

Report

	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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	
# contigs (>= 10000 bp)	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	
# contigs (>= 50000 bp)	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Total length (>= 5000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 10000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 25000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
Total length (>= 50000 bp)	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
# contigs	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
Largest contig	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
Total length	24075406	24070890	24072753	24062203	24060263	24054195	28130867	24074923	24071344	24072870	24062184	24061558	24055354	28131695	24074822	24070715	24072827	24063225	24060618	24054198	28131333
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	44.79	44.78	51.10	44.80	44.80	44.80	44.80	44.79	44.79	51.10	44.80	44.80	44.80	44.80	44.79	44.78	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	4045595	4045617	4045595	4045588	4045225	4045305	4756113	4045604	4045620	4045593	4045591	4045221	4045309	4756067	4045604	4045624	4045591	4045594	4045221	4045286	4756051
NG50	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	6788581
N75	2845426	2845369	2845429	2845431	2845288	2845343	2990676	2845426	2845369	2845430	2845431	2845286	2845339	2990627	2845426	2845369	2845430	2845431	2845286	2845339	2990627
NG75	4766016	4765867	4765431	4765364	4764829	4764690	6787718	4765469	4765339	4765413	4765389	4765359	4764750	6788581	4765404	4765326	4765369	4765362	4764572	4764639	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	20	21	21	21	21	21	21	21	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	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
# local misassemblies	37	38	37	36	37	37	47	36	37	36	37	39	37	57	36	37	37	37	36	36	61
# 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	19039882	19035265	19036186	19026164	19026909	19021351	23177684	19041520	19037334	19036707	19026673	19025975	19020290	23185358	19040425	19035465	19036565	19026915	19024358	19019018	23187263
Genome fraction (%)	97.703	97.701	97.701	97.703	97.703	97.701	97.655	97.703	97.701	97.703	97.701	97.701	97.701	97.660	97.703	97.701	97.701	97.701	97.703	97.703	97.644
Duplication ratio	1.077	1.077	1.077	1.077	1.076	1.076	1.060	1.076	1.076	1.077	1.077	1.077	1.077	1.058	1.077	1.077	1.077	1.077	1.077	1.077	1.058
# 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	441.84	439.33	443.54	442.18	442.53	441.17	487.89	438.27	436.76	442.40	441.08	445.81	447.09	478.64	441.29	439.63	442.75	442.56	448.34	446.29	481.85
# indels per 100 kbp	21.02	18.75	15.29	14.97	15.29	14.97	230.16	20.63	18.11	15.46	14.97	18.11	38.08	234.49	21.28	18.54	14.99	15.12	18.30	35.56	234.16
Largest alignment	1409355	1409277	1408949	1408887	1408915	1408742	1009756	1408933	1408887	1408949	1408914	1408923	1408777	850481	1408818	1408785	1408816	1408821	1408632	1408656	1104930
Total aligned length	5030118	5032604	5033614	5030715	5028102	5030018	4950556	5028052	5031044	5030826	5032547	5032650	5032154	4941345	5029058	5032284	5033297	5033346	5030888	5029885	4941743
NGA50	1103287	1105635	1105652	1103275	1103068	1105468	586871	1103284	1105633	1103273	1105649	1105948	1105488	412111	1103294	1105646	1105651	1105651	1103091	1103091	583107
NGA75	393567	393566	393561	393563	393550	393564	376875	393567	393566	393562	393562	393499	393558	303485	393570	393563	393561	393563	393544	393541	376965
LGA50	2	2	2	2	2	2	3	2	2	2	2	2	2	4	2	2	2	2	2	2	3
LGA75	5	5	5	5	5	5	6	5	5	5	5	5	5	7	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_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_3_raw
# misassemblies	21	21	21	21	21	21	20	21	21	21	21	21	21	21	21	21	21	21	21	21	19
# contig misassemblies	21	21	21	21	21	21	20	21	21	21	21	21	21	21	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	19	20	20	20	20	20	20	20	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	4766016	4765867	4765431	4765364	4764829	4764690	4764018	4765469	4765339	4765413	4765389	4765359	4764750	4763884	4765404	4765326	4765369	4765362	4764572	4764639	4763513
# 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	30	12	12	12	12	12	12	36	12	12	12	12	12	12	34
# local misassemblies	37	38	37	36	37	37	47	36	37	36	37	39	37	57	36	37	37	37	36	36	61
# 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	39	42	42	42	42	42	42	38	42	42	42	42	42	42	35
# 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	20663	20545	20742	20679	20695	20631	22805	20496	20425	20689	20627	20848	20908	22374	20637	20559	20705	20696	20967	20871	22520
# indels	983	877	715	700	1763	1624	10758	965	847	723	700	1781	1603	10961	995	867	701	707	1791	1663	10944
# indels (<= 5 bp)	881	777	618	603	1665	1526	10561	863	748	625	603	1683	1506	10764	896	766	605	611	1693	1566	10746
# indels (> 5 bp)	102	100	97	97	98	98	197	102	99	98	97	98	97	197	99	101	96	96	98	97	198
Indels length	6315	6104	5914	5927	7156	6916	19948	6278	6053	6014	5853	7117	6913	20448	6276	6102	5833	5835	7187	7025	19942

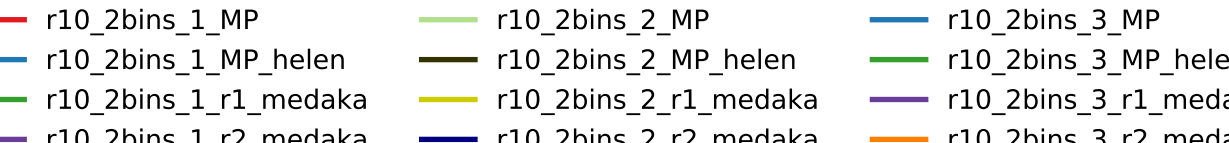
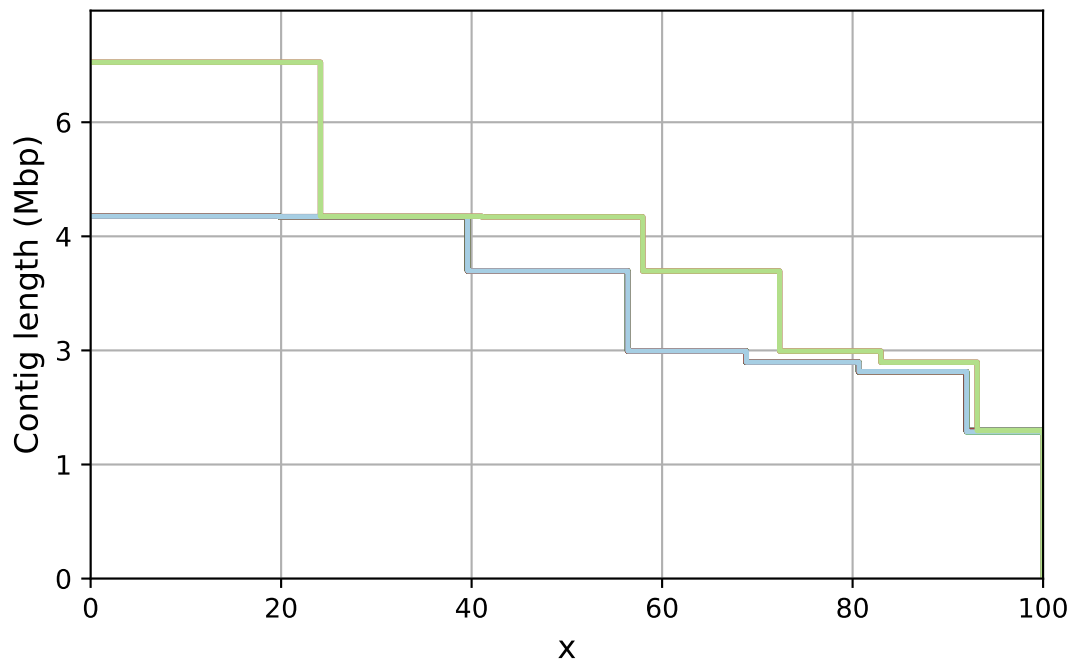
All statistics are based on contigs of size >= 5000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

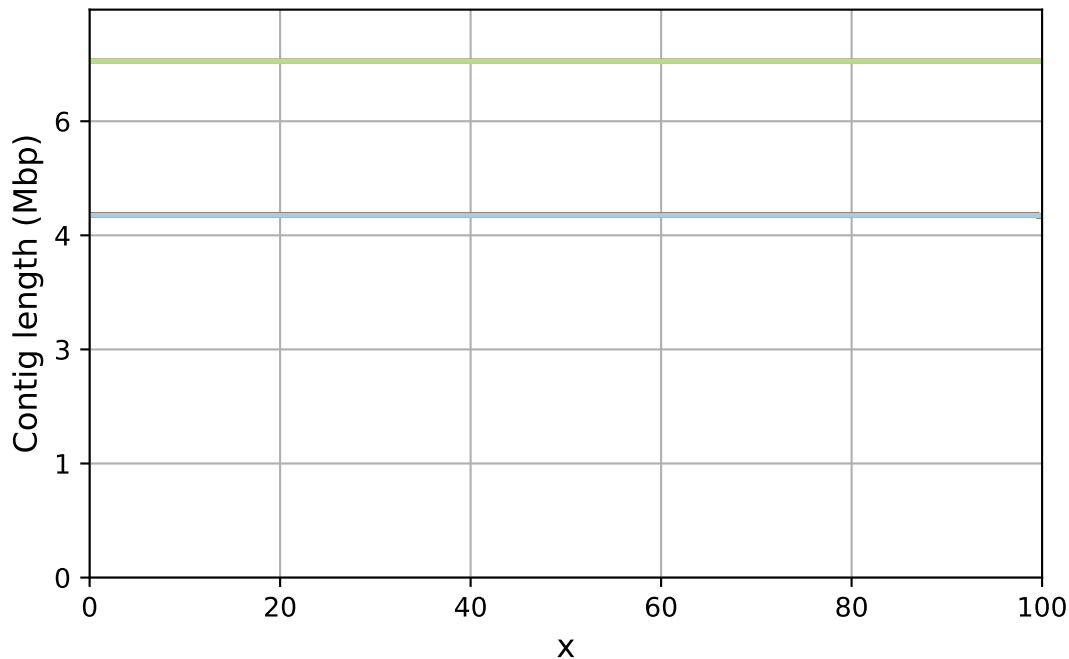
	r10_2bins_1_MP	r10_2bins_1_MP_helen	r10_2bins_1_r1_medaka	r10_2bins_1_r2_medaka	r10_2bins_1_racon_r1	r10_2bins_1_racon_r2	r10_2bins_1_raw	r10_2bins_2_MP	r10_2bins_2_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_2_racon_r2	r10_2bins_2_raw	r10_2bins_3_MP	r10_2bins_3_MP_helen	r10_2bins_3_r1_medaka	r10_2bins_3_r2_medaka	r10_2bins_3_racon_r1	r10_2bins_3_racon_r2	r10_2bins_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	19039882	19035265	19036186	19026164	19026909	19021351	23177684	19041520	19037334	19036707	19026673	19025975	19020290	23185358	19040425	19035465	19036565	19026915	19024358	19019018	23187263
# 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  $\geq 5000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

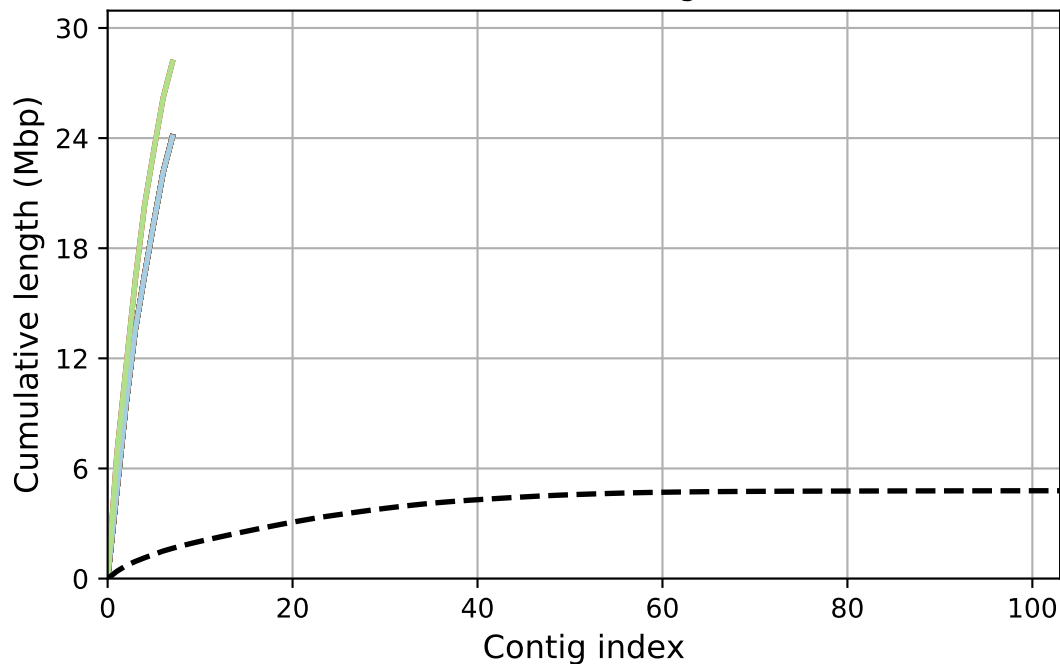


# NGx



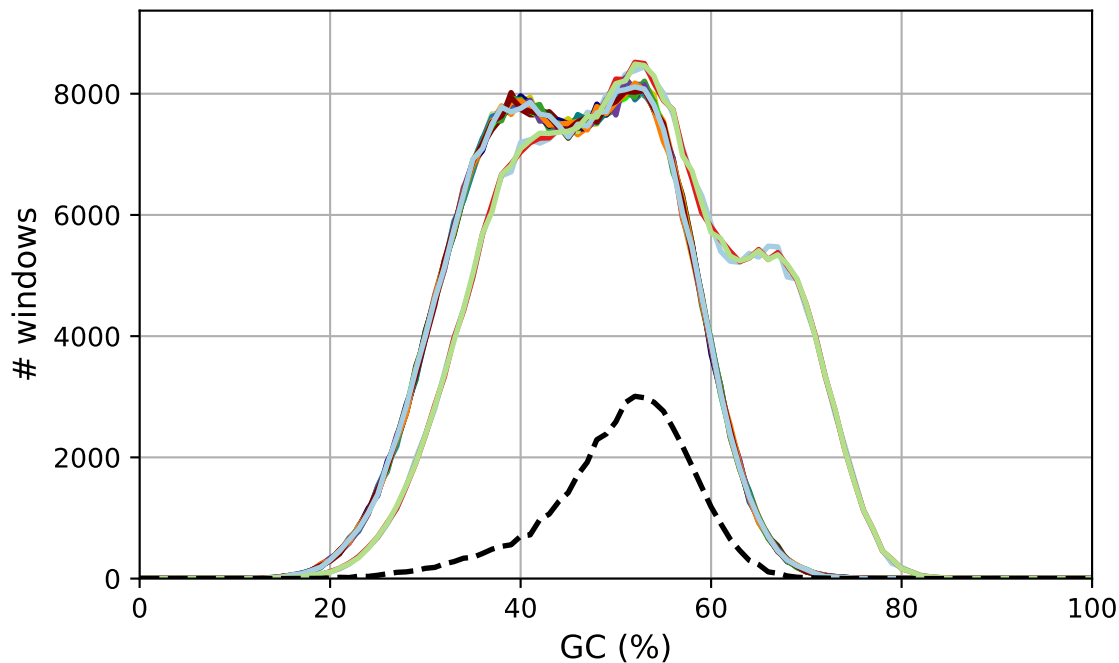
— r10\_2bins\_1\_MP      — r10\_2bins\_2\_MP      — r10\_2bins\_3\_MP  
— r10\_2bins\_1\_MP\_helen      — r10\_2bins\_2\_MP\_helen      — r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_1\_r1\_medaka      — r10\_2bins\_2\_r1\_medaka      — r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_1\_r2\_medaka      — r10\_2bins\_2\_r2\_medaka      — r10\_2bins\_3\_r2\_medaka

# Cumulative length



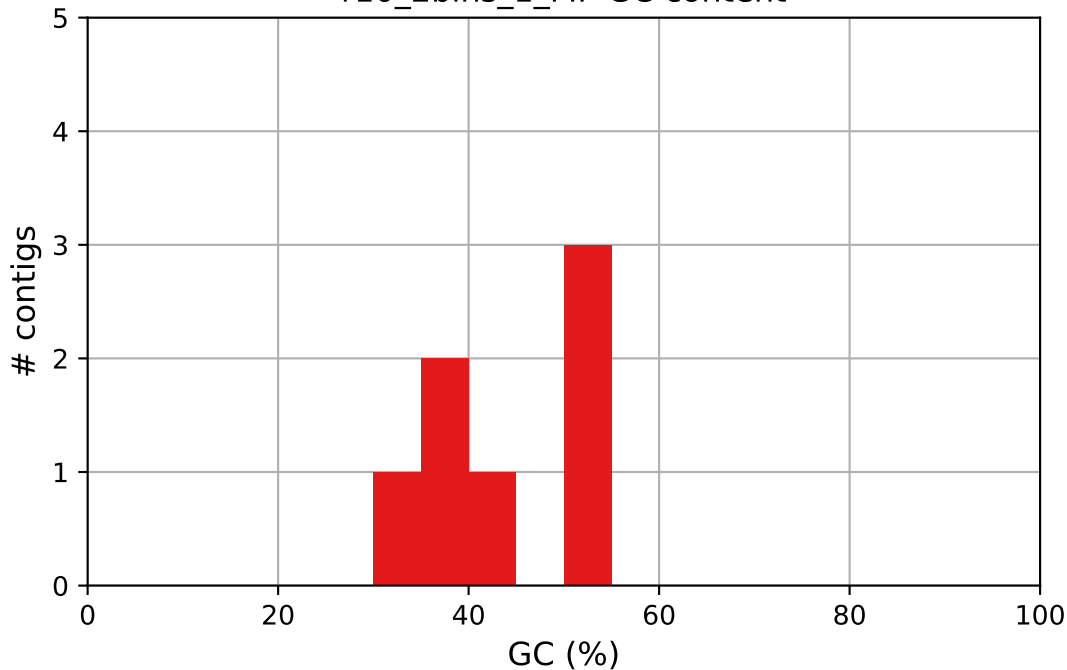
— r10\_2bins\_1\_MP  
— r10\_2bins\_1\_MP\_helen  
— r10\_2bins\_1\_r1\_medaka  
— r10\_2bins\_1\_r2\_medaka  
— r10\_2bins\_2\_MP\_helen  
— r10\_2bins\_2\_r1\_medaka  
— r10\_2bins\_2\_r2\_medaka  
— r10\_2bins\_2\_racon\_r1  
— r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_3\_r2\_medaka  
— r10\_2bins\_3\_racon\_r1

GC content



r10_2bins_1_MP	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_MP_helen	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r1_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_racon_r1	r10_2bins_3_racon_r1

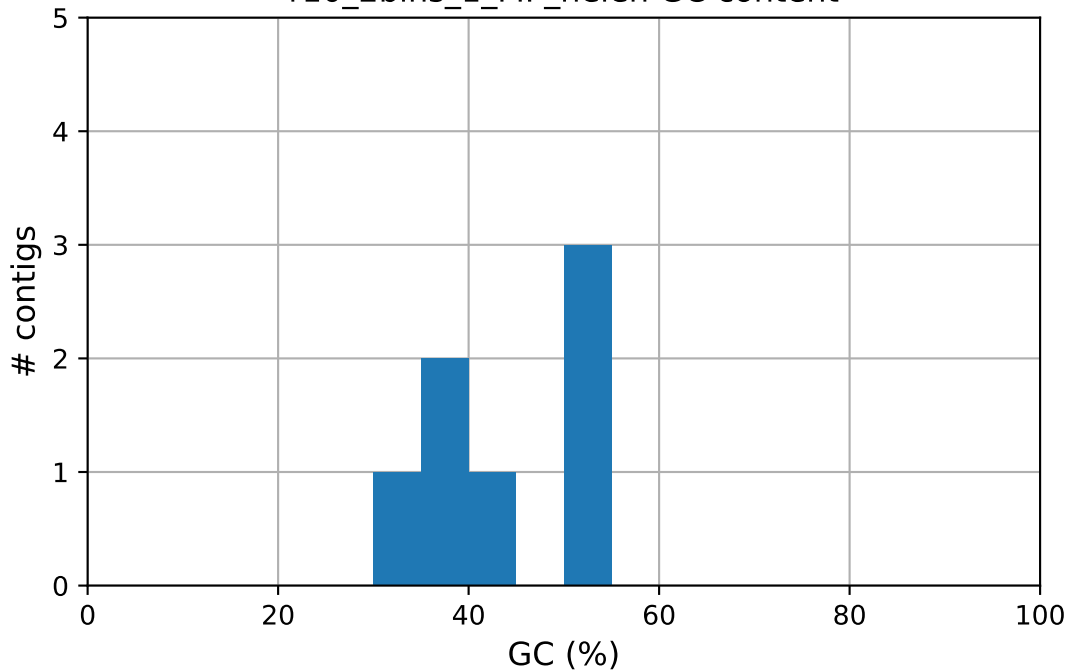
r10\_2bins\_1\_MP GC content



r10\_2bins\_1\_MP

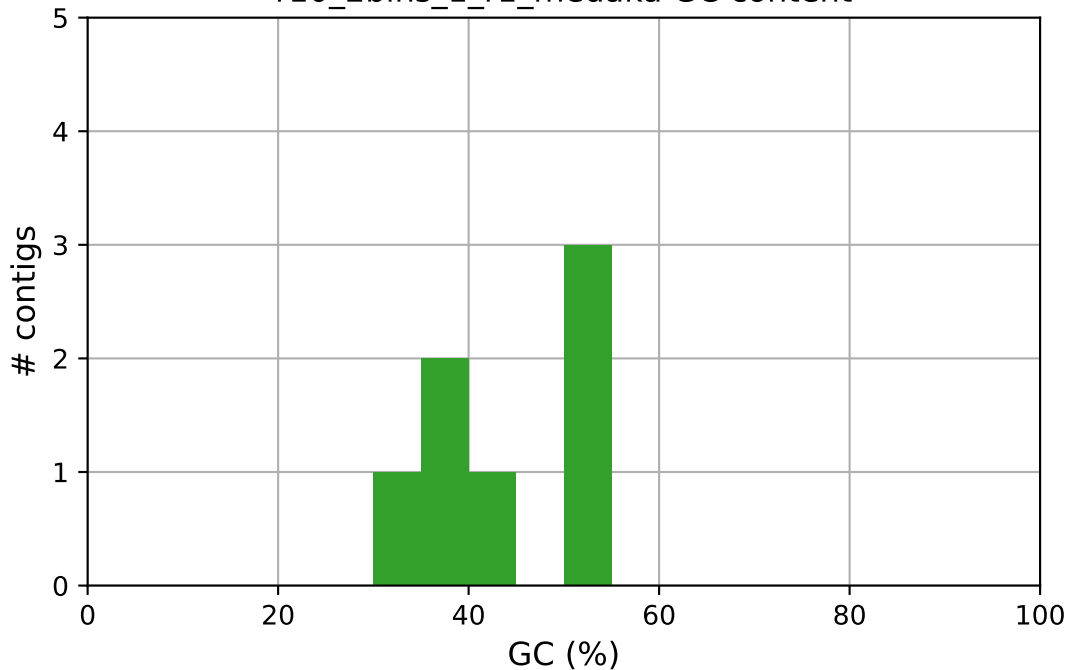


r10\_2bins\_1\_MP\_helen GC content



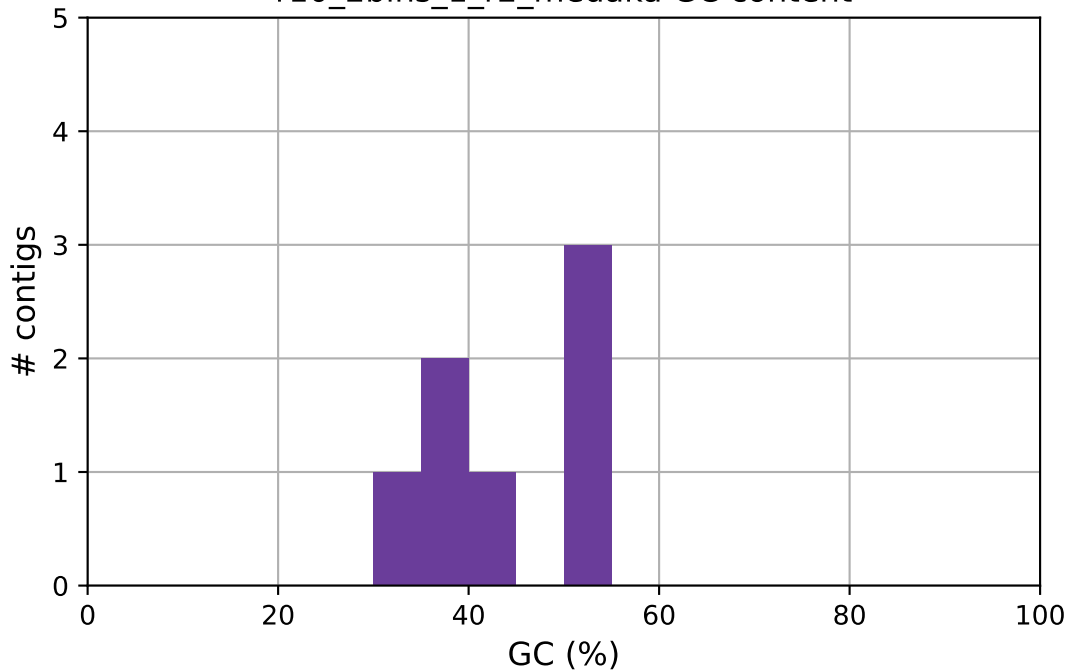
r10\_2bins\_1\_MP\_helen

r10\_2bins\_1\_r1\_medaka GC content



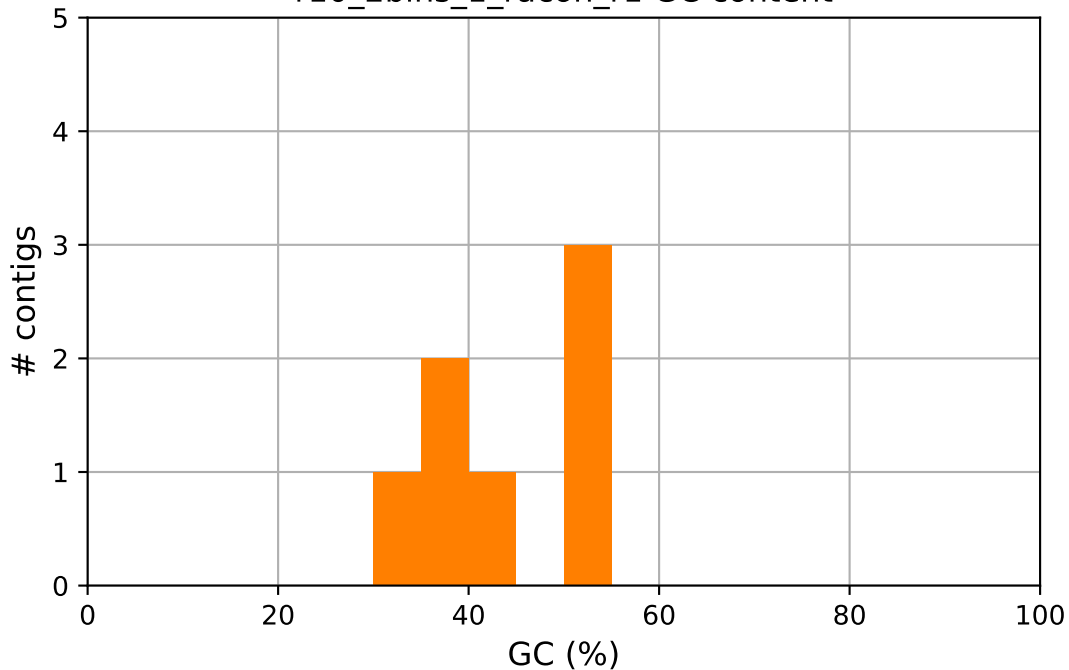
r10\_2bins\_1\_r1\_medaka

r10\_2bins\_1\_r2\_medaka GC content



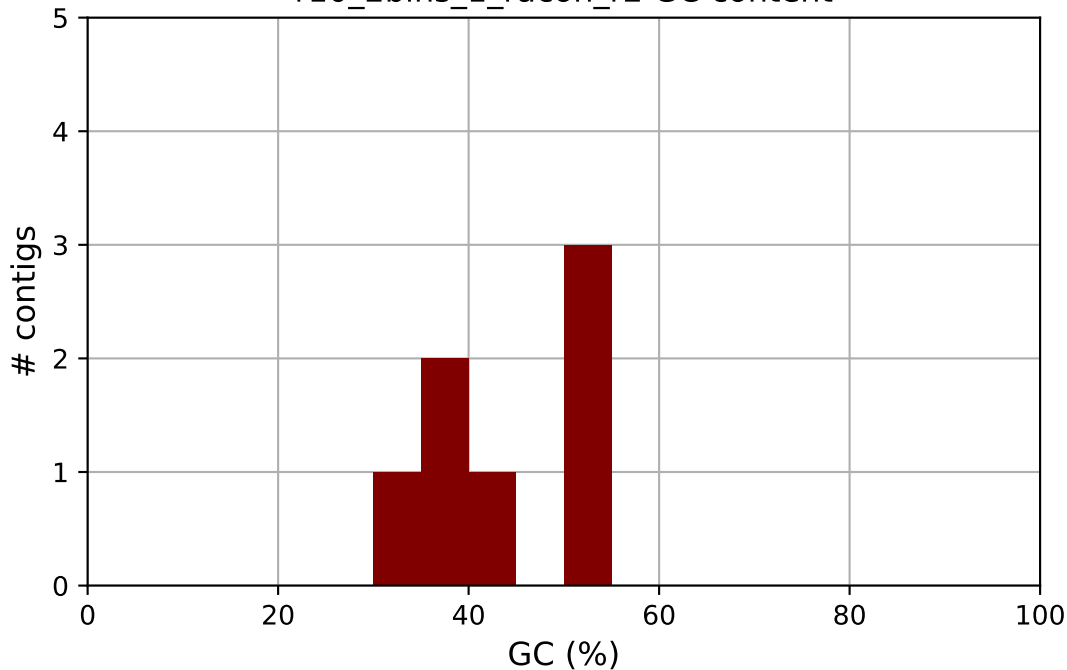
r10\_2bins\_1\_r2\_medaka

r10\_2bins\_1\_racon\_r1 GC content



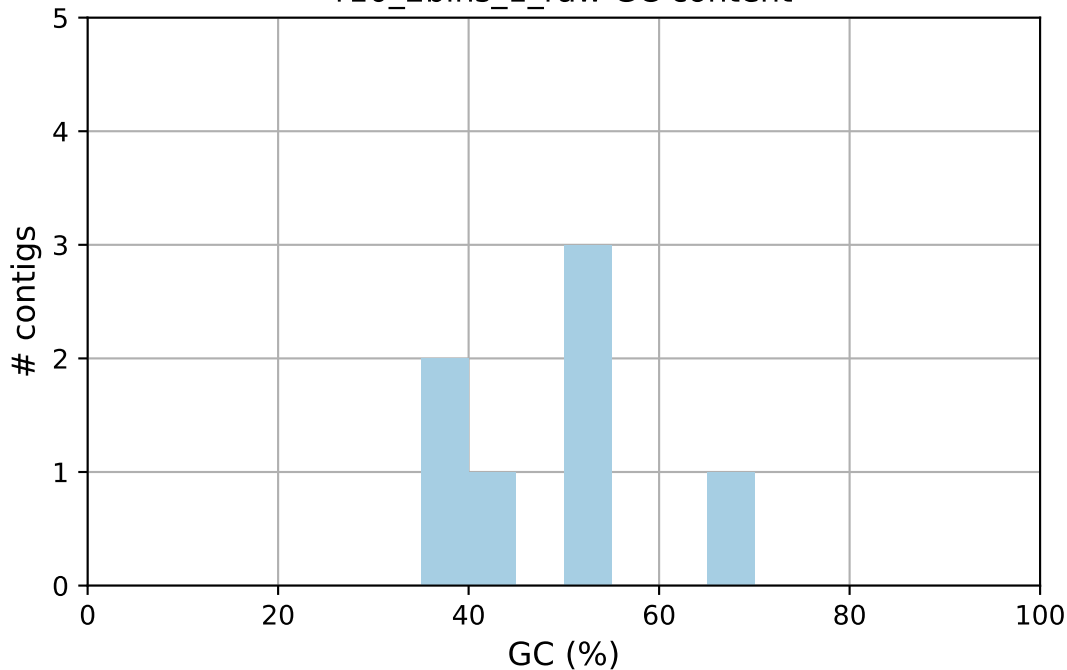
r10\_2bins\_1\_racon\_r1

r10\_2bins\_1\_racon\_r2 GC content



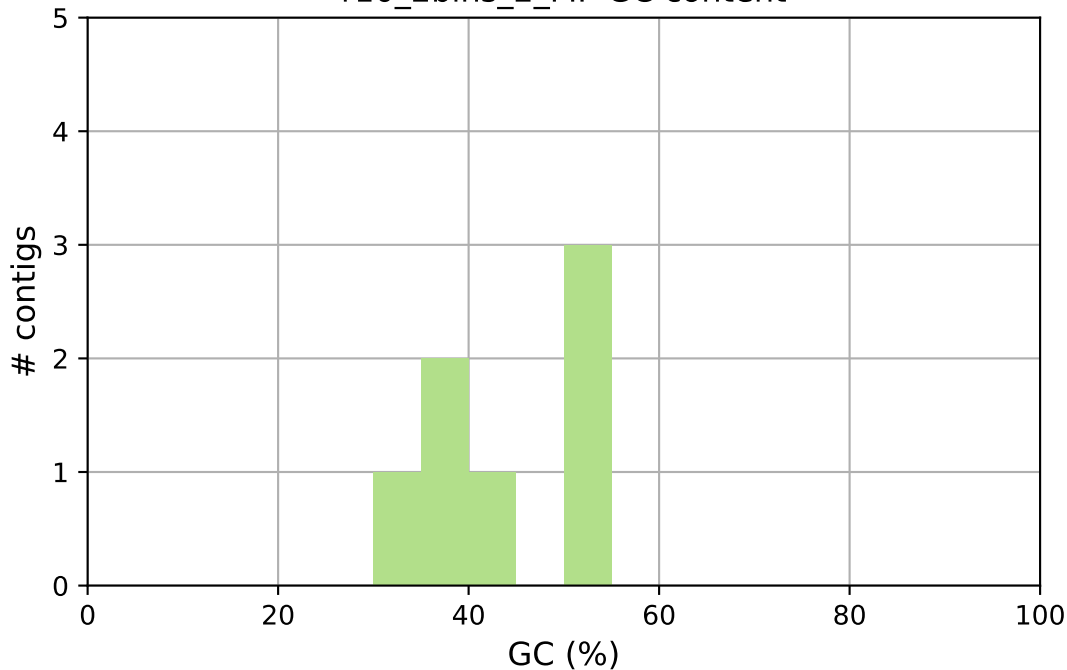
r10\_2bins\_1\_racon\_r2

r10\_2bins\_1\_raw GC content



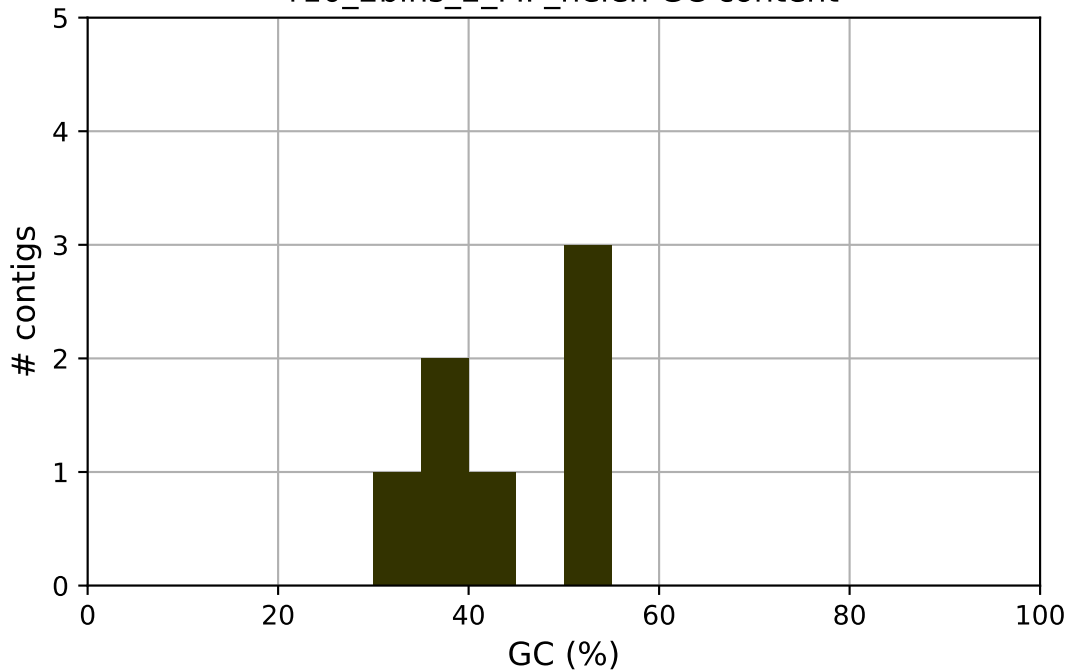
r10\_2bins\_1\_raw

r10\_2bins\_2\_MP GC content



r10\_2bins\_2\_MP

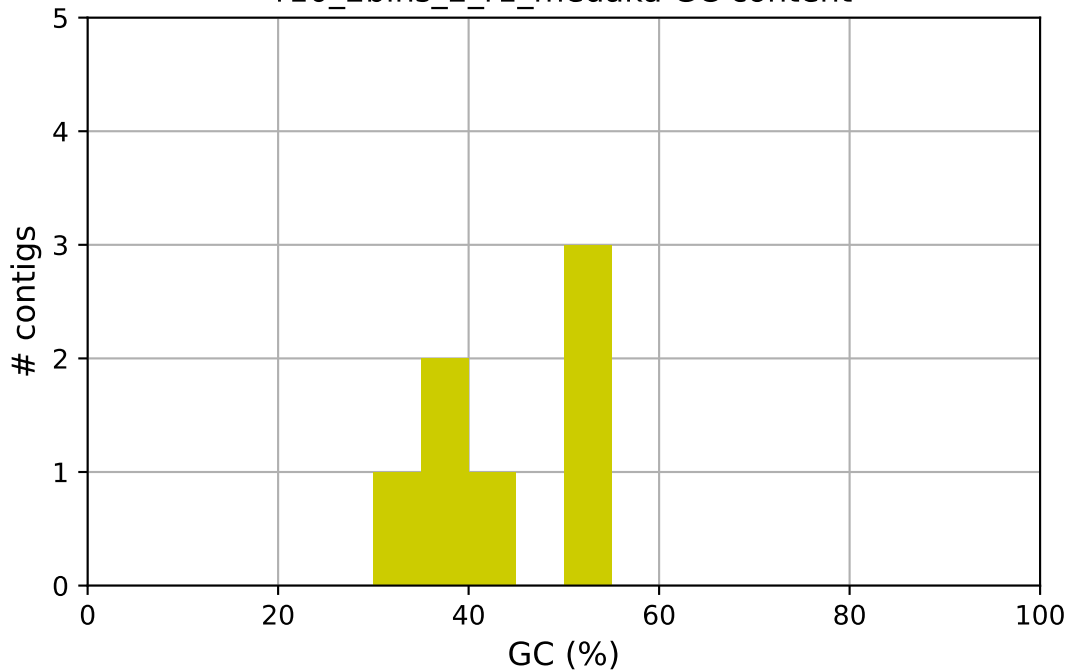
r10\_2bins\_2\_MP\_helen GC content



r10\_2bins\_2\_MP\_helen

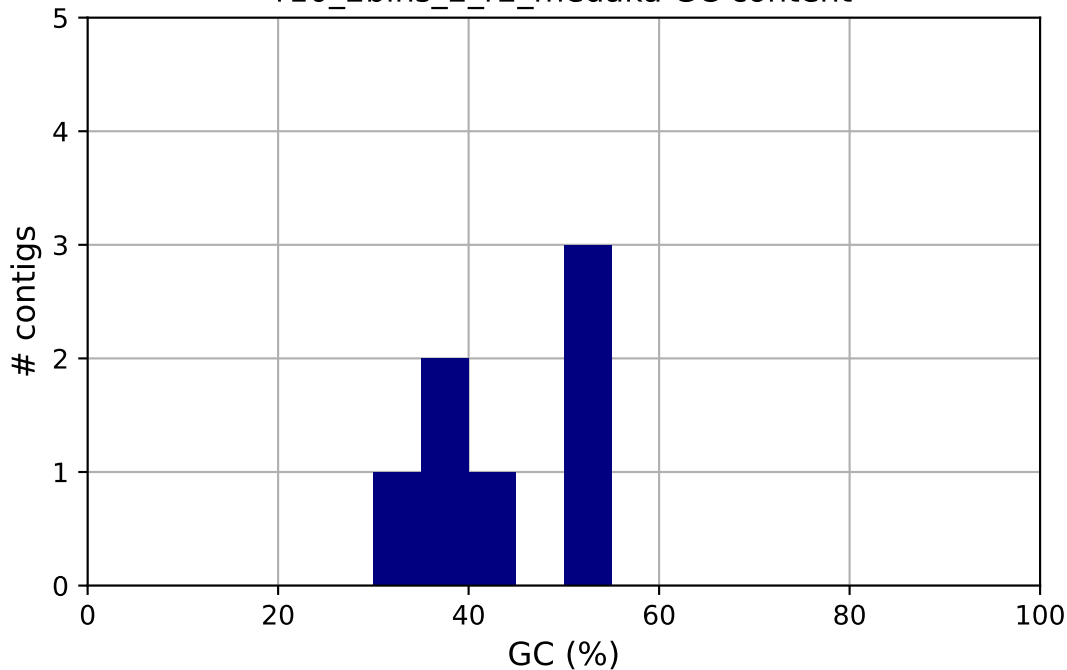


r10\_2bins\_2\_r1\_medaka GC content



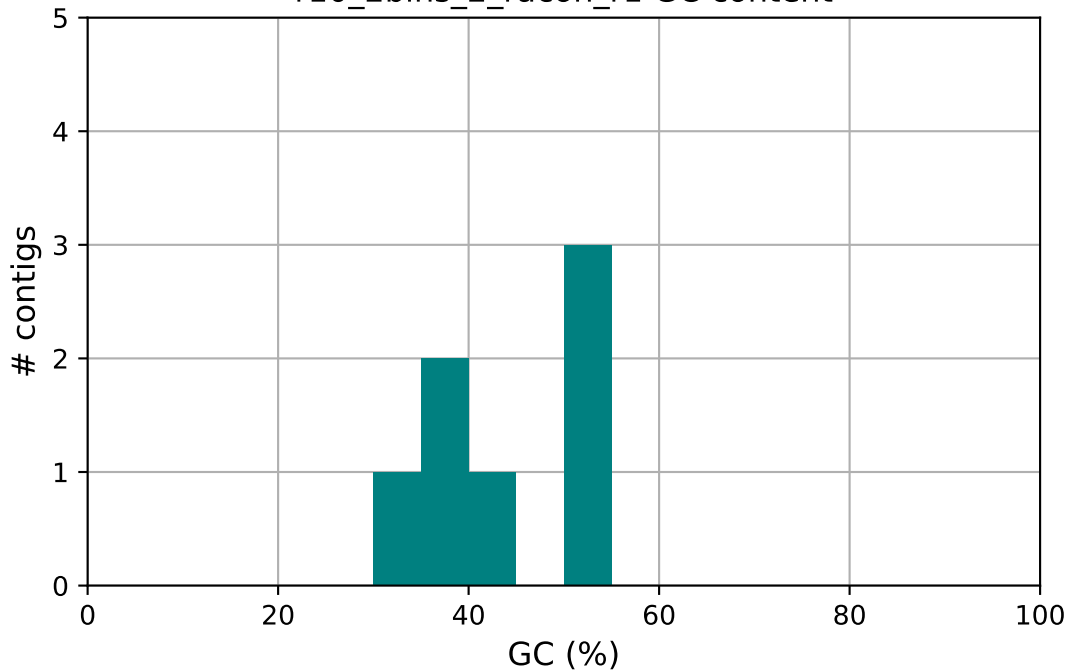
r10\_2bins\_2\_r1\_medaka

r10\_2bins\_2\_r2\_medaka GC content



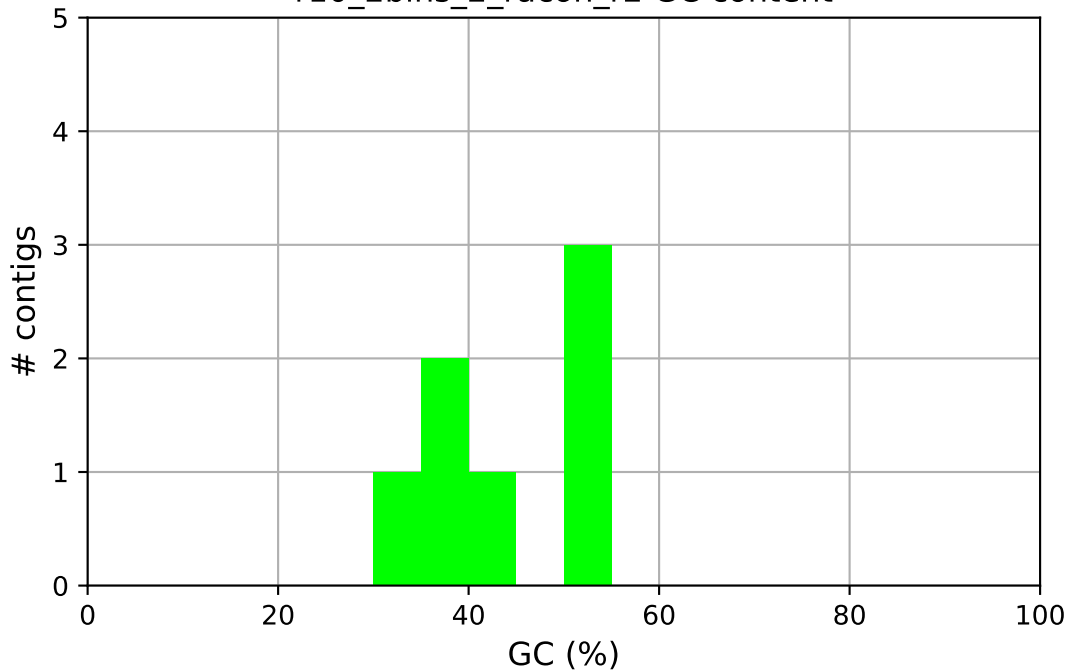
r10\_2bins\_2\_r2\_medaka

r10\_2bins\_2\_racon\_r1 GC content



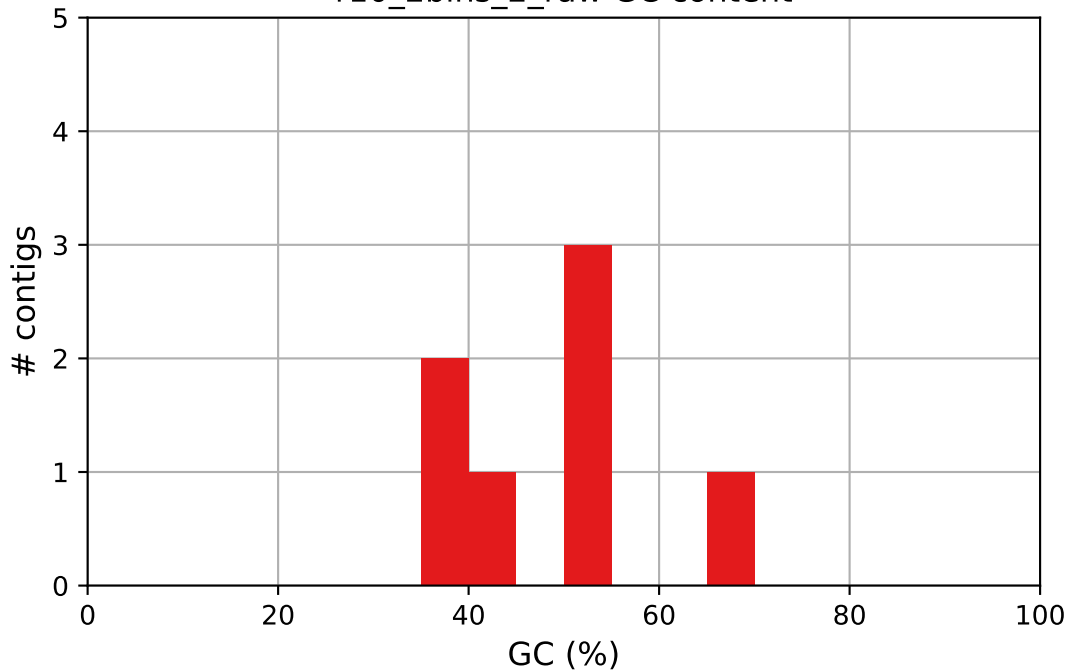
r10\_2bins\_2\_racon\_r1

r10\_2bins\_2\_racon\_r2 GC content



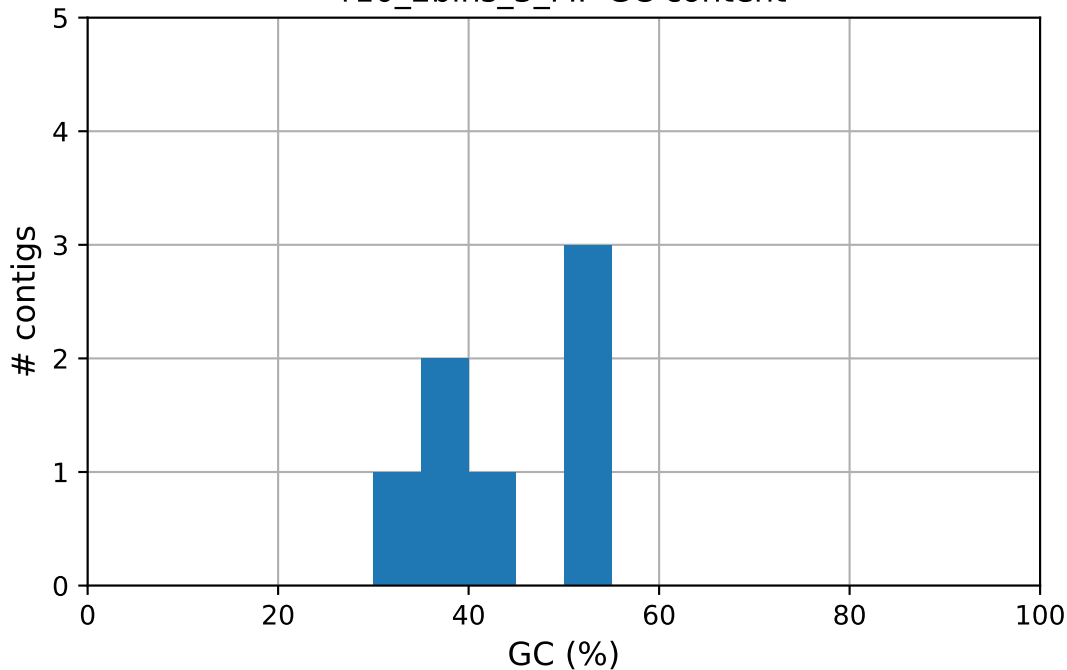
■ r10\_2bins\_2\_racon\_r2

r10\_2bins\_2\_raw GC content



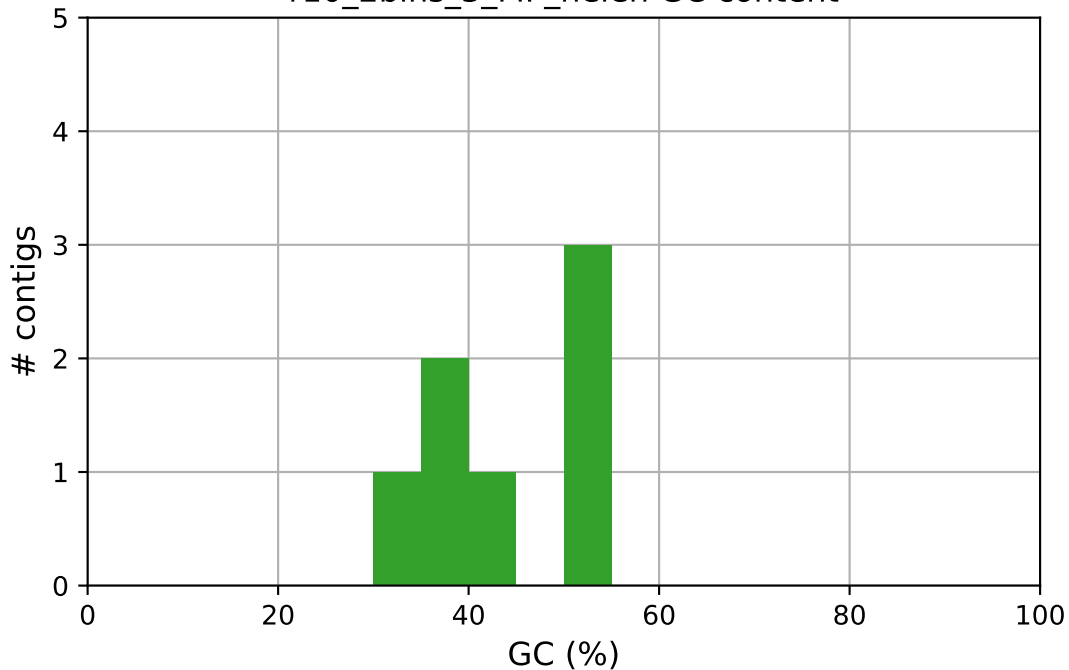
r10\_2bins\_2\_raw

r10\_2bins\_3\_MP GC content



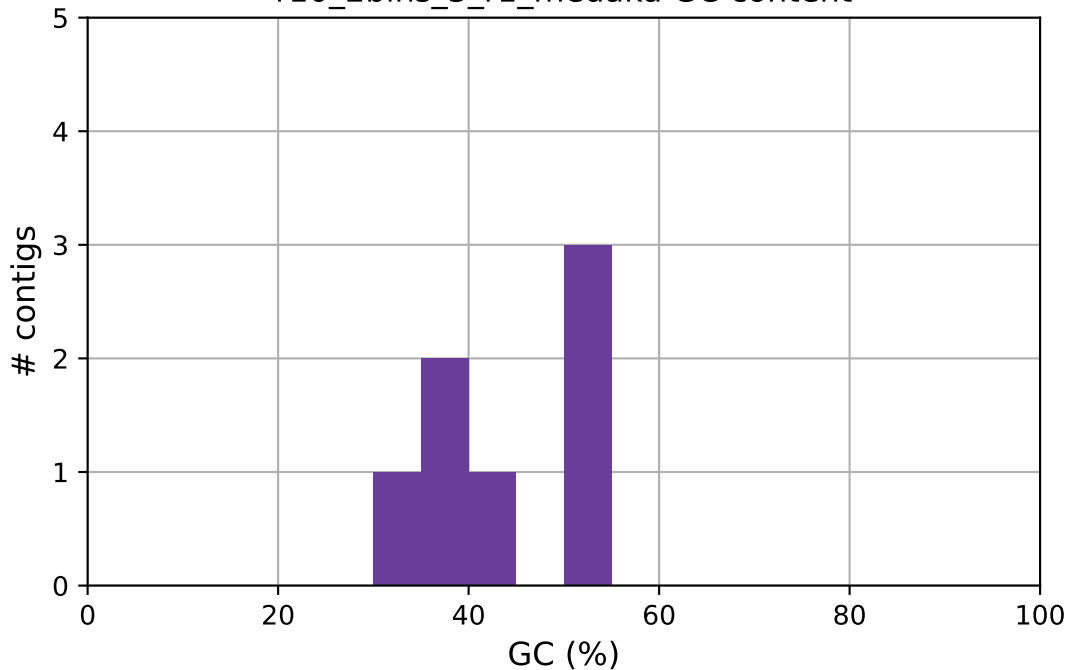
r10\_2bins\_3\_MP

r10\_2bins\_3\_MP\_helen GC content



r10\_2bins\_3\_MP\_helen

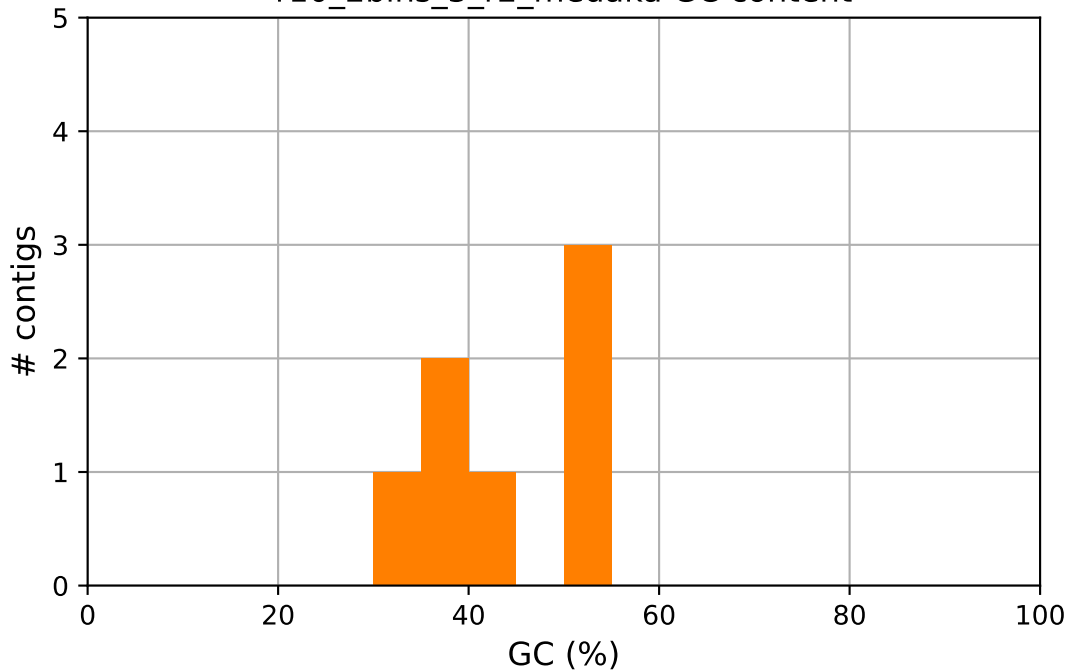
r10\_2bins\_3\_r1\_medaka GC content



r10\_2bins\_3\_r1\_medaka

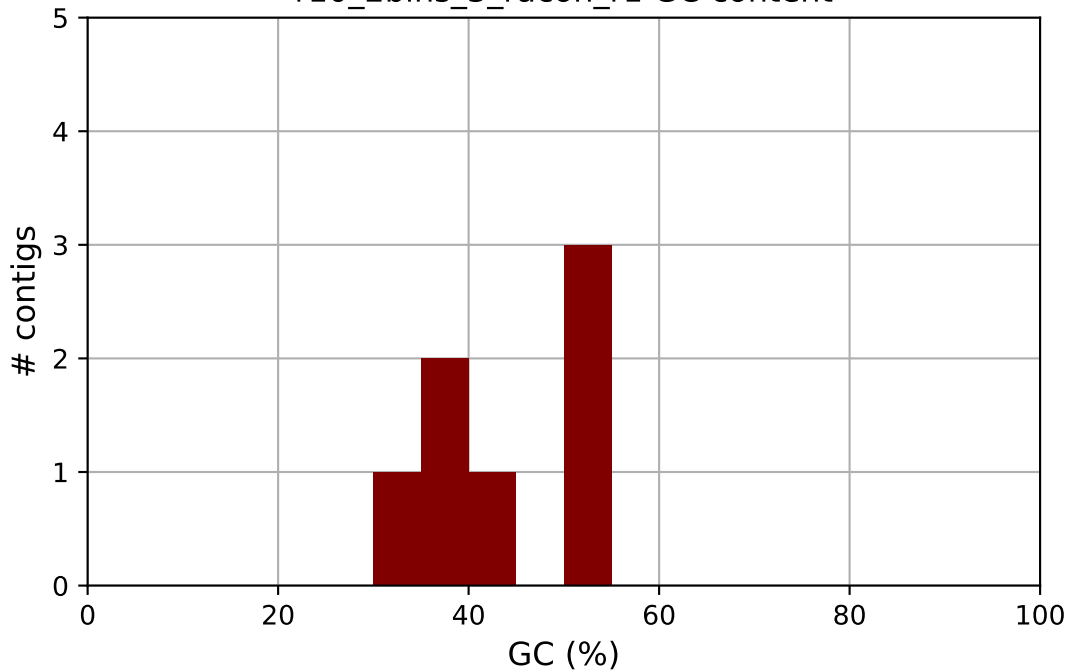


r10\_2bins\_3\_r2\_medaka GC content



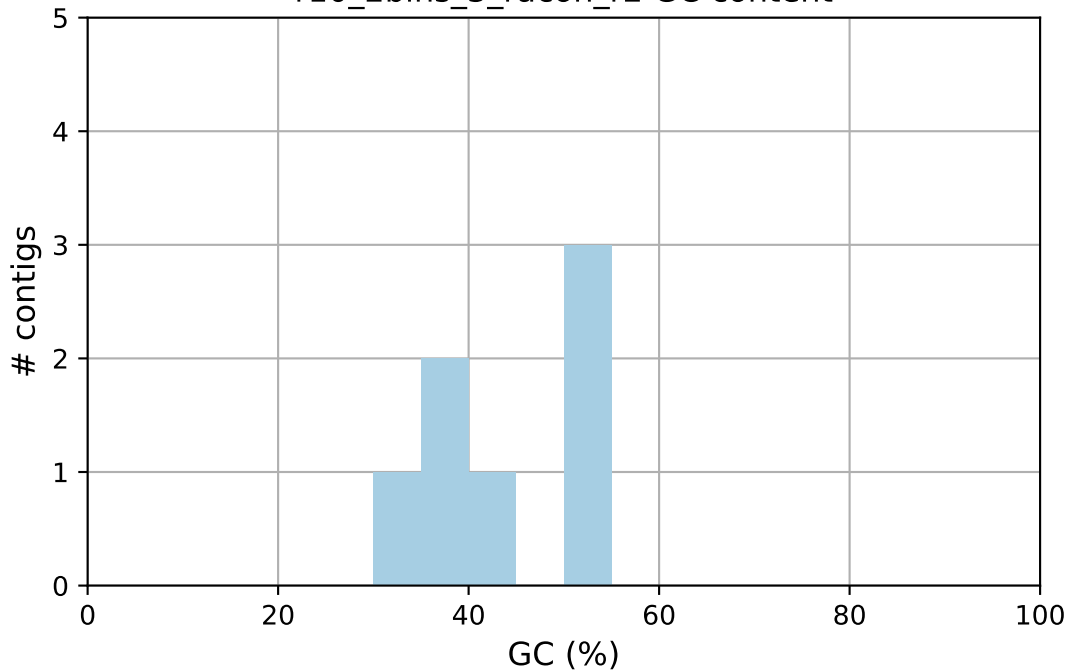
r10\_2bins\_3\_r2\_medaka

r10\_2bins\_3\_racon\_r1 GC content



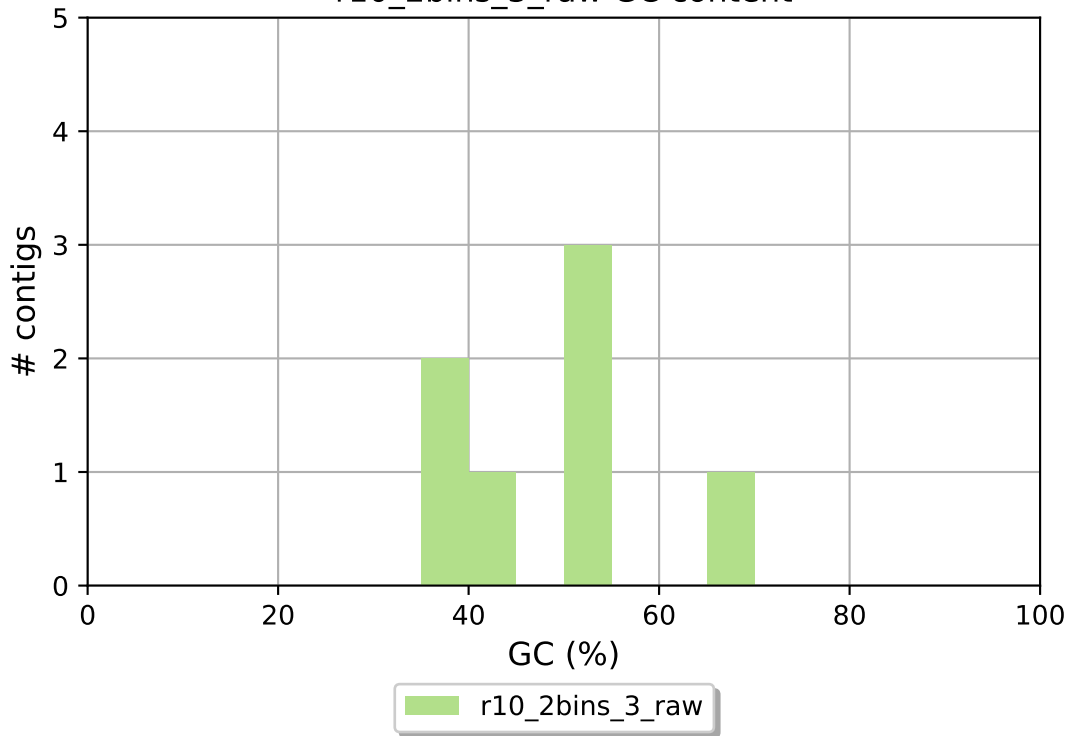
r10\_2bins\_3\_racon\_r1

r10\_2bins\_3\_racon\_r2 GC content

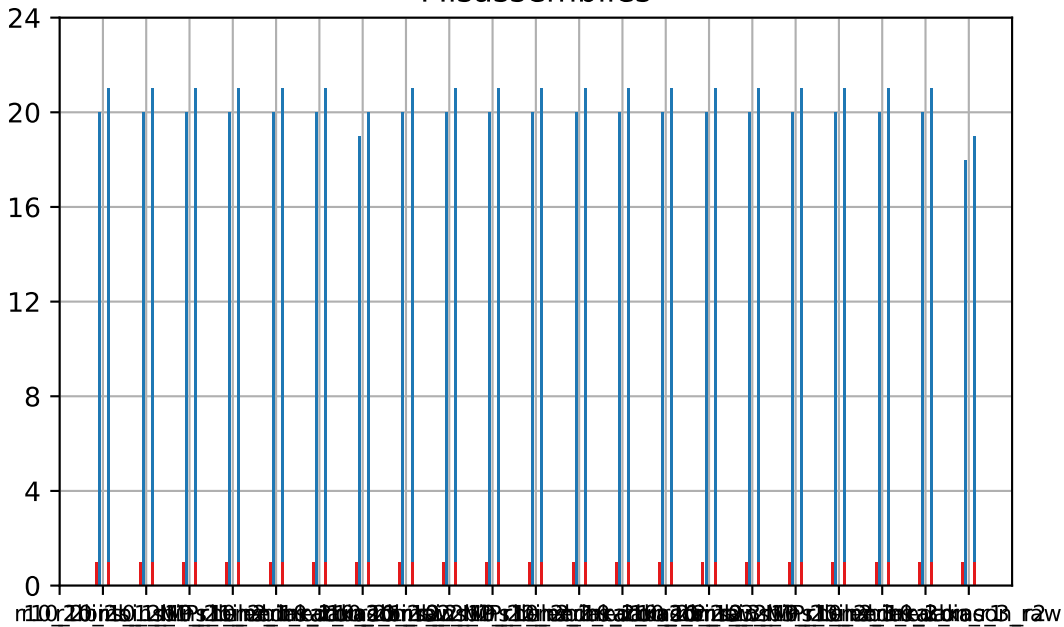


r10\_2bins\_3\_racon\_r2

r10\_2bins\_3\_raw GC content



# Misassemblies



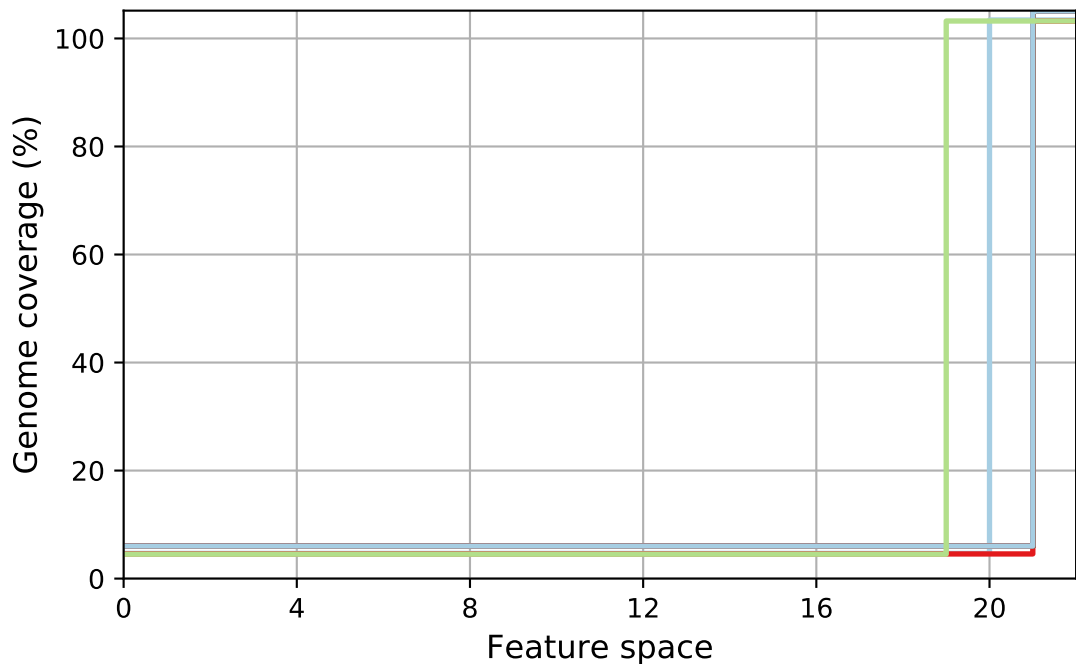
114

```
# relocations
```

11

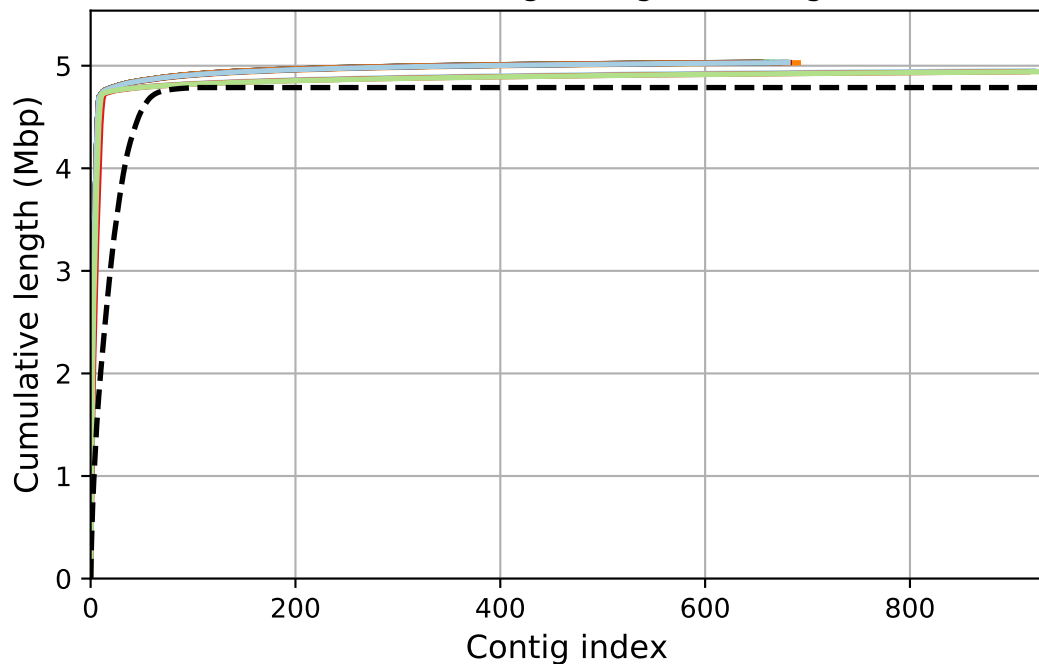
## # translocations

# FRCurve (misassemblies)



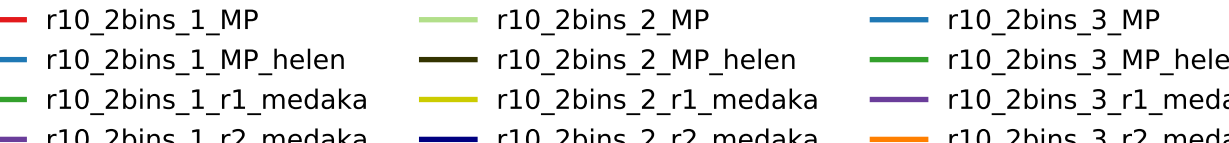
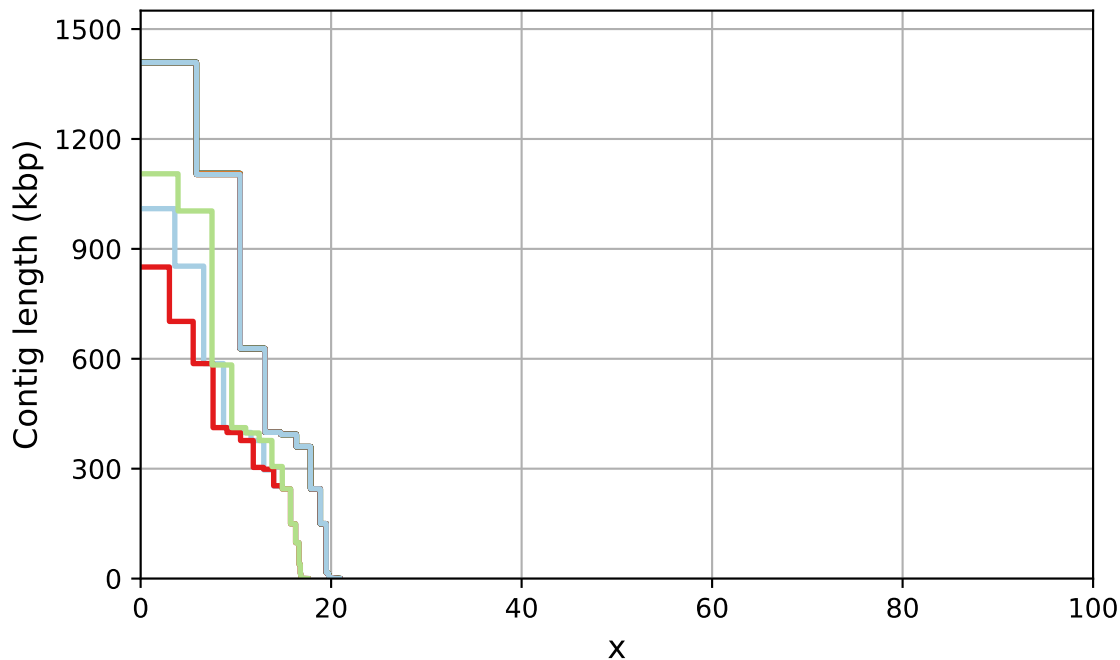
r10_2bins_1_MP	r10_2bins_2_MP	r10_2bins_3_MP
r10_2bins_1_MP_helen	r10_2bins_2_MP_helen	r10_2bins_3_MP_helen
r10_2bins_1_r1_medaka	r10_2bins_2_r1_medaka	r10_2bins_3_r1_medaka
r10_2bins_1_r2_medaka	r10_2bins_2_r2_medaka	r10_2bins_3_r2_medaka

Cumulative length (aligned contigs)



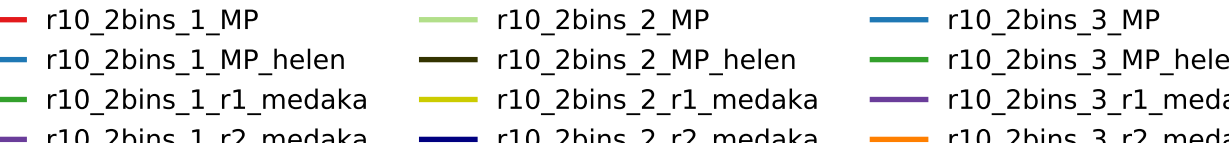
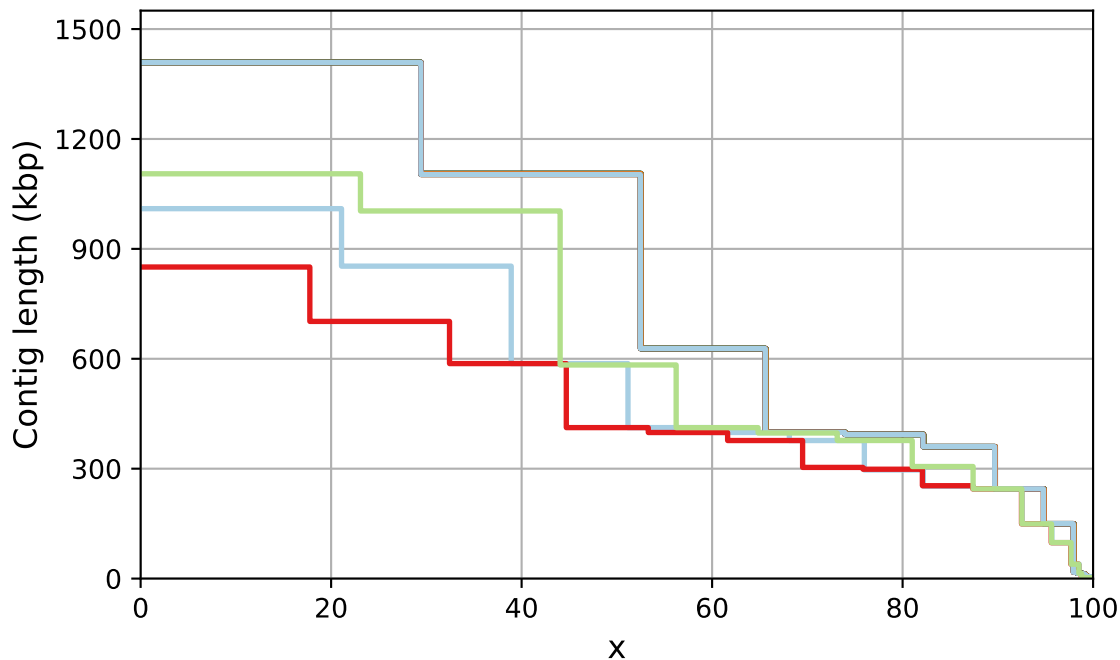
— r10\_2bins\_1\_MP      — r10\_2bins\_2\_MP\_helen      — r10\_2bins\_3\_MP\_helen  
— r10\_2bins\_1\_MP\_helen      — r10\_2bins\_2\_r1\_medaka      — r10\_2bins\_3\_r1\_medaka  
— r10\_2bins\_1\_r1\_medaka      — r10\_2bins\_2\_r2\_medaka      — r10\_2bins\_3\_r2\_medaka  
— r10\_2bins\_1\_r2\_medaka      — r10\_2bins\_2\_racon\_r1      — r10\_2bins\_3\_racon\_r1

# NAx





# NGAx



Genome fraction, %

100

99

98

