

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	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)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 10000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 25000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Total length (>= 50000 bp)	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
Total length	24074745	24070729	24072155	24064354	24061185	24054036	24061588	24074631	24069339	24071923	24062244	24061038	24054829	24060476	24074724	24069480	24072032	24064645	24060108	24055808	24060952
Reference length	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
GC (%)	44.80	44.80	44.80	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	44.79	44.77	44.80	44.80	44.80	44.80	44.79	44.79	44.77
Reference GC (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
N50	4045595	4045615	4045602	4045598	4045293	4045319	4043044	4045596	4045616	4045587	4045593	4045258	4045323	4042479	4045596	4045613	4045582	4045587	4045248	4045358	4043002
NG50	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
N75	2845436	2845374	2845428	2845430	2845286	2845307	2843860	2845427	2845364	2845435	2845433	2845287	2845362	2843855	2845427	2845365	2845437	2845434	2845286	2845324	2843844
NG75	4765396	4765339	4765361	4765365	4764689	4764726	4763575	4765403	4765334	4765359	4765364	4764683	4764682	4763493	4765471	4765411	4765372	4765365	4764770	4764744	4763941
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	74	73	73	77	73	80	77	74	73	76	79	75	82	75	74	74	76	78	79	83	77
# 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	1947326	1946182	1945604	1937700	1935646	1928318	1945672	1947356	1945118	1945358	1936107	1935574	1929159	1945498	1947365	1944965	1945429	1938538	1934631	1930127	1945410
# local misassemblies	11	15	27	30	44	39	33	11	14	25	28	43	35	30	12	16	21	30	46	32	33
# 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	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 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	
Unaligned length	22082720	22079951	22085137	22085618	22080726	22080016	22114139	22082419	22080080	22084183	22083488	22079927	22077481	22105466	22082736	22081091	22083283	22085685	22079579	22078522	22111837
Genome fraction (%)	99.943	99.889	99.926	99.895	99.897	99.875	99.875	99.943	99.832	99.925	99.936	99.913	99.888	99.862	99.936	99.828	99.872	99.932	99.870	99.869	99.860
Duplication ratio	1.104	1.104	1.101	1.097	1.098	1.095	1.080	1.104	1.104	1.102	1.097	1.098	1.097	1.084	1.104	1.103	1.103	1.097	1.098	1.097	1.081
# 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	
# mismatches per 100 kbp	266.98	267.34	289.03	291.17	267.21	267.38	360.39	267.36	266.22	300.95	283.79	270.05	272.00	372.64	265.66	264.01	318.25	275.04	267.89	268.23	362.05
# indels per 100 kbp	11.36	15.36	14.25	14.03	57.45	53.02	345.30	11.75	10.76	16.85	12.91	52.95	51.57	351.95	11.64	14.93	18.91	10.75	56.68	53.52	349.90
Largest alignment	177205	177204	177198	176920	176816	176760	176983	177205	177205	173114	176980	173004	176835	176989	177206	177206	173025	173046	172882	172972	177003
Total aligned length	1985939	1987024	1980994	1972765	1976871	1968214	1943991	1986126	1983173	1981709	1972702	1976523	1971181	1951560	1988234	1982248	1985090	1972955	1974626	1971413	1945734
NGA50	89790	88849	89788	81510	81489	81364	69730	89789	87700	89895	85401	89780	79258	69730	89790	87652	79490	81501	79400	81451	69730
NGA75	35033	35503	35031	35032	35015	35015	34946	35033	35032	34836	34837	34825	34811	34946	35505	35032	35032	35032	34825	34811	34946
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	
LGA75	17	16	17	17	17	17	18	17	17	17	17	17	18	18	16	17	18	17	18	18	

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

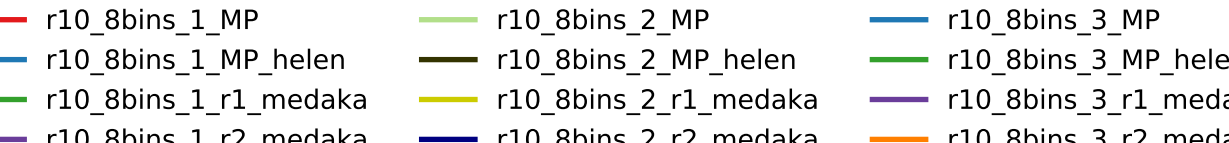
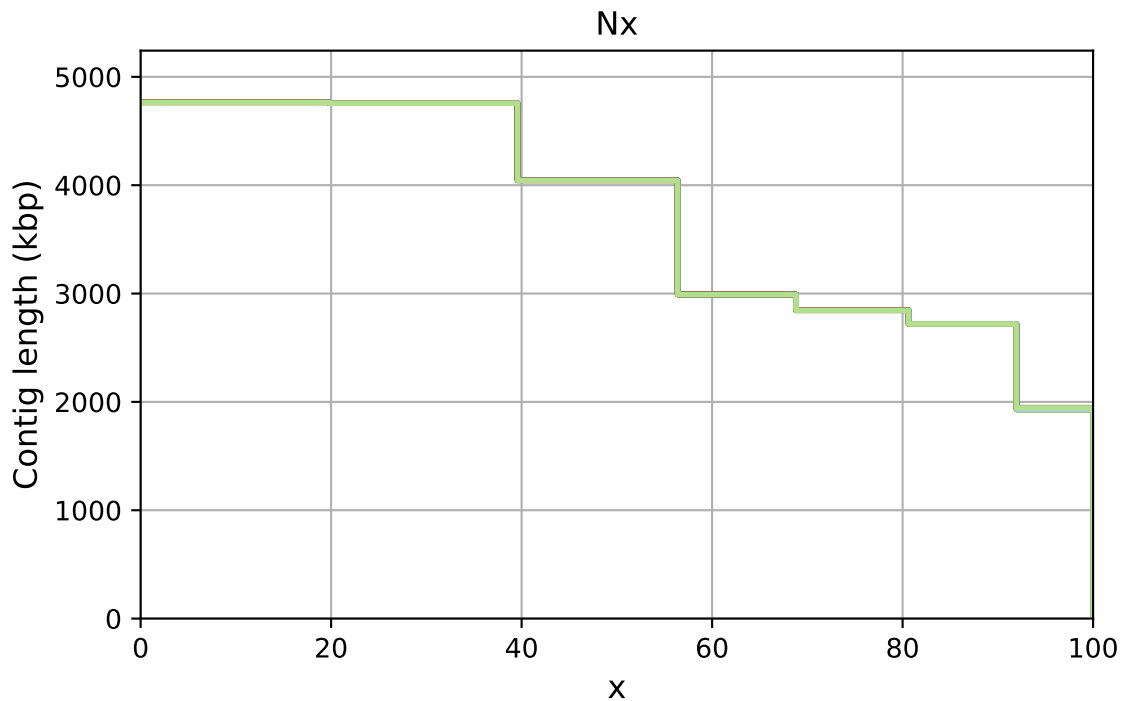
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# misassemblies	74	73	73	77	73	80	77	74	73	76	79	75	82	75	74	74	76	78	79	83	77
# contig misassemblies	74	73	73	77	73	80	77	74	73	76	79	75	82	75	74	74	76	78	79	83	77
# c. relocations	4	3	3	5	3	6	4	4	3	3	7	3	6	4	4	3	3	5	3	5	4
# c. translocations	70	70	70	72	70	74	73	70	70	73	72	72	76	71	70	71	73	73	76	78	73
# 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	1947326	1946182	1945604	1937700	1935646	1928318	1945672	1947356	1945118	1945358	1936107	1935574	1929159	1945498	1947365	1944965	1945429	1938538	1934631	1930127	1945410
# 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	36	36	34	36	36	34	46	36	38	32	36	34	28	42	36	38	32	38	32	28	46
# local misassemblies	11	15	27	30	44	39	33	11	14	25	28	43	35	30	12	16	21	30	46	32	33
# 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	66	66	65	66	63	63	36	66	66	65	63	65	62	40	66	65	63	65	62	61	40
# 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	4817	4821	5214	5251	4819	4821	6498	4824	4798	5429	5120	4871	4905	6718	4793	4758	5738	4962	4830	4836	6527
# indels	205	277	257	253	1036	956	6226	212	194	304	233	955	930	6345	210	269	341	194	1022	965	6308
# indels (<= 5 bp)	155	227	206	199	956	886	6124	161	139	257	175	882	856	6244	161	208	293	143	955	898	6206
# indels (> 5 bp)	50	50	51	54	80	70	102	51	55	47	58	73	74	101	49	61	48	51	67	67	102
Indels length	2705	2757	2808	2881	5168	4754	11068	2731	2747	2830	3095	4820	4879	11281	2605	3006	2789	2729	4912	4306	11182

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).

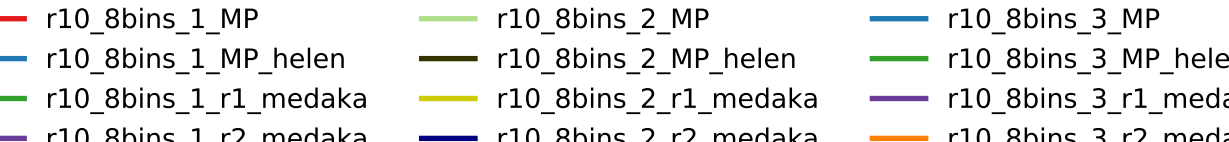
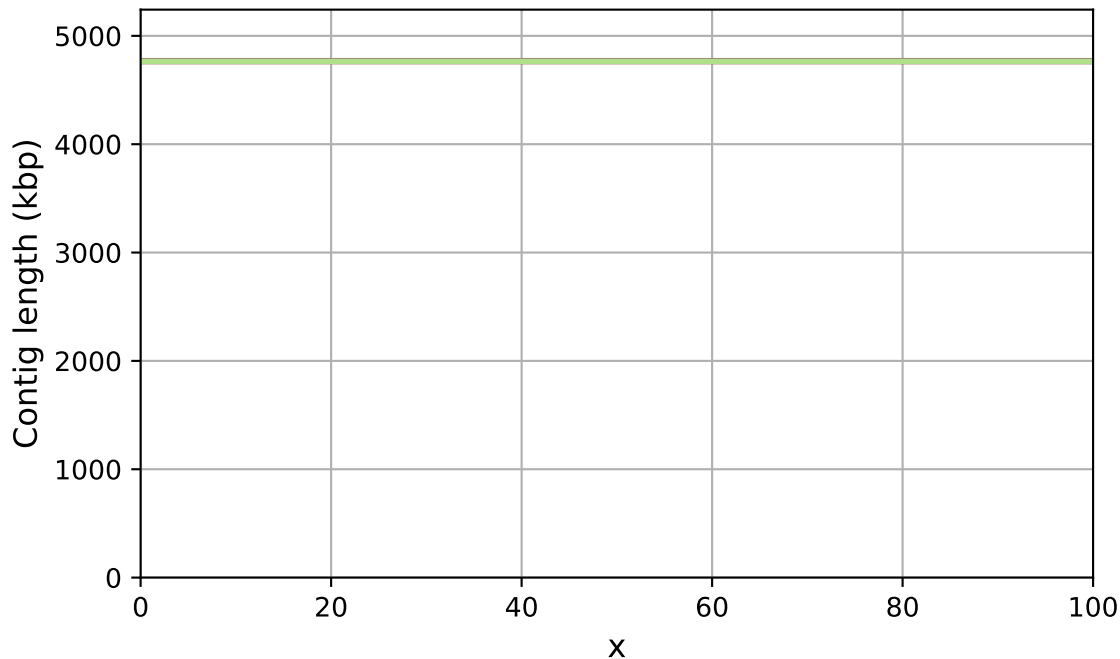
Unaligned report

	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	7	7	7	7	7	7	7	7
Partially unaligned length	22082720	22079951	22085137	22085618	22080726	22080016	22114139	22082419	22080080	22084183	22083488	22079927	22077481	22105466	22082736	22081091	22083283	22085685	22079579	22078522	22111837
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

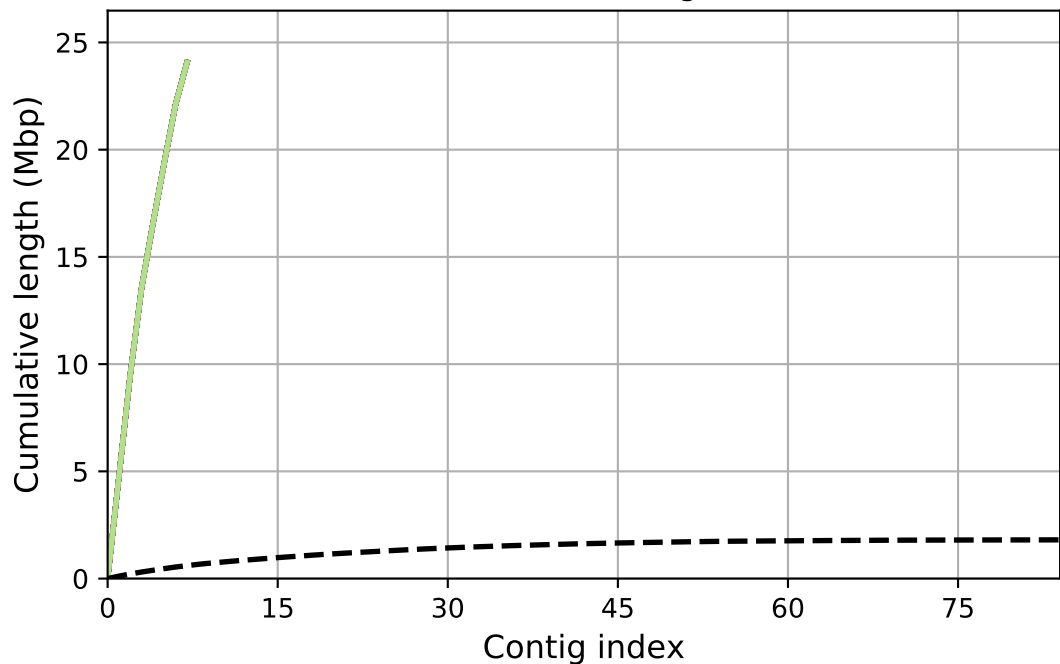
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

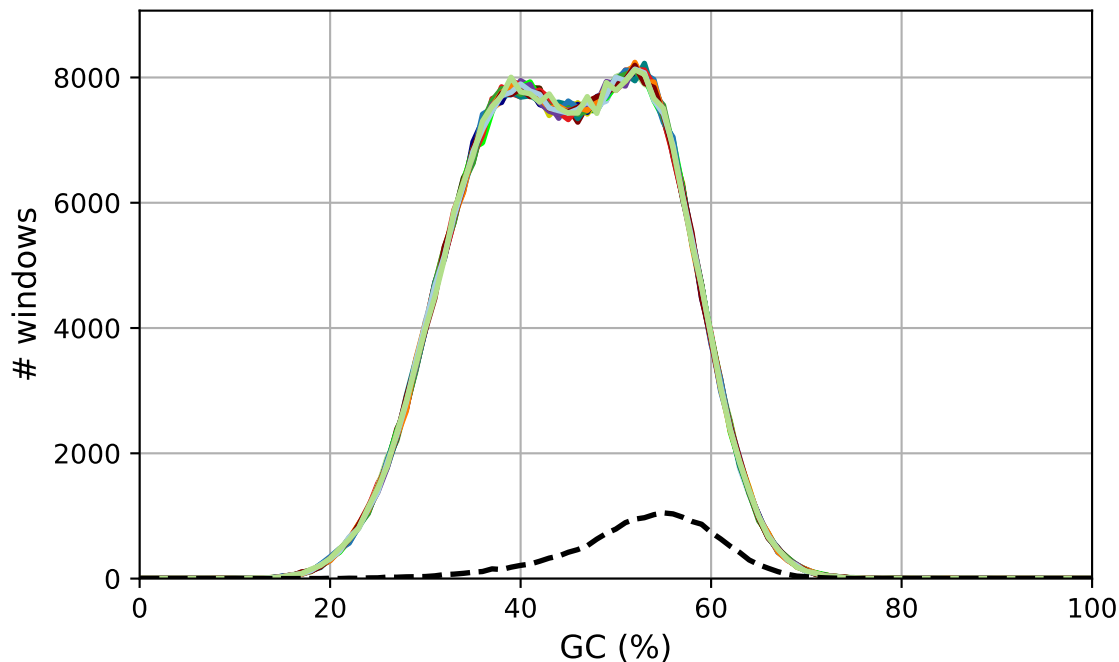


Cumulative length



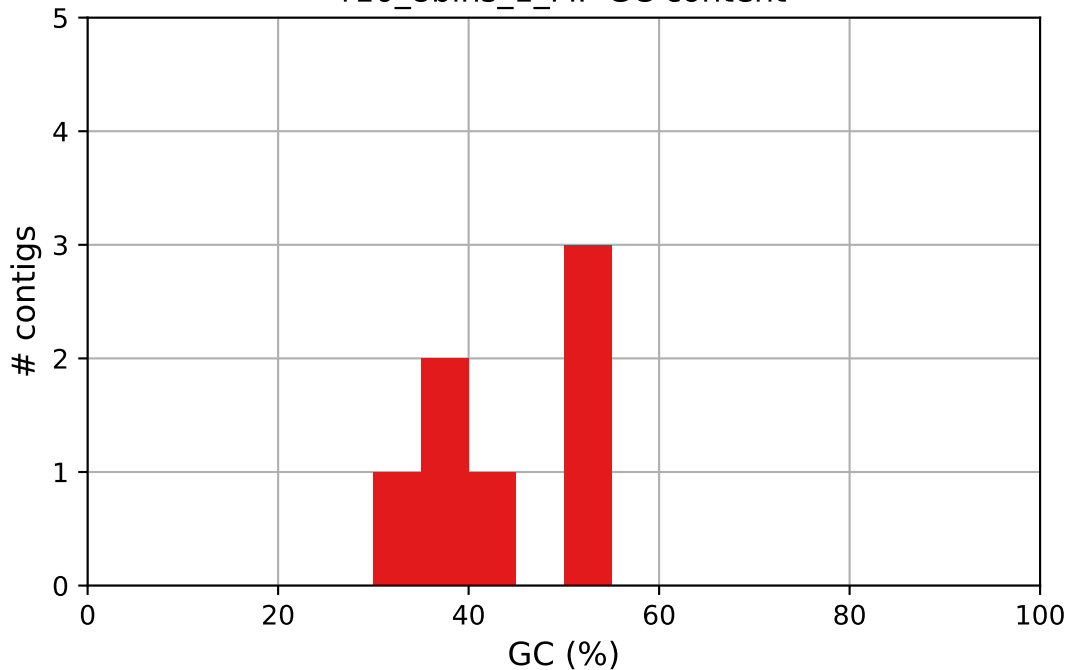
— r10_8bins_1_MP
— r10_8bins_1_MP_helen
— r10_8bins_1_r1_medaka
— r10_8bins_1_r2_medaka
— r10_8bins_2_MP_helen
— r10_8bins_2_r1_medaka
— r10_8bins_2_r2_medaka
— r10_8bins_2_racon_r1
— r10_8bins_3_MP_helen
— r10_8bins_3_r1_medaka
— r10_8bins_3_r2_medaka
— r10_8bins_3_racon_r1

