

Report

	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# contigs (>= 5000 bp)	8	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	8
# contigs (>= 25000 bp)	8	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	8
Total length (>= 5000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 10000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 25000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 50000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792240	6792237	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
Total length	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.51	49.51	49.51	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.50	49.49	49.49	49.49	49.49	49.50	49.49	49.48	49.48	49.48
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21
N50	4757946	4757846	4757780	4758962	4758994	4758970	4758583	4758586	4758587	4758100	4758114	4758101	4757934	4757908	4757887	4757853	4757839	4757857	4755983	4756088	4755683
NG50	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792237	6792231	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
N75	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992072	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261
NG75	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792237	6792231	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
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	5
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# misassemblies	6	6	6	8	6	8	6	6	6	6	6	6	6	6	6	6	6	6	9	10	10
# 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	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792237	6792231	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
# local misassemblies	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	29	24	24
# 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	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	6	7	7	6	7	6
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24042643	24046657	24044196	24047730	24049851	24048222	24045077	24048537	24046109	24037819	24041340	24039429	24032724	24039288	24033116	24028398	24034056	24026484	24077032	24079252	24076394
Genome fraction (%)	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.894	99.863	99.864	99.875
Duplication ratio	1.015	1.014	1.014	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.014	1.014	1.015	1.014	1.014	1.008	1.008	1.008
# 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	56.29	55.48	55.20	59.25	57.91	58.56	56.56	55.35	55.77	56.02	55.89	55.29	58.46	56.66	57.57	58.25	58.34	57.51	64.74	64.86	65.35
# indels per 100 kbp	5.45	5.18	3.81	5.88	5.49	5.71	3.59	3.66	3.59	3.59	3.76	3.57	14.16	13.66	13.78	12.50	13.03	12.96	97.03	96.80	97.39
Largest alignment	1643815	1643826	2052278	1643836	1643839	1643777	1643845	1643844	2052326	1643846	1643841	2052324	1643669	1643678	2052173	1643691	1643705	2052196	2098266	2098268	2098661
Total aligned length	6815252	6814518	6814997	6815859	6814586	6815908	6816004	6814815	6815627	6815624	6815298	6815326	6814861	6813236	6814529	6814619	6814534	6814444	6768420	6768571	6770126
NGA50	1274462	1274461	1643773	1274471	1274471	1188534	1274468	1274469	1643772	1274472	1274470	1643777	1274332	1274331	1643599	1274366	1274358	1643642	1471342	1471391	1471541
NGA75	1070325	1070325	1070208	1070339	1070339	1070192	1070330	1070333	1070188	1070330	1070331	1070186	1070260	1070256	1070099	1070257	1070262	1070117	610112	610115	569700
LGA50	3	3	2	3	3	3	3	3	2	3	3	2	3	3	2	3	3	2	2	2	2
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4

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

	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	6	6	6	8	6	8	6	6	6	6	6	6	6	6	6	6	6	6	9	10	10
# contig misassemblies	6	6	6	8	6	8	6	6	6	6	6	6	6	6	6	6	6	6	9	10	10
# c. relocations	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	6	6	6	7	6	7	6	6	6	6	6	6	6	6	6	6	6	6	9	10	10
# 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	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792237	6792231	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
# 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	18	18	18	16	18	16	18	18	18	18	18	18	18	18	18	18	18	18	33	34	34
# local misassemblies	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	29	29	24
# 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	21	21	21	20	21	20	21	21	21	21	21	21	21	21	21	21	21	21	16	16	16
# unaligned mis. contigs	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	6	7	7	6	7	6
# mismatches	3783	3729	3710	3982	3892	3936	3801	3720	3748	3765	3756	3716	3929	3808	3869	3915	3921	3865	4350	4358	4391
# indels	366	348	256	395	369	384	241	246	241	241	253	240	952	918	926	840	876	871	6519	6504	6544
# indels (<= 5 bp)	265	250	161	298	273	289	148	152	148	148	159	147	858	822	833	746	779	776	6398	6383	6420
# indels (> 5 bp)	101	98	95	97	96	95	93	94	93	93	94	93	94	96	93	94	97	95	121	121	124
Indels length	5444	5418	5294	5480	5417	5428	5202	5264	5243	5202	5270	5239	6032	6045	6039	5876	6008	5993	12832	12818	12975

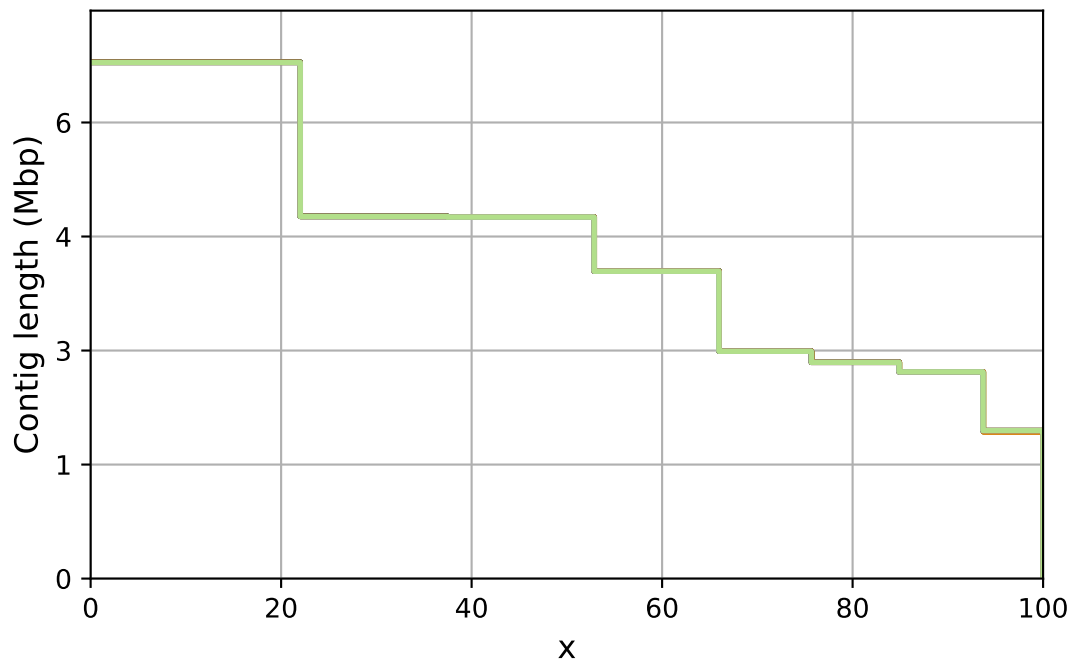
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

### Unaligned report

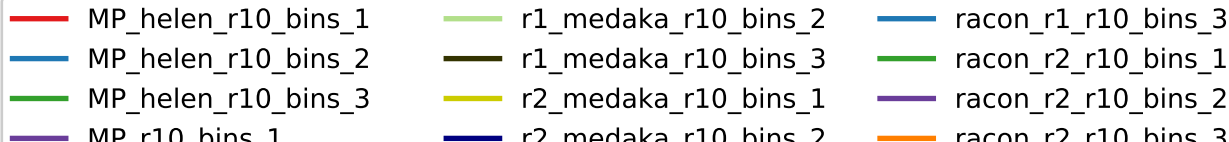
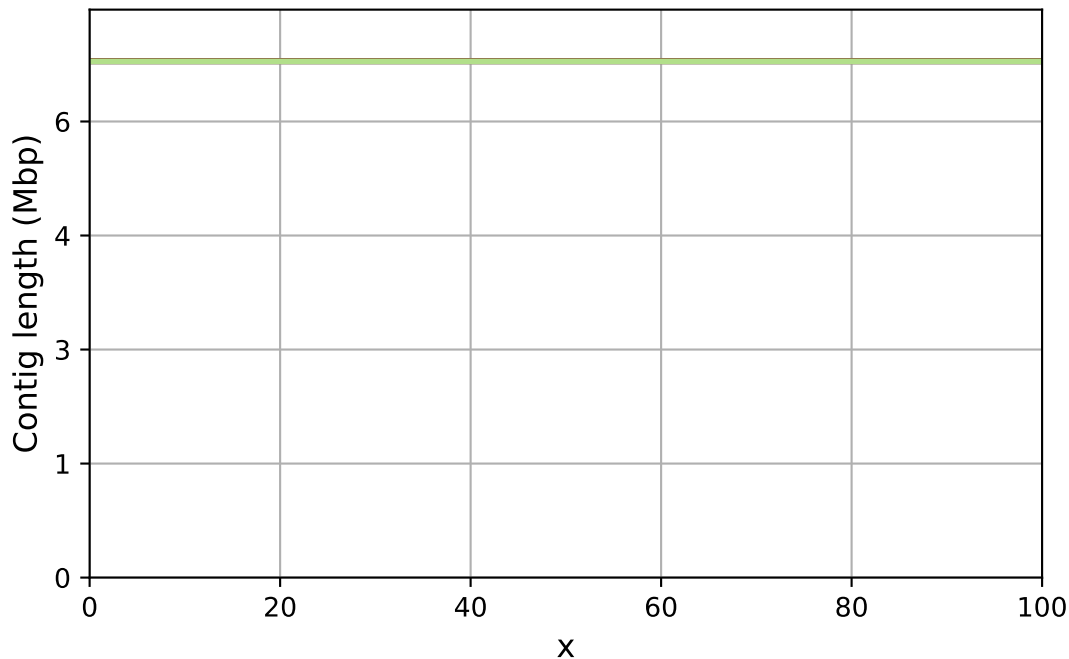
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# 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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24042643	24046657	24044196	24047730	24049851	24048222	24045077	24048537	24046109	24037819	24041340	24039429	24032724	24039288	24033116	24028398	24034056	24026484	24077032	24079252	24076394
# 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).

