Report

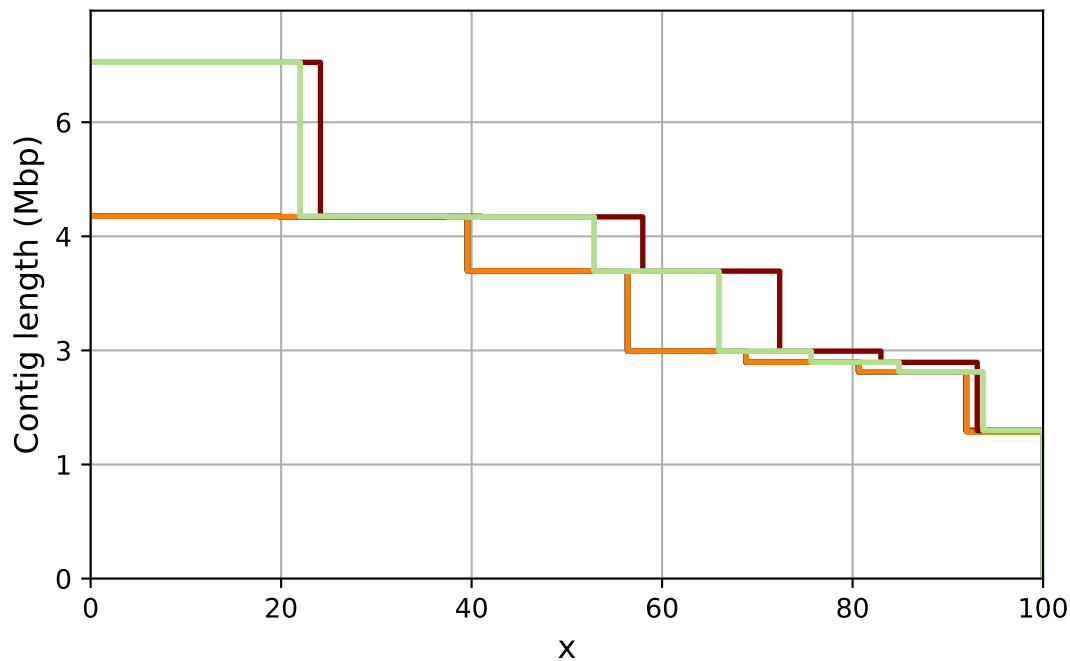|	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Total length (>= 5000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30849039
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30849039
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30849039
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30849039
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Largest contig	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614
Total length	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	28129504	30850309	30849039
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	44.81	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.79	44.79	44.79	44.79	44.79	44.79	51.10	49.48	49.48
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	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4755983	4756088	4755683
NG50	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614
N75	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2990633	2990279	2990261
NG75	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	6787702	6787718	6788614
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	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	19	18	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	4757946	4757846	4757780	4758962	4758994	4758970	4758583	4758586	4758587	4758100	4758114	4758101	4757934	4757908	4757887	4757853	4757839	4757857	4755983	4756088	4755683
# local misassemblies	8	8	8	8	8	8	8	8	8	8	8	8	7	8	8	8	8	8	27	20	29
# 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 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	19033512	19036360	19034564	19038552	19039878	19038661	19034885	19040241	19035546	19027937	19034057	19029383	19019441	19029778	19024350	19019476	19022840	19013503	23169749	25896359	25889982
Genome fraction (%)	98.920	98.919	98.918	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.920	98.889	98.896	98.886
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.074	1.075	1.075	1.075	1.074	1.075	1.076	1.074	1.074	1.075	1.075	1.059	1.057	1.059
# N's per 100 kbp	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	0.00	0.00
# mismatches per 100 kbp	408.49	411.12	408.50	411.22	410.90	411.03	410.90	404.93	410.22	410.65	404.95	409.60	422.53	410.28	411.74	412.40	416.30	420.87	466.68	461.98	468.02
# indels per 100 kbp	16.01	15.86	16.18	21.00	21.38	21.02	11.57	11.25	11.52	11.61	11.29	11.55	35.53	35.49	36.00	33.53	34.02	33.35	218.87	225.11	221.18
Largest alignment	1342442	1342445	1342449	1342515	1342521	1342523	1342471	1342475	1342468	1342476	1342476	1342473	1342204	1342272	1342278	1342287	1342296	1342285	1341367	1341457	1341035
Total aligned length	5033641	5034084	5033421	5034252	5033711	5034221	5035364	5032281	5034898	5032189	5029290	5031603	5037945	5032521	5032641	5033259	5035445	5036642	4957920	4951768	4957224
NGA50	745356	745357	745355	745404	745409	745404	745366	745369	745372	745367	745370	745370	745267	745290	745264	745274	745273	745261	745147	744987	745147
NGA75	611507	611510	611506	611515	611515	611517	611515	611515	611517	611515	611515	611516	611428	611426	611433	611436	611448	611448	407846	433868	407847
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	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