GC content



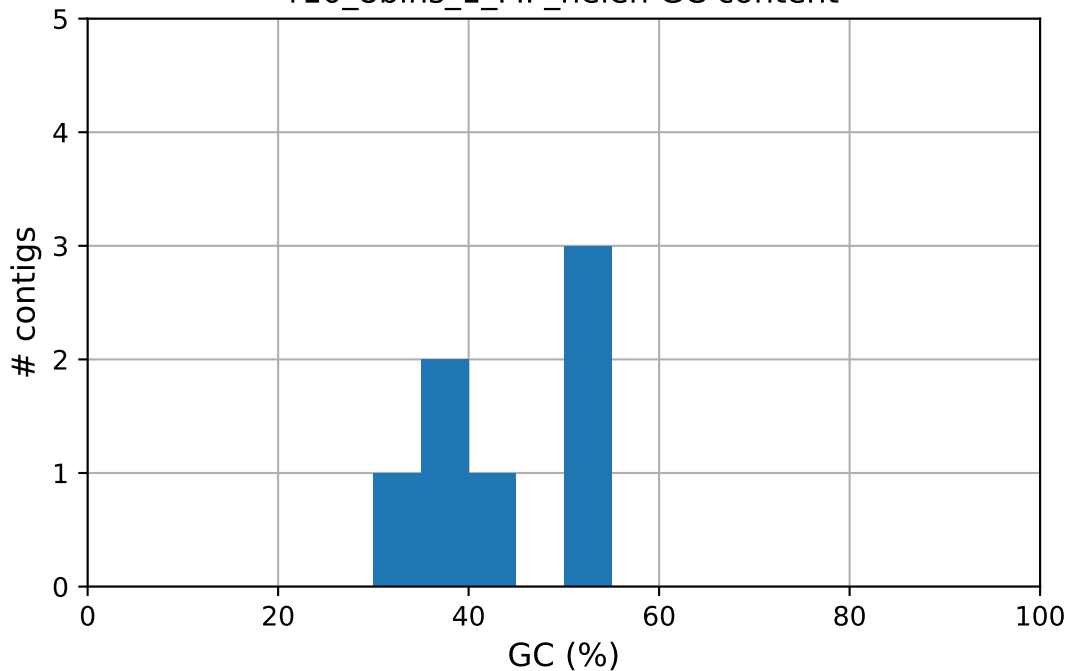
— r10_8bins_1_MP — r10_8bins_2_MP_helen — r10_8bins_3_MP_helen
— r10_8bins_1_MP_helen — r10_8bins_2_r1_medaka — r10_8bins_3_r1_medaka
— r10_8bins_1_r1_medaka — r10_8bins_2_r2_medaka — r10_8bins_3_r2_medaka
— r10_8bins_1_r2_medaka — r10_8bins_2_racon_r1 — r10_8bins_3_racon_r1

r10_8bins_1_MP GC content



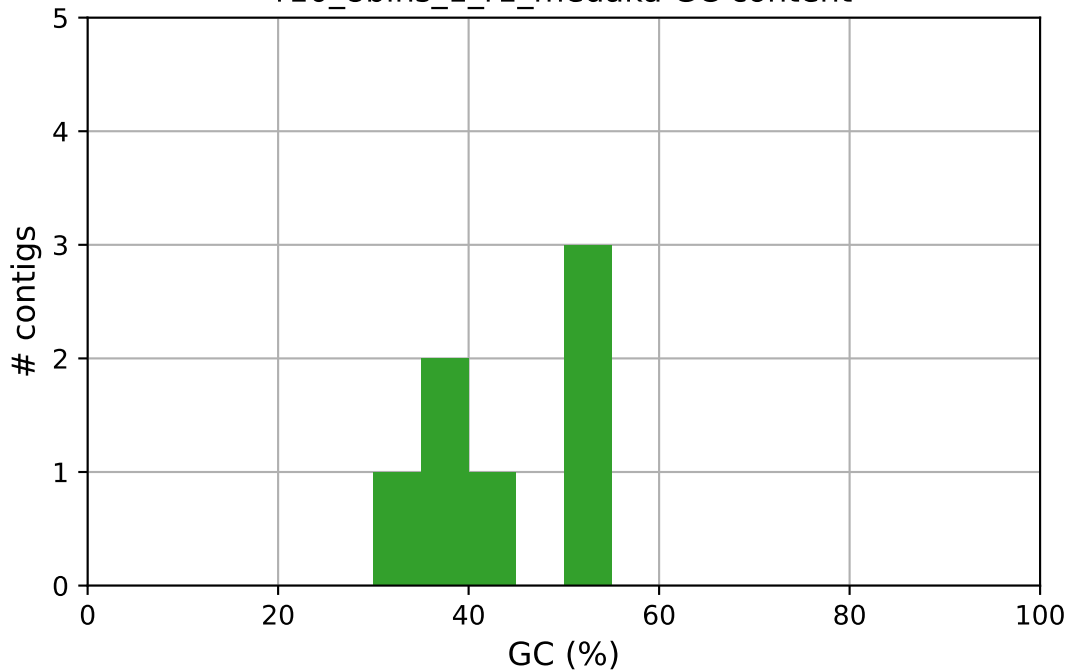
r10_8bins_1_MP

r10_8bins_1_MP_helen GC content



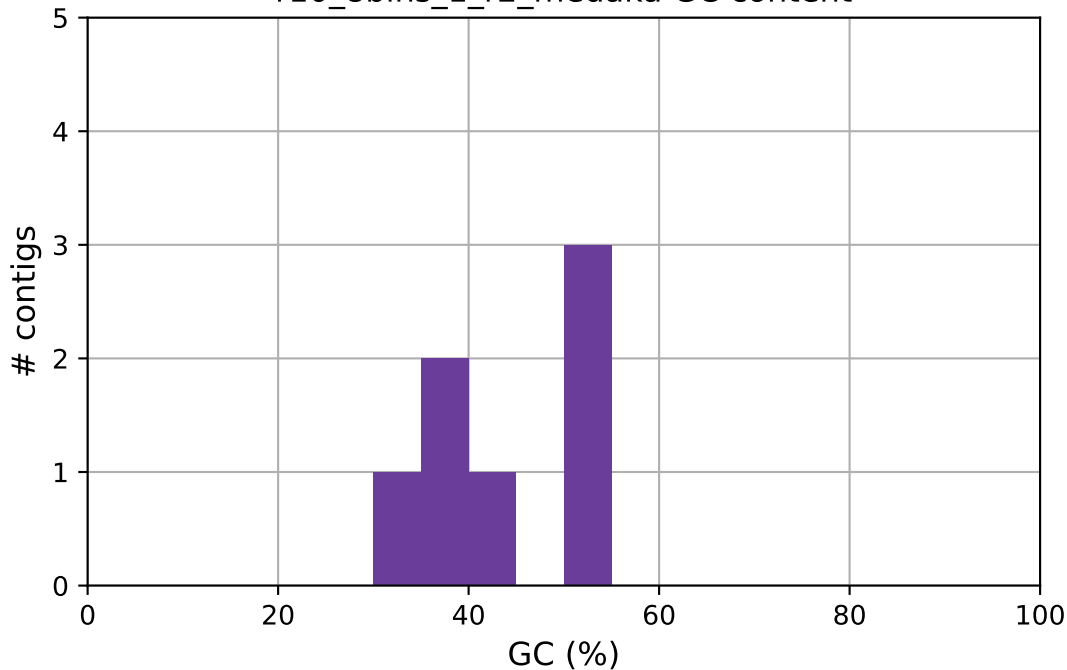
r10_8bins_1_MP_helen

r10_8bins_1_r1_medaka GC content



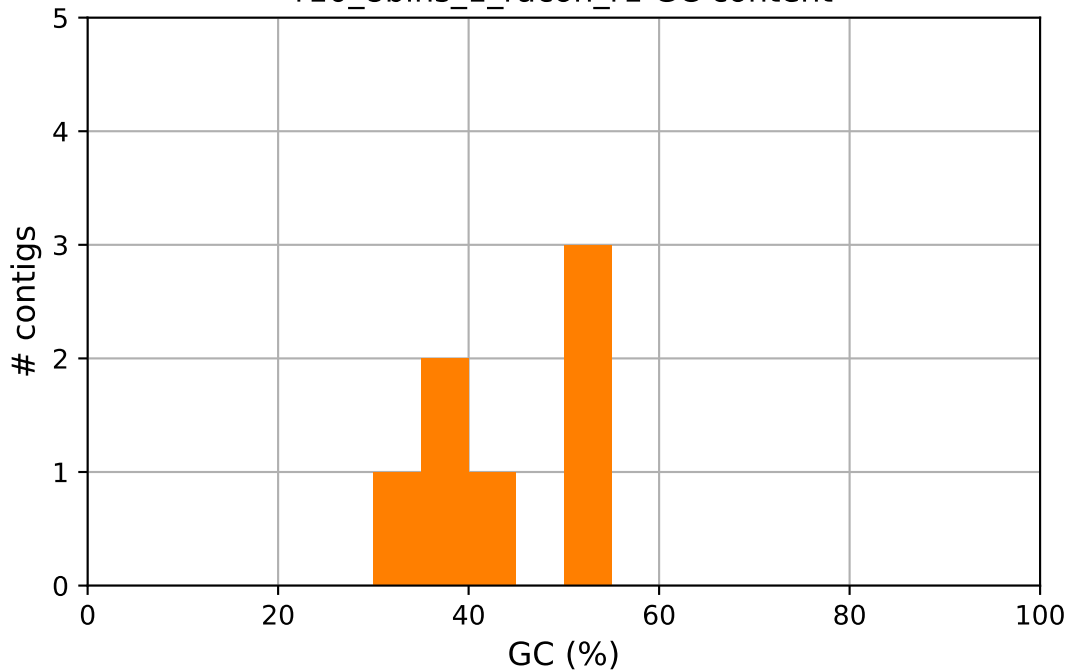
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r10_8bins_1_r2_medaka GC content



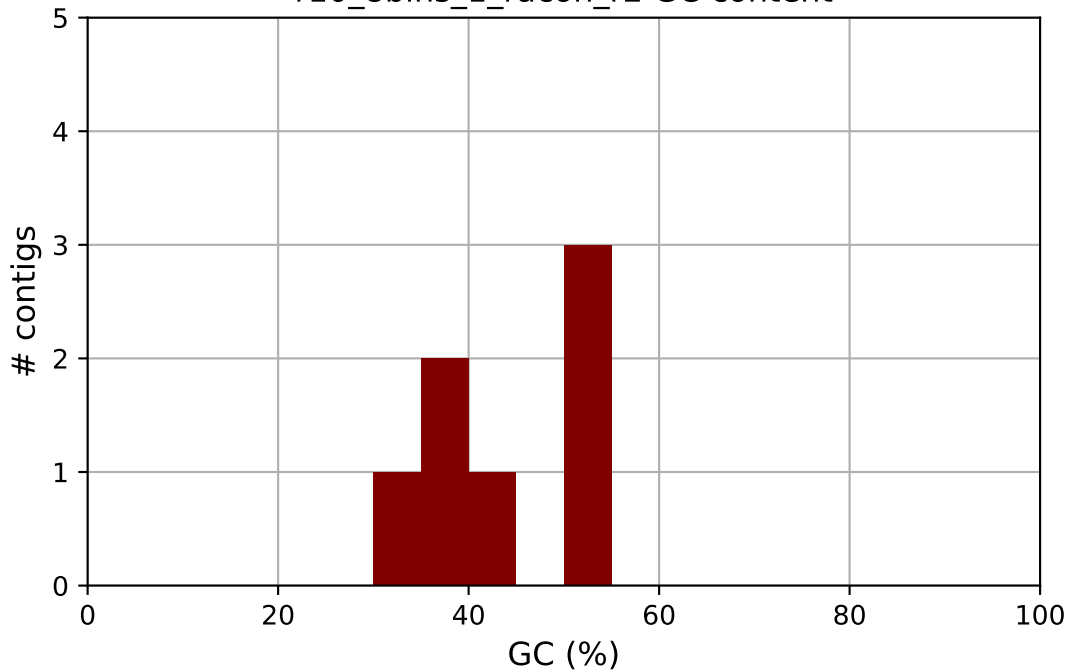
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r10_8bins_1_racon_r1 GC content



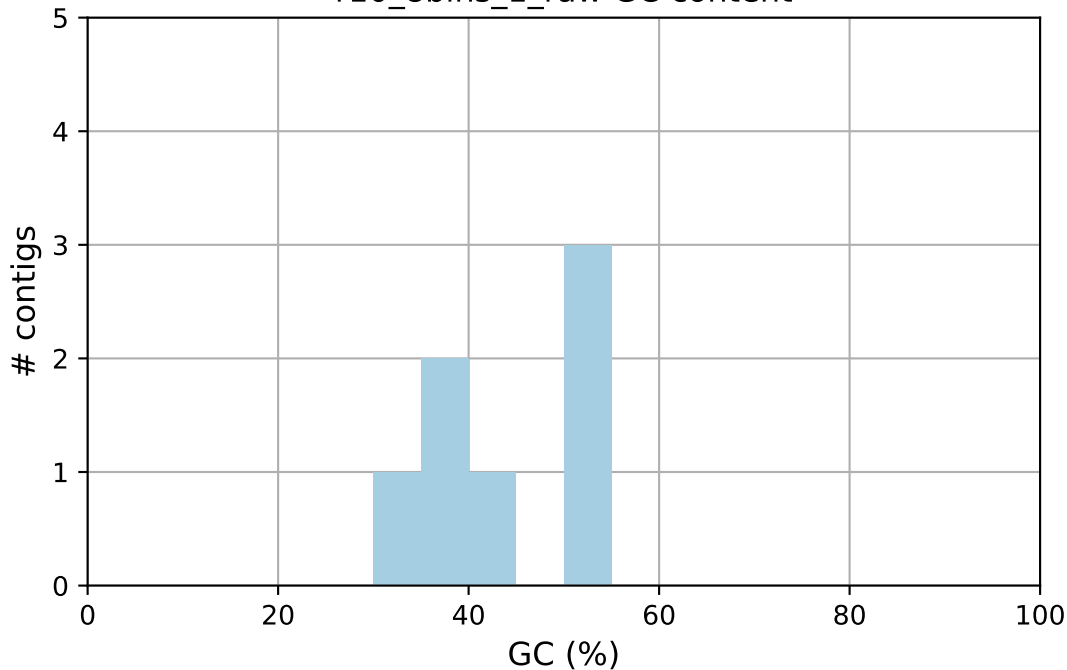
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r10_8bins_1_racon_r2 GC content



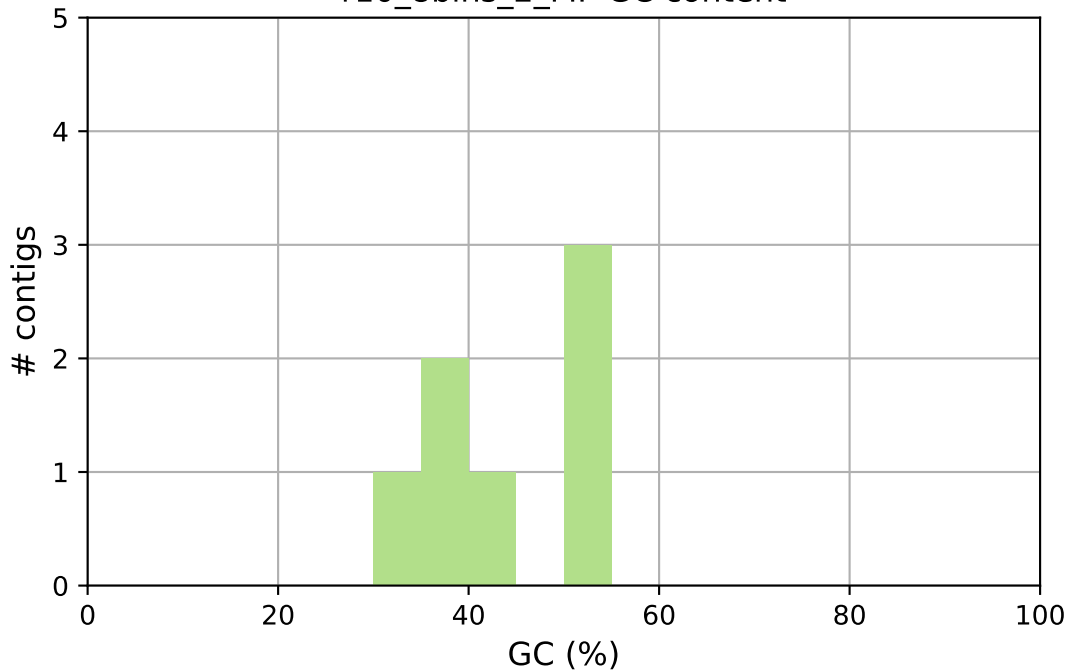
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r10_8bins_1_raw GC content



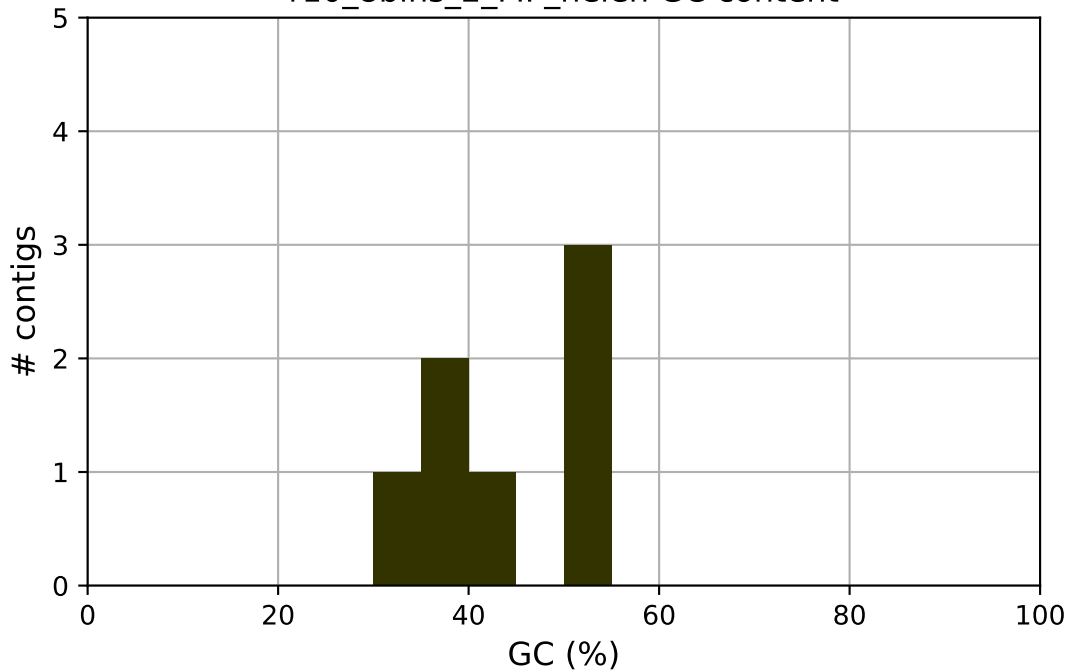
r10_8bins_1_raw

r10_8bins_2_MP GC content



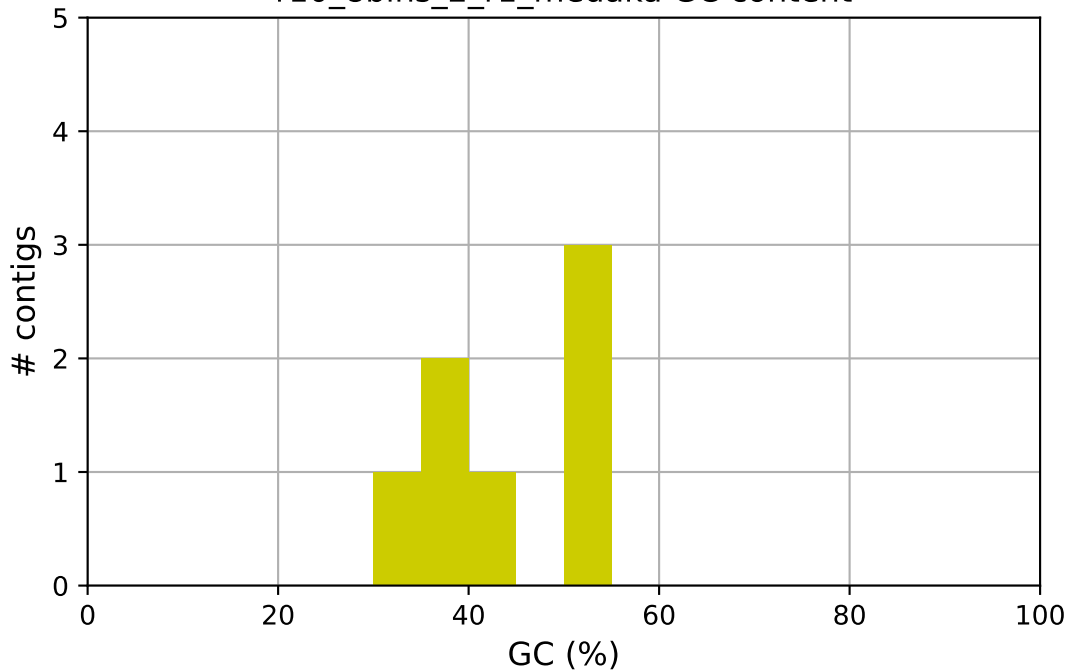
r10_8bins_2_MP

r10_8bins_2_MP_helen GC content



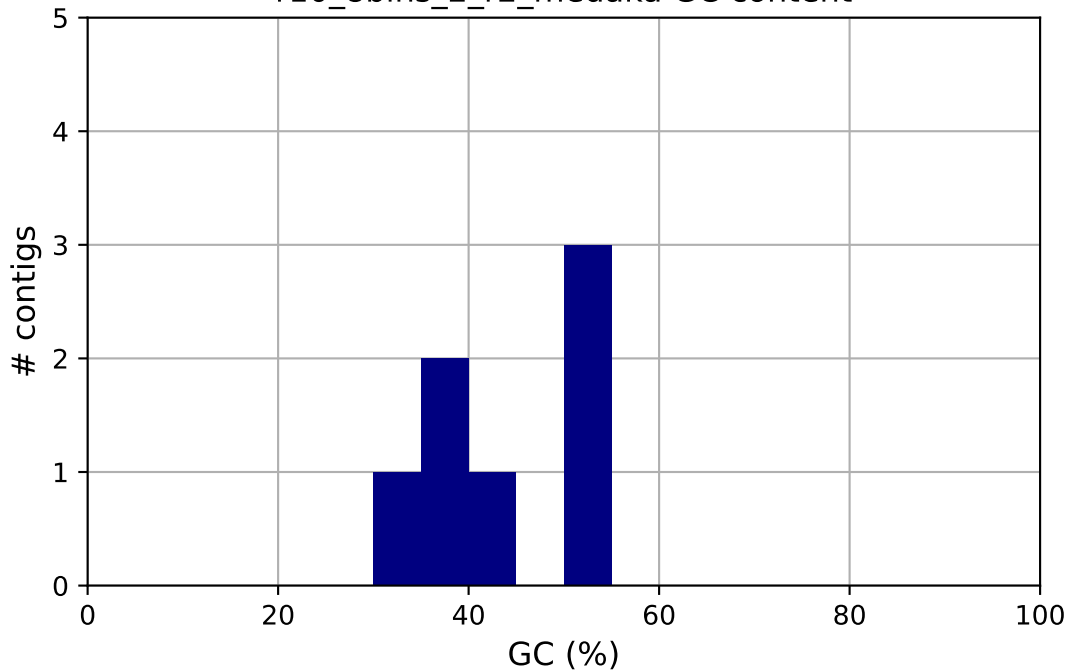
r10_8bins_2_MP_helen

r10_8bins_2_r1_medaka GC content



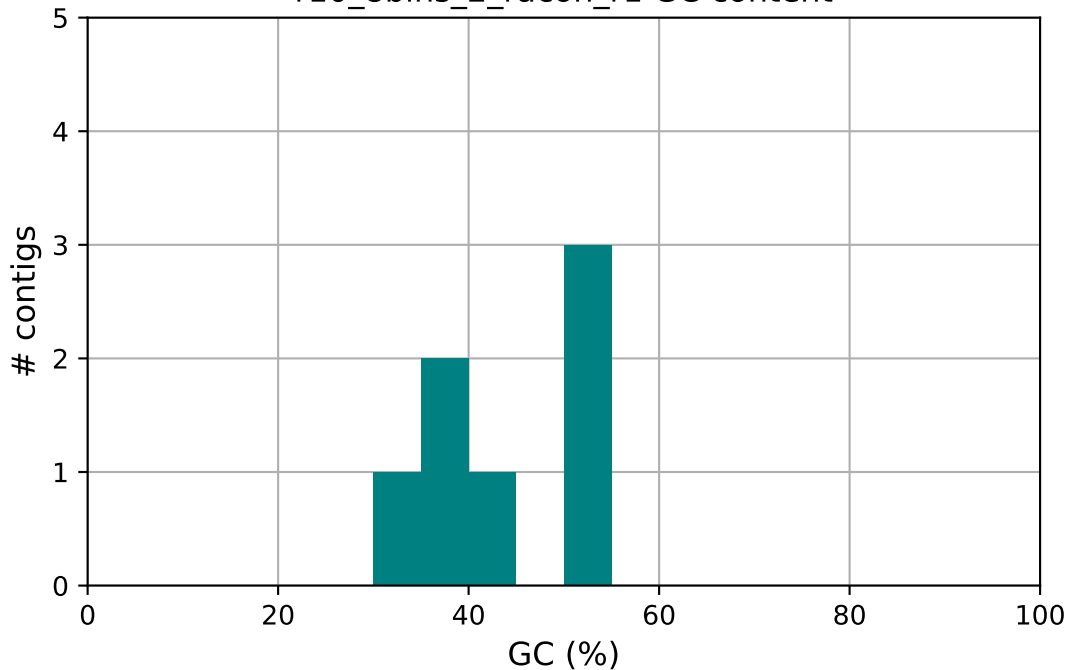
r10_8bins_2_r1_medaka

r10_8bins_2_r2_medaka GC content



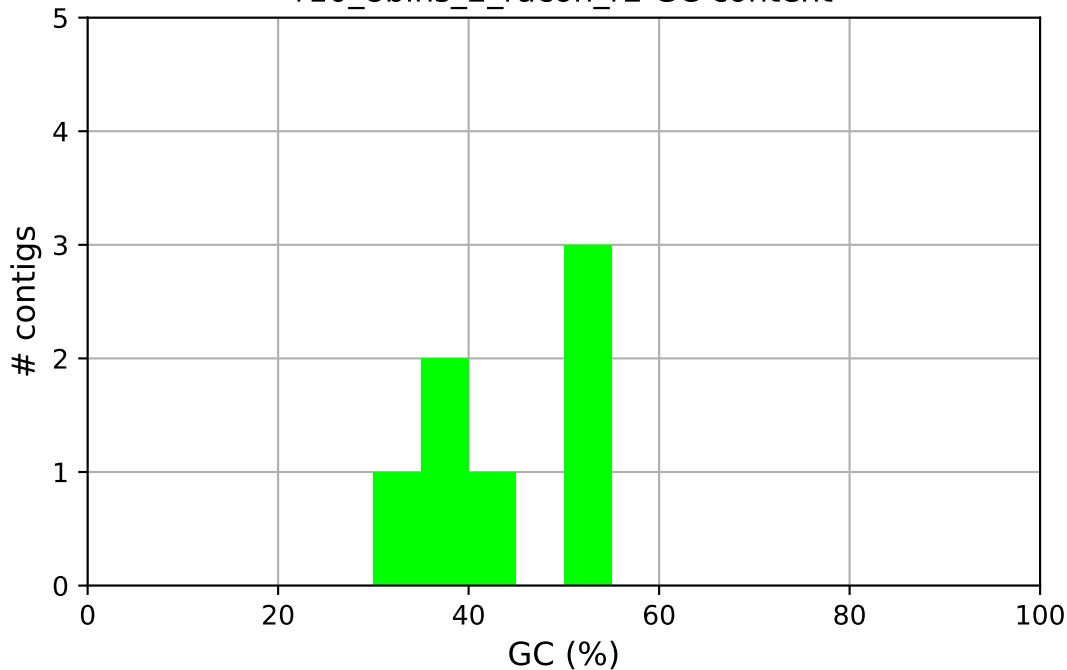
r10_8bins_2_r2_medaka

r10_8bins_2_racon_r1 GC content



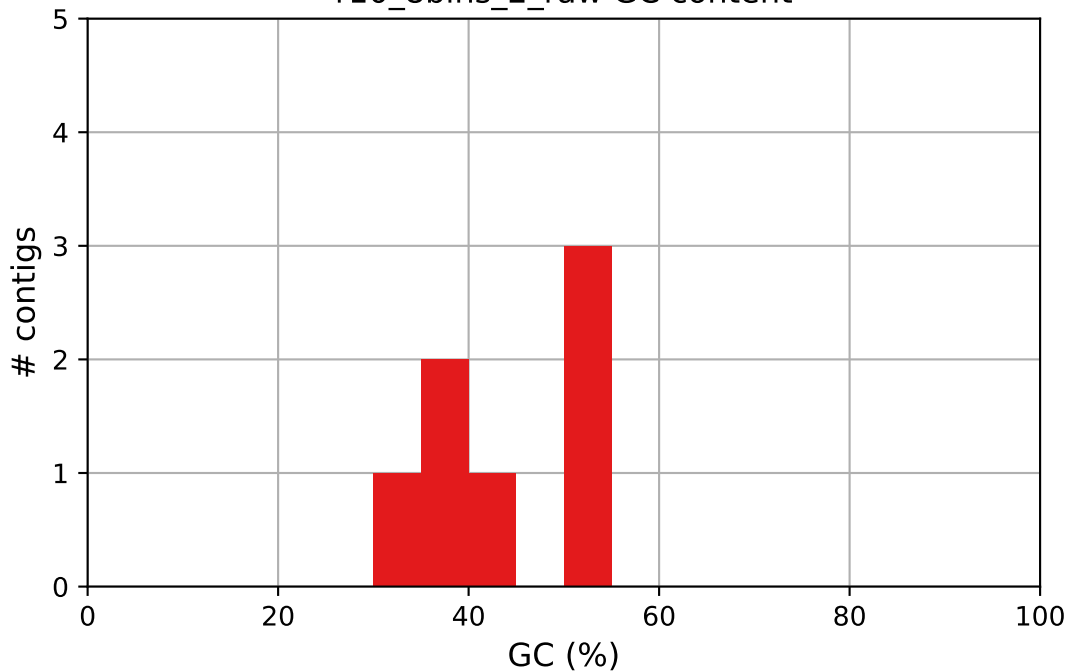
r10_8bins_2_racon_r1

r10_8bins_2_racon_r2 GC content



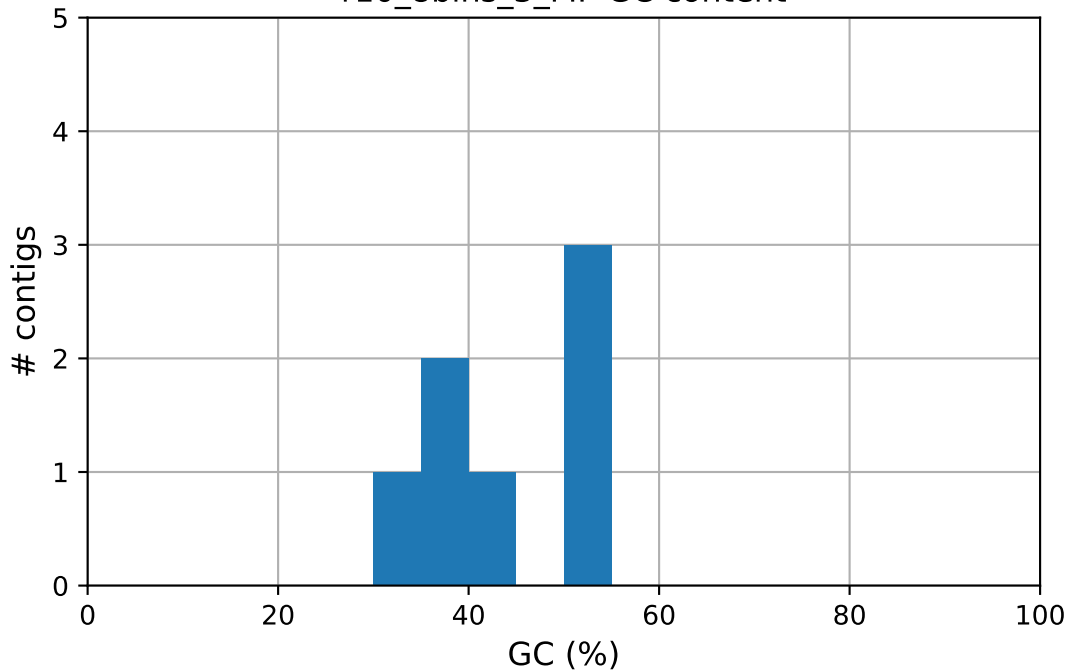
r10_8bins_2_racon_r2

r10_8bins_2_raw GC content



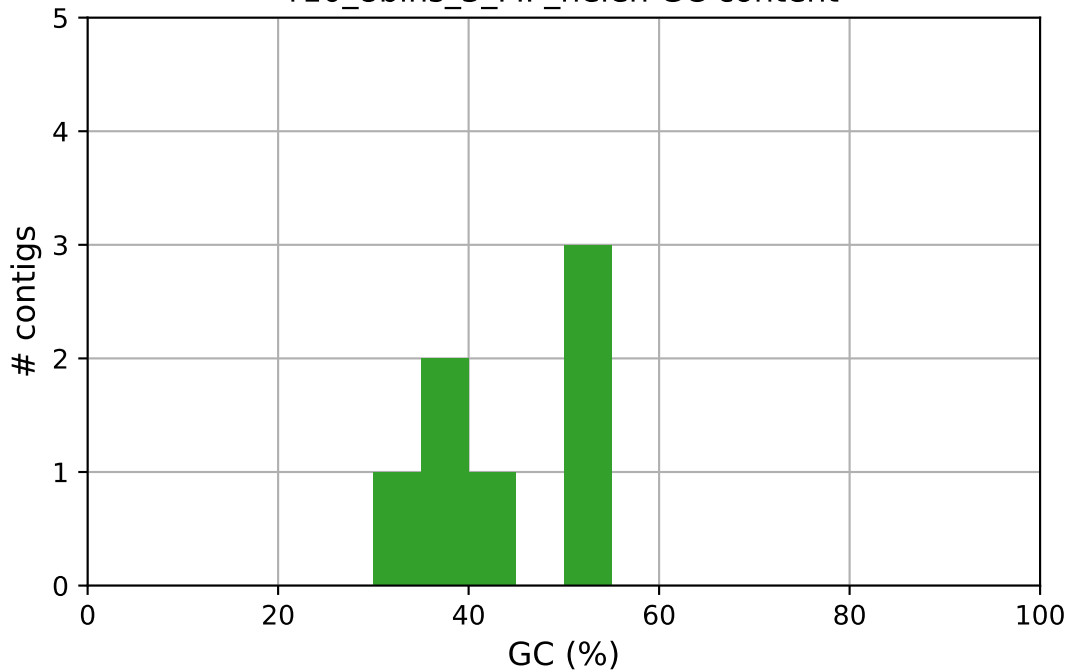
r10_8bins_2_raw

r10_8bins_3_MP GC content



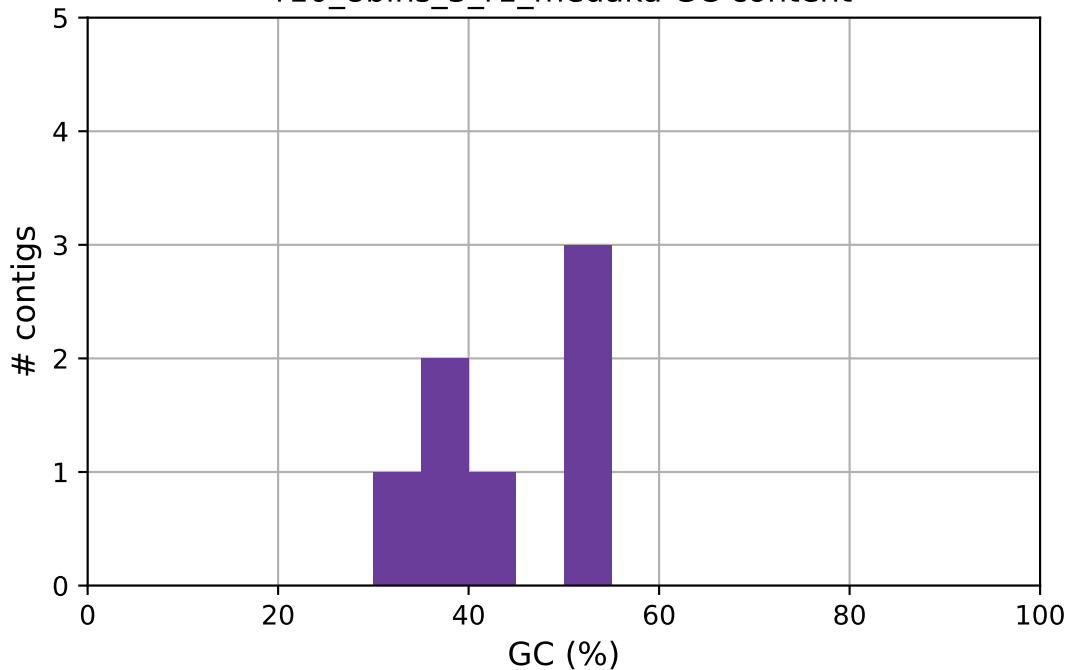
r10_8bins_3_MP

r10_8bins_3_MP_helen GC content



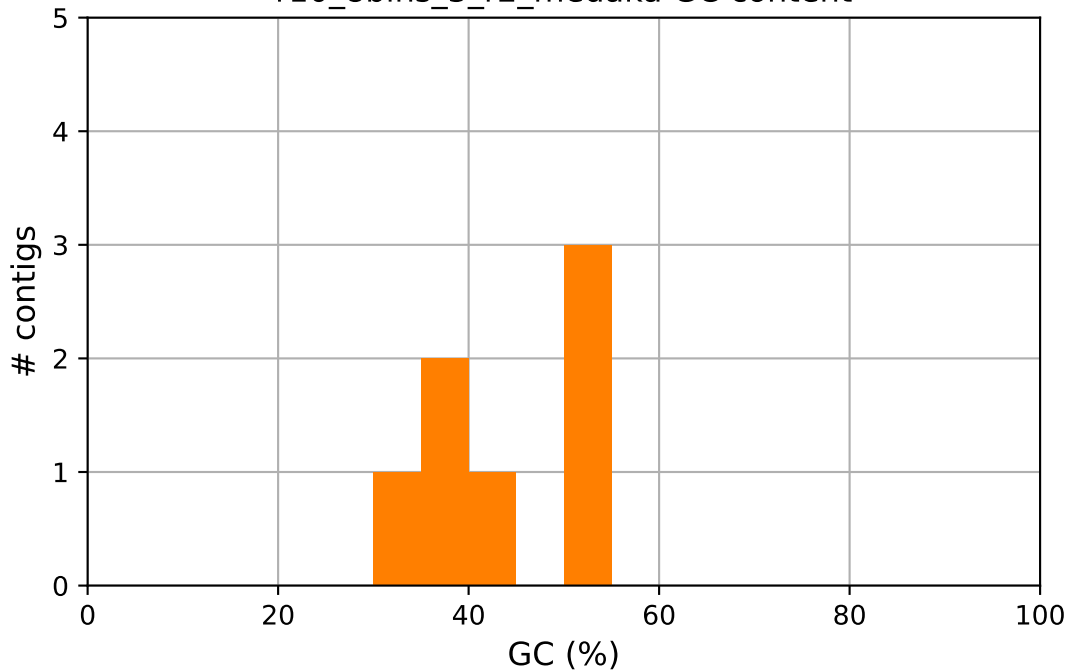
r10_8bins_3_MP_helen

r10_8bins_3_r1_medaka GC content



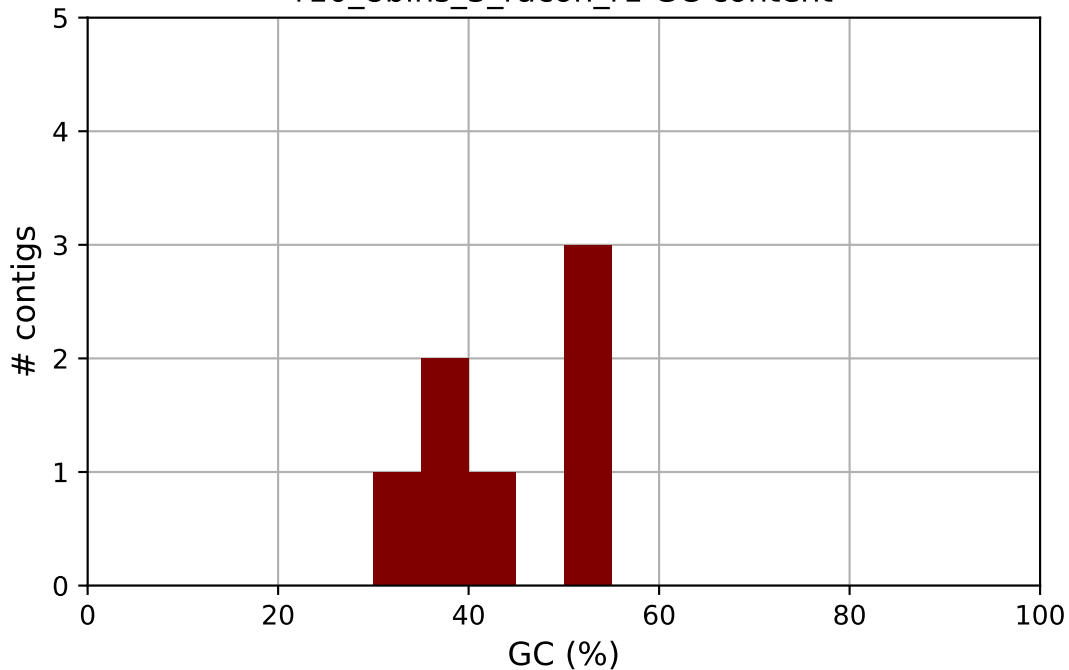
r10_8bins_3_r1_medaka

r10_8bins_3_r2_medaka GC content



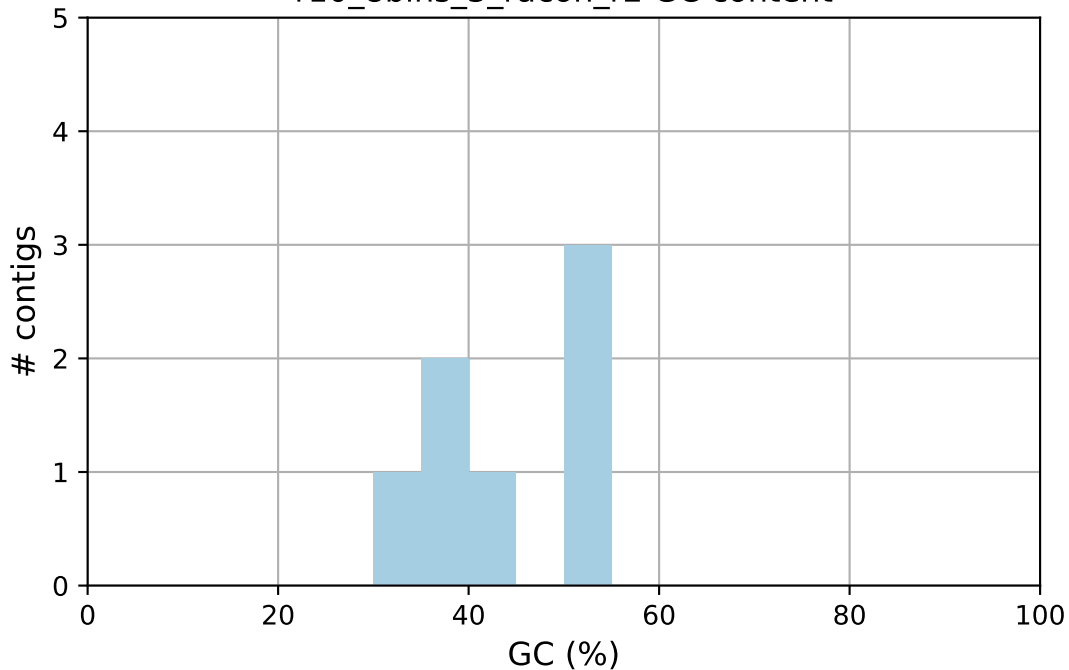
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r10_8bins_3_racon_r1 GC content



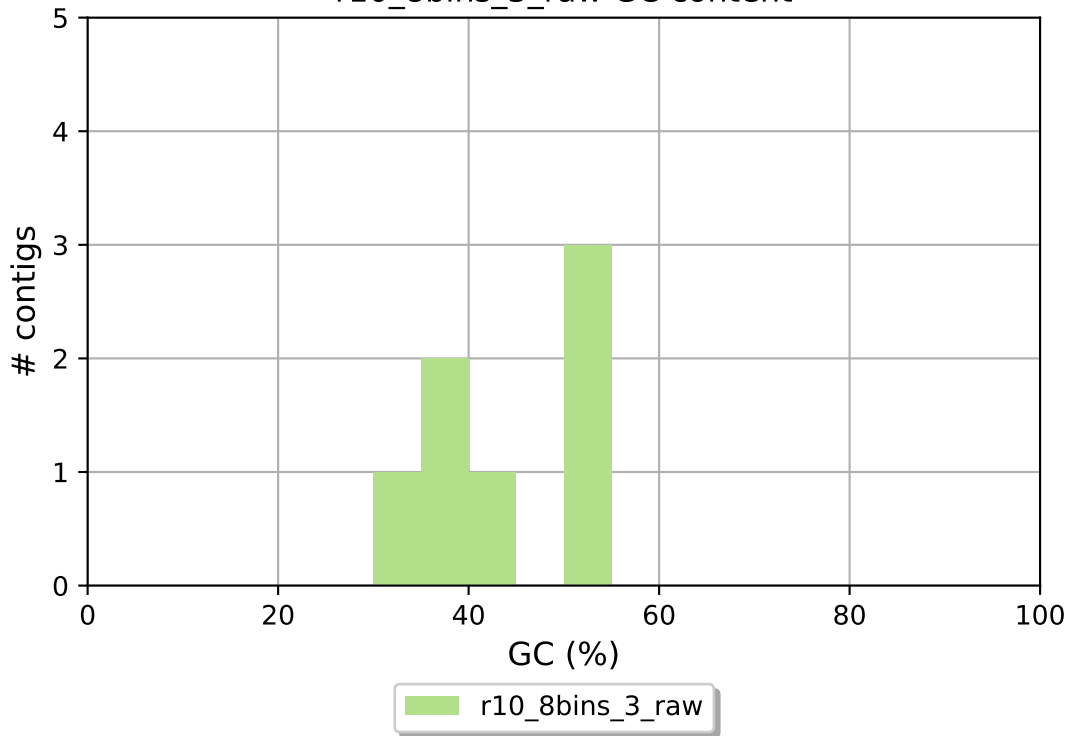
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r10_8bins_3_racon_r2 GC content

