

Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw	
# contigs (>= 0 bp)	8	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	8	
# contigs (>= 5000 bp)	8	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	8	
# contigs (>= 25000 bp)	8	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	8	
Total length (>= 0 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Total length (>= 1000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Total length (>= 5000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Total length (>= 10000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Total length (>= 25000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Total length (>= 50000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Largest contig	6792205	6792208	6792382	6792380	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6791549	6791658	6788581	
Total length	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	
N50	4758902	4757799	4759020	4758488	4757908	4757843	4755996	4758906	4758018	4759008	4758481	4757940	4757851	4755926	4757804	4759024	4758498	4757988	4757863	4756050	
N75	2992069	2992056	2992173	2992163	2991926	2991944	2990670	2992084	2992067	2992181	2992179	2991904	2991942	2990627	2992085	2992068	2992180	2992178	2991937	2991954	2990634
L50	3	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	5	
# misassemblies	170	169	171	177	170	170	180	173	171	168	169	175	168	177	173	170	168	171	168	174	174
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
Misassembled contigs length	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	3086614	30855149	30852655	30845216	30849517		
# local misassemblies	116	117	132	131	149	140	204	116	118	132	134	149	142	211	116	117	132	133	148	139	208
# 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	
# unaligned mis. contigs	0	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 + 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	78588	78989	81776	80026	77699	76041	136933	78932	78363	82131	80539	78081	76507	139774	78459	78365	81158	79524	77848	76770	139620
Genome fraction (%)	99.399	99.397	99.397	99.398	99.396	99.395	99.374	99.400	99.398	99.397	99.396	99.394	99.373	99.400	99.399	99.398	99.399	99.398	99.397	99.371	
Duplication ratio	1.044	1.044	1.043	1.043	1.042	1.043	1.027	1.043	1.044	1.043	1.043	1.042	1.043	1.028	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	0.00	0.00	
# mismatches per 100 kbp	174.70	167.29	179.17	178.10	174.24	180.07	273.15	174.57	167.98	178.91	178.01	174.34	179.64	269.89	176.43	168.48	180.55	176.95	179.22	177.92	273.37
# indels per 100 kbp	38.17	22.69	42.70	43.14	65.91	62.28	310.12	37.79	22.88	42.85	42.66	66.10	62.89	304.78	38.13</td						

Misassemblies report

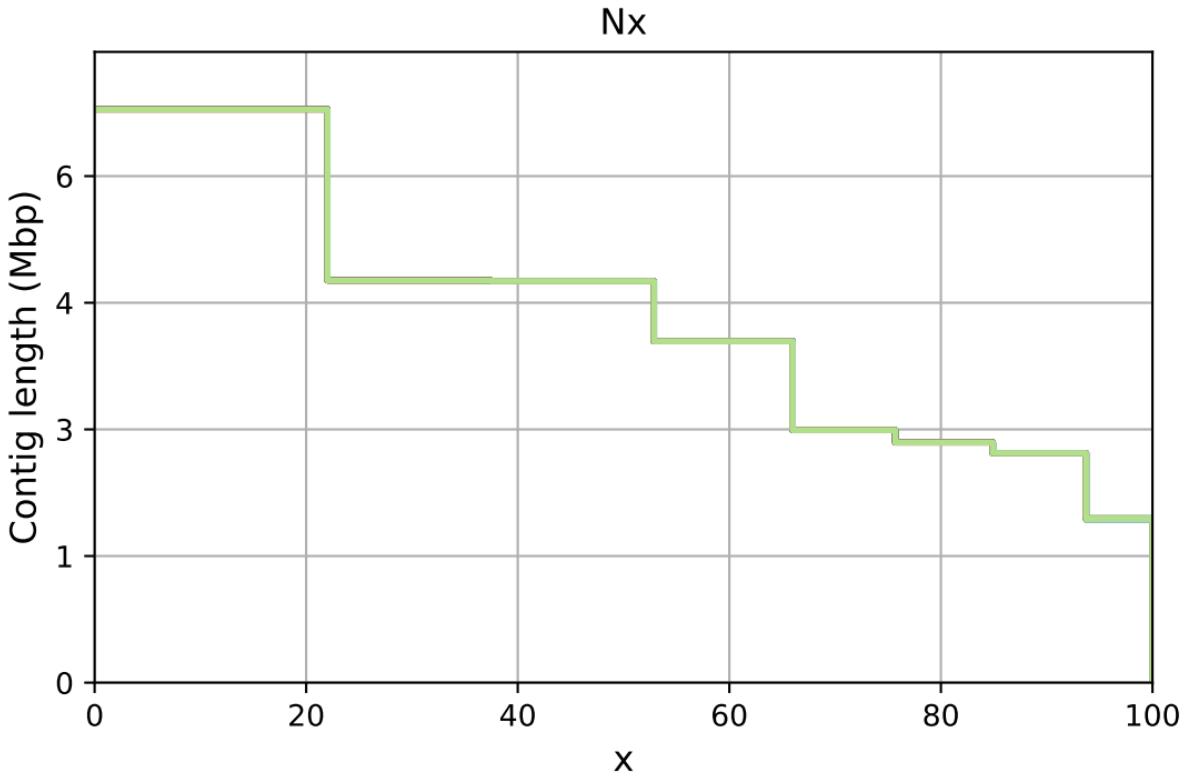
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw		
# misassemblies	170	169	171	177	170	180	173	171	168	169	175	168	177	173	170	168	171	168	174		
# contig misassemblies	170	169	171	177	170	180	173	171	168	169	175	168	177	173	170	168	171	168	174		
# c. relocations	5	4	5	10	5	10	5	6	4	9	4	9	5	6	4	8	4	8	5		
# c. translocations	163	163	164	165	163	168	164	163	162	164	162	166	162	162	162	161	162	164	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	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		
# 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	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
# 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	94	94	94	90	168	98	98	96	94	98	90	174	98	98	96	98	92	164	
# local misassemblies	116	117	132	131	149	140	204	116	118	132	134	149	142	211	116	117	132	133	148	139	208
# 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	251	251	250	171	252	253	252	250	251	253	251	251	252	250	250	251	177	
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# mismatches	52981	50732	54333	54011	52838	54606	82816	52942	50942	54256	53983	52869	54475	81825	53504	51093	54754	53661	54351	53955	82878
# indels	11575	6880	12949	13084	19986	18887	94025	11461	6939	12995	12936	20045	19072	92404	11563	7224	13156	13079	20178	19140	93179
# indels (<= 5 bp)	10910	6213	12355	12489	19336	18234	92781	10814	6265	12331	19376	18426	91173	10902	6554	12560	12475	19534	18494	91948	
# indels (> 5 bp)	665	667	594	595	650	653	1244	647	674	595	605	669	1231	661	670	596	604	644	646	1231	
Indels length	45983	41146	46178	46756	57764	55609	55606	45780	41215	46338	46955	58486	56452	156361	45840	41480	46720	46677	58128	55982	157439

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_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	8	
Partially unaligned length	78588	78989	81776	80026	77699	76041	136933	78932	78363	82131	80539	78081	76507	139774	78459	78158	79524	77848	76770	139620
# N's	0	10	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).

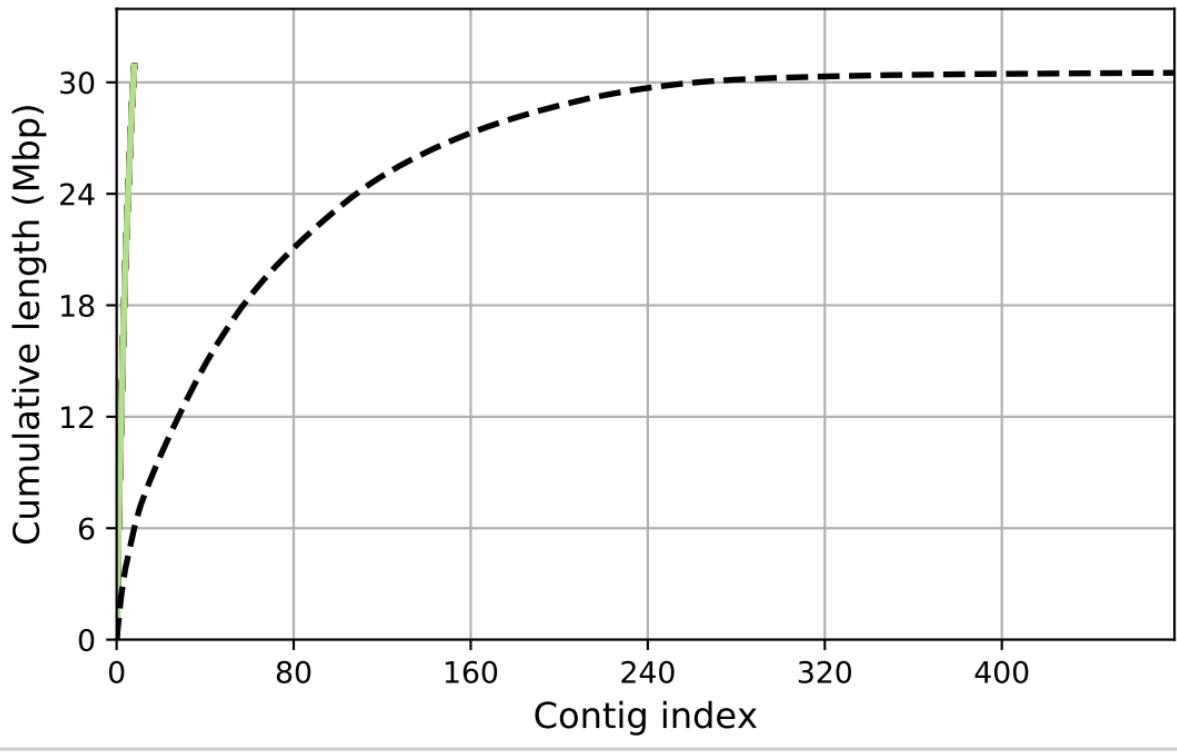


r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_helen
r10_1bin_v4_3_r1_medaka
r10_1bin_v4_3_r2_medaka

Cumulative length

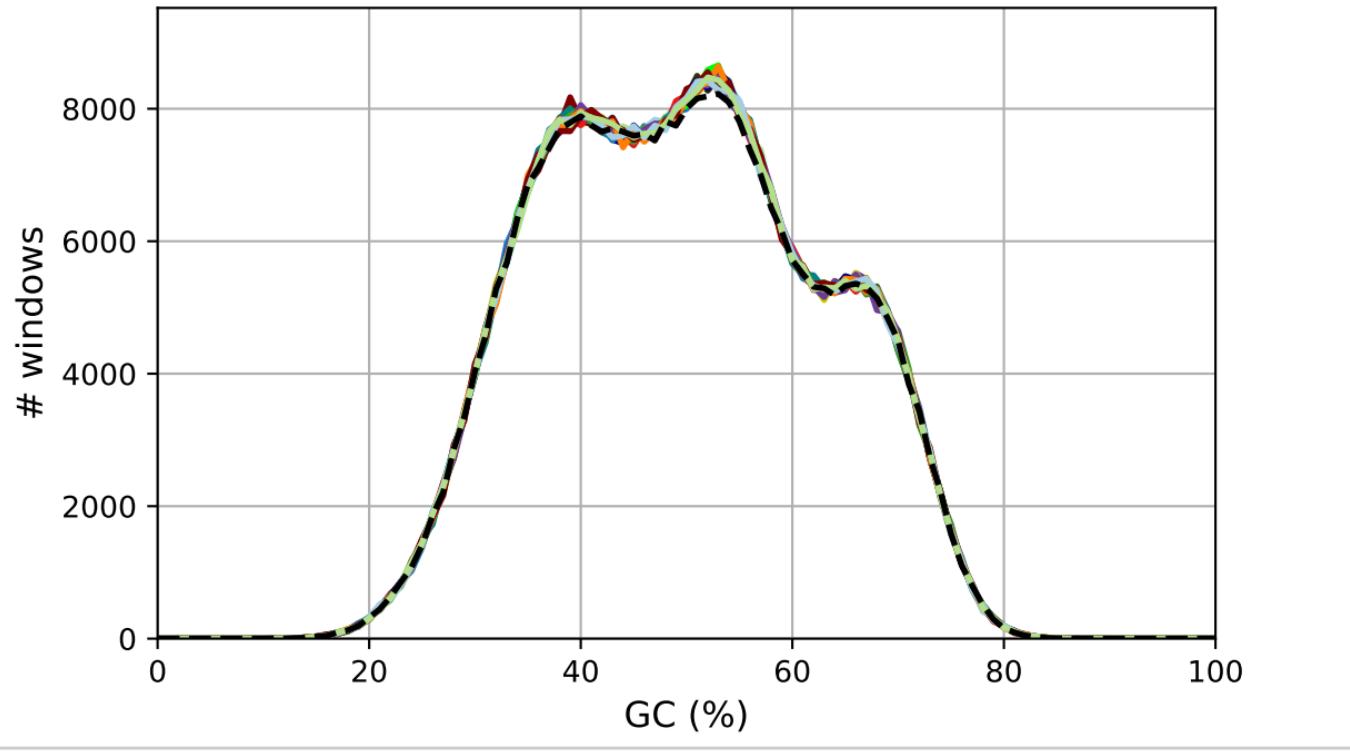


r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_2_racon_r1

r10_1bin_v4_3_MP_helen
r10_1bin_v4_3_r1_medaka
r10_1bin_v4_3_r2_medaka
r10_1bin_v4_3_racon_r1

