Report

	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# 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)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 10000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 25000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Total length (>= 50000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
Total length	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	24062559	24061175	24061500
Reference length	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517	1805517
GC (%)	44.81	44.80	44.81	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.80	44.79	44.79	44.79	44.79	44.78	44.79	44.77	44.77	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	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4043031	4042943	4042477
NG50	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
N75	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2843358	2843843	2843366
NG75	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	4763429	4763874	4763424
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	75	73	75	74	74	74	74	76	74	74	82	75	74	76	74	77	83	79	76	75	76
# 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	1947899	1945703	1947905	1948632	1947378	1948619	1948337	1945464	1948309	1942334	1933725	1945619	1938546	1934980	1939919	1935799	1927743	1936941	1947584	1945502	1947491
# local misassemblies	12	14	13	11	11	11	23	29	18	27	25	25	45	43	42	34	39	33	28	29	28
# 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	22079400	22080830	22079301	22082014	22083090	22082058	22083303	22085751	22082523	22083679	22085454	22083524	22080962	22080072	22079956	22079750	22078655	22079212	22108393	22106210	22104512
Genome fraction (%)	99.934	99.858	99.934	99.943	99.943	99.943	99.926	99.928	99.934	99.922	99.870	99.886	99.908	99.913	99.902	99.901	99.815	99.845	99.869	99.861	99.867
Duplication ratio	1.105	1.104	1.105	1.105	1.104	1.105	1.104	1.101	1.104	1.100	1.095	1.103	1.099	1.098	1.101	1.099	1.096	1.100	1.084	1.084	1.085
# 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	263.62	265.43	263.90	263.37	267.75	266.64	307.99	290.85	305.19	281.72	280.48	289.14	266.57	270.83	270.63	270.19	269.54	264.74	372.17	373.09	382.94
# indels per 100 kbp	11.92	10.54	12.08	12.08	11.75	11.58	14.80	13.53	14.19	12.03	10.48	10.70	57.44	56.94	57.44	53.17	54.44	50.76	354.03	353.73	354.76
Largest alignment	177187	177211	177186	177188	177208	177188	177182	173119	177183	177184	177198	174104	176931	173003	176990	176969	176979	174000	176965	177003	176965
Total aligned length	1986914	1983807	1986952	1988052	1986237	1988553	1985686	1980360	1986471	1978775	1968538	1982335	1974953	1973821	1979586	1975731	1971091	1976151	1948623	1951544	1951445
NGA50	69796	88201	69794	81537	89790	81536	81506	89788	81506	81470	81428	81470	81445	89773	81445	81437	69433	81437	69751	69730	69751
NGA75	35503	35032	35504	35503	35032	35504	35504	34836	35504	35415	35033	35417	35488	34825	35488	35349	34932	35370	35172	34946	35172
LGA50	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	9	8	8	8	8
LGA75	18	17	18	17	17	17	17	17	17	17	17	17	17	17	17	17	18	17	18	18	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

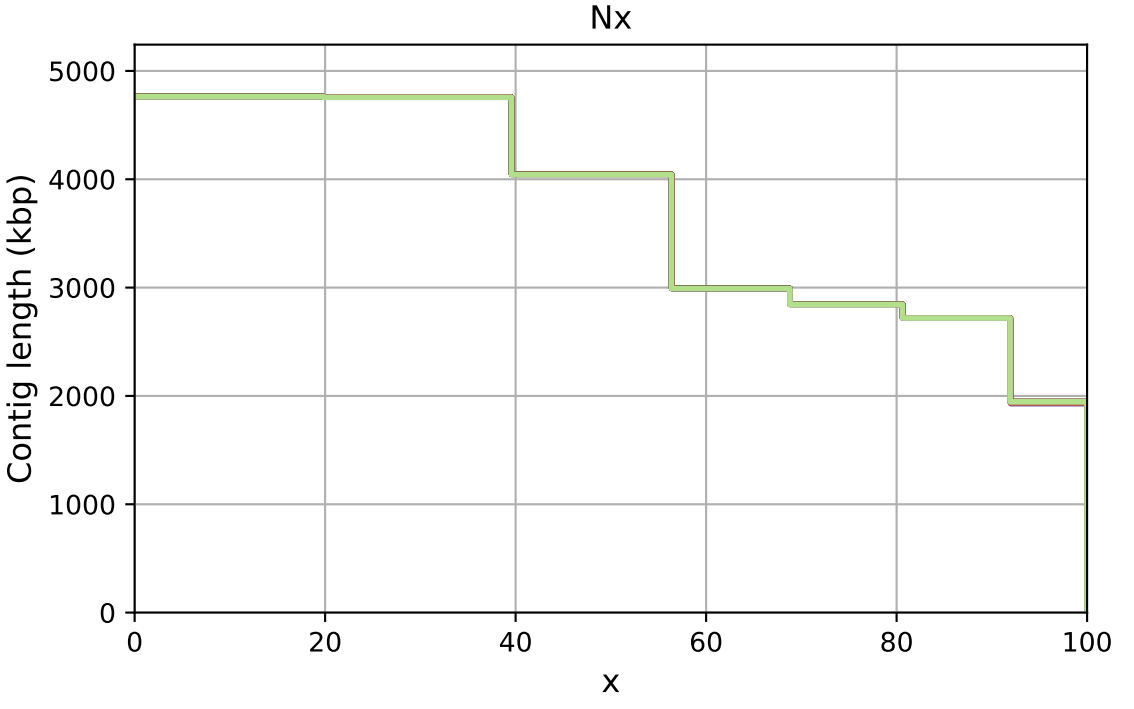
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	75	73	75	74	74	74	74	76	74	74	82	75	74	76	74	77	83	79	76	75	76
# contig misassemblies	75	73	75	74	74	74	74	76	74	74	82	75	74	76	74	77	83	79	76	75	76
# c. relocations	4	3	4	4	4	4	4	3	4	4	9	4	4	3	4	4	6	4	5	4	5
# c. translocations	71	70	71	70	70	70	70	73	70	70	73	71	70	73	70	73	77	75	71	71	71
# 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	1947899	1945703	1947905	1948632	1947378	1948619	1948337	1945464	1948309	1942334	1933725	1945619	1938546	1934980	1939919	1935799	1927743	1936941	1947584	1945502	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	36	34	34	36	34	34	32	34	34	36	38	36	34	36	32	28	30	42	42	42
# local misassemblies	12	14	13	11	11	11	23	29	18	27	25	25	45	43	42	34	39	33	28	29	28
# 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	65	66	65	66	66	66	66	64	66	66	65	66	65	62	64	62	63	63	42	41	41
# 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	4756	4785	4761	4752	4831	4811	5556	5247	5506	5082	5057	5214	4808	4885	4881	4873	4857	4772	6710	6726	6904
# indels	215	190	218	218	212	209	267	244	256	217	189	193	1036	1027	1036	959	981	915	6383	6377	6396
# indels (<= 5 bp)	167	141	170	168	163	160	218	194	204	168	140	146	961	948	959	893	913	843	6294	6275	6302
# indels (> 5 bp)	48	49	48	50	49	49	49	50	52	49	49	47	75	79	77	66	68	72	89	102	94
Indels length	2577	2704	2580	2737	2729	2717	2712	2821	2772	2731	2726	2583	5127	5171	4952	4575	4544	5007	11288	11323	11364

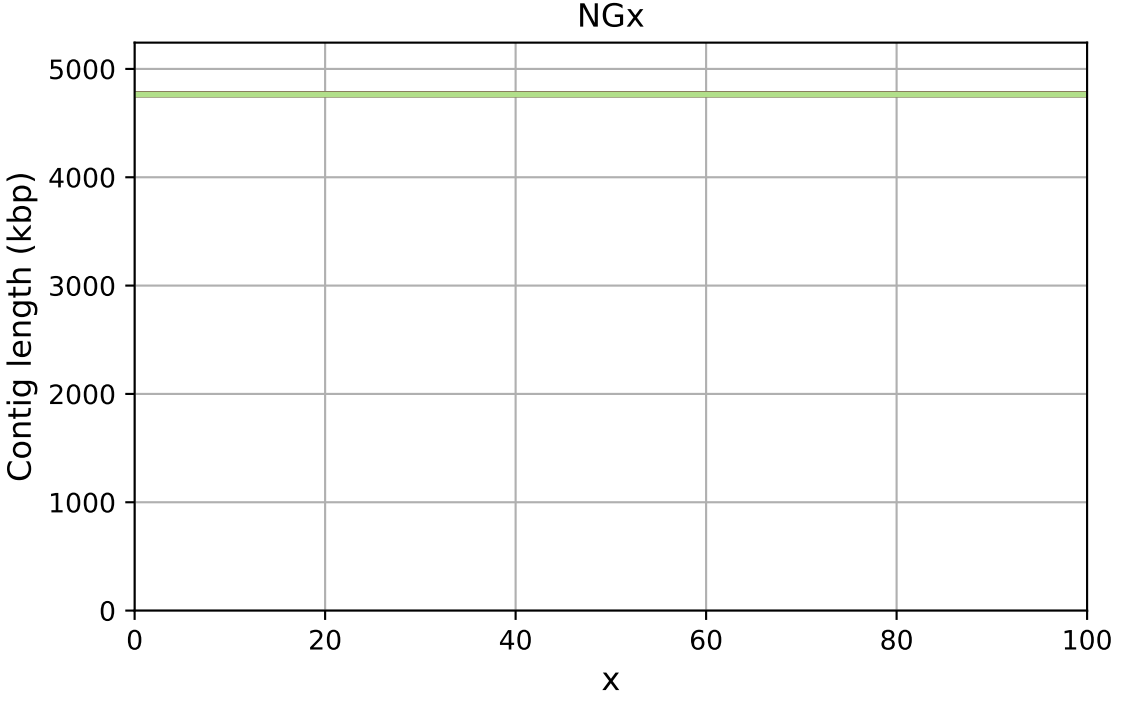
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

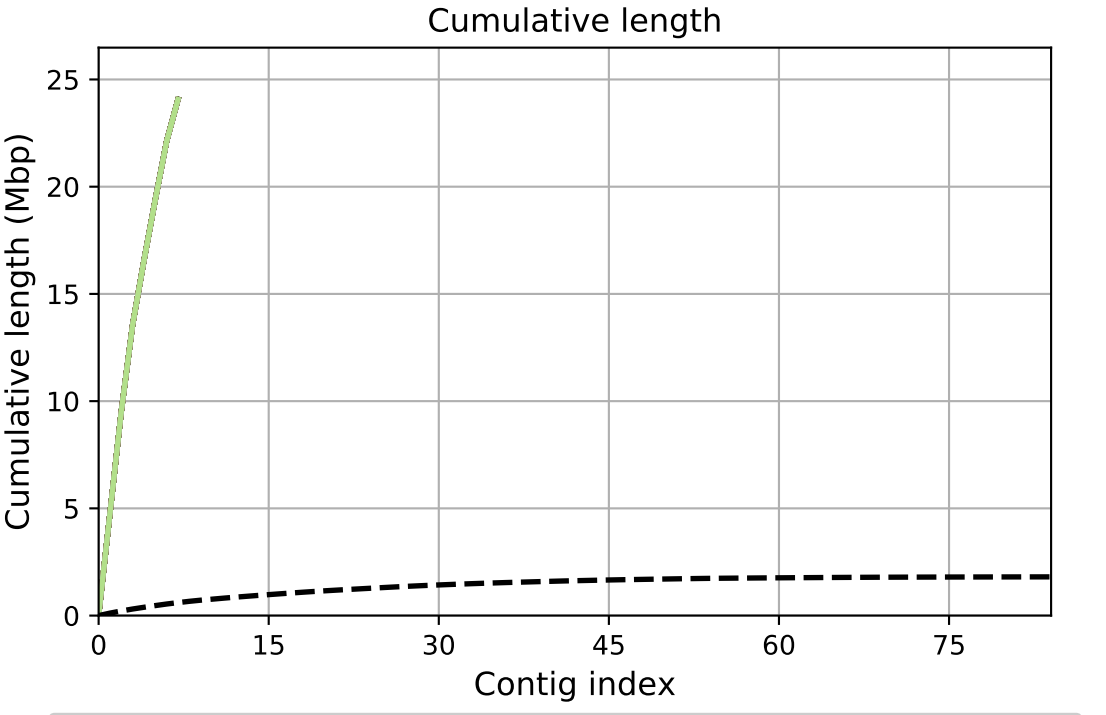
Unaligned report

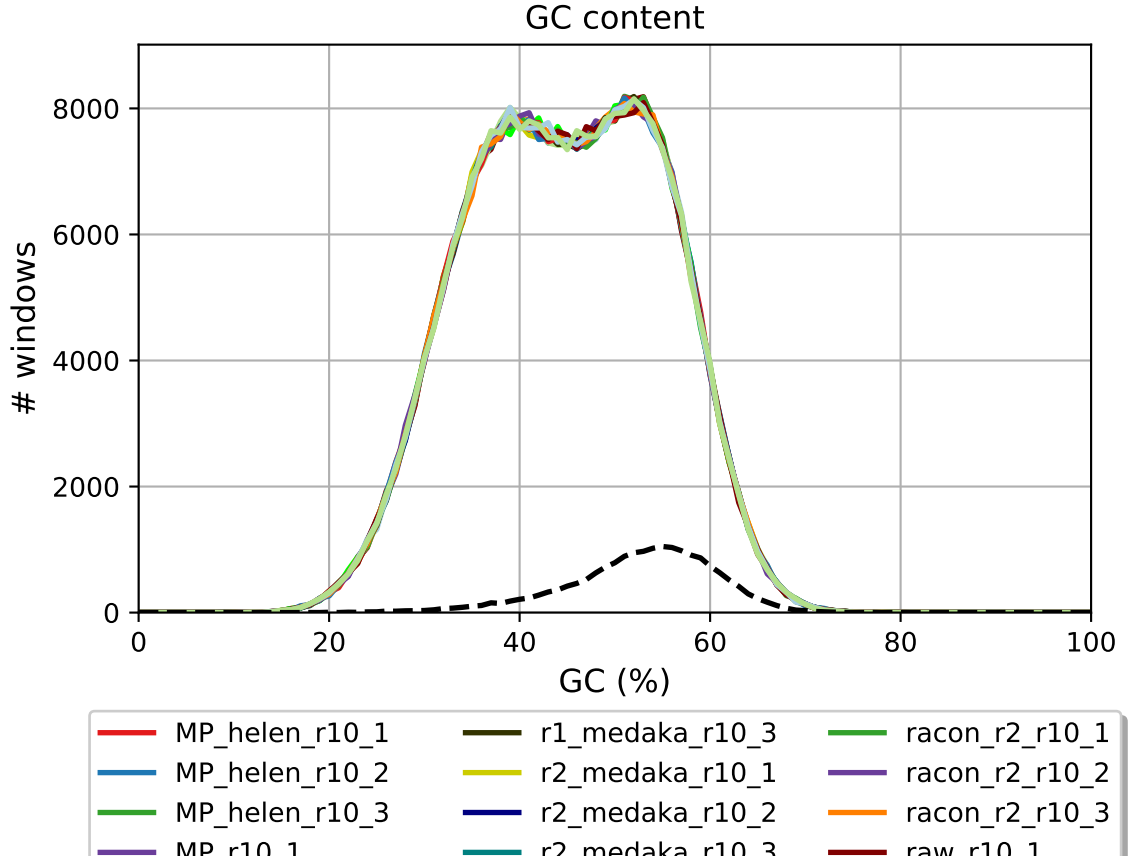
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	22079400	22080830	22079301	22082014	22083090	22082058	22083303	22085751	22082523	22083679	22085454	22083524	22080962	22080072	22079956	22079750	22078655	22079212	22108393	22106210	22104512
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

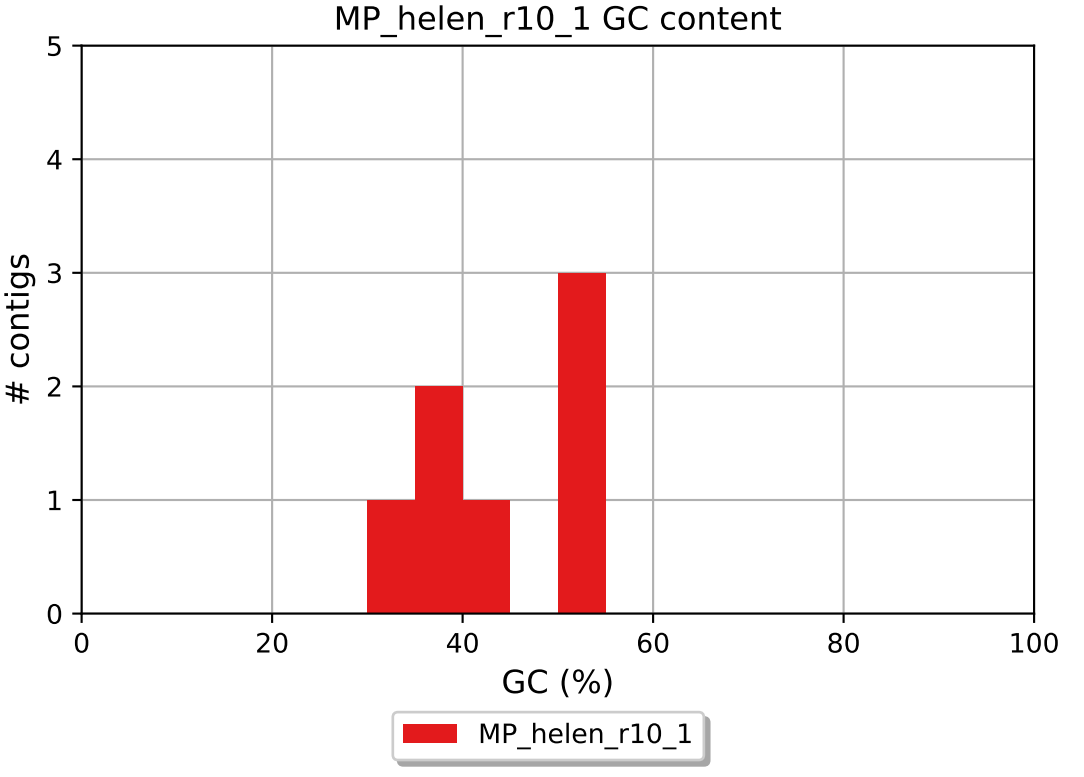
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

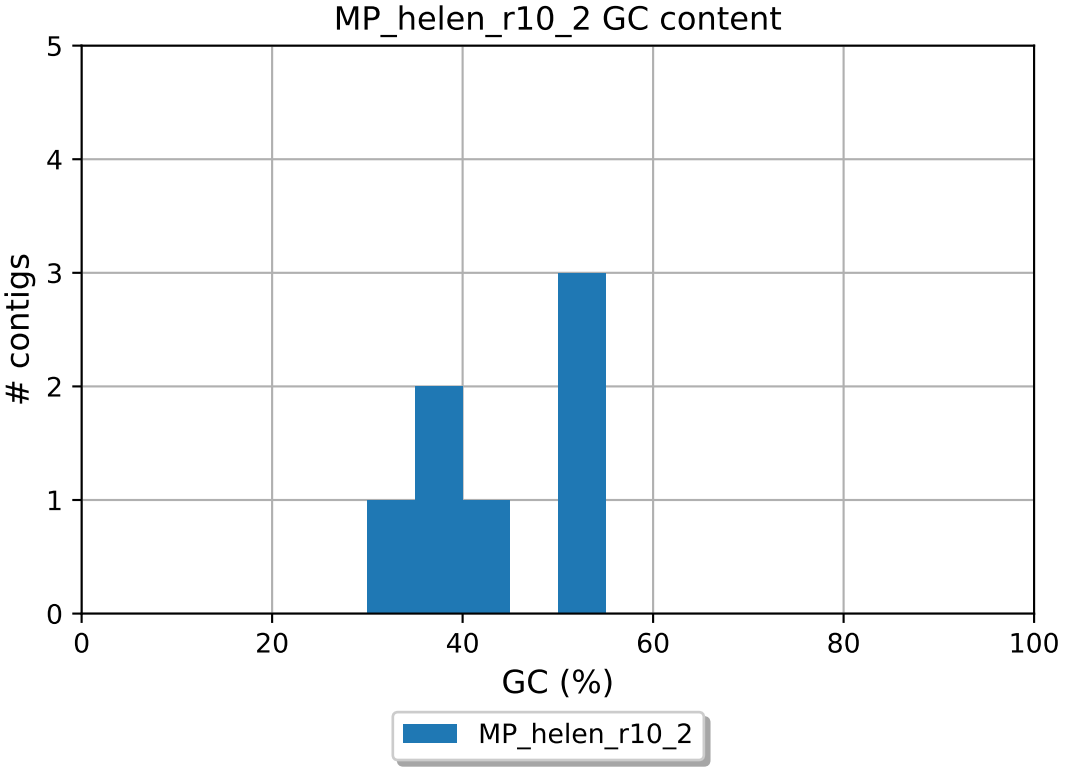

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3

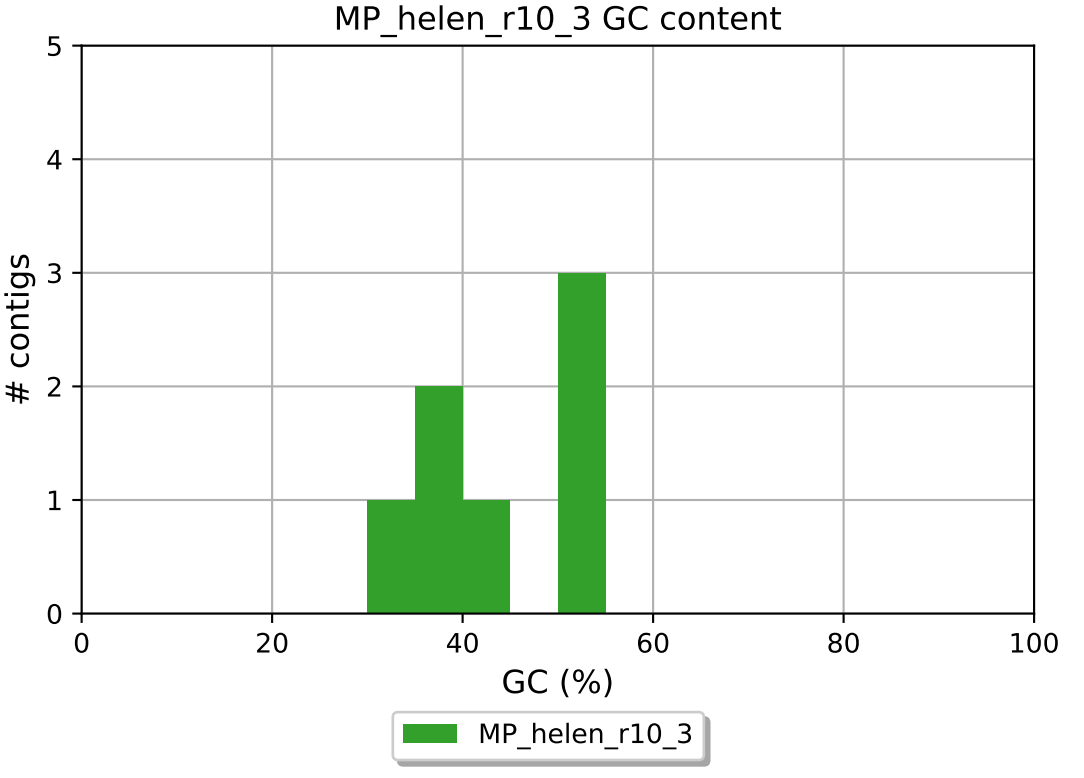

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2

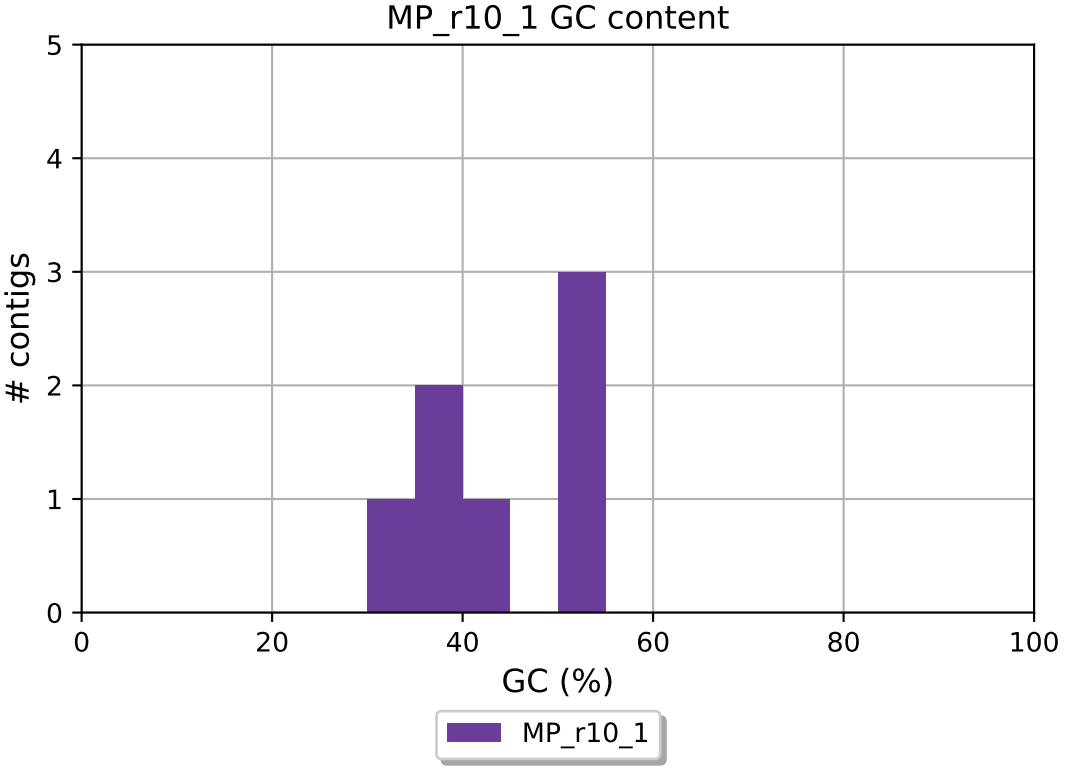

Cumulative length
Cumulative length (Mbp)
0
5
10
15
20
25
0
15
30
45
60
75
Contig index
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1

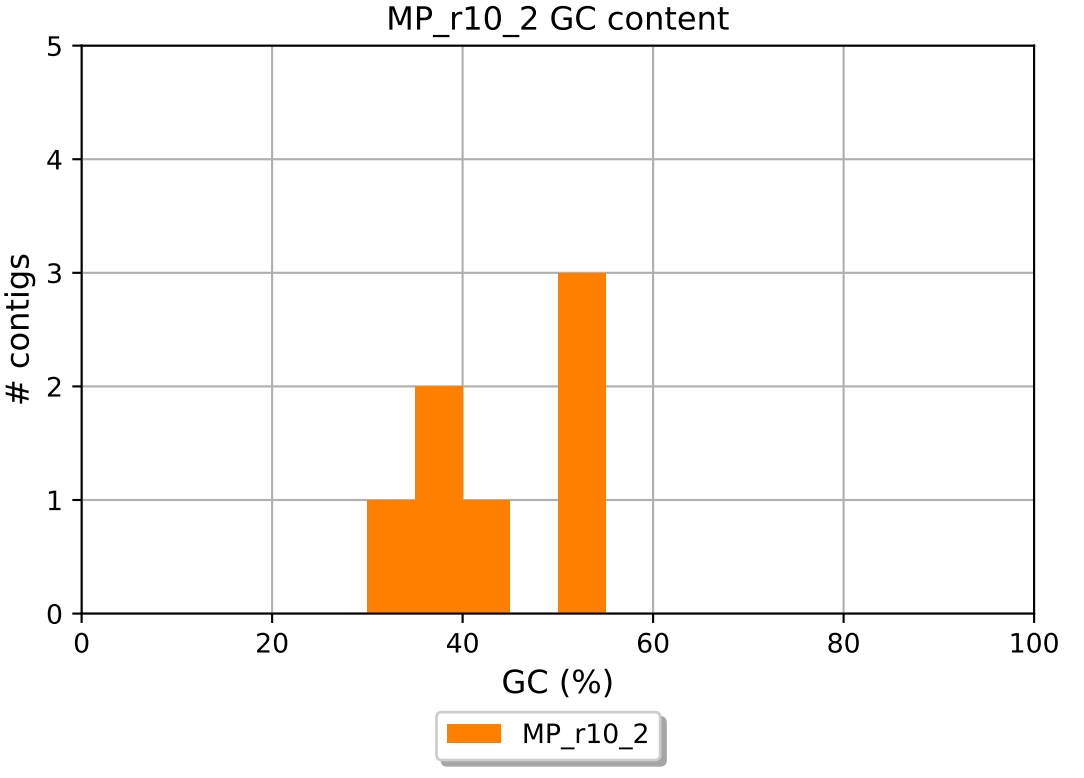

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3

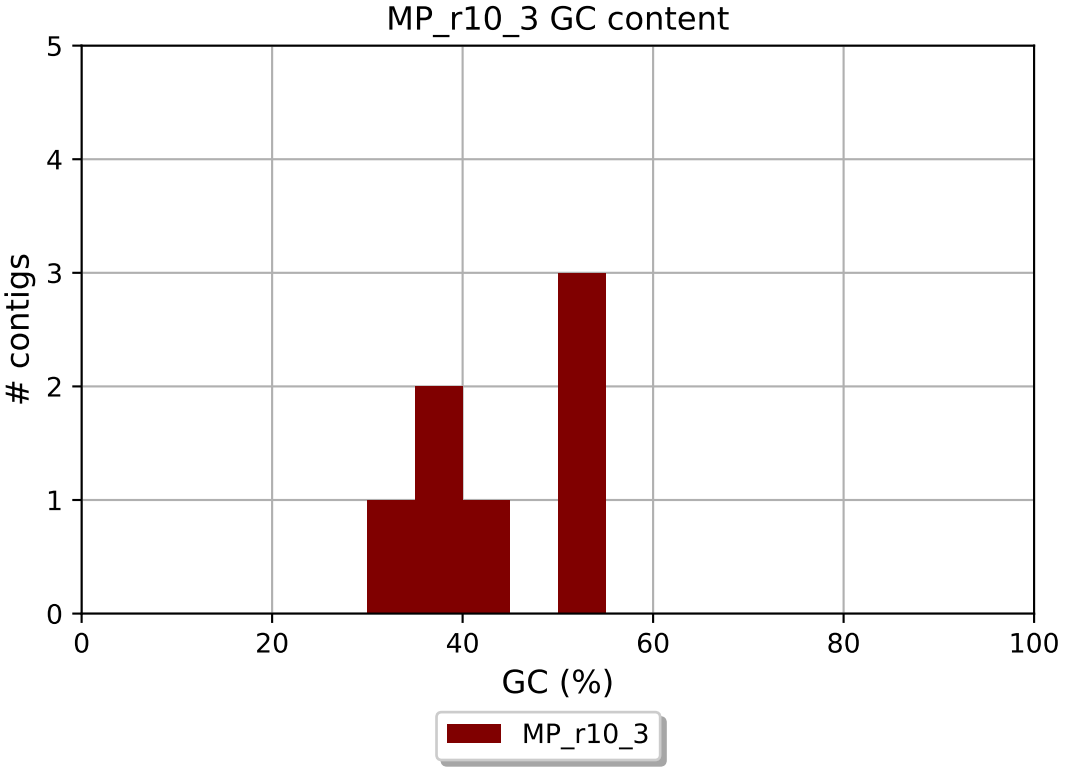

MP_helen_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_1

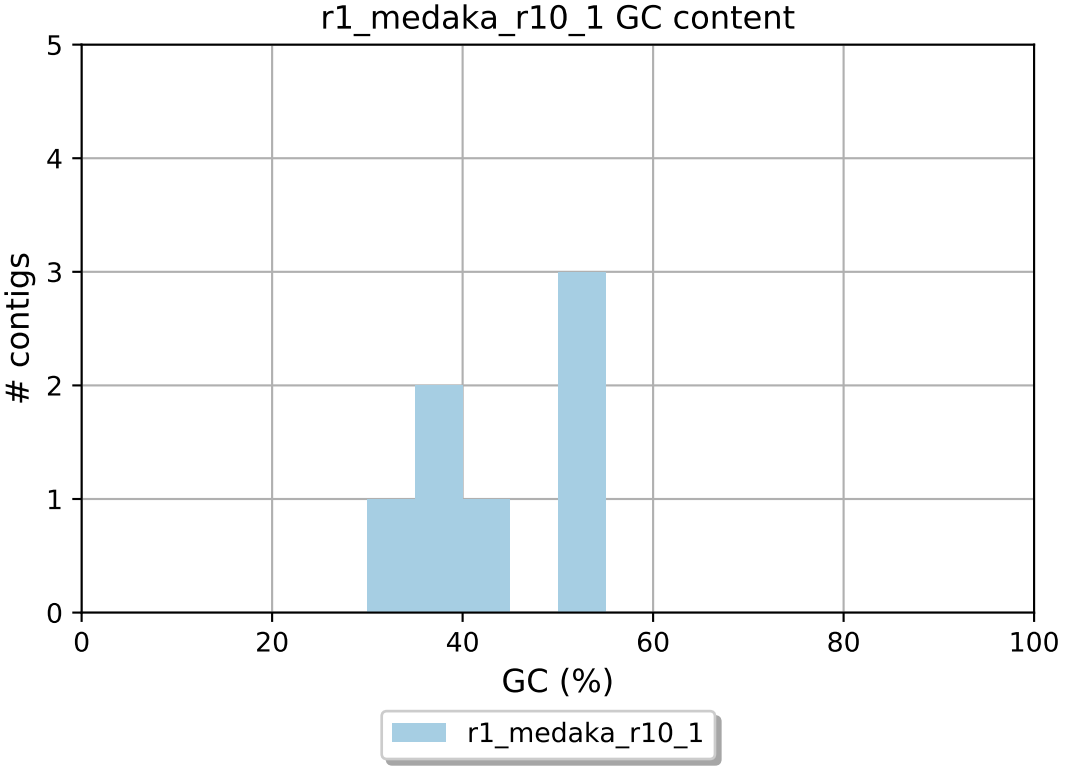

MP_helen_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_2

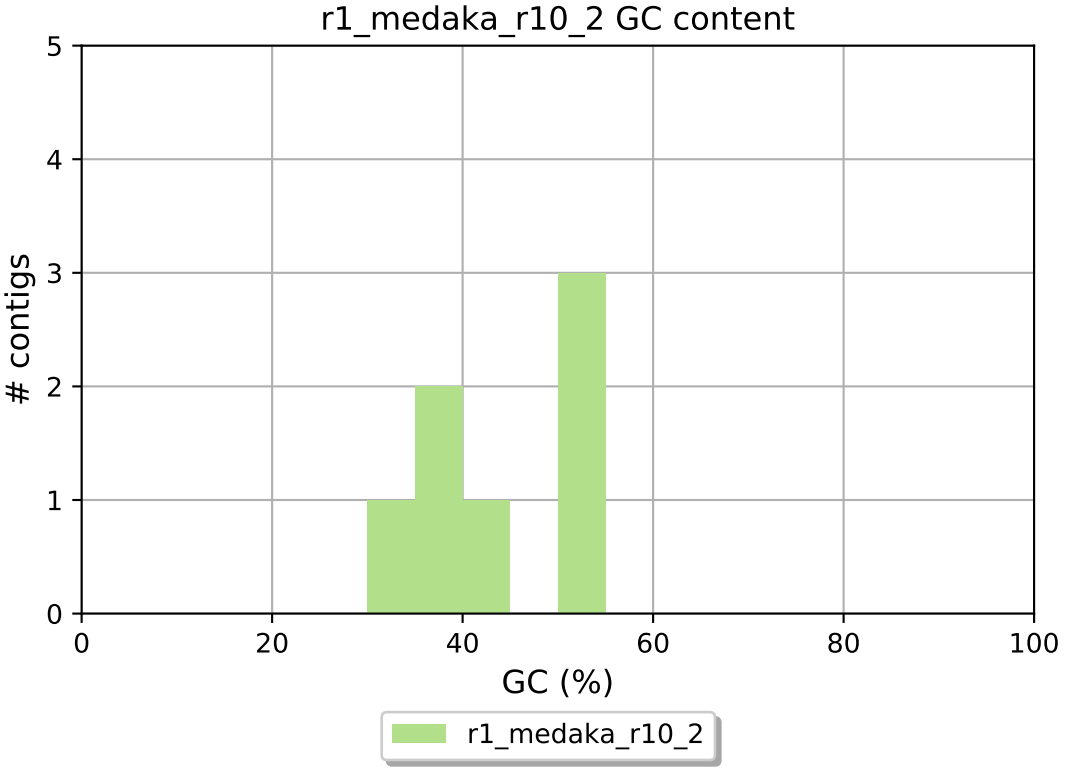

MP_helen_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_3

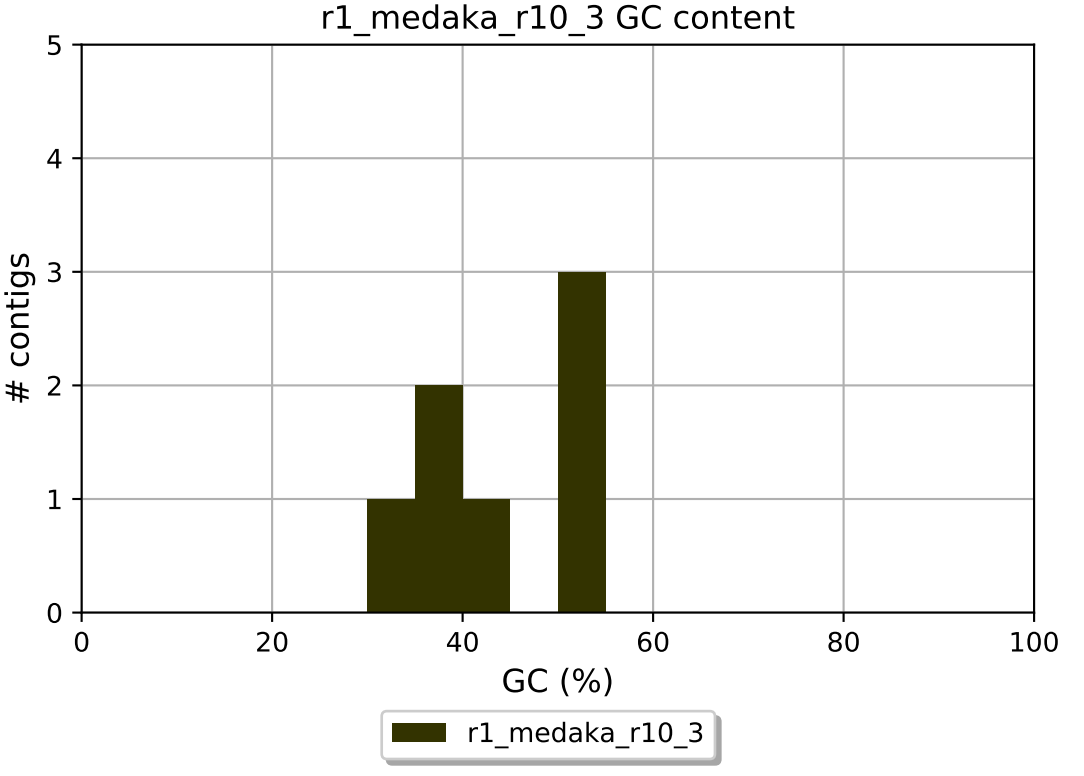

MP_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_1

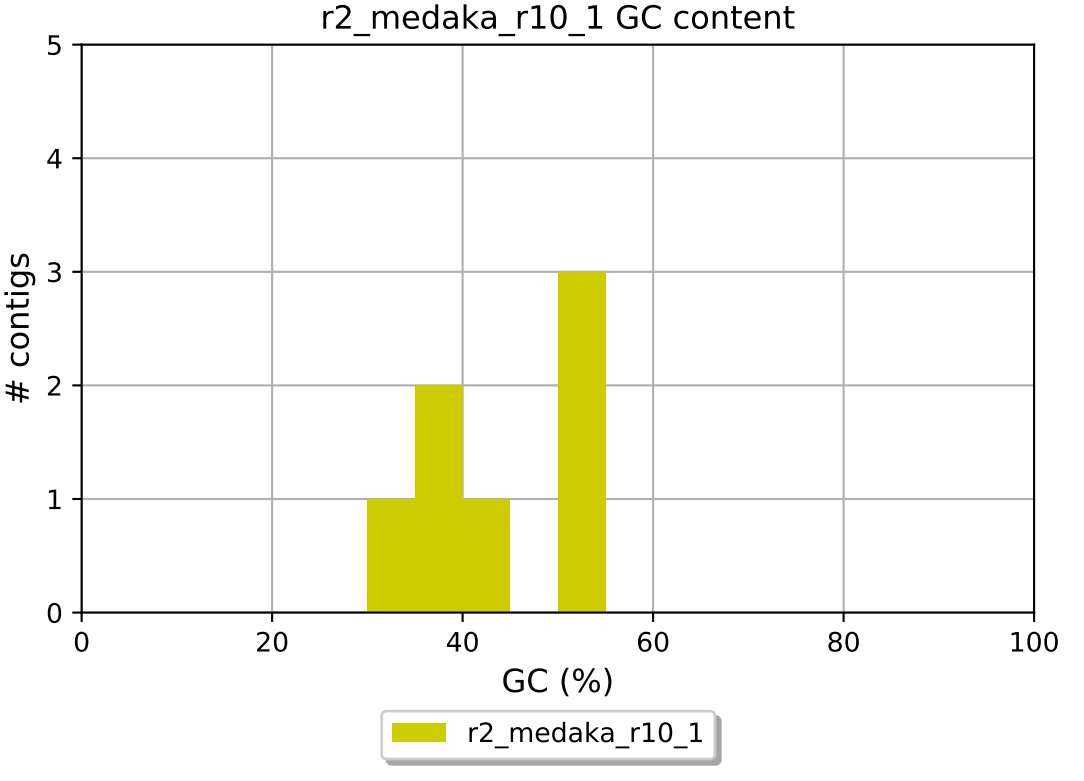

MP_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_2

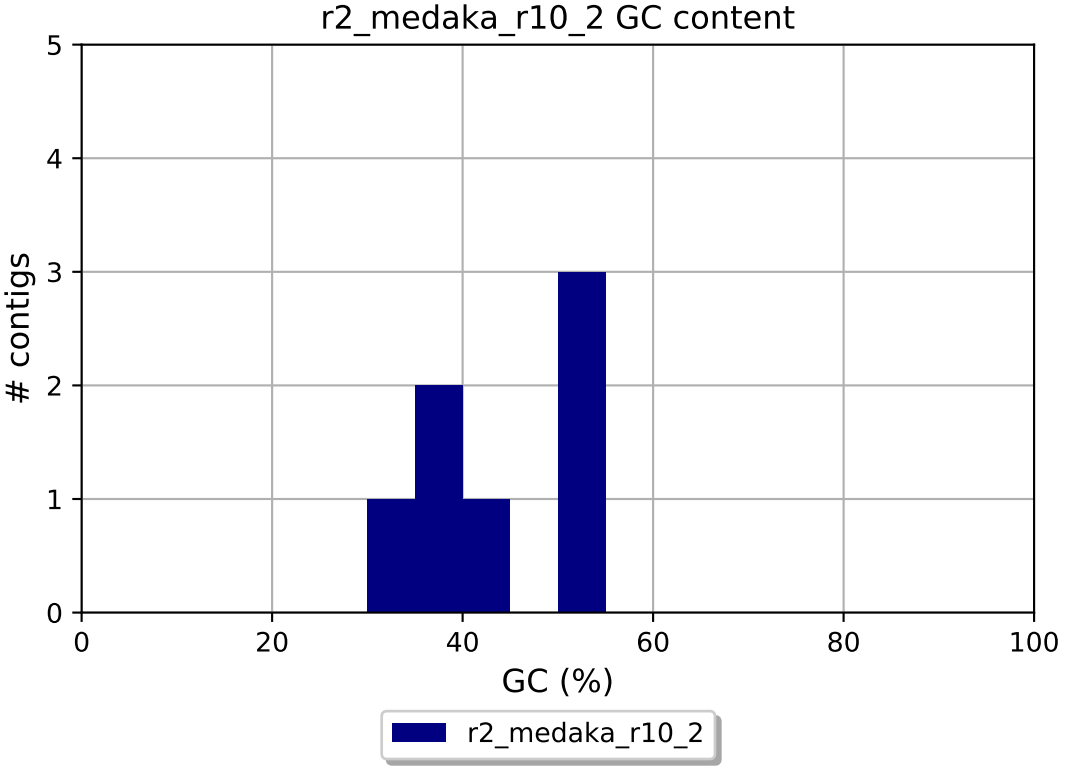

MP_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_3

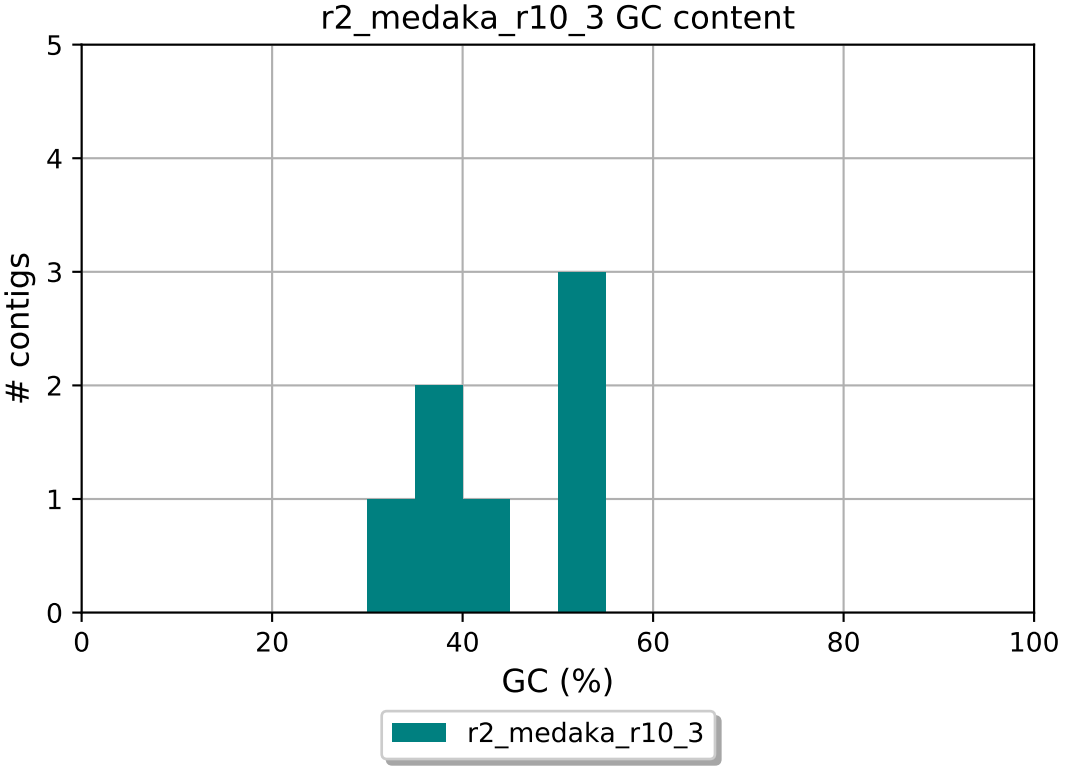

r1_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_1

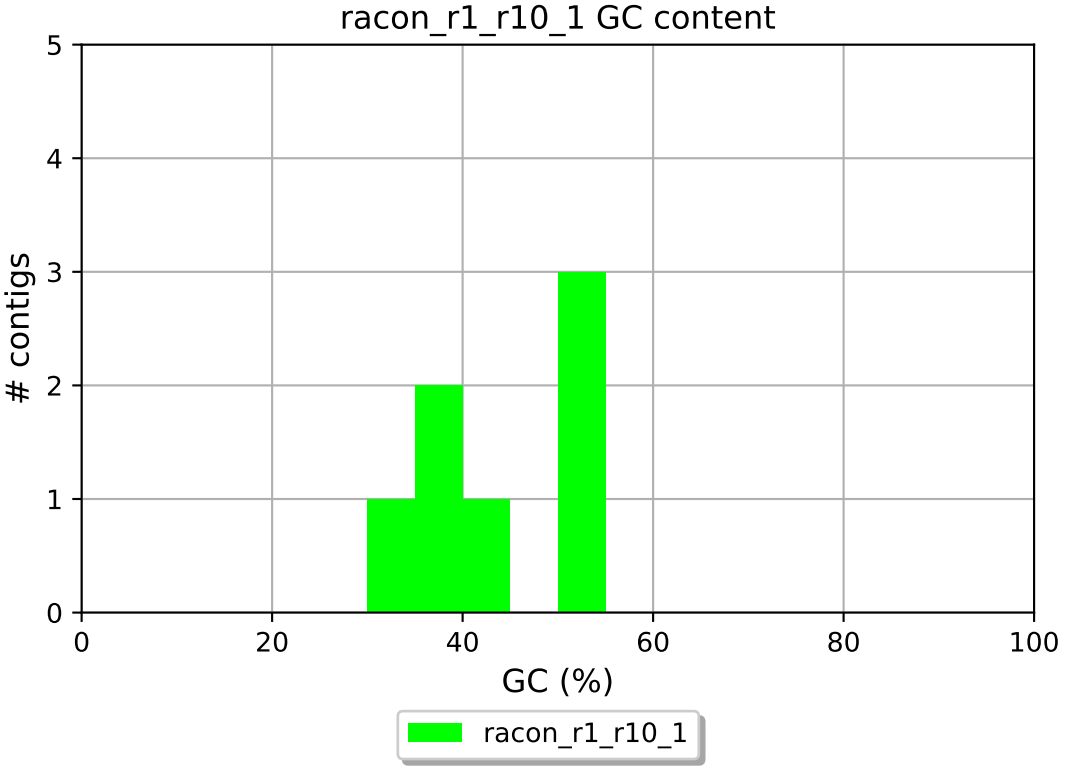

r1_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_2

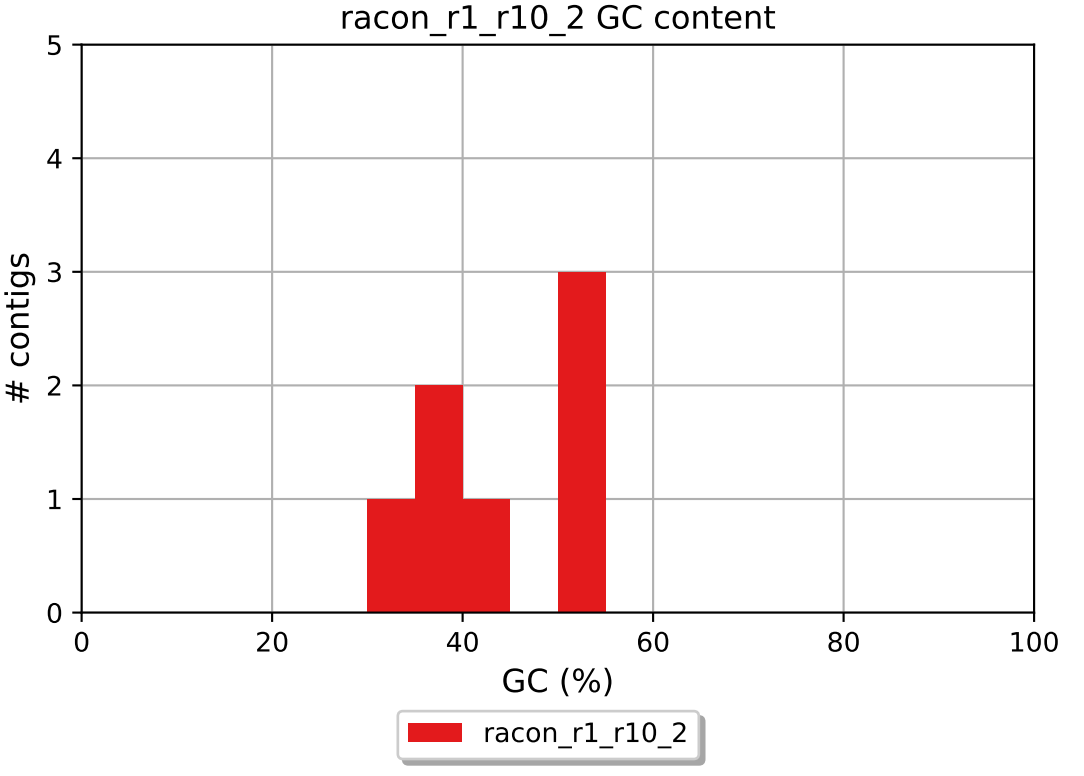

r1_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_3

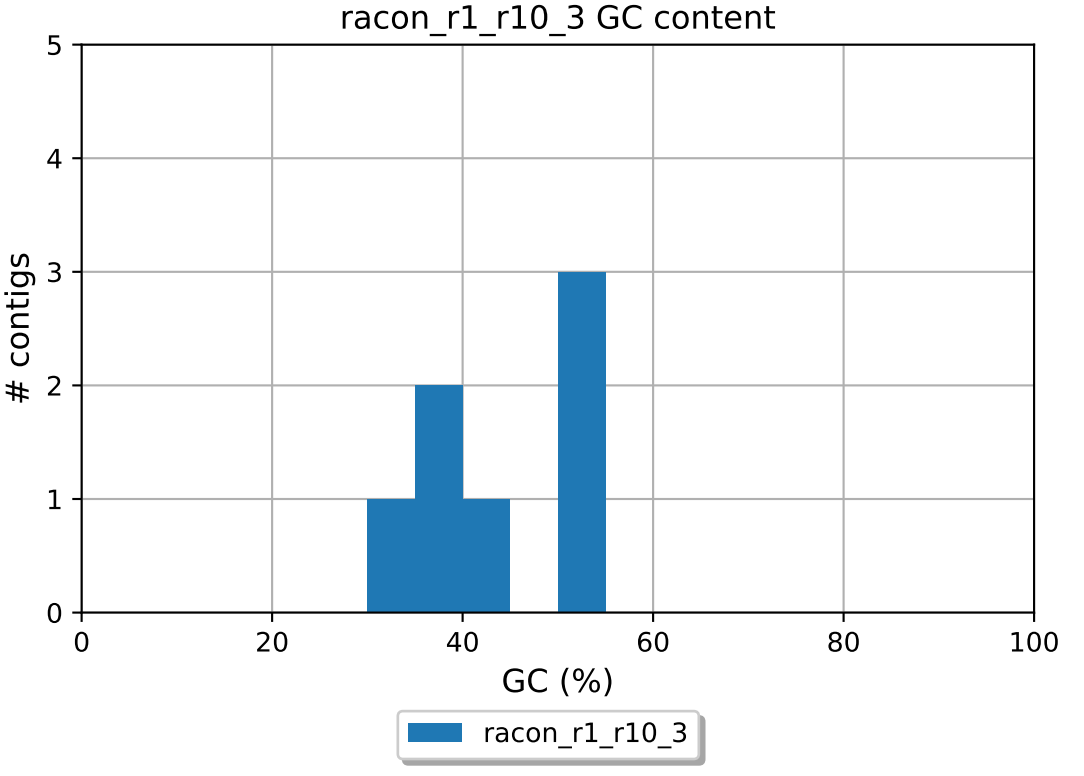

r2_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_1

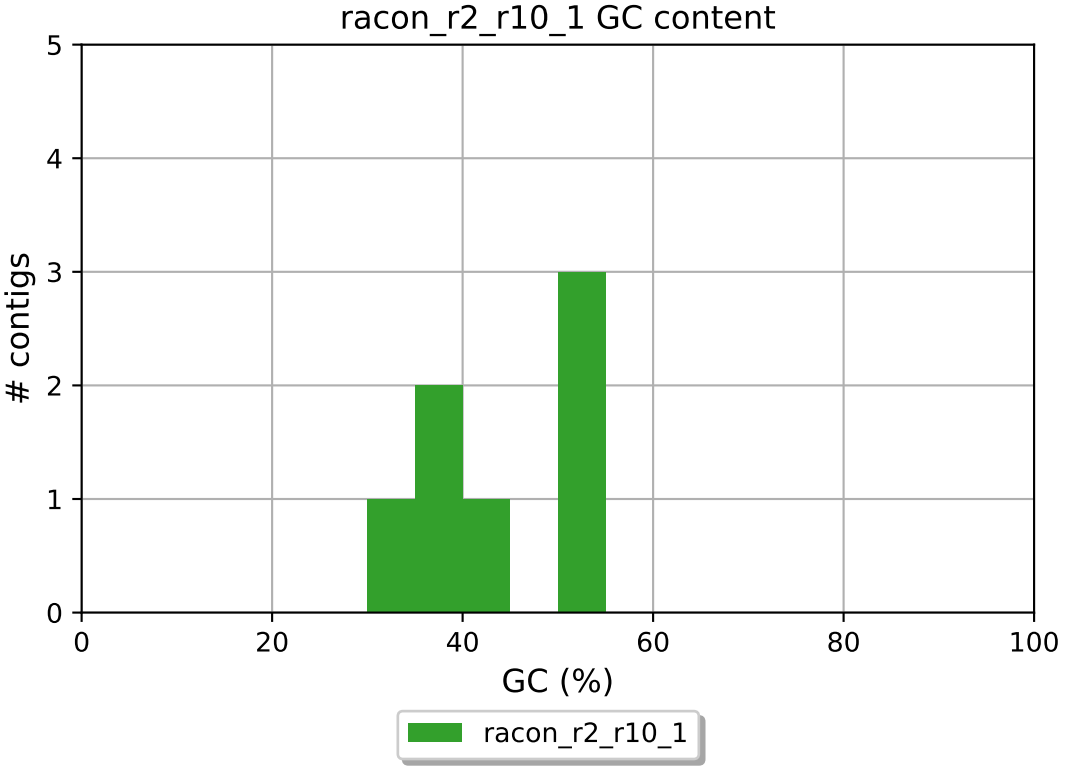

r2_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_2

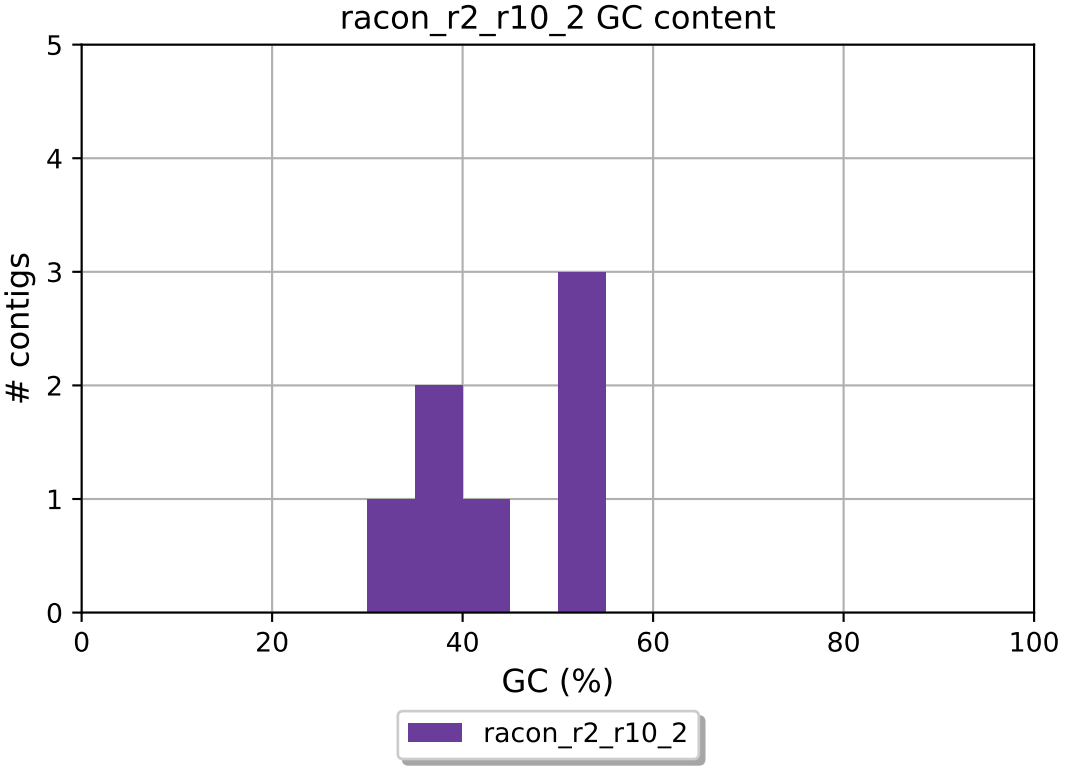

r2_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_3

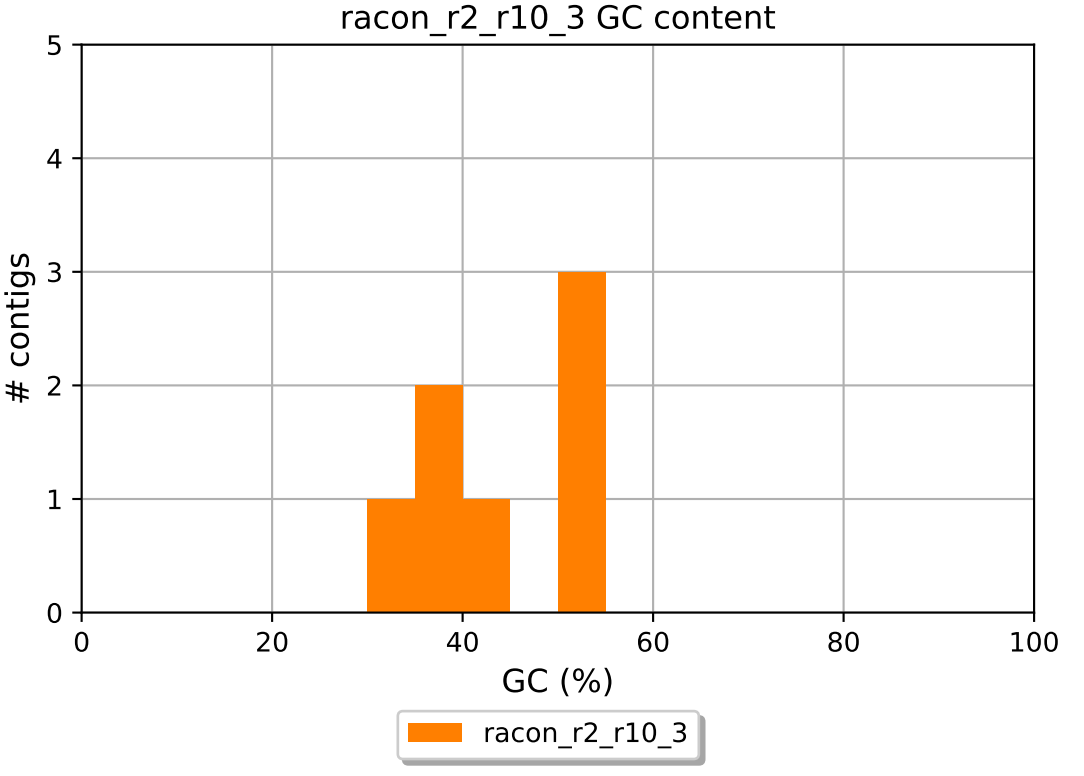

racon_r1_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_1

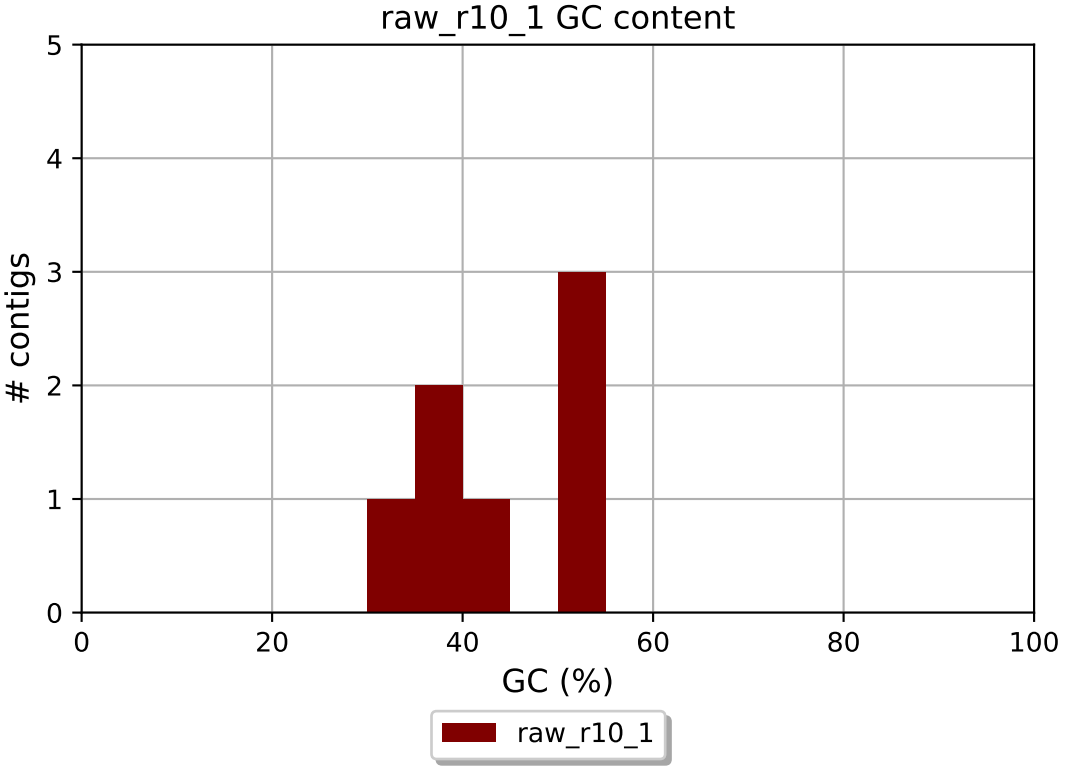

racon_r1_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_2

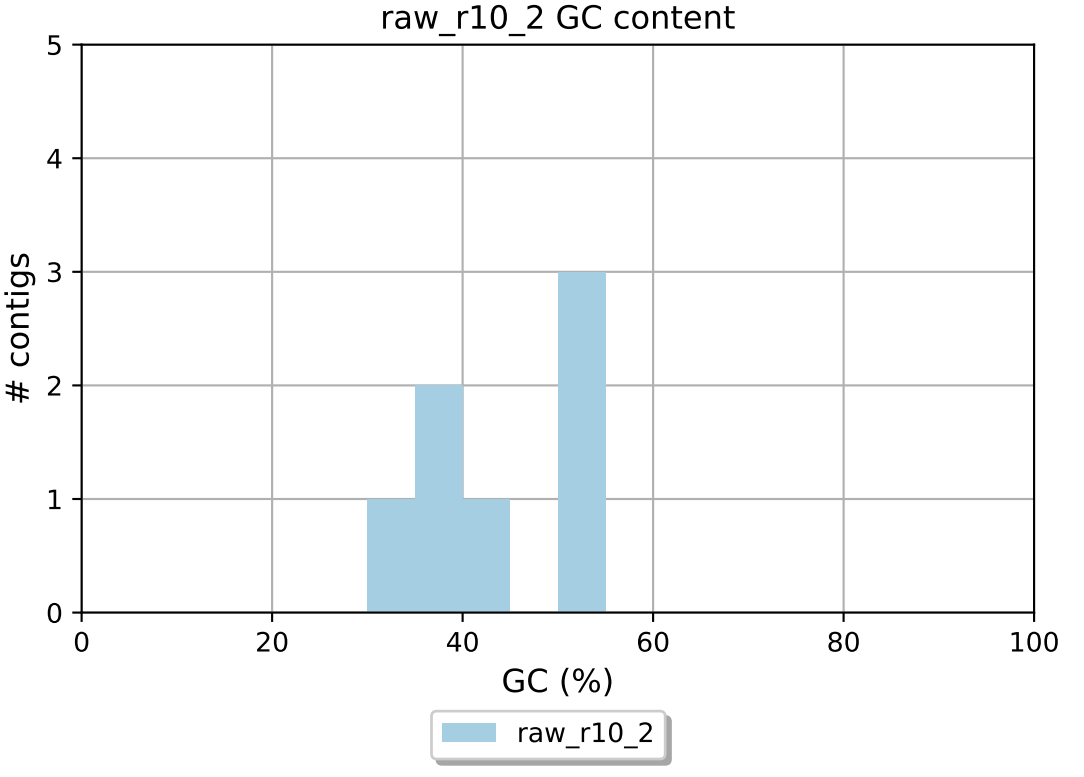

racon_r1_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_3

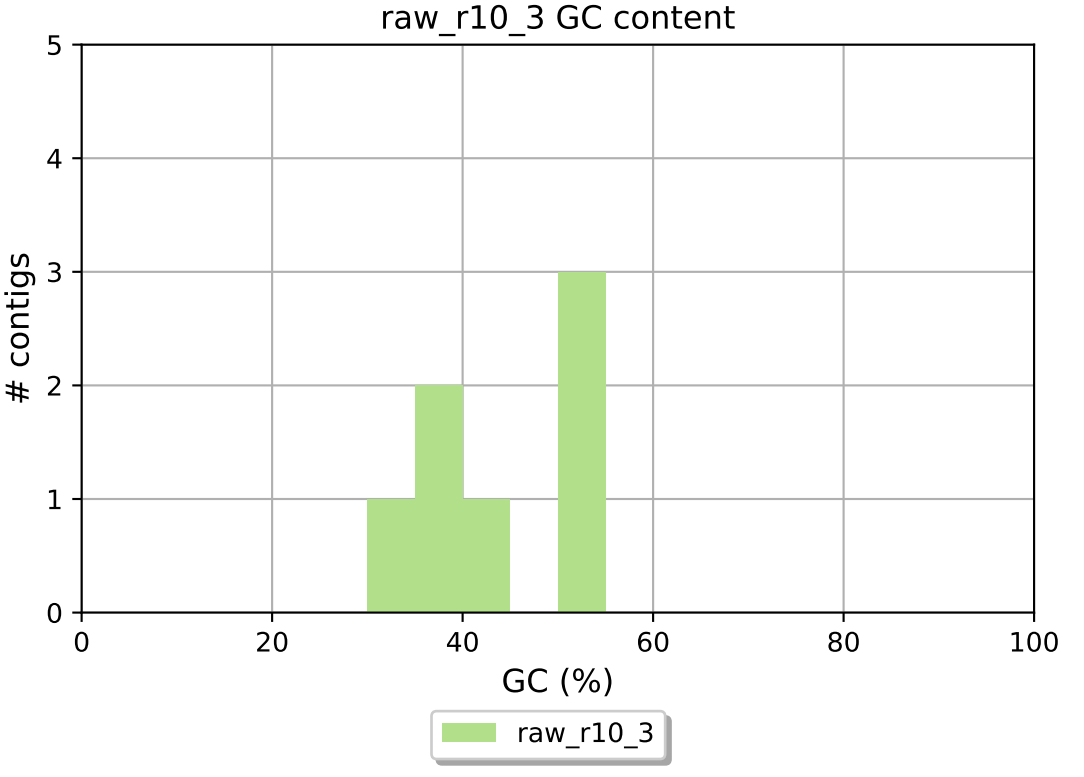

racon_r2_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_1

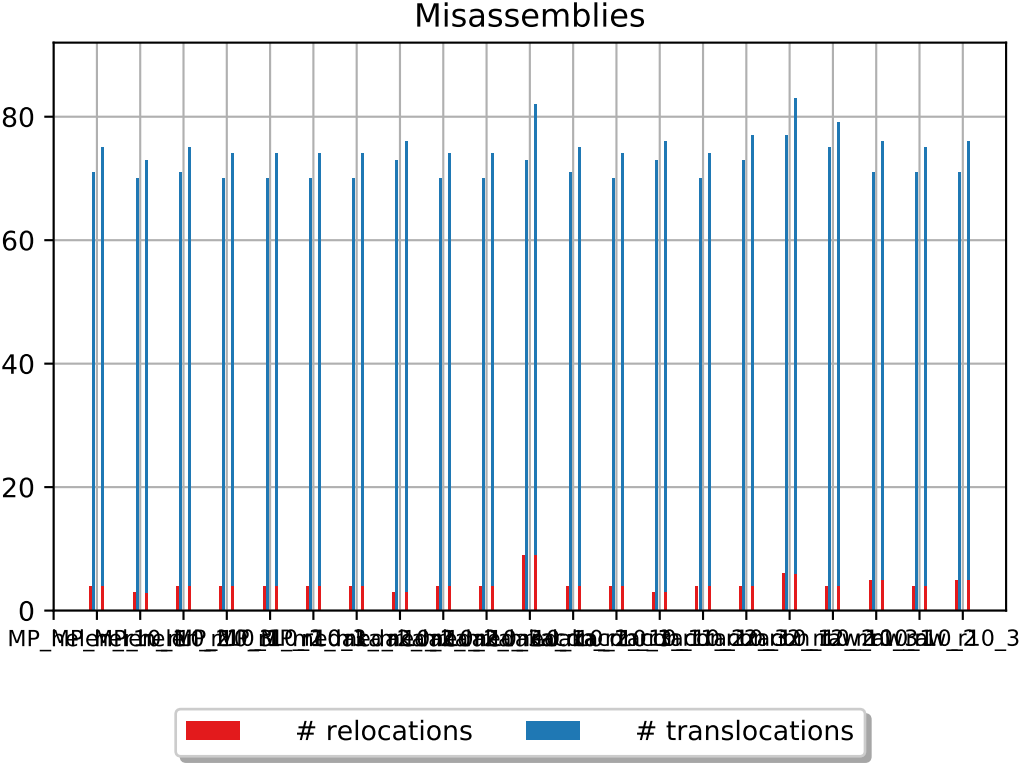

racon_r2_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_2

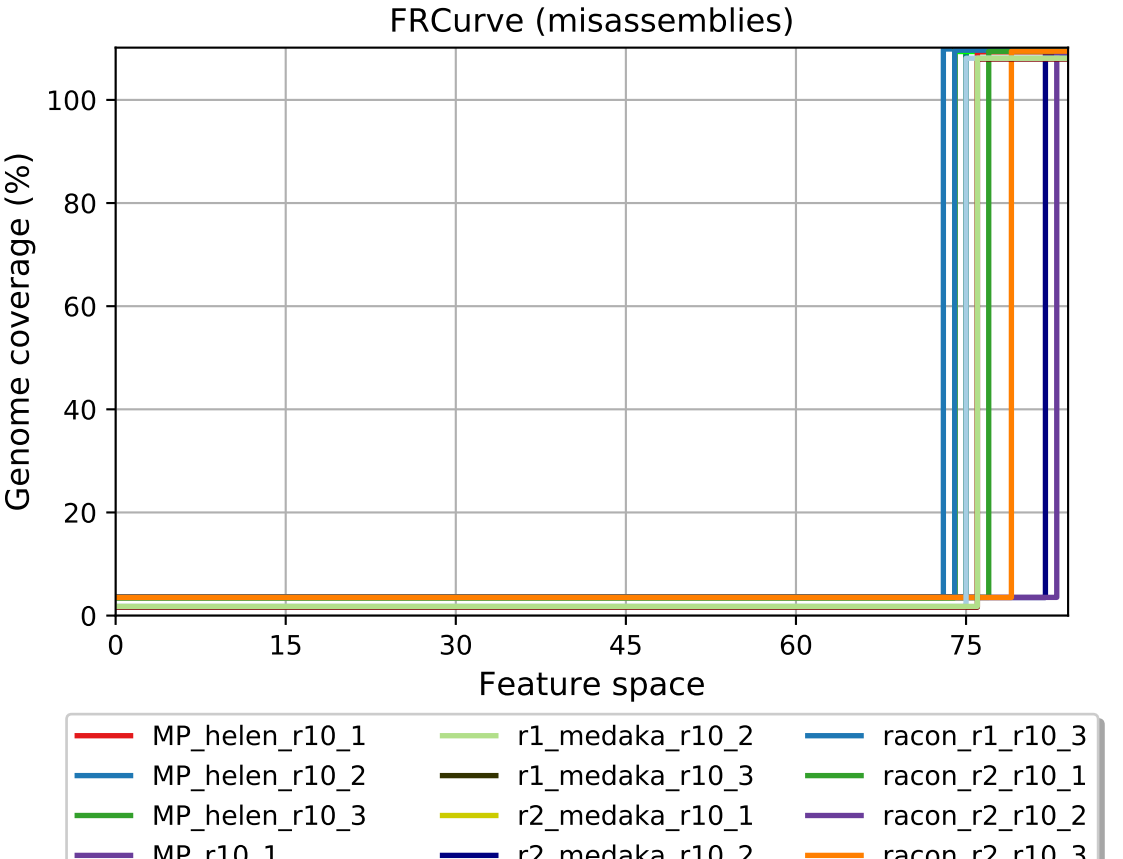

racon_r2_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_3

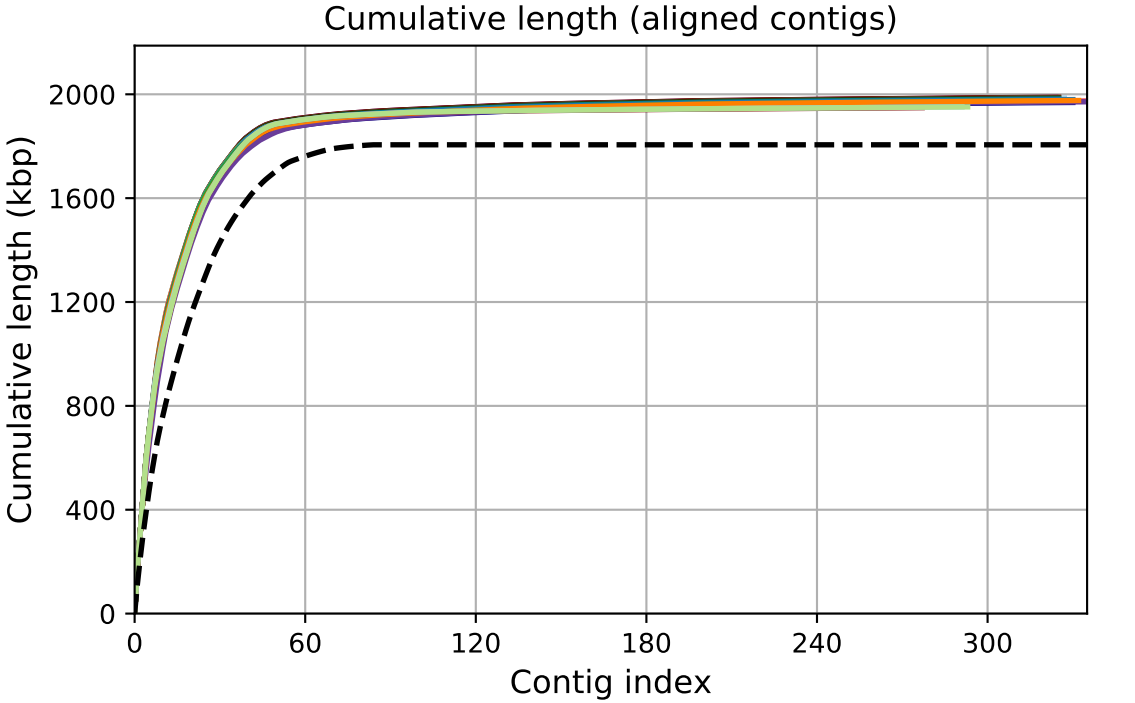

raw_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_1

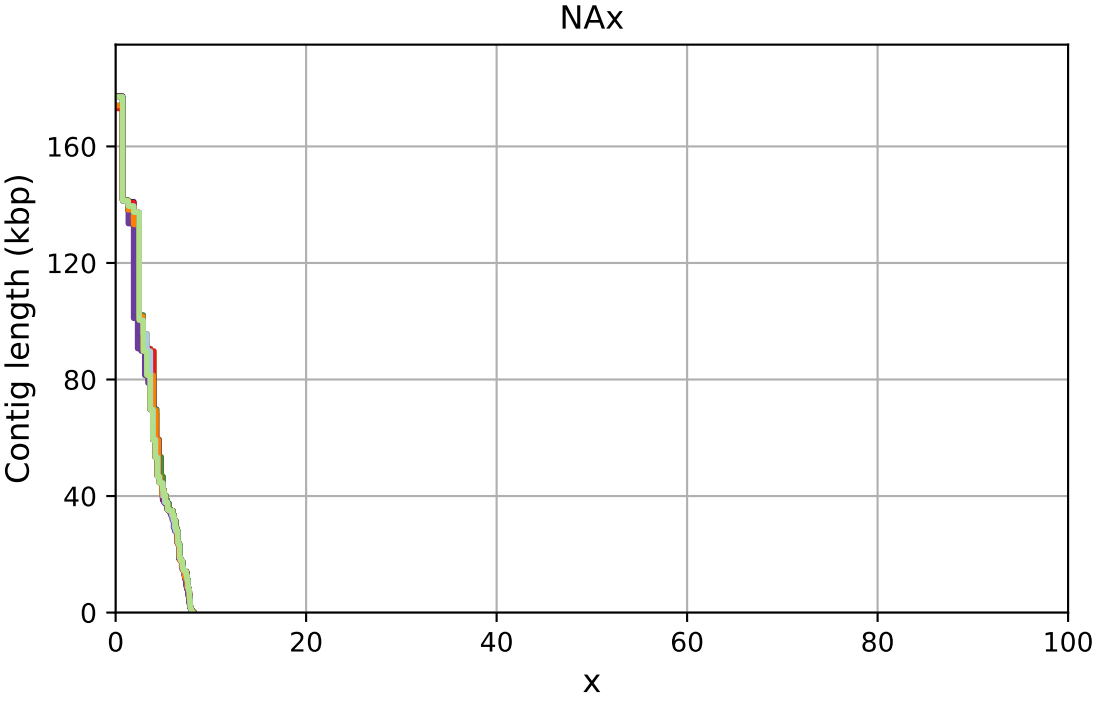

raw_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_2

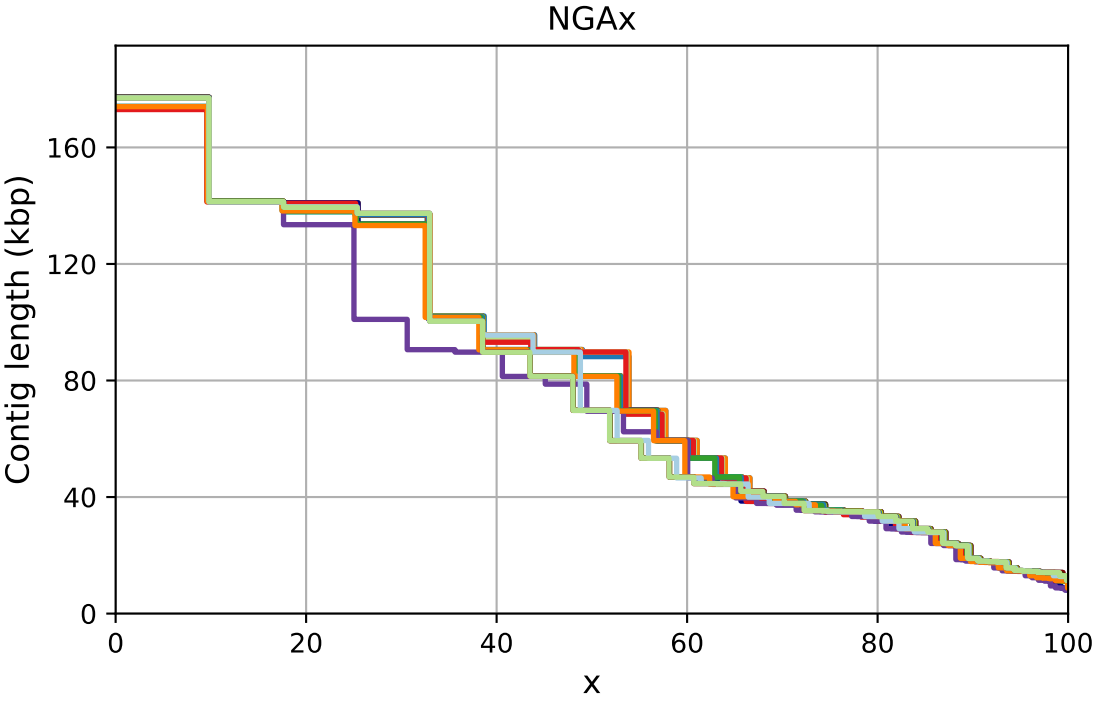

raw_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_3

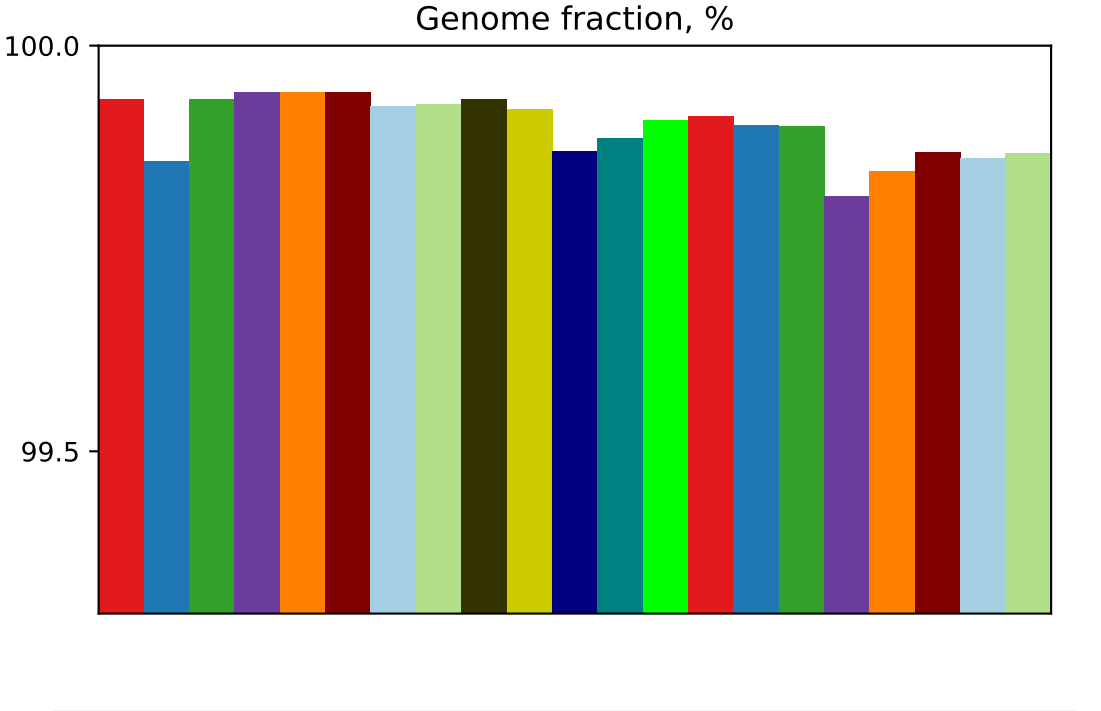

Misassemblies
80
60
40
20
0
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
Feature space
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
60
120
180
240
300
Contig index
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1


NAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2


NGAx
Contig length (kbp)
0
40
80
120
160
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3


Genome fraction, %
100.0
99.5
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3