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 (>= 0 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 1000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 5000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 10000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 25000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
# contigs (>= 50000 bp)	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total length (>= 0 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 1000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 5000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 10000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 25000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Total length (>= 50000 bp)	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792153	6792196	6792204	6792195	6792258	6792206	6792241	6792240	6792231	6792247	6792237	6792231	6791608	6791632	6791594	6791690	6791710	6791707	6787702	6787718	6788614
Total length	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4757946	4757846	4757780	4758962	4758994	4758970	4758583	4758586	4758587	4758100	4758114	4758101	4757934	4757908	4757887	4757853	4757839	4757857	4755983	4756088	4755683
N75	2992064	2992055	2992078	2992084	2992059	2992095	2992070	2992047	2992077	2992072	2992049	2992076	2991922	2991946	2991934	2991954	2991964	2991975	2990633	2990279	2990261
L50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
L75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
# misassemblies	168	170	169	171	168	171	171	168	170	169	171	170	174	168	175	170	173	171	173	172	174
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Misassembled contigs length	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
# local misassemblies	120	114	118	116	115	116	129	129	127	140	131	137	154	148	154	141	135	147	211	210	220
# 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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# 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	79565	78195	78875	79117	78323	79121	81460	80932	82331	83674	80168	84789	77362	78353	76984	77636	76509	78011	138521	136824	144818
Genome fraction (%)	99.394	99.400	99.398	99.400	99.400	99.399	99.398	99.400	99.398	99.398	99.399	99.399	99.397	99.398	99.396	99.396	99.398	99.396	99.369	99.371	99.371
Duplication ratio	1.044	1.044	1.044	1.044	1.043	1.043	1.044	1.044	1.044	1.043	1.043	1.043	1.043	1.043	1.043	1.043	1.043	1.043	1.028	1.027	1.028
# 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	168.17	166.00	167.75	176.47	173.47	174.92	178.85	177.70	178.75	174.32	173.20	175.00	177.22	175.15	176.37	177.93	175.97	178.72	269.69	272.89	272.56
# indels per 100 kbp	24.42	21.37	21.94	38.67	38.32	38.65	26.56	26.89	27.16	26.23	26.12	26.79	62.03	61.89	61.93	57.85	58.56	57.14	305.23	308.79	306.54
Largest alignment	2559993	2395781	2593982	2560095	2395774	2594051	2560100	2395776	2594057	2560100	2395777	2594055	2559973	2395662	2593934	2560012	2395671	2593947	2555544	2389434	2590031
Total aligned length	30746119	30740559	30751251	30749875	30742915	30753462	30747605	30739946	30748203	30735289	30731381	30736256	30738378	30731783	30742614	30734140	30729618	30731685	30681327	30672256	30675980
NA50	948383	948350	948302	949048	948286	948950	948968	948851	948875	948989	948885	948890	949226	949109	949153	949271	949166	949165	788152	777743	788149
NA75	399301	394041	381438	399298	394054	381657	399301	394045	381619	399302	394045	381615	399233	393984	373882	399242	394006	381605	345502	381477	373536
LA50	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
LA75	23	25	23	23	25	24	23	25	23	23	25	23	23	25	23	23	25	23	26	26	26

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

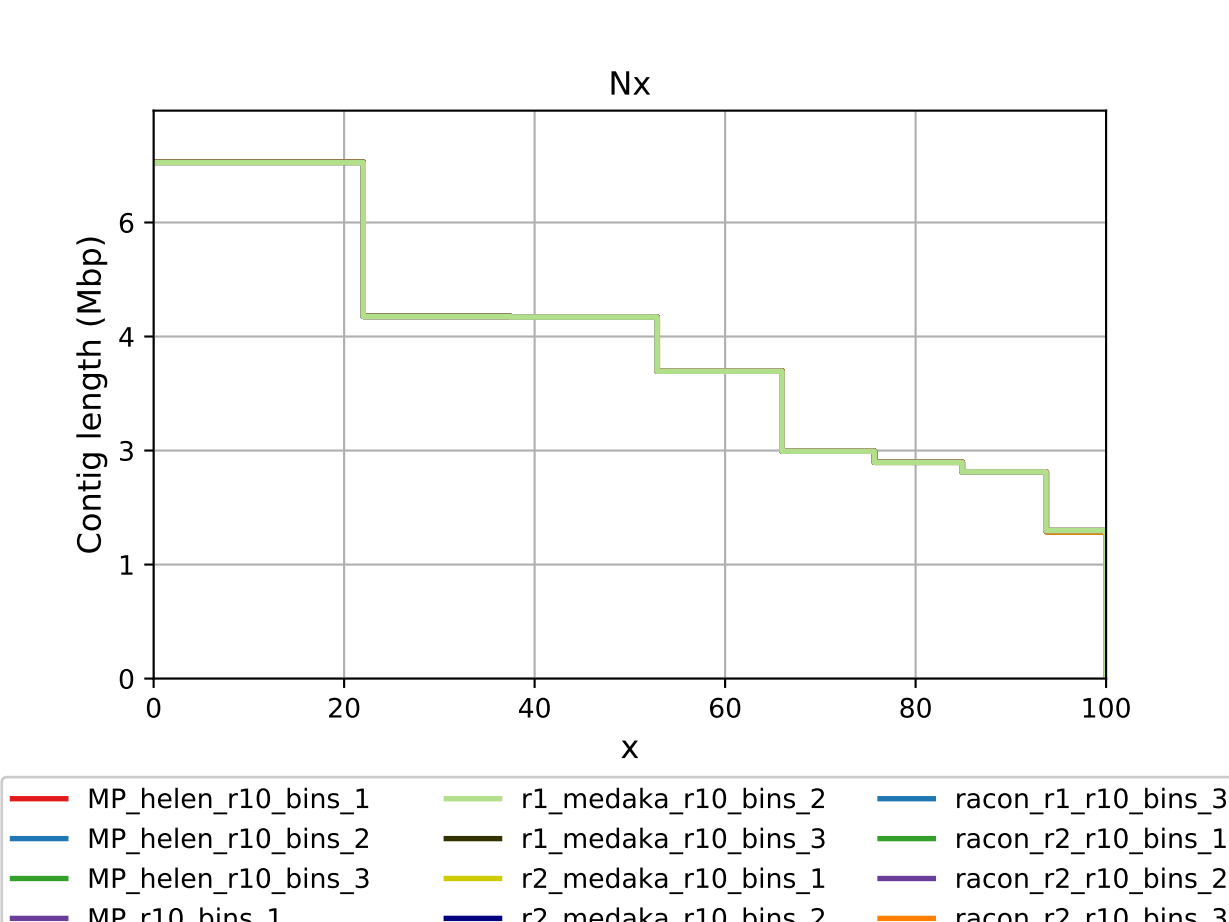
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	racon_r2_r10_bins_2	racon_r2_r10_bins_3	raw_r10_bins_1	raw_r10_bins_2	raw_r10_bins_3
# misassemblies	168	170	169	171	168	171	171	168	170	169	171	170	174	168	175	170	173	171	173	172	174
# contig misassemblies	168	170	169	171	168	171	171	168	170	169	171	170	174	168	175	170	173	171	173	172	174
# c. relocations	4	5	4	6	5	6	4	5	4	5	6	5	4	5	4	5	6	5	5	6	5
# c. translocations	162	163	163	163	161	163	165	161	164	162	163	163	168	161	169	163	165	164	164	162	165
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# c. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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
# 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
# s. interspecies translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Misassembled contigs length	30861647	30864927	30862476	30867341	30868189	30867430	30864833	30867104	30865019	30857195	30860390	30858038	30851337	30856276	30850927	30846769	30852342	30844210	30847938	30850309	30849039
# possibly misassembled contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# possible misassemblies	98	96	98	98	98	98	96	96	98	102	96	98	96	100	92	96	92	96	169	166	177
# local misassemblies	120	114	118	116	115	116	129	129	127	140	131	137	154	148	154	141	135	147	211	210	220
# 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	251	252	251	252	253	252	250	251	250	253	252	252	248	247	248	251	247	249	178	181	173
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# mismatches	50998	50343	50872	53517	52607	53047	54237	53891	54207	52863	52524	53072	53742	53116	53486	53957	53365	54197	81762	82733	82635
# indels	7405	6480	6655	11727	11621	11720	8054	8154	8236	7955	7922	8124	18811	18769	18781	17543	17759	17328	92537	93619	92935
# indels (<= 5 bp)	6722	5834	6000	11073	10974	11072	7462	7549	7643	7361	7320	7533	18181	18102	18154	16910	17101	16687	91315	92409	91728
# indels (> 5 bp)	683	646	655	654	647	648	592	605	593	594	602	591	630	667	627	633	658	641	1222	1210	1207
Indels length	42042	40462	40455	46191	45867	45751	40692	41364	41072	40540	40765	40643	55906	56587	55359	53952	55510	53006	155914	158186	156087

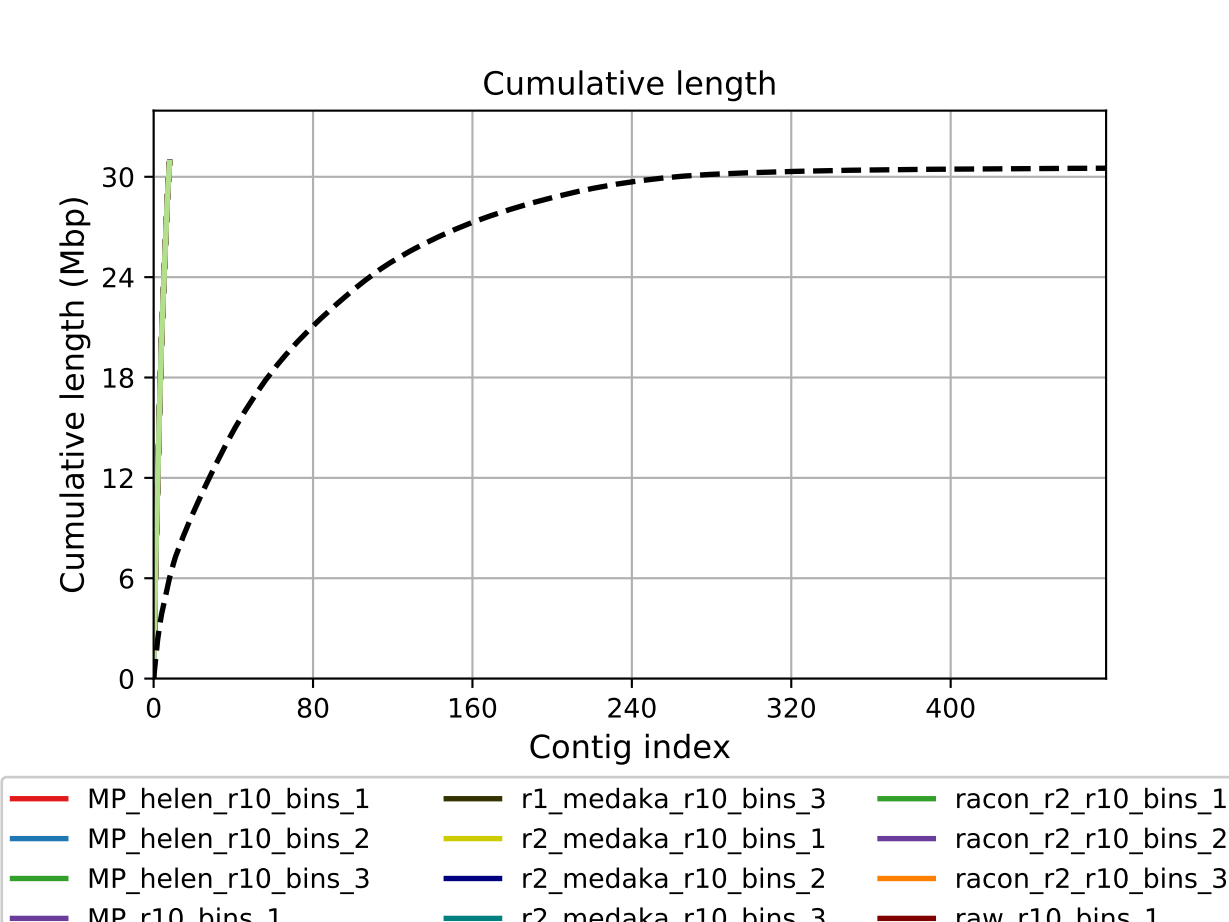
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

