Report

	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# 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 (>= 5000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
Total length (>= 10000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
Total length (>= 25000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
Total length (>= 50000 bp)	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
# contigs	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Largest contig	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792391	6792395	6791556	6791638	6787718
Total length	30867105	30862332	30864140	30855723	30852485	30847715	30848193	30866747	30862810	30867513	30858217	30852216	30847455	30848654	30870433	30862880	30870915	30863583	30855714	30850694	30851667
Reference length	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151	6728151
GC (%)	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48	49.50	49.51	49.50	49.50	49.49	49.49	49.48
Reference GC (%)	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21	66.21
N50	4758942	4758045	4758082	4757996	4757676	4757433	4756098	4758934	4757811	4759010	4758465	4757950	4757851	4756089	4758933	4757839	4759025	4758469	4757998	4757867	4756074
NG50	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792391	6792395	6791556	6791638	6787718
N75	2992085	2992067	2992074	2992074	2991917	2991951	2990633	2992084	2992067	2992184	2992173	2991893	2991931	2990628	2992084	2992068	2992178	2992176	2991922	2991951	2990626
NG75	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792391	6792395	6791556	6791638	6787718
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	8	6	6	6	6	6	10	8	6	6	6	6	6	10	6	6	6	6	6	6	10
# 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	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792391	6792395	6791556	6791638	6787718
# local misassemblies	11	11	11	11	11	11	28	11	11	11	11	11	12	29	11	11	11	11	11	11	29
# 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	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	6	6
# unaligned contigs	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	24046975	24042790	24043929	24035604	24033094	24028472	24076786	24047237	24043942	24048404	24039283	24033441	24028774	24077732	24051441	24043921	24052067	24044933	24037196	24032079	24080254
Genome fraction (%)	99.894	99.894	99.894	99.894	99.895	99.894	99.867	99.894	99.894	99.894	99.894	99.894	99.894	99.864	99.894	99.894	99.894	99.894	99.894	99.894	99.864
Duplication ratio	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008	1.015	1.015	1.015	1.015	1.015	1.015	1.008
# N's per 100 kbp	0.00	0.03	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	0.32
# mismatches per 100 kbp	59.40	56.44	57.09	57.06	59.31	58.91	65.65	58.80	56.09	56.88	56.69	58.92	58.52	64.58	58.33	56.17	56.50	56.35	58.13	58.58	65.29
# indels per 100 kbp	5.71	3.41	3.68	3.60	14.97	14.31	97.14	5.49	5.13	6.56	6.38	15.49	14.21	96.85	5.48	5.13	6.28	6.46	15.16	14.25	96.80
Largest alignment	1547073	2052317	2052329	2052330	2052131	2052150	1826402	1546954	2052186	2052258	2052252	2052053	2052076	1664908	1643841	1643830	1643876	1643878	1643635	1643680	2098268
Total aligned length	6816775	6816194	6816873	6816781	6816059	6815905	6766612	6815813	6815171	6815412	6815237	6815078	6814984	6768491	6815239	6815207	6815096	6814898	6814766	6814863	6768827
NGA50	1274873	1371005	1371014	1371015	1370872	1370886	940304	1209489	1209480	1209520	1209516	1209345	1209366	940651	1274471	1274461	1274503	1274502	1274310	1274344	1471391
NGA75	1070200	1070195	1070190	1070189	1070104	1070107	569562	1070337	1070324	1070369	1070366	1070242	1070249	569184	1070337	1070325	1070363	1070364	1070253	1070241	610115
LGA50	3	2	2	2	2	2	3	3	3	3	3	3	3	3	3	3	3	3	3	3	2
LGA75	4	4	4	4	4	4	5	4	4	4	4	4	4	5	4	4	4	4	4	4	4

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

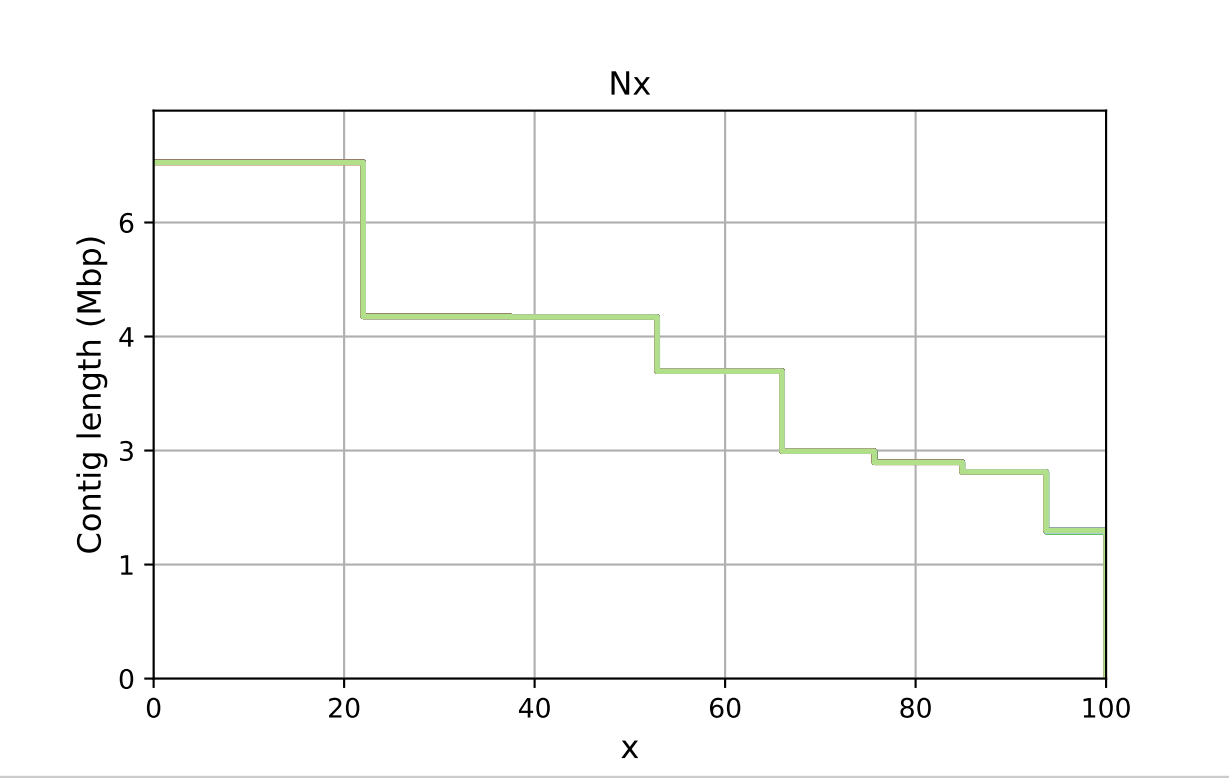
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_3_raw
# misassemblies	8	6	6	6	6	6	10	8	6	6	6	6	6	10	6	6	6	6	6	6	10
# contig misassemblies	8	6	6	6	6	6	10	8	6	6	6	6	6	10	6	6	6	6	6	6	10
# c. relocations	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	7	6	6	6	6	6	10	7	6	6	6	6	6	10	6	6	6	6	6	6	10
# 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	6792277	6792242	6792252	6792253	6791585	6791667	6787707	6792257	6792199	6792399	6792386	6791581	6791672	6787721	6792253	6792197	6792391	6792395	6791556	6791638	6787718
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# possible misassemblies	16	18	18	18	18	18	34	16	18	18	18	18	18	34	18	18	18	18	18	18	34
# local misassemblies	11	11	11	11	11	11	28	11	11	11	11	11	12	29	11	11	11	11	11	11	29
# 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	20	21	21	21	21	21	16	20	21	21	21	21	20	16	21	21	21	21	21	21	16
# unaligned mis. contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	6	7	7	7	7	7	6	6
# mismatches	3992	3793	3837	3835	3986	3959	4411	3952	3770	3823	3810	3960	3933	4339	3920	3775	3797	3787	3907	3937	4387
# indels	384	229	247	242	1006	962	6527	369	345	441	429	1041	955	6507	368	345	422	434	1019	958	6504
# indels (<= 5 bp)	288	134	153	148	912	867	6403	274	248	348	336	948	862	6389	272	247	328	340	923	864	6383
# indels (> 5 bp)	96	95	94	94	94	95	124	95	97	93	93	93	93	118	96	98	94	94	96	94	121
Indels length	5432	5261	5260	5255	6141	6080	12979	5361	5364	5410	5394	6118	6010	12747	5411	5411	5446	5456	6141	6071	12818

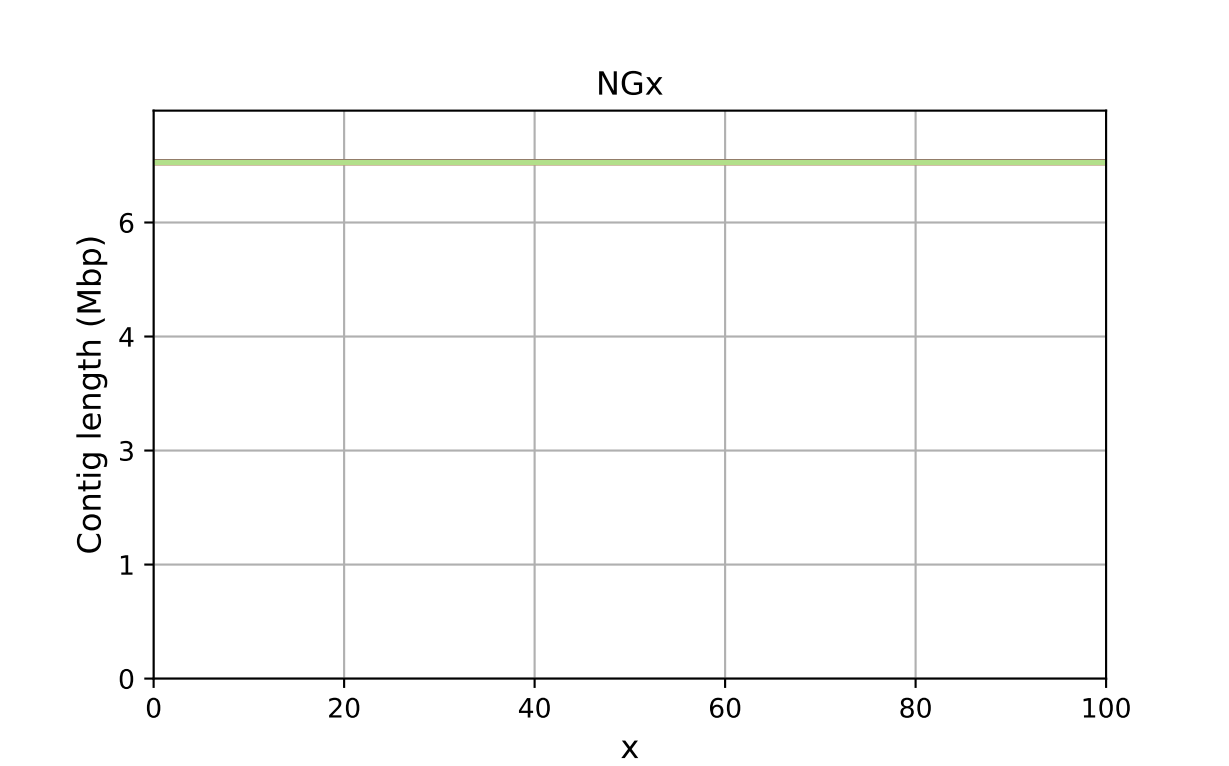
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

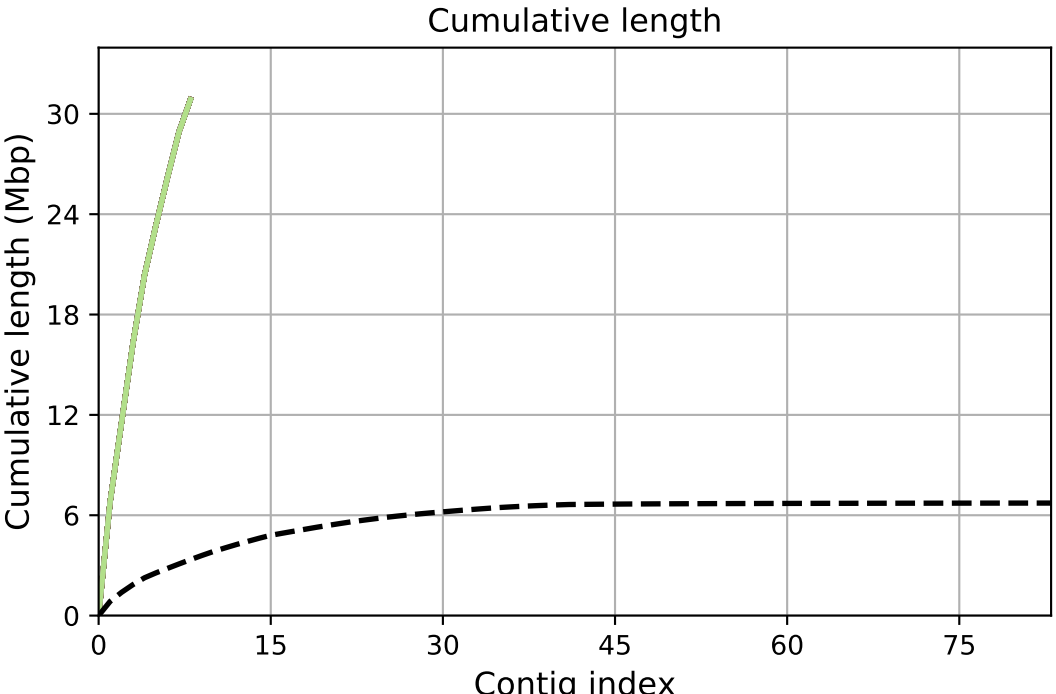
Unaligned report

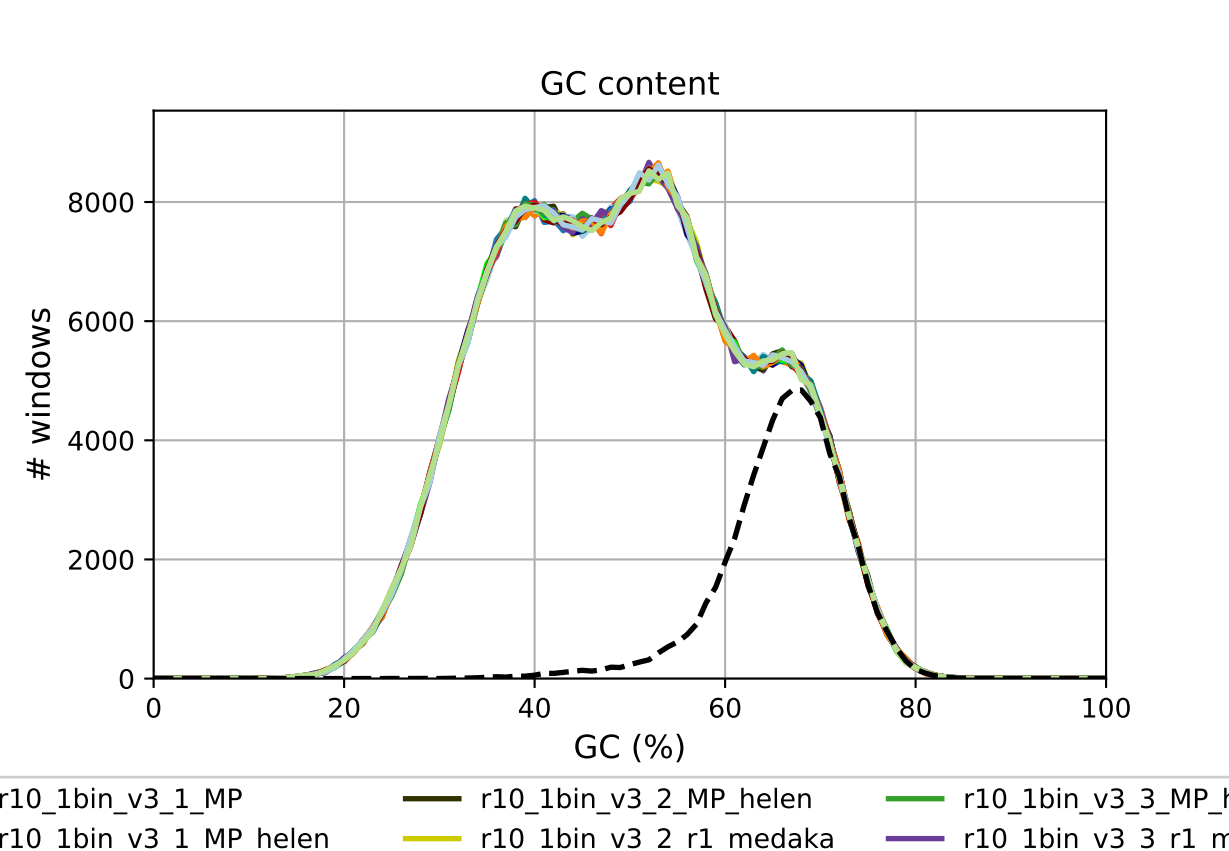
	r10_1bin_v3_1_MP	r10_1bin_v3_1_MP_helen	r10_1bin_v3_1_r1_medaka	r10_1bin_v3_1_r2_medaka	r10_1bin_v3_1_racon_r1	r10_1bin_v3_1_racon_r2	r10_1bin_v3_1_raw	r10_1bin_v3_2_MP	r10_1bin_v3_2_MP_helen	r10_1bin_v3_2_r1_medaka	r10_1bin_v3_2_r2_medaka	r10_1bin_v3_2_racon_r1	r10_1bin_v3_2_racon_r2	r10_1bin_v3_2_raw	r10_1bin_v3_3_MP	r10_1bin_v3_3_MP_helen	r10_1bin_v3_3_r1_medaka	r10_1bin_v3_3_r2_medaka	r10_1bin_v3_3_racon_r1	r10_1bin_v3_3_racon_r2	r10_1bin_v3_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	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Partially unaligned length	24046975	24042790	24043929	24035604	24033094	24028472	24076786	24047237	24043942	24048404	24039283	24033441	24028774	24077732	24051441	24043921	24052067	24044933	24037196	24032079	24080254
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	100

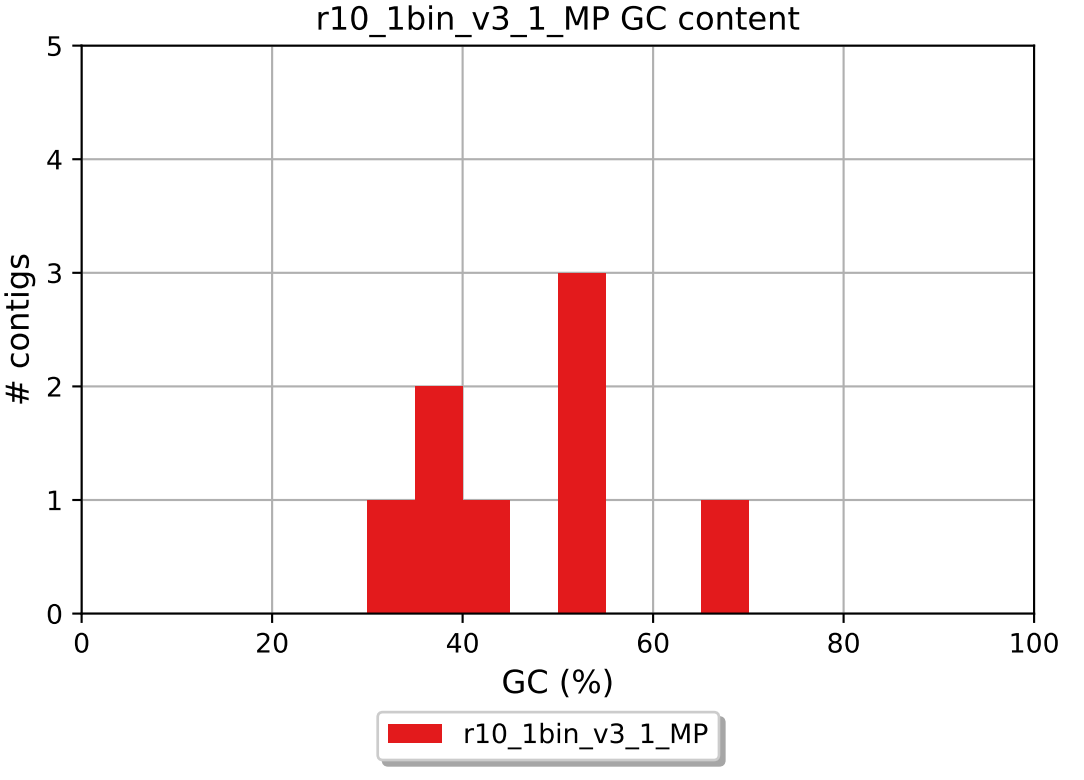
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

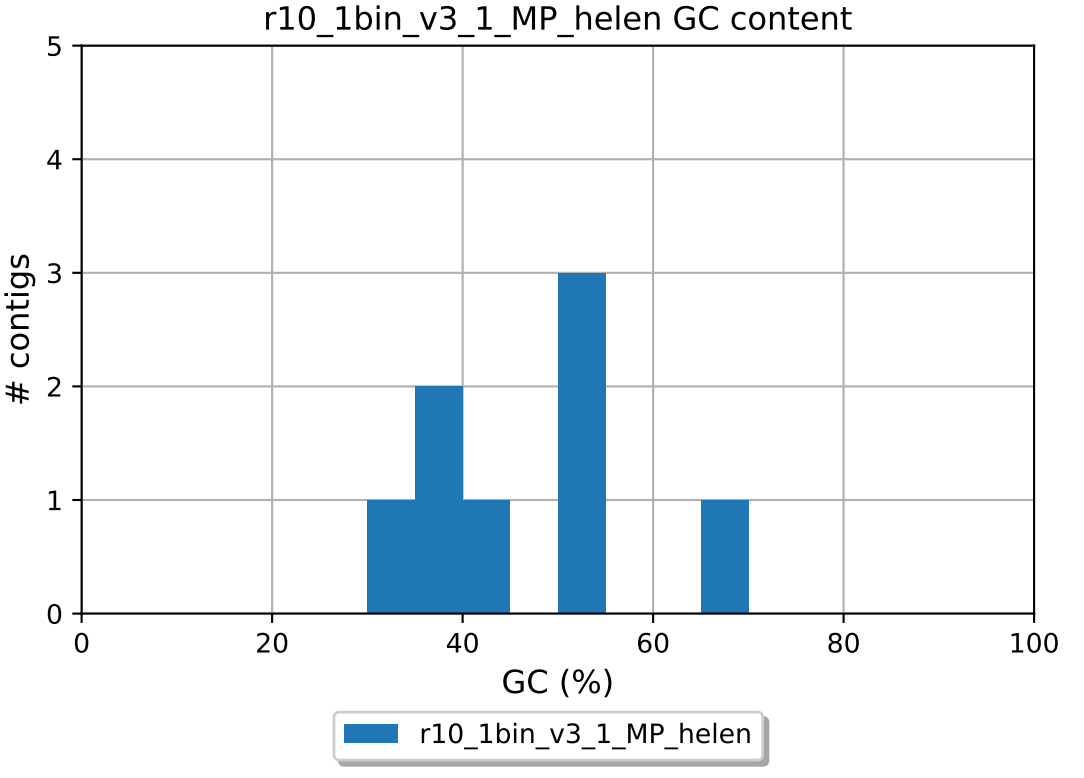

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

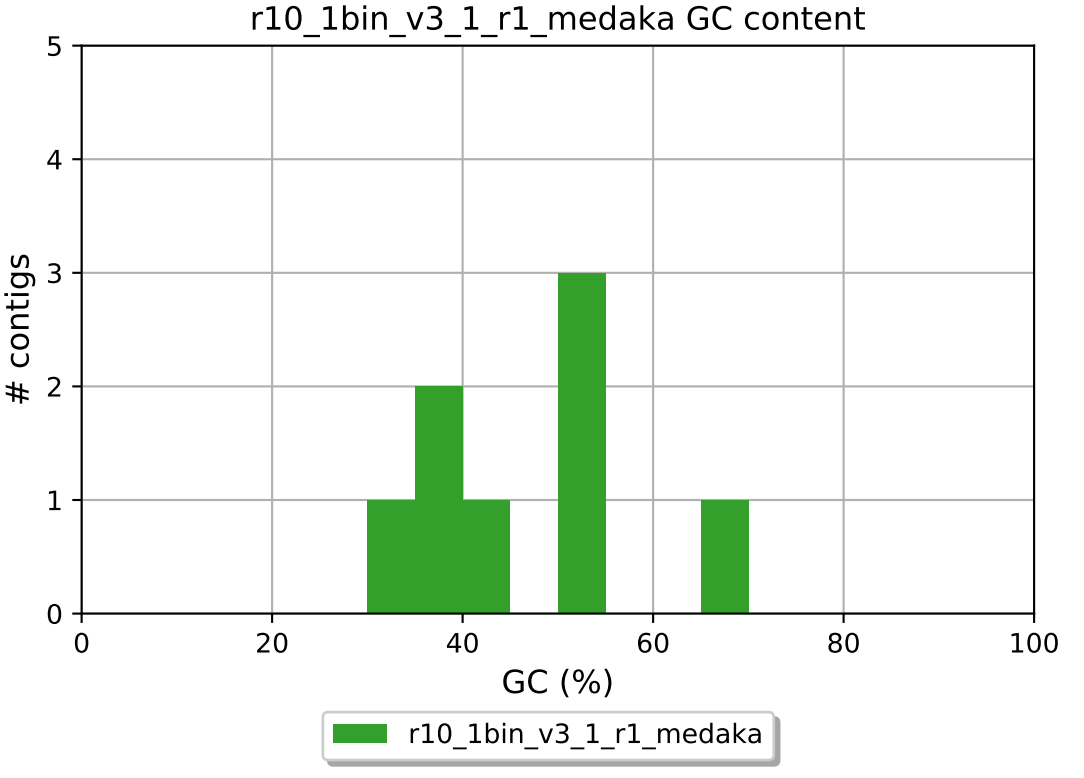

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m

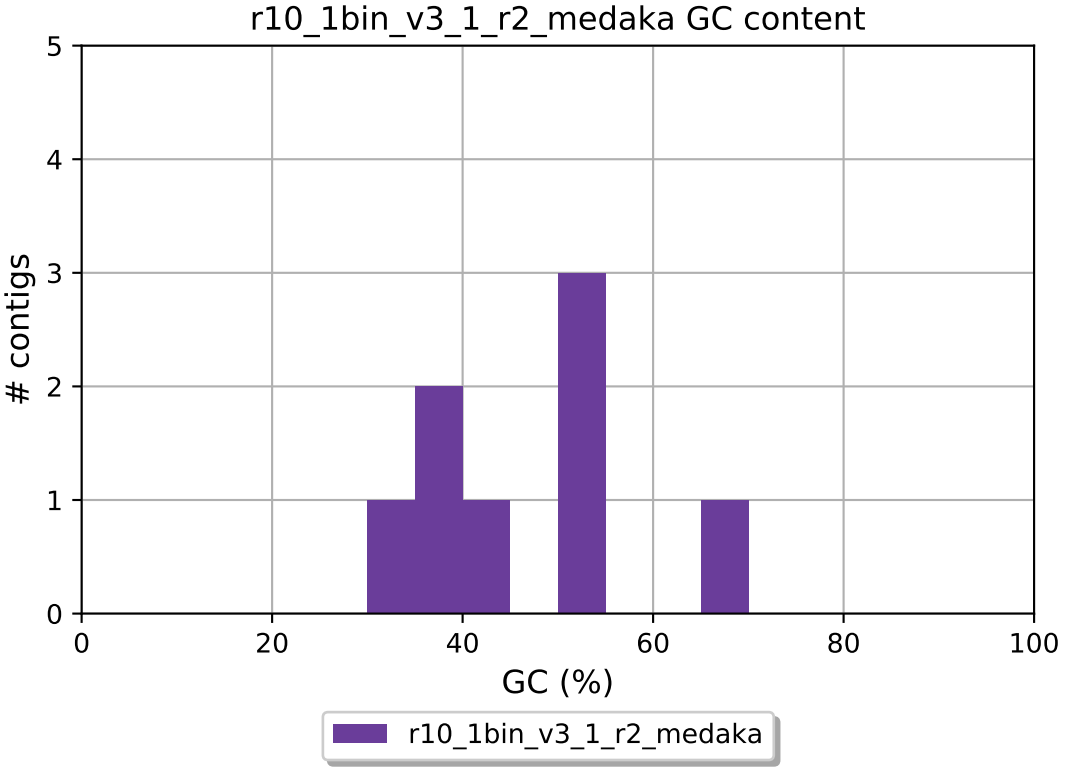

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
15
30
45
60
75
Contig index
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

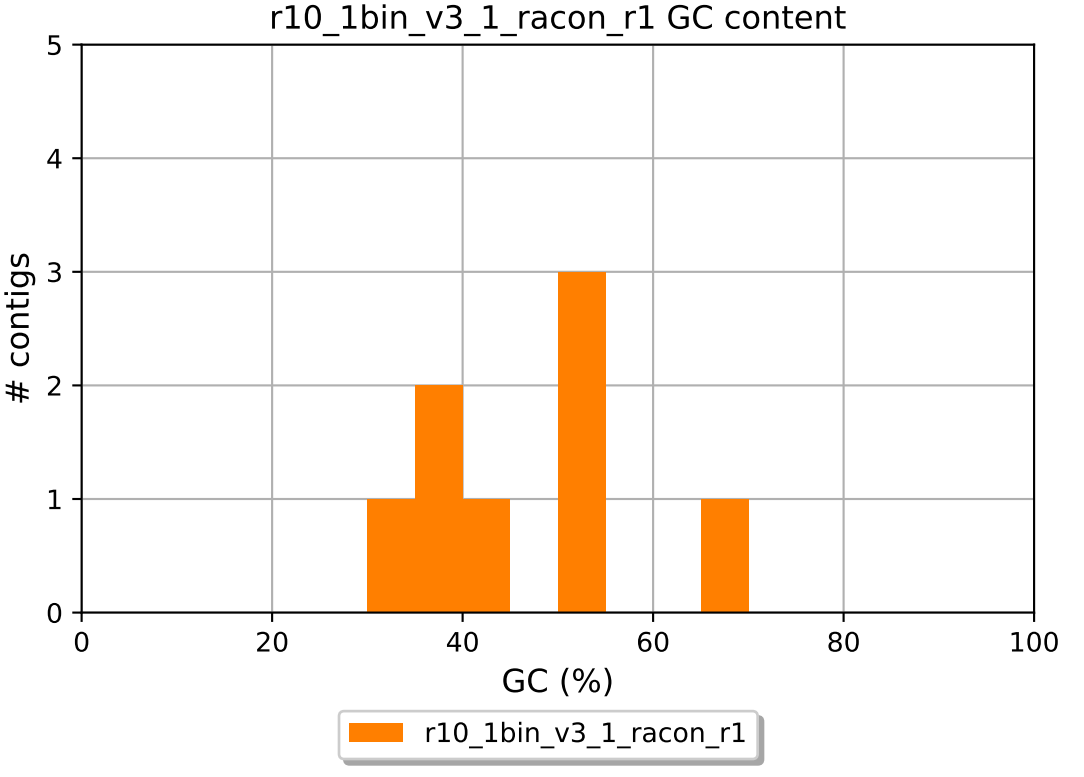

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m

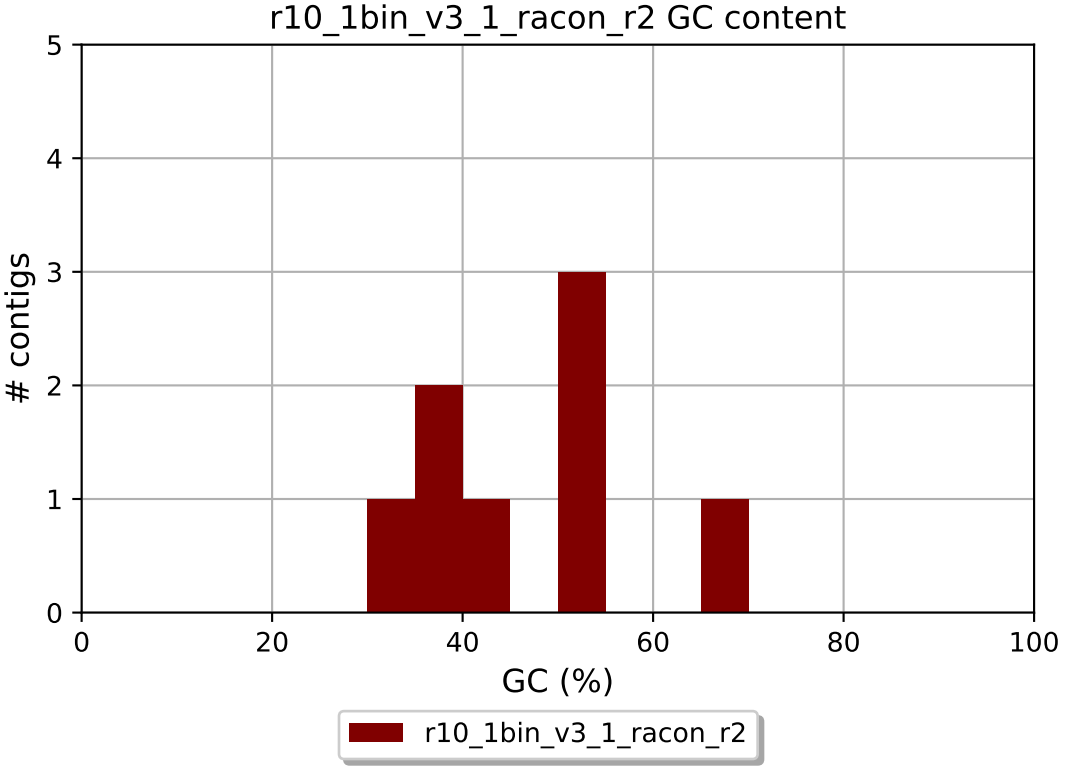

r10_1bin_v3_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP

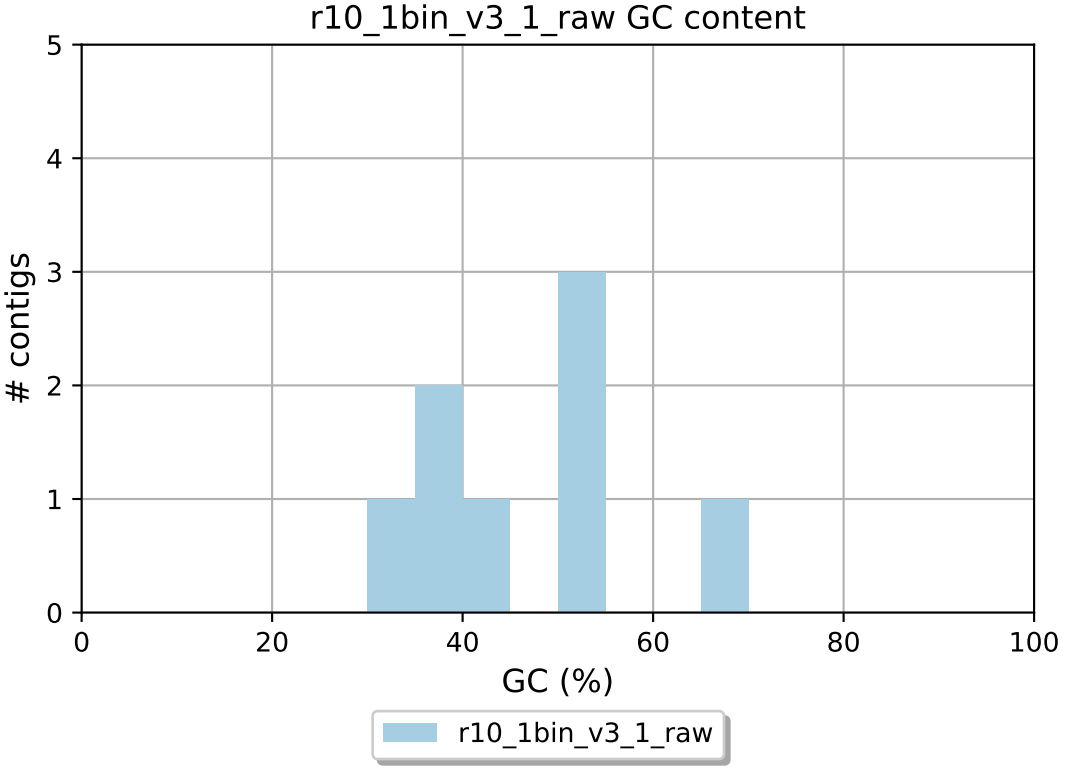

r10_1bin_v3_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_MP_helen

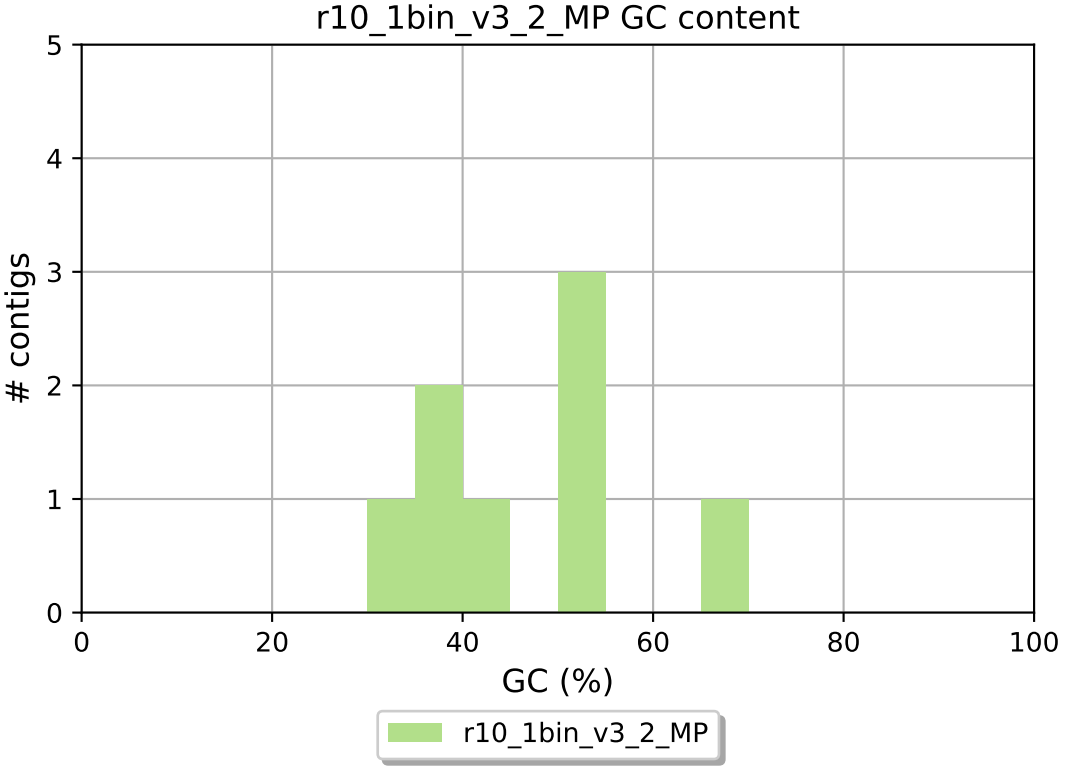

r10_1bin_v3_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r1_medaka

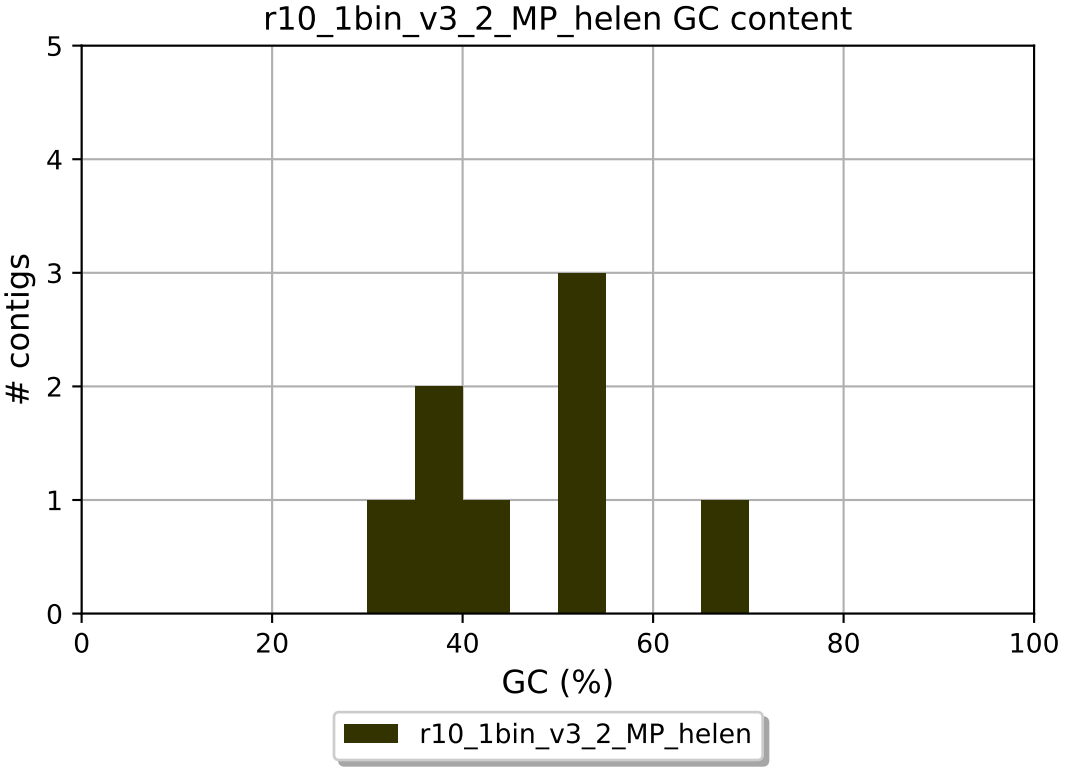

r10_1bin_v3_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_r2_medaka

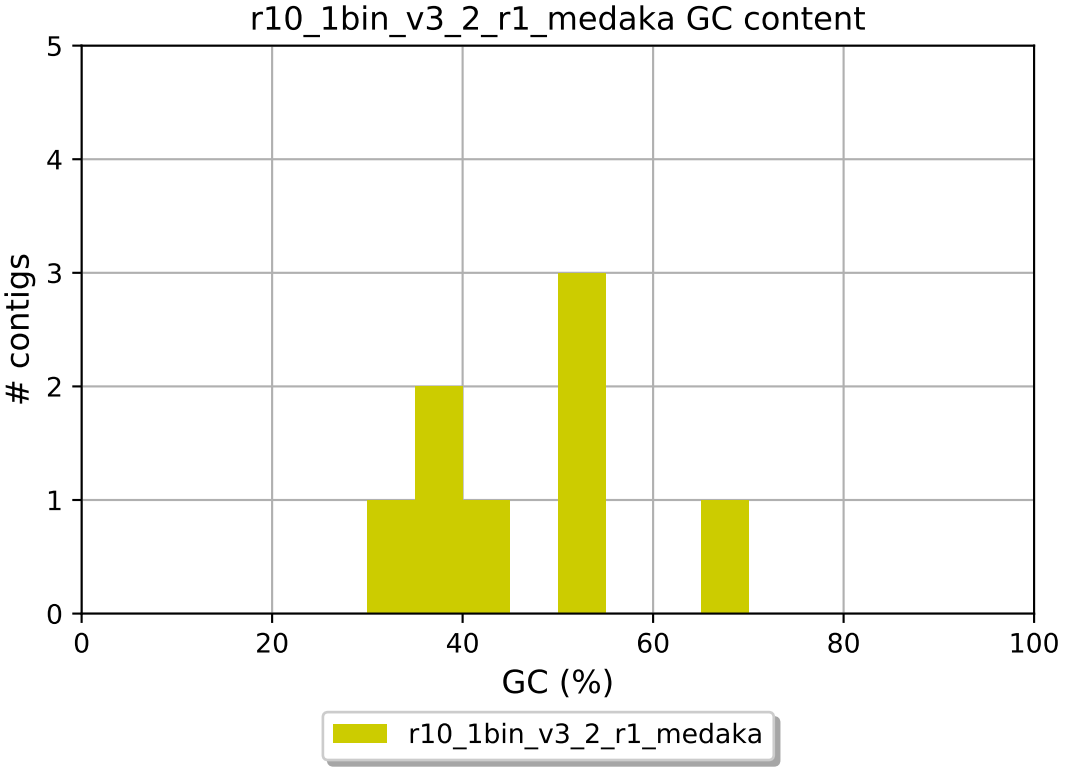

r10_1bin_v3_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r1

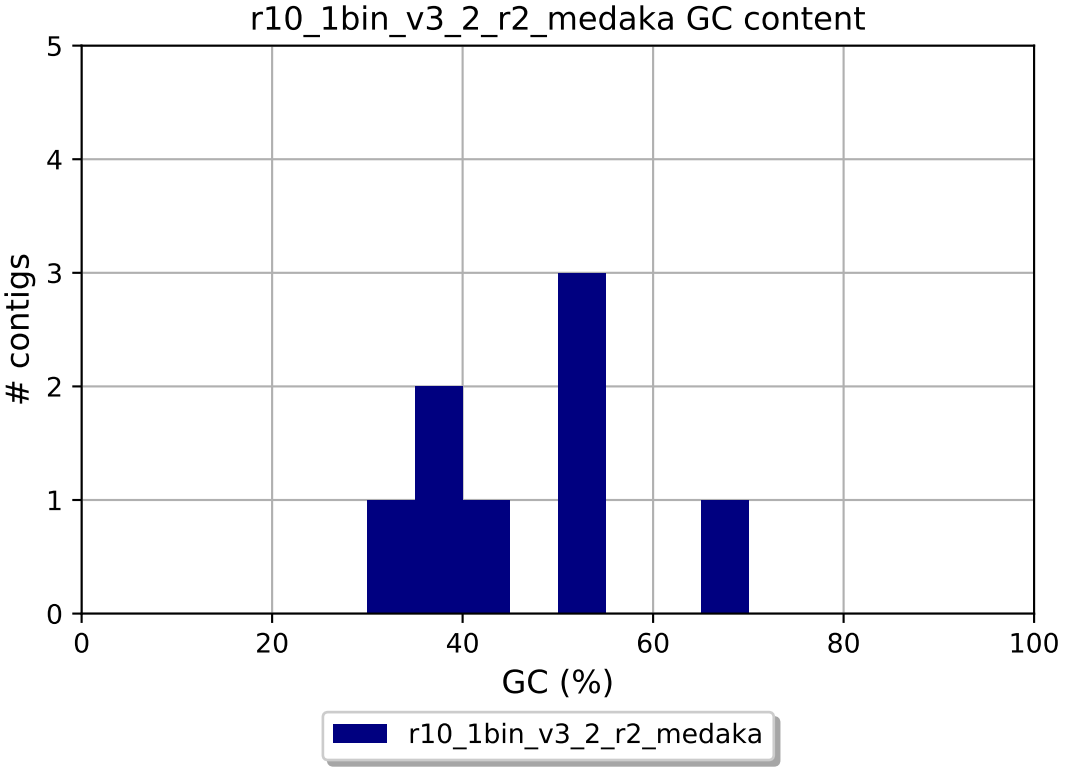

r10_1bin_v3_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_racon_r2

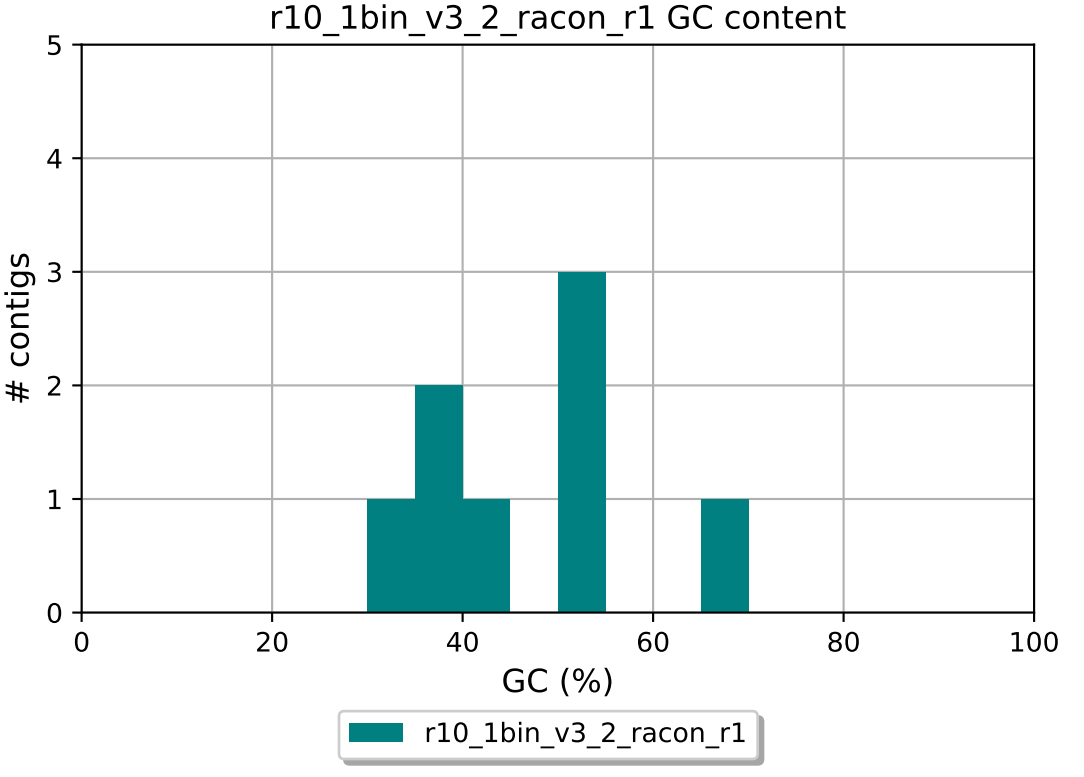

r10_1bin_v3_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_1_raw

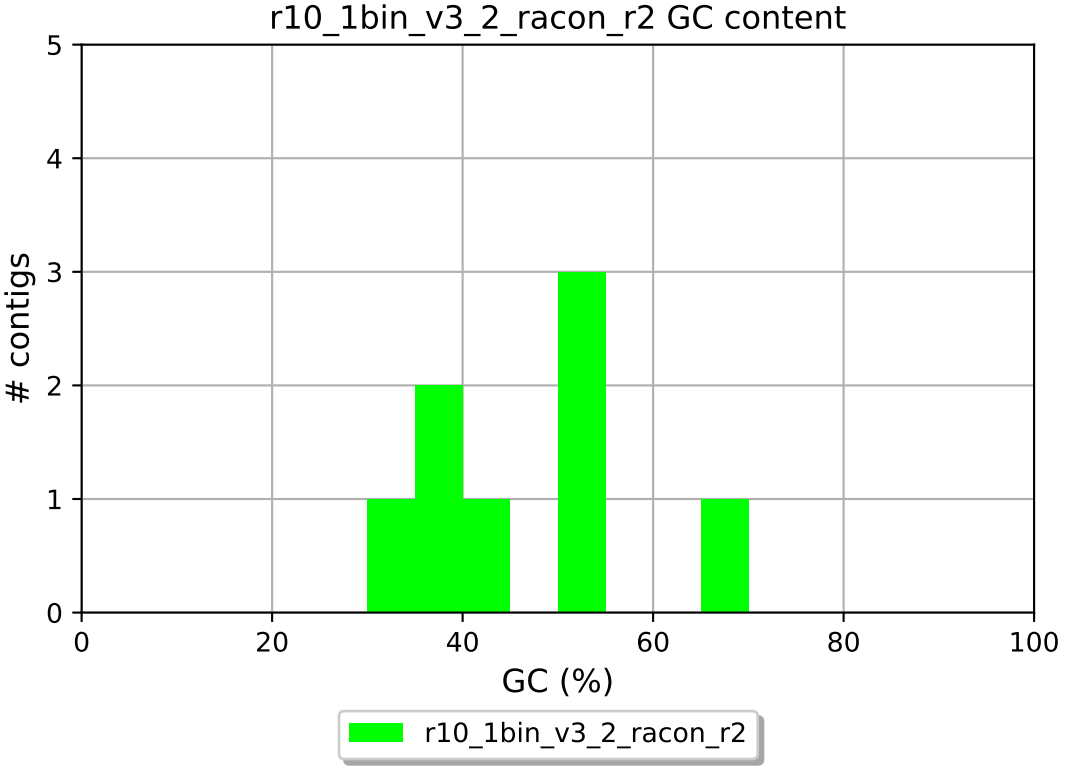

r10_1bin_v3_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP

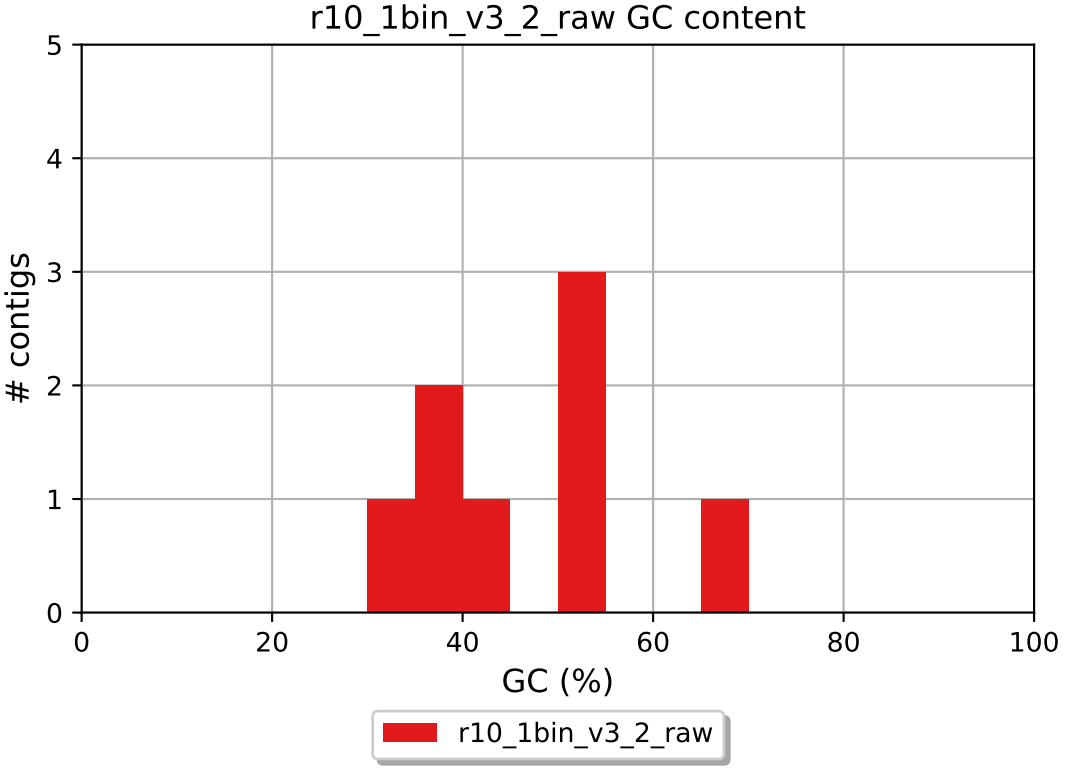

r10_1bin_v3_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_MP_helen

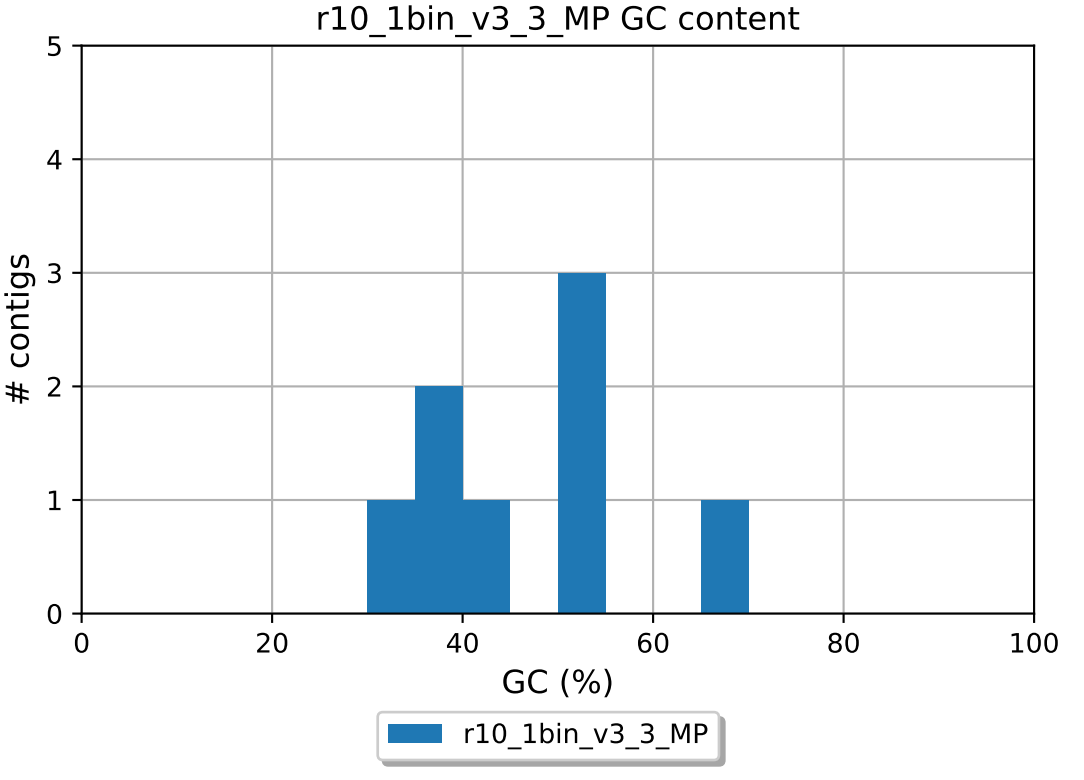

r10_1bin_v3_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r1_medaka

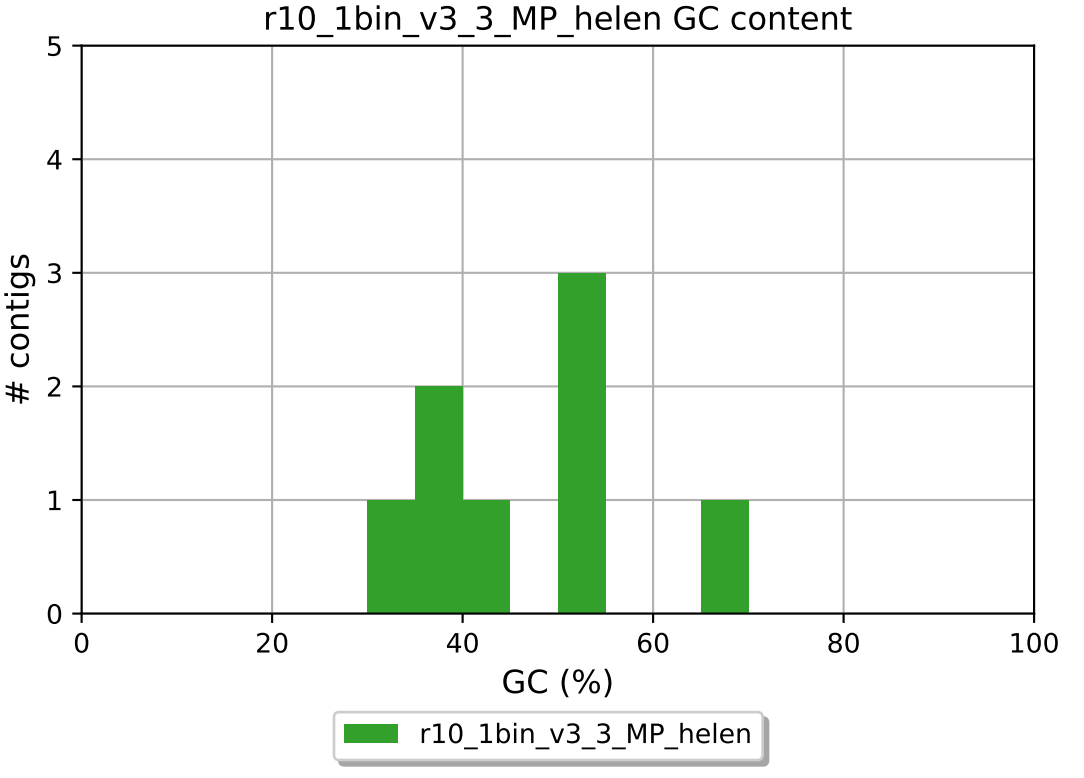

r10_1bin_v3_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_r2_medaka

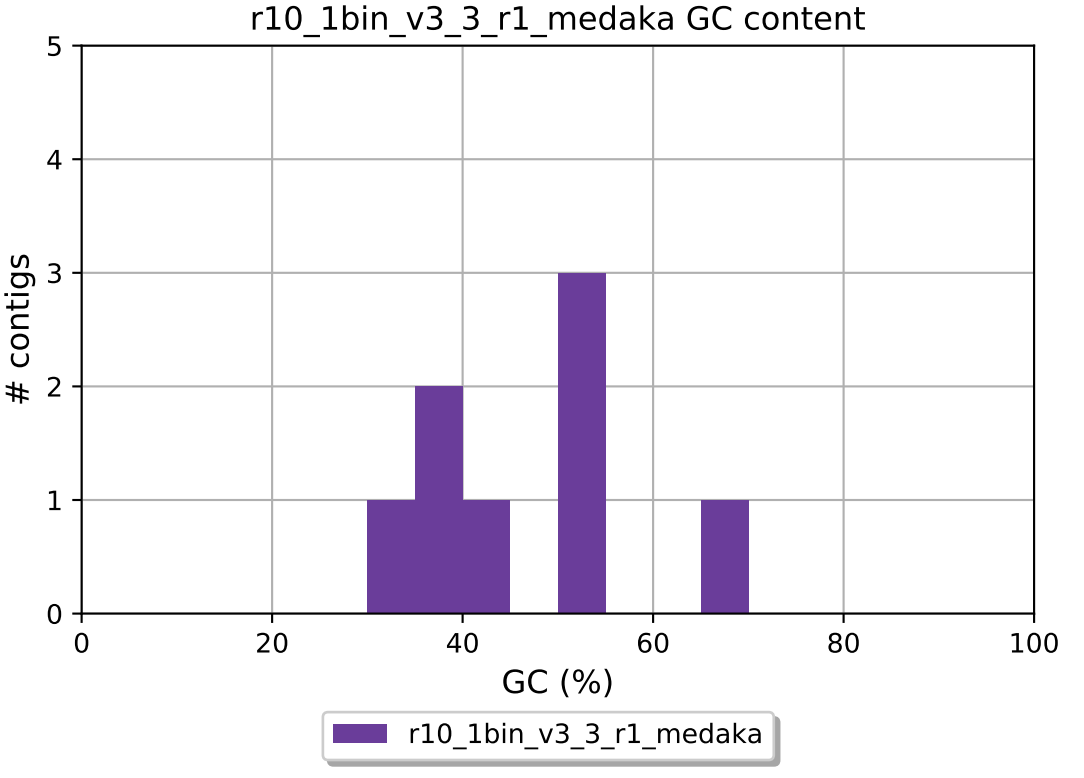

r10_1bin_v3_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r1

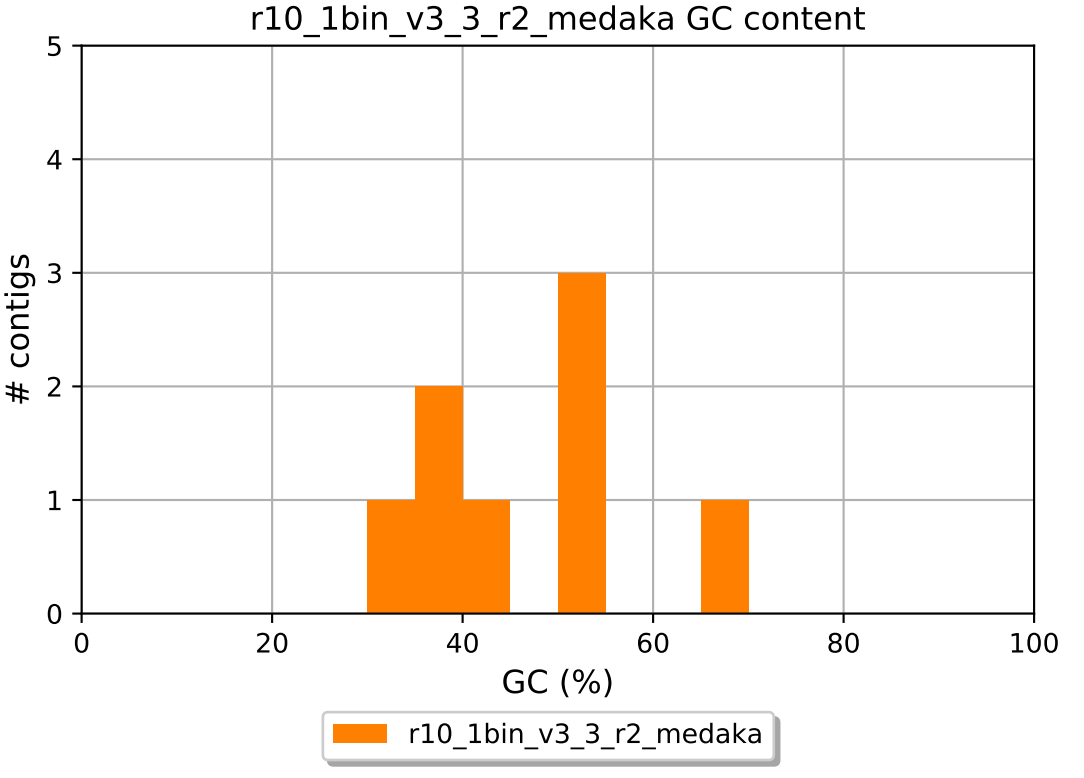

r10_1bin_v3_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_racon_r2

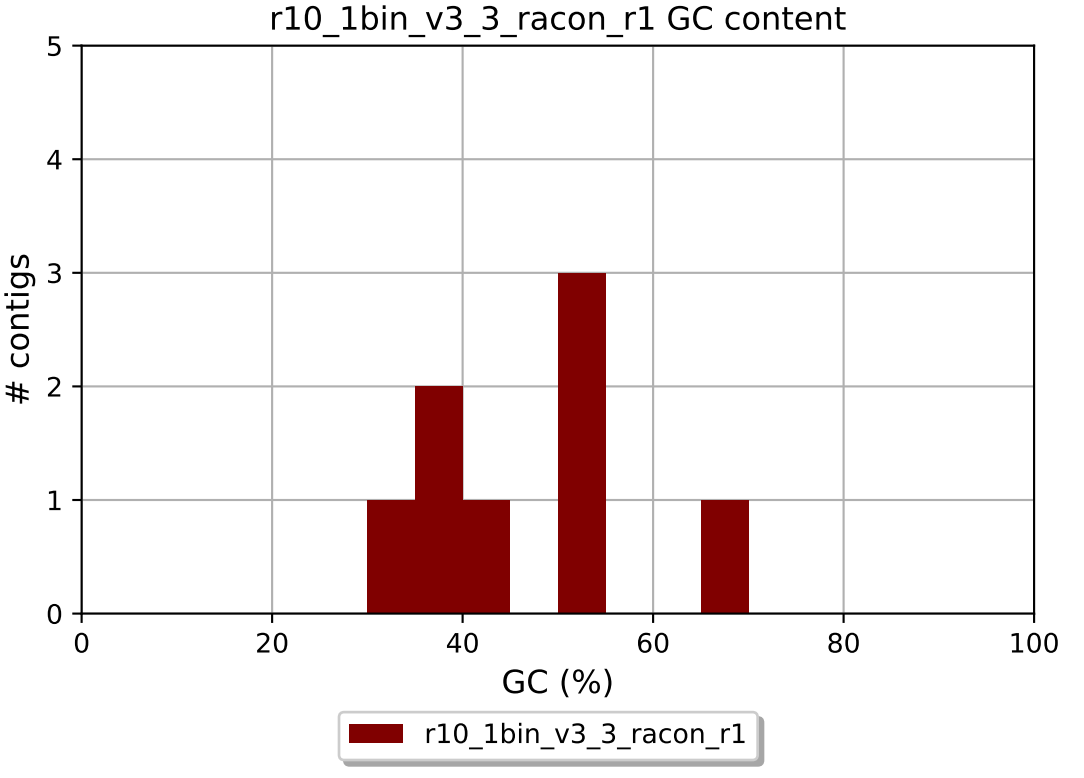

r10_1bin_v3_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_2_raw

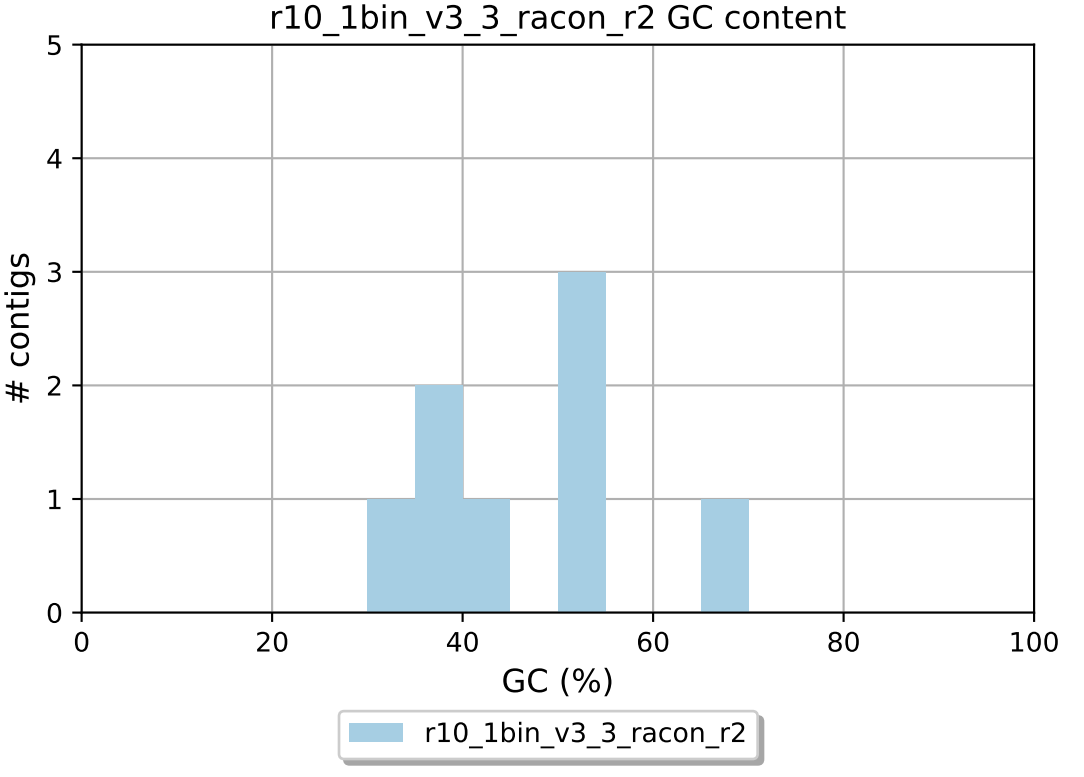

r10_1bin_v3_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP

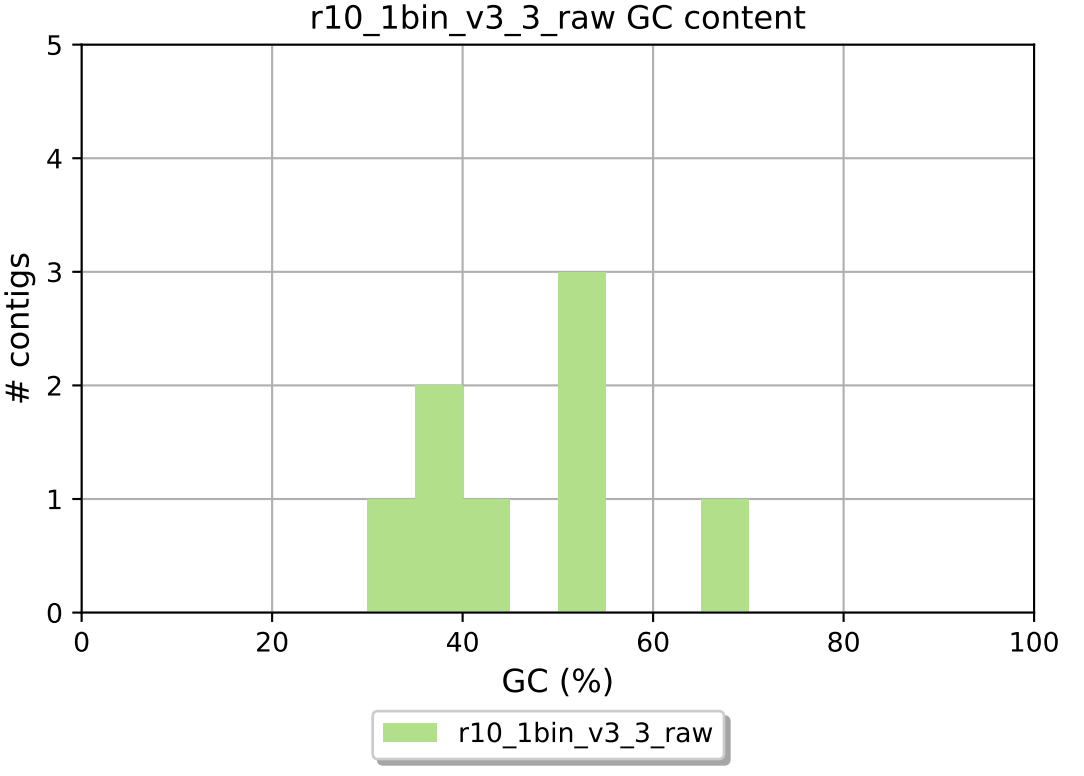

r10_1bin_v3_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_MP_helen

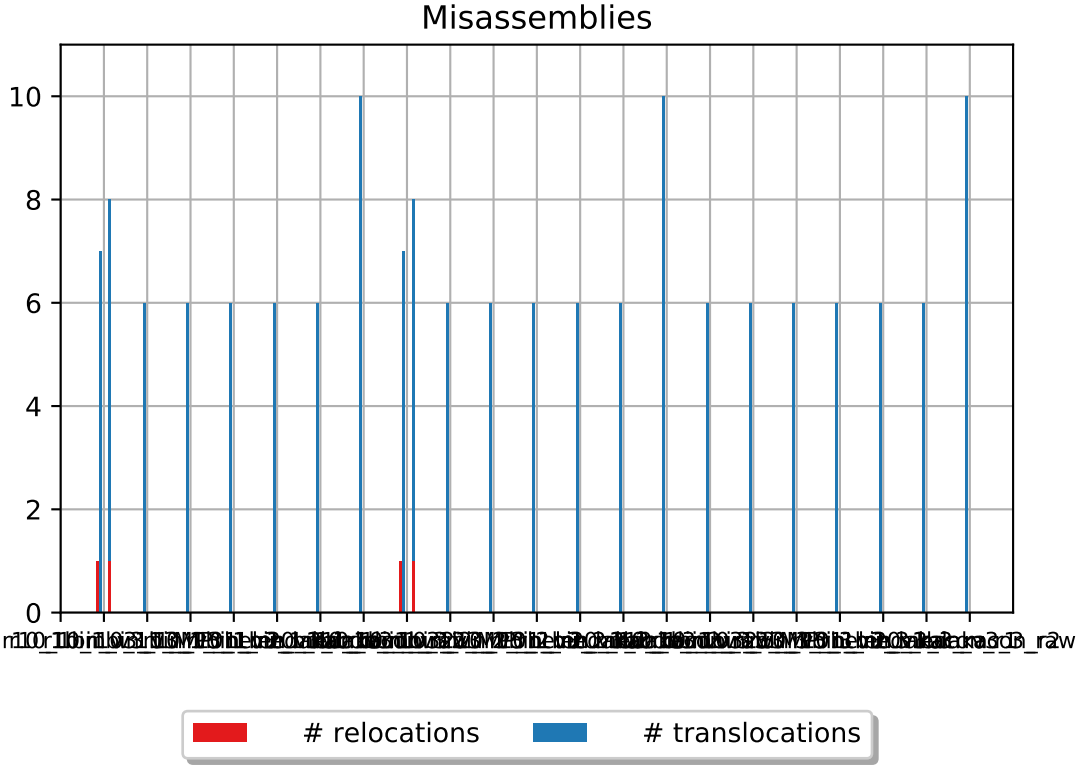

r10_1bin_v3_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r1_medaka

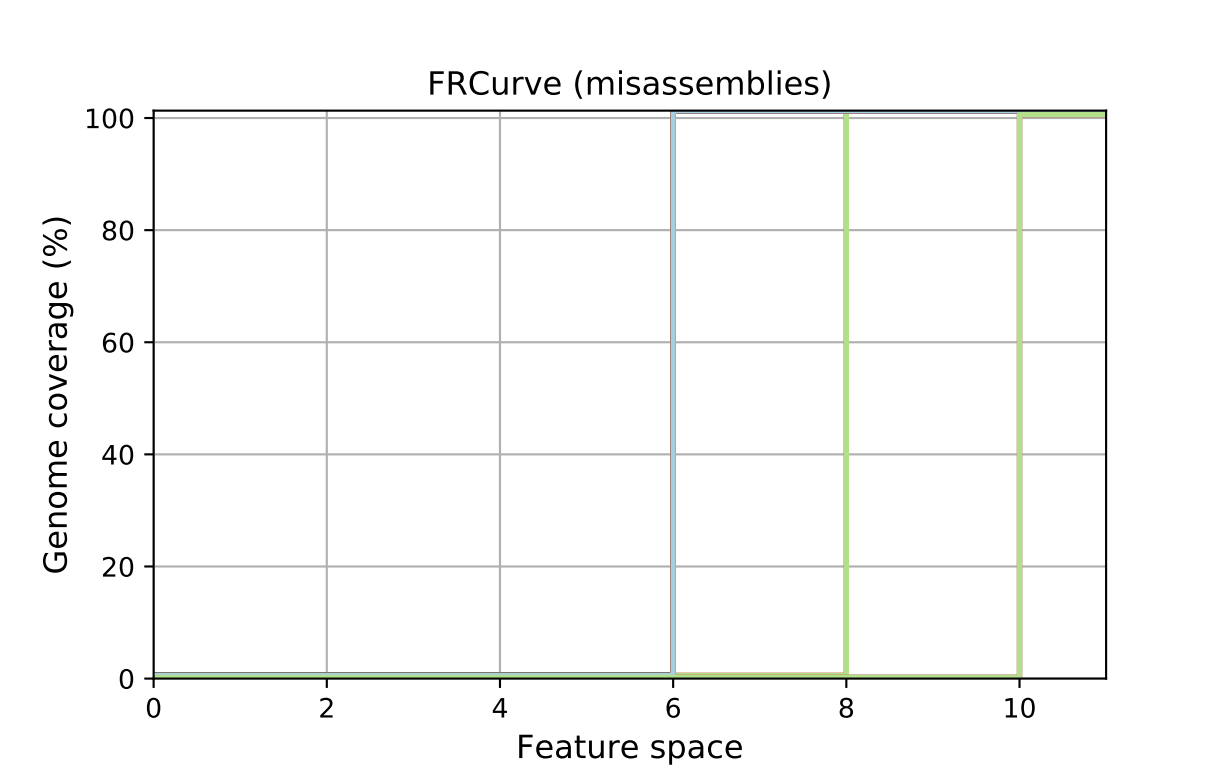

r10_1bin_v3_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_r2_medaka

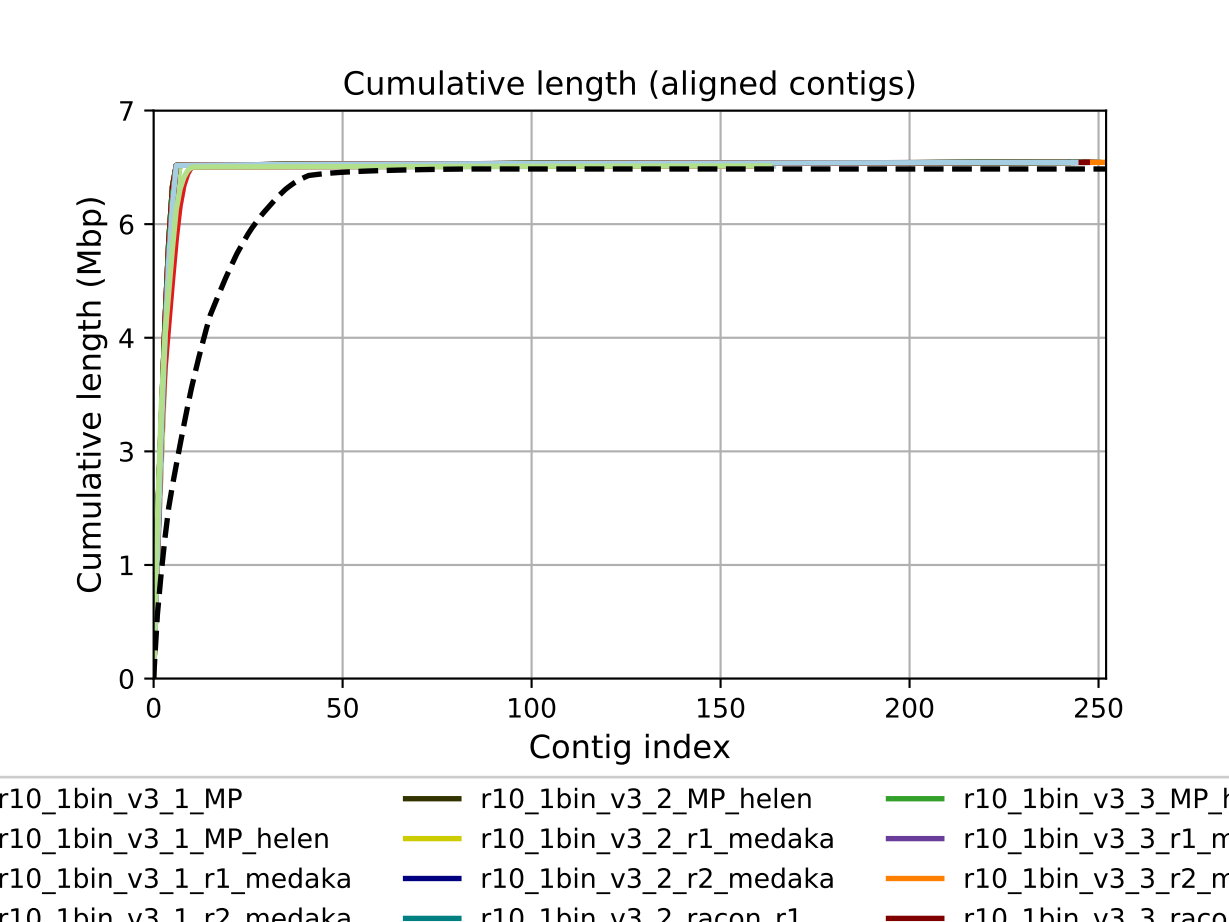

r10_1bin_v3_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r1

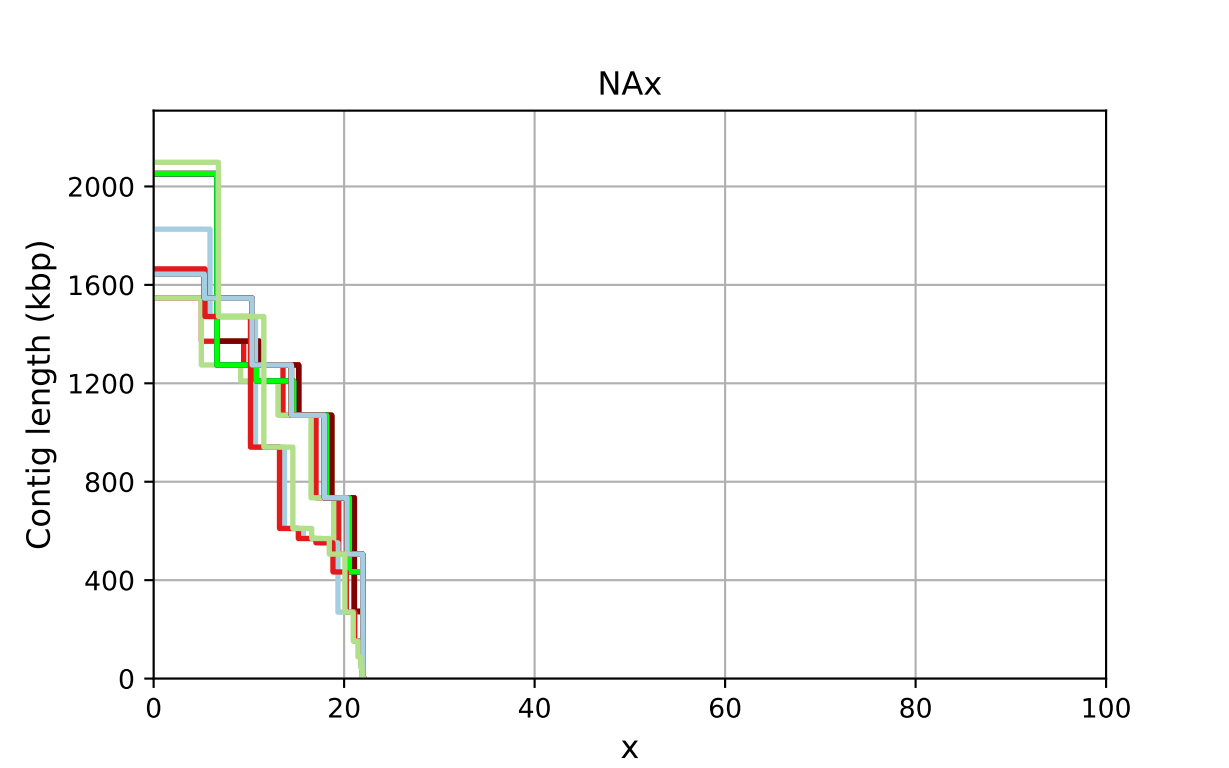

r10_1bin_v3_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_racon_r2

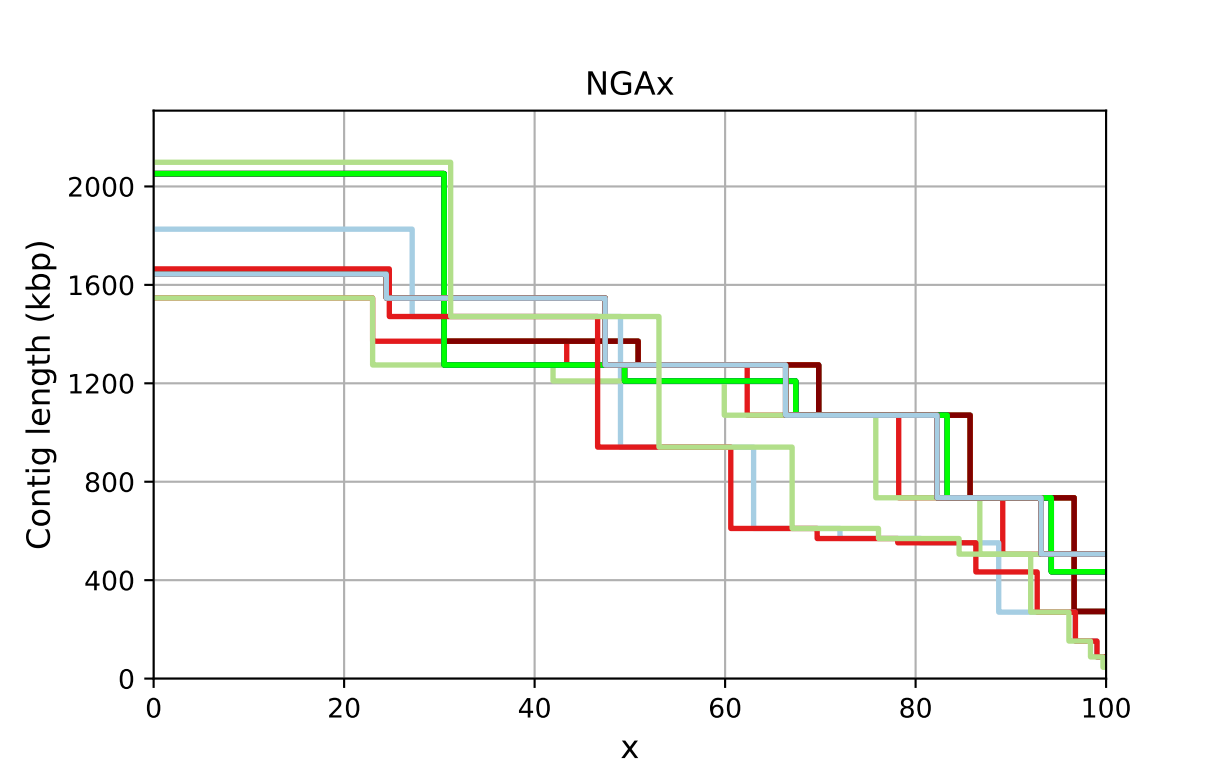

r10_1bin_v3_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v3_3_raw

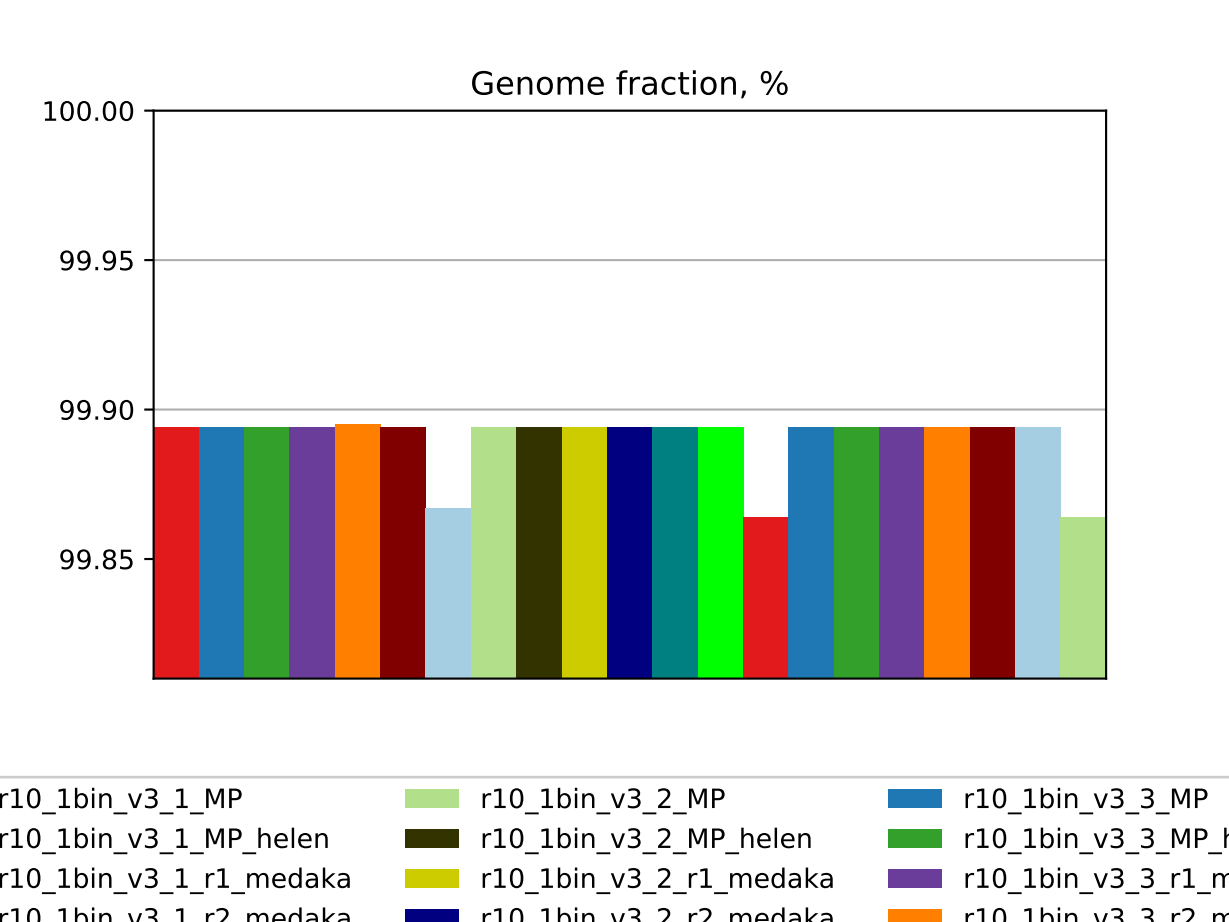

Misassemblies
10
8
6
4
2
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
3
4
6
7
0
50
100
150
200
250
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_2_r2_medaka
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m
r10_1bin_v3_3_r2_m


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m


Genome fraction, %
100.00
99.95
99.90
99.85
r10_1bin_v3_1_MP
r10_1bin_v3_1_MP_helen
r10_1bin_v3_1_r1_medaka
r10_1bin_v3_2_MP
r10_1bin_v3_2_MP_helen
r10_1bin_v3_2_r1_medaka
r10_1bin_v3_3_MP
r10_1bin_v3_3_MP_h
r10_1bin_v3_3_r1_m