

Report

	C-51k-ha	C-61k-ha	C-71k-ha	C-81k-ha	C-91k-ha	C-101k-ha	C-111k-ha	C-121k-ha	C-131k-ha	C-def-ha	canu	F-51k-ha	F-61k-ha	F-71k-ha	F-81k-ha	F-91k-ha	F-101k-ha	F-111k-ha	F-121k-ha	F-131k-ha	F-def-ha	R-51k-ha	R-61k-ha	R-71k-ha	R-81k-ha	R-91k-ha	R-101k-ha	R-111k-ha	R-121k-ha	R-131k-ha	R-def-ha	
# contigs (>= 0 bp)	22	28	23	20	17	21	15	16	17	24	3	11	12	9	11	11	9	9	9	9	11	13	12	13	14	7	11	8	10	6	15	
# contigs (>= 1000 bp)	11	20	16	14	16	18	14	16	15	13	3	8	10	6	11	11	9	9	9	8	9	8	7	9	13	7	11	8	10	6	9	
# contigs (>= 5000 bp)	8	11	10	9	8	8	8	10	10	10	2	4	5	5	5	5	4	5	4	4	6	5	5	7	7	4	7	4	6	3	6	
# contigs (>= 10000 bp)	3	5	5	5	5	4	4	6	8	4	1	3	3	4	3	3	3	3	3	3	3	3	3	4	5	2	4	3	4	2	3	
# contigs (>= 25000 bp)	3	4	4	3	3	3	3	4	2	2	1	2	2	2	2	2	2	2	2	2	2	2	3	3	3	2	2	3	3	1	2	
# contigs (>= 50000 bp)	1	2	2	1	1	0	1	2	1	1	1	0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	
Total length (>= 0 bp)	185646	286068	266628	212872	208978	205931	230839	267657	221066	192185	108981	118157	126962	128713	124375	125573	139068	123043	119998	118015	142606	137681	171639	196674	192538	171216	196503	188440	222421	133455	144605	
Total length (>= 1000 bp)	178955	280656	261958	209414	208384	204193	230115	267657	219615	186034	108981	116073	125103	125921	124375	125573	139068	123043	119998	117058	141400	134682	168189	193770	192027	171216	196503	188440	222421	133455	141338	
Total length (>= 5000 bp)	168831	255653	242774	197309	180973	177320	209920	247701	203512	175658	104381	101378	109258	121104	108746	109042	123751	109986	104619	104093	131056	124355	160344	187280	177120	162003	185303	176283	211160	124017	131074	
Total length (>= 10000 bp)	128809	208379	206332	162940	159119	149284	179112	213884	190460	129983	97559	93776	96511	113662	96183	96198	116083	97132	97186	96351	111882	110622	146189	166251	163180	147156	164214	168565	197484	116262	111681	
Total length (>= 25000 bp)	128809	190118	188052	124283	130588	138972	168569	186052	97426	87238	97559	69892	72621	70849	72263	72277	97137	73201	73210	72365	87928	93859	146189	149542	129589	147156	130590	168565	180653	97287	87723	
Total length (>= 50000 bp)	58166	113588	111490	58305	59332	0	97237	108337	58350	51558	97559	0	0	0	0	0	62886	0	0	0	52248	58159	58209	61552	58254	97191	97233	97233	97275	97287	52043	
# contigs	22	28	23	20	17	21	45	16	17	24	3	11	12	9	11	11	9	9	9	9	11	13	12	13	14	7	11	8	10	6	15	
Largest contig	58166	57154	59457	58305	59332	49982	97237	58298	58350	51558	97559	35742	38005	37541	38012	38026	62886	38954	38962	38117	52248	58159	58209	61552	58254	97191	97233	97233	97275	97287	52043	
Total length	185646	286068	266628	212872	208978	205931	692517	267657	221066	192185	108981	118157	126962	128713	124375	125573	139068	123043	119998	118015	142606	137681	171639	196674	192538	171216	196503	188440	222421	133455	144605	
Reference length	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	134226	
GC (%)	53.46	53.80	54.05	53.63	53.64	53.37	53.90	53.31	53.21	53.07	56.07	56.28	56.20	55.95	56.13	56.33	56.04	56.21	56.41	56.30	55.63	55.56	55.65	55.59	55.60	56.03	55.68	56.23	55.65	55.85	55.30	
Reference GC (%)	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23	
N50	35742	38524	38546	27994	33272	39060	38060	39103	20075	33272	23961	97559	34150	34616	33308	34251	34251	34251	34247	34248	34248	35680	35700	49974	49974	38026	97191	33357	97233	49984	97287	35680
NG50	35742	56434	52033	37984	37984	49930	97237	50039	39076	35680	97559	34150	34616	33308	34251	34251	34251	34247	34248	34248	35680	35700	49974	49974	38026	97191	97233	97233	97275	97287	35680	
N75	9093	9679	18280	16791	10430	9278	10543	16833	13759	9140	97559	23884	23890	18871	23920	23921	18946	23931	23976	23986	23954	16763	38006	38016	16800	49965	16813	33272	33394	18975	23958	
NG75	34901	56434	52033	27994	33272	39060	97237	50039	20075	23961	6822	7602	7600	18871	7386	7666	18946	7666	7433	7742	23954	16763	49974	49974	33309	49965	33357	38060	49984	18975	23958	
L50	2	3	3	3	3	3	5	3	3	3	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2	1	2	1	2
LG50	2	2	2	2	2	2	1	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	1	1	1	2
L75	5	6	5	5	5	5	11	5	6	6	1	3	3	4	3	3	3	3	3	3	3	3	3	3	4	2	3	3	3	2	3	
LG75	3	2	2	3	3	3	2	2	3	3	2	4	4	4	4	4	3	4	4	4	3	3	2	2	3	2	2	2	2	2	3	
# misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# local misassemblies	5	6	6	4	1	1	6	4	3	3	7	4	4	7	3	4	3	3	2	5	2	4	4	4	4	4	2	2	3	2	3	2
# 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	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	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# unaligned contigs	10 + 0 part	13 + 0 part	9 + 0 part	10 + 0 part	8 + 0 part	11 + 0 part	18 + 0 part	6 + 0 part	6 + 0 part	12 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	1 + 0 part	3 + 0 part	3 + 0 part	2 + 0 part	1 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	5 + 0 part	
Unaligned length	31045	40577	30275	31981	37035	39323	111123	47002	43744	31436	0	0	0	0	0	0	0	0	0	0	663	1586	1586	1017	511	0	0	0	0	0	2647	
Genome fraction (%)	88.448	88.262	84.846	84.575	86.445	82.906	92.195	85.527	88.984	83.844	80.228	84.550	86.943	55.995	84.510	87.478	86.751	84.939	84.770	87.488	83.638	88.560	89.384	84.622	89.460	84.961	89.565	85.159	89.587	85.091	83.767	
Duplication ratio	1.302	2.072	2.075	1.593	1.482	1.497	4.698	1.922	1.485	1.428	1.012	1.041	1.088	1.713	1.096	1.069	1.194	1.079	1.055	1.005	1.264	1.145	1.417	1.723	1.599	1.501	1.635	1.649	1.850	1.168	1.263	
# 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	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
# mismatches per 100 kbp	1304.75	2144.83	2277.72	1759.15	1534.93	1574.39	4964.89	2186.43	1497.84	1361.29	1123.63	1062.67	1182.52	2280.47	1230.66	1182.95	1255.55	1183.23	1154.83	1146.20	1244.39	1224.02	1471.95	1930.71	1723.88	1581.90	1735.15	1698.07	2021.64	1197.75	1260.26	
# indels per 100 kbp	103.61	168.82	157.17	126.85	131.00	159.06	433.94	163.76	126.42	111.07	348.23	95.16	95.12	162.32	91.68	101.35	113.36	97.36	102.83	91.97	107.78	94.22	129.19	147.91	145.74	149.95	153.88	154.85	167.15	105.94	112.06	
Largest alignment	57969	57002	58837	58041	59068	49912	96972	58039	58076	51551	95825	35742	38000	36941	38008	38018	62881	38913	38924	38112	51945	58007	57979	60945	57999	96930	96972	96972	97014	97129	51855	
Total aligned length	154144	244577	235210	179764	171525	166148	579042	219475	176676	160385	107210	117862	126160	127632	123722	124936	138592	122536	119553	117409	141345	135616	169452	194664	191199	170755	195667	187900				

Misassemblies report

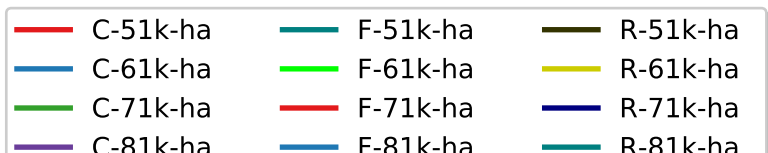
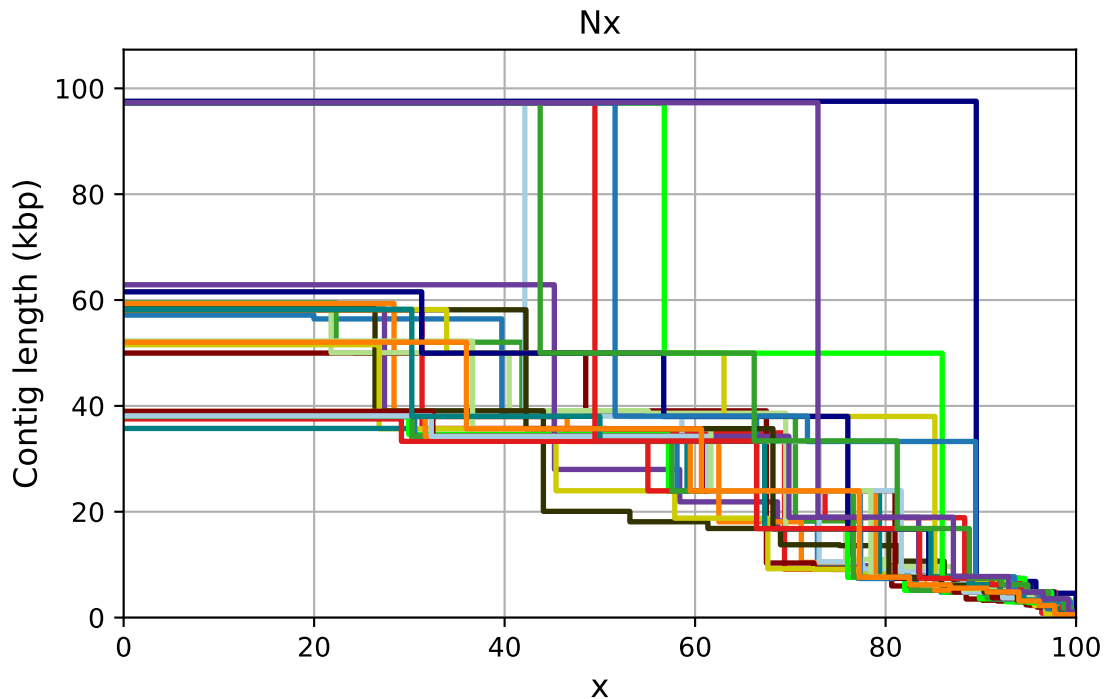
	C-51k-ha	C-61k-ha	C-71k-ha	C-81k-ha	C-91k-ha	C-101k-ha	C-111k-ha	C-121k-ha	C-131k-ha	C-def-ha	canu	F-51k-ha	F-61k-ha	F-71k-ha	F-81k-ha	F-91k-ha	F-101k-ha	F-111k-ha	F-121k-ha	F-131k-ha	F-def-ha	R-51k-ha	R-61k-ha	R-71k-ha	R-81k-ha	R-91k-ha	R-101k-ha	R-111k-ha	R-121k-ha	R-131k-ha	R-def-ha
# misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# c. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# c. inversions	0	0	0	0	0	0	0	0	0	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	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	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	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	0	0	0	0	0	0	0	0	0	
# misassembled contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Misassembled contigs length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# local misassemblies	5	6	6	4	1	1	6	4	3	3	7	4	4	7	3	4	3	3	2	5	2	4	4	4	4	2	2	3	2	3	2
# 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	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	0	0	0	0	0	0	0	0	0	
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
# mismatches	1549	2541	2594	1997	1781	1752	6144	2510	1789	1532	1210	1206	1380	1714	1396	1389	1462	1349	1314	1346	1397	1455	1766	2193	2070	1804	2086	1941	2431	1368	1417
# indels	123	200	179	144	152	177	537	188	151	125	375	108	111	122	104	119	132	111	117	108	121	112	155	168	175	171	185	177	201	121	126
# indels (<= 5 bp)	109	176	154	128	133	156	468	164	133	116	360	100	99	110	91	106	119	96	103	97	108	103	138	148	157	150	164	155	175	105	110
# indels (> 5 bp)	14	24	25	16	19	21	69	24	18	9	15	8	12	12	13	13	13	15	14	11	13	9	17	20	18	21	21	22	26	16	16
Indels length	641	870	974	658	773	1076	3411	1009	912	560	1053	499	568	580	618	640	721	780	782	532	650	408	793	916	919	1033	1023	1127	1187	732	650

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

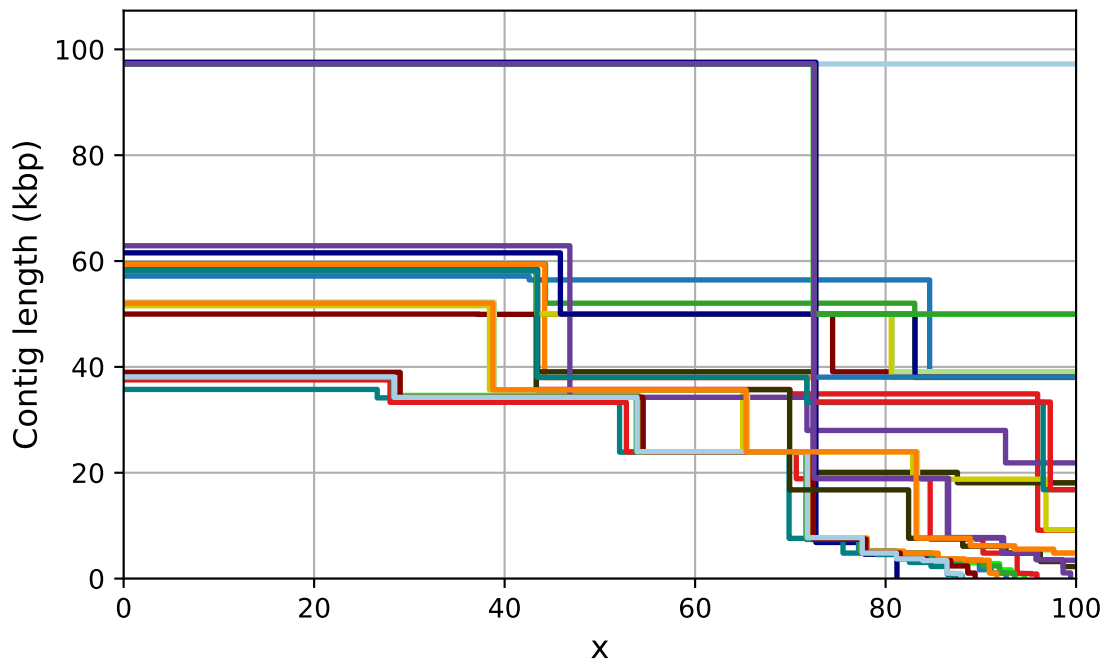
Unaligned report

	C-51k-ha	C-61k-ha	C-71k-ha	C-81k-ha	C-91k-ha	C-101k-ha	C-111k-ha	C-121k-ha	C-131k-ha	C-def-ha	canu	F-51k-ha	F-61k-ha	F-71k-ha	F-81k-ha	F-91k-ha	F-101k-ha	F-111k-ha	F-121k-ha	F-131k-ha	F-def-ha	R-51k-ha	R-61k-ha	R-71k-ha	R-81k-ha	R-91k-ha	R-101k-ha	R-111k-ha	R-121k-ha	R-131k-ha	R-def-ha
# fully unaligned contigs	10	13	9	10	8	11	18	6	6	12	0	0	0	0	0	0	0	0	0	0	1	3	3	2	1	0	0	0	0	0	5
Fully unaligned length	31045	40577	30275	31981	37035	39323	111123	47002	43744	31436	0	0	0	0	0	0	0	0	0	0	663	1586	1586	1017	511	0	0	0	0	0	2647
# partially unaligned contigs	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# N's	0	0	0	0	0	0	0	0	0	0	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 ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

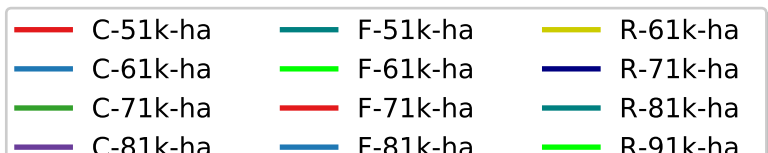
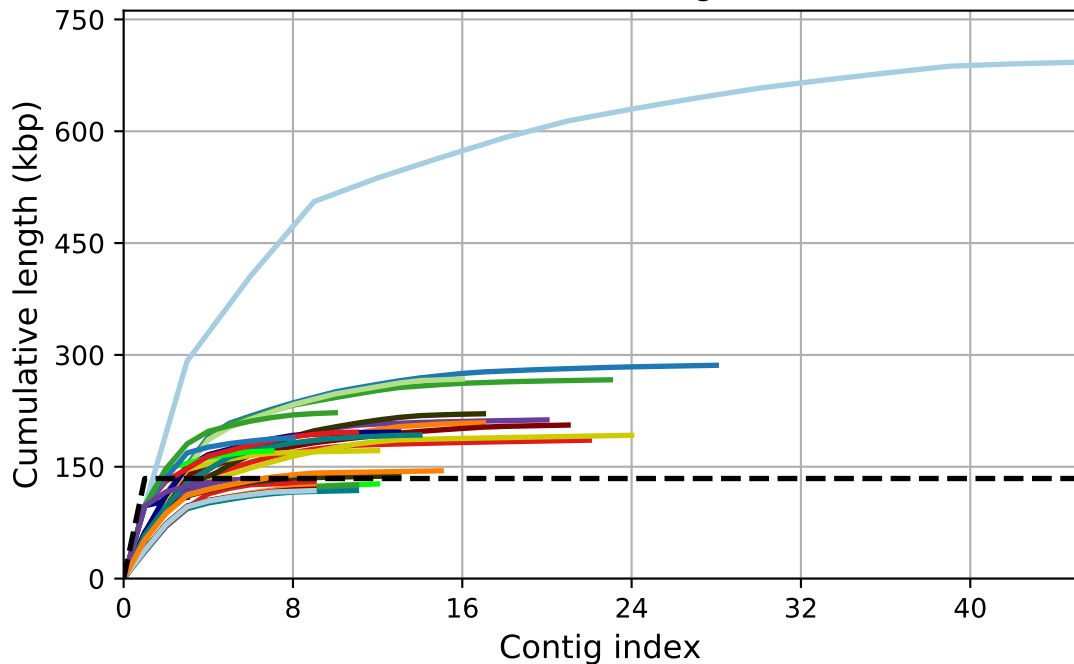


NGx

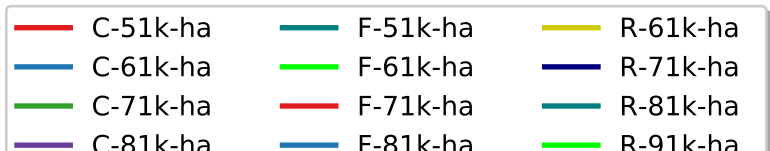
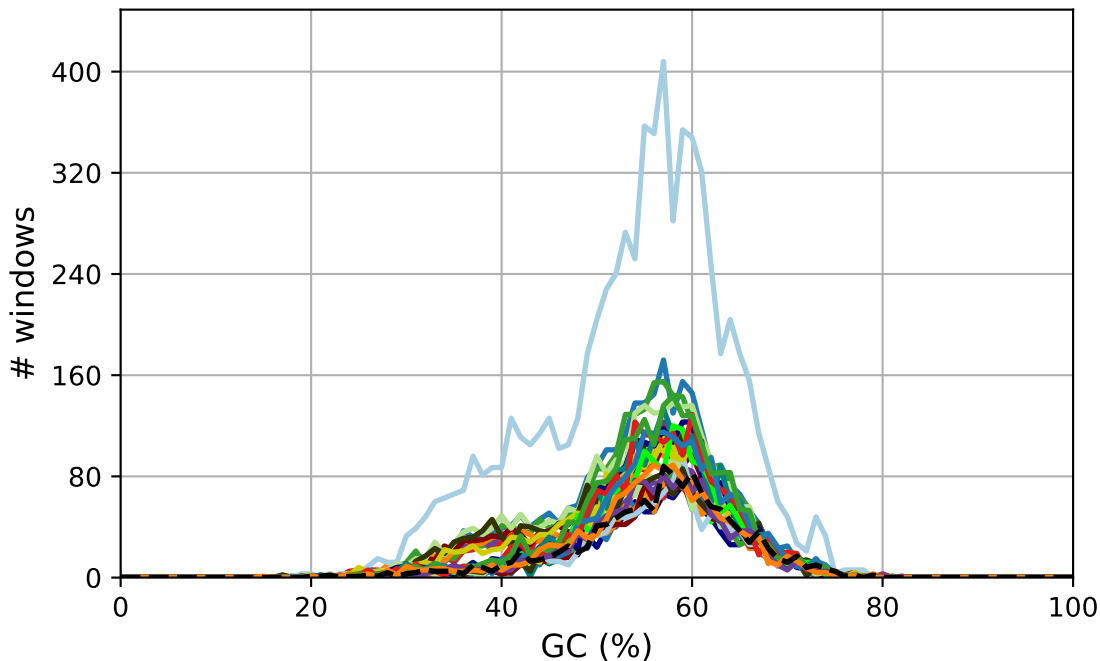


- | | | |
|--|---|---|
| — C-51k-ha | — F-51k-ha | — R-51k-ha |
| — C-61k-ha | — F-61k-ha | — R-61k-ha |
| — C-71k-ha | — F-71k-ha | — R-71k-ha |
| — C-81k-ha | — F-81k-ha | — R-81k-ha |

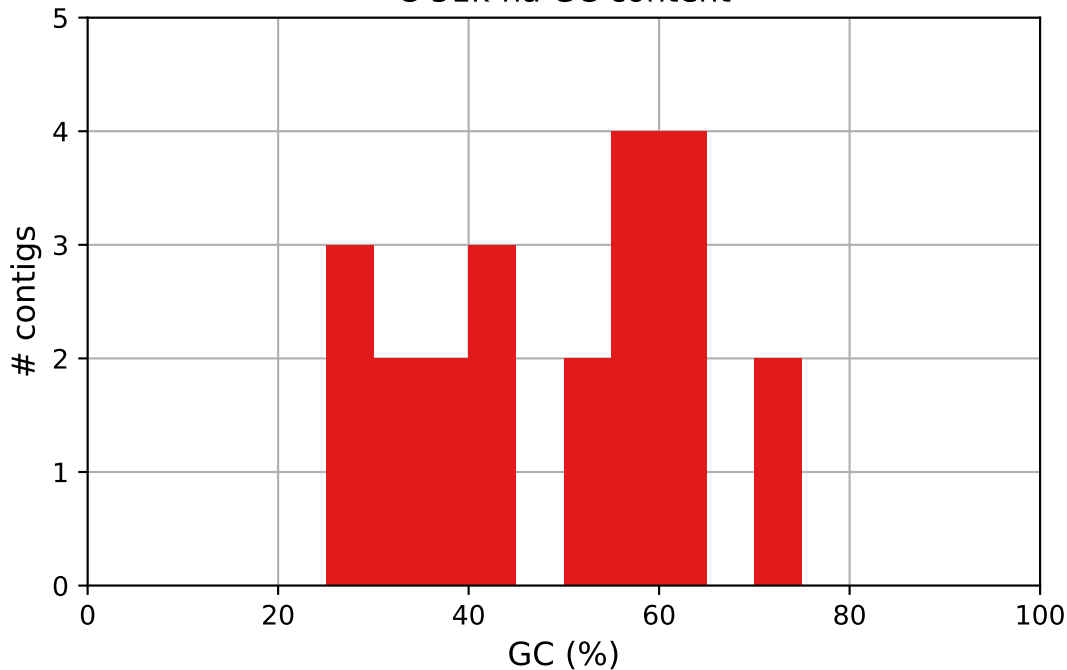
Cumulative length



GC content

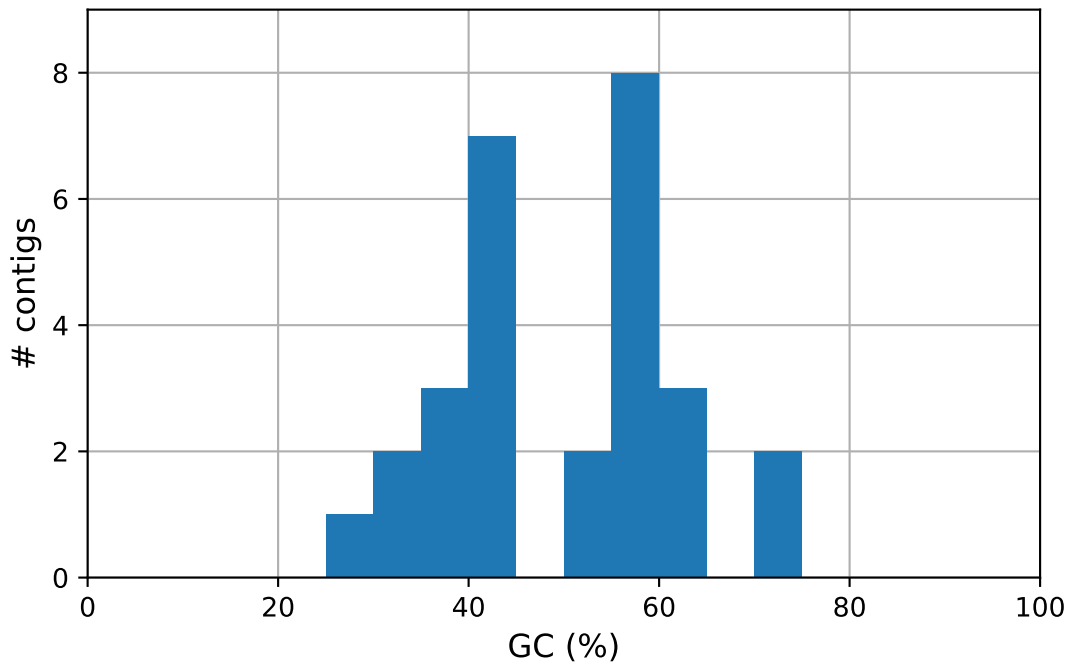


C-51k-ha GC content



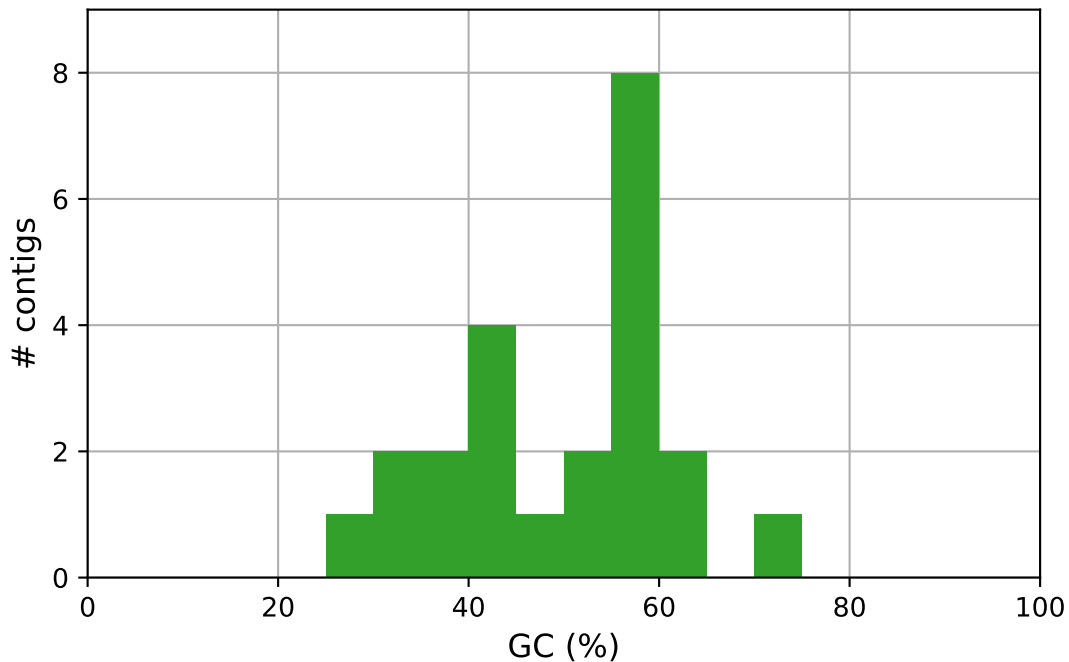
C-51k-ha

C-61k-ha GC content



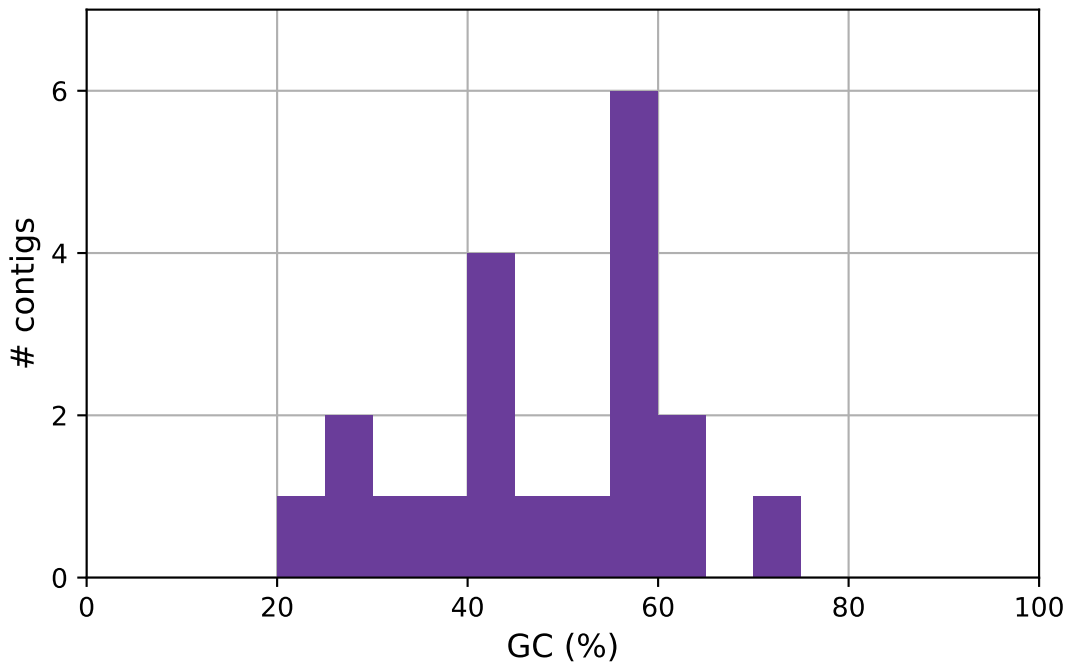
C-61k-ha

C-71k-ha GC content



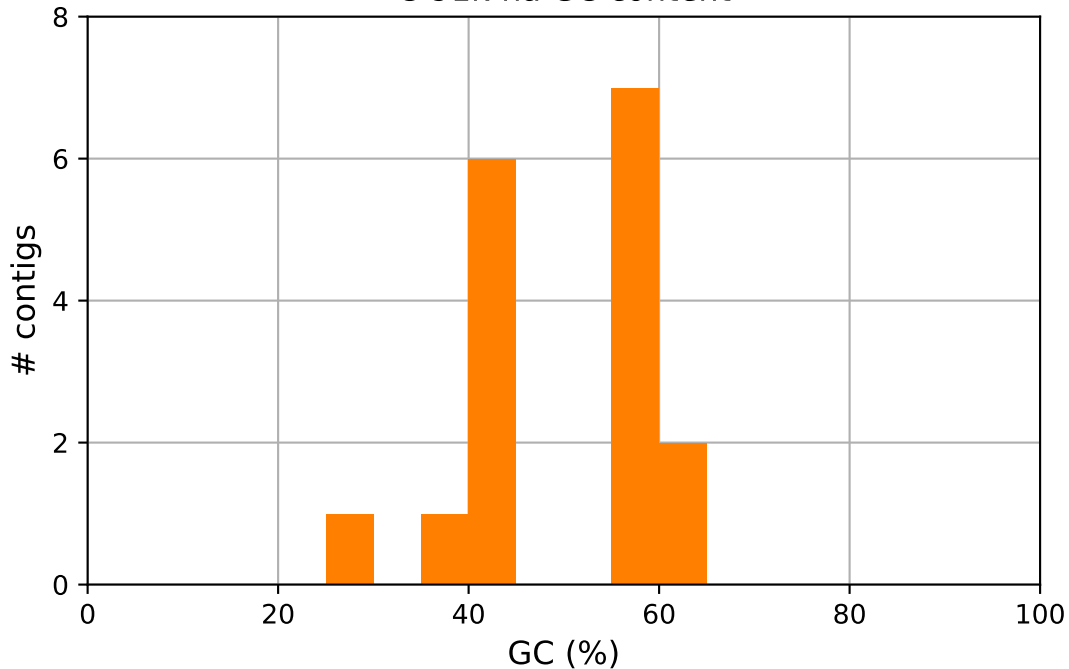
C-71k-ha

C-81k-ha GC content



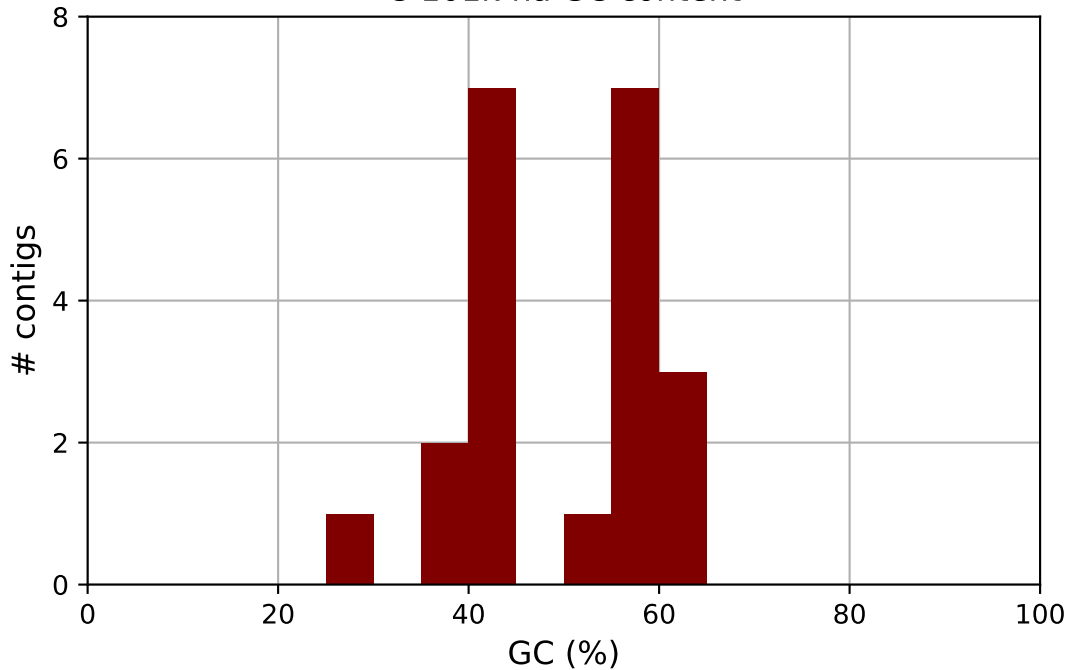
C-81k-ha

C-91k-ha GC content



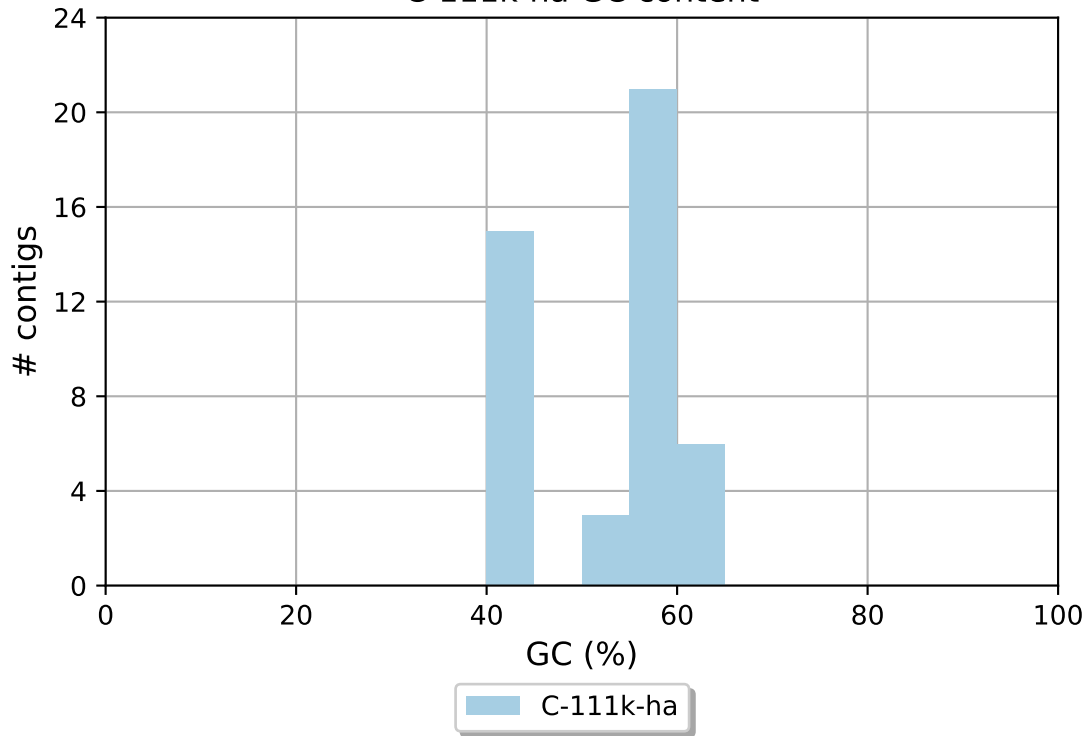
C-91k-ha

C-101k-ha GC content

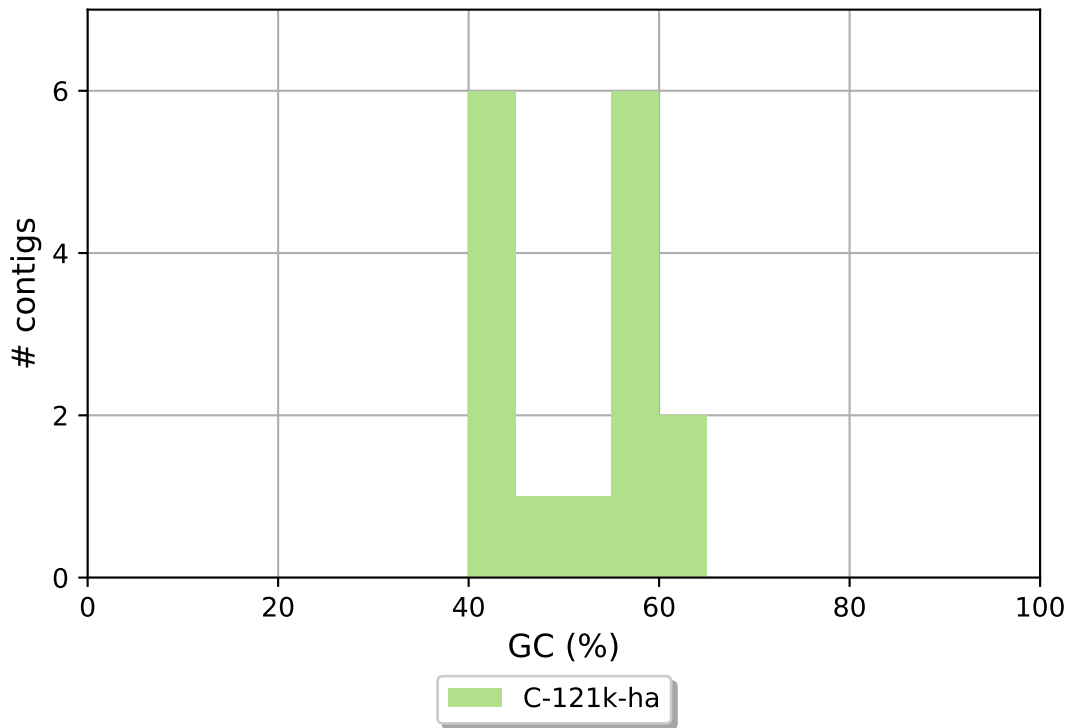


C-101k-ha

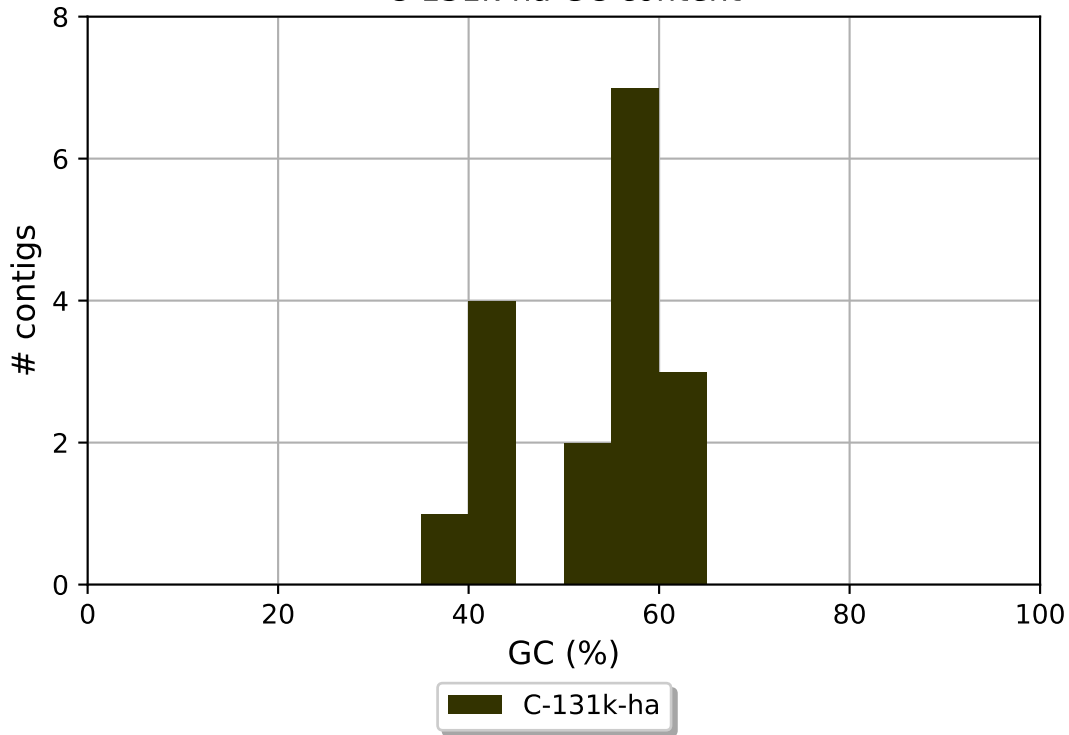
C-111k-ha GC content



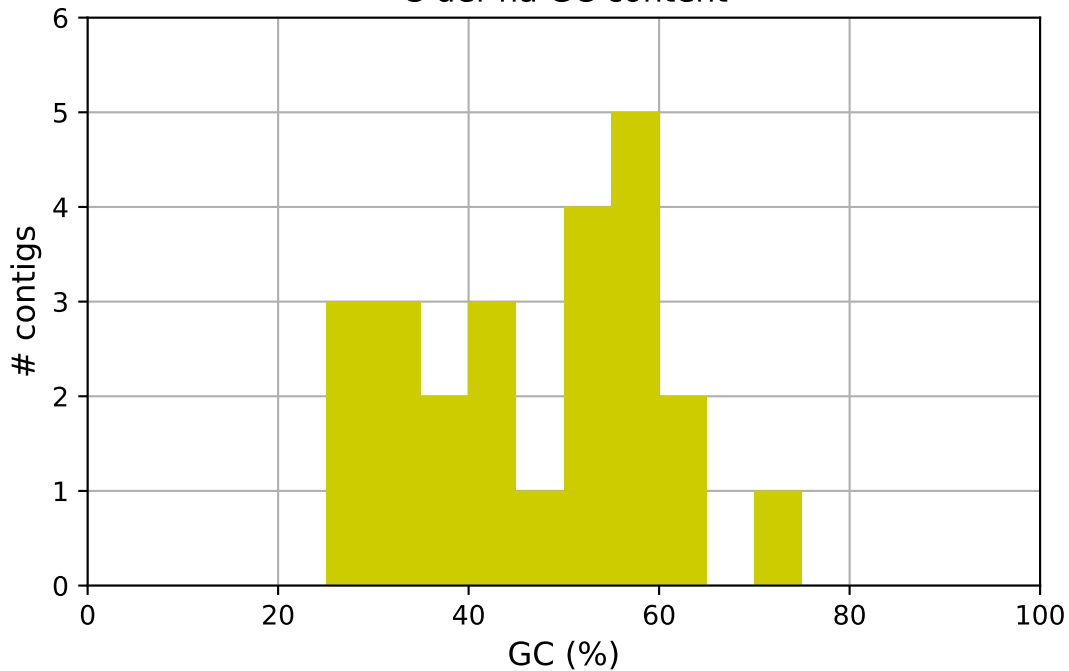
C-121k-ha GC content



C-131k-ha GC content

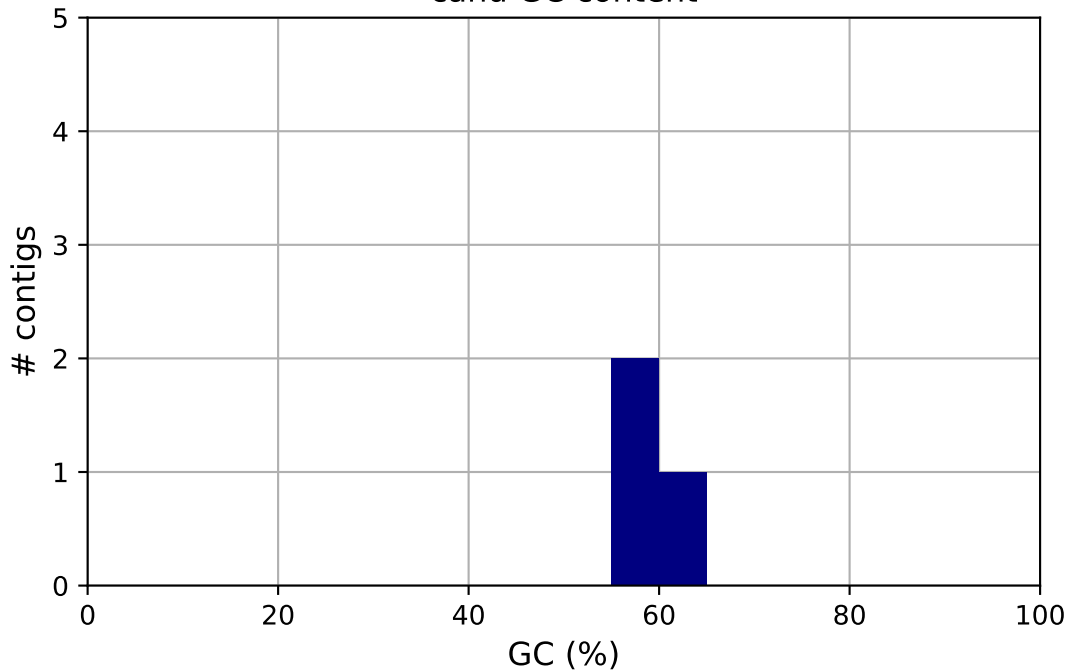


C-def-ha GC content



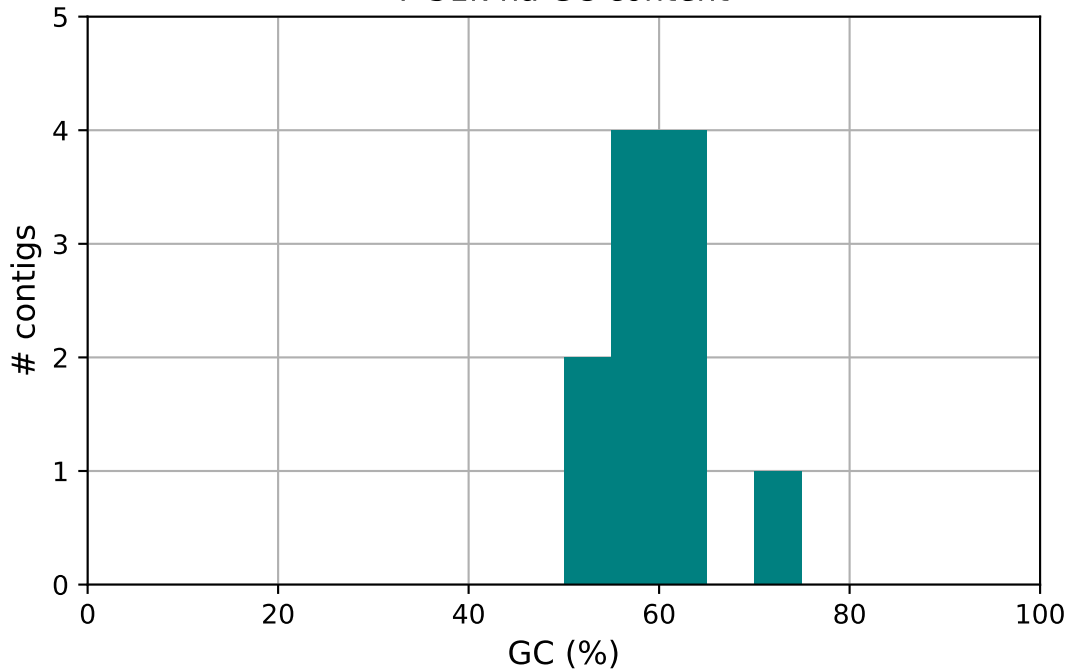
C-def-ha

canu GC content



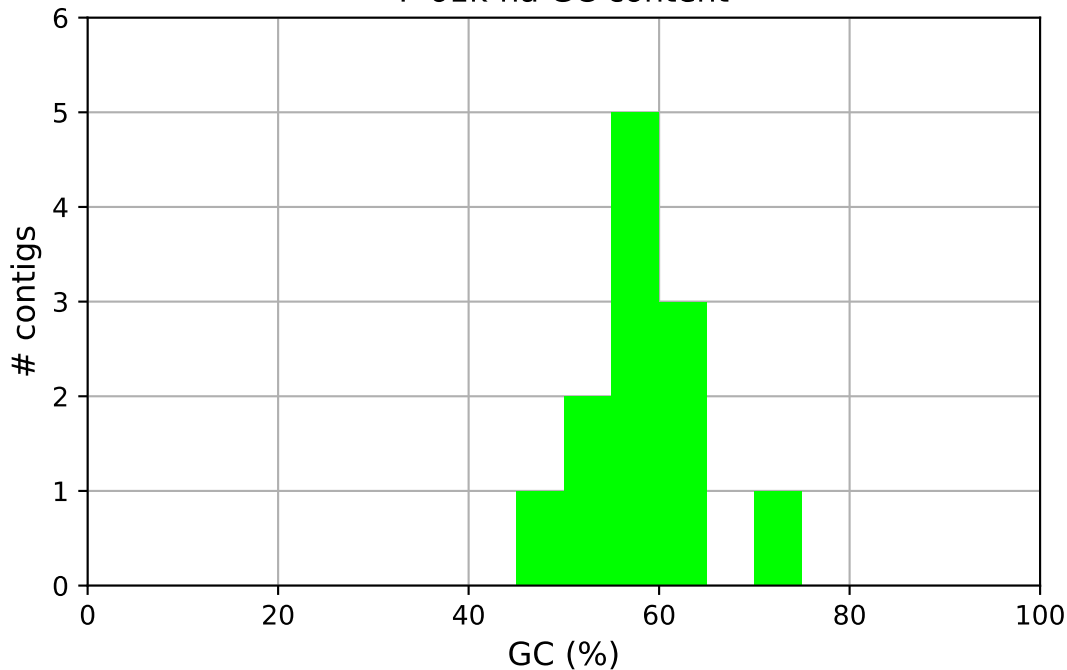
canu

F-51k-ha GC content



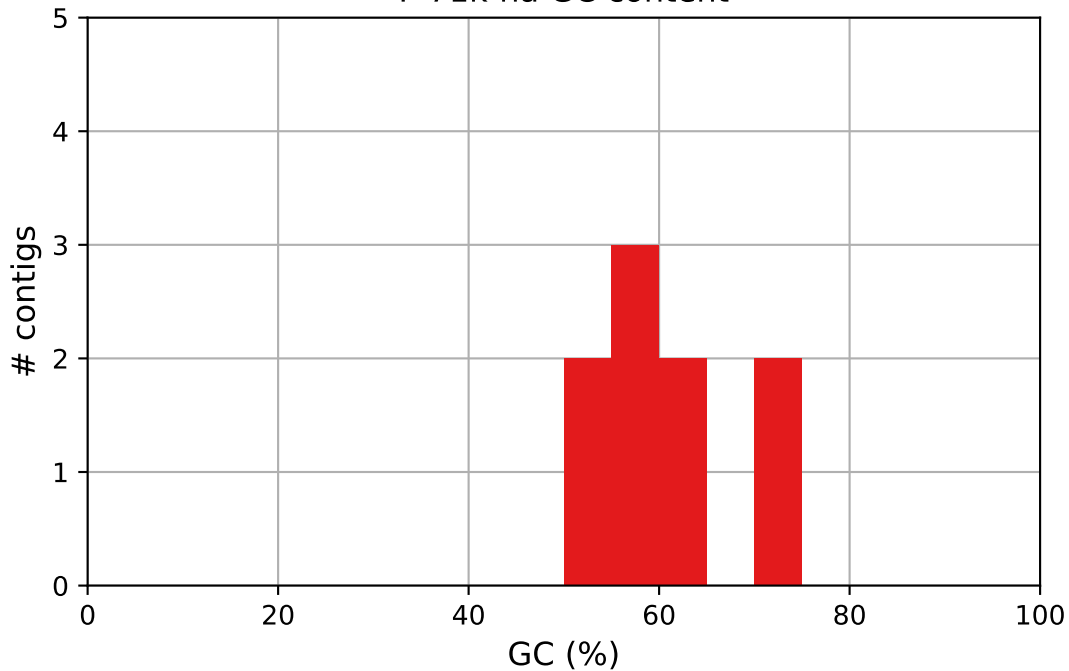
F-51k-ha

F-61k-ha GC content



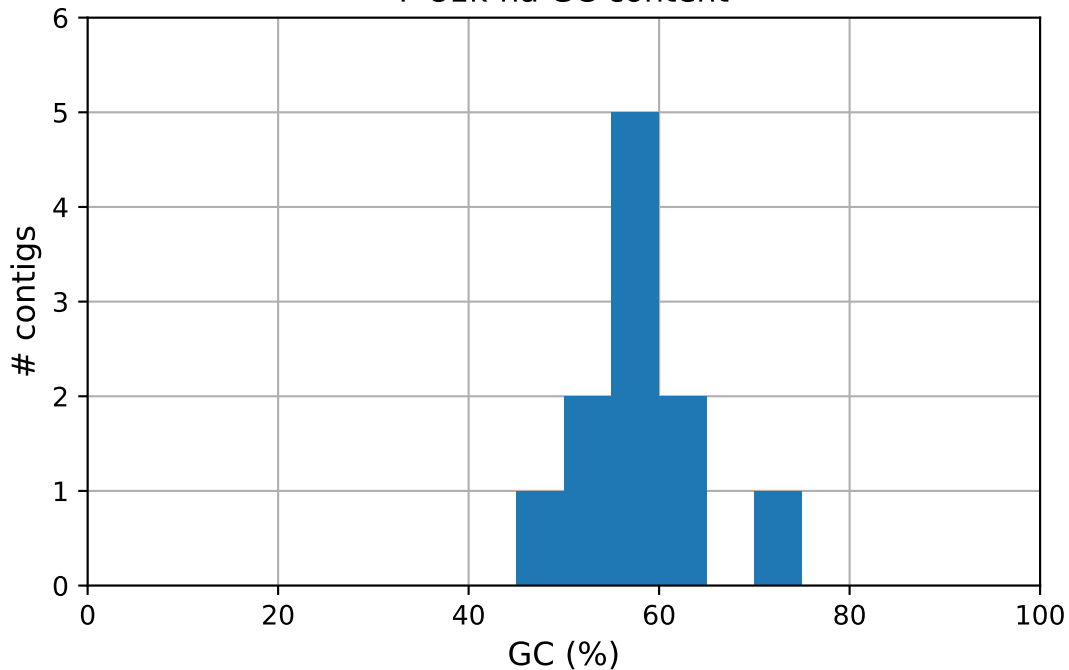
 F-61k-ha

F-71k-ha GC content



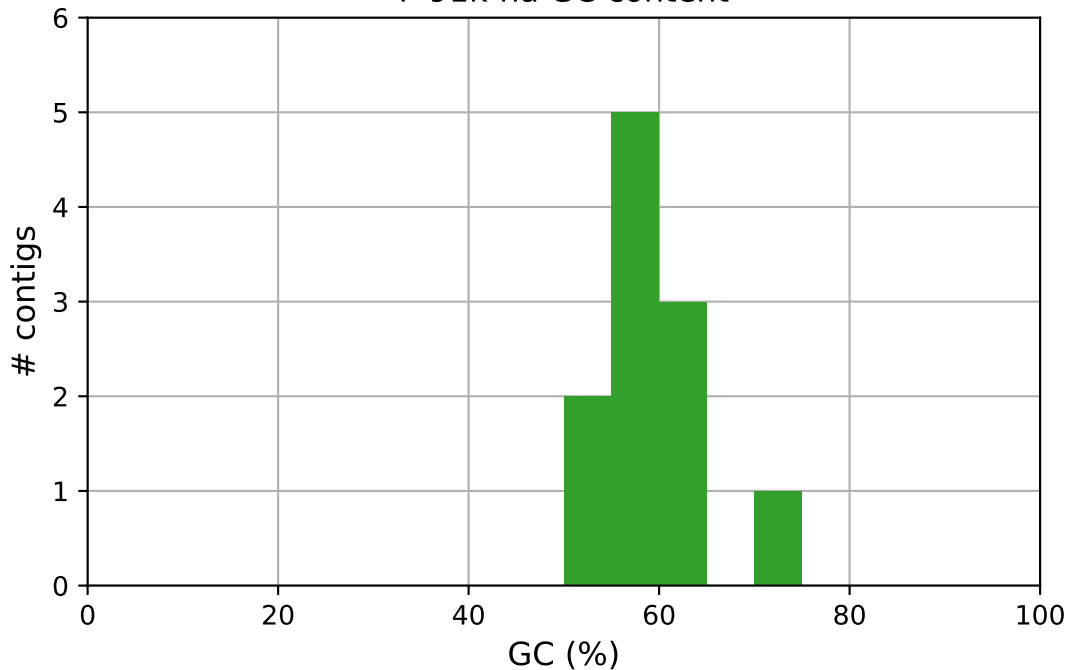
 F-71k-ha

F-81k-ha GC content



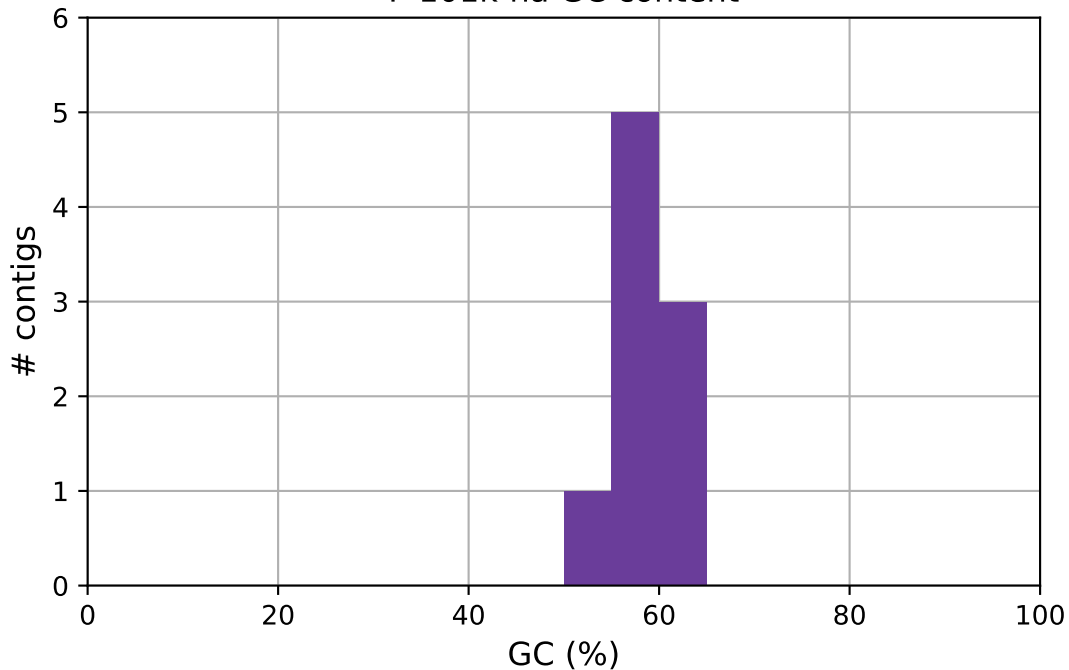
F-81k-ha

F-91k-ha GC content



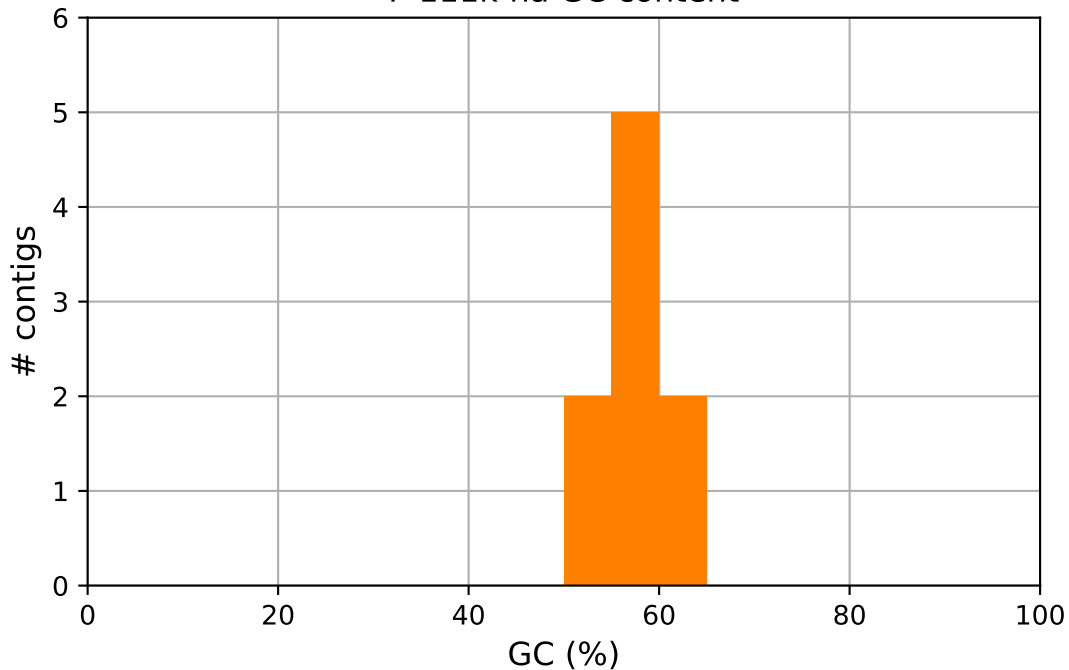
F-91k-ha

F-101k-ha GC content



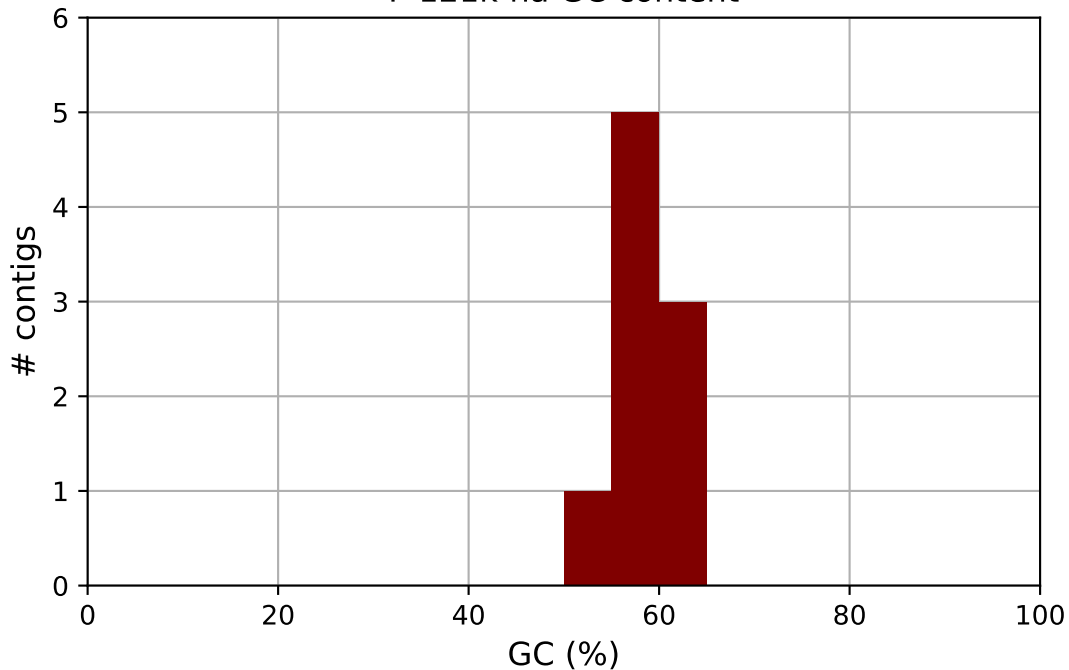
F-101k-ha

F-111k-ha GC content



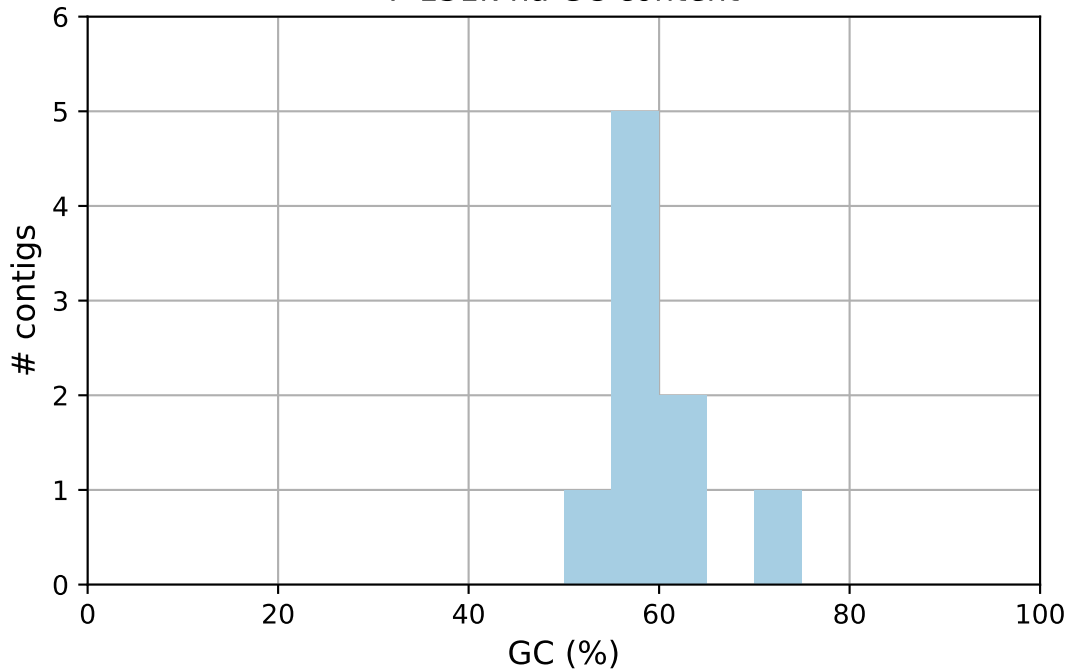
F-111k-ha

F-121k-ha GC content



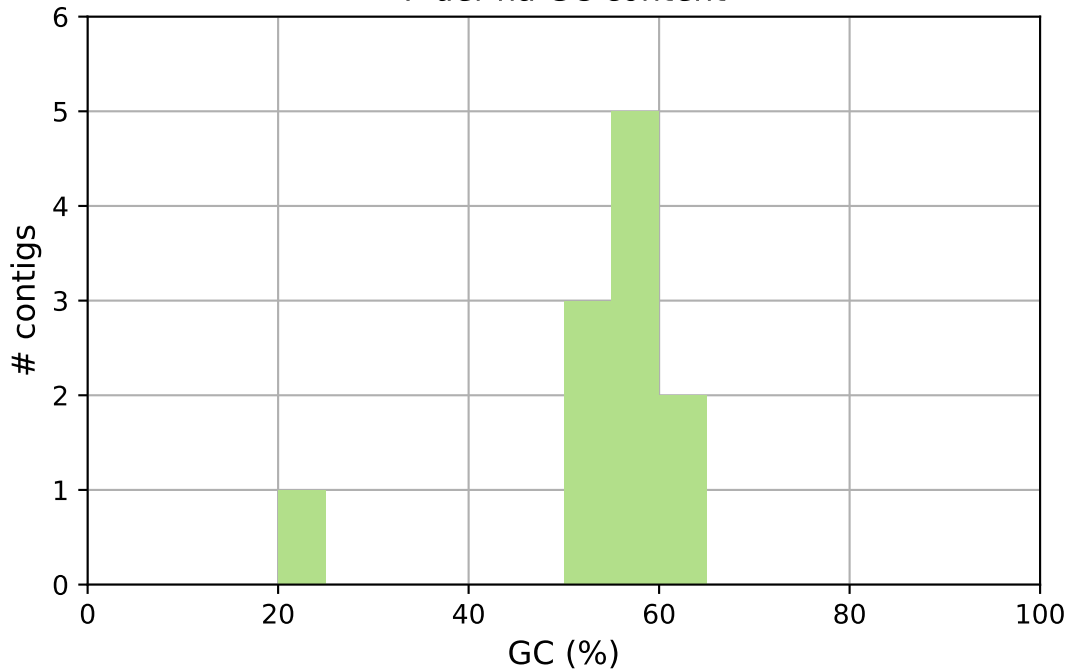
F-121k-ha

F-131k-ha GC content



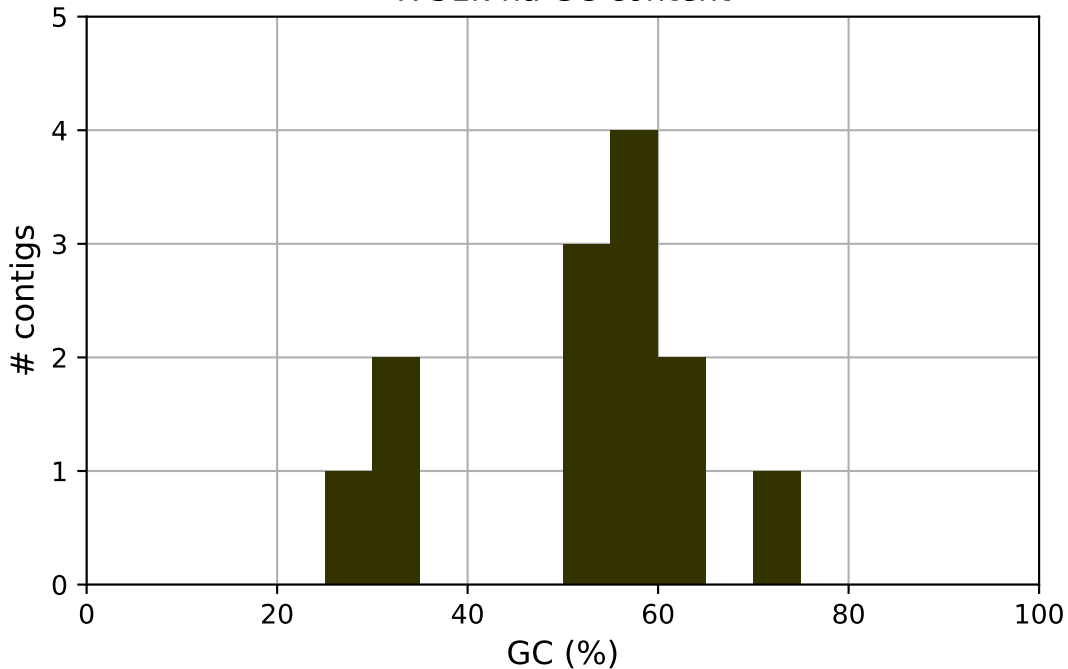
F-131k-ha

F-def-ha GC content



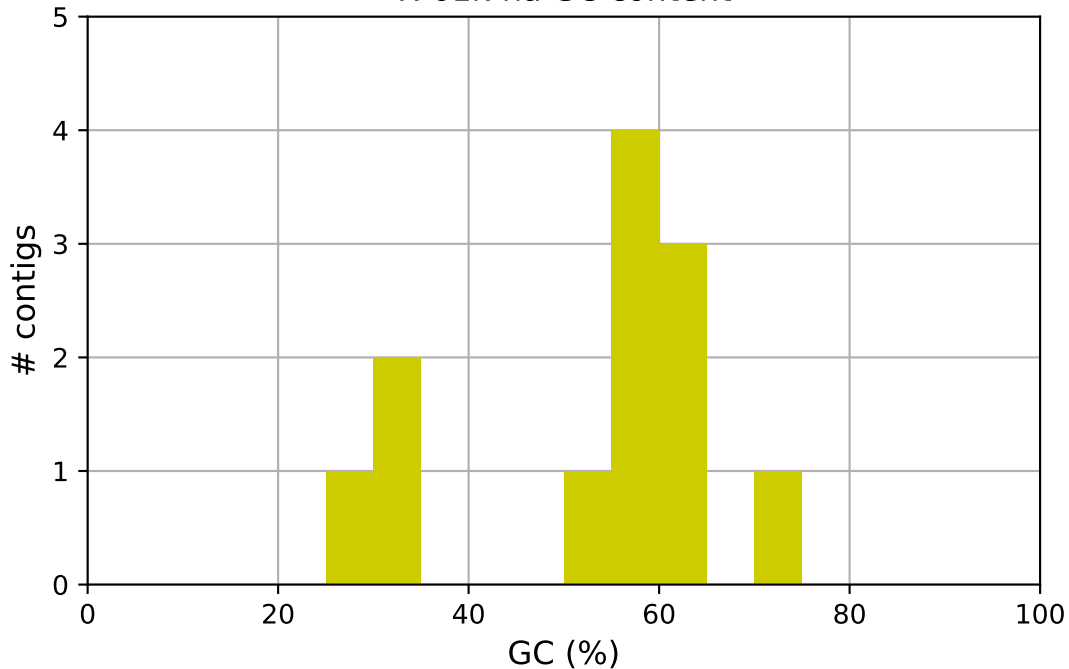
F-def-ha

R-51k-ha GC content



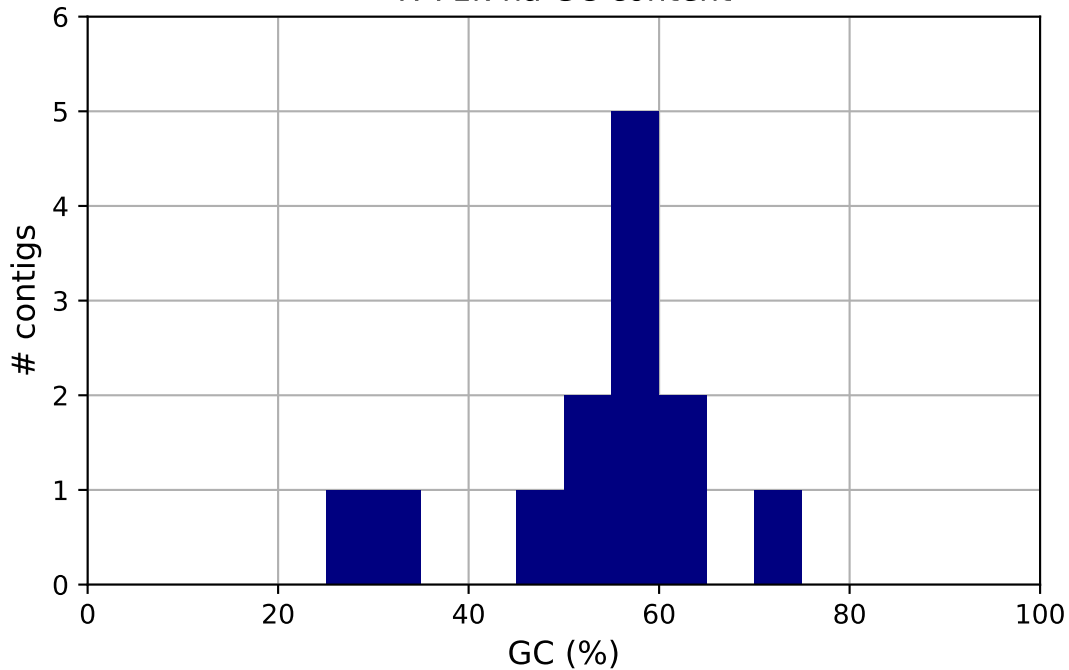
R-51k-ha

R-61k-ha GC content



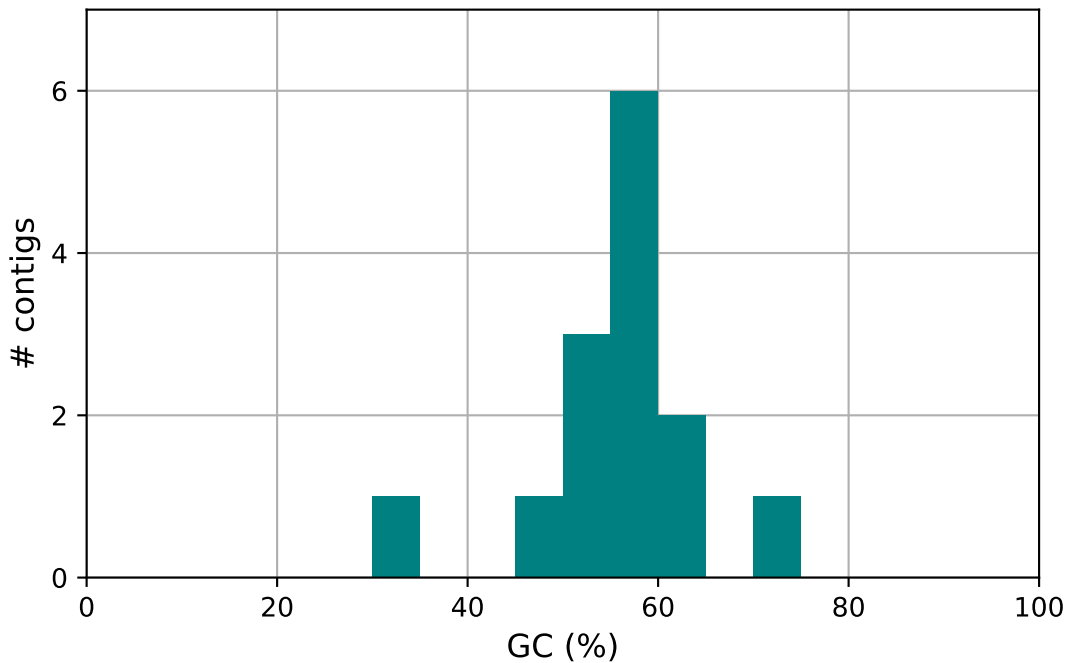
R-61k-ha

R-71k-ha GC content



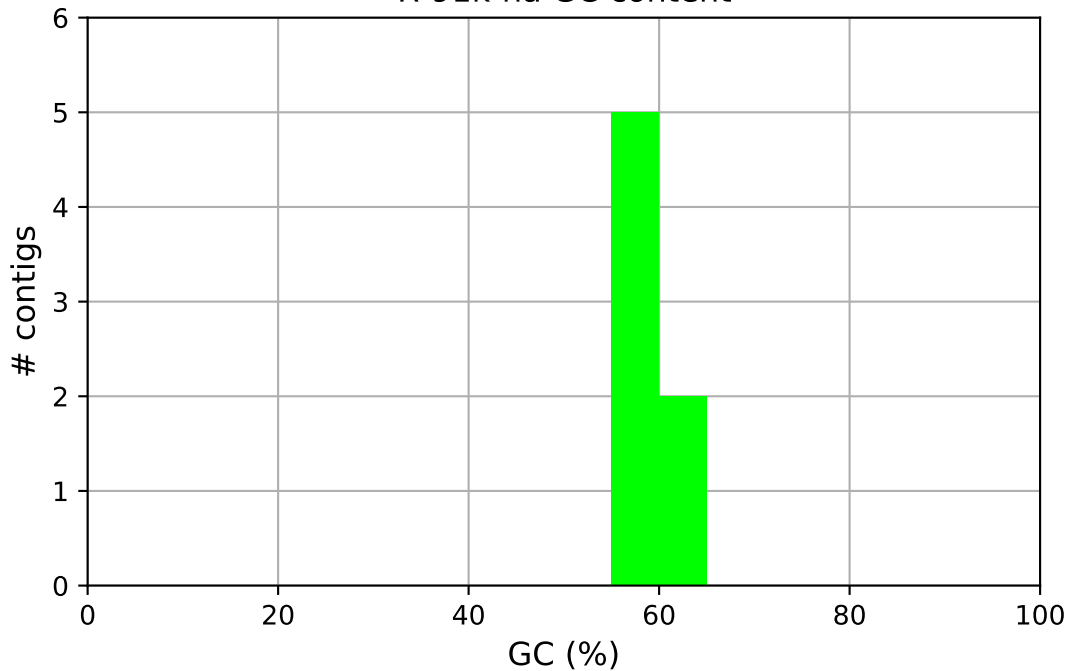
■ R-71k-ha

R-81k-ha GC content



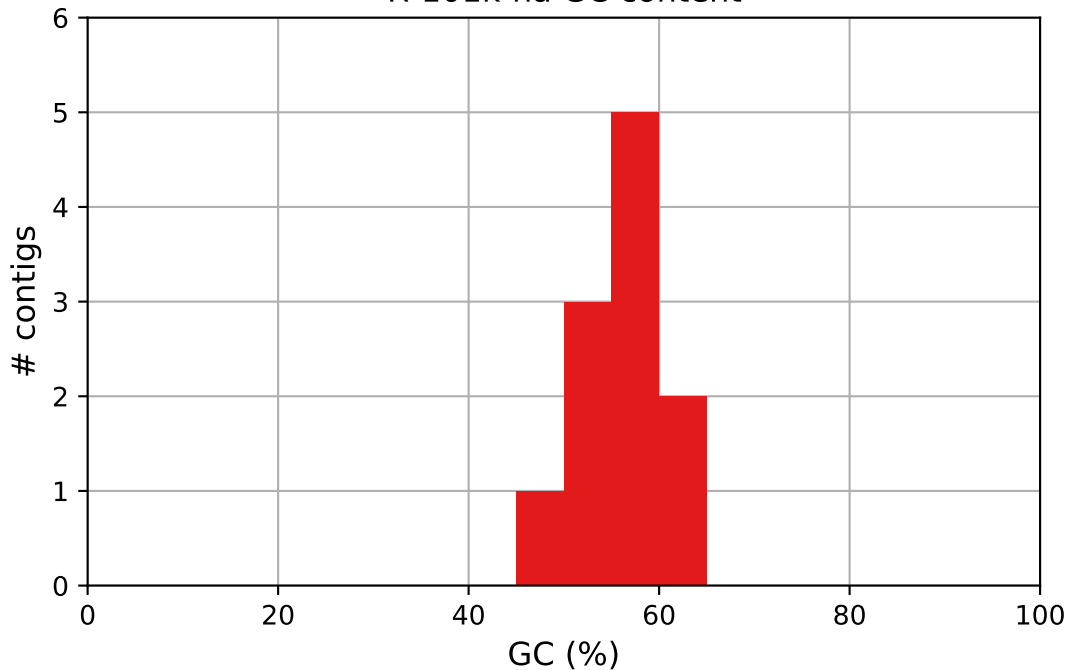
R-81k-ha

R-91k-ha GC content



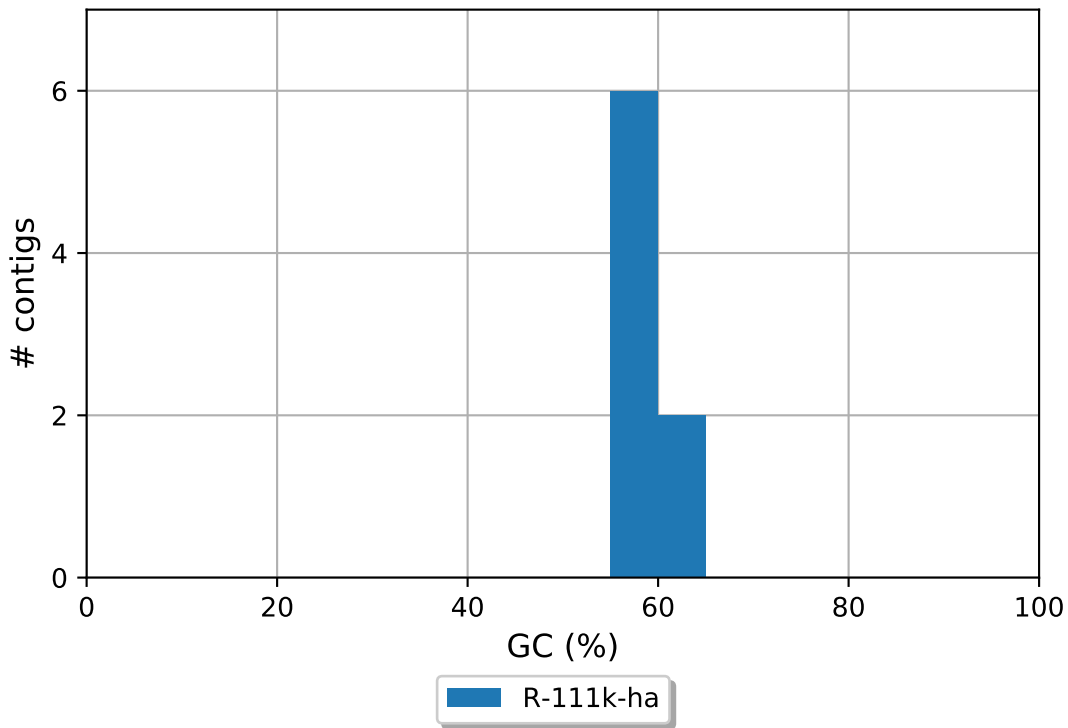
 R-91k-ha

R-101k-ha GC content

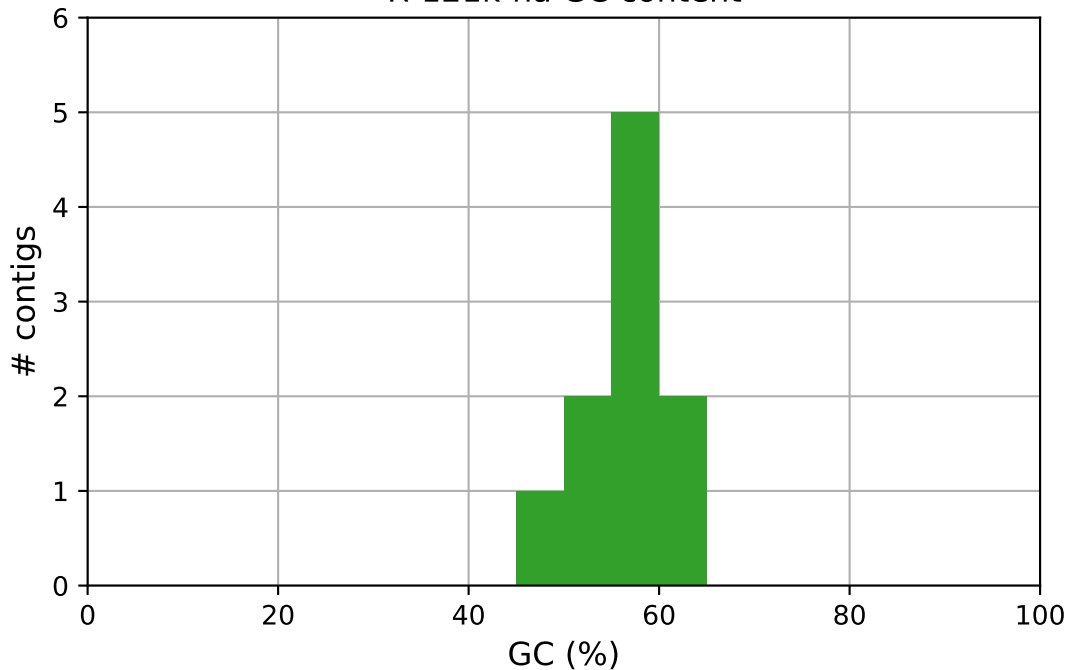


R-101k-ha

R-111k-ha GC content

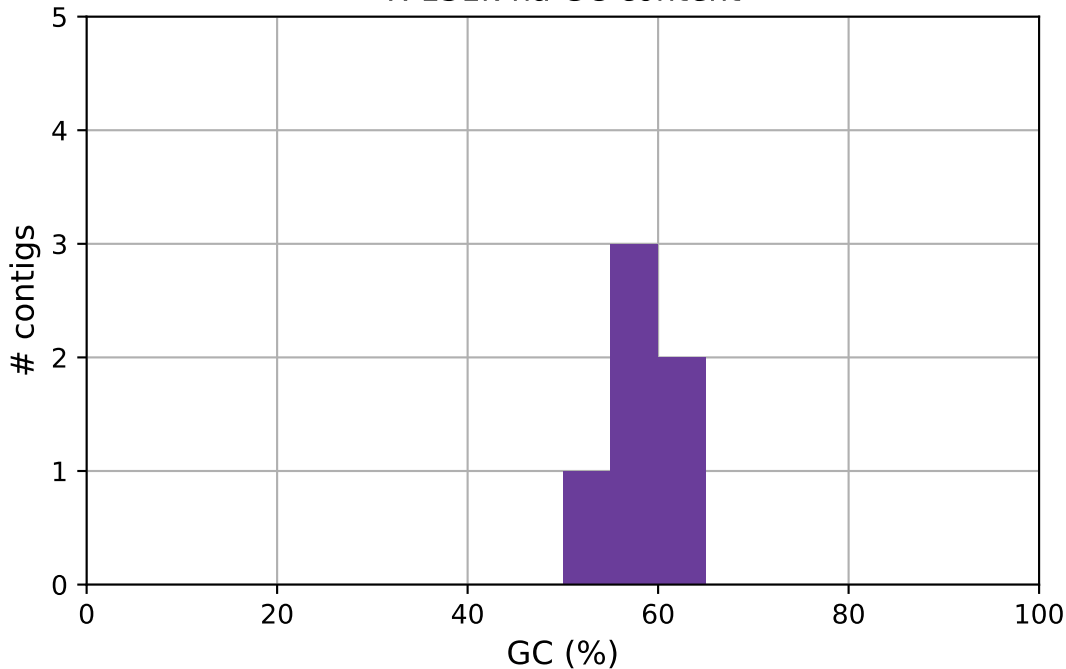


R-121k-ha GC content



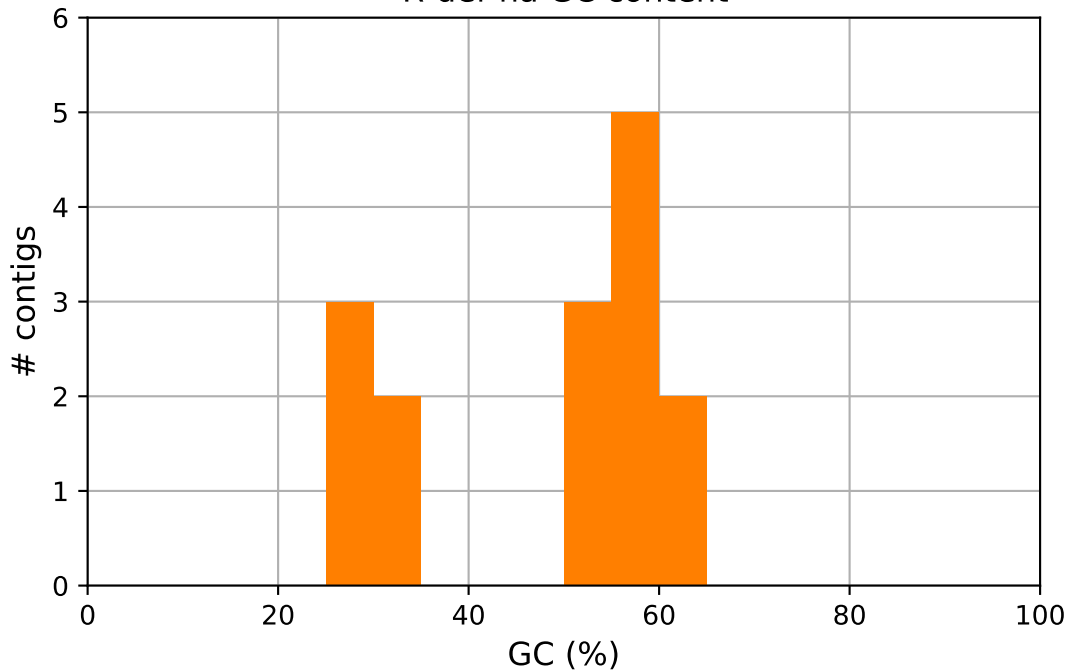
R-121k-ha

R-131k-ha GC content



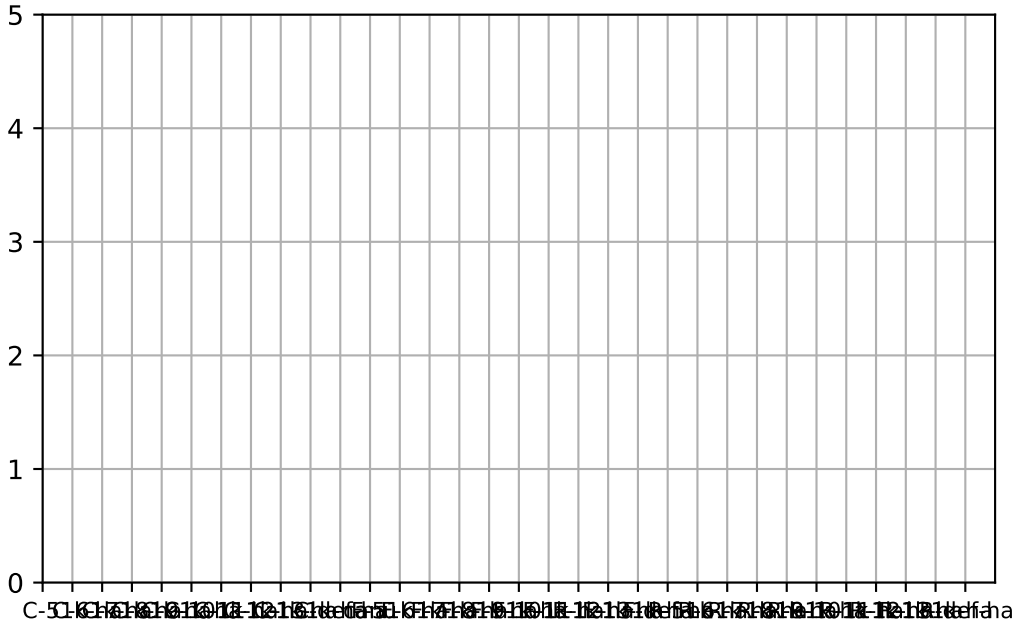
R-131k-ha

R-def-ha GC content

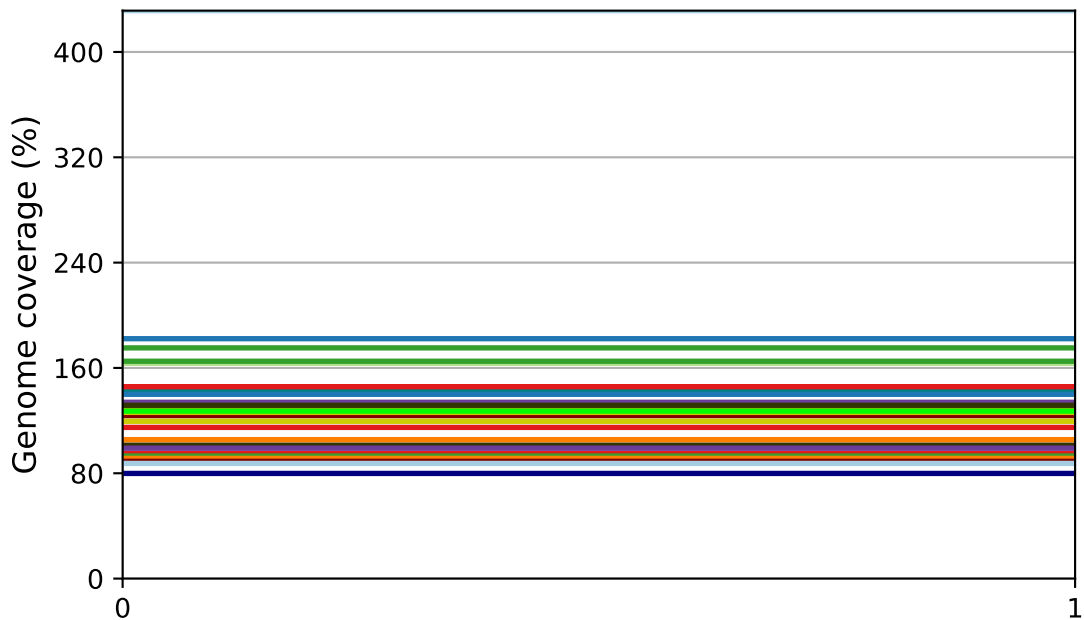


 R-def-ha

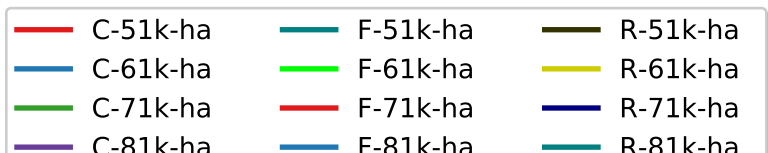
Misassemblies



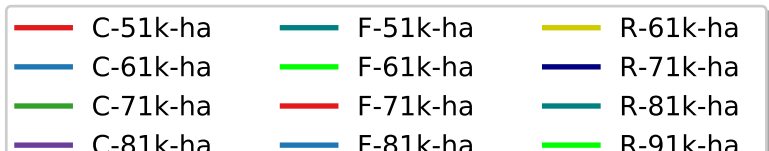
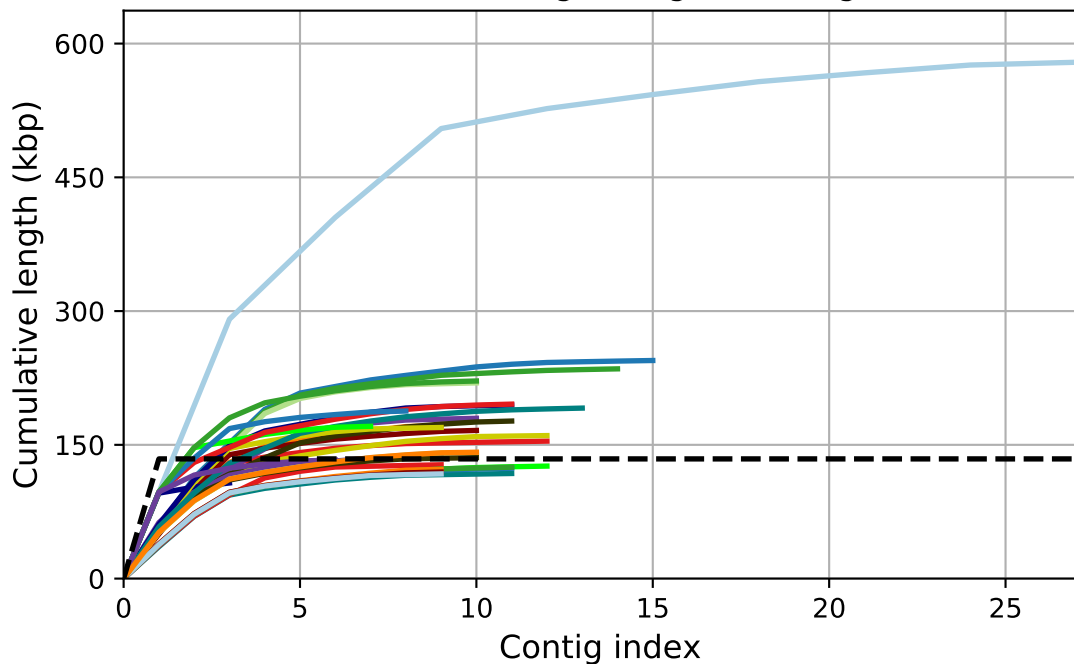
FRCurve (misassemblies)



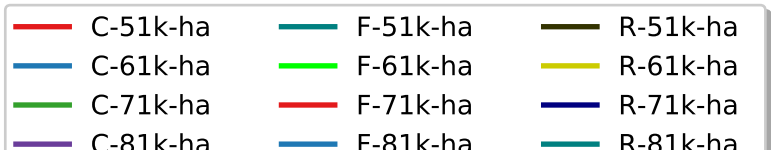
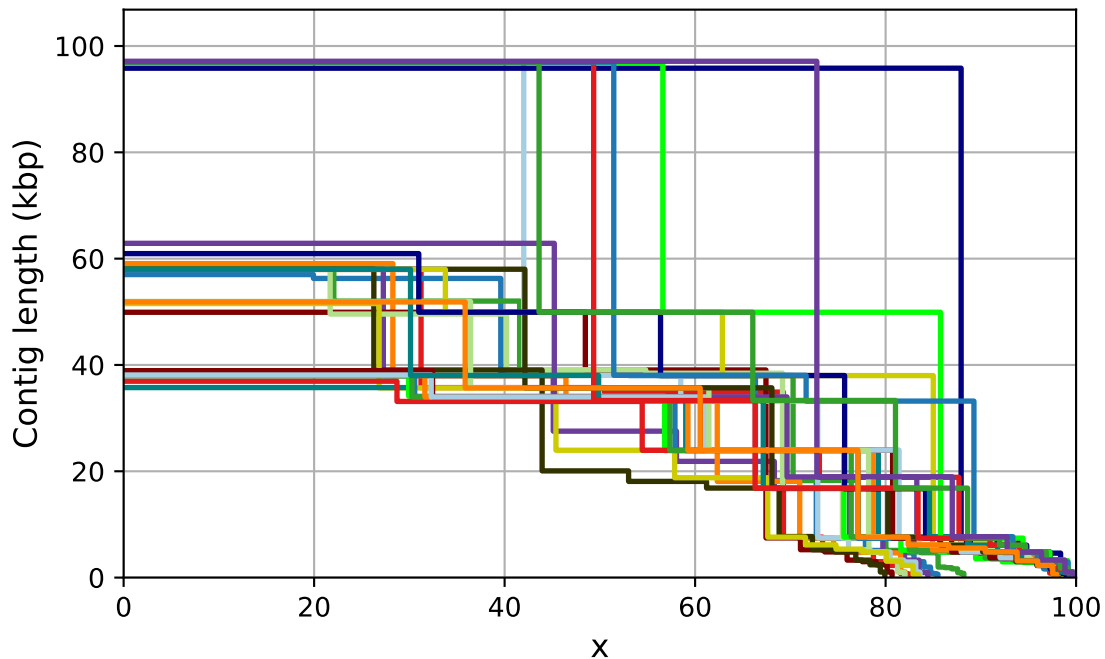
Feature space



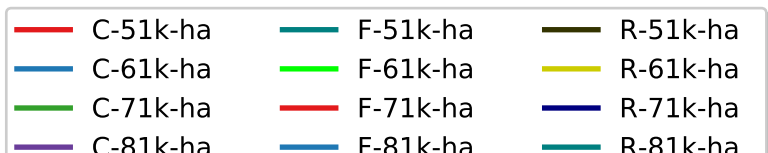
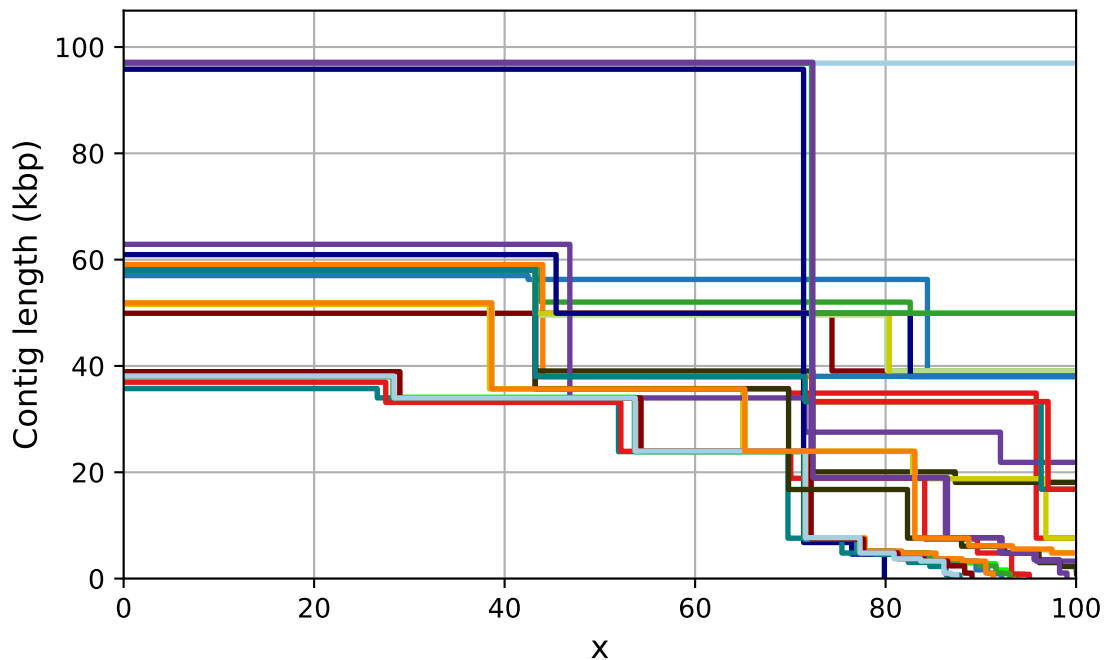
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