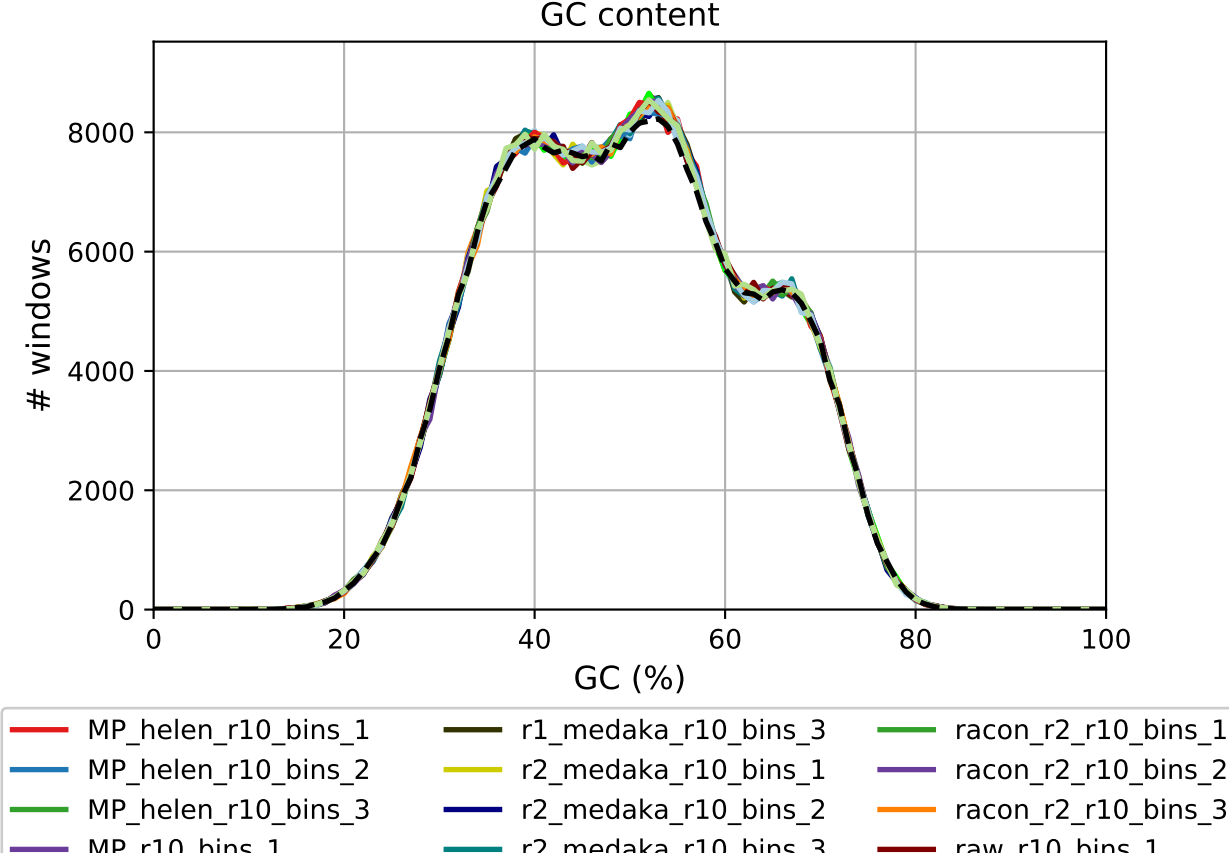
Unaligned report

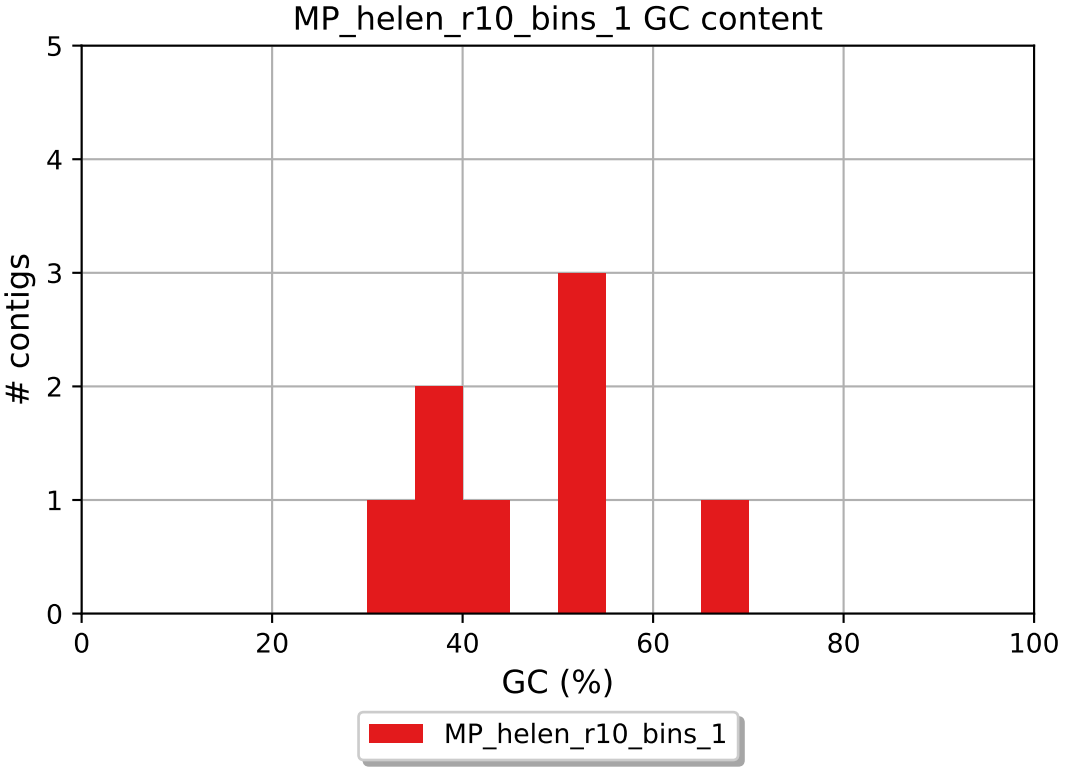
	MP_helen_r10_bins_1	MP_helen_r10_bins_2	MP_helen_r10_bins_3	MP_r10_bins_1	MP_r10_bins_2	MP_r10_bins_3	r1_medaka_r10_bins_1	r1_medaka_r10_bins_2	r1_medaka_r10_bins_3	r2_medaka_r10_bins_1	r2_medaka_r10_bins_2	r2_medaka_r10_bins_3	racon_r1_r10_bins_1	racon_r1_r10_bins_2	racon_r1_r10_bins_3	racon_r2_r10_bins_1	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	79565	78195	78875	79117	78323	79121	81460	80932	82331	83674	80168	84789	77362	78353	76984	77636	76509	78011	138521	136824	144818
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

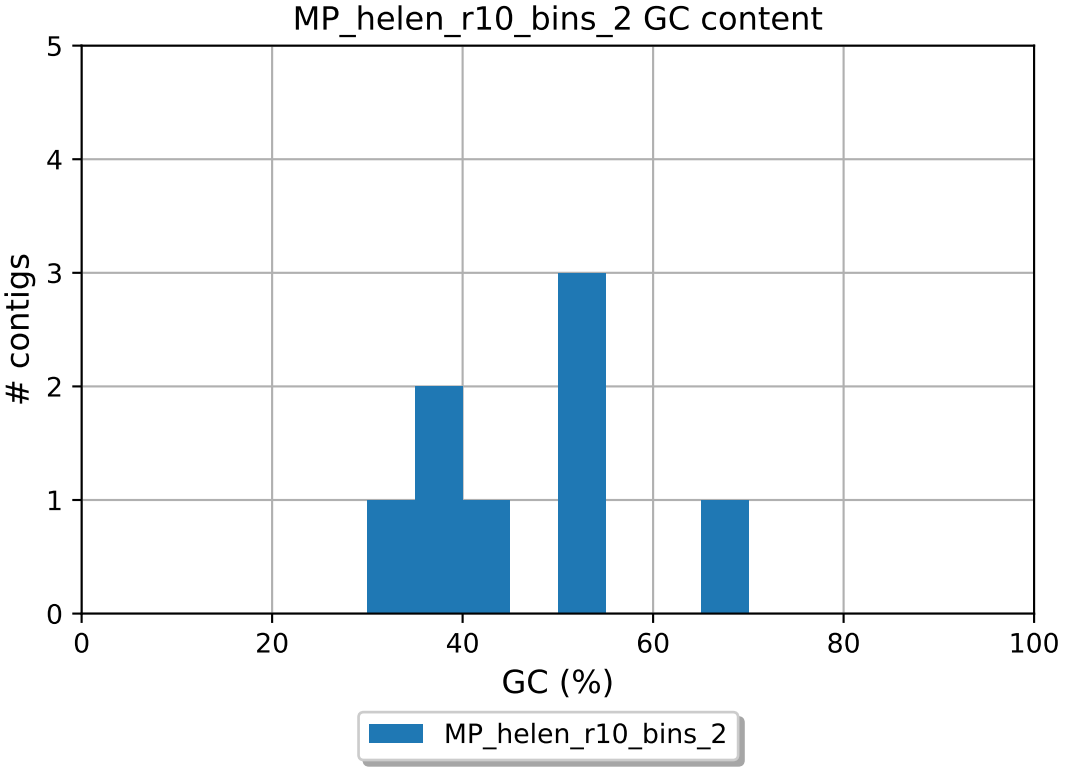
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

