Report

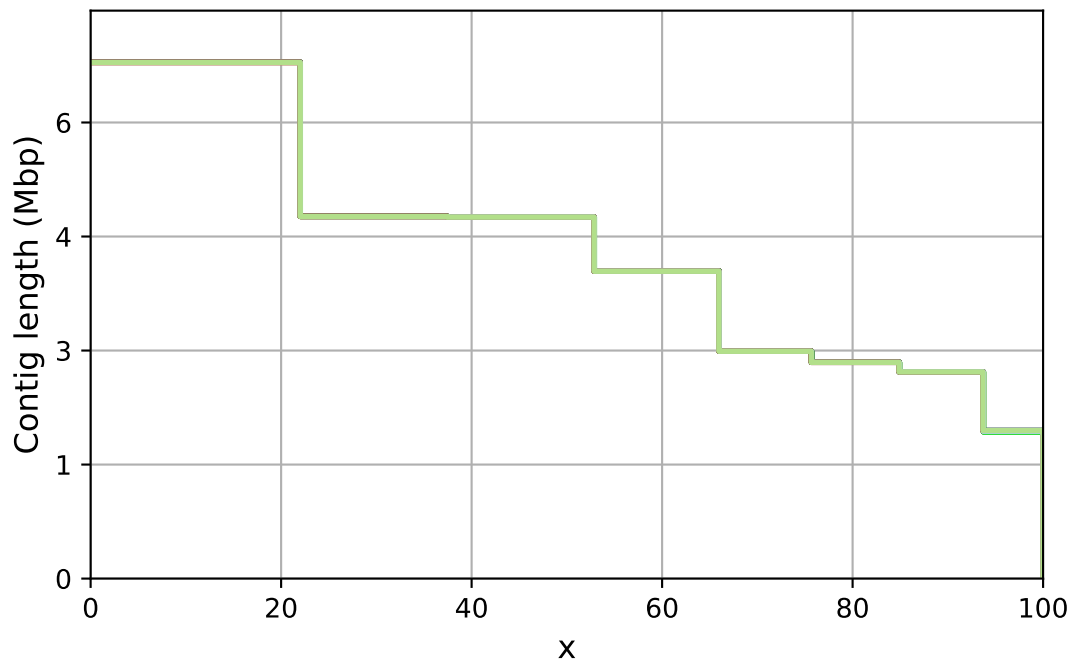|	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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	8
# contigs (>= 1000 bp)	8	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	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 (>= 0 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 1000 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 5000 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 10000 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 25000 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Total length (>= 50000 bp)	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792277	6792242	6792250	6792256	6791584	6791674	6787707	6792192	6792152	6792241	6792246	6791553	6791665	6787702	6792242	6792185	6792243	6792245	6791548	6791645	6788581
Total length	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4758918	4757927	4758579	4758111	4757861	4757813	4755626	4758939	4757856	4758583	4758093	4757899	4757820	4756102	4758920	4757780	4758582	4758118	4757872	4757851	4755682
N75	2992095	2992079	2992073	2992075	2991950	2991981	2990263	2992085	2992067	2992071	2992073	2991978	2991952	2990631	2992051	2992049	2992047	2992047	2991957	2991941	2990406
L50	3	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	5
# misassemblies	171	168	171	173	174	174	175	171	169	169	176	170	177	172	170	170	168	173	168	174	176
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Misassembled contigs length	30867141	30861676	30864248	30855517	30851576	30847638	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867787	30864288	30867356	30861838	30856703	30852242	30851275
# local misassemblies	116	121	127	131	152	138	218	115	119	136	130	146	145	211	114	113	122	124	142	139	213
# 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	0	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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	79123	80182	80803	81232	77326	76833	143089	78620	78897	82450	81228	78832	77254	136980	77562	78324	79894	81584	77903	76296	141107
Genome fraction (%)	99.400	99.391	99.398	99.399	99.397	99.398	99.369	99.400	99.394	99.398	99.399	99.398	99.397	99.371	99.400	99.399	99.399	99.398	99.398	99.397	99.371
Duplication ratio	1.044	1.044	1.044	1.044	1.043	1.043	1.027	1.044	1.044	1.043	1.043	1.043	1.043	1.028	1.043	1.044	1.044	1.044	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	0.00
# mismatches per 100 kbp	174.27	167.43	179.24	174.69	177.69	177.69	269.71	176.29	168.84	176.48	175.72	176.00	179.51	273.88	173.76	166.51	178.24	176.26	177.38	179.99	273.34
# indels per 100 kbp	37.92	21.94	26.72	26.37	66.38	62.55	306.68	38.24	24.33	26.33	26.07	66.46	62.55	308.66	37.68	22.14	27.15	26.61	67.85	63.49	308.71
Largest alignment	2390996	2390977	2390992	2390989	2390887	2390903	2387862	2594052	2593983	2594054	2594056	2593927	2593981	2589950	2593981	2589950	2719510	2719511	2719432	2719419	2717896
Total aligned length	30749952	30746518	30746264	30730860	30739690	30738884	30672992	30749721	30747155	30745961	30733711	30735039	30731189	30683558	30746057	30741910	30743302	30733693	30734715	30730585	30673973
NA50	804862	948326	948857	948885	949243	949272	777677	948988	948359	948963	948282	949353	948871	788148	948280	948893	949279	948895	949279	947277	777733
NA75	399299	399300	399301	399305	399219	399233	345599	381587	381348	381551	381557	381677	381714	373736	394049	394043	394044	394045	393973	393984	369878
LA50	12	11	11	11	11	11	12	11	11	11	11	11	11	11	10	10	10	10	10	10	11
LA75	24	23	23	23	23	27	24	24	24	24	24	24	24	25	23	22	22	22	22	22	25

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

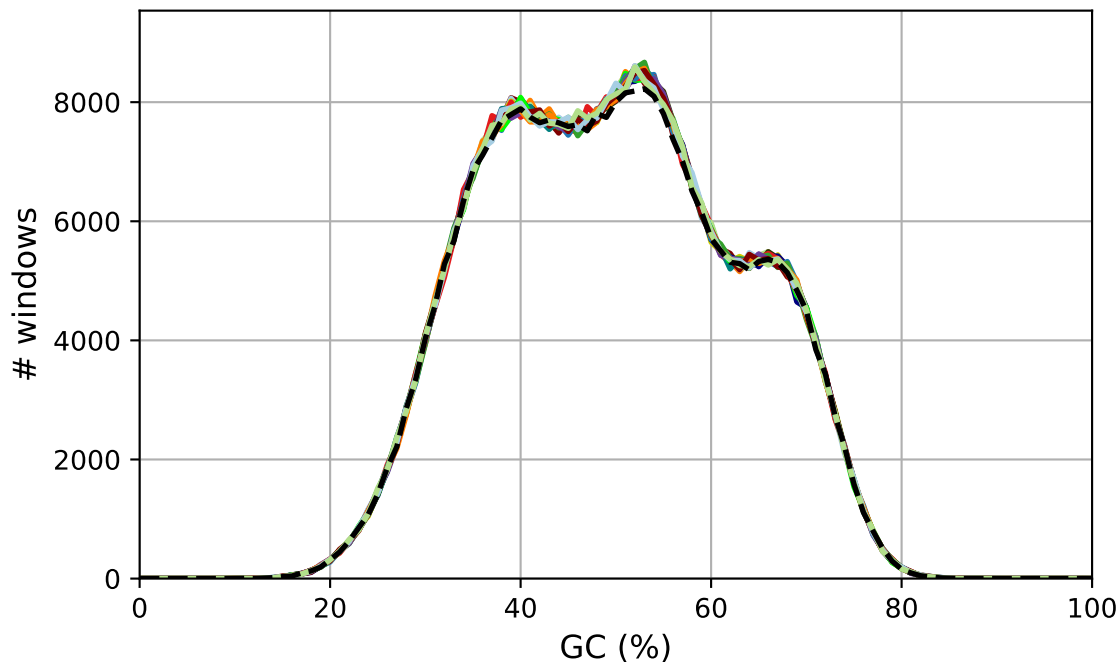|	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# misassemblies 173	171	168	171	173	174	174	175	171	169	169	176	170	177	172	170	170	168	173	168	174	176
# contig misassemblies	171	168	171	173	174	174	175	171	169	169	176	170	177	172	170	170	168	173	168	174	176
# c. relocations	6	4	4	6	4	6	5	6	4	4	9	4	9	5	6	5	5	7	5	5	6
# c. translocations	163	162	165	165	168	166	166	163	163	163	165	164	166	163	162	163	161	164	161	167	166
# c. inversions	2	2	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	2	0	0	0	0	0	0	2	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	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
# s. interspecies translocations	0	0	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	8	8
Misassembled contigs length	30867141	30861676	30864248	30856517	30851576	30847368	30847730	30866597	30861823	30864057	30853121	30851361	30844132	30848669	30867356	30864288	30856838	30859703	30856703	30852242	30851275
# possibly misassembled contigs 7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# possible misassemblies 4	98	102	94	98	94	92	174	98	98	96	98	98	94	167	96	98	96	94	98	92	173
# local misassemblies 1	116	121	127	131	152	138	218	115	119	136	130	146	145	211	114	113	122	124	142	139	213
# 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	252	251	250	252	248	248	174	252	253	252	252	250	249	179	252	252	253	253	250	246	172
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# mismatches	52850	50772	54355	52976	53887	53887	81767	53463	51200	53520	53288	53373	54436	83035	52696	50497	54055	53452	53791	54583	82871
# indels	11501	6654	8104	7997	20130	18969	92976	11596	7379	7985	7907	20153	18970	93579	11426	6714	8233	8071	20576	19254	93592
# indels (<= 5 bp)	10852	5985	7508	7384	19493	18320	91747	10928	6689	7385	7310	19503	18335	92348	10767	6055	7627	7466	19899	18599	92399
# indels (> 5 bp)	649	669	596	613	637	649	1229	668	690	600	597	650	635	1231	659	659	606	605	677	655	1193
Indels length	45828	40929	40991	41020	57729	56080	156862	46131	41731	40539	40620	58096	55505	158088	45650	40784	41179	40905	59218	56704	156644

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_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	79123	80182	80803	181232	77326	76833	143089	78620	78897	82450	81228	78832	77254	136980	77562	78324	79894	81584	77903	76296	141107
# N's	0	10	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).

Nx

Contig length (Mbp) vs **x**

Legend:

r10_1bin_v2_1_MP — r10_1bin_v2_2_MP — r10_1bin_v2_3_MP

r10_1bin_v2_1_MP_helen — r10_1bin_v2_2_MP_helen — r10_1bin_v2_3_MP_h

r10_1bin_v2_1_r1_medaka — r10_1bin_v2_2_r1_medaka — r10_1bin_v2_3_r1_m

r10_1bin_v2_1_r2_medaka — r10_1bin_v2_2_r2_medaka — r10_1bin_v2_3_r2_m

Cumulative length

r10_1bin_v2_1_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_3_MP_h
r10_1bin_v2_1_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_3_r1_m
r10_1bin_v2_1_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_3_r2_m
r10_1bin_v2_1_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_3_raco

GC content

Legend:
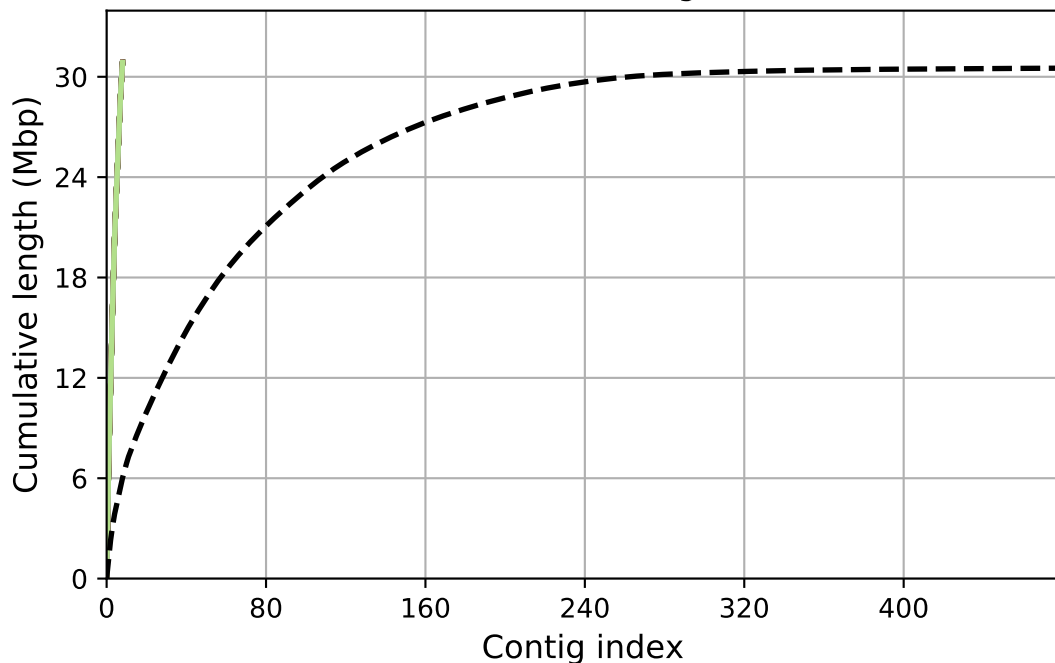
- r10_1bin_v2_1_MP
- r10_1bin_v2_1_MP_helen
- r10_1bin_v2_1_r1_medaka
- r10_1bin_v2_1_r2_medaka
- r10_1bin_v2_2_MP_helen
- r10_1bin_v2_2_r1_medaka
- r10_1bin_v2_2_r2_medaka
- r10_1bin_v2_2_racon_r1
- r10_1bin_v2_3_MP_h
- r10_1bin_v2_3_r1_m
- r10_1bin_v2_3_r2_m
- r10_1bin_v2_3_raco

Axis: # windows vs GC (%)

r10_1bin_v2_1_MP GC content
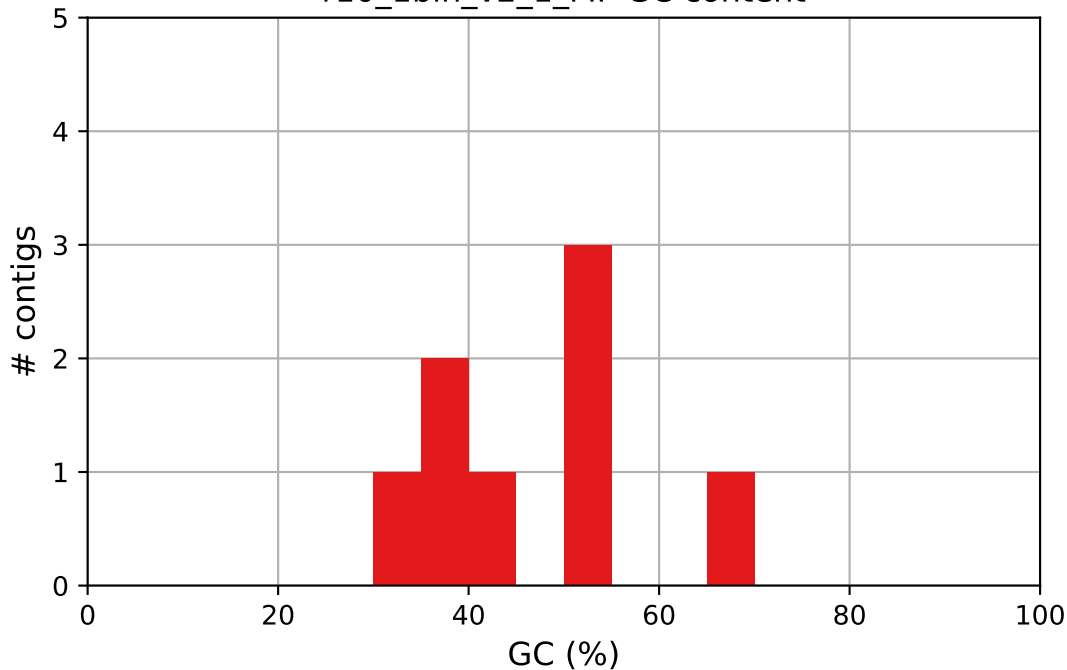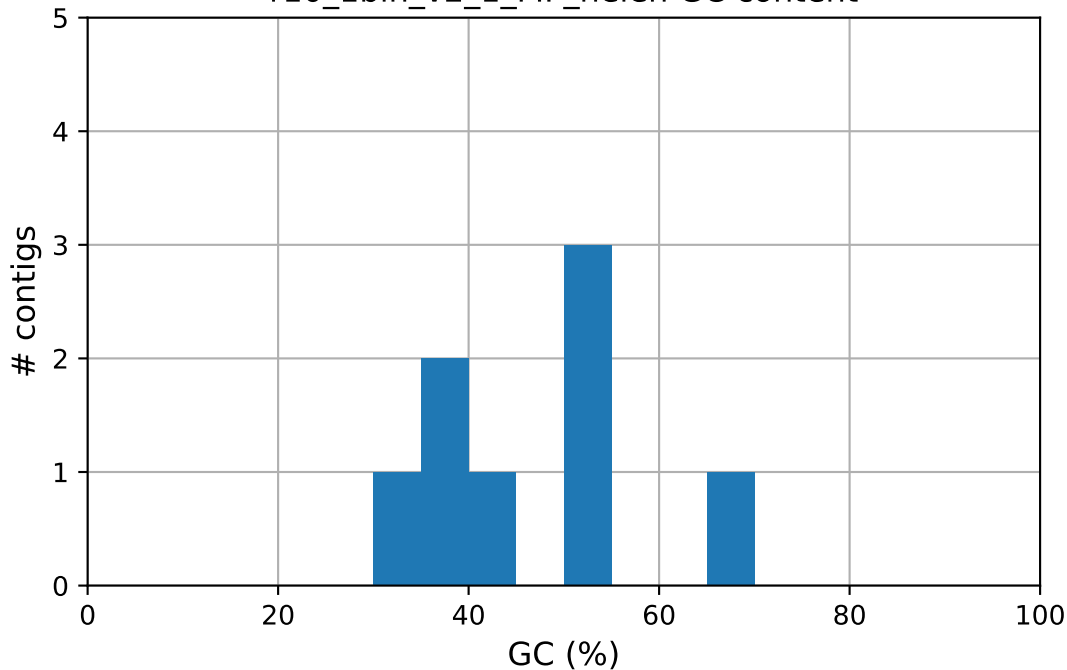
r10_1bin_v2_1_r1_medaka GC content
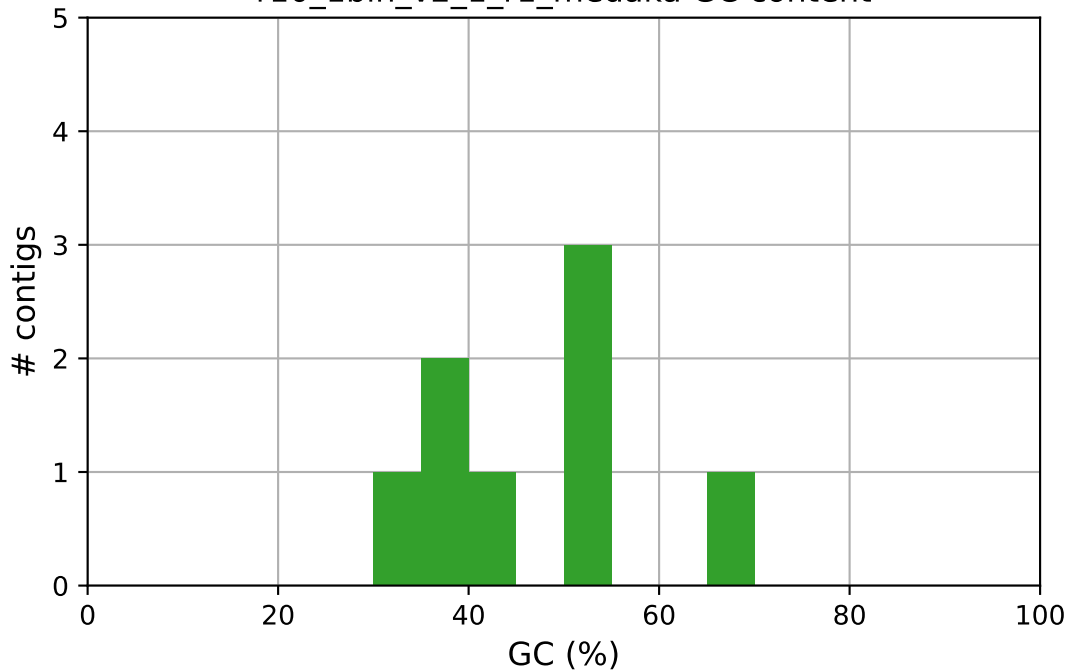
r10_1bin_v2_1_r2_medaka GC content
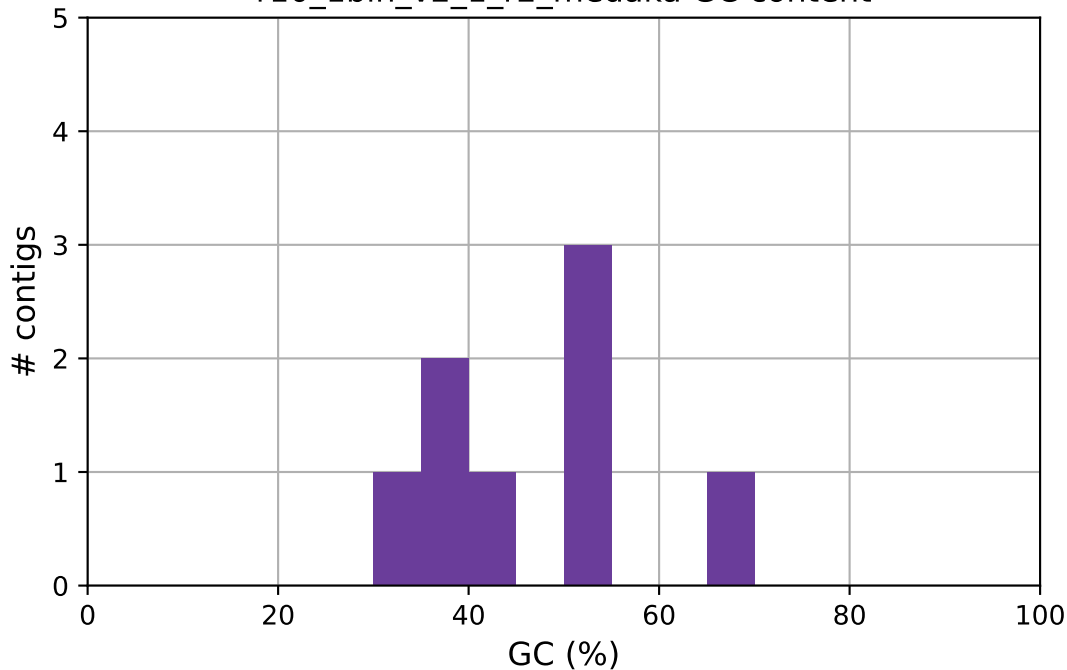
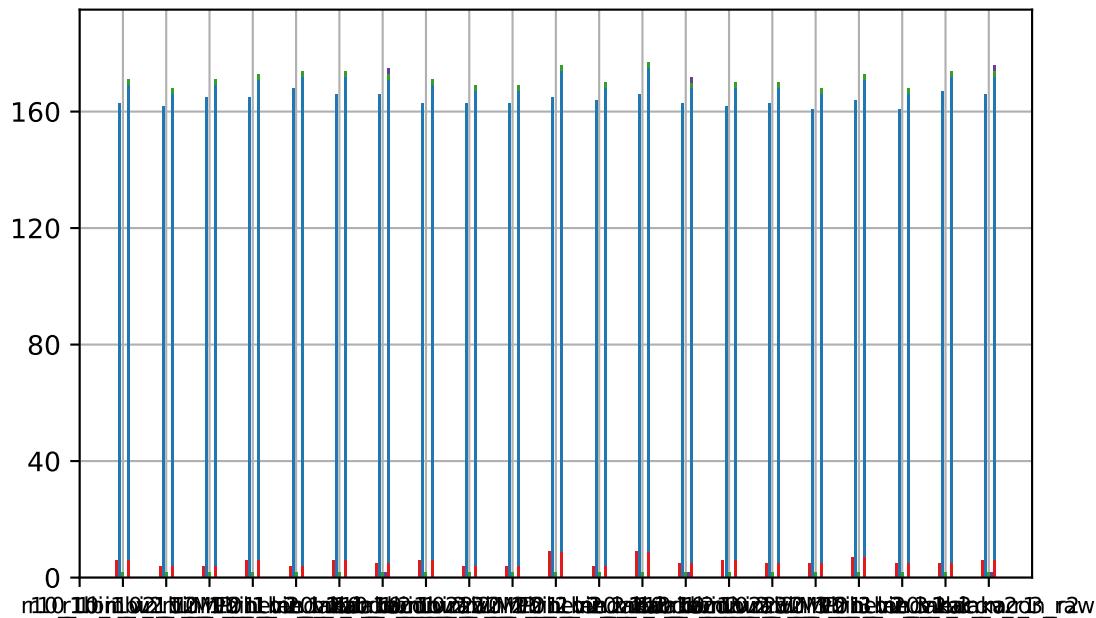r10_1bin_v2_1_racon_r1 GC content
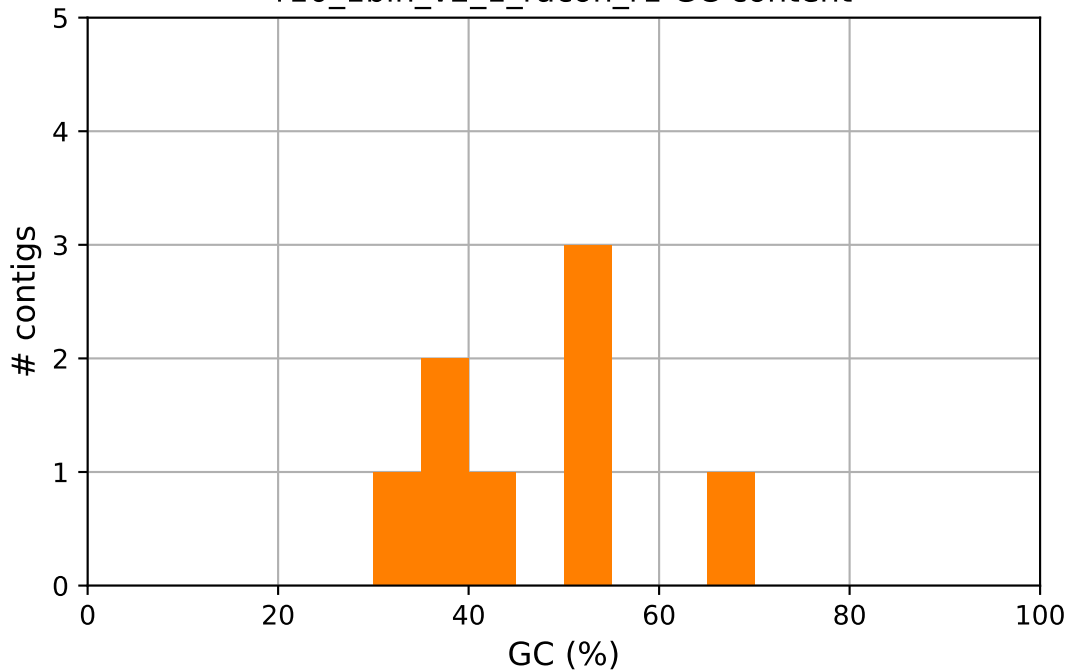
r10_1bin_v2_1_racon_r2 GC content
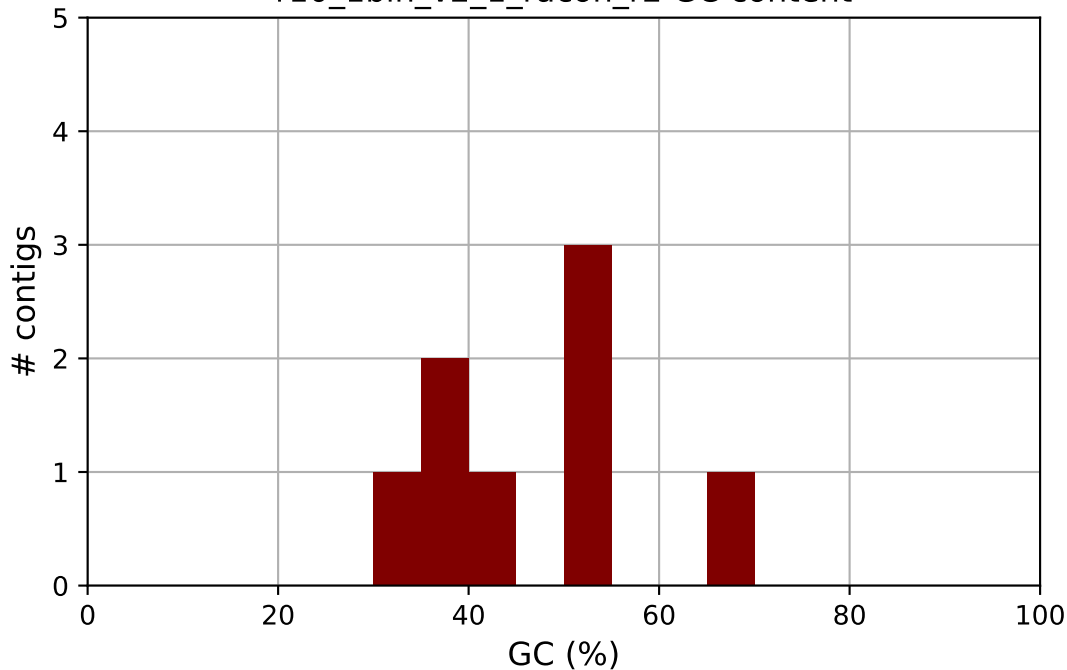
r10_1bin_v2_1_raw GC content
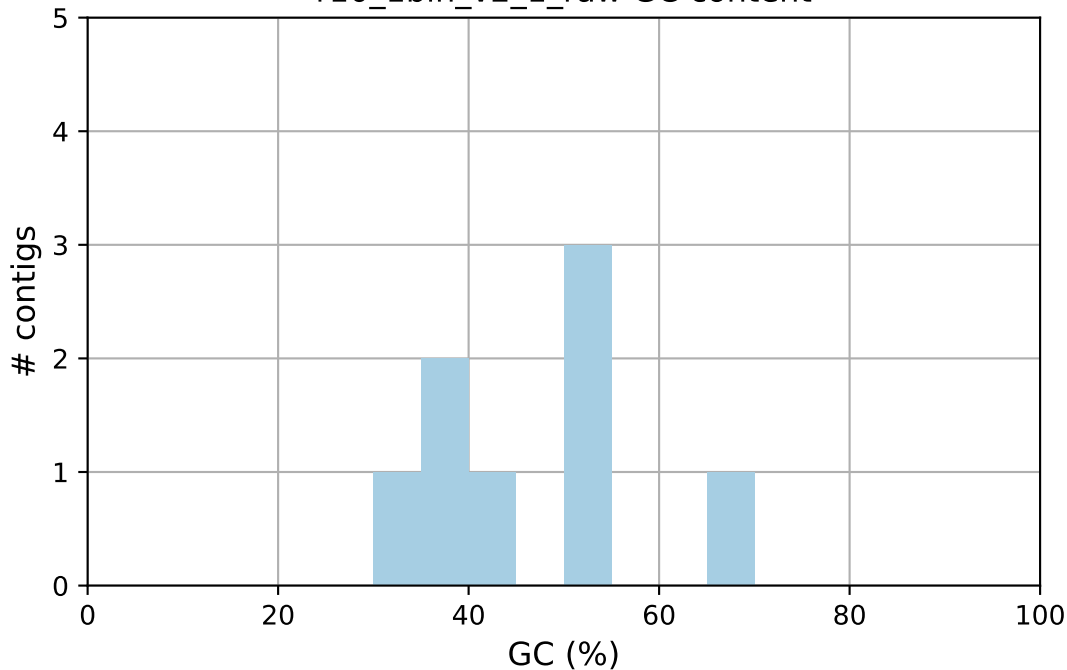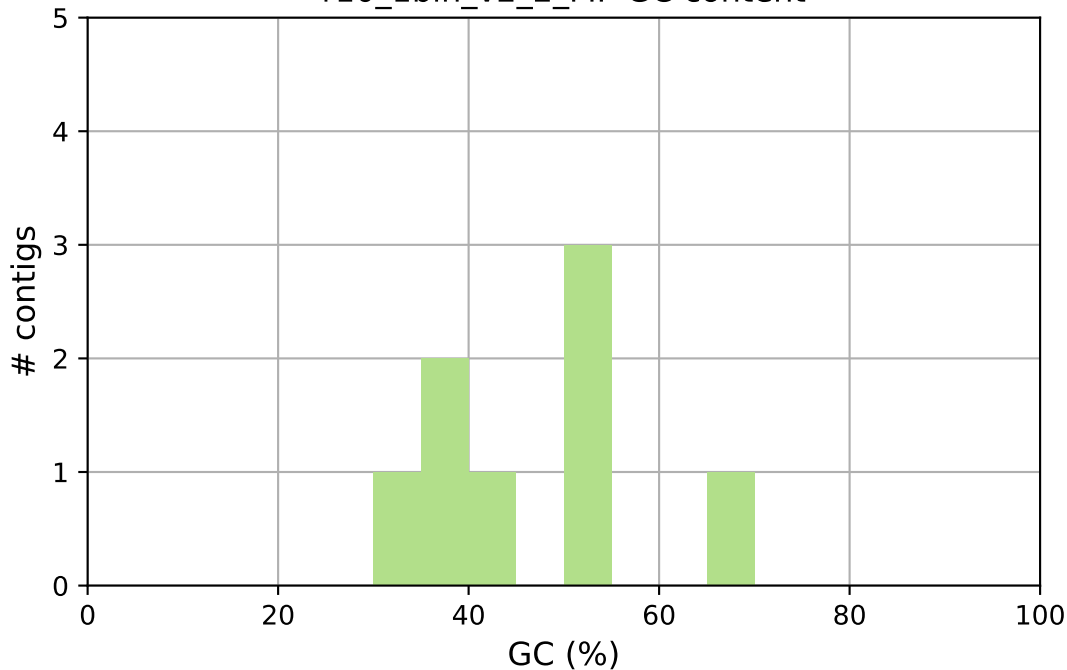
r10_1bin_v2_2_MP_helen GC content
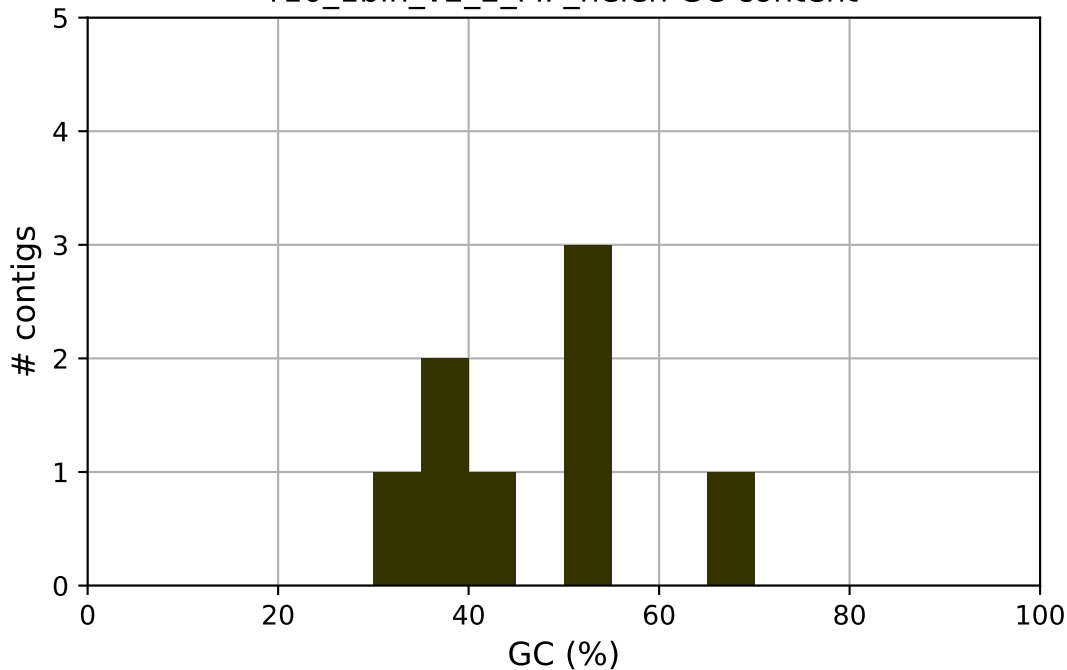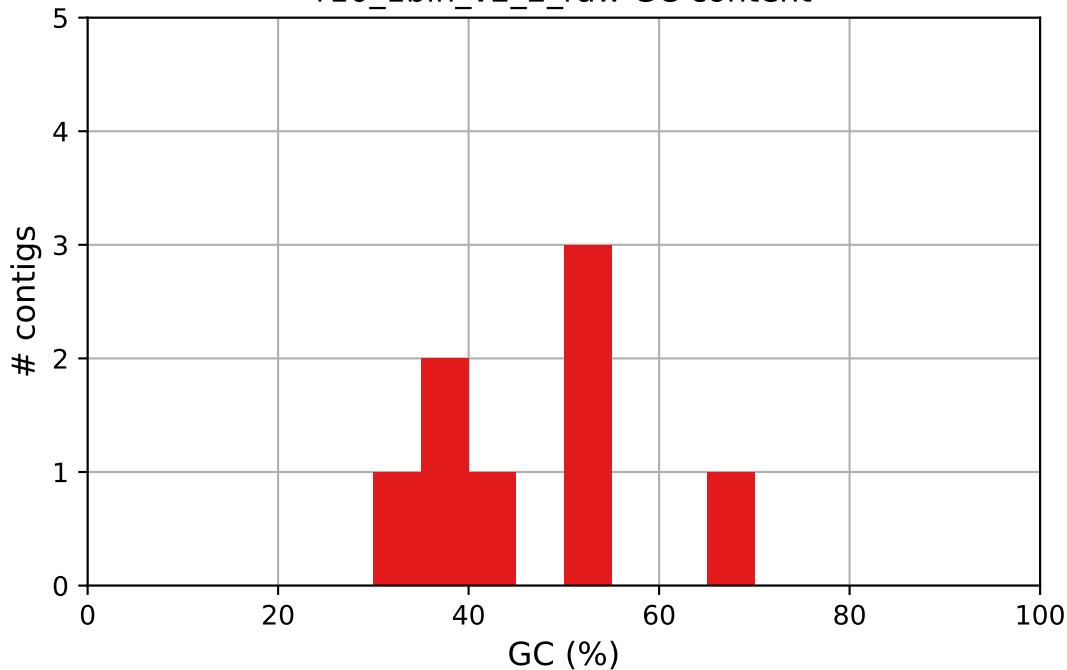
r10_1bin_v2_2_r1_medaka GC content

