Report

	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
Total length	24074864	24069434	24071998	24064261	24059992	24055964	24060023	24074405	24069671	24071816	24060875	24059808	24052467	24060967	24075545	24072103	24075113	24069593	24065155	24060597	24062694
Reference length	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	44.77	44.80	44.80	44.80	44.80	44.78	44.78	44.77	44.80	44.81	44.80	44.80	44.79	44.79	44.77
Reference GC (%)	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72	52.72
N50	4045598	4045624	4045593	4045588	4045161	4045292	4043043	4045604	4045480	4045604	4045608	4045229	4045315	4042940	4045596	4045614	4045597	4045593	4045228	4045344	4043027
NG50	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
N75	2845425	2845362	2845428	2845425	2845303	2845317	2843846	2845427	2845365	2845431	2845433	2845282	2845346	2843855	2845434	2845416	2845426	2845429	2845240	2845336	2843848
NG75	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
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	74	73	76	78	80	79	77	74	73	74	81	75	82	75	74	75	74	79	74	80	78
# 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	1947358	1945184	1945421	1938102	1934600	1930264	1945410	1947367	1945631	1945233	1934696	1934507	1926766	1945527	1948617	1947910	1948308	1943446	1939324	1934869	1947491
# local misassemblies	11	15	23	26	47	32	33	11	15	31	26	43	39	30	12	12	19	22	39	37	32
# 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 + 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	22082588	22081257	22083968	22083903	22078526	22078691	22110892	22081954	22079236	22085585	22084165	22079813	22079475	22107683	22081711	22079681	22083431	22084583	22080859	22078889	22113481
Genome fraction (%)	99.943	99.828	99.879	99.938	99.869	99.906	99.860	99.943	99.855	99.915	99.931	99.892	99.885	99.859	99.936	99.935	99.934	99.874	99.902	99.839	99.867
Duplication ratio	1.104	1.103	1.103	1.098	1.099	1.096	1.081	1.104	1.104	1.101	1.096	1.098	1.094	1.083	1.105	1.104	1.104	1.101	1.100	1.099	1.081
# 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	267.75	262.85	312.96	283.06	273.39	270.35	361.22	268.47	267.32	296.38	283.92	272.94	268.35	367.71	263.50	261.79	304.30	295.00	269.19	269.86	366.02
# indels per 100 kbp	11.92	13.98	16.19	13.58	56.69	55.39	350.01	11.86	10.60	14.03	11.47	58.28	53.13	353.40	11.53	12.25	13.86	14.59	60.82	53.59	350.10
Largest alignment	177205	177205	173026	172971	172889	172861	177003	177204	177203	173115	173023	172987	172948	177003	177186	177187	177181	177181	176880	177039	176961
Total aligned length	1986190	1982026	1982047	1974362	1975571	1971321	1945749	1986365	1986681	1980310	1970711	1974217	1967019	1949881	1987946	1986592	1985801	1979191	1978486	1974615	1943668
NGA50	89790	87725	79490	81625	68560	81471	69730	89793	88233	89867	81637	81586	81534	69730	81535	69795	81506	81468	81455	81441	69751
NGA75	35034	35032	35043	35032	34818	34964	34946	35032	35503	34836	35031	34818	35000	34945	35502	35503	35503	35491	35479	35438	35172
LGA50	8	8	8	8	9	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
LGA75	17	17	18	17	18	17	18	17	16	17	17	17	17	18	17	18	17	17	17	17	18

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

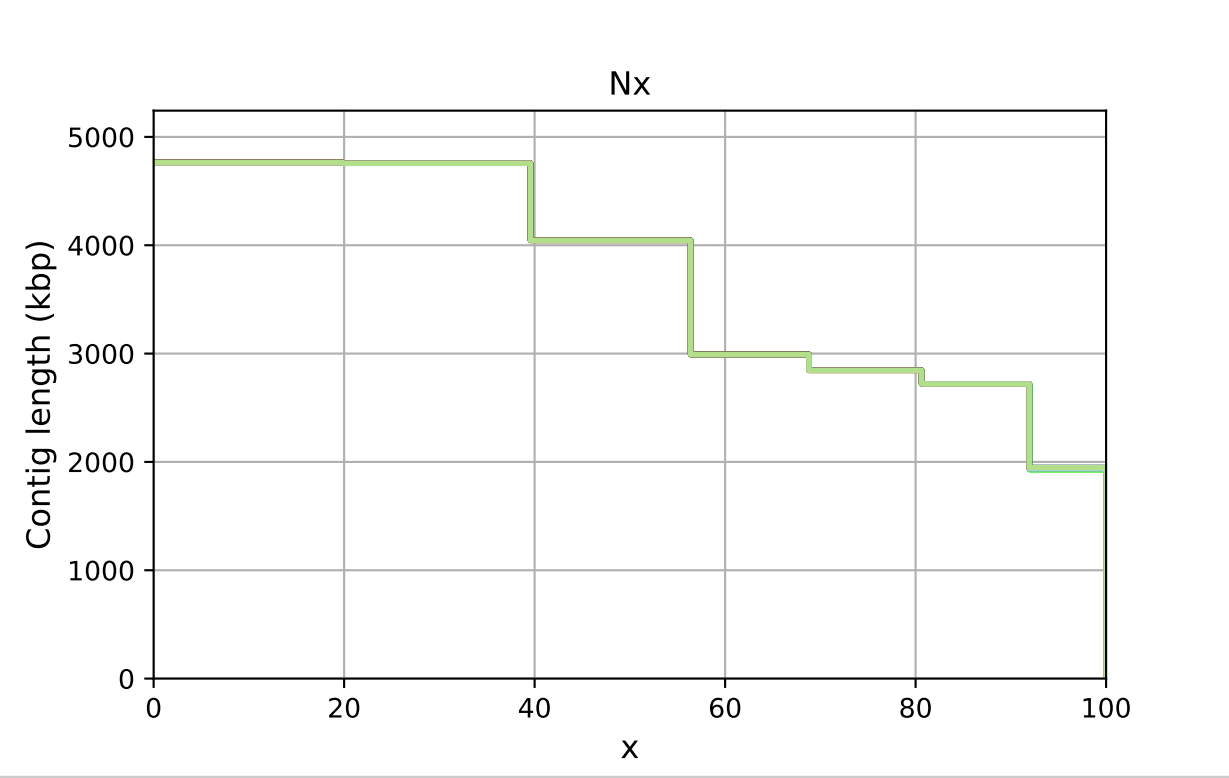
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_3_raw
# misassemblies	74	73	76	78	80	79	77	74	73	74	81	75	82	75	74	75	74	79	74	80	78
# contig misassemblies	74	73	76	78	80	79	77	74	73	74	81	75	82	75	74	75	74	79	74	80	78
# c. relocations	4	3	3	5	3	5	4	4	3	3	8	3	8	4	4	4	4	6	4	4	5
# c. translocations	70	70	73	73	77	74	73	70	70	71	73	72	74	71	70	71	70	73	70	76	73
# 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	1947358	1945184	1945421	1938102	1934600	1930264	1945410	1947367	1945631	1945233	1934696	1934507	1926766	1945527	1948617	1947910	1948308	1943446	1939324	1934869	1947491
# 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	36	40	32	36	32	30	46	36	36	34	36	36	32	44	34	36	34	32	36	30	46
# local misassemblies	11	15	23	26	47	32	33	11	15	31	26	43	39	30	12	12	19	22	39	37	32
# 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	66	64	63	65	61	61	40	66	66	65	65	63	63	41	66	65	66	66	64	60	40
# 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	4831	4737	5643	5107	4929	4876	6512	4844	4819	5346	5122	4922	4839	6629	4754	4723	5490	5319	4855	4864	6599
# indels	215	252	292	245	1022	999	6310	214	191	253	207	1051	958	6371	208	221	250	263	1097	966	6312
# indels (<= 5 bp)	164	195	244	188	957	922	6208	164	138	200	159	979	891	6269	160	174	198	212	1016	892	6220
# indels (> 5 bp)	51	57	48	57	65	77	102	50	53	53	48	72	67	102	48	47	52	51	81	74	92
Indels length	2740	2924	2806	2900	4511	4912	11185	2727	2614	2782	2651	4864	4446	11243	2590	2573	2698	2627	5251	4737	11172

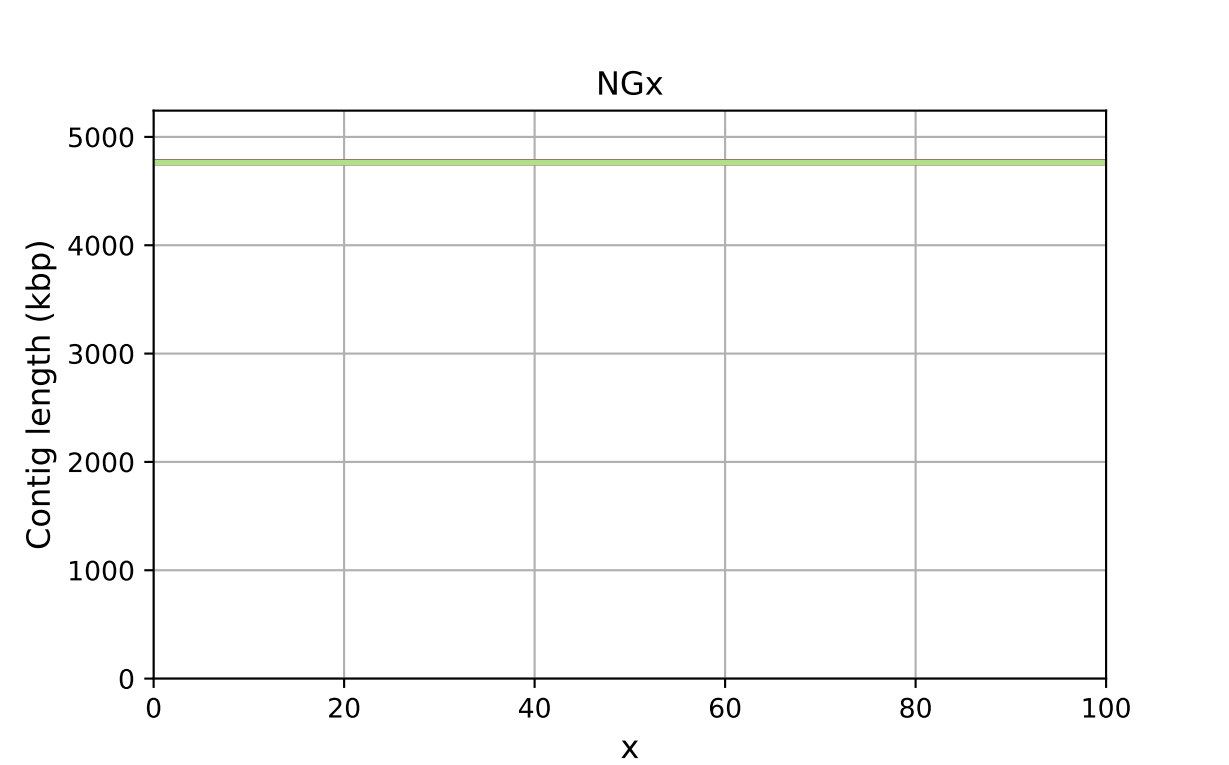
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

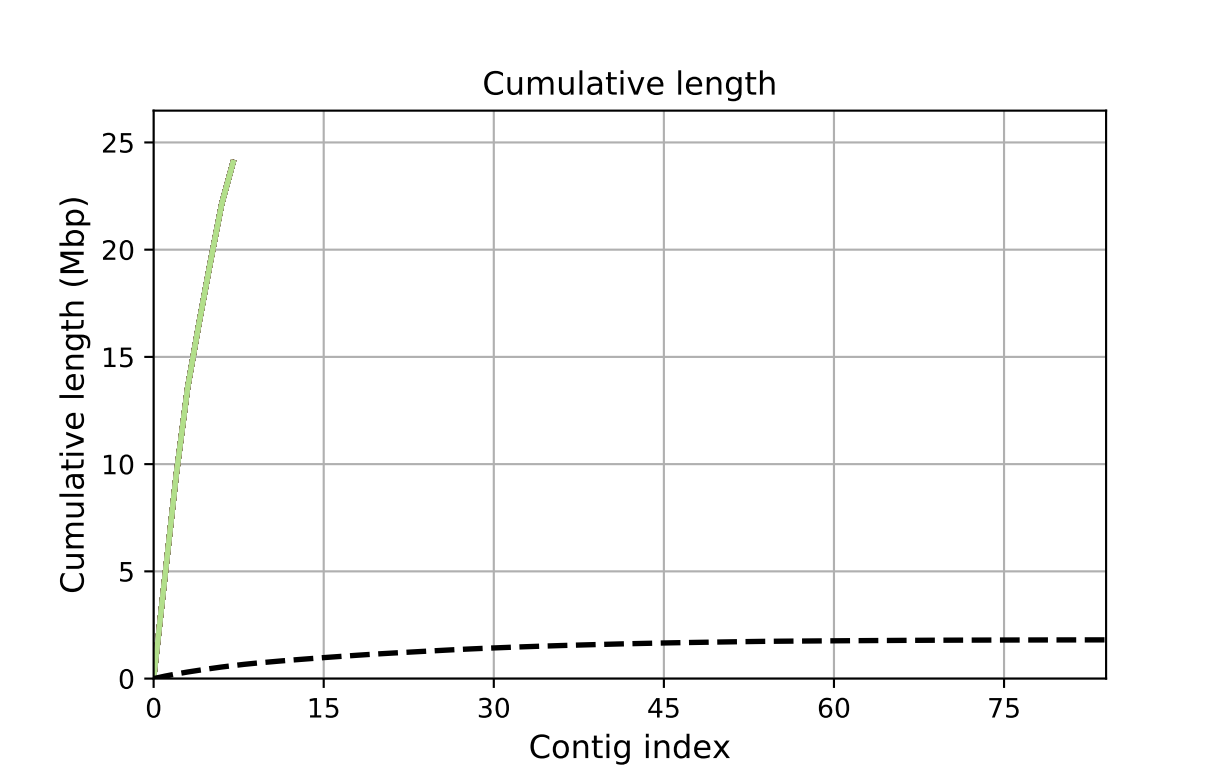
Unaligned report

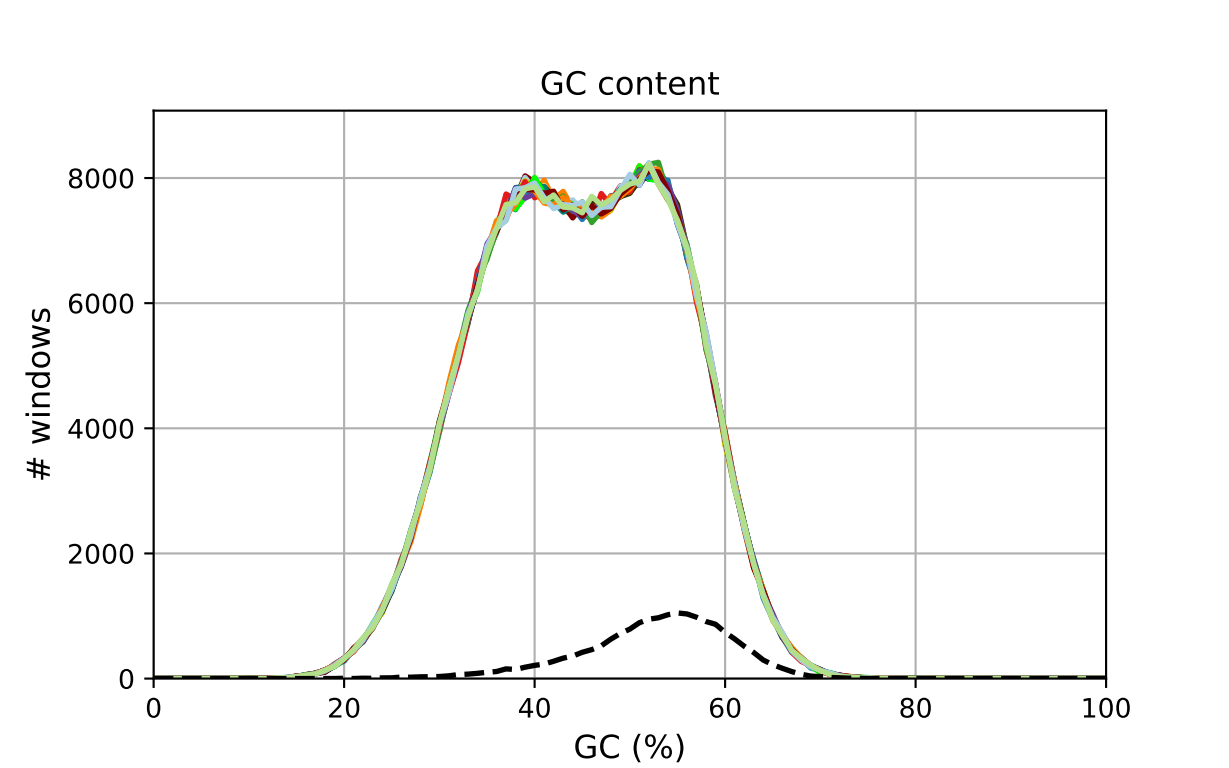
	r10_1bin_v2_1_MP	r10_1bin_v2_1_MP_helen	r10_1bin_v2_1_r1_medaka	r10_1bin_v2_1_r2_medaka	r10_1bin_v2_1_racon_r1	r10_1bin_v2_1_racon_r2	r10_1bin_v2_1_raw	r10_1bin_v2_2_MP	r10_1bin_v2_2_MP_helen	r10_1bin_v2_2_r1_medaka	r10_1bin_v2_2_r2_medaka	r10_1bin_v2_2_racon_r1	r10_1bin_v2_2_racon_r2	r10_1bin_v2_2_raw	r10_1bin_v2_3_MP	r10_1bin_v2_3_MP_helen	r10_1bin_v2_3_r1_medaka	r10_1bin_v2_3_r2_medaka	r10_1bin_v2_3_racon_r1	r10_1bin_v2_3_racon_r2	r10_1bin_v2_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	22082588	22081257	22083968	22083903	22078526	22078691	22110892	22081954	22079236	22085585	22084165	22079813	22079475	22107683	22081711	22079681	22083431	22084583	22080859	22078889	22113481
# N's	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

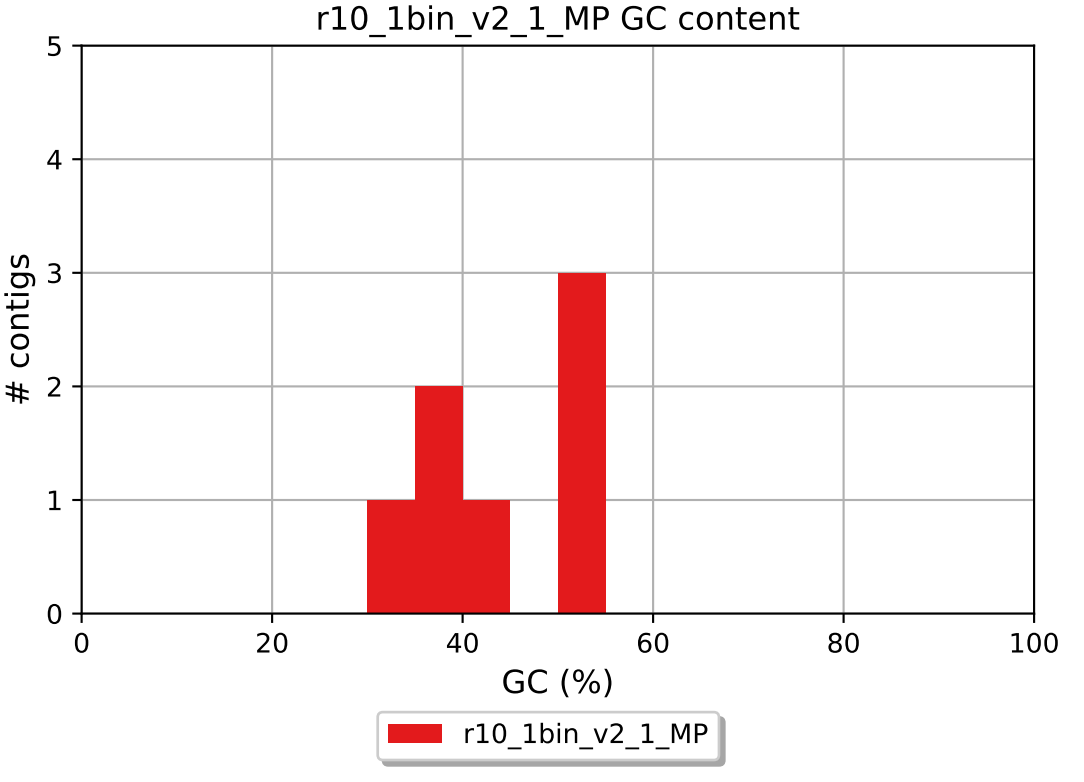
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

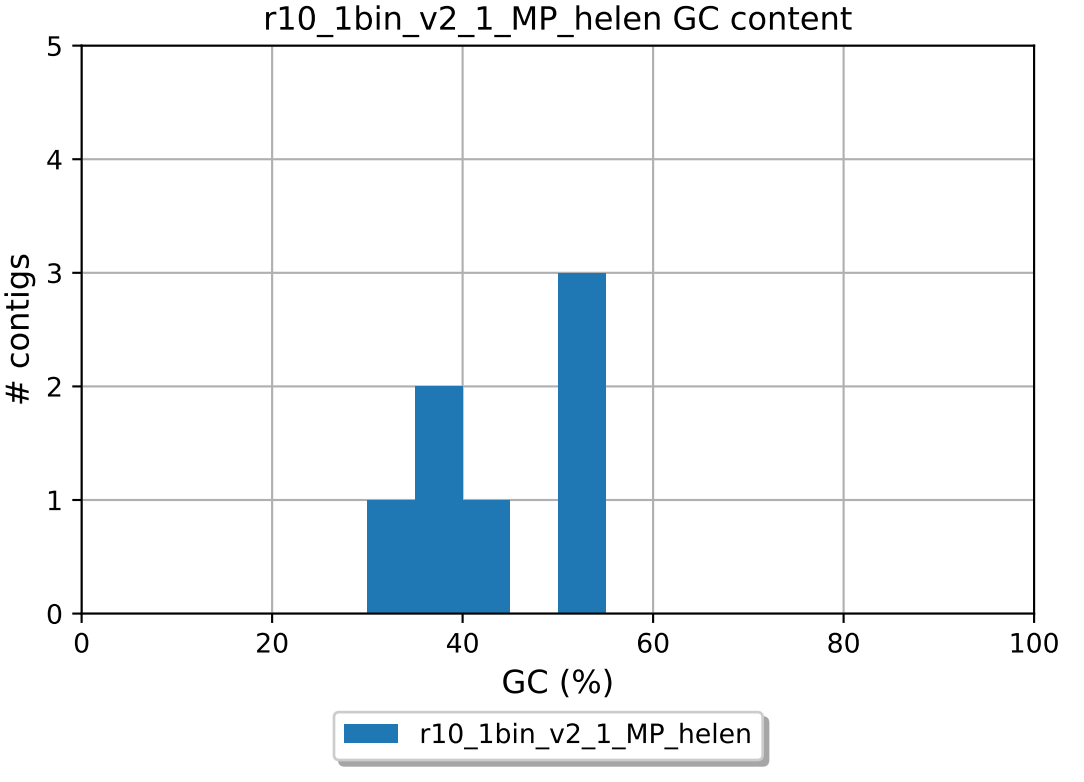

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

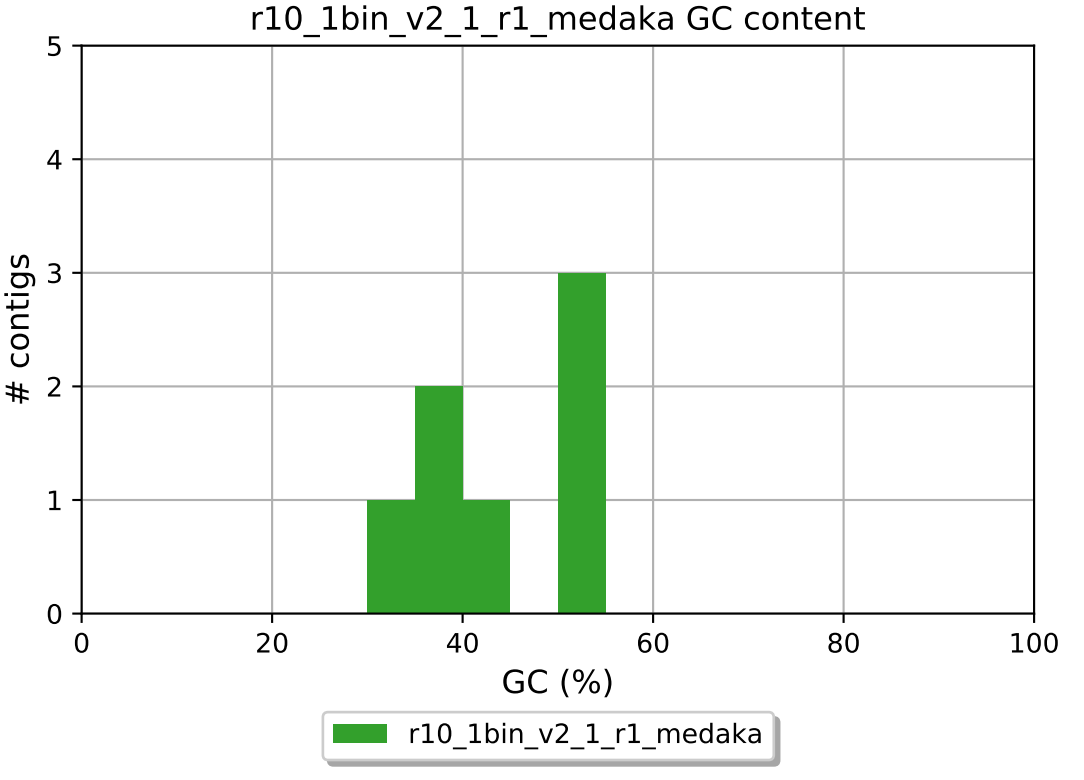

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m

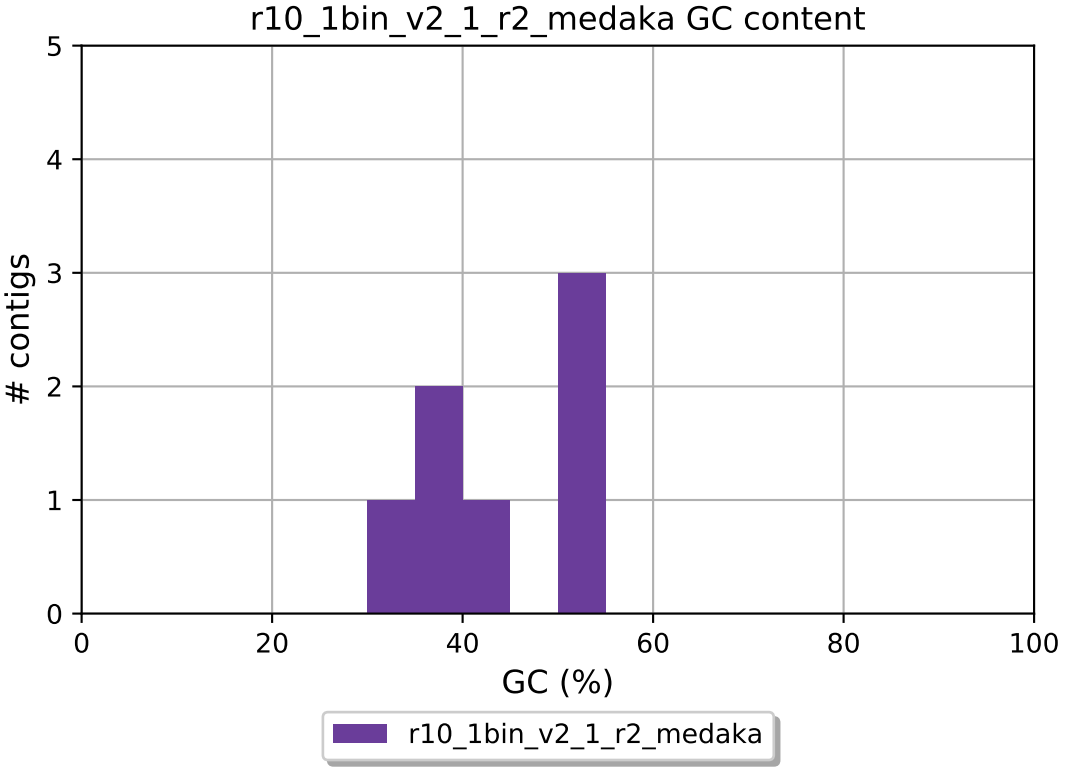

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
15
30
45
60
75
Contig index
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

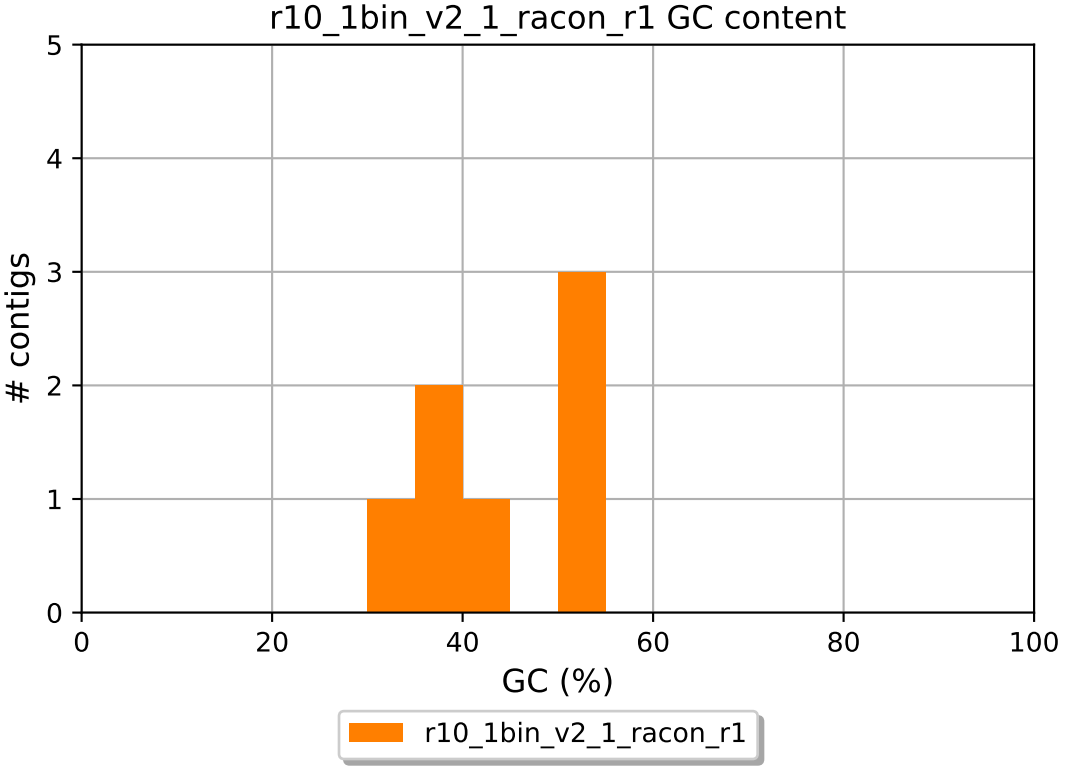

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m

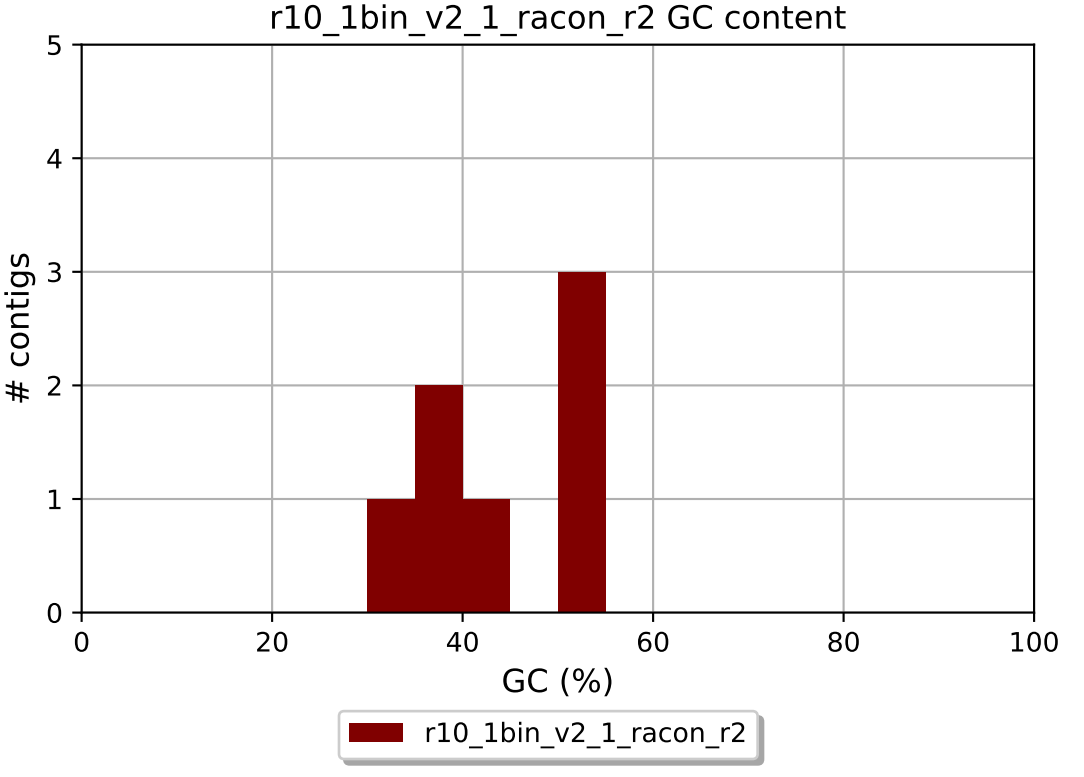

r10_1bin_v2_1_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP

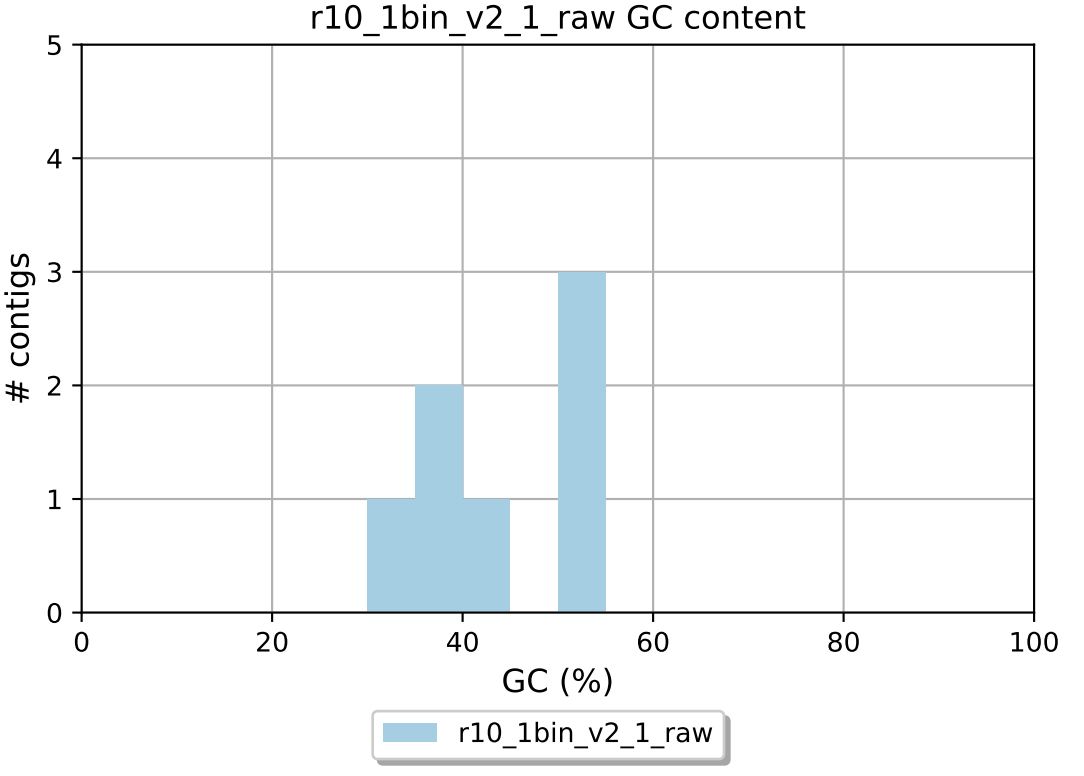

r10_1bin_v2_1_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_MP_helen

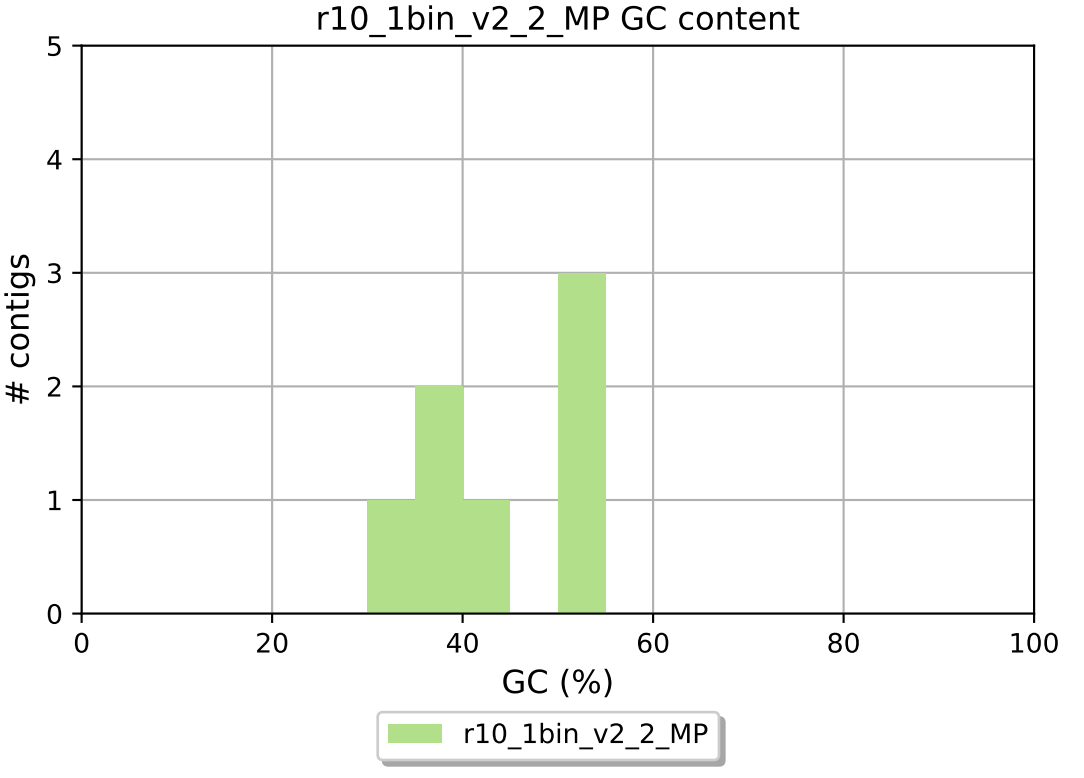

r10_1bin_v2_1_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r1_medaka

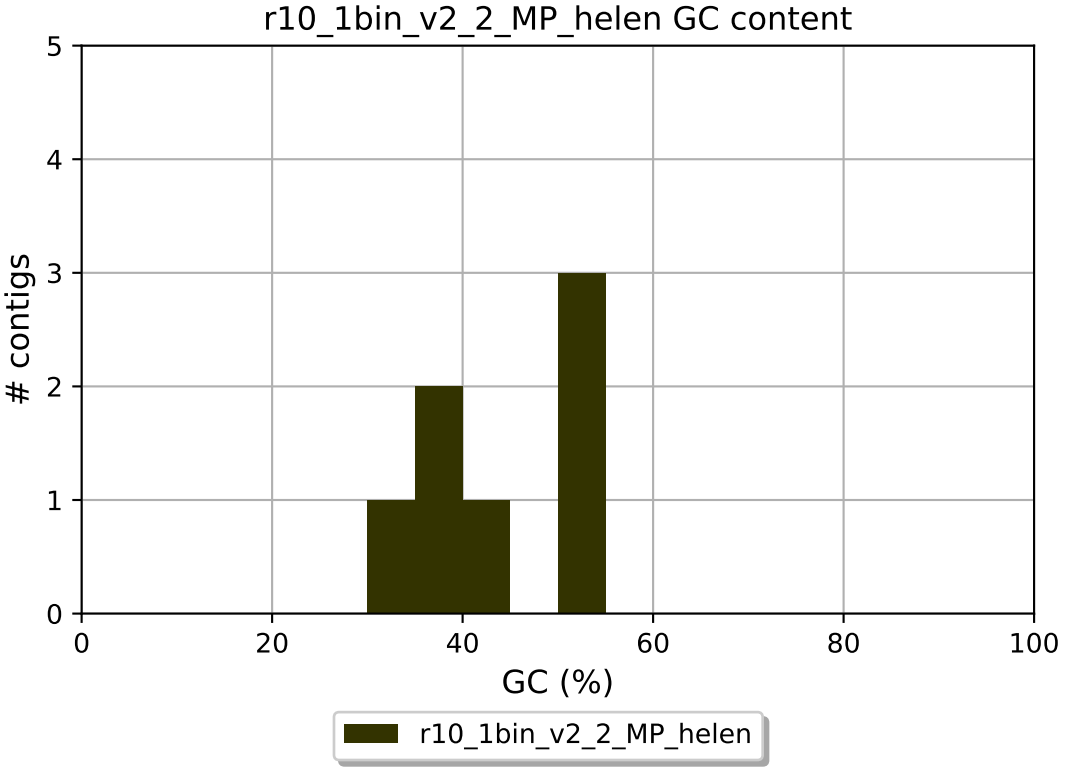

r10_1bin_v2_1_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_r2_medaka

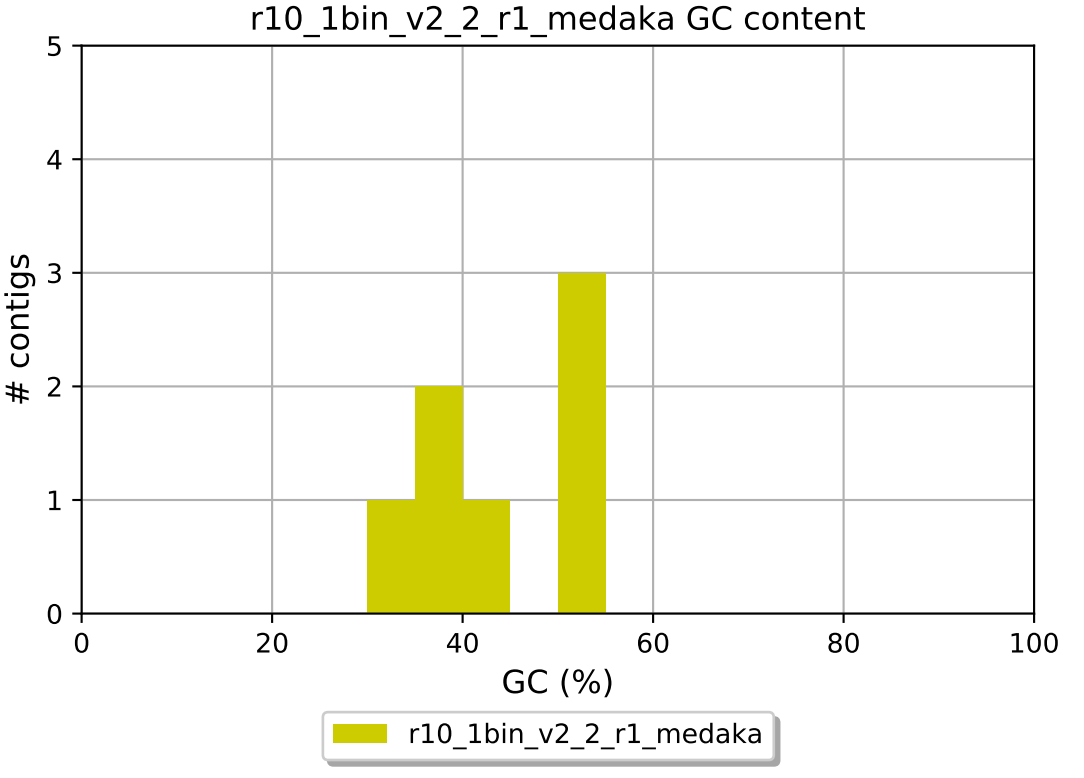

r10_1bin_v2_1_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r1

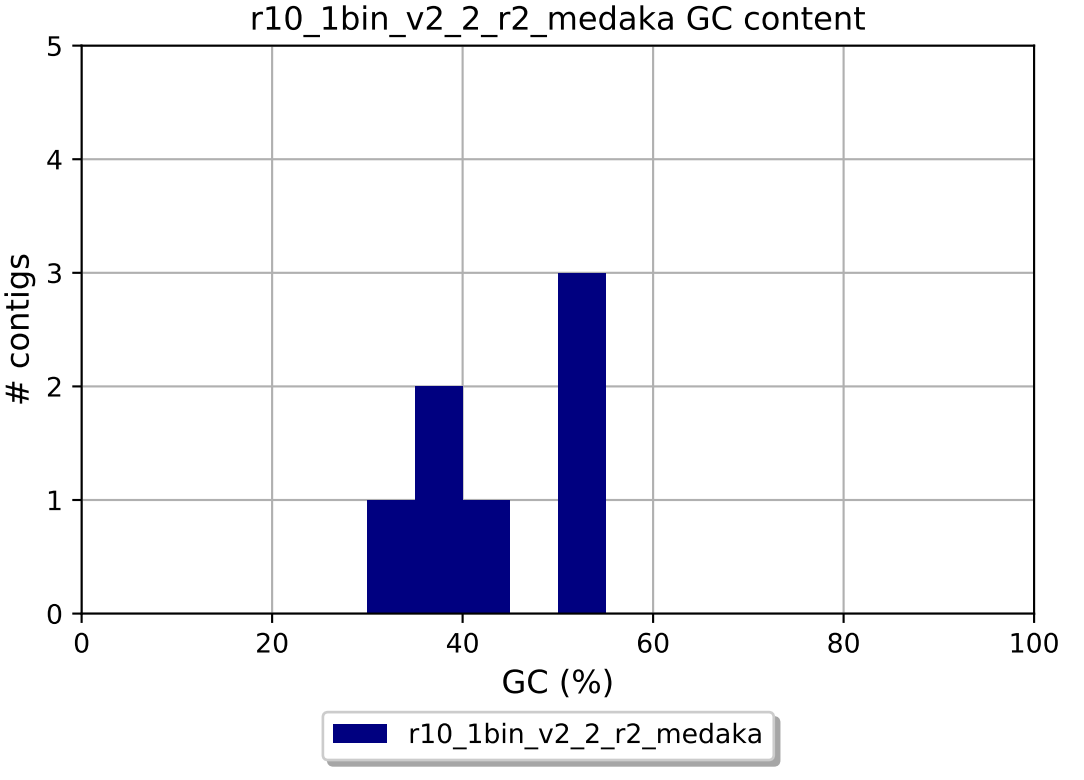

r10_1bin_v2_1_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_racon_r2

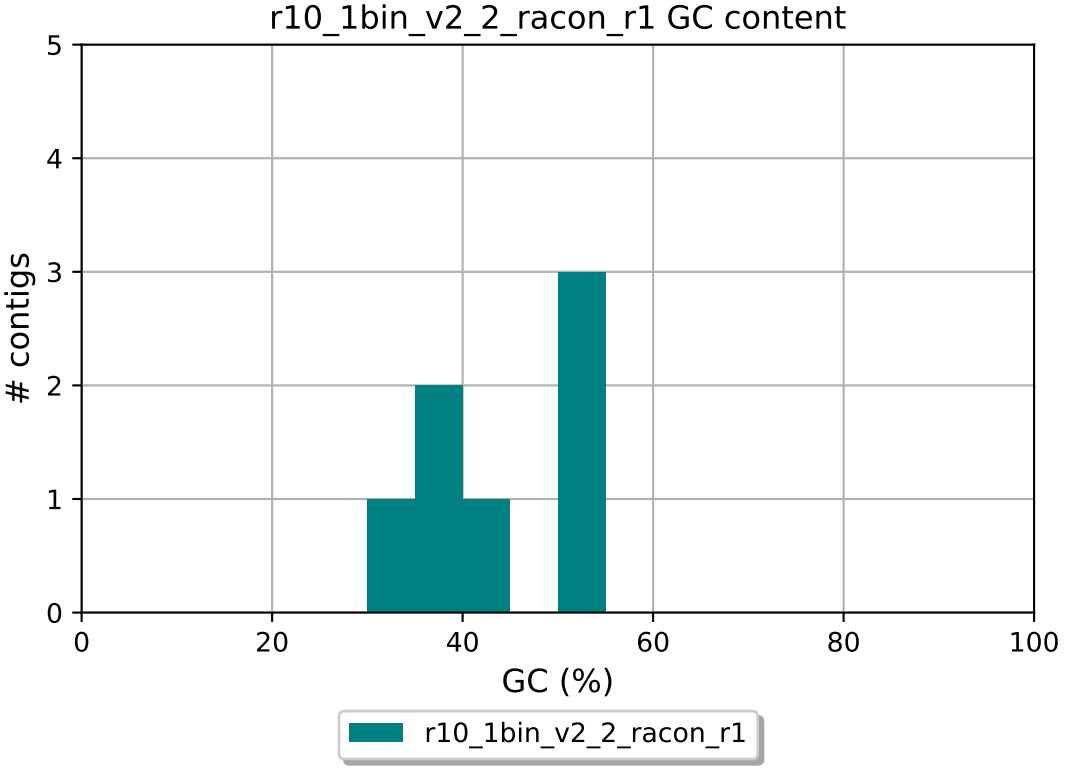

r10_1bin_v2_1_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_1_raw

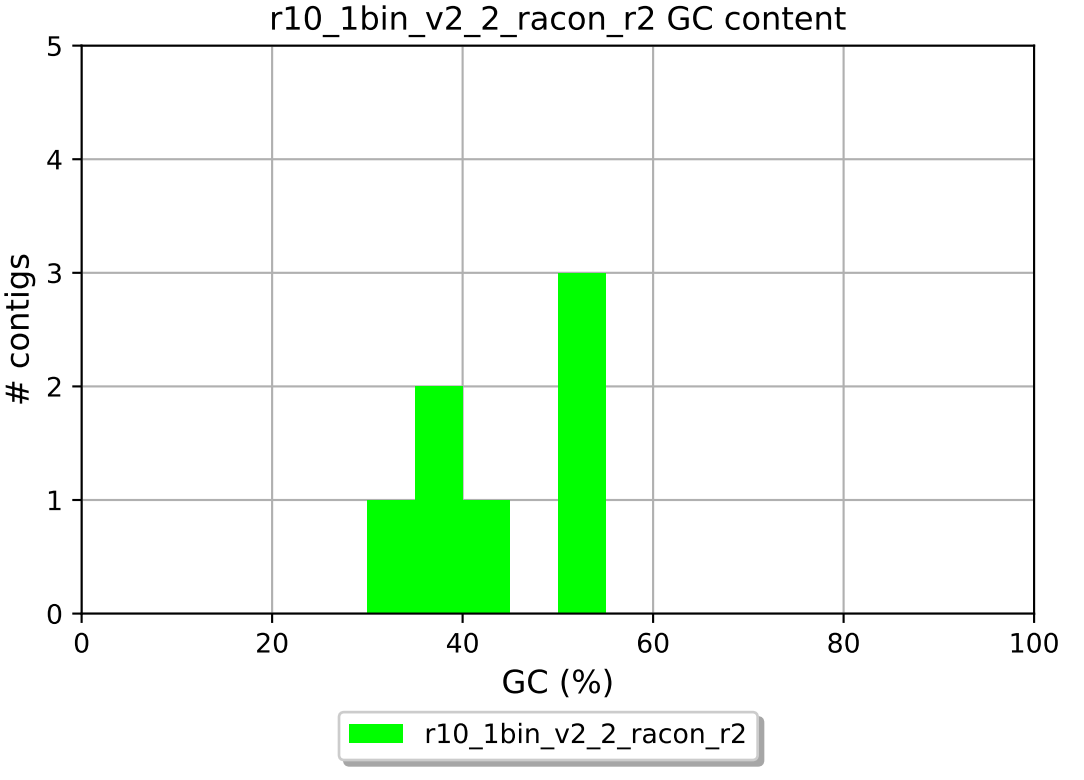

r10_1bin_v2_2_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP

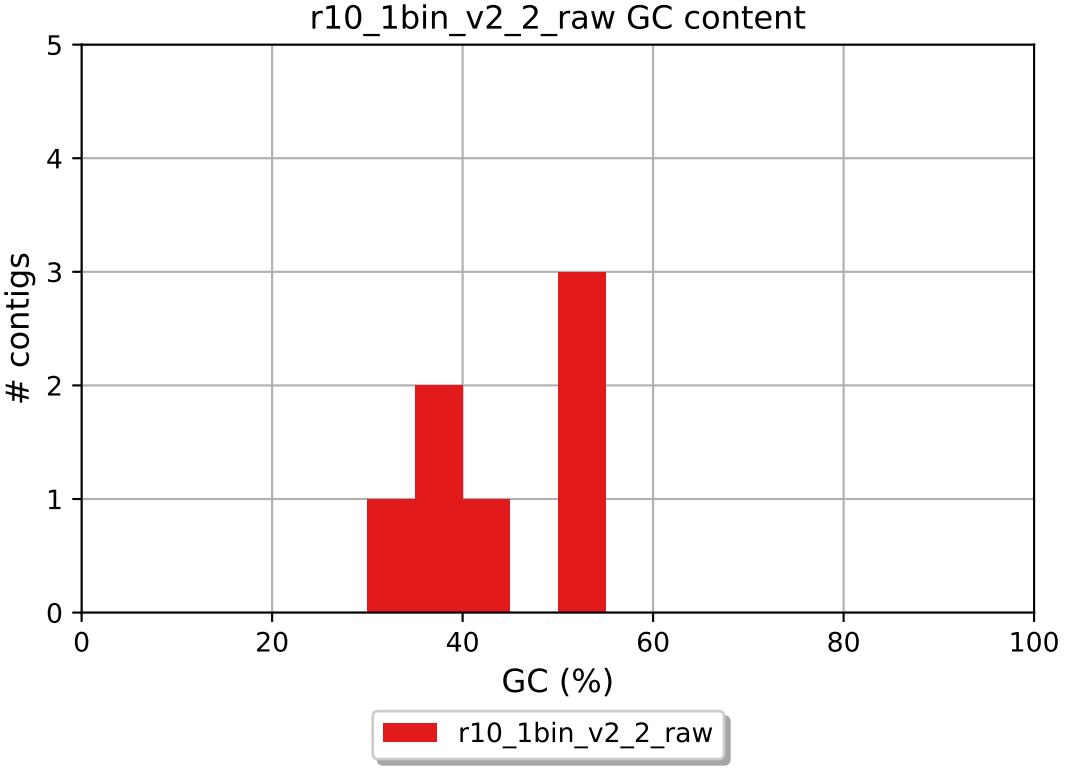

r10_1bin_v2_2_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_MP_helen

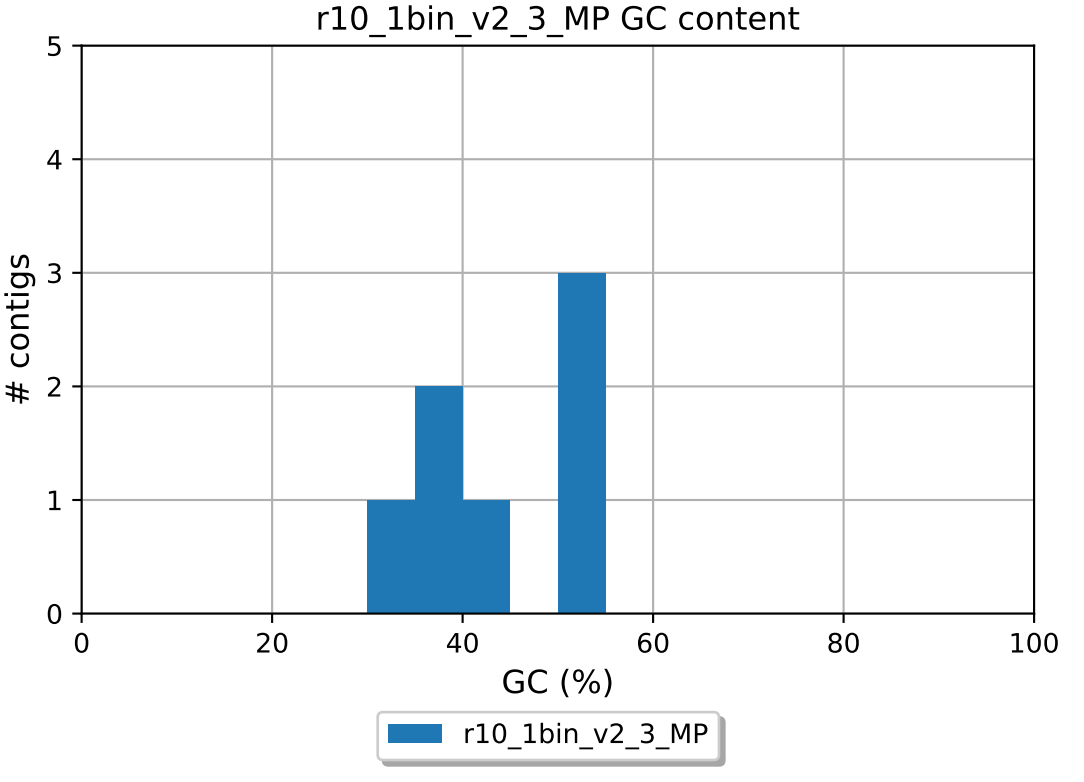

r10_1bin_v2_2_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r1_medaka

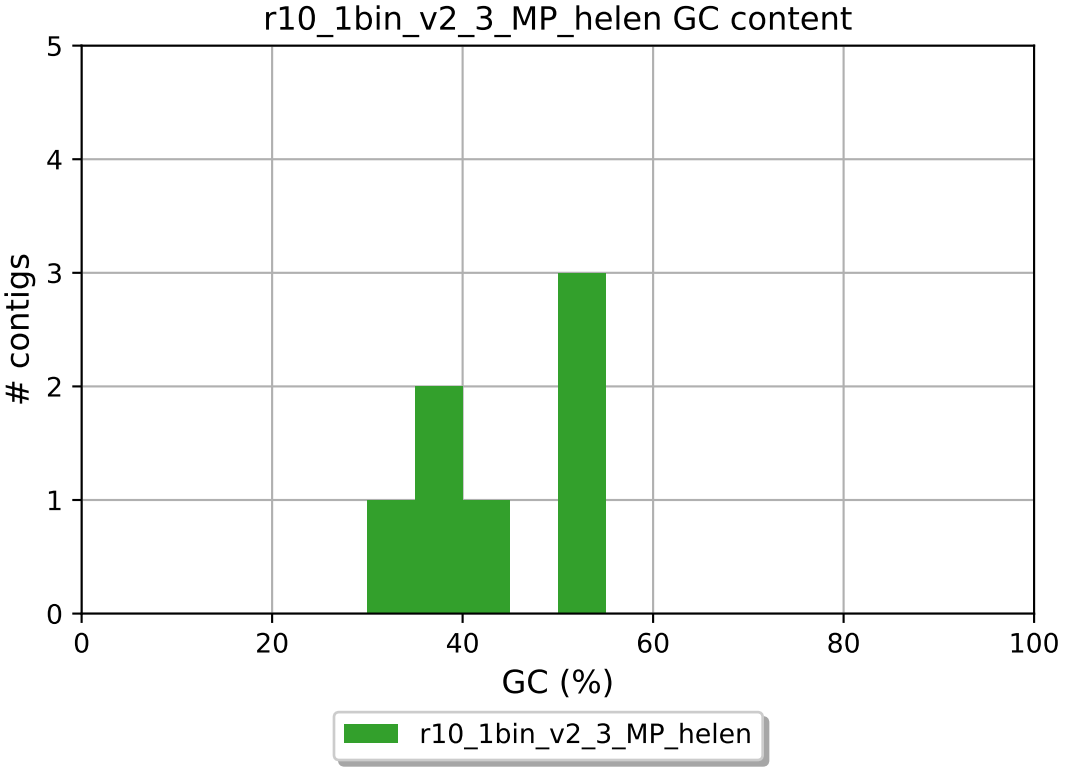

r10_1bin_v2_2_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_r2_medaka

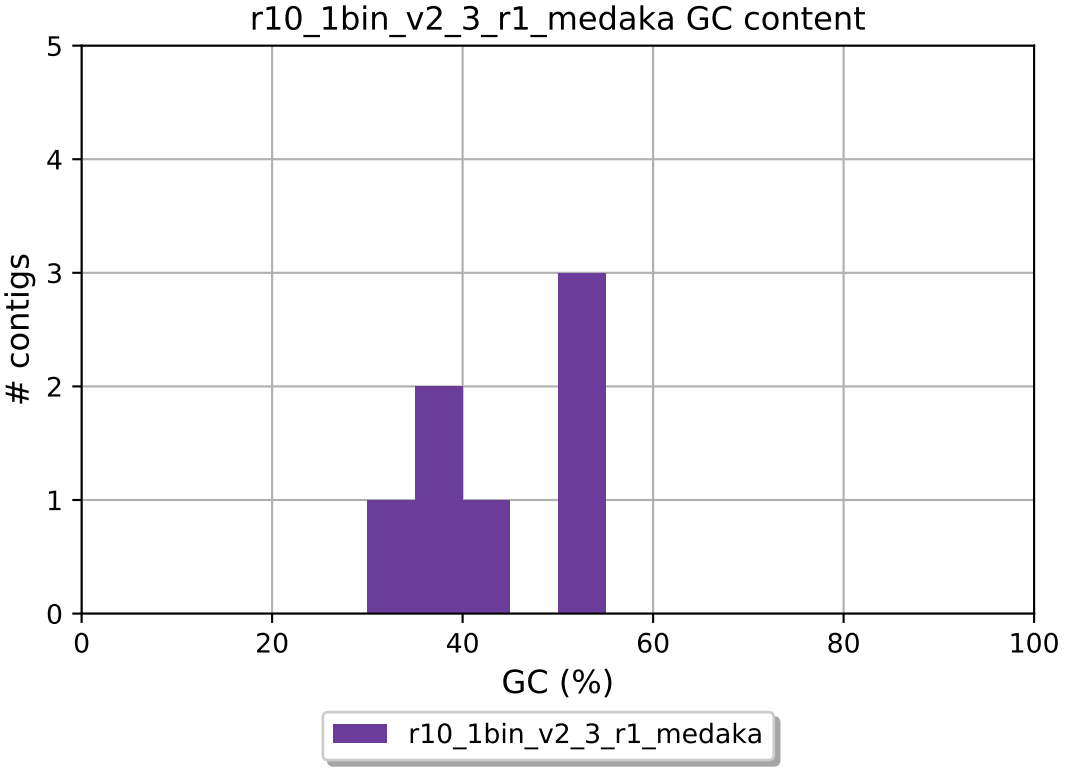

r10_1bin_v2_2_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r1

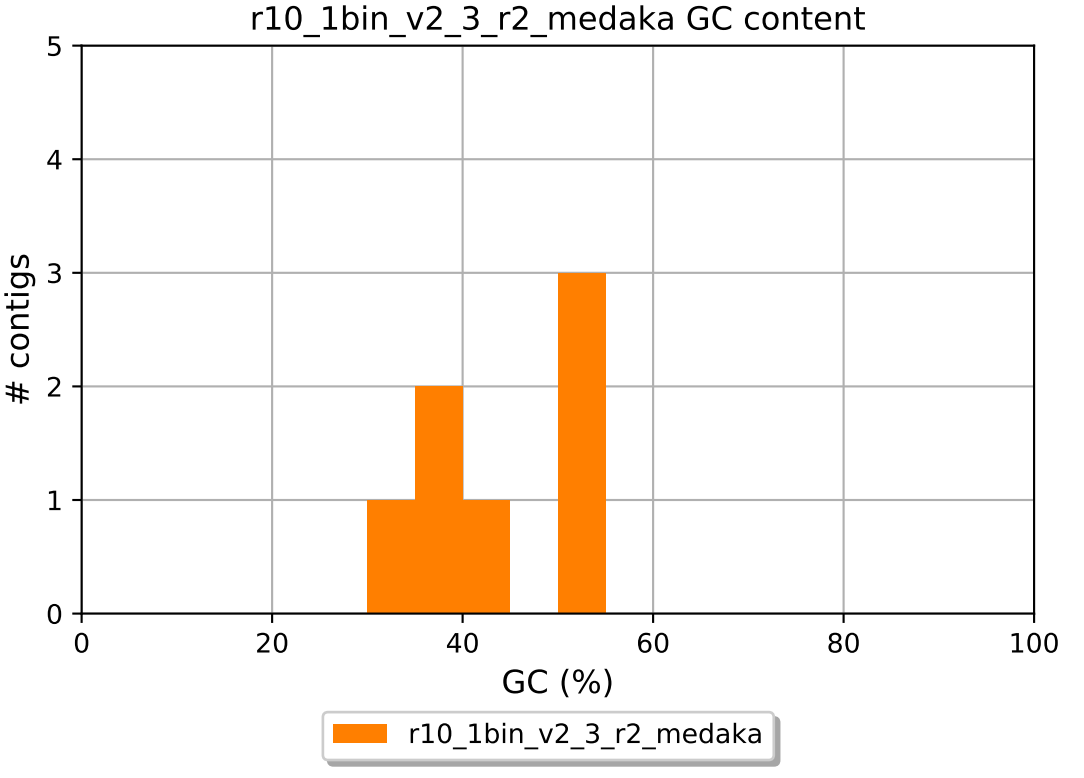

r10_1bin_v2_2_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_racon_r2

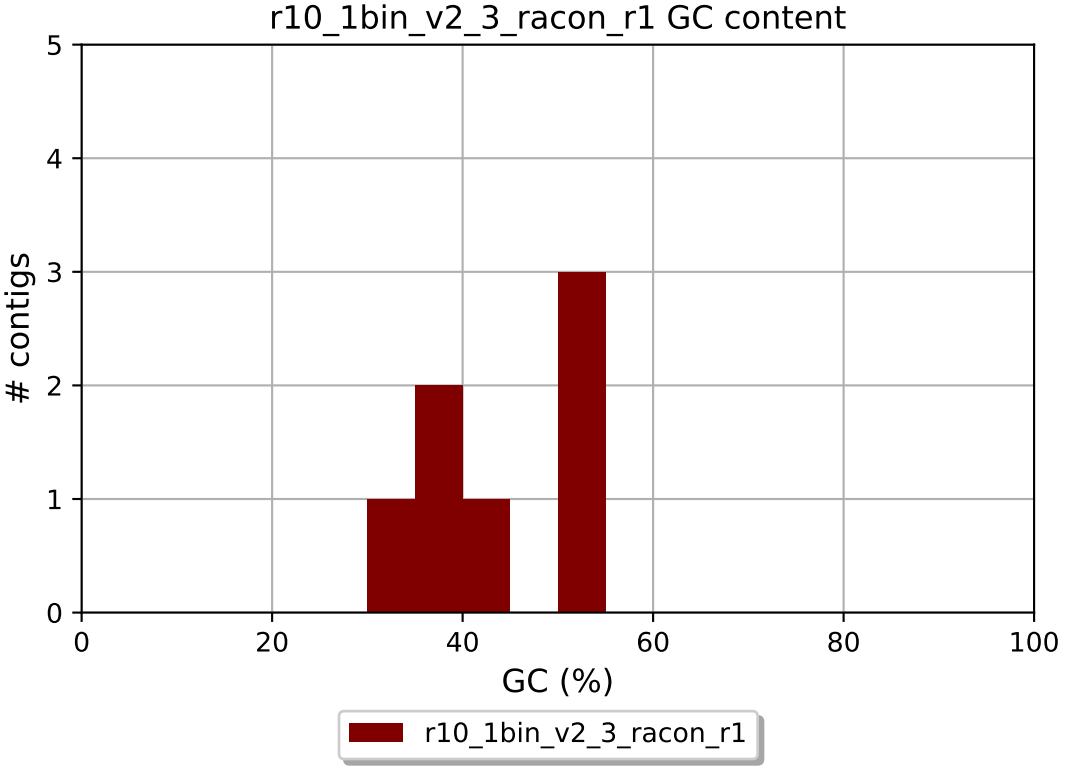

r10_1bin_v2_2_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_2_raw

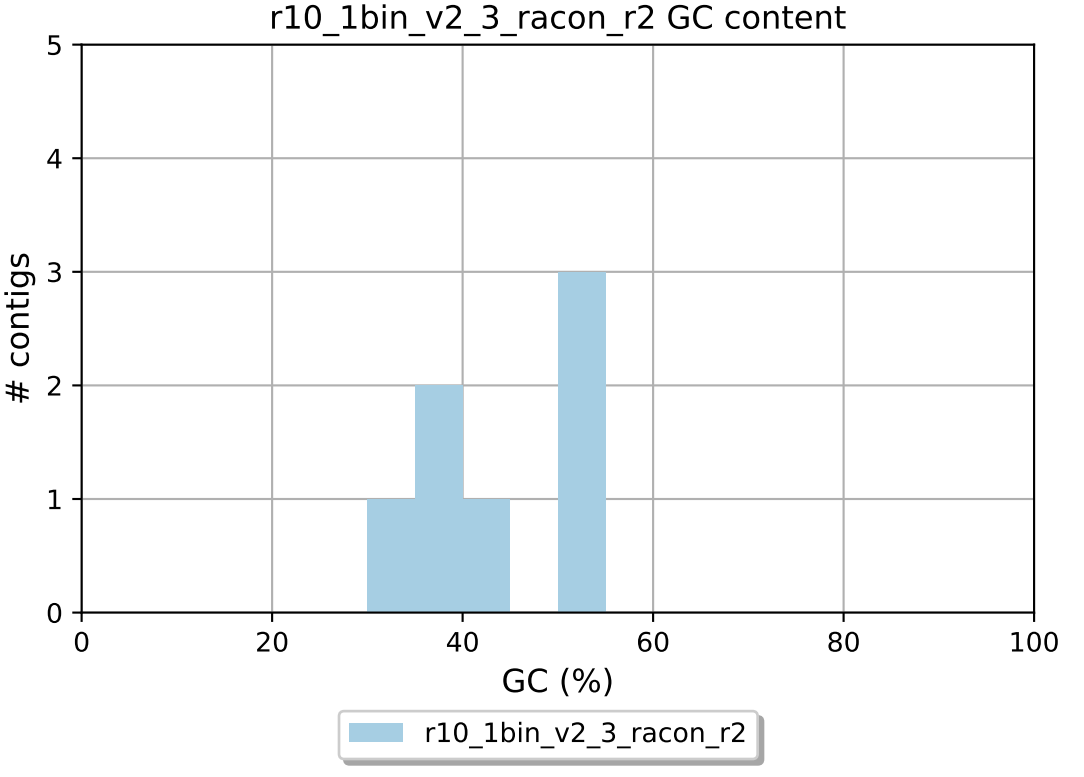

r10_1bin_v2_3_MP GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP

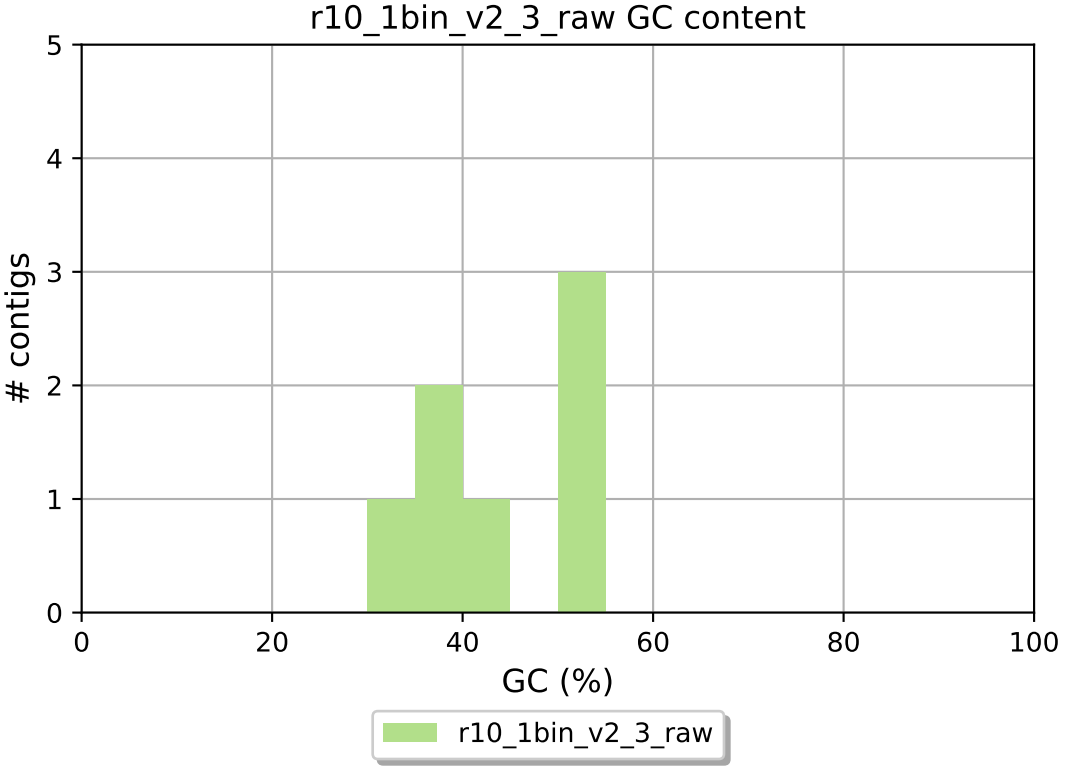

r10_1bin_v2_3_MP_helen GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_MP_helen

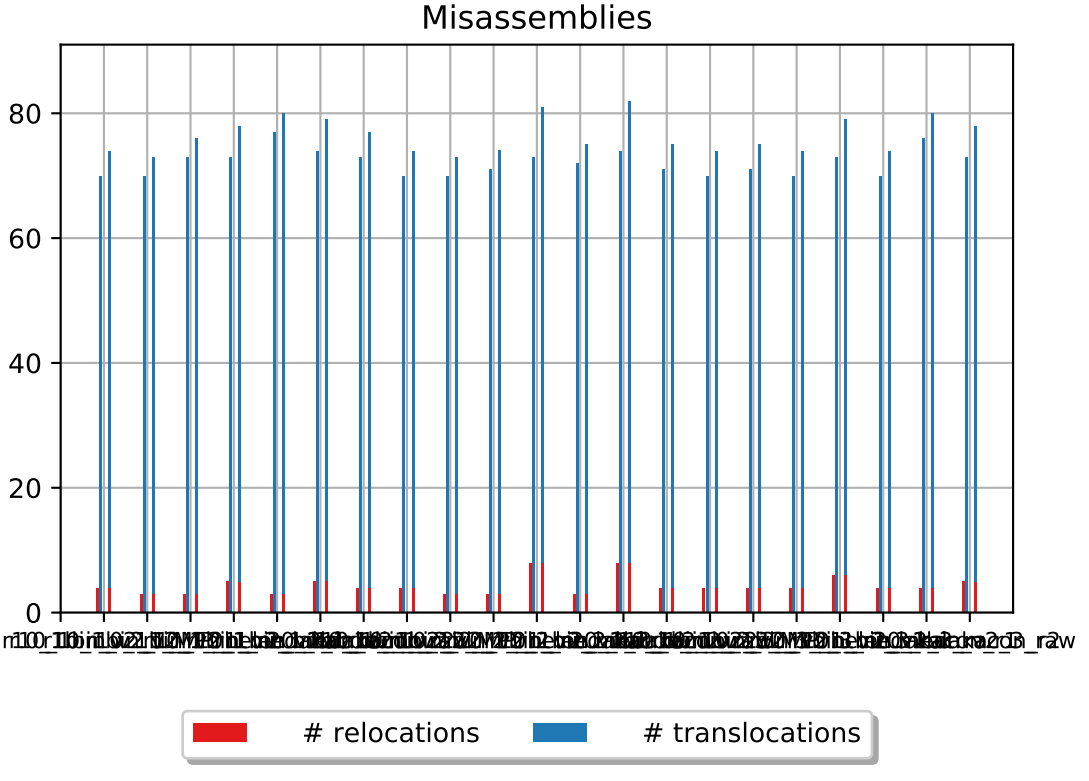

r10_1bin_v2_3_r1_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r1_medaka

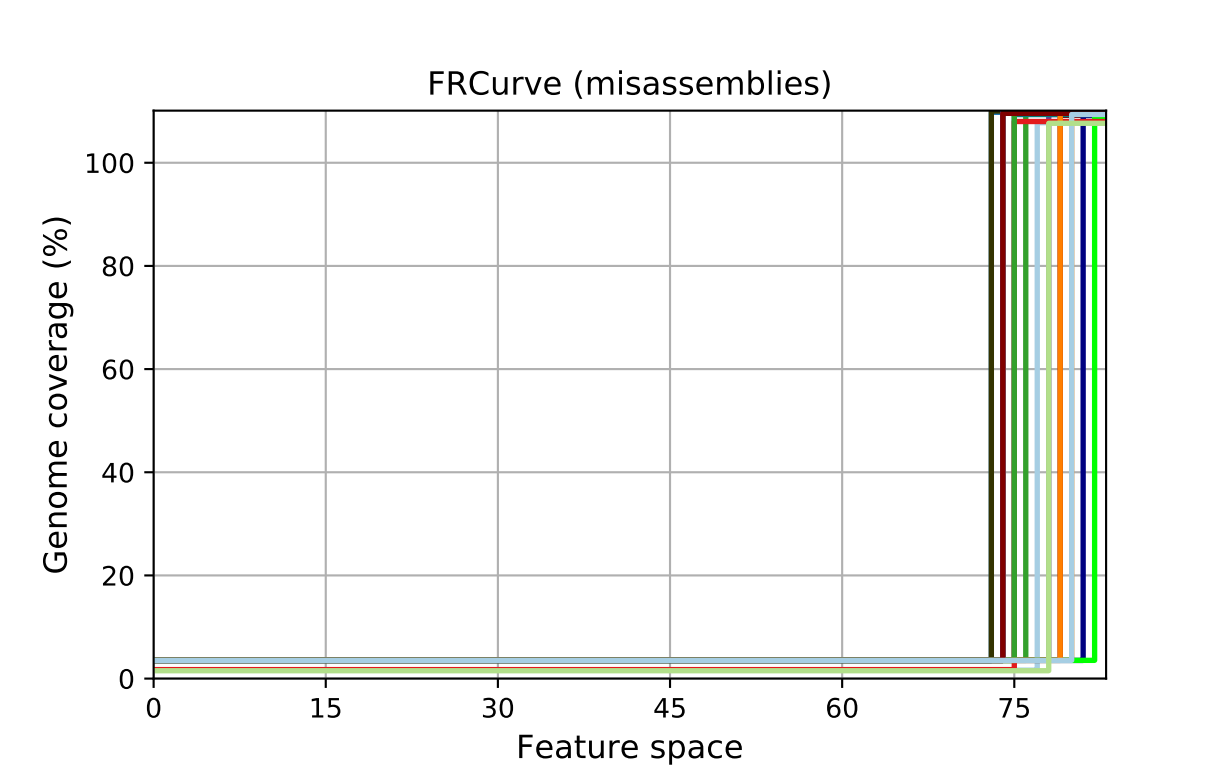

r10_1bin_v2_3_r2_medaka GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_r2_medaka

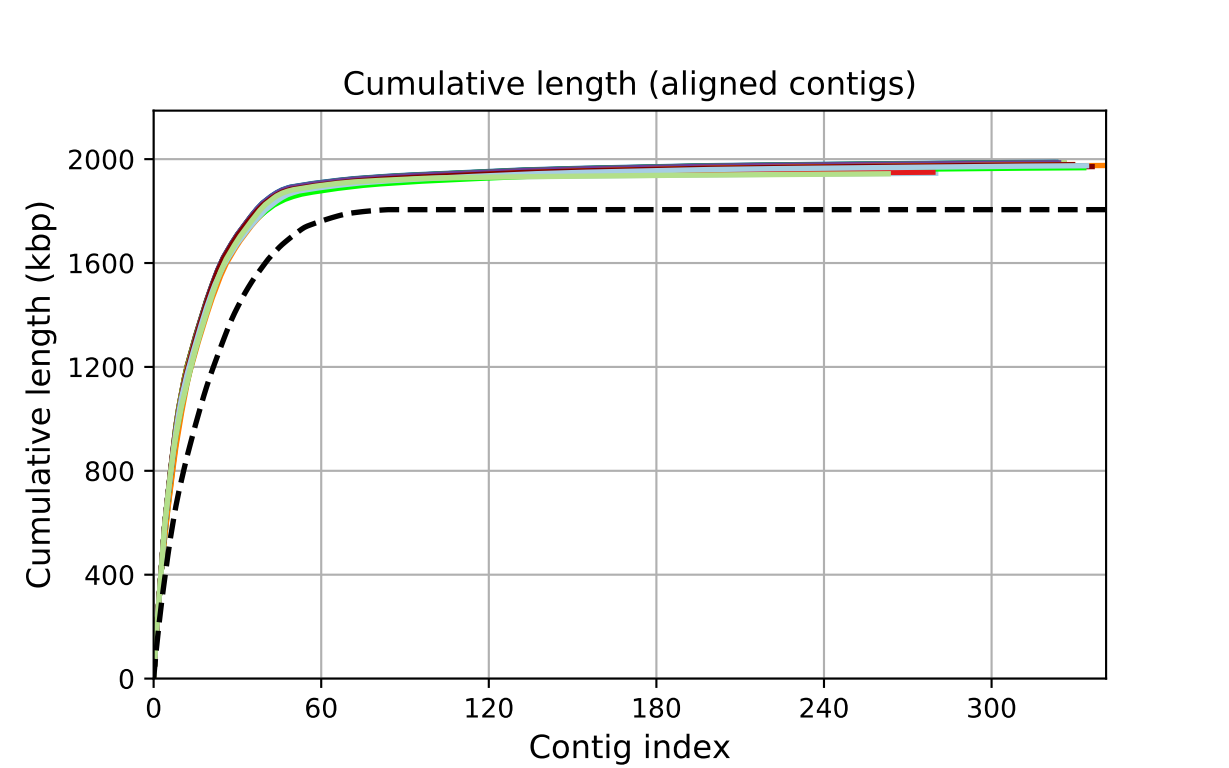

r10_1bin_v2_3_racon_r1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r1

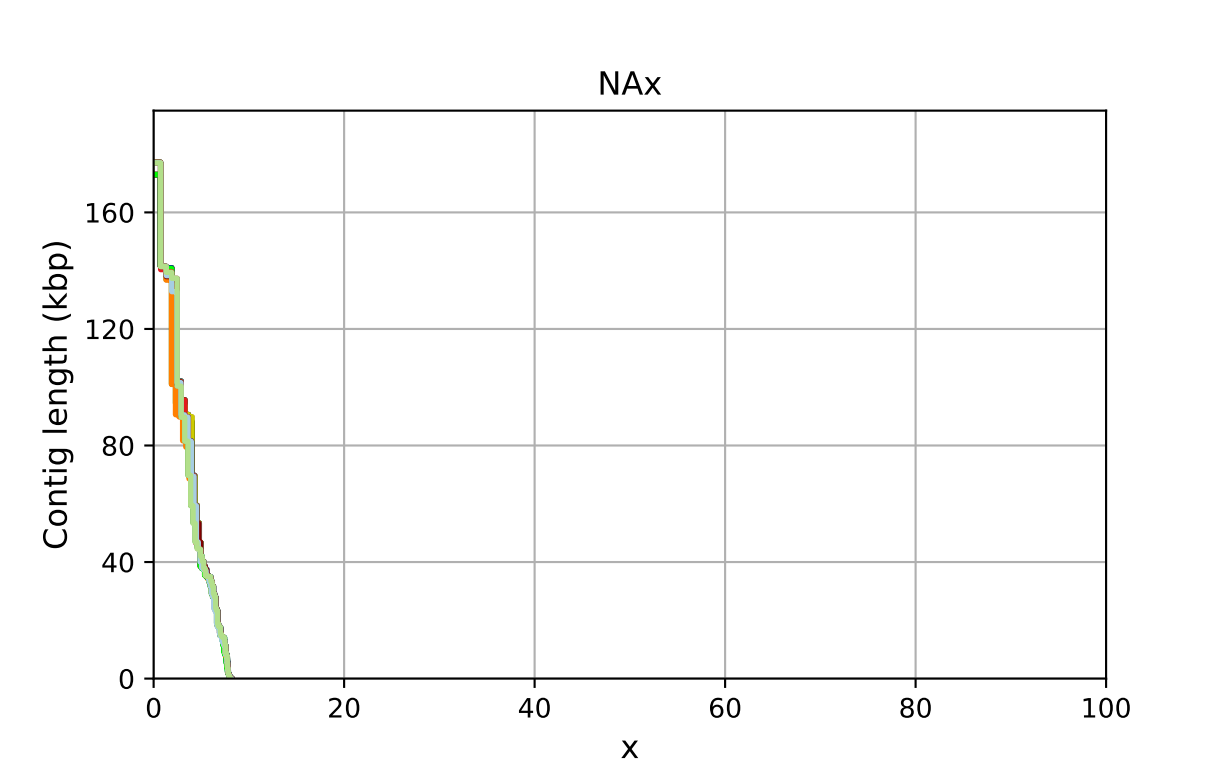

r10_1bin_v2_3_racon_r2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_racon_r2

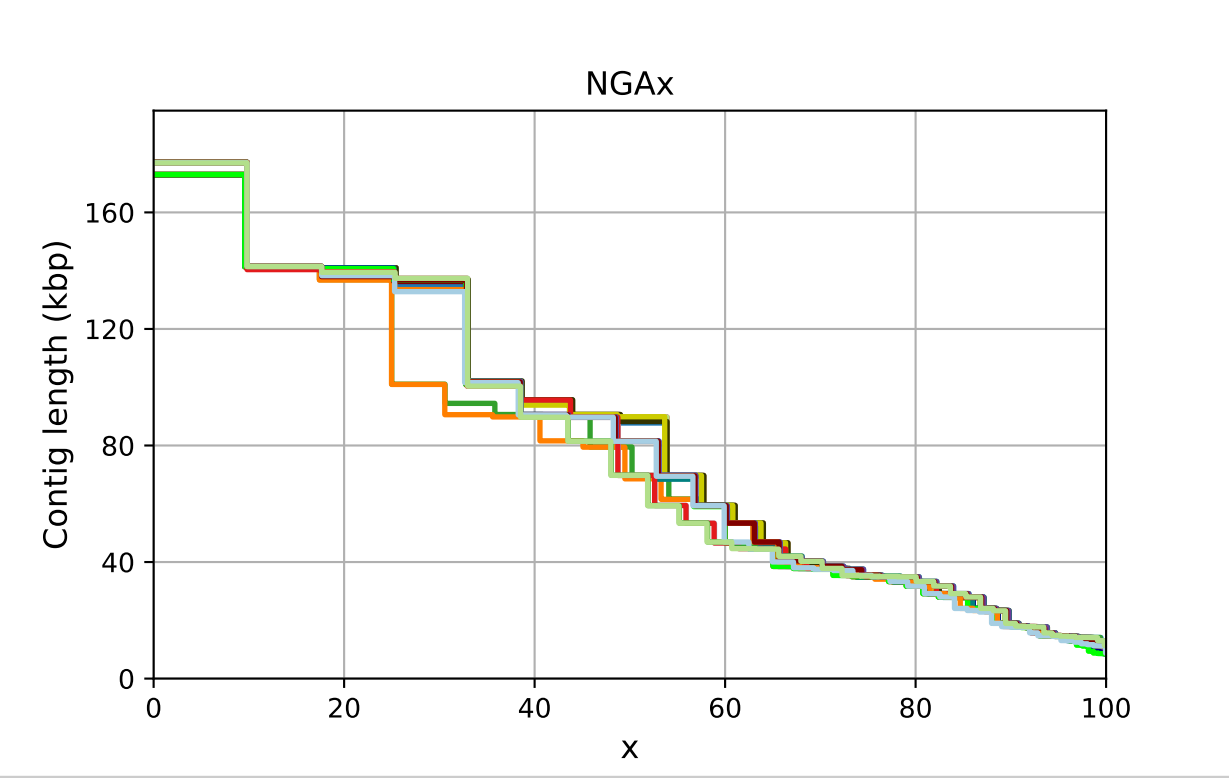

r10_1bin_v2_3_raw GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r10_1bin_v2_3_raw

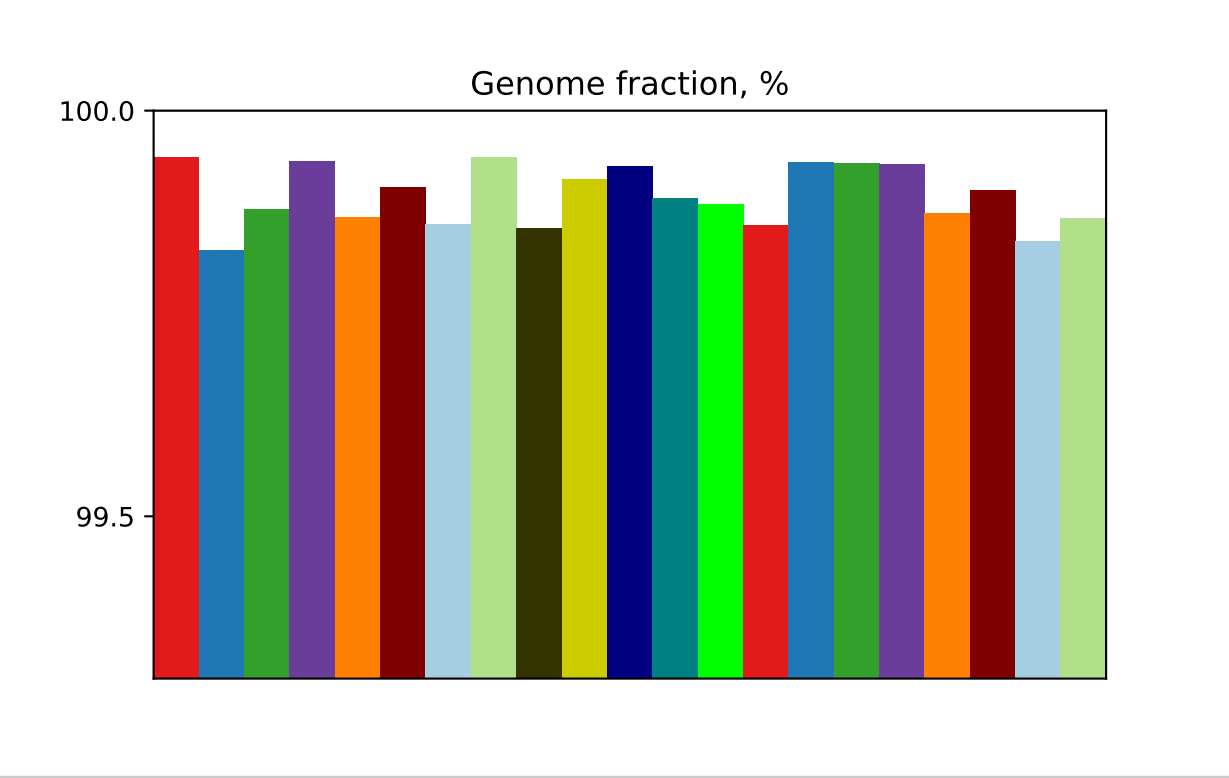

Misassemblies
80
60
40
20
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
Feature space
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
60
120
180
240
300
Contig index
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_2_r2_medaka
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m
r10_1bin_v2_3_r2_m


NAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m


NGAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m


Genome fraction, %
100.0
99.5
r10_1bin_v2_1_MP
r10_1bin_v2_1_MP_helen
r10_1bin_v2_1_r1_medaka
r10_1bin_v2_2_MP
r10_1bin_v2_2_MP_helen
r10_1bin_v2_2_r1_medaka
r10_1bin_v2_3_MP
r10_1bin_v2_3_MP_h
r10_1bin_v2_3_r1_m