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	8	8	8
# contigs (>= 10000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 25000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Total length (>= 5000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	30851140	30849756	30850081
Total length (>= 10000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	30851140	30849756	30850081
Total length (>= 25000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	30851140	30849756	30850081
Total length (>= 50000 bp)	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	30851140	30849756	30850081
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	8
Largest contig	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	6788581
Total length	24072144	24070716	24072083	24075954	24075406	24076499	24074829	24072142	24074875	24068354	24059914	24071745	24063908	24060798	24065303	24061249	24053400	24062516	30851140	30849756	30850081
Reference length	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570	2958570
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	49.48	49.48	49.48
Reference GC (%)	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84	37.84
N50	4045616	4045633	4045623	4045594	4045600	4045599	4045600	4045603	4045599	4045597	4045604	4045600	4045299	4045286	4045284	4045354	4045343	4045342	4756101	4755953	4755682
NG50	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	6788581
N75	2845381	2845365	2845381	2845424	2845426	2845425	2845435	2845435	2845432	2845432	2845433	2845433	2845317	2845303	2845316	2845298	2845330	2845342	2990626	2990624	2990626
NG75	4765293	4765903	4765296	4765362	4766035	4765940	4765290	4765413	4765355	4765312	4765387	4765372	4764581	4764920	4764661	4764695	4764766	4764706	6788581	6788581	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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992057	2992066	2992057	2992056	2992083	2992056	2992047	2992072	2992048	2992047	2992073	2992046	2991930	2991945	2991935	2991941	2991986	2991949	2990626	2990624	2990626
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	14	12	12
# 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	7	7	7
# 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 + 8 part	0 + 8 part	0 + 8 part
Unaligned length	20951800	20950458	20951816	20958091	20957318	20957702	20955190	20952764	20955134	20948340	20941662	20951823	20945612	20941987	20945431	20943447	20934413	20944384	27792768	27789921	27790618
Genome fraction (%)	99.986	99.984	99.986	99.986	99.984	99.986	99.986	99.984	99.986	99.986	99.984	99.986	99.986	99.984	99.986	99.986	99.984	99.986	99.983	99.983	99.985
Duplication ratio	1.055	1.055	1.055	1.054	1.054	1.055	1.055	1.055	1.055	1.055	1.054	1.055	1.054	1.055	1.055	1.054	1.055	1.054	1.034	1.035	1.035
# 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	236.32	236.19	236.02	229.63	230.38	231.99	232.16	231.73	232.81	233.65	227.70	233.58	229.39	231.46	234.80	228.88	231.39	228.61	145.71	146.86	145.67
# indels per 100 kbp	22.11	22.28	22.08	22.01	21.91	21.94	22.28	22.15	21.64	21.78	21.61	22.08	32.60	31.58	31.82	29.49	29.28	30.60	116.25	116.29	115.85
Largest alignment	2719483	1569029	2719483	2719482	1569036	2719482	2719473	1569031	2719474	2719473	1569033	2719472	2719362	1568971	2719367	2719393	1569000	2719396	2718083	1568343	2718129
Total aligned length	3118956	3119784	3118879	3116475	3117614	3117409	3118251	3118904	3118353	3118626	3117778	3118534	3116908	3118338	3118484	3116421	3118514	3116744	3056997	3059397	3058091
NGA50	2719483	1569029	2719483	2719482	1569036	2719482	2719473	1569031	2719474	2719473	1569033	2719472	2719362	1568971	2719367	2719393	1569000	2719396	2718083	1568343	2718129
NGA75	2719483	1410494	2719483	2719482	1410523	2719482	2719473	1410517	2719474	2719473	1410516	2719472	2719362	1410449	2719367	2719393	1410463	2719396	2718083	1409710	2718129
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	2	1	1	2	1	1	2	1	1	2	1	1	2	1	1	2	1	1	2	1

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

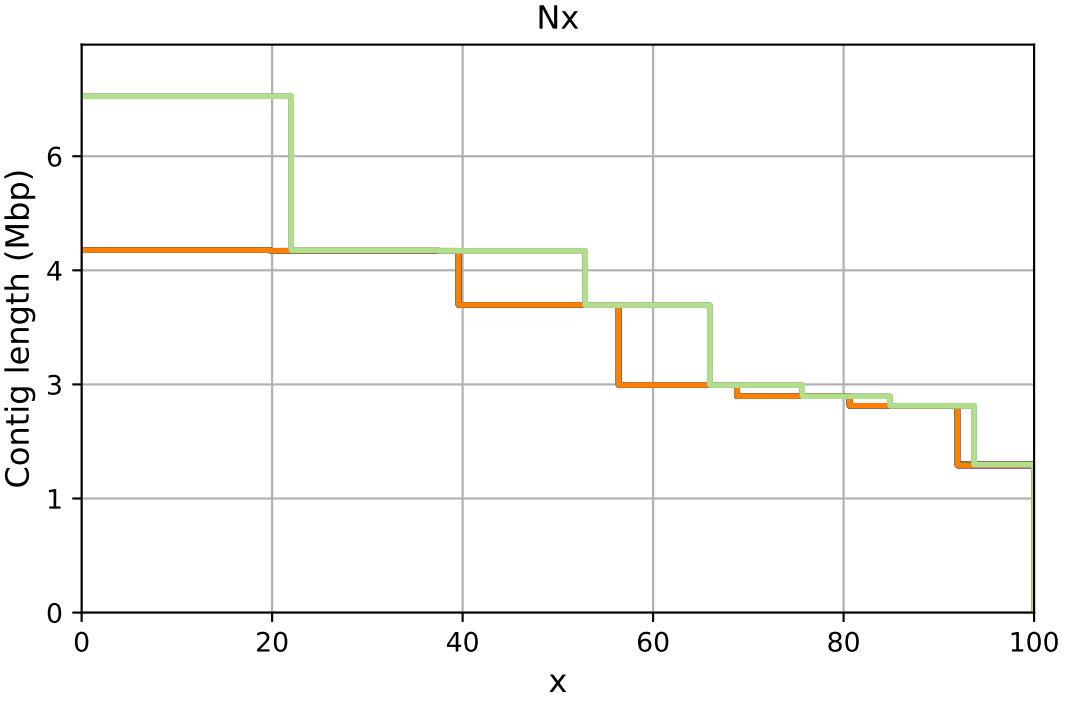
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# contig misassemblies	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	2992057	2992066	2992057	2992056	2992083	2992056	2992047	2992072	2992048	2992047	2992073	2992046	2991930	2991945	2991935	2991941	2991986	2991949	2990626	2990624	2990626
# possibly misassembled contigs	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2
# possible misassemblies	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	9	9	9
# local misassemblies	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	14	12	12
# 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	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	10	11	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	7	7	7
# mismatches	6989	6985	6980	6791	6813	6861	6866	6853	6885	6910	6734	6908	6784	6845	6944	6769	6843	6761	4309	4343	4308
# indels	654	659	653	651	648	649	659	655	640	644	639	653	964	934	941	872	866	905	3438	3439	3426
# indels (<= 5 bp)	629	634	628	626	624	624	634	630	616	620	615	628	938	908	916	848	842	878	3409	3410	3396
# indels (> 5 bp)	25	25	25	25	24	25	25	25	24	24	24	25	26	26	25	24	24	27	29	29	30
Indels length	1960	1967	1958	1956	1947	1952	1974	1970	1931	1935	1930	1968	2399	2342	2345	2237	2232	2306	5307	5340	5342

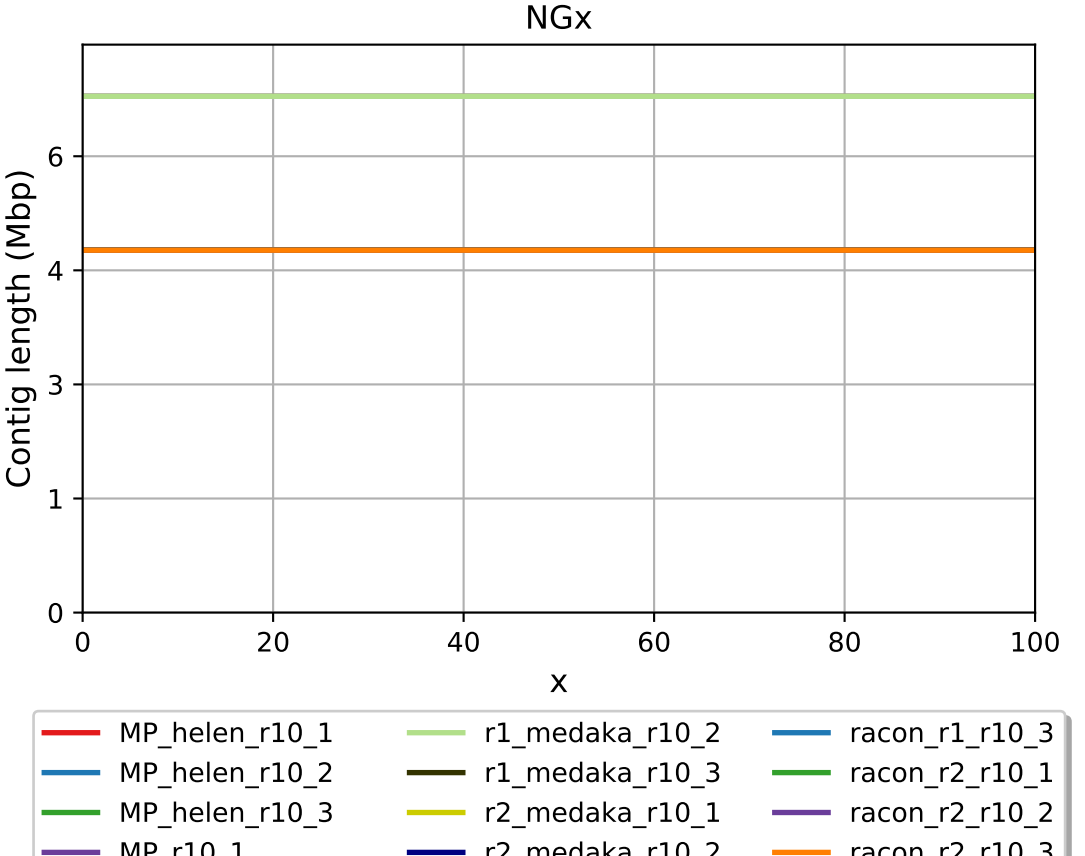
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

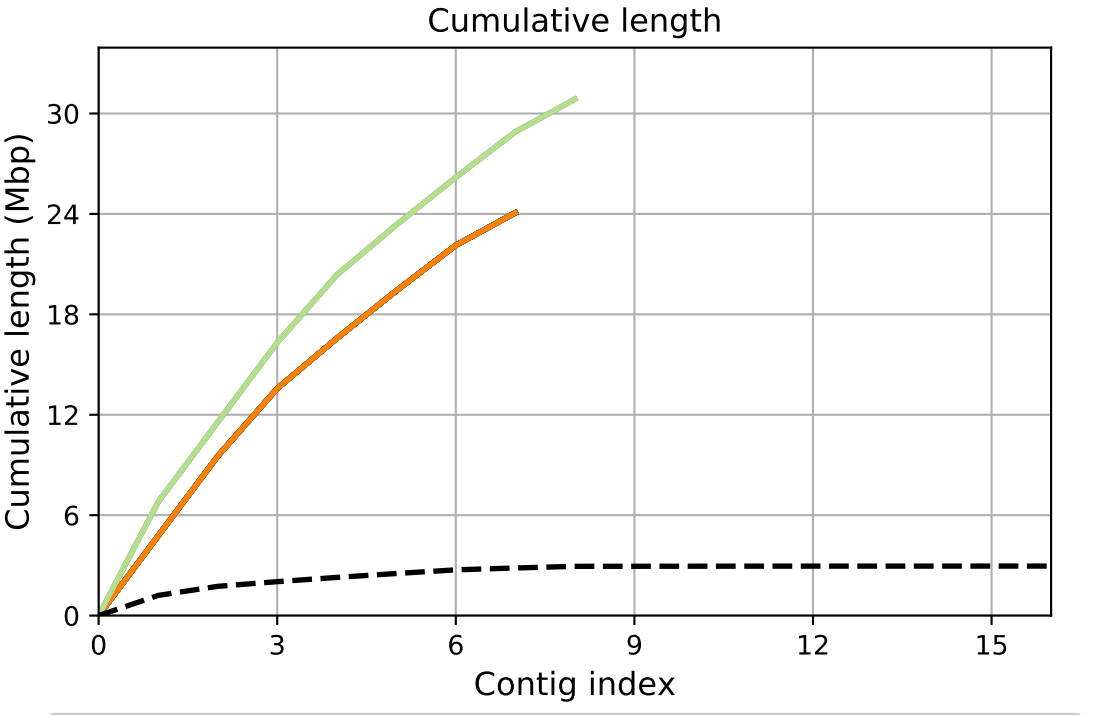
Unaligned report

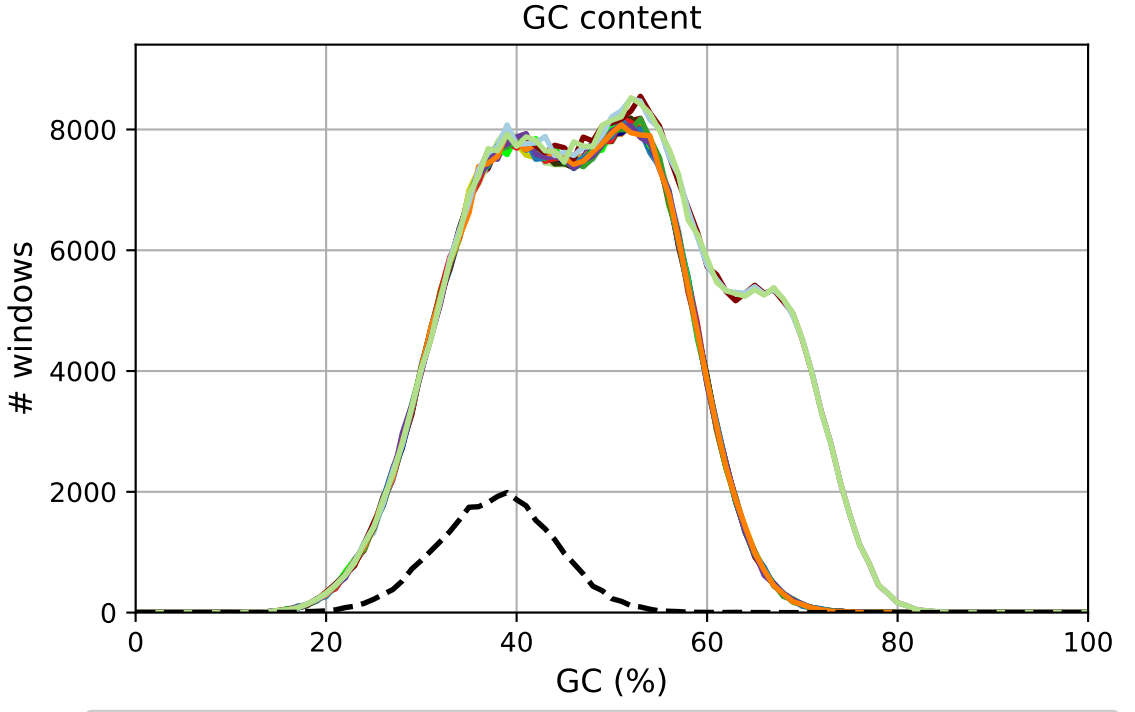
	MP_helen_r10_1	MP_helen_r10_2	MP_helen_r10_3	MP_r10_1	MP_r10_2	MP_r10_3	r1_medaka_r10_1	r1_medaka_r10_2	r1_medaka_r10_3	r2_medaka_r10_1	r2_medaka_r10_2	r2_medaka_r10_3	racon_r1_r10_1	racon_r1_r10_2	racon_r1_r10_3	racon_r2_r10_1	racon_r2_r10_2	racon_r2_r10_3	raw_r10_1	raw_r10_2	raw_r10_3
# fully unaligned 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	8	8	8
Partially unaligned length	20951800	20950458	20951816	20958091	20957318	20957702	20955190	20952764	20955134	20948340	20941662	20951823	20945612	20941987	20945431	20943447	20934413	20944384	27792768	27789921	27790618
# N's	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

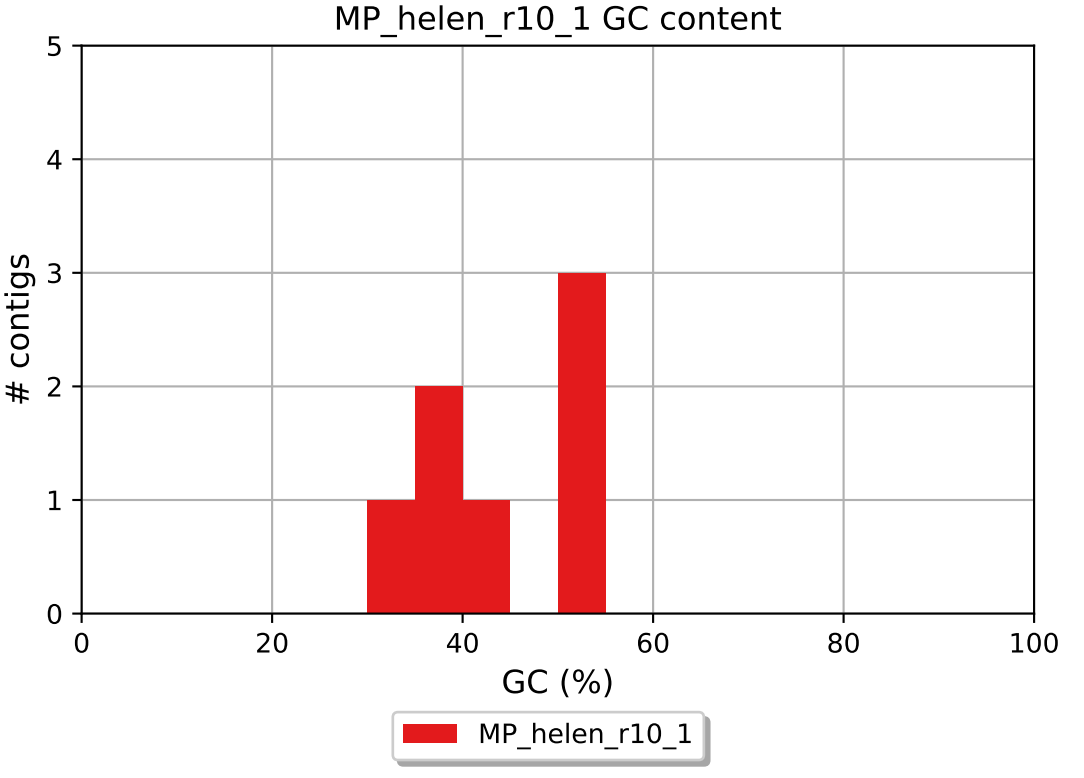
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

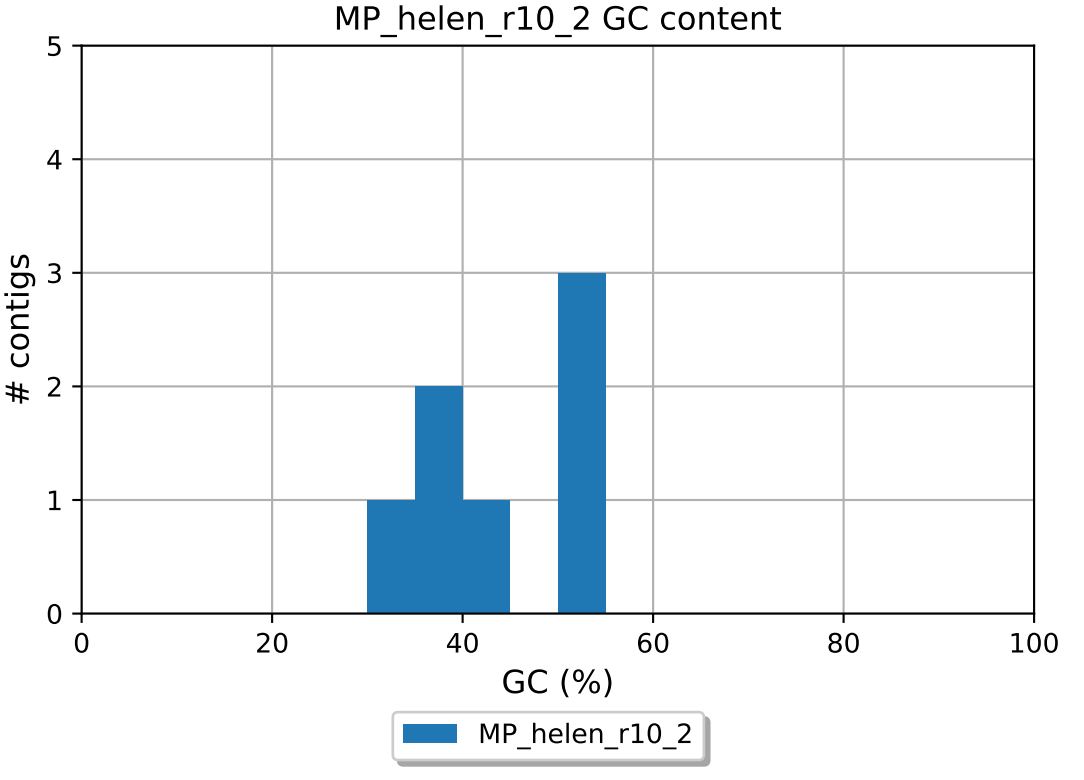

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3

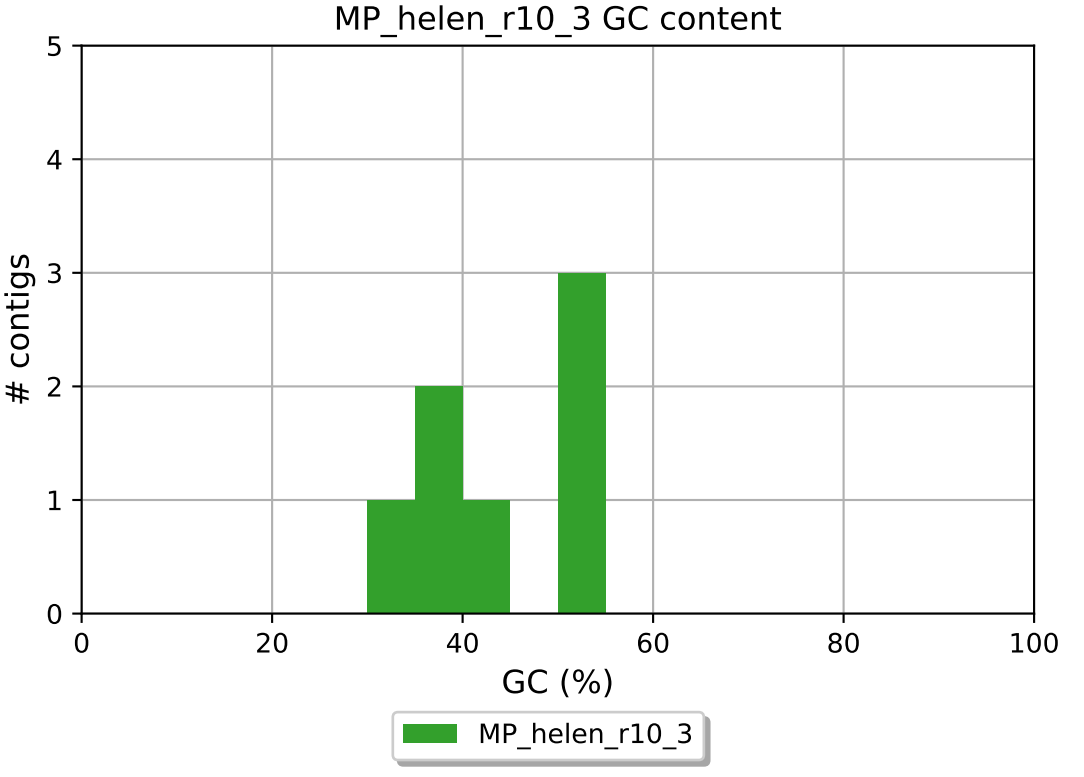

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_2
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
racon_r1_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3

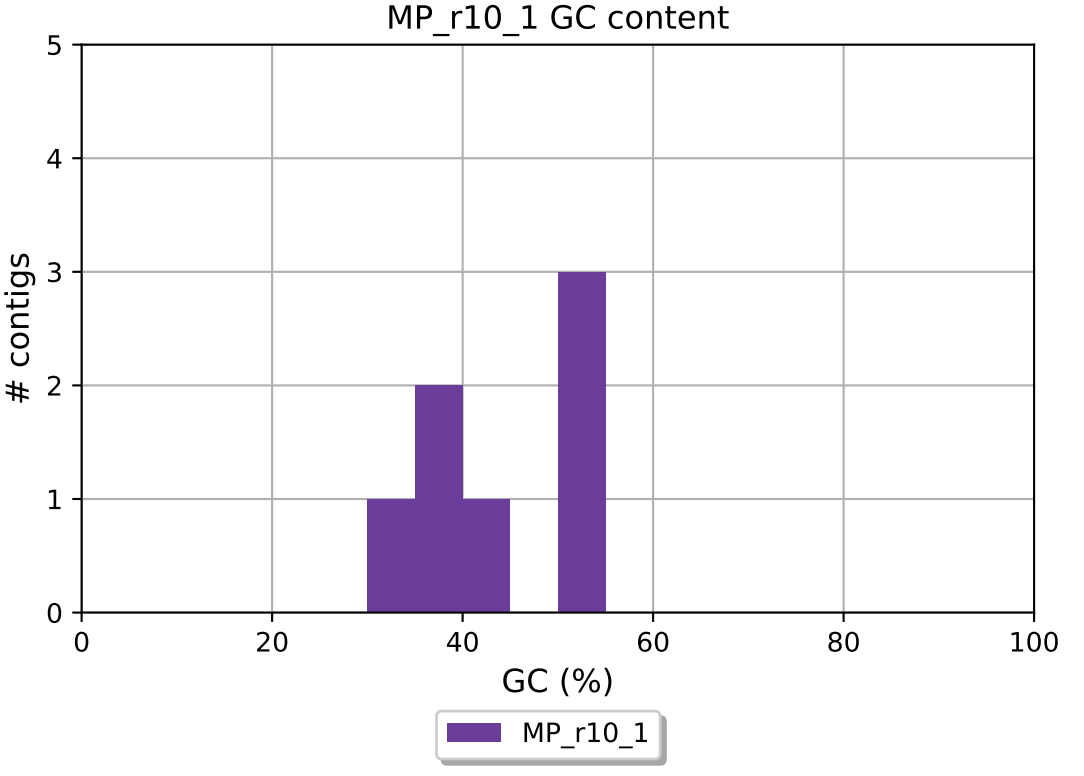

Cumulative length
Cumulative length (Mbp)
0
6
12
18
24
30
0
3
6
9
12
15
Contig index
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1

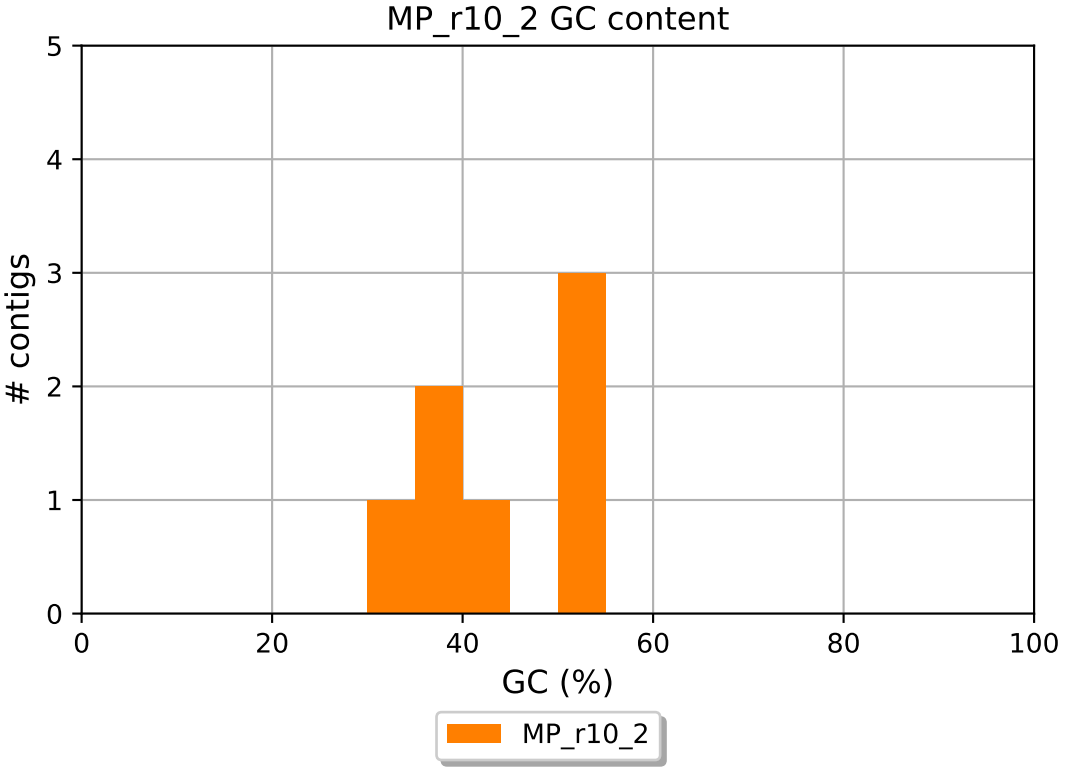

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
MP_helen_r10_1
MP_helen_r10_2
MP_helen_r10_3
MP_r10_1
r1_medaka_r10_3
r2_medaka_r10_1
r2_medaka_r10_2
r2_medaka_r10_3
racon_r2_r10_1
racon_r2_r10_2
racon_r2_r10_3
raw_r10_1

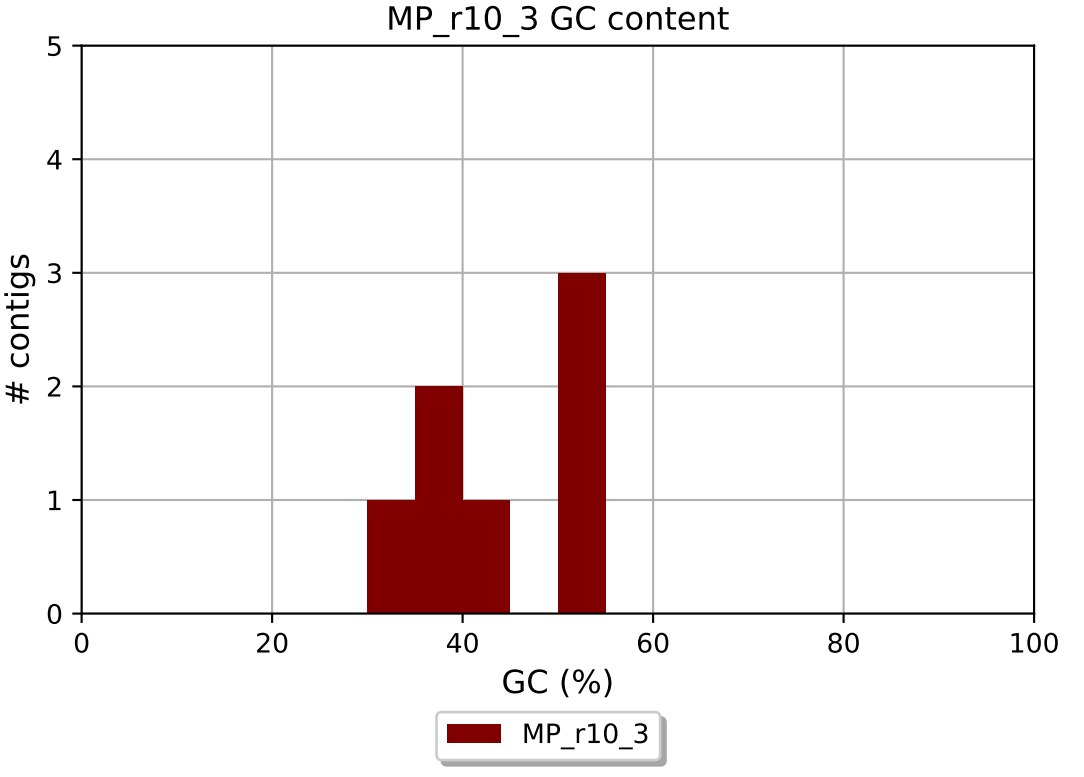

MP_helen_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_1

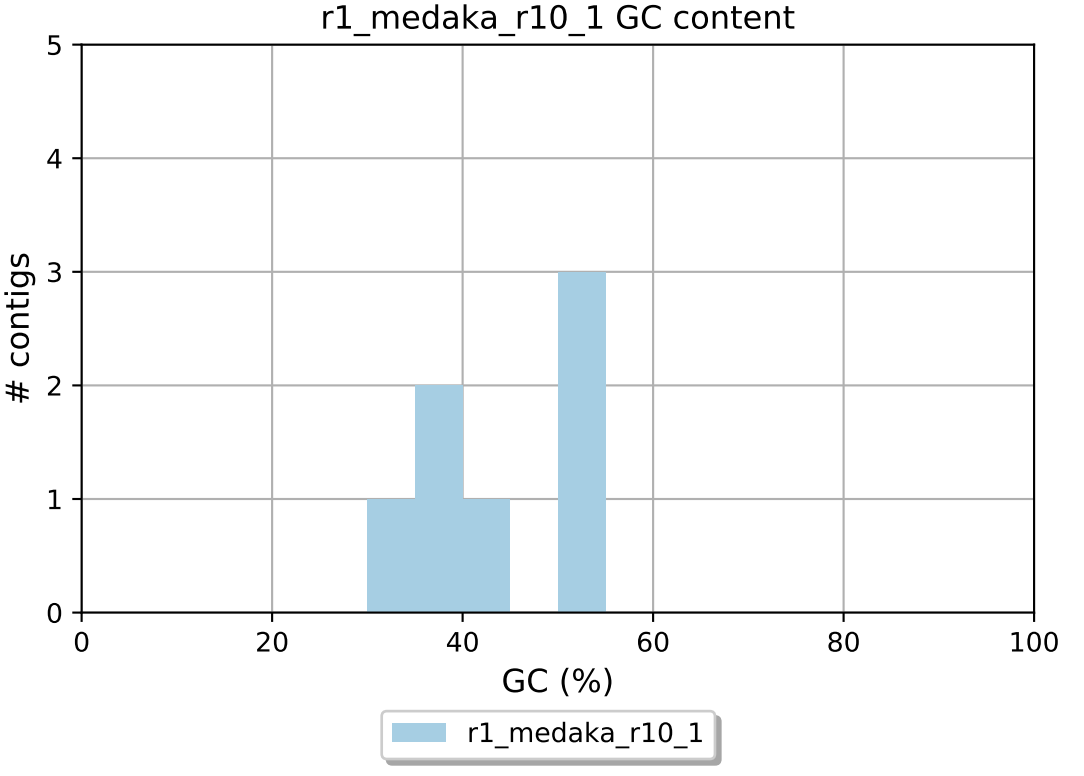

MP_helen_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_2

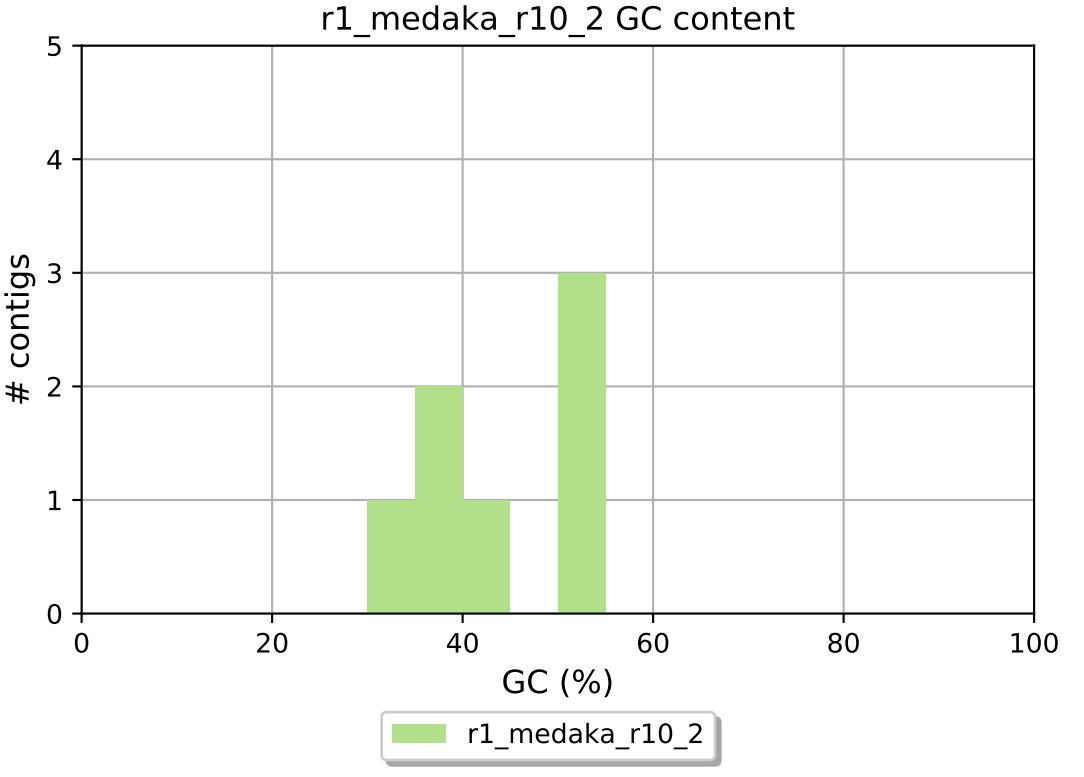

MP_helen_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_helen_r10_3

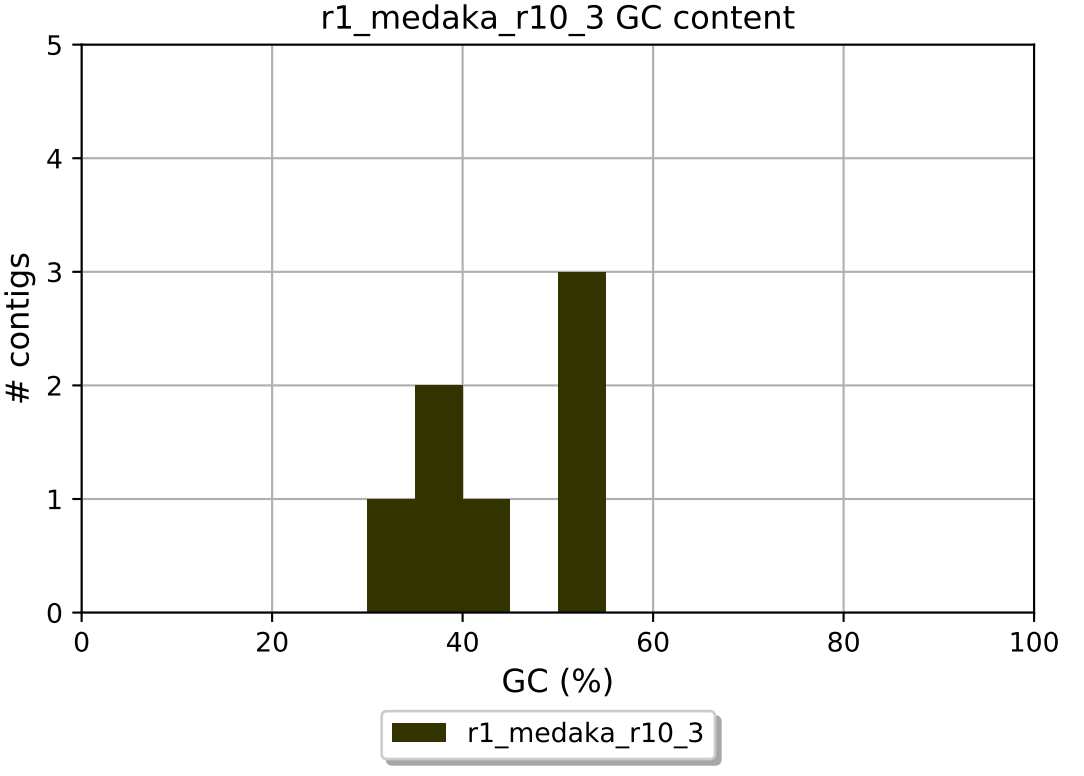

MP_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_1

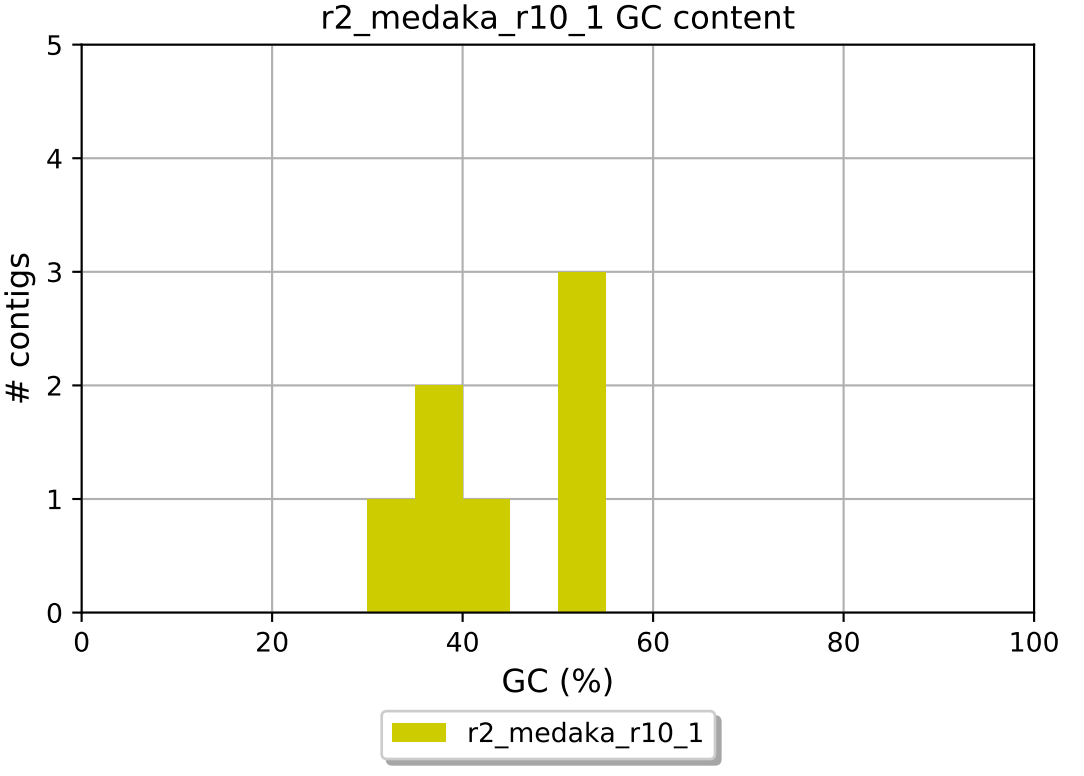

MP_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_2

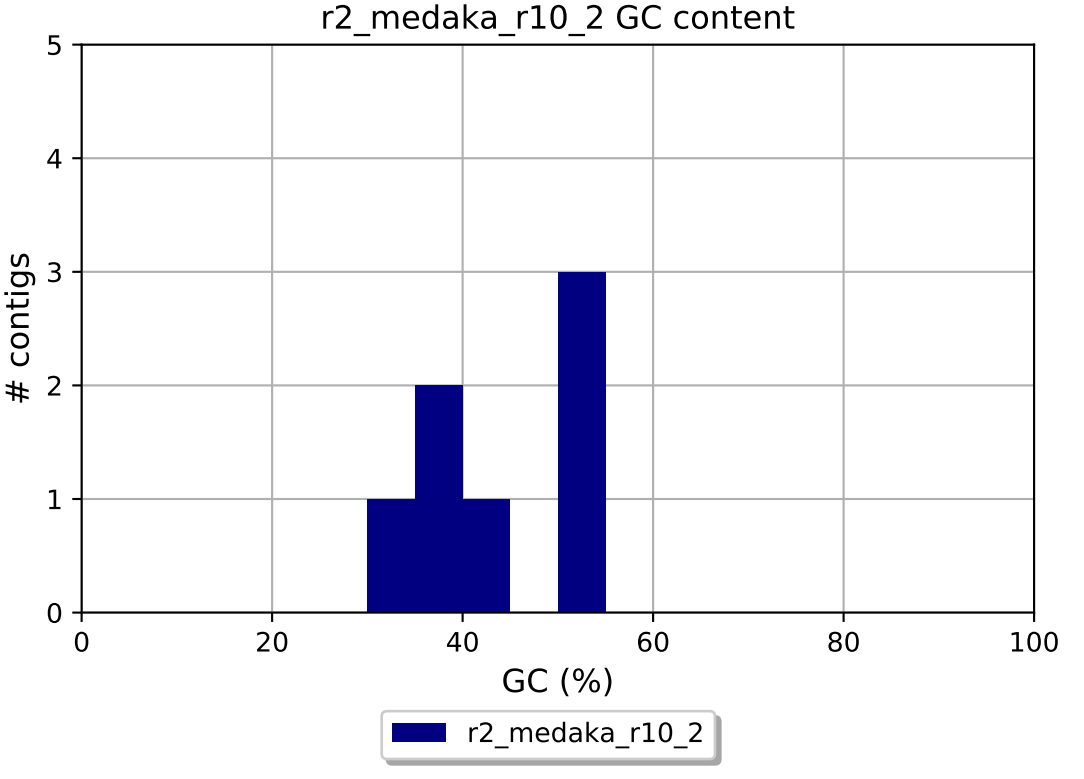

MP_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
MP_r10_3

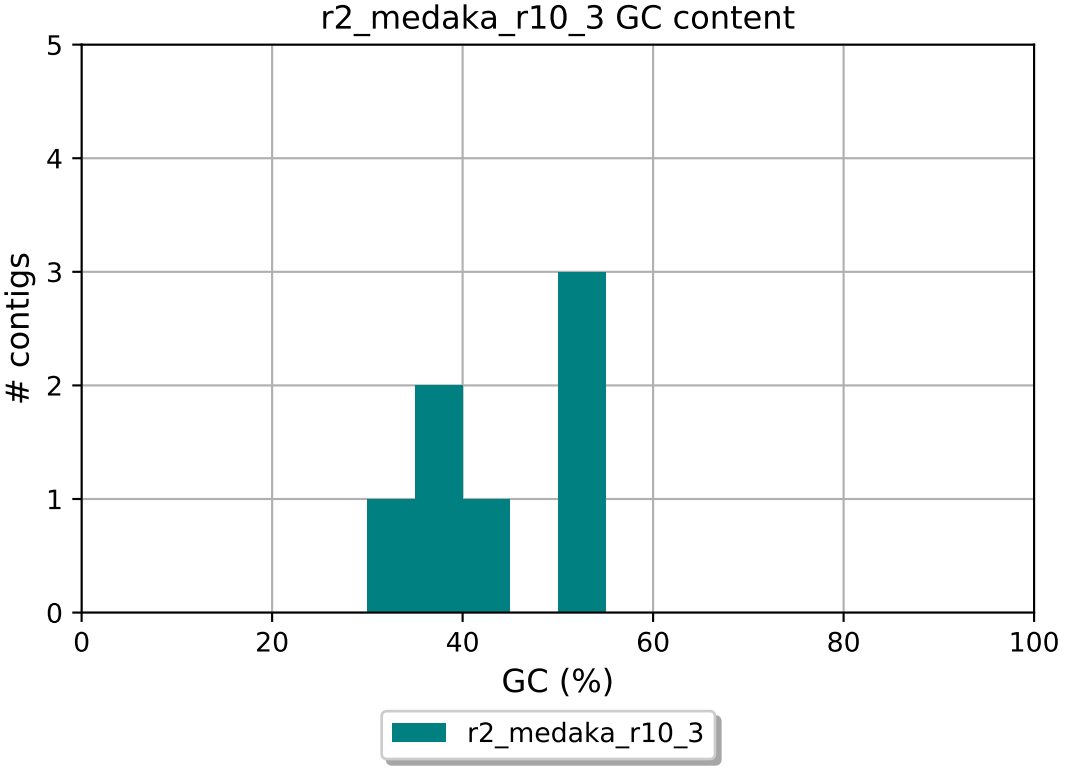

r1_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_1

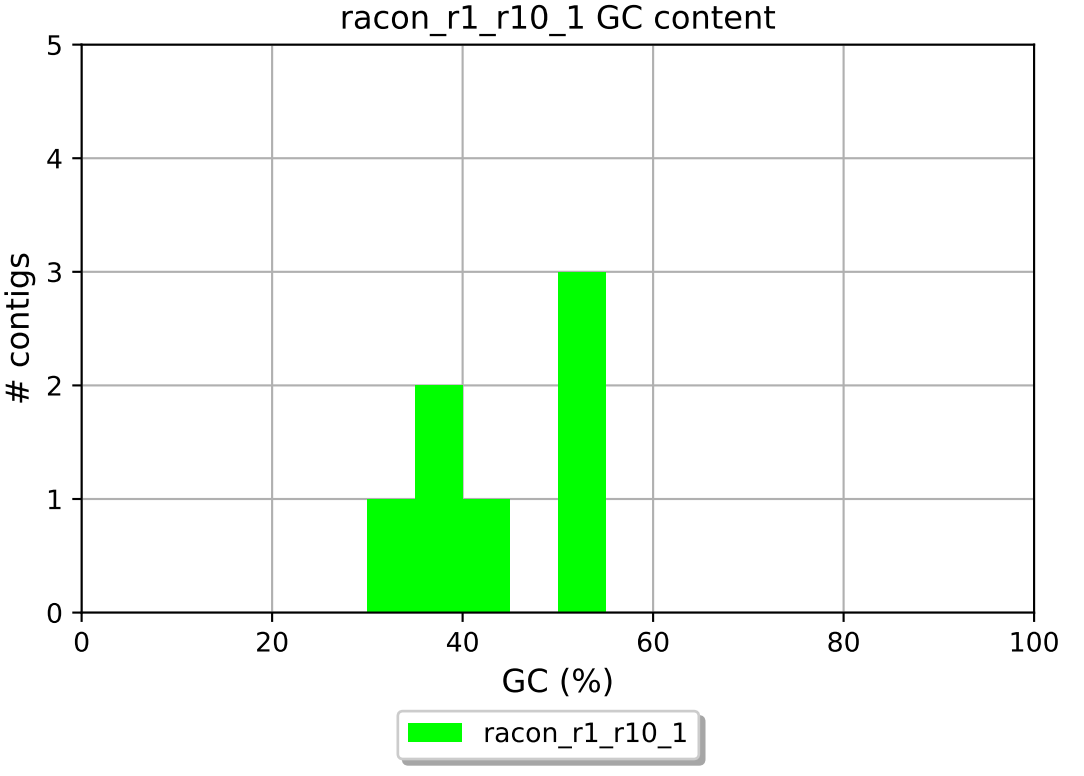

r1_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_2

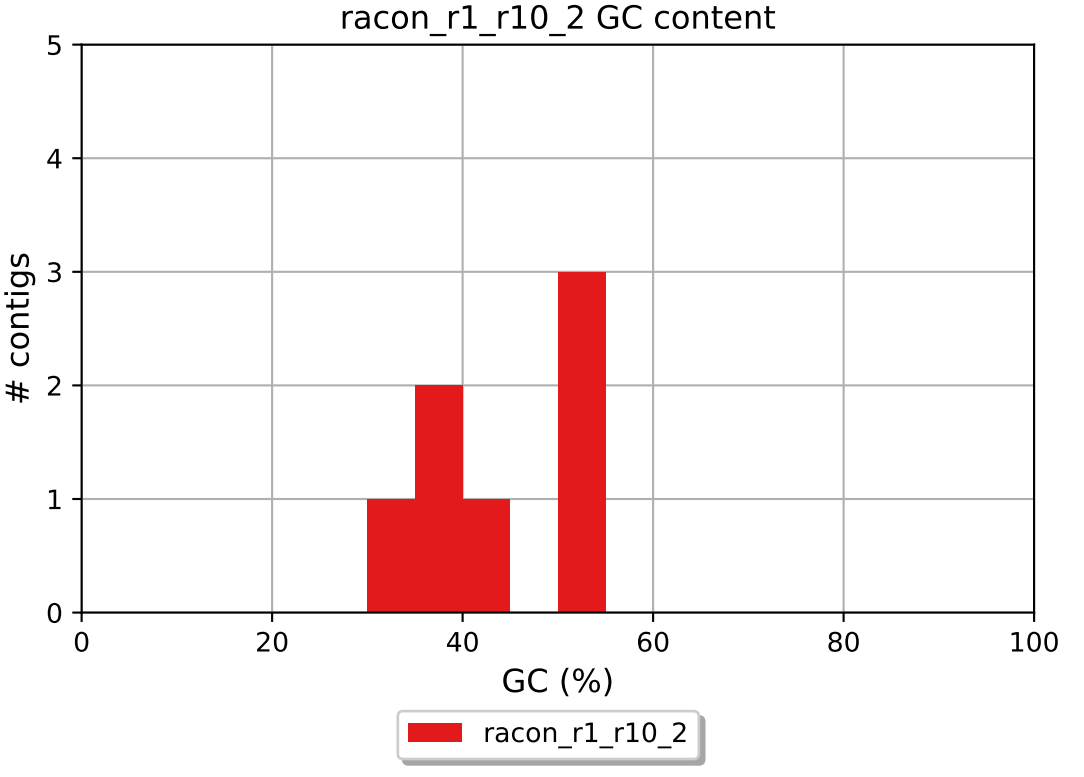

r1_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r1_medaka_r10_3

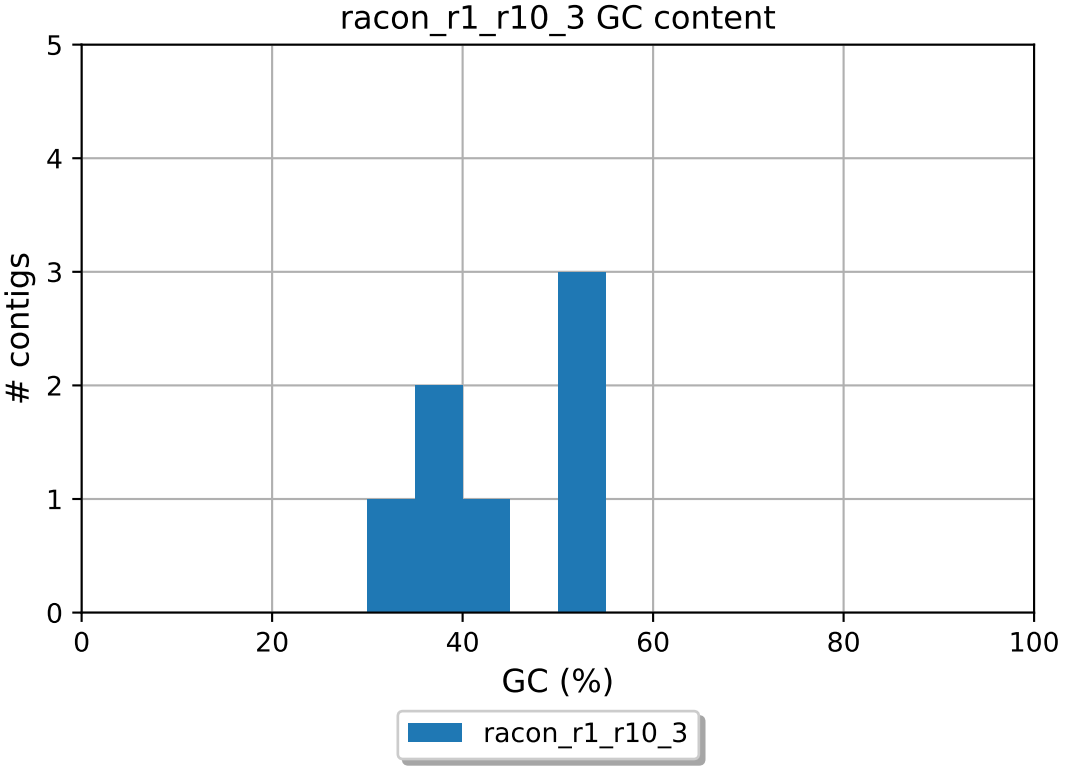

r2_medaka_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_1

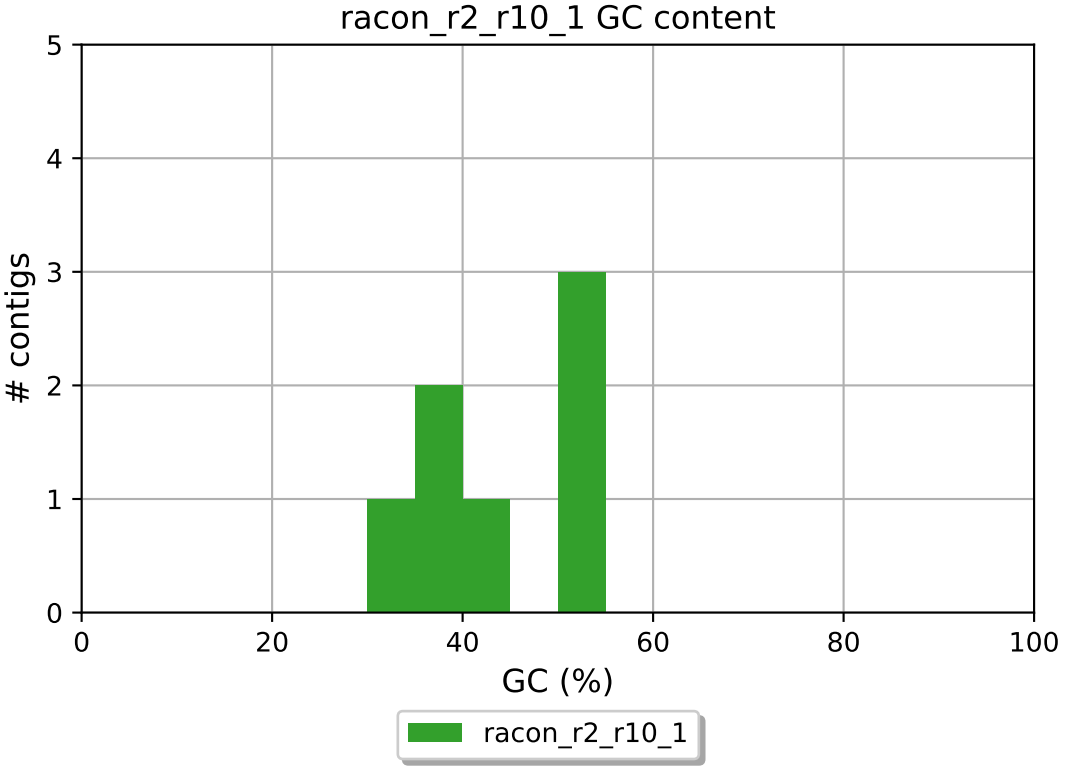

r2_medaka_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_2

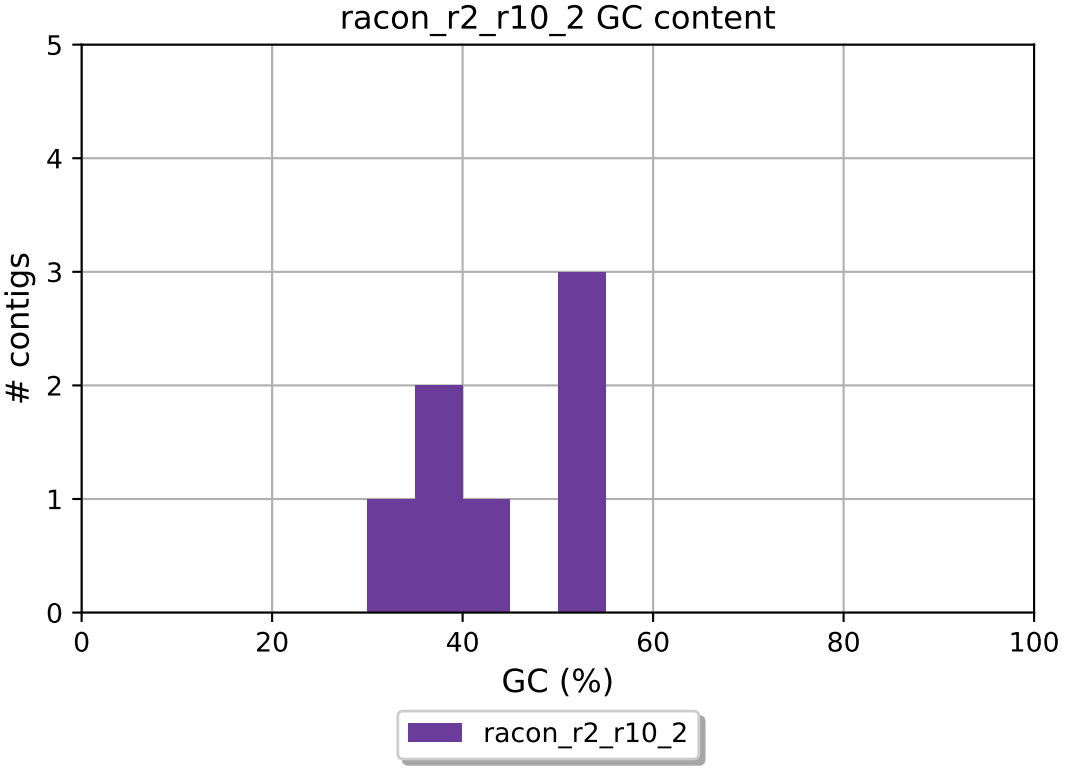

r2_medaka_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
r2_medaka_r10_3

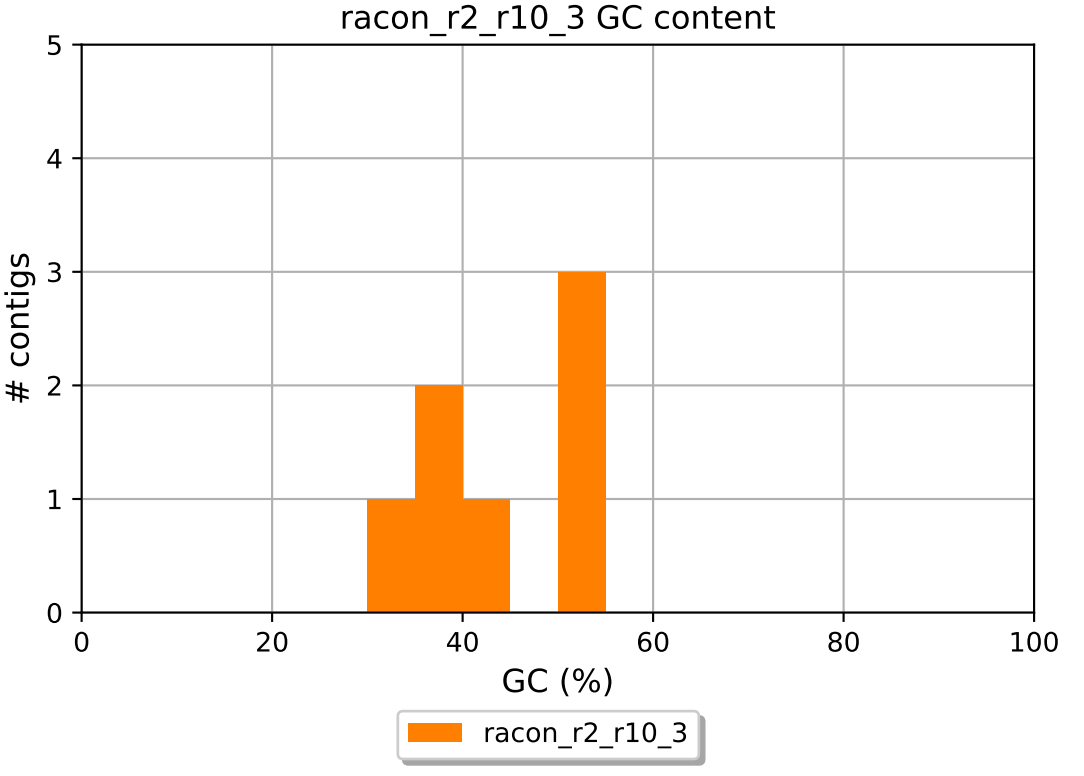

racon_r1_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_1

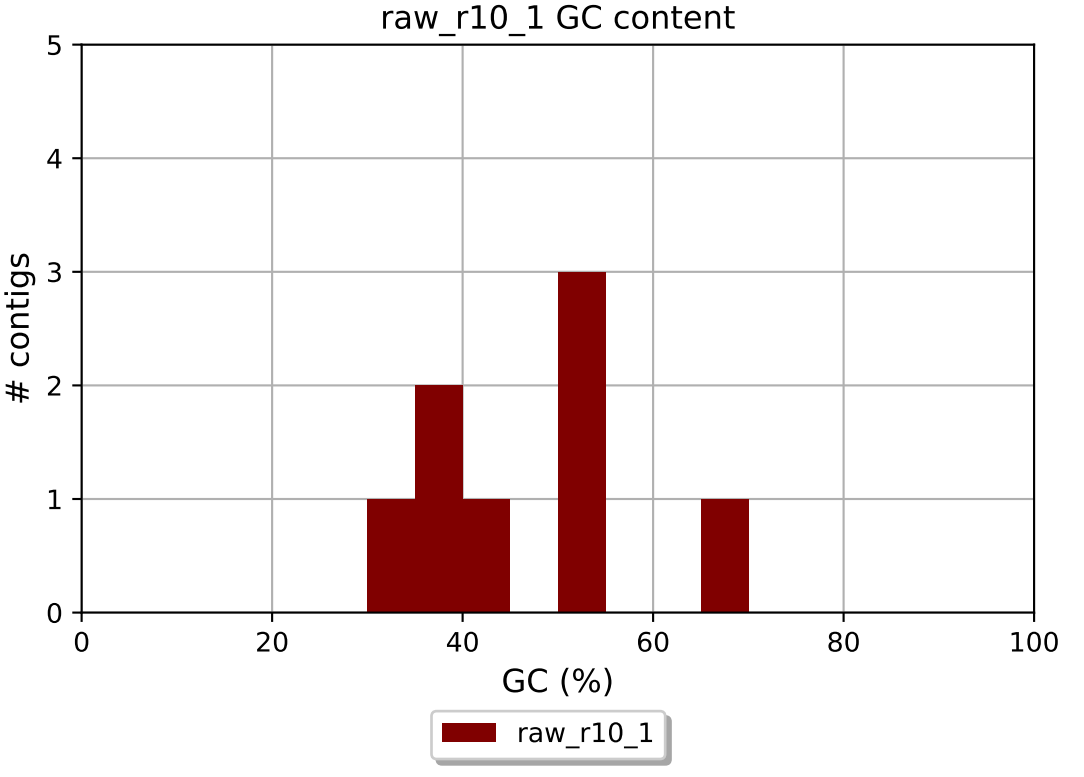

racon_r1_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_2

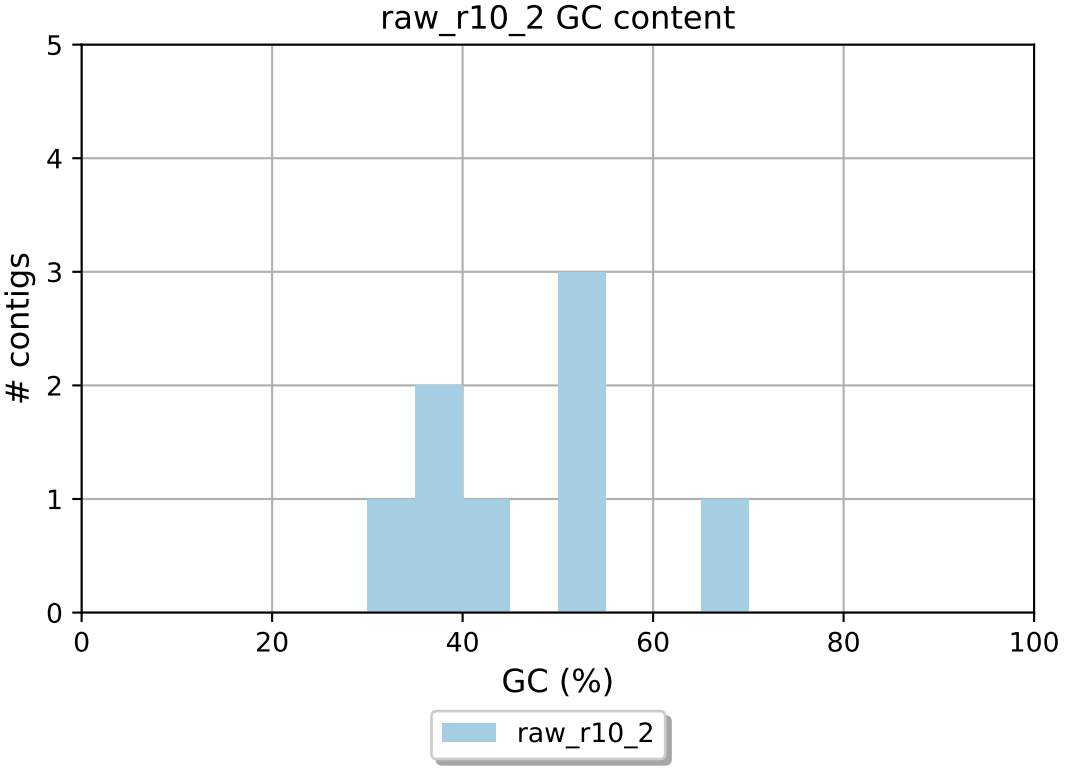

racon_r1_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r1_r10_3

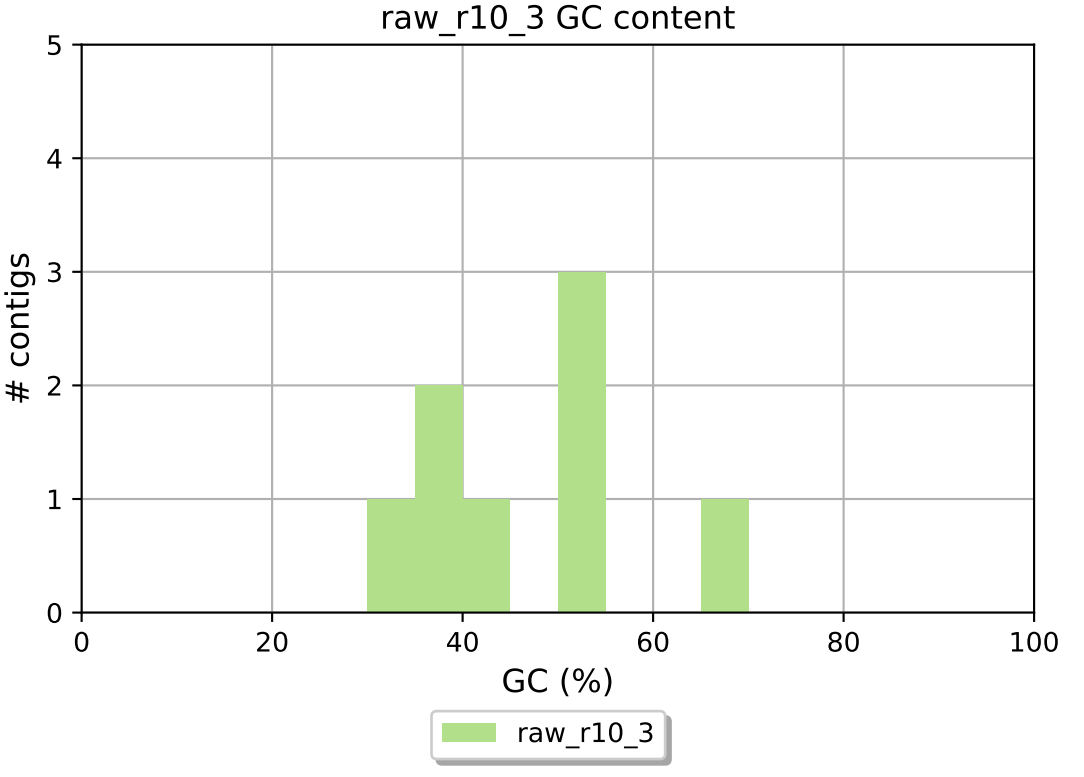

racon_r2_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_1

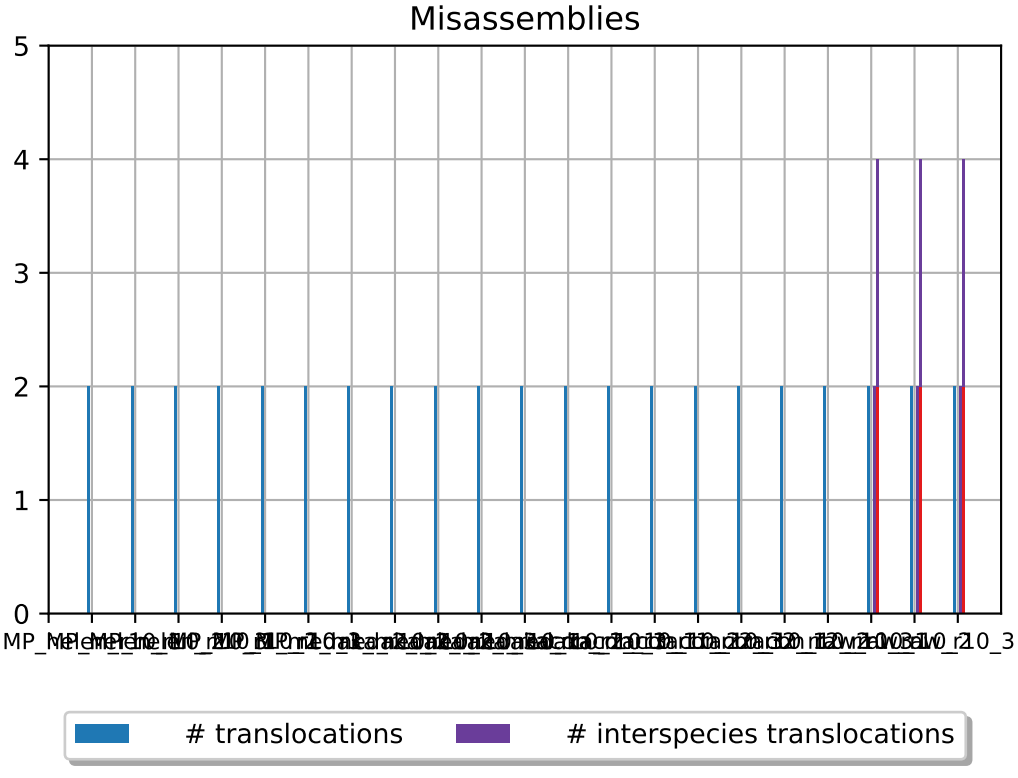

racon_r2_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_2

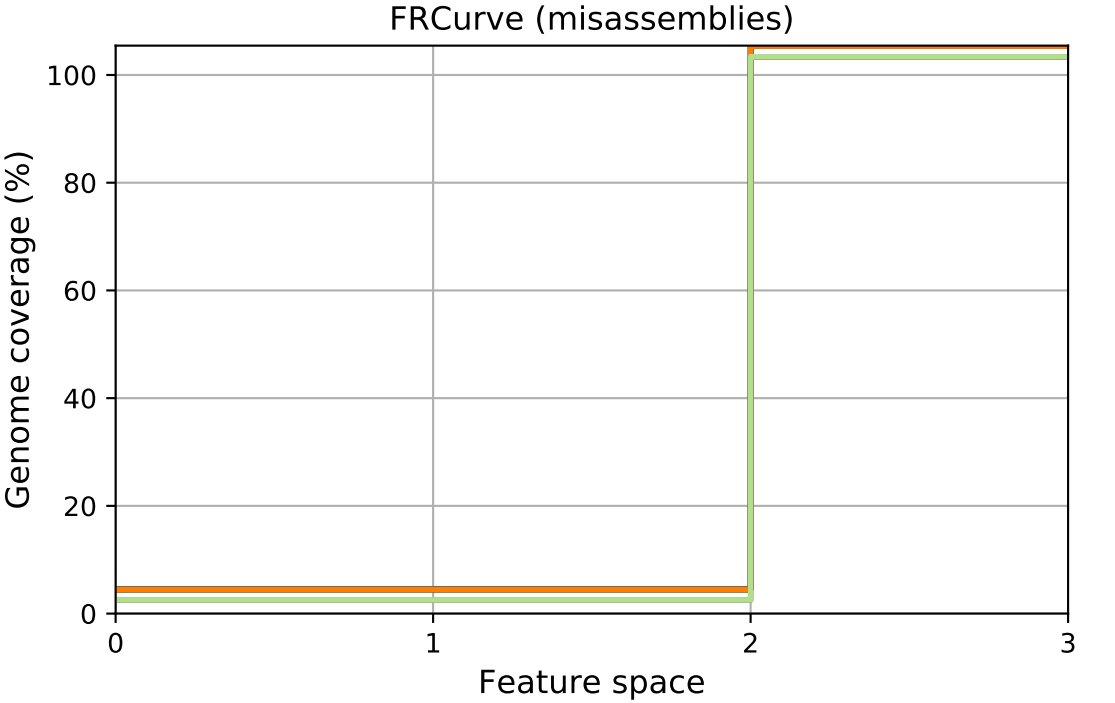

racon_r2_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
racon_r2_r10_3

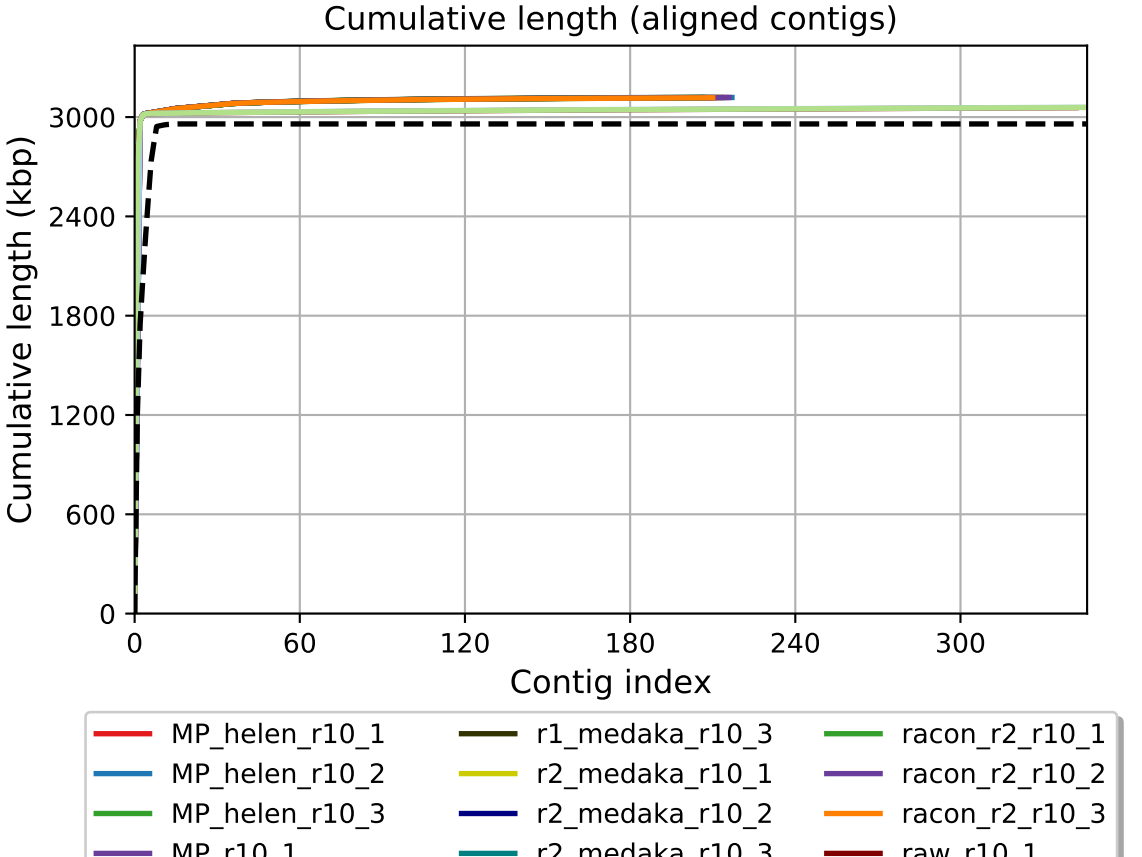

raw_r10_1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_1

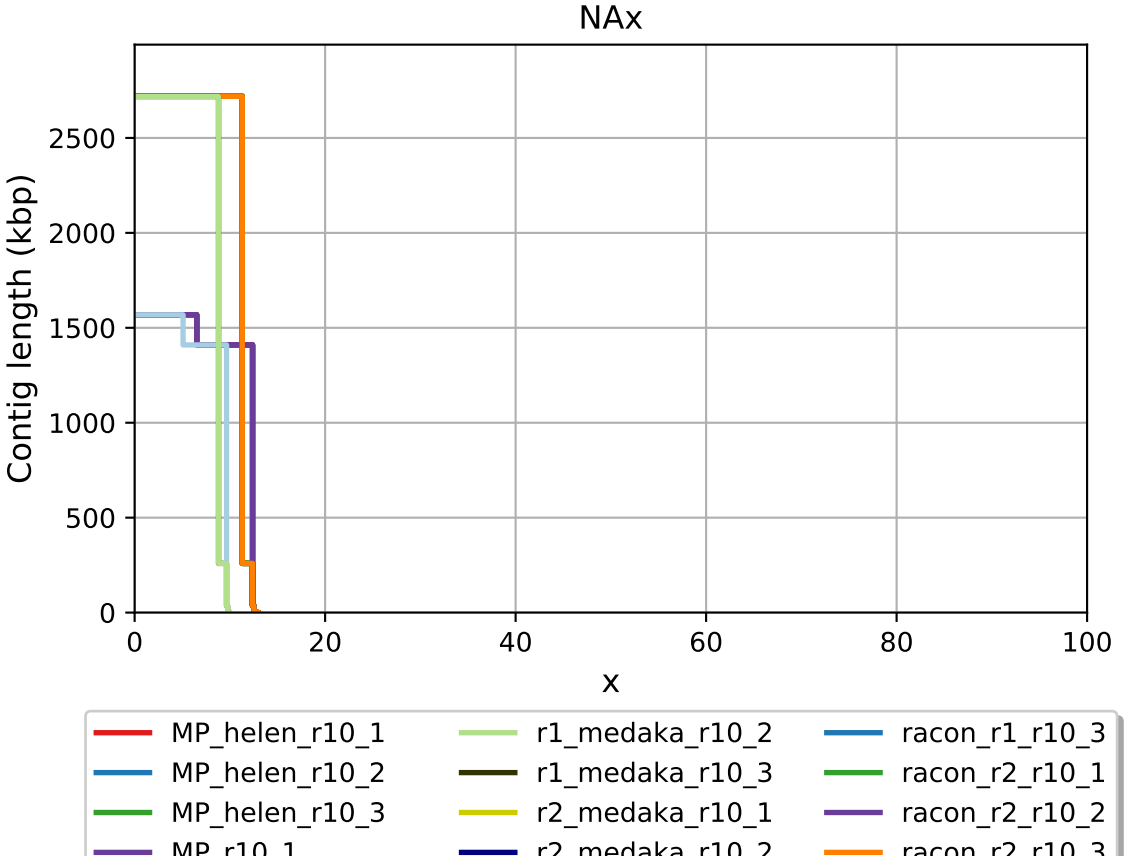

raw_r10_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_2

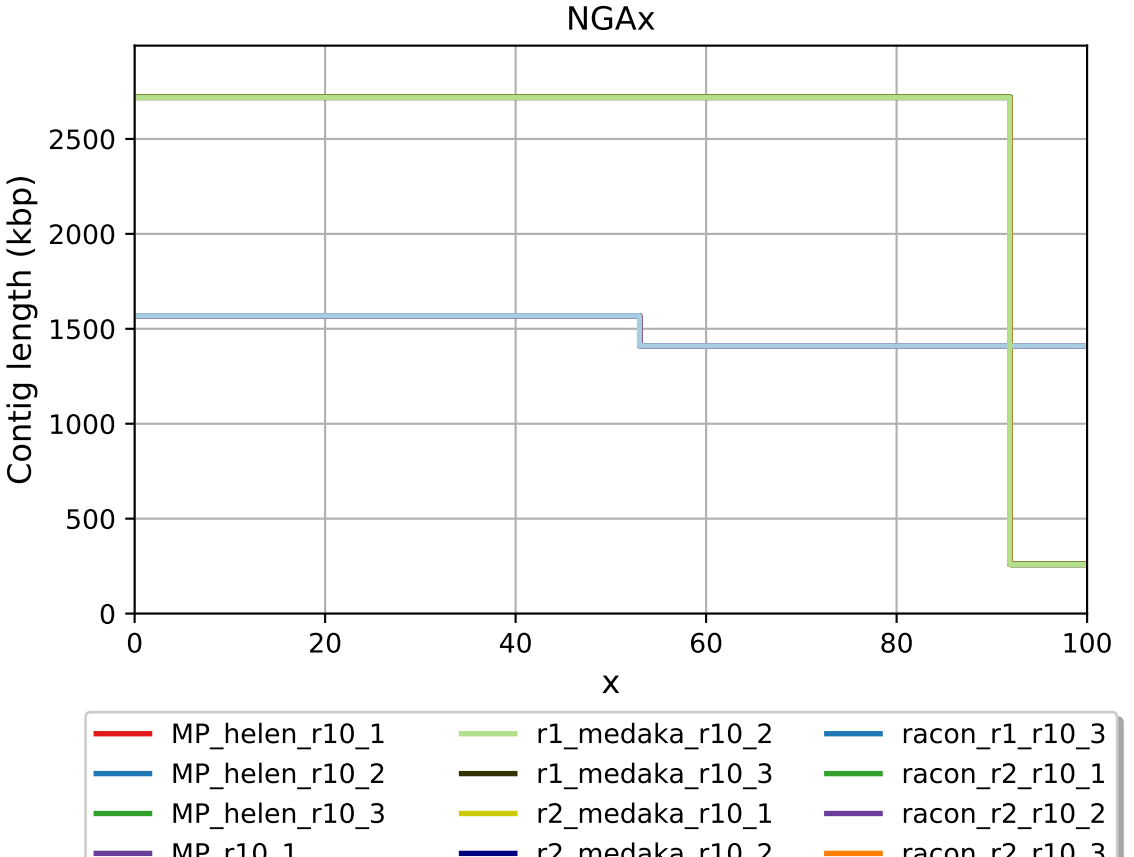

raw_r10_3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
raw_r10_3

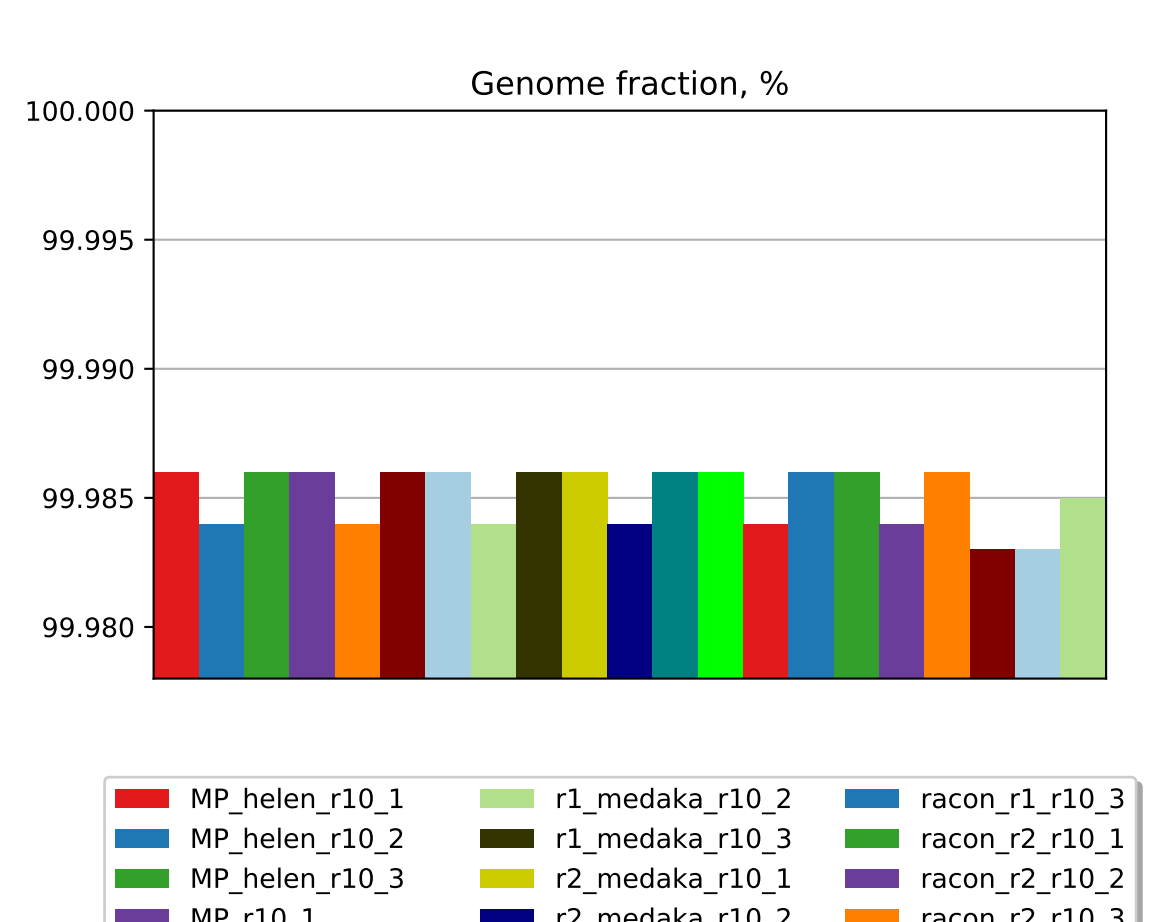

Misassemblies
5
4
3
2
1
0
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
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)
3000
2400
1800
1200
600
0
0
60
120
180
240
300
Contig index
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


NAx
Contig length (kbp)
2500
2000
1500
1000
500
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


NGAx
Contig length (kbp)
2500
2000
1500
1000
500
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


Genome fraction, %
100.000
99.995
99.990
99.985
99.980
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