

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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	30850202	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	30849244
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	30850202	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	30849244
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	30850202	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	30849244
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	30850202	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	30849244
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
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	30850202	24074631	24069339	24071923	24062244	24061038	24054829	30849057	24074724	24069480	24072032	24064645	24060108	24055808	30849244
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
GC (%)	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	49.48	44.80	44.80	44.80	44.80	44.79	44.79	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
N50	4045595	4045595	4045598	4045598	4045598	4045598	4755933	4045596	4045596	4045587	4045593	4045258	4045323	4756088	4045596	4045596	4045582	4045582	4045587	4045248	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	2845428	2845430	2845286	2845307	2990636	2845427	2845364	2845435	2845433	2845287	2845362	2990626	2845427	2845365	2845437	2845434	2845286	2845324	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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992094	2992072	2992073	2992074	2991951	2991999	2990636	2992084	2992066	2992073	2992074	2991957	2991981	2990626	2992095	2992076	2992076	2992073	2991935	2991970	2990261
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	12	7	7	7	7	7	7	13
# 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	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# unaligned contigs	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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	20956806	20950389	20952398	20945237	20942136	20934494	27793894	20956560	20949086	20952561	20942641	20942342	20934999	27788298	20956826	20949795	20952339	20945766	20941973	20937303	27794223
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.983	99.984	99.984	99.984	99.984	99.984	99.984	99.975
Duplication ratio	1.054	1.055	1.055	1.055	1.055	1.055	1.033	1.054	1.055	1.055	1.055	1.055	1.055	1.035	1.054	1.055	1.055	1.055	1.054	1.054	1.033
# 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	229.56	236.33	232.81	230.58	230.75	232.81	141.48	230.14	236.02	230.54	231.93	229.97	234.30	149.16	229.46	234.60	232.20	229.33	228.82	229.43	138.08
# indels per 100 kbp	22.05	22.28	21.64	21.64	29.76	29.38	116.49	22.15	22.42	22.32	21.61	22.79	21.61	22.08	22.28	21.78	22.15	22.28	31.41	30.53	113.56
Largest alignment	1569037	1569031	1569033	1569033	1568975	1568997	1568351	1569037	1569030	1569033	1569033	1568984	1568977	1568344	1569036	1569032	1569034	1569033	1568941	1568999	1568099
Total aligned length	3117465	3119866	3119283	3118643	3118576	3119068	3055925	3117597	3119779	3118888	3119129	3118223	3119357	3060321	3117424	3119211	3119219	3118405	3117662	3118031	3054593
NGA50	1569037	1569031	1569033	1569033	1568975	1568997	1568351	1569037	1569030	1569033	1569033	1568984	1568977	1568344	1569036	1569032	1569034	1569033	1568941	1568999	1568099
NGA75	1410533	1410498	1410516	1410517	1410450	1410479	1409726	1410523	1410493	1410516	1410517	1410450	1410482	1409711	1410535	1410501	1410518	1410516	1410474	1410448	1409675
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2

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_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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992094	2992072	2992073	2992074	2991951	2991999	2990636	2992084	2992066	2992073	2992074	2991957	2991981	2990626	2992095	2992076	2992076	2992073	2991935	2991970	2990261
# possibly misassembled contigs	1	1	1	1	1	1	2	1	1	1	1	1	1	2	1	1	1	1	1	1	2
# possible misassemblies	8	8	8	8	8	8	9	8	8	8	8	8	8	9	8	8	8	8	8	8	9
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	12	7	7	7	7	7	7	13
# 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	16	16	16	16	16	16	10	16	16	16	16	16	16	11	16	16	16	16	16	16	11
# unaligned mis. contigs	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6789	6989	6885	6819	6824	6885	4184	6806	6980	6818	6859	6801	6929	4411	6786	6938	6867	6782	6767	6785	4083
# indels	652	659	640	640	880	869	3445	655	663	660	639	910	881	3434	653	659	644	655	929	903	3358
# indels (<= 5 bp)	627	633	616	616	856	843	3417	631	638	635	615	885	853	3405	628	633	620	630	904	878	3331
# indels (> 5 bp)	25	26	24	24	24	26	28	24	25	25	24	25	28	29	25	26	24	25	25	25	27
Indels length	1964	1974	1931	1931	2269	2240	5296	1960	1973	1978	1930	2331	2295	5322	1966	1975	1936	1970	2323	2312	5240

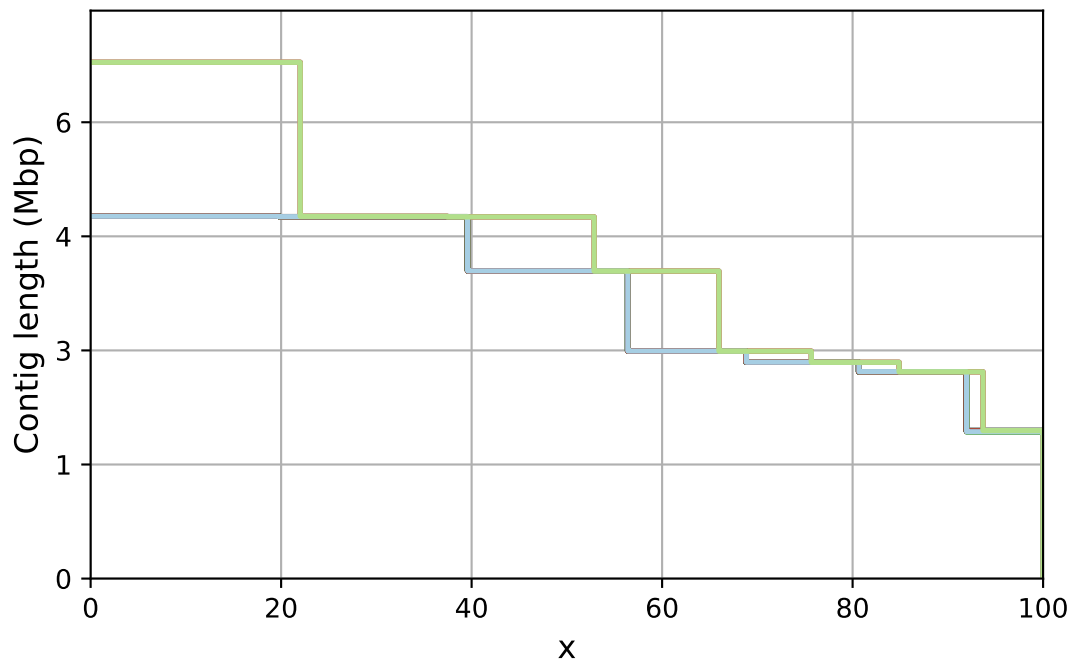
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	20956806	20950389	20952398	20945237	20942136	20934494	27793894	20956560	20949086	20952561	20942641	20942342	20934999	27788298	20956826	20949795	20952339	20945766	20941973	20937303	27794223
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

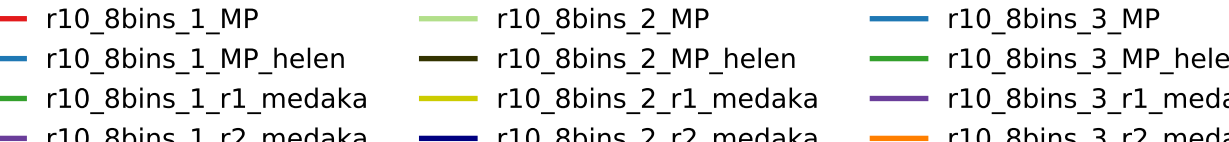
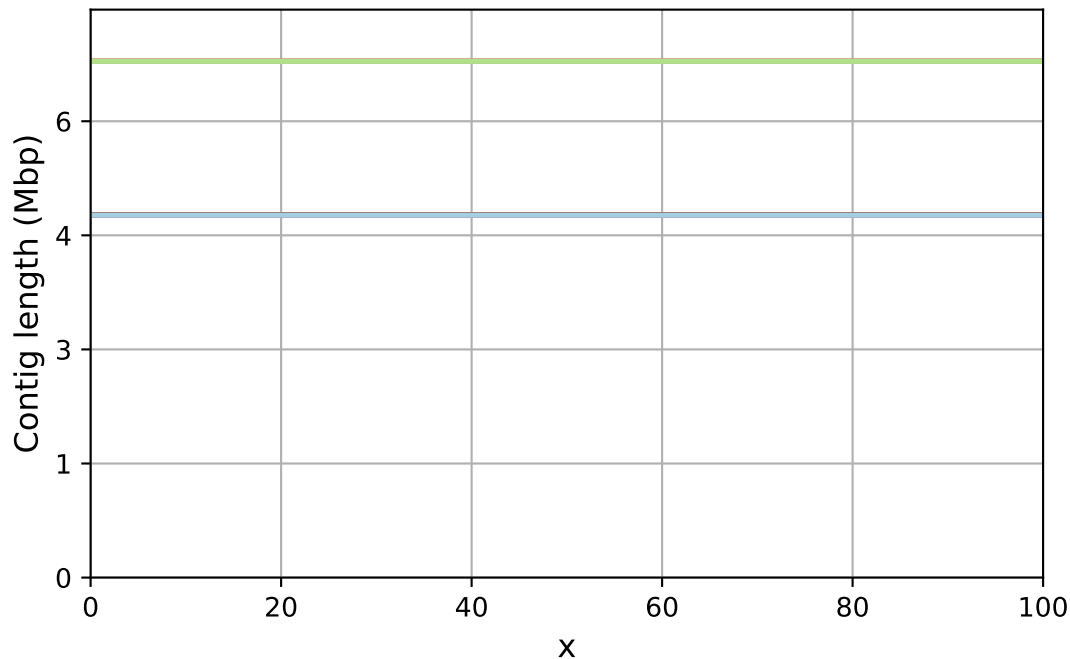
All statistics are based on contigs of size  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

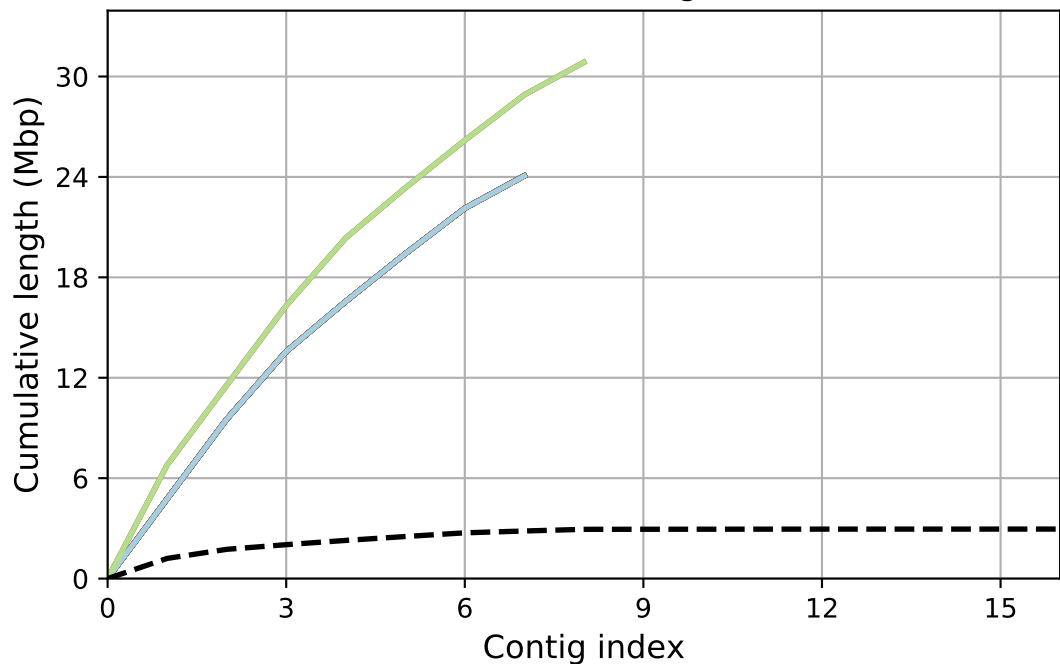


— r10\_8bins\_1\_MP      — r10\_8bins\_2\_MP      — r10\_8bins\_3\_MP  
— r10\_8bins\_1\_MP\_helen      — r10\_8bins\_2\_MP\_helen      — r10\_8bins\_3\_MP\_helen  
— r10\_8bins\_1\_r1\_medaka      — r10\_8bins\_2\_r1\_medaka      — r10\_8bins\_3\_r1\_medaka  
— r10\_8bins\_1\_r2\_medaka      — r10\_8bins\_2\_r2\_medaka      — r10\_8bins\_3\_r2\_medaka

# NGx

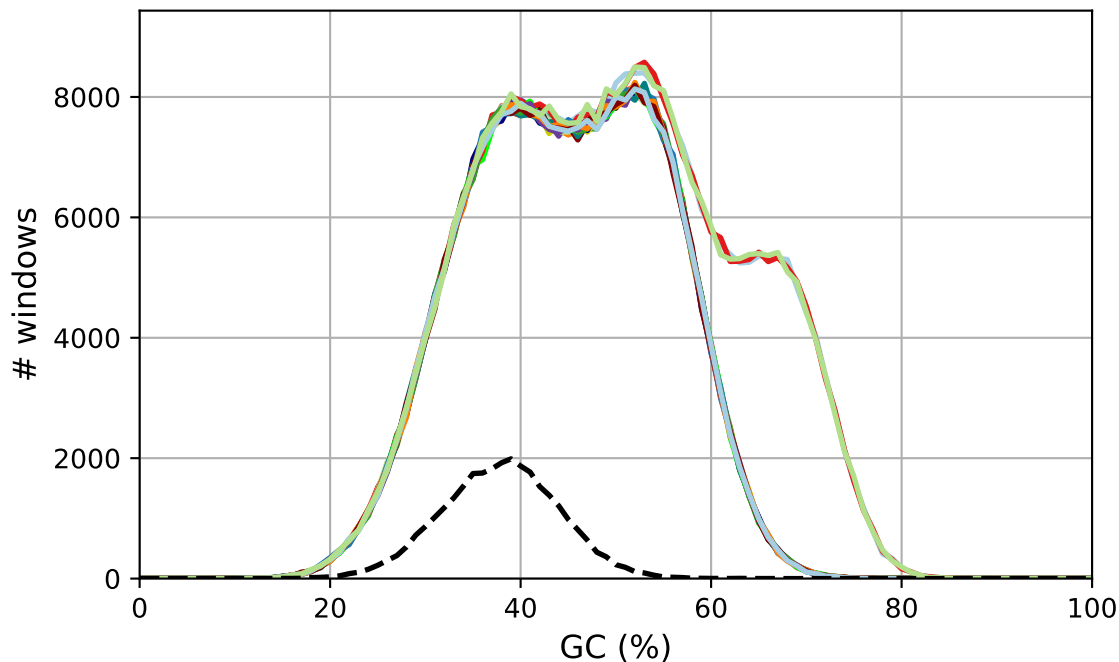


# Cumulative length



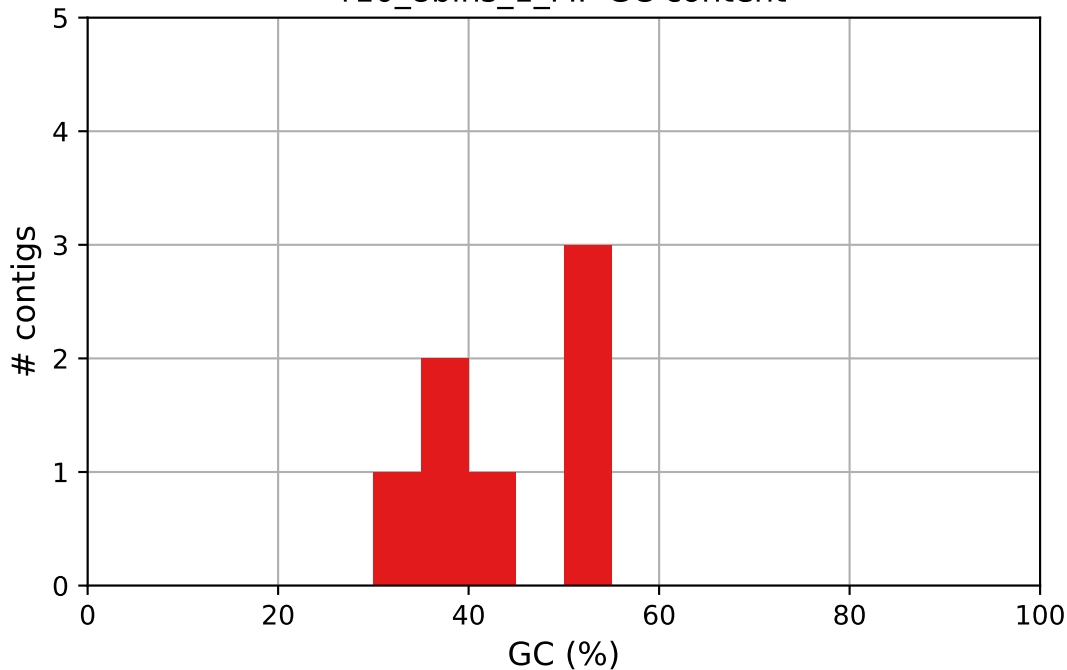
— r10\_8bins\_1\_MP  
— r10\_8bins\_1\_MP\_helen  
— r10\_8bins\_1\_r1\_medaka  
— r10\_8bins\_1\_r2\_medaka  
— r10\_8bins\_2\_MP\_helen  
— r10\_8bins\_2\_r1\_medaka  
— r10\_8bins\_2\_r2\_medaka  
— r10\_8bins\_2\_racon\_r1  
— r10\_8bins\_3\_MP\_helen  
— r10\_8bins\_3\_r1\_medaka  
— r10\_8bins\_3\_r2\_medaka  
— 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\_medaka  
— r10\_8bins\_1\_r1\_medaka      — r10\_8bins\_2\_r2\_medaka      — r10\_8bins\_3\_r2\_medaka  
— r10\_8bins\_1\_r2\_medaka      — r10\_8bins\_2\_racon\_r1      — r10\_8bins\_3\_racon\_r1

