

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 (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
Total length	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77	44.80	44.81	44.80	44.80	44.79	44.79	44.77
Reference GC (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
N50	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	4045608	4045229	4045315	4042940	4045596	4045614	4045597	4045593	4045228	4045344	4043027
NG50	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
N75	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845336	2845240	2845336	2843848
NG75	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
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	14	14	14	14	14	14	13	14	14	14	14	14	14	13	14	14	14	14	14	14	14
# 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	2719597	2717966	2719541	2719590	2720576	2720615	2718428	2719618	2717942	2719541	2719616	2720432	2720646	2718430	2719555	2717972	2719594	2719599	2720567	2720658	2718818
# local misassemblies	10	10	9	10	9	9	20	9	9	9	9	9	9	20	9	9	8	8	9	9	19
# 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	5	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# 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 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	21275184	21271369	21272515	21264526	21261875	21256848	21322161	21274830	21271766	21273207	21261392	21263246	21251966	21319606	21276777	21274939	21276207	21271604	21266299	21259924	21322355
Genome fraction (%)	99.544	99.544	99.544	99.544	99.544	99.544	99.538	99.546	99.546	99.546	99.546	99.546	99.546	99.538	99.544	99.544	99.544	99.544	99.544	99.544	99.542
Duplication ratio	1.046	1.045	1.046	1.046	1.045	1.046	1.023	1.045	1.045	1.045	1.046	1.045	1.046	1.045	1.046	1.046	1.045	1.046	1.046	1.046	1.024
# N's per 100 kbp	0.00	0.04	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	285.92	254.62	291.08	290.00	293.81	295.64	239.47	286.85	257.08	286.29	291.04	285.43	301.68	247.05	282.23	249.35	286.00	281.93	295.86	300.87	253.91
# indels per 100 kbp	110.28	36.24	76.02	76.51	113.15	112.96	158.10	110.83	43.48	74.97	76.47	111.84	113.00	158.44	109.30	36.20	78.75	76.36	116.44	114.72	166.69
Largest alignment	948911	948326	948729	948885	949115	949144	1350532	948860	948231	948835	948866	949154	949225	1350628	948871	948280	948767	948765	949279	949277	1350546
Total aligned length	2797987	2796557	2797987	2798237	2796620	2797619	2736761	2797598	2795931	2796634	2797507	2794585	2797269	2739446	2795665	2797269	2797408	2796491	2797357	2799174	2739173
NGA50	480596	480303	480562	480561	480718	480741	1350532	480537	480269	480493	480521	480640	480678	1350628	480545	480260	480568	480554	480717	480743	1350546
NGA75	297928	297766	297941	297940	298042	298058	297825	381468	381229	381432	381438	381558	381595	381298	381472	381287	381501	381495	381608	381620	381395
LGA50	2	2	2	2	2	2	1	2	2	2	2	2	2	1	2	2	2	2	2	2	1
LGA75	4	4	4	4	4	4	3	4	4	4	4	4	4	3	4	4	4	4	4	4	3

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

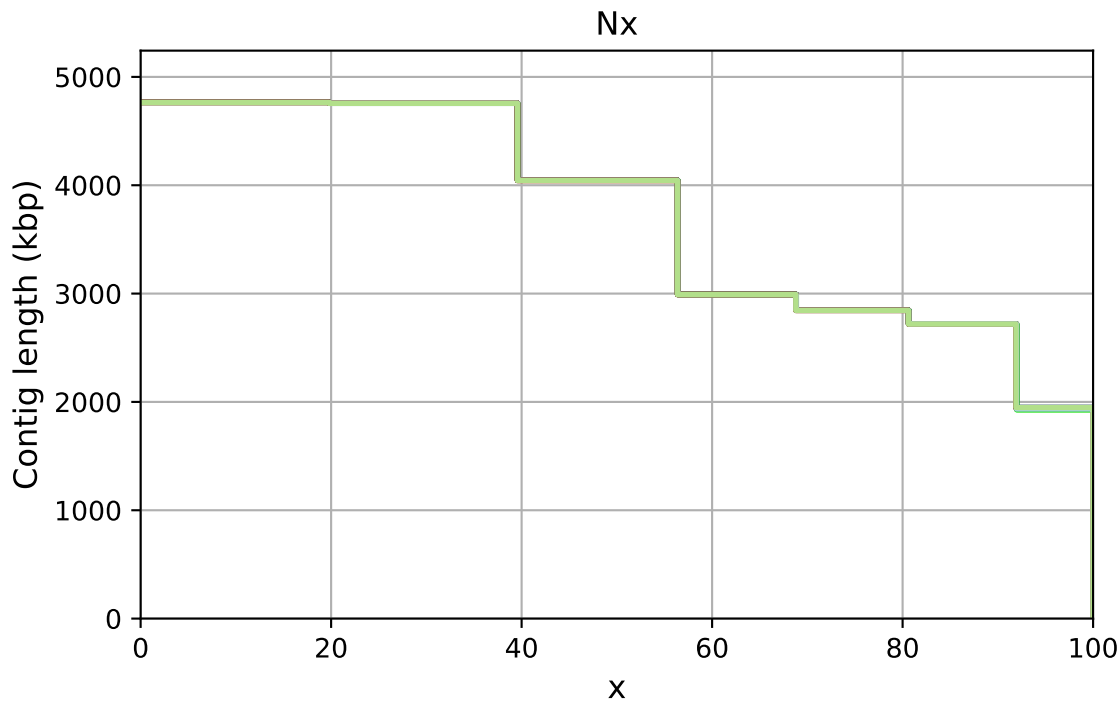
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# misassemblies	14	14	14	14	14	14	13	14	14	14	14	14	14	13	14	14	14	14	14	14	14
# contig misassemblies	14	14	14	14	14	14	13	14	14	14	14	14	14	13	14	14	14	14	14	14	14
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	14	14	14	14	14	14	13	14	14	14	14	14	14	13	14	14	14	14	14	14	14
# 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	2719597	2717966	2719541	2719590	2720576	2720615	2718428	2719618	2717942	2719541	2719616	2720432	2720646	2718430	2719555	2717972	2719594	2719599	2720567	2720658	2718818
# 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	10	10	10	10	10	10	16	10	10	10	10	10	10	16	10	10	10	10	10	10	19
# local misassemblies	10	10	9	10	9	9	20	9	9	9	9	9	9	20	9	9	8	8	9	9	19
# 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	26	26	26	26	26	26	24	26	26	26	26	26	26	24	26	26	26	26	26	26	22
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# mismatches	7654	6816	7792	7763	7865	7914	6410	7679	6882	7664	7791	7641	8076	6613	7555	6675	7656	7547	7920	8054	6797
# indels	2952	970	2035	2048	3029	3024	4232	2967	1164	2007	2047	2994	3025	4241	2926	969	2108	2044	3117	3071	4462
# indels (<= 5 bp)	2885	904	1984	1997	2979	2973	4171	2893	1099	1956	1995	2943	2972	4181	2852	905	2056	1993	3062	3017	4406
# indels (> 5 bp)	67	66	51	51	50	51	61	74	65	51	52	51	53	60	74	64	52	51	55	54	56
Indels length	6848	4687	5388	5385	6828	6722	8352	6905	4943	5330	5393	6743	6764	8348	6823	4681	5461	5376	6887	6832	8548

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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21275184	21271369	21272515	21264526	21261875	21256848	21322161	21274830	21271766	21273207	21261392	21263246	21251966	21319606	21276777	21274939	21276207	21271604	21266299	21259924	21322355
# 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  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



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

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

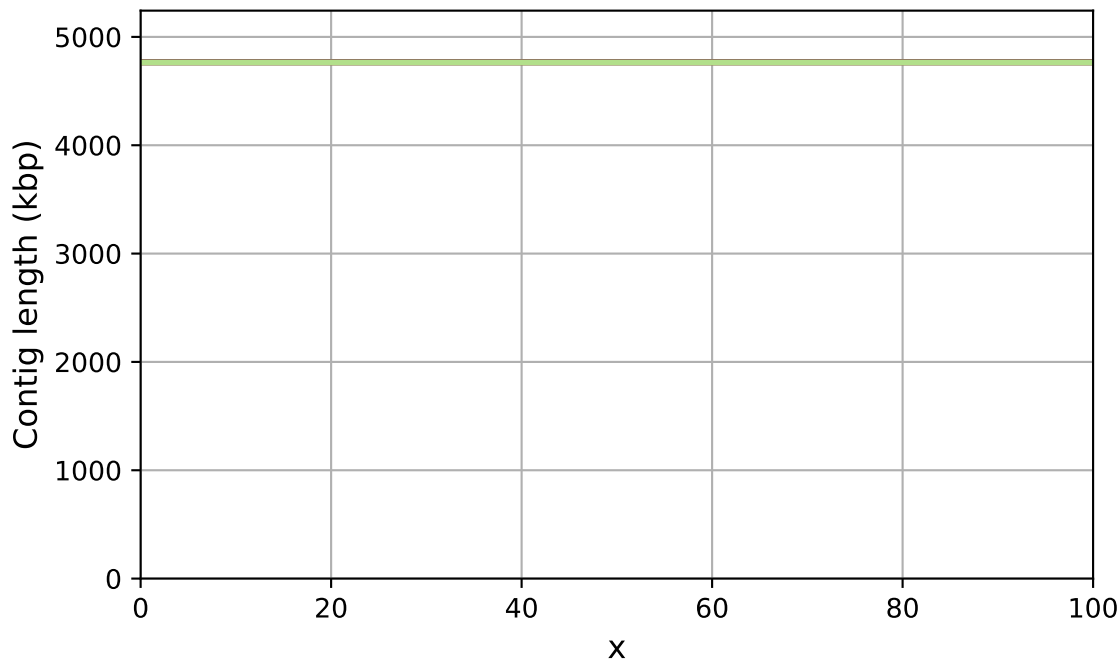
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

# NGx



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\_helen

r10\_1bin\_v2\_1\_r1\_medaka

r10\_1bin\_v2\_2\_r1\_medaka

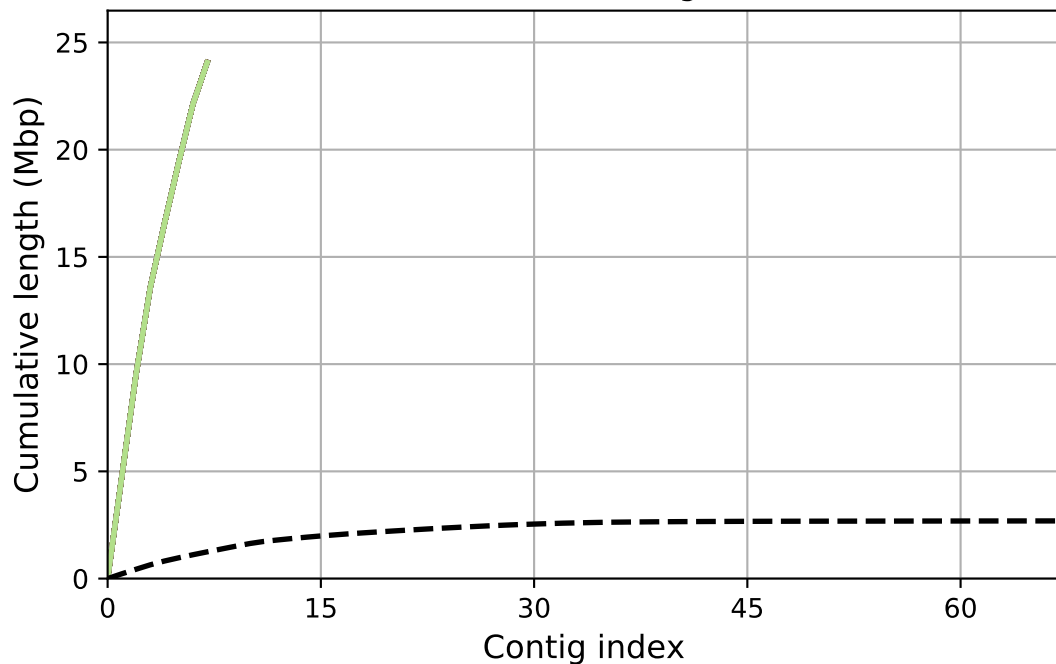
r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

Cumulative length



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

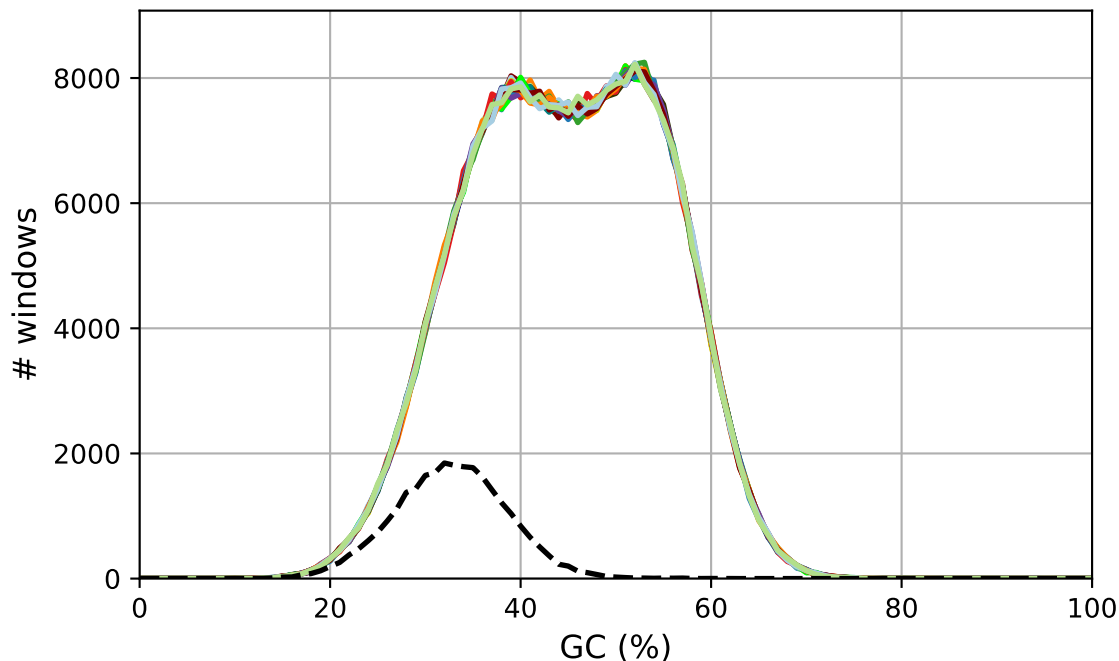
r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1

GC content



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

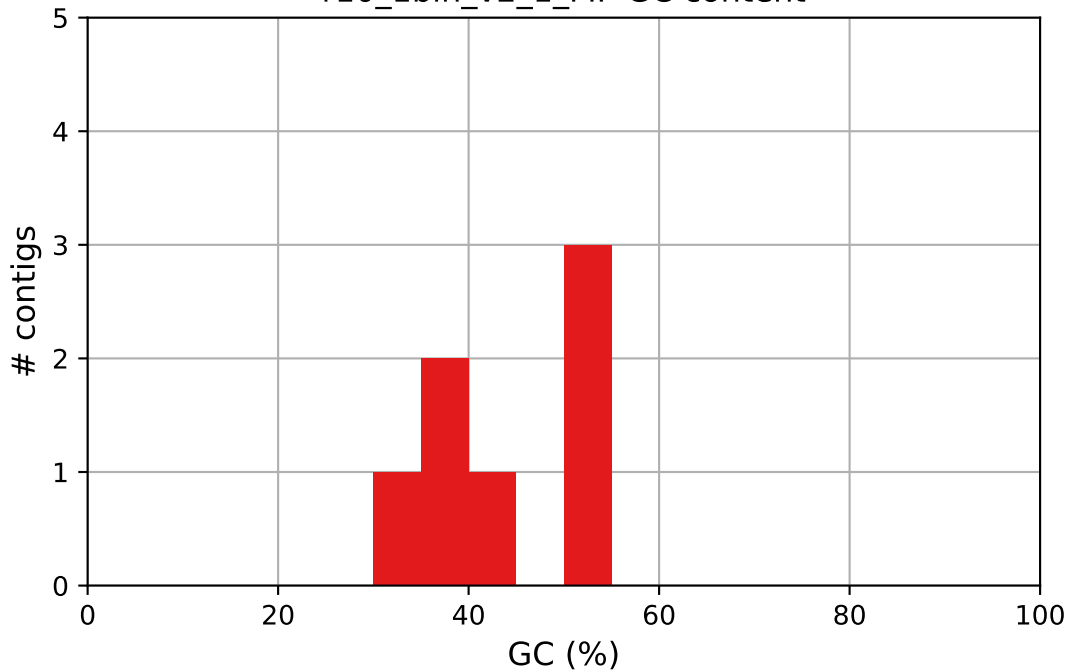
r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1

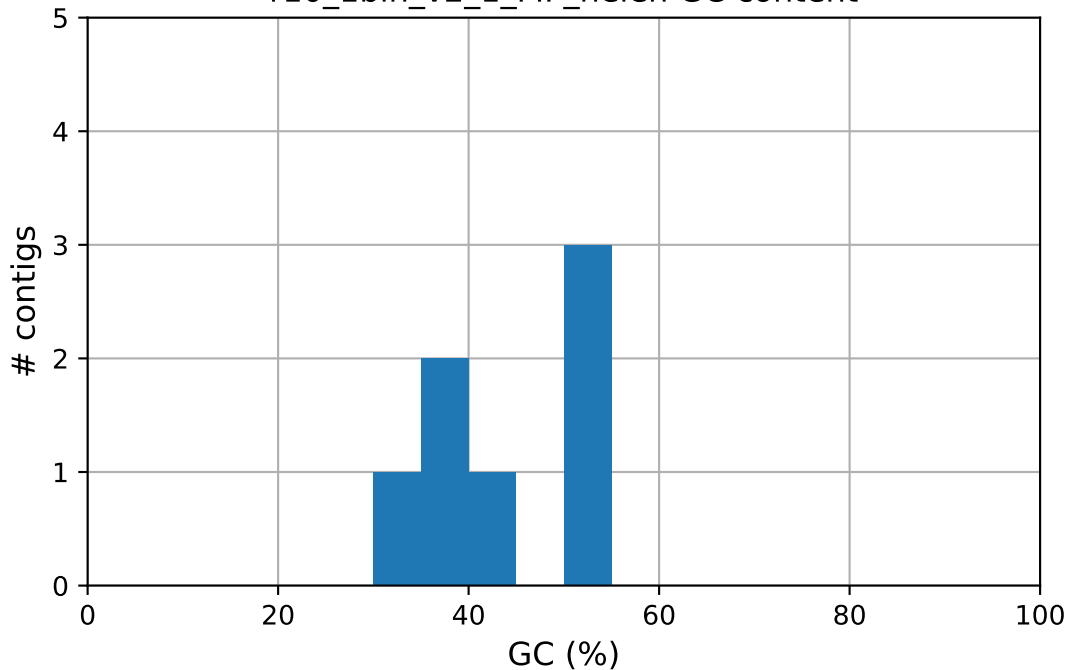
r10\_1bin\_v2\_1\_MP GC content



r10\_1bin\_v2\_1\_MP

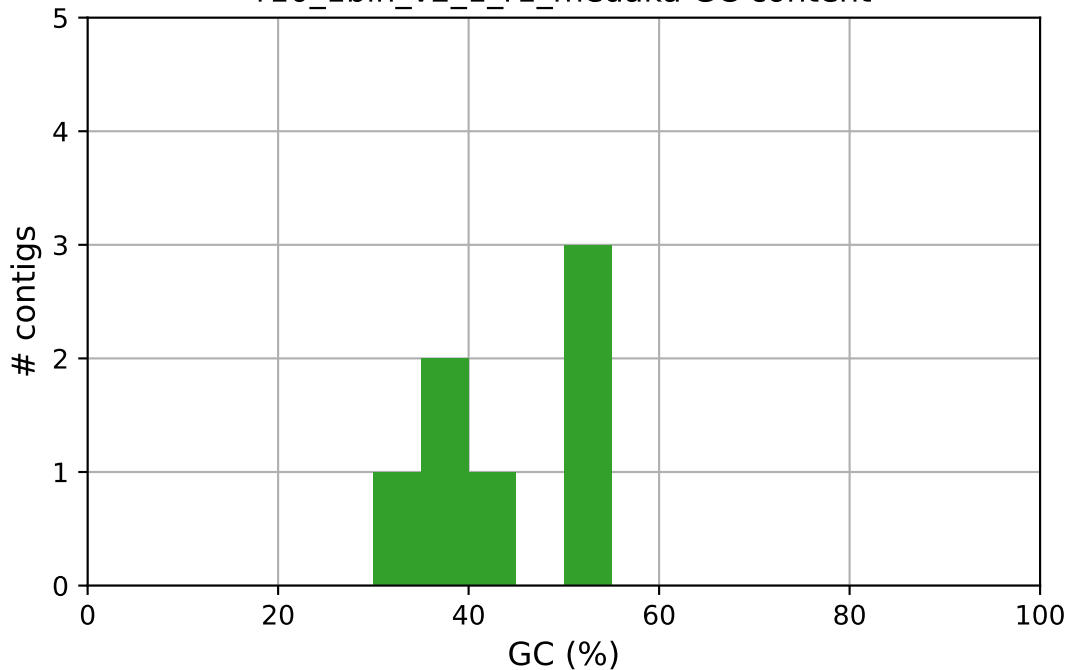


r10\_1bin\_v2\_1\_MP\_helen GC content



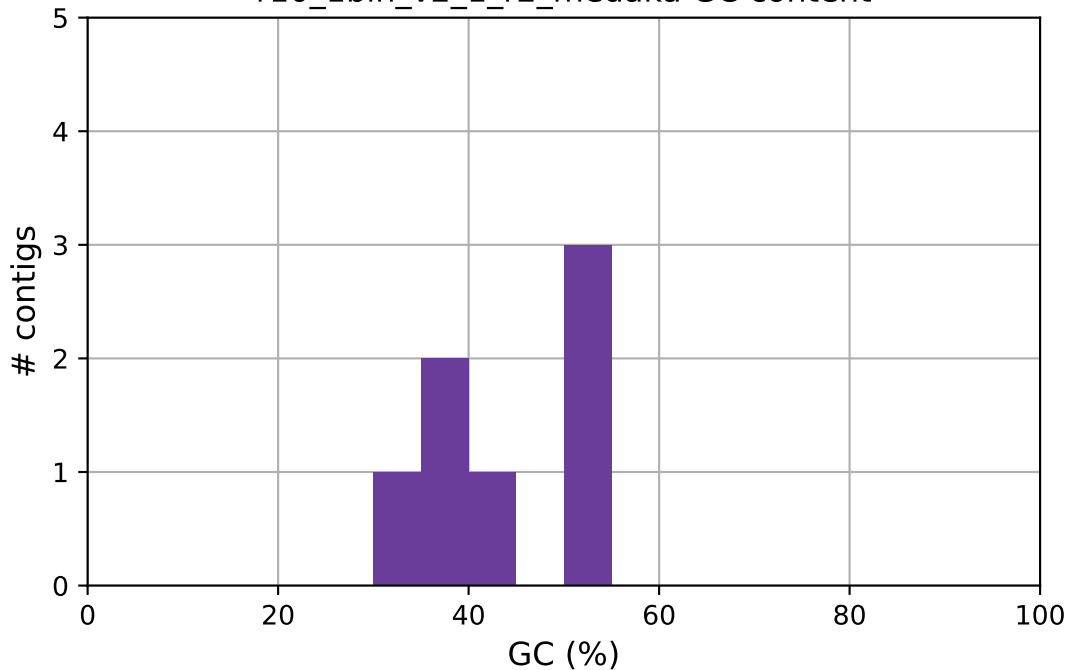
r10\_1bin\_v2\_1\_MP\_helen

r10\_1bin\_v2\_1\_r1\_medaka GC content



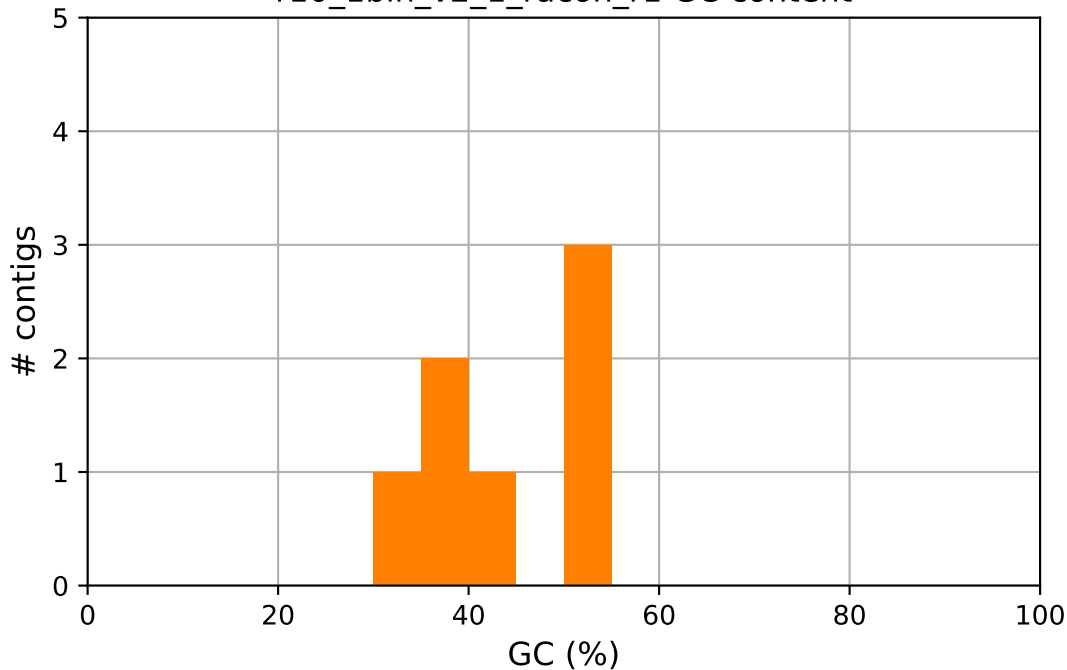
r10\_1bin\_v2\_1\_r1\_medaka

r10\_1bin\_v2\_1\_r2\_medaka GC content



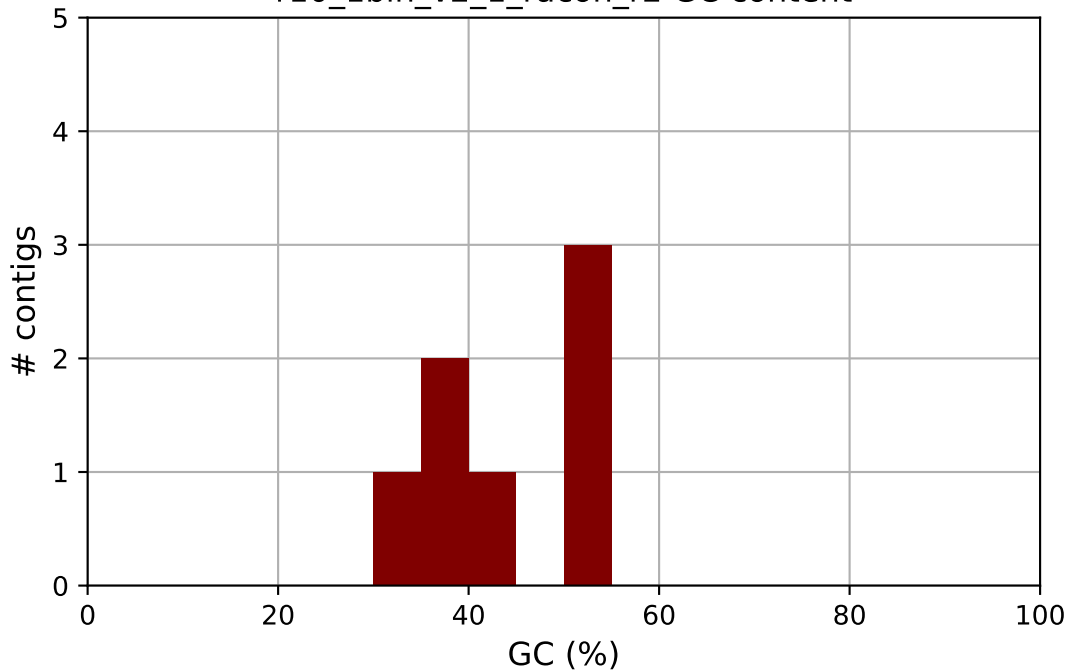
r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_1\_racon\_r1 GC content



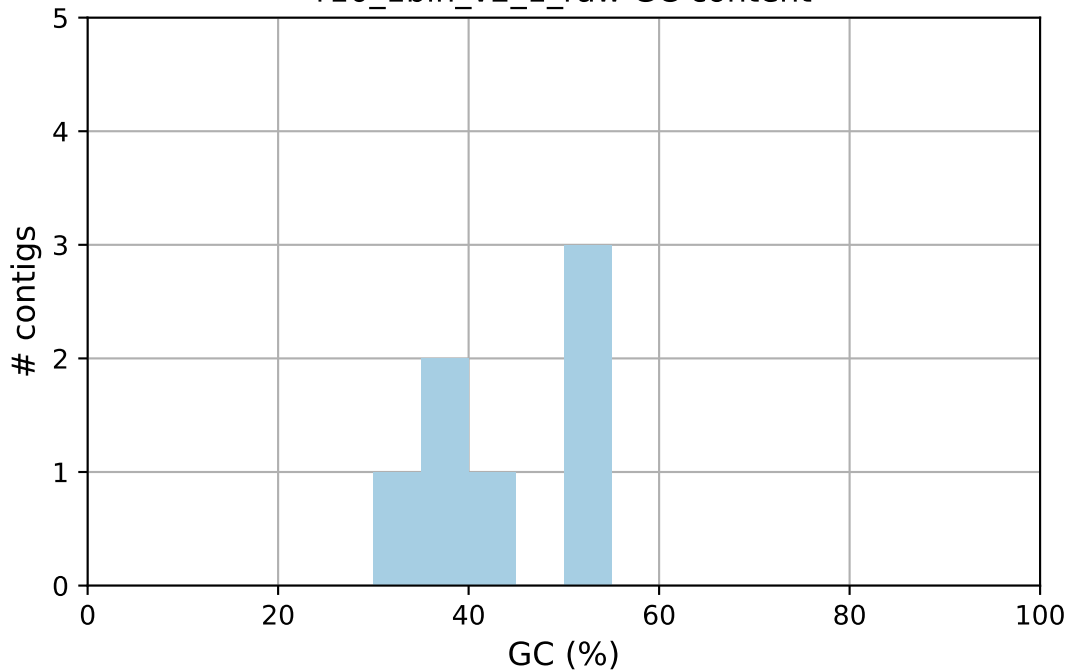
r10\_1bin\_v2\_1\_racon\_r1

r10\_1bin\_v2\_1\_racon\_r2 GC content



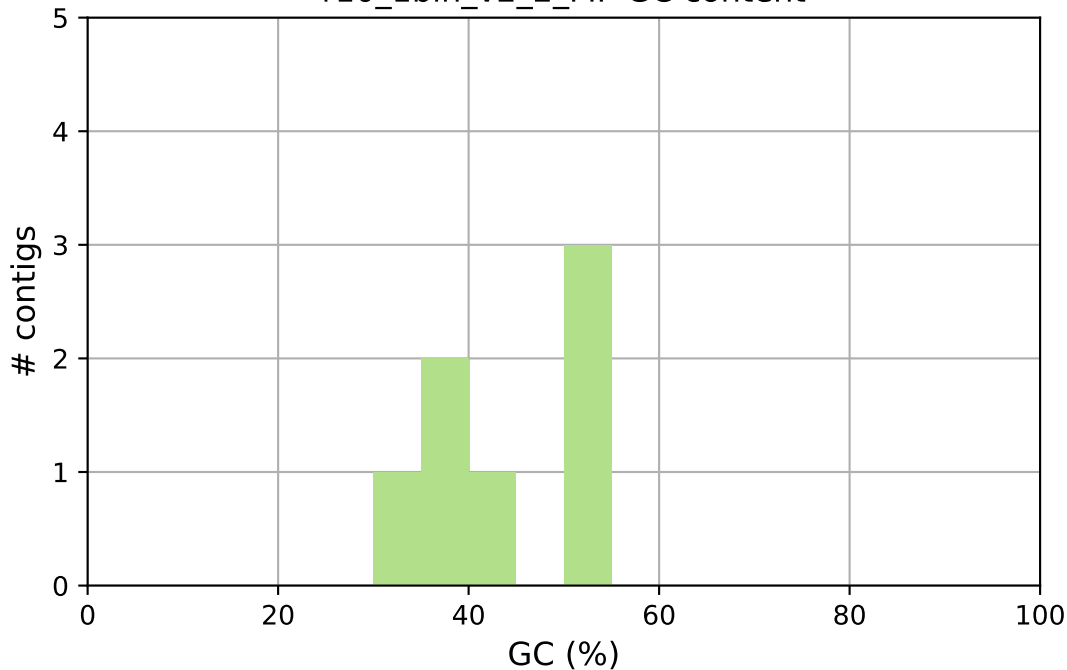
r10\_1bin\_v2\_1\_racon\_r2

r10\_1bin\_v2\_1\_raw GC content



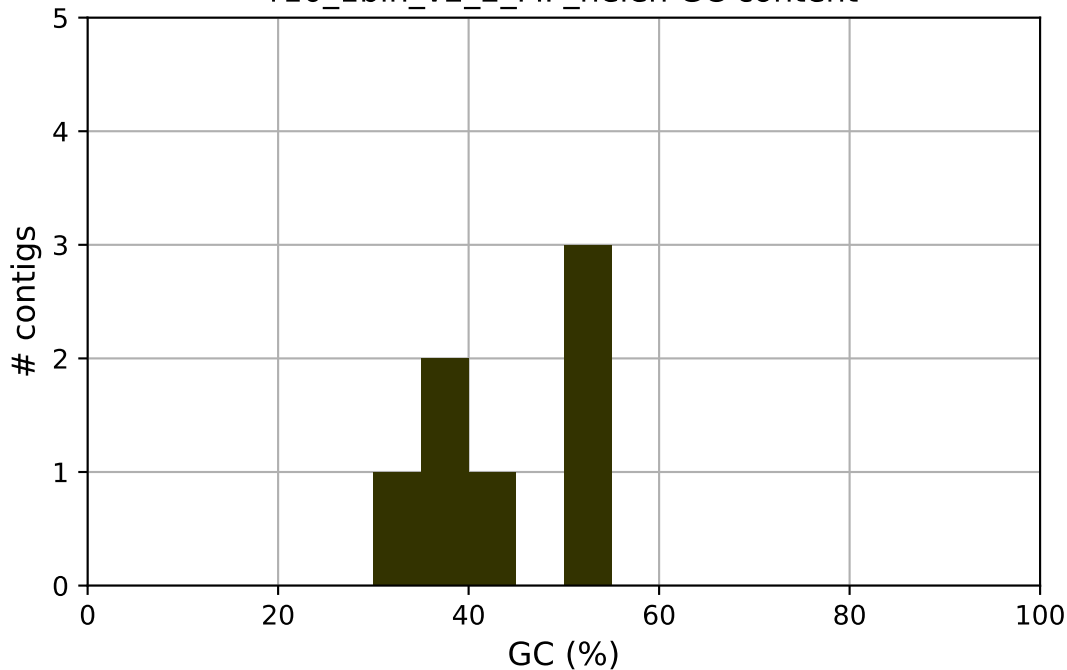
r10\_1bin\_v2\_1\_raw

r10\_1bin\_v2\_2\_MP GC content



r10\_1bin\_v2\_2\_MP

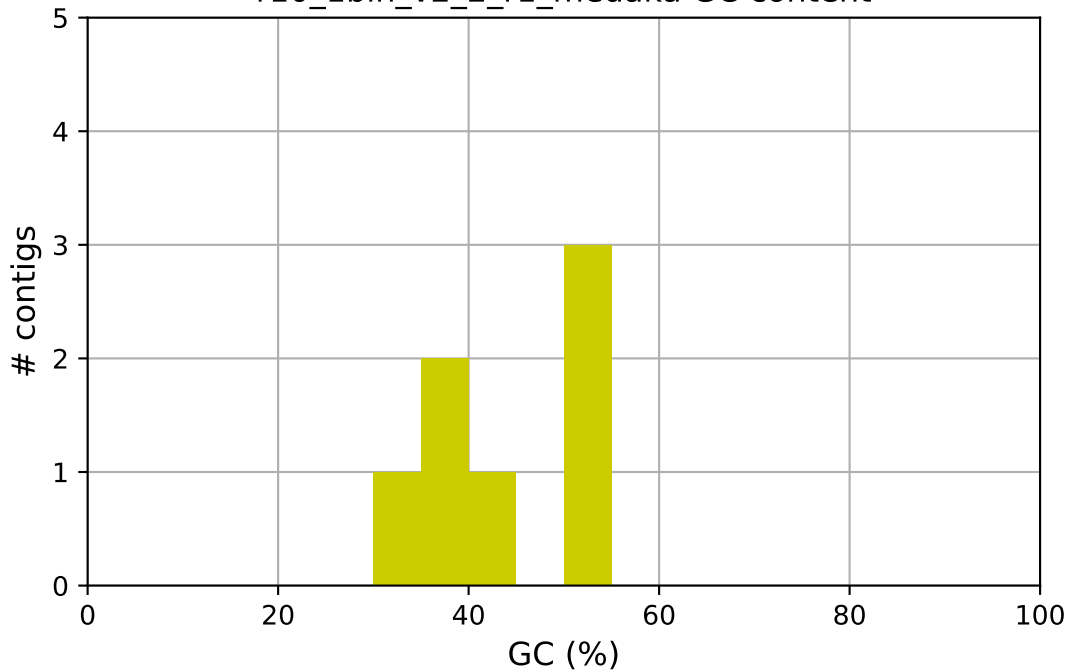
r10\_1bin\_v2\_2\_MP\_helen GC content



r10\_1bin\_v2\_2\_MP\_helen

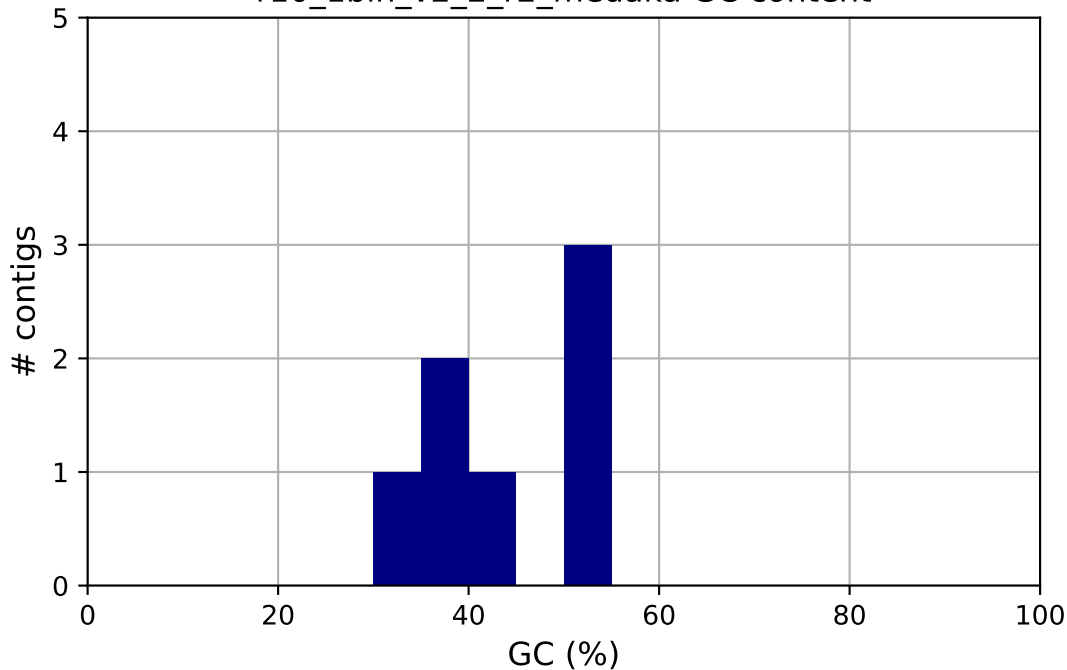


r10\_1bin\_v2\_2\_r1\_medaka GC content



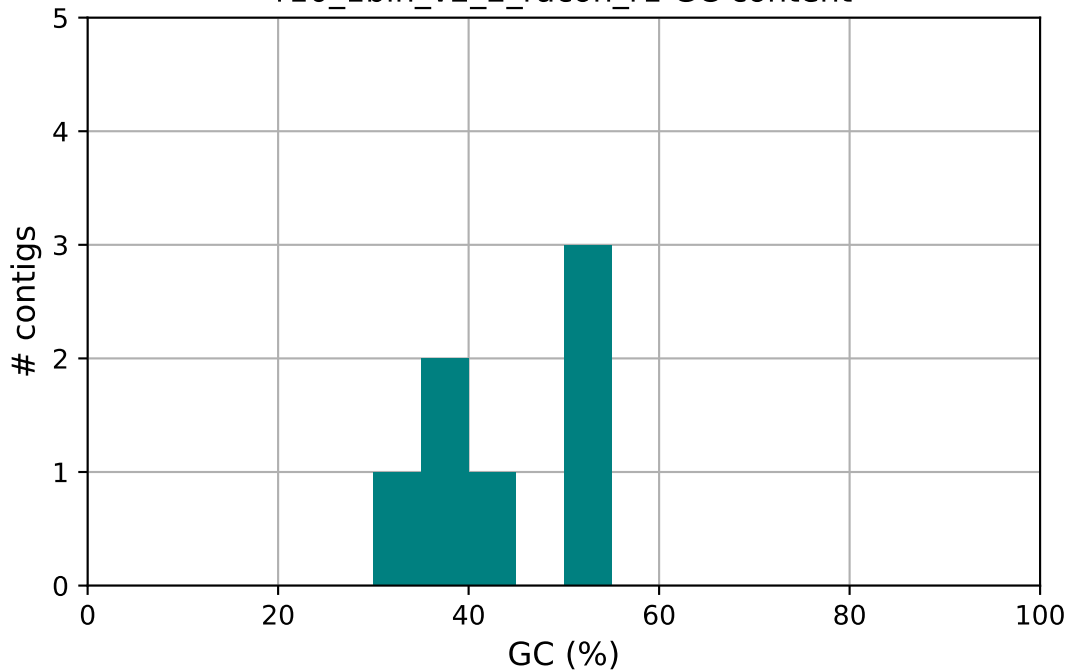
r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka GC content



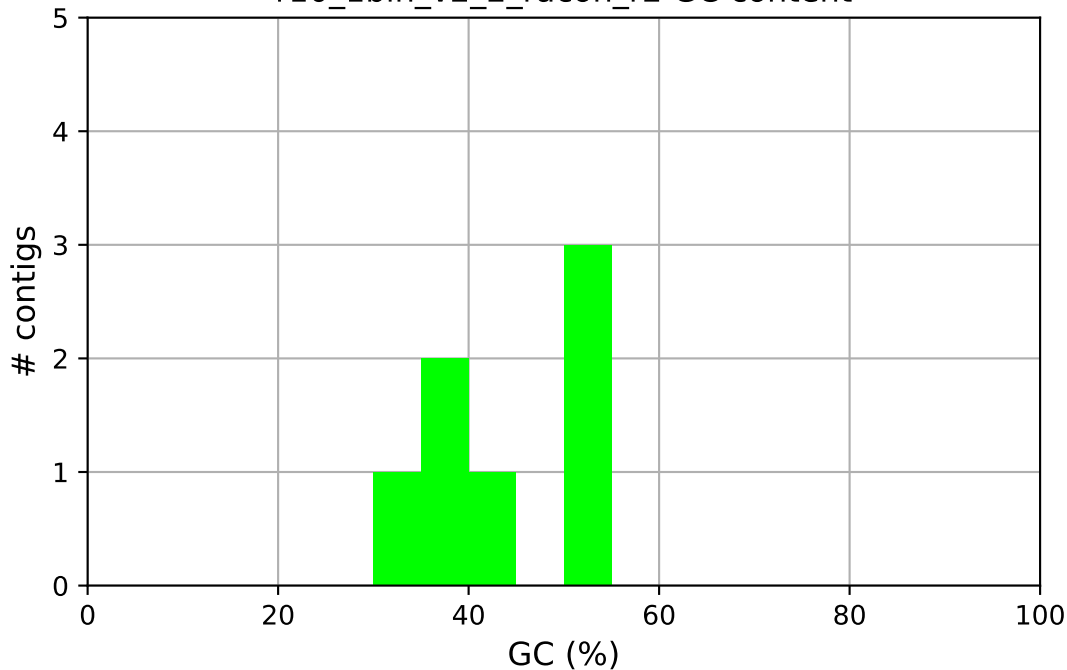
r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_2\_racon\_r1 GC content



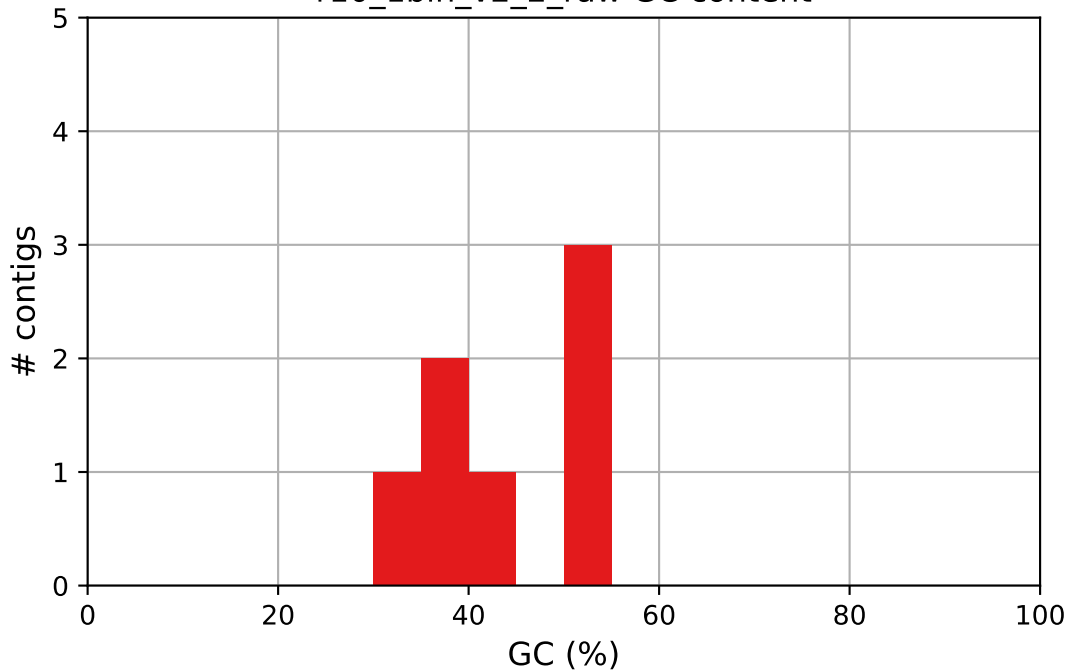
r10\_1bin\_v2\_2\_racon\_r1

r10\_1bin\_v2\_2\_racon\_r2 GC content



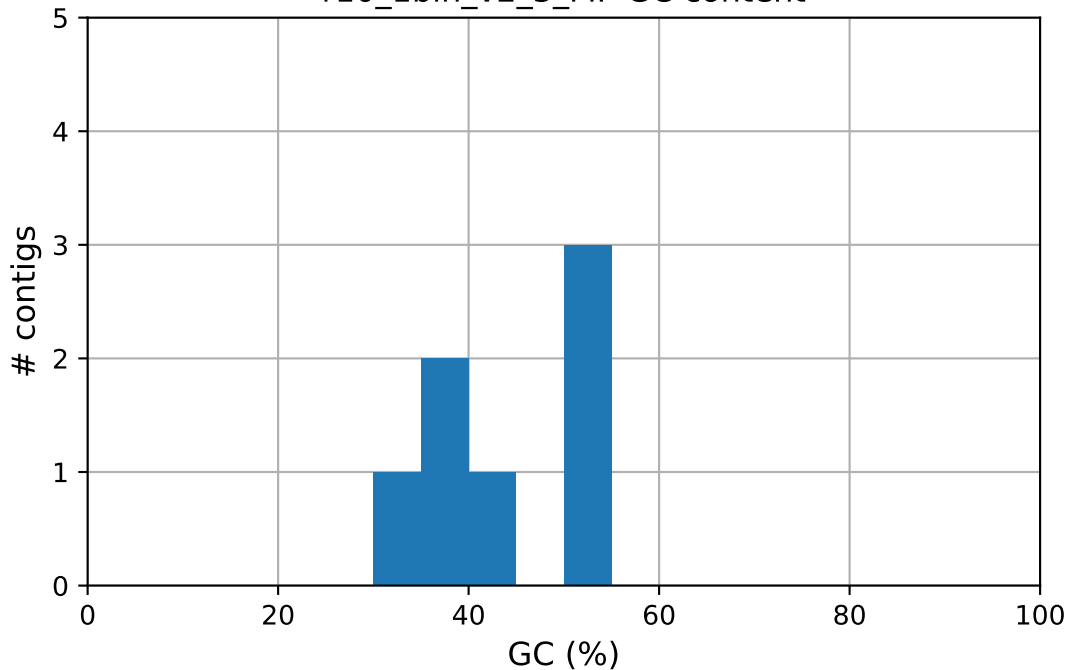
r10\_1bin\_v2\_2\_racon\_r2

r10\_1bin\_v2\_2\_raw GC content



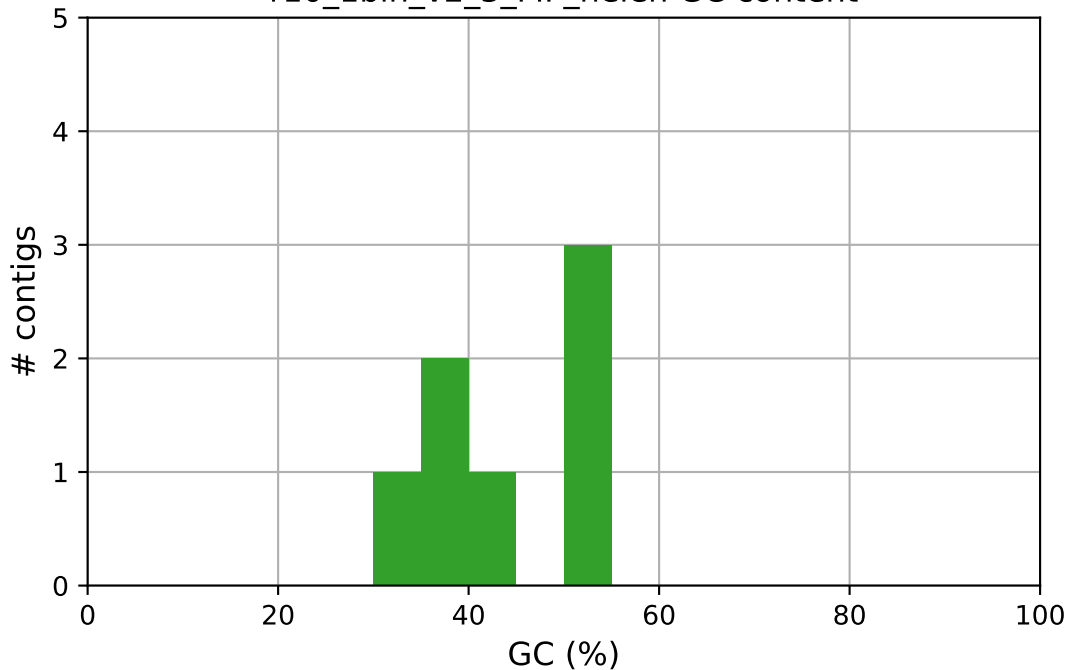
r10\_1bin\_v2\_2\_raw

r10\_1bin\_v2\_3\_MP GC content



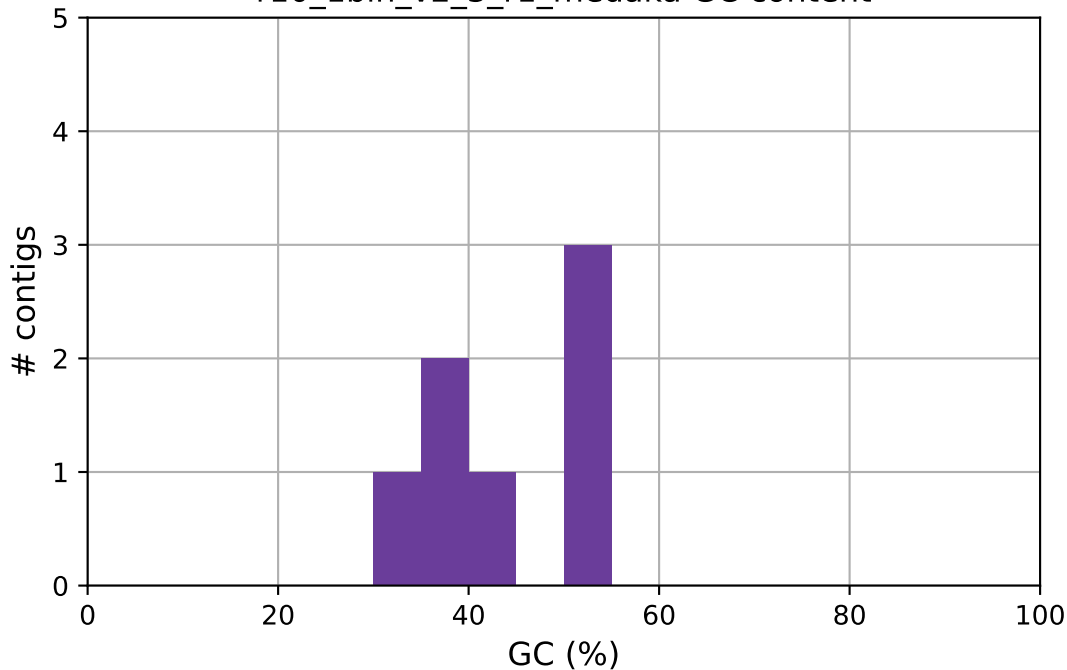
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen GC content



r10\_1bin\_v2\_3\_MP\_helen

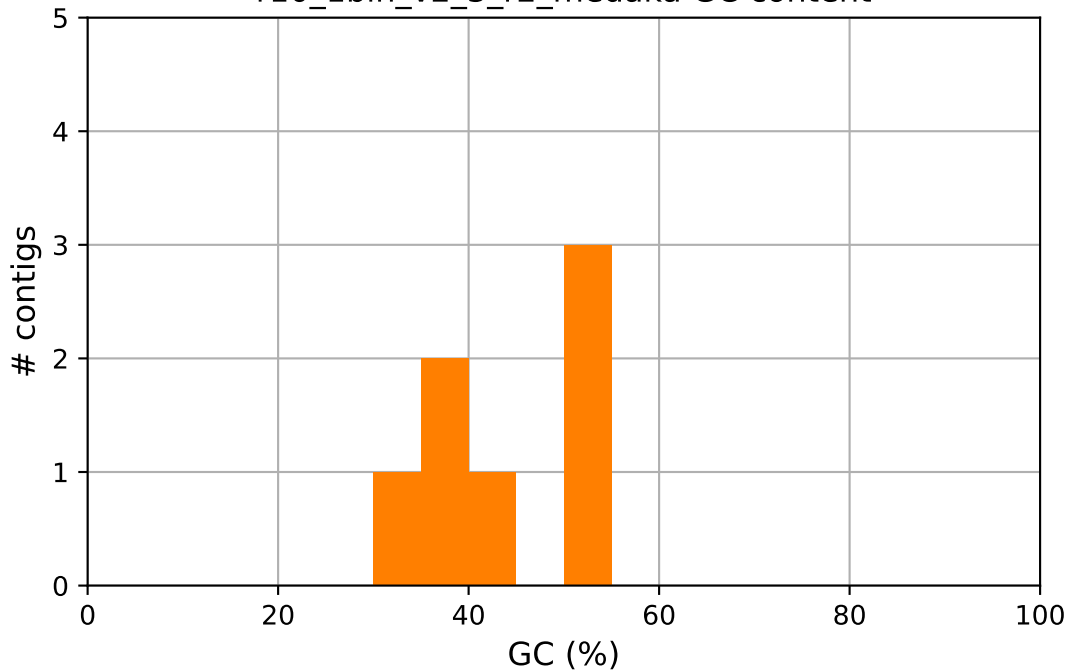
r10\_1bin\_v2\_3\_r1\_medaka GC content



r10\_1bin\_v2\_3\_r1\_medaka

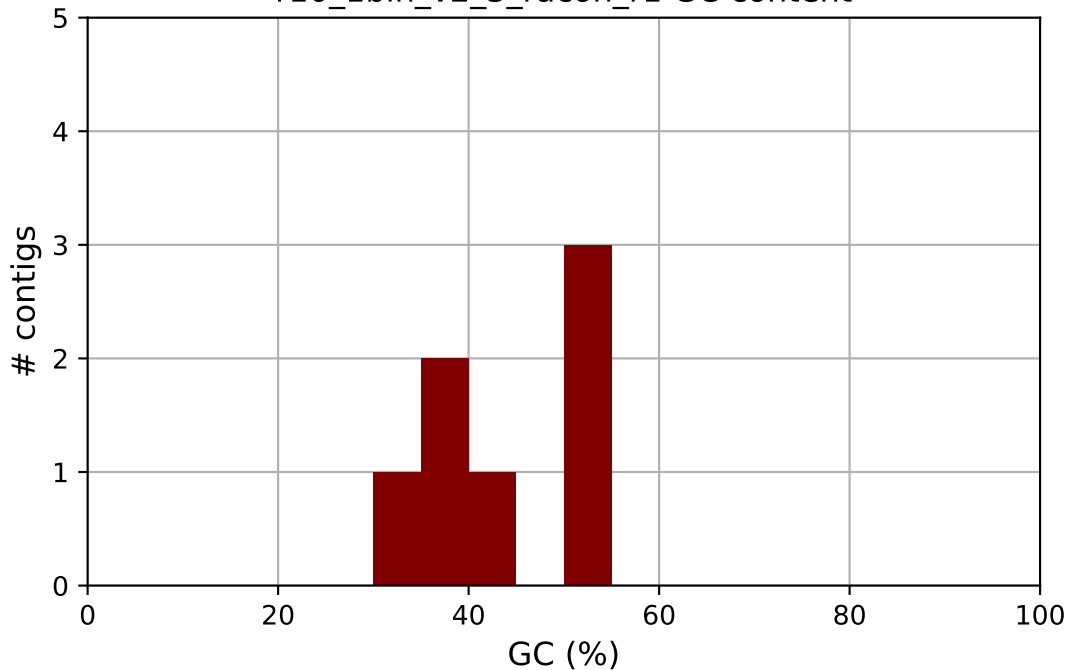


r10\_1bin\_v2\_3\_r2\_medaka GC content



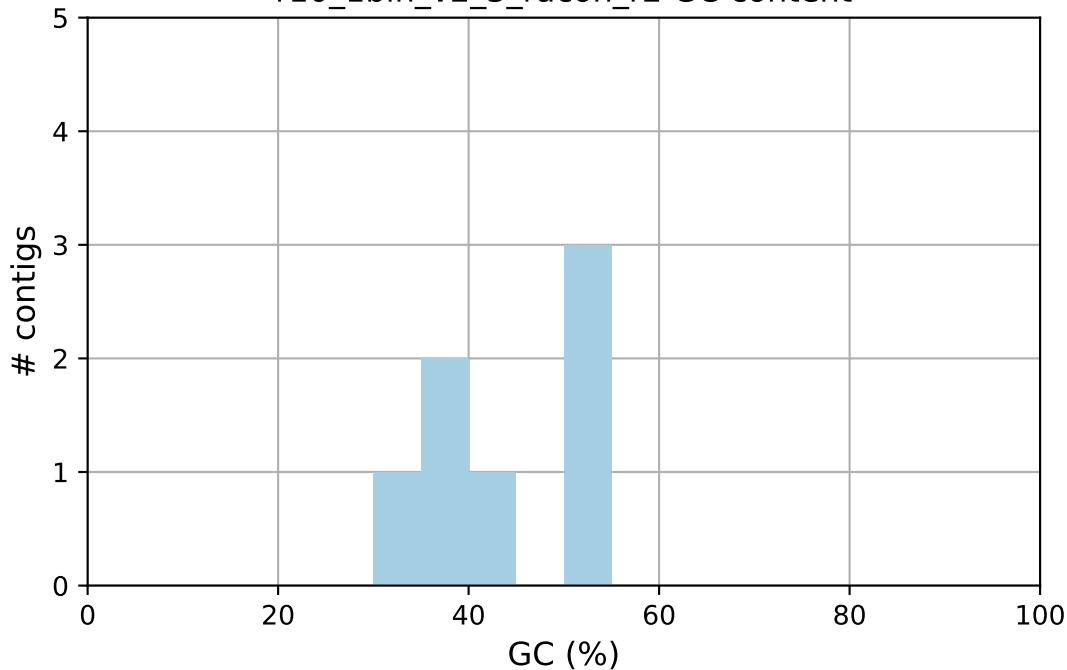
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1 GC content



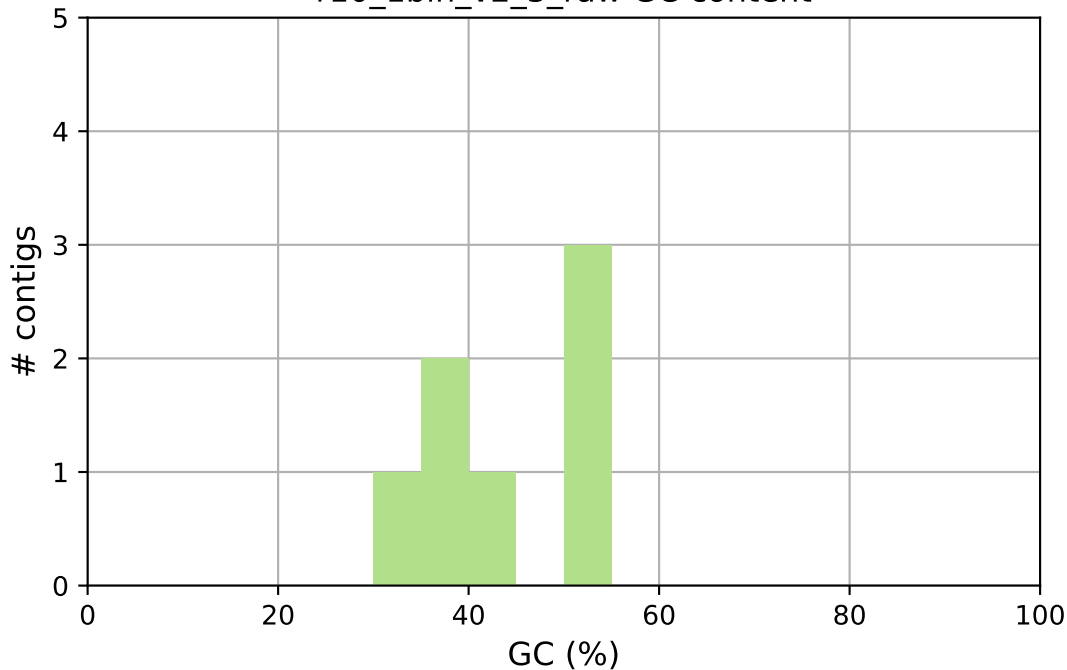
r10\_1bin\_v2\_3\_racon\_r1

r10\_1bin\_v2\_3\_racon\_r2 GC content



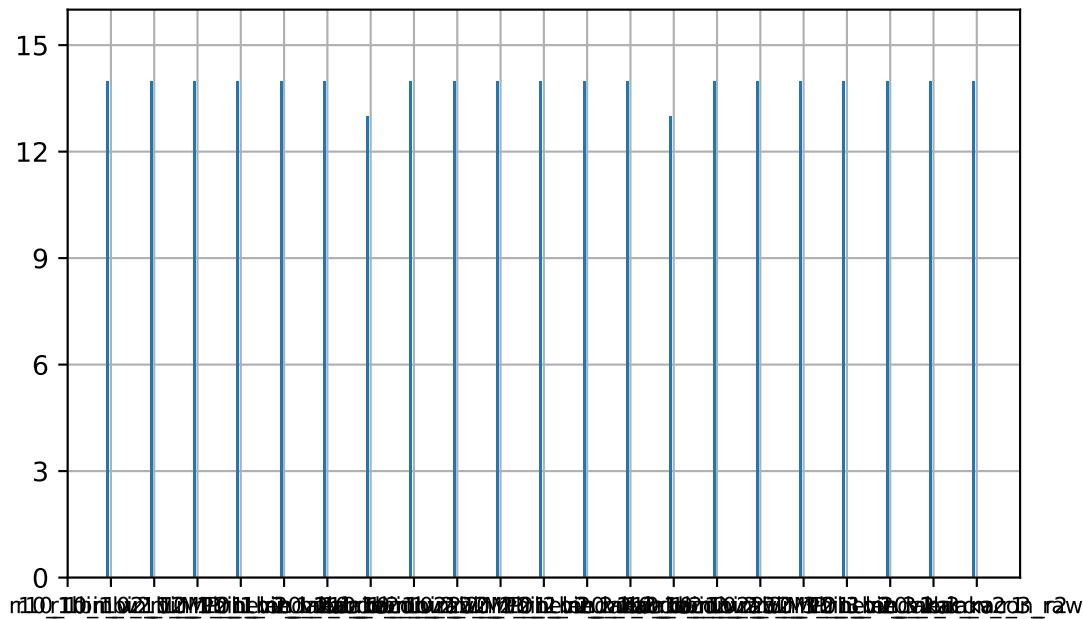
r10\_1bin\_v2\_3\_racon\_r2

r10\_1bin\_v2\_3\_raw GC content



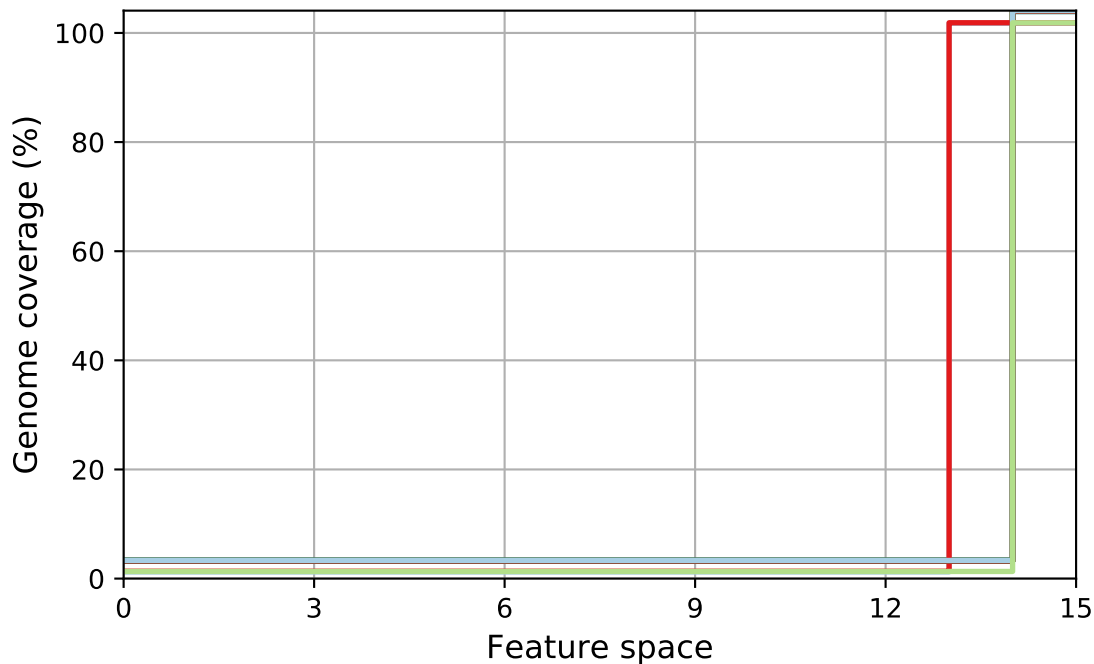
r10\_1bin\_v2\_3\_raw

# Misassemblies



# translocations

### FRCurve (misassemblies)



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

— r10\_1bin\_v2\_2\_MP\_helen

— r10 1bin v2 2 r1 medaka

— r10 1bin y2 2 r2 medaka

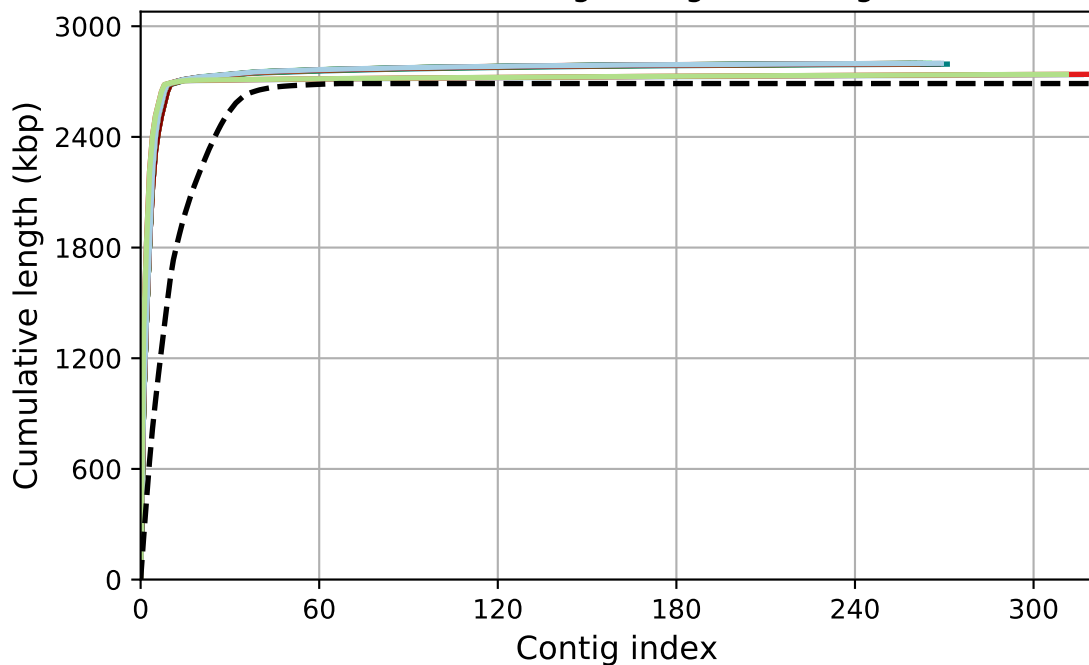
— r10\_1bin\_v2\_3\_MP

— r10\_1bin\_v2\_3\_MP\_h

— r10 1bin v2 3 r1 m

— r10 1bin v2 3 r2 m

Cumulative length (aligned contigs)



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

