

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	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 10000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 25000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Total length (>= 50000 bp)	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
# 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	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
Total length	24074864	24069434	24071998	24064261	24059992	24055964	28129302	24074405	24069671	24071816	24060875	24059808	24052467	28130239	24075545	24072103	24075113	24069593	24065155	24060597	28132457
Reference length	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036	4787036
GC (%)	44.80	44.80	44.80	44.80	44.78	44.78	51.10	44.80	44.80	44.80	44.80	44.78	44.78	51.10	44.80	44.81	44.80	44.80	44.79	44.79	51.10
Reference GC (%)	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45	50.45
N50	4045598	4045624	4045593	4045588	4045161	4045292	4755626	4045604	4045480	4045604	4045608	4045229	4045315	4756102	4045596	4045614	4045597	4045593	4045228	4045344	4755682
NG50	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	6788581
N75	2845425	2845362	2845428	2845425	2845303	2845317	2990263	2845427	2845365	2845431	2845433	2845282	2845346	2990631	2845434	2845416	2845426	2845429	2845240	2845336	2990406
NG75	4765873	4765292	4765363	4765370	4764541	4764622	6787707	4765365	4765330	4765353	4765356	4764481	4764622	6787702	4765372	4765362	4765559	4765361	4764967	4764598	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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# 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	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
# local misassemblies	37	37	37	37	36	37	57	36	36	36	36	36	36	60	36	36	37	36	37	36	57
# 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	19039975	19036084	19035102	19028735	19022681	19014810	23168496	19039376	19034339	19035890	19025050	19025332	19015811	23183119	19040423	19036903	19040929	19034396	19031832	19021731	23171535
Genome fraction (%)	97.703	97.701	97.701	97.701	97.703	97.701	97.663	97.703	97.703	97.703	97.703	97.703	97.703	97.665	97.703	97.703	97.703	97.703	97.703	97.703	97.663
Duplication ratio	1.077	1.076	1.077	1.077	1.077	1.077	1.078	1.061	1.077	1.077	1.077	1.077	1.077	1.058	1.077	1.077	1.076	1.077	1.076	1.077	1.061
# 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	441.74	435.89	444.16	440.95	451.02	457.89	503.78	442.36	439.66	442.33	441.46	443.02	448.79	484.25	442.06	439.28	438.27	441.01	440.54	453.50	503.85
# indels per 100 kbp	20.23	18.05	14.90	14.88	40.12	36.59	238.22	20.29	18.13	15.35	14.90	40.76	36.93	236.68	20.38	16.53	15.44	15.16	40.97	37.59	238.22
Largest alignment	1408864	1408814	1408884	1408889	1408682	1408699	1104888	1408812	1408783	1408811	1408819	1408861	1408646	1102535	1414841	1414814	1414828	1414827	1414597	1414606	1102144
Total aligned length	5029495	5030374	5032931	5032574	5032131	5038294	4958510	5029690	5029993	5030600	5030488	5029267	5031469	4942341	5028701	5028791	5027774	5028787	5027012	5032561	4955729
NGA50	1103283	1105646	1105652	1105648	1103083	1105452	586344	1103277	1103269	1103272	1103273	1103073	1103096	586349	1102966	1102966	1103054	1102961	1103243	1102811	586484
NGA75	393562	393563	393563	393563	393537	393557	376841	393562	393564	393566	393564	393531	393534	376968	394049	394043	394044	394045	393973	393984	369878
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	3	2	2	2	2	2	2	3
LGA75	5	5	5	5	5	5	6	5	5	5	5	5	5	6	5	5	5	5	5	5	6

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	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# contig misassemblies	21	21	21	21	21	21	19	21	21	21	21	21	21	19	21	21	21	21	21	21	19
# c. relocations	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
# c. translocations	20	20	20	20	20	20	18	20	20	20	20	20	20	18	20	20	20	20	20	20	18
# 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	4765873	4765292	4765363	4765370	4764541	4764622	4763407	4765365	4765330	4765353	4765356	4764481	4764622	4763482	4765372	4765362	4765559	4765361	4764967	4764598	4763422
# 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	12	12	12	12	12	12	32	12	12	12	12	12	12	34	12	12	12	12	12	12	32
# local misassemblies	37	37	37	37	36	37	57	36	36	36	36	36	36	60	36	36	37	36	37	36	57
# 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	42	42	42	42	42	42	36	42	42	42	42	42	42	35	42	42	42	42	42	42	36
# 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	20658	20384	20771	20621	21092	21413	23550	20687	20561	20686	20645	20718	20988	22637	20673	20543	20496	20624	20602	21208	23553
# indels	946	844	697	696	1876	1711	11136	949	848	718	697	1906	1727	11064	953	773	722	709	1916	1758	11136
# indels (<= 5 bp)	848	745	601	600	1778	1615	10936	850	749	621	600	1809	1629	10863	852	672	624	611	1818	1659	10937
# indels (> 5 bp)	98	99	96	96	98	96	200	99	99	97	97	97	98	201	101	101	98	98	98	99	199
Indels length	6195	6055	5824	5825	7256	6963	20315	6216	6145	5946	5919	7291	7095	20371	6221	6044	5943	5939	7314	7127	20306

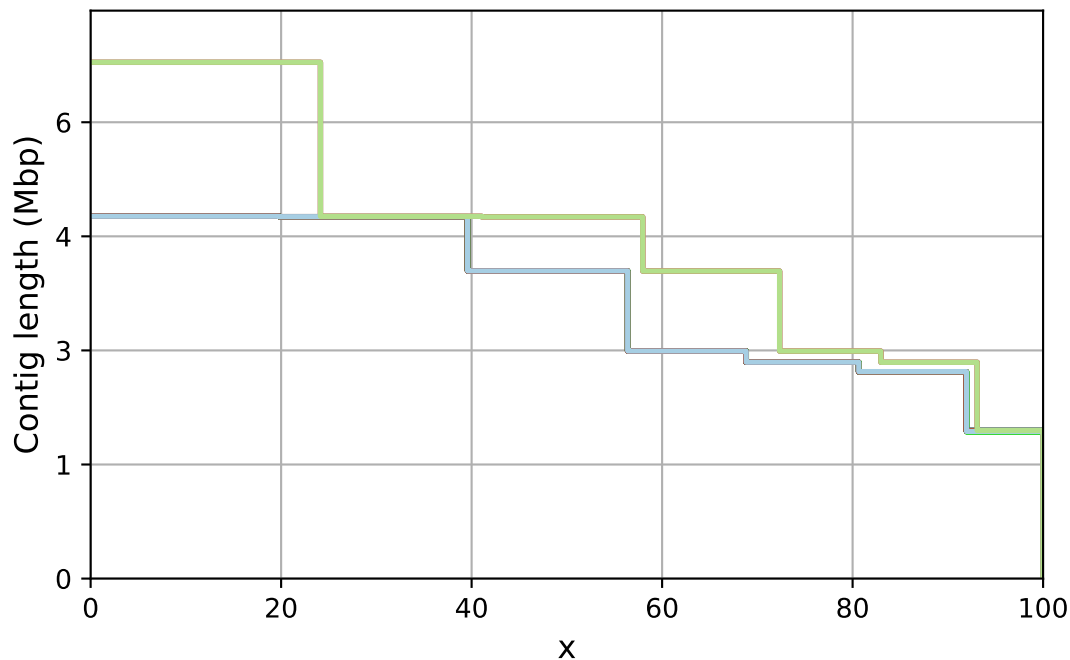
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	19039975	19036084	19035102	19028735	19022681	19014810	23168496	19039376	19034339	19035890	19025050	19025332	19015811	23183119	19040423	19036903	19040929	19034396	19031832	19021731	23171535
# 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  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



r10\_1bin\_v2\_1\_MP

r10\_1bin\_v2\_2\_MP

r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_1\_MP\_helen

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_1\_r1\_medaka

r10\_1bin\_v2\_2\_r1\_medaka

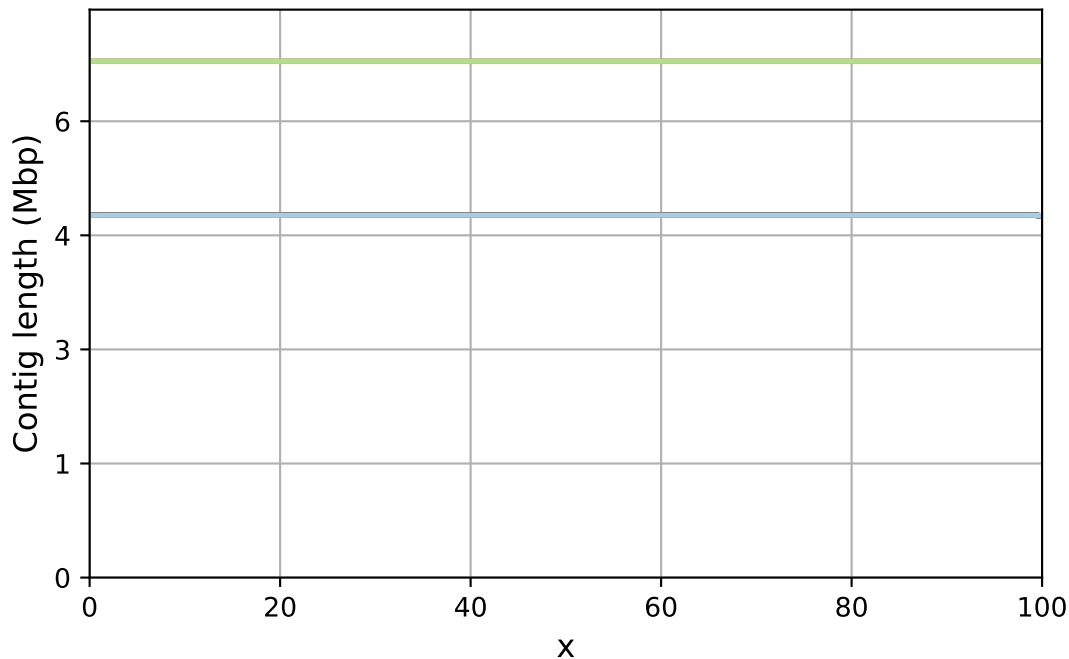
r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

# NGx



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\_2\_MP

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

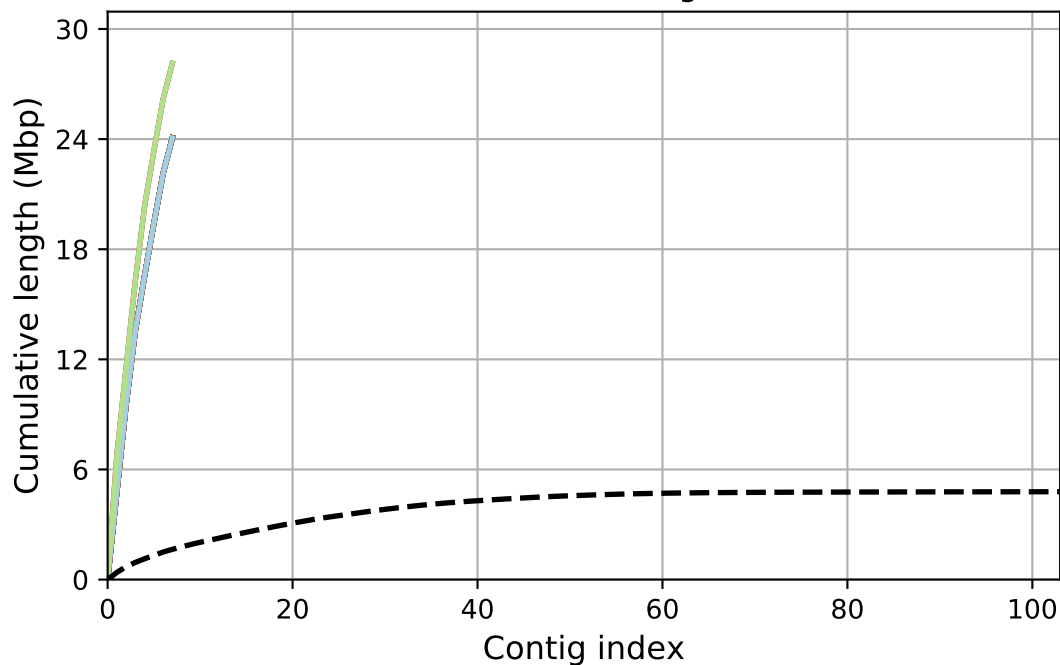
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

Cumulative length



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\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_2\_racon\_r1

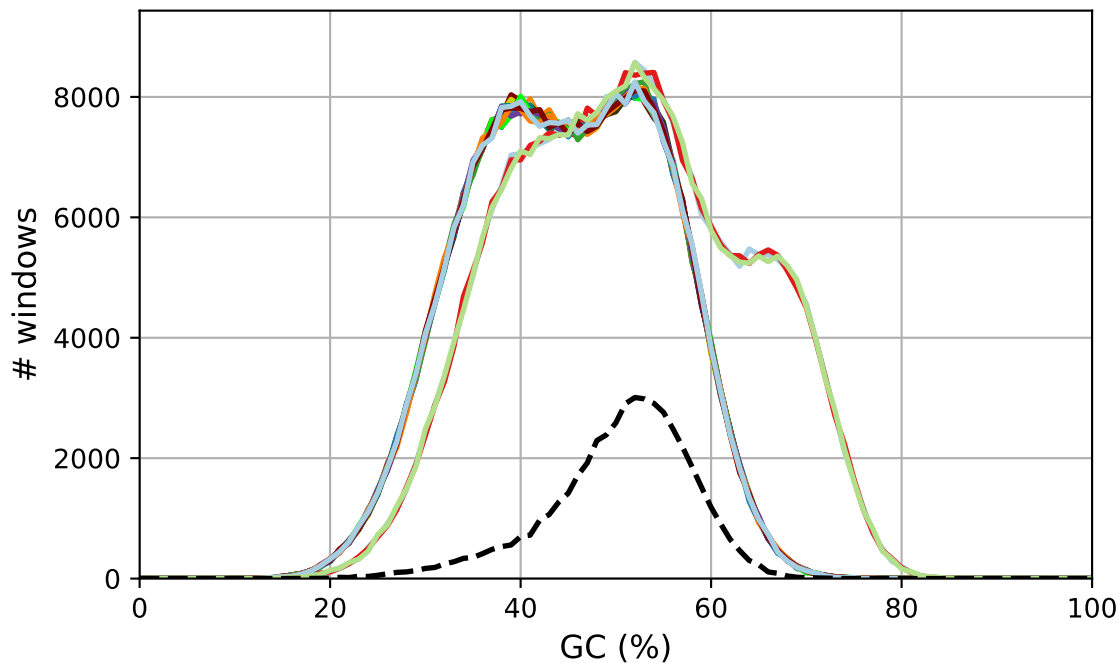
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r10\_1bin\_v2\_3\_r1\_medaka

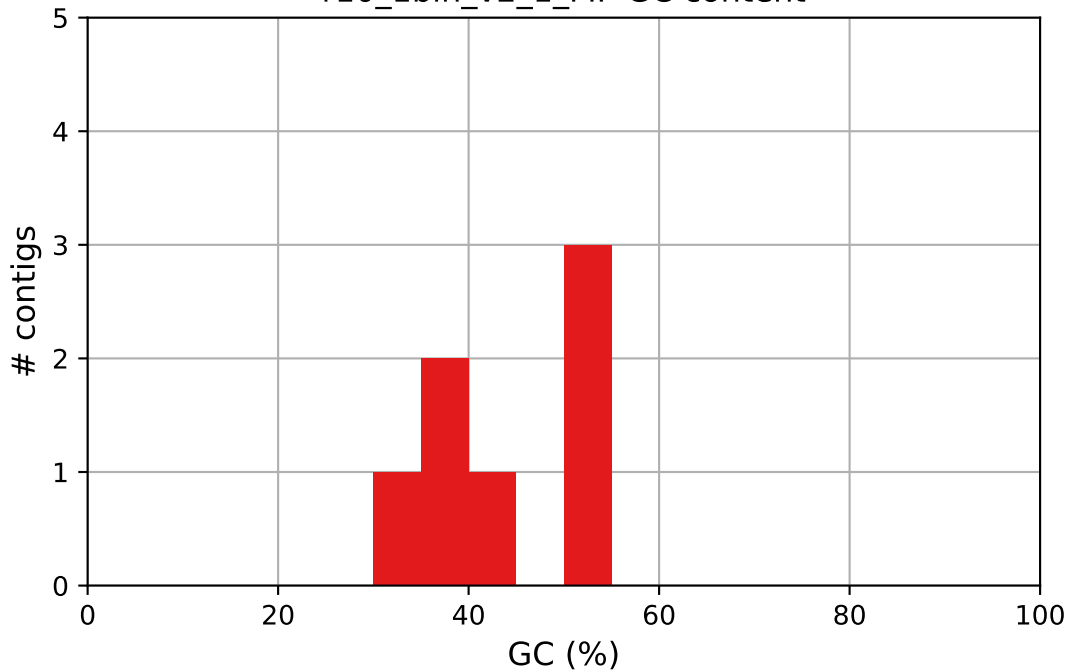
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1

GC content



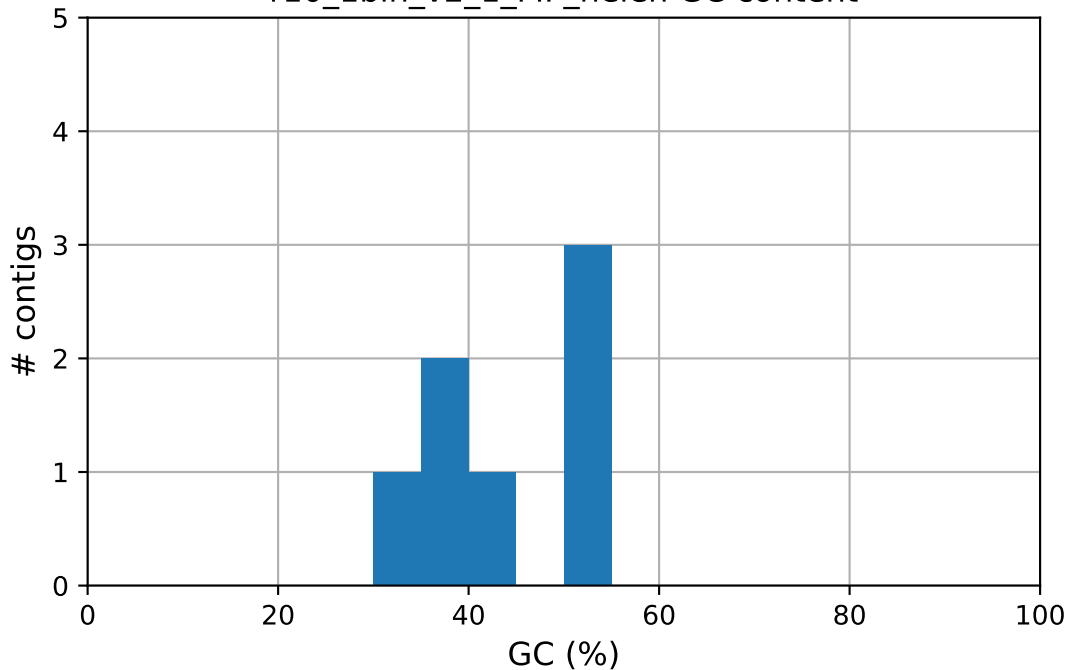
r10\_1bin\_v2\_1\_MP GC content



r10\_1bin\_v2\_1\_MP

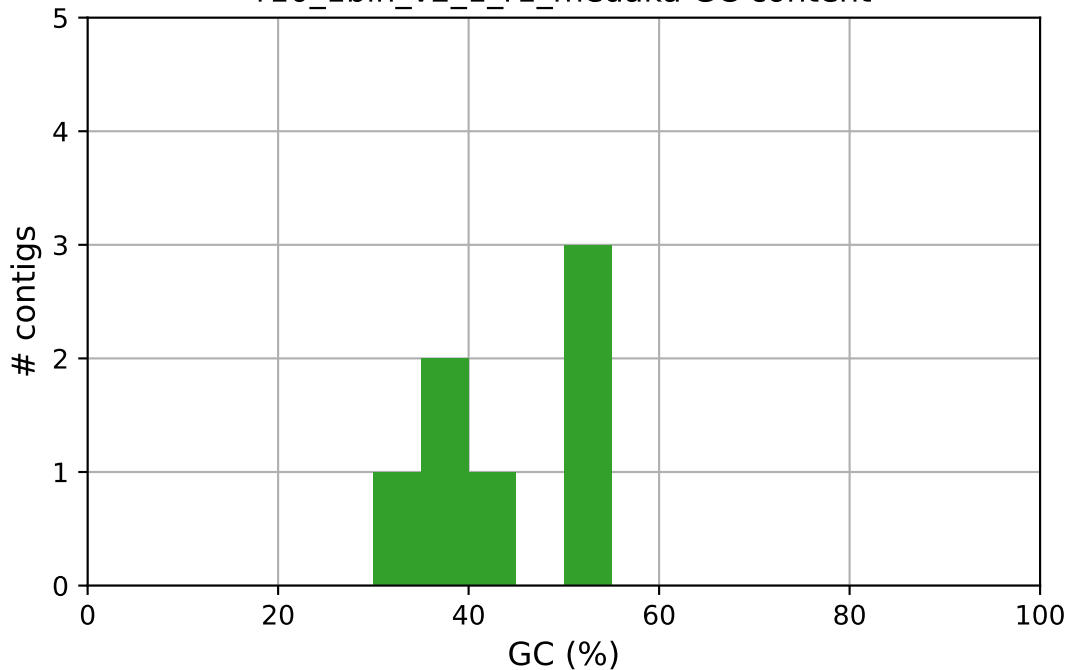


r10\_1bin\_v2\_1\_MP\_helen GC content



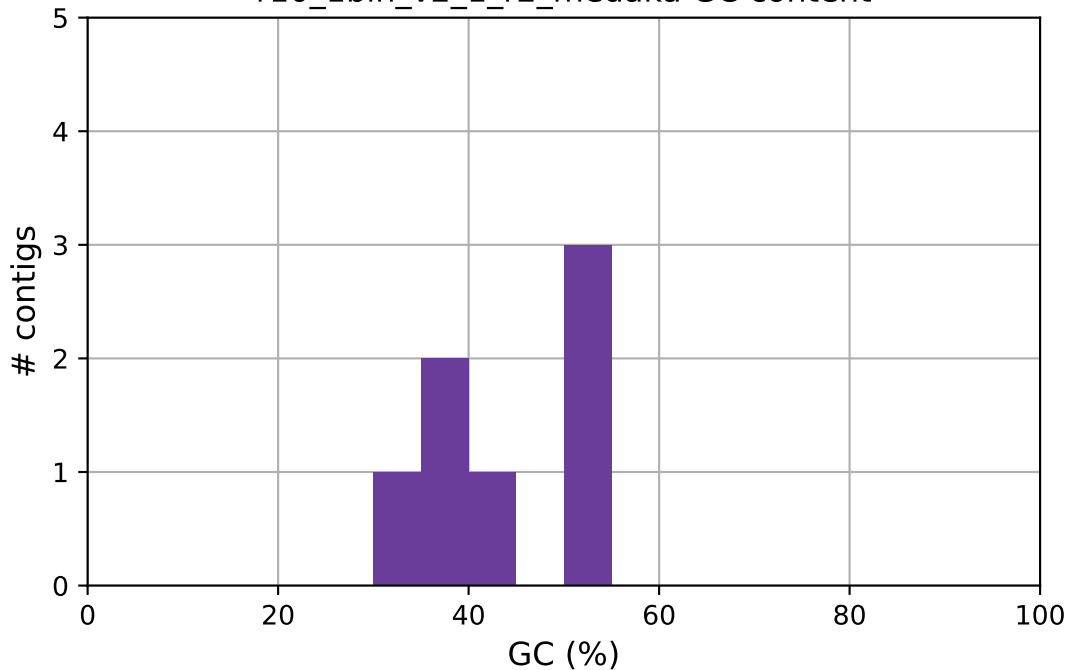
r10\_1bin\_v2\_1\_MP\_helen

r10\_1bin\_v2\_1\_r1\_medaka GC content



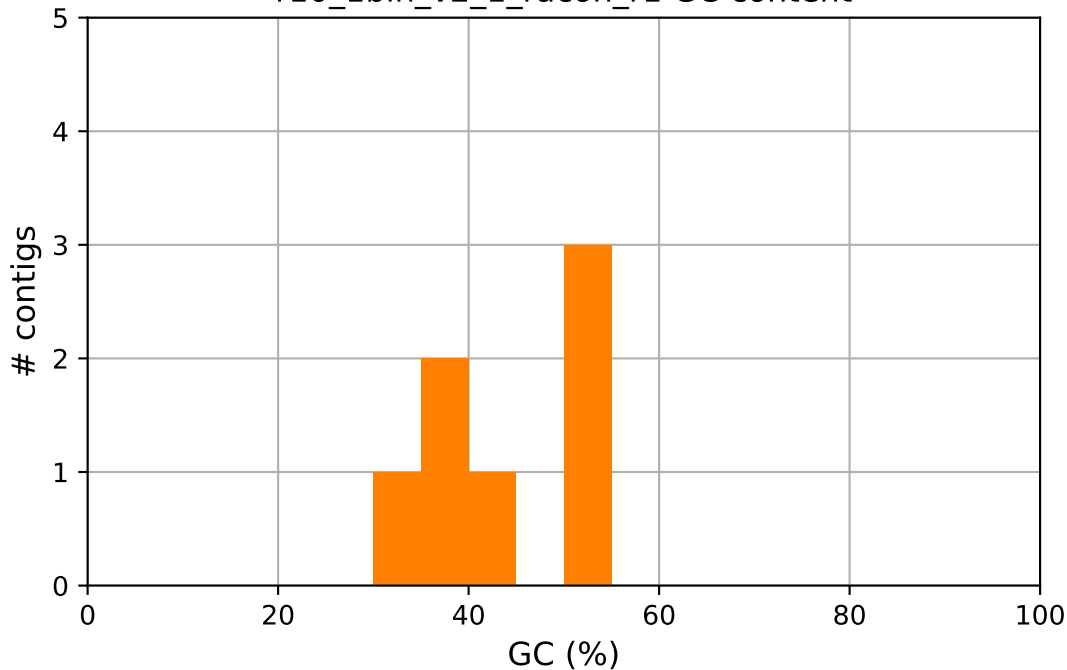
r10\_1bin\_v2\_1\_r1\_medaka

r10\_1bin\_v2\_1\_r2\_medaka GC content



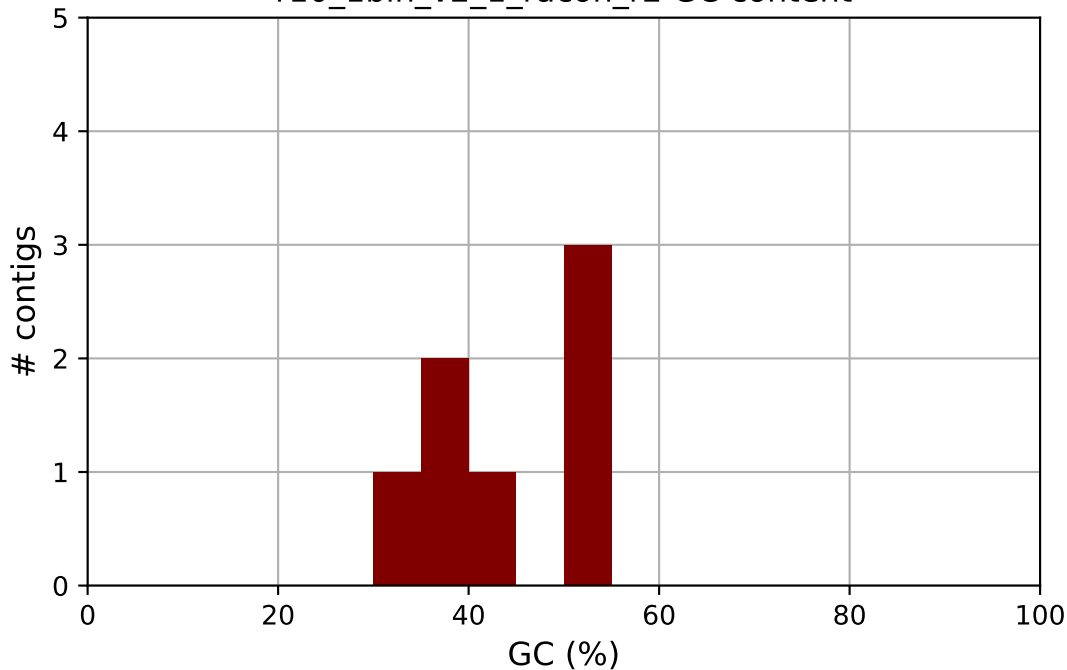
r10\_1bin\_v2\_1\_r2\_medaka

r10\_1bin\_v2\_1\_racon\_r1 GC content



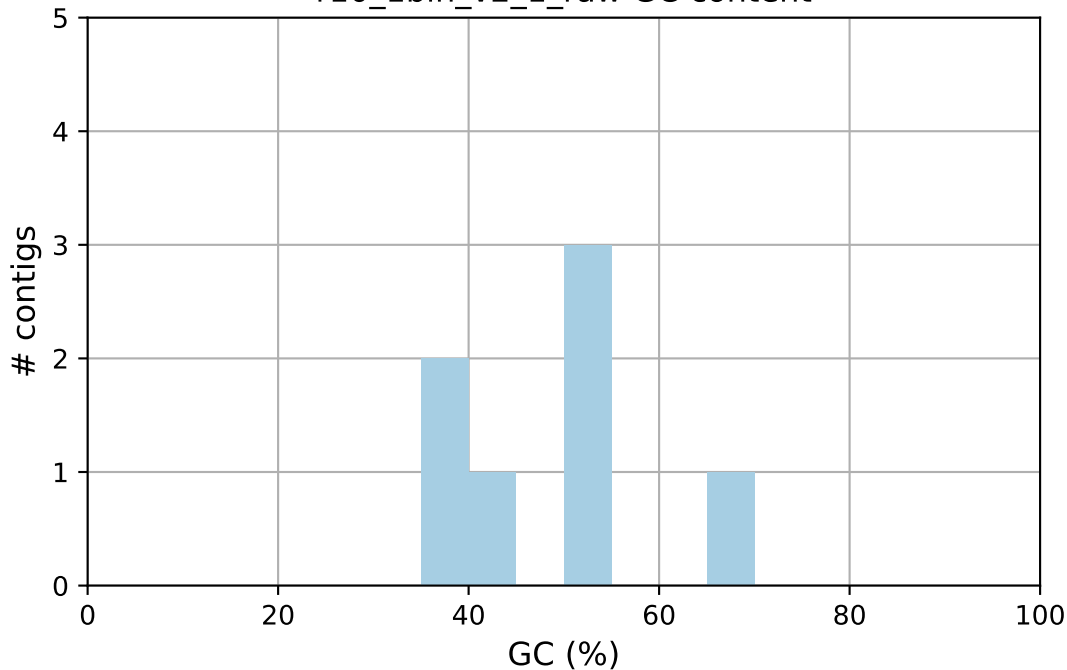
r10\_1bin\_v2\_1\_racon\_r1

r10\_1bin\_v2\_1\_racon\_r2 GC content



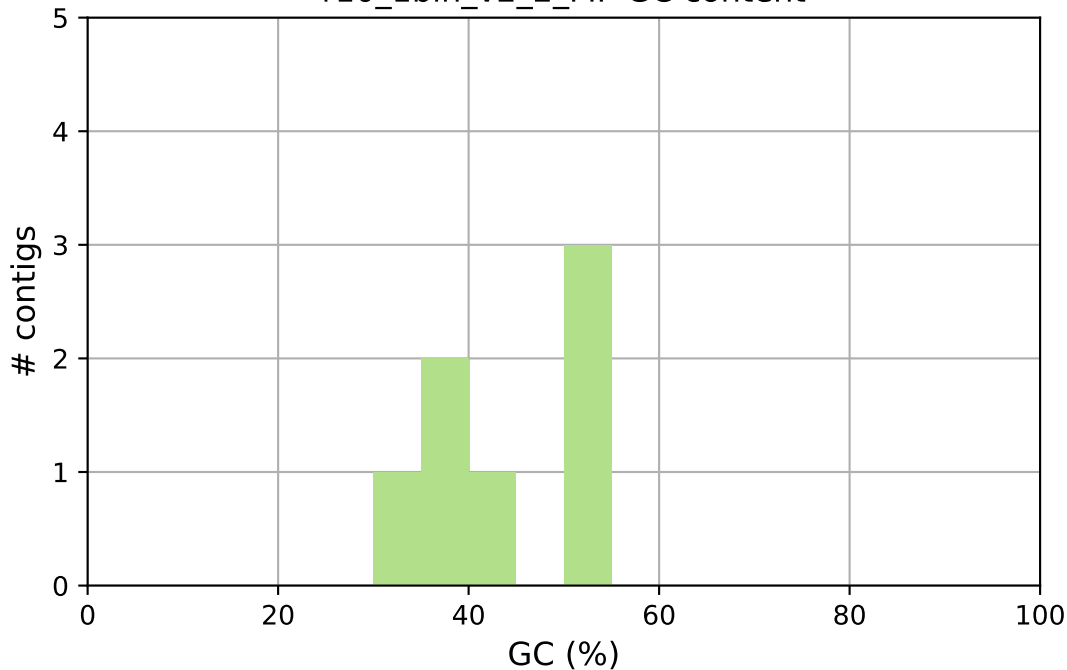
r10\_1bin\_v2\_1\_racon\_r2

r10\_1bin\_v2\_1\_raw GC content



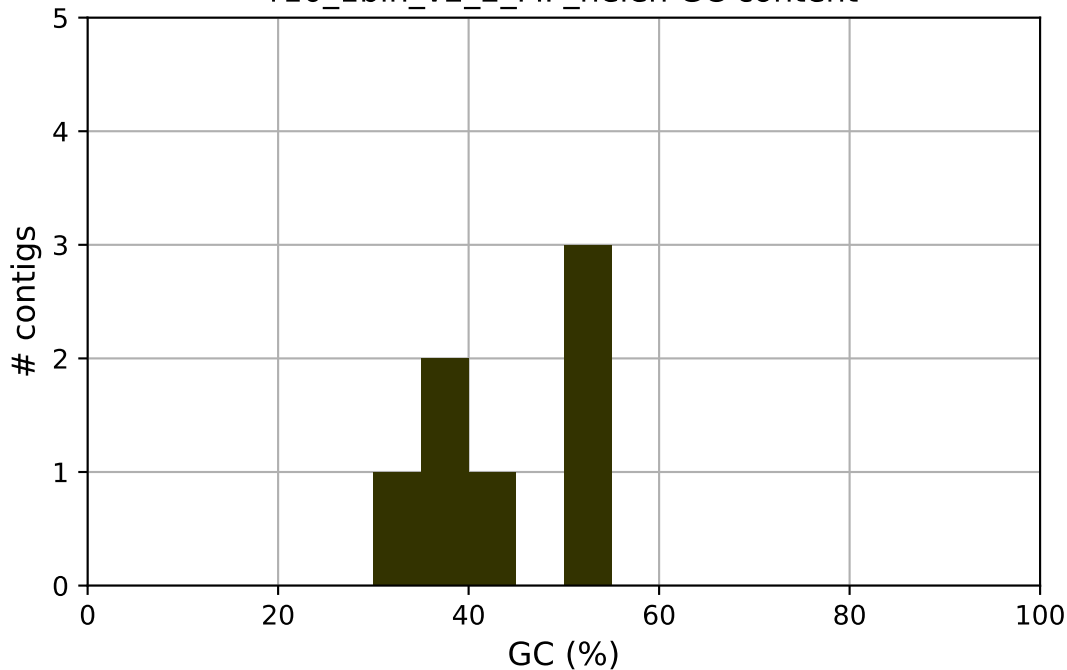
r10\_1bin\_v2\_1\_raw

r10\_1bin\_v2\_2\_MP GC content



r10\_1bin\_v2\_2\_MP

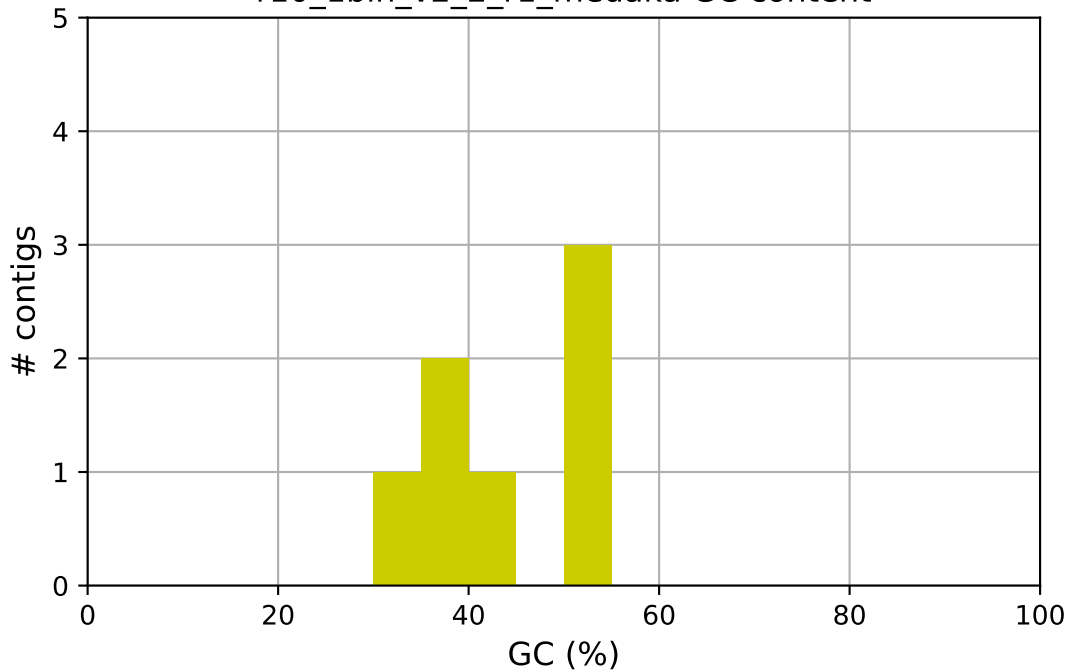
r10\_1bin\_v2\_2\_MP\_helen GC content



r10\_1bin\_v2\_2\_MP\_helen

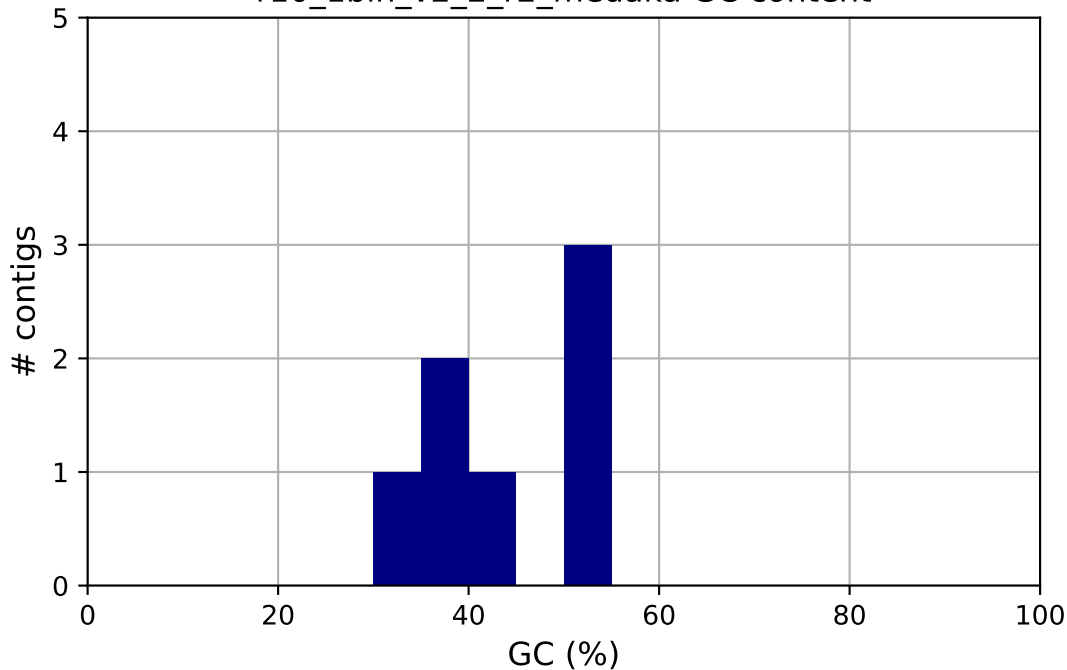


r10\_1bin\_v2\_2\_r1\_medaka GC content



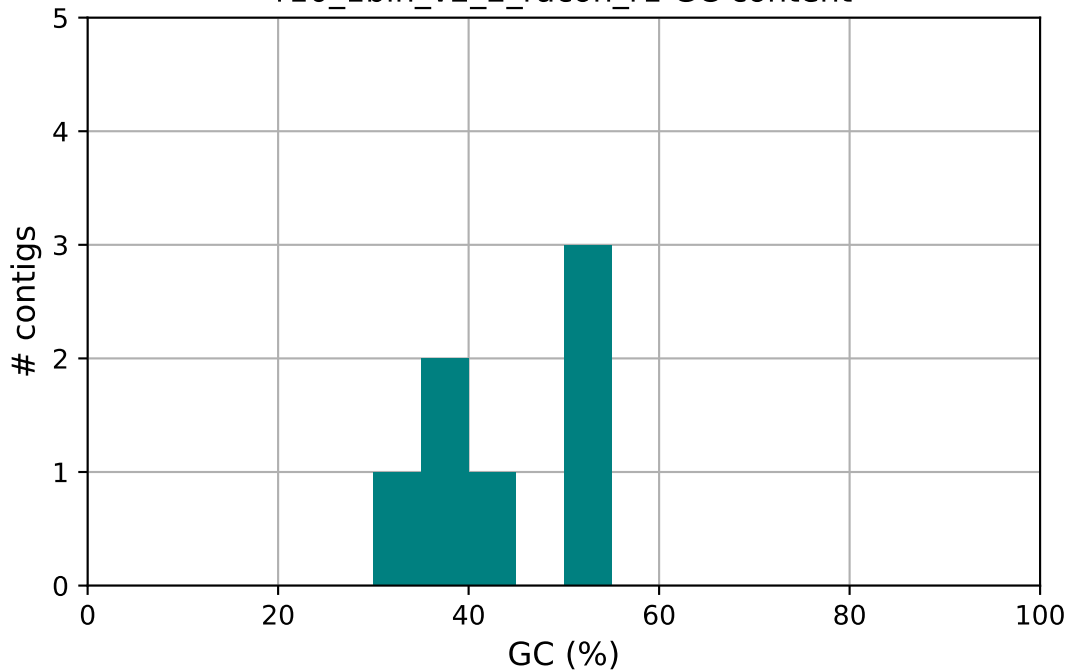
r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka GC content



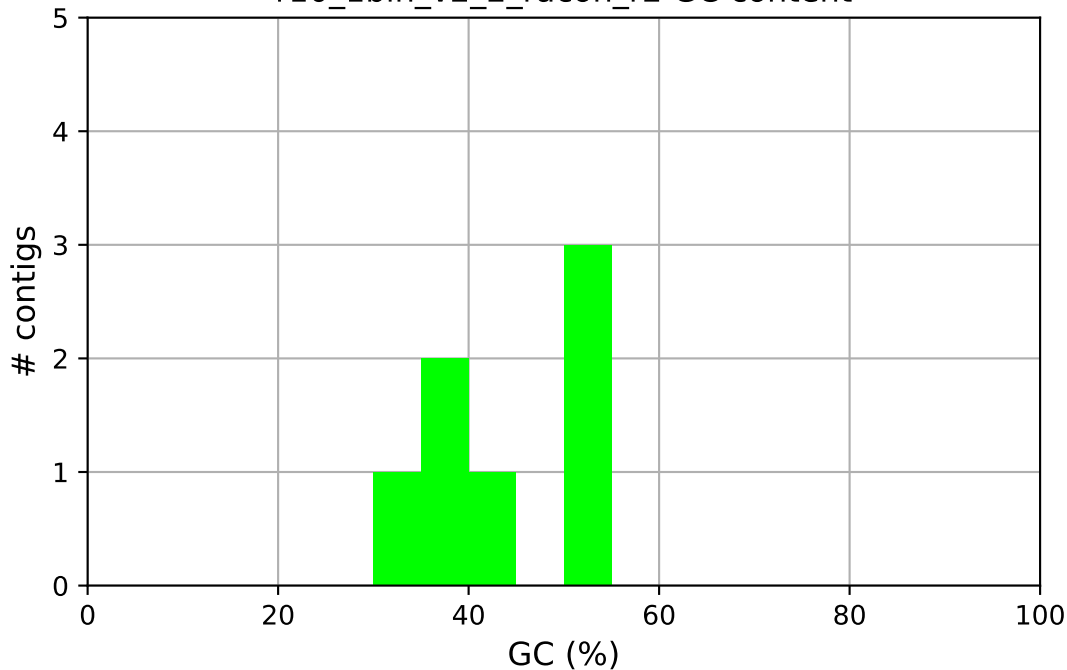
r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_2\_racon\_r1 GC content



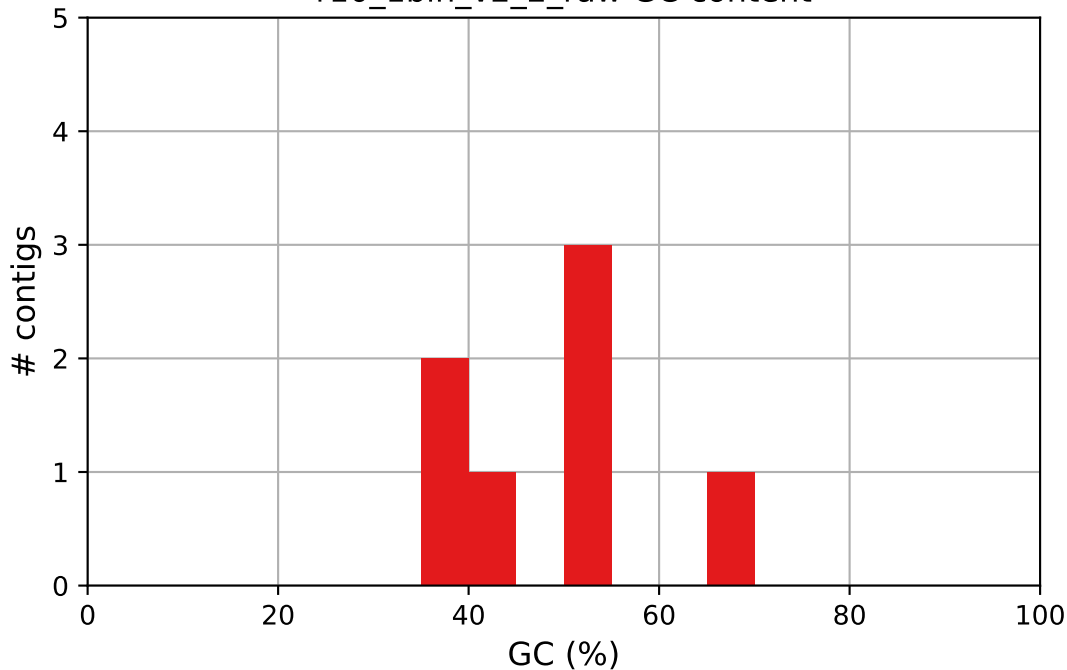
r10\_1bin\_v2\_2\_racon\_r1

r10\_1bin\_v2\_2\_racon\_r2 GC content



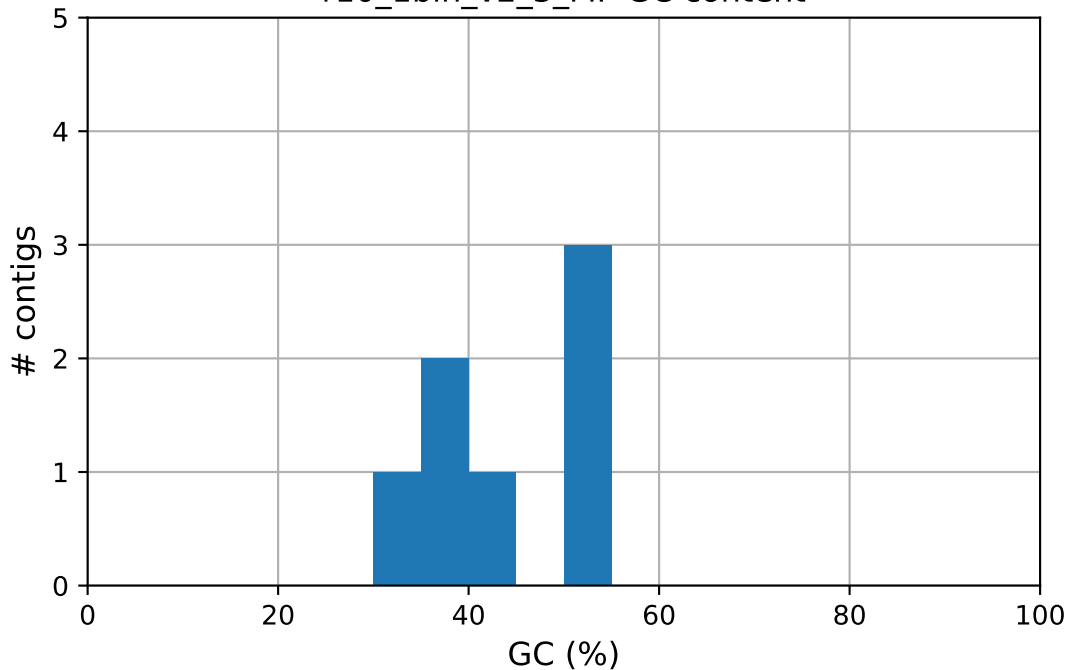
r10\_1bin\_v2\_2\_racon\_r2

r10\_1bin\_v2\_2\_raw GC content



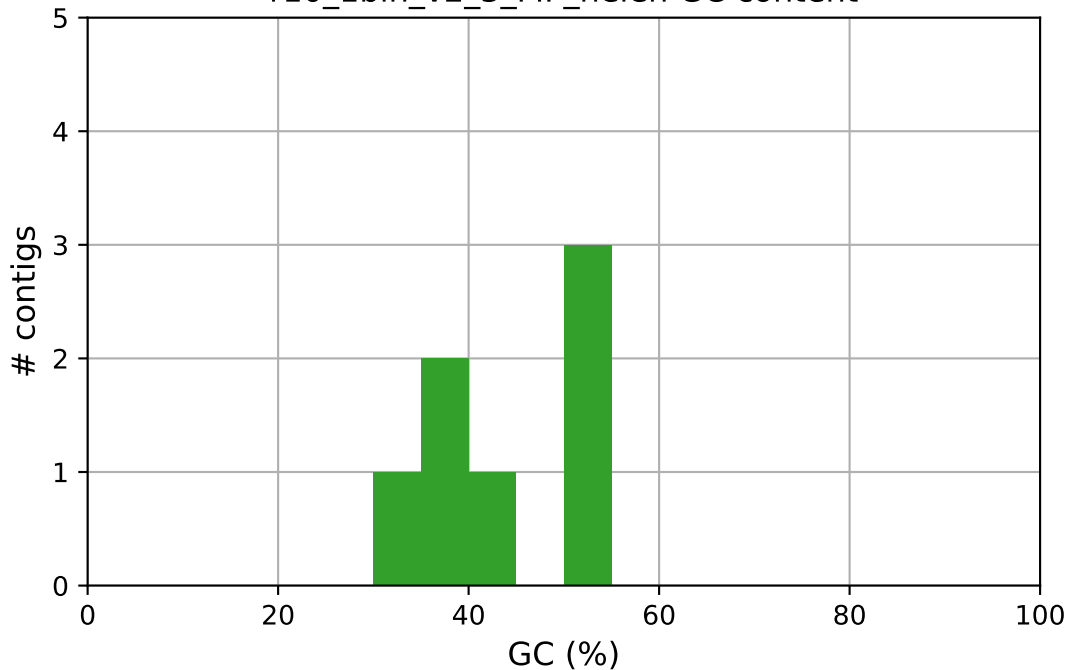
r10\_1bin\_v2\_2\_raw

r10\_1bin\_v2\_3\_MP GC content



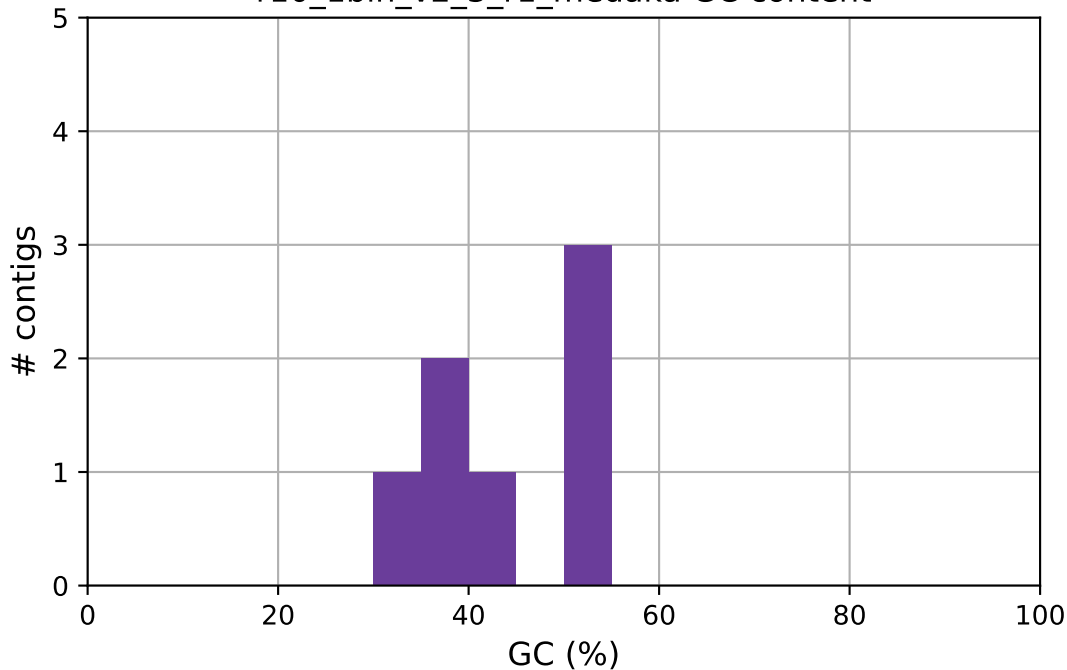
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen GC content



r10\_1bin\_v2\_3\_MP\_helen

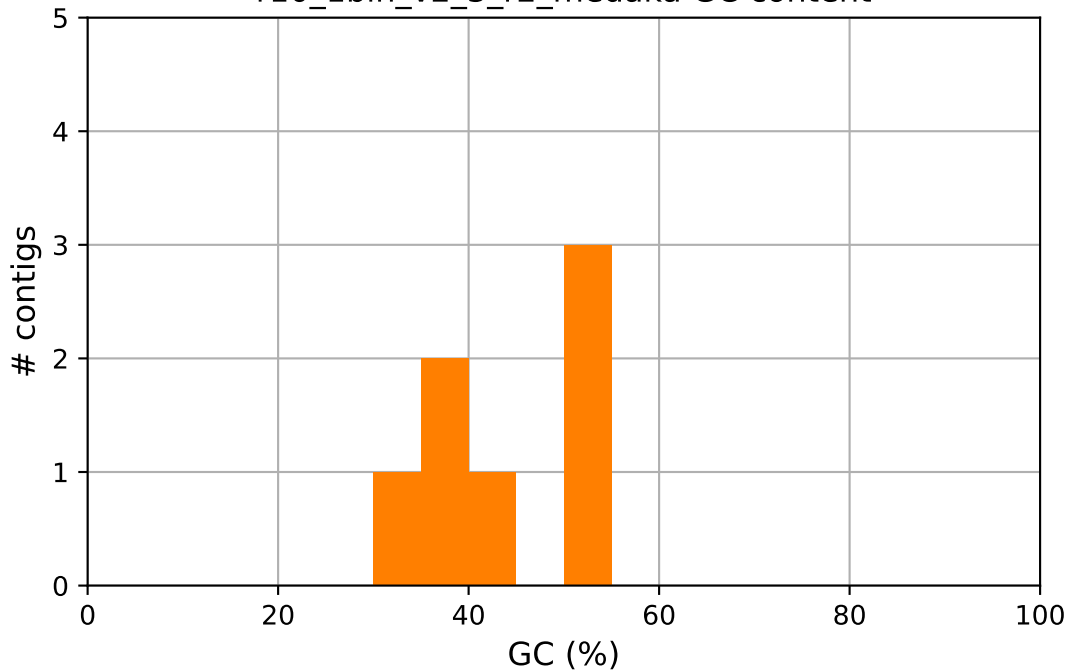
r10\_1bin\_v2\_3\_r1\_medaka GC content



r10\_1bin\_v2\_3\_r1\_medaka

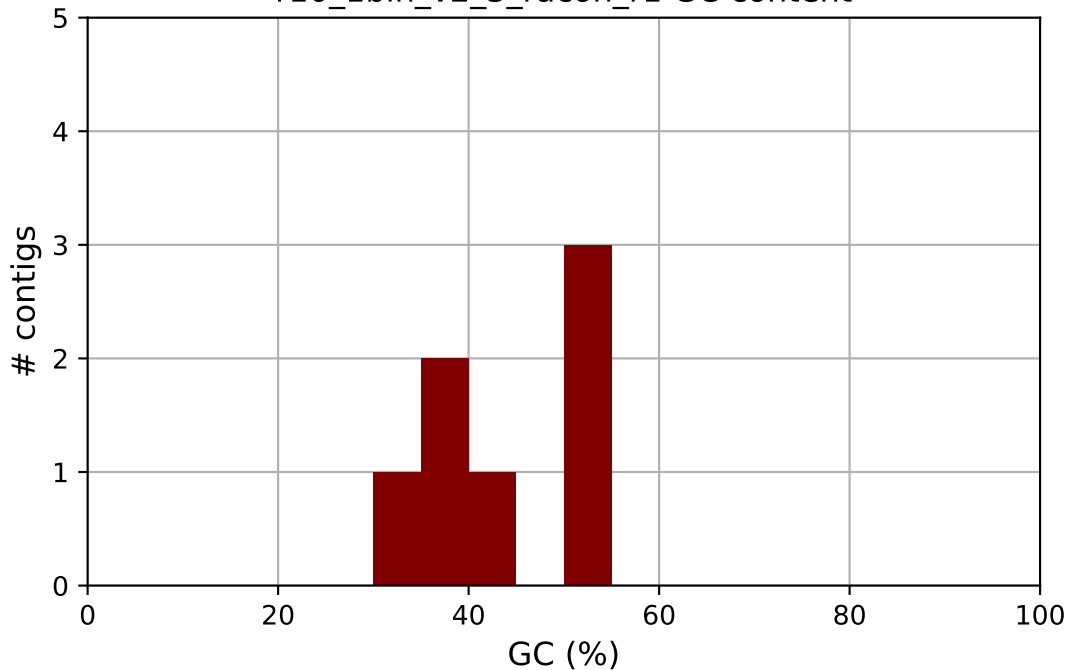


r10\_1bin\_v2\_3\_r2\_medaka GC content



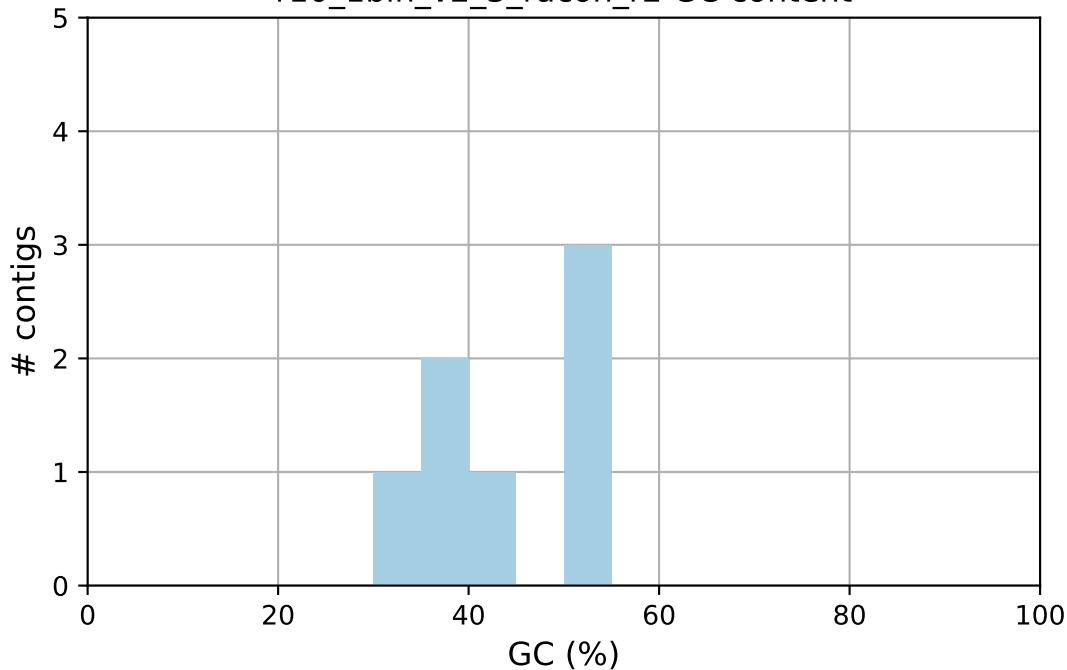
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1 GC content



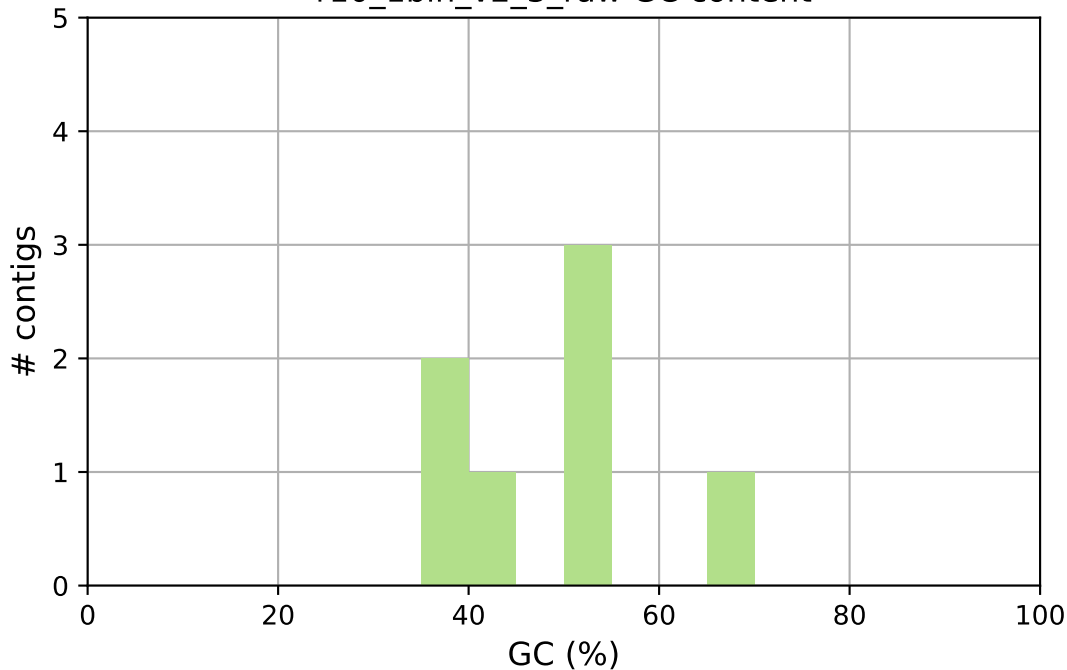
r10\_1bin\_v2\_3\_racon\_r1

r10\_1bin\_v2\_3\_racon\_r2 GC content



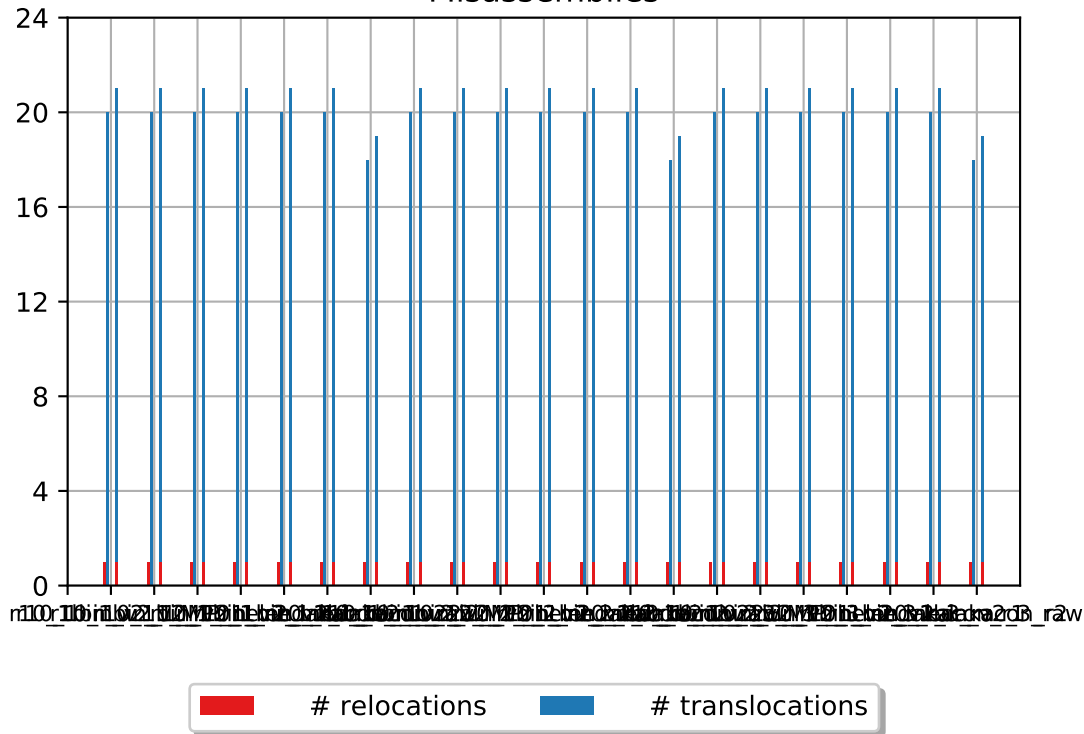
r10\_1bin\_v2\_3\_racon\_r2

r10\_1bin\_v2\_3\_raw GC content

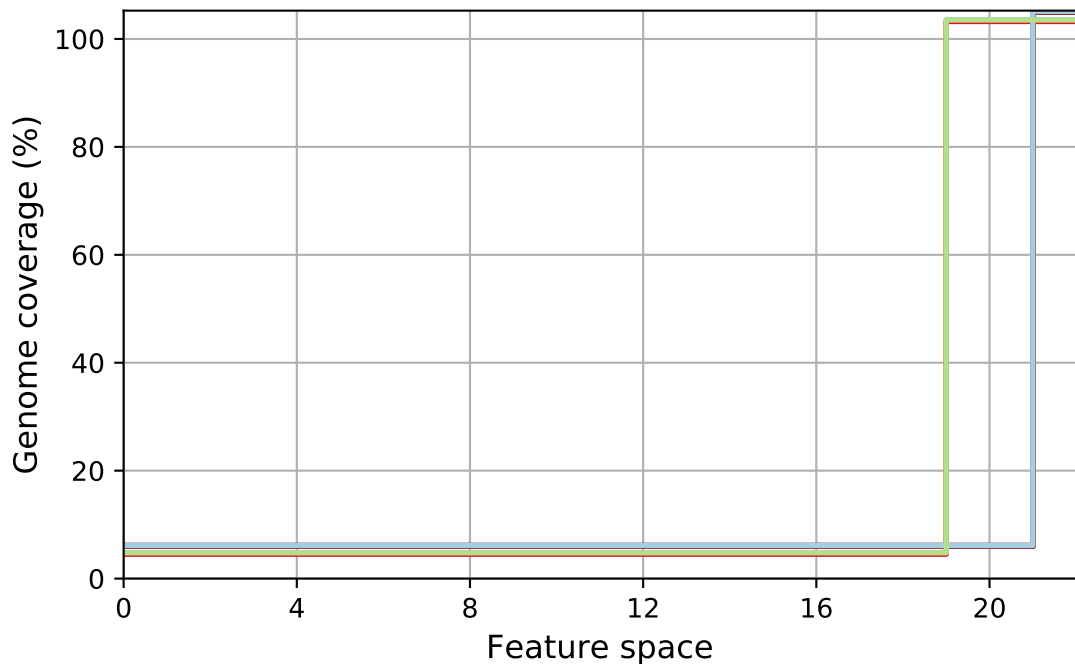


r10\_1bin\_v2\_3\_raw

# Misassemblies



FRCurve (misassemblies)



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\_2\_MP

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

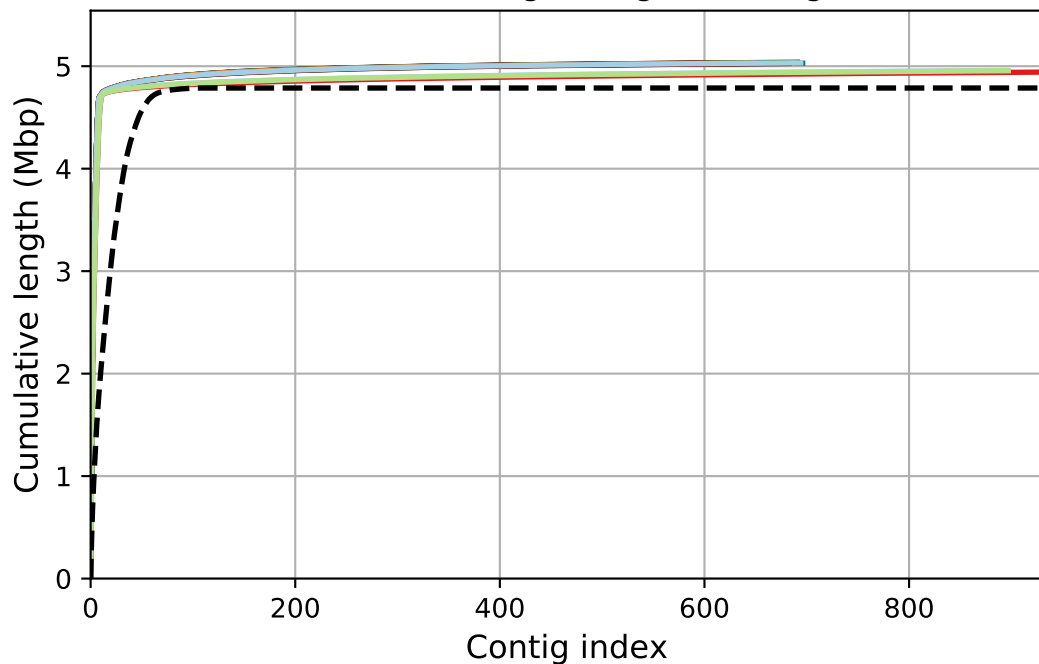
r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

Cumulative length (aligned contigs)



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\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_2\_racon\_r1

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

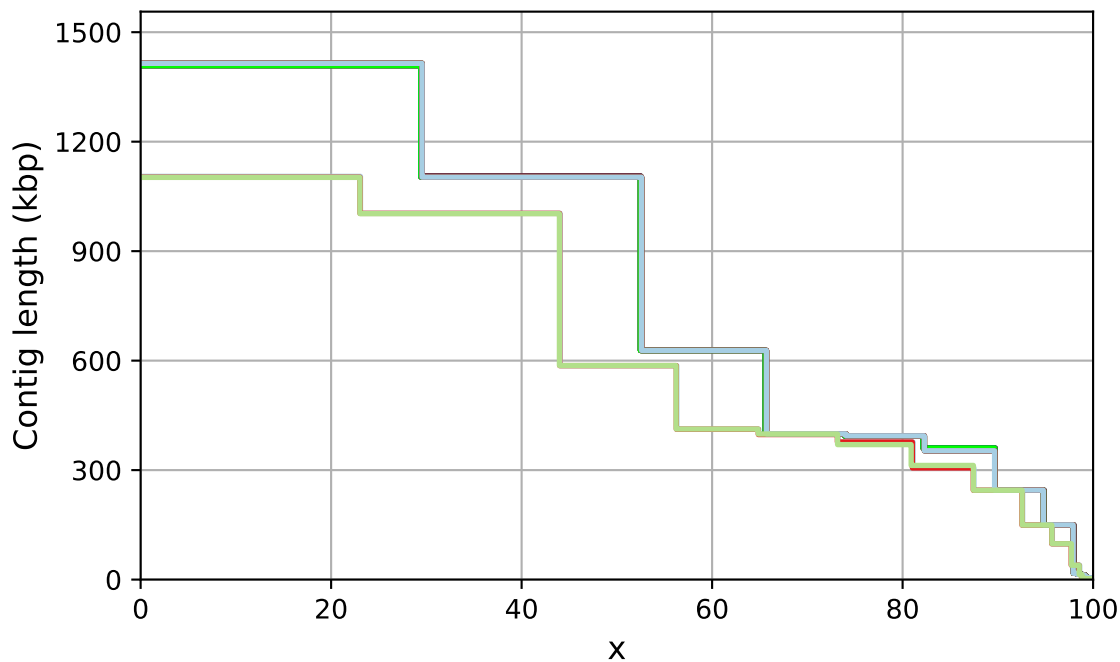
r10\_1bin\_v2\_3\_r2\_medaka

r10\_1bin\_v2\_3\_racon\_r1





# NGAx



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\_2\_MP

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka

Genome fraction, %



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\_2\_MP

r10\_1bin\_v2\_2\_MP\_helen

r10\_1bin\_v2\_2\_r1\_medaka

r10\_1bin\_v2\_2\_r2\_medaka

r10\_1bin\_v2\_3\_MP

r10\_1bin\_v2\_3\_MP\_helen

r10\_1bin\_v2\_3\_r1\_medaka

r10\_1bin\_v2\_3\_r2\_medaka