

Report

	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# contigs (>= 5000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 10000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 25000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 50000 bp)	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total length (>= 5000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 10000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 25000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Total length (>= 50000 bp)	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
# contigs	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
Total length	30866559	30861633	30864249	30853622	30851421	30845671	28005820	30866756	30862760	30864301	30855523	30851886	30847576	30849158	30866651	30863115	30864187	30847828	30851884	30843598	30848199
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.50	49.51	49.50	49.50	49.49	49.50	50.69	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21
N50	4758939	4757800	4758594	4758071	4757983	4757672	4756051	4758953	4757846	4758592	4758065	4757922	4757649	4756088	4758954	4757856	4758593	4758140	4757950	4757852	4756101
NG50	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
N75	2992083	2992068	2992071	2992068	2991898	2991964	2990667	2992084	2992066	2992071	2992072	2991914	2991953	2990633	2992084	2992066	2992071	2992073	2991916	2991960	2990633
NG75	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
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	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# 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	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	11	29	11	11	11	11	11	11	29
# 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	7	7	7	7	7	7	6	7	7	7	7	7	7	6	7	7	7	7	7	7	7
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 7 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24046874	24042487	24044291	24033589	24032131	24026773	21233862	24047726	24043803	24044012	24035756	24032504	24029144	24078261	24047588	24044048	24044416	24028070	24033065	24024838	24076495
Genome fraction (%)	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.894	99.894	99.894	99.894	99.894	99.894	99.864	99.894	99.894	99.894	99.894	99.894	99.894	99.864
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008
# N's per 100 kbp	0.00	0.03	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	58.73	56.18	56.60	56.66	59.56	58.80	64.65	58.40	56.18	57.18	56.51	59.43	58.33	64.73	58.41	56.24	56.56	56.51	58.71	58.89	65.49
# indels per 100 kbp	5.42	5.06	3.60	3.59	14.58	13.45	97.24	5.49	5.15	3.62	3.60	14.27	13.50	96.80	5.48	5.15	3.63	3.62	14.30	13.53	96.71
Largest alignment	1643838	2052185	2052212	2052213	2052073	2052095	2098630	1643840	1643830	1643848	1643848	1643640	1643676	2098268	1643840	1643830	1643848	1643848	1643640	1643676	2098268
Total aligned length	6815933	6815384	6816206	6816281	6815538	6815146	6769483	6815278	6815205	6816537	6816015	6815630	6814680	6768411	6815311	6815315	6816019	6816006	6815067	6815008	6769218
NGA50	1274461	1643838	1643848	1643851	1643660	1471418	1274461	1274471	1274461	1274469	1274471	1274322	1274362	1274471	1274461	1274461	1274469	1274461	1274322	1274362	1471391
NGA75	1070337	1070326	1070328	1070333	1070244	1070262	610213	1070338	1070325	1070332	1070330	1070257	1070255	610115	1070338	1070325	1070332	1070330	1070257	1070255	610115
LGA50	3	2	2	2	2	2	2	3	3	3	3	3	3	2	3	3	3	3	3	3	2
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4

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

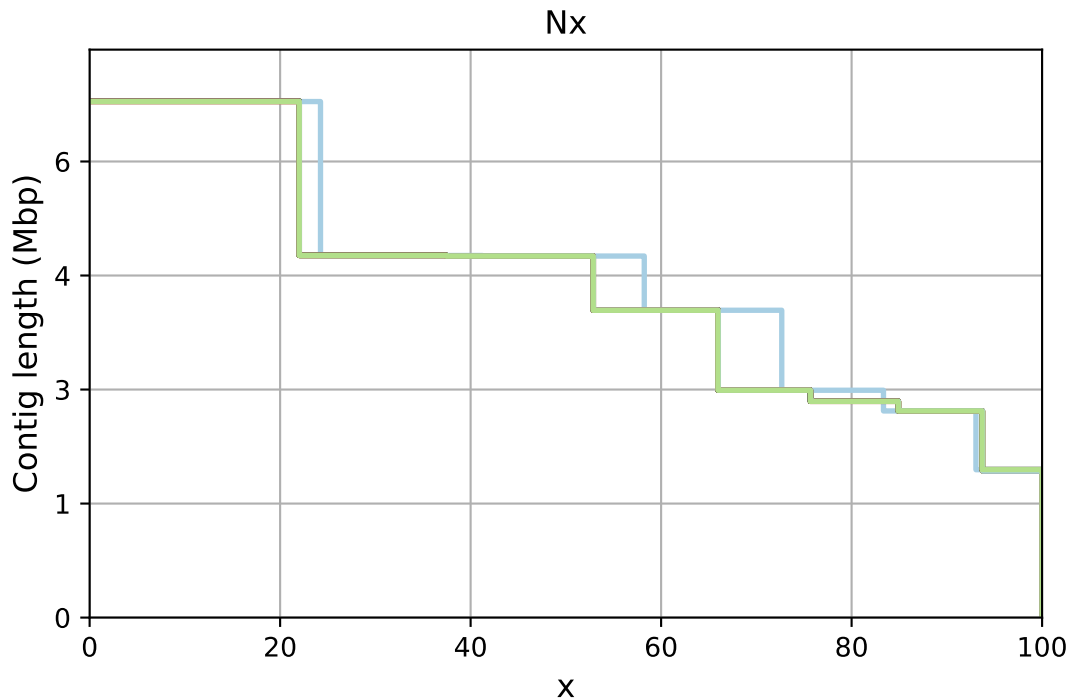
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_v2_3_raw
# misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# contig misassemblies	8	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# c. relocations	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	7	6	6	6	6	6	10	6	6	6	6	6	6	10	6	6	6	6	6	6	10
# 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	6792242	6792185	6792244	6792252	6791600	6791732	6788581	6792252	6792198	6792245	6792243	6791577	6791686	6787718	6792252	6792198	6792245	6792243	6791577	6791686	6787718
# 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	16	18	18	18	18	18	34	18	18	18	18	18	18	34	18	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	25	11	11	11	11	11	11	29	11	11	11	11	11	11	29
# 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	20	21	21	21	21	21	16	21	21	21	21	21	21	16	21	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	6	7	7	7	7	7	7	6	7	7	7	7	7	7	7
# mismatches	3947	3776	3804	3808	4003	3952	4344	3925	3776	3843	3798	3994	3920	4349	3926	3780	3801	3798	3946	3958	4400
# indels	364	340	242	241	980	904	6534	369	346	243	242	959	907	6504	368	346	244	243	961	909	6498
# indels (<= 5 bp)	269	243	148	147	886	808	6411	273	248	149	148	864	812	6383	272	248	150	149	866	814	6377
# indels (> 5 bp)	95	97	94	94	94	96	123	96	98	94	94	95	95	121	96	98	94	94	95	95	121
Indels length	5394	5400	5259	5258	6103	6027	12929	5412	5412	5261	5258	6074	6021	12818	5411	5412	5262	5259	6076	6023	12810

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_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	r10_2bins_v2_3_MP	r10_2bins_v2_3_MP_helen	r10_2bins_v2_3_r1_medaka	r10_2bins_v2_3_r2_medaka	r10_2bins_v2_3_racon_r1	r10_2bins_v2_3_racon_r2	r10_2bins_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	8	8	8	8	8	8	7	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24046874	24042487	24044291	24033589	24032131	24026773	21233862	24047726	24043803	24044012	24035756	24032504	24029144	24078261	24047588	24044048	24044416	24028070	24033065	24024838	24076495
# 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).



0\_2bins\_v2\_1\_MP

r10\_2bins\_v2\_2\_MP

r10\_2bins\_v2\_3\_MP

0\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_3\_MP\_helen

0\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_2\_r1\_medaka

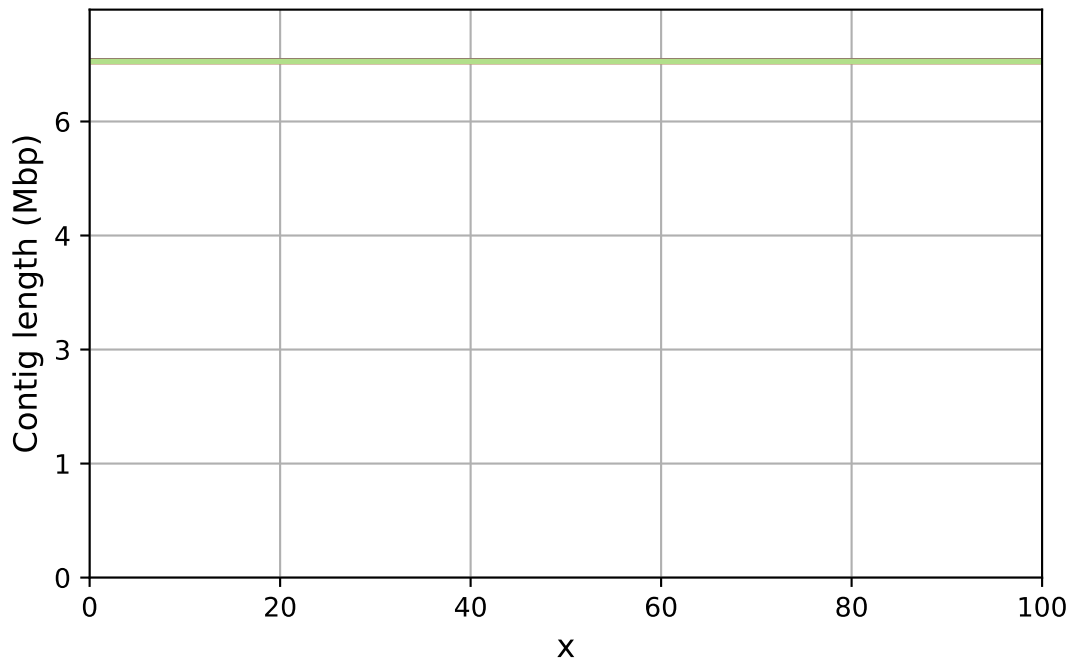
r10\_2bins\_v2\_3\_r1\_medaka

0\_2bins\_v2\_1\_r2\_medaka

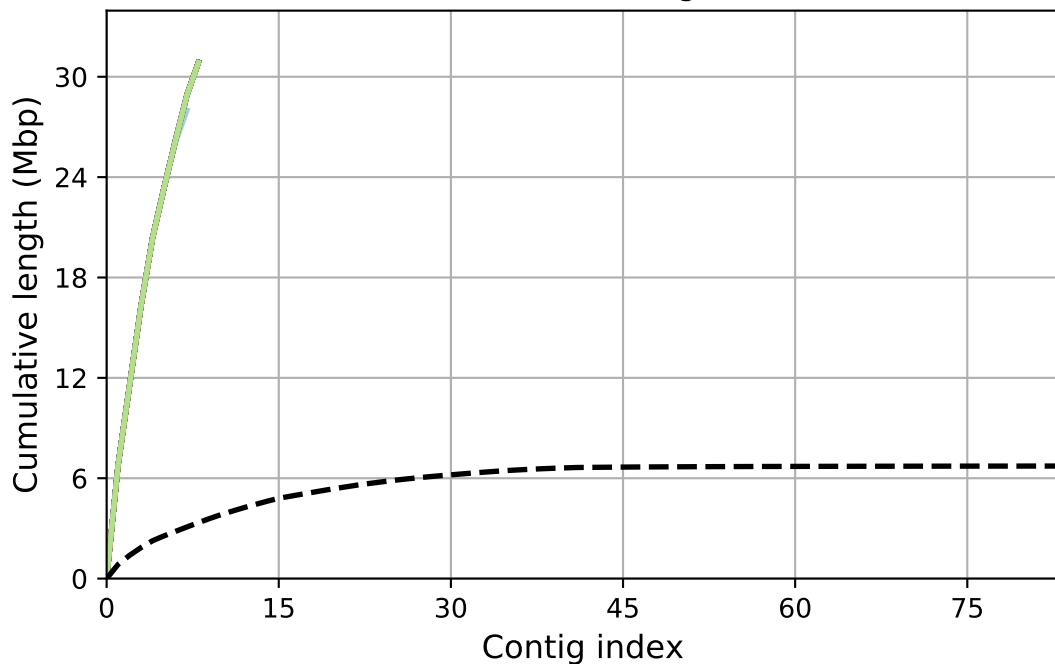
r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_r2\_medaka

# NGx



# Cumulative length



0\_2bins\_v2\_1\_MP

0\_2bins\_v2\_1\_MP\_helen

0\_2bins\_v2\_1\_r1\_medaka

0\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_2\_racon\_r1

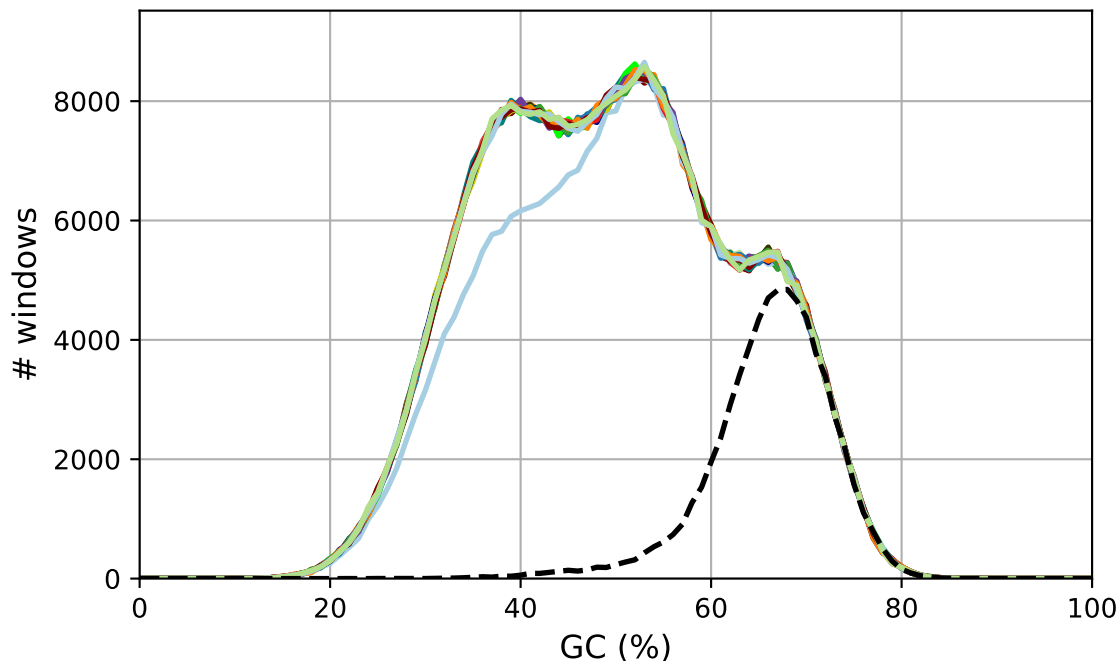
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_r1

r10\_2bins\_v2\_3\_r2

r10\_2bins\_v2\_3\_racon\_r1

GC content



r10\_2bins\_v2\_1\_MP

r10\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_2\_racon\_r1

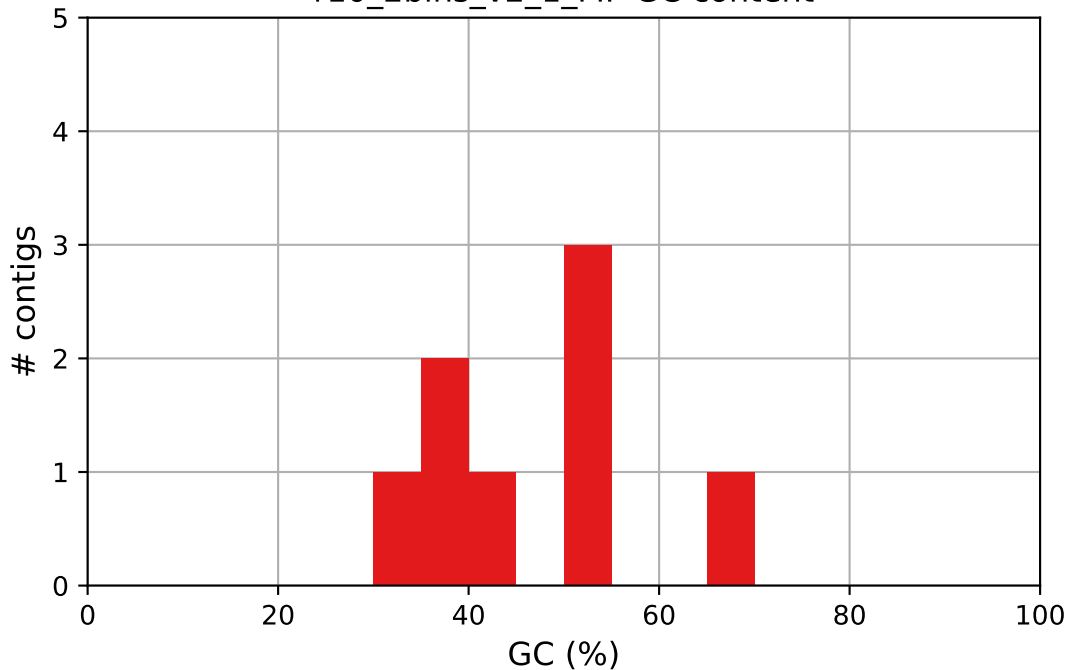
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_r1

r10\_2bins\_v2\_3\_r2

r10\_2bins\_v2\_3\_racon\_r1

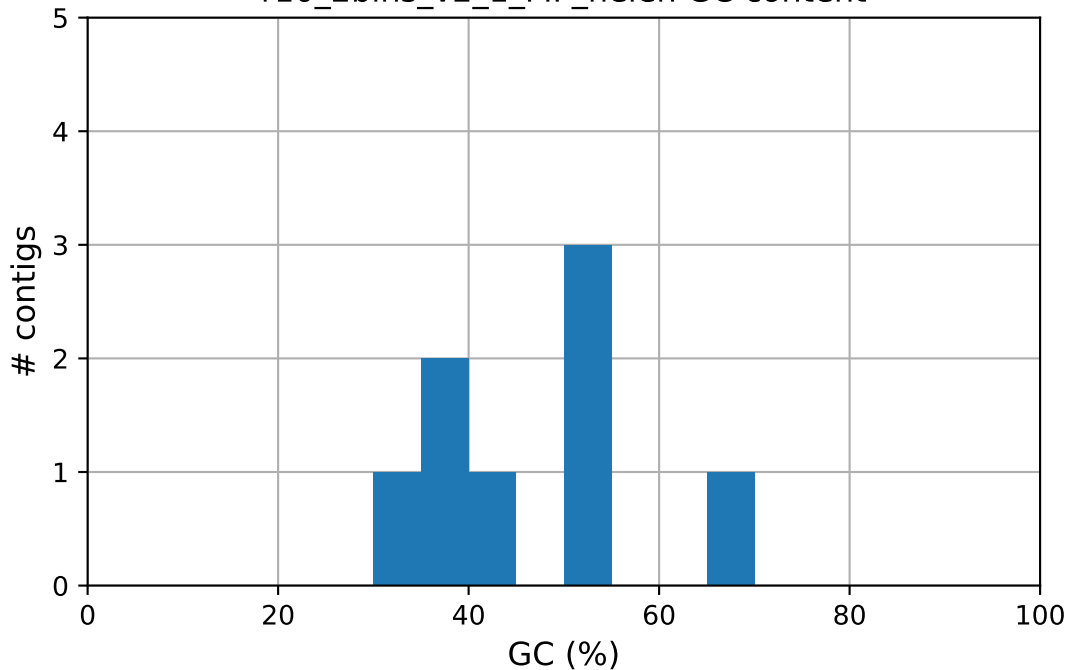
r10\_2bins\_v2\_1\_MP GC content



r10\_2bins\_v2\_1\_MP

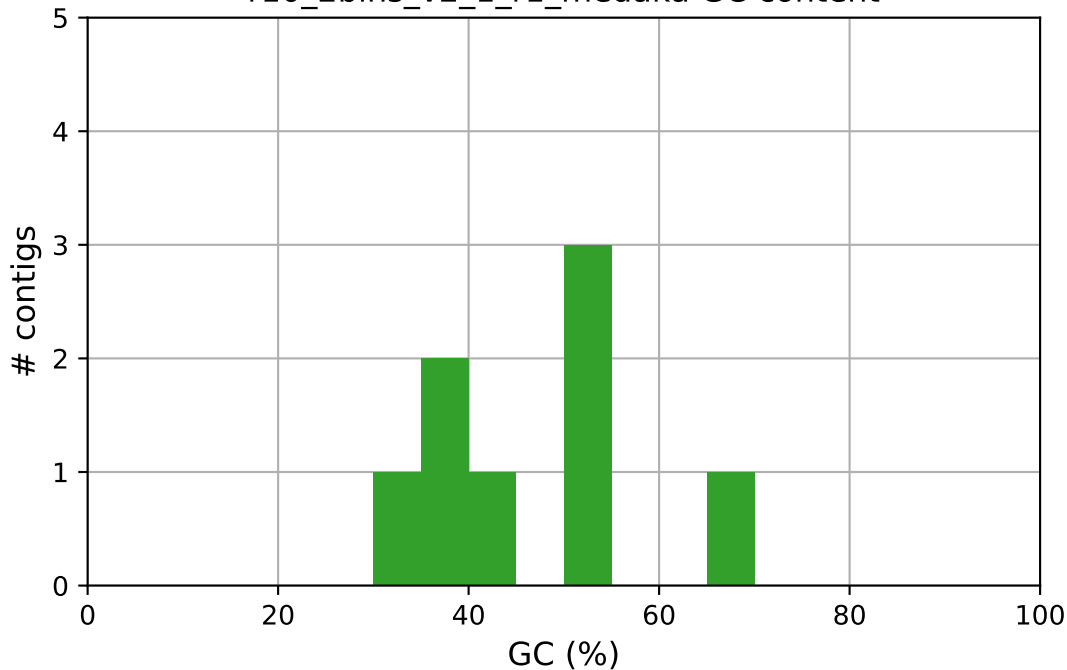


r10\_2bins\_v2\_1\_MP\_helen GC content



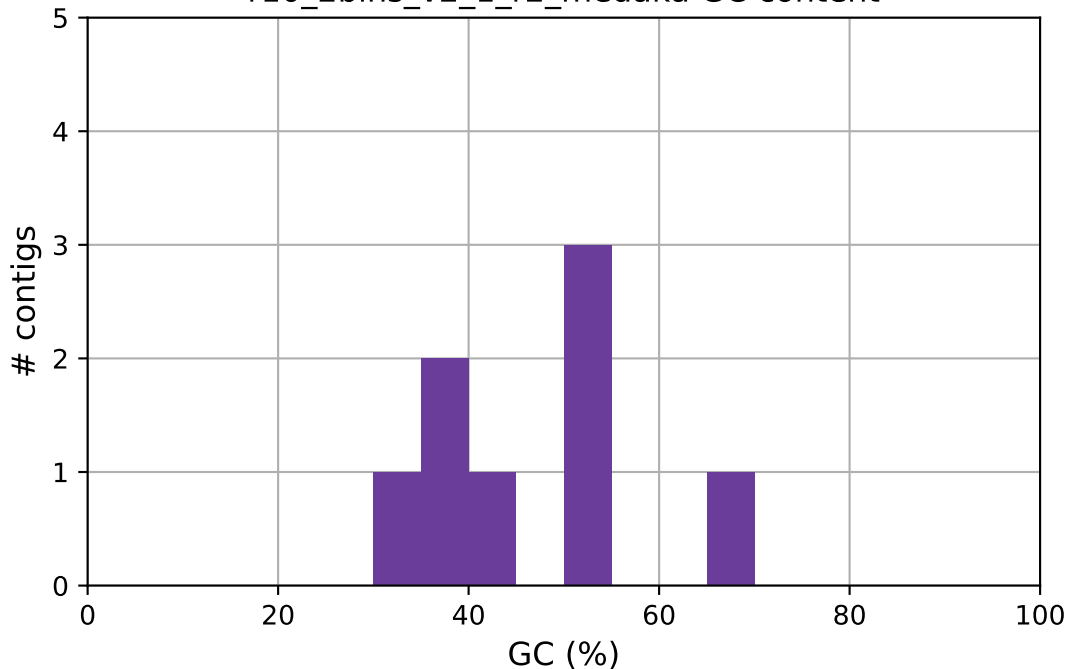
r10\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_1\_r1\_medaka GC content



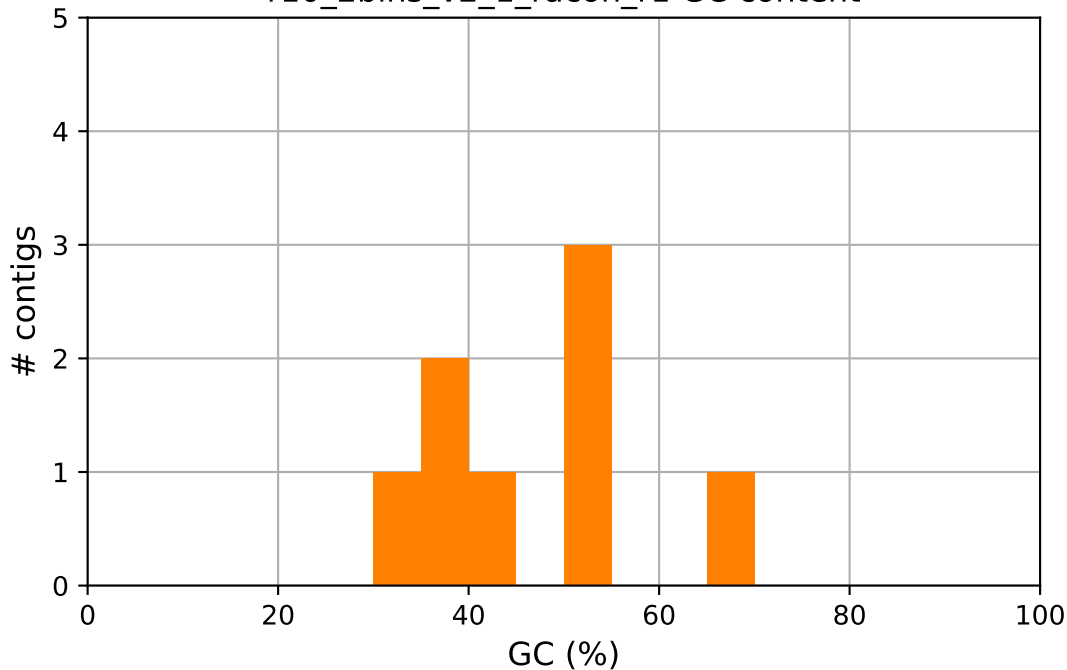
r10\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_1\_r2\_medaka GC content



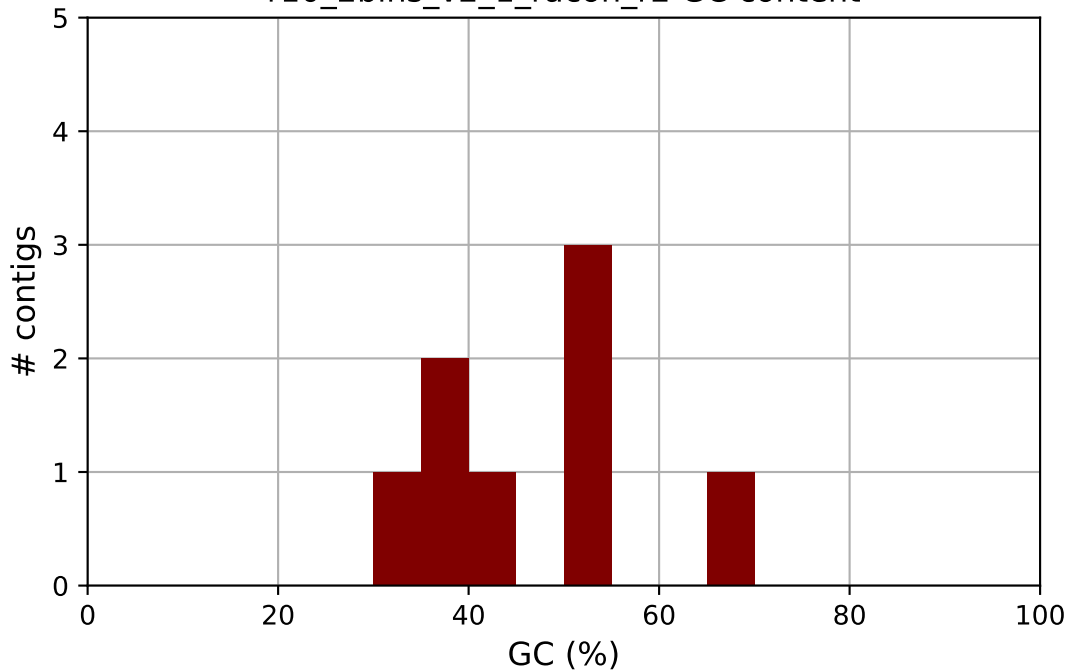
r10\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_1\_racon\_r1 GC content



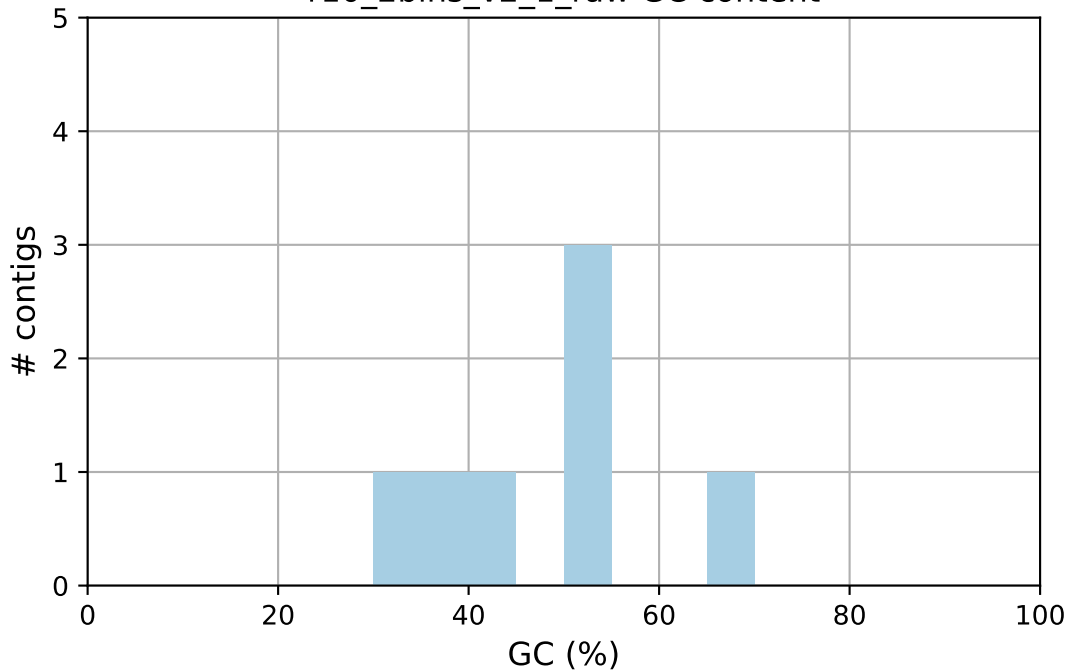
r10\_2bins\_v2\_1\_racon\_r1

r10\_2bins\_v2\_1\_racon\_r2 GC content



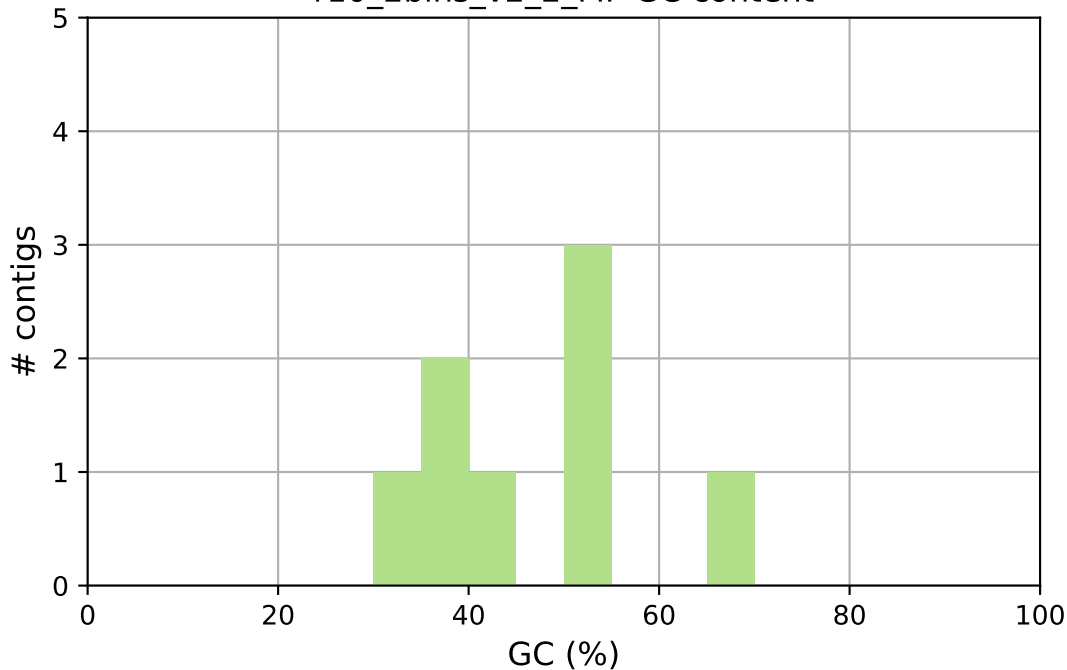
r10\_2bins\_v2\_1\_racon\_r2

r10\_2bins\_v2\_1\_raw GC content



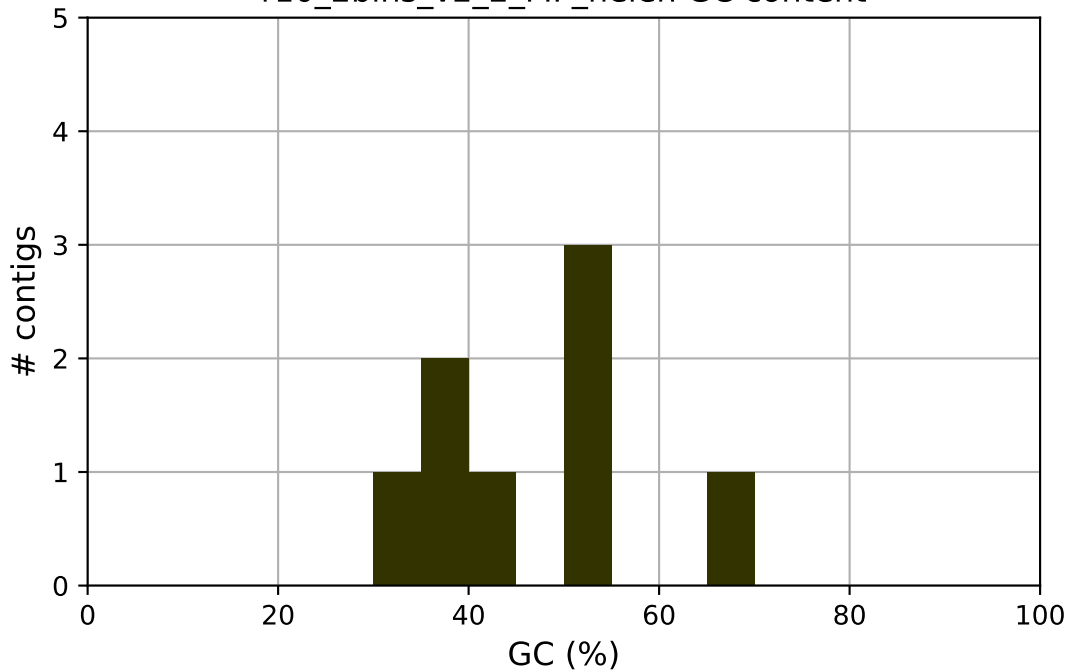
r10\_2bins\_v2\_1\_raw

r10\_2bins\_v2\_2\_MP GC content



r10\_2bins\_v2\_2\_MP

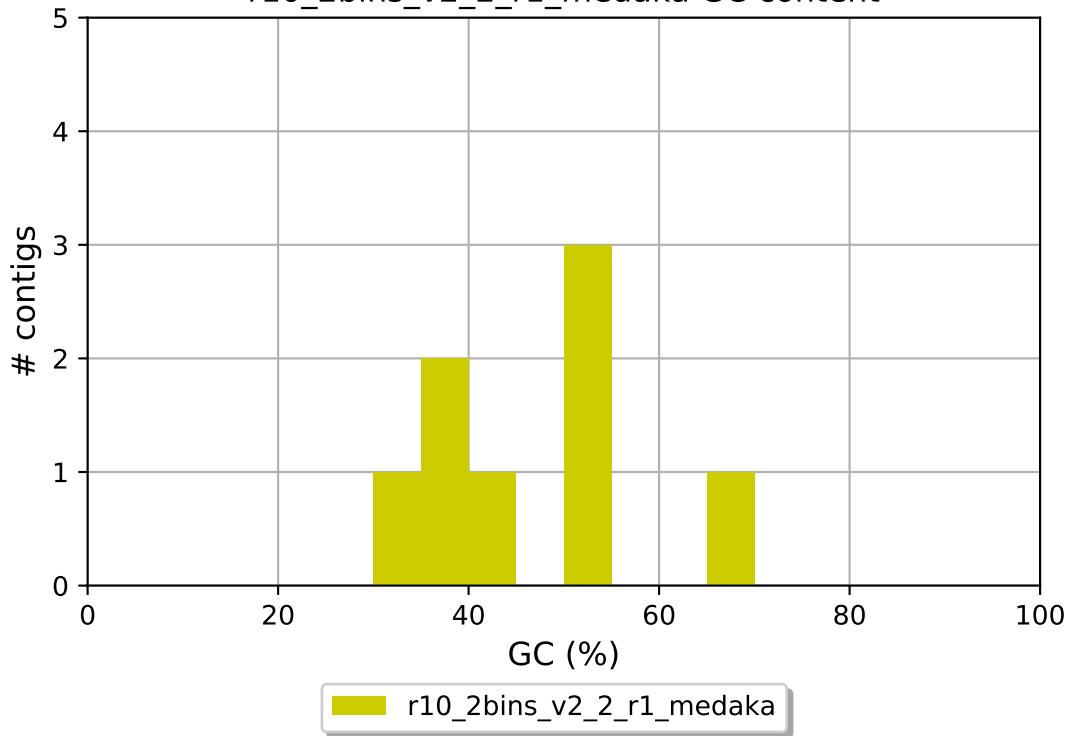
