

Report

	69-1	131-1	117-2	4-2	7-2	4-1	134-2	79-2	134-1	80-1	7-1	11-1
# contigs (>= 0 bp)	3077	3651	2810	2762	2892	2886	3977	3053	3142	4374	2512	3368
# contigs (>= 1000 bp)	3077	3651	2810	2762	2892	2886	3977	3053	3142	4374	2512	3368
# contigs (>= 5000 bp)	3034	3583	2764	2692	2847	2824	3917	3003	3093	4298	2476	3300
# contigs (>= 10000 bp)	2652	2975	2352	2260	2489	2400	3441	2601	2669	3794	2135	2858
# contigs (>= 25000 bp)	2112	2176	1835	1712	1928	1878	2732	2011	2063	3044	1700	2235
# contigs (>= 50000 bp)	1724	1723	1478	1377	1544	1571	2205	1619	1658	2419	1396	1801
Total length (>= 0 bp)	727390278	741972642	732119004	737644925	732453614	730824717	729140748	730361544	731863475	720959413	732454342	728550441
Total length (>= 1000 bp)	727390278	741972642	732119004	737644925	732453614	730824717	729140748	730361544	731863475	720959413	732454342	728550441
Total length (>= 5000 bp)	727194307	741670402	731911910	737325828	732249698	730549578	728872266	730138754	731653955	720617167	732301371	728249213
Total length (>= 10000 bp)	724432183	737367207	728953094	734248805	729675154	727452559	725484046	727226685	728608772	716985763	729824896	725125738
Total length (>= 25000 bp)	715606484	724360480	720350958	725265239	720369086	718975837	713767746	717606344	718779490	704573330	722552085	714885638
Total length (>= 50000 bp)	701784840	708516718	707651040	713393073	706760228	707906448	695242695	703771067	704116687	682004702	711527268	699240390
# contigs	3077	3647	2808	2759	2890	2883	3973	3051	3134	4370	2509	3365
Largest contig	6080511	5589066	5059334	6376848	4099264	5635124	3835876	6658276	4138056	3238833	5851261	4525370
Total length	727390278	741963499	732113747	737637241	732448405	730816425	729131624	730357166	731842804	720948860	732447291	728542858
Reference length	734057086	734057086	734057086	734057086	734057086	734057086	734057086	734057086	734057086	734057086	734057086	734057086
GC (%)	40.59	40.72	40.73	40.71	40.69	40.66	40.75	40.62	40.71	40.49	40.69	40.56
Reference GC (%)	40.84	40.84	40.84	40.84	40.84	40.84	40.84	40.84	40.84	40.84	40.84	40.84
N50	708738	737055	903899	971613	845096	802725	475444	742721	747064	404886	942347	624727
NG50	701776	760902	903202	981023	844726	797058	470988	740010	743484	395849	942347	620071
N90	135723	114467	158734	173477	148107	151668	98008	142636	131389	90072	172910	124149
NG90	125013	127005	152043	182060	145239	147423	93985	137087	128389	75983	170443	114600
L50	292	273	227	205	250	259	426	278	274	514	217	316
LG50	297	267	228	203	251	261	432	281	276	530	217	321
L90	1170	1197	957	864	1004	1034	1668	1091	1123	1937	878	1260
LG90	1216	1139	969	846	1014	1053	1714	1115	1138	2079	887	1301
# misassemblies	3508	4329	4854	4404	4256	4021	4825	3740	4250	2608	4200	3218
# misassembled contigs	1153	1098	1136	1014	1134	1092	1490	1083	1166	1167	1024	1037
Misassembled contigs length	572944670	550260247	610866120	627209679	606086631	592002443	520433751	571182881	584385643	442684353	620929268	537255616
# local misassemblies	56036	52375	46690	48857	49280	50934	45197	53227	49134	62158	49627	59404
# scaffold gap ext. mis.	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
# possible TEs	3302	4204	3762	3800	3518	3660	3730	3328	3534	2306	3564	2886
# unaligned mis. contigs	600	970	590	630	617	587	687	632	610	973	544	700
# unaligned contigs	395 + 2654 part	548 + 3009 part	322 + 2407 part	439 + 2273 part	357 + 2478 part	383 + 2439 part	359 + 3441 part	445 + 2575 part	376 + 2675 part	650 + 3708 part	278 + 2186 part	557 + 2783 part
Unaligned length	154149946	178050369	111106346	124494633	124847277	131473023	107583242	145692301	124762382	229390229	124267298	182815162
Genome fraction (%)	78.996	76.930	84.922	84.044	83.409	82.319	84.886	80.509	83.221	67.956	83.448	75.300
Duplication ratio	0.989	0.999	0.997	0.994	0.993	0.992	0.998	0.990	0.994	0.986	0.993	0.988
# 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
# mismatches per 100 kbp	1598.75	1411.75	1132.46	1240.50	1297.78	1373.31	1069.98	1512.73	1271.78	1868.20	1311.65	1726.82
# indels per 100 kbp	1360.35	1008.41	995.35	1125.20	1166.51	1209.13	936.28	1329.31	1084.02	1498.52	1164.84	1409.92
# genomic features	5675 + 16400 part	7227 + 14877 part	8524 + 13870 part	7689 + 14668 part	7493 + 14805 part	7003 + 15232 part	8783 + 13530 part	6174 + 15935 part	7620 + 14634 part	3825 + 17584 part	7332 + 14948 part	4863 + 17004 part
Largest alignment	1823612	2231101	2195961	2781976	1761859	2340443	1698873	2384437	2042573	1304457	2243072	1541261
Total aligned length	573096833	563763739	620809739	612988975	607409964	599170757	621355180	584535579	606908341	491501885	608014583	545652612
NA50	220342	180572	270130	279257	253015	259311	209441	235007	245116	105372	265102	180262
NGA50	217551	183503	269002	281643	252421	255515	206967	232602	244876	100537	264148	177143
NA90	-	-	-	-	-	-	-	-	-	-	-	-
NGA90	-	-	-	-	-	-	-	-	-	-	-	-
LA50	830	951	712	678	744	746	923	780	779	1485	702	953
LGA50	845	929	716	672	747	753	935	788	783	1549	705	968
LA90	-	-	-	-	-	-	-	-	-	-	-	-
LGA90	-	-	-	-	-	-	-	-	-	-	-	-

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	69-1	131-1	117-2	4-2	7-2	4-1	134-2	79-2	134-1	80-1	7-1	11-1
# misassemblies	3508	4329	4854	4404	4256	4021	4825	3740	4250	2608	4200	3218
# contig misassemblies	3508	4329	4854	4404	4256	4021	4825	3740	4250	2608	4200	3218
# c. relocations	1673	1611	1824	1774	1799	1706	1721	1649	1723	1366	1750	1599
# c. translocations	1810	2696	3004	2605	2434	2294	3085	2068	2507	1221	2425	1601
# c. inversions	25	22	26	25	23	21	19	23	20	21	25	18
# scaffold misassemblies	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
# s. translocations	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
# misassembled contigs	1153	1098	1136	1014	1134	1092	1490	1083	1166	1167	1024	1037
Misassembled contigs length	572944670	550260247	610866120	627209679	606086631	592002443	520433751	571182881	584385643	442684353	620929268	537255616
# local misassemblies	56036	52375	46690	48857	49280	50934	45197	53227	49134	62158	49627	59404
# scaffold gap ext. mis.	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
# possible TEs	3302	4204	3762	3800	3518	3660	3730	3328	3534	2306	3564	2886
# unaligned mis. contigs	600	970	590	630	617	587	687	632	610	973	544	700
# mismatches	9162381	7958924	7030429	7604128	7882861	8228444	6648402	8842437	7718522	9182244	7975019	9422459
# indels	7796151	5685040	6179250	6897324	7085502	7244733	5817646	7770276	6579011	7365255	7082393	7693274
# indels (<= 5 bp)	7586301	5467905	5961975	6680341	6869114	7029909	5602008	7556826	6363687	7186016	6866087	7492753
# indels (> 5 bp)	209850	217135	217275	216983	216388	214824	215638	213450	215324	179239	216306	200521
Indels length	13681330	11753609	12860768	13413043	13480079	13462638	12588124	13833690	12974594	12263336	13465894	13210611

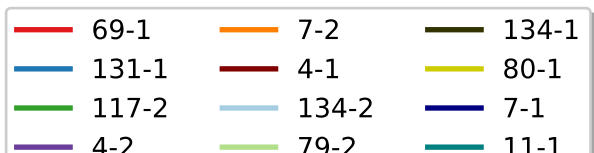
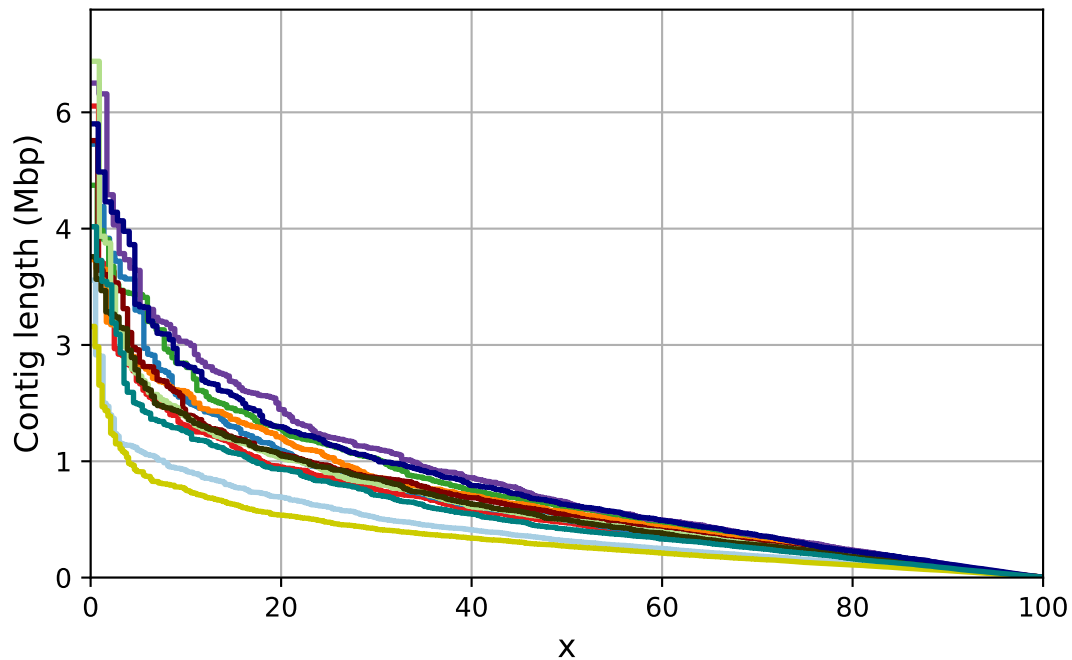
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

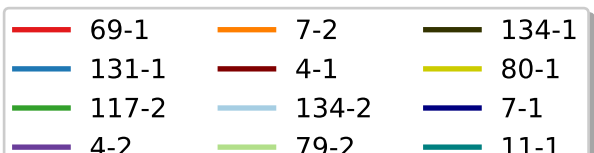
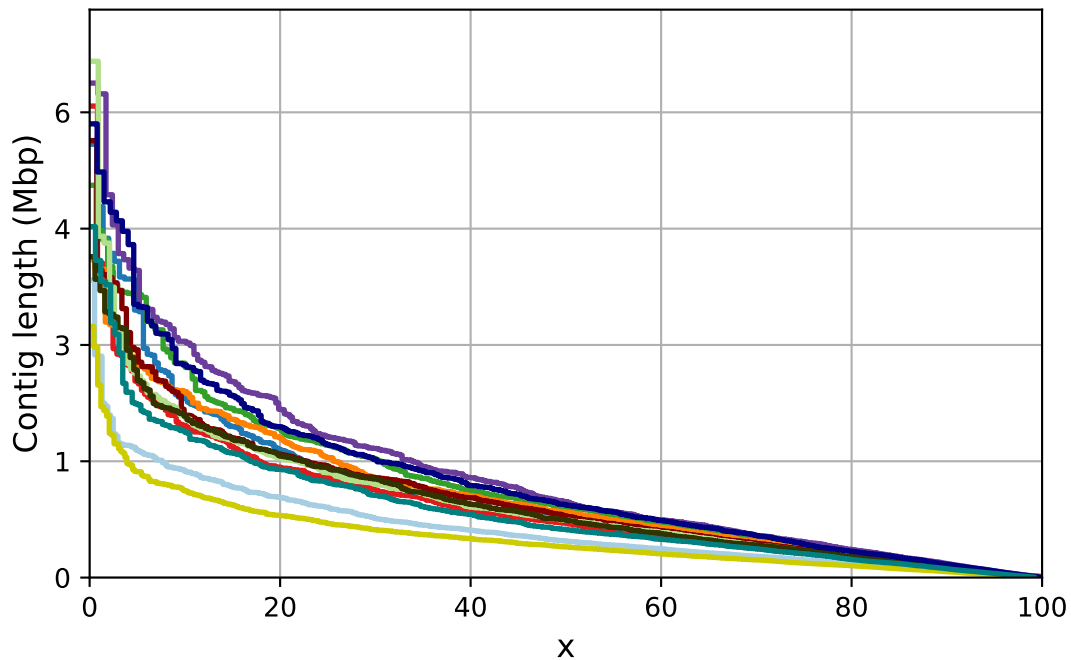
	69-1	131-1	117-2	4-2	7-2	4-1	134-2	79-2	134-1	80-1	7-1	11-1
# fully unaligned contigs	395	548	322	439	357	383	359	445	376	650	278	557
Fully unaligned length	4858813	6048042	3512706	5083785	3973564	3817010	3938691	5381483	4415133	8234029	3038114	7161291
# partially unaligned contigs	2654	3009	2407	2273	2478	2439	3441	2575	2675	3708	2186	2783
Partially unaligned length	149291133	172002327	107593640	119410848	120873713	127656013	103644551	140310818	120347249	221156200	121229184	175653871
# N's	0	0	0	0	0	0	0	0	0	0	0	0

All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

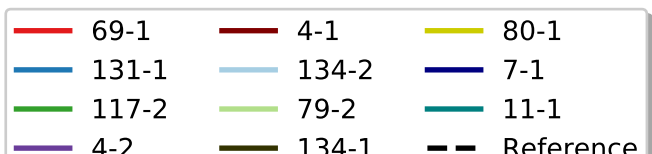
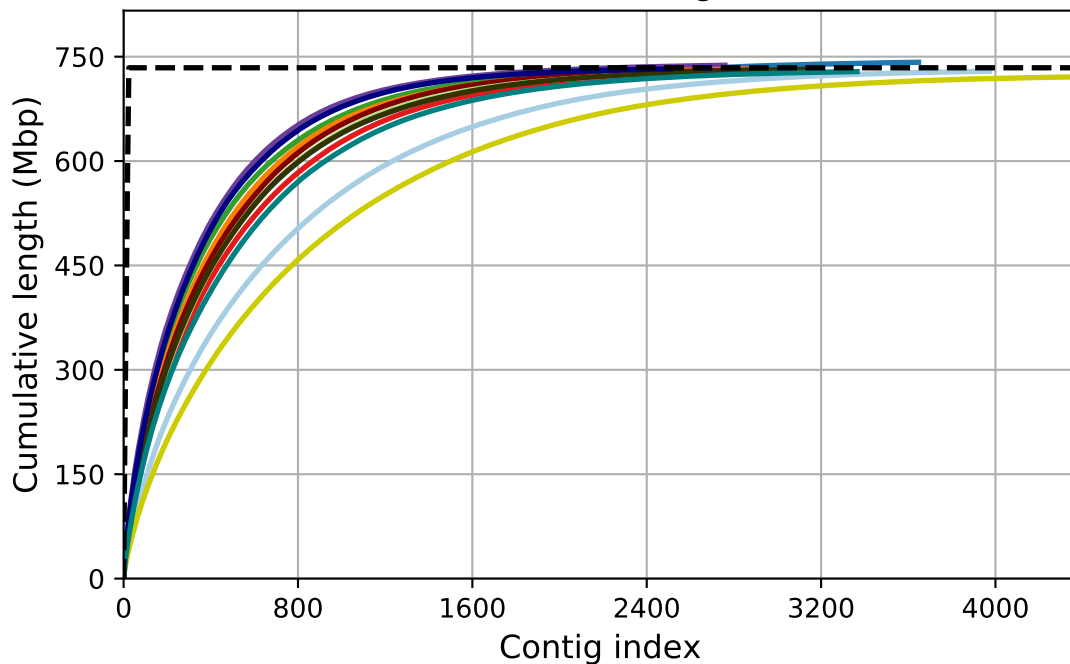
Nx



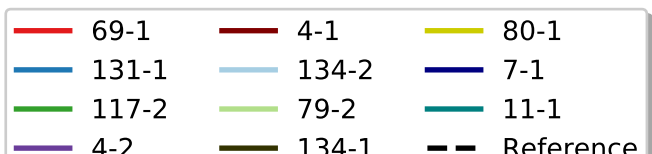
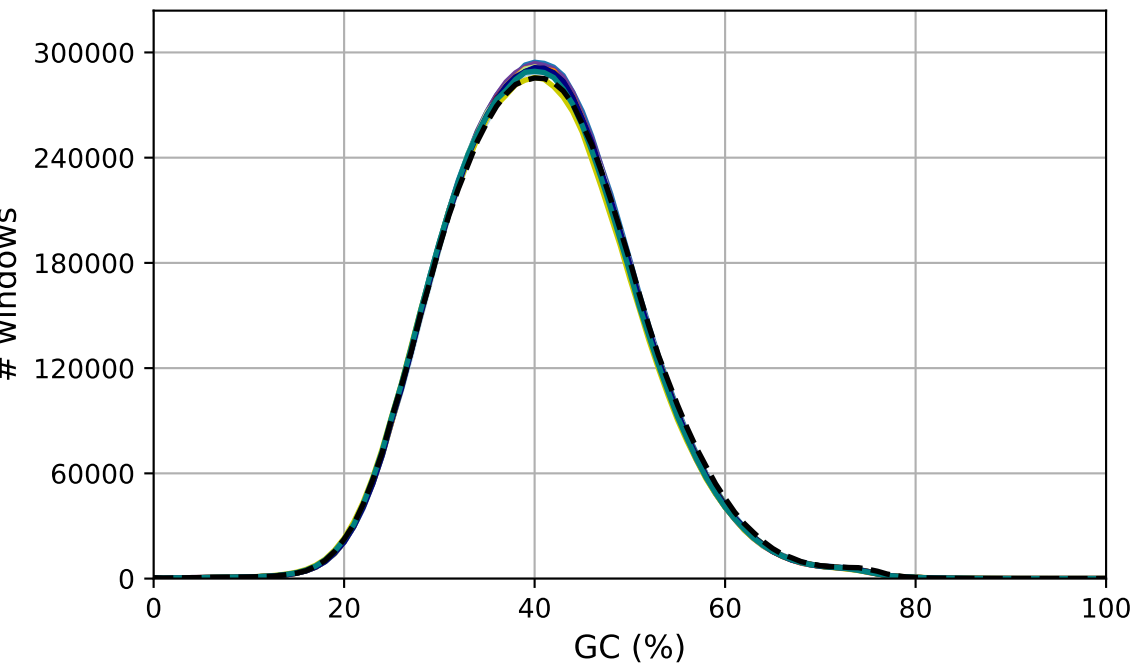
NGx



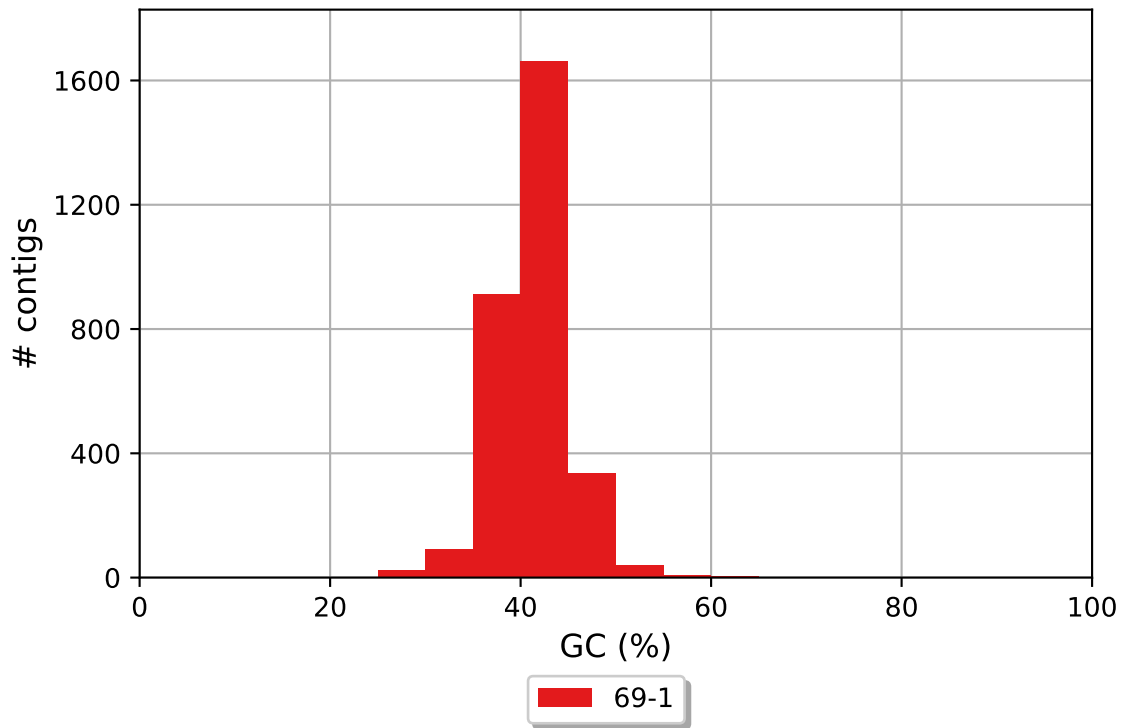
Cumulative length



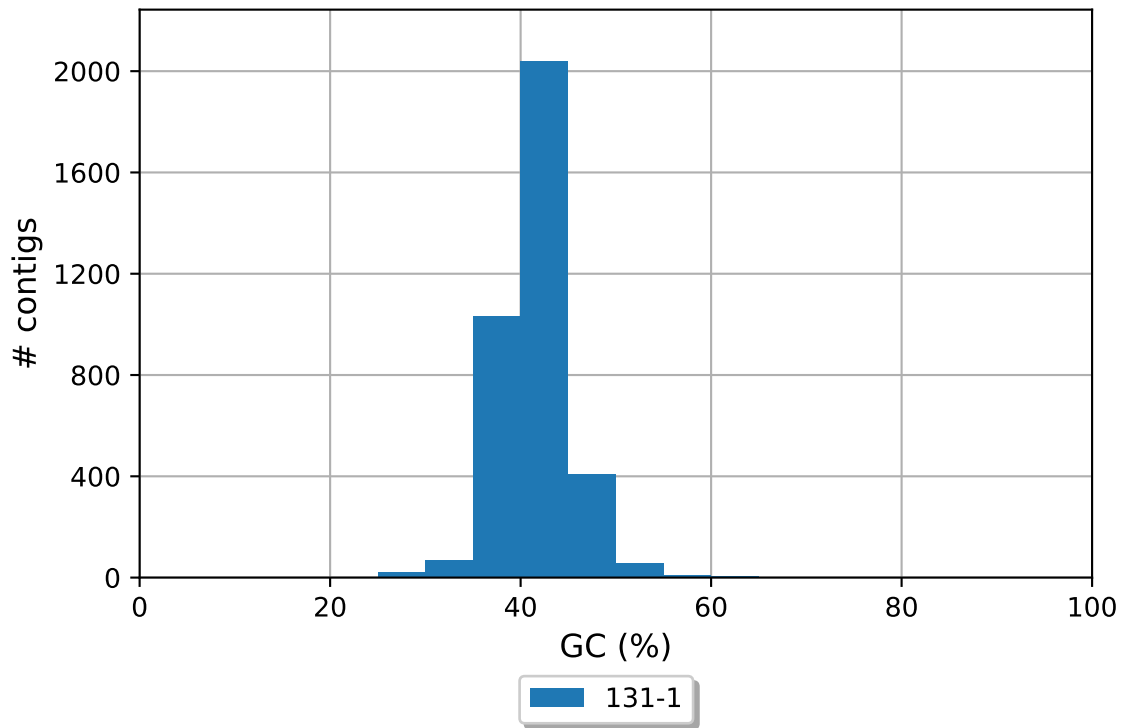
GC content



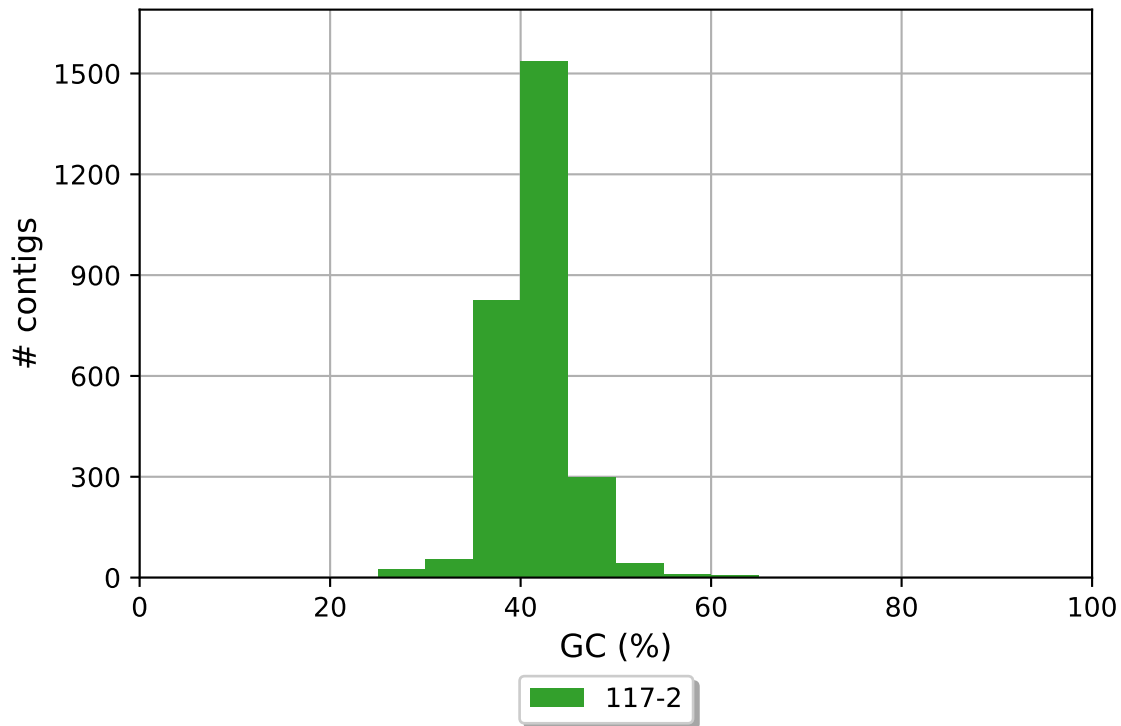
69-1 GC content



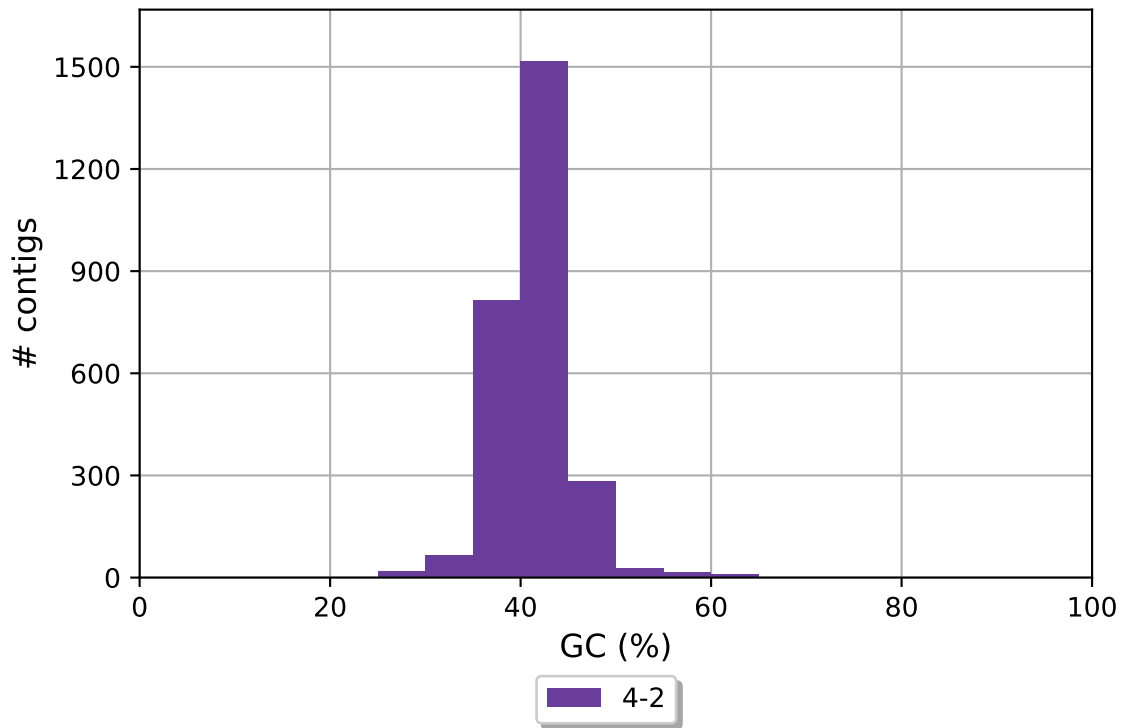
131-1 GC content



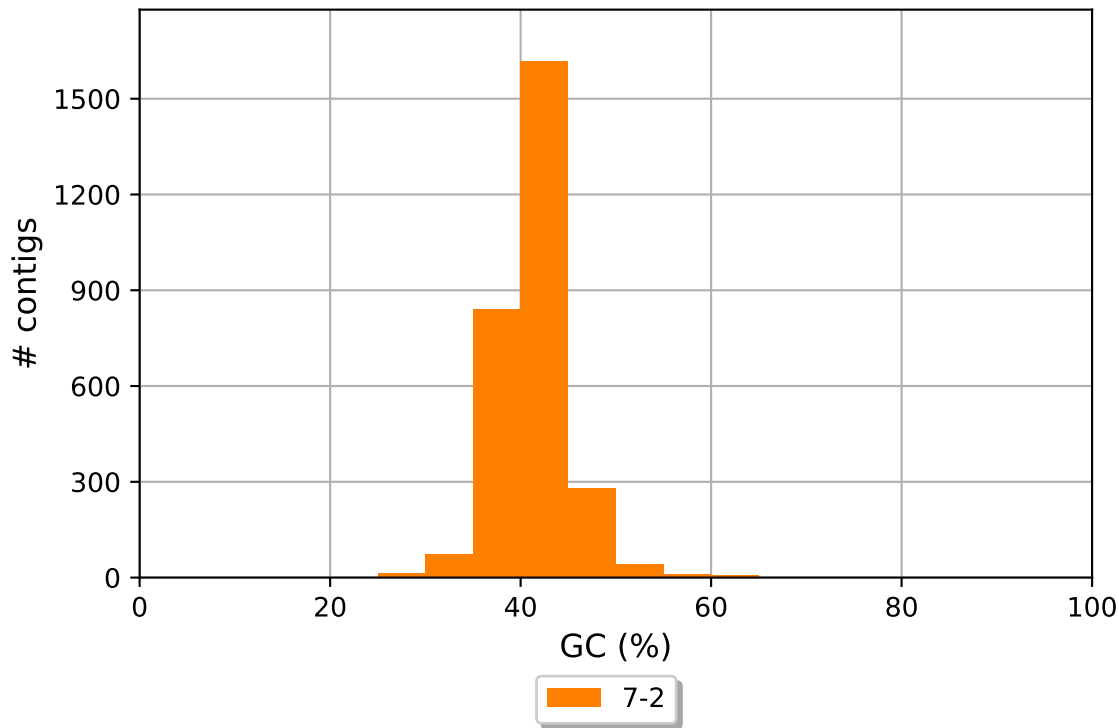
117-2 GC content



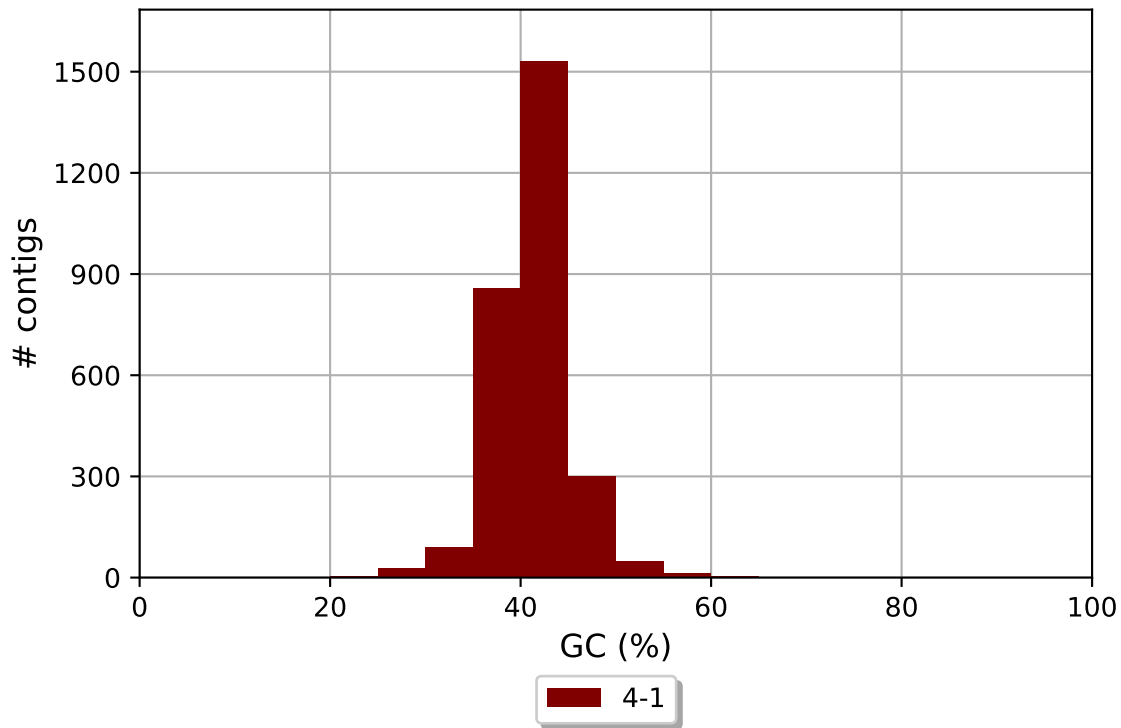
4-2 GC content



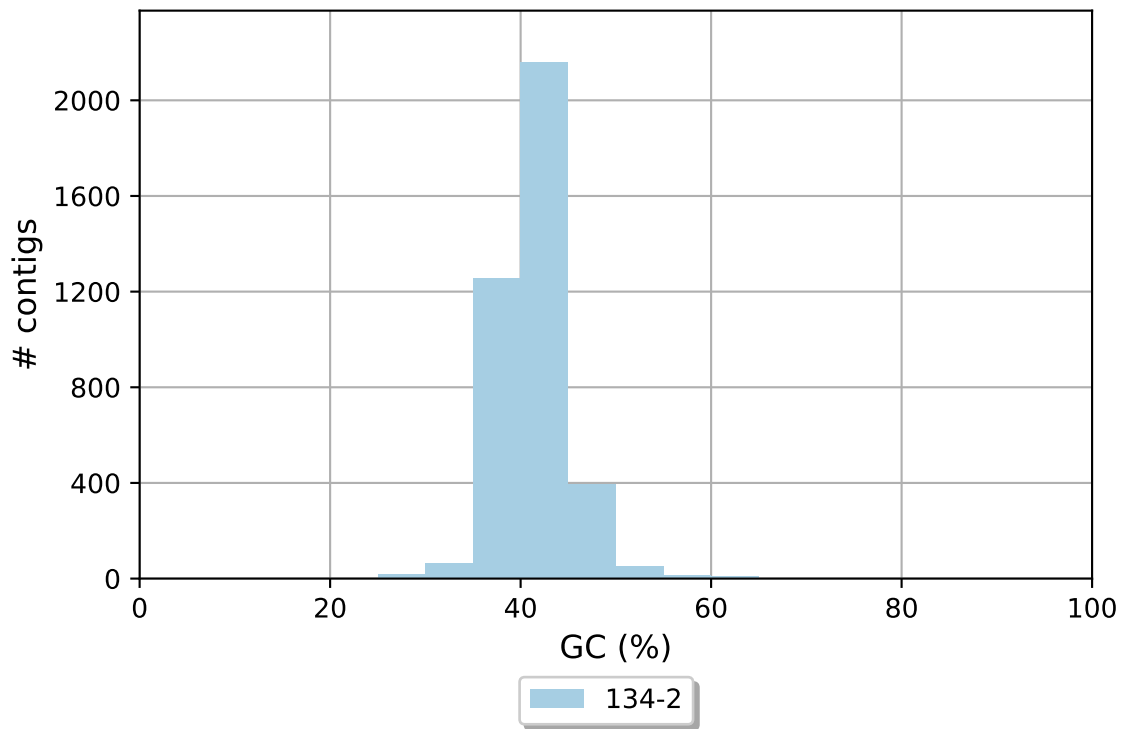
7-2 GC content



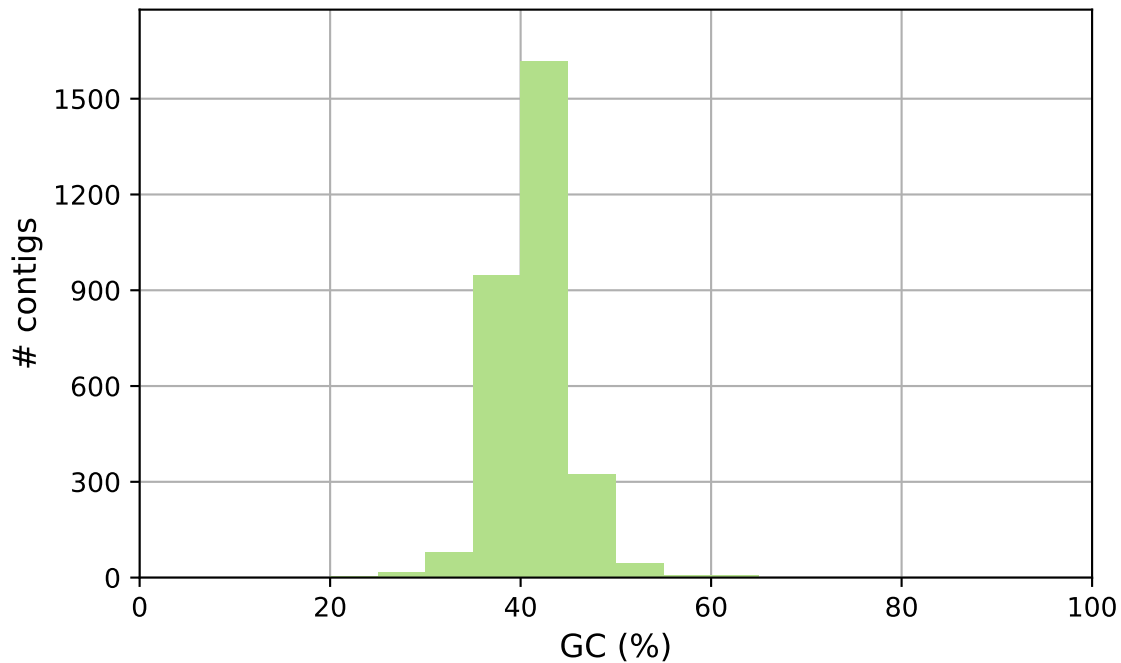
4-1 GC content



134-2 GC content

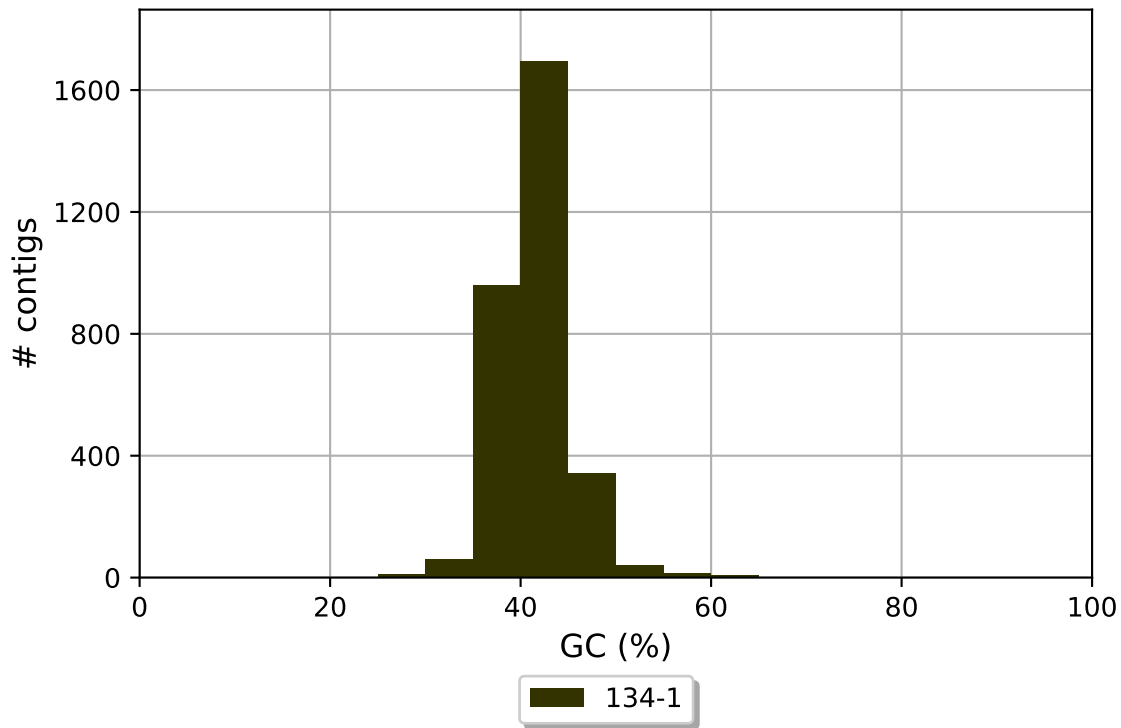


79-2 GC content

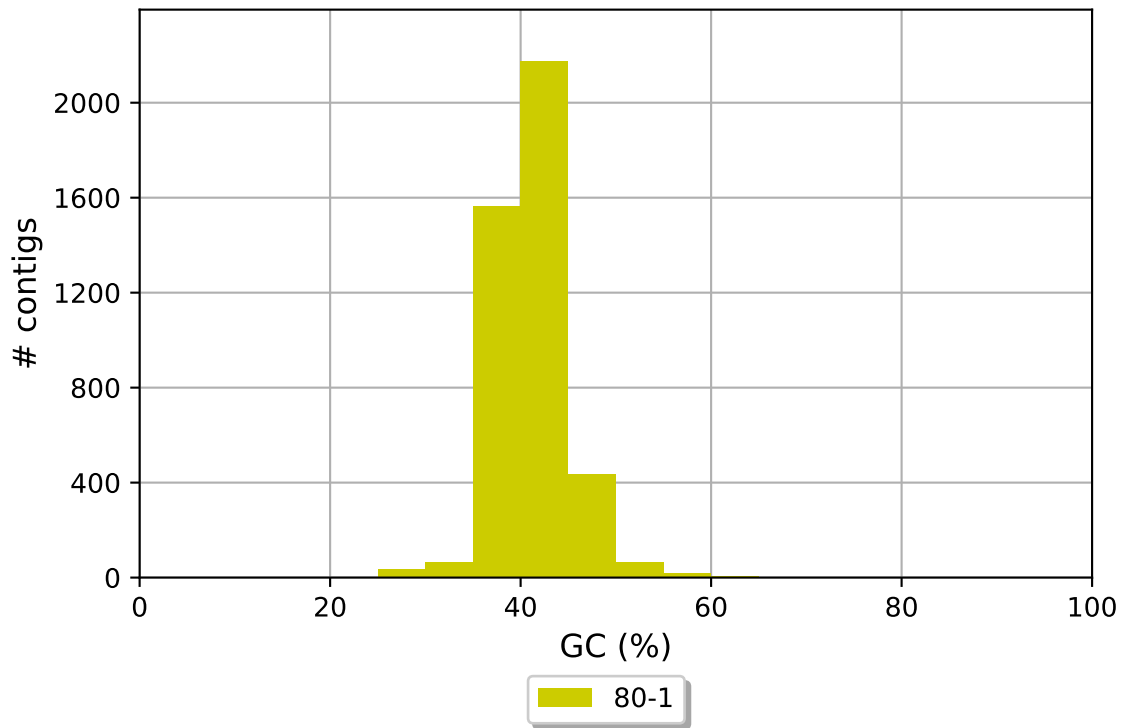


79-2

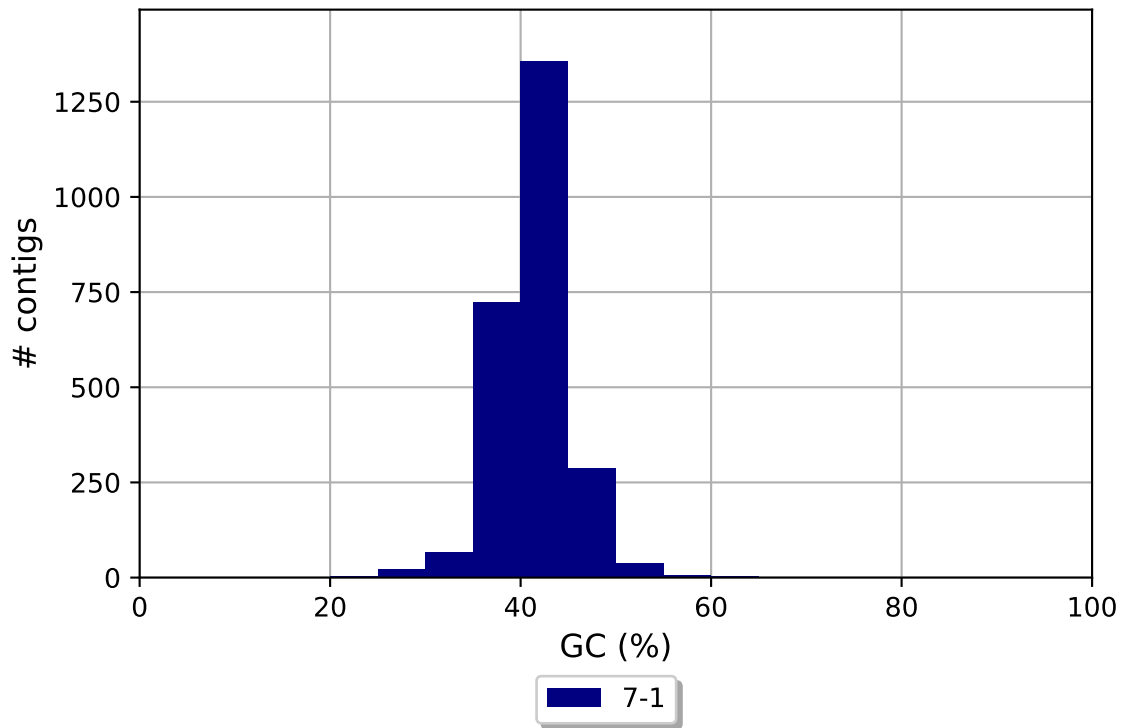
134-1 GC content



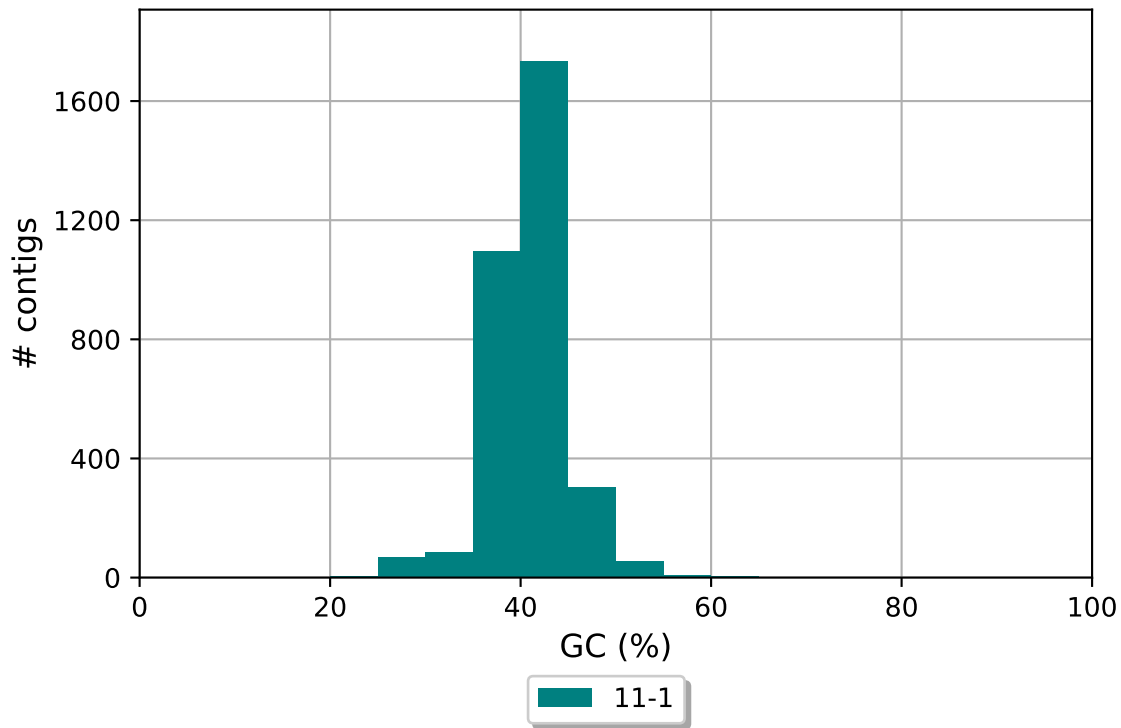
80-1 GC content



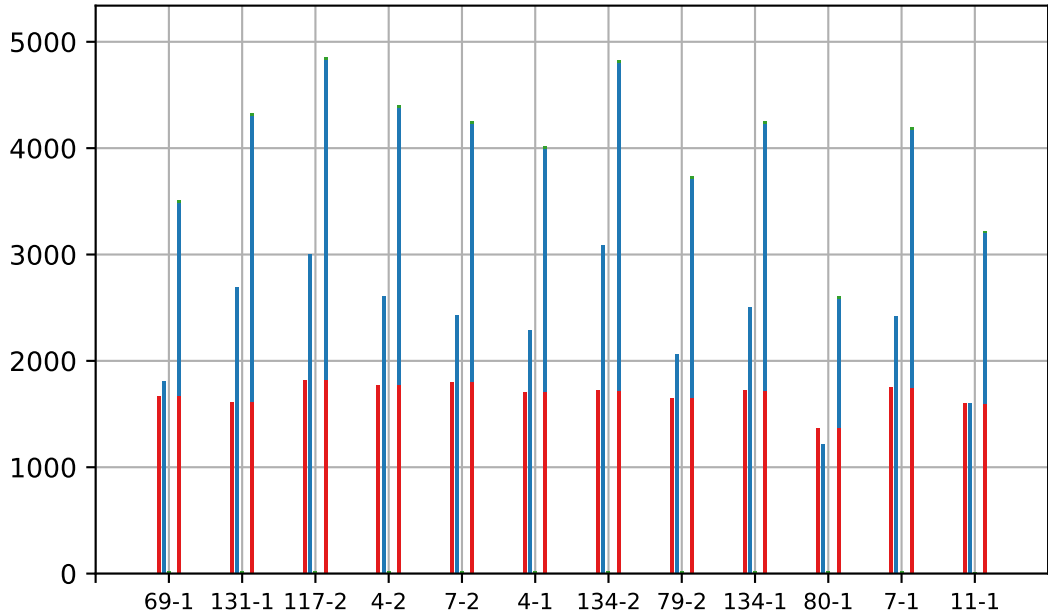
7-1 GC content



11-1 GC content

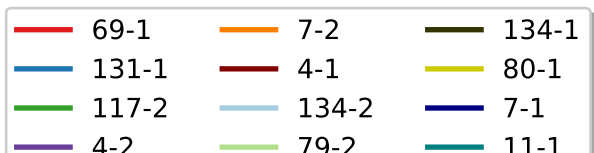
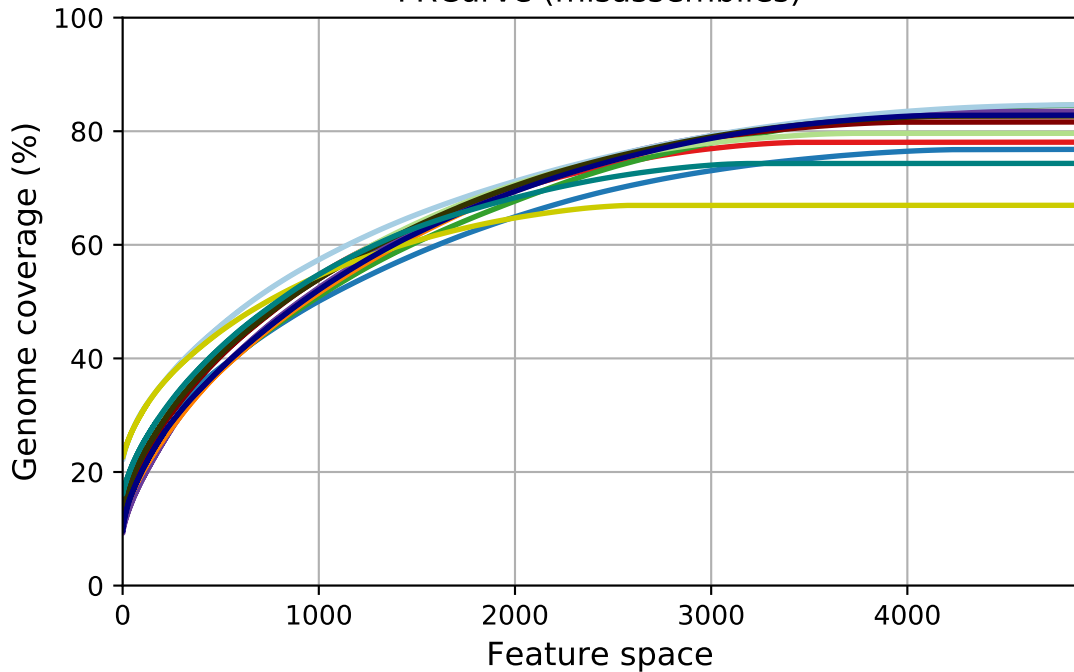


Misassemblies

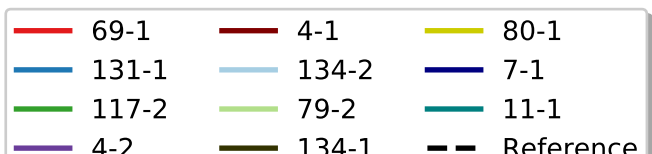
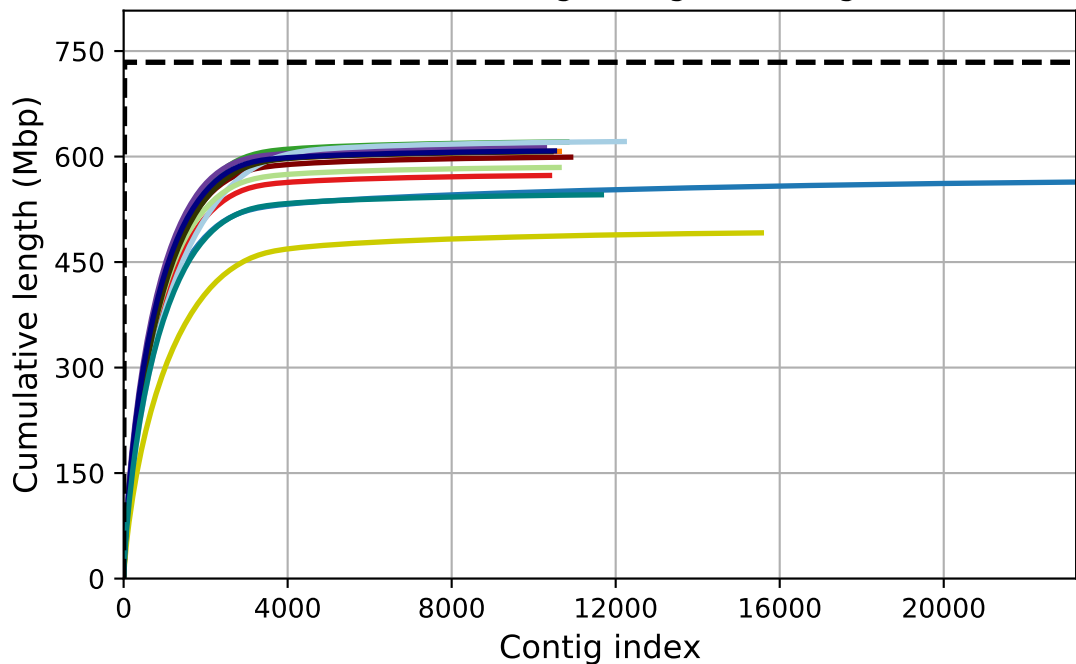


■ # relocations ■ # translocations ■ # inversions

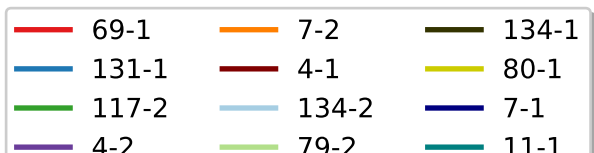
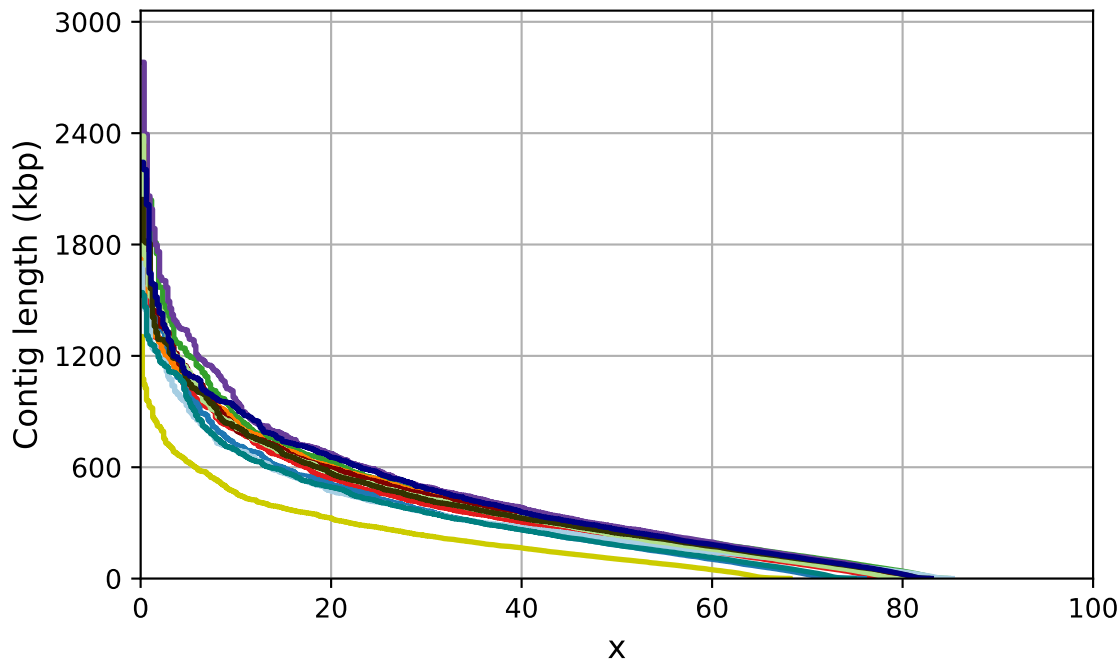
FRCurve (misassemblies)



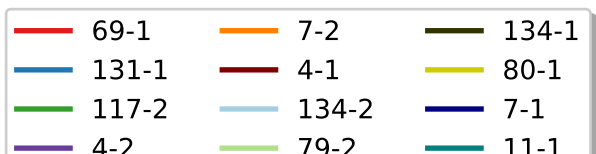
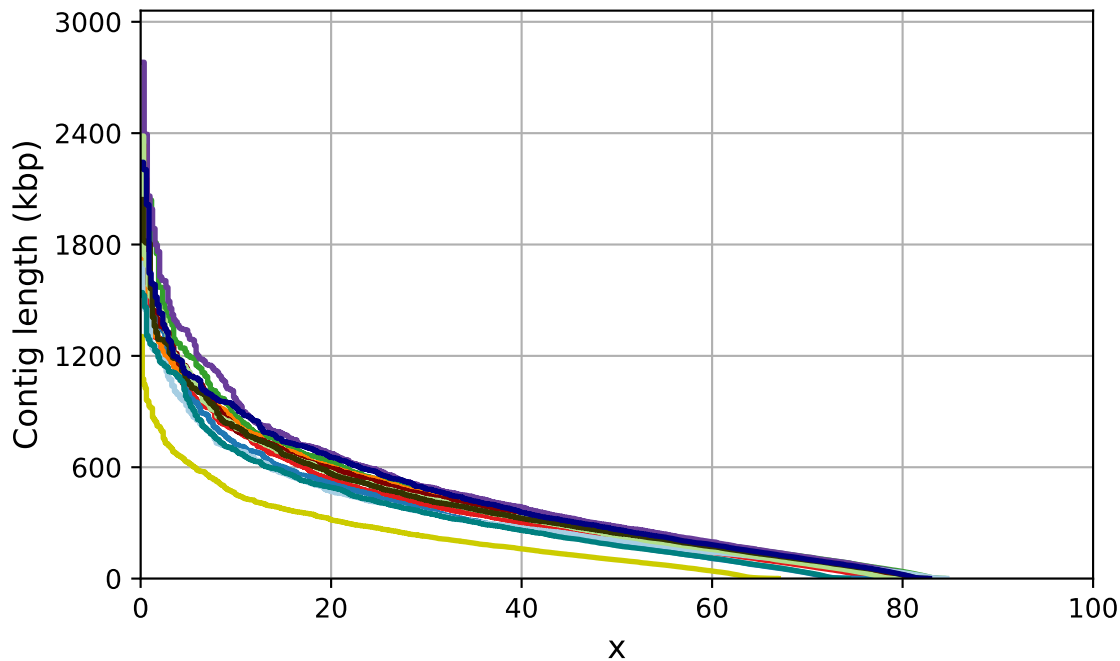
Cumulative length (aligned contigs)



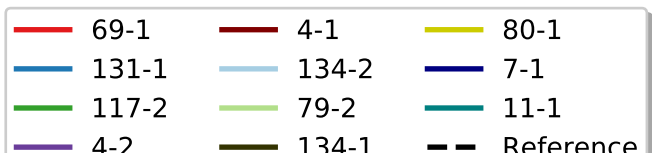
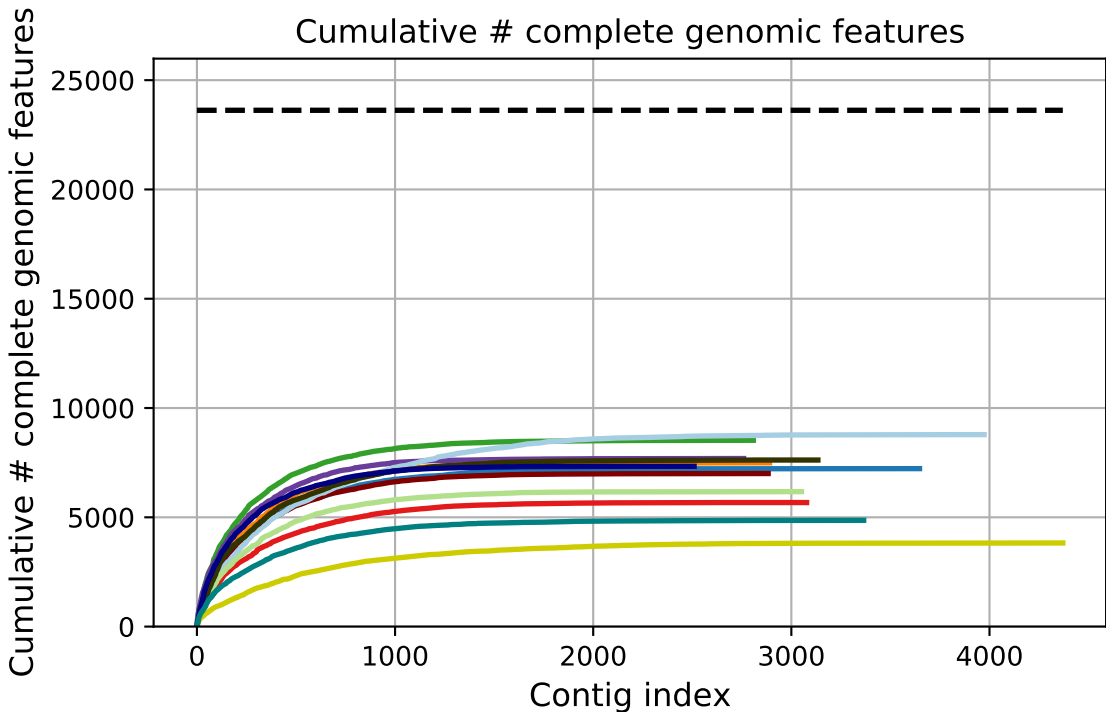
NAx



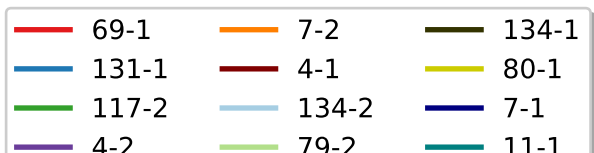
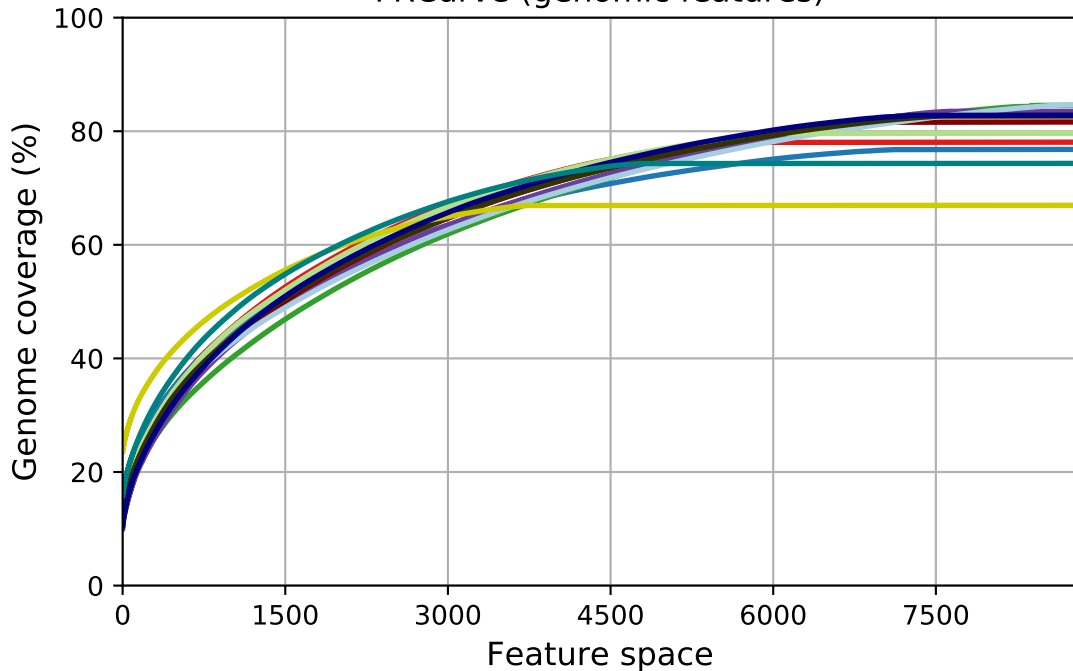
NGAx



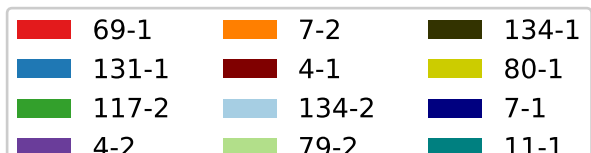
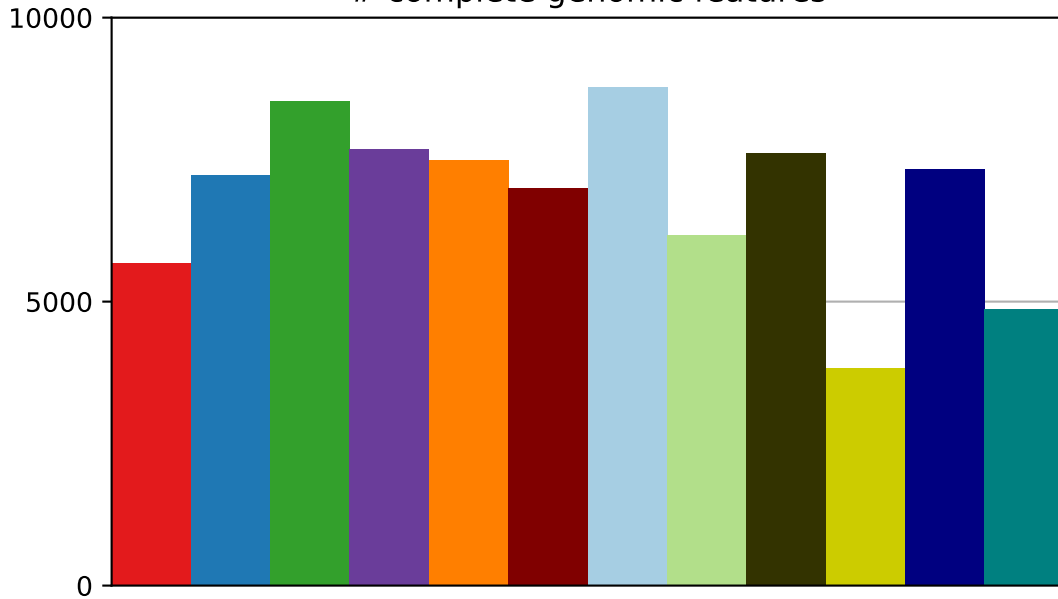
Cumulative # complete genomic features



FRCurve (genomic features)



complete genomic features



Genome fraction, %