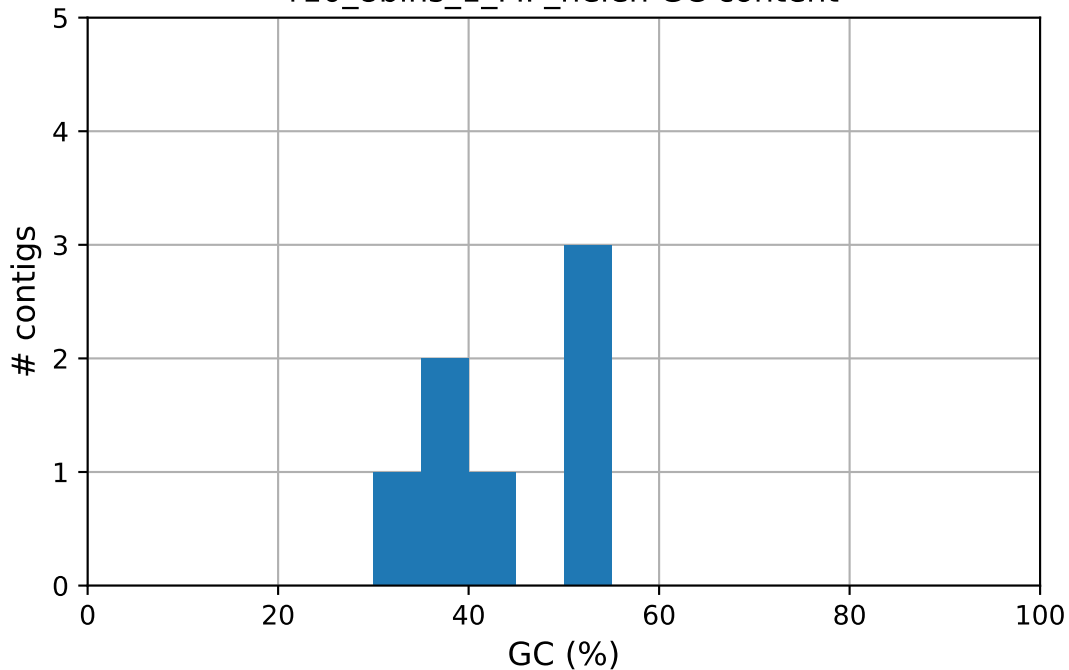
r10\_8bins\_1\_MP GC content



r10\_8bins\_1\_MP

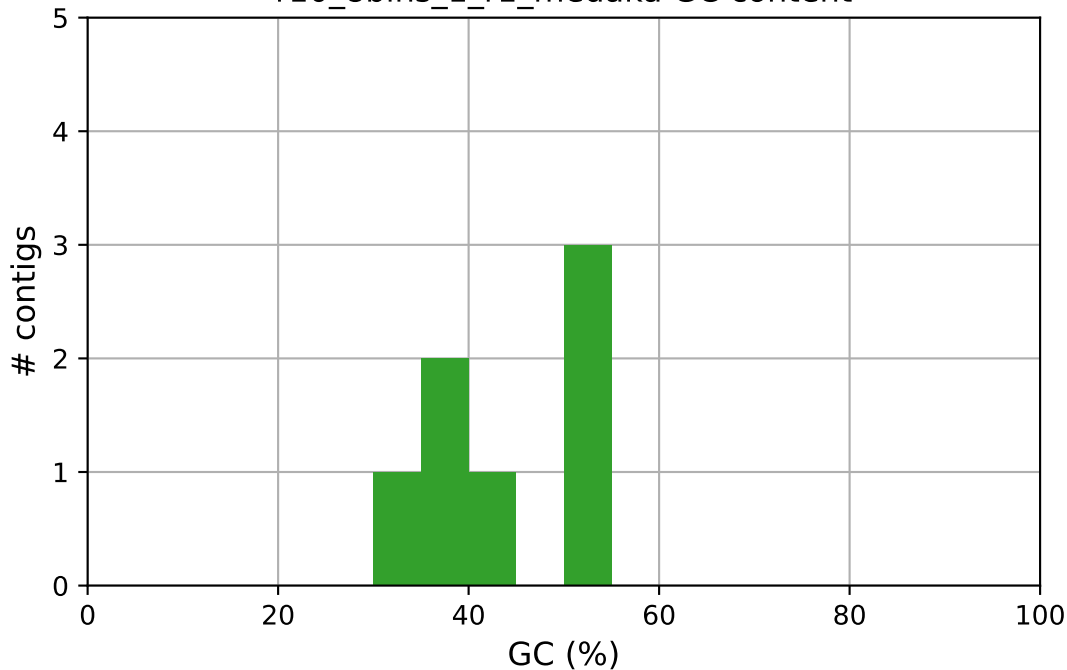


r10\_8bins\_1\_MP\_helen GC content



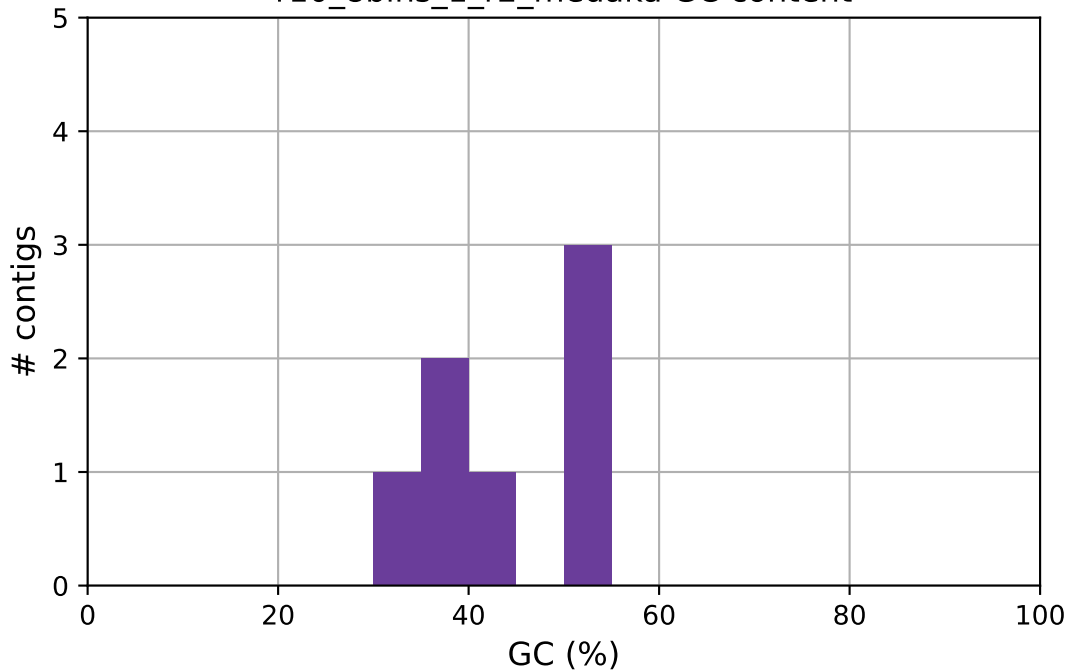
r10\_8bins\_1\_MP\_helen

r10\_8bins\_1\_r1\_medaka GC content



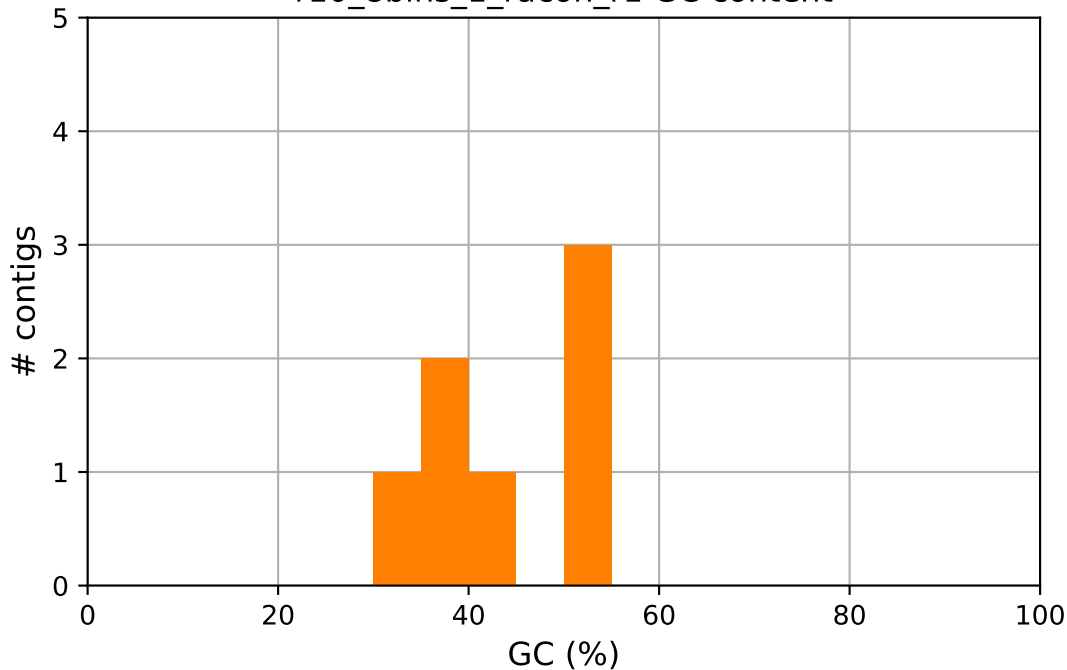
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r10\_8bins\_1\_r2\_medaka GC content



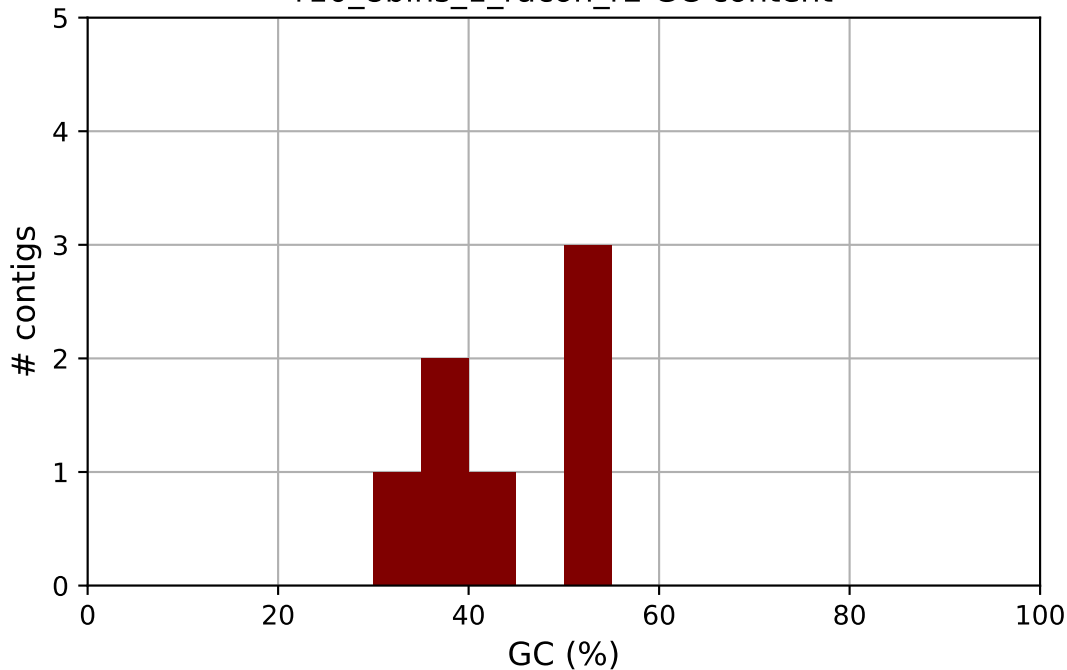
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r10\_8bins\_1\_racon\_r1 GC content



