

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	30847938	30850309	30849039
Total length (>= 10000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039
Total length (>= 25000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	30850309	30849039
Total length (>= 50000 bp)	24069494	24072731	24070272	24075146	24075931	24075224	24072592	24074864	24072788	24064948	24068153	24065807	24059729	24064644	24059333	24055079	24060632	24052503	30847938	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	30847938	30850309	30849039
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
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	49.48	49.48	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992077	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	12	13	13
# 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	7	7	7
# 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	20949559	20952921	20950876	20956341	20958826	20957201	20953011	20954417	20952911	20946491	20948236	20947143	20940672	20945302	20941576	20936510	20941874	20934991	27788635	27793928	27794257
Genome fraction (%)	99.984	99.986	99.984	99.984	99.986	99.984	99.984	99.986	99.984	99.986	99.984	99.986	99.984	99.986	99.984	99.984	99.986	99.984	99.983	99.977	99.975
Duplication ratio	1.055	1.055	1.055	1.055	1.054	1.054	1.055	1.055	1.055	1.054	1.055	1.055	1.055	1.055	1.054	1.055	1.055	1.054	1.034	1.034	1.033
# 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	235.55	234.29	233.18	231.73	226.96	229.77	231.90	235.58	233.01	228.11	233.65	229.80	231.59	231.99	226.49	229.83	231.18	226.35	145.74	141.18	137.40
# indels per 100 kbp	22.35	21.07	22.11	22.01	20.83	22.08	22.15	22.69	21.91	22.11	21.88	21.71	30.74	31.01	31.48	29.72	28.37	29.62	115.78	114.10	115.05
Largest alignment	1569028	2022617	1569034	1569037	2022620	1569036	1569032	2022616	1569034	1569033	2022615	1569033	1568975	2022540	1568946	1568967	2022543	1568978	1568349	2021412	1568099
Total aligned length	3119461	3118422	3118922	3118331	3115717	3117549	3119107	3119060	3119403	3117983	3118530	3118190	3118583	3117974	3117285	3118095	3117370	3117040	3058865	3055011	3054354
NGA50	1569028	2022617	1569034	1569037	2022620	1569036	1569032	2022616	1569034	1569033	2022615	1569033	1568975	2022540	1568946	1568967	2022543	1568978	1568349	2021412	1568099
NGA75	1410493	956030	1410501	1410523	956031	1410535	1410514	956024	1410519	1410515	956027	1410519	1410424	956018	1410468	1410464	956010	1410473	1409713	955493	1409675
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2

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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992077	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2
# possible misassemblies	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	9	9	9
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	12	13	13
# 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	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	15	16	11	11	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	7	7
# mismatches	6966	6929	6896	6853	6712	6795	6858	6967	6891	6746	6910	6796	6849	6861	6698	6797	6837	6694	4310	4175	4063
# indels	661	623	654	651	616	653	655	671	648	654	647	642	909	917	931	879	839	876	3424	3374	3402
# indels (<= 5 bp)	636	601	628	627	593	628	630	645	624	629	623	618	884	890	907	854	815	852	3396	3346	3375
# indels (> 5 bp)	25	22	26	24	23	25	25	26	24	25	24	24	25	27	24	25	24	24	28	28	27
Indels length	1971	1895	1967	1955	1885	1961	1971	2011	1943	1969	1938	1933	2321	2331	2323	2237	2185	2249	5313	5297	5306

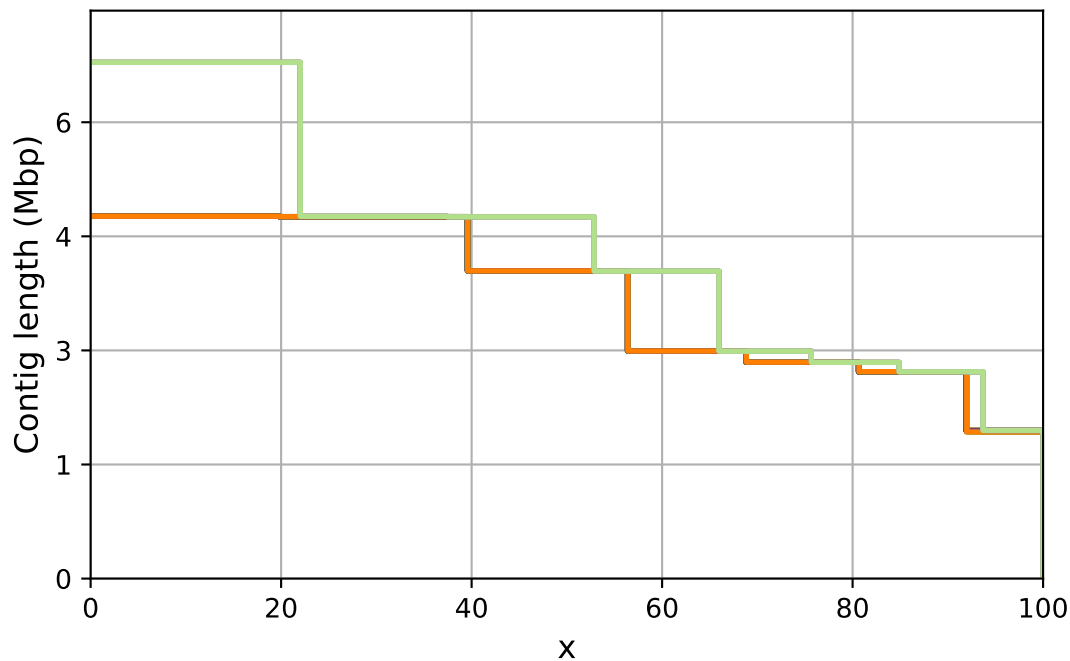
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	8	8	8
Partially unaligned length	20949559	20952921	20950876	20956341	20958826	20957201	20953011	20954417	20952911	20946491	20948236	20947143	20940672	20945302	20941576	20936510	20941874	20934991	27788635	27793928	27794257
# 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

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

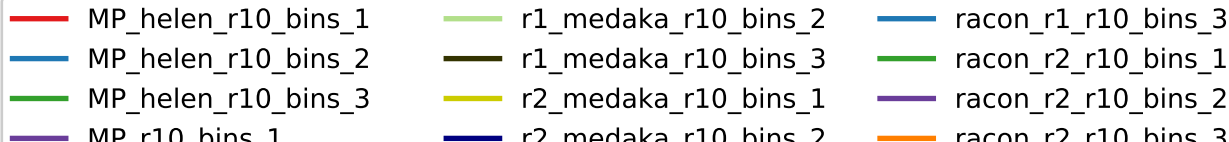
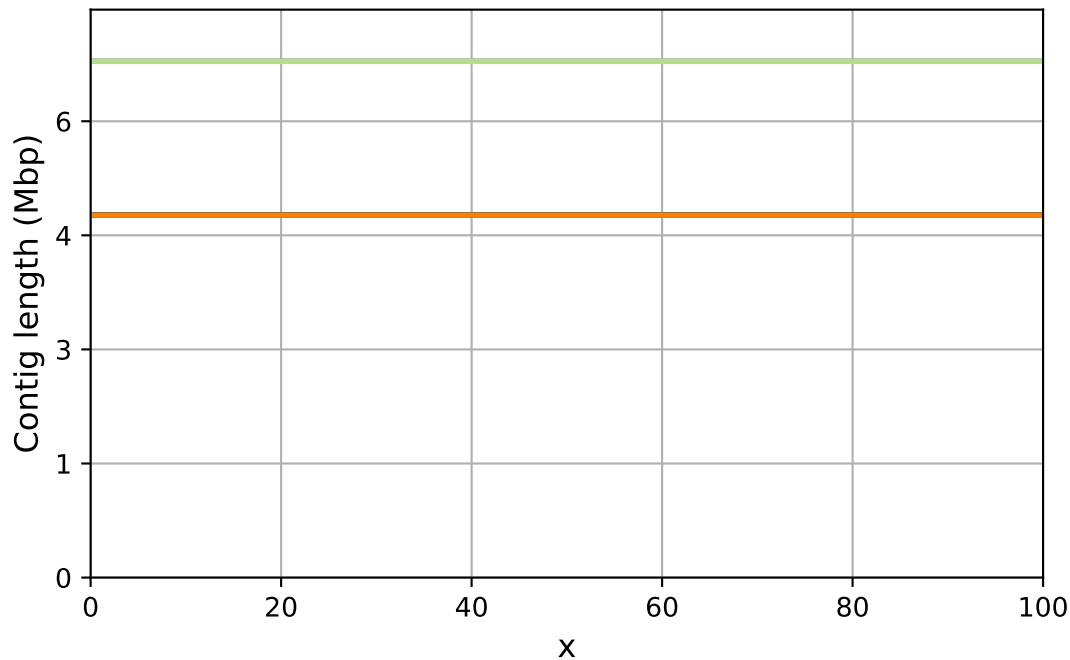
racon_r1_r10_bins_3

racon_r2_r10_bins_1

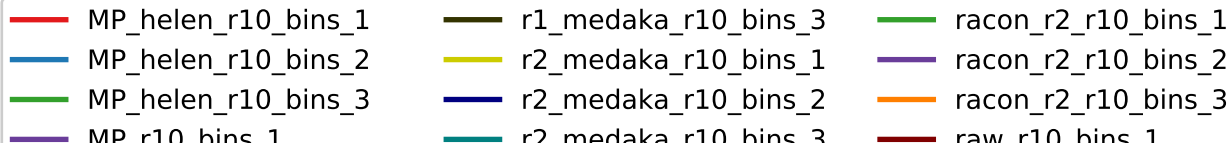
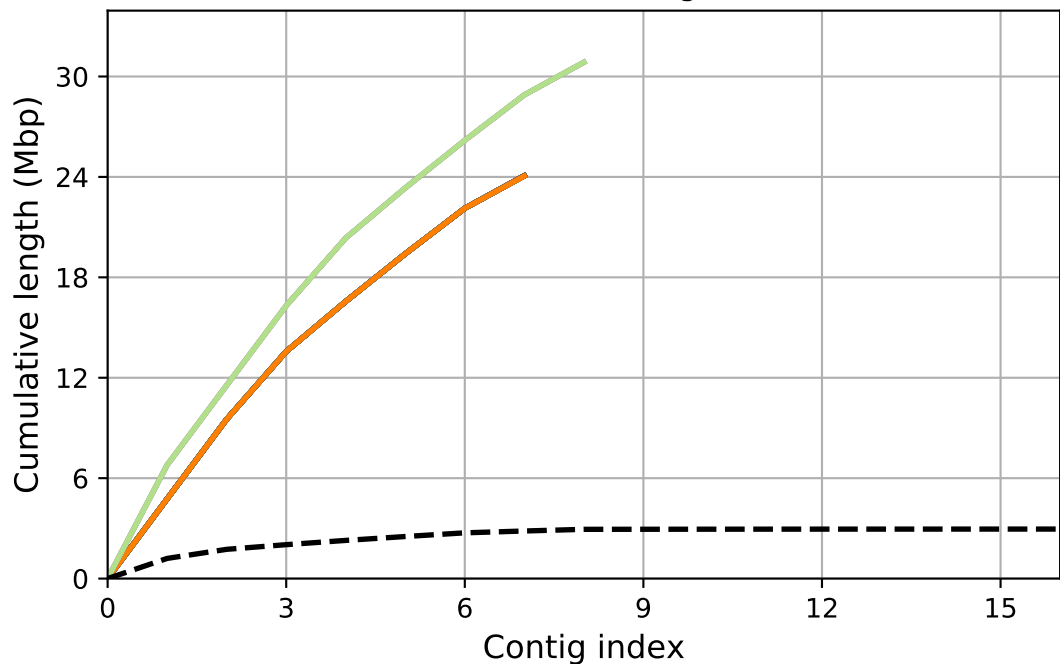
racon_r2_r10_bins_2

racon_r2_r10_bins_3

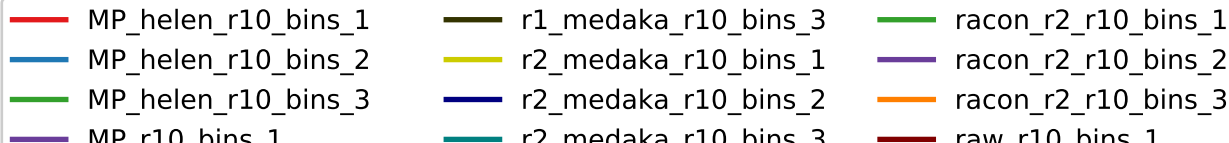
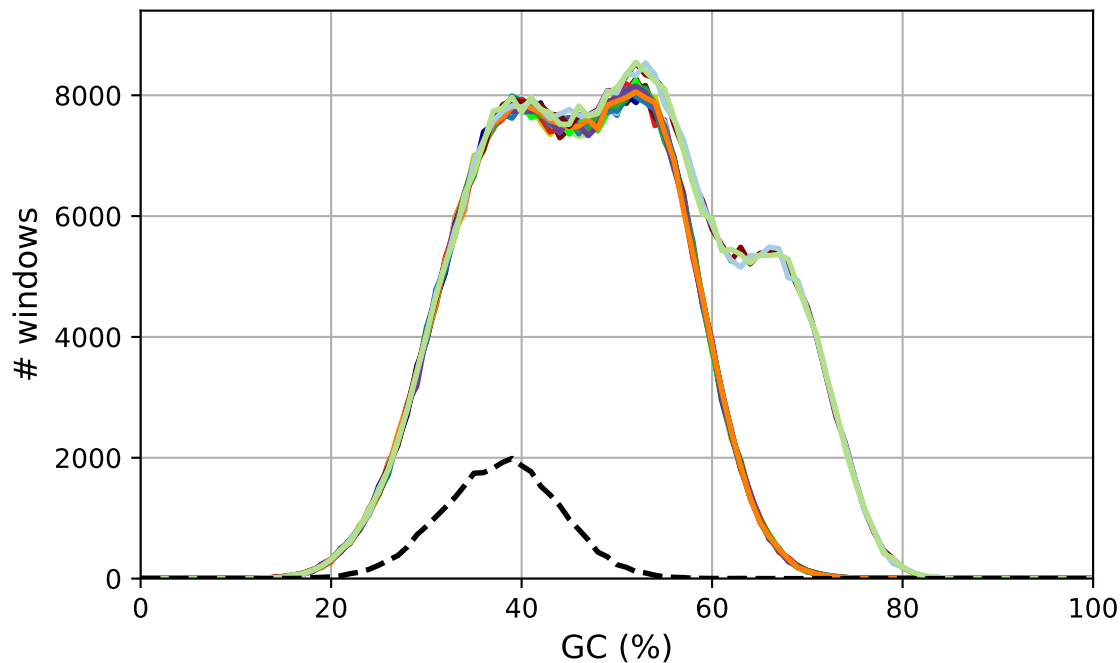
NGx



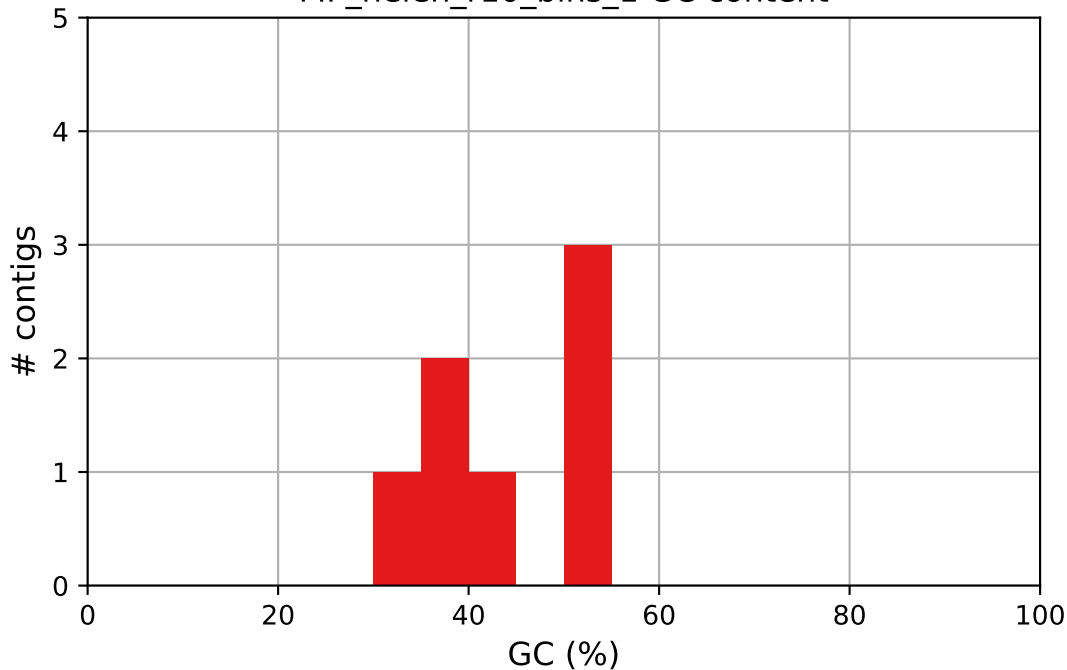
Cumulative length



GC content

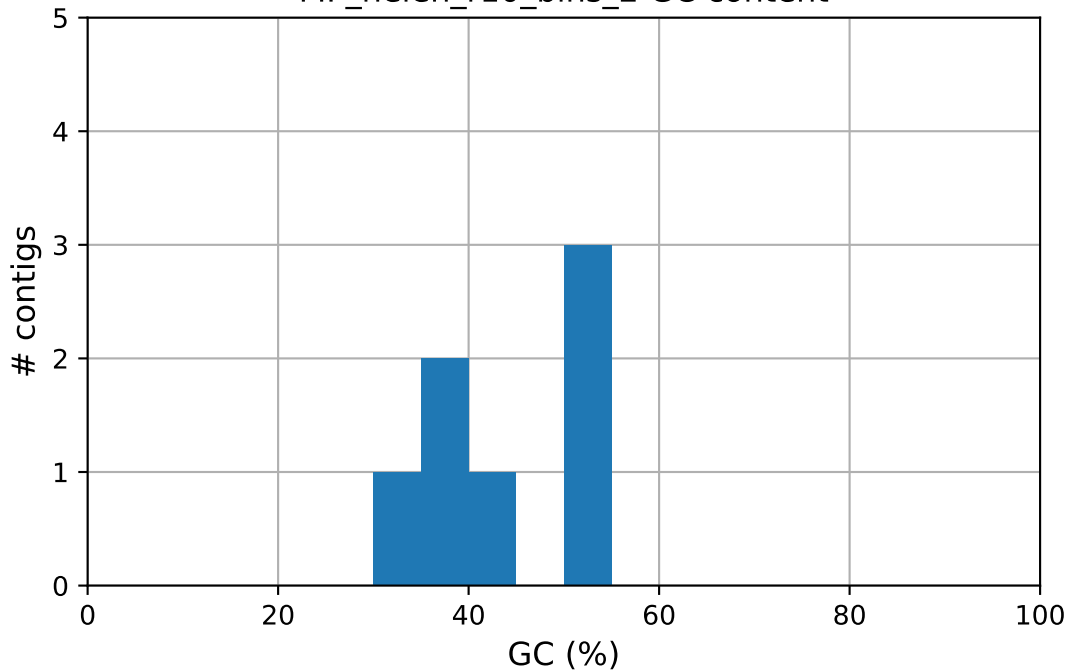


MP_helen_r10_bins_1 GC content



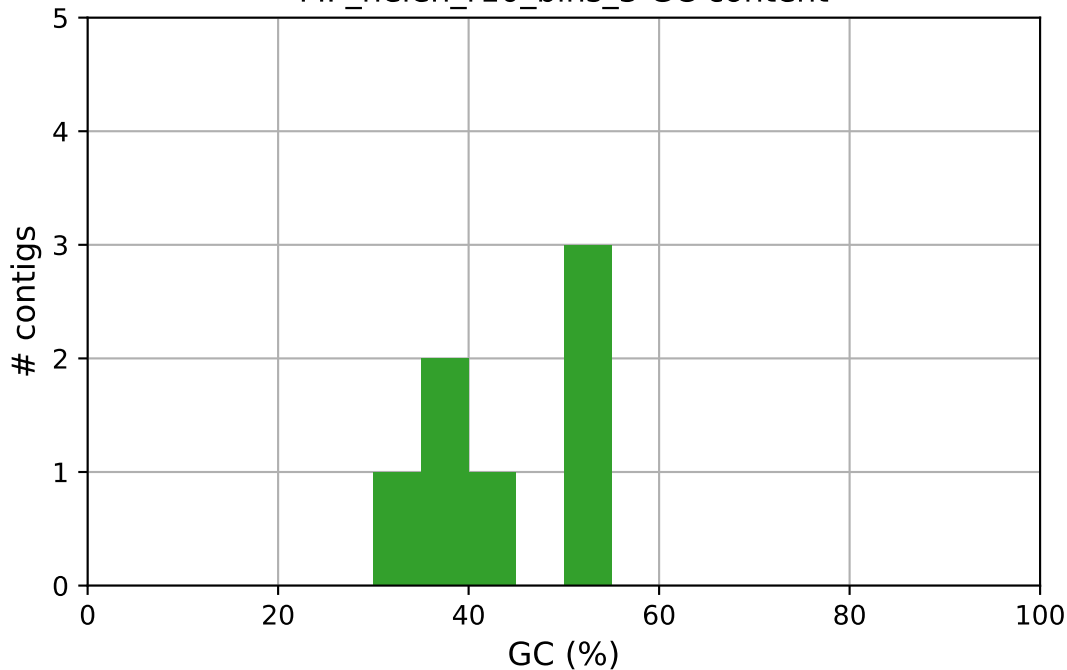
MP_helen_r10_bins_1

MP_helen_r10_bins_2 GC content



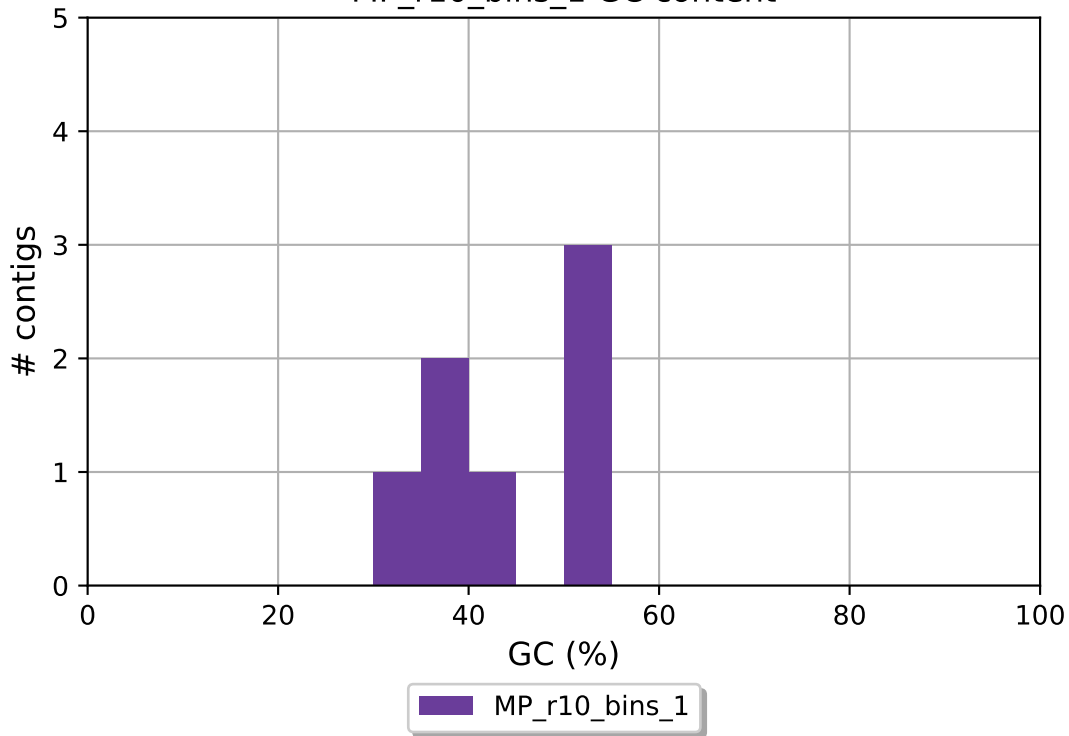
MP_helen_r10_bins_2

MP_helen_r10_bins_3 GC content

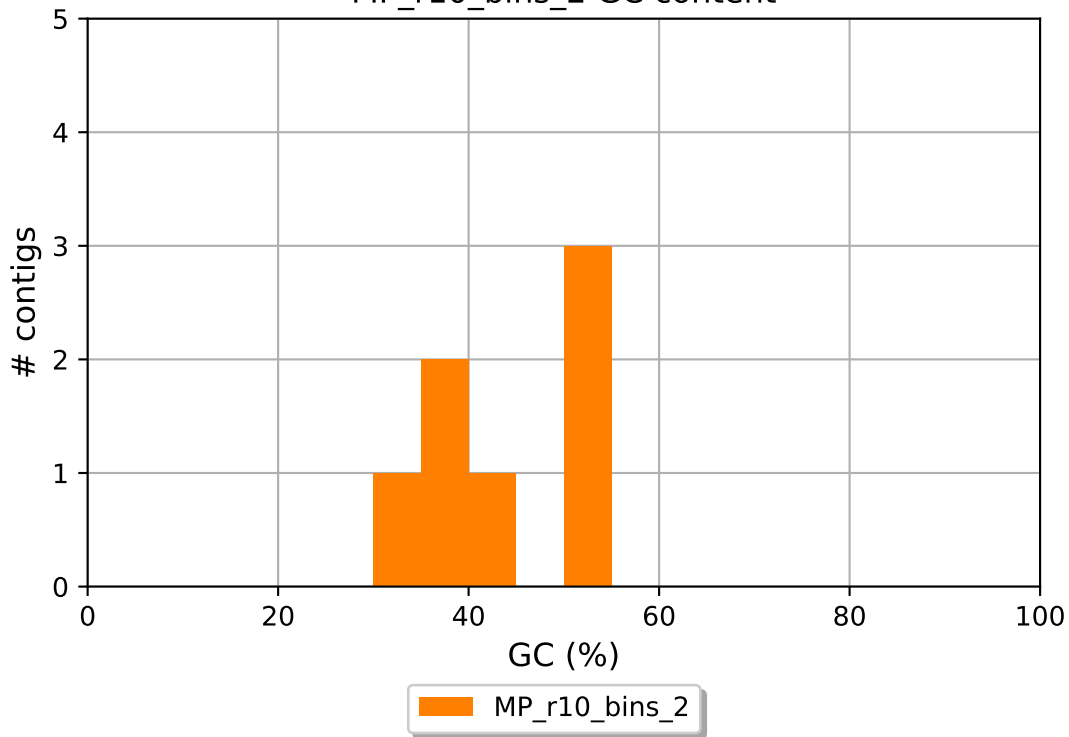


MP_helen_r10_bins_3

