

# Report

	NEK_END	NEK_START	NEK_clone_2	NEK_clone_3	NEK_clone_4	NEK_clone_5
# contigs (>= 0 bp)	101286	115992	154553	139634	137263	154920
# contigs (>= 1000 bp)	5257	5686	5068	4946	4878	4932
# contigs (>= 5000 bp)	1215	1263	960	887	1058	1015
# contigs (>= 10000 bp)	616	631	445	423	474	451
# contigs (>= 25000 bp)	253	263	218	233	217	212
# contigs (>= 50000 bp)	123	93	133	135	124	129
Total length (>= 0 bp)	47306720	48728197	53528328	51339271	52614670	54075679
Total length (>= 1000 bp)	32744369	32302034	31763272	31246106	32283764	31979138
Total length (>= 5000 bp)	24198904	22934762	23181693	22725901	24144765	23607497
Total length (>= 10000 bp)	19988606	18601941	19705289	19548943	20121164	19735987
Total length (>= 25000 bp)	14527416	13049209	16285659	16617049	16261208	16166927
Total length (>= 50000 bp)	9792306	7059213	13231279	12977535	12889604	13187050
# contigs	8451	9388	9895	9726	9692	9882
Largest contig	244352	190878	311525	305493	313583	313212
Total length	34983361	34900198	35068276	34510083	35541370	35322680
Reference length	35826294	35826294	35826294	35826294	35826294	35826294
GC (%)	44.56	44.61	44.37	44.53	44.42	44.40
Reference GC (%)	45.49	45.49	45.49	45.49	45.49	45.49
N50	15026	12068	17619	20532	17179	16472
NG50	14133	11170	16095	17135	16447	15442
N75	3587	3064	2964	2923	3317	3188
NG75	3235	2745	2728	2485	3199	2994
L50	412	526	278	262	292	287
LG50	441	566	300	297	301	303
L75	1700	2098	1782	1722	1680	1741
LG75	1886	2338	1982	2090	1746	1863
# misassemblies	341	319	262	270	286	252
# misassembled contigs	282	271	216	213	237	209
Misassembled contigs length	2378619	1802798	2607917	2332715	2954030	2654193
# local misassemblies	471	523	496	435	496	496
# scaffold gap ext. mis.	27	26	32	26	22	24
# scaffold gap loc. mis.	291	350	451	363	559	571
# unaligned mis. contigs	939	933	903	876	917	916
# unaligned contigs	2894 + 2317 part	3254 + 2347 part	4461 + 2335 part	4355 + 2281 part	4358 + 2204 part	4495 + 2179 part
Unaligned length	11218777	11151306	11420571	10919331	11828240	11659068
Genome fraction (%)	63.574	63.242	63.263	63.179	63.328	63.224
Duplication ratio	1.044	1.048	1.044	1.043	1.045	1.045
# N's per 100 kbp	111.51	128.65	175.06	136.63	194.70	206.92
# mismatches per 100 kbp	1133.77	1145.83	1101.86	1086.74	1103.00	1104.79
# indels per 100 kbp	157.62	153.26	158.49	160.94	159.51	158.83
# genomic features	41764 + 8988 part	40914 + 9755 part	41858 + 8635 part	42259 + 8264 part	41552 + 9209 part	41550 + 9113 part
Largest alignment	226229	190641	305895	304995	306963	303798
Total aligned length	23340628	23262575	23144344	23099213	23230872	23158330
NA50	11988	8542	15468	18567	14015	13498
NGA50	10442	7294	13112	14828	13340	11996
LA50	444	574	300	282	322	315
LGA50	481	632	326	322	332	335

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).

## Misassemblies report

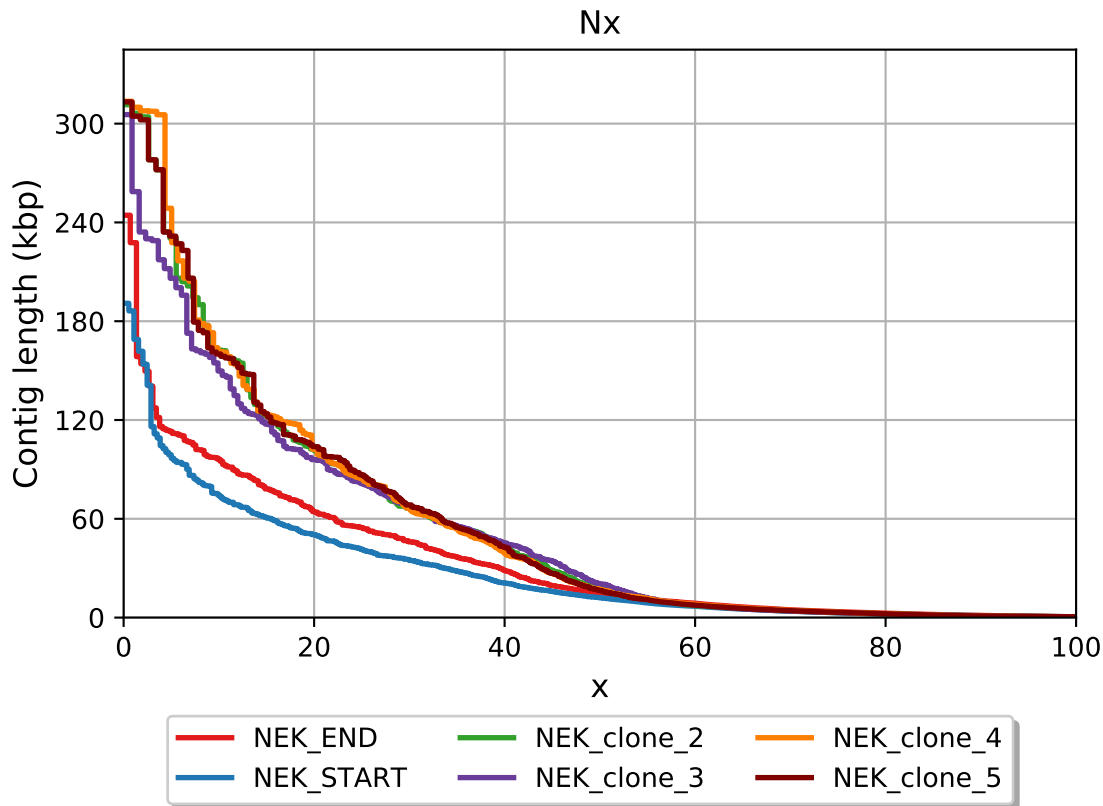
	NEK_END	NEK_START	NEK_clone_2	NEK_clone_3	NEK_clone_4	NEK_clone_5
# misassemblies	341	319	262	270	286	252
# contig misassemblies	339	316	256	265	282	250
# c. relocations	103	96	75	88	85	85
# c. translocations	236	218	181	177	197	165
# c. inversions	0	2	0	0	0	0
# scaffold misassemblies	2	3	6	5	4	2
# s. relocations	2	3	3	4	2	2
# s. translocations	0	0	3	1	2	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	282	271	216	213	237	209
Misassembled contigs length	2378619	1802798	2607917	2332715	2954030	2654193
# local misassemblies	471	523	496	435	496	496
# scaffold gap ext. mis.	27	26	32	26	22	24
# scaffold gap loc. mis.	291	350	451	363	559	571
# unaligned mis. contigs	939	933	903	876	917	916
# mismatches	258163	259546	249669	245918	250183	250179
# indels	35891	34716	35911	36420	36180	35967
# indels (<= 5 bp)	30454	29530	30393	30760	30559	30474
# indels (> 5 bp)	5437	5186	5518	5660	5621	5493
Indels length	130050	126468	133883	136512	135930	135529

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

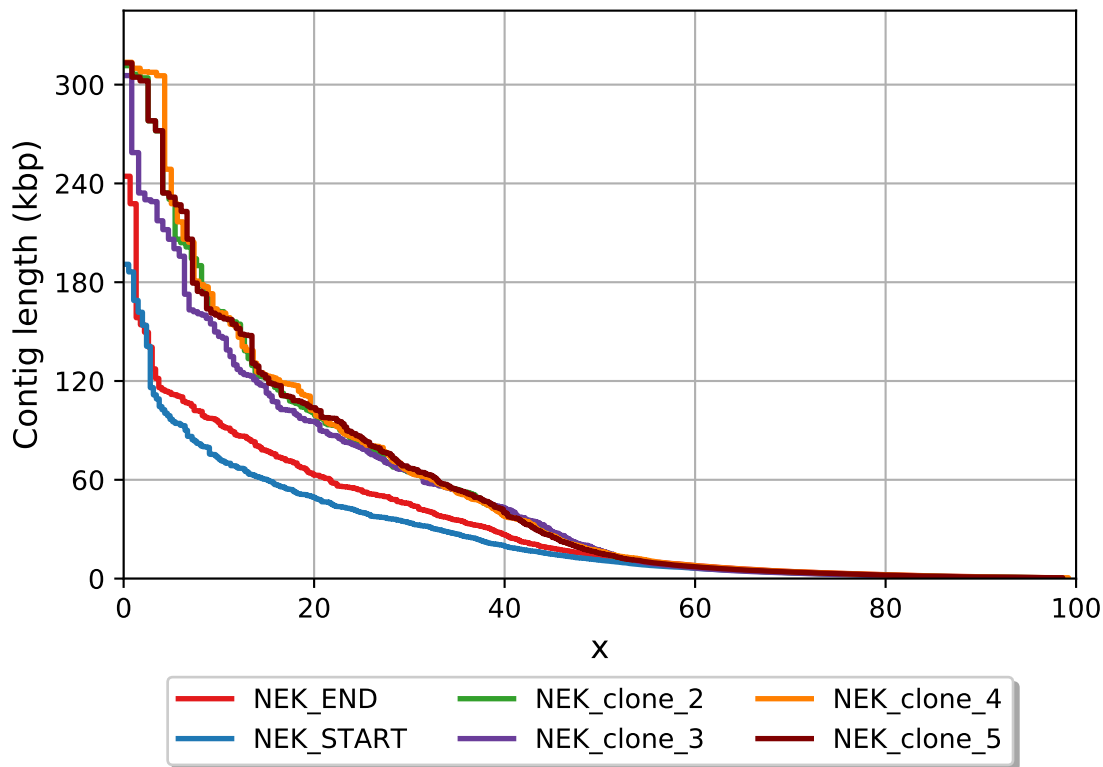
## Unaligned report

	NEK_END	NEK_START	NEK_clone_2	NEK_clone_3	NEK_clone_4	NEK_clone_5
# fully unaligned contigs	2894	3254	4461	4355	4358	4495
Fully unaligned length	4319816	4772776	5486086	5351342	5242776	5411829
# partially unaligned contigs	2317	2347	2335	2281	2204	2179
Partially unaligned length	6898961	6378530	5934485	5567989	6585464	6247239
# N's	39010	44900	61390	47150	69200	73088

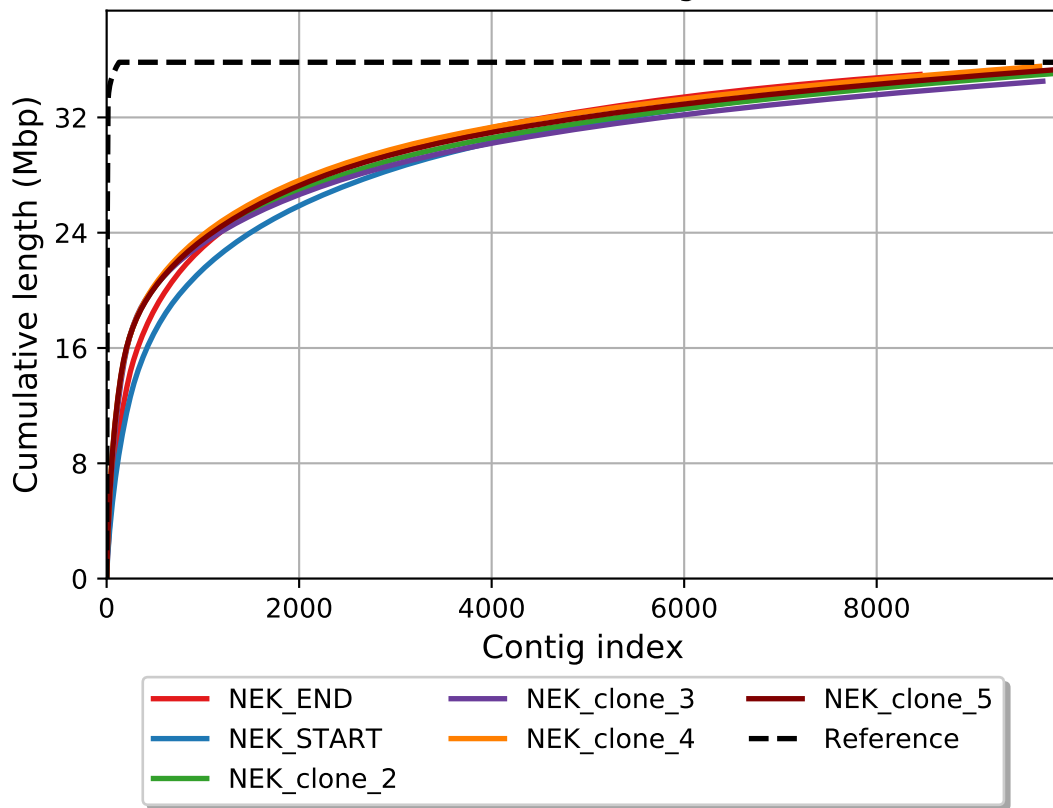
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



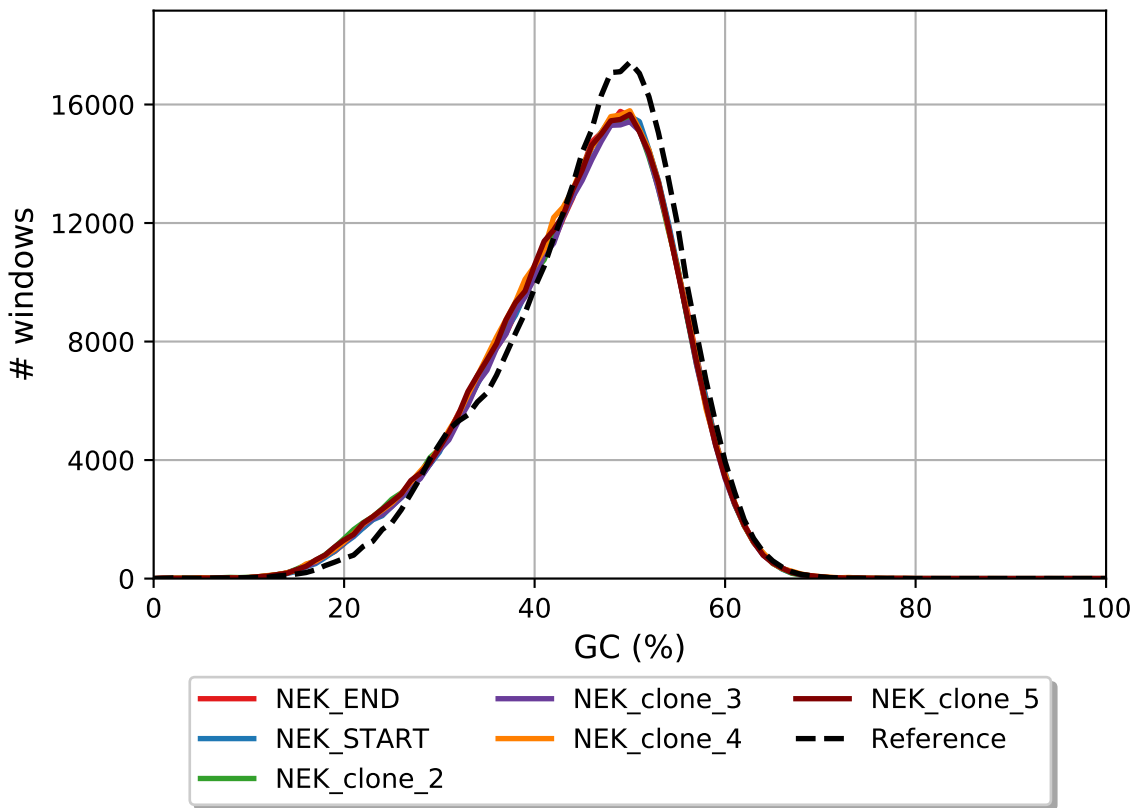
# NGx



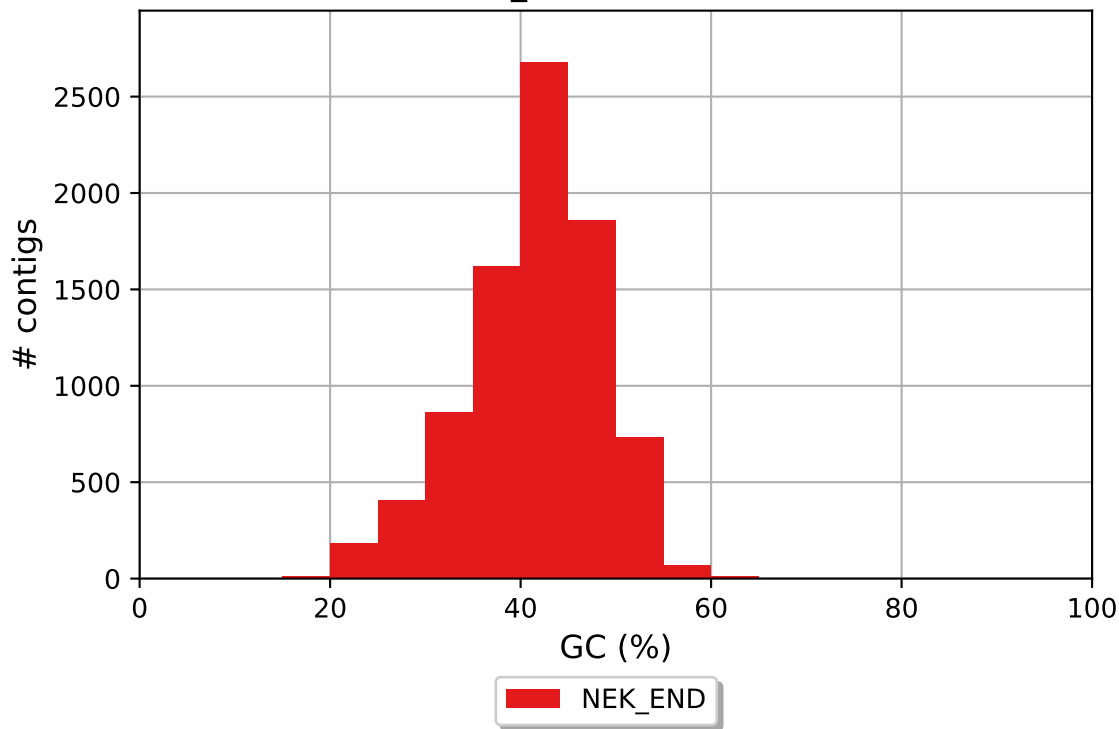
Cumulative length



GC content

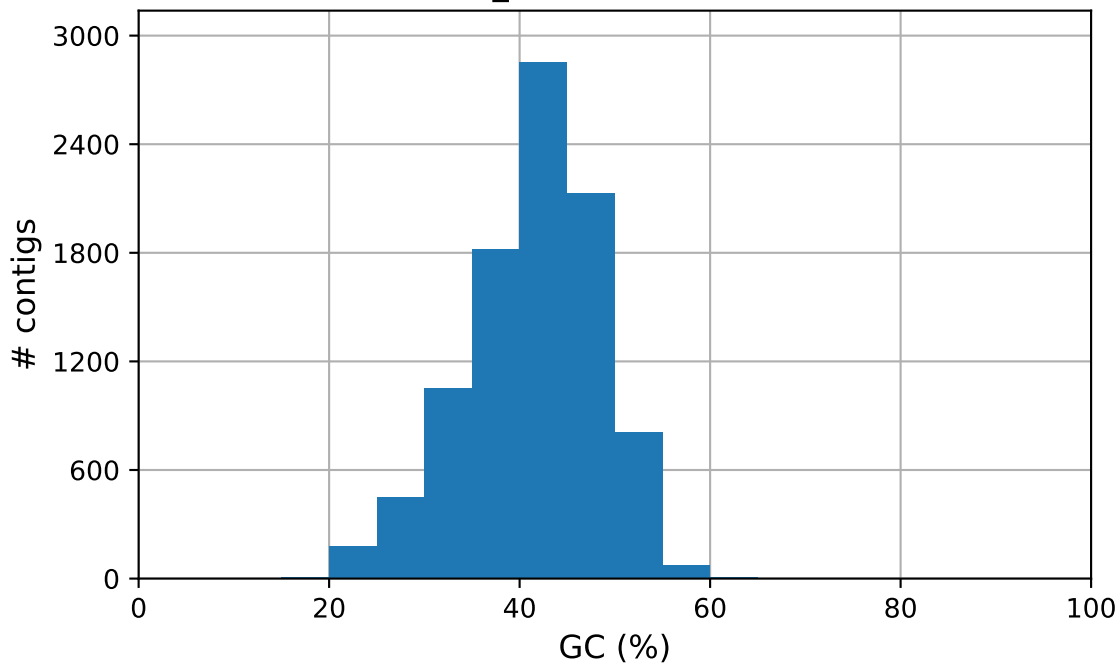


NEK\_END GC content



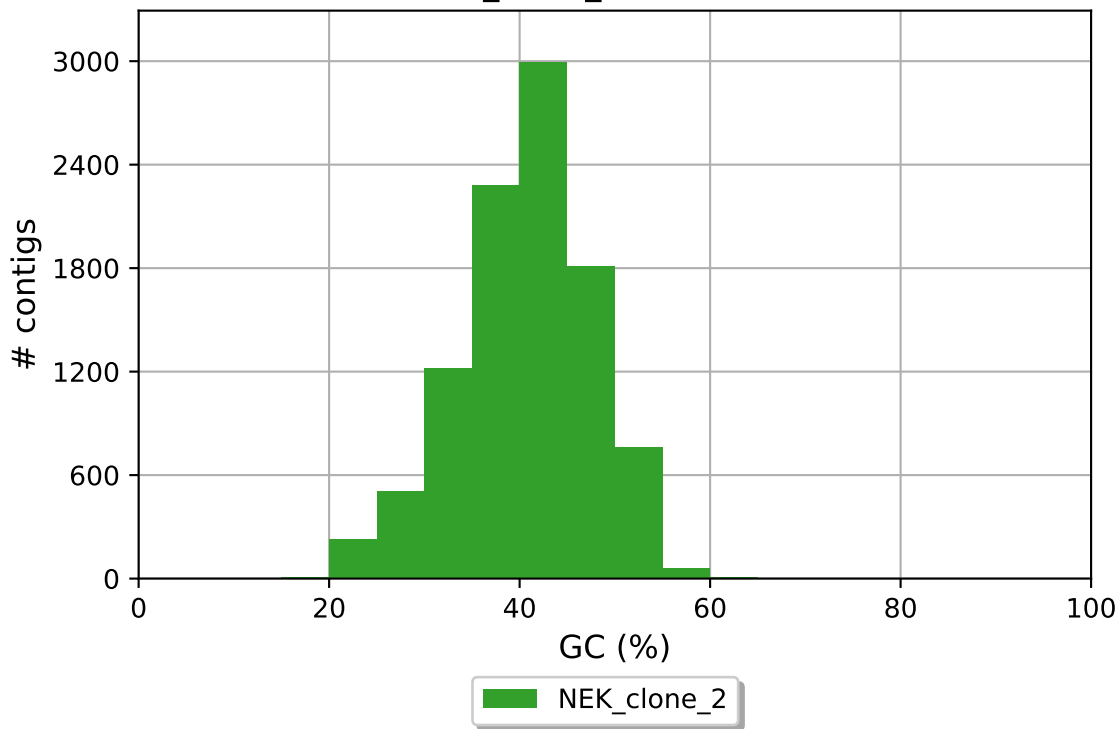


NEK\_START GC content

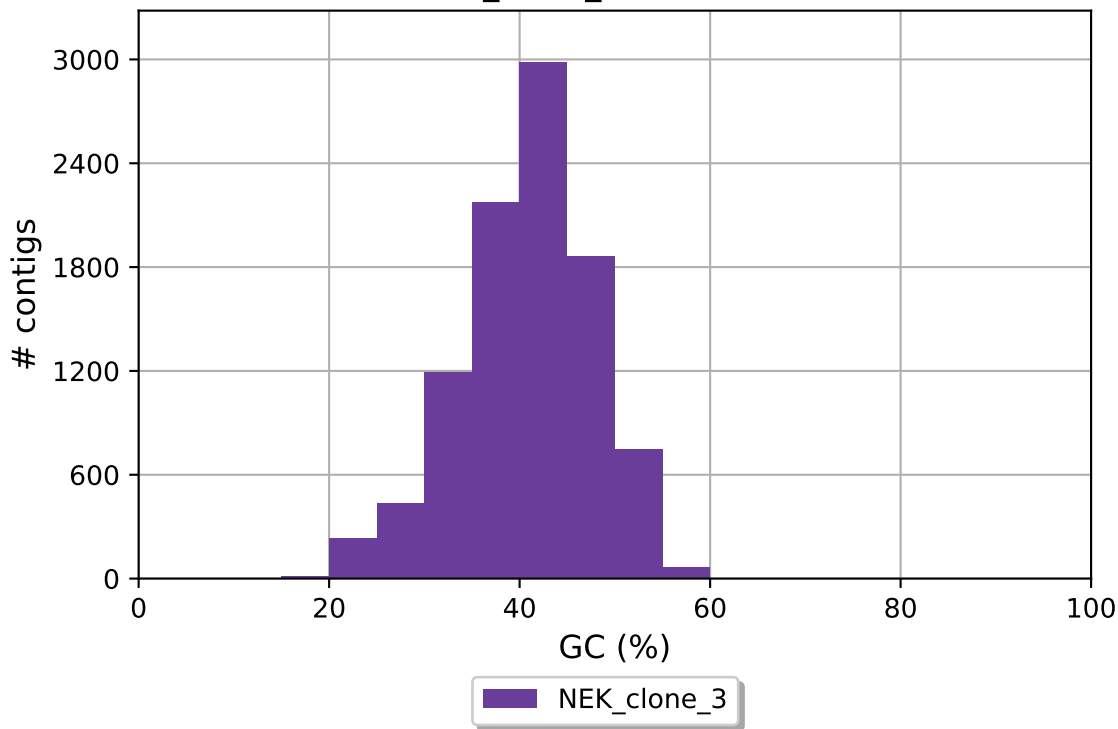


NEK\_START

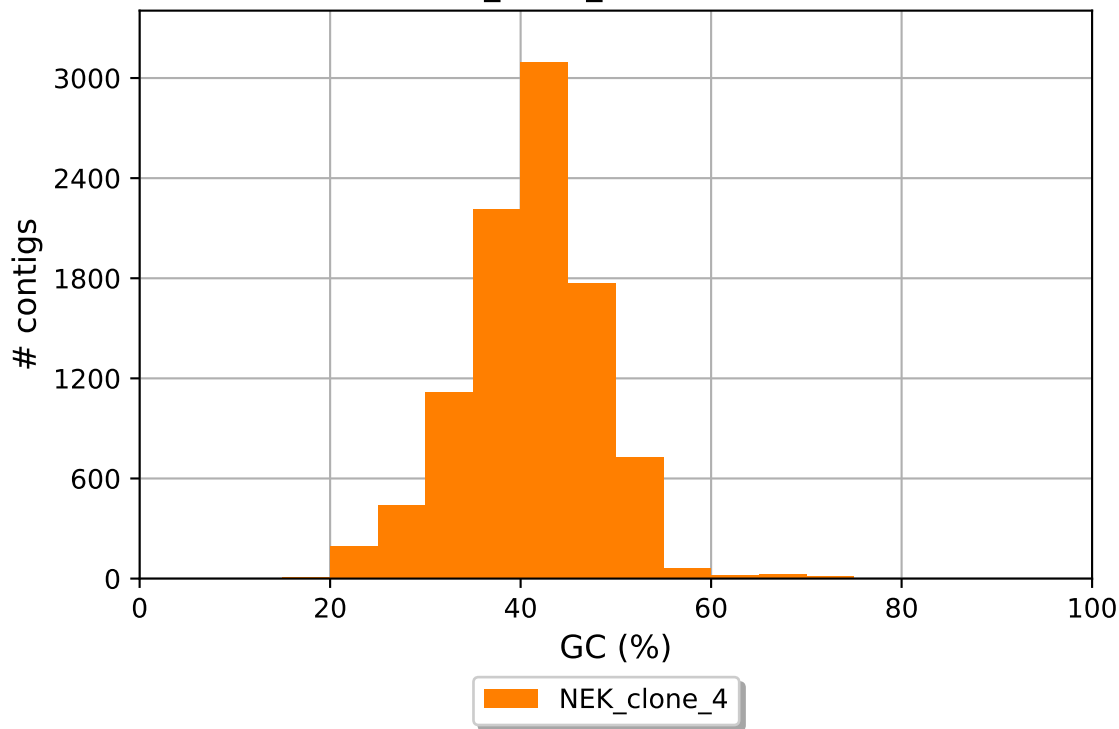
NEK\_clone\_2 GC content



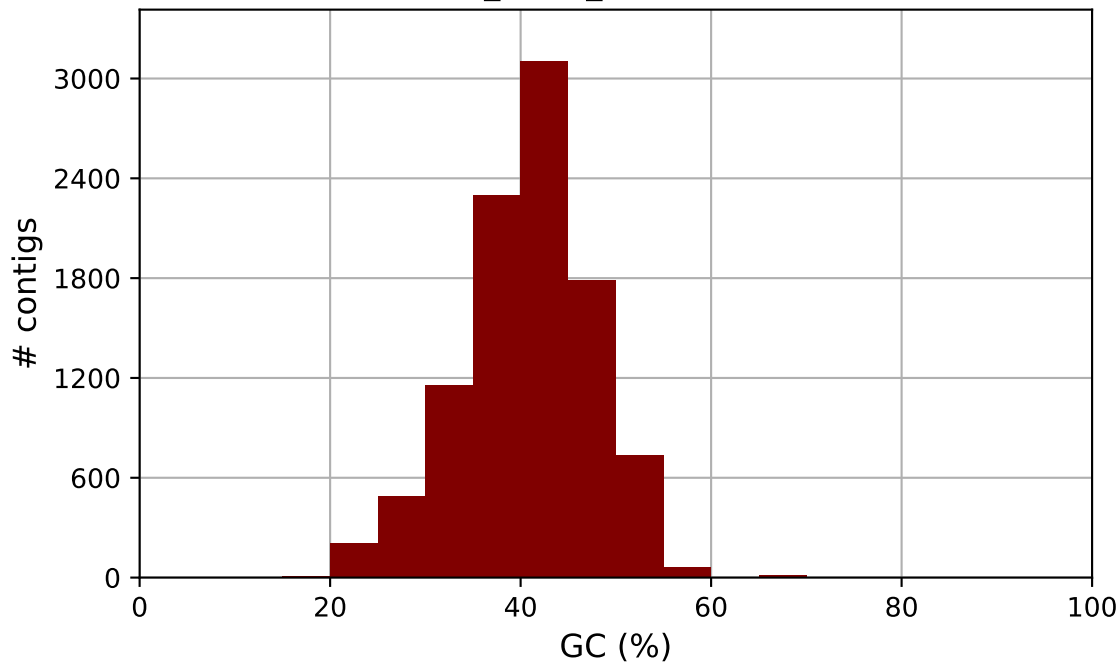
NEK\_clone\_3 GC content



NEK\_clone\_4 GC content

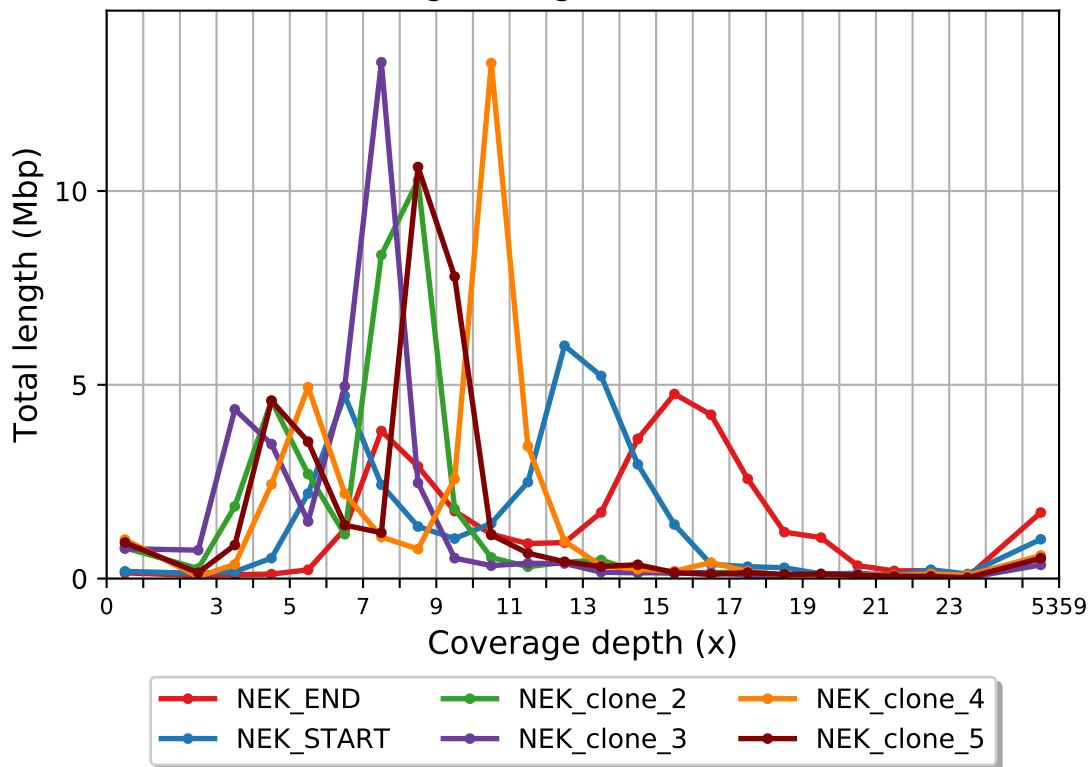


NEK\_clone\_5 GC content

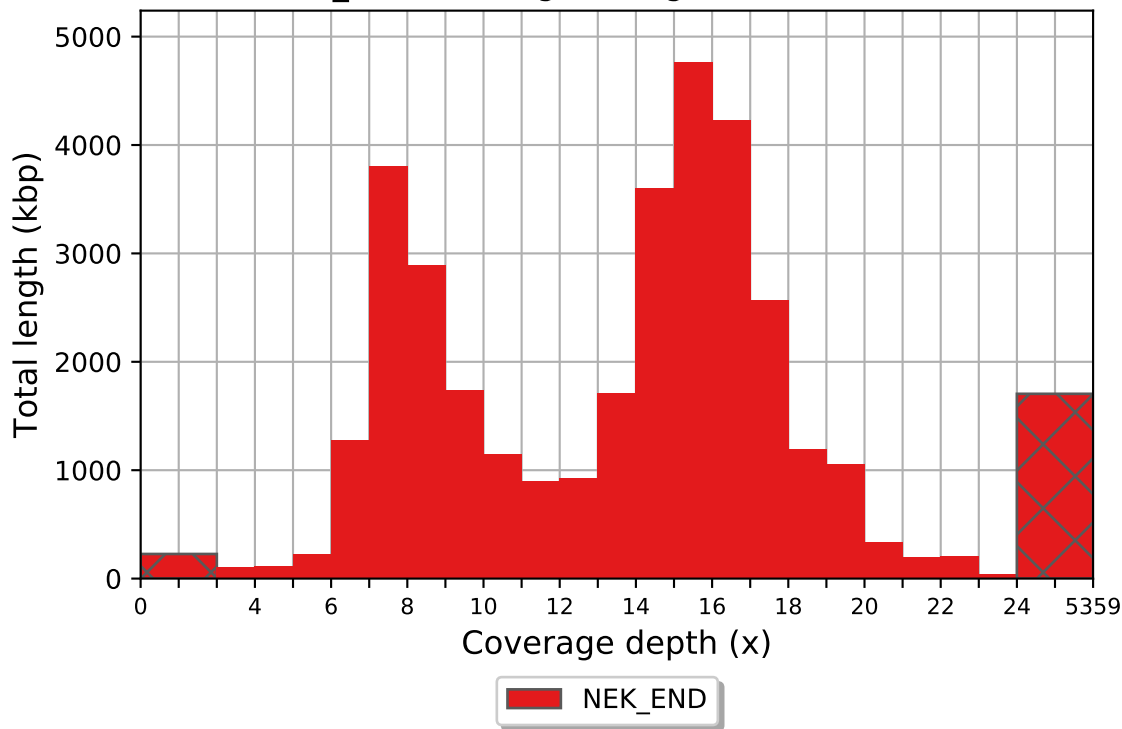


NEK\_clone\_5

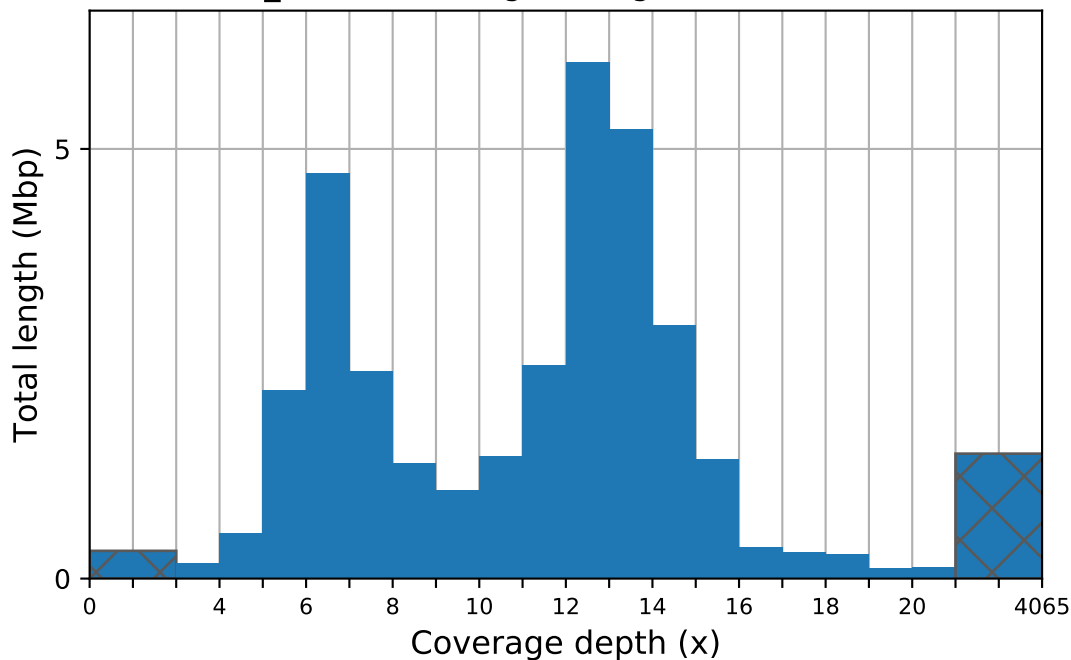
Coverage histogram (bin size: 1x)



NEK\_END coverage histogram (bin size: 1x)



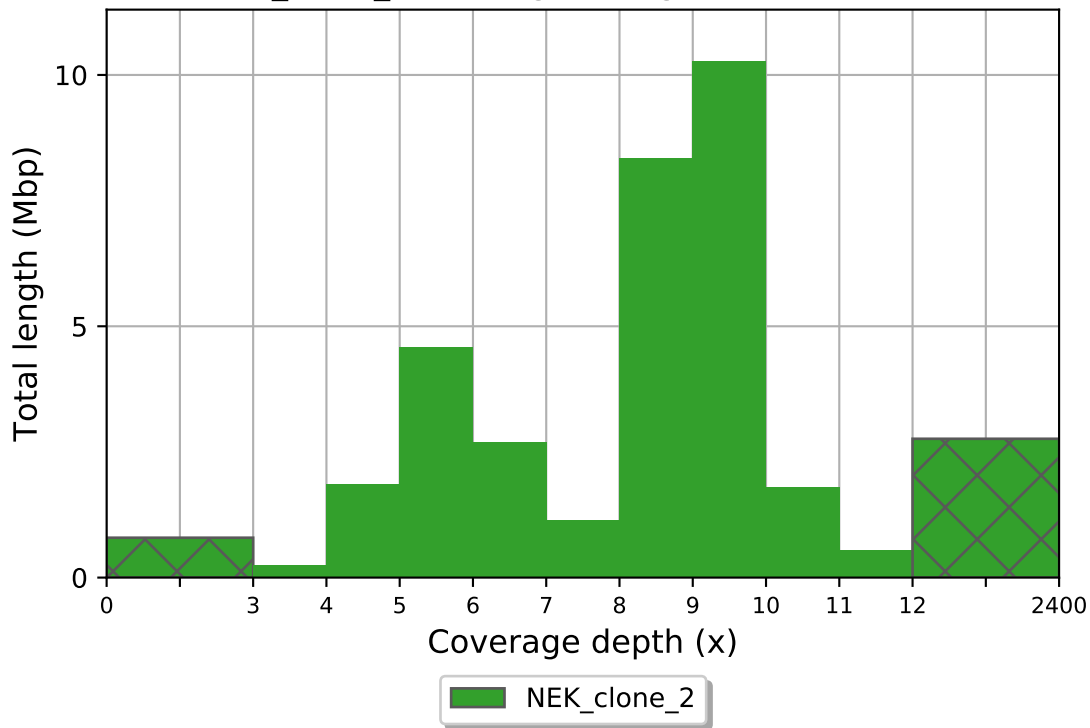
NEK\_START coverage histogram (bin size: 1x)



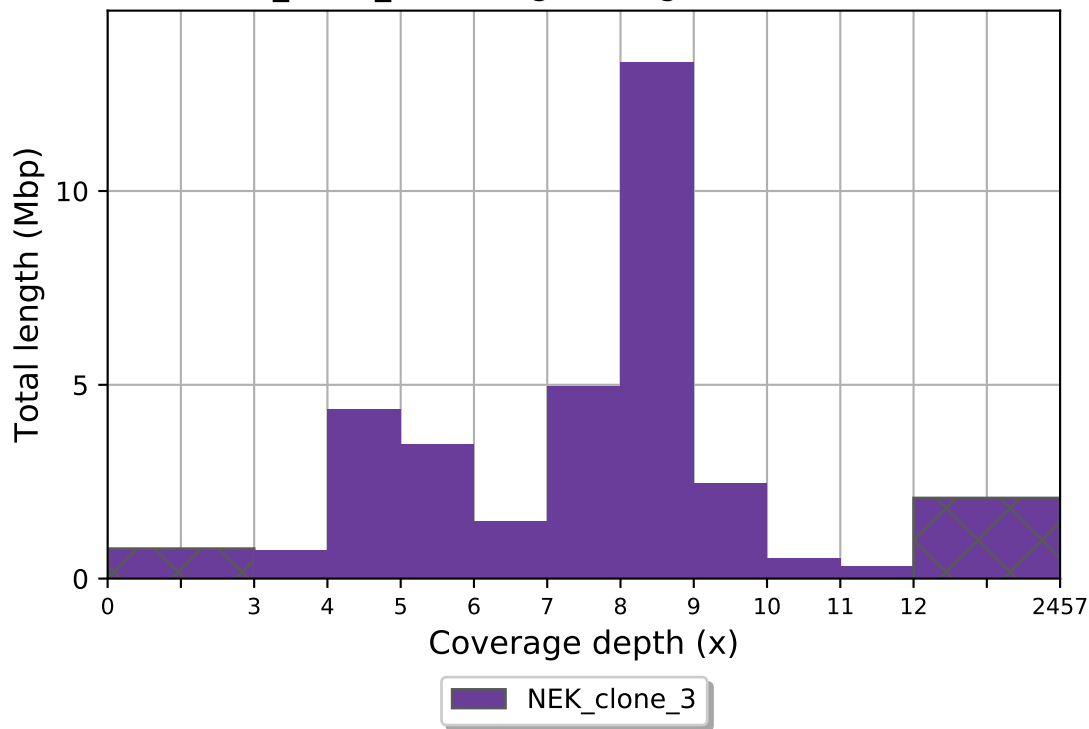
NEK\_START



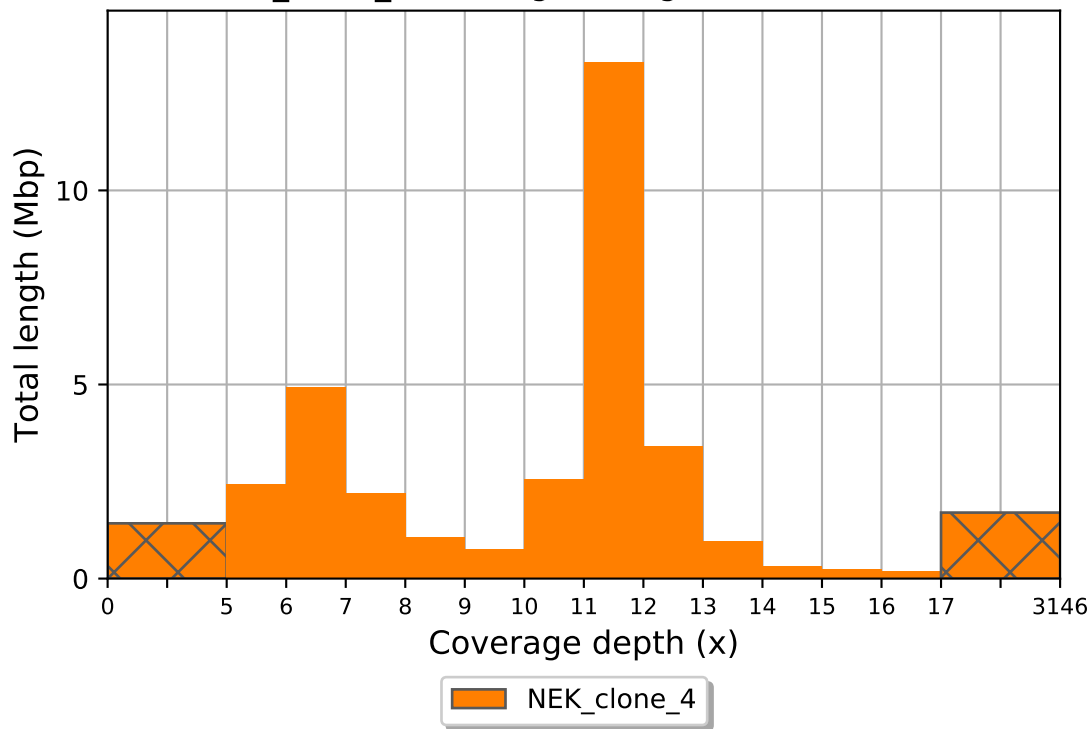
NEK\_clone\_2 coverage histogram (bin size: 1x)



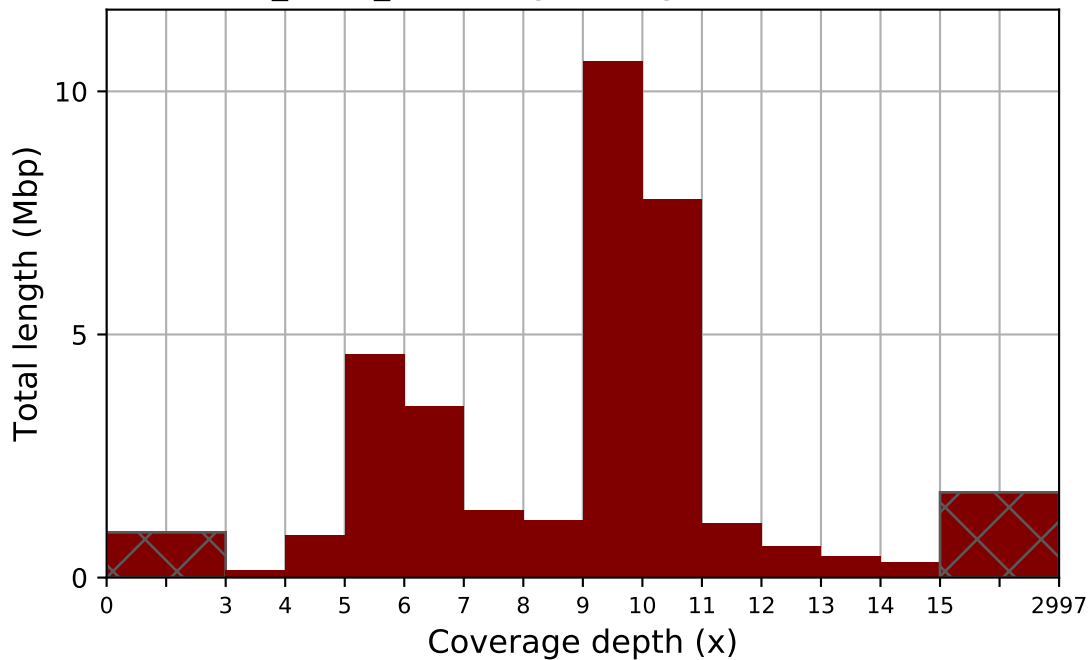
NEK\_clone\_3 coverage histogram (bin size: 1x)



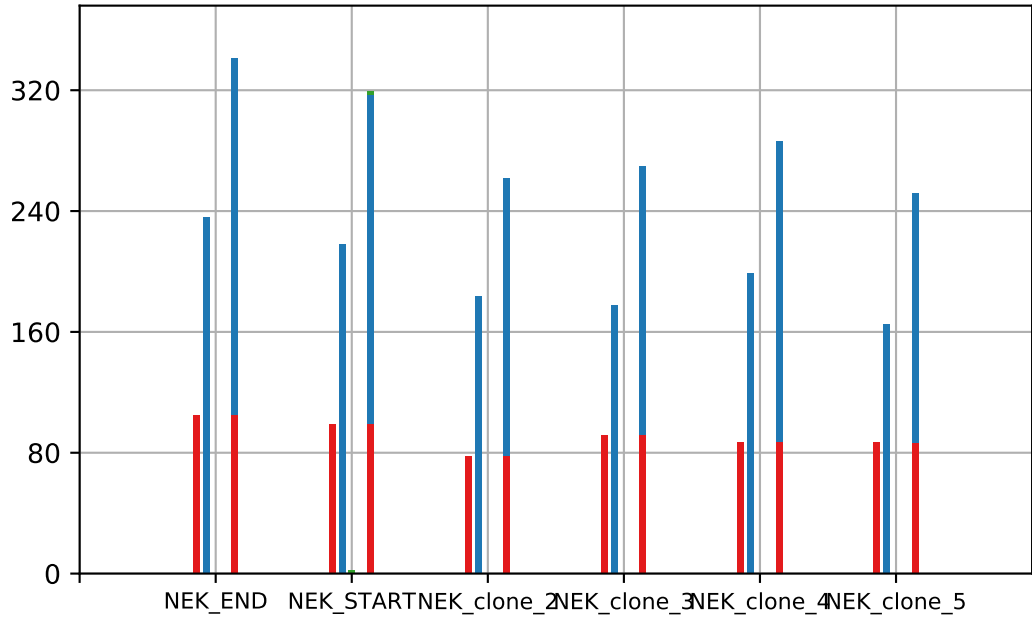
NEK\_clone\_4 coverage histogram (bin size: 1x)



NEK\_clone\_5 coverage histogram (bin size: 1x)



## Misassemblies



# relocations

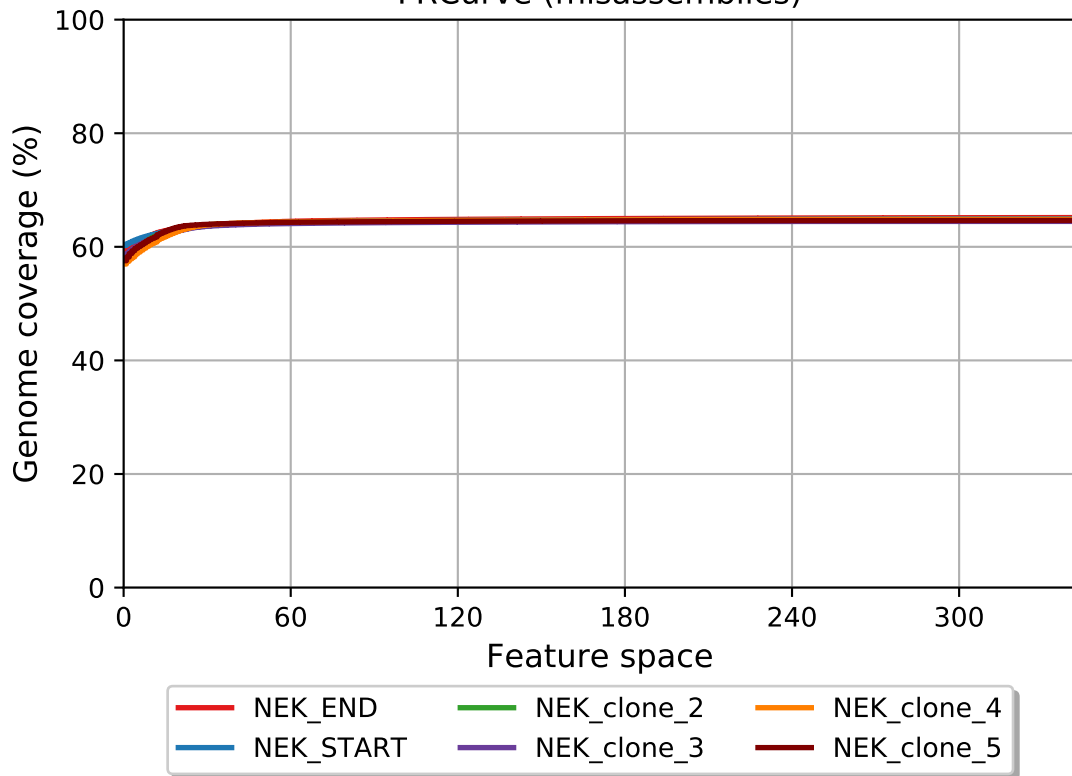


# translocations

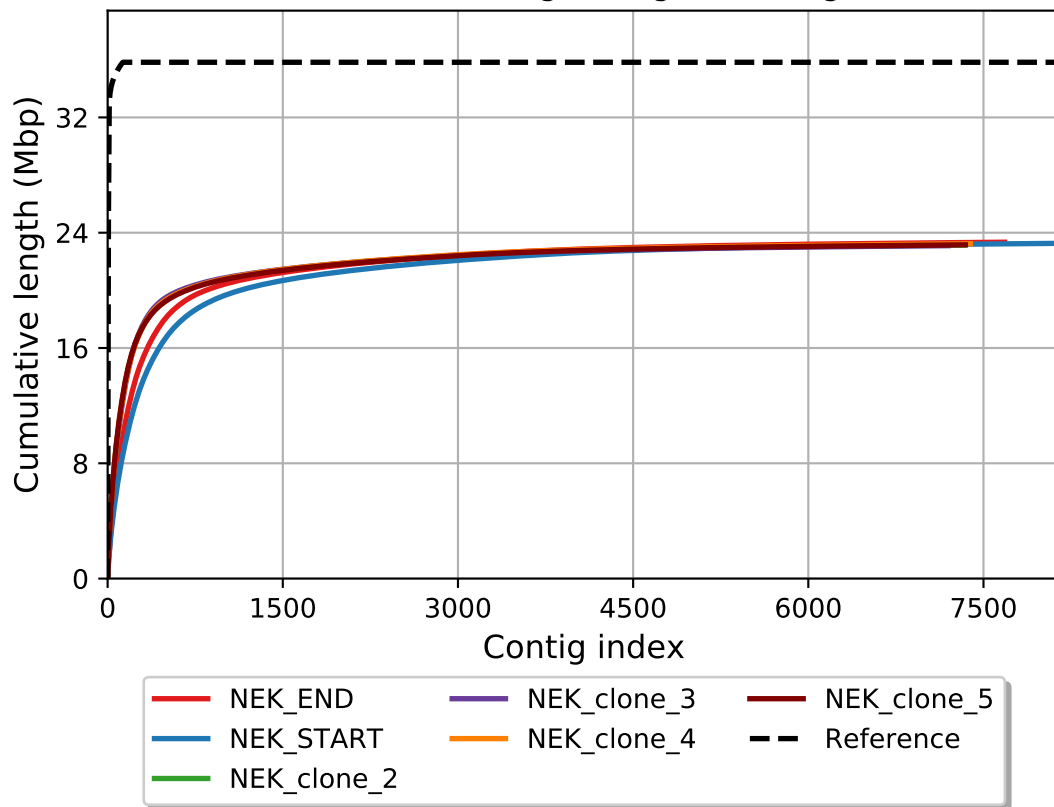


# inversions

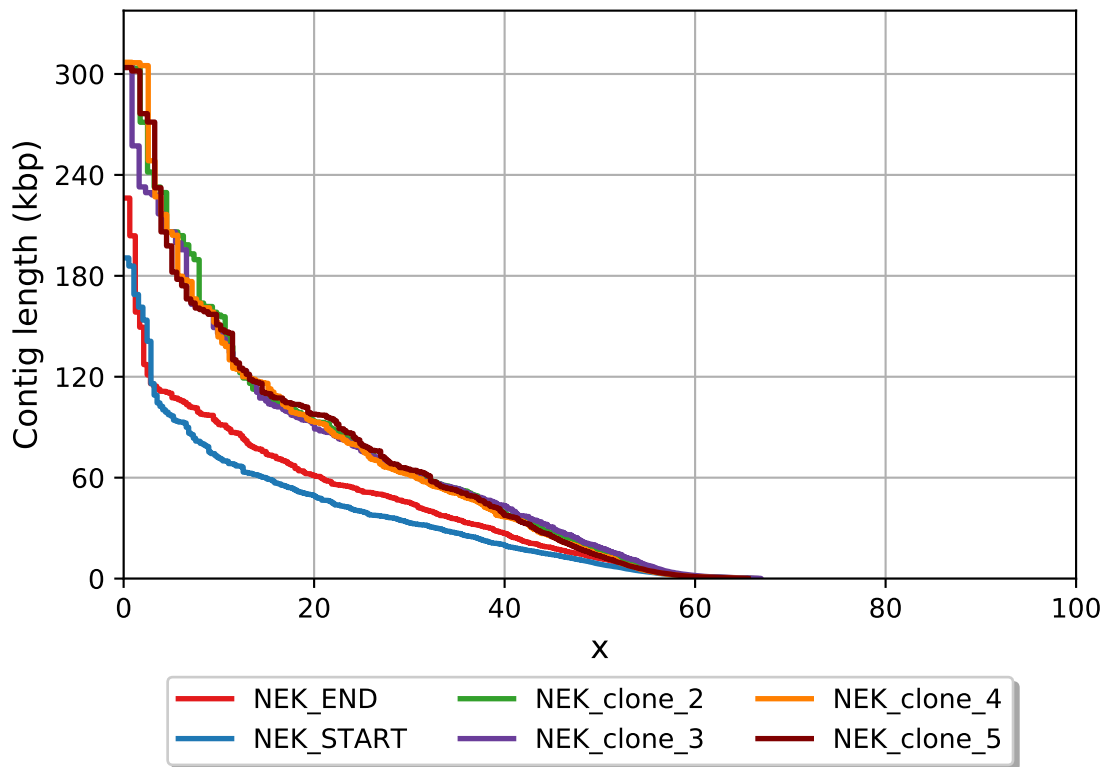
FRCurve (misassemblies)



Cumulative length (aligned contigs)

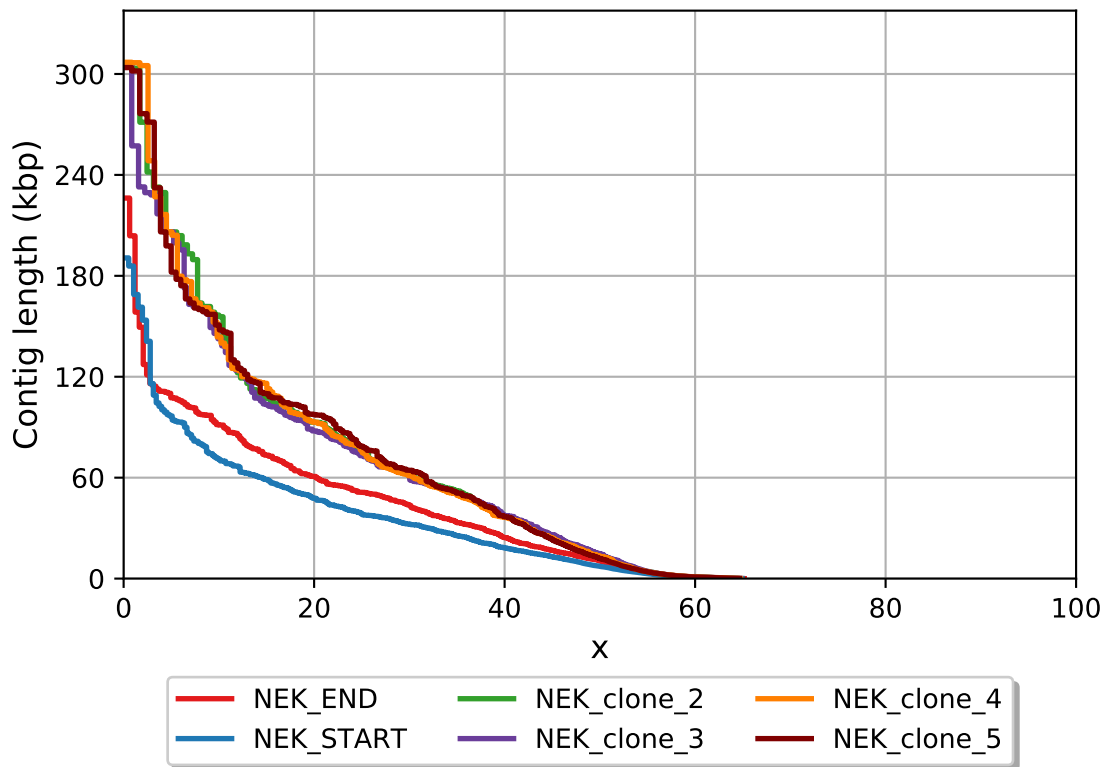


NAx



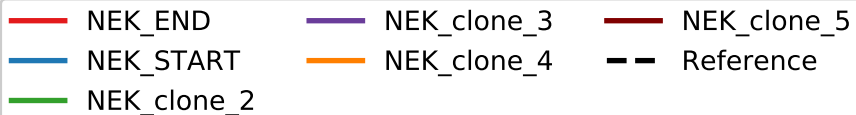
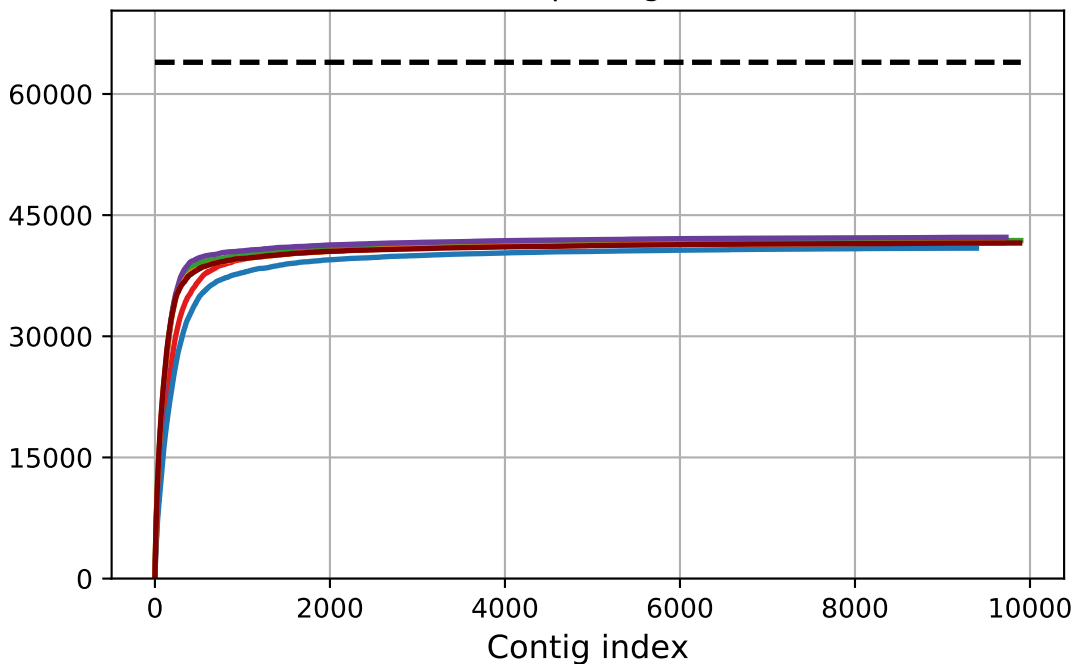


# NGAx

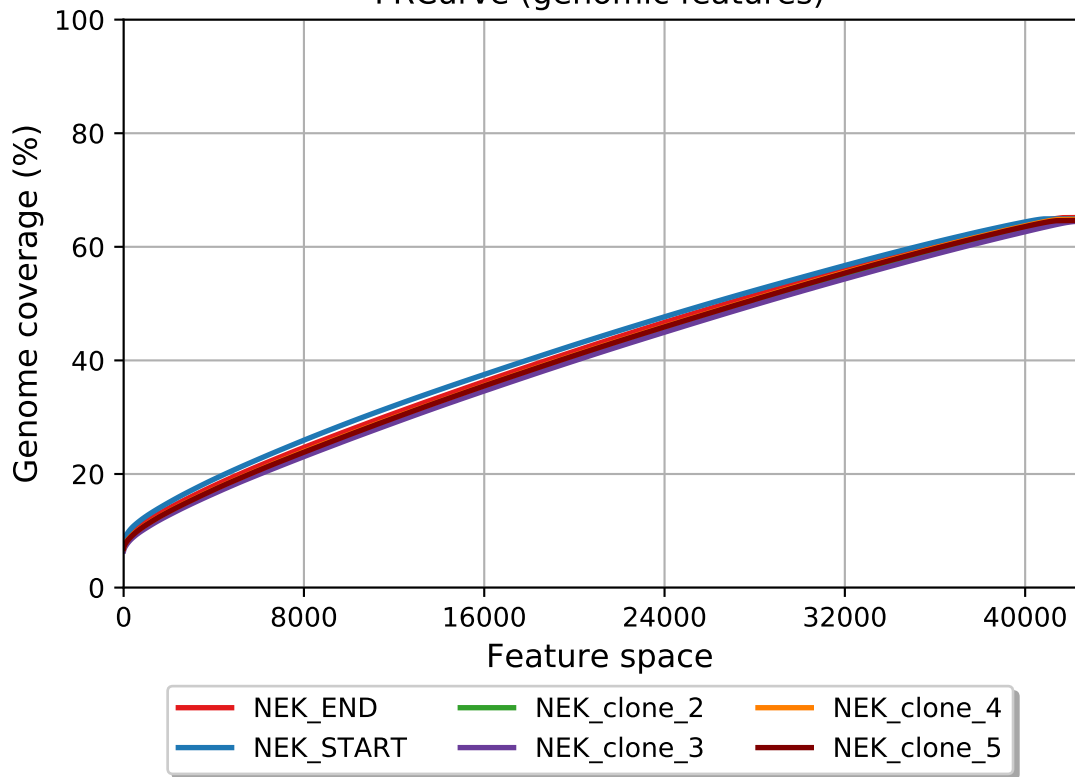


Cumulative # complete genomic features

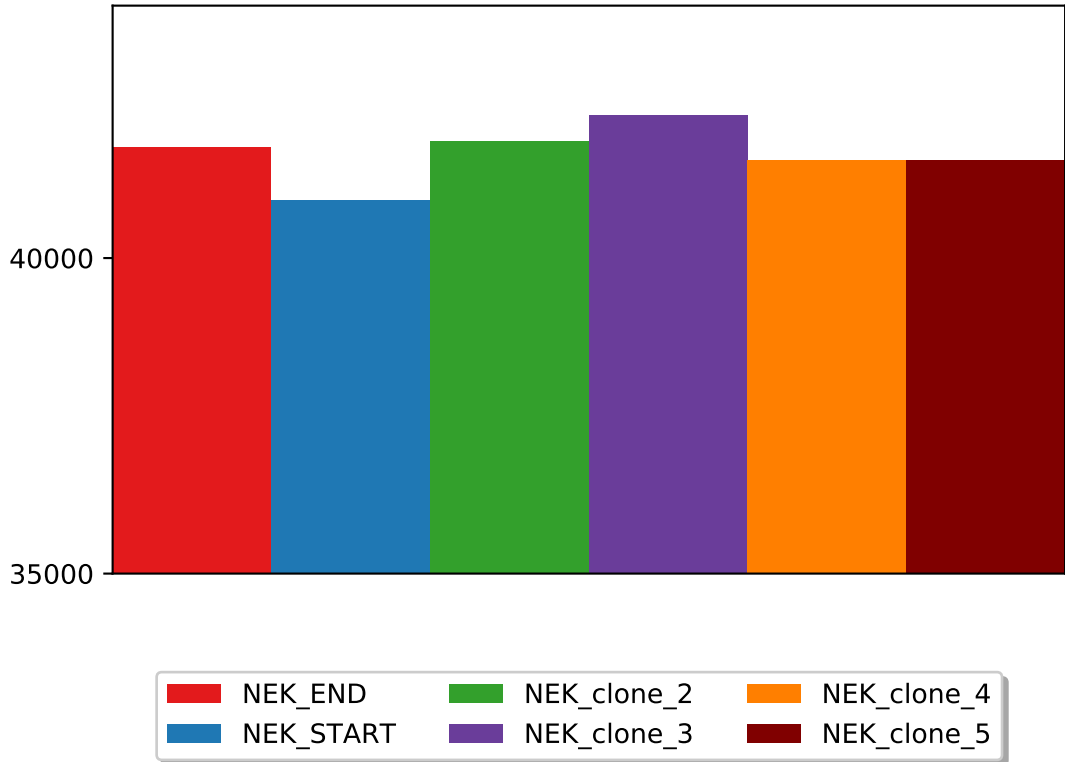
Cumulative # complete genomic features



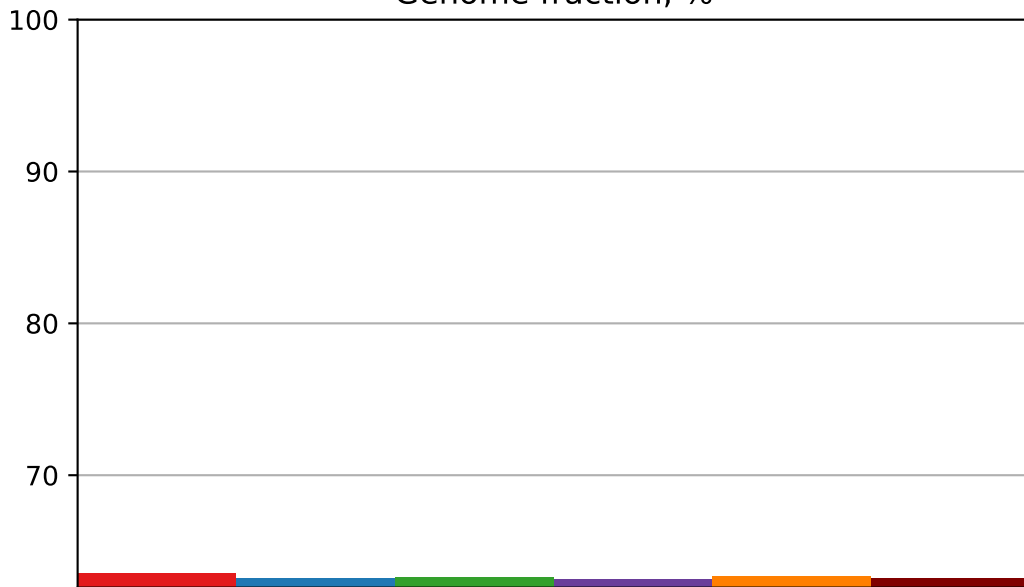
FRCurve (genomic features)



# complete genomic features



Genome fraction, %



<span style="color: red;">■</span> NEK_END	<span style="color: green;">■</span> NEK_clone_2	<span style="color: orange;">■</span> NEK_clone_4
<span style="color: blue;">■</span> NEK_START	<span style="color: purple;">■</span> NEK_clone_3	<span style="color: darkred;">■</span> NEK_clone_5