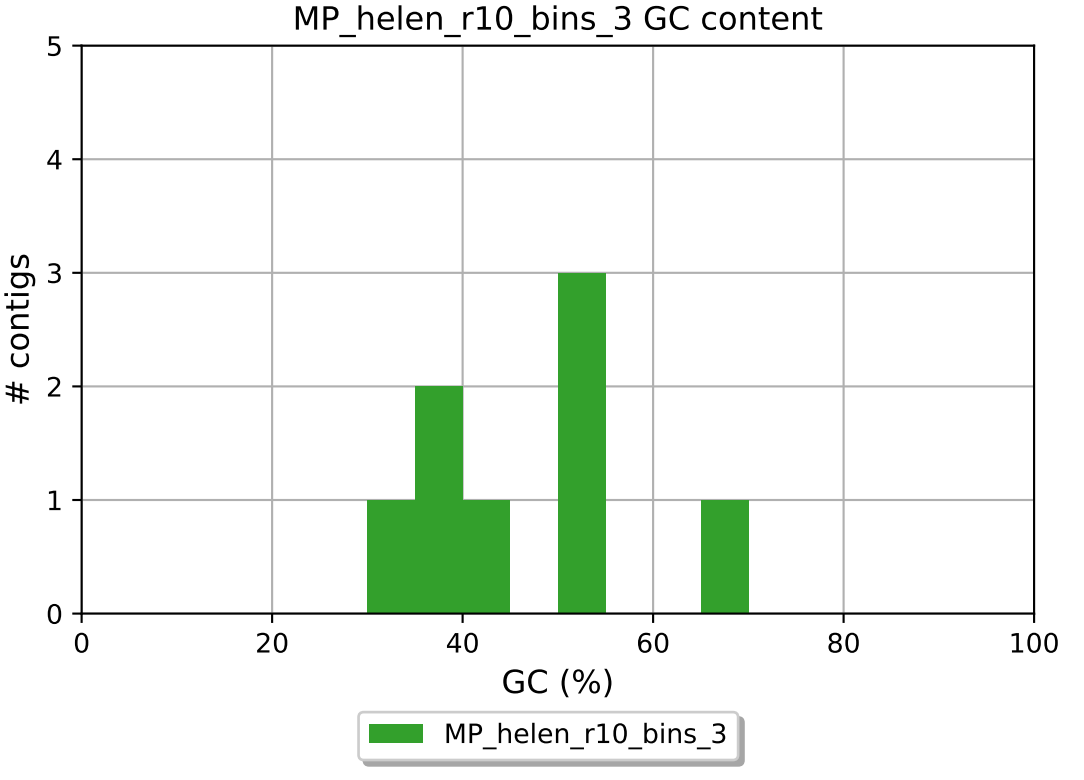

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
r1_medaka_r10_bins_2
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
racon_r1_r10_bins_3
racon_r2_r10_bins_1
racon_r2_r10_bins_2

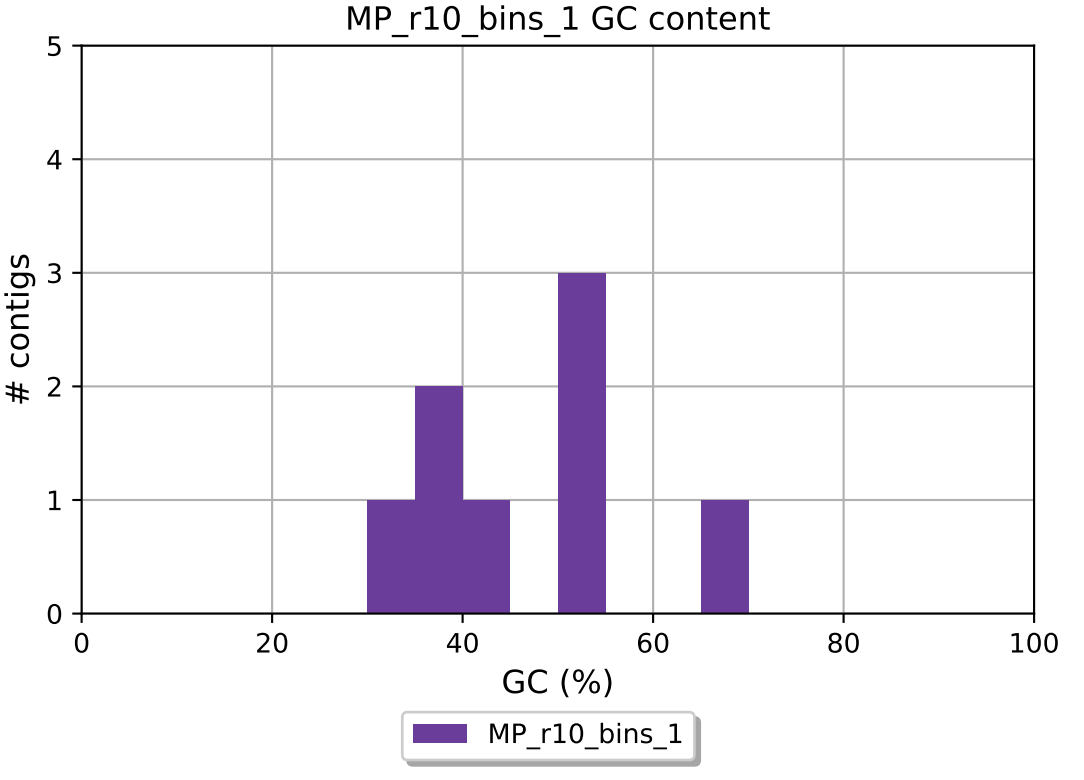

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
80
160
240
320
400
Contig index
MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
MP_r10_bins_1
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
r2_medaka_r10_bins_2
r2_medaka_r10_bins_3
racon_r2_r10_bins_1
racon_r2_r10_bins_2
racon_r2_r10_bins_3
raw_r10_bins_1

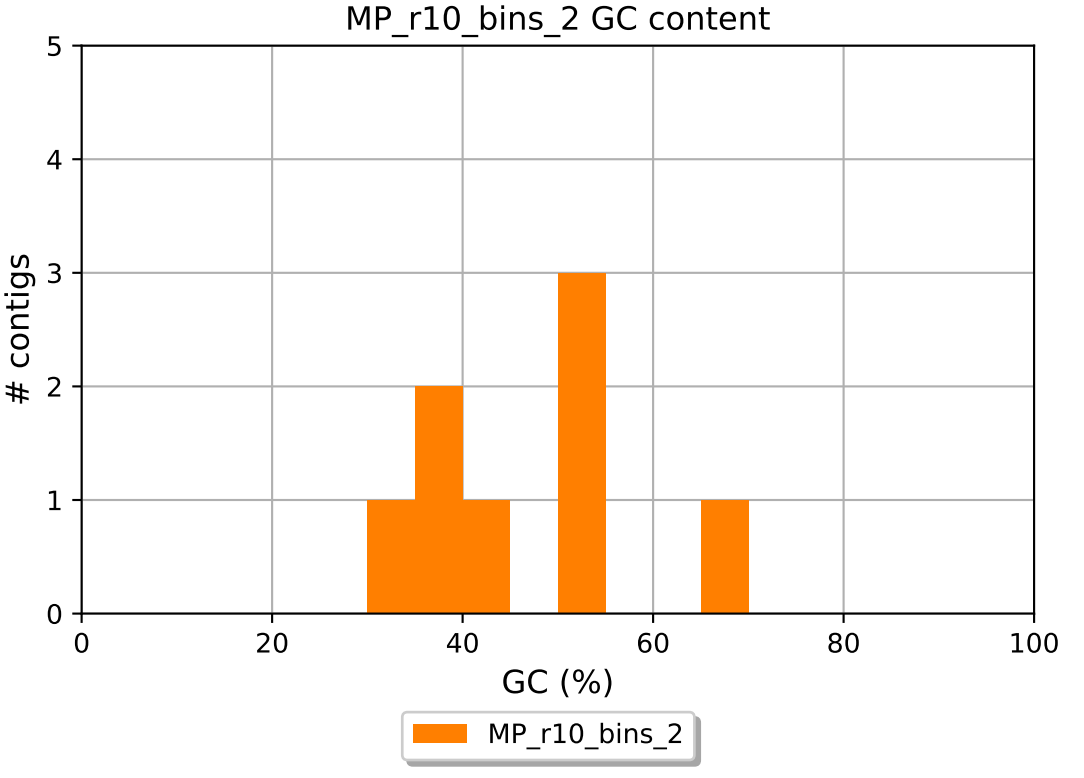

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
r2_medaka_r10_bins_2
racon_r2_r10_bins_1
racon_r2_r10_bins_2
racon_r2_r10_bins_3

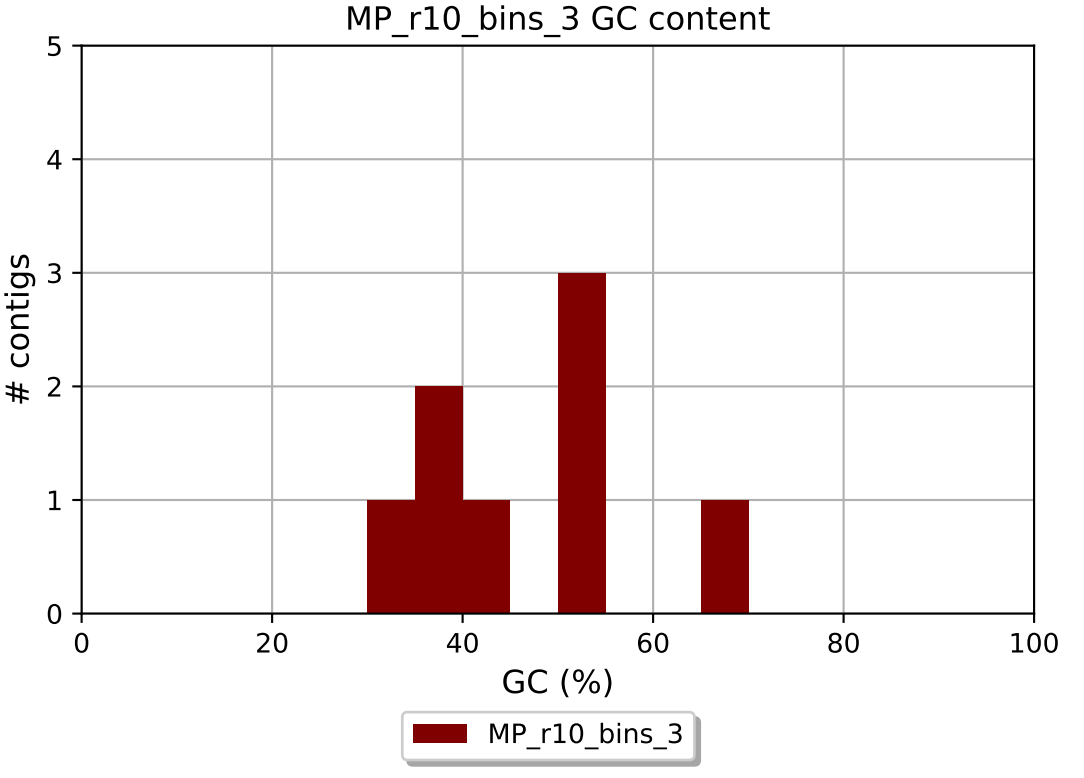

MP_helen_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_bins_1

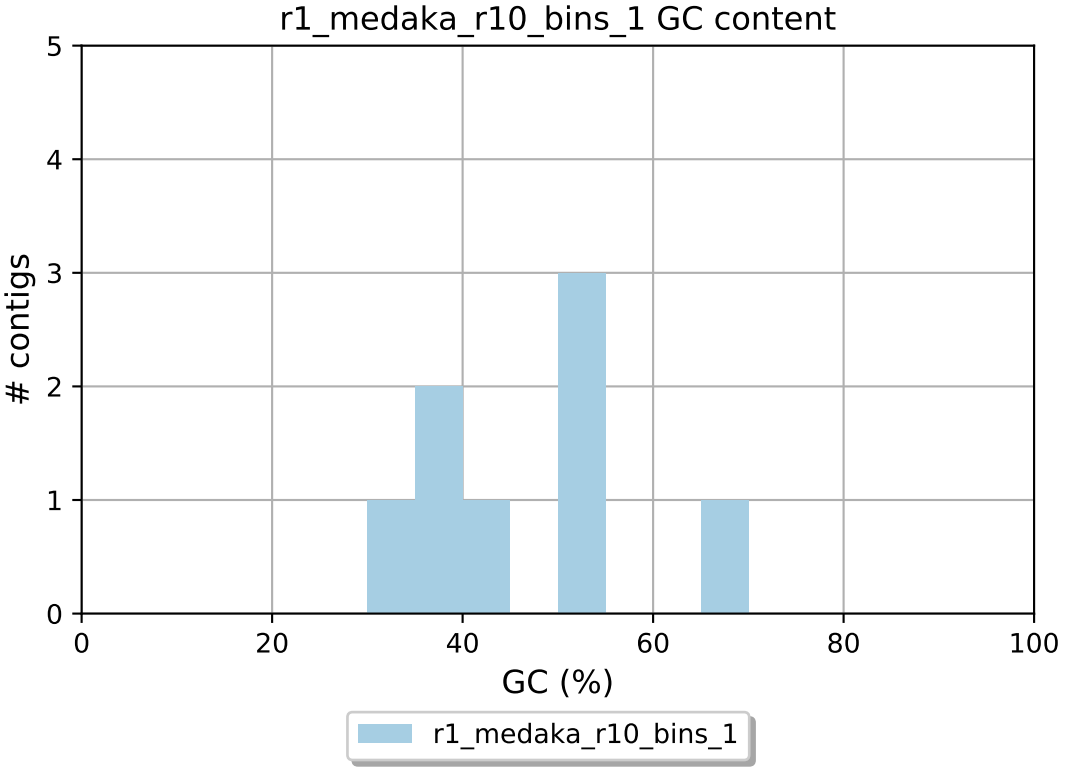

MP_helen_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_bins_2

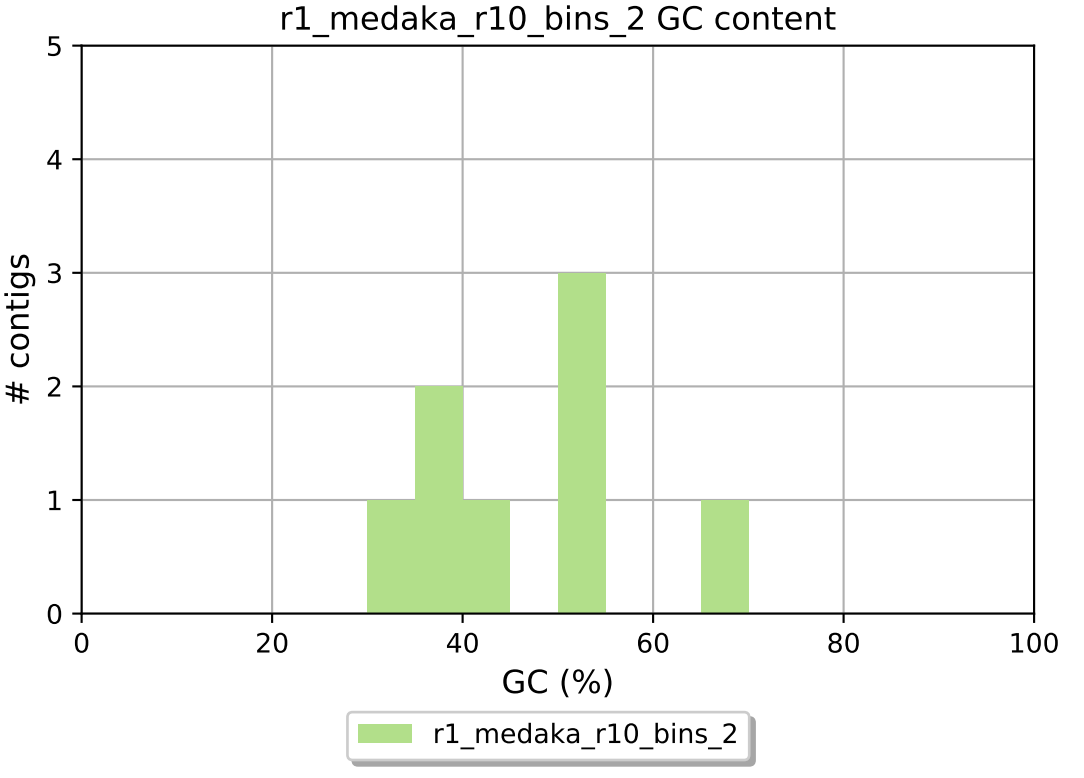

MP_helen_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_bins_3

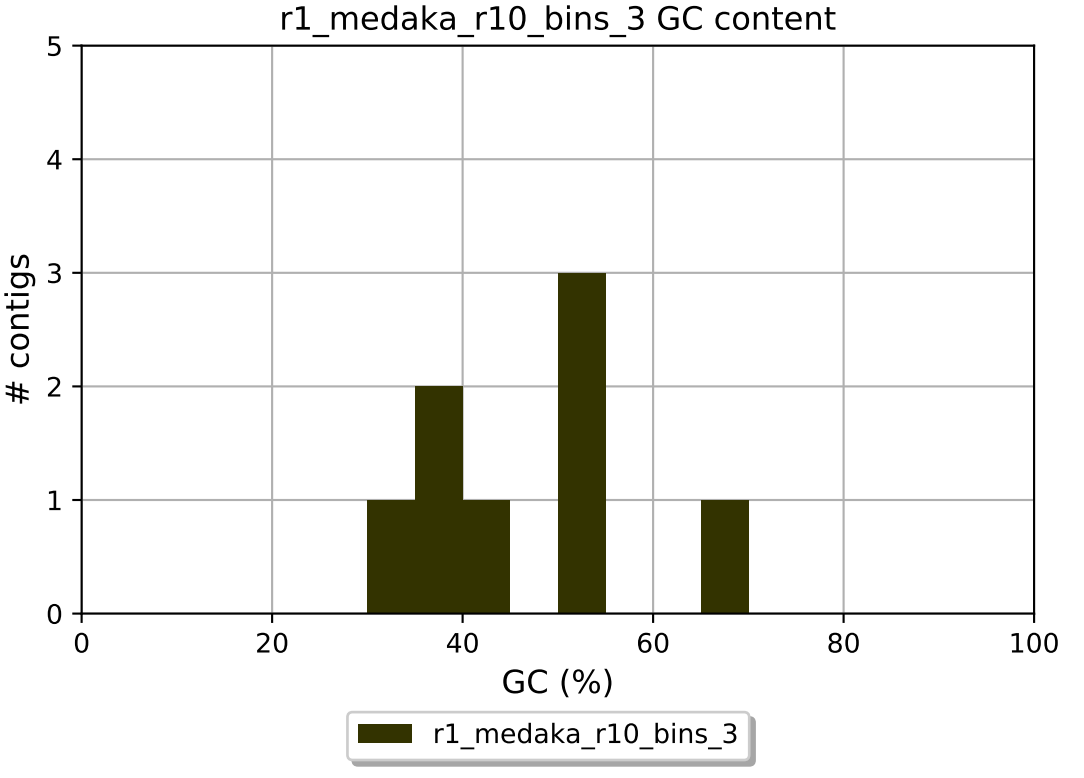

MP_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_bins_1

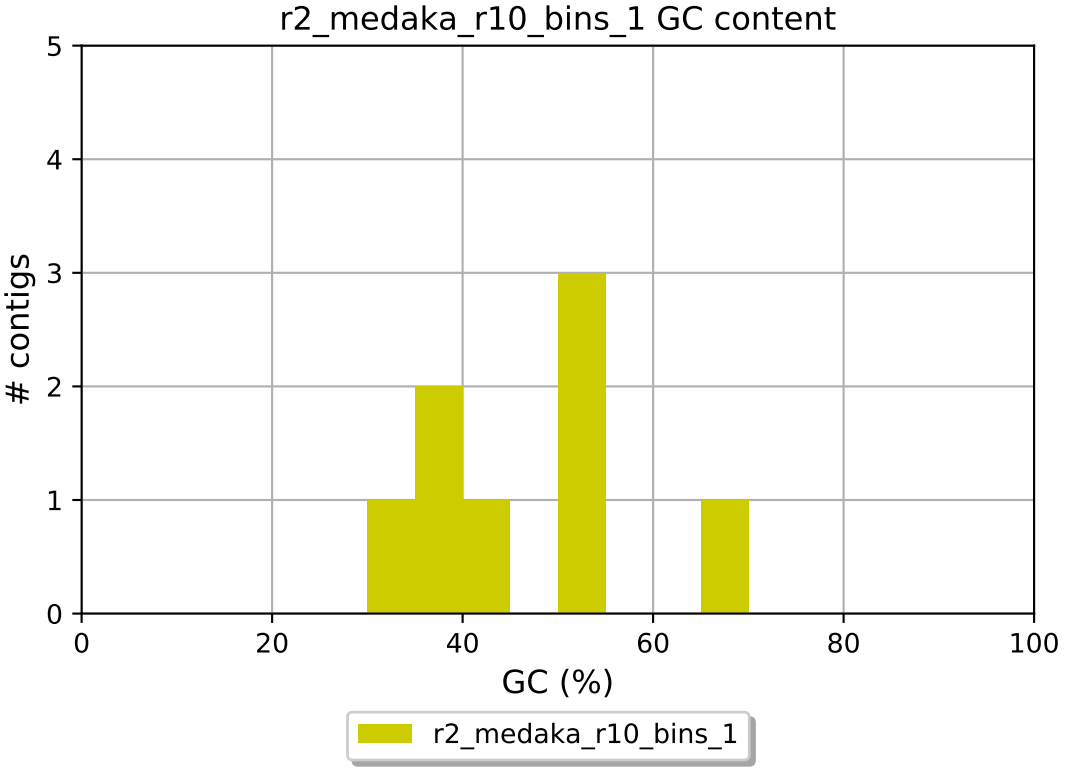

MP_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_bins_2

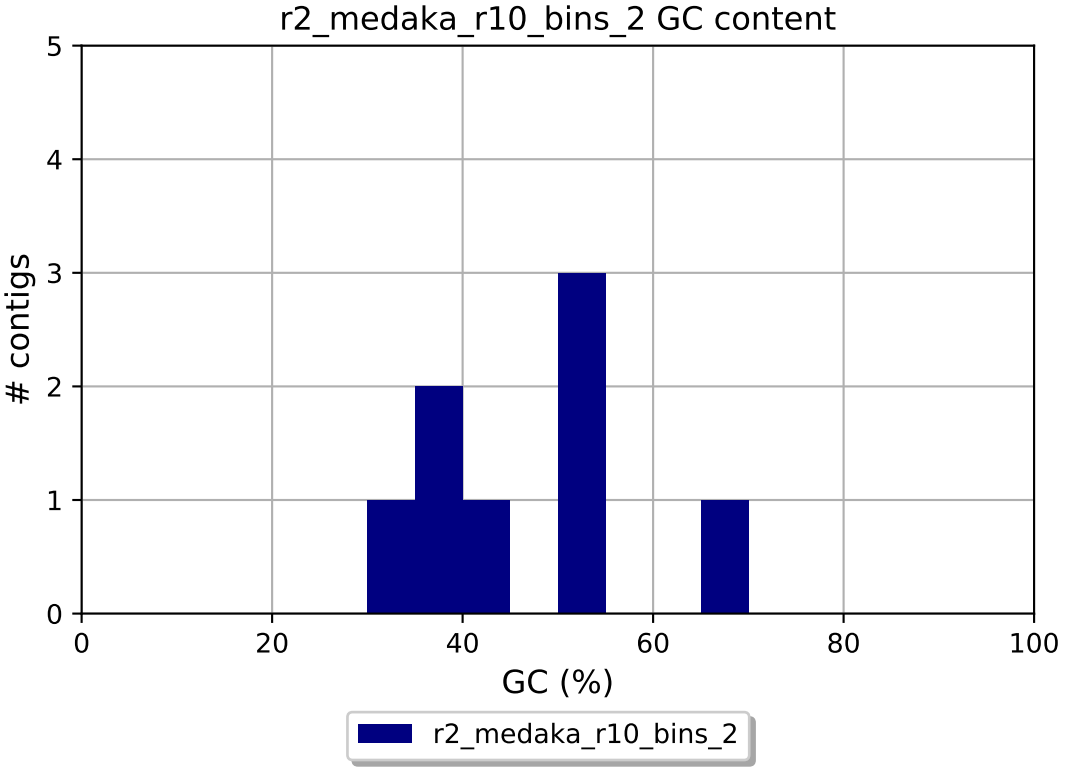

MP_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_bins_3

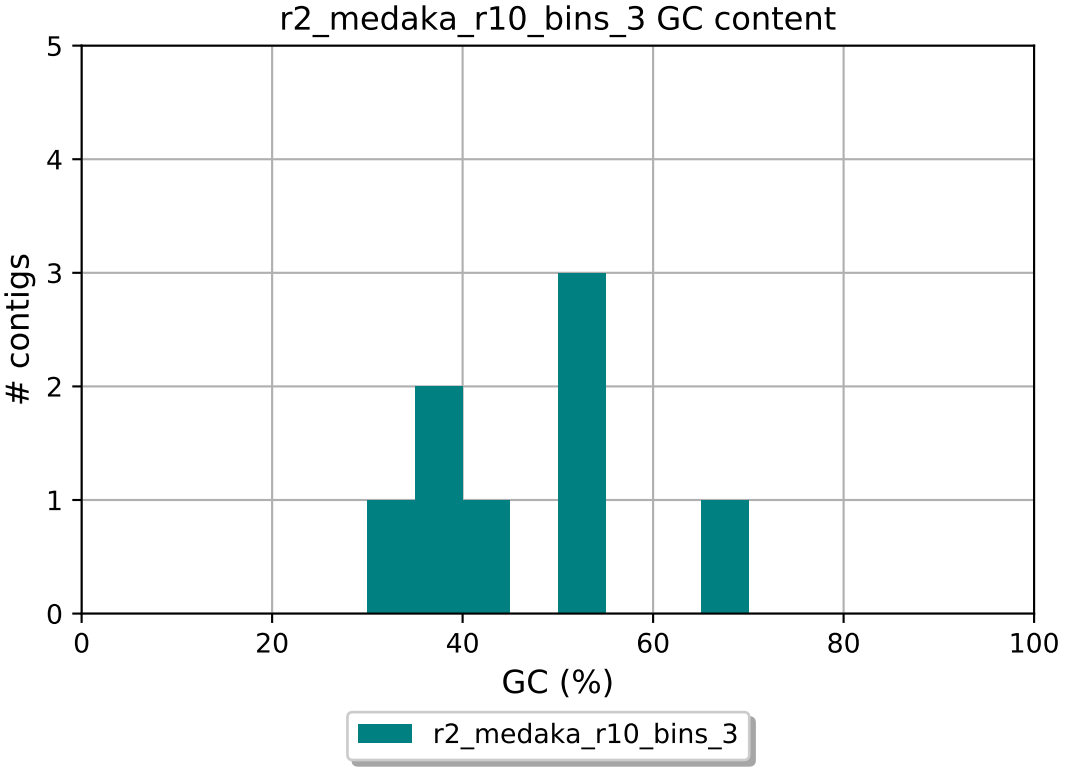

r1_medaka_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_bins_1

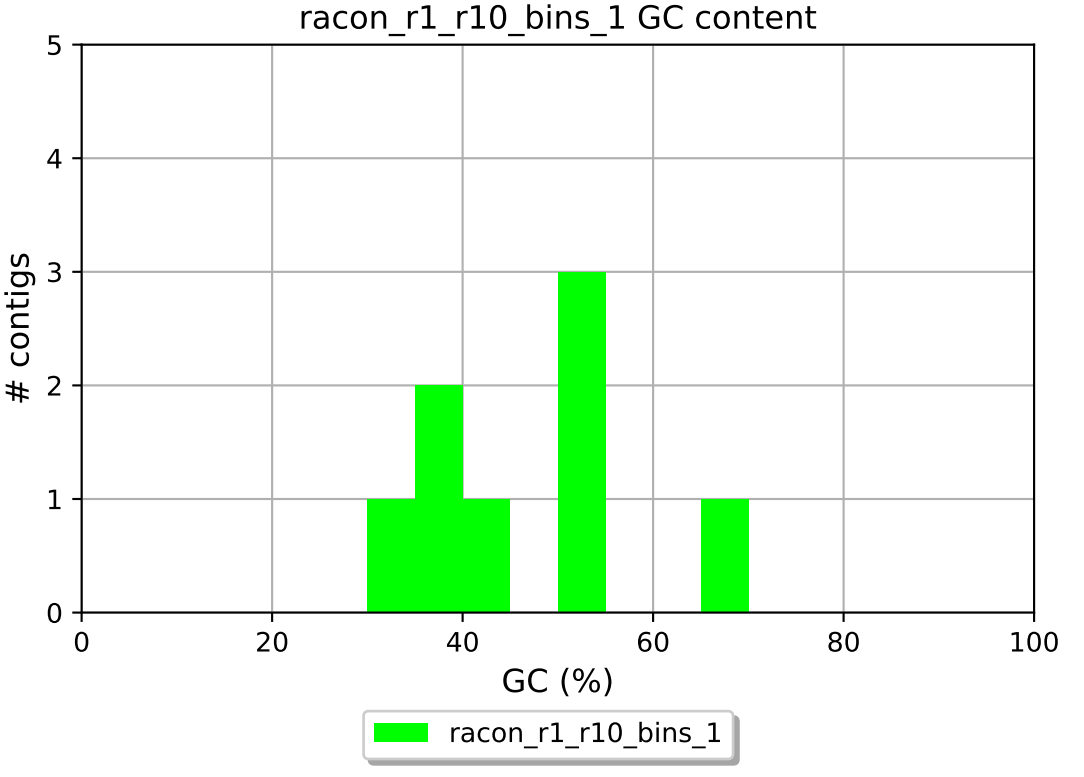

r1_medaka_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_bins_2

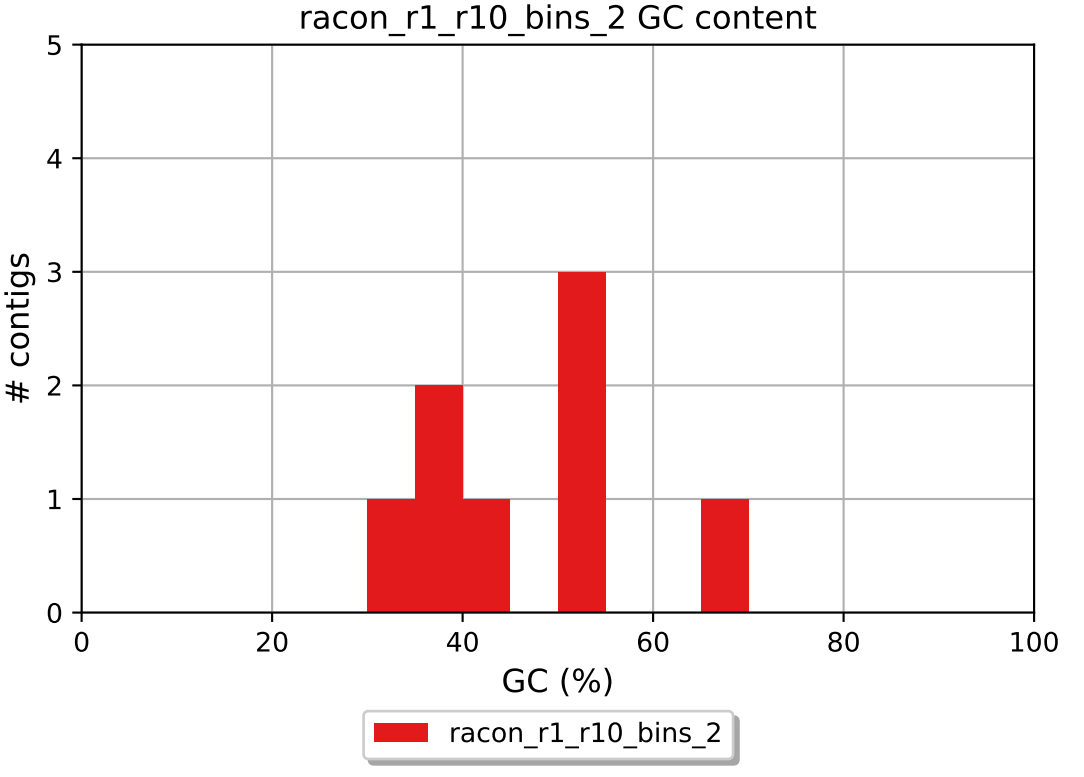

r1_medaka_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_bins_3

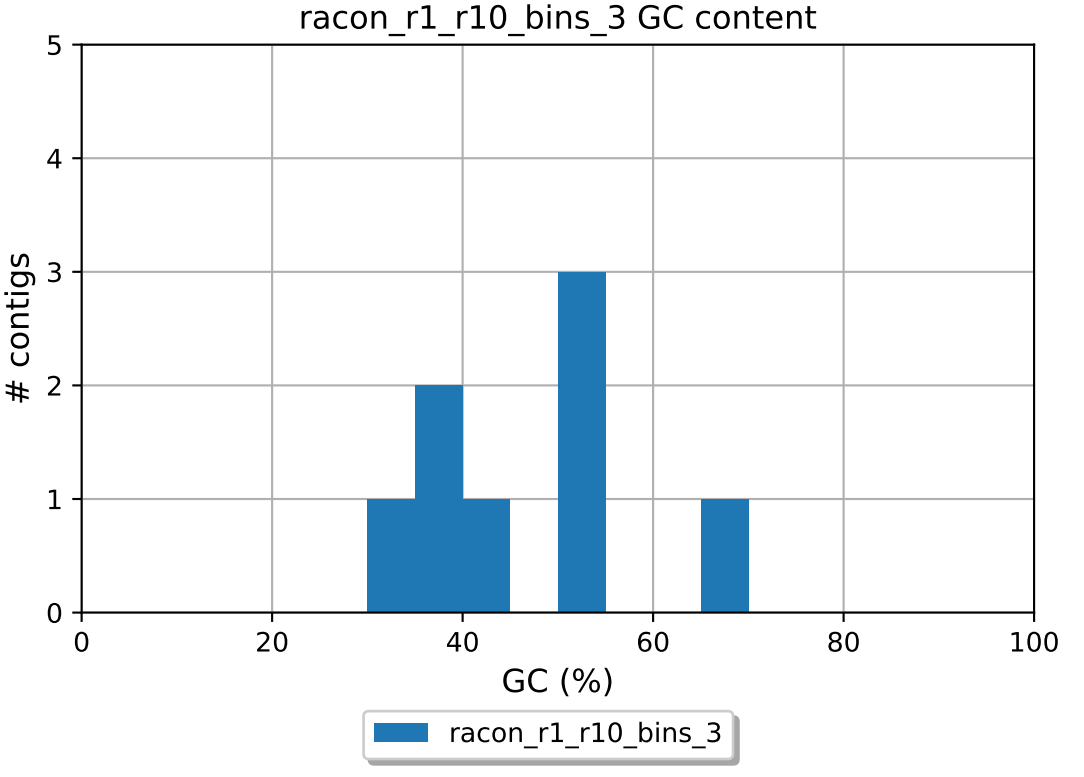

r2_medaka_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_bins_1

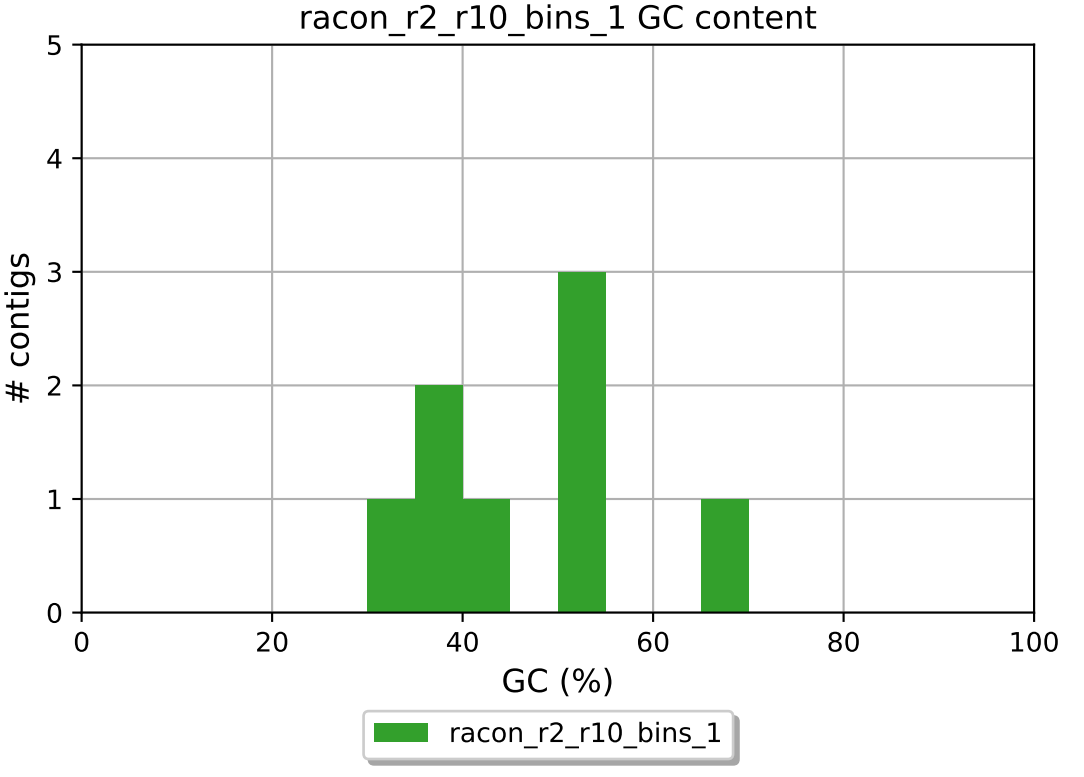

r2_medaka_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_bins_2

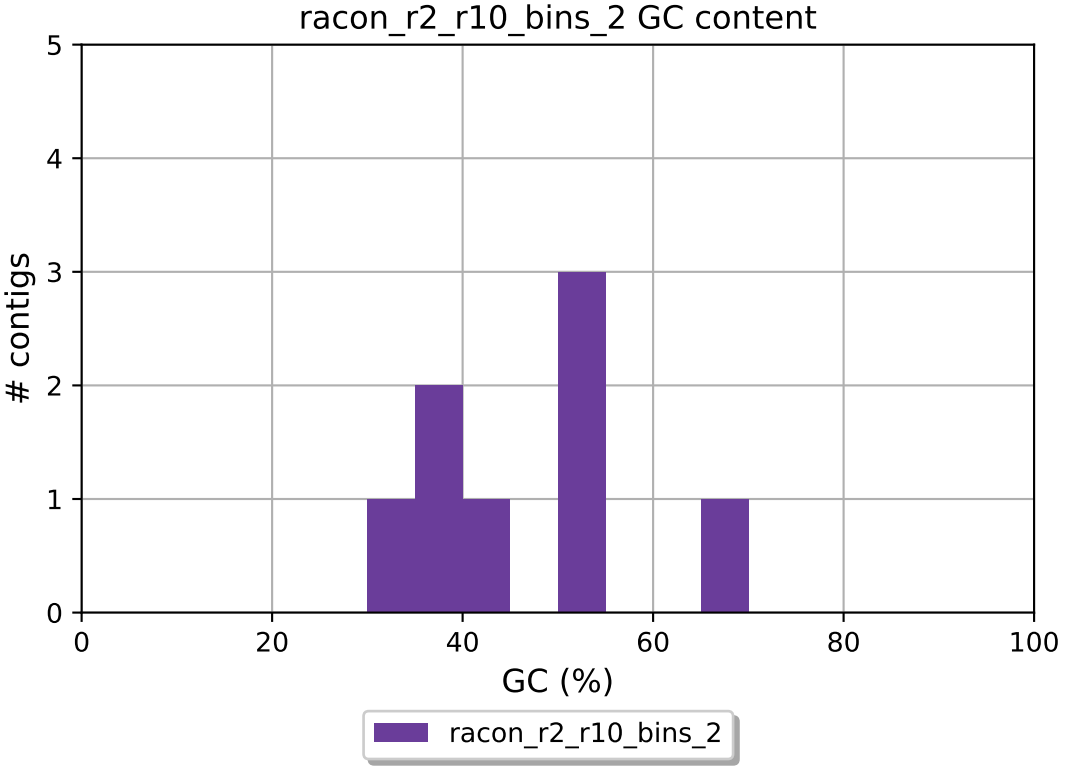

r2_medaka_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_bins_3

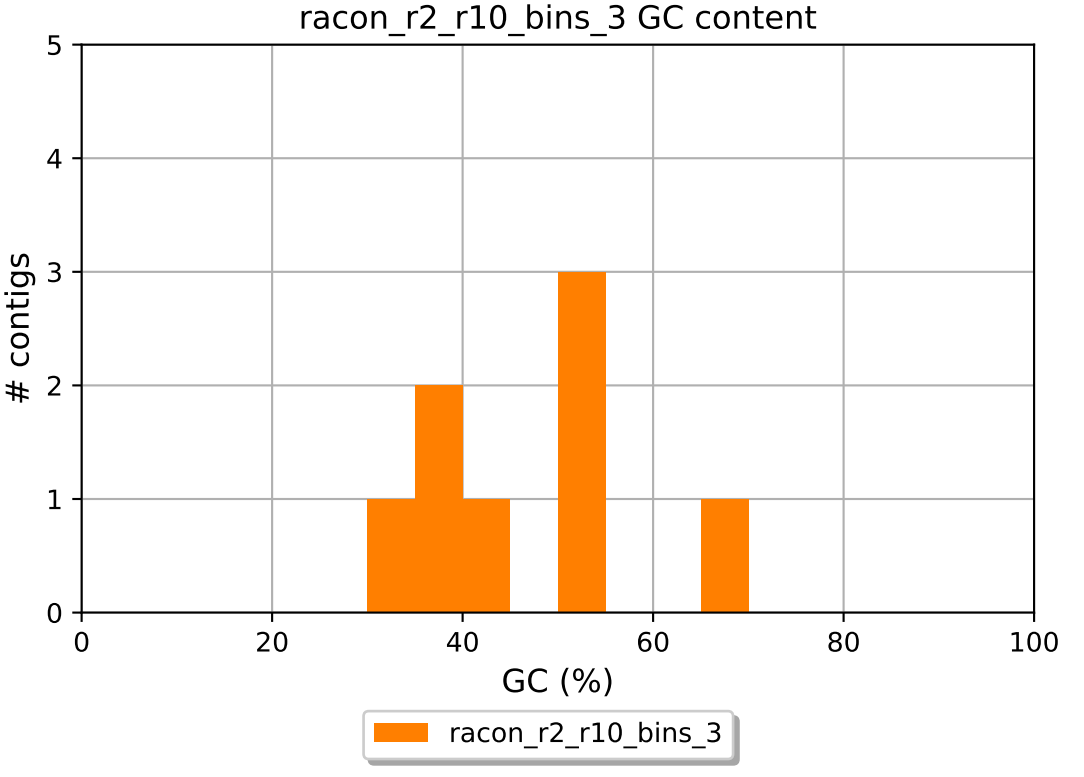

racon_r1_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_bins_1

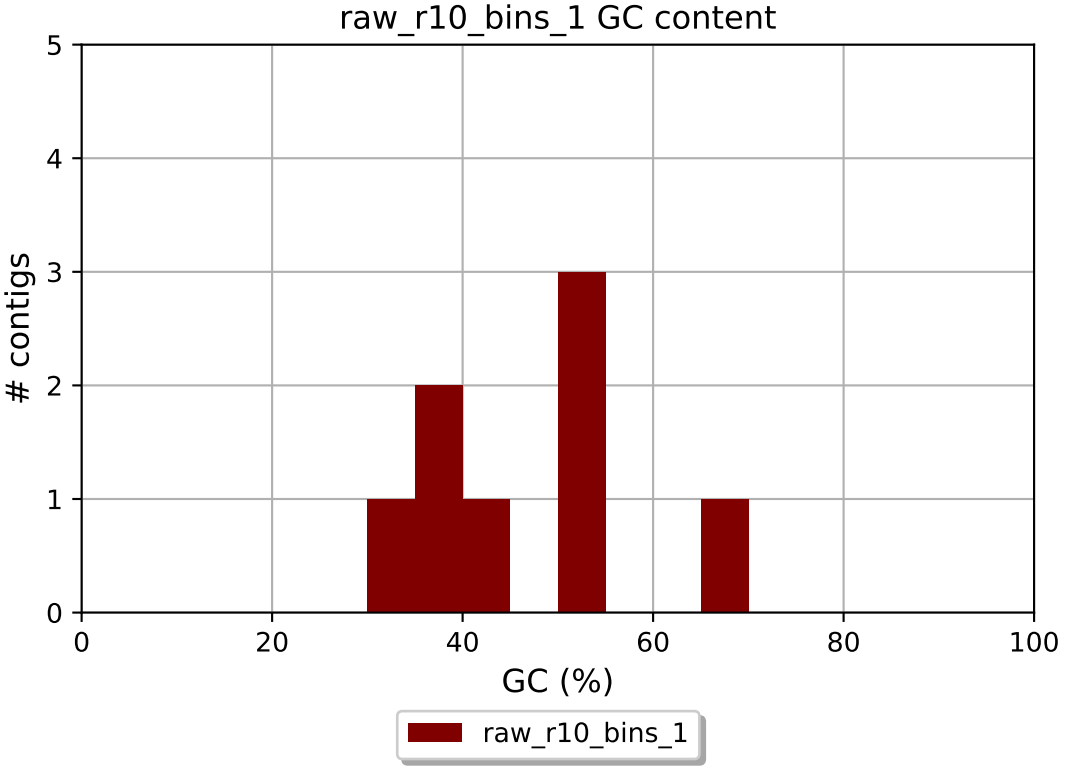

racon_r1_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_bins_2

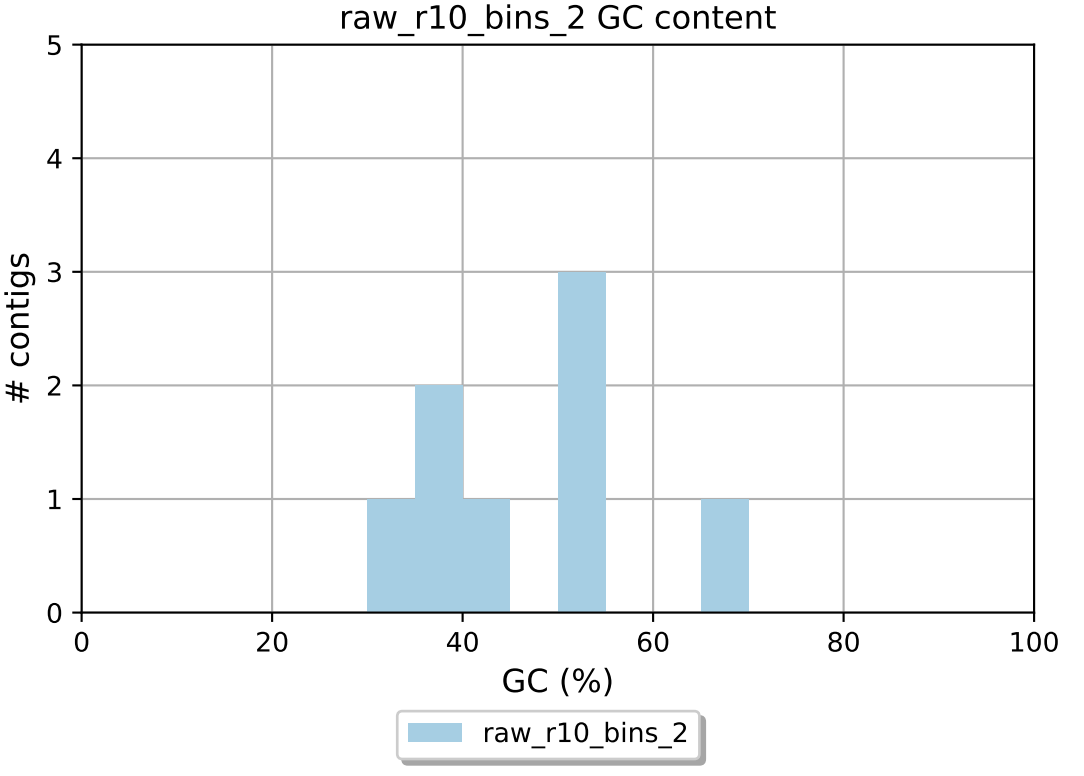

racon_r1_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_bins_3

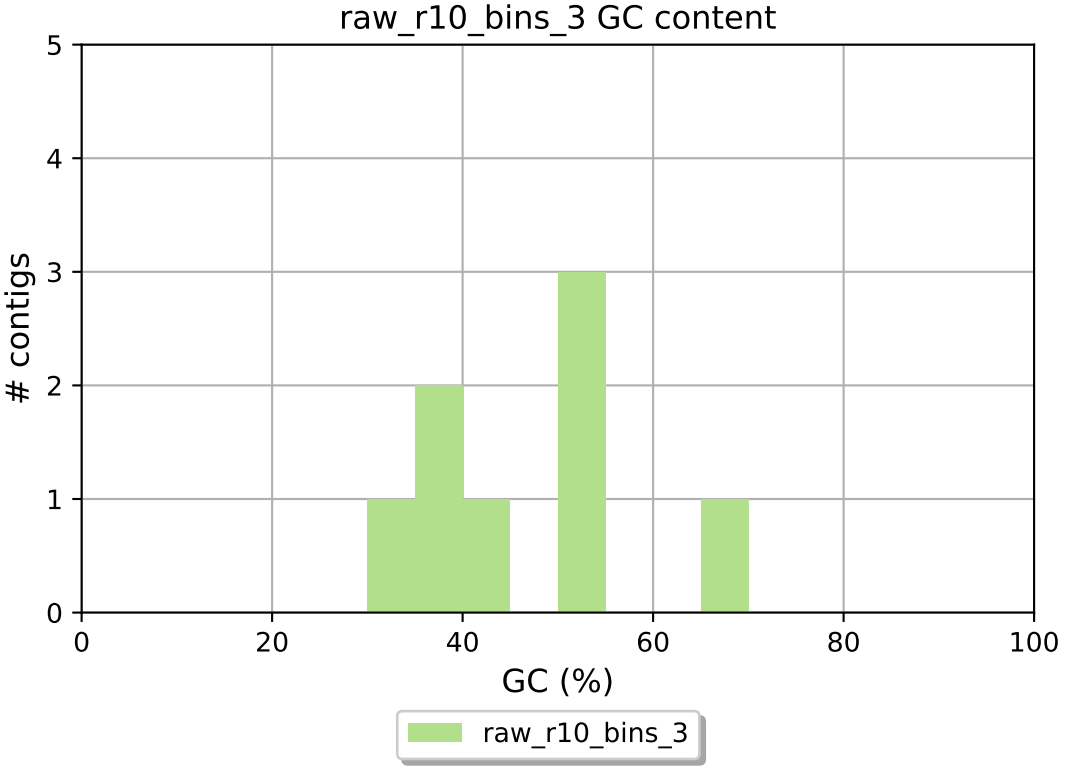

racon_r2_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_bins_1

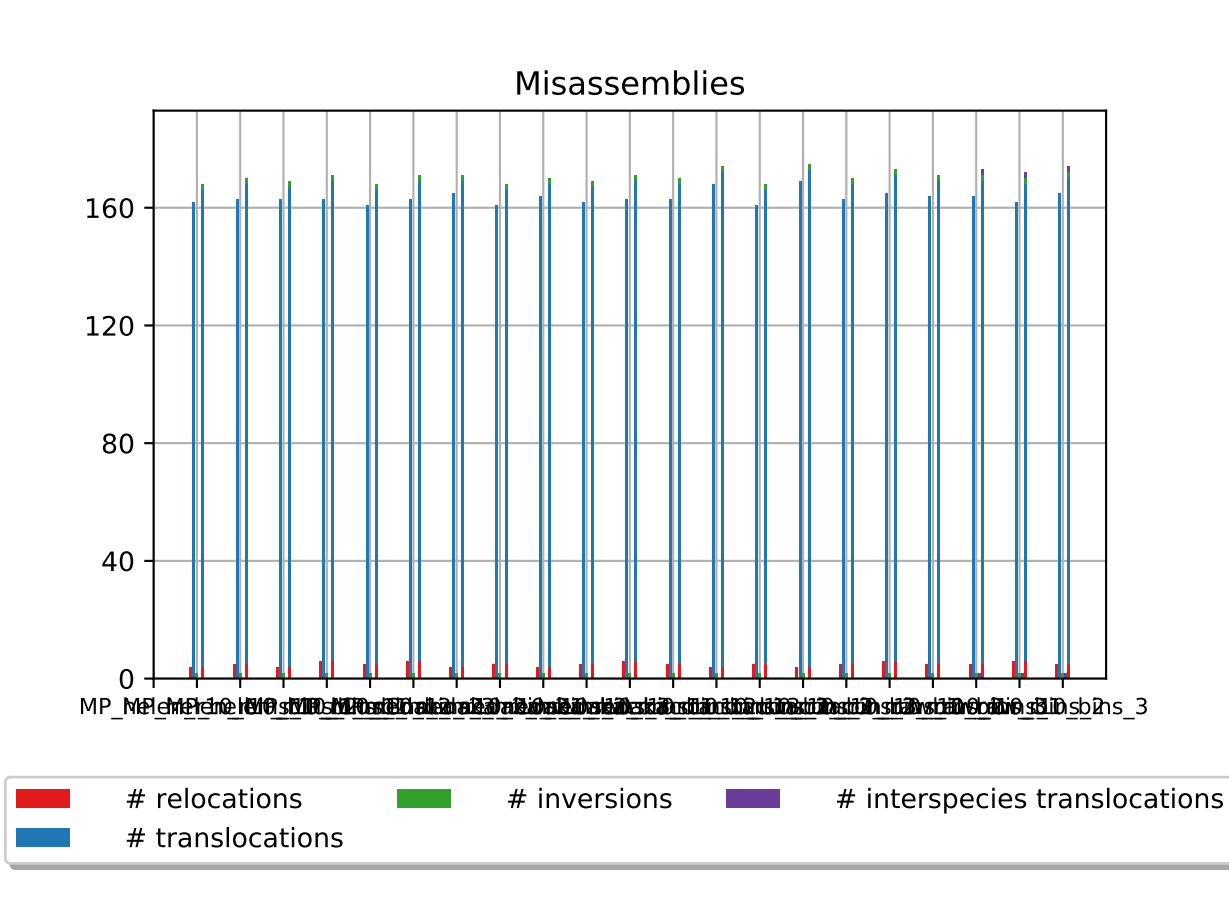

racon_r2_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_bins_2

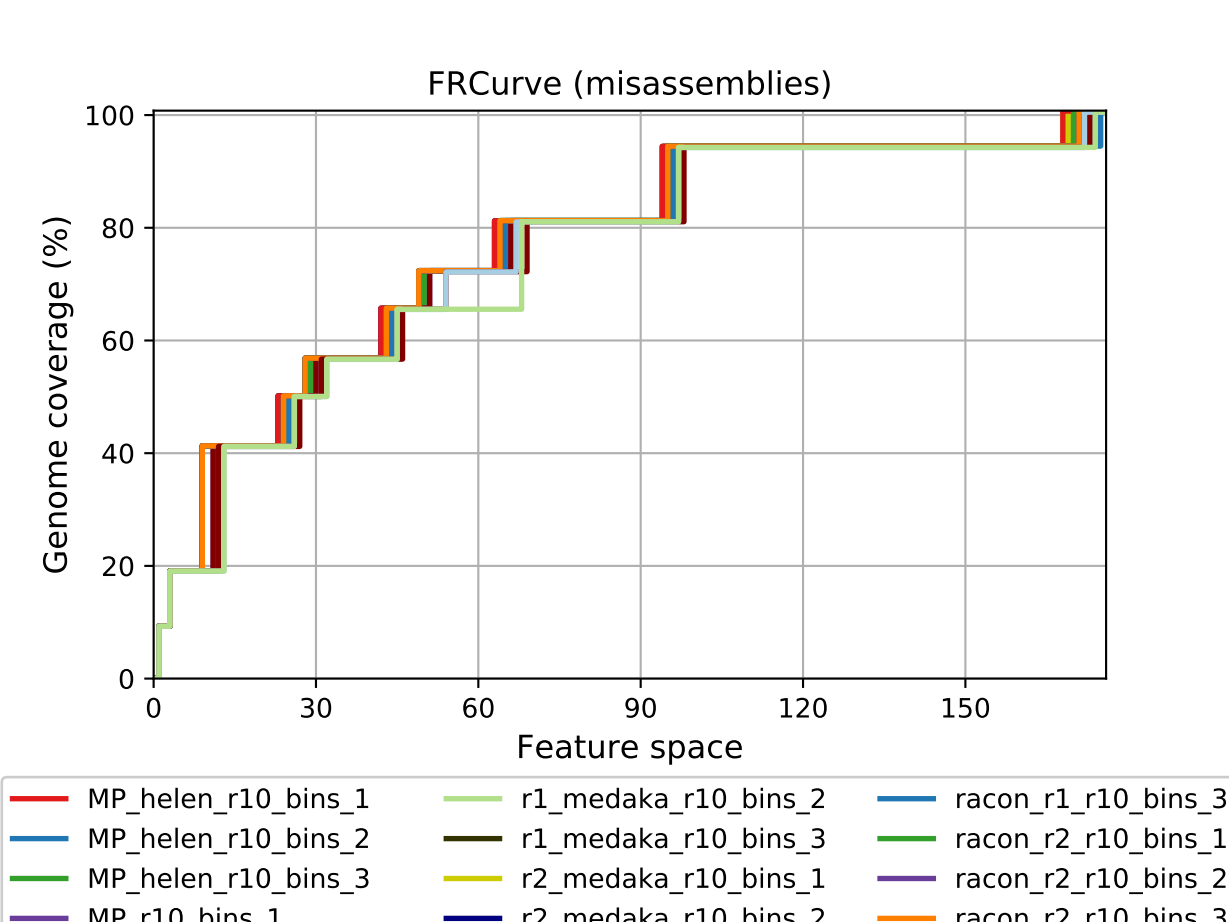

racon_r2_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_bins_3

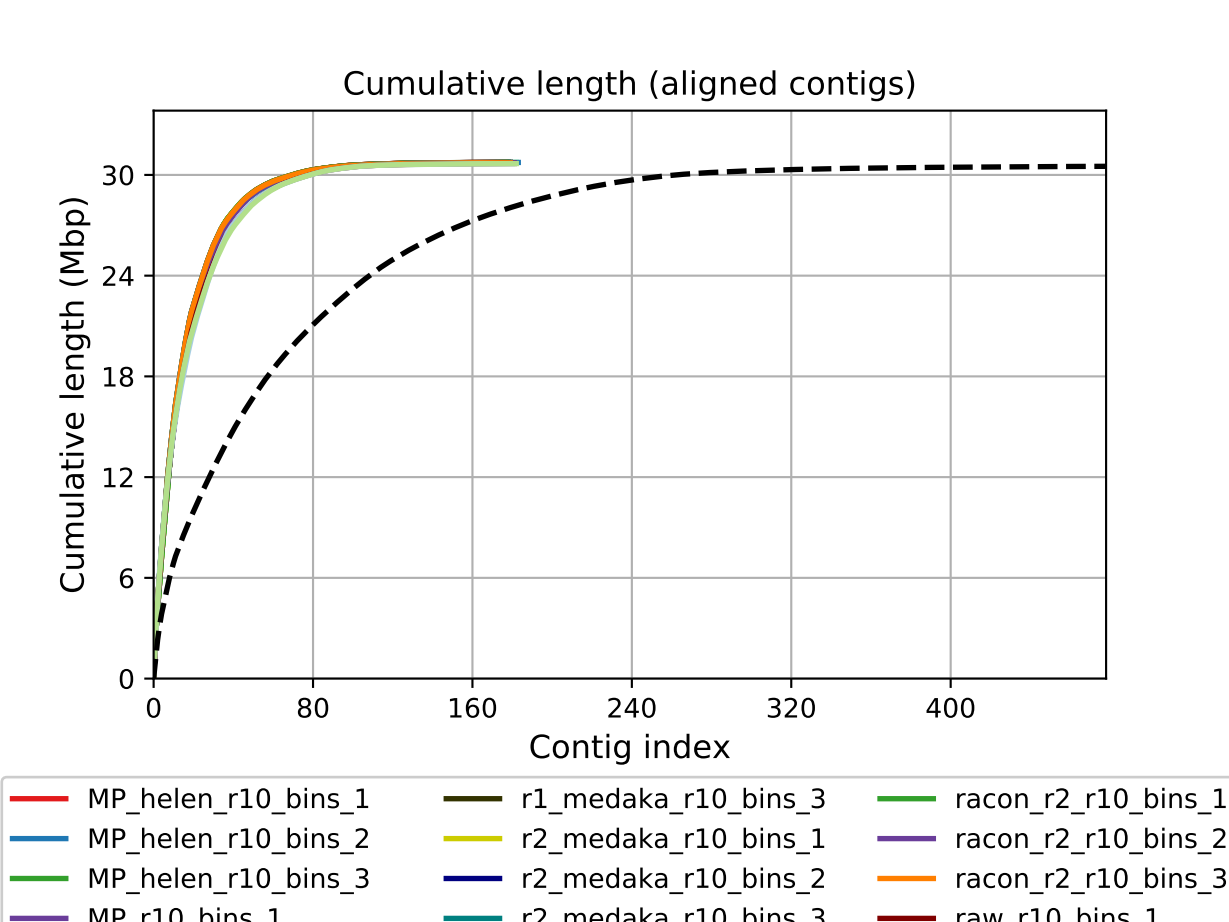

raw_r10_bins_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_bins_1

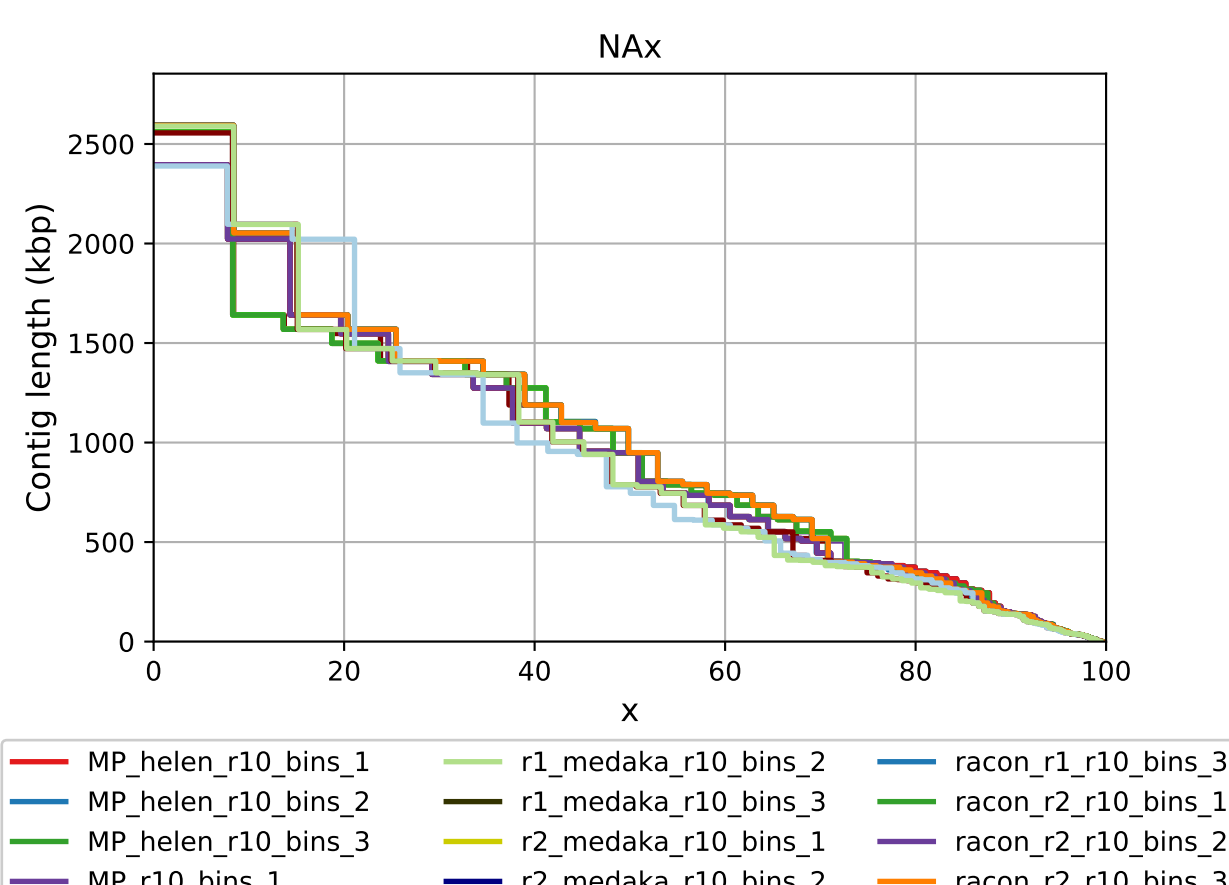

raw_r10_bins_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_bins_2

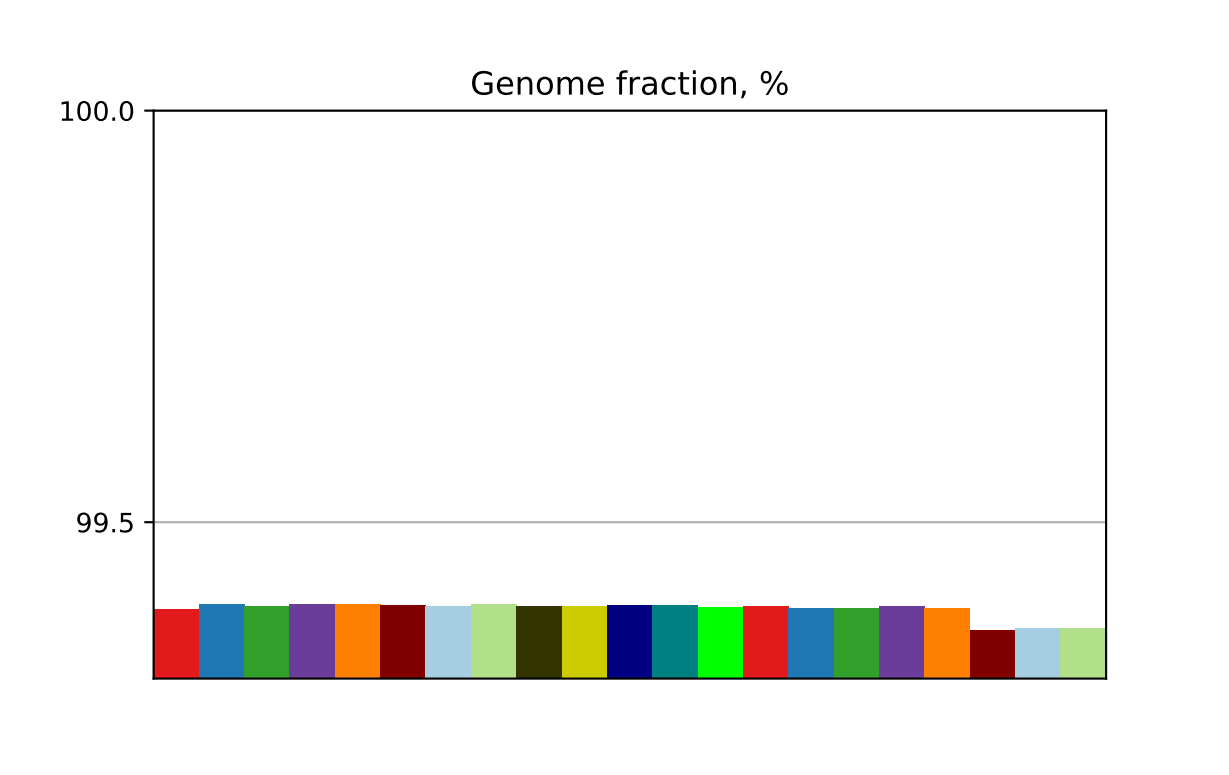

raw_r10_bins_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_bins_3


Misassemblies
160
120
80
40
0
relocations
inversions
interspecies translocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
30
60
90
120
150
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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
6
12
18
24
30
0
80
160
240
320
400
Contig index
MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
MP_r10_bins_1
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
r2_medaka_r10_bins_2
r2_medaka_r10_bins_3
racon_r2_r10_bins_1
racon_r2_r10_bins_2
racon_r2_r10_bins_3
raw_r10_bins_1


NAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
MP_helen_r10_bins_1
MP_helen_r10_bins_2
MP_helen_r10_bins_3
r1_medaka_r10_bins_2
r1_medaka_r10_bins_3
r2_medaka_r10_bins_1
racon_r1_r10_bins_3
racon_r2_r10_bins_1
racon_r2_r10_bins_2


Genome fraction, %
100.0
99.5
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