

Report

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_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)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 1000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 5000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 10000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 25000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 50000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
Total length	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758592	4758065	4757922	4757649	4756088	4758954	4757856	4758593	4758140	4757950	4757852	4756101
N75	2992083	2992068	2992071	2992074	2991898	2991964	2990667	2992084	2992066	2992071	2992072	2991914	2991953	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633
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	169	169	169	174	169	172	168	172	168	169	171	169	172	176	168	168	169	177	168	175	172
# 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	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# local misassemblies	118	117	138	131	149	139	208	115	116	132	133	149	135	211	115	117	134	130	150	145	204
# 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	1	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	78429	78867	82596	81033	78571	78067	141701	79248	78734	81756	80845	78355	77917	136441	79252	78804	81829	80999	78252	77033	134441
Genome fraction (%)	99.400	99.393	99.398	99.397	99.398	99.396	99.370	99.400	99.397	99.399	99.399	99.398	99.399	99.371	99.400	99.399	99.398	99.398	99.398	99.396	99.370
Duplication ratio	1.044	1.044	1.043	1.043	1.043	1.043	1.027	1.044	1.044	1.044	1.043	1.043	1.043	1.028	1.044	1.044	1.043	1.043	1.043	1.043	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	176.22	168.20	176.25	175.31	179.29	179.06	270.98	175.53	167.54	178.27	174.58	176.13	176.89	274.19	175.99	168.64	175.32	173.93	176.43	176.69	274.68
# indels per 100 kbp	38.29	24.09	26.35	26.63	63.57	59.60	309.19	38.10	23.02	27.10	26.36	62.95	59.92	310.40	38.18	23.88	26.52	26.39	63.08	59.58	308.51
Largest alignment	2390995	2390975	2390993	2390991	2390867	2390936	2387840	2390995	2390975	2390992	2390994	2390894	2390901	2387942	2390995	2390978	2390995	2390990	2390895	2390906	2387930
Total aligned length	30757047	30749353	30748342	30739190	30742141	30736356	30682147	30741473	30738065	30736691	30728759	30726623	30674984	30749160	30748514	30746660	30730897	30740025	30730863	30683073	
NA50	948799	948170	948783	948793	949039	949083	777743	948896	948227	948794	948812	949149	949090	948178	948794	948763	948784	948763	949082	949108	777741
NA75	399300	399300	399301	399300	399235	399235	381417	394048	394042	394044	394044	393977	393997	369917	399300	399300	399302	399302	399226	402942	381417
LA50	11	11	11	11	11	11	12	11	11	11	11	11	11	12	11	11	11	11	11	11	12
LA75	24	23	23	23	23	23	26	24	24	24	24	24	24	28	24	24	24	24	24	23	26

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

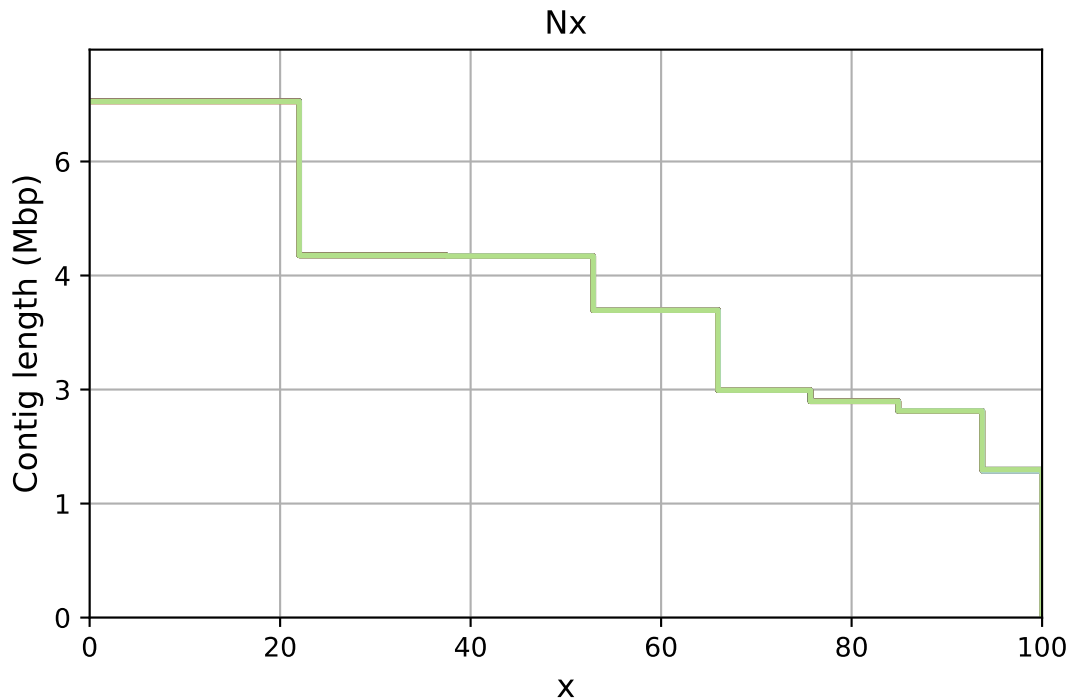
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# misassemblies	169	169	169	174	169	178	172	168	168	169	171	169	172	176	168	168	169	177	168	175	172
# contig misassemblies	169	169	169	174	169	178	172	168	168	169	171	169	172	176	168	168	169	177	168	175	172
# c. relocations	5	5	4	9	4	9	5	5	4	4	6	4	6	5	5	4	4	10	4	7	5
# c. translocations	162	162	163	163	163	167	163	161	162	163	163	163	164	167	161	162	163	165	162	166	163
# 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	30866559	30861633	30864249	30853622	30851421	30845671	30849678	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# 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	98	98	96	98	98	96	168	100	98	96	96	96	96	168	100	98	96	96	98	94	164
# local misassemblies	118	117	138	131	149	139	208	115	116	132	133	149	135	211	115	117	134	130	150	145	204
# 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	1	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	253	250	252	249	249	172	253	253	250	251	250	250	173	253	253	250	251	251	248	181
# 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	53441	51005	53448	53163	54372	54301	82153	53232	50808	54062	52943	53413	53645	83129	53370	51141	53166	52746	53505	53583	83275
# indels	11611	7304	7990	8075	19279	18073	93739	11555	6980	8217	7994	19089	18171	94105	11578	7241	8043	8004	19128	18068	93530
# indels (<= 5 bp)	10951	6630	7393	7474	18618	17440	92494	10903	6320	7613	7391	18438	17513	92885	10910	6575	7452	7411	18475	17433	92300
# indels (> 5 bp)	660	674	597	601	661	633	1245	652	660	604	603	651	658	1220	668	666	591	593	653	635	1230
Indels length	45792	41705	40616	41121	56997	54561	158364	45916	41322	41318	40914	57107	55122	158766	46106	41387	40634	40565	56803	55379	158210

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_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_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	78429	78867	82596	81033	78571	78067	141701	79248	78734	81756	80845	78355	77917	136441	79252	78804	81829	80999	78252	77033	134441
# 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).



r0_2bins_v2_1_MP

r0_2bins_v2_1_MP_helen

r0_2bins_v2_1_r1_medaka

r0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

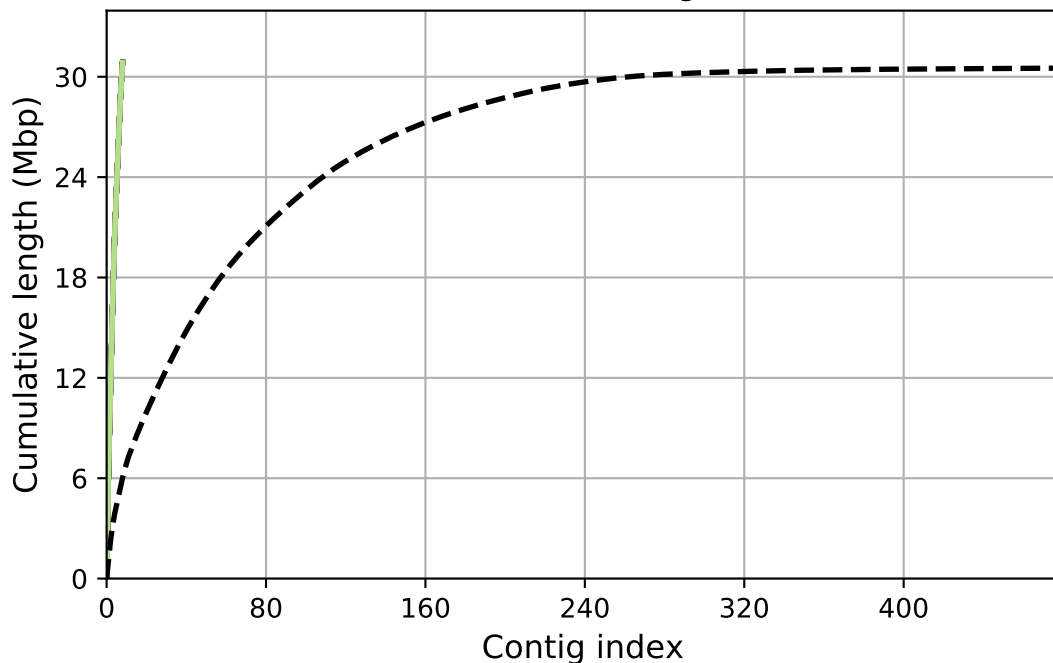
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

