

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)	7	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	7
# contigs (>= 25000 bp)	7	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	7
Total length (>= 5000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 10000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 25000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Total length (>= 50000 bp)	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
Total length	24074317	24069448	24072005	24061370	24059821	24053939	24061097	24074504	24070562	24072056	24063280	24060309	24055890	24061440	24074399	24070917	24071942	24055585	24060307	24051912	24060481
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
GC (%)	44.80	44.80	44.80	44.79	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	44.78	44.77
Reference GC (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
N50	4045600	4045625	4045591	4045593	4045204	4045287	4043049	4045597	4045613	4045604	4045605	4045243	4045295	4043007	4045597	4045617	4045586	4045593	4045248	4045340	4042483
NG50	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
N75	2845424	2845372	2845429	2845427	2845272	2845846	2843858	2845424	2845368	2845428	2845430	2845282	2845321	2843857	2845424	2845363	2845431	2845427	2845312	2845321	2843845
NG75	4765357	4765332	4765357	4765355	4764584	4764687	4763514	4765355	4765369	4765398	4765353	4764761	4764686	4763493	4765363	4765342	4765361	4765354	4764595	4764670	4763481
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	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	13
# 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	2719574	2717922	2719543	2719562	2720329	2720423	2718431	2719745	2717983	2719603	2719633	2720494	2720498	2718867	2719589	2717938	2719539	2719544	2720372	2720459	2718437
# local misassemblies	10	9	9	9	10	10	20	9	9	9	9	9	10	19	9	9	9	9	10	9	19
# 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	4	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# 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	21274658	21271555	21273233	21261883	21263760	21253836	21322606	21275861	21273678	21273285	21265050	21263380	21257264	21320082	21274857	21273023	21273407	21256346	21265173	21252622	21318452
Genome fraction (%)	99.537	99.537	99.537	99.537	99.537	99.537	99.538	99.537	99.537	99.537	99.537	99.537	99.537	99.542	99.537	99.537	99.537	99.537	99.537	99.537	99.538
Duplication ratio	1.046	1.045	1.046	1.046	1.045	1.046	1.023	1.046	1.045	1.046	1.045	1.045	1.046	1.024	1.046	1.045	1.045	1.046	1.044	1.046	1.024
# 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	286.80	257.07	286.73	289.01	284.67	299.50	244.40	283.37	252.13	287.36	283.85	285.16	291.14	255.89	286.77	257.36	286.21	290.13	279.14	298.68	250.71
# indels per 100 kbp	110.77	43.93	75.61	76.62	109.72	112.41	159.44	111.25	41.73	76.88	77.22	110.51	109.83	166.01	110.73	43.93	75.28	76.88	109.12	112.26	159.22
Largest alignment	948799	948042	948655	948665	949039	949083	948372	948768	948099	948666	948684	949021	949090	948394	948666	948050	948656	948635	949082	948980	948372
Total aligned length	2797737	2795964	2796861	2797576	2794149	2798191	2736576	2796730	2794965	2796860	2796319	2795018	2796714	2739435	2797620	2795975	2796624	2797328	2793222	2797379	2740114
NGA50	480523	480630	480492	480508	480497	480630	480397	480508	480257	480508	480637	480504	480637	480577	480493	480271	480493	480509	480653	480398	480398
NGA75	381462	381229	381409	381430	381516	381564	381299	381465	381235	381423	381427	381537	381557	381350	381468	381236	381411	381422	381519	381575	381299
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	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

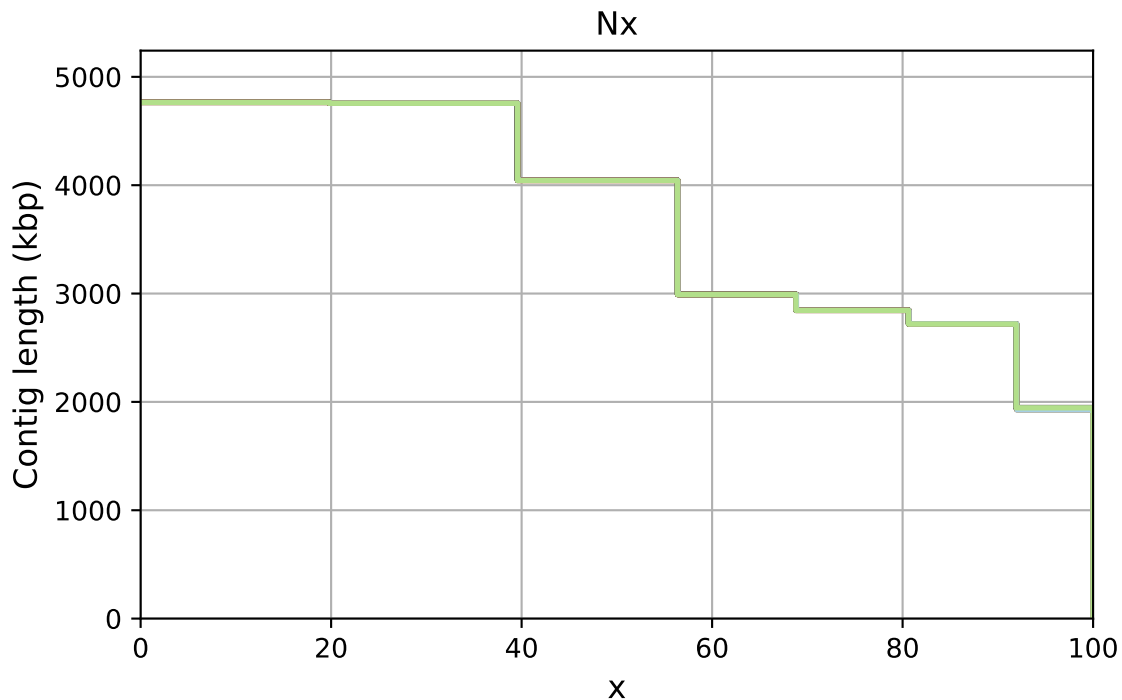
	r10_2bins_v2_1_MP	r10_2bins_v2_1_MP_helen	r10_2bins_v2_1_r1_medaka	r10_2bins_v2_1_r2_medaka	r10_2bins_v2_1_racon_r1	r10_2bins_v2_1_racon_r2	r10_2bins_v2_1_raw	r10_2bins_v2_2_MP	r10_2bins_v2_2_MP_helen	r10_2bins_v2_2_r1_medaka	r10_2bins_v2_2_r2_medaka	r10_2bins_v2_2_racon_r1	r10_2bins_v2_2_racon_r2	r10_2bins_v2_2_raw	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	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	13
# contig misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	15	13	13	13	13	13	13	13
# 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	13	13	13	13	13	13	13	15	13	13	13	13	13	13	13
# 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	2719574	2717922	2719543	2719562	2720329	2720423	2718431	2719745	2717983	2719603	2719633	2720494	2720498	2718867	2719589	2717938	2719539	2719544	2720372	2720459	2718437
# 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	10	10	10	10	10	10	18	10	10	10	10	10	10	20	10	10	10	10	10	10	16
# local misassemblies	10	9	9	9	10	10	20	9	9	9	9	9	10	19	9	9	9	9	10	9	19
# 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	26	26	26	26	26	26	23	26	26	26	26	26	26	22	26	26	26	26	26	26	25
# unaligned mis. contigs	6	6	6	6	6	6	4	6	6	6	6	6	6	5	6	6	6	6	6	6	5
# mismatches	7677	6881	7675	7736	7620	8017	6542	7585	6749	7692	7598	7633	7793	6850	7676	6889	7661	7766	7472	7995	6711
# indels	2965	1176	2024	2051	2937	3009	4268	2978	1117	2058	2067	2958	2940	4444	2964	1176	2015	2058	2921	3005	4262
# indels (<= 5 bp)	2889	1110	1973	2000	2884	2955	4205	2911	1054	2007	2016	2906	2887	4389	2888	1110	1964	2006	2869	2953	4202
# indels (> 5 bp)	76	66	51	51	53	54	63	67	63	51	51	52	53	55	76	66	51	52	52	52	60
Indels length	6931	4974	5351	5372	6680	6687	8388	6853	4886	5389	5399	6731	6659	8526	6929	4979	5341	5404	6672	6718	8364

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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21274658	21271555	21273233	21261883	21263760	21253836	21322606	21275861	21273678	21273285	21265050	21263380	21257264	21320082	21274857	21273023	21273407	21256346	21265173	21252622	21318452
# 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).



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

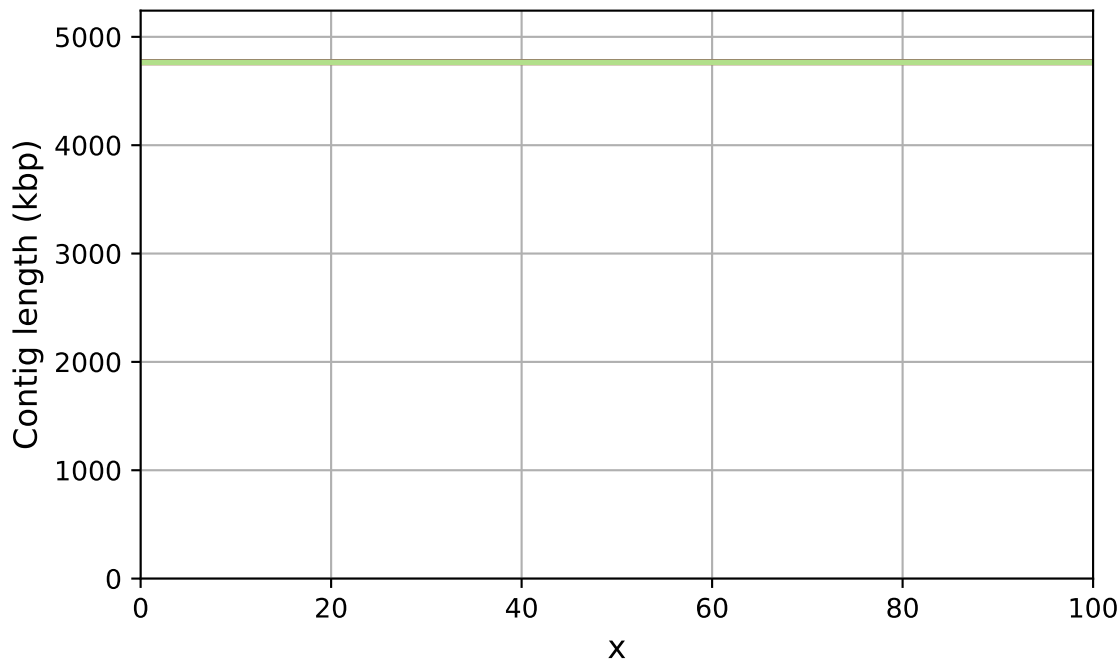
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_MP\_helen