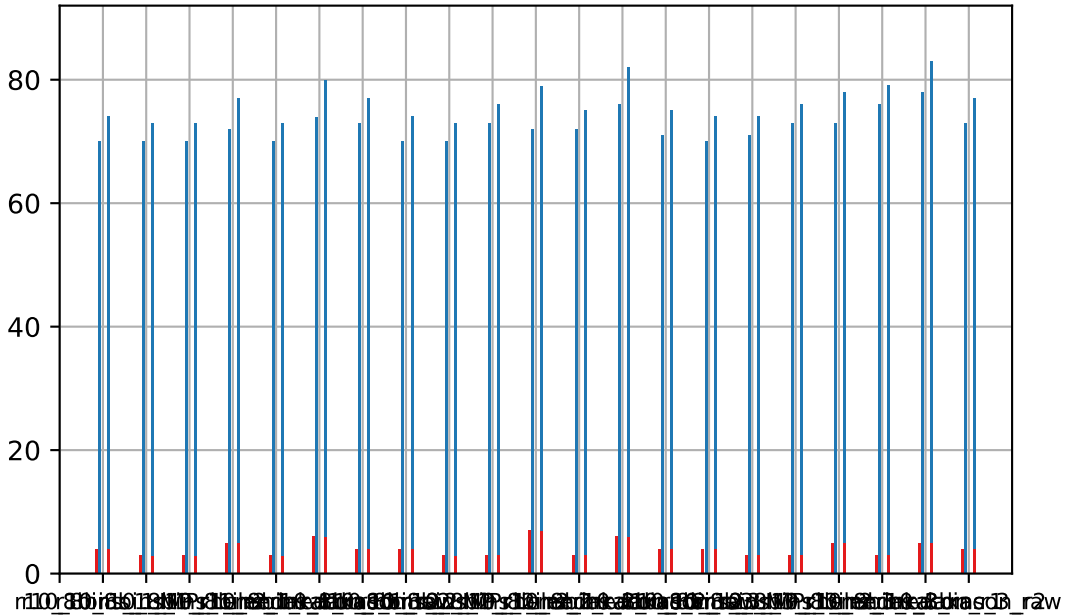


r10_8bins_3_racon_r2

r10_8bins_3_raw GC content



Misassemblies

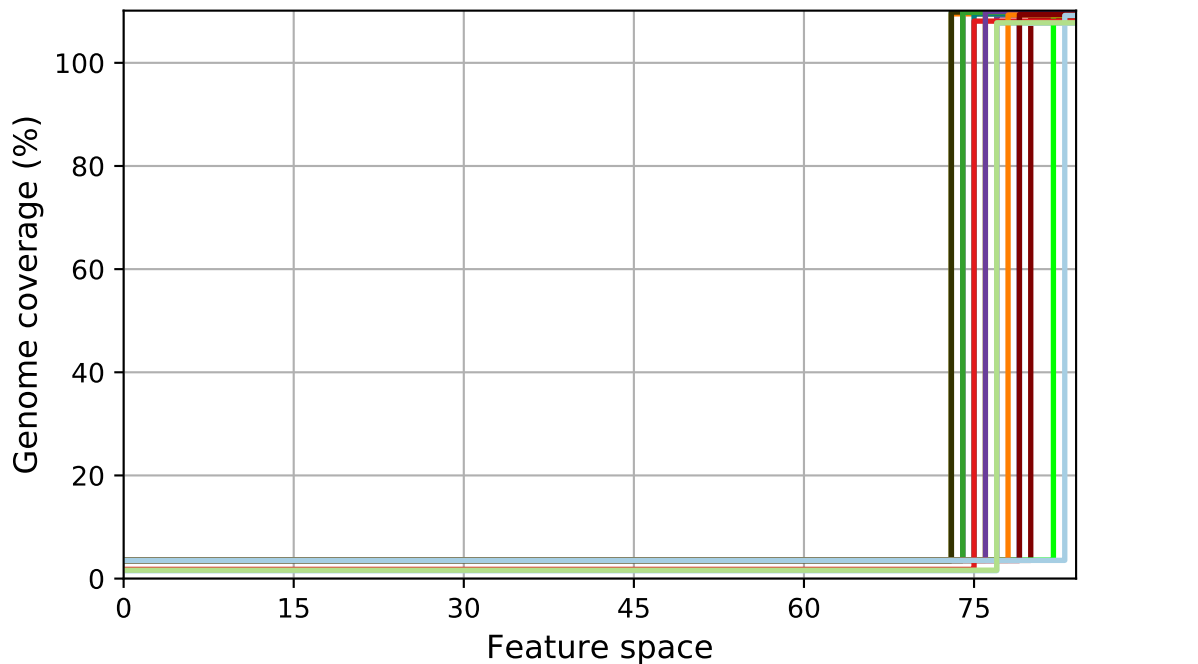


114

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# relocations
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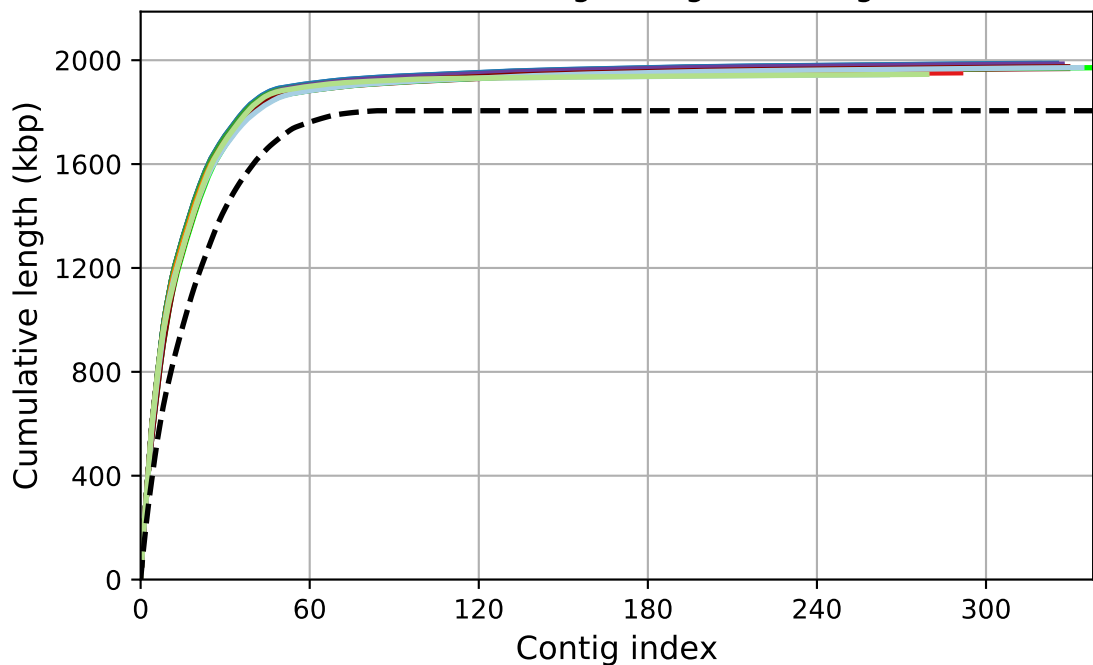

translocations

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)



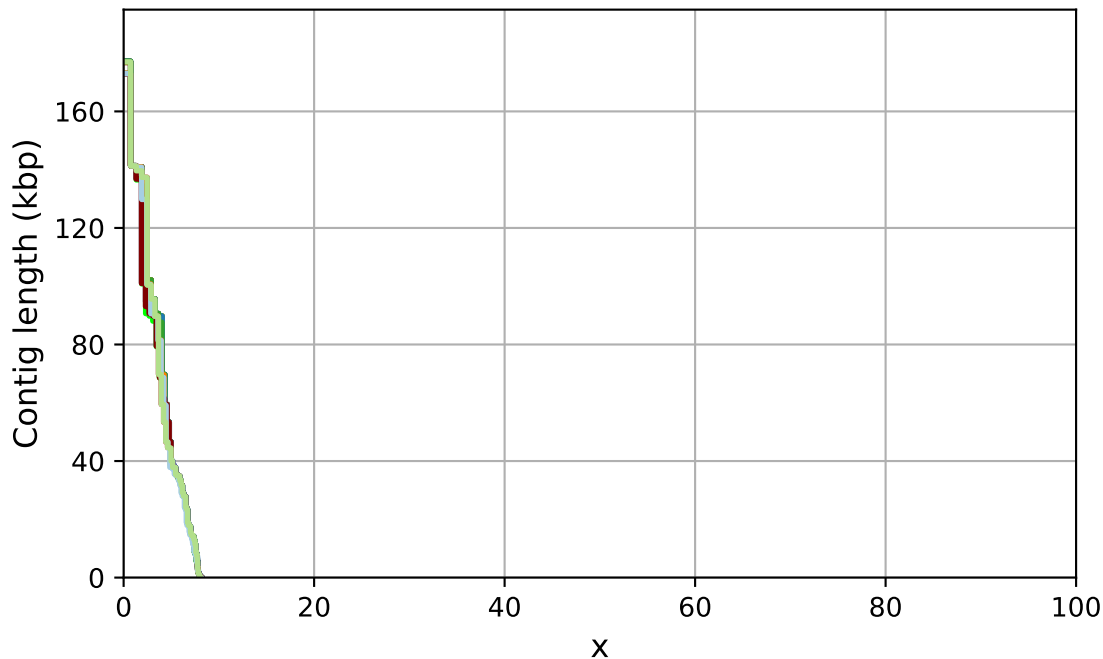
— r10_8bins_1_MP
 — r10_8bins_2_MP_helen
 — r10_8bins_3_MP_helen

— 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

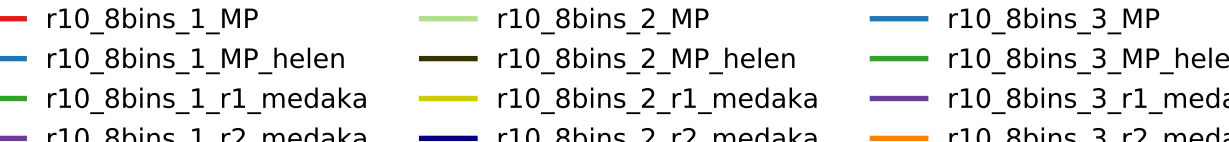
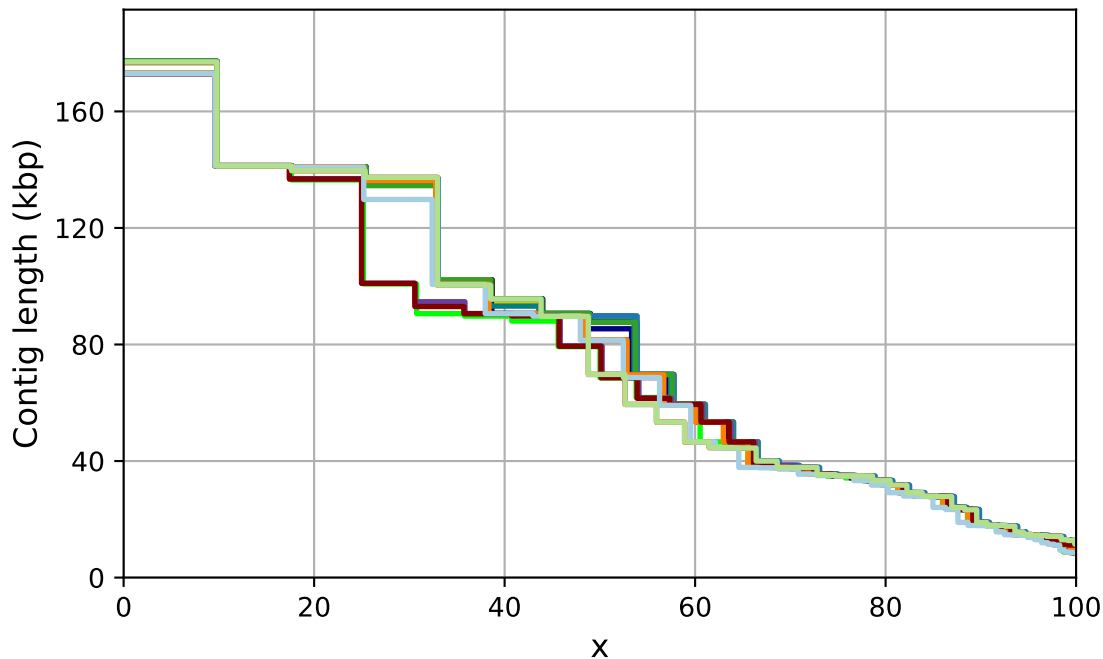
— r10_8bins_1_r2_medaka
 — r10_8bins_2_racon_r1
 — r10_8bins_3_racon_r1

NAX



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

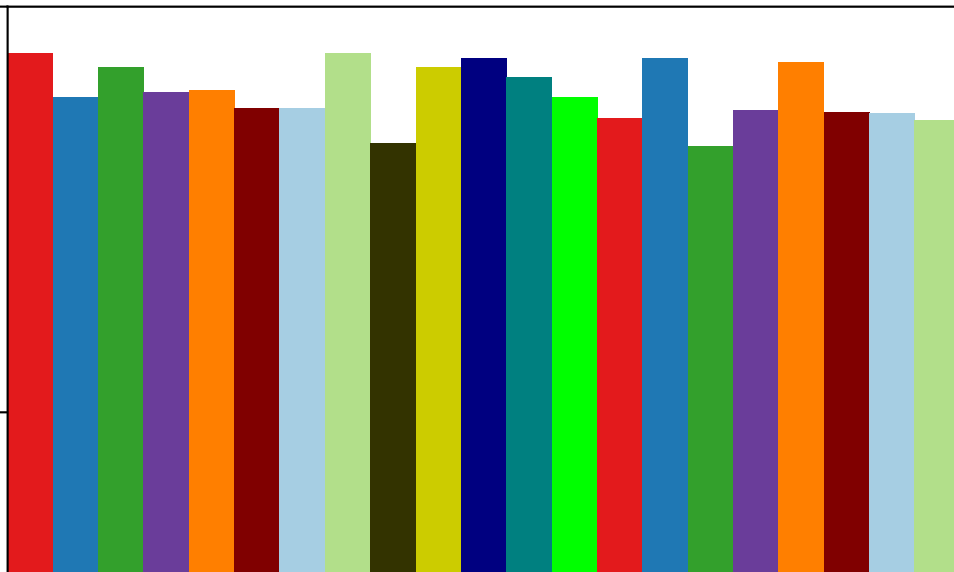
NGAx



Genome fraction, %

100.0

99.5



■ 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