

Report

	GCA_003344945.1	GCA_009761105.1	GCA_012275225.1	GCA_012365075.1	GCA_023718355.1	GCA_030015405.1
# contigs (>= 0 bp)	396	239	958	1079	191	340
# contigs (>= 1000 bp)	396	239	578	897	183	337
# contigs (>= 5000 bp)	209	190	297	510	137	114
# contigs (>= 10000 bp)	156	161	235	377	122	69
# contigs (>= 25000 bp)	106	132	172	236	107	37
# contigs (>= 50000 bp)	80	111	134	176	93	22
Total length (>= 0 bp)	37511876	38180955	38127725	37388807	36421613	37795174
Total length (>= 1000 bp)	37511876	38180955	37876750	37257724	36414626	37793685
Total length (>= 5000 bp)	37093637	38058310	37260300	36356245	36304265	37360731
Total length (>= 10000 bp)	36727208	37851351	36808551	35432605	36198704	37039229
Total length (>= 25000 bp)	35997202	37356481	35743902	33172663	35933578	36546851
Total length (>= 50000 bp)	35066793	36597329	34420215	31034950	35456935	35996980
# contigs	396	239	953	1079	191	338
Largest contig	2162797	2008345	978104	704754	1803798	9205284
Total length	37511876	38180955	38126481	37388807	36421613	37794437
Reference length	37795174	37795174	37795174	37795174	37795174	37795174
GC (%)	49.66	48.27	49.25	49.46	49.37	49.38
Reference GC (%)	49.38	49.38	49.38	49.38	49.38	49.38
N50	757052	456288	319661	183962	603759	5092470
NG50	754018	464240	319822	182246	567302	5092470
N90	101550	118627	52440	21214	128277	1231058
NG90	86985	138169	58321	18800	104770	1231058
auN	788682.2	640440.3	375066.7	222044.4	687337.2	5109541.1
auNG	782770.6	646977.3	378354.5	219657.0	662357.9	5109441.5
LS0	17	23	36	60	20	3
LG50	18	22	35	61	21	3
LS90	61	83	132	257	65	8
LG90	64	80	127	275	75	8
# misassemblies	282	523	429	186	298	0
# misassembled contigs	100	110	203	143	87	0
Misassembled contigs length	32298781	33623479	28777884	9292459	31937031	0
# local misassemblies	379	491	371	154	358	0
# scaffold gap ext. mis.	4	0	0	0	0	0
# scaffold gap loc. mis.	12	2	6	0	0	0
# unaligned mis. contigs	48	27	28	16	10	0
# unaligned contigs	54 + 194 part	32 + 167 part	309 + 236 part	81 + 100 part	13 + 104 part	0 + 0 part
Unaligned length	3342340	6235003	3200231	706722	2426136	0
Genome fraction (%)	90.281	84.576	92.134	96.887	90.009	99.998
Duplication ratio	1.001	1.000	1.003	1.002	1.000	1.001
# N's per 100 kbp	90.20	1.24	38.91	0.10	1.51	122.77
# mismatches per 100 kbp	1177.98	1984.67	1099.63	37.77	1175.28	0.00
# indels per 100 kbp	129.20	226.57	121.51	4.60	129.26	0.00
# genomic features	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Largest alignment	1332178	669313	538497	547803	1177966	9205284
Total aligned length	34130398	31934905	34870975	36654495	33981819	37794437
NA50	225632	96514	148446	165440	175001	5092470
NGA50	225383	97796	149303	164079	163833	5092470
NA90	2461	-	2820	17419	20381	1231058
NGA90	1095	-	4719	14923	-	1231058
auNA	327162.0	132723.5	178937.6	189682.3	219292.4	5109541.1
auNGA	324709.7	134078.2	180506.2	187642.8	211322.8	5109441.5
LA50	45	102	74	69	63	3
LGA50	46	100	73	71	67	3
LA90	387	-	523	298	267	8
LGA90	542	-	441	321	-	8

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

	GCA_003344945.1	GCA_009761105.1	GCA_012275225.1	GCA_012365075.1	GCA_023718355.1	GCA_030015405.1
# misassemblies	282	523	429	186	298	0
# contig misassemblies	273	523	429	186	298	0
# c. relocations	181	365	210	18	200	0
# c. translocations	85	141	198	164	84	0
# c. inversions	7	17	21	4	14	0
# scaffold misassemblies	9	0	0	0	0	0
# s. relocations	3	0	0	0	0	0
# s. translocations	6	0	0	0	0	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	100	110	203	143	87	0
Misassembled contigs length	32298781	33623479	28777884	9292459	31937031	0
# local misassemblies	379	491	371	154	358	0
# scaffold gap ext. mis.	4	0	0	0	0	0
# scaffold gap loc. mis.	12	2	6	0	0	0
# unaligned mis. contigs	48	27	28	16	10	0
# mismatches	402049	633804	383450	13846	399381	0
# indels	44098	72354	42373	1685	43924	0
# indels (<= 5 bp)	38922	63633	37529	1274	38824	0
# indels (> 5 bp)	5176	8721	4844	411	5100	0
Indels length	185945	275192	165268	21807	176522	0

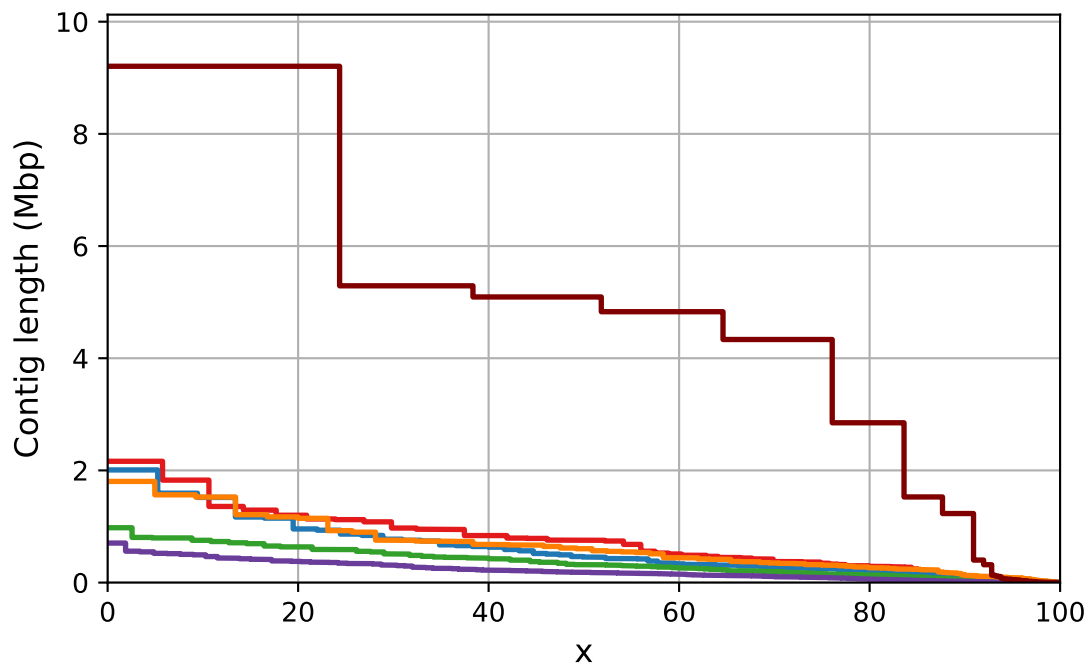
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	GCA_003344945.1	GCA_009761105.1	GCA_012275225.1	GCA_012365075.1	GCA_023718355.1	GCA_030015405.1
# fully unaligned contigs	54	32	309	81	13	0
Fully unaligned length	158993	184946	465017	248234	81722	0
# partially unaligned contigs	194	167	236	100	104	0
Partially unaligned length	3183347	6050057	2735214	458488	2344414	0
# N's	33835	472	14834	39	551	46400

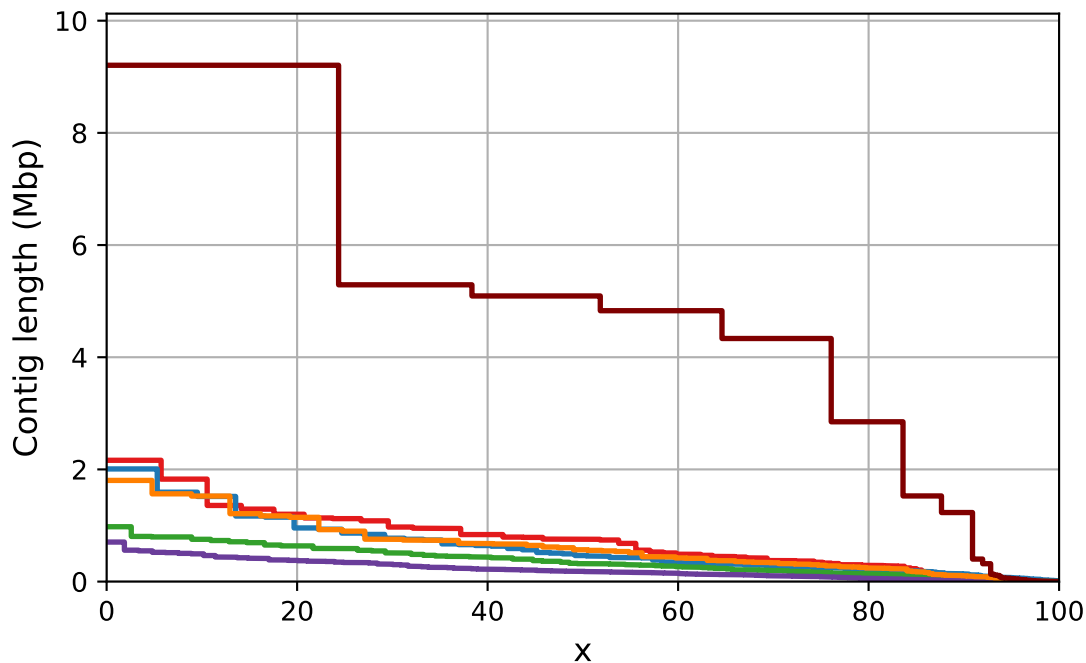
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



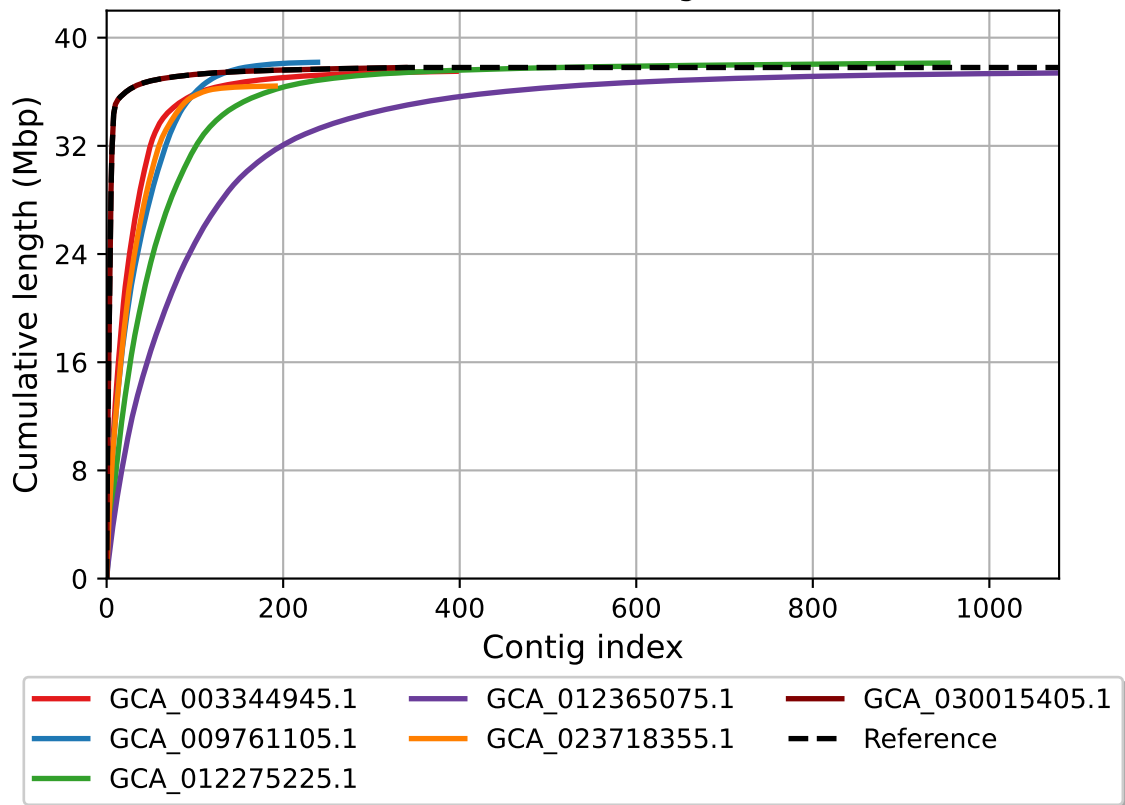
GCA_003344945.1 GCA_012275225.1 GCA_023718355.1
GCA_009761105.1 GCA_012365075.1 GCA_030015405.1

NGx

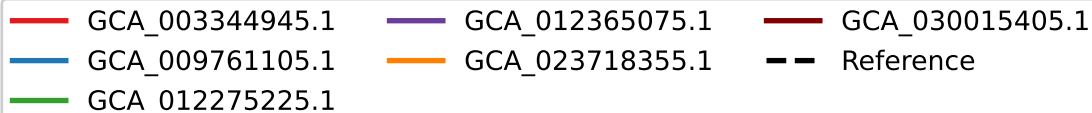
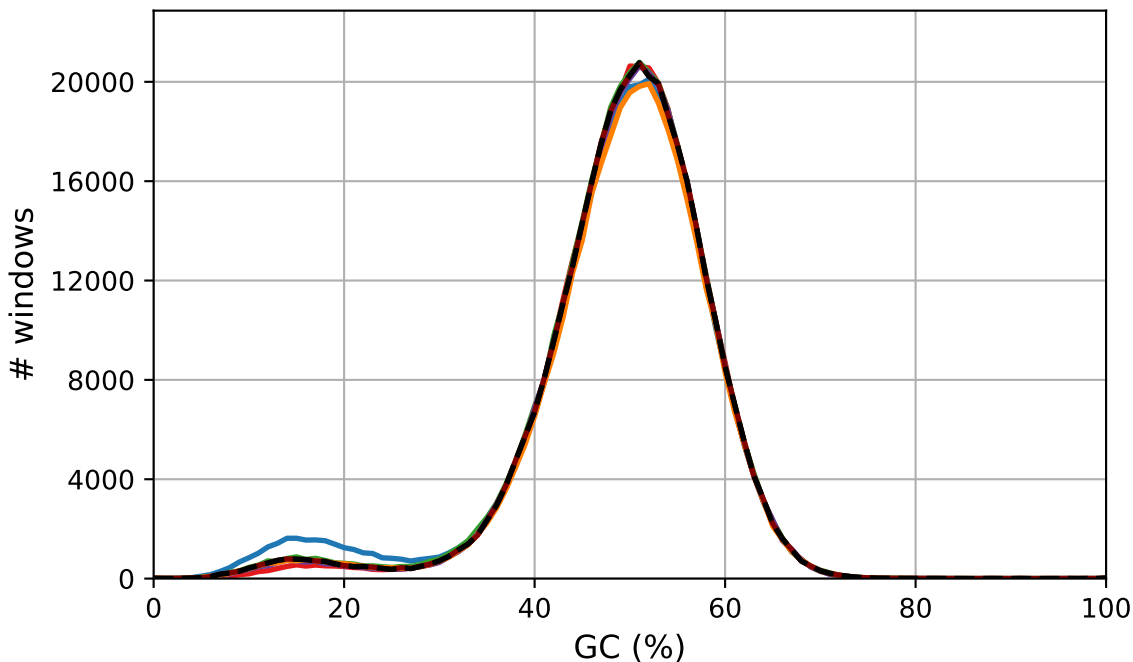


GCA_003344945.1	GCA_012275225.1	GCA_023718355.1
GCA_009761105.1	GCA_012365075.1	GCA_030015405.1

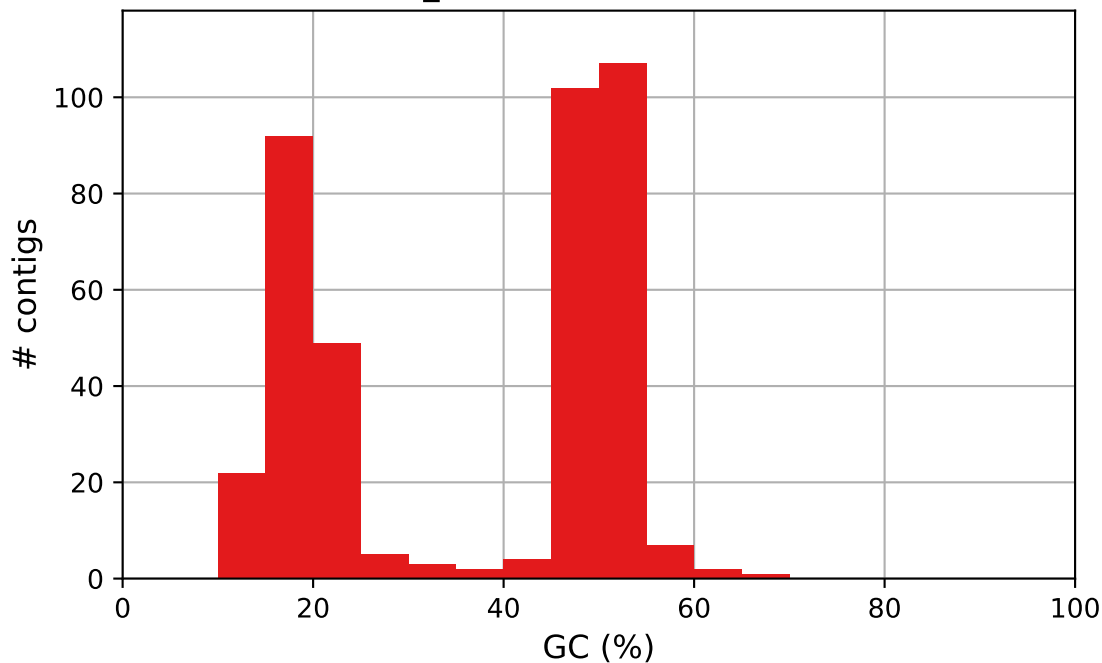
Cumulative length



GC content

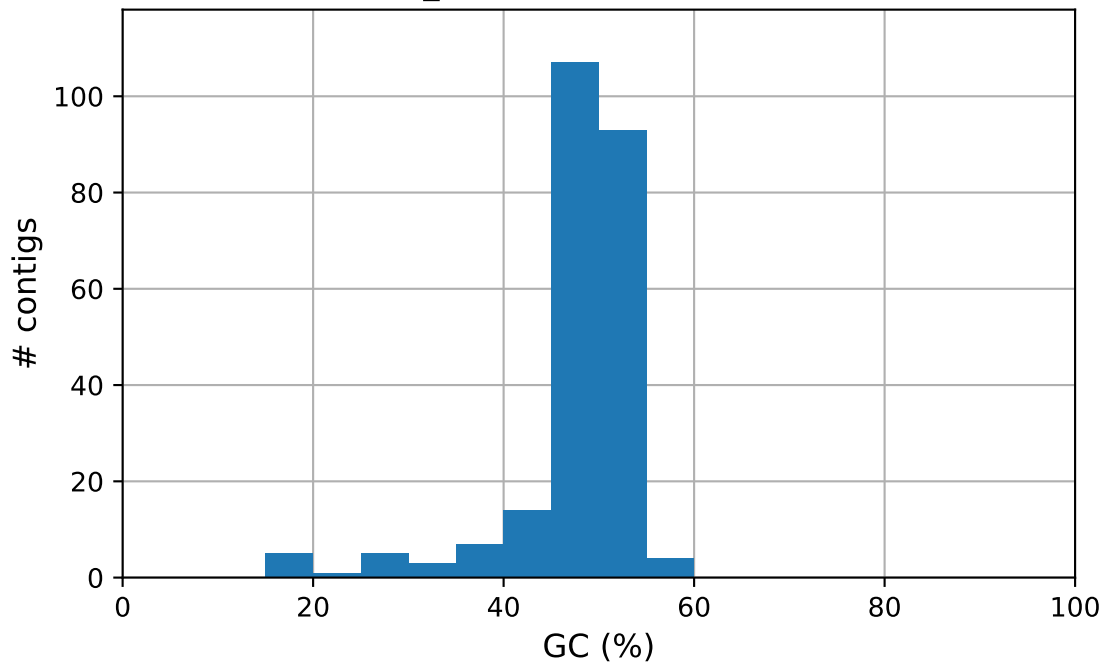


GCA_003344945.1 GC content



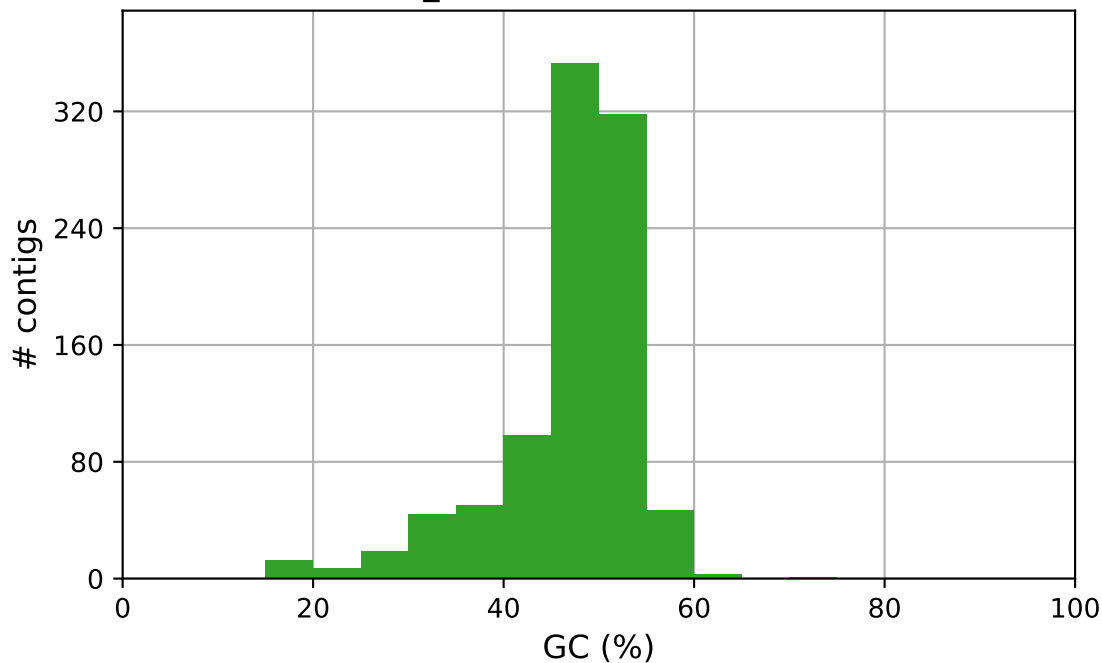
GCA_003344945.1

GCA_009761105.1 GC content



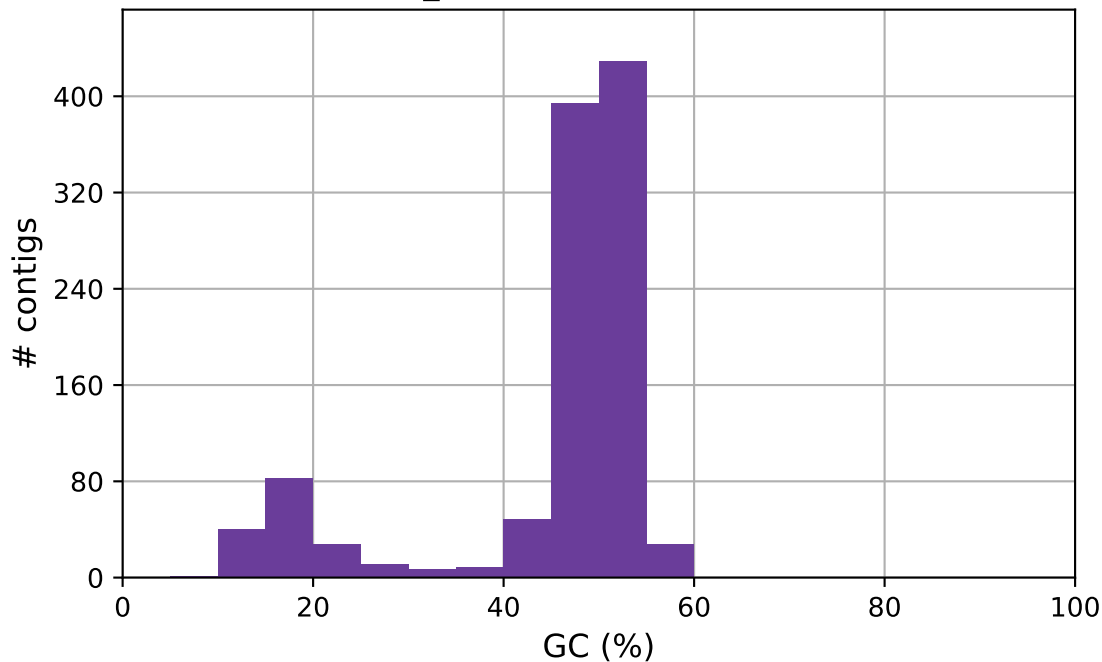
GCA_009761105.1

GCA_012275225.1 GC content



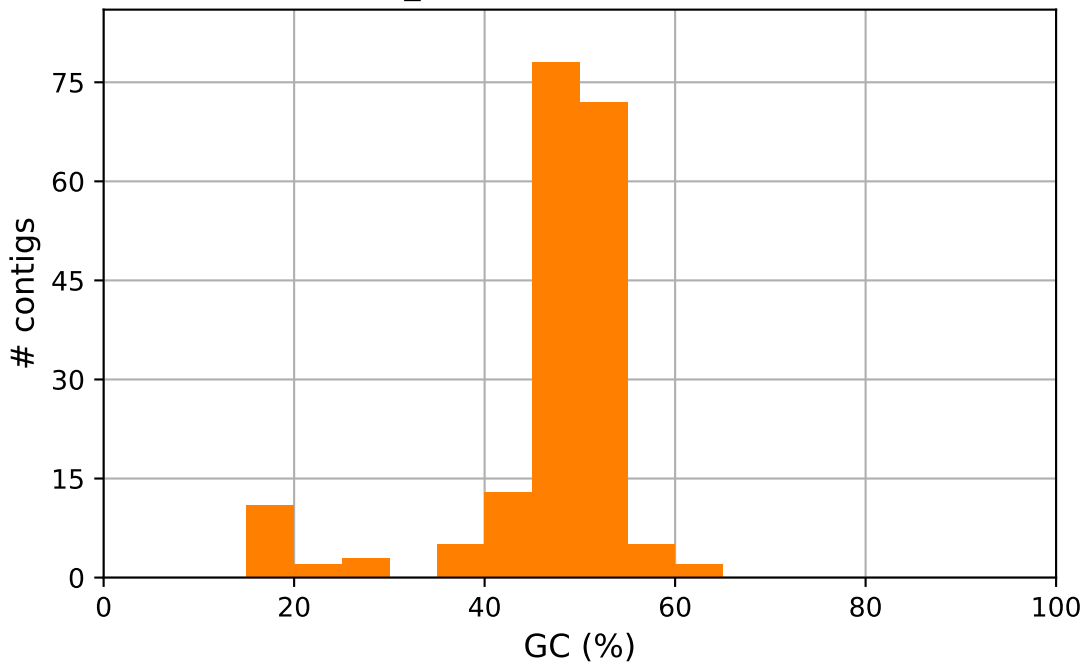
GCA_012275225.1

GCA_012365075.1 GC content



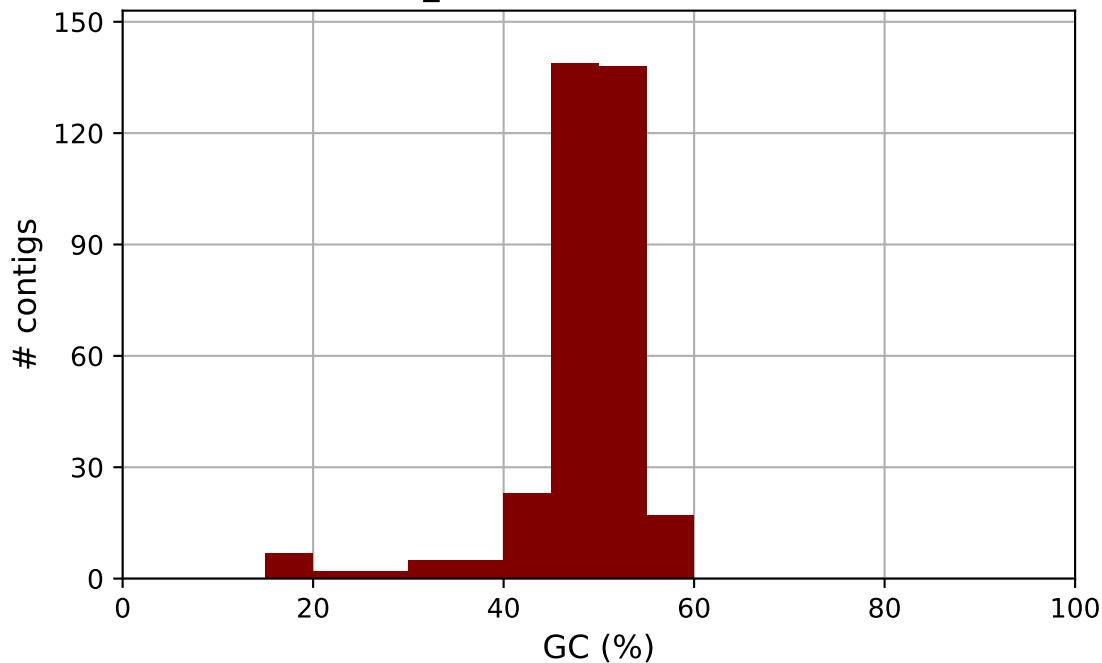
GCA_012365075.1

GCA_023718355.1 GC content



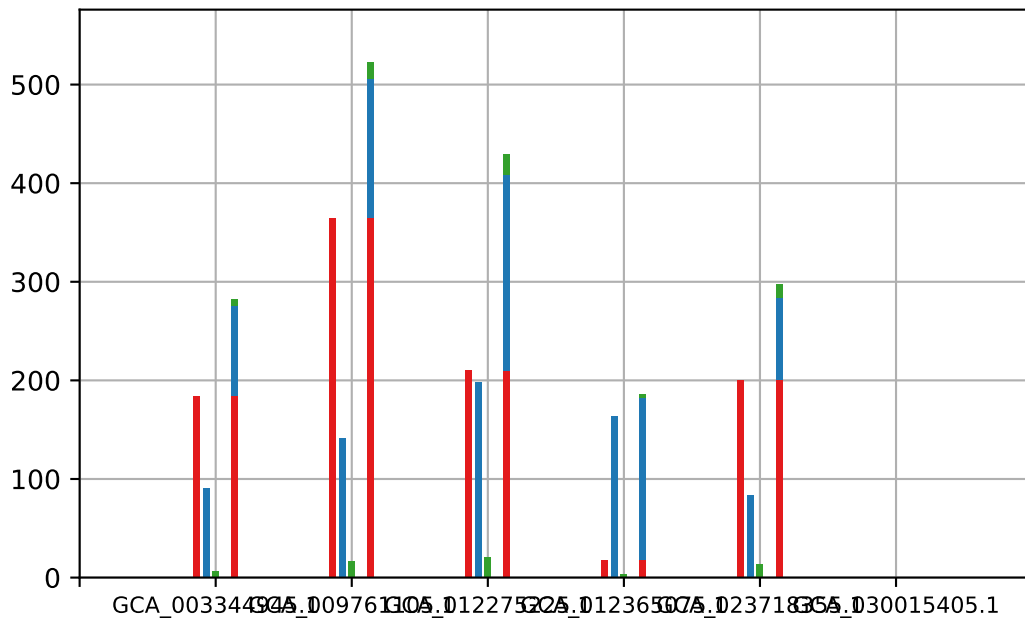
GCA_023718355.1

GCA_030015405.1 GC content



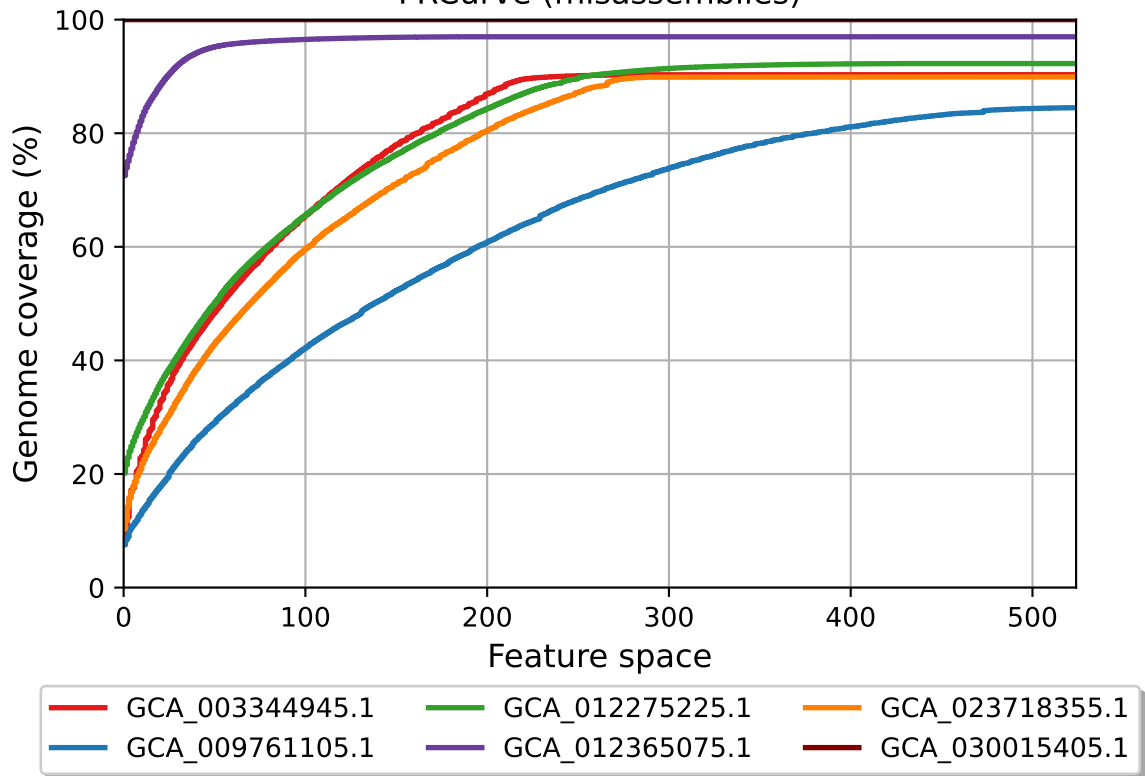
GCA_030015405.1

Misassemblies

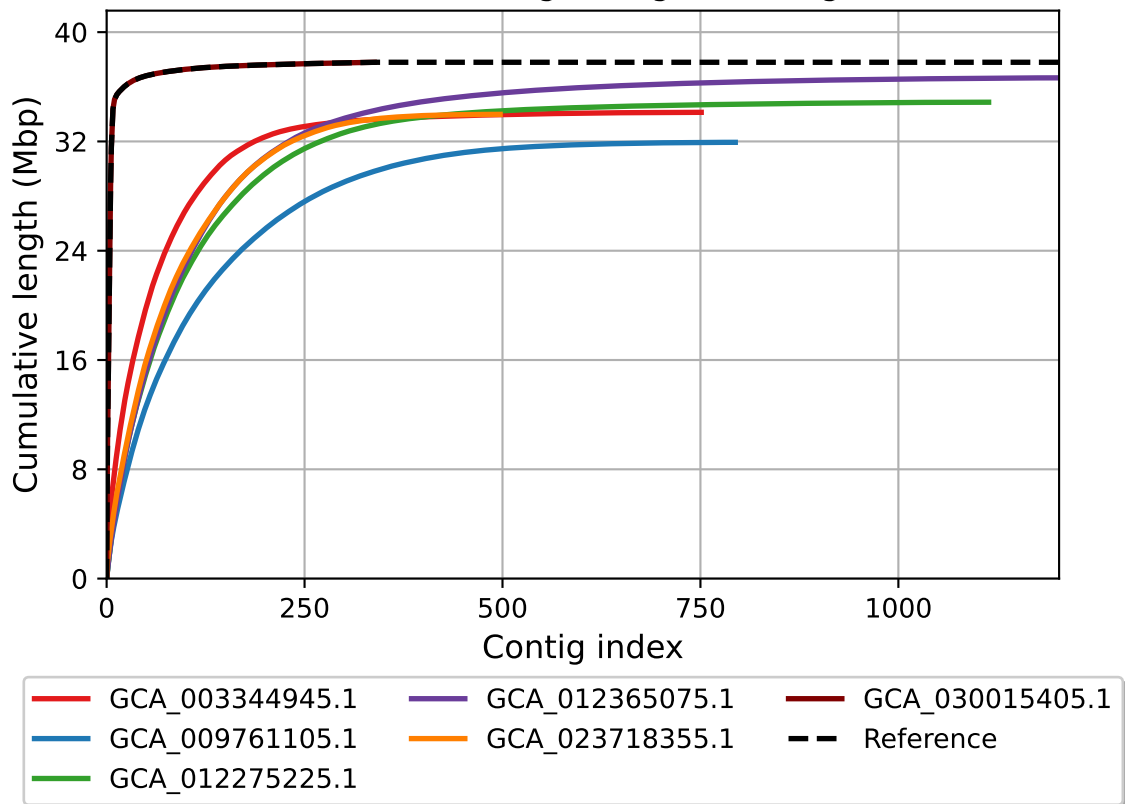


■ # relocations
 ■ # translocations
 ■ # inversions

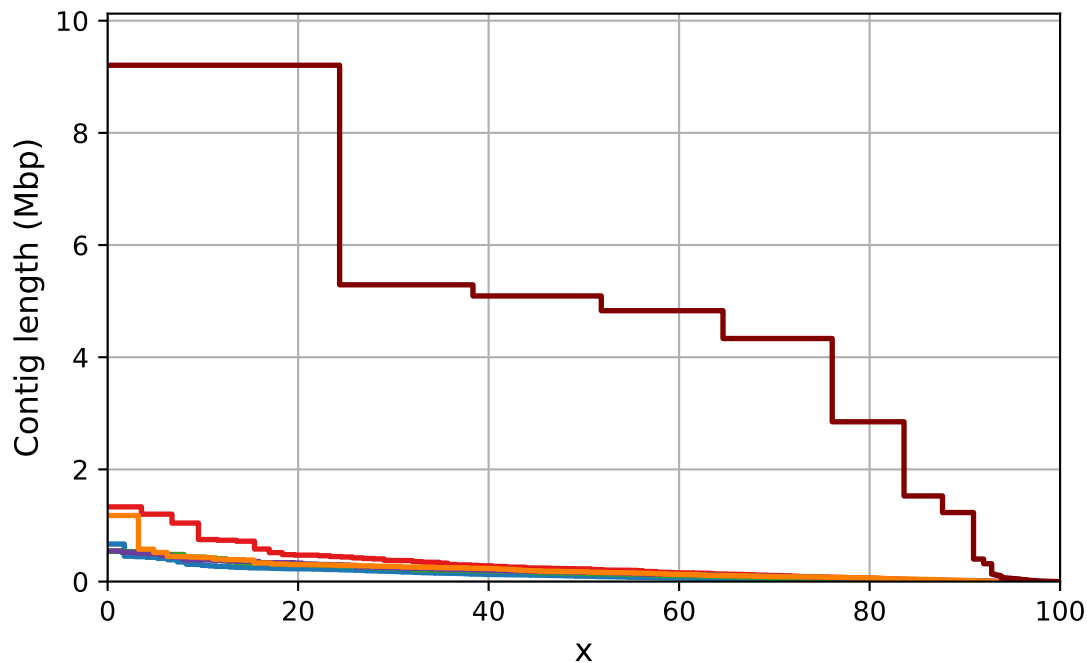
FRCurve (misassemblies)



Cumulative length (aligned contigs)

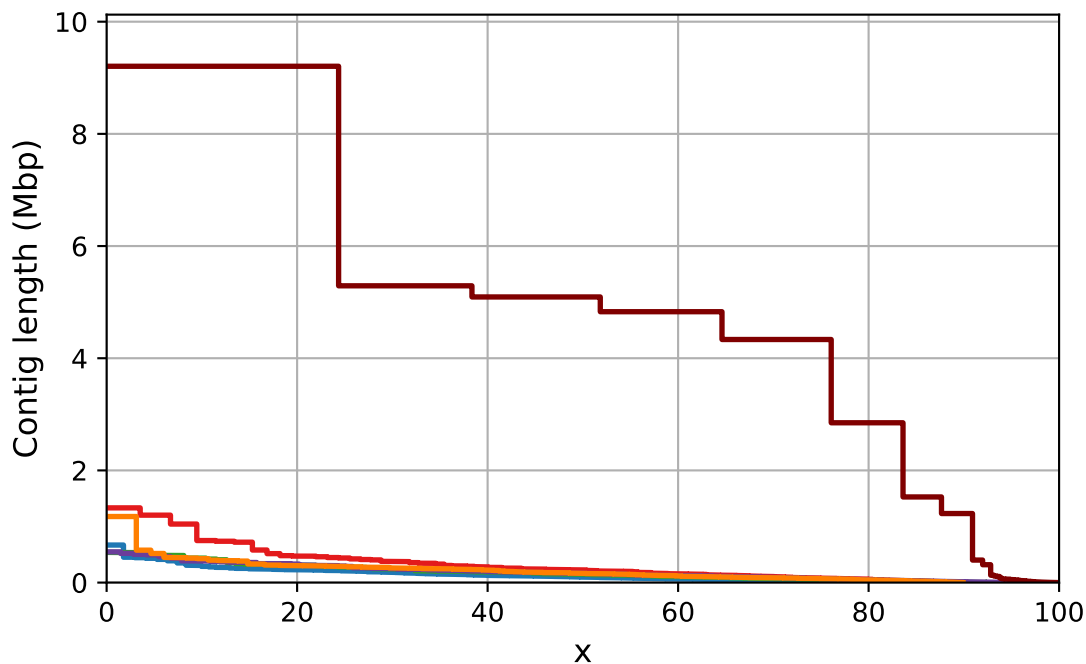


NAx



GCA_003344945.1	GCA_012275225.1	GCA_023718355.1
GCA_009761105.1	GCA_012365075.1	GCA_030015405.1

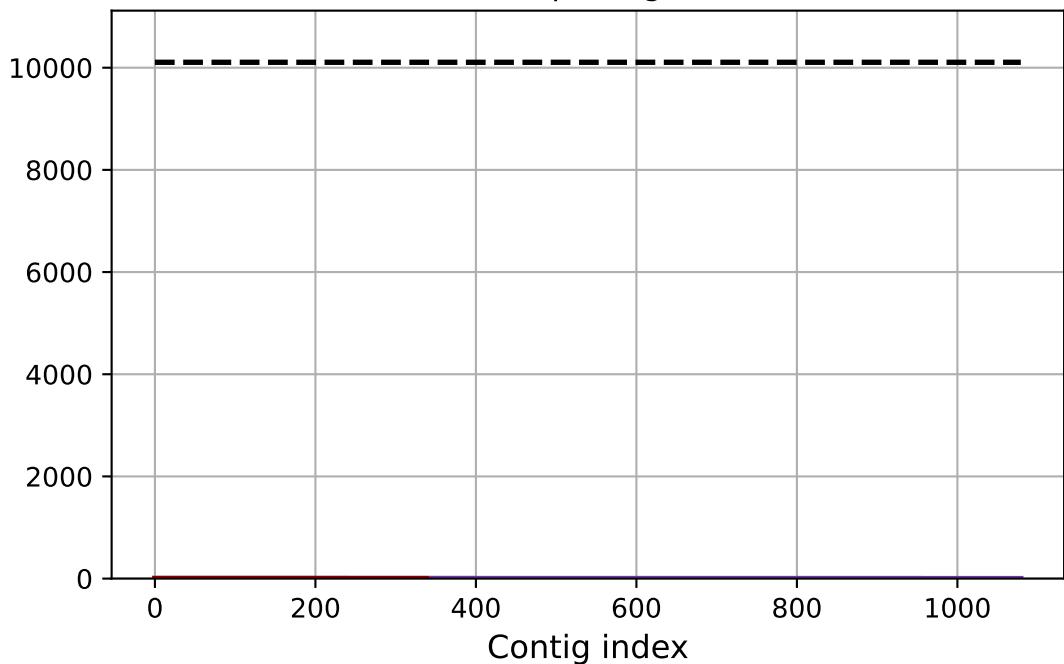
NGAx



GCA_003344945.1	GCA_012275225.1	GCA_023718355.1
GCA_009761105.1	GCA_012365075.1	GCA_030015405.1

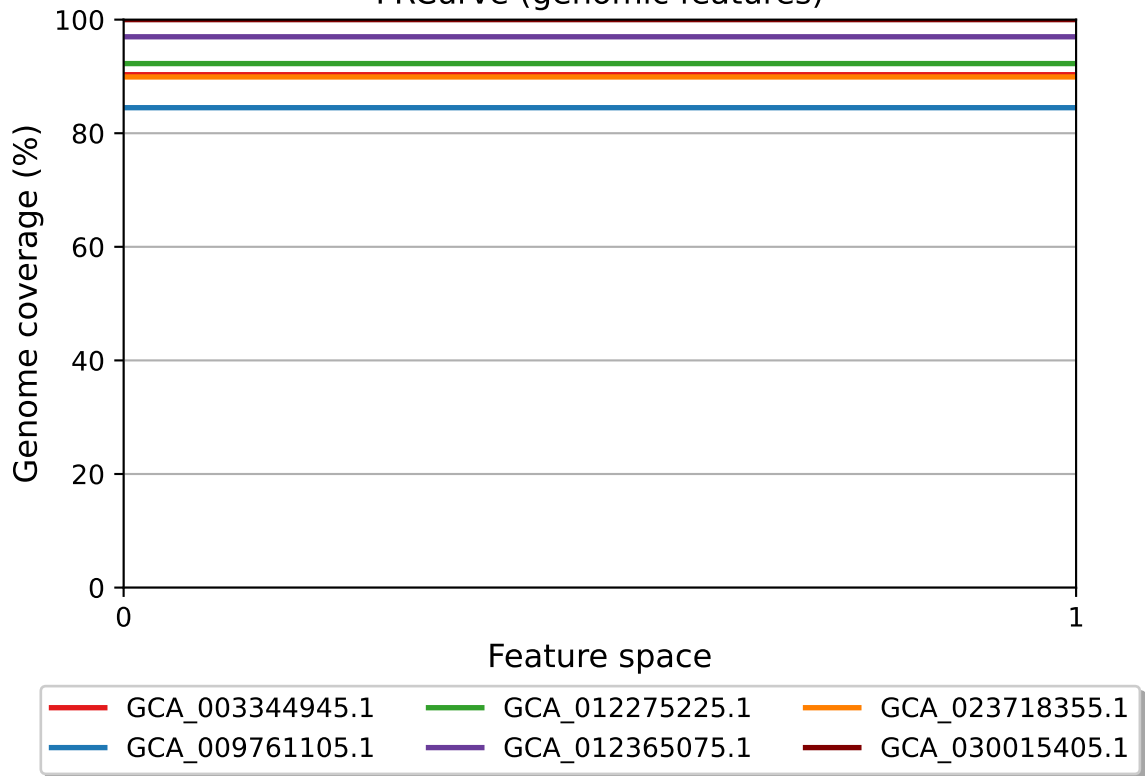
Cumulative # complete genomic features

Cumulative # complete genomic features



GCA_003344945.1	GCA_012365075.1	GCA_030015405.1
GCA_009761105.1	GCA_023718355.1	Reference
GCA_012275225.1		

FRCurve (genomic features)



complete genomic features

