

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)	692	857	490	641	511	422	388	420	682	960	525	812
# contigs (>= 5000 bp)	20	118	0	115	0	115	0	116	8	102	4	122
# contigs (>= 10000 bp)	0	39	0	40	0	52	0	47	0	31	0	33
# contigs (>= 25000 bp)	0	2	0	9	0	12	0	11	0	4	0	2
# contigs (>= 50000 bp)	0	0	0	2	0	3	0	1	0	1	0	0
Total length (>= 1000 bp)	1280473	2688527	727933	2517740	755401	2760993	557136	2198718	1183614	2776390	849444	2545163
Total length (>= 5000 bp)	117617	1120403	0	1378461	0	2030940	0	1473139	47413	1022542	22822	1119308
Total length (>= 10000 bp)	0	587059	0	870320	0	1583033	0	986029	0	539950	0	541782
Total length (>= 25000 bp)	0	78286	0	401773	0	975027	0	450118	0	184026	0	63722
Total length (>= 50000 bp)	0	0	0	180988	0	687555	0	94911	0	84933	0	0
# contigs	2885	3247	2919	2015	2708	1316	2730	938	3202	3861	2845	2842
Largest contig	7853	43497	4361	122265	4065	516683	4655	94911	7733	84933	6603	37343
Total length	2408099	3812066	2023376	3185402	1965545	3183308	1824752	2444847	2489927	4115203	2084212	3517417
Reference length	2296803	2296803	2296803	2296803	2296803	2296803	2296803	2296803	2296803	2296803	2296803	2296803
GC (%)	37.12	37.39	37.51	37.99	37.46	41.33	37.44	37.88	37.23	37.45	37.30	37.28
Reference GC (%)	36.89	36.89	36.89	36.89	36.89	36.89	36.89	36.89	36.89	36.89	36.89	36.89
N50	1078	2411	788	3761	826	9999	734	7521	951	1997	846	2478
NG50	1142	4825	699	6769	710	19348	606	8348	1031	4408	767	4924
N75	584	793	506	1288	534	2806	500	2851	541	724	526	883
NG75	634	2963	414	3256	417	8371	343	3582	618	2683	445	2569
L50	619	344	811	165	762	53	806	75	746	446	735	306
LG50	569	124	995	75	978	20	1161	65	648	130	867	128
L75	1384	1051	1620	527	1501	209	1561	208	1619	1325	1522	911
LG75	1247	275	2066	203	2025	68	2412	174	1370	302	1853	291
# misassemblies	7	24	1	16	3	17	4	9	11	27	7	17
# misassembled contigs	7	24	1	16	3	15	4	9	11	26	7	17
Misassembled contigs length	9802	82950	512	107290	3109	196733	3721	73558	11330	63047	4985	77822
# local misassemblies	5	21	2	9	1	8	2	11	4	17	5	16
# 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	1	25	2	10	2	6	2	3	2	28	1	14
# unaligned contigs	4 + 40 part	9 + 163 part	3 + 12 part	8 + 93 part	1 + 11 part	6 + 57 part	2 + 14 part	3 + 46 part	6 + 32 part	12 + 169 part	6 + 15 part	15 + 140 part
Unaligned length	47552	519710	10152	497262	13417	824392	13205	339429	38928	596478	17783	384208
Genome fraction (%)	81.755	89.722	74.875	85.417	74.935	82.896	70.551	81.009	81.690	89.863	75.782	88.896
Duplication ratio	1.261	1.603	1.174	1.374	1.138	1.243	1.121	1.135	1.310	1.710	1.191	1.539
# 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	1683.29	2493.07	1470.61	2143.93	1444.95	2007.59	1338.69	1786.03	1687.21	2639.29	1539.06	2356.62
# indels per 100 kbp	14.00	25.99	11.14	20.81	11.19	20.81	10.83	20.59	12.78	24.88	12.05	23.14
Largest alignment	7851	21617	4290	32140	4025	37919	4627	41962	7657	27640	6491	22424
Total aligned length	2280072	3250959	1893813	2666374	1848260	2338768	1703672	2087105	2337856	3475073	1962828	3090456
NA50	995	1373	717	2162	761	2692	671	4732	869	1107	772	1702
NGA50	1056	3470	628	3873	655	5767	538	5200	946	2855	699	3781
NA75	489	394	429	449	468	-	427	1019	447	360	452	465
NGA75	544	1735	339	1738	337	2030	-	1631	532	1596	374	1788
LA50	656	542	862	294	807	205	859	120	796	742	778	413
LGA50	602	184	1065	140	1044	94	1252	105	689	221	923	164
LA75	1523	1946	1779	1177	1632	-	1713	380	1802	2494	1663	1453
LGA75	1361	422	2317	361	2258	261	-	294	1505	491	2051	392

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

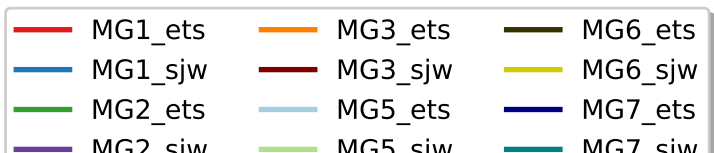
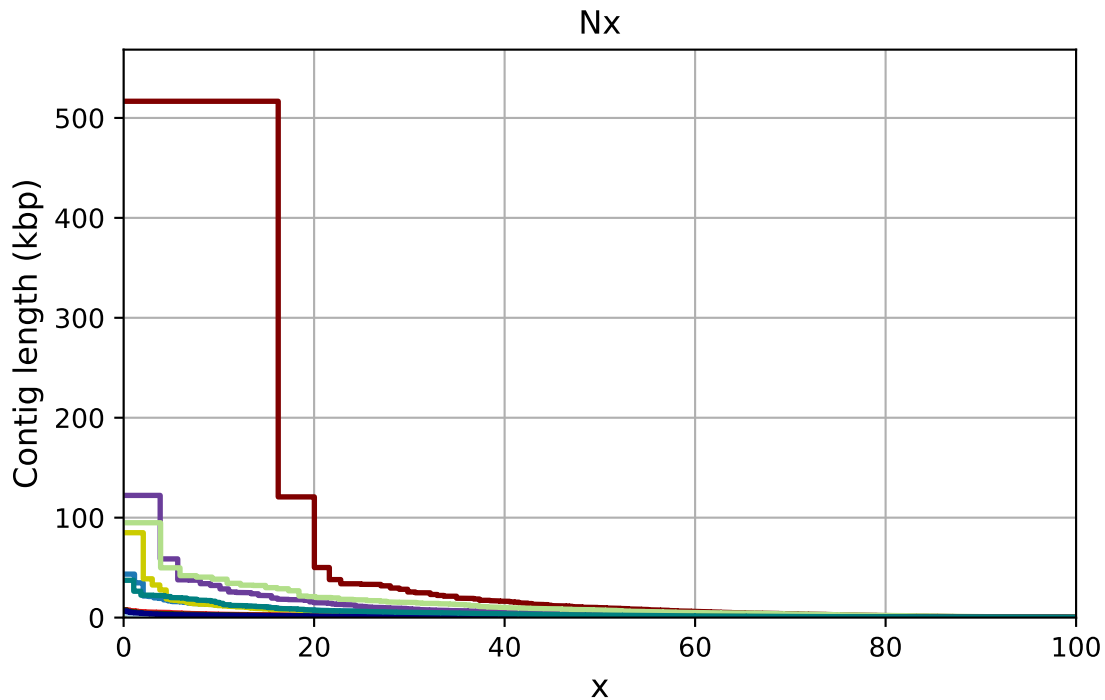
	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# misassemblies	7	24	1	16	3	17	4	9	11	27	7	17
# contig misassemblies	7	24	1	16	3	17	4	9	11	27	7	17
# c. relocations	7	19	1	15	3	15	0	8	10	23	4	15
# c. translocations	0	0	0	0	0	0	0	0	0	0	0	0
# c. inversions	0	5	0	1	0	2	4	1	1	4	3	2
# 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	7	24	1	16	3	15	4	9	11	26	7	17
Misassembled contigs length	9802	82950	512	107290	3109	196733	3721	73558	11330	63047	4985	77822
# possibly misassembled contigs	27	105	10	56	6	36	11	25	29	117	13	97
# possible misassemblies	27	117	10	64	6	45	11	30	29	130	13	105
# local misassemblies	5	21	2	9	1	8	2	11	4	17	5	16
# 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	1	25	2	10	2	6	2	3	2	28	1	14
# mismatches	31510	51216	25212	41930	24792	38105	21625	33128	31558	54305	26705	47967
# indels	262	534	191	407	192	395	175	382	239	512	209	471
# indels (<= 5 bp)	250	498	180	366	179	361	165	355	220	474	191	437
# indels (> 5 bp)	12	36	11	41	13	34	10	27	19	38	18	34
Indels length	408	1223	346	1166	384	1165	390	978	560	1257	563	1261

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).

