

Report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_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)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	28132710	28131320	28131647
Total length (>= 10000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	28132710	28131320	28131647
Total length (>= 25000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	28132710	28131320	28131647
Total length (>= 50000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	28132710	28131320	28131647
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	6788581
Total length	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	28132710	28131320	28131647
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
GC (%)	44.81	44.80	44.81	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	44.78	44.79	51.10	51.10	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	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4756101	4755953	4755682
NG50	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	6788581
N75	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2990626	2990624	2990626
NG75	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	6788581
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	21	21	21	21	21	21	21	21	21	21	21	21	19	19	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	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
# local misassemblies	36	37	37	36	37	37	36	36	36	36	37	36	36	37	36	36	36	36	61	48	57
# 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	19037503	19038179	19037191	19044228	19042871	19043951	19039034	19035704	19040429	19032199	19023615	19037445	19031850	19022978	19035297	19023685	19015199	19027551	23185721	23179076	23170795
Genome fraction (%)	97.703	97.703	97.701	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.701	97.703	97.703	97.703	97.703	97.703	97.703	97.703	97.661	97.667	97.663
Duplication ratio	1.077	1.076	1.077	1.076	1.076	1.076	1.077	1.077	1.077	1.077	1.077	1.076	1.076	1.077	1.076	1.077	1.077	1.077	1.058	1.059	1.061
# 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	438.57	432.65	438.86	435.36	436.13	437.42	442.21	442.87	438.49	442.63	442.54	438.25	439.38	451.64	434.70	452.13	452.32	445.58	484.30	484.19	503.74
# indels per 100 kbp	17.26	18.26	18.18	20.46	20.91	20.96	15.87	15.65	15.14	15.61	15.05	14.73	36.35	36.37	36.09	32.59	33.91	33.70	236.64	238.81	238.03
Largest alignment	1414788	1409105	1408813	1414847	1409411	1408886	1414826	1408941	1408883	1414828	1408918	1408887	1414644	1408924	1408712	1414640	1408775	1408698	1102167	1311196	1104870
Total aligned length	5028232	5027143	5031914	5025305	5027153	5027154	5029385	5031101	5029109	5029774	5033335	5028963	5025617	5032474	5024723	5031169	5032885	5029695	4941665	4947237	4958552
NGA50	1102964	1103266	1105651	1102965	1103287	1103294	1102953	1103270	1103279	1102960	1105647	1103284	1102776	1103102	1103098	1102840	1103126	1103150	586489	586884	586344
NGA75	394044	393567	393564	394057	393568	393570	394044	393564	393559	394045	393564	393562	393993	393561	393549	394011	393550	393544	369864	376836	376858
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	3	3	3
LGA75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	6	6	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

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	19	19	19
# contig misassemblies	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	19	19	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	20	20	20	20	20	20	20	20	20	20	20	20	18	18	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	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
# 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	12	12	12	12	12	12	12	12	12	12	12	12	34	28	32
# local misassemblies	36	37	37	36	37	37	36	36	36	36	37	36	36	37	36	36	36	36	61	48	57
# 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	42	42	42	42	42	42	42	42	42	42	41	42	35	39	36
# 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	20510	20233	20523	20360	20396	20456	20680	20711	20506	20700	20695	20495	20548	21121	20329	21144	21153	20838	22639	22635	23548
# indels	807	854	850	957	978	980	742	732	708	730	704	689	1700	1701	1688	1524	1586	1576	11062	11164	11127
# indels (<= 5 bp)	706	755	751	857	877	882	645	634	611	633	607	592	1603	1603	1591	1427	1487	1478	10862	10964	10928
# indels (> 5 bp)	101	99	99	100	101	98	97	98	97	97	97	97	97	98	97	97	99	98	200	200	199
Indels length	6112	6140	6070	6220	6294	6239	5976	6021	5919	5962	5860	5899	7102	7124	7084	6881	6982	6941	20270	20739	20311

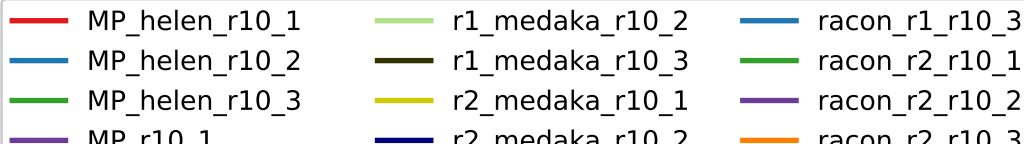
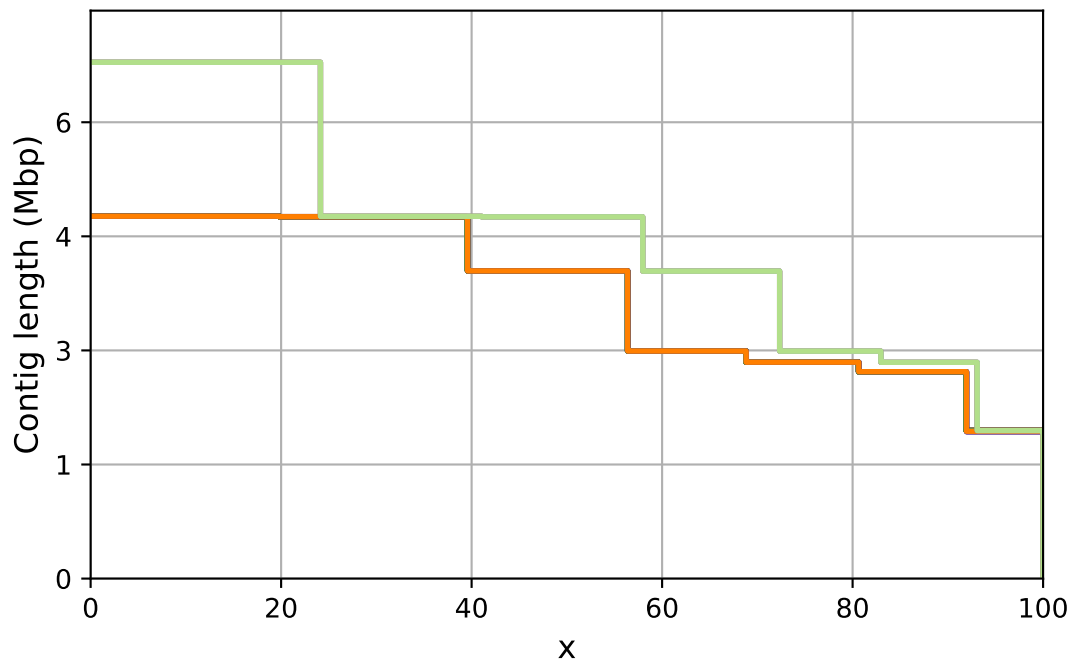
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

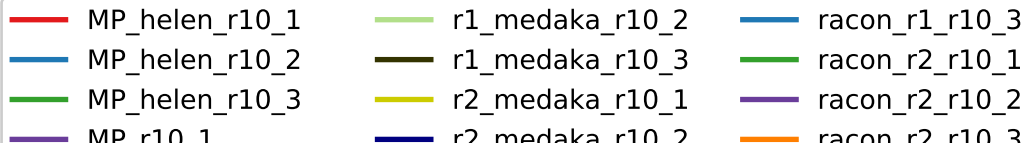
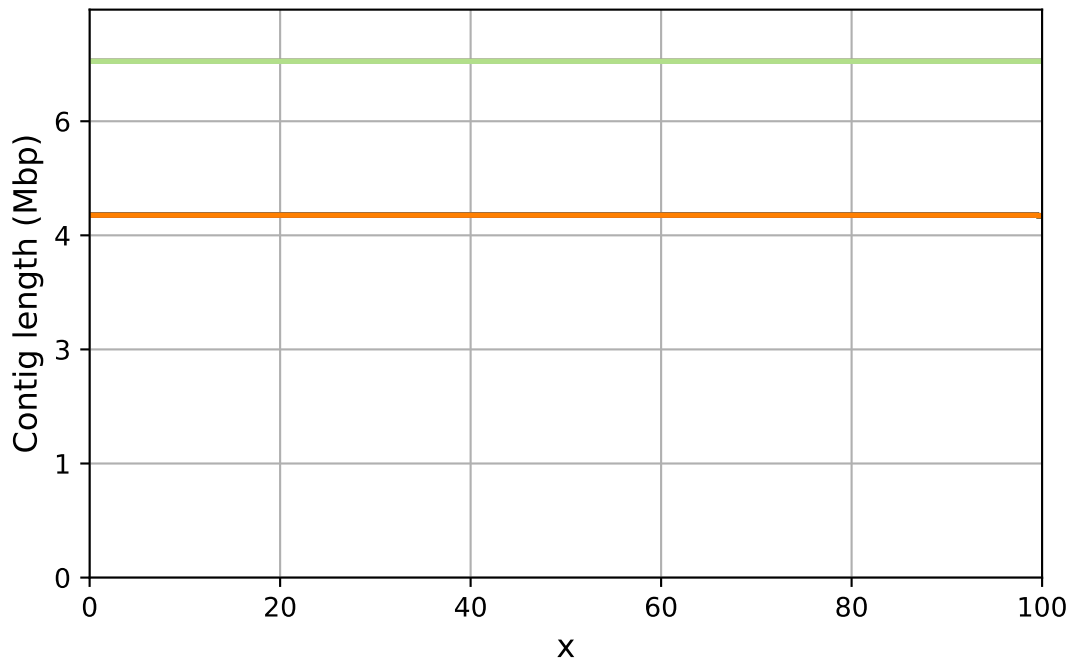
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	19037503	19038179	19037191	19044228	19042871	19043951	19039034	19035704	19040429	19032199	19023615	19037445	19031850	19022978	19035297	19023685	19015199	19027551	23185721	23179076	23170795
# 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).

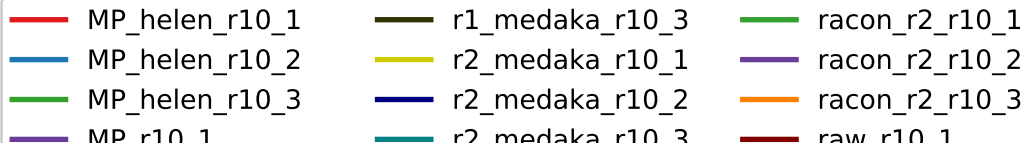
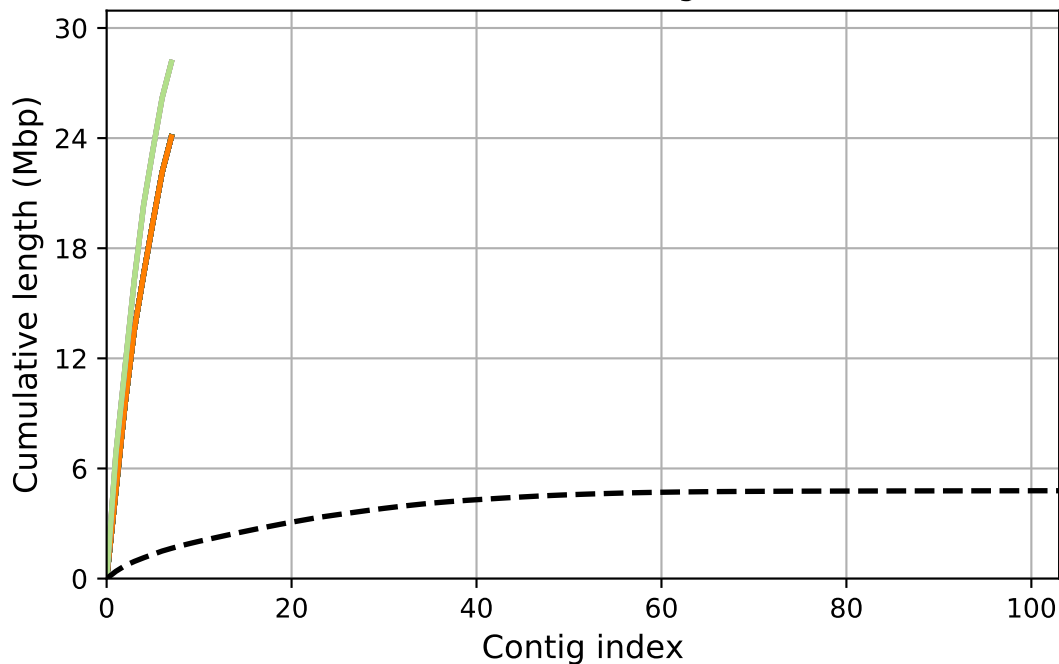
Nx



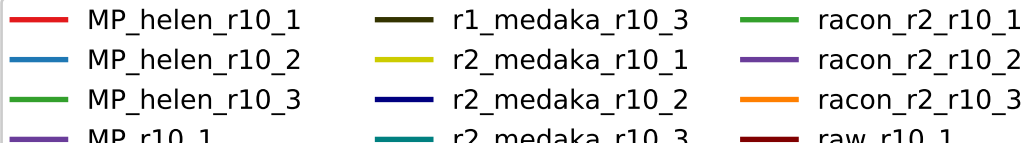
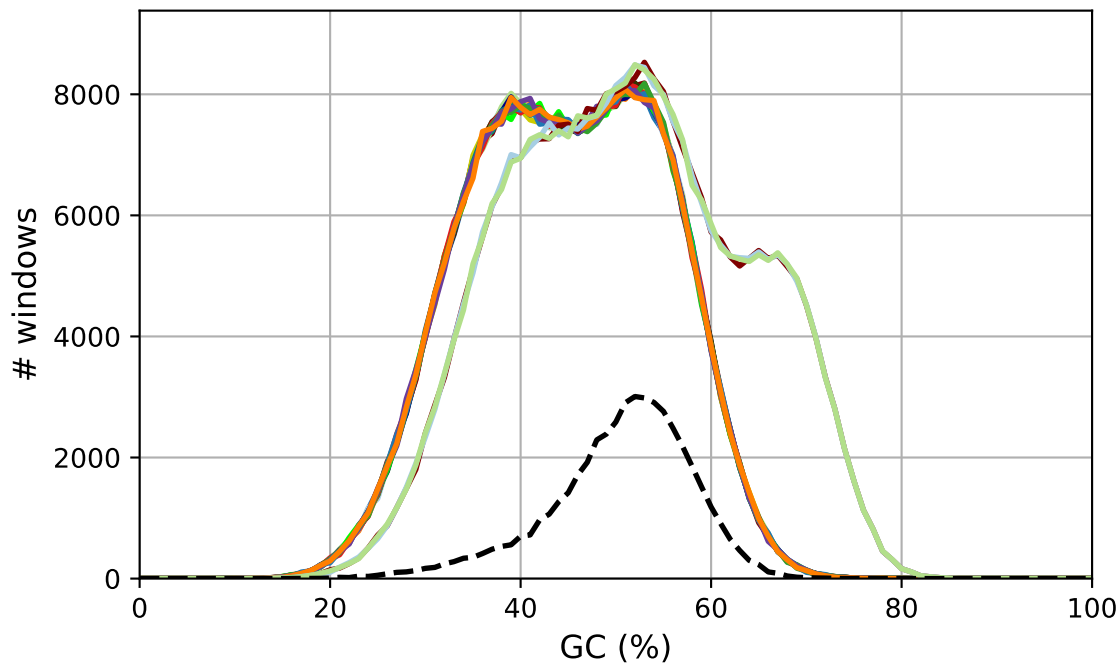
NGx



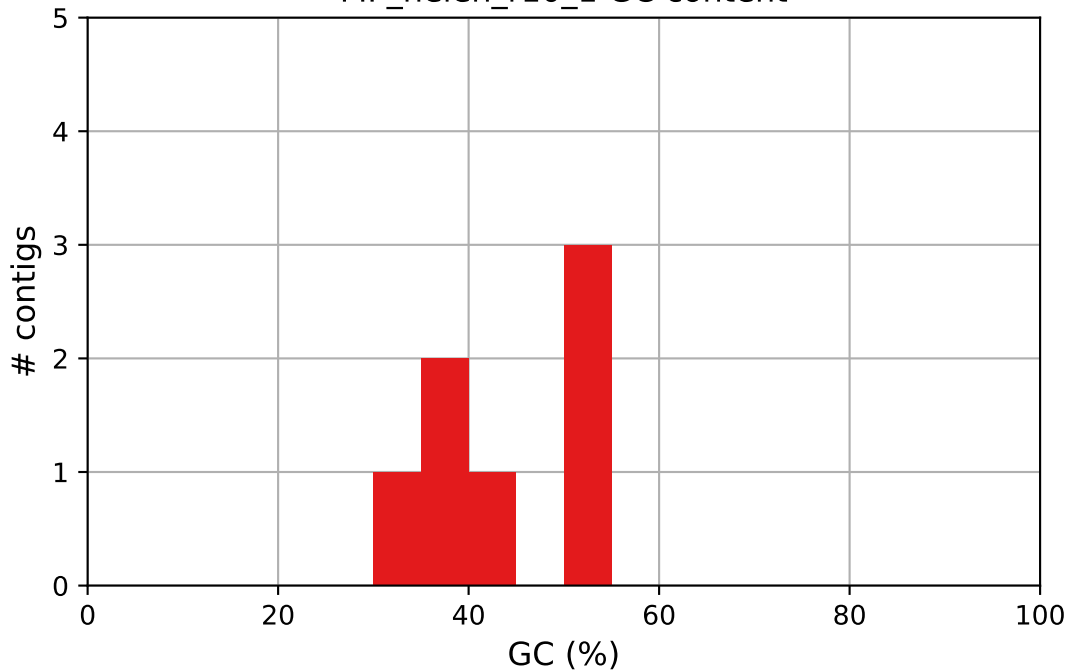
Cumulative length



GC content

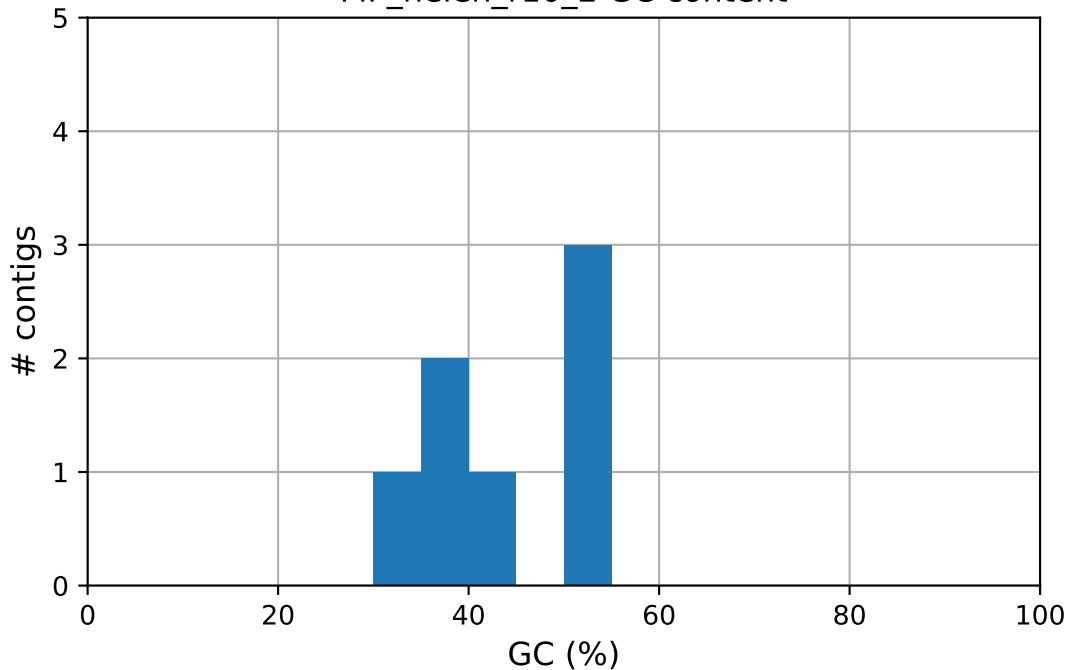


MP_helen_r10_1 GC content



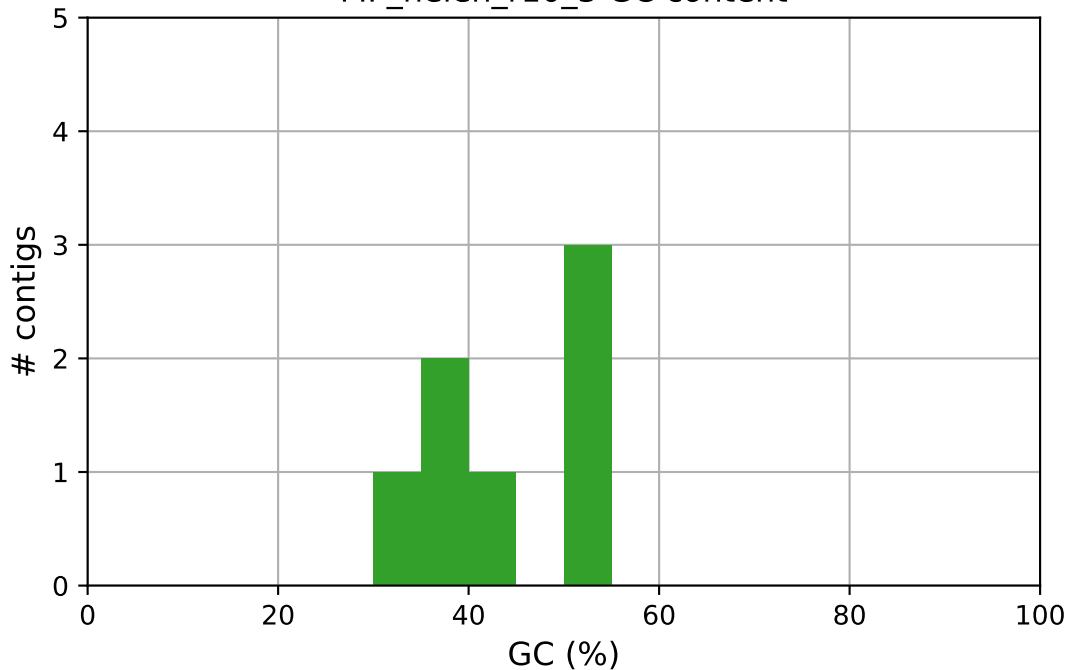
MP_helen_r10_1

MP_helen_r10_2 GC content



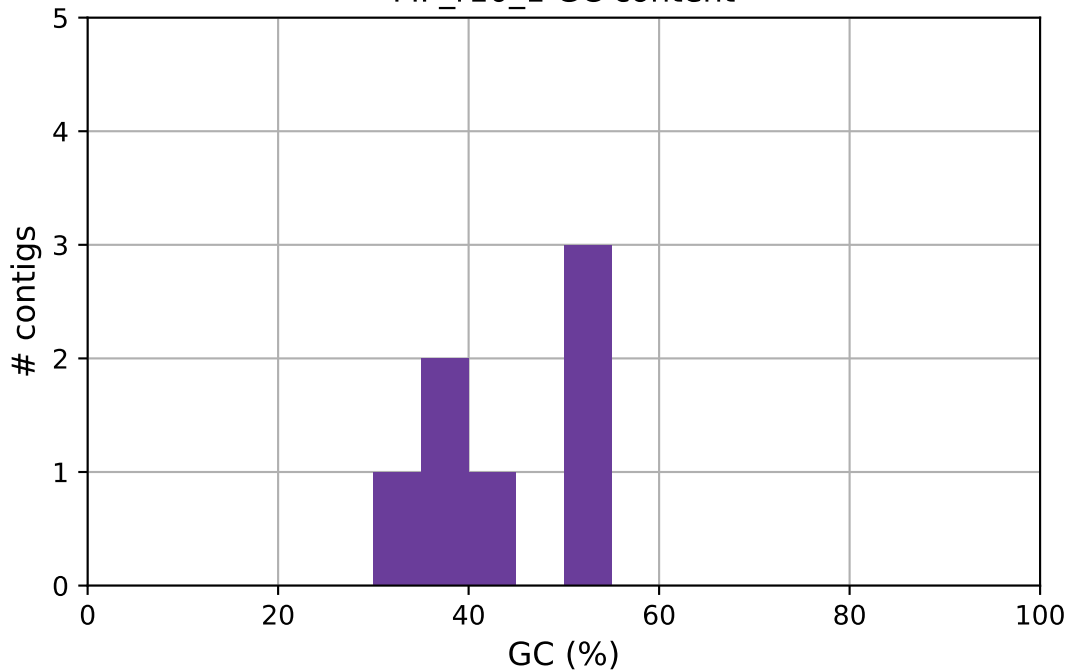
MP_helen_r10_2

MP_helen_r10_3 GC content



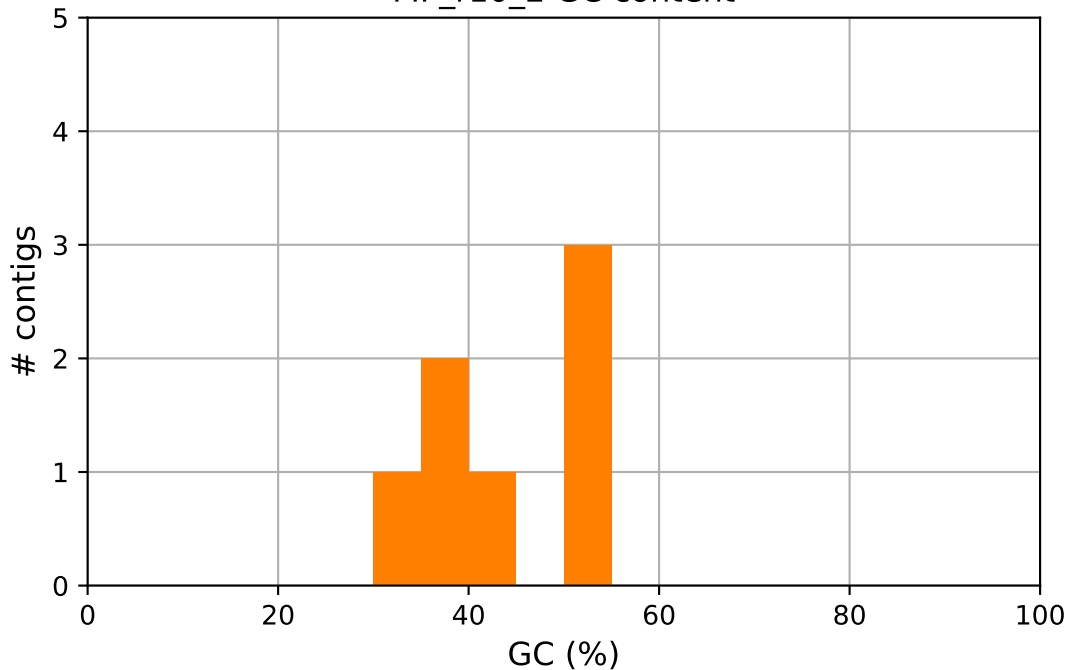
MP_helen_r10_3

MP_r10_1 GC content



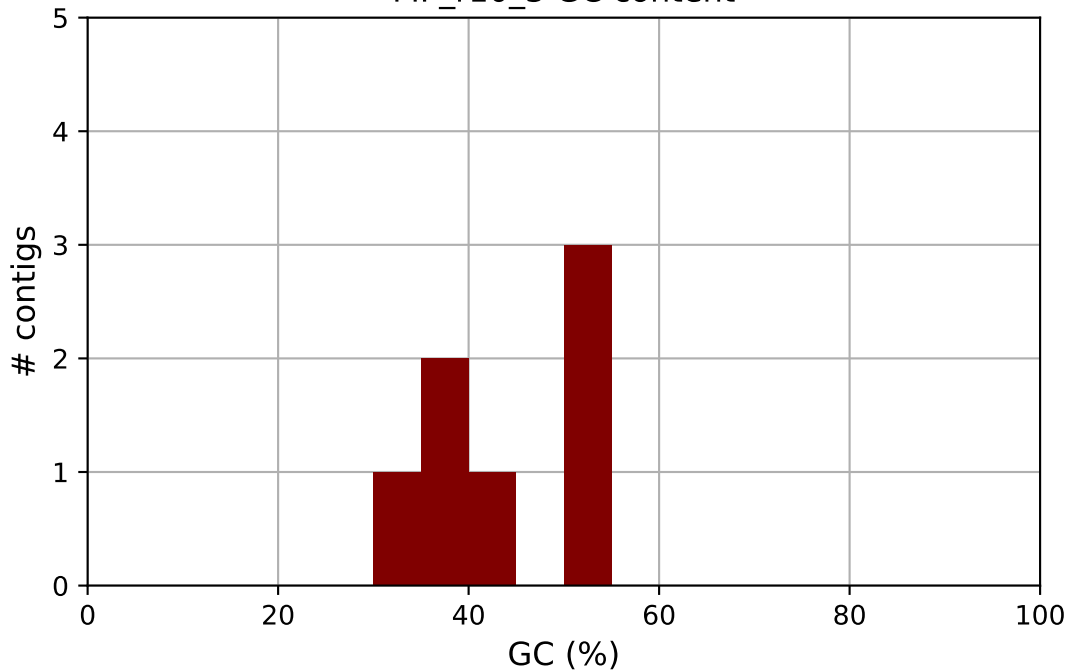
MP_r10_1

MP_r10_2 GC content



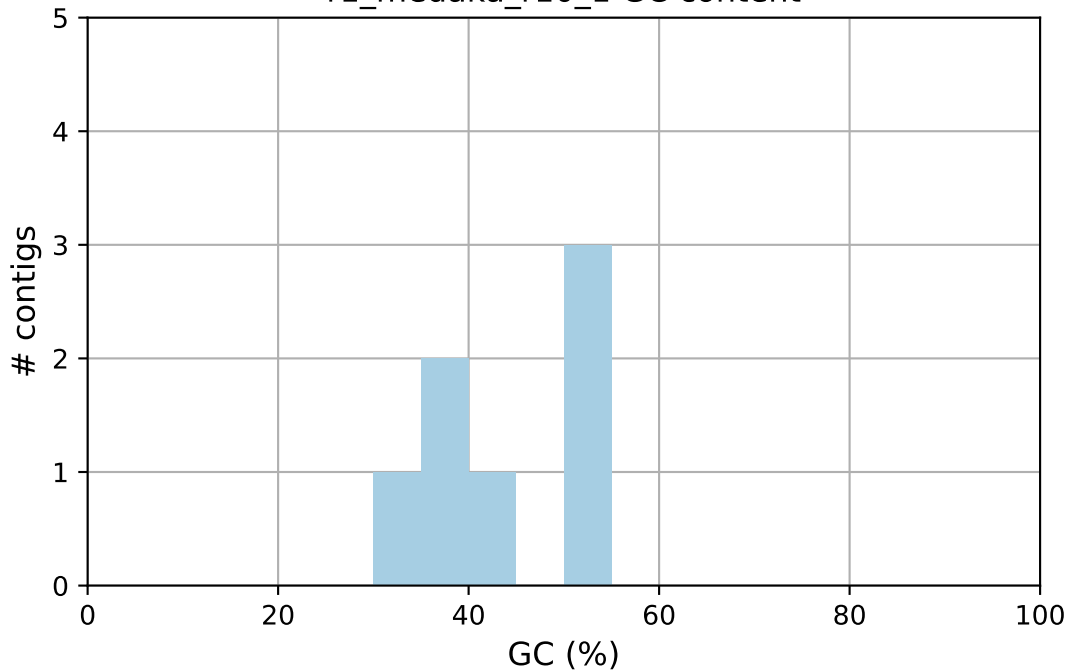
MP_r10_2

MP_r10_3 GC content



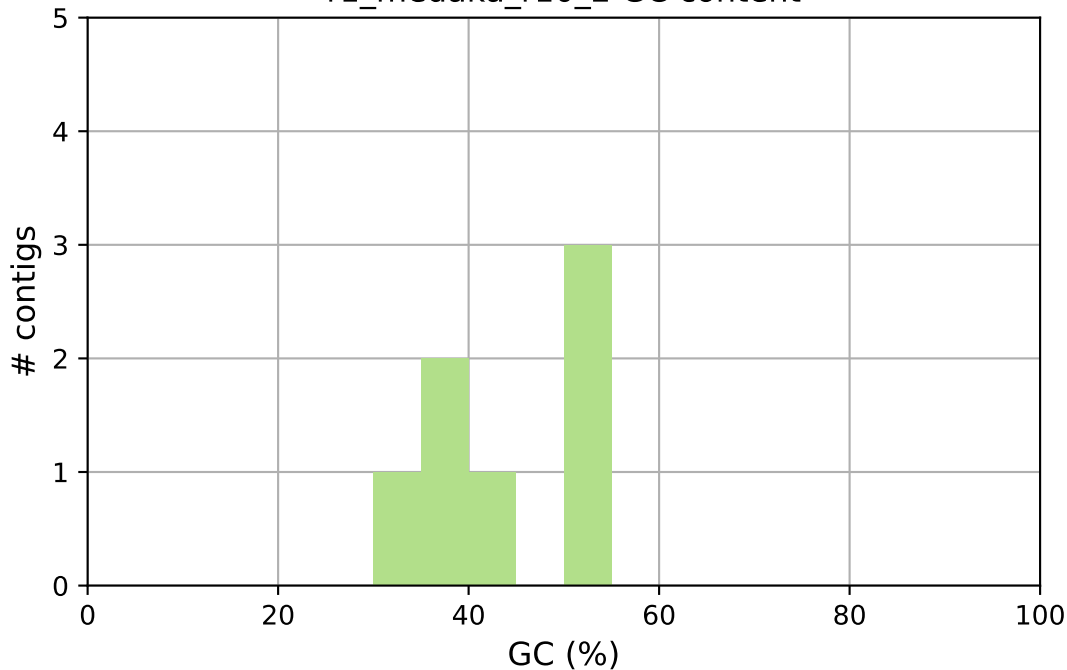
MP_r10_3

r1_medaka_r10_1 GC content



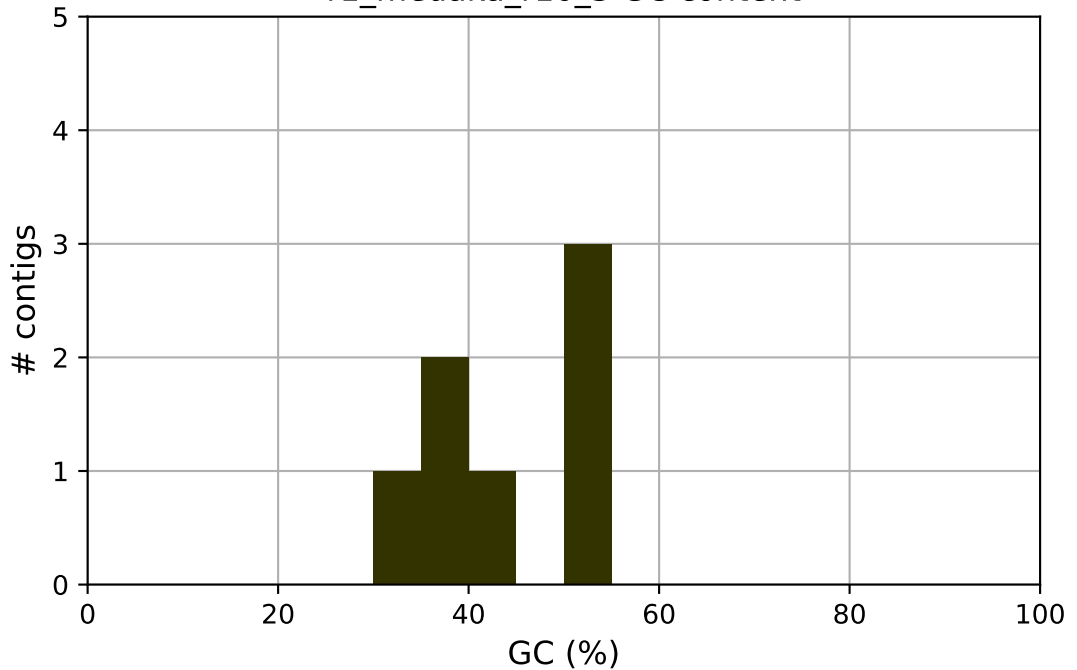
r1_medaka_r10_1

r1_medaka_r10_2 GC content



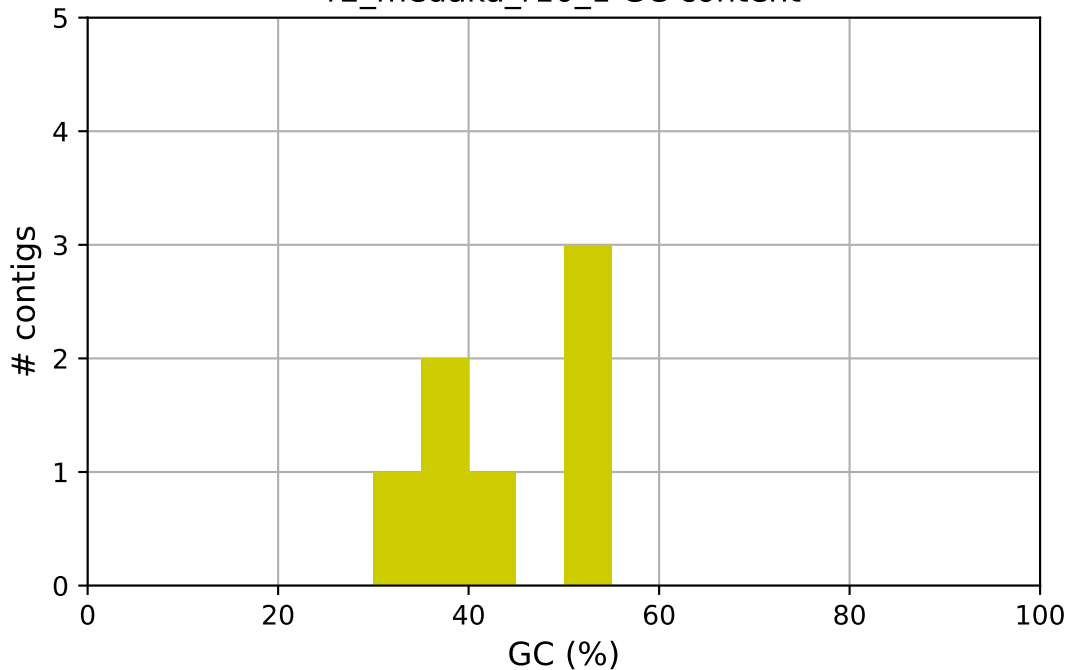
r1_medaka_r10_2

r1_medaka_r10_3 GC content



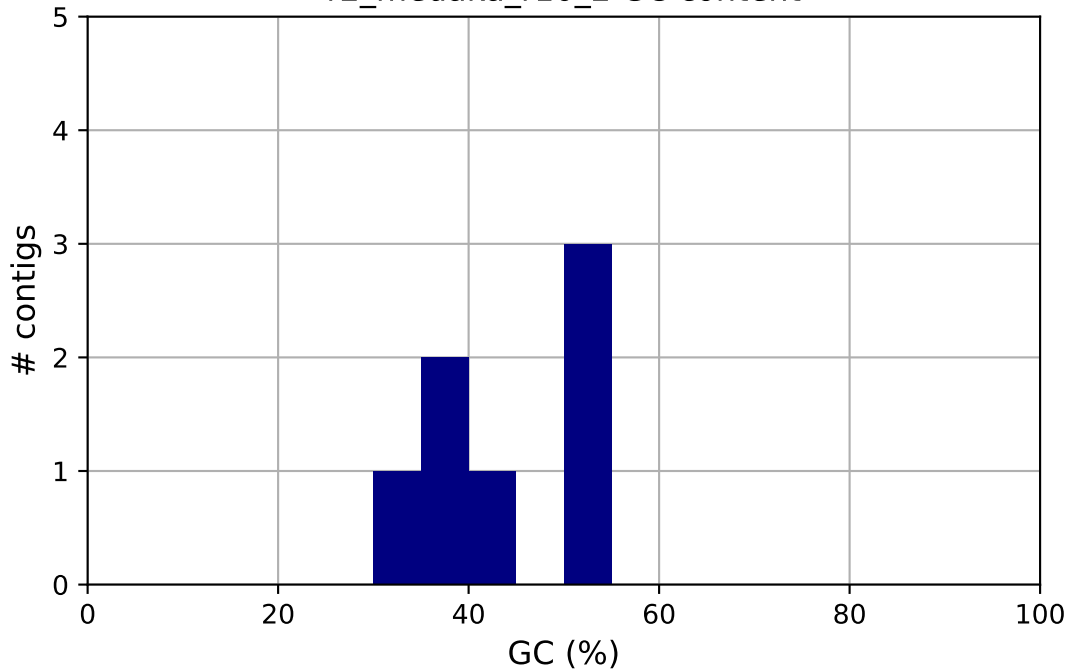
r1_medaka_r10_3

r2_medaka_r10_1 GC content



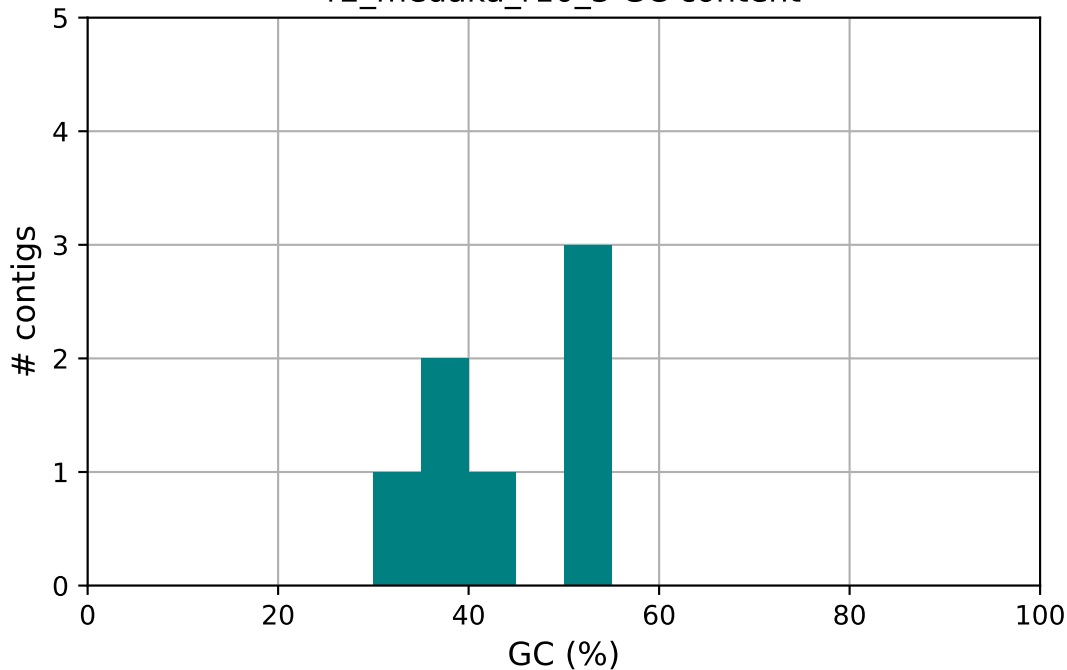
r2_medaka_r10_1

r2_medaka_r10_2 GC content



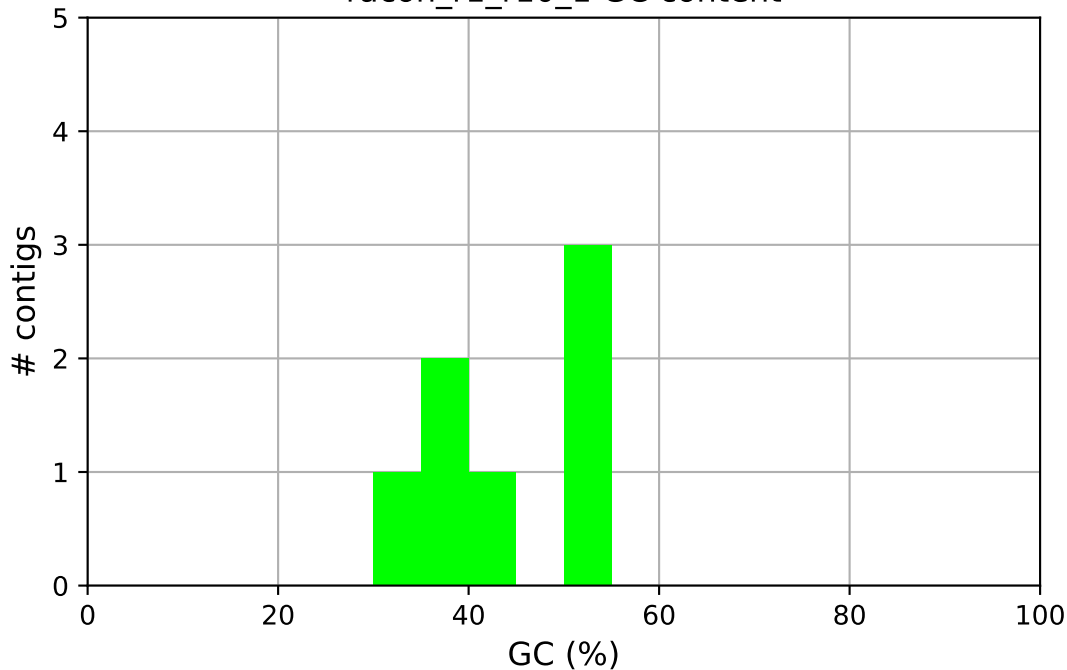
r2_medaka_r10_2

r2_medaka_r10_3 GC content



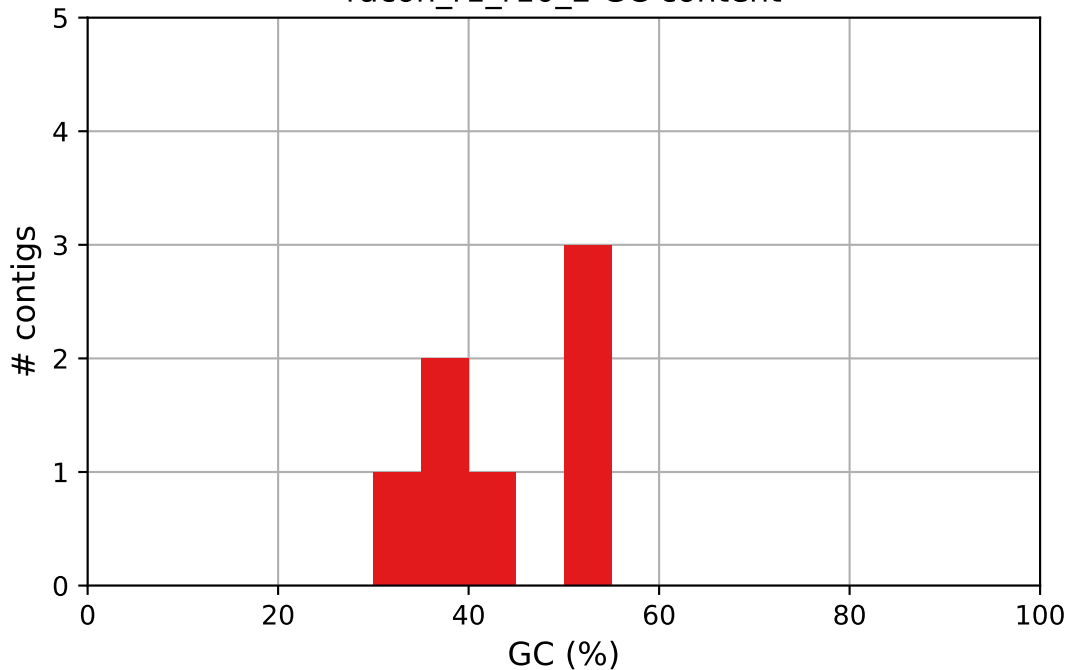
r2_medaka_r10_3

racon_r1_r10_1 GC content



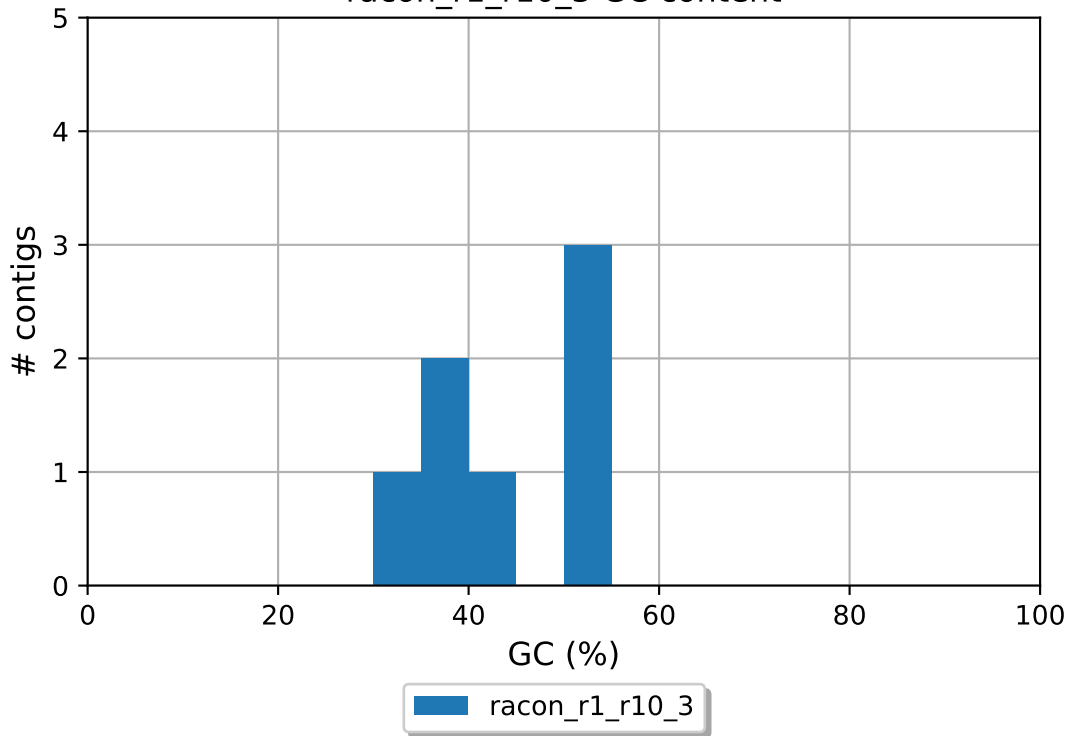
racon_r1_r10_1

racon_r1_r10_2 GC content

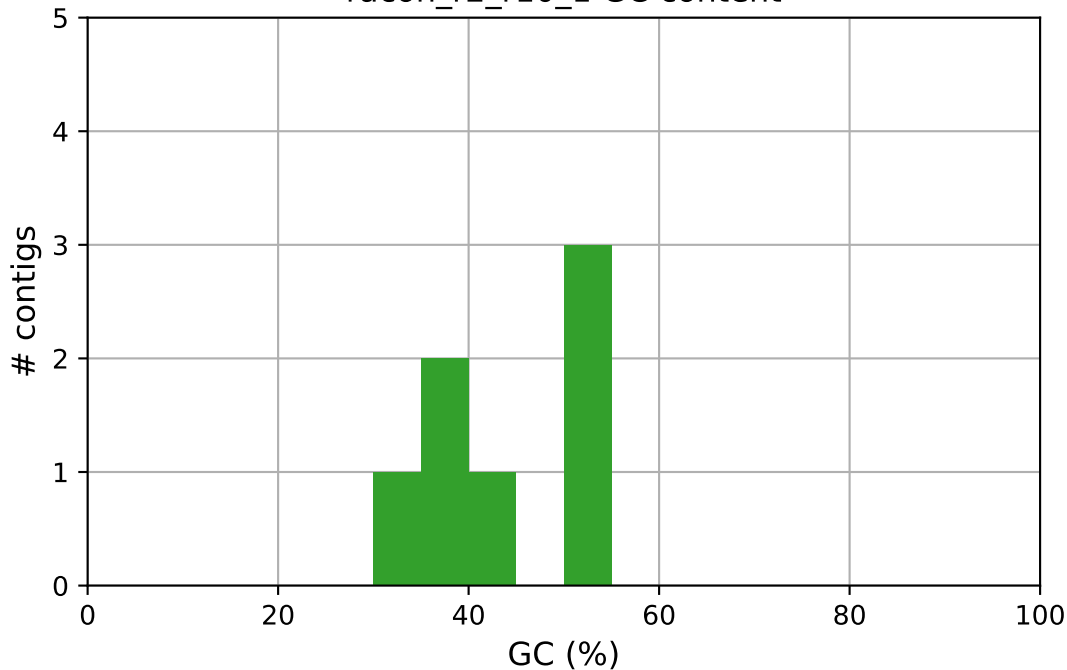


racon_r1_r10_2

racon_r1_r10_3 GC content

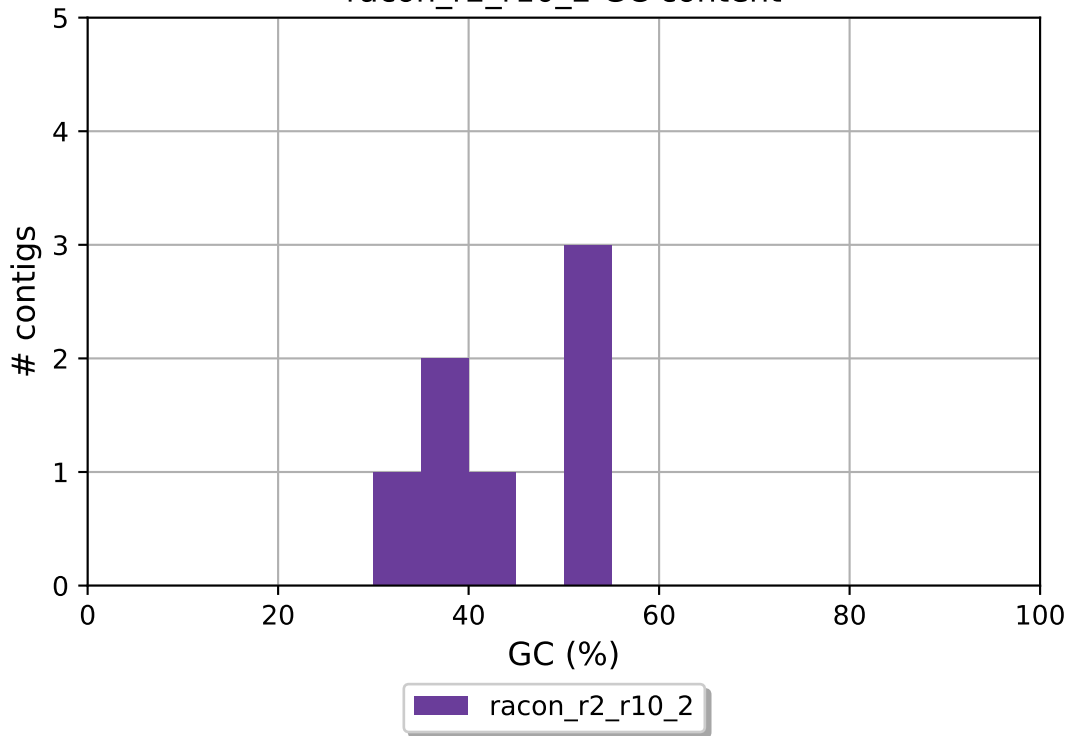


racon_r2_r10_1 GC content

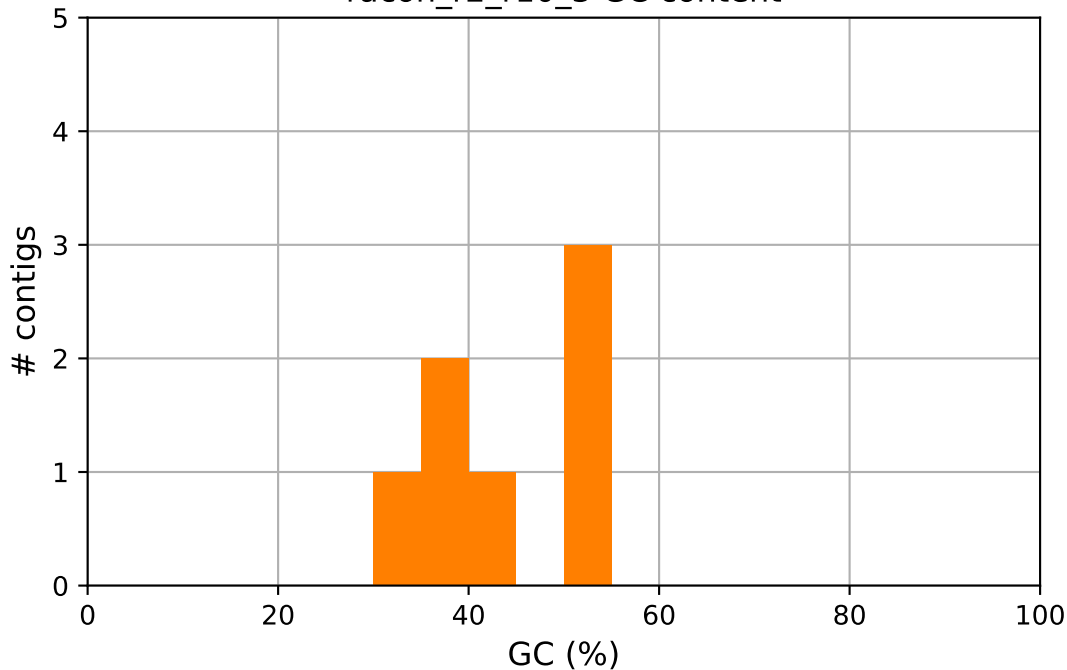


racon_r2_r10_1

racon_r2_r10_2 GC content

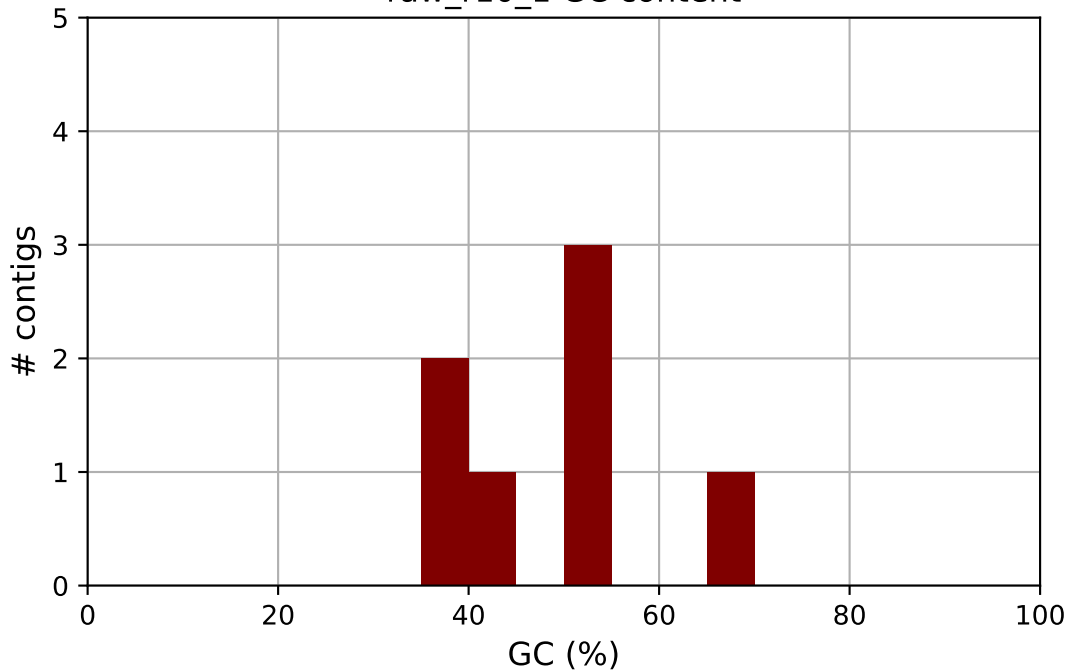


racon_r2_r10_3 GC content



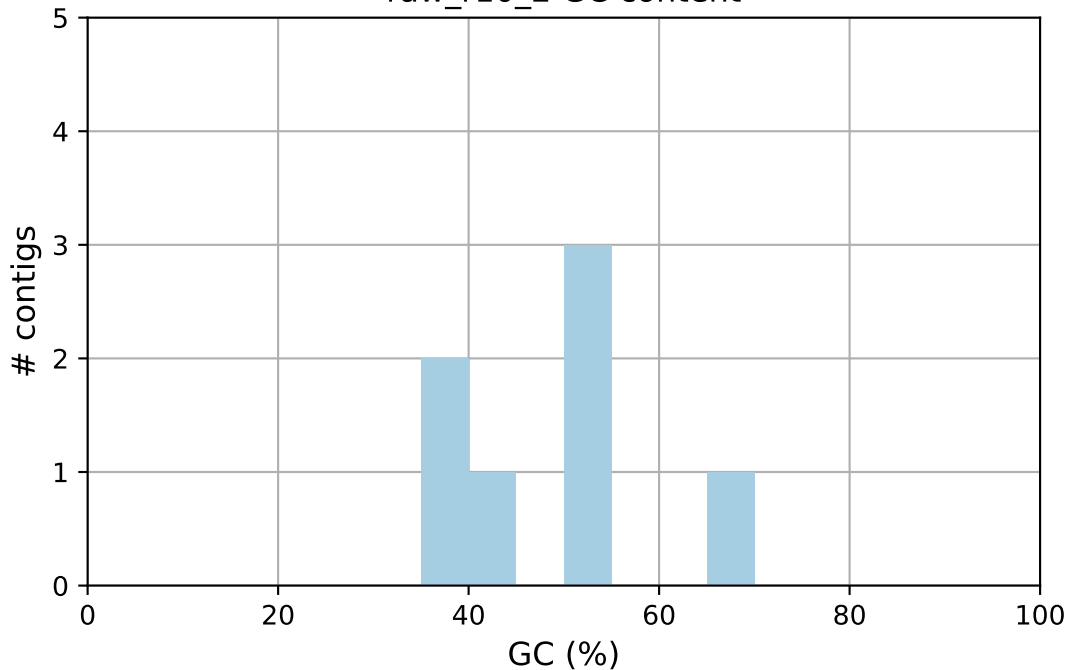
racon_r2_r10_3

raw_r10_1 GC content



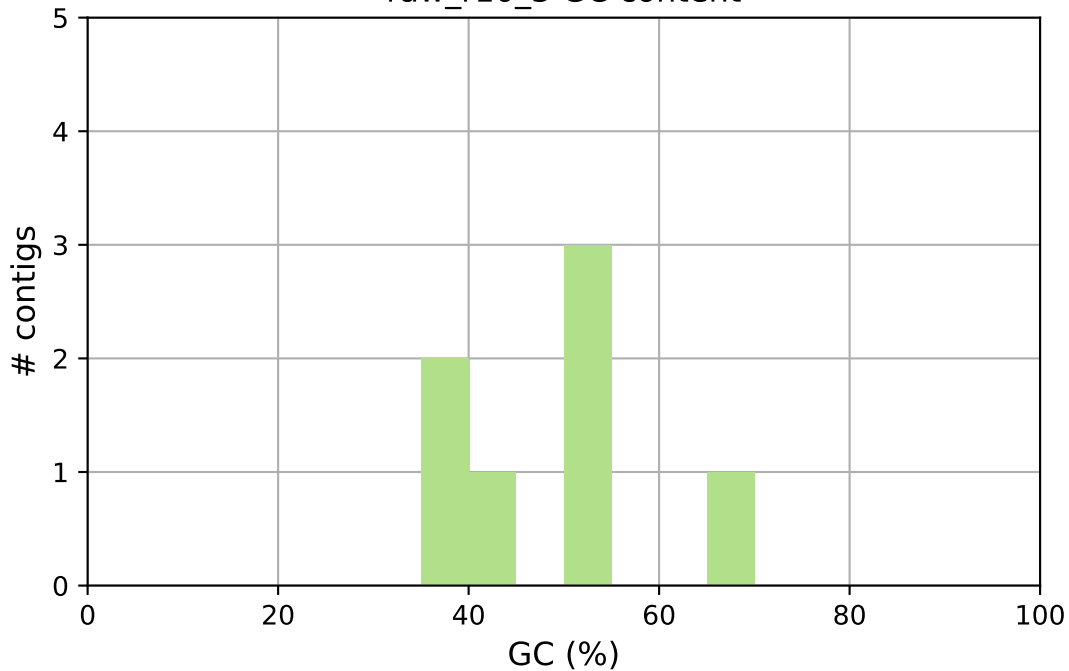
raw_r10_1

raw_r10_2 GC content



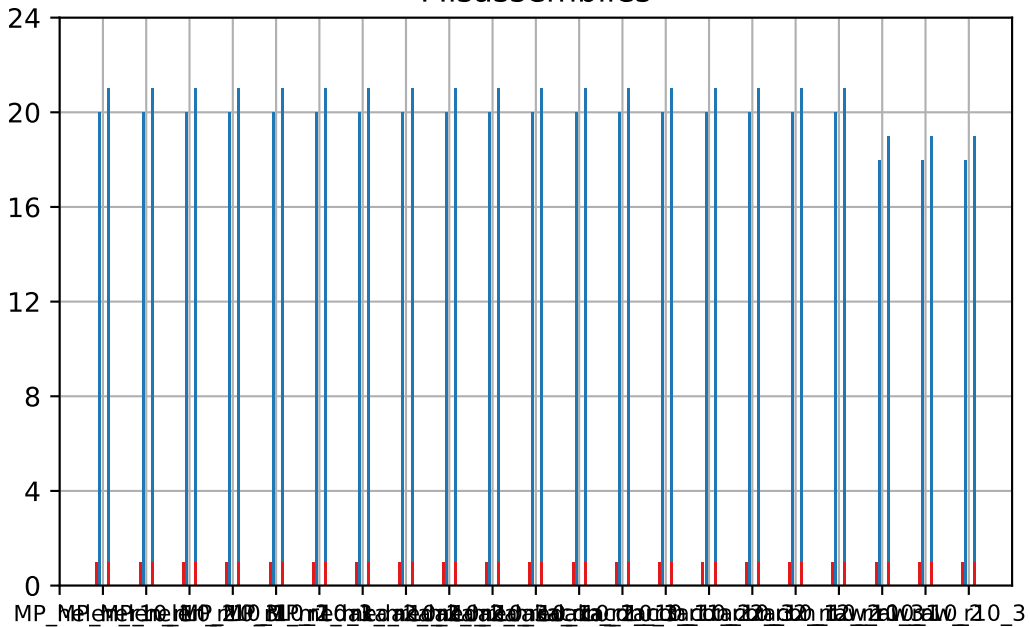
raw_r10_2

raw_r10_3 GC content



raw_r10_3

Misassemblies

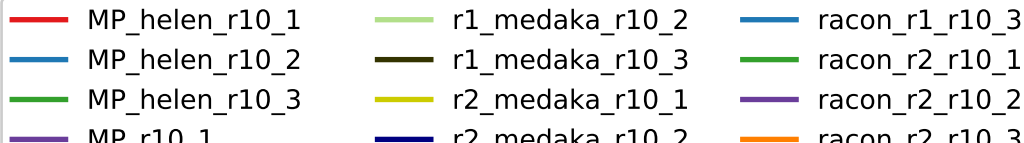
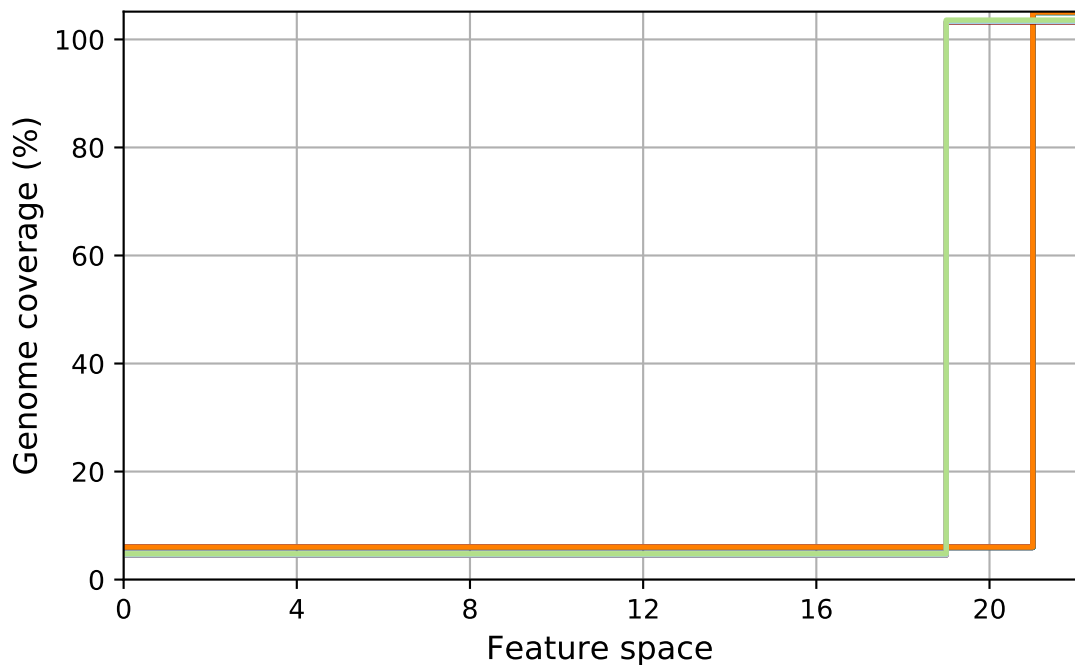


```
# relocations
```

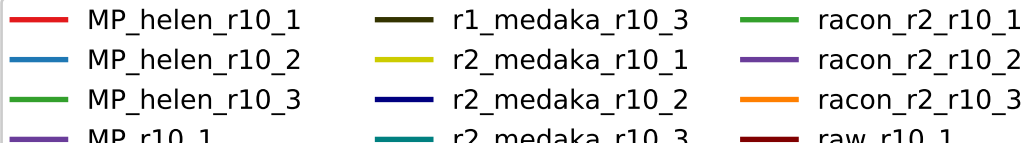
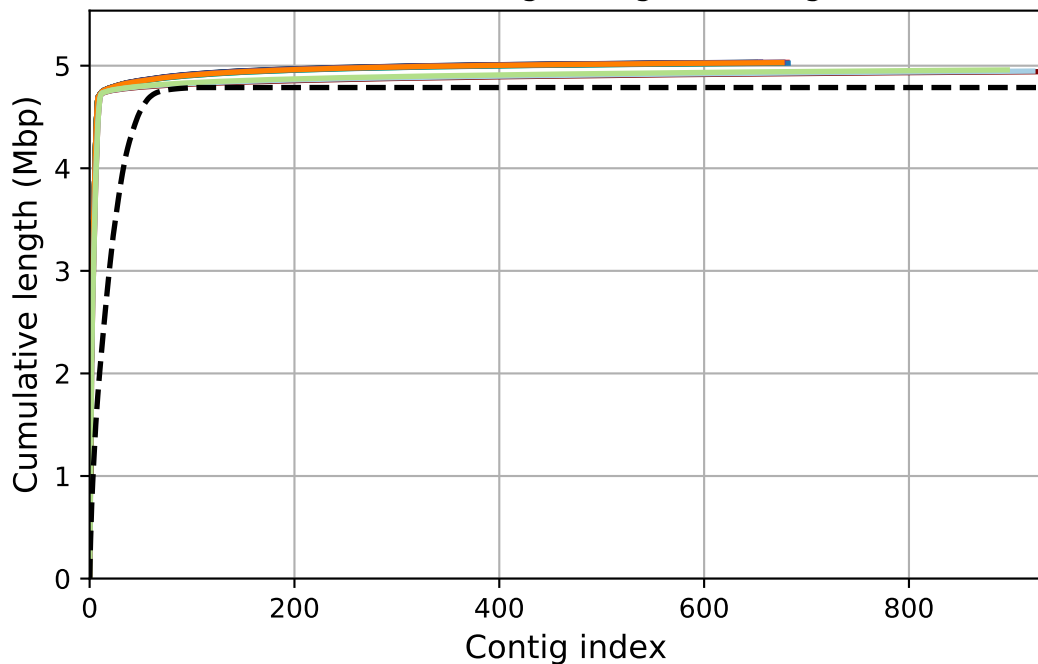
11

translocations

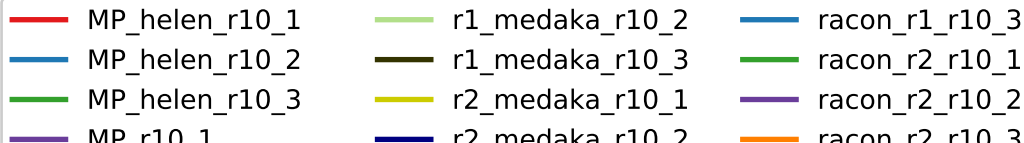
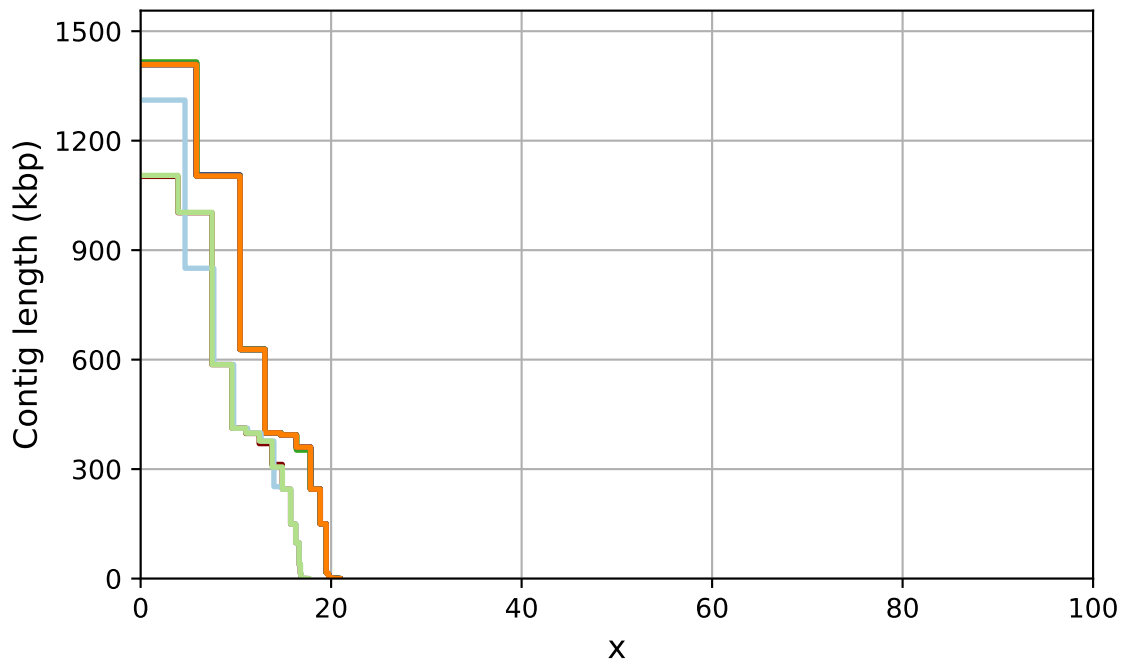
FRCurve (misassemblies)



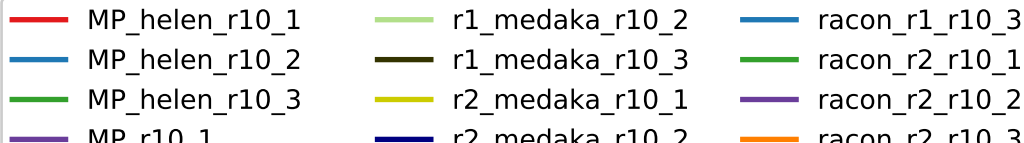
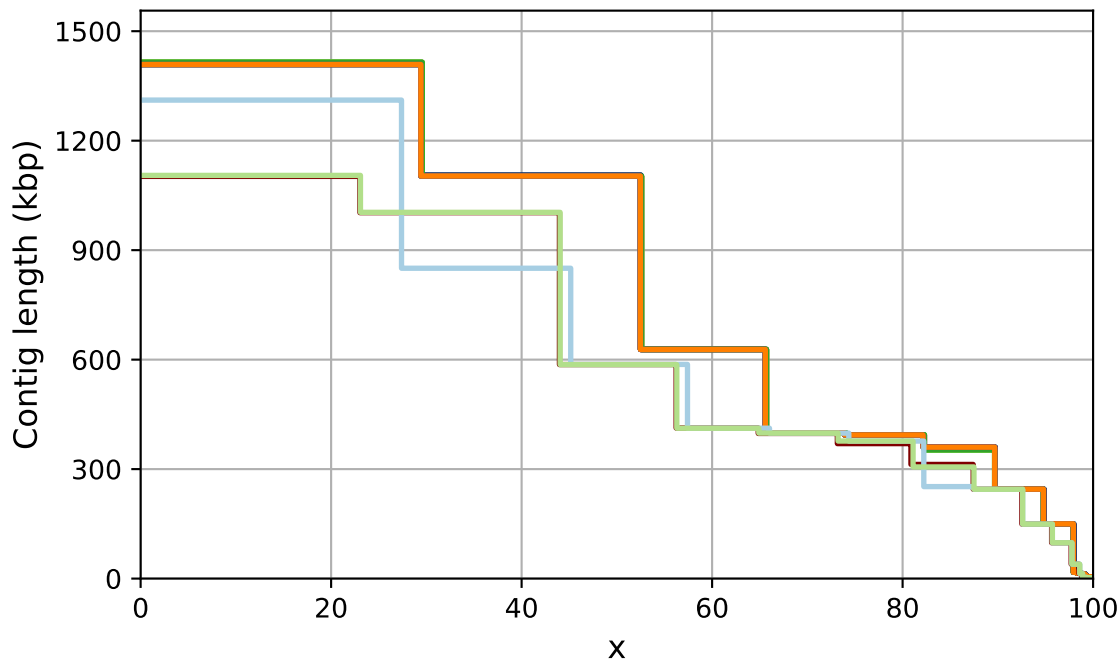
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

