

Report

	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# contigs (>= 1000 bp)	576	1110	371	784	493	719	101	817	418	898	232	848
# contigs (>= 5000 bp)	0	197	0	175	0	218	0	44	0	174	0	184
# contigs (>= 10000 bp)	0	49	0	45	0	87	0	28	0	55	0	54
# contigs (>= 25000 bp)	0	10	0	10	0	16	0	13	0	9	0	11
# contigs (>= 50000 bp)	0	5	0	4	0	7	0	8	0	5	0	3
Total length (>= 1000 bp)	802853	4650409	490418	3646235	666577	4437855	127612	2935158	563718	3650642	289152	3404294
Total length (>= 5000 bp)	0	2680023	0	2190456	0	3282225	0	1485847	0	2047700	0	1943899
Total length (>= 10000 bp)	0	1686843	0	1319553	0	2339417	0	1384255	0	1245178	0	1063633
Total length (>= 25000 bp)	0	1078091	0	799594	0	1296948	0	1150445	0	561147	0	469684
Total length (>= 50000 bp)	0	915444	0	580112	0	1031573	0	1001634	0	428067	0	196256
# contigs	3770	3020	3691	2081	3684	1969	2633	1961	3966	2758	3671	2373
Largest contig	3771	370211	2871	329477	3249	248889	3098	193415	3793	115025	2434	67374
Total length	2503583	5600353	2237516	4280858	2377305	5056949	1331382	3602542	2424450	4561220	2055500	4147737
Reference length	2544614	2544614	2544614	2544614	2544614	2544614	2544614	2544614	2544614	2544614	2544614	2544614
GC (%)	32.80	32.40	33.09	31.78	32.99	32.34	32.96	33.11	33.21	32.15	32.87	32.34
Reference GC (%)	31.79	31.79	31.79	31.79	31.79	31.79	31.79	31.79	31.79	31.79	31.79	31.79
N50	743	4593	646	5117	708	8739	510	3014	653	4063	588	4497
NG50	734	19043	588	11335	672	25016	315	14379	631	9711	506	8261
N75	492	1624	460	2042	482	2937	389	1277	458	1405	430	1522
NG75	484	8309	397	5999	442	14053	-	2620	433	5546	341	5122
L50	1103	223	1172	166	1119	108	906	128	1234	226	1232	212
LG50	1131	19	1422	41	1240	16	2442	19	1328	58	1683	77
L75	2146	758	2205	485	2137	353	1657	610	2345	705	2260	614
LG75	2209	74	2743	123	2409	51	-	166	2547	148	3212	177
# misassemblies	37	79	19	60	26	66	19	46	28	75	22	77
# misassembled contigs	37	70	19	57	26	59	18	43	27	71	22	71
Misassembled contigs length	36555	242311	15341	316778	27322	348184	11603	72388	26864	307773	16355	271316
# local misassemblies	18	75	14	70	7	71	7	15	15	65	7	65
# 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
# unaligned mis. contigs	9	72	8	53	14	47	3	16	10	63	7	49
# unaligned contigs	24 + 106 part	64 + 481 part	27 + 76 part	22 + 330 part	27 + 79 part	33 + 361 part	14 + 32 part	15 + 167 part	30 + 67 part	25 + 357 part	25 + 35 part	32 + 325 part
Unaligned length	114655	2335169	80098	1497361	87779	2215743	35058	1639726	76354	1345110	41181	1154264
Genome fraction (%)	75.541	85.774	70.076	83.834	74.296	85.027	45.632	71.713	74.107	85.696	67.005	85.260
Duplication ratio	1.244	1.497	1.211	1.306	1.212	1.314	1.117	1.076	1.246	1.476	1.182	1.381
# 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	2035.36	2940.76	2047.47	2817.02	1924.77	2641.21	1654.65	1888.32	1914.33	2810.31	1888.13	2747.49
# indels per 100 kbp	37.90	62.62	32.88	57.27	34.14	64.01	24.65	37.18	31.73	58.60	30.22	58.48
Largest alignment	3633	18818	2819	33804	2929	31861	2087	5815	3286	18545	2377	33492
Total aligned length	2159738	3151238	1925737	2682118	2061107	2758824	1181760	1887279	2085516	3109043	1817120	2893964
NA50	595	401	526	883	584	395	439	355	532	902	498	1246
NGA50	584	3340	471	3579	546	5547	-	960	510	3709	419	3943
NA75	347	-	333	-	351	-	321	-	330	-	342	-
NGA75	339	1644	154	1475	309	2048	-	-	305	1716	-	1692
LA50	1289	1690	1362	666	1293	1097	1034	1582	1446	739	1373	545
LGA50	1323	218	1671	197	1441	133	-	706	1562	189	1908	184
LA75	2666	-	2692	-	2619	-	1924	-	2900	-	2621	-
LGA75	2756	493	3525	461	2999	323	-	-	3184	440	-	432

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

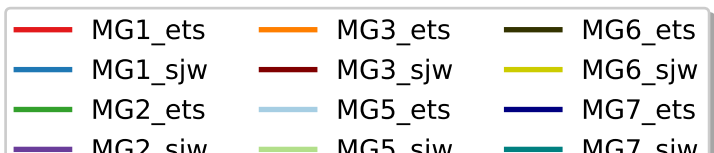
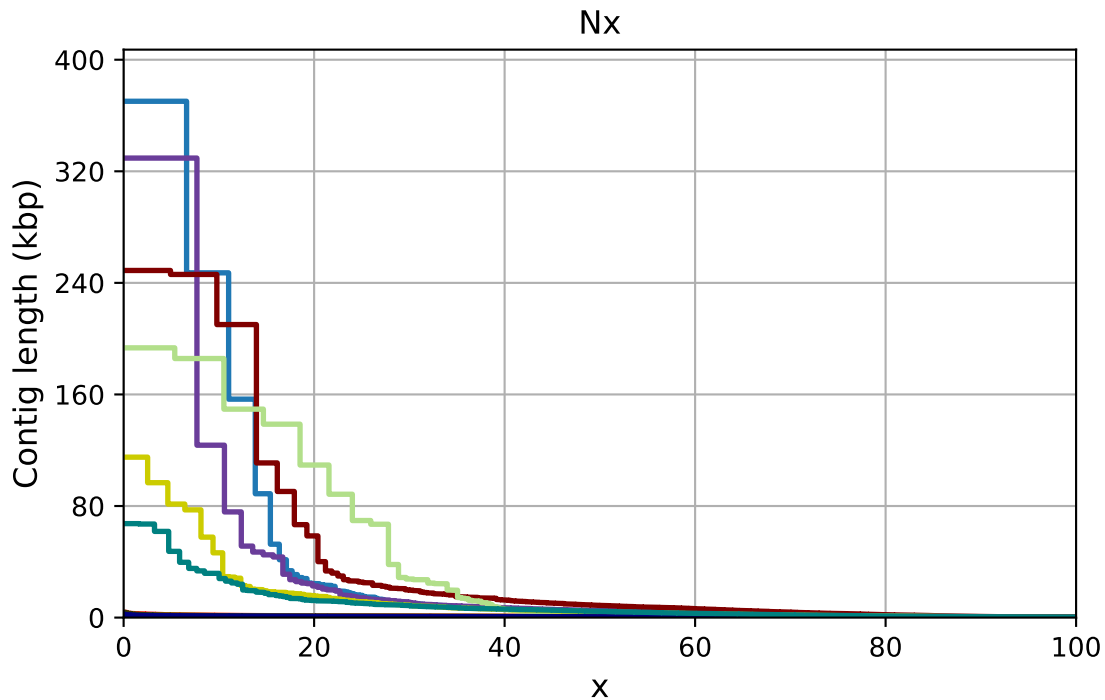
	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# misassemblies	37	79	19	60	26	66	19	46	28	75	22	77
# contig misassemblies	37	79	19	60	26	66	19	46	28	75	22	77
# c. relocations	16	36	9	22	12	27	7	16	11	28	8	36
# c. translocations	20	39	8	36	13	34	10	26	16	38	13	37
# c. inversions	1	4	2	2	1	5	2	4	1	9	1	4
# 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	37	70	19	57	26	59	18	43	27	71	22	71
Misassembled contigs length	36555	242311	15341	316778	27322	348184	11603	72388	26864	307773	16355	271316
# possibly misassembled contigs	106	443	77	287	74	323	31	152	67	307	35	283
# possible misassemblies	108	536	81	358	76	406	32	189	68	372	35	350
# local misassemblies	18	75	14	70	7	71	7	15	15	65	7	65
# 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
# unaligned mis. contigs	9	72	8	53	14	47	3	16	10	63	7	49
# mismatches	39100	64146	36487	60057	36366	57110	19201	34437	36077	61245	32173	59571
# indels	728	1366	586	1221	645	1384	286	678	598	1277	515	1268
# indels (<= 5 bp)	689	1270	547	1128	602	1278	266	630	554	1174	483	1173
# indels (> 5 bp)	39	96	39	93	43	106	20	48	44	103	32	95
Indels length	1558	3401	1435	3268	1606	3555	684	1611	1447	3513	972	3286