GC content



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racoon_r1

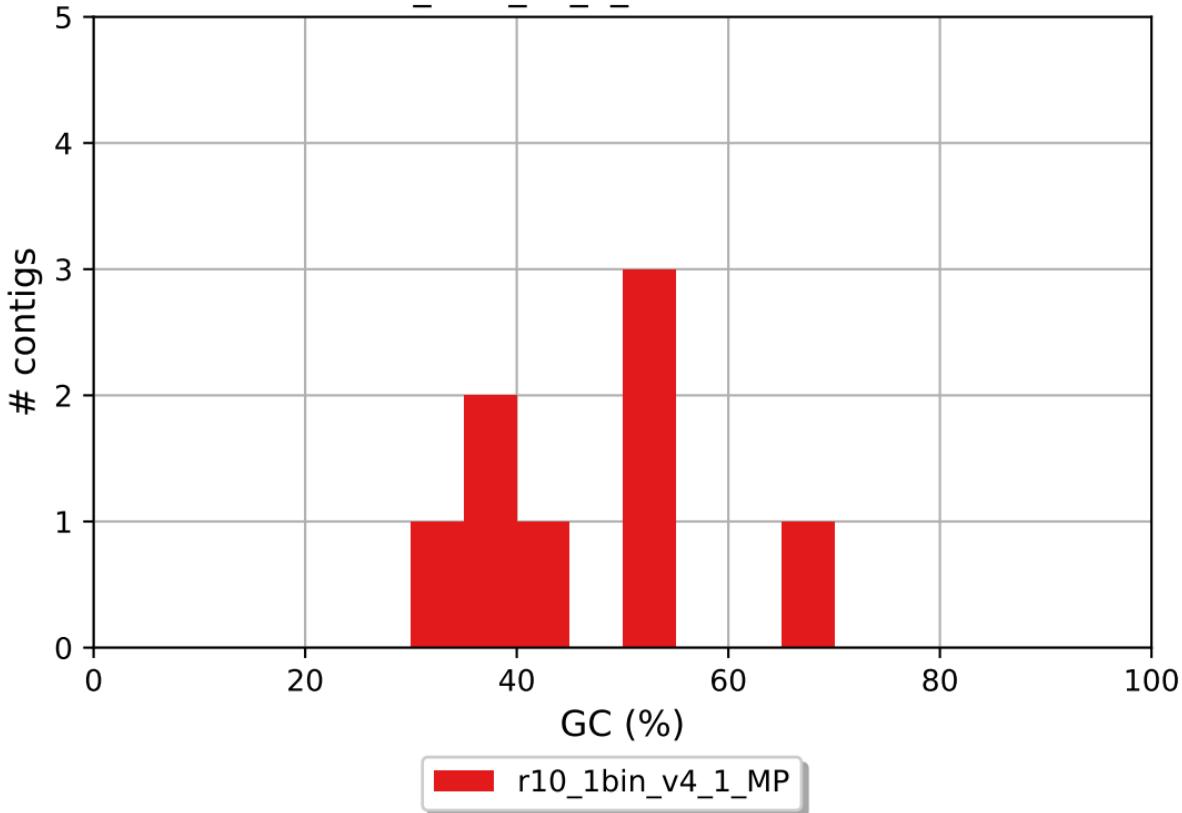
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r10_1bin_v4_3_r1_medaka

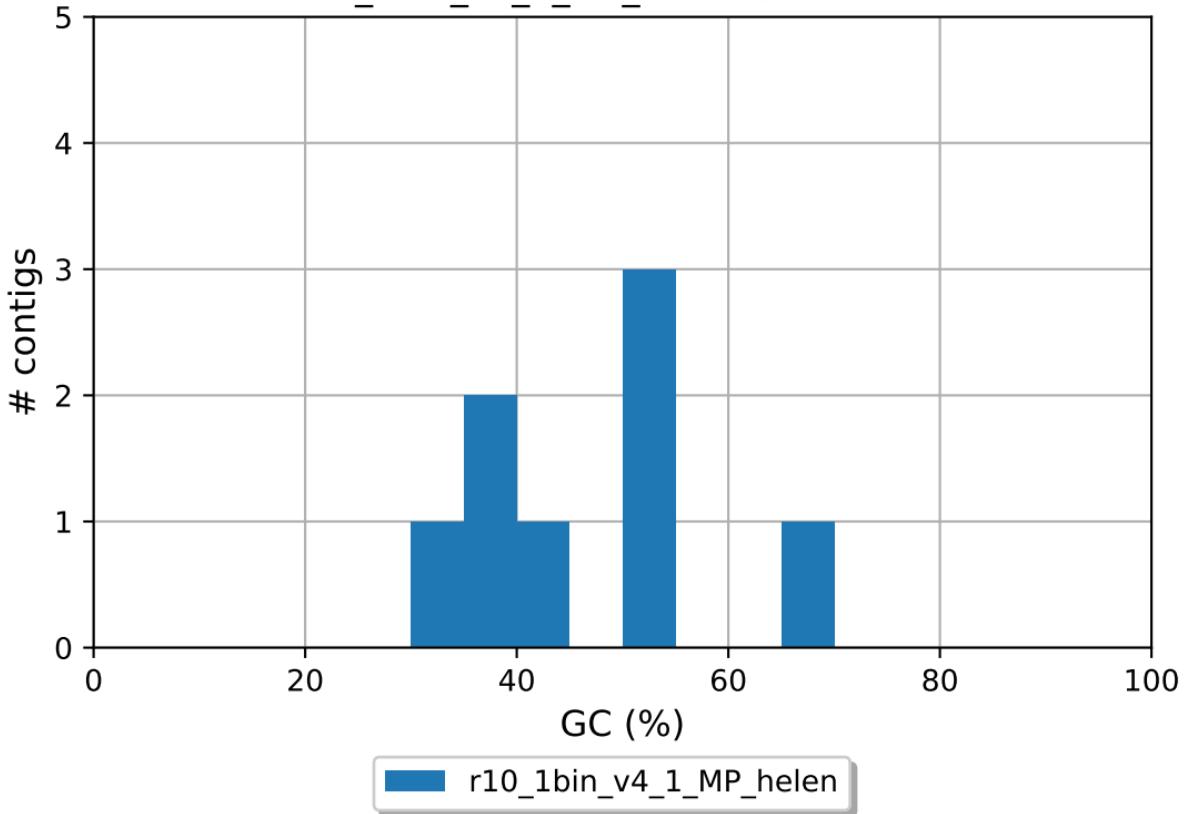
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r10_1bin_v4_3_racoon_r1

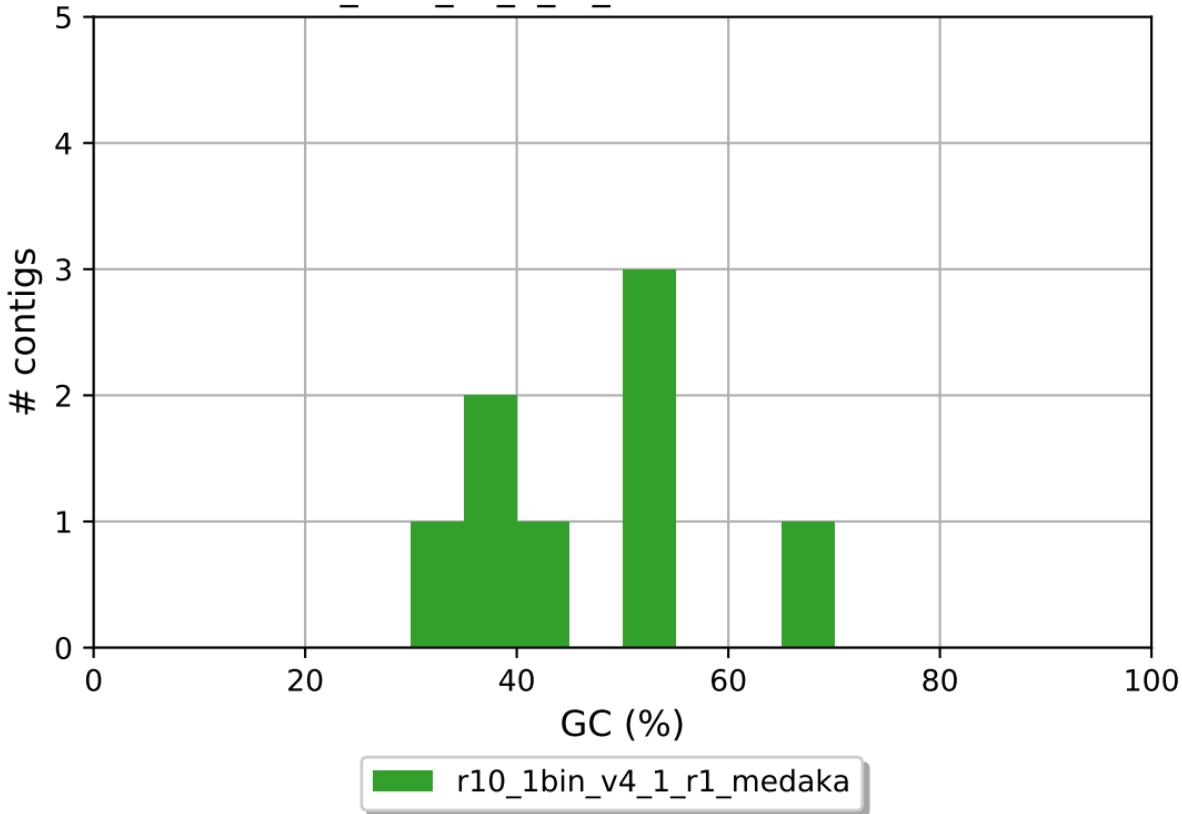
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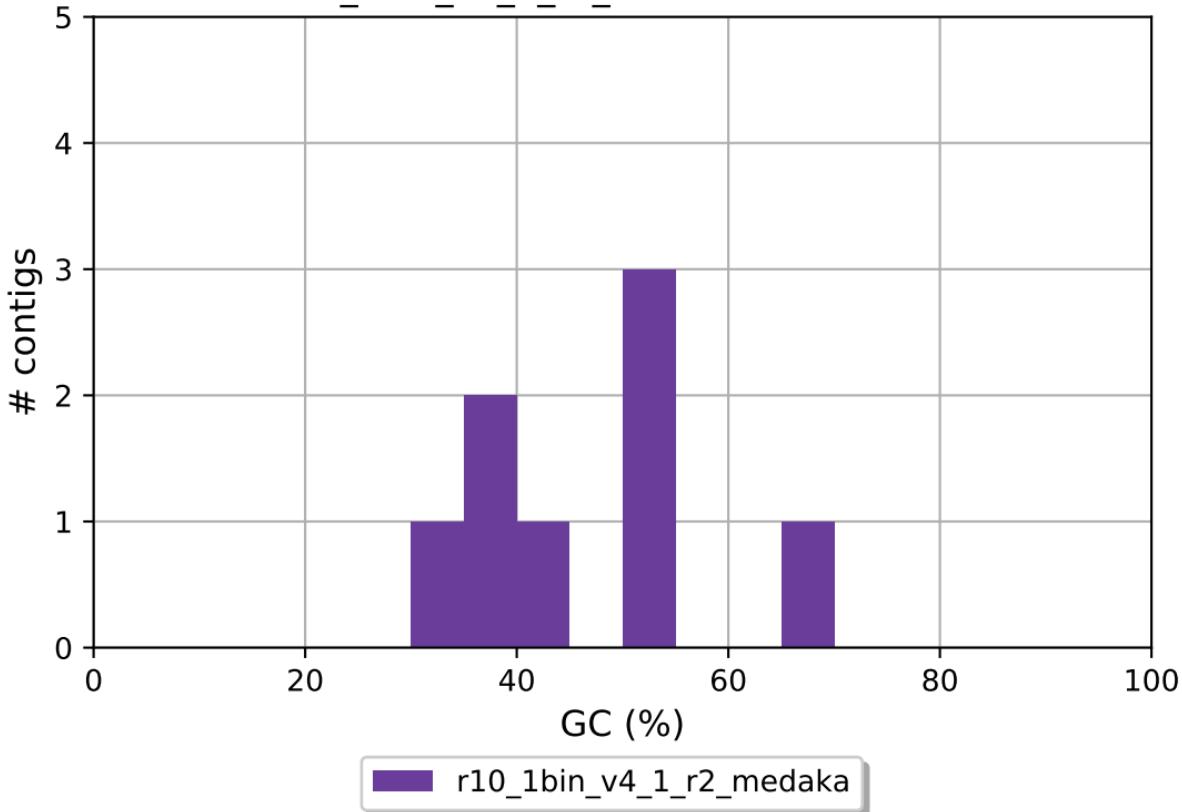
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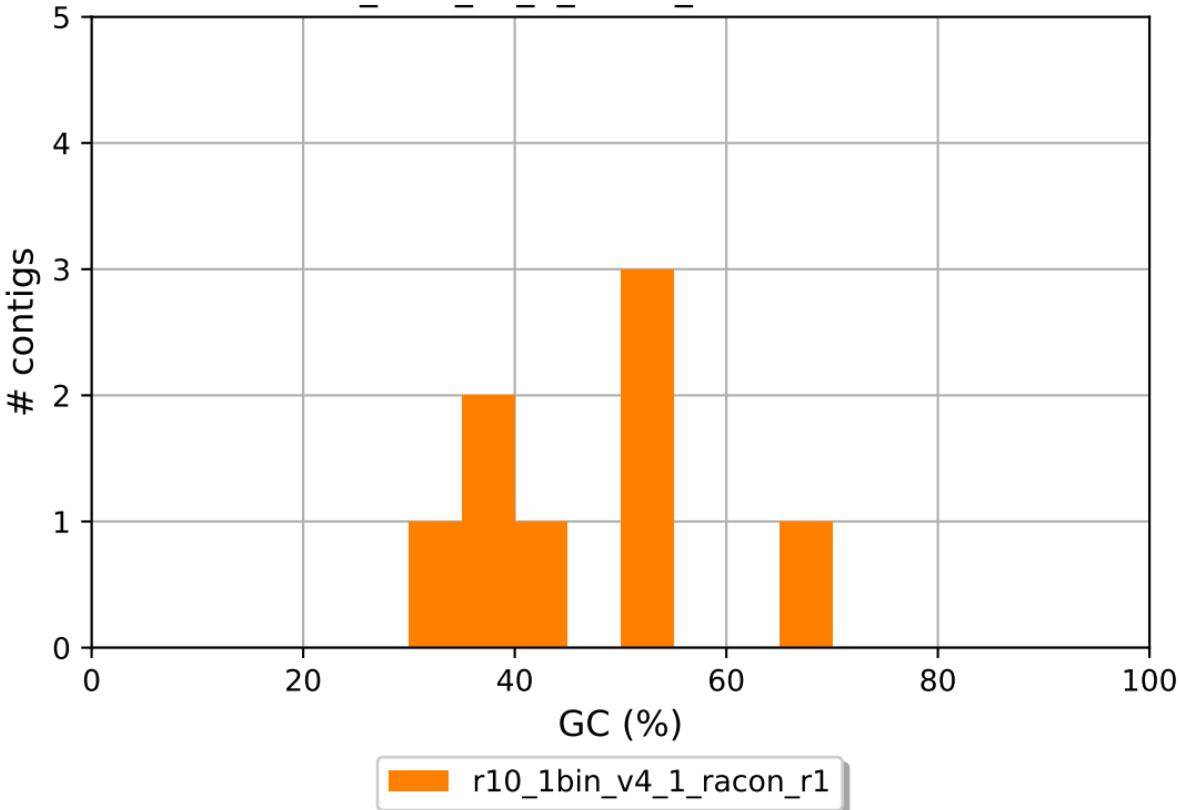
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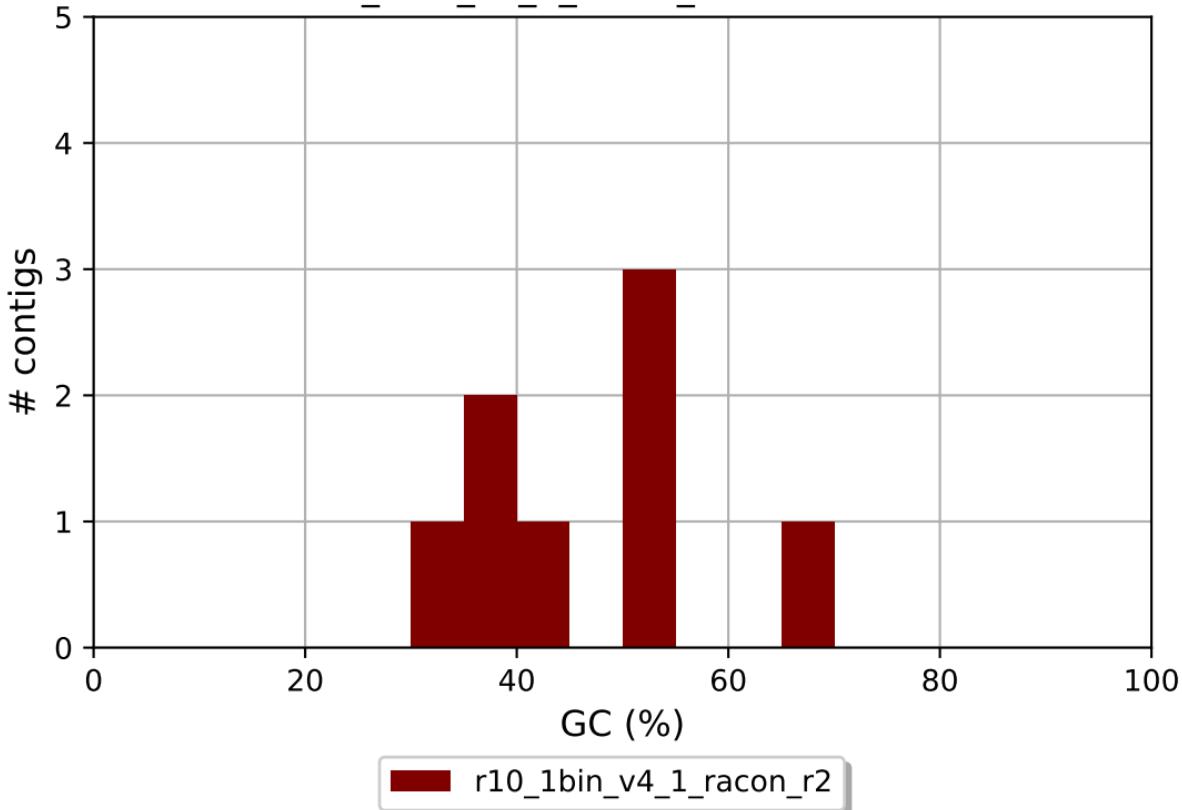
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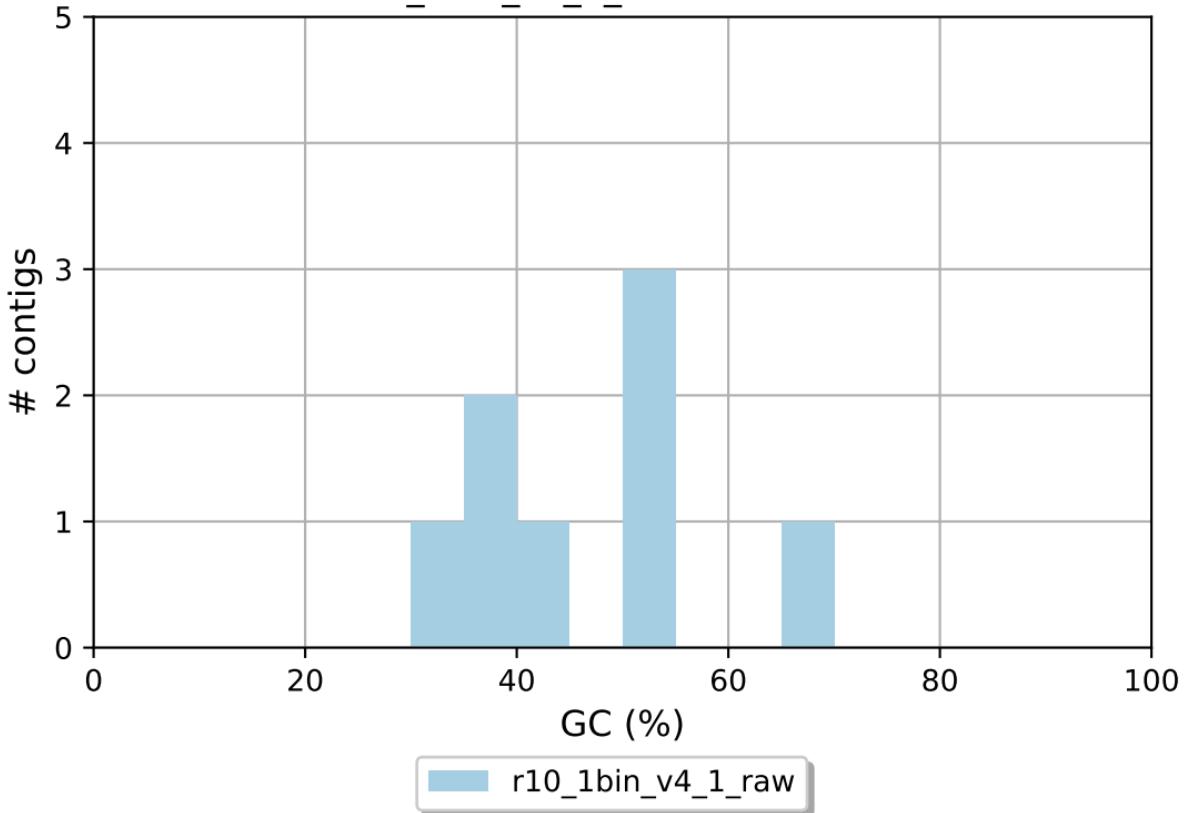
r10_1bin_v4_1_racon_r1 GC content



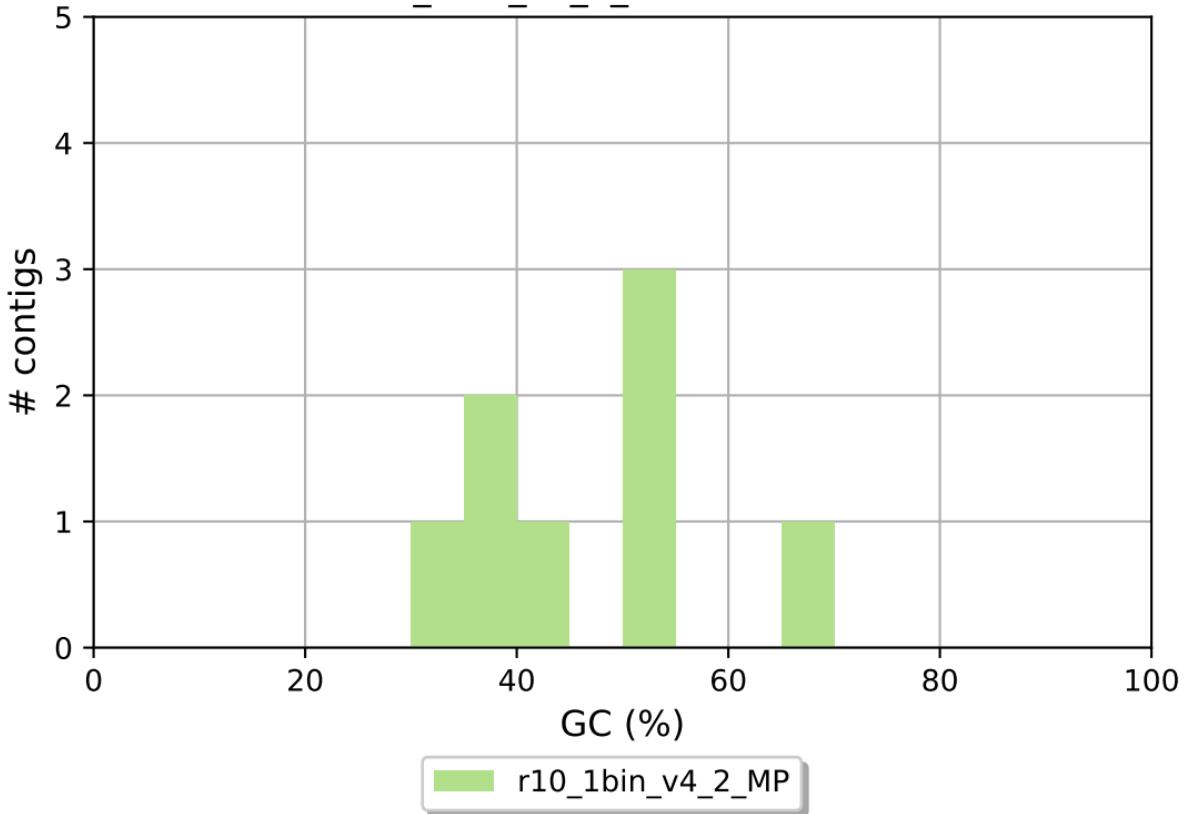
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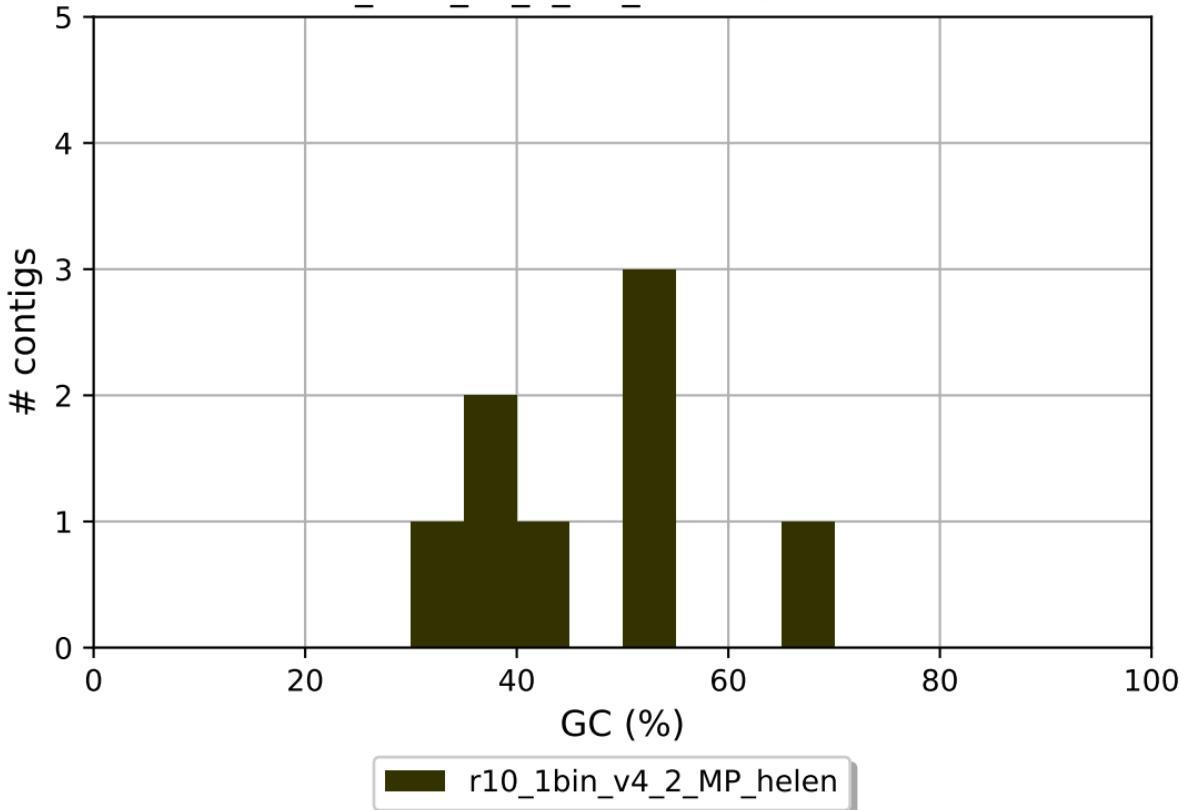
r10_1bin_v4_1_raw GC content



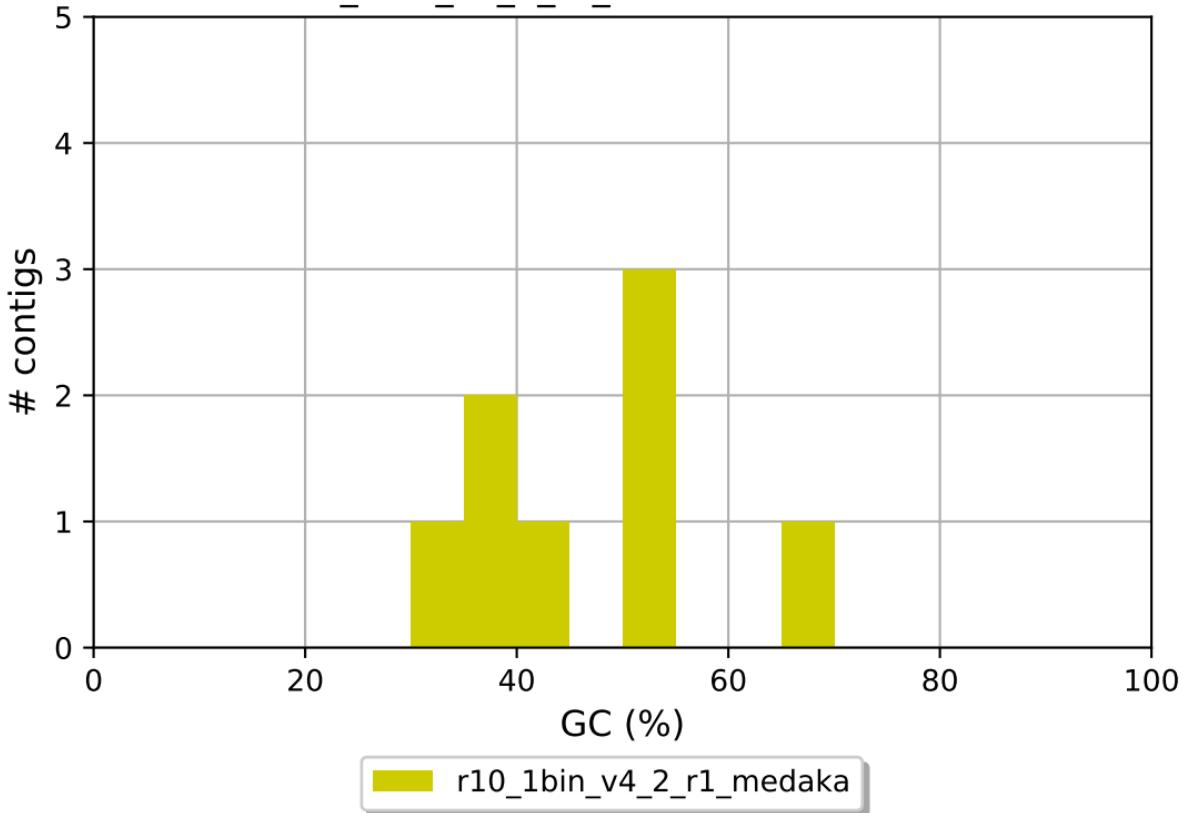
r10_1bin_v4_2_MP GC content



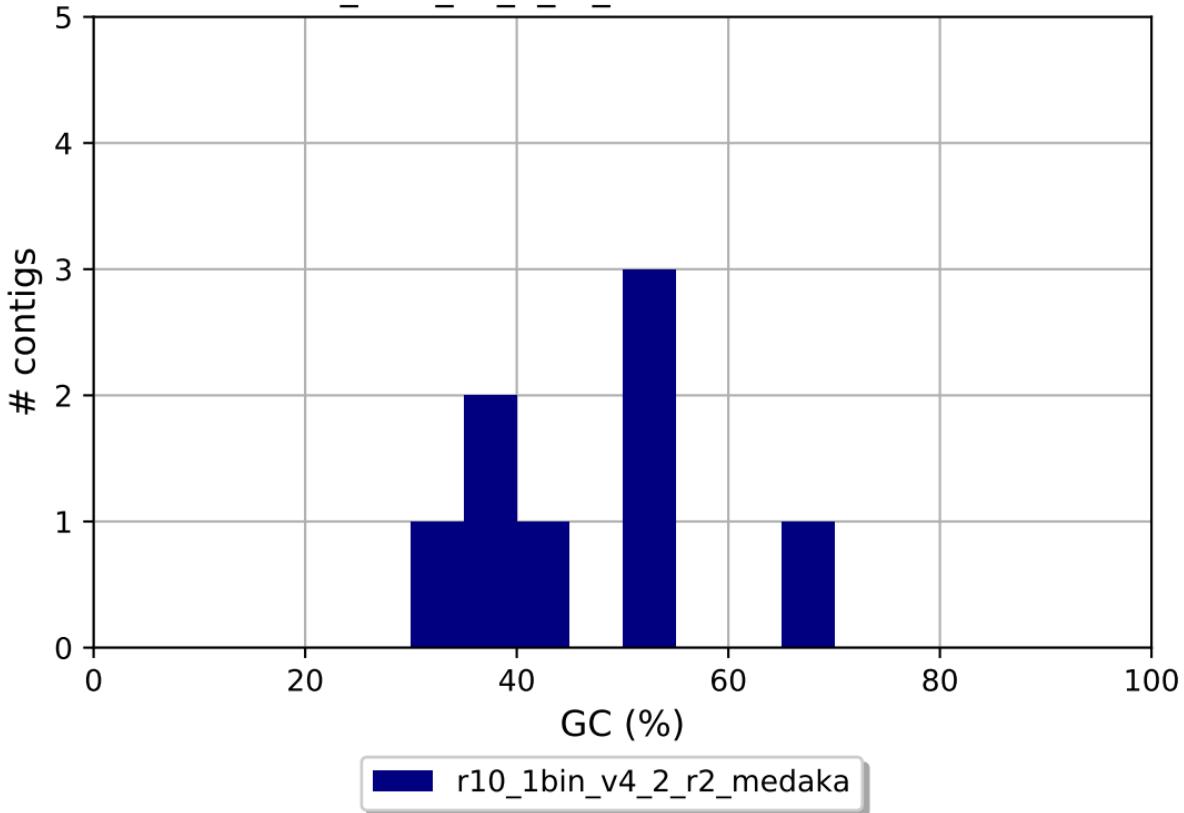
r10_1bin_v4_2_MP_helen GC content



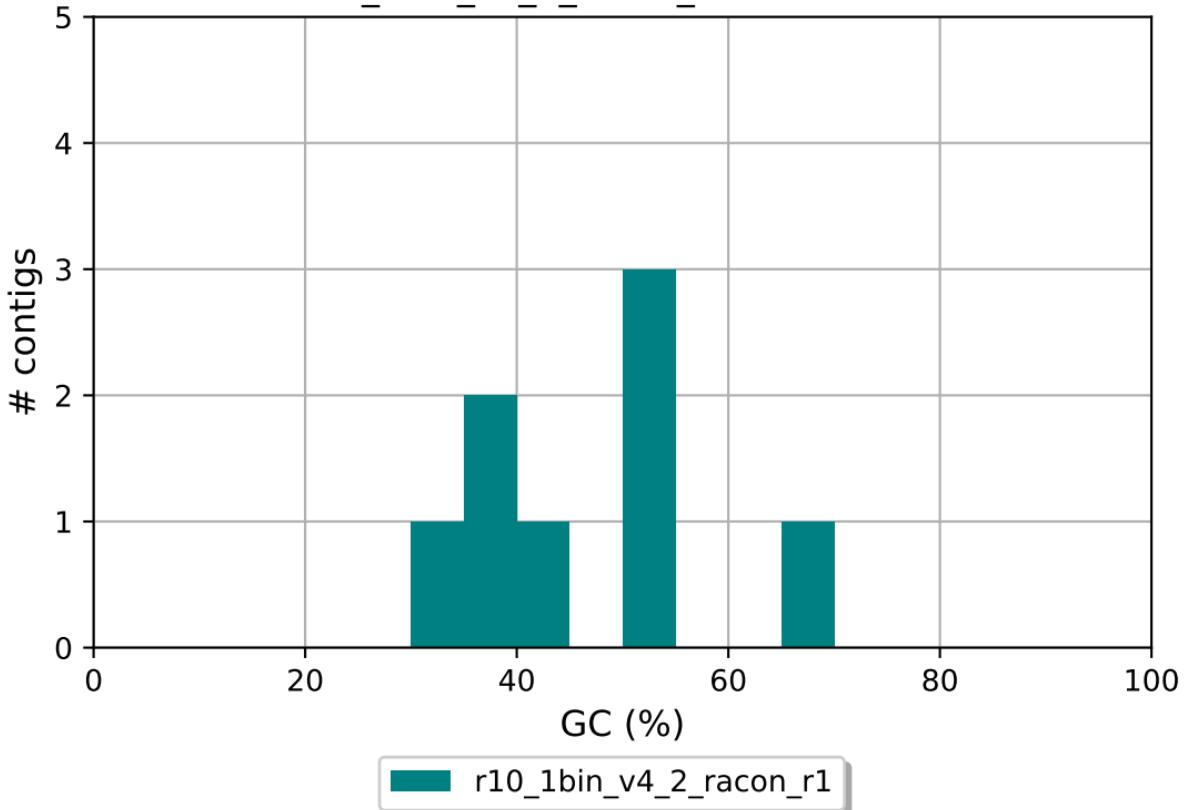
r10_1bin_v4_2_r1_medaka GC content



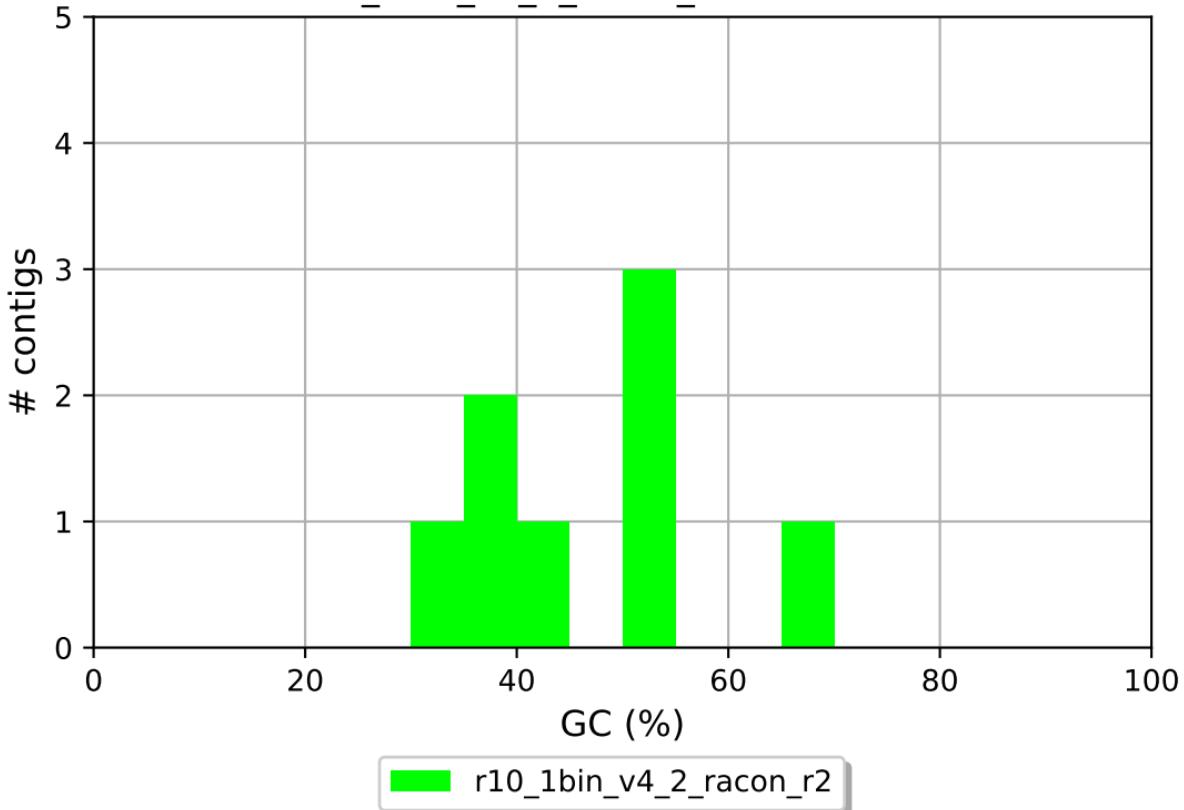
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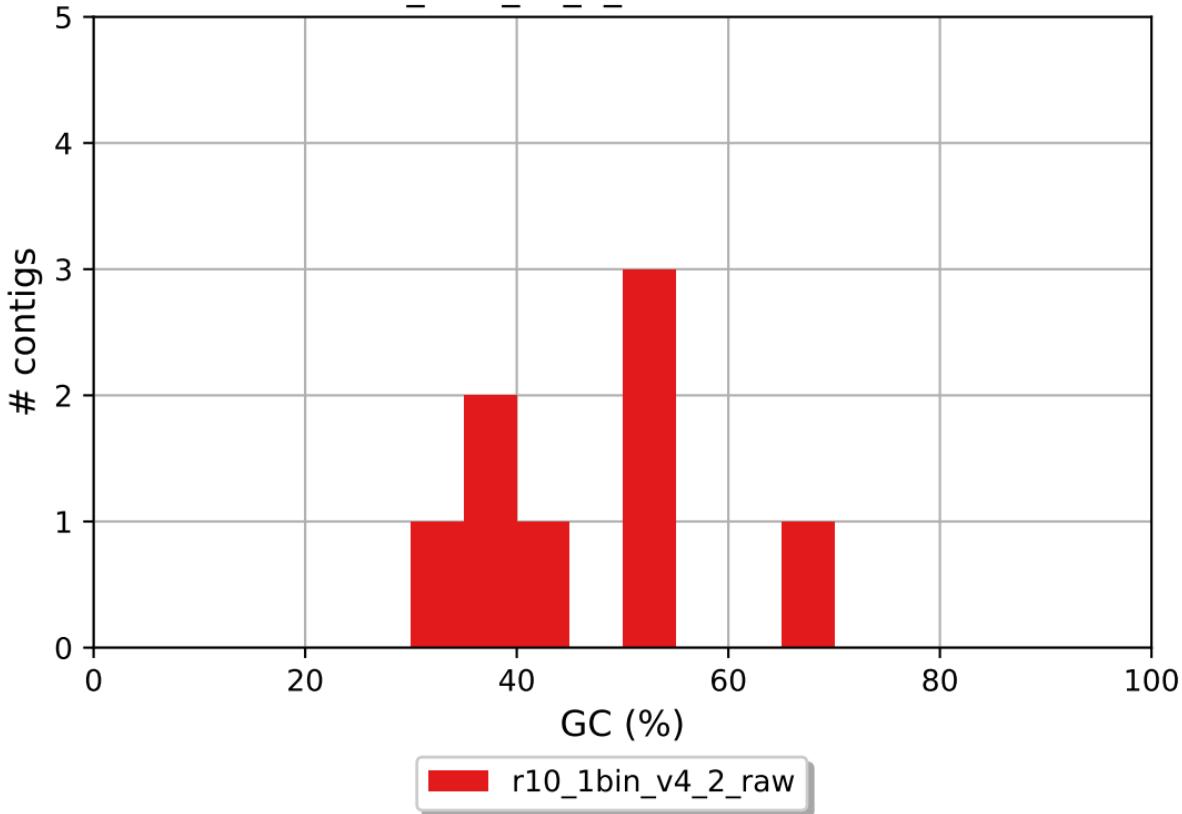
r10_1bin_v4_2_racon_r1 GC content