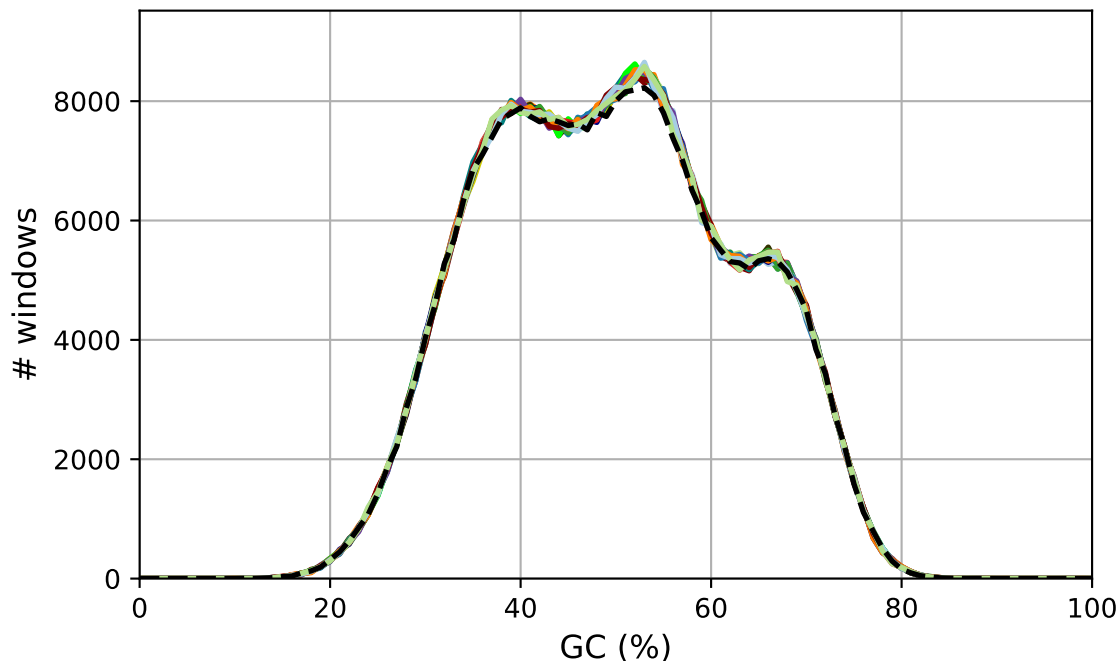
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racon_r1

GC content



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

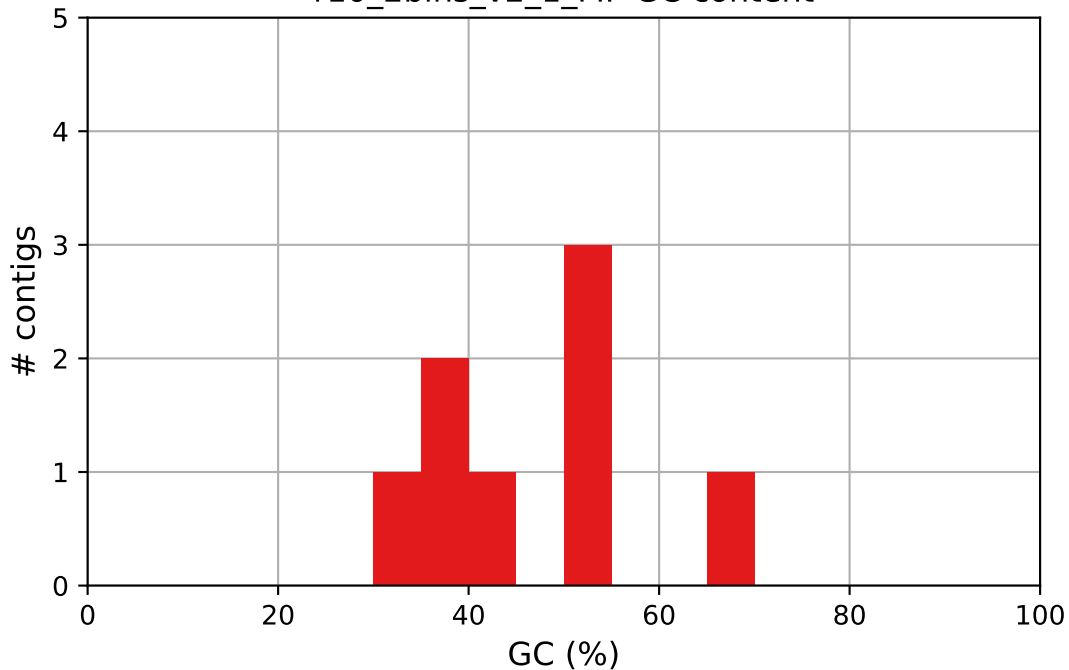
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

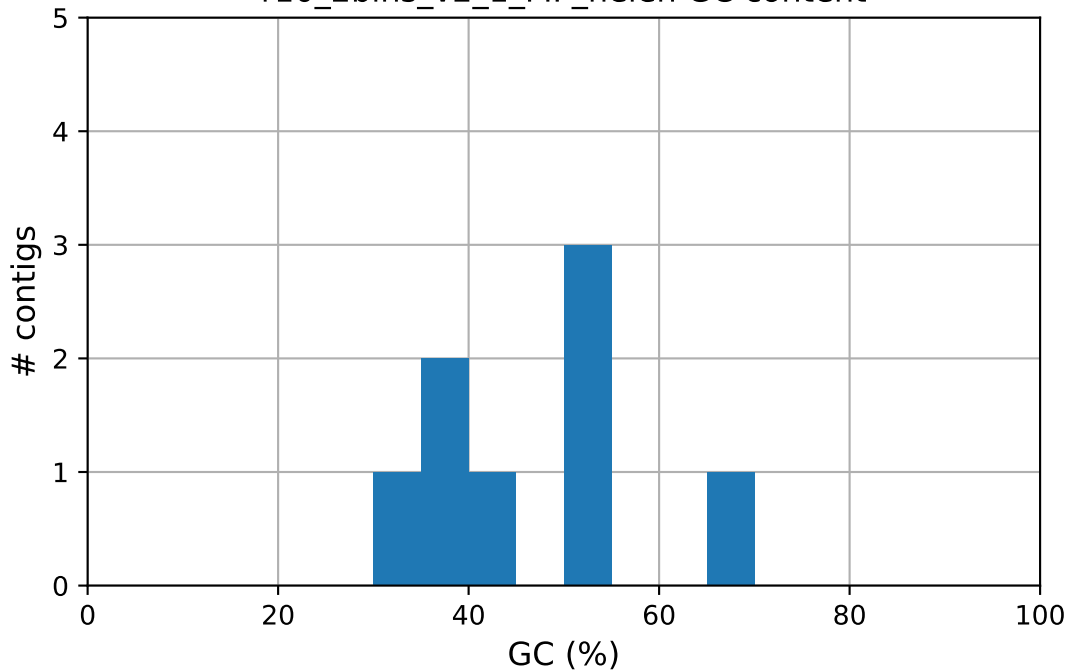
r10_2bins_v2_3_racon_r1

r10_2bins_v2_1_MP GC content



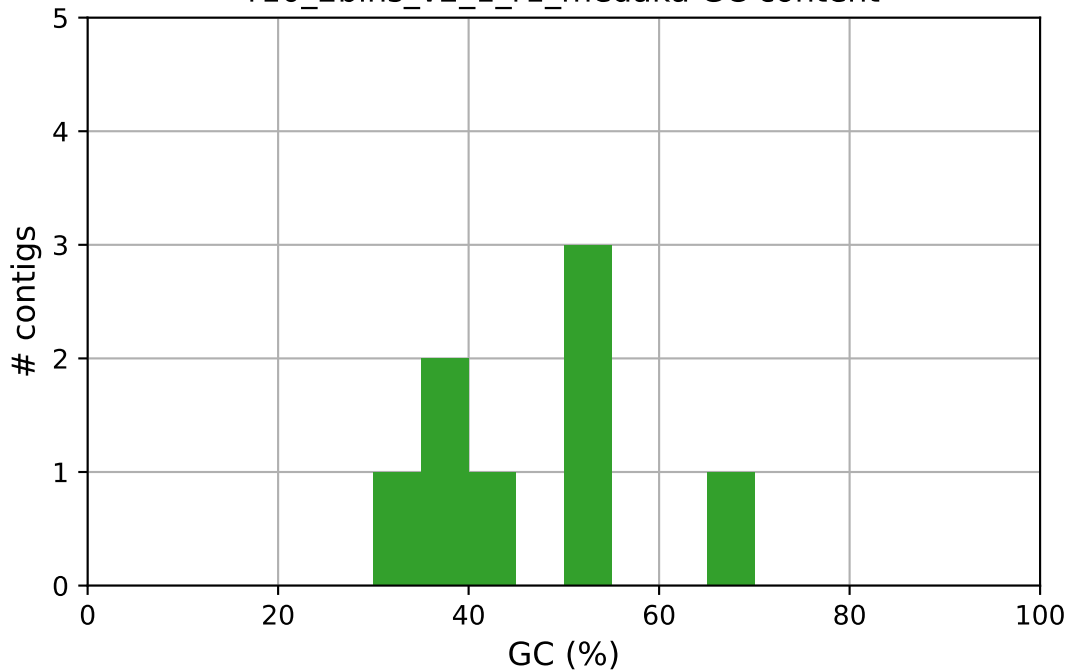
r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen GC content



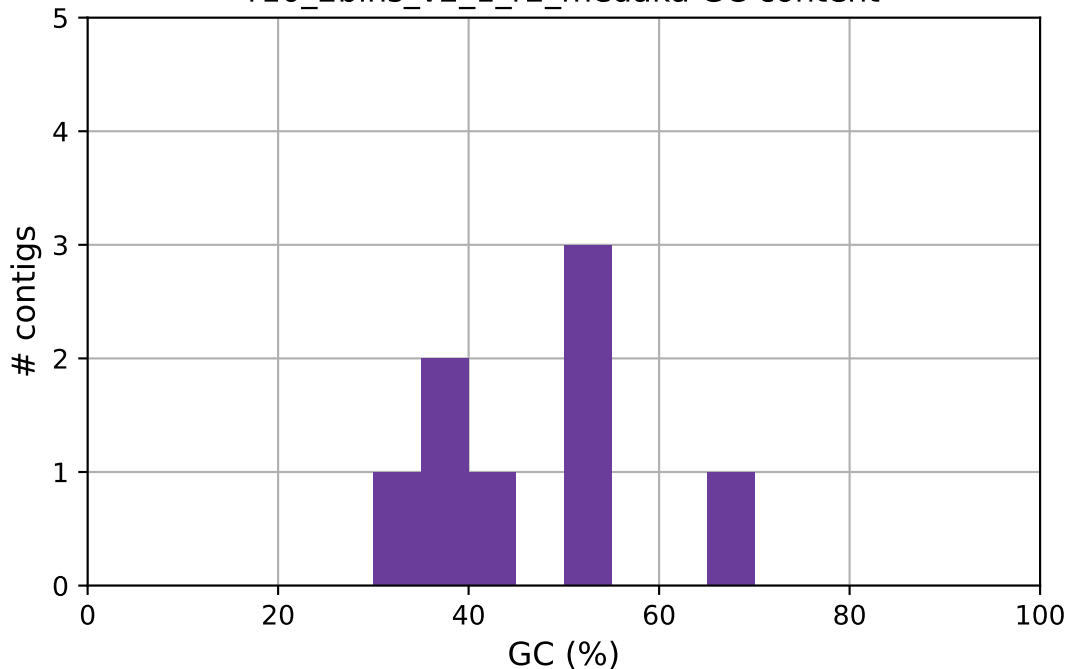
r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka GC content



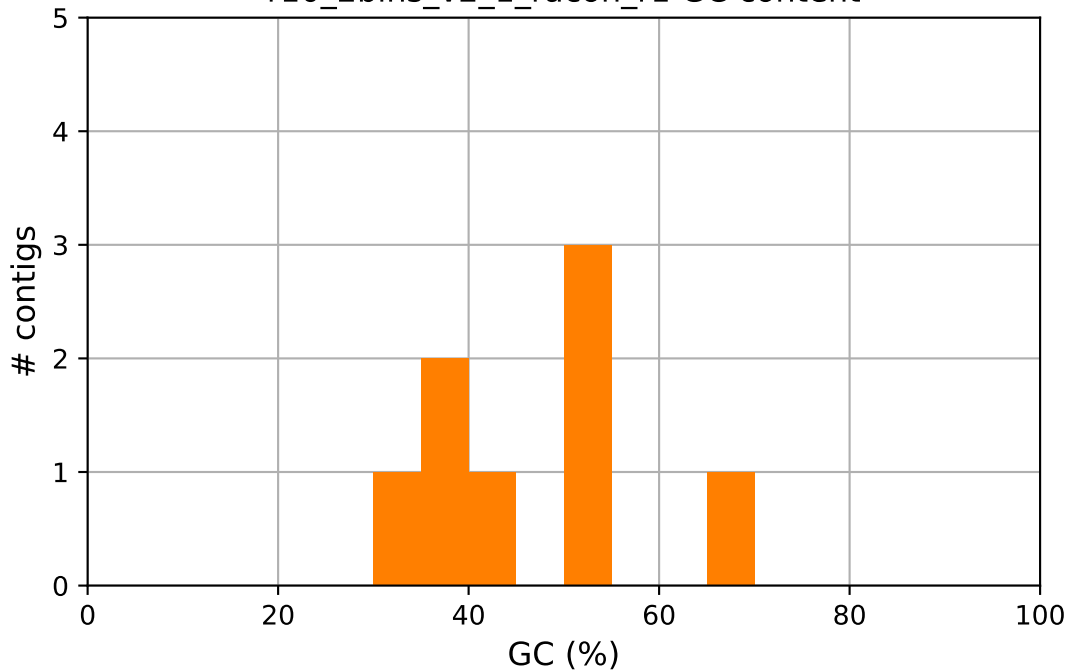
r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka GC content



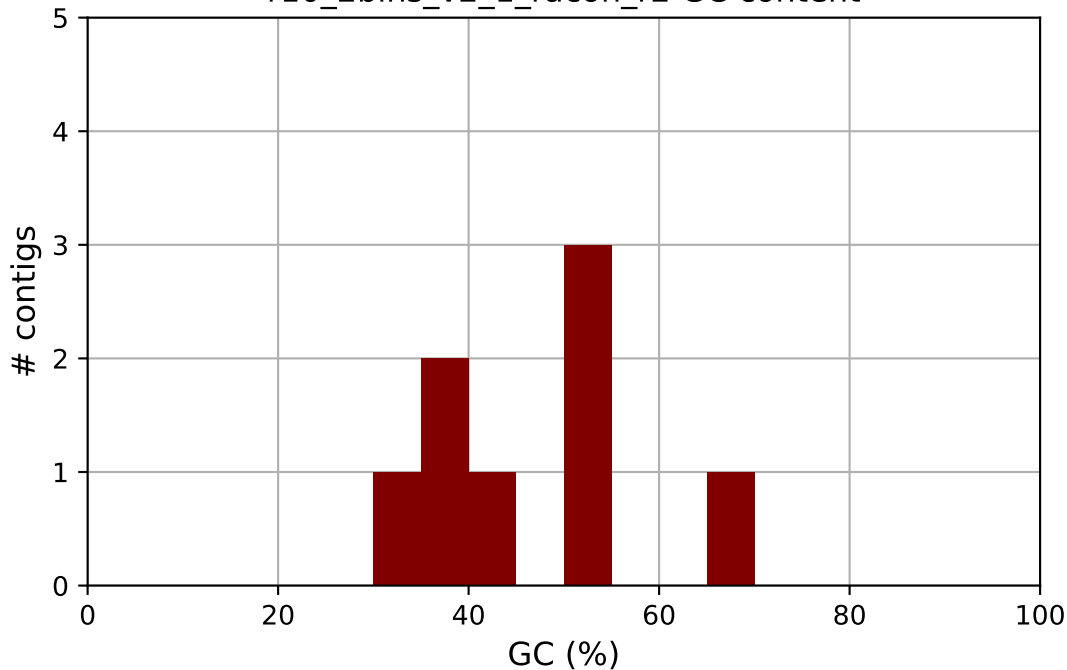
r10_2bins_v2_1_r2_medaka

r10_2bins_v2_1_racon_r1 GC content



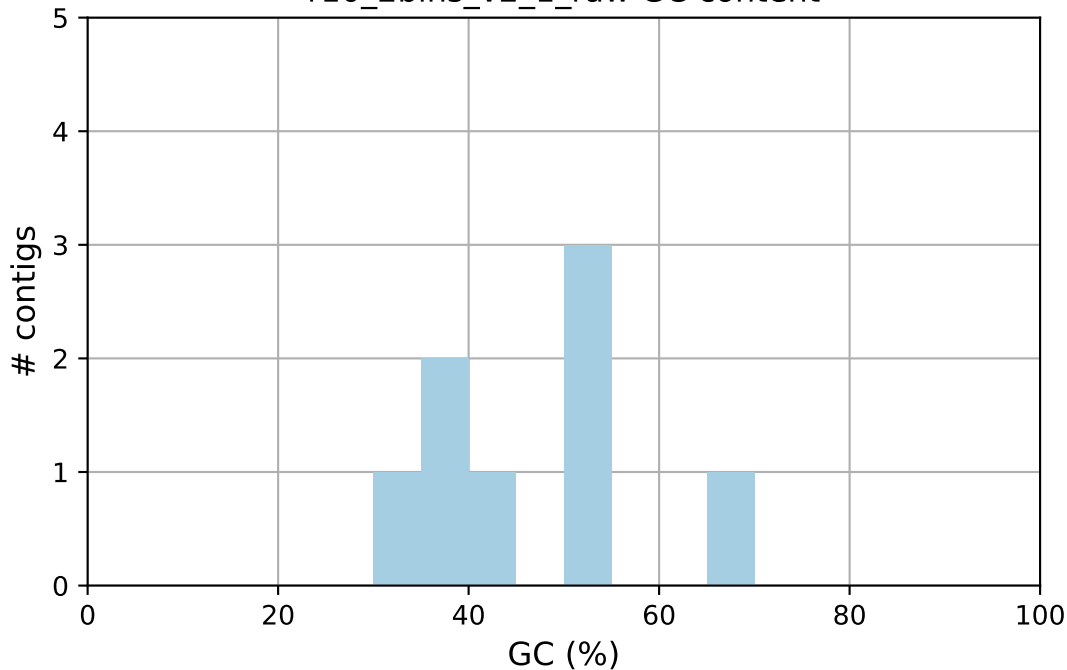
r10_2bins_v2_1_racon_r1

r10_2bins_v2_1_racon_r2 GC content



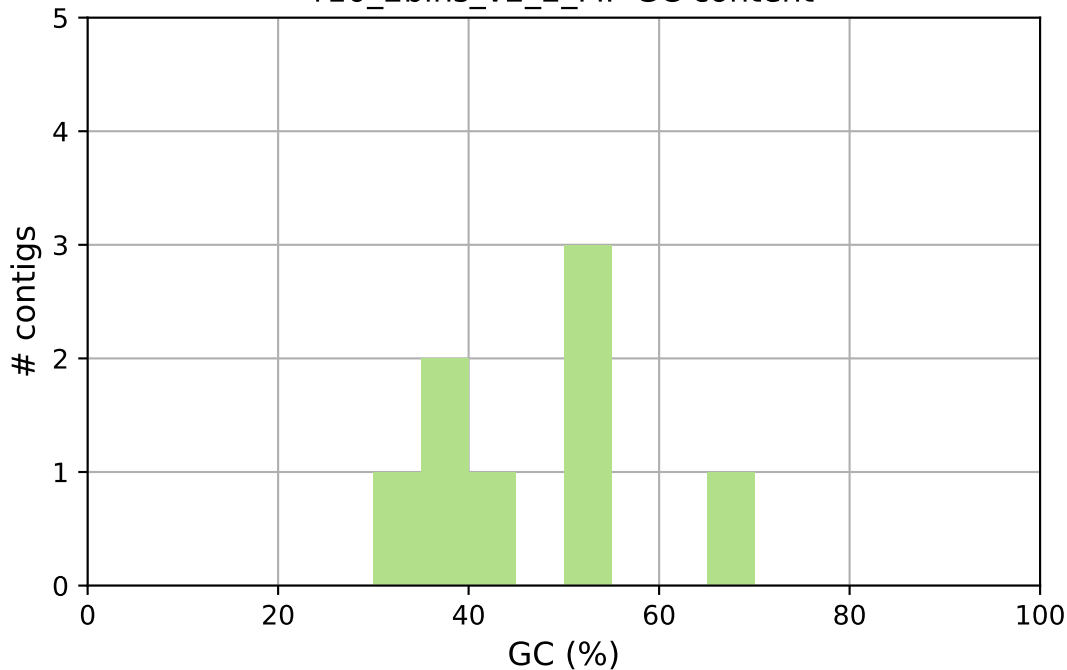
r10_2bins_v2_1_racon_r2

r10_2bins_v2_1_raw GC content



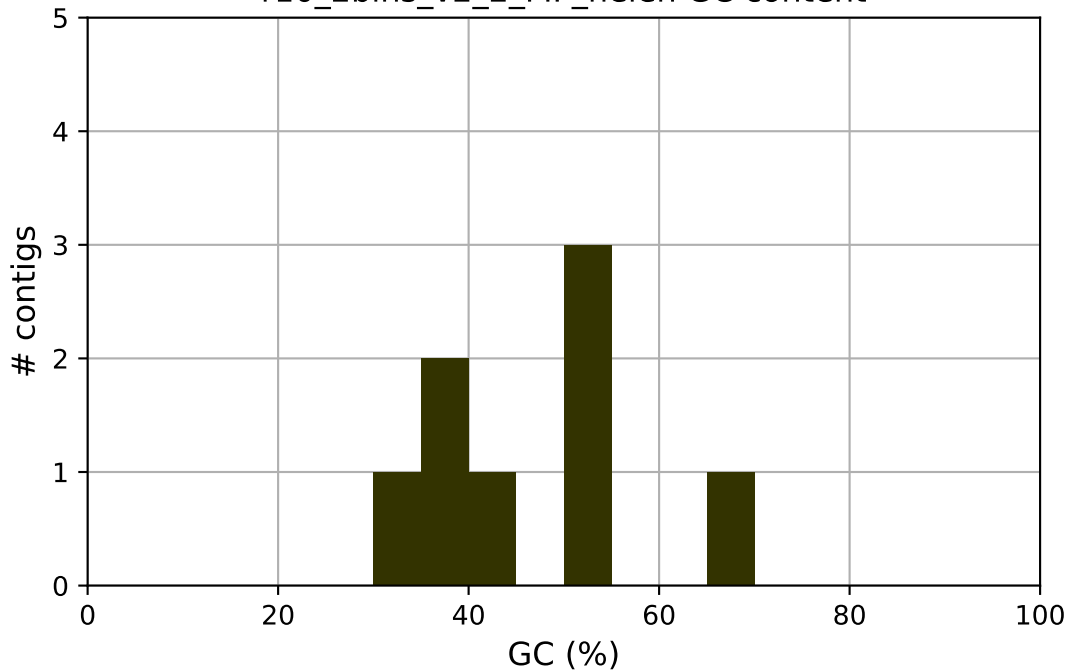
r10_2bins_v2_1_raw

r10_2bins_v2_2_MP GC content



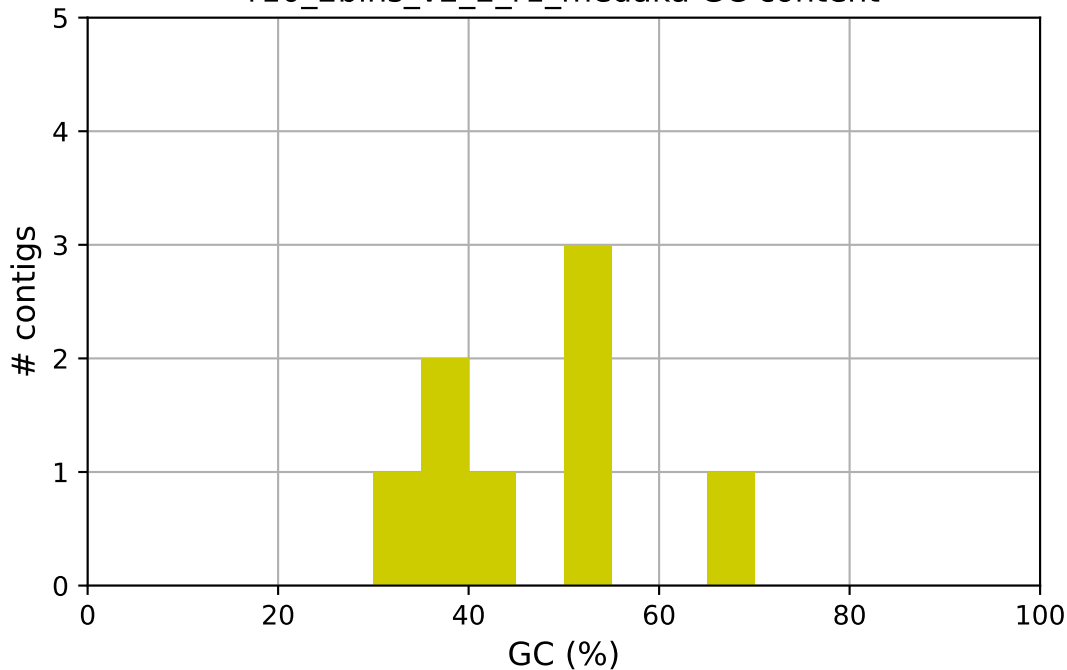
r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen GC content



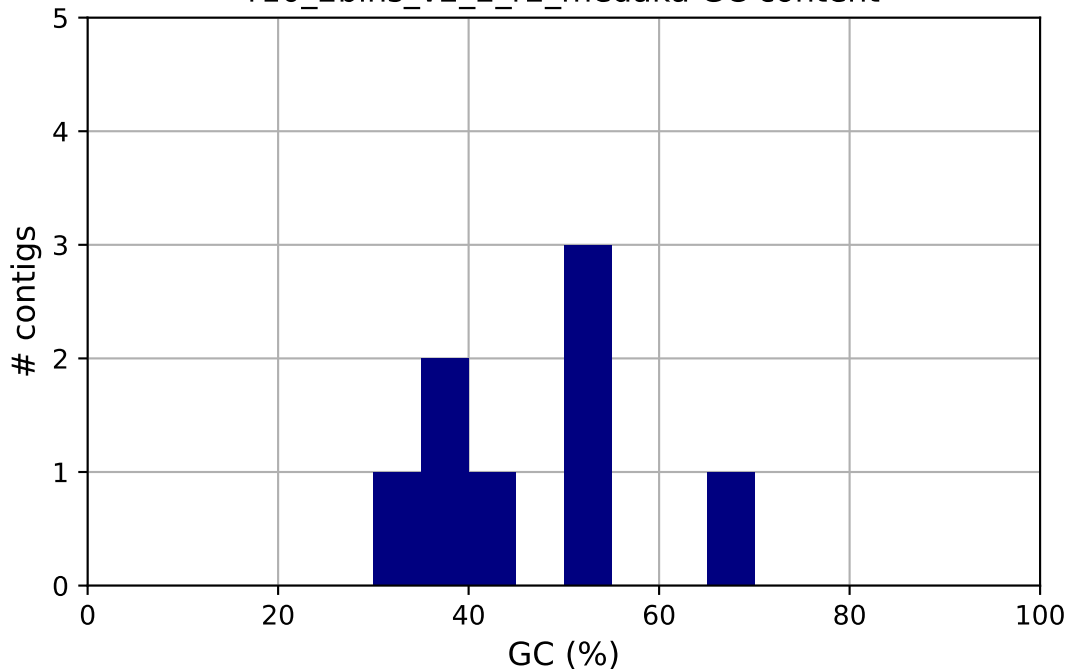
r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka GC content



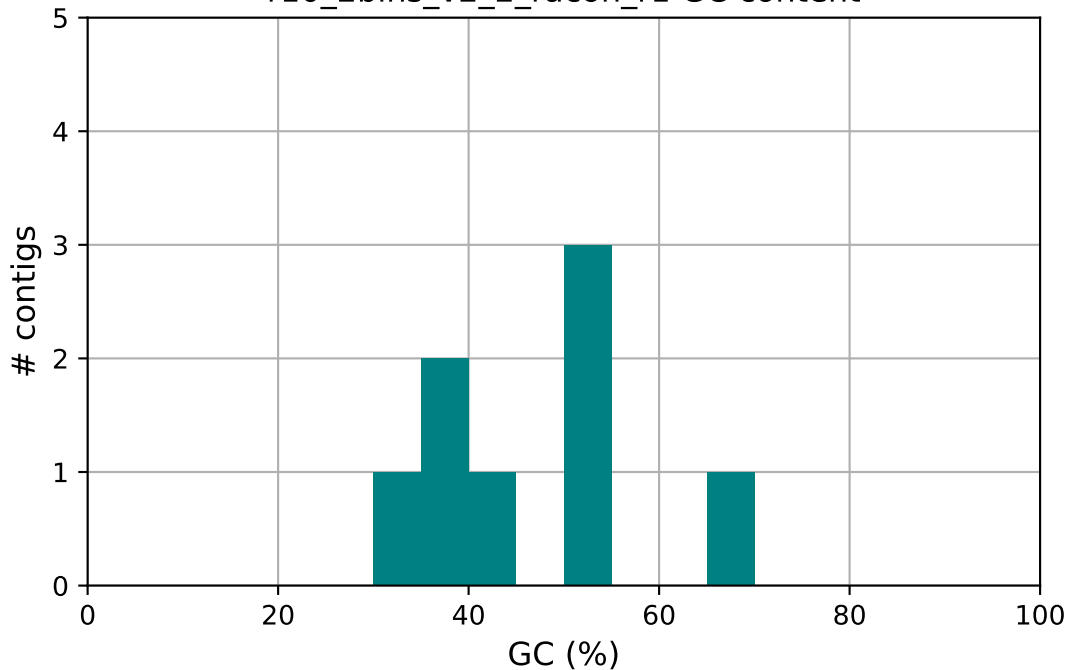
r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka GC content



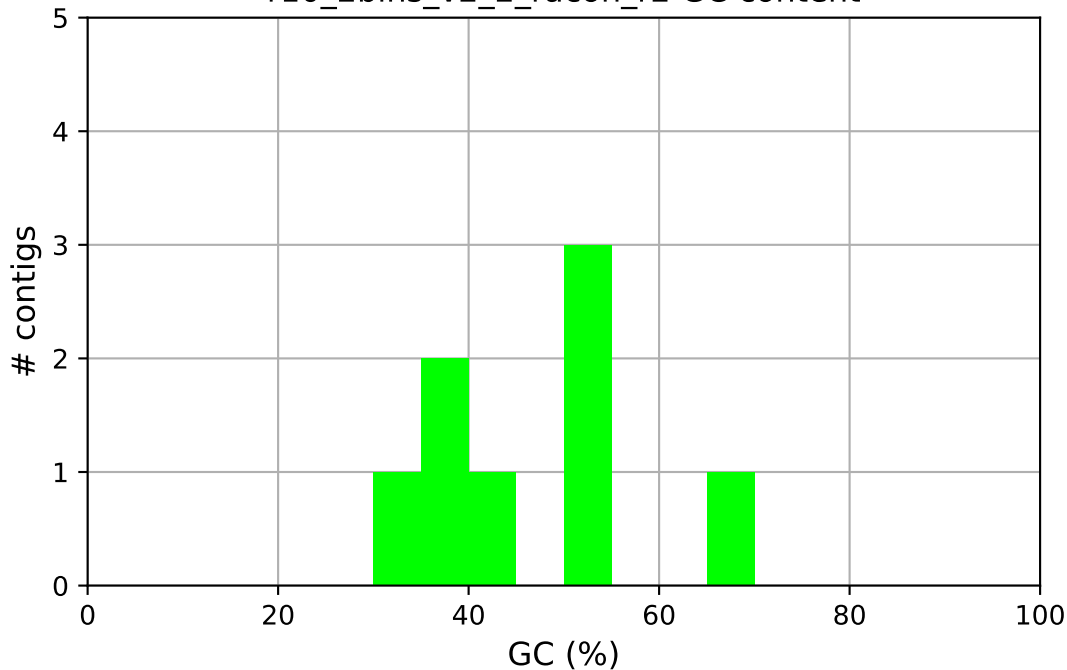
r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1 GC content



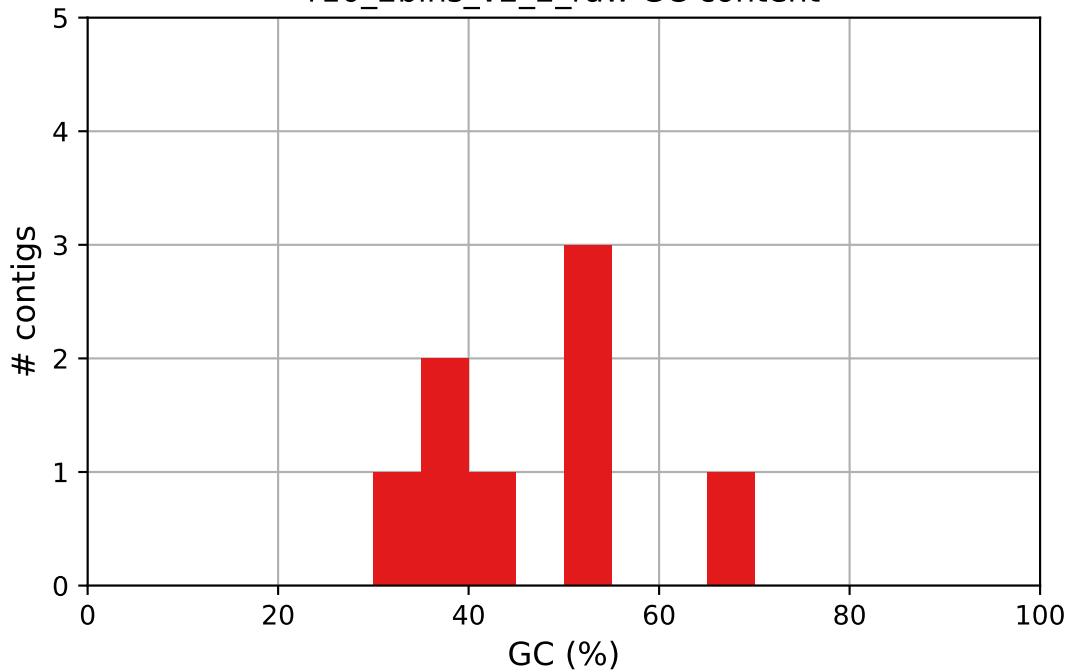
r10_2bins_v2_2_racon_r1

r10_2bins_v2_2_racon_r2 GC content



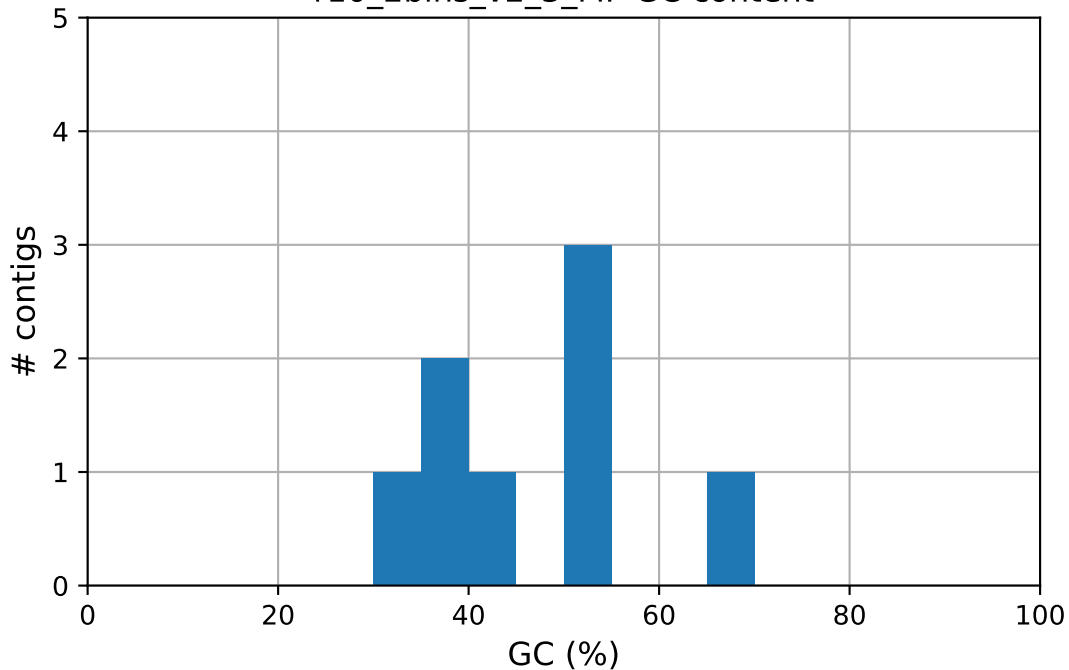
r10_2bins_v2_2_racon_r2

r10_2bins_v2_2_raw GC content



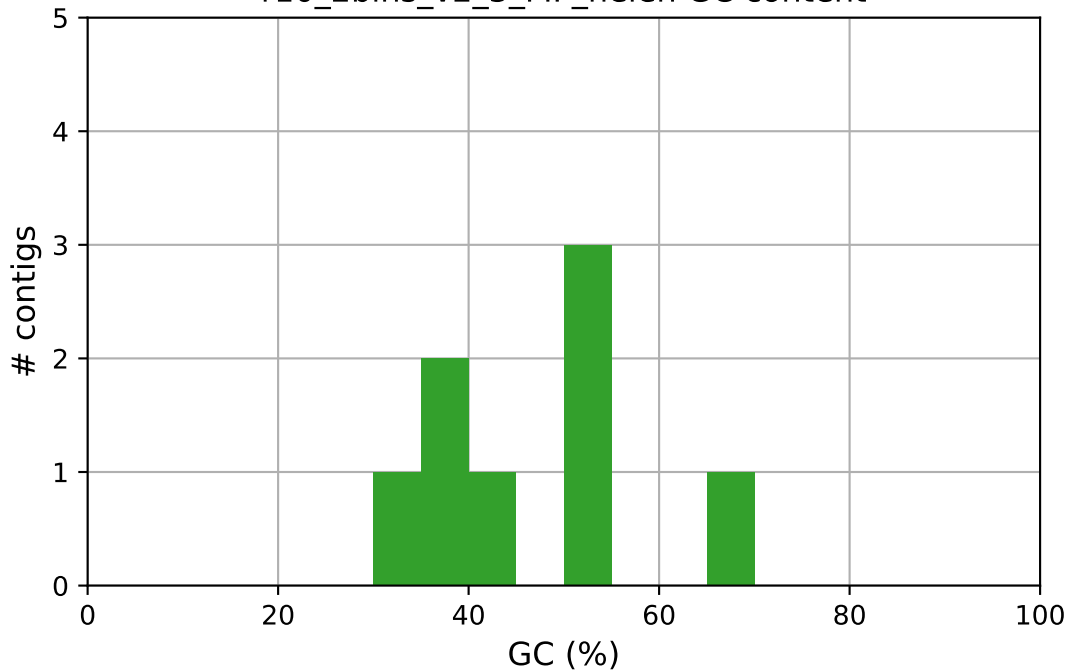
r10_2bins_v2_2_raw

r10_2bins_v2_3_MP GC content



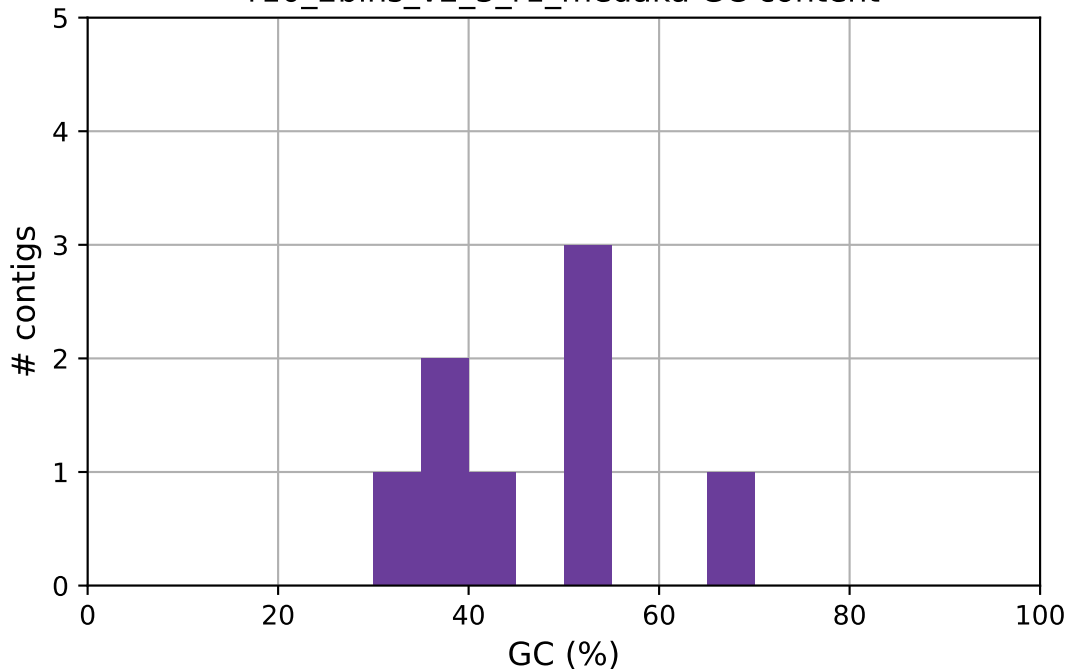
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen GC content



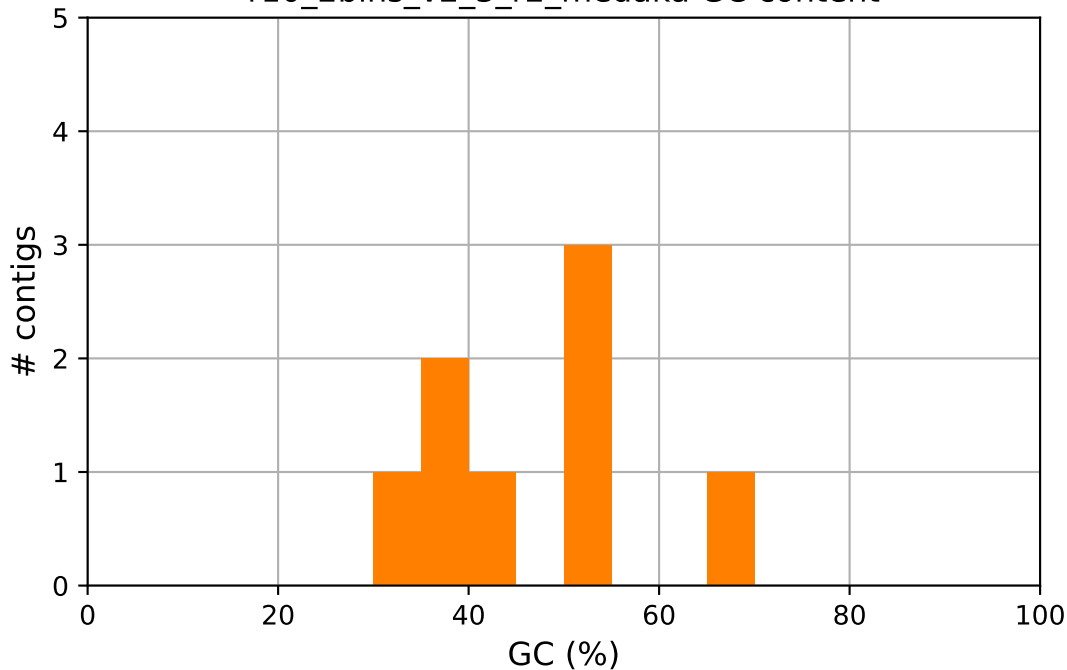
r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka GC content



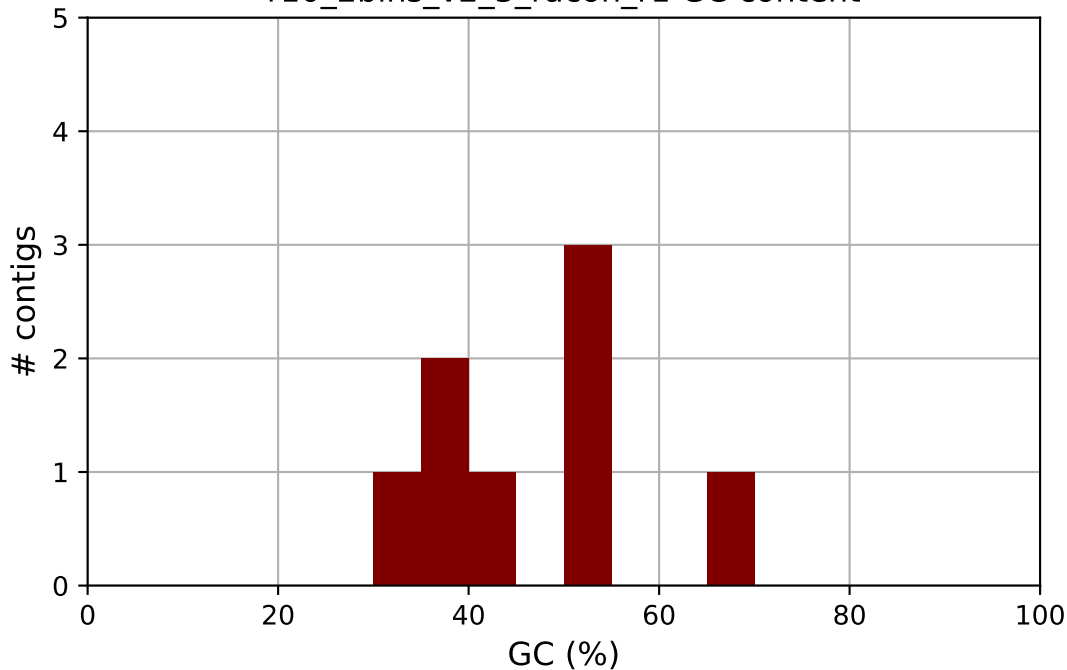
r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka GC content



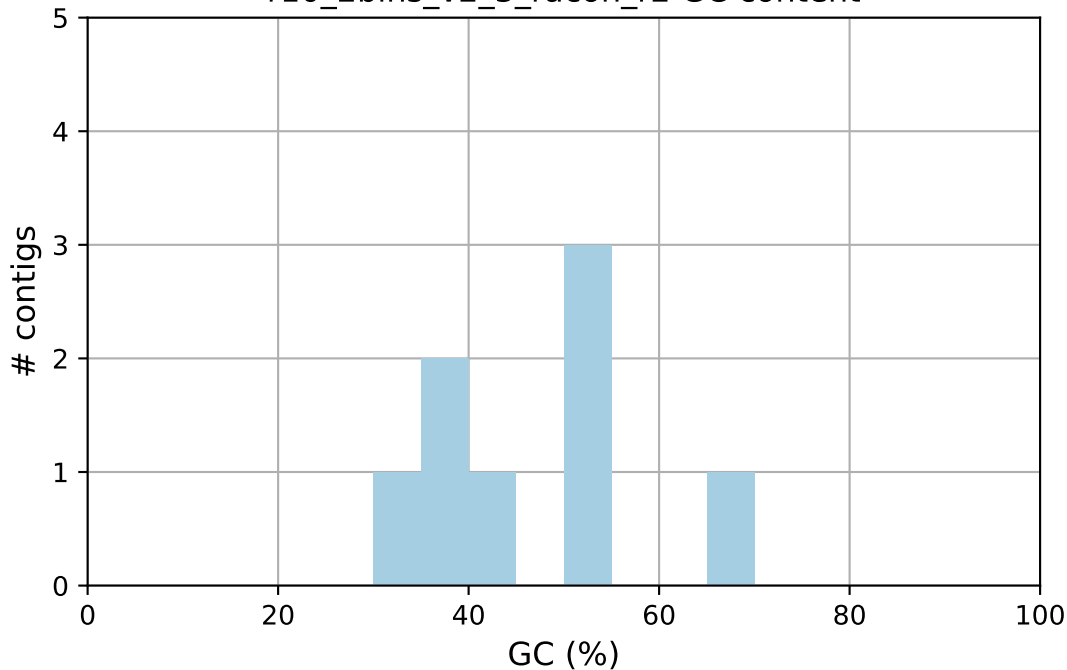
r10_2bins_v2_3_r2_medaka

r10_2bins_v2_3_racon_r1 GC content



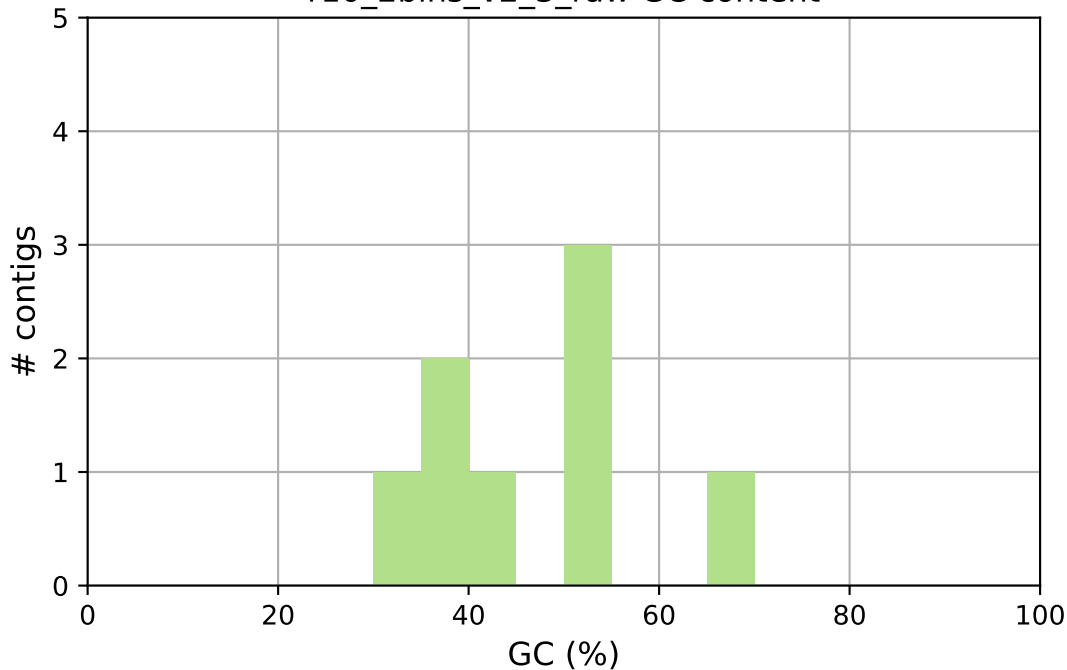
r10_2bins_v2_3_racon_r1

r10_2bins_v2_3_racon_r2 GC content



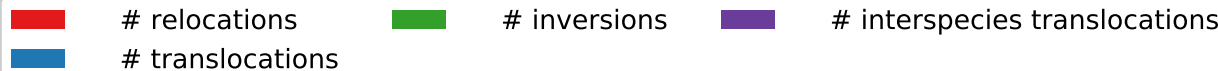
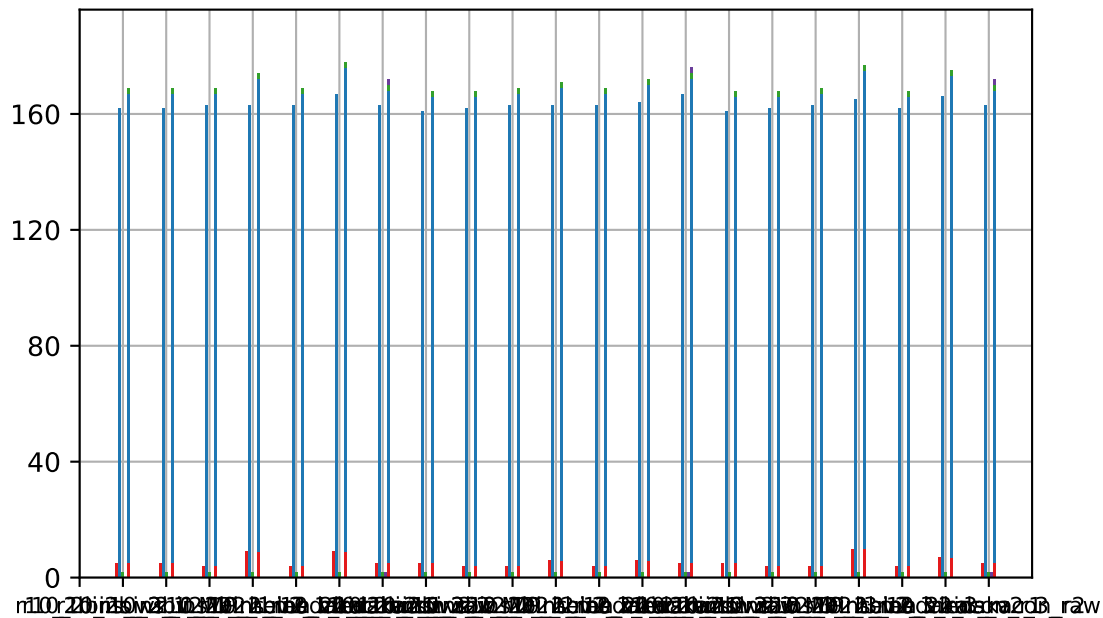
r10_2bins_v2_3_racon_r2

r10_2bins_v2_3_raw GC content

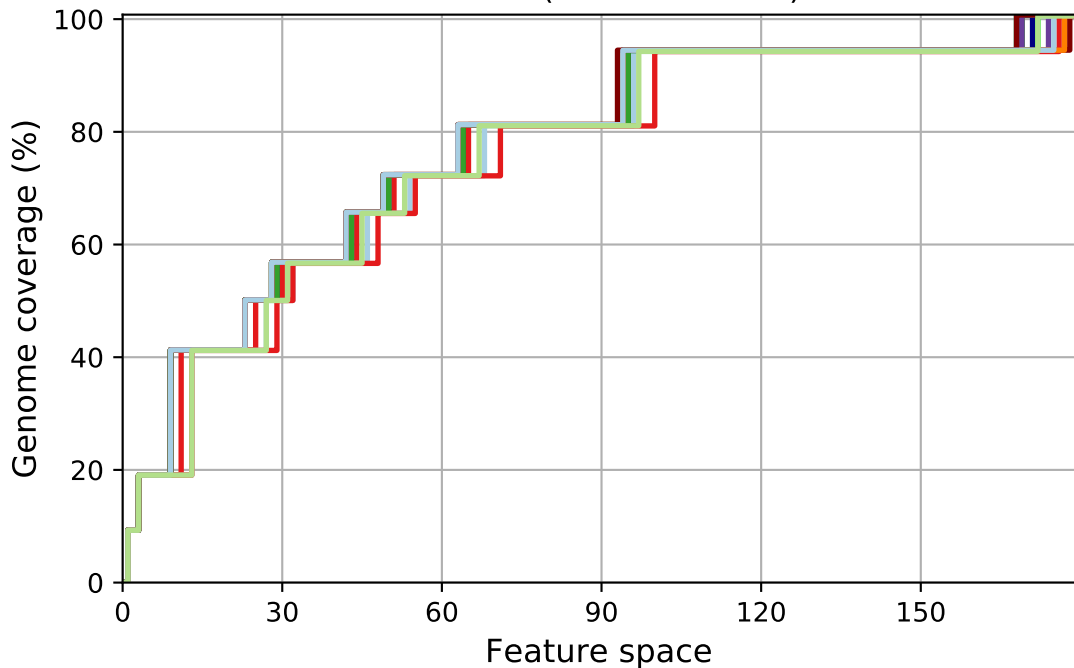


r10_2bins_v2_3_raw

Misassemblies



FRCurve (misassemblies)



r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

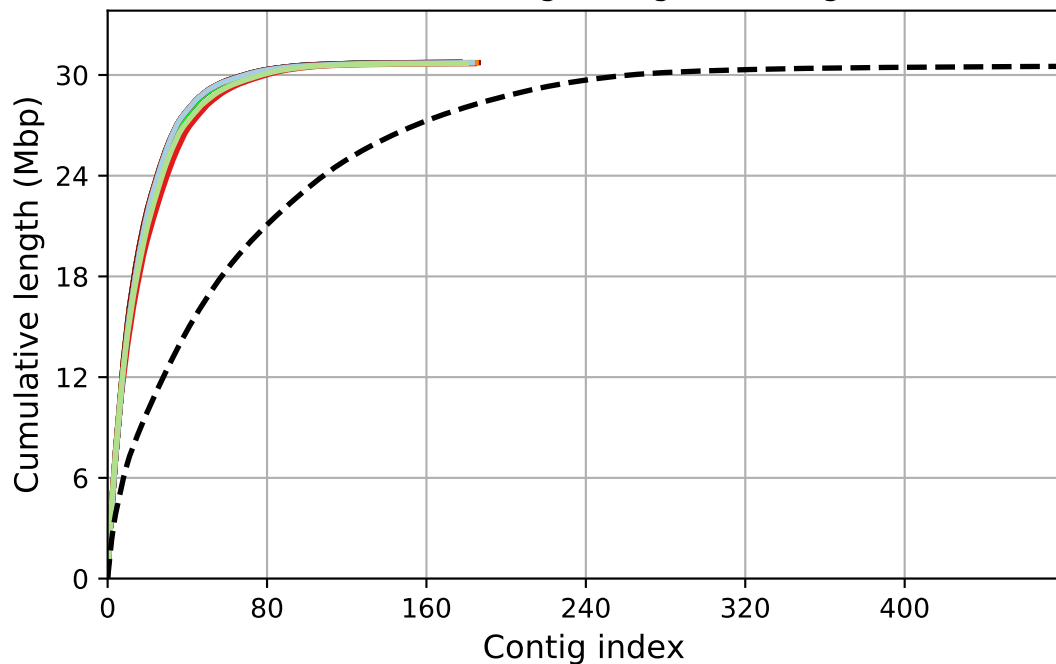
r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka

Cumulative length (aligned contigs)



0_2bins_v2_1_MP

0_2bins_v2_1_MP_helen

0_2bins_v2_1_r1_medaka

0_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_2_racon_r1

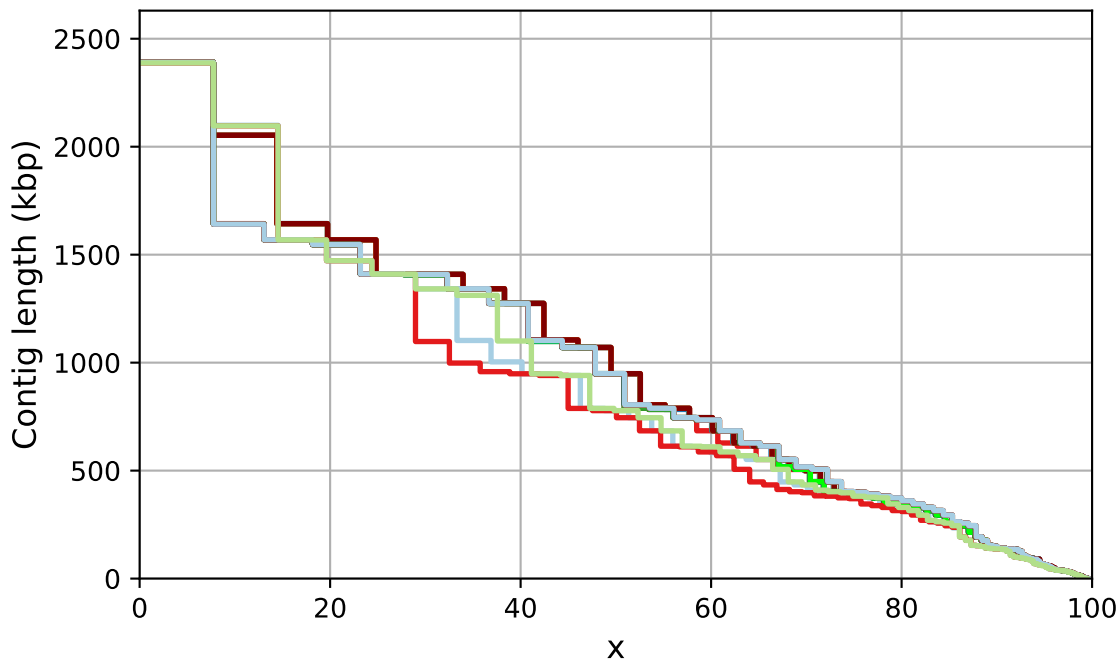
r10_2bins_v2_3_MP

r10_2bins_v2_3_r1

r10_2bins_v2_3_r2

r10_2bins_v2_3_racon_r1

NAx



r10_2bins_v2_1_MP

r10_2bins_v2_2_MP

r10_2bins_v2_3_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_2_MP_helen

r10_2bins_v2_3_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_r2_medaka

Genome fraction, %

100.0

99.5



r10_2bins_v2_1_MP

r10_2bins_v2_1_MP_helen

r10_2bins_v2_1_r1_medaka

r10_2bins_v2_1_r2_medaka

r10_2bins_v2_2_MP

r10_2bins_v2_2_MP_helen

r10_2bins_v2_2_r1_medaka

r10_2bins_v2_2_r2_medaka

r10_2bins_v2_3_MP

r10_2bins_v2_3_MP_helen

r10_2bins_v2_3_r1_medaka

r10_2bins_v2_3_r2_medaka