

Report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765367	4765367	4765367	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
Total length	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	4043032
NG50	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
N75	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
NG75	4765367	4765367	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	20
# 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	5	6	6	6	6	6	6	6	6	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part
Unaligned length	21097375	21091297	21093348	21086501	21088634	21081227	21152186	21097079	21091552	21095755	21083996	21089161	21080389	21151019	21097843	21090496	21093253	21086982	21087208	21080758	21152503
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.930	99.954	99.954	99.954	99.954	99.954	99.954	99.948	99.954	99.954	99.954	99.954	99.954	99.954	99.949
Duplication ratio	1.056	1.057	1.057	1.057	1.055	1.055	1.032	1.056	1.057	1.056	1.056	1.054	1.056	1.033	1.056	1.057	1.057	1.057	1.055	1.056	1.032
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	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
# mismatches per 100 kbp	248.76	255.78	252.30	250.21	231.69	239.35	155.51	249.18	253.44	247.09	247.51	229.24	242.83	153.32	249.29	252.59	253.12	250.95	232.19	243.36	148.85
# indels per 100 kbp	15.72	15.61	14.12	13.45	21.50	21.08	131.95	15.65	15.79	13.80	13.77	21.61	21.61	127.03	15.97	15.72	14.16	13.91	20.37	21.64	126.50
Largest alignment	2560115	2560015	2560118	2560122	2559977	2560026	2555531	2390859	2390838	2390855	2390858	2390735	2390788	2387737	2390859	2390842	2390857	2390855	2390748	2390779	2387793
Total aligned length	2971690	2973422	2973434	2972354	2966936	2969023	2907000	2971749	2973223	2971523	2971890	2965669	2970008	2908499	2971737	2972784	2973513	2972652	2967459	2970193	2907357
NGA50	2560115	2560015	2560118	2560122	2559977	2560026	2555531	2390859	2390838	2390855	2390858	2390735	2390788	2387737	2390859	2390842	2390857	2390855	2390748	2390779	2387793
NGA75	2560115	2560015	2560118	2560122	2559977	2560026	2555531	2390859	2390838	2390855	2390858	2390735	2390788	2387737	2390859	2390842	2390857	2390855	2390748	2390779	2387793
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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

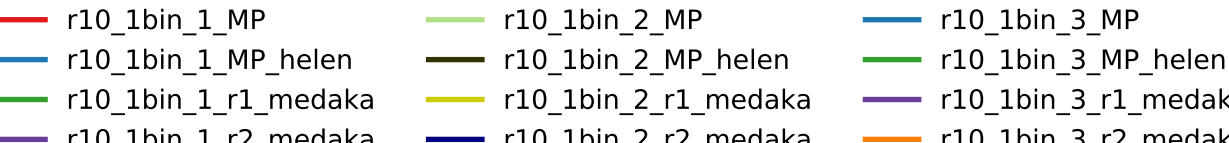
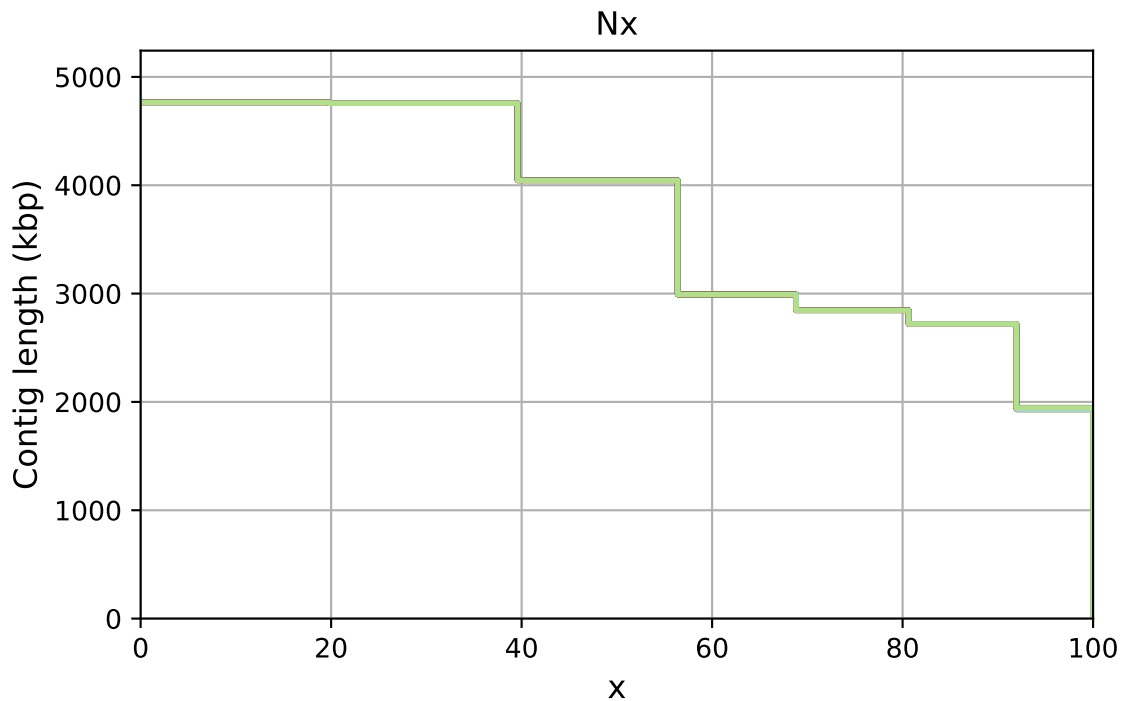
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# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. 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	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	0	0	6	0	0	0	0	0	0	6
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	20
# 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	19	18	19	19	19	19	10	19	19	19	19	19	19	10	19	19	19	19	19	19	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	5	6	6	6	6	6	6	6	6	6
# mismatches	7011	7209	7111	7052	6530	6746	4382	7023	7143	6964	6976	6461	6844	4321	7026	7119	7134	7073	6544	6859	4195
# indels	443	440	398	379	606	594	3718	441	445	389	388	609	609	3580	450	443	399	392	574	610	3565
# indels (<= 5 bp)	402	397	359	338	567	555	3677	400	403	350	347	572	568	3542	409	399	360	351	536	569	3530
# indels (> 5 bp)	41	43	39	41	39	39	41	41	42	39	41	37	41	38	41	44	39	41	38	41	35
Indels length	2461	2473	2351	2336	2575	2583	6421	2459	2476	2326	2348	2570	2657	6281	2474	2479	2353	2370	2537	2619	6151

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).

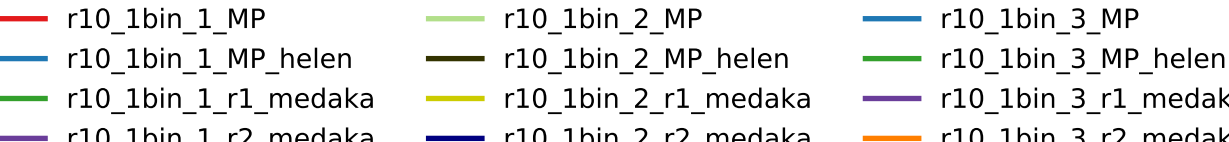
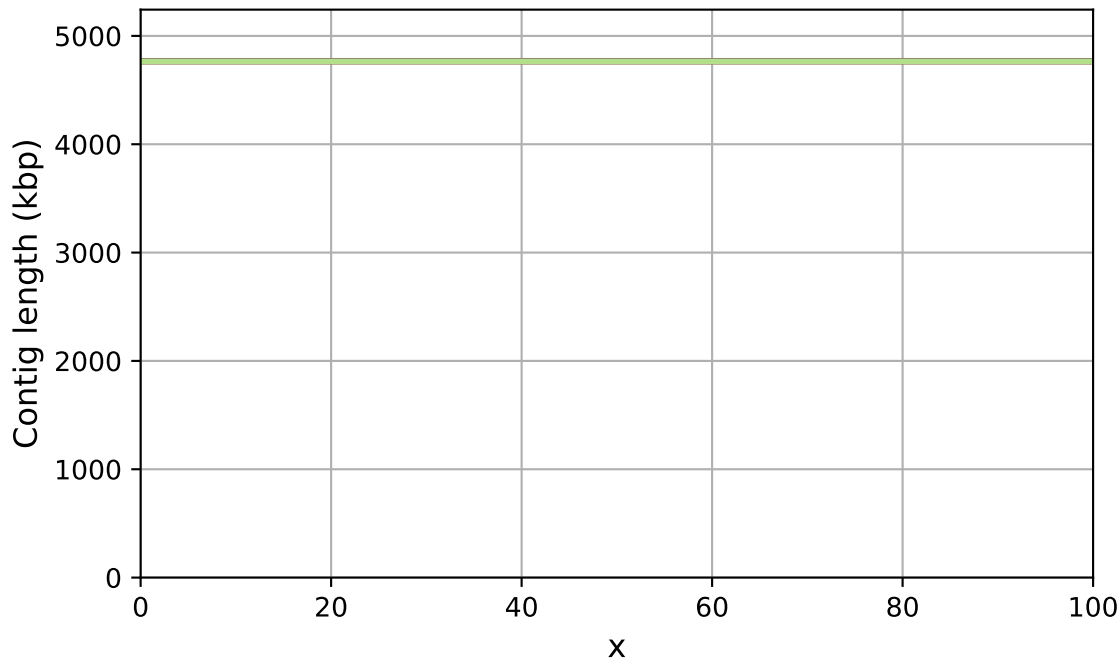
# Unaligned report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
Partially unaligned length	21097375	21091297	21093348	21086501	21088634	21081227	21152186	21097079	21091552	21095755	21083996	21089161	21080389	21151019	21097843	21090496	21093253	21086982	21087208	21080758	21152503
# N's	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0

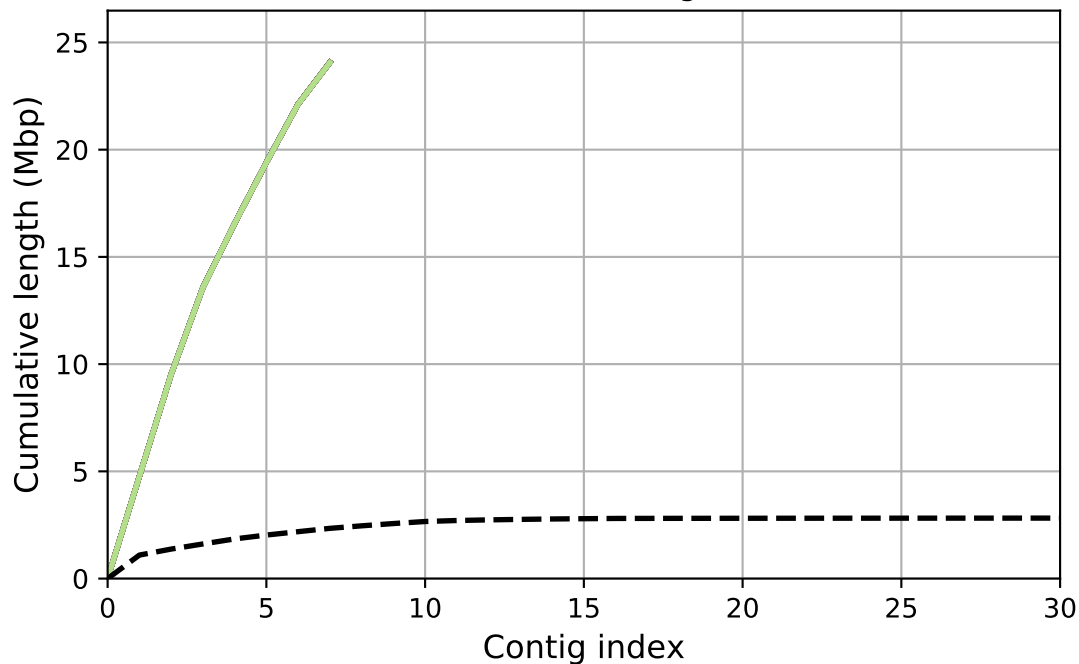
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



# NGx

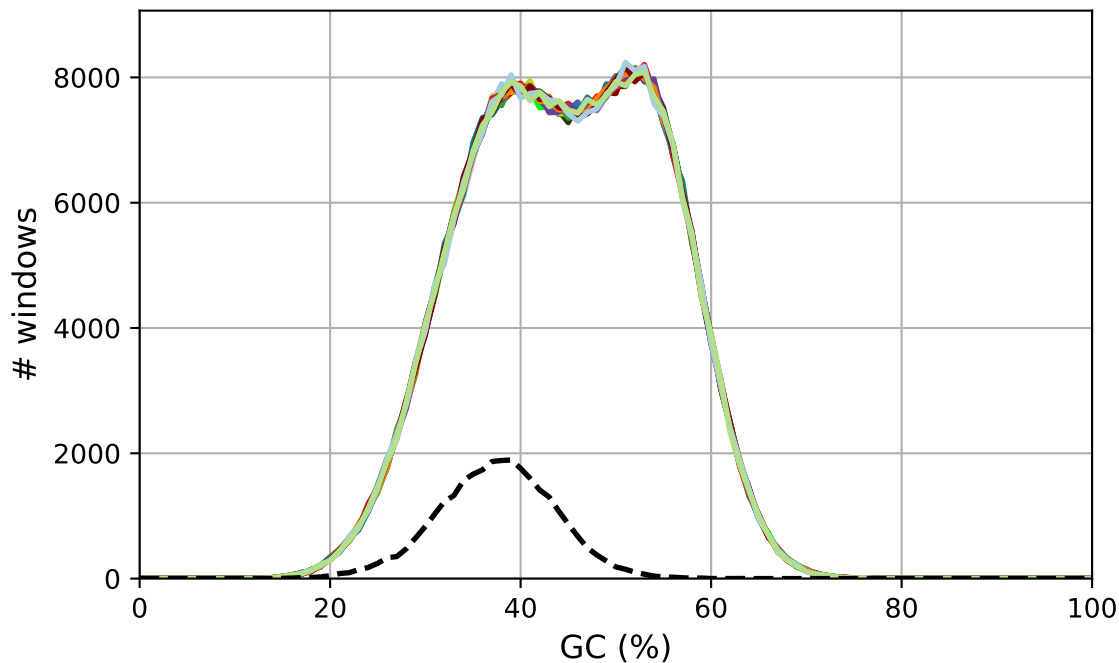


Cumulative length



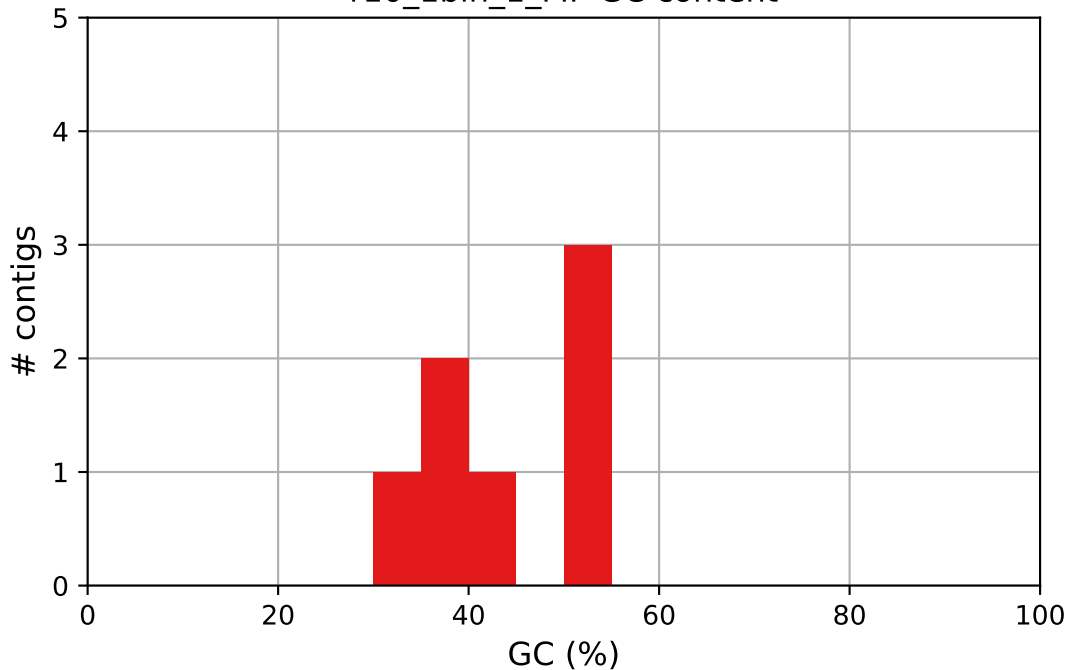
r10_1bin_1_MP	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak
r10_1bin_1_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_3_racon_r1

GC content



r10_1bin_1_MP	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medak
r10_1bin_1_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medak
r10_1bin_1_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_3_racon_r1

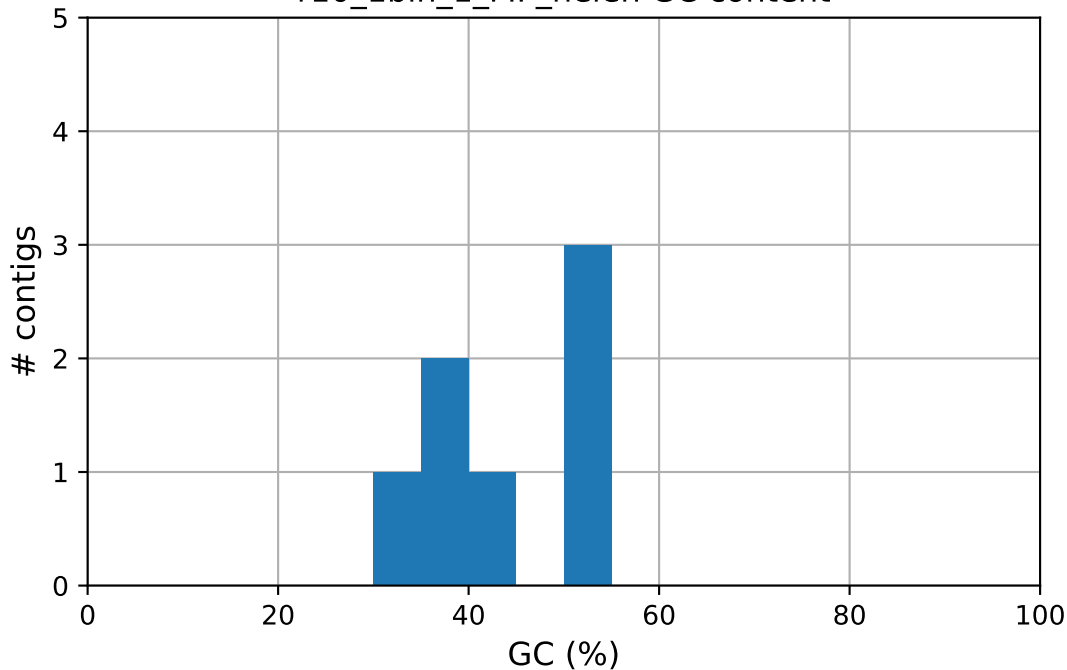
r10\_1bin\_1\_MP GC content



r10\_1bin\_1\_MP

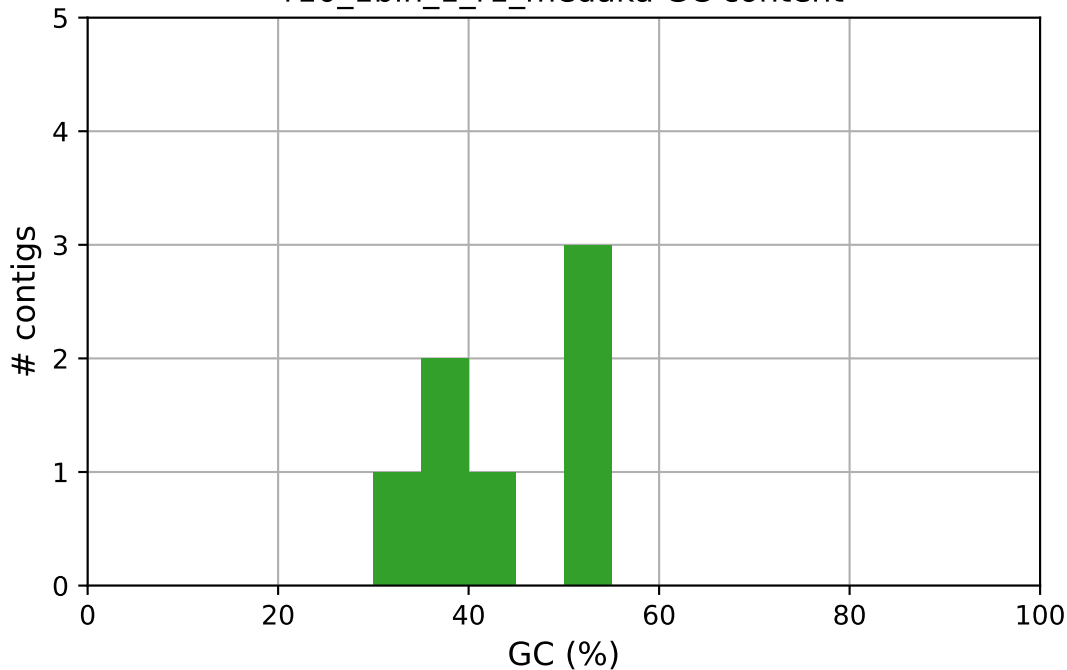


r10\_1bin\_1\_MP\_helen GC content



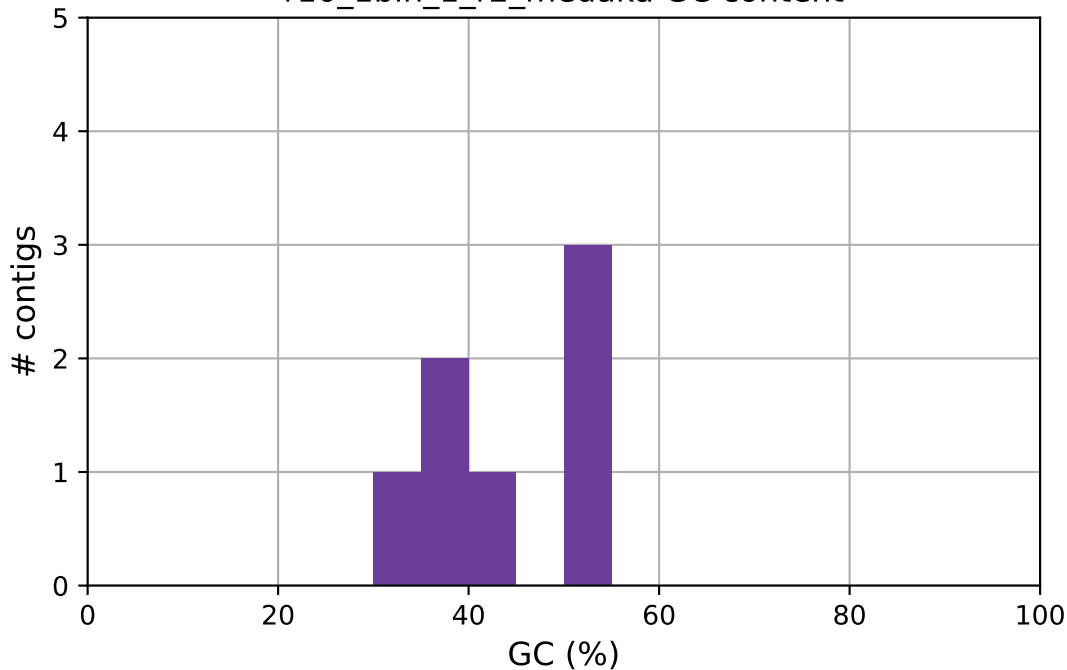
r10\_1bin\_1\_MP\_helen

r10\_1bin\_1\_r1\_medaka GC content



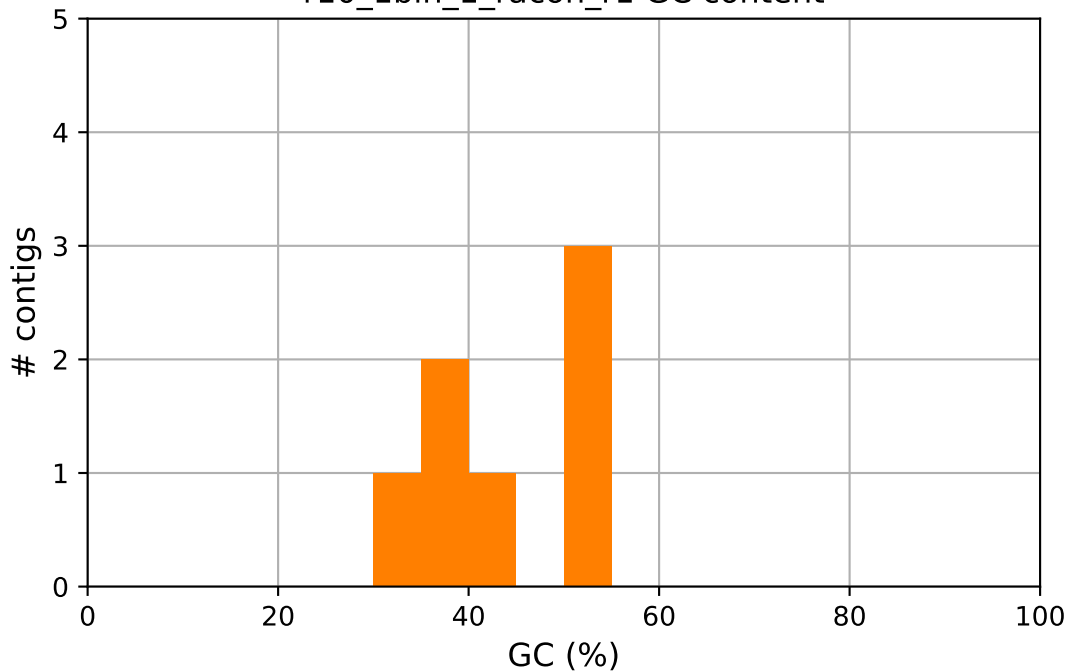
r10\_1bin\_1\_r1\_medaka

r10\_1bin\_1\_r2\_medaka GC content



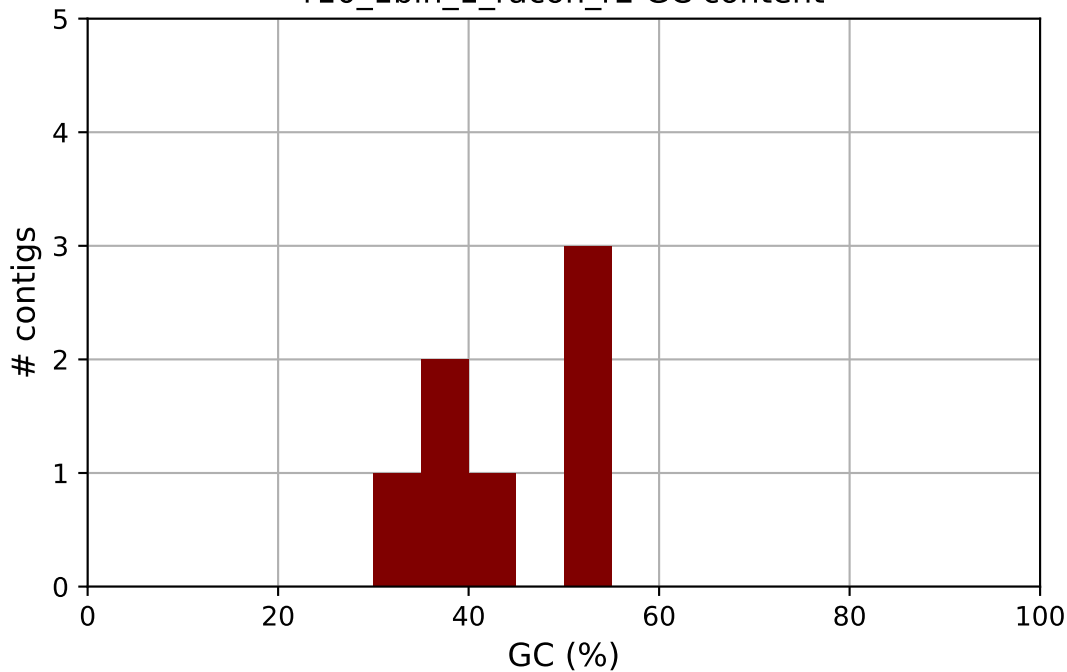
r10\_1bin\_1\_r2\_medaka

r10\_1bin\_1\_racon\_r1 GC content



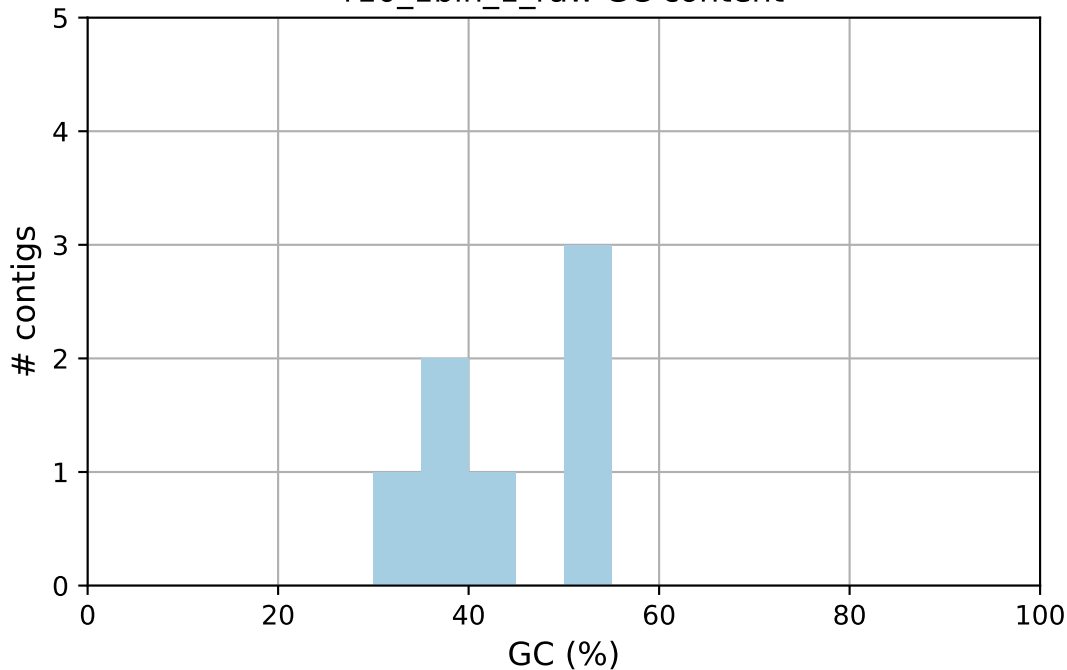
r10\_1bin\_1\_racon\_r1

r10\_1bin\_1\_racon\_r2 GC content



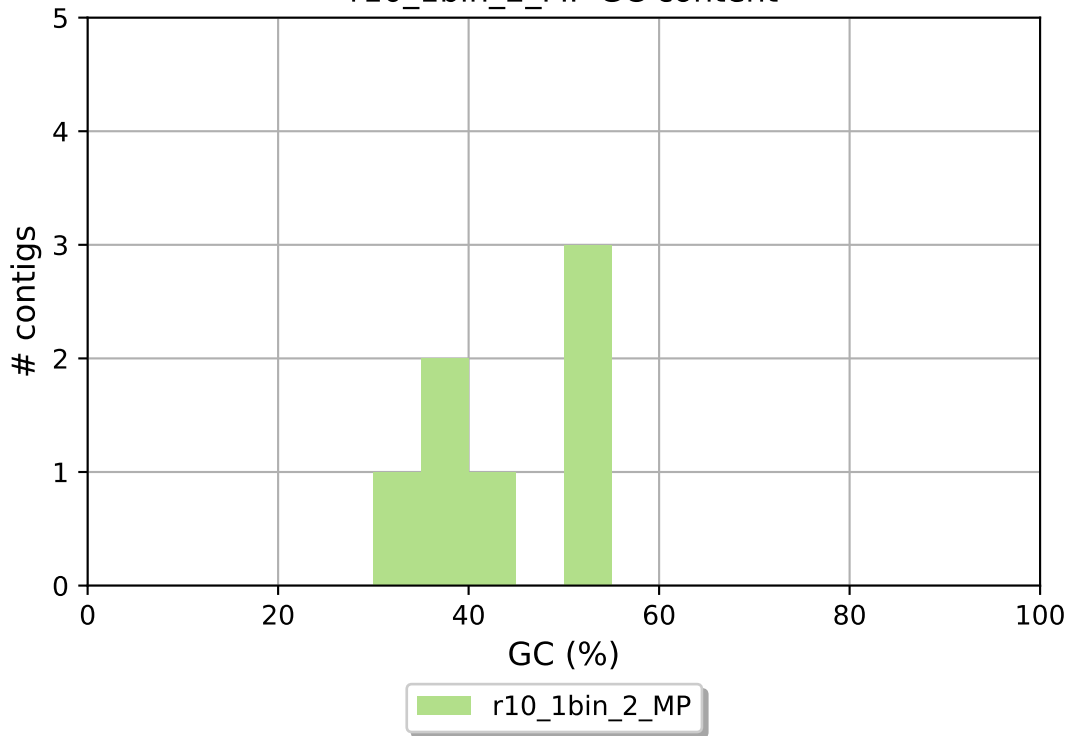
r10\_1bin\_1\_racon\_r2

r10\_1bin\_1\_raw GC content

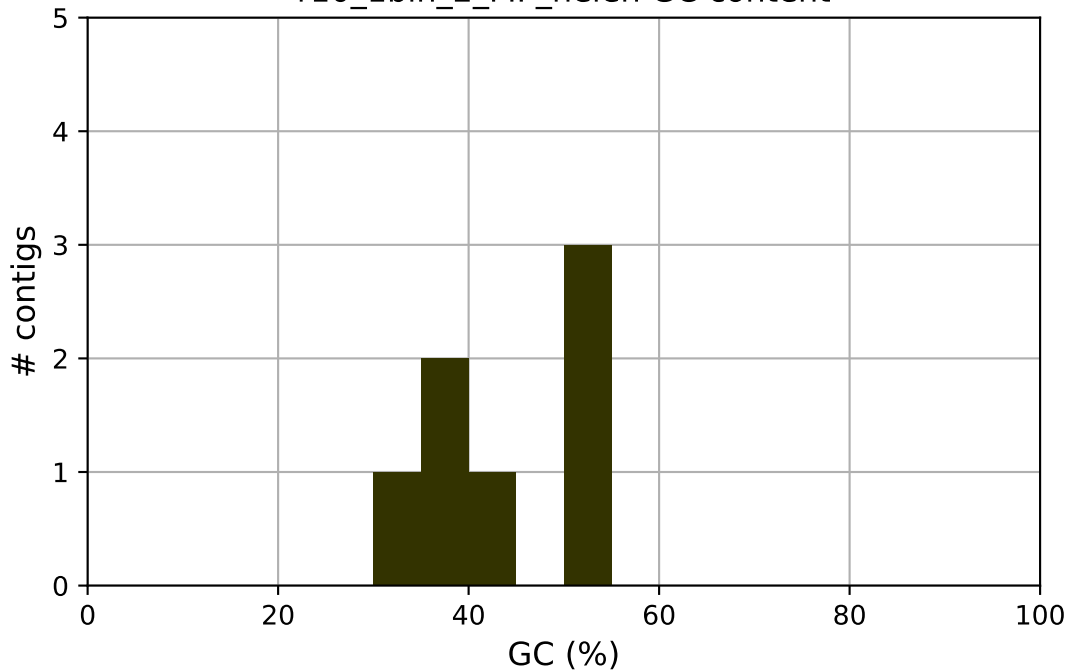


r10\_1bin\_1\_raw

r10\_1bin\_2\_MP GC content



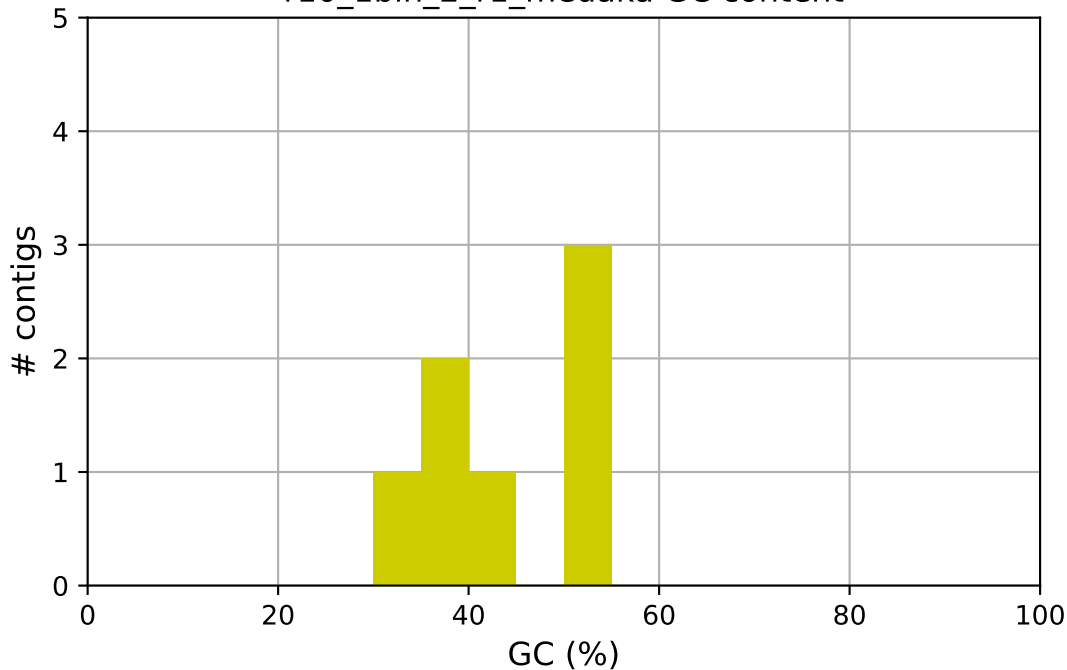
r10\_1bin\_2\_MP\_helen GC content



■ r10\_1bin\_2\_MP\_helen

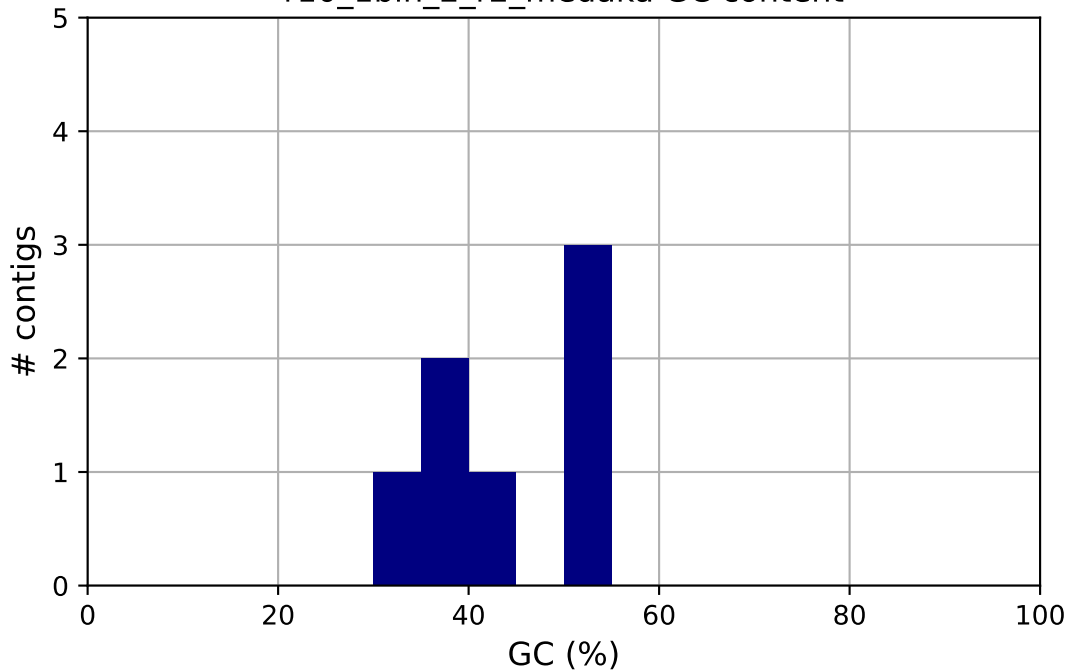


r10\_1bin\_2\_r1\_medaka GC content



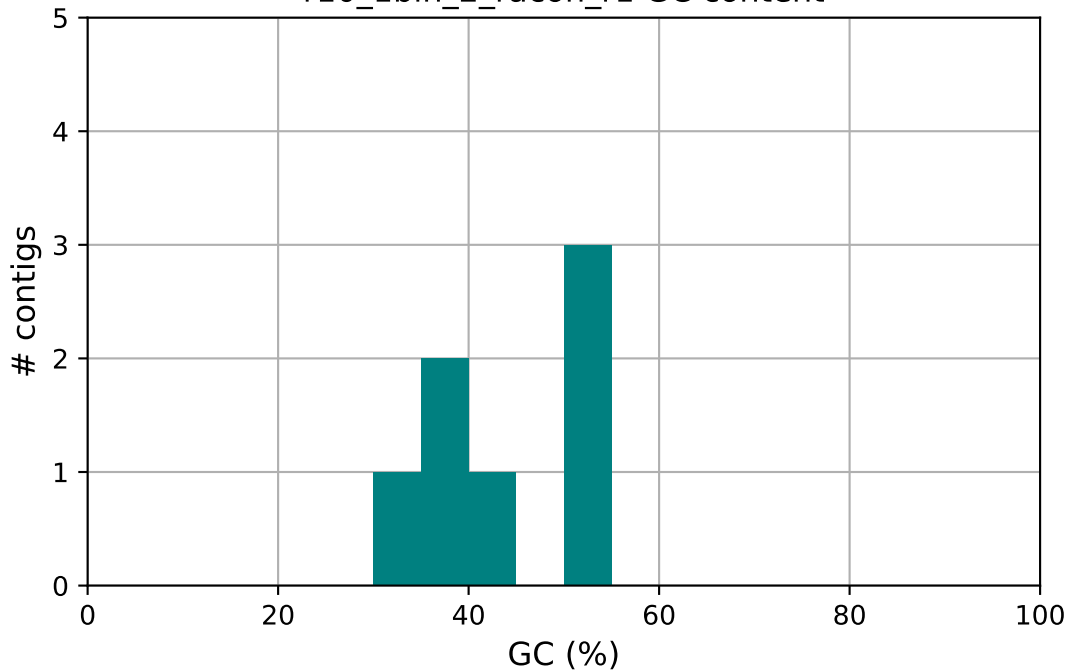
r10\_1bin\_2\_r1\_medaka

r10\_1bin\_2\_r2\_medaka GC content



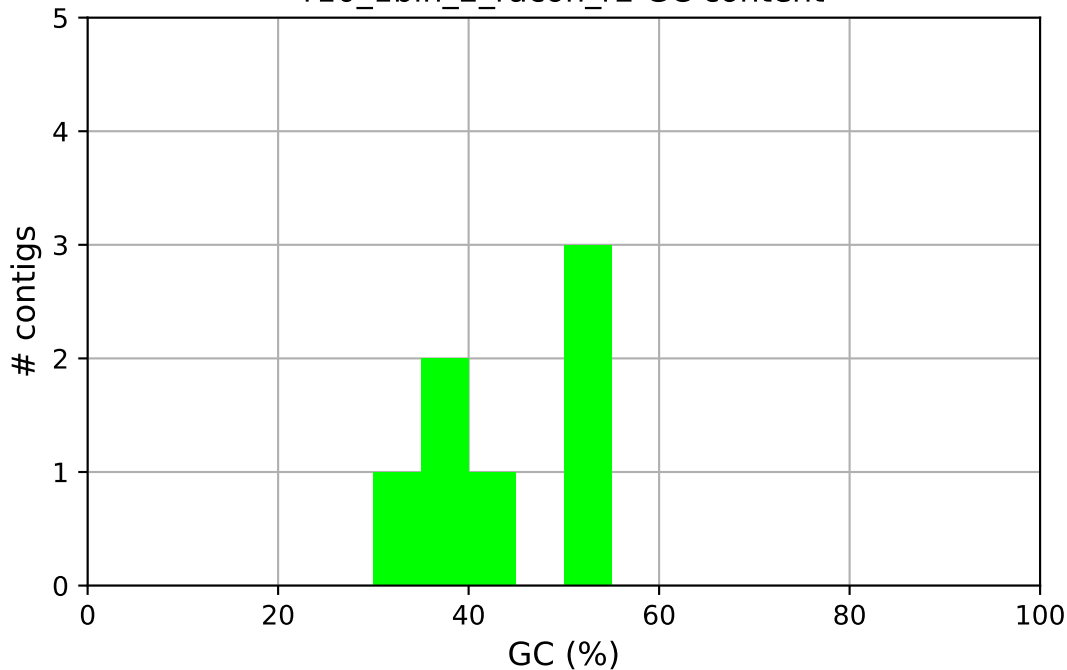
r10\_1bin\_2\_r2\_medaka

r10\_1bin\_2\_racon\_r1 GC content



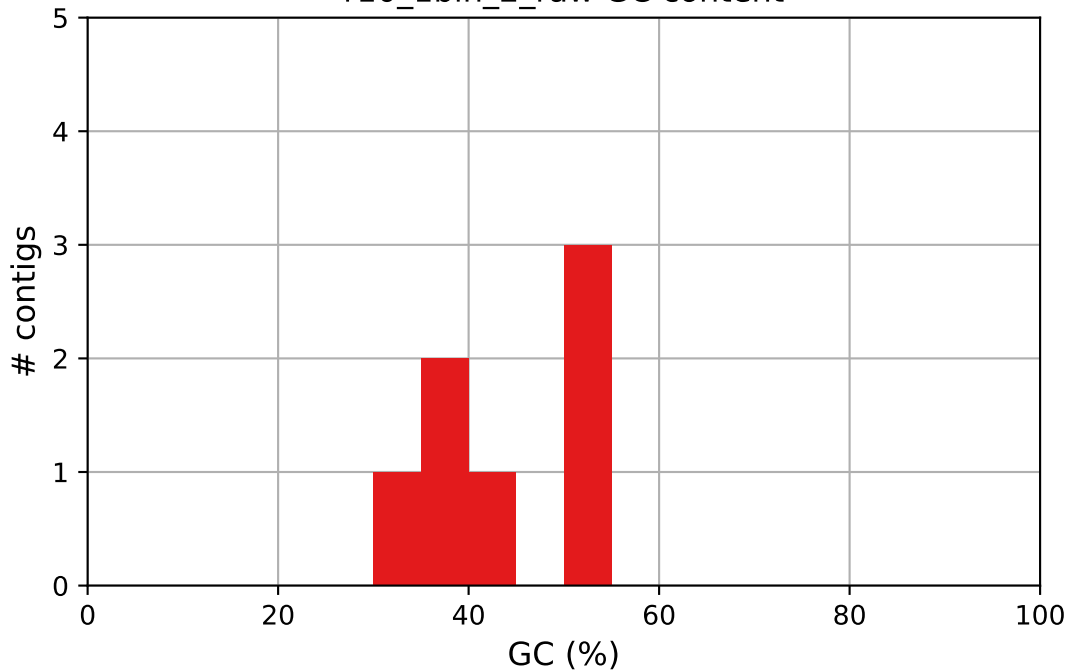
r10\_1bin\_2\_racon\_r1

r10\_1bin\_2\_racon\_r2 GC content



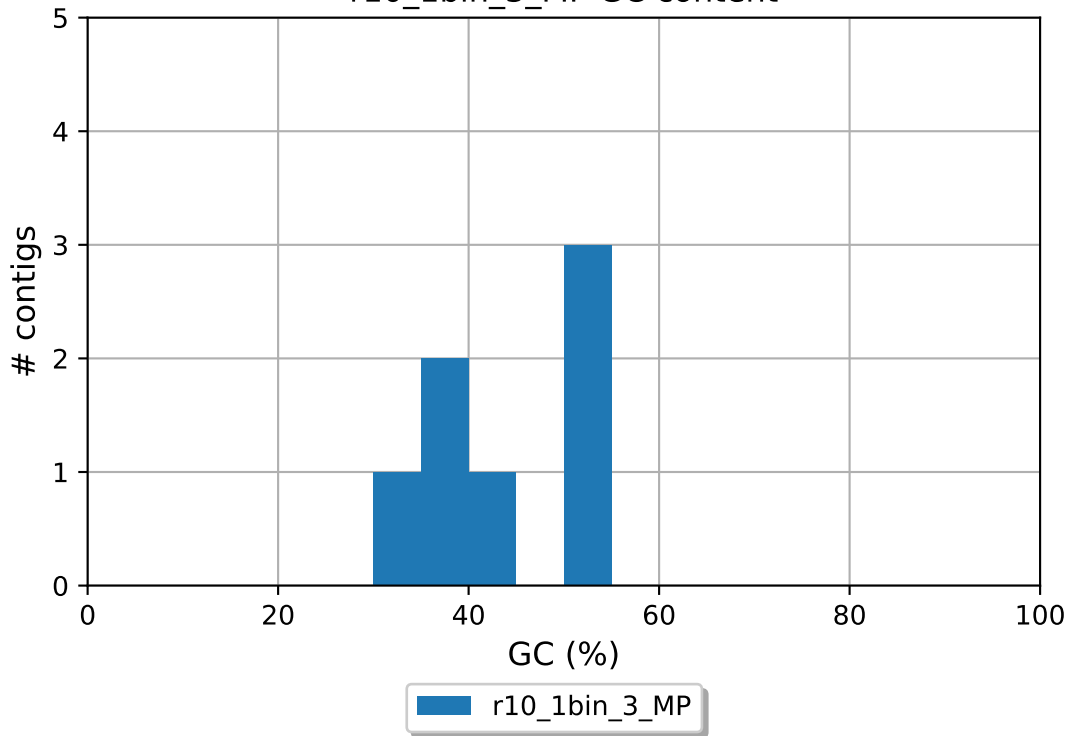
█ r10\_1bin\_2\_racon\_r2

r10\_1bin\_2\_raw GC content

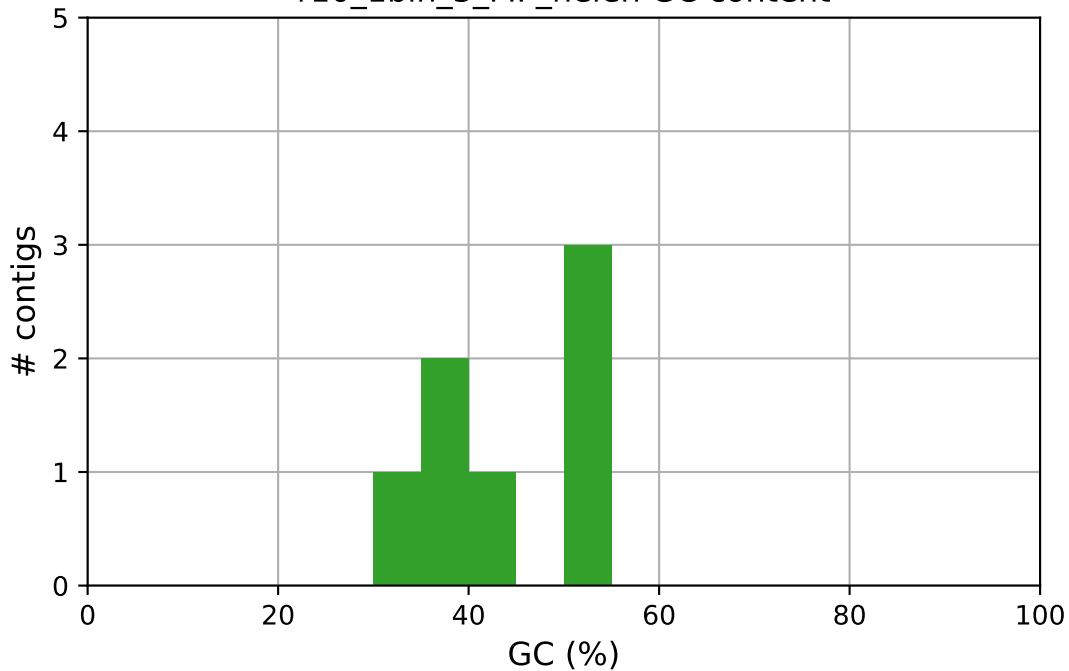


r10\_1bin\_2\_raw

r10\_1bin\_3\_MP GC content

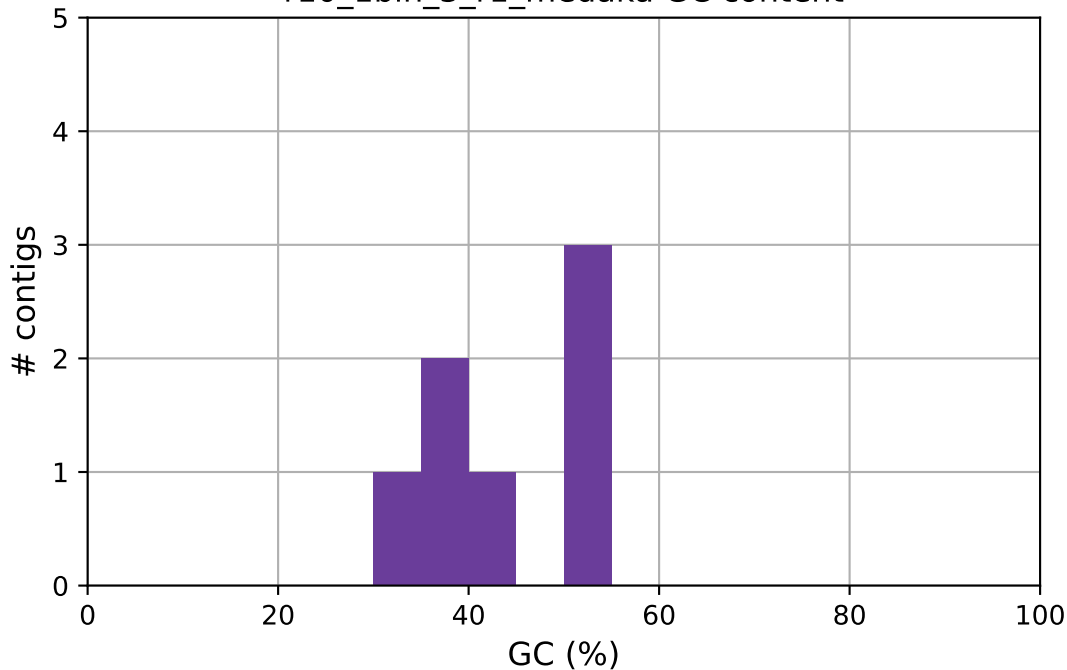


r10\_1bin\_3\_MP\_helen GC content



r10\_1bin\_3\_MP\_helen

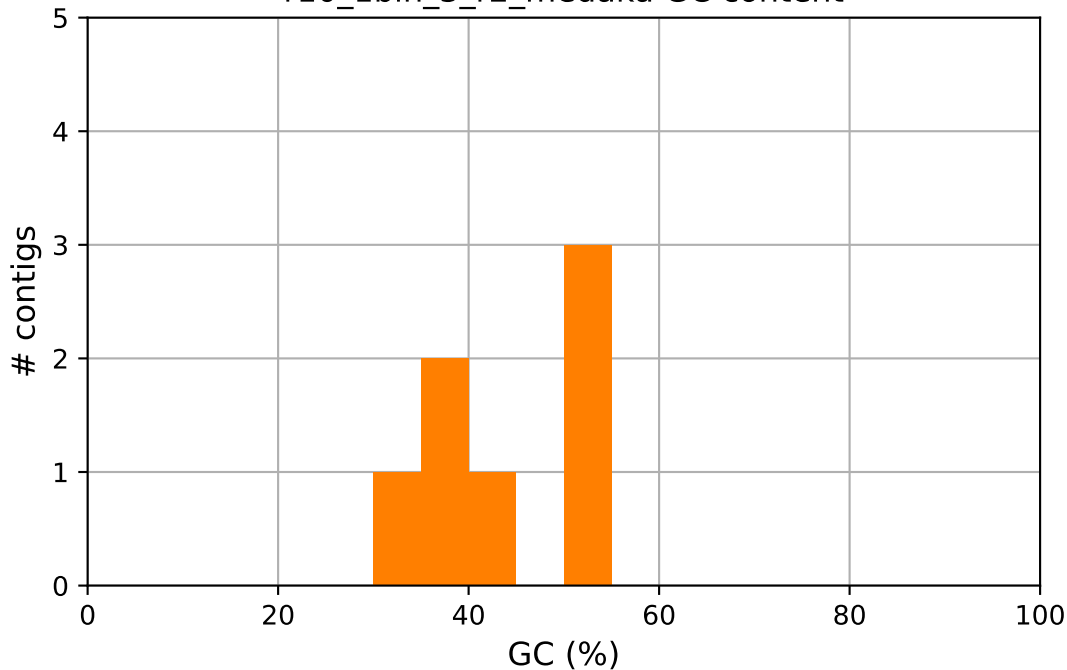
r10\_1bin\_3\_r1\_medaka GC content



r10\_1bin\_3\_r1\_medaka

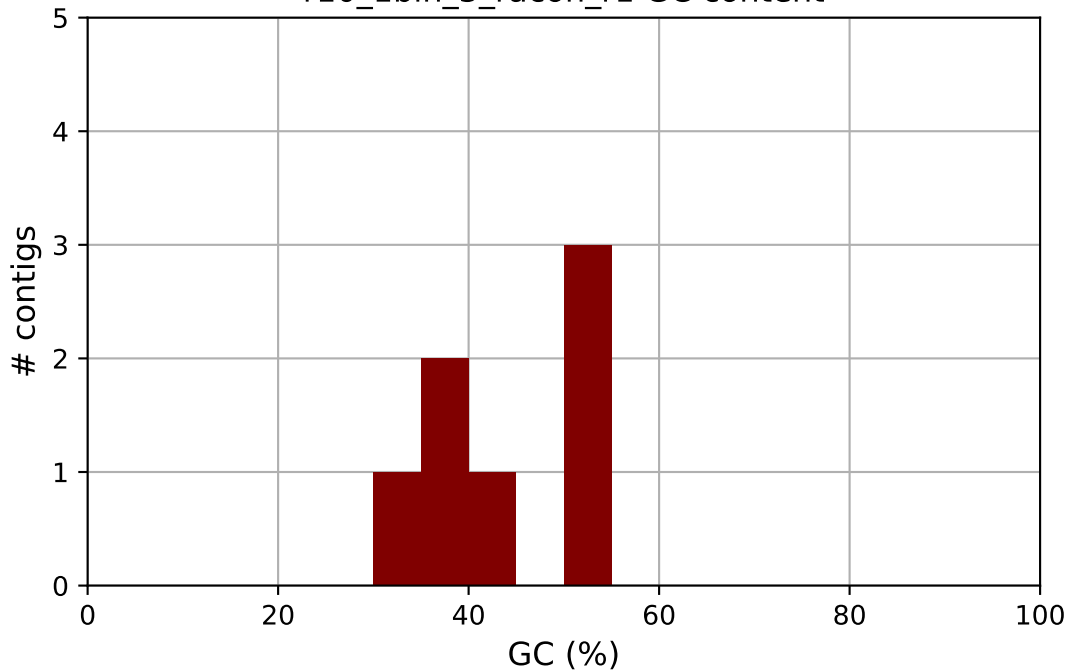


r10\_1bin\_3\_r2\_medaka GC content



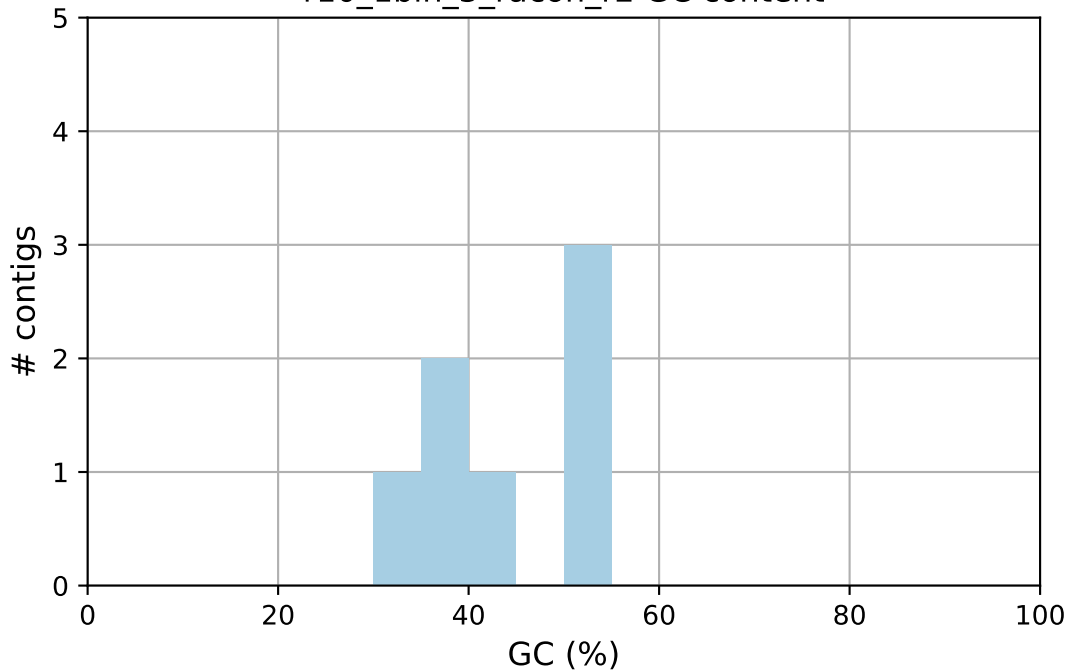
r10\_1bin\_3\_r2\_medaka

r10\_1bin\_3\_racon\_r1 GC content



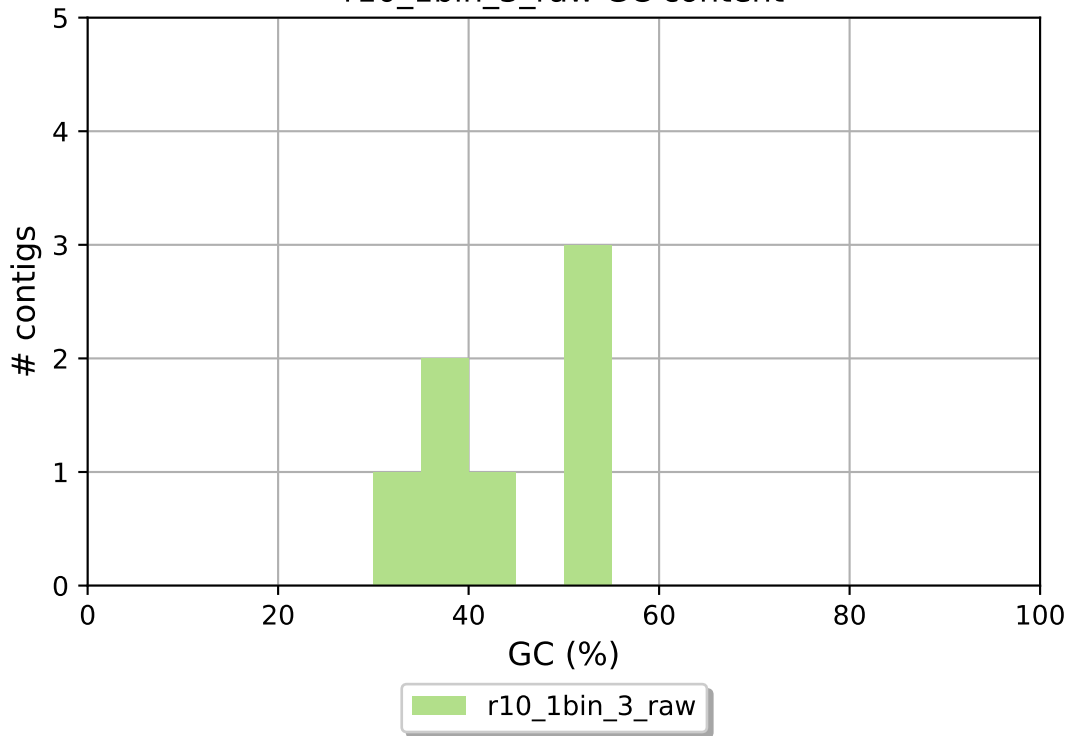
r10\_1bin\_3\_racon\_r1

r10\_1bin\_3\_racon\_r2 GC content

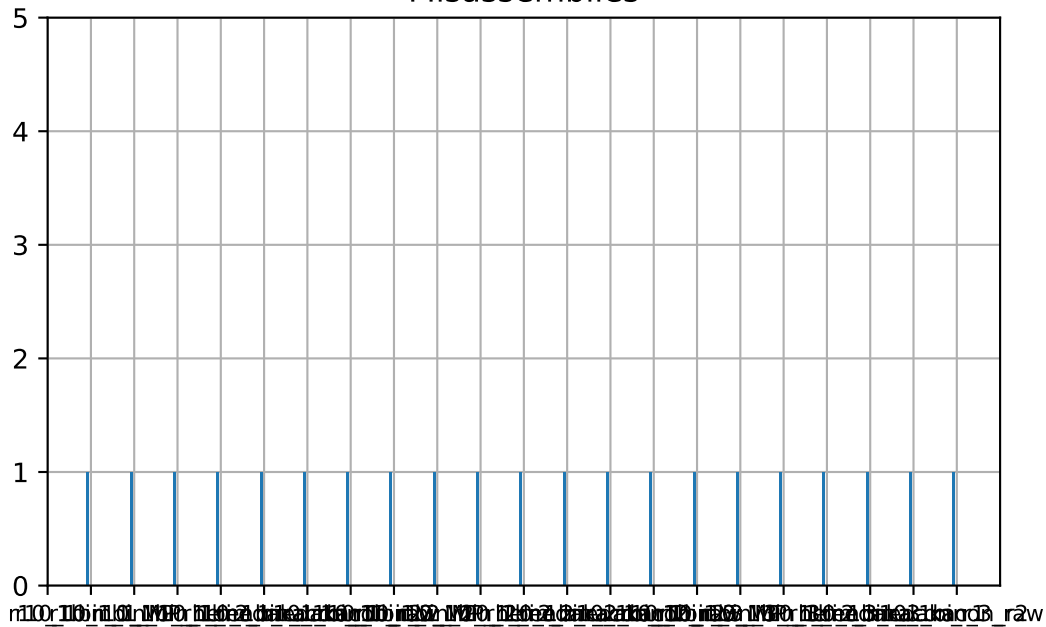


r10\_1bin\_3\_racon\_r2

r10\_1bin\_3\_raw GC content

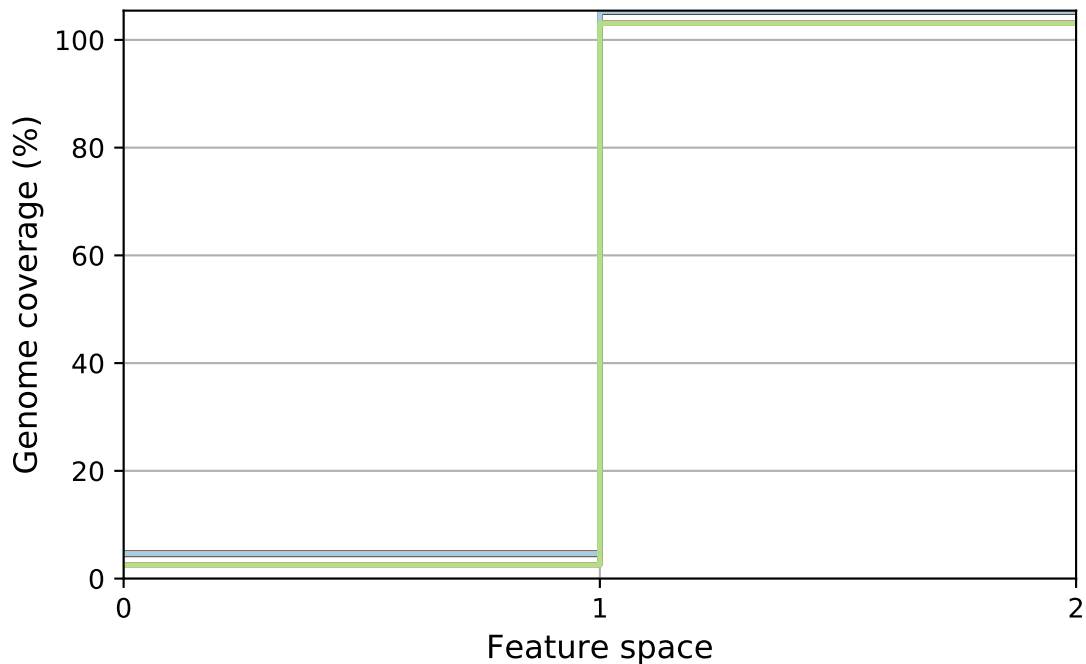


## Misassemblies



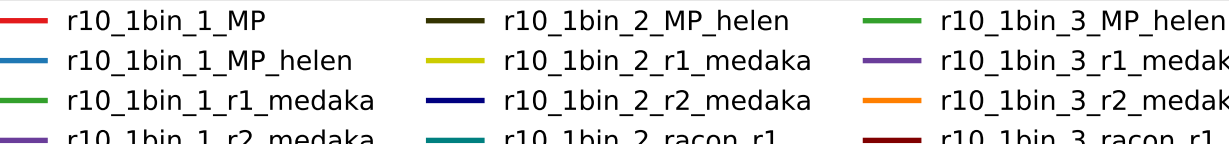
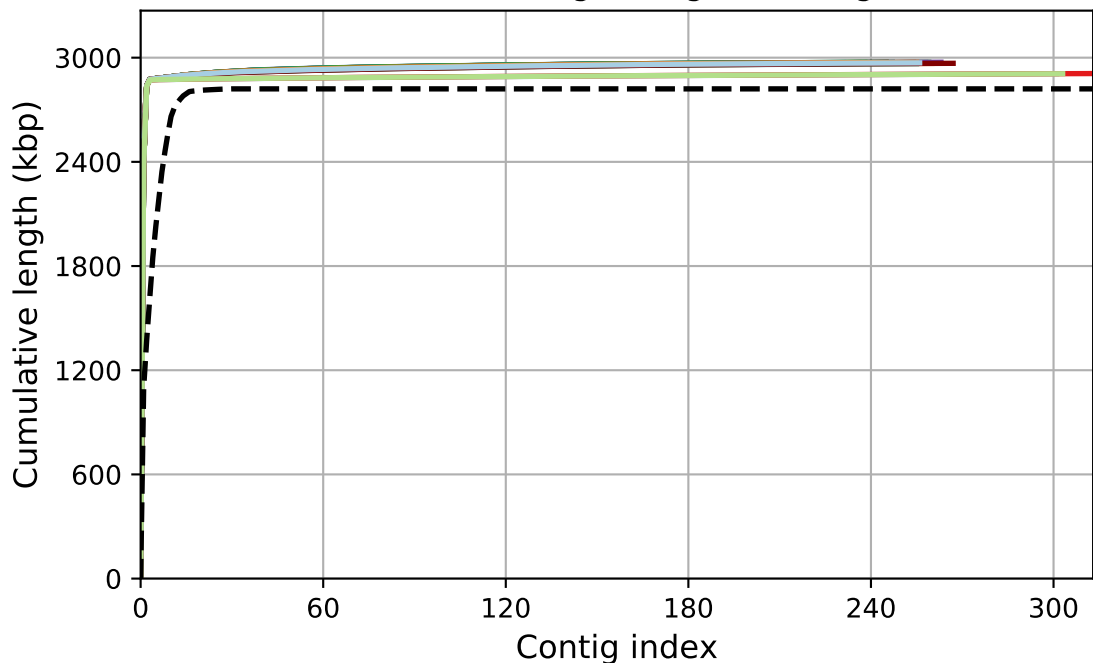
# translocations

FRCurve (misassemblies)

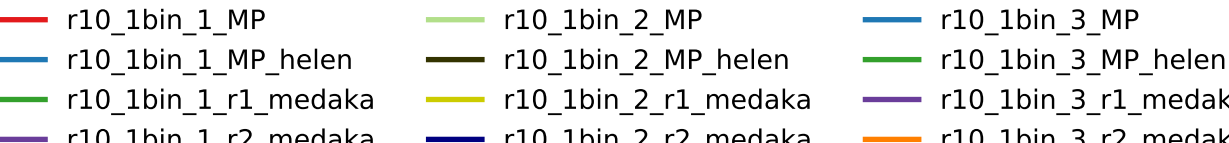
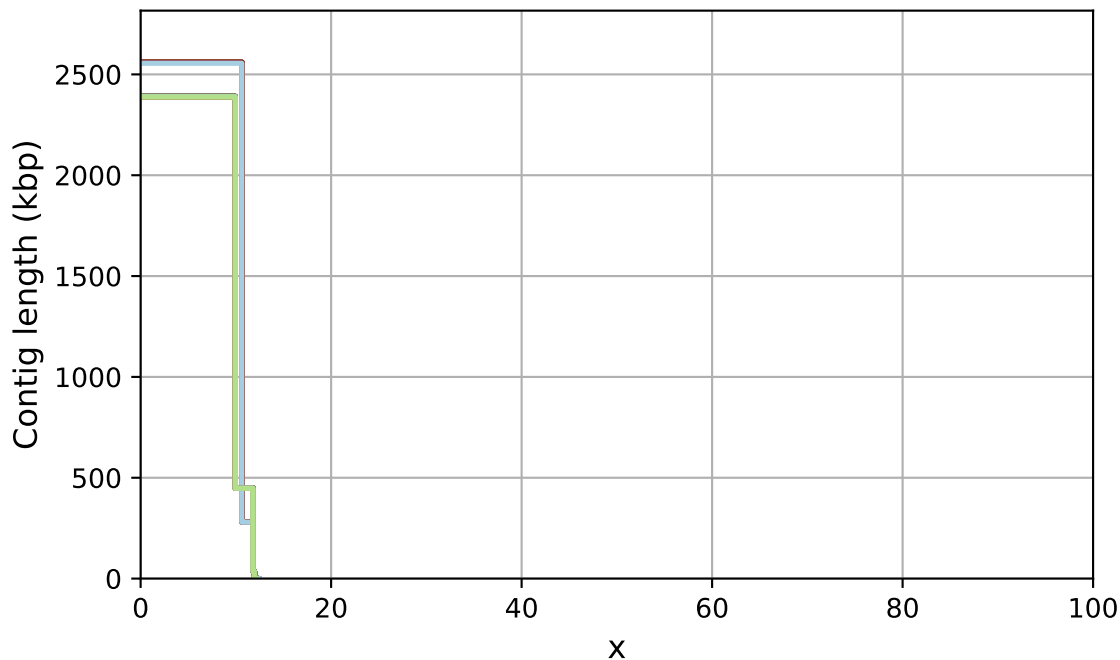


— r10\_1bin\_1\_MP      — r10\_1bin\_2\_MP      — r10\_1bin\_3\_MP  
— r10\_1bin\_1\_MP\_helen      — r10\_1bin\_2\_MP\_helen      — r10\_1bin\_3\_MP\_helen  
— r10\_1bin\_1\_r1\_medaka      — r10\_1bin\_2\_r1\_medaka      — r10\_1bin\_3\_r1\_medak  
— r10\_1bin\_1\_r2\_medaka      — r10\_1bin\_2\_r2\_medaka      — r10\_1bin\_3\_r2\_medak

Cumulative length (aligned contigs)

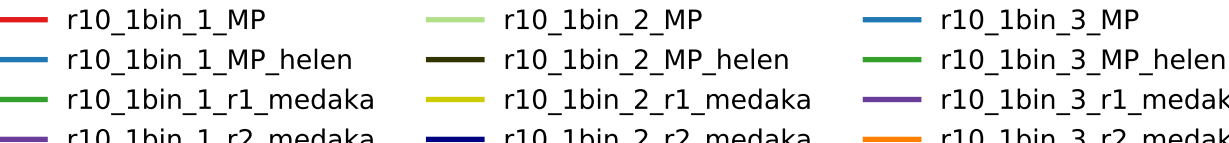
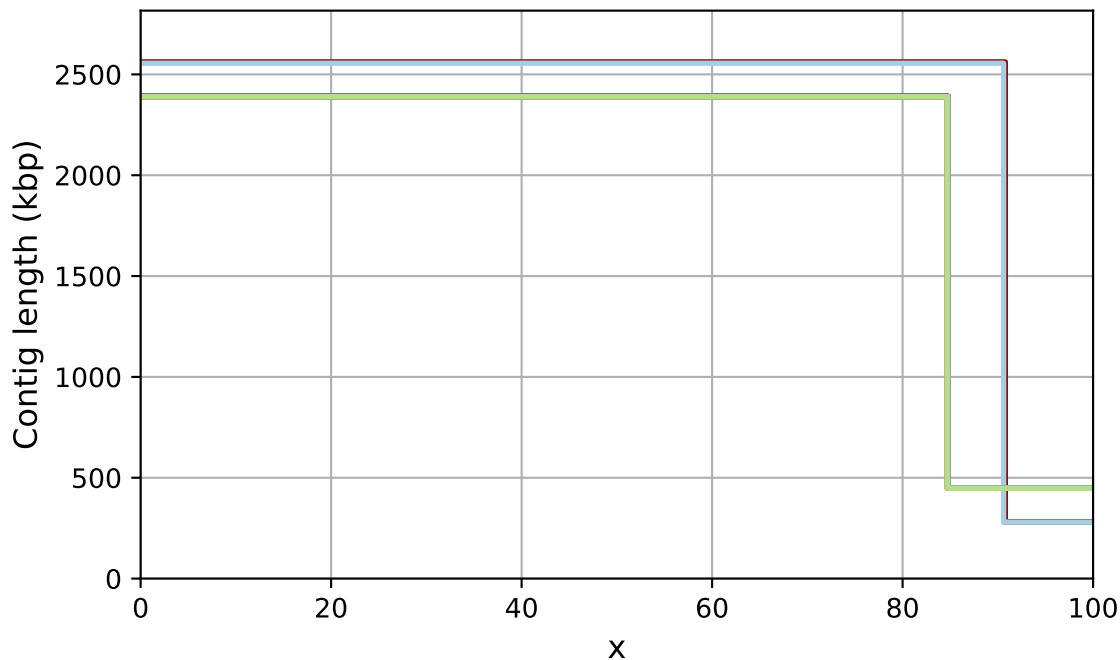


NAX





# NGAx



100.00



- r10\_1bin\_3\_MP
- r10\_1bin\_3\_MP\_helen
- r10\_1bin\_3\_r1\_medak
- r10\_1bin\_3\_r2\_medak