

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	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357
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 (%)	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	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	16	15	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	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	4757850	4758004	4757772	4758987	4759001	4758968	4758591	4758589	4758585	4758094	4758113	4758100	4757969	4758019	4757945	4757915	4757917	4757899	4756101	4755953	4755682
# local misassemblies	8	8	8	8	8	8	8	8	8	7	8	7	9	8	8	8	8	8	20	22	28
# 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	19035741	19036395	19037087	19040709	19036842	19041453	19039557	19034814	19038047	19034042	19023312	19035426	19027818	19022248	19028473	19024517	19016007	19027981	23179358	23172242	23173126
Genome fraction (%)	98.918	98.920	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	98.896	98.893	98.886
Duplication ratio	1.075	1.074	1.075	1.075	1.075	1.074	1.075	1.075	1.075	1.074	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.074	1.057	1.059	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	411.43	403.99	407.24	409.99	415.45	409.20	406.61	410.11	409.56	405.50	409.73	409.67	415.19	420.10	415.85	416.79	417.11	412.48	460.72	467.60	468.34
# indels per 100 kbp	15.88	15.56	16.20	21.38	21.68	21.04	11.35	11.55	11.74	11.33	11.48	11.59	36.30	35.17	36.32	34.02	33.27	33.78	224.94	230.39	222.08
Largest alignment	1342442	1342439	1342445	1342514	1342526	1342523	1342474	1342473	1342470	1342473	1342472	1342473	1342280	1342309	1342278	1342298	1342314	1342322	1341458	1341467	1341035
Total aligned length	5034116	5031980	5032709	5032903	5036222	5032704	5032930	5034985	5034485	5029542	5031803	5031548	5033748	5036205	5034488	5034385	5035048	5032238	4951170	4957070	4956698
NGA50	745355	745359	745356	745409	745414	745402	745373	745370	745370	745375	745371	745372	745276	745293	745281	745271	745292	745290	744998	744860	745147
NGA75	611507	611506	611505	611518	611517	611516	611515	611515	611516	611515	611514	611516	611430	611448	611427	611449	611444	611438	433871	433978	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_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	16	15	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	19	19
# contig misassemblies	16	15	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	19	19
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	14	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	16	17	17
# c. inversions	2	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	0
# s. relocations	0	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	0
# s. inversions	0	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	1
Misassembled contigs length	4757850	4758004	4757772	4758987	4759001	4758968	4758591	4758589	4758585	4758094	4758113	4758100	4757969	4758019	4757945	4757915	4757917	4757899	4756101	4755953	4755682	
# possibly misassembled contigs	1	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	4	4	4	4	4	4	4	14	14	18
# local misassemblies	8	8	8	8	8	8	8	8	8	7	8	7	9	8	8	8	8	8	20	22	28	
# 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	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	0
# misassemblies caused by fragmented reference	14	14	14	14	14	14	14	14	14	14	14	14	13	14	14	14	14	14	11	10	8	
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	19279	18931	19083	19212	19468	19175	19054	19218	19192	19002	19200	19197	19456	19686	19487	19531	19546	19329	21584	21906	21939	
# indels	744	729	759	1002	1016	986	532	541	550	531	538	543	1701	1648	1702	1594	1559	1583	10538	10793	10403	
# indels (<= 5 bp)	645	634	661	906	919	892	443	451	460	440	447	451	1610	1555	1609	1503	1469	1492	10362	10621	10232	
# indels (> 5 bp)	99	95	98	96	97	94	89	90	90	91	91	92	91	93	93	91	90	91	176	172	171	
Indels length	5273	5245	5294	5545	5575	5500	4955	4972	4984	5056	5001	5073	6296	6250	6319	6164	6107	6136	19244	19522	18654	

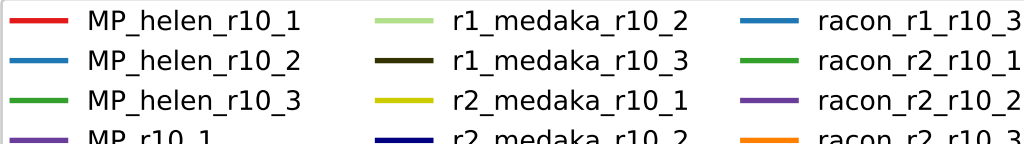
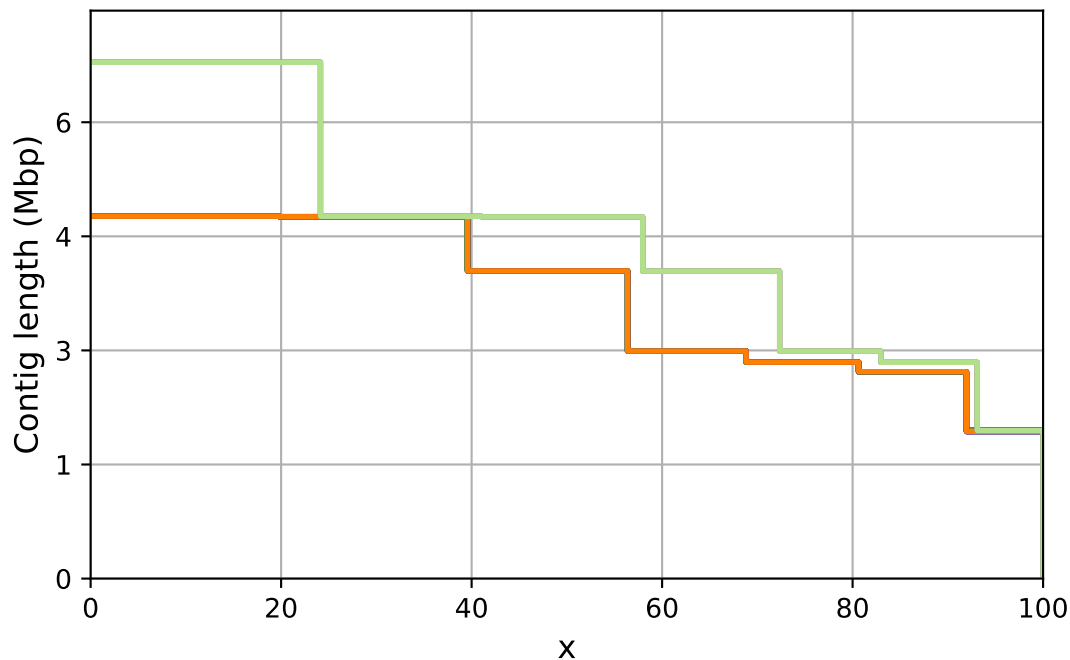
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

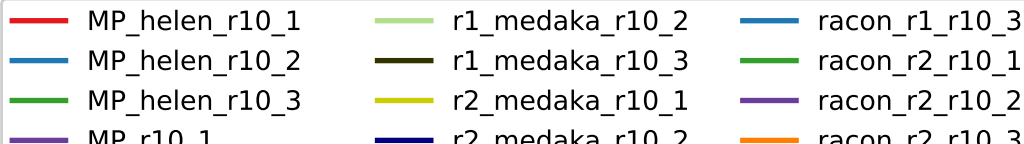
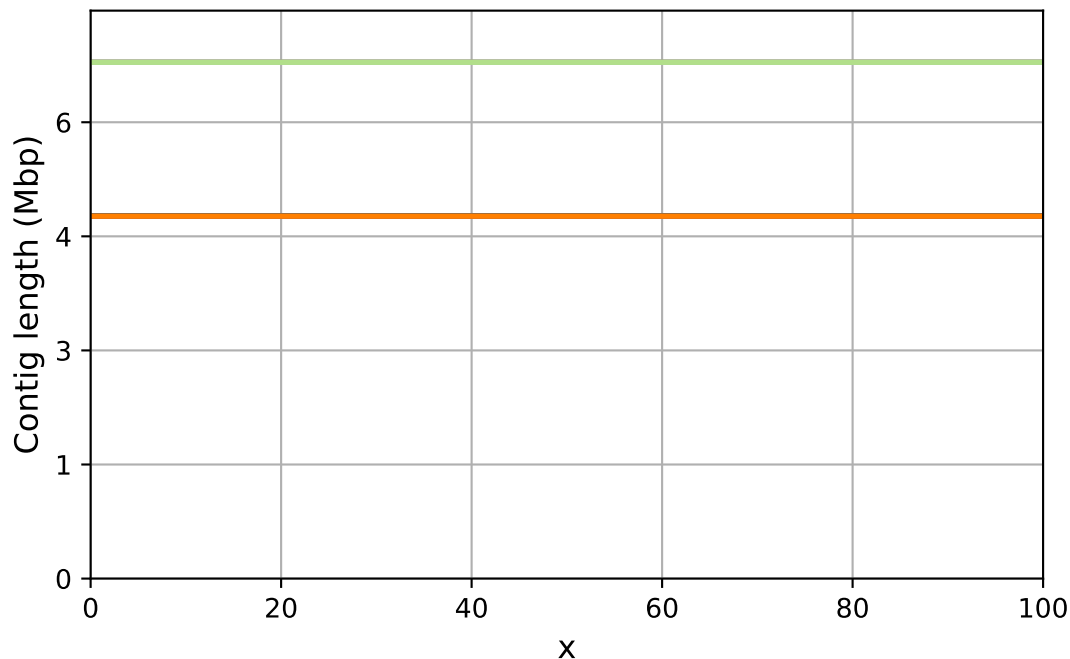
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	19035741	19036395	19037087	19040709	19036842	19041453	19039557	19034814	19038047	19034042	19023312	19035426	19027818	19022248	19028473	19024517	19016007	19027981	23179358	23172242	23173126
# 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).

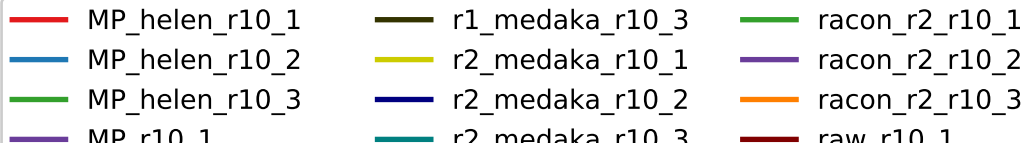
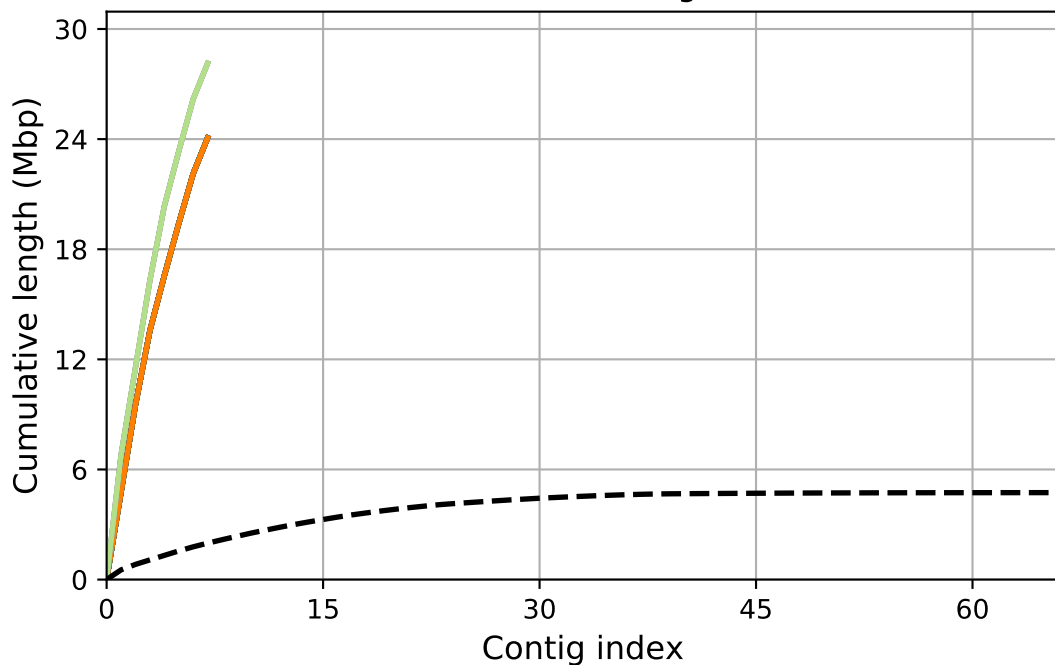
Nx



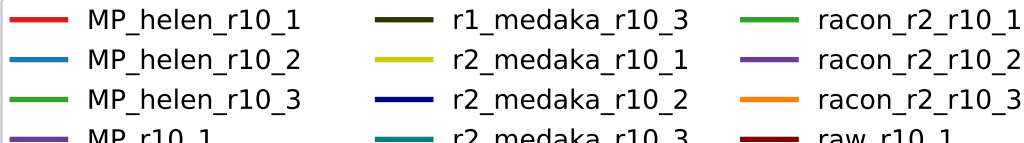
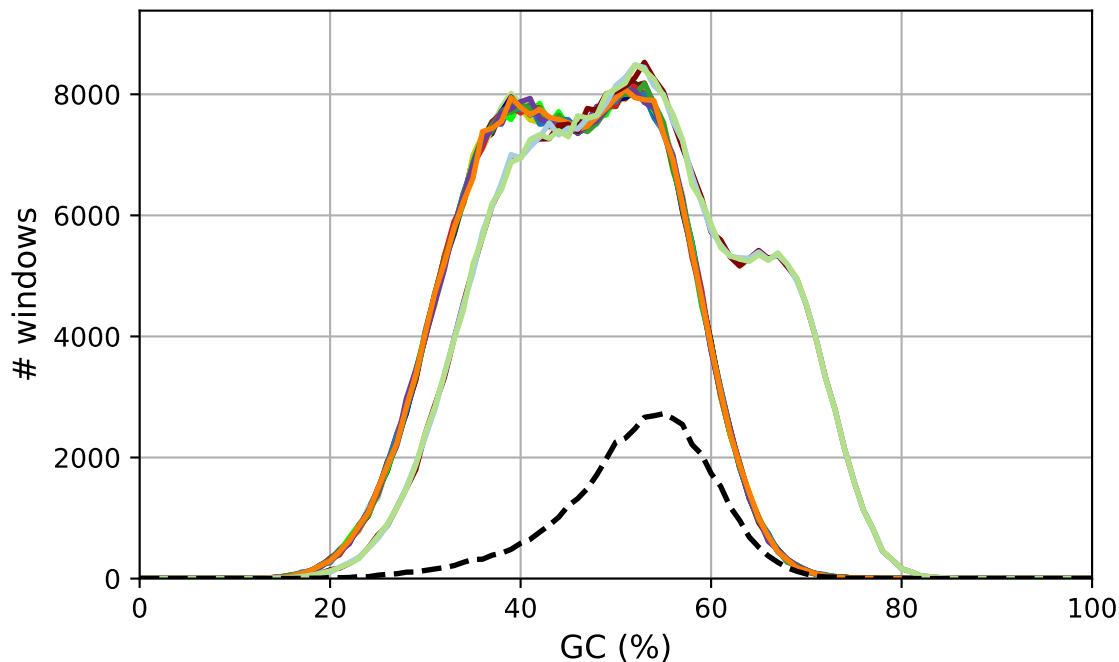
NGx



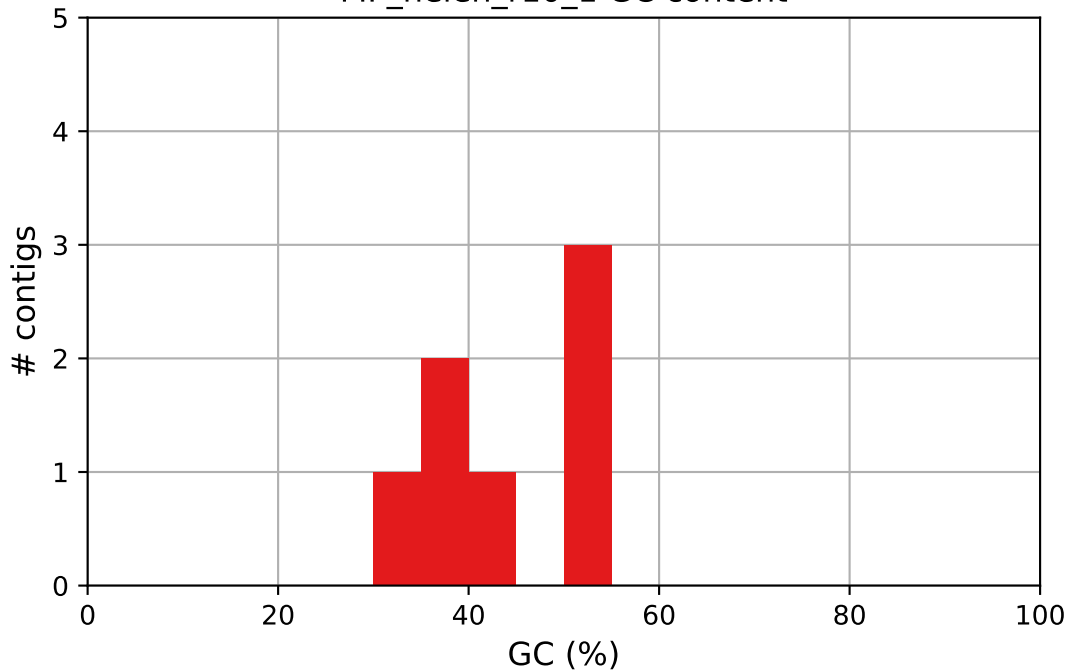
Cumulative length



GC content

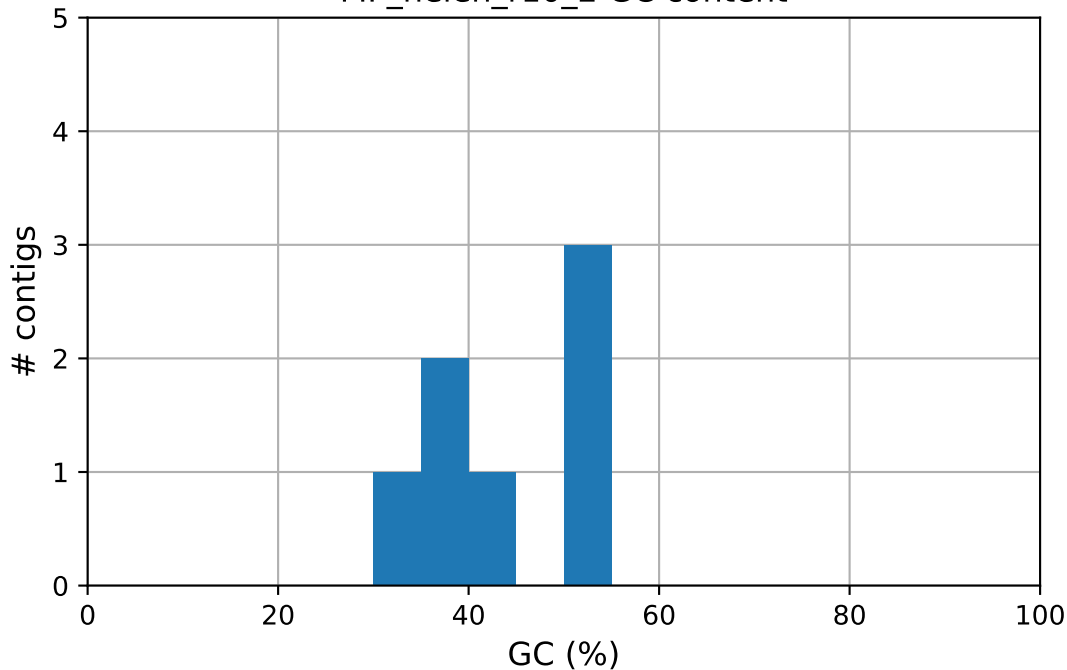


MP_helen_r10_1 GC content



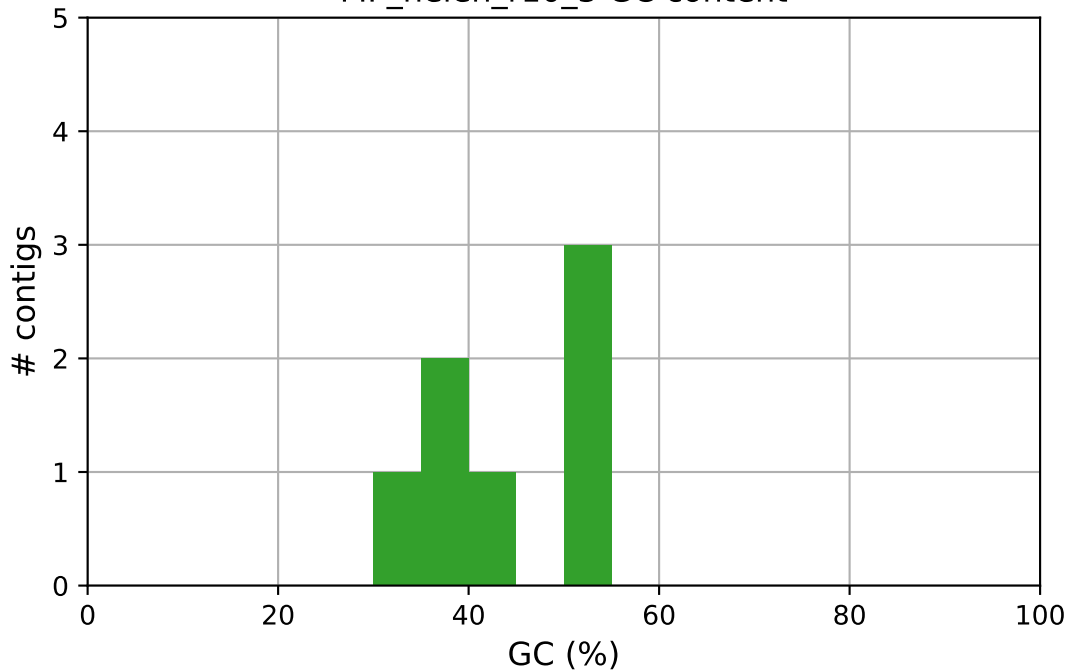
MP_helen_r10_1

MP_helen_r10_2 GC content



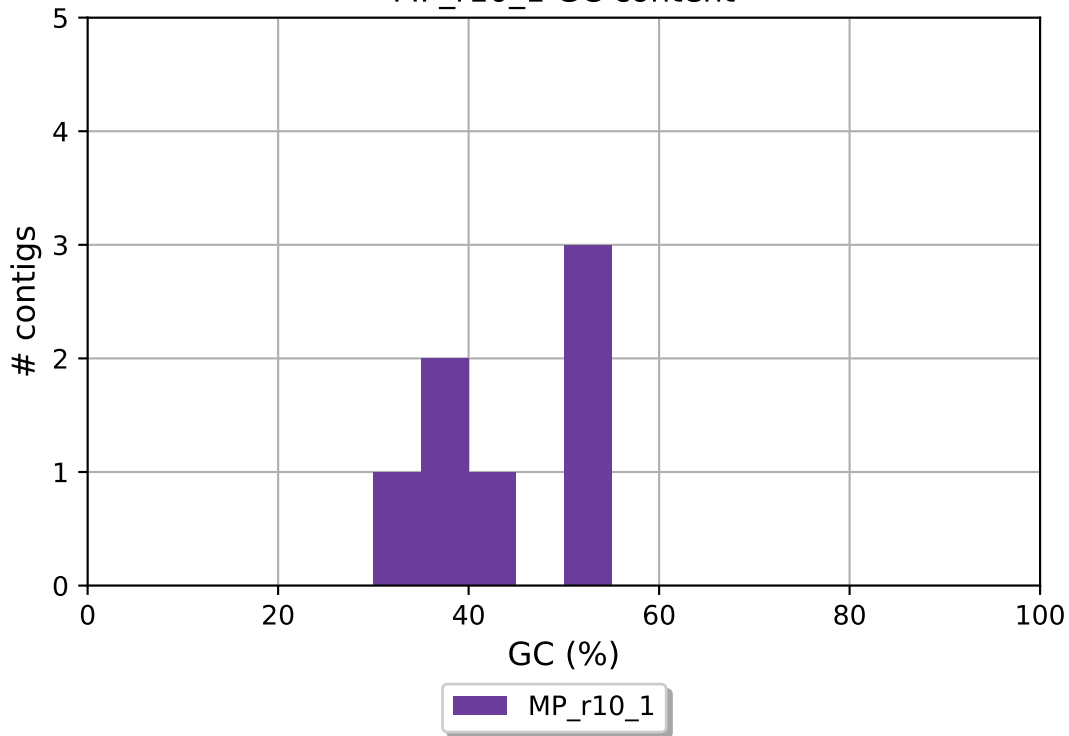
MP_helen_r10_2

MP_helen_r10_3 GC content

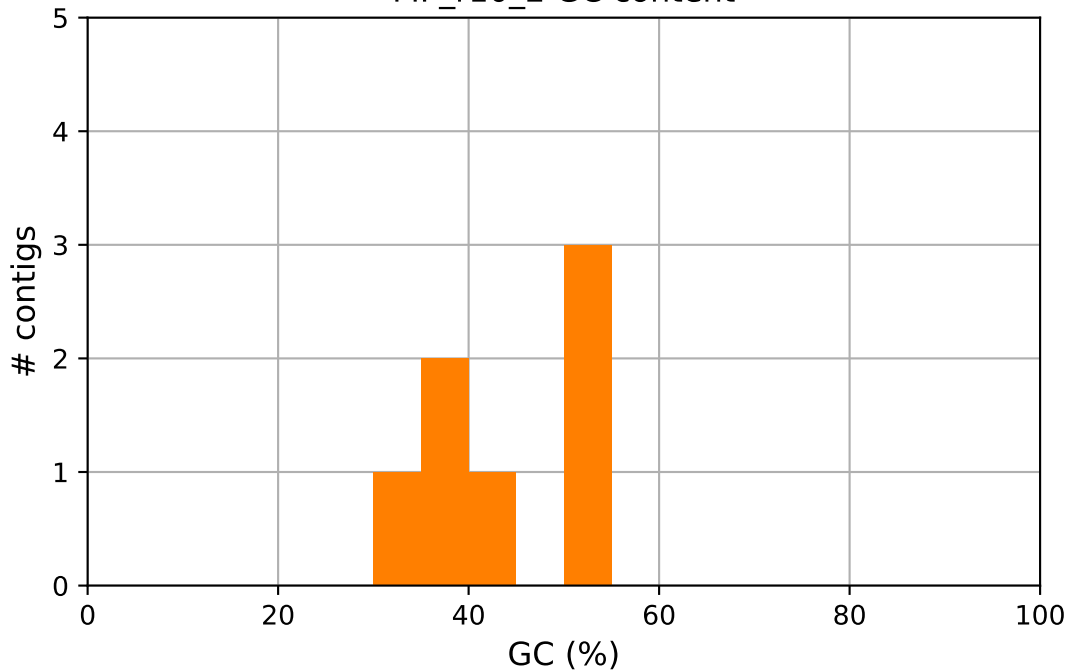


MP_helen_r10_3

MP_r10_1 GC content

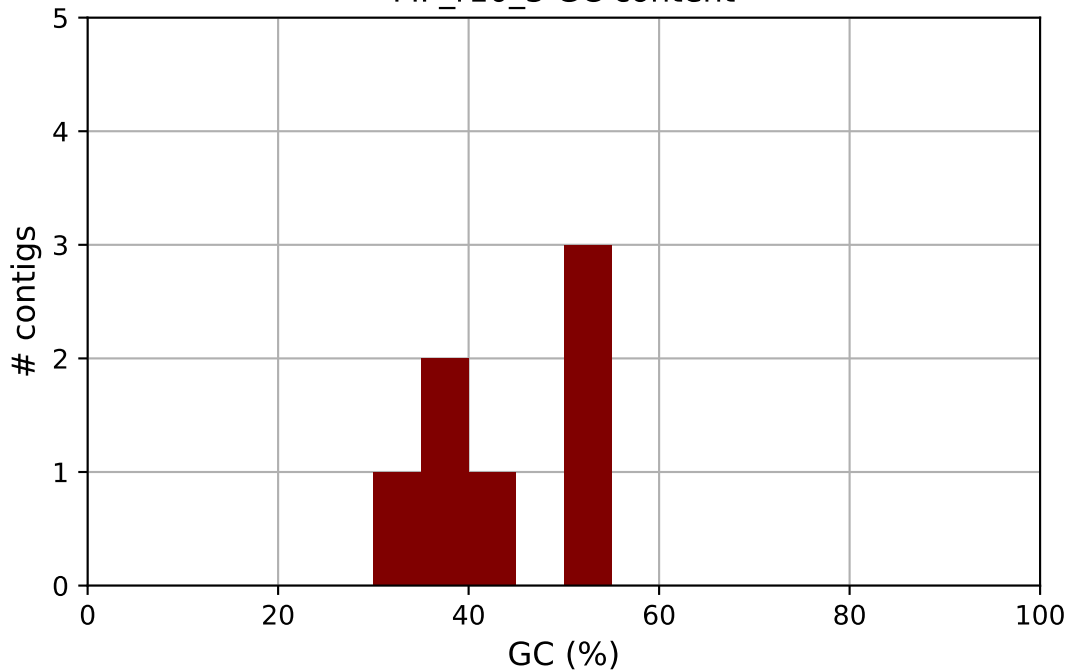


MP_r10_2 GC content



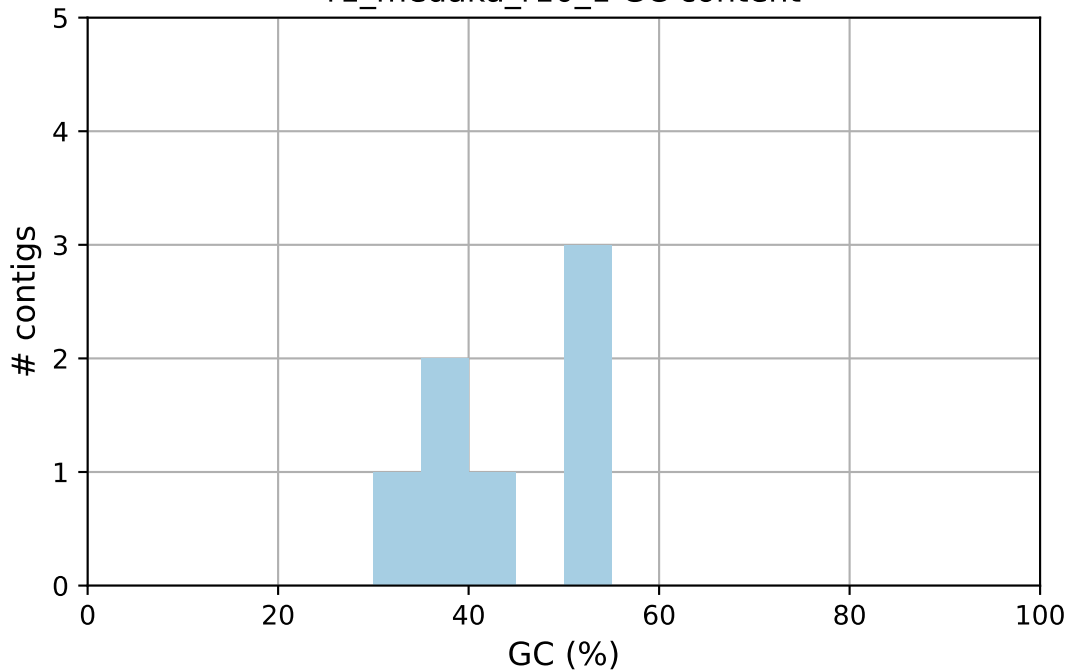
MP_r10_2

MP_r10_3 GC content



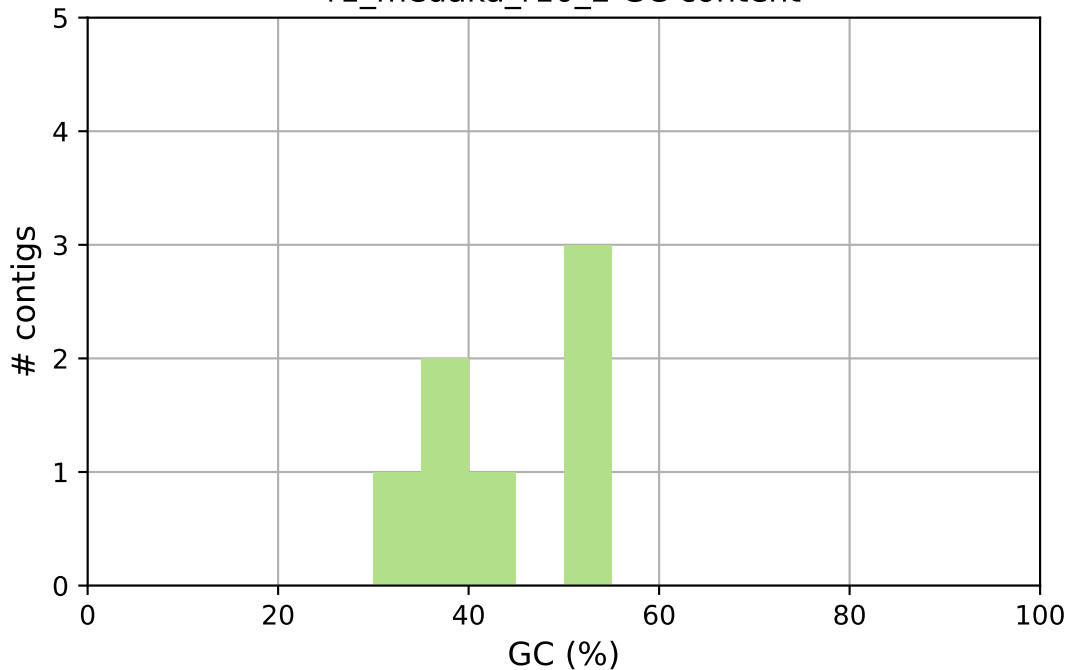
MP_r10_3

r1_medaka_r10_1 GC content



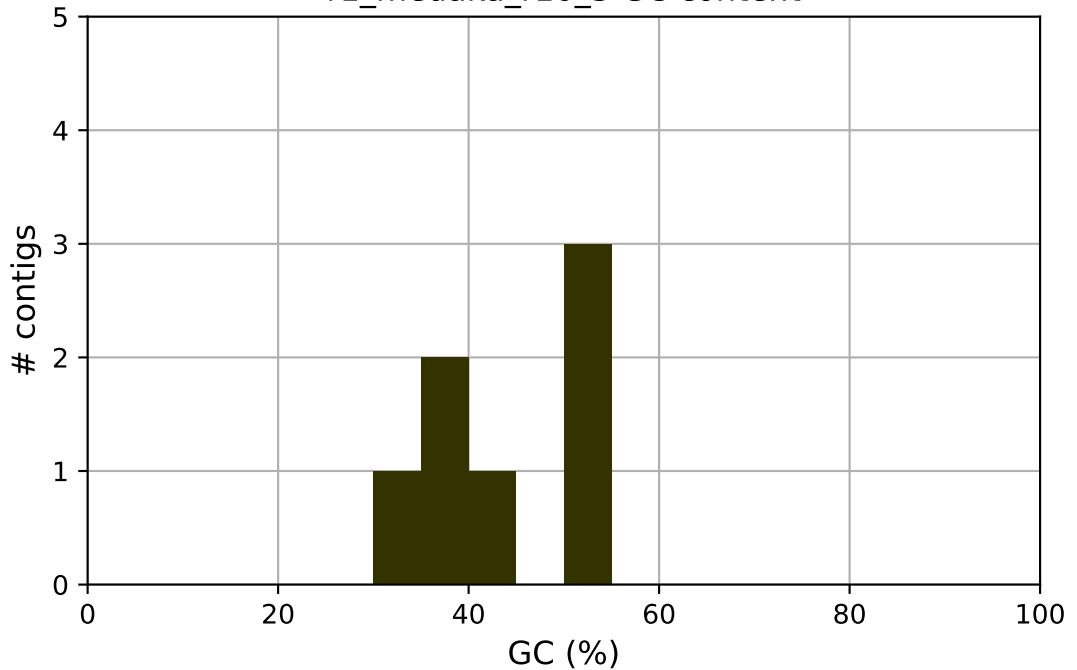
r1_medaka_r10_1

r1_medaka_r10_2 GC content



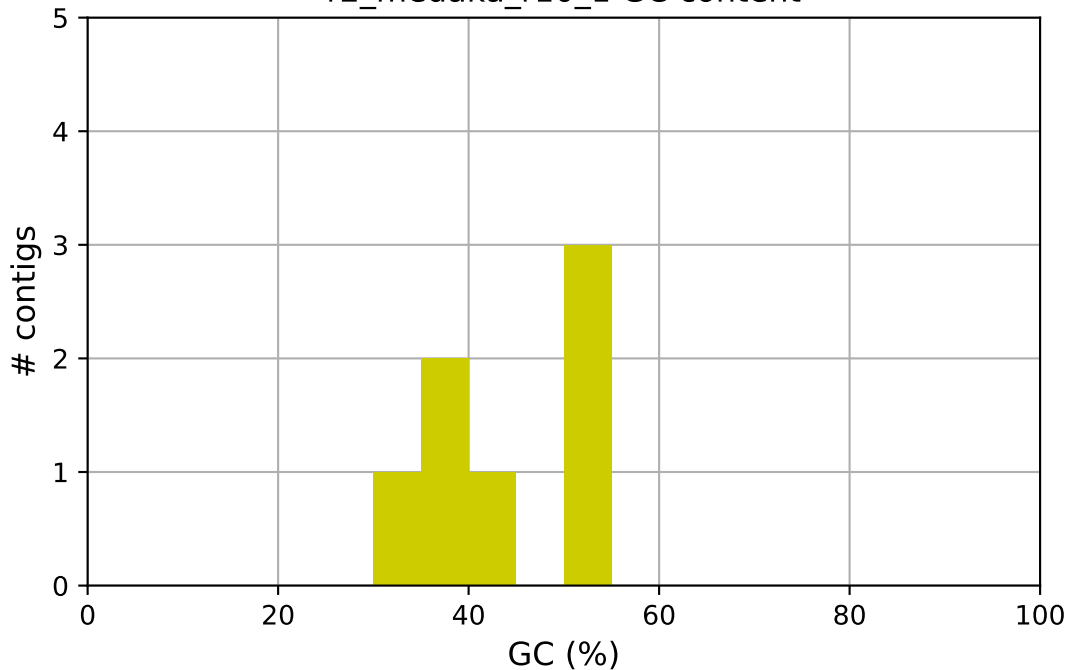