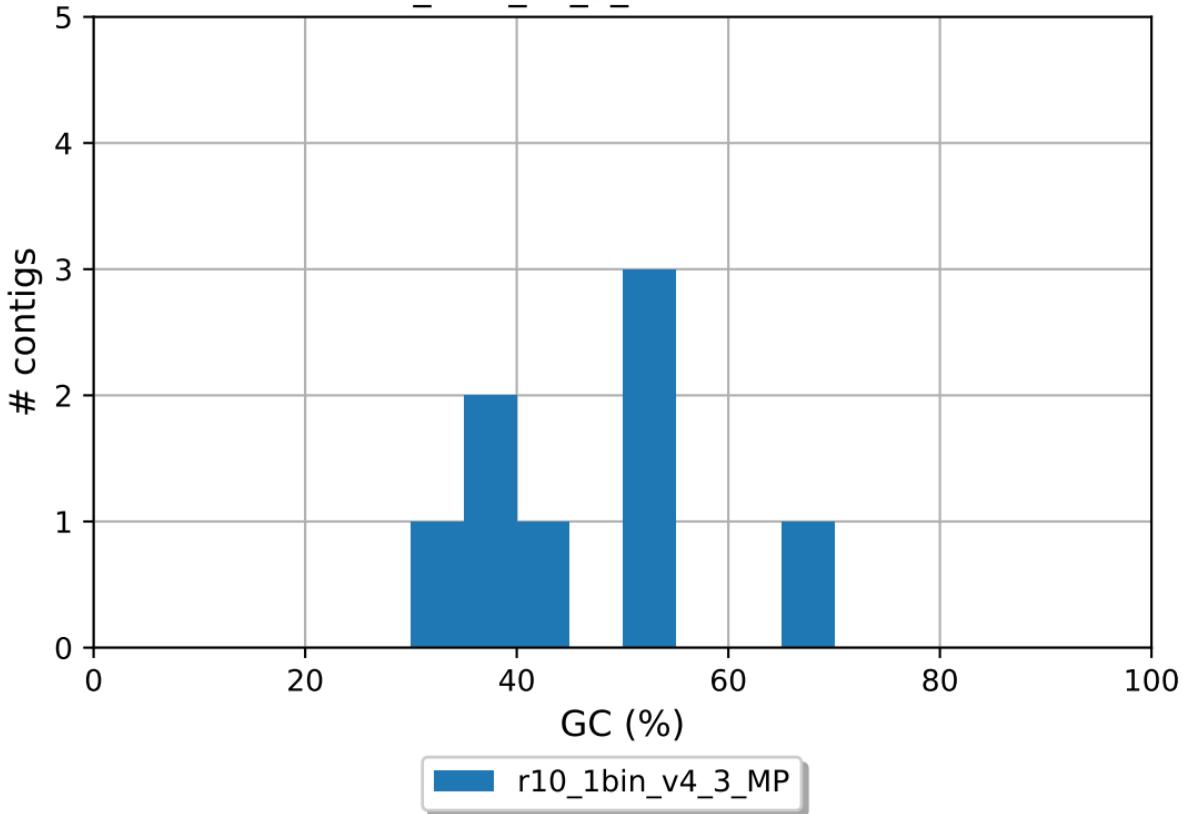
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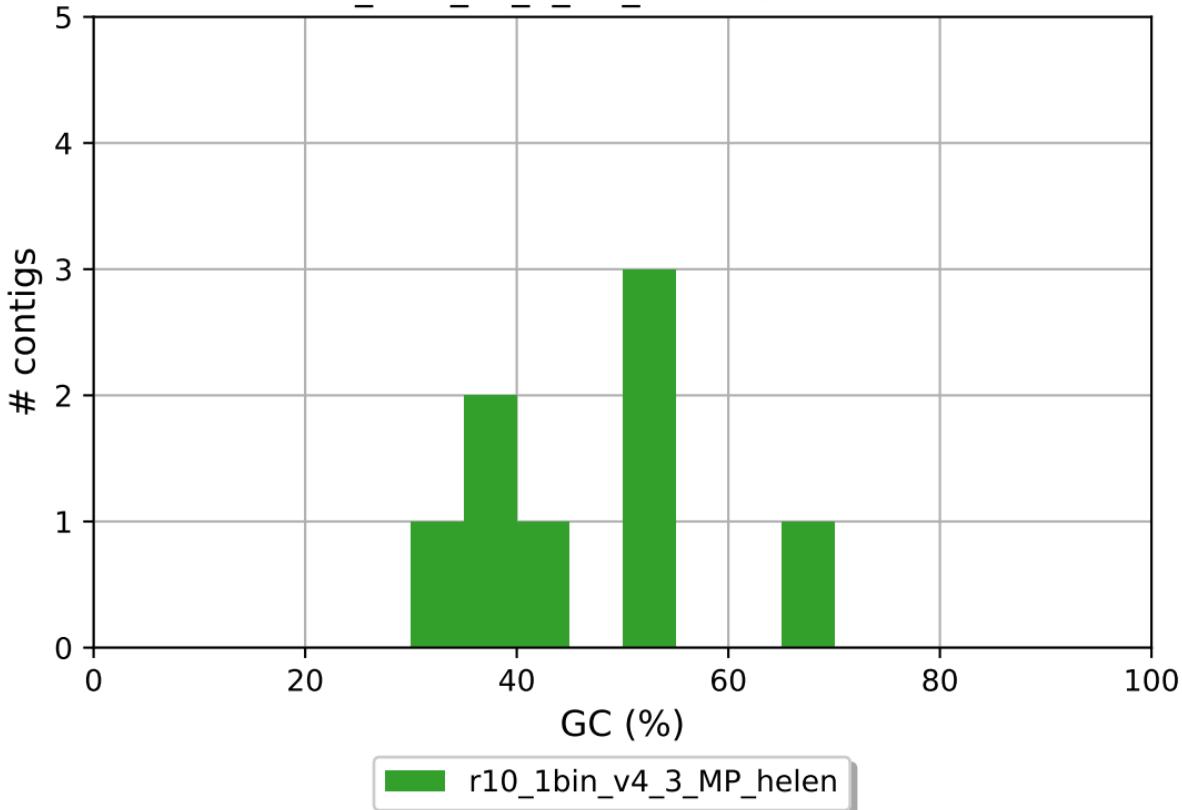
r10_1bin_v4_2_raw GC content



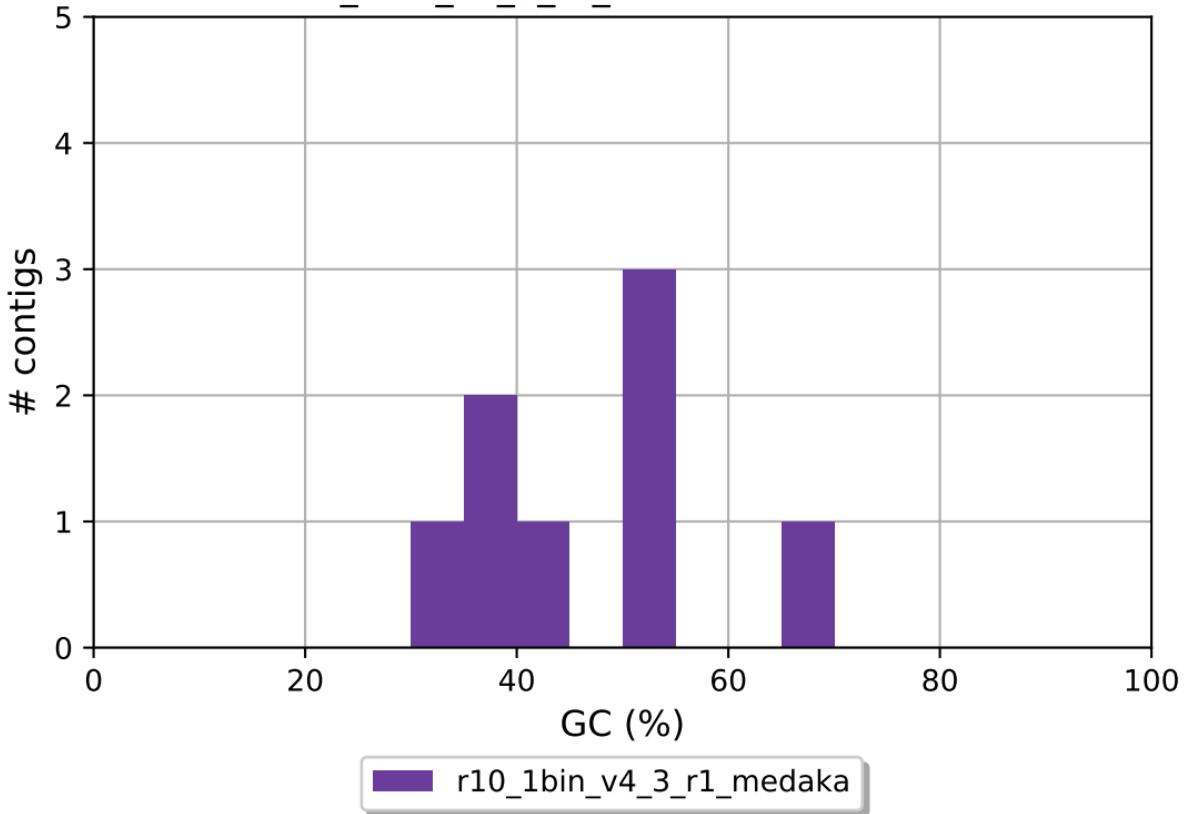
r10_1bin_v4_3_MP GC content



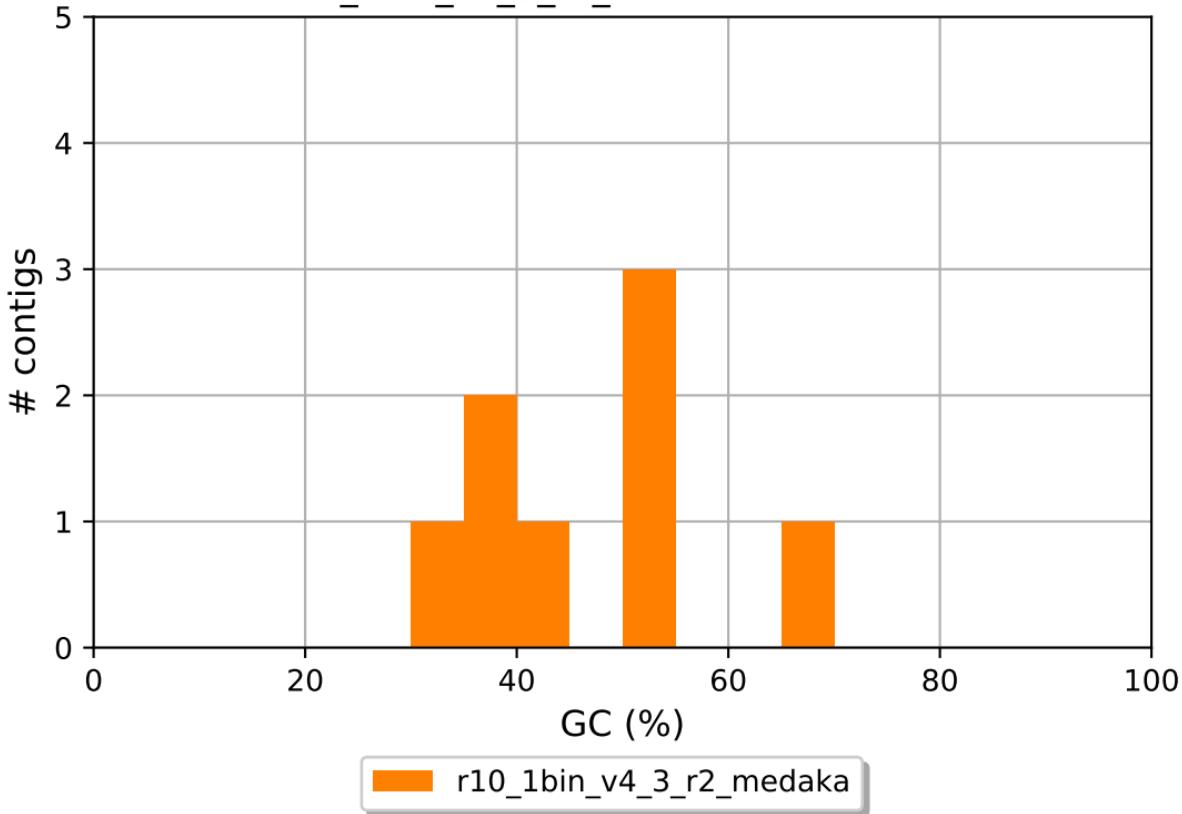
r10_1bin_v4_3_MP_helen GC content



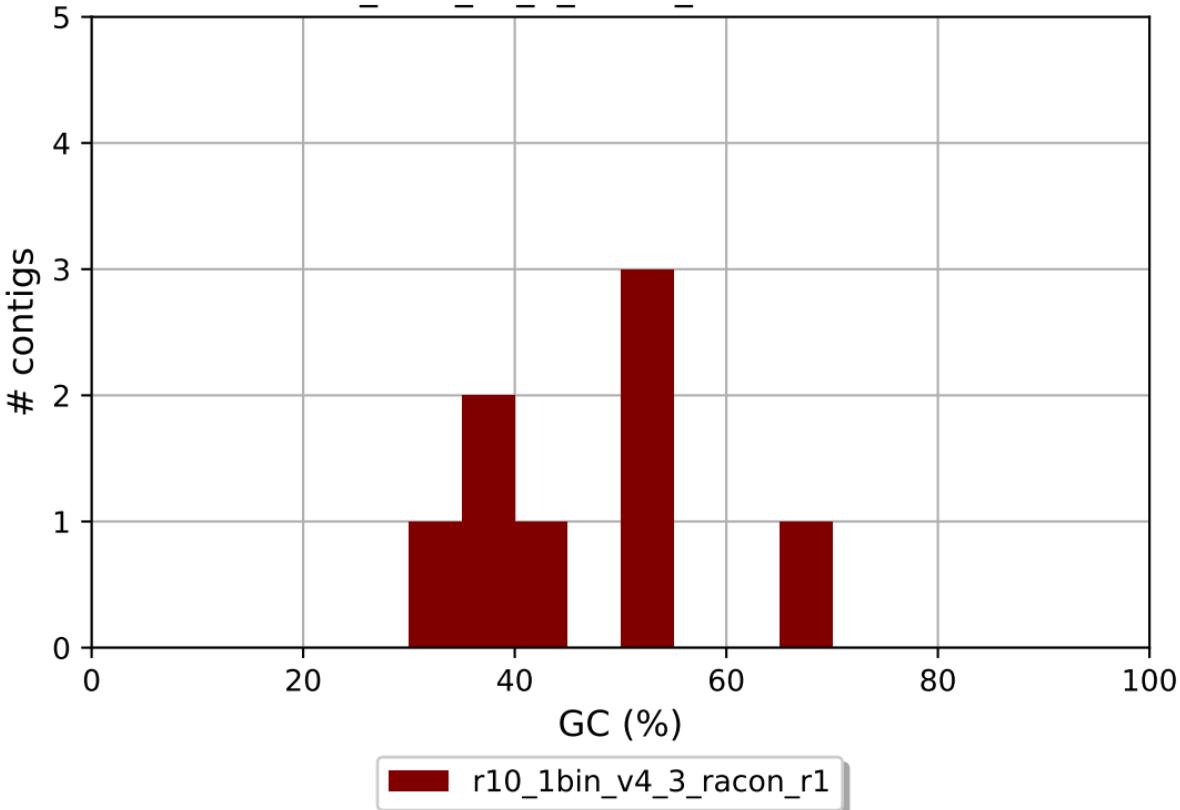
r10_1bin_v4_3_r1_medaka GC content



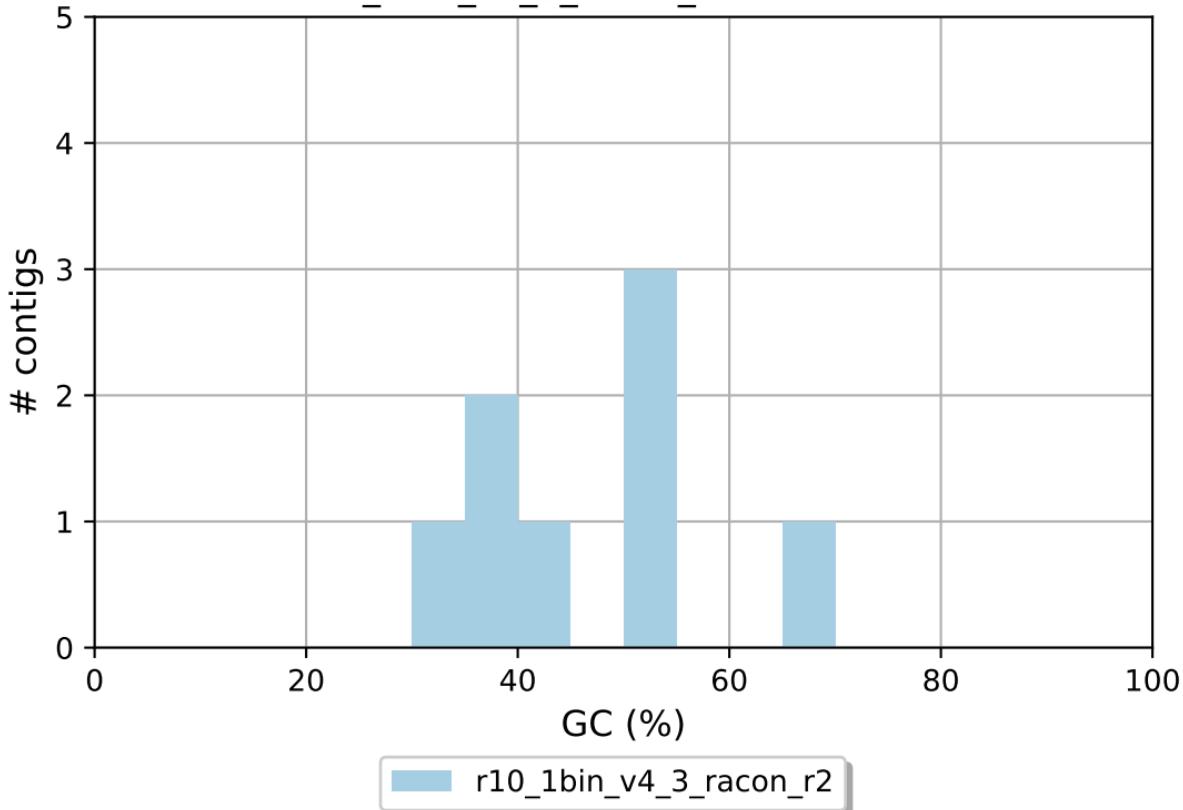
r10_1bin_v4_3_r2_medaka GC content



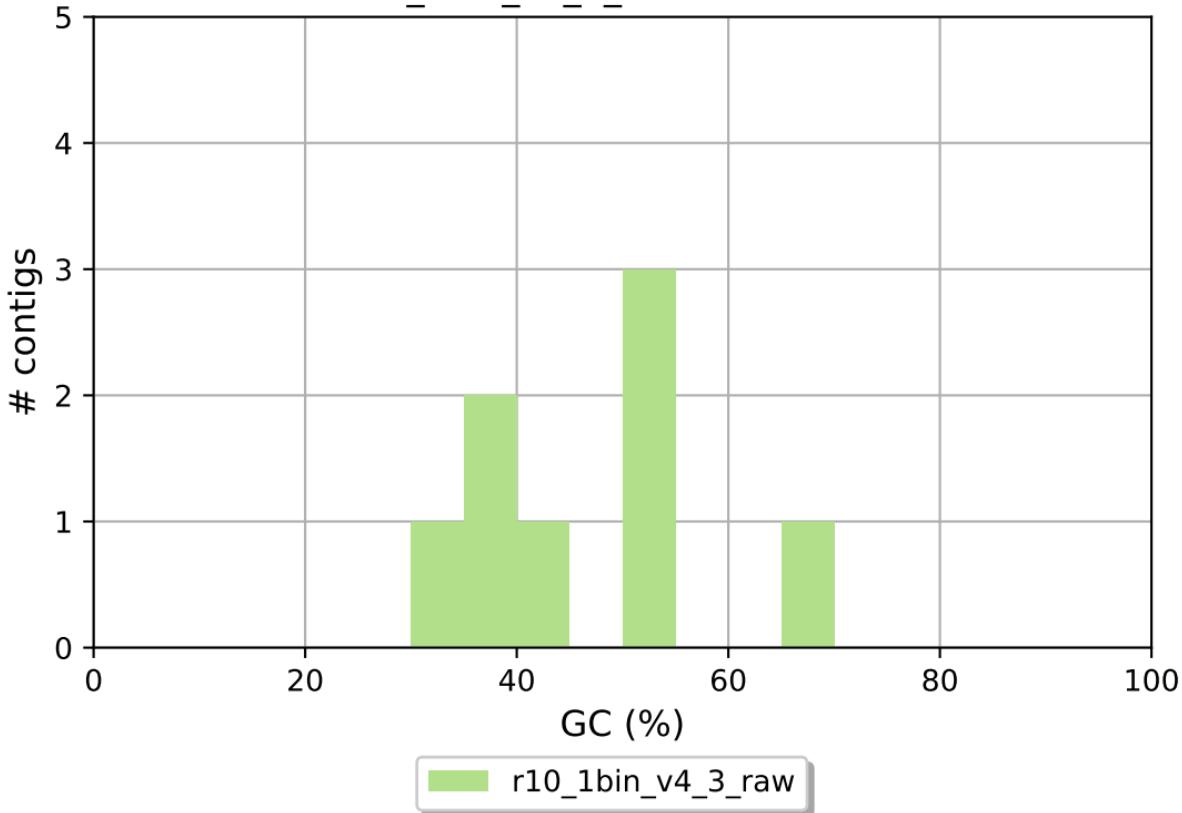
r10_1bin_v4_3_racon_r1 GC content



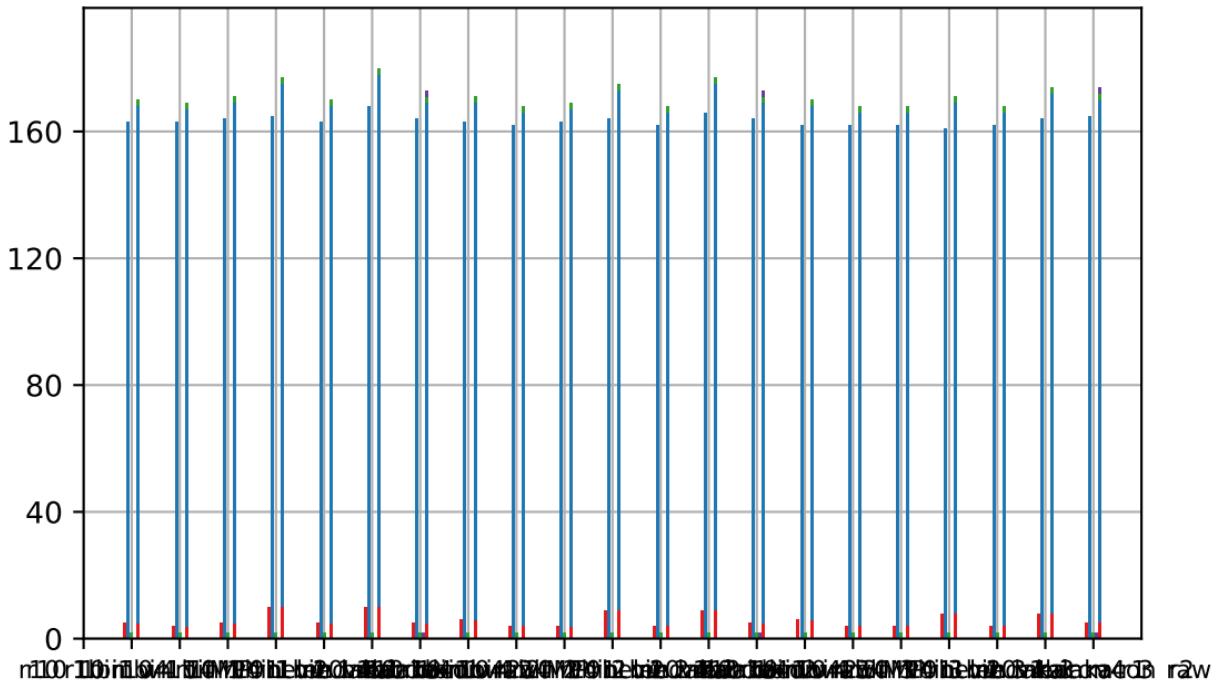
r10_1bin_v4_3_racon_r2 GC content



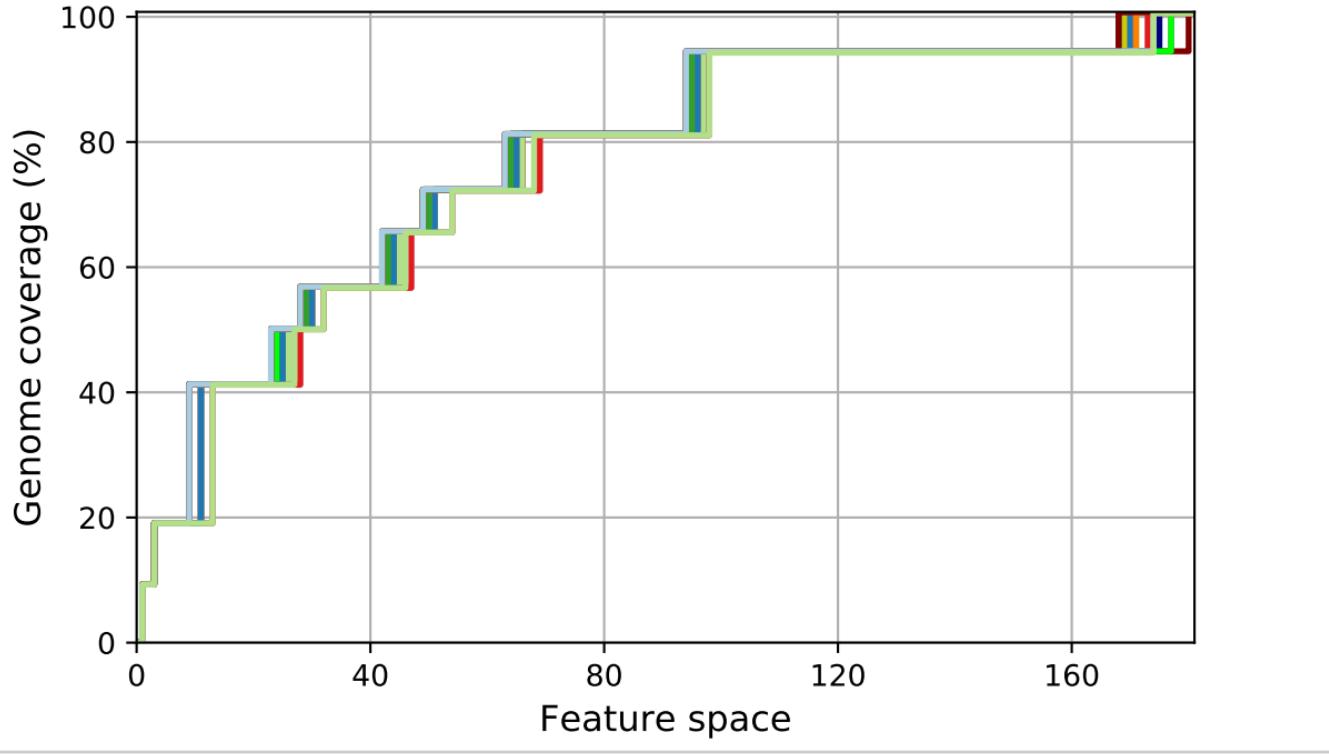
r10_1bin_v4_3_raw GC content



Misassemblies



FRCurve (misassemblies)



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP_helen

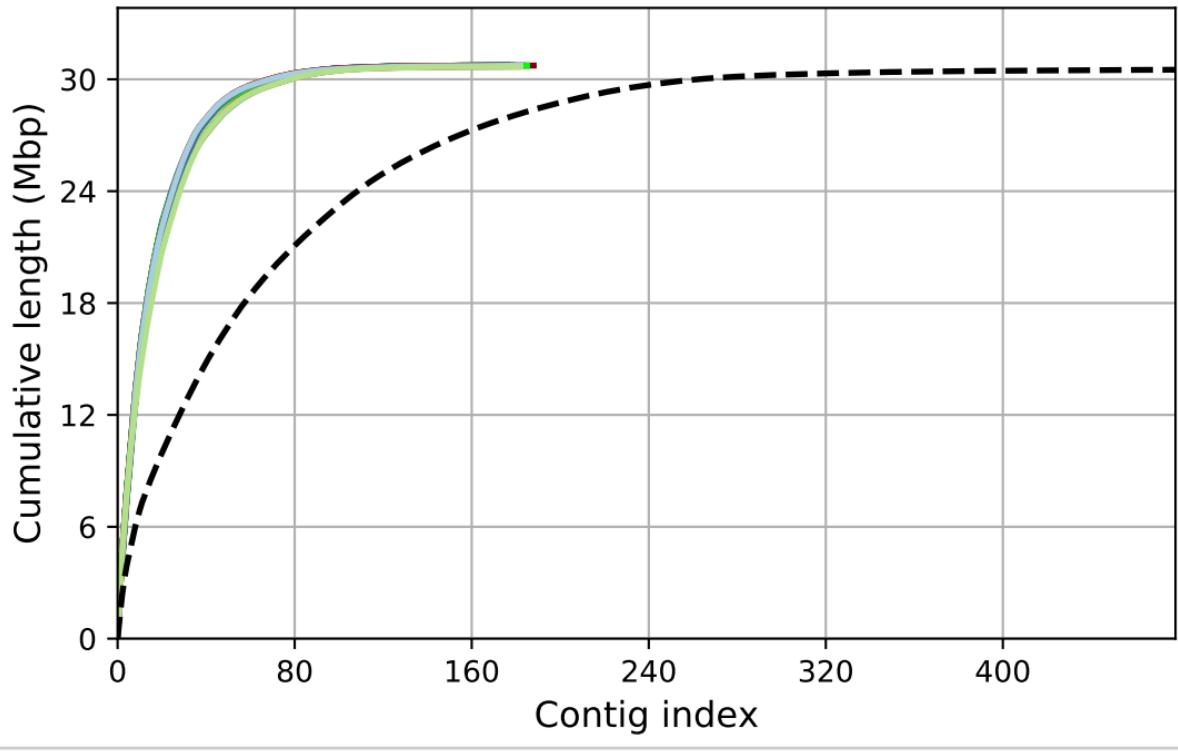
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_4_MP_helen

r10_1bin_v4_4_r1_medaka

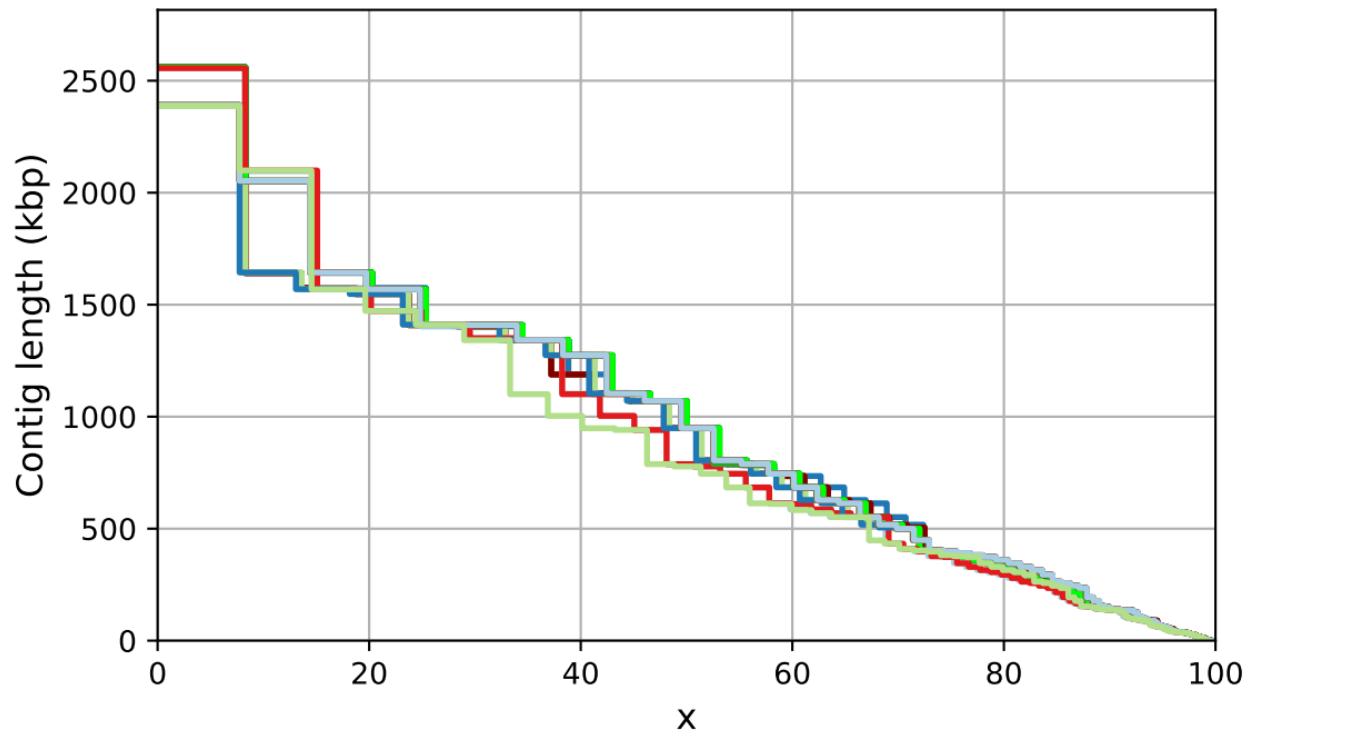
Cumulative length (aligned contigs)



Legend:

- r10_1bin_v4_1_MP
- r10_1bin_v4_1_MP_helen
- r10_1bin_v4_1_r1_medaka
- r10_1bin_v4_1_r2_medaka
- r10_1bin_v4_2_MP_helen
- r10_1bin_v4_2_r1_medaka
- r10_1bin_v4_2_r2_medaka
- r10_1bin_v4_2_racoon_r1
- r10_1bin_v4_3_MP_helen
- r10_1bin_v4_3_r1_medaka
- r10_1bin_v4_3_r2_medaka
- r10_1bin_v4_3_racoon_r1

NAx



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

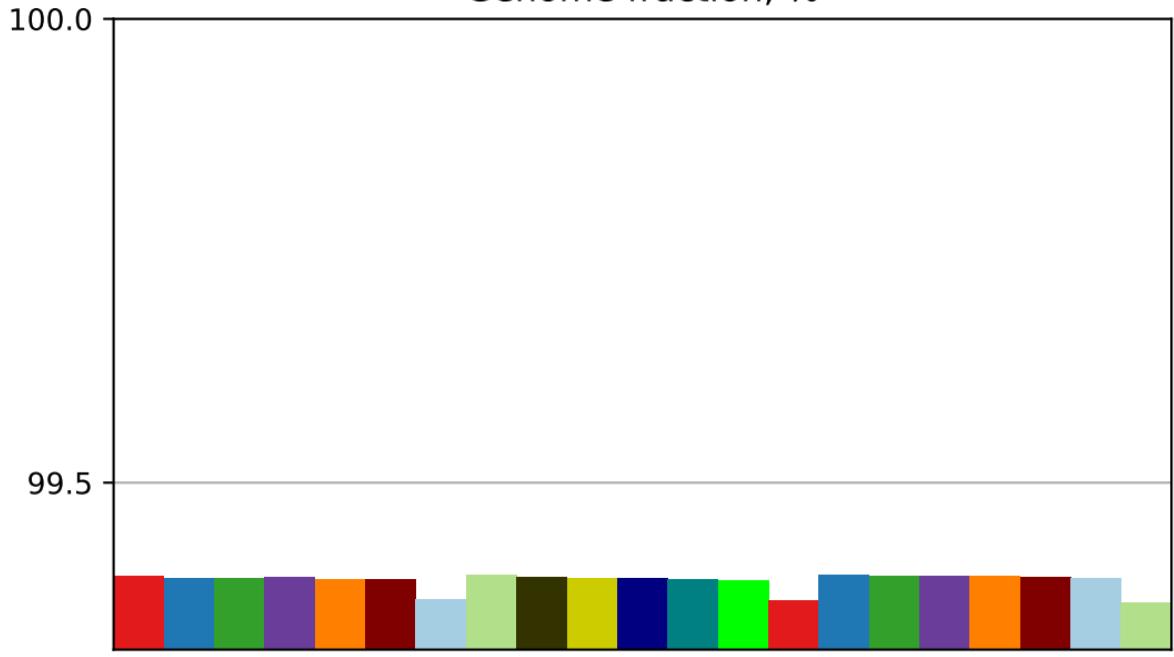
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

Genome fraction, %



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka