

	Report																				
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
Total length	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Reference length	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	51.10	44.80	44.80	44.80	44.80	44.78	44.78	51.10	44.80	44.81	44.80	44.80	44.79	44.79	51.10
Reference GC (%)	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15
N50	4045598	4045624	4045593	4045588	4045161	4045292	4755626	4045604	4045480	4045604	4045608	4045229	4045315	4756102	4045596	4045614	4045597	4045593	4045228	4045344	4755682
NG50	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
N75	2845425	2845362	2845428	2845425	2845303	2845317	2990263	2845427	2845365	2845431	2845433	2845282	2845346	2990631	2845434	2845416	2845426	2845336	2845240	2845336	2990406
NG75	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	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	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# 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	4758918	4757927	4758579	4758111	4757861	4757873	4755626	4758939	4757856	4758583	4758093	4757899	4757820	4756102	4758920	4757780	4758582	4758118	4757872	4757851	4755682
# local misassemblies	8	9	8	8	8	8	28	8	8	8	8	8	8	20	8	8	8	8	8	8	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	6	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	0 + 7 part
Unaligned length	19038396	19033833	19034794	19027982	19021662	19019281	23171792	19037719	19032986	19034729	19024798	19023643	19012064	23176396	19040392	19037087	19041070	19034869	19028086	19024205	23175080
Genome fraction (%)	98.918	98.920	98.920	98.920	98.920	98.920	98.886	98.918	98.918	98.920	98.920	98.920	98.920	98.896	98.918	98.918	98.920	98.920	98.920	98.886	
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.058	1.075	1.075	1.075	1.075	1.075	1.076	1.057	1.075	1.075	1.074	1.074	1.075	1.058	
# N's per 100 kbp	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	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	411.02	408.37	410.28	409.37	417.43	415.19	467.00	411.11	409.72	409.77	408.92	412.72	422.24	461.59	408.93	408.57	404.25	406.61	416.47	415.71	466.72
# indels per 100 kbp	20.44	15.39	11.50	11.40	40.12	37.92	220.52	20.76	15.90	11.50	11.37	39.88	38.22	224.89	20.47	16.13	11.29	11.14	40.65	38.45	220.60
Largest alignment	1342515	1342456	1342472	1342474	1342282	1342315	1341035	1342502	1342444	1342470	1342472	1342248	1342303	1341458	1342515	1342456	1342469	1342476	1342260	1342299	1341035
Total aligned length	5034126	5033226	5034861	5031472	5035986	5034340	4955673	5034344	5034398	5034745	5033733	5033814	5038059	4951661	5032811	5032729	5031701	5032382	5034711	5034049	4955540
NGA50	745380	745348	745366	745365	745247	745284	745147	745393	745369	745369	745369	745249	745249	744999	745380	745347	745370	745370	745267	745280	745146
NGA75	611517	611510	611515	611516	611431	611452	407847	611514	611510	611514	611515	611430	611437	433871	611519	611509	611518	611516	611423	611452	407847
LGA50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LGA75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5

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_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# misassemblies	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# contig misassemblies	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# 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	13	13	13	13	13	13	17	13	14	13	13	13	13	16	13	14	13	13	13	13	17
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	4758918	4757927	4758579	4758111	4757861	4757873	4755626	4758939	4757856	4758583	4758093	4757899	4757820	4756102	4758920	4757780	4758582	4758118	4757872	4757851	4755682
# 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	6	4	4	4	4	4	18	6	4	4	4	4	4	14	6	4	4	4	4	4	18
# local misassemblies	8	9	8	8	8	8	28	8	8	8	8	8	8	20	8	8	8	8	8	8	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	14	14	14	14	14	14	8	14	14	14	14	14	14	11	14	14	14	14	14	14	7
# 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	19260	19136	19226	19183	19561	19456	21876	19264	19199	19202	19162	19340	19786	21625	19162	19145	18943	19054	19516	19480	21863
# indels	958	721	539	534	1880	1777	10330	973	745	539	533	1869	1791	10536	959	756	529	522	1905	1802	10334
# indels (<= 5 bp)	863	624	449	443	1788	1687	10161	877	645	449	443	1779	1701	10360	864	656	440	433	1812	1710	10164
# indels (> 5 bp)	95	97	90	91	92	90	169	96	100	90	90	90	90	176	95	100	89	89	93	92	170
Indels length	5483	5303	4971	4987	6482	6330	18477	5519	5271	4972	4965	6458	6344	19243	5482	5307	4955	4945	6526	6366	18535

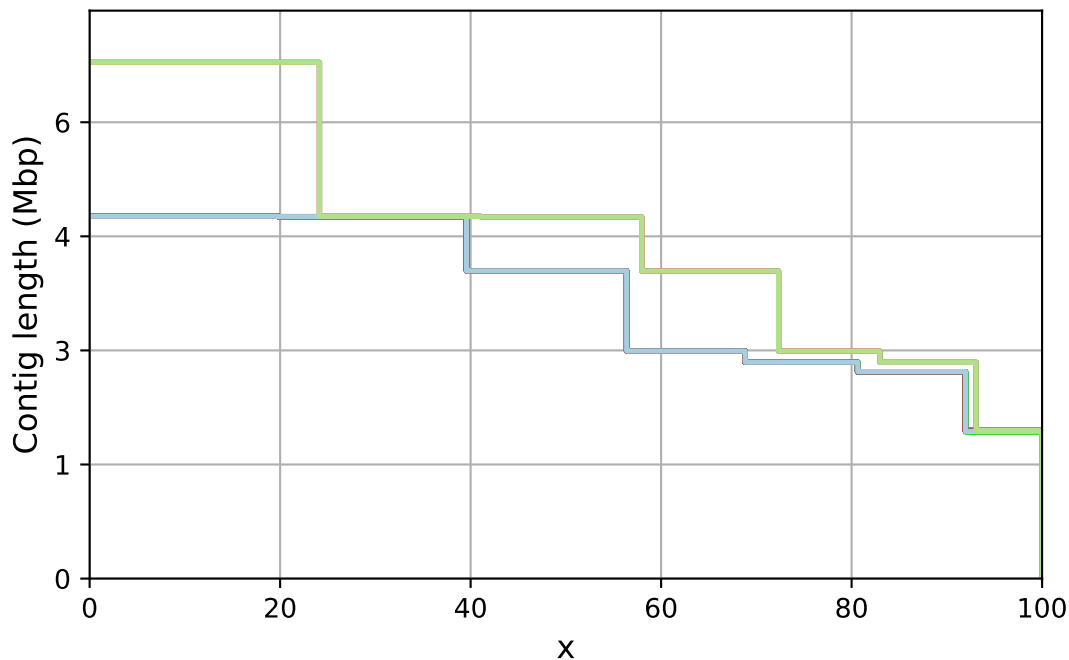
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19038396	19033833	19034794	19027982	19021662	19019281	23171792	19037719	19032986	19034729	19024798	19023643	19012064	23176396	19040392	19037087	19041070	19034869	19028086	19024205	23175080
# 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_v2_1_MP

r10_1bin_v2_2_MP

r10_1bin_v2_3_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_2_MP_helen

r10_1bin_v2_3_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_2_r1_medaka

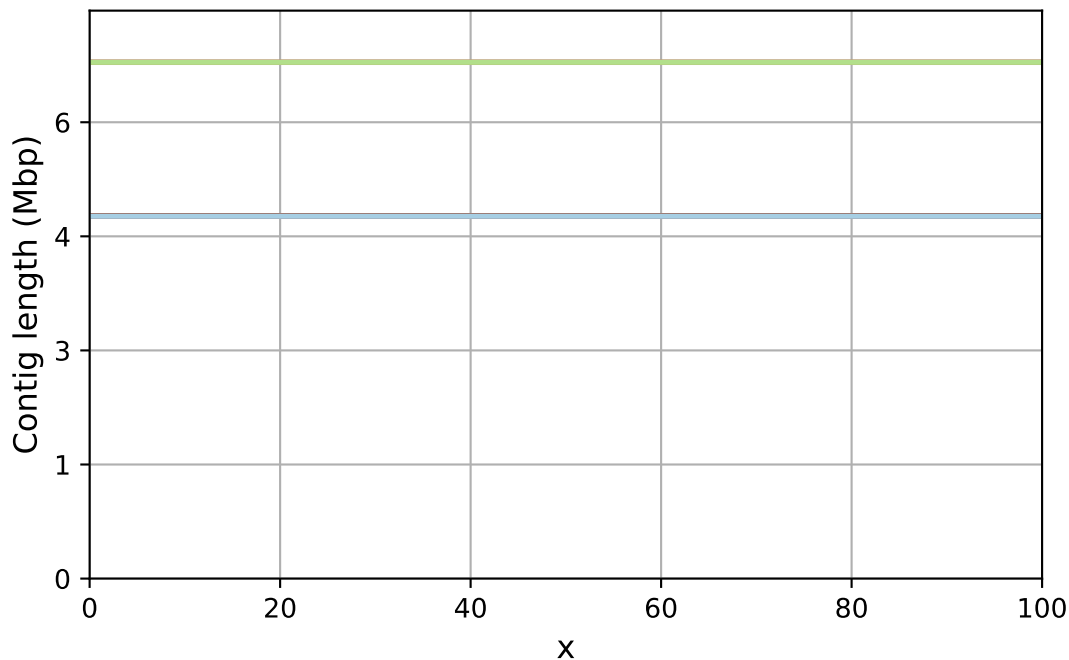
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_1_r2_medaka

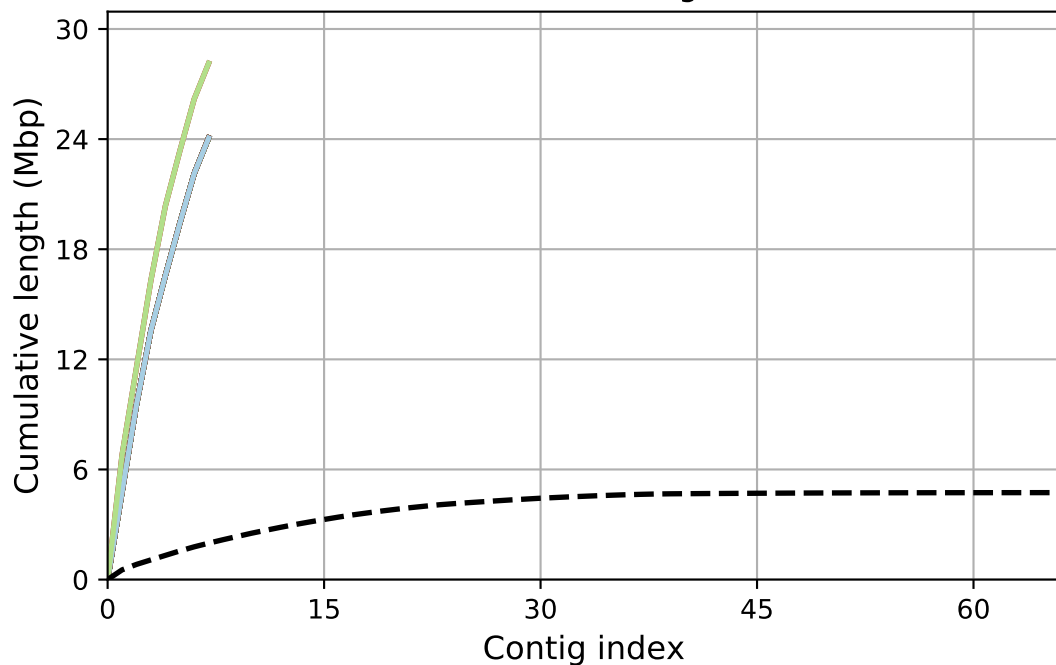
r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_r2_medaka

NGx



Cumulative length



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1

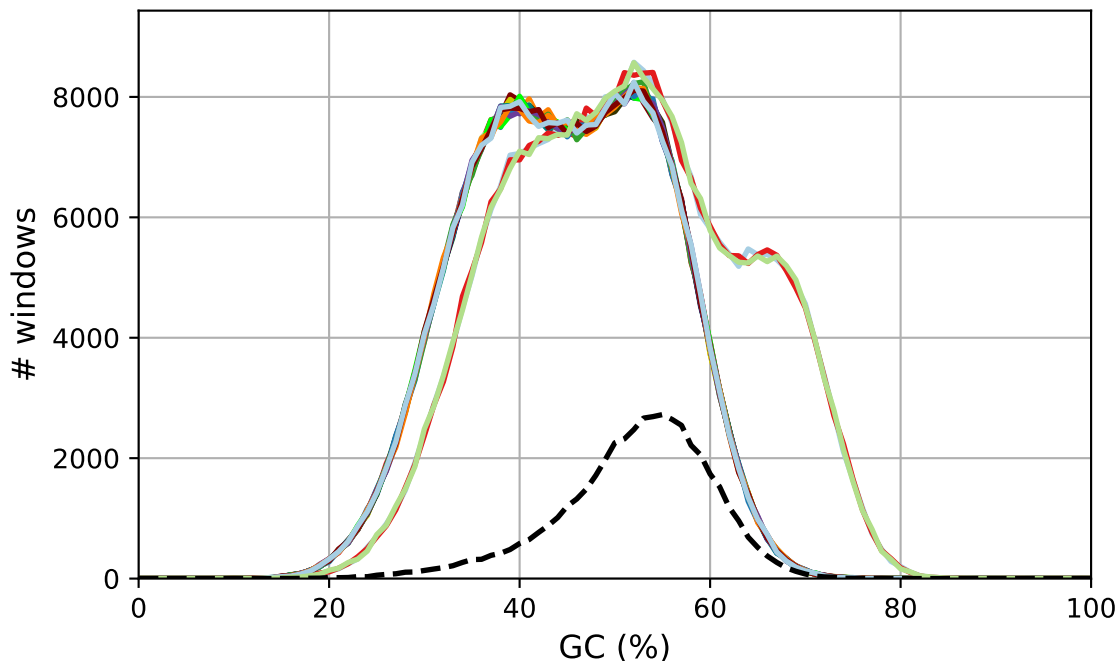
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1

GC content



r10_1bin_v2_1_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_3_MP_h

r10_1bin_v2_1_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_3_r1_m

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_2_r2_medaka

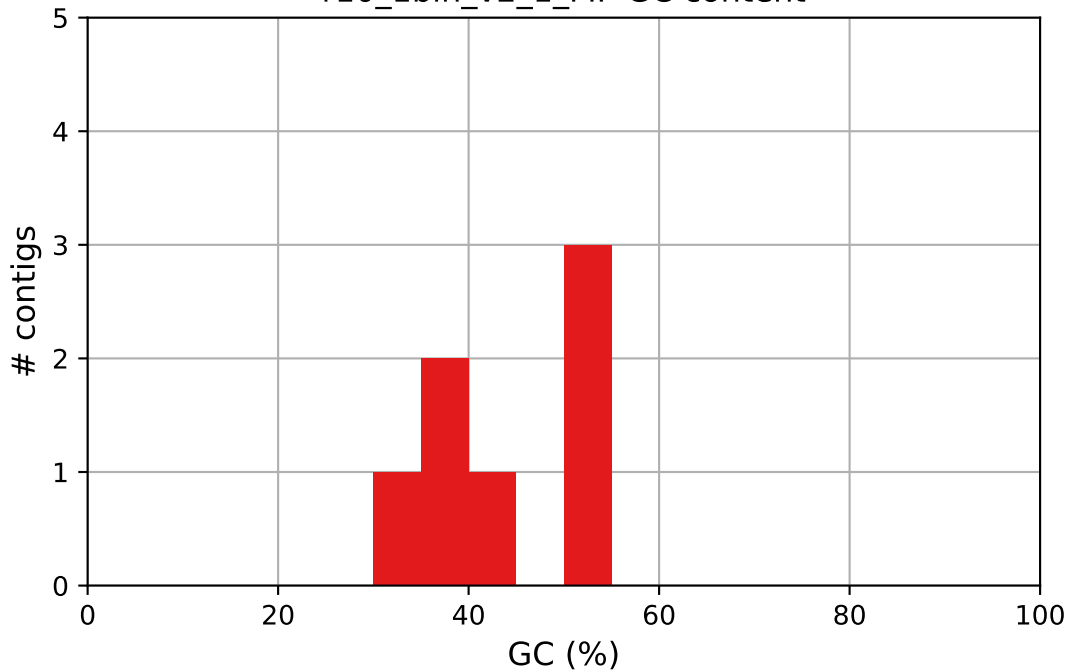
r10_1bin_v2_3_r2_m

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_racon_r1

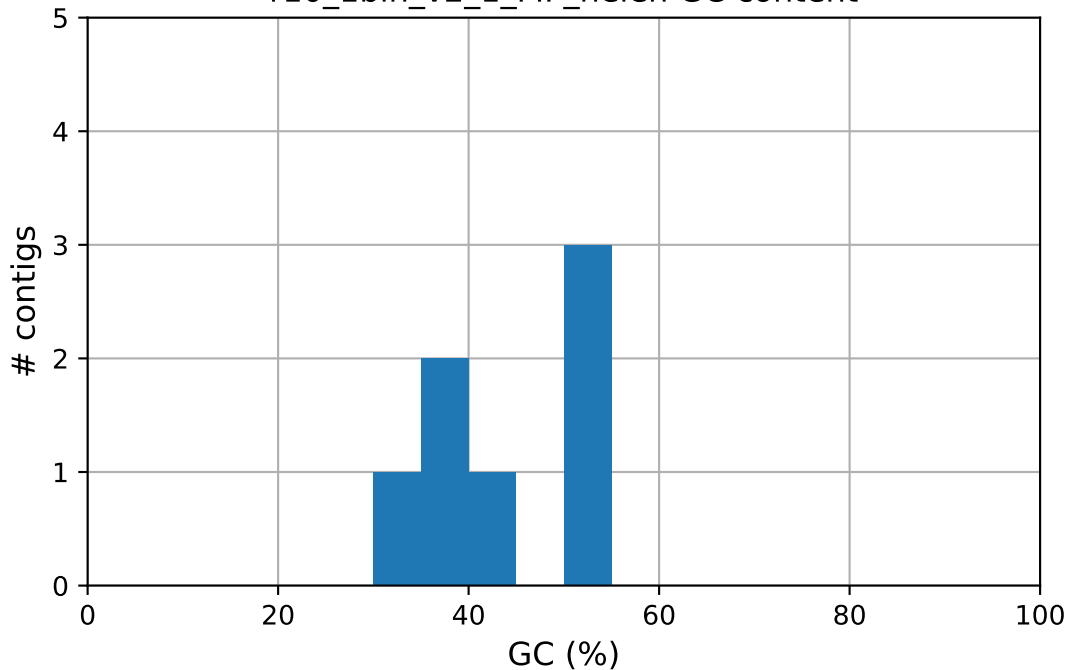
r10_1bin_v2_3_racon_r1

r10_1bin_v2_1_MP GC content



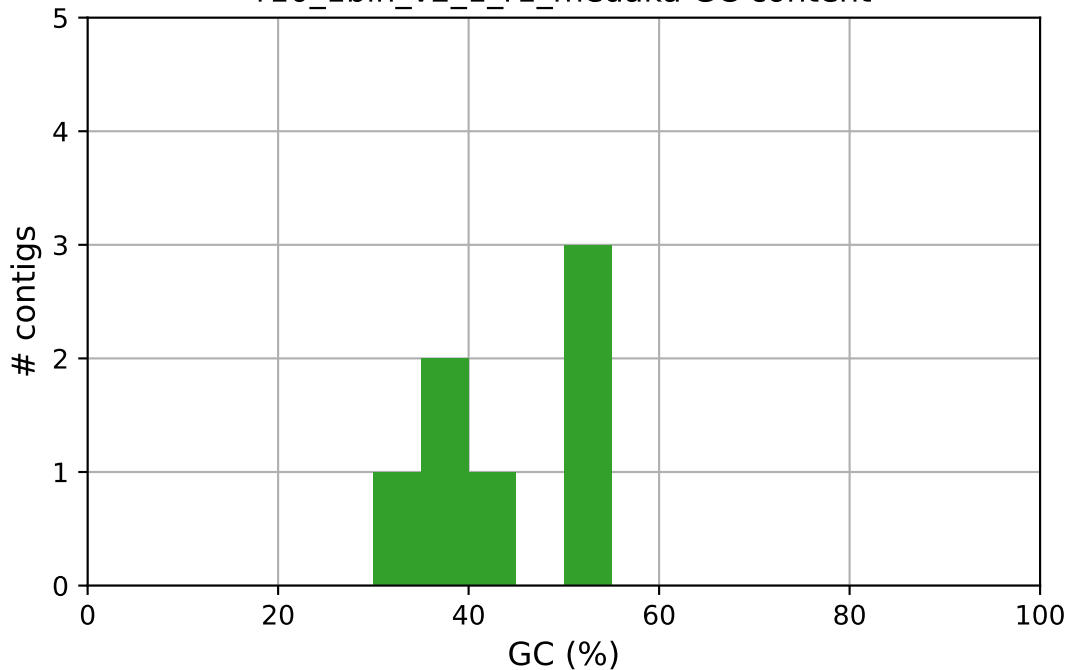
r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen GC content



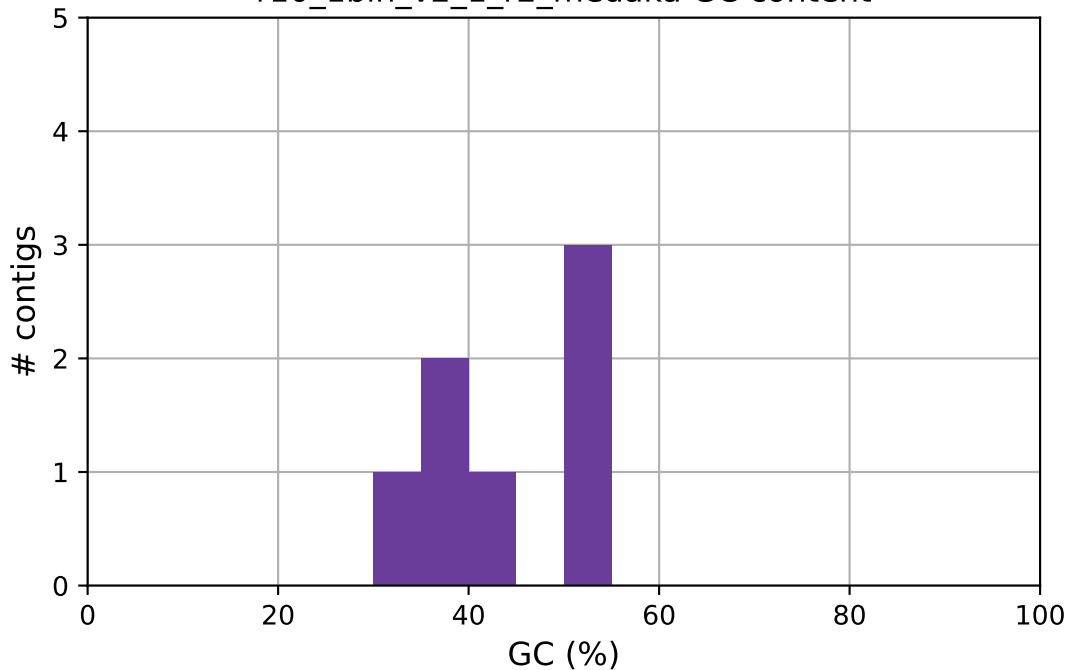
r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka GC content



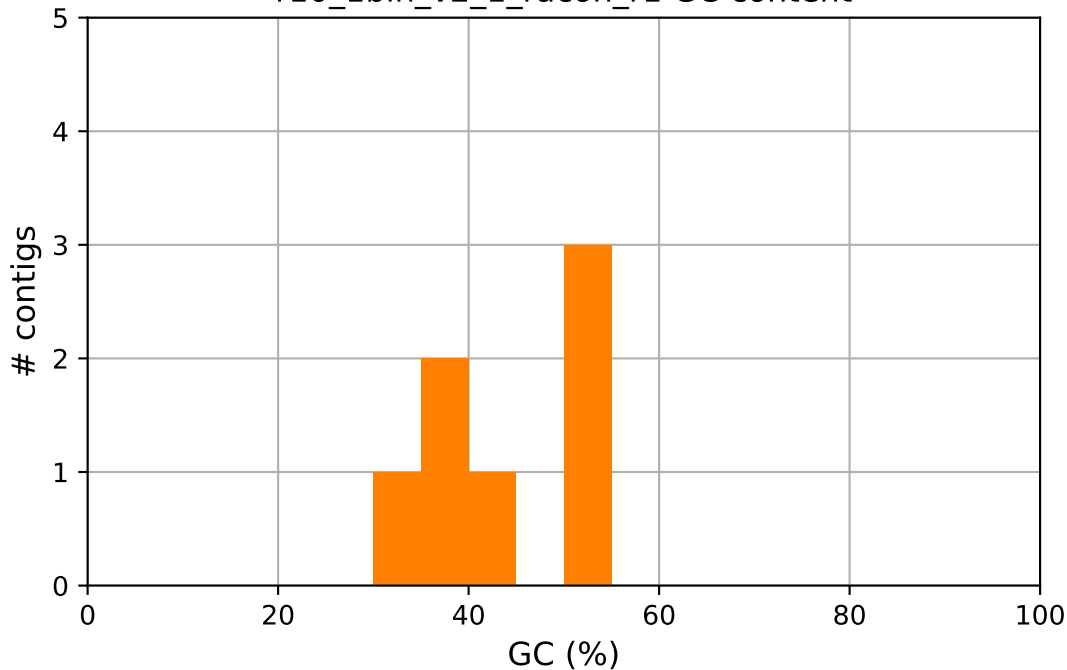
r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka GC content



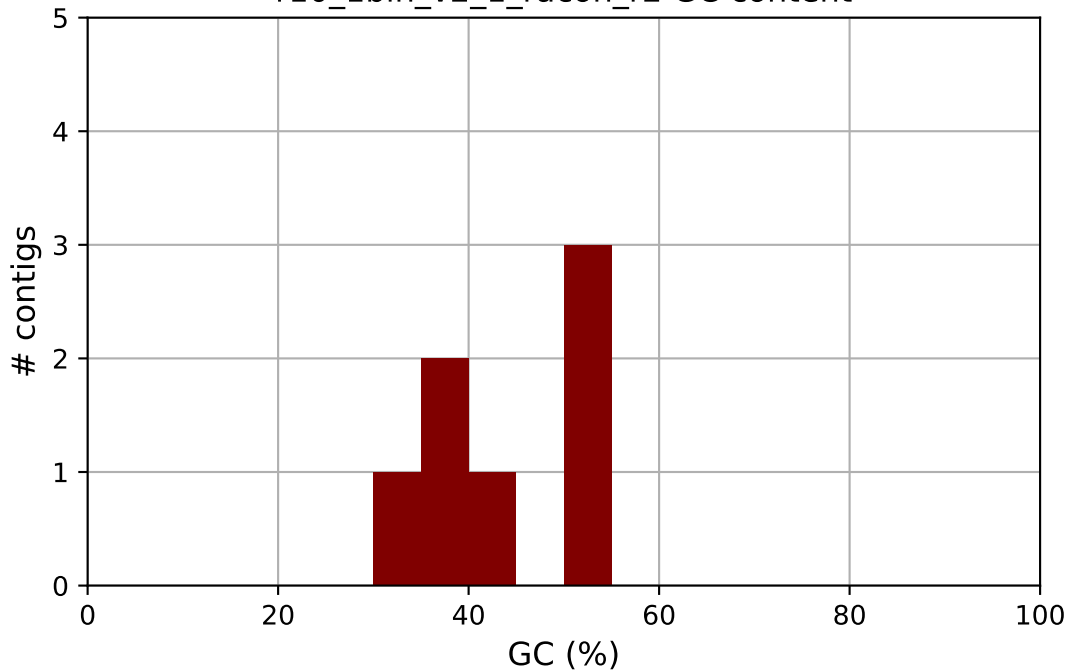
r10_1bin_v2_1_r2_medaka

r10_1bin_v2_1_racon_r1 GC content



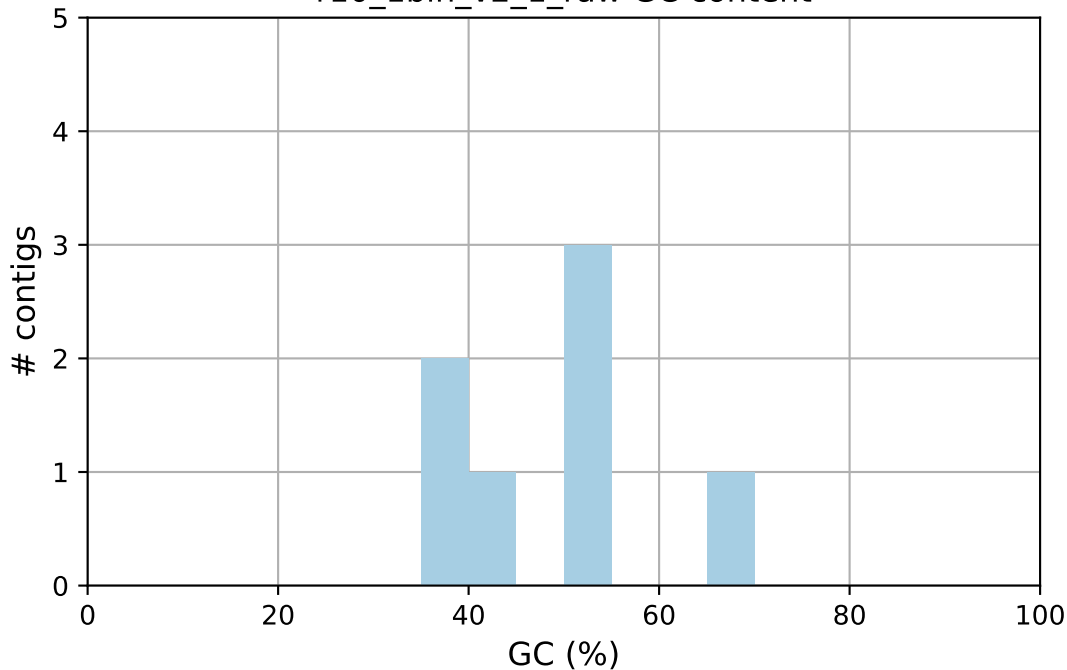
r10_1bin_v2_1_racon_r1

r10_1bin_v2_1_racon_r2 GC content



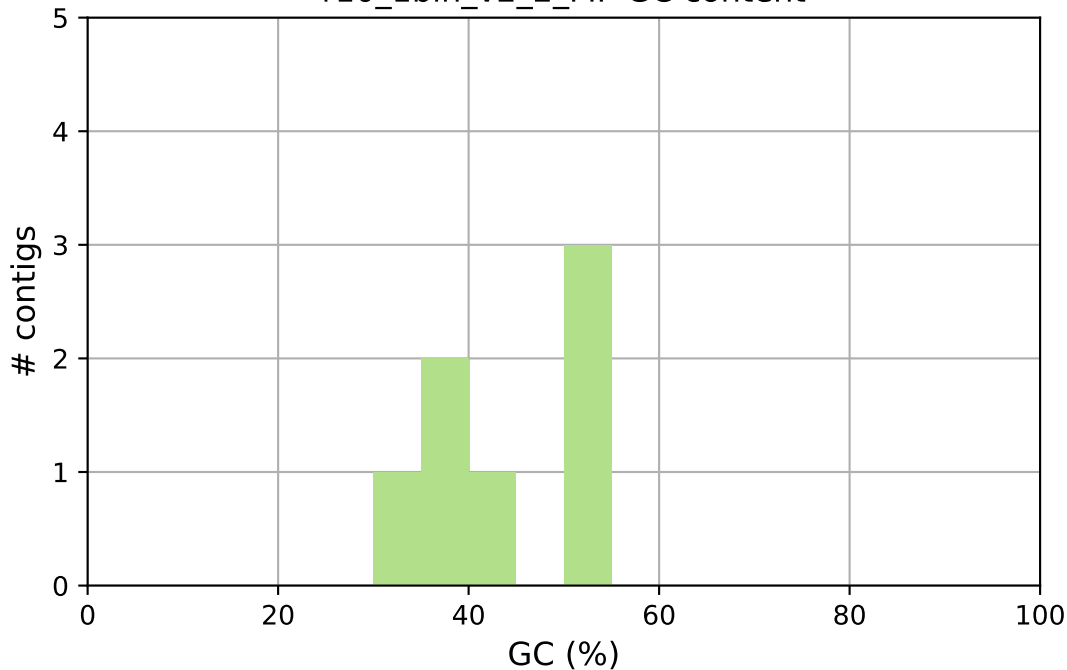
r10_1bin_v2_1_racon_r2

r10_1bin_v2_1_raw GC content



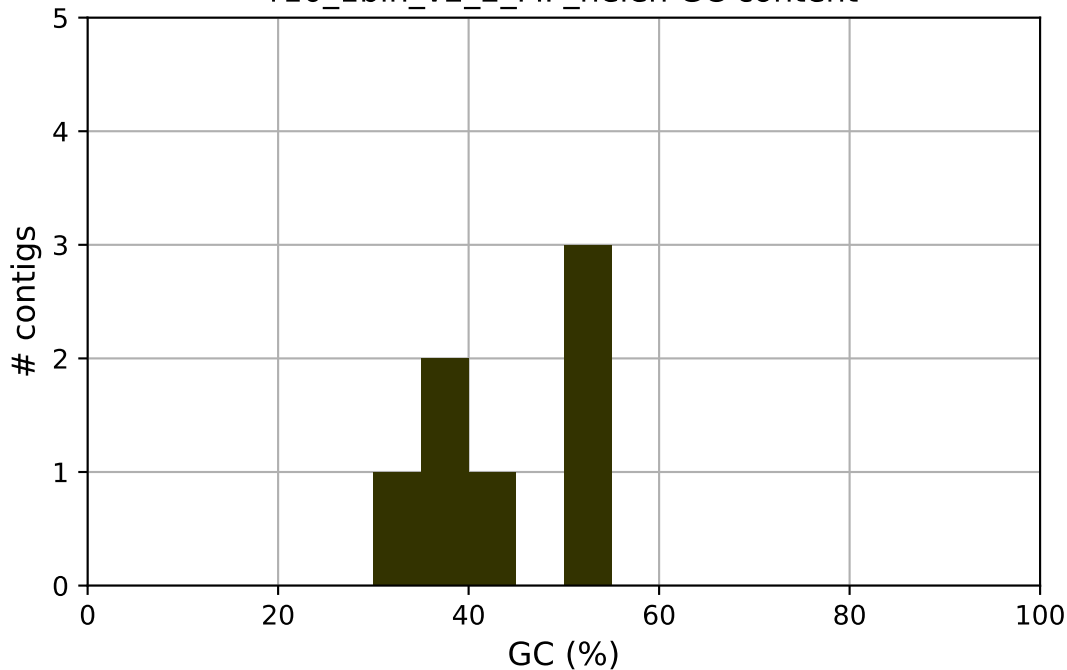
r10_1bin_v2_1_raw

r10_1bin_v2_2_MP GC content



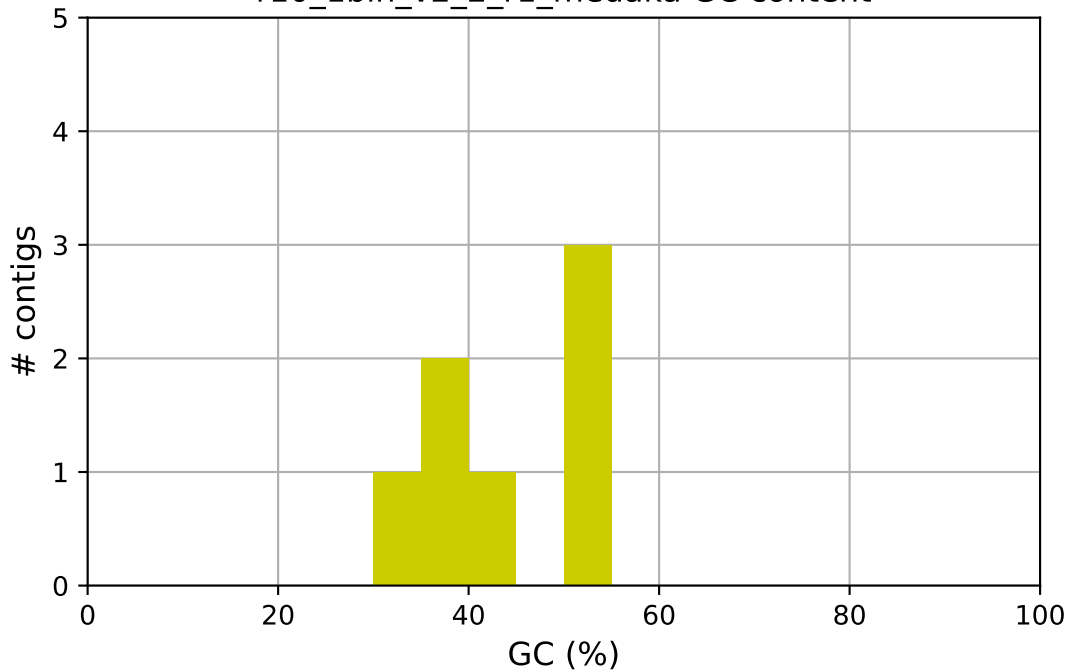
r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen GC content



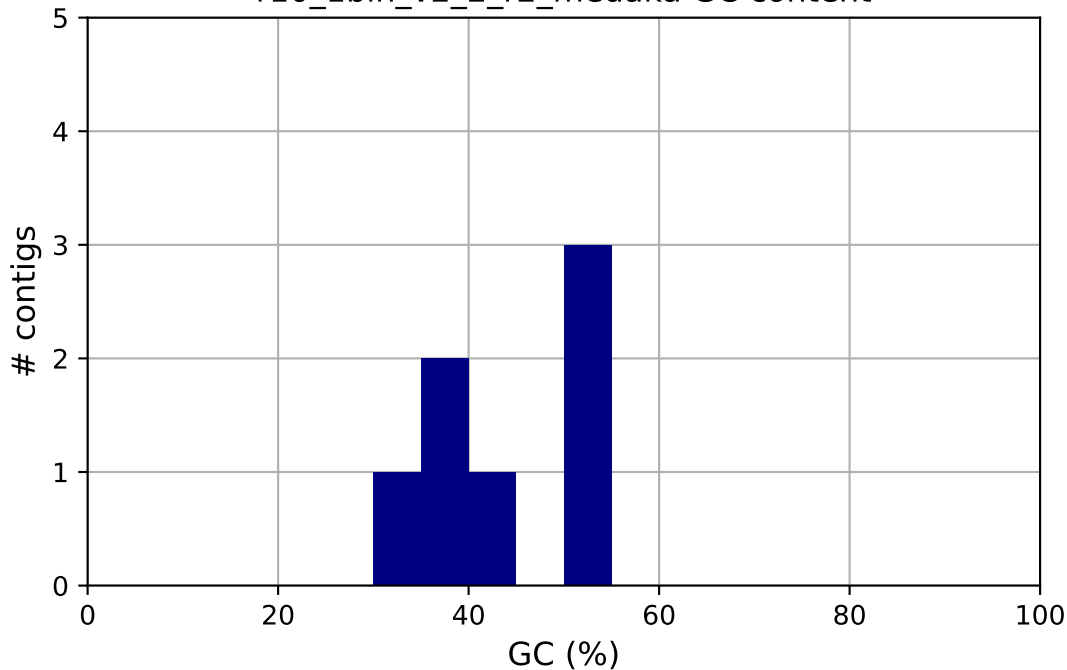
r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka GC content



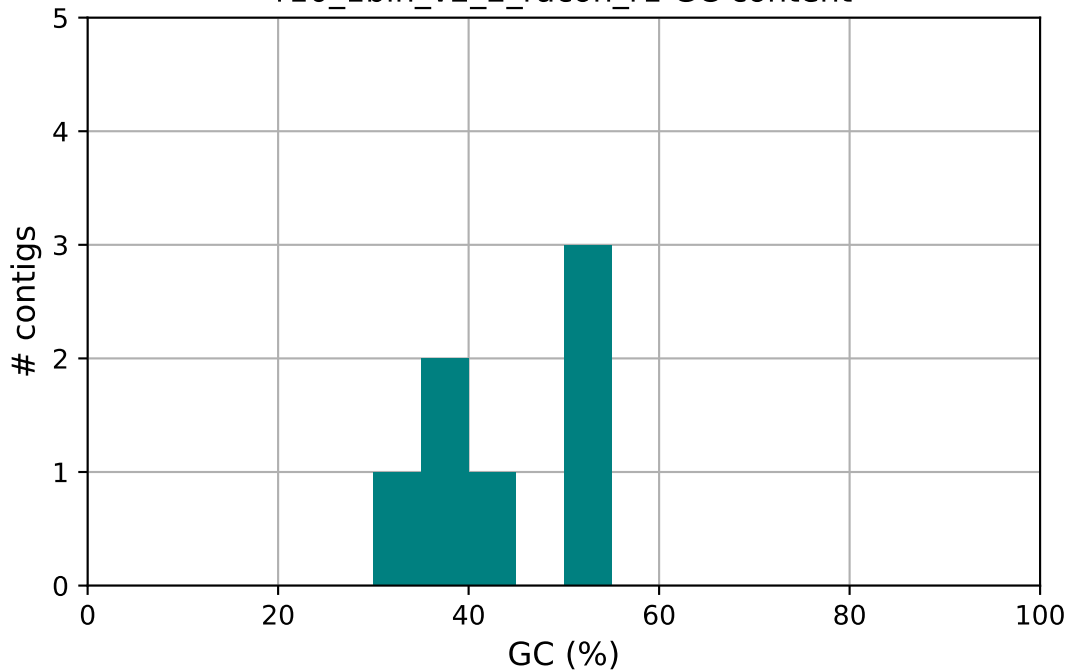
r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka GC content



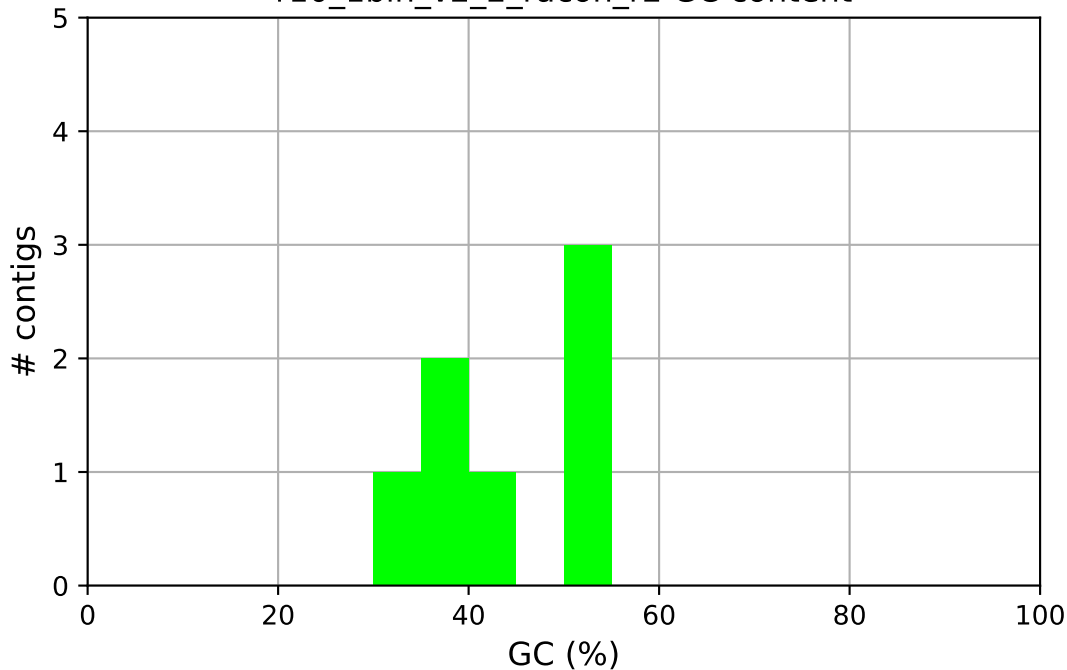
r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1 GC content



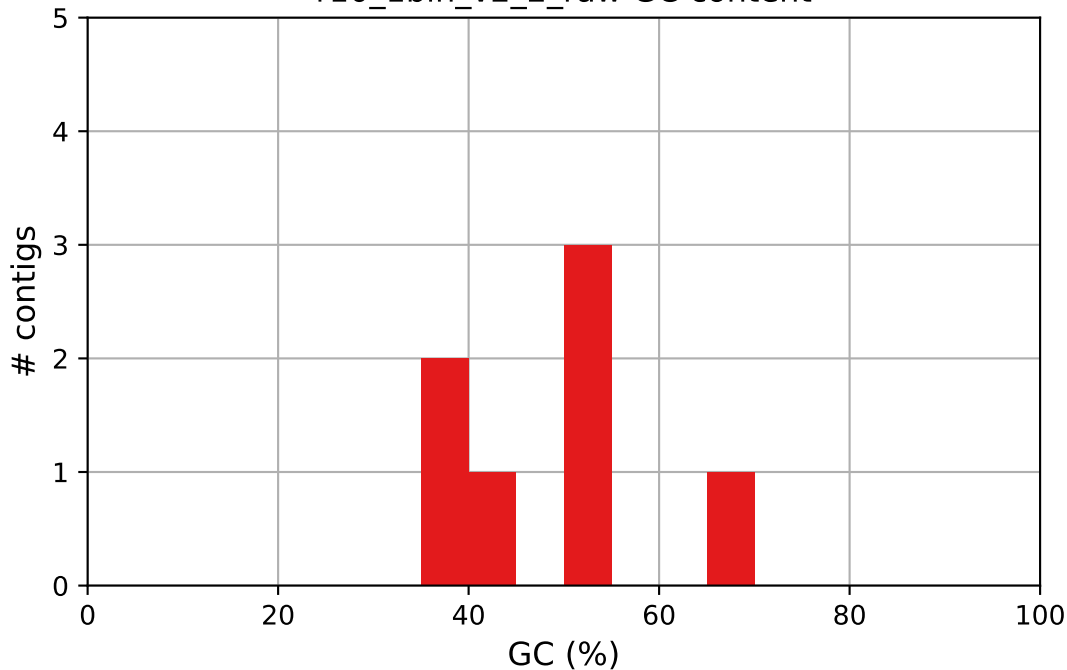
r10_1bin_v2_2_racon_r1

r10_1bin_v2_2_racon_r2 GC content



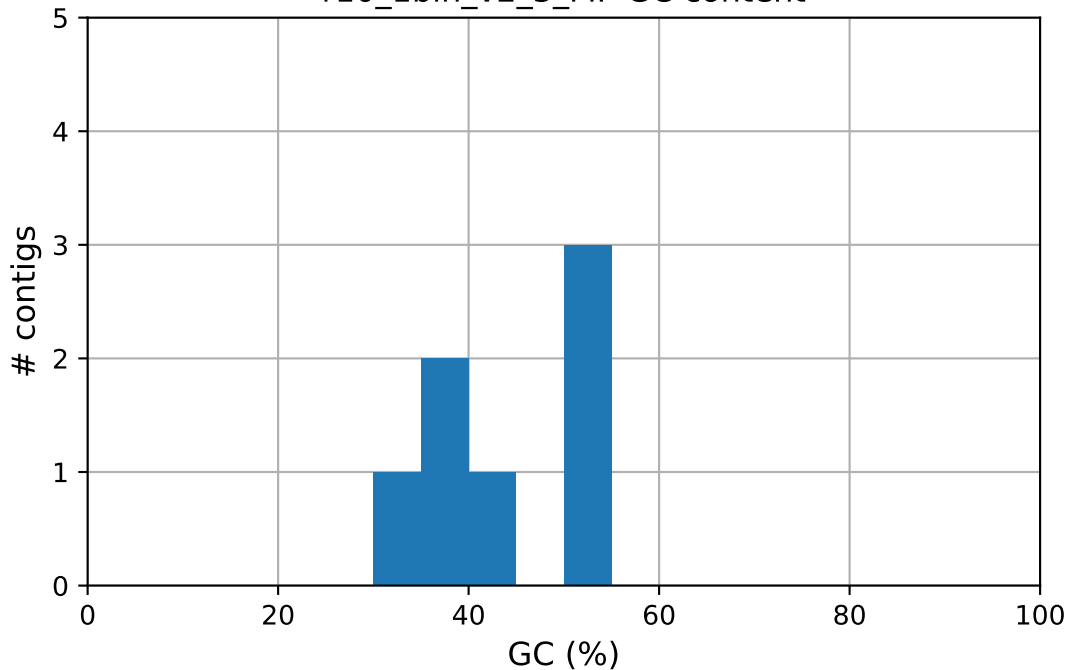
r10_1bin_v2_2_racon_r2

r10_1bin_v2_2_raw GC content



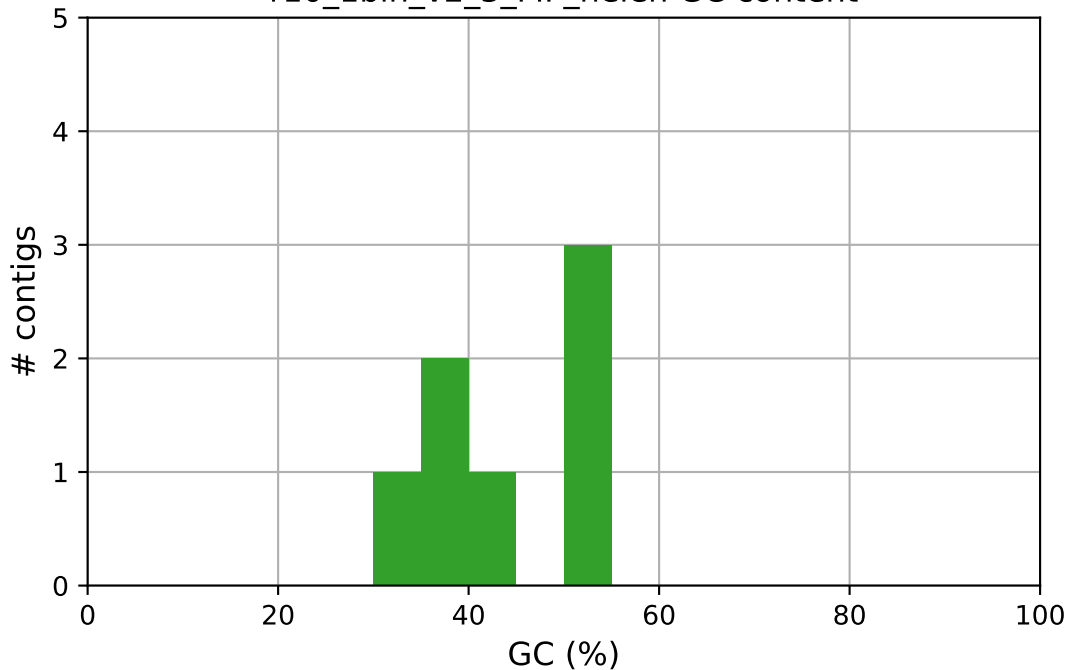
r10_1bin_v2_2_raw

r10_1bin_v2_3_MP GC content



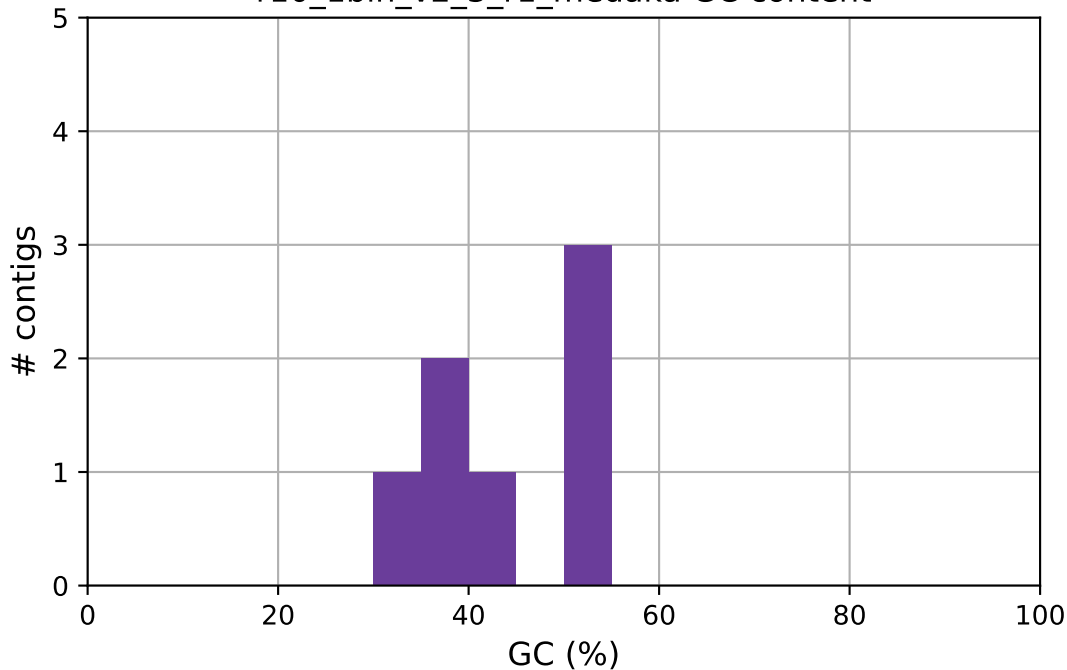
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen GC content



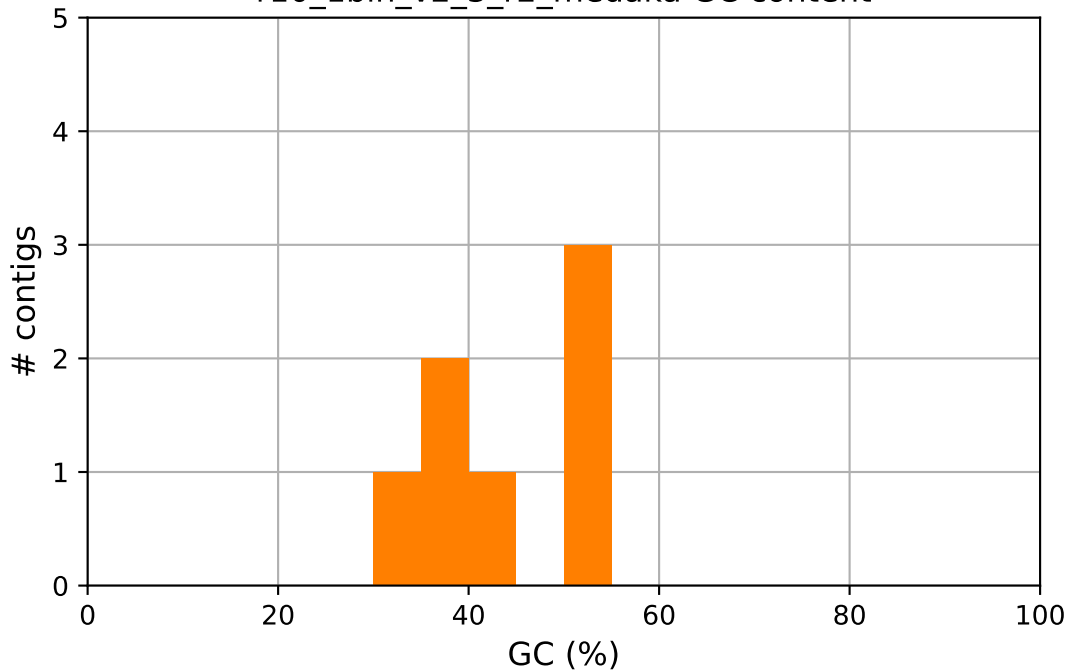
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka GC content



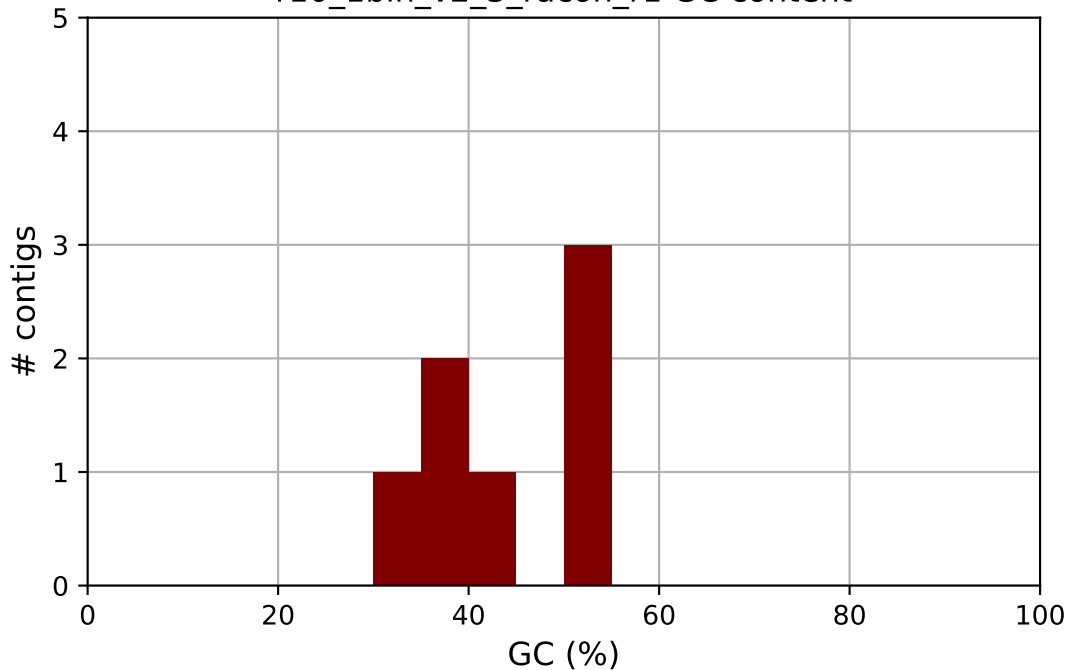
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka GC content



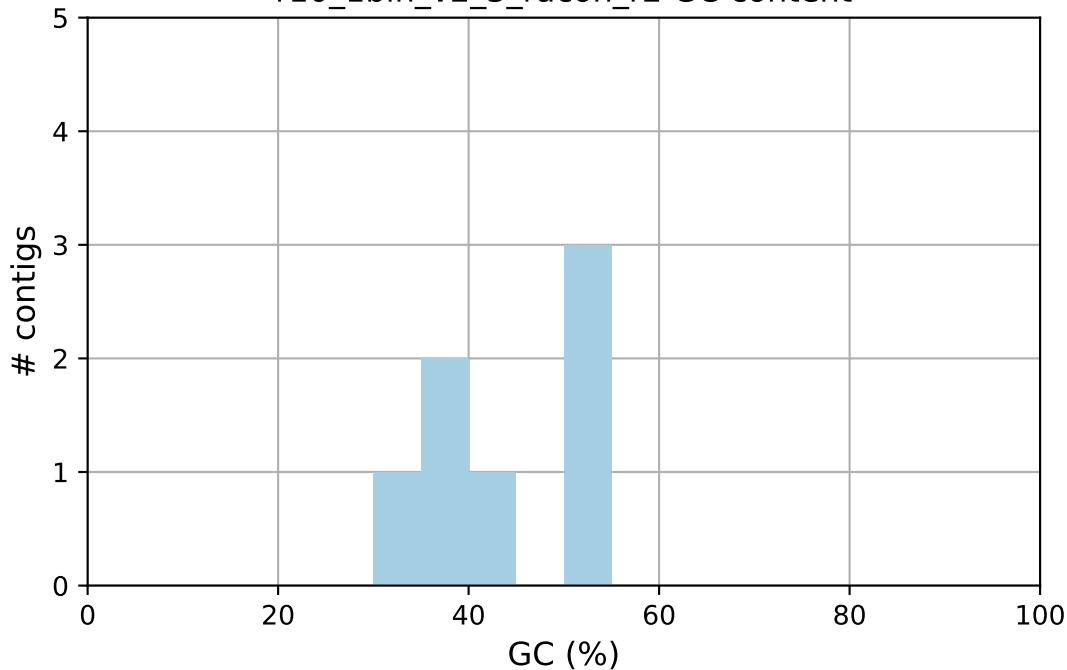
r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1 GC content



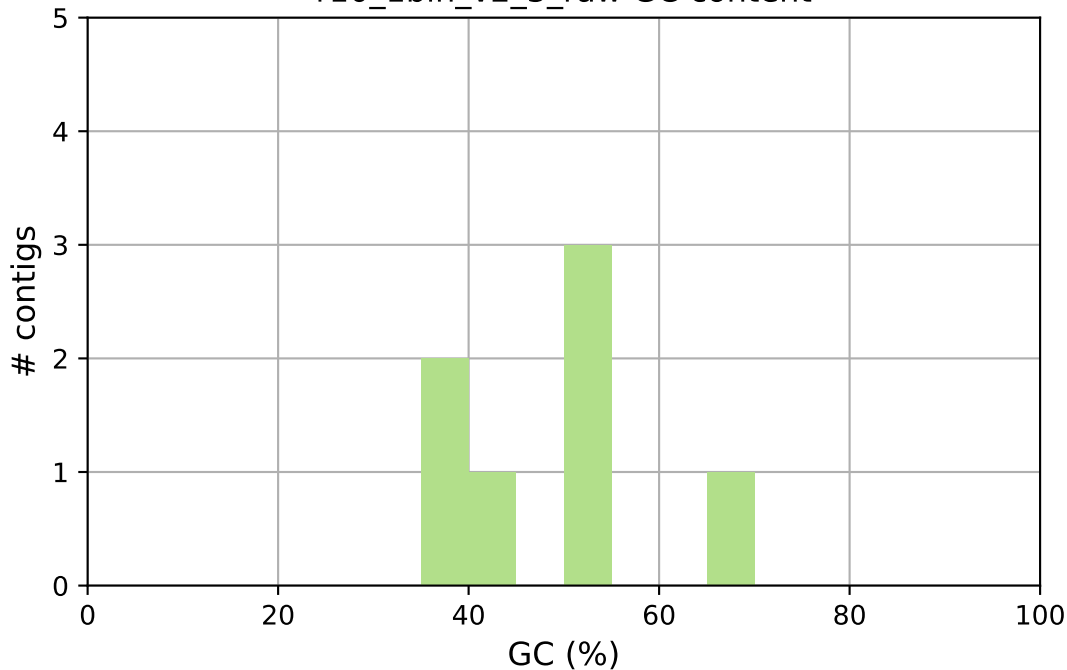
r10_1bin_v2_3_racon_r1

r10_1bin_v2_3_racon_r2 GC content



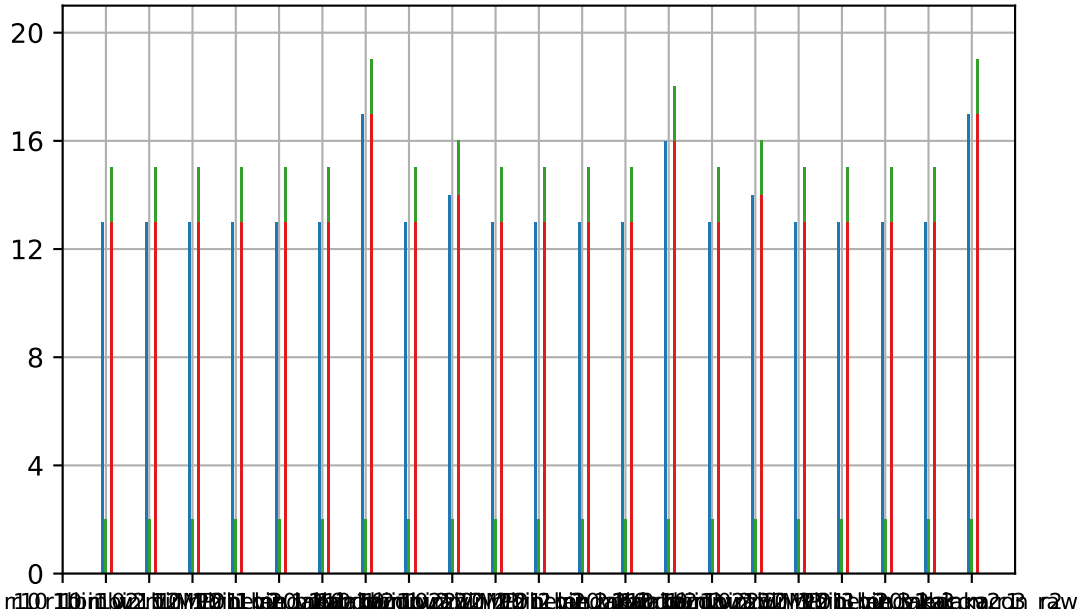
r10_1bin_v2_3_racon_r2

r10_1bin_v2_3_raw GC content



r10_1bin_v2_3_raw

Misassemblies



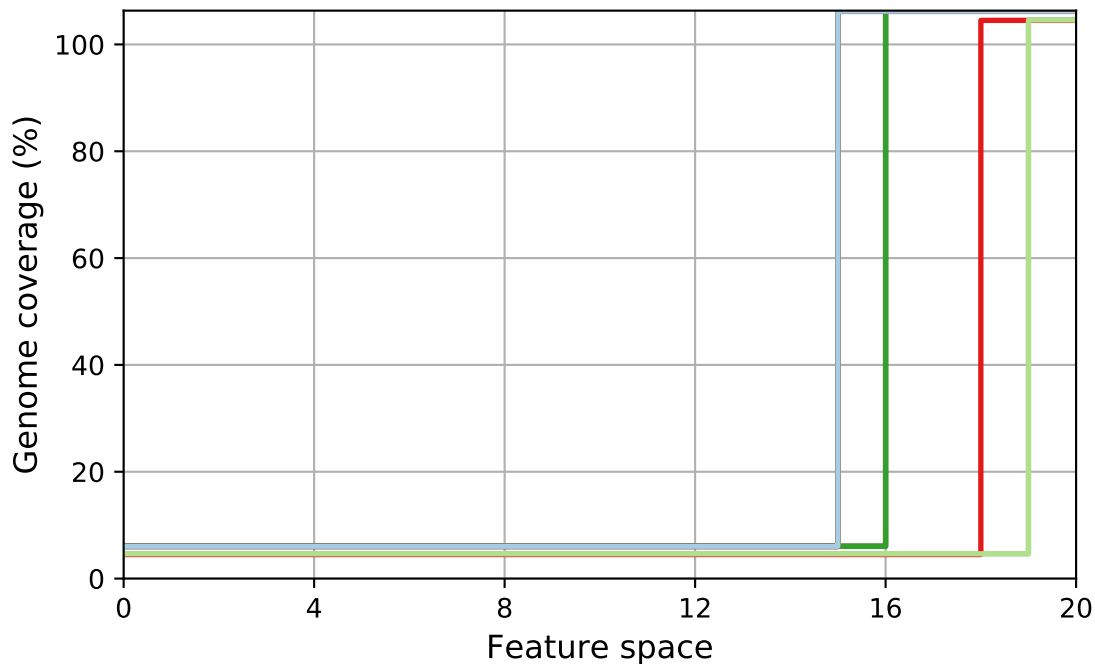
10

translocations



inversions

FRCurve (misassemblies)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

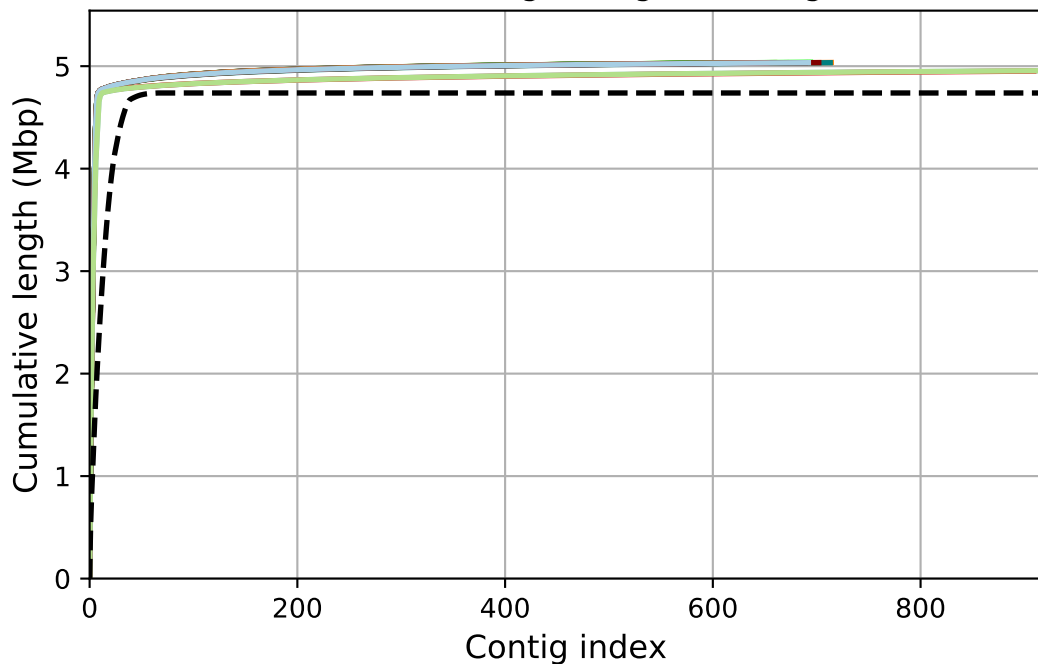
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_2_racon_r1

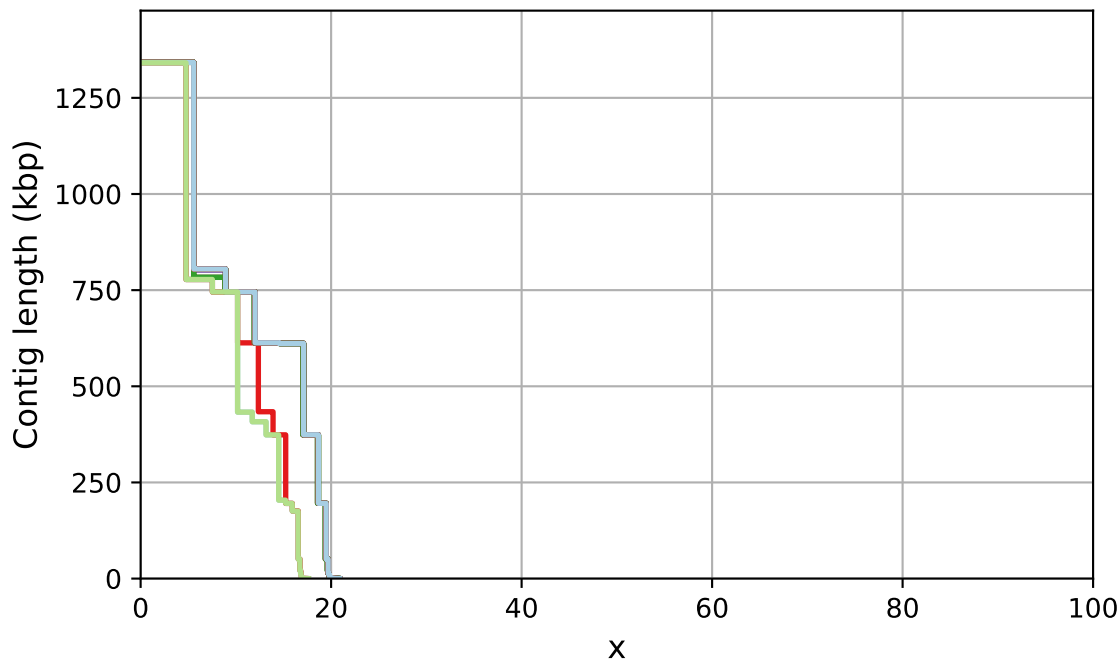
r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

r10_1bin_v2_3_racon_r1

NAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

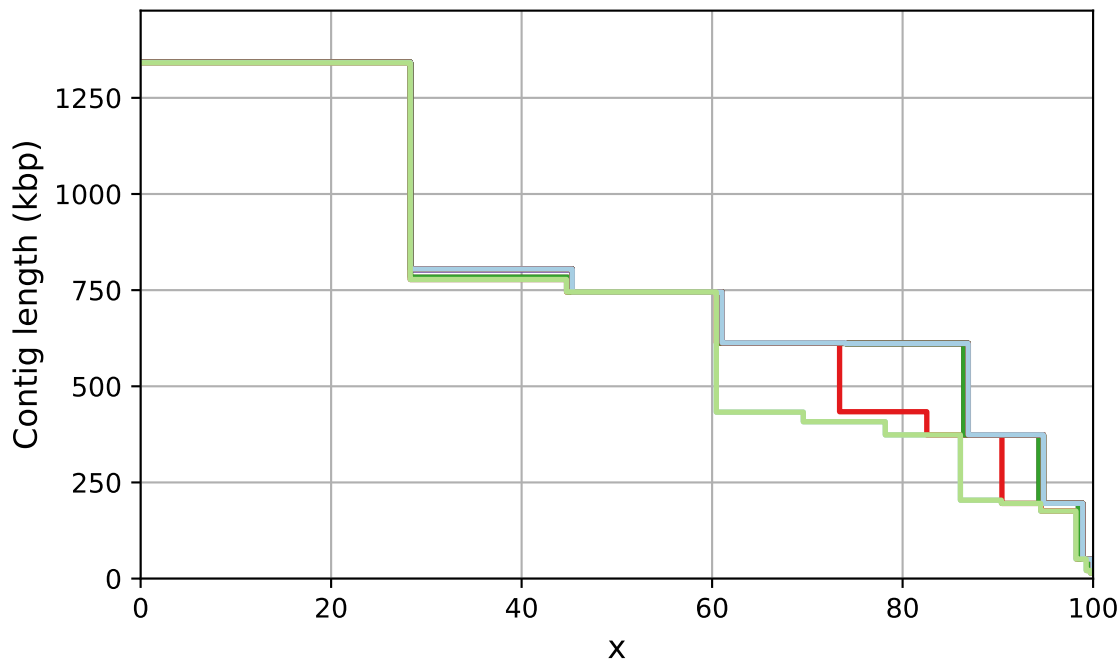
r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

NGAx



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

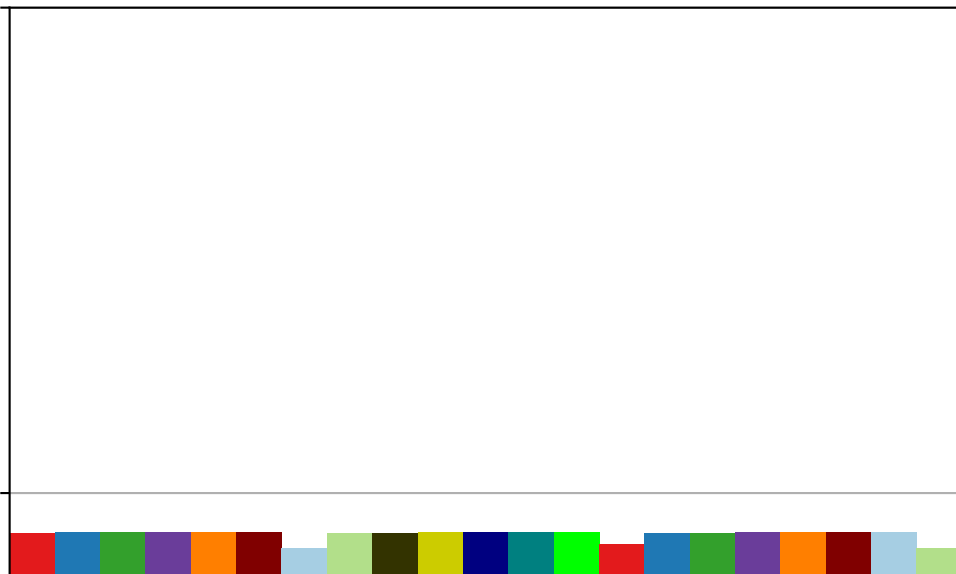
r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka

Genome fraction, %

100

99



r10_1bin_v2_1_MP

r10_1bin_v2_1_MP_helen

r10_1bin_v2_1_r1_medaka

r10_1bin_v2_1_r2_medaka

r10_1bin_v2_2_MP

r10_1bin_v2_2_MP_helen

r10_1bin_v2_2_r1_medaka

r10_1bin_v2_2_r2_medaka

r10_1bin_v2_3_MP

r10_1bin_v2_3_MP_helen

r10_1bin_v2_3_r1_medaka

r10_1bin_v2_3_r2_medaka