Report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# 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)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 1000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 5000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 10000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 25000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Total length (>= 50000 bp)	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792253	6792196	6792240	6792242	6791560	6791674	6787718	6792241	6792182	6792245	6792248	6791611	6791688	6788581	6792241	6792182	6792244	6792249	6791613	6791620	6788581
Total length	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
Reference length	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959	30512959
N50	4758965	4757933	4758577	4758103	4757936	4757875	4756113	4758986	4758029	4758599	4758140	4757918	4757909	4756067	4758962	4757806	4758586	4758100	4757923	4757852	4756051
N75	2992084	2992068	2992075	2992072	2991900	2991958	2990676	2992084	2992066	2992074	2992072	2991919	2991966	2990627	2992084	2992066	2992074	2992073	2991919	2991966	2990627
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	167	168	172	167	174	176	170	167	167	171	168	172	177	170	168	167	170	168	174	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	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
# local misassemblies	117	121	136	135	149	140	203	115	116	132	136	152	141	206	117	119	133	137	150	141	207
# 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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 8 part
Unaligned length	79301	79024	82721	82427	78902	77927	140331	78460	78392	81958	80540	78032	77044	140179	78460	78655	82194	81821	78115	77252	140623
Genome fraction (%)	99.400	99.395	99.399	99.398	99.398	99.397	99.370	99.400	99.400	99.398	99.397	99.397	99.395	99.374	99.400	99.397	99.398	99.398	99.397	99.396	99.372
Duplication ratio	1.044	1.044	1.043	1.044	1.043	1.043	1.028	1.044	1.044	1.044	1.043	1.043	1.043	1.027	1.044	1.044	1.044	1.043	1.043	1.043	1.027
# 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	175.41	168.53	175.77	175.01	175.33	179.74	270.00	176.66	168.47	176.96	175.56	177.03	178.16	271.65	176.70	168.43	176.49	174.97	177.61	179.37	273.80
# indels per 100 kbp	38.49	23.74	26.70	26.23	62.95	59.78	305.83	38.54	23.64	26.60	26.55	63.98	58.94	308.72	38.64	23.73	26.50	26.26	64.10	58.04	309.25
Largest alignment	2390997	2390976	2390994	2390996	2390889	2390913	2387942	2390997	2390976	2390995	2390996	2390889	2390911	2387942	2390997	2390976	2390995	2390996	2390889	2390911	2387942
Total aligned length	30752499	30750611	30746527	30733907	30739809	30732404	30681021	30752876	30749307	30747422	30743007	30746957	30734466	30684220	30757538	30750836	30747094	30737851	30743611	30737745	30681288
NA50	948963	948260	948811	948796	949071	949118	777689	948962	948258	948799	948787	949124	949124	699762	948964	948259	948799	948791	949124	949113	777743
NA75	399305	399300	399305	399302	399225	399227	376875	399306	399299	399302	399301	399230	399231	373707	399303	399301	399302	399302	399239	399238	381469
LA50	11	11	11	11	11	11	12	11	11	11	11	11	11	13	11	11	11	11	11	11	12
LA75	24	24	24	24	24	24	27	24	23	23	23	23	23	28	24	23	23	23	23	23	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

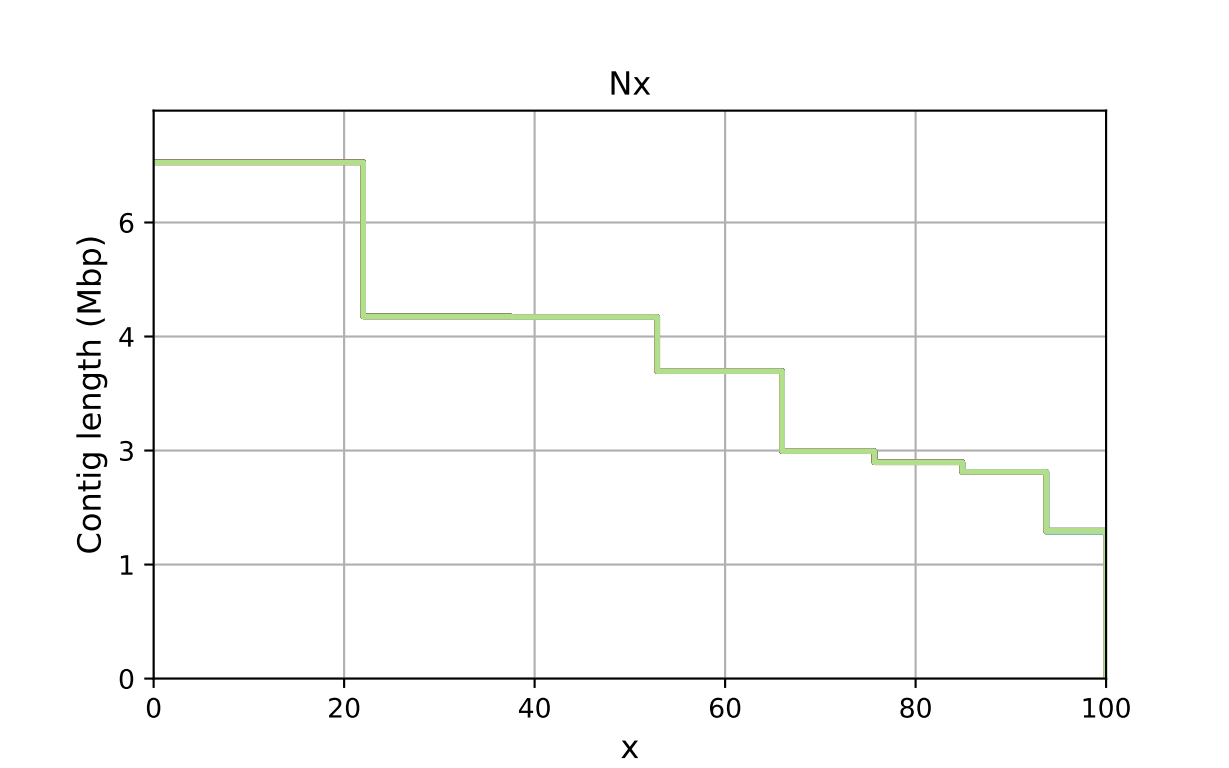
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# misassemblies	168	167	168	172	167	174	176	170	167	167	171	168	172	177	170	168	167	170	168	174	174
# contig misassemblies	168	167	168	172	167	174	176	170	167	167	171	168	172	177	170	168	167	170	168	174	174
# c. relocations	5	4	4	8	4	9	5	6	4	4	7	4	7	5	6	4	4	6	4	7	5
# c. translocations	161	161	162	162	161	163	167	162	161	161	162	162	163	168	162	162	161	162	162	165	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	2	0	0	0	0	0	0	2	0	0	0	0	0	0	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	30867659	30863086	30864993	30854445	30851823	30845869	30849737	30867164	30863526	30865115	30854432	30853169	30847042	30850562	30867063	30862897	30865071	30855474	30852231	30845818	30850200
# possibly misassembled contigs	7	7	7	7	7	7	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
# possible misassemblies	100	98	98	102	98	96	166	98	98	98	98	100	94	172	98	98	96	98	100	94	170
# local misassemblies	117	121	136	135	149	140	203	115	116	132	136	152	141	206	117	119	133	137	150	141	207
# 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	253	253	251	252	250	250	176	252	253	251	252	249	250	172	252	253	252	252	249	251	171
# 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	53196	51107	53303	53074	53170	54508	81857	53576	51091	53664	53240	53684	54026	82359	53587	51076	53521	53062	53860	54394	83010
# indels	11673	7199	8097	7954	19089	18128	92718	11688	7169	8068	8050	19402	17872	93600	11717	7195	8036	7965	19438	17601	93758
# indels (<= 5 bp)	11023	6558	7498	7352	18443	17481	91507	11045	6522	7471	7457	18747	17239	92393	11080	6536	7435	7363	18779	16961	92528
# indels (> 5 bp)	650	641	599	602	646	647	1211	643	647	597	593	655	633	1207	637	659	601	602	659	640	1230
Indels length	45771	41100	40888	40954	56401	55059	156481	45904	41301	41088	40840	57155	54534	158278	45494	41297	41029	41047	57392	54271	158210

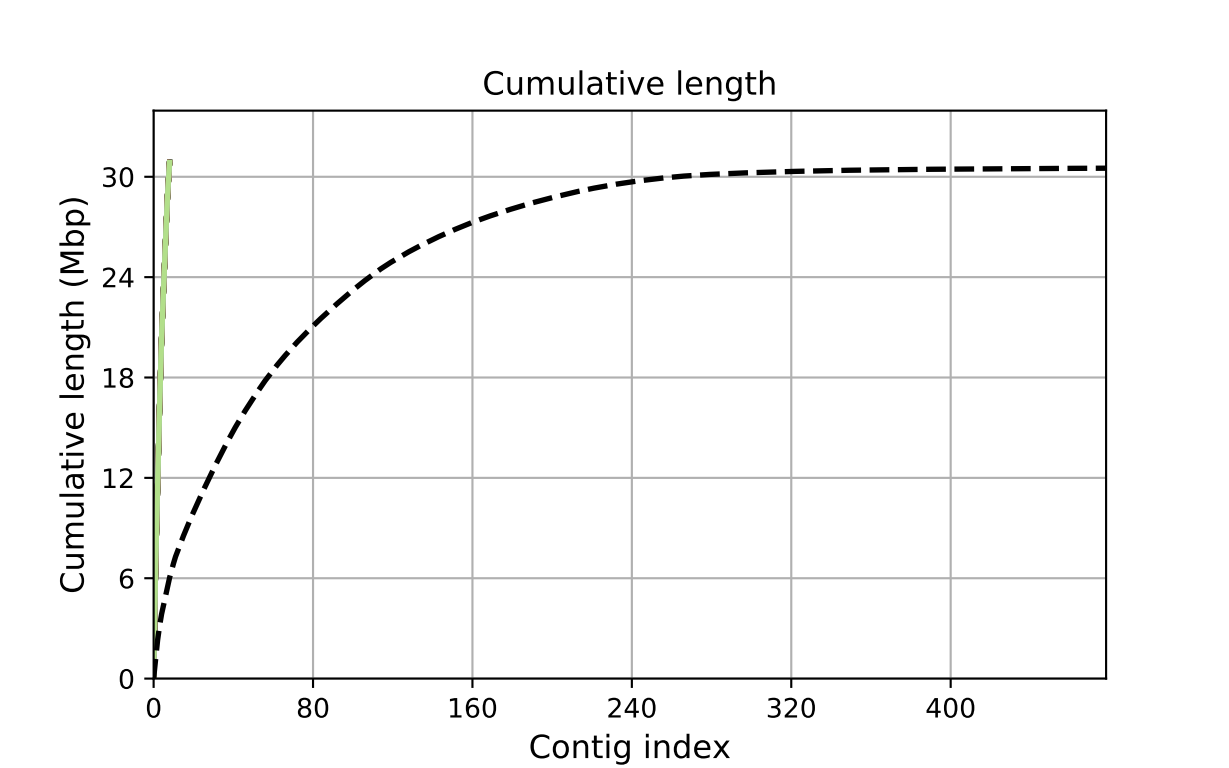
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

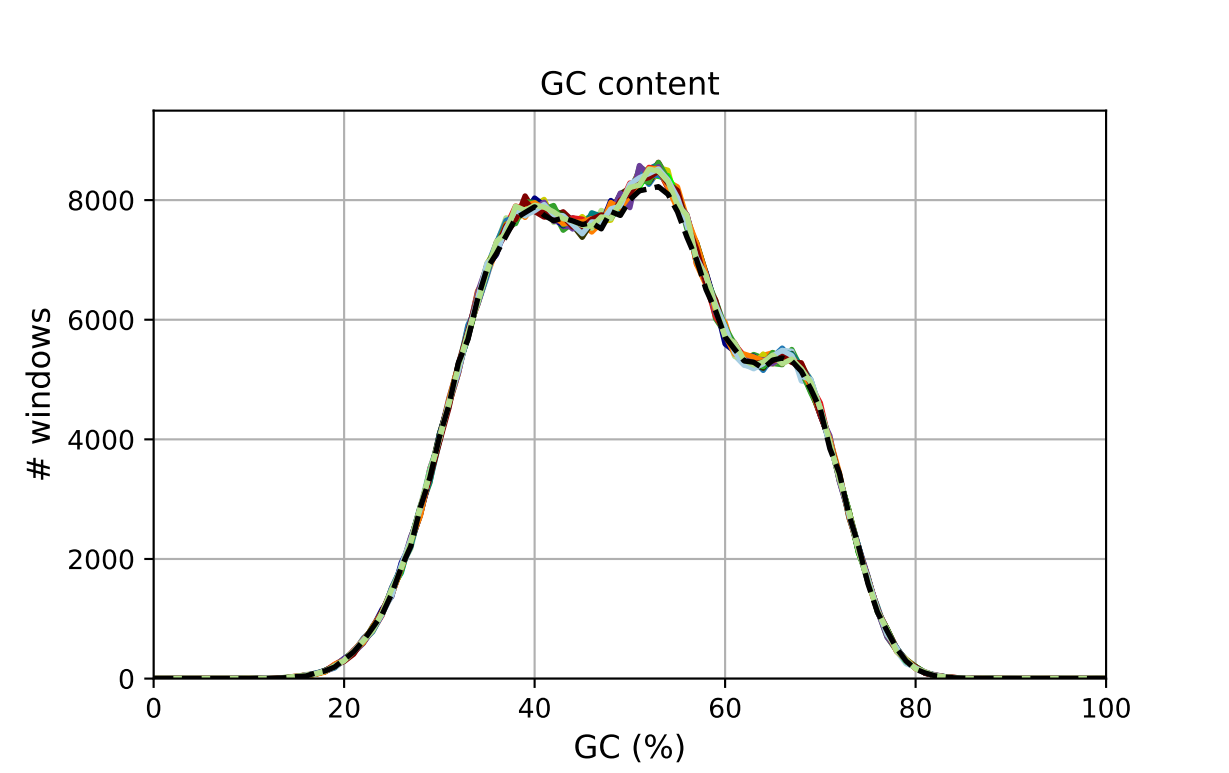
Unaligned report

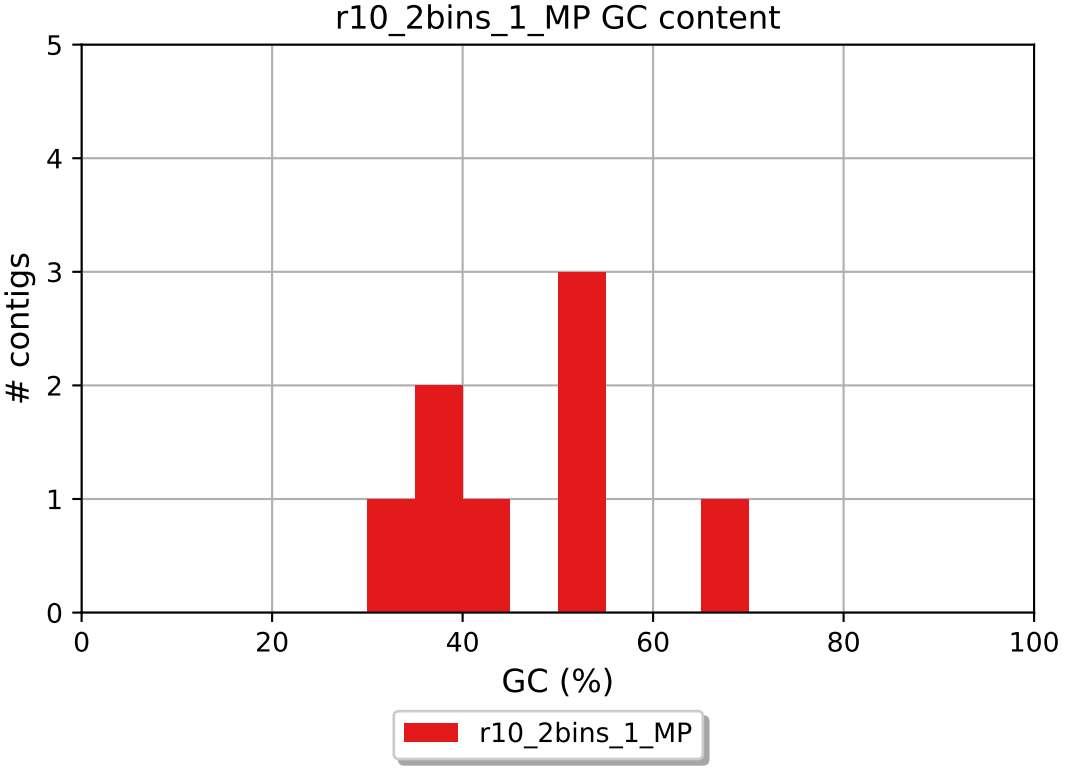
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# 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	8	7	7	7	7	7	7	8	7	7	7	7	7	7	8
Partially unaligned length	79301	79024	82721	82427	78902	77927	140331	78460	78392	81958	80540	78032	77044	140179	78460	78655	82194	81821	78115	77252	140623
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

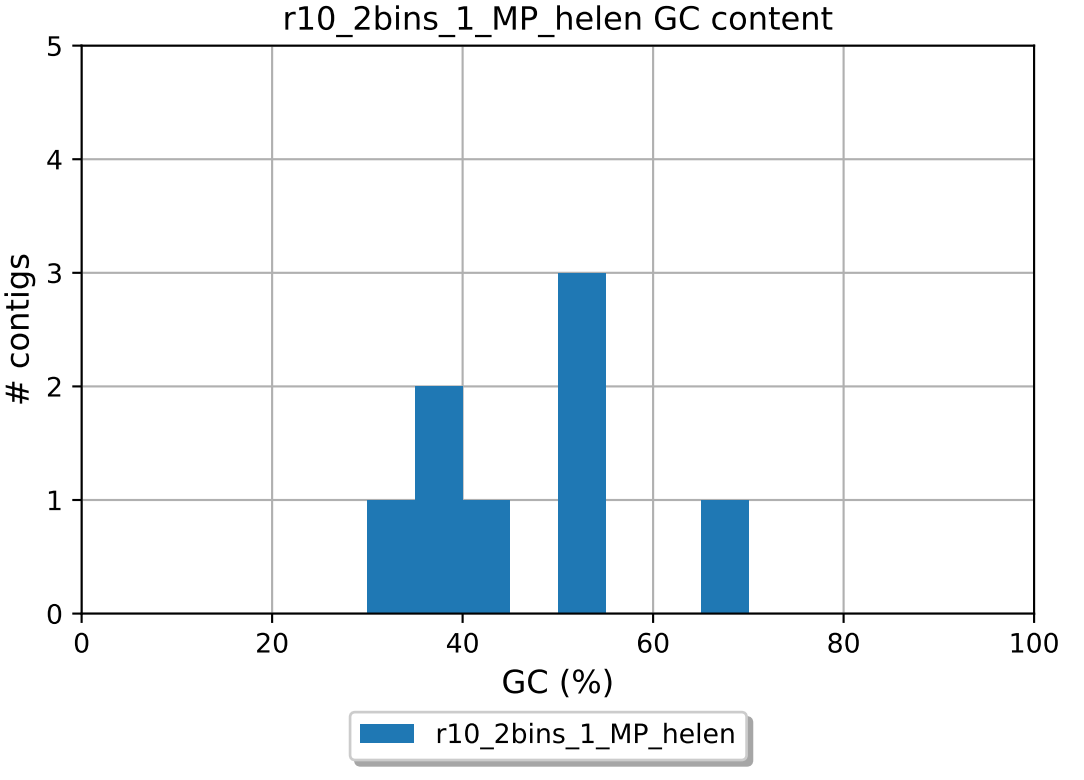
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

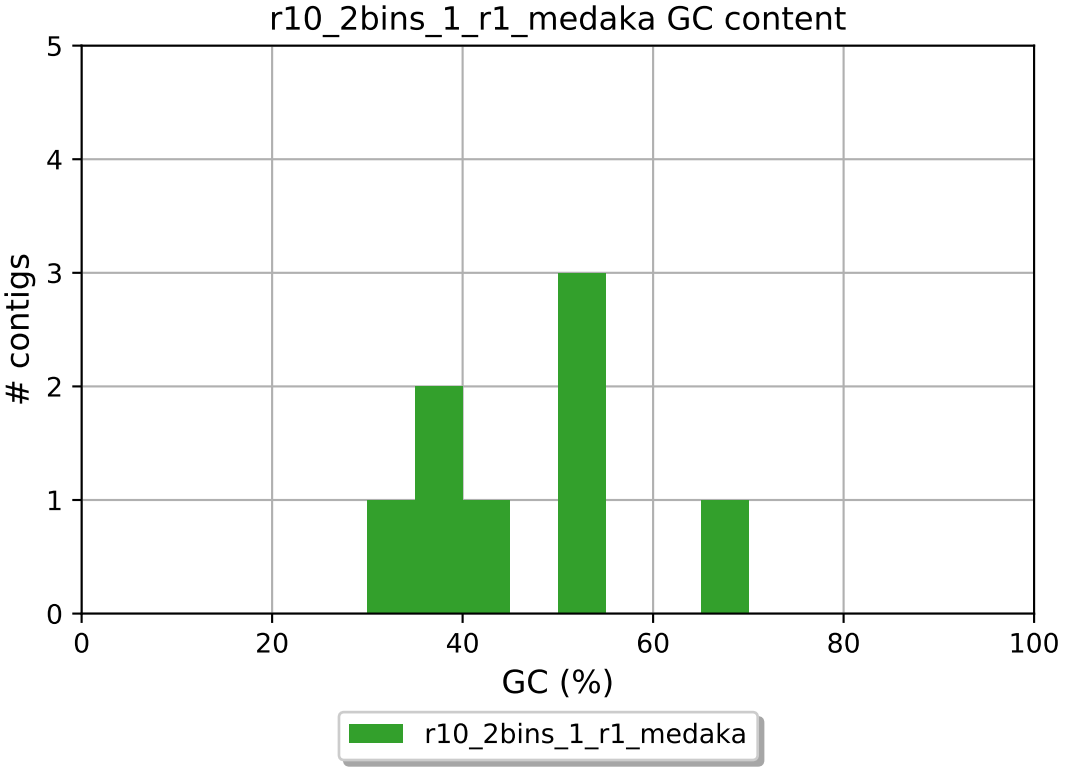

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_3_MP
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda

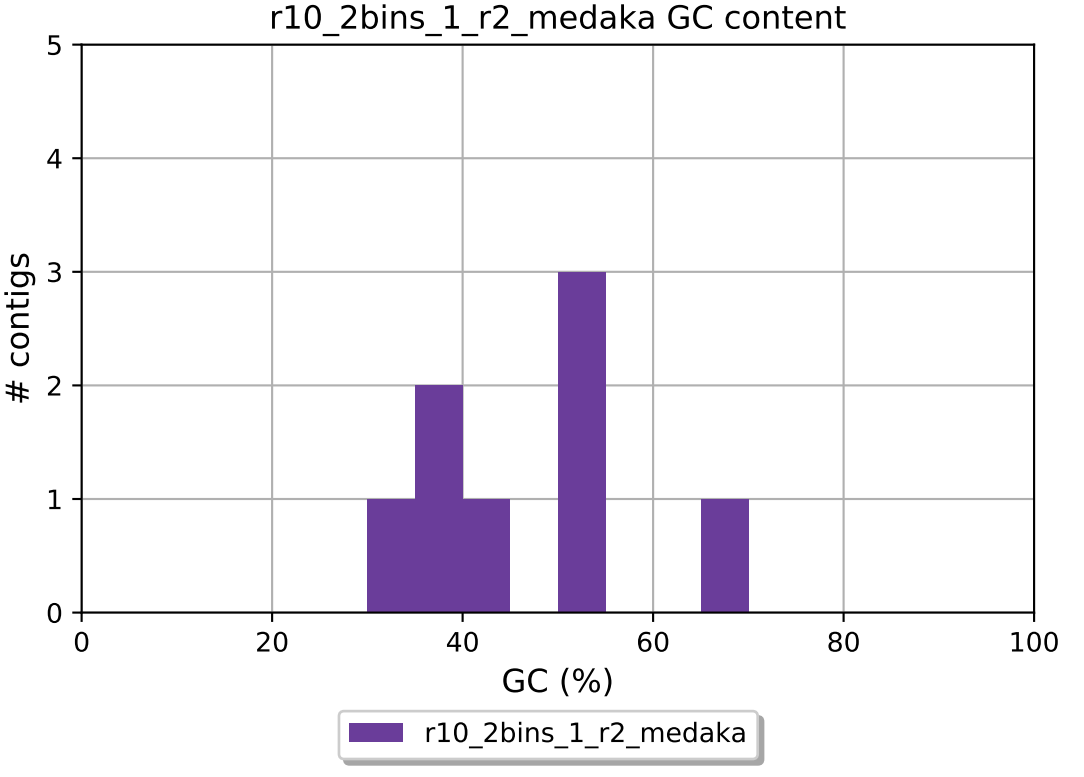

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
80
160
240
320
400
Contig index
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_2_r2_medaka
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda
r10_2bins_3_r2_meda

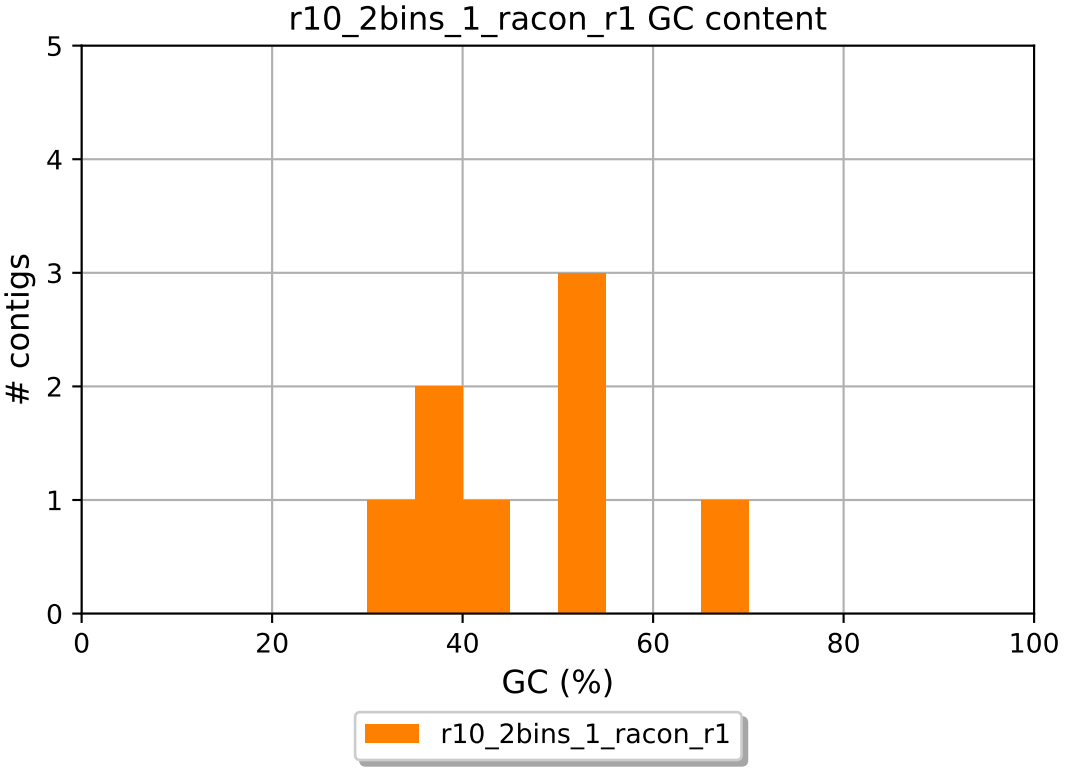

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_2_r2_medaka
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda
r10_2bins_3_r2_meda

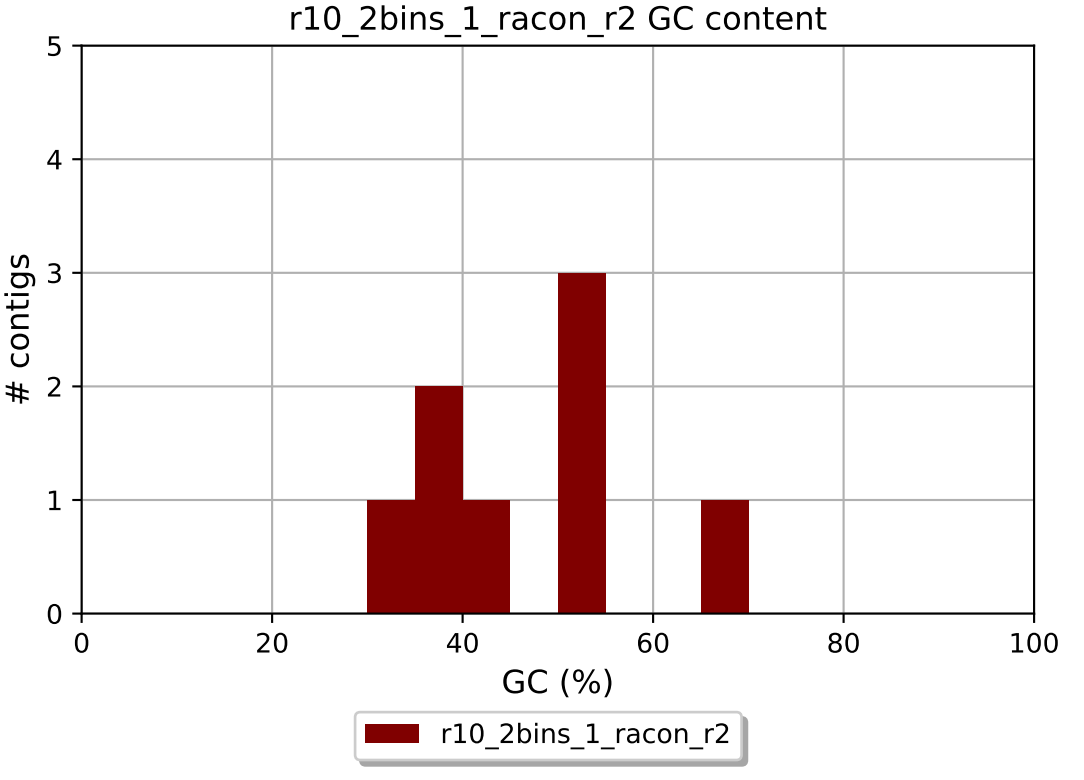

r10_2bins_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_MP

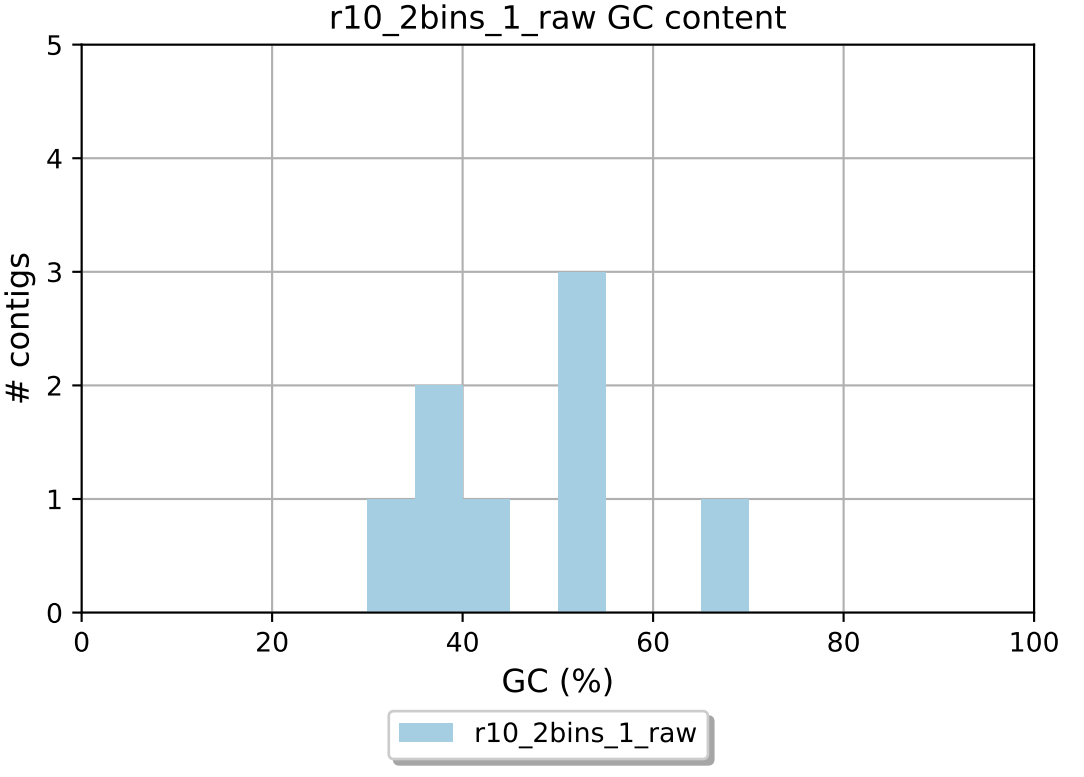

r10_2bins_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_MP_helen

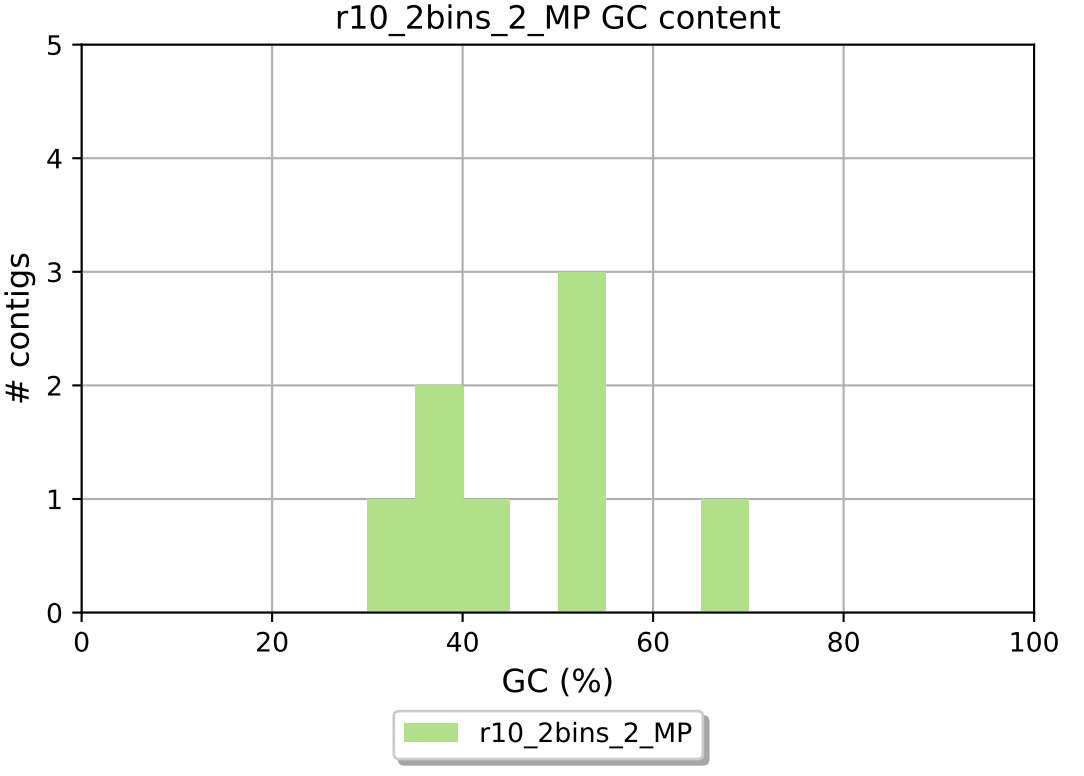

r10_2bins_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_r1_medaka

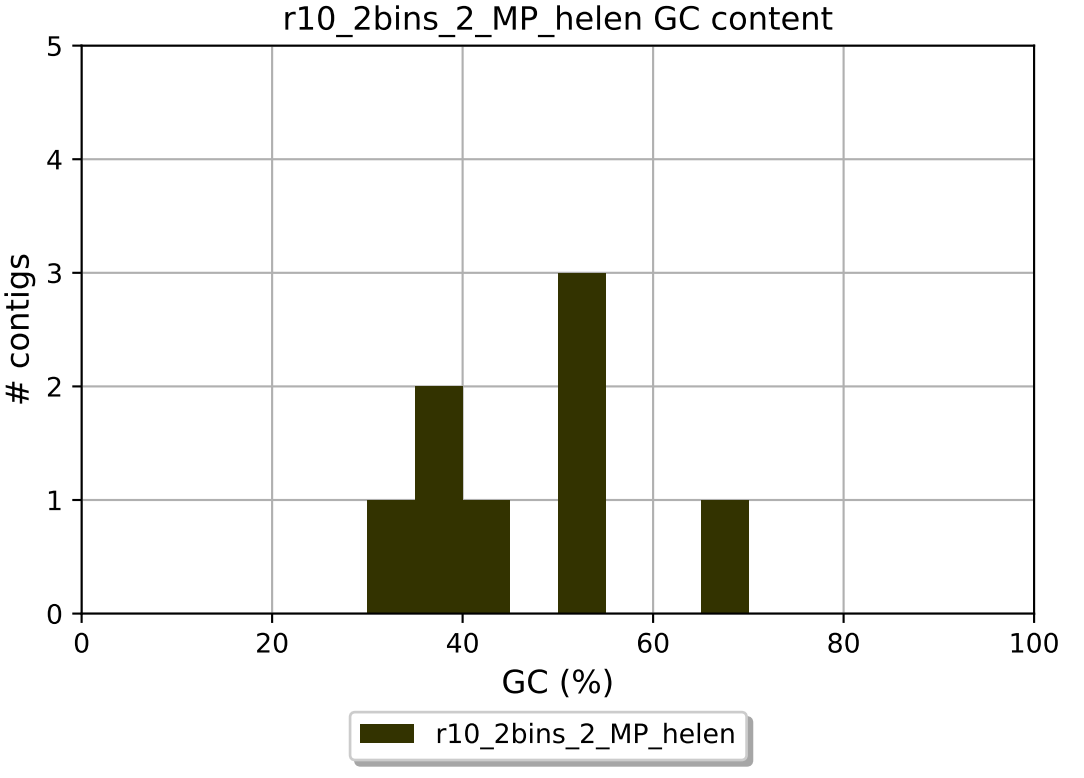

r10_2bins_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_r2_medaka

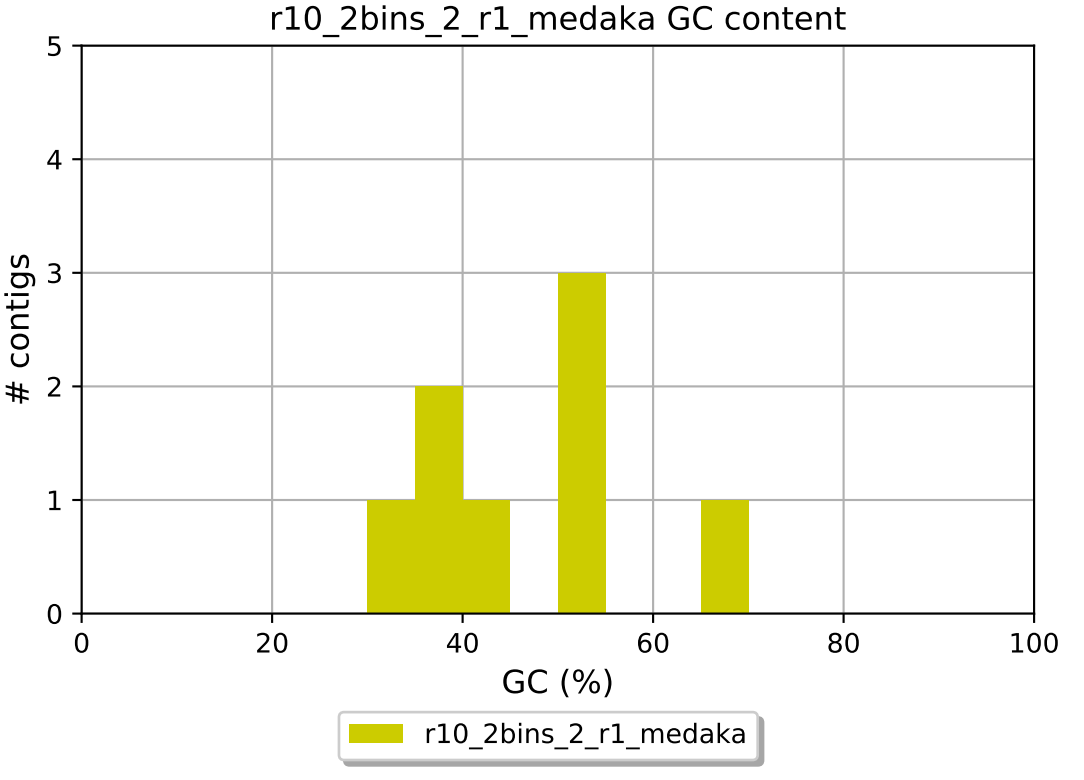

r10_2bins_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_racon_r1

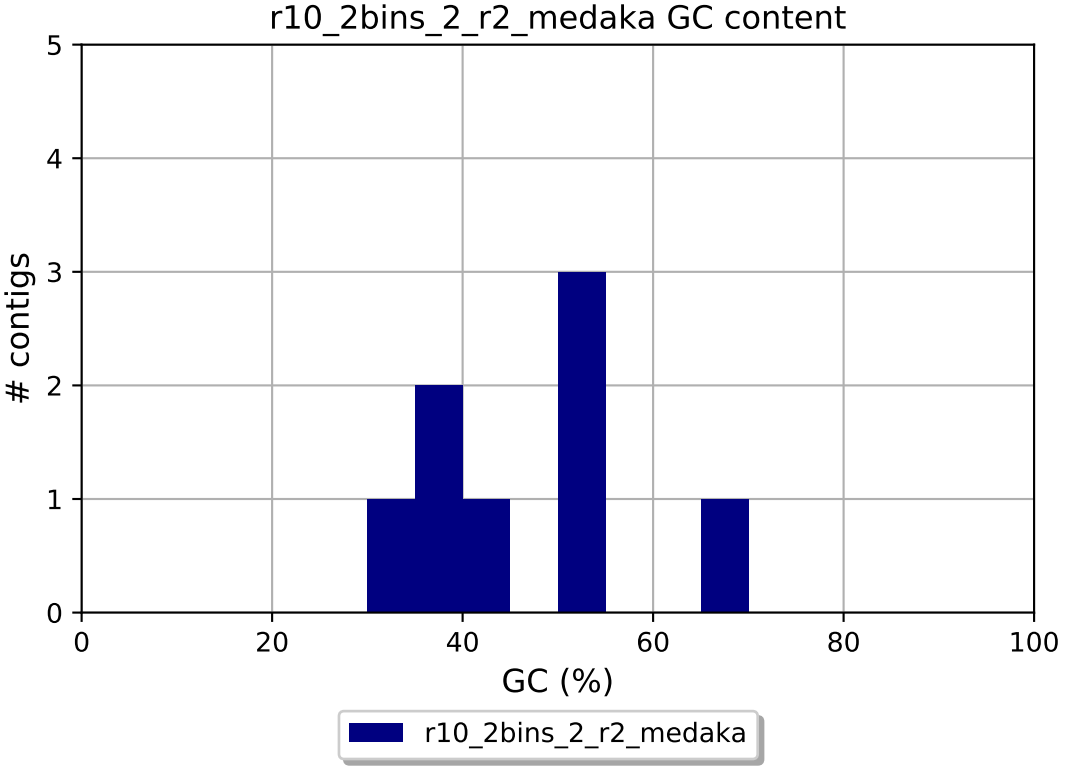

r10_2bins_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_racon_r2

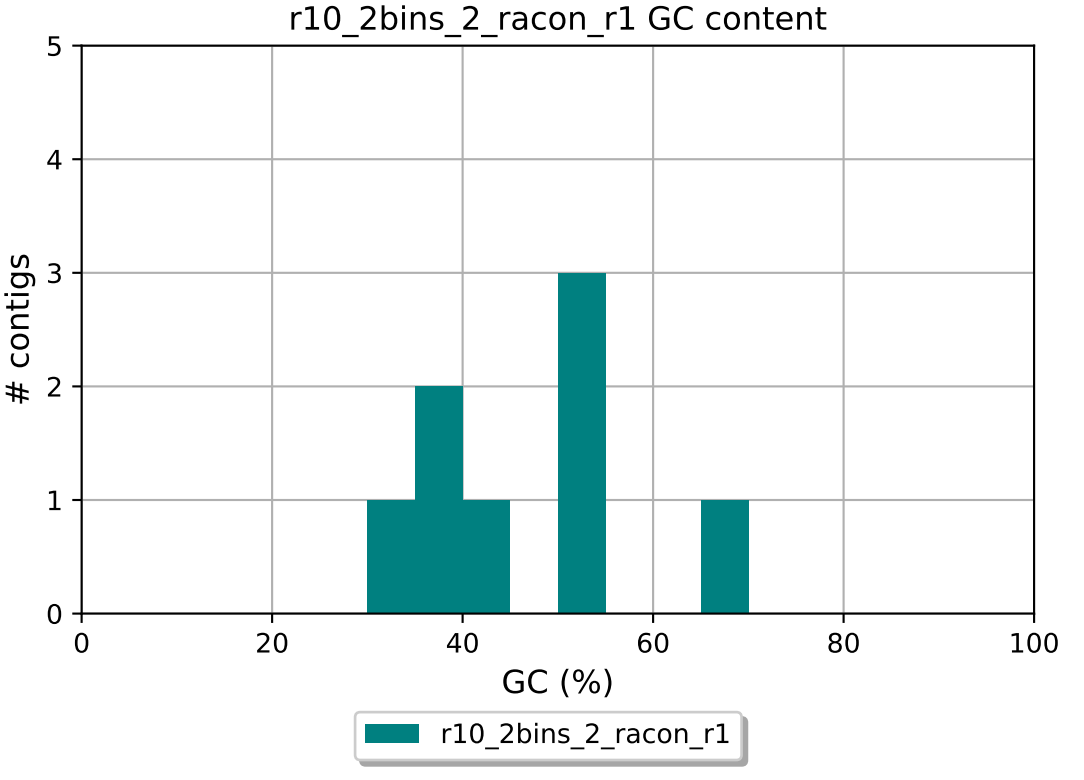

r10_2bins_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_1_raw

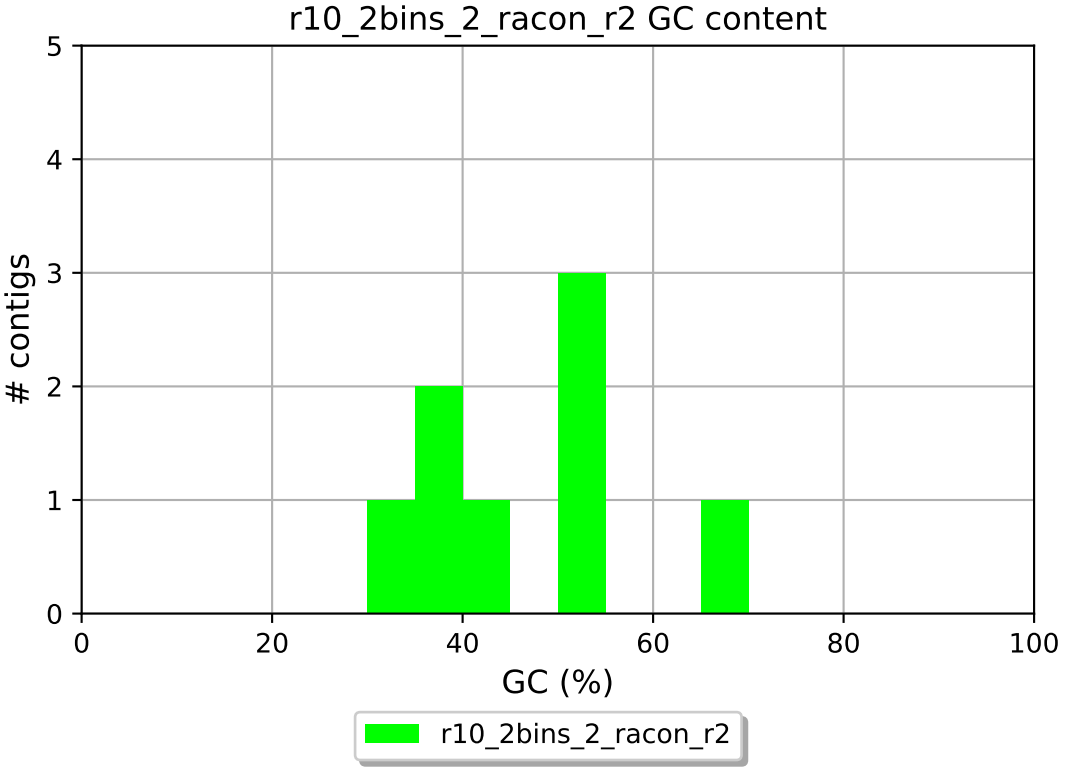

r10_2bins_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_MP

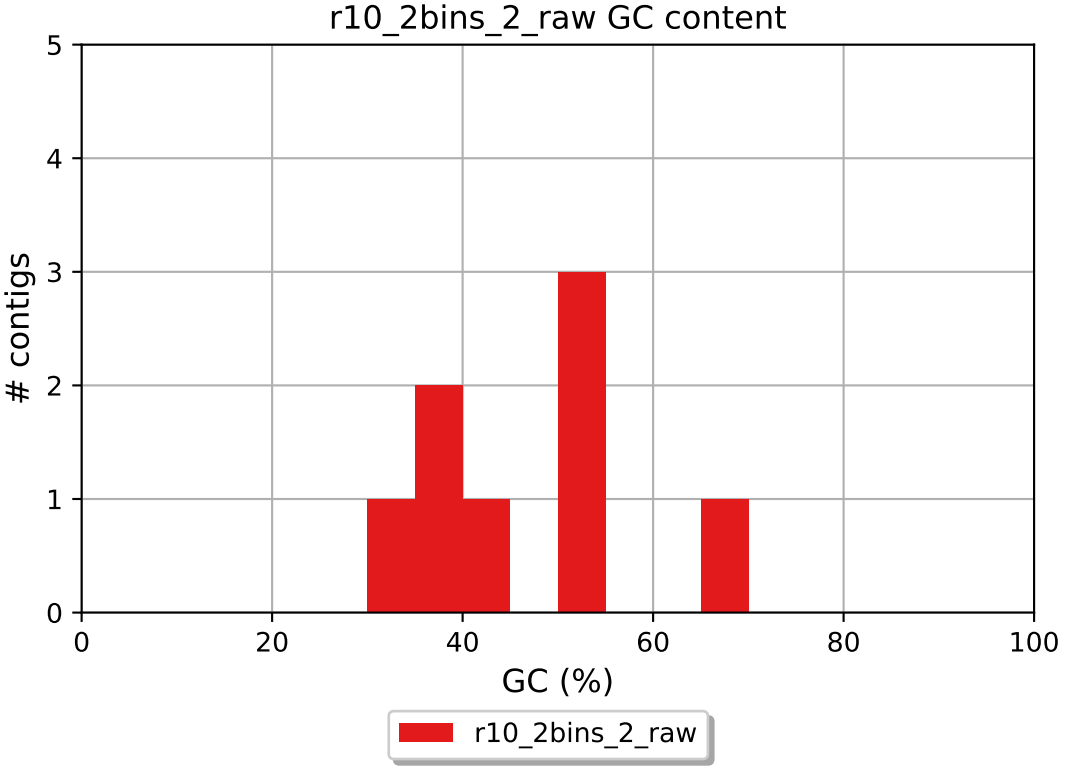

r10_2bins_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_MP_helen

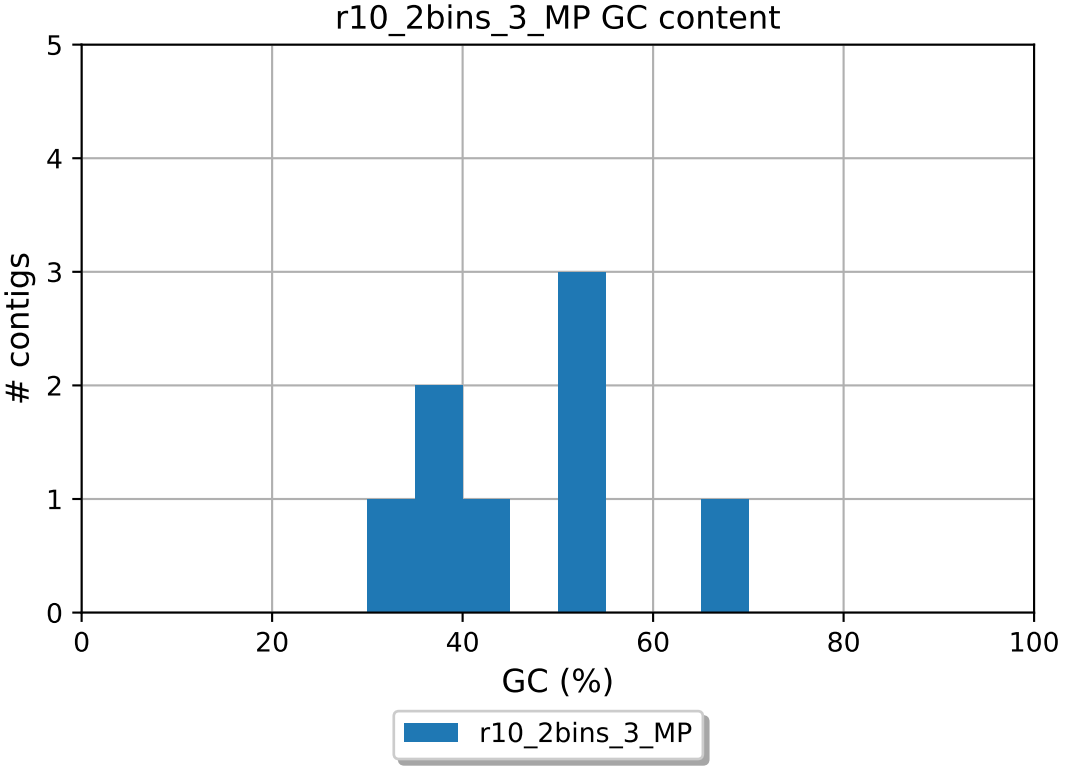

r10_2bins_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_r1_medaka

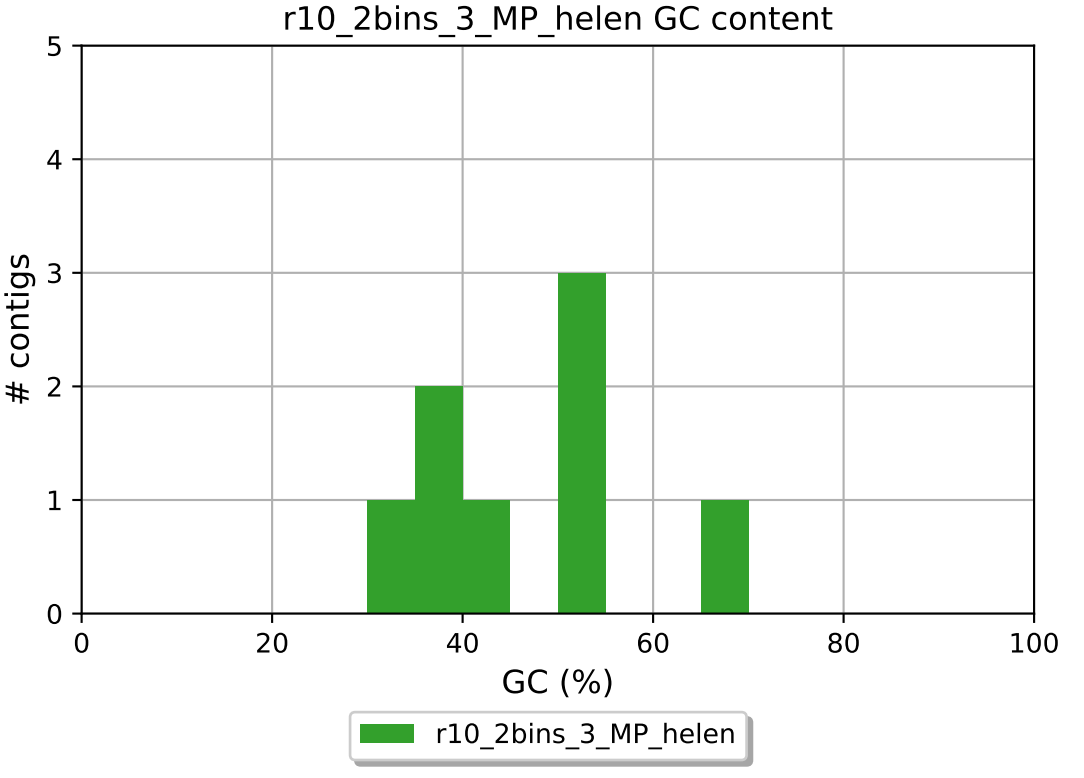

r10_2bins_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_r2_medaka

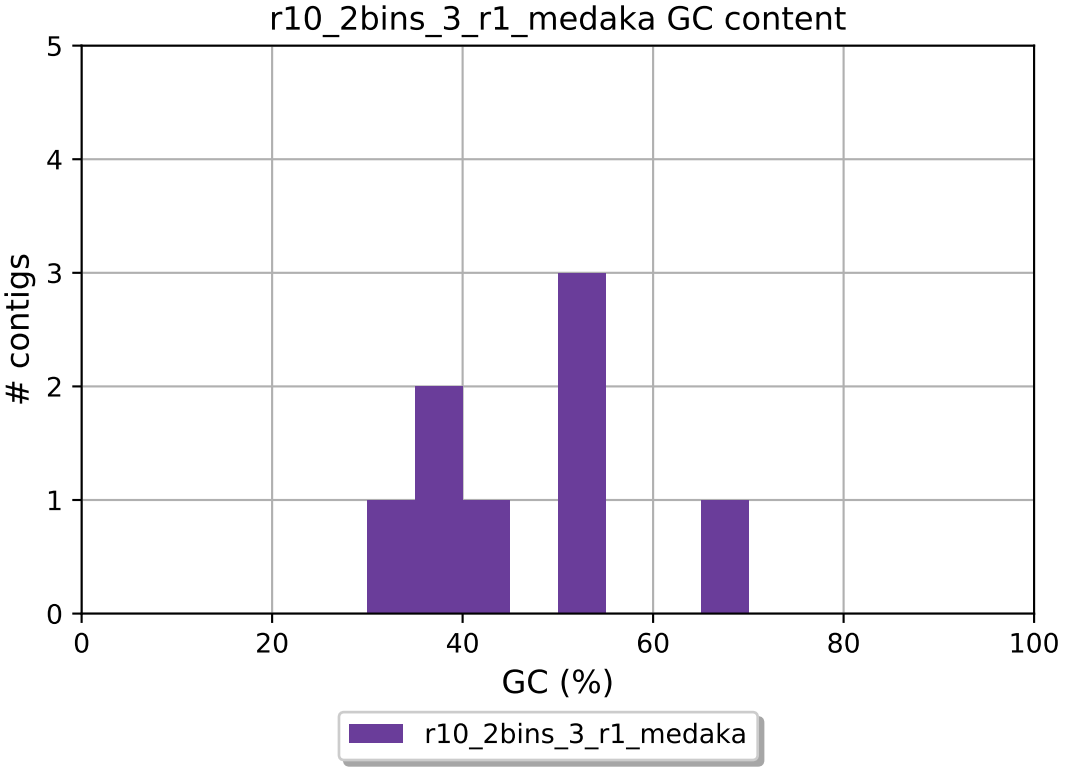

r10_2bins_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_racon_r1

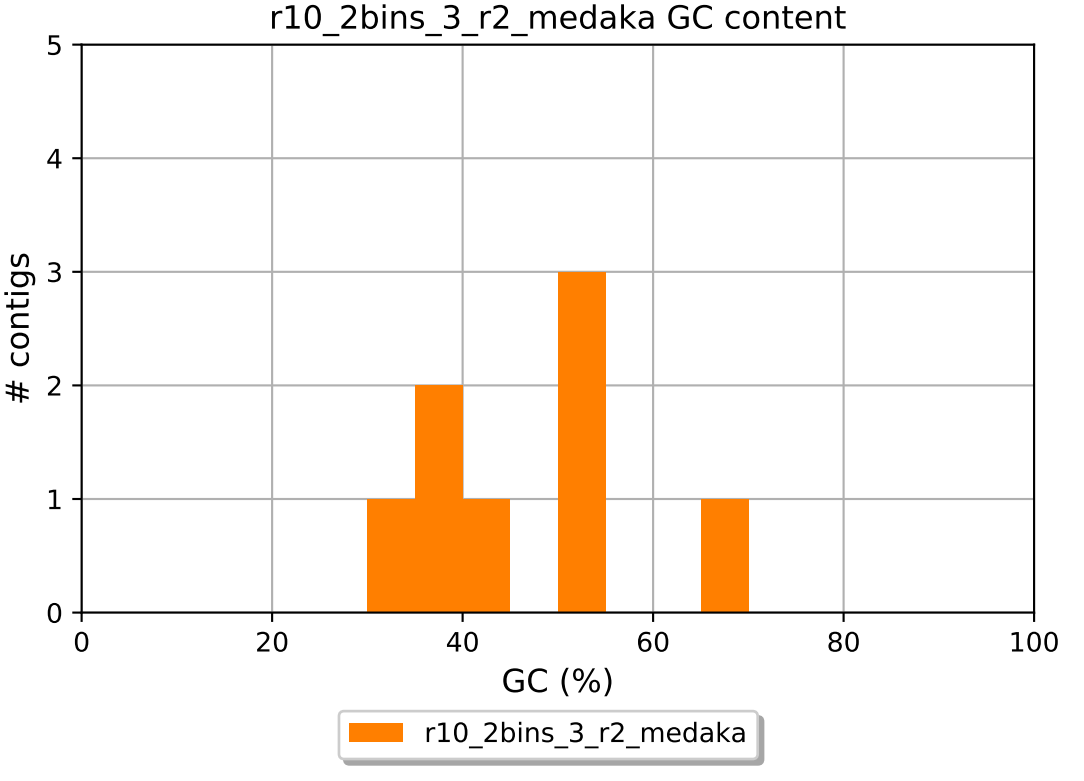

r10_2bins_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_racon_r2

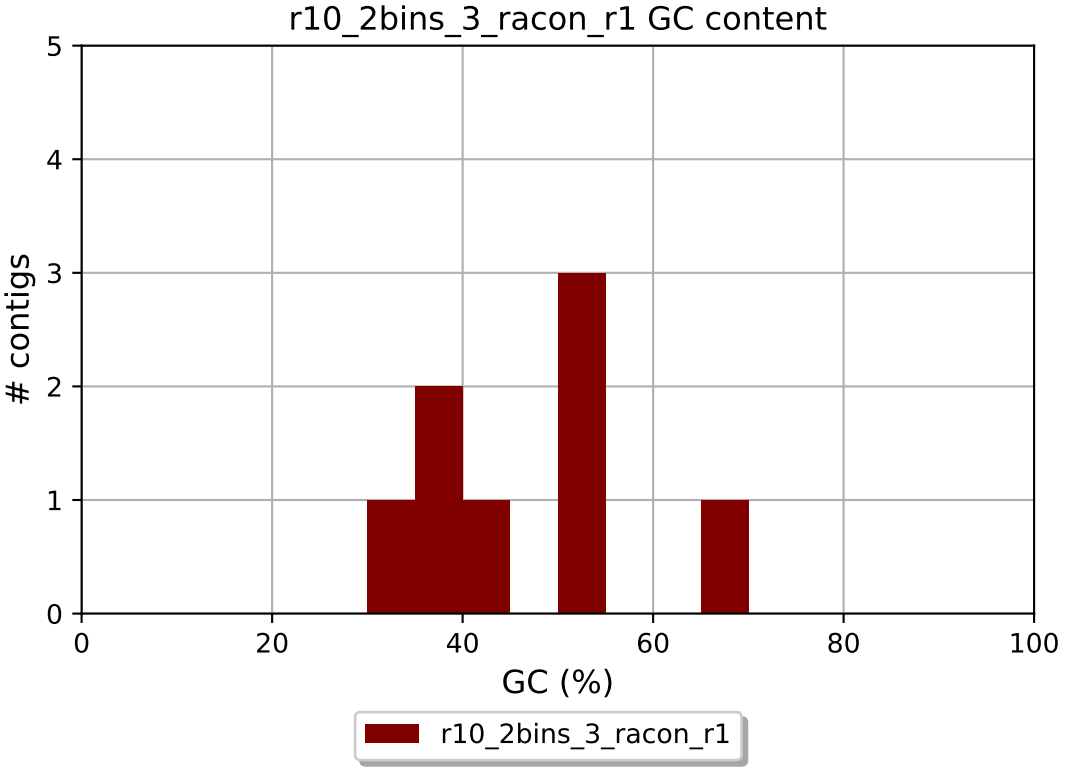

r10_2bins_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_2_raw

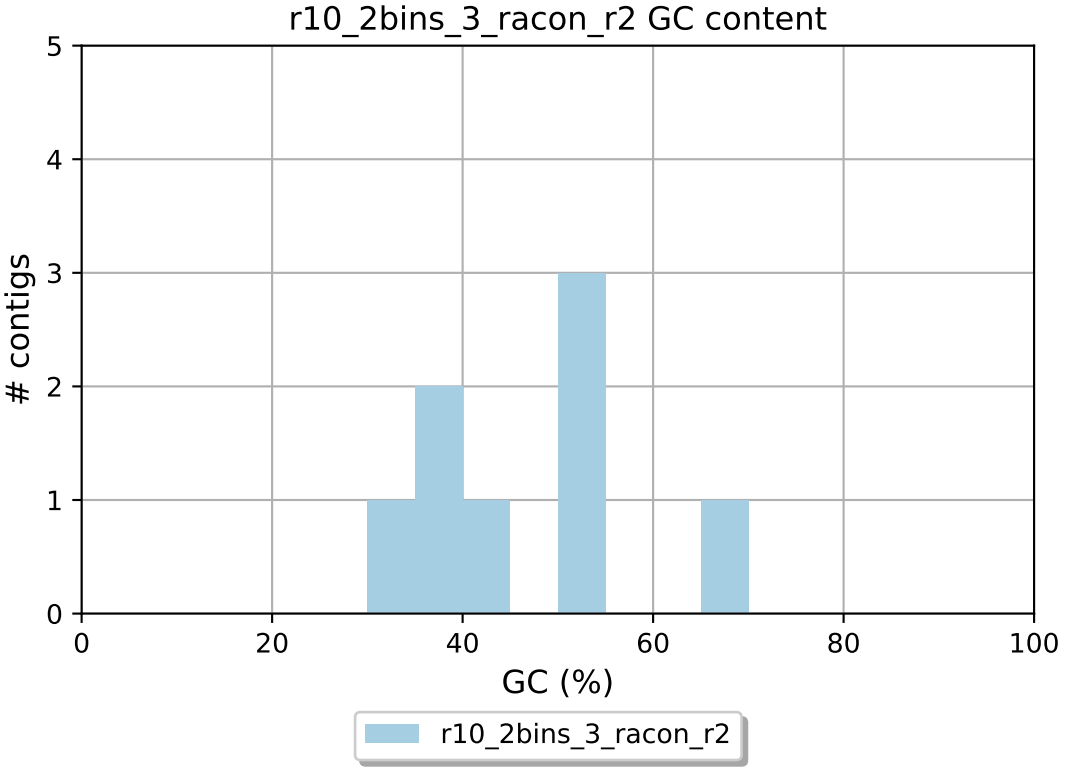

r10_2bins_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_MP

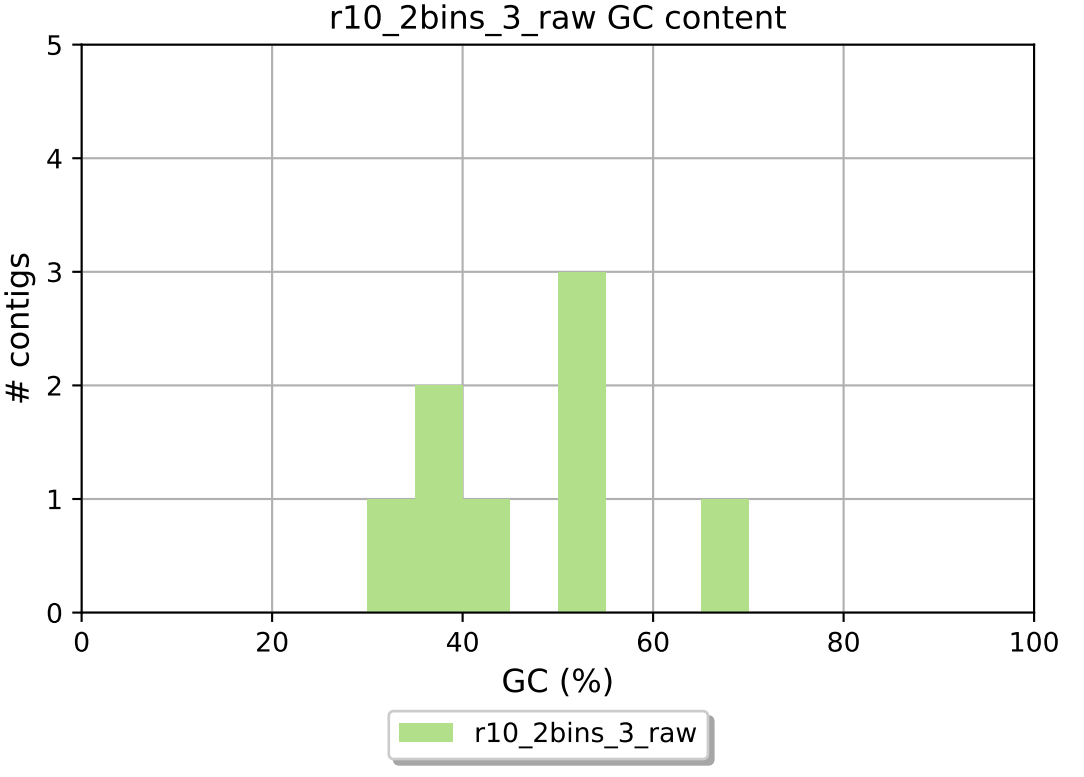

r10_2bins_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_MP_helen

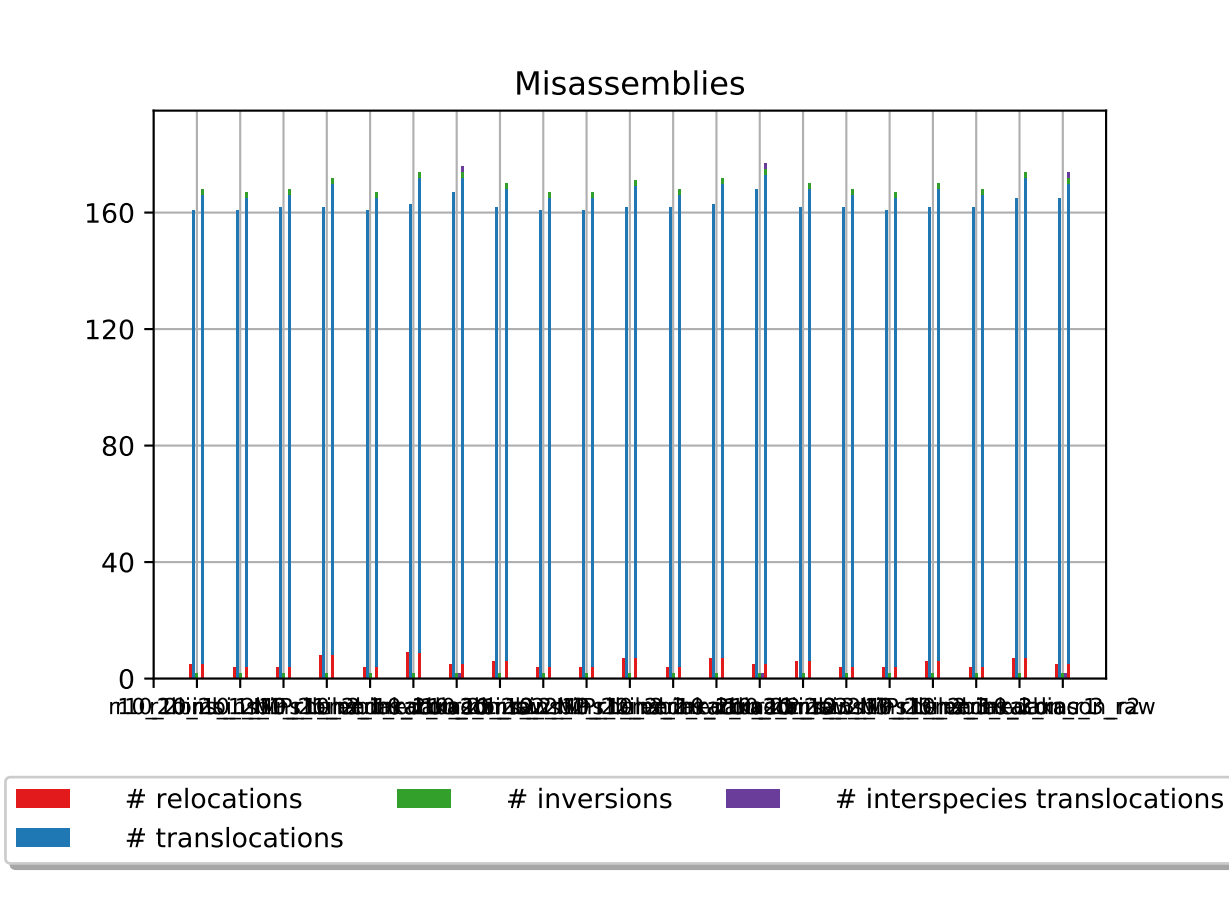

r10_2bins_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_r1_medaka

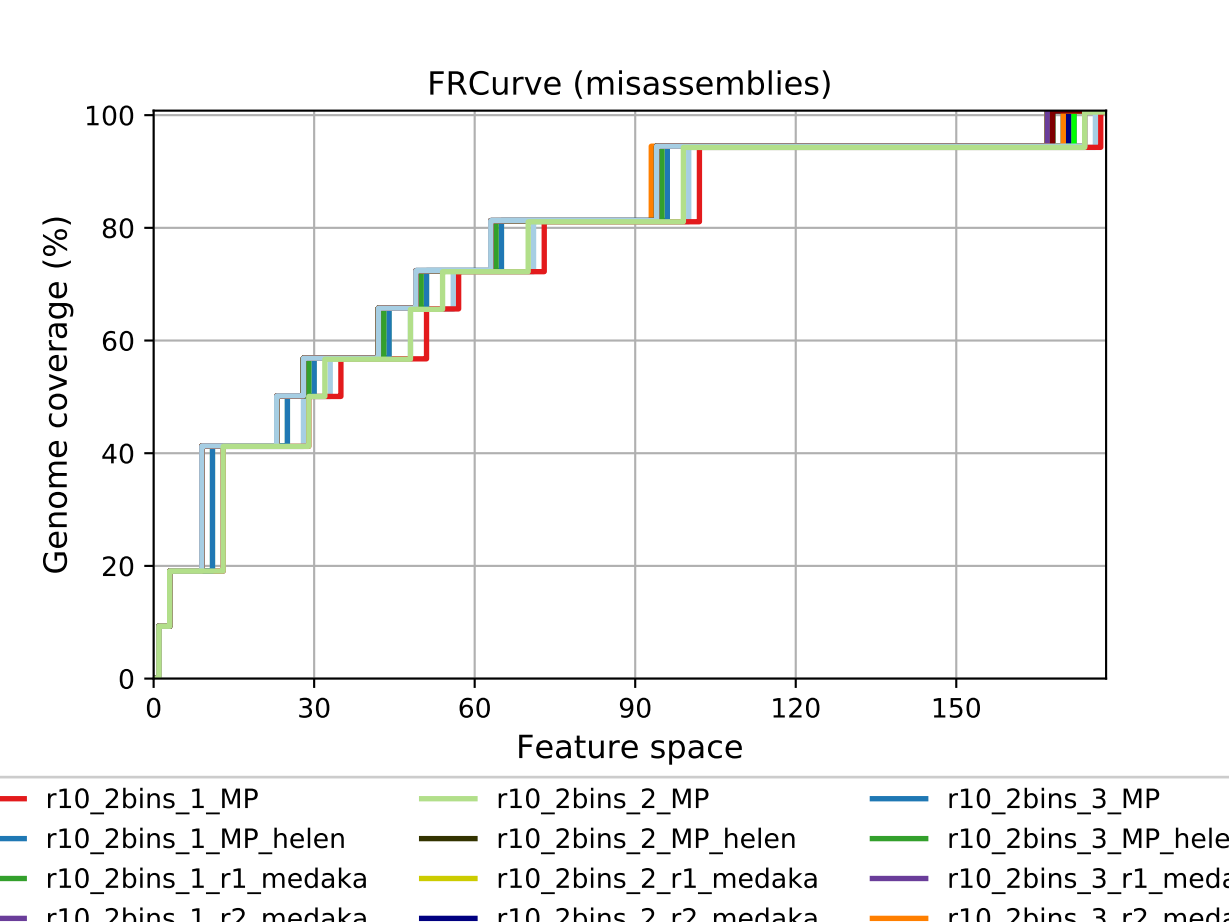

r10_2bins_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_r2_medaka

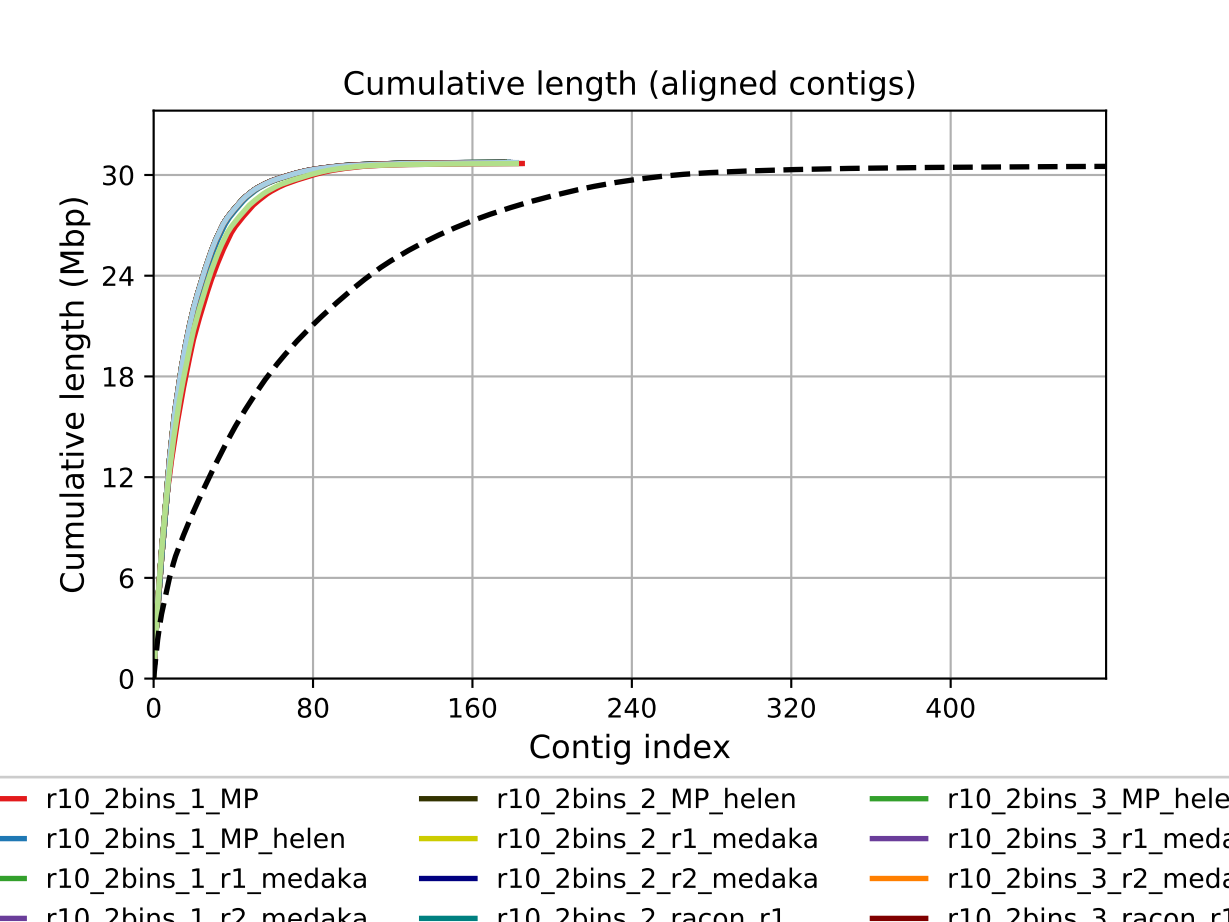

r10_2bins_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_racon_r1

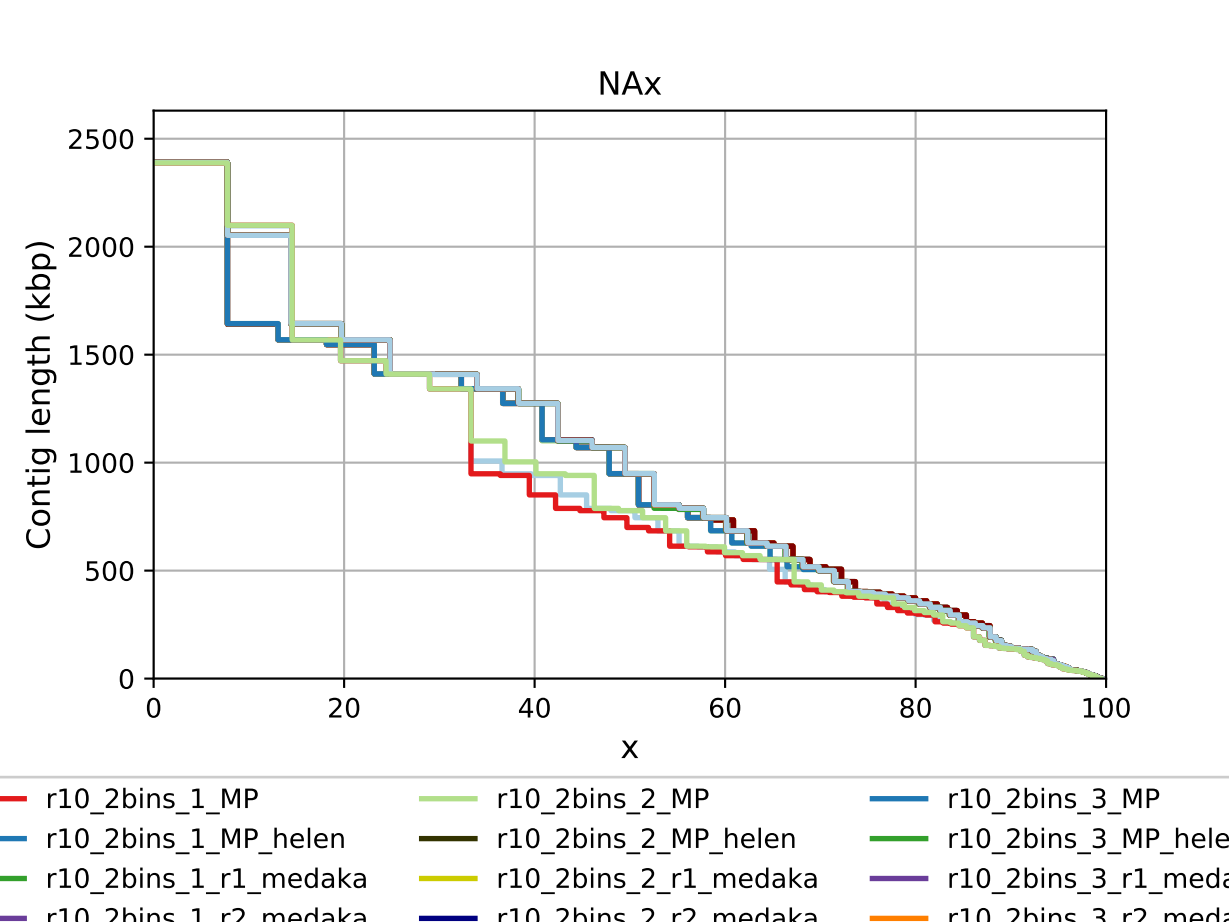

r10_2bins_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_racon_r2

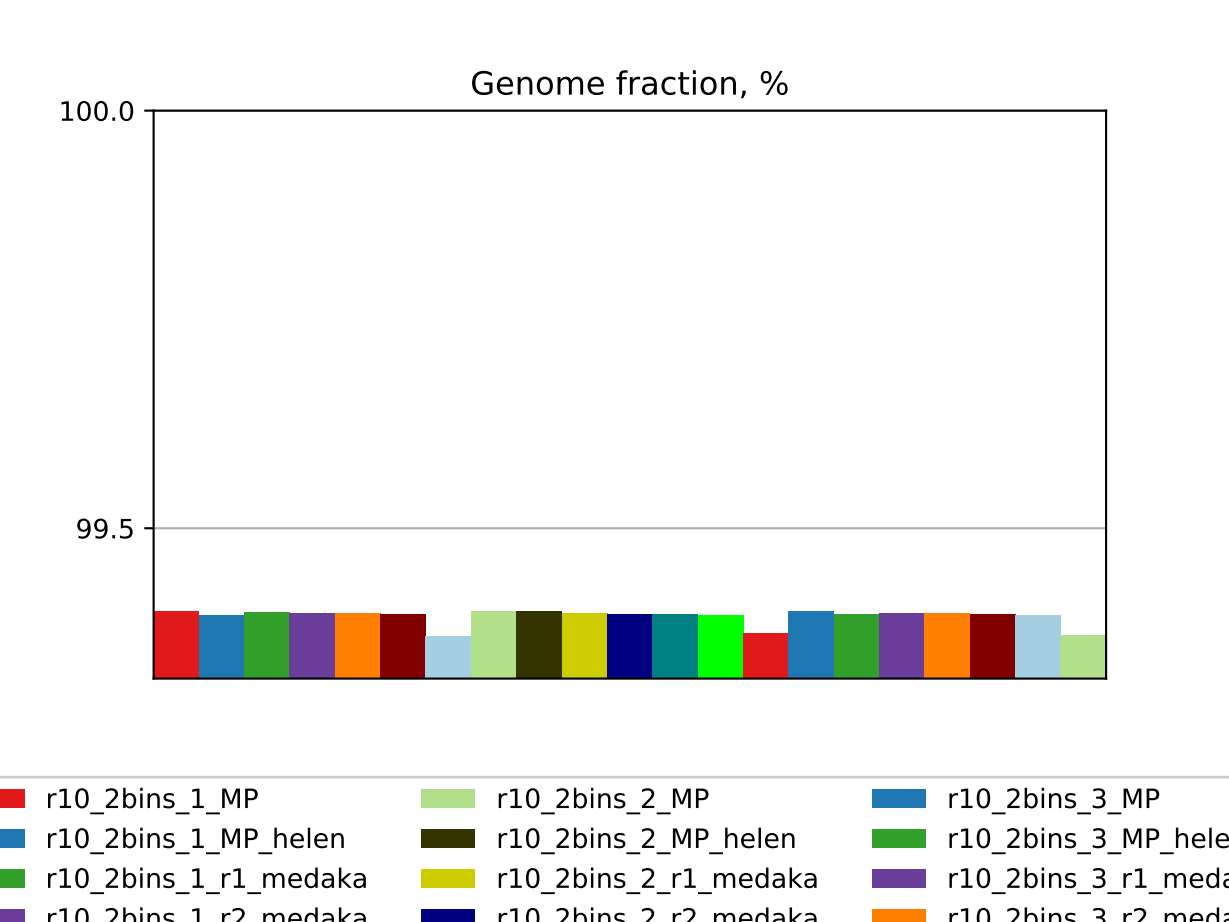

r10_2bins_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_2bins_3_raw


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
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_3_MP
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
6
12
18
24
30
0
80
160
240
320
400
Contig index
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_2_r2_medaka
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda
r10_2bins_3_r2_meda


NAx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_3_MP
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda


Genome fraction, %
100.0
99.5
r10_2bins_1_MP
r10_2bins_1_MP_helen
r10_2bins_1_r1_medaka
r10_2bins_2_MP
r10_2bins_2_MP_helen
r10_2bins_2_r1_medaka
r10_2bins_3_MP
r10_2bins_3_MP_hele
r10_2bins_3_r1_meda