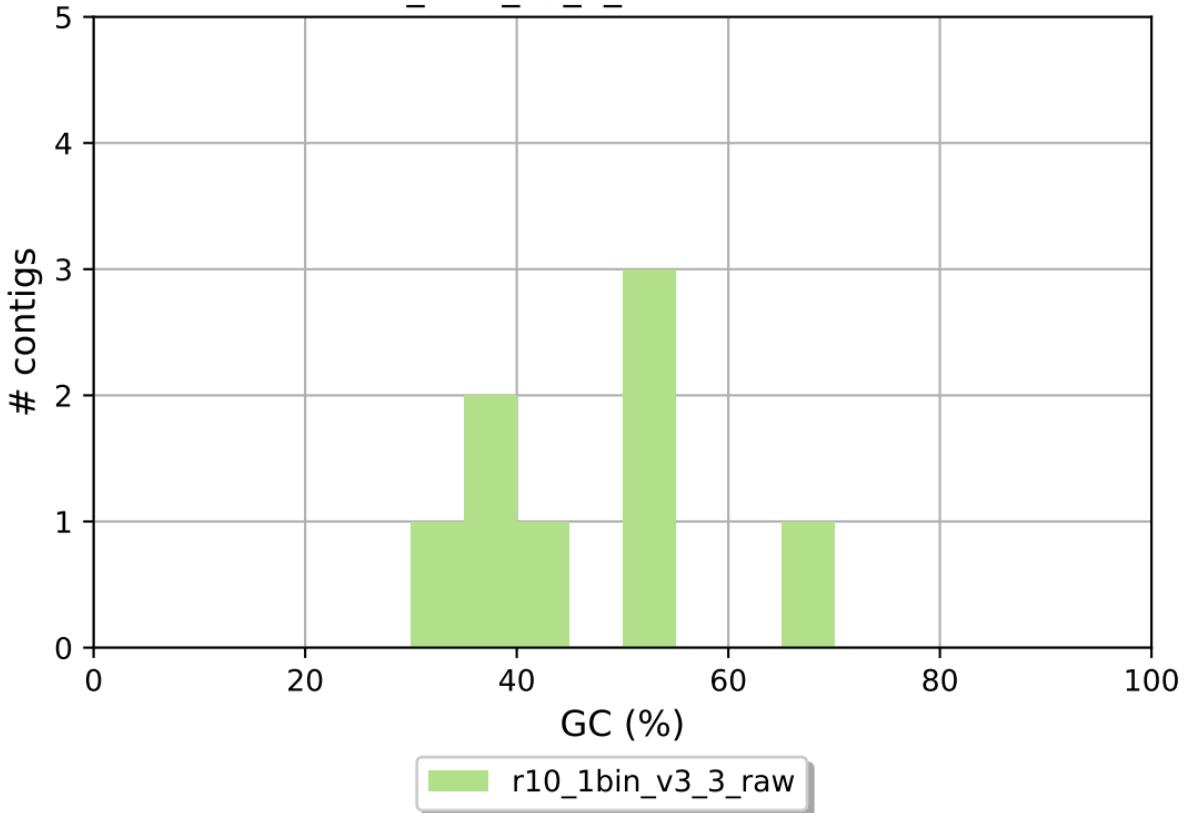
r10_1bin_v3_3_racon_r1 GC content



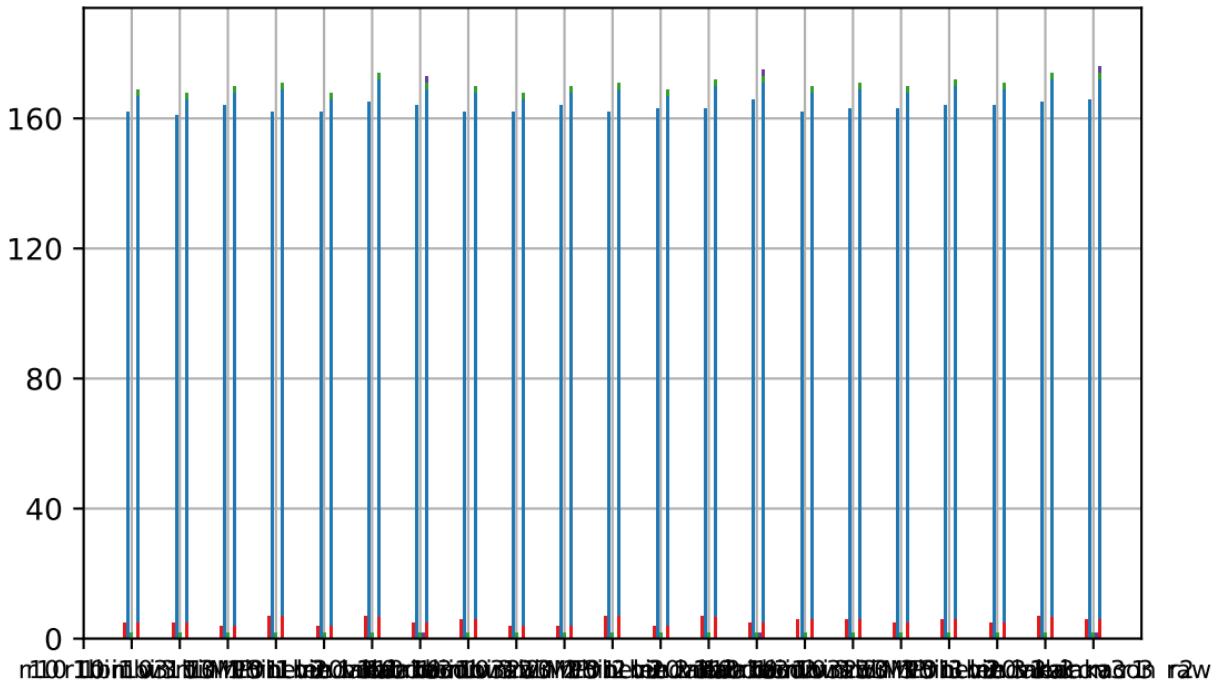
r10_1bin_v3_3_racon_r2 GC content



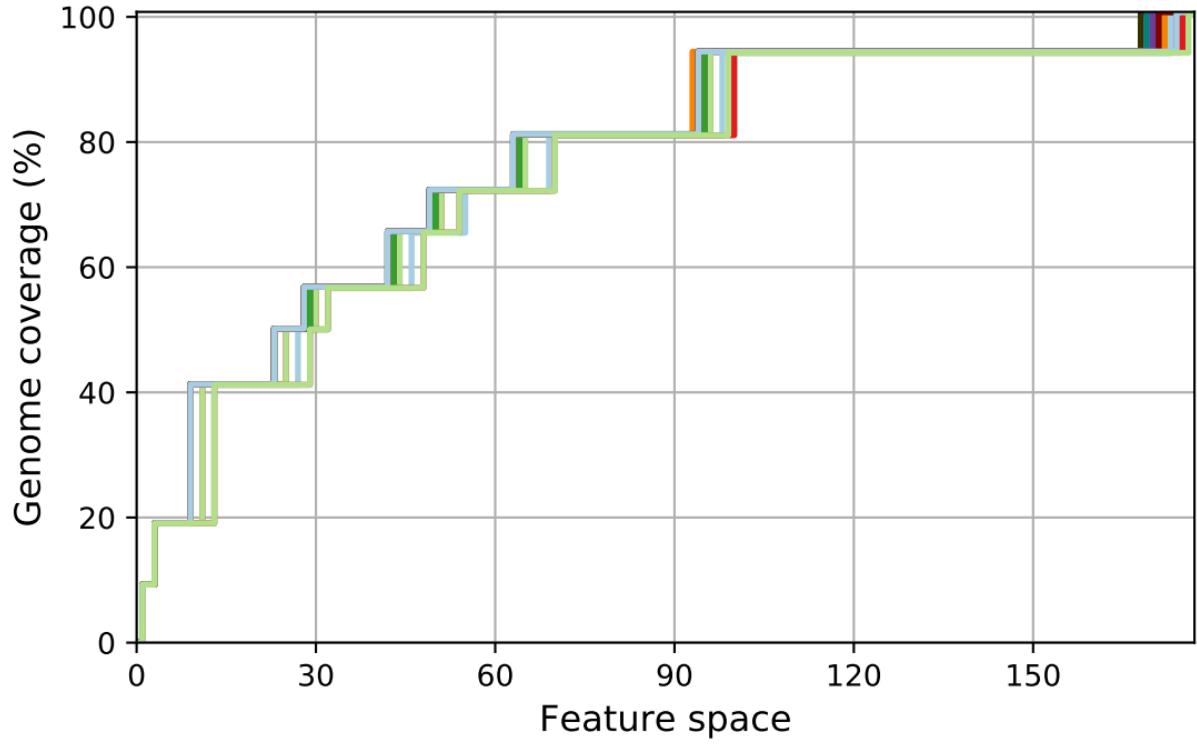
r10_1bin_v3_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

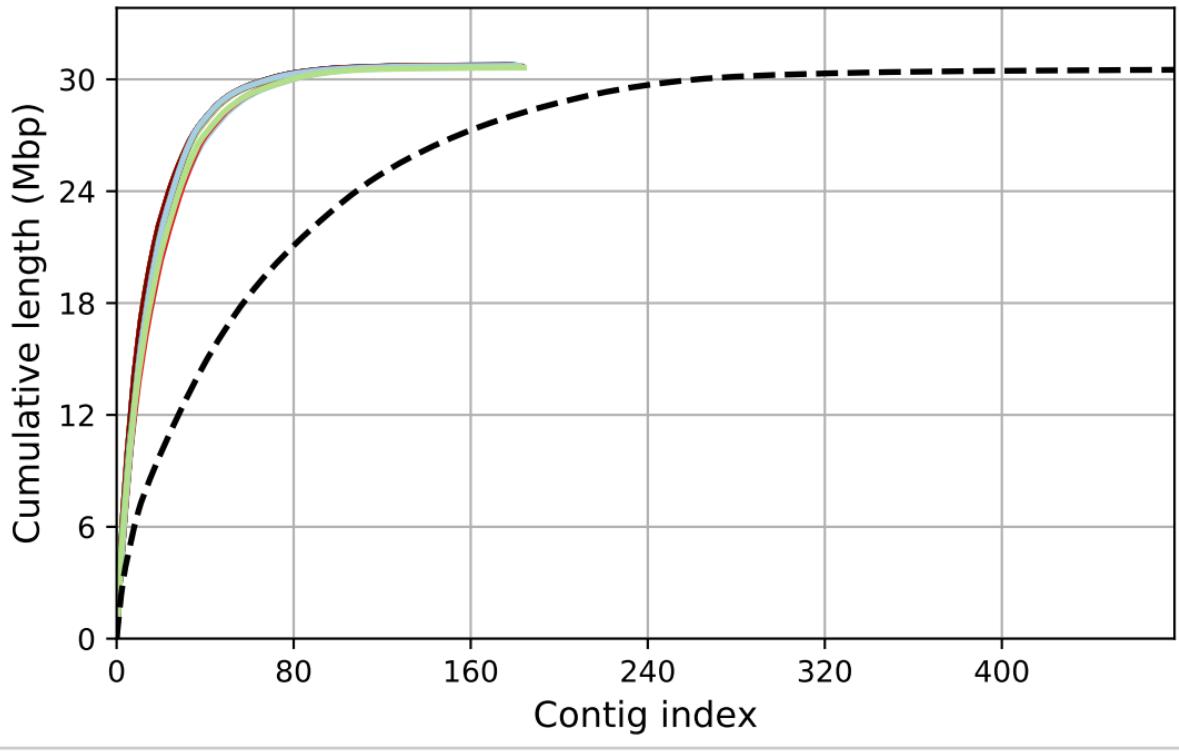
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_H

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length (aligned contigs)

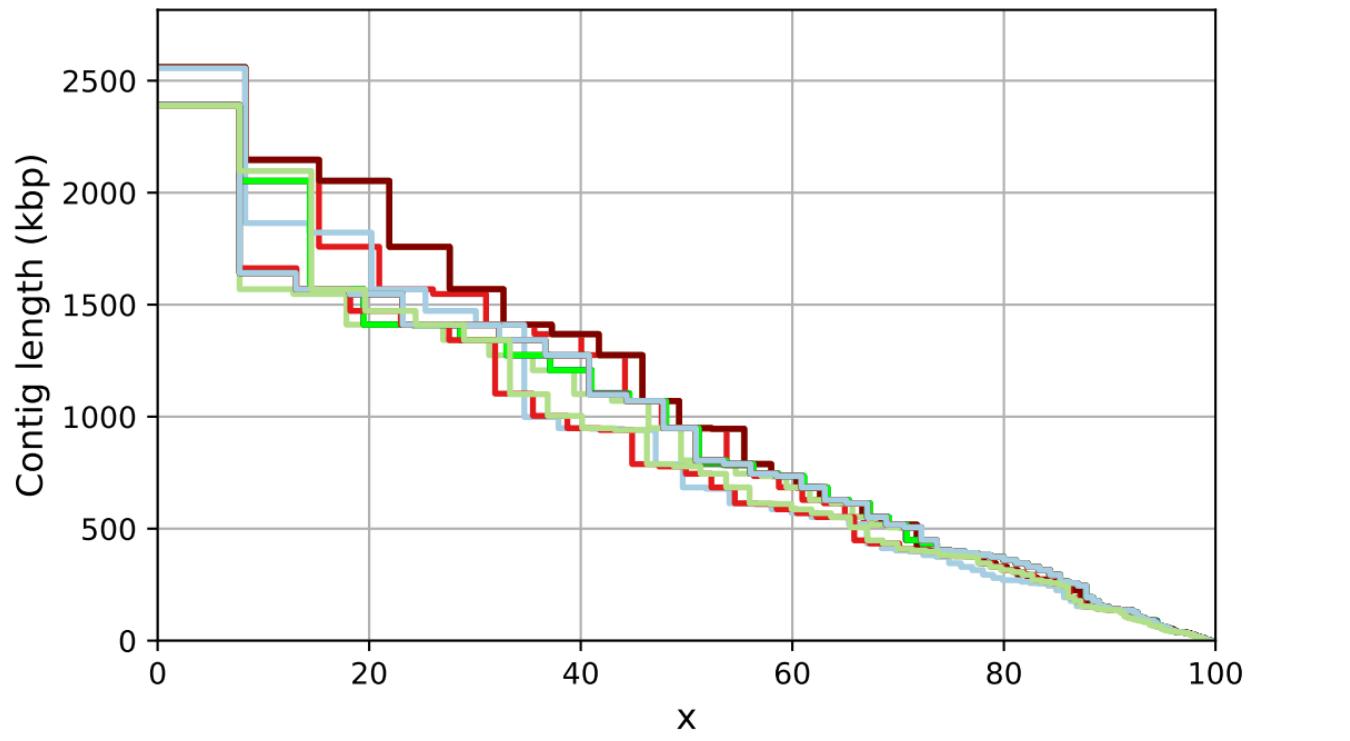


r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_2_racon_r1

r10_1bin_v3_3_MP_helen
r10_1bin_v3_3_r1_medaka
r10_1bin_v3_3_r2_medaka
r10_1bin_v3_3_racon_r1

NAx

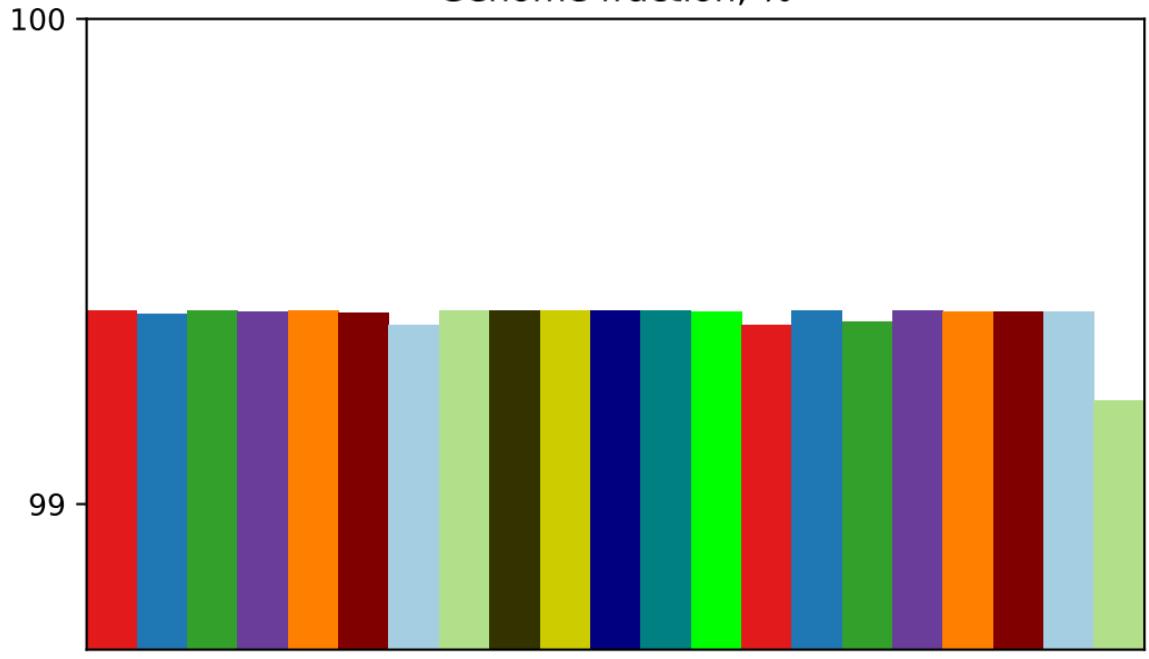


r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_helen
r10_1bin_v3_3_r1_medaka
r10_1bin_v3_3_r2_medaka

Genome fraction, %



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka