Report

	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# 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)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 10000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 25000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Total length (>= 50000 bp)	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
Total length	24074494	24070200	24072211	24064284	24060998	24055678	24060917	24074257	24070195	24072707	24061315	24060258	24055824	24061249	24075009	24068751	24072195	24065063	24060094	24056380	24061591
Reference length	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205	2689205
GC (%)	44.80	44.80	44.80	44.80	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77
Reference GC (%)	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69	32.69
N50	4045598	4045621	4045594	4045589	4045227	4045309	4043006	4045598	4045629	4045591	4045590	4045220	4045285	4043036	4045598	4045626	4045592	4045592	4045212	4045306	4043032
NG50	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
N75	2845422	2845369	2845428	2845432	2845260	2845328	2843368	2845425	2845372	2845428	2845431	2845275	2845354	2843858	2845425	2845364	2845429	2845427	2845297	2845324	2843845
NG75	4765367	4765335	4765354	4765366	4764519	4764885	4763493	4765367	4765342	4765360	4765365	4764481	4764611	4763481	4765870	4765291	4765346	4765353	4764528	4764900	4763766
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	13	13	13	13	13	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	15
# 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	2719717	2717967	2719596	2719631	2720606	2720621	2718836	2719580	2717932	2719533	2719556	2720595	2720631	2718436	2719746	2717979	2719620	2719614	2720627	2720623	2718867
# local misassemblies	9	9	10	10	10	9	21	9	9	9	9	10	9	20	10	10	10	10	10	10	19
# 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	5	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# 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 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	21274945	21272394	21273393	21264885	21262974	21256165	21321354	21274720	21273304	21273244	21261562	21263785	21255162	21320856	21275235	21270684	21273194	21265762	21262104	21257623	21320346
Genome fraction (%)	99.537	99.537	99.537	99.537	99.537	99.537	99.535	99.537	99.537	99.537	99.537	99.537	99.537	99.538	99.537	99.537	99.537	99.537	99.537	99.537	99.542
Duplication ratio	1.046	1.045	1.046	1.046	1.045	1.046	1.023	1.046	1.045	1.046	1.046	1.045	1.046	1.024	1.046	1.045	1.046	1.046	1.045	1.046	1.024
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	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	287.74	257.29	286.80	289.57	290.69	298.09	251.80	286.65	252.21	292.71	292.33	287.03	304.32	247.09	288.26	257.25	287.29	288.67	289.31	291.81	255.33
# indels per 100 kbp	112.04	42.40	75.43	77.78	114.28	115.81	165.05	110.58	42.93	74.75	75.84	110.28	113.27	158.70	112.30	42.55	76.25	77.07	113.94	114.02	166.05
Largest alignment	948765	948104	948808	948817	949190	949066	948394	948668	948052	948657	948645	949192	949045	948372	948892	948228	948809	948796	949173	949147	948394
Total aligned length	2797636	2795887	2796896	2797478	2796102	2797591	2737632	2797615	2794963	2797543	2797833	2794544	2798741	2738478	2797861	2796148	2797081	2797380	2796070	2796835	2739322
NGA50	480550	480253	480493	480514	480637	480649	480377	480526	480259	480492	480509	480707	480718	480392	480550	480258	480504	480492	480649	480632	480377
NGA75	381443	381233	381432	381430	381568	381577	381322	381461	381225	381425	381442	381538	381590	381299	381471	381234	381435	381447	381577	381623	381350
LGA50	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
LGA75	4	4	4	4	4	4	4	4	4	4	4	4	4	4	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

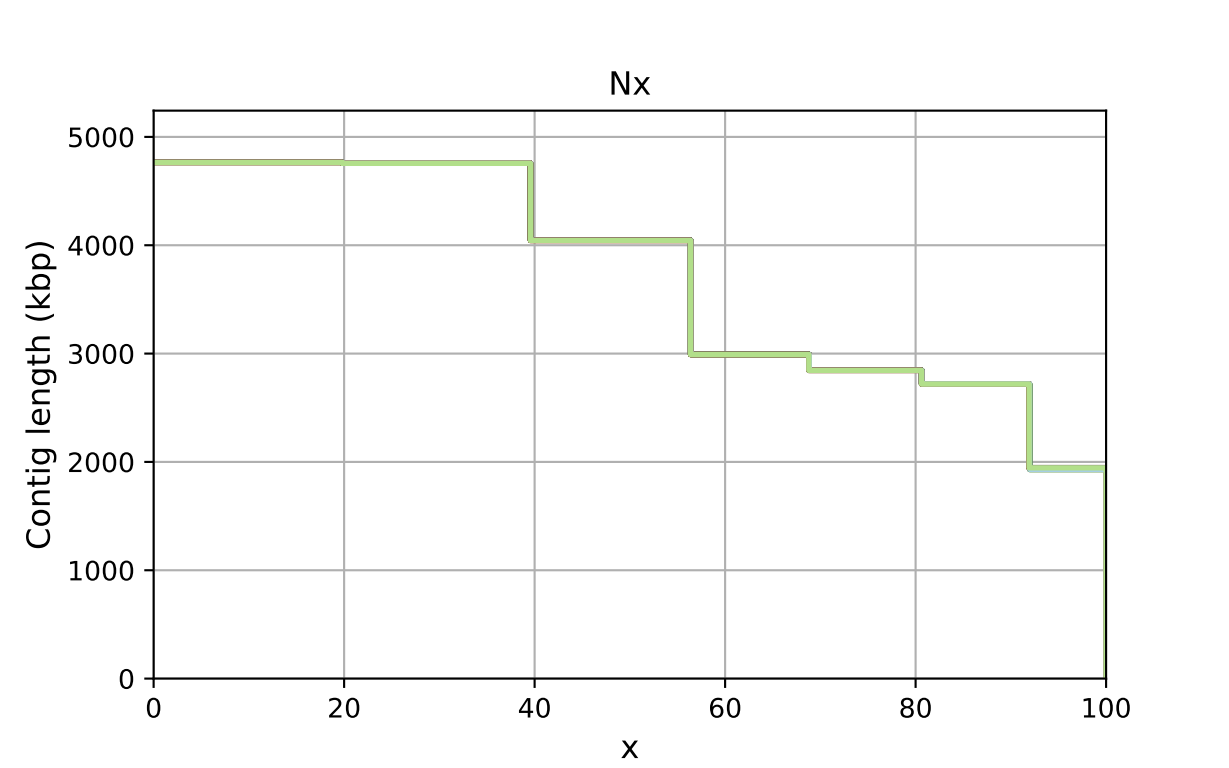
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_3_raw
# misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	15
# contig misassemblies	13	13	13	13	13	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	15
# 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	13	13	13	13	13	13	14	13	13	13	13	13	13	13	13	13	13	13	13	13	15
# 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	2719717	2717967	2719596	2719631	2720606	2720621	2718836	2719580	2717932	2719533	2719556	2720595	2720631	2718436	2719746	2717979	2719620	2719614	2720627	2720623	2718867
# 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	10	10	10	10	10	10	18	10	10	10	10	10	10	16	10	10	10	10	10	10	20
# local misassemblies	9	9	10	10	10	9	21	9	9	9	9	10	9	20	10	10	10	10	10	10	19
# 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	26	26	26	26	26	26	21	26	26	26	26	26	26	25	26	26	26	26	26	26	22
# unaligned mis. contigs	6	6	6	6	6	6	5	6	6	6	6	6	6	5	6	6	6	6	6	6	4
# mismatches	7702	6887	7677	7751	7781	7979	6740	7673	6751	7835	7825	7683	8146	6614	7716	6886	7690	7727	7744	7811	6835
# indels	2999	1135	2019	2082	3059	3100	4418	2960	1149	2001	2030	2952	3032	4248	3006	1139	2041	2063	3050	3052	4445
# indels (<= 5 bp)	2928	1069	1968	2031	3004	3047	4361	2886	1084	1950	1979	2897	2980	4187	2938	1076	1990	2012	2996	3000	4390
# indels (> 5 bp)	71	66	51	51	55	53	57	74	65	51	51	55	52	61	68	63	51	51	54	52	55
Indels length	6908	4925	5356	5426	6824	6843	8505	6922	4937	5336	5367	6744	6762	8365	6889	4913	5369	5389	6821	6739	8527

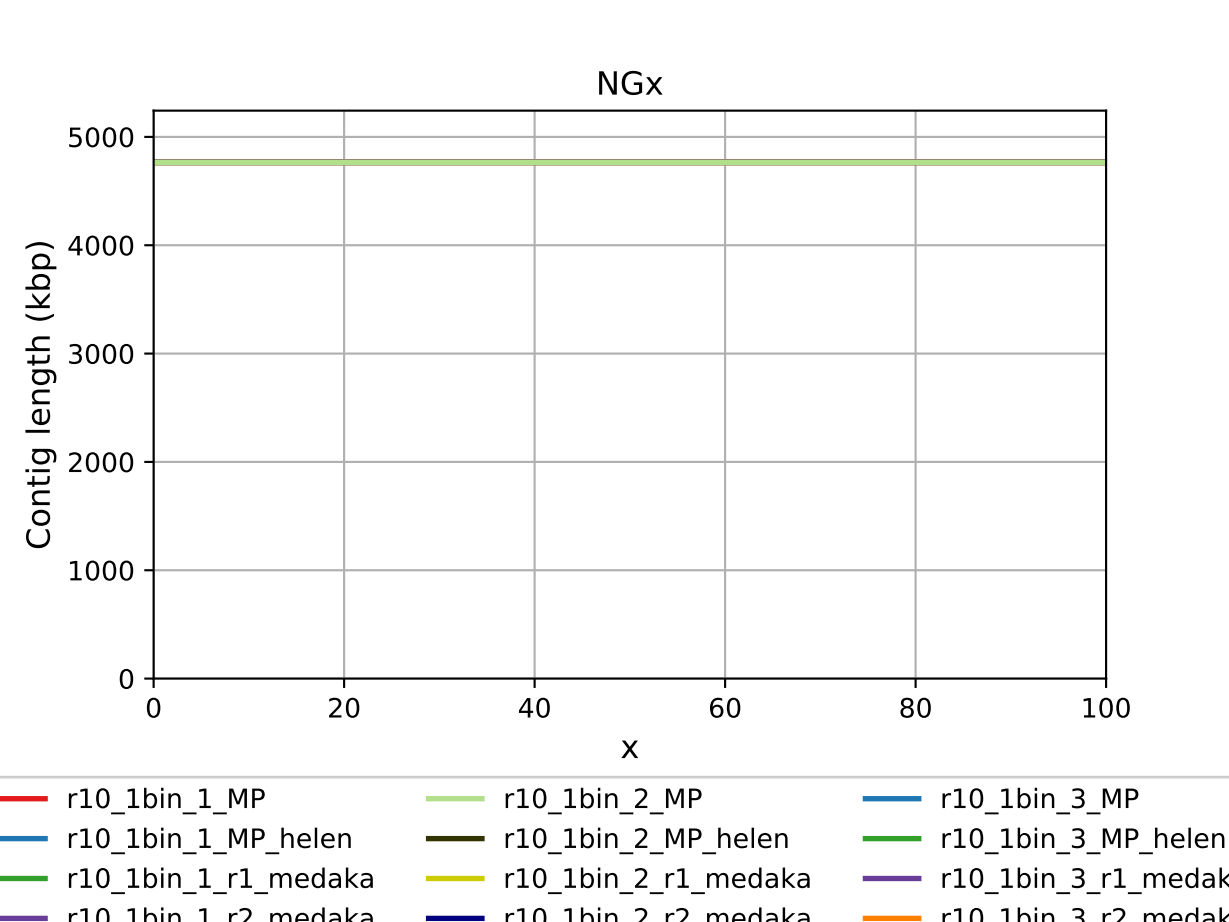
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

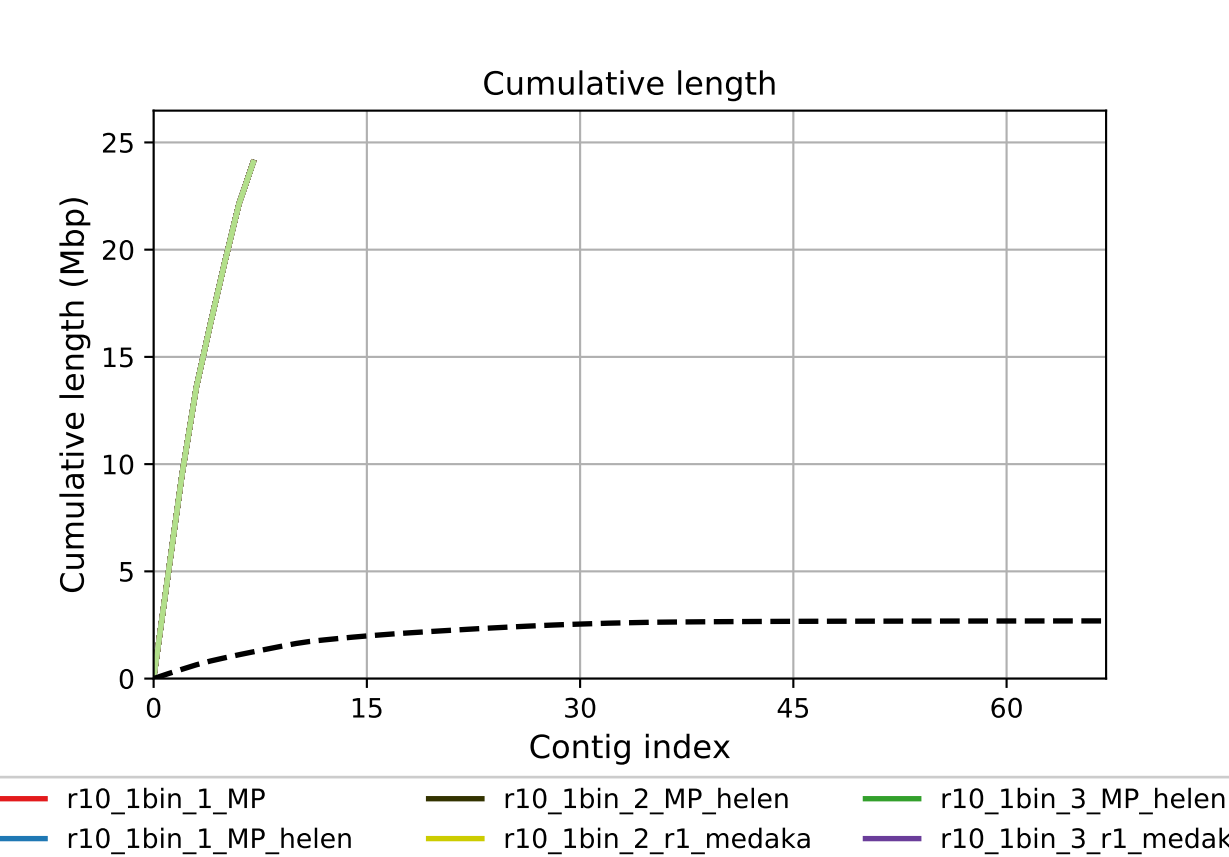
Unaligned report

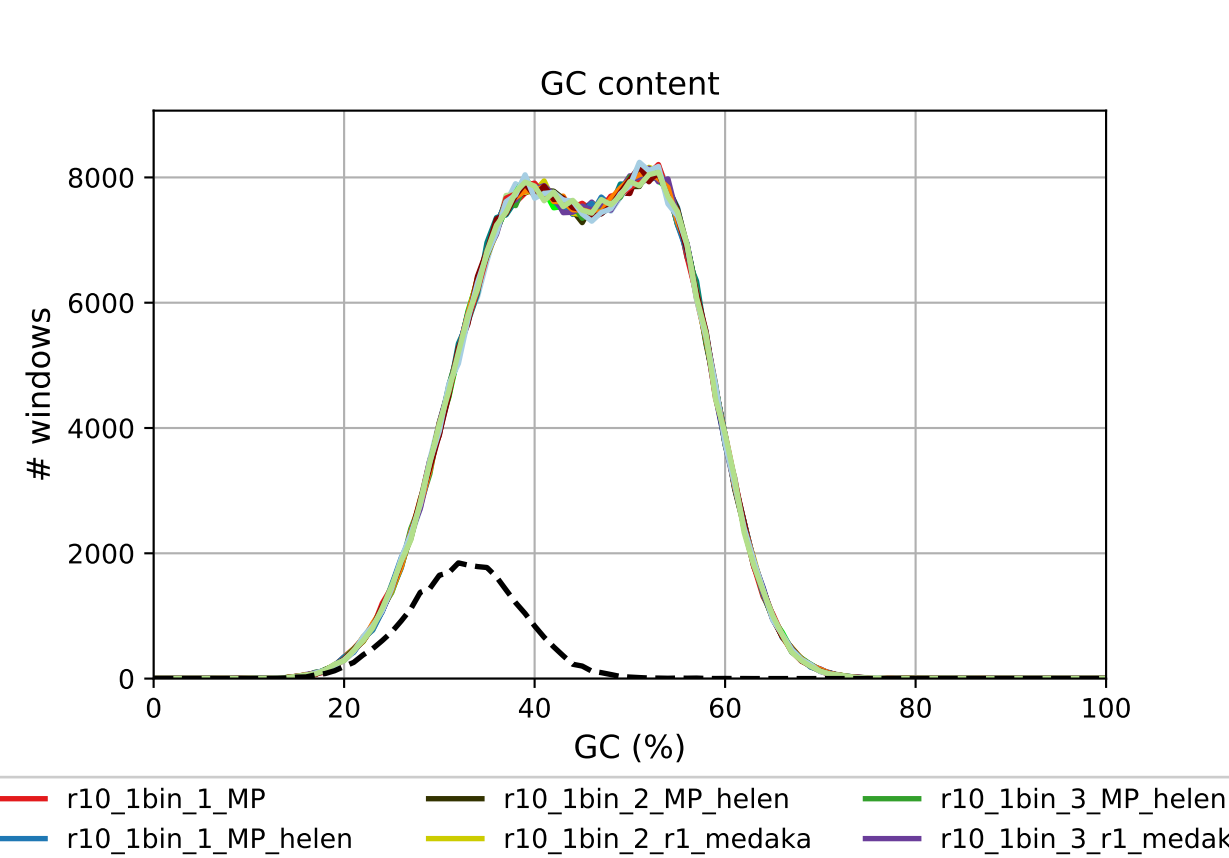
	r10_1bin_1_MP	r10_1bin_1_MP_helen	r10_1bin_1_r1_medaka	r10_1bin_1_r2_medaka	r10_1bin_1_racon_r1	r10_1bin_1_racon_r2	r10_1bin_1_raw	r10_1bin_2_MP	r10_1bin_2_MP_helen	r10_1bin_2_r1_medaka	r10_1bin_2_r2_medaka	r10_1bin_2_racon_r1	r10_1bin_2_racon_r2	r10_1bin_2_raw	r10_1bin_3_MP	r10_1bin_3_MP_helen	r10_1bin_3_r1_medaka	r10_1bin_3_r2_medaka	r10_1bin_3_racon_r1	r10_1bin_3_racon_r2	r10_1bin_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	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Partially unaligned length	21274945	21272394	21273393	21264885	21262974	21256165	21321354	21274720	21273304	21273244	21261562	21263785	21255162	21320856	21275235	21270684	21273194	21265762	21262104	21257623	21320346
# N's	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0

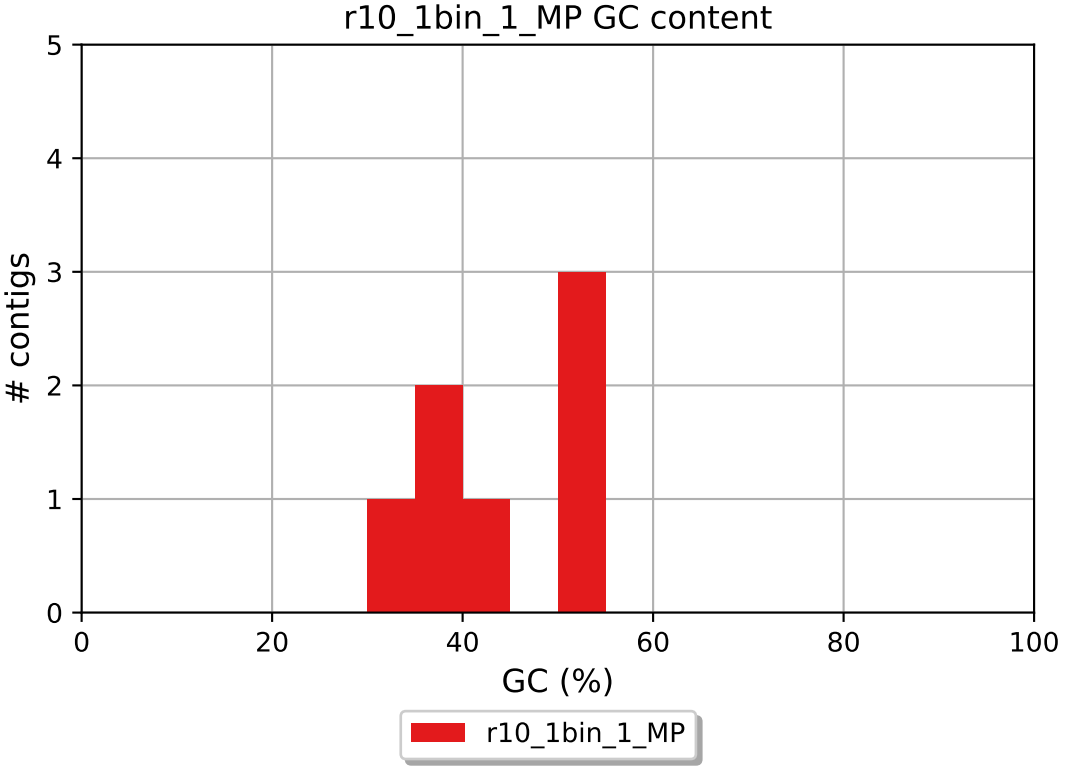
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

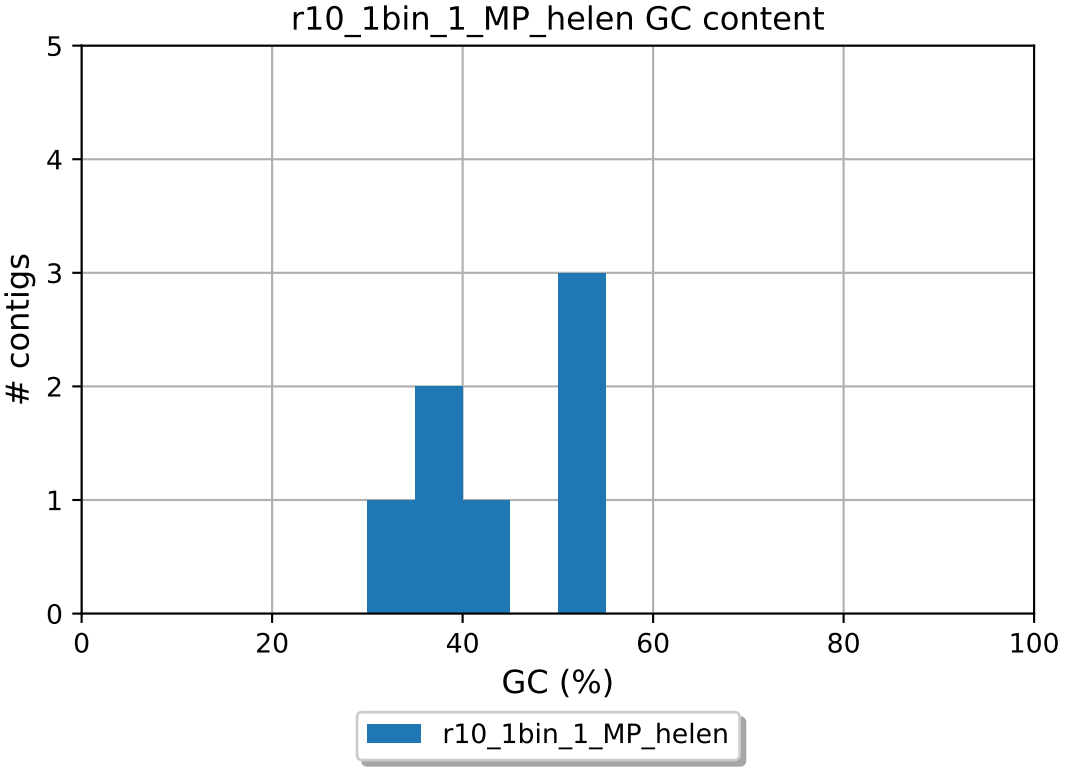

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak

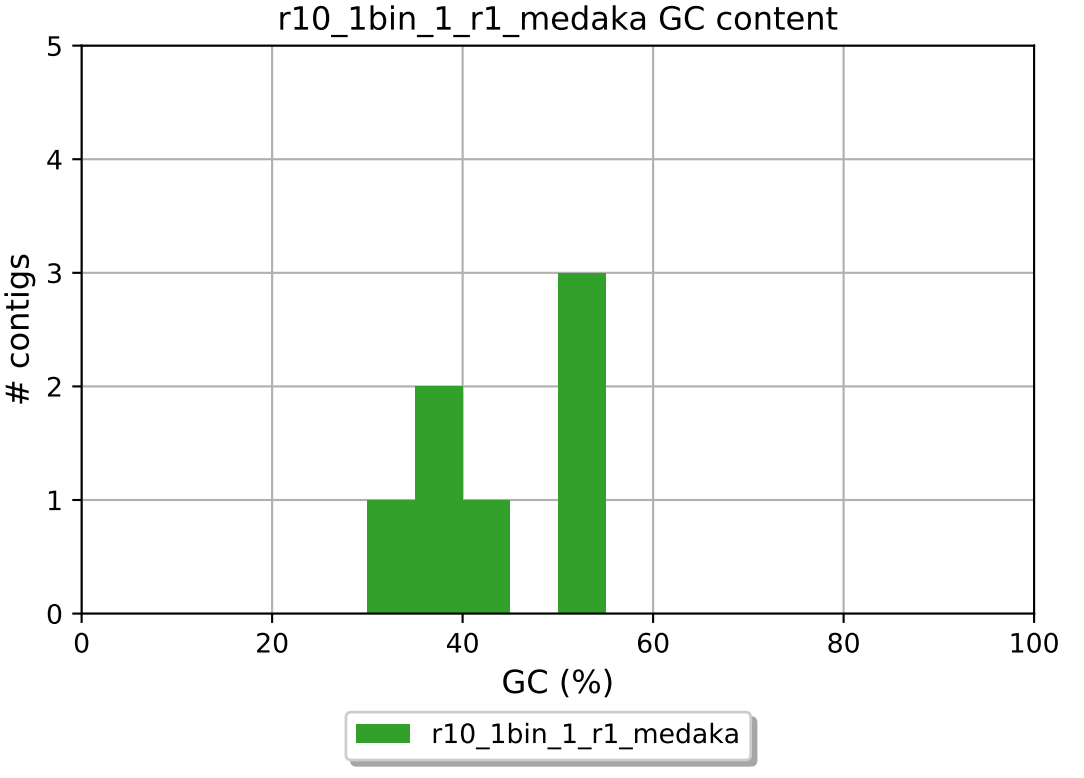

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak

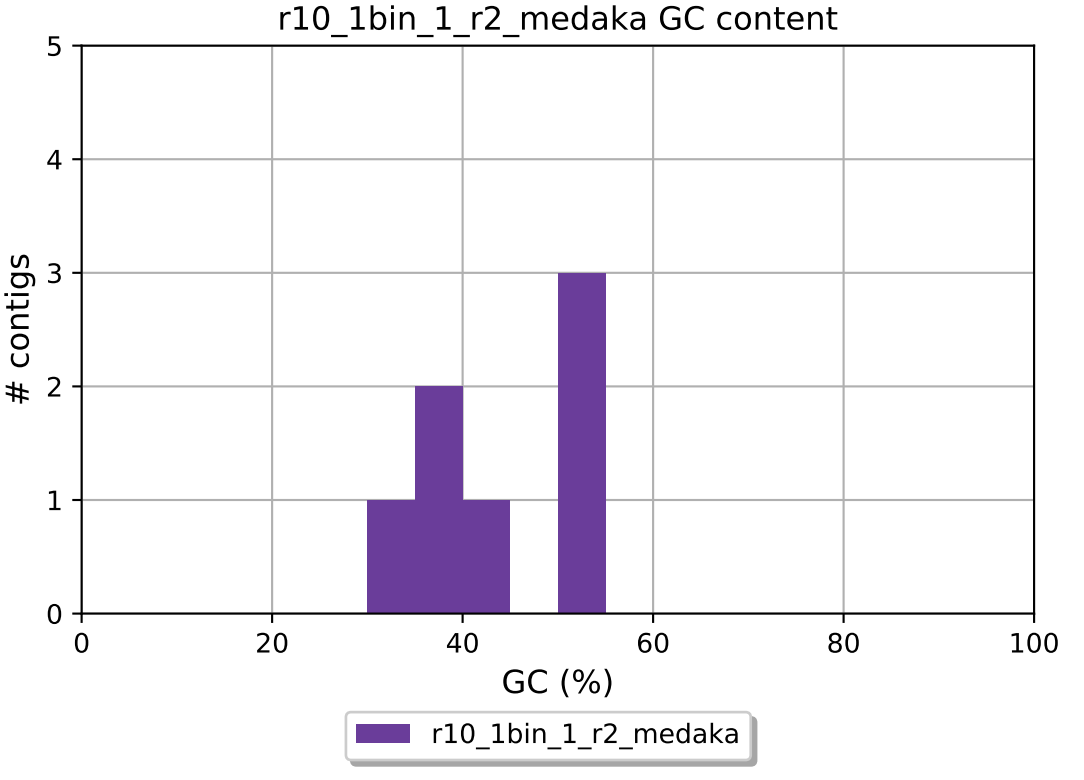

Cumulative length
Cumulative length (Mbp)
0
5
10
15
20
25
0
15
30
45
60
Contig index
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak
r10_1bin_3_r2_medak

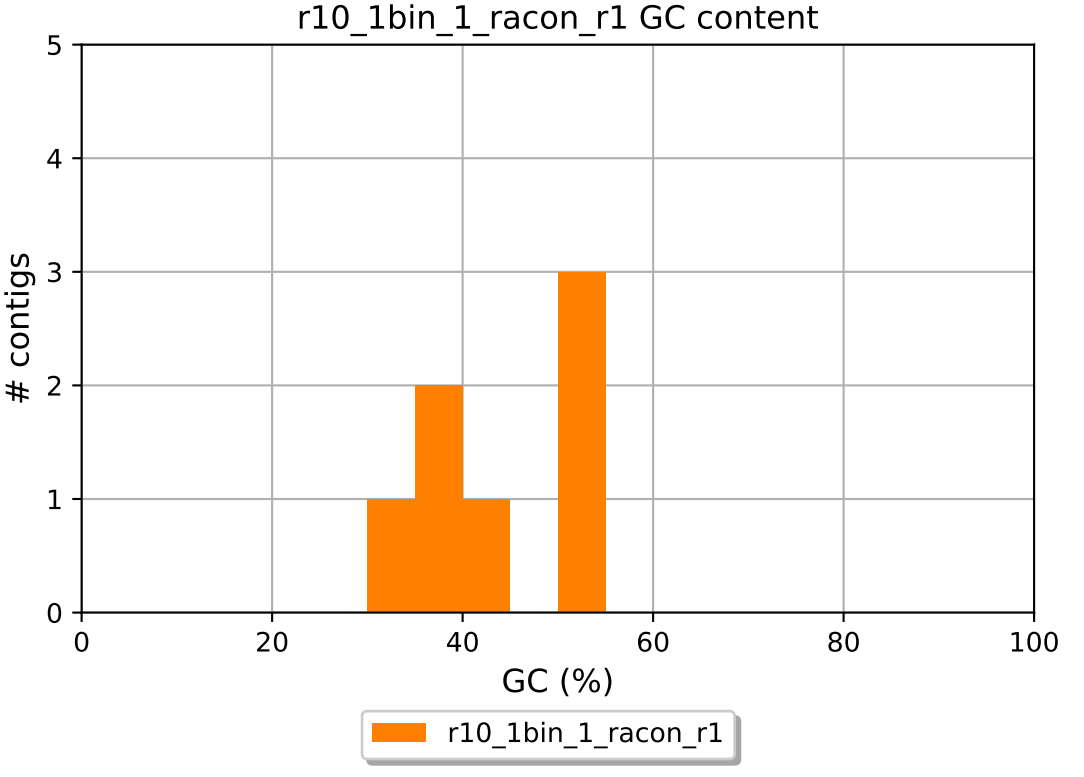

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak
r10_1bin_3_r2_medak

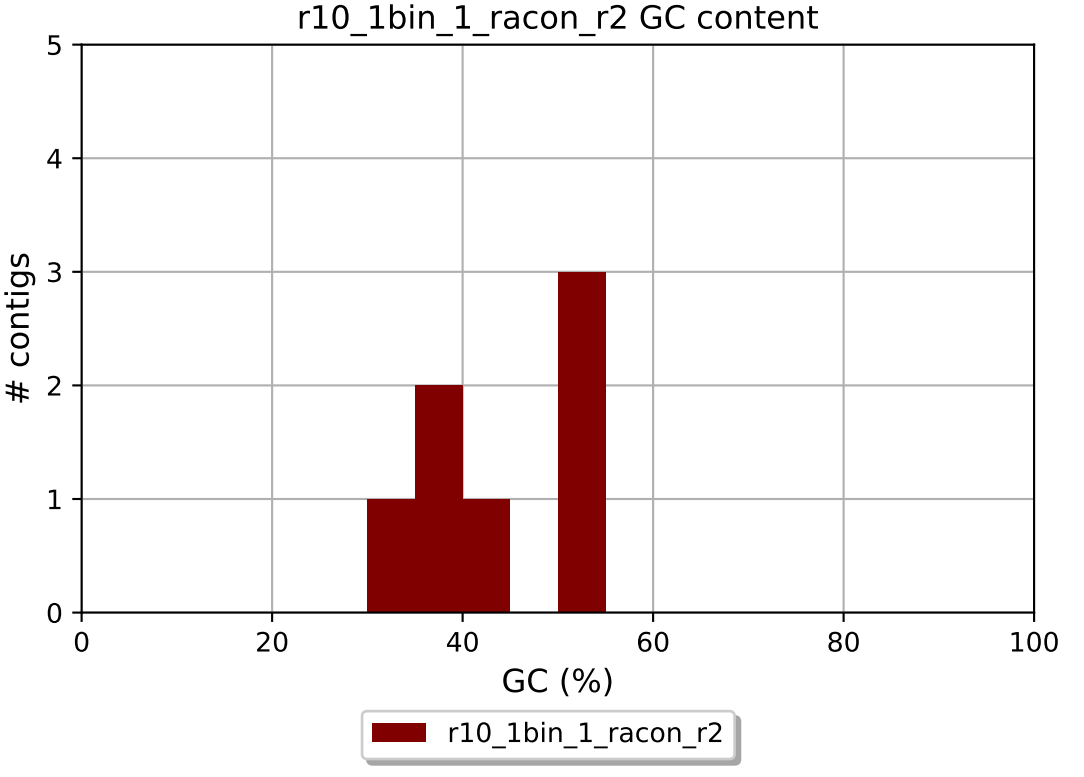

r10_1bin_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_MP

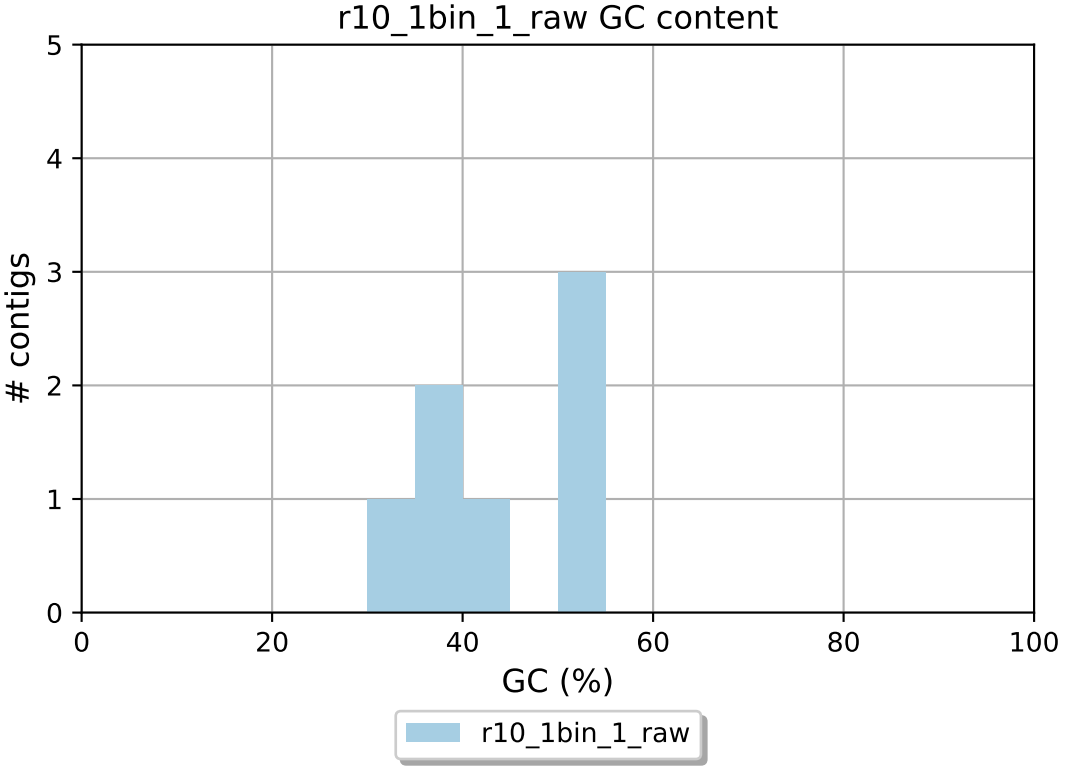

r10_1bin_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_MP_helen

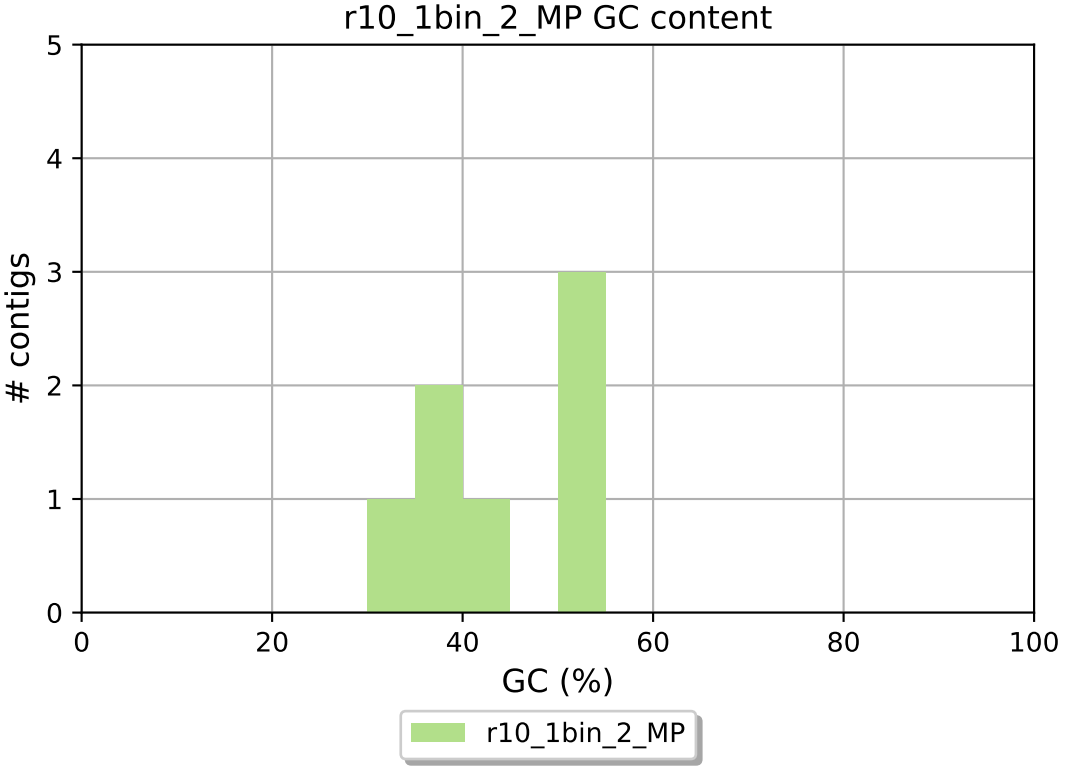

r10_1bin_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_r1_medaka

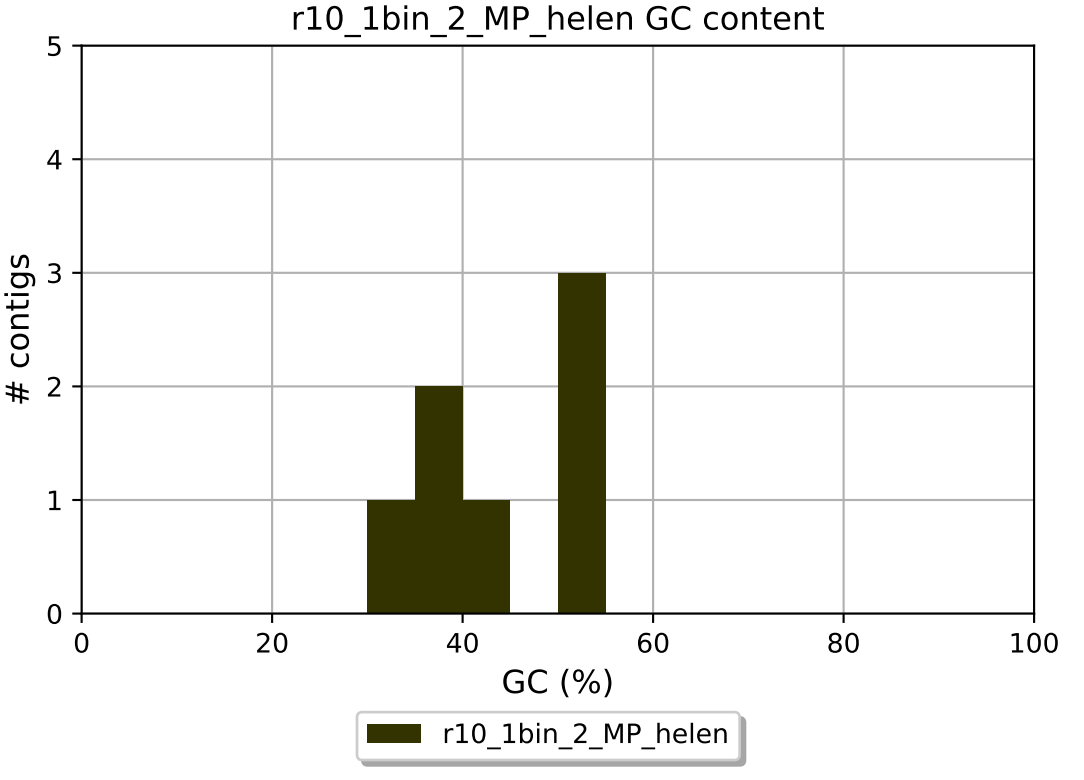

r10_1bin_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_r2_medaka

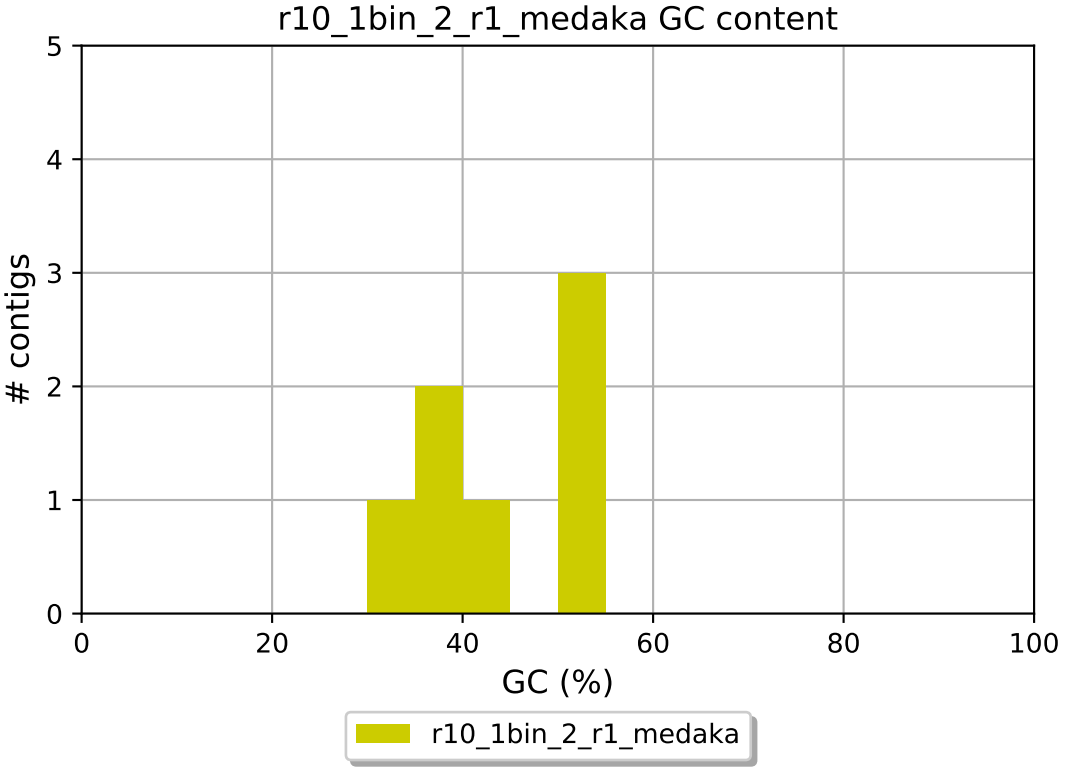

r10_1bin_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_racon_r1

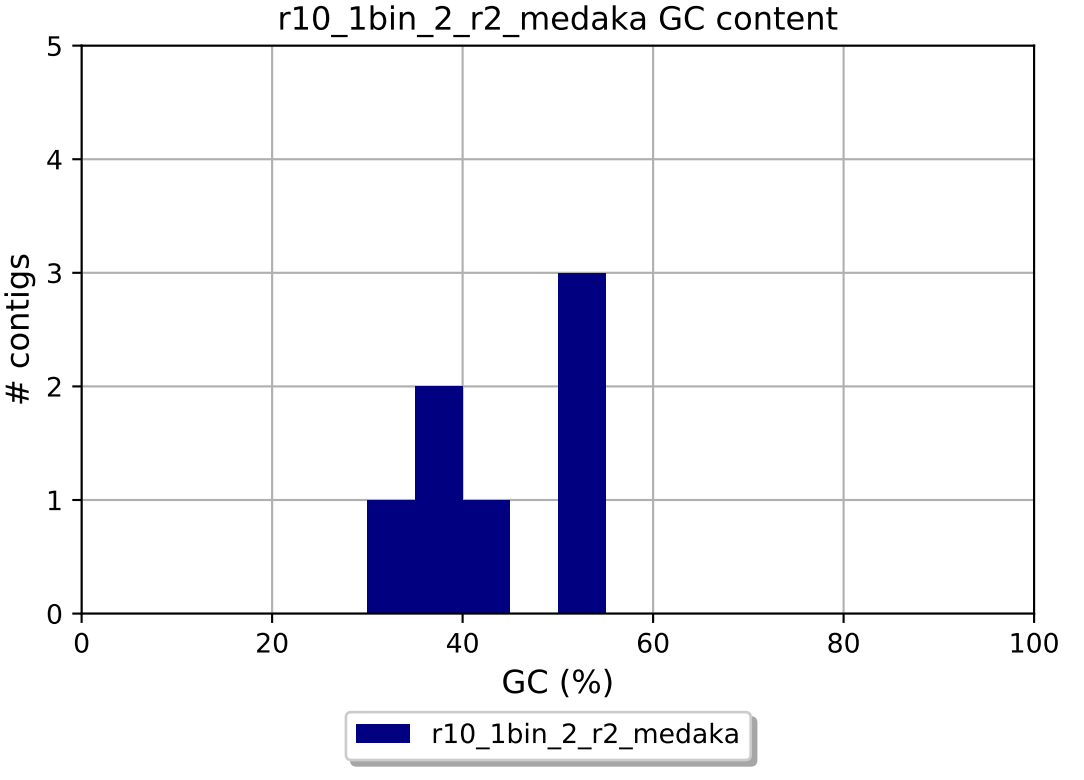

r10_1bin_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_racon_r2

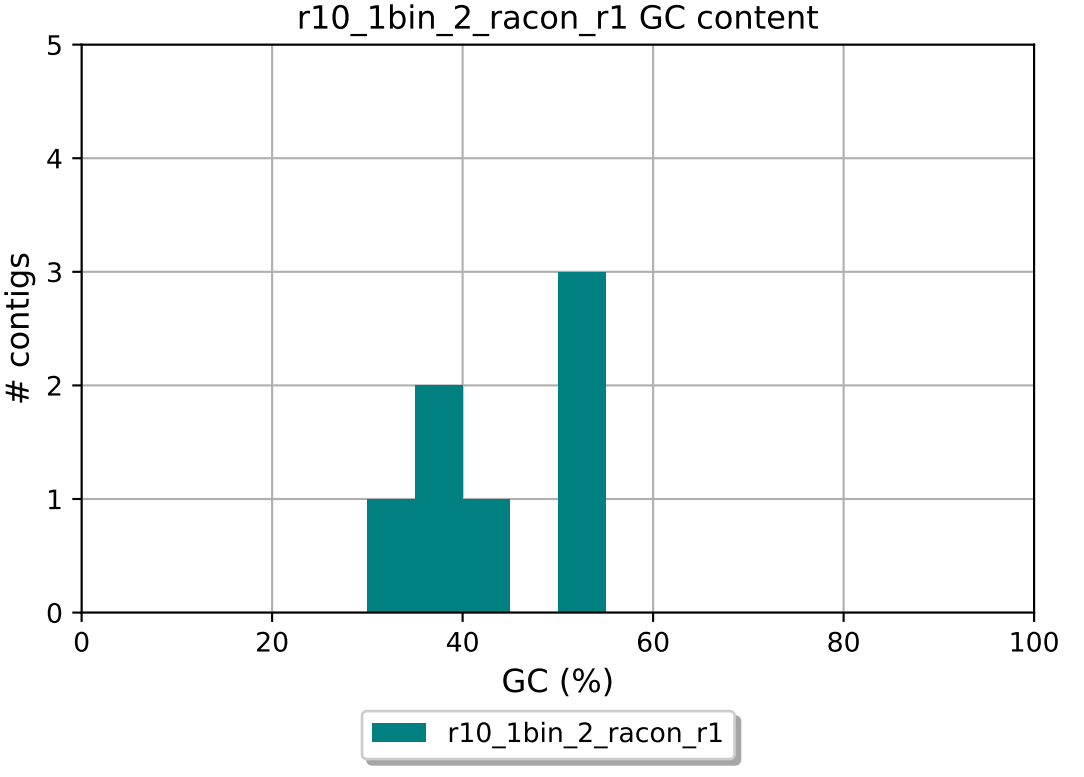

r10_1bin_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_1_raw

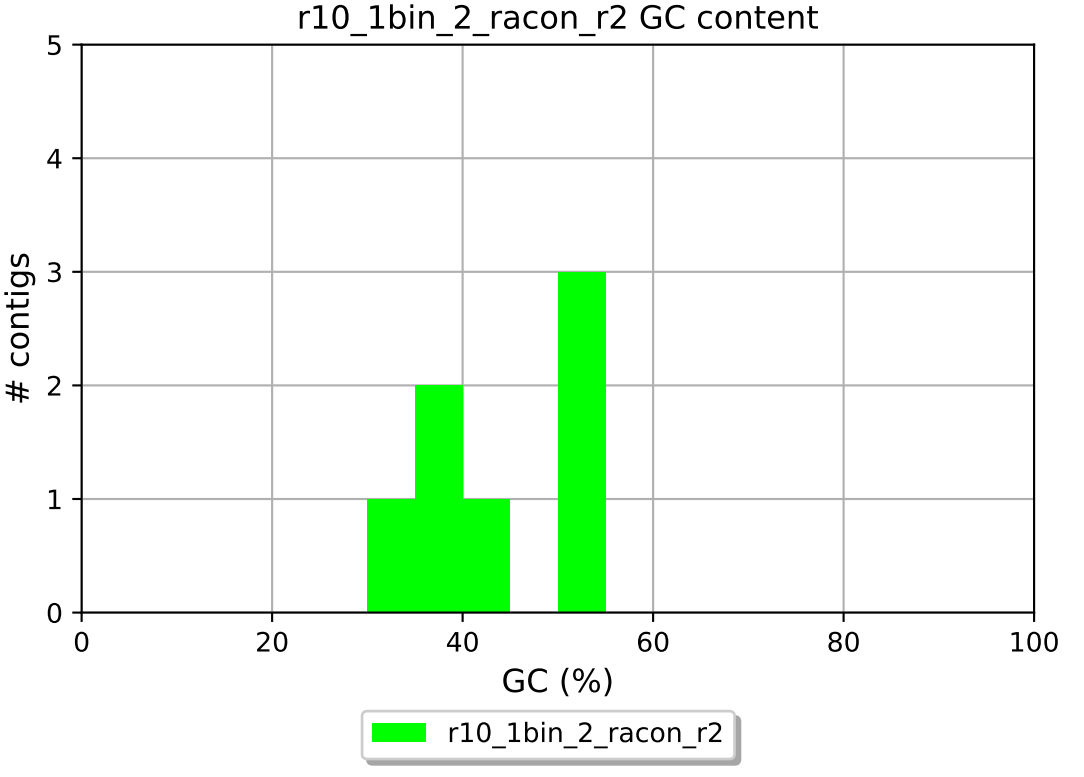

r10_1bin_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_MP

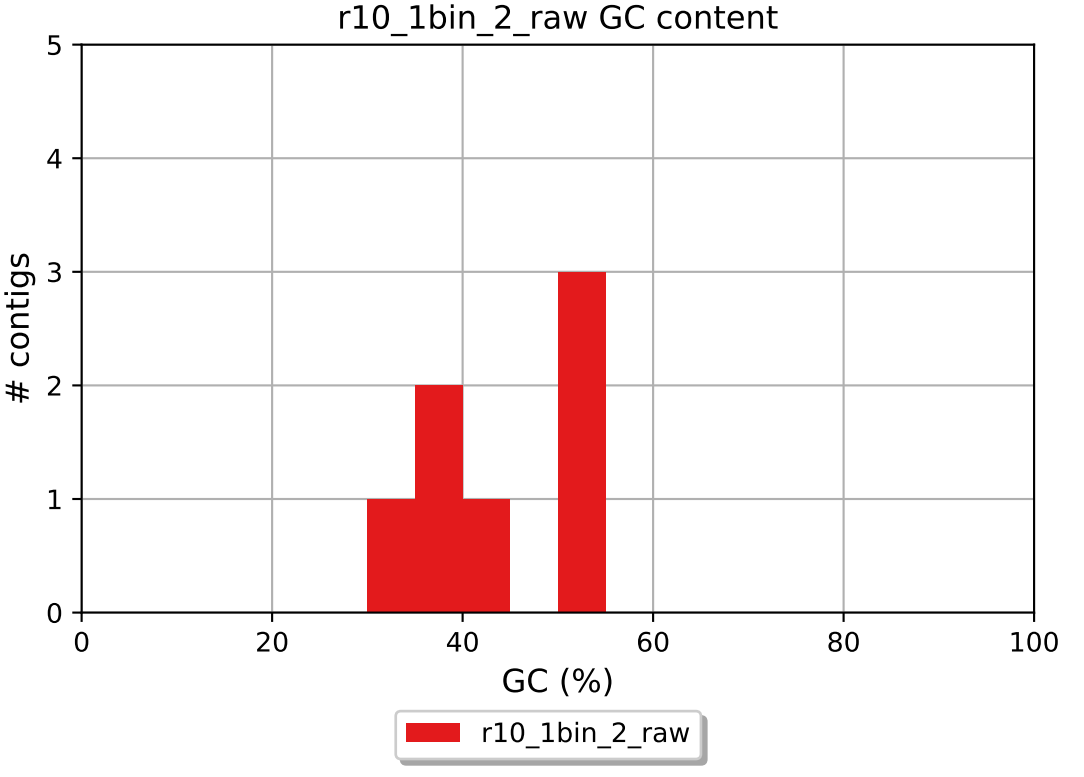

r10_1bin_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_MP_helen

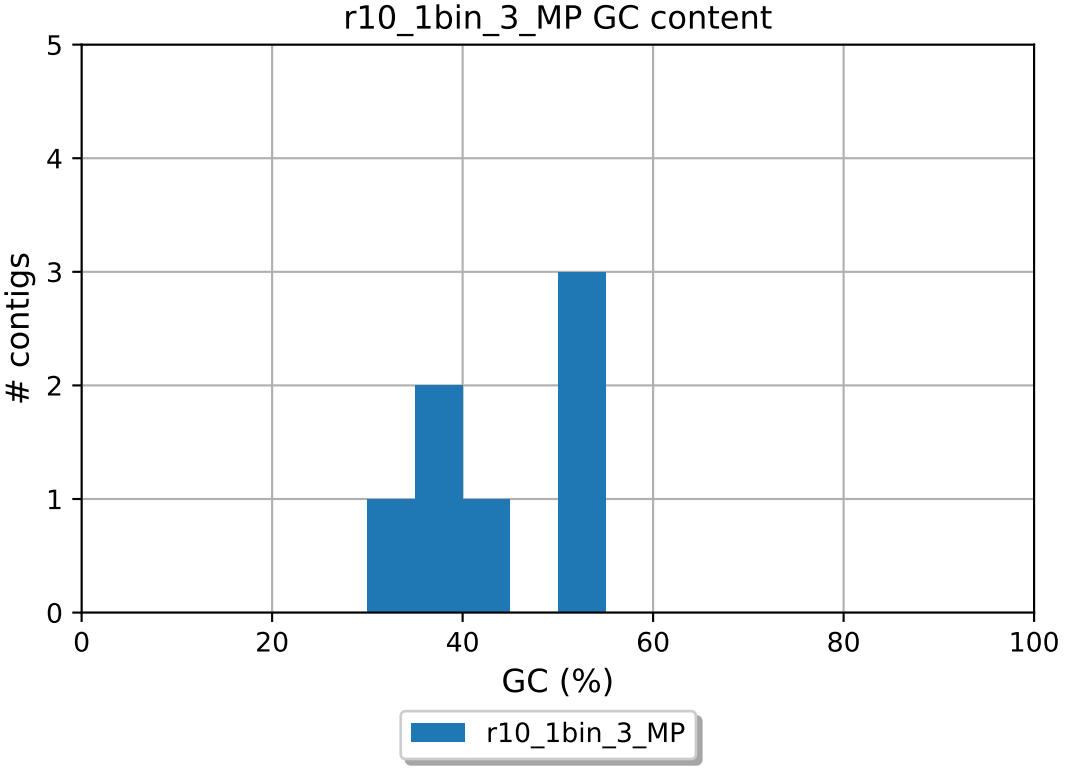

r10_1bin_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_r1_medaka

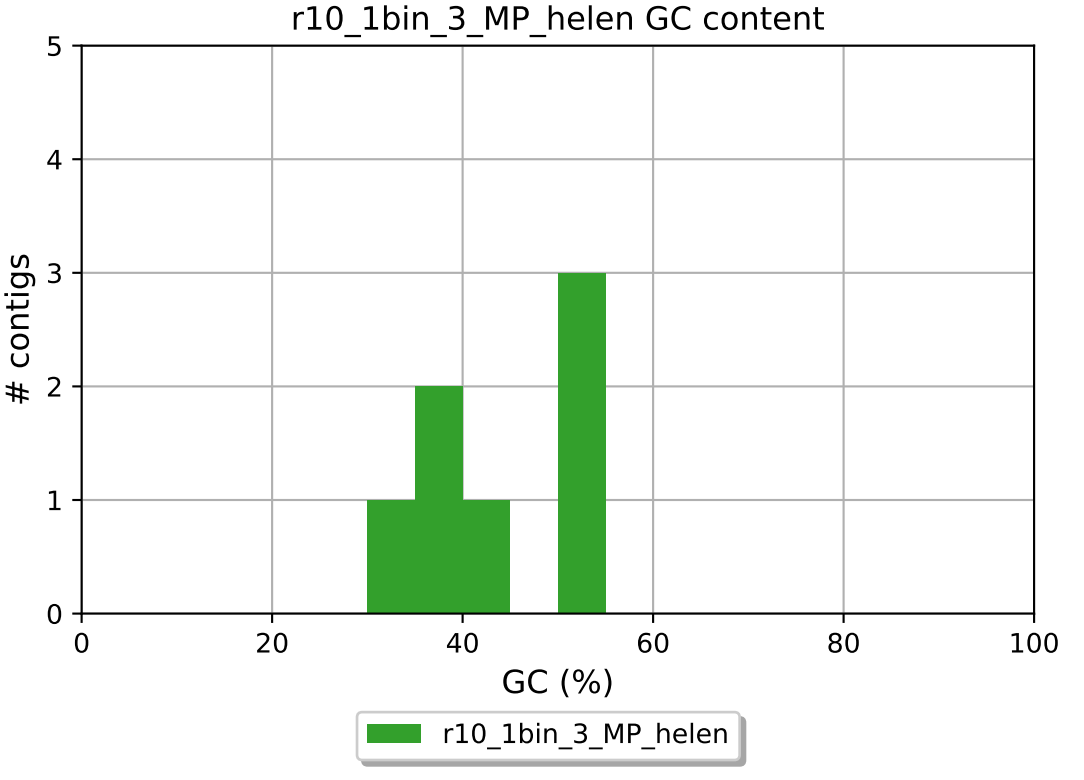

r10_1bin_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_r2_medaka

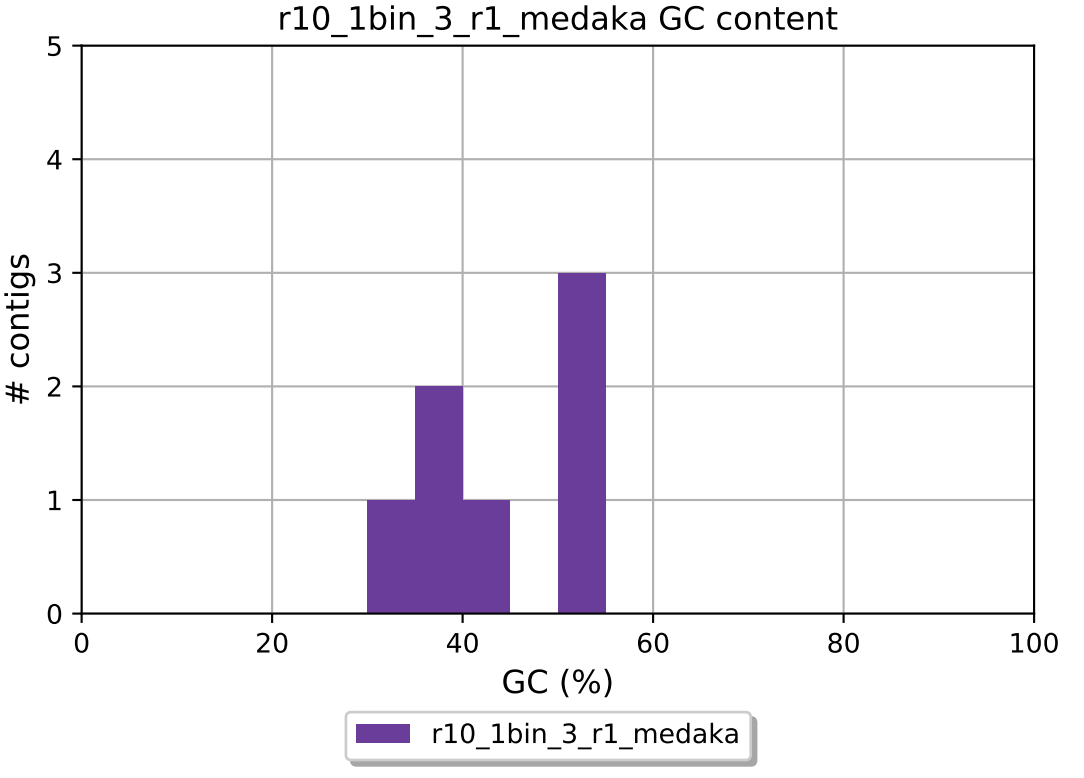

r10_1bin_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_racon_r1

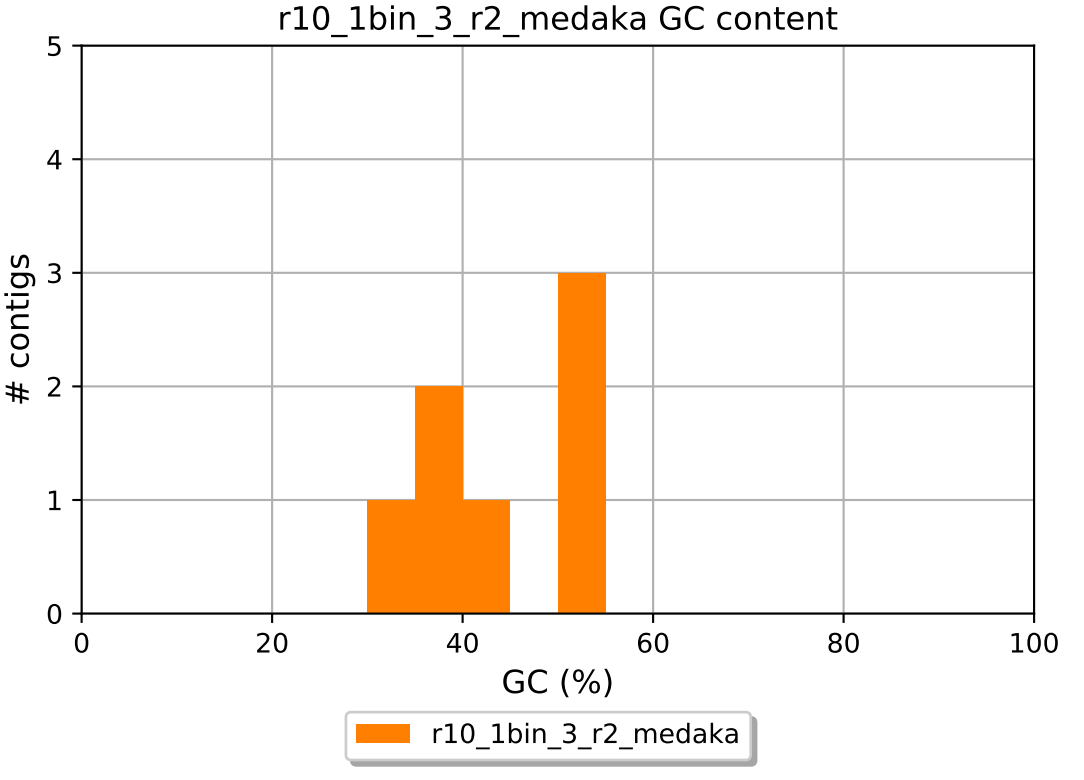

r10_1bin_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_racon_r2

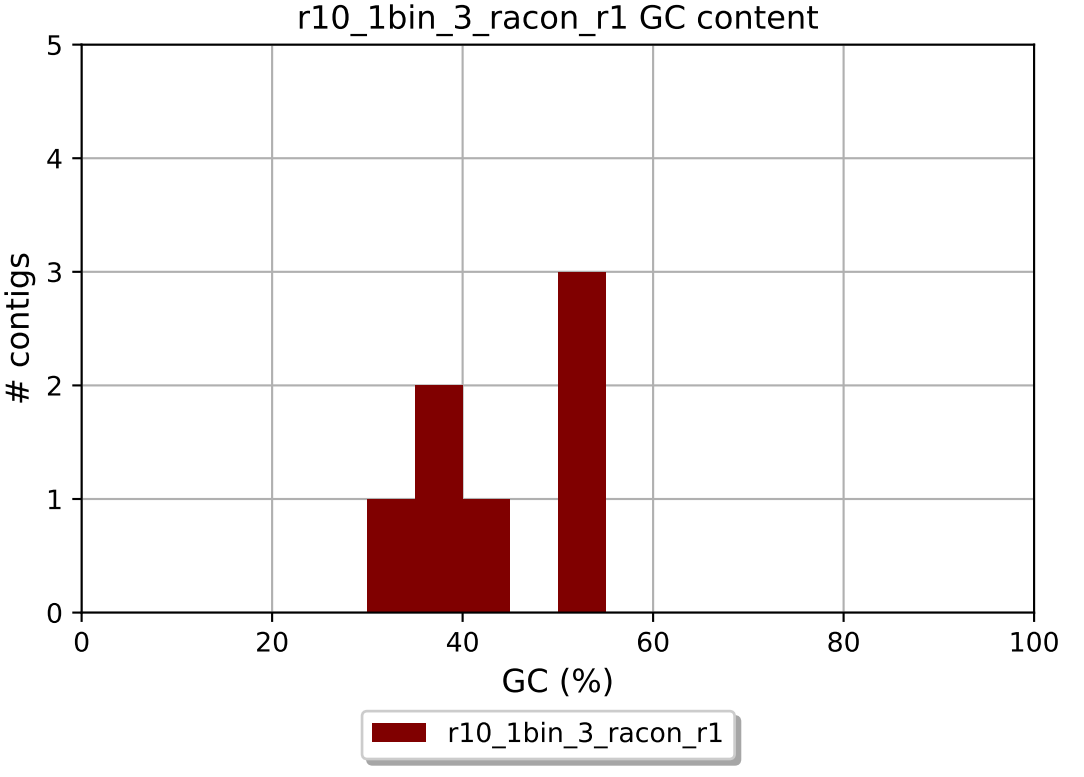

r10_1bin_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_2_raw

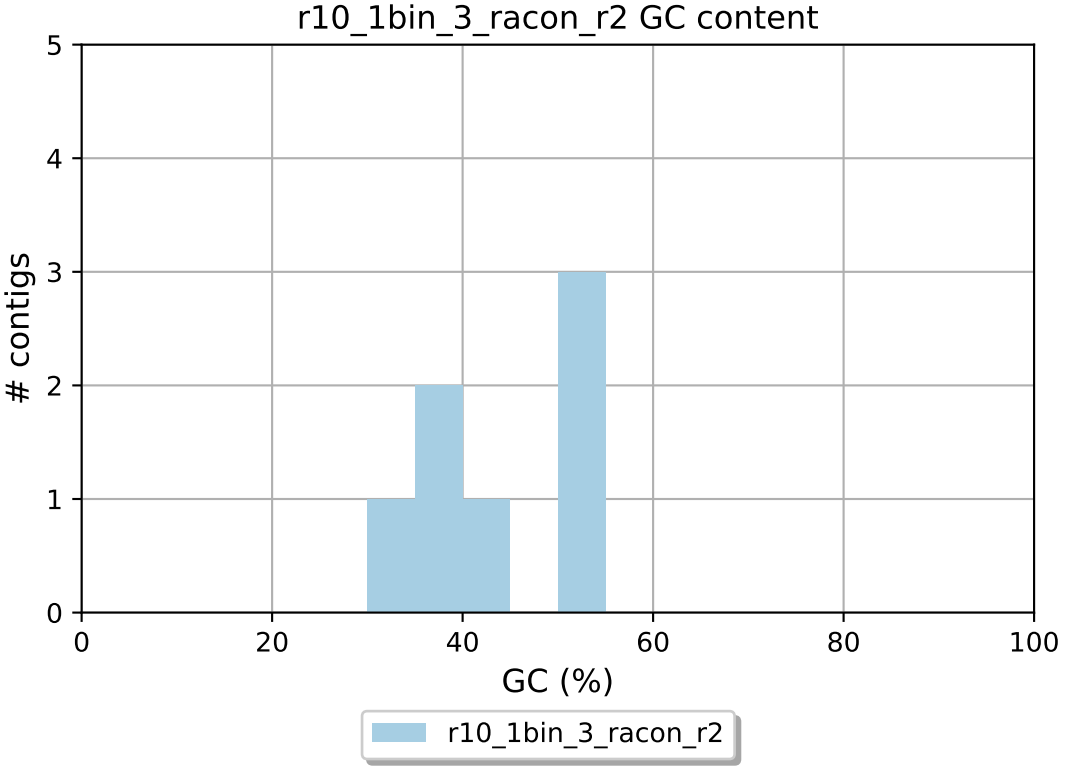

r10_1bin_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_MP

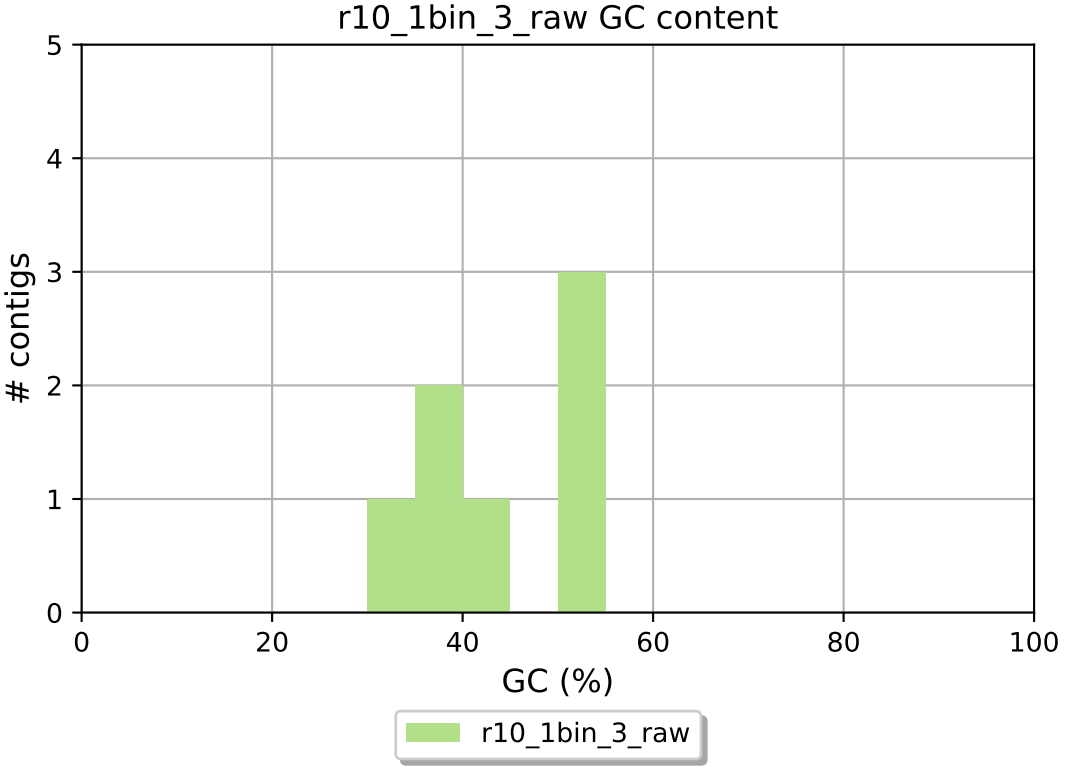

r10_1bin_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_MP_helen

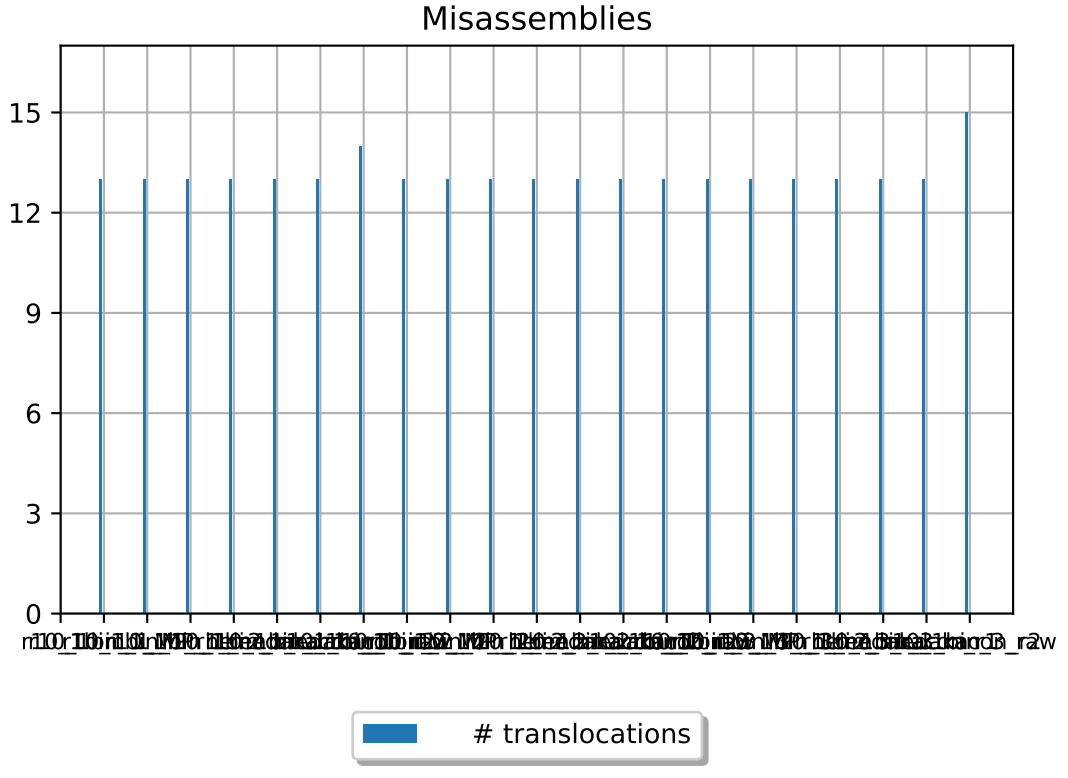

r10_1bin_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_r1_medaka

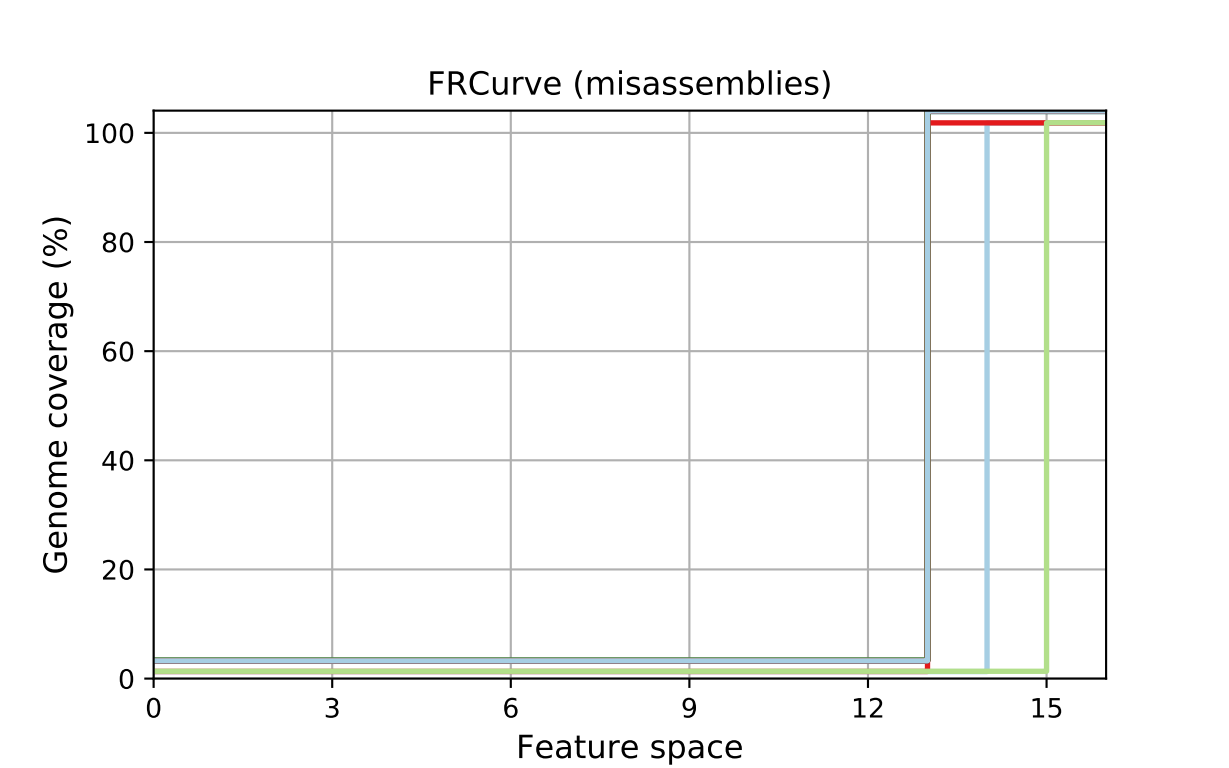

r10_1bin_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_r2_medaka

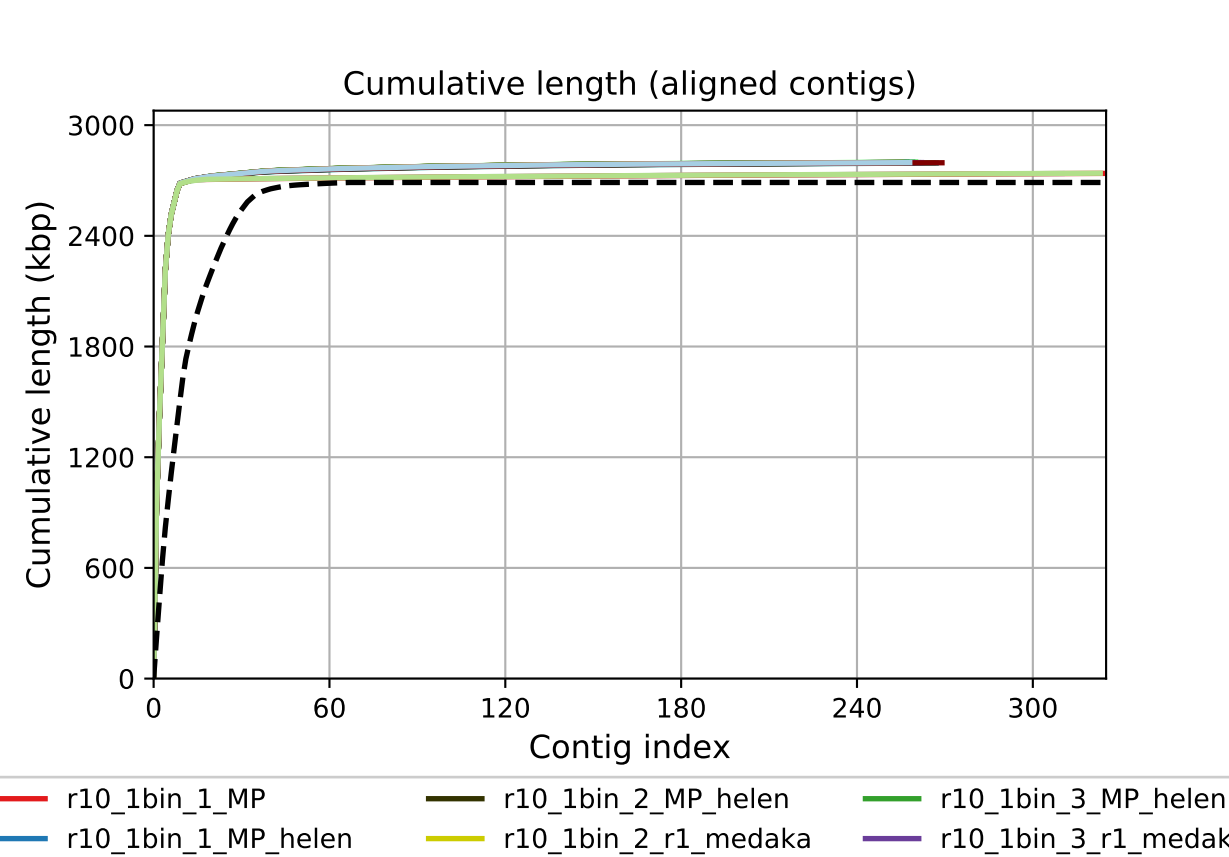

r10_1bin_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_racon_r1

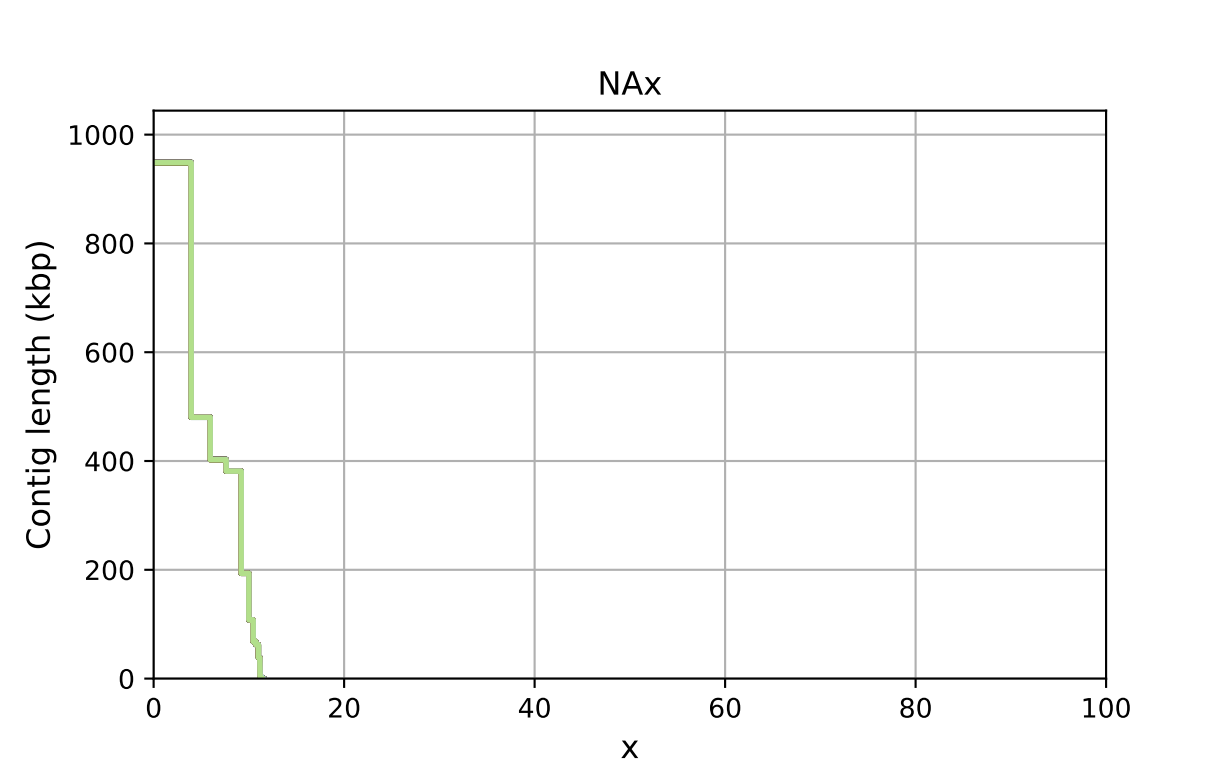

r10_1bin_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_racon_r2

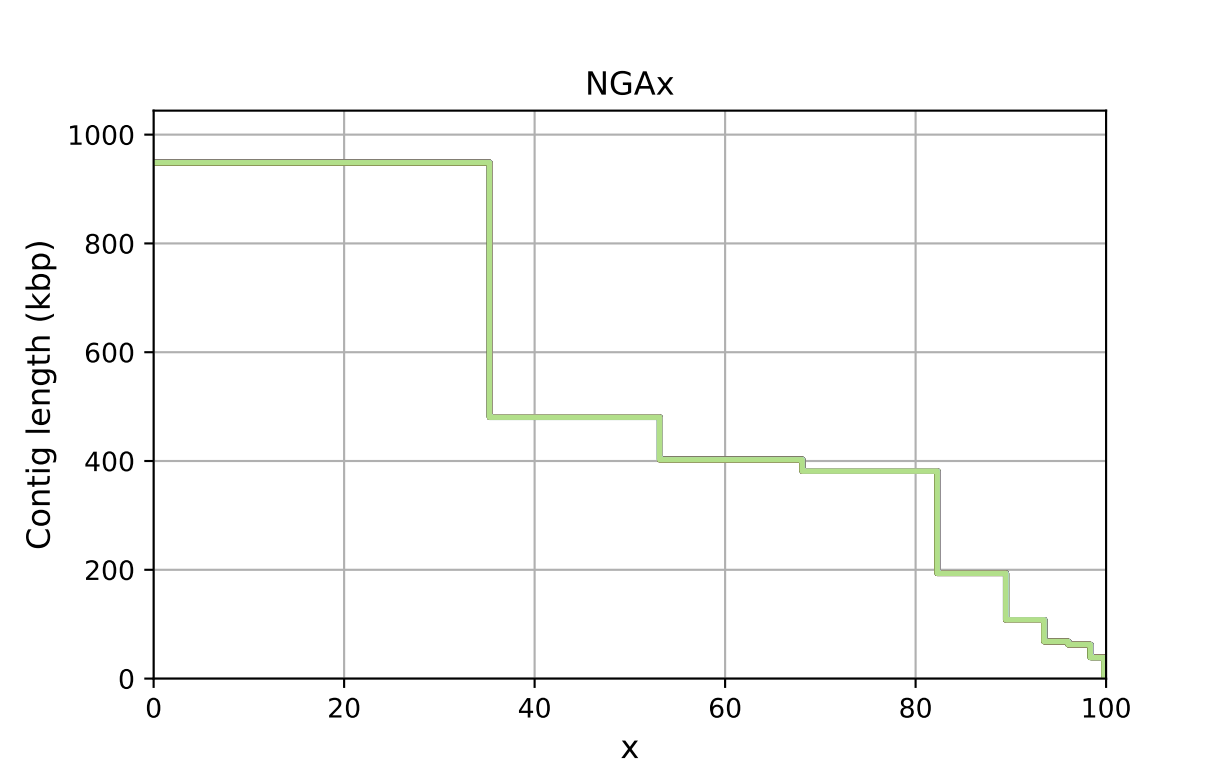

r10_1bin_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_3_raw

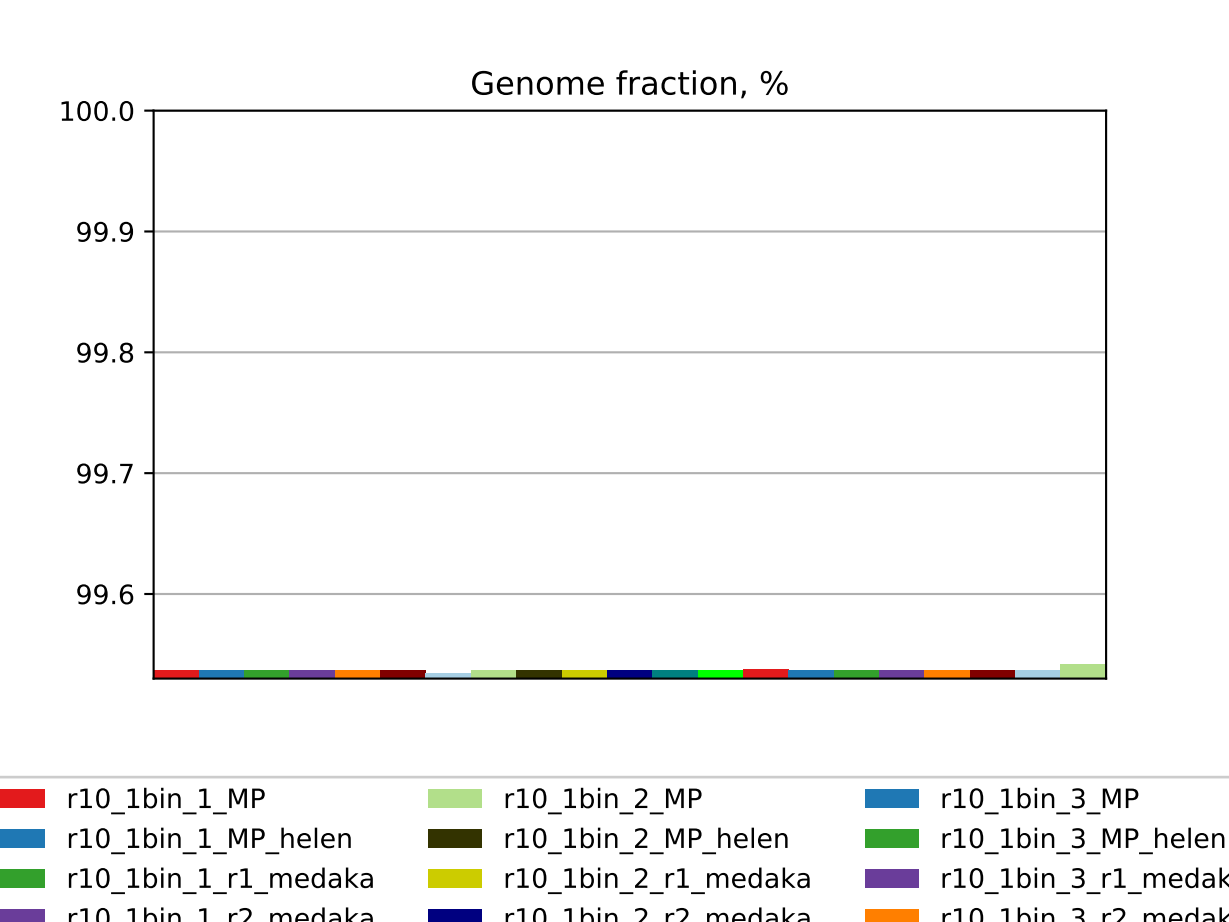

Misassemblies
15
12
9
6
3
0
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
60
120
180
240
300
Contig index
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_2_r2_medaka
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak
r10_1bin_3_r2_medak


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak


Genome fraction, %
100.0
99.9
99.8
99.7
99.6
r10_1bin_1_MP
r10_1bin_1_MP_helen
r10_1bin_1_r1_medaka
r10_1bin_2_MP
r10_1bin_2_MP_helen
r10_1bin_2_r1_medaka
r10_1bin_3_MP
r10_1bin_3_MP_helen
r10_1bin_3_r1_medak