

Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total length (>= 5000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
Total length (>= 10000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
Total length (>= 25000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
Total length (>= 50000 bp)	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792205	6792208	6792382	6792380	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6792392	6791549	6791658	6788581
Total length	30866444	30863055	30868172	30857647	30851994	30845980	30850127	30867072	30862764	30868268	30857590	30852101	30844741	30850012	30866614	30862713	30867461	30855149	30852655	30845216	30849517
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	49.49	49.48	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	4758902	4757799	4759020	4758488	4757908	4757843	4755996	4758906	4758018	4759008	4758481	4757940	4757851	4755926	4758924	4757804	4759024	4758498	4757988	4757863	4756050
NG50	6792205	6792208	6792382	6791578	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6792392	6791549	6791658	6788581
N75	2992069	2992056	2992173	2992056	2991926	2991944	2990670	2992084	2992067	2992181	2992179	2991904	2991942	2990627	2992085	2992068	2992180	2991937	2991954	2992178	2990634
NG75	6792205	6792208	6792382	6792380	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6792392	6791549	6791658	6788581
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	8	8	8	8	10	8	6	6	6	6	6	10	8	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	6792205	6792208	6792382	6792380	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6792392	6791549	6791658	6788581
# local misassemblies	11	11	11	11	11	11	24	11	11	11	11	11	11	25	11	11	11	11	11	11	25
# 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	7	7	7	7	6	7	7	6	7	7	7	6	7	7	7
# unaligned contigs	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	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24046899	24044035	24048788	24038073	24032909	24026947	24078447	24047244	24043534	24049295	24038848	24033071	24025959	24077959	24046907	24043562	24048050	24036158	24033853	24026199	24077085
Genome fraction (%)	99.894	99.894	99.894	99.894	99.894	99.894	99.877	99.893	99.893	99.893	99.893	99.893	99.893	99.878	99.893	99.893	99.893	99.893	99.893	99.893	99.878
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	58.79	55.90	57.14	57.20	59.17	58.59	64.59	58.88	56.21	56.62	56.32	59.13	58.73	64.69	58.76	56.18	57.14	56.59	58.64	58.91	65.28
# indels per 100 kbp	5.67	3.84	6.41	6.35	15.16	14.11	97.33	5.42	5.06	6.40	6.37	15.73	14.76	97.25	5.42	5.04	6.40	6.37	15.68	14.79	97.24
Largest alignment	1643774	2052283	1643818	1643819	1643611	1643625	2098661	1643839	2052185	2052252	2052255	2052050	2052085	2098630	1643839	2052185	2052252	2052255	2052050	2052083	2098630
Total aligned length	6816245	6815727	6816084	6816274	6815792	6816734	6769161	6815478	6815221	6815030	6814990	6815278	6815030	6769578	6815955	6815399	6815659	6815239	6815050	6815265	6769957
NGA50	1188531	1643773	1188552	1188554	1188415	1188411	1471541	1274461	1643838	1643872	1643872	1643649	1643667	1471418	1643838	1643872	1643838	1643872	1643649	1643667	1471418
NGA75	1070191	1070208	1070221	1070219	1070088	1070099	569700	1070336	1070326	1070367	1070366	1070234	1070253	610213	1070336	1070326	1070367	1070366	1070234	1070253	610213
LGA50	3	2	3	3	3	3	2	3	2	2	2	2	2	2	3	2	2	2	2	2	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_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# misassemblies	8	6	8	8	8	8	10	8	6	6	6	6	6	10	8	6	6	6	6	6	10
# contig misassemblies	8	6	8	8	8	8	10	8	6	6	6	6	6	10	8	6	6	6	6	6	10
# c. relocations	1	0	1	1	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
# c. translocations	7	6	7	7	7	7	10	7	6	6	6	6	6	10	7	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	6792205	6792208	6792382	6792380	6791578	6791619	6788614	6792242	6792185	6792389	6792392	6791549	6791659	6788581	6792242	6792185	6792389	6792392	6791549	6791658	6788581
# 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	16	16	16	16	34	16	18	18	18	18	18	34	16	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	24	11	11	11	11	11	11	25	11	11	11	11	11	11	25
# 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	20	20	20	20	16	20	21	21	21	21	21	16	20	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	7	7	7	7	6	7	7	6	7	7	7	6	7	7	7
# mismatches	3951	3757	3840	3844	3977	3938	4340	3957	3778	3805	3785	3974	3947	4347	3949	3776	3840	3803	3941	3959	4387
# indels	381	258	431	427	1019	948	6540	364	340	430	428	1057	992	6535	364	339	430	428	1054	994	6534
# indels (<= 5 bp)	286	163	338	334	925	855	6416	269	243	336	334	963	897	6412	269	242	336	334	960	899	6411
# indels (> 5 bp)	95	95	93	93	94	93	124	95	97	94	94	94	95	123	95	97	94	94	94	95	123
Indels length	5422	5292	5436	5434	6142	6040	12965	5394	5401	5447	5445	6177	6103	12930	5394	5399	5447	5445	6174	6106	12929

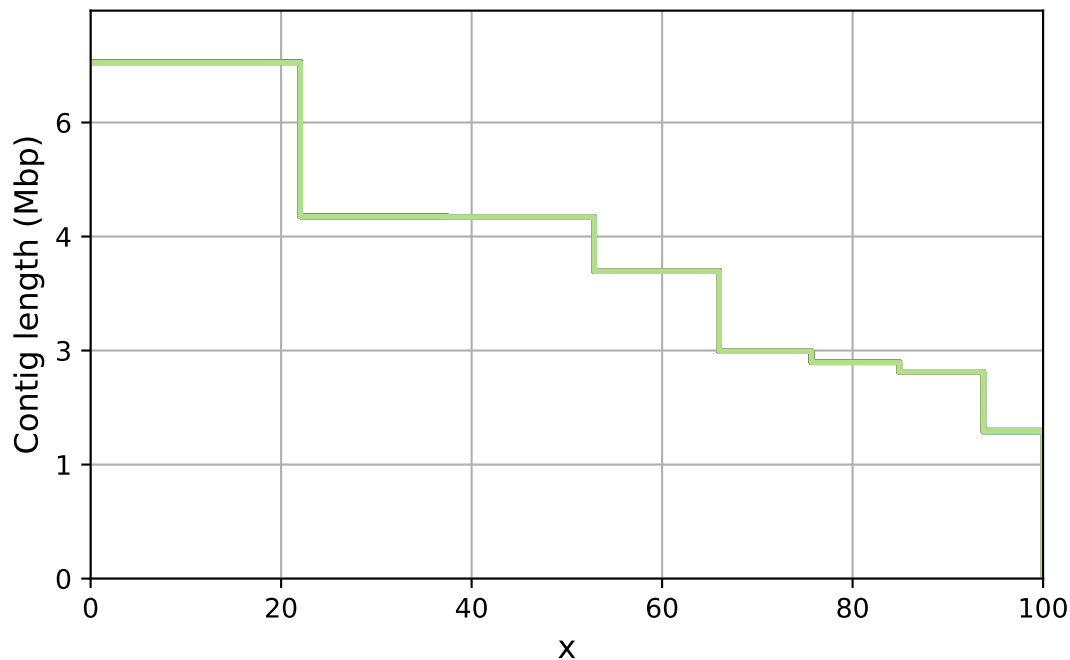
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24046899	24044035	24048788	24038073	24032909	24026947	24078447	24047244	24043534	24049295	24038848	24033071	24025959	24077959	24046907	24043562	24048050	24036158	24033853	24026199	24077085
# 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).

Nx



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

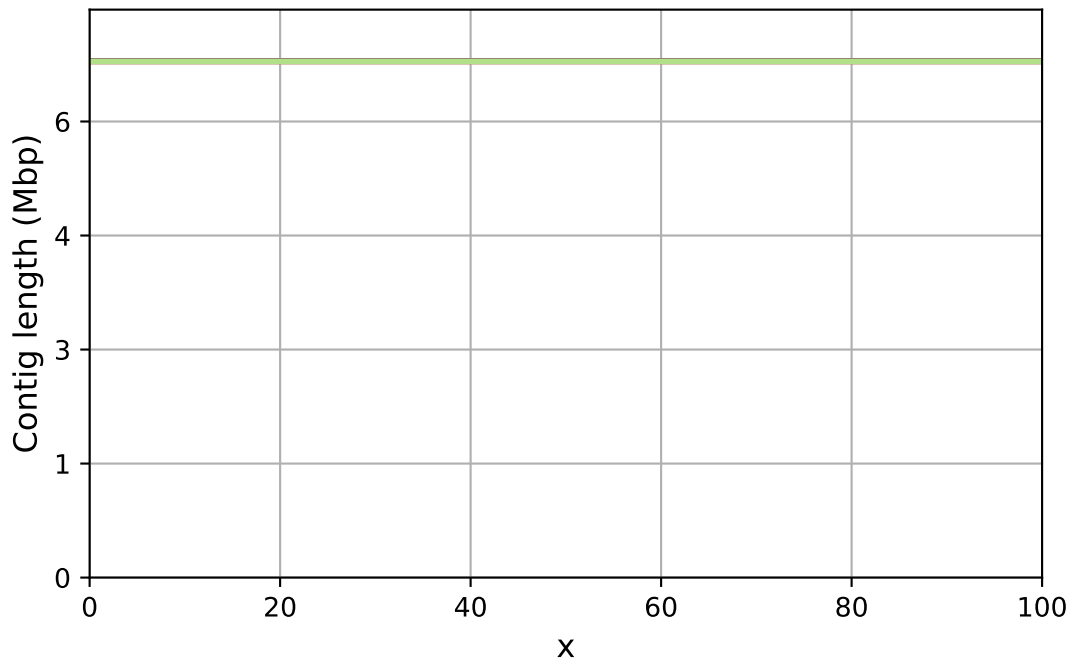
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r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

NGx



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

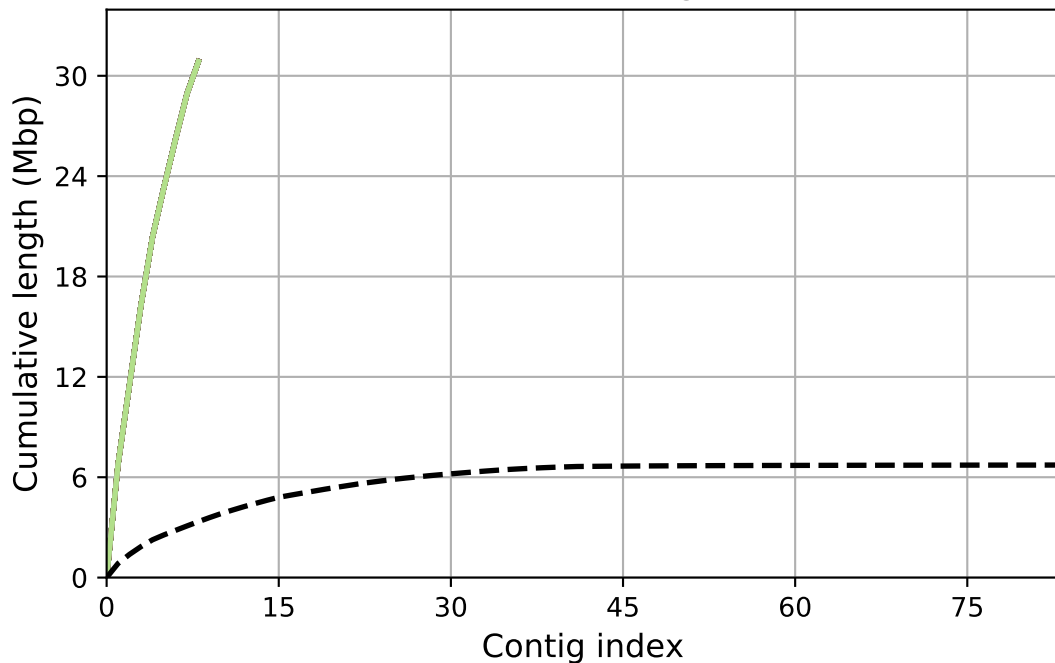
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r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

Cumulative length



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

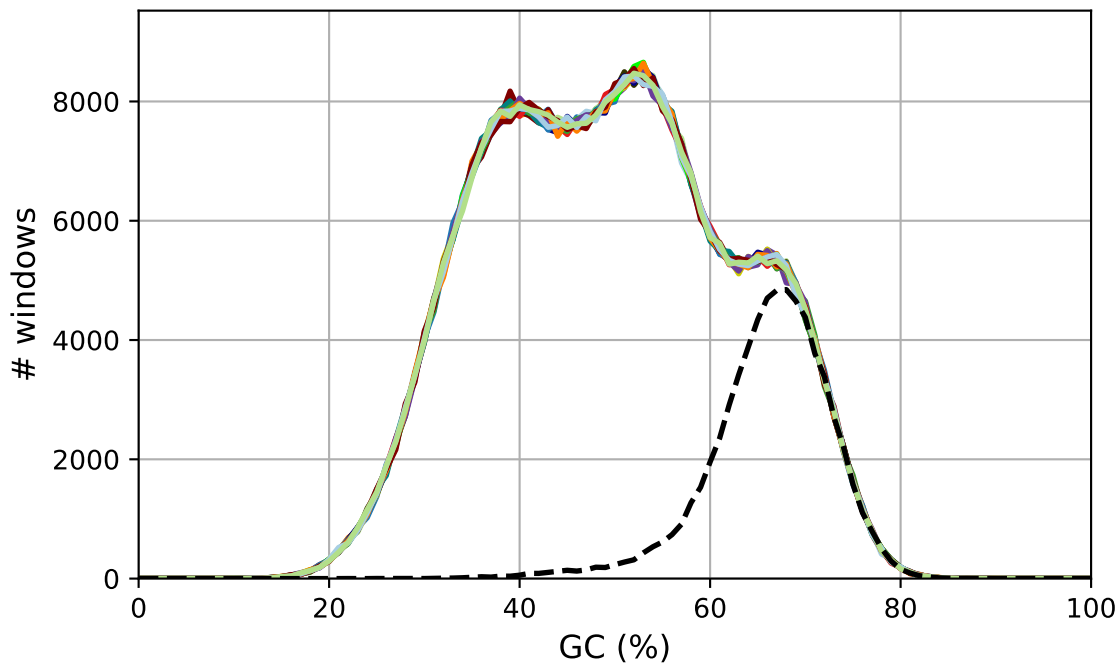
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

GC content



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

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r10 1bin v4 1 r1 medaka
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r10 1bin v4 1 r2 medaka

— r10_1bin_v4_2_MP_helen

— r10_1bin_v4_2_r1_medaka

— r10 1bin v4 2 r2 medaka

— r10 1bin v4 2 racon r1

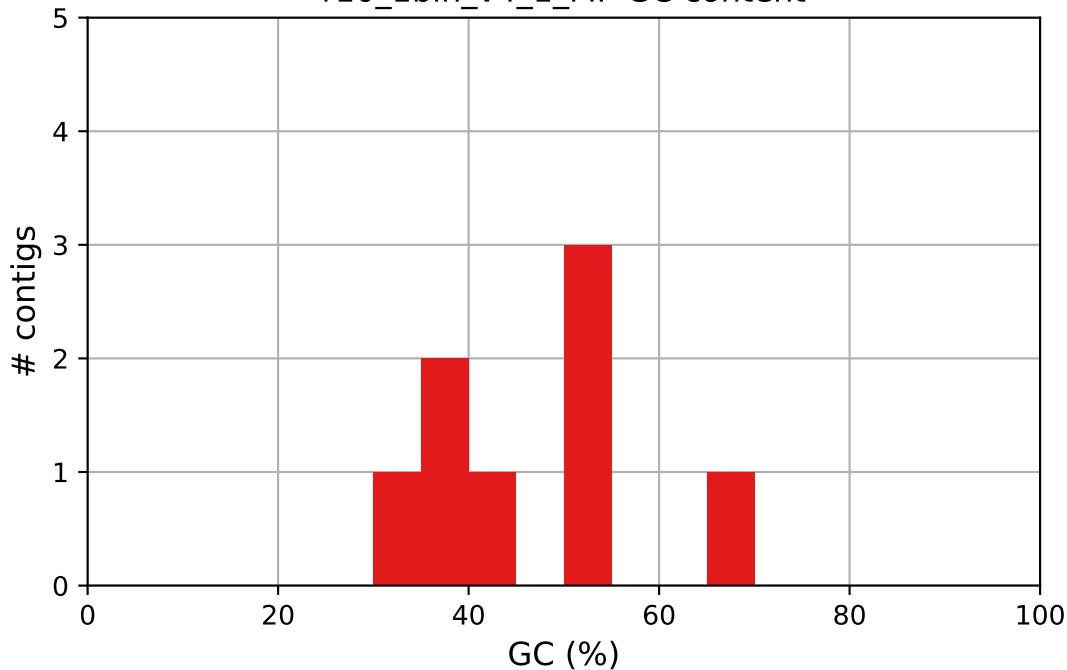
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— r10_1bin_v4_3_r1_m

— r10 1bin v4 3 r2 m

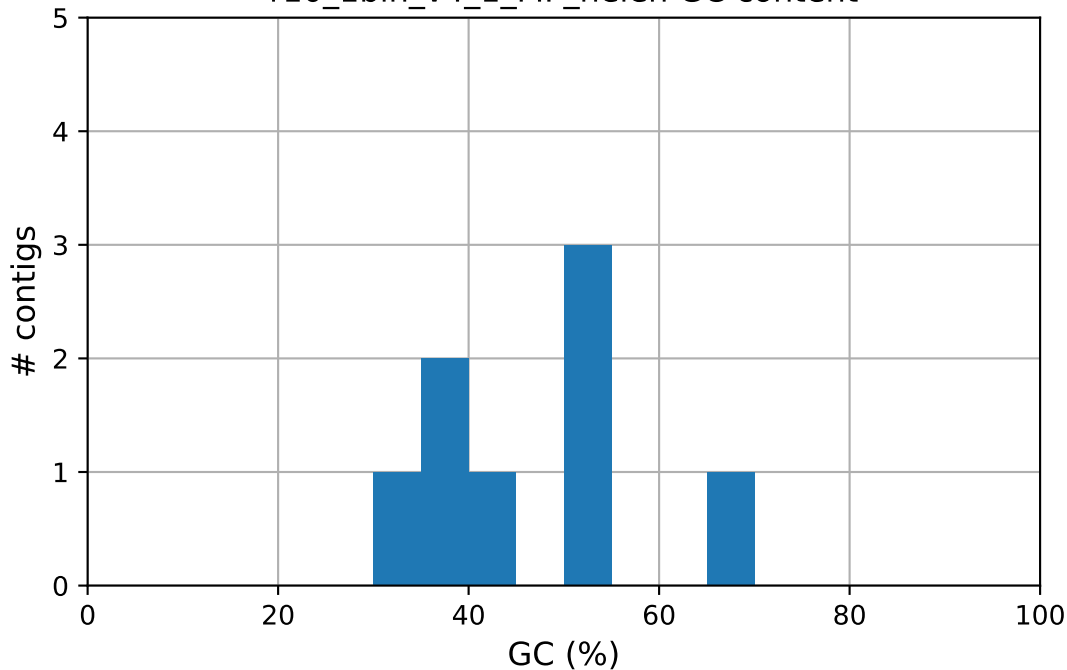
— r10 1bin v4 3 raco

r10_1bin_v4_1_MP GC content



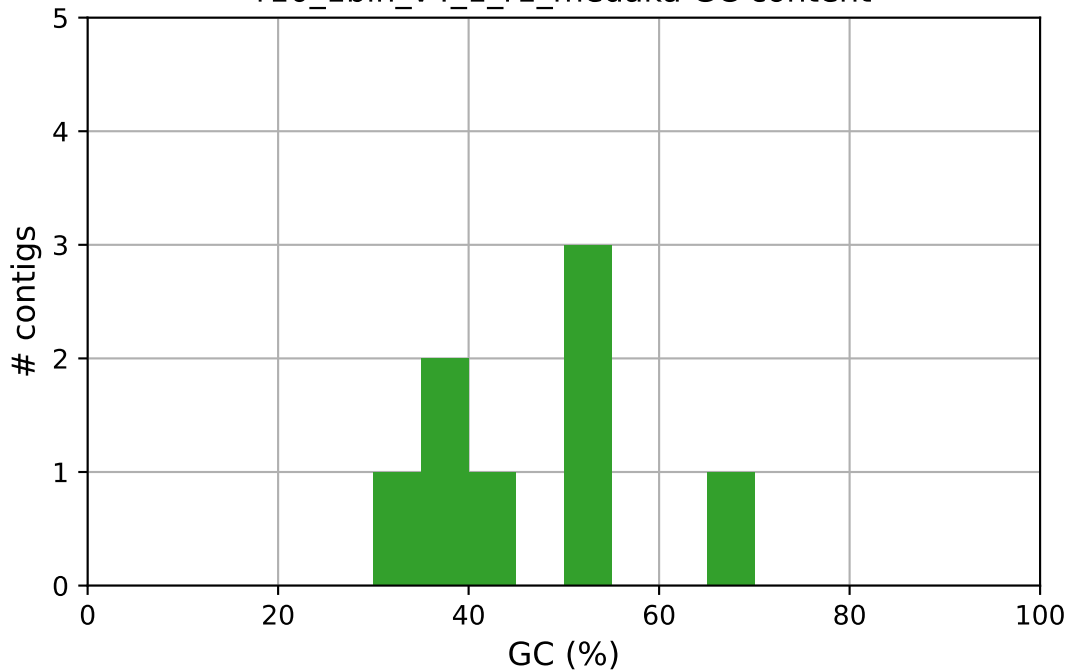
r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen GC content



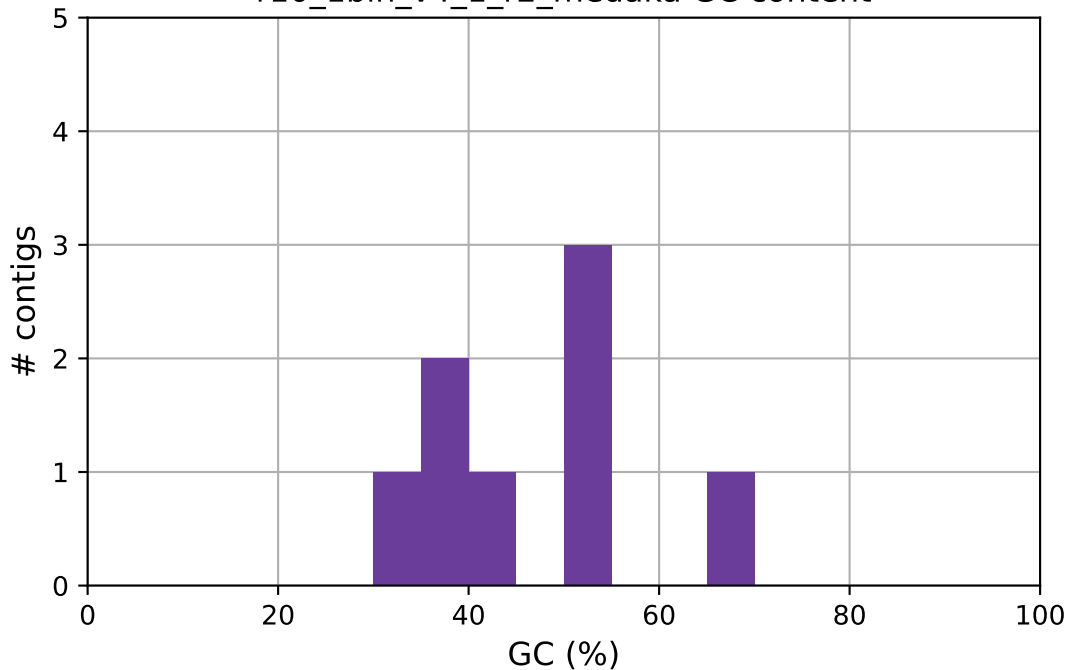
r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka GC content



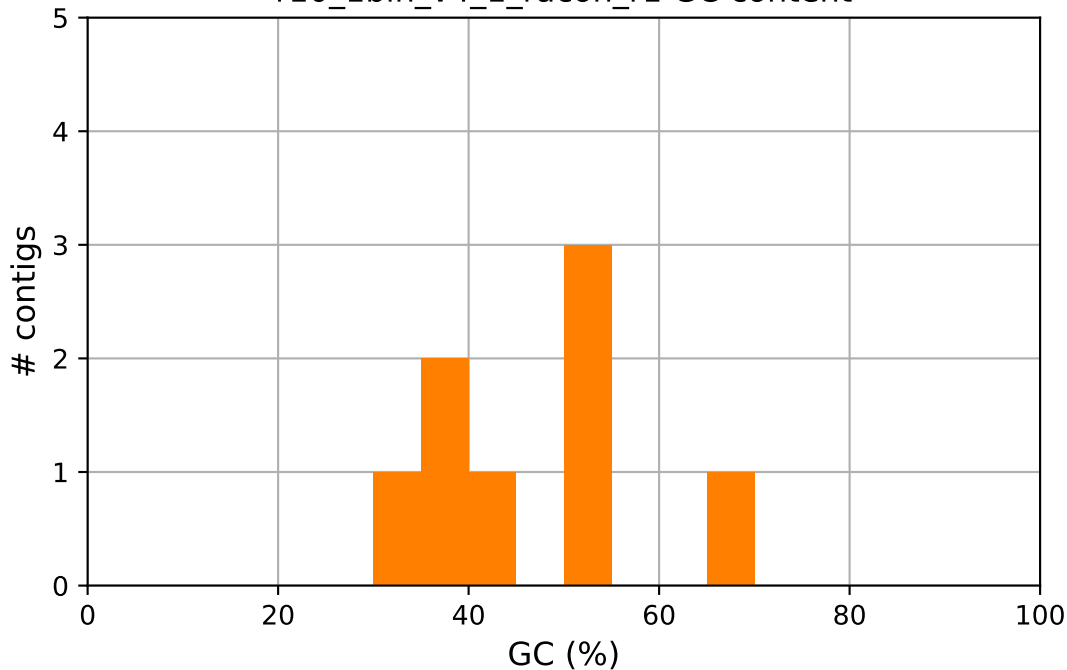
r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka GC content



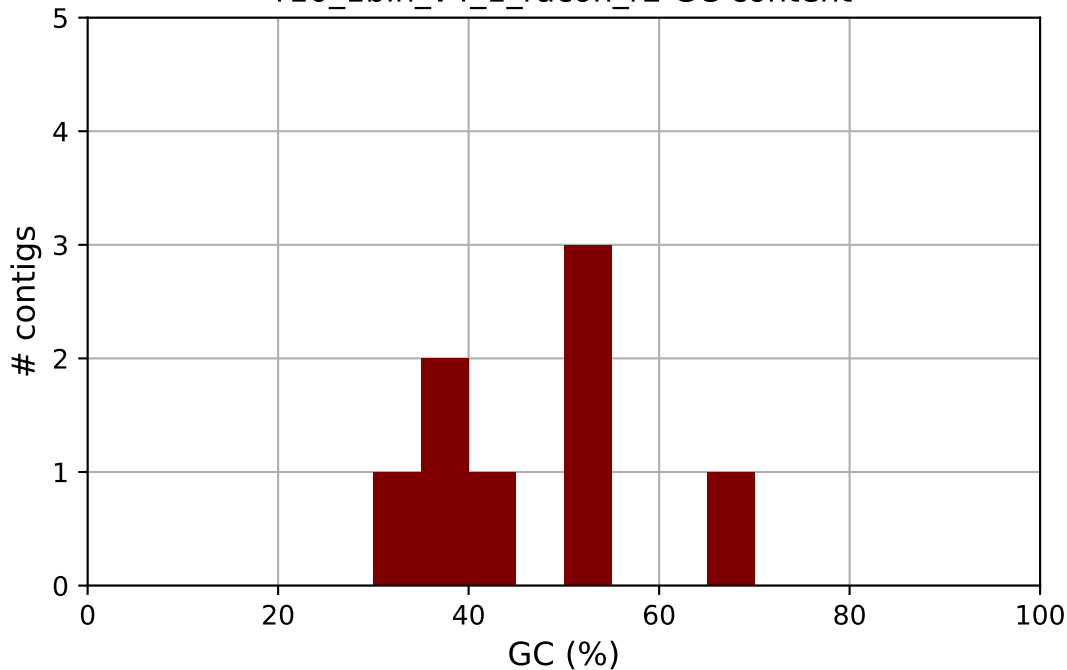
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_1_racon_r1 GC content



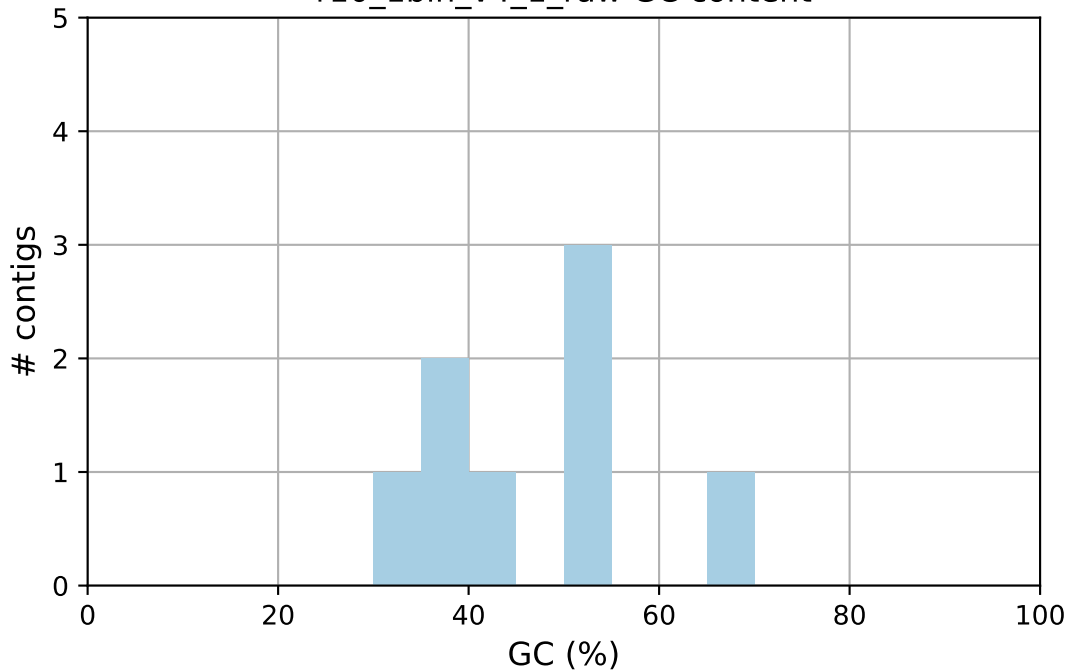
r10_1bin_v4_1_racon_r1

r10_1bin_v4_1_racon_r2 GC content



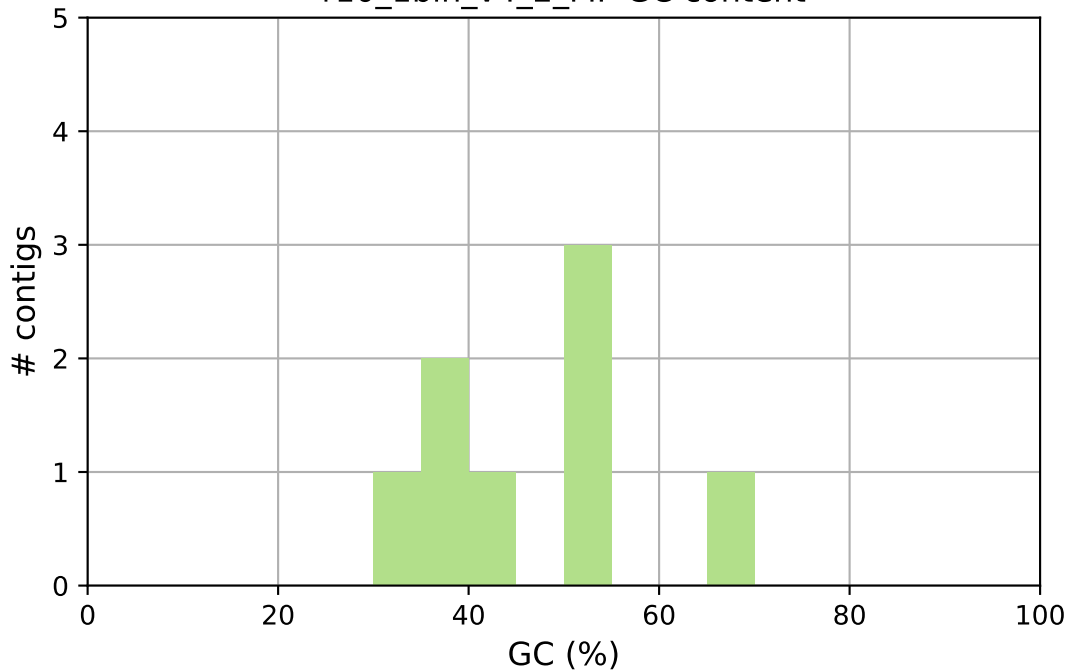
r10_1bin_v4_1_racon_r2

r10_1bin_v4_1_raw GC content



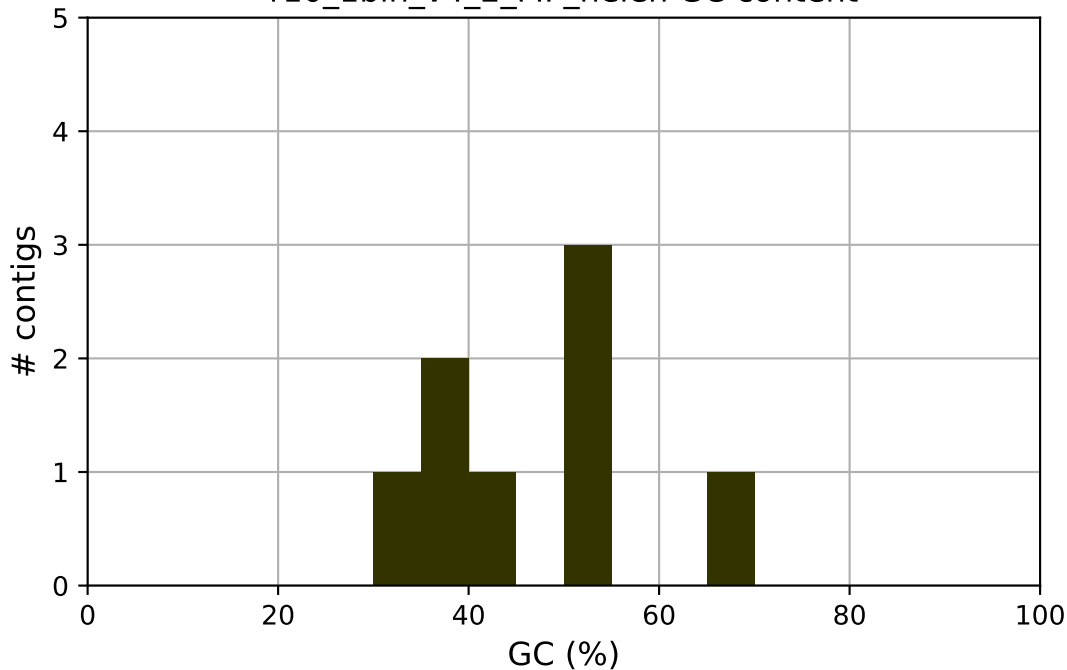
r10_1bin_v4_1_raw

r10_1bin_v4_2_MP GC content



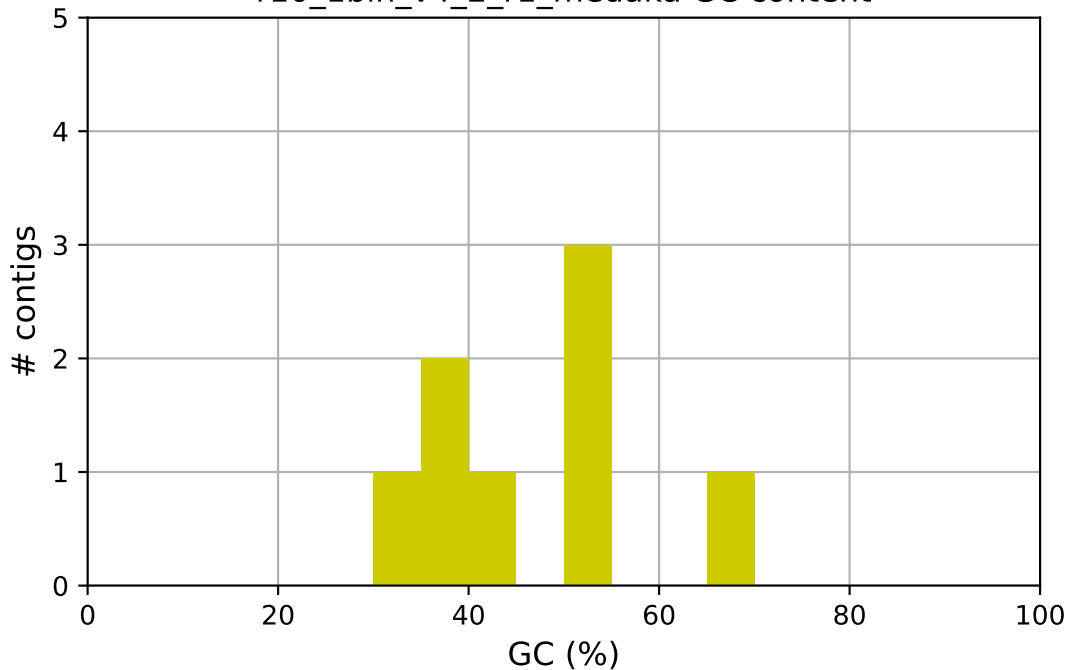
r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen GC content



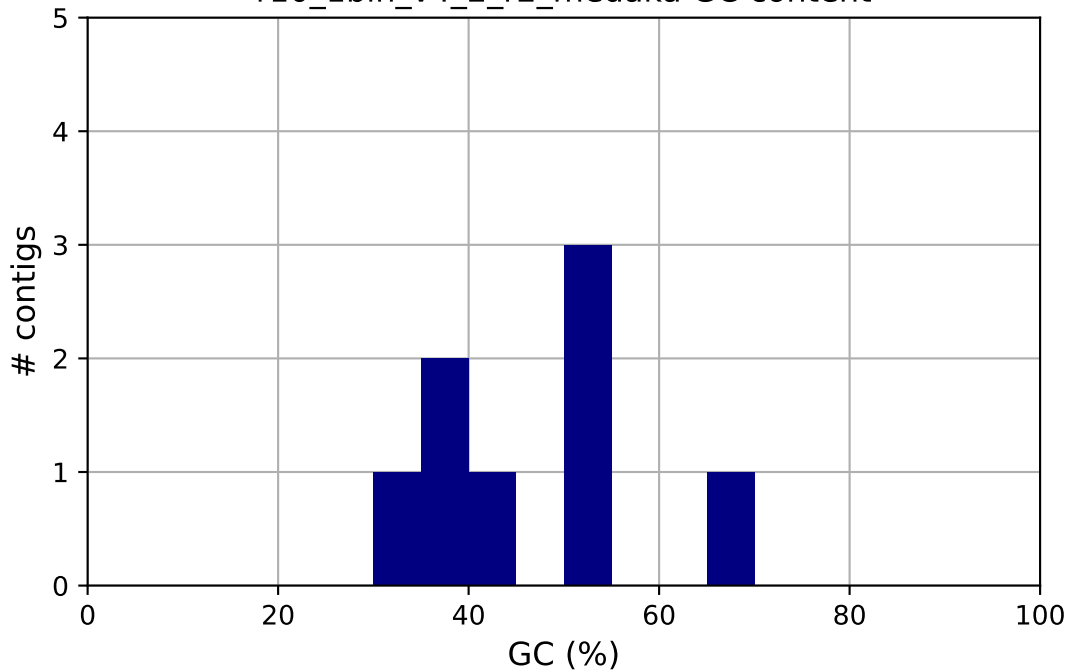
r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka GC content



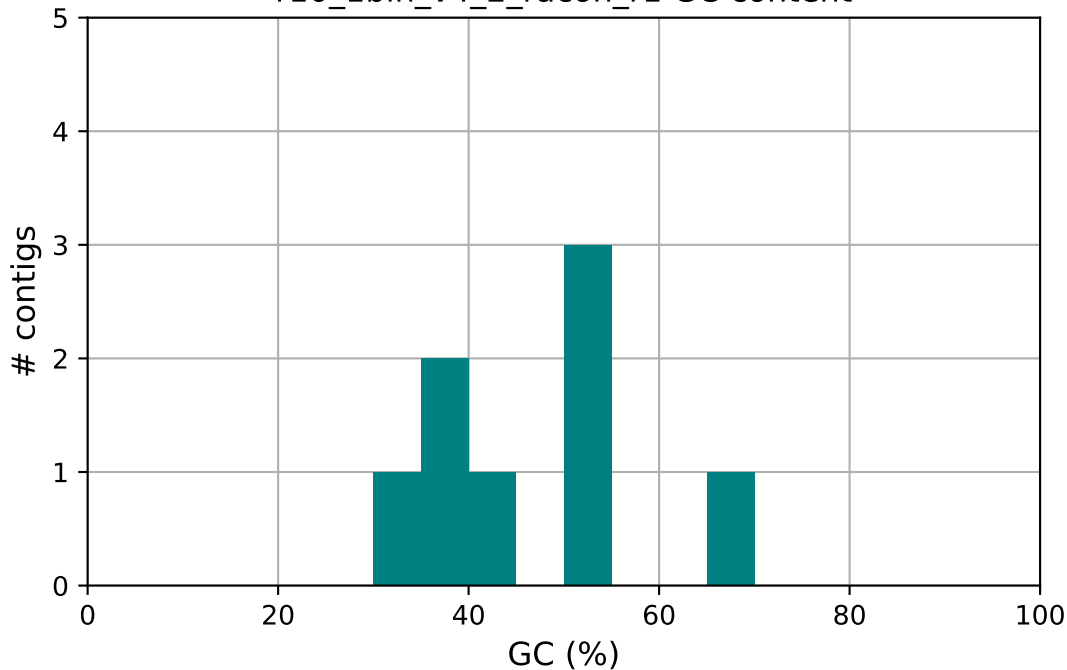
r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka GC content



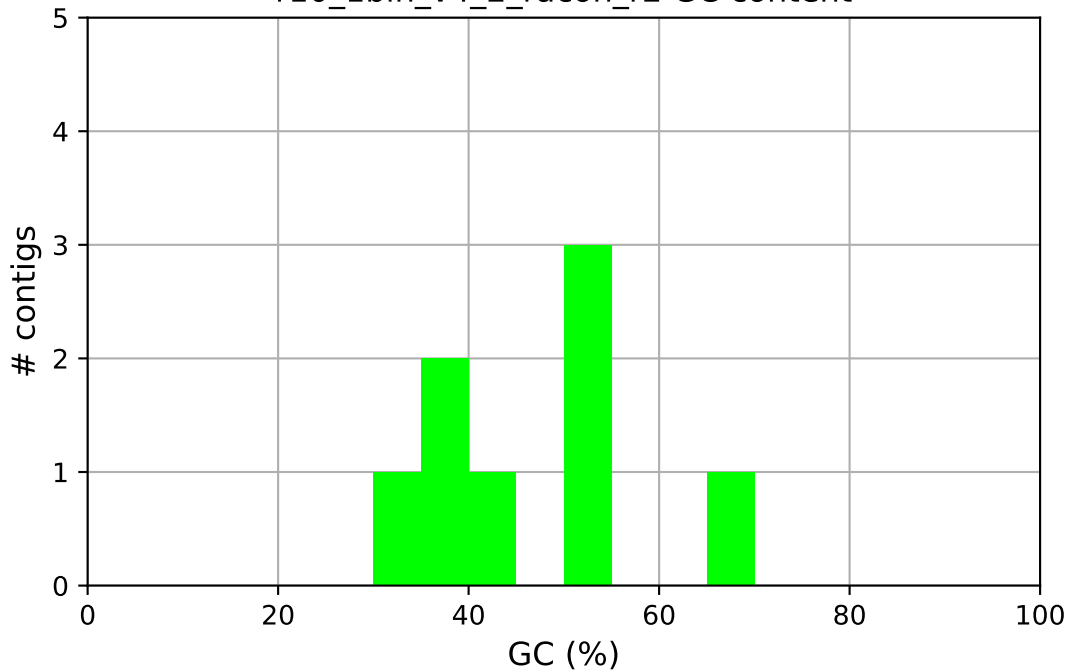
r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1 GC content



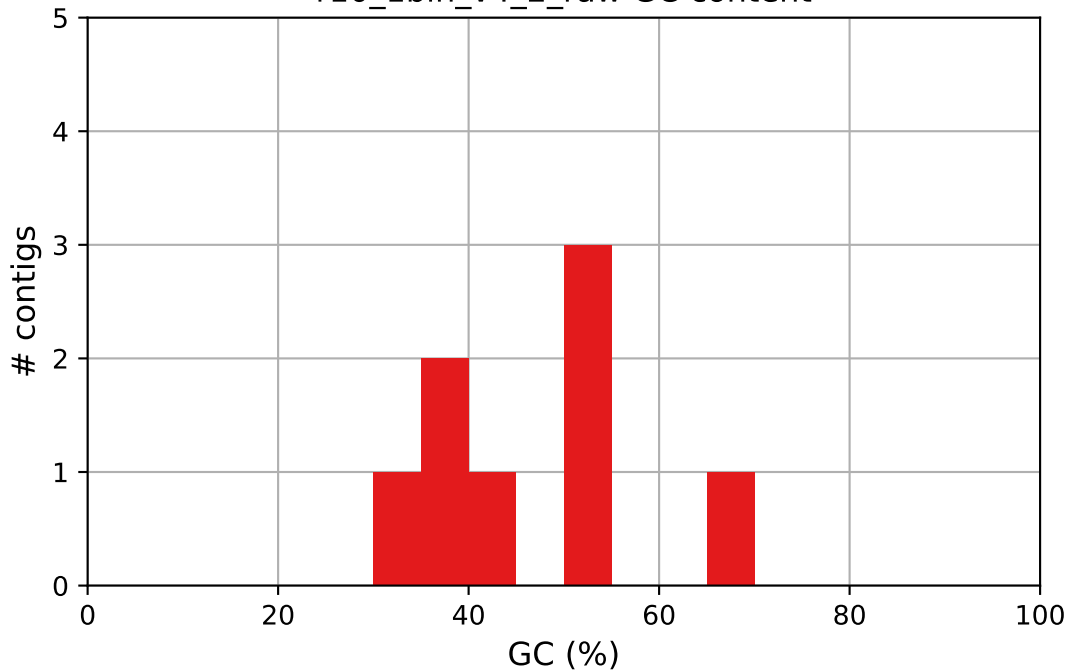
r10_1bin_v4_2_racon_r1

r10_1bin_v4_2_racon_r2 GC content



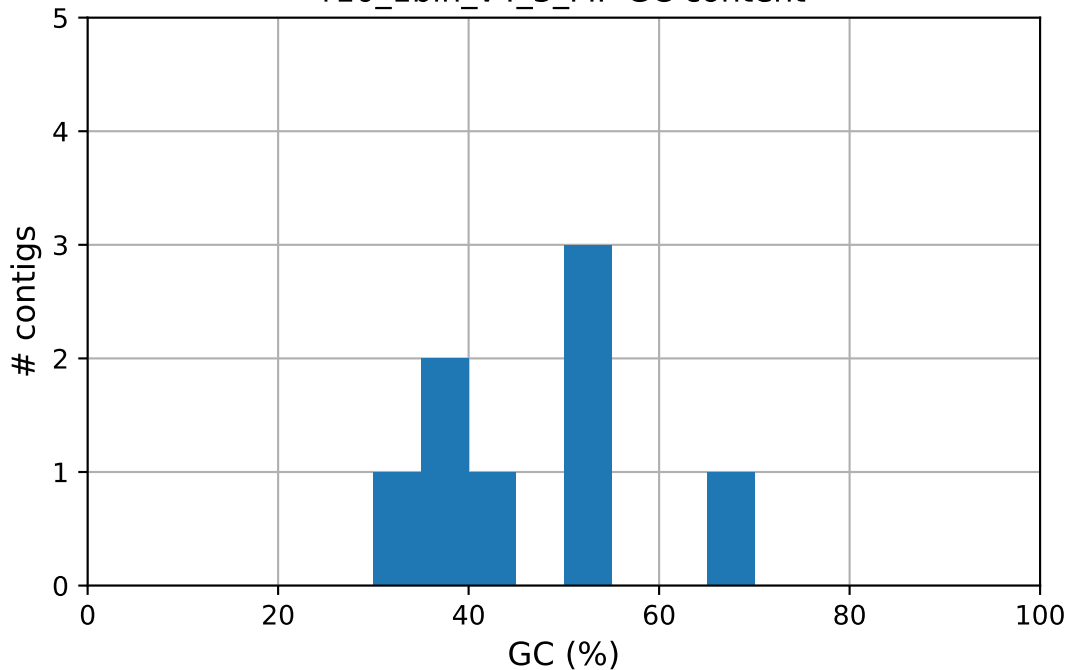
r10_1bin_v4_2_racon_r2

r10_1bin_v4_2_raw GC content



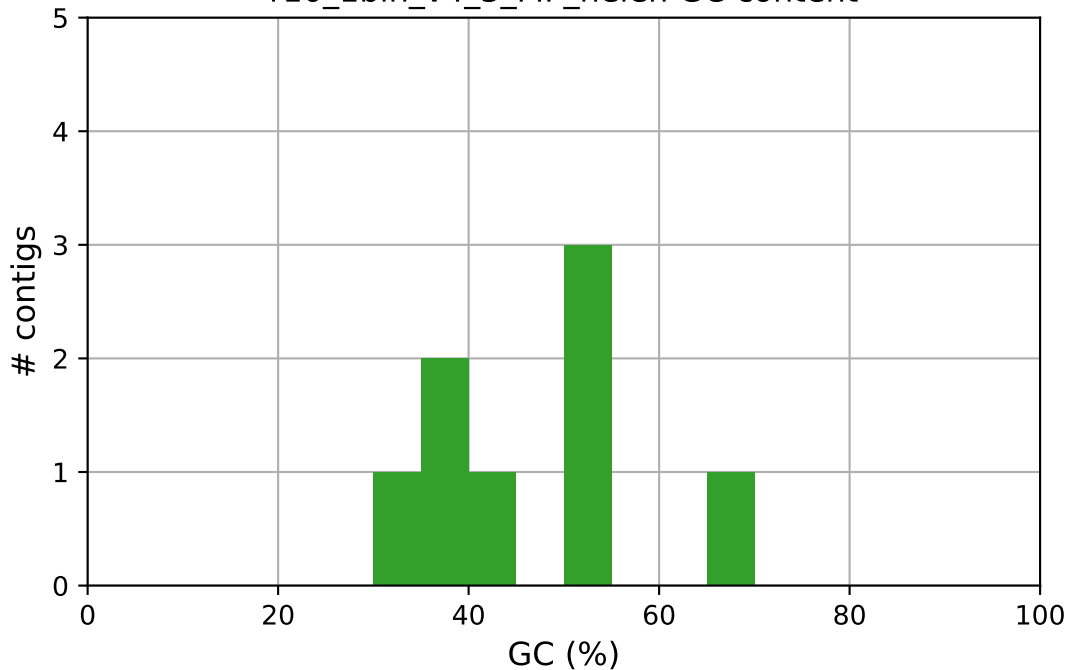
r10_1bin_v4_2_raw

r10_1bin_v4_3_MP GC content



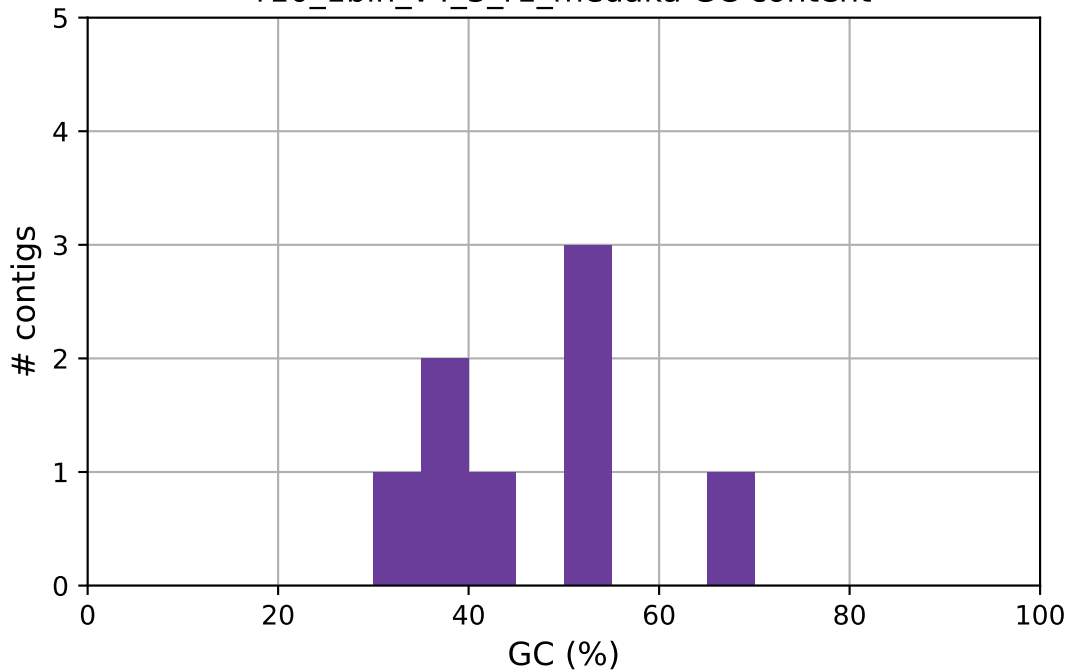
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen GC content



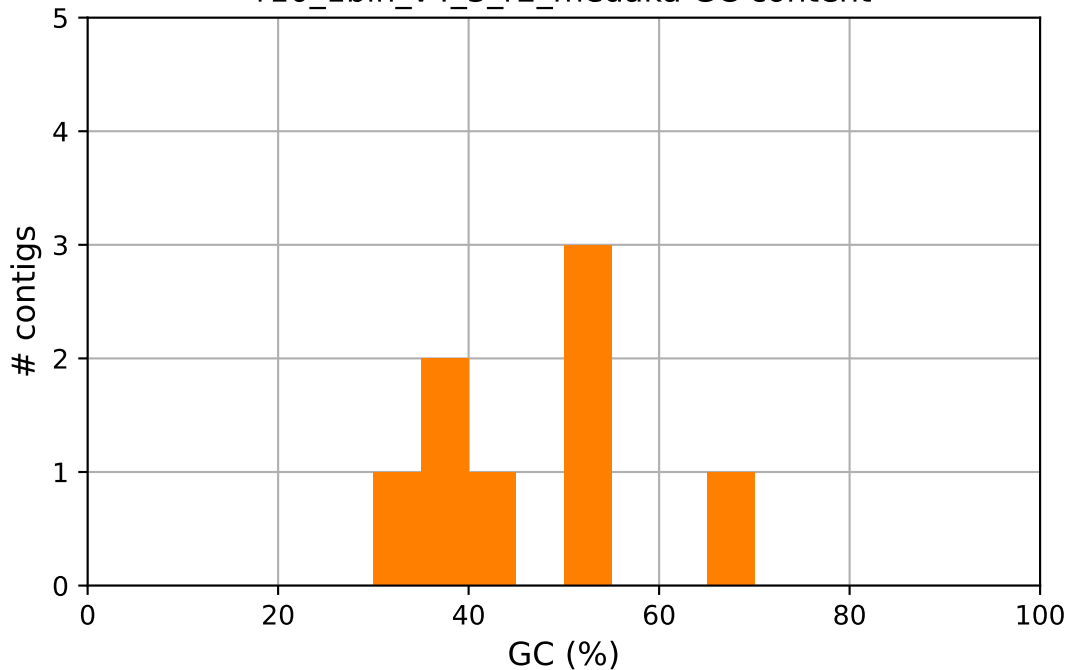
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka GC content



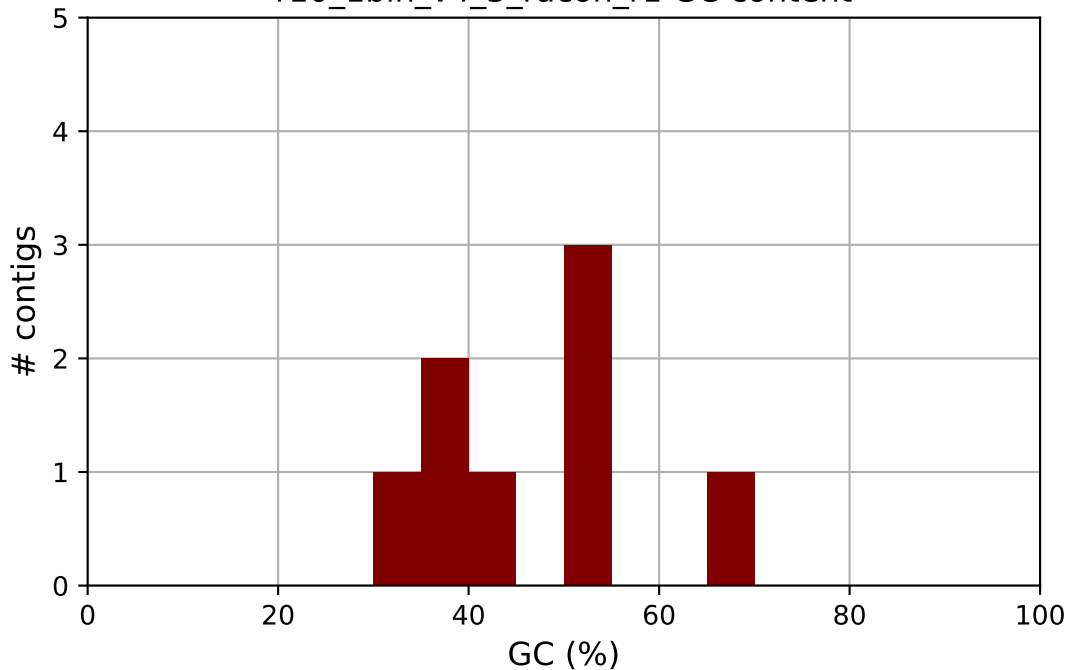
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka GC content



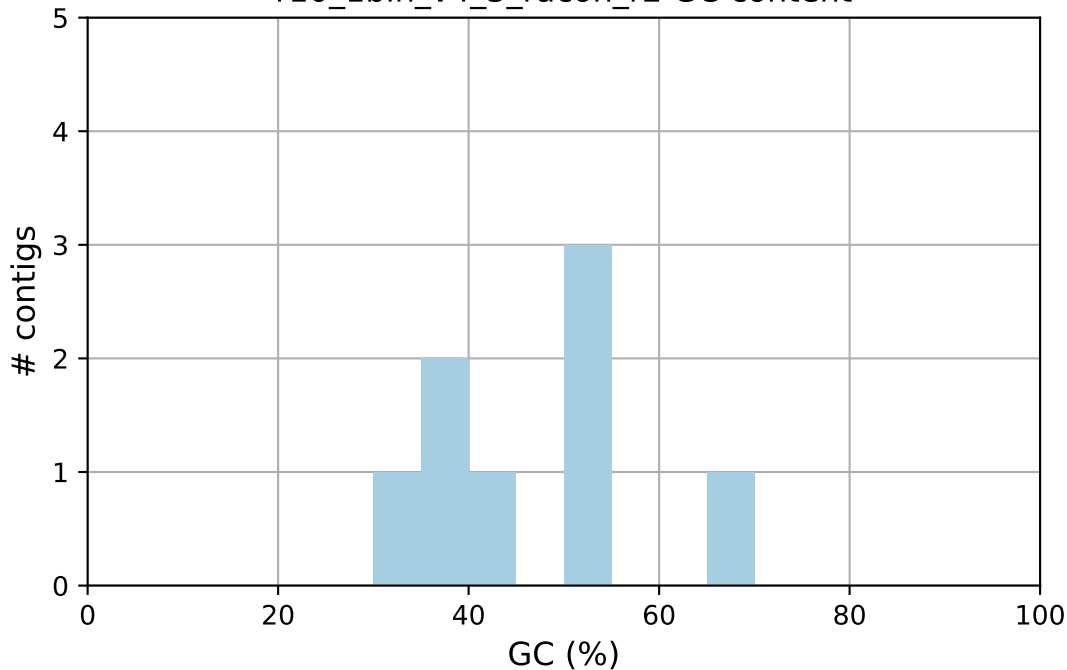
r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1 GC content



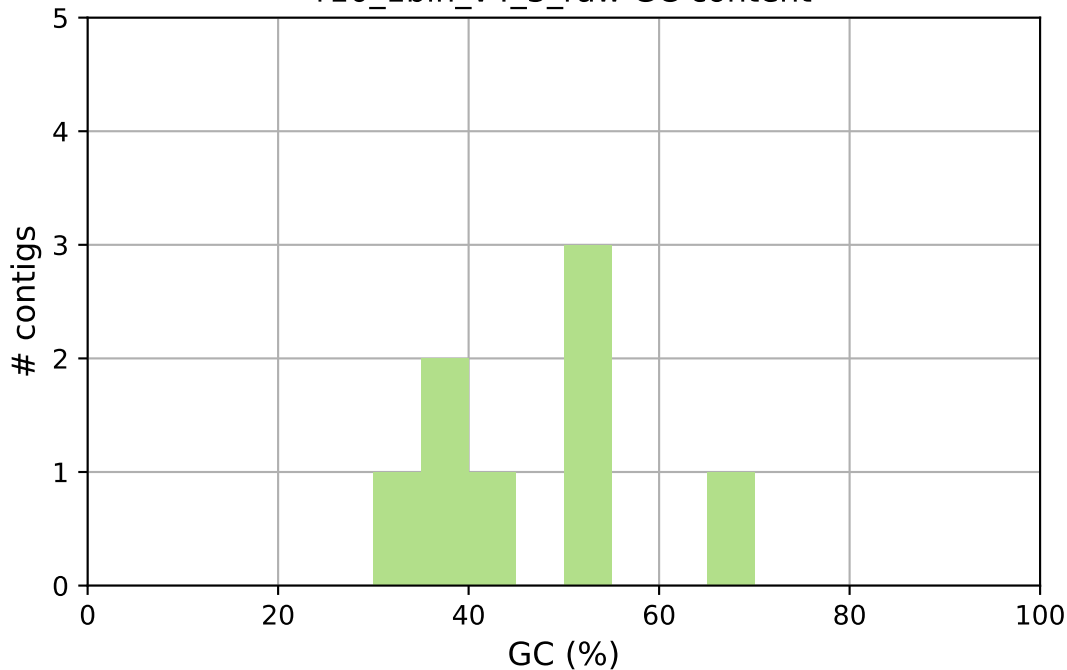
r10_1bin_v4_3_racon_r1

r10_1bin_v4_3_racon_r2 GC content



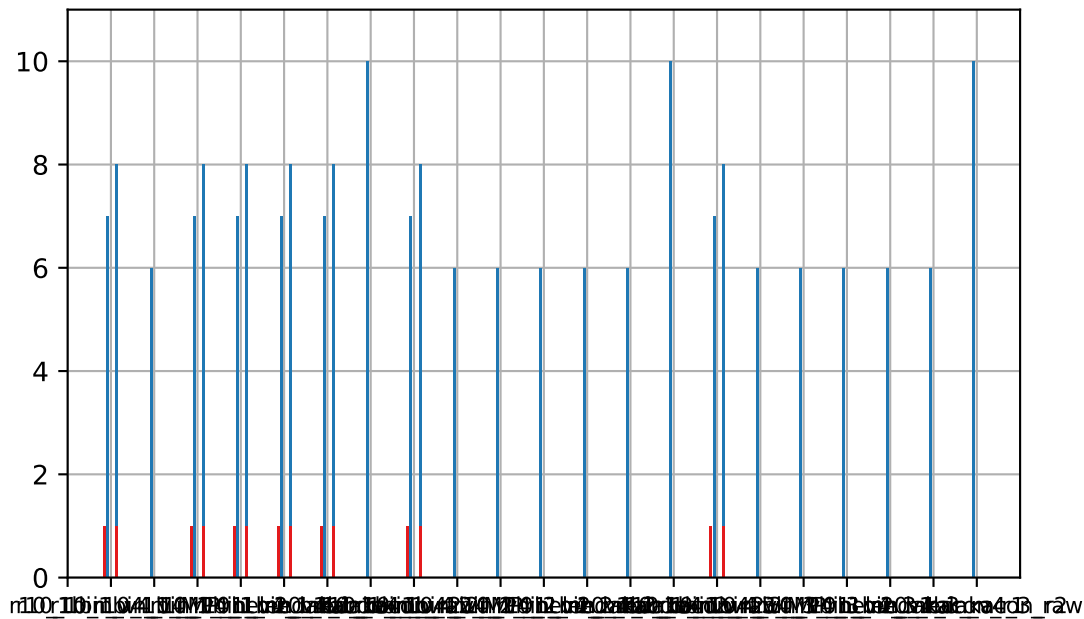
r10_1bin_v4_3_racon_r2

r10_1bin_v4_3_raw GC content



r10_1bin_v4_3_raw

Misassemblies

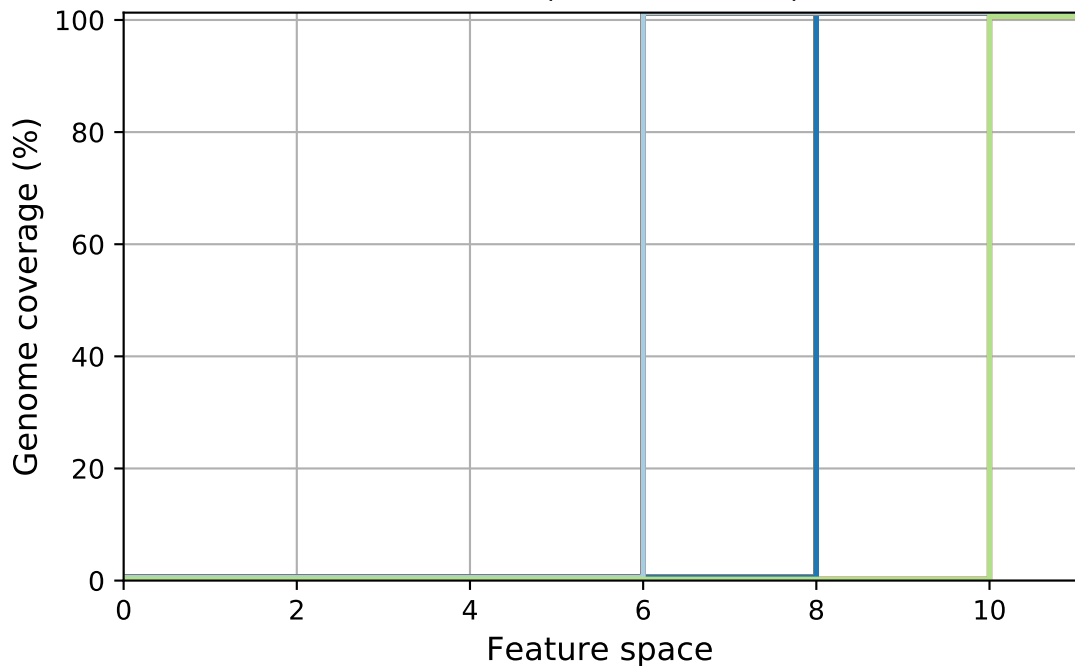


relocations



translocations

FRCurve (misassemblies)



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

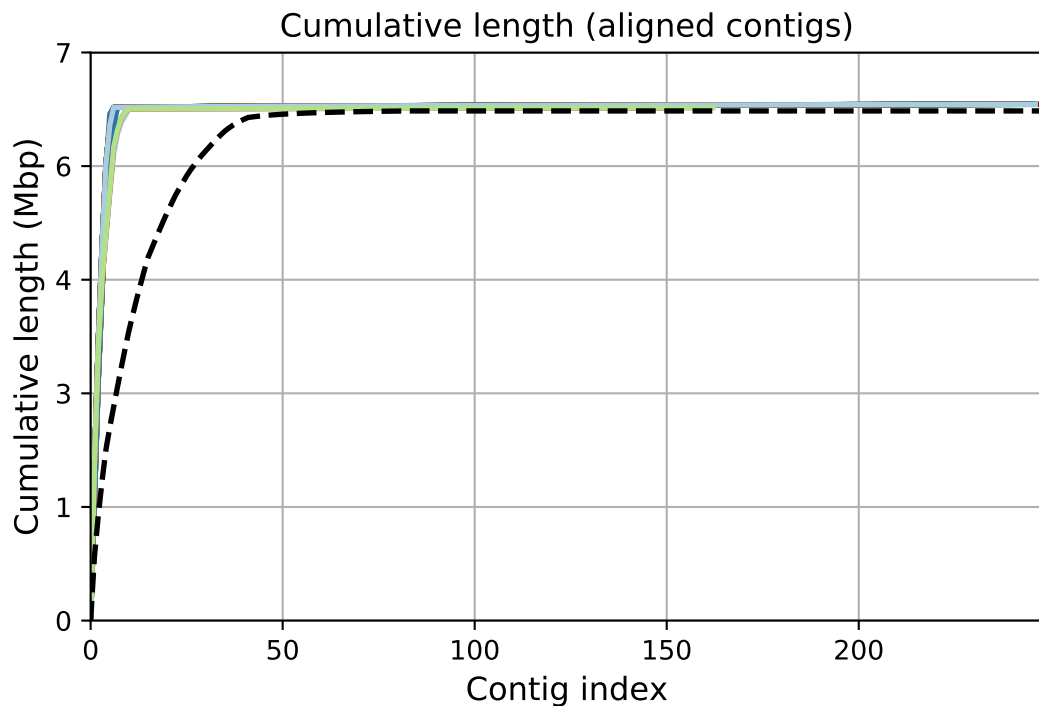
r10_1bin_v4_2_r1_medaka

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

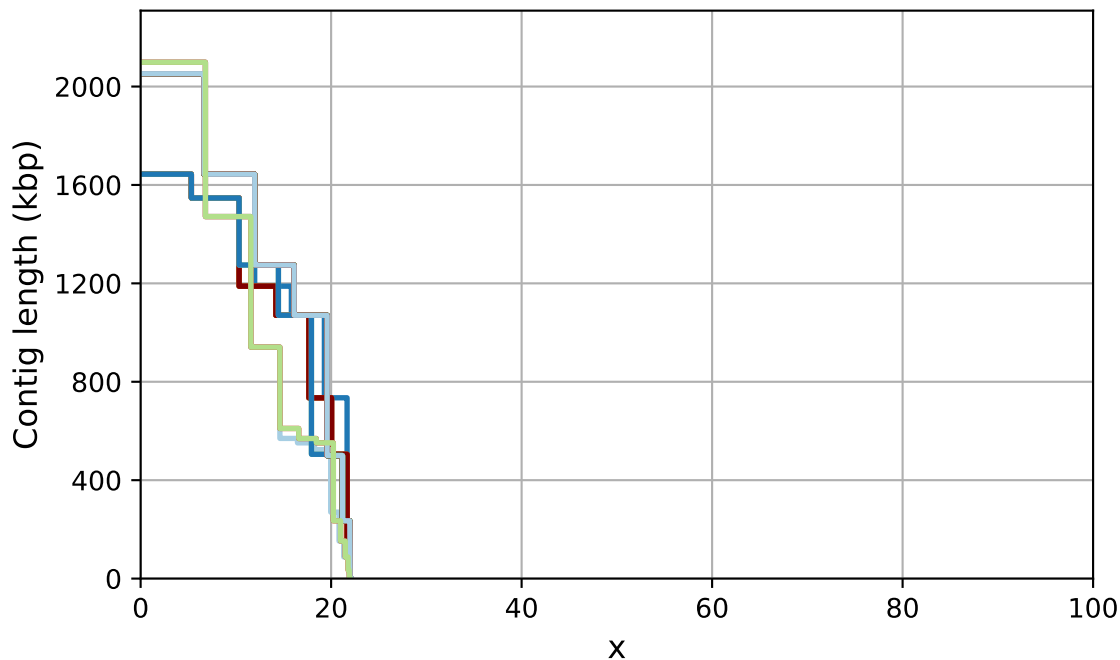
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

NAx



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

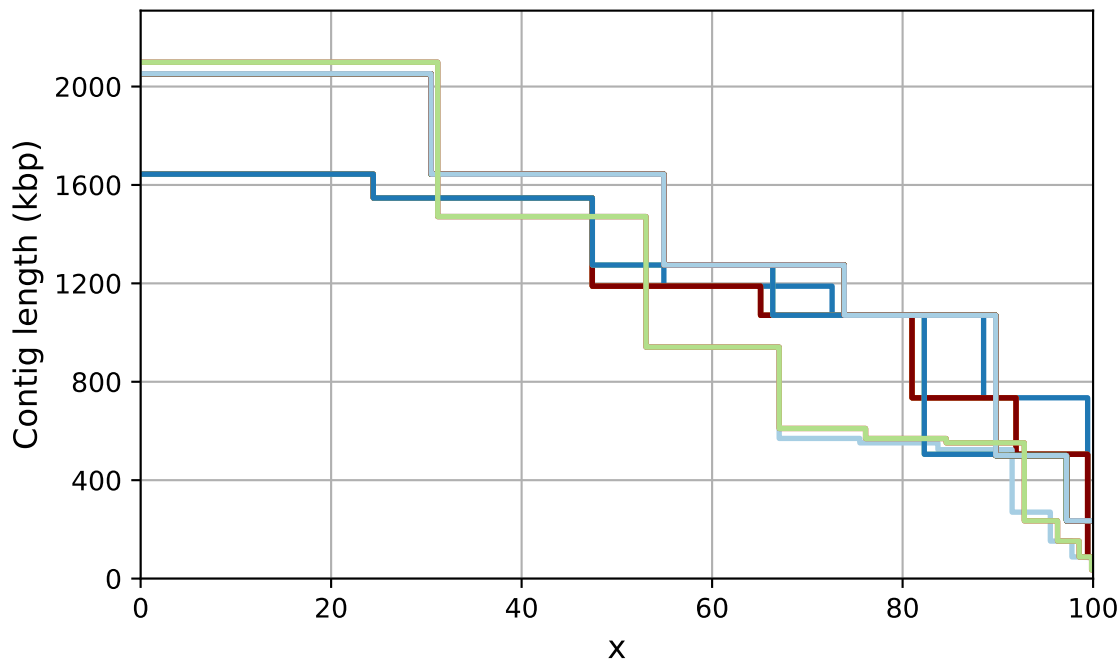
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

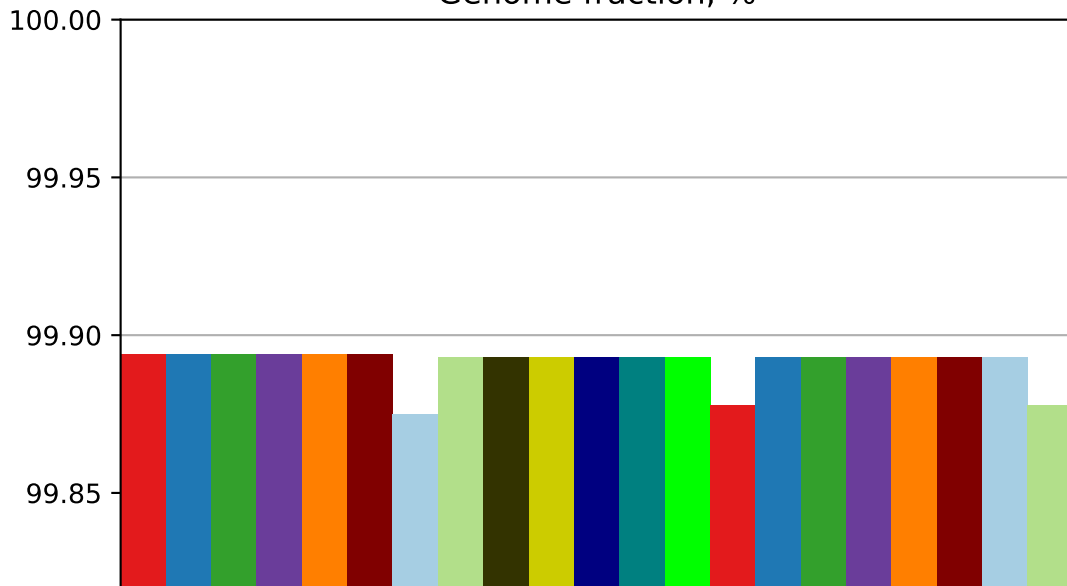
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

NGAx



Genome fraction, %



r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka