

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	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357	4738357
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 (%)	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15	52.15
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	2845303	2845263	2845303	2990670	2845424	2845368	2845573	2845324	2845566	2845324	2990627	2845425	2845368	2845425	2845368	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	15	16	15	15	15	15	18	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# 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	4758902	4757799	4759020	4758488	4757908	4757843	4755996	4758906	4758018	4759008	4758481	4757940	4757851	4755926	4758924	4757804	4759024	4758498	4757988	4757863	4756050
# local misassemblies	8	8	8	7	8	8	19	8	8	8	7	8	8	27	8	8	8	7	8	8	22
# 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	19035966	19033364	19036335	19025938	19021731	19018187	23177888	19038353	19034535	19036611	19025782	19020584	19014756	25889054	19037050	19033913	19035526	19022933	19025677	19014891	23176099
Genome fraction (%)	98.918	98.917	98.920	98.920	98.920	98.920	98.895	98.918	98.920	98.920	98.920	98.920	98.891	98.920	98.918	98.919	98.920	98.920	98.920	98.896	98.896
Duplication ratio	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.076	1.075	1.075	1.075	1.075	1.076	1.075	1.075	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	415.25	412.37	416.26	417.11	417.80	413.57	460.08	411.55	408.81	415.71	417.22	422.04	418.12	467.04	412.64	409.84	416.52	417.80	410.99	418.67	463.79
# indels per 100 kbp	21.58	16.50	23.35	23.43	40.25	38.22	224.49	20.79	15.24	23.11	23.28	40.20	38.18	219.31	21.17	16.26	23.26	23.50	39.82	37.86	224.77
Largest alignment	1342517	1342449	1342630	1342625	1342280	1342286	1341459	1342509	1342448	1342621	1342631	1342297	1342306	1341360	1342502	1342445	1342633	1342633	1342298	1342306	1341434
Total aligned length	5035931	5035186	5037112	5036986	5036341	5033831	4951182	5034135	5033702	5036925	5037073	5037640	5035983	4959058	5034980	5034328	5037203	5037481	5036323	4952803	4952803
NGA50	745380	745358	745424	745418	745282	745278	744951	745380	745348	745429	745430	745272	745277	745086	745392	745355	745426	745423	745279	745273	744978
NGA75	611514	611512	611578	611579	611420	611436	433917	611516	611509	611571	611574	611437	611440	432790	611500	611467	611578	611580	611449	611446	433863
LGA50	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
LGA75	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5

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	15	16	15	15	15	15	18	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# contig misassemblies	15	16	15	15	15	15	18	15	15	15	15	15	15	18	15	16	15	15	15	15	18
# 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	14	13	13	13	13	16	13	13	13	13	13	13	16	13	14	13	13	13	13	16
# c. inversions	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
# 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	4758902	4757799	4759020	4758488	4757908	4757843	4755996	4758906	4758018	4759008	4758481	4757940	4757851	4755926	4758924	4757804	4759024	4758498	4757988	4757863	4756050
# 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	6	4	4	4	4	4	14	6	4	4	4	4	4	16	6	4	4	4	4	4	14
# local misassemblies	8	8	8	7	8	8	19	8	8	8	7	8	8	27	8	8	8	7	8	8	22
# 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	14	14	14	14	14	14	11	14	14	14	14	14	14	7	14	14	14	14	14	14	10
# 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	19458	19323	19506	19546	19578	19380	21554	19285	19157	19480	19551	19777	19593	21879	19336	19205	19518	19578	19259	19619	21728
# indels	1011	773	1094	1098	1886	1791	10517	974	714	1083	1091	1884	1789	10274	992	762	1090	1101	1866	1774	10530
# indels (<= 5 bp)	914	672	1004	1007	1794	1701	10335	879	619	993	1000	1793	1699	10101	895	660	1000	1010	1775	1684	10354
# indels (> 5 bp)	97	101	90	91	92	90	182	95	95	90	91	91	90	173	97	102	90	91	91	90	176
Indels length	5578	5348	5548	5613	6518	6355	19338	5533	5237	5526	5600	6516	6348	18601	5557	5343	5549	5615	6455	6326	19193

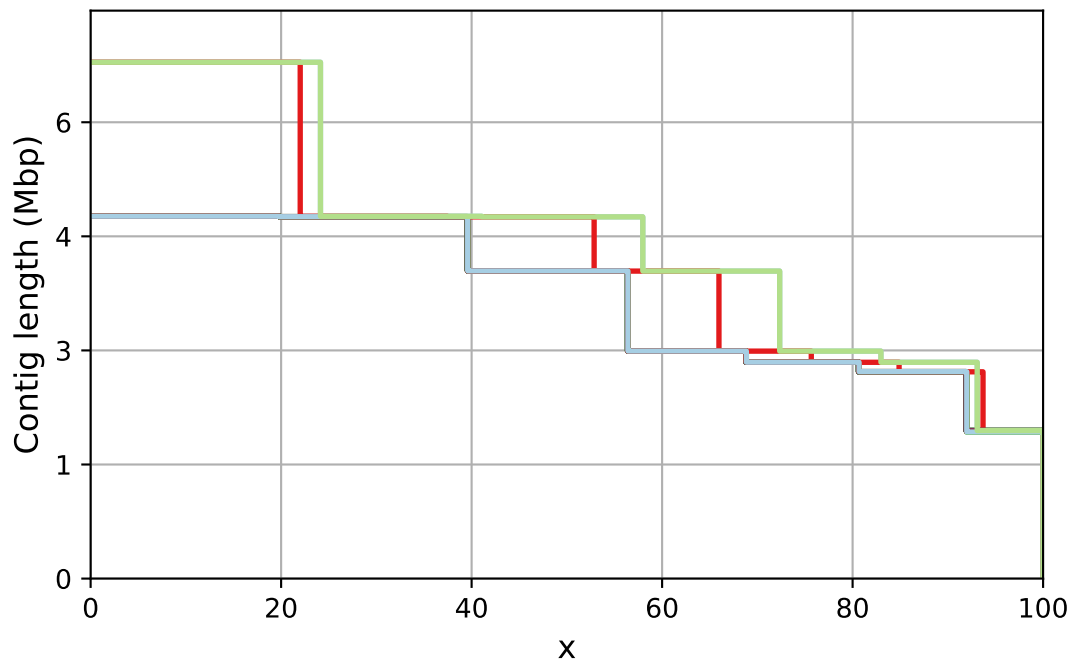
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	19035966	19033364	19036335	19025938	19021731	19018187	23177888	19038353	19034535	19036611	19025782	19020584	19014756	25889054	19037050	19033913	19035526	19022933	19025677	19014891	23176099
# 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



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

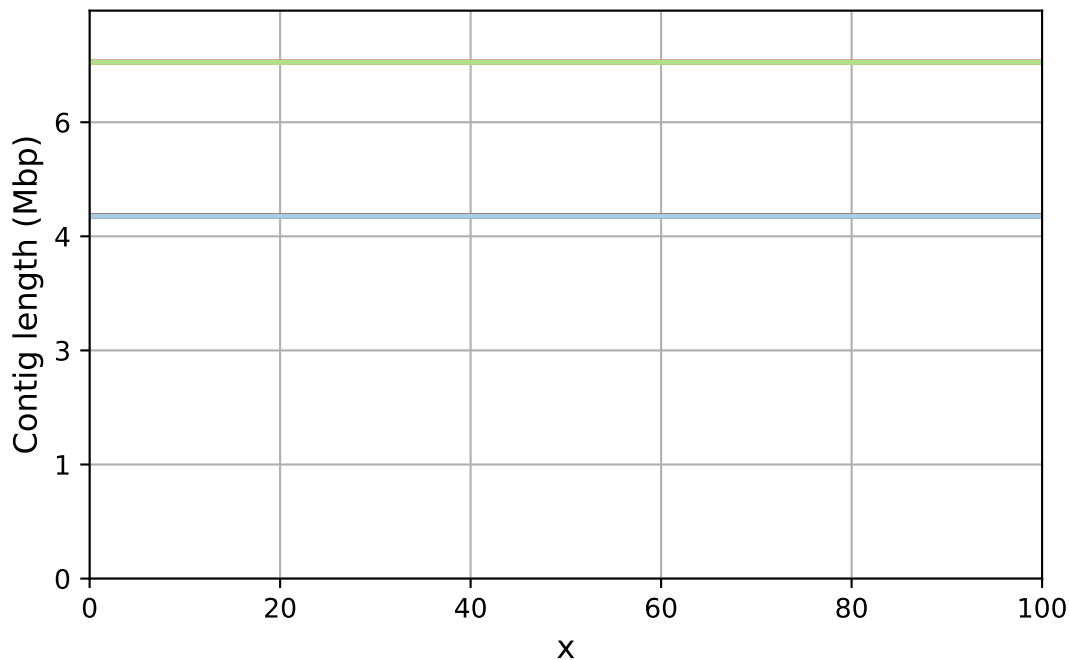
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

NGx



r10_1bin_v4_1_MP

r10_1bin_v4_2_MP

r10_1bin_v4_3_MP

r10_1bin_v4_1_MP_helen

r10_1bin_v4_2_MP_helen

r10_1bin_v4_3_MP_helen

r10_1bin_v4_1_r1_medaka

r10_1bin_v4_2_r1_medaka

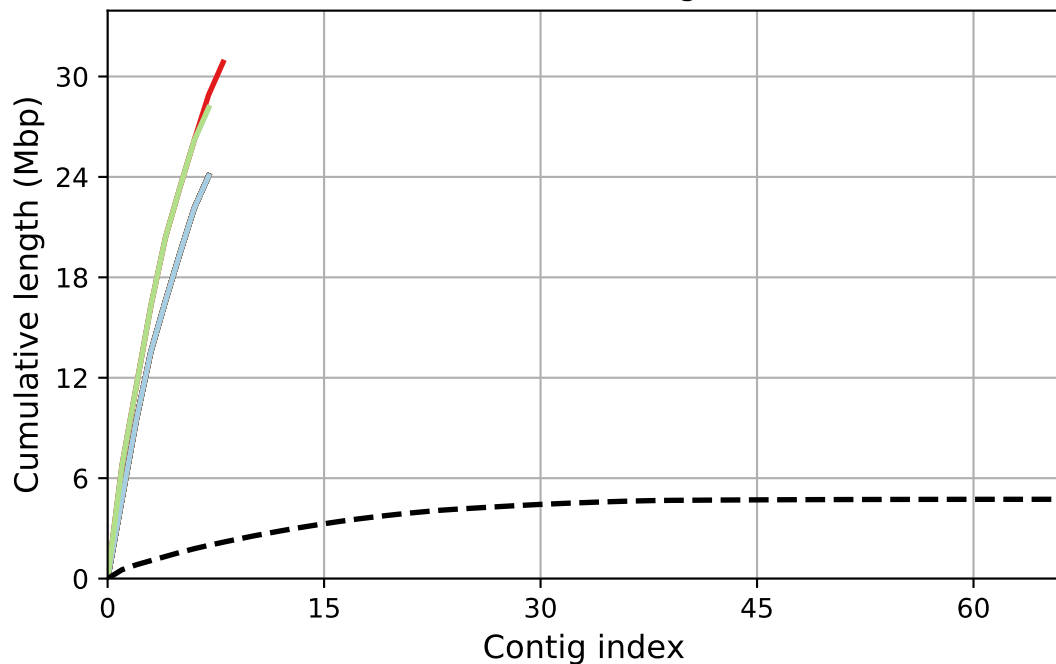
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

Cumulative length



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_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

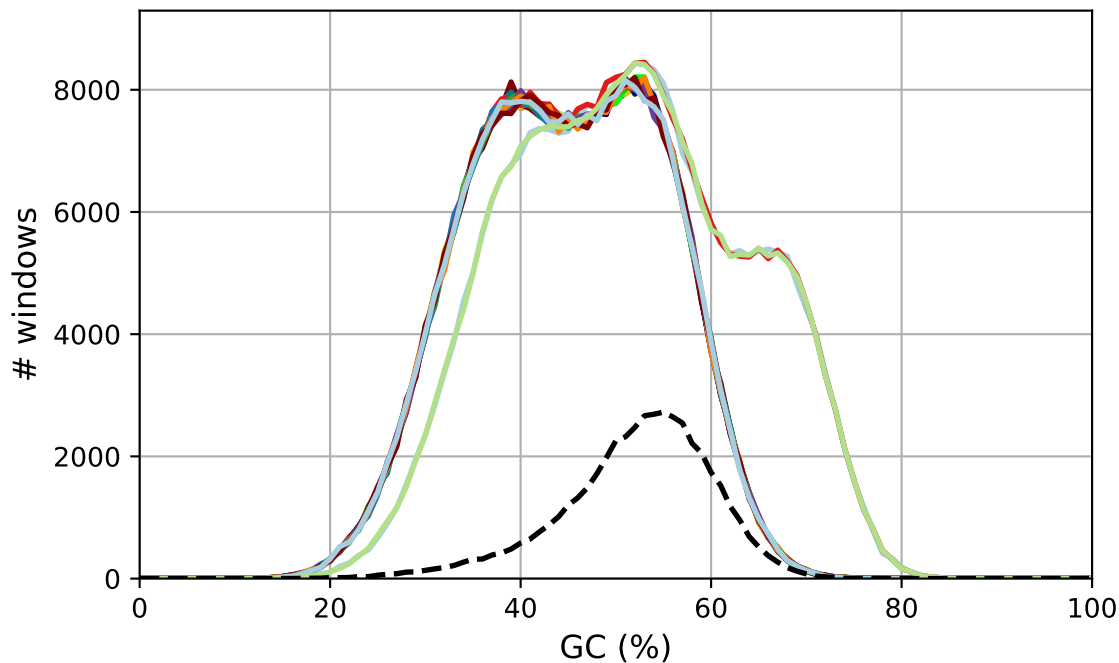
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

GC content



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_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

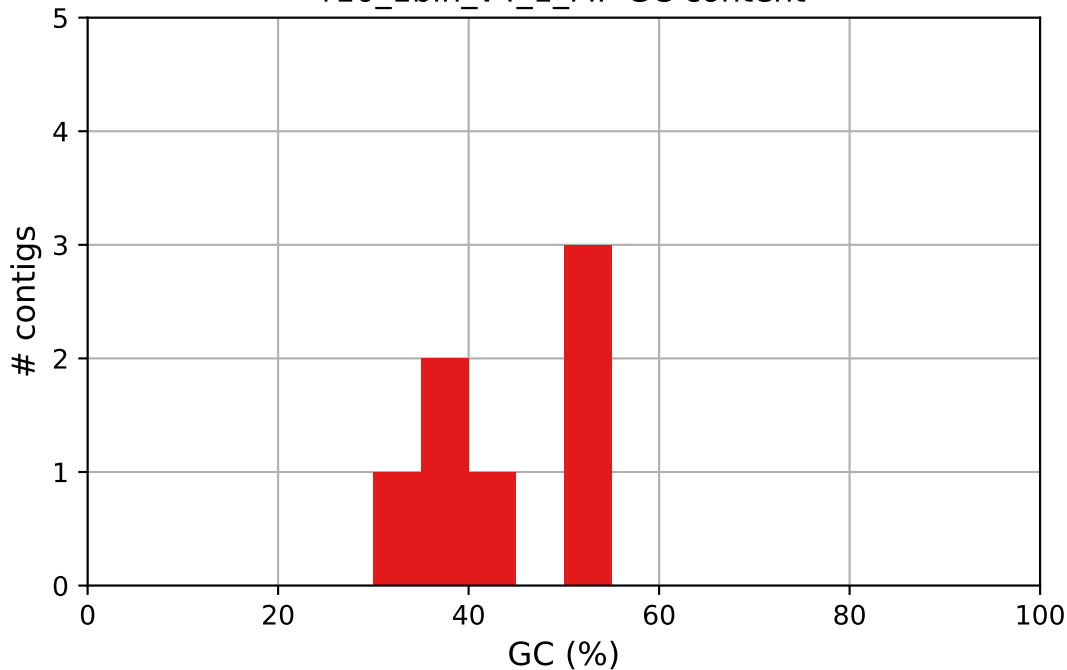
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

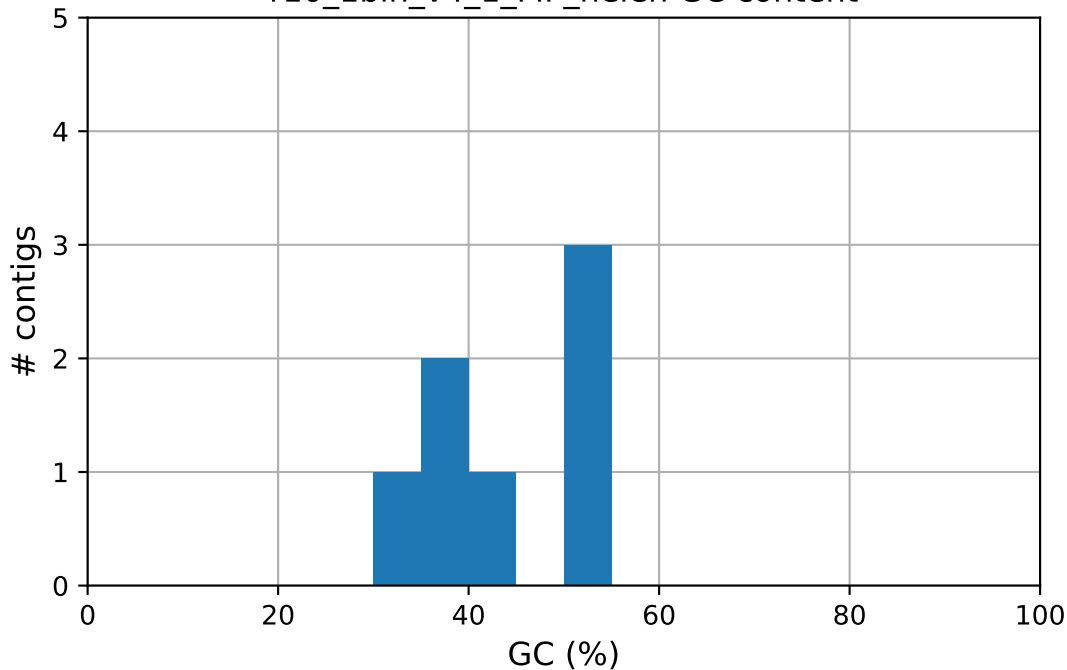
r10_1bin_v4_3_r2_medaka

r10_1bin_v4_1_MP GC content



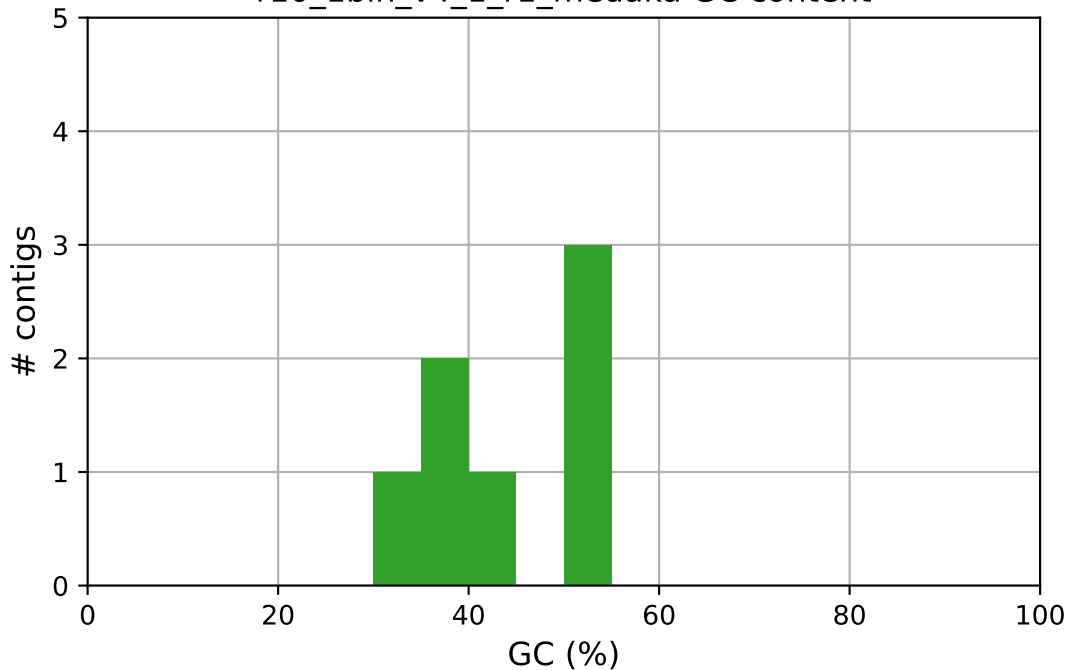
r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen GC content



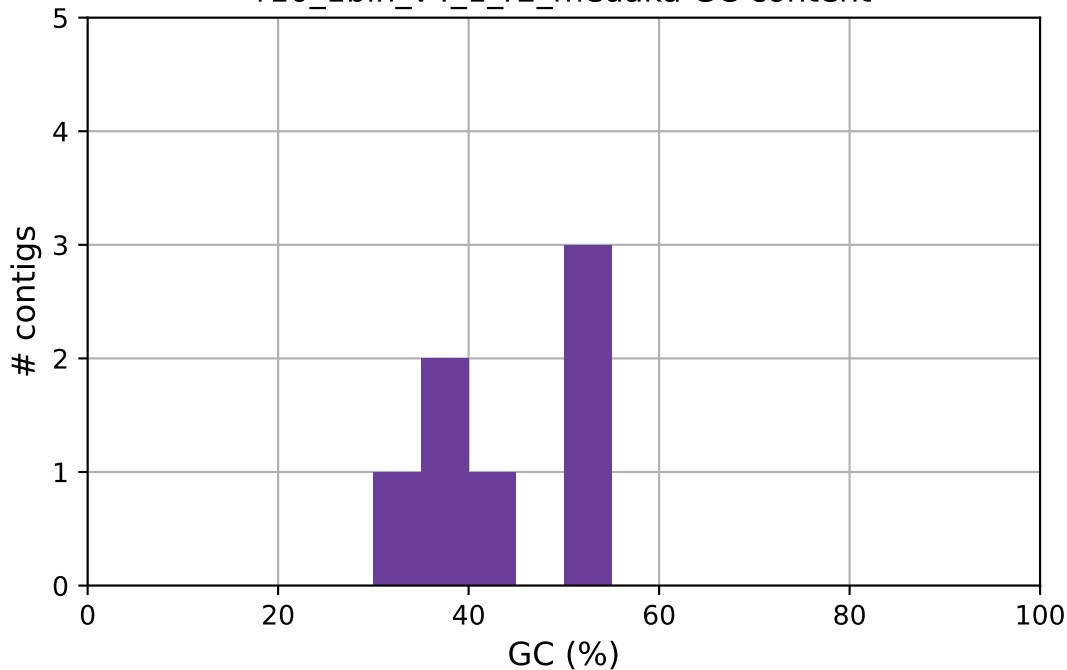
r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka GC content



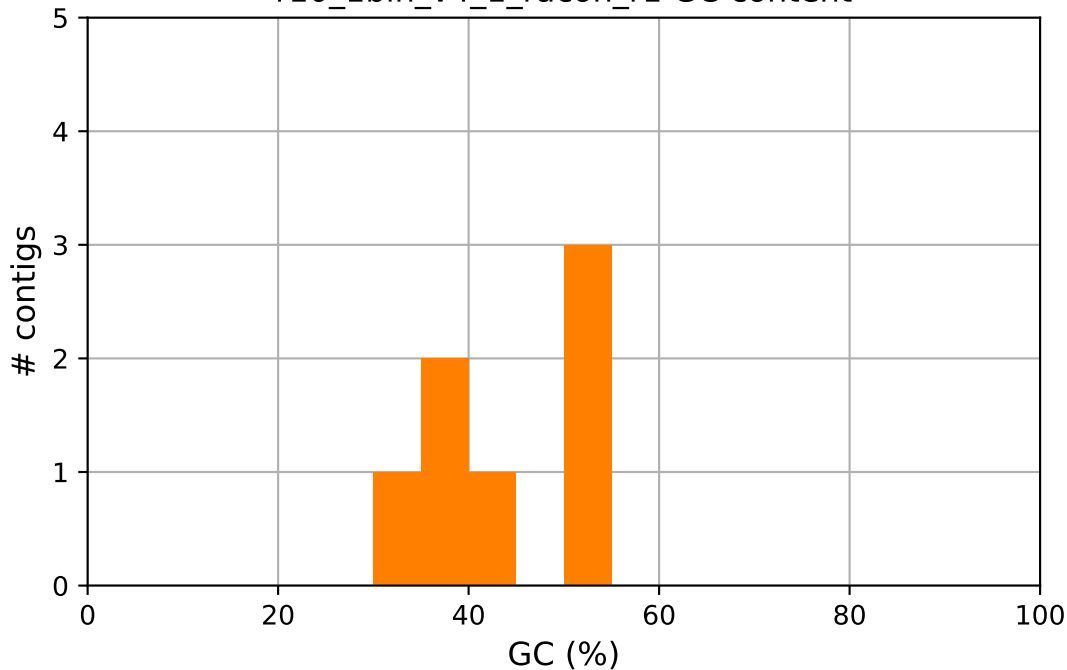
r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka GC content



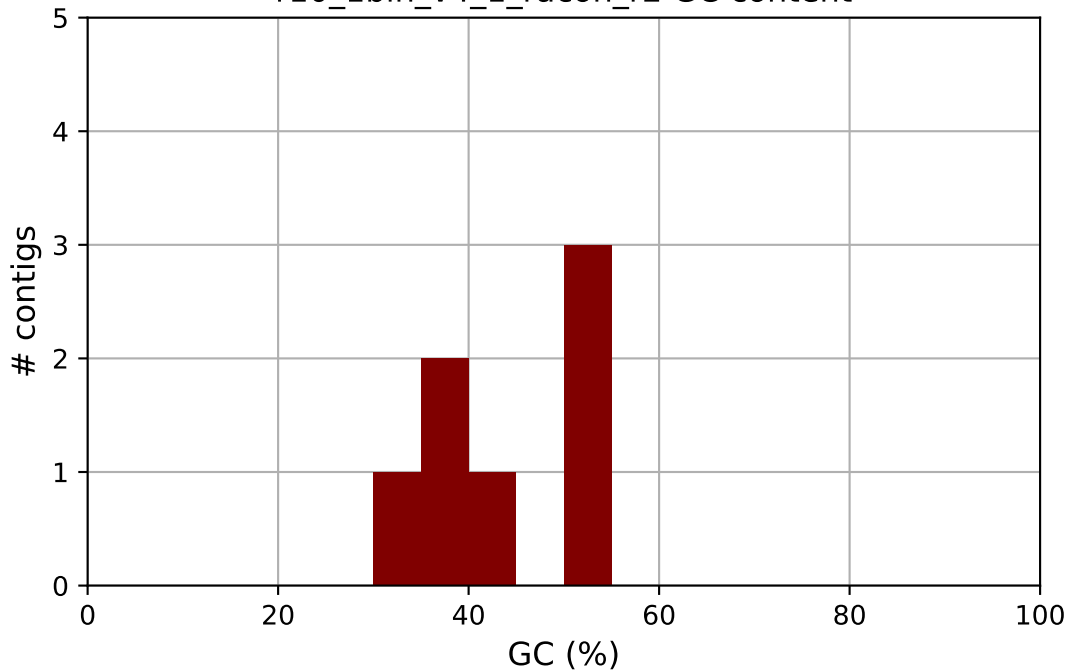
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_1_racon_r1 GC content



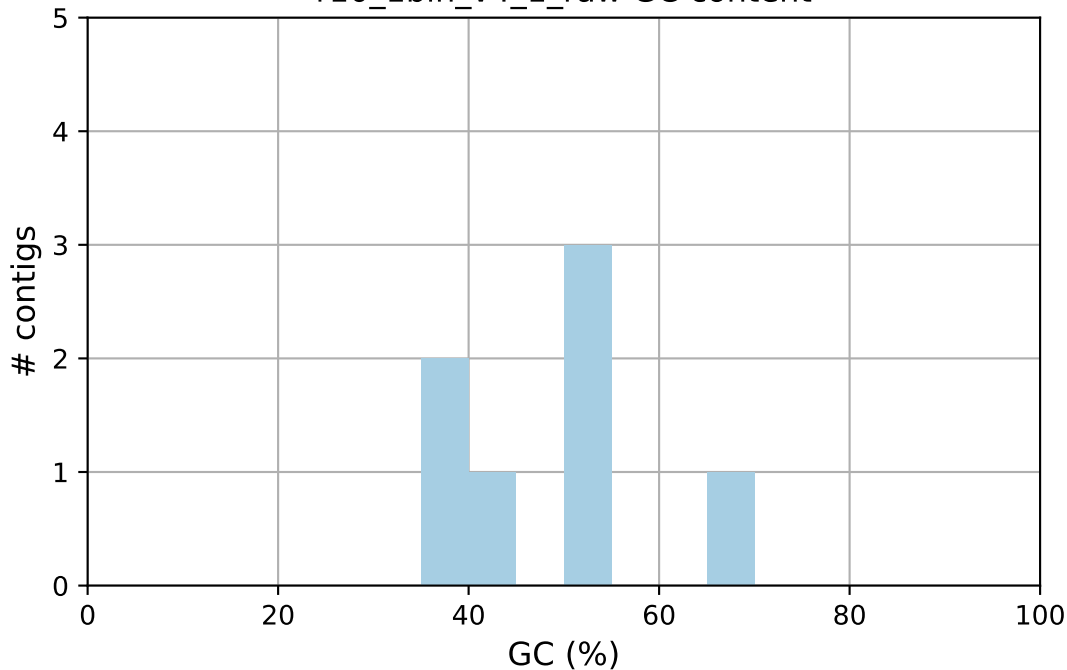
r10_1bin_v4_1_racon_r1

r10_1bin_v4_1_racon_r2 GC content



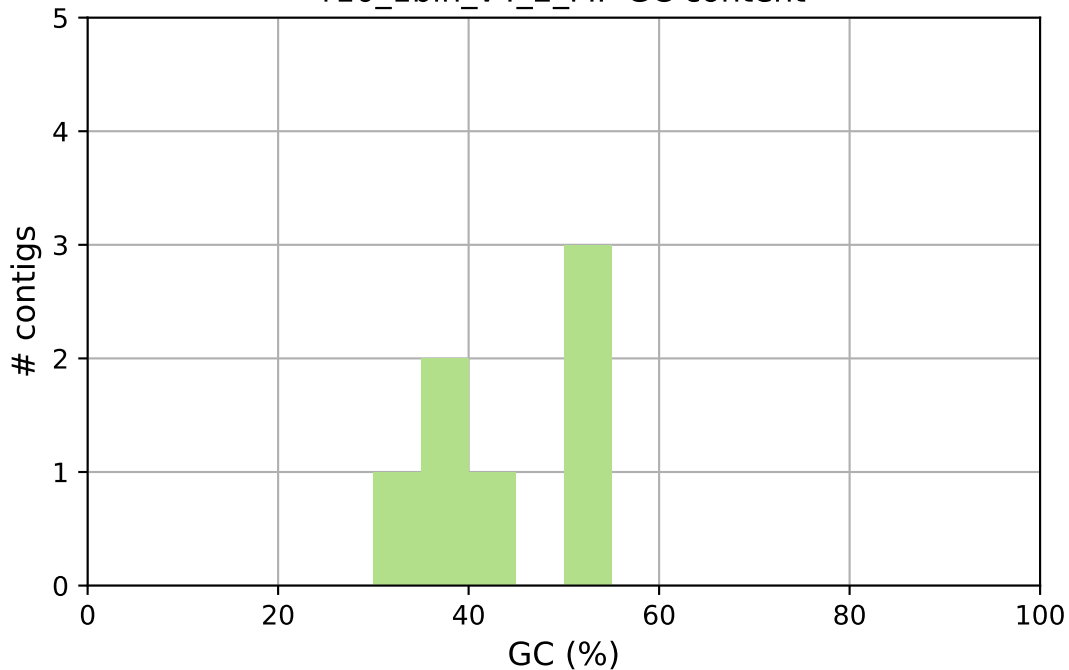
r10_1bin_v4_1_racon_r2

r10_1bin_v4_1_raw GC content



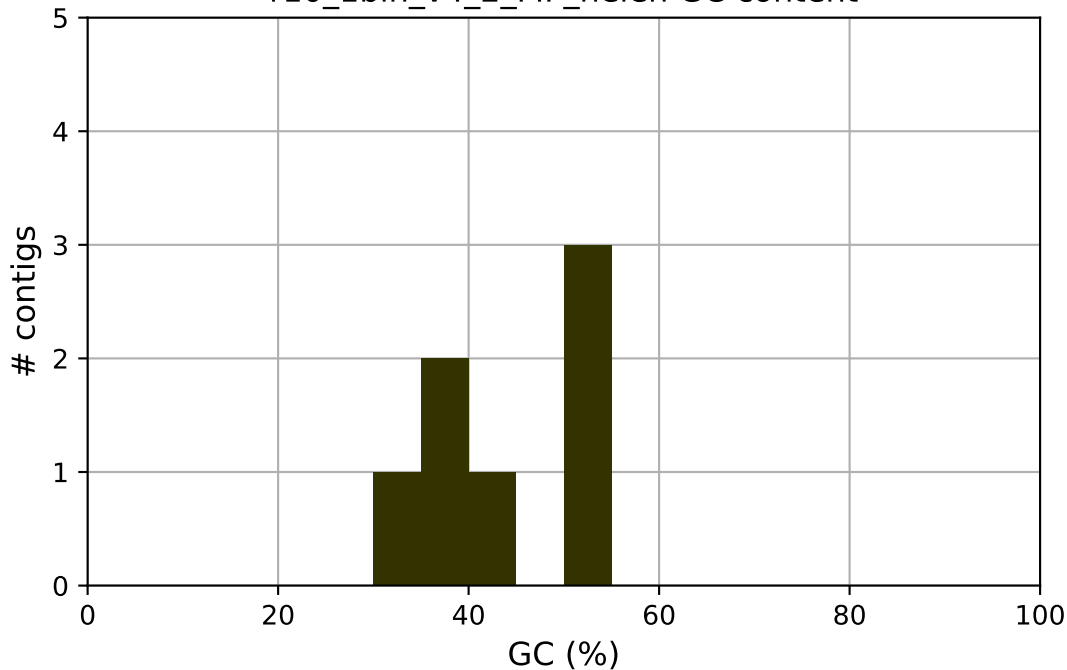
r10_1bin_v4_1_raw

r10_1bin_v4_2_MP GC content



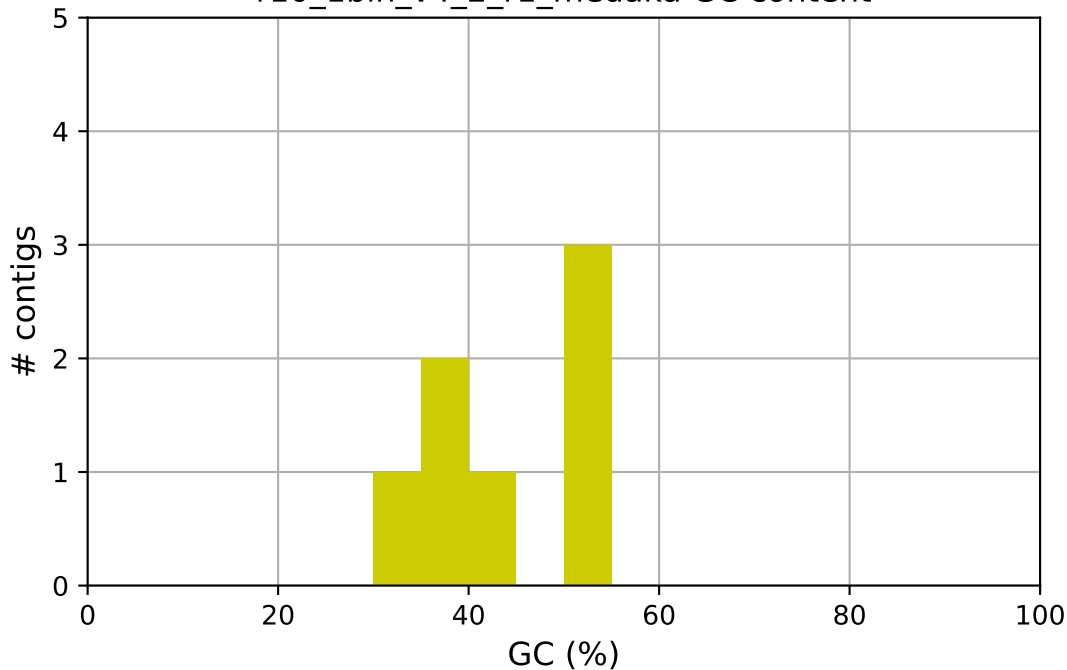
r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen GC content



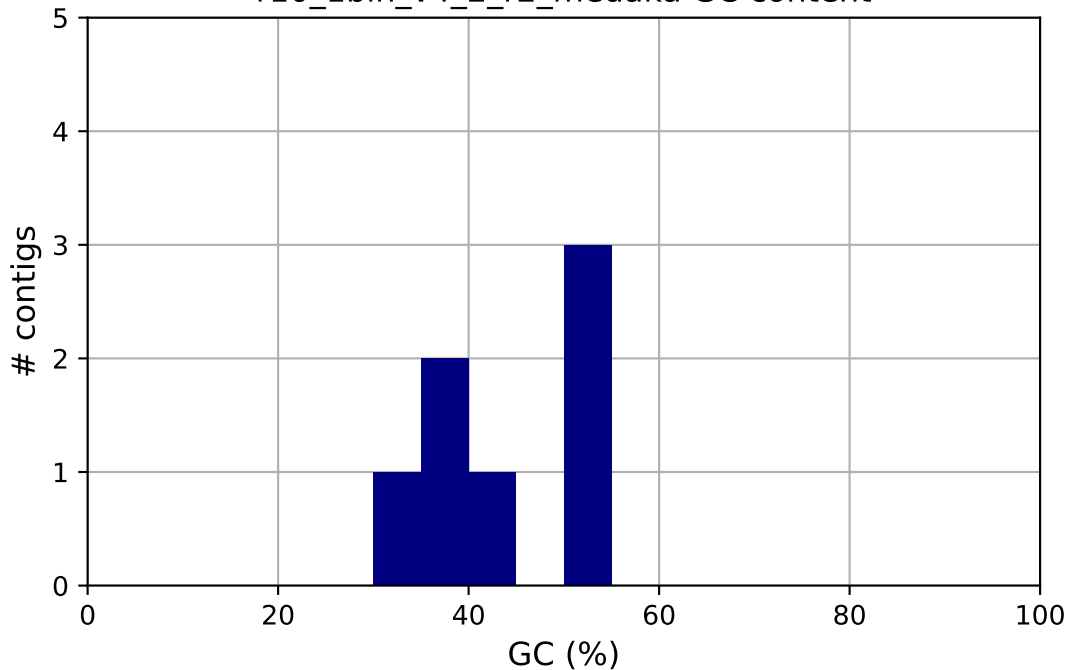
r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka GC content



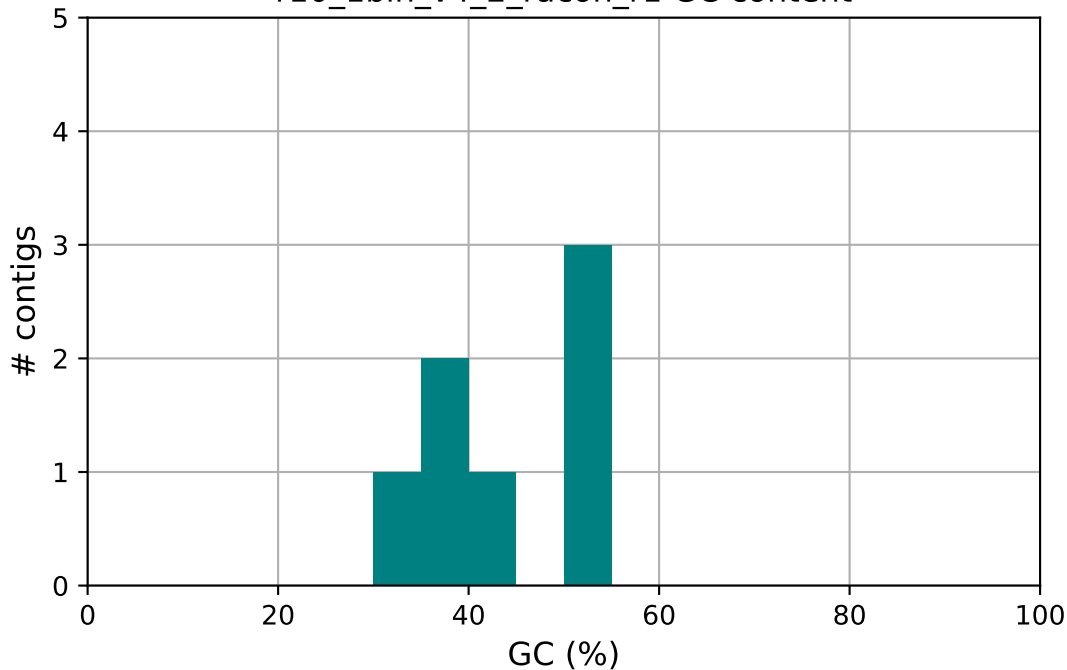
r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka GC content



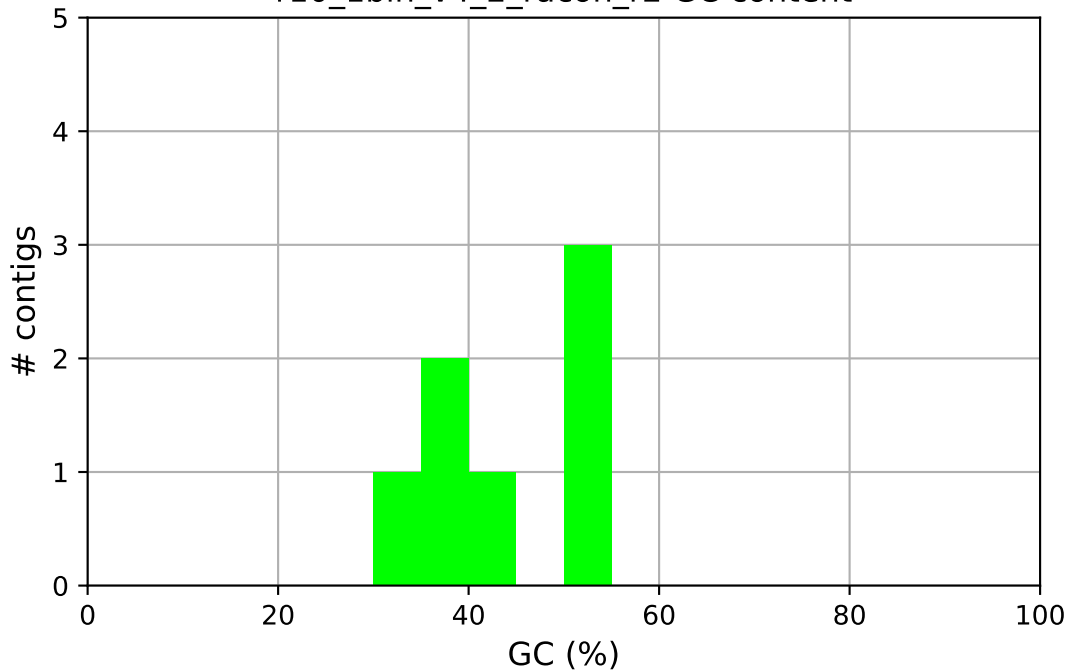
r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1 GC content



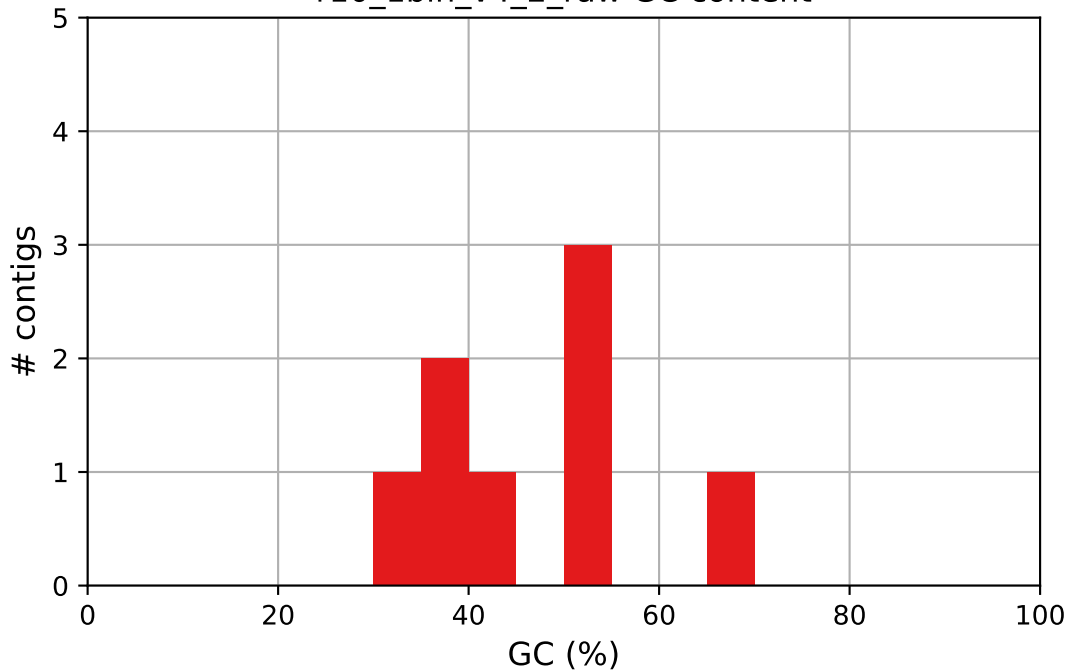
r10_1bin_v4_2_racon_r1

r10_1bin_v4_2_racon_r2 GC content



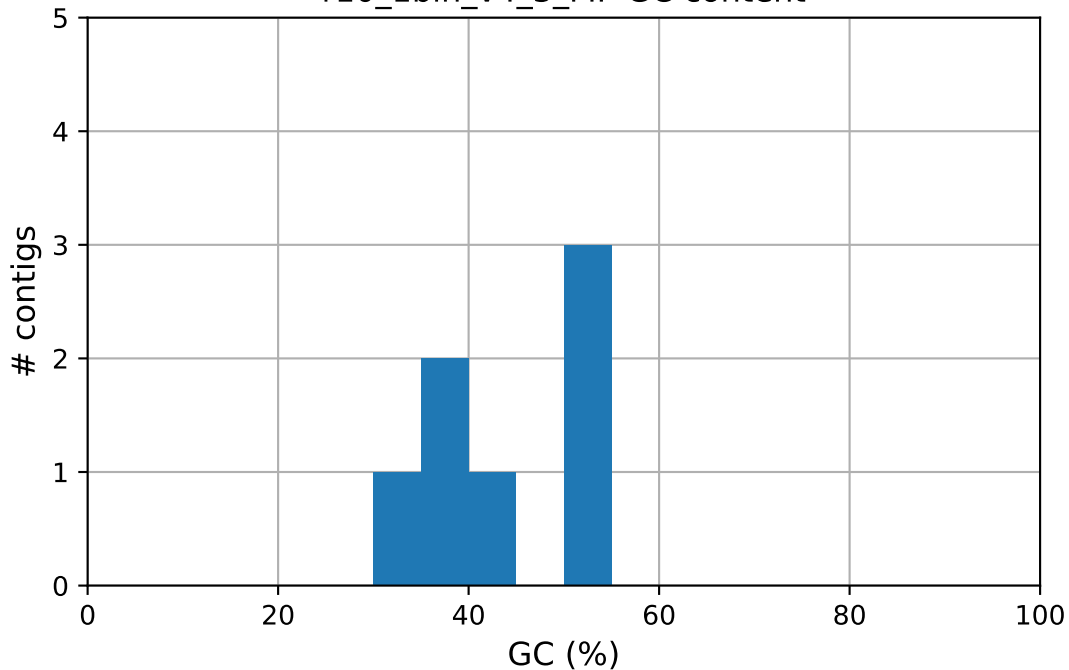
r10_1bin_v4_2_racon_r2

r10_1bin_v4_2_raw GC content



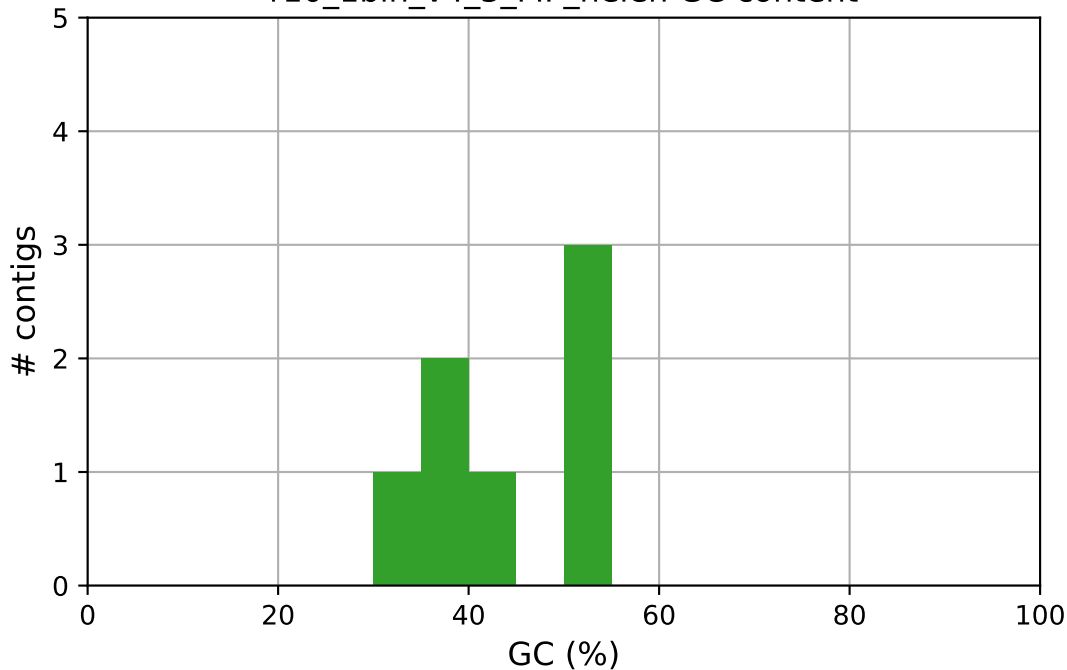
r10_1bin_v4_2_raw

r10_1bin_v4_3_MP GC content



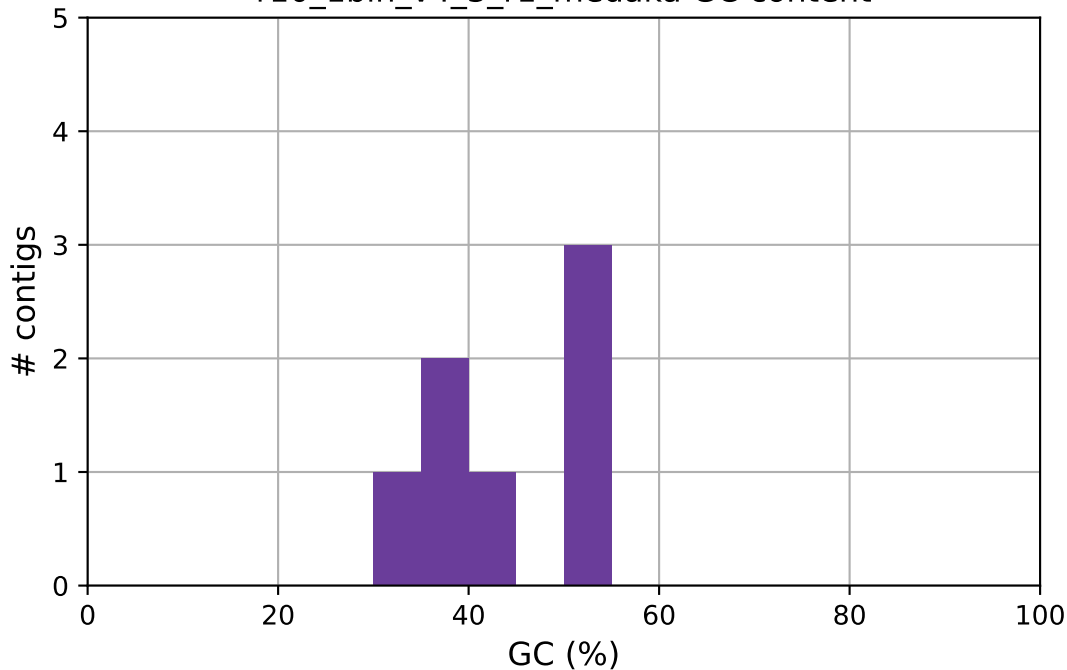
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen GC content



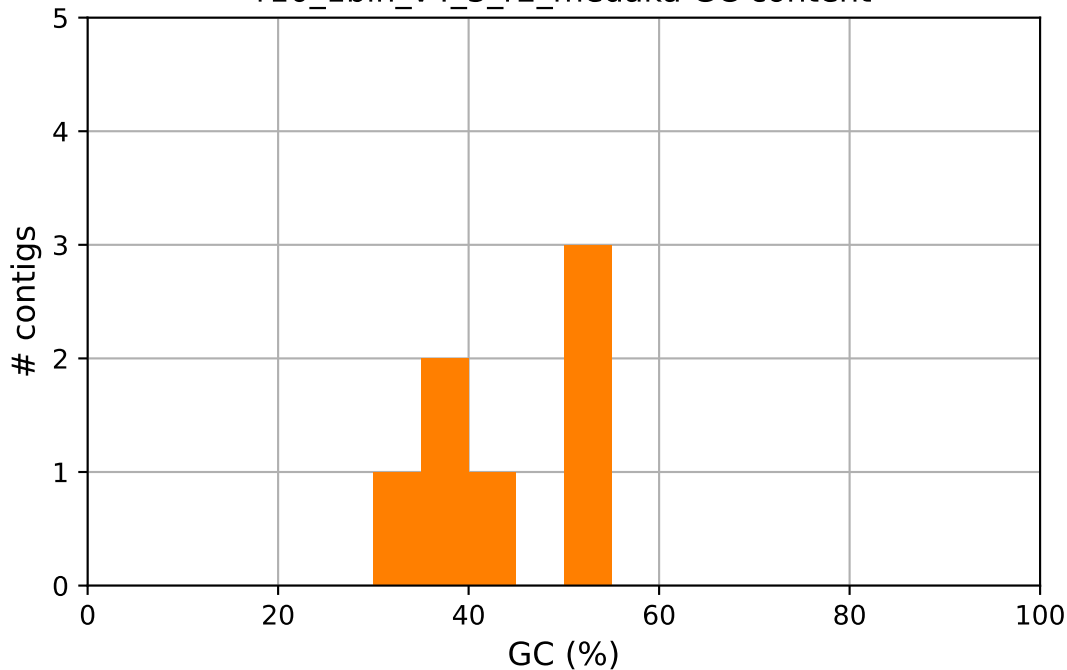
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka GC content



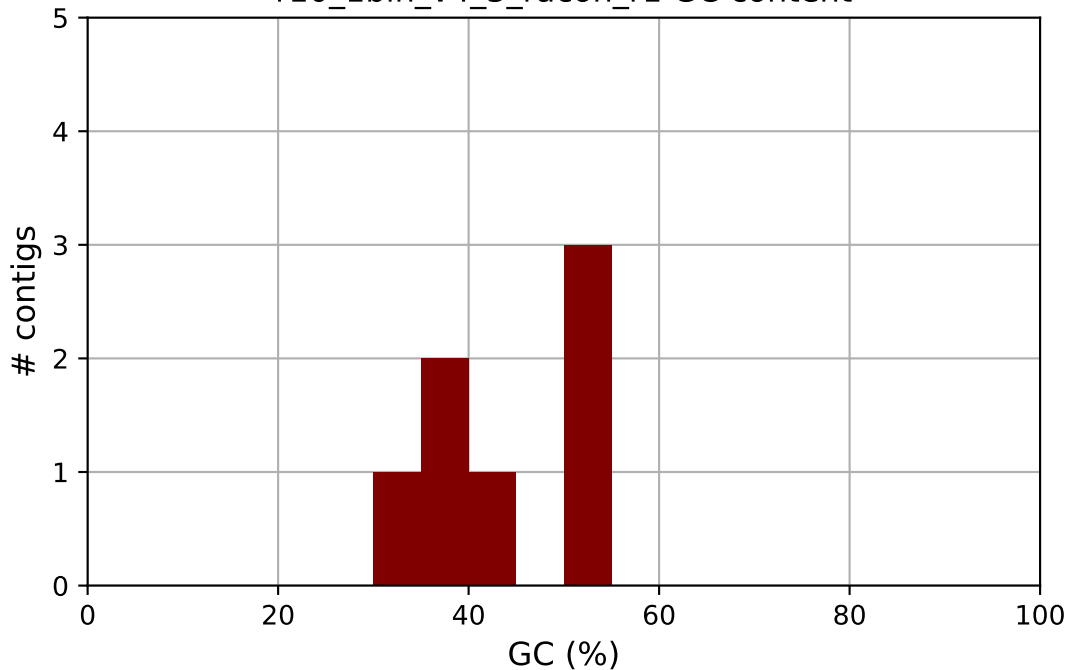
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka GC content



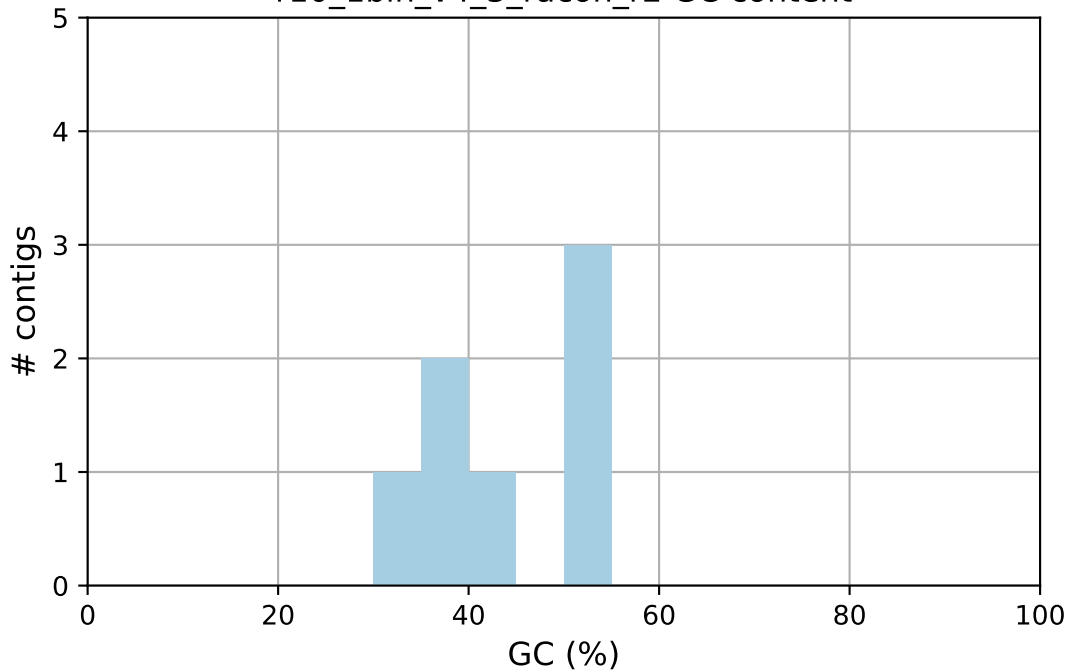
r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1 GC content



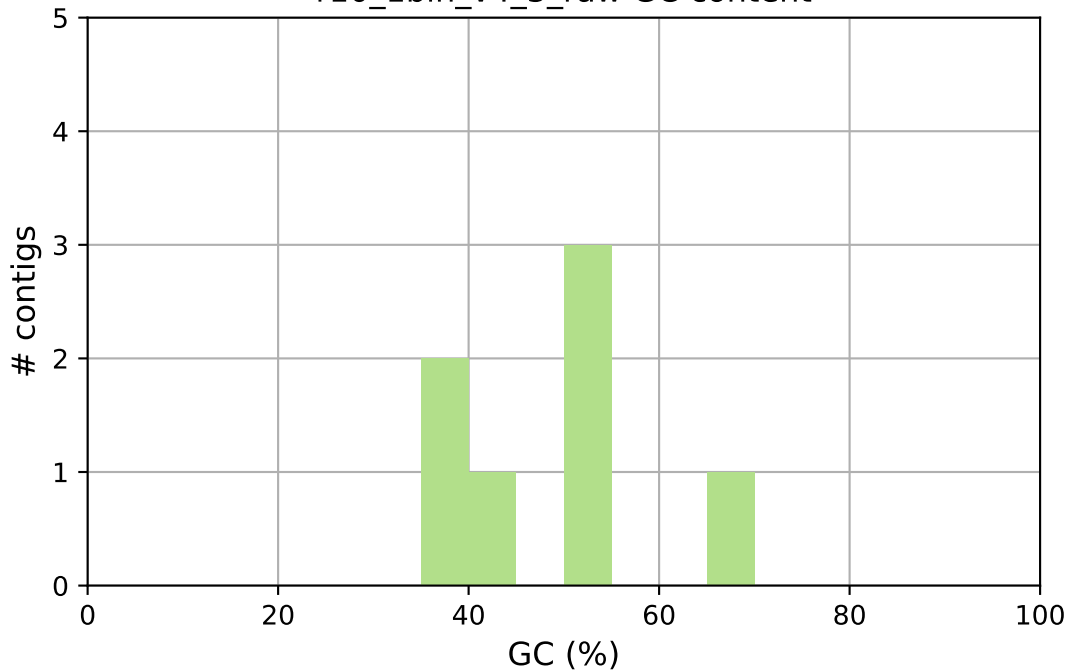
r10_1bin_v4_3_racon_r1

r10_1bin_v4_3_racon_r2 GC content



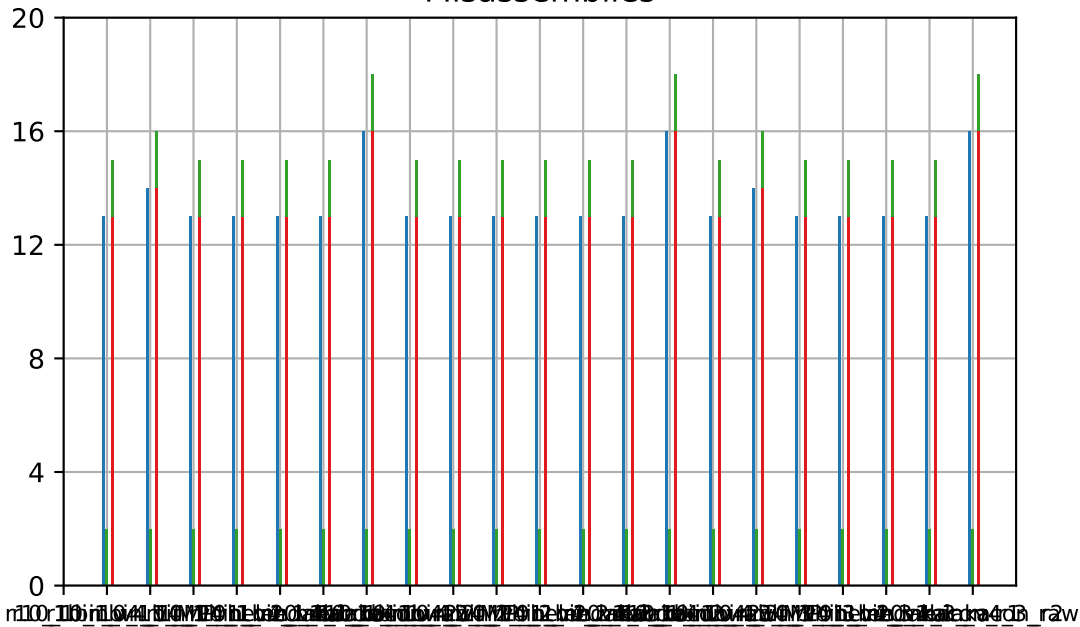
r10_1bin_v4_3_racon_r2

r10_1bin_v4_3_raw GC content



r10_1bin_v4_3_raw

Misassemblies



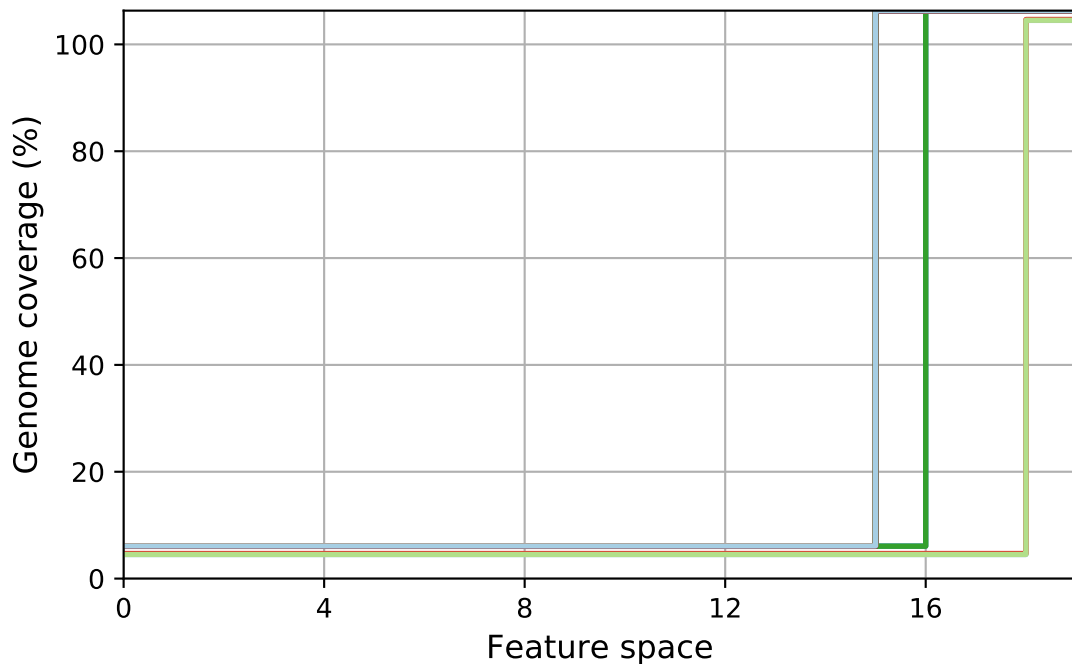
5

translocations



```
# inversions
```

FRCurve (misassemblies)



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_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

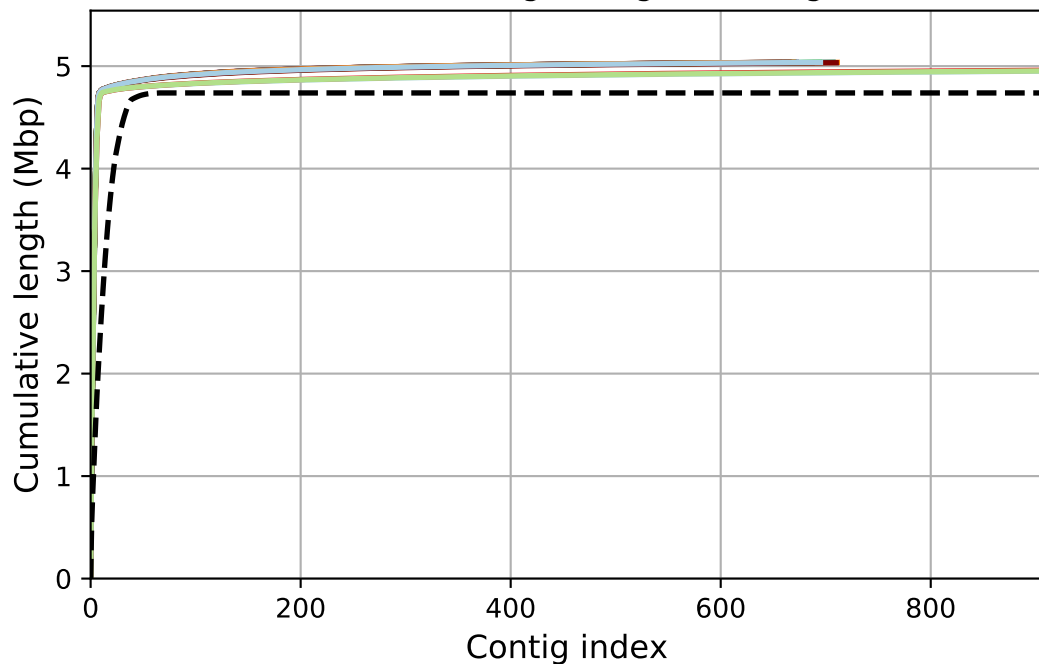
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

Cumulative length (aligned contigs)



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_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1

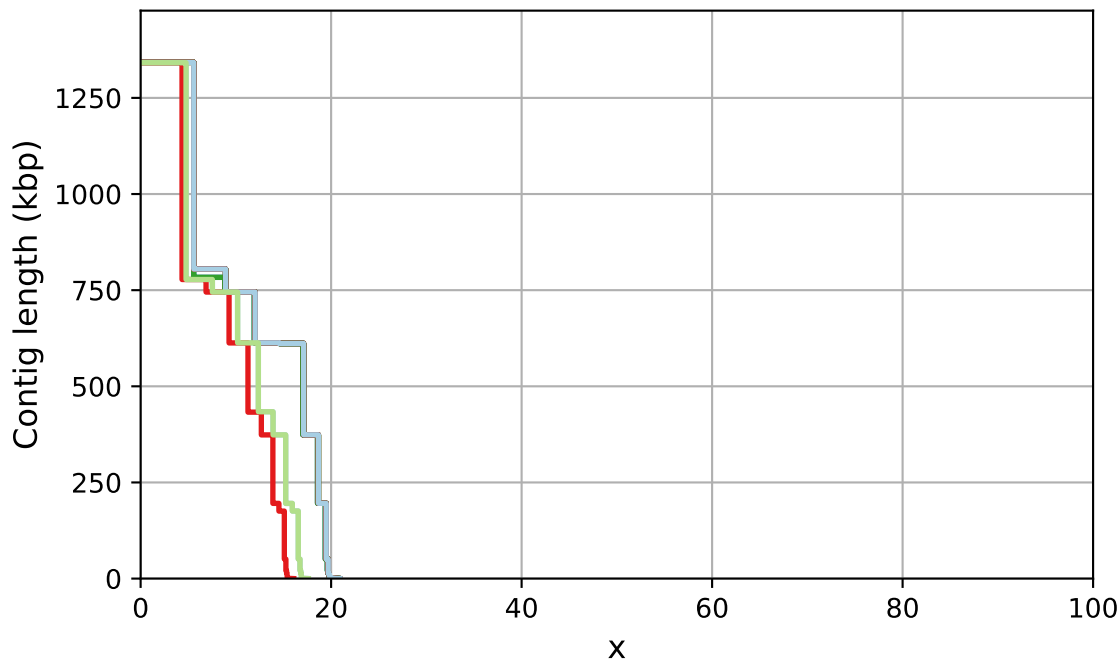
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1

NAx



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_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

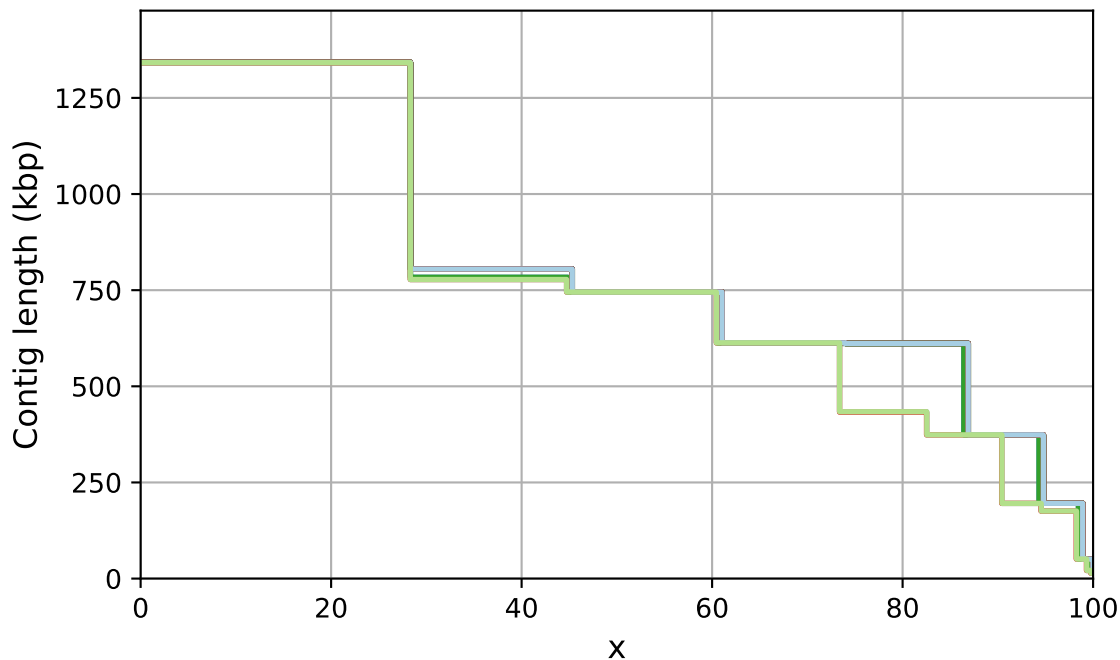
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

NGAx



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_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

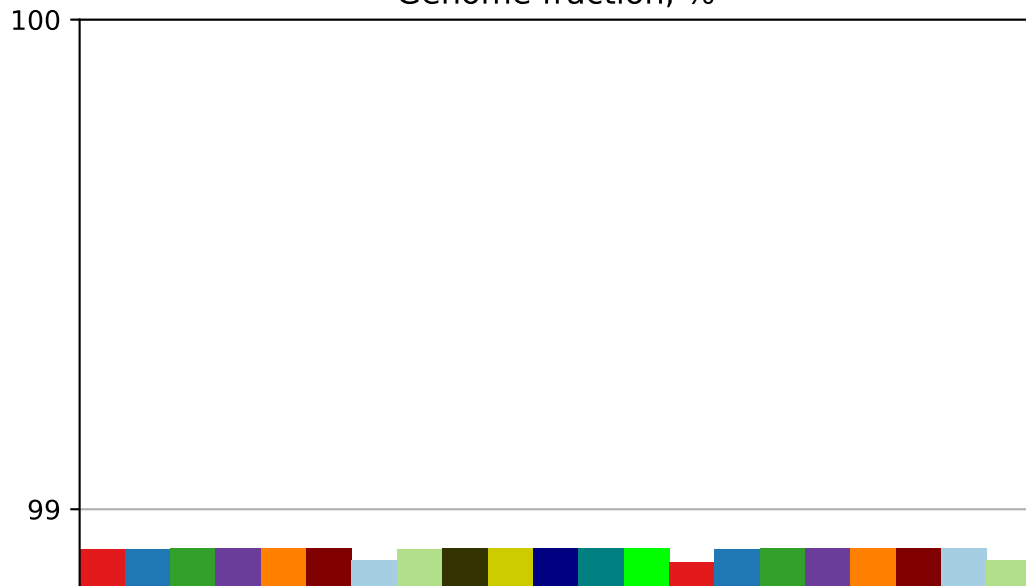
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

Genome fraction, %



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_2_MP

r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka