Report

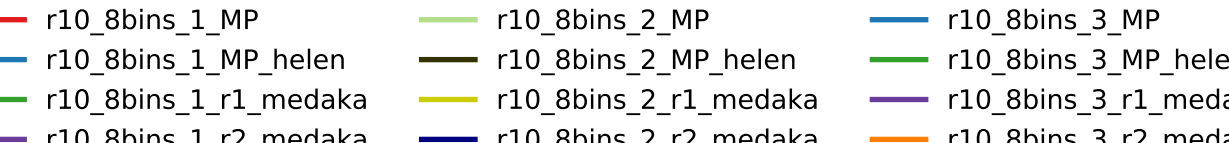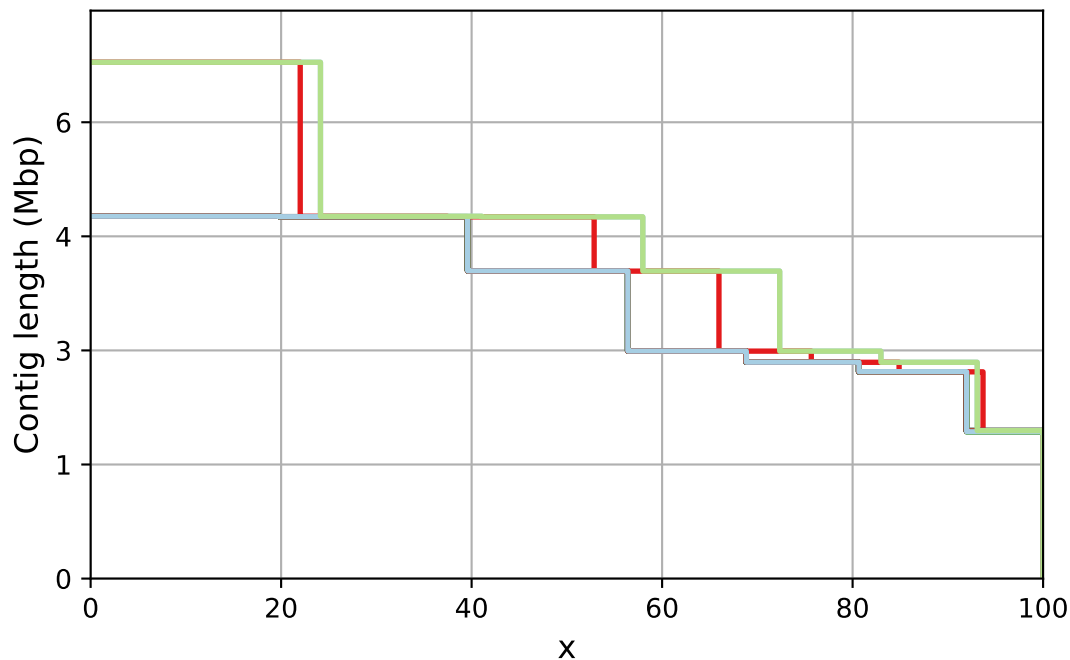|	r10_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	28130815
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	28130815
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	28130815
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	28130815
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Largest contig	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764683	4764682	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292
Total length	24074745	24070729	24072155	24064354	24061185	24054036	28131334	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	28130815
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
GC (%)	44.80	44.80	44.80	44.80	44.79	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.79	49.48	44.80	44.80	44.80	44.80	44.79	44.79	51.10
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45
N50	4045595	4045615	4045602	4045598	4045293	4045319	4755933	4045596	4045616	4045587	4045593	4045258	4045228	4756088	4045596	4045613	4045582	4045587	4045248	4045593	4756065
NG50	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764683	4764682	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292
N75	2845436	2845374	2845424	2845430	2845286	2845307	2990636	2845427	2845364	2845435	2845433	2845287	2845362	2990626	2845437	2845286	2845434	2845365	2845324	2845286	2990261
NG75	4765396	4765339	4765361	4765365	4764689	4764726	6788614	4765403	4765334	4765359	4765364	4764683	4764682	6788581	4765471	4765411	4765372	4765365	4764770	4764744	6788292
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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# 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	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
# local misassemblies	36	36	36	36	36	36	57	37	36	37	37	36	36	60	36	36	36	36	37	36	50
# 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	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# 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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	19040505	19035392	19036412	19028914	19026122	19019095	23174629	19040491	19034214	19035522	19026126	19022699	19018419	25901605	19042627	19036995	19036124	19028944	19028251	19019480	23177631
Genome fraction (%)	97.703	97.703	97.703	97.703	97.703	97.703	97.663	97.701	97.703	97.701	97.701	97.703	97.703	97.665	97.703	97.703	97.703	97.703	97.703	97.703	97.667
Duplication ratio	1.076	1.077	1.077	1.077	1.077	1.077	1.060	1.076	1.077	1.077	1.077	1.077	1.077	1.058	1.076	1.076	1.077	1.077	1.076	1.077	1.060
# 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	440.09	439.64	442.08	441.69	445.67	446.59	493.41	439.84	439.36	442.81	442.41	449.93	449.16	484.70	435.47	432.93	442.06	441.65	439.79	449.39	477.81
# indels per 100 kbp	20.72	17.88	15.08	14.69	35.65	33.19	231.87	20.78	18.11	15.16	15.01	35.60	33.12	236.85	20.44	16.76	15.87	15.78	37.31	33.46	234.75
Largest alignment	1769075	1769068	1769076	1769075	1768838	1768853	1104940	1408820	1408784	1408817	1408818	1408647	1408657	1102546	1414863	1414845	1414832	1414839	1414665	1414862	1317831
Total aligned length	5028944	5030053	5030449	5030158	5029878	5029746	4954414	5031162	5029786	5033437	5033154	5033049	5031223	4942673	5025688	5026076	5029498	5029291	5025531	5029949	4948104
NGA50	1103290	1103273	1103272	1103272	1103115	1103124	682839	1105658	1103270	1105646	1105649	1103118	1103114	586349	1102980	1102956	1102786	1102785	1102780	1102786	586997
NGA75	399303	399301	399304	399307	399254	399241	412061	393569	393564	393562	393562	393555	393550	376968	394051	394047	394042	394044	393983	394000	369859
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	3	2	2	2	2	2	2	3
LGA75	4	4	4	4	4	5	5	5	5	5	5	5	5	6	5	5	5	5	5	5	6

