

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	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)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 10000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 25000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Total length (>= 50000 bp)	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
Largest contig	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
Total length	24074239	24070847	24075790	24065267	24060416	24054361	24061513	24074830	24070579	24075879	24065198	24060552	24053082	24061431	24074372	24070528	24075072	24062757	24061106	24053558	24060936
Reference length	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294	2820294
GC (%)	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.79	44.78	44.77	44.80	44.80	44.80	44.79	44.78	44.78	44.77
Reference GC (%)	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44	37.44
N50	4045594	4045614	4045830	4045830	4045233	4045289	4042947	4045599	4045618	4045837	4045836	4045198	4045283	4042978	4045594	4045616	4045840	4045837	4045212	4045325	4042951
NG50	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
N75	2845424	2845373	2845569	2845303	2845263	2845303	2843857	2845424	2845368	2845573	2845566	2845303	2845324	2843857	2845425	2845368	2845568	2845313	2843857		
NG75	4765380	4765358	4765659	4765647	4764472	4764668	4763504	4765857	4765290	4765665	4765638	4764540	4764597	4763606	4765360	4765338	4765695	4765649	4764493	4764872	4763509
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	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# 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	2845424	2845373	2845569	2845565	2845263	2845303	2843857	2845424	2845368	2845573	2845566	2845303	2845324	2843857	2845425	2845368	2845568	2845560	2845287	2845313	2843857
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	20
# 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	5	6	5	6	6
# unaligned contigs	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 6 part	0 + 7 part
Unaligned length	21096644	21093803	21097770	21088186	21088322	21078268	21152484	21097744	21093393	21097618	21087627	21087037	21077720	21152048	21097245	21092484	21097723	21086783	21087781	21077271	21149899
Genome fraction (%)	99.954	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.954	99.949	99.954	99.954	99.954	99.954	99.954	99.954	99.949
Duplication ratio	1.056	1.056	1.057	1.056	1.055	1.056	1.032	1.056	1.057	1.056	1.056	1.055	1.056	1.032	1.056	1.057	1.056	1.056	1.055	1.056	1.033
# 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	249.57	247.58	250.42	248.79	229.77	244.46	148.32	248.15	249.54	251.77	250.10	234.78	242.58	148.78	248.40	251.38	248.93	244.71	236.05	245.21	152.97
# indels per 100 kbp	15.29	14.90	19.48	18.77	22.07	20.54	125.89	15.29	15.58	20.22	19.09	21.11	22.89	125.40	15.65	15.75	19.59	18.91	23.42	21.89	125.61
Largest alignment	2560117	2560082	2560238	2560235	2559977	2560017	2556100	2560120	2560017	2560247	2560240	2560005	2560018	2556103	2390859	2390838	2390971	2390963	2390760	2390767	2387805
Total aligned length	2972166	2971621	2970668	2971652	2966665	2970668	2971652	297298	2971657	2972832	2969934	2972142	2968087	297652	2971698	2972639	2971919	2970545	2967907	2970859	2909306
NGA50	2560117	2560082	2560238	2560235	2559977	2560017	256100	2560120	2560017	2560247	2560240	2560005	2560018	2556103	2390859	2390838	2390971	2390963	2390760	2390767	2387805
NGA75	2560117	2560082	2560238	2560235	2559977	2560017	256100	2560120	2560017	2560247	2560240	2560005	2560018	2556103	2390859	2390838	2390971	2390963	2390760	2390767	2387805
LGA50	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
LGA75	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	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

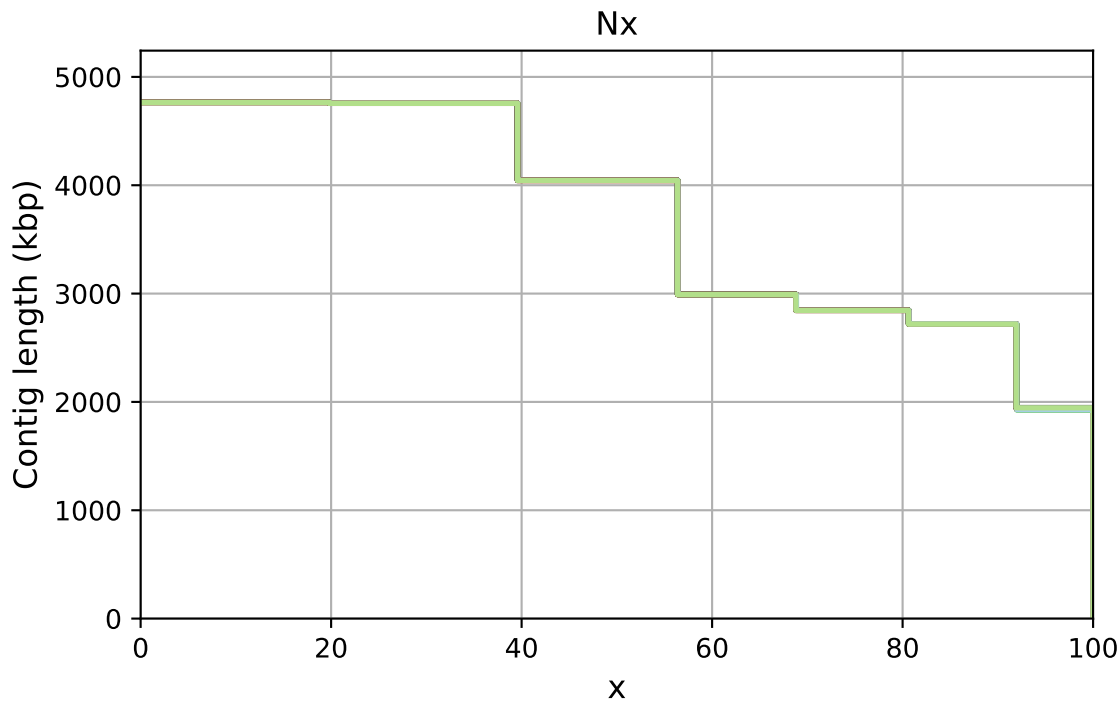
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# misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# contig misassemblies	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. translocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. 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	2845424	2845373	2845569	2845565	2845263	2845303	2843857	2845424	2845368	2845573	2845566	2845303	2845324	2843857	2845425	2845368	2845568	2845560	2845287	2845313	2843857
# possibly misassembled contigs	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
# possible misassemblies	0	0	0	0	0	0	6	0	0	0	0	0	0	6	0	0	0	0	0	0	6
# local misassemblies	16	16	16	16	16	16	20	16	16	16	16	16	16	20	16	16	16	16	16	16	20
# 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	19	19	19	19	19	19	11	19	19	19	19	19	19	11	19	19	19	19	19	19	11
# unaligned mis. contigs	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	5	6	5	6	6
# mismatches	7034	6978	7058	7012	6476	6890	4180	6994	7033	7096	7049	6617	6837	4193	7001	7085	7016	6897	6653	6911	4311
# indels	431	420	549	529	622	579	3548	431	439	570	538	595	645	3534	441	444	552	533	660	617	3540
# indels (<= 5 bp)	390	378	508	490	583	540	3512	390	396	529	497	555	606	3498	400	402	511	492	618	578	3504
# indels (> 5 bp)	41	42	41	39	39	39	36	41	43	41	41	40	39	36	41	42	41	41	42	39	36
Indels length	2440	2436	2529	2486	2591	2557	6142	2440	2469	2570	2530	2587	2691	6122	2459	2474	2531	2517	2716	2639	6130

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	6	6	6	6	6	6	7	6	6	6	6	6	6	7	6	6	6	6	6	6	7
Partially unaligned length	21096644	21093803	21097770	21088186	21088322	21078268	21152484	21097744	21093393	21097618	21087627	21087037	21077720	21152048	21097245	21092484	21097723	21086783	21087781	21077271	21149899
# 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).



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

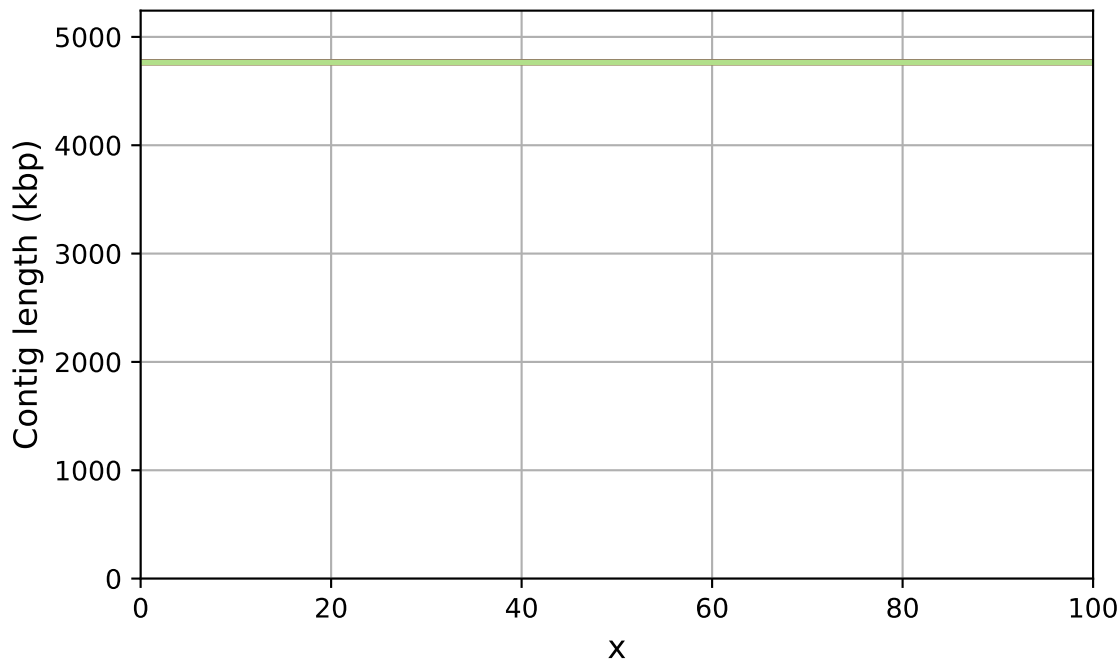
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka

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

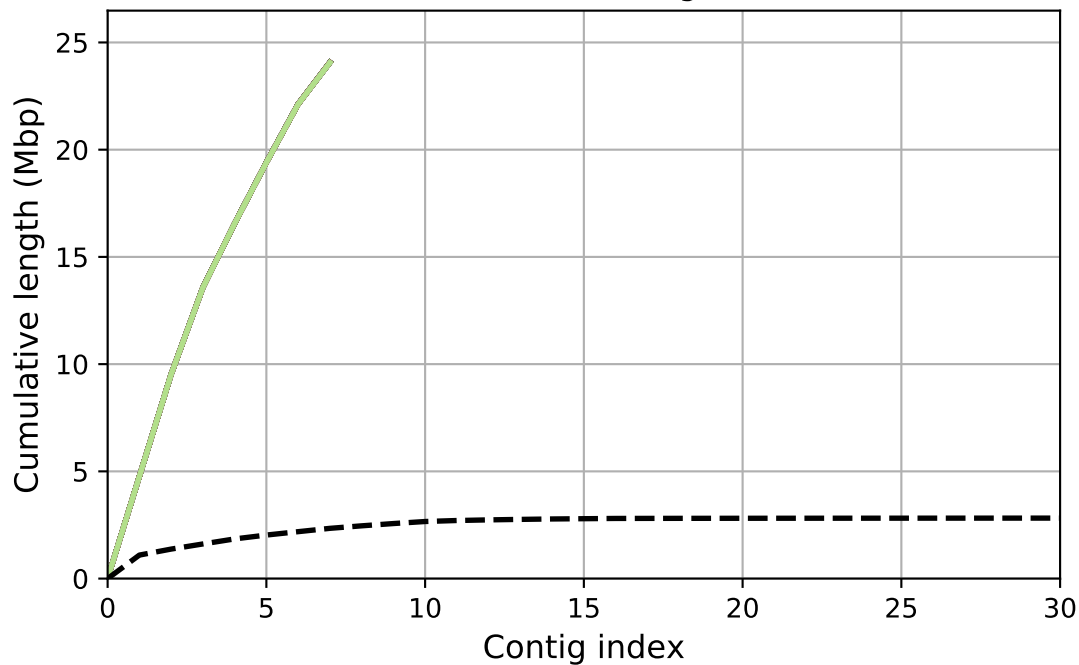
r10_1bin_v4_3_r1_medaka

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

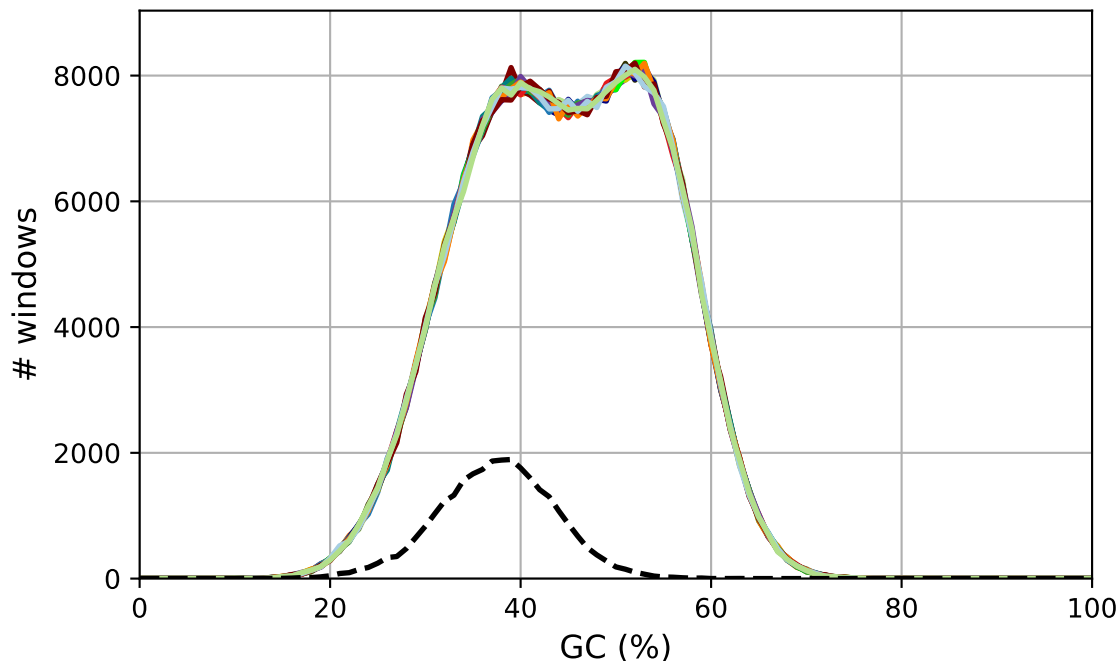
r10_1bin_v4_3_MP_helen

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

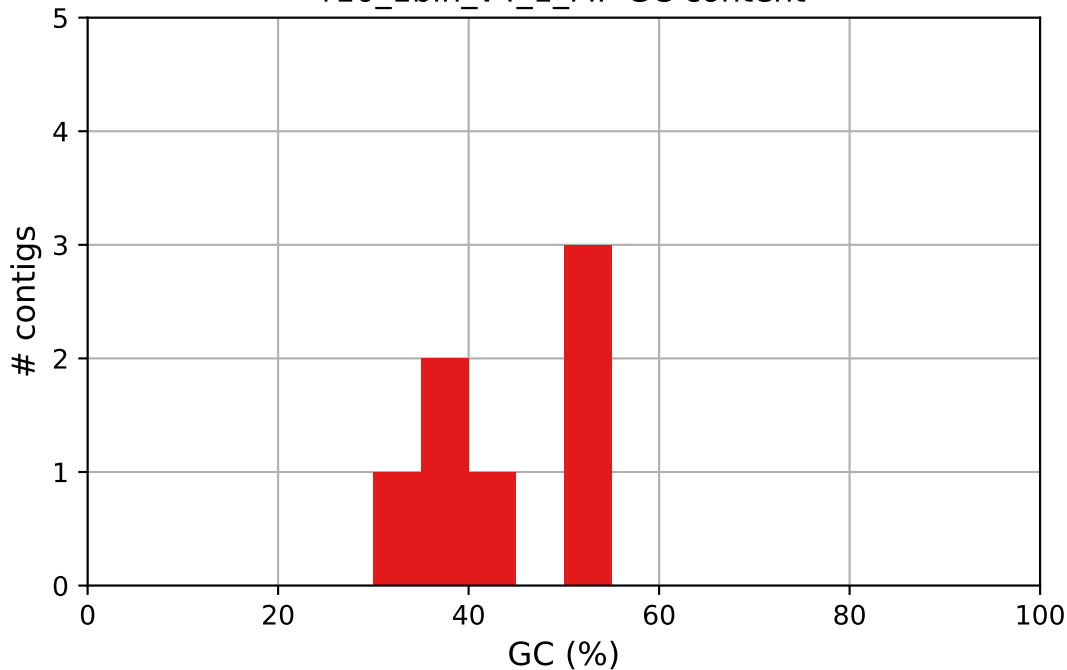
r10_1bin_v4_3_MP_h

r10_1bin_v4_3_r1_m

r10_1bin_v4_3_r2_m

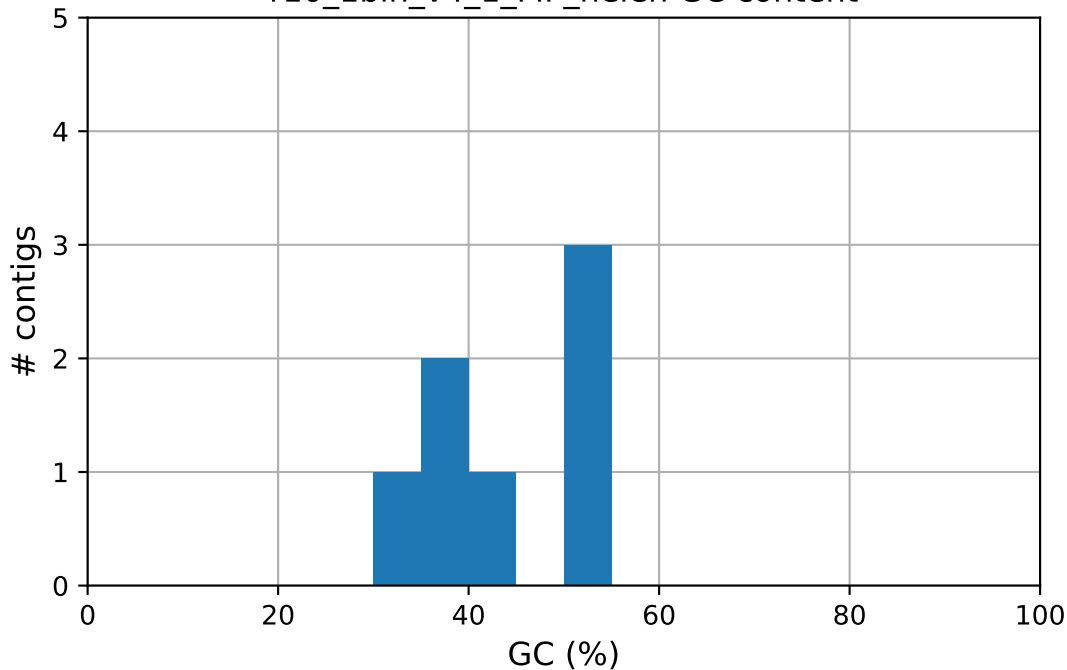
r10_1bin_v4_3_raco

r10_1bin_v4_1_MP GC content



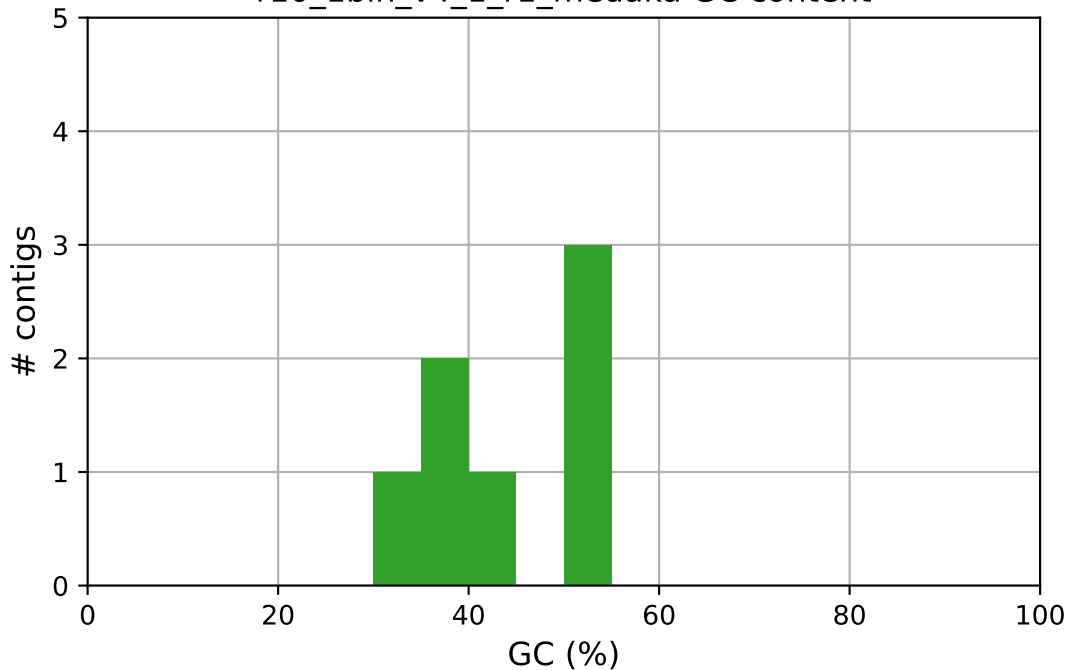
r10_1bin_v4_1_MP

r10_1bin_v4_1_MP_helen GC content



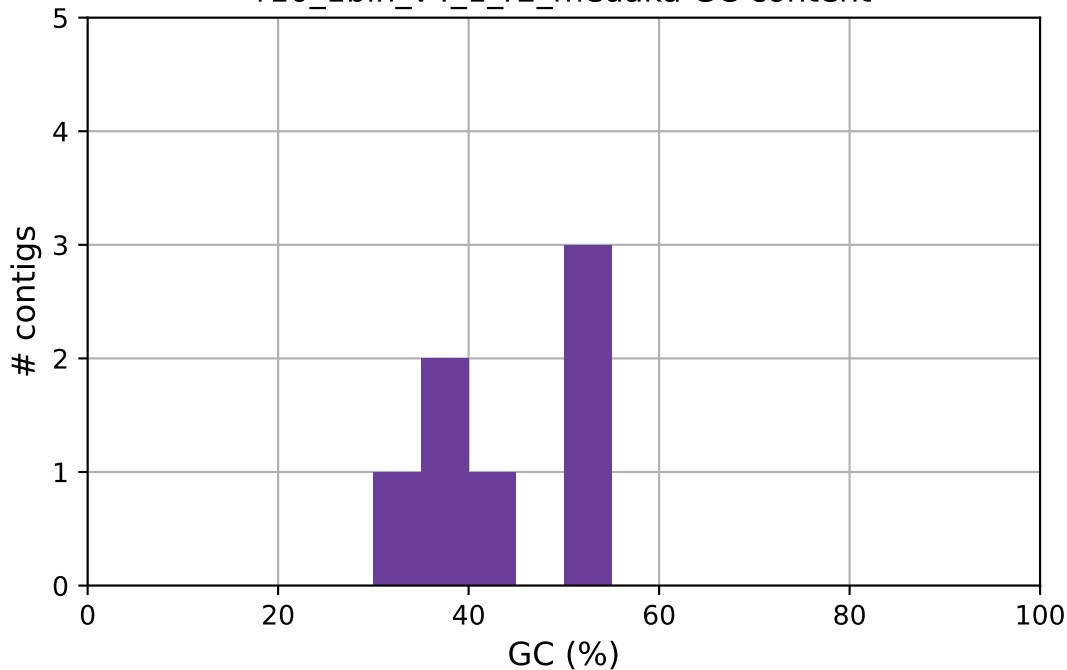
r10_1bin_v4_1_MP_helen

r10_1bin_v4_1_r1_medaka GC content



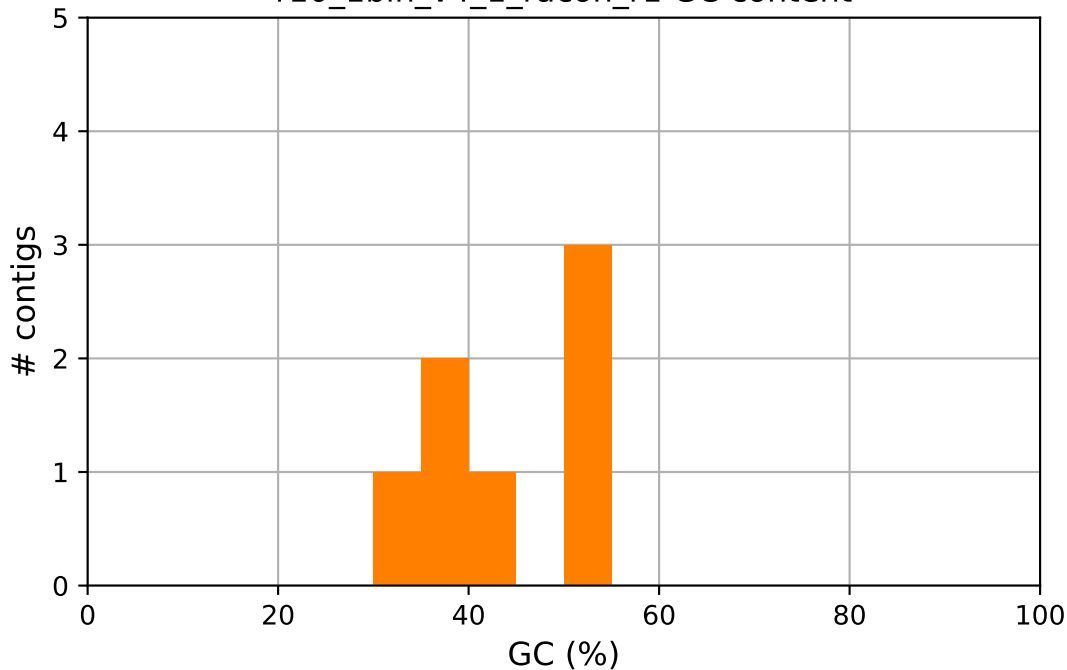
r10_1bin_v4_1_r1_medaka

r10_1bin_v4_1_r2_medaka GC content



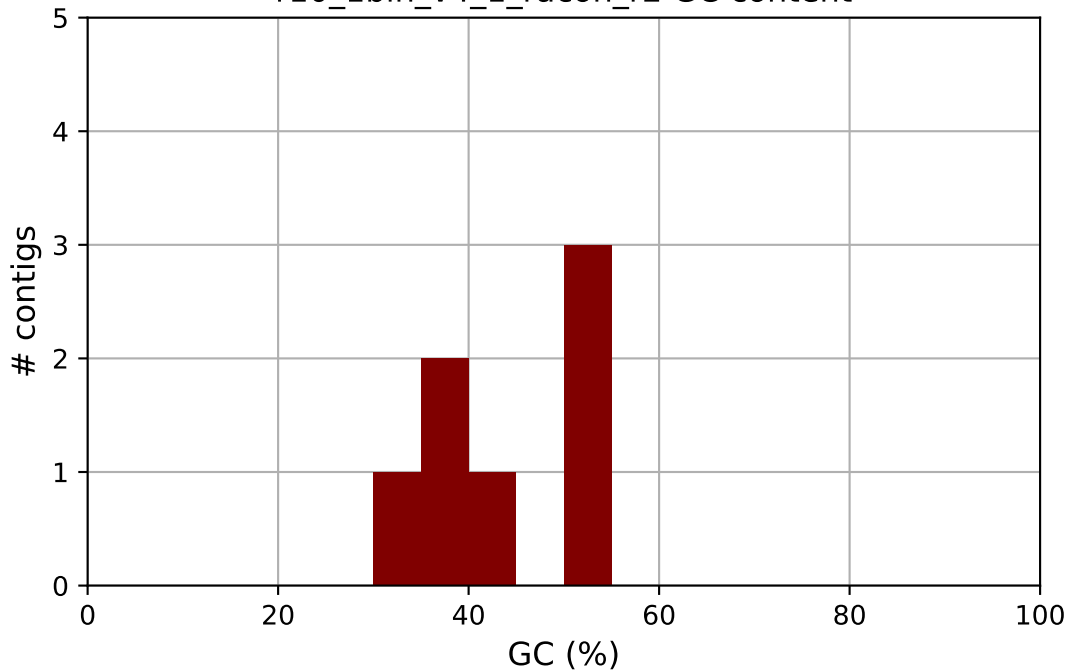
r10_1bin_v4_1_r2_medaka

r10_1bin_v4_1_racon_r1 GC content



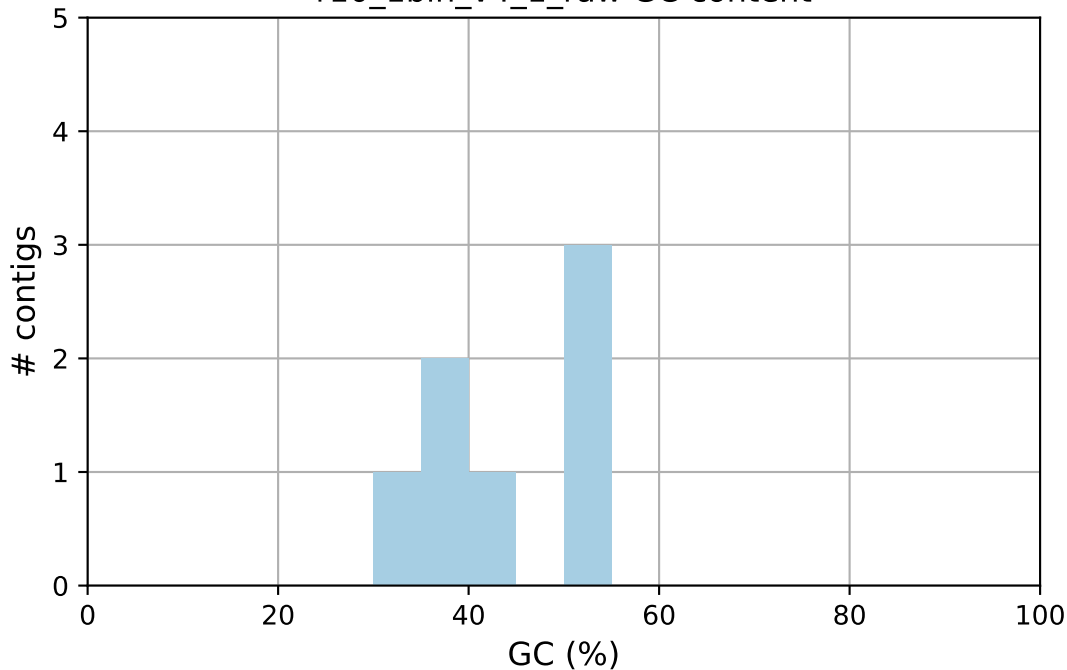
r10_1bin_v4_1_racon_r1

r10_1bin_v4_1_racon_r2 GC content



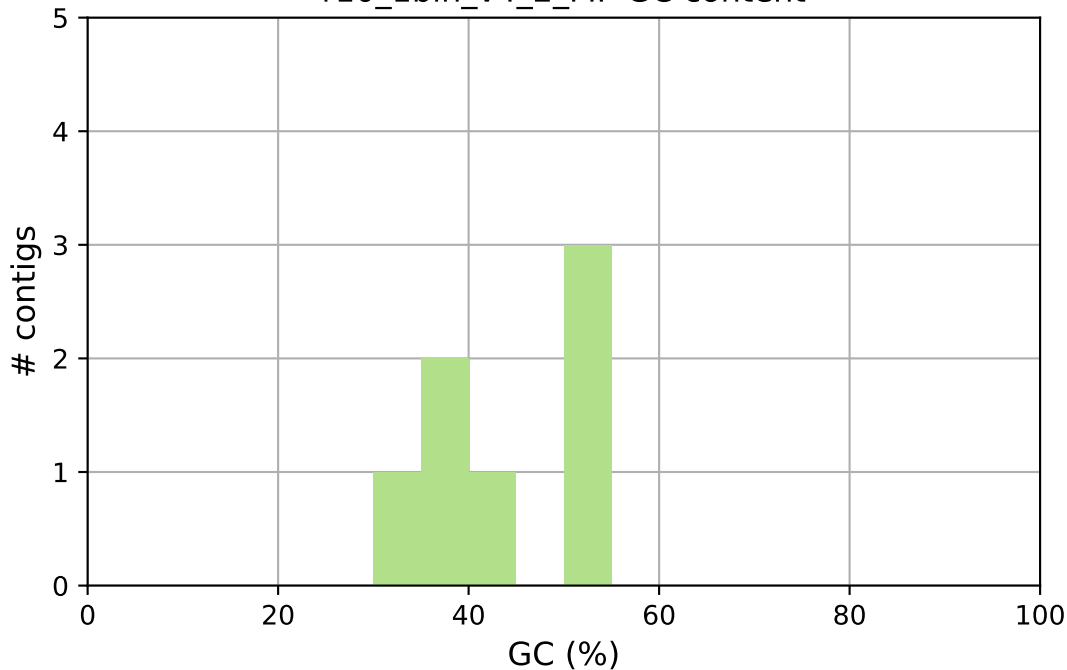
r10_1bin_v4_1_racon_r2

r10_1bin_v4_1_raw GC content



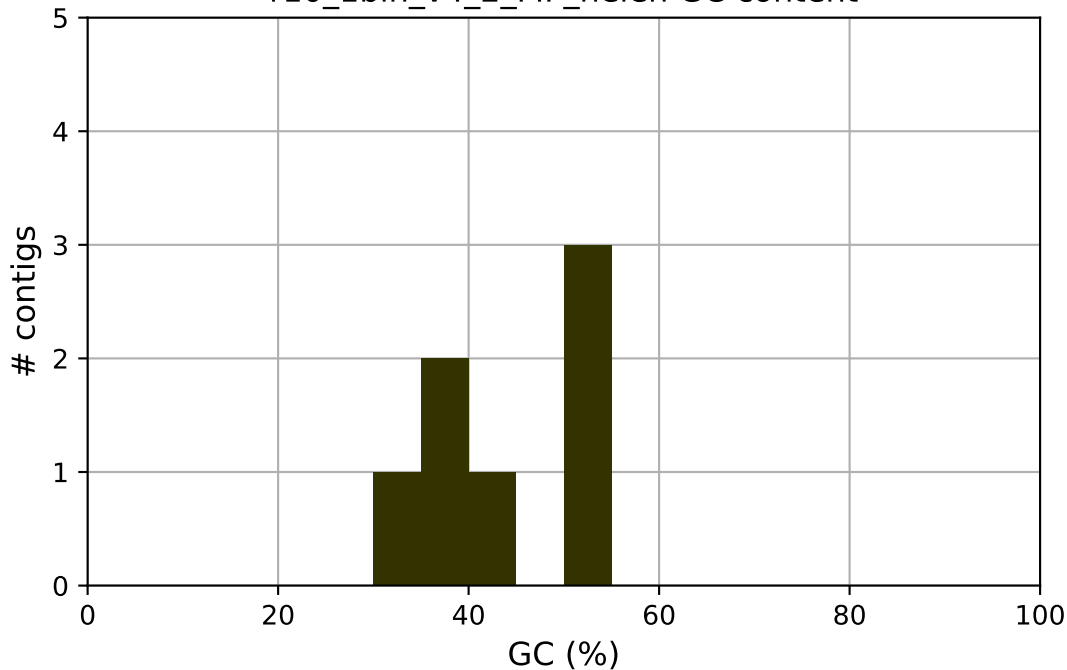
r10_1bin_v4_1_raw

r10_1bin_v4_2_MP GC content



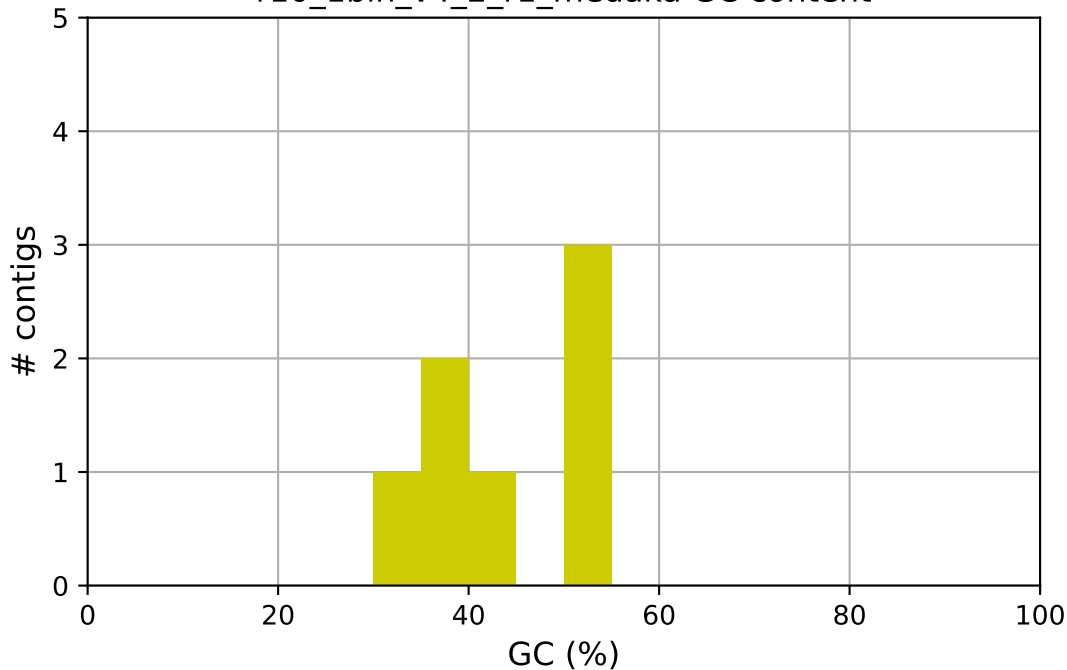
r10_1bin_v4_2_MP

r10_1bin_v4_2_MP_helen GC content



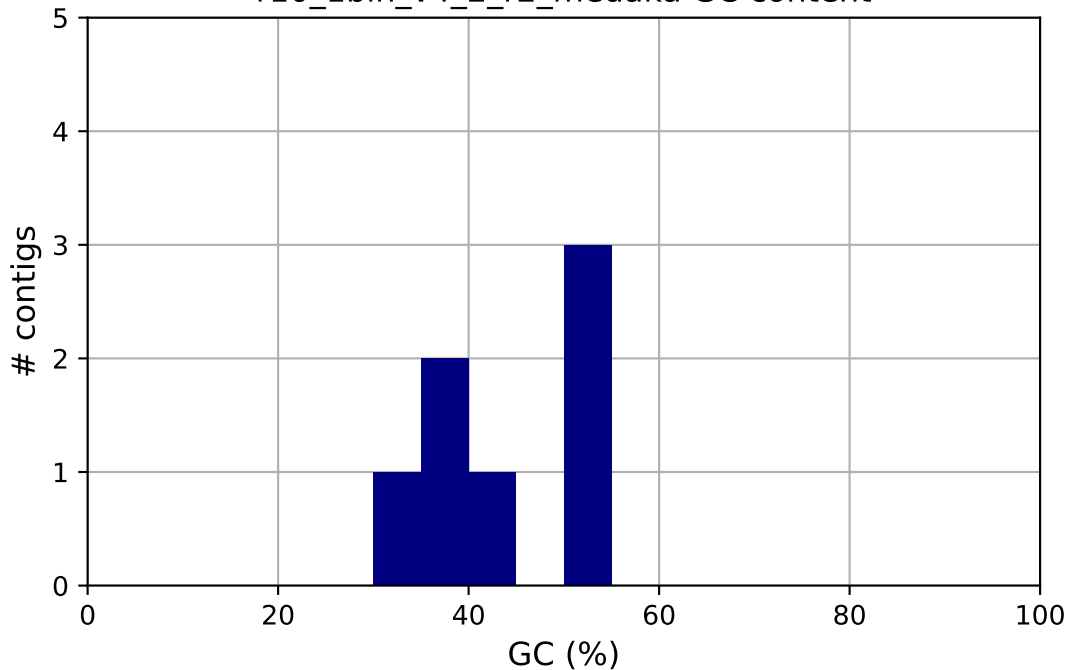
r10_1bin_v4_2_MP_helen

r10_1bin_v4_2_r1_medaka GC content



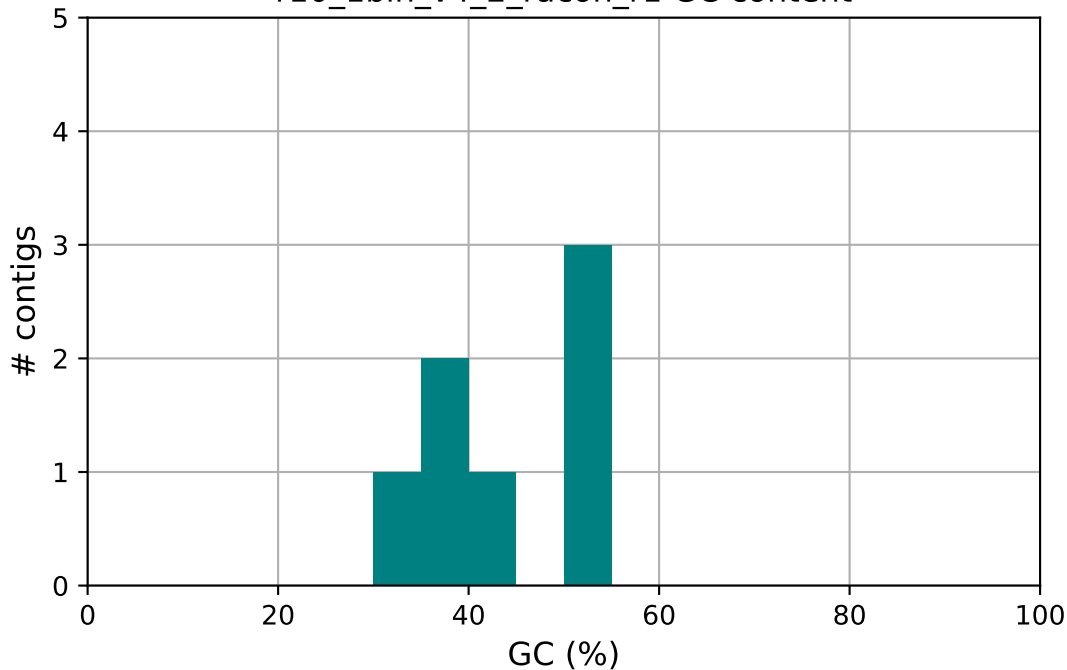
r10_1bin_v4_2_r1_medaka

r10_1bin_v4_2_r2_medaka GC content



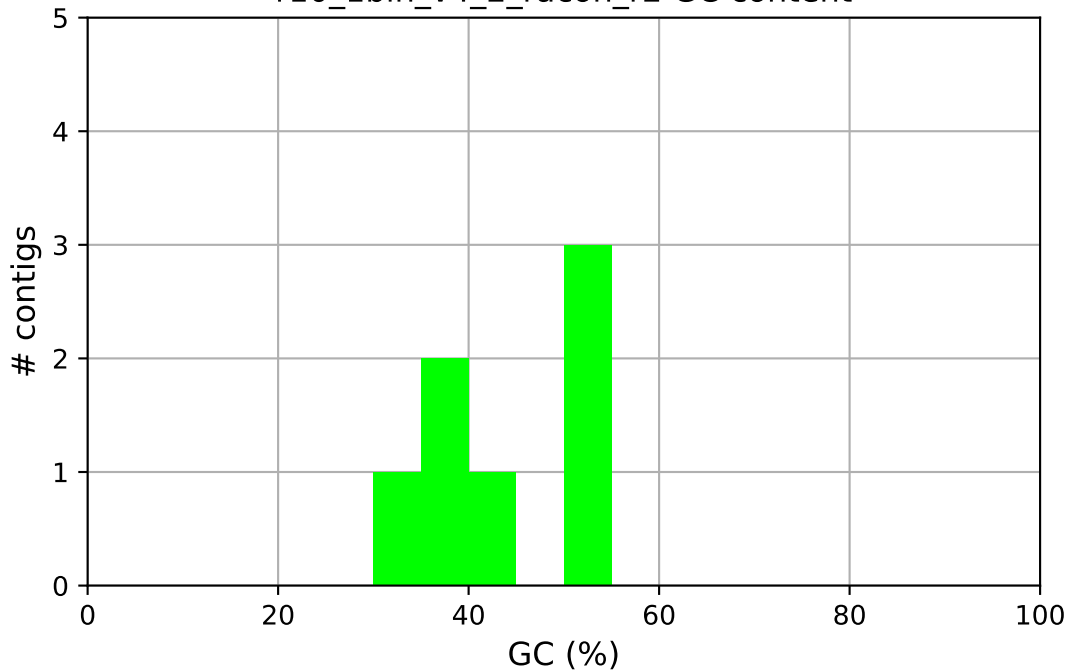
r10_1bin_v4_2_r2_medaka

r10_1bin_v4_2_racon_r1 GC content



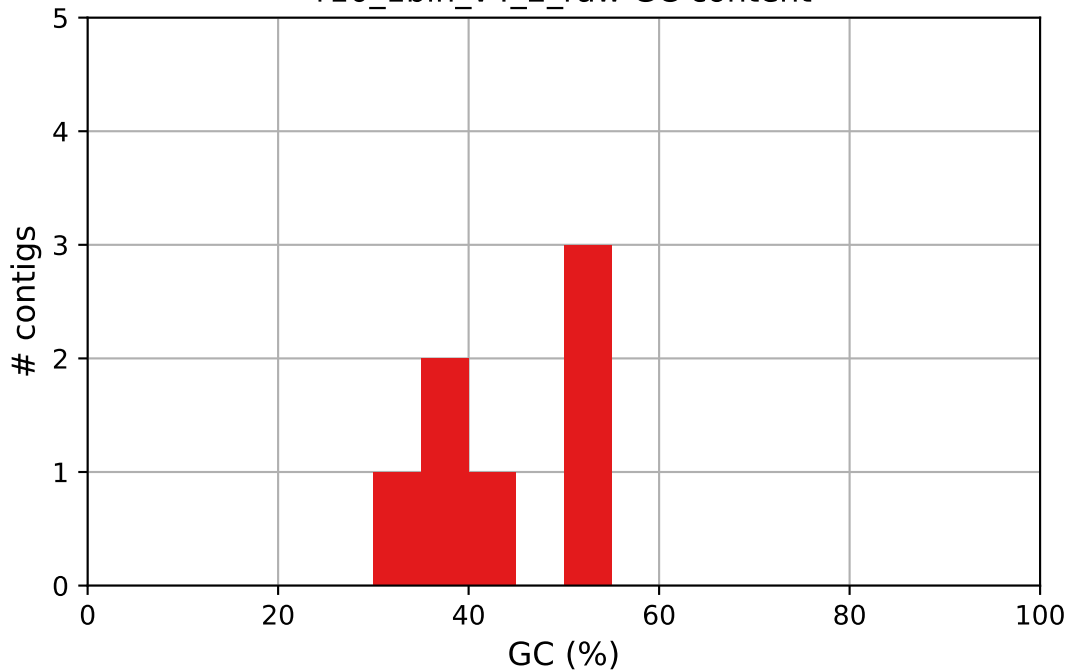
r10_1bin_v4_2_racon_r1

r10_1bin_v4_2_racon_r2 GC content



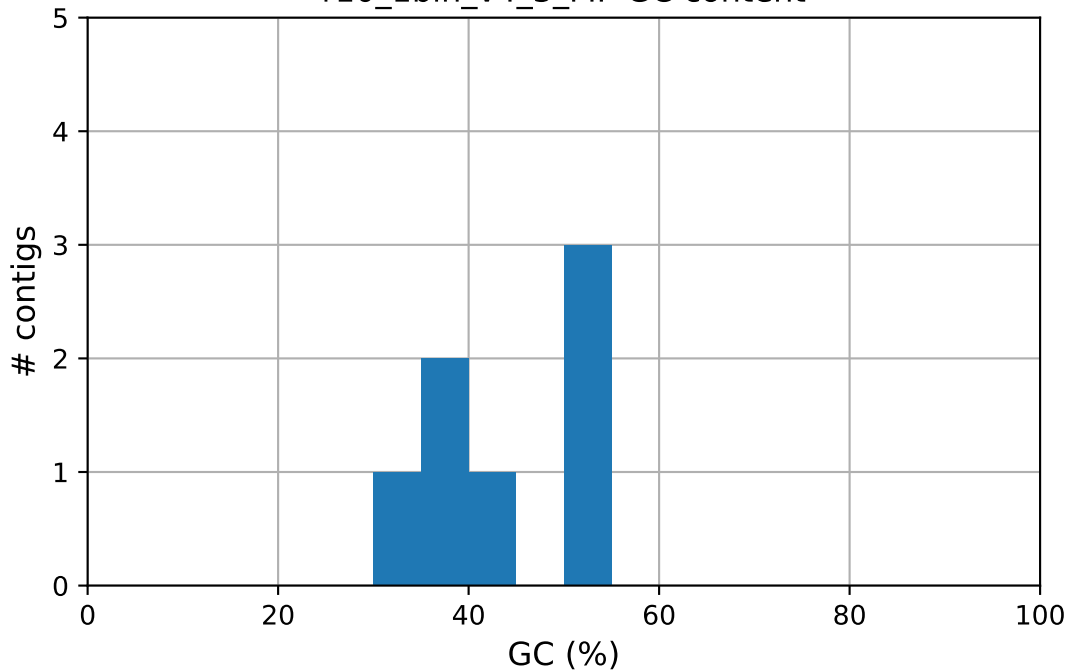
r10_1bin_v4_2_racon_r2

r10_1bin_v4_2_raw GC content



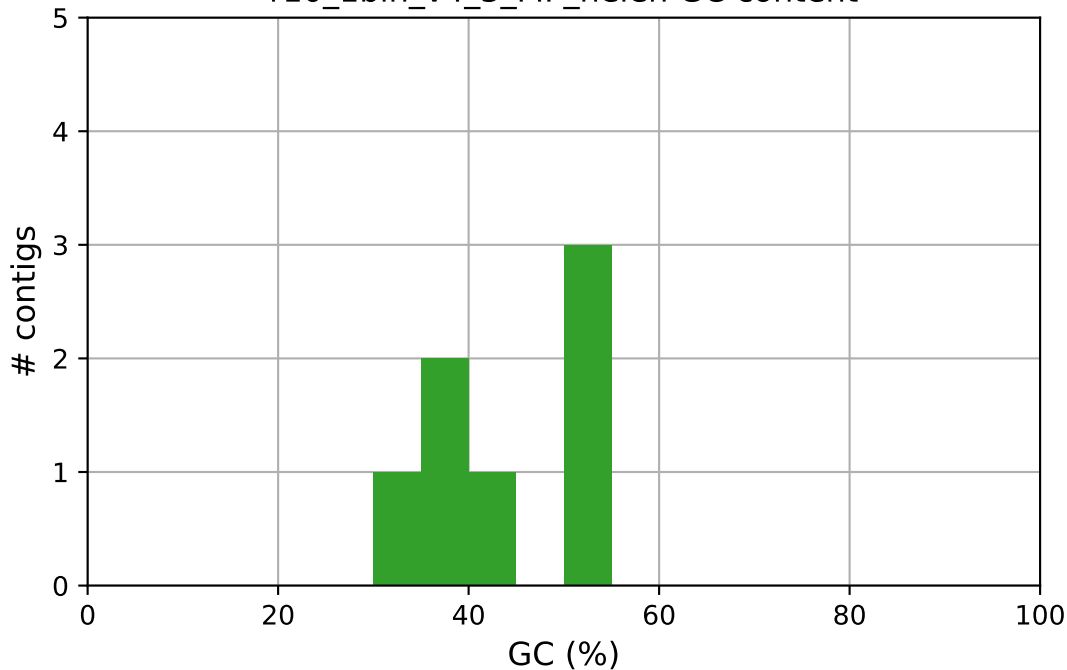
r10_1bin_v4_2_raw

r10_1bin_v4_3_MP GC content



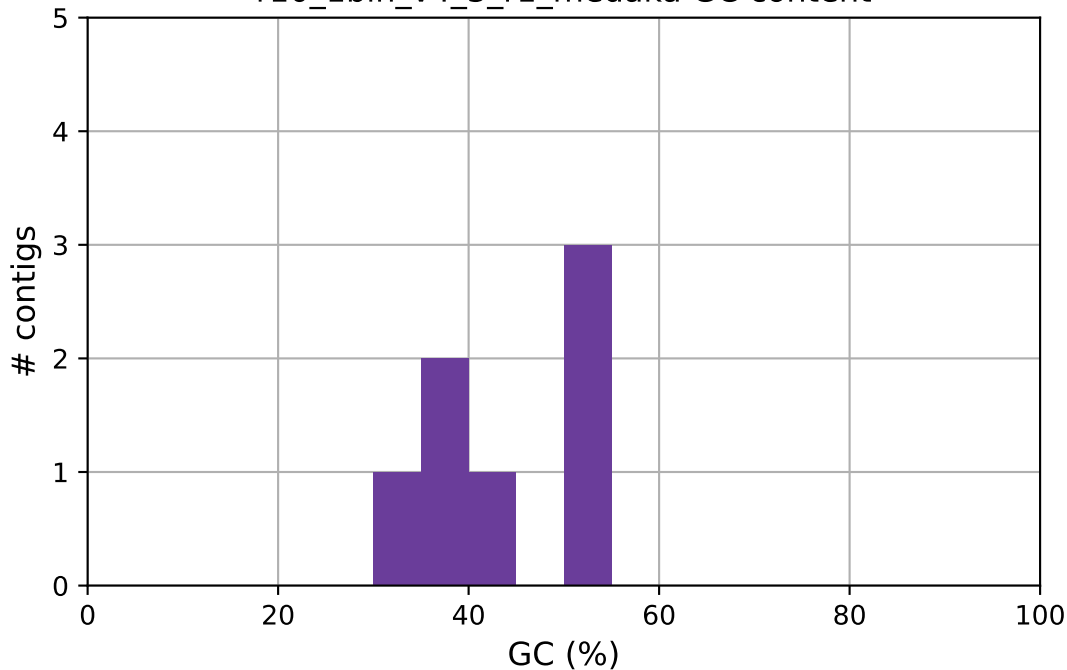
r10_1bin_v4_3_MP

r10_1bin_v4_3_MP_helen GC content



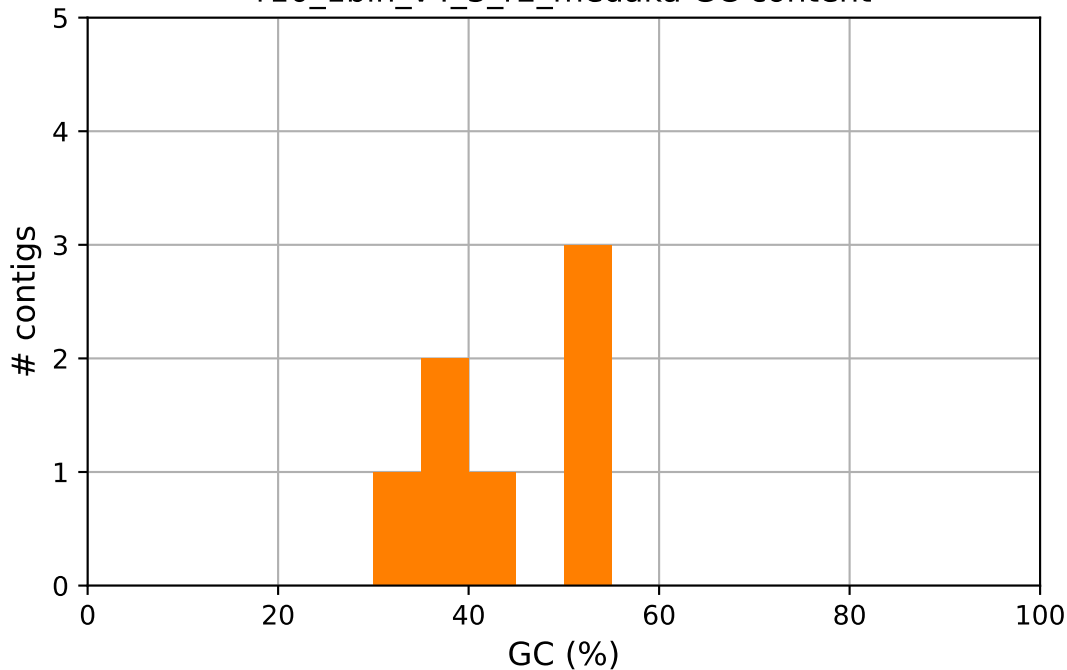
r10_1bin_v4_3_MP_helen

r10_1bin_v4_3_r1_medaka GC content



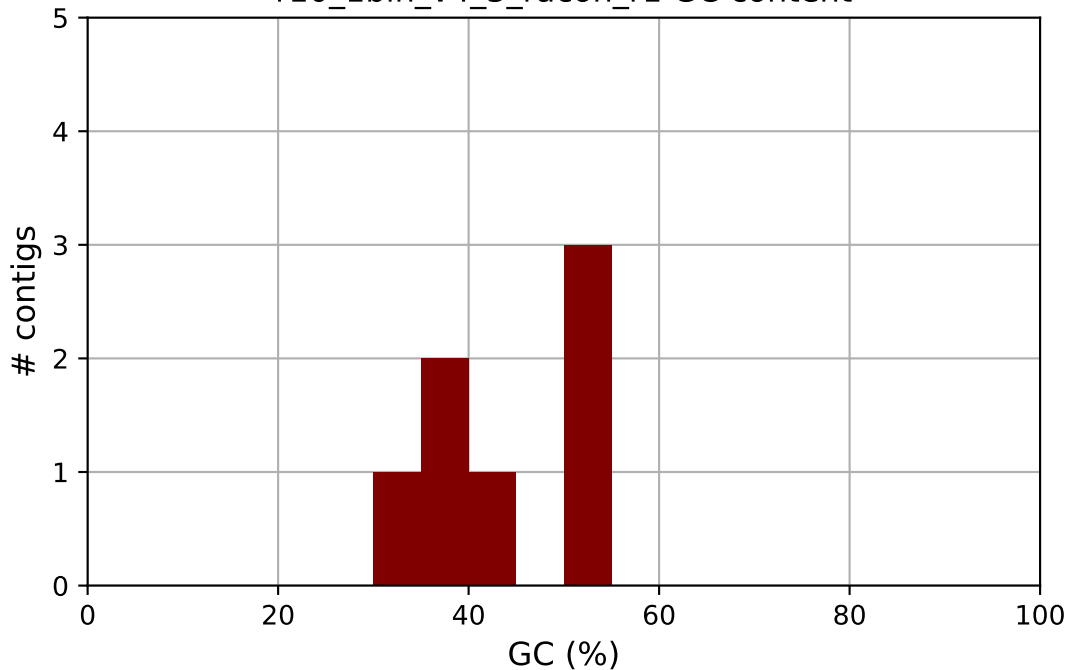
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_3_r2_medaka GC content



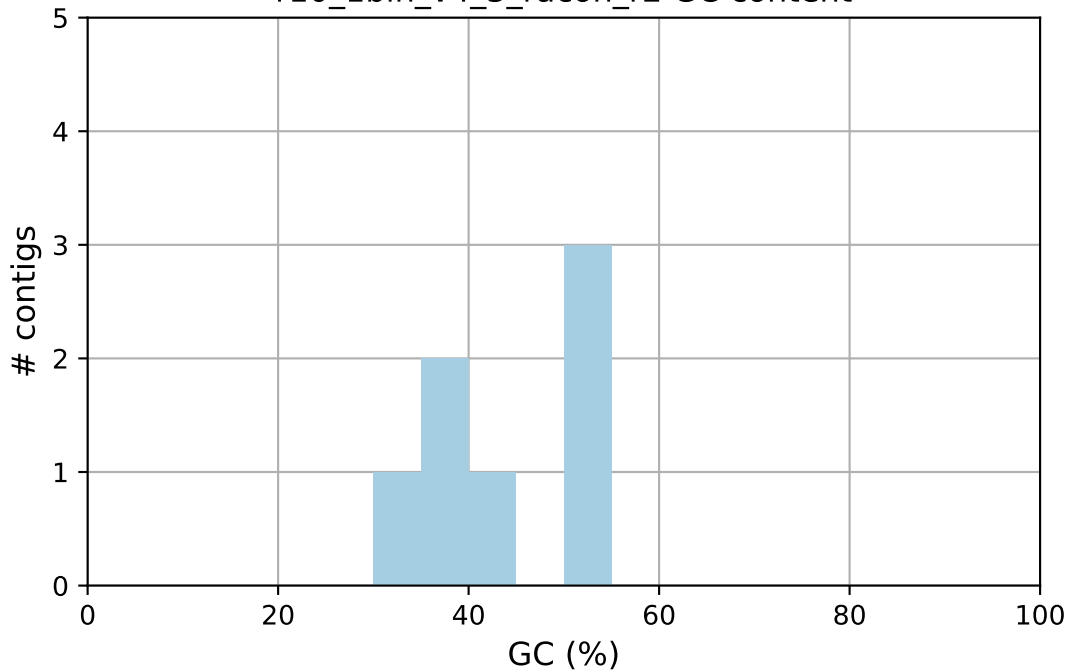
r10_1bin_v4_3_r2_medaka

r10_1bin_v4_3_racon_r1 GC content



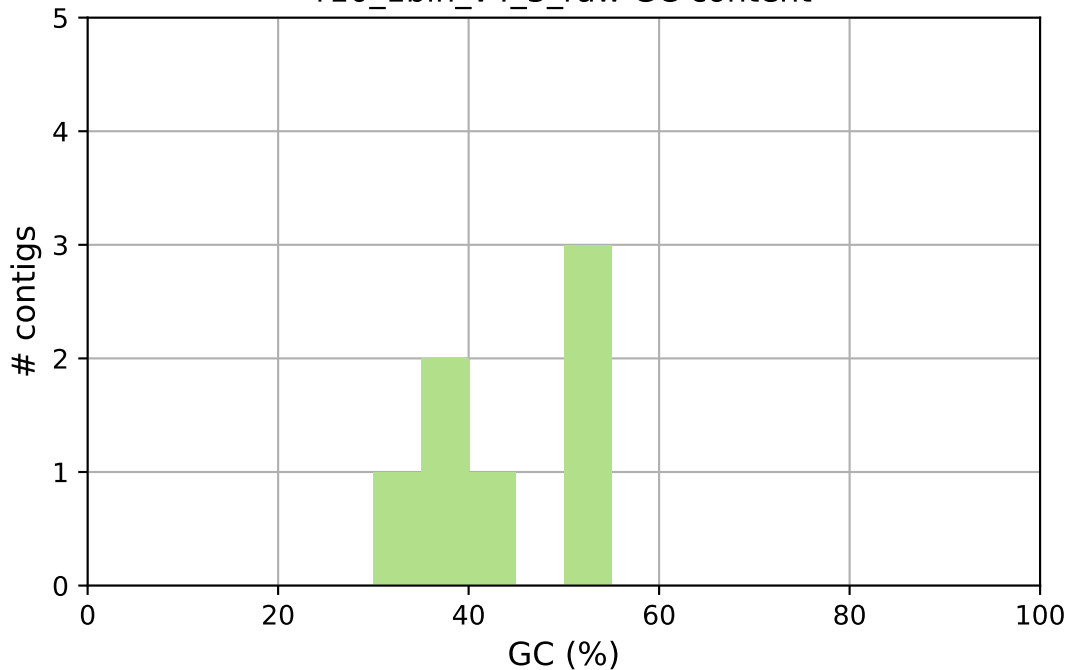
r10_1bin_v4_3_racon_r1

r10_1bin_v4_3_racon_r2 GC content



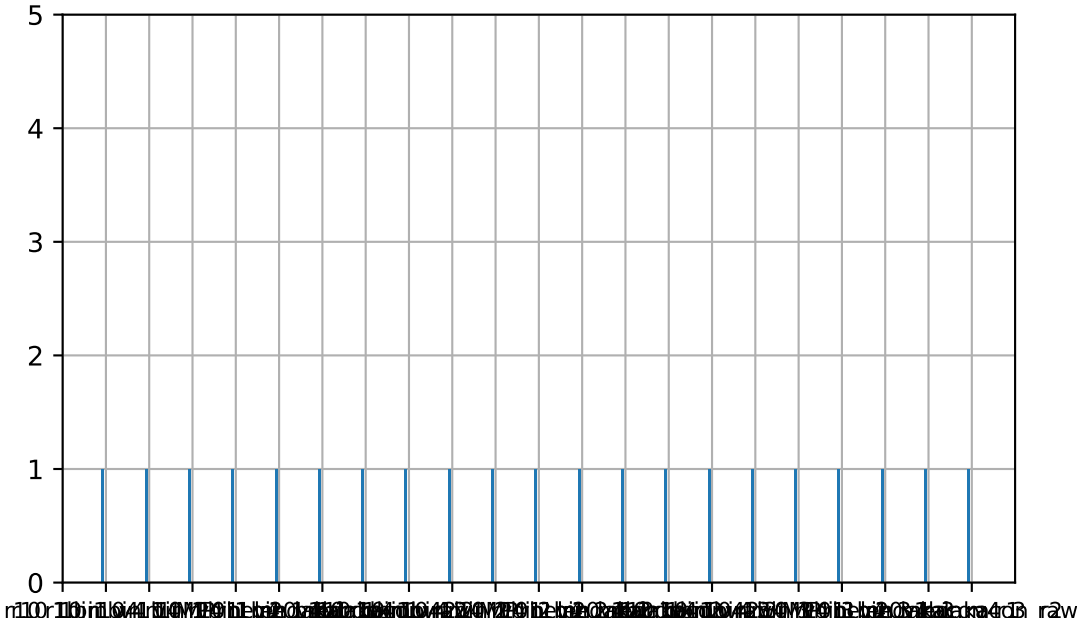
r10_1bin_v4_3_racon_r2

r10_1bin_v4_3_raw GC content



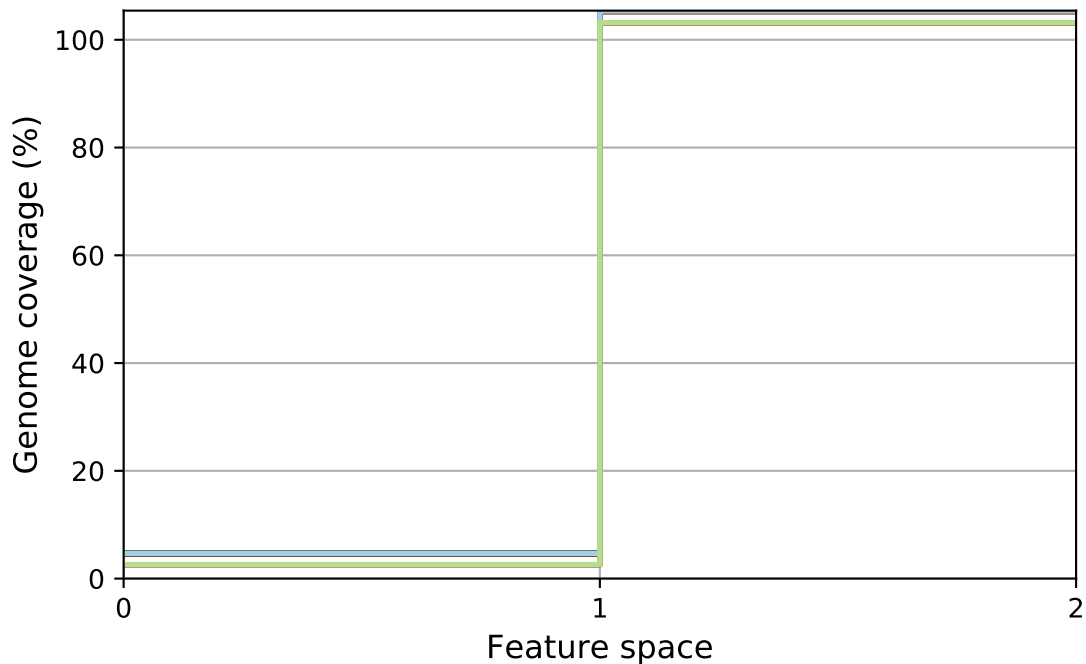
r10_1bin_v4_3_raw

Misassemblies



translocations

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

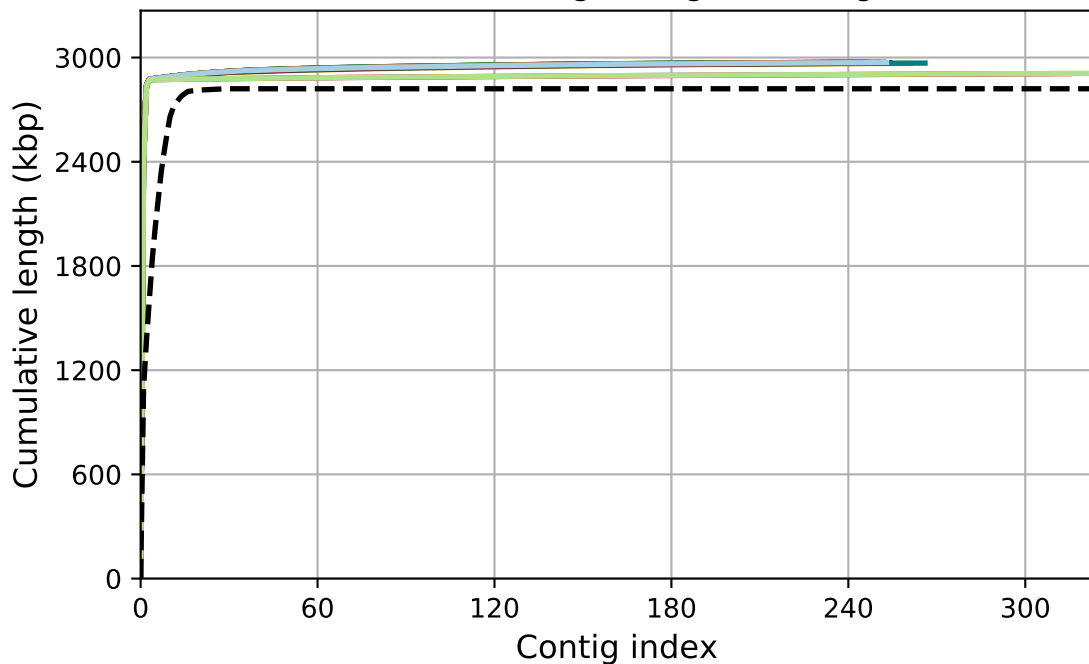
r10_1bin_v4_3_MP

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

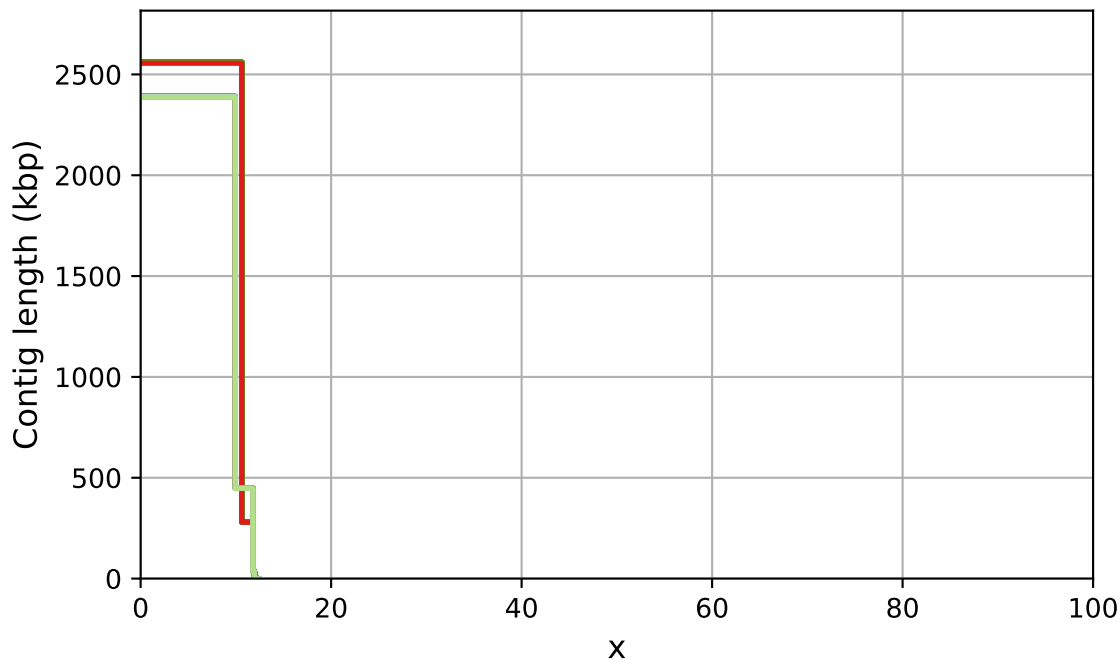
r10_1bin_v4_3_MP_helen

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

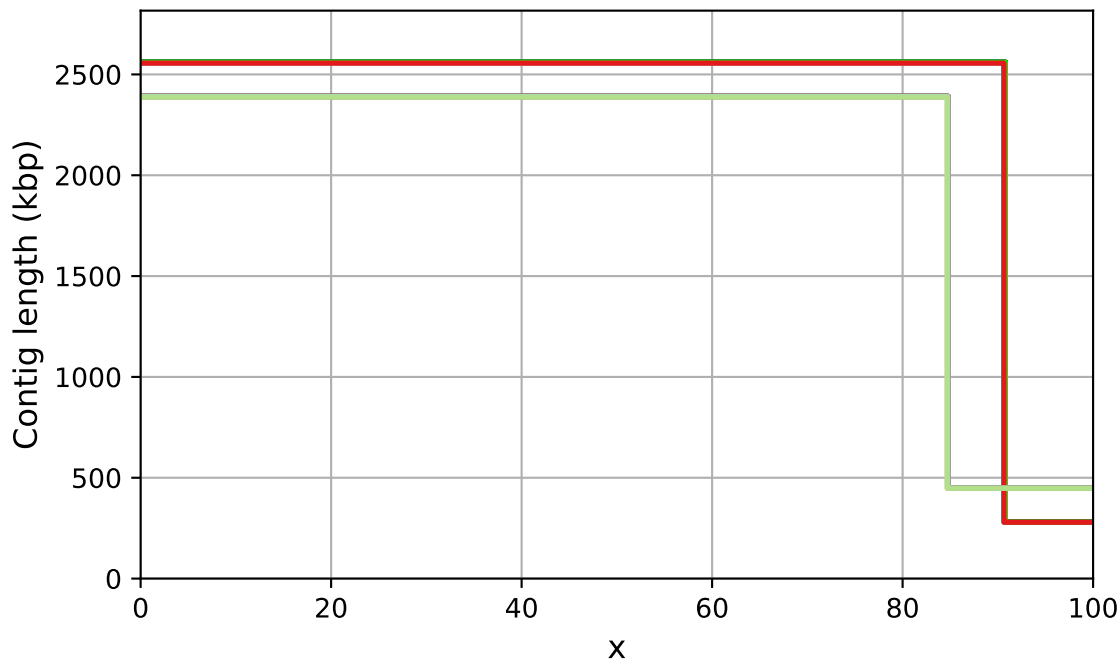
r10_1bin_v4_3_MP

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_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

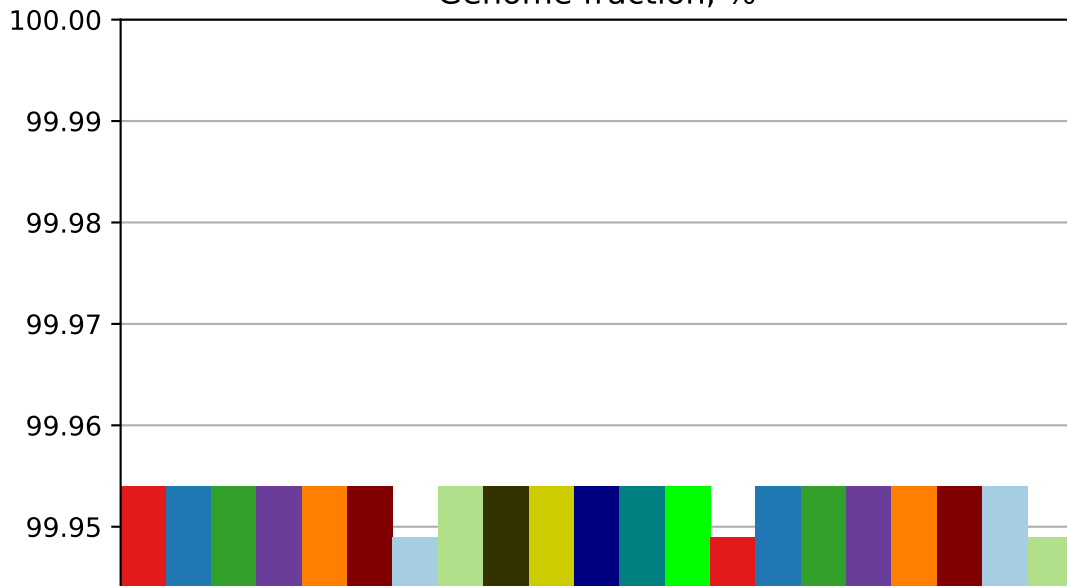
r10_1bin_v4_3_r1_medaka

r10_1bin_v4_1_r2_medaka

r10_1bin_v4_2_r2_medaka

r10_1bin_v4_3_r2_medaka

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