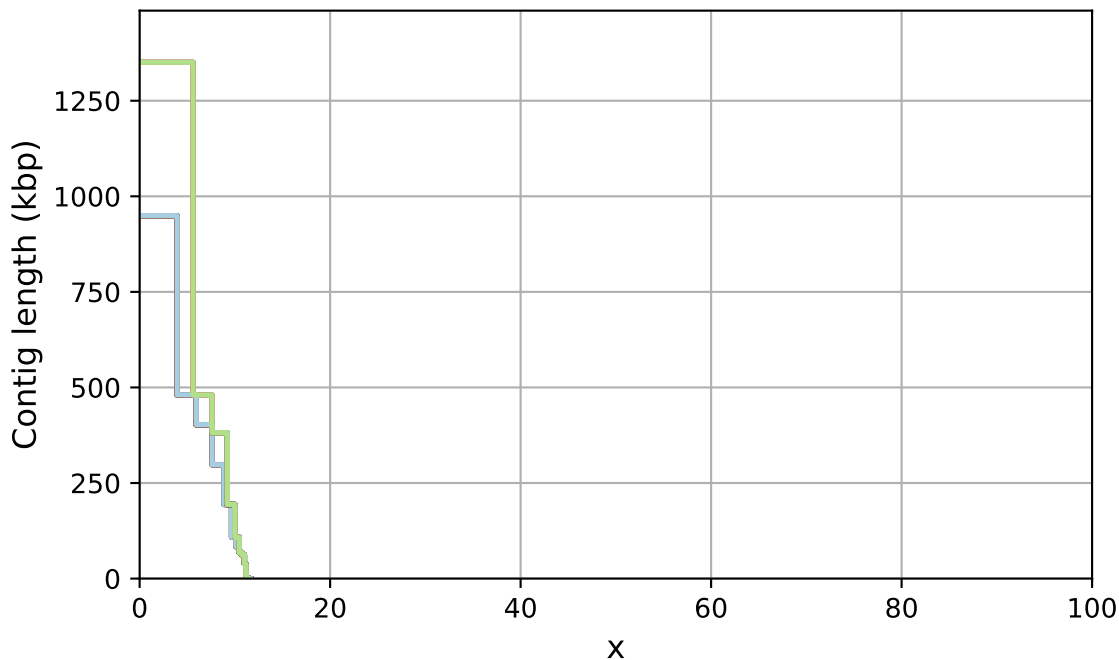
r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1

NAx



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\_helen

r10\_1bin\_v2\_1\_r1\_medaka

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_3\_r1\_medaka

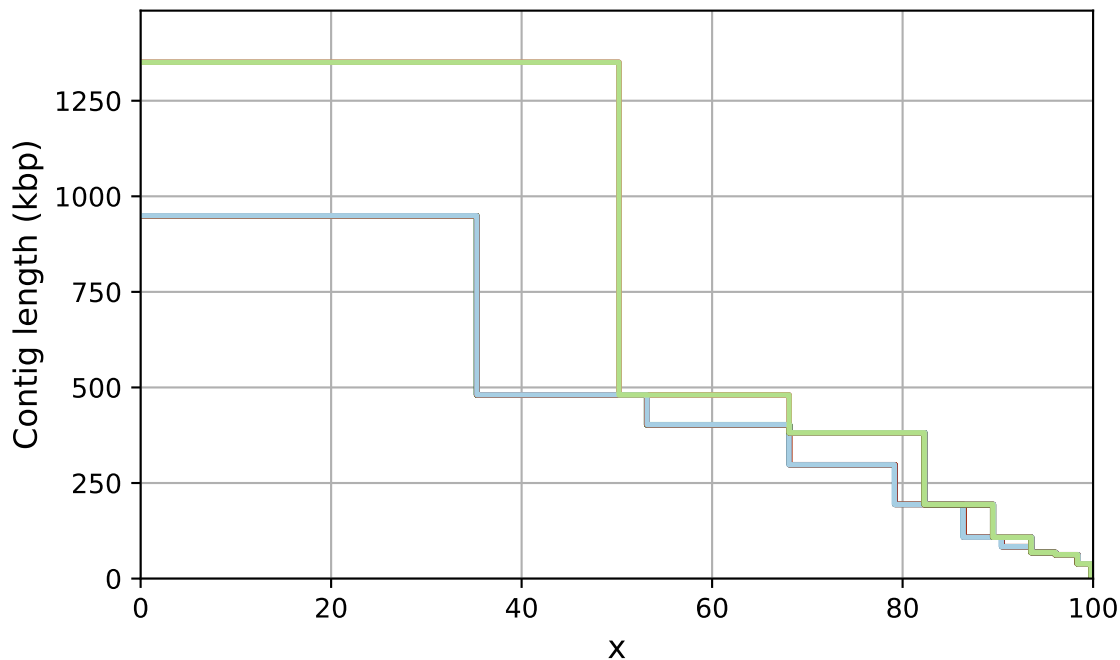
r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_r2\_medaka



# NGAx



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

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

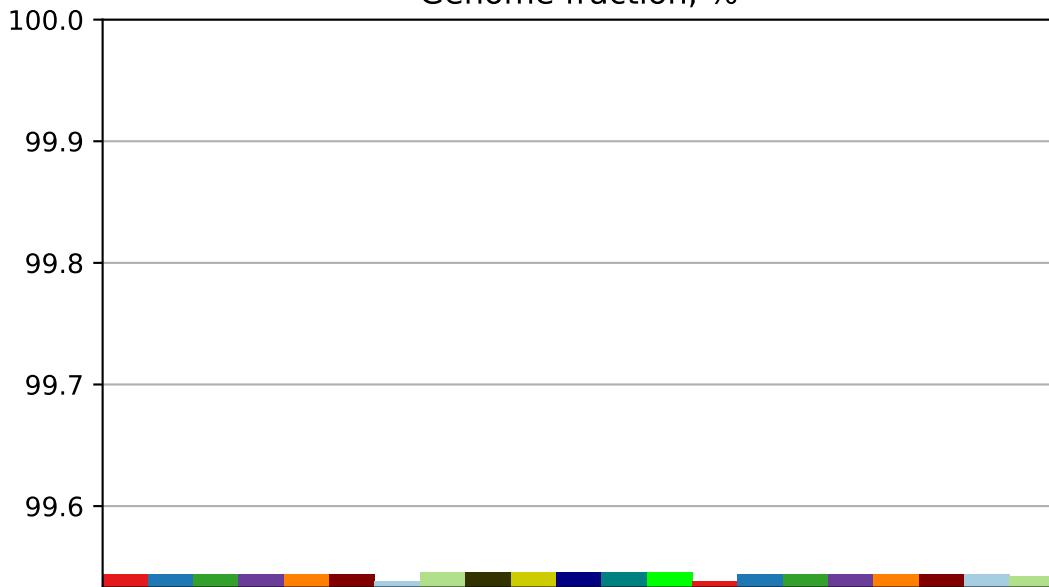
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

Genome fraction, %



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

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka