Report

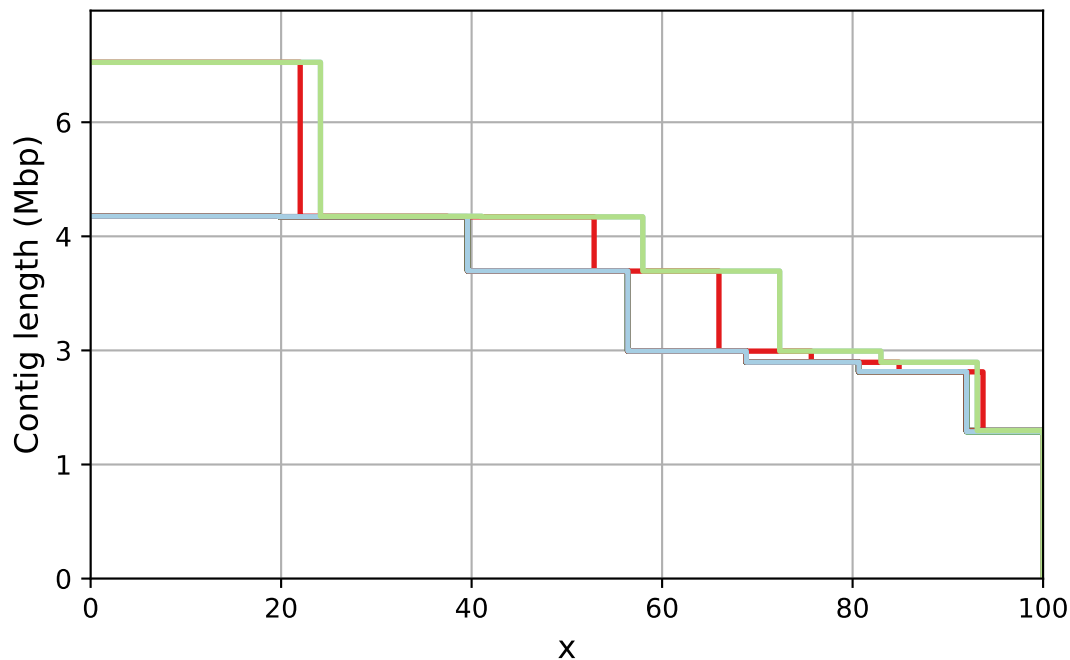|	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	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	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
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	44.78	44.78	44.78	51.10
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45
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	21	21	21	21	21	21	19	21	21	21	21	21	21	18	21	21	21	21	21	21	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	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
# local misassemblies	36	36	37	37	36	38	60	36	36	37	36	36	36	57	37	36	37	37	36	37	61
# 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	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	19039379	19035026	19035485	19028017	19024918	19015446	23183477	19038854	19034932	19036605	19025705	19027461	19016574	25899660	19041077	19035277	19036197	19029497	19023217	19018182	23181201
Genome fraction (%)	97.703	97.703	97.701	97.701	97.703	97.701	97.665	97.703	97.703	97.701	97.703	97.703	97.703	97.663	97.703	97.703	97.701	97.701	97.703	97.703	97.664
Duplication ratio	1.077	1.077	1.077	1.077	1.077	1.078	1.058	1.077	1.077	1.077	1.077	1.077	1.076	1.078	1.059	1.076	1.076	1.077	1.077	1.077	1.059
# 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	442.70	439.45	443.16	442.28	445.54	455.37	484.61	443.08	439.64	442.31	441.27	440.28	453.82	481.34	440.05	435.92	442.49	441.12	448.56	450.78	491.63
# indels per 100 kbp	20.31	18.11	15.23	14.78	39.71	36.89	236.83	20.31	17.94	15.20	15.05	40.78	36.76	236.19	20.63	18.54	15.20	14.86	40.54	36.91	241.45
Largest alignment	1408812	1408784	1408811	1408819	1408601	1408646	1102546	1408813	1408790	1408816	1408822	1408626	1408649	1311433	1408800	1408654	1408813	1408811	1408608	1408654	1102626
Total aligned length	5029788	5029835	5033790	5033291	5030902	5037405	4942385	5030076	5029914	5030776	5032646	5027574	5034052	4946879	5028526	5028135	5033033	5032602	5031647	5032999	4944437
NGA50	1103278	1103268	1105649	1105646	1103075	1105456	586349	1103277	1103269	1103273	1105643	1103085	1103096	1104907	1103280	1103275	1105646	1105646	1103087	1103077	586350
NGA75	393562	393565	393563	393565	393542	393556	376968	393562	393563	393564	393564	393535	393551	397472	393562	393564	393565	393545	393556	393556	376968
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	2	2	2	2	2	2	2	3
LGA75	5	5	5	5	5	5	6	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
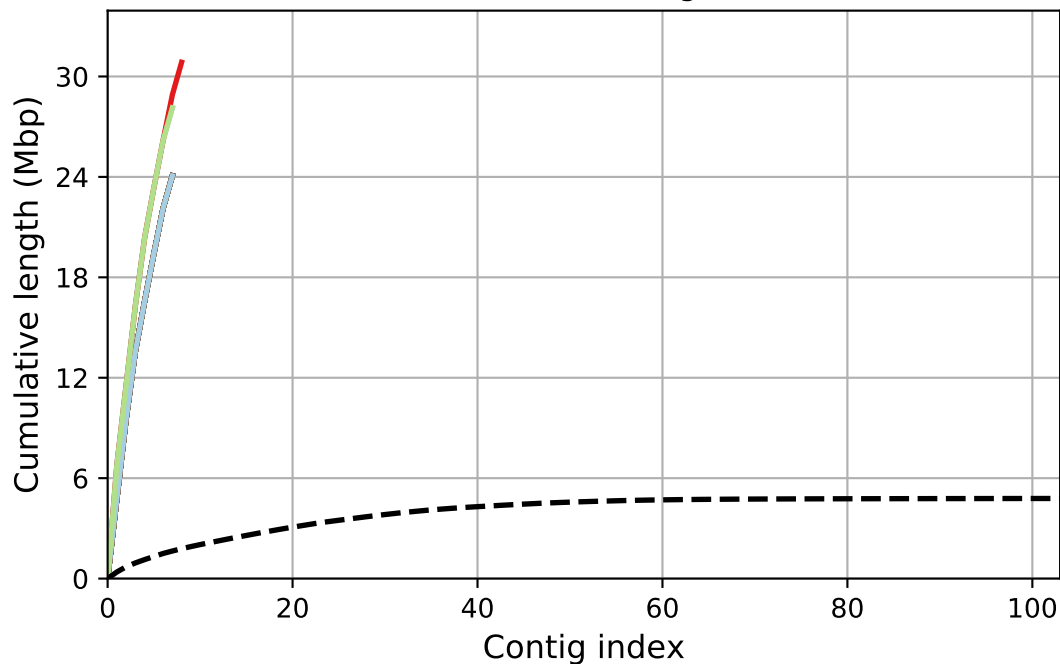
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	18	21	21	21	21	21	21	19
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	18	21	21	21	21	21	21	19
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	17	20	20	20	20	20	20	18
# 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	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764811	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
# 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	12	12	12	12	12	12	34	12	12	12	12	12	12	32	12	12	12	12	12	12	34
# local misassemblies	36	36	37	37	36	38	60	36	36	36	37	36	36	57	37	36	37	37	36	37	61
# 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	42	42	42	42	42	42	35	42	42	42	42	42	42	35	42	42	42	42	42	42	35
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	7	6	6	6	6	6	6	6
# mismatches	20703	20551	20724	20683	20836	21295	22654	20721	20560	20685	20636	20590	21223	22501	20579	20386	20693	20629	20977	21081	22982
# indels	950	847	712	691	1857	1725	11071	950	839	711	704	1907	1719	11041	965	867	711	695	1896	1726	11287
# indels (<= 5 bp)	851	748	616	595	1760	1629	10870	851	740	614	608	1809	1620	10841	866	764	615	599	1798	1628	11084
# indels (> 5 bp)	99	99	96	96	97	96	201	99	99	97	96	98	99	200	99	103	96	96	98	98	203
Indels length	6218	6143	5838	5817	7254	6979	20404	6218	6133	5937	5830	7296	7081	20238	6237	6227	5836	5820	7294	7097	20753

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	19039379	19035026	19035485	19028017	19024918	19015446	23183477	19038854	19034932	19036605	19025705	19027461	19016574	25899660	19041077	19035277	19036197	19029497	19023217	19018182	23181201
# N's	0	0	0	0	0	0	10	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

Contig length (Mbp) vs x

Legend:
- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_1_r2_medaka
- r10_1bin_2_MP
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_3_MP
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medak
- r10_1bin_3_r2_medak
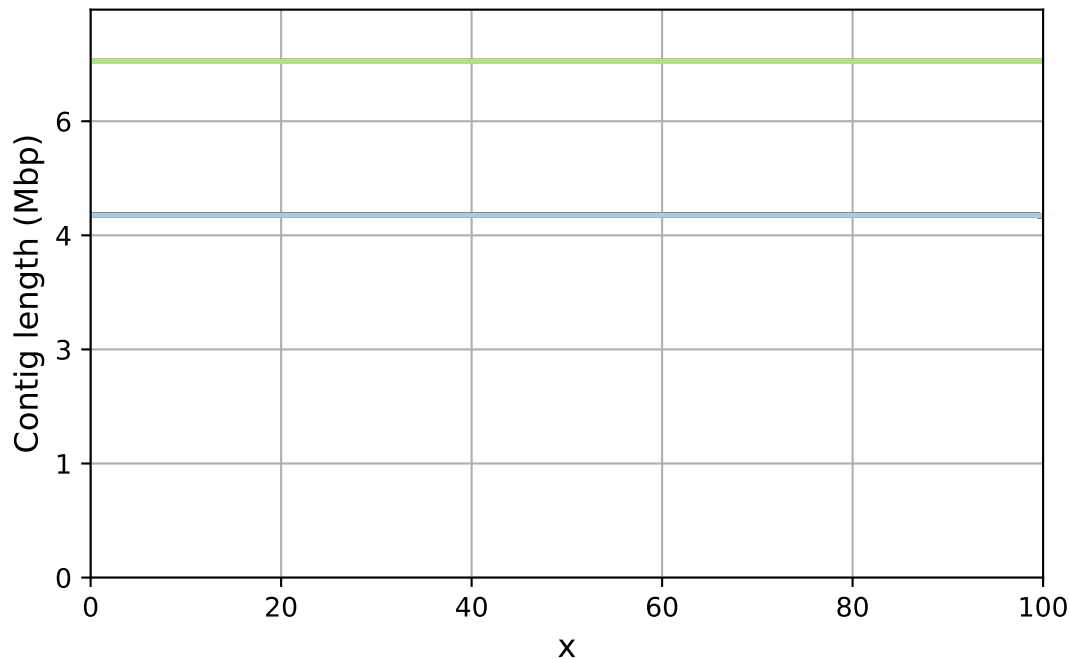
NGx

▬ 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_medak
▬ r10_1bin_1_r2_medaka	▬ r10_1bin_2_r2_medaka	▬ r10_1bin_3_r2_medak

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_medak
— r10_1bin_1_r1_medaka	— r10_1bin_2_r2_medaka	— r10_1bin_3_r2_medak
— r10_1bin_1_r2_medaka	— r10_1bin_2_racon_r1	— r10_1bin_3_racon_r1

GC content

Legend:
- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_1_r2_medaka
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_2_racon_r1
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medak
- r10_1bin_3_r2_medak
- r10_1bin_3_racon_r1
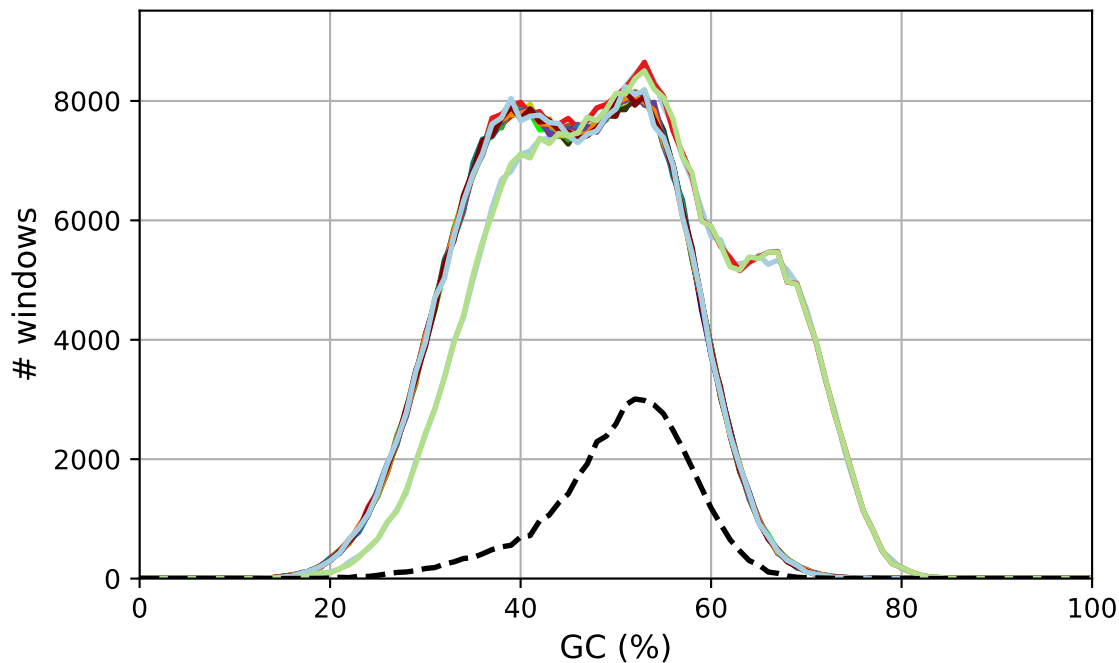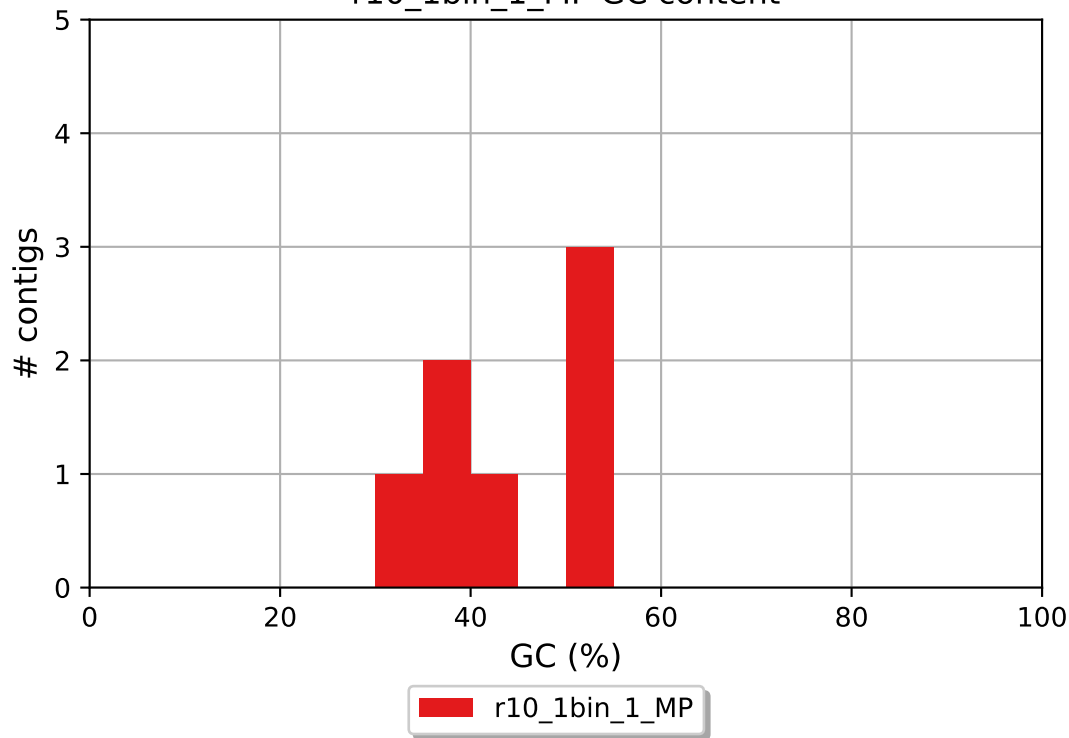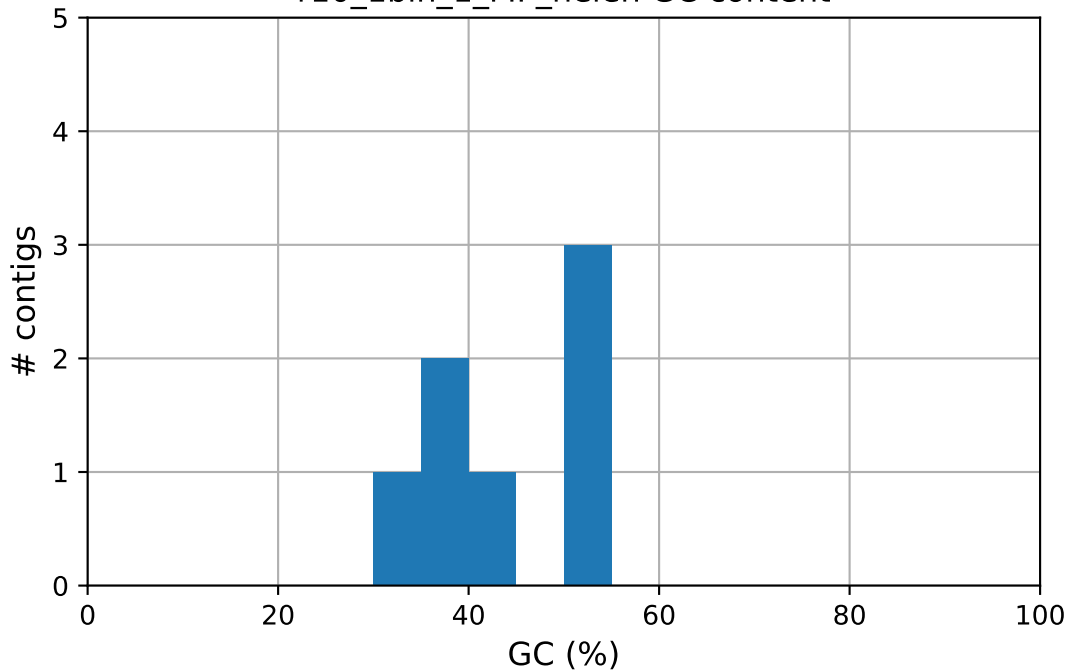
r10_1bin_1_r1_medaka GC content
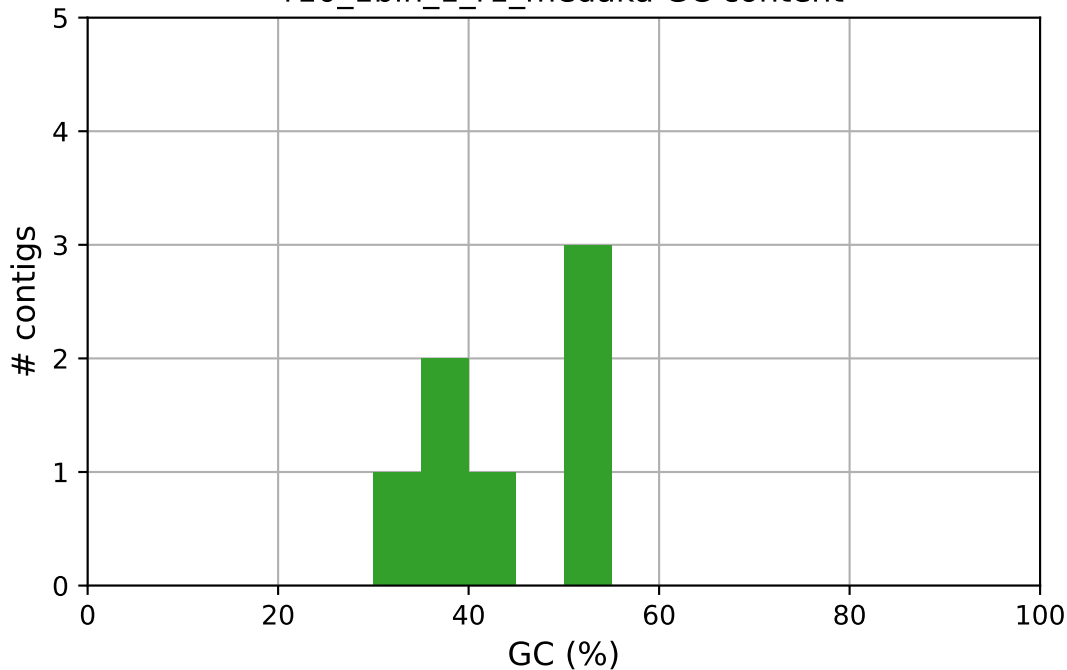
r10_1bin_1_r2_medaka GC content
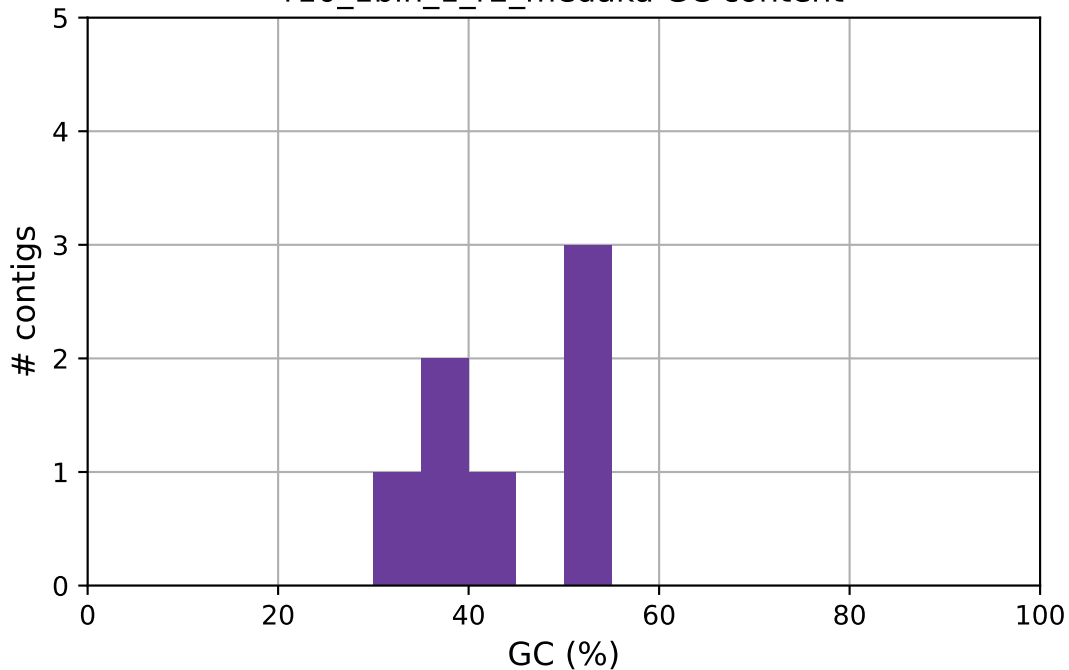
r10_1bin_1_racon_r1 GC content
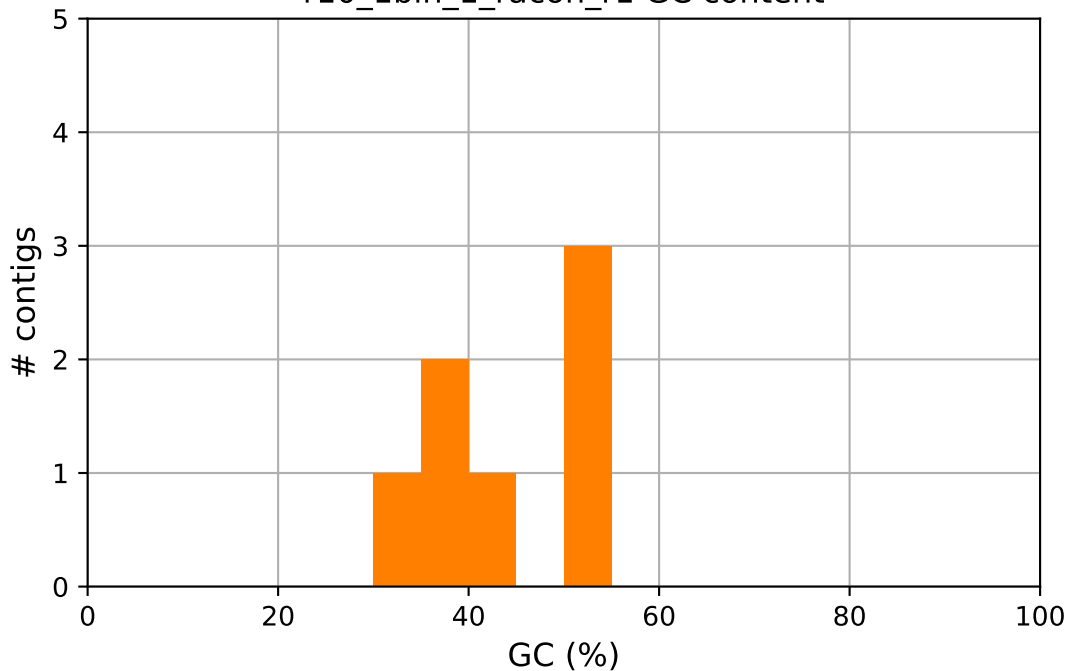
r10_1bin_1_racon_r2 GC content
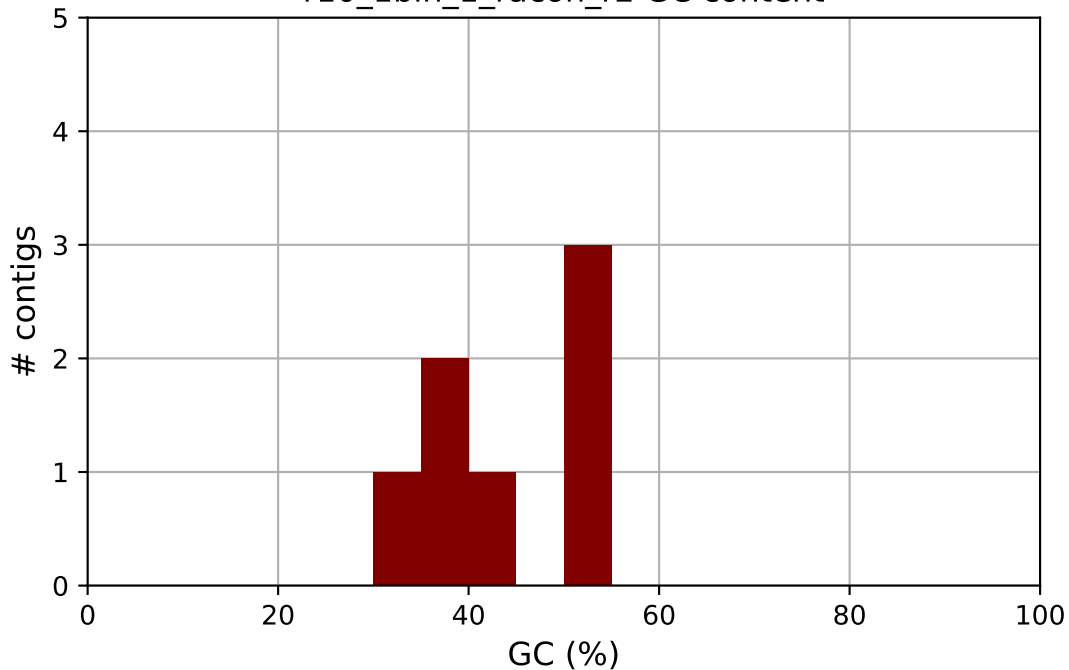
r10_1bin_1_raw GC content
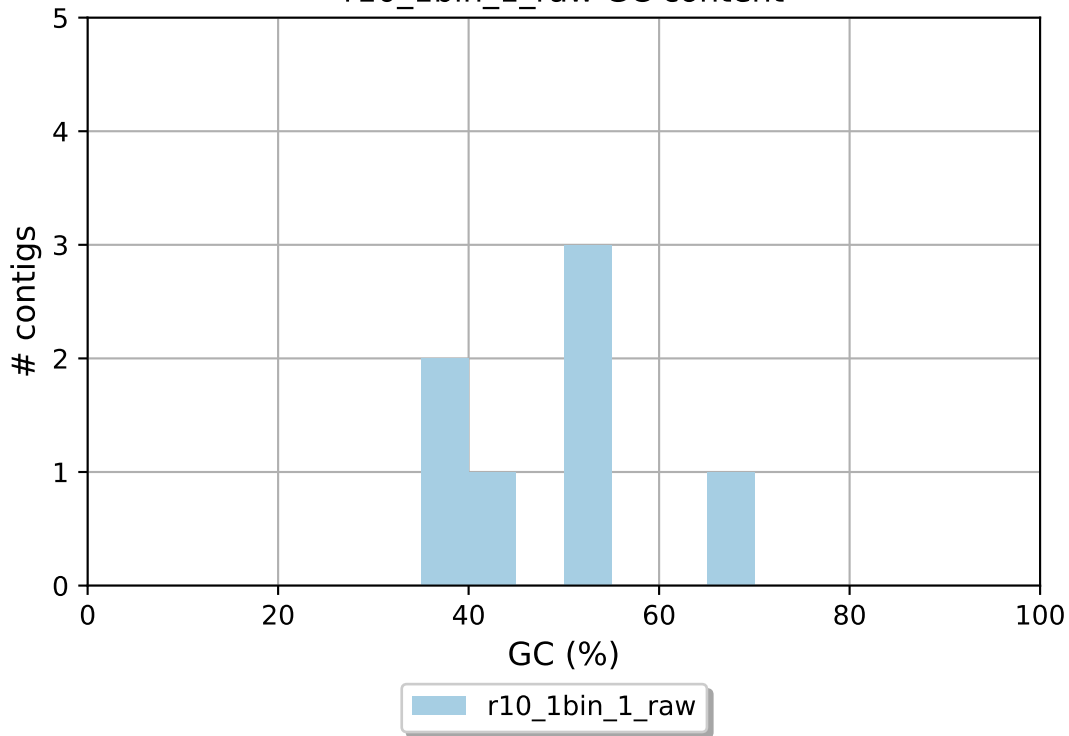
r10_1bin_2_MP GC content
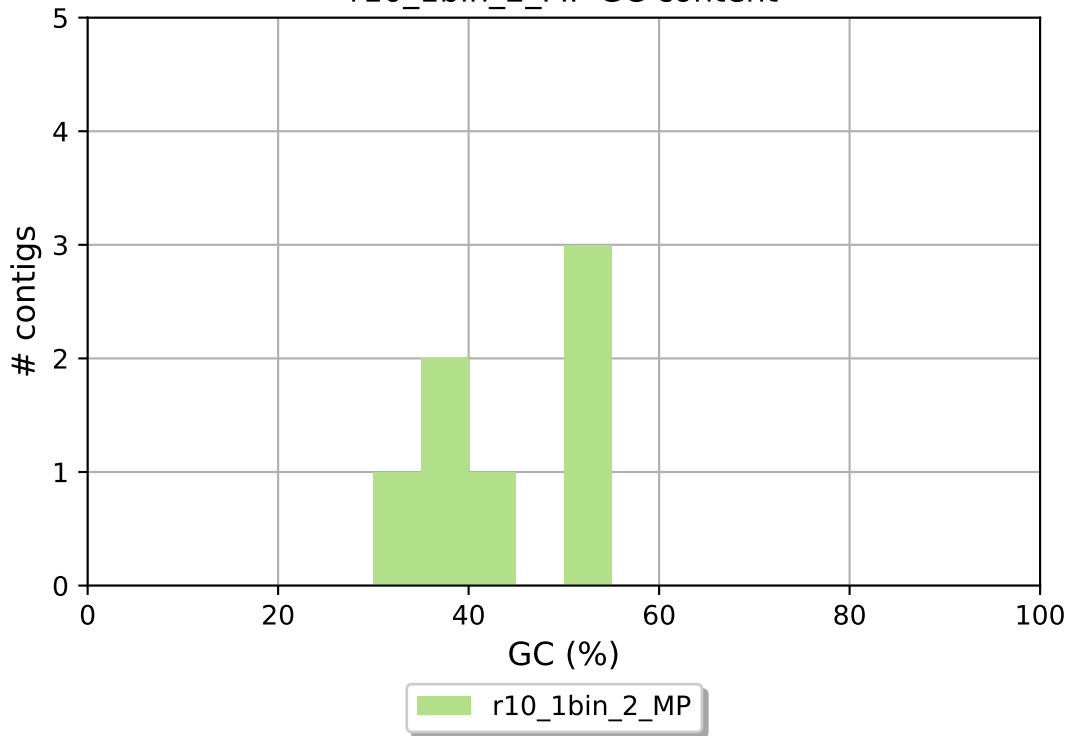
r10_1bin_2_MP_helen GC content
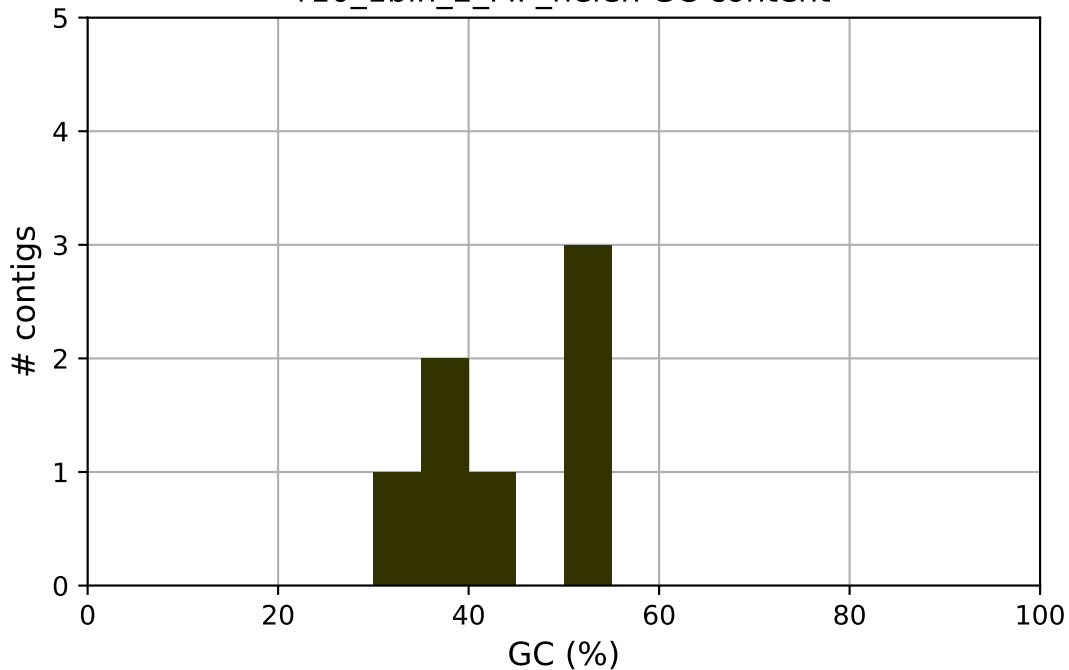
r10_1bin_2_r1_medaka GC content
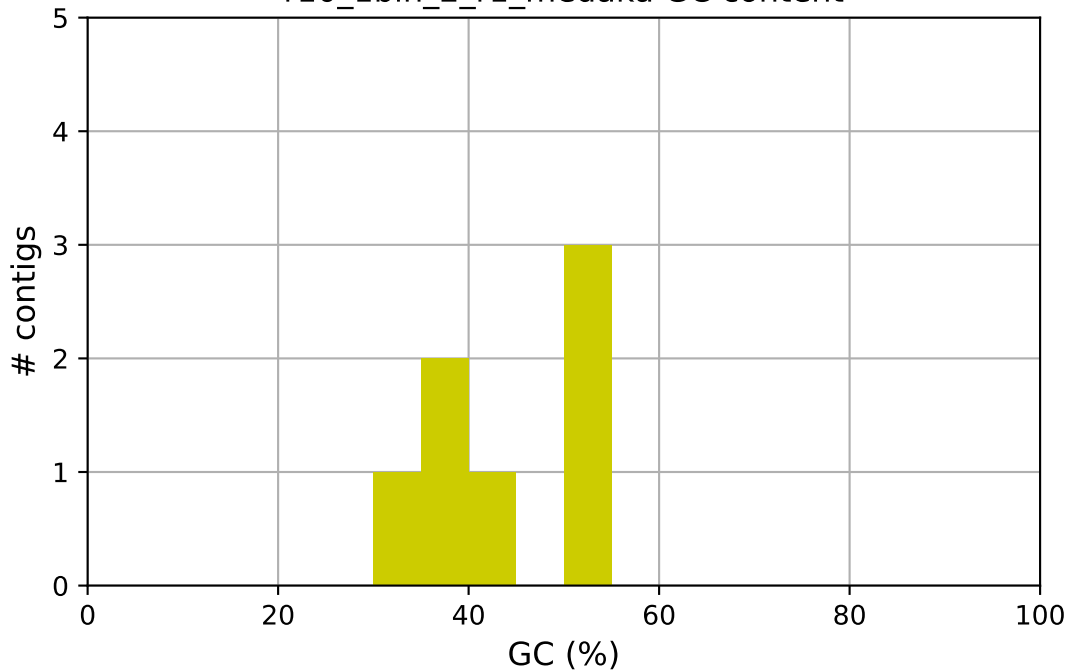
r10_1bin_2_r2_medaka GC content
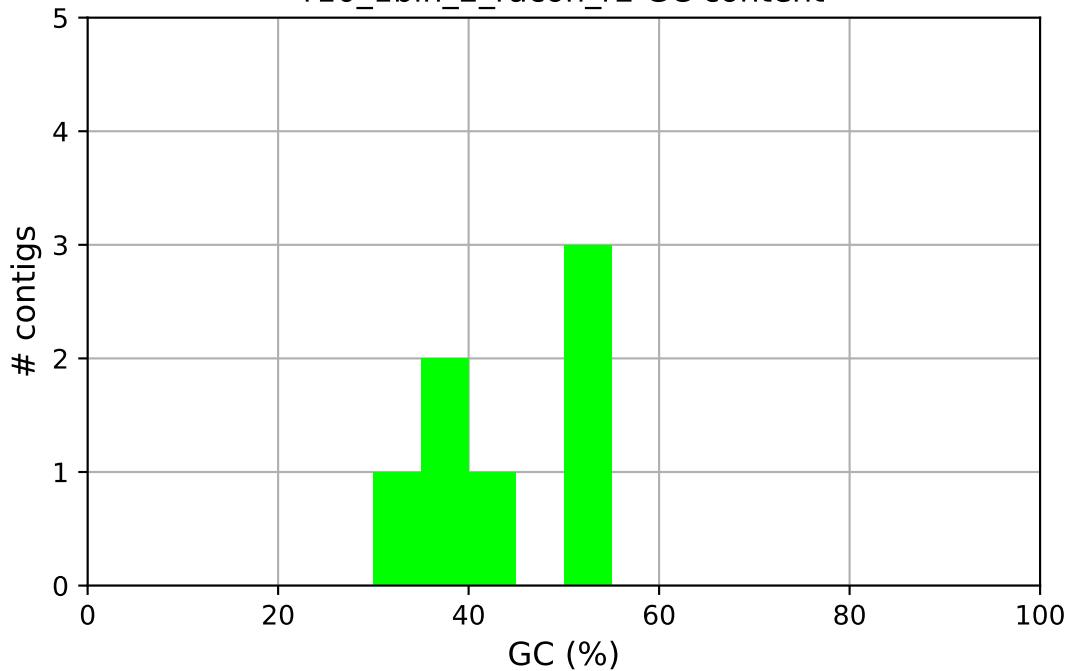
r10_1bin_2_raw GC content
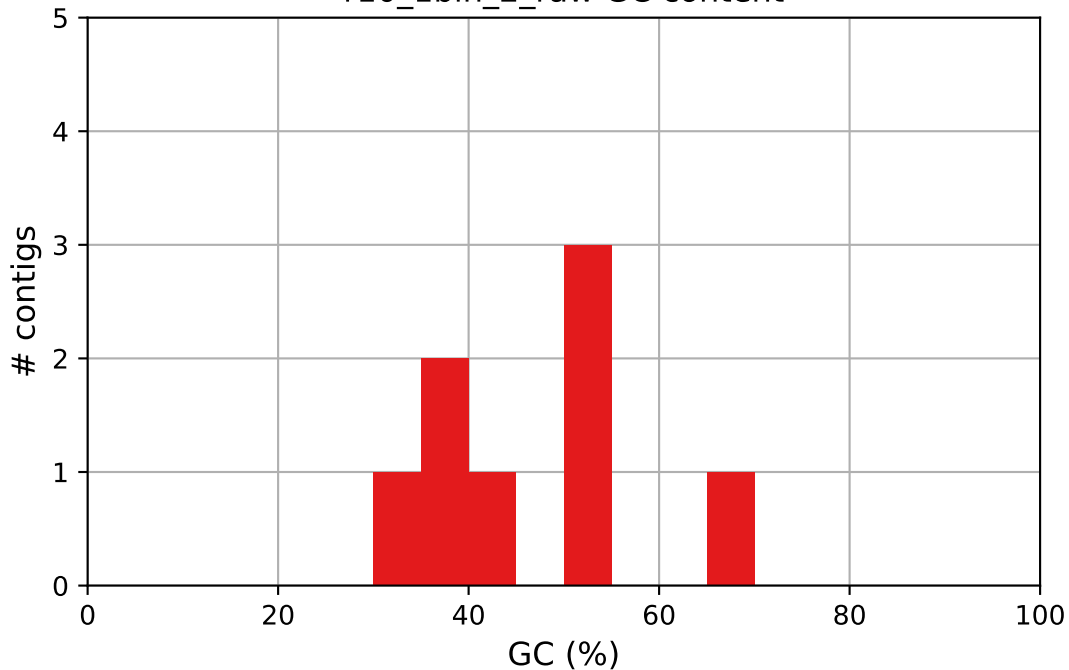
r10_1bin_3_MP GC content
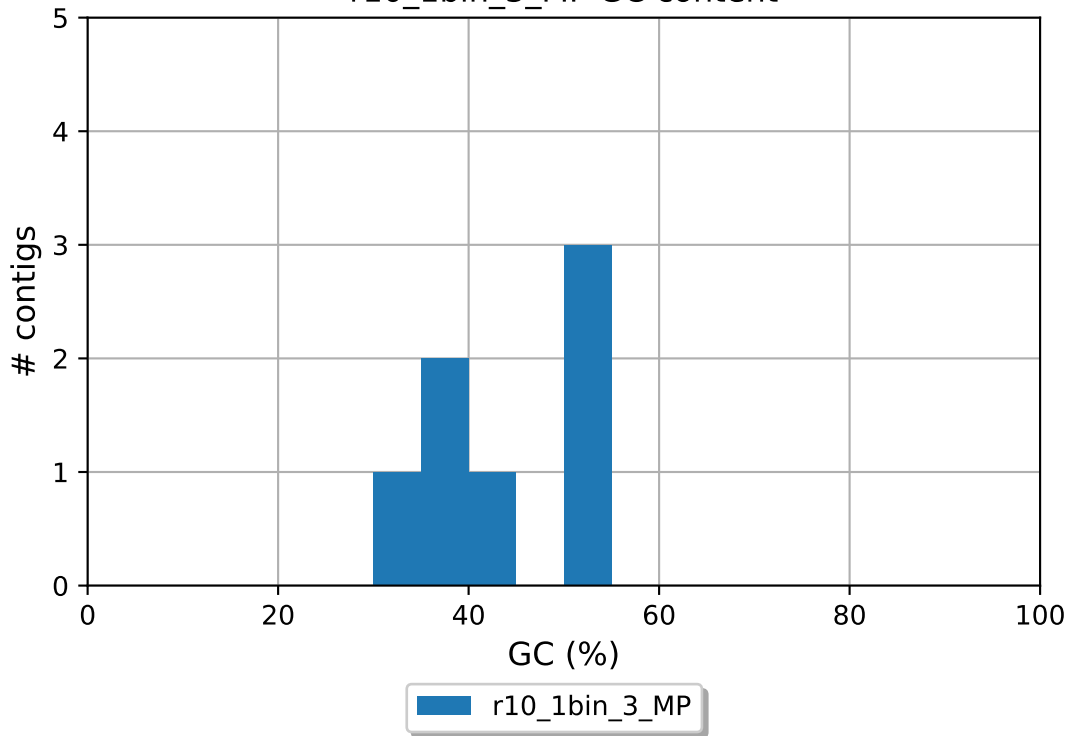
r10_1bin_3_MP_helen GC content
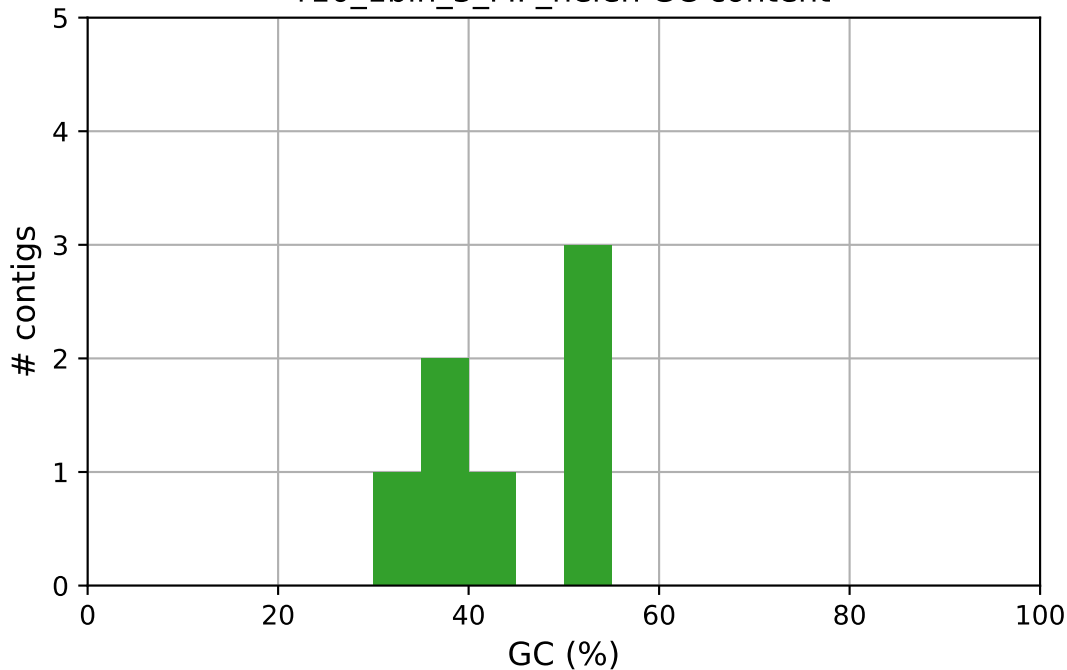
r10_1bin_3_r1_medaka GC content
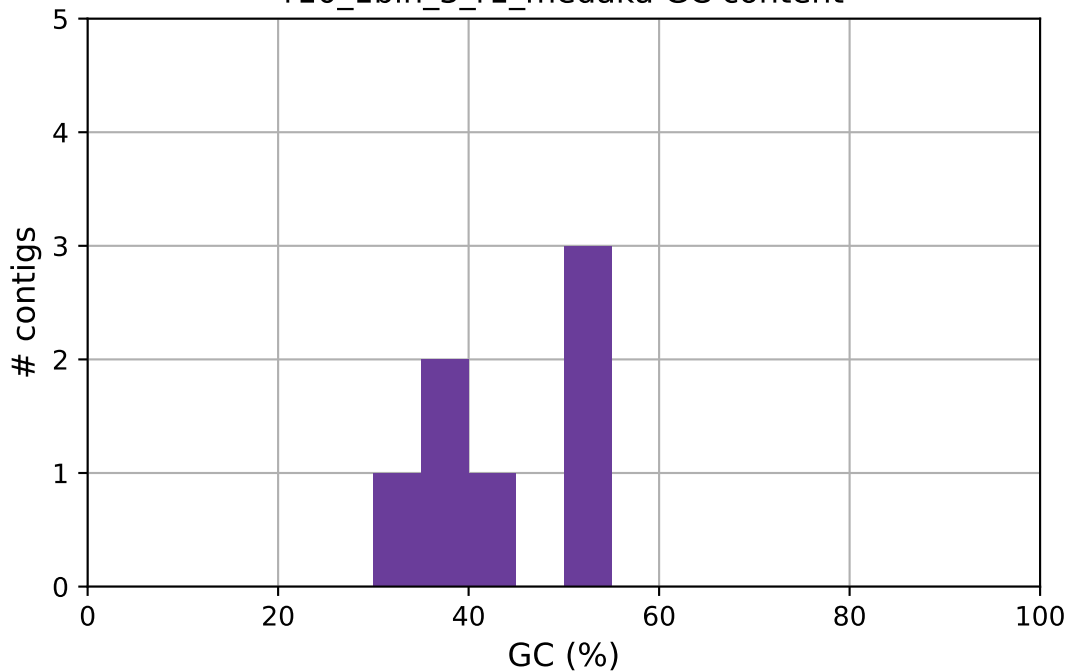
r10_1bin_3_r2_medaka GC content
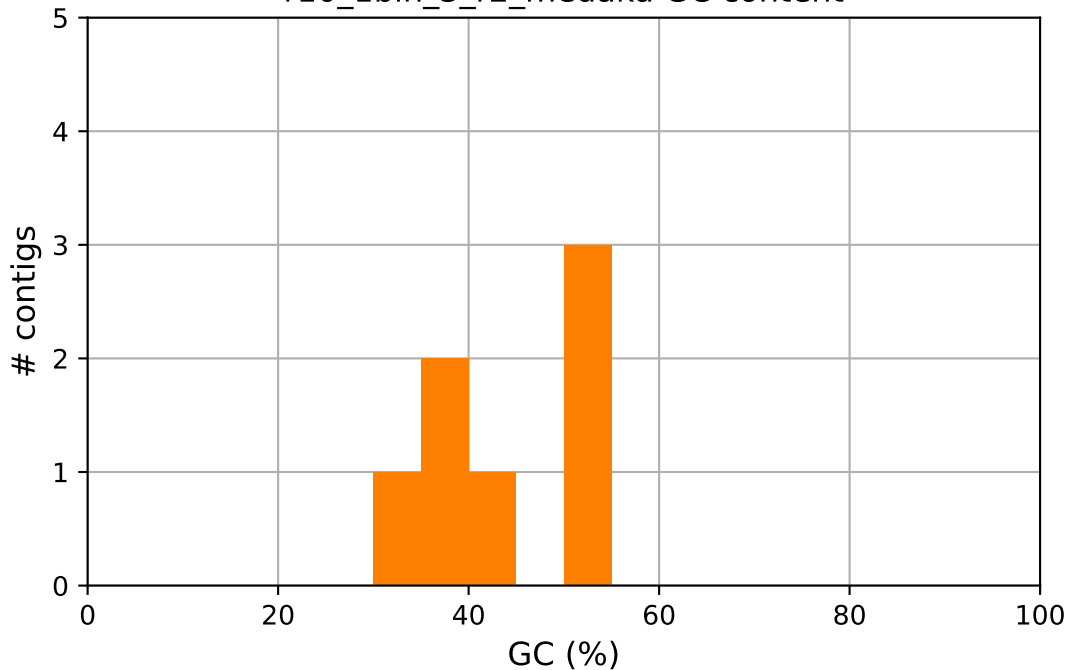
r10_1bin_3_racon_r1 GC content
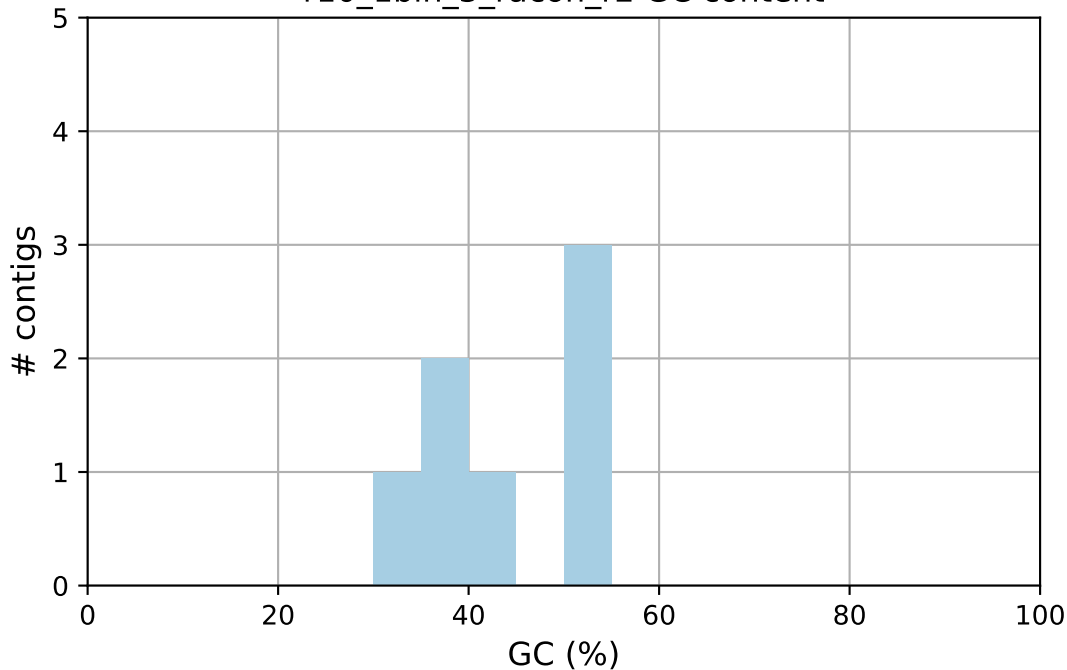
r10_1bin_3_raw GC content

Misassemblies
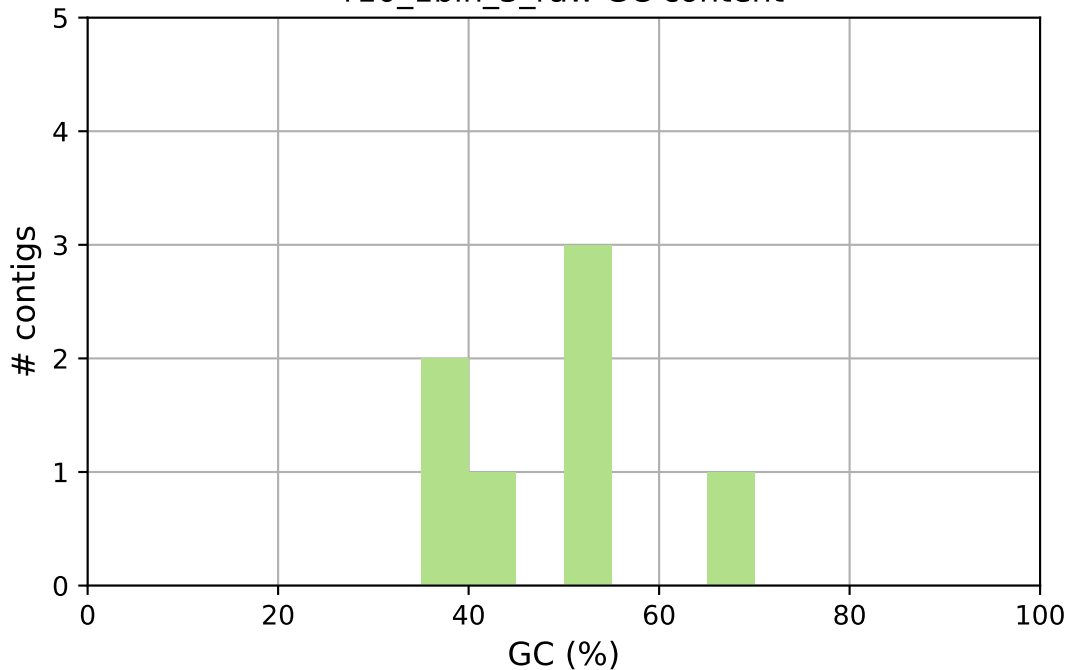
Legend:
- # relocations
- # translocations
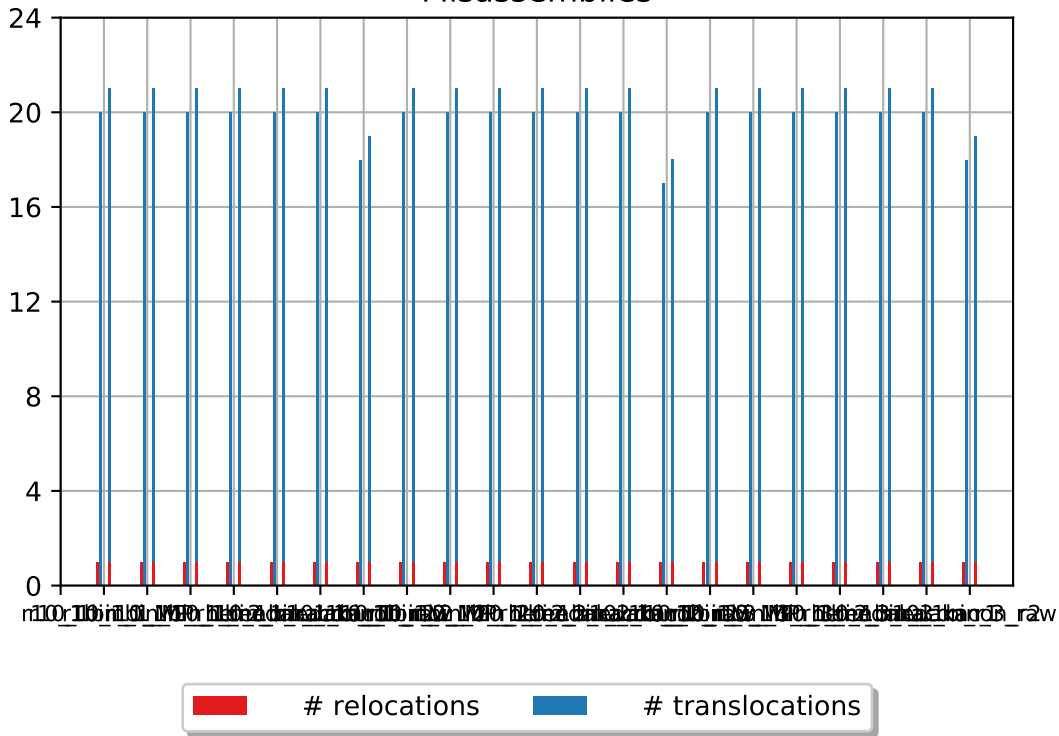
FRCurve (misassemblies)
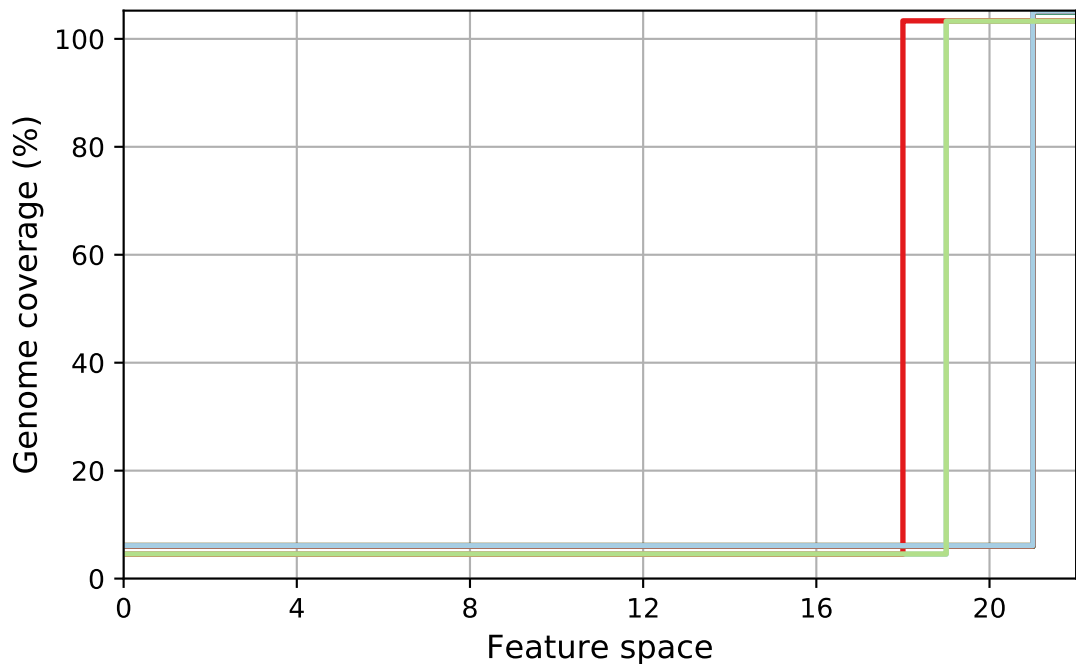
── r10_1bin_1_MP	── r10_1bin_2_MP	── r10_1bin_3_MP
── r10_1bin_1_MP_helen	── r10_1bin_2_MP_helen	── r10_1bin_3_MP_helen
── r10_1bin_1_r1_medaka	── r10_1bin_2_r1_medaka	── r10_1bin_3_r1_medak
── r10_1bin_1_r2_medaka	── r10_1bin_2_r2_medaka	── r10_1bin_3_r2_medak

Cumulative length (aligned contigs)

Legend:
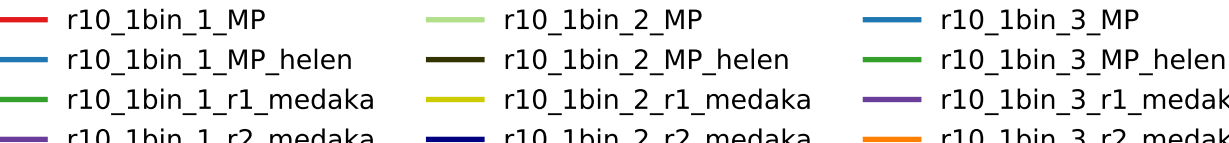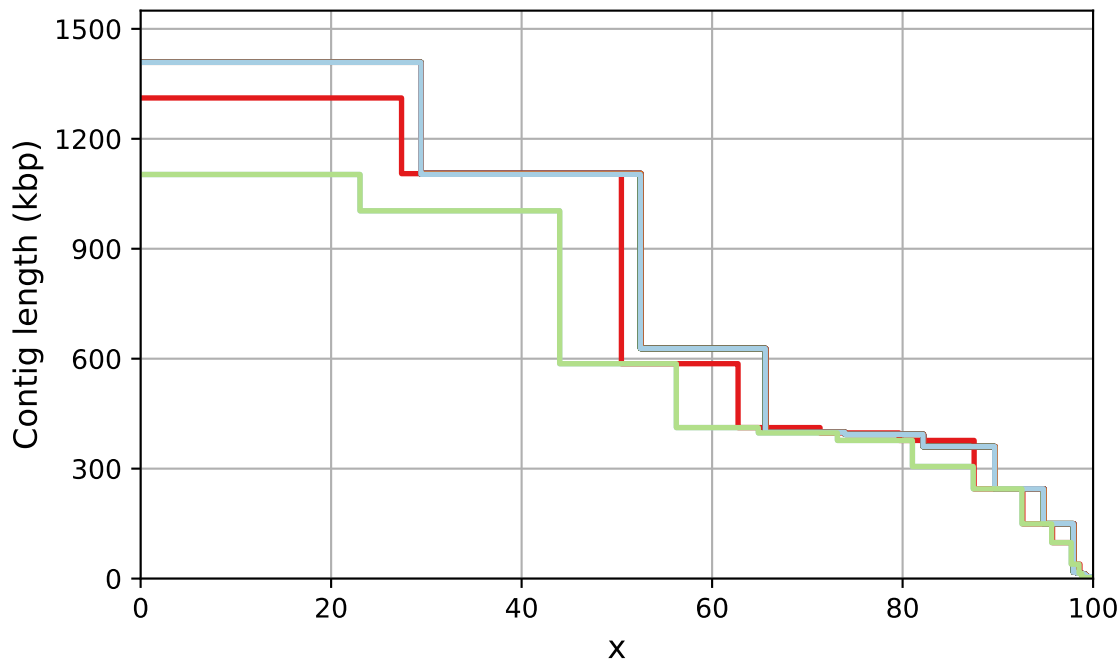
- r10_1bin_1_MP
- r10_1bin_1_MP_helen
- r10_1bin_1_r1_medaka
- r10_1bin_1_r2_medaka
- r10_1bin_2_MP_helen
- r10_1bin_2_r1_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_2_racon_r1
- r10_1bin_3_MP_helen
- r10_1bin_3_r1_medak
- r10_1bin_3_r2_medak
- r10_1bin_3_racon_r1

NAx

—— 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_medak
—— r10_1bin_1_r2_medaka	—— r10_1bin_2_r2_medaka	—— r10_1bin_3_r2_medak

NGAx

— 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_medak
— r10_1bin_1_r2_medaka		— r10_1bin_2_r2_medaka	— r10_1bin_3_r2_medak

Genome fraction, %

Legend:
- 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_medak
- r10_1bin_1_r2_medaka
- r10_1bin_2_r2_medaka
- r10_1bin_3_r2_medak