All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
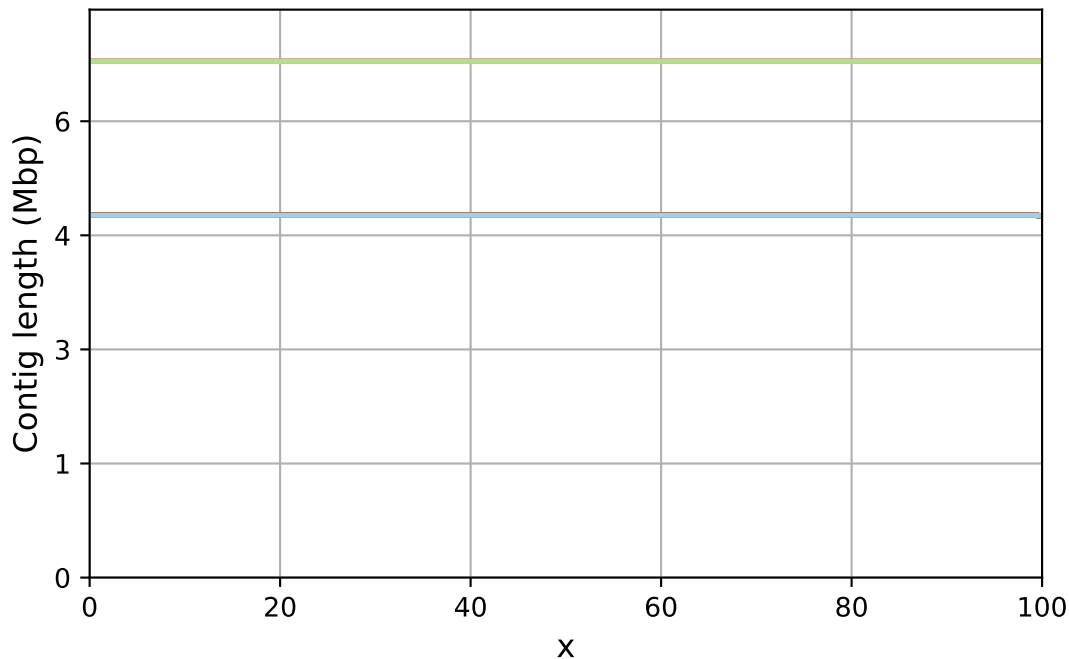(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
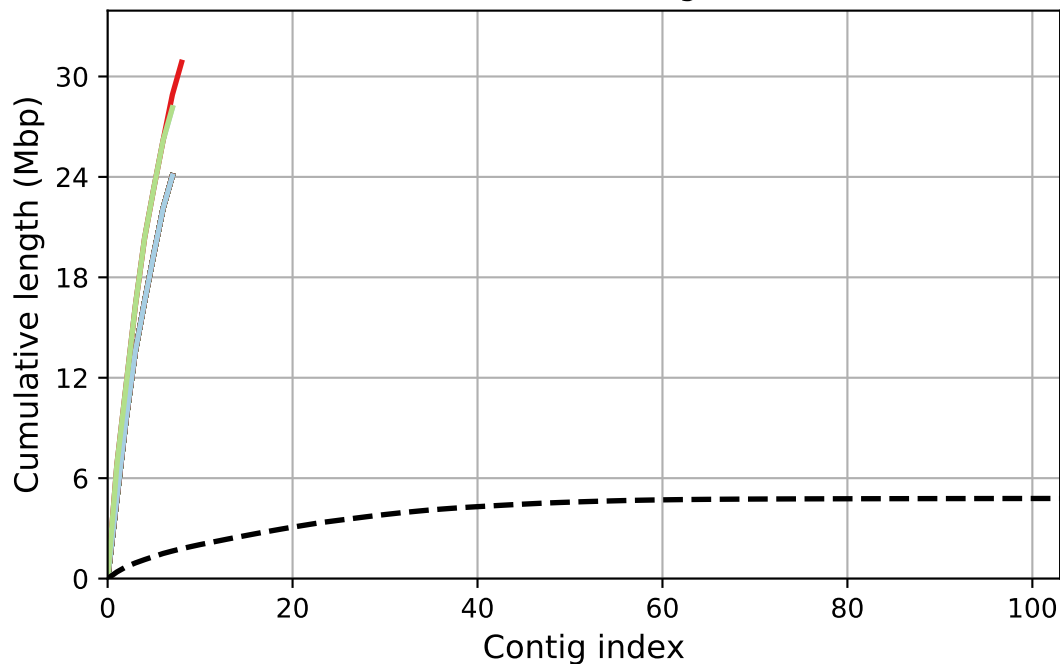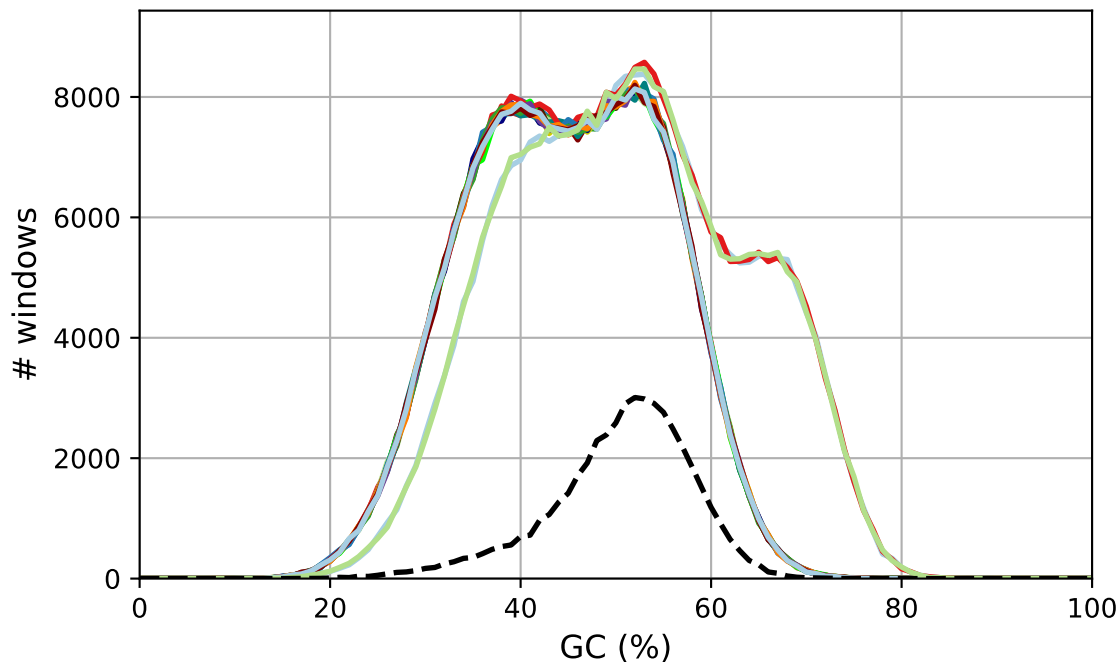
Misassemblies report
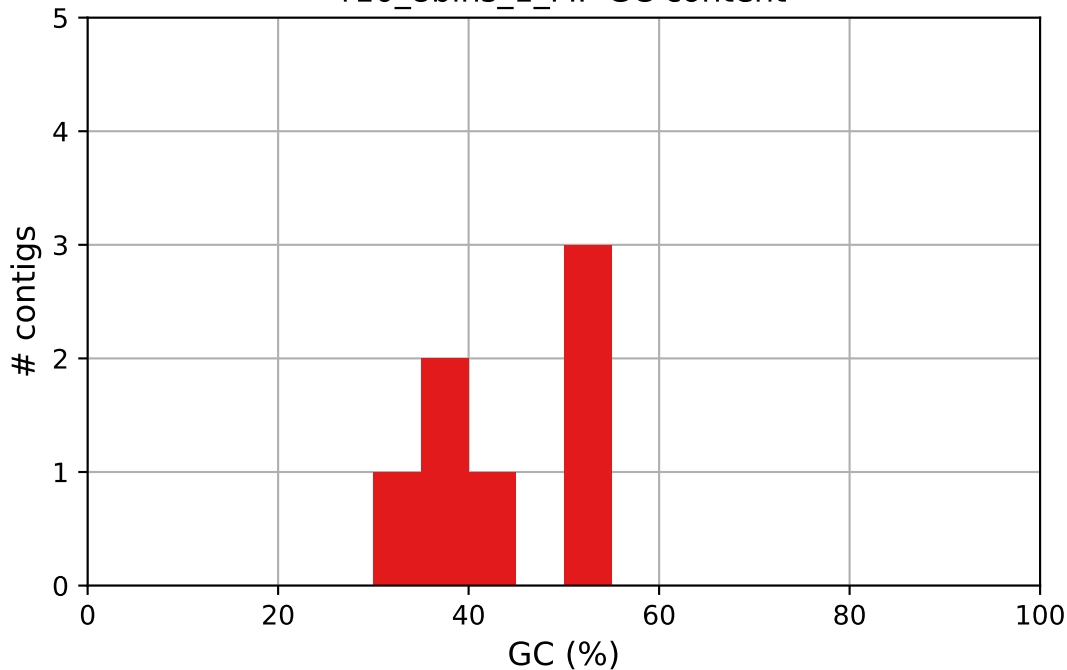
r10_8bins_3_r2	r10_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_3_raw
# misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	18	20	20	20	20	20	20	18
# 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	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
# 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	12	12	12	12	12	12	32	12	12	12	12	12	12	34	12	12	12	12	12	12	28
# local misassemblies	36	36	36	36	36	36	57	37	36	37	37	36	36	60	36	36	36	36	37	36	50
# 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	42	42	42	42	42	42	36	42	42	42	42	42	42	35	42	42	42	42	42	42	38
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	20581	20560	20674	20656	20842	20885	23065	20569	20547	20708	20689	21041	21005	22658	20365	20246	20673	20654	20567	21016	22337
# indels	969	836	705	687	1667	1552	10839	972	847	709	702	1665	1549	11072	956	784	742	738	1745	1565	10974
# indels (<= 5 bp)	872	738	609	591	1570	1455	10646	874	748	613	606	1567	1452	10871	853	686	644	641	1647	1467	10777
# indels (> 5 bp)	97	98	96	96	97	97	193	98	99	96	96	98	97	201	103	98	98	97	98	98	197
Indels length	6164	6059	5874	5855	7020	6871	19825	6132	6146	5833	5831	7060	6915	20402	6284	6066	6014	5975	7134	6973	20473

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_8bins_1_MP	r10_8bins_1_MP_helen	r10_8bins_1_r1_medaka	r10_8bins_1_r2_medaka	r10_8bins_1_racon_r1	r10_8bins_1_racon_r2	r10_8bins_1_raw	r10_8bins_2_MP	r10_8bins_2_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_2_racon_r2	r10_8bins_2_raw	r10_8bins_3_MP	r10_8bins_3_MP_helen	r10_8bins_3_r1_medaka	r10_8bins_3_r2_medaka	r10_8bins_3_racon_r1	r10_8bins_3_racon_r2	r10_8bins_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	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Partially unaligned length	19040505	19035392	19036412	19028914	19026122	19019095	23174629	19040491	19034214	19035522	19026126	19022699	19018419	25901605	19042627	19036995	19036124	19028944	19028251	19019480	23177631
# 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

Contig length (Mbp)		

NGx

| Contig length (Mbp) vs x |

r10_8bins_1_MP
r10_8bins_1_MP_helen
r10_8bins_1_r1_medaka
r10_8bins_1_r2_medaka

r10_8bins_2_MP
r10_8bins_2_MP_helen
r10_8bins_2_r1_medaka
r10_8bins_2_r2_medaka

r10_8bins_3_MP
r10_8bins_3_MP_hele
r10_8bins_3_r1_meda
r10_8bins_3_r2_meda

Cumulative length

Legend		
r10_8bins_1_MP	r10_8bins_2_MP_helen	r10_8bins_3_MP_hele
r10_8bins_1_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_3_r1_meda
r10_8bins_1_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_meda
r10_8bins_1_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_3_racon_r1

GC content

r10_8bins_1_MP	r10_8bins_2_MP_helen	r10_8bins_3_MP_helen
r10_8bins_1_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_3_r1_meda
r10_8bins_1_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_meda
r10_8bins_1_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_3_racon_r1

r10_8bins_1_MP GC content

r10_8bins_1_MP_helen GC content
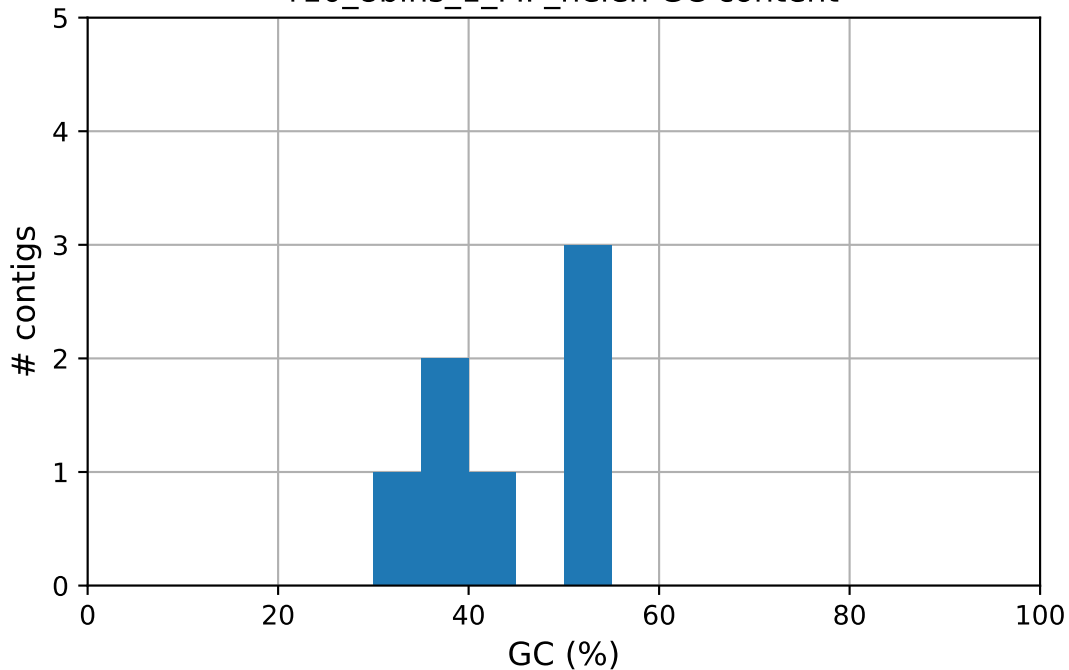
r10_8bins_1_r1_medaka GC content
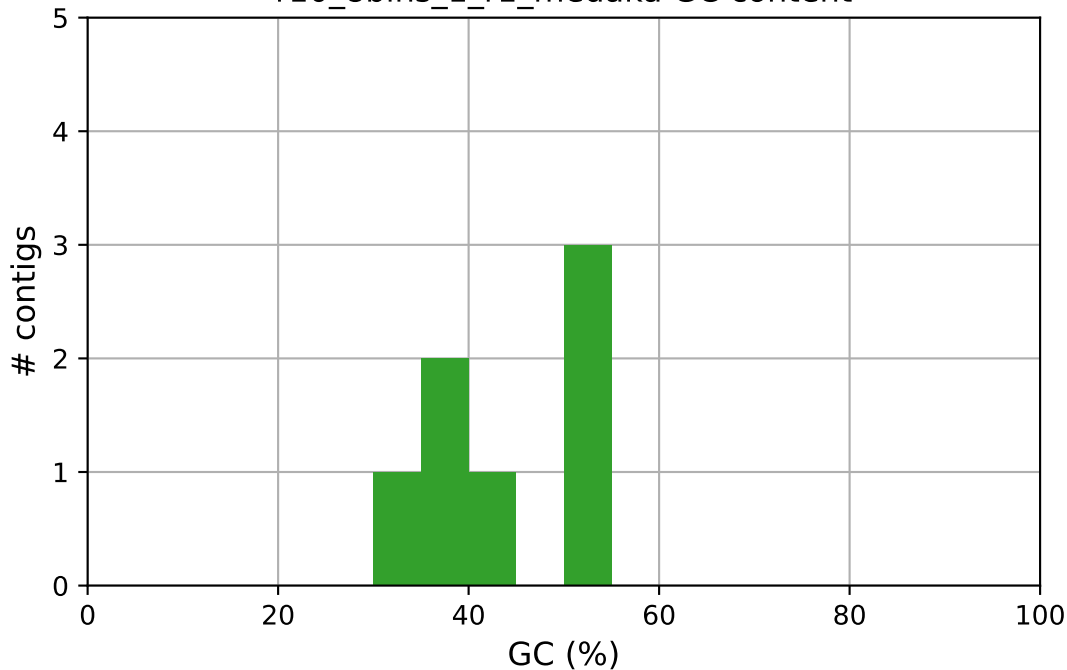
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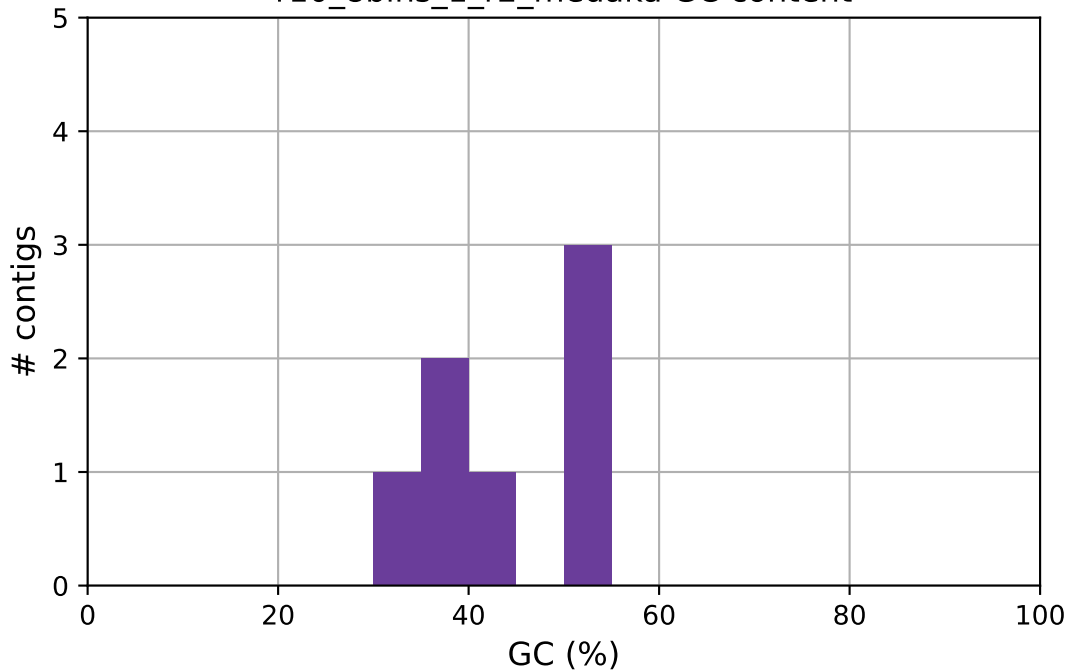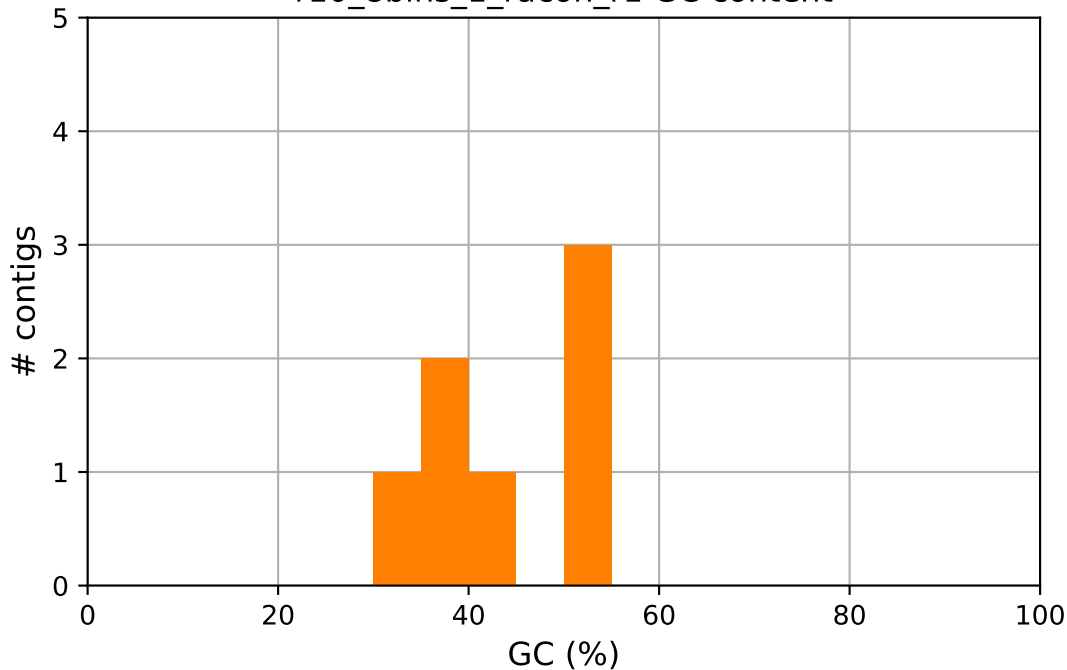
r10_8bins_1_racon_r2 GC content
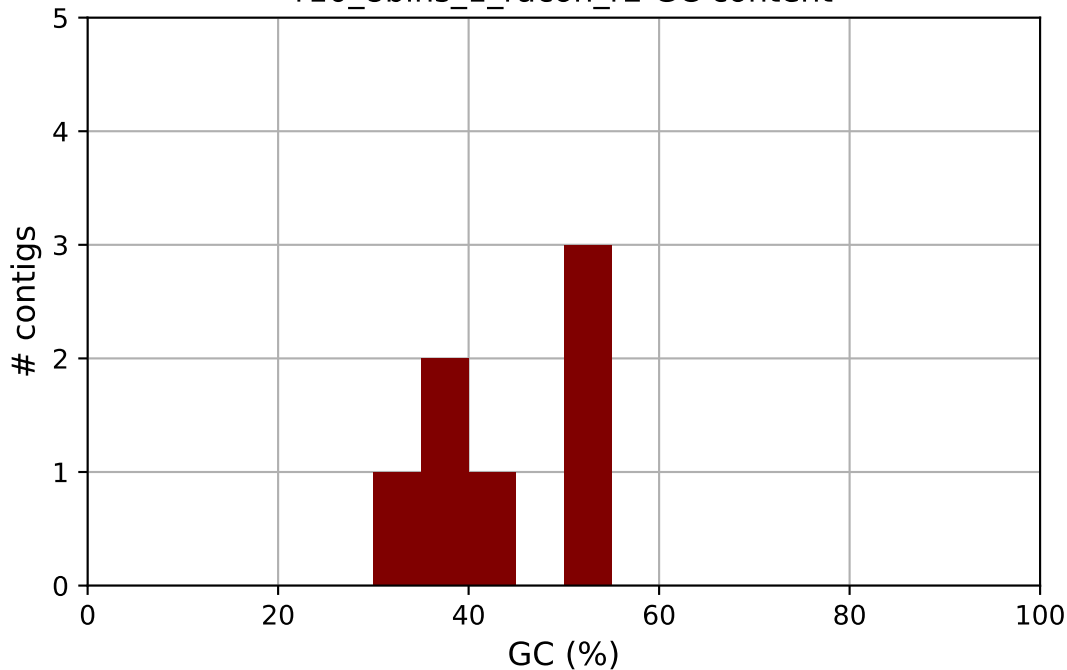
r10_8bins_1_raw GC content
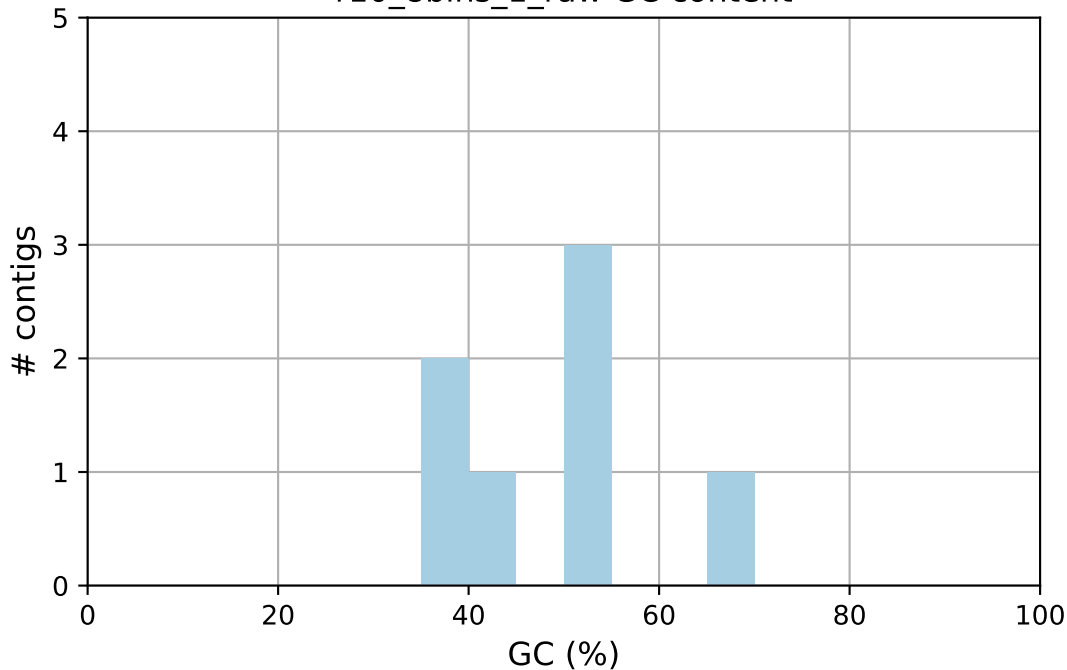
r10_8bins_2_MP GC content
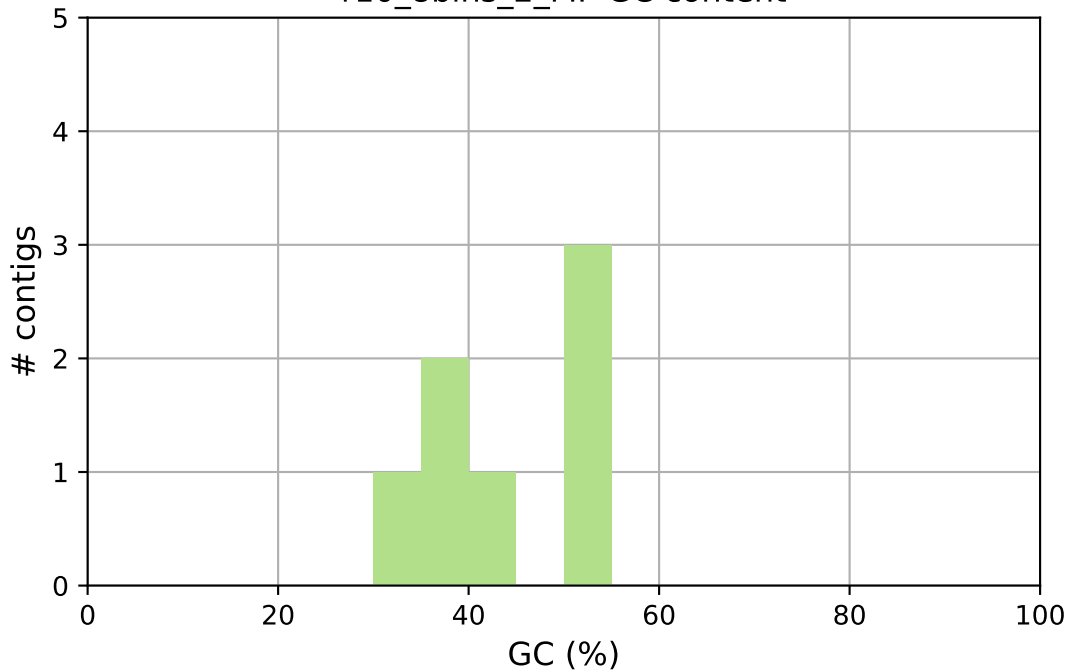
r10_8bins_2_MP_helen GC content
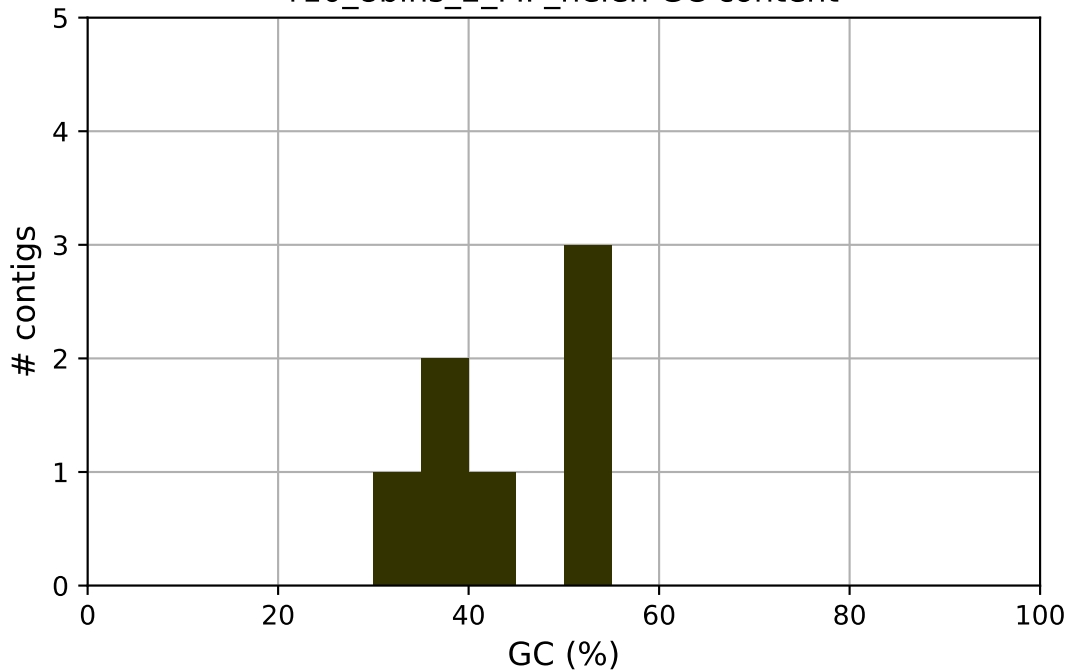
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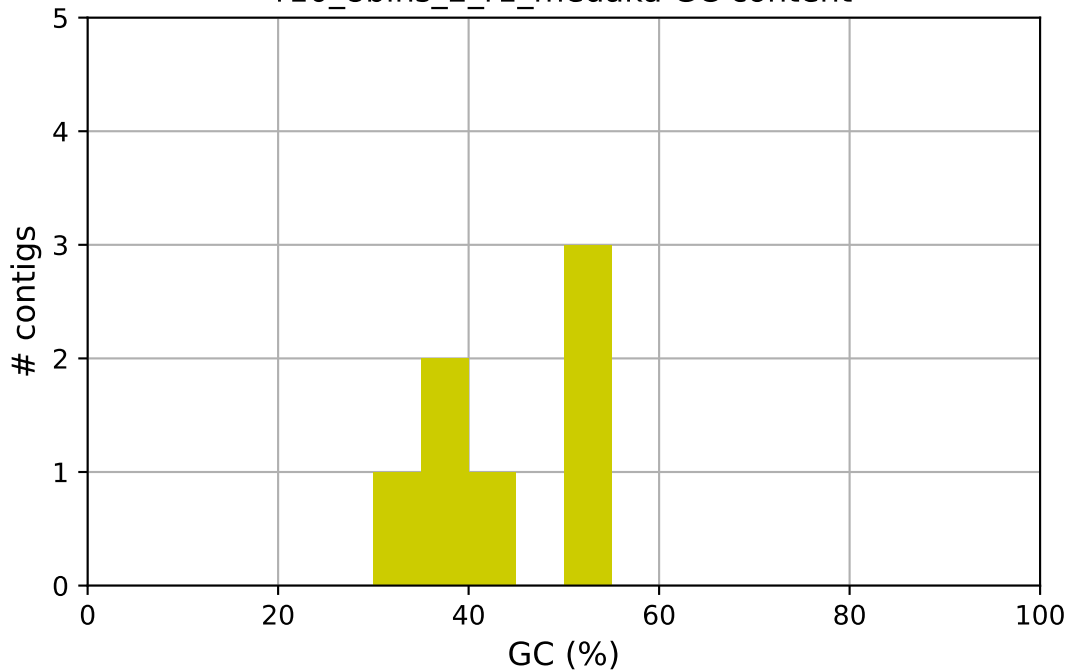
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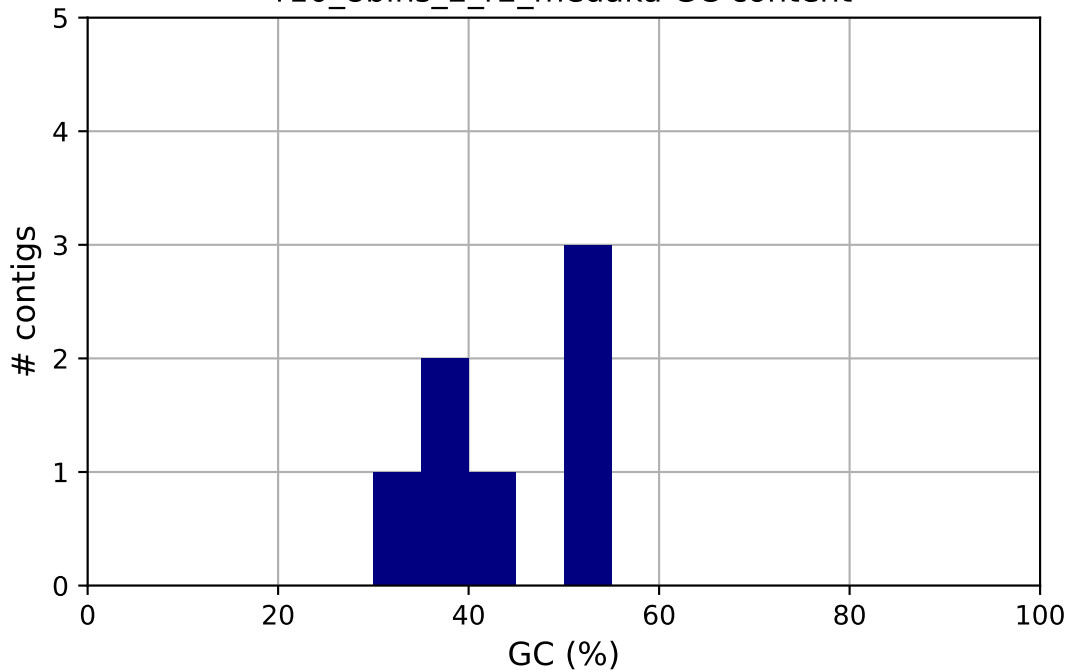
r10_8bins_2_racon_r1 GC content
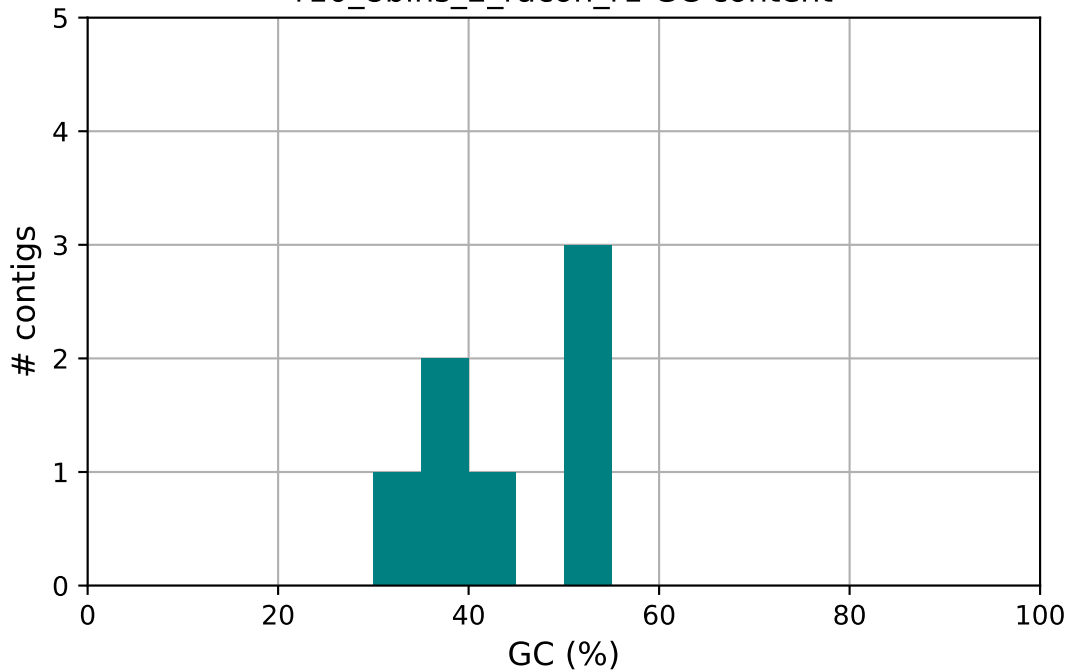
r10_8bins_2_racon_r2 GC content
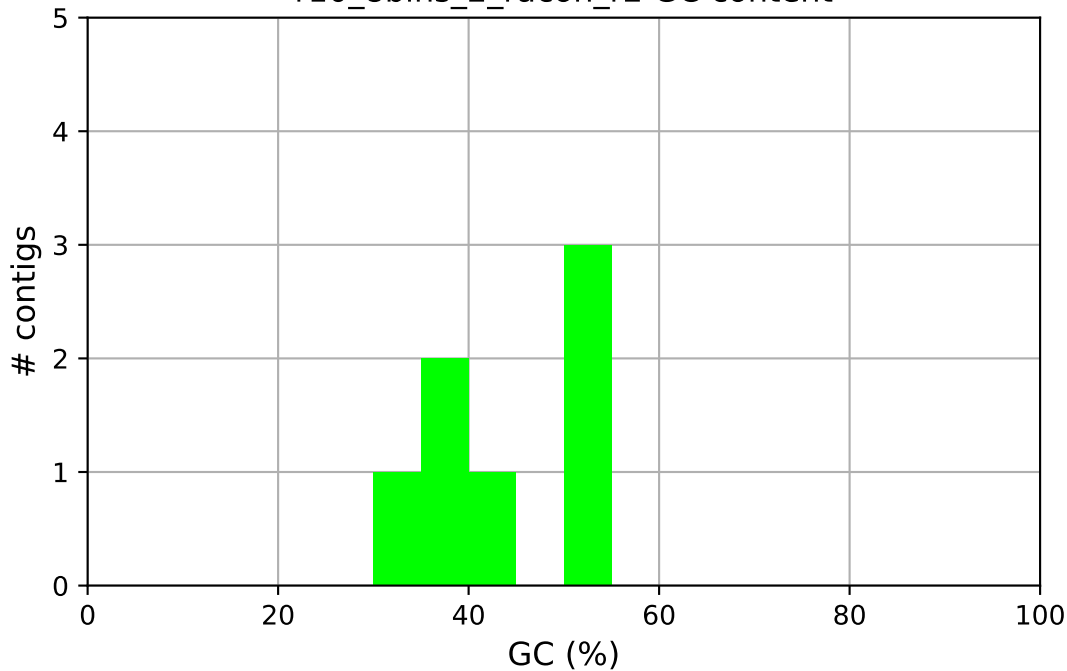
r10_8bins_2_raw GC content
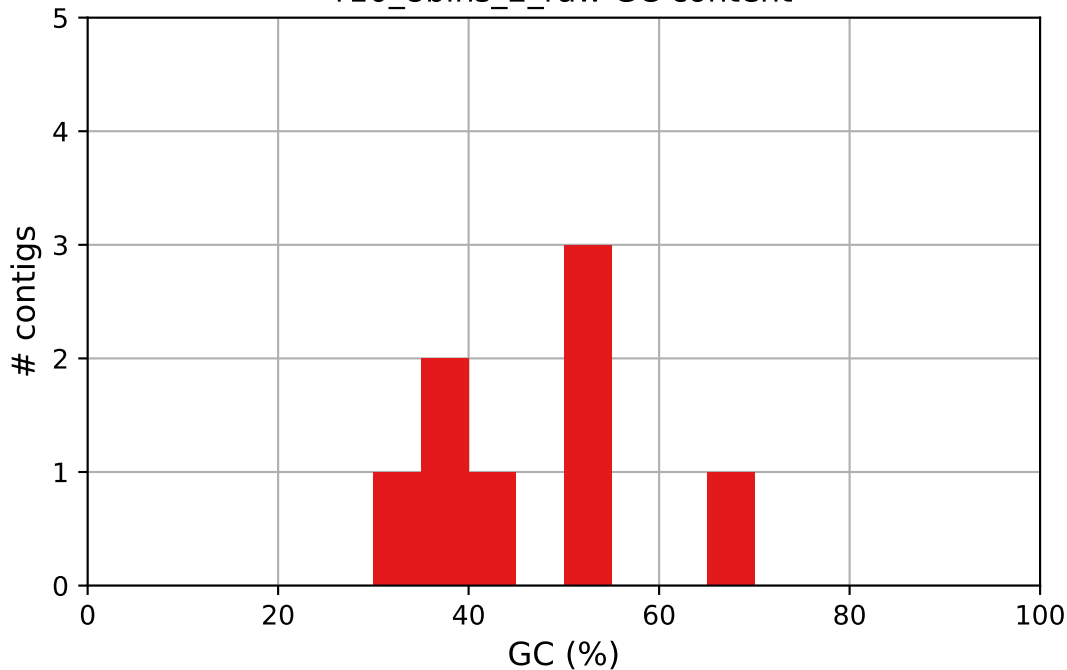
r10_8bins_3_MP GC content
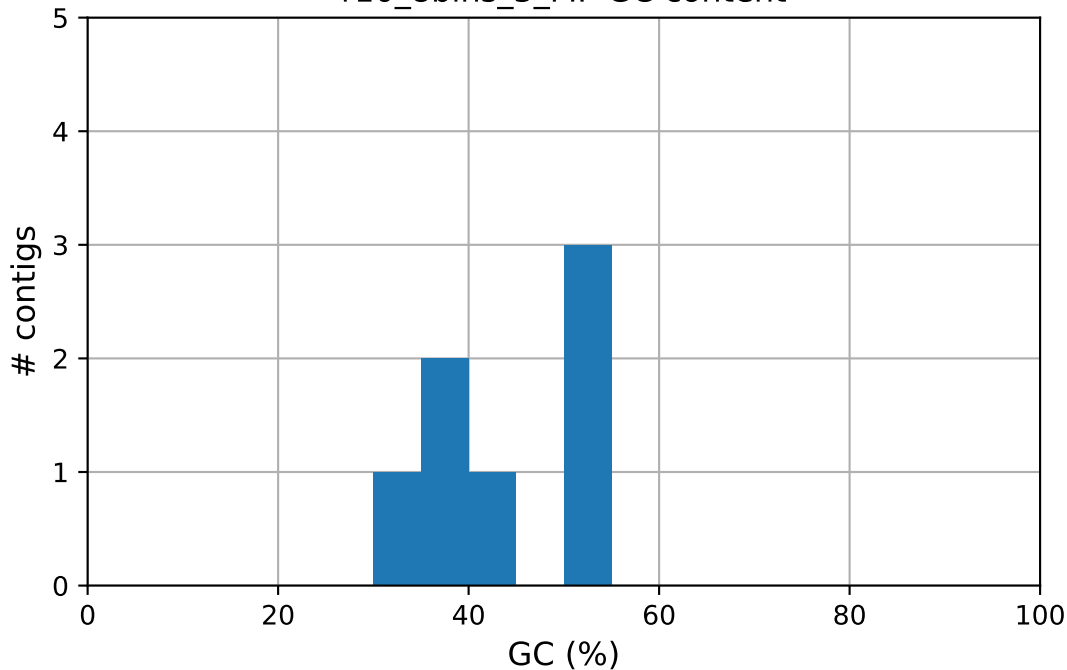
r10_8bins_3_MP_helen GC content
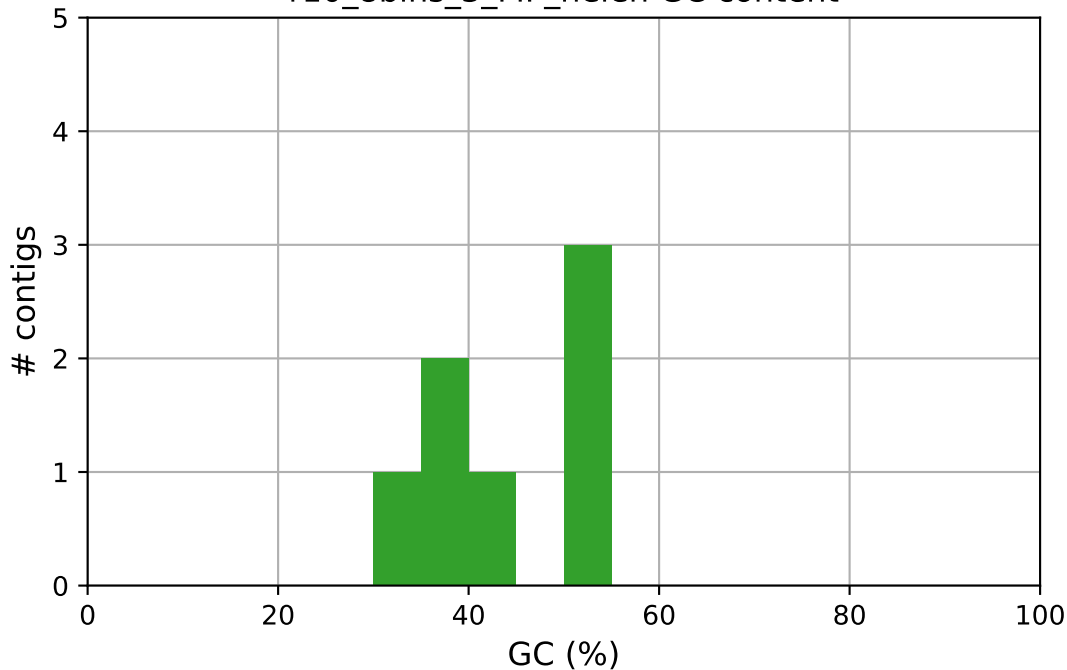
r10_8bins_3_r1_medaka GC content
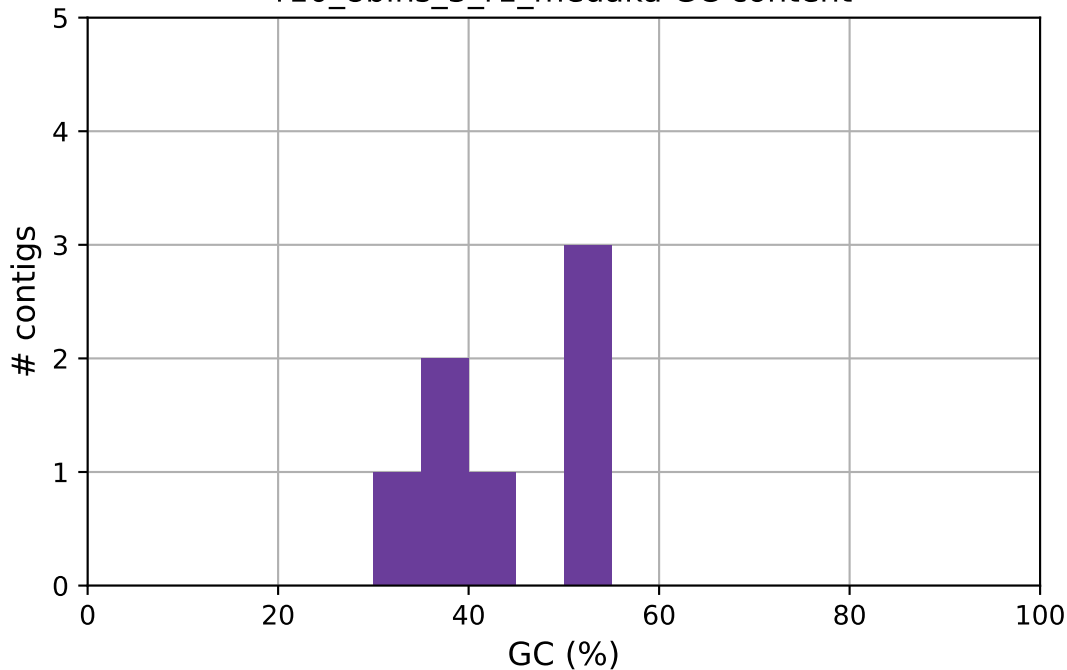
r10_8bins_3_r2_medaka GC content
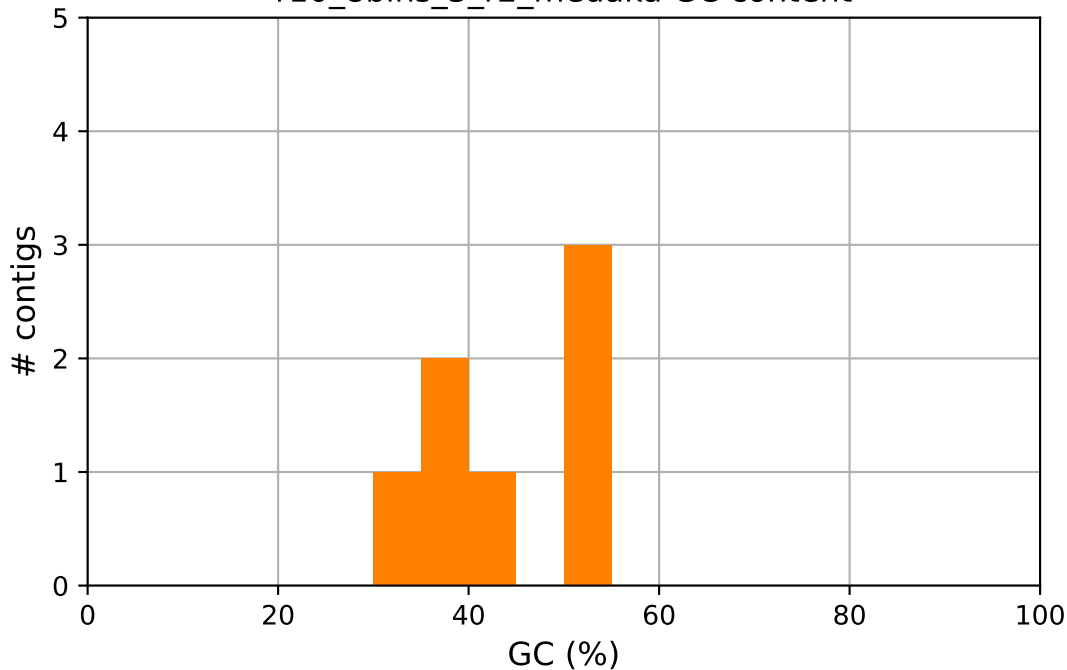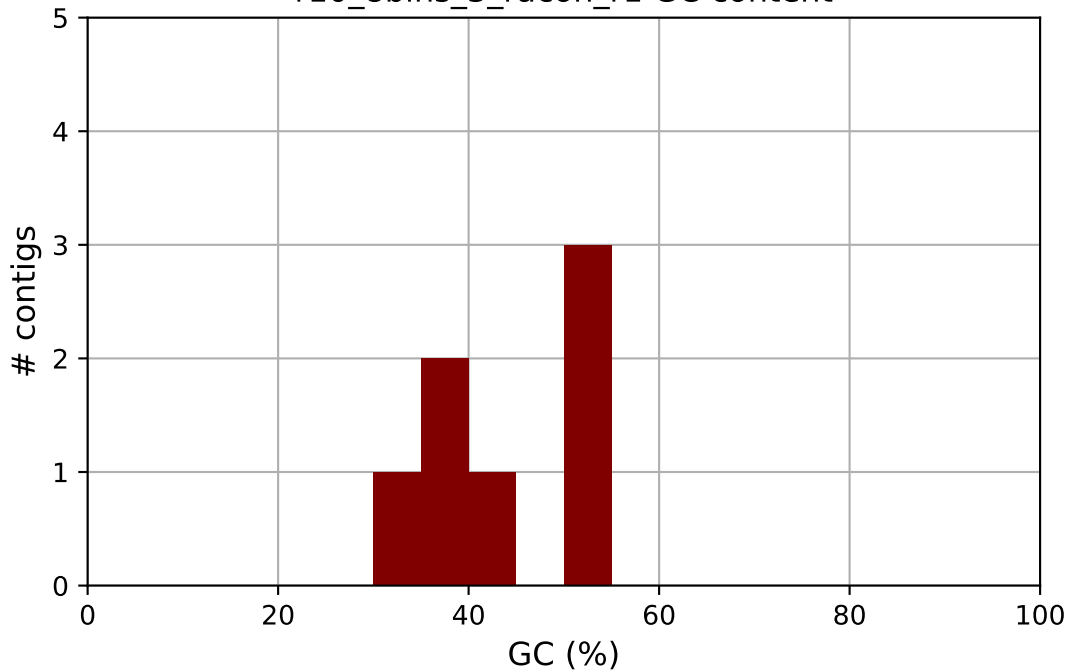
r10_8bins_3_racon_r1 GC content