r10_1bin_v2_3_MP GC content
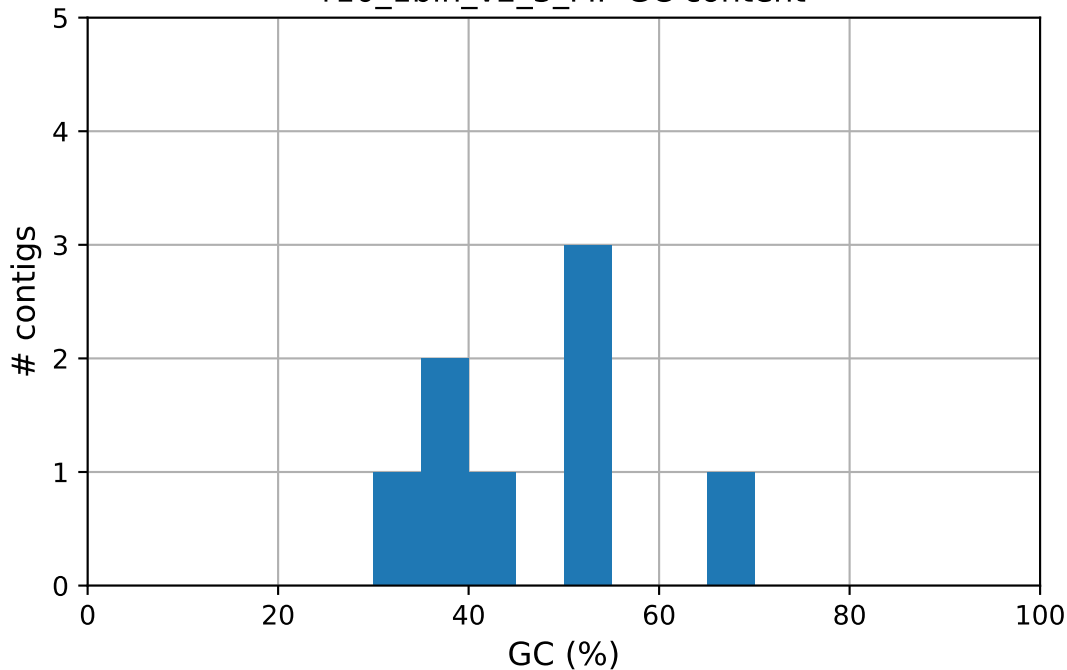
r10_1bin_v2_3_MP_helen GC content
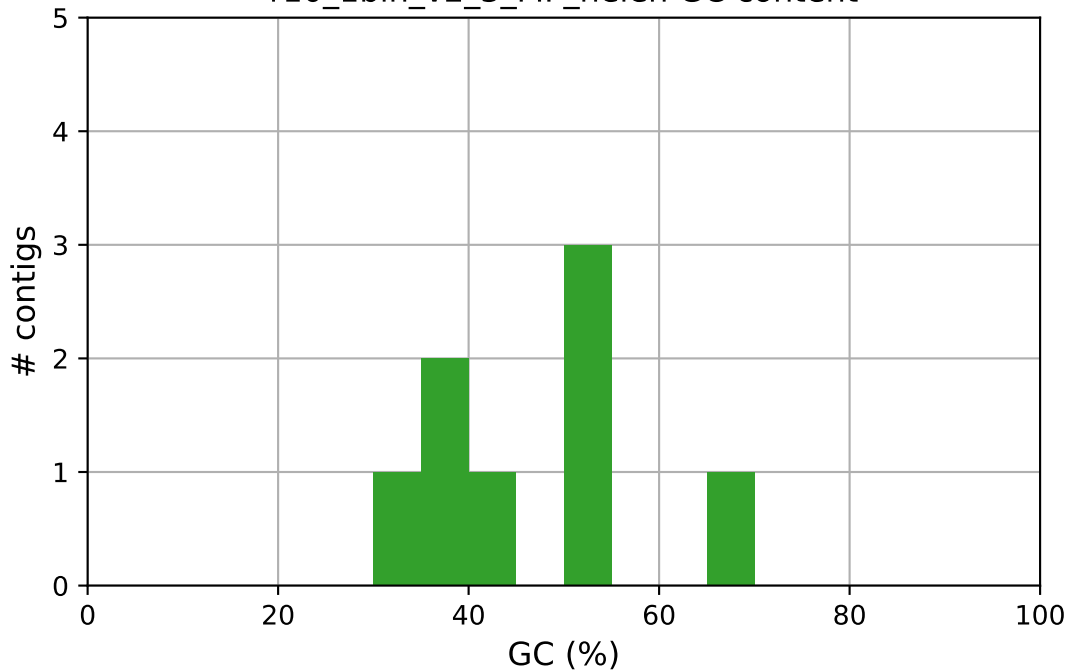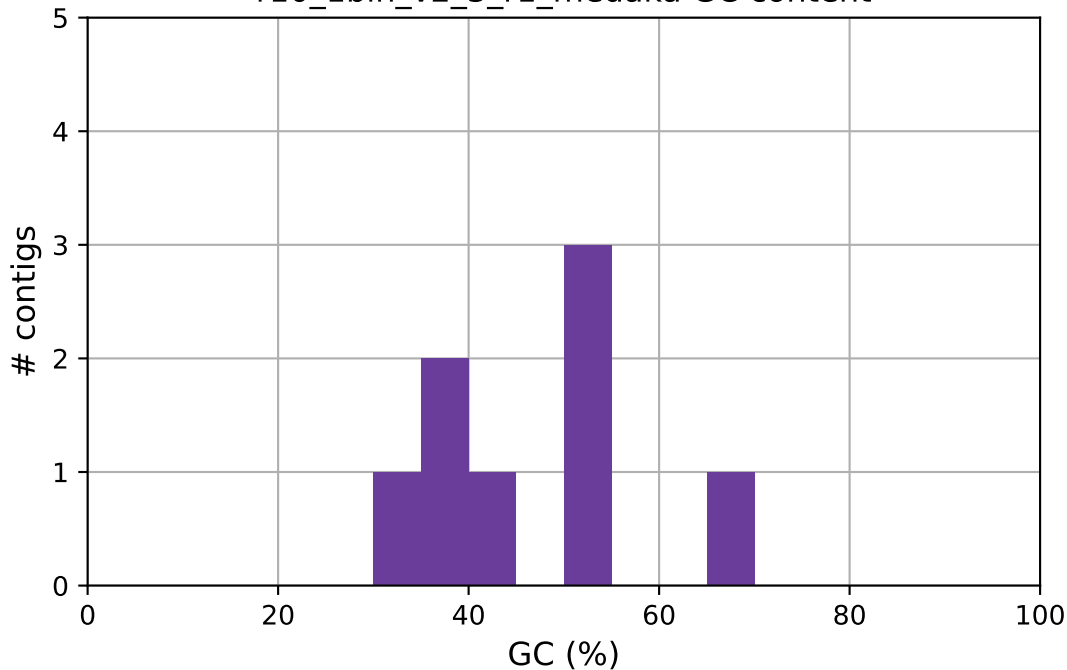
r10_1bin_v2_3_r2_medaka GC content
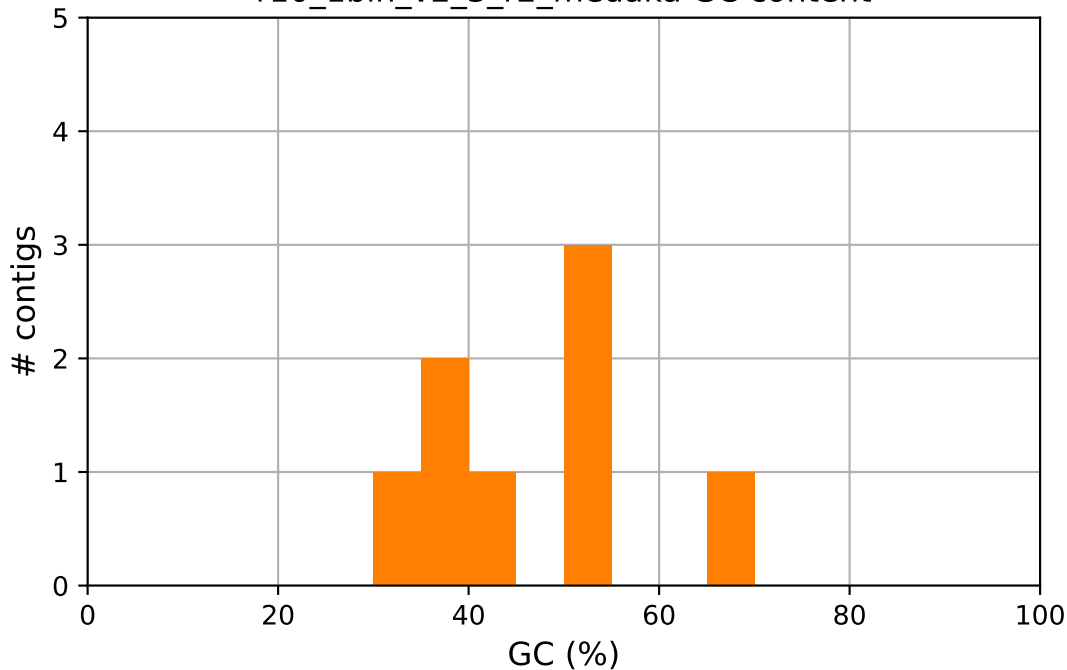
r10_1bin_v2_3_racon_r1 GC content
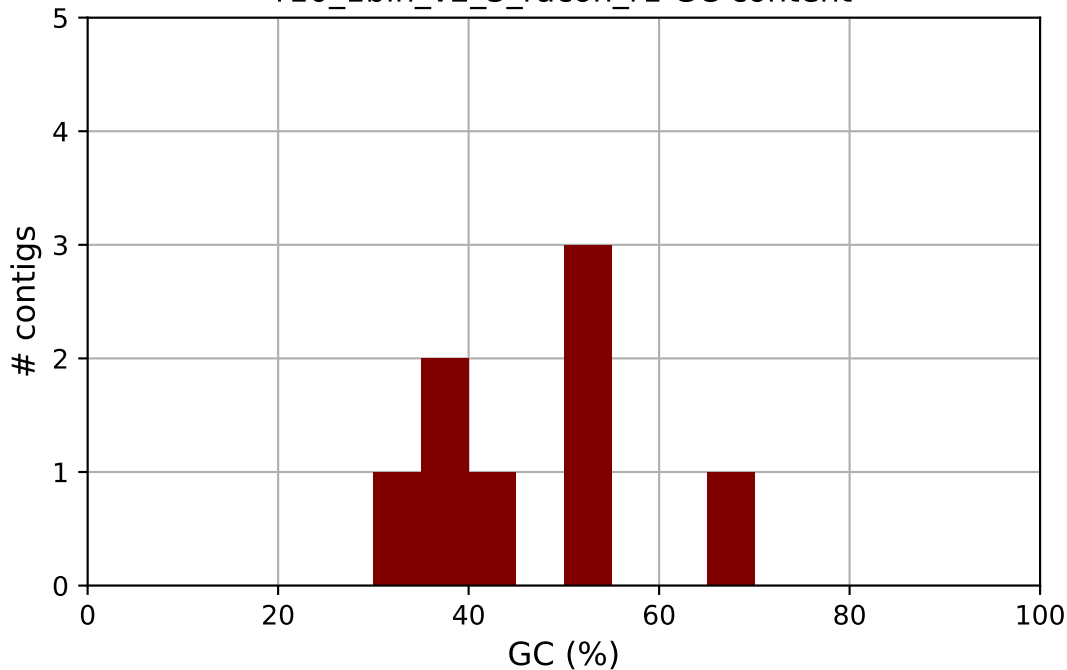
r10_1bin_v2_3_racon_r2 GC content
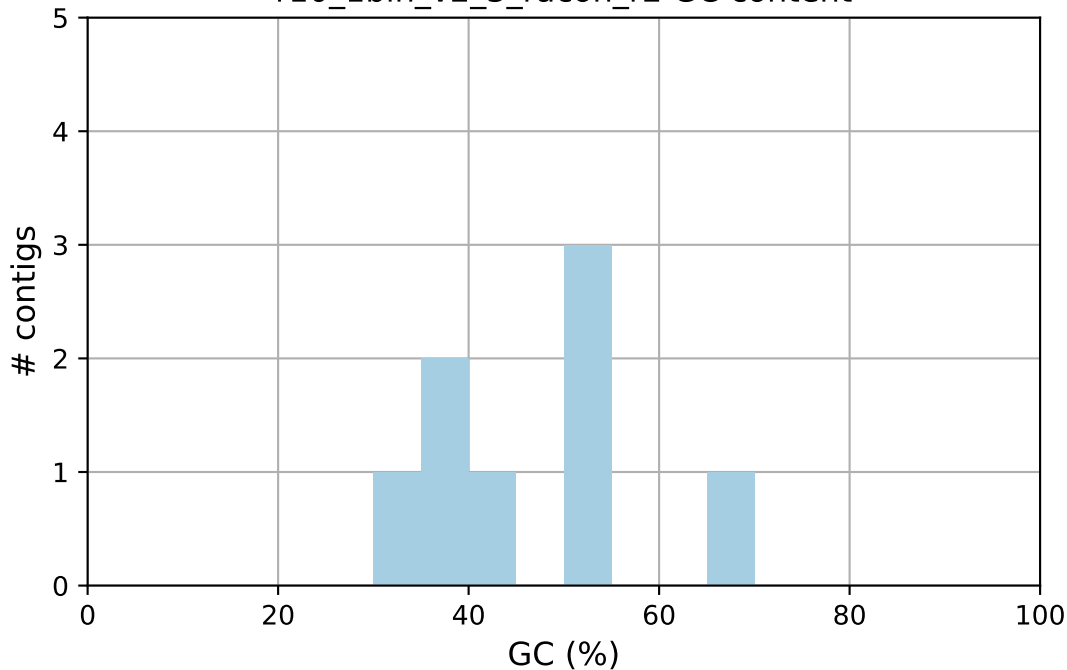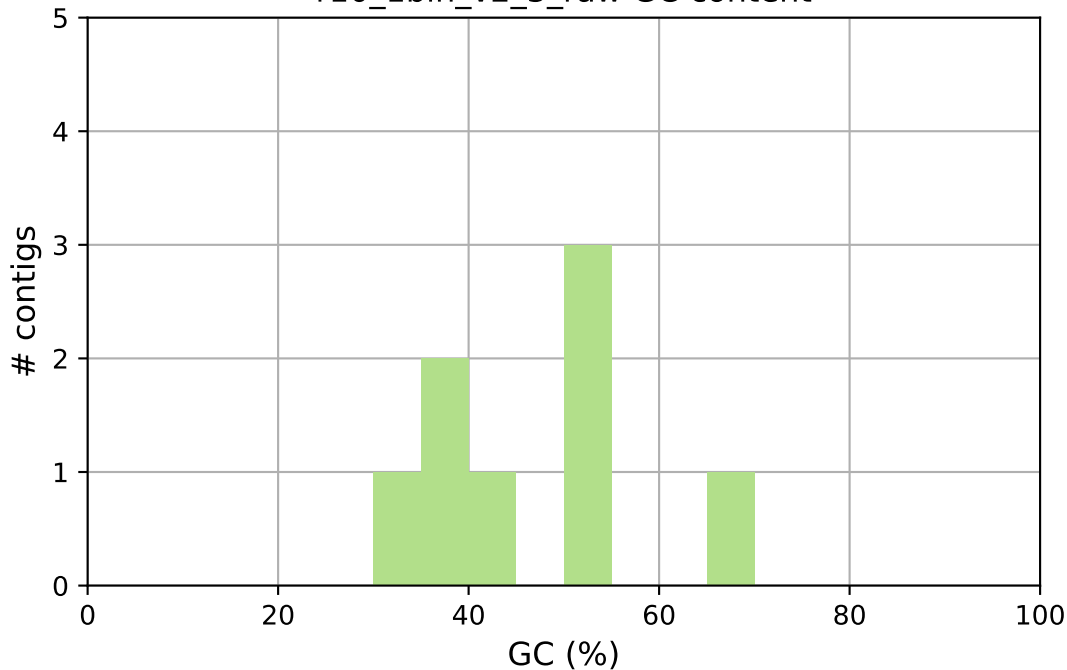
Misassemblies

Legend:
- # relocations
- # inversions
- # interspecies translocations
- # translocations

FRCurve (misassemblies)
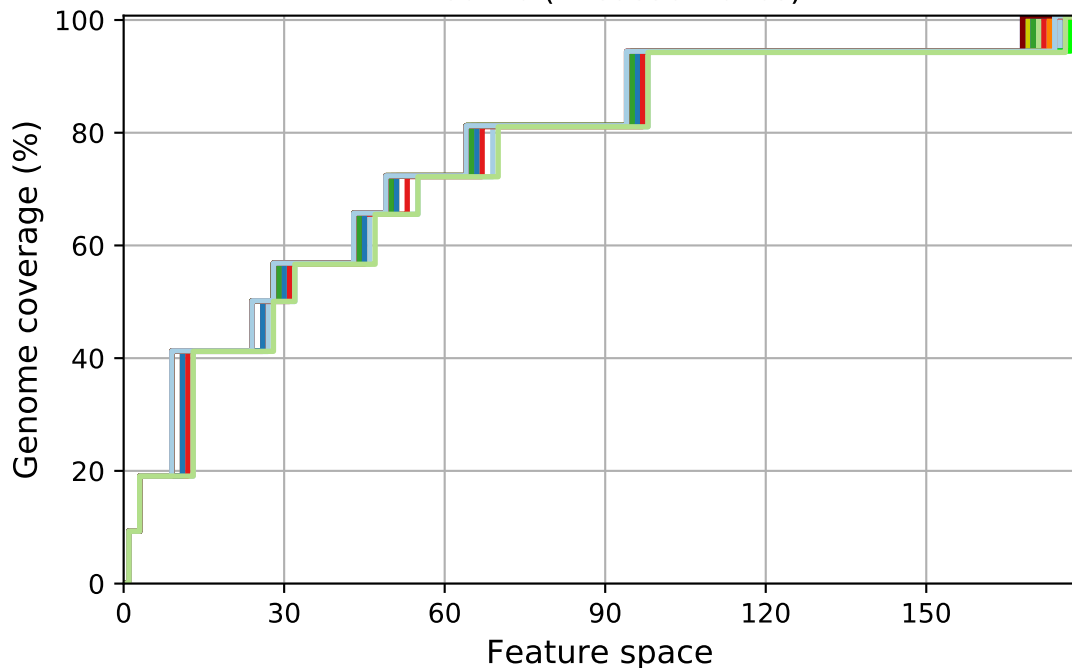
Legend:
- r10_1bin_v2_1_MP
- r10_1bin_v2_2_MP
- r10_1bin_v2_3_MP
- r10_1bin_v2_1_MP_helen
- r10_1bin_v2_2_MP_helen
- r10_1bin_v2_3_MP_h
- r10_1bin_v2_1_r1_medaka
- r10_1bin_v2_2_r1_medaka
- r10_1bin_v2_3_r1_m
- r10_1bin_v2_1_r2_medaka
- r10_1bin_v2_2_r2_medaka
- r10_1bin_v2_3_r2_m

Cumulative length (aligned contigs)

Legend:

r10_1bin_v2_1_MP   r10_1bin_v2_2_MP_helen   r10_1bin_v2_3_MP_h

r10_1bin_v2_1_MP_helen   r10_1bin_v2_2_r1_medaka   r10_1bin_v2_3_r1_m

r10_1bin_v2_1_r1_medaka   r10_1bin_v2_2_r2_medaka   r10_1bin_v2_3_r2_m

r10_1bin_v2_1_r2_medaka   r10_1bin_v2_2_racon_r1   r10_1bin_v2_3_raco

NAx

Contig length (kbp) vs x

r10_1bin_v2_1_MP	r10_1bin_v2_2_MP	r10_1bin_v2_3_MP
r10_1bin_v2_1_MP_helen	r10_1bin_v2_2_MP_helen	r10_1bin_v2_3_MP_h
r10_1bin_v2_1_r1_medaka	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_3_r1_m
r10_1bin_v2_1_r2_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_3_r2_m

Genome fraction, %