

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)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 10000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 25000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 50000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total length (>= 5000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	28006130	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 10000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	28006130	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 25000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	28006130	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Total length (>= 50000 bp)	30866736	30862385	30864454	30856532	30852547	30847337	28006130	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
# contigs	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792242	6792248	6792243	6792185	6791549	6791659	6788581	6792253	6792197	6792241	6792253	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
Total length	30866736	30862385	30864454	30856532	30852547	30847337	28006130	30866510	30862392	30864952	30853556	30851814	30847462	30848967	30867262	30860948	30864440	30857304	30851650	30848018	30849309
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.50	49.51	49.50	49.50	49.49	49.49	50.69	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	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	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	4756002
NG50	6792242	6792185	6792243	6792248	6791549	6791659	6788581	6792253	6792197	6792245	6792241	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
N75	2992084	2992067	2992075	2992074	2991894	2991958	2990628	2992085	2992067	2992074	2992073	2991915	2991980	2990633	2992084	2992069	2992075	2992075	2991930	2991998	2990669
NG75	6792242	6792185	6792243	6792248	6791549	6791659	6788581	6792253	6792197	6792245	6792241	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
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	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	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	6792242	6792185	6792243	6792248	6791549	6791659	6788581	6792253	6792197	6792245	6792241	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	11	29	11	11	11	11	11	11	29
# 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	5	7	7	7	6	7	6	7	7	7	7	7	7	7	6
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 7 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	24046925	24043250	24044496	24036870	24033659	24028137	21234710	24047423	24043332	24045182	24034276	24033602	24029057	24077281	24048374	24042085	24044672	24037472	24033069	24029095	24077965
Genome fraction (%)	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.894	99.894	99.894	99.894	99.894	99.894	99.864	99.894	99.894	99.894	99.894	99.894	99.894	99.864
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.014	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	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
# mismatches per 100 kbp	58.94	56.18	56.63	56.15	58.98	59.23	64.03	58.44	56.20	56.53	55.93	58.01	58.03	65.32	58.25	56.11	56.54	56.58	58.47	58.92	65.22
# indels per 100 kbp	5.42	5.06	3.65	3.60	15.68	14.75	97.15	5.48	5.13	3.63	3.60	15.18	14.27	96.71	5.48	5.13	3.63	3.60	15.18	14.27	96.89
Largest alignment	1643839	2052185	2052213	2052213	2052050	2052085	2098630	1643841	1643830	1643850	1643848	1643635	1643680	2098268	1643841	1643830	1643850	1643848	1643635	1643680	2098268
Total aligned length	6816059	6815383	6816206	6815910	6815136	6815448	6768945	6815335	6815298	6816018	6815528	6814460	6814653	6769200	6815136	6815111	6816016	6816080	6814829	6815171	6768858
NGA50	1274461	1643838	1643849	1643849	1643649	1643667	1471418	1274471	1274461	1274469	1274469	1274310	1274344	1471391	1274471	1274461	1274469	1274469	1274310	1274344	1471391
NGA75	1070336	1070326	1070328	1070330	1070234	1070253	610213	1070337	1070325	1070331	1070329	1070253	1070241	610115	1070337	1070325	1070331	1070329	1070253	1070241	610115
LGA50	3	2	2	2	2	2	2	3	3	3	3	3	3	2	3	3	3	3	3	3	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

	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
# misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# contig misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# c. relocations	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	7	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	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	6792242	6792185	6792243	6792248	6791549	6791659	6788581	6792253	6792197	6792245	6792241	6791556	6791638	6787718	6792253	6792197	6792245	6792241	6791556	6791638	6787718
# 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	16	18	18	18	18	18	34	18	18	18	18	18	18	34	18	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	11	29	11	11	11	11	11	11	29
# 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	20	21	21	21	21	21	16	21	21	21	21	21	21	16	21	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	5	7	7	7	6	7	6	7	7	7	7	7	7	7	6
# mismatches	3961	3776	3806	3774	3964	3981	4303	3928	3777	3799	3759	3899	3900	4389	3915	3771	3800	3803	3930	3960	4382
# indels	364	340	245	242	1054	991	6528	368	345	244	242	1020	959	6498	368	345	244	242	1020	959	6510
# indels (<= 5 bp)	269	243	151	148	960	896	6405	272	247	150	148	924	865	6377	272	247	150	148	924	865	6389
# indels (> 5 bp)	95	97	94	94	94	95	123	96	98	94	94	96	94	121	96	98	94	94	96	94	121
Indels length	5394	5400	5261	5258	6174	6102	12917	5411	5411	5261	5259	6142	6072	12810	5411	5411	5261	5259	6142	6072	12830

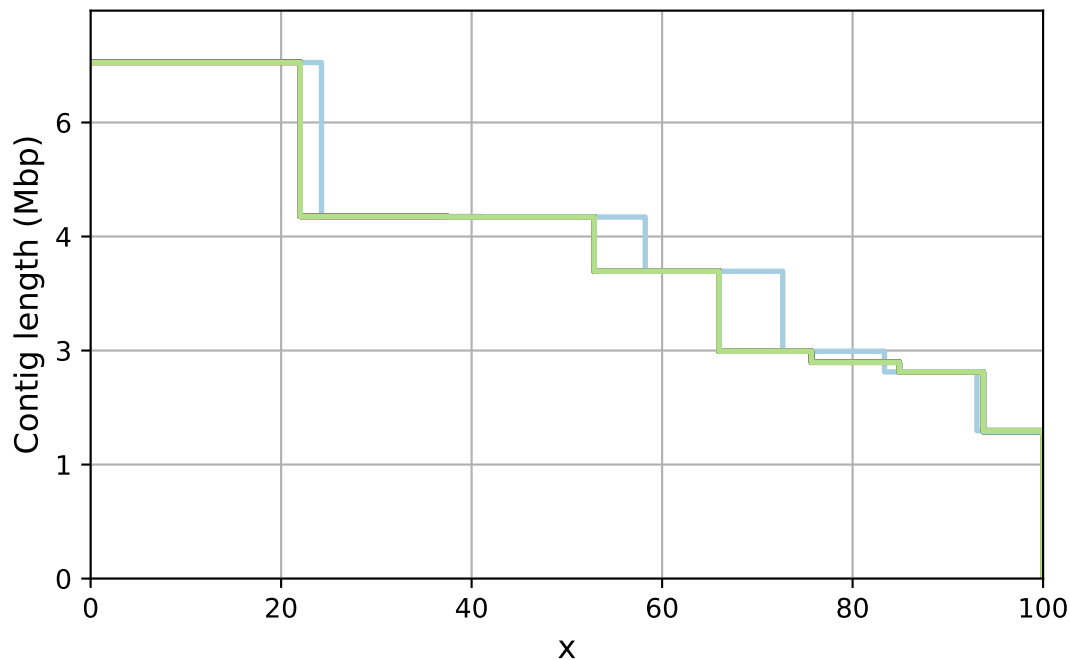
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

# Unaligned report

	r10_1bin_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
# 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	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24046925	24043250	24044496	24036870	24033659	24028137	21234710	24047423	24043332	24045182	24034276	24033602	24029057	24077281	24048374	24042085	24044672	24037472	24033069	24029095	24077965
# N's	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0

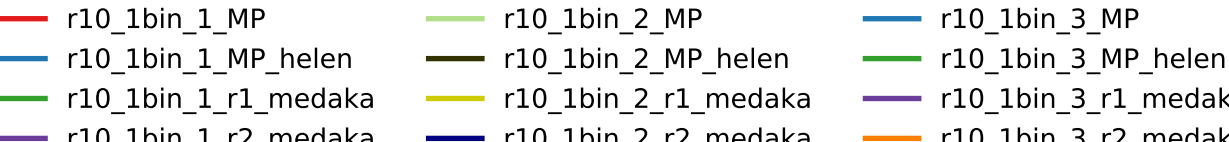
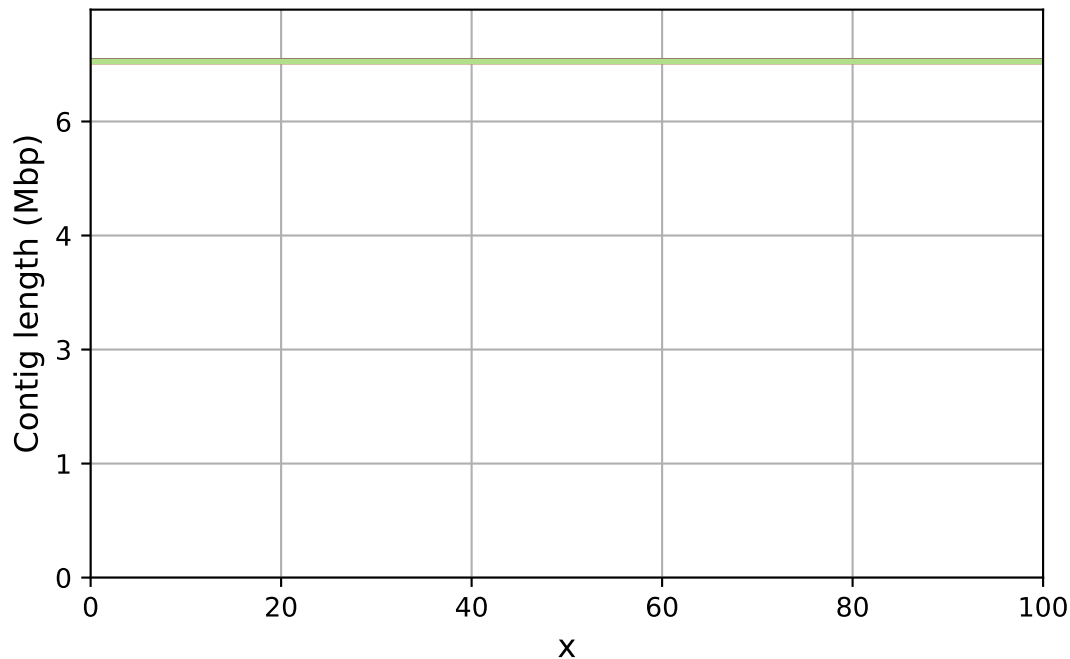
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

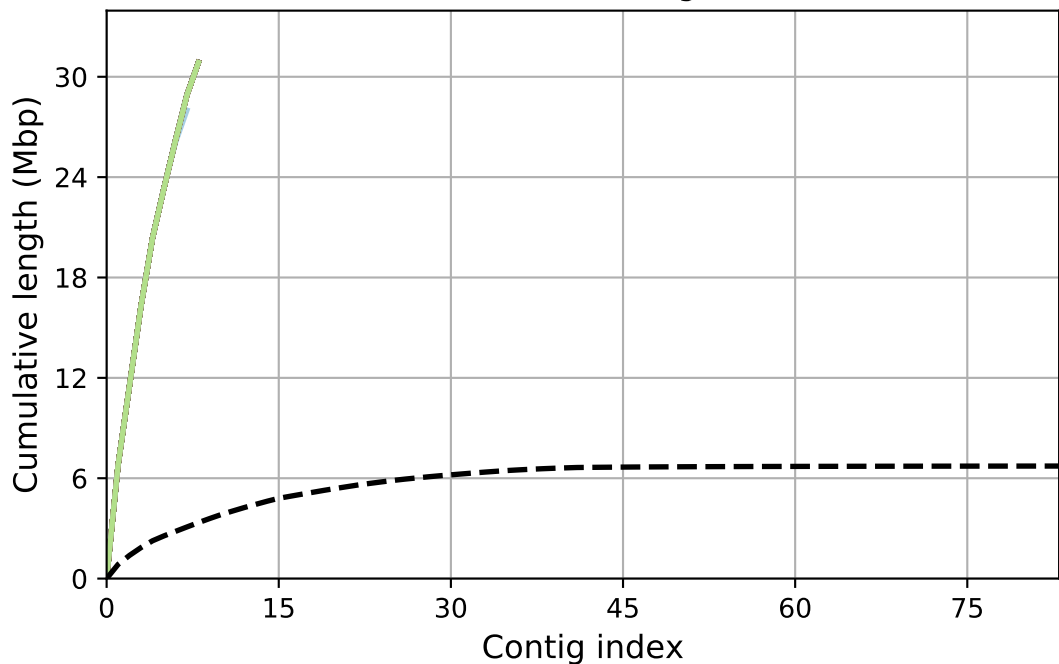


r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medaka
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medaka

# NGx

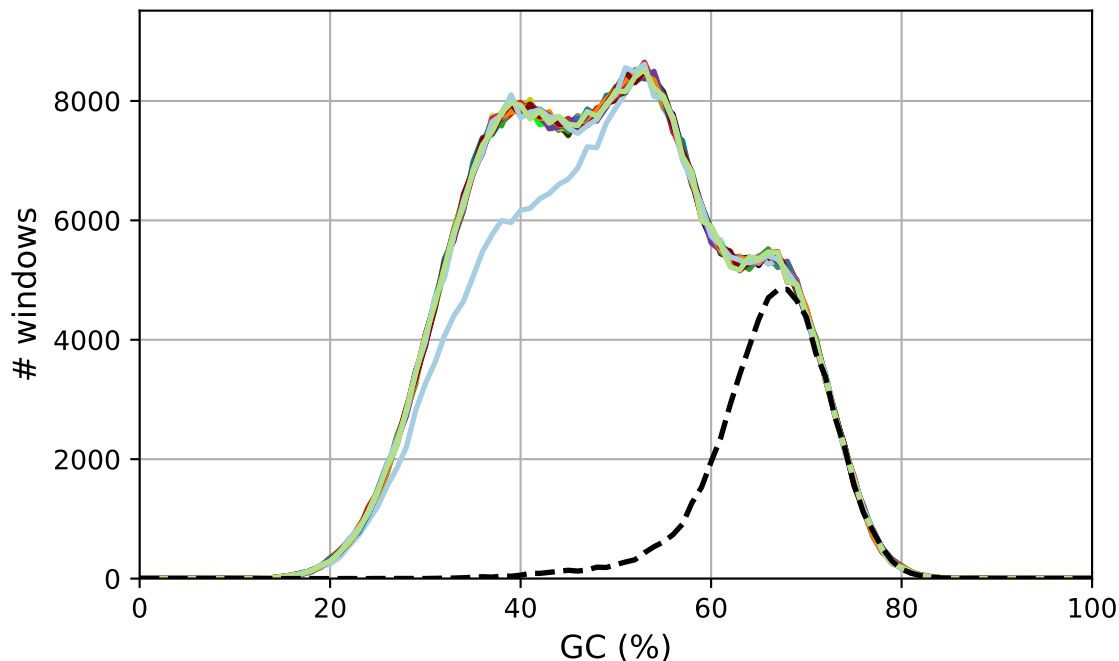


Cumulative length



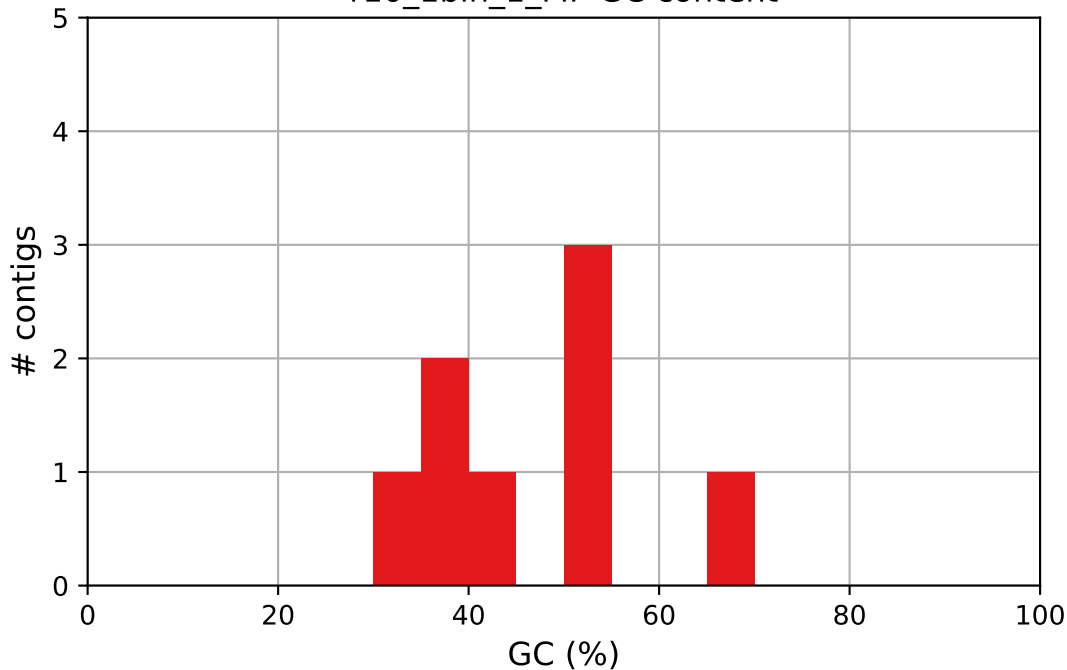
r10_1bin_1_MP	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak
r10_1bin_1_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_3_racon_r1

GC content



— r10\_1bin\_1\_MP      — r10\_1bin\_2\_MP\_helen      — r10\_1bin\_3\_MP\_helen  
— r10\_1bin\_1\_MP\_helen      — r10\_1bin\_2\_r1\_medaka      — r10\_1bin\_3\_r1\_medaka  
— r10\_1bin\_1\_r1\_medaka      — r10\_1bin\_2\_r2\_medaka      — r10\_1bin\_3\_r2\_medaka  
— r10\_1bin\_1\_r2\_medaka      — r10\_1bin\_2\_racon\_r1      — r10\_1bin\_3\_racon\_r1

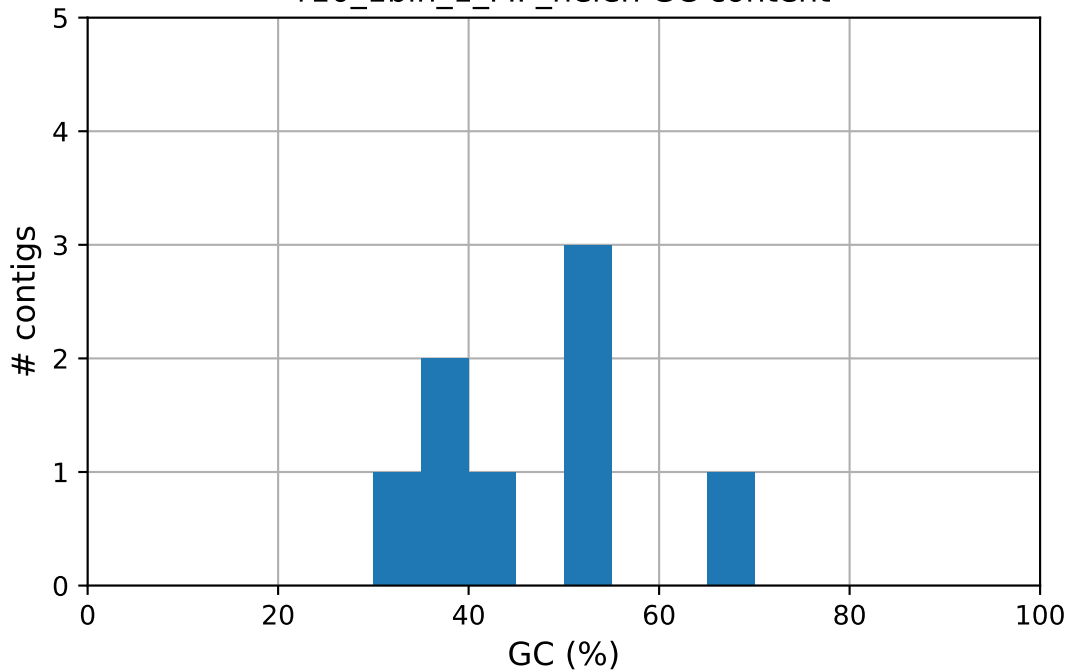
r10\_1bin\_1\_MP GC content



r10\_1bin\_1\_MP

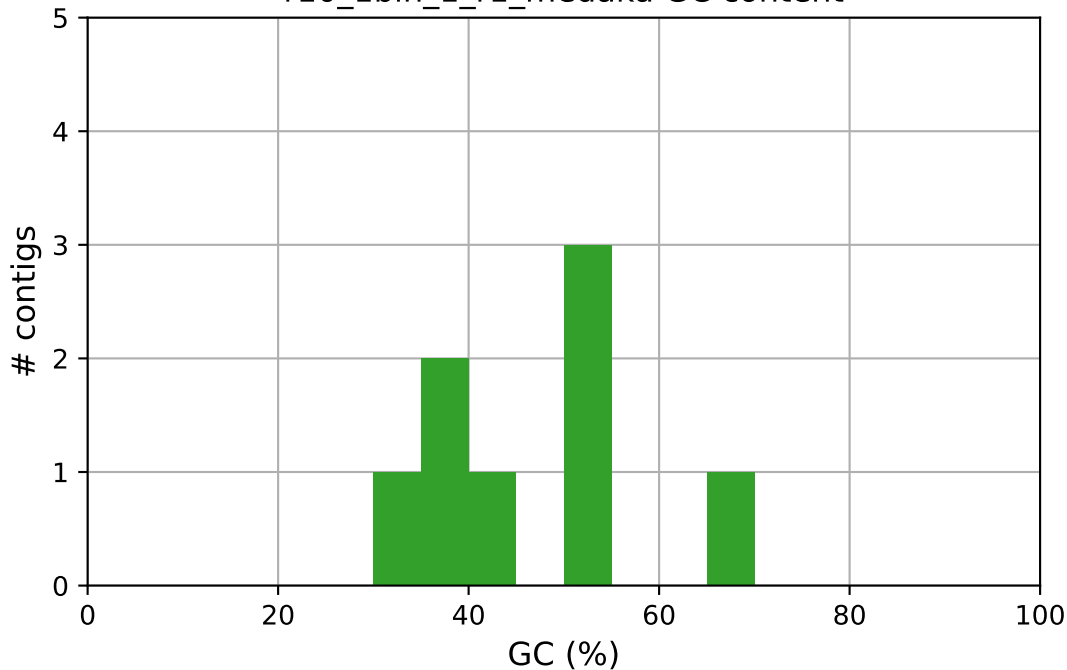


r10\_1bin\_1\_MP\_helen GC content



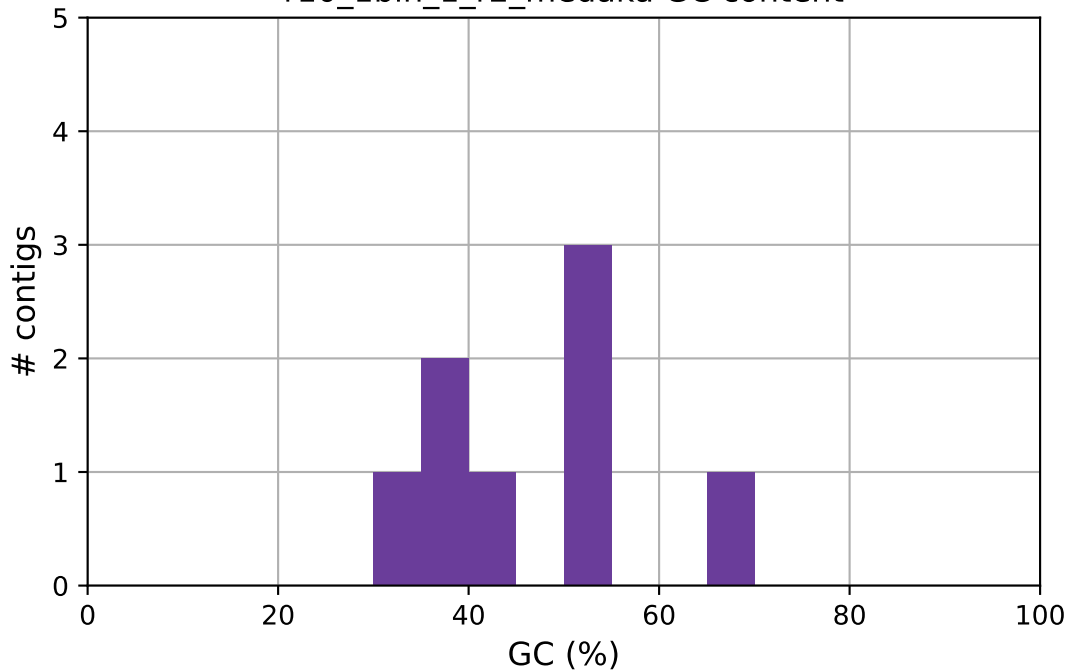
r10\_1bin\_1\_MP\_helen

r10\_1bin\_1\_r1\_medaka GC content



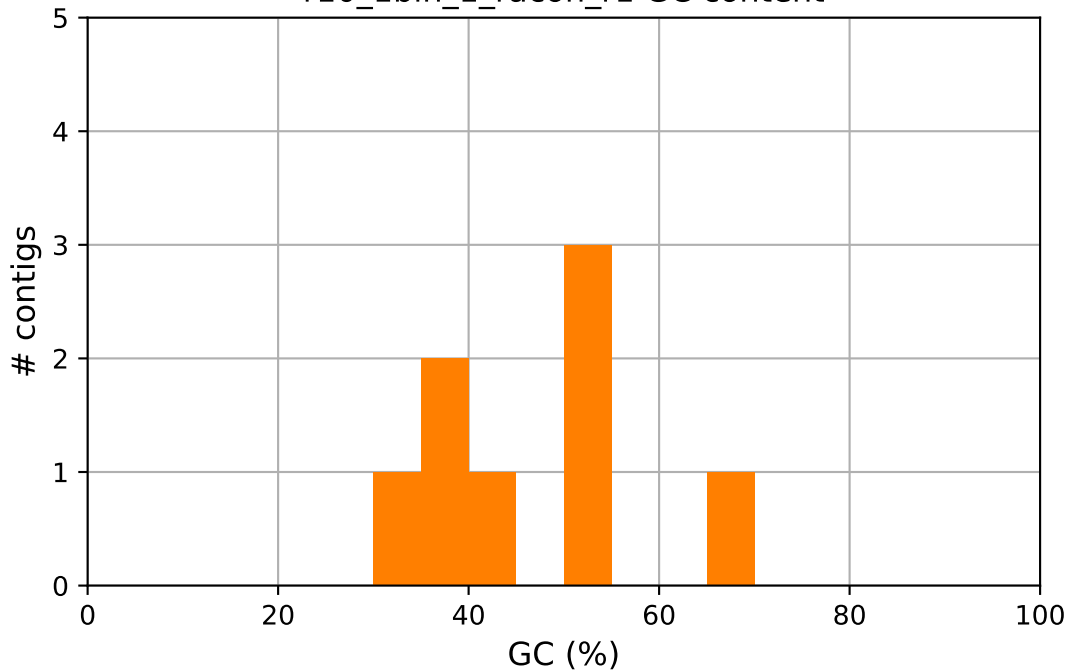
r10\_1bin\_1\_r1\_medaka

r10\_1bin\_1\_r2\_medaka GC content



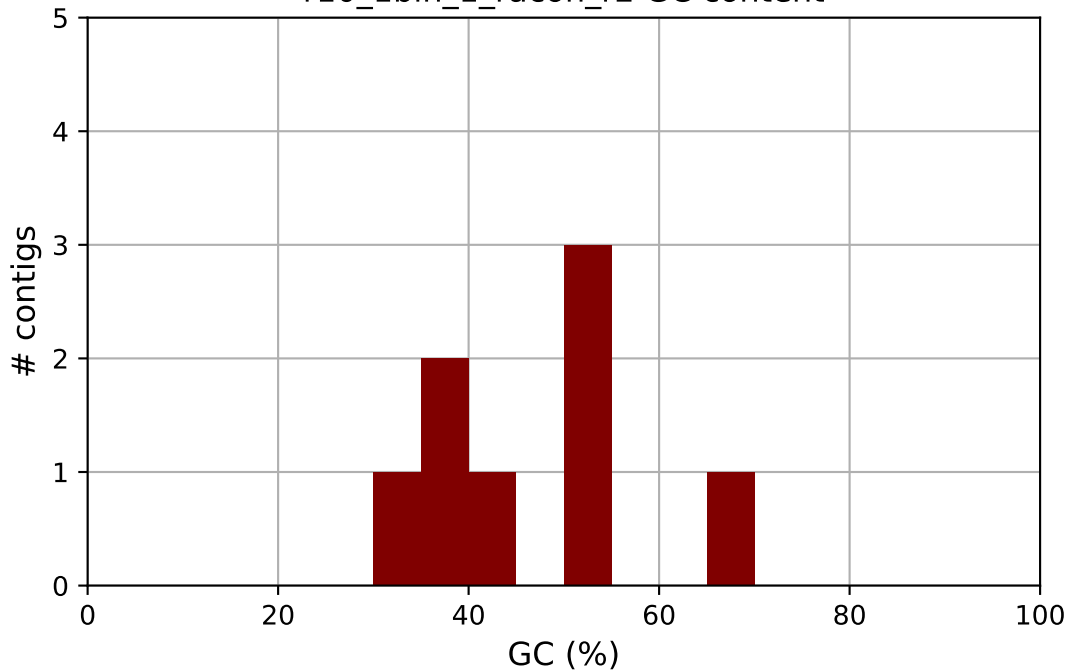
r10\_1bin\_1\_r2\_medaka

