

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	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)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
Total length (>= 10000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
Total length (>= 25000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
Total length (>= 50000 bp)	24074828	24070090	24071888	24063470	24060900	24056048	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
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	28129756	24074490	24070611	24075114	24065831	24060635	24055783	28129787	24078180	24070683	24078524	24071188	24064158	24059056	28132800
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	44.79	44.78	51.10	44.80	44.80	44.80	44.79	44.79	44.78	51.10	44.80	44.81	44.80	44.79	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	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	2845429	2845295	2845304	2990633	2845423	2845301	2845564	2845571	2845301	2845564	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	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	18
# 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	4758942	4758045	4758082	4757996	4757676	4757433	4756098	4758934	4757811	4759010	4758465	4757950	4757851	4756089	4758933	4757839	4759025	4758469	4757998	4757867	4756074
# local misassemblies	8	8	7	7	8	7	20	8	8	8	7	8	8	22	8	8	8	7	8	8	20
# 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	19036922	19032575	19037152	19028552	19022583	19014683	23175629	19037407	19034250	19036354	19027194	19025633	19017988	23176116	19041213	19034298	19039111	19031709	19026842	19018766	23177021
Genome fraction (%)	98.918	98.920	98.920	98.920	98.920	98.920	98.894	98.918	98.919	98.920	98.920	98.920	98.920	98.896	98.918	98.919	98.920	98.920	98.920	98.920	98.896
Duplication ratio	1.075	1.075	1.074	1.074	1.075	1.076	1.057	1.075	1.075	1.075	1.075	1.075	1.075	1.057	1.075	1.075	1.075	1.075	1.075	1.076	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	0.36
# mismatches per 100 kbp	415.61	412.85	406.27	406.74	419.10	426.16	461.64	412.19	409.33	413.98	415.58	409.69	416.88	462.06	411.57	409.16	416.13	417.50	416.09	422.81	464.52
# indels per 100 kbp	21.11	15.22	11.16	11.22	40.50	37.17	224.45	21.15	16.26	23.00	22.81	39.52	37.20	224.32	20.87	15.96	23.30	22.96	39.69	36.90	225.45
Largest alignment	2147343	2147007	2147107	2147023	2147099	2146784	1864181	1342502	1342445	1342625	1342628	1342266	1342305	1341457	1342502	1342444	1342628	1342618	1342279	1342297	1341457
Total aligned length	5035509	5035108	5032339	5032521	5035917	5038966	4951958	5034741	5036417	5036294	5034617	5032658	5035452	4951489	5034624	5034098	5037070	5037135	5034971	5037946	4953501
NGA50	613187	613135	613152	613150	613070	613072	612982	745393	745356	745429	745422	745296	745265	744988	745393	745355	745435	745424	745286	745274	744979
NGA75	520322	520294	520304	520304	520214	520249	373736	611508	611476	611574	611566	611445	611452	433868	611507	611503	611578	611575	611454	611450	433862
LGA50	2	2	2	2	2	2	2	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LGA75	4	4	4	4	4	4	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_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	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	18
# contig misassemblies	15	15	15	15	15	15	19	15	16	15	15	15	15	18	15	16	15	15	15	15	18
# 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	16
# 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	4758942	4758045	4758082	4757996	4757676	4757433	4756098	4758934	4757811	4759010	4758465	4757950	4757851	4756089	4758933	4757839	4759025	4758469	4757998	4757867	4756074
# 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	14	6	4	4	4	4	4	14	6	4	4	4	4	4	14
# local misassemblies	8	8	7	7	8	7	20	8	8	8	7	8	8	22	8	8	8	7	8	8	20
# 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	11	14	14	14	14	14	14	10	14	14	14	14	14	14	11
# 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	19475	19346	19038	19060	19639	19970	21627	19315	19181	19399	19474	19198	19535	21647	19286	19173	19500	19564	19498	19813	21762
# indels	989	713	523	526	1898	1742	10515	991	762	1078	1069	1852	1743	10509	978	748	1092	1076	1860	1729	10562
# indels (<= 5 bp)	890	617	432	436	1807	1650	10334	895	661	988	978	1759	1652	10332	881	648	1002	985	1768	1639	10386
# indels (> 5 bp)	99	96	91	90	91	92	181	96	101	90	91	93	91	177	97	100	90	91	92	90	176
Indels length	5605	5283	5081	5003	6546	6358	19306	5552	5335	5531	5577	6473	6306	19191	5528	5302	5553	5585	6485	6279	19264

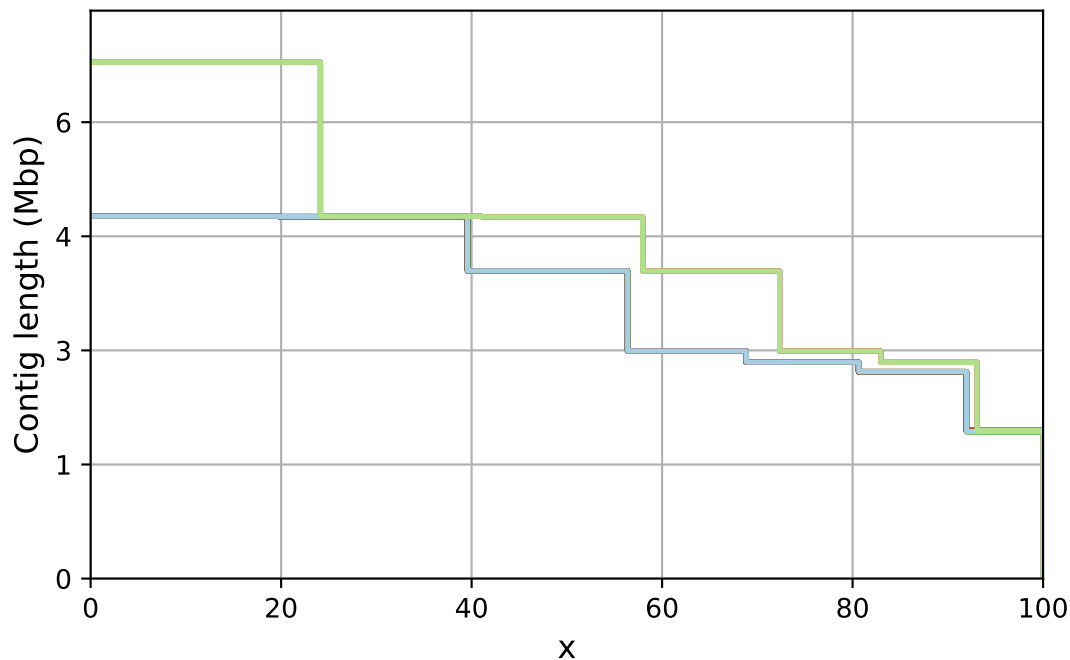
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	19036922	19032575	19037152	19028552	19022583	19014683	23175629	19037407	19034250	19036354	19027194	19025633	19017988	23176116	19041213	19034298	19039111	19031709	19026842	19018766	23177021
# 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

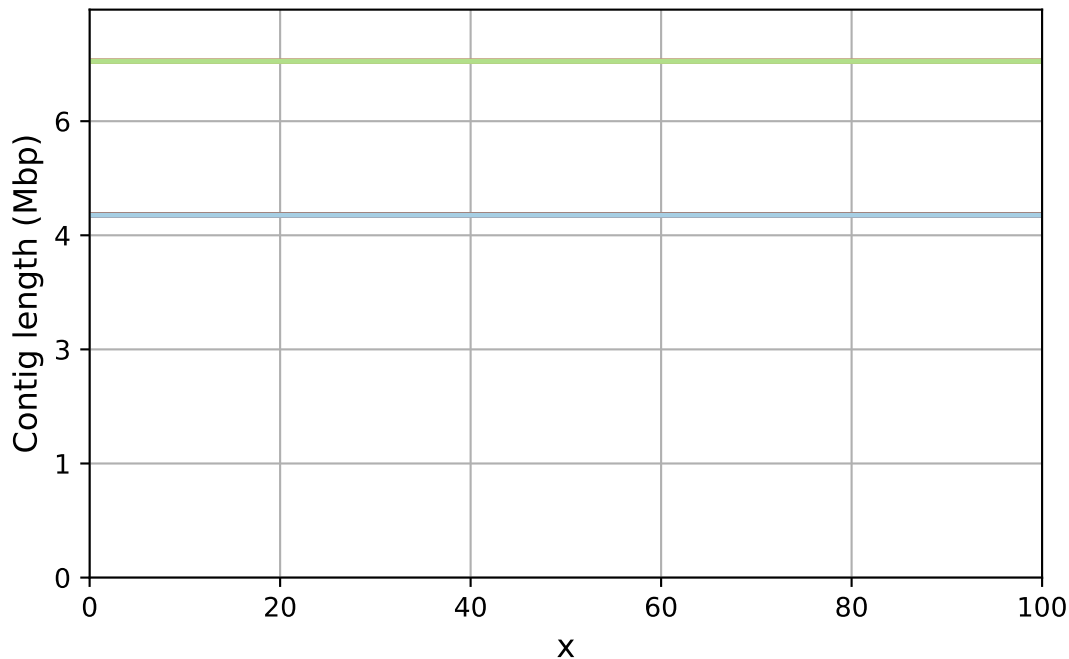
r10_1bin_v3_3_r1_medaka

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_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

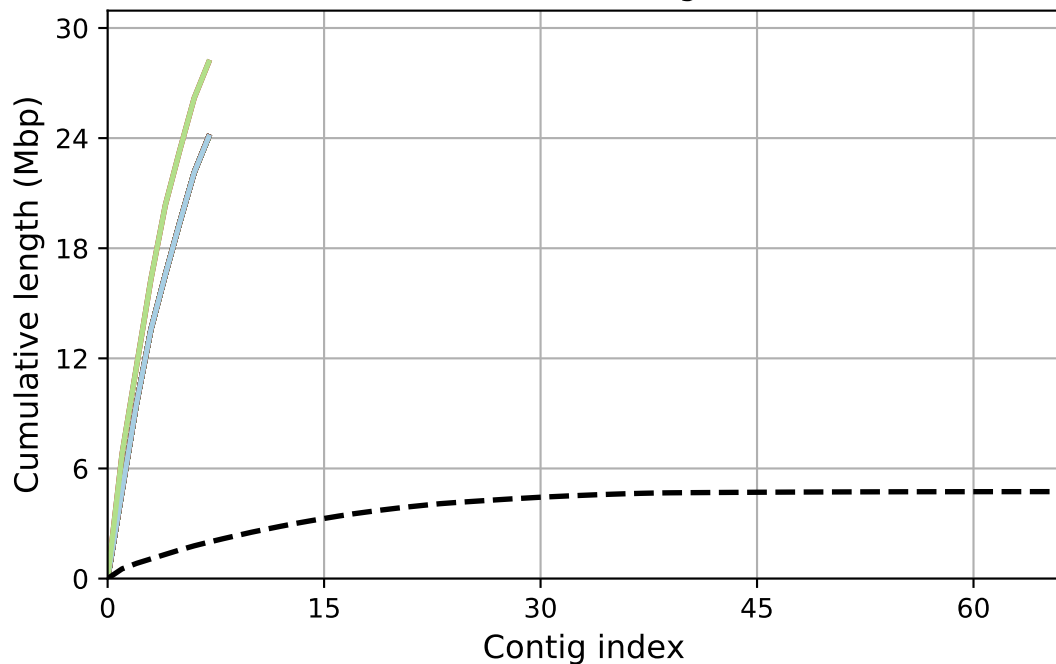
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Cumulative length



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

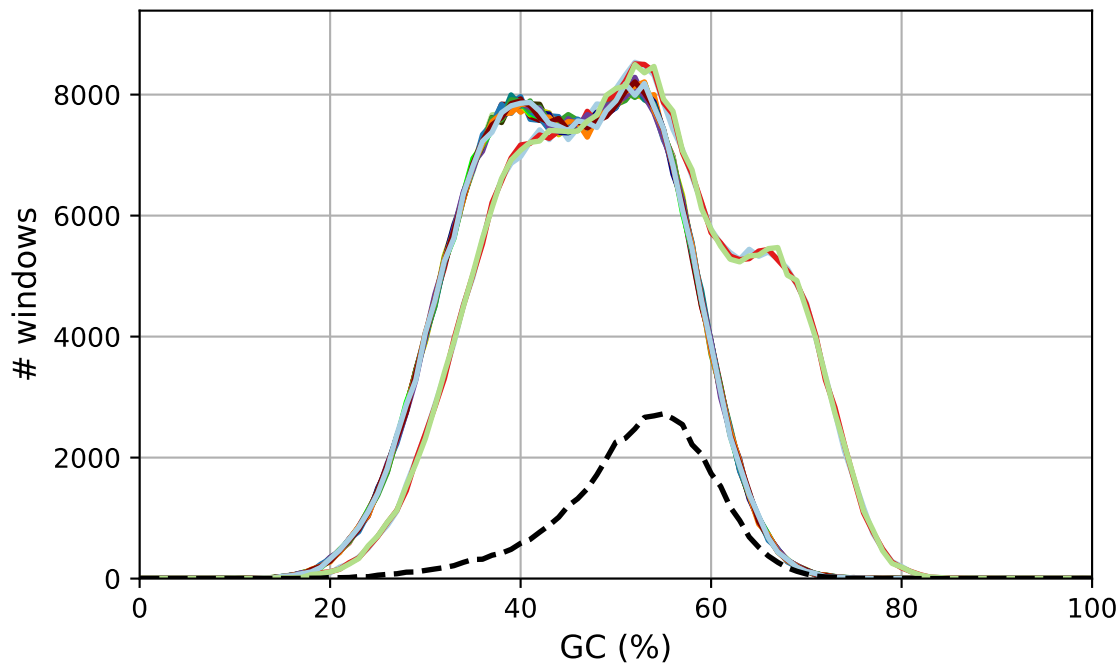
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1

GC content



r10_1bin_v3_1_MP

r10_1bin_v3_2_MP_helen

r10_1bin_v3_3_MP_h

r10_1bin_v3_1_MP_helen

r10_1bin_v3_2_r1_medaka

r10_1bin_v3_3_r1_m

r10_1bin_v3_1_r1_medaka

r10_1bin_v3_2_r2_medaka

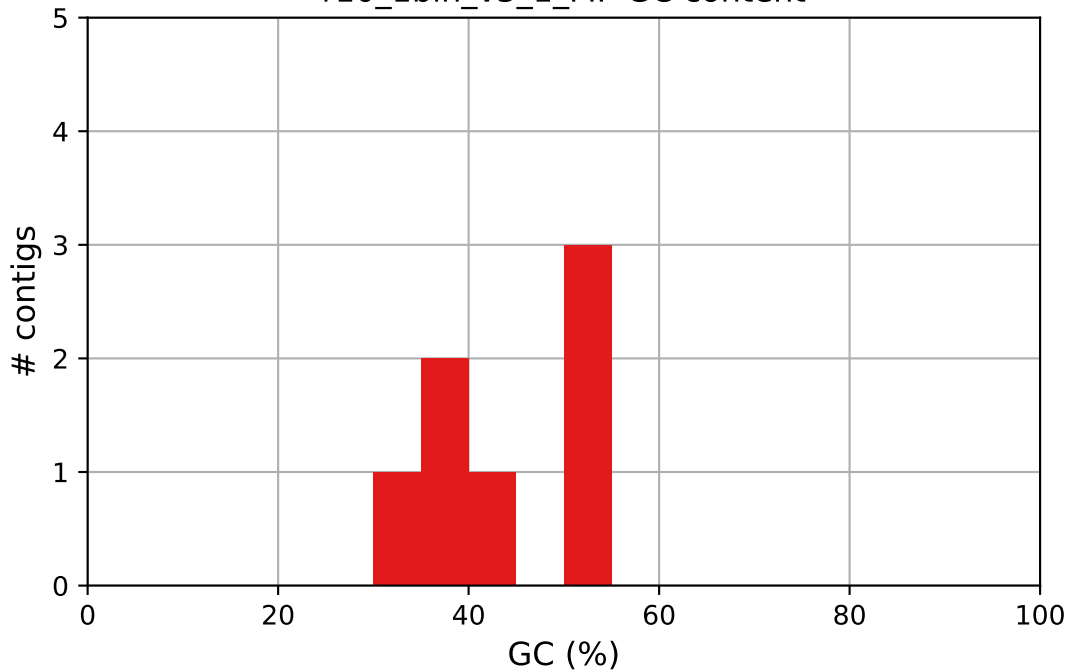
r10_1bin_v3_3_r2_m

r10_1bin_v3_1_r2_medaka

r10_1bin_v3_2_racon_r1

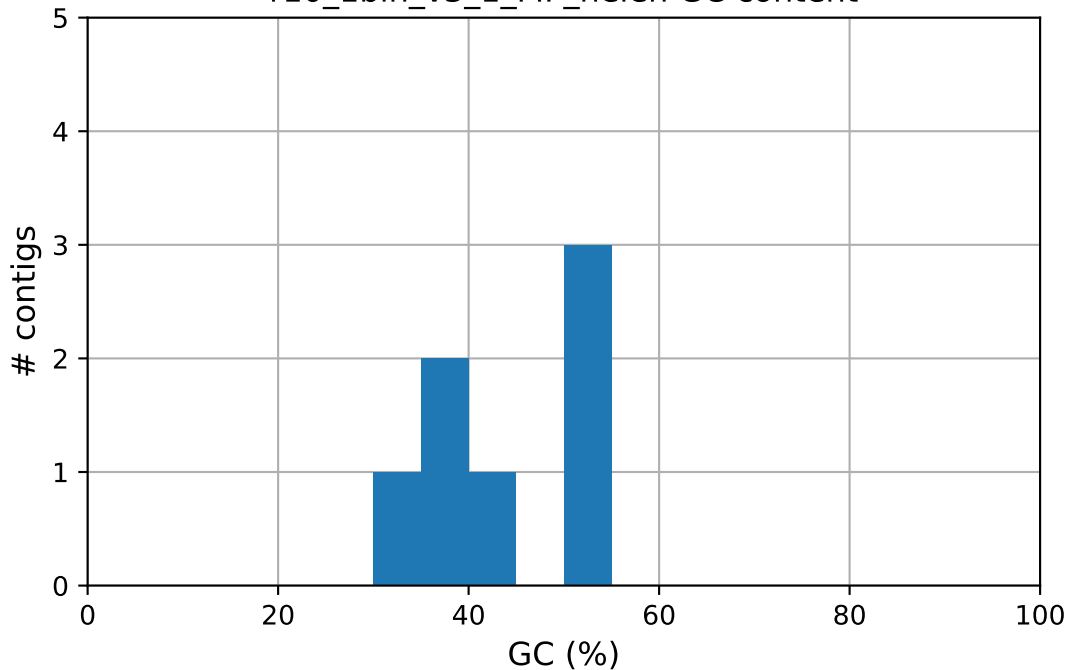
r10_1bin_v3_3_racon_r1

r10_1bin_v3_1_MP GC content



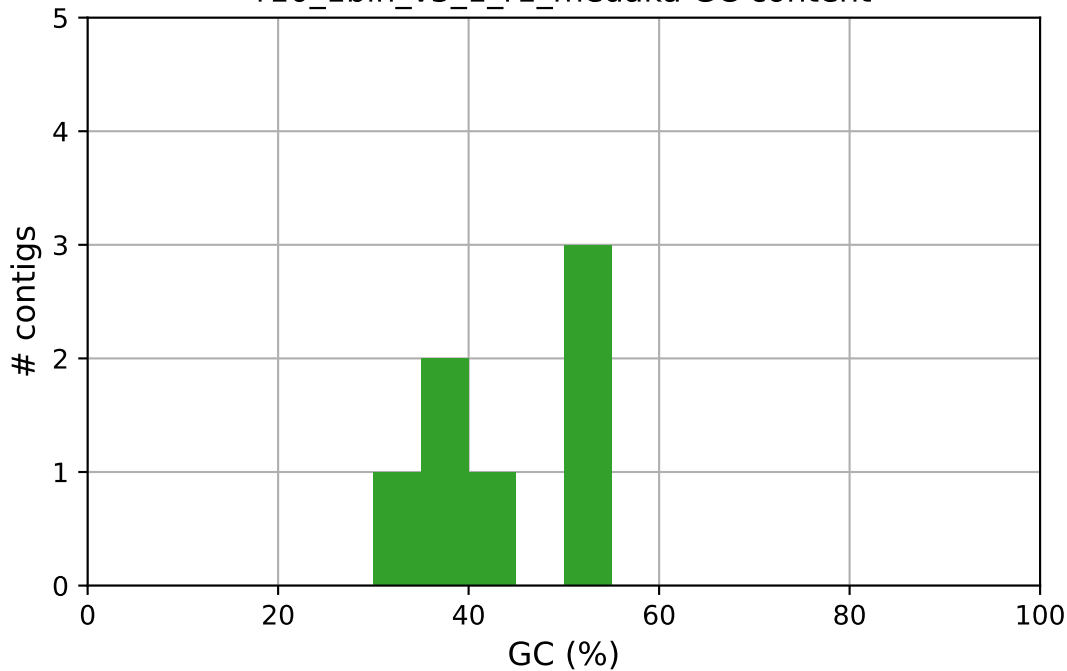
r10_1bin_v3_1_MP

r10_1bin_v3_1_MP_helen GC content



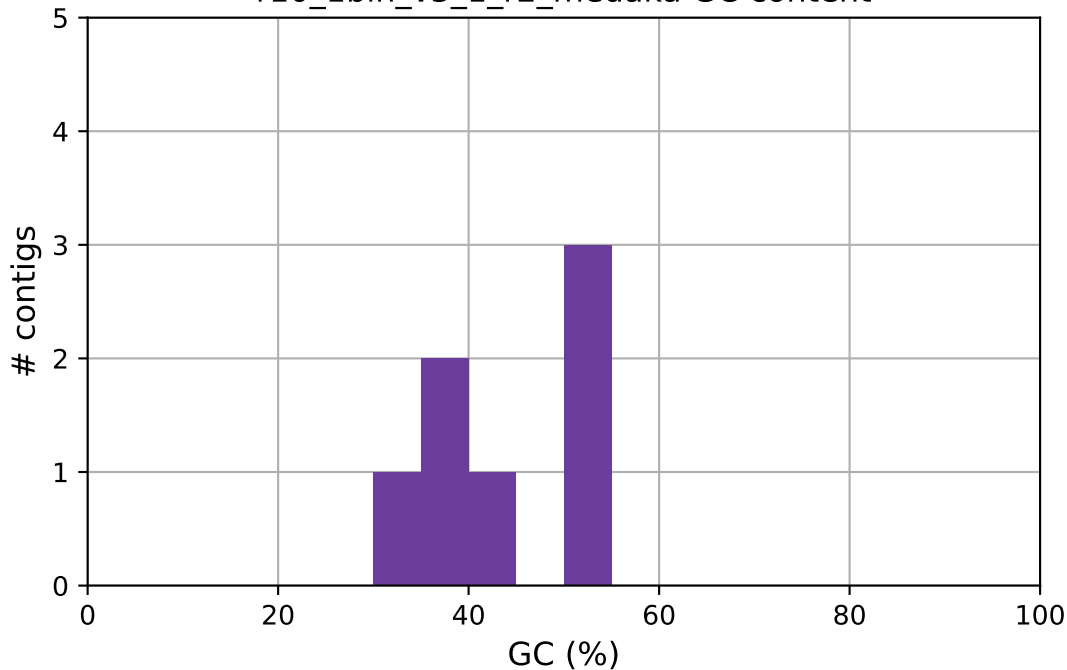
r10_1bin_v3_1_MP_helen

r10_1bin_v3_1_r1_medaka GC content



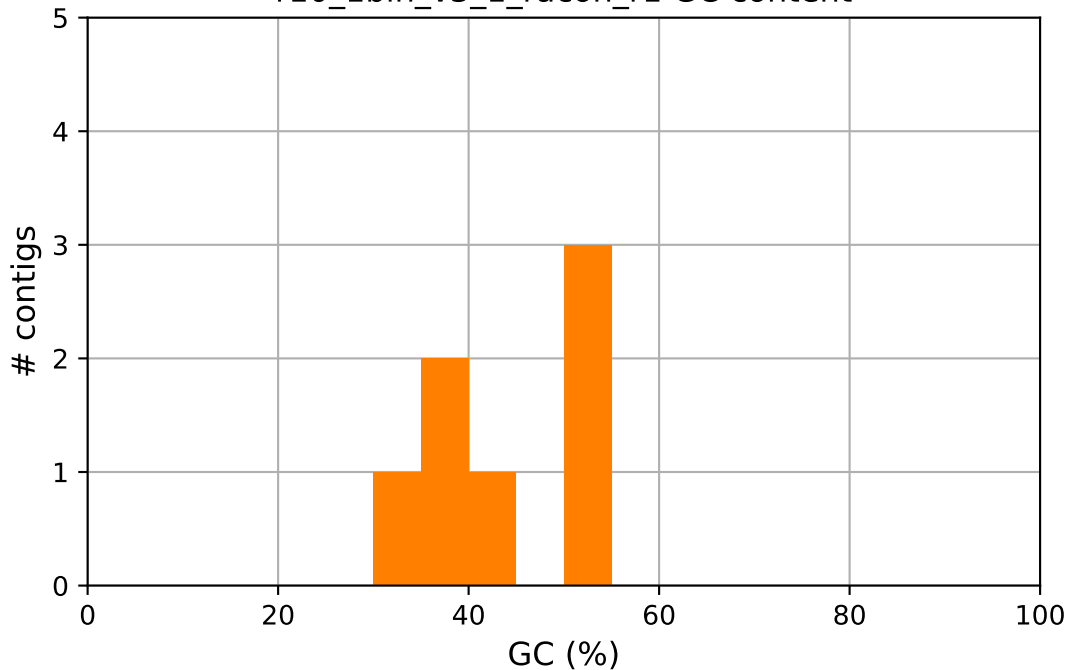
r10_1bin_v3_1_r1_medaka

r10_1bin_v3_1_r2_medaka GC content



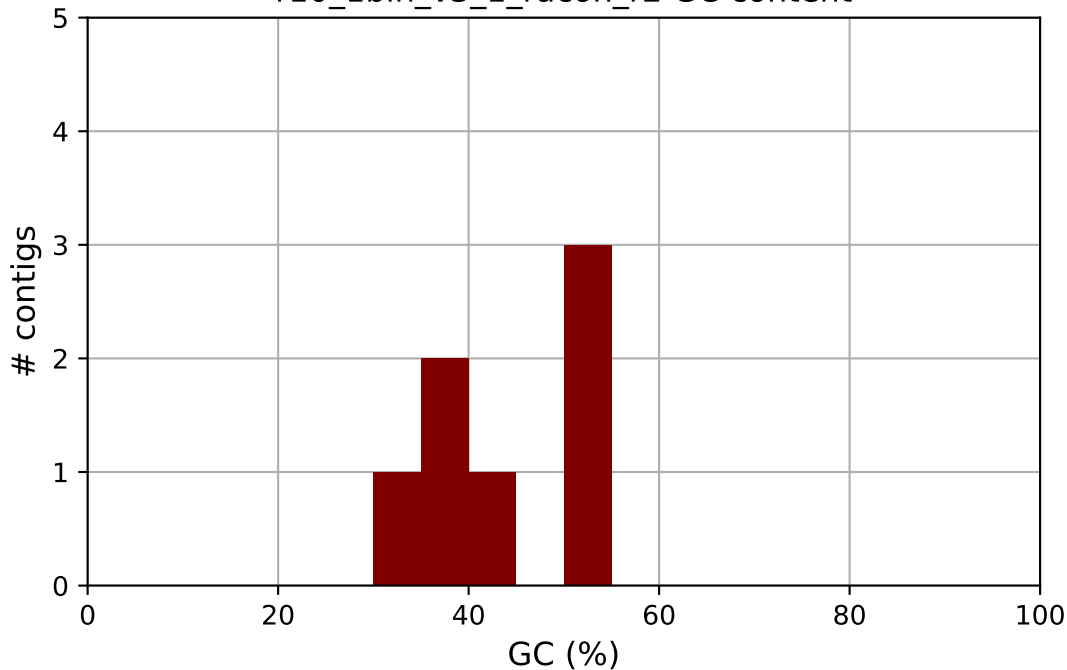
r10_1bin_v3_1_r2_medaka

r10_1bin_v3_1_racon_r1 GC content



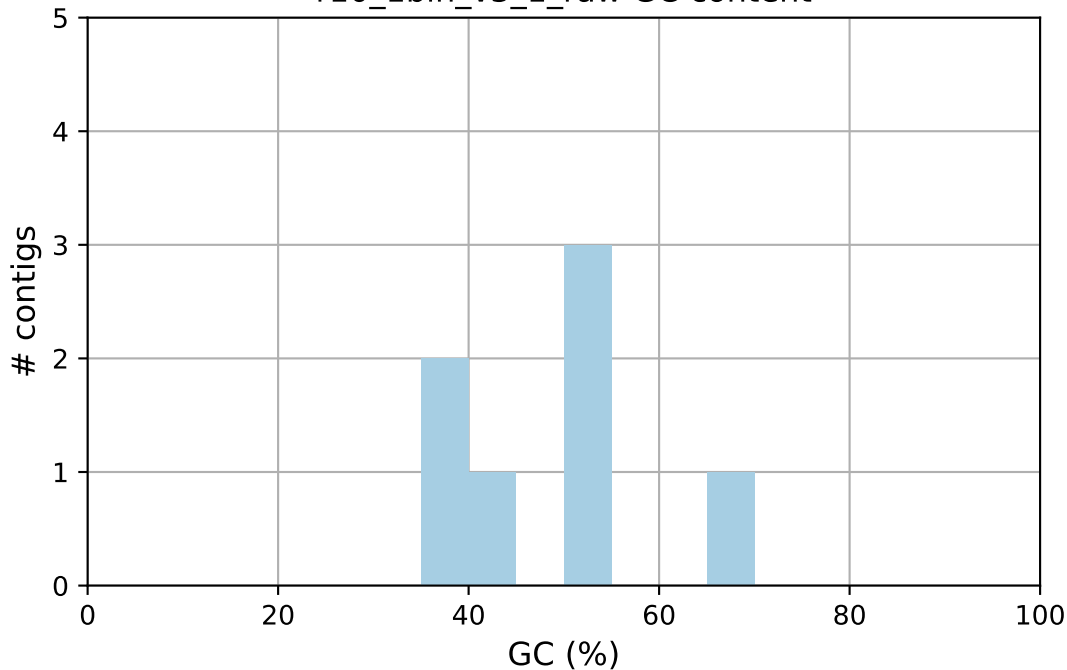
r10_1bin_v3_1_racon_r1

r10_1bin_v3_1_racon_r2 GC content



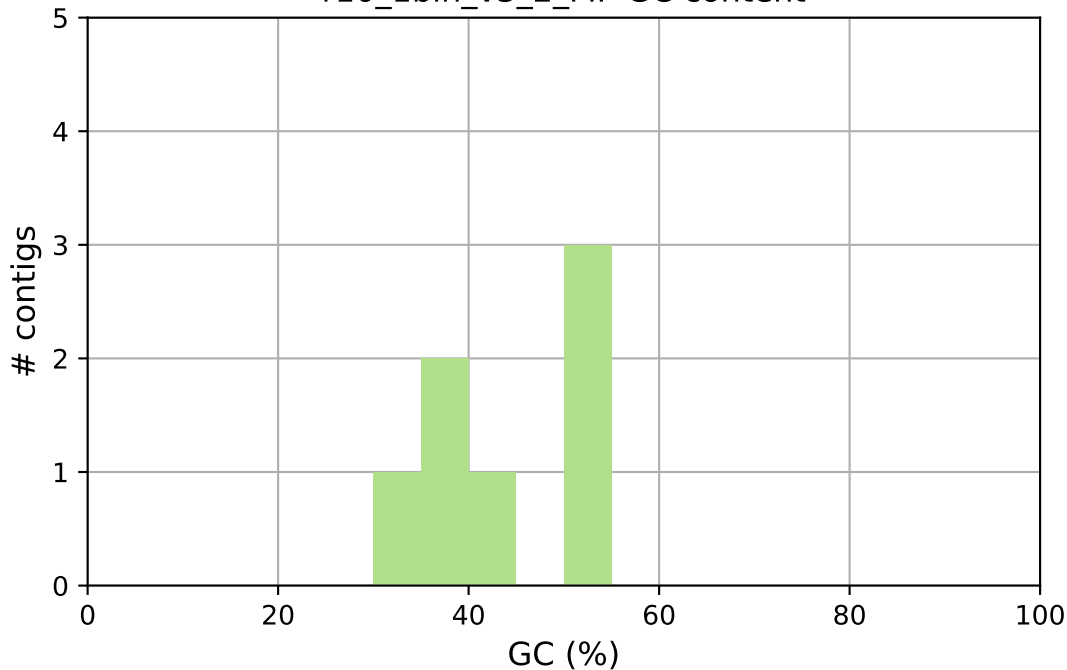
r10_1bin_v3_1_racon_r2

r10_1bin_v3_1_raw GC content



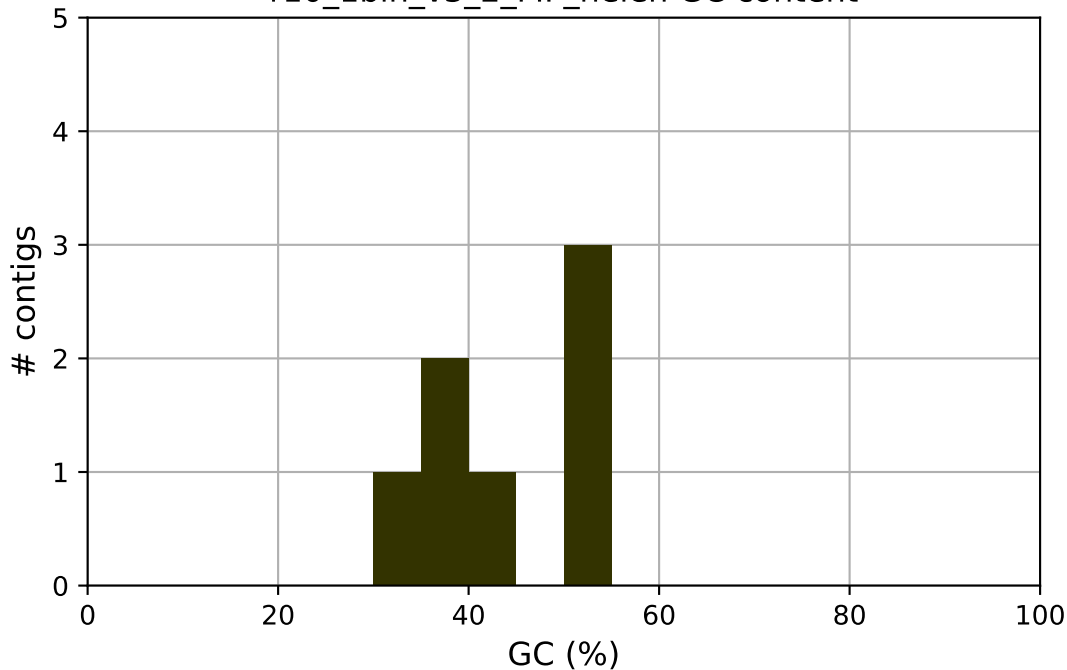
r10_1bin_v3_1_raw

r10_1bin_v3_2_MP GC content



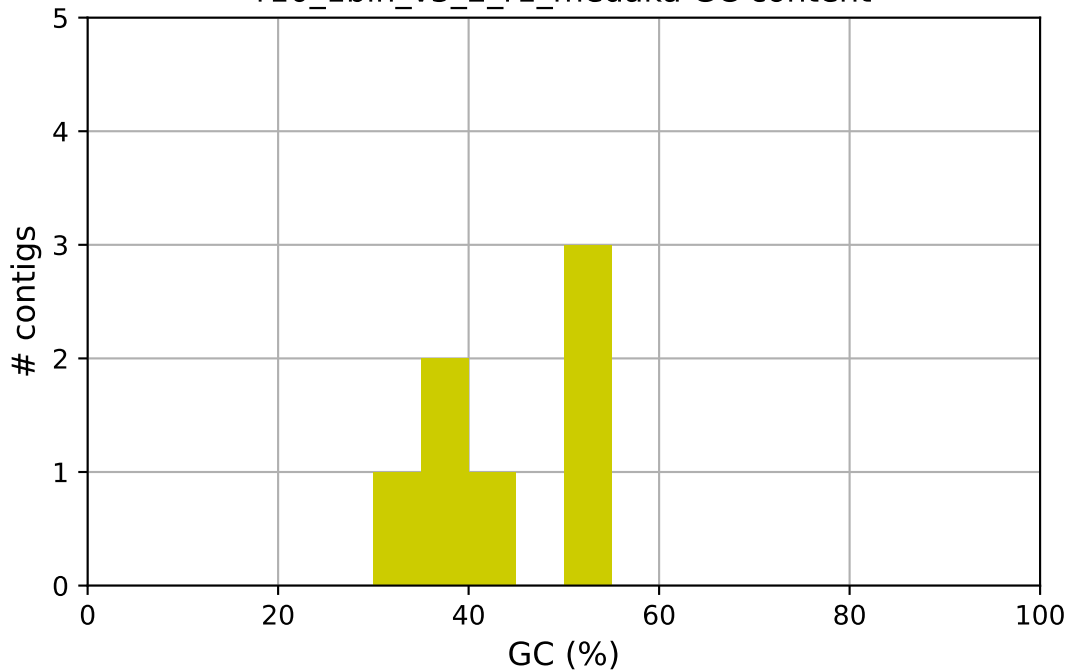
r10_1bin_v3_2_MP

r10_1bin_v3_2_MP_helen GC content



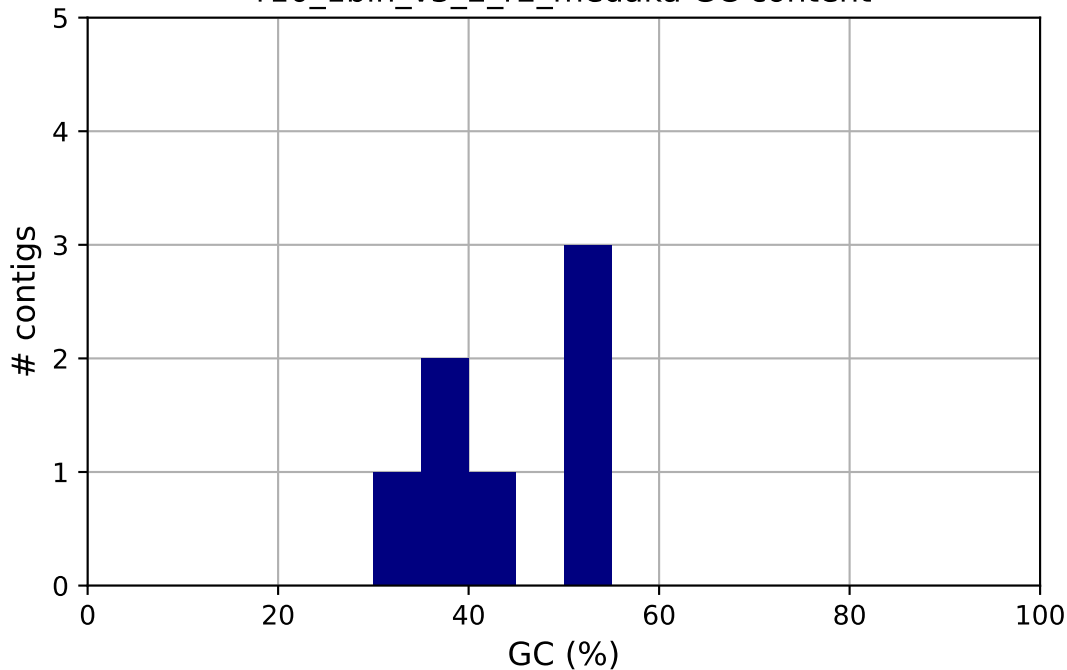
r10_1bin_v3_2_MP_helen

r10_1bin_v3_2_r1_medaka GC content



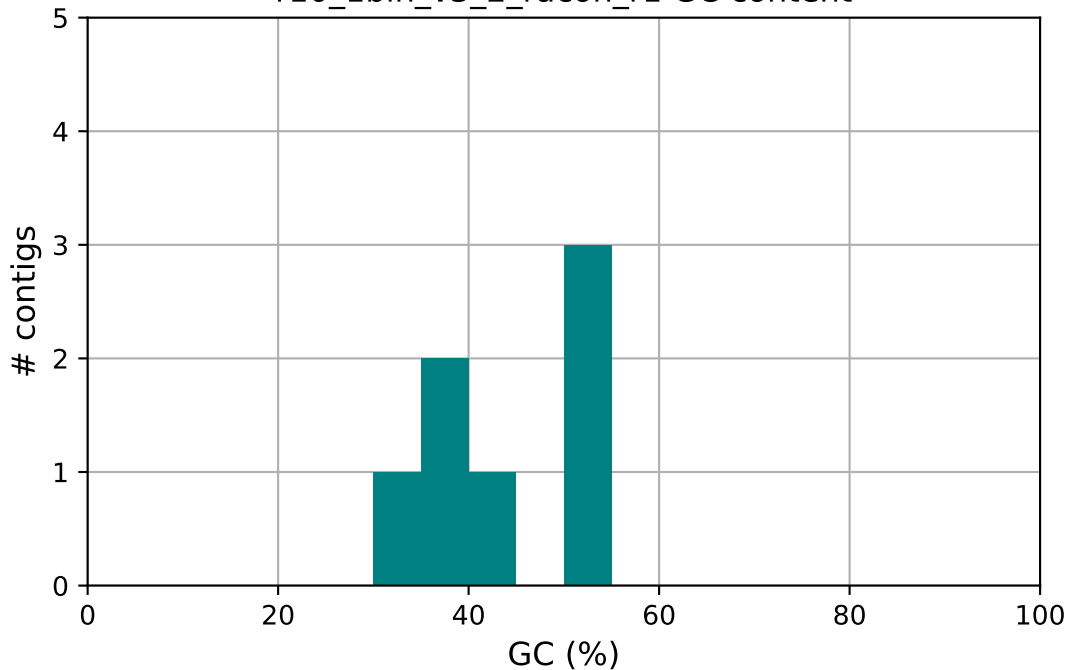
r10_1bin_v3_2_r1_medaka

r10_1bin_v3_2_r2_medaka GC content



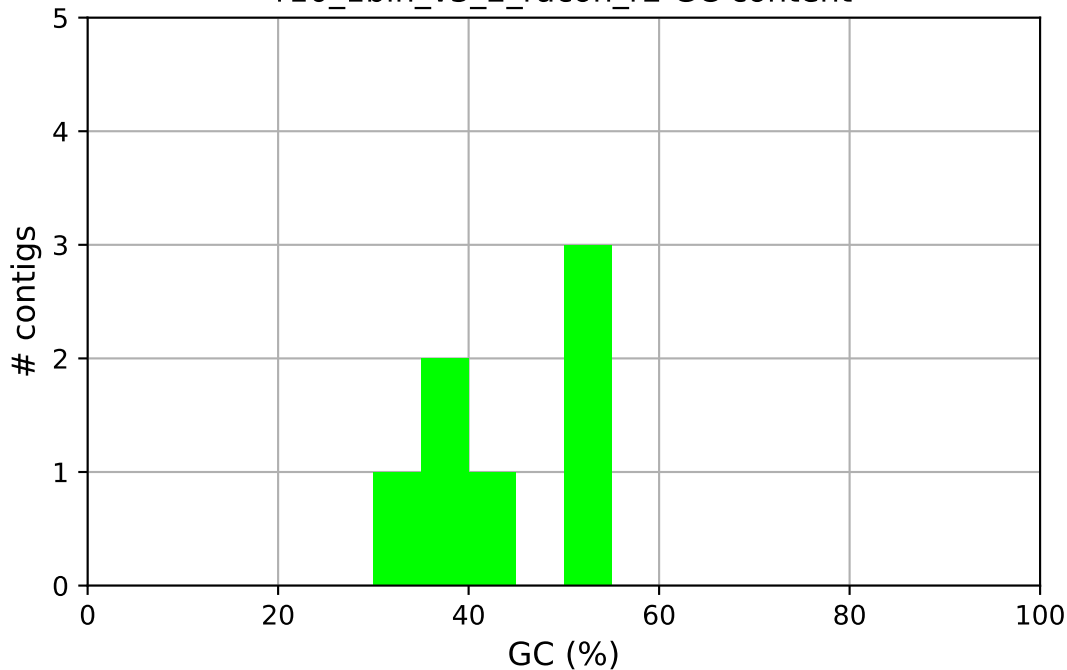
r10_1bin_v3_2_r2_medaka

r10_1bin_v3_2_racon_r1 GC content



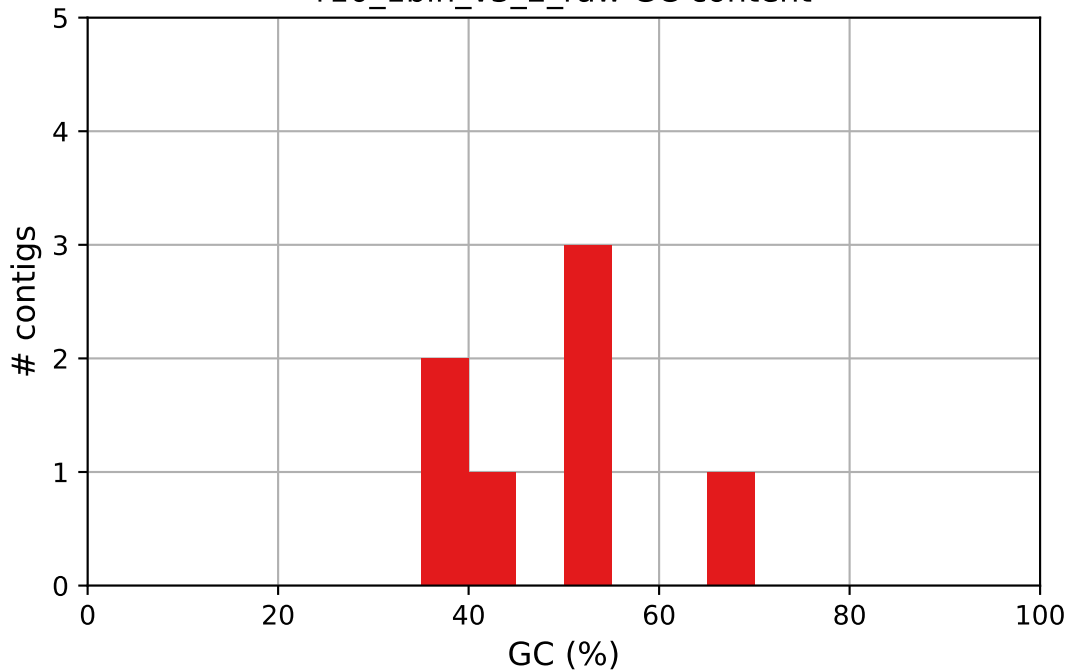
r10_1bin_v3_2_racon_r1

r10_1bin_v3_2_racon_r2 GC content



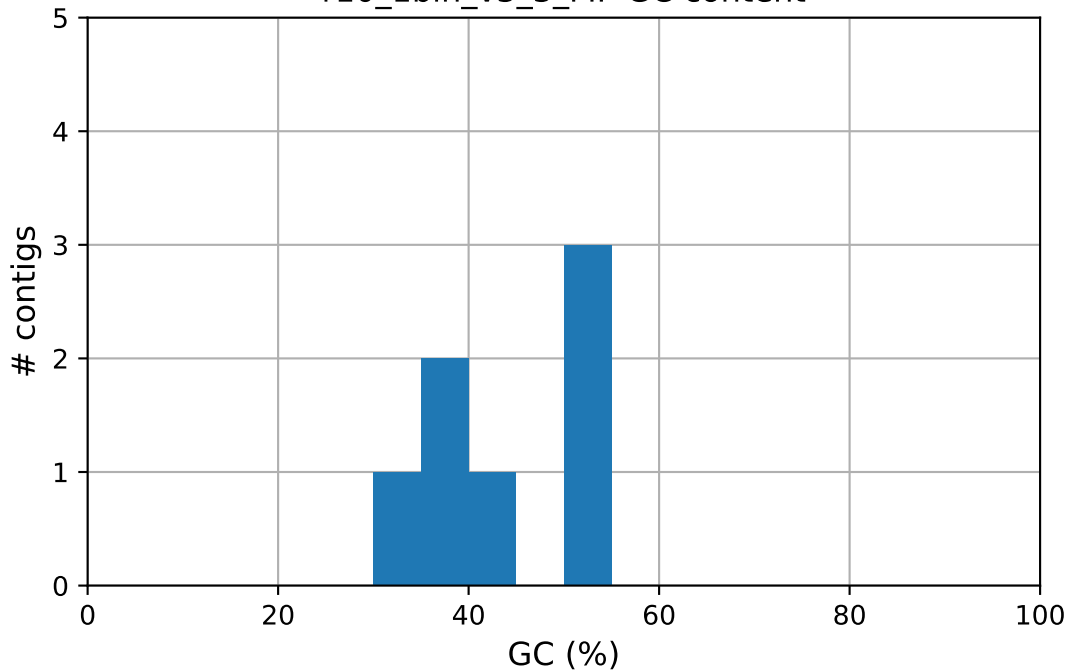
r10_1bin_v3_2_racon_r2

r10_1bin_v3_2_raw GC content



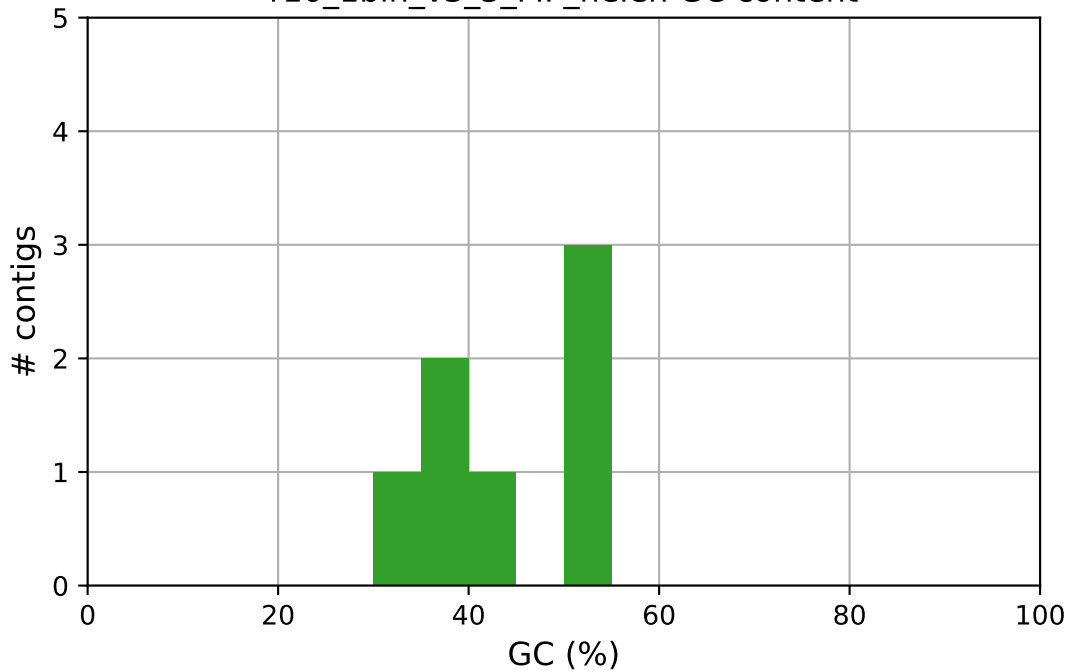
r10_1bin_v3_2_raw

r10_1bin_v3_3_MP GC content



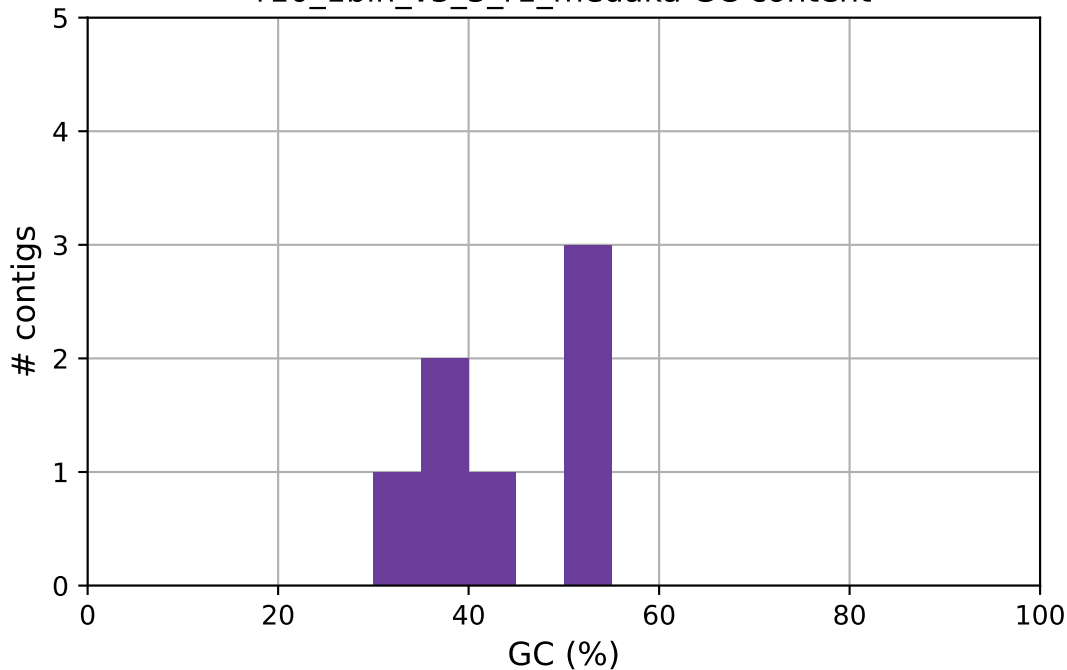
r10_1bin_v3_3_MP

r10_1bin_v3_3_MP_helen GC content



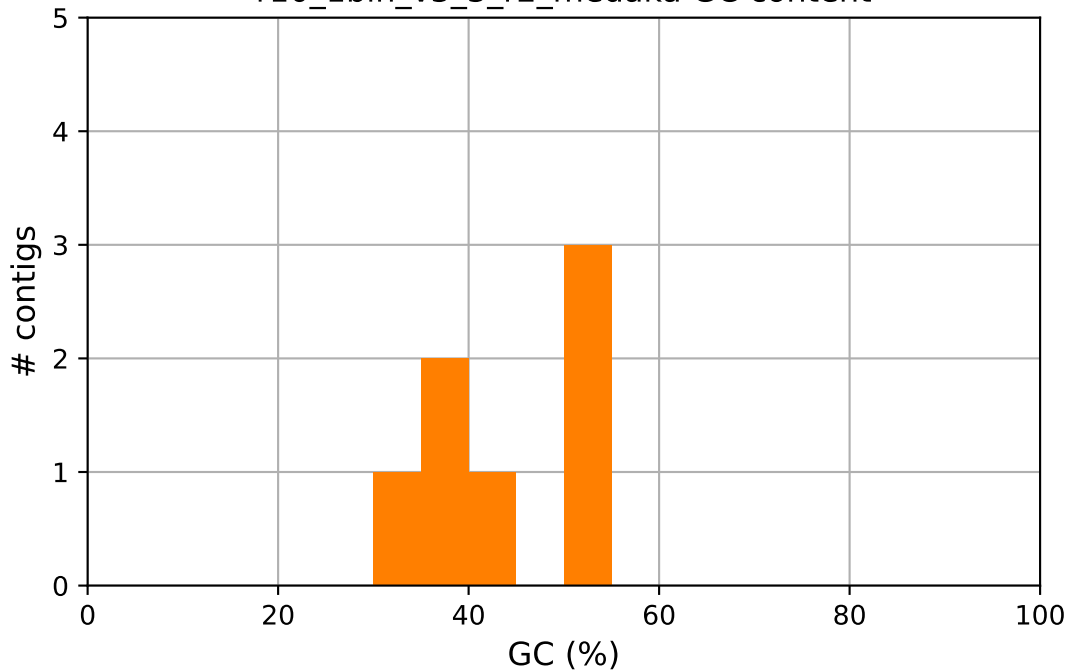
r10_1bin_v3_3_MP_helen

r10_1bin_v3_3_r1_medaka GC content



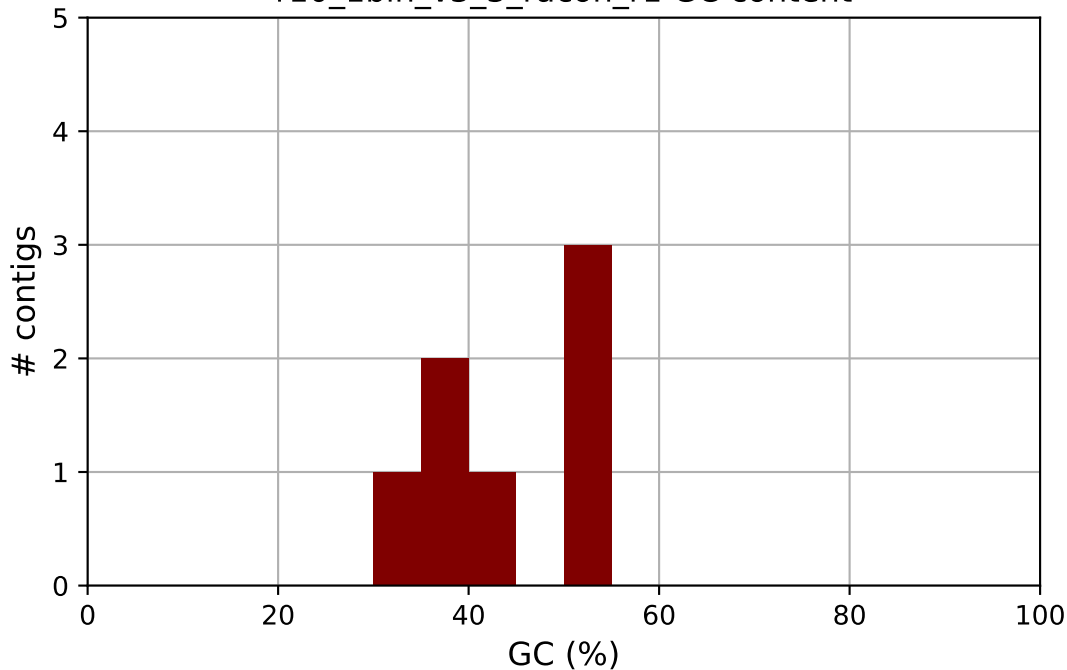
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka GC content



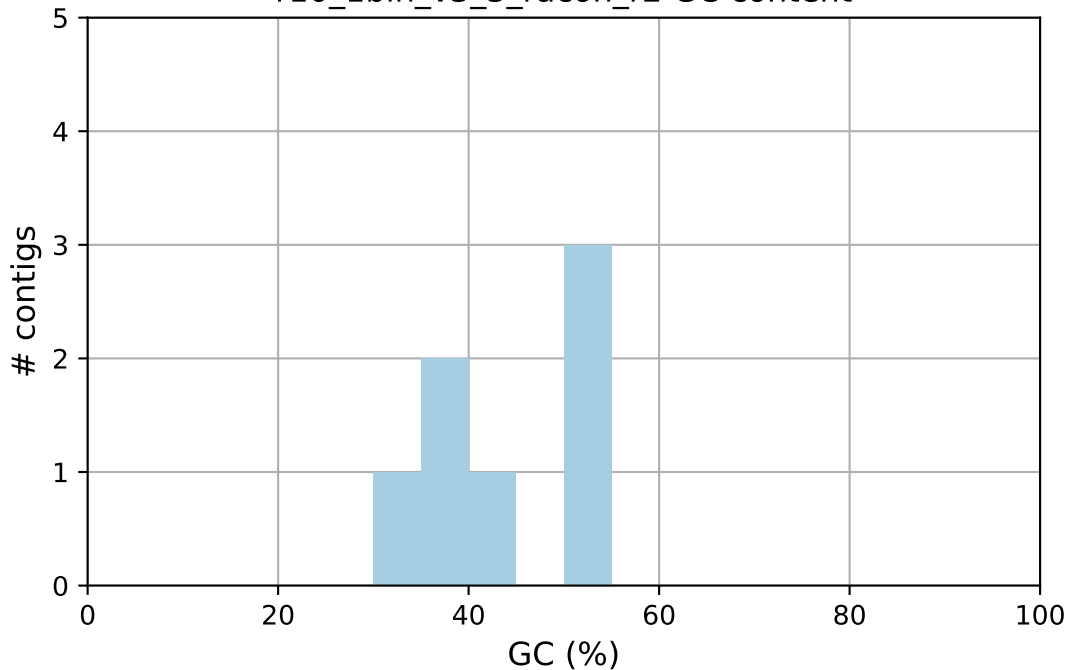
r10_1bin_v3_3_r2_medaka

r10_1bin_v3_3_racon_r1 GC content



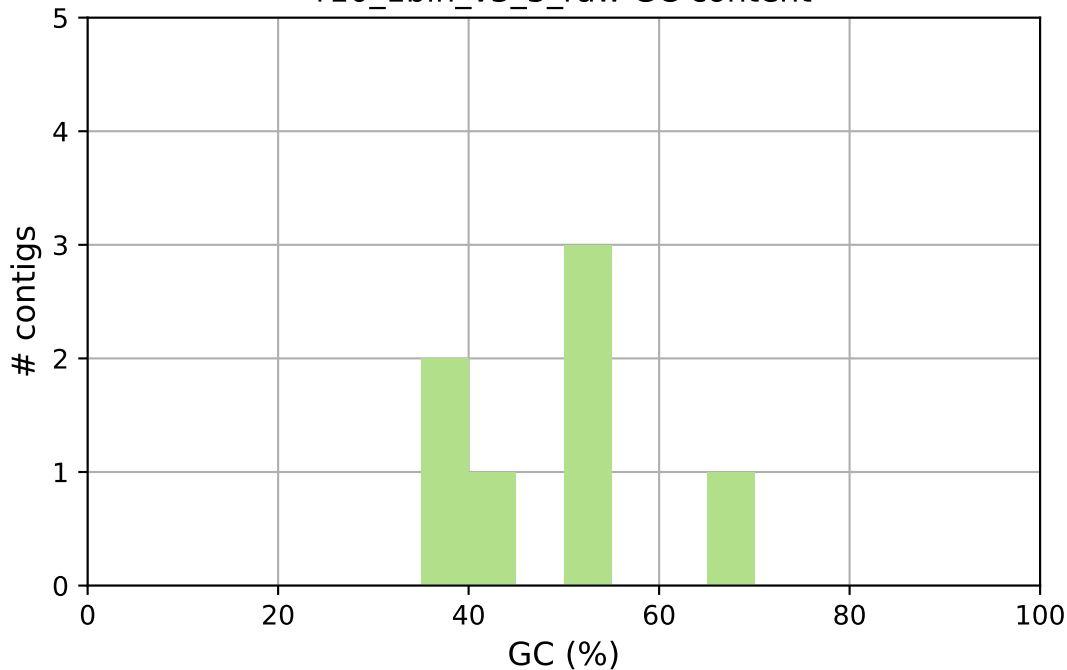
r10_1bin_v3_3_racon_r1

r10_1bin_v3_3_racon_r2 GC content



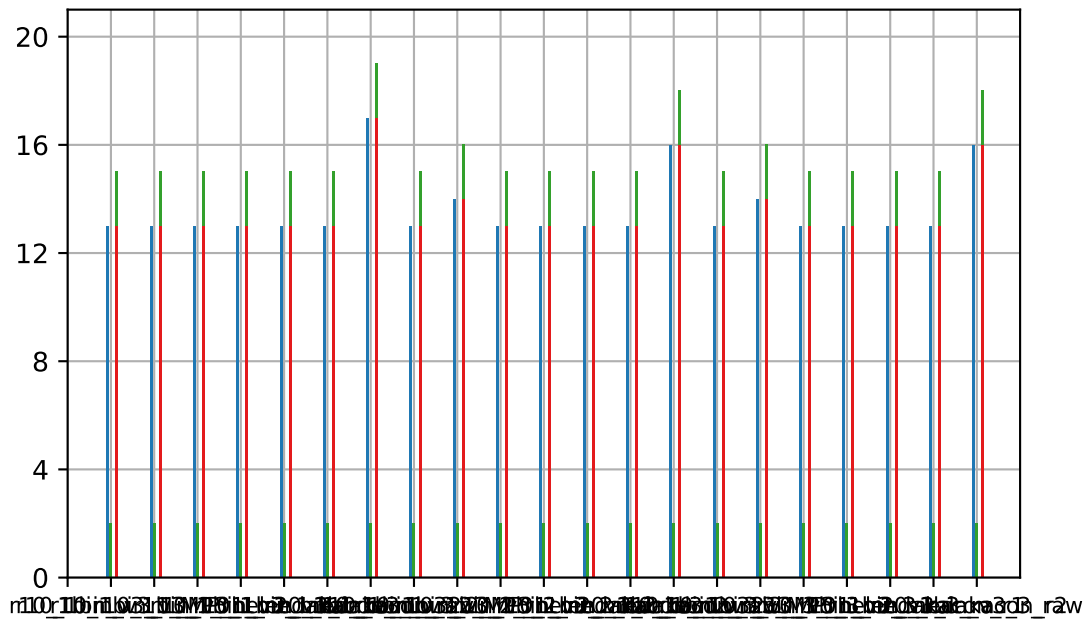
r10_1bin_v3_3_racon_r2

r10_1bin_v3_3_raw GC content

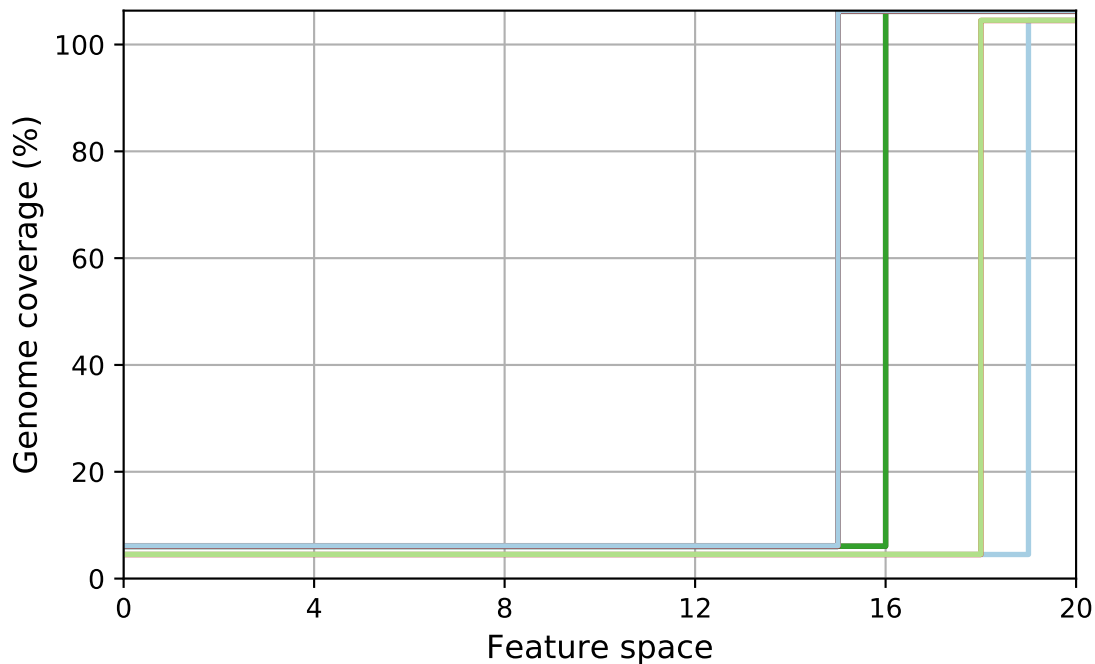


r10_1bin_v3_3_raw

Misassemblies



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

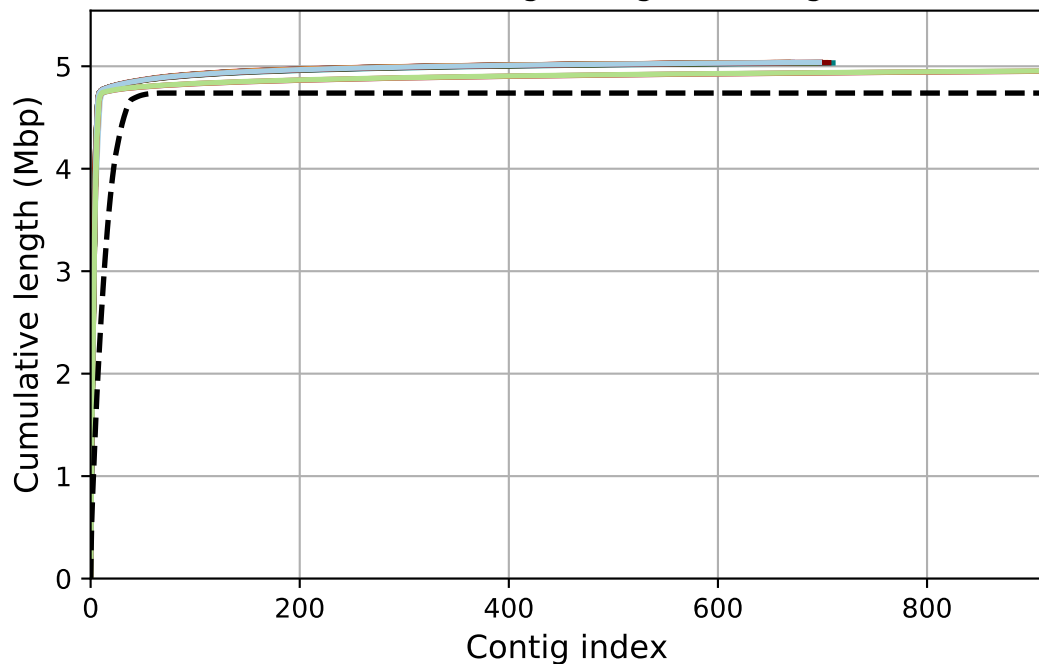
r10_1bin_v3_3_MP

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

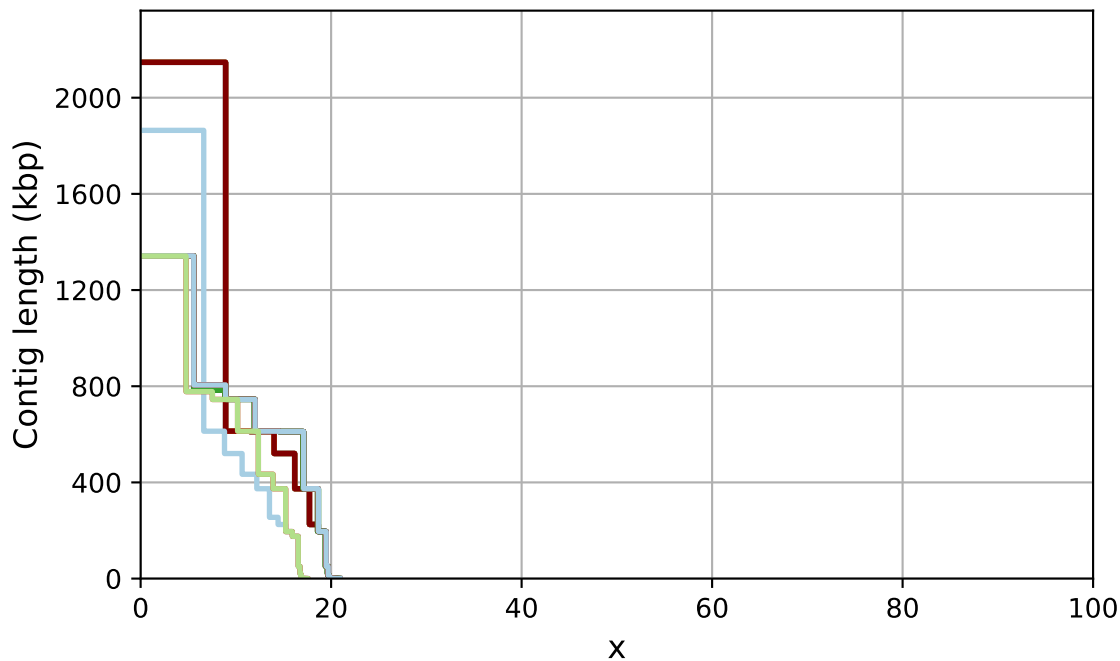
r10_1bin_v3_3_MP_helen

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

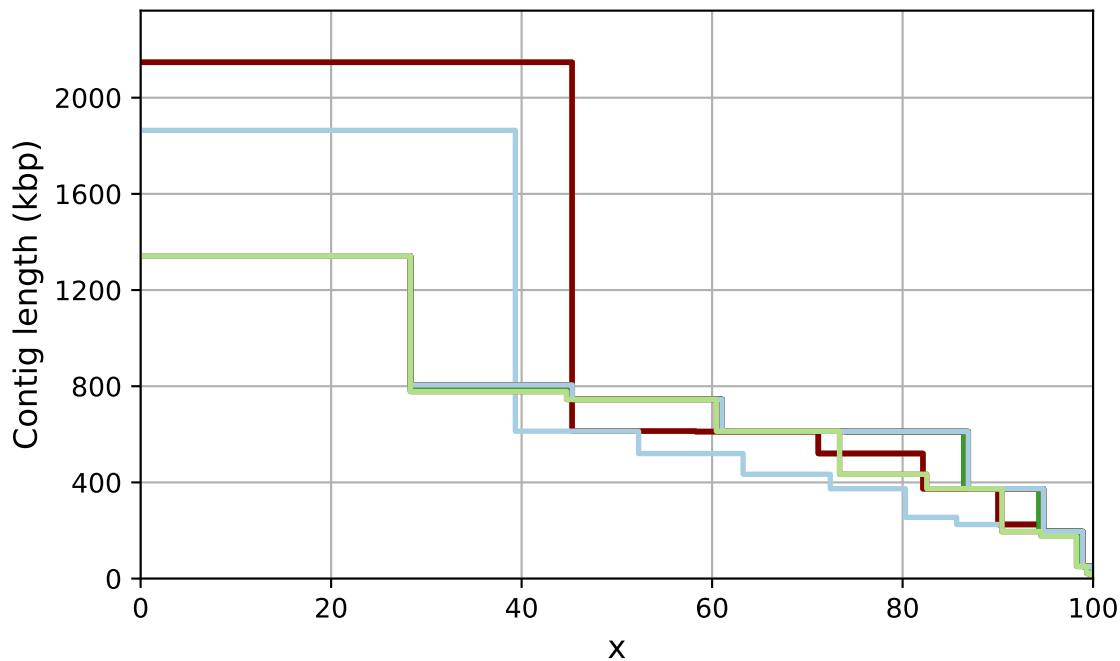
r10_1bin_v3_3_MP

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

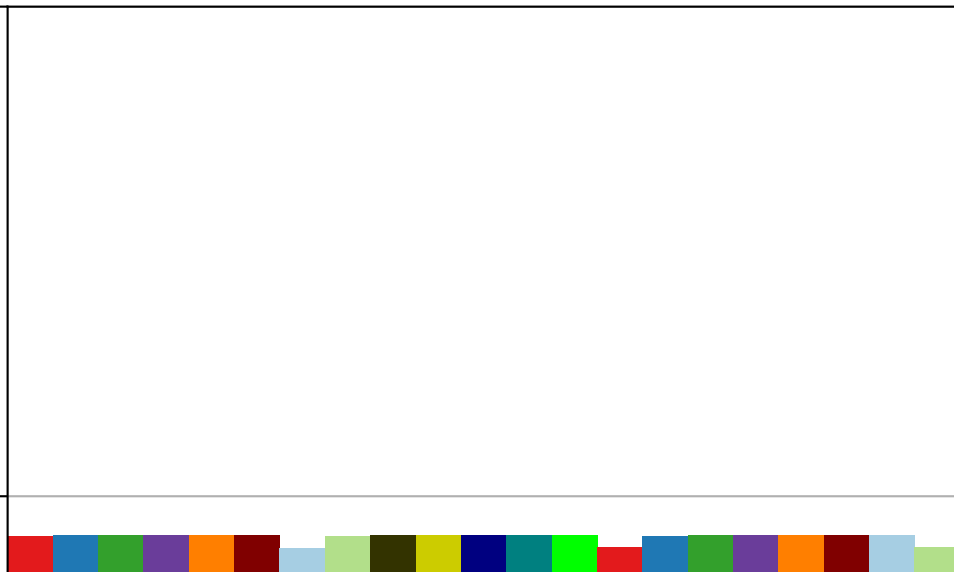
r10_1bin_v3_3_r1_medaka

r10_1bin_v3_3_r2_medaka

Genome fraction, %

100

99



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