

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	
# contigs (>= 10000 bp)	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	
# contigs (>= 50000 bp)	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	
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	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
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 (%)	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82
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	2845365	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	
LG50	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	
LG75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
# misassemblies	34	34	34	34	34	34	31	34	34	34	34	34	34	32	33	33	33	33	33	30	
# misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Misassembled contigs length	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	4045608	4045229	4045315	4042940	4045596	4045614	4045597	4045593	4045228	4045344	4043027
# local misassemblies	13	13	13	13	13	13	19	13	13	13	13	13	14	17	13	13	13	13	13	16	
# scaffold gap ext. mis.	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	
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	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	
Unaligned length	19977169	19974309	19975362	19967757	19962982	19959156	20001076	19976530	19973307	19975868	19964584	19962199	19955344	19999168	19978065	19975780	19977848	19973498	19968251	19963630	20004206
Genome fraction (%)	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.999	99.999	99.999	99.999	99.999	99.999	99.996	99.998	99.998	99.998	99.998	99.998	99.992	
Duplication ratio	1.028	1.027	1.028	1.028	1.028	1.028	1.018	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.028	1.028	1.028	1.028	1.018	
# 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	
# mismatches per 100 kbp	97.60	94.11	96.04	95.74	98.30	98.10	88.92	98.00	96.22	95.46	95.89	99.60	99.38	86.16	97.20	95.59	97.07	95.69	97.15	97.35	
# indels per 100 kbp	11.27	11.04	10.44	10.54	23.99	20.47	104.70	11.29	12.70	10.46	10.34	23.38	20.35	103.60	11.19	11.27	10.64	10.46	22.98	20.37	
Largest alignment	788689	788690	788691	788688	788606	788620	788112	788681	788687	788691	788690	788627	788626	788148	788615	788613	788616	788615	788578	788053	
Total aligned length	4097143	4094617	4096138	4096006	4096513	4096310	4057959	4097378	4095921	4095451	4095794	4097111	4096626	4060790	4097162	4096059	4097001	4095831	4096584	4096702	
NGA50	329474	329468	329466	329465	329433	329450	329353	315065	315070	315066	315066	315027	315041	314876	329413	329412	329410	329410	329383	329401	
NGA75	257050	257051	257051	257051	257022	257026	256895	257050	257052	257051	257052	257027	257027	256896	257050	257054	257050	257050	257018	257028	
LGA50	4	4	4	4	4	4	4	5	5	5	5	5	5	5	4	4	4	4	4	4	
LGA75	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	

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

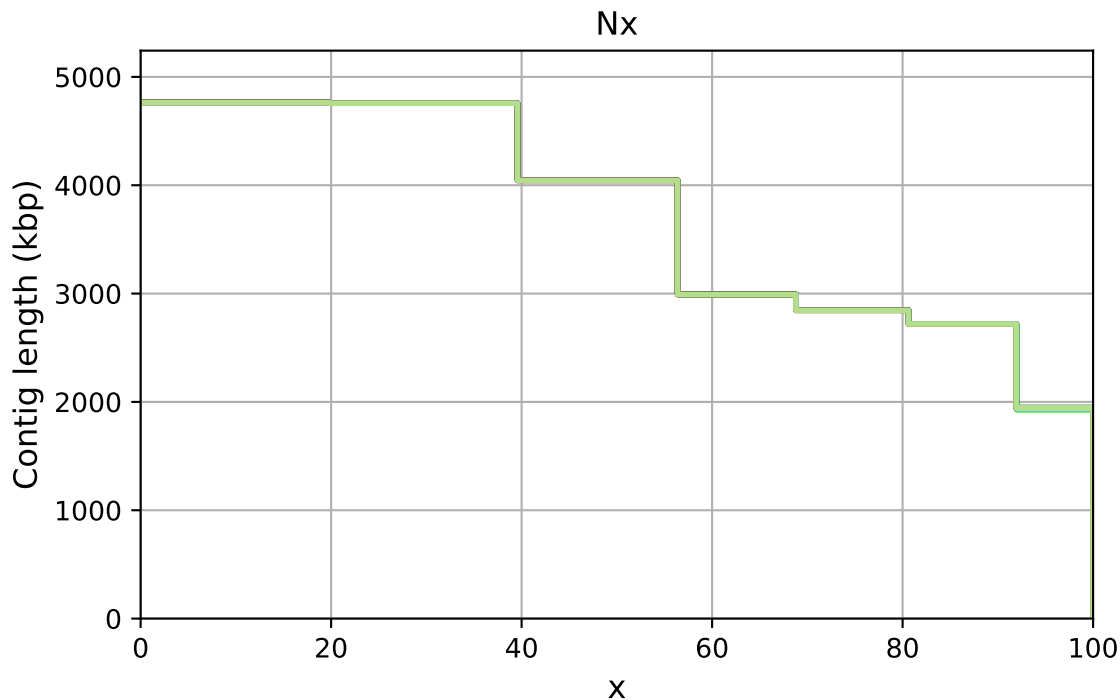
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	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	34	34	34	34	34	34	31	34	34	34	34	34	34	32	33	33	33	33	33	33	30
# contig misassemblies	34	34	34	34	34	34	31	34	34	34	34	34	34	32	33	33	33	33	33	33	30
# 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	34	34	34	34	34	34	31	34	34	34	34	34	34	32	33	33	33	33	33	33	30
# 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	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	4045608	4045229	4045315	4042940	4045596	4045614	4045597	4045593	4045228	4045344	4043027
# 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	13	10	10	10	10	10	10	11	10	10	10	10	10	10	9
# local misassemblies	13	13	13	13	13	13	19	13	13	13	13	13	14	17	13	13	13	13	13	13	16
# 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	49	49	49	49	49	49	30	49	49	49	49	49	48	32	49	49	49	49	48	48	31
# 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	3890	3751	3828	3816	3918	3910	3544	3906	3835	3805	3822	3970	3961	3434	3874	3810	3869	3814	3872	3880	3251
# indels	449	440	416	420	956	816	4173	450	506	417	412	932	811	4129	446	449	424	417	916	812	4153
# indels (<= 5 bp)	400	392	367	371	906	767	4112	399	448	369	364	882	763	4072	397	400	375	369	866	762	4094
# indels (> 5 bp)	49	48	49	49	50	49	61	51	58	48	48	50	48	57	49	49	49	48	50	50	59
Indels length	2591	2571	2552	2556	3197	3038	7351	2608	2760	2537	2532	3176	3006	7216	2581	2595	2559	2536	3185	3029	7240

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	19977169	19974309	19975362	19967757	19962982	19959156	20001076	19976530	19973307	19975868	19964584	19962199	19955344	19999168	19978065	19975780	19977848	19973498	19968251	19963630	20004206
# 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).



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

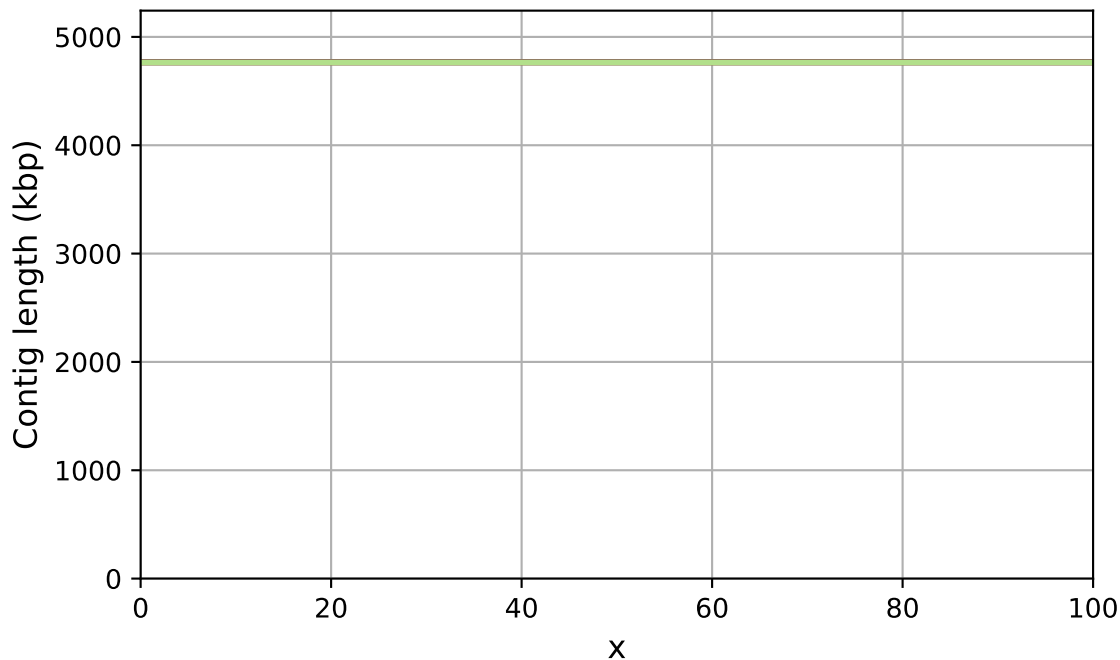
r10\_1bin\_v2\_3\_MP

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\_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

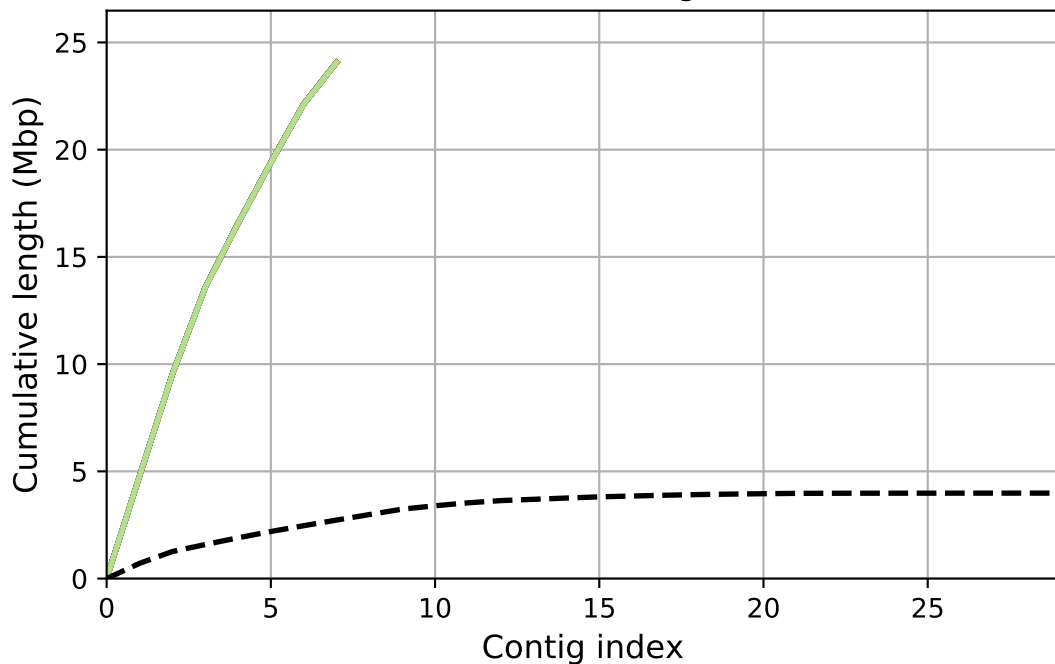
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

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

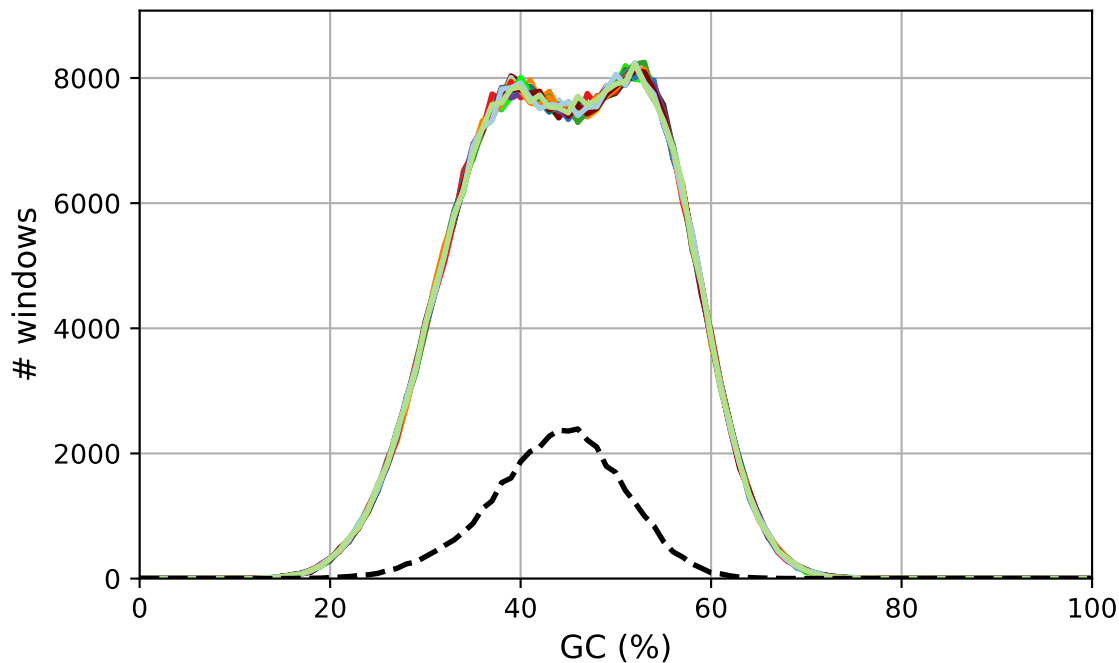
r10\_1bin\_v2\_3\_MP\_helen

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

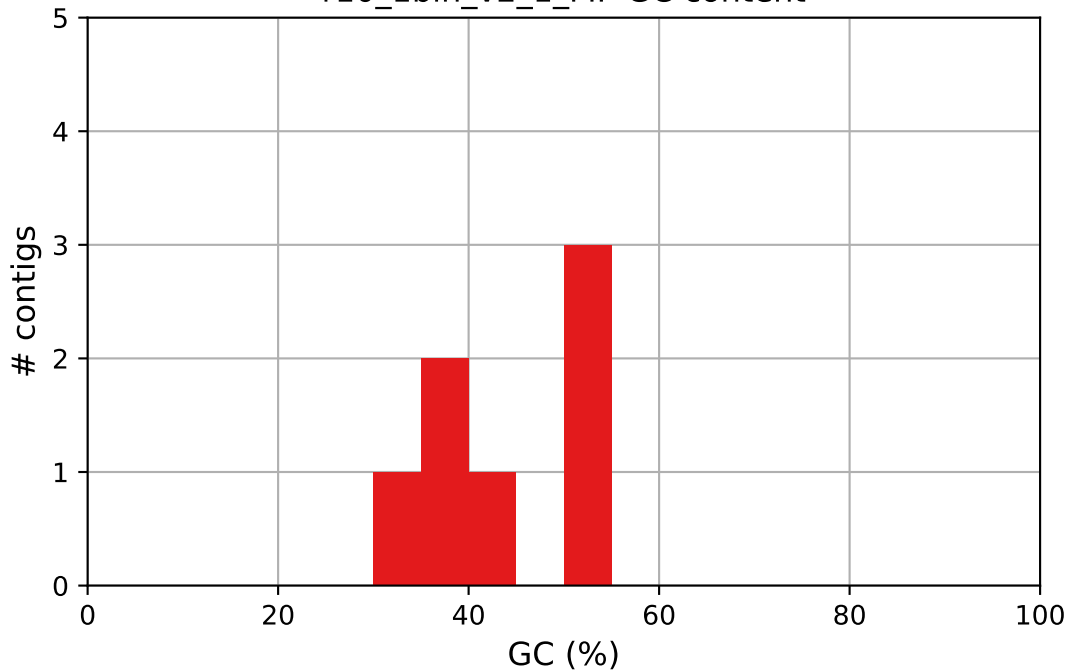
r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1

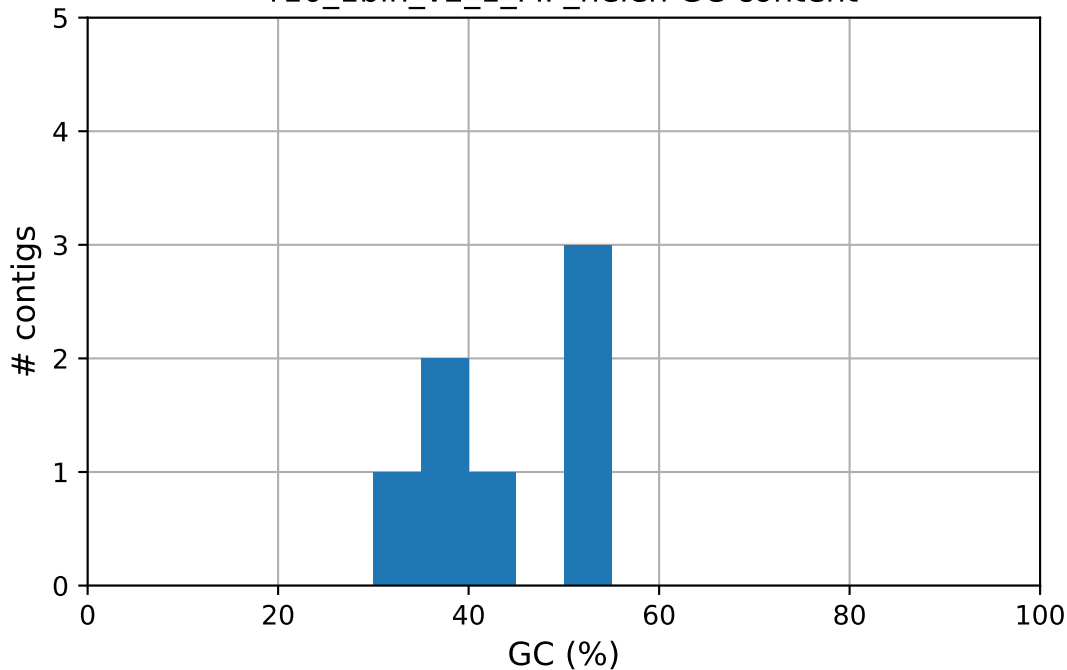
r10\_1bin\_v2\_1\_MP GC content



r10\_1bin\_v2\_1\_MP

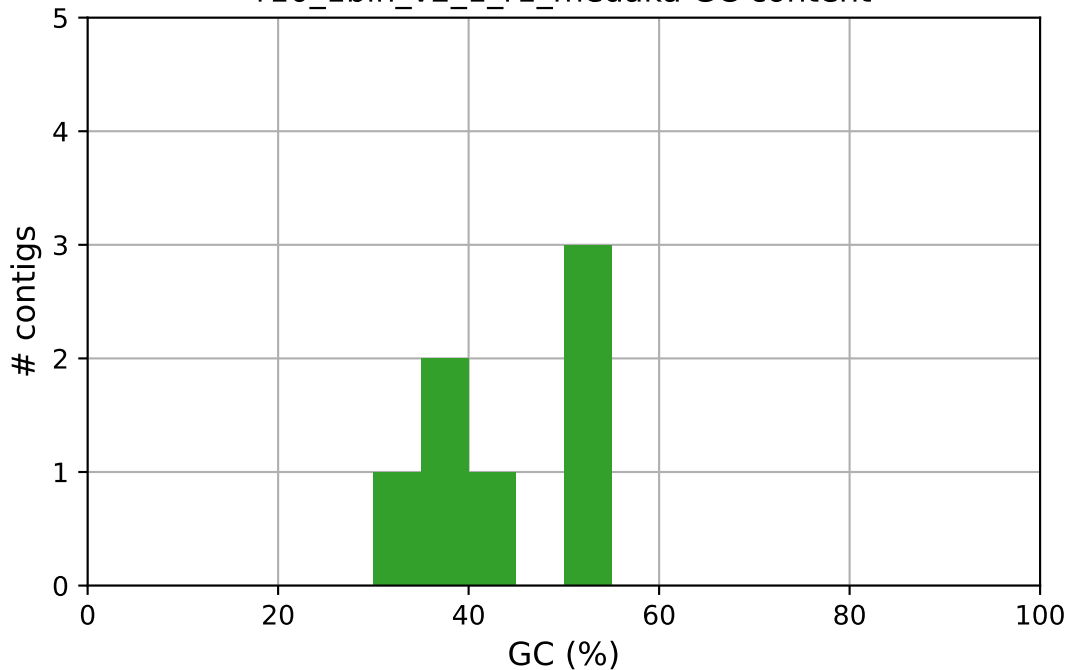


r10\_1bin\_v2\_1\_MP\_helen GC content



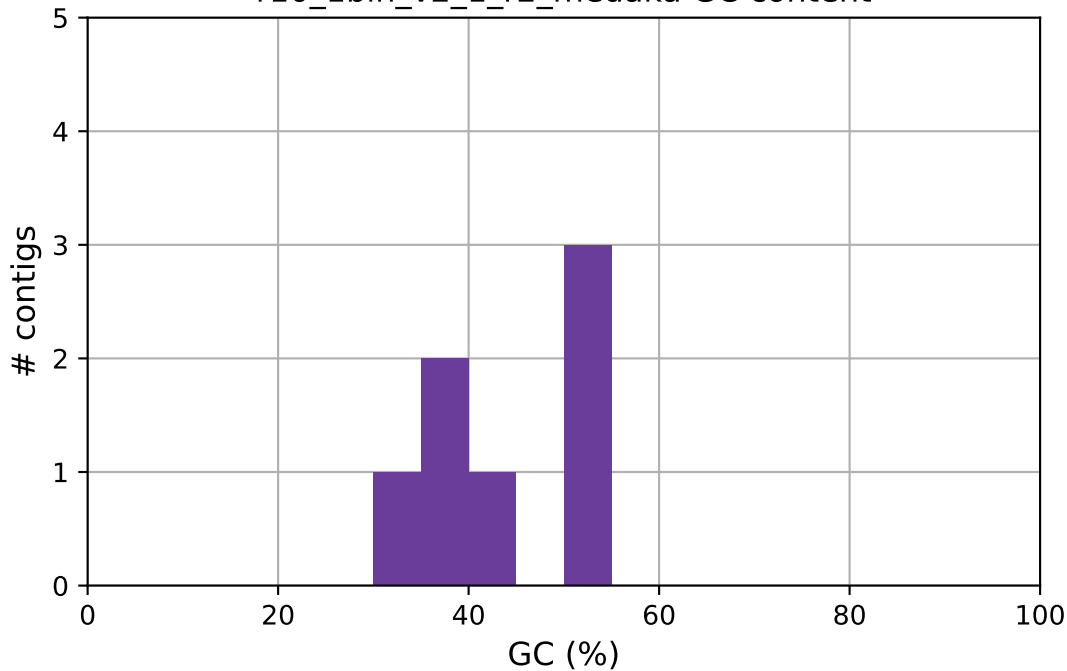
r10\_1bin\_v2\_1\_MP\_helen

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



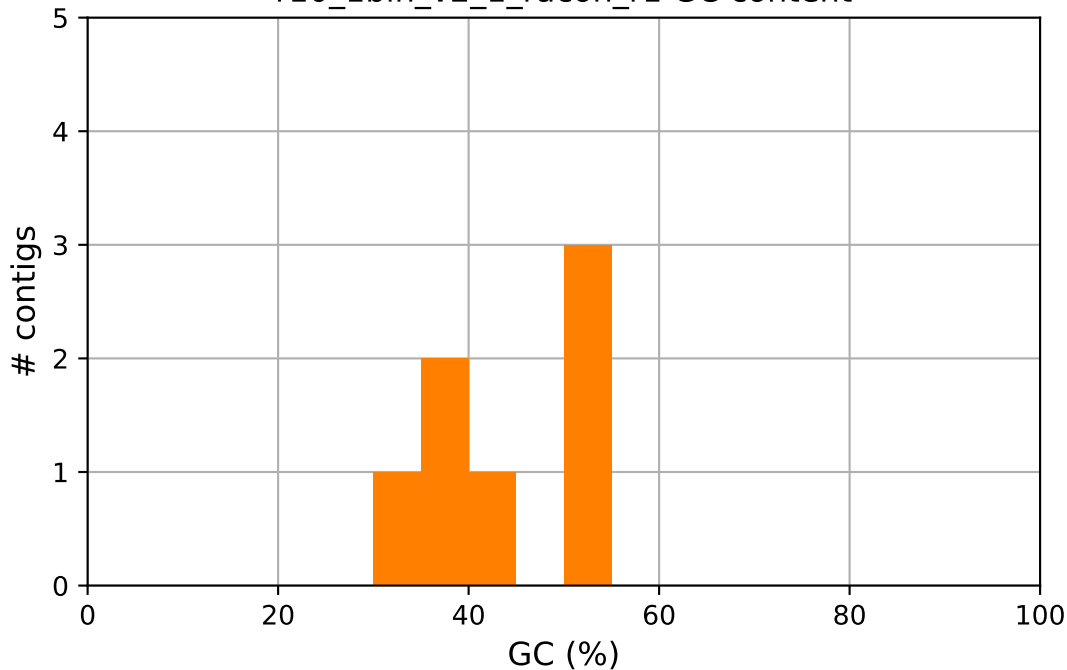
r10\_1bin\_v2\_1\_r1\_medaka

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



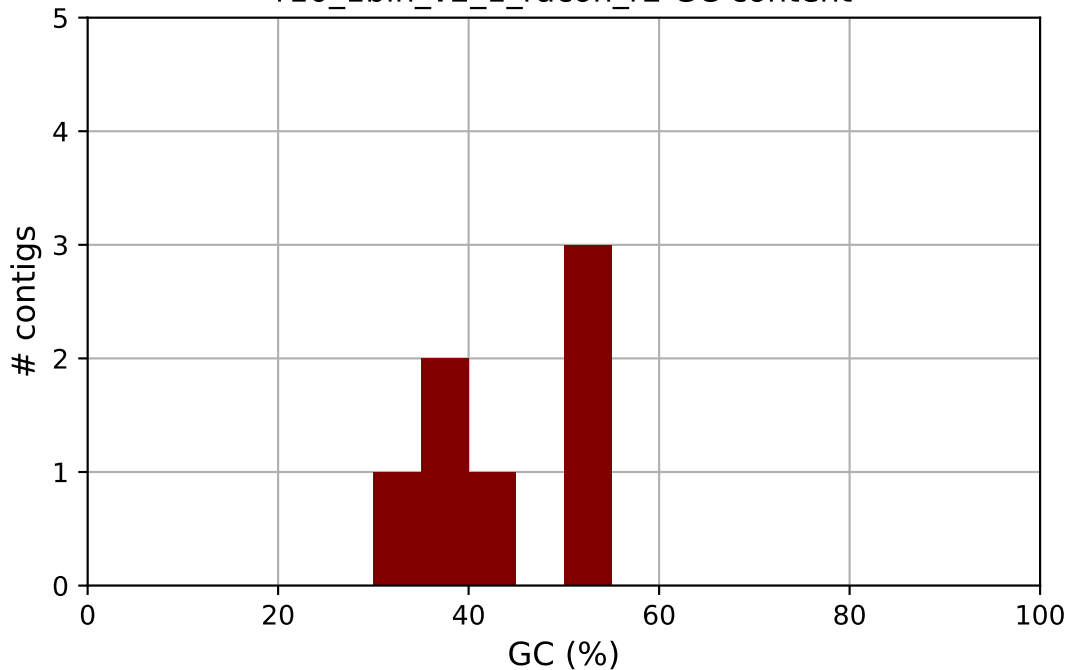
r10\_1bin\_v2\_1\_r2\_medaka

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



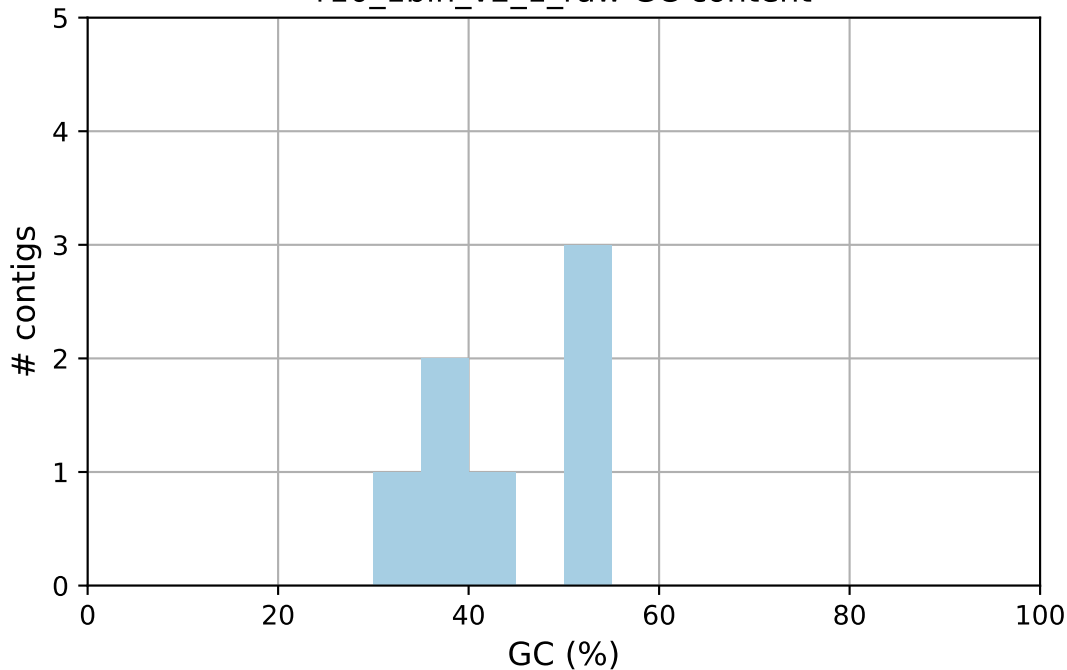
r10\_1bin\_v2\_1\_racon\_r1

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



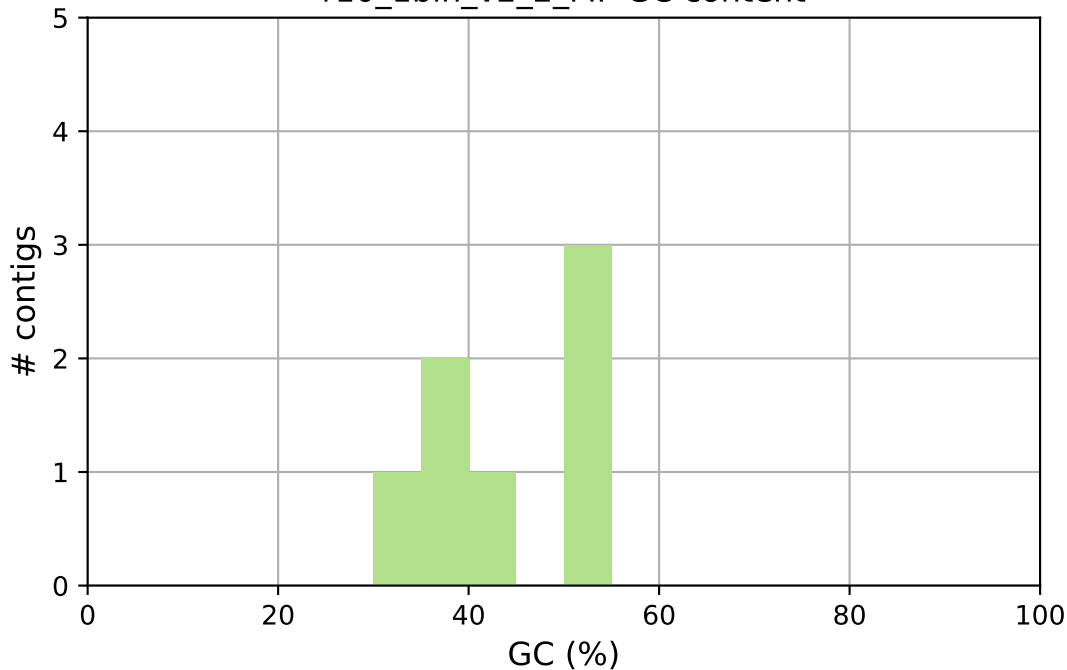
r10\_1bin\_v2\_1\_racon\_r2

r10\_1bin\_v2\_1\_raw GC content



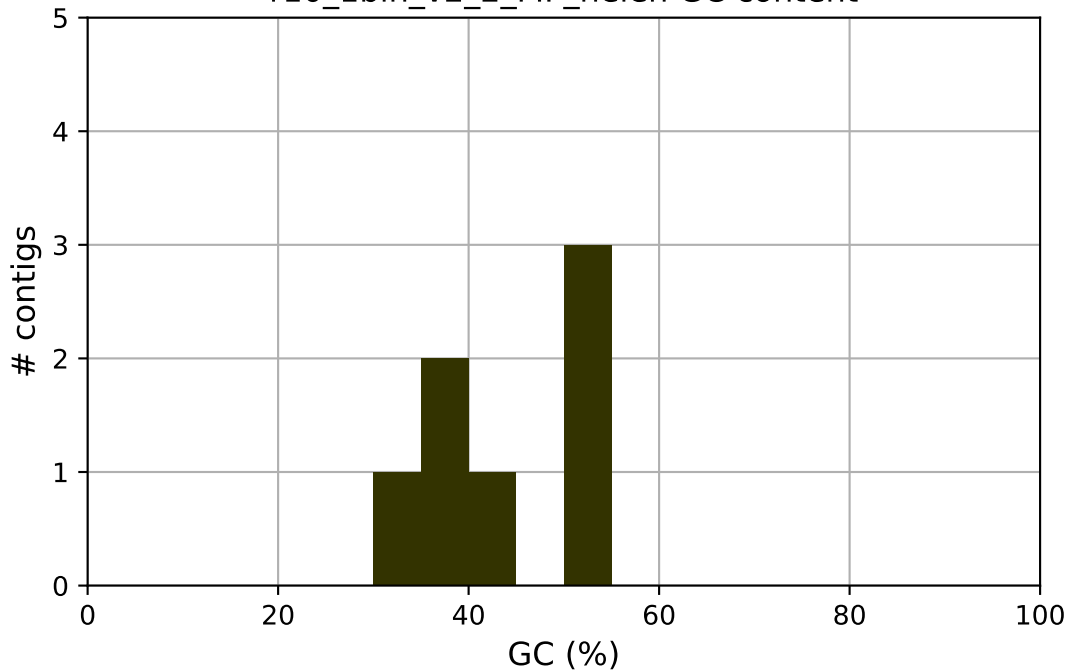
r10\_1bin\_v2\_1\_raw

r10\_1bin\_v2\_2\_MP GC content



r10\_1bin\_v2\_2\_MP

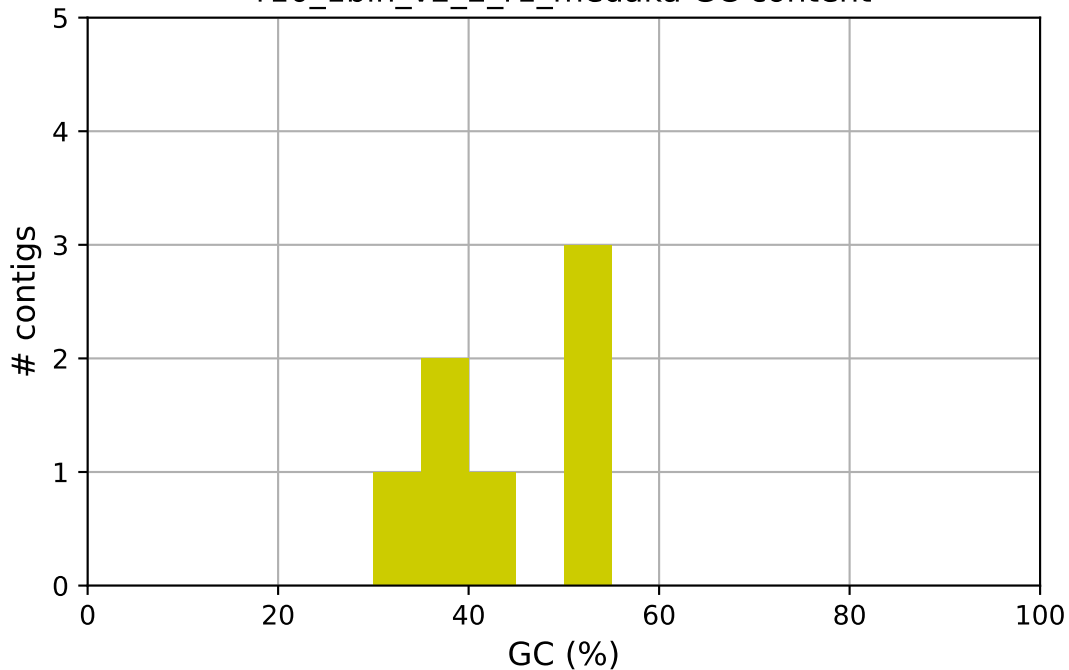
r10\_1bin\_v2\_2\_MP\_helen GC content



r10\_1bin\_v2\_2\_MP\_helen

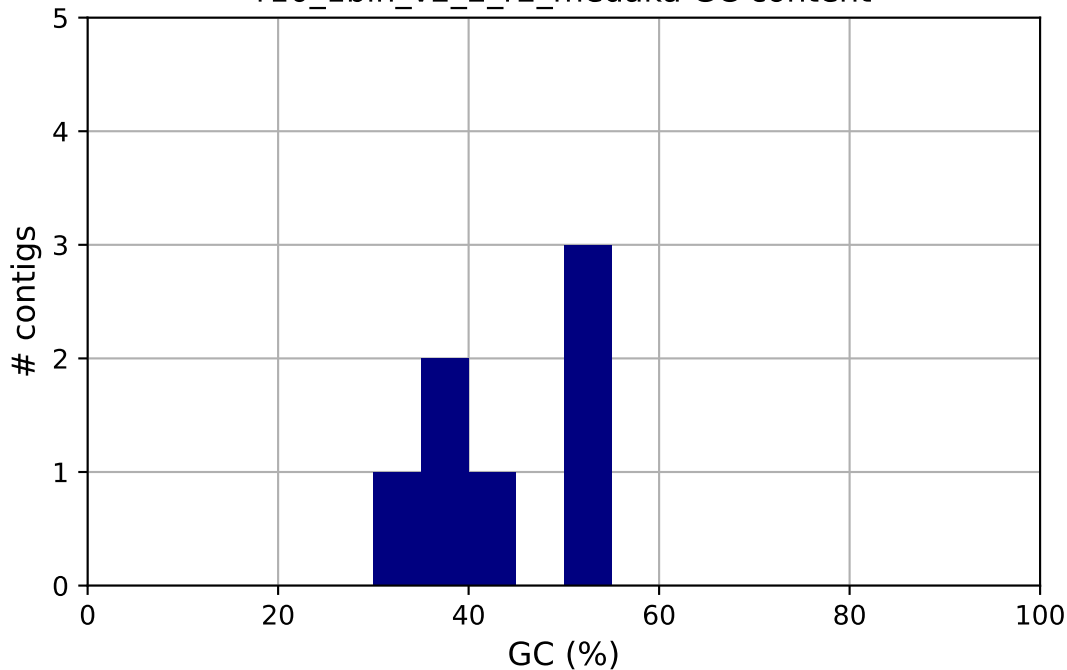


r10\_1bin\_v2\_2\_r1\_medaka GC content



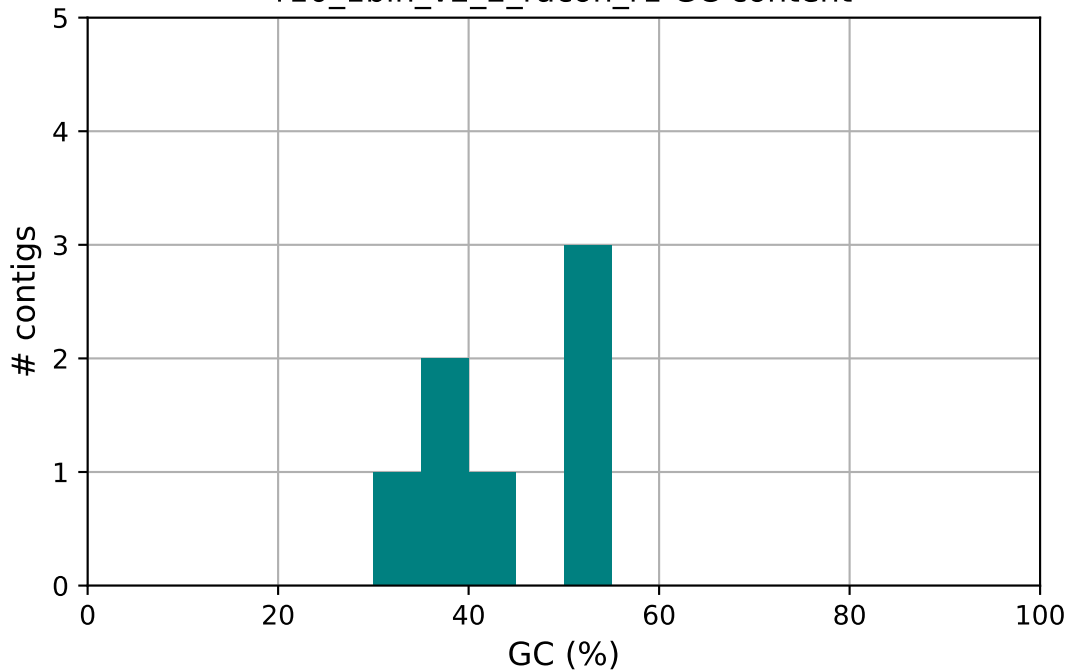
r10\_1bin\_v2\_2\_r1\_medaka

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



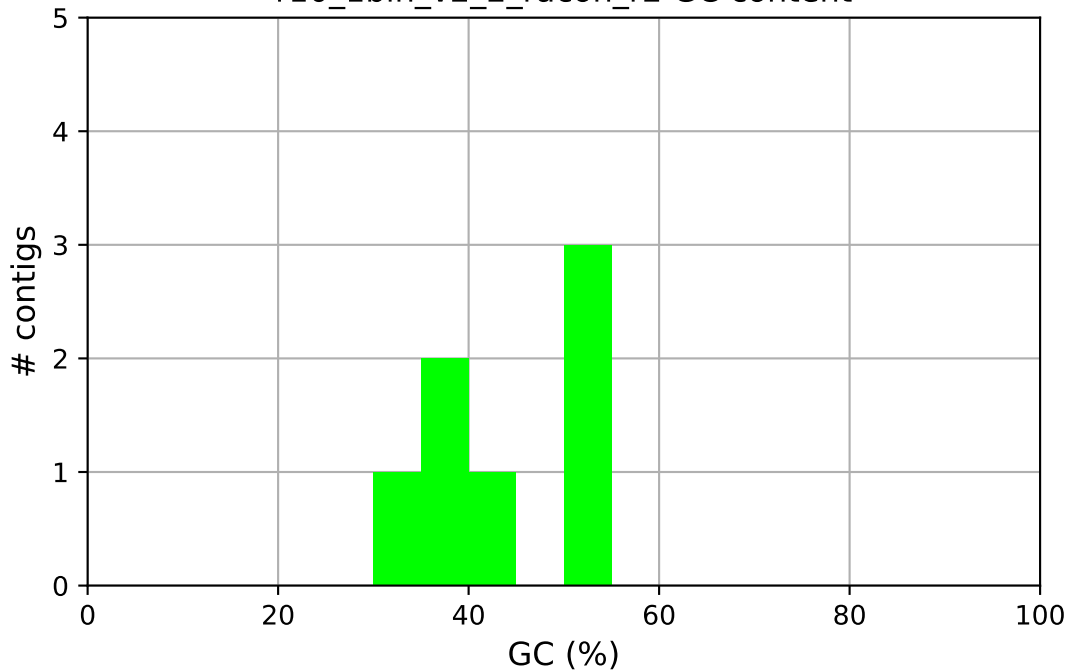
r10\_1bin\_v2\_2\_r2\_medaka

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



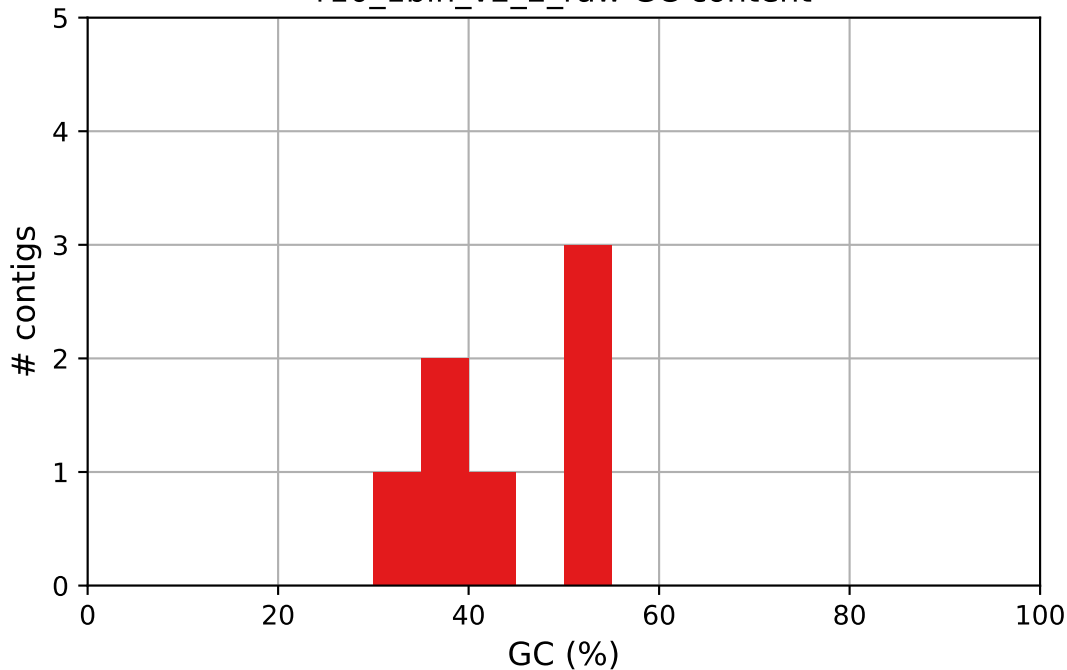
r10\_1bin\_v2\_2\_racon\_r1

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



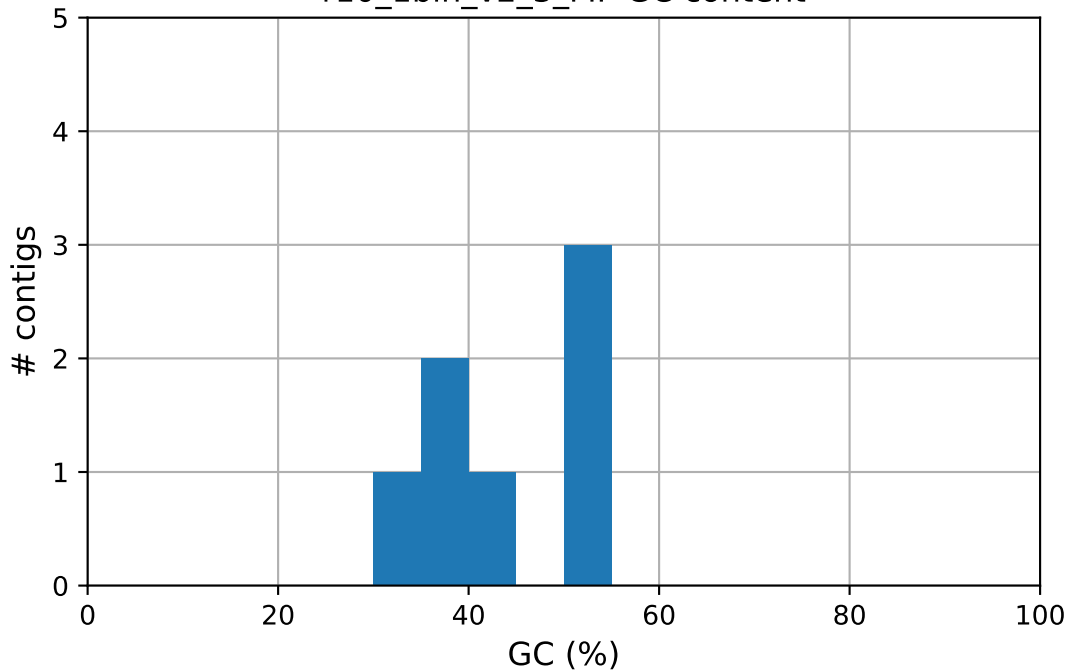
r10\_1bin\_v2\_2\_racon\_r2

r10\_1bin\_v2\_2\_raw GC content



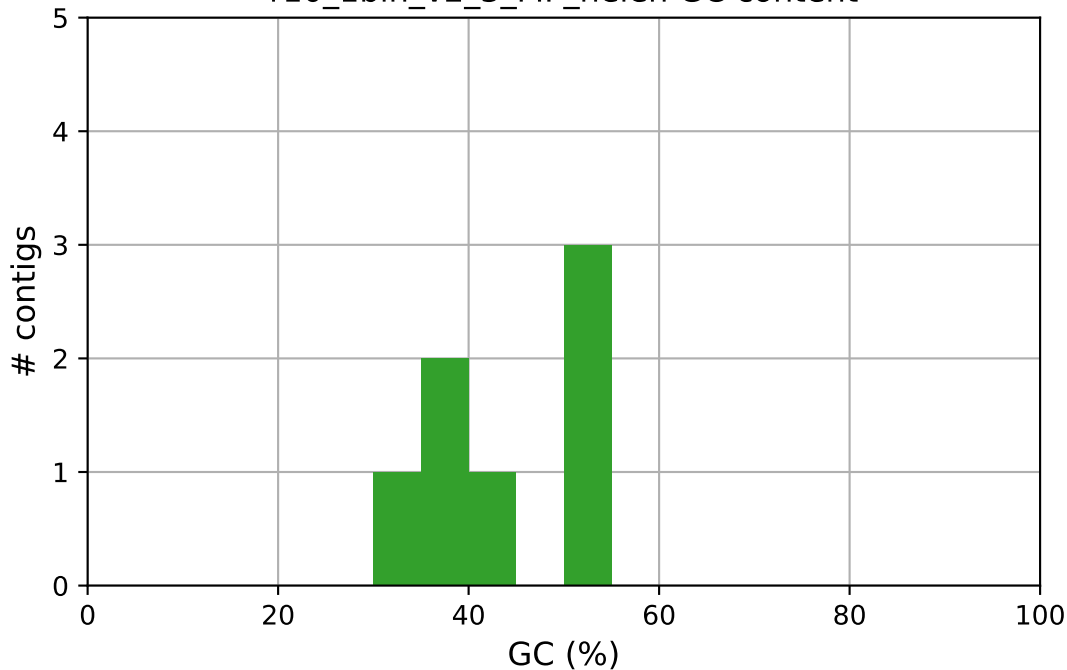
r10\_1bin\_v2\_2\_raw

r10\_1bin\_v2\_3\_MP GC content



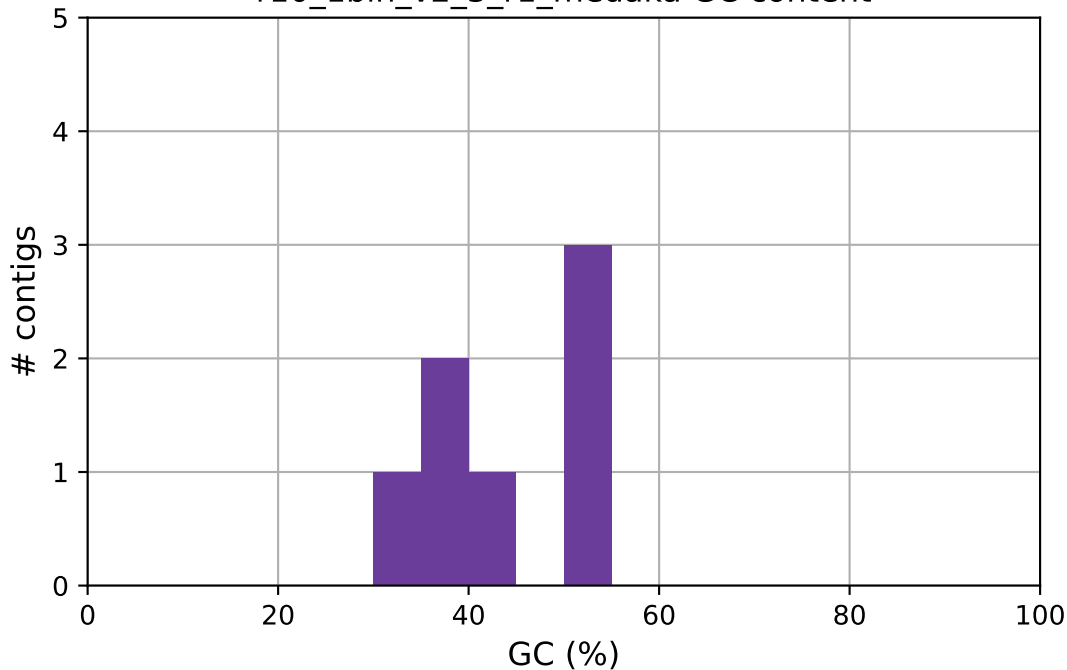
r10\_1bin\_v2\_3\_MP

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



r10\_1bin\_v2\_3\_MP\_helen

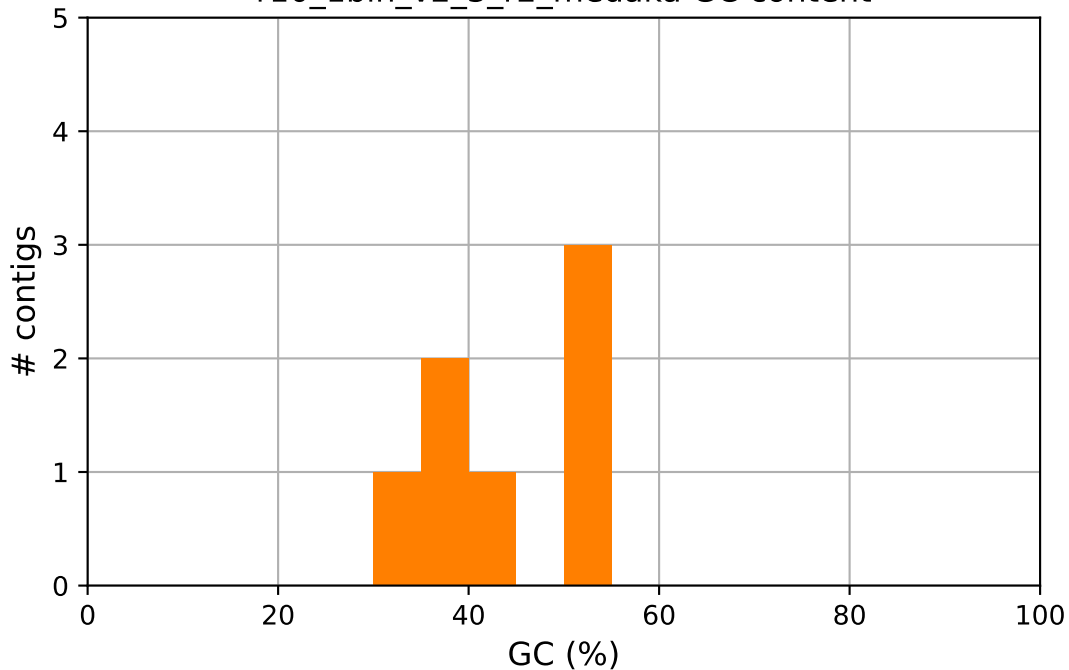
r10\_1bin\_v2\_3\_r1\_medaka GC content



r10\_1bin\_v2\_3\_r1\_medaka

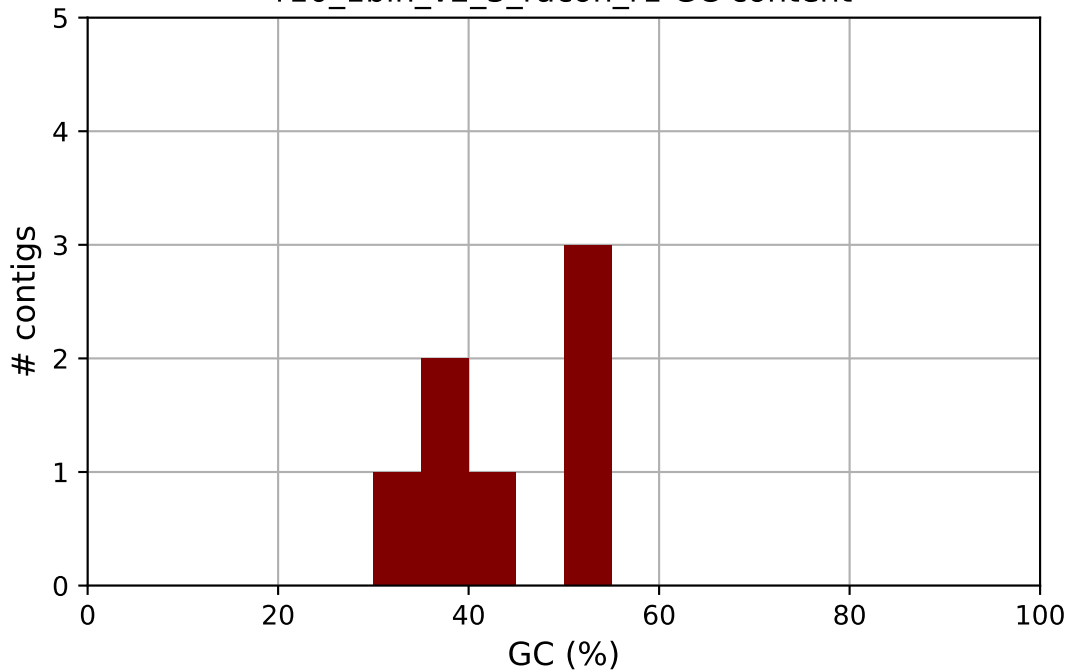


r10\_1bin\_v2\_3\_r2\_medaka GC content



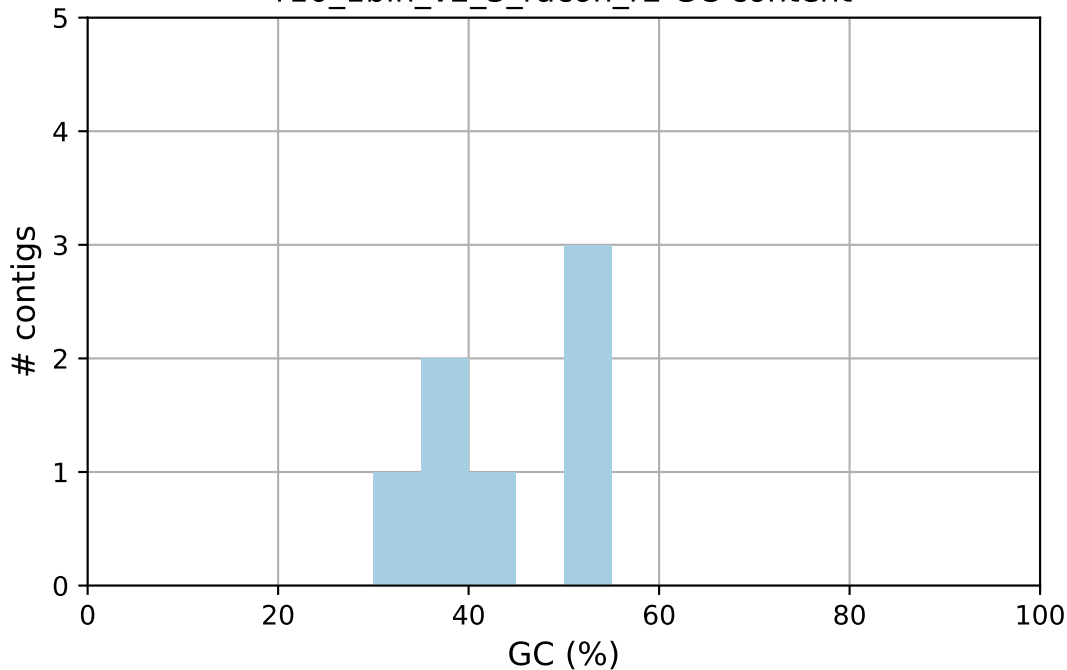
r10\_1bin\_v2\_3\_r2\_medaka

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



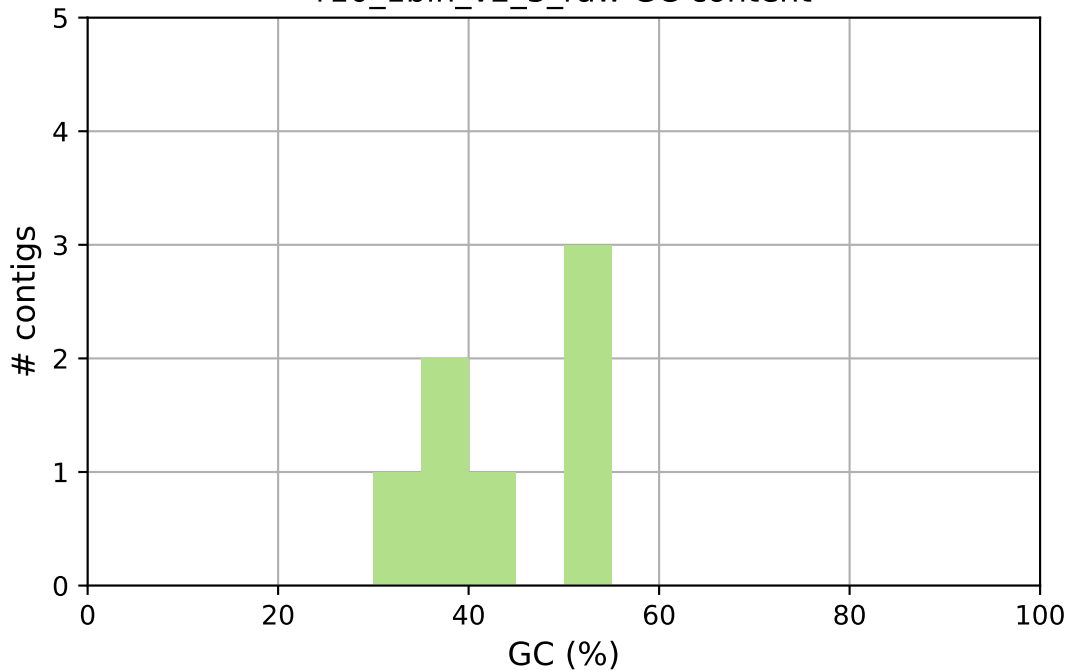
r10\_1bin\_v2\_3\_racon\_r1

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



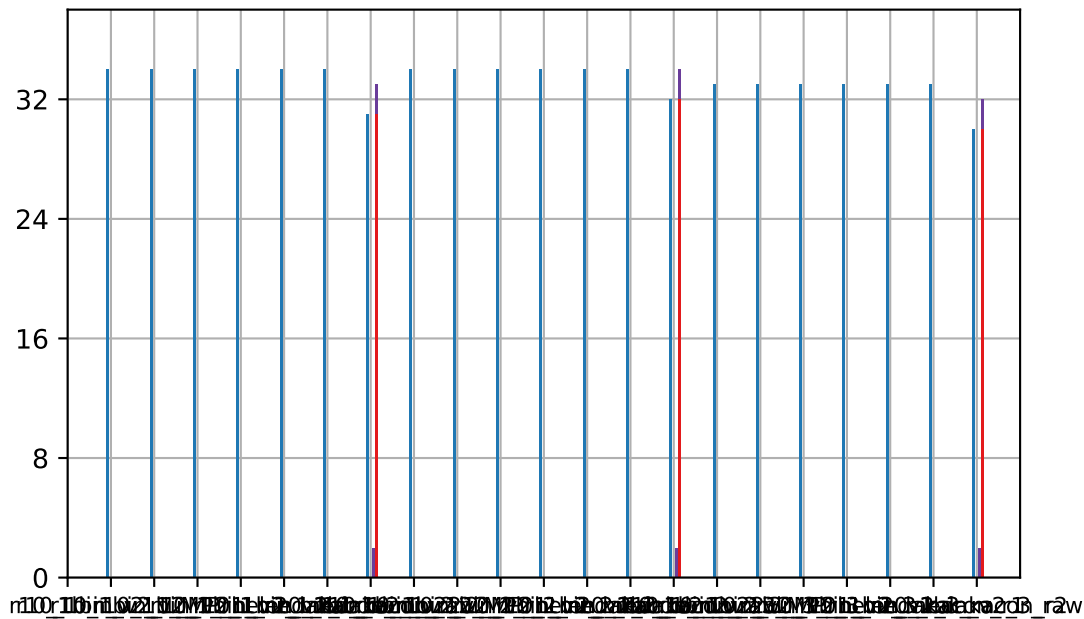
r10\_1bin\_v2\_3\_racon\_r2

r10\_1bin\_v2\_3\_raw GC content



r10\_1bin\_v2\_3\_raw

# Misassemblies

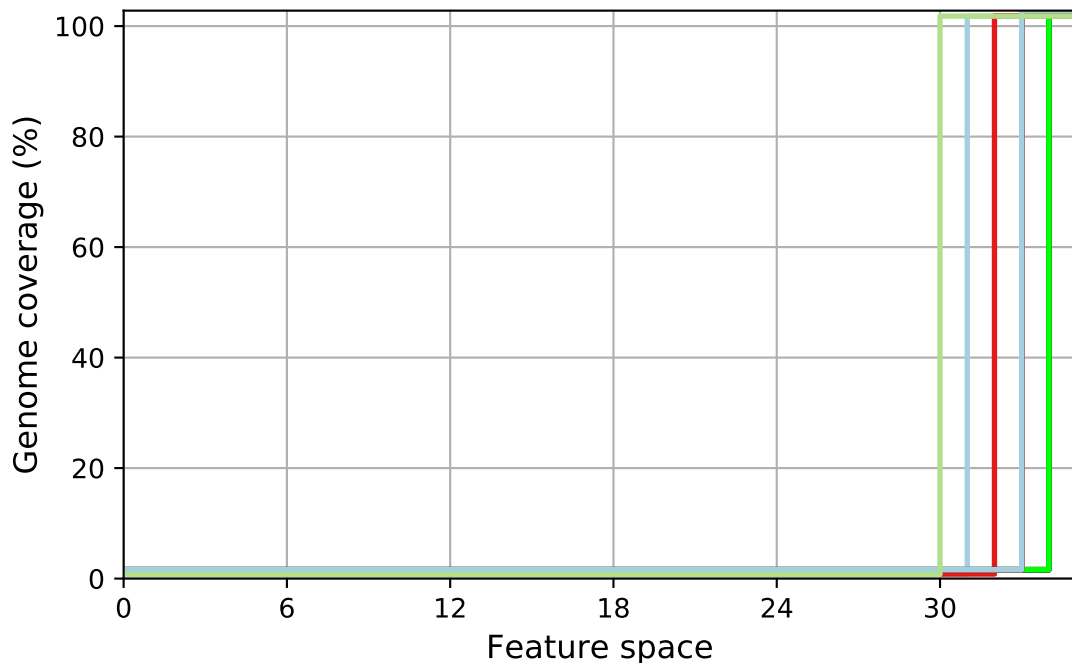


# translocations



# interspecies 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\_v2\_2\_r2\_medaka

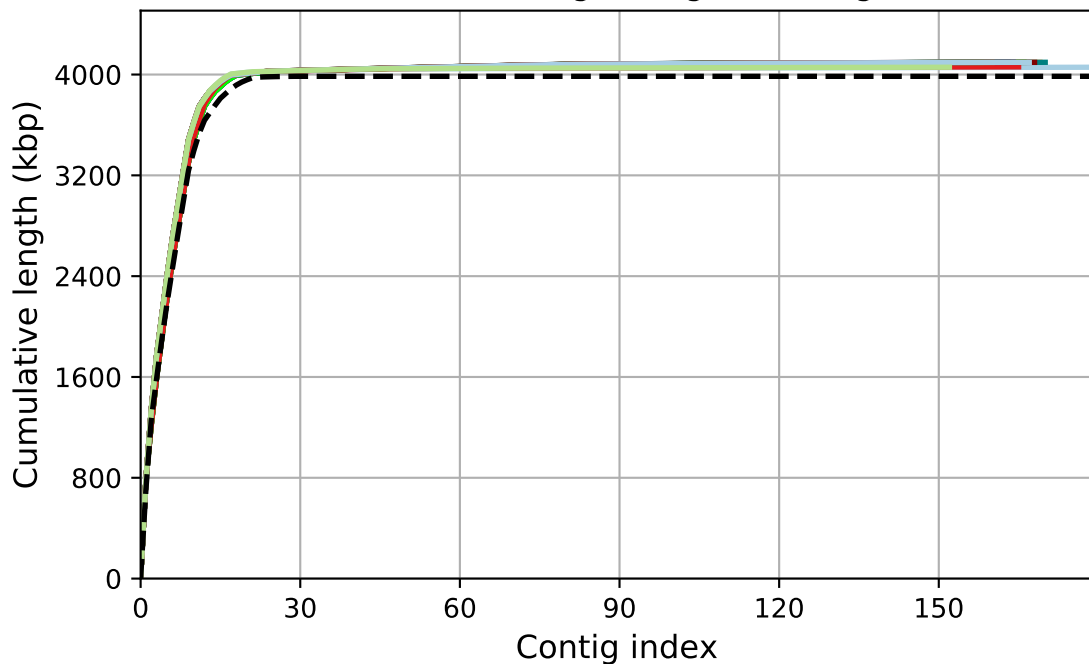
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

# 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

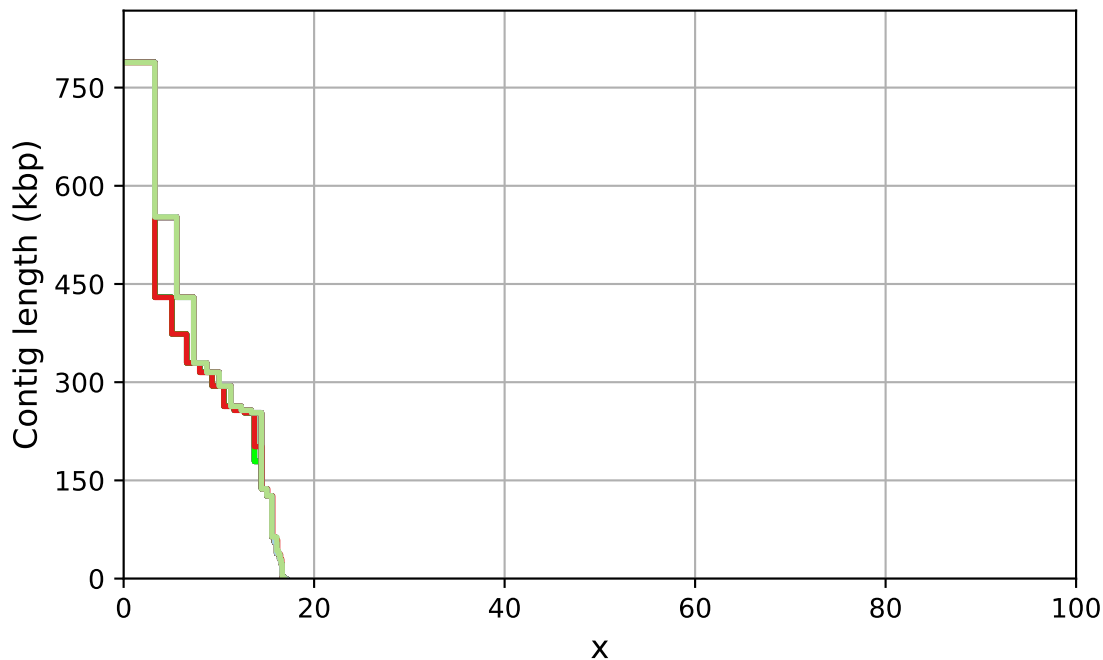
r10\_1bin\_v2\_3\_MP\_helen

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

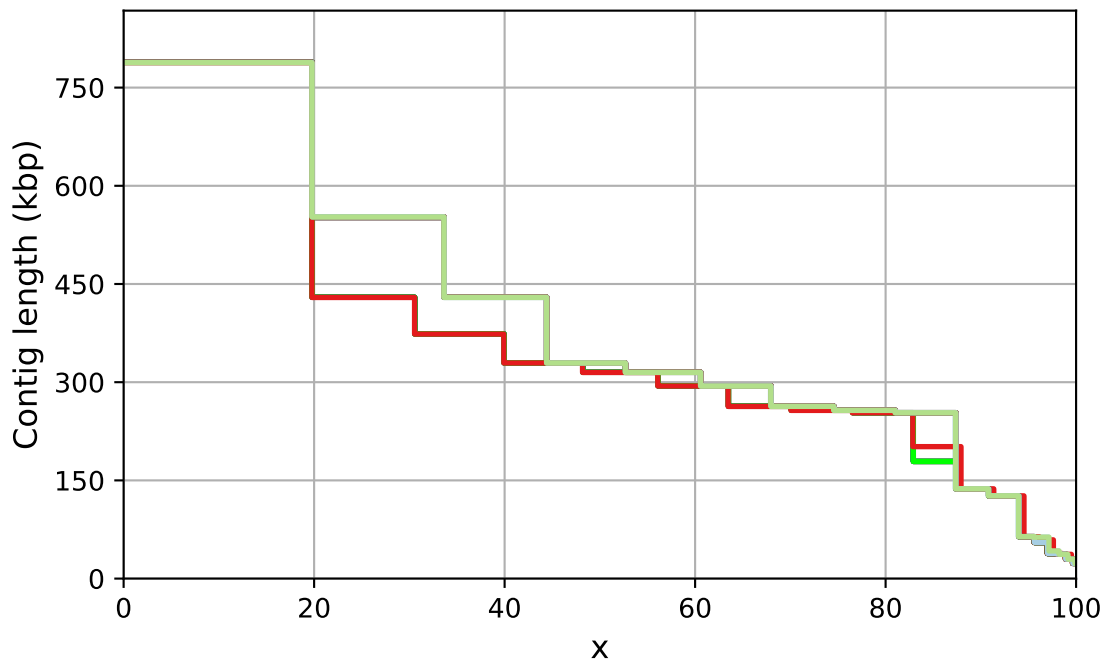
r10\_1bin\_v2\_1\_r2\_medaka

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

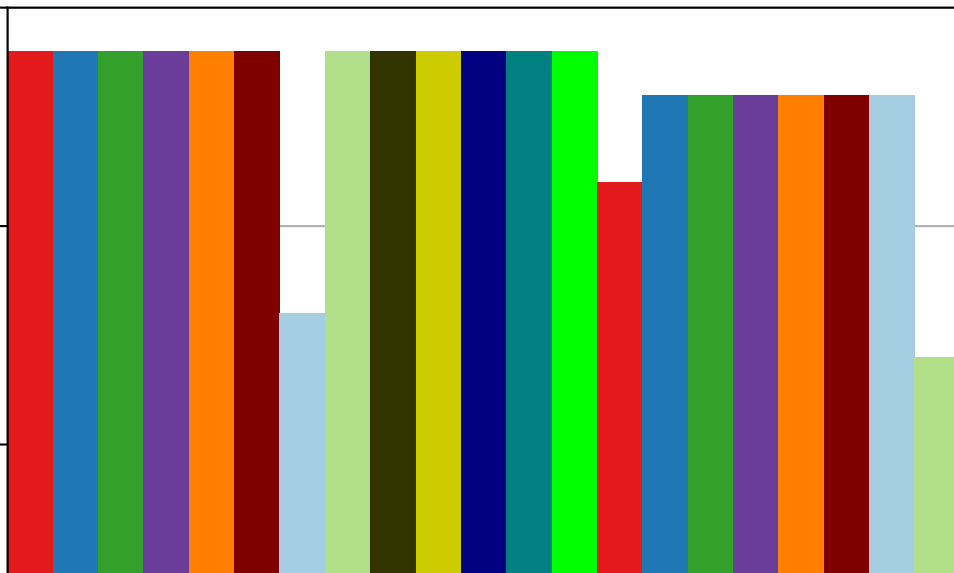
Genome fraction, %

+9.999e1

0.010

0.005

0.000



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