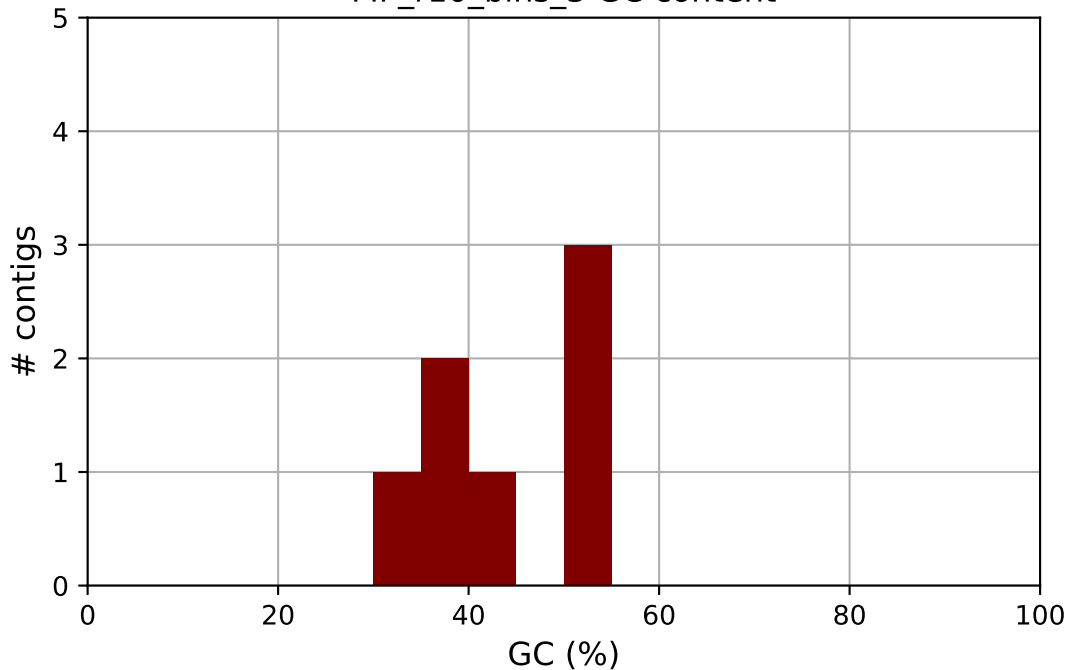
MP_r10_bins_1 GC content



MP_r10_bins_2 GC content

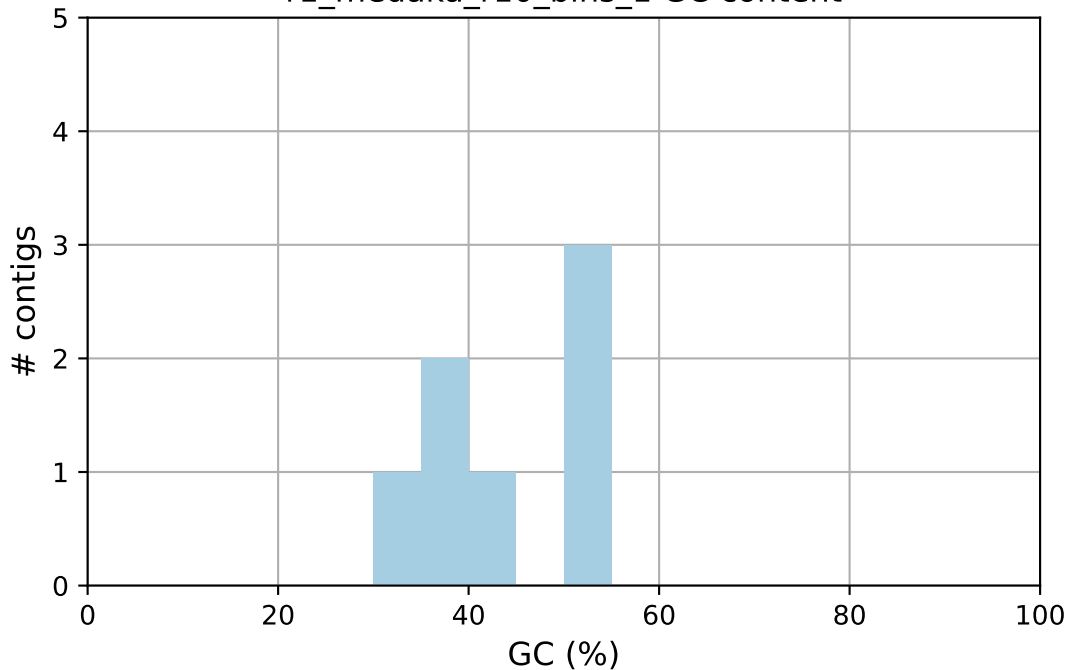


MP_r10_bins_3 GC content



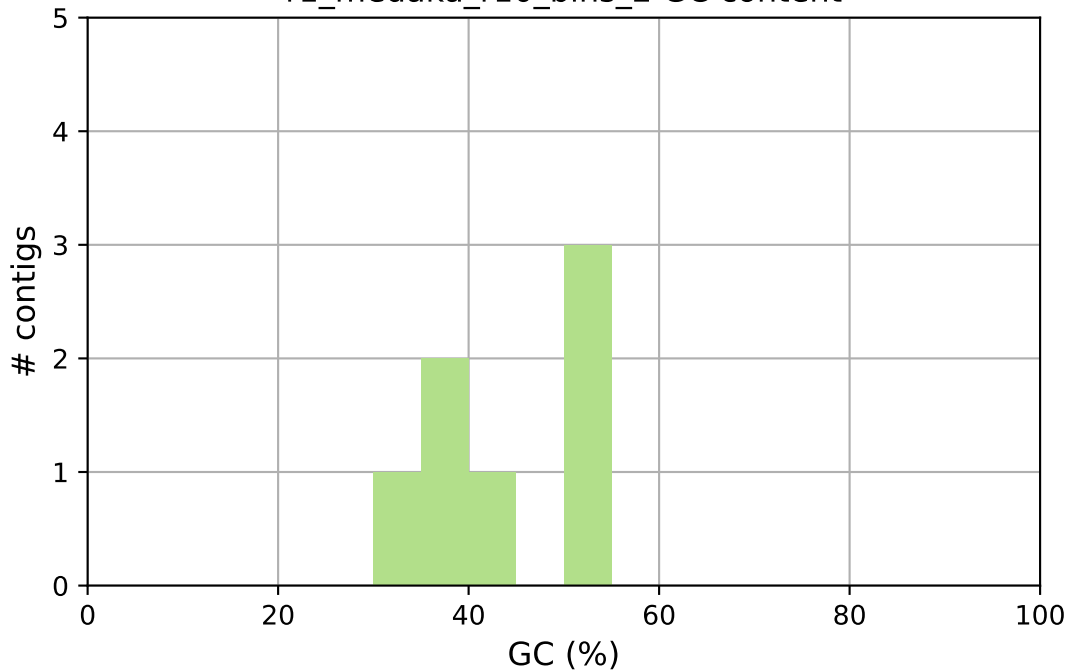
MP_r10_bins_3

r1_medaka_r10_bins_1 GC content



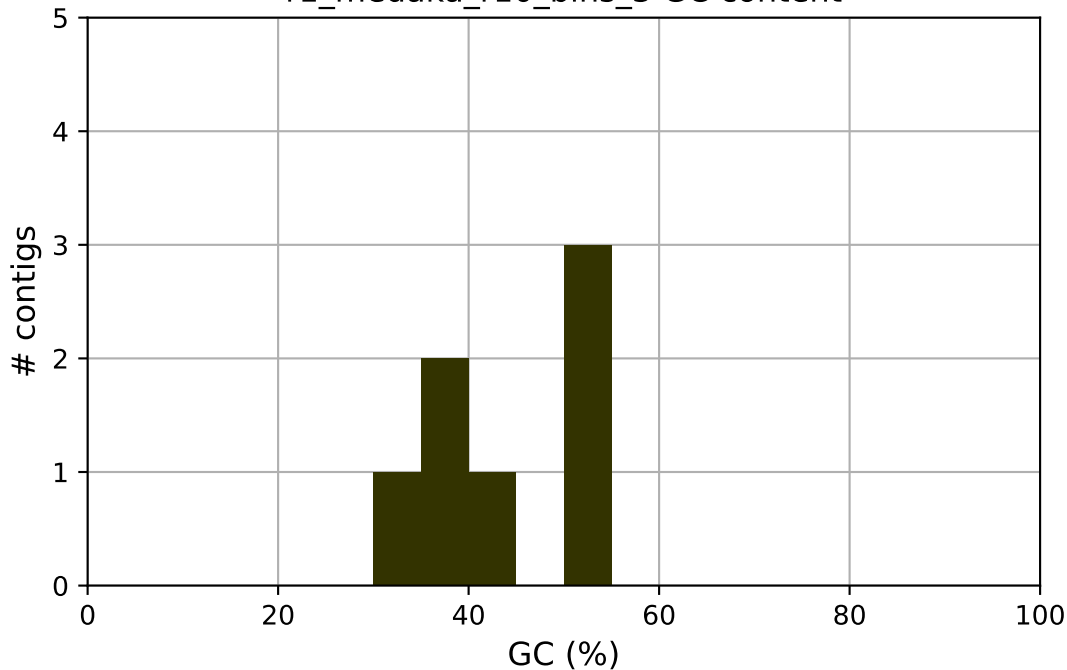
r1_medaka_r10_bins_1

r1_medaka_r10_bins_2 GC content



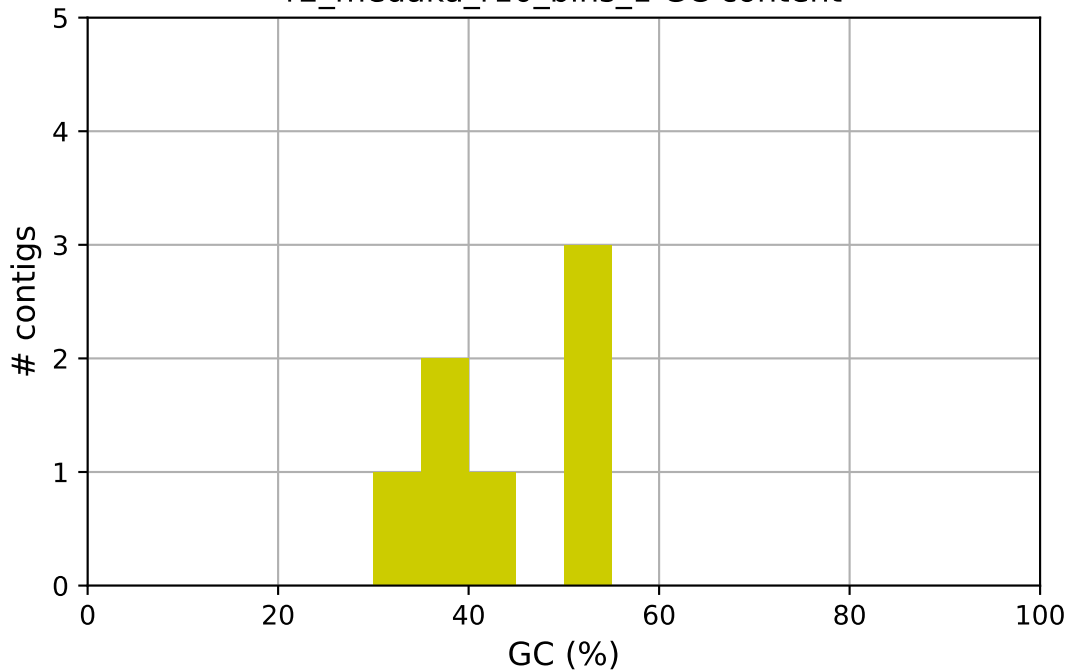
r1_medaka_r10_bins_2

r1_medaka_r10_bins_3 GC content



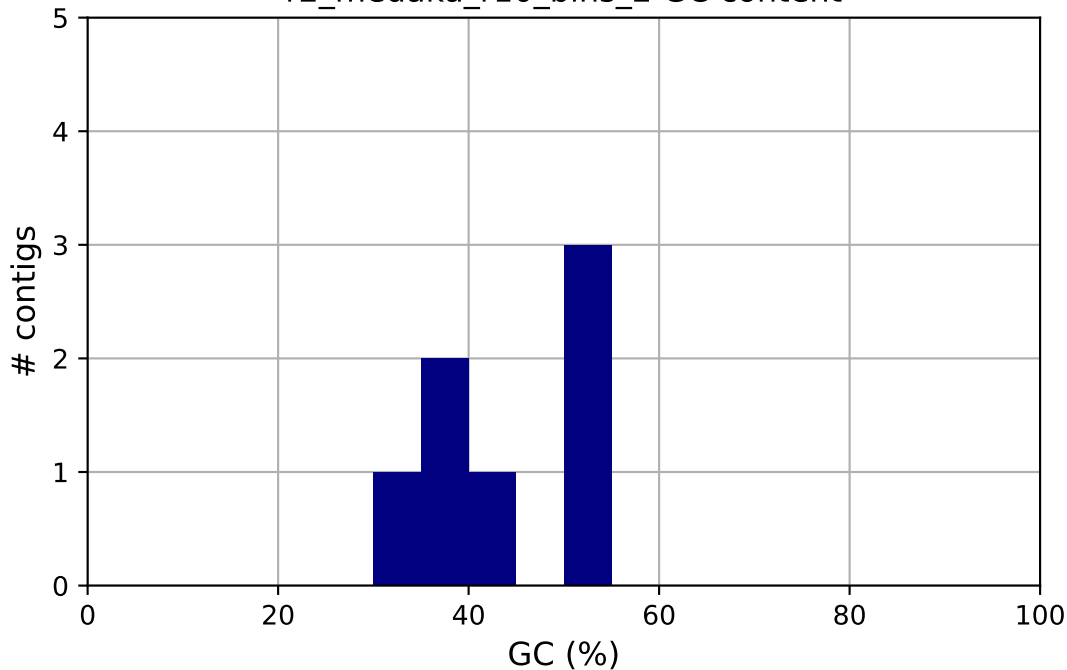
r1_medaka_r10_bins_3

r2_medaka_r10_bins_1 GC content



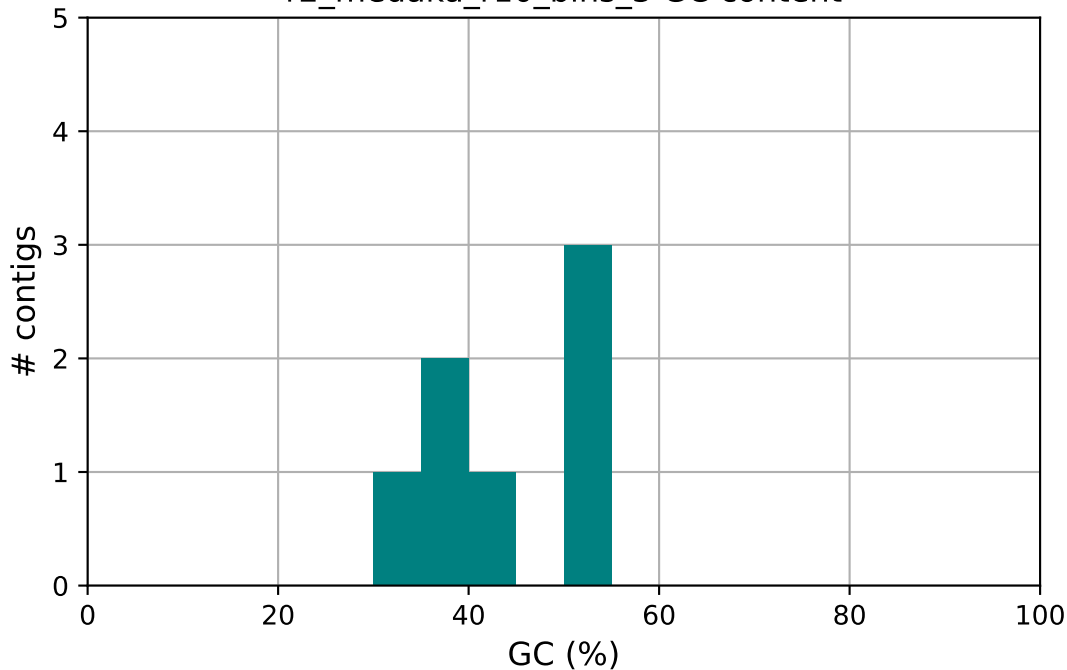
r2_medaka_r10_bins_1

r2_medaka_r10_bins_2 GC content



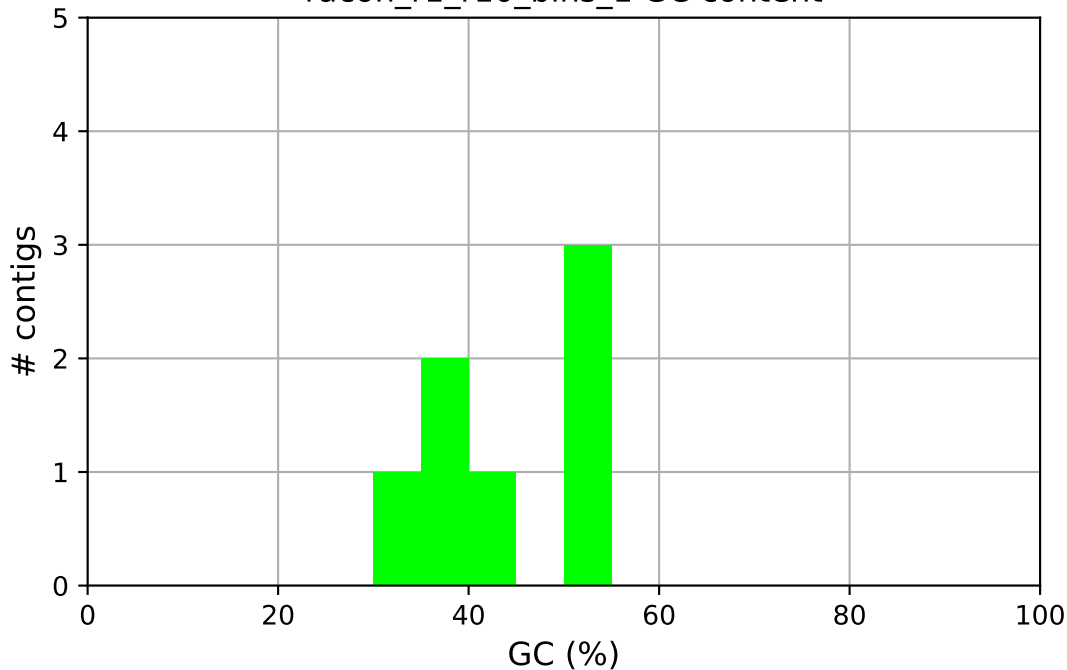
r2_medaka_r10_bins_2

r2_medaka_r10_bins_3 GC content



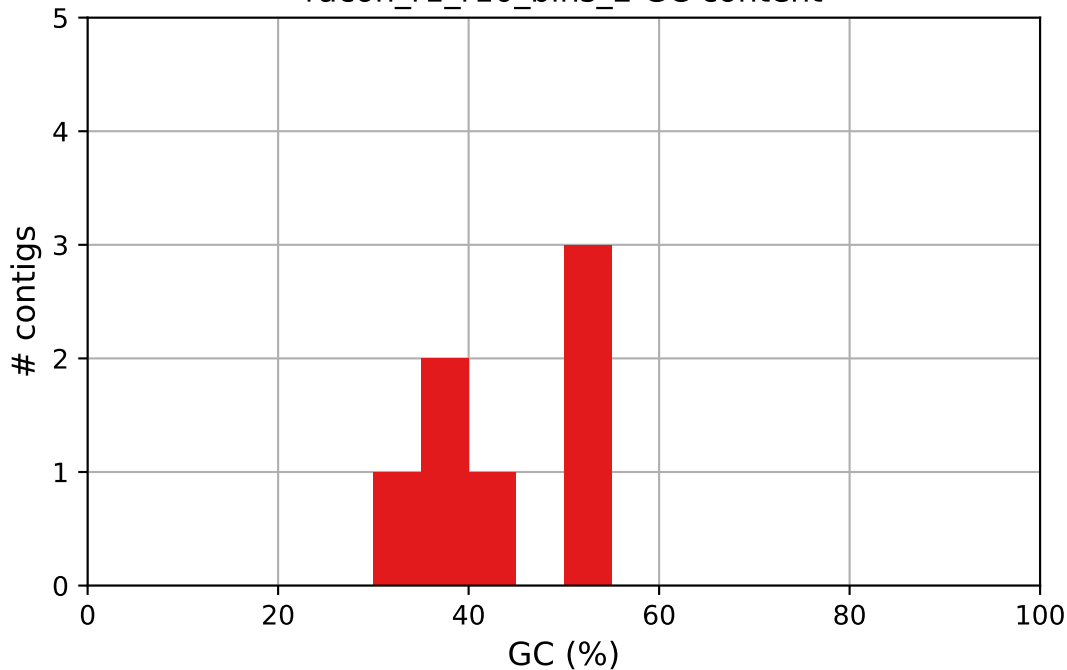
r2_medaka_r10_bins_3

racon_r1_r10_bins_1 GC content



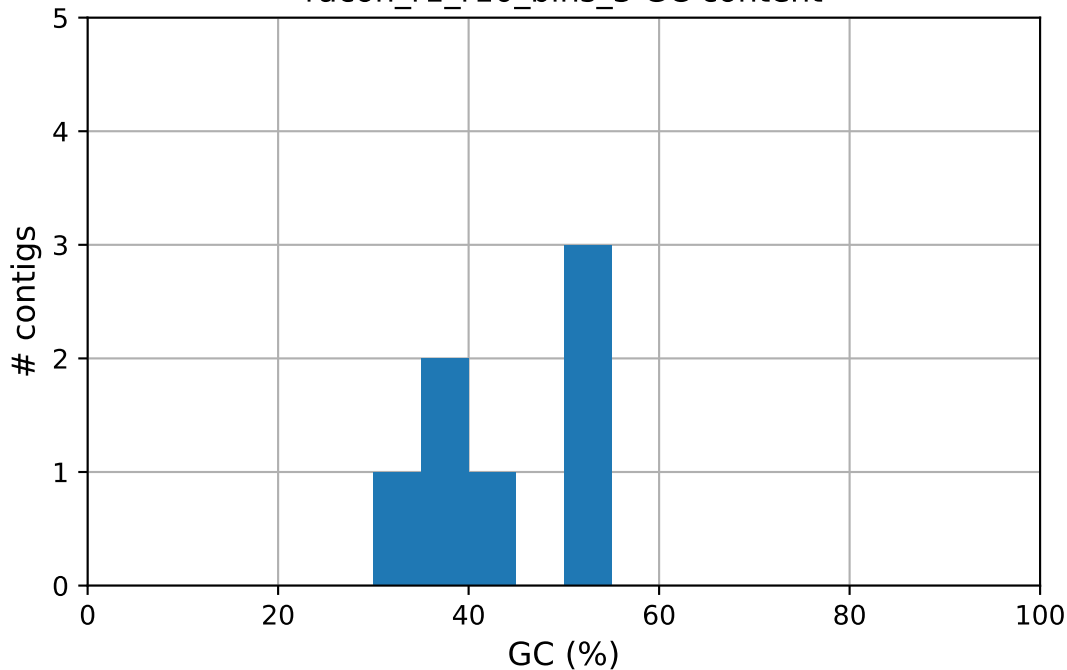
racon_r1_r10_bins_1

racon_r1_r10_bins_2 GC content



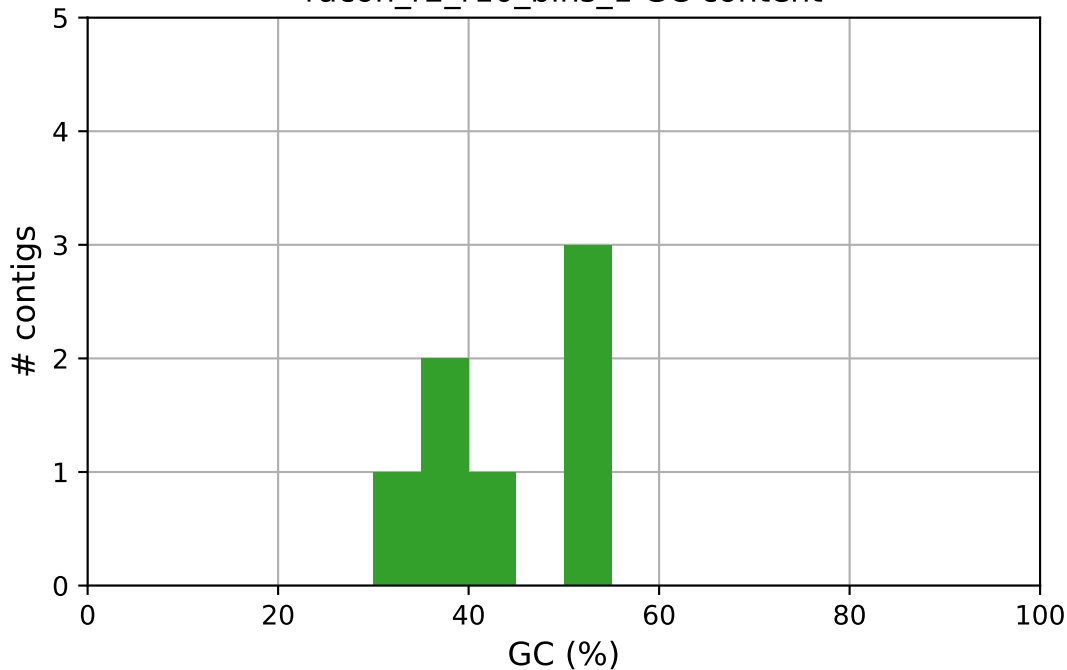
racon_r1_r10_bins_2

racon_r1_r10_bins_3 GC content



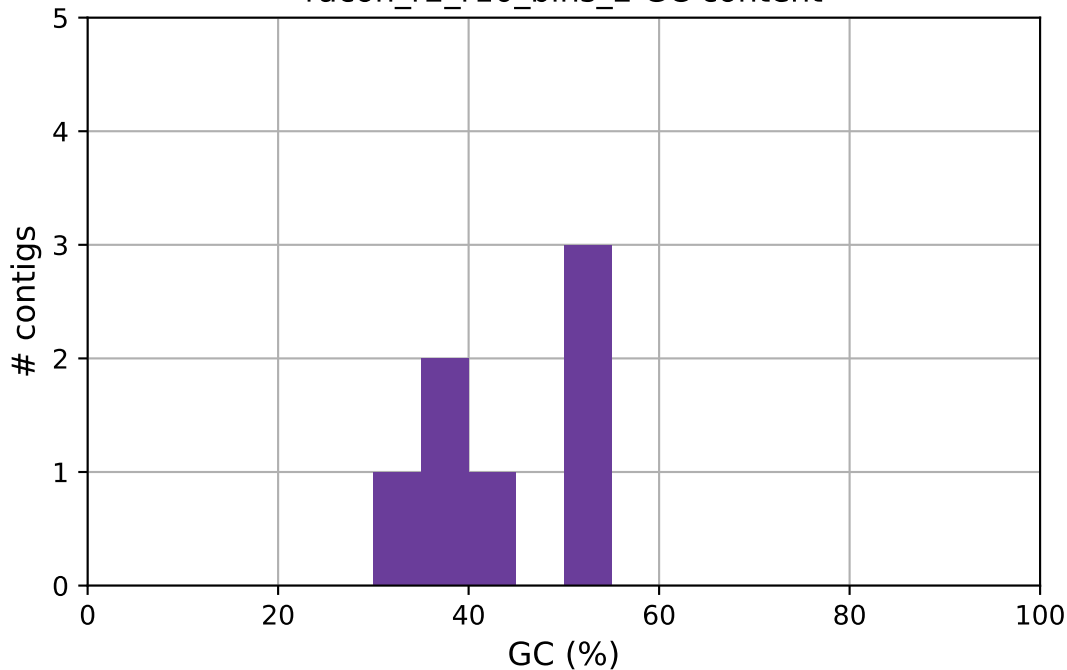
racon_r1_r10_bins_3

racon_r2_r10_bins_1 GC content



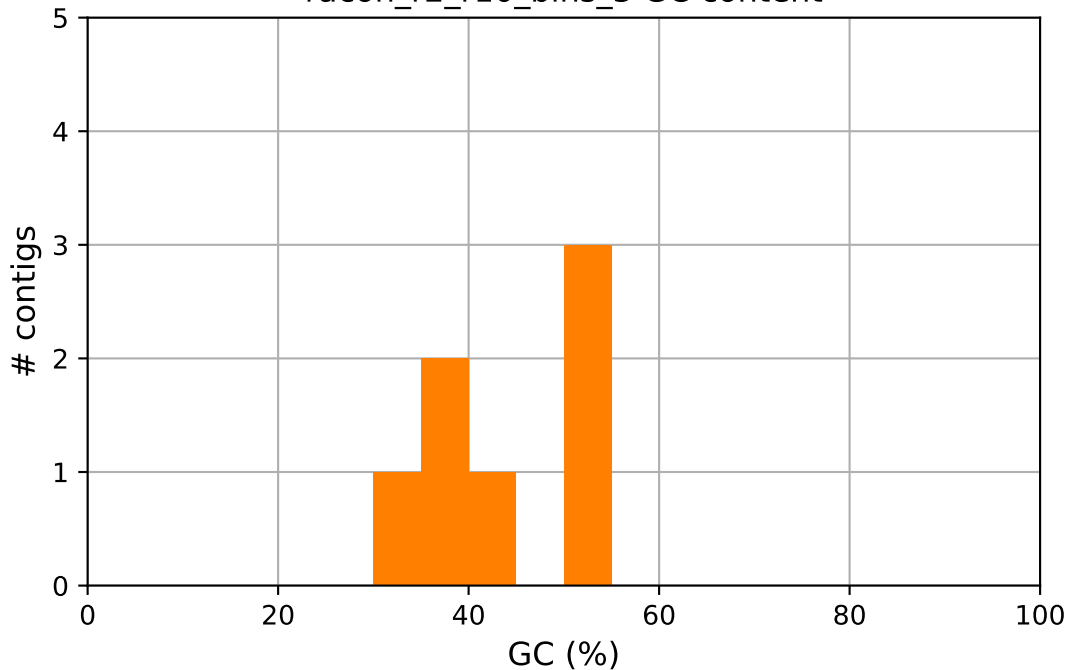
racon_r2_r10_bins_1

racon_r2_r10_bins_2 GC content



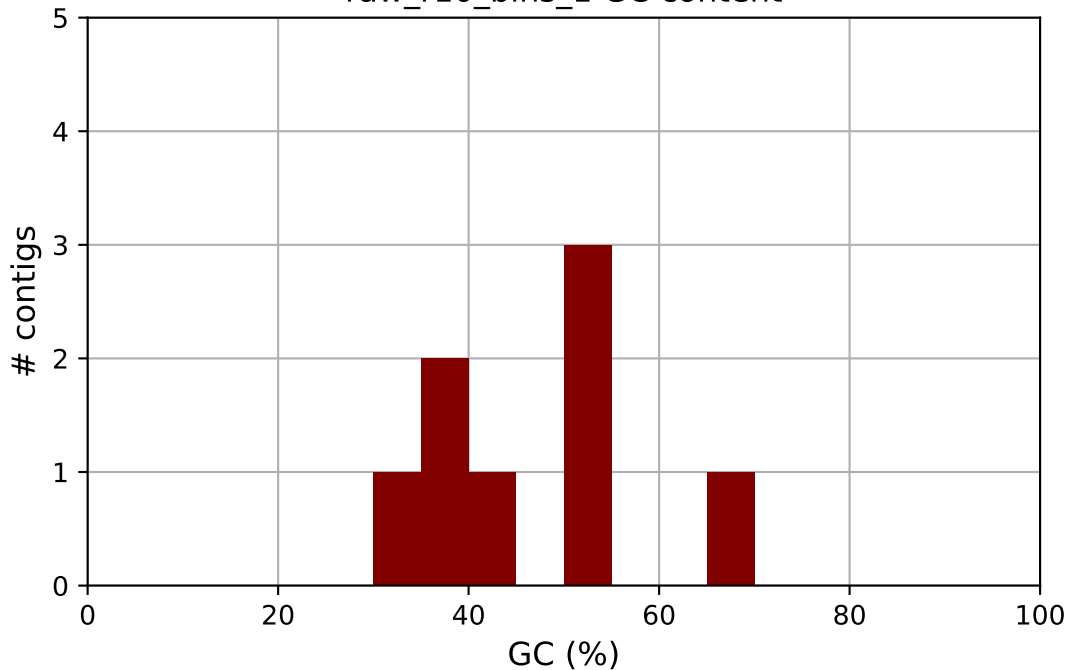
racon_r2_r10_bins_2

racon_r2_r10_bins_3 GC content



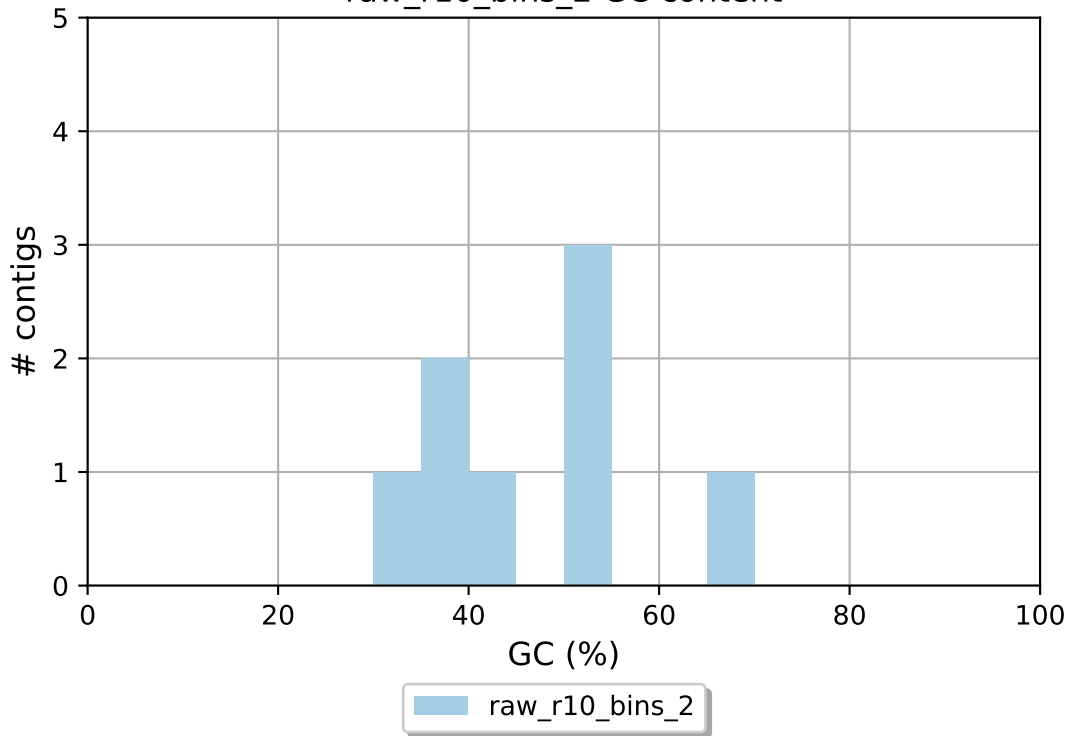
racon_r2_r10_bins_3

raw_r10_bins_1 GC content

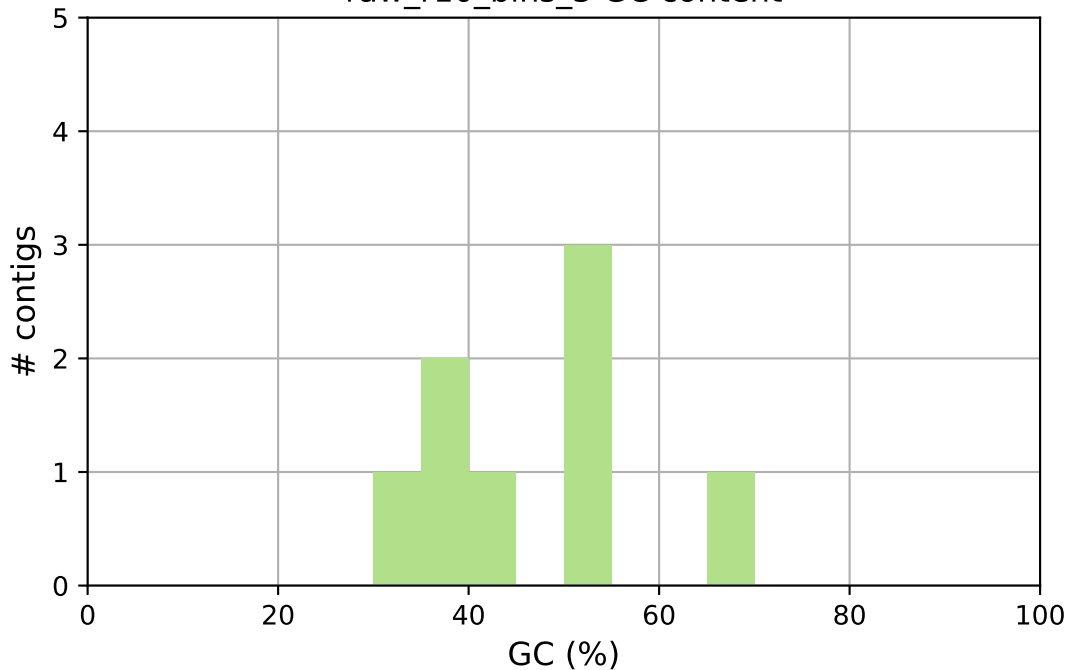


raw_r10_bins_1

raw_r10_bins_2 GC content

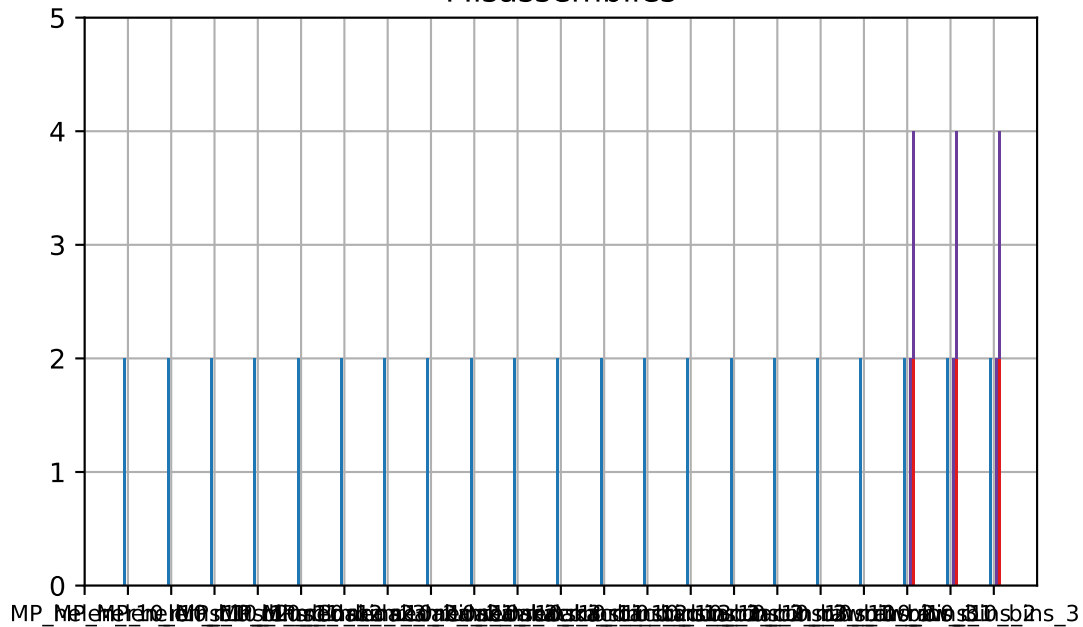


raw_r10_bins_3 GC content

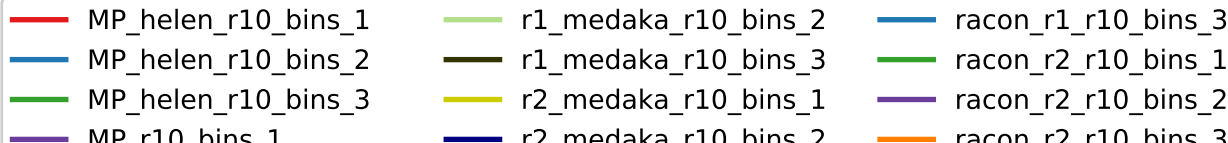
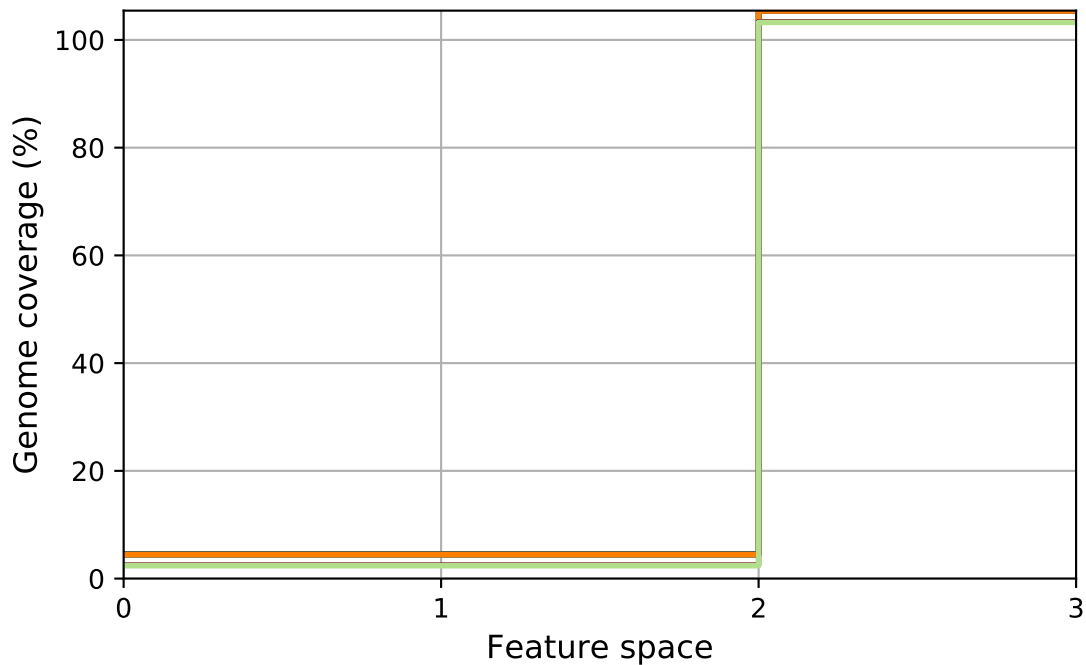


raw_r10_bins_3

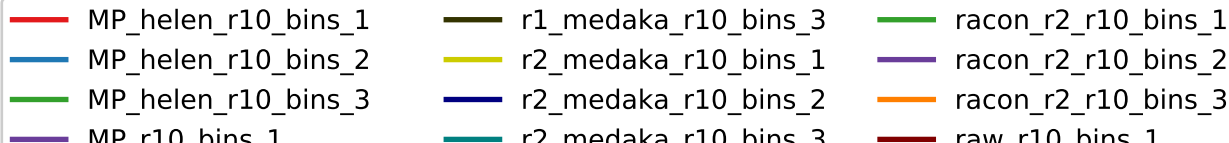
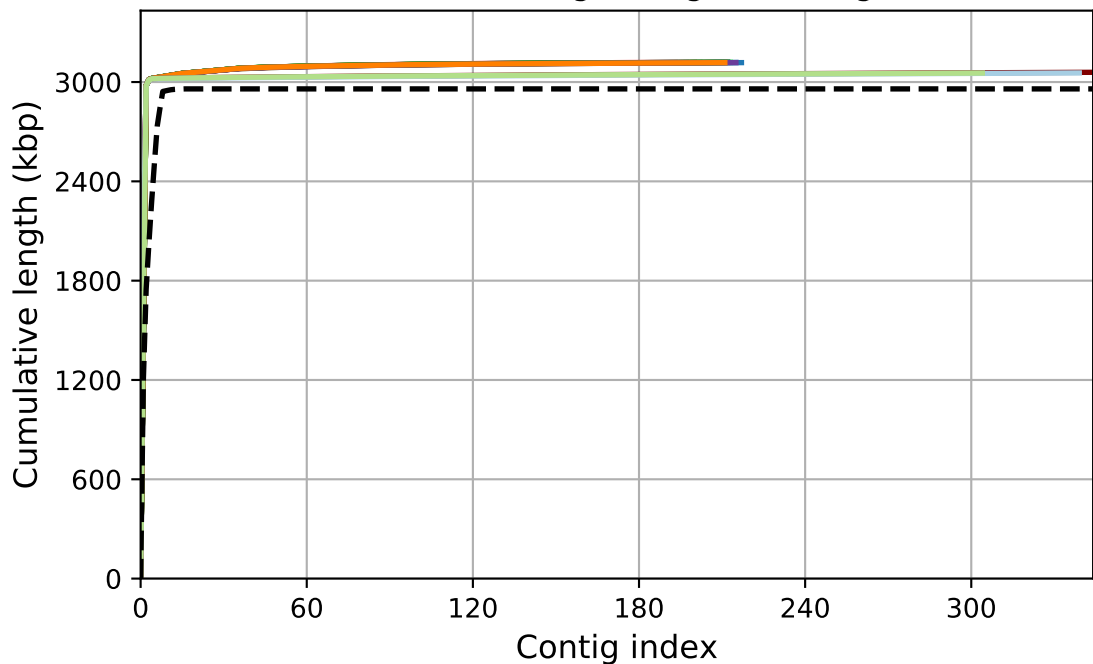
Misassemblies



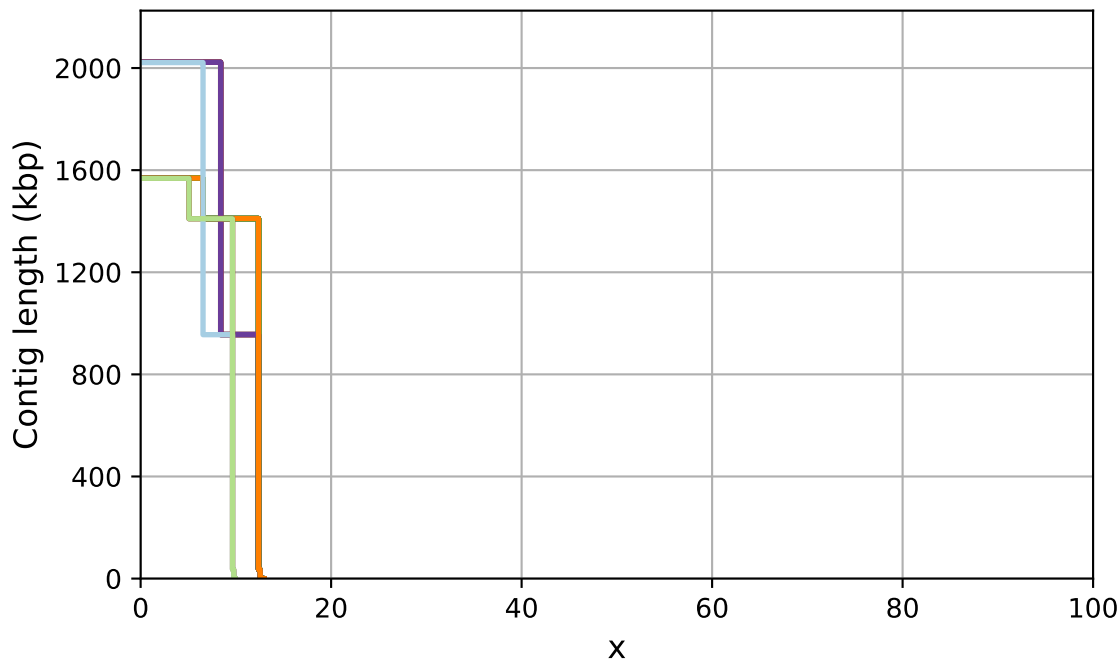
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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

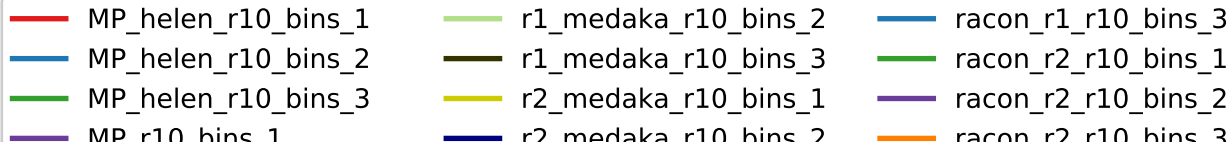
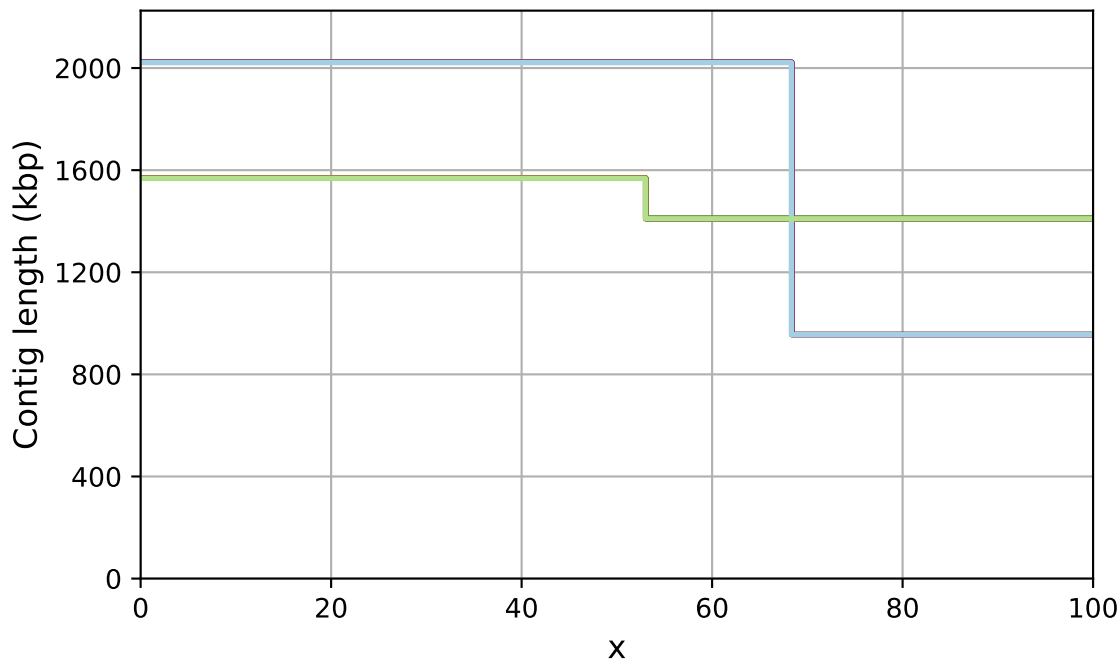
racon_r1_r10_bins_3

racon_r2_r10_bins_1

racon_r2_r10_bins_2

racon_r2_r10_bins_3

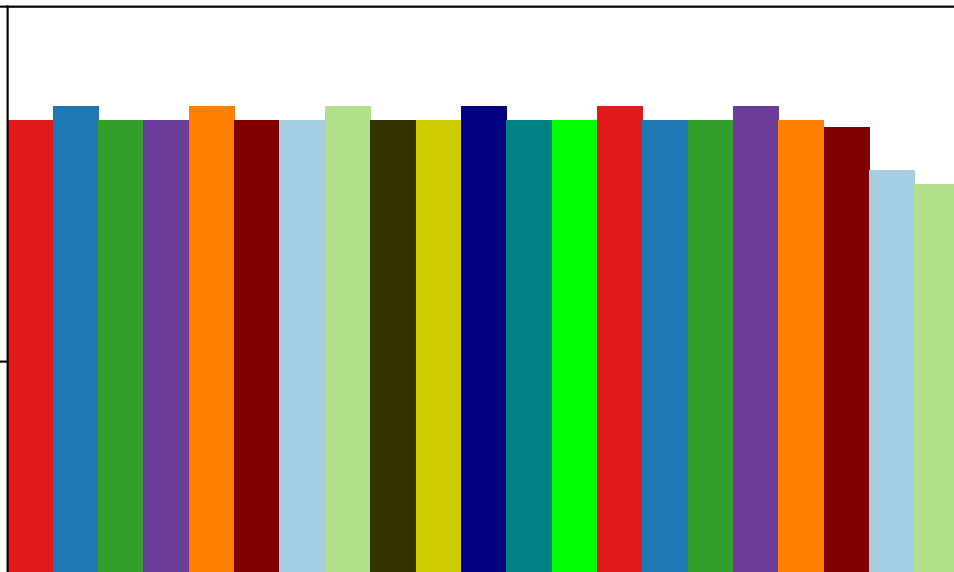
NGAx



Genome fraction, %

100.00

99.95



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