r10\_1bin\_1\_racon\_r1 GC content



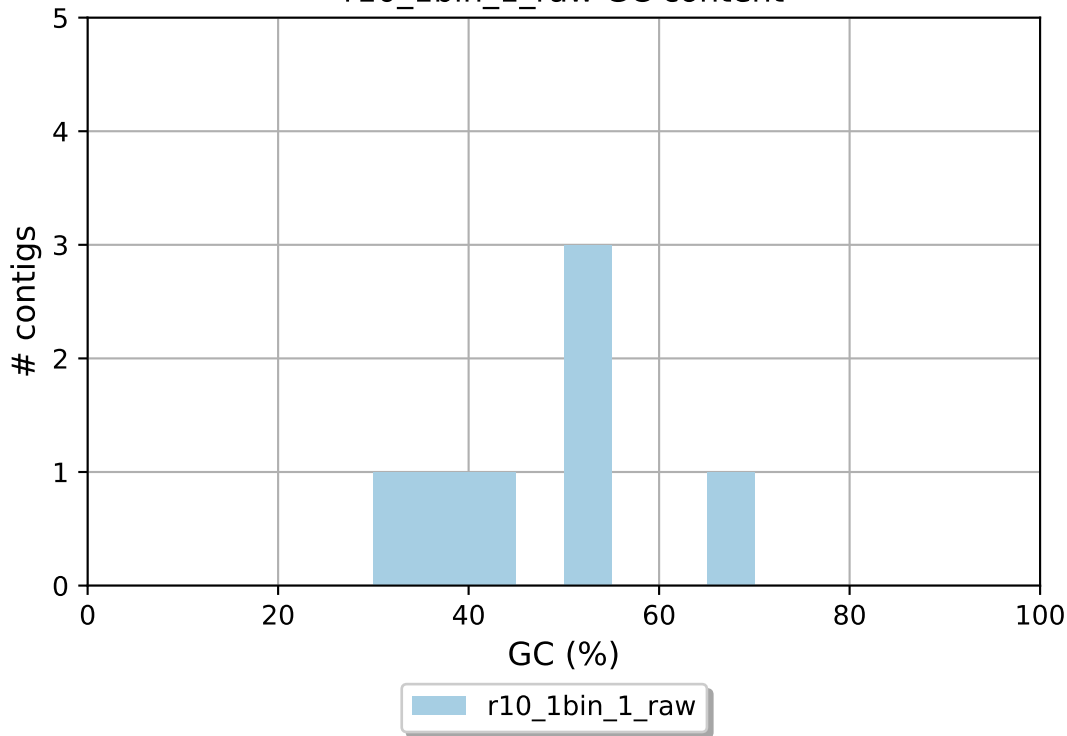
r10\_1bin\_1\_racon\_r1

r10\_1bin\_1\_racon\_r2 GC content

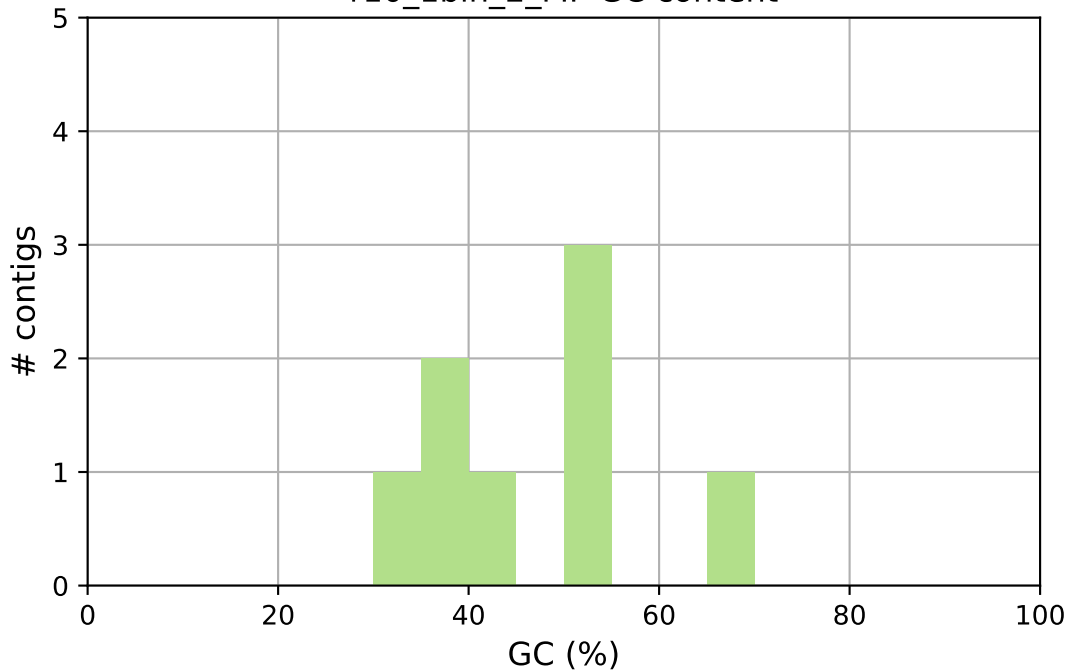


r10\_1bin\_1\_racon\_r2

r10\_1bin\_1\_raw GC content

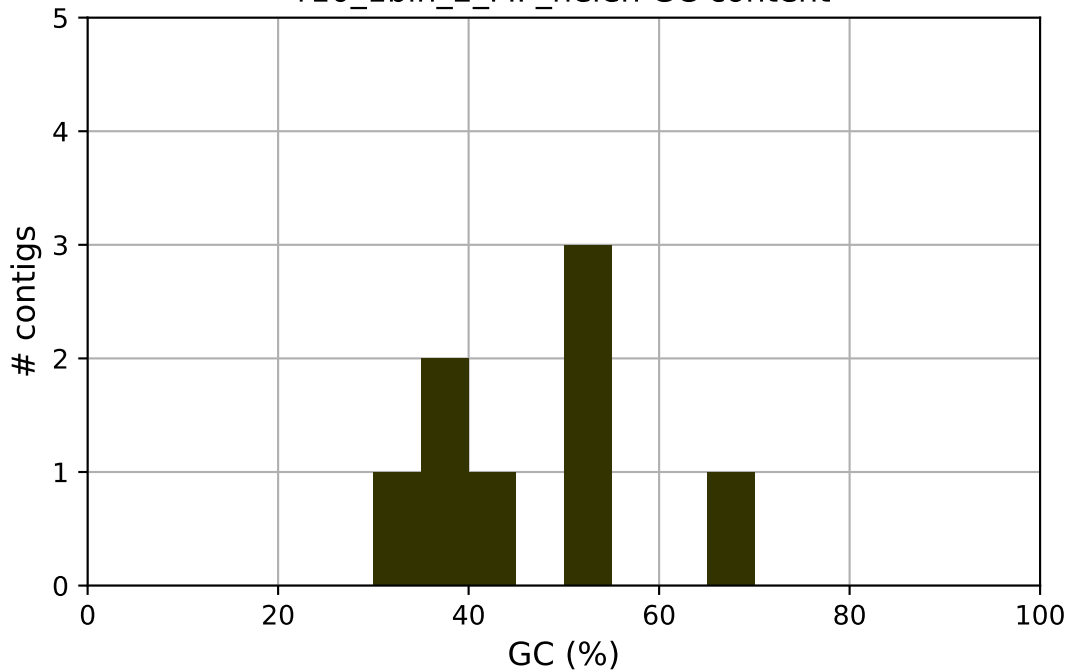


r10\_1bin\_2\_MP GC content



r10\_1bin\_2\_MP

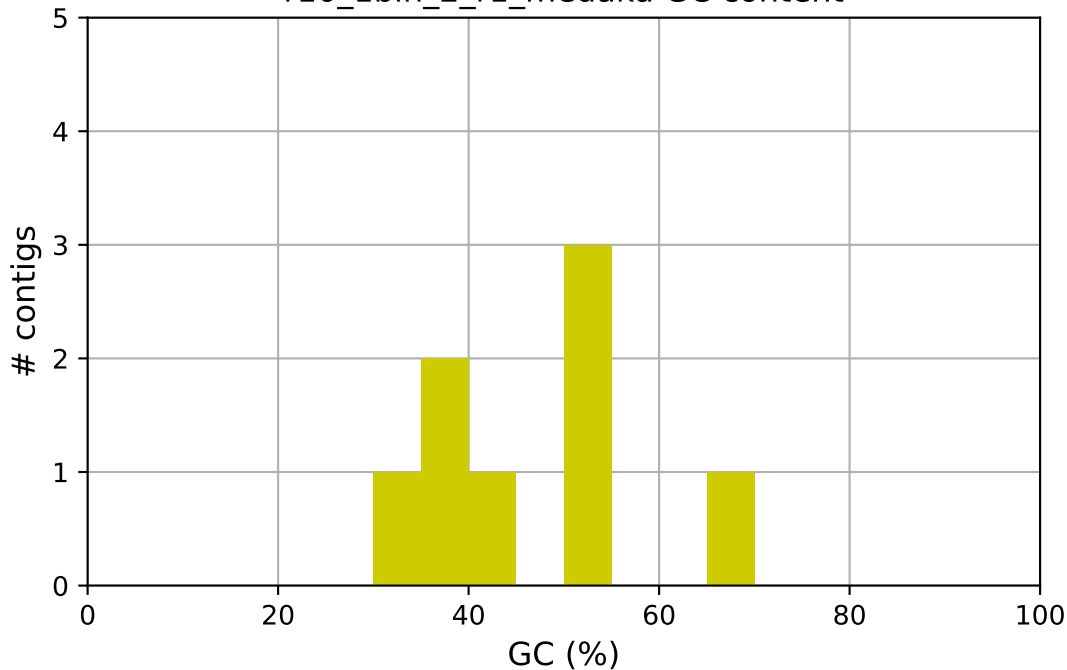
r10\_1bin\_2\_MP\_helen GC content



■ r10\_1bin\_2\_MP\_helen

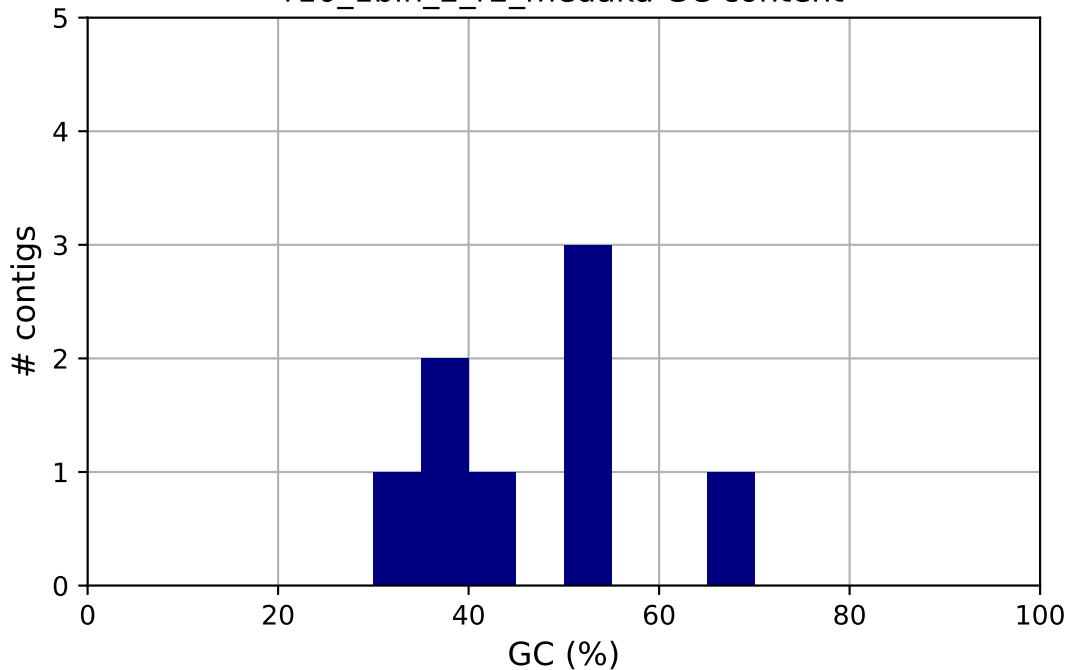


r10\_1bin\_2\_r1\_medaka GC content



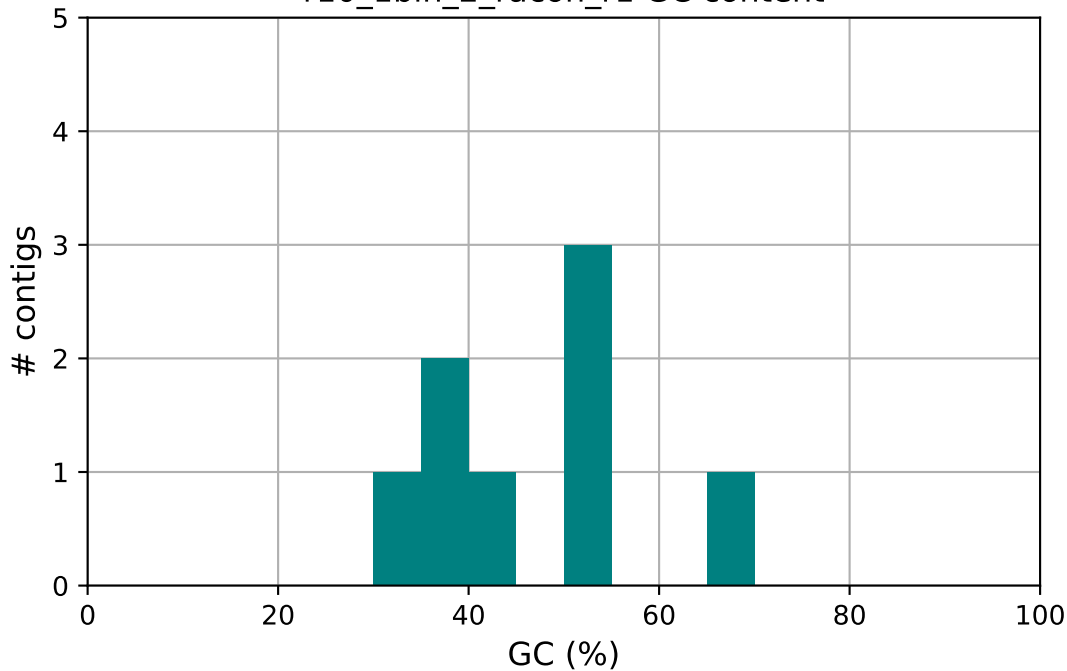
r10\_1bin\_2\_r1\_medaka

r10\_1bin\_2\_r2\_medaka GC content



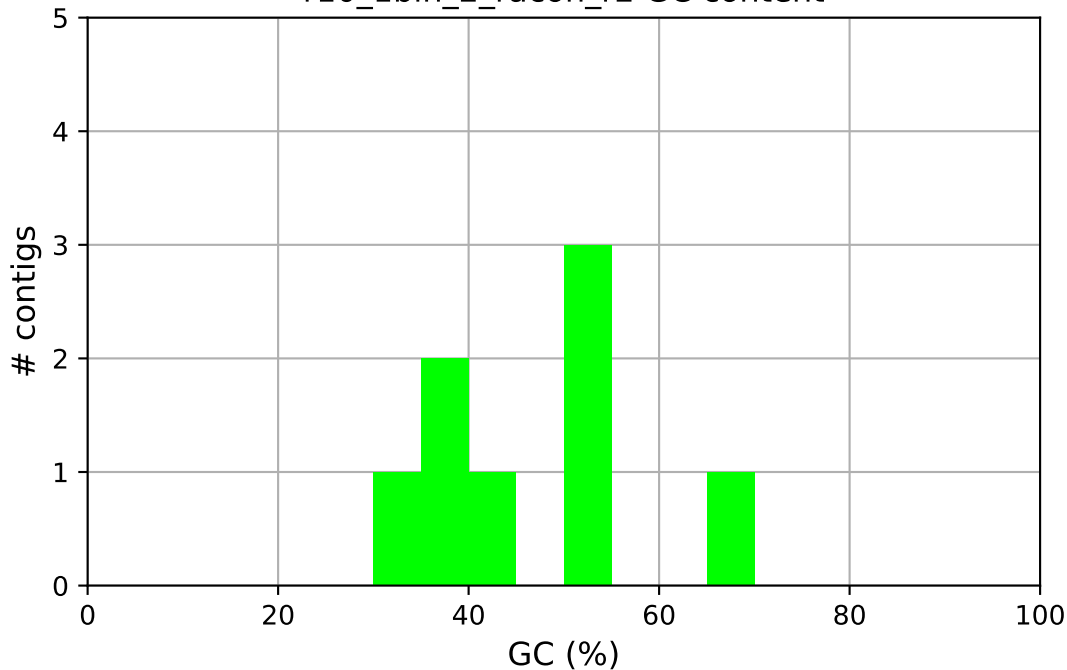
r10\_1bin\_2\_r2\_medaka

r10\_1bin\_2\_racon\_r1 GC content



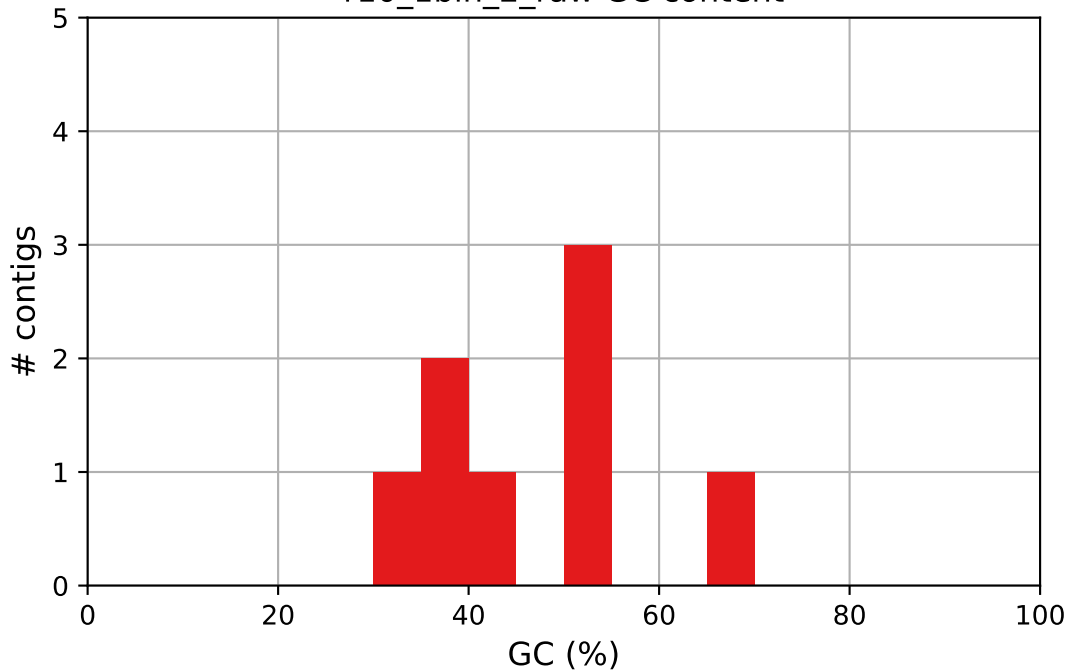
r10\_1bin\_2\_racon\_r1

r10\_1bin\_2\_racon\_r2 GC content



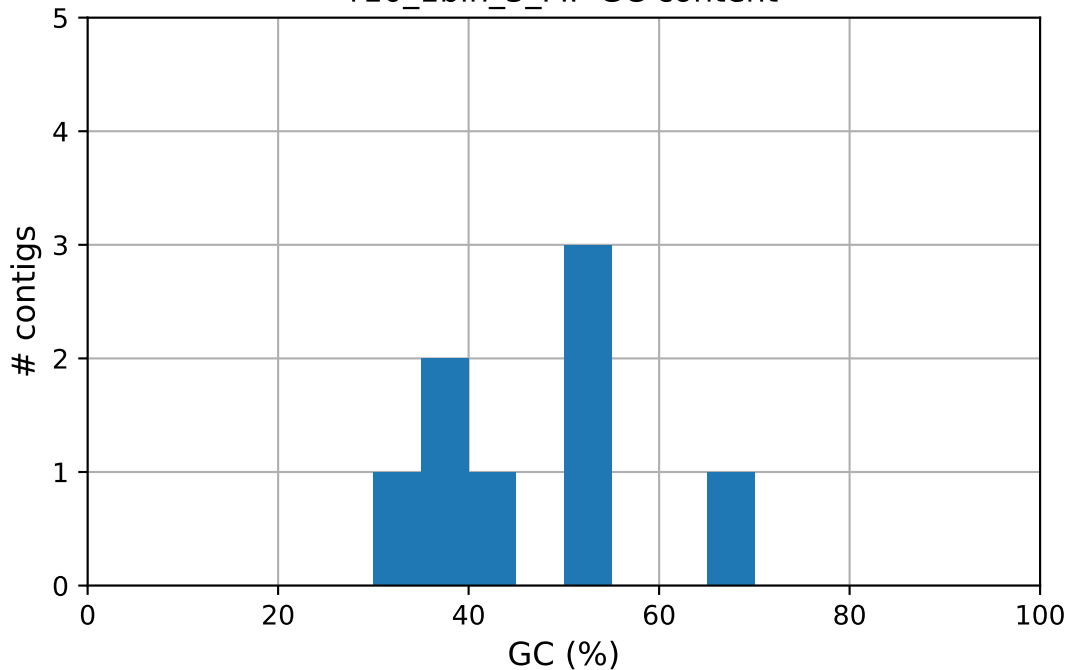
r10\_1bin\_2\_racon\_r2

r10\_1bin\_2\_raw GC content



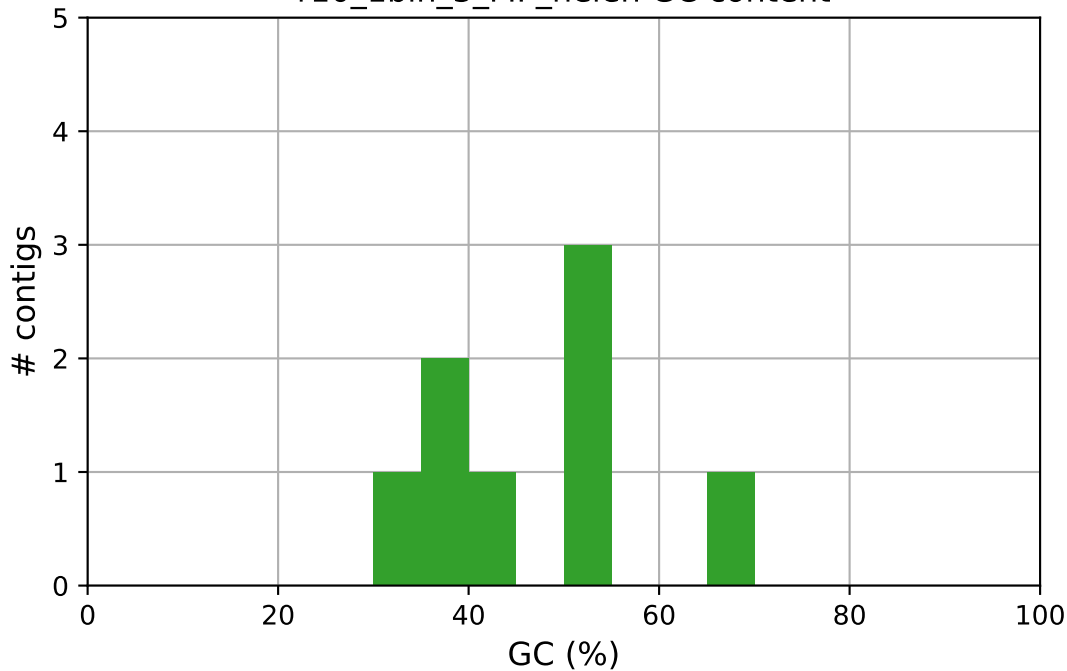
r10\_1bin\_2\_raw

r10\_1bin\_3\_MP GC content



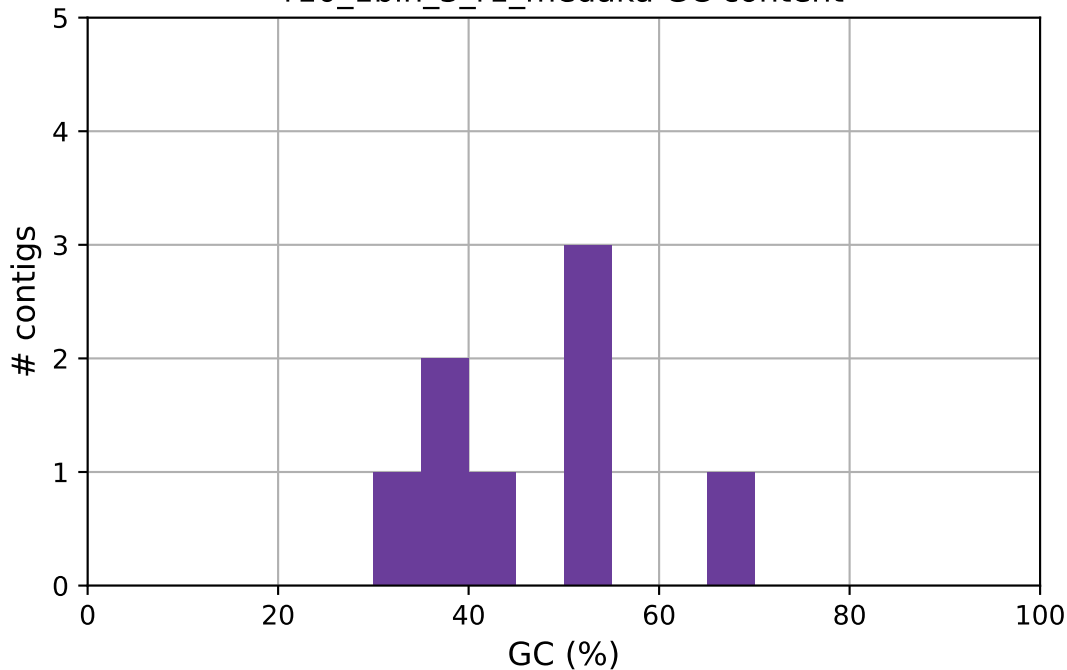
r10\_1bin\_3\_MP

r10\_1bin\_3\_MP\_helen GC content



r10\_1bin\_3\_MP\_helen

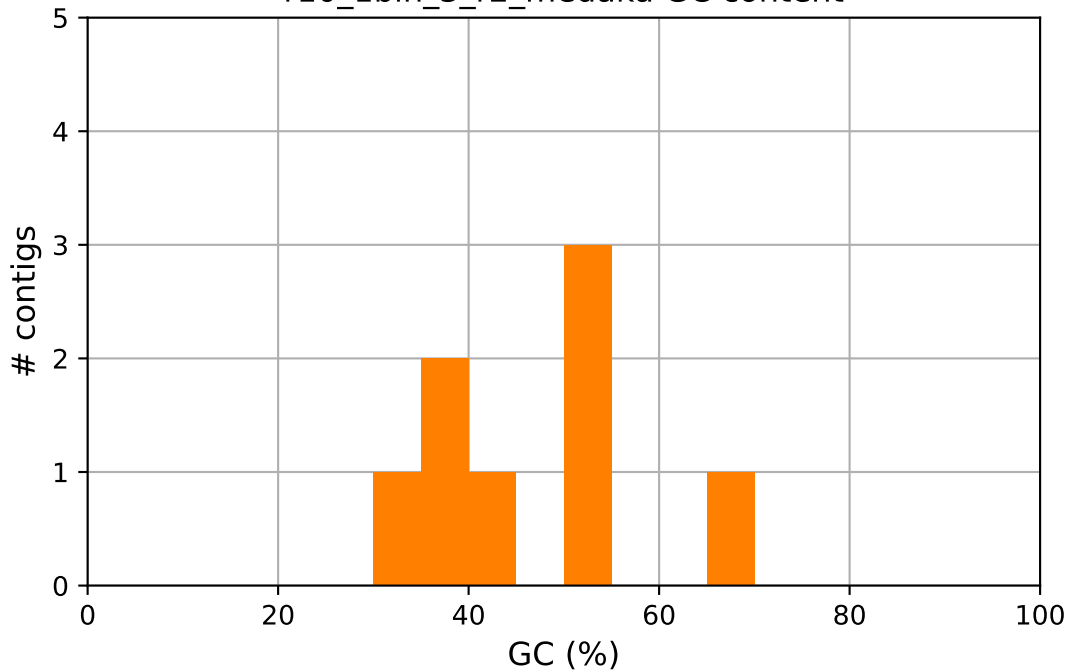
r10\_1bin\_3\_r1\_medaka GC content



r10\_1bin\_3\_r1\_medaka

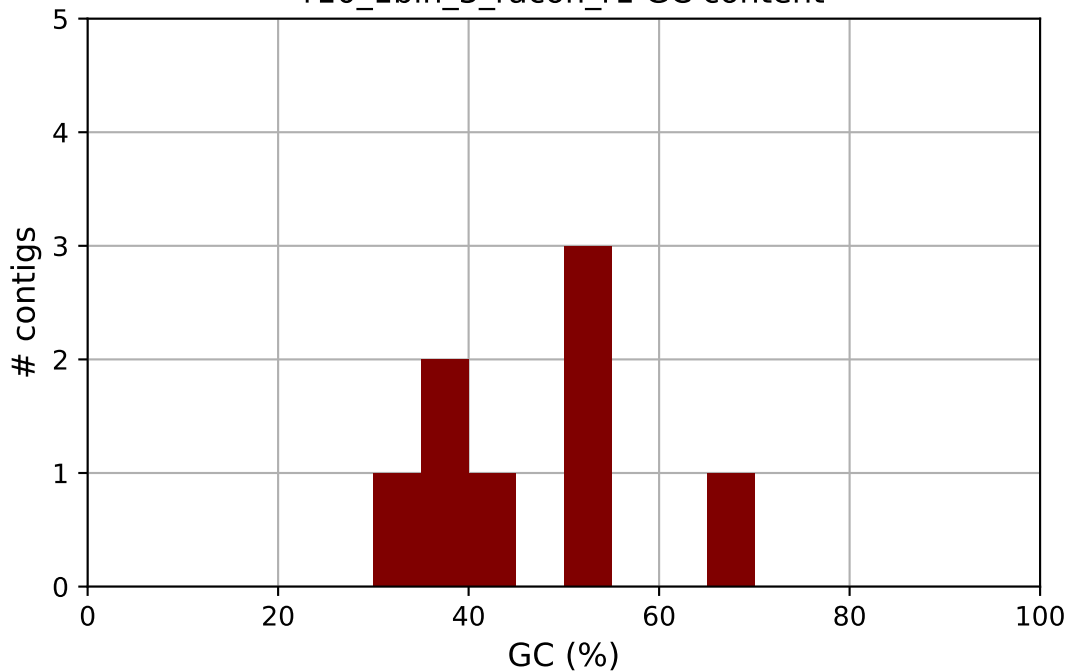


r10\_1bin\_3\_r2\_medaka GC content



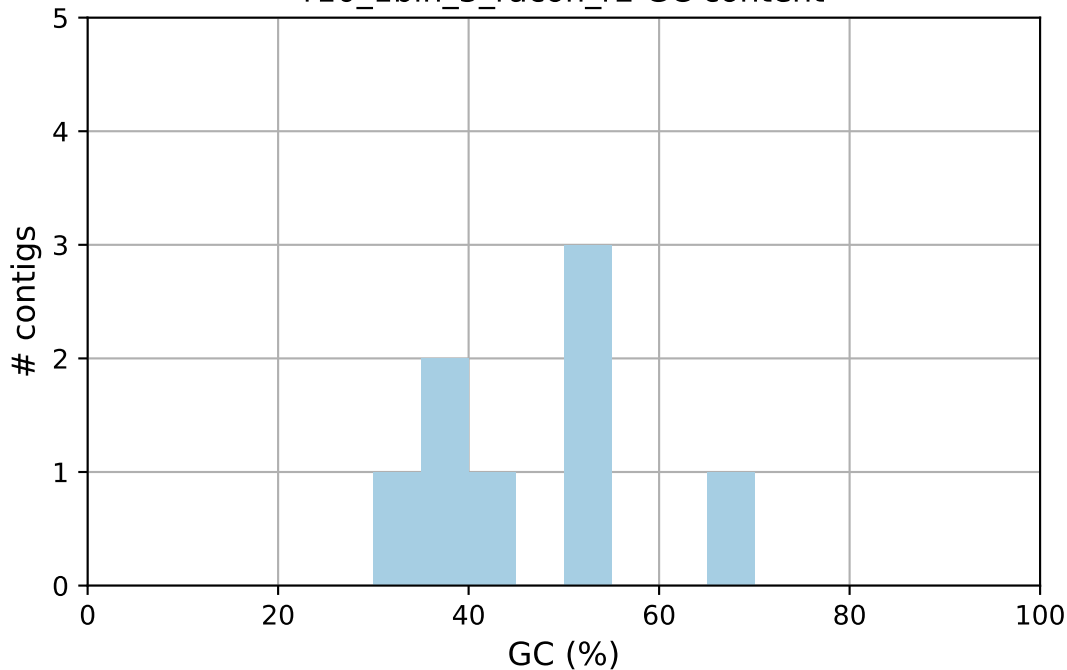
r10\_1bin\_3\_r2\_medaka

r10\_1bin\_3\_racon\_r1 GC content



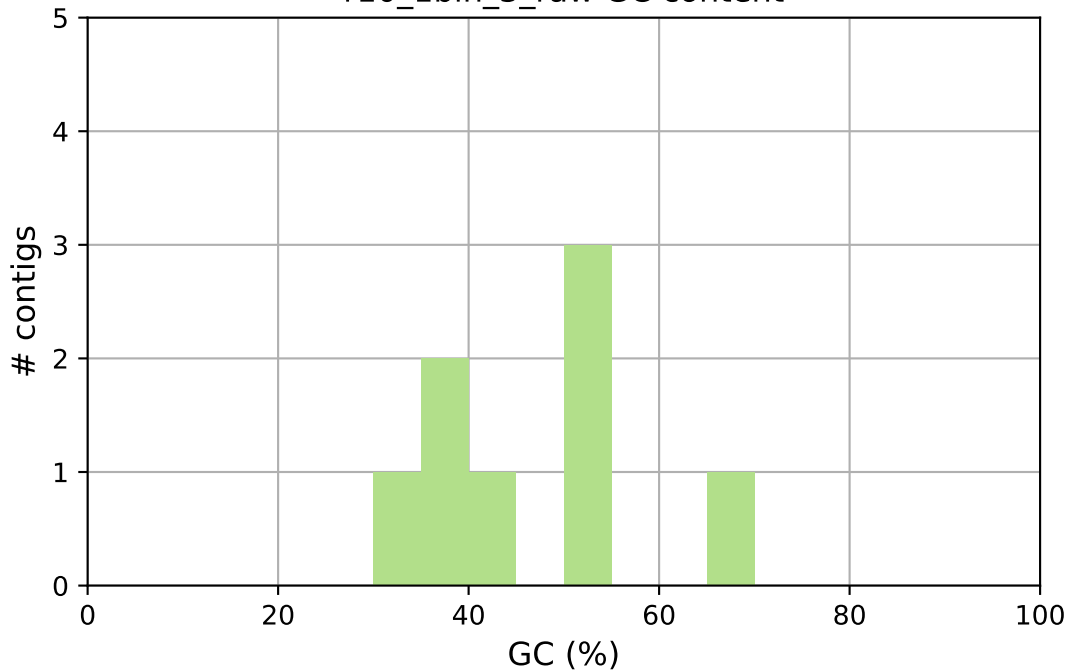
r10\_1bin\_3\_racon\_r1

r10\_1bin\_3\_racon\_r2 GC content



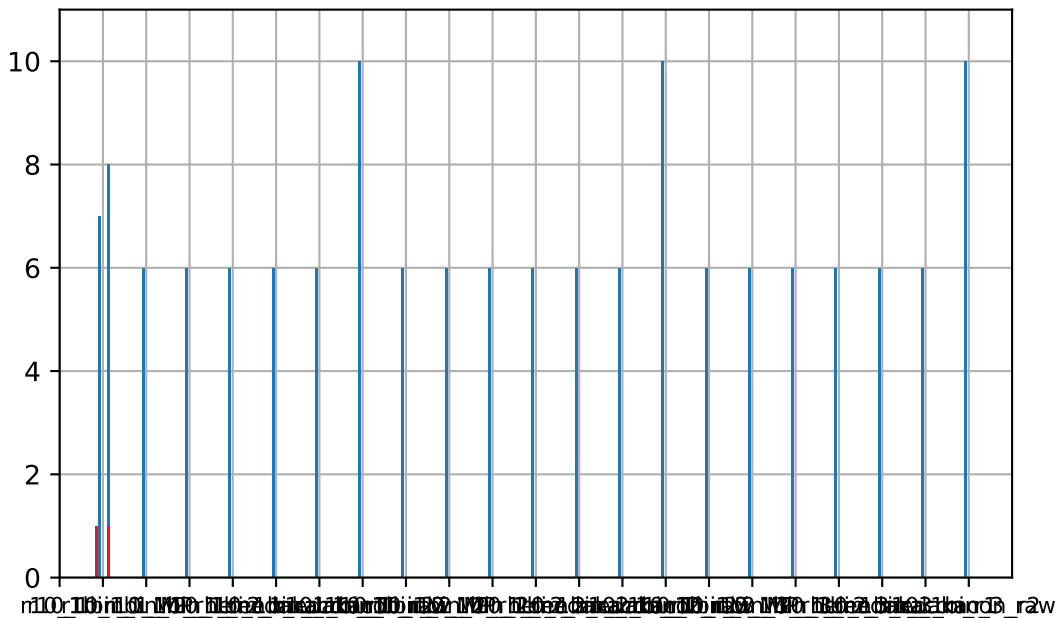
r10\_1bin\_3\_racon\_r2

r10\_1bin\_3\_raw GC content



r10\_1bin\_3\_raw

# Misassemblies



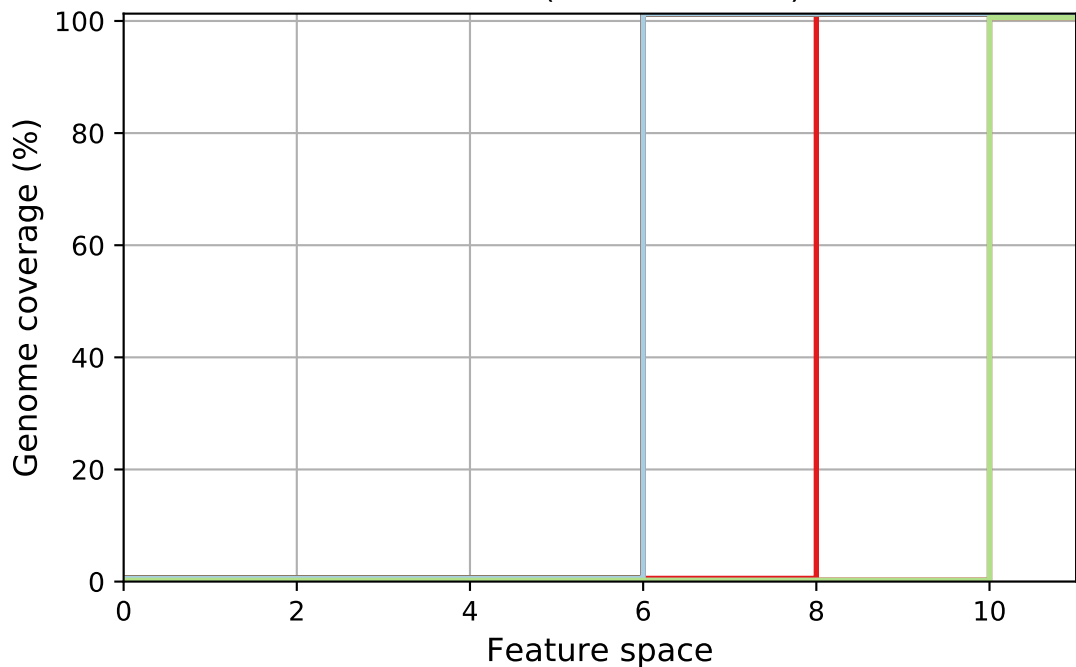
\_\_\_\_\_

```
# relocations
```

11

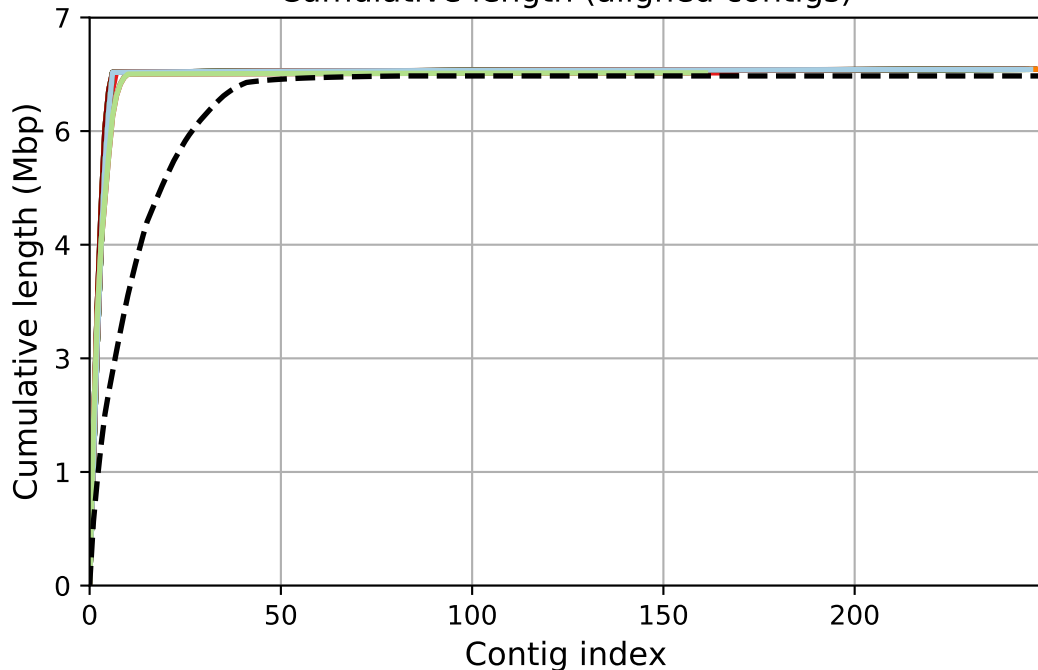
# translocations

FRCurve (misassemblies)



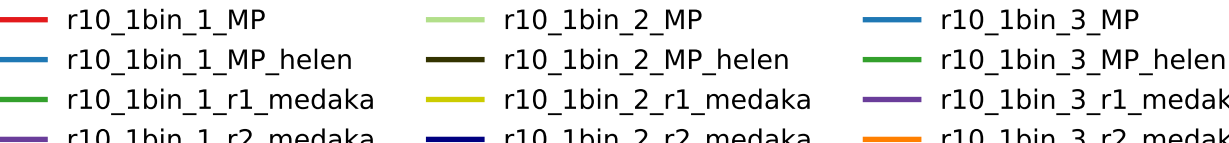
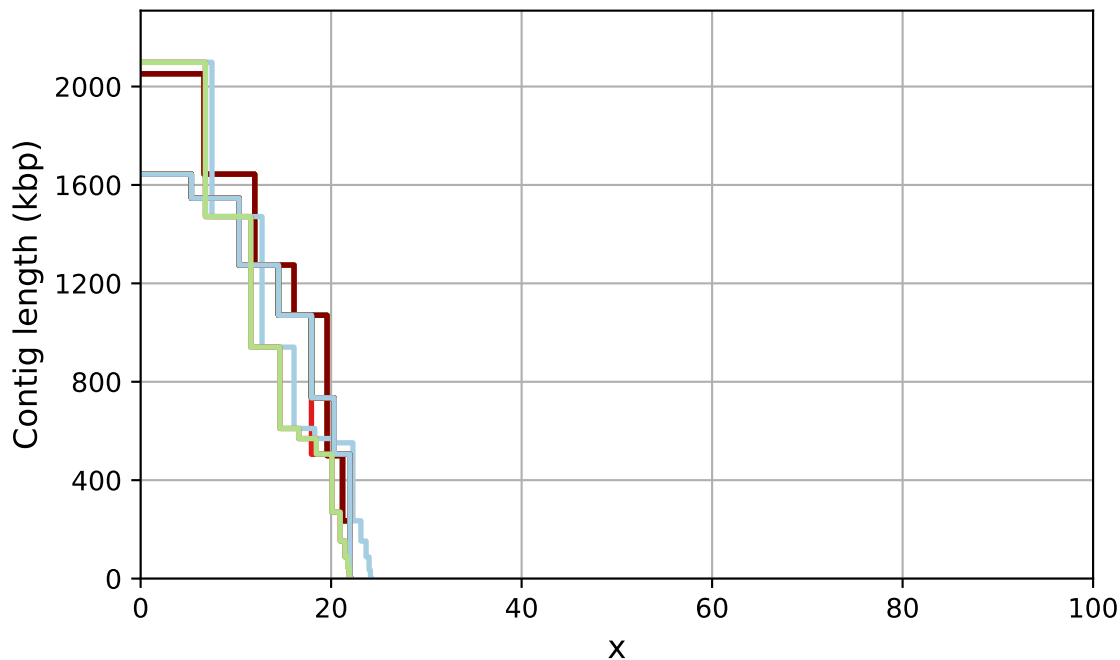
— r10\_1bin\_1\_MP      — r10\_1bin\_2\_MP      — r10\_1bin\_3\_MP  
— r10\_1bin\_1\_MP\_helen      — r10\_1bin\_2\_MP\_helen      — r10\_1bin\_3\_MP\_helen  
— r10\_1bin\_1\_r1\_medaka      — r10\_1bin\_2\_r1\_medaka      — r10\_1bin\_3\_r1\_medak  
— r10\_1bin\_1\_r2\_medaka      — r10\_1bin\_2\_r2\_medaka      — r10\_1bin\_3\_r2\_medak

Cumulative length (aligned contigs)



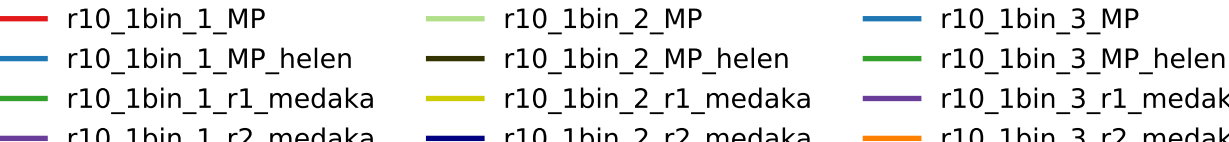
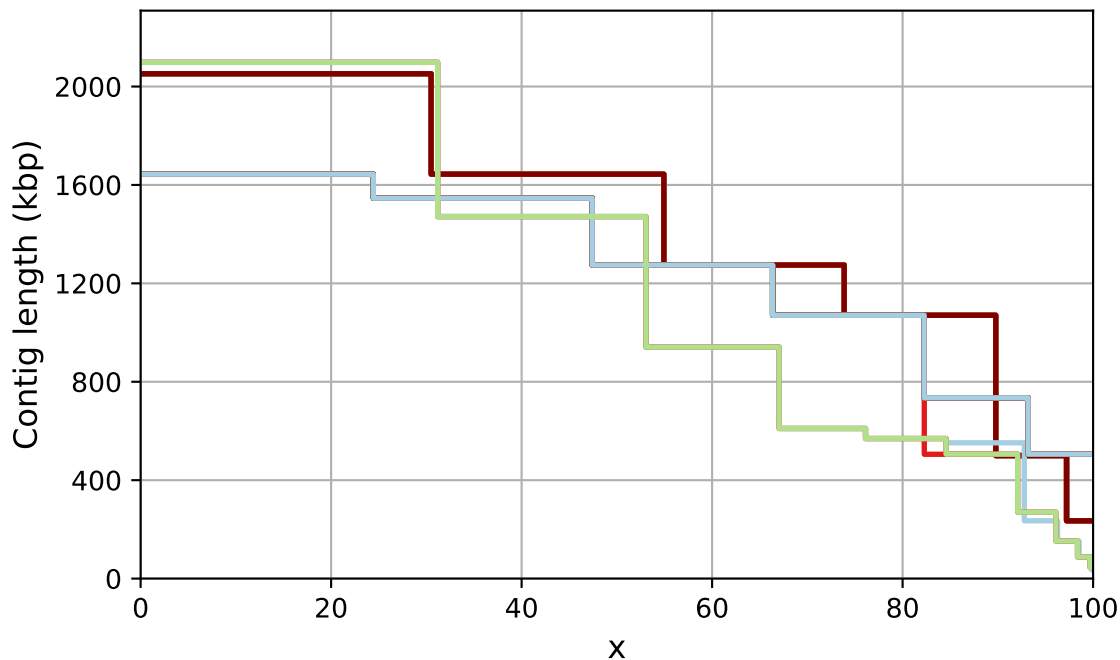
— r10\_1bin\_1\_MP      — r10\_1bin\_2\_MP\_helen      — r10\_1bin\_3\_MP\_helen  
— r10\_1bin\_1\_MP\_helen      — r10\_1bin\_2\_r1\_medaka      — r10\_1bin\_3\_r1\_medaka  
— r10\_1bin\_1\_r1\_medaka      — r10\_1bin\_2\_r2\_medaka      — r10\_1bin\_3\_r2\_medaka  
— r10\_1bin\_1\_r2\_medaka      — r10\_1bin\_2\_racon\_r1      — r10\_1bin\_3\_racon\_r1

NAX





# NGAx



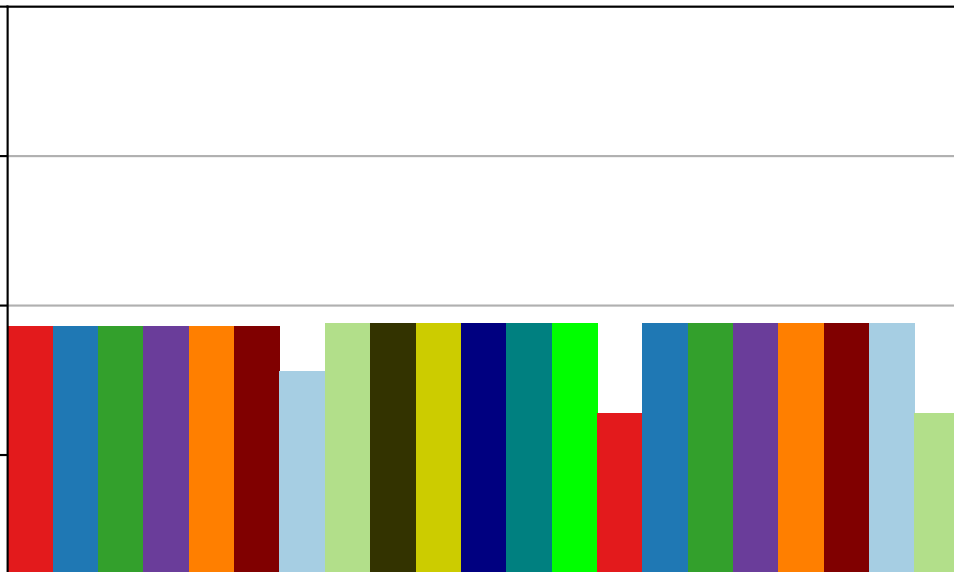
Genome fraction, %

100.00

99.95

99.90

99.85



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\_medaka

r10\_1bin\_3\_r2\_medaka