

Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Total length (>= 5000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24060635	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24060635	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24060635	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24060635	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667
# contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Largest contig	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	6787718
Total length	24074828	24070090	24071888	24063470	24060900	24056048	30848193	24074490	24070611	24075114	24065831	24060635	24055783	30848654	24078180	24070683	24078524	24071188	24064158	24059056	30851667
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	49.48	44.80	44.80	44.80	44.79	44.79	44.78	49.48	44.80	44.81	44.80	44.79	44.79	44.79	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
N50	4045594	4045616	4045591	4045596	4045200	4045302	4756098	4045598	4045623	4045846	4045845	4045161	4045304	4756089	4045599	4045602	4045842	4045840	4045210	4045276	4756074
NG50	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	6787718
N75	2845421	2845364	2845429	2845364	2845295	2845304	2990633	2845423	2845360	2845571	2845423	2845301	2845301	2990628	2845422	2845361	2845572	2845563	2845260	2845299	2990626
NG75	4765884	4765881	4765833	4765837	4765031	4765076	6787707	4765366	4765332	4765684	4765663	4764521	4764646	6787721	4765358	4765330	4765688	4765655	4764491	4764636	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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992173	2991893	2991931	2990628	2992084	2992068	2992178	2992176	2991922	2991951	2990626
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	12	7	7	7	7	7	7	12
# 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	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# unaligned contigs	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	20956540	20949552	20952382	20945364	20942573	20937602	27788160	20956888	20950605	20957178	20948833	20942016	20936441	27792561	20960694	20950789	20961124	20955176	20945168	20939944	27795908
Genome fraction (%)	99.984	99.984	99.984	99.984	99.984	99.984	99.981	99.984	99.984	99.984	99.984	99.984	99.984	99.983	99.984	99.984	99.984	99.984	99.984	99.984	99.983
Duplication ratio	1.054	1.055	1.055	1.054	1.054	1.054	1.035	1.054	1.055	1.054	1.054	1.055	1.055	1.033	1.054	1.055	1.054	1.054	1.055	1.055	1.033
# 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	0.32
# mismatches per 100 kbp	230.85	236.83	231.46	226.72	227.97	229.63	148.14	228.75	235.55	228.65	225.20	228.96	232.07	140.97	228.45	235.21	226.52	223.04	230.41	232.00	139.82
# indels per 100 kbp	22.08	22.38	22.38	21.54	31.92	29.72	116.05	21.30	21.71	26.27	25.60	31.89	29.62	115.61	21.30	21.78	26.17	25.36	33.54	29.45	115.78
Largest alignment	1569038	1569031	1569032	1569032	1568962	1568962	1568349	1569037	1569031	1569095	1569093	1568941	1568951	1568344	1569037	1569031	1569093	1569095	1568946	1568971	1568343
Total aligned length	3117814	3120054	3117932	3117632	3117853	3117972	3059650	3117462	3119532	3118868	3116524	3118145	3118638	3055655	3117011	3119420	3116926	3115538	3118518	3118638	3055221
NGA50	1569038	1569031	1569032	1569032	1568962	1568962	1568349	1569037	1569031	1569095	1569093	1568941	1568951	1568344	1569037	1569031	1569093	1569095	1568946	1568971	1568343
NGA75	1410523	1410493	1410518	1410518	1410429	1410466	1409725	1410523	1410493	1410565	1410556	1410429	1410455	1409713	1410523	1410494	1410561	1410557	1410452	1410458	1409712
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2

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_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992173	2991893	2991931	2990628	2992084	2992068	2992178	2992176	2991922	2991951	2990626
# possibly misassembled contigs	1	1	1	1	1	1	2	1	1	1	1	1	1	2	1	1	1	1	1	1	2
# possible misassemblies	8	8	8	8	8	8	9	8	8	8	8	8	8	9	8	8	8	8	8	8	9
# local misassemblies	7	7	7	7	7	7	14	7	7	7	7	7	7	12	7	7	7	7	7	7	12
# 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	16	16	16	16	16	16	10	16	16	16	16	16	16	11	16	16	16	16	16	16	11
# unaligned mis. contigs	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
# mismatches	6827	7004	6845	6705	6742	6791	4381	6765	6966	6762	6660	6771	6863	4169	6756	6956	6699	6596	6814	6861	4135
# indels	653	662	662	637	944	879	3432	630	642	777	757	943	876	3419	630	644	774	750	992	871	3424
# indels (<= 5 bp)	629	637	637	613	919	855	3405	607	618	752	732	918	851	3390	607	620	749	726	966	847	3395
# indels (> 5 bp)	24	25	25	24	25	24	27	23	24	25	25	25	25	29	23	24	25	24	26	24	29
Indels length	1955	1971	1978	1928	2356	2238	5280	1920	1937	2098	2073	2348	2232	5300	1920	1939	2094	2044	2438	2231	5318

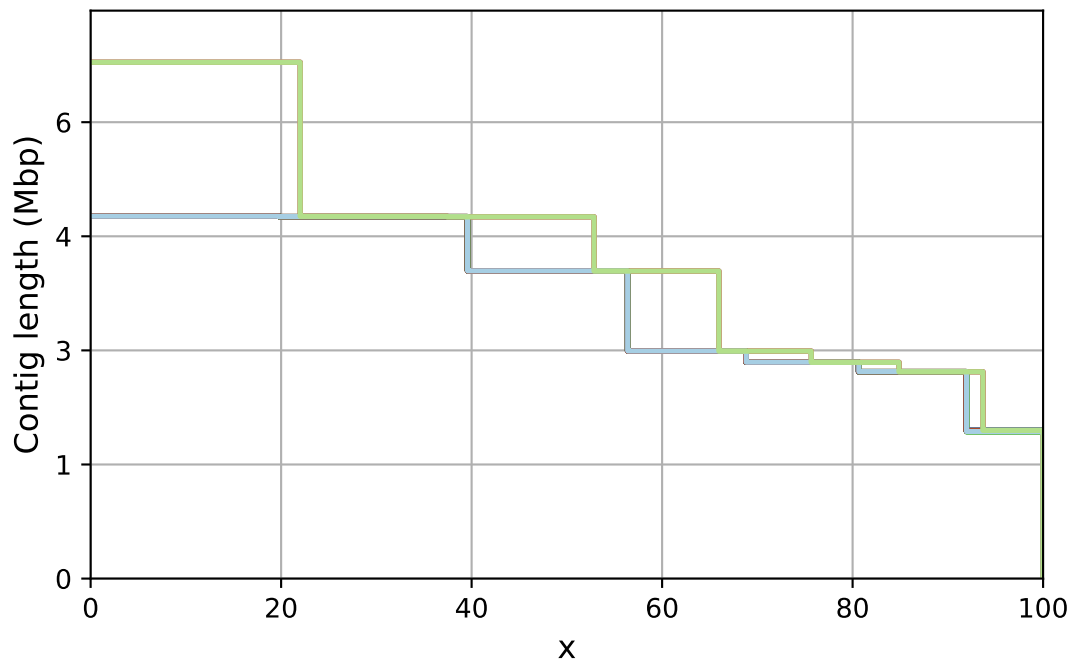
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	20956540	20949552	20952382	20945364	20942573	20937602	27788160	20956888	20950605	20957178	20948833	20942016	20936441	27792561	20960694	20950789	20961124	20955176	20945168	20939944	27795908
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	100

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_v3_1_MP

r10_1bin_v3_2_MP

r10_1bin_v3_3_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r1_medaka

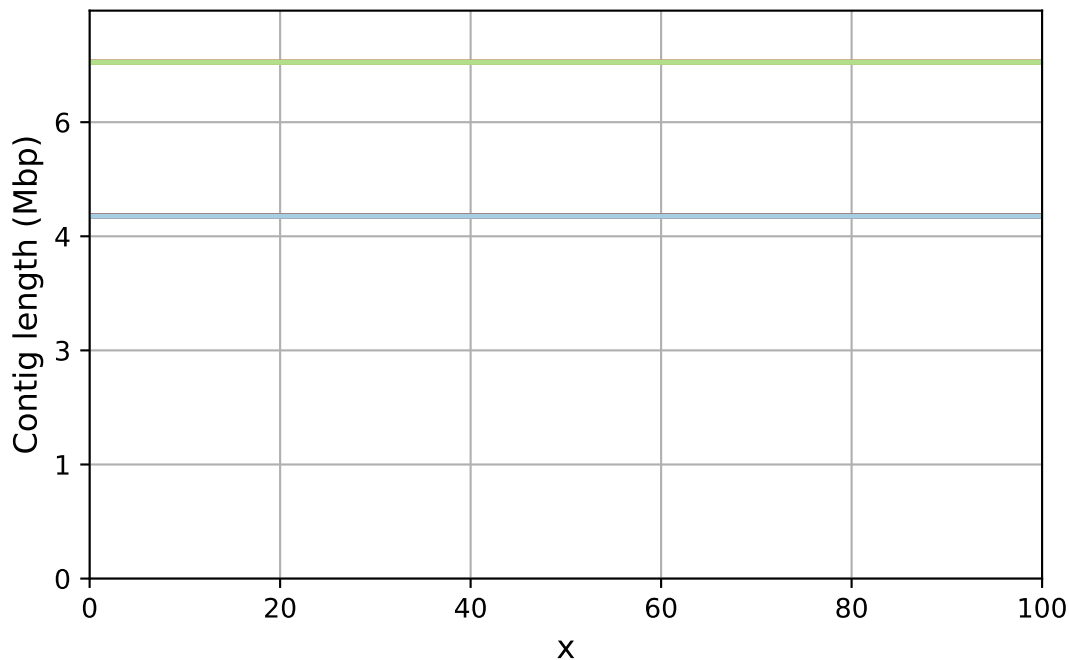
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_r2_medaka

NGx



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP

r10_1bin_v3_3_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r1_medaka

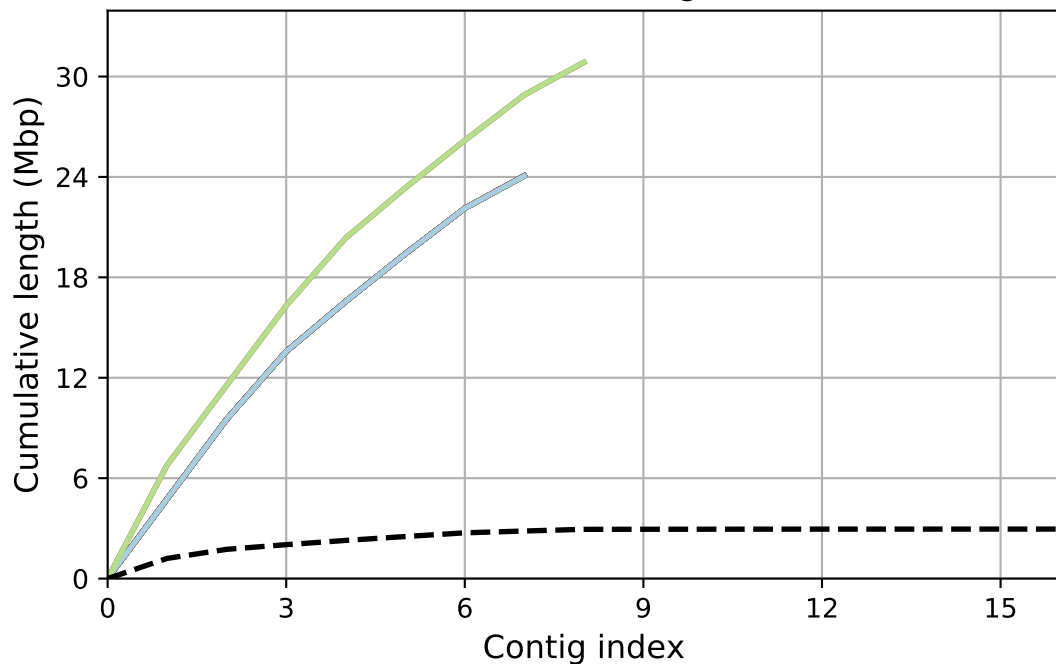
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_helen

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r2_medaka

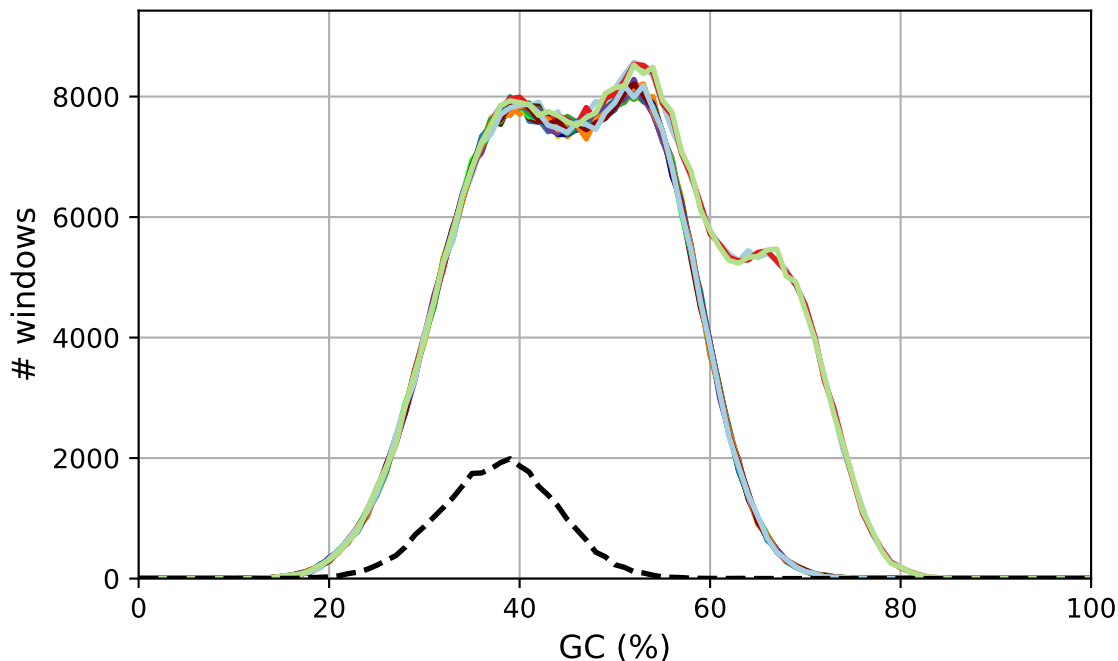
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_racon_r1

r10_1bin_v3_3_racon_r1

GC content



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1

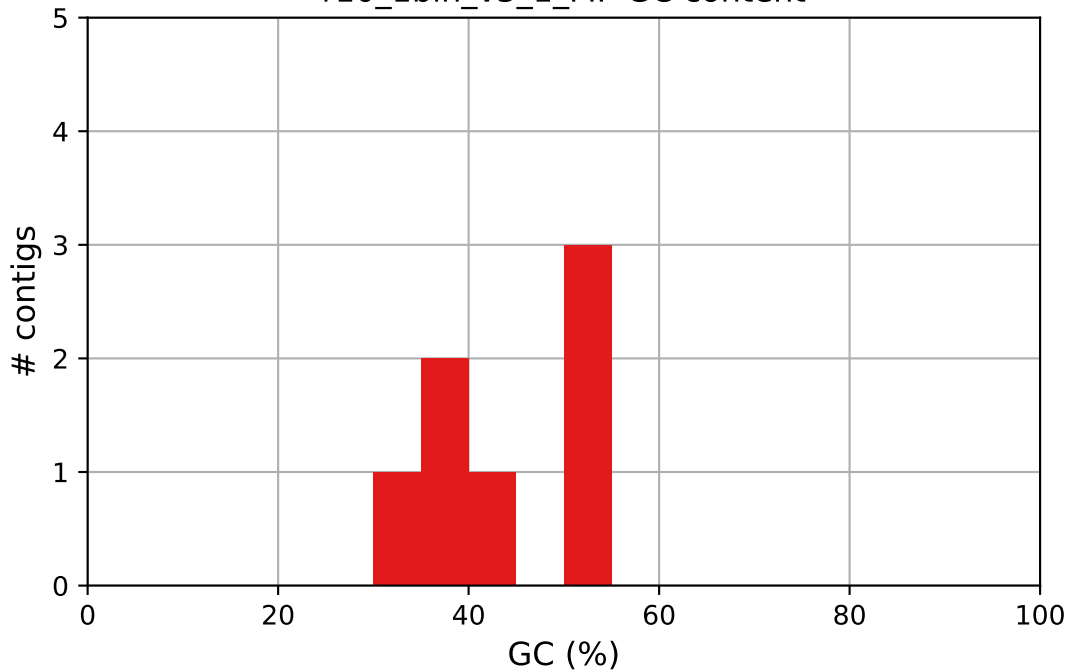
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

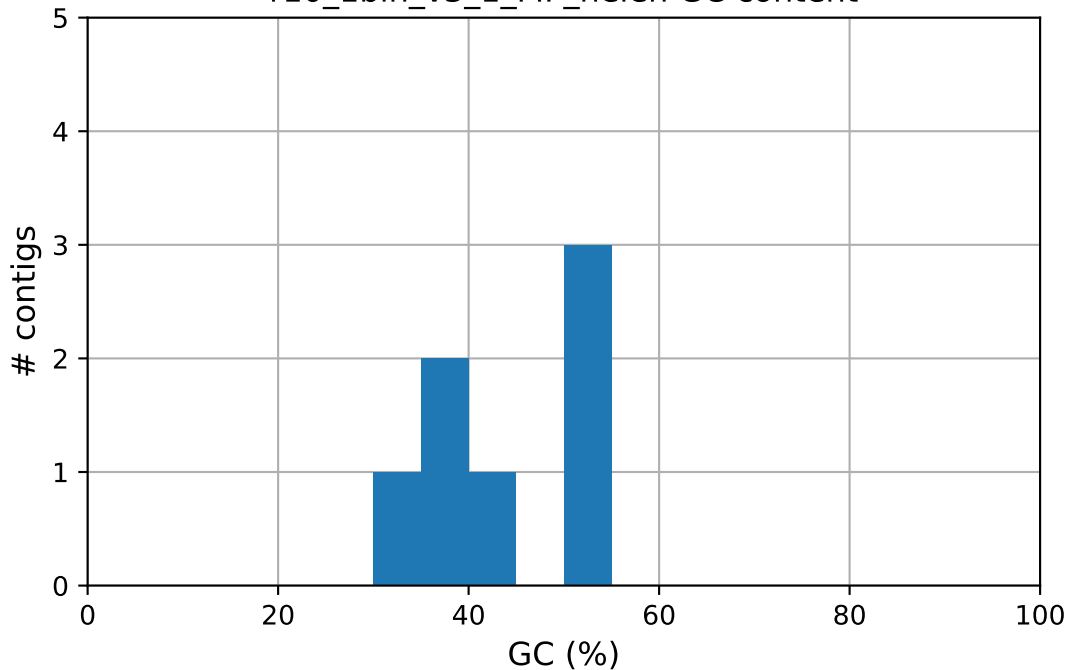
r10_1bin_v3_3_racon_r1

r10_1bin_v3_1_MP GC content



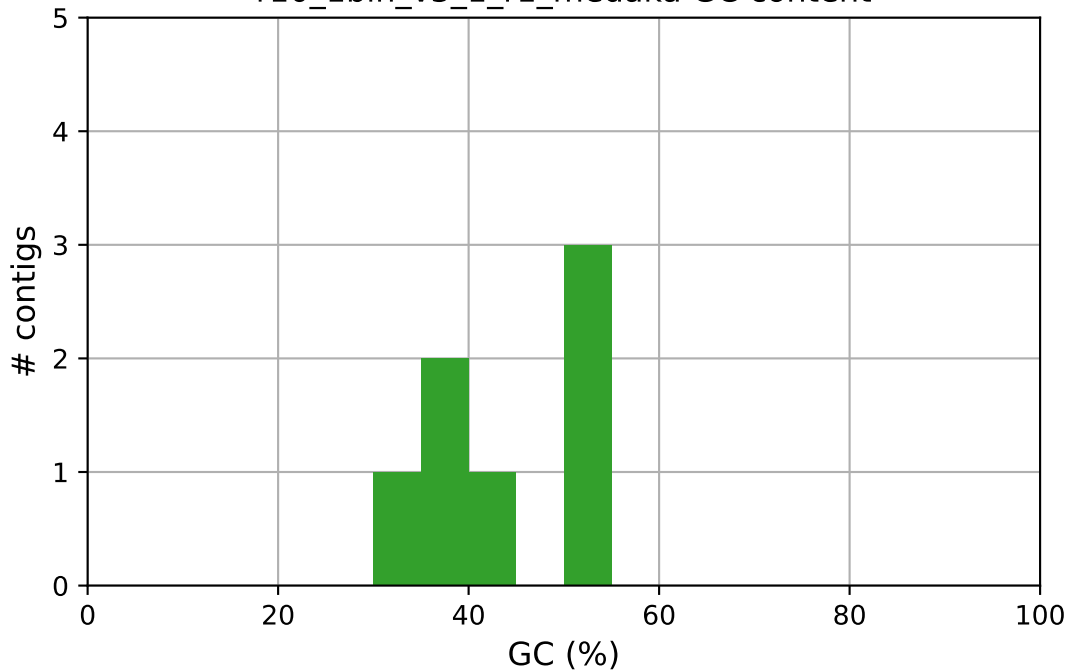
r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen GC content



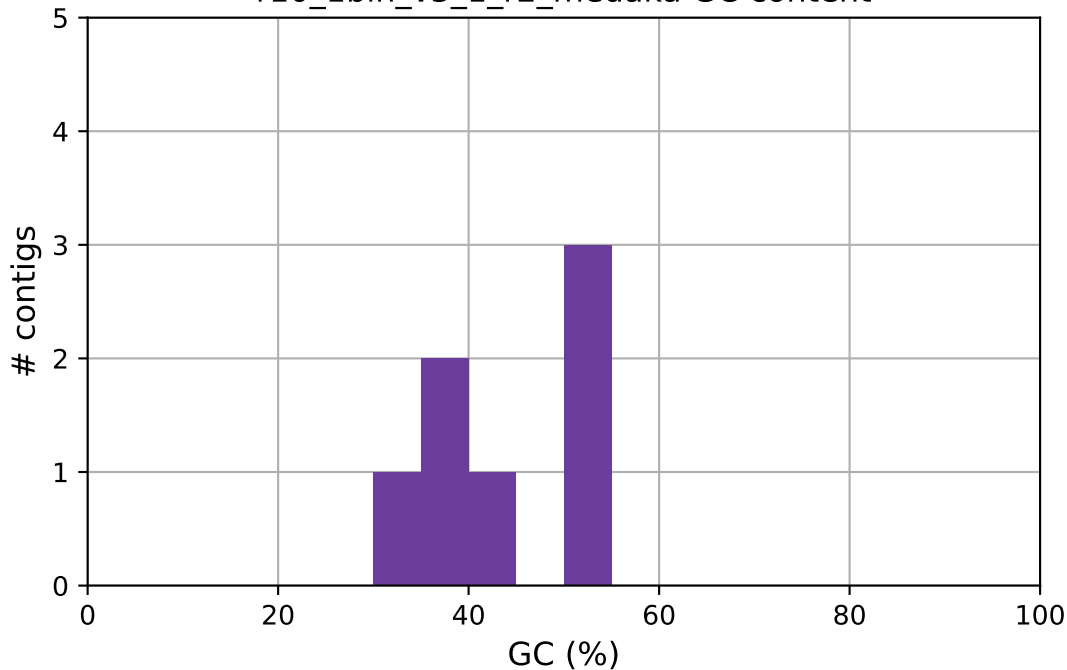
r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka GC content



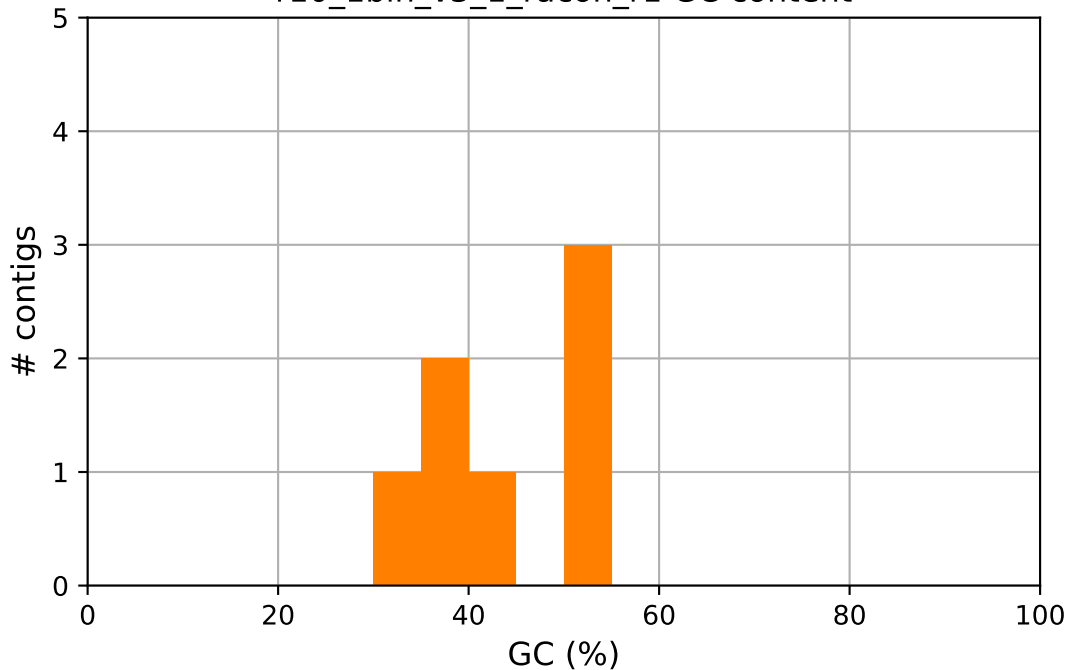
r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka GC content



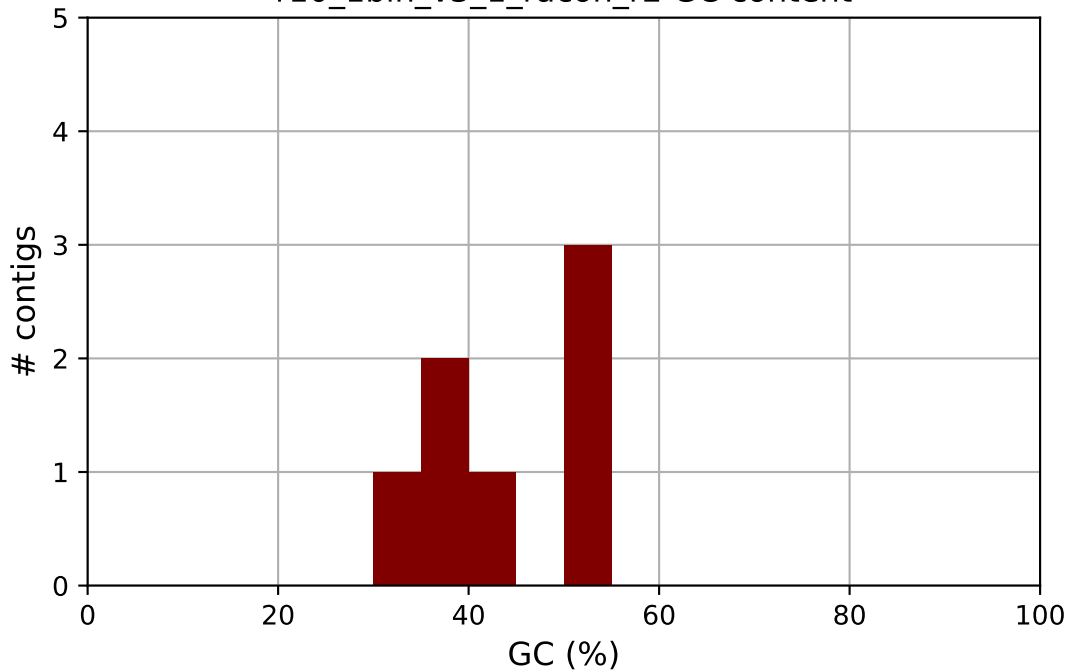
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_1_racon_r1 GC content



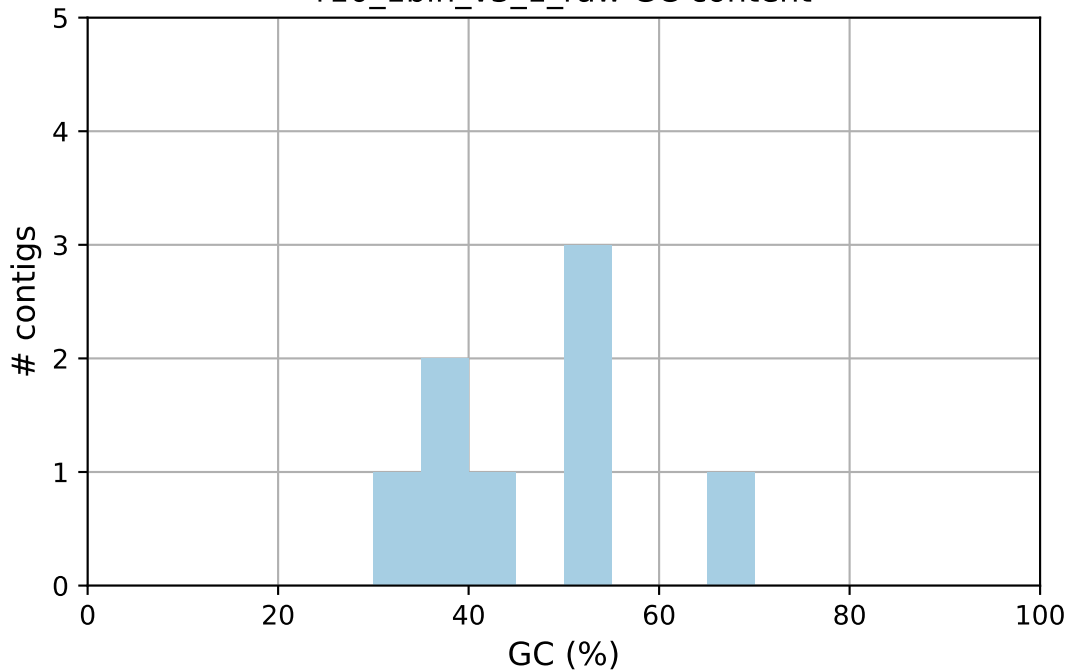
r10_1bin_v3_1_racon_r1

r10_1bin_v3_1_racon_r2 GC content



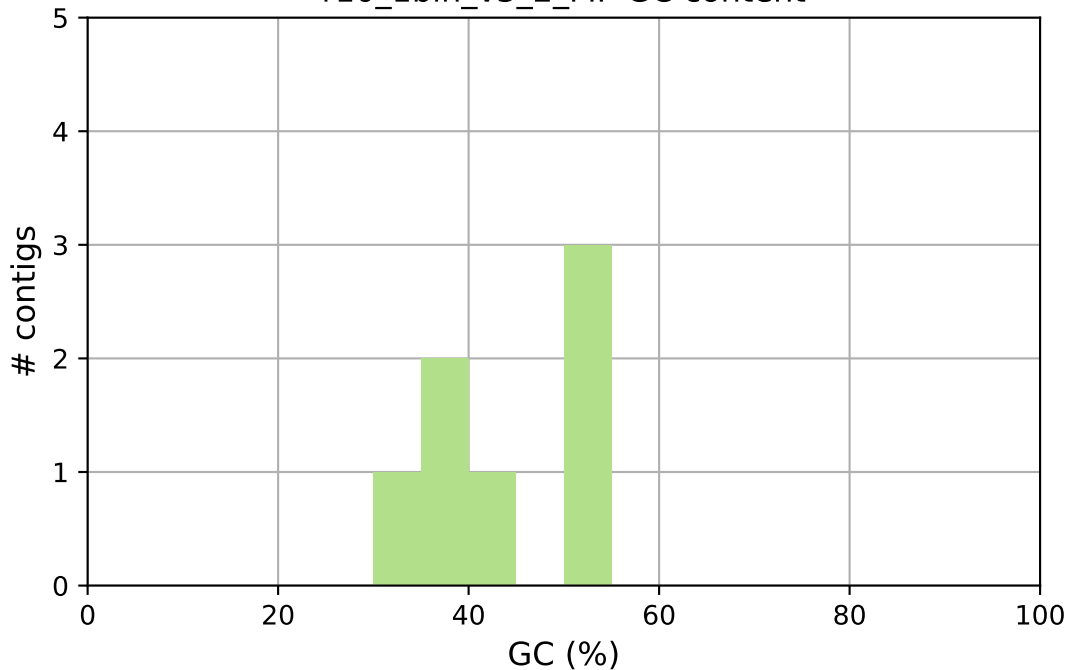
r10_1bin_v3_1_racon_r2

r10_1bin_v3_1_raw GC content



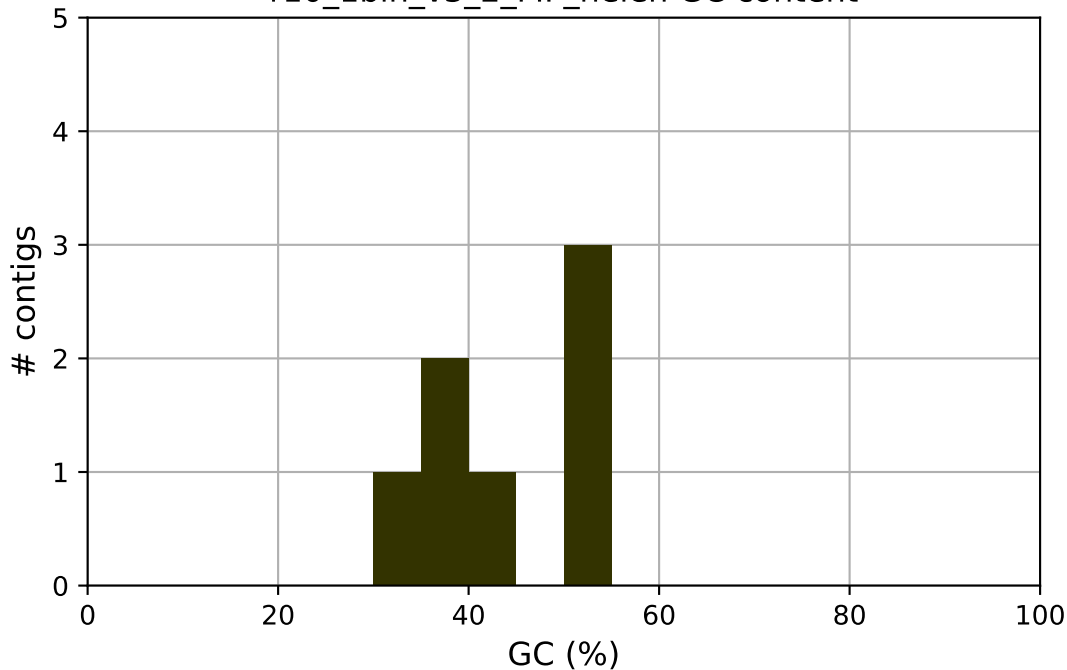
r10_1bin_v3_1_raw

r10_1bin_v3_2_MP GC content



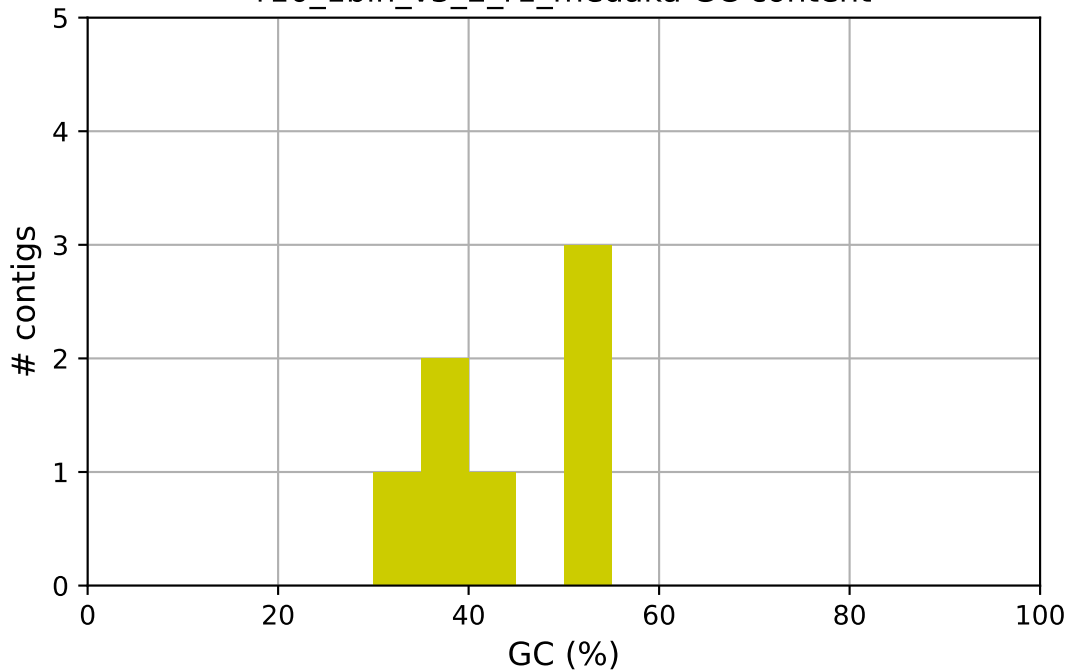
r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen GC content



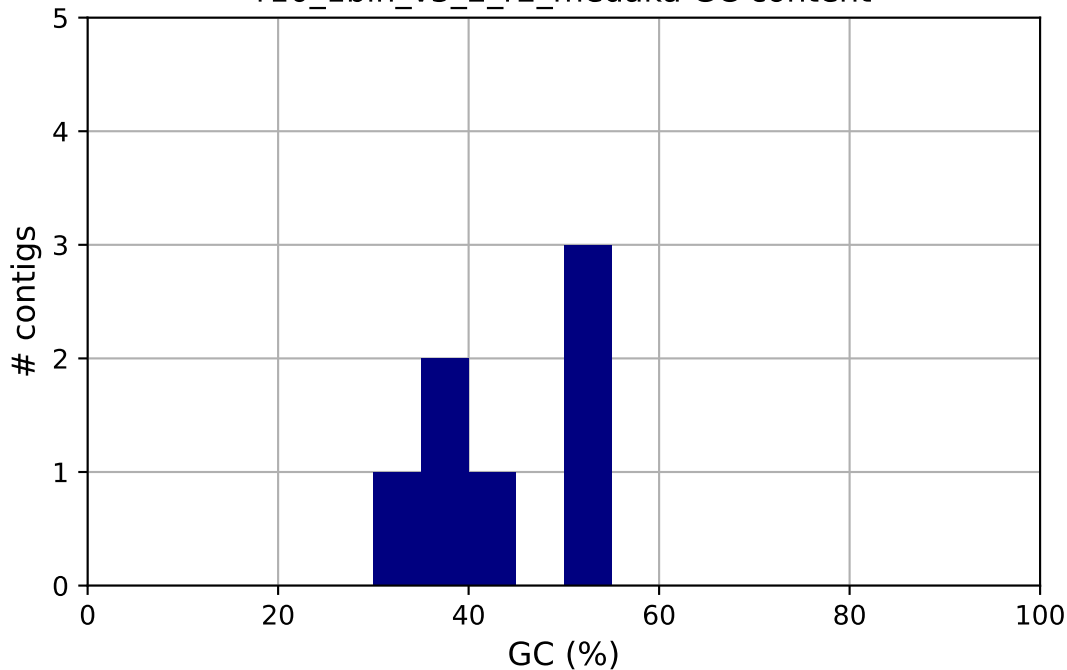
r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka GC content



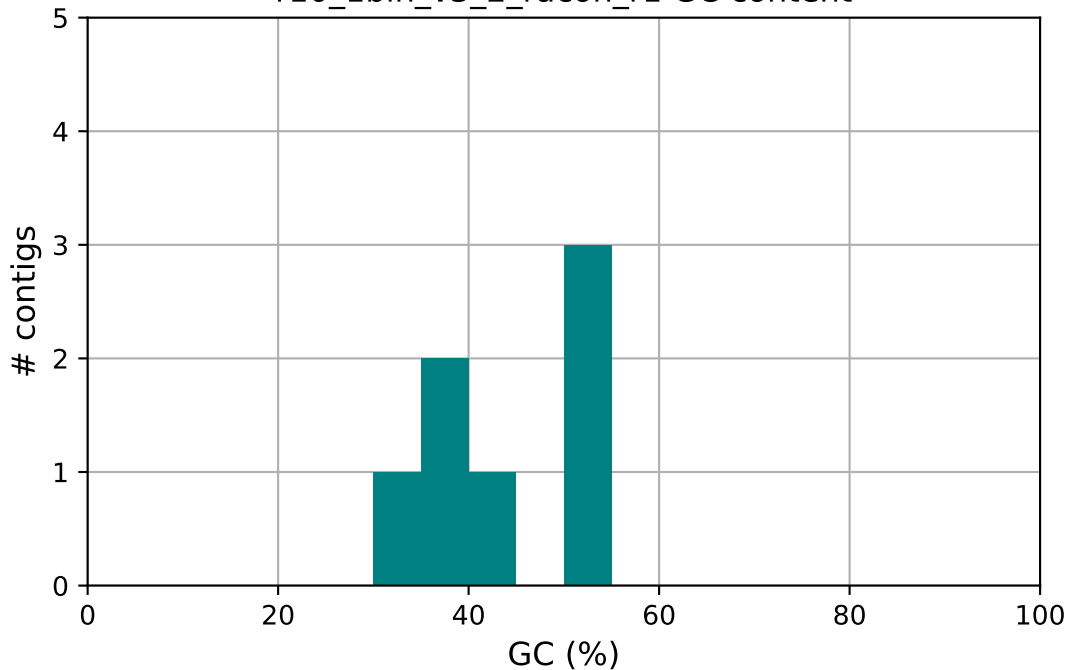
r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka GC content



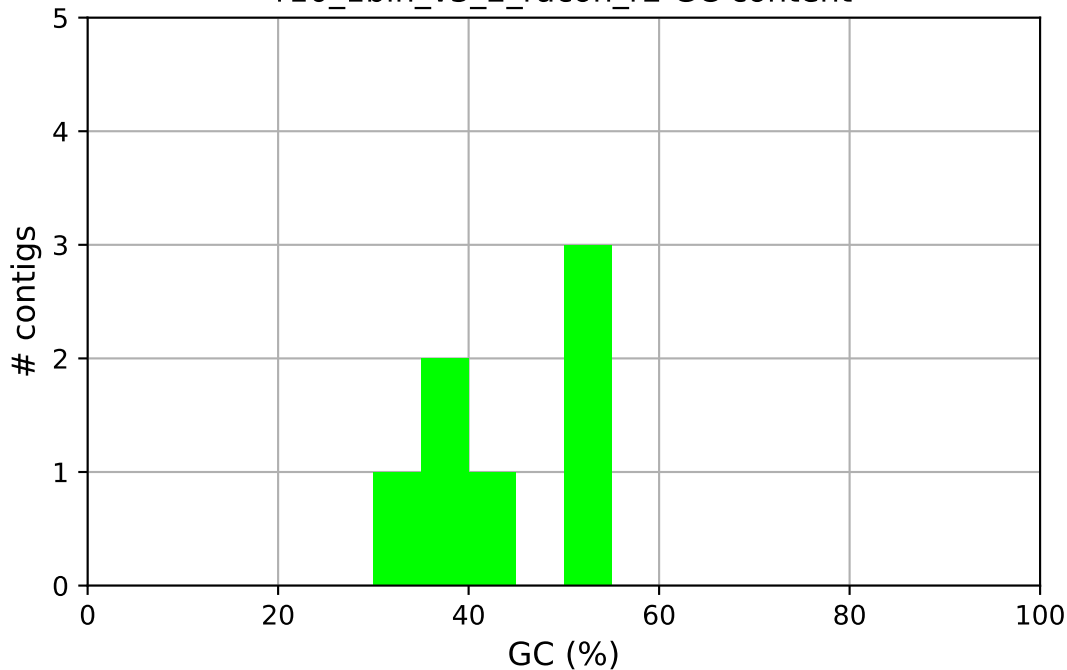
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1 GC content



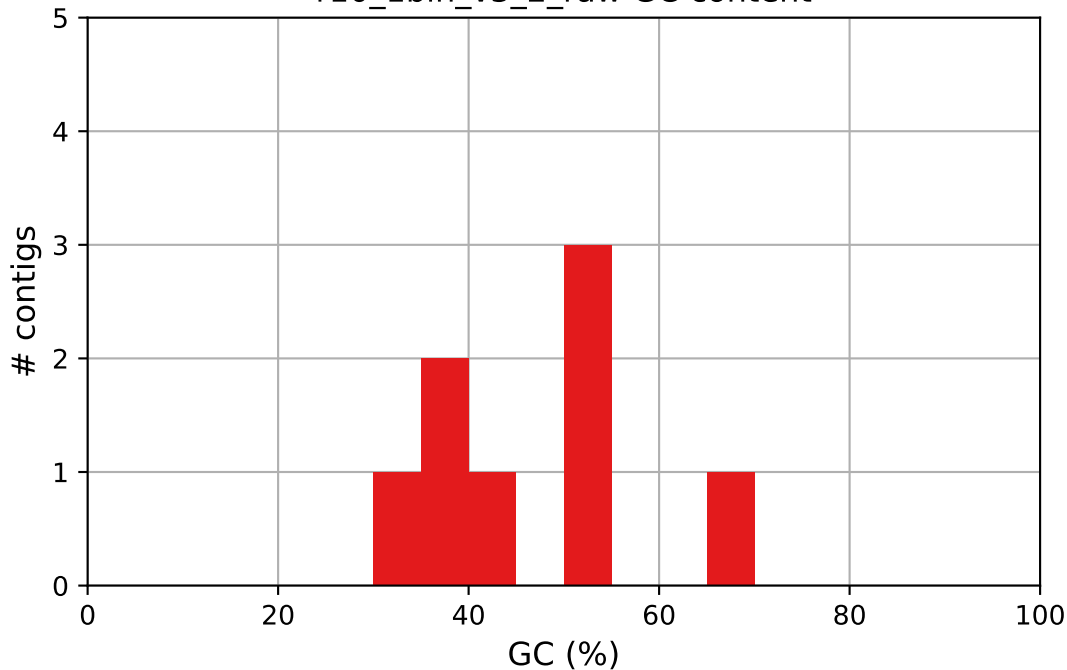
r10_1bin_v3_2_racon_r1

r10_1bin_v3_2_racon_r2 GC content



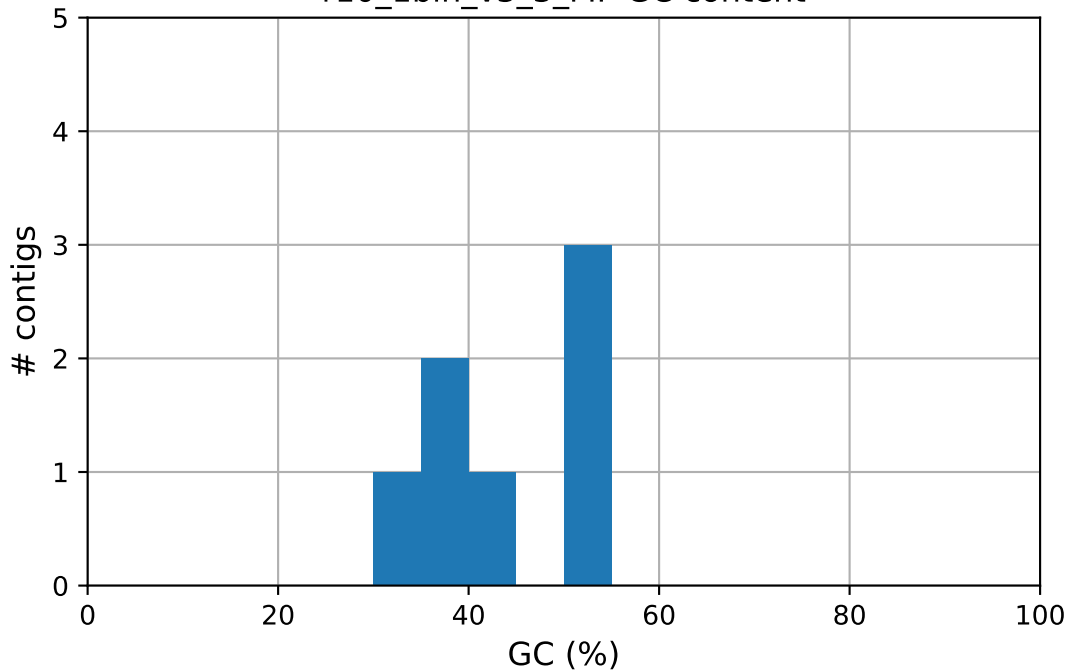
r10_1bin_v3_2_racon_r2

r10_1bin_v3_2_raw GC content



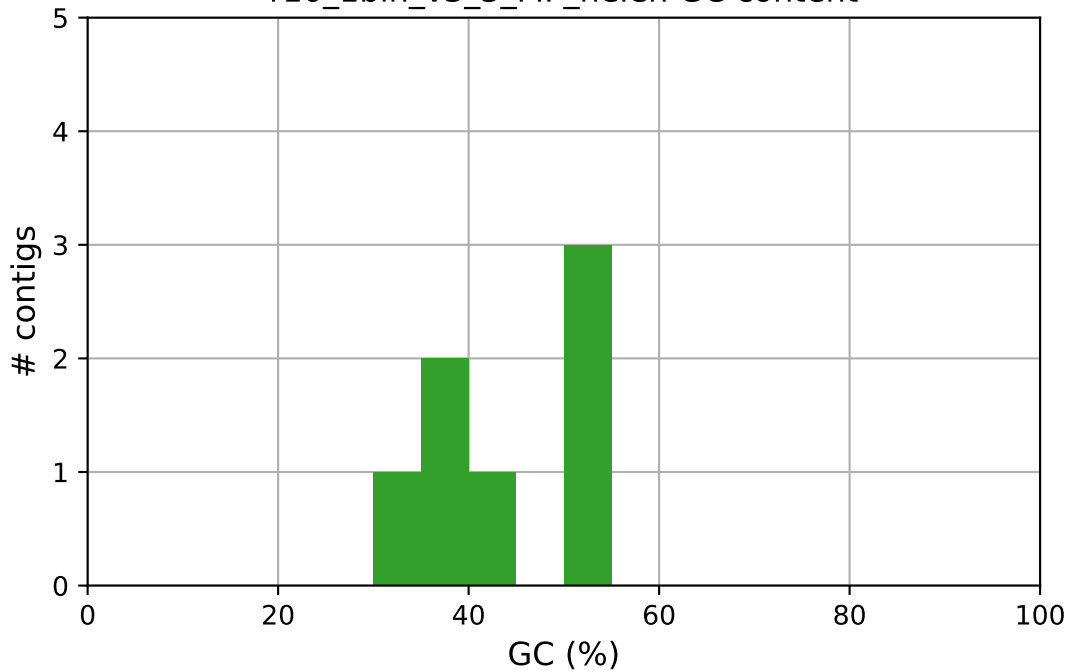
r10_1bin_v3_2_raw

r10_1bin_v3_3_MP GC content



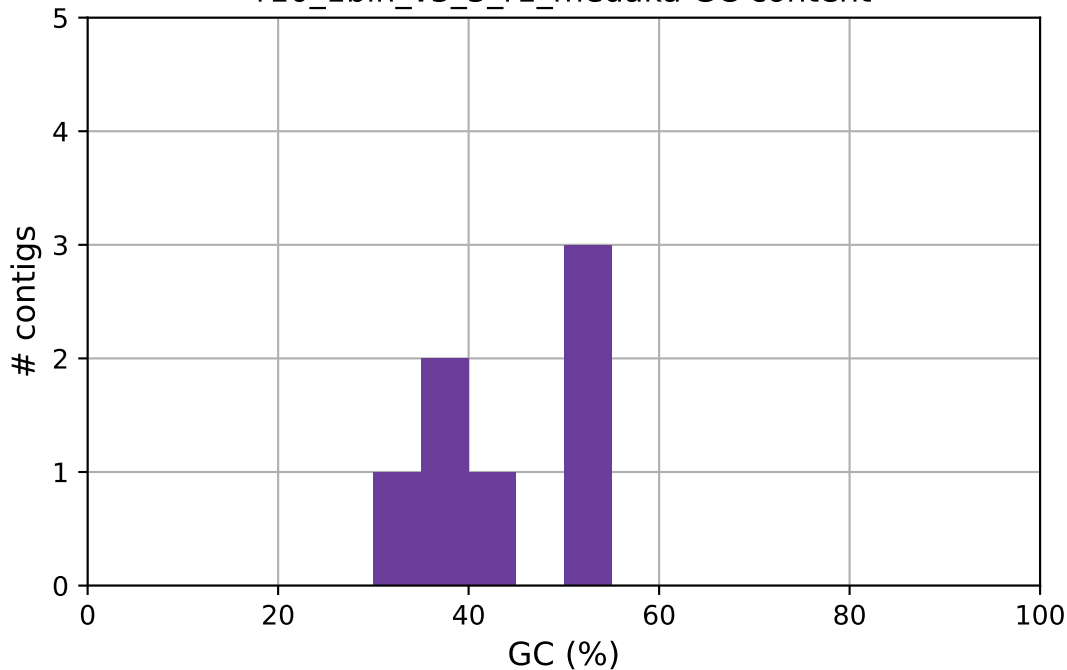
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen GC content



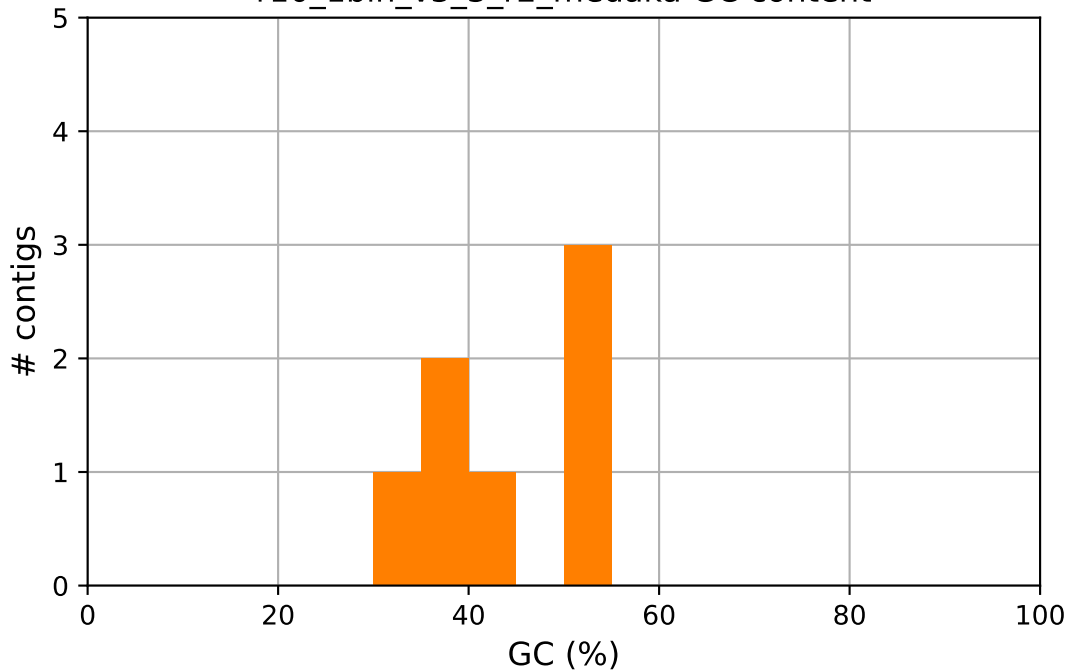
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka GC content



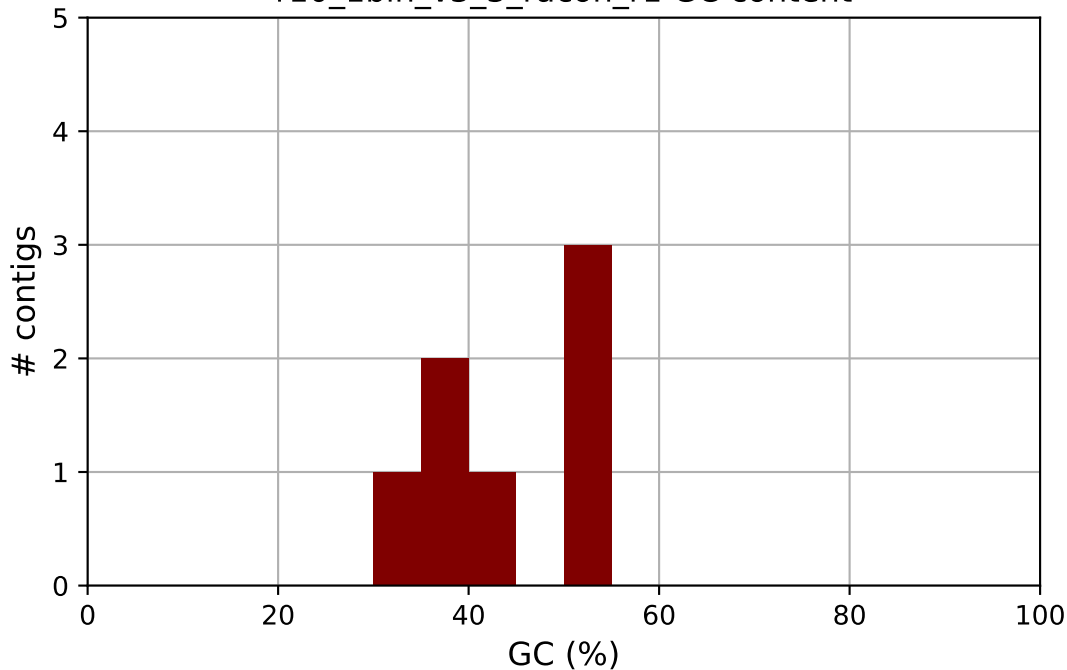
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka GC content



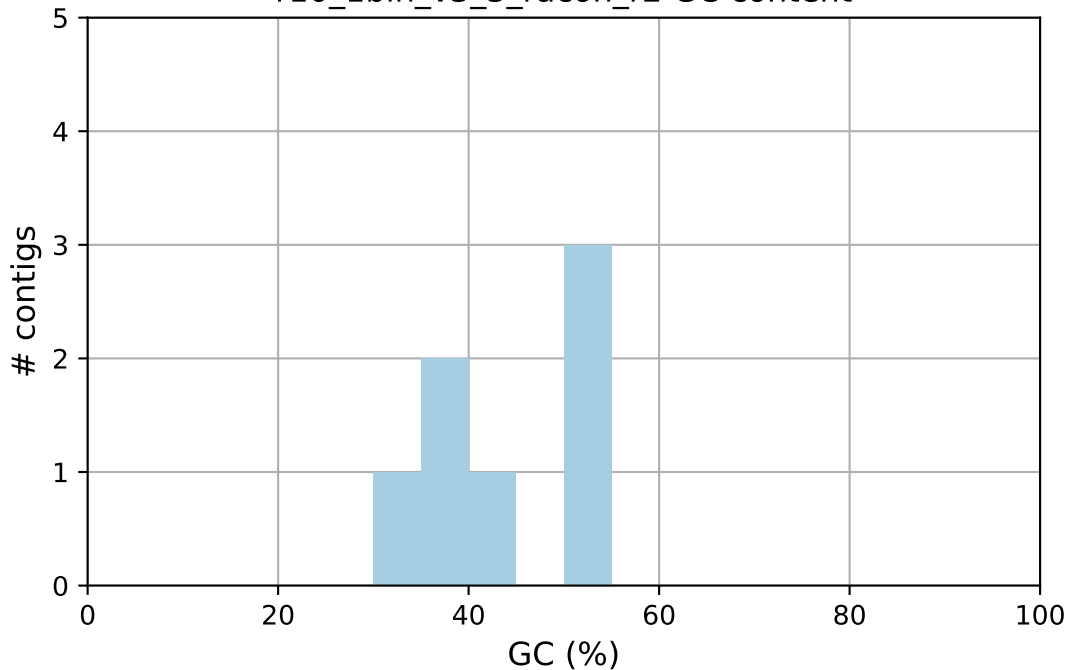
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1 GC content



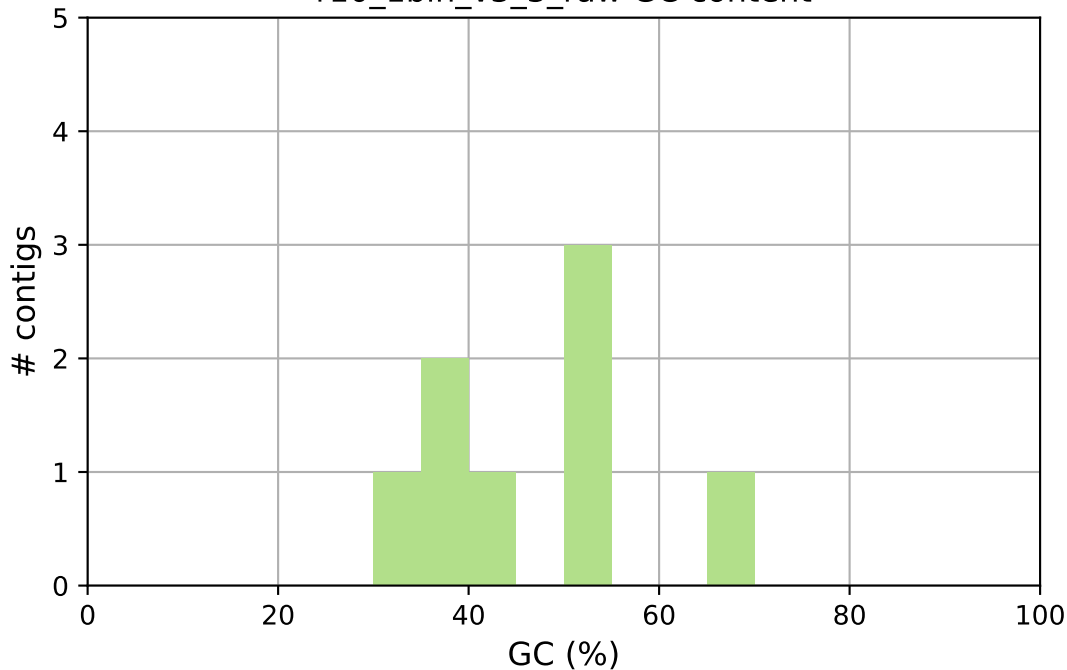
r10_1bin_v3_3_racon_r1

r10_1bin_v3_3_racon_r2 GC content



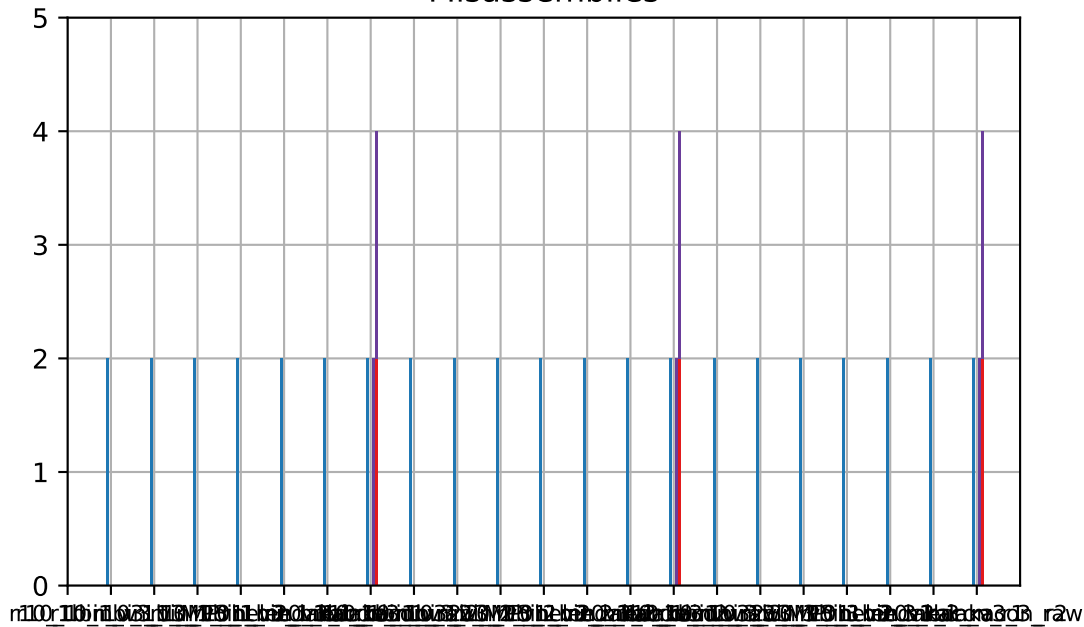
r10_1bin_v3_3_racon_r2

r10_1bin_v3_3_raw GC content



r10_1bin_v3_3_raw

Misassemblies

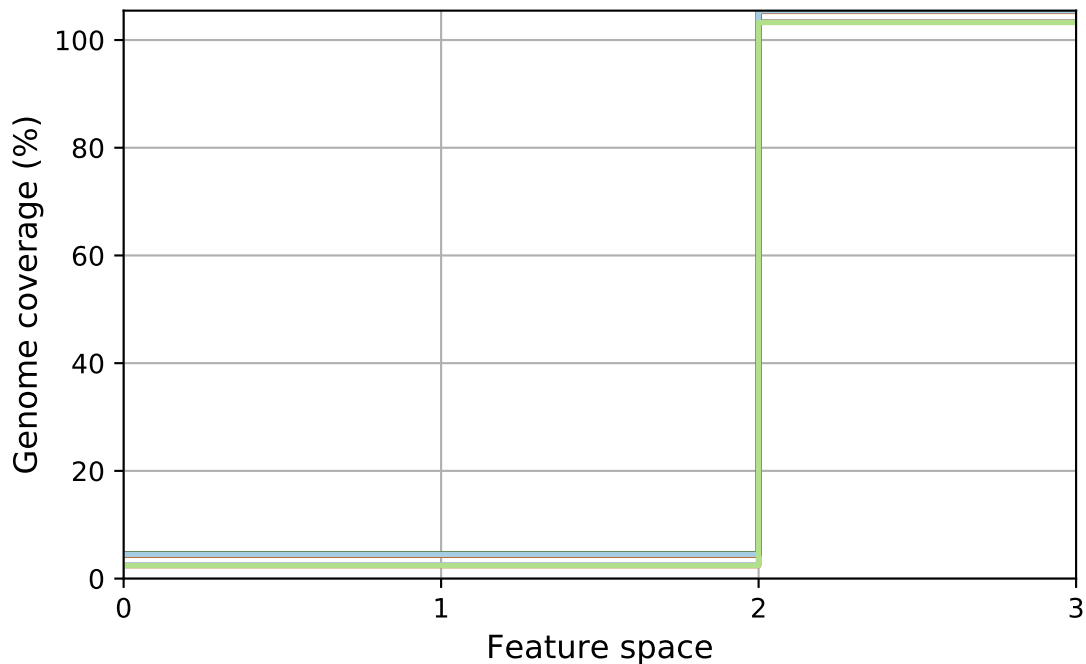


translocations



interspecies translocations

FRCurve (misassemblies)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

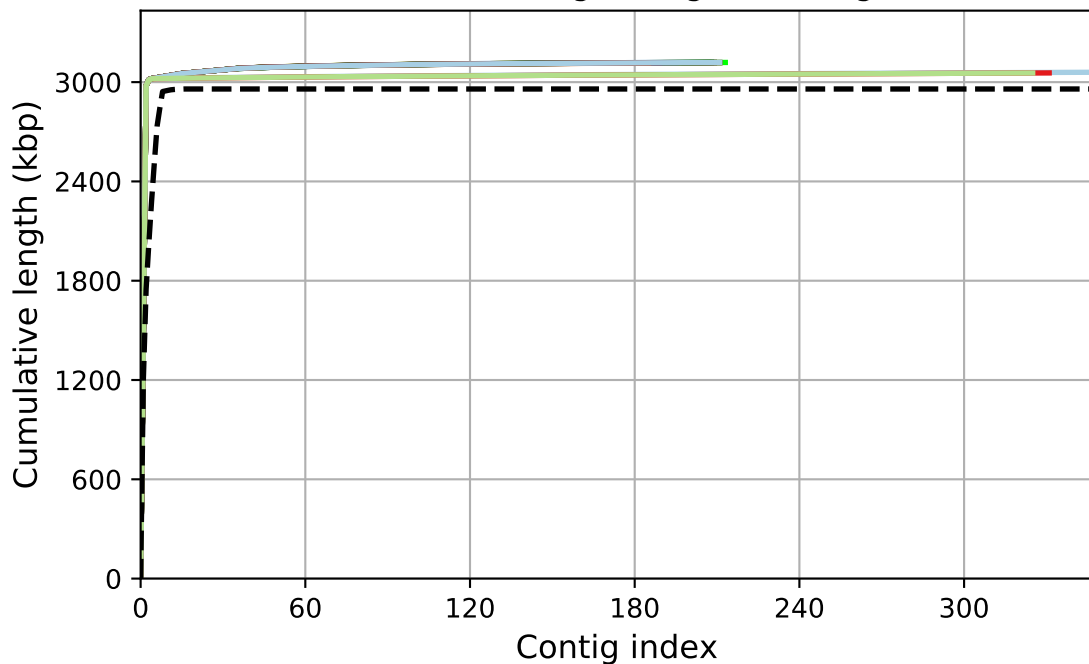
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length (aligned contigs)



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1

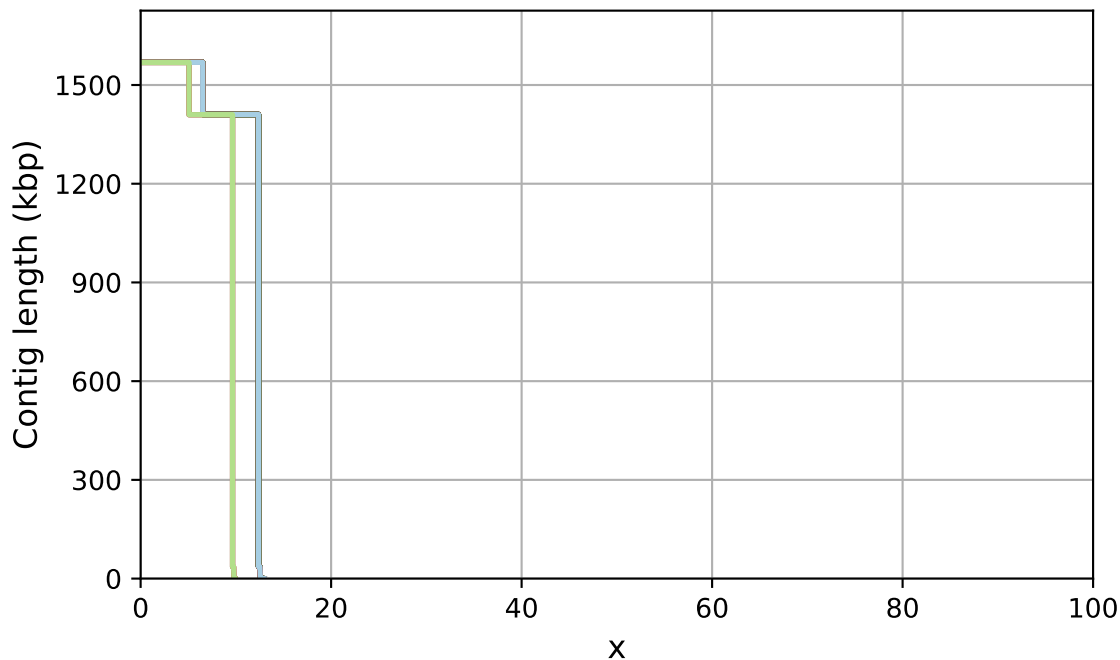
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1

NAx



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

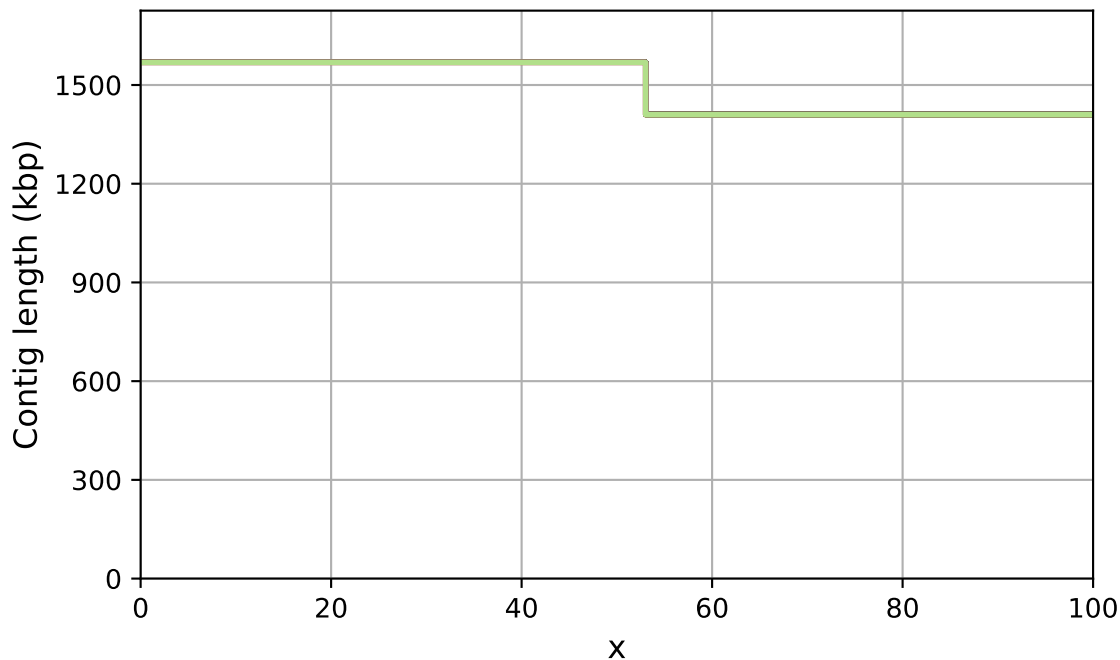
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

NGAx



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

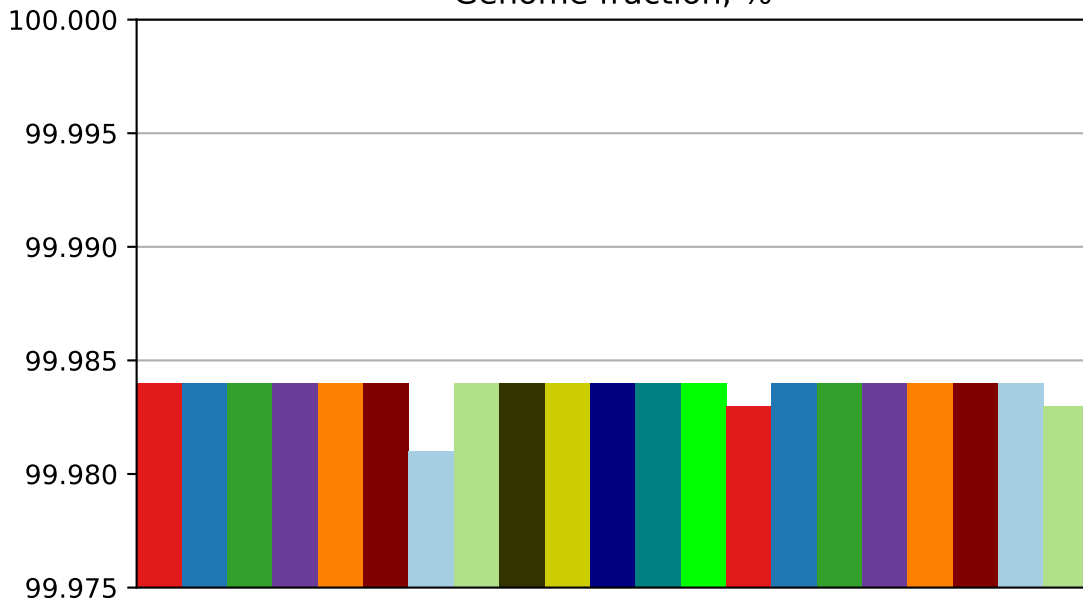
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Genome fraction, %



r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka

r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka