

Report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130442
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130442
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130442
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130442
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
Total length	24074494	24070200	24072211	24064284	24060998	24055678	28130662	24074257	24070195	24072707	24061315	24060258	24055824	30848967	24075009	24068751	24072195	24065063	24060094	24056380	28130442
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	49.48	44.80	44.80	44.80	44.80	44.78	44.78	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	4045621	4045594	4045589	4045227	4045309	4756088	4045598	4045629	4045591	4045590	4045220	4045285	4756101	4045598	4045626	4045592	4045592	4045212	4045306	4756002
NG50	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	6787718
N75	2845422	2845369	2845428	2845432	2845260	2845328	2990628	2845425	2845372	2845428	2845431	2845275	2845354	2990633	2845425	2845364	2845429	2845427	2845297	2845324	2990669
NG75	4765367	4765335	4765354	4765366	4764519	4764885	6788581	4765367	4765342	4765360	4765365	4764481	4764611	6787718	4765870	4765291	4765346	4765353	4764528	4764900	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	16	15	15	15	15	18	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	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	4756002
# local misassemblies	8	8	8	8	8	8	20	8	8	8	8	8	8	20	8	8	8	8	8	8	22
# 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	5	6	6	6	6	6	6	7	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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	19037478	1903877	19035115	19028637	19026237	19017760	23177473	19036921	19033715	19035671	19025060	19024071	19017509	25891898	19037922	19032421	19035692	19028950	19022053	19019148	23175187
Genome fraction (%)	98.918	98.919	98.920	98.920	98.920	98.920	98.896	98.918	98.918	98.920	98.920	98.920	98.920	98.896	98.918	98.918	98.920	98.920	98.920	98.920	98.894
Duplication ratio	1.075	1.075	1.075	1.075	1.074	1.075	1.057	1.075	1.075	1.075	1.075	1.075	1.075	1.058	1.075	1.075	1.075	1.075	1.075	1.075	1.058
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	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
# mismatches per 100 kbp	411.75	409.10	409.69	408.09	409.15	417.50	460.80	412.30	409.53	409.71	409.11	413.93	418.39	463.96	412.19	409.34	408.92	408.88	417.09	416.43	466.59
# indels per 100 kbp	20.81	15.96	11.42	11.29	39.48	37.84	225.09	20.76	15.92	11.55	11.40	40.52	37.58	226.79	21.26	16.26	11.48	11.42	40.16	37.26	229.70
Largest alignment	1342502	1342446	1342474	1342473	1342283	1342302	1341457	1342502	1342444	1342475	1342474	1342274	1342300	1341458	1342502	1342446	1342473	1342473	1342271	1342282	958286
Total aligned length	5034674	5034036	5034753	5030825	5032416	5035574	4951007	5034994	5034183	5034694	5033911	5033848	5035972	4954941	5034745	5034043	5034160	5033769	5035696	5034889	4953133
NGA50	745392	745356	745368	745370	745273	745278	744987	745392	745353	745371	745370	745265	745286	744998	745398	745356	745370	745371	745280	745283	744899
NGA75	611514	611511	611516	611516	611442	611449	433868	611514	611510	611514	611515	611428	611450	433871	611508	611476	611514	611515	611430	611443	383173
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	6

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_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	15	16	15	15	15	15	18	15	16	15	15	15	15	18	15	16	15	15	15	15	19
# contig misassemblies	15	16	15	15	15	15	18	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	14	13	13	13	13	16	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	4758939	4757842	4758592	4758097	4757948	4757880	4756088	4758938	4757859	4758591	4758127	4757960	4757842	4756101	4758939	4757830	4758588	4758127	4757931	4757812	4756002
# 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	8	8	8	8	20	8	8	8	8	8	8	20	8	8	8	8	8	8	22
# 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	11	14	14	14	14	14	14	10
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	7	6	6	6	6	6	6	6
# mismatches	19294	19170	19198	19123	19173	19564	21588	19320	19190	19199	19171	19397	19606	21736	19315	19181	19162	19160	19545	19514	21859
# indels	975	748	535	529	1850	1773	10545	973	746	541	534	1899	1761	10625	996	762	538	535	1882	1746	10761
# indels (<= 5 bp)	879	649	445	438	1758	1683	10369	877	646	451	444	1808	1670	10449	899	660	448	445	1791	1655	10582
# indels (> 5 bp)	96	99	90	91	92	90	176	96	100	90	90	91	91	176	97	102	90	90	91	91	179
Indels length	5521	5292	4966	4968	6451	6318	19245	5519	5271	4972	4965	6537	6287	19367	5562	5316	4969	4967	6492	6283	19619

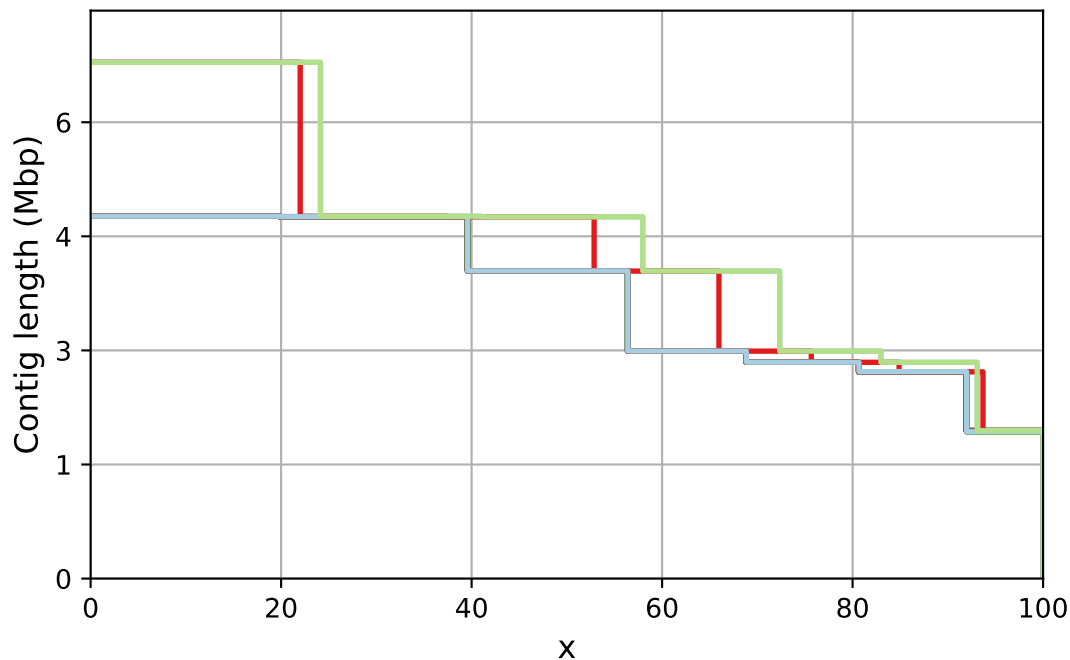
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	8	7	7	7	7	7	7	7
Partially unaligned length	19037478	19033877	19035115	19028637	19026237	19017760	23177473	19036921	19033715	19035671	19025060	19024071	19017509	25891898	19037922	19032421	19035692	19028950	19022053	19019148	23175187
# N's	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0

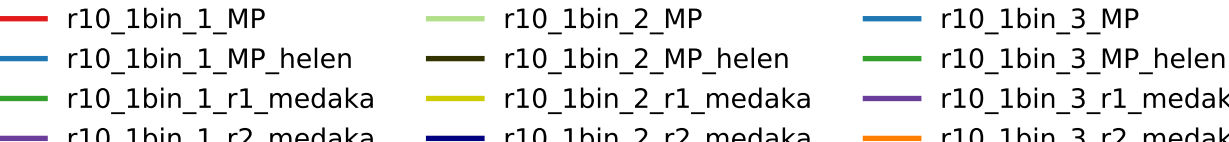
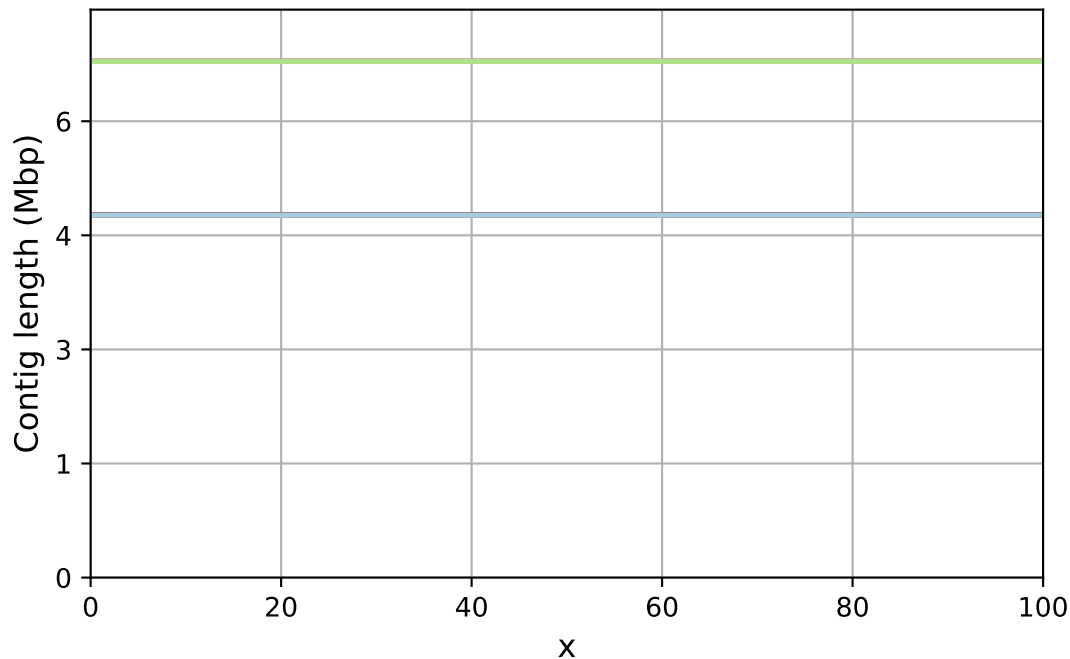
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

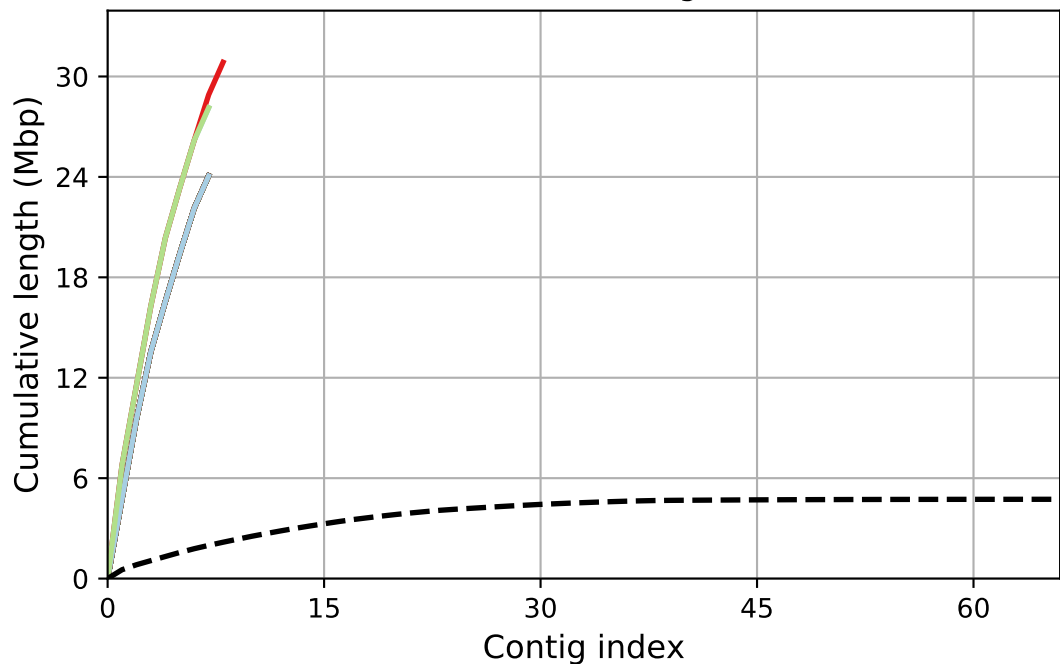


r10_1bin_1_MP	r10_1bin_2_MP	r10_1bin_3_MP
r10_1bin_1_MP_helen	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_r1_medaka	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medaka
r10_1bin_1_r2_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medaka

NGx

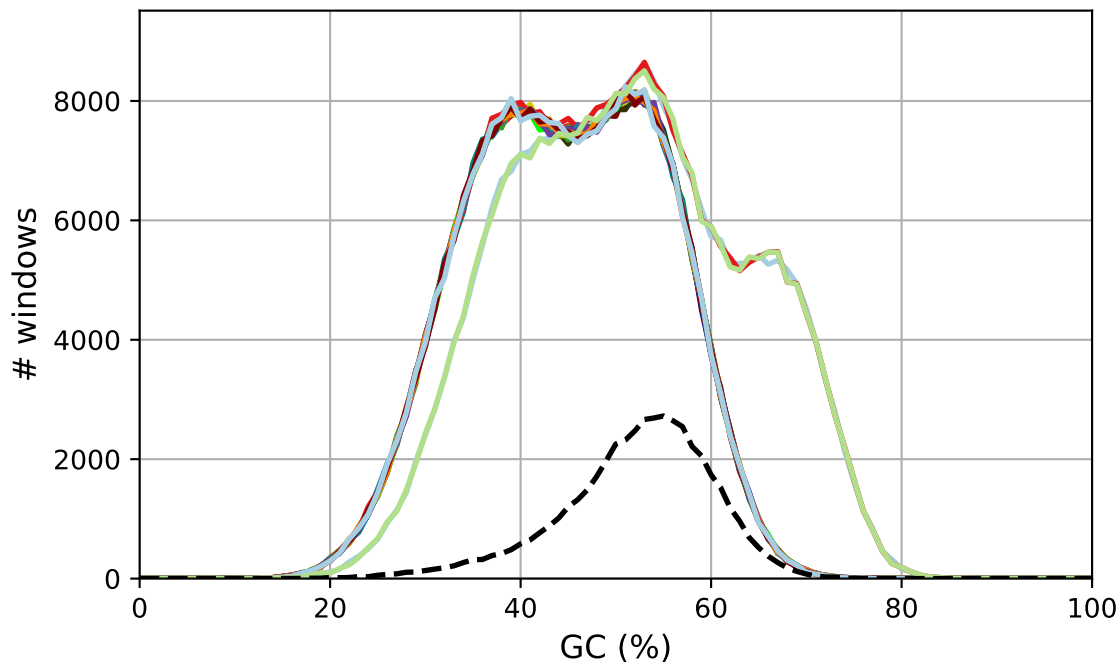


Cumulative length

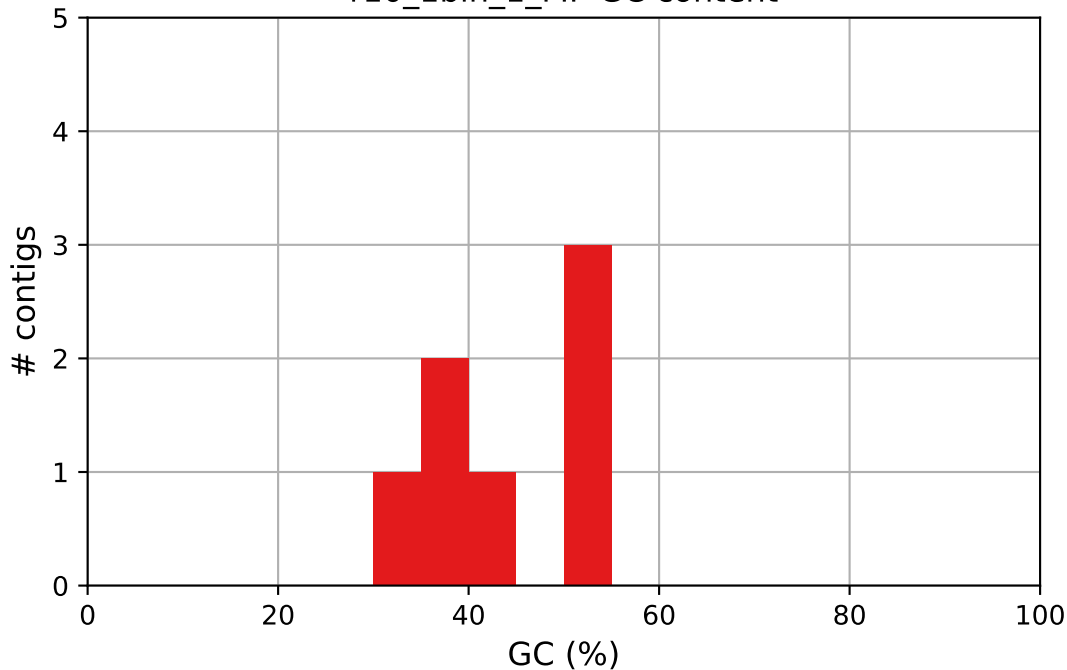


r10_1bin_1_MP	r10_1bin_2_MP_helen	r10_1bin_3_MP_helen
r10_1bin_1_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_3_r1_medaka
r10_1bin_1_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_3_r2_medaka
r10_1bin_1_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_3_racon_r1

GC content

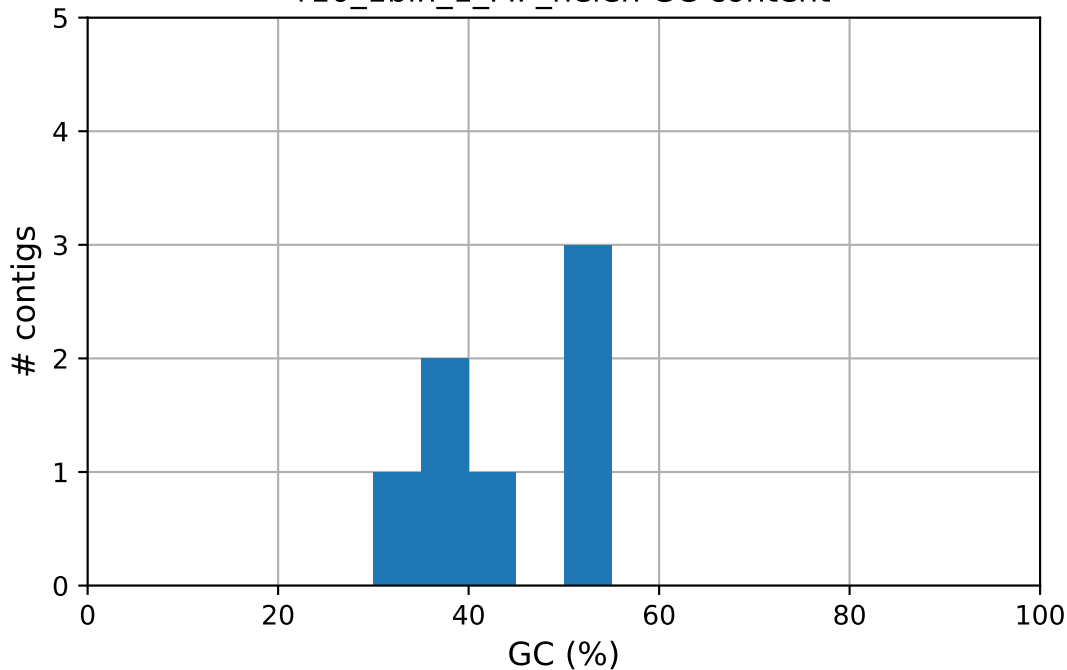


r10_1bin_1_MP GC content



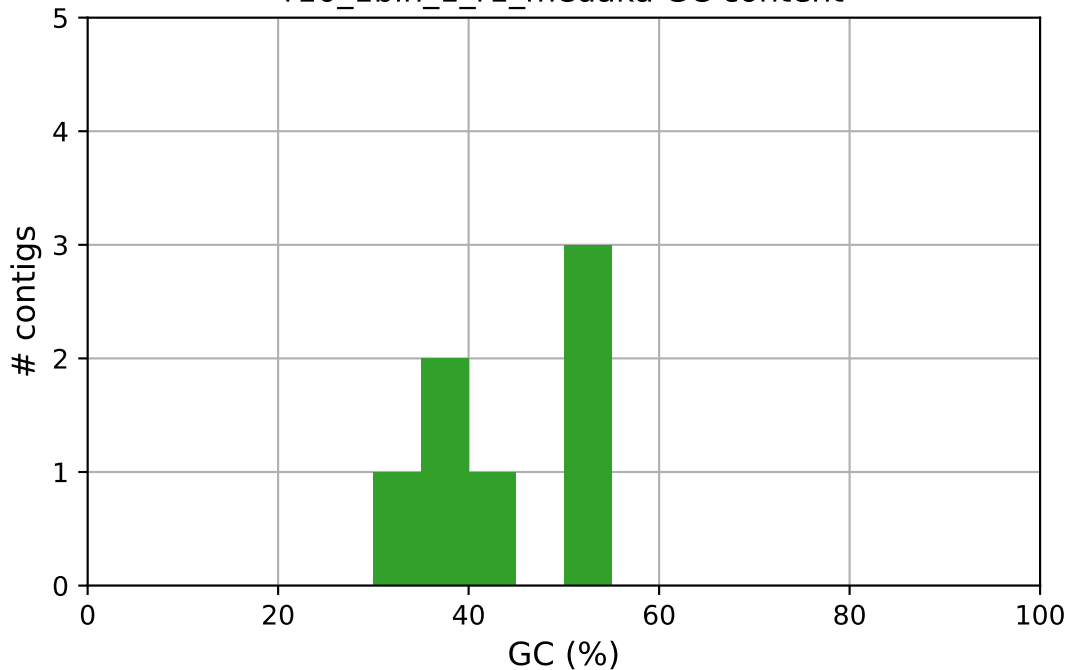
r10_1bin_1_MP

r10_1bin_1_MP_helen GC content



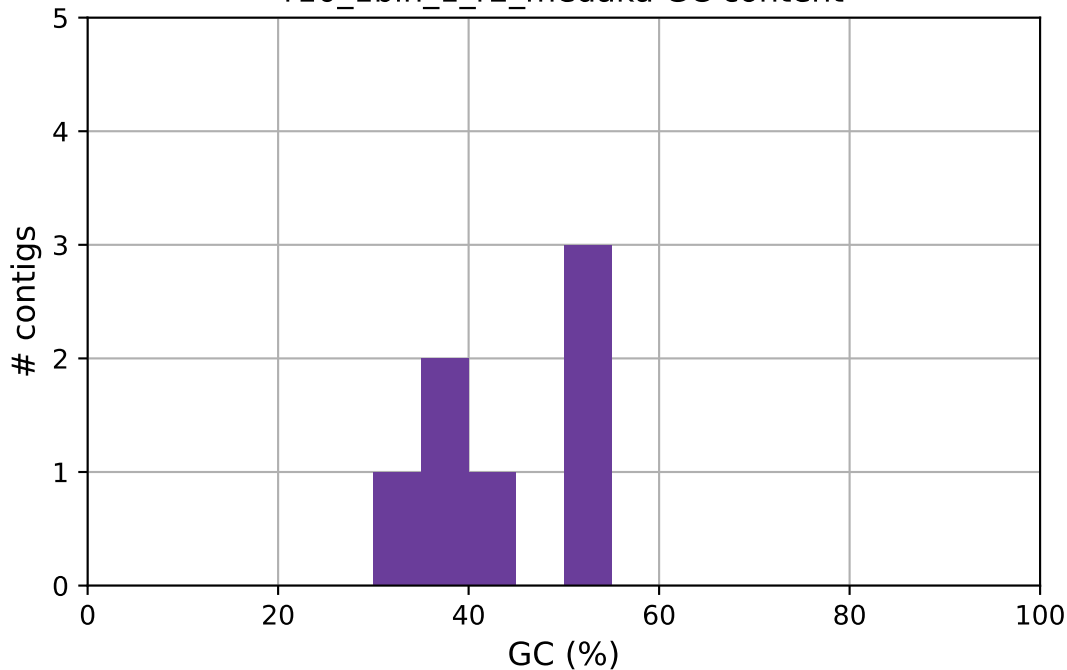
r10_1bin_1_MP_helen

r10_1bin_1_r1_medaka GC content



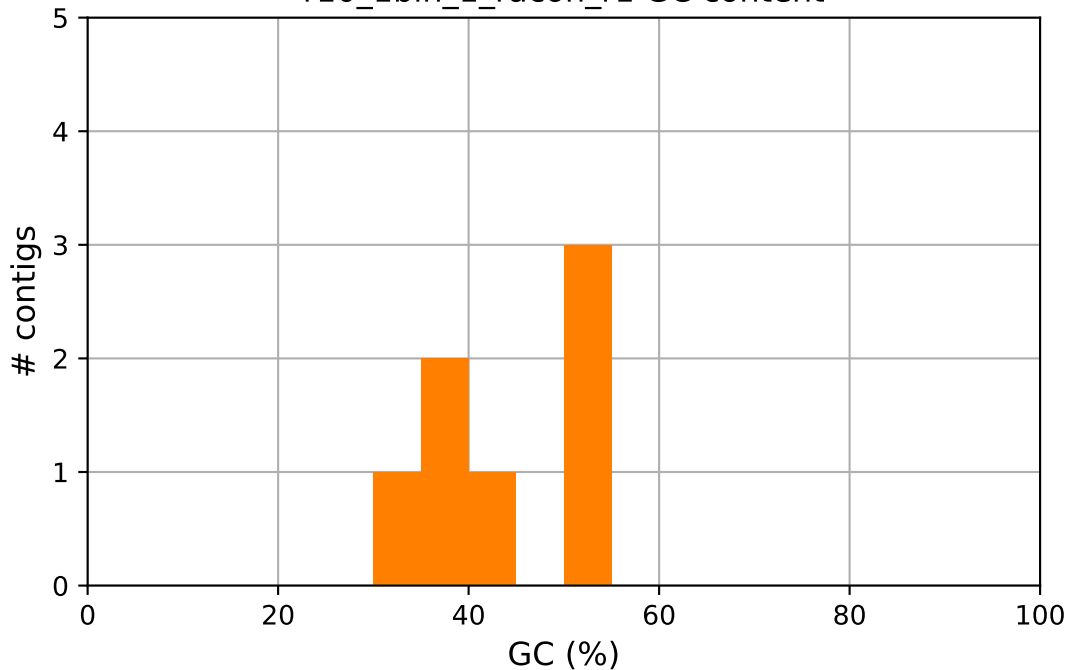
r10_1bin_1_r1_medaka

r10_1bin_1_r2_medaka GC content



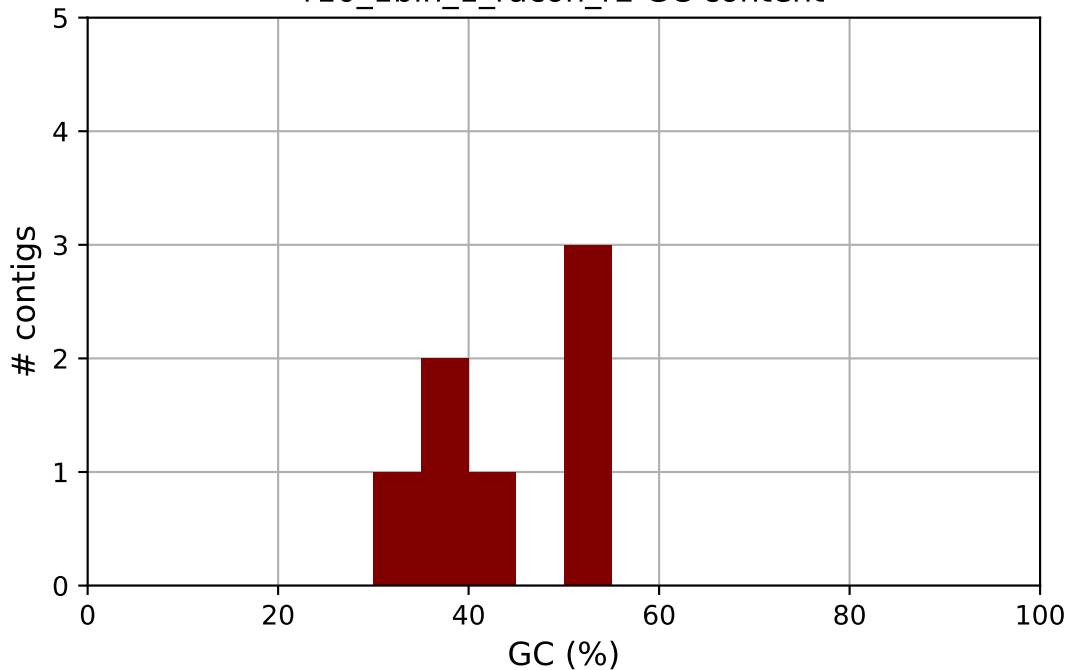
r10_1bin_1_r2_medaka

r10_1bin_1_racon_r1 GC content



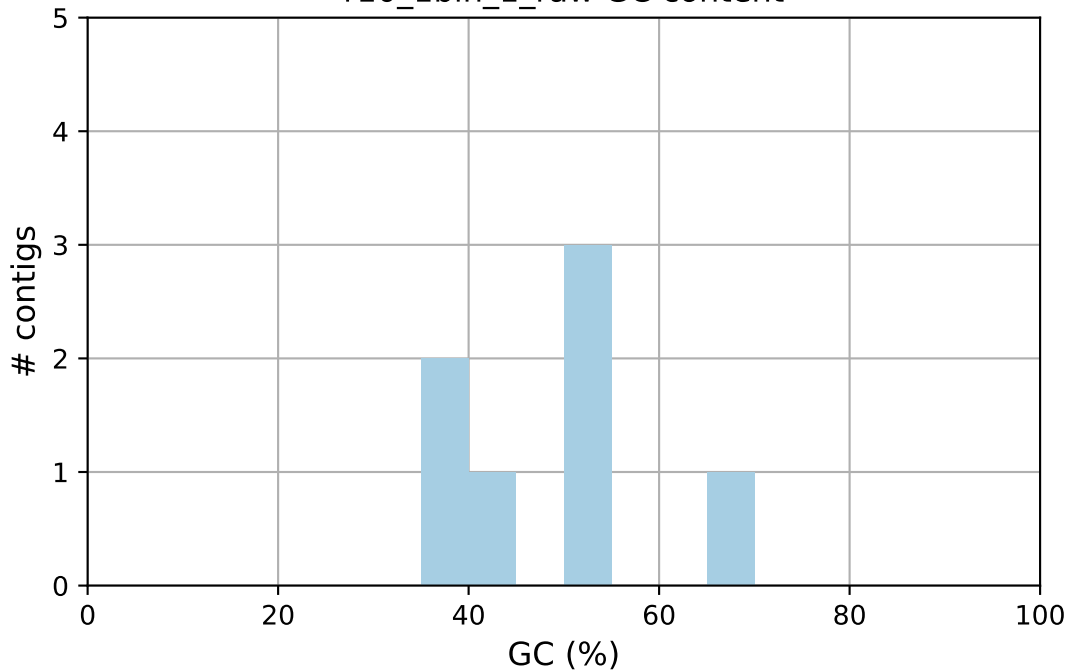
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r10_1bin_1_racon_r2 GC content



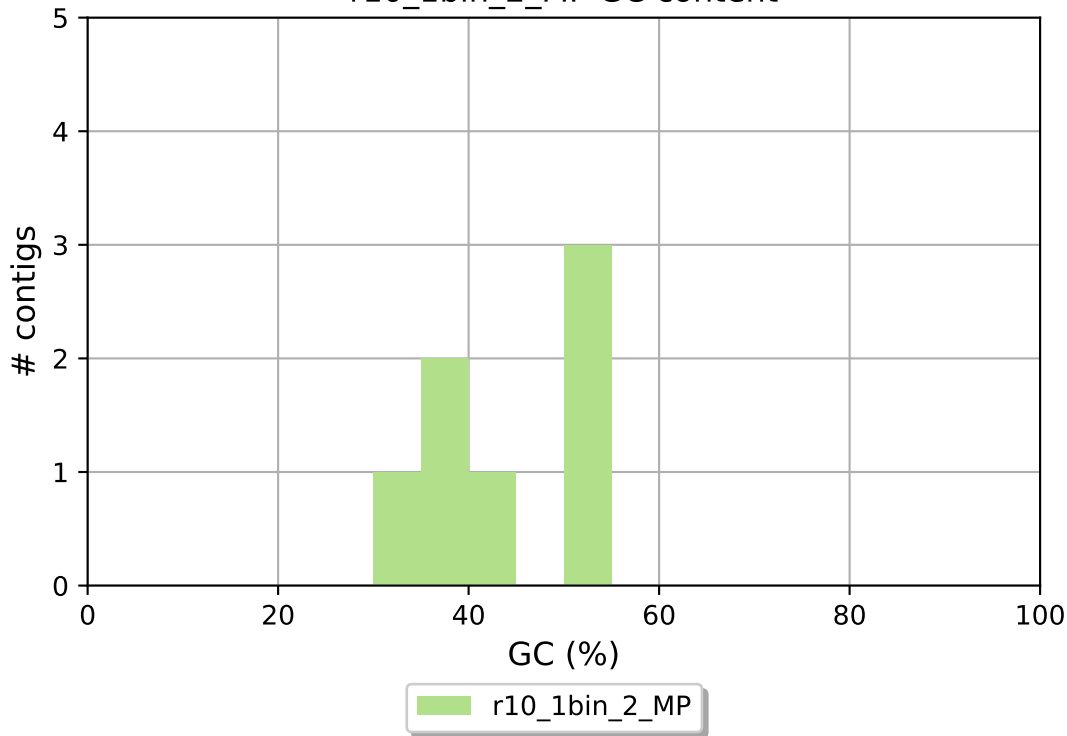
r10_1bin_1_racon_r2

r10_1bin_1_raw GC content

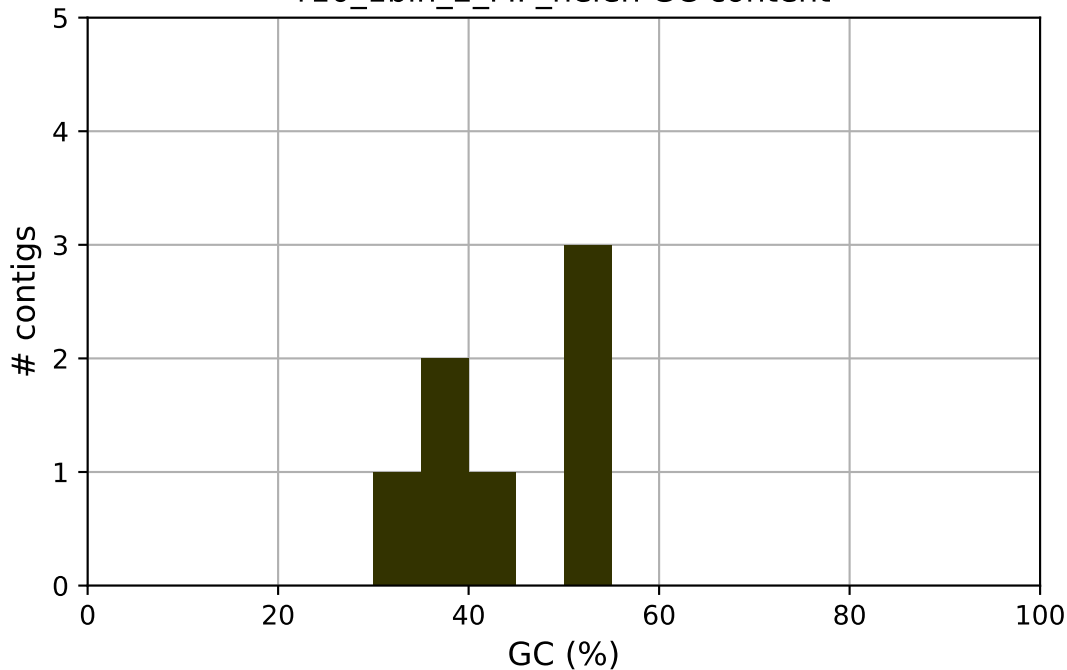


r10_1bin_1_raw

r10_1bin_2_MP GC content

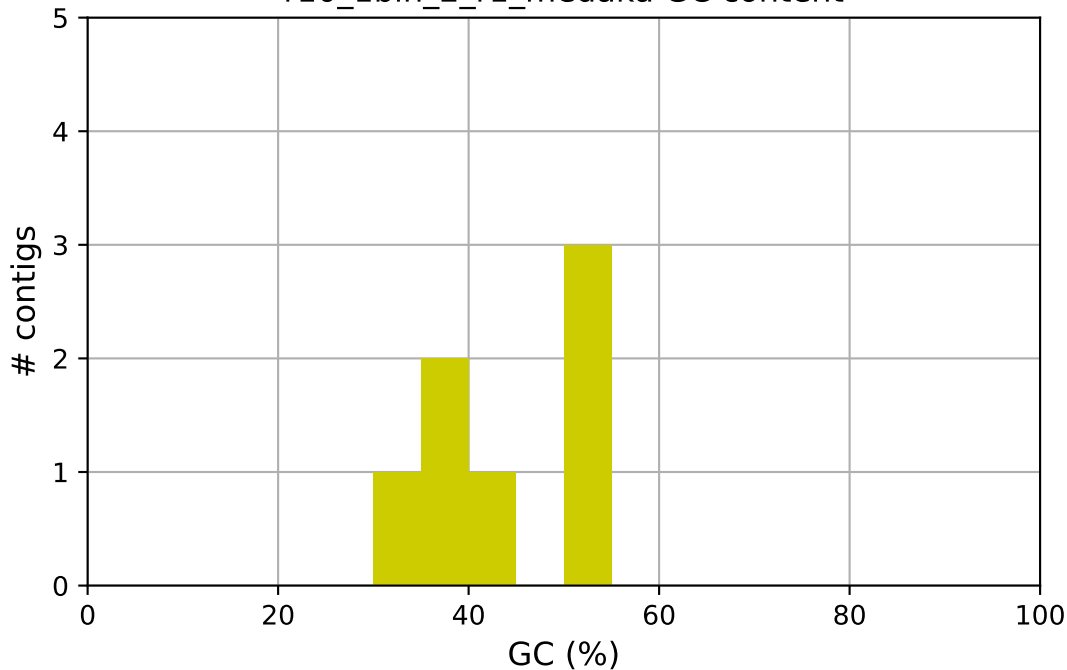


r10_1bin_2_MP_helen GC content



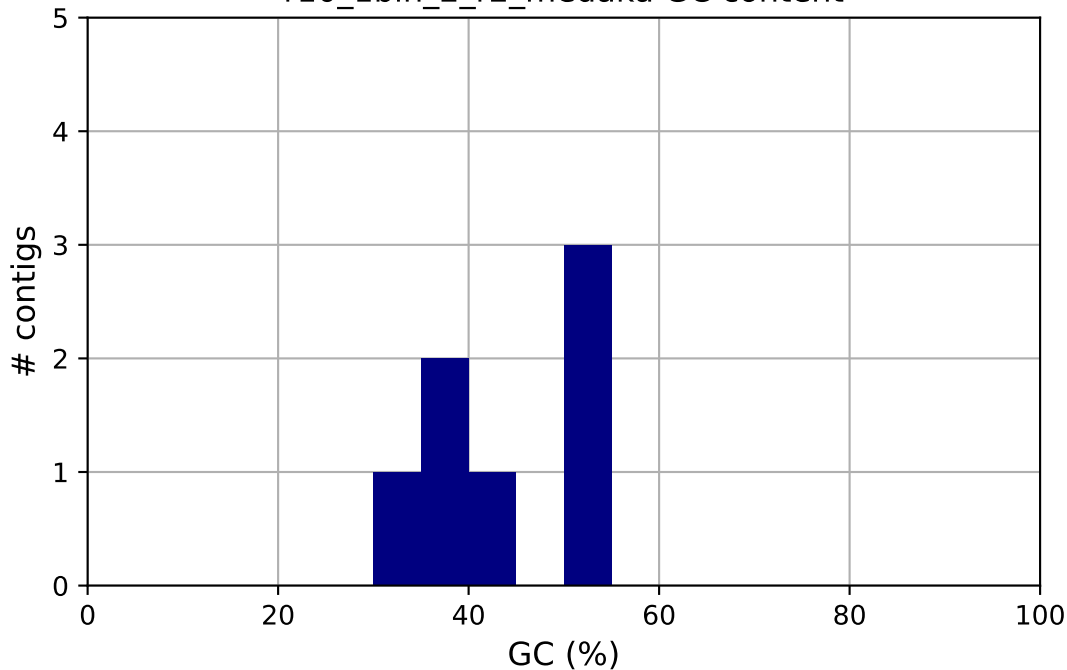
■ r10_1bin_2_MP_helen

r10_1bin_2_r1_medaka GC content



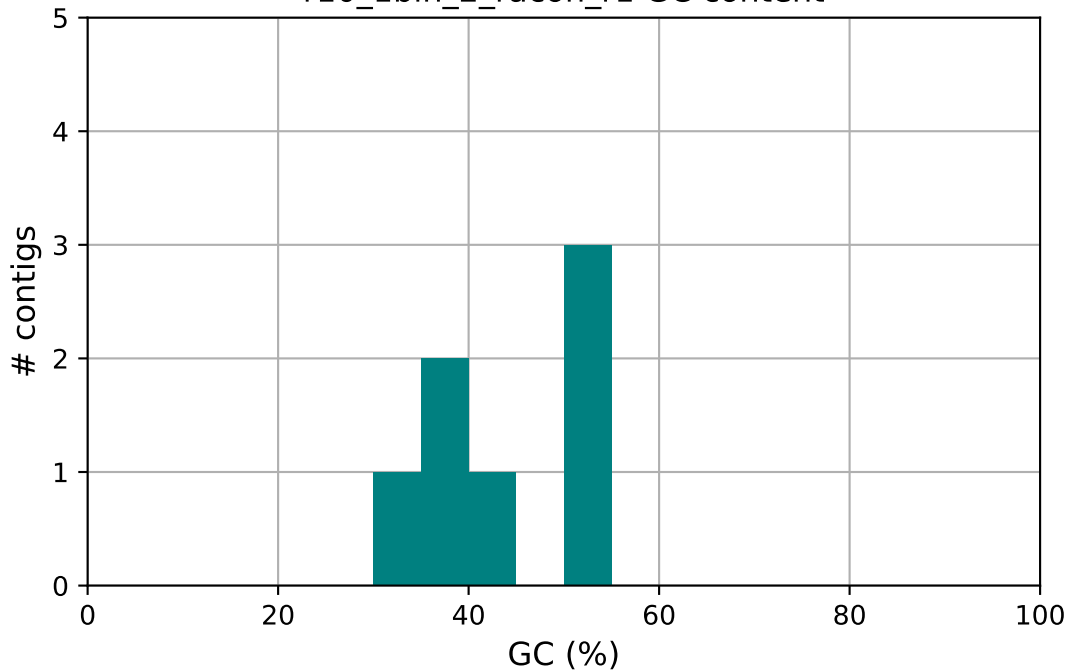
r10_1bin_2_r1_medaka

r10_1bin_2_r2_medaka GC content



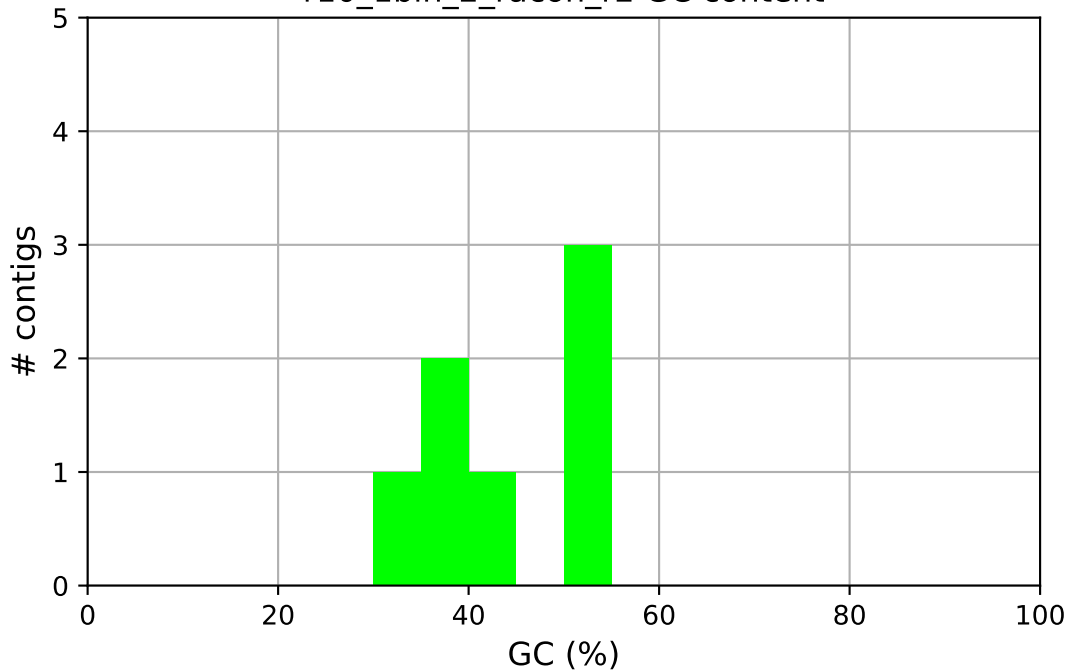
r10_1bin_2_r2_medaka

r10_1bin_2_racon_r1 GC content



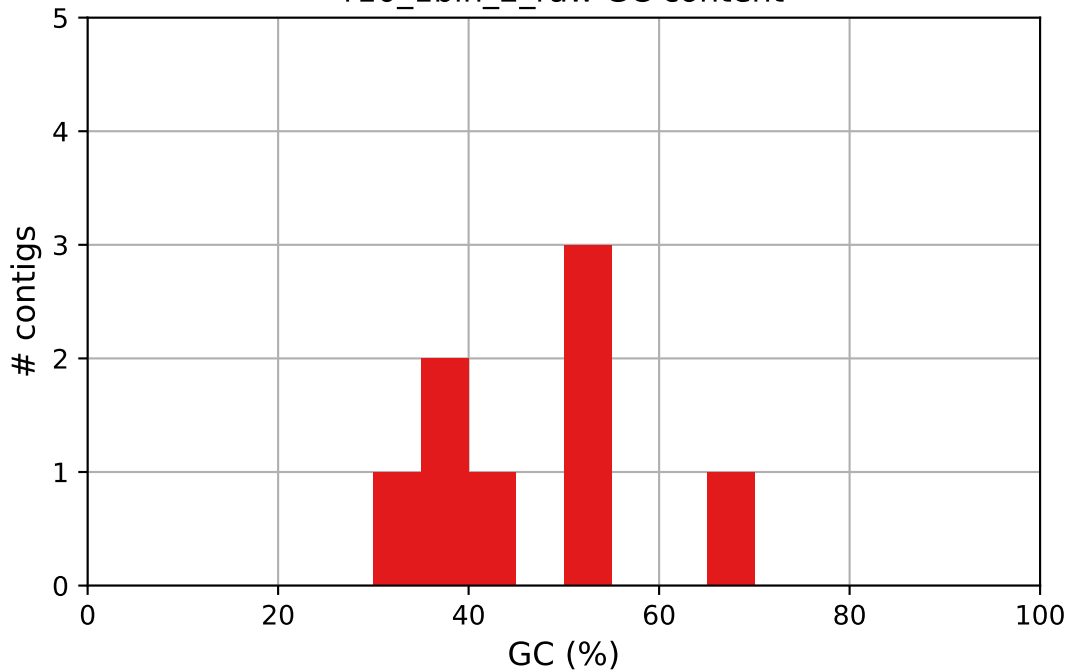
r10_1bin_2_racon_r1

r10_1bin_2_racon_r2 GC content



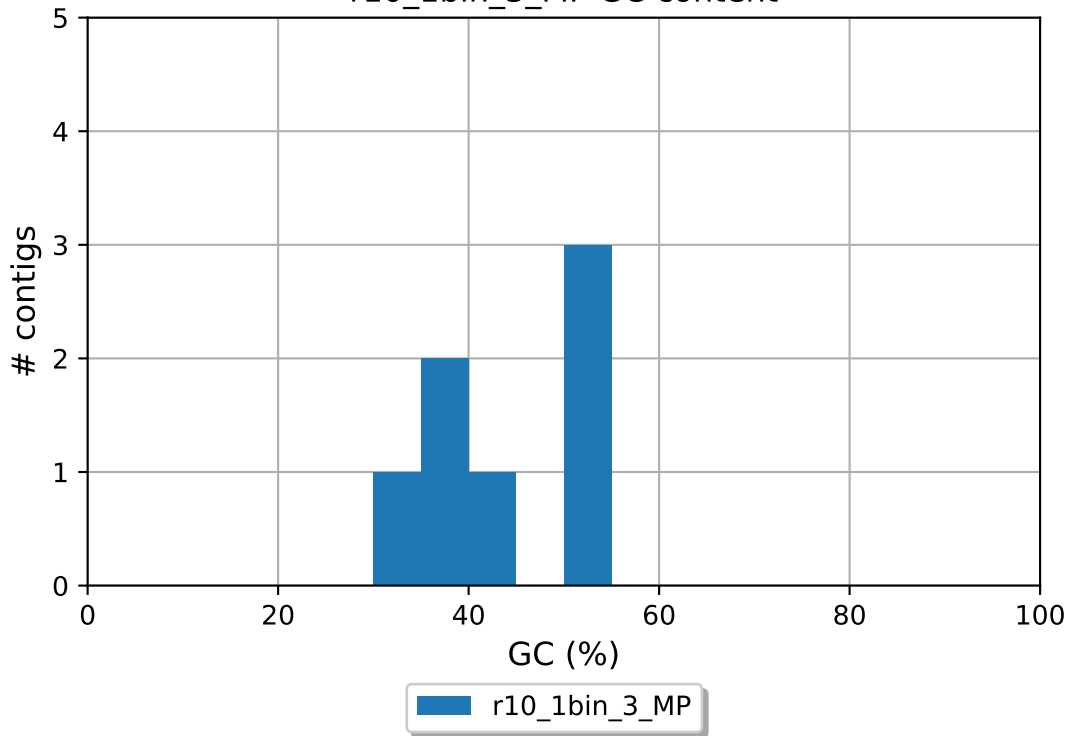
 r10_1bin_2_racon_r2

r10_1bin_2_raw GC content

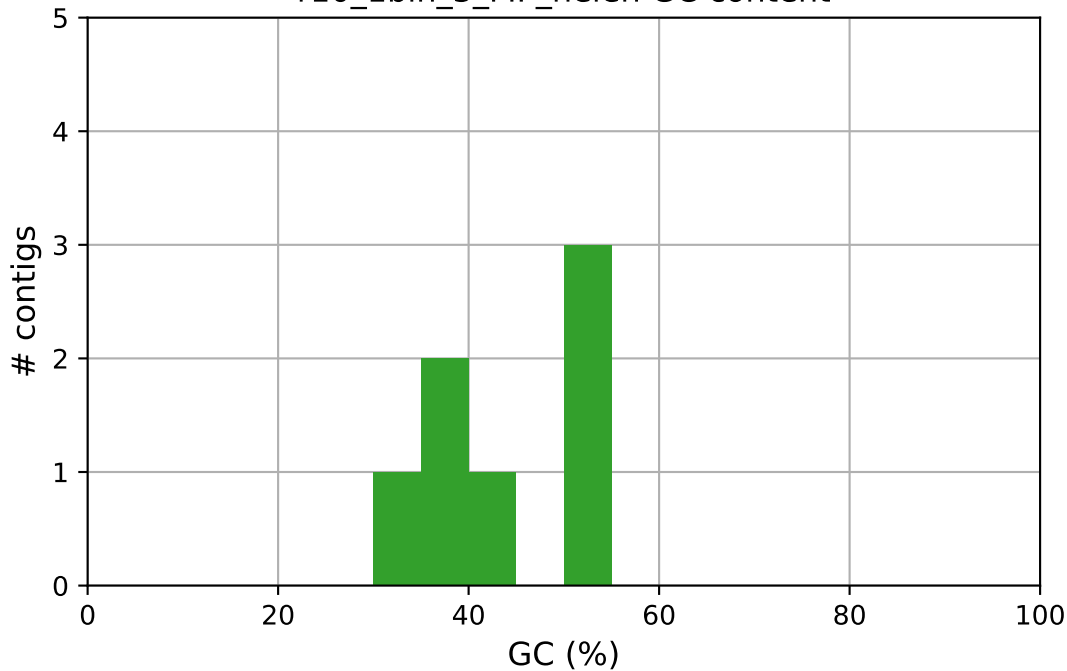


r10_1bin_2_raw

r10_1bin_3_MP GC content

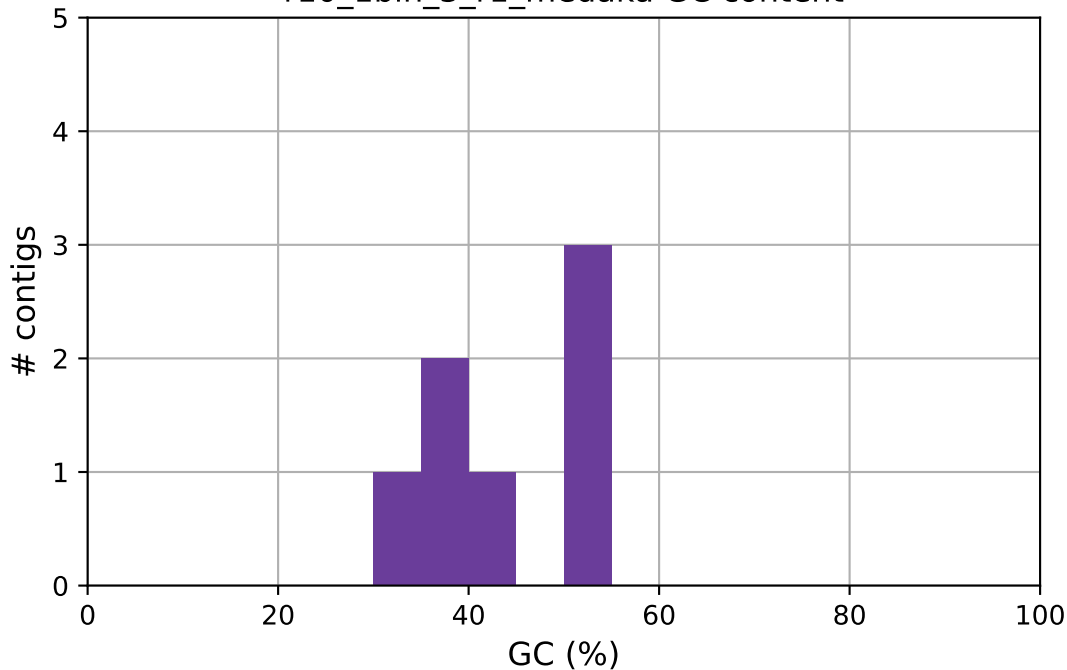


r10_1bin_3_MP_helen GC content



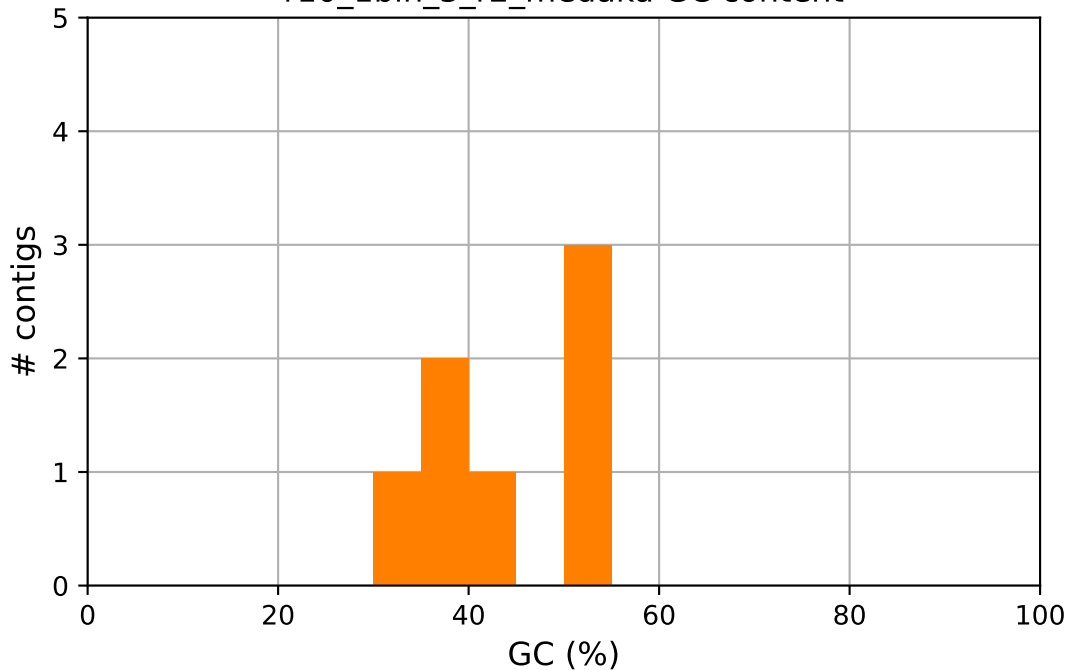
r10_1bin_3_MP_helen

r10_1bin_3_r1_medaka GC content



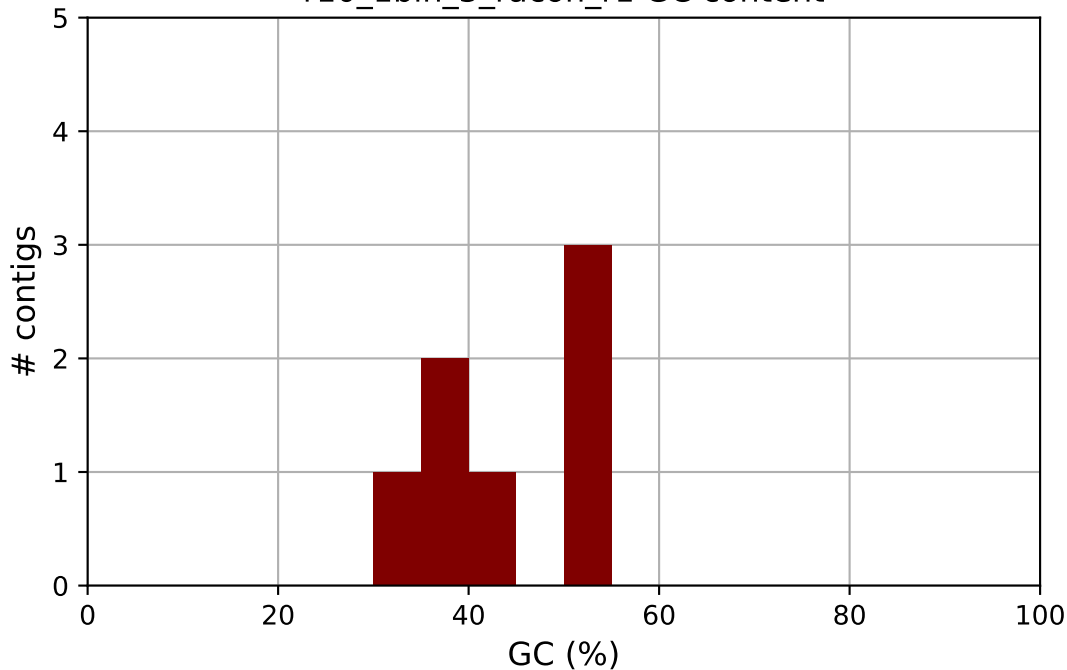
r10_1bin_3_r1_medaka

r10_1bin_3_r2_medaka GC content



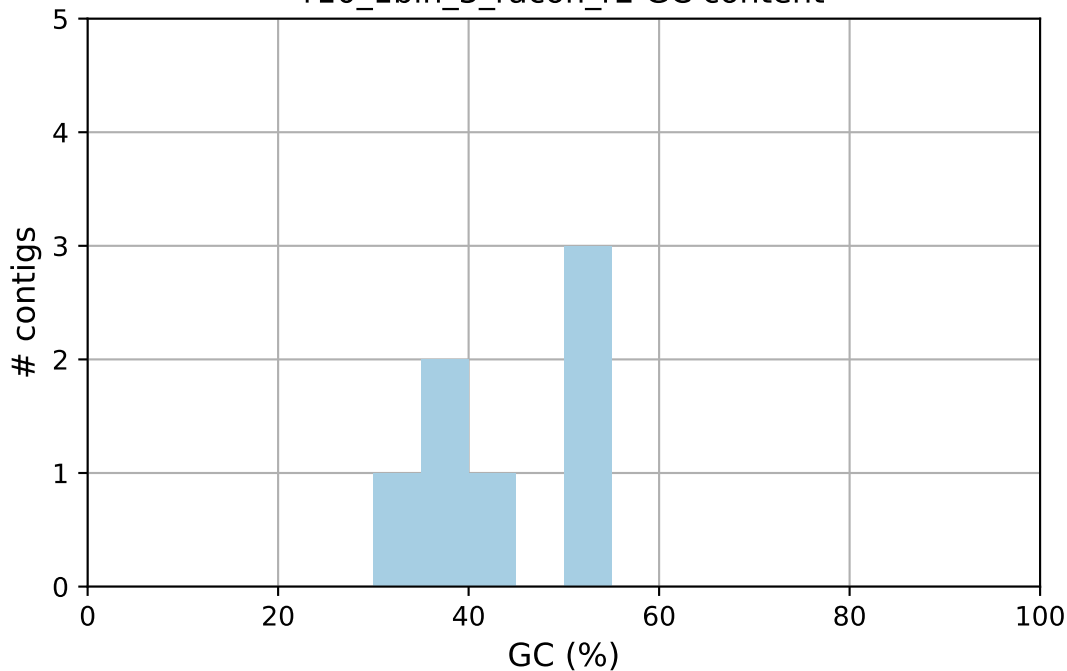
r10_1bin_3_r2_medaka

r10_1bin_3_racon_r1 GC content



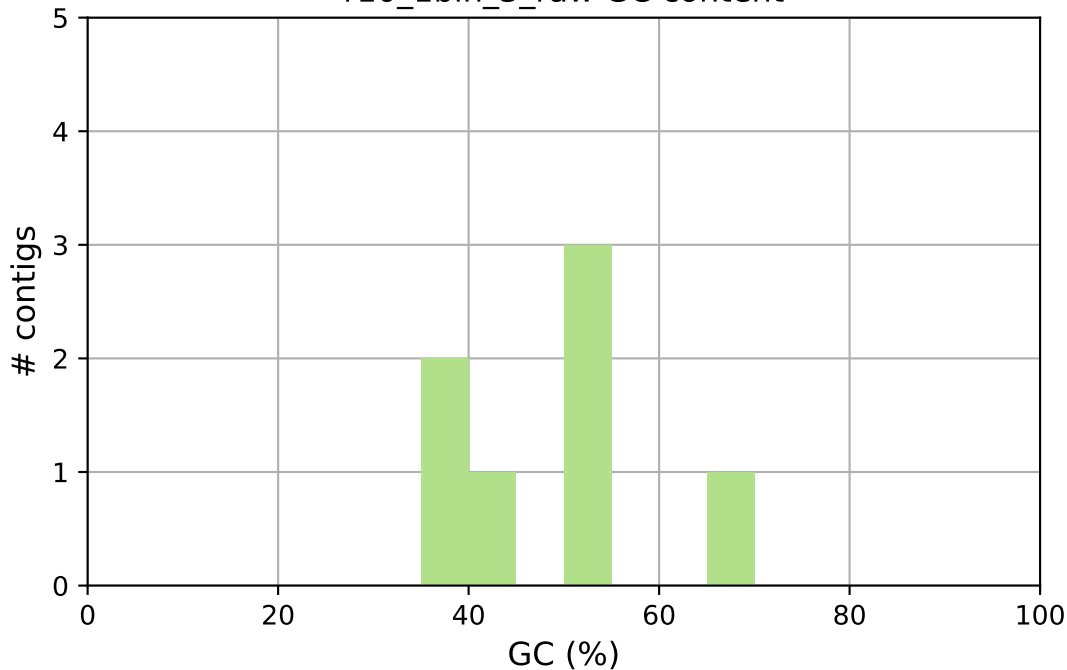
r10_1bin_3_racon_r1

r10_1bin_3_racon_r2 GC content



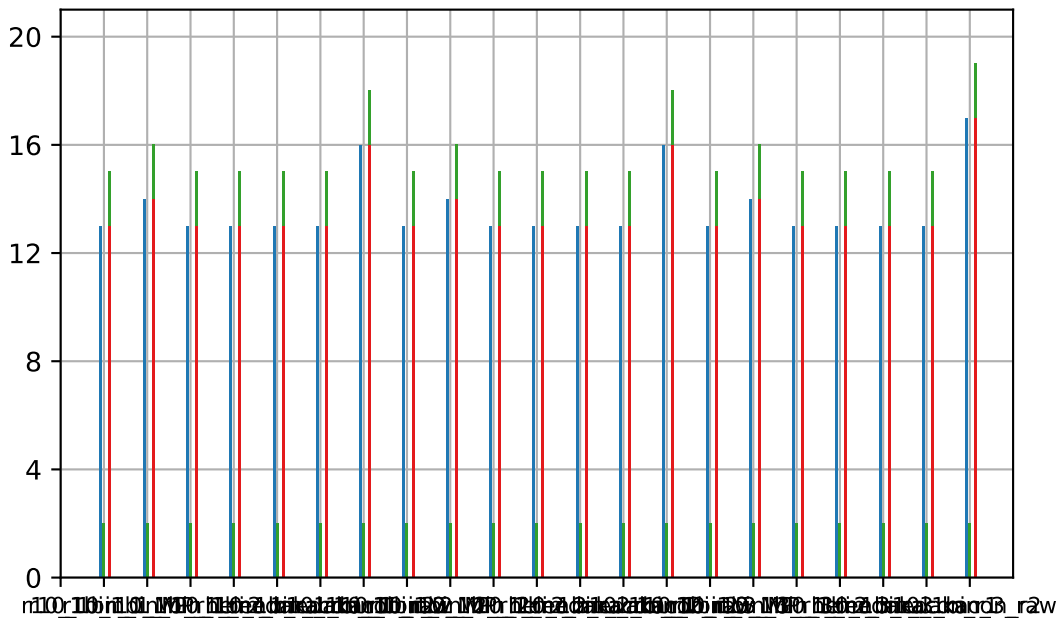
r10_1bin_3_racon_r2

r10_1bin_3_raw GC content

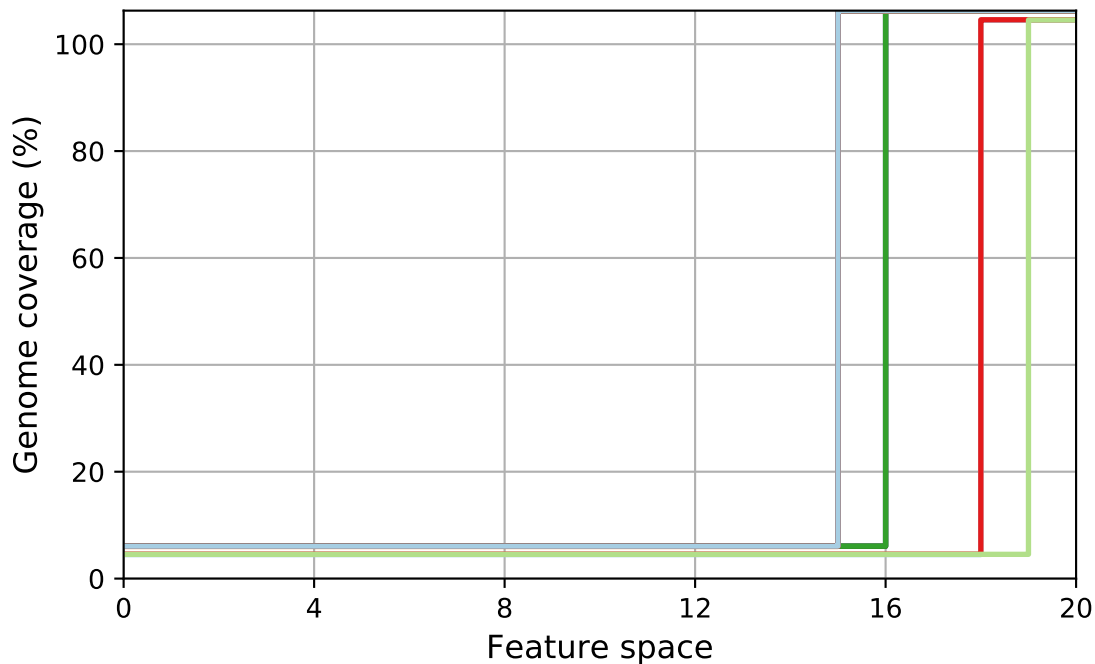


r10_1bin_3_raw

Misassemblies

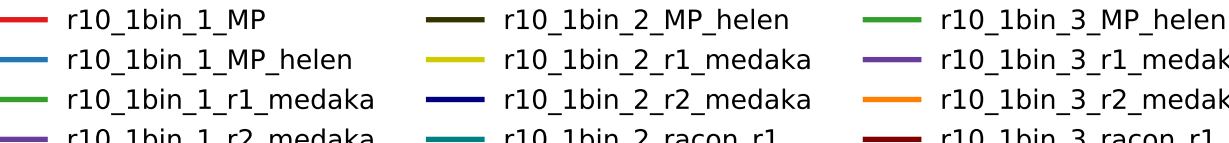
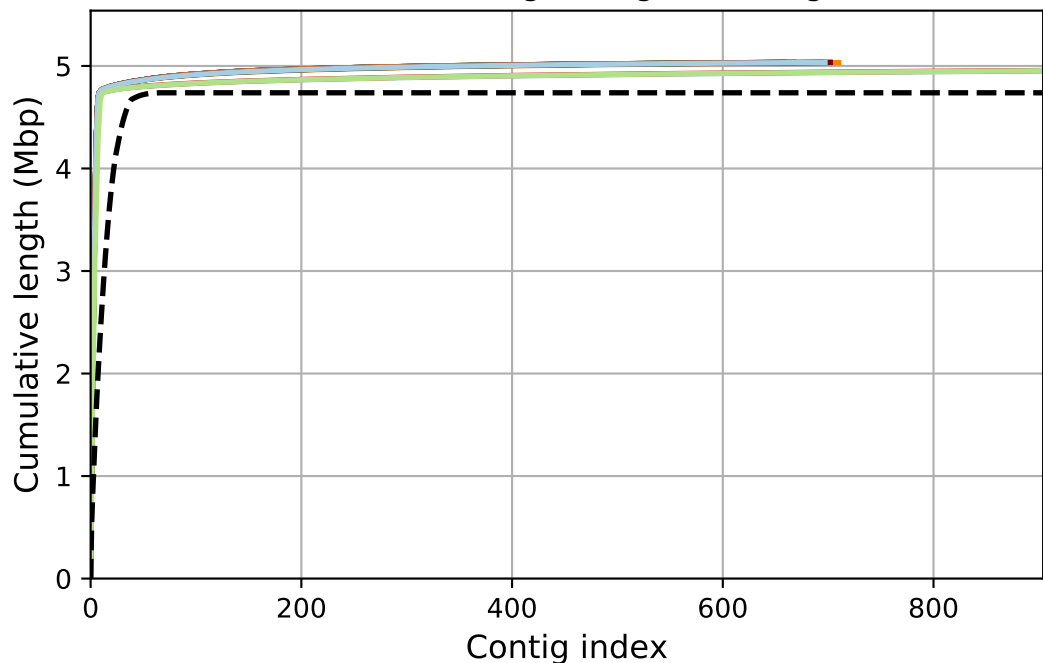


FRCurve (misassemblies)

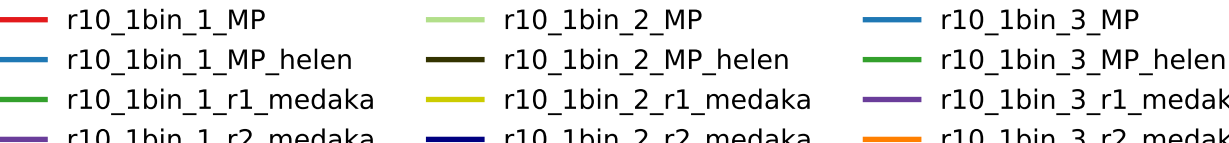
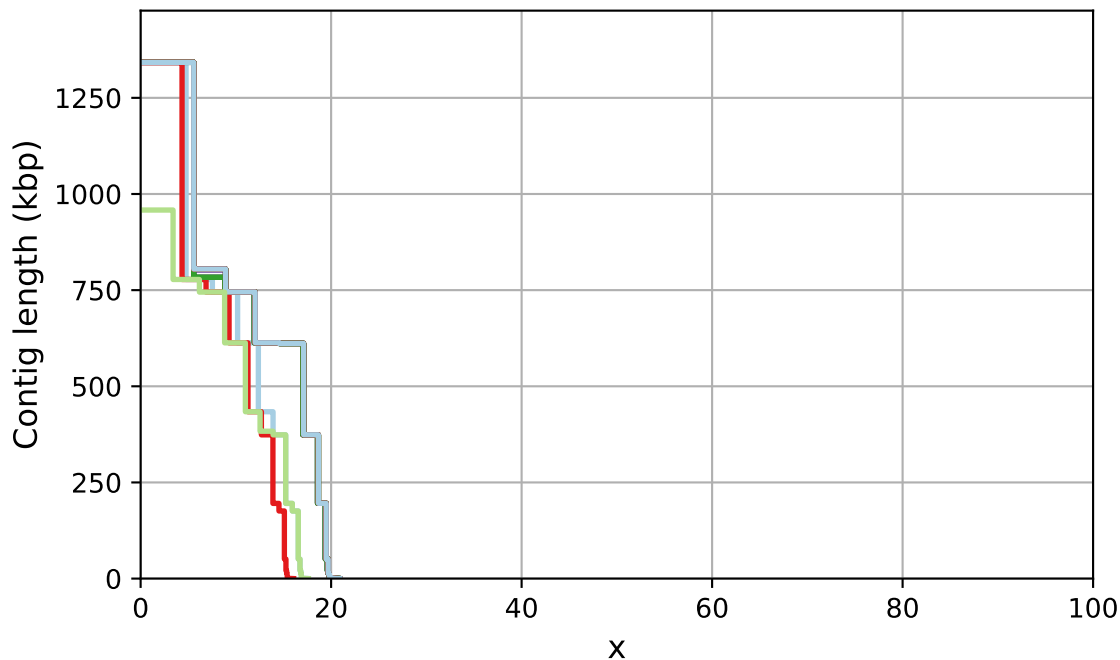


— r10_1bin_1_MP — r10_1bin_2_MP — r10_1bin_3_MP
— r10_1bin_1_MP_helen — r10_1bin_2_MP_helen — r10_1bin_3_MP_helen
— r10_1bin_1_r1_medaka — r10_1bin_2_r1_medaka — r10_1bin_3_r1_medaka
— r10_1bin_1_r2_medaka — r10_1bin_2_r2_medaka — r10_1bin_3_r2_medaka

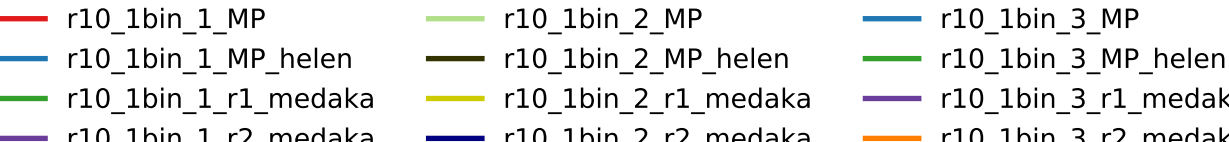
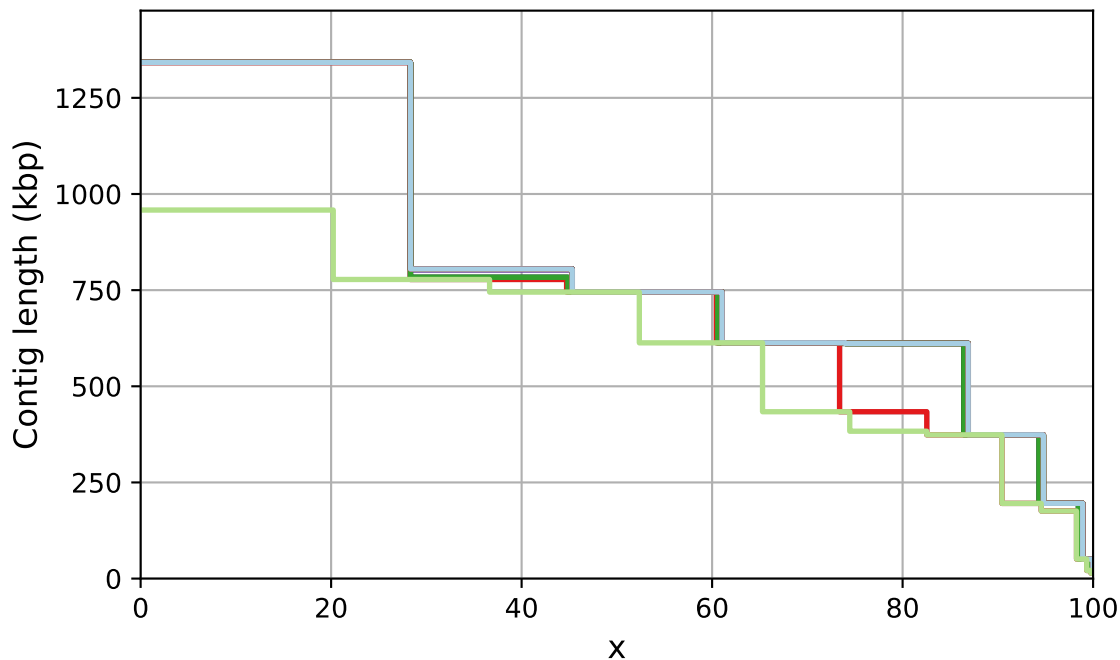
Cumulative length (aligned contigs)



NAX



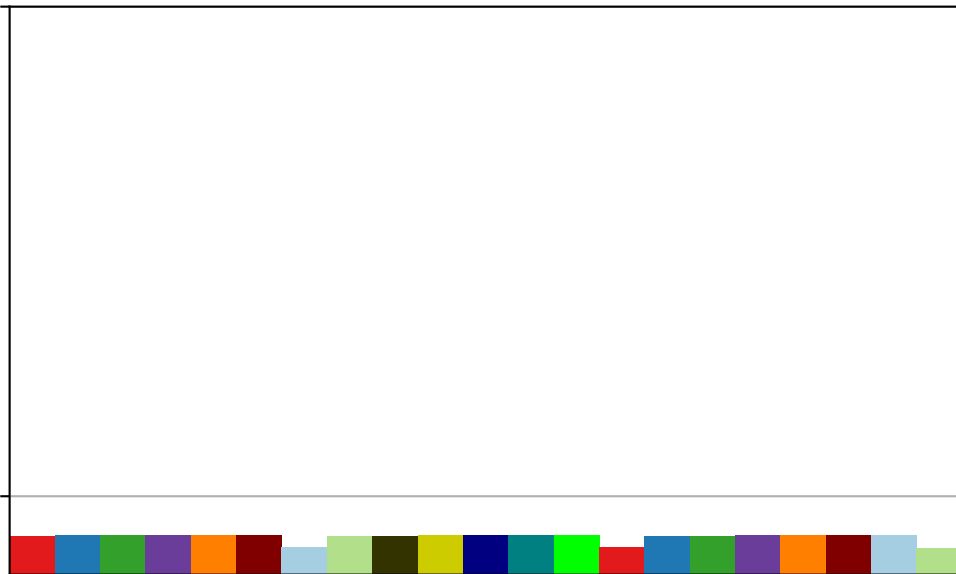
NGAx



Genome fraction, %

100

99



■ r10_1bin_1_MP	■ r10_1bin_2_MP	■ r10_1bin_3_MP
■ r10_1bin_1_MP_helen	■ r10_1bin_2_MP_helen	■ r10_1bin_3_MP_helen
■ r10_1bin_1_r1_medaka	■ r10_1bin_2_r1_medaka	■ r10_1bin_3_r1_medaka
■ r10_1bin_1_r2_medaka	■ r10_1bin_2_r2_medaka	■ r10_1bin_3_r2_medaka