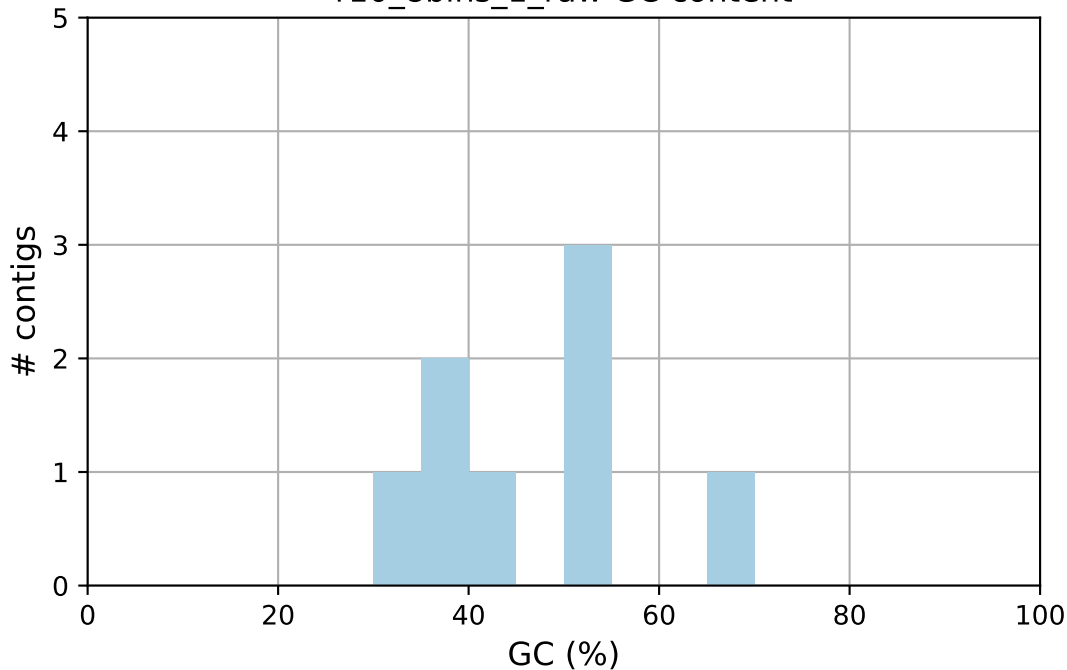
r10\_8bins\_1\_racon\_r1

r10\_8bins\_1\_racon\_r2 GC content



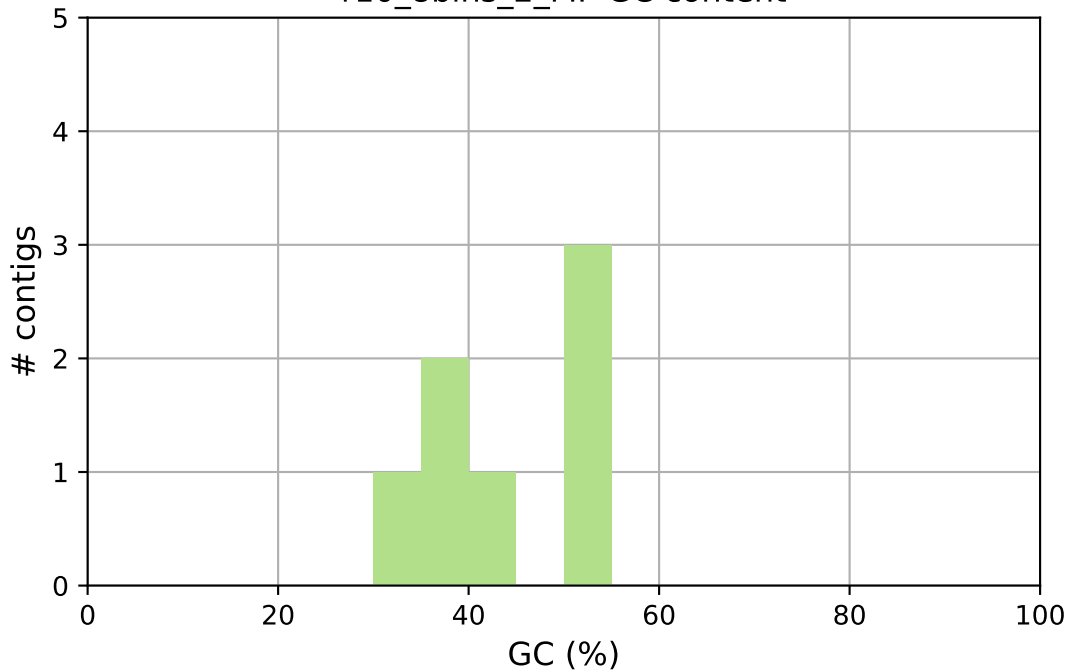
r10\_8bins\_1\_racon\_r2

r10\_8bins\_1\_raw GC content



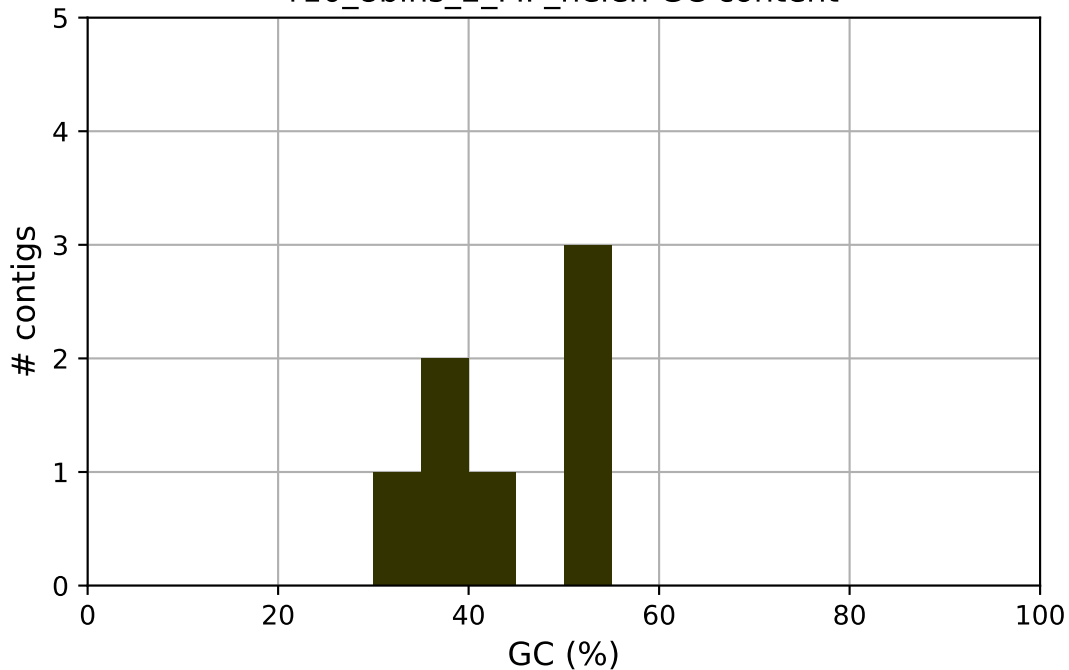
r10\_8bins\_1\_raw

r10\_8bins\_2\_MP GC content



r10\_8bins\_2\_MP

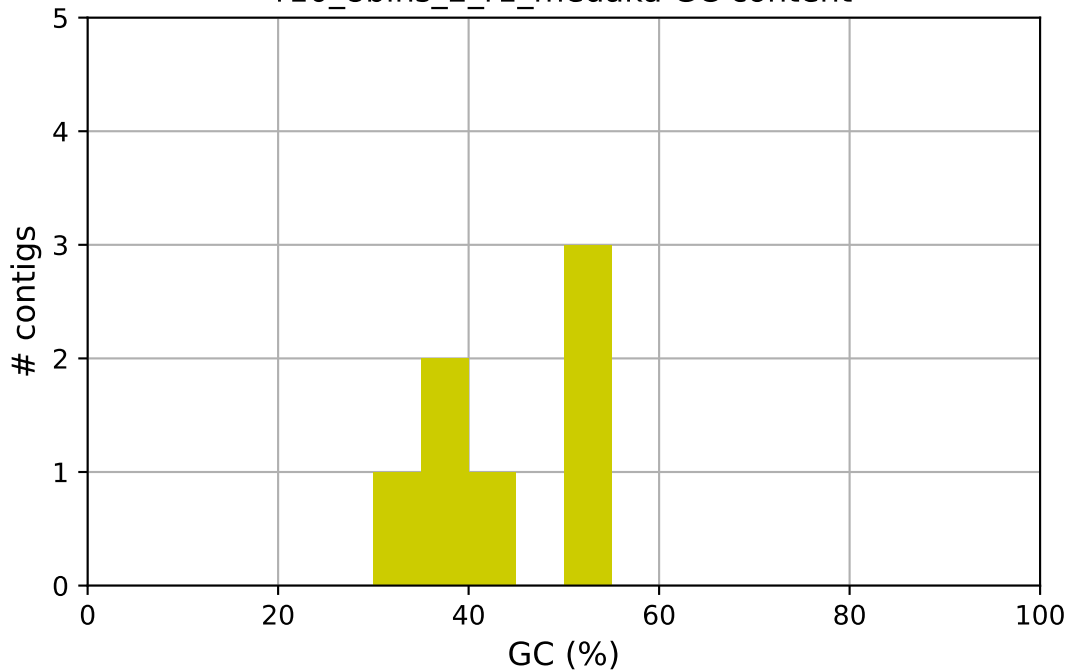
r10\_8bins\_2\_MP\_helen GC content



r10\_8bins\_2\_MP\_helen

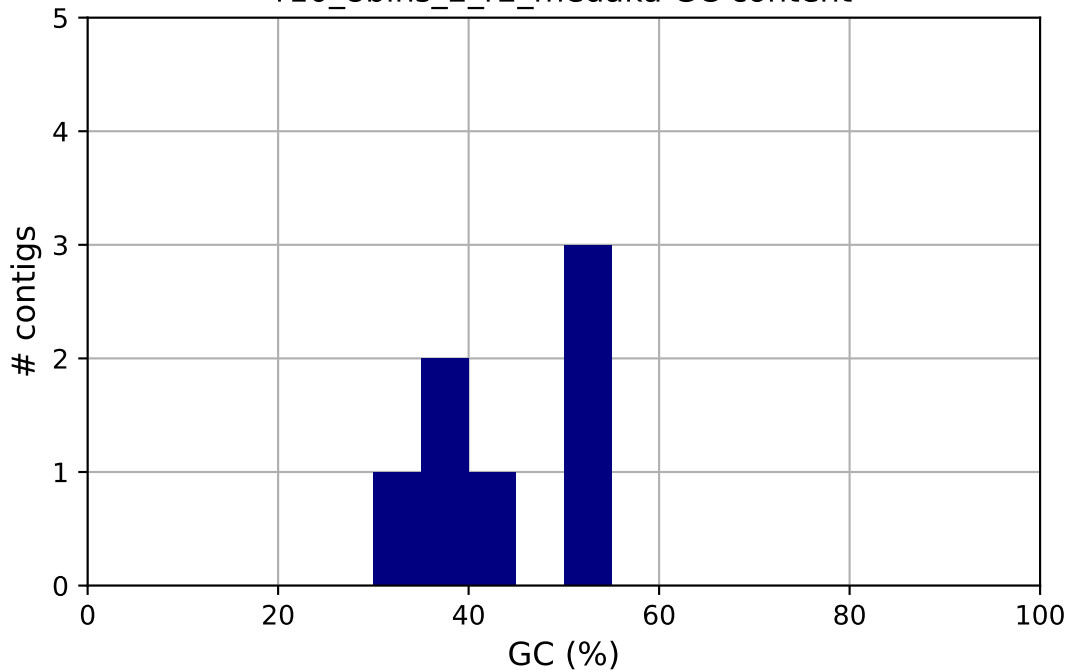


r10\_8bins\_2\_r1\_medaka GC content



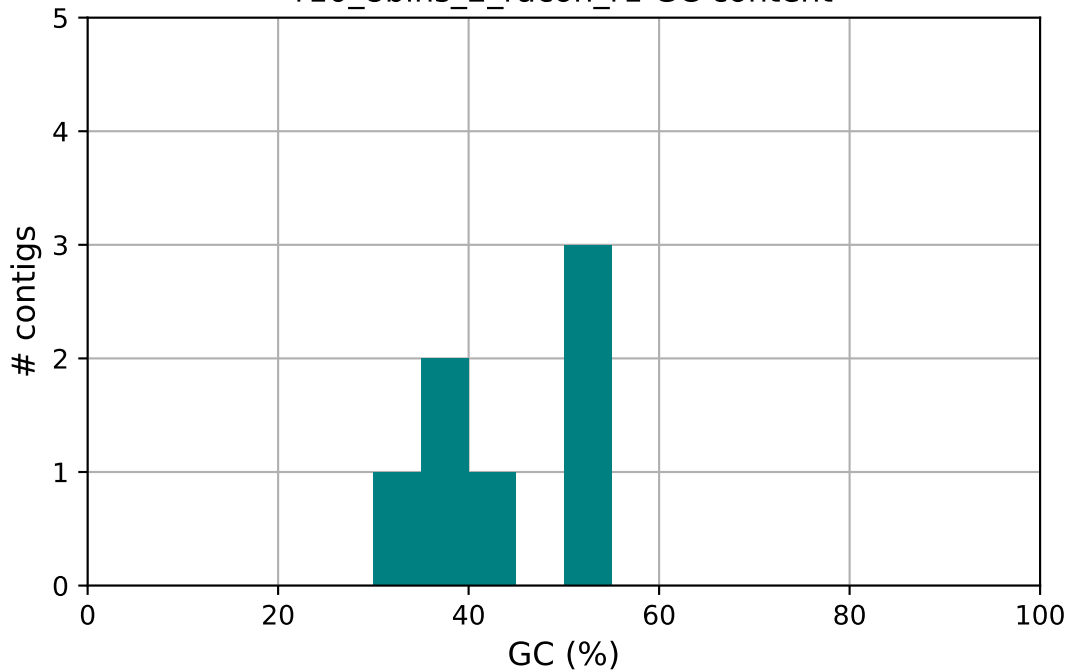
r10\_8bins\_2\_r1\_medaka

r10\_8bins\_2\_r2\_medaka GC content



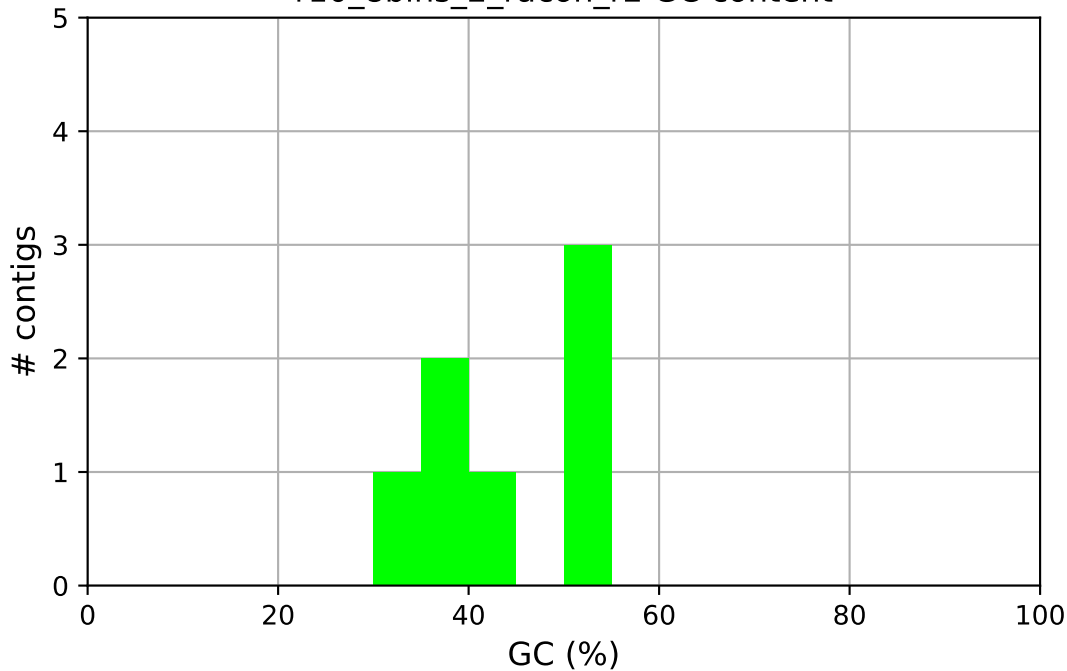
r10\_8bins\_2\_r2\_medaka

r10\_8bins\_2\_racon\_r1 GC content



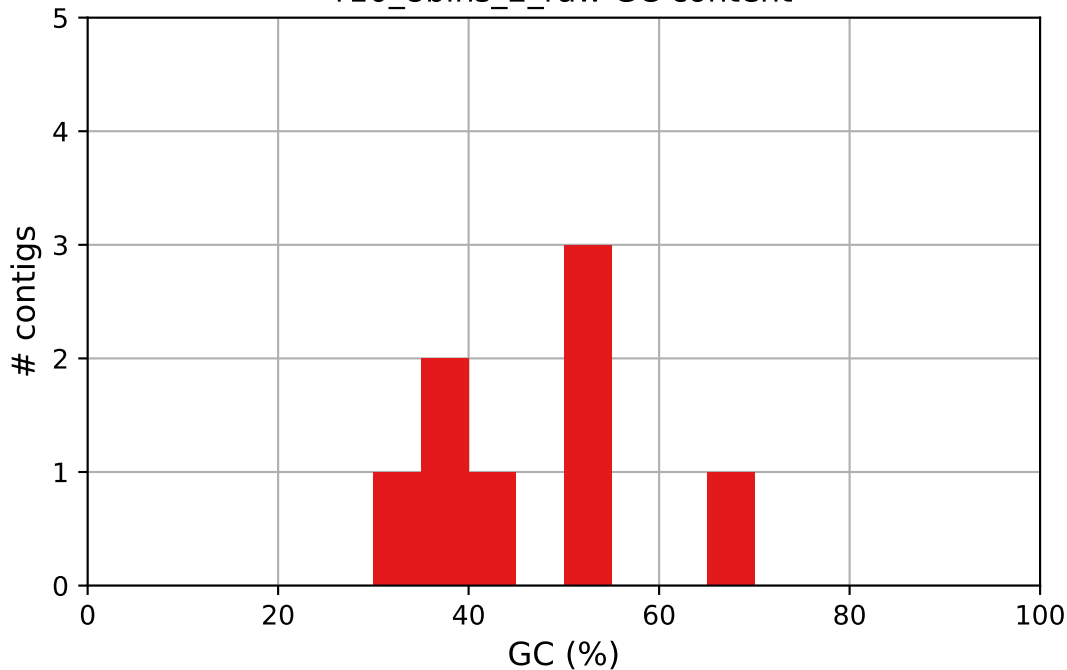
r10\_8bins\_2\_racon\_r1

r10\_8bins\_2\_racon\_r2 GC content



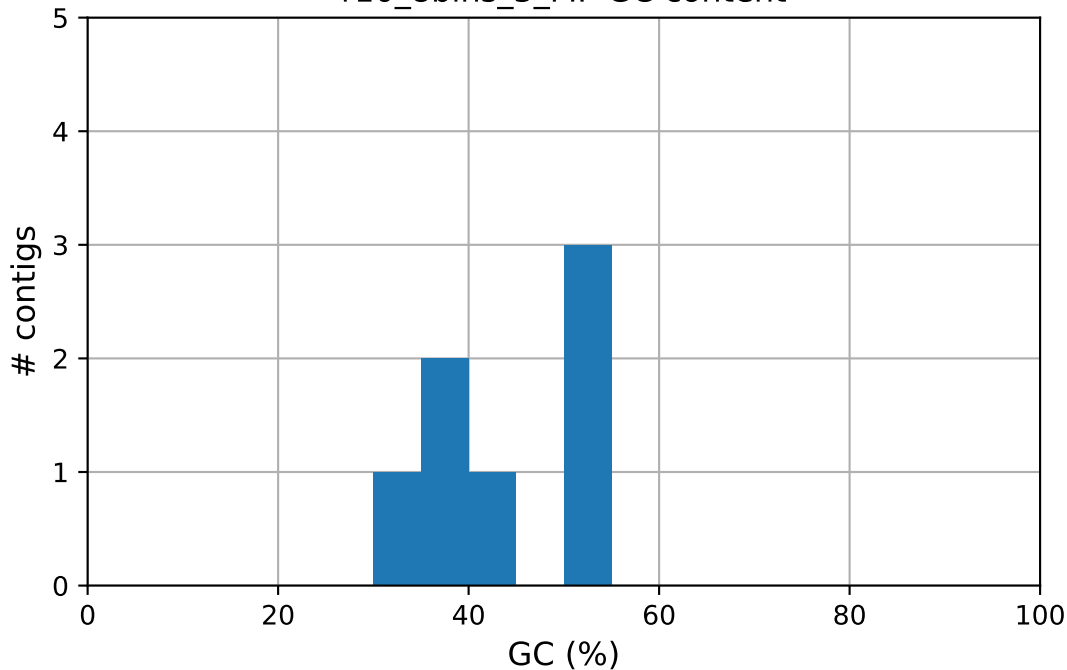
 r10\_8bins\_2\_racon\_r2

r10\_8bins\_2\_raw GC content



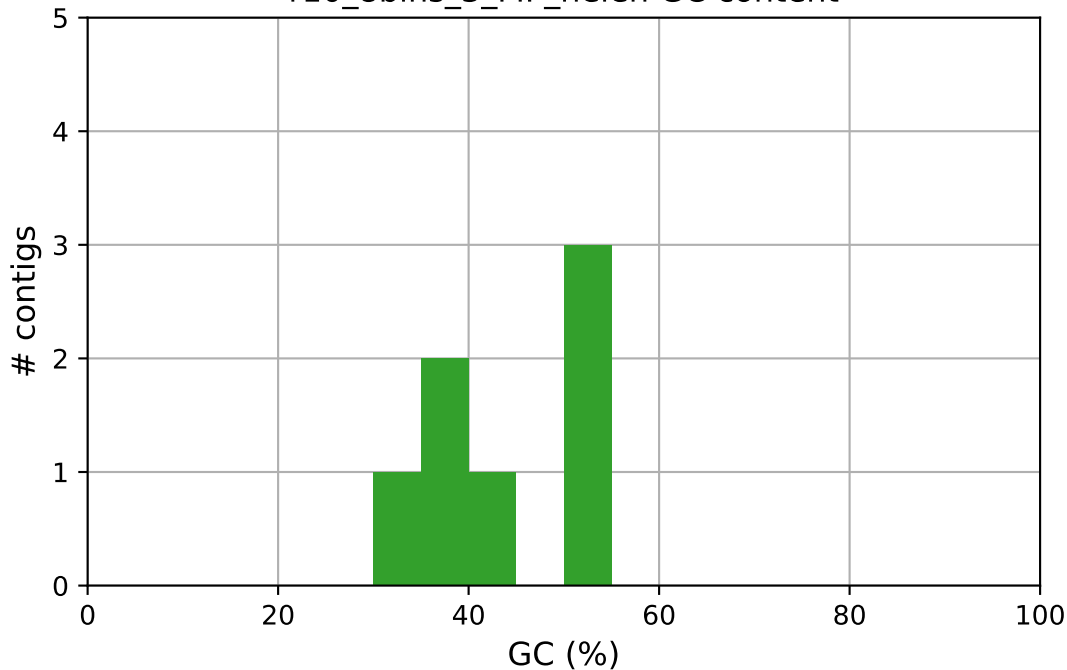
r10\_8bins\_2\_raw