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

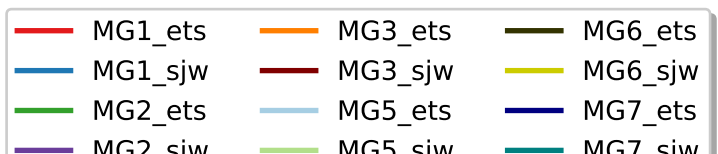
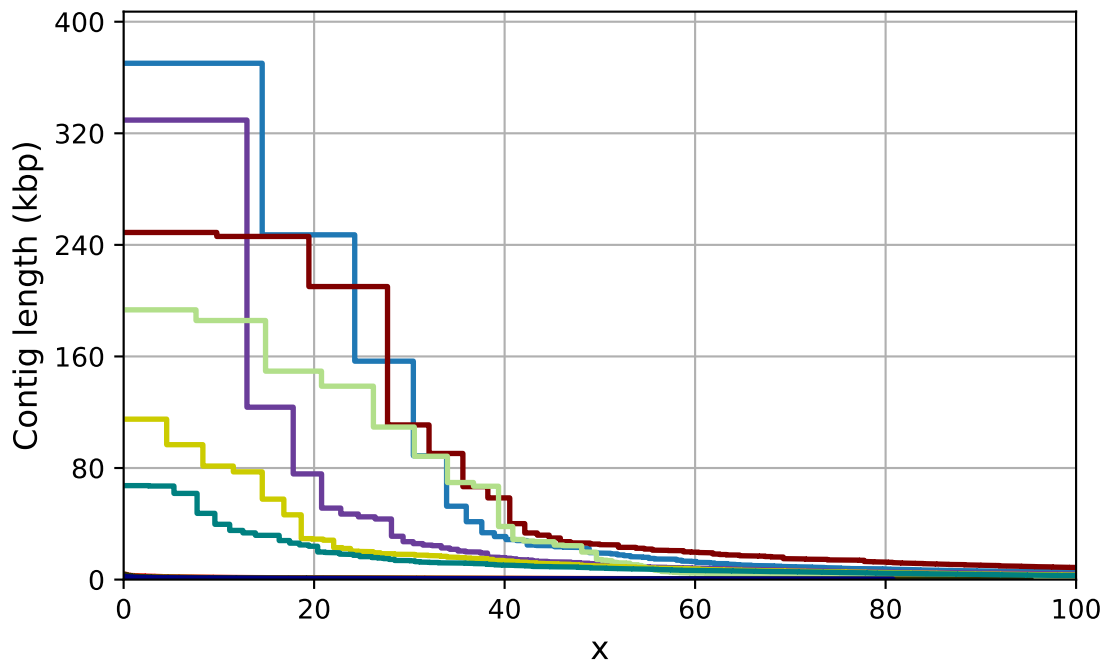
Unaligned report

	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# fully unaligned contigs	24	64	27	22	27	33	14	15	30	25	25	32
Fully unaligned length	17718	182198	16123	24378	17097	245647	7985	14939	16905	22635	16347	25016
# partially unaligned contigs	106	481	76	330	79	361	32	167	67	357	35	325
Partially unaligned length	96937	2152971	63975	1472983	70682	1970096	27073	1624787	59449	1322475	24834	1129248
# N's	0	0	0	0	0	0	0	0	0	0	0	0

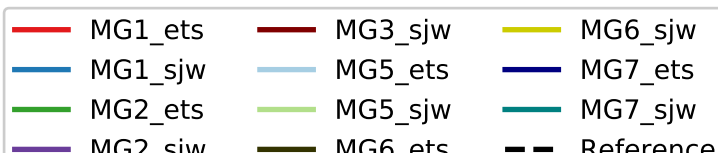
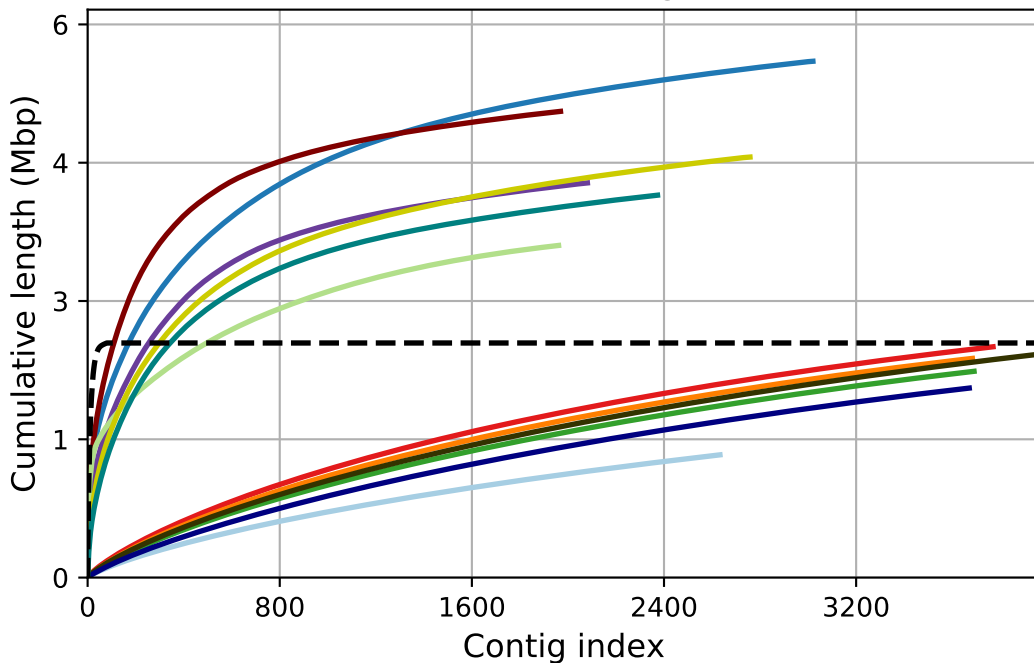
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



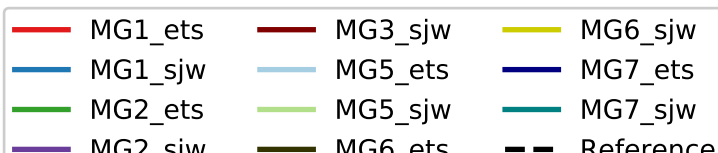
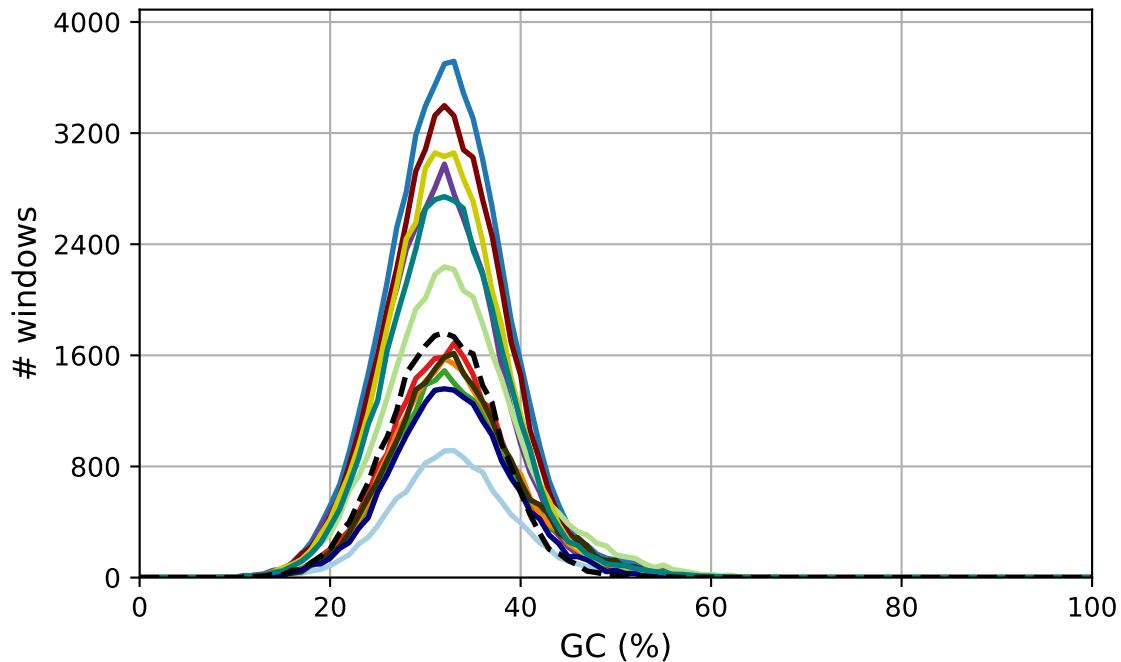
NGx



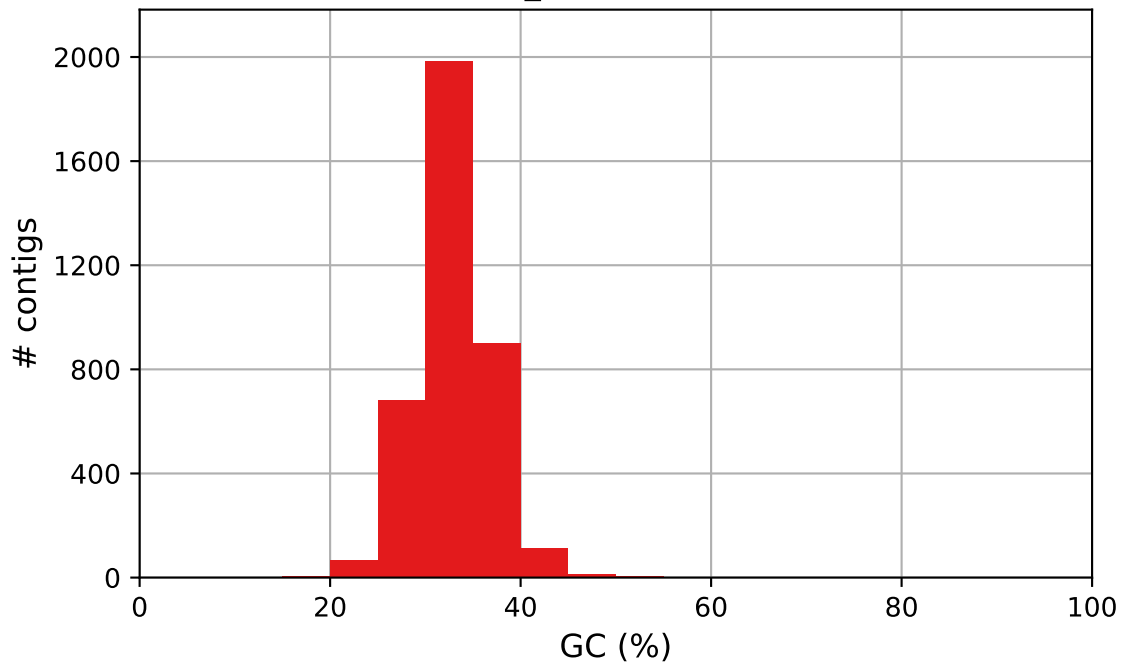
Cumulative length



GC content

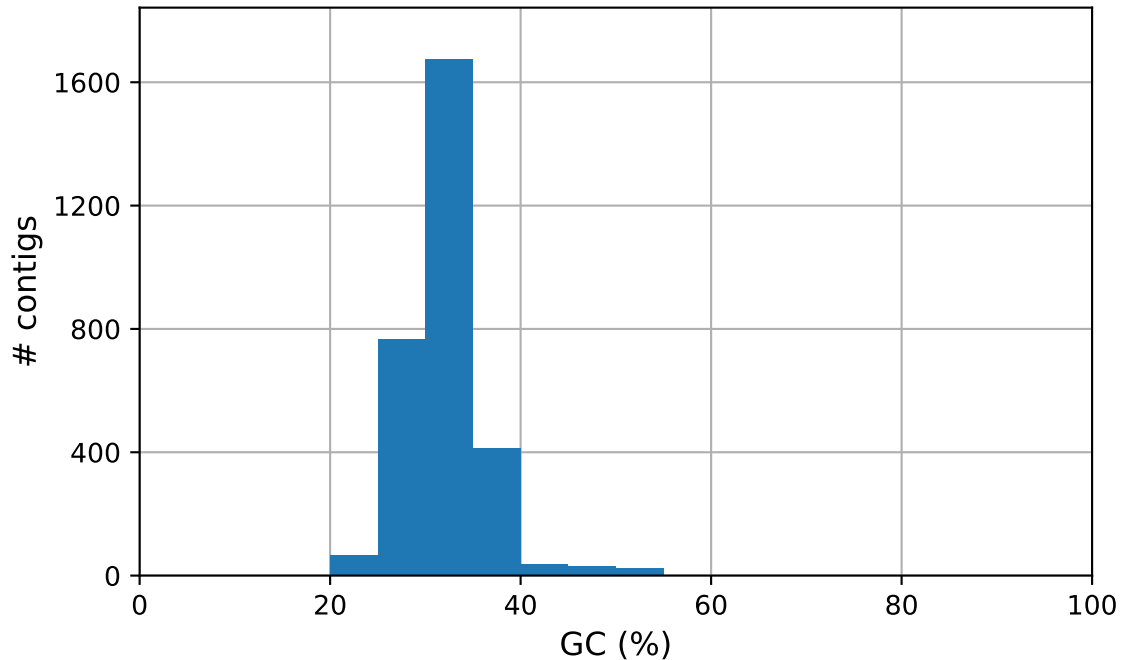


MG1_ets GC content



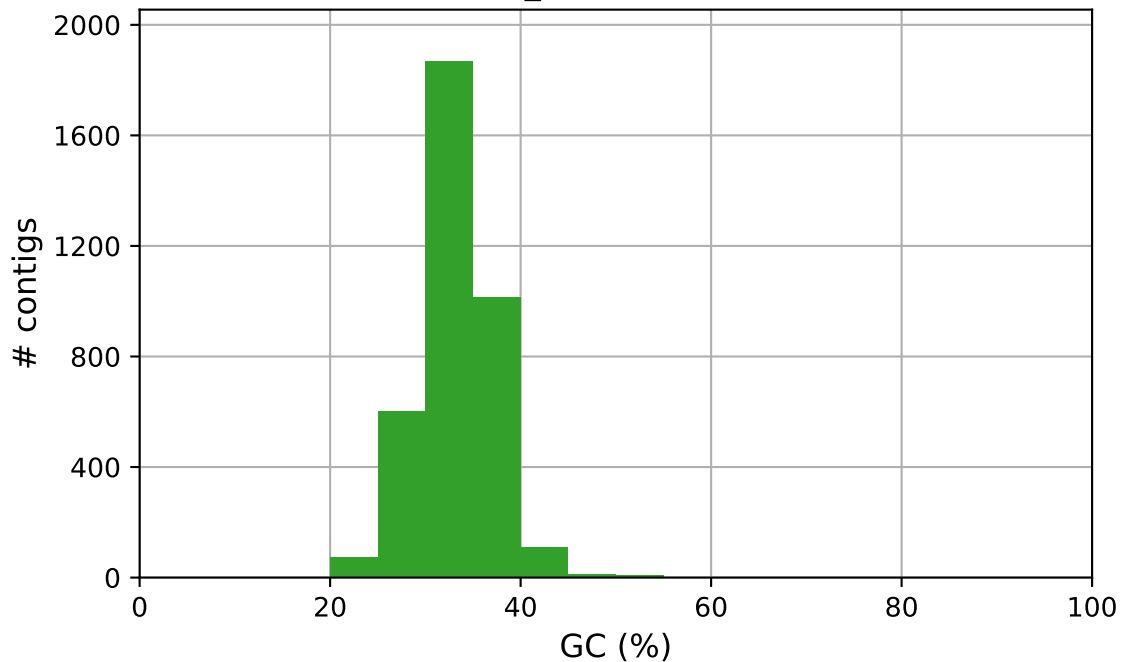
MG1_ets

MG1_sjw GC content



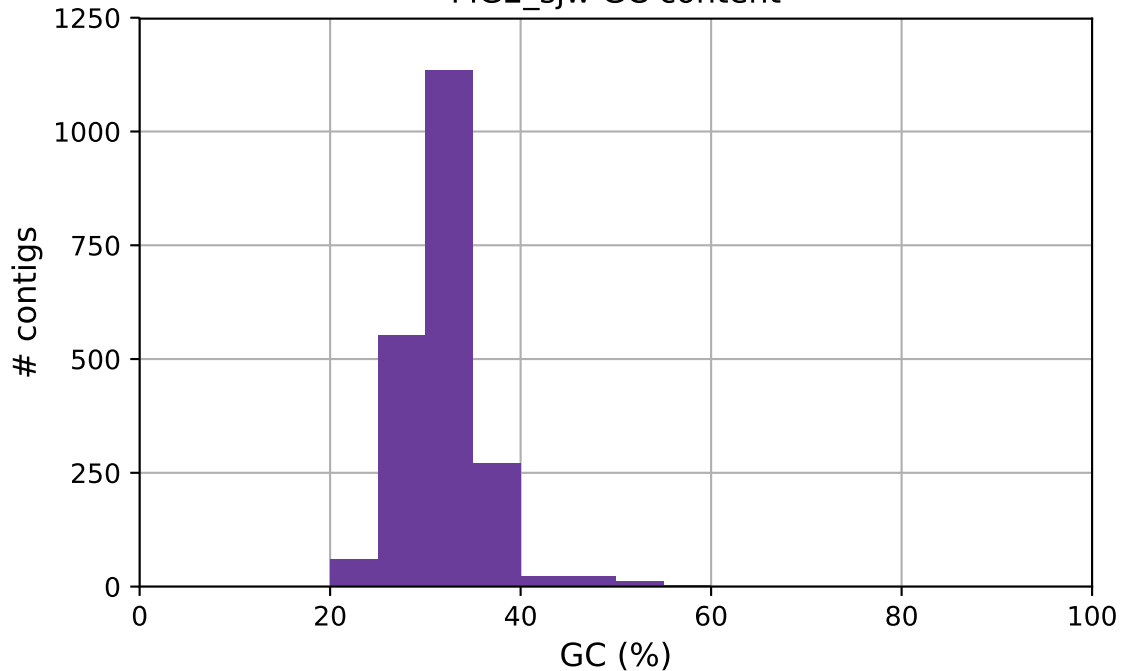
MG1_sjw

MG2_ets GC content



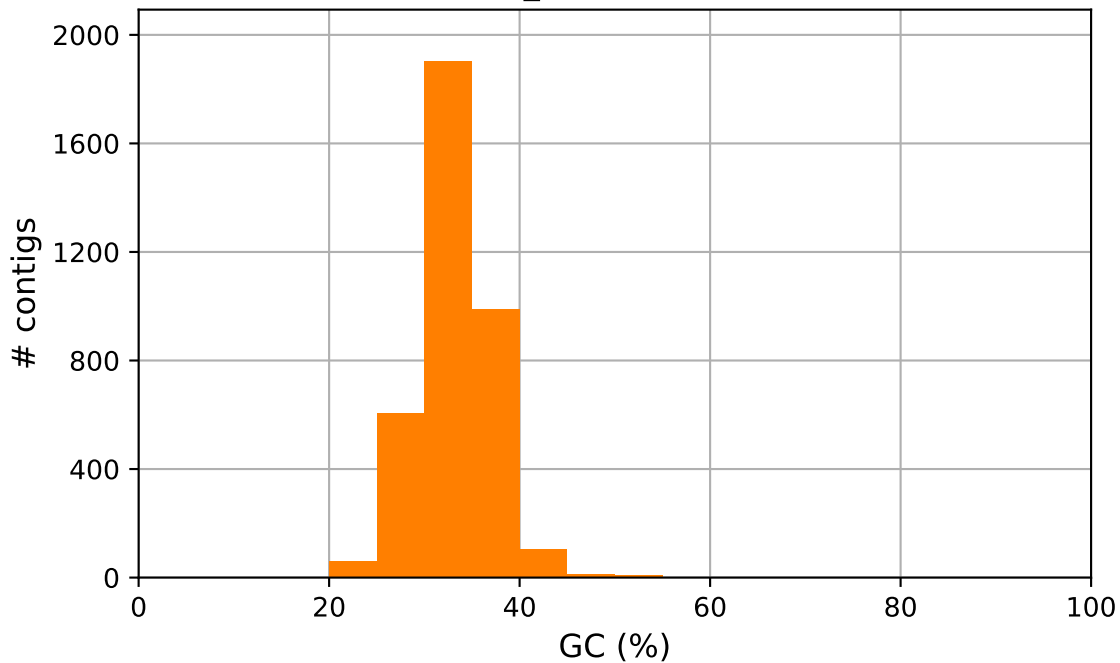
MG2_ets

MG2_sjw GC content



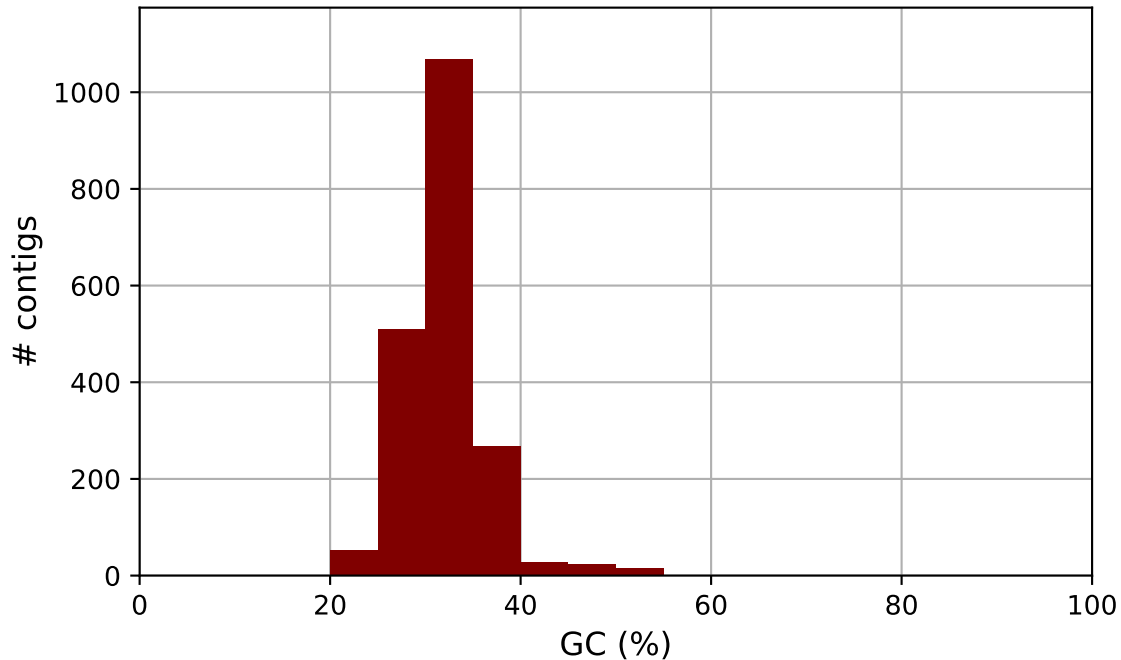
MG2_sjw

MG3_ets GC content



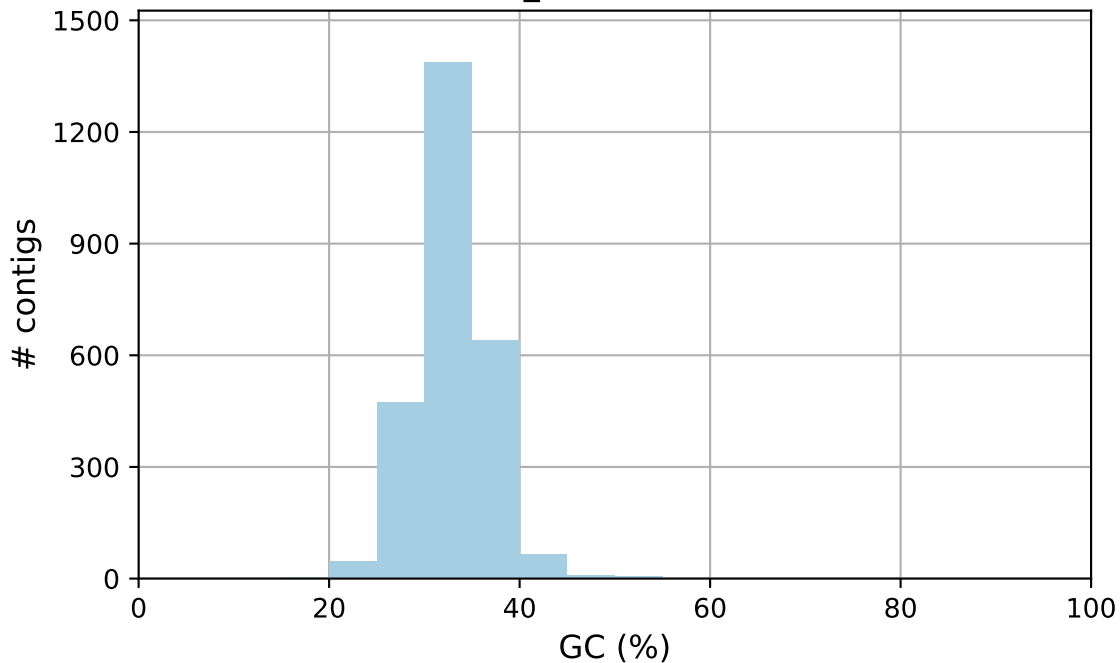
MG3_ets

MG3_sjw GC content



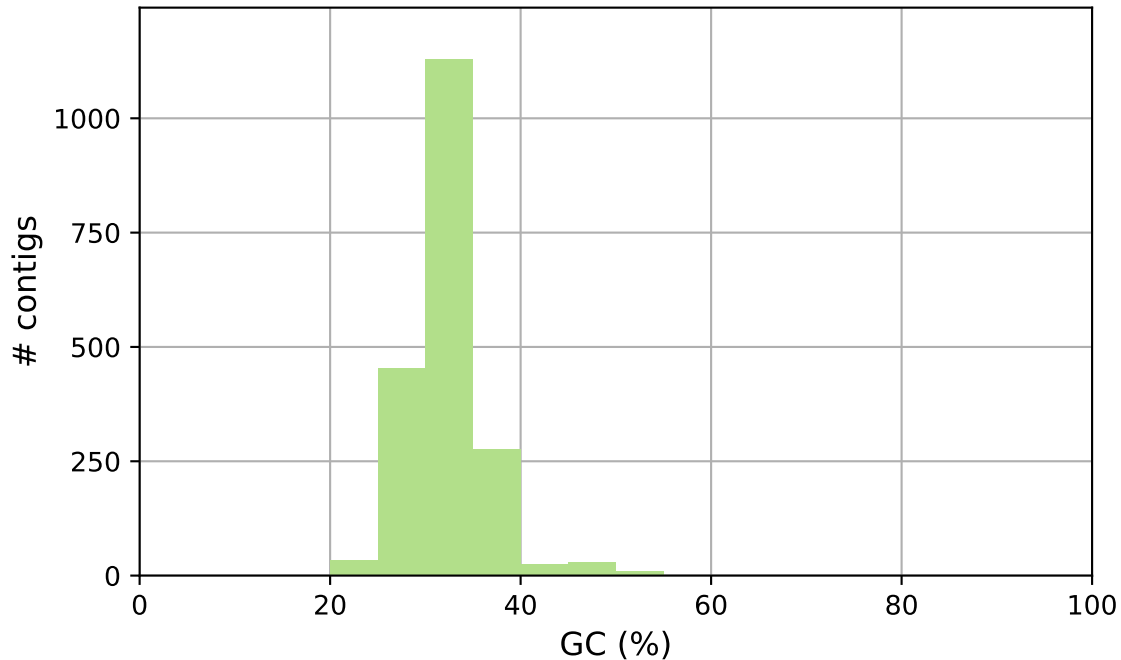
MG3_sjw

MG5_ets GC content



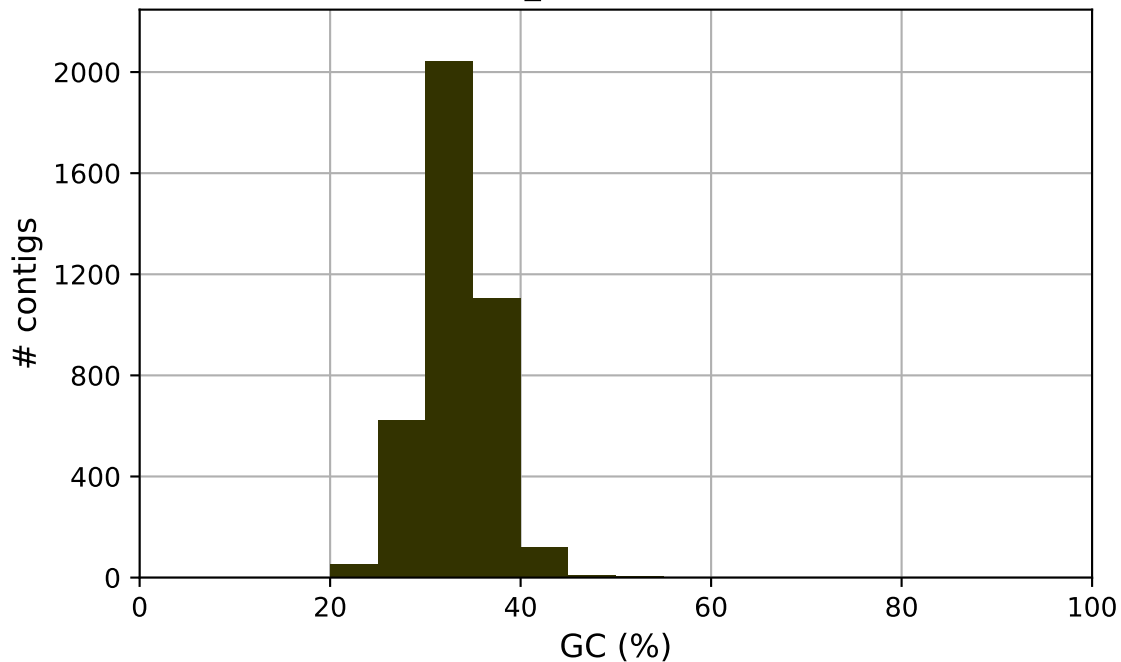
MG5_ets

MG5_sjw GC content



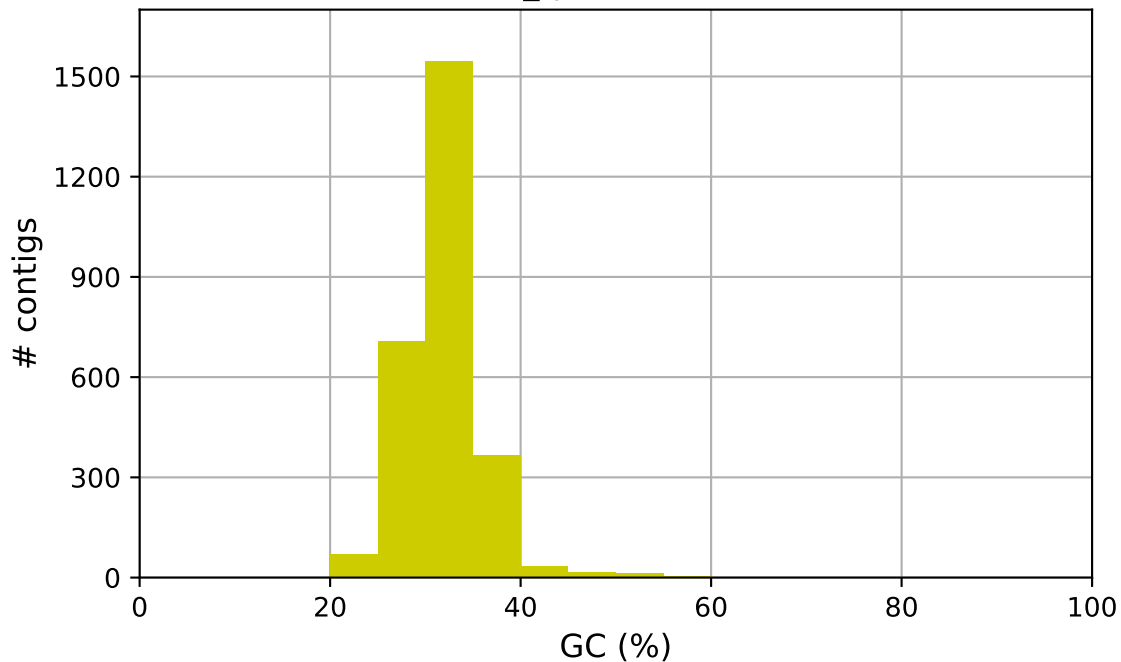
MG5_sjw

MG6_ets GC content



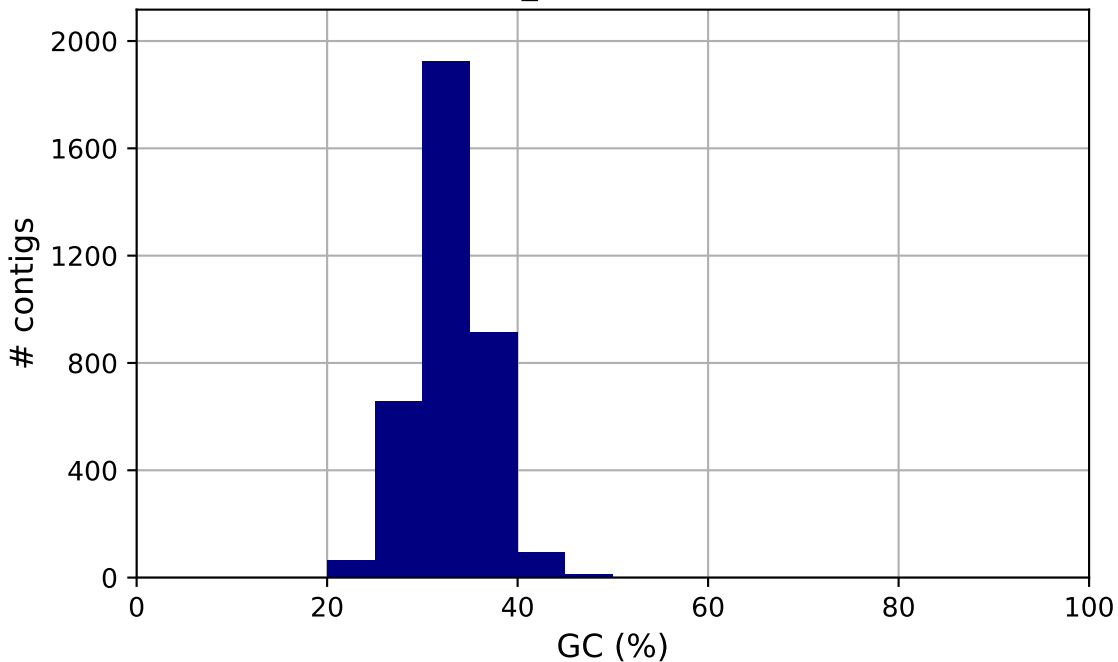
MG6_ets

MG6_sjw GC content



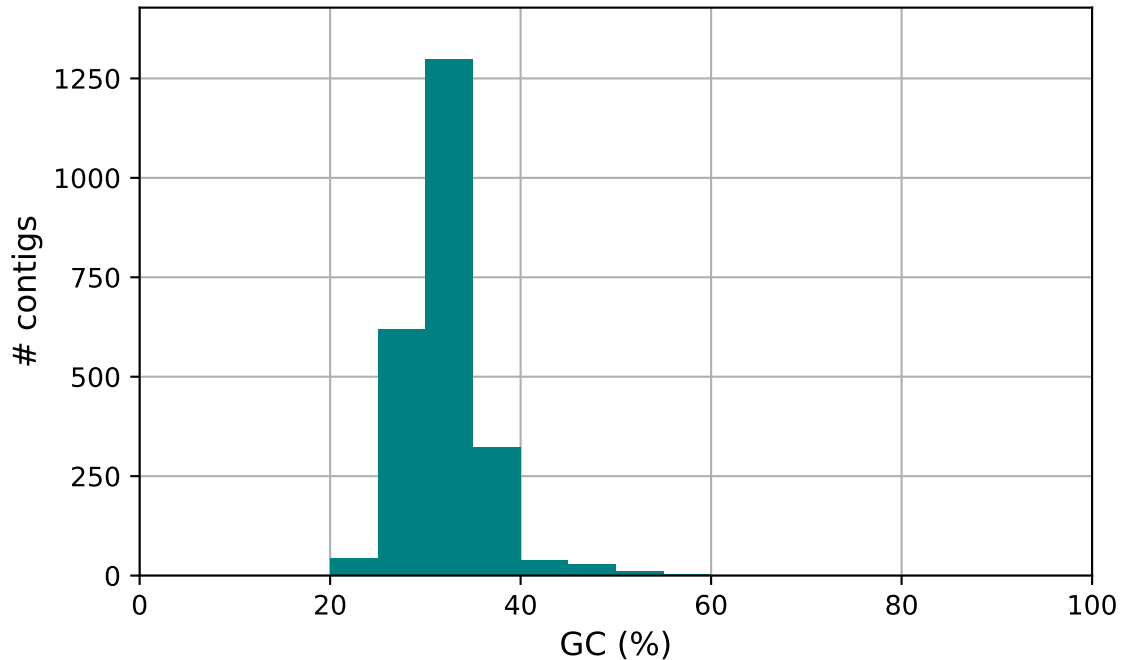
MG6_sjw

MG7_ets GC content



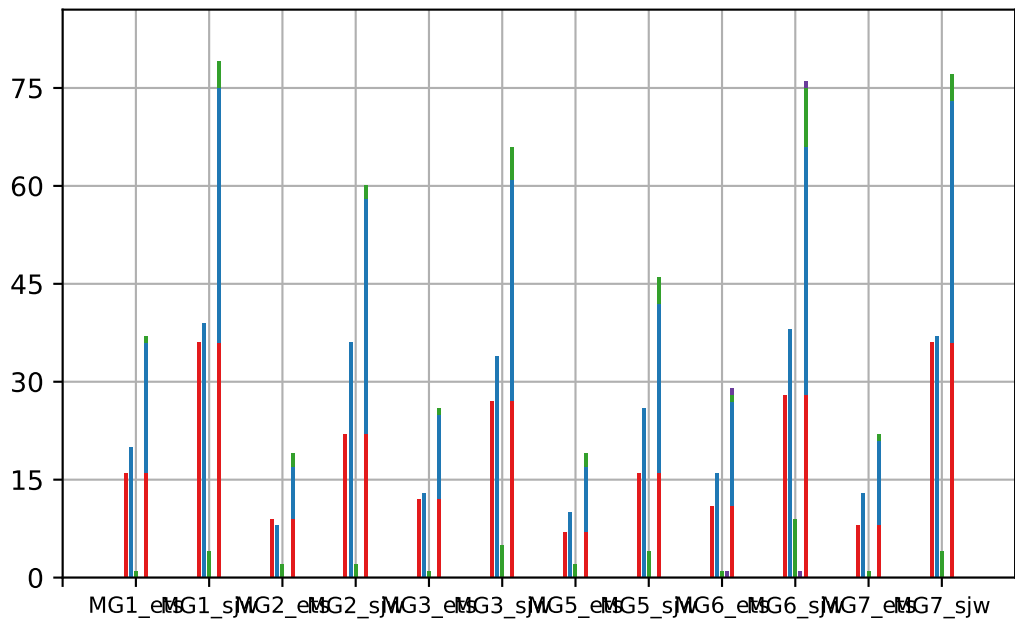
MG7_ets

MG7_sjw GC content

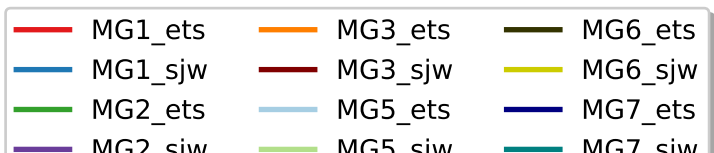
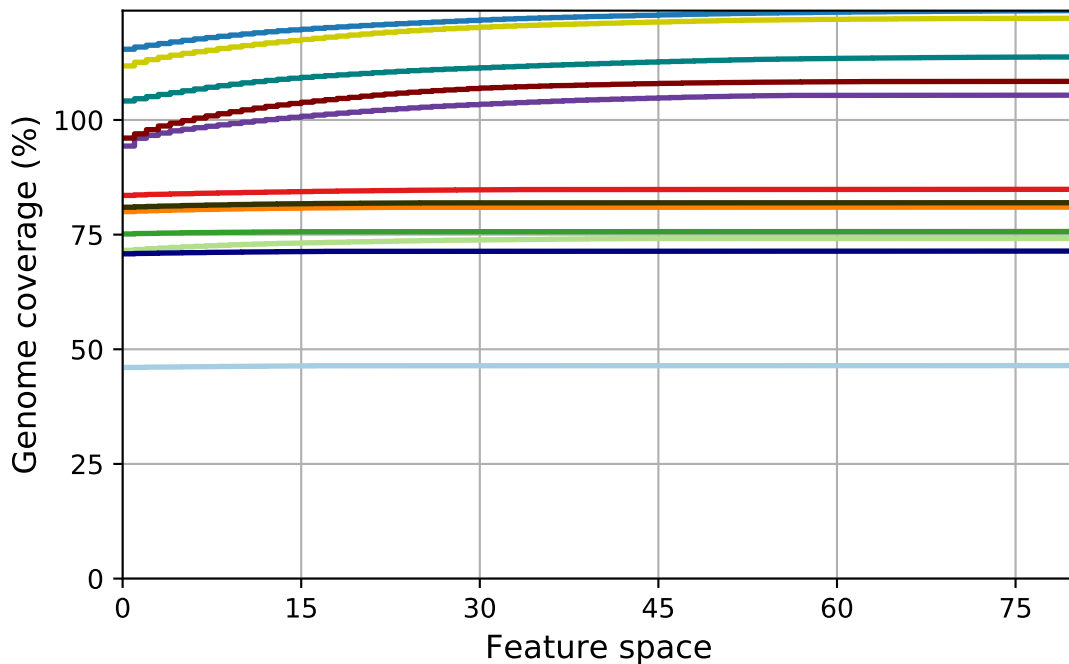


MG7_sjw

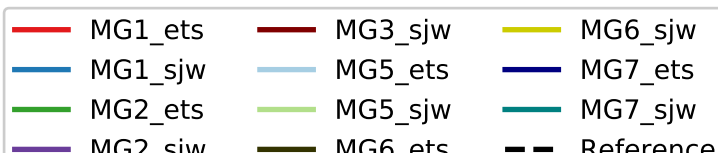
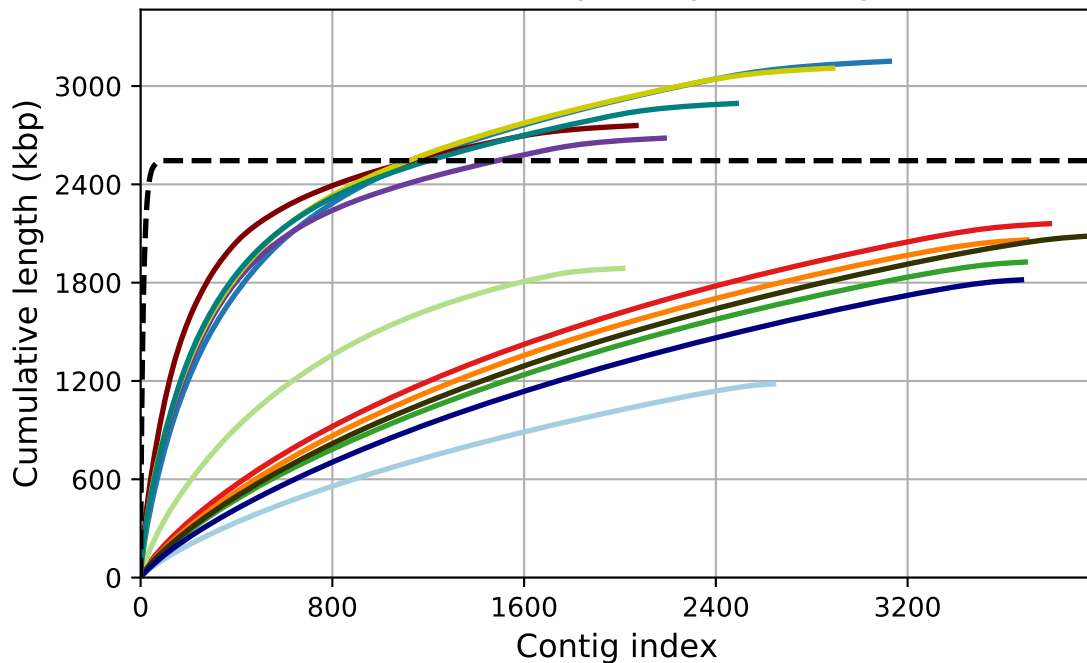
Misassemblies



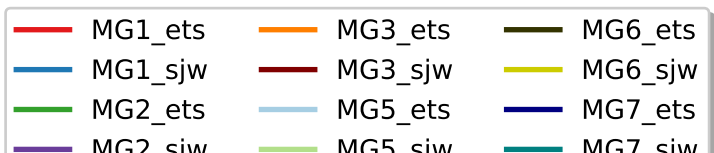
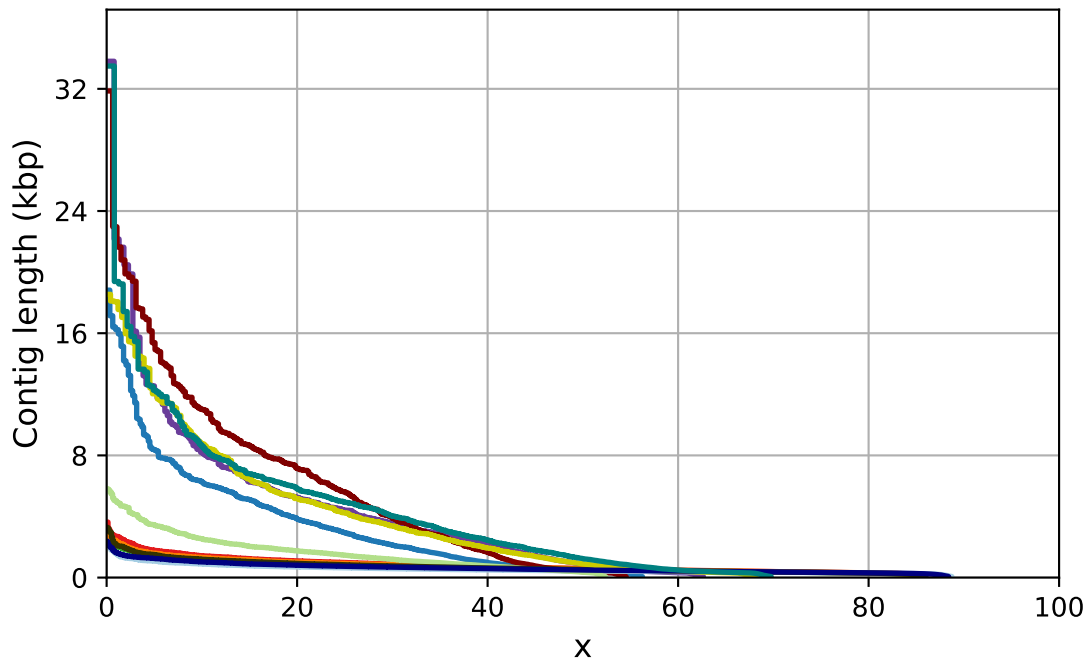
FRCurve (misassemblies)



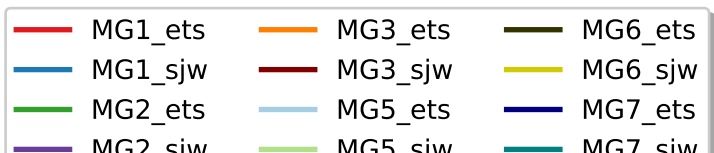
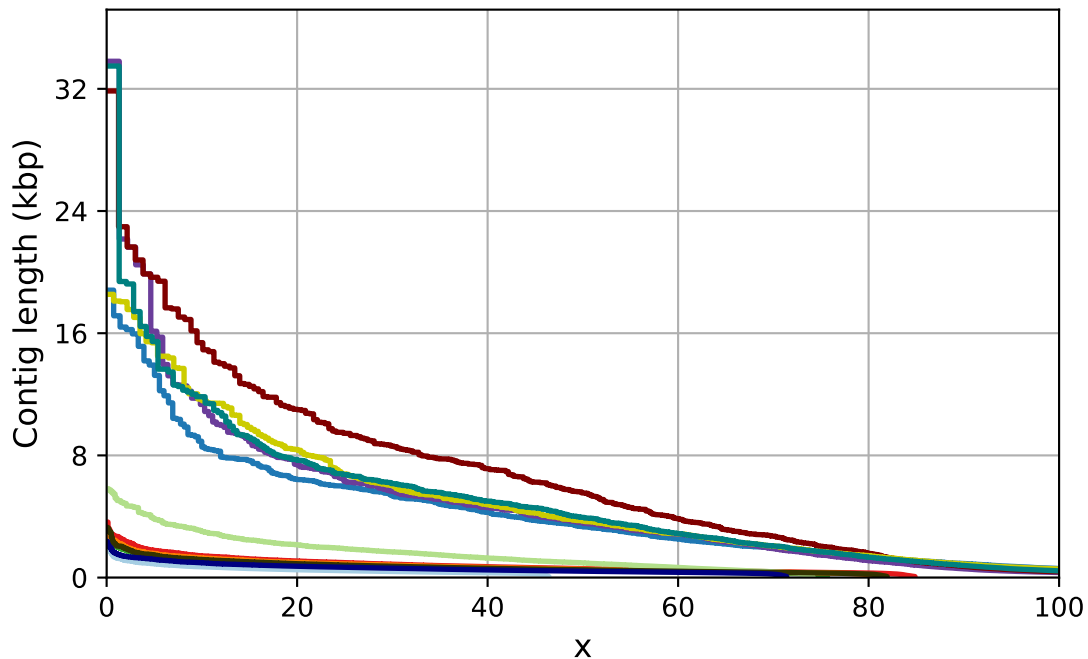
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