r1_medaka_r10_2

r1_medaka_r10_3 GC content



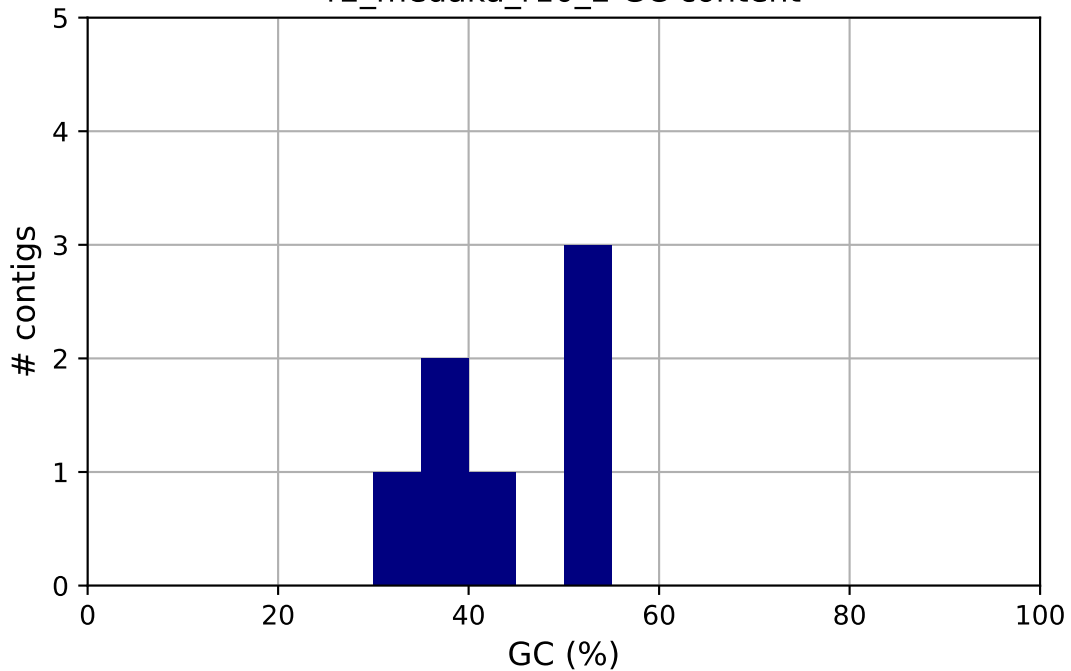
r1_medaka_r10_3

r2_medaka_r10_1 GC content



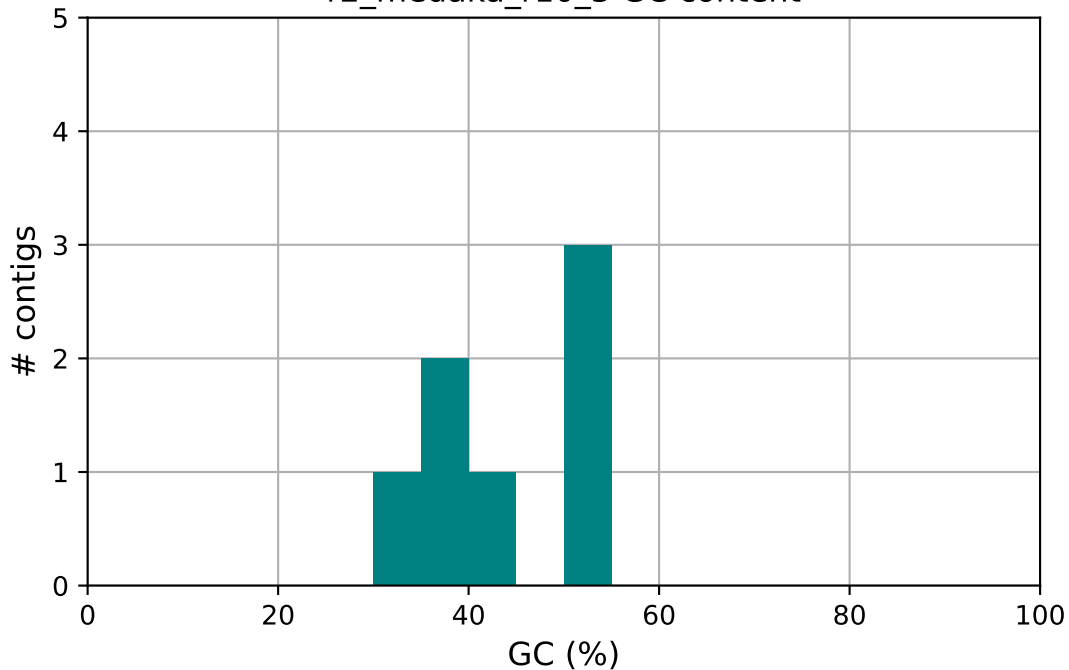
r2_medaka_r10_1

r2_medaka_r10_2 GC content



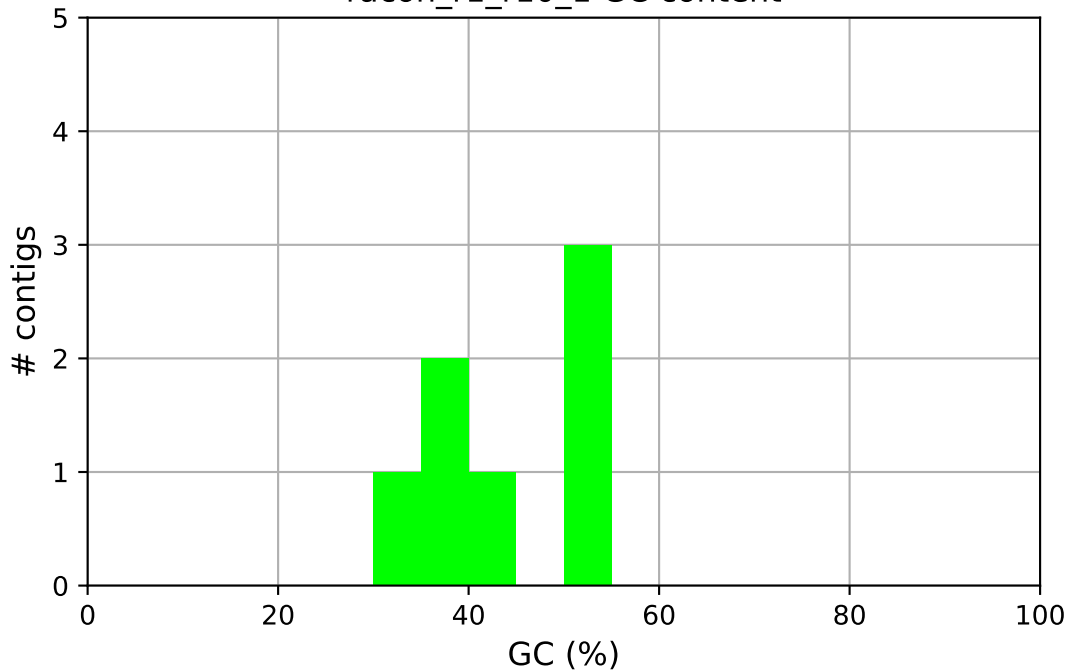
r2_medaka_r10_2

r2_medaka_r10_3 GC content



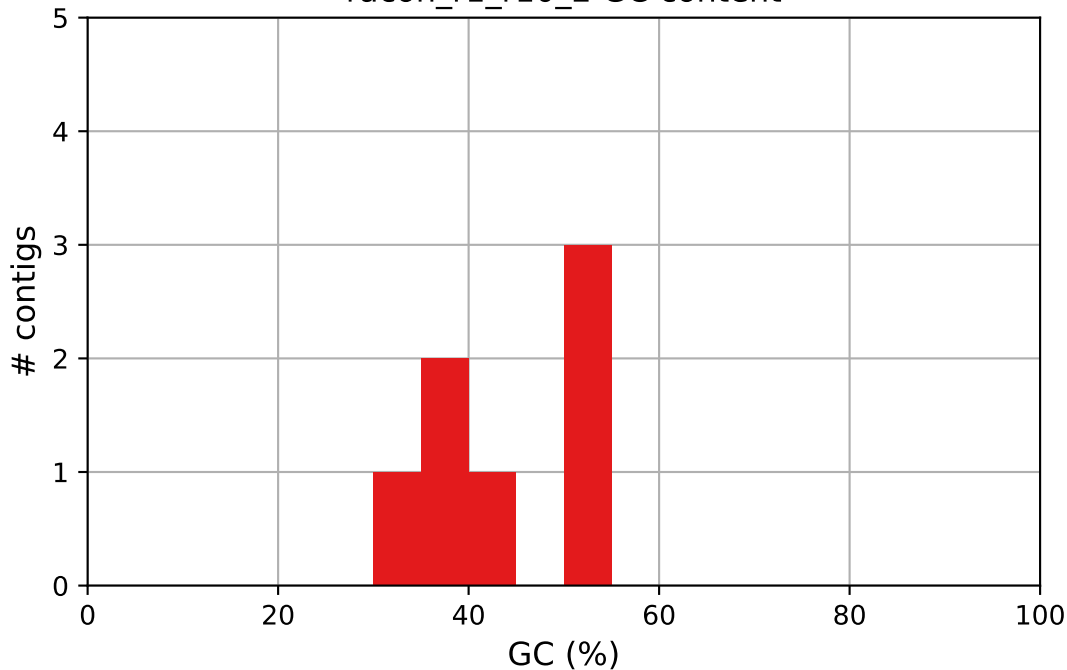
r2_medaka_r10_3

racon_r1_r10_1 GC content



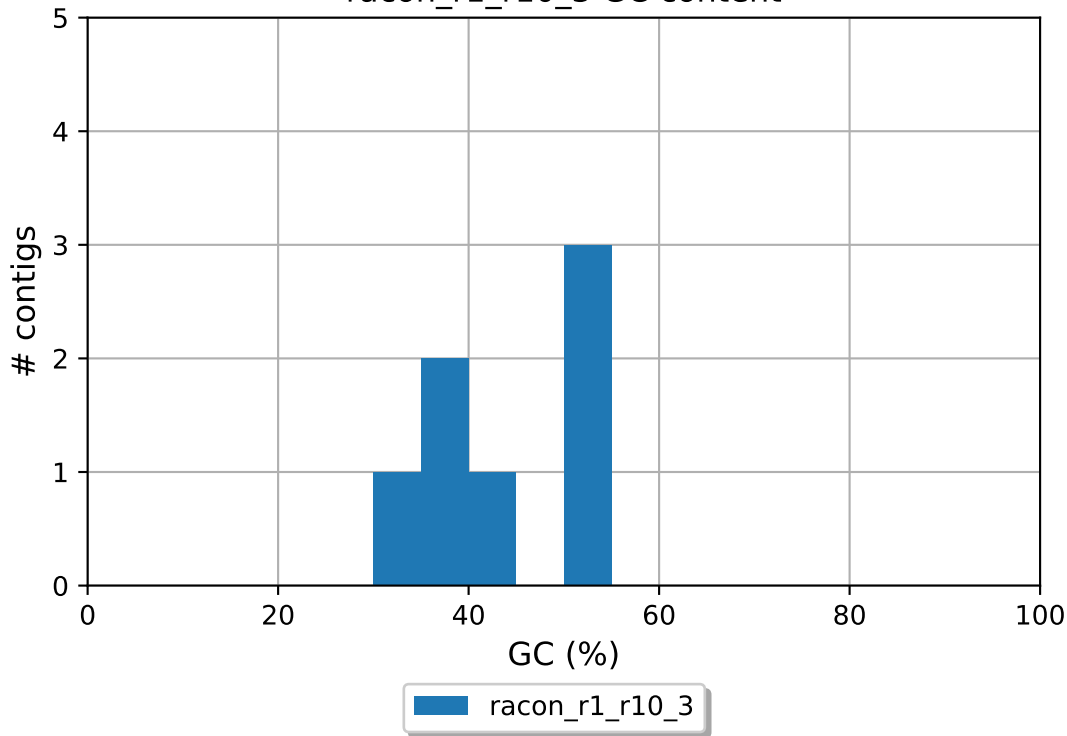
racon_r1_r10_1

racon_r1_r10_2 GC content

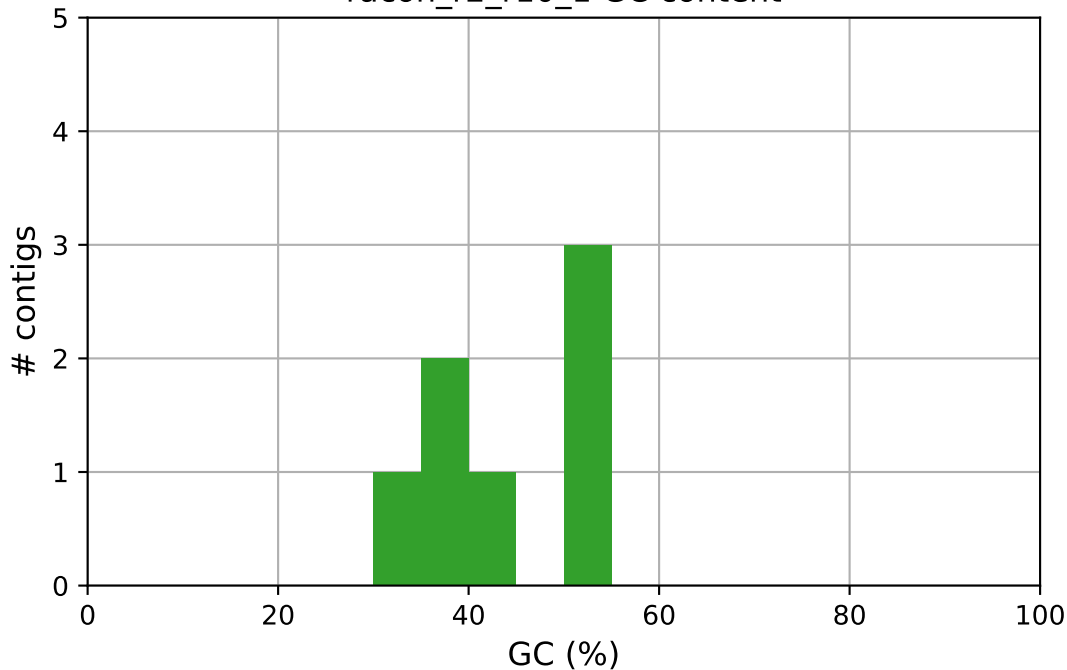


racon_r1_r10_2

racon_r1_r10_3 GC content

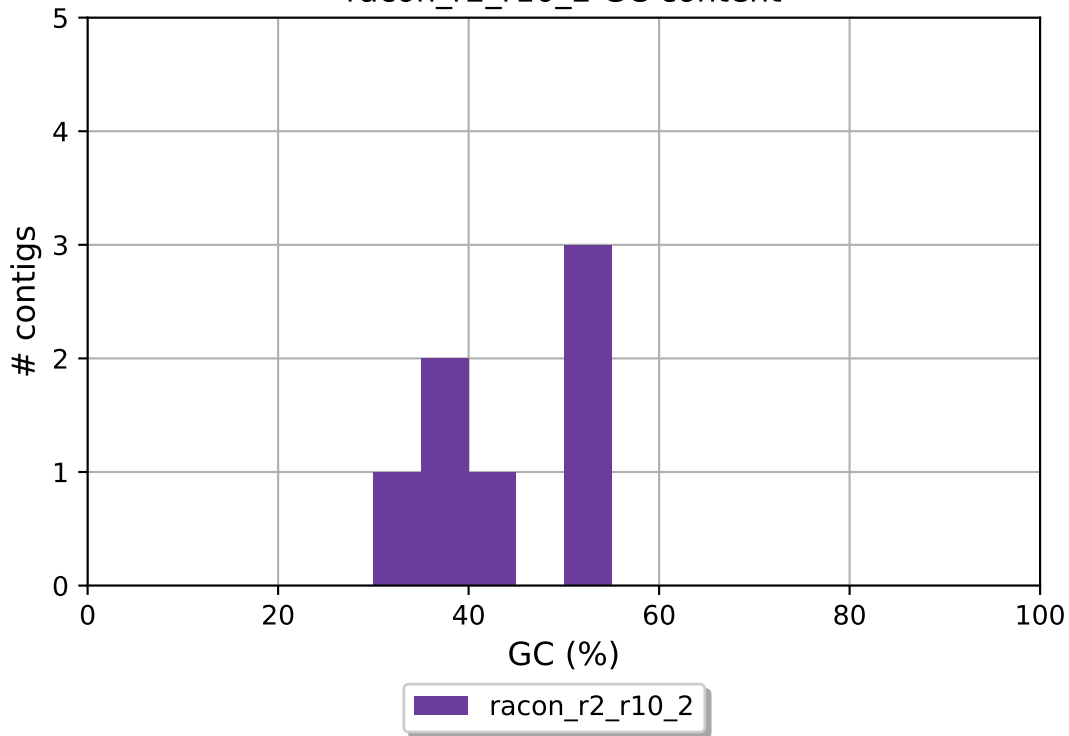


racon_r2_r10_1 GC content

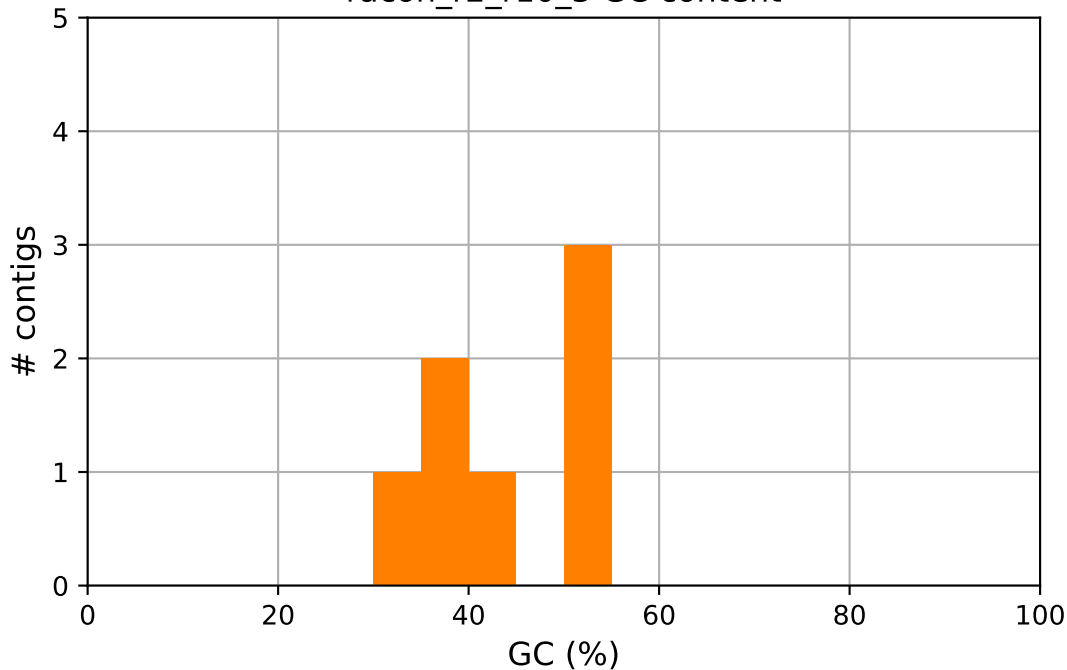


racon_r2_r10_1

racon_r2_r10_2 GC content

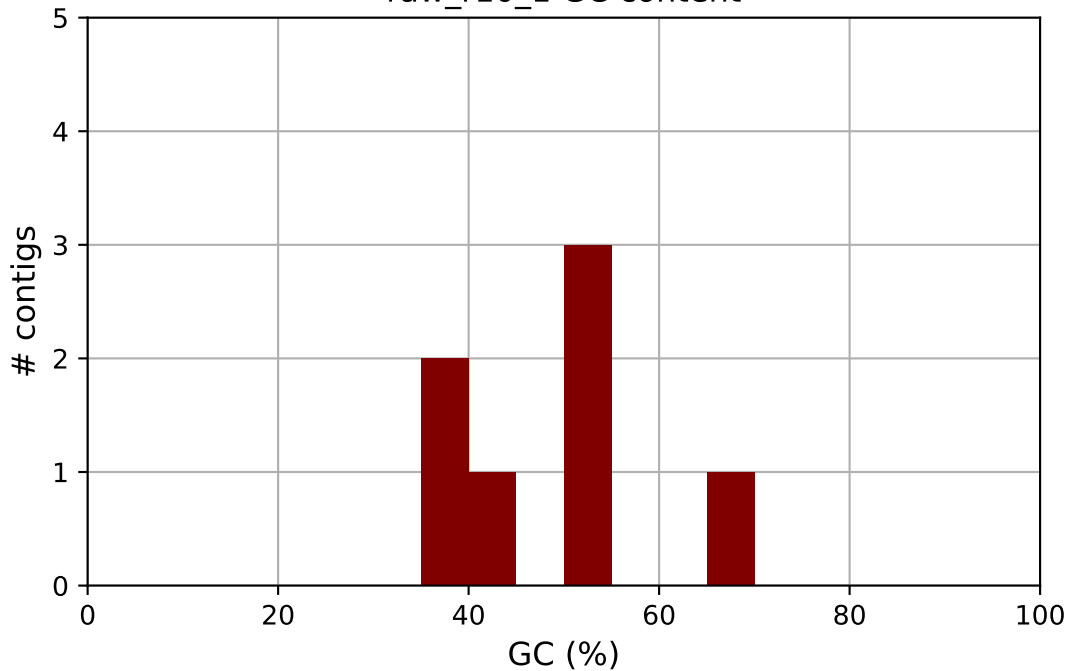


racon_r2_r10_3 GC content



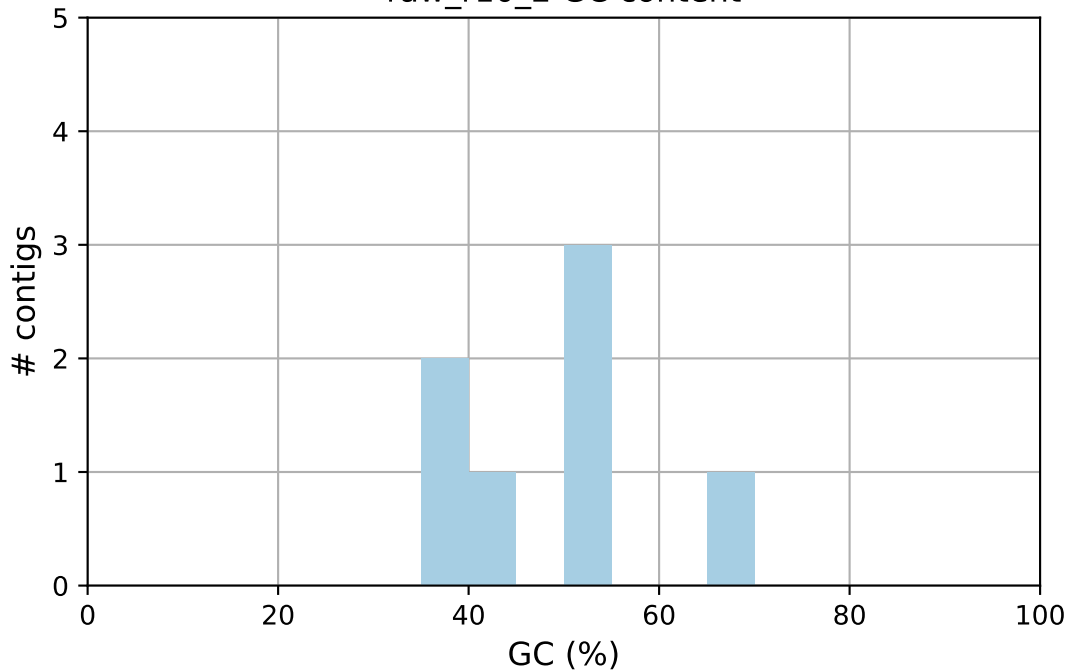
racon_r2_r10_3

raw_r10_1 GC content



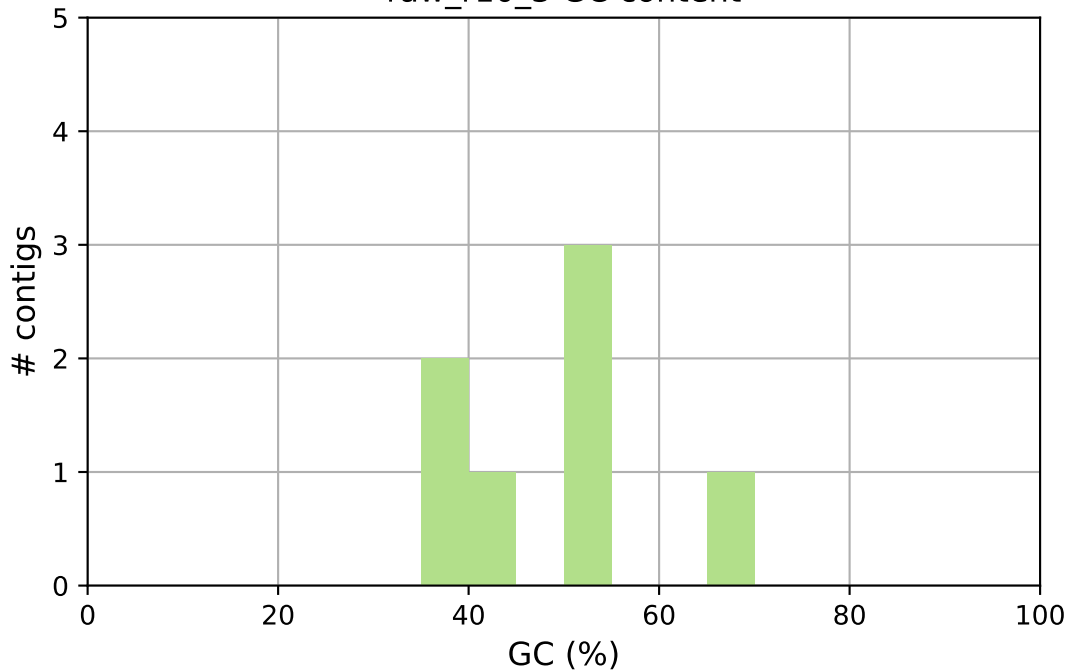
raw_r10_1

raw_r10_2 GC content



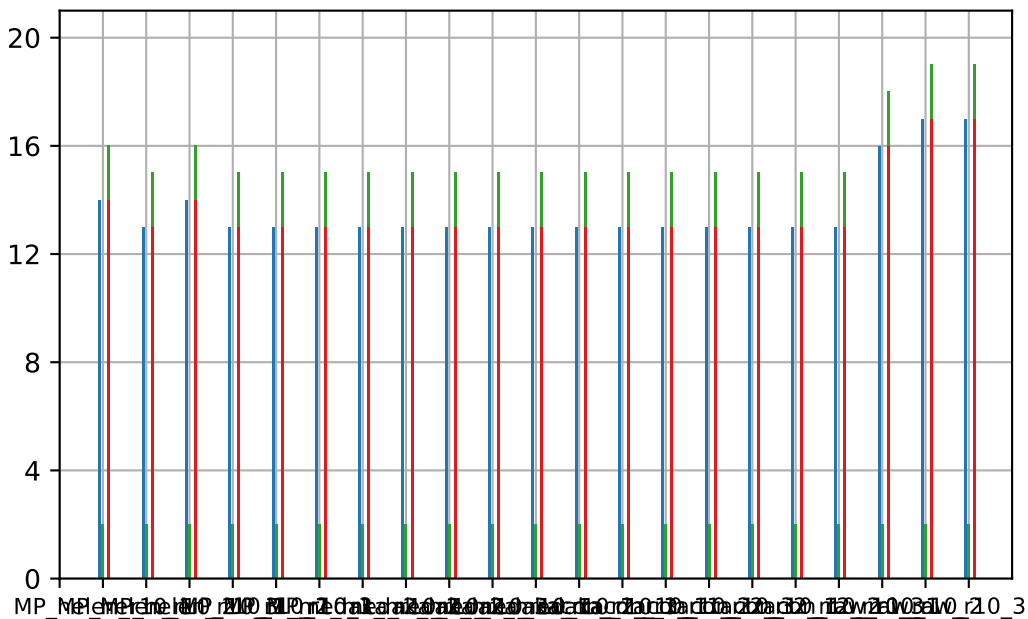
raw_r10_2

raw_r10_3 GC content

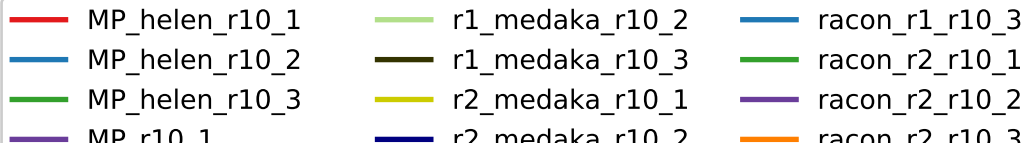
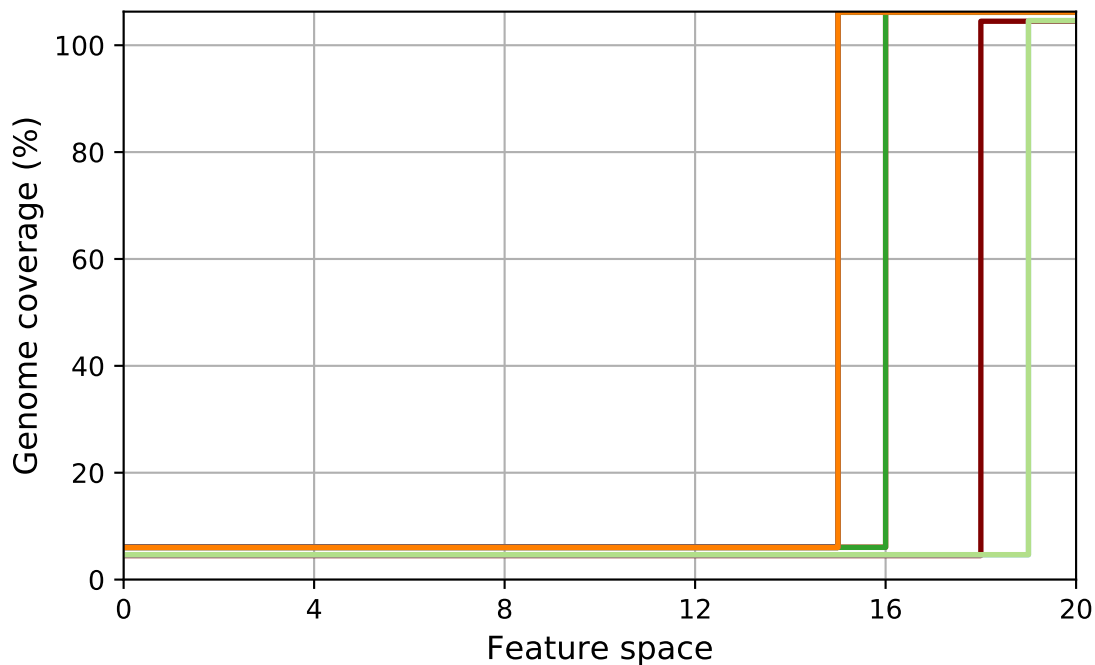


raw_r10_3

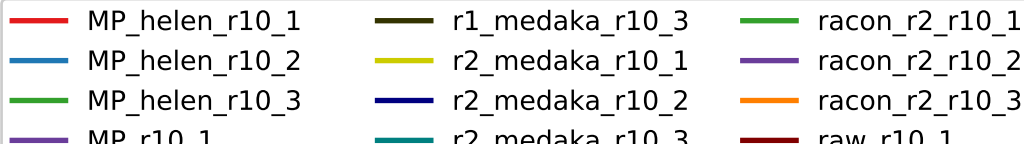
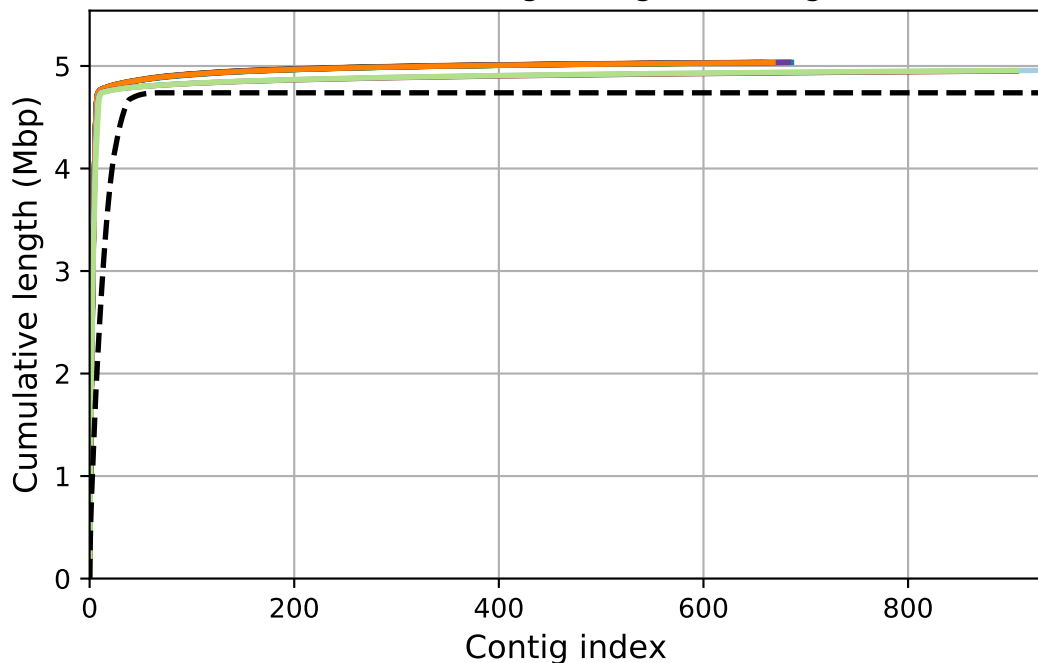
Misassemblies



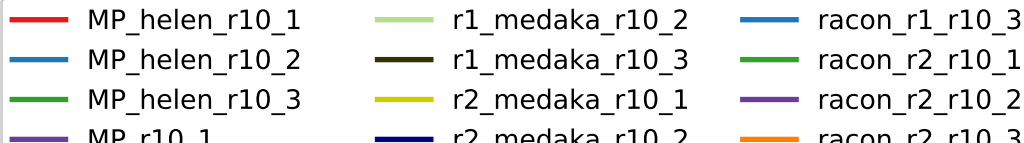
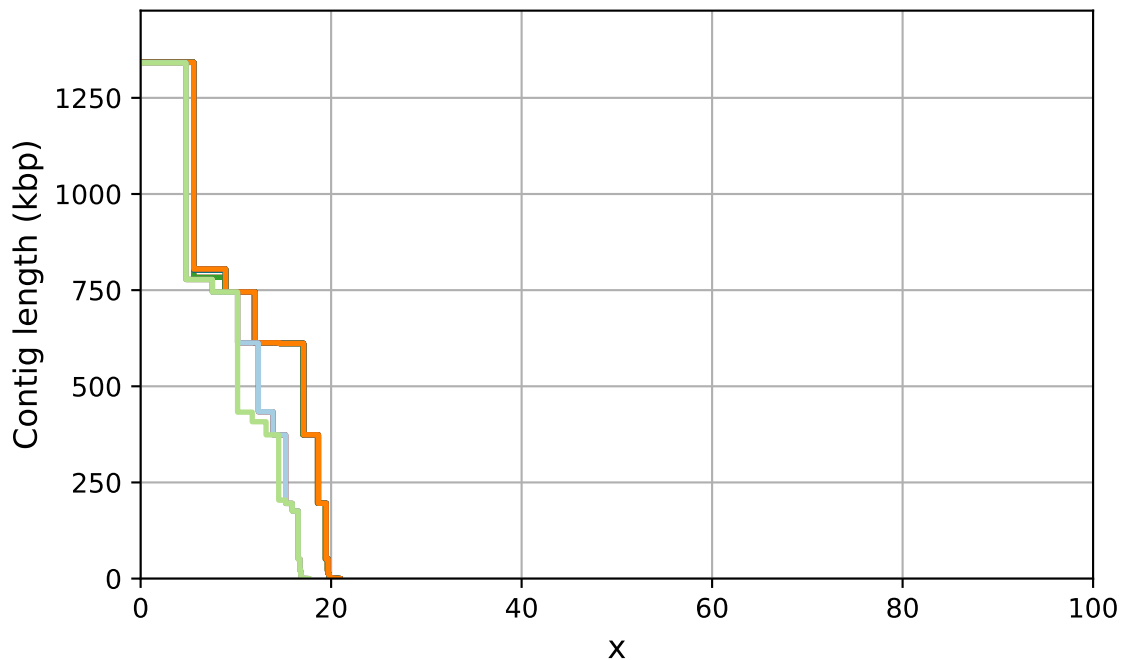
FRCurve (misassemblies)



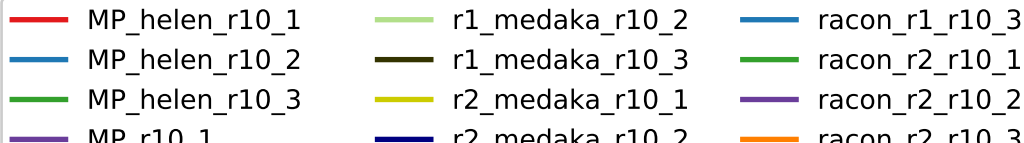
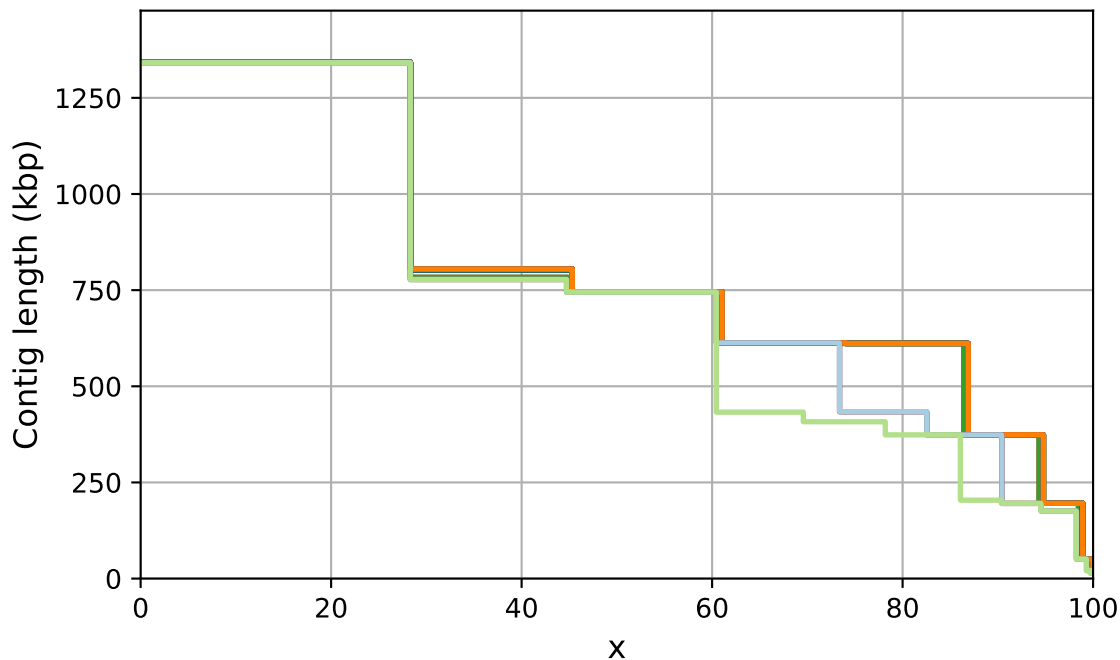
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

