

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	24062559	24061175	24061500
Total length (>= 10000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 25000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 50000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
# 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	4763429	4763874	4763424
Total length	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
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	44.77	44.77	44.77
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4043031	4042943	4042477
NG50	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
N75	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2843358	2843843	2843366
NG75	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2843358	2843843	2843366
# local misassemblies	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	21	20	21
# 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	5	6	6	6	6	6	6	5	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	21094534	21093007	21094962	21099150	21098261	21099468	21097110	21094764	21096732	21089872	21081977	21093488	21090751	21087724	21090506	21083807	21076351	21085887	21153285	21150527	21152169
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.954	99.930	99.949	99.931
Duplication ratio	1.056	1.057	1.056	1.056	1.056	1.056	1.057	1.056	1.057	1.057	1.057	1.057	1.055	1.055	1.055	1.056	1.056	1.056	1.032	1.033	1.032
# 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	249.18	249.89	247.34	248.12	248.68	248.22	249.68	248.72	250.99	251.88	250.78	251.88	234.03	234.60	240.45	250.03	248.76	247.94	152.00	151.55	149.73
# indels per 100 kbp	14.94	15.75	15.04	15.54	15.51	15.61	14.30	14.09	14.16	14.12	13.59	14.41	20.90	21.57	22.03	22.18	22.96	22.10	127.55	125.47	126.62
Largest alignment	2594042	2594005	2594042	2594071	2594073	2594072	2594080	2594080	2594077	2594077	2594078	2594078	2593978	2593970	2593977	2593960	2593995	2594002	2589370	2589961	2589447
Total aligned length	2972248	2972326	2971759	2971428	2971769	2971655	2972343	2972002	2972767	2973106	2972561	2972881	2967781	2967700	2969422	2972067	2971674	2971254	2907588	2908962	2907645
NGA50	2594042	2594005	2594042	2594071	2594073	2594072	2594080	2594080	2594077	2594077	2594078	2594078	2593978	2593970	2593977	2593960	2593995	2594002	2589370	2589961	2589447
NGA75	2594042	2594005	2594042	2594071	2594073	2594072	2594080	2594080	2594077	2594077	2594078	2594078	2593978	2593970	2593977	2593960	2593995	2594002	2589370	2589961	2589447
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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

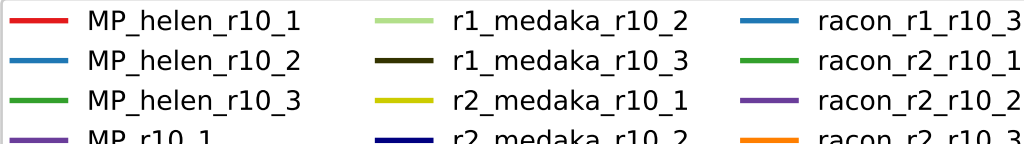
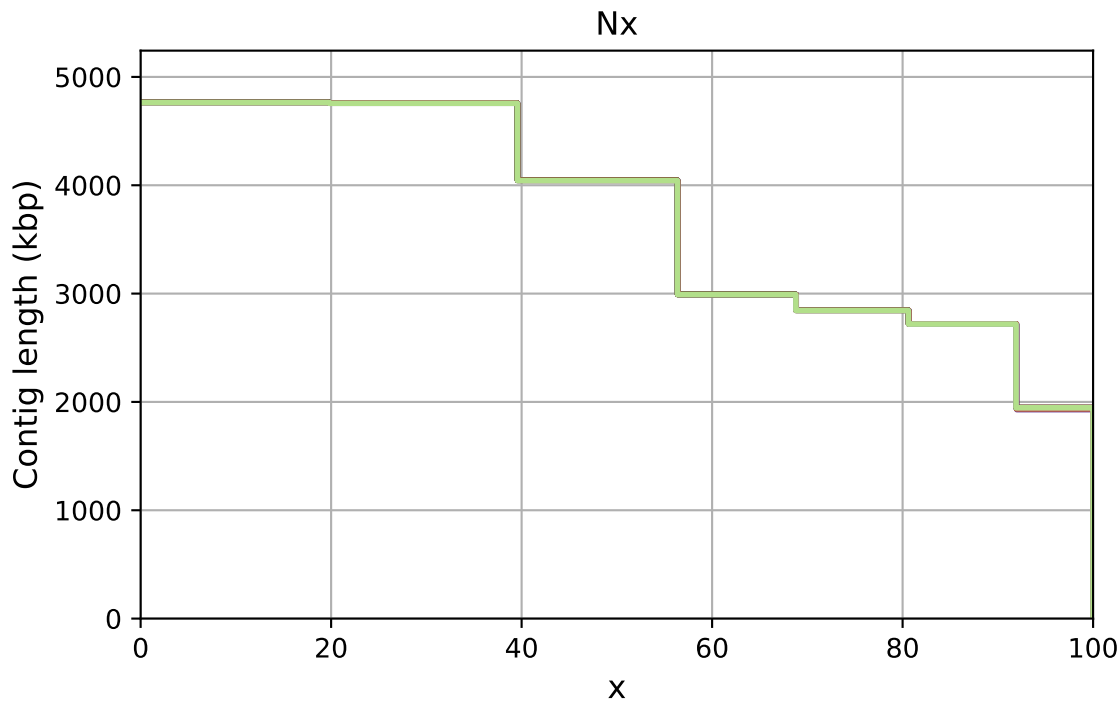
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2843358	2843843	2843366
# possibly misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
# possible misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	6	6
# local misassemblies	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	21	20	21
# 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	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	10	11	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6
# mismatches	7023	7043	6971	6993	7009	6996	7037	7010	7074	7099	7068	7099	6596	6612	6777	7047	7011	6988	4283	4271	4219
# indels	421	444	424	438	437	440	403	397	399	398	383	406	589	608	621	625	647	623	3594	3536	3568
# indels (<= 5 bp)	381	403	384	398	397	400	363	357	359	358	344	366	552	571	585	588	609	585	3557	3502	3532
# indels (> 5 bp)	40	41	40	40	40	40	40	40	40	40	39	40	37	37	36	37	38	38	37	34	36
Indels length	2381	2417	2385	2399	2398	2401	2333	2313	2328	2327	2296	2341	2512	2525	2564	2598	2620	2570	6231	6061	6103

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).

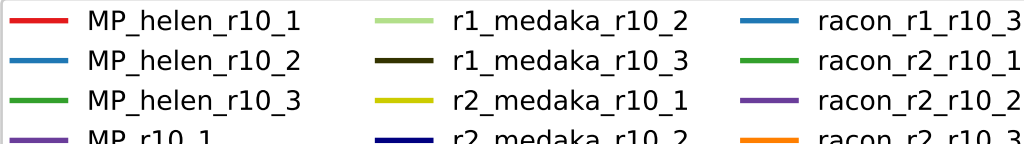
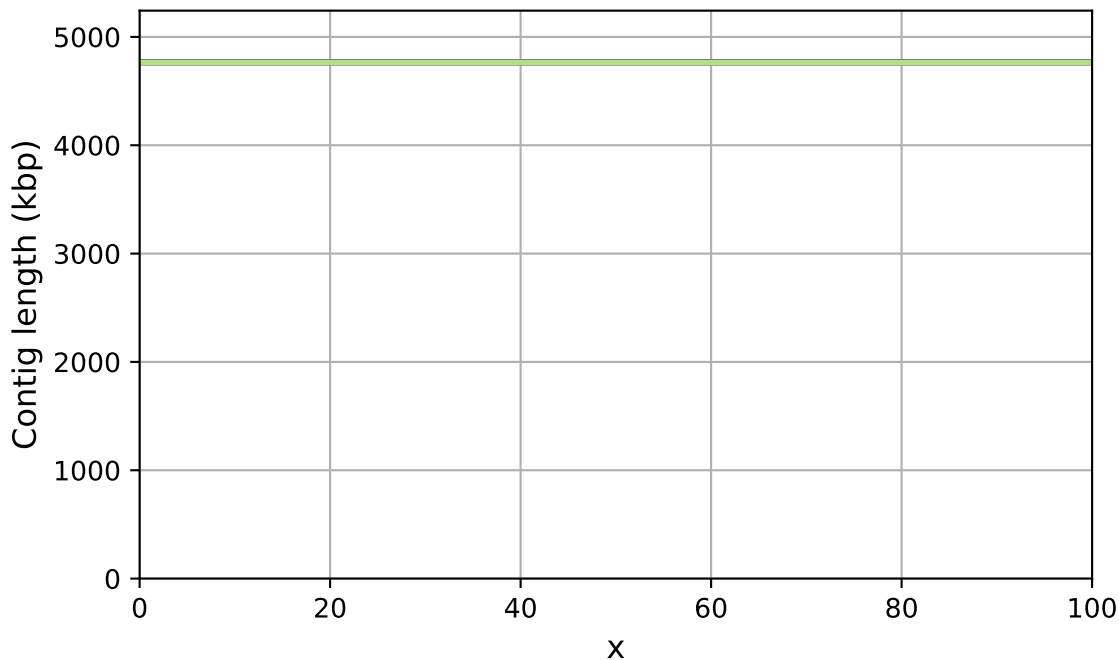
Unaligned report

	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	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	7	7
Partially unaligned length	21094534	21093007	21094962	21099150	21098261	21099468	21097110	21094764	21096732	21089872	21081977	21093488	21090751	21087724	21090506	21083807	21076351	21085887	21153285	21150527	21152169
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

