

Report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# 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)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 1000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 5000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 10000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 25000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Total length (>= 50000 bp)	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792182	6792182	6792182	6792248	6792248	6792248	6792245	6792245	6792245	6792246	6792246	6792246	6791651	6791651	6791651	6791761	6791761	6791761	6788581	6788581	6788581
Total length	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4757850	4758004	4757772	4758987	4759001	4758968	4758591	4758589	4758585	4758094	4758113	4758100	4757969	4758019	4757945	4757915	4757917	4757899	4756101	4755953	4755682
N75	2992057	2992066	2992057	2992056	2992083	2992056	2992047	2992072	2992048	2992047	2992073	2992046	2991930	2991945	2991935	2991941	2991986	2991949	2990626	2990624	2990626
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	170	168	170	170	171	170	168	171	168	168	177	169	168	171	168	171	178	173	172	173	174
# 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	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
# local misassemblies	114	121	117	115	116	117	126	134	122	130	130	128	149	148	145	139	144	139	206	196	209
# 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 + 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 + 7 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	78334	79238	78141	77559	78440	77994	80389	81606	79327	80339	81948	80562	77865	77619	77776	77778	76436	76731	136362	133018	137278
Genome fraction (%)	99.399	99.394	99.399	99.400	99.400	99.400	99.399	99.399	99.399	99.399	99.395	99.399	99.398	99.398	99.398	99.397	99.395	99.397	99.371	99.373	99.368
Duplication ratio	1.044	1.044	1.044	1.044	1.044	1.044	1.044	1.043	1.044	1.044	1.043	1.044	1.043	1.043	1.043	1.043	1.043	1.043	1.027	1.028	1.028
# 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	167.14	168.33	167.79	175.57	176.79	176.43	177.79	175.84	177.91	175.14	174.97	176.56	178.87	177.74	178.06	180.59	178.51	179.28	273.77	275.46	273.62
# indels per 100 kbp	23.20	23.57	23.67	38.49	38.54	38.64	27.16	26.83	26.75	26.41	26.16	26.24	62.35	61.70	62.07	58.03	57.67	58.07	309.74	311.18	307.46
Largest alignment	2719520	2593983	2719520	2719519	2594051	2719519	2719510	2594058	2719511	2719510	2594056	2719509	2719399	2593948	2719404	2719430	2593973	2719433	2718120	2589938	2718166
Total aligned length	30741396	30752516	30751752	30745916	30753243	30756160	30742019	30749368	30753312	30733107	30734452	30746514	30730889	30738104	30744934	30730647	30736448	30737040	30677538	30690651	30685123
NA50	948395	1070324	948397	949083	949084	949081	948951	1070329	948995	948963	1070329	948996	949205	1070253	949230	949216	1070270	949250	777741	788154	777733
NA75	394044	381362	391214	394057	381621	391220	394044	381538	391209	394045	381556	391212	393993	381631	391199	394011	381663	391194	369864	373707	373676
LA50	10	10	10	10	11	10	10	10	10	10	10	10	10	10	10	10	10	10	11	11	11
LA75	22	23	22	23	24	23	22	23	22	22	23	22	22	23	22	22	23	22	25	25	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

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	170	168	170	170	171	170	168	171	168	168	177	169	168	171	168	171	178	173	172	173	174
# contig misassemblies	170	168	170	170	171	170	168	171	168	168	177	169	168	171	168	171	178	173	172	173	174
# c. relocations	5	4	5	6	6	6	5	4	5	5	10	5	5	4	5	5	7	5	6	5	6
# c. translocations	163	162	163	162	163	162	161	165	161	161	165	162	161	165	161	164	169	166	162	164	164
# 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	0	0	0	0	0	0	0	0	0	0	0	0	2	2	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	30864326	30862898	30864265	30868202	30867654	30868747	30867074	30864387	30867120	30860600	30852160	30863991	30855559	30852449	30856954	30853010	30845161	30854277	30851140	30849756	30850081
# possibly misassembled contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# possible misassemblies	98	98	96	96	98	96	96	94	96	96	98	100	98	96	98	94	90	92	166	160	166
# local misassemblies	114	121	117	115	116	117	126	134	122	130	130	128	149	148	145	139	144	139	206	196	209
# 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	253	252	252	252	252	253	251	253	253	252	253	250	249	250	249	249	250	178	183	179
# 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	50687	51047	50884	53243	53613	53504	53916	53326	53952	53113	53061	53545	54244	53901	53999	54764	54132	54367	83001	83514	82951
# indels	7035	7147	7177	11674	11689	11718	8237	8135	8112	8009	7934	7958	18909	18712	18822	17598	17489	17611	93904	94345	93211
# indels (<= 5 bp)	6379	6505	6525	11026	11037	11077	7638	7537	7511	7411	7336	7364	18255	18047	18163	16965	16849	16959	92688	93126	92000
# indels (> 5 bp)	656	642	652	648	652	641	599	598	601	598	598	594	654	665	659	633	640	652	1216	1219	1211
Indels length	41151	40882	41156	45874	45977	45700	41219	41050	40941	40950	40759	40685	57370	56924	57003	54371	54254	55312	158337	159179	156651

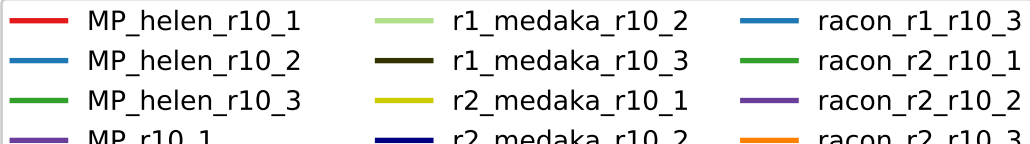
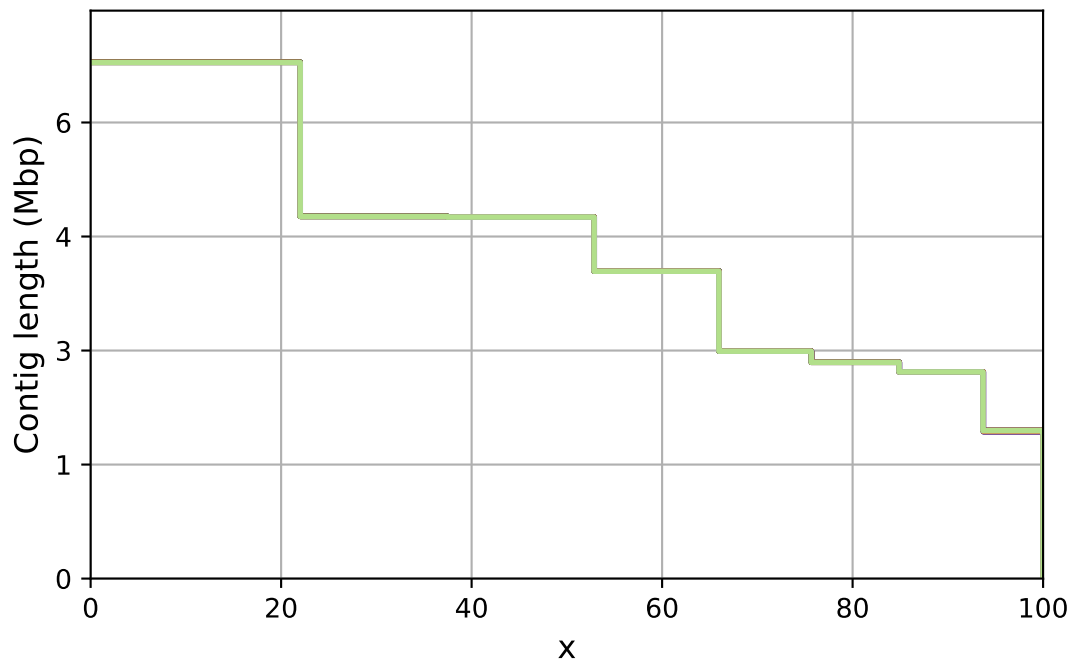
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

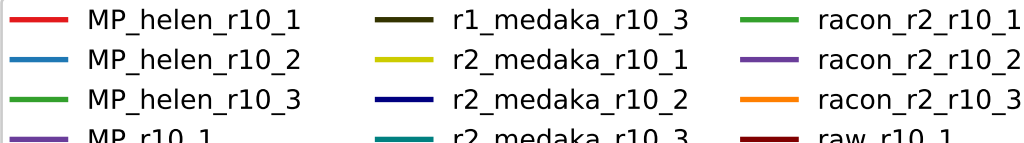
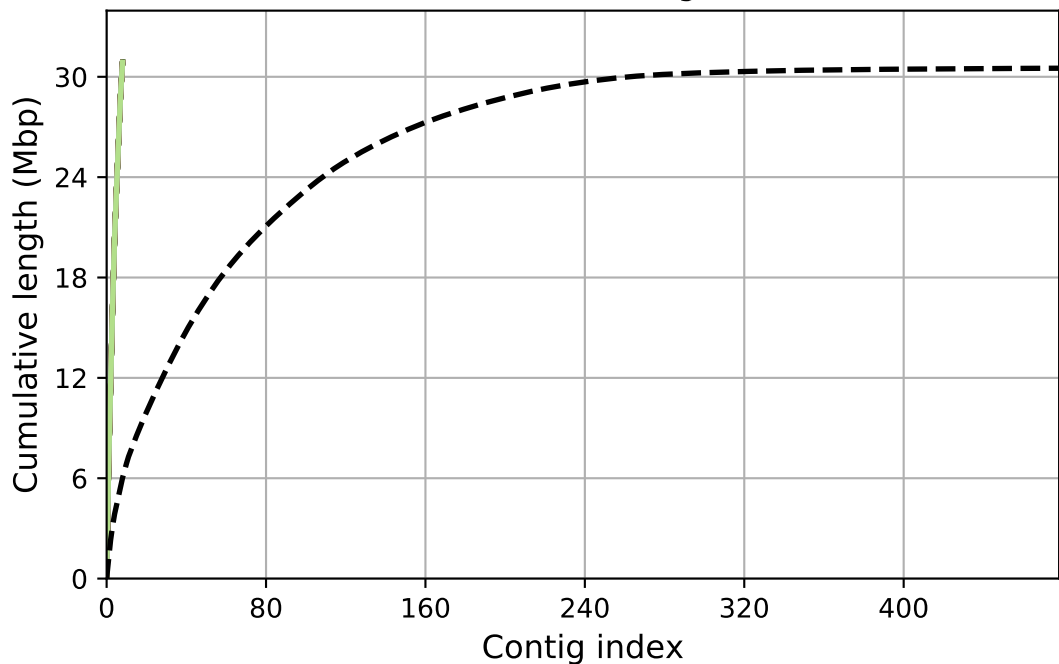
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Partially unaligned length	78334	79238	78141	77559	78440	77994	80389	81606	79327	80339	81948	80562	77865	77619	77776	77778	76436	76731	136362	133018	137278
# 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 ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

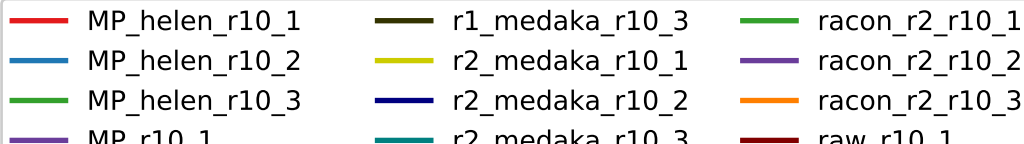
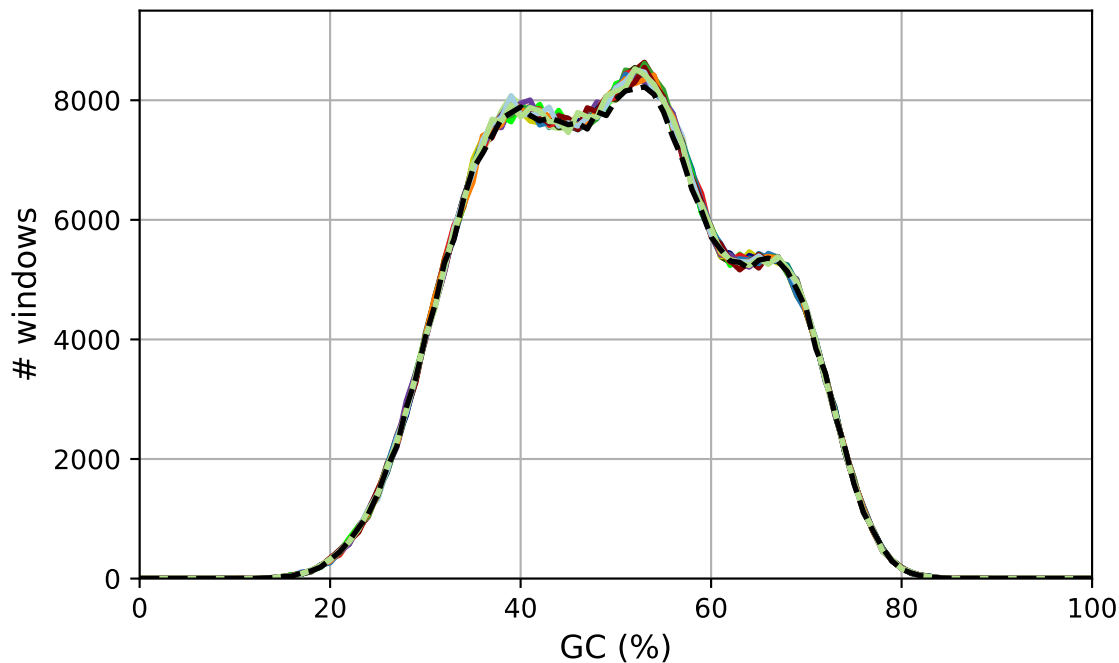
Nx