r10\_8bins\_3\_MP GC content



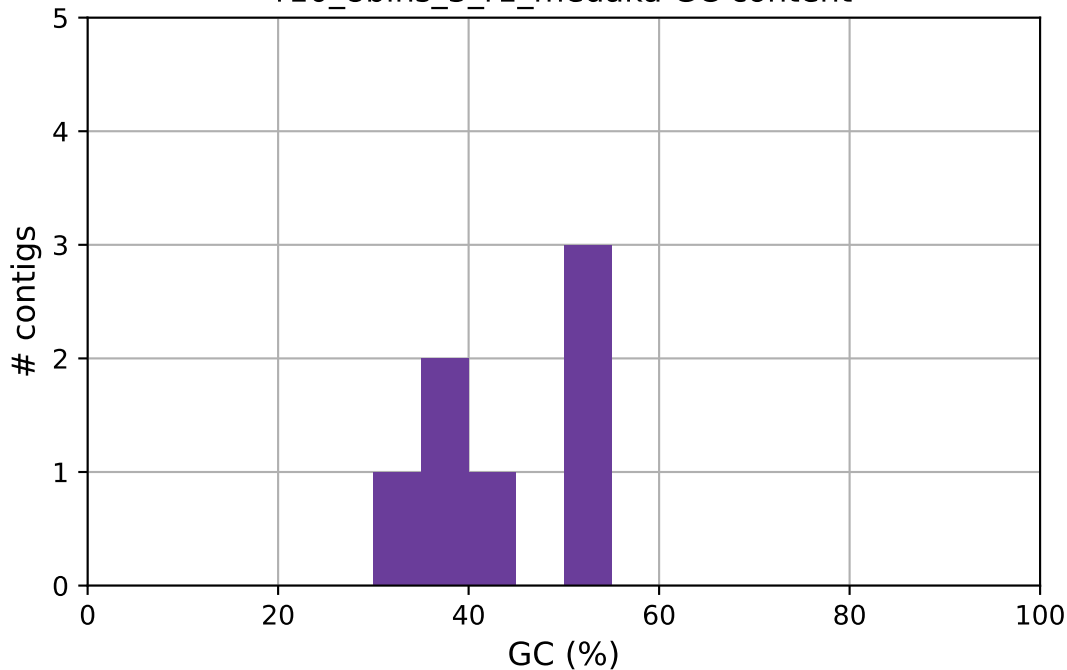
r10\_8bins\_3\_MP

r10\_8bins\_3\_MP\_helen GC content



r10\_8bins\_3\_MP\_helen

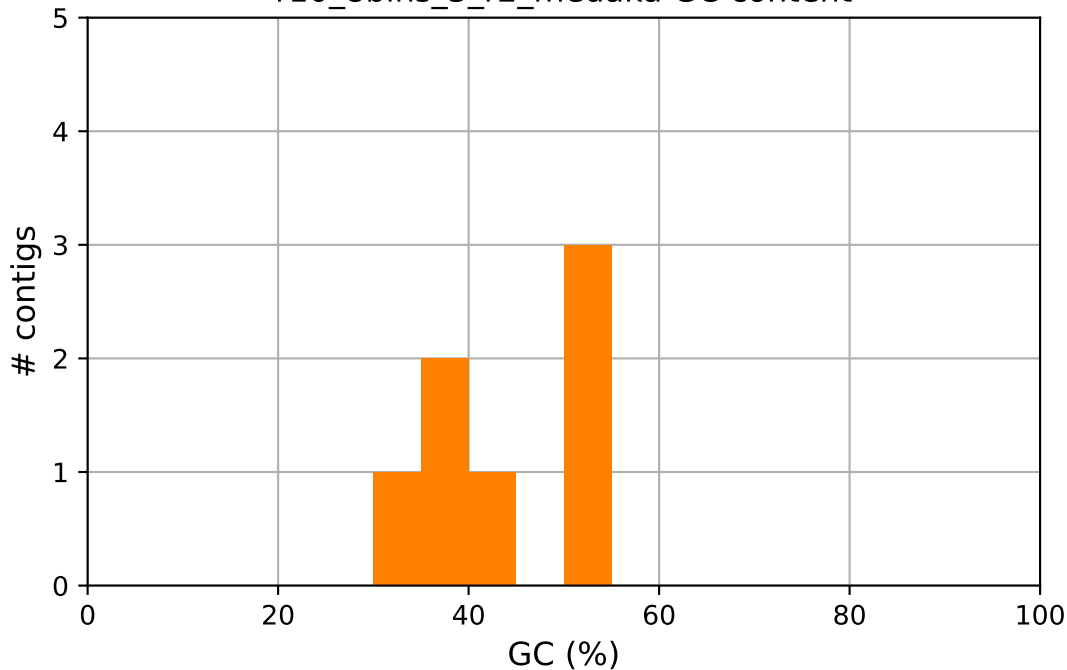
r10\_8bins\_3\_r1\_medaka GC content



r10\_8bins\_3\_r1\_medaka

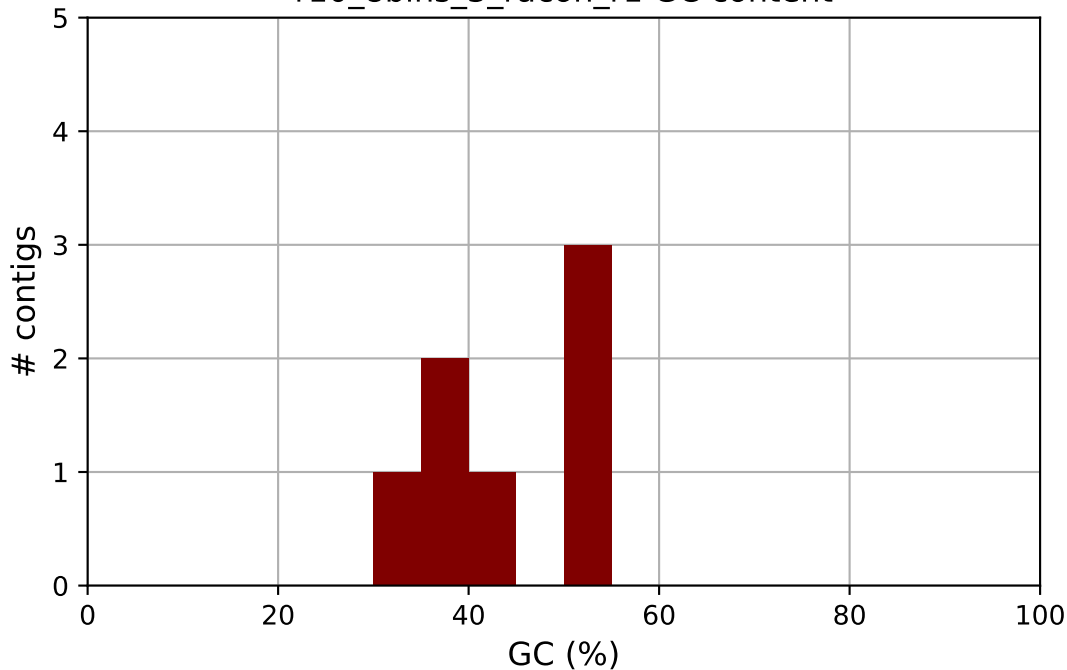


r10\_8bins\_3\_r2\_medaka GC content



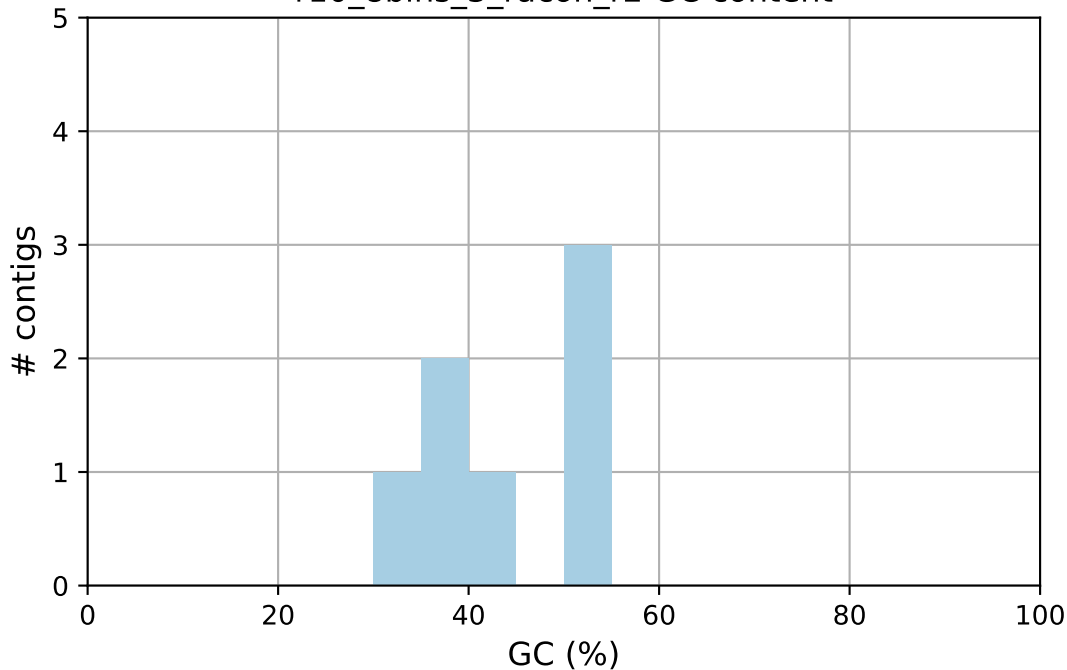
r10\_8bins\_3\_r2\_medaka

r10\_8bins\_3\_racon\_r1 GC content



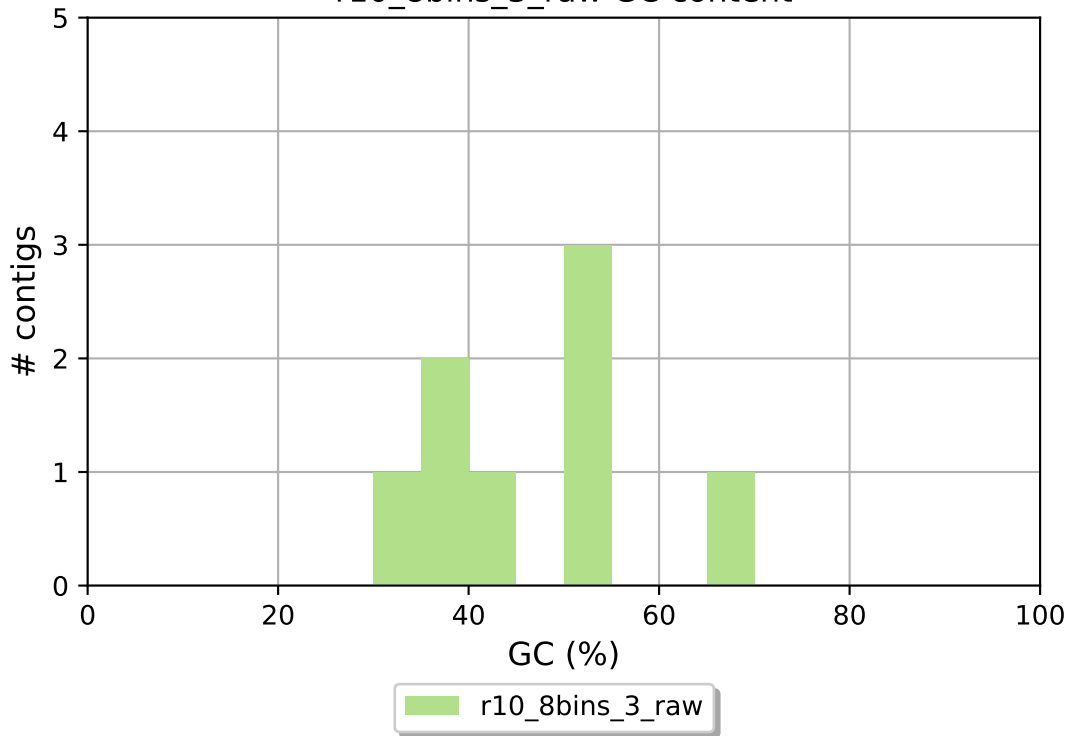
r10\_8bins\_3\_racon\_r1

r10\_8bins\_3\_racon\_r2 GC content

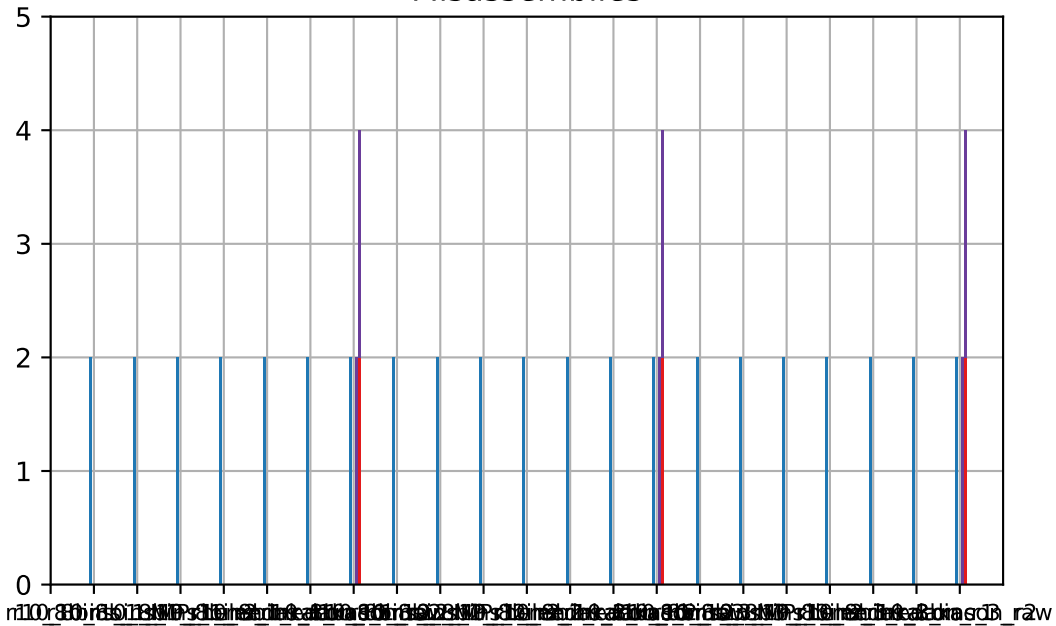


r10\_8bins\_3\_racon\_r2

r10\_8bins\_3\_raw GC content



# Misassemblies



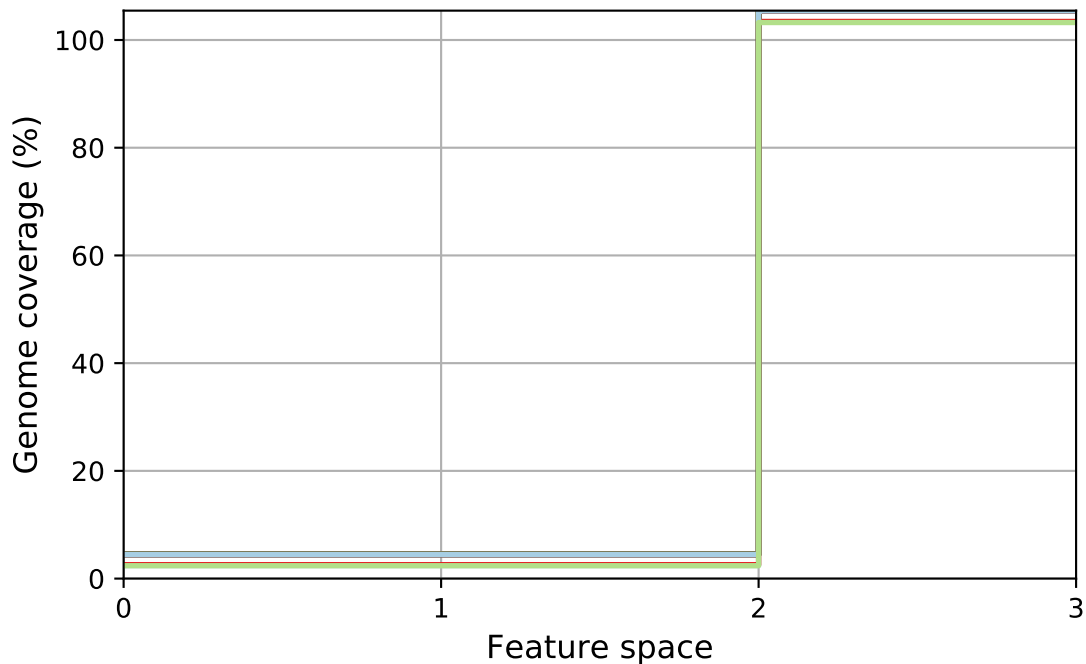
114

# translocations

10

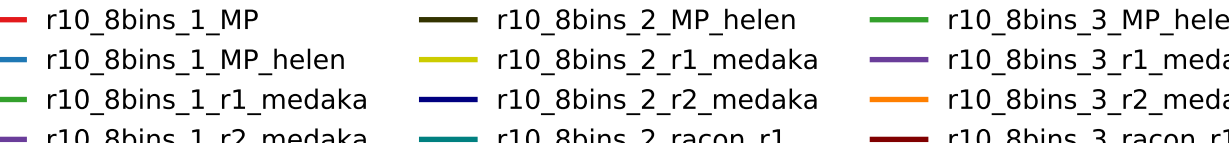
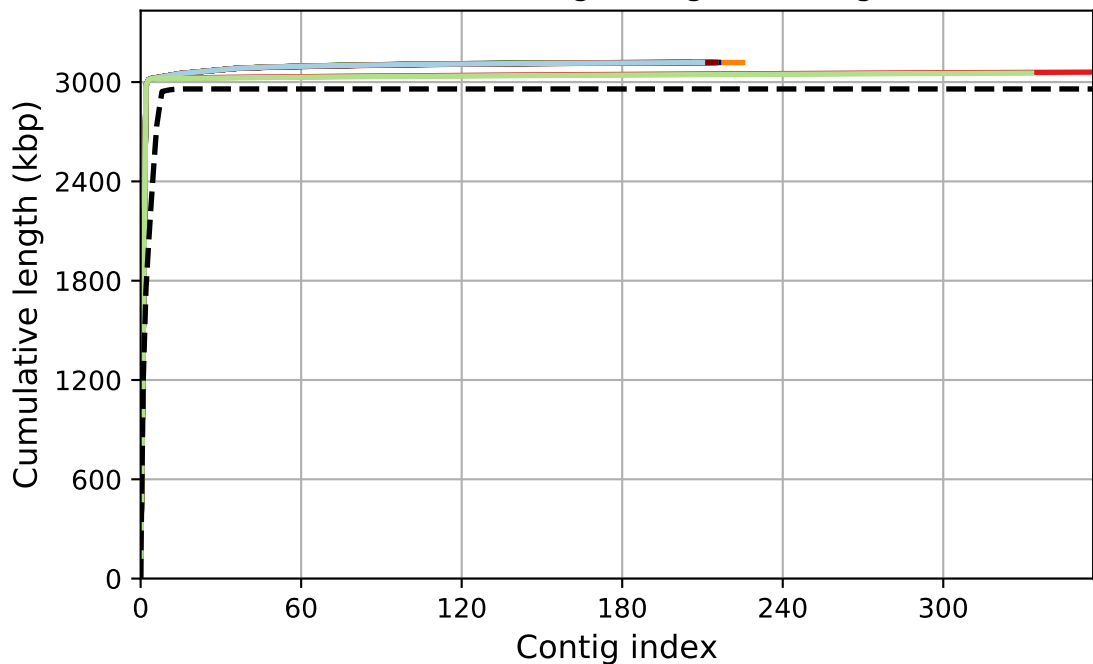
# interspecies translocations

# FRCurve (misassemblies)

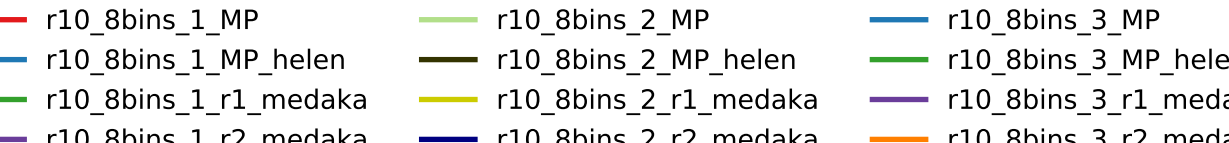
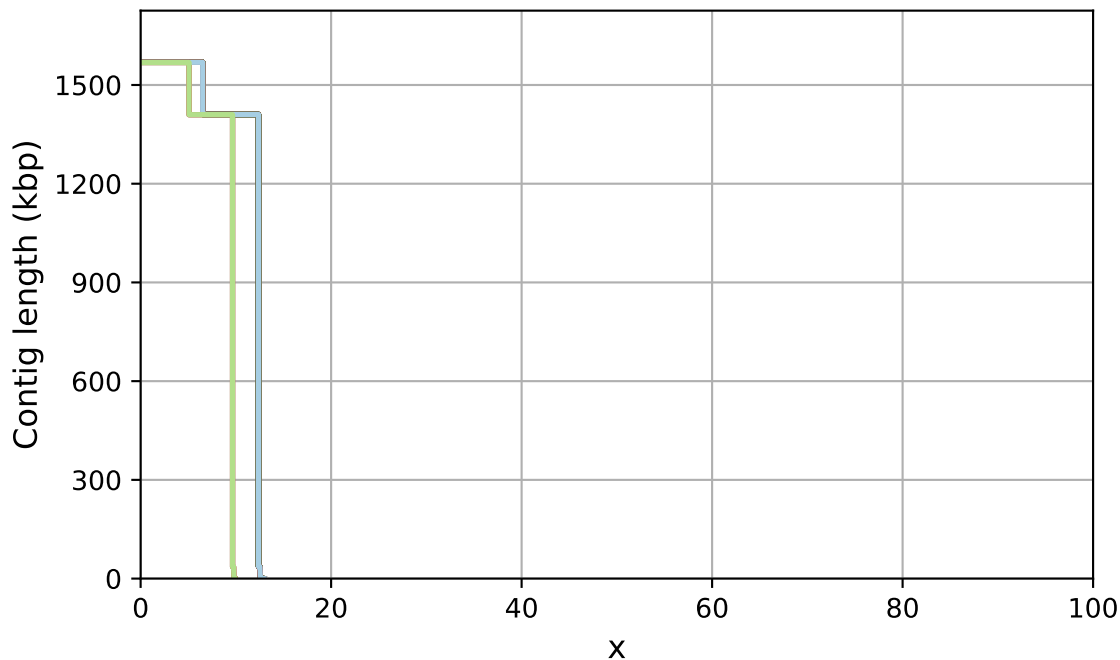


— r10\_8bins\_1\_MP      — r10\_8bins\_2\_MP      — r10\_8bins\_3\_MP  
— r10\_8bins\_1\_MP\_helen      — r10\_8bins\_2\_MP\_helen      — r10\_8bins\_3\_MP\_helen  
— r10\_8bins\_1\_r1\_medaka      — r10\_8bins\_2\_r1\_medaka      — r10\_8bins\_3\_r1\_medaka  
— r10\_8bins\_1\_r2\_medaka      — r10\_8bins\_2\_r2\_medaka      — r10\_8bins\_3\_r2\_medaka

Cumulative length (aligned contigs)

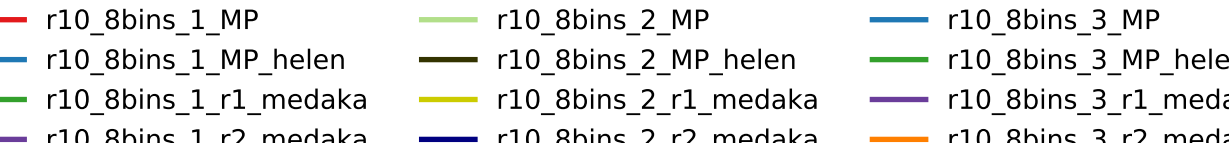
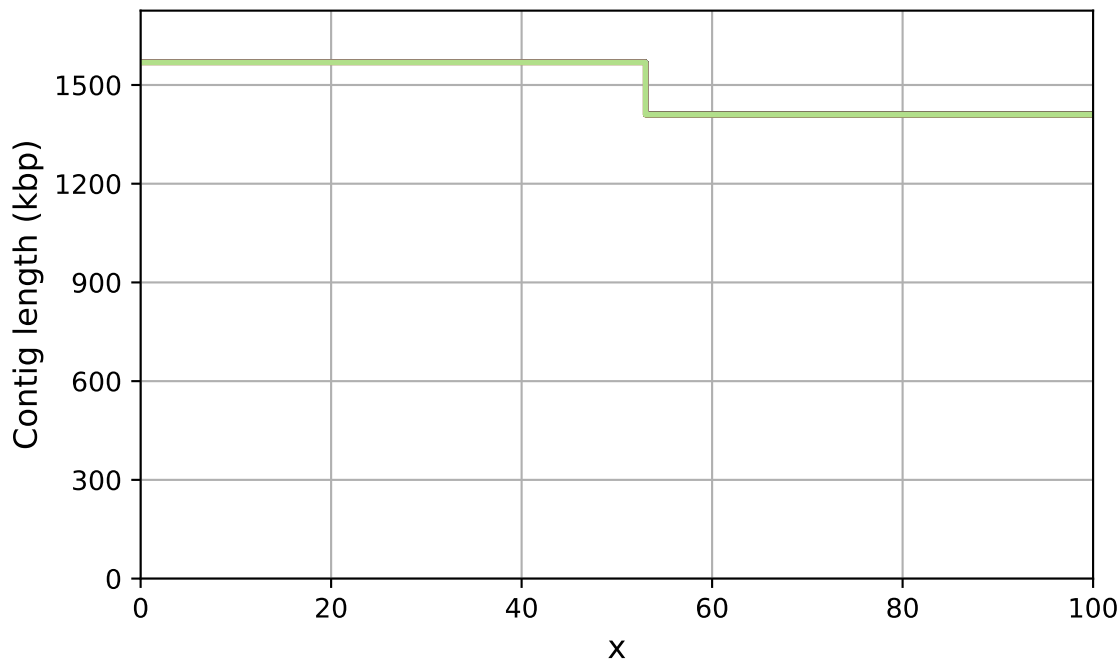


NAX





# NGAx



Genome fraction, %

100.00

99.99

99.98

99.97