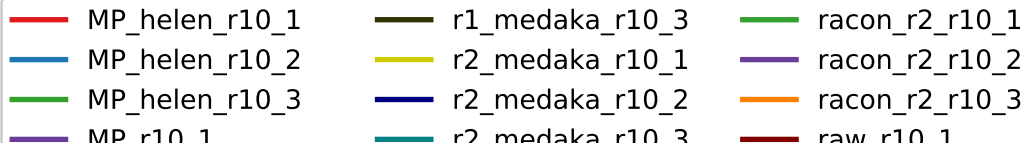
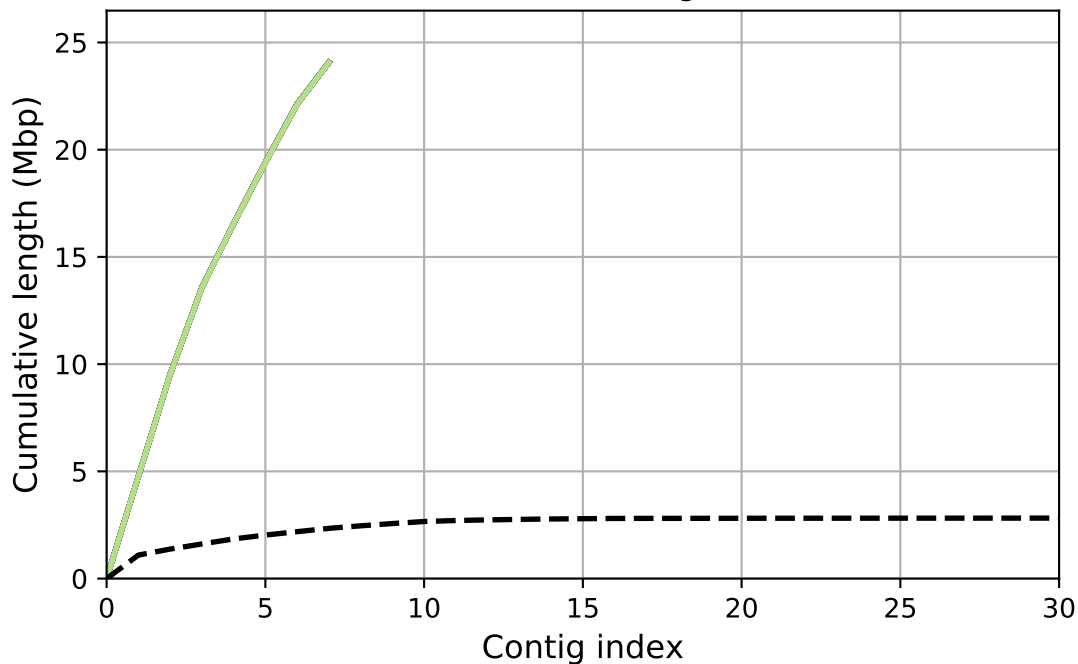
All statistics are based on contigs of size ≥ 5000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



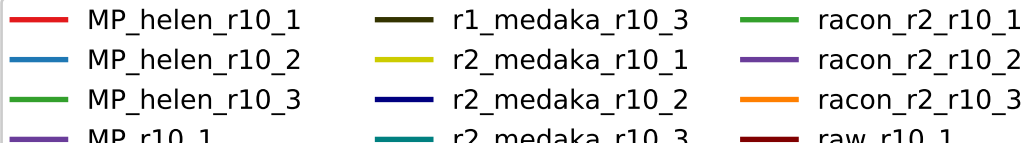
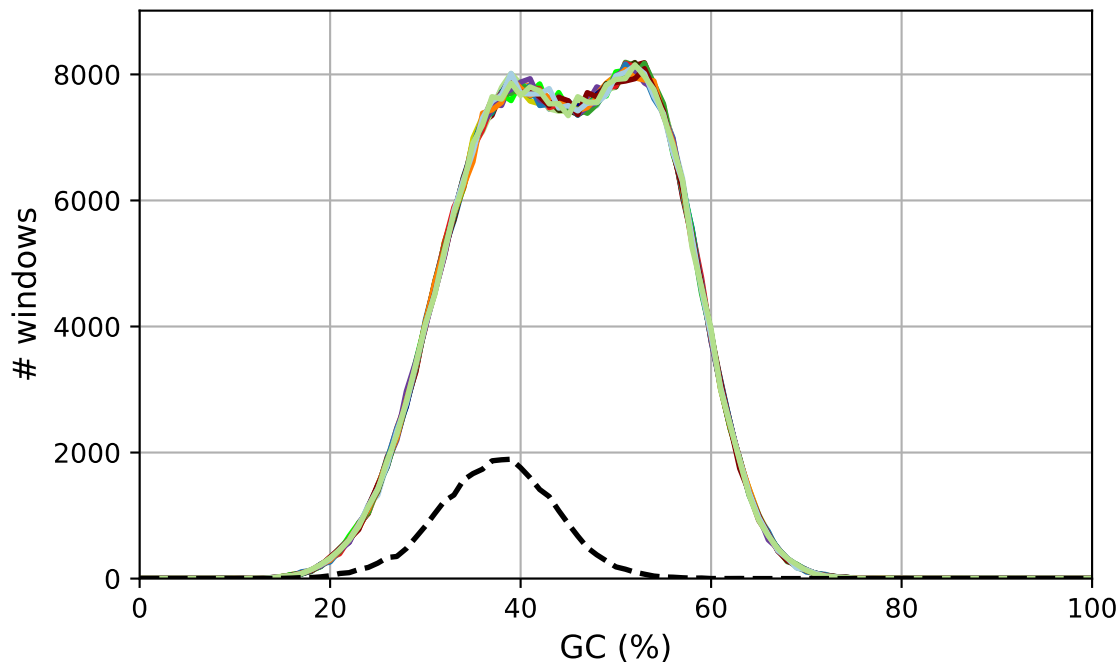
NGx



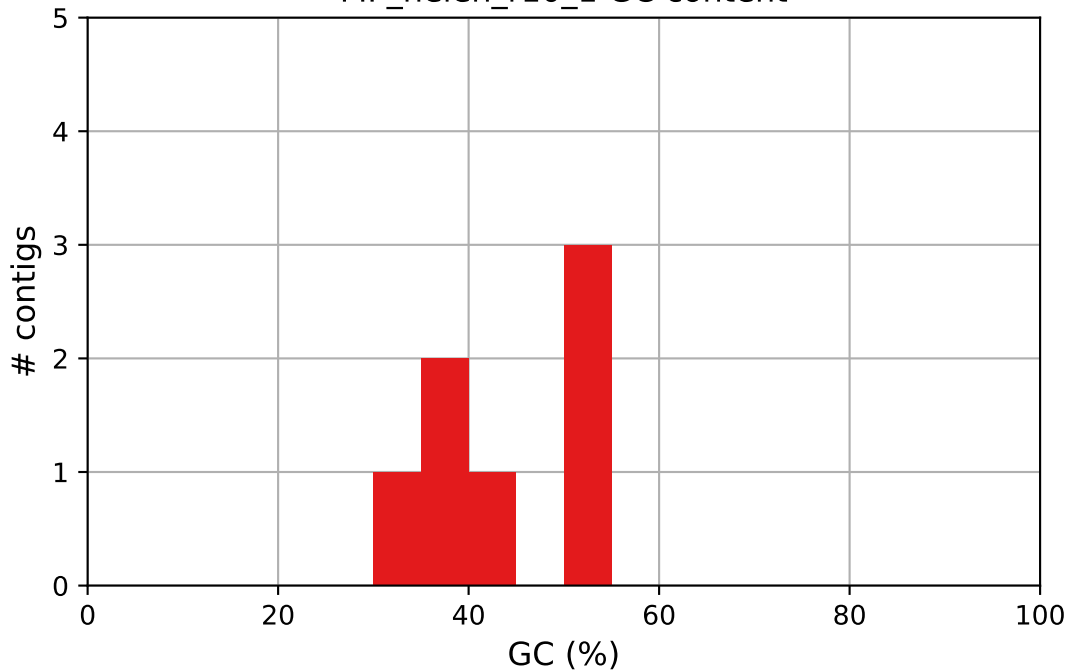
Cumulative length



GC content

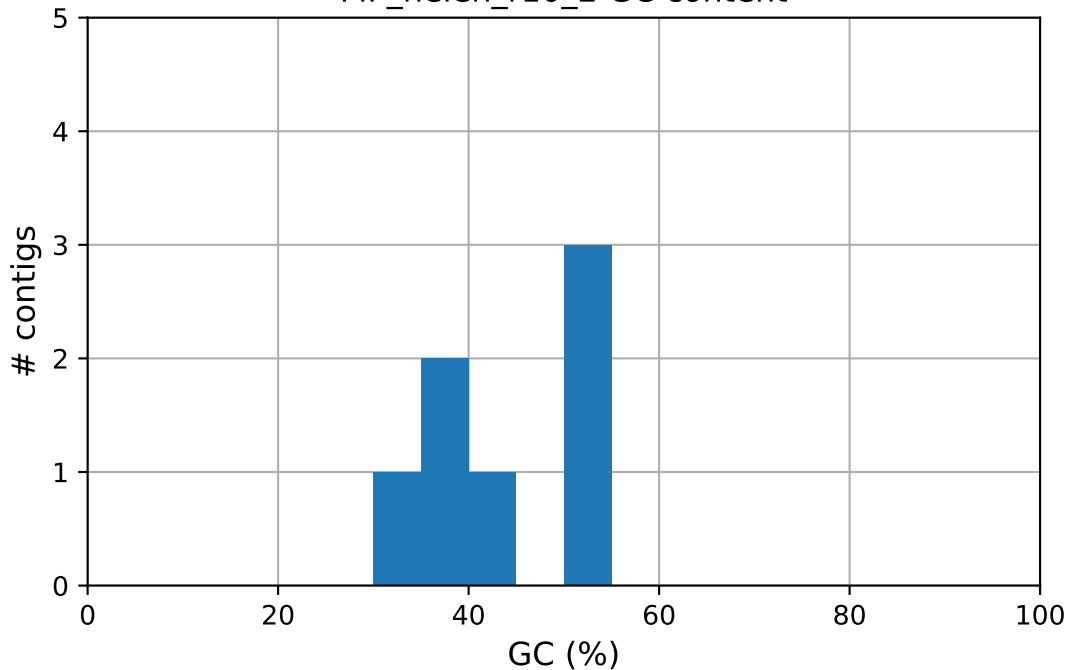


MP_helen_r10_1 GC content



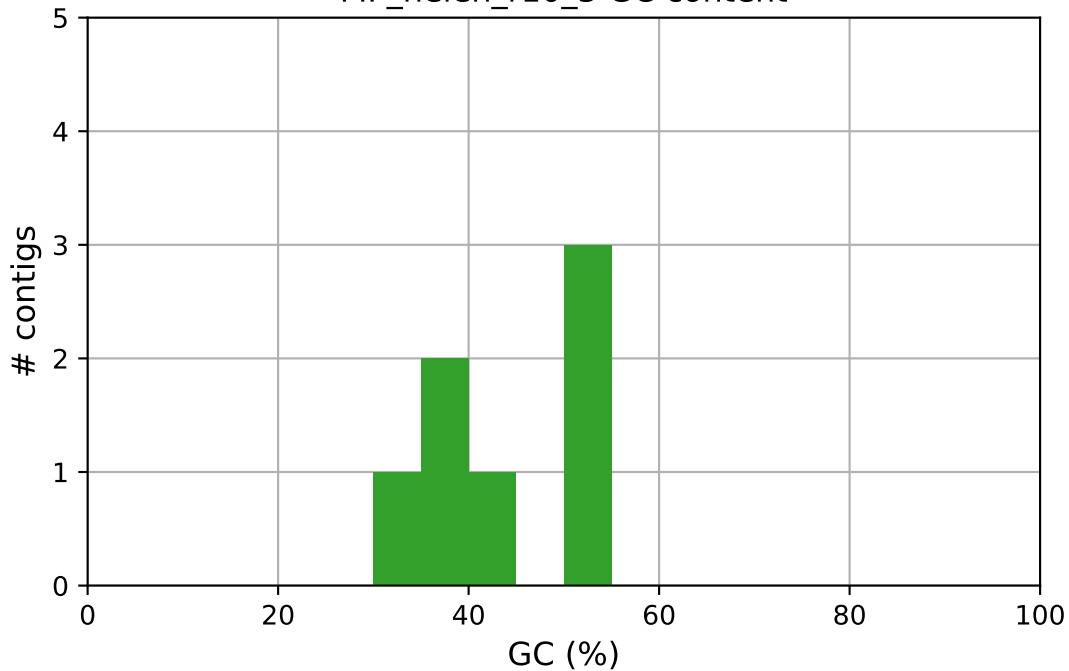
MP_helen_r10_1

MP_helen_r10_2 GC content



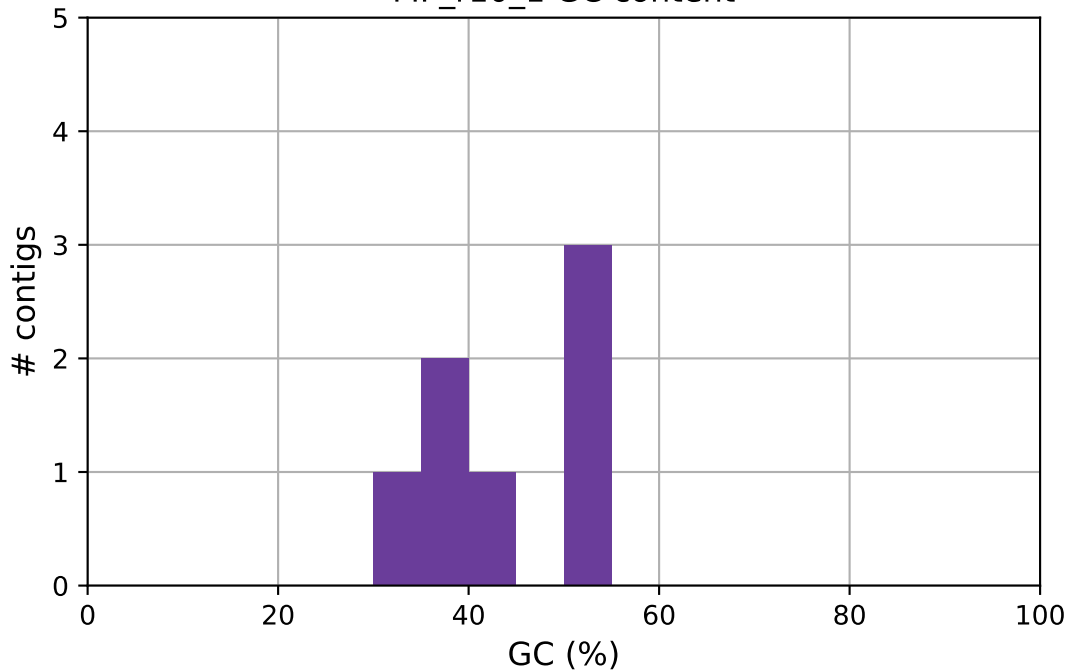
MP_helen_r10_2

MP_helen_r10_3 GC content



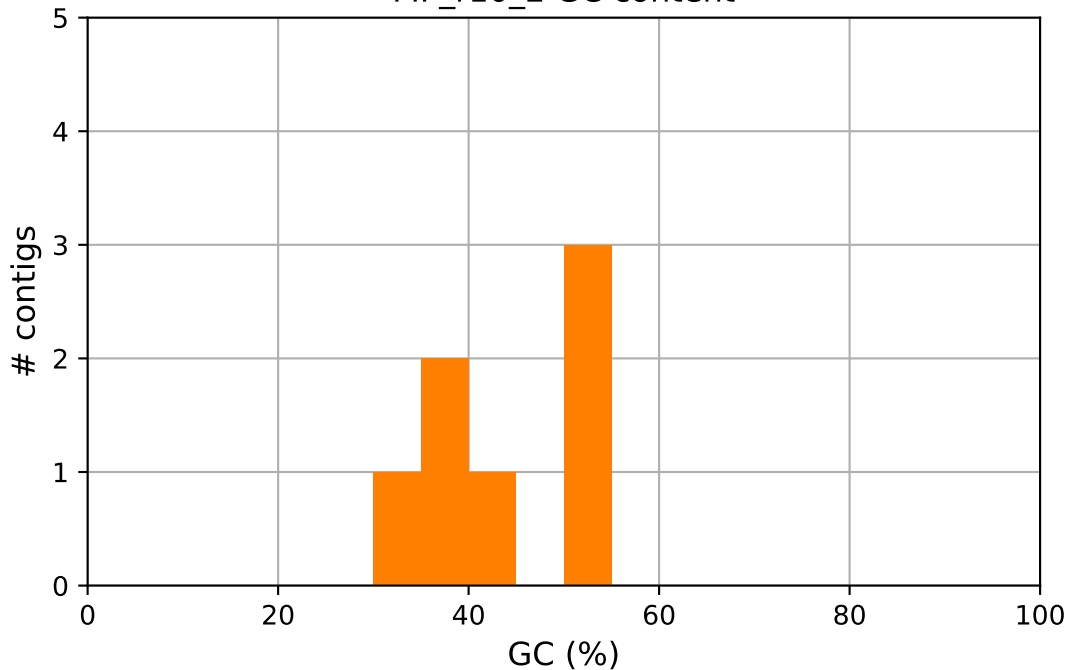
MP_helen_r10_3

MP_r10_1 GC content



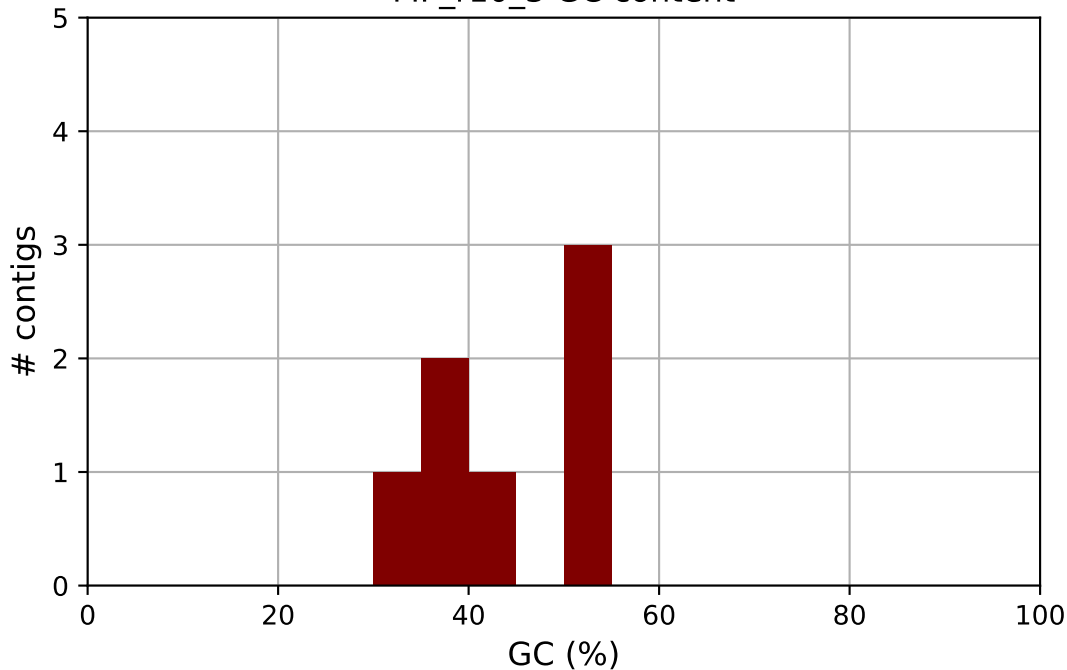
MP_r10_1

MP_r10_2 GC content



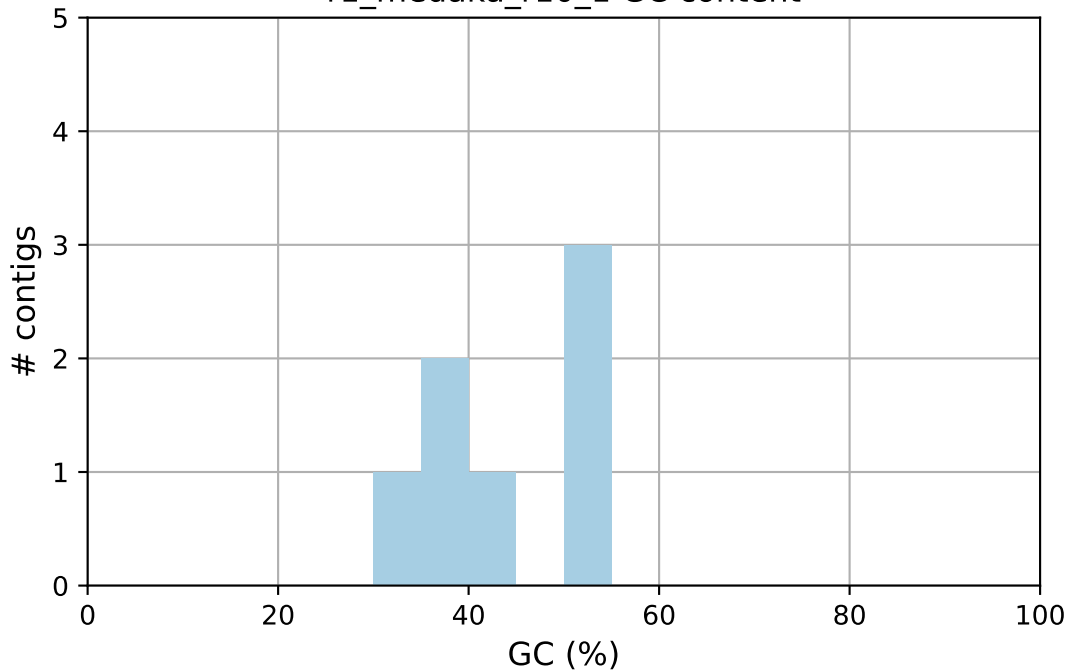
MP_r10_2

MP_r10_3 GC content



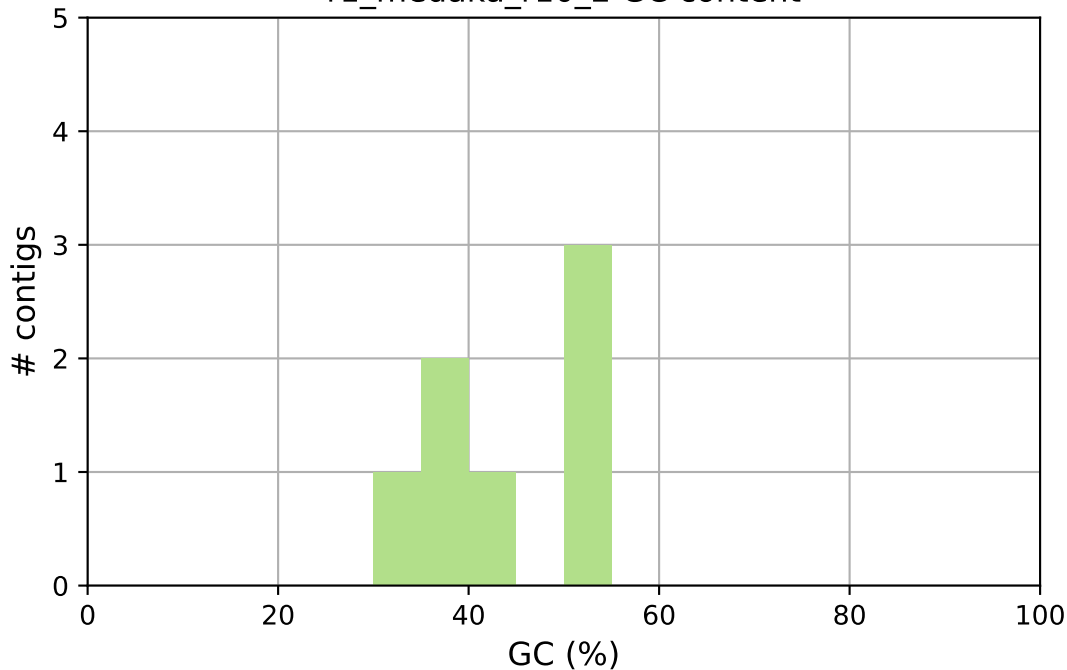
MP_r10_3

r1_medaka_r10_1 GC content



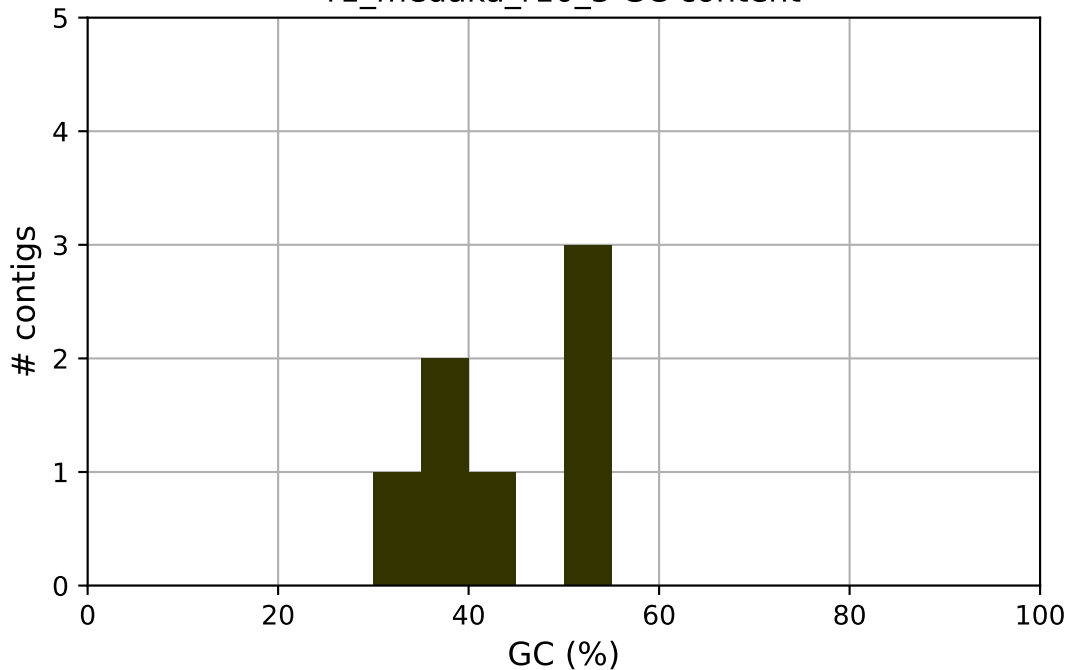
r1_medaka_r10_1

r1_medaka_r10_2 GC content



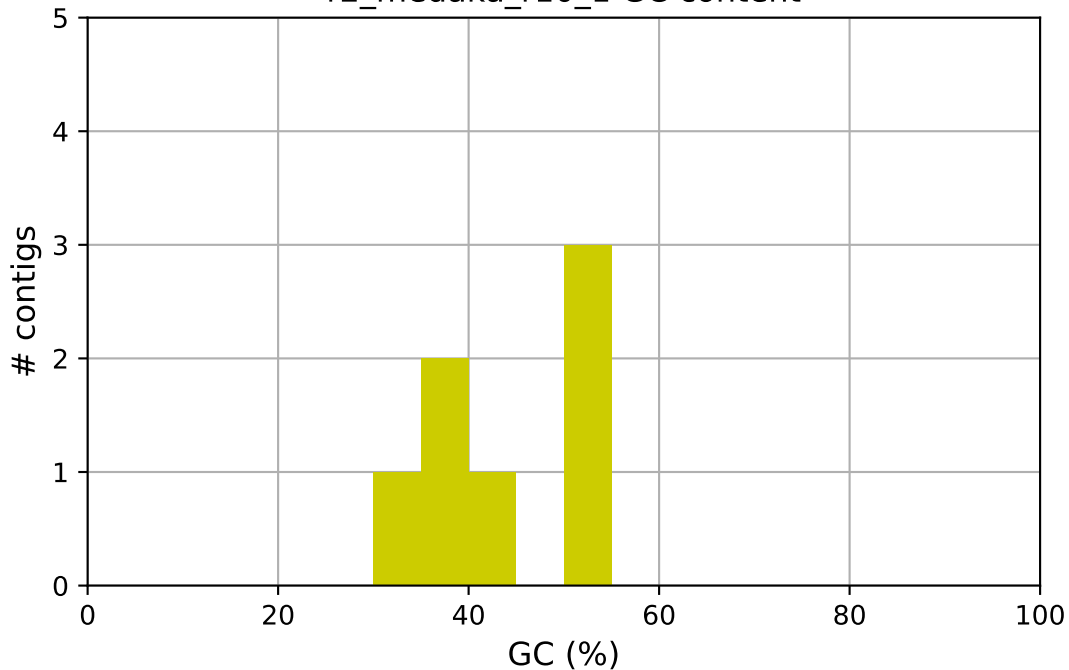
r1_medaka_r10_2

r1_medaka_r10_3 GC content



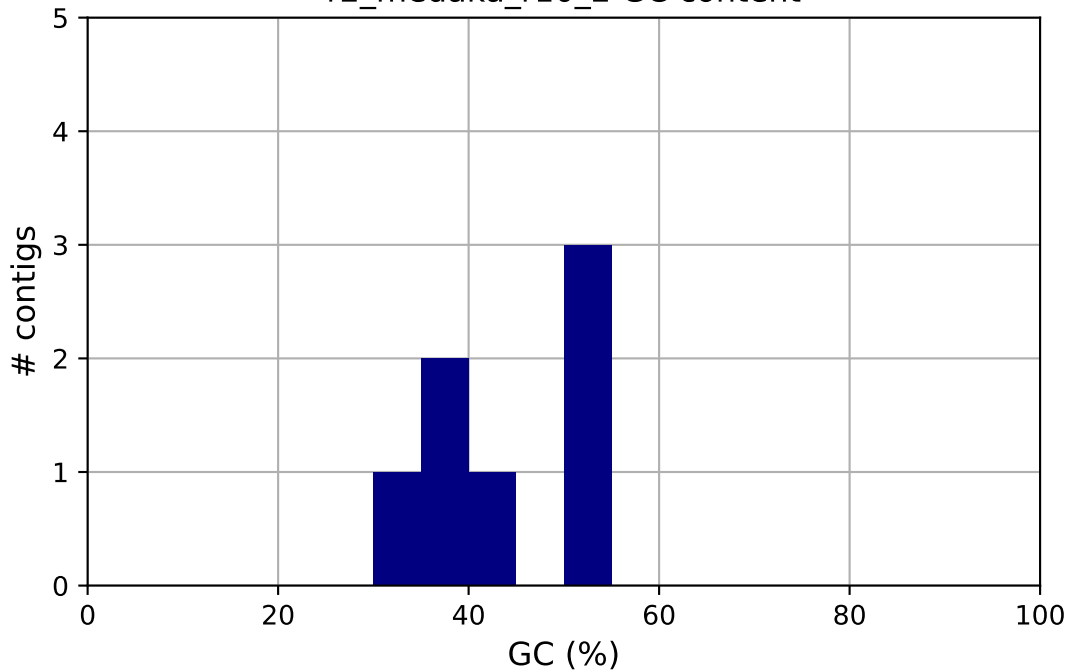
r1_medaka_r10_3

r2_medaka_r10_1 GC content



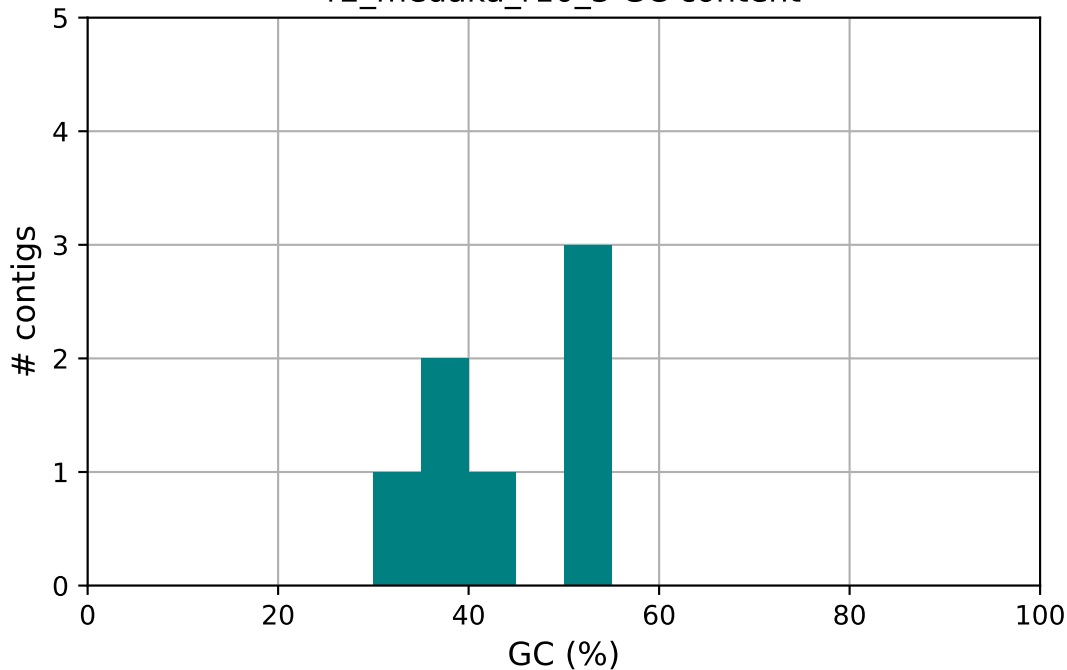
r2_medaka_r10_1

r2_medaka_r10_2 GC content



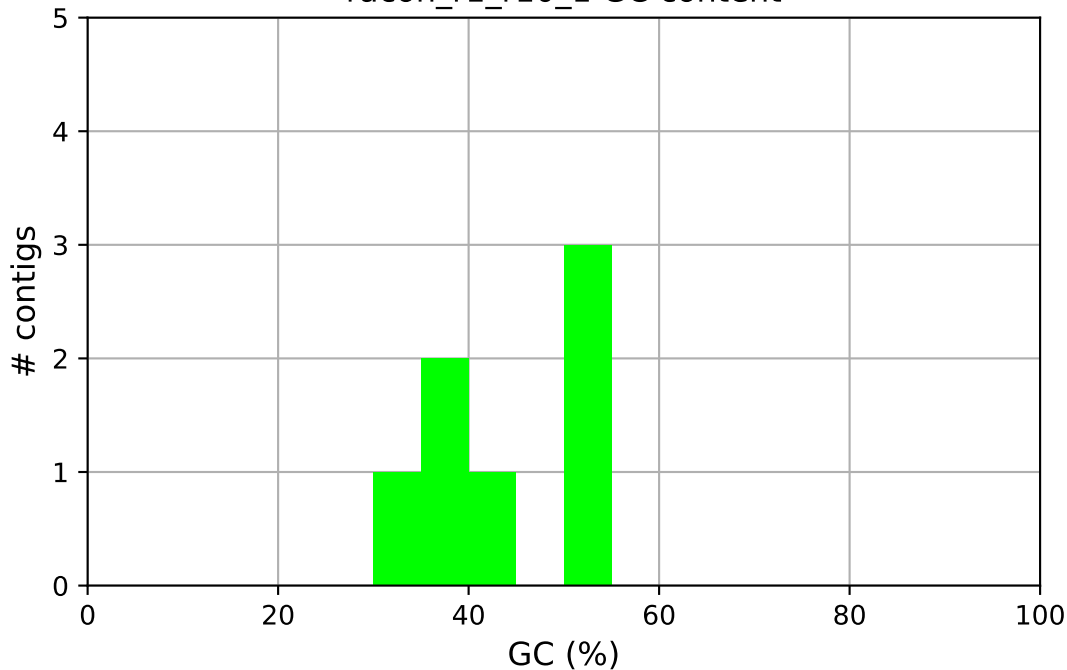
r2_medaka_r10_2

r2_medaka_r10_3 GC content



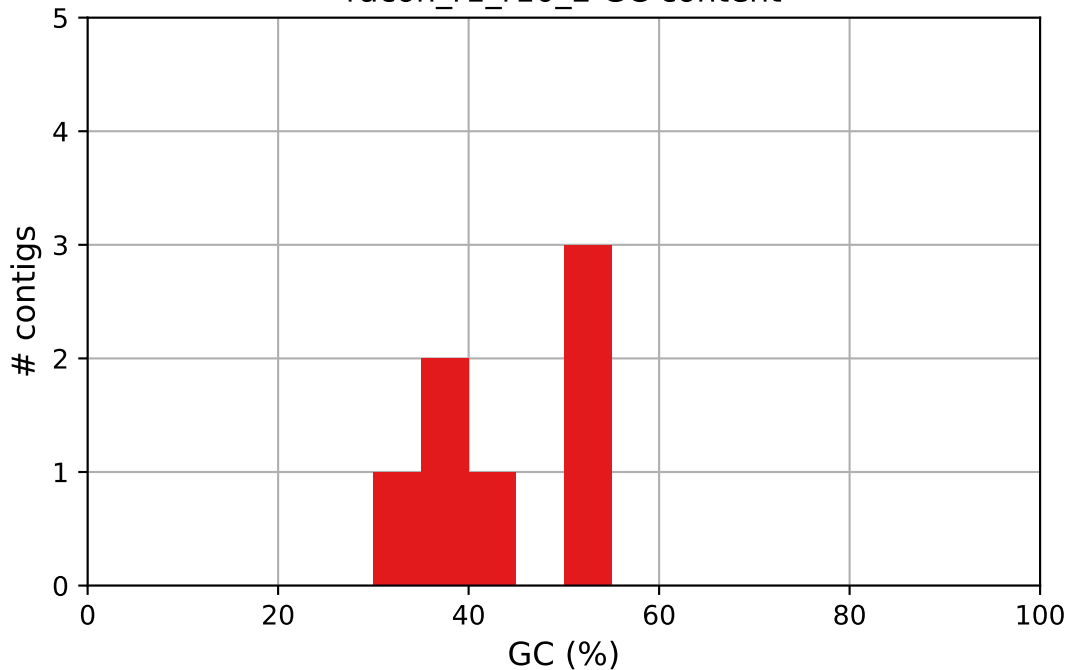
r2_medaka_r10_3

racon_r1_r10_1 GC content



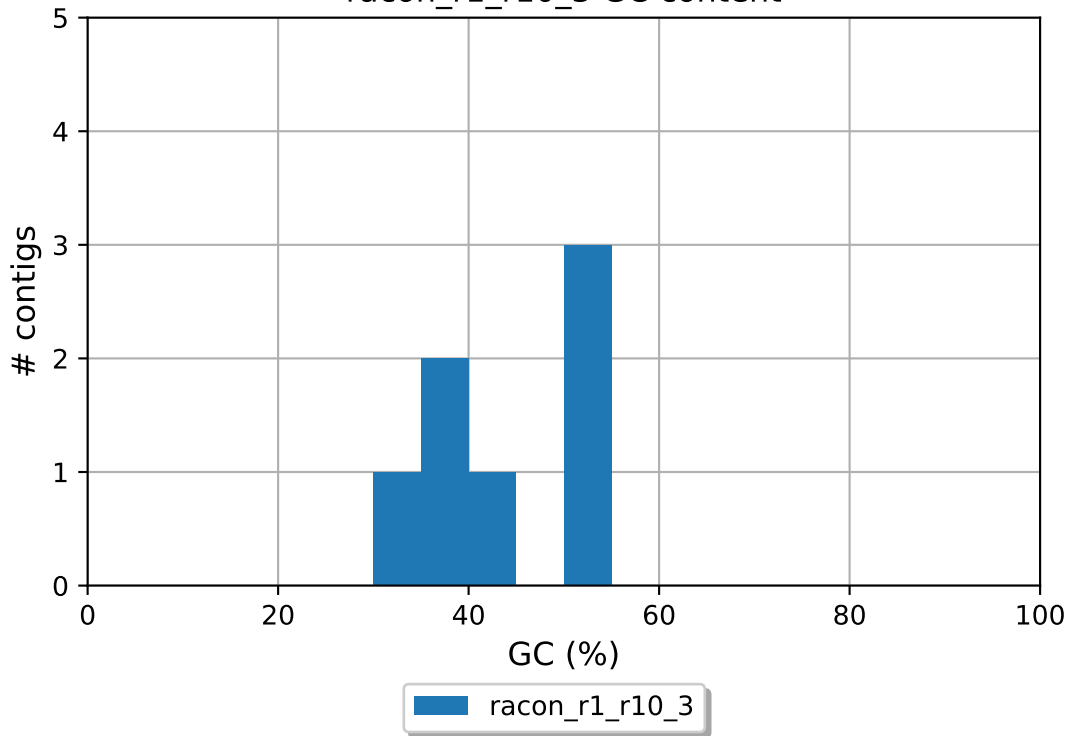
racon_r1_r10_1

racon_r1_r10_2 GC content

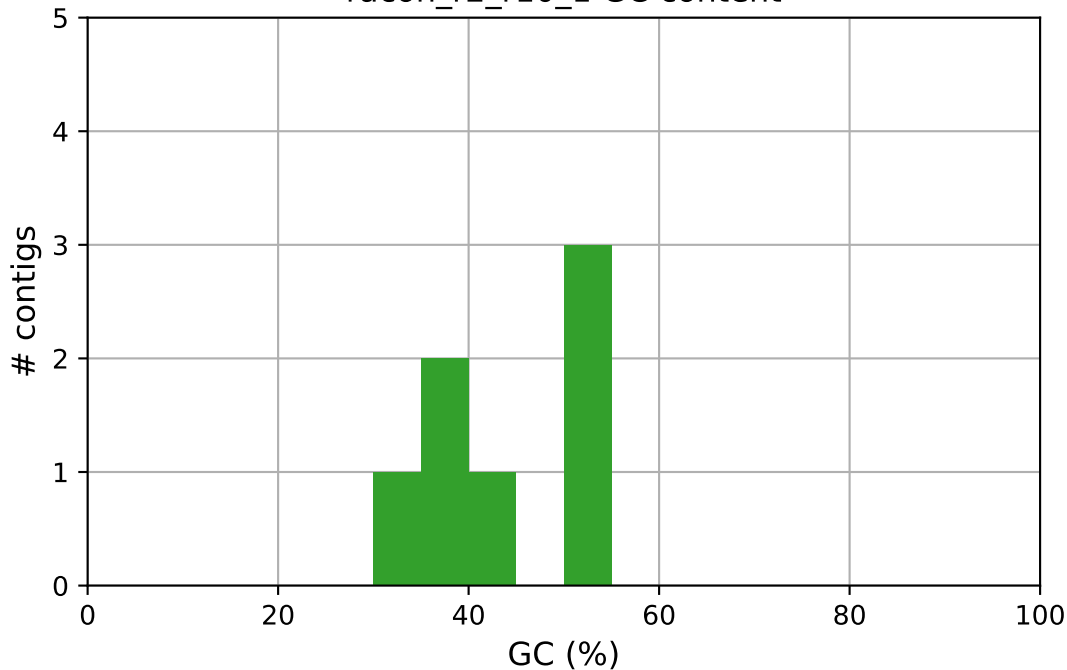


racon_r1_r10_2

racon_r1_r10_3 GC content

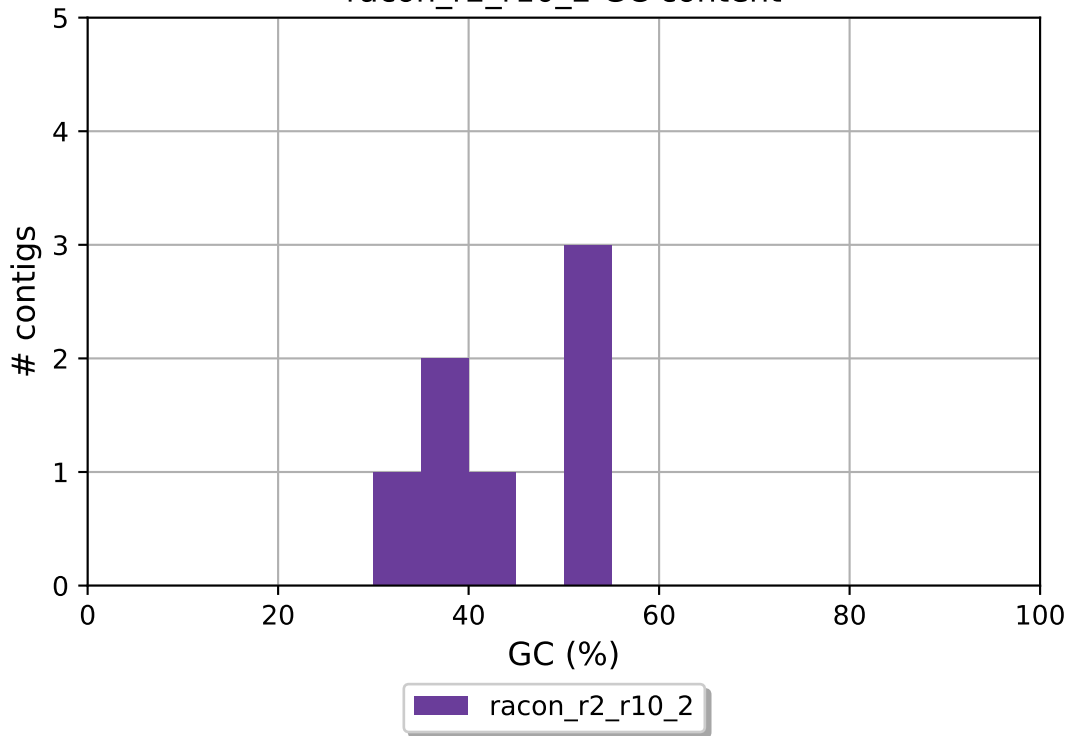


racon_r2_r10_1 GC content

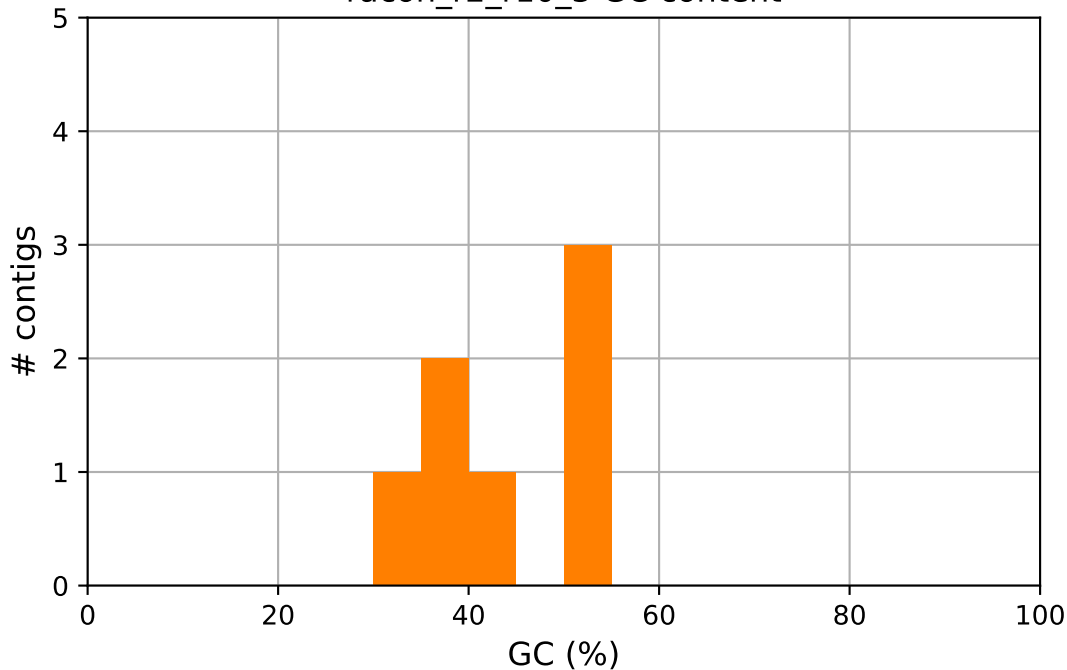


racon_r2_r10_1

racon_r2_r10_2 GC content

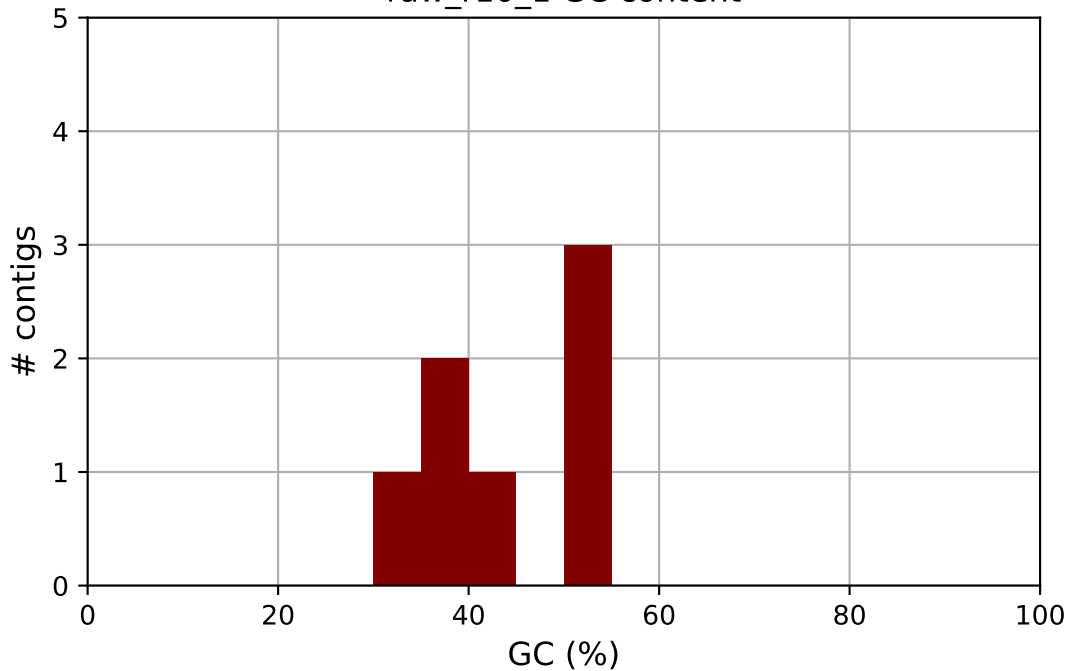


racon_r2_r10_3 GC content



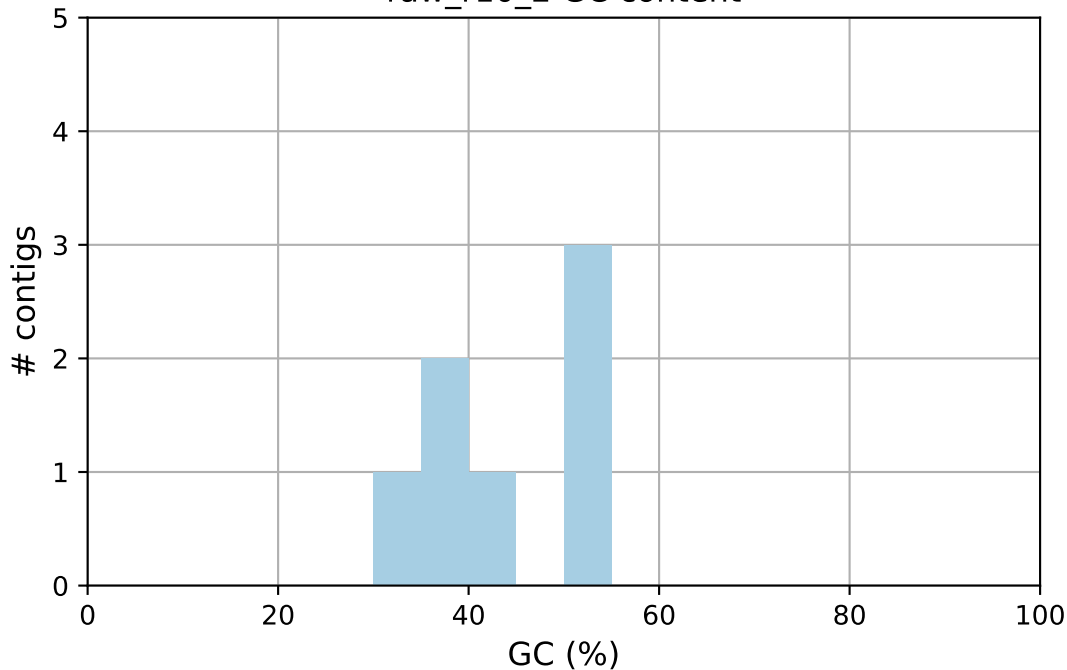
racon_r2_r10_3

raw_r10_1 GC content



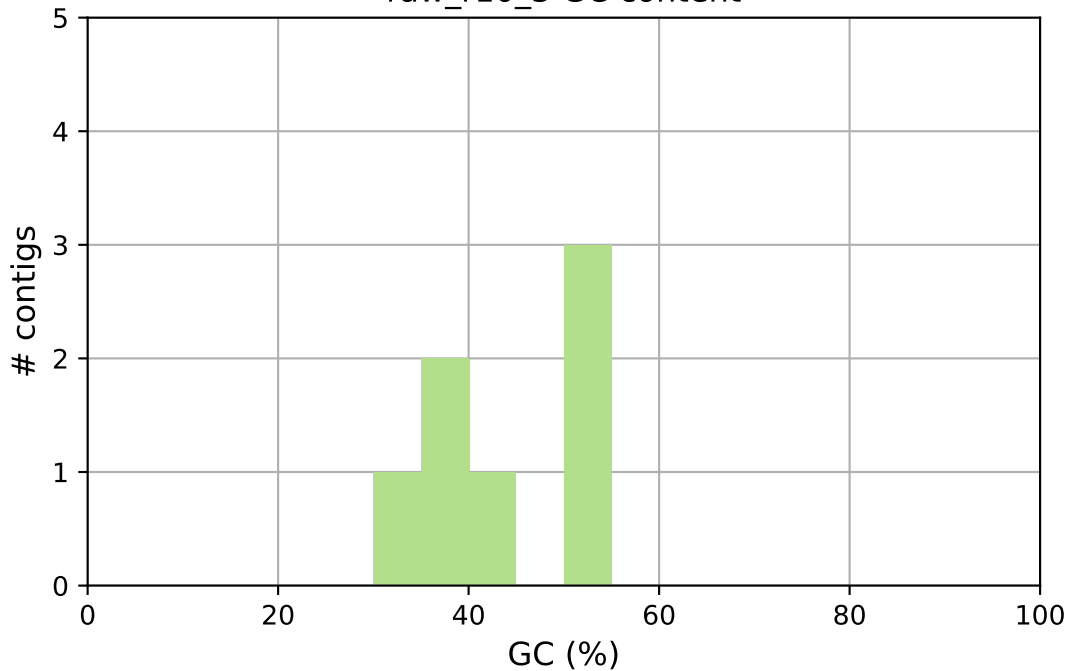
raw_r10_1

raw_r10_2 GC content



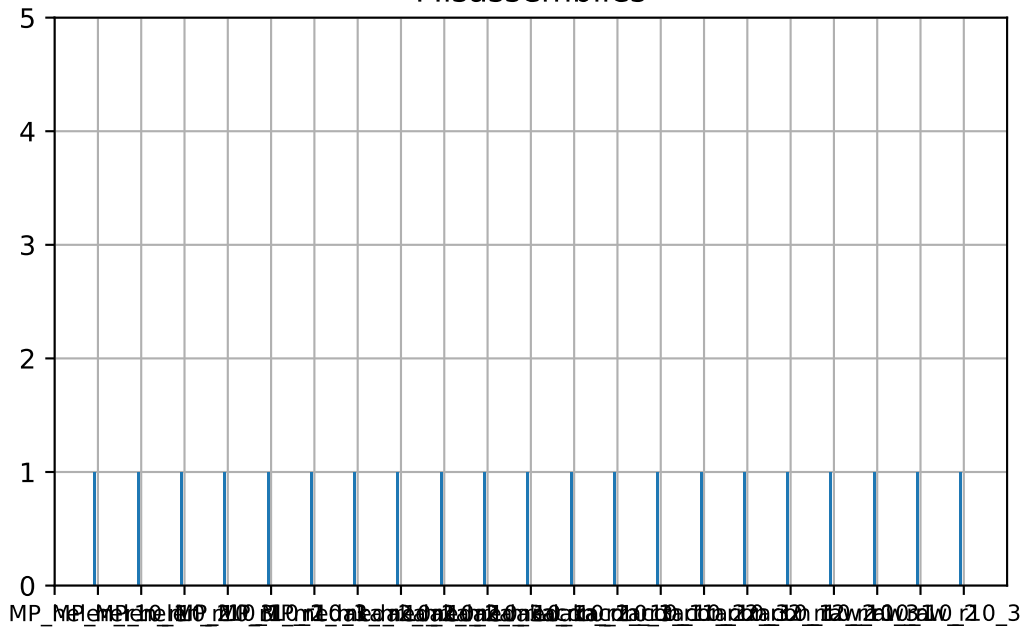
raw_r10_2

raw_r10_3 GC content



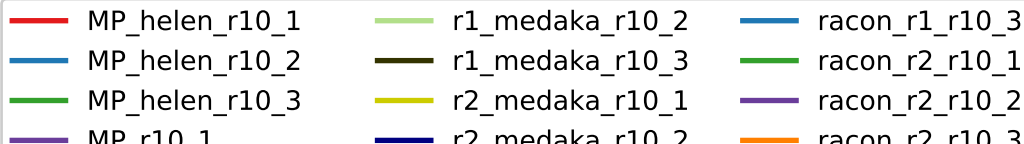
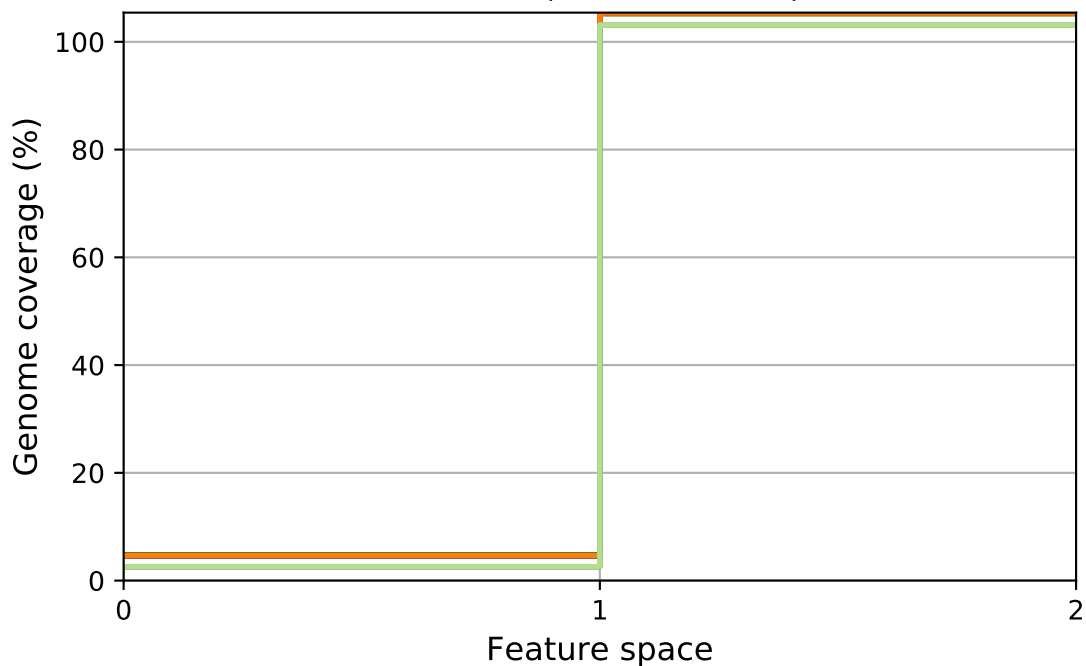
raw_r10_3

Misassemblies

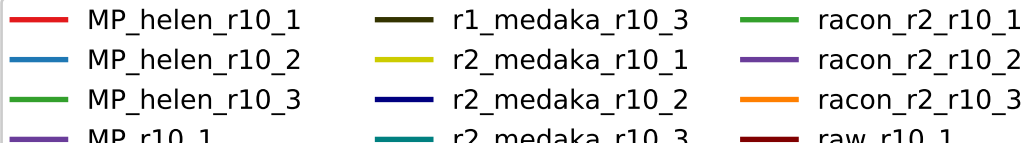
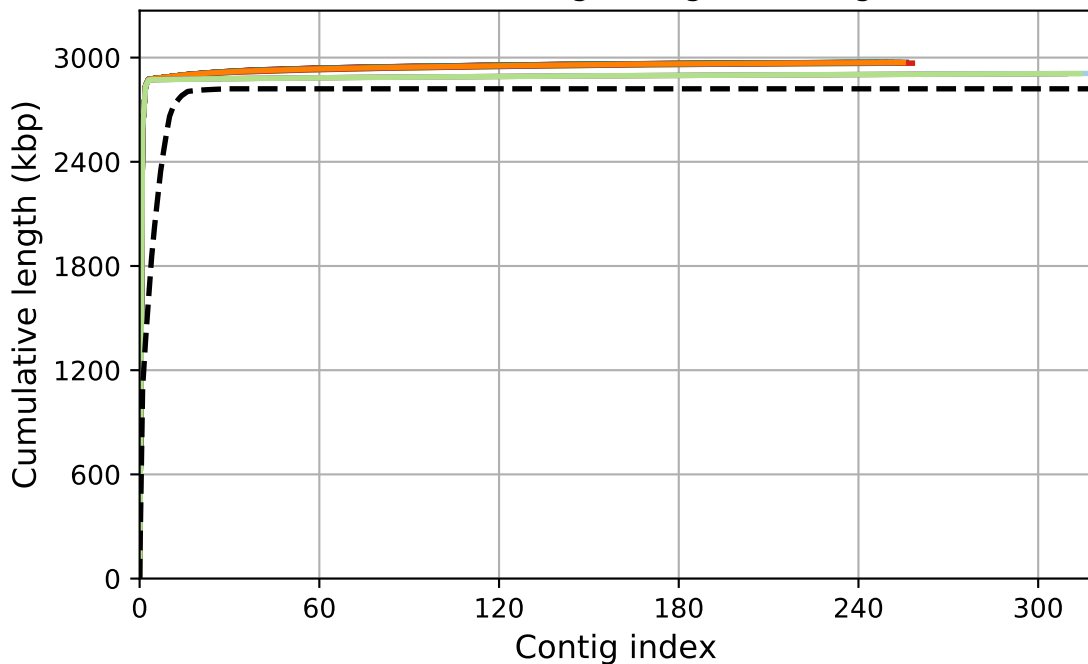


translocations

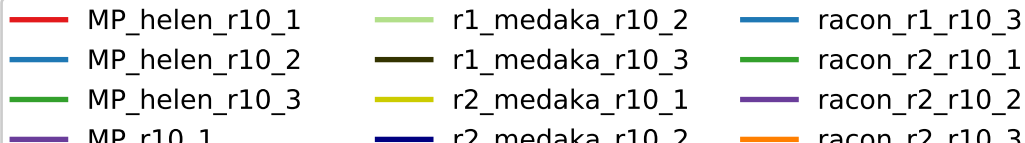
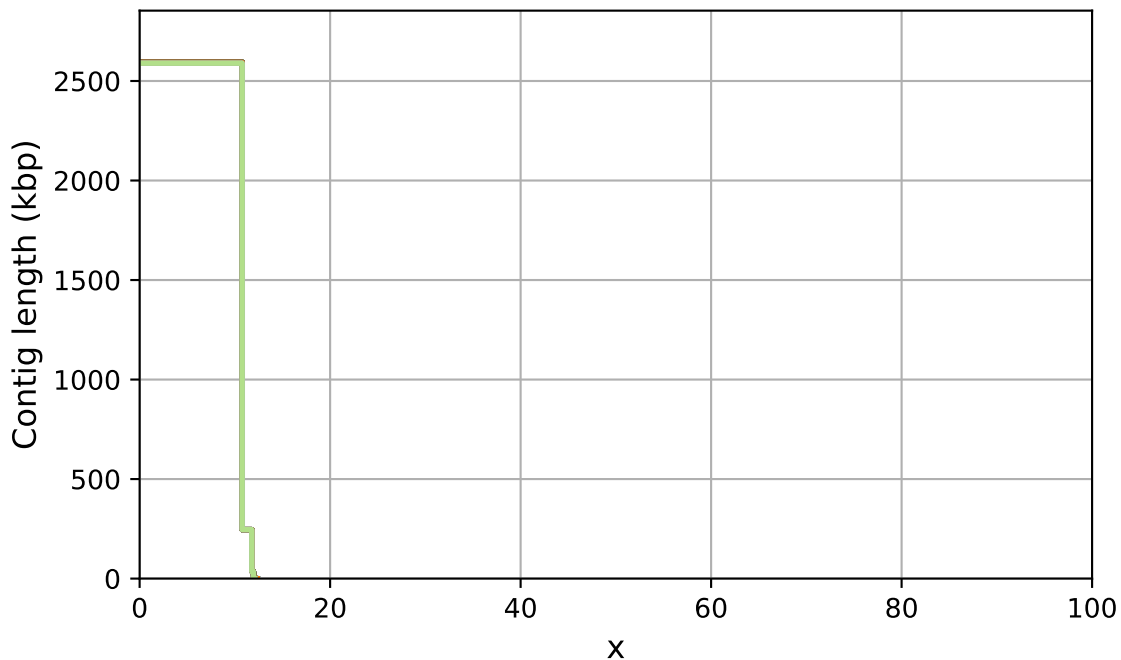
FRCurve (misassemblies)



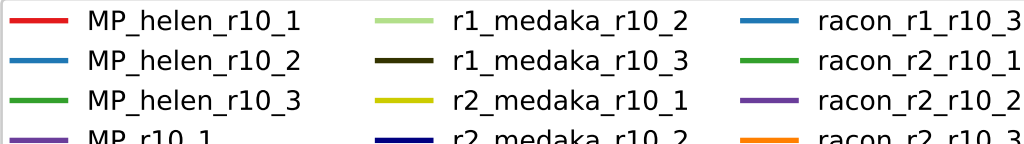
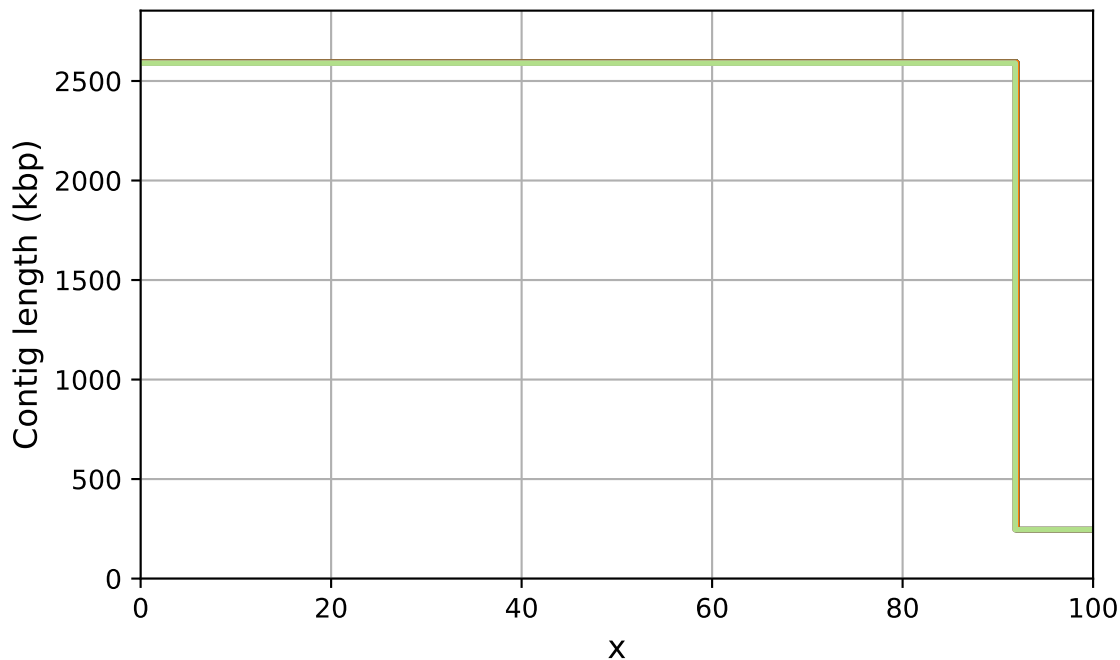
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