r10\_2bins\_v2\_2\_MP\_helen GC content



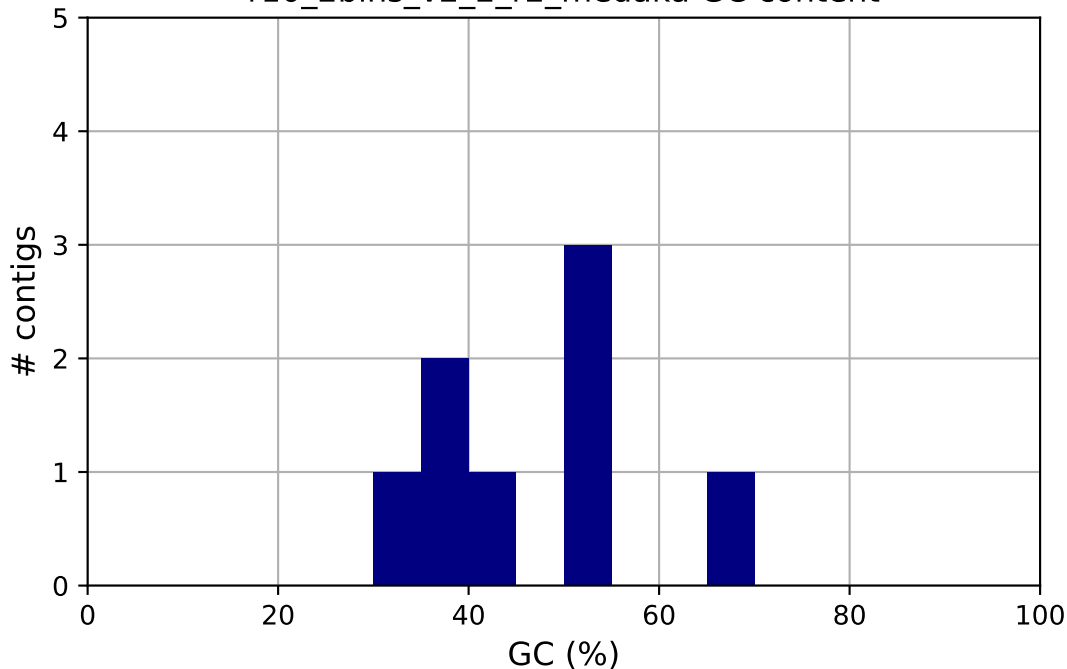
r10\_2bins\_v2\_2\_MP\_helen



r10\_2bins\_v2\_2\_r1\_medaka GC content

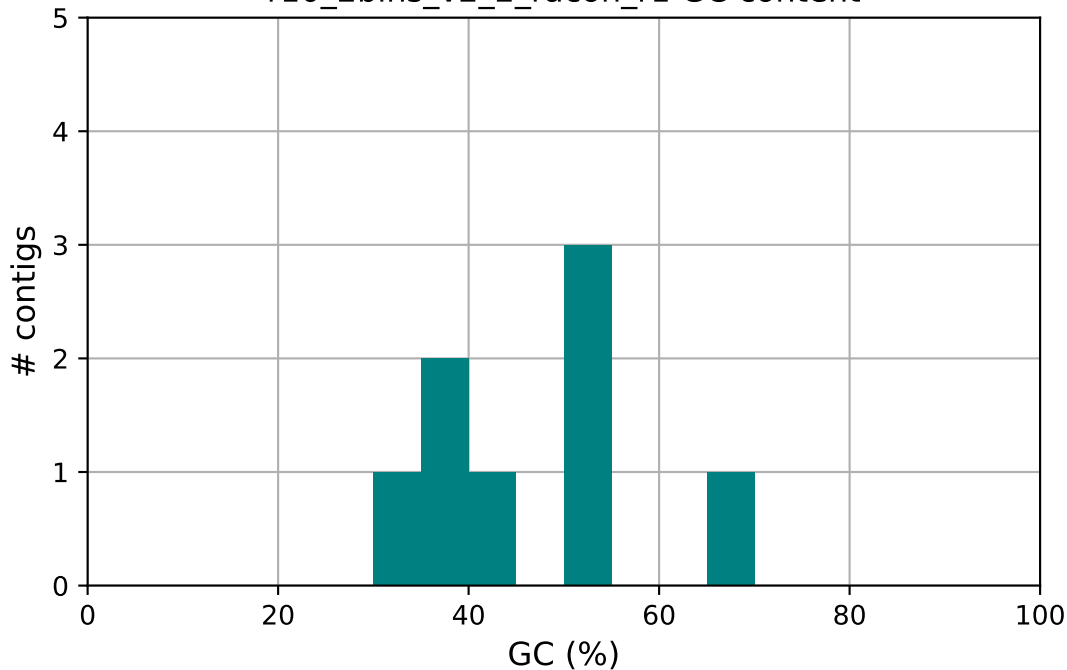


r10\_2bins\_v2\_2\_r2\_medaka GC content



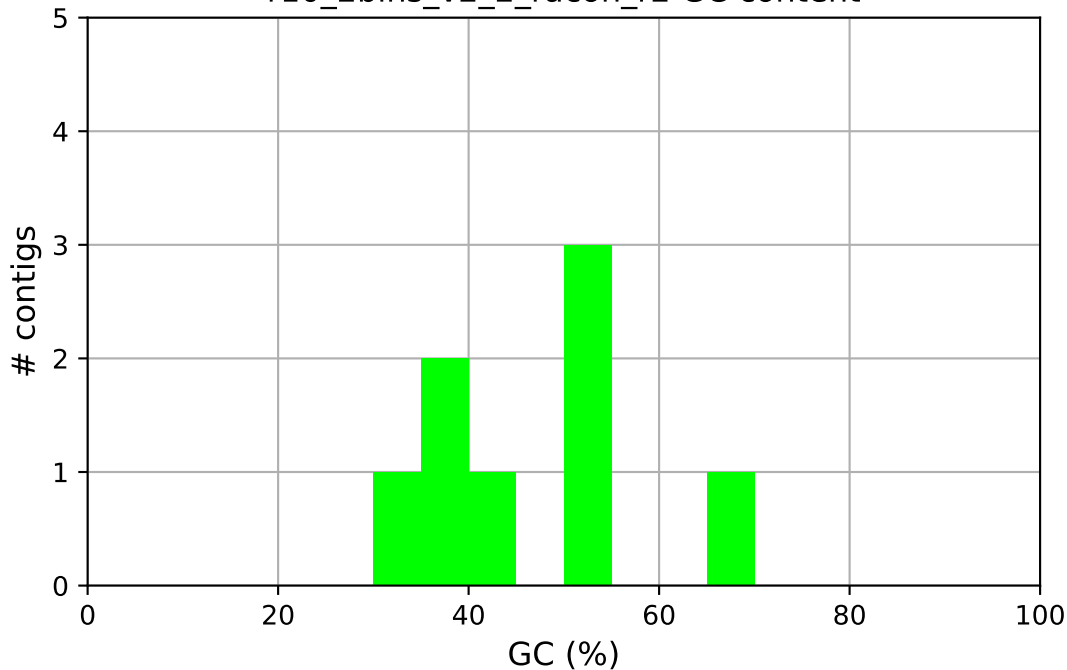
r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_2\_racon\_r1 GC content



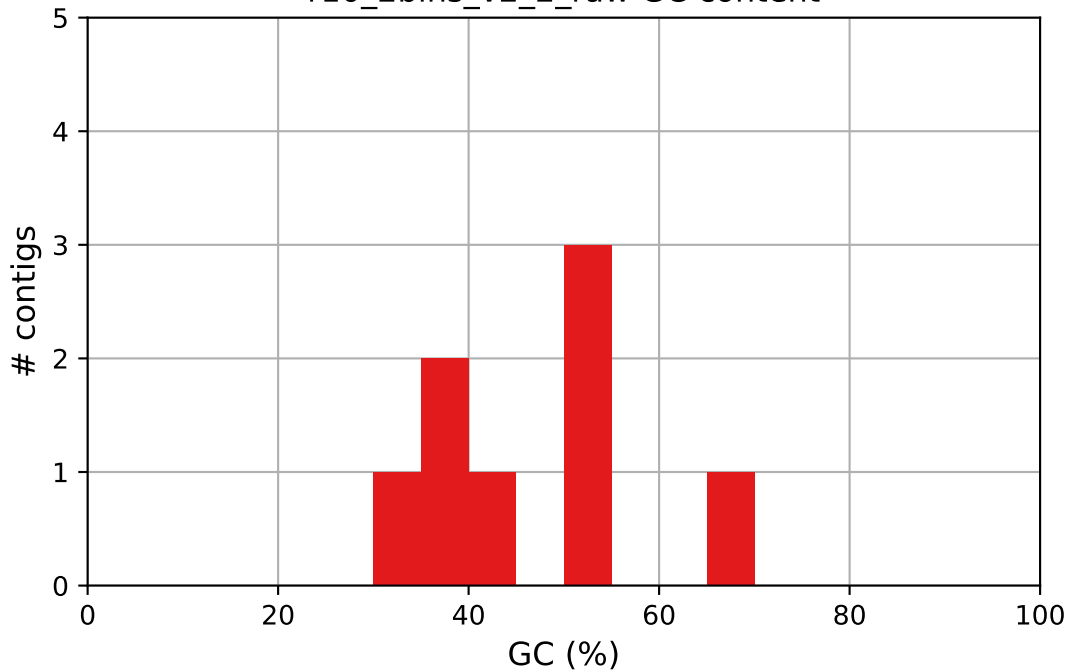
r10\_2bins\_v2\_2\_racon\_r1

r10\_2bins\_v2\_2\_racon\_r2 GC content



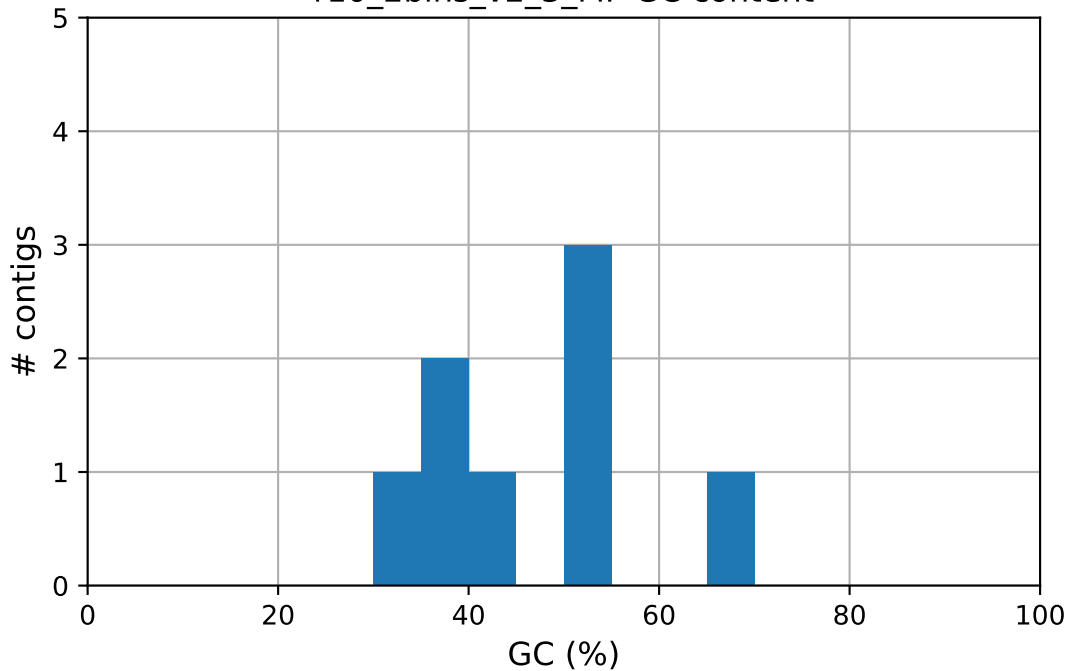
r10\_2bins\_v2\_2\_racon\_r2

r10\_2bins\_v2\_2\_raw GC content



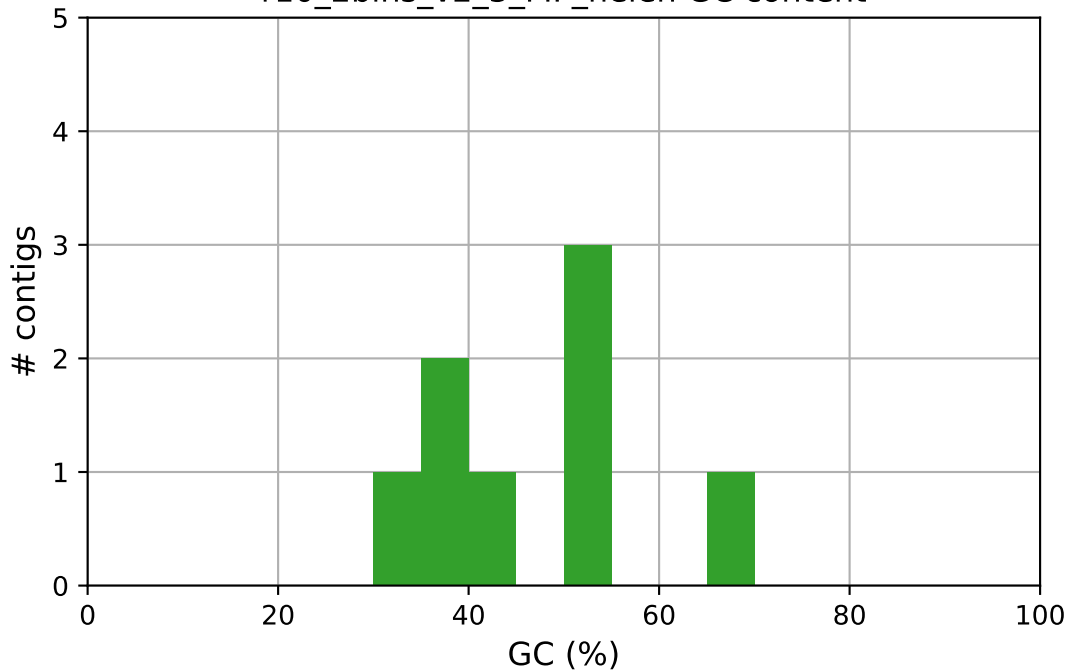
r10\_2bins\_v2\_2\_raw

r10\_2bins\_v2\_3\_MP GC content



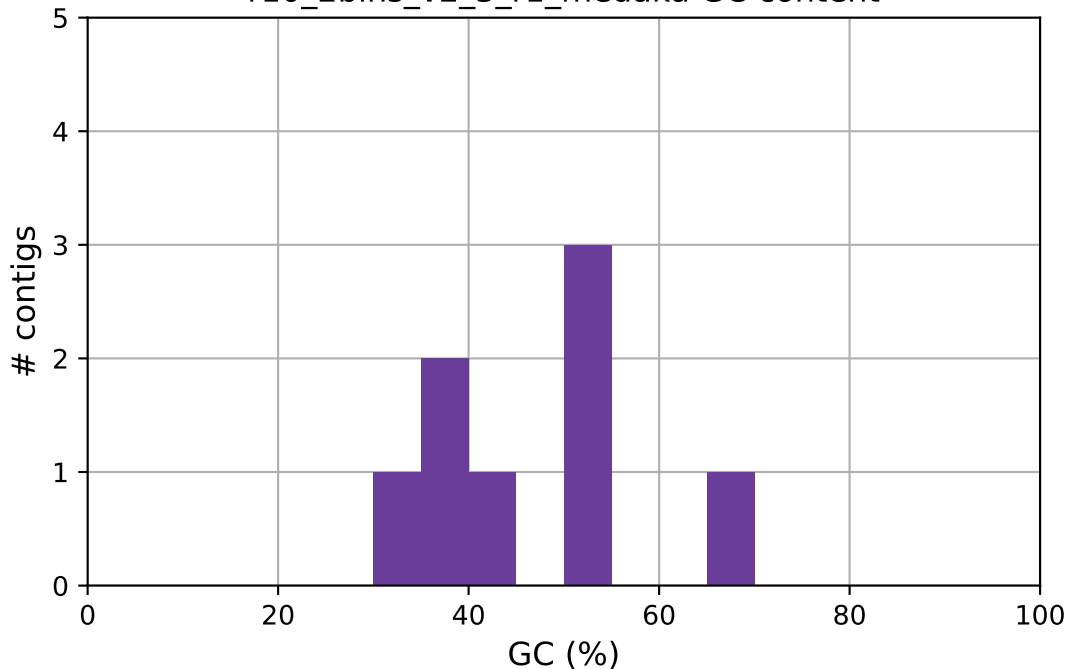
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_MP\_helen GC content



r10\_2bins\_v2\_3\_MP\_helen

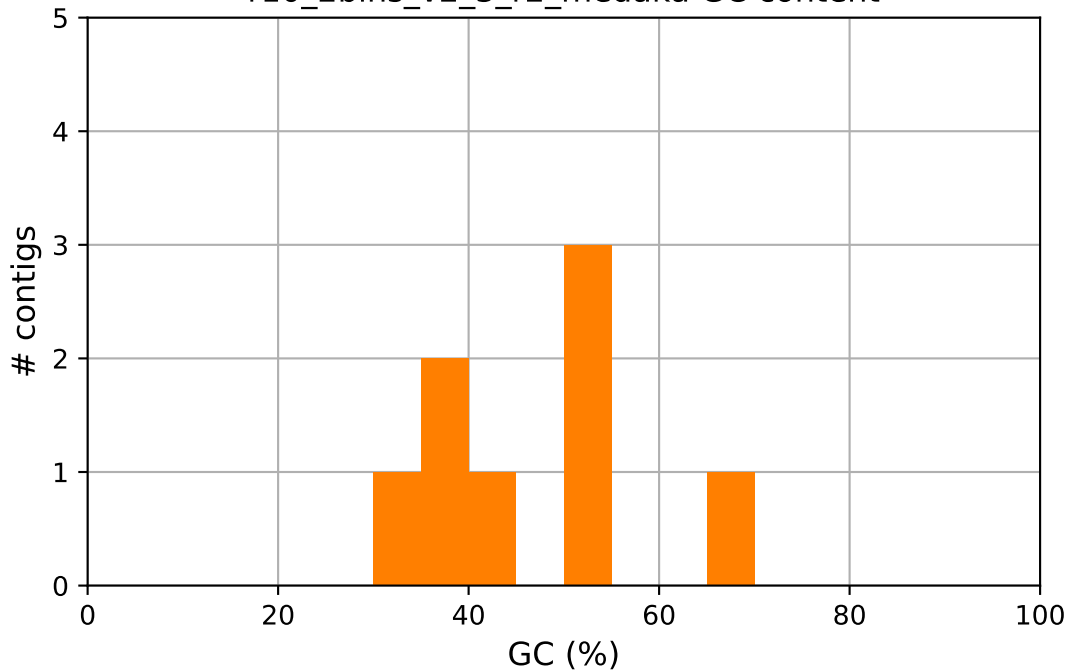
r10\_2bins\_v2\_3\_r1\_medaka GC content



r10\_2bins\_v2\_3\_r1\_medaka

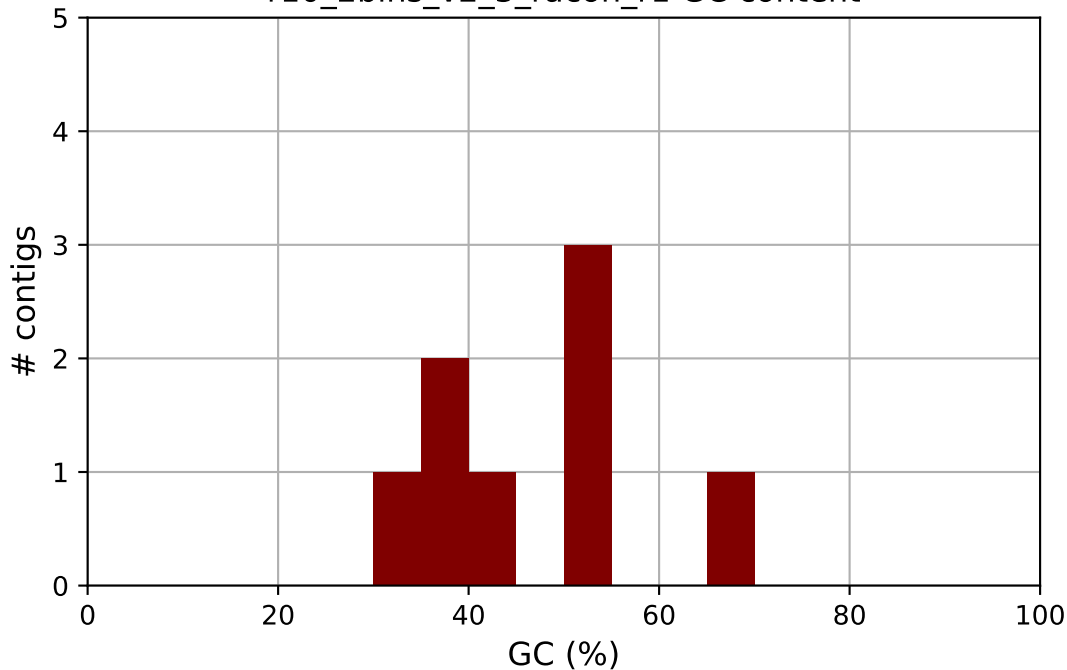


r10\_2bins\_v2\_3\_r2\_medaka GC content



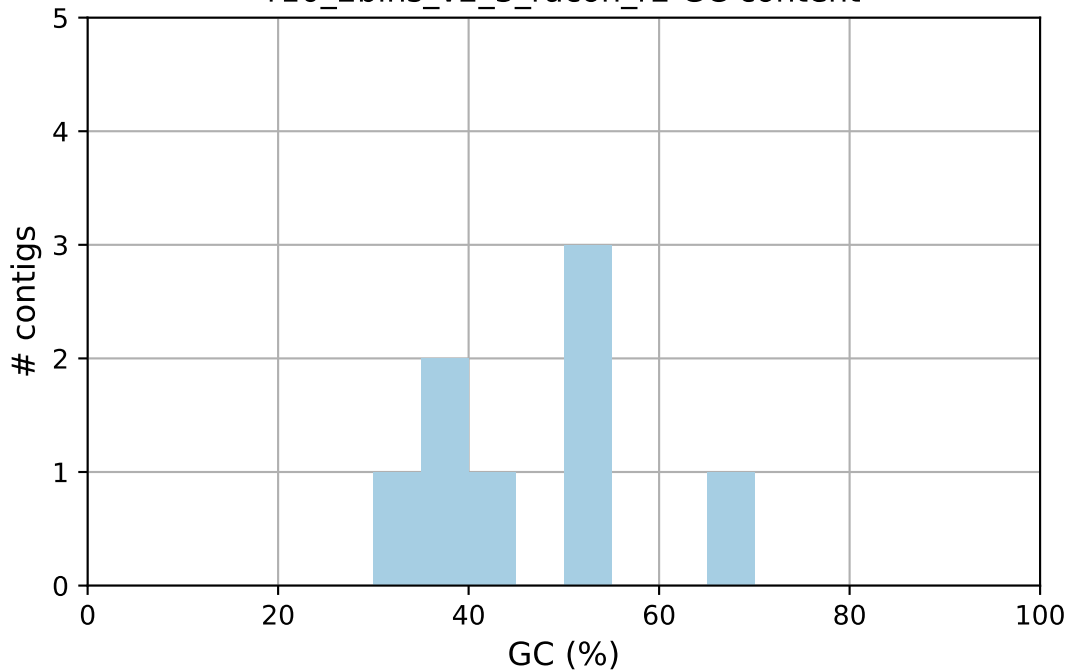
r10\_2bins\_v2\_3\_r2\_medaka

r10\_2bins\_v2\_3\_racon\_r1 GC content



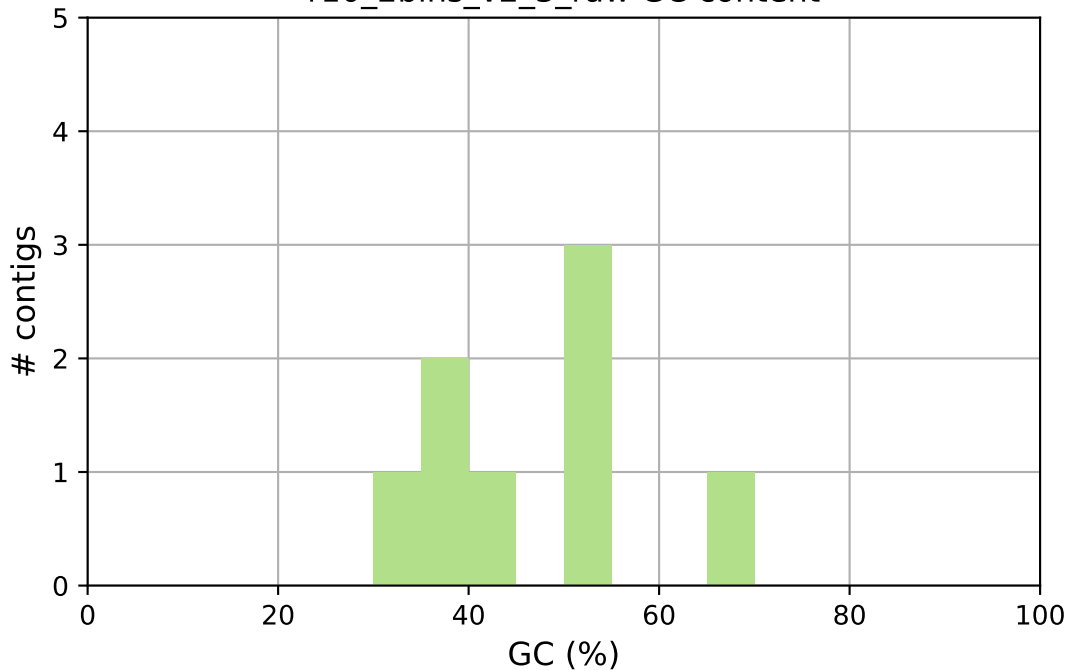
r10\_2bins\_v2\_3\_racon\_r1

r10\_2bins\_v2\_3\_racon\_r2 GC content



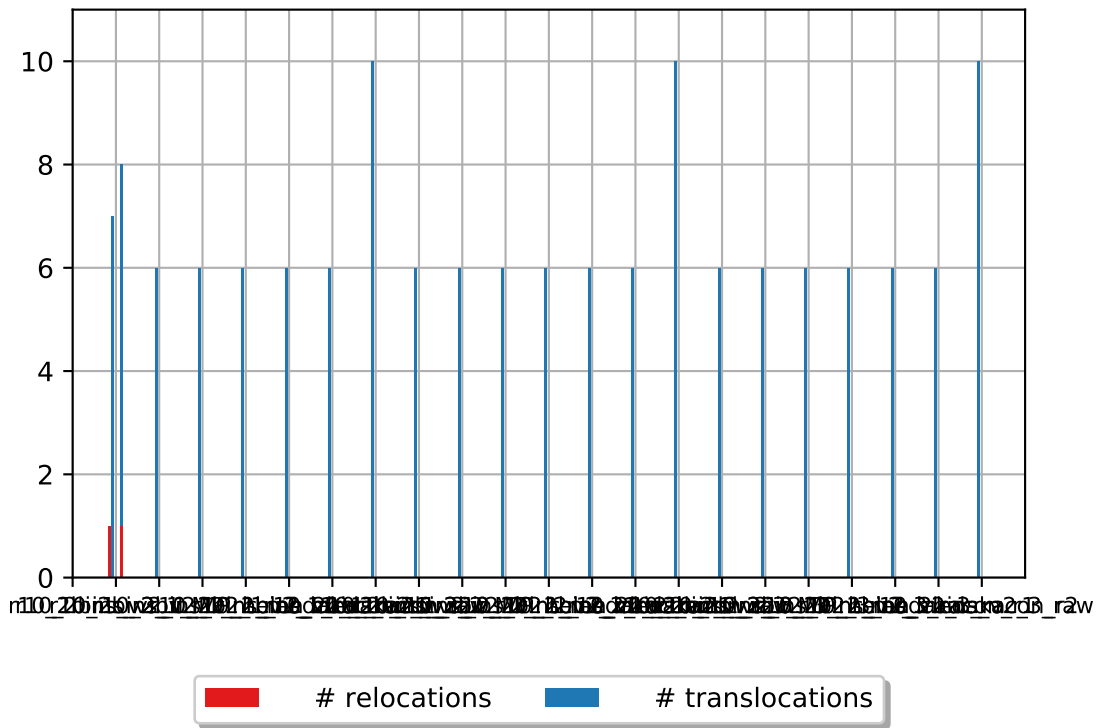
r10\_2bins\_v2\_3\_racon\_r2

r10\_2bins\_v2\_3\_raw GC content

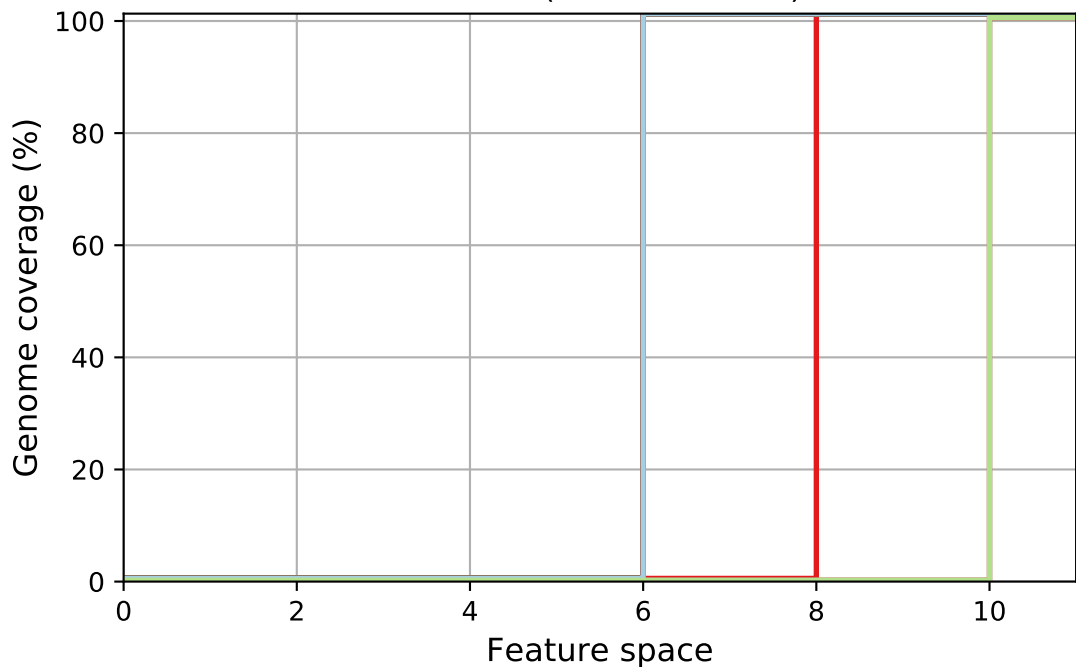


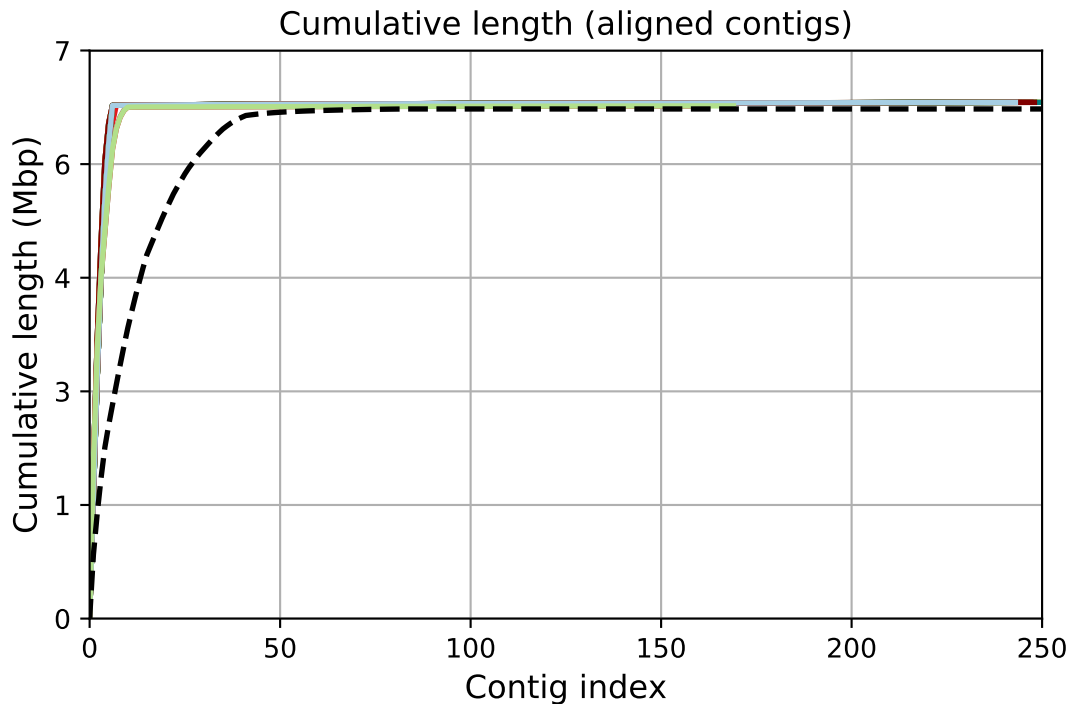
r10\_2bins\_v2\_3\_raw

# Misassemblies



FRCurve (misassemblies)





r10\_2bins\_v2\_1\_MP

r10\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_2\_racon\_r1

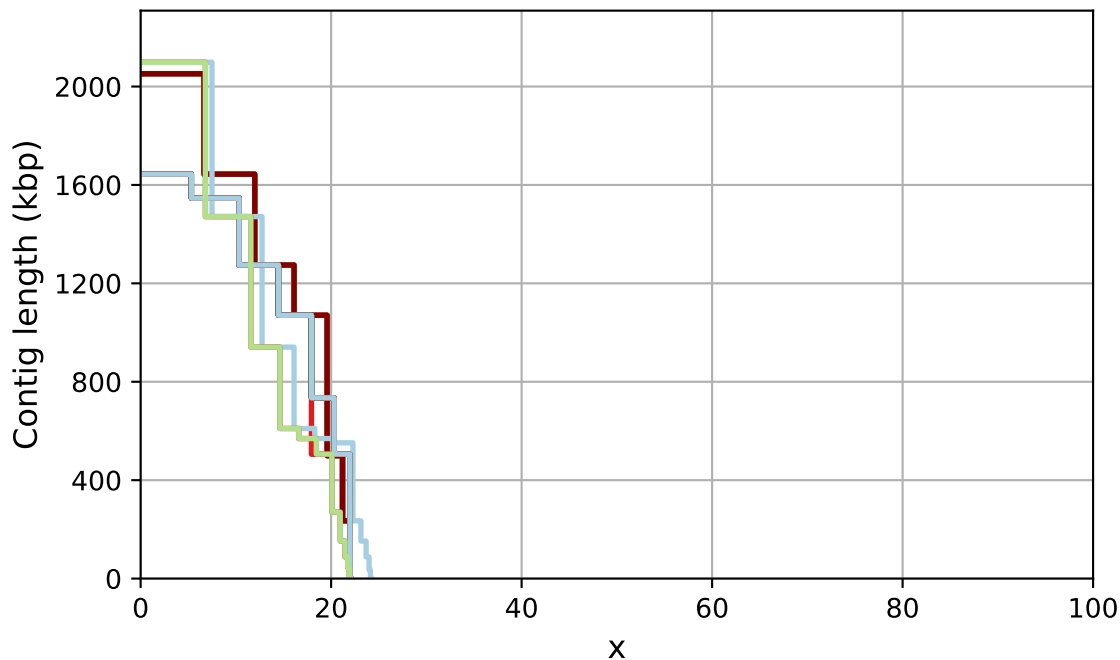
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_r1

r10\_2bins\_v2\_3\_r2

r10\_2bins\_v2\_3\_racon\_r1

# NAx



r10\_2bins\_v2\_1\_MP

r10\_2bins\_v2\_2\_MP

r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_3\_MP\_helen

r10\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_3\_r1\_medaka

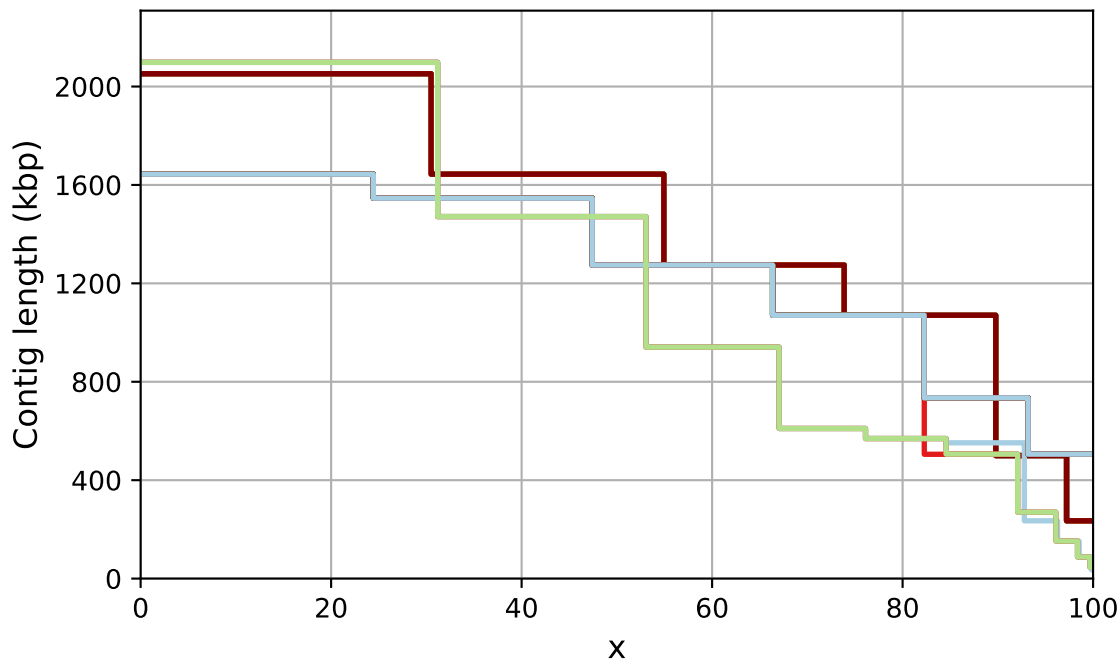
r10\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_r2\_medaka



# NGAx



0\_2bins\_v2\_1\_MP

0\_2bins\_v2\_1\_MP\_helen

0\_2bins\_v2\_1\_r1\_medaka

0\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_MP

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_MP\_helen

r10\_2bins\_v2\_3\_r1\_medaka

r10\_2bins\_v2\_3\_r2\_medaka

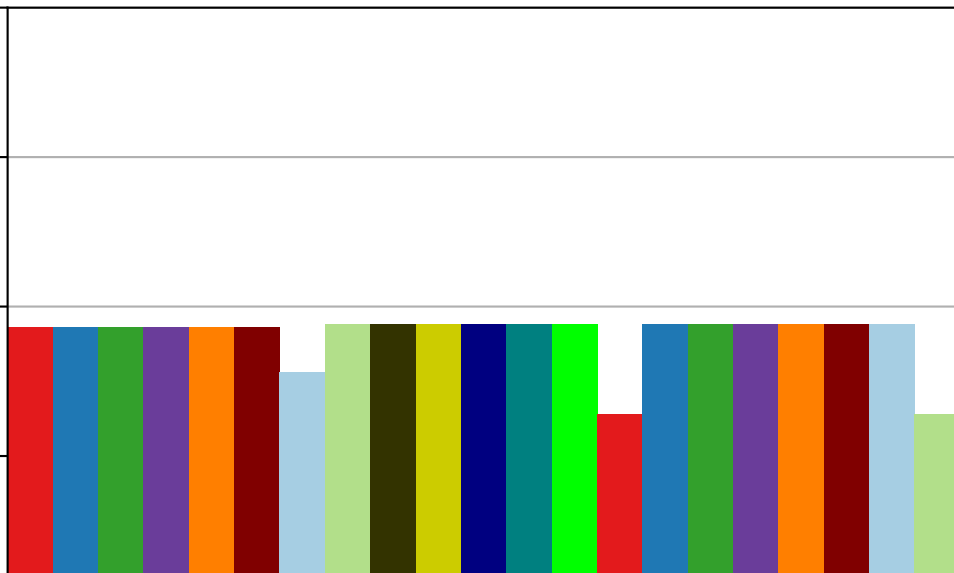
Genome fraction, %

100.00

99.95

99.90

99.85



r10\_2bins\_v2\_1\_MP

r10\_2bins\_v2\_1\_MP\_helen

r10\_2bins\_v2\_1\_r1\_medaka

r10\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_MP

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_MP\_helen

r10\_2bins\_v2\_3\_r1\_medaka

r10\_2bins\_v2\_3\_r2\_medaka