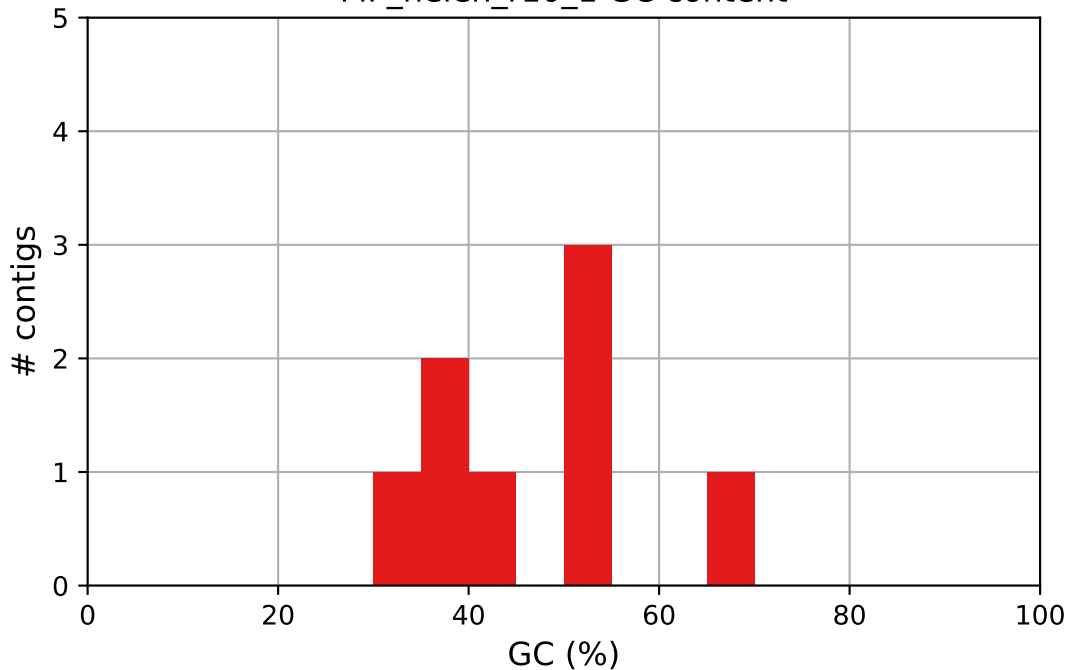
Cumulative length



GC content

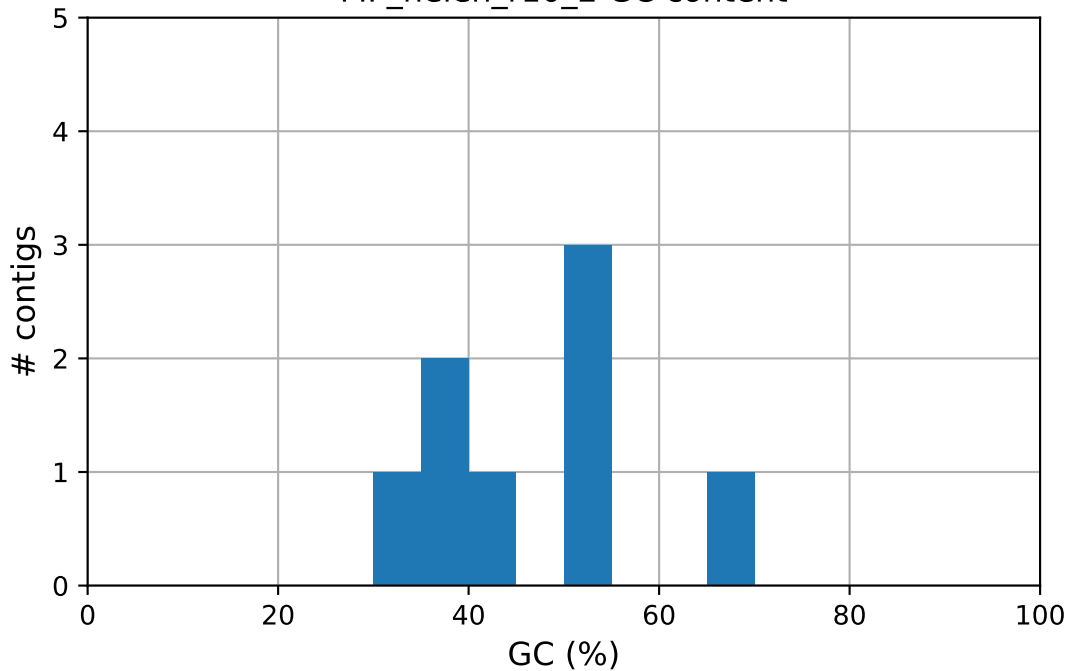


MP_helen_r10_1 GC content



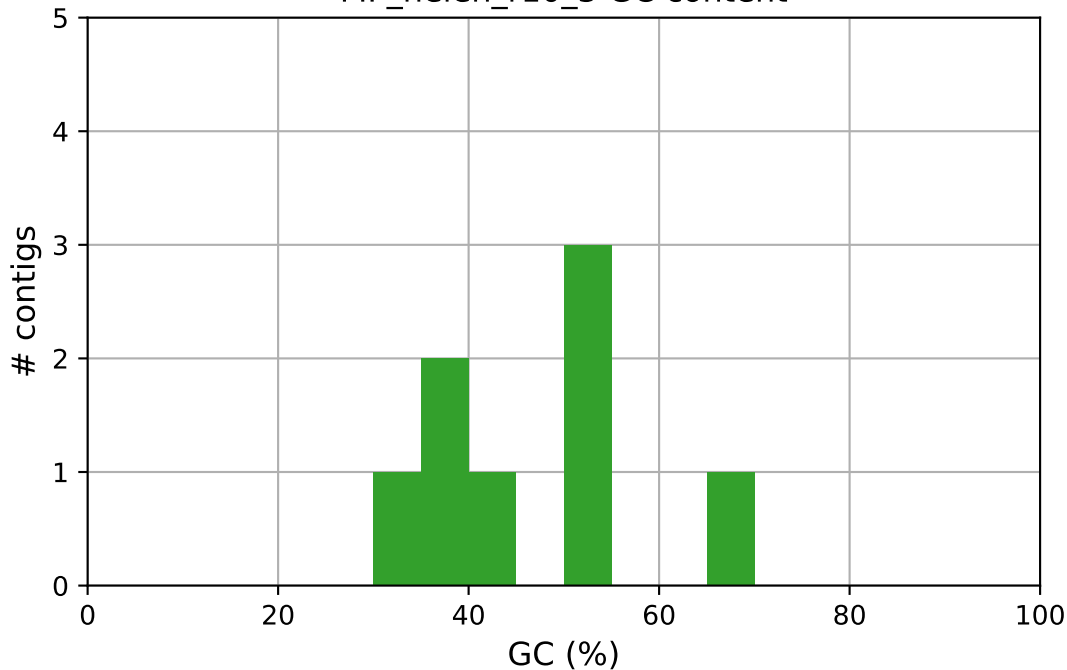
MP_helen_r10_1

MP_helen_r10_2 GC content



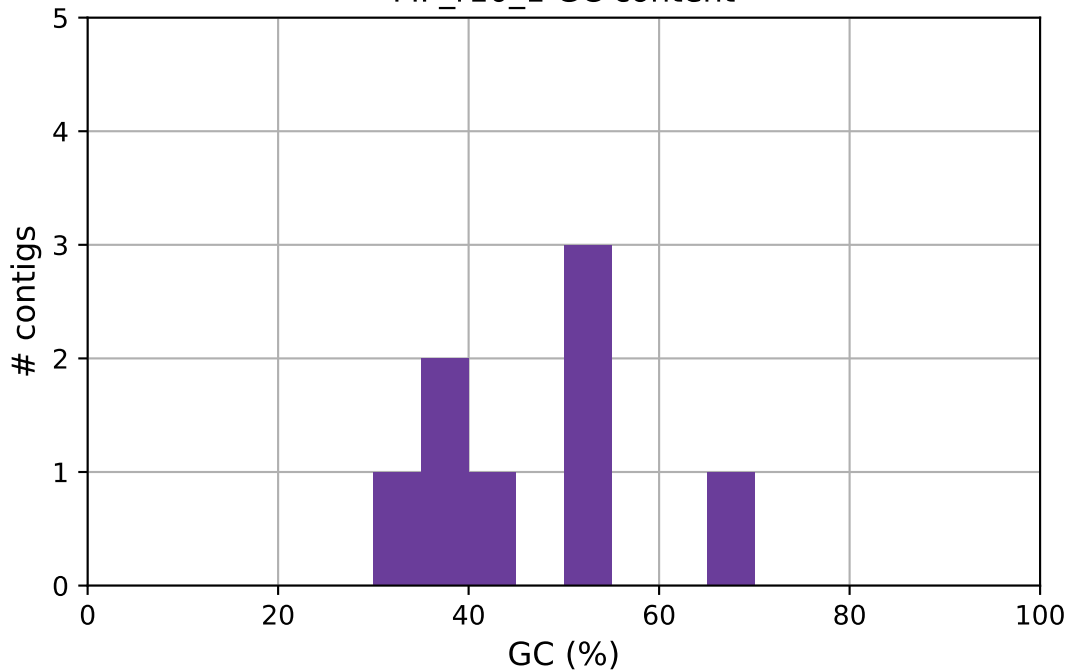
MP_helen_r10_2

MP_helen_r10_3 GC content



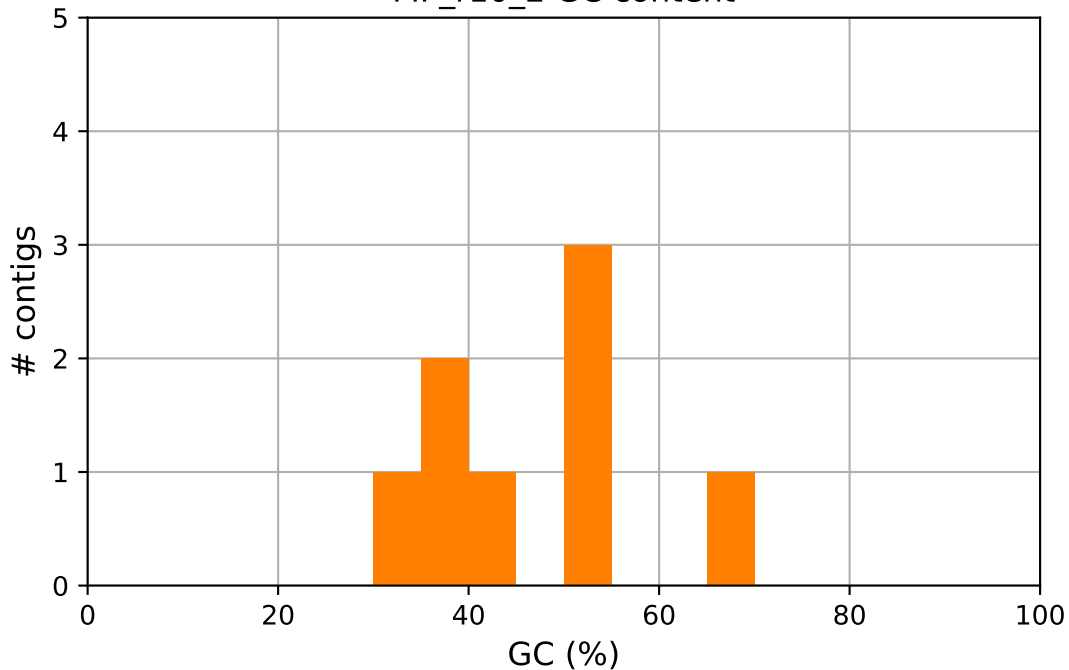
MP_helen_r10_3

MP_r10_1 GC content



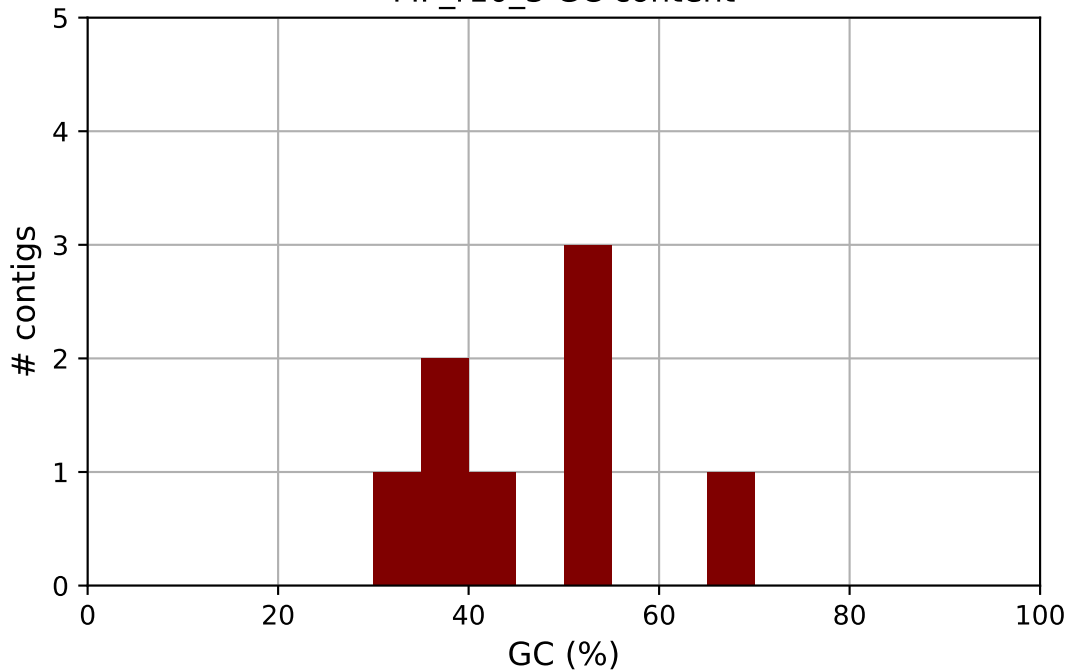
MP_r10_1

MP_r10_2 GC content



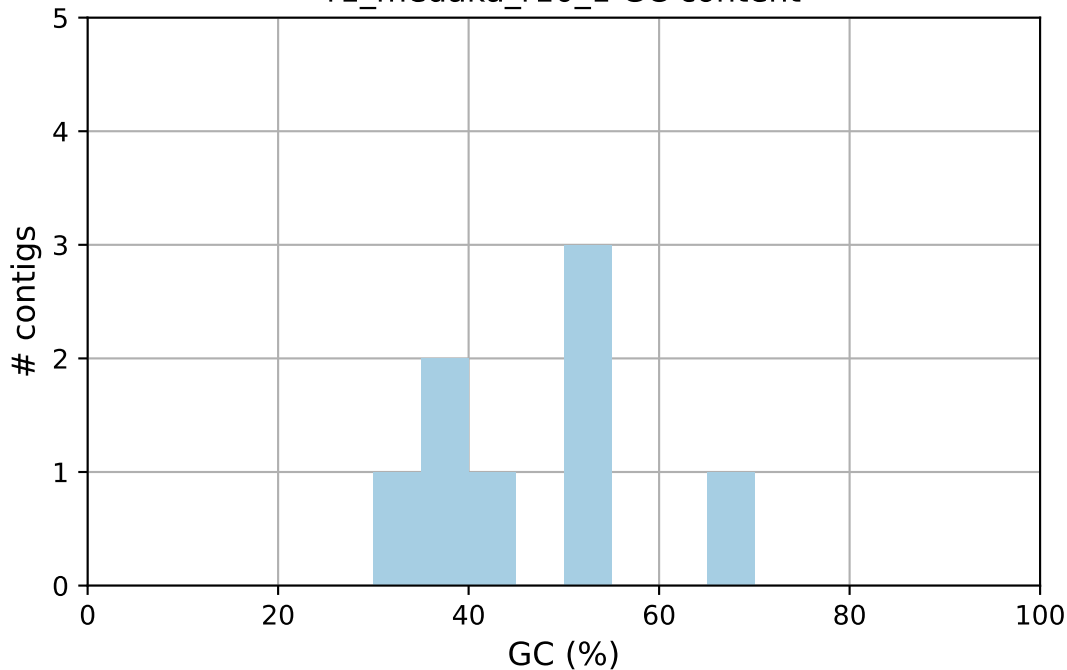
MP_r10_2

MP_r10_3 GC content



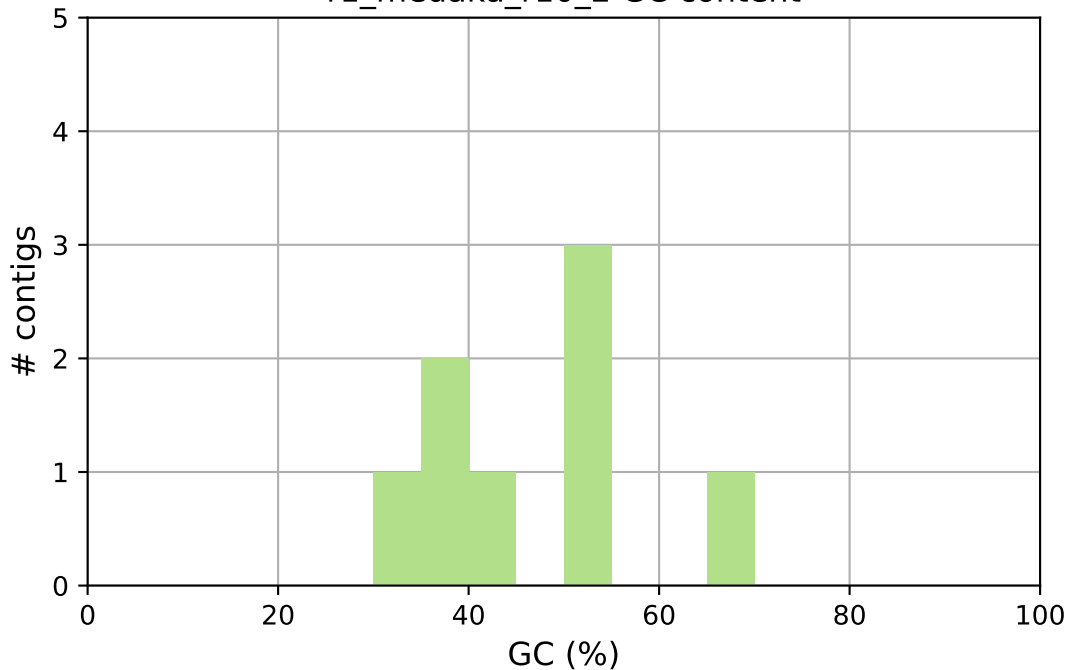
MP_r10_3

r1_medaka_r10_1 GC content



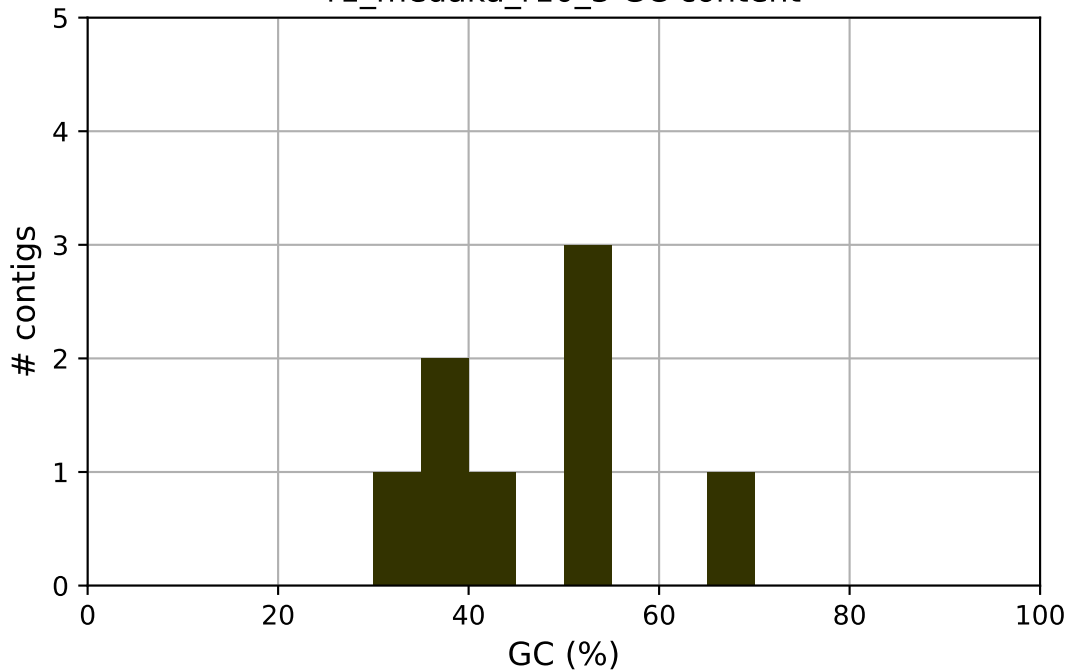
r1_medaka_r10_1

r1_medaka_r10_2 GC content



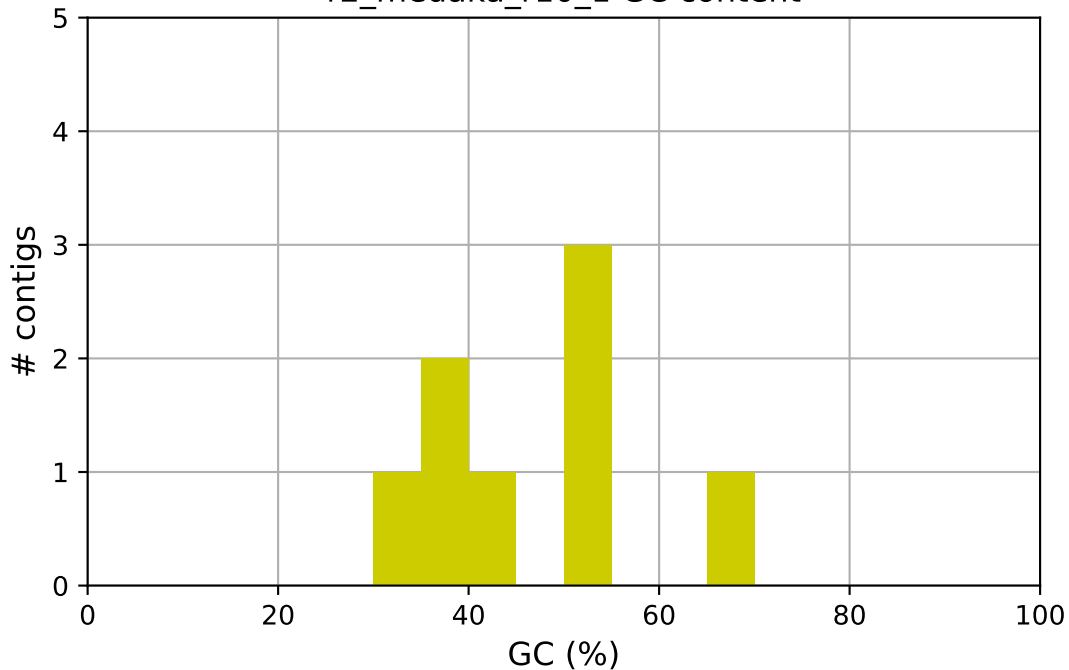
r1_medaka_r10_2

r1_medaka_r10_3 GC content



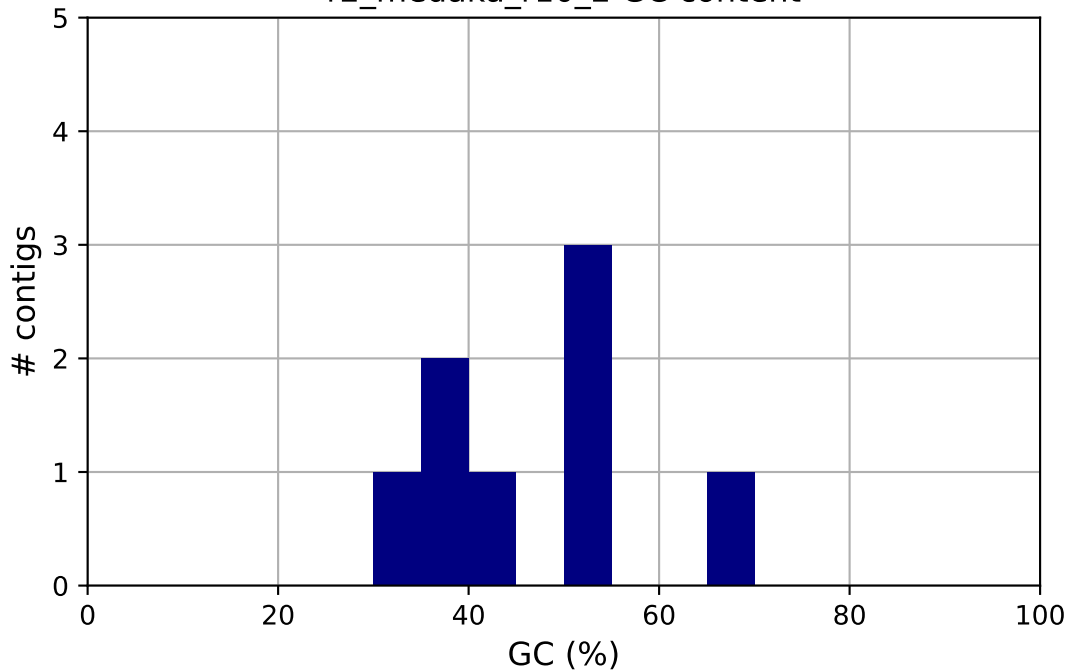
r1_medaka_r10_3

r2_medaka_r10_1 GC content



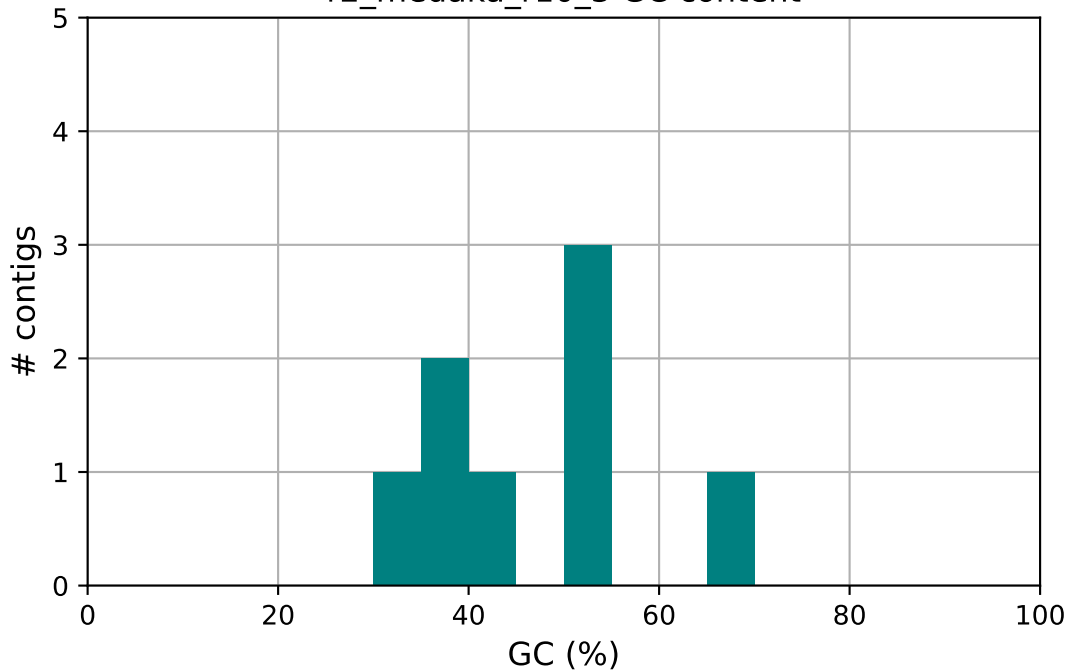
r2_medaka_r10_1

r2_medaka_r10_2 GC content



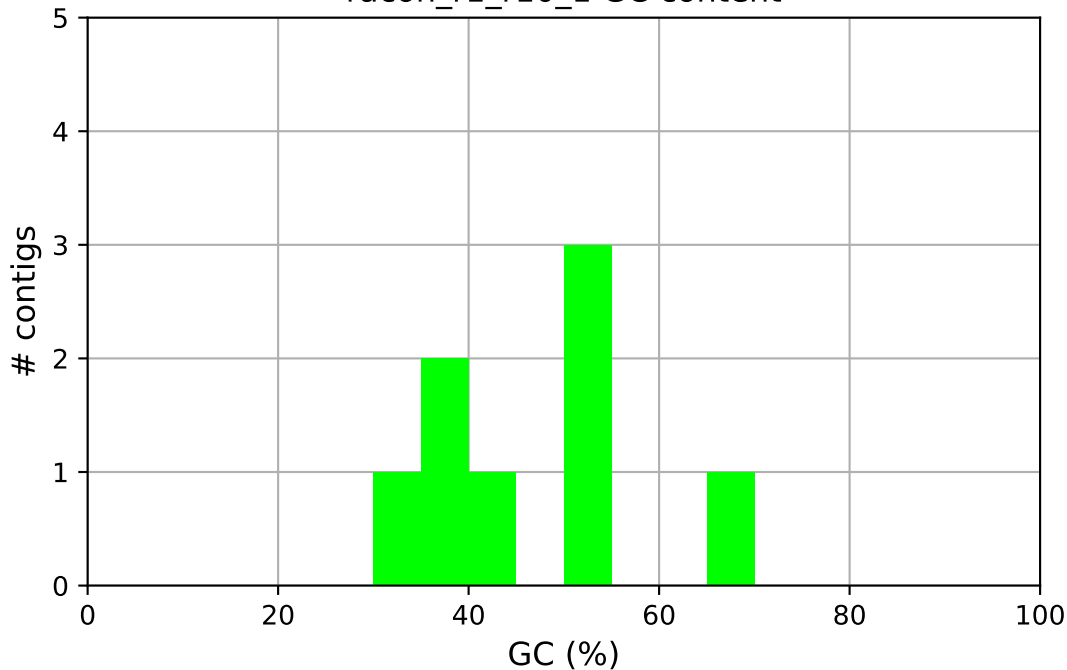
r2_medaka_r10_2

r2_medaka_r10_3 GC content



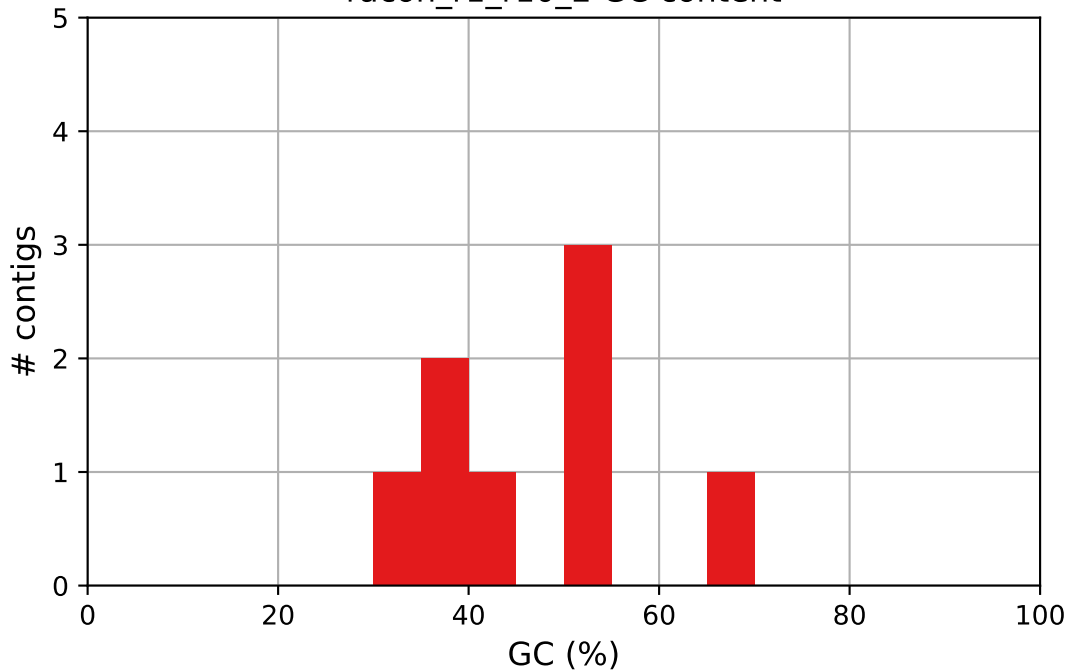
r2_medaka_r10_3

racon_r1_r10_1 GC content



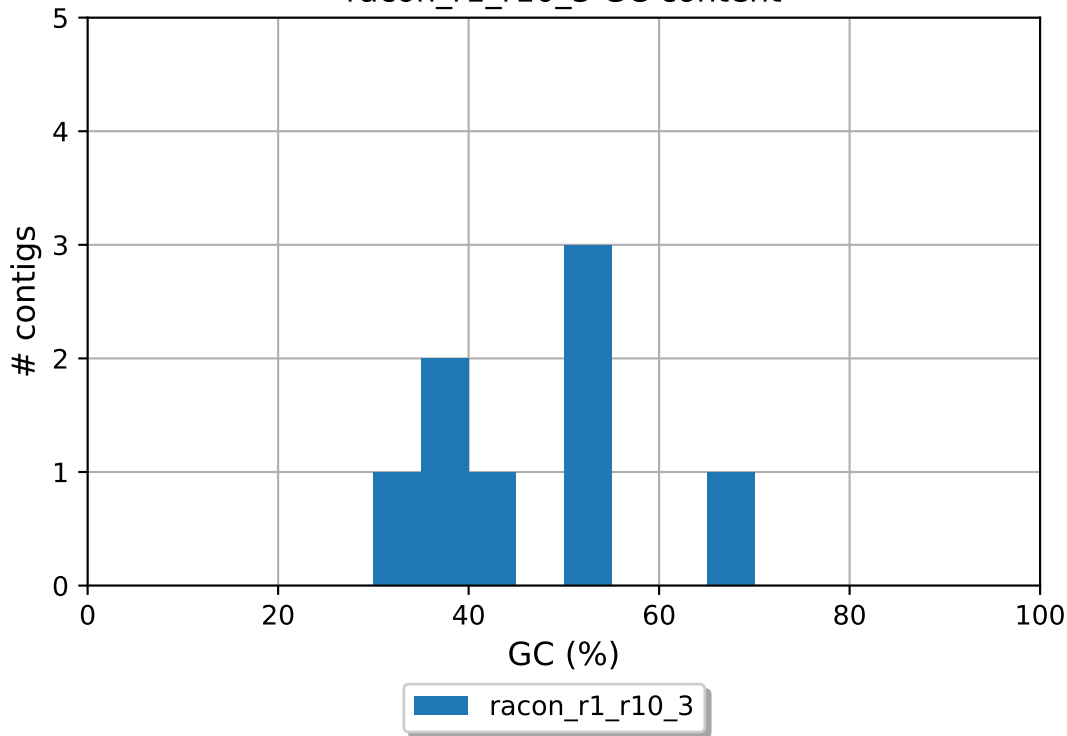
racon_r1_r10_1

racon_r1_r10_2 GC content

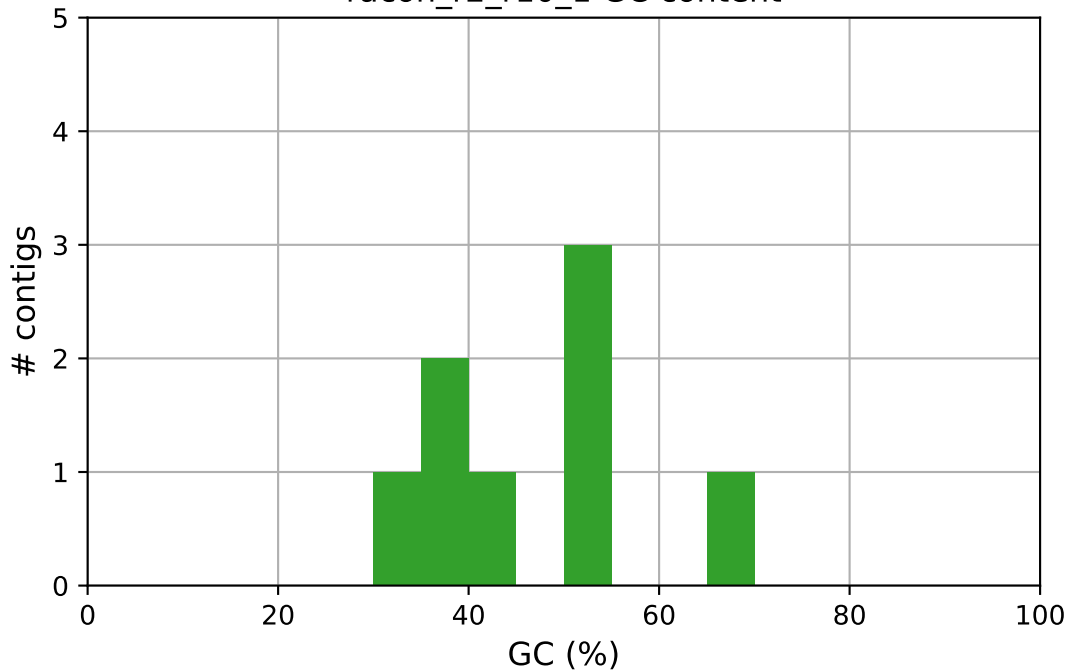


racon_r1_r10_2

racon_r1_r10_3 GC content

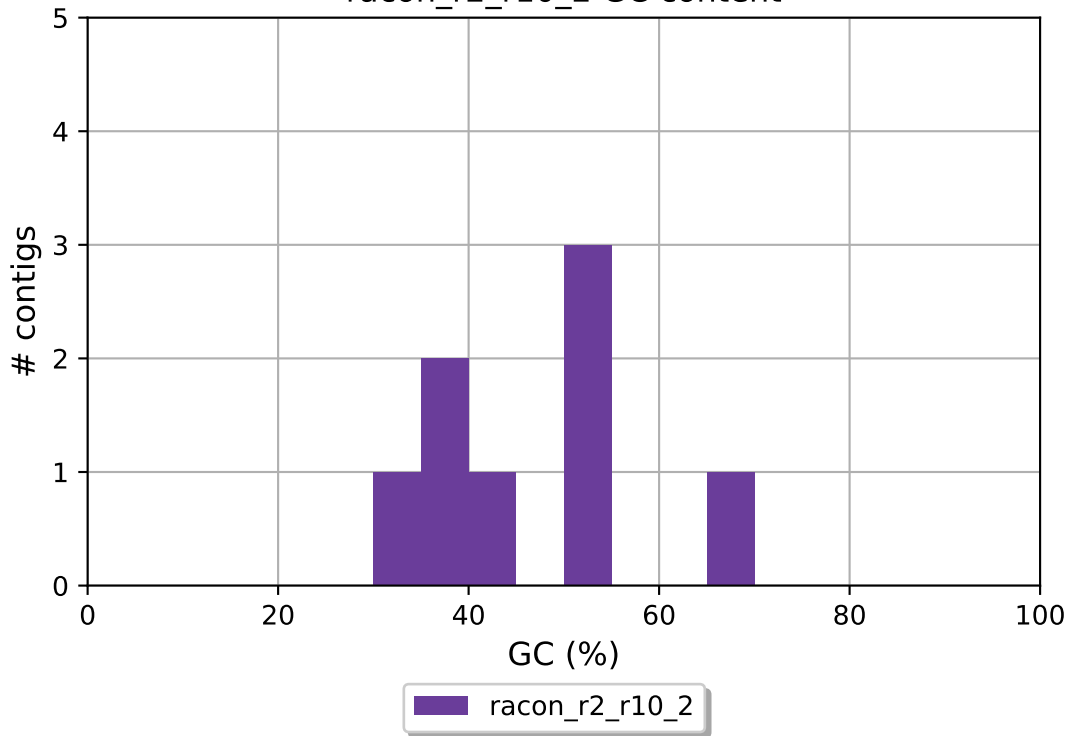


racon_r2_r10_1 GC content

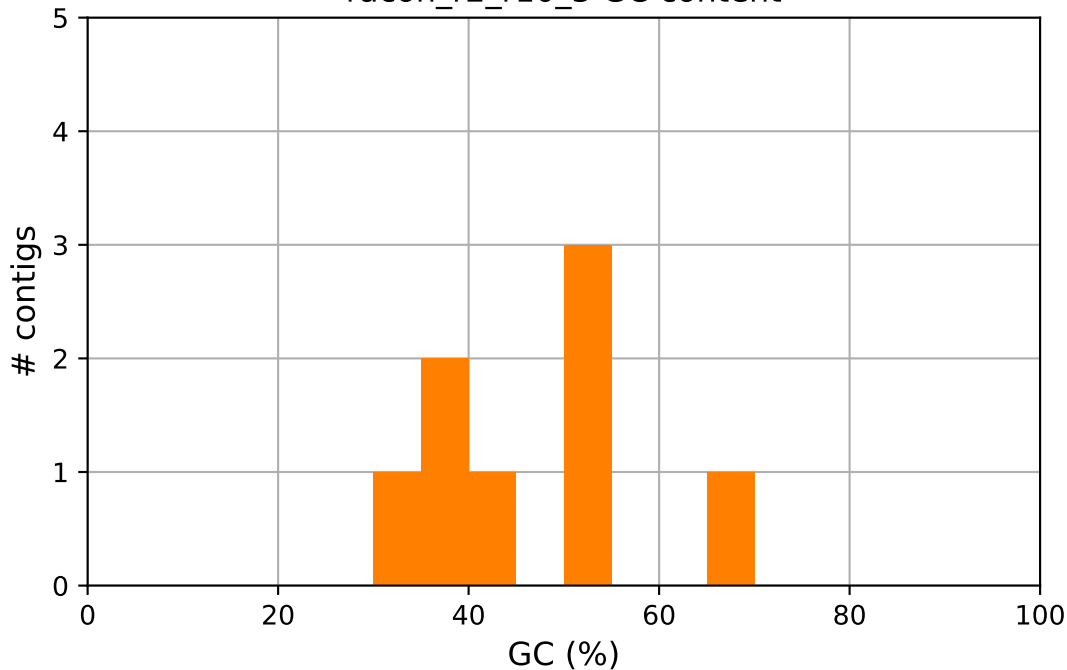


racon_r2_r10_1

racon_r2_r10_2 GC content

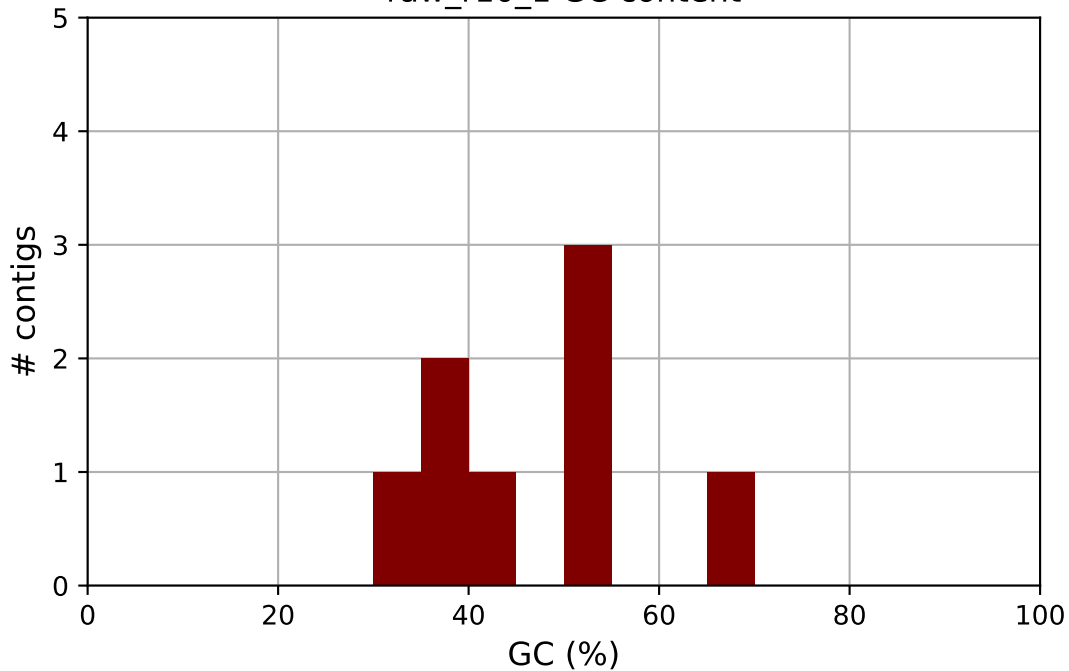


racon_r2_r10_3 GC content



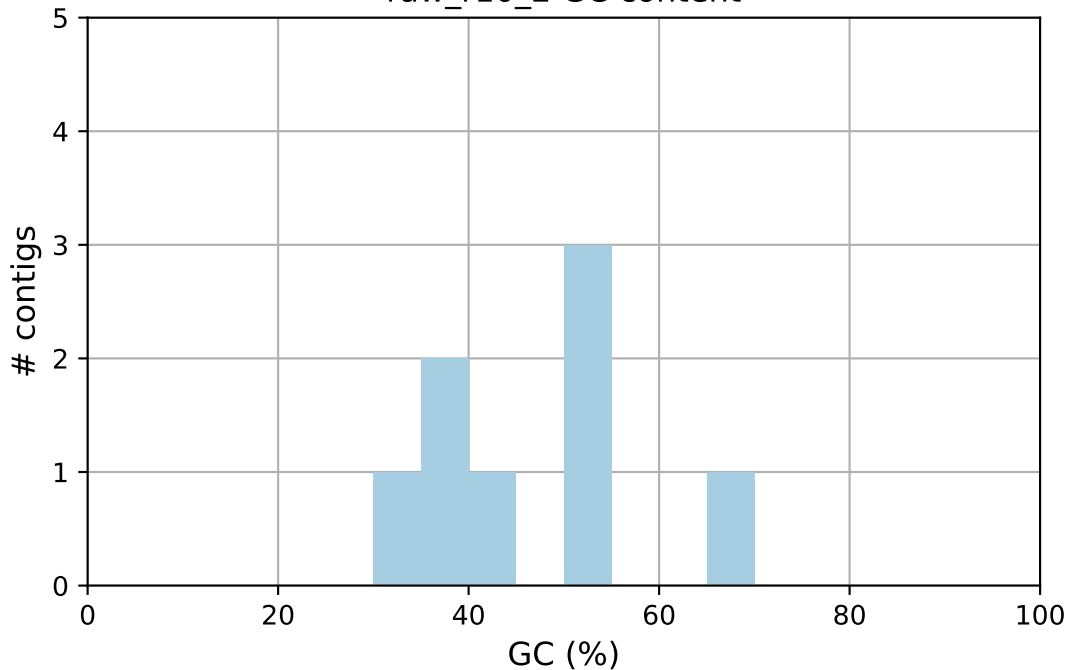
racon_r2_r10_3

raw_r10_1 GC content



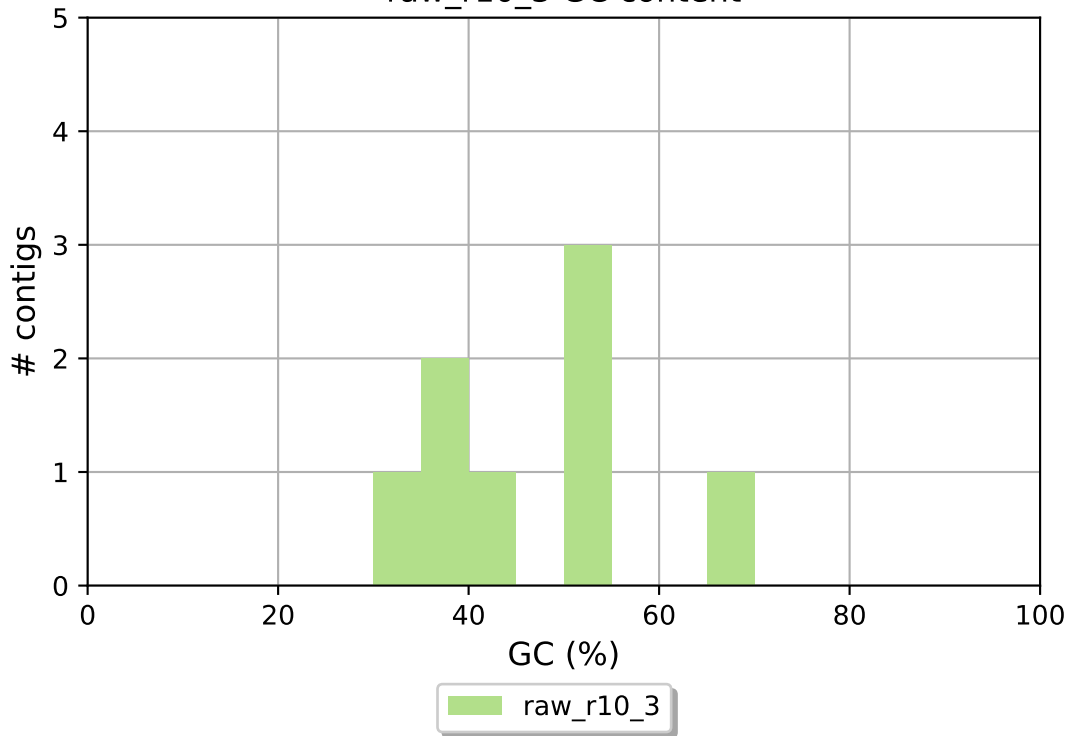
raw_r10_1

raw_r10_2 GC content

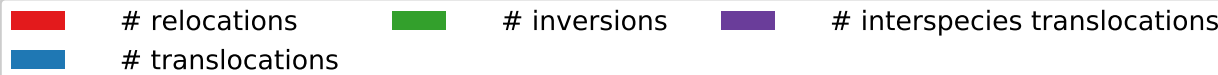
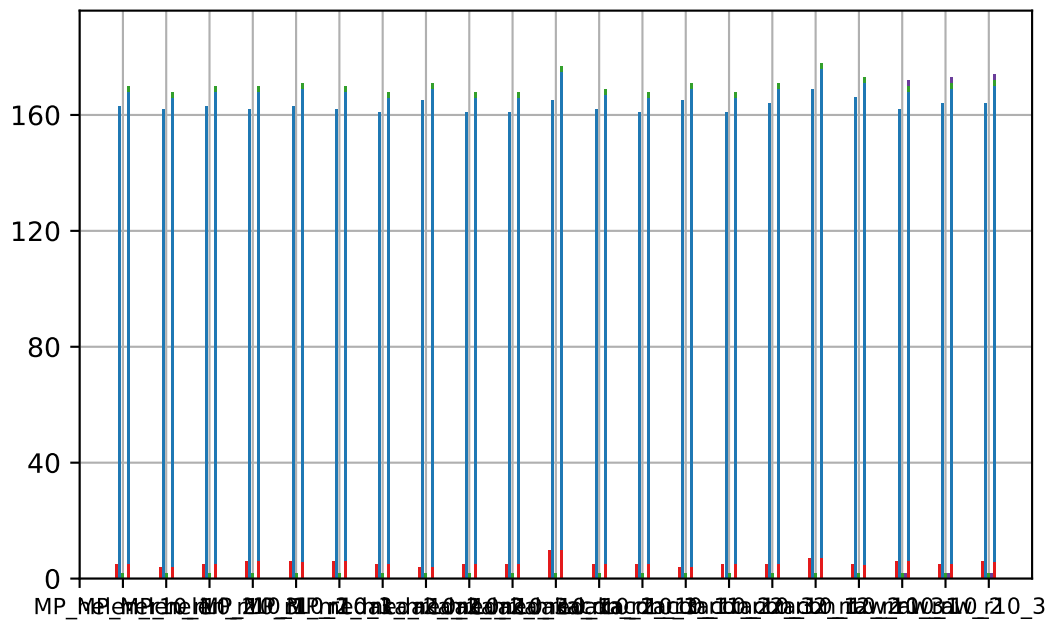


raw_r10_2

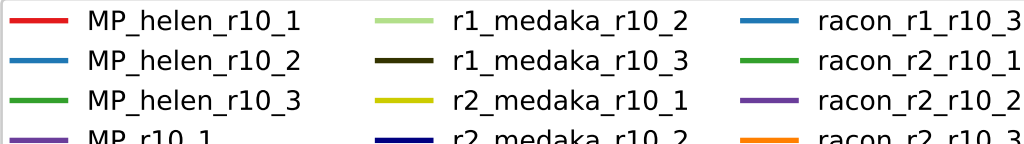
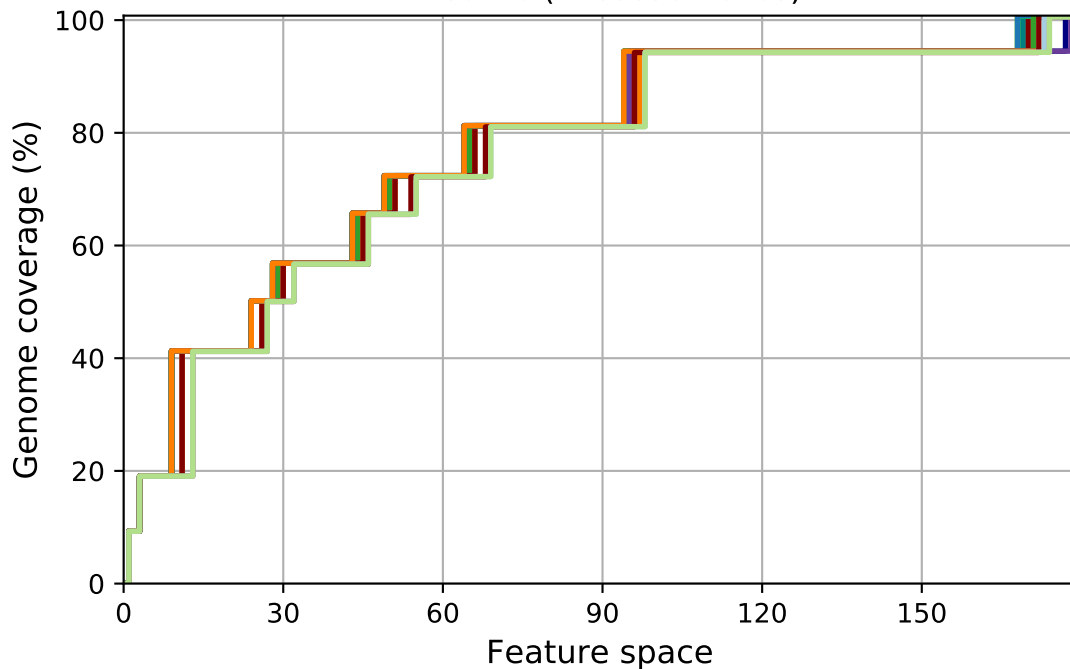
raw_r10_3 GC content



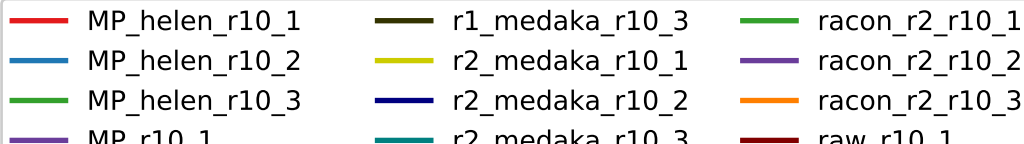
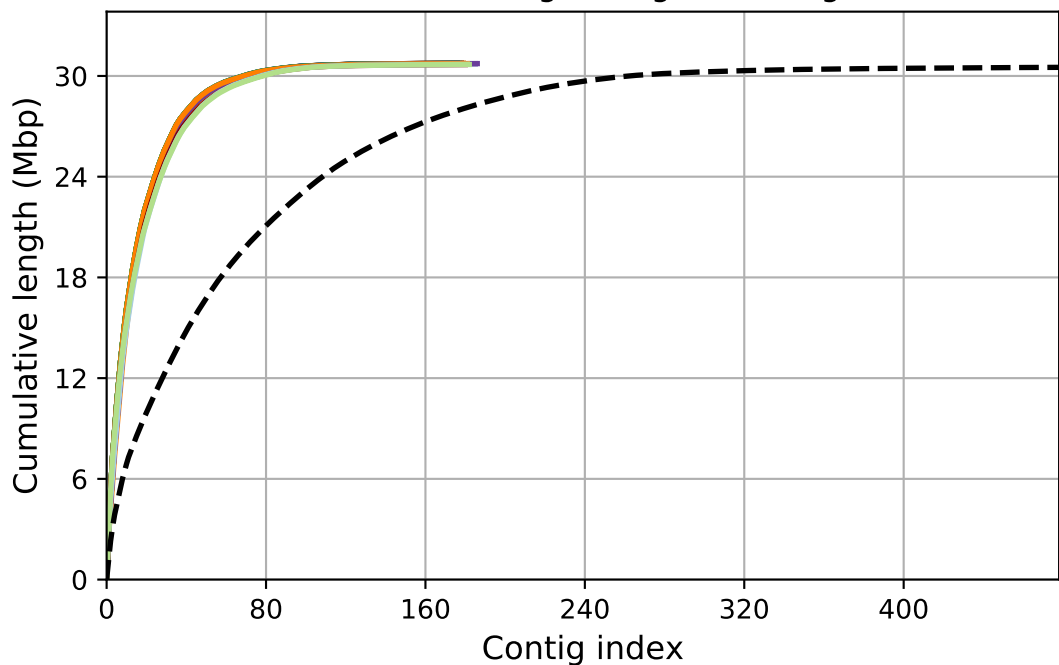
Misassemblies



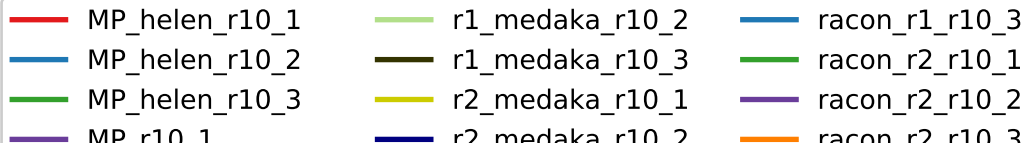
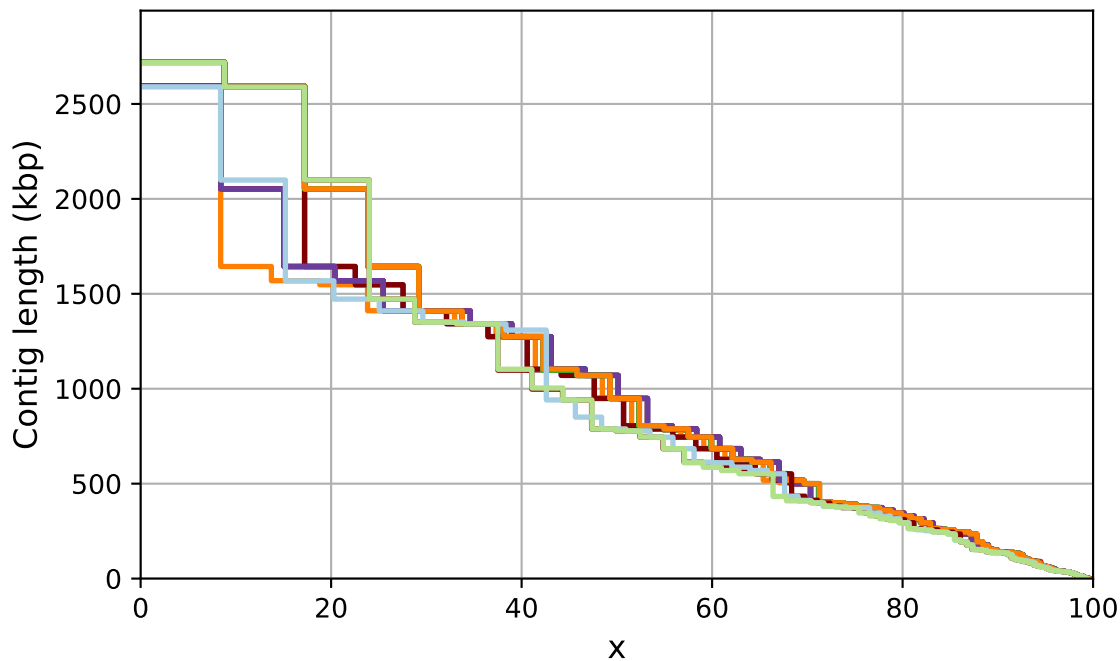
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



Genome fraction, %

