Report

	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# contigs (>= 5000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Total length (>= 5000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	28131261	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	28131080
Total length (>= 10000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	28131261	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	28131080
Total length (>= 25000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	28131261	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	28131080
Total length (>= 50000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	28131261	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	28131080
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	8	7	7	7	7	7	7	7
Largest contig	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	6788581
Total length	24074239	24070847	24075790	24065267	24060416	24054361	28131261	24074830	24070579	24075879	24065198	24060552	24053082	30850012	24074372	24070528	24075072	24062757	24061106	24053558	28131080
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
GC (%)	44.80	44.80	44.80	44.79	44.79	44.78	51.10	44.80	44.80	44.80	44.79	44.79	44.78	49.48	44.80	44.80	44.80	44.79	44.78	44.78	51.10
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45
N50	4045594	4045614	4045830	4045830	4045233	4045289	4755996	4045599	4045618	4045837	4045836	4045198	4045283	4755926	4045594	4045616	4045840	4045837	4045212	4045325	4756050
NG50	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	6788581
N75	2845424	2845373	2845569	2845565	2845263	2845303	2990670	2845424	2845368	2845573	2845566	2845303	2845324	2990627	2845425	2845368	2845568	2845560	2845287	2845313	2990634
NG75	4765380	4765358	4765659	4765647	4764472	4764668	6788614	4765857	4765290	4765665	4765638	4764540	4764597	6788581	4765360	4765338	4765695	4765649	4764493	4764872	6788581
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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# 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	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
# local misassemblies	36	36	36	37	36	37	58	37	36	37	37	37	36	55	36	36	37	37	36	38	61
# 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	6	6	6
# 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 + 8 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	19038707	19035805	19038701	19030255	19024960	19016740	23182737	19039665	19035014	19037635	19027690	19022491	19014448	25890284	19038572	19035353	19038620	19025354	19029919	19012658	23187093
Genome fraction (%)	97.703	97.703	97.703	97.701	97.703	97.701	97.668	97.703	97.703	97.701	97.701	97.701	97.703	97.666	97.703	97.703	97.701	97.701	97.703	97.701	97.644
Duplication ratio	1.077	1.077	1.077	1.077	1.077	1.077	1.059	1.077	1.077	1.077	1.077	1.077	1.077	1.061	1.077	1.077	1.077	1.077	1.076	1.078	1.058
# N's per 100 kbp	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	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	443.32	439.21	445.48	441.57	444.77	450.96	486.97	442.59	440.26	448.37	446.88	451.78	454.05	497.89	444.05	439.53	443.71	445.87	435.24	456.54	481.85
# indels per 100 kbp	20.40	17.92	21.08	20.85	39.94	36.37	239.35	20.40	18.05	21.19	20.55	40.80	37.01	234.71	20.66	18.35	21.79	21.06	41.16	36.67	234.14
Largest alignment	1408828	1408802	1408908	1408894	1408596	1408655	1102556	1408860	1408818	1408977	1408968	1408722	1408715	1104965	1408812	1408786	1408918	1408900	1408606	1408661	1104926
Total aligned length	5030193	5029734	5031751	5032046	5030259	5034794	4943675	5029783	5030238	5035302	5034554	5035276	5033402	4957379	5030449	5029848	5033498	5034466	5025956	5038103	4941660
NGA50	1103278	1103269	1103328	1105700	1103072	1105485	586349	1103285	1103272	1105706	1105701	1105447	1103071	586347	1103280	1103271	1105713	1105699	1103076	1105453	583107
NGA75	393562	393566	393580	393580	393533	393552	376967	393562	393564	393579	393580	393561	393566	376858	393562	393564	393580	393577	393545	393550	376966
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	3	2	2	2	2	2	2	3
LGA75	5	5	5	5	5	5	6	5	5	5	5	5	5	6	5	5	5	5	5	5	6

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

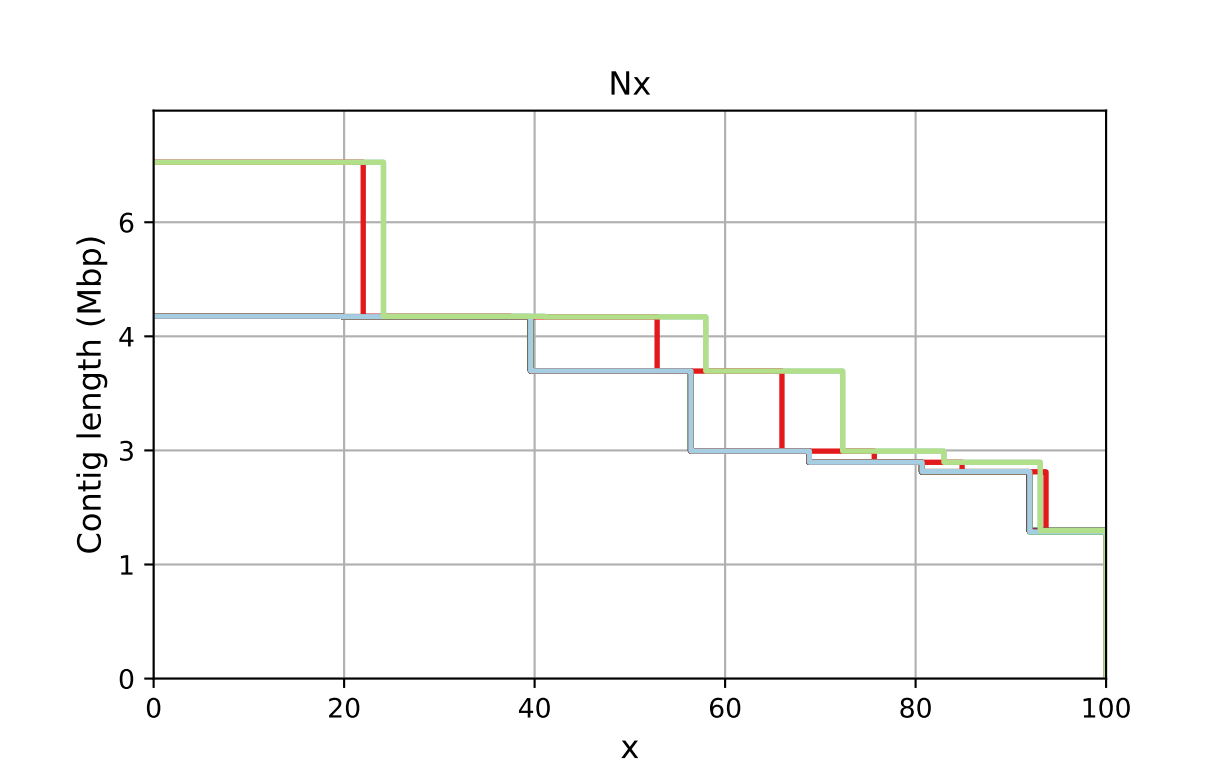
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_3_raw
# misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	18	20	20	20	20	20	20	18
# 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	4765380	4765358	4765659	4765647	4764472	4764468	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
# 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	12	12	12	12	12	12	34	12	12	12	12	12	12	32	12	12	12	12	12	12	34
# local misassemblies	36	36	36	37	36	37	58	37	36	37	37	37	36	55	36	36	37	37	36	38	61
# 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	42	42	42	42	42	42	36	42	42	42	42	42	42	37	42	42	42	42	42	42	35
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6
# mismatches	20732	20540	20833	20650	20800	21089	22765	20698	20589	20968	20898	21127	21234	23275	20766	20555	20750	20851	20354	21350	22520
# indels	954	838	986	975	1868	1701	11189	954	844	991	961	1908	1731	10972	966	858	1019	985	1925	1715	10943
# indels (<= 5 bp)	854	738	889	879	1771	1605	10983	856	743	895	865	1809	1634	10774	867	756	923	889	1828	1618	10745
# indels (> 5 bp)	100	100	97	96	97	96	206	98	101	96	96	99	97	198	99	102	96	96	97	97	198
Indels length	6236	6141	6237	6117	7246	6966	20687	6210	6162	6137	6107	7275	7082	20201	6245	6187	6183	6129	7338	6961	19939

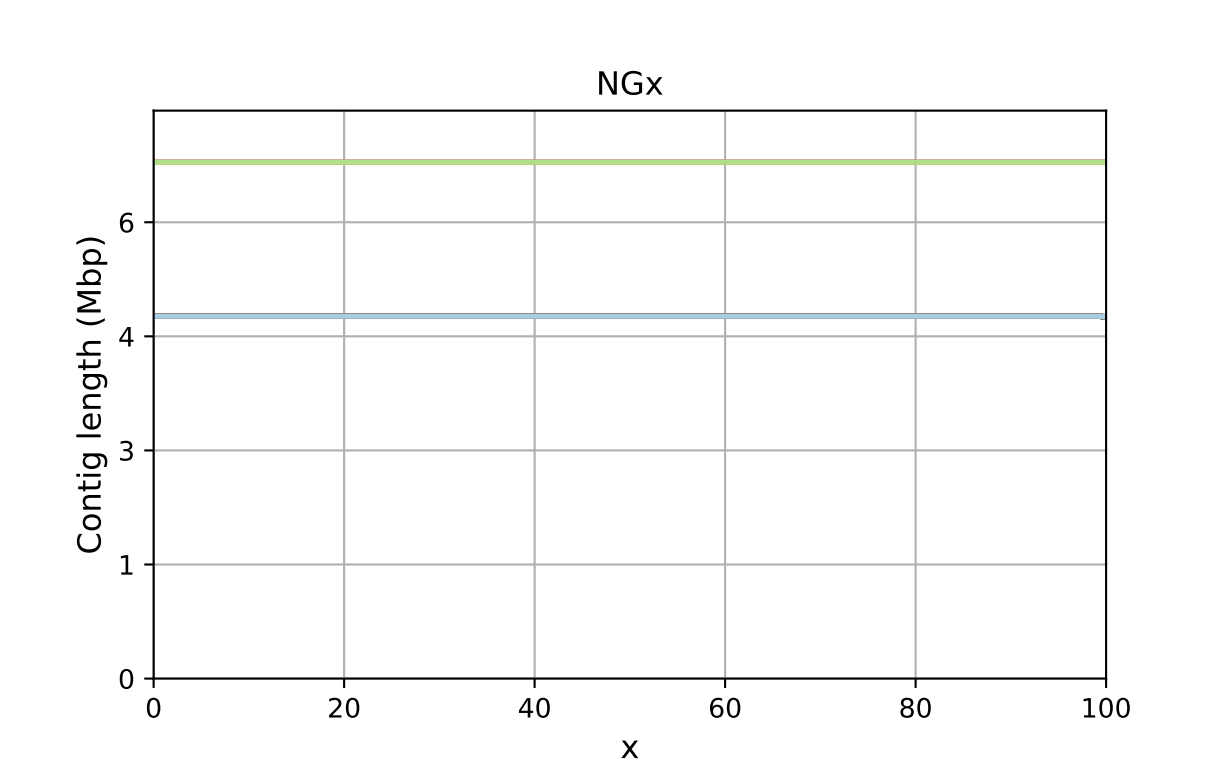
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

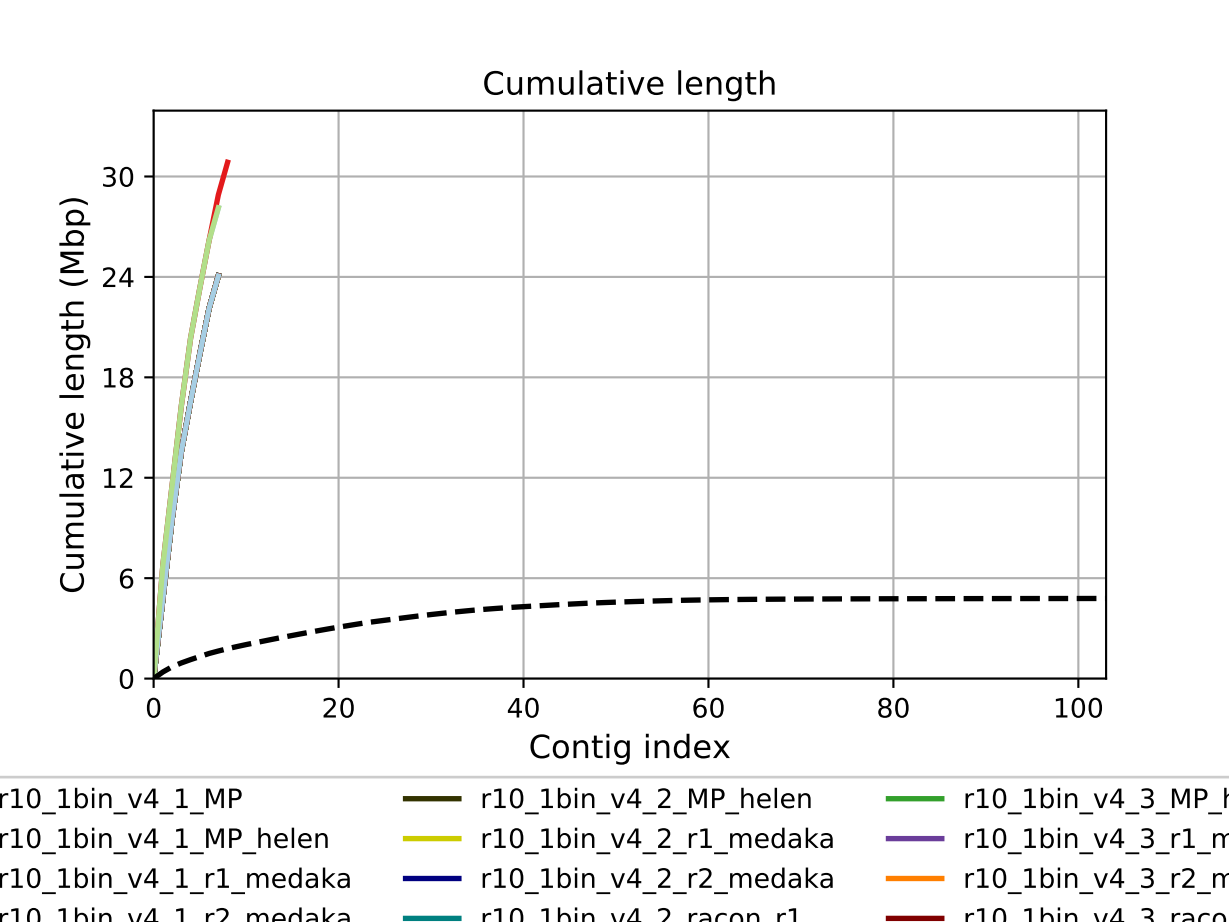
Unaligned report

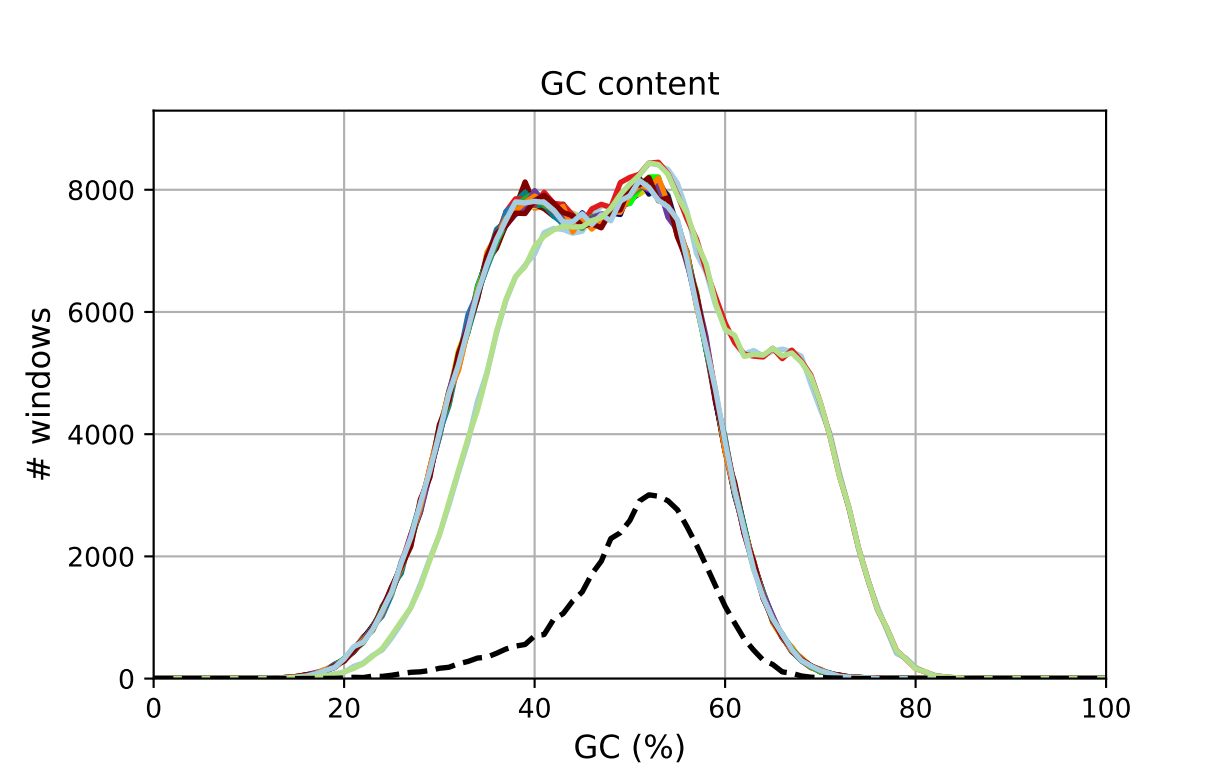
	r10_1bin_v4_1_MP	r10_1bin_v4_1_MP_helen	r10_1bin_v4_1_r1_medaka	r10_1bin_v4_1_r2_medaka	r10_1bin_v4_1_racon_r1	r10_1bin_v4_1_racon_r2	r10_1bin_v4_1_raw	r10_1bin_v4_2_MP	r10_1bin_v4_2_MP_helen	r10_1bin_v4_2_r1_medaka	r10_1bin_v4_2_r2_medaka	r10_1bin_v4_2_racon_r1	r10_1bin_v4_2_racon_r2	r10_1bin_v4_2_raw	r10_1bin_v4_3_MP	r10_1bin_v4_3_MP_helen	r10_1bin_v4_3_r1_medaka	r10_1bin_v4_3_r2_medaka	r10_1bin_v4_3_racon_r1	r10_1bin_v4_3_racon_r2	r10_1bin_v4_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	8	7	7	7	7	7	7	7
Partially unaligned length	19038707	19035805	19038701	19030255	19024960	19016740	23182737	19039665	19035014	19037635	19027690	19022491	19014448	25890284	19038572	19035353	19038620	19025354	19029919	19012658	23187093
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

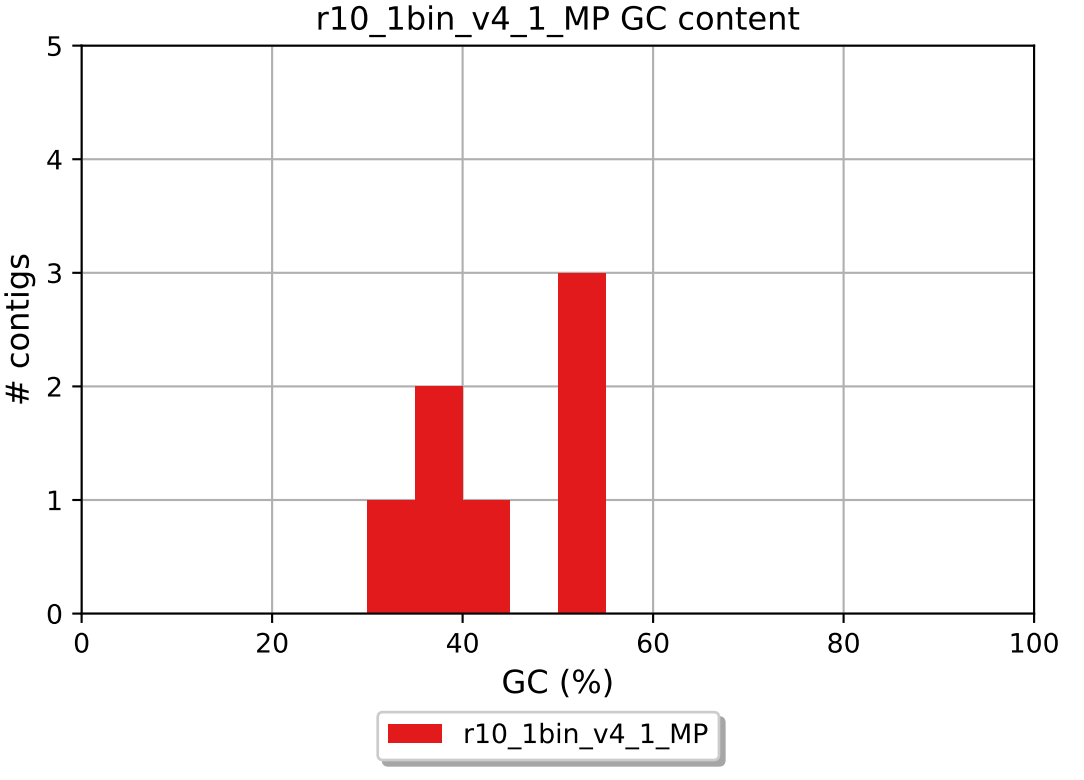
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

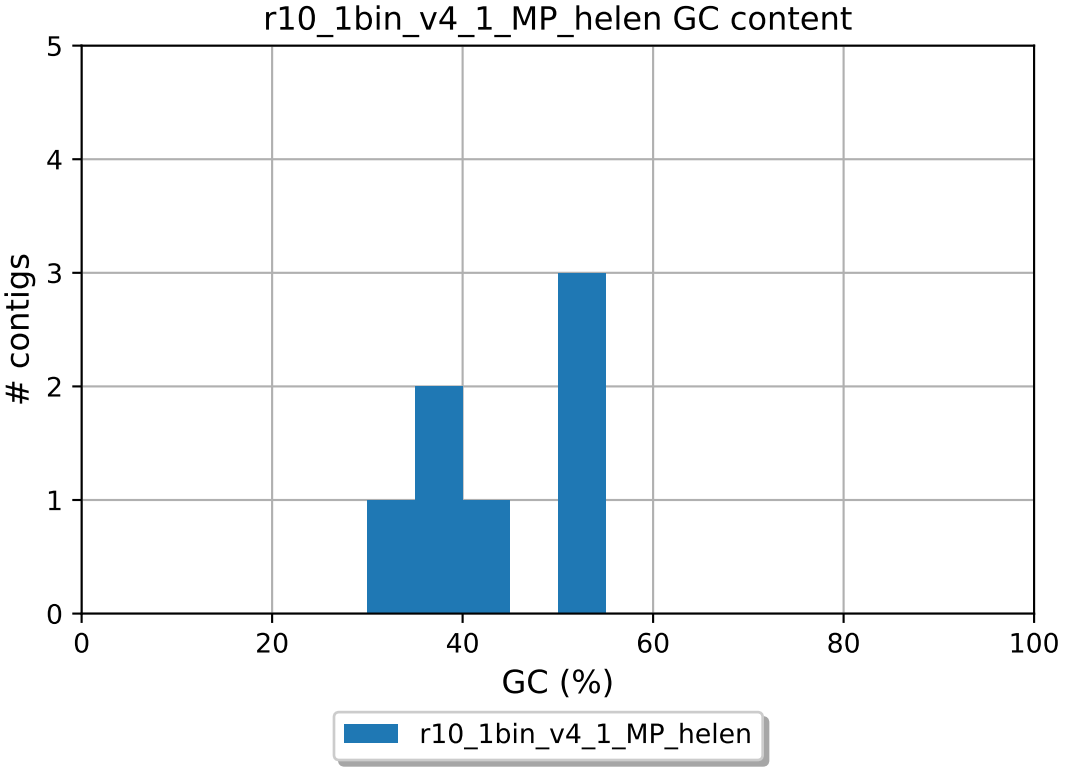

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m

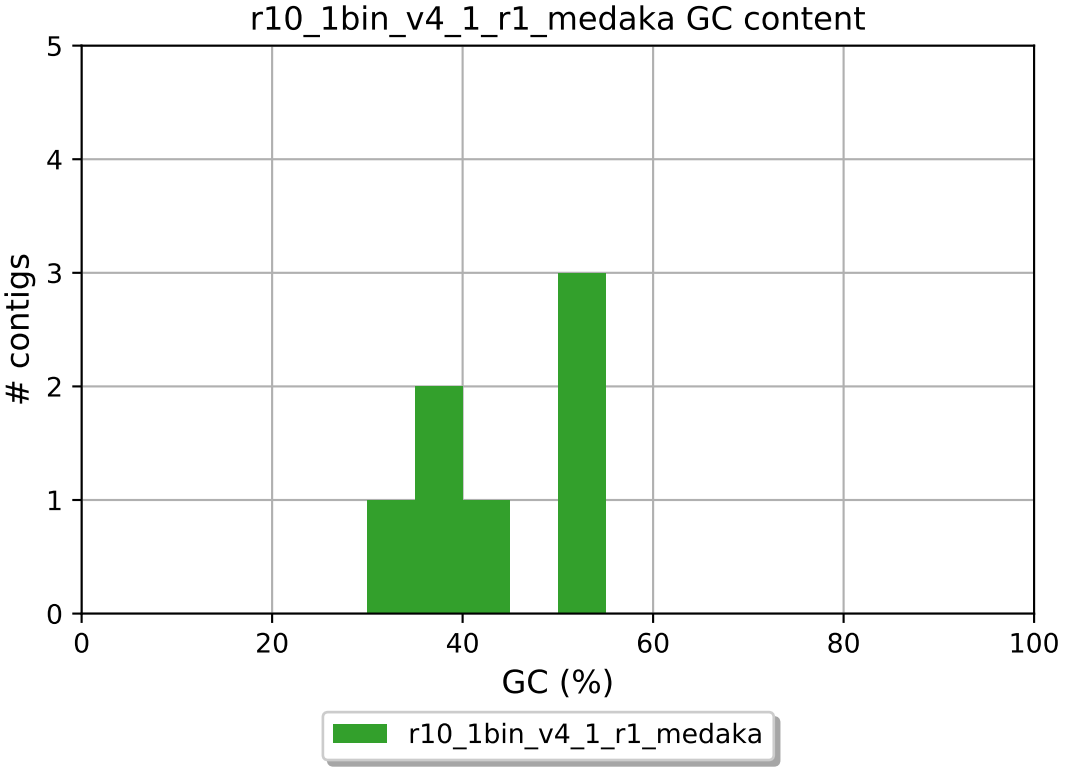

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
X
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_r1_m

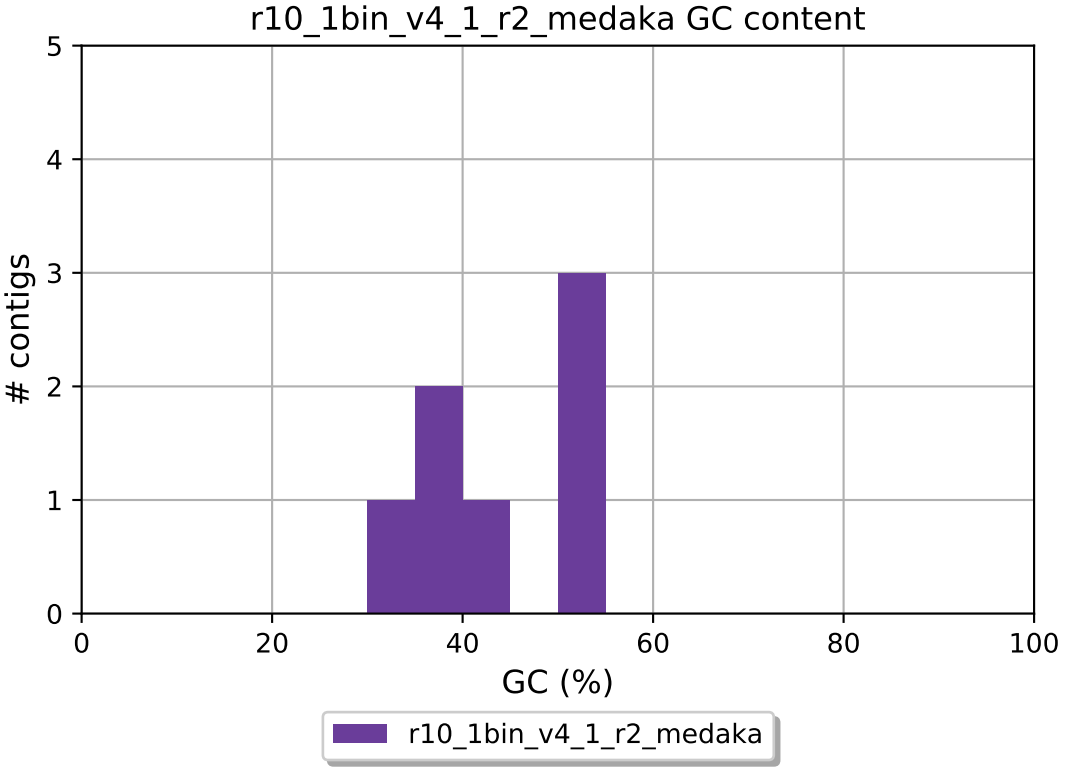

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
Contig index
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

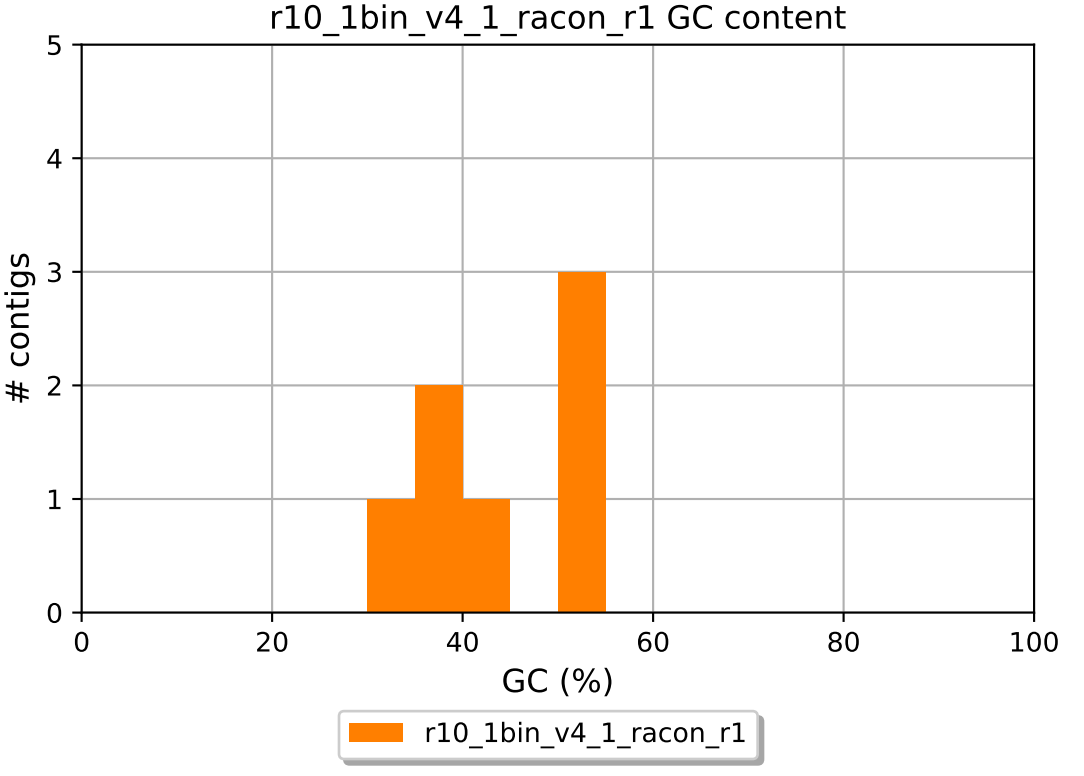

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m

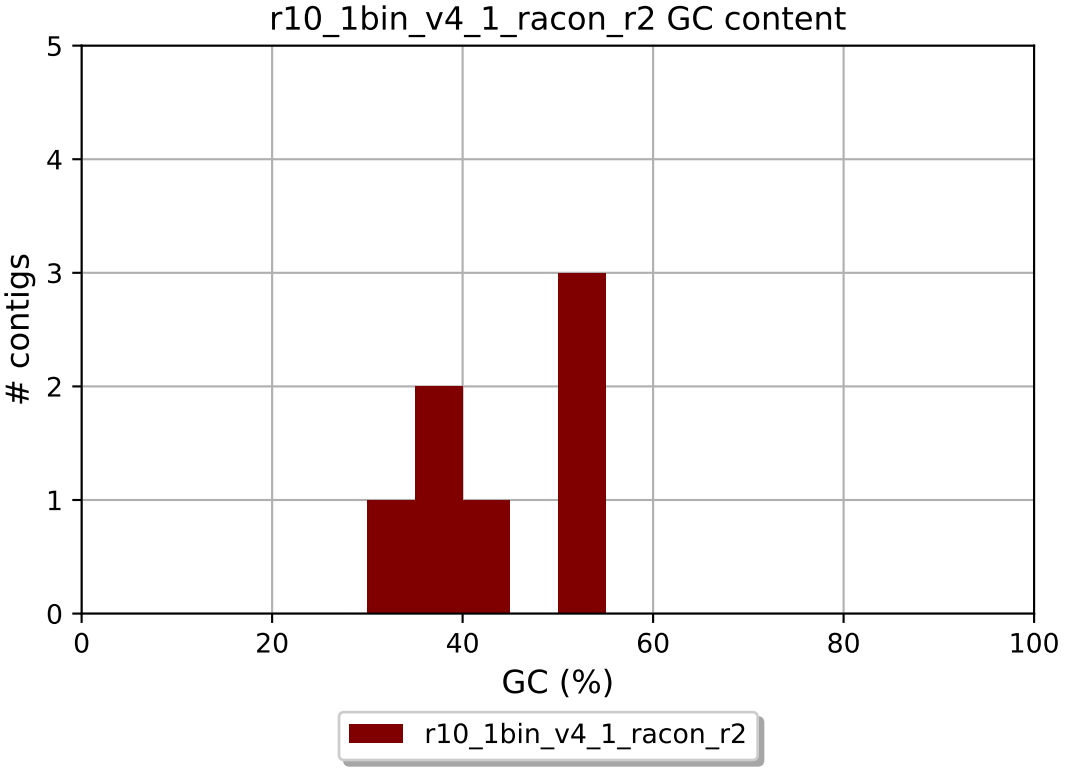

r10_1bin_v4_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP

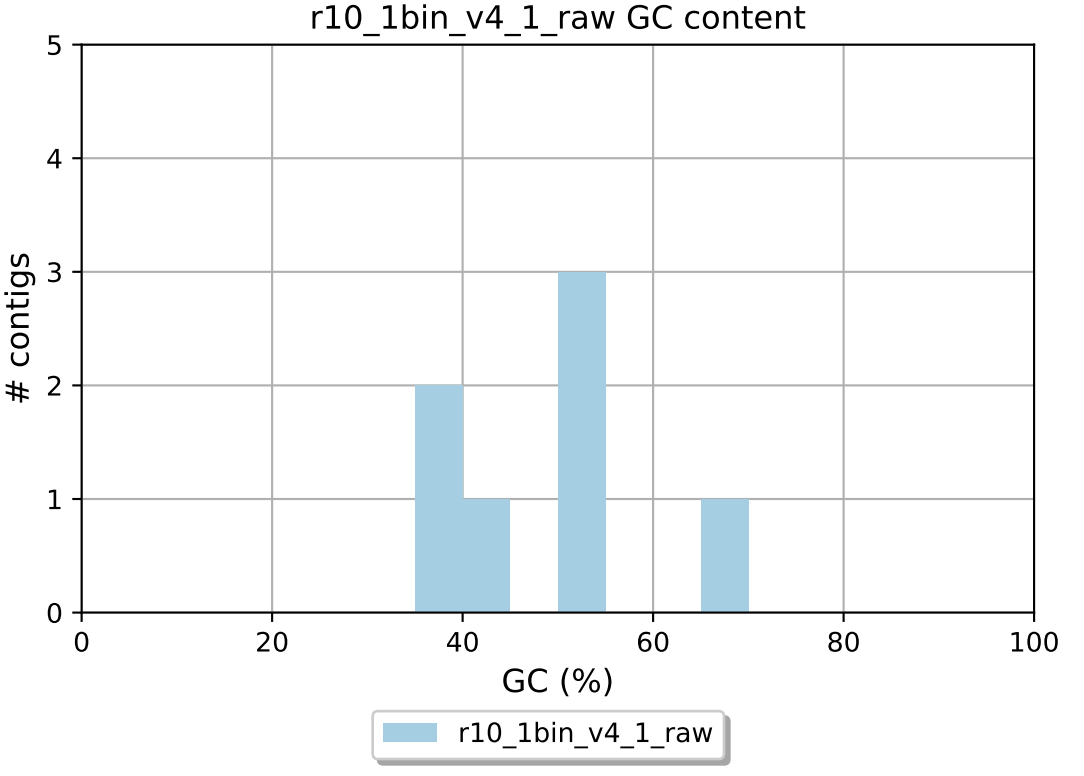

r10_1bin_v4_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_MP_helen

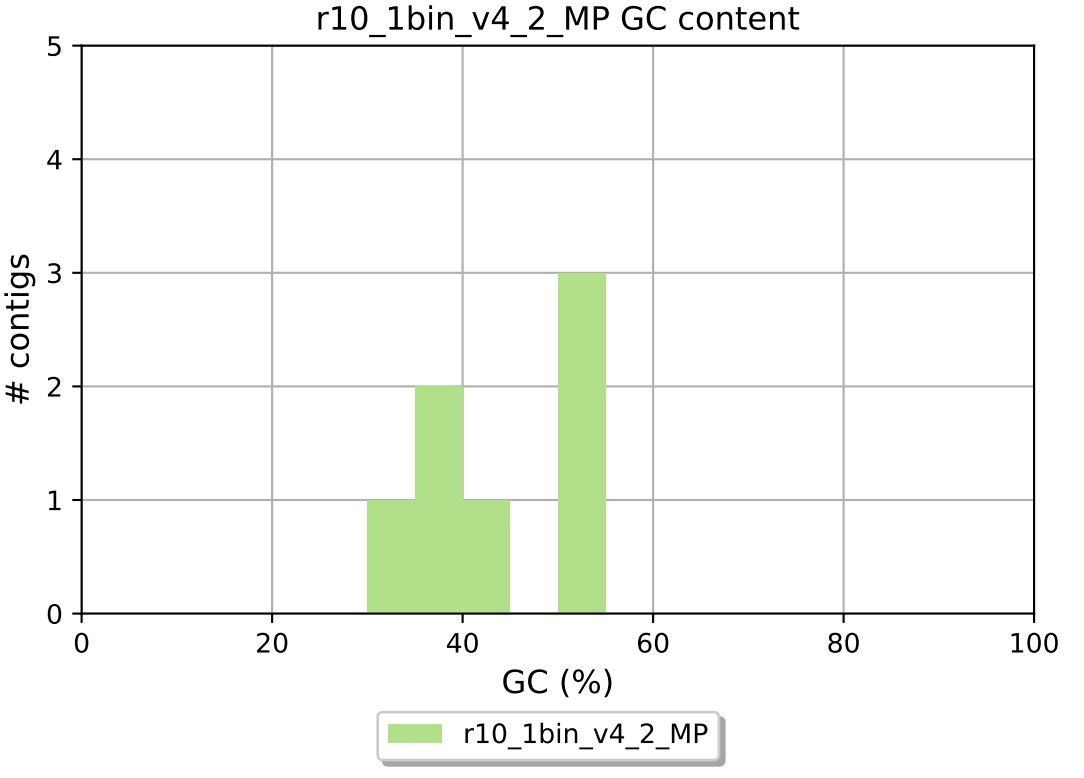

r10_1bin_v4_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r1_medaka

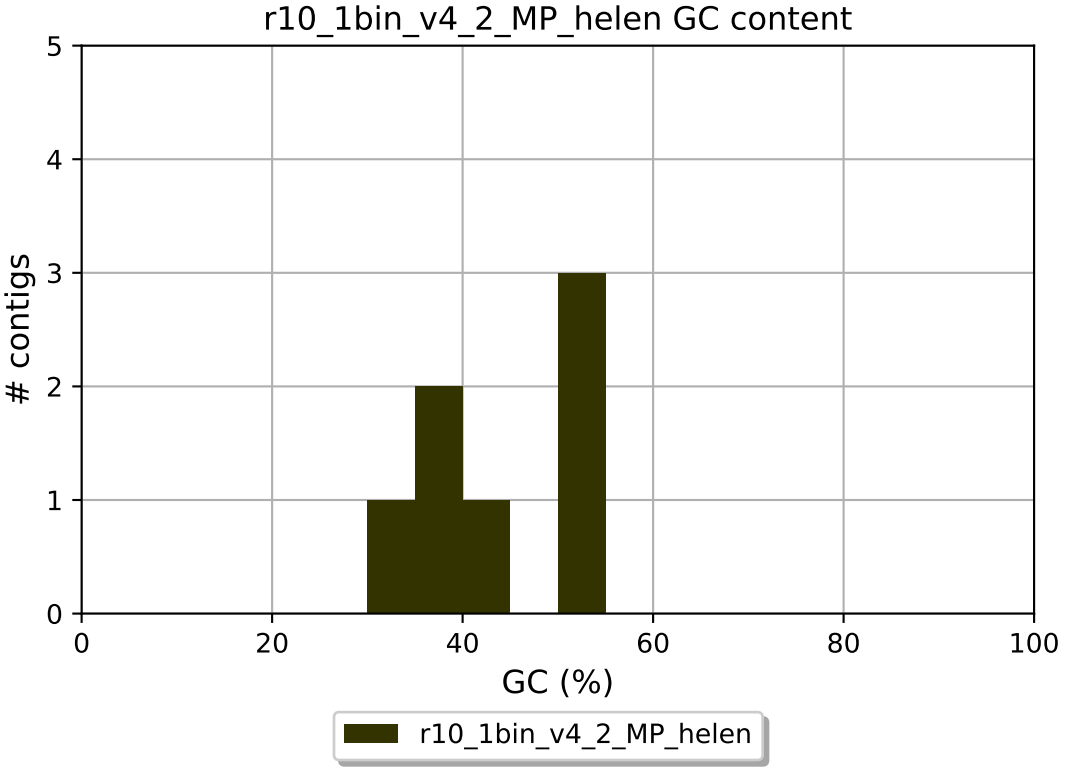

r10_1bin_v4_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_r2_medaka

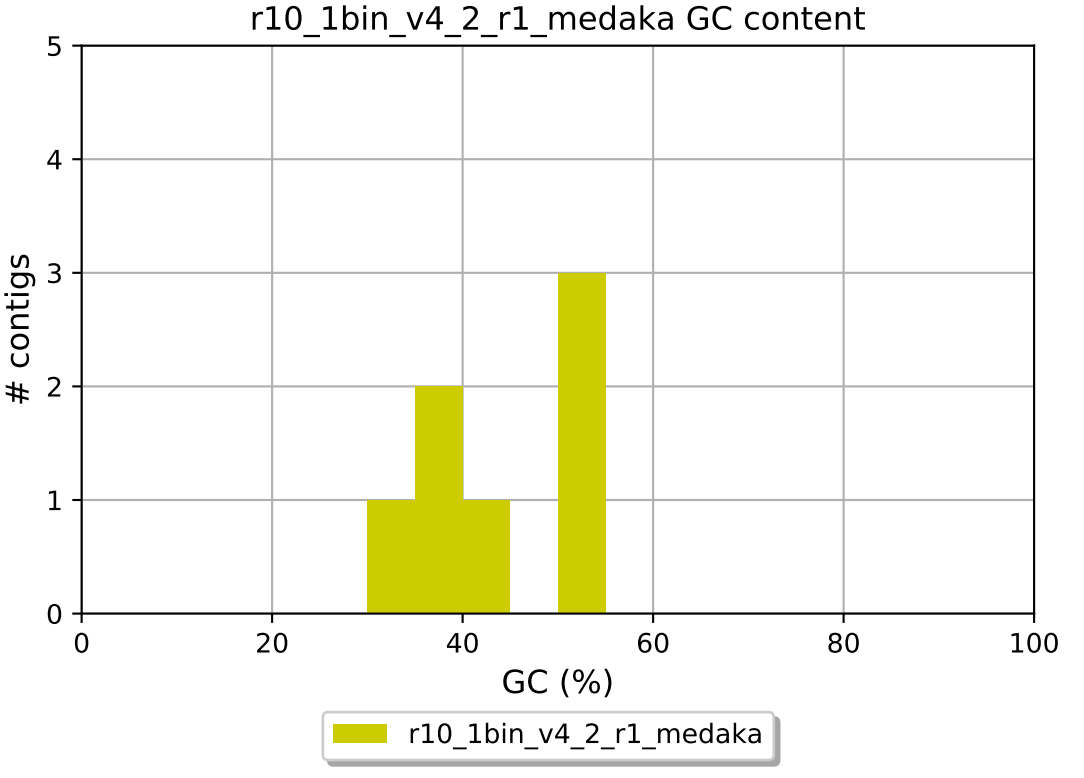

r10_1bin_v4_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r1

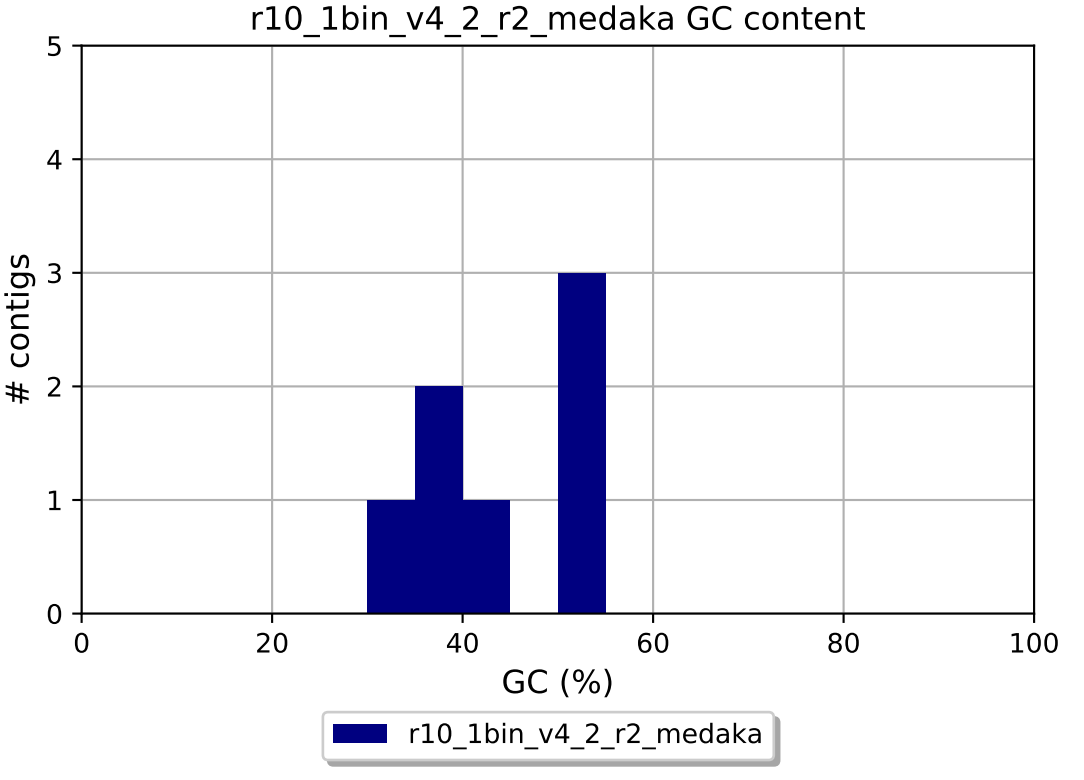

r10_1bin_v4_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_racon_r2

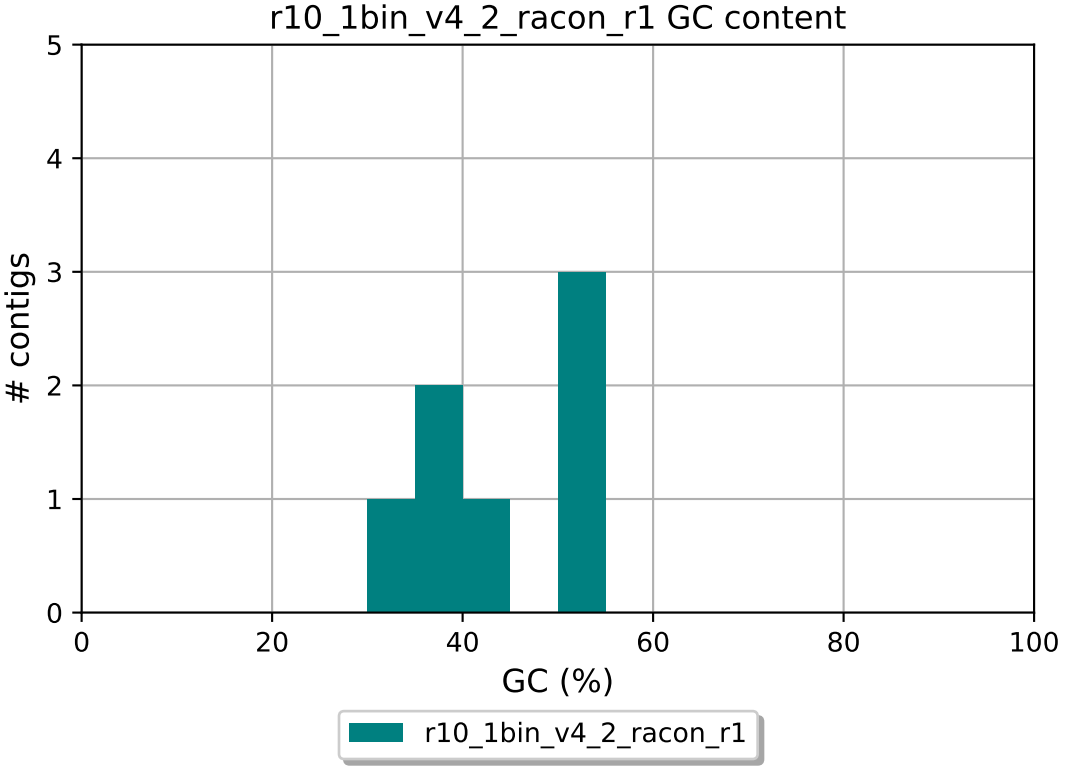

r10_1bin_v4_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_1_raw

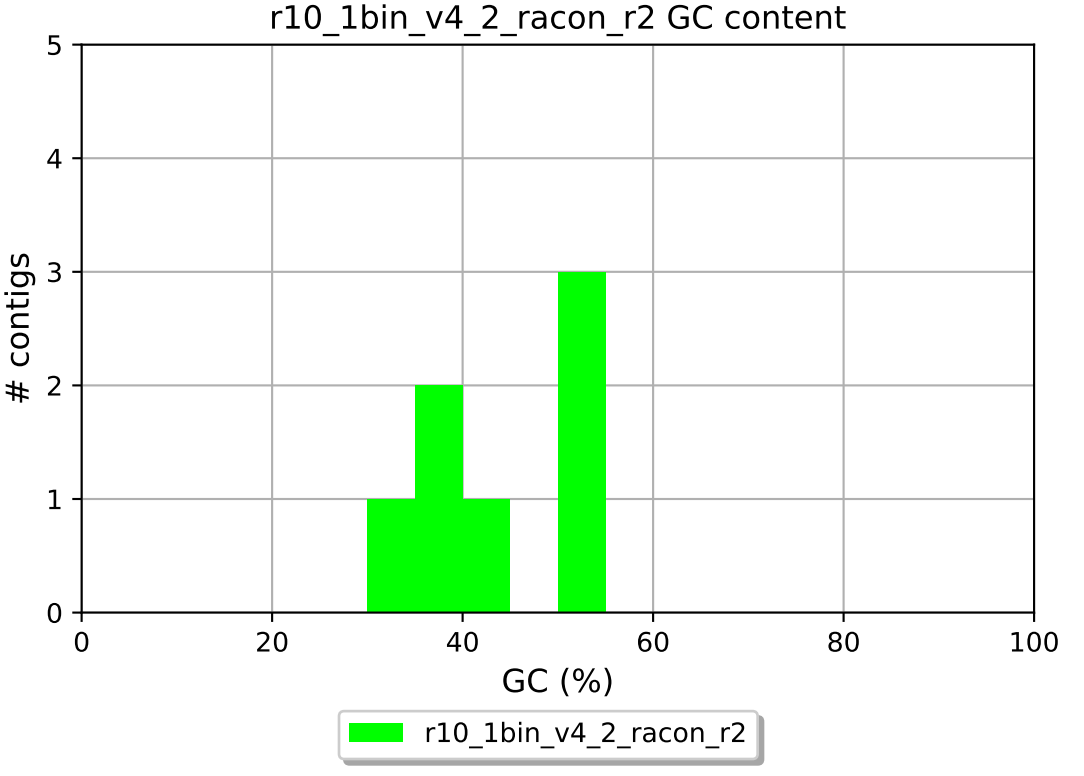

r10_1bin_v4_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP

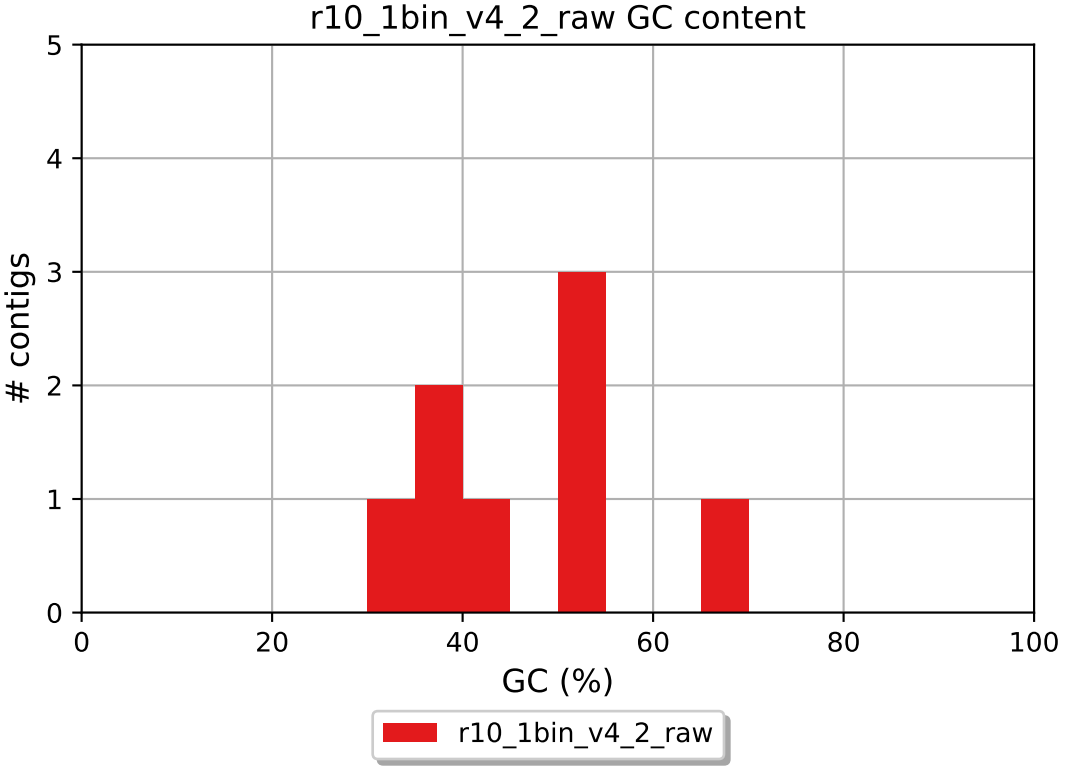

r10_1bin_v4_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_MP_helen

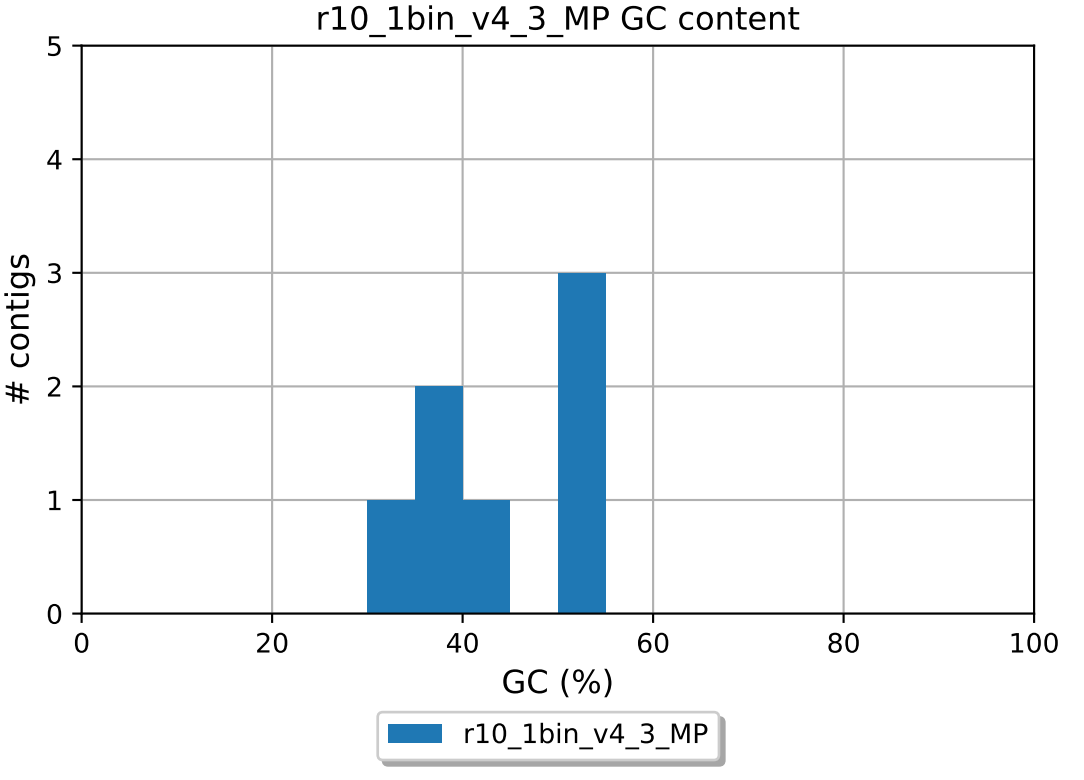

r10_1bin_v4_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r1_medaka

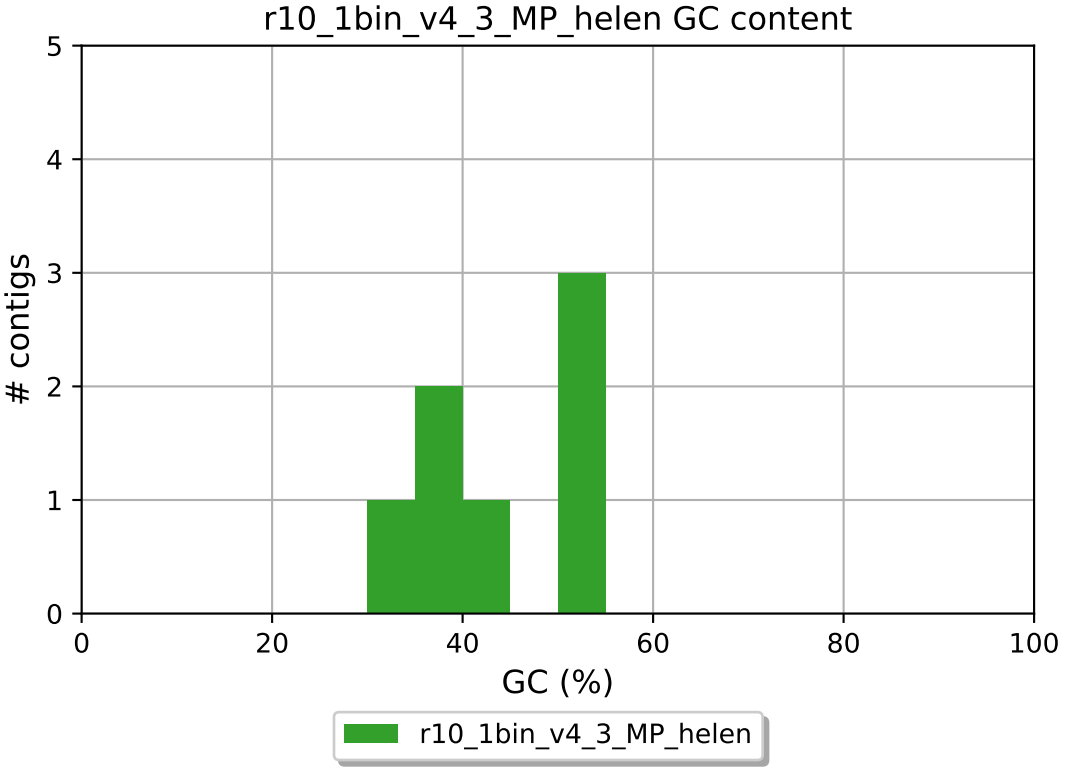

r10_1bin_v4_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_r2_medaka

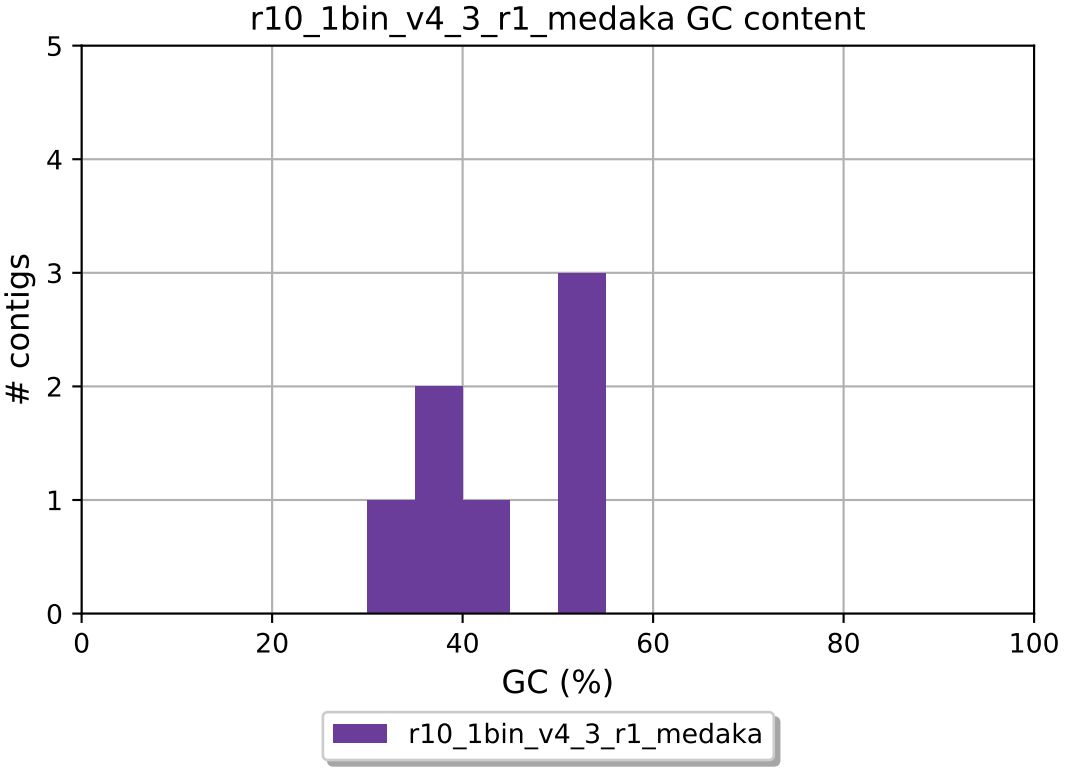

r10_1bin_v4_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r1

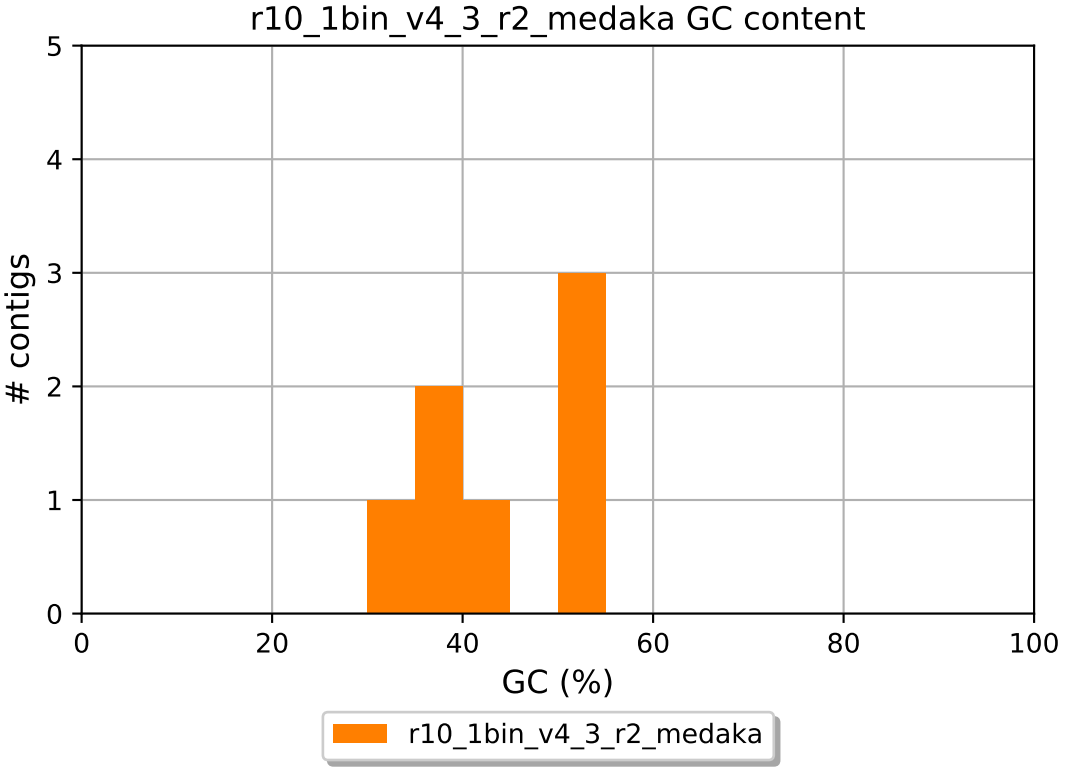

r10_1bin_v4_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_racon_r2

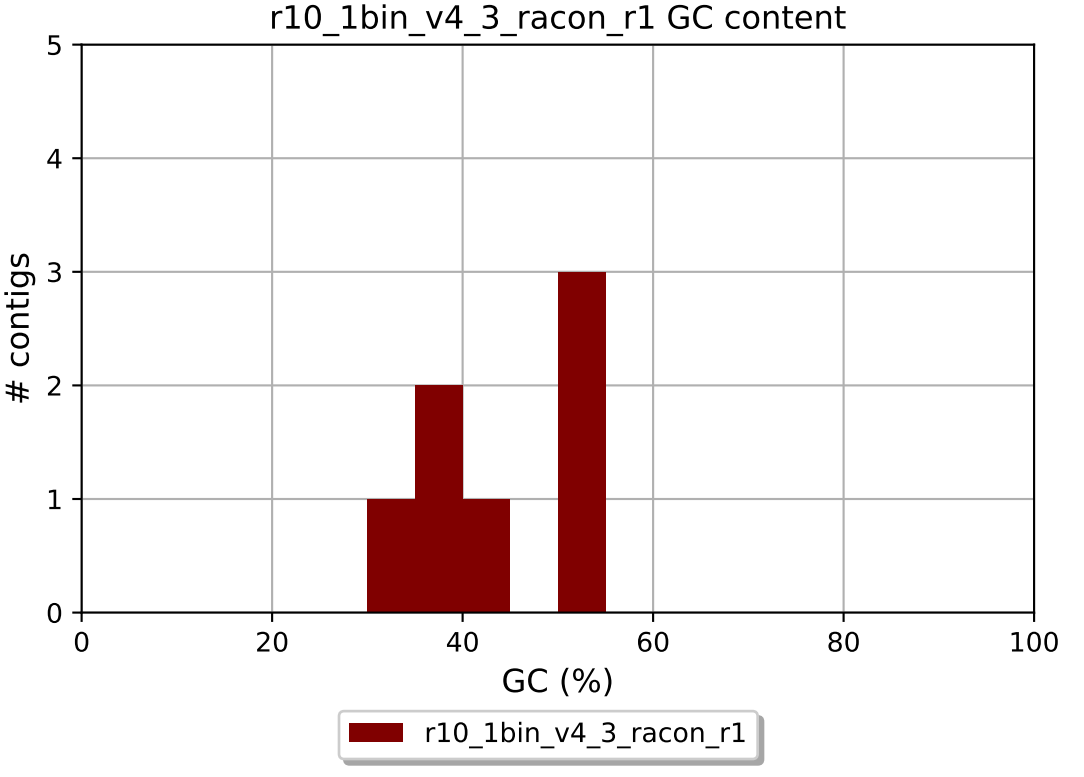

r10_1bin_v4_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_2_raw

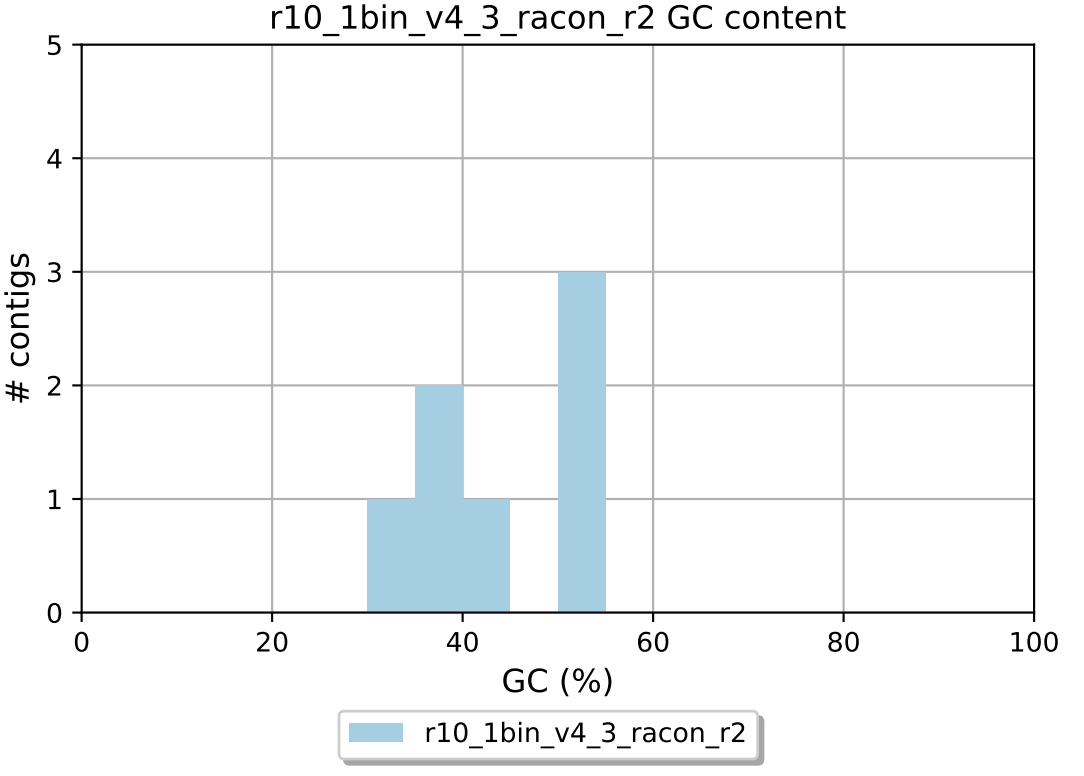

r10_1bin_v4_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP

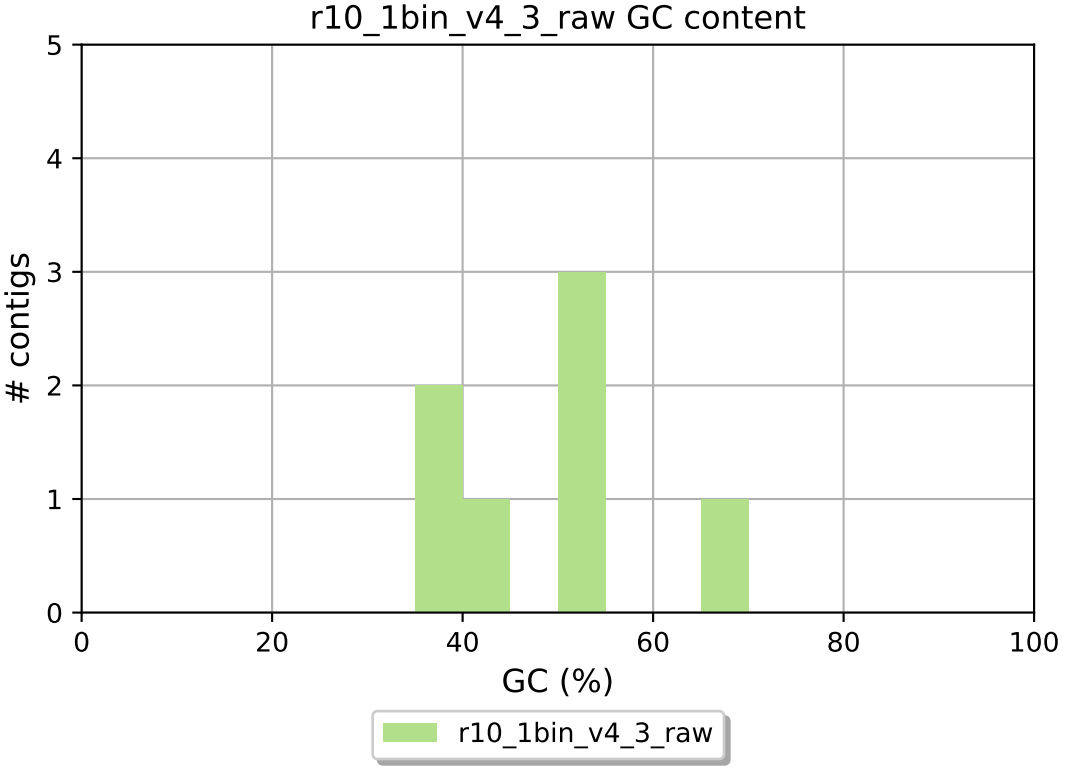

r10_1bin_v4_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_MP_helen

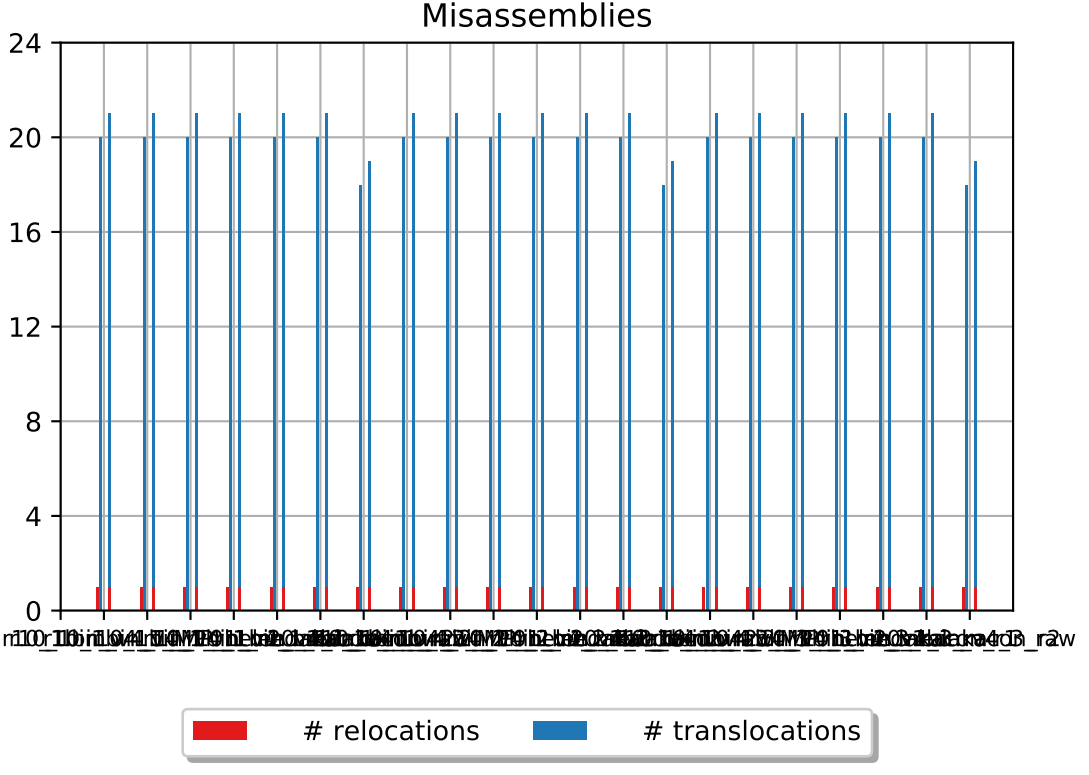

r10_1bin_v4_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r1_medaka

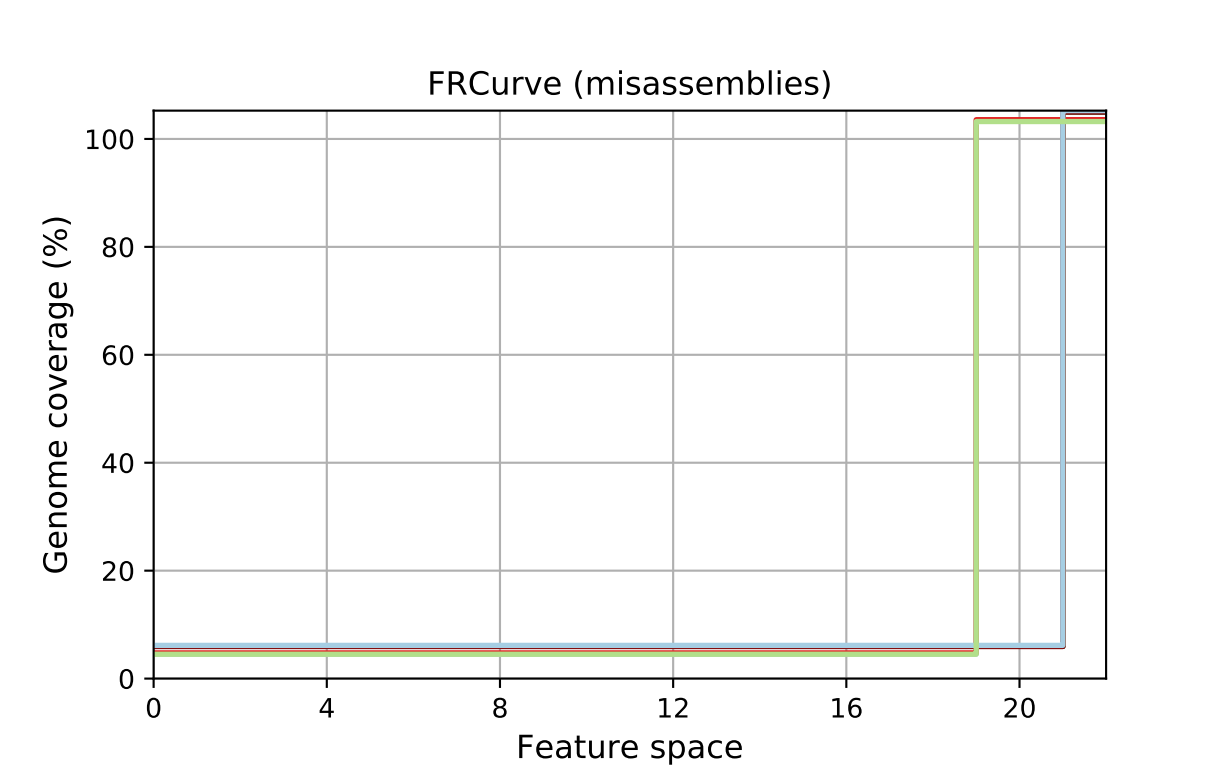

r10_1bin_v4_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_r2_medaka

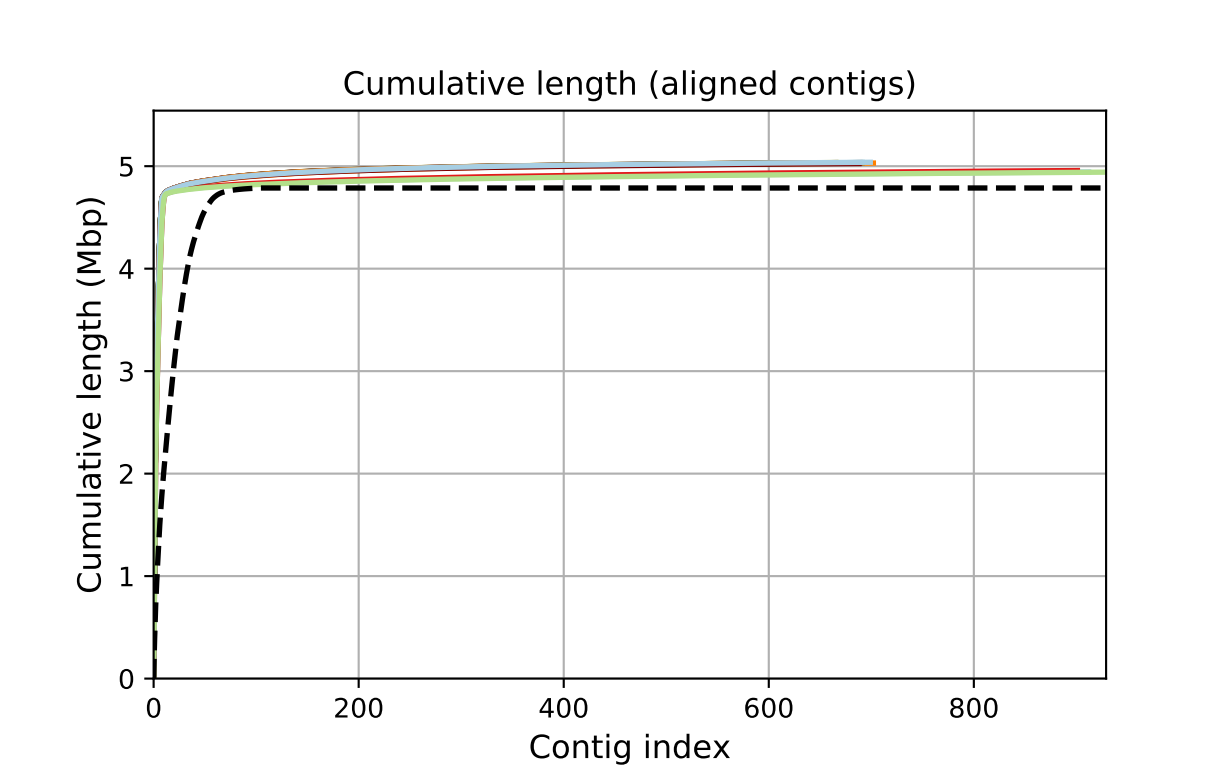

r10_1bin_v4_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r1

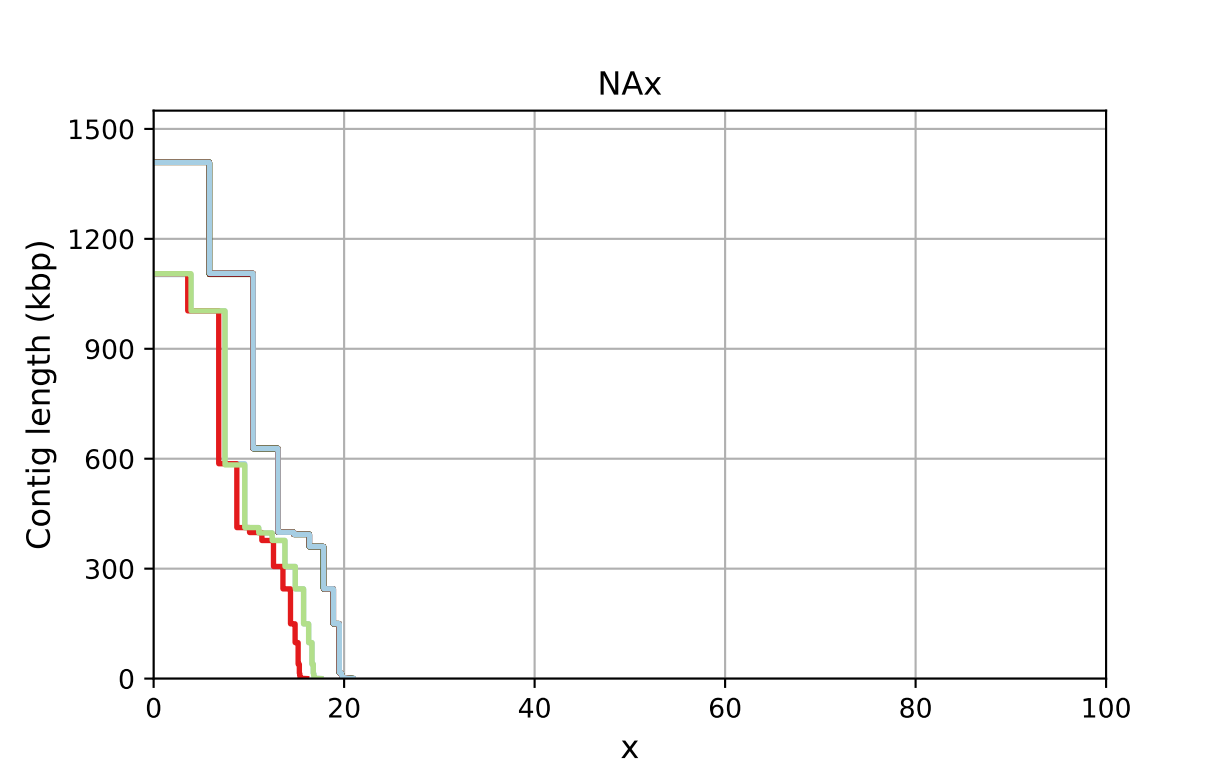

r10_1bin_v4_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_racon_r2

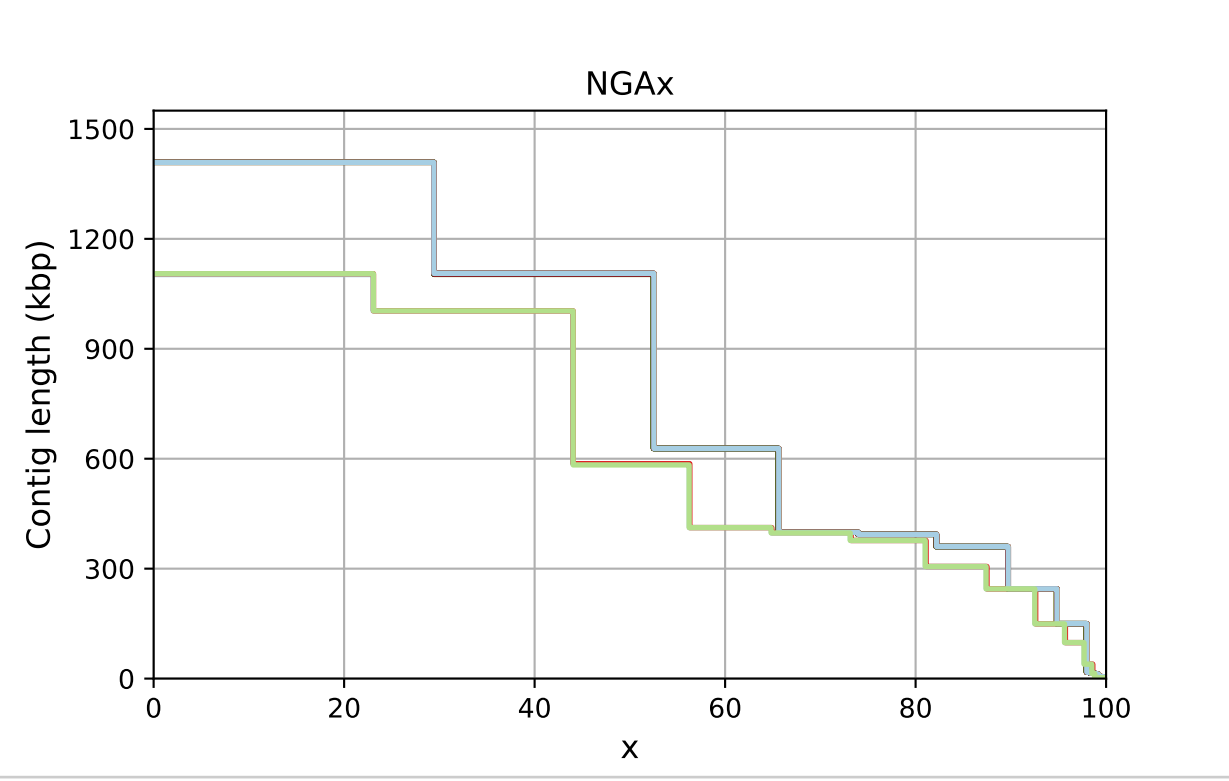

r10_1bin_v4_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v4_3_raw

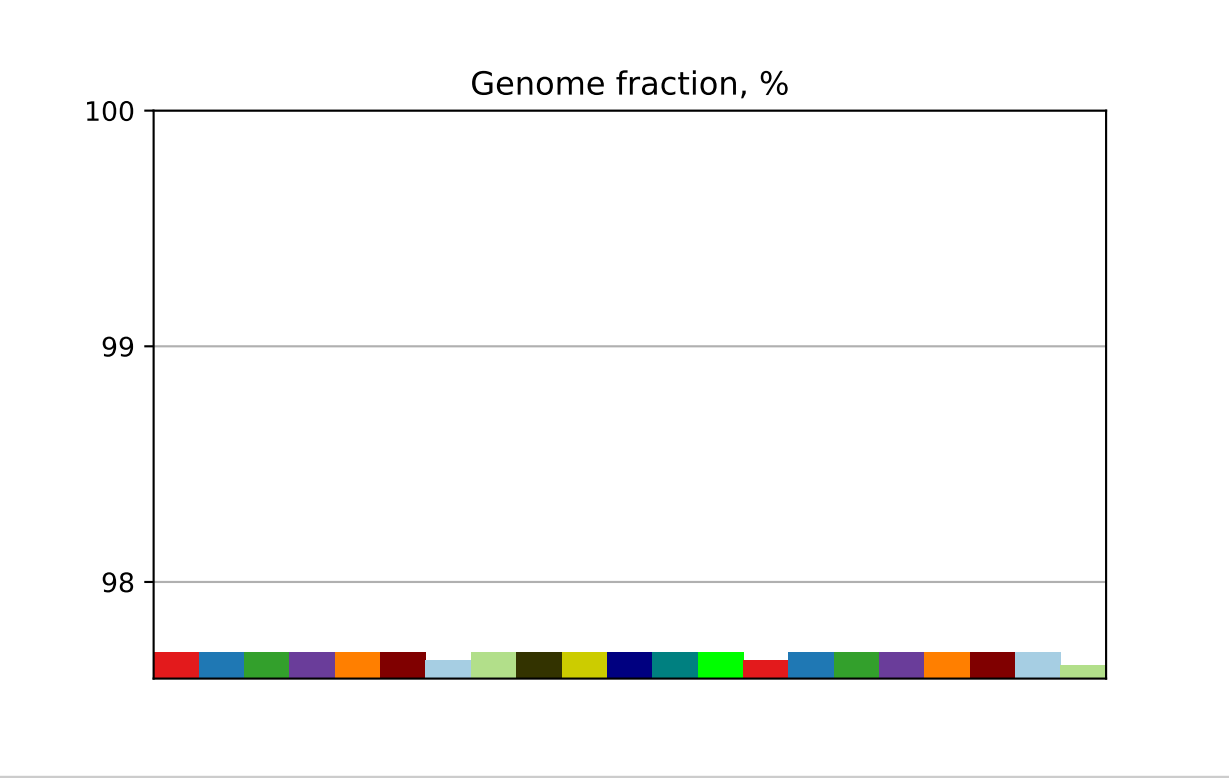

Misassemblies
24
20
16
12
8
4
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
200
400
600
800
Contig index
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_2_r2_medaka
r10_1bin_v4_2_racon_r1
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m
r10_1bin_v4_3_r2_m


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m


Genome fraction, %
100
99
98
r10_1bin_v4_1_MP
r10_1bin_v4_1_MP_helen
r10_1bin_v4_1_r1_medaka
r10_1bin_v4_2_MP
r10_1bin_v4_2_MP_helen
r10_1bin_v4_2_r1_medaka
r10_1bin_v4_3_MP
r10_1bin_v4_3_MP_h
r10_1bin_v4_3_r1_m