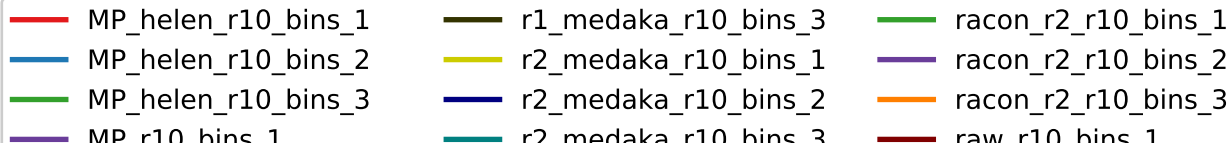
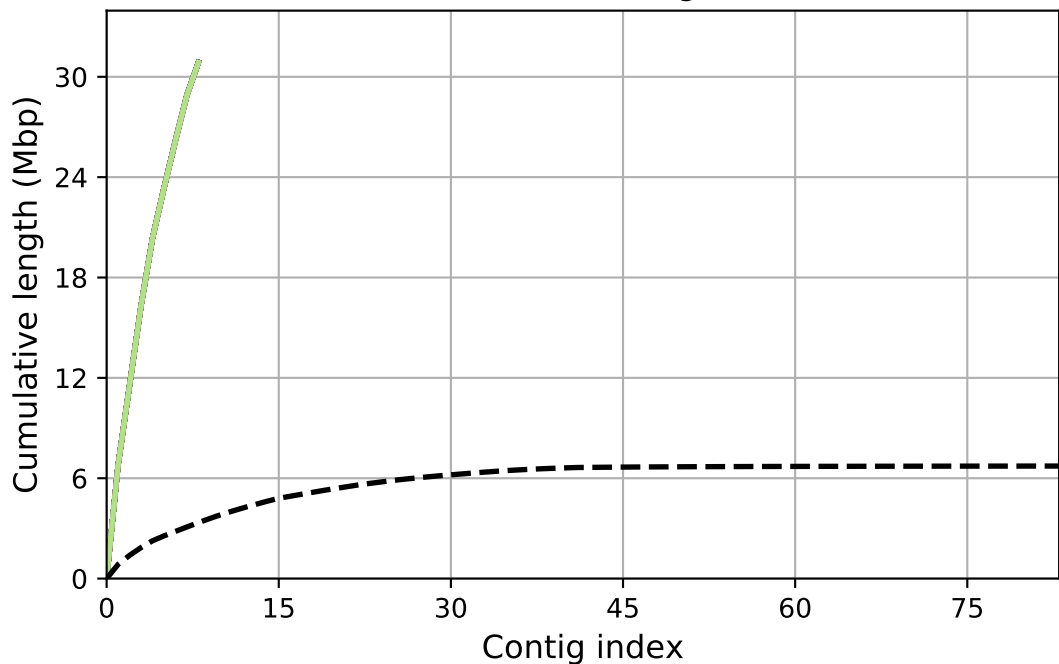
Nx



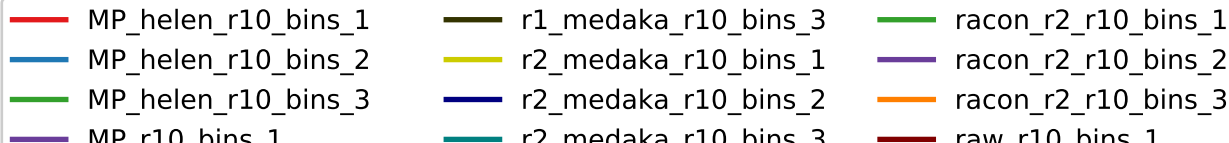
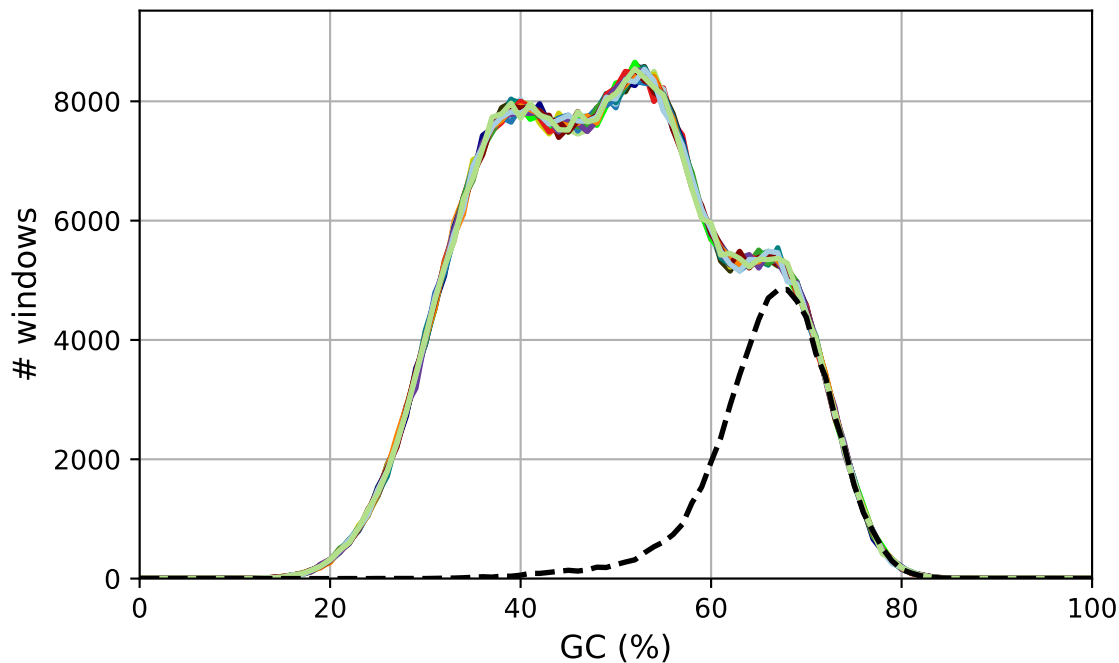
# NGx



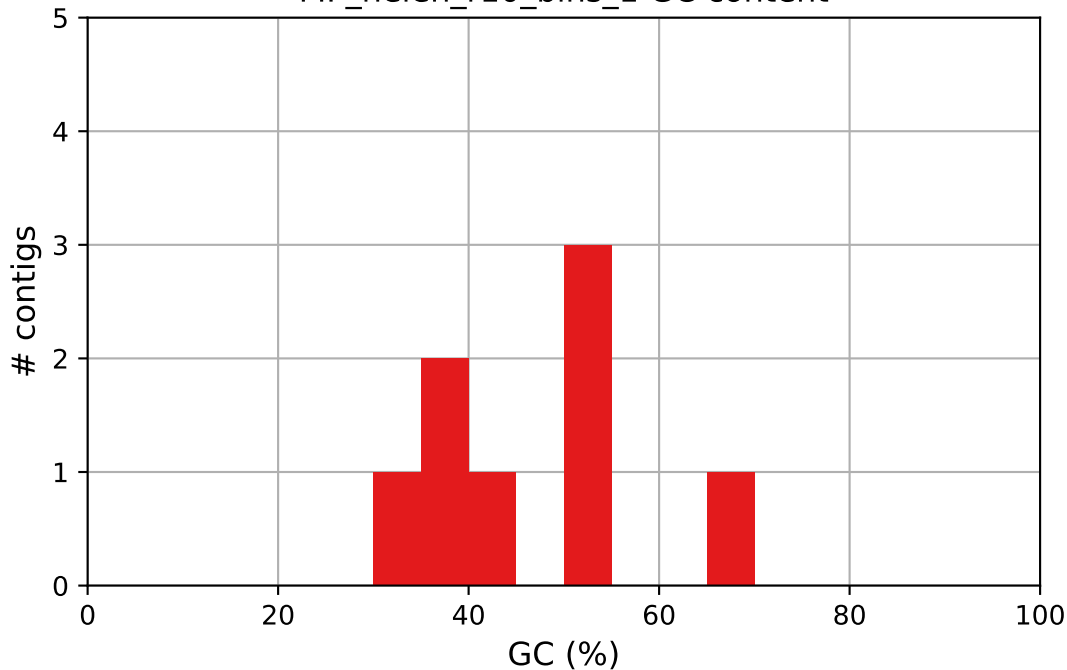
# Cumulative length



GC content



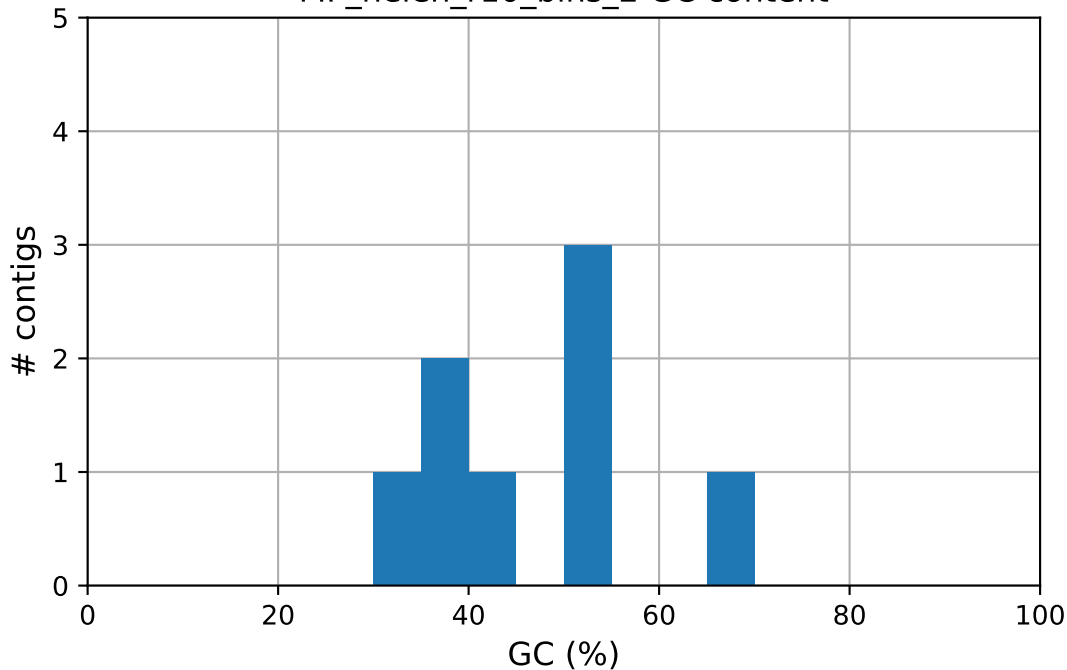
MP\_helen\_r10\_bins\_1 GC content



MP\_helen\_r10\_bins\_1

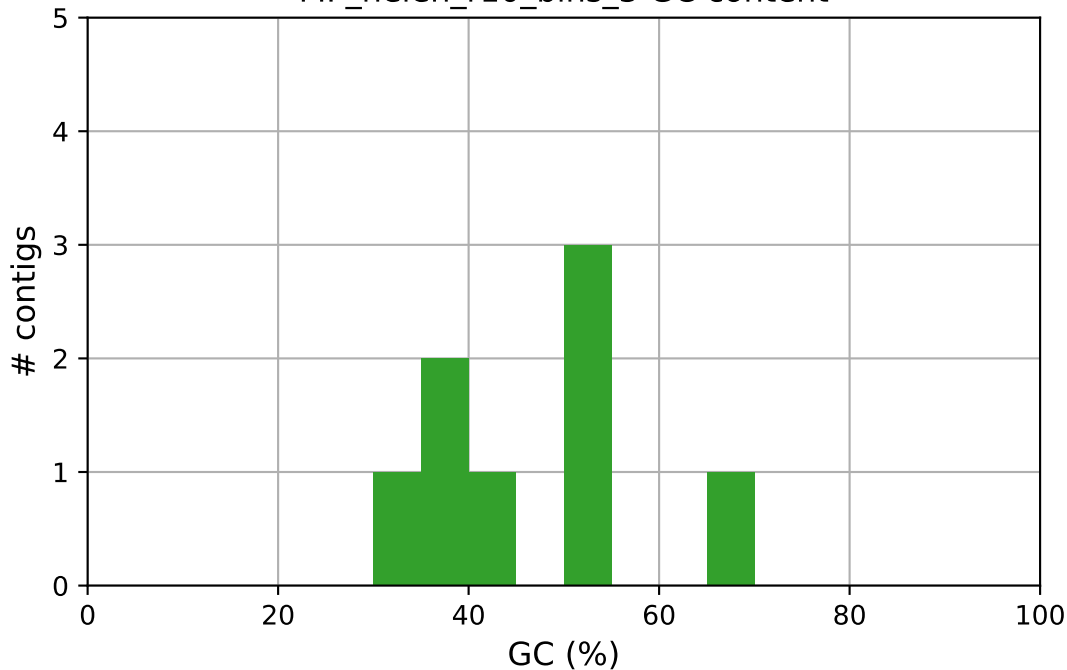


MP\_helen\_r10\_bins\_2 GC content



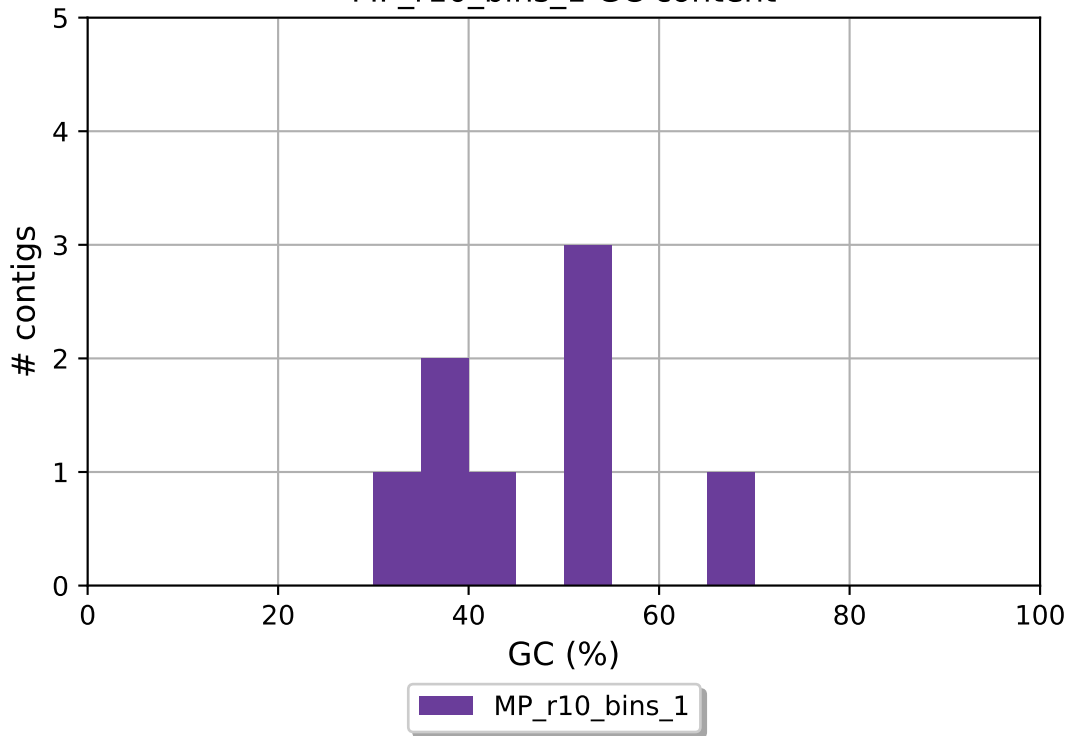
MP\_helen\_r10\_bins\_2

MP\_helen\_r10\_bins\_3 GC content

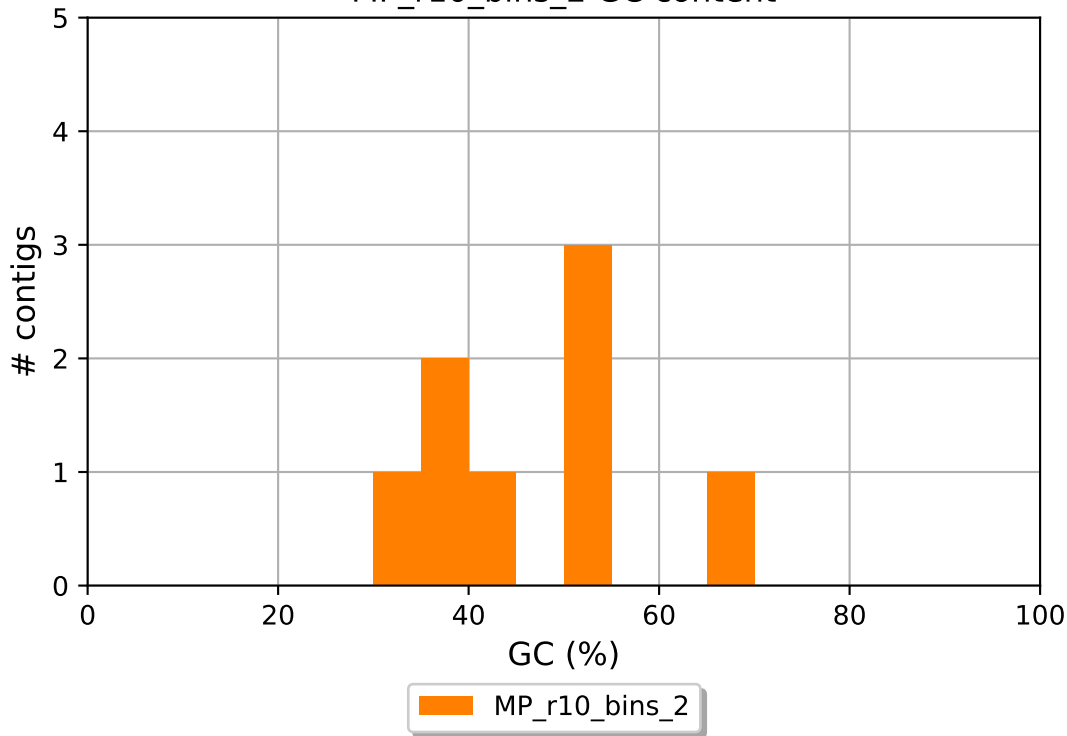


MP\_helen\_r10\_bins\_3