r10_8bins_3_racon_r2 GC content
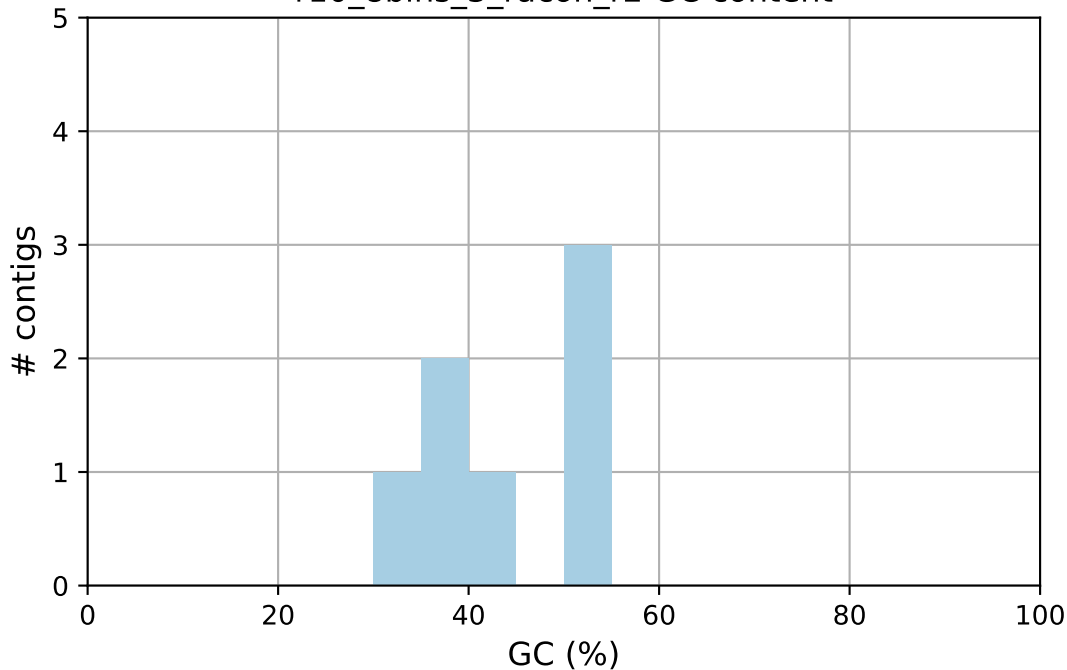
r10_8bins_3_raw GC content
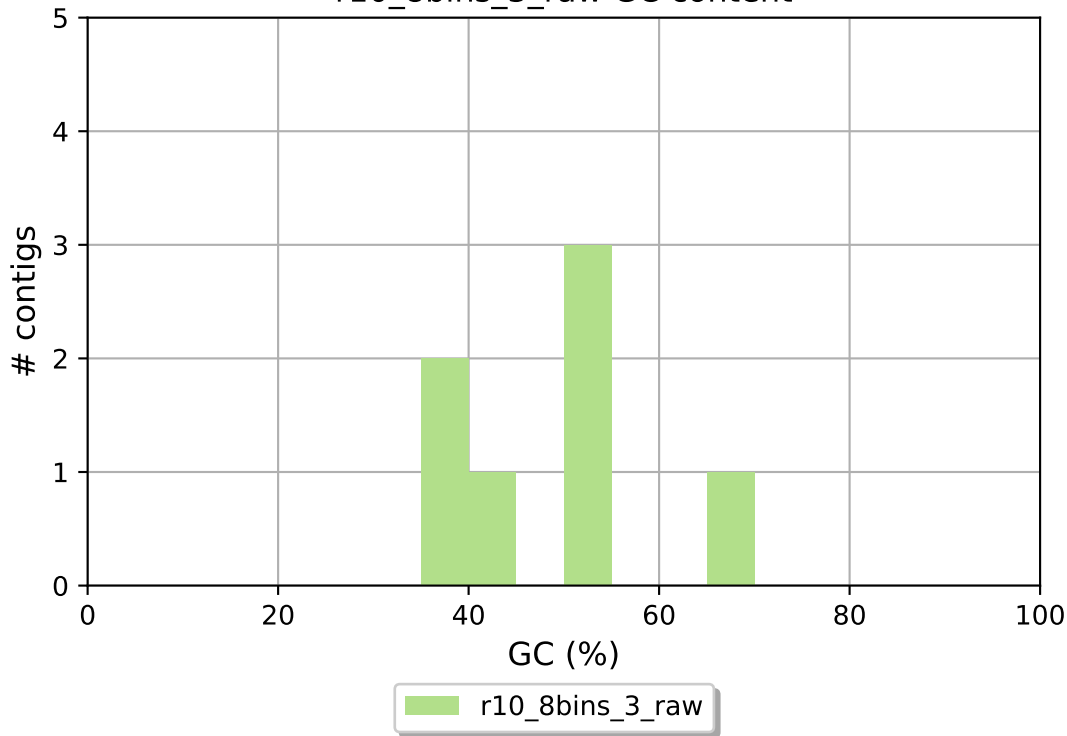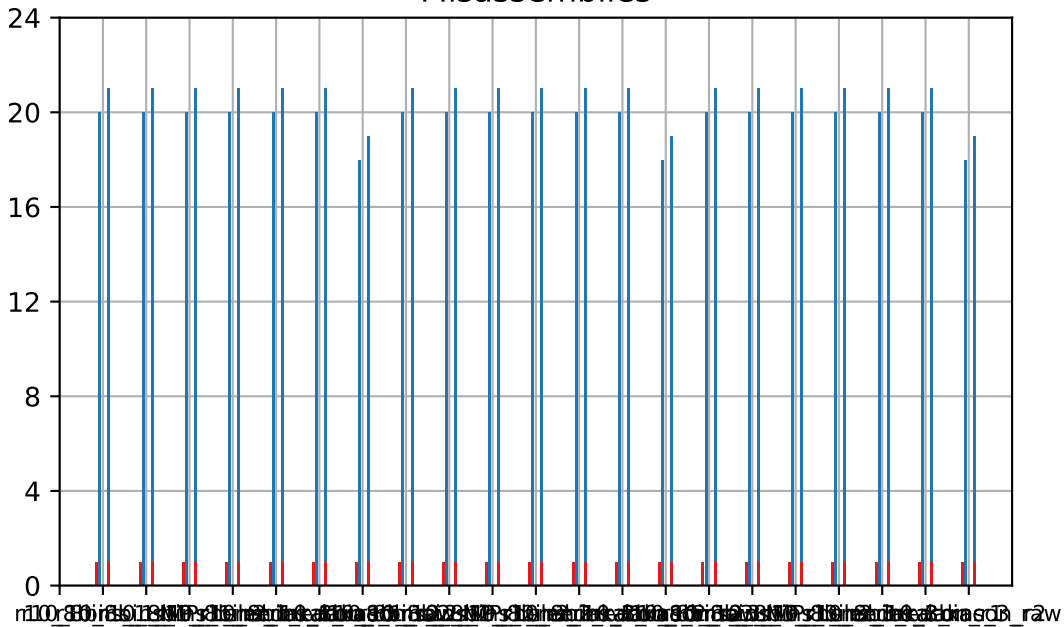
Misassemblies

FRCurve (misassemblies)
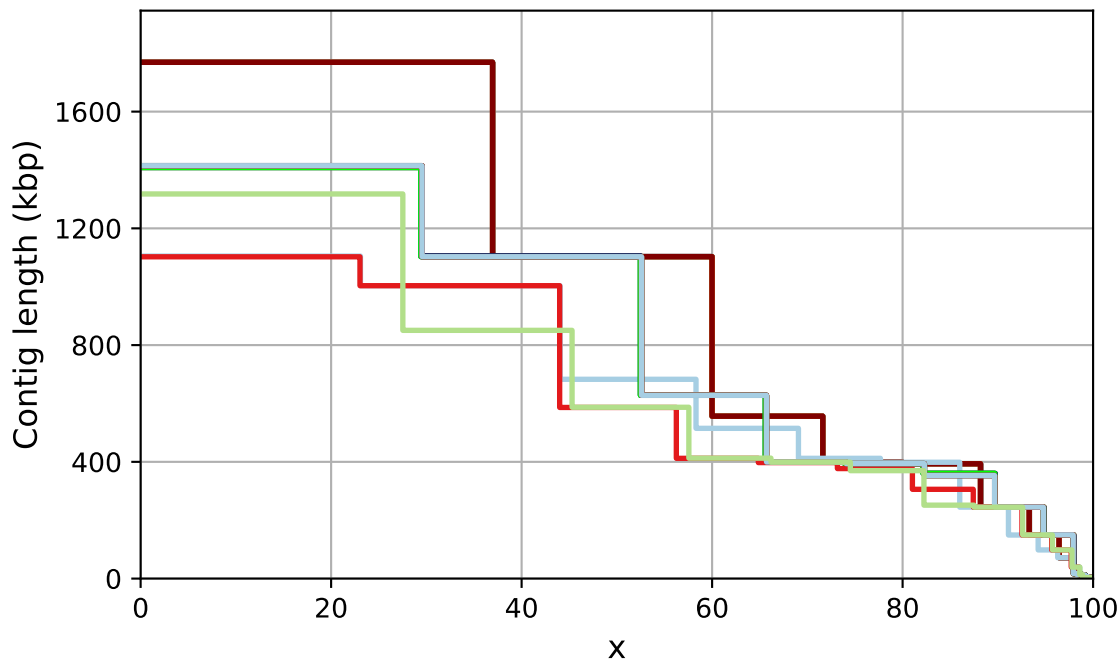
r10_8bins_1_MP	r10_8bins_2_MP	r10_8bins_3_MP
r10_8bins_1_MP_helen	r10_8bins_2_MP_helen	r10_8bins_3_MP_hele
r10_8bins_1_r1_medaka	r10_8bins_2_r1_medaka	r10_8bins_3_r1_meda
r10_8bins_1_r2_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_meda
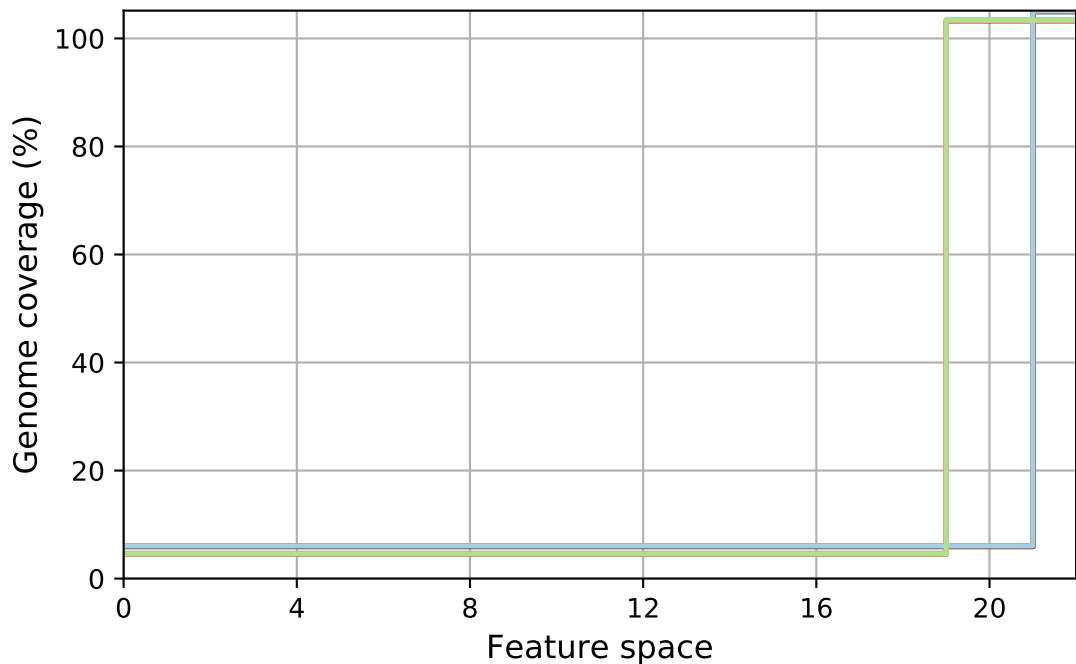
Cumulative length (aligned contigs)

r10_8bins_1_MP	r10_8bins_2_MP_helen	r10_8bins_3_MP_helen
r10_8bins_1_MP_helen	r10_8bins_2_r1_medaka	r10_8bins_3_r1_meda
r10_8bins_1_r1_medaka	r10_8bins_2_r2_medaka	r10_8bins_3_r2_meda
r10_8bins_1_r2_medaka	r10_8bins_2_racon_r1	r10_8bins_3_racon_r1

NAx

Contig length (kbp)

x

- r10_8bins_1_MP
- r10_8bins_1_MP_helen
- r10_8bins_1_r1_medaka
- r10_8bins_1_r2_medaka
- r10_8bins_2_MP
- r10_8bins_2_MP_helen
- r10_8bins_2_r1_medaka
- r10_8bins_2_r2_medaka
- r10_8bins_3_MP
- r10_8bins_3_MP_hele
- r10_8bins_3_r1_meda
- r10_8bins_3_r2_meda

NGAx

Genome fraction, %