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	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	7
# contigs (>= 25000 bp)	7	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	7
Total length (>= 5000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
Total length	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	24060236	24062591	24060425
Reference length	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829	3985829
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	44.77	44.77	44.77
Reference GC (%)	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82	43.82
N50	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4042946	4043032	4042936
NG50	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
N75	2845363	2845435	2845364	2845421	2845426	2845426	2845430	2845432	2845434	2845429	2845433	2845432	2845290	2845293	2845290	2845315	2845310	2845306	2843359	2843856	2843855
NG75	4765299	4765370	4765301	4765922	4765391	4765920	4765362	4765395	4765360	4765364	4765350	4765359	4764643	4764770	4764652	4764716	4764723	4764656	4763471	4763493	4763422
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	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	31	32	31
# 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	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4042946	4043032	4042936
# local misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	17	18	18
# 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	5	5	5
# 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	19974162	19976128	19974972	19977168	19977463	19977318	19976037	19977816	19975947	19968217	19971589	19969936	19962159	19967864	19962560	19957381	19963756	19956863	19999507	20002106	20001739
Genome fraction (%)	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.999	99.993	99.996	99.996
Duplication ratio	1.027	1.028	1.027	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.028	1.019	1.019	1.018
# 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	94.41	95.94	94.21	98.00	98.85	97.85	95.77	97.05	96.22	96.19	96.09	95.11	99.20	99.20	97.65	98.02	99.55	97.17	96.47	85.23	85.46
# indels per 100 kbp	10.91	11.62	11.19	11.19	11.44	11.42	10.41	10.64	10.54	10.51	10.64	10.34	21.23	21.73	21.65	19.85	19.92	20.22	102.62	106.18	106.41
Largest alignment	788687	552725	788687	788681	552723	788681	788689	552721	788690	788690	552723	788691	788627	552675	788636	788646	552660	788614	788152	552394	788149
Total aligned length	4094787	4096058	4094803	4097433	4097923	4097355	4096010	4096557	4096344	4096186	4096019	4095482	4097127	4096289	4096276	4097207	4096331	4095143	4059712	4059477	4057707
NGA50	329468	329467	315070	329482	329480	315065	329464	329466	315066	329465	329466	315066	329417	329449	315047	329449	329453	315035	329347	329353	314876
NGA75	257052	257051	257049	257047	257050	257049	257051	257051	257051	257051	257051	257052	257020	257031	257028	257028	257036	257029	256893	256898	256896
LGA50	4	5	5	4	4	5	4	5	5	4	5	5	4	4	5	4	4	5	4	5	5
LGA75	8	8	8	9	8	8	9	8	8	9	8	8	9	8	8	9	8	8	9	8	8

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).
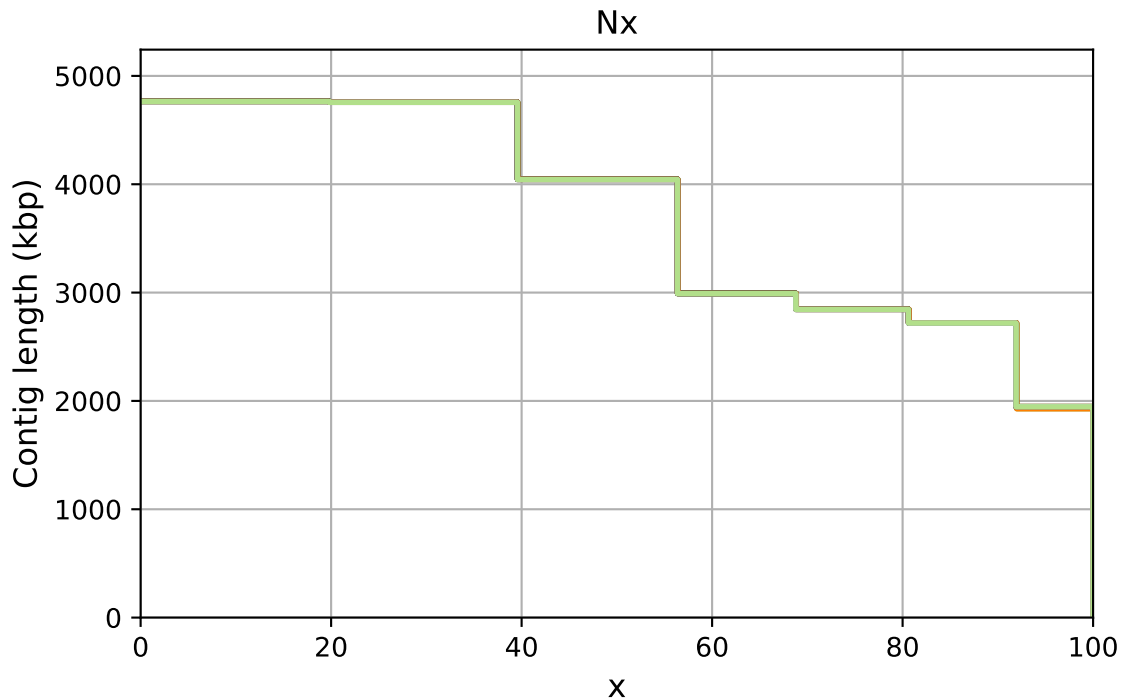
Misassemblies report

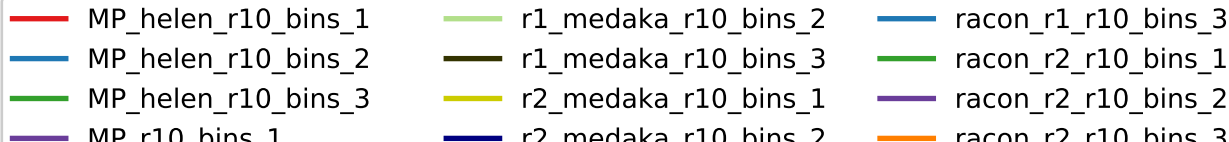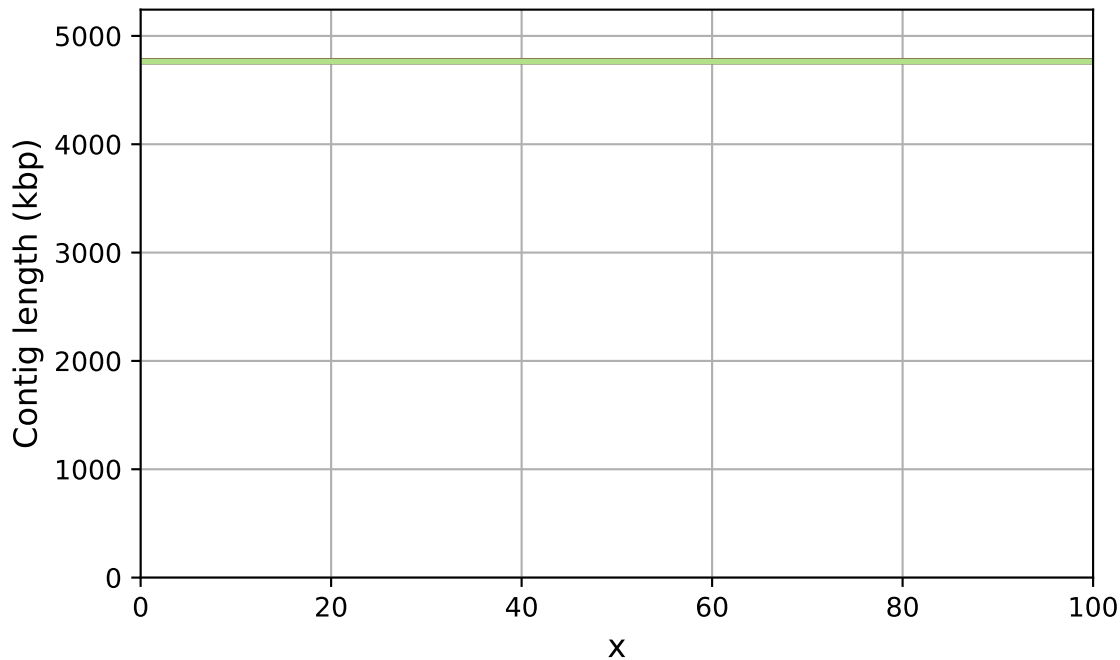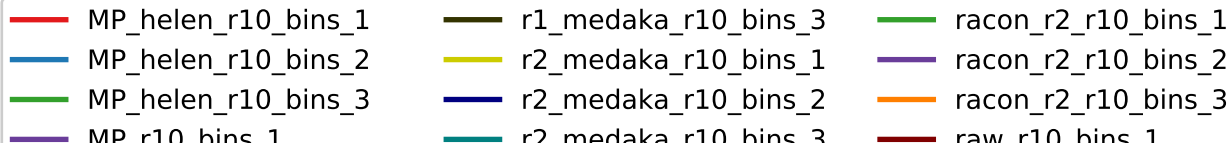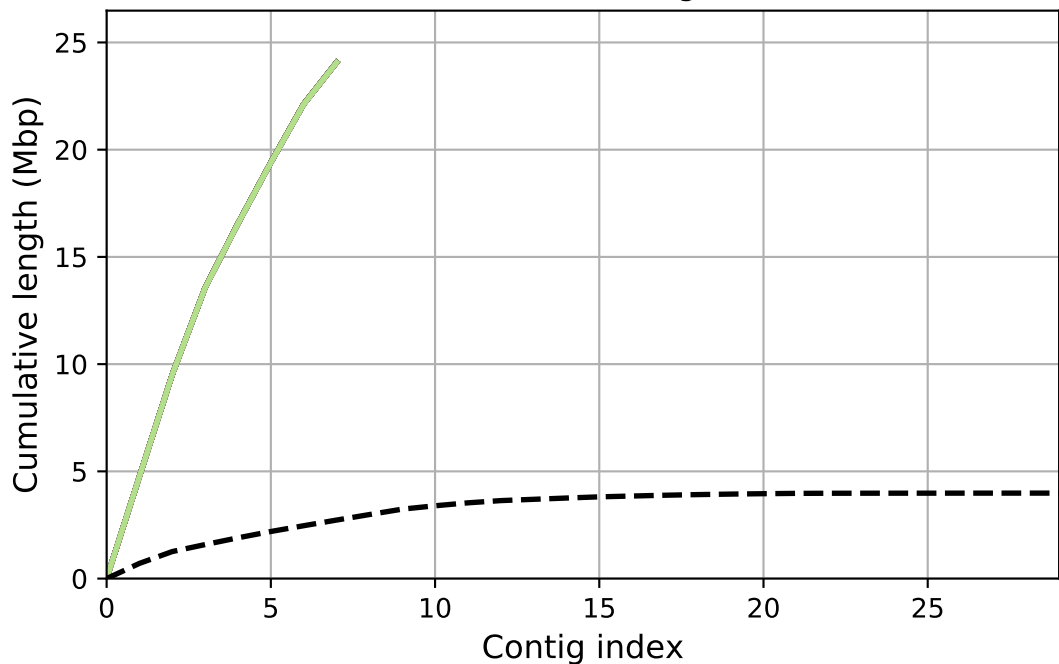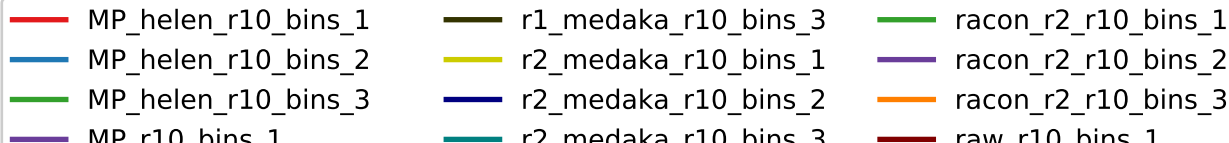|	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	31	32	31
# contig misassemblies	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	31	32	31
# 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	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	31	32	31
# 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	4045615	4045634	4045636	4045594	4045608	4045601	4045589	4045607	4045601	4045589	4045605	4045604	4045233	4045287	4045256	4045364	4045333	4045318	4042946	4043032	4042936
# 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	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	11	13
# local misassemblies	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	17	18	18
# 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	49	49	49	49	49	49	49	49	49	49	49	49	48	49	49	49	49	49	33	31	30
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5	5
# mismatches	3763	3824	3755	3914	3940	3900	3817	3868	3835	3834	3830	3791	3954	3892	3907	3968	3873	3845	3397	3577	3406
# indels	435	463	446	446	456	455	415	424	420	419	424	412	846	866	863	791	794	806	4090	4232	4241
# indels (<= 5 bp)	386	414	397	395	406	404	366	375	371	370	375	364	797	815	813	742	744	758	4035	4173	4187
# indels (> 5 bp)	49	49	49	51	50	51	49	49	49	49	49	48	49	51	50	49	50	48	55	59	54
Indels length	2570	2624	2586	2602	2617	2613	2553	2561	2557	2556	2562	2532	3072	3114	3125	2992	3022	3005	7094	7287	7248

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

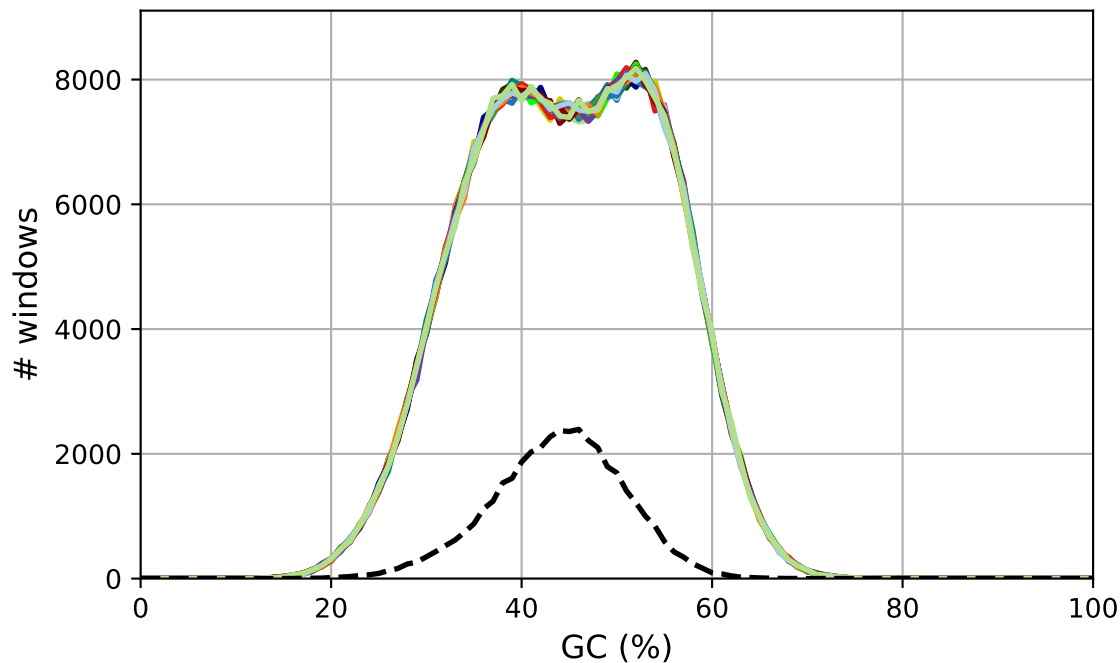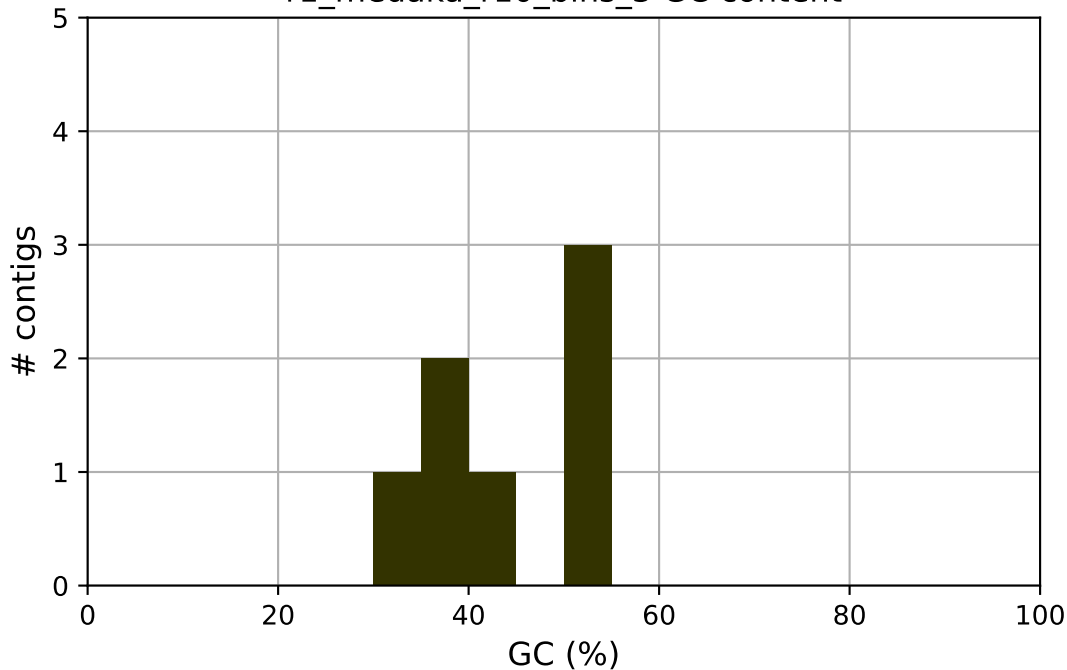|	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	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	7	7
Partially unaligned length	19974162	19976128	19974972	19977168	19977463	19977318	19976037	19977816	19975947	19968217	19971589	19969936	19962159	19967864	19962560	19957381	19963756	19956863	19999507	20002106	20001739
# 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

Contig length (kbp) vs 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

NGx

Contig length (kbp)

x

—— 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

—— 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

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
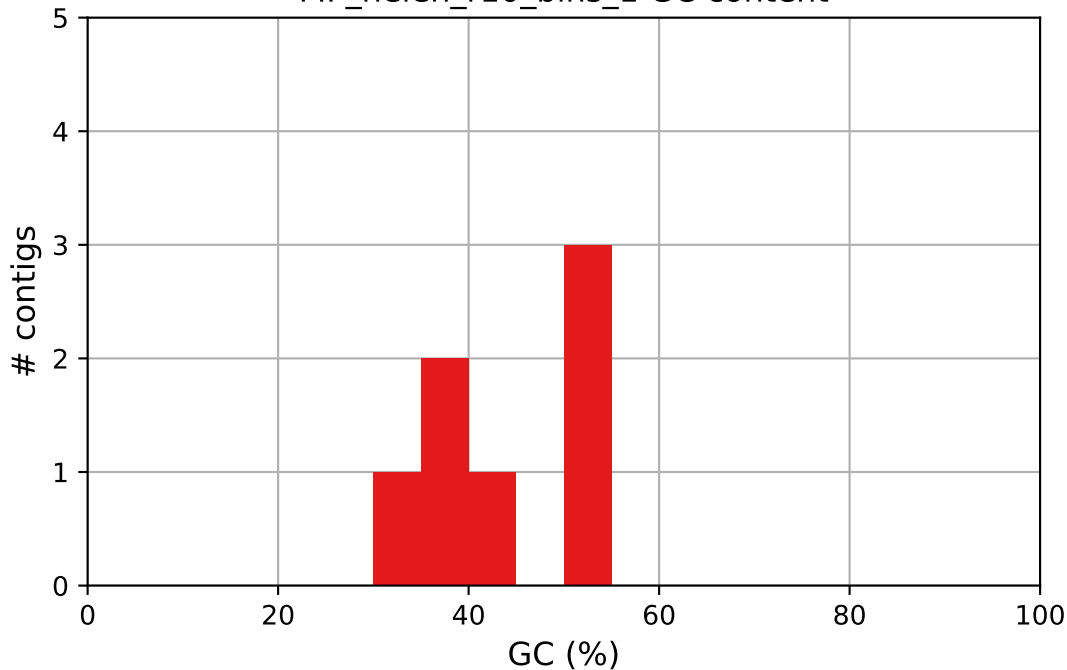
MP_helen_r10_bins_2 GC content
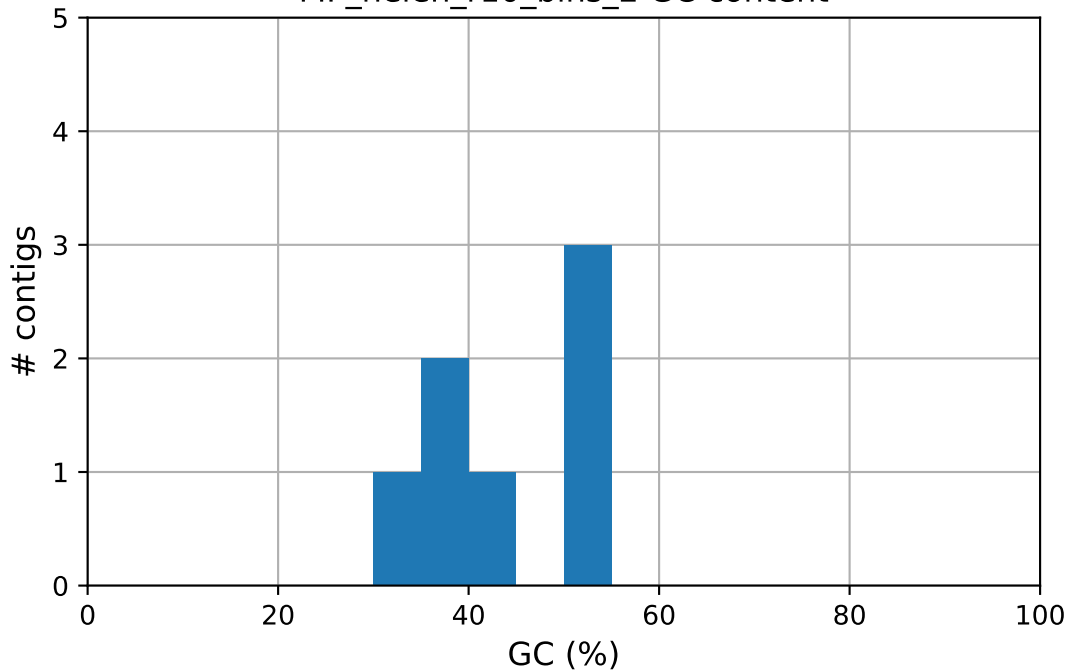
MP_helen_r10_bins_3 GC content
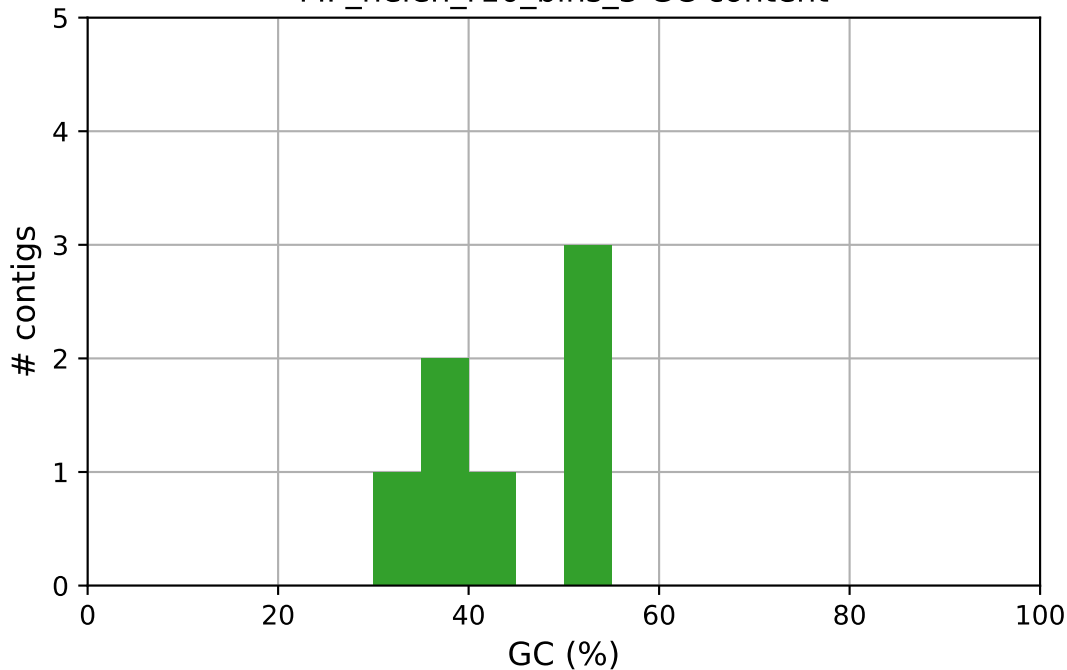
MP_r10_bins_1 GC content
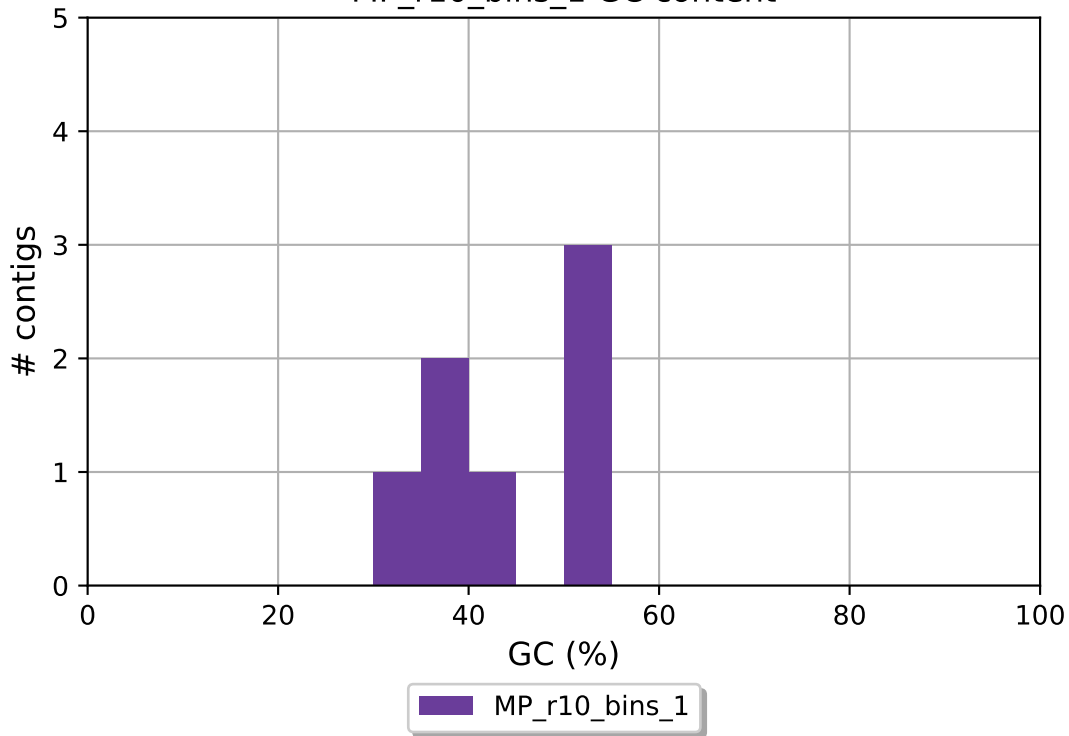
MP_r10_bins_2 GC content
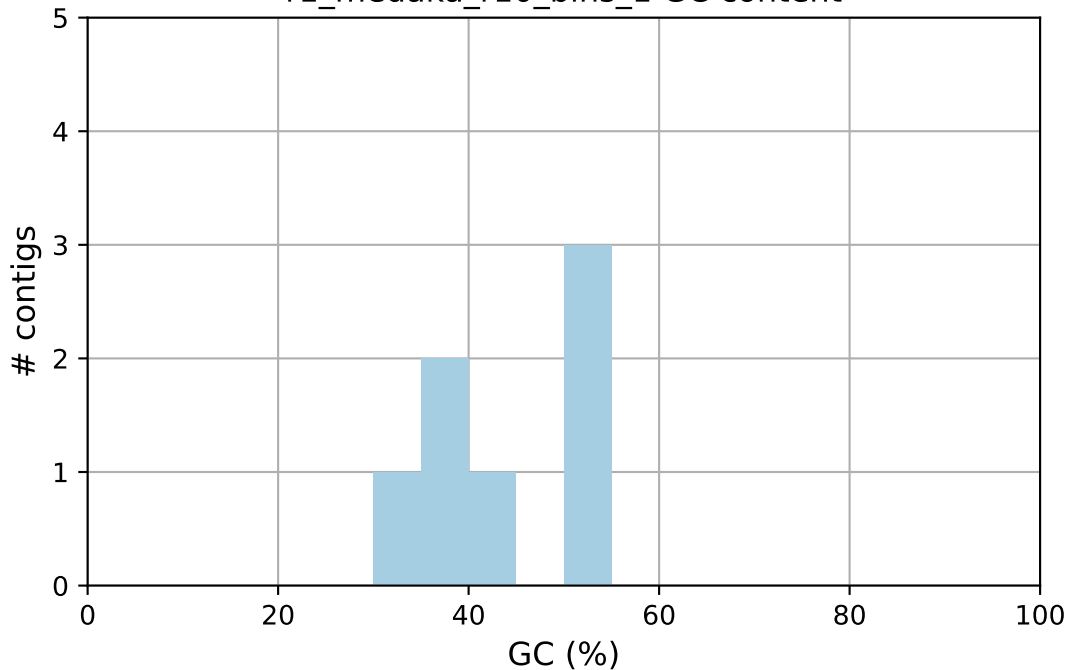
MP_r10_bins_3 GC content
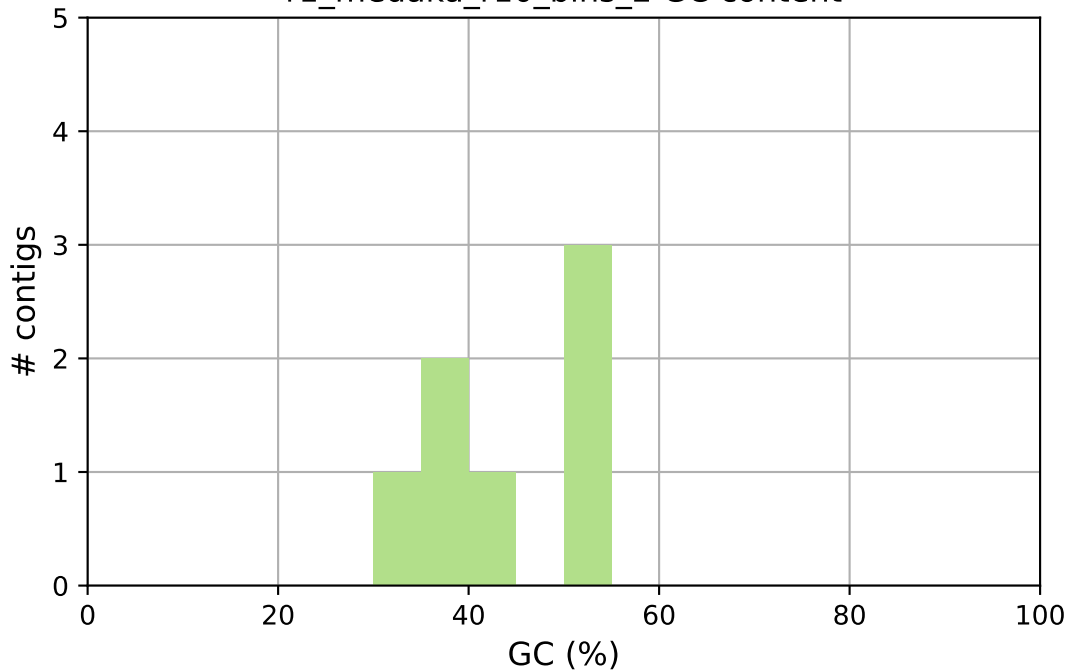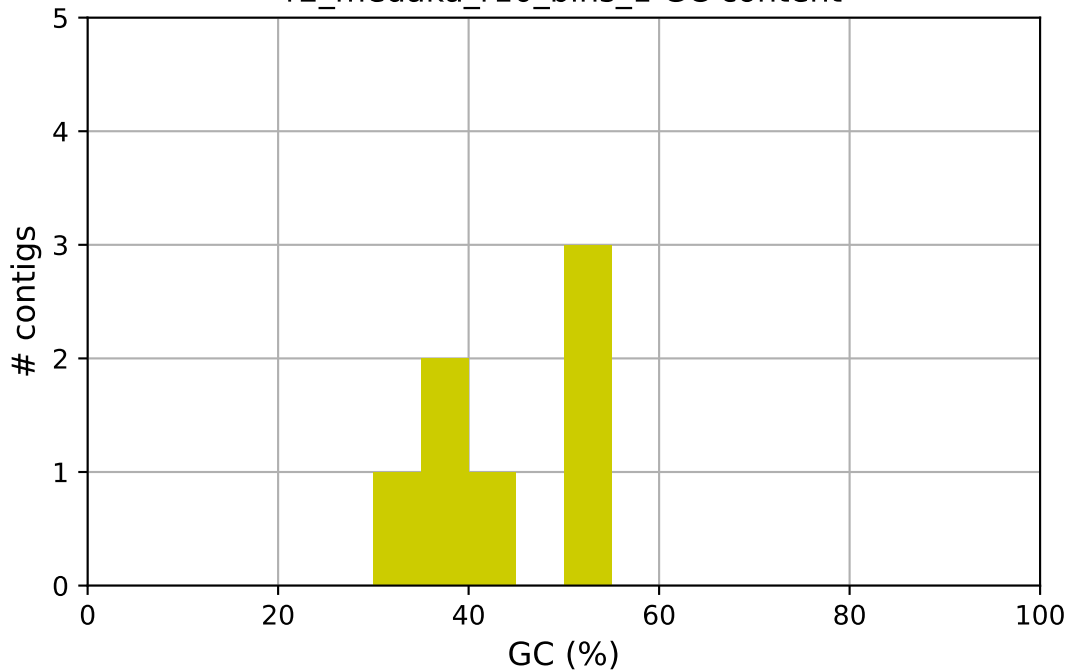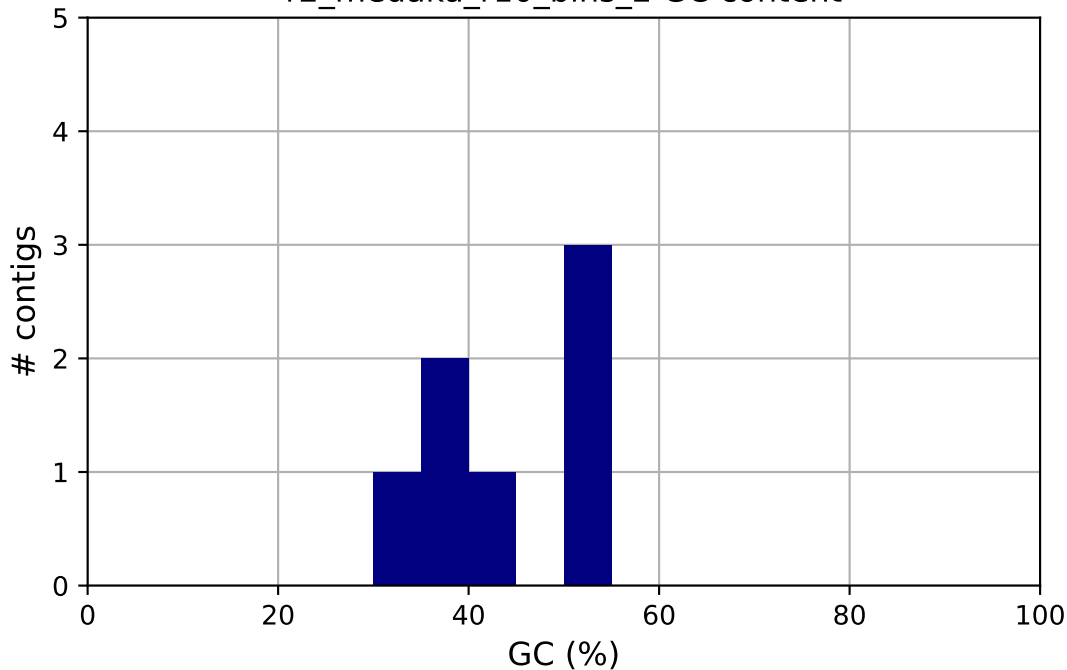
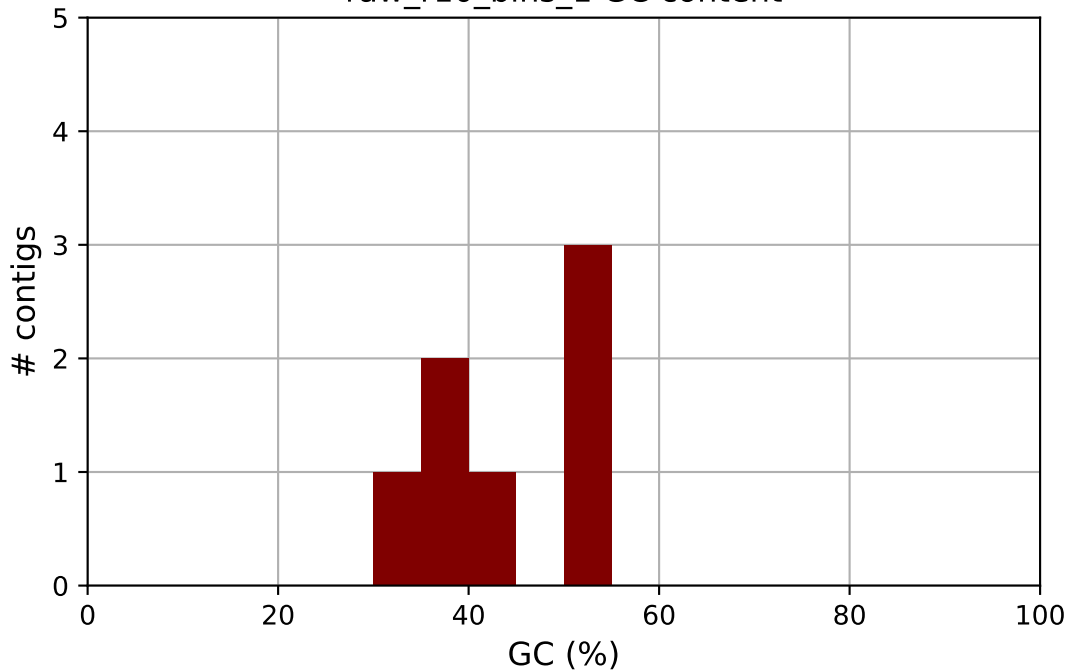r1_medaka_r10_bins_3 GC content
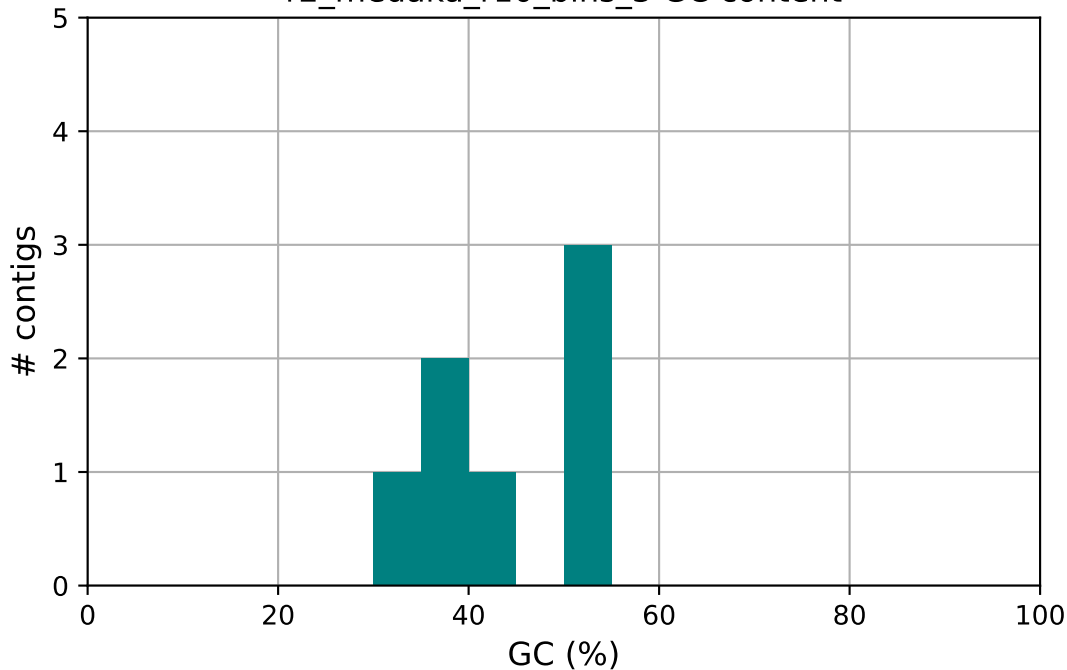
racon_r1_r10_bins_1 GC content
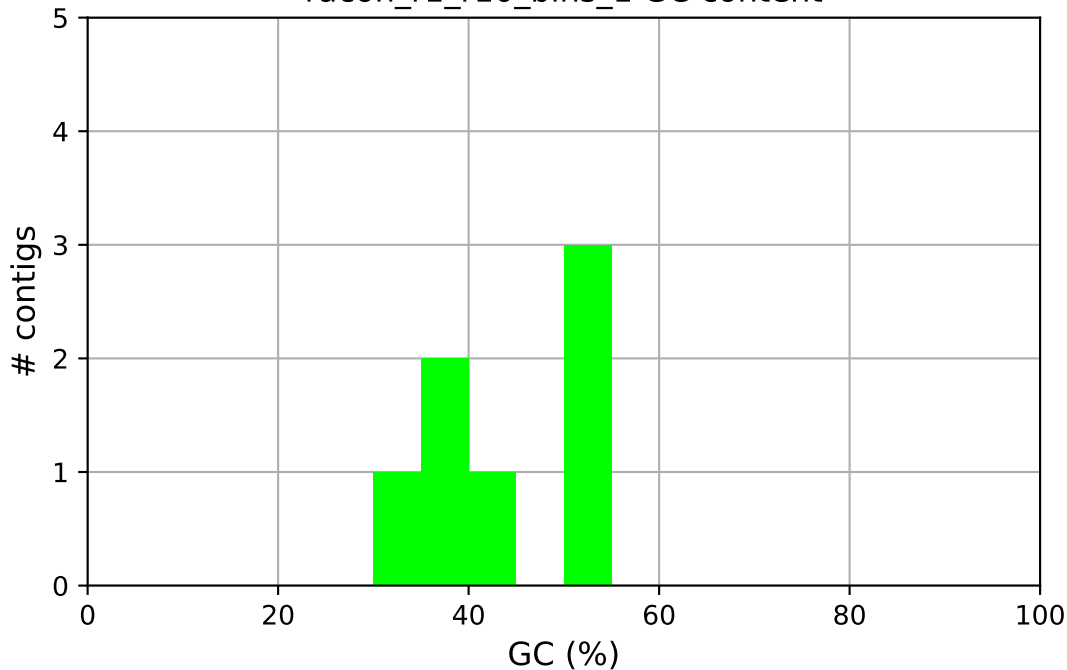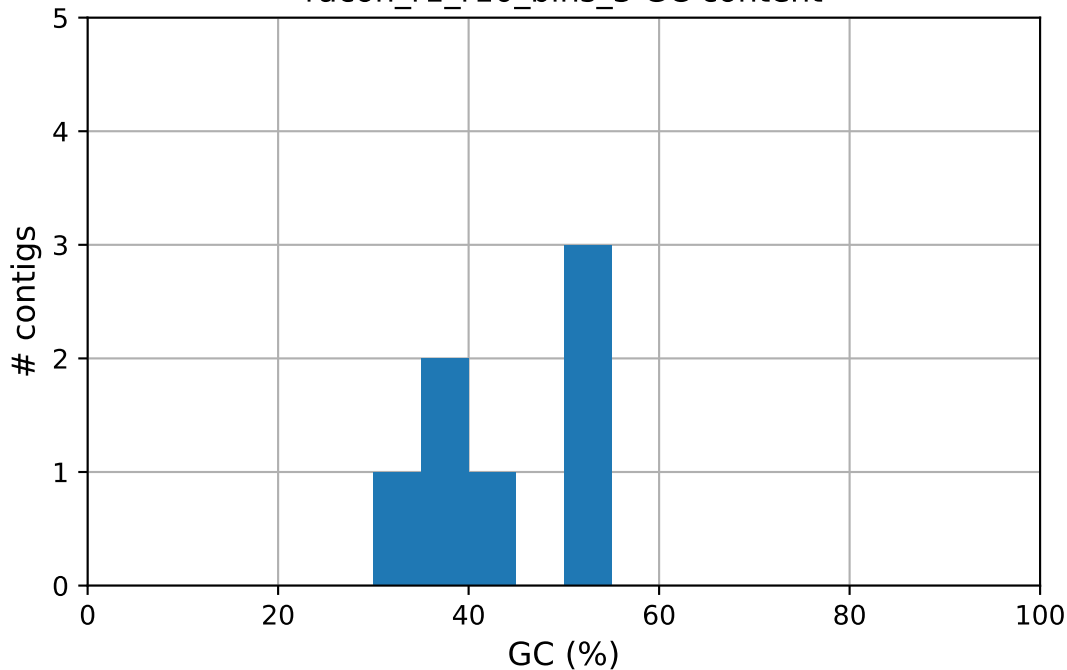
racon_r2_r10_bins_1 GC content
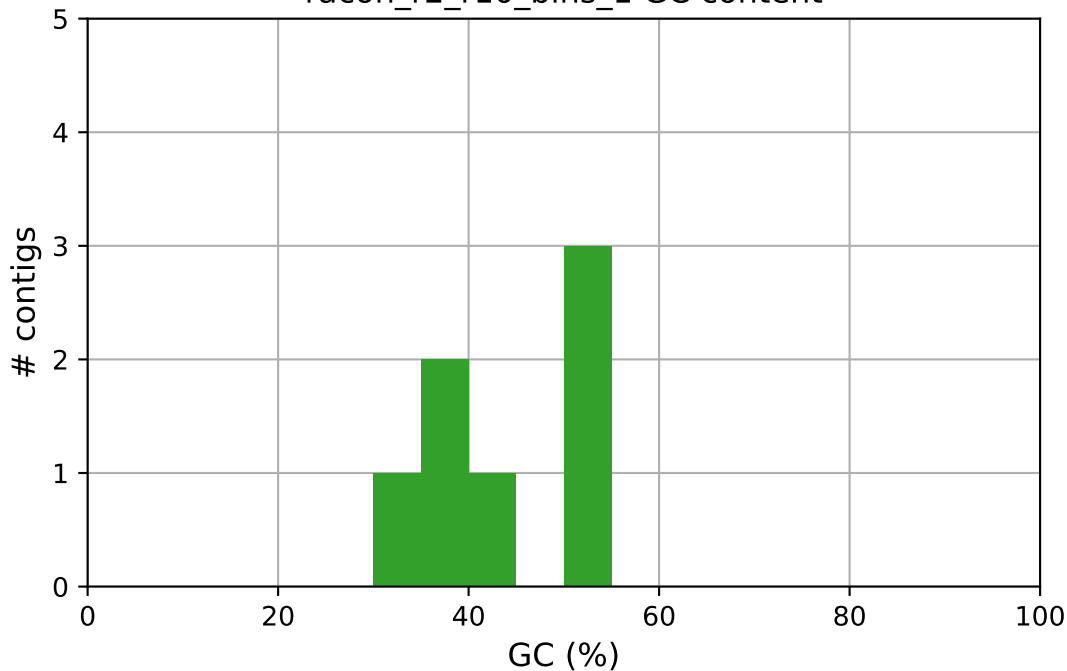
racon_r2_r10_bins_2 GC content
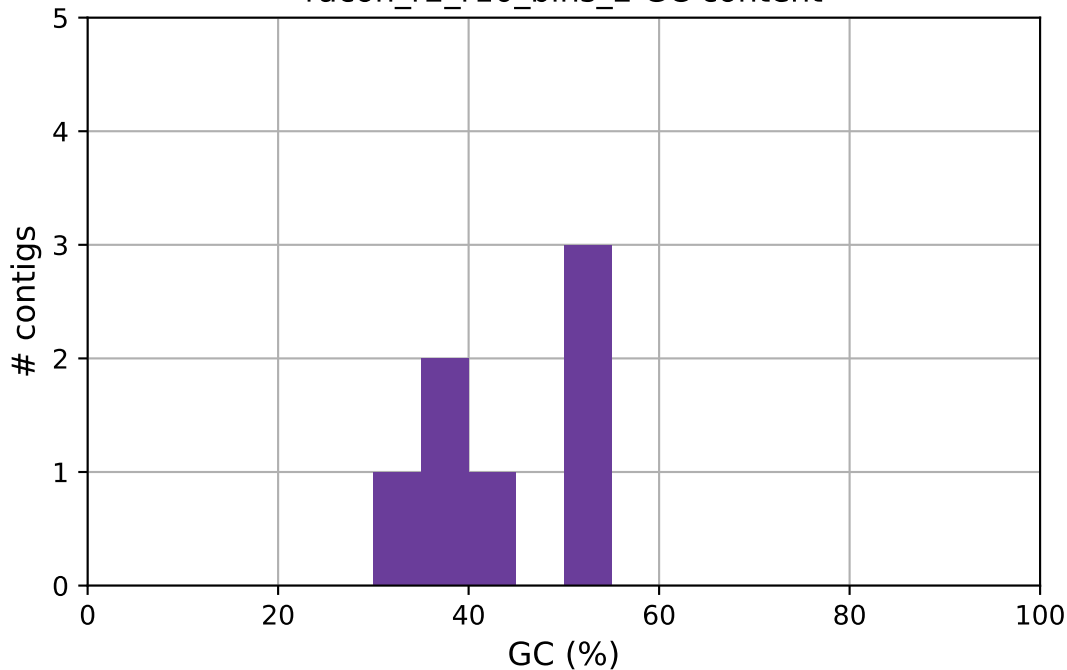
racon_r2_r10_bins_3 GC content
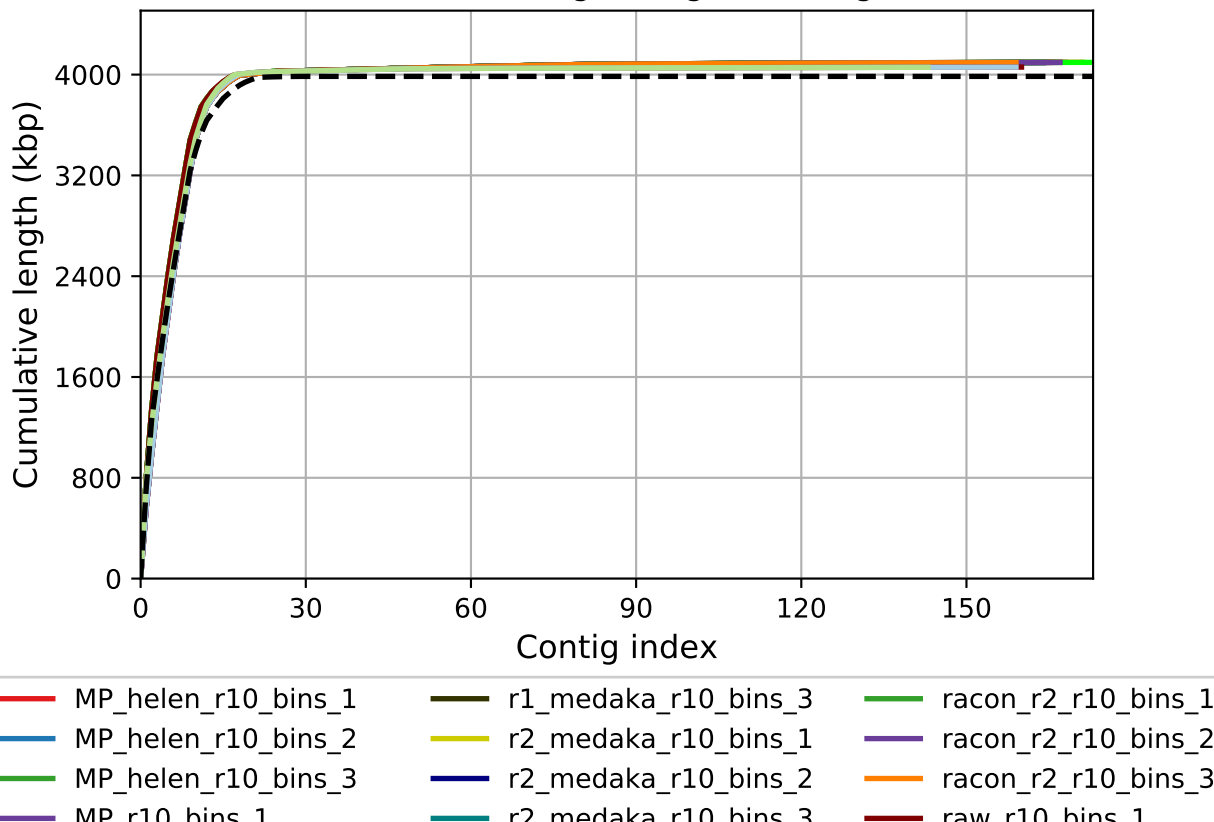
raw_r10_bins_2 GC content
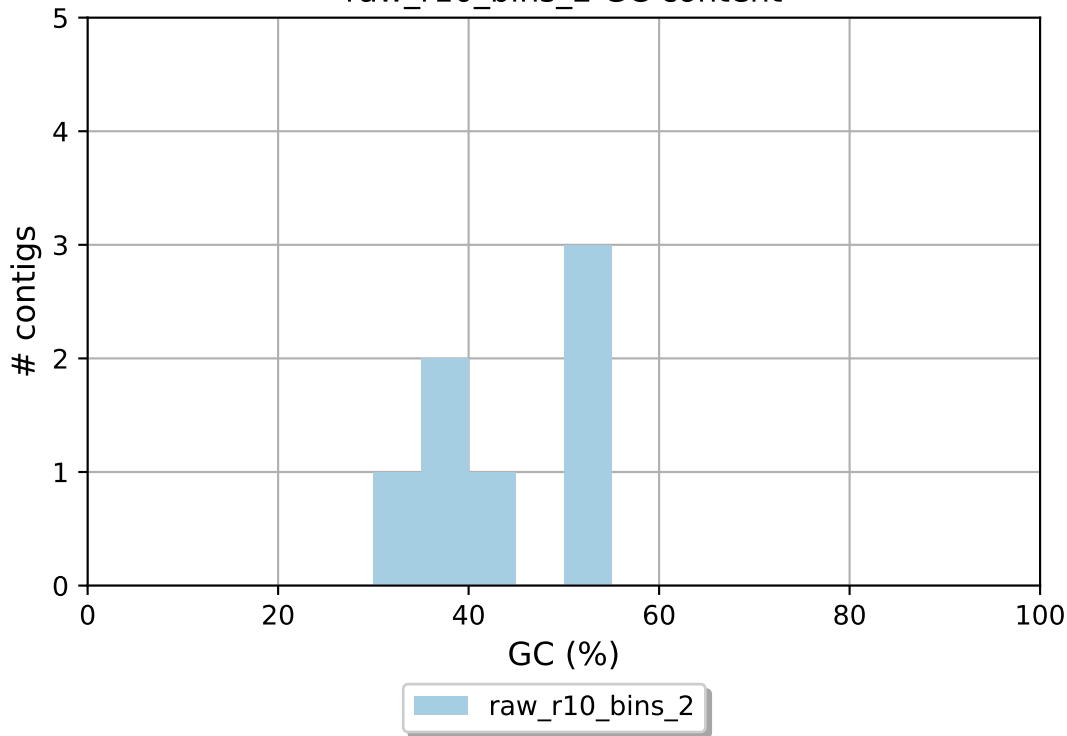
Misassemblies
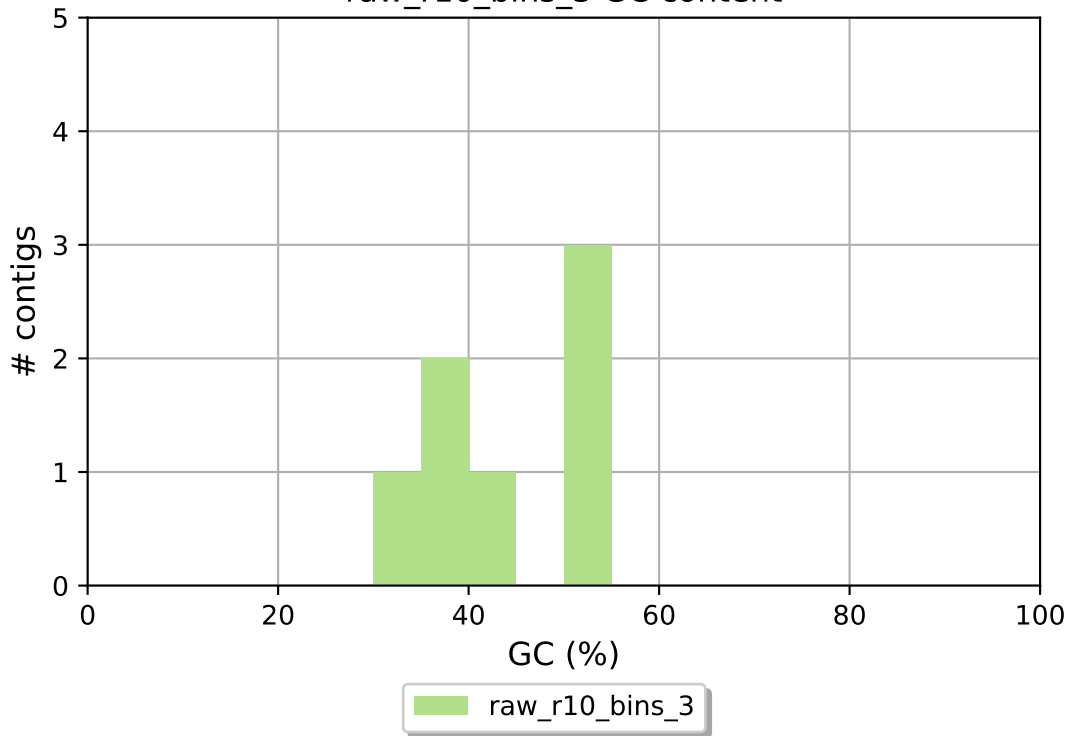
translocations   # interspecies translocations

FRCurve (misassemblies)

—— 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
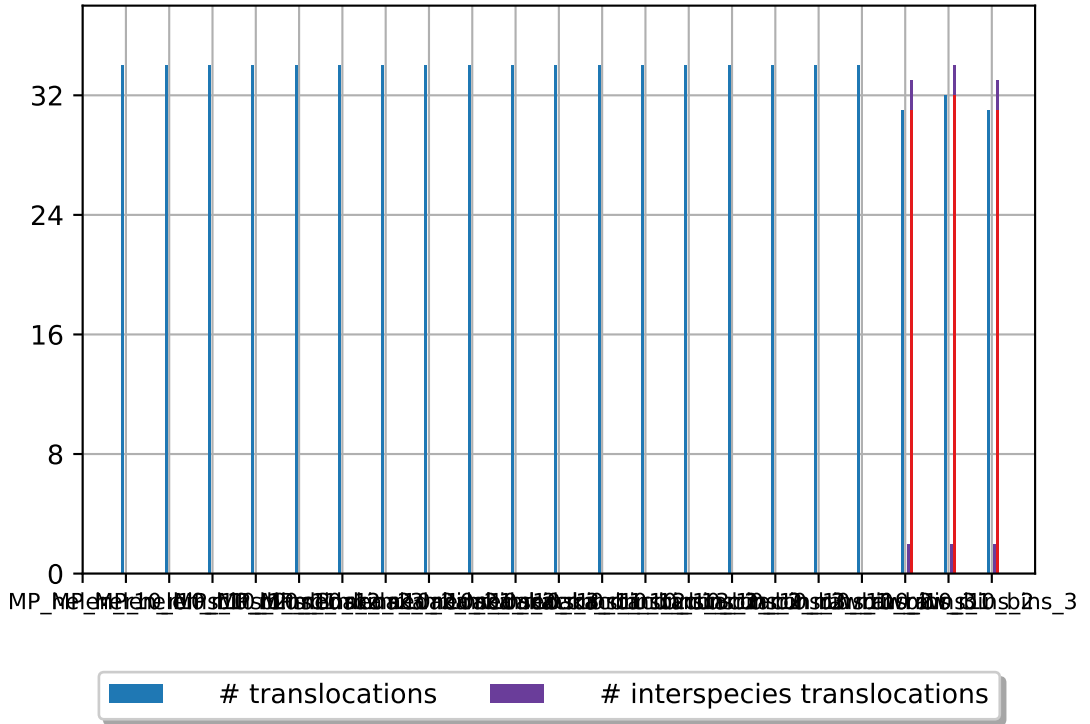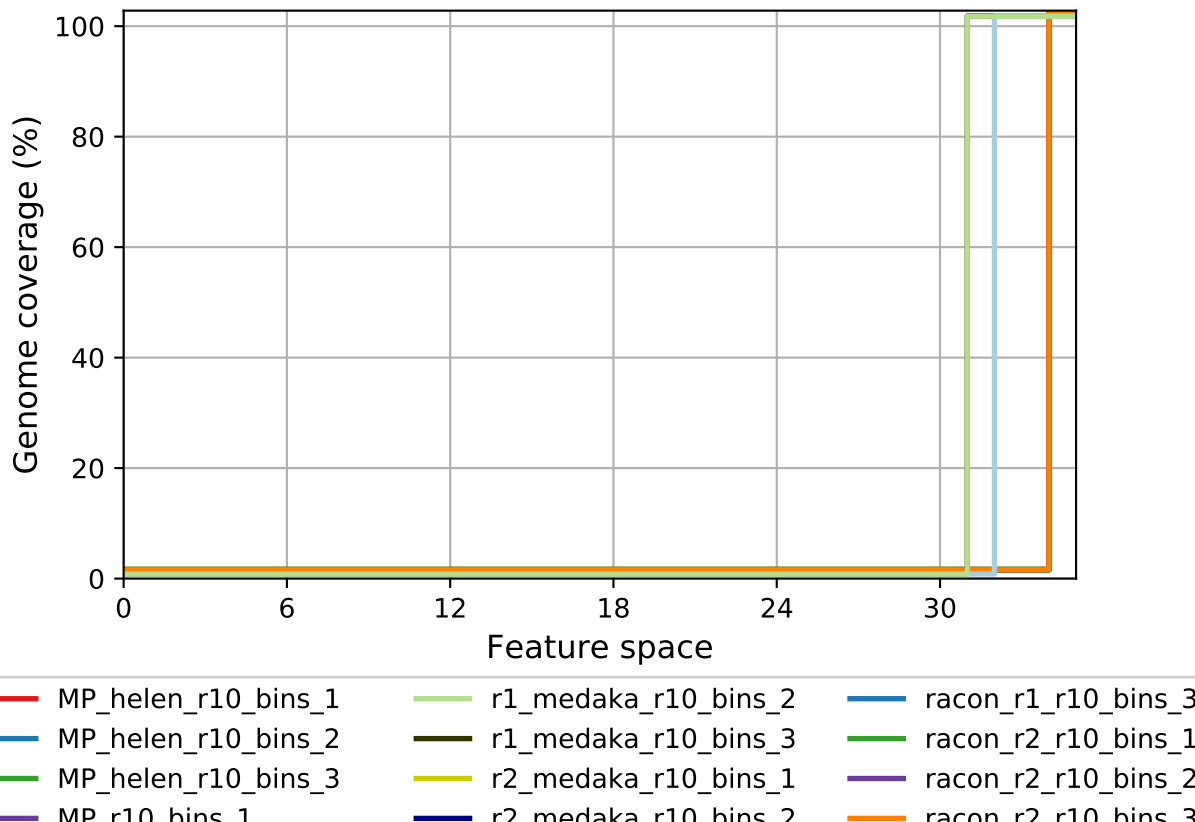
Cumulative length (aligned contigs)
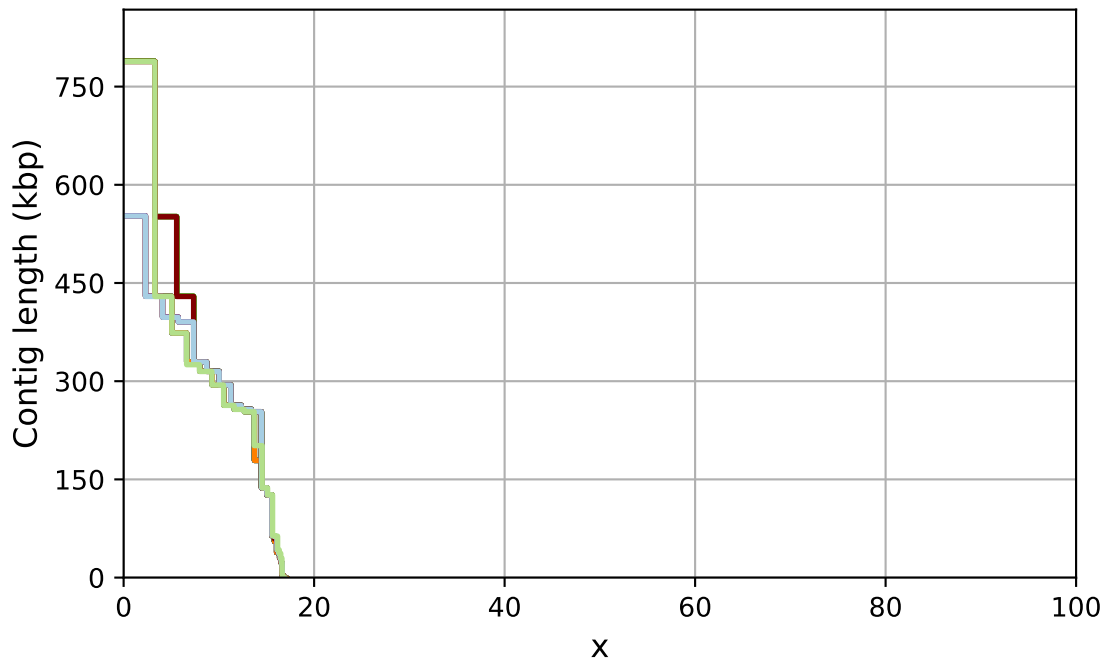
Legend		
MP_helen_r10_bins_1	r1_medaka_r10_bins_3	racon_r2_r10_bins_1
MP_helen_r10_bins_2	r2_medaka_r10_bins_1	racon_r2_r10_bins_2
MP_helen_r10_bins_3	r2_medaka_r10_bins_2	racon_r2_r10_bins_3
MP_r10_bins_1	r2_medaka_r10_bins_3	raw_r10_bins_1

NAx

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

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, %

Legend		
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