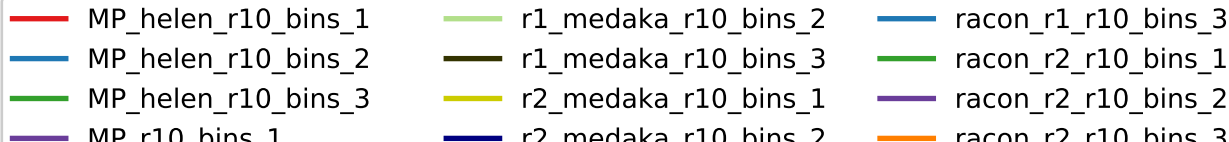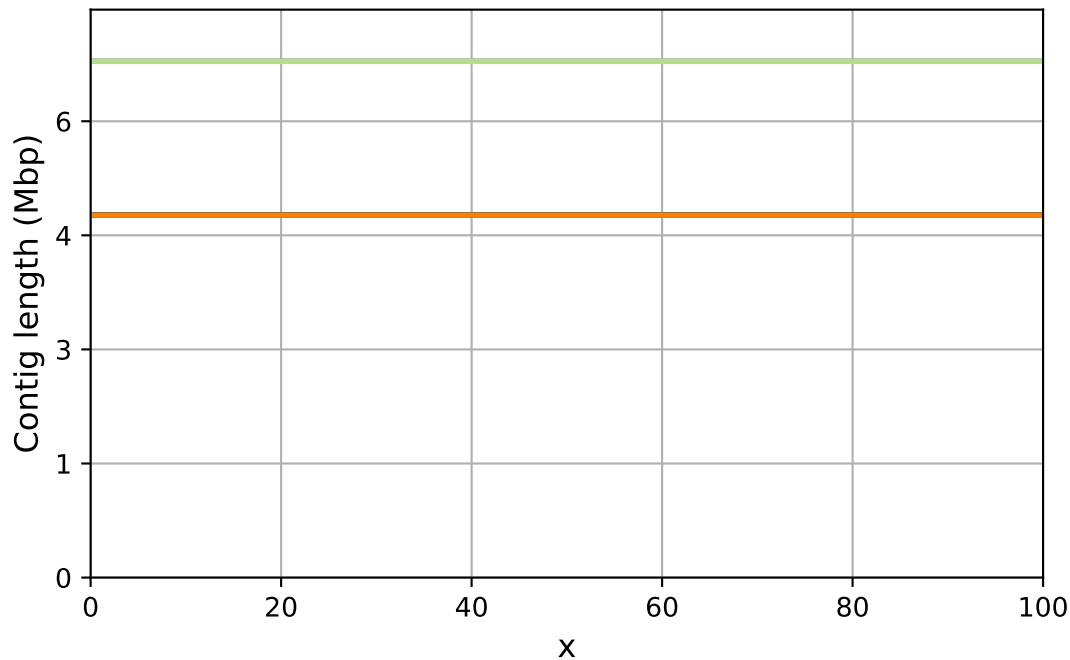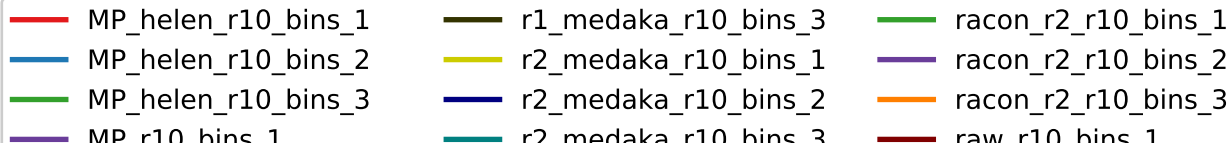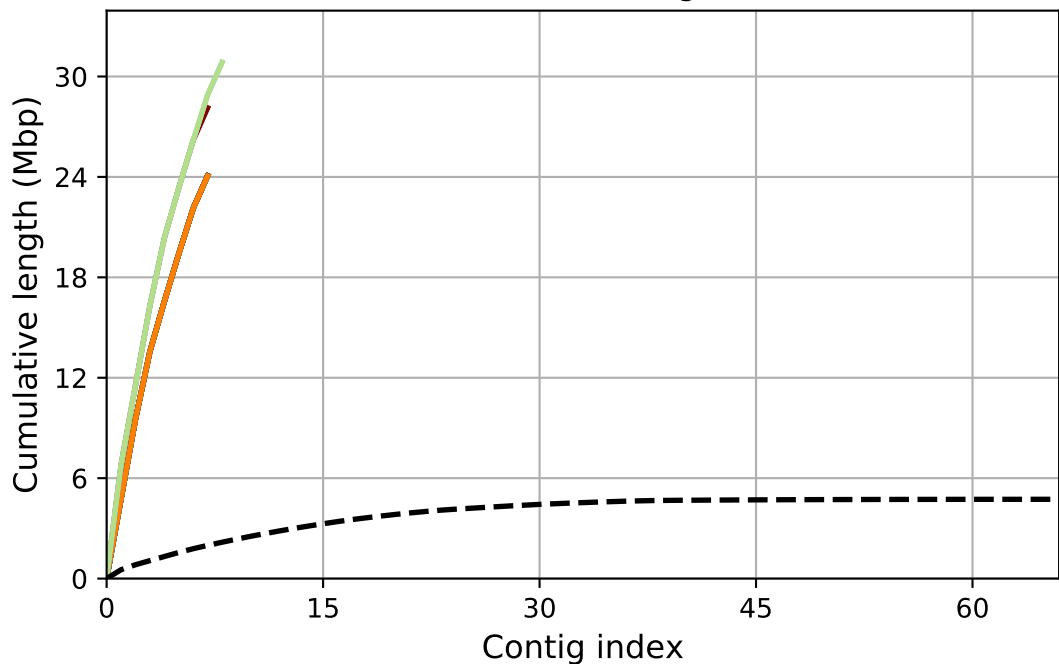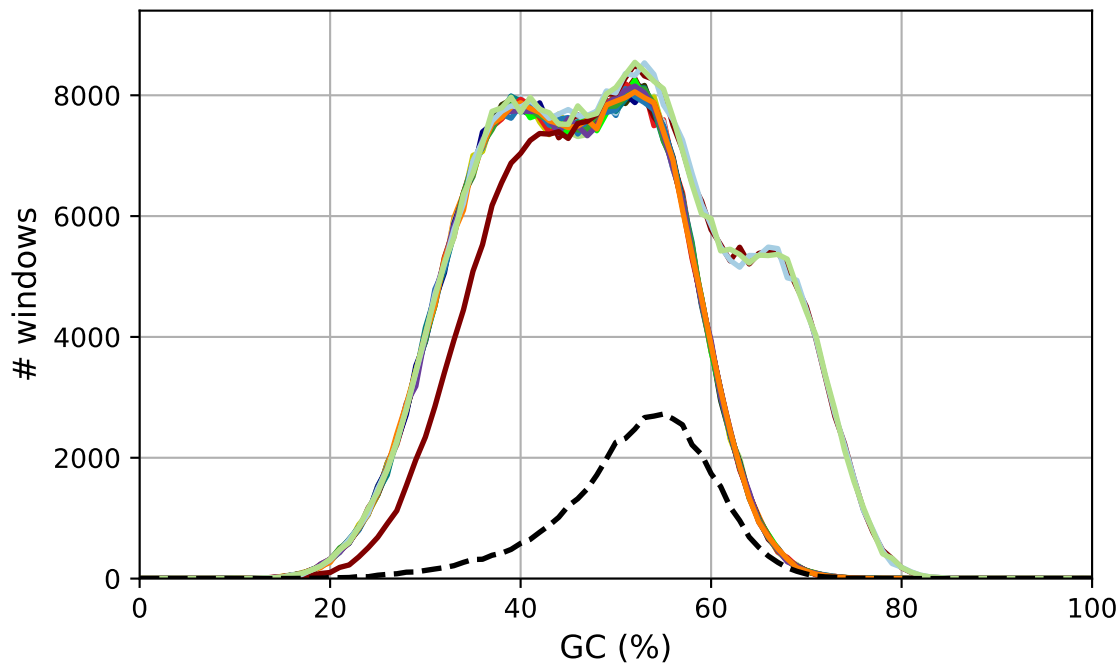|	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	15	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	19	18	19
# contig misassemblies	15	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	19	18	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	14	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	17	16	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	4757946	4757846	4757780	4758962	4758994	4758970	4758583	4758586	4758587	4758100	4758114	4758101	4757934	4757908	4757887	4757853	4757839	4757857	4755983	4756088	4755683
# 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	4	4	4	6	6	6	4	4	4	4	4	4	6	4	4	4	4	4	18	14	18
# local misassemblies	8	8	8	8	8	8	8	8	8	8	8	8	7	8	8	8	8	8	27	20	29
# 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	14	14	14	14	14	14	14	14	14	14	14	14	8	11	7
# 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	19142	19265	19142	19270	19255	19261	19255	18975	19223	19243	18976	19194	19800	19226	19294	19325	19508	19722	21862	21643	21924
# indels	750	743	758	984	1002	985	542	527	540	544	529	541	1665	1663	1687	1571	1594	1563	10253	10546	10361
# indels (<= 5 bp)	652	644	660	890	906	891	452	438	450	453	439	450	1573	1572	1595	1481	1504	1473	10083	10370	10191
# indels (> 5 bp)	98	99	98	94	96	94	90	89	90	91	90	91	92	91	92	90	90	90	170	176	170
Indels length	5315	5286	5291	5504	5546	5502	4976	4951	4972	4985	4975	4981	6275	6256	6274	6109	6152	6102	18404	19245	18569

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

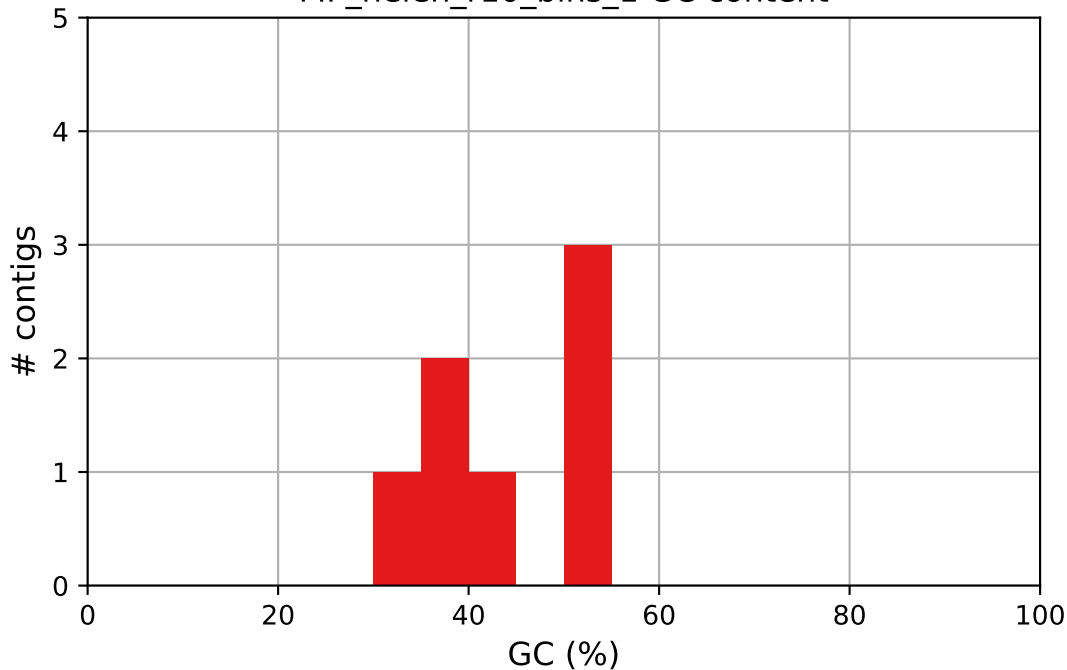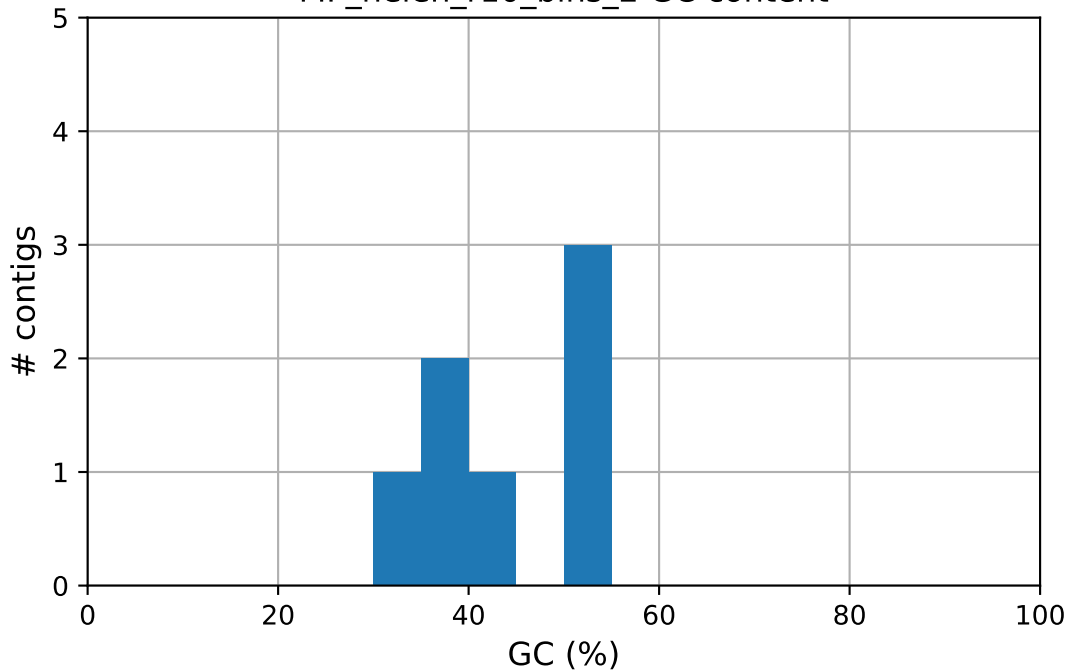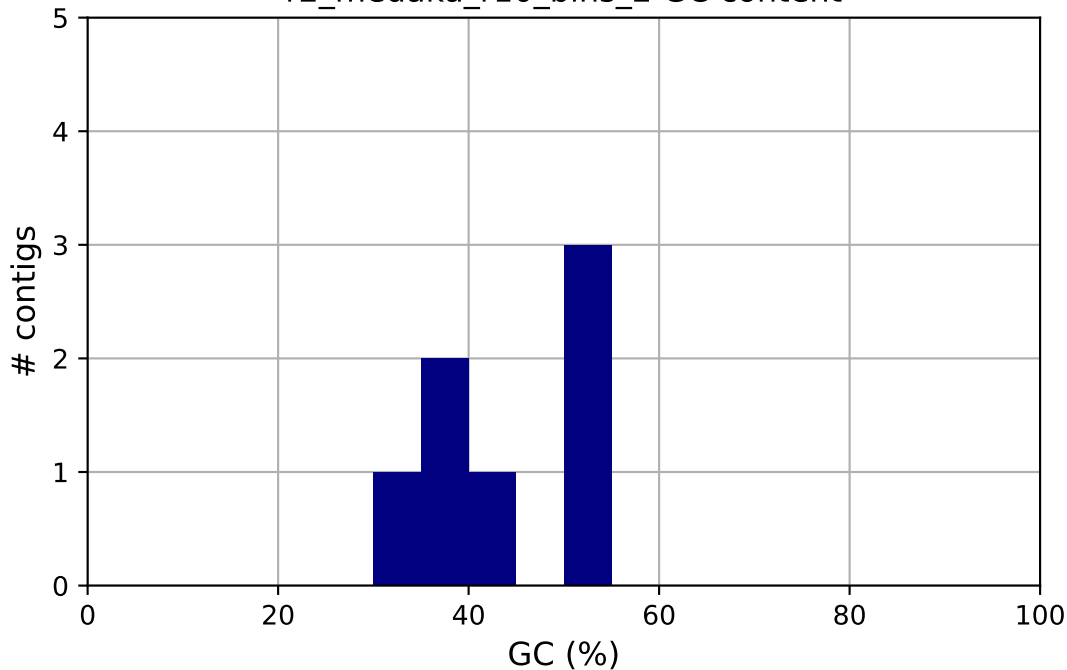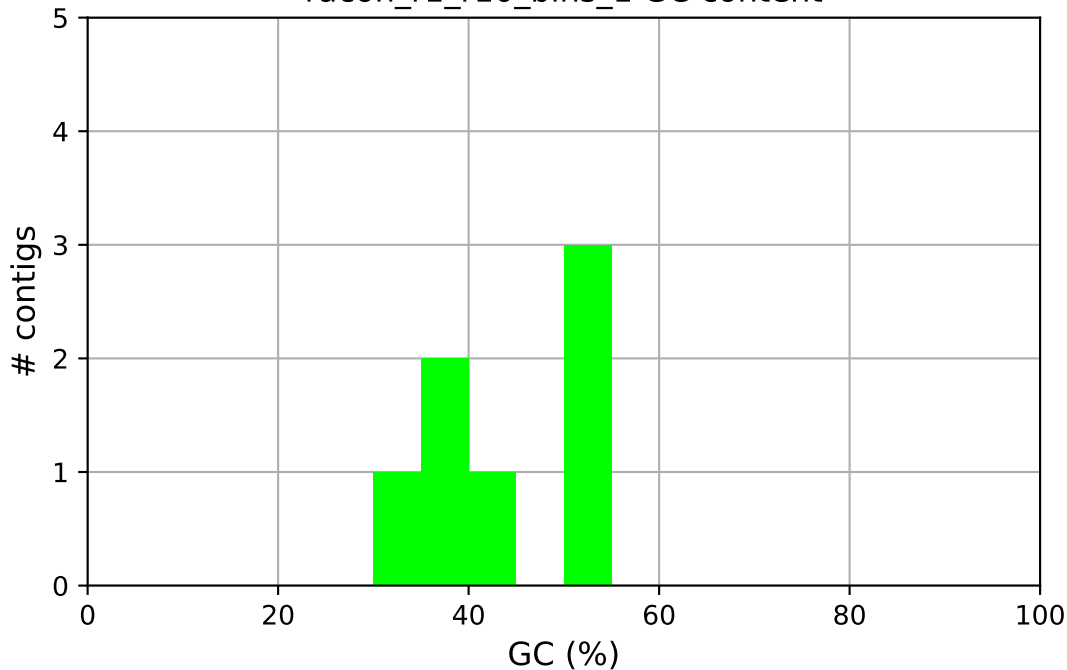|	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# 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	8	8
Partially unaligned length	19033512	19036360	19034564	19038552	19039878	19038661	19034885	19040241	19035546	19027937	19034057	19029383	19019441	19029778	19024350	19019476	19022840	19013503	23169749	25896359	25889982
# N's	0	0	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).

Nx

MP_helen_r10_bins_1	r1_medaka_r10_bins_2	racon_r1_r10_bins_3
MP_helen_r10_bins_2	r1_medaka_r10_bins_3	racon_r2_r10_bins_1
MP_helen_r10_bins_3	r2_medaka_r10_bins_1	racon_r2_r10_bins_2
MP_r10_bins_1	r2_medaka_r10_bins_2	racon_r2_r10_bins_3

NGx

Contig length (Mbp)

— MP_helen_r10_bins_1	— r1_medaka_r10_bins_2	— racon_r1_r10_bins_3
— MP_helen_r10_bins_2	— r1_medaka_r10_bins_3	— racon_r2_r10_bins_1
— MP_helen_r10_bins_3	— r2_medaka_r10_bins_1	— racon_r2_r10_bins_2
— MP_r10_bins_1	— r2_medaka_r10_bins_2	— racon_r2_r10_bins_3

Cumulative length

Cumulative length (Mbp)	
30	
24	
18	
12	
6	
0	

Contig index: 0, 15, 30, 45, 60

GC content

MP_helen_r10_bins_1	r1_medaka_r10_bins_3	racon_r2_r10_bins_1
MP_helen_r10_bins_2	r2_medaka_r10_bins_1	racon_r2_r10_bins_2
MP_helen_r10_bins_3	r2_medaka_r10_bins_2	racon_r2_r10_bins_3
MP_r10_bins_1	r2_medaka_r10_bins_3	raw_r10_bins_1

MP_helen_r10_bins_1 GC content

MP_helen_r10_bins_3 GC content
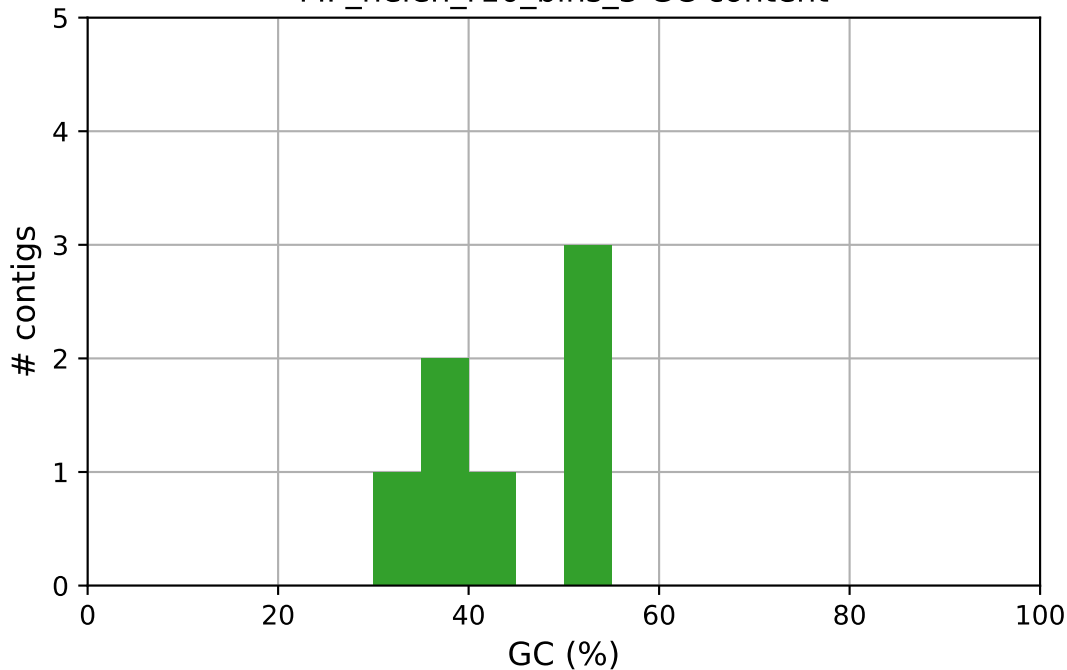
MP_r10_bins_1 GC content

MP_r10_bins_2 GC content
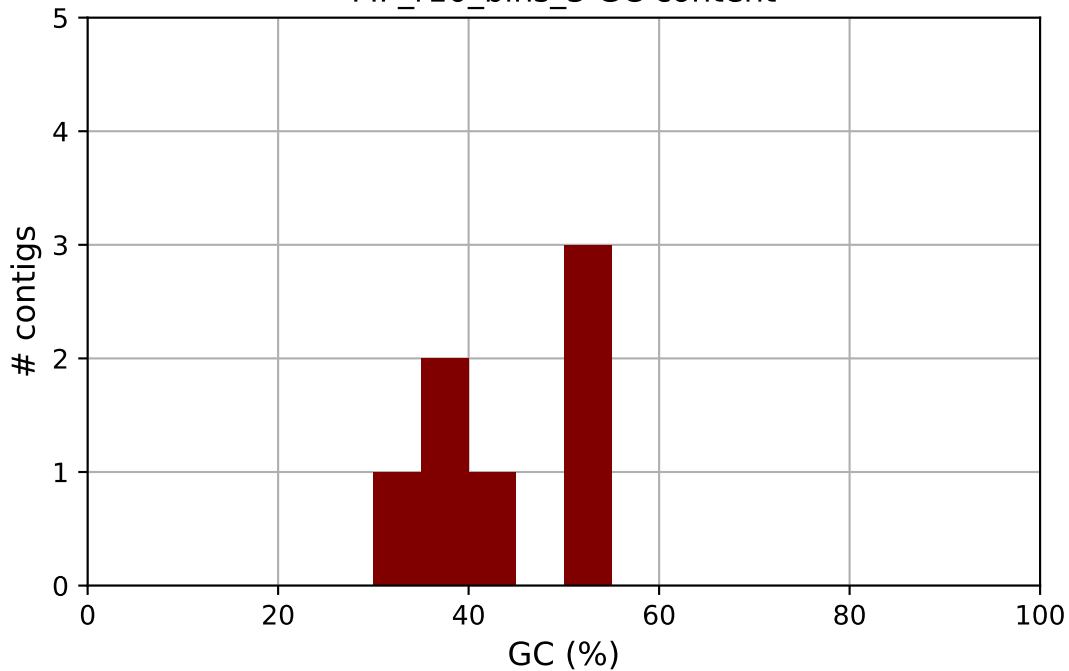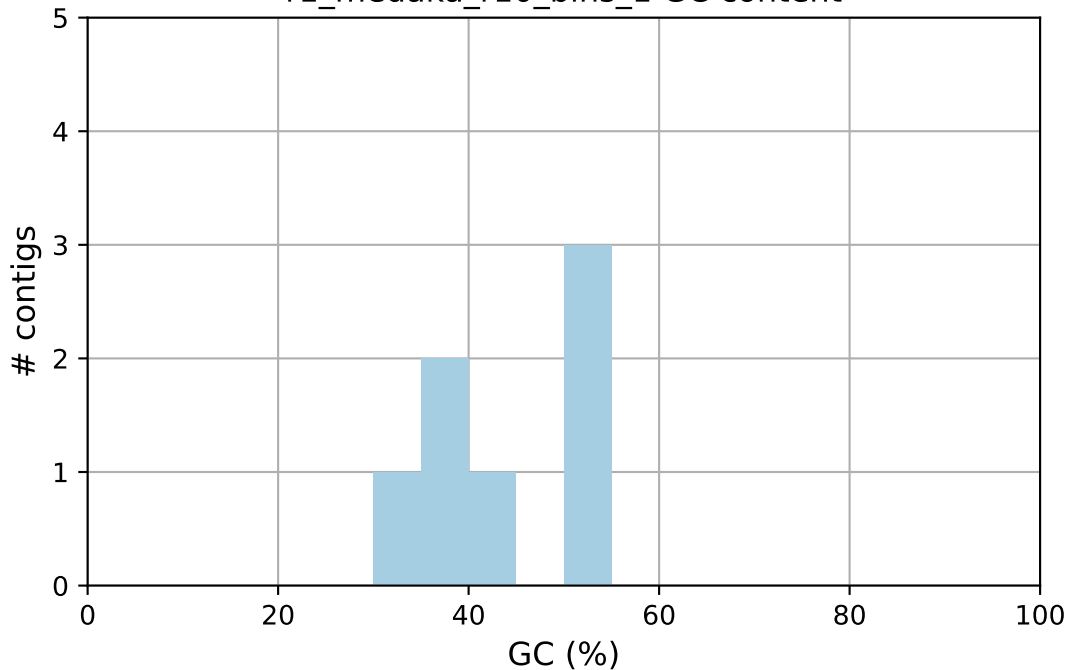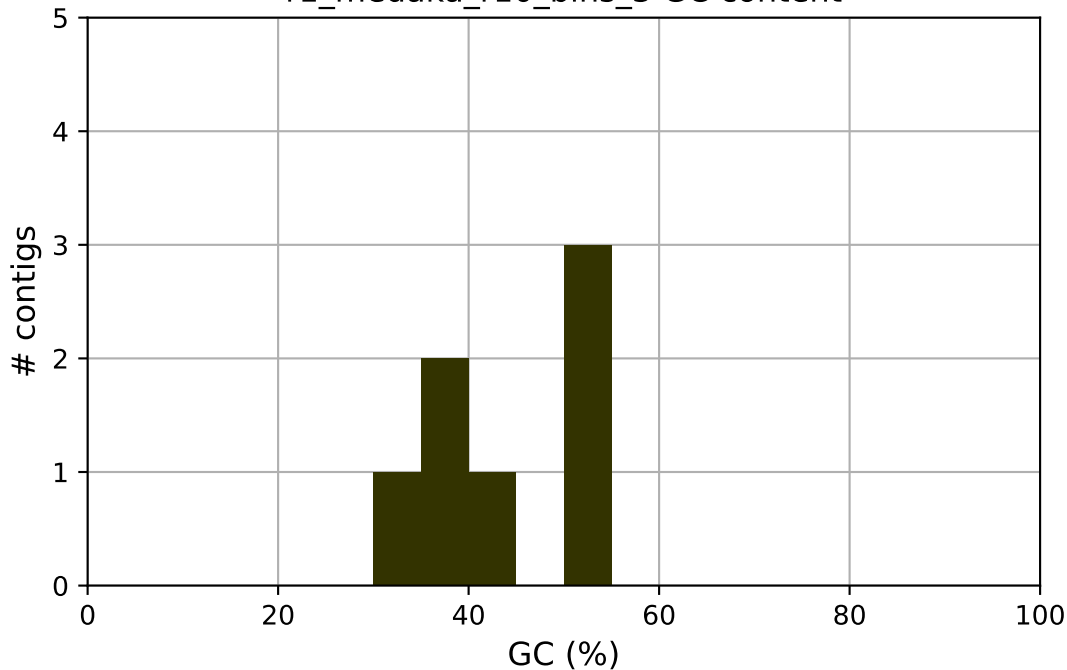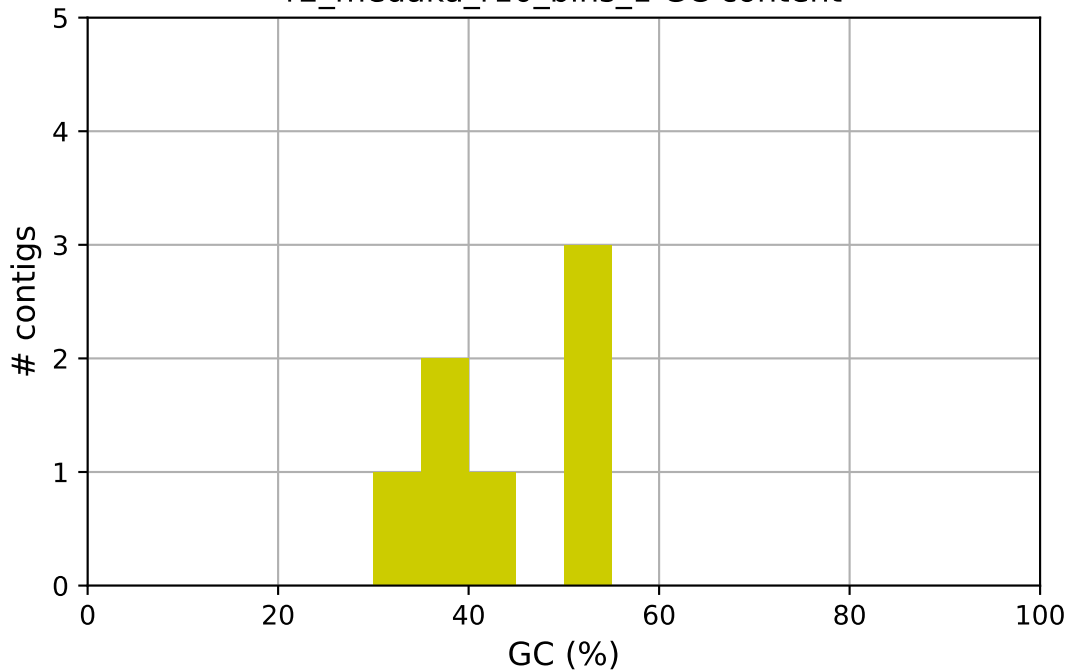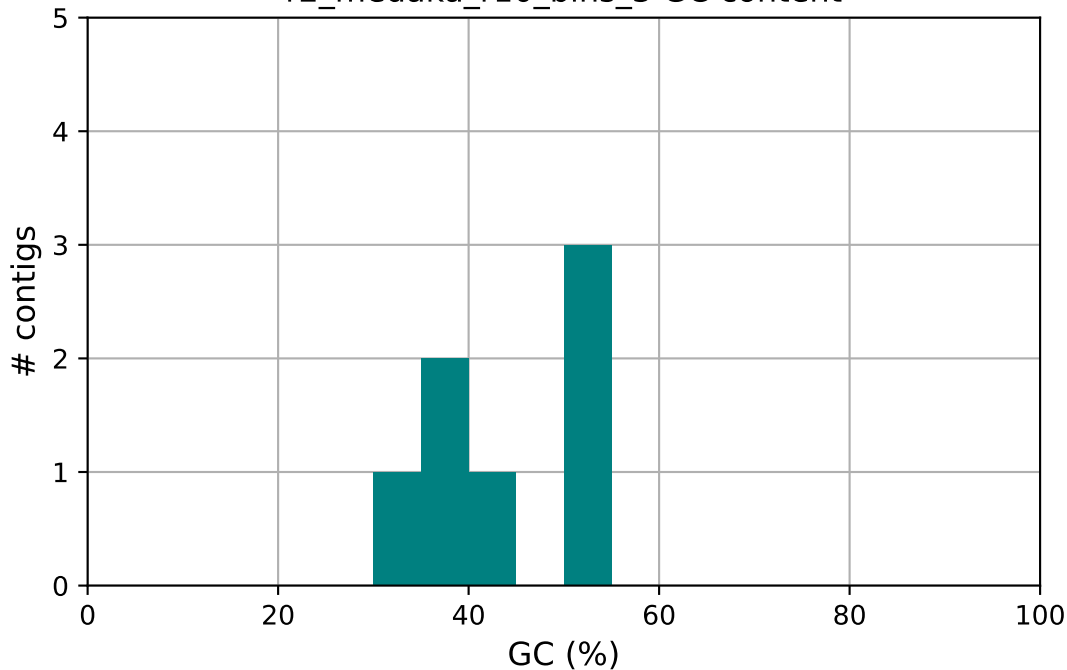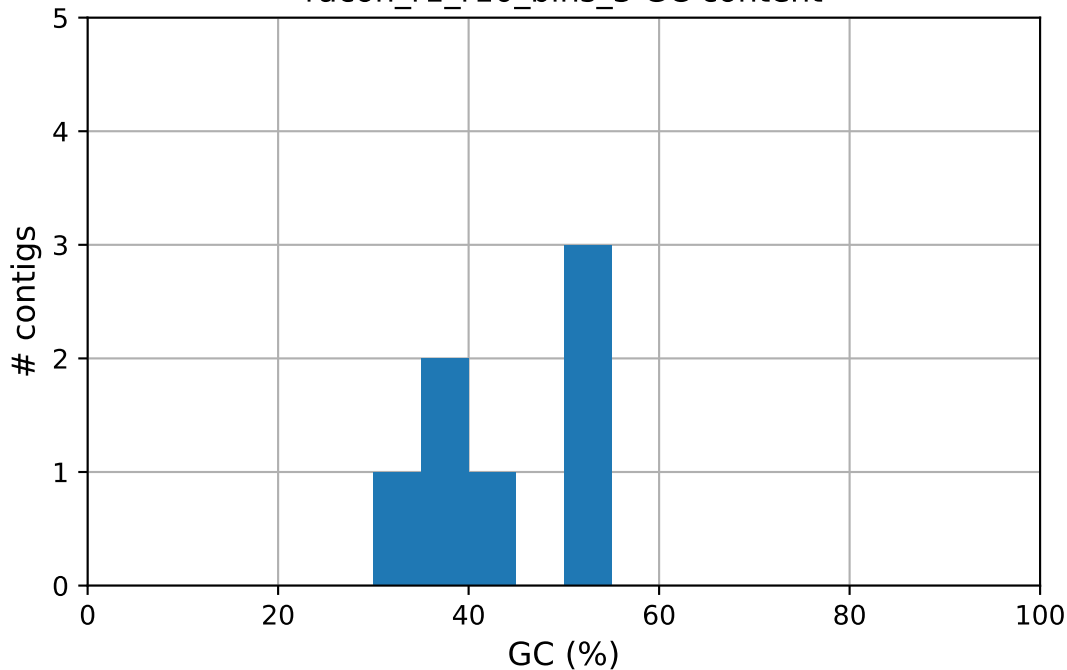
racon_r2_r10_bins_2 GC content
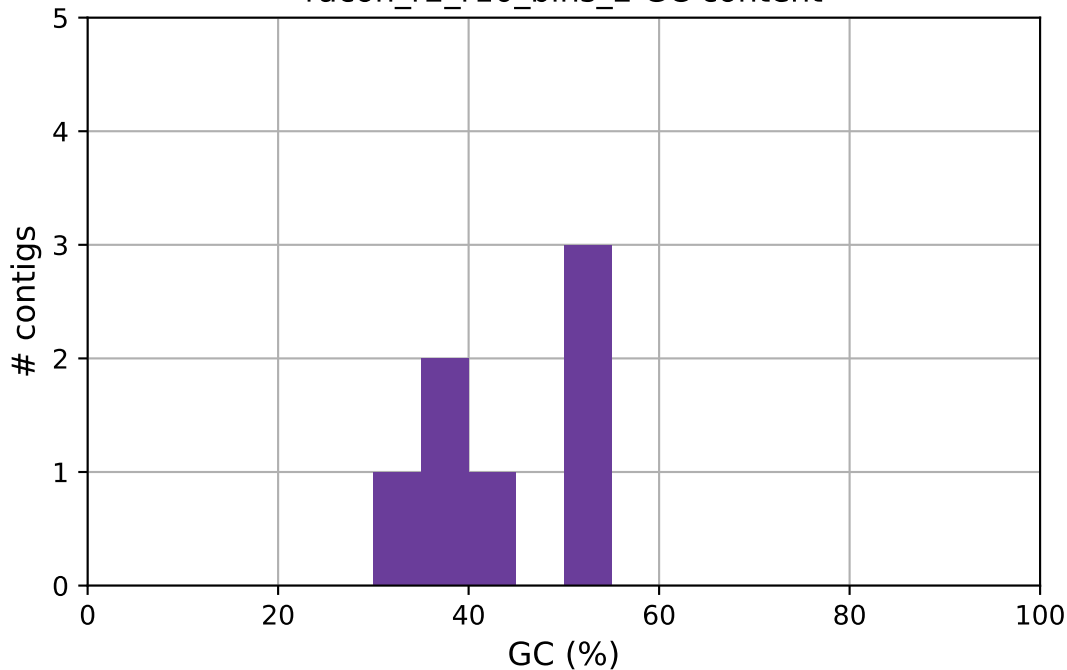
racon_r2_r10_bins_3 GC content
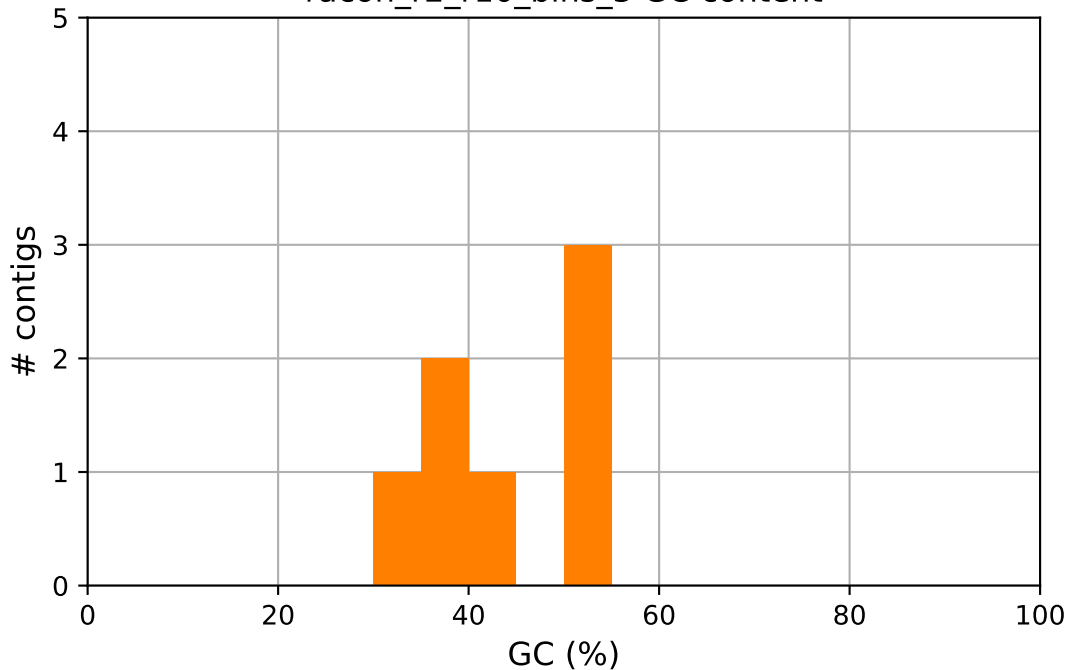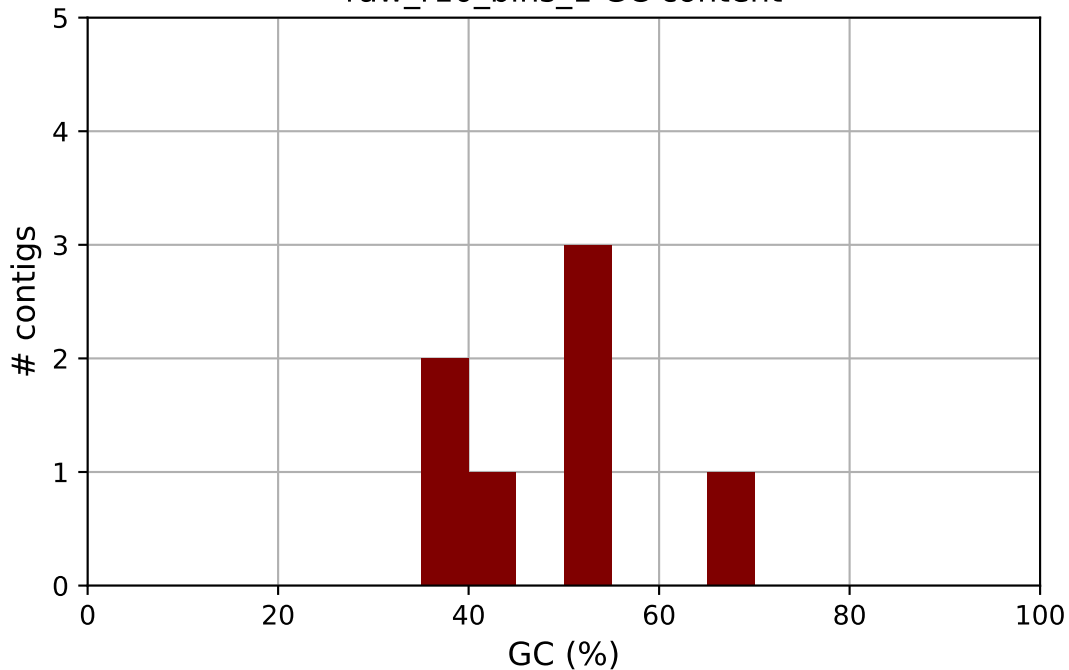
raw_r10_bins_2 GC content
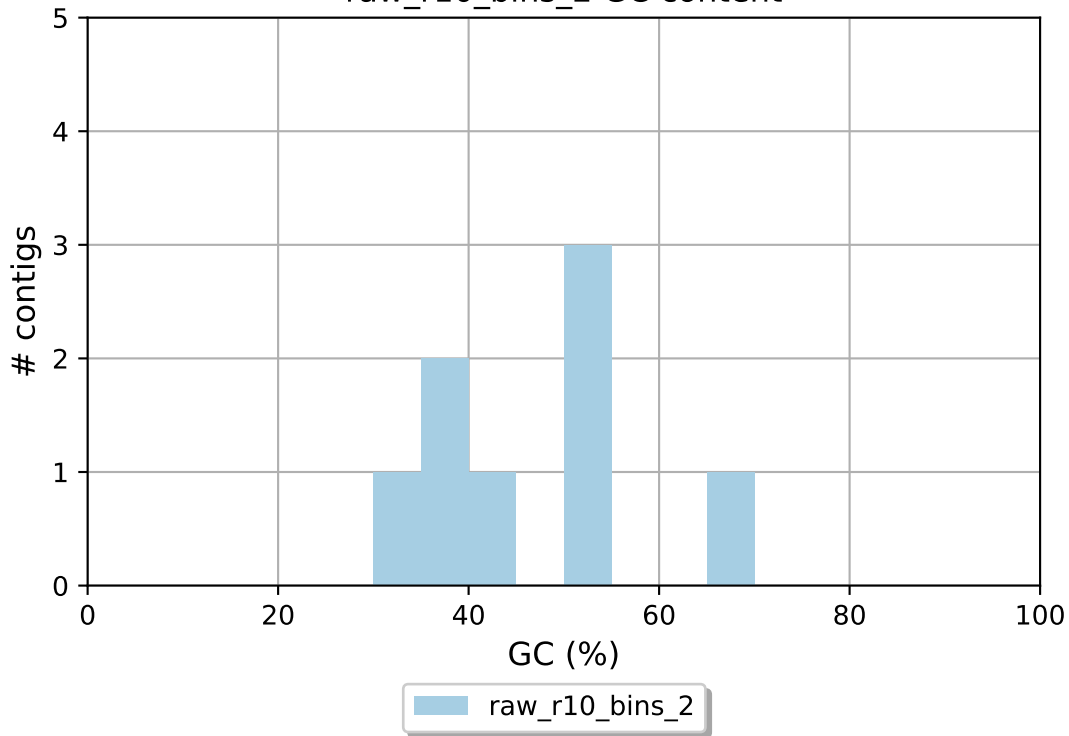
raw_r10_bins_3 GC content

Misassemblies
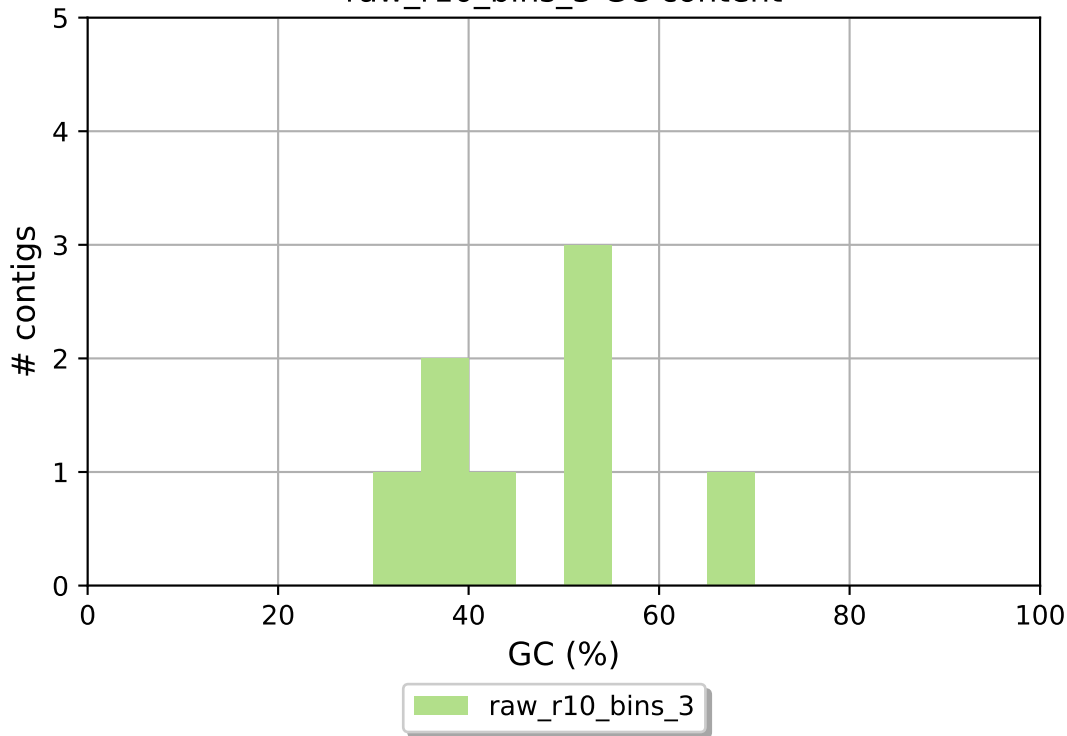
translocations   # inversions
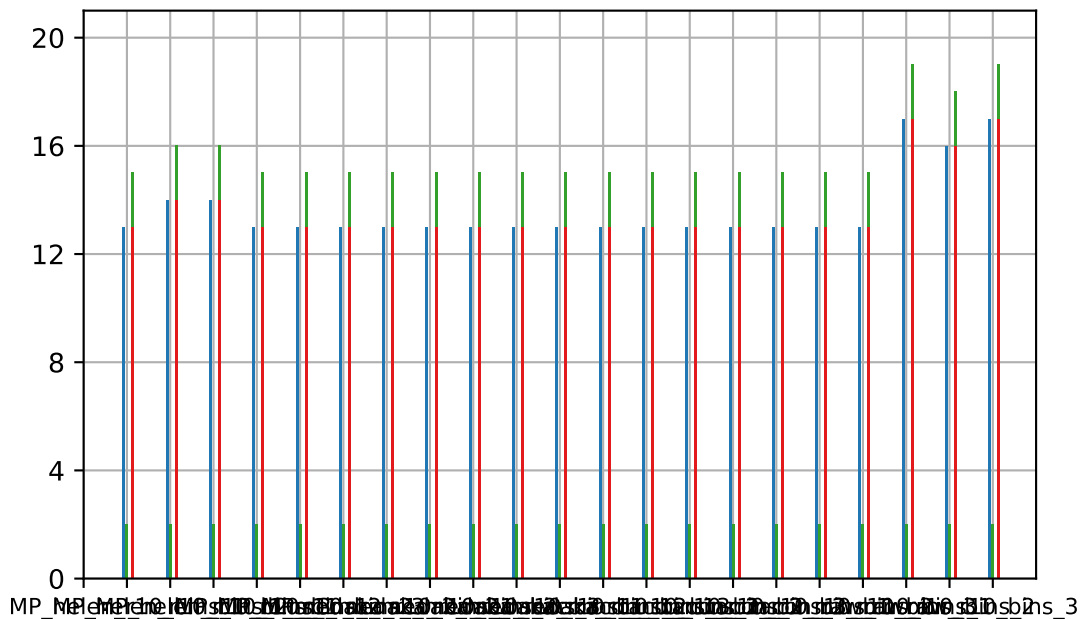
FRCurve (misassemblies)
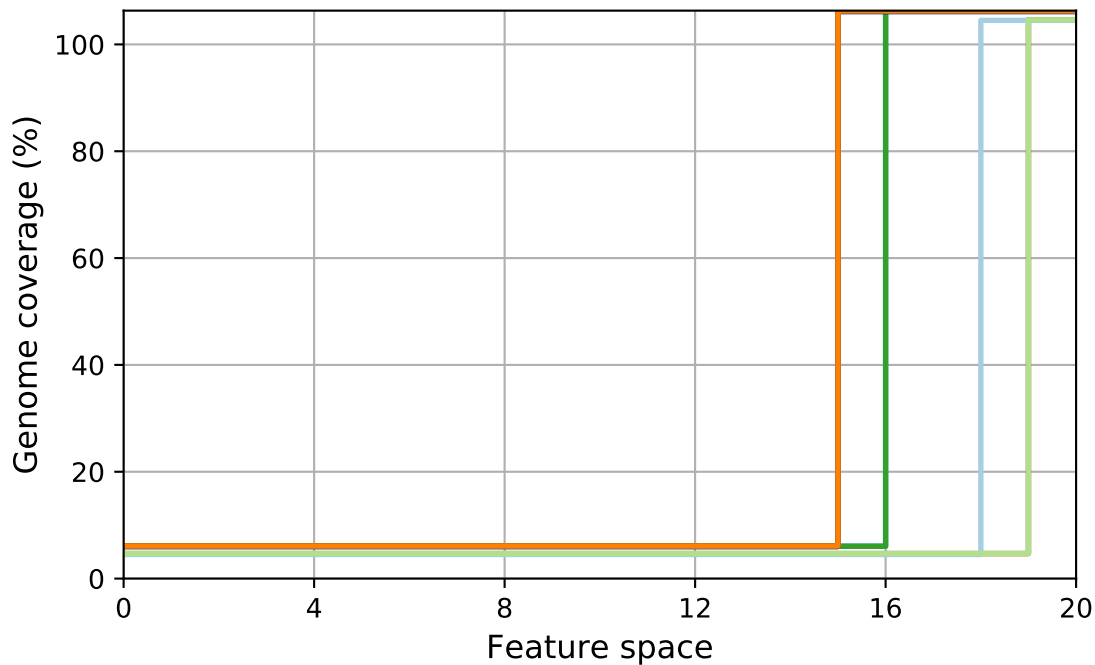
Legend:
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

Cumulative length (aligned contigs)

Contig index	Cumulative length (Mbp)

Legend:
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- r2_medaka_r10_bins_3
- racon_r2_r10_bins_1
- racon_r2_r10_bins_2
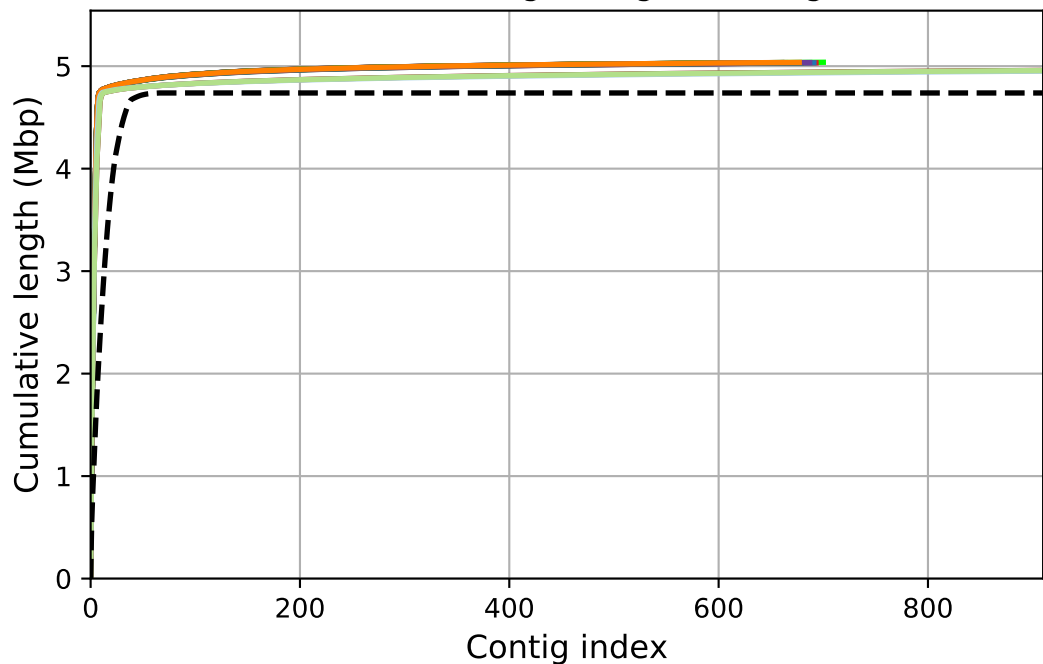- racon_r2_r10_bins_3
- raw_r10_bins_1
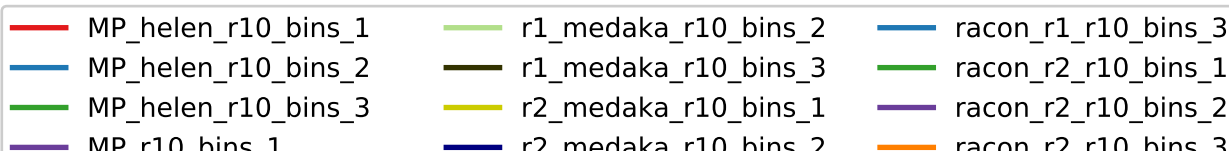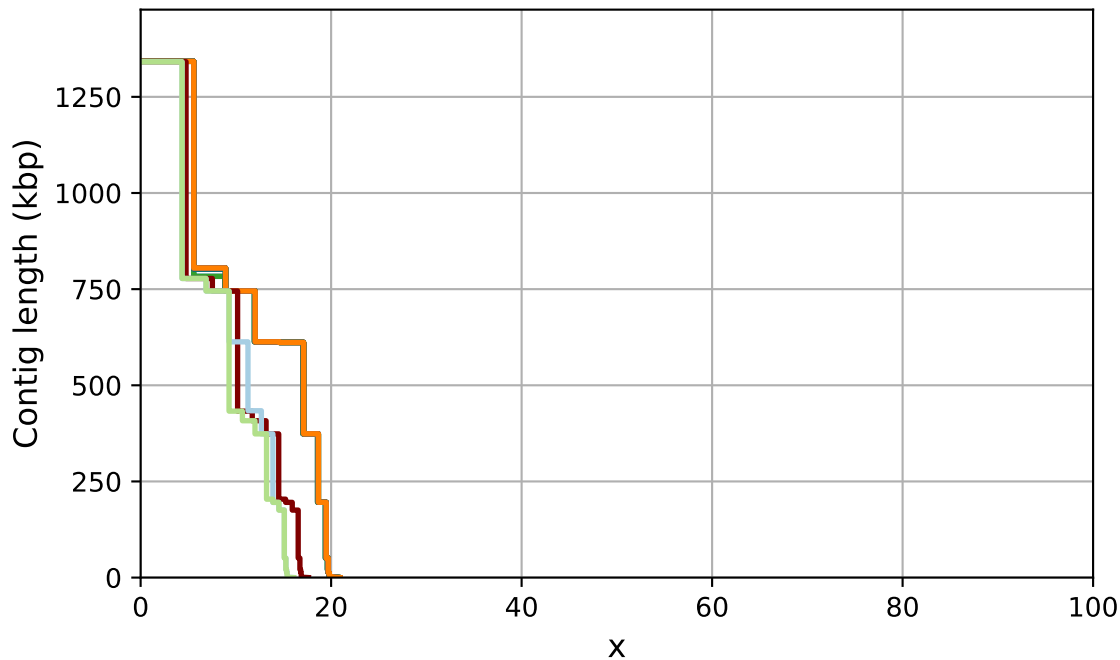
NAx

| Contig length (kbp) | x |

Legend:
- MP_helen_r10_bins_1
- MP_helen_r10_bins_2
- MP_helen_r10_bins_3
- MP_r10_bins_1
- r1_medaka_r10_bins_2
- r1_medaka_r10_bins_3
- r2_medaka_r10_bins_1
- r2_medaka_r10_bins_2
- racon_r1_r10_bins_3
- racon_r2_r10_bins_1
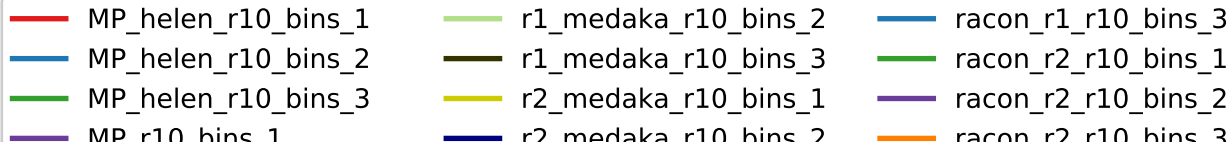- racon_r2_r10_bins_2
- racon_r2_r10_bins_3

NGAx

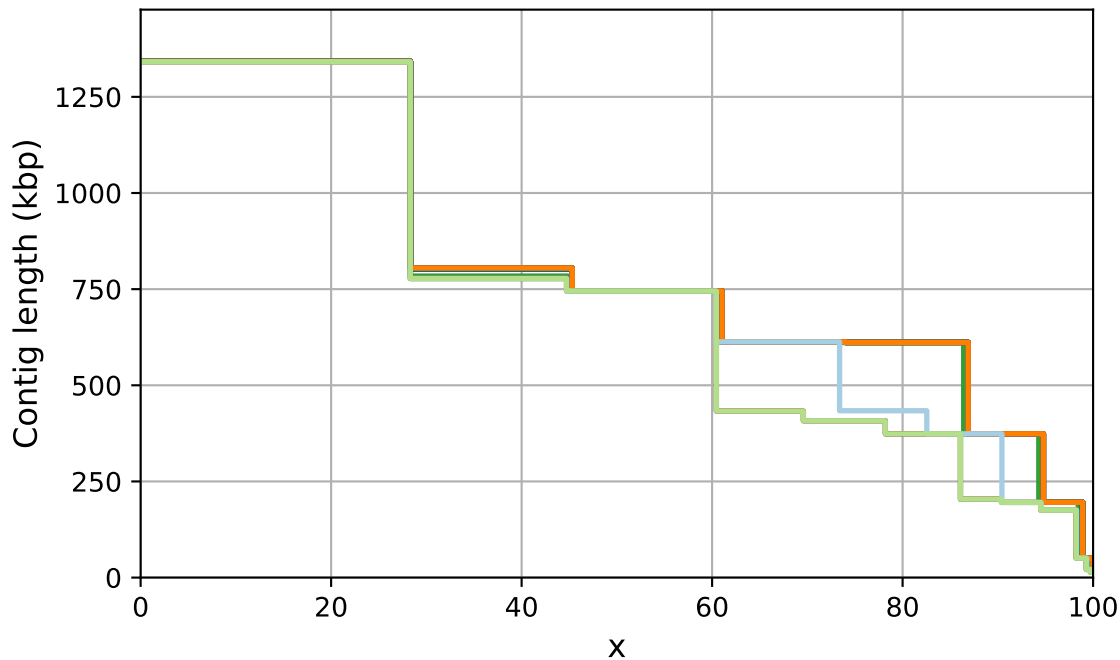| MP_helen_r10_bins_1 | r1_medaka_r10_bins_2 | racon_r1_r10_bins_3 |
MP_helen_r10_bins_2	r1_medaka_r10_bins_3	racon_r2_r10_bins_1
MP_helen_r10_bins_3	r2_medaka_r10_bins_1	racon_r2_r10_bins_2
MP_r10_bins_1	r2_medaka_r10_bins_2	racon_r2_r10_bins_3

Genome fraction, %

🟥 MP_helen_r10_bins_1	🟩 r1_medaka_r10_bins_2	🟦 racon_r1_r10_bins_3
🟦 MP_helen_r10_bins_2	⬛ r1_medaka_r10_bins_3	🟩 racon_r2_r10_bins_1
🟩 MP_helen_r10_bins_3	🟨 r2_medaka_r10_bins_1	🟪 racon_r2_r10_bins_2
🟪 MP_r10_bins_1	🟦 r2_medaka_r10_bins_2	🟧 racon_r2_r10_bins_3