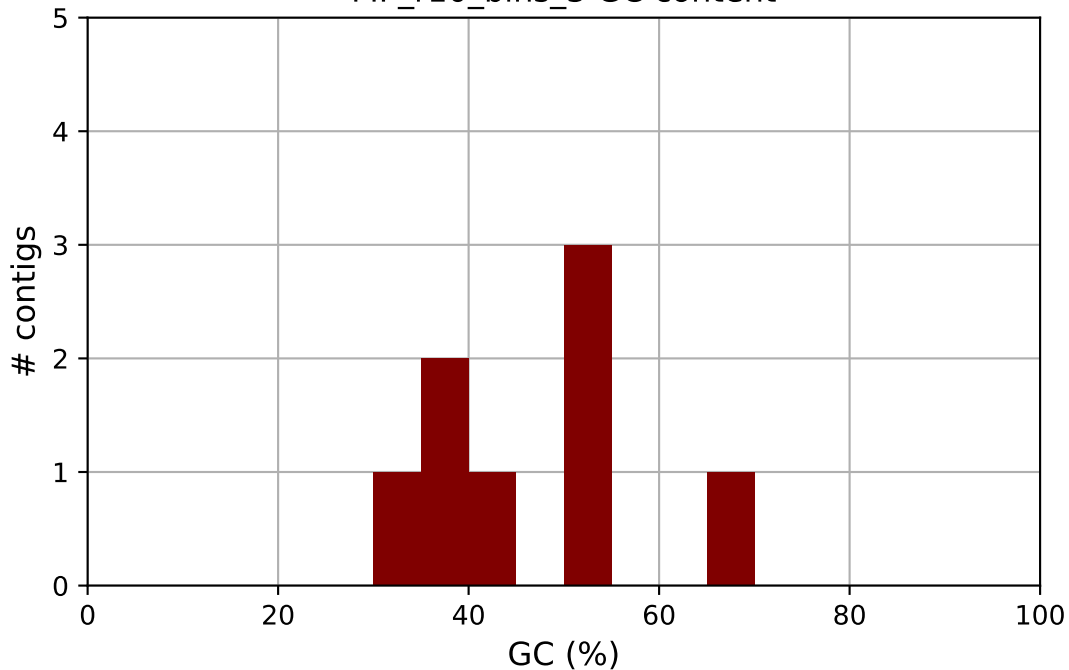
MP\_r10\_bins\_1 GC content



MP\_r10\_bins\_2 GC content

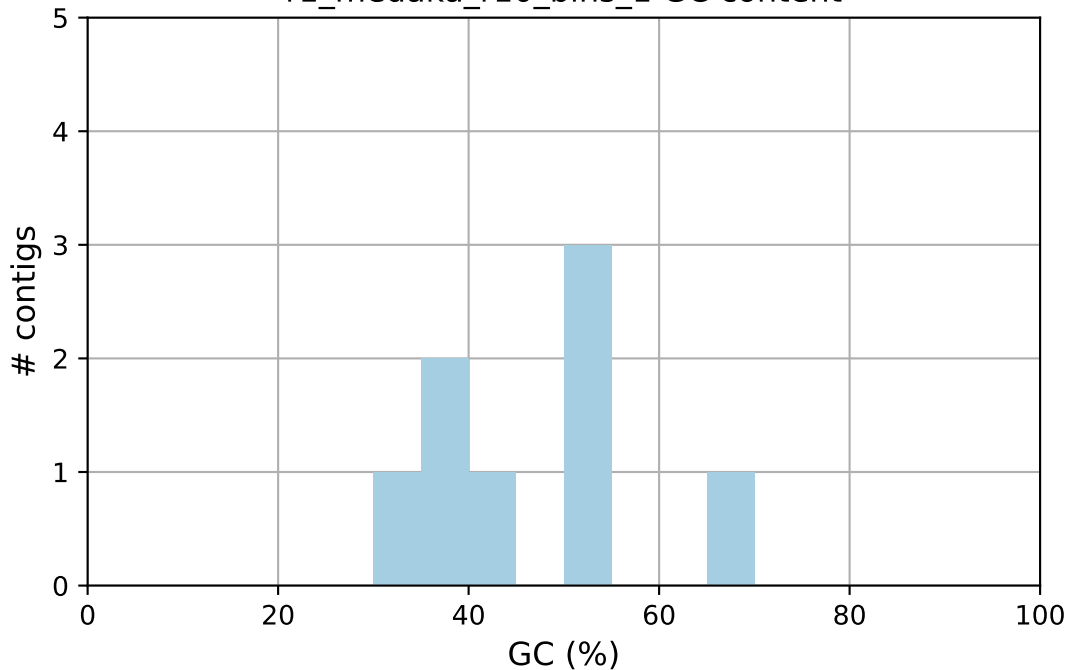


MP\_r10\_bins\_3 GC content



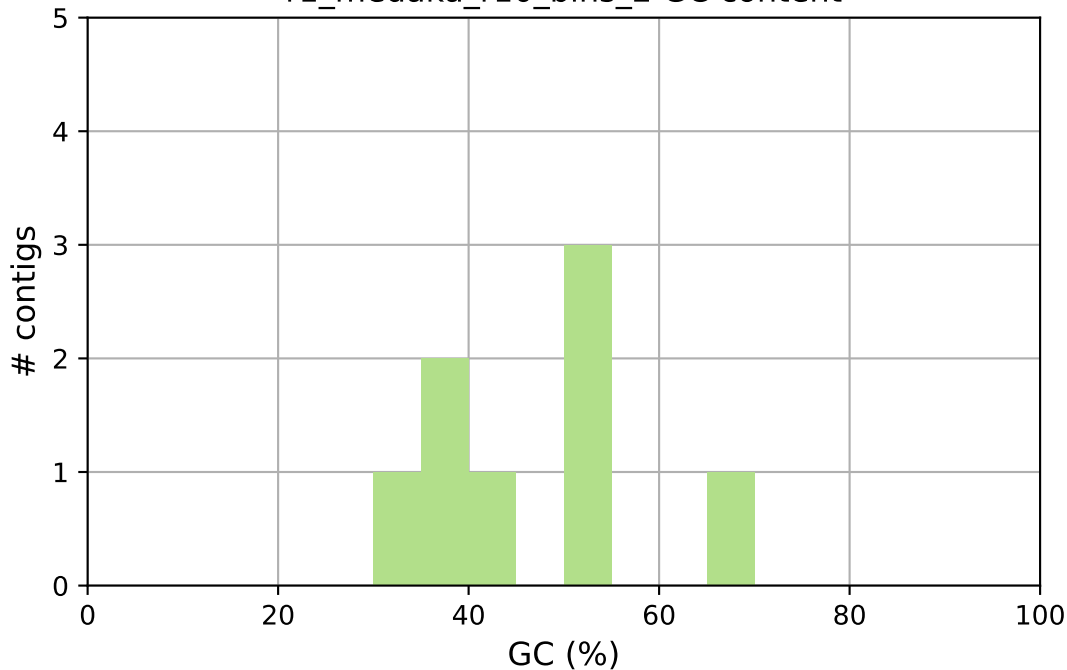
MP\_r10\_bins\_3

r1\_medaka\_r10\_bins\_1 GC content



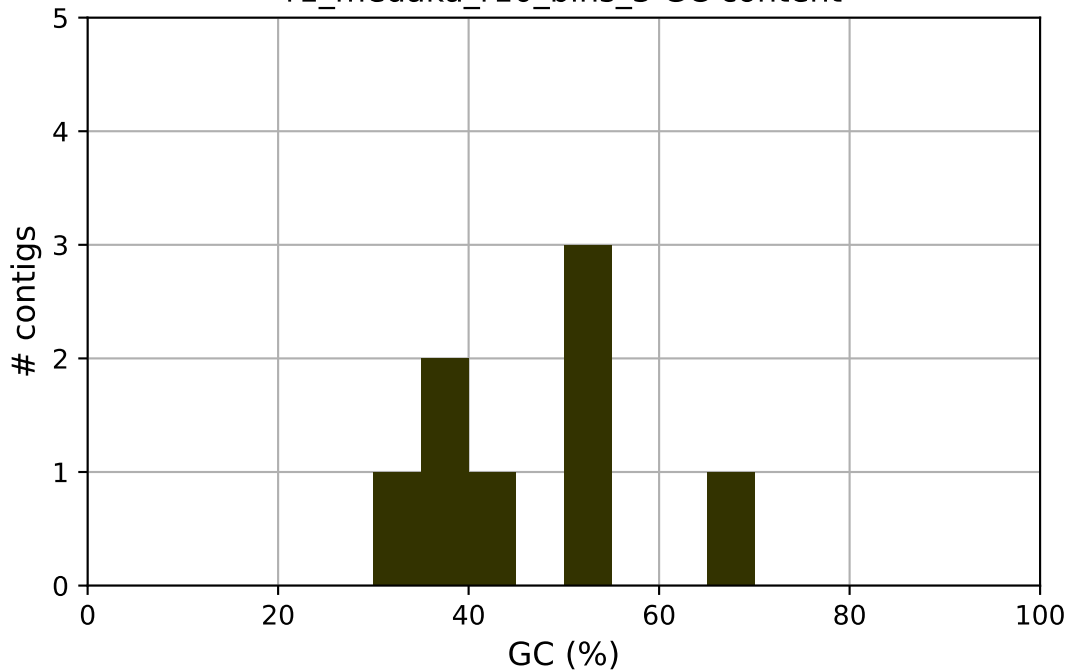
r1\_medaka\_r10\_bins\_1

r1\_medaka\_r10\_bins\_2 GC content



r1\_medaka\_r10\_bins\_2

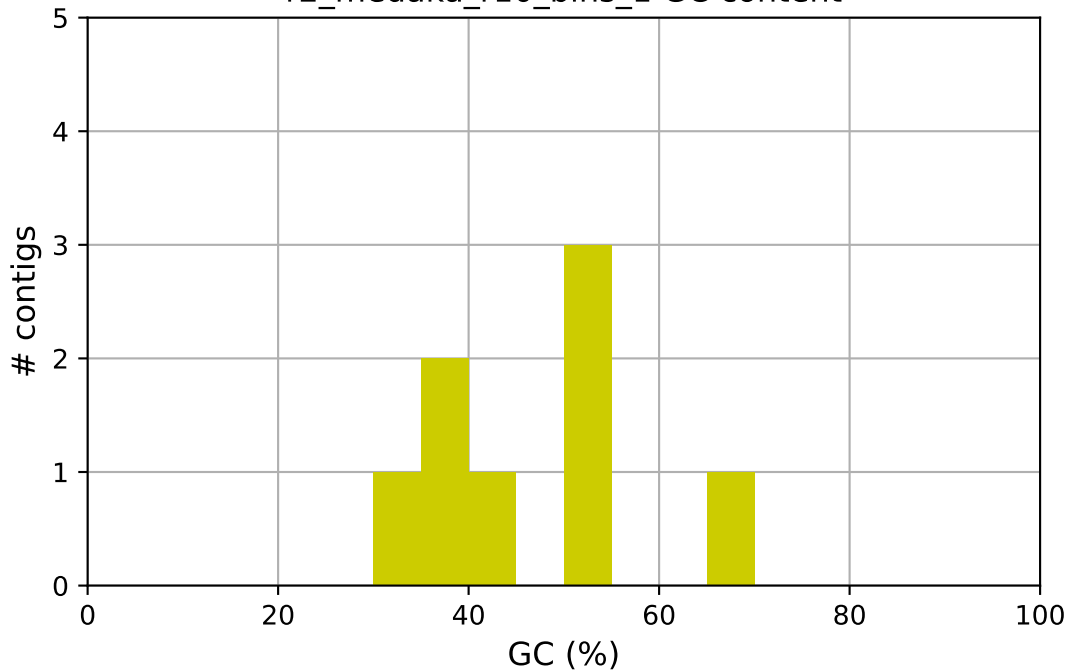
r1\_medaka\_r10\_bins\_3 GC content



r1\_medaka\_r10\_bins\_3

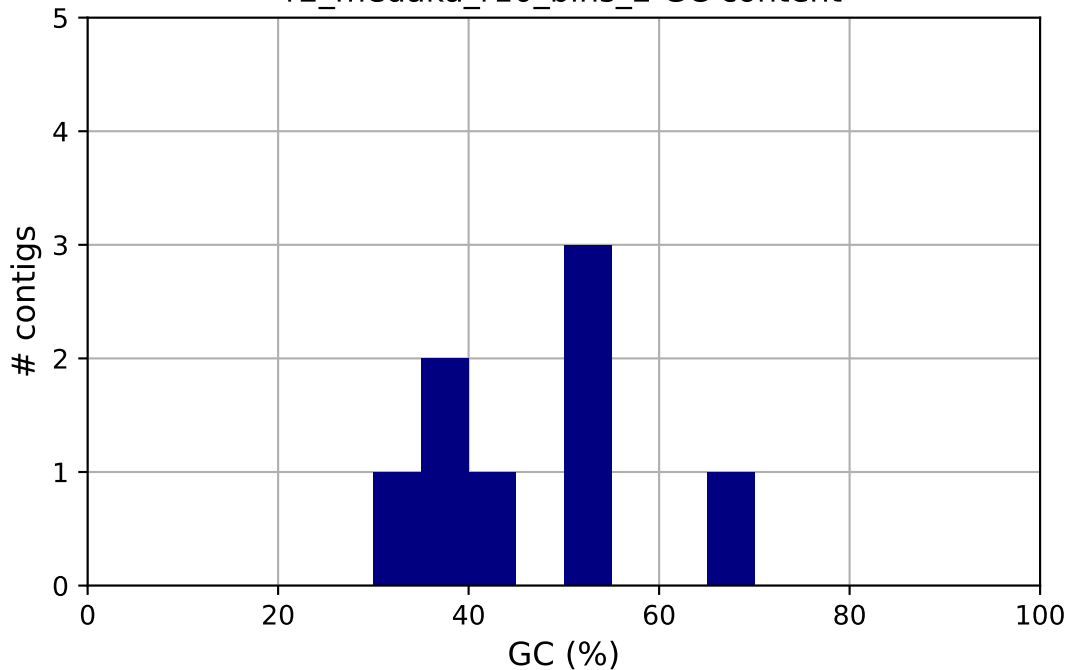


r2\_medaka\_r10\_bins\_1 GC content



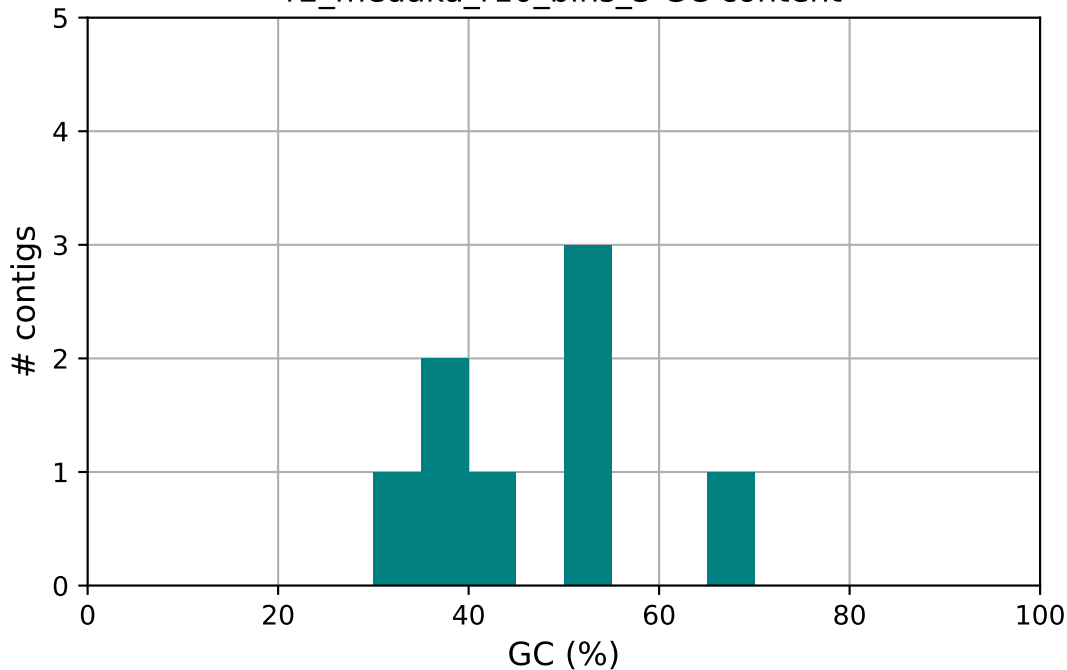
r2\_medaka\_r10\_bins\_1

r2\_medaka\_r10\_bins\_2 GC content



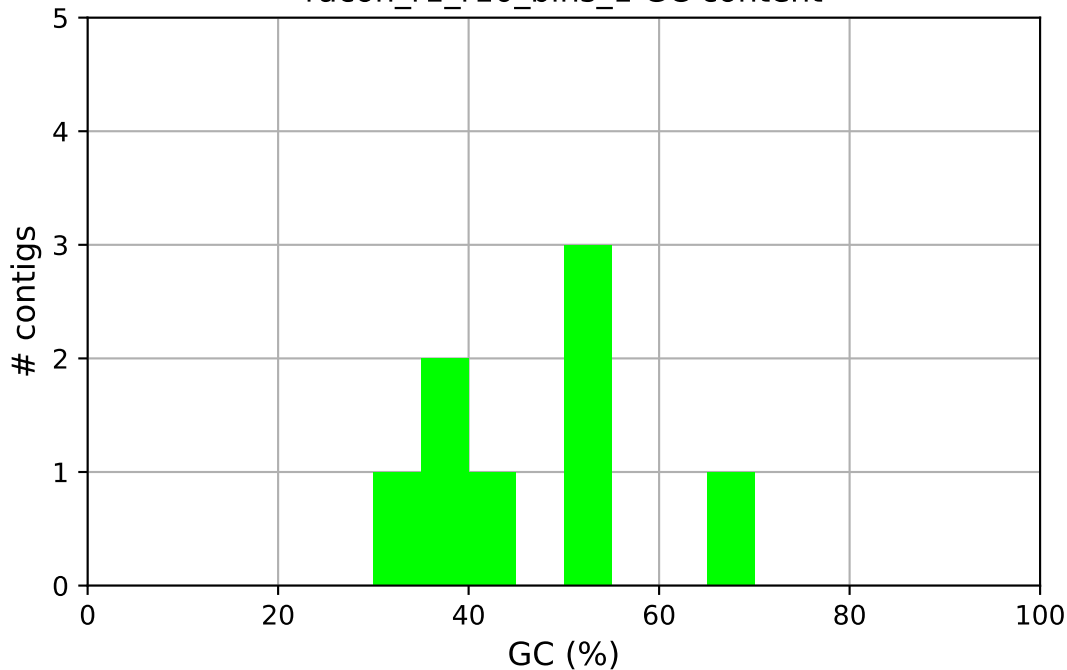
r2\_medaka\_r10\_bins\_2

r2\_medaka\_r10\_bins\_3 GC content



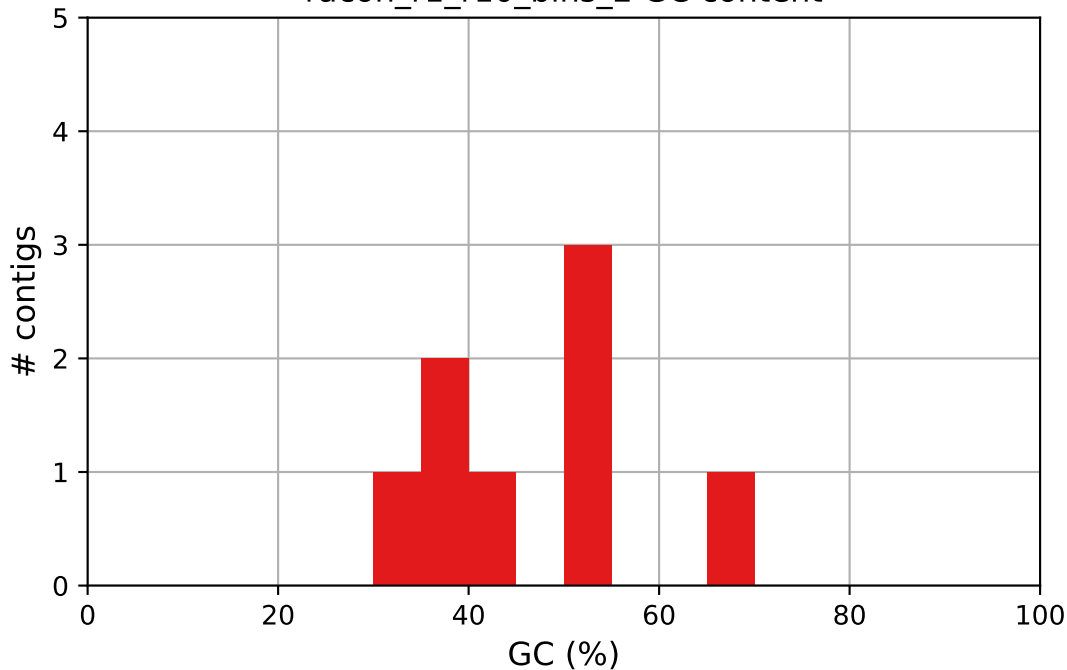
r2\_medaka\_r10\_bins\_3

racon\_r1\_r10\_bins\_1 GC content



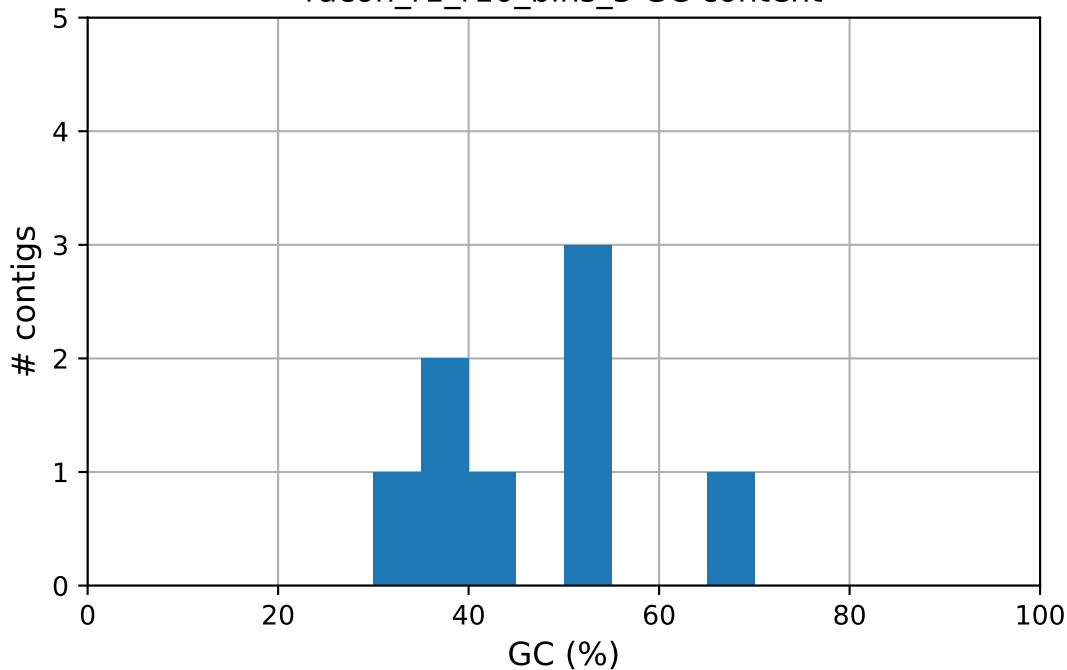
racon\_r1\_r10\_bins\_1

racon\_r1\_r10\_bins\_2 GC content



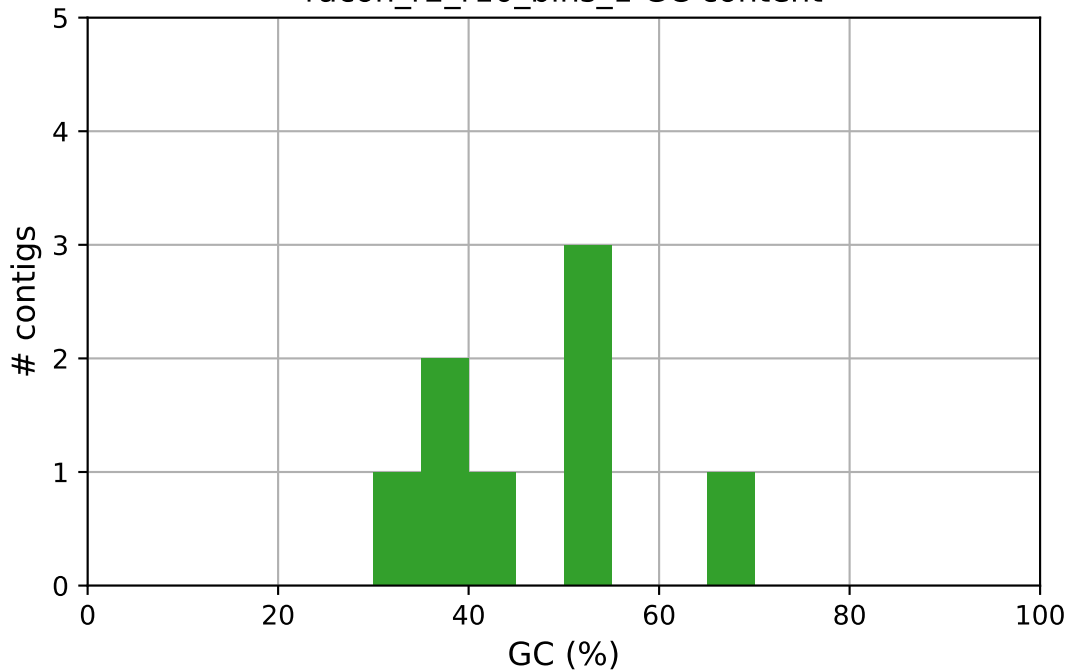
racon\_r1\_r10\_bins\_2

racon\_r1\_r10\_bins\_3 GC content



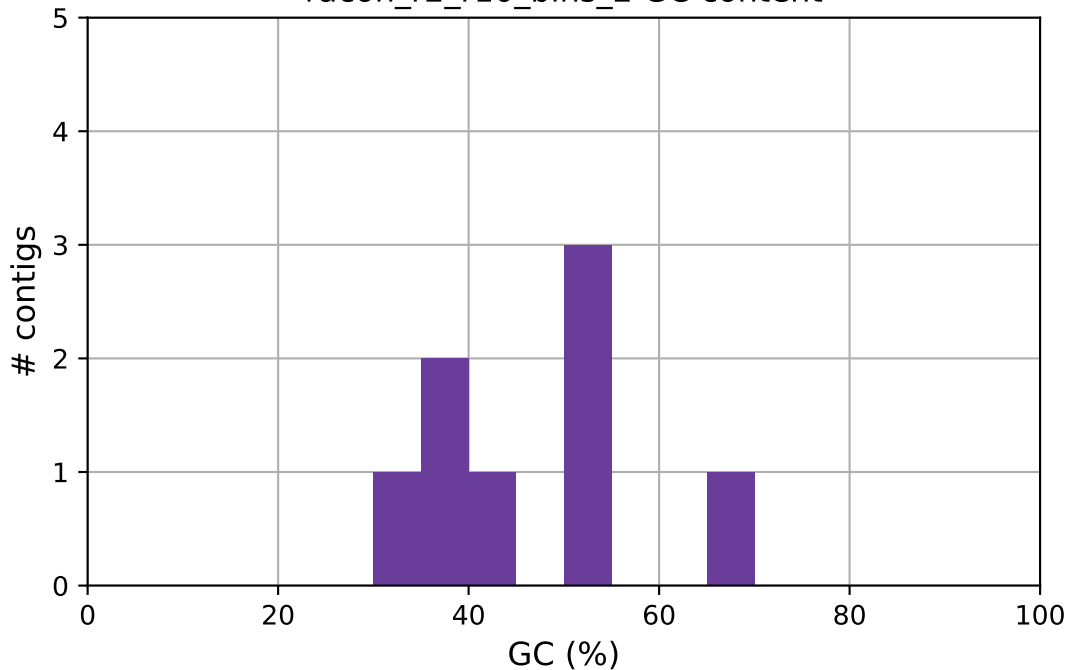
racon\_r1\_r10\_bins\_3

racon\_r2\_r10\_bins\_1 GC content



racon\_r2\_r10\_bins\_1

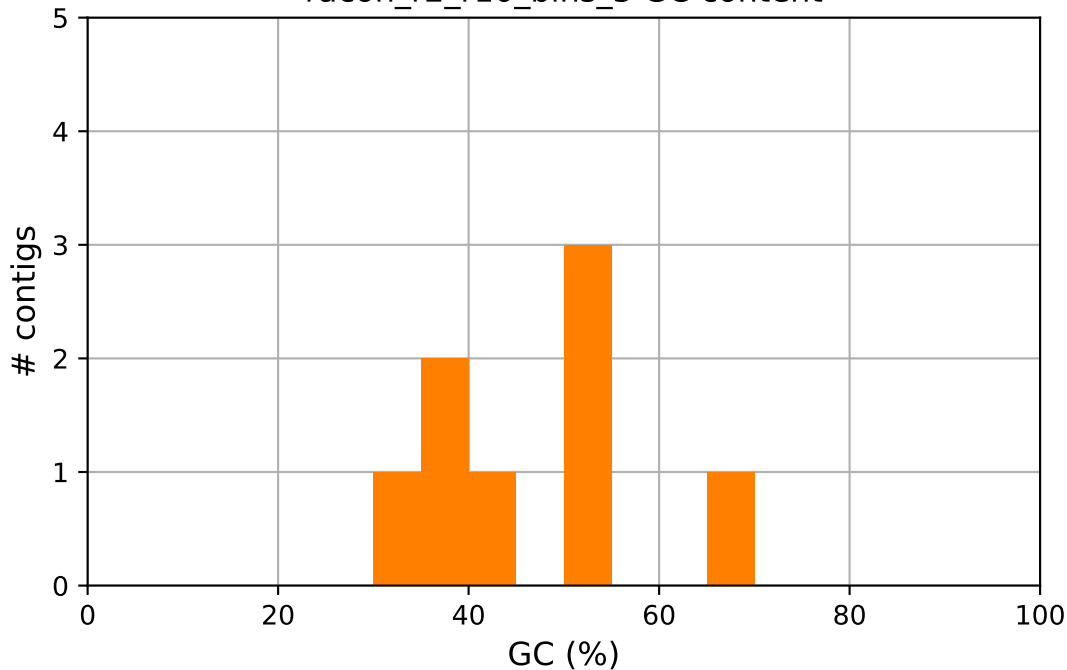
racon\_r2\_r10\_bins\_2 GC content



racon\_r2\_r10\_bins\_2

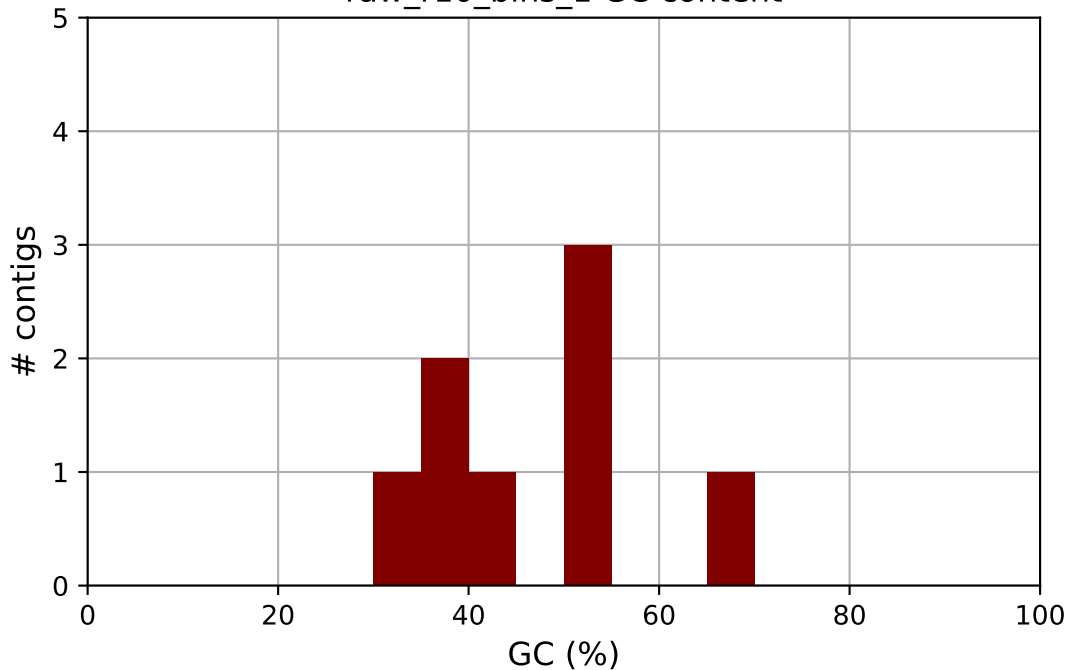


racon\_r2\_r10\_bins\_3 GC content



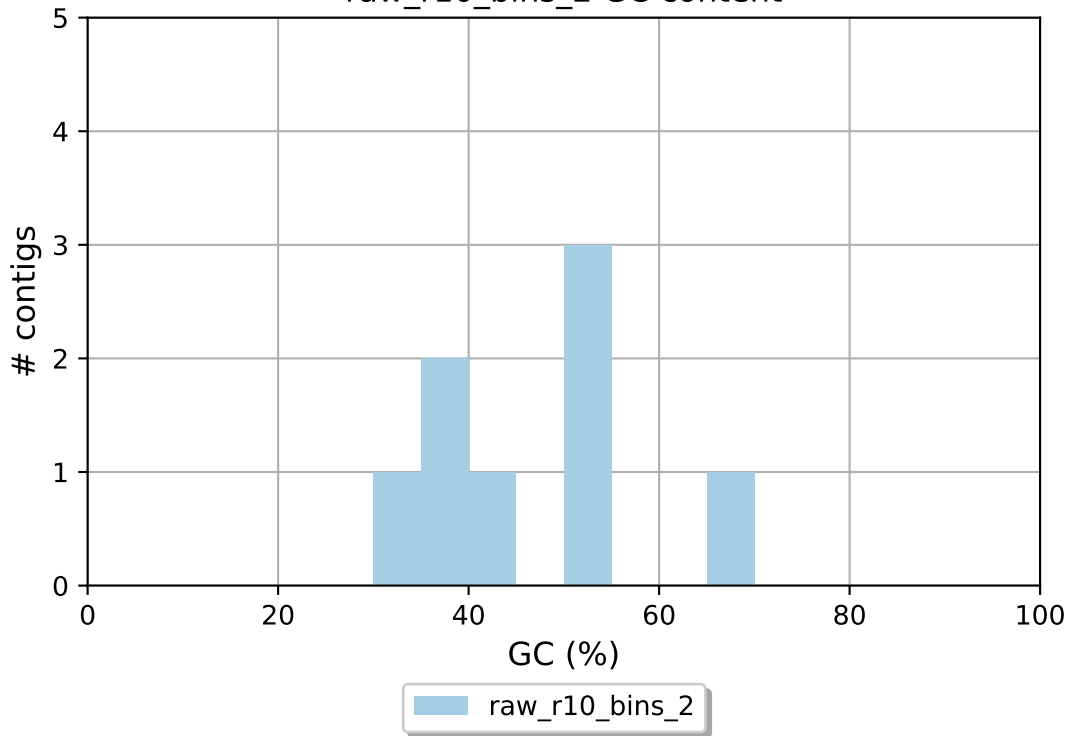
racon\_r2\_r10\_bins\_3

raw\_r10\_bins\_1 GC content

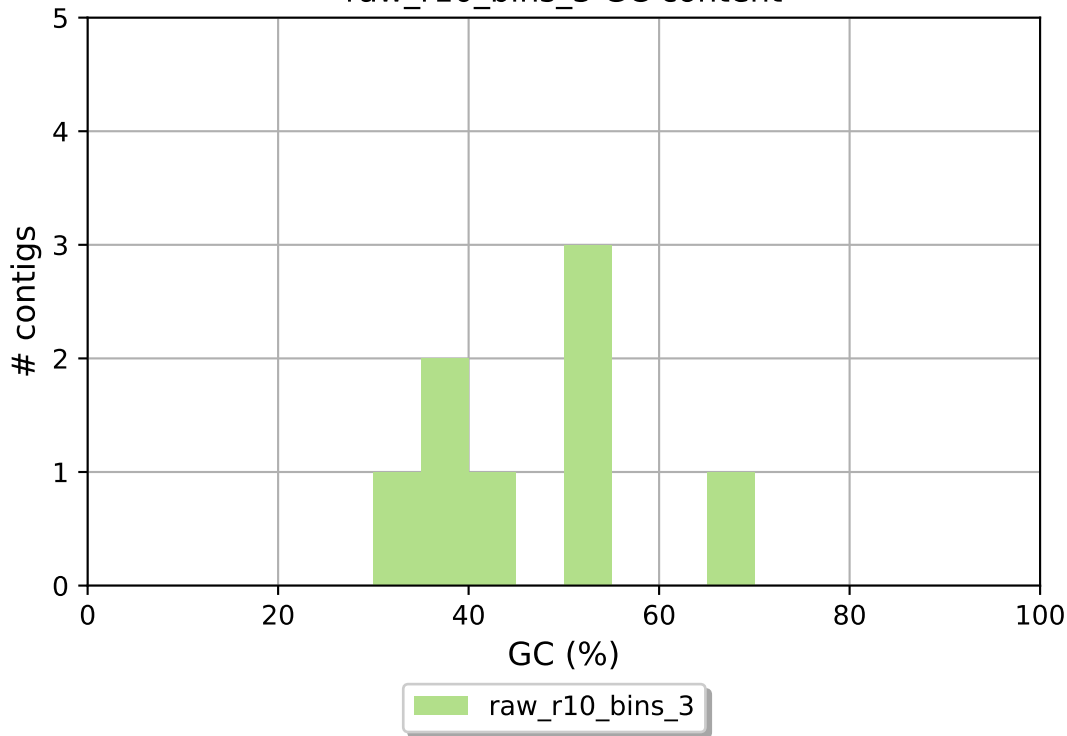


raw\_r10\_bins\_1

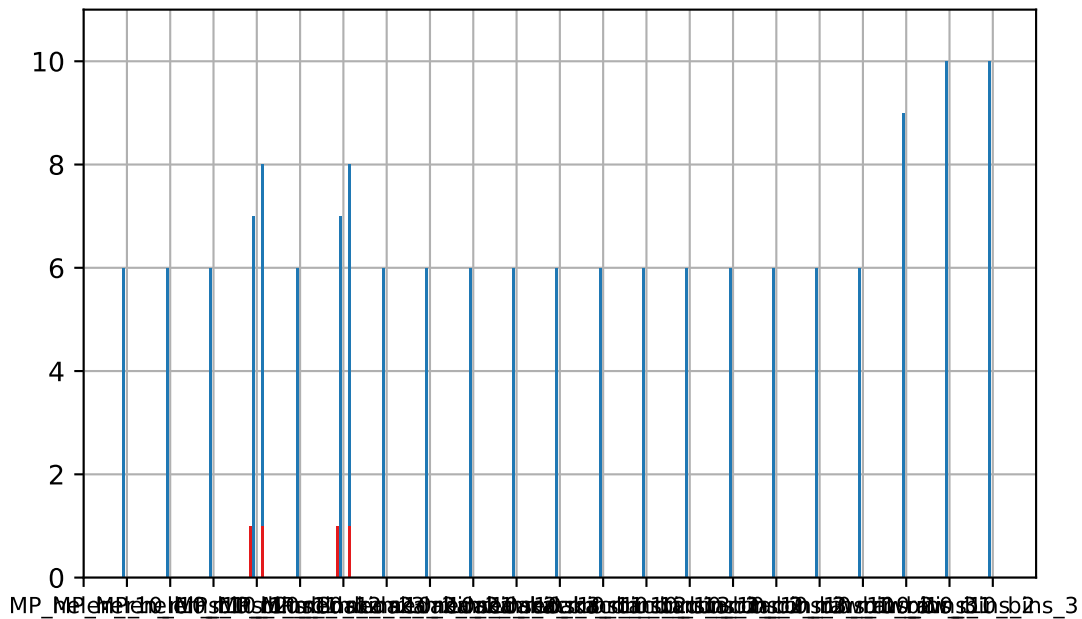
raw\_r10\_bins\_2 GC content



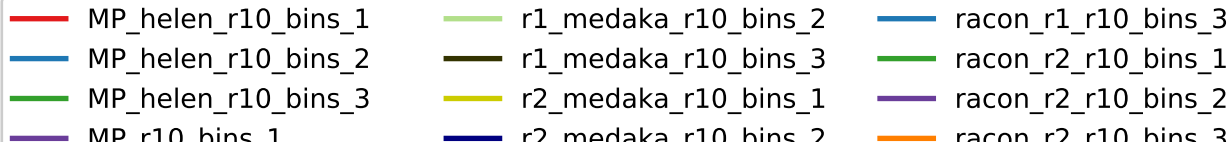
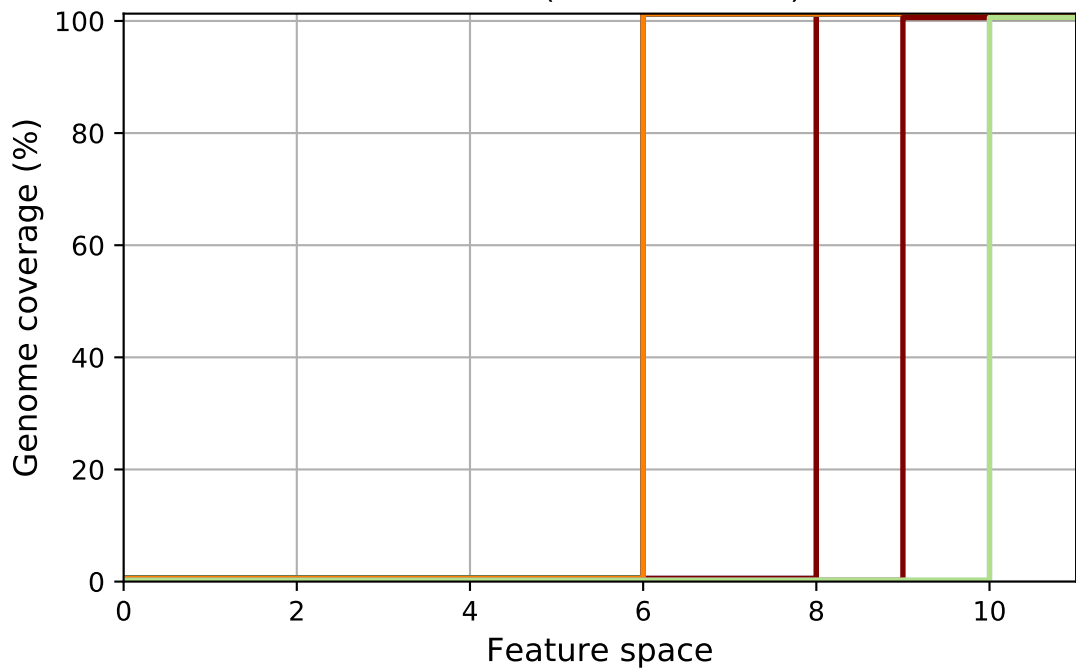
raw\_r10\_bins\_3 GC content

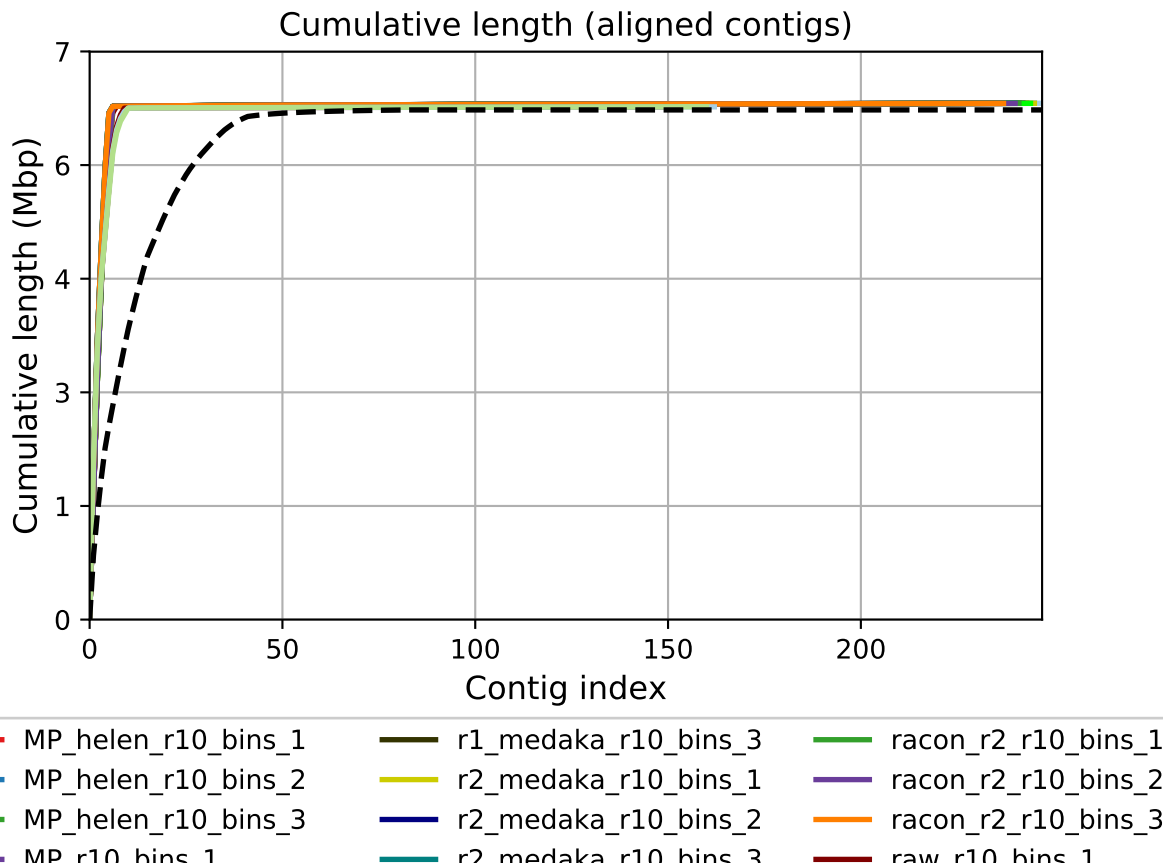


# Misassemblies

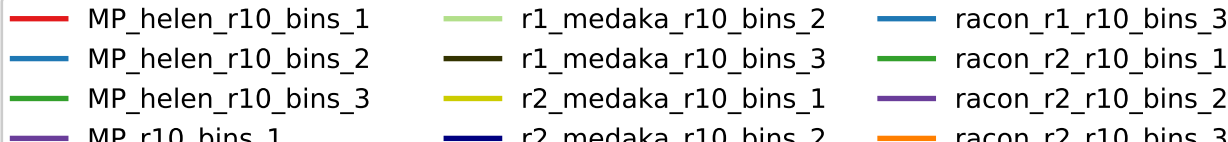
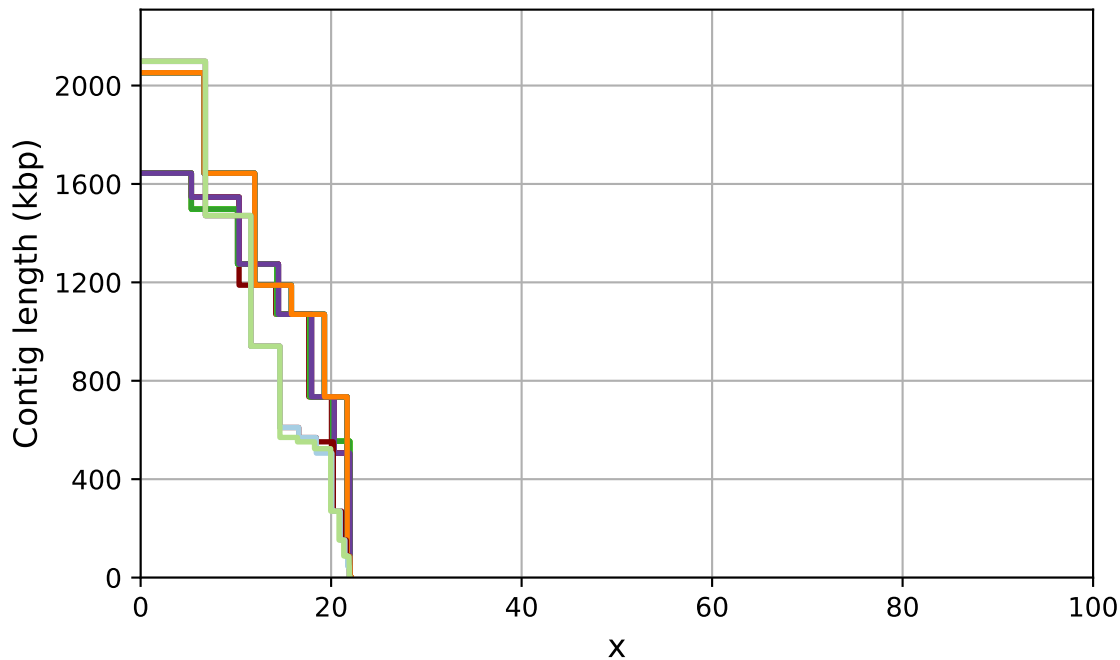


FRCurve (misassemblies)



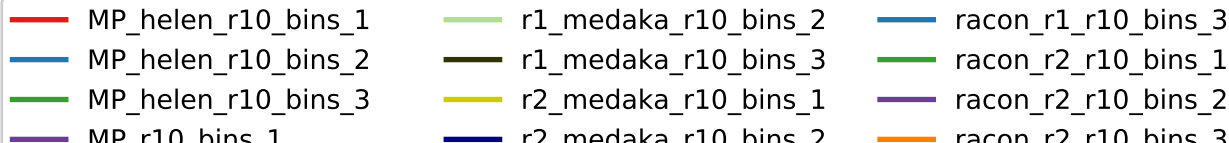
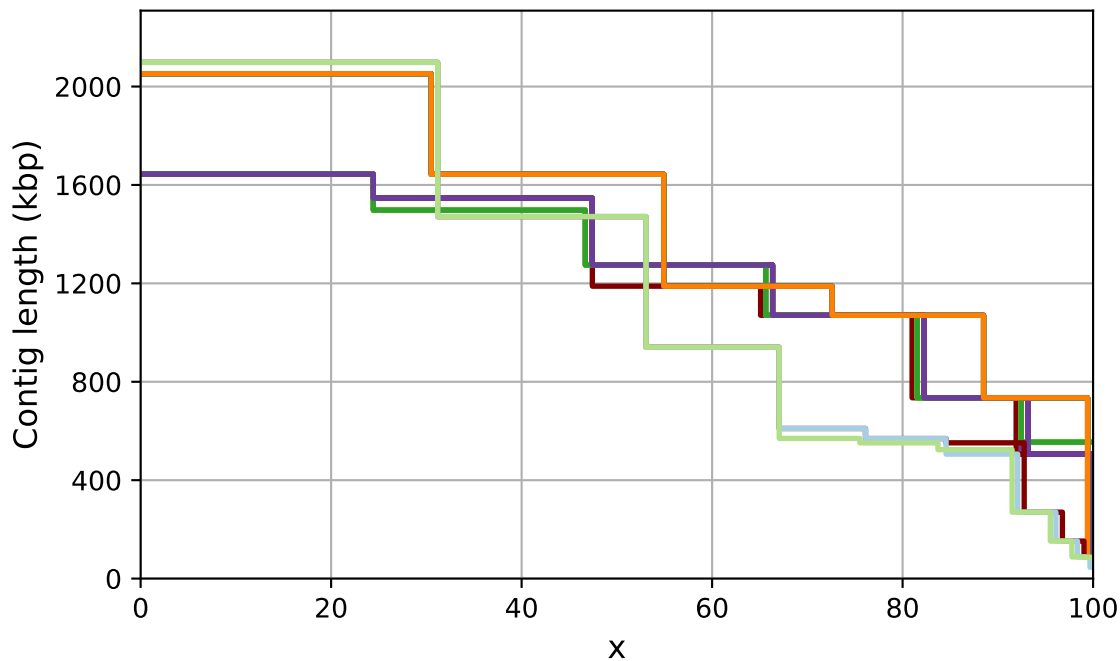


NAx





# NGAx



100.00



- racon\_r1\_r10\_bins\_3
- racon\_r2\_r10\_bins\_1
- racon\_r2\_r10\_bins\_2
- racon\_r2\_r10\_bins\_3