r10\_2bins\_v2\_3\_r1\_medaka

r10\_2bins\_v2\_3\_r2\_medaka

# NGx



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

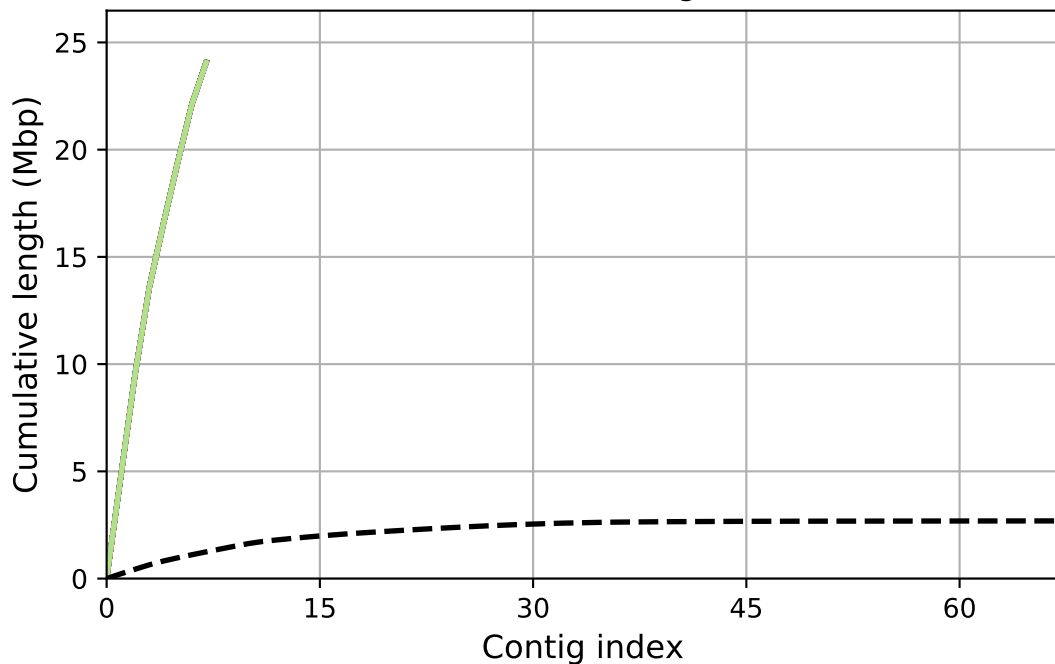
r10\_2bins\_v2\_3\_r1\_medaka

0\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_r2\_medaka

# 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

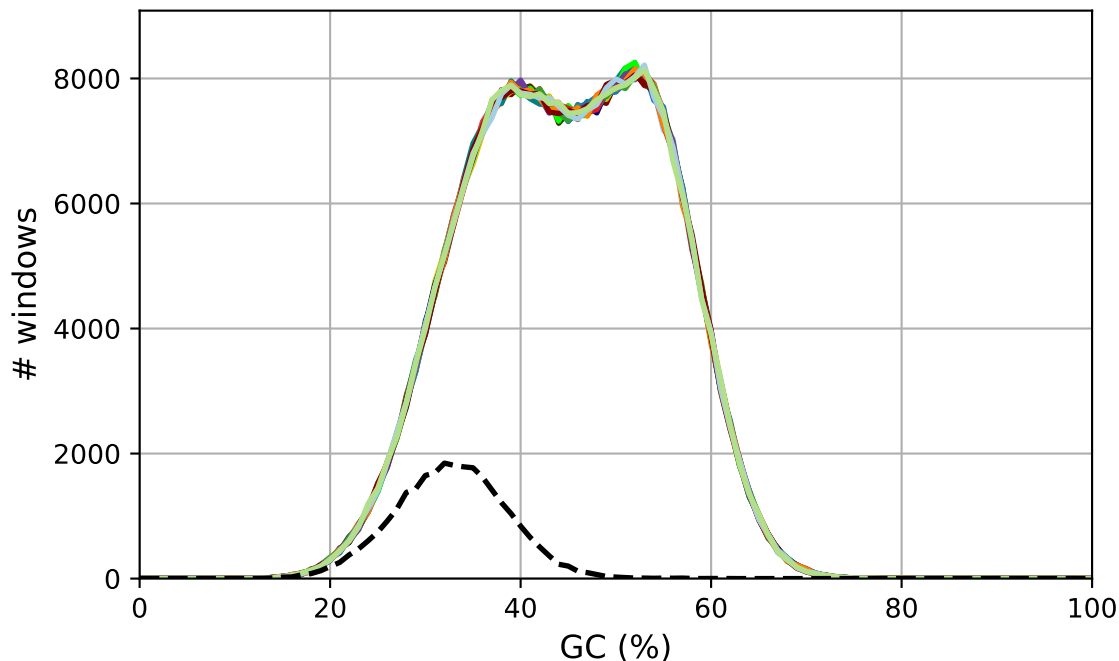
r10\_2bins\_v2\_3\_MP

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

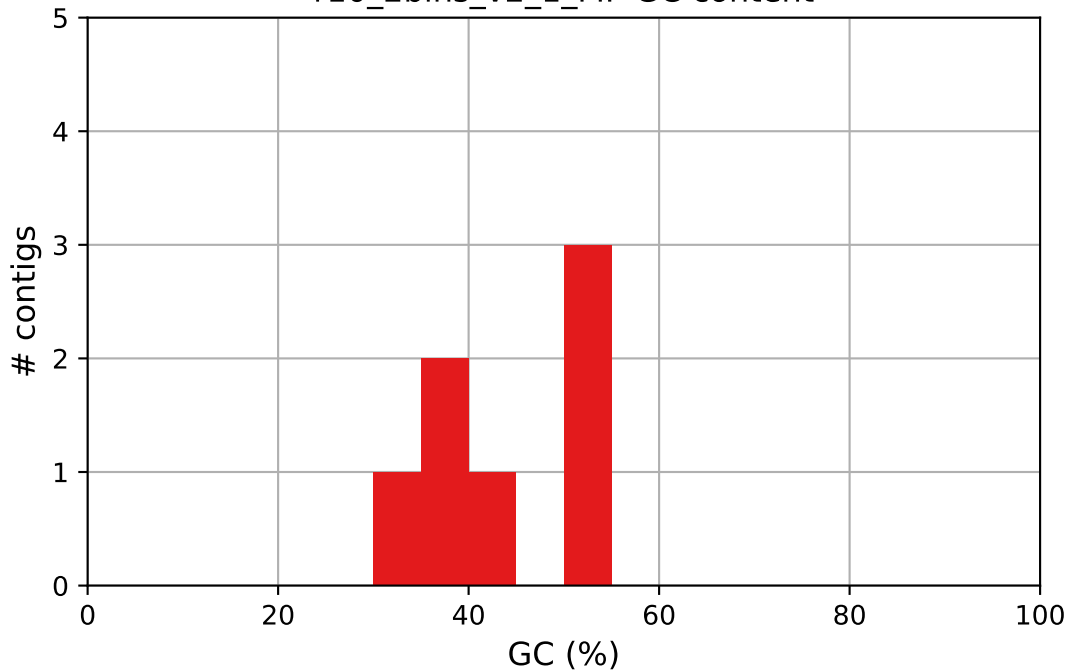
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_r1

r10\_2bins\_v2\_3\_r2

r10\_2bins\_v2\_3\_racon\_r1

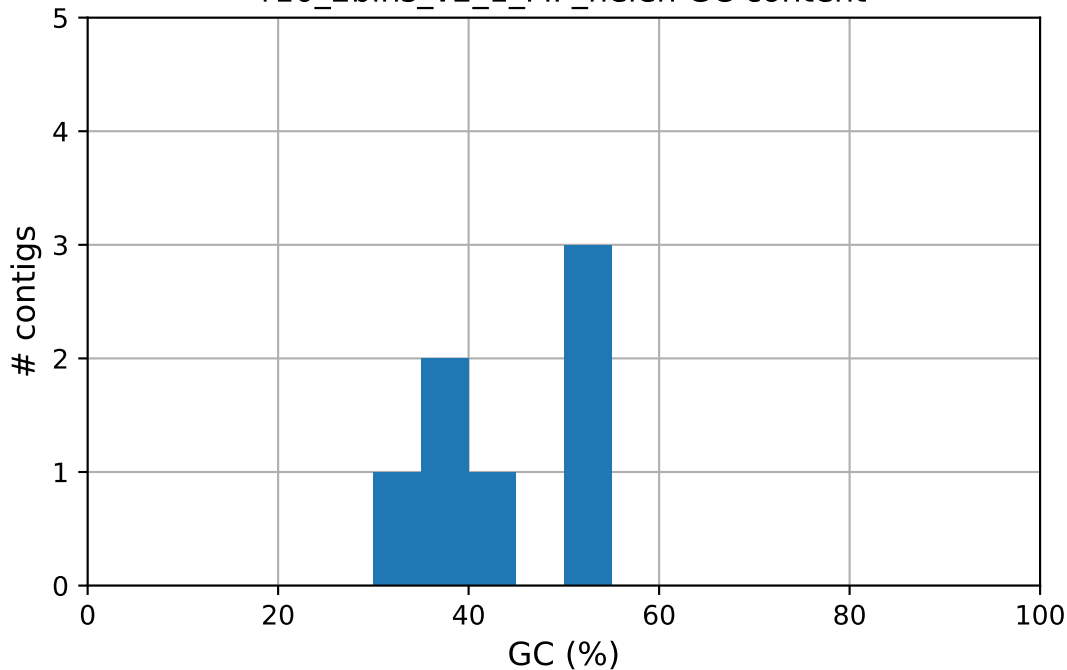
r10\_2bins\_v2\_1\_MP GC content



r10\_2bins\_v2\_1\_MP

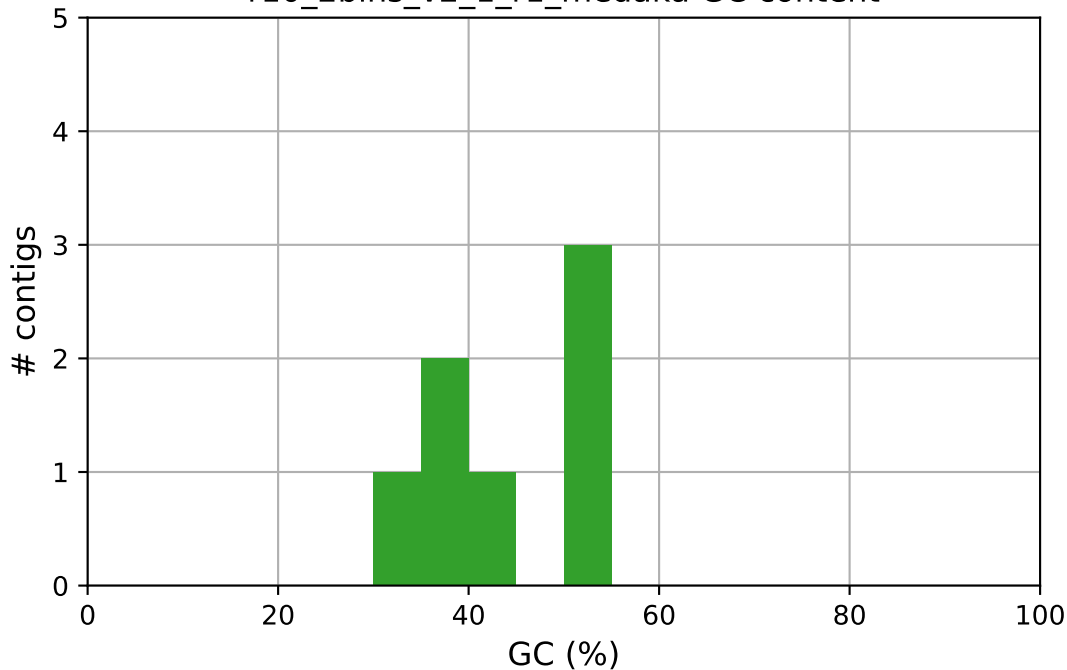


r10\_2bins\_v2\_1\_MP\_helen GC content



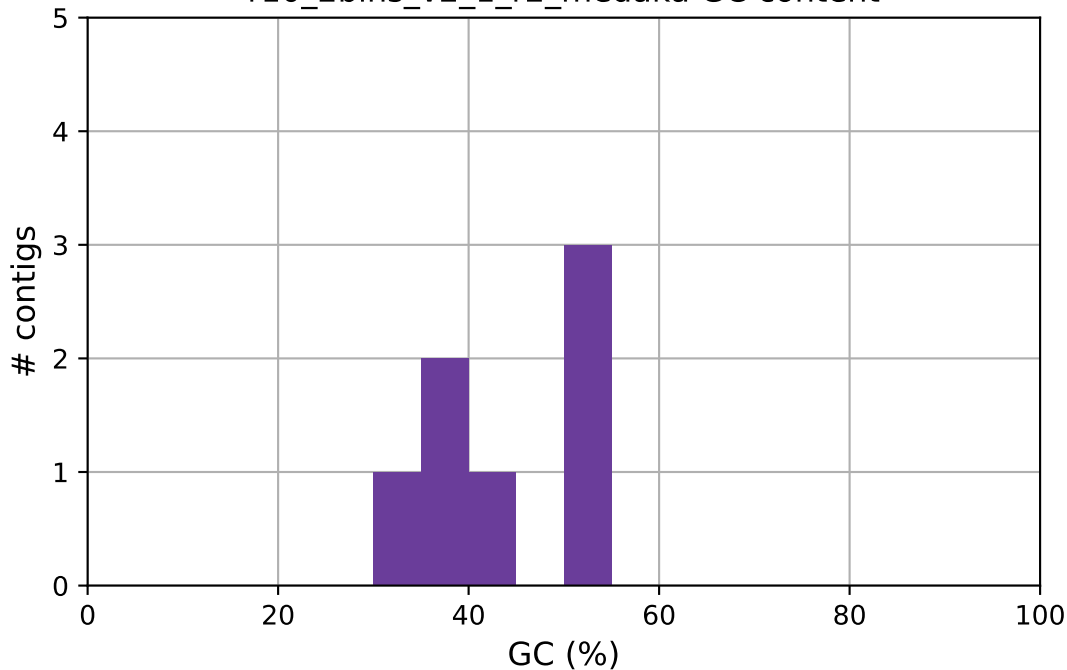
r10\_2bins\_v2\_1\_MP\_helen

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



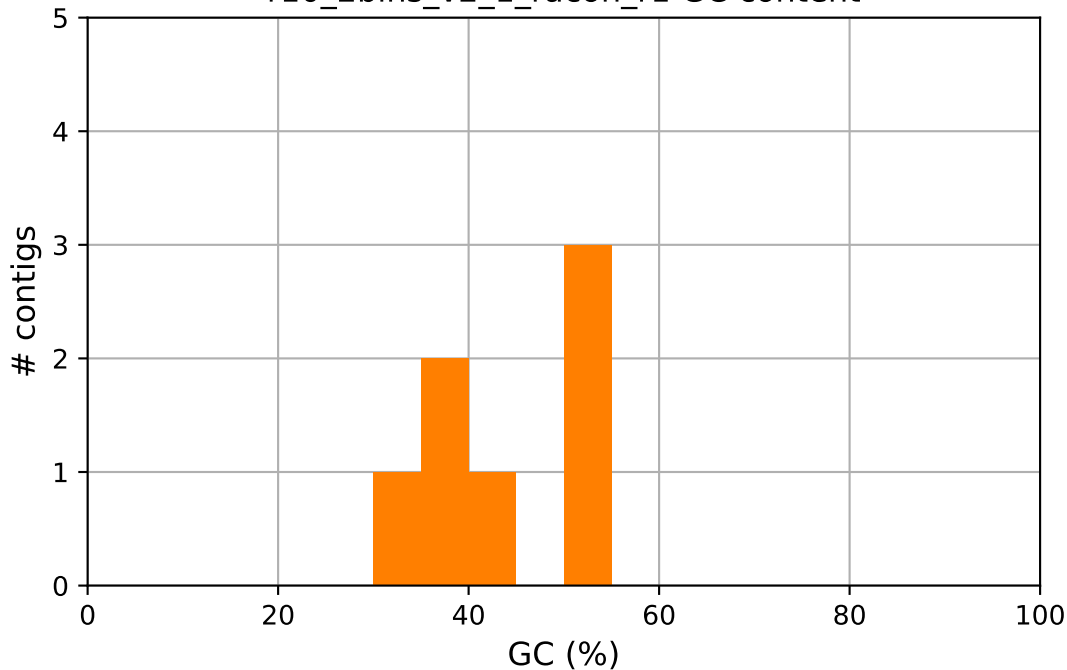
r10\_2bins\_v2\_1\_r1\_medaka

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



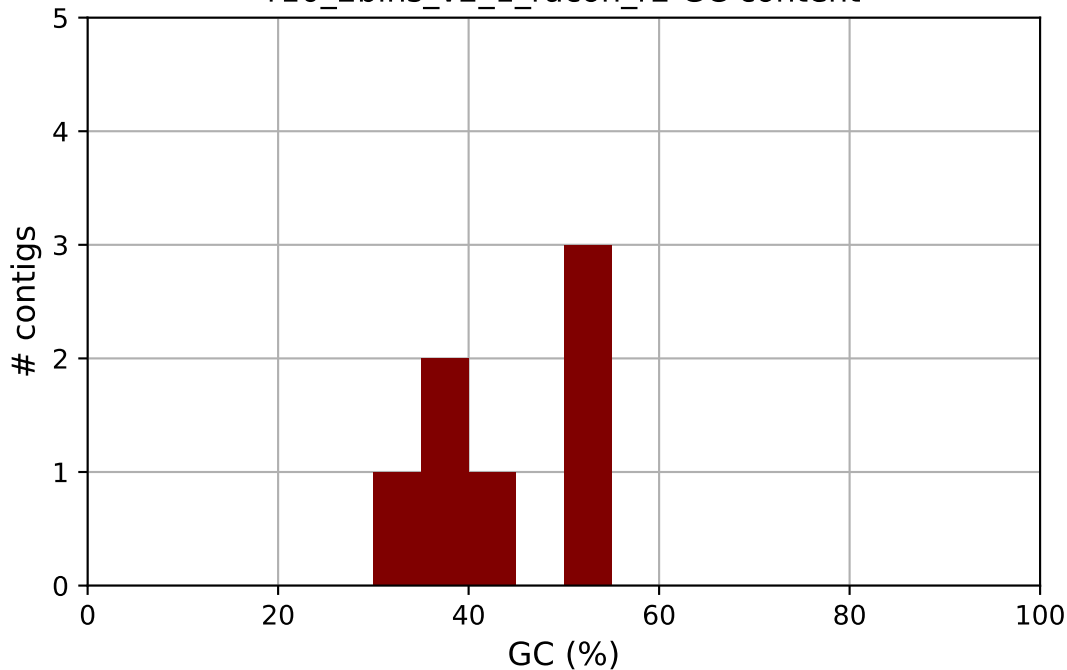
r10\_2bins\_v2\_1\_r2\_medaka

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



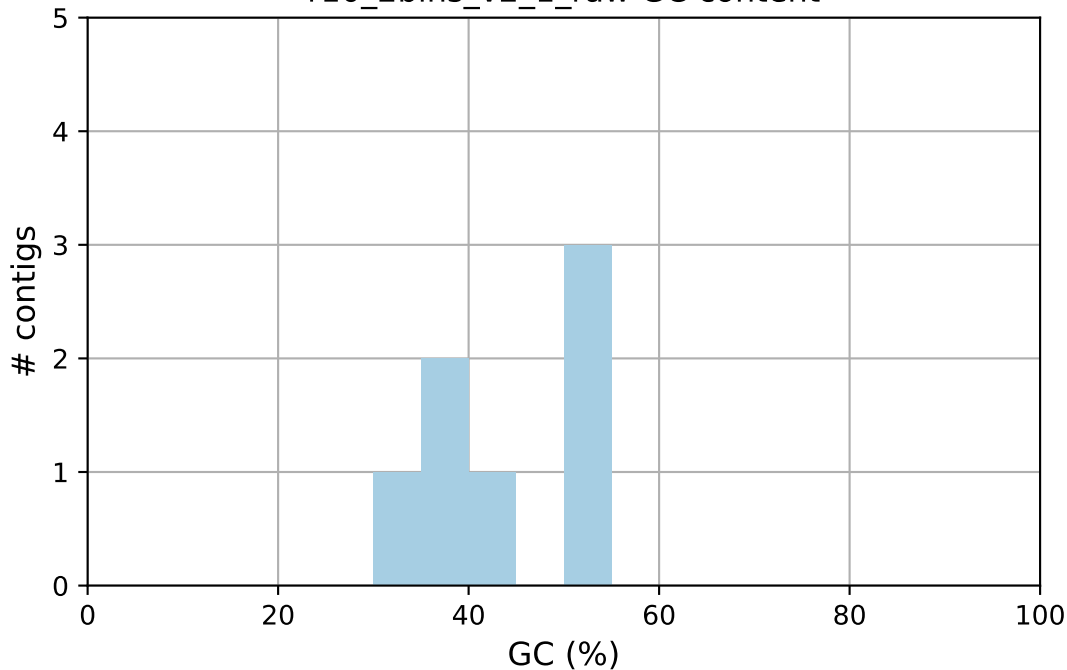
r10\_2bins\_v2\_1\_racon\_r1

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



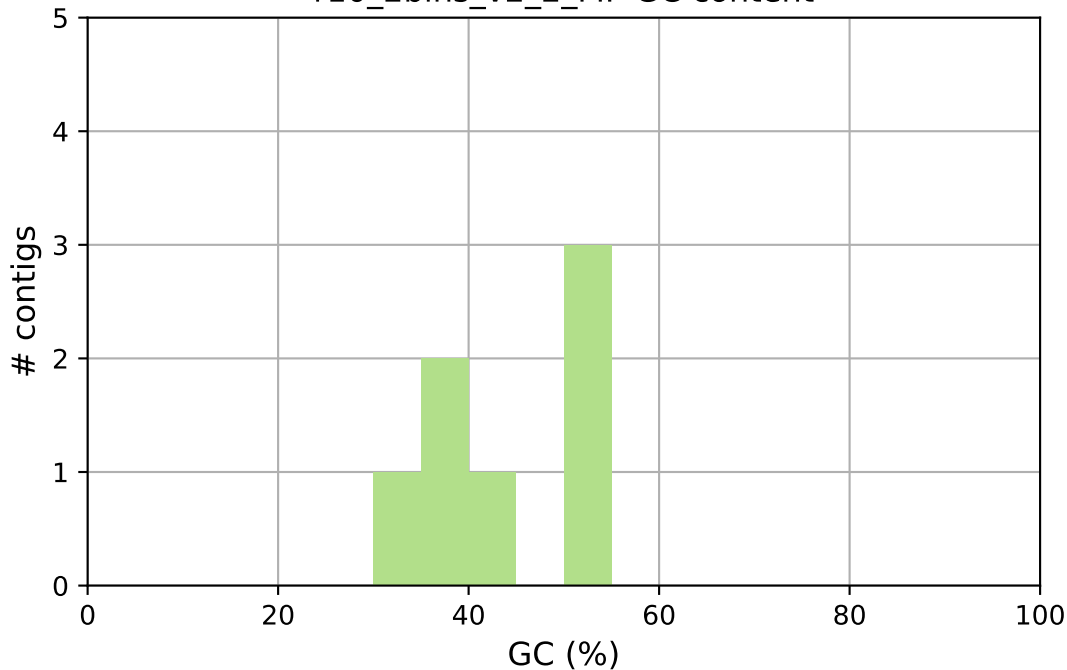
r10\_2bins\_v2\_1\_racon\_r2

r10\_2bins\_v2\_1\_raw GC content



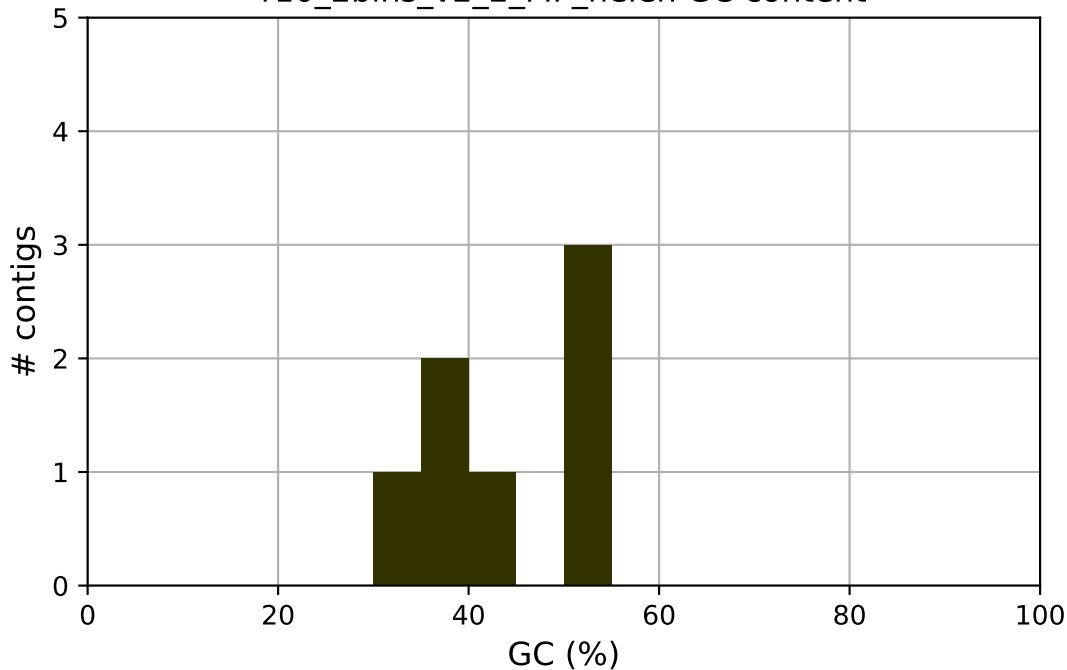
r10\_2bins\_v2\_1\_raw

r10\_2bins\_v2\_2\_MP GC content



r10\_2bins\_v2\_2\_MP

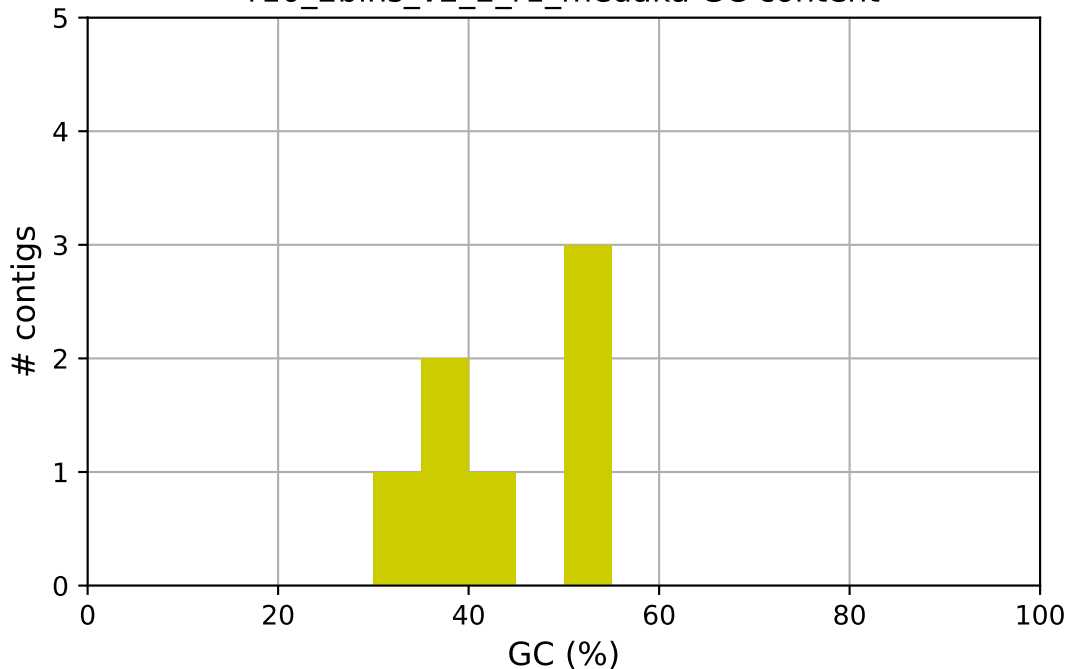
r10\_2bins\_v2\_2\_MP\_helen GC content



r10\_2bins\_v2\_2\_MP\_helen

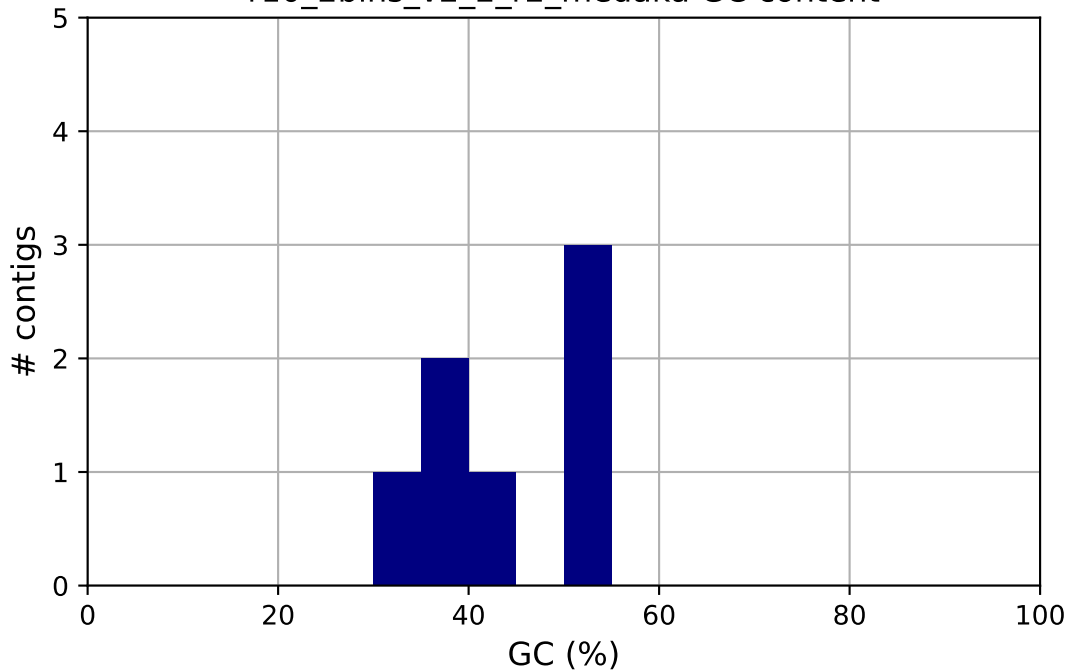


r10\_2bins\_v2\_2\_r1\_medaka GC content



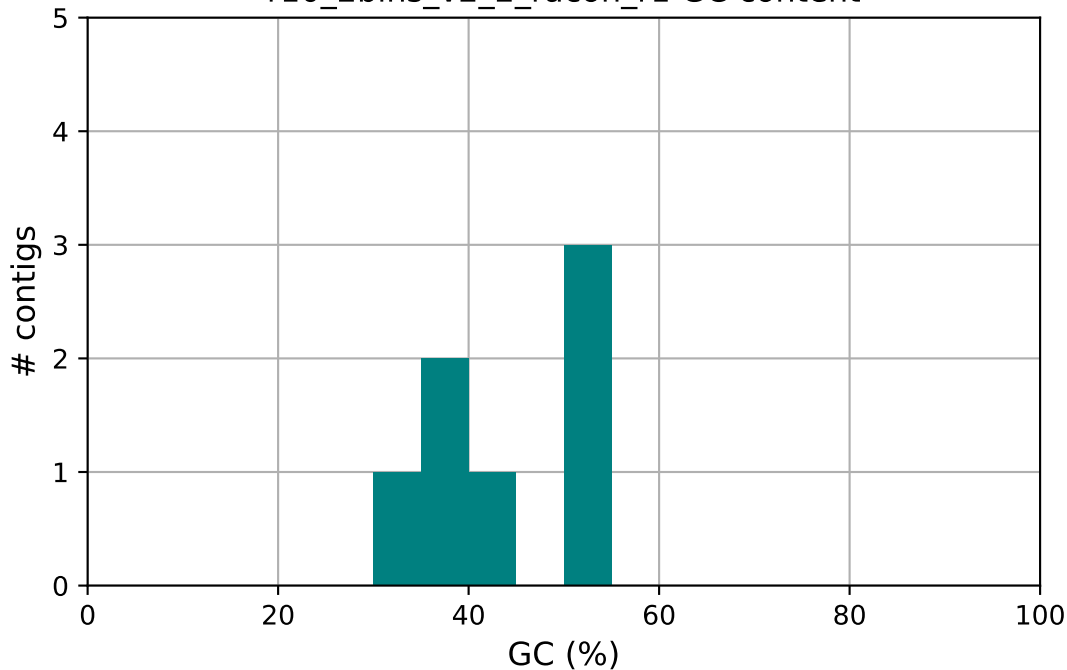
r10\_2bins\_v2\_2\_r1\_medaka

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



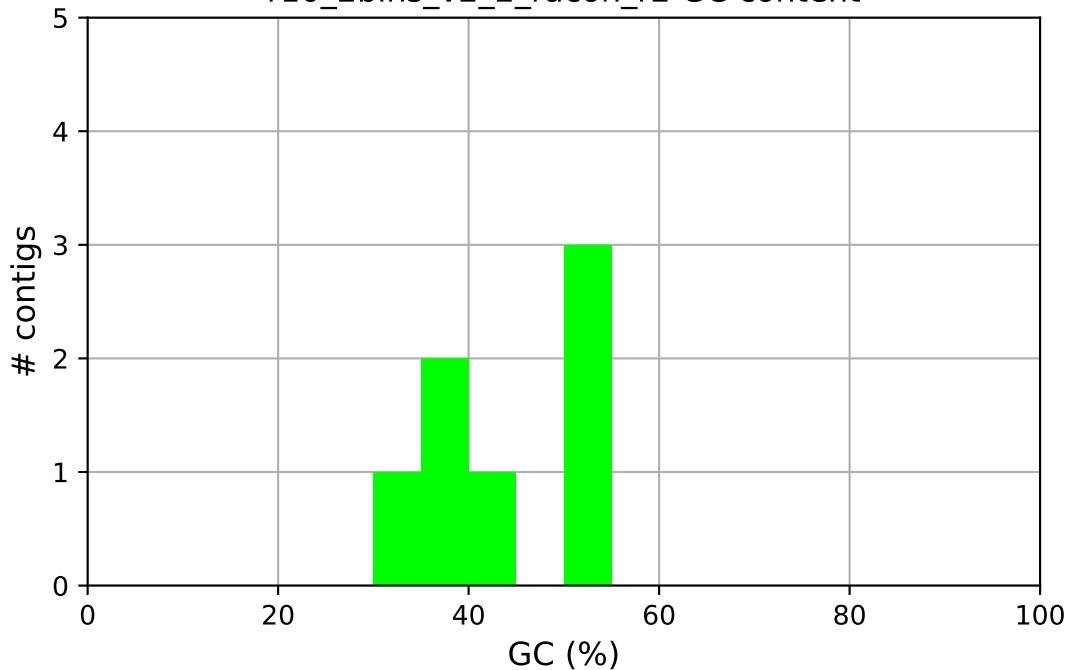
r10\_2bins\_v2\_2\_r2\_medaka

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



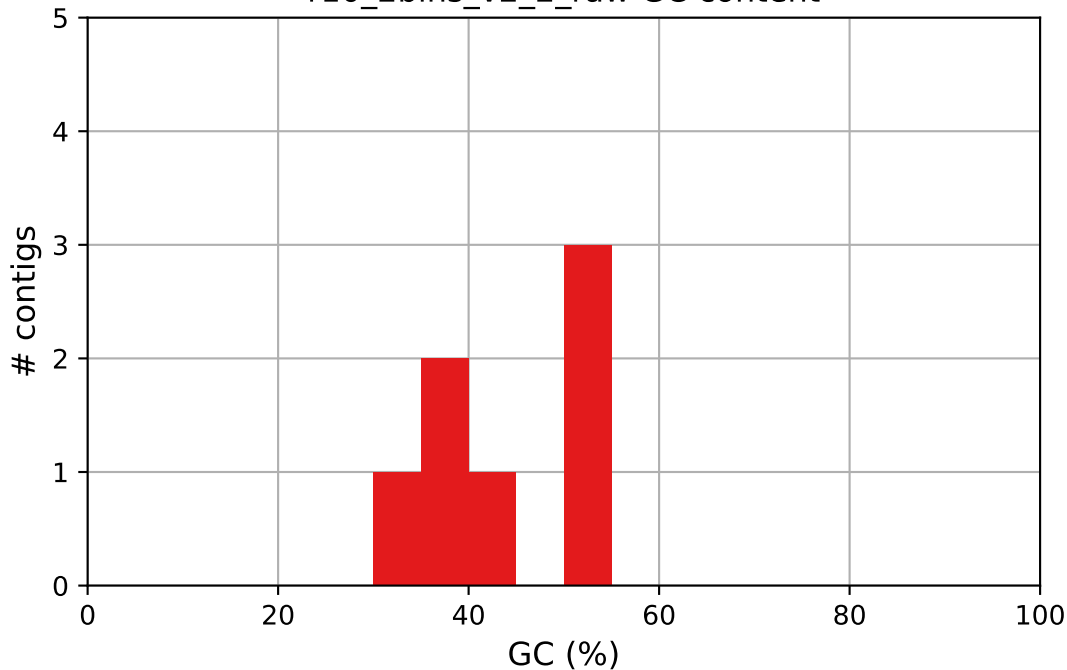
r10\_2bins\_v2\_2\_racon\_r1

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



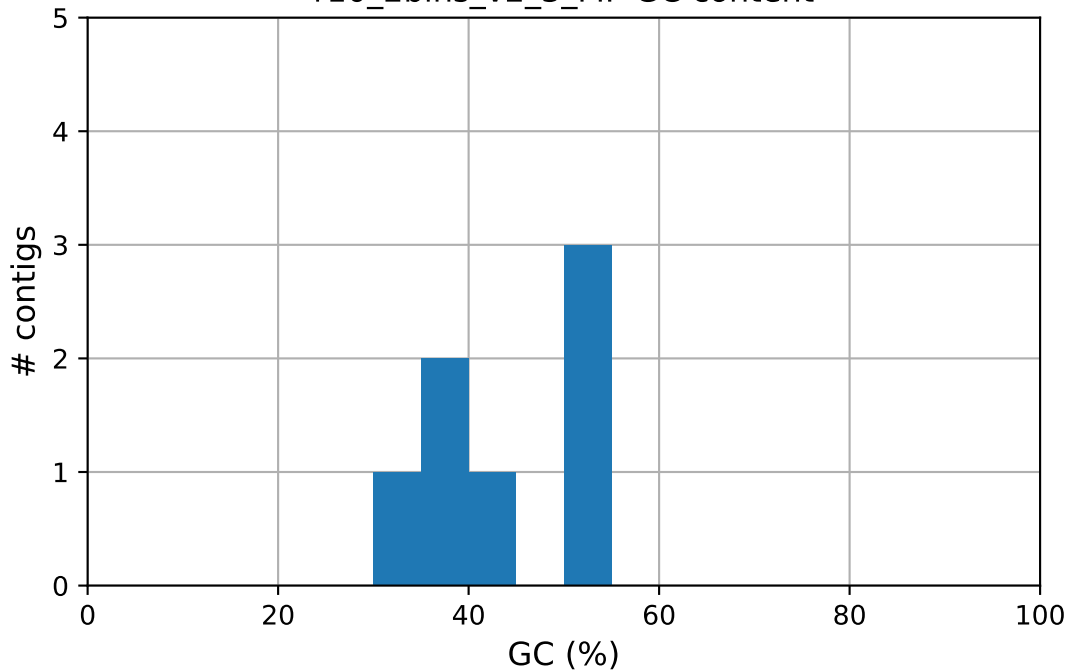
■ r10\_2bins\_v2\_2\_racon\_r2

r10\_2bins\_v2\_2\_raw GC content



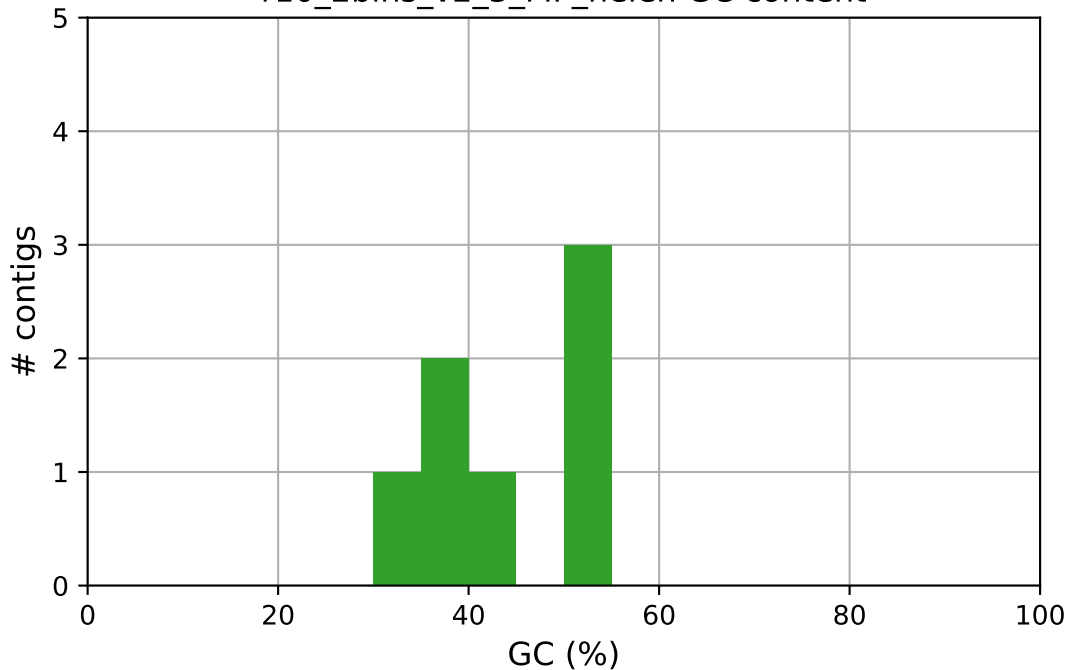
r10\_2bins\_v2\_2\_raw

r10\_2bins\_v2\_3\_MP GC content



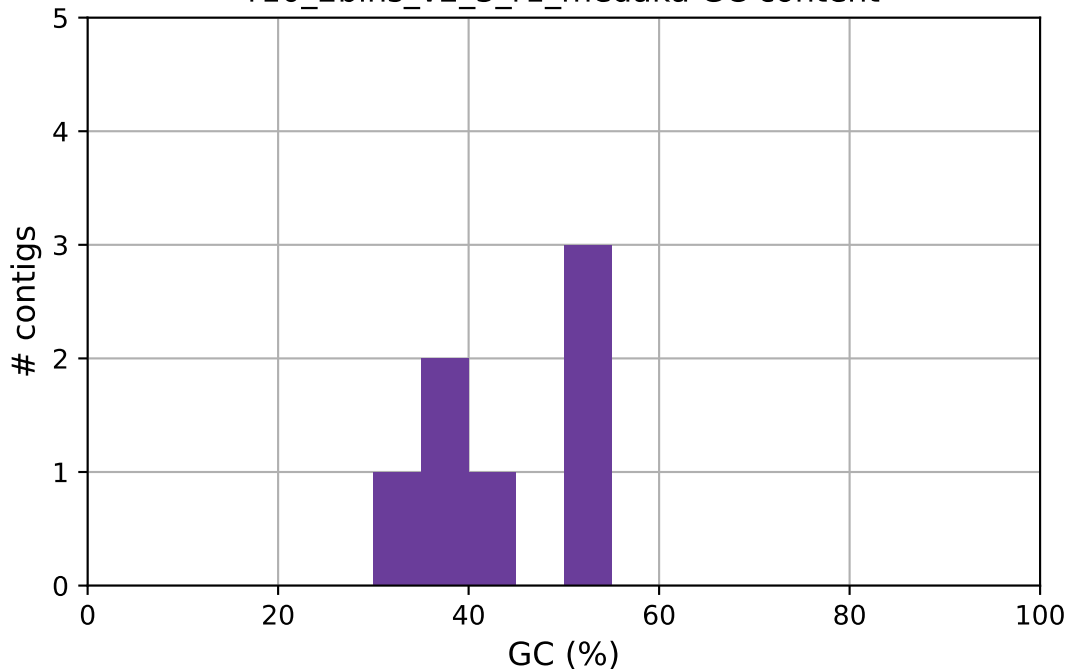
r10\_2bins\_v2\_3\_MP

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



r10\_2bins\_v2\_3\_MP\_helen

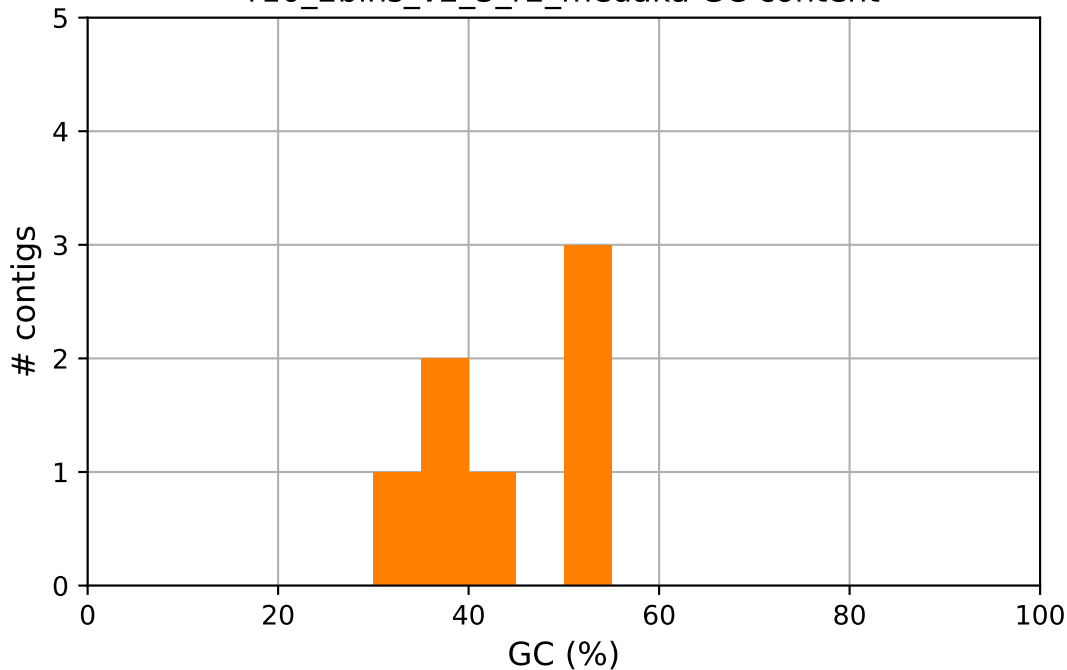
r10\_2bins\_v2\_3\_r1\_medaka GC content



r10\_2bins\_v2\_3\_r1\_medaka

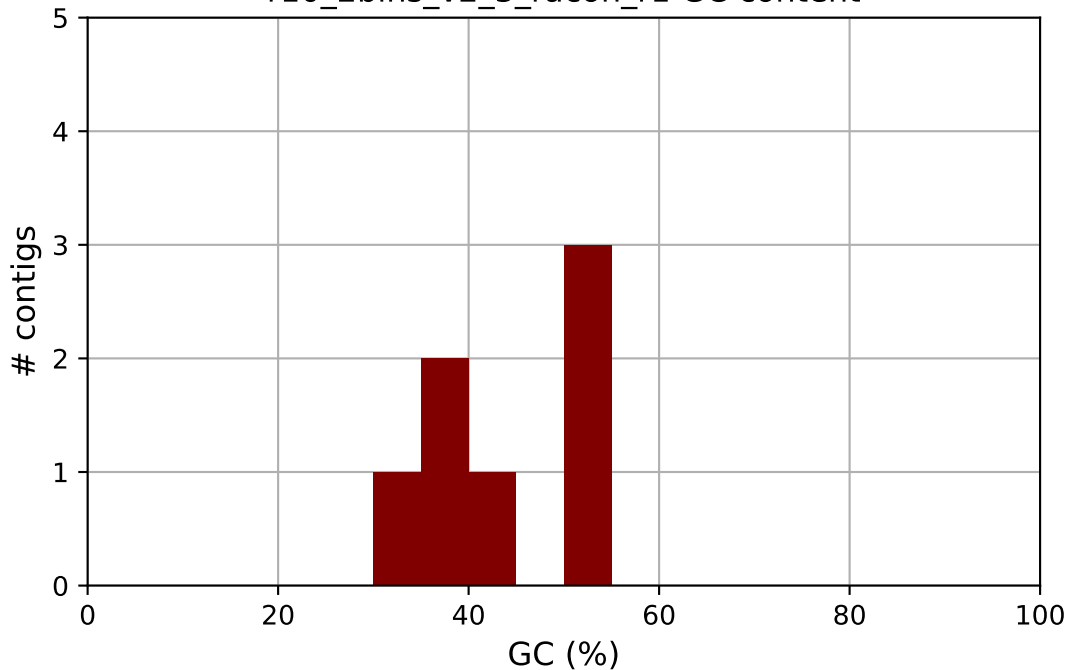


r10\_2bins\_v2\_3\_r2\_medaka GC content



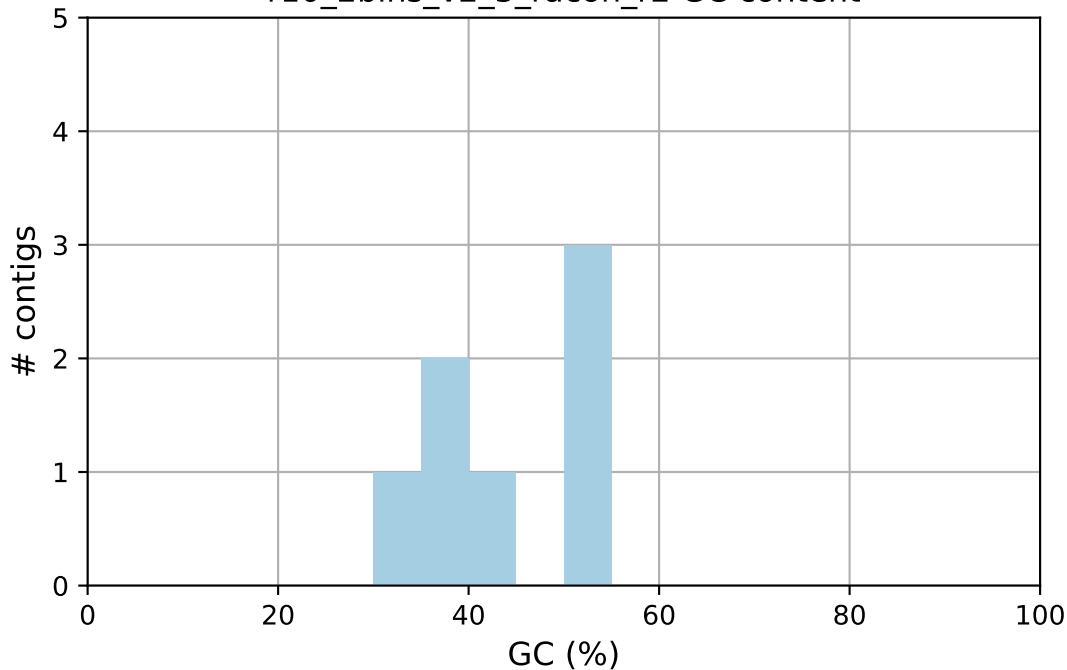
r10\_2bins\_v2\_3\_r2\_medaka

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



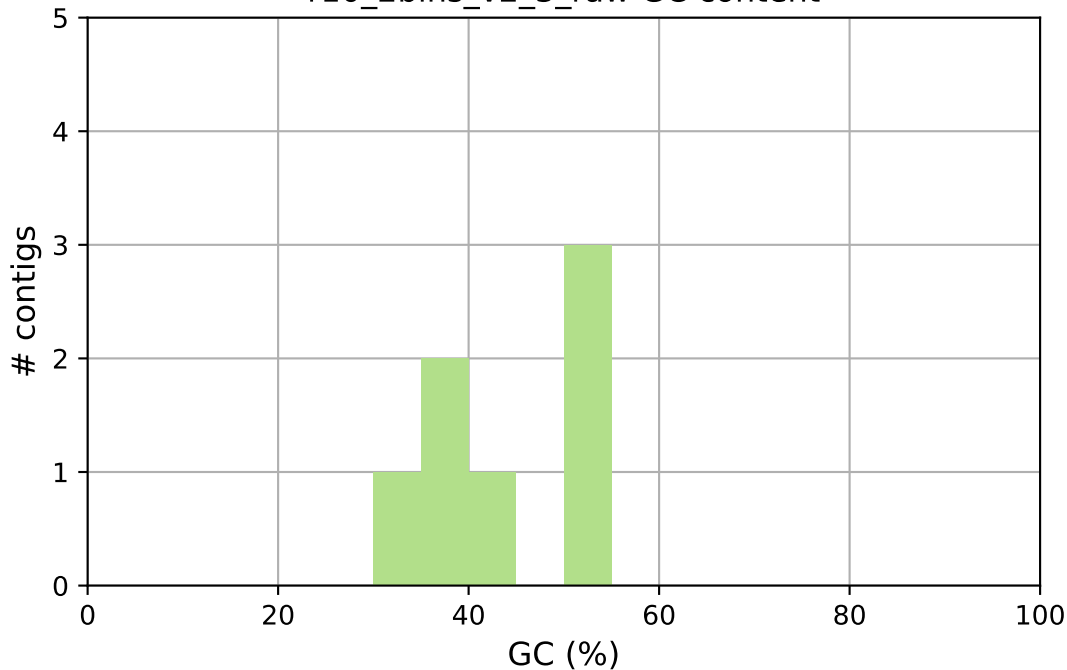
r10\_2bins\_v2\_3\_racon\_r1

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



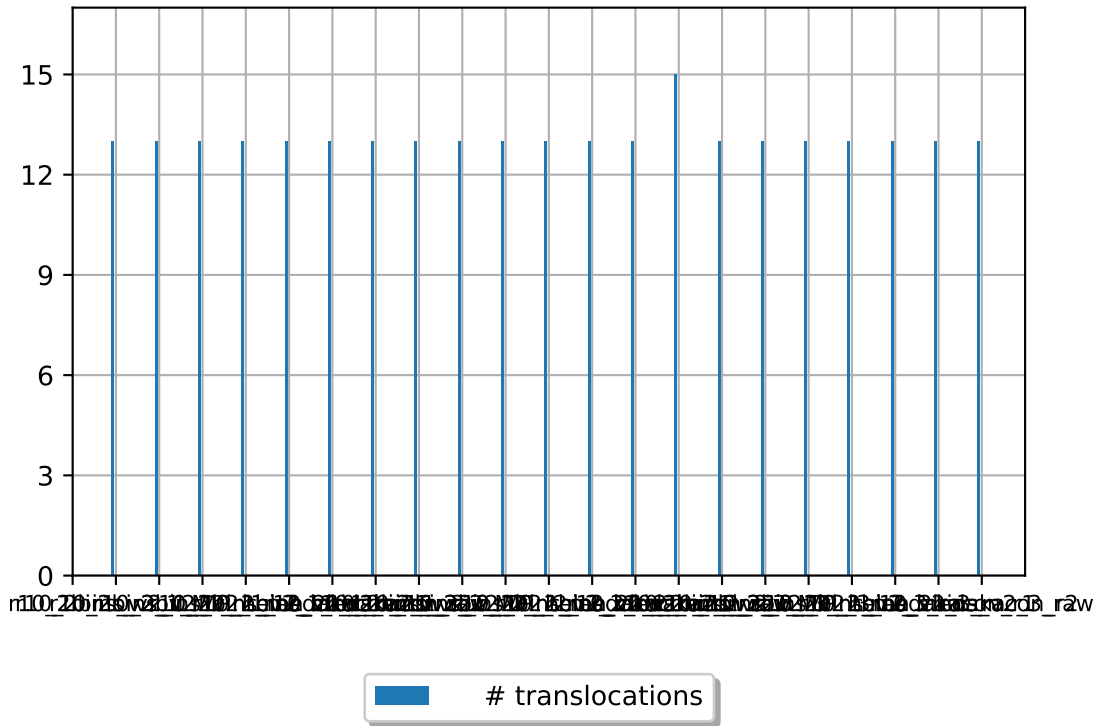
r10\_2bins\_v2\_3\_racon\_r2

r10\_2bins\_v2\_3\_raw GC content

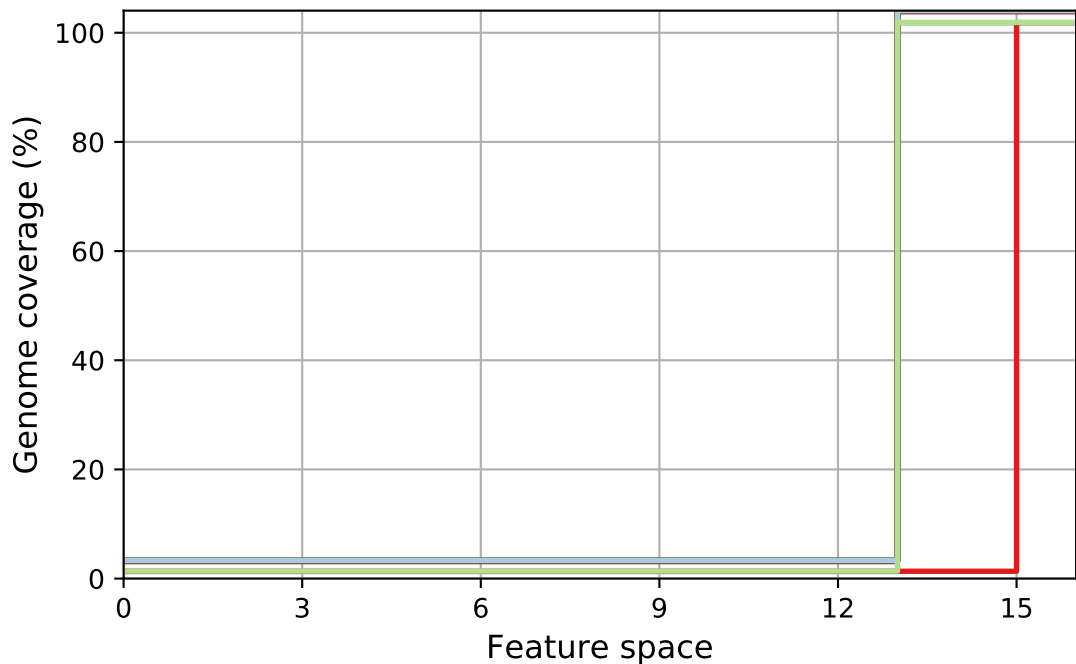


r10\_2bins\_v2\_3\_raw

# 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

r10\_2bins\_v2\_2\_MP\_helen

r10\_2bins\_v2\_2\_r1\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

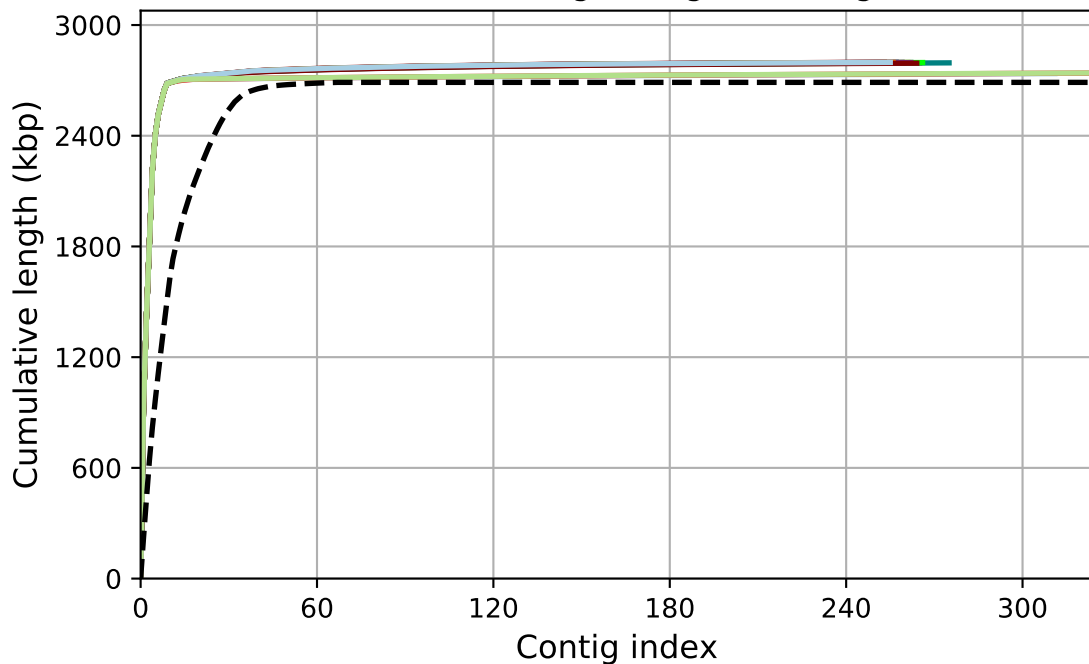
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_MP\_helen

r10\_2bins\_v2\_3\_r1\_medaka

r10\_2bins\_v2\_3\_r2\_medaka

# Cumulative length (aligned contigs)



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

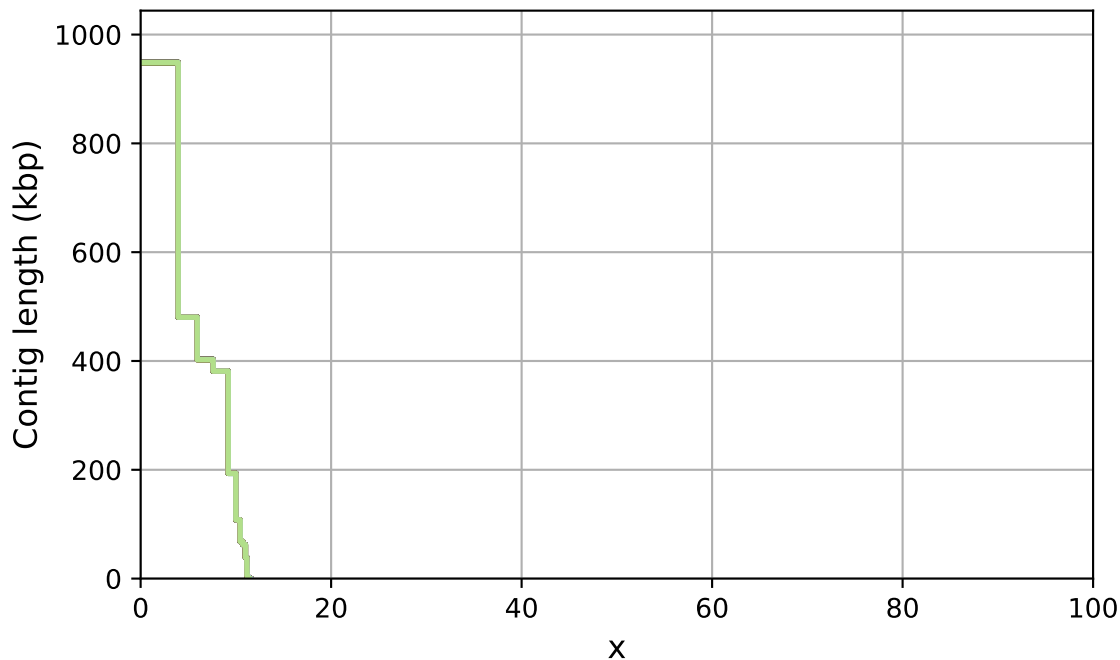
r10\_2bins\_v2\_3\_MP

r10\_2bins\_v2\_3\_r1

r10\_2bins\_v2\_3\_r2

r10\_2bins\_v2\_3\_racon\_r1

NAx



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

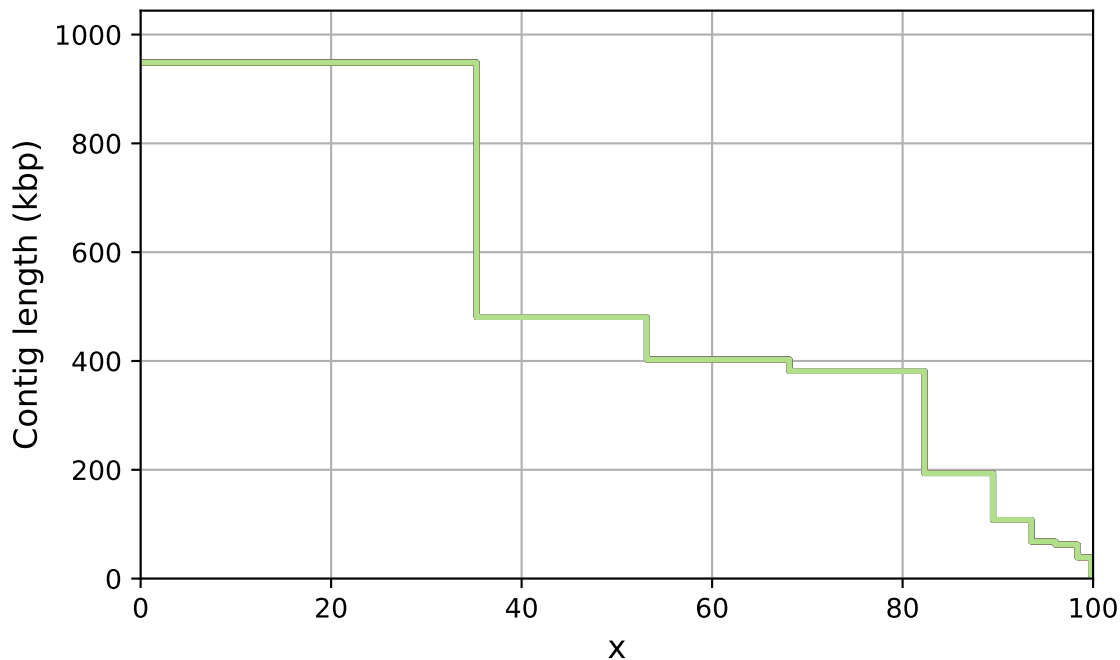
0\_2bins\_v2\_1\_r2\_medaka

r10\_2bins\_v2\_2\_r2\_medaka

r10\_2bins\_v2\_3\_r2\_medaka



# NGAx



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

Genome fraction, %

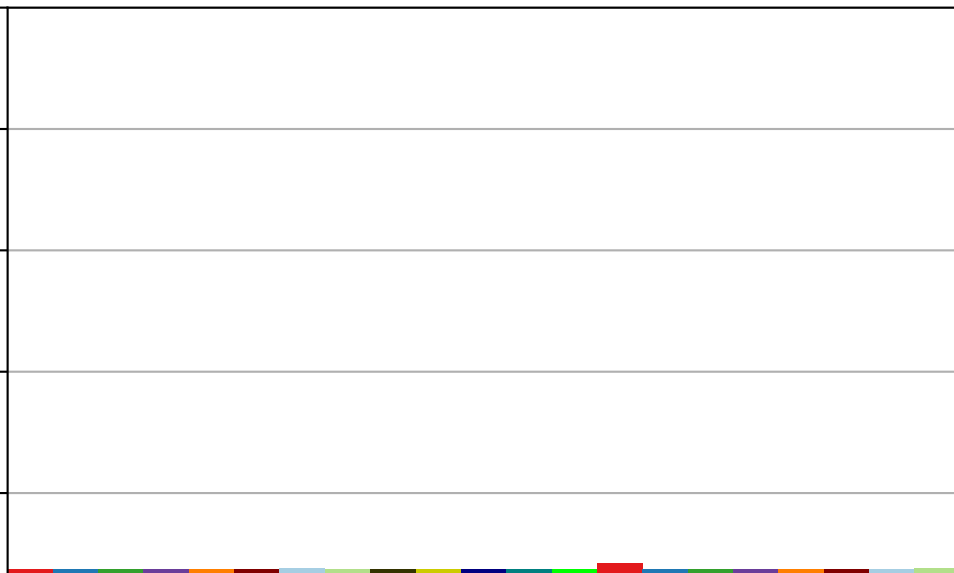
100.0

99.9

99.8

99.7

99.6



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