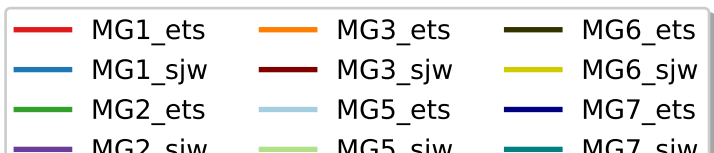
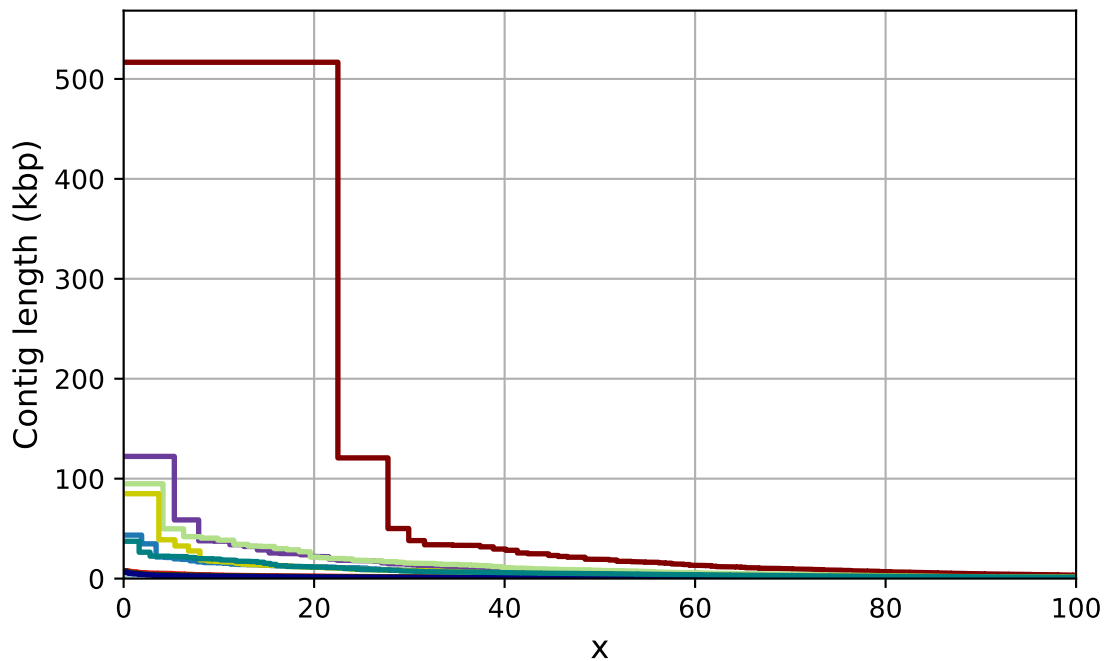
Unaligned report

	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	4	9	3	8	1	6	2	3	6	12	6	15
Fully unaligned length	2581	11430	1329	16934	403	519440	853	2359	4150	16004	3057	16293
# partially unaligned contigs	40	163	12	93	11	57	14	46	32	169	15	140
Partially unaligned length	44971	508280	8823	480328	13014	304952	12352	337070	34778	580474	14726	367915
# N's	0	0	0	0	0	0	0	0	0	0	0	0

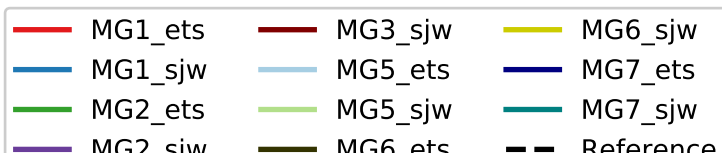
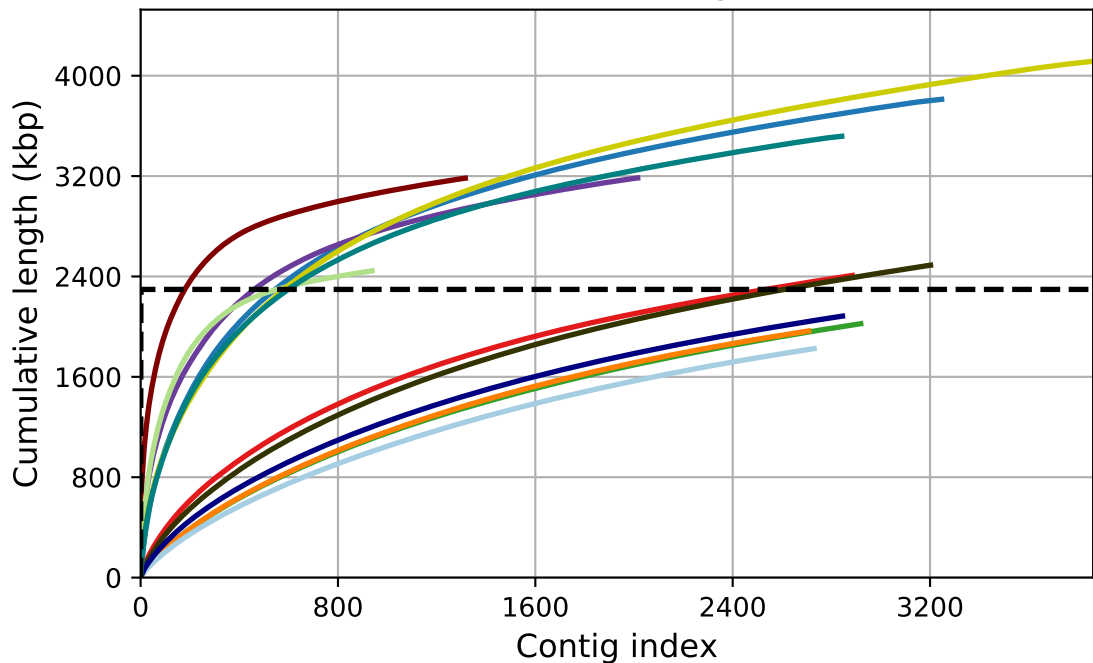
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



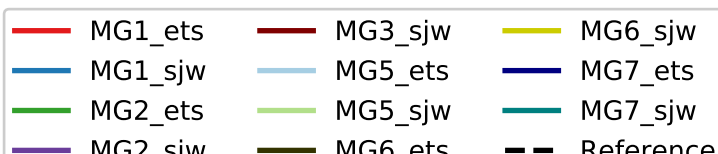
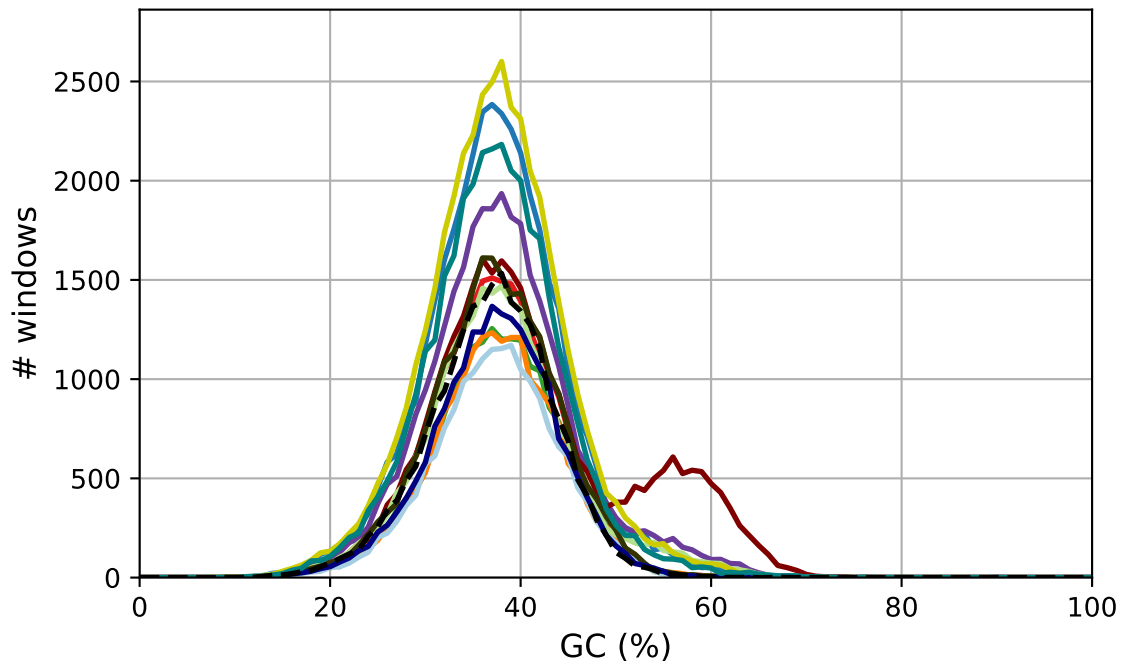
NGx



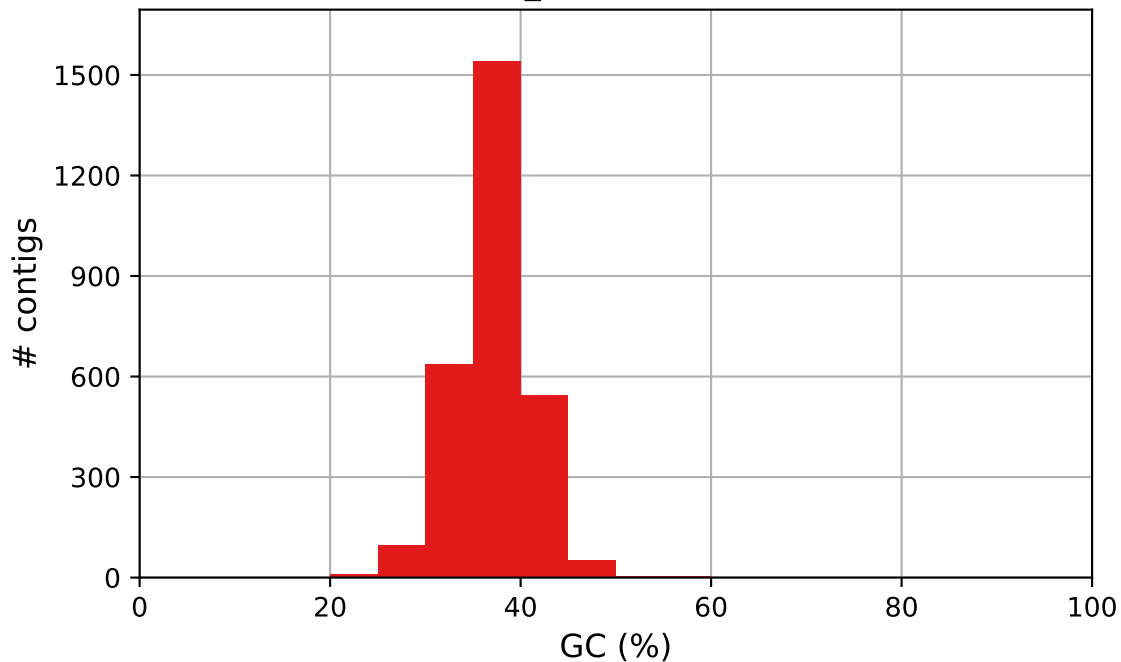
Cumulative length



GC content

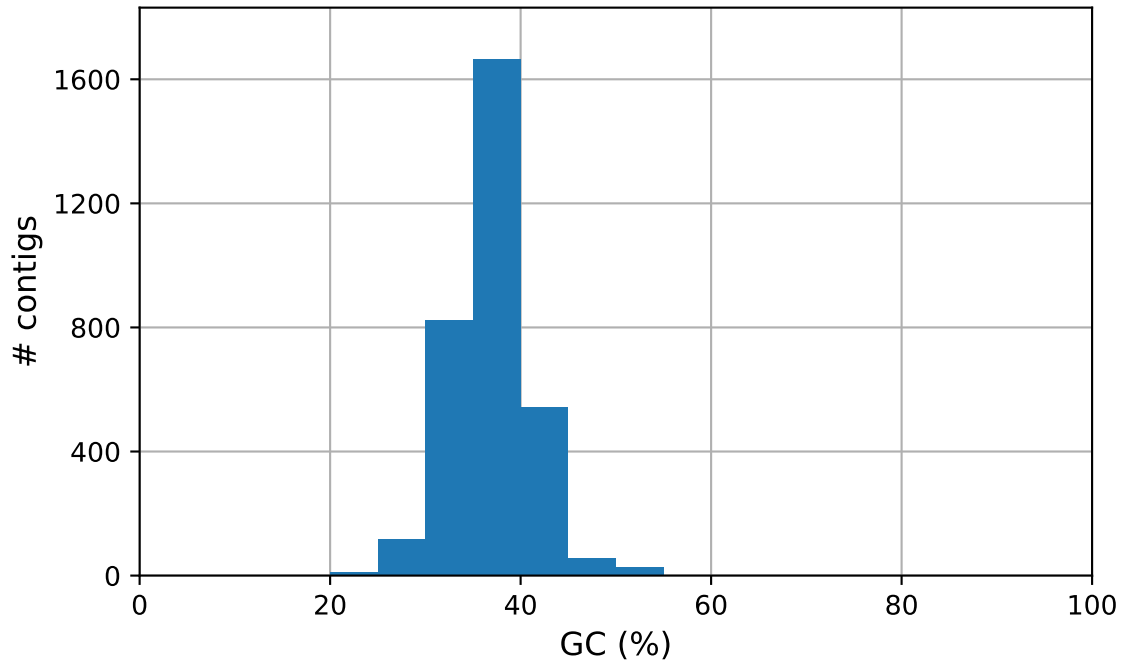


MG1_ets GC content



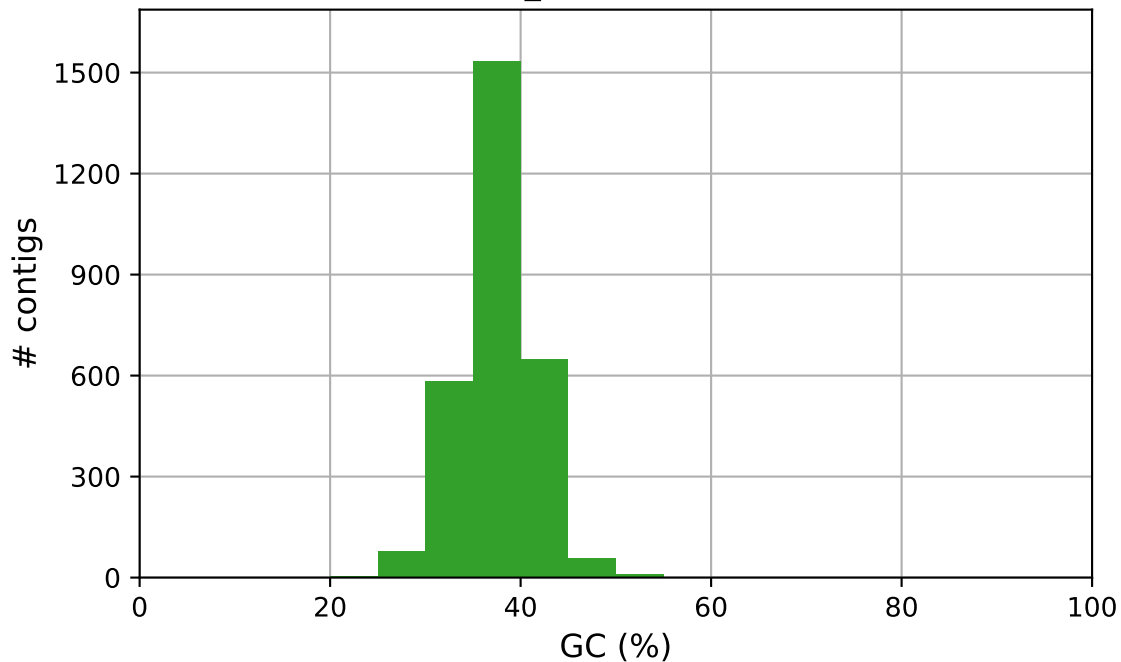
MG1_ets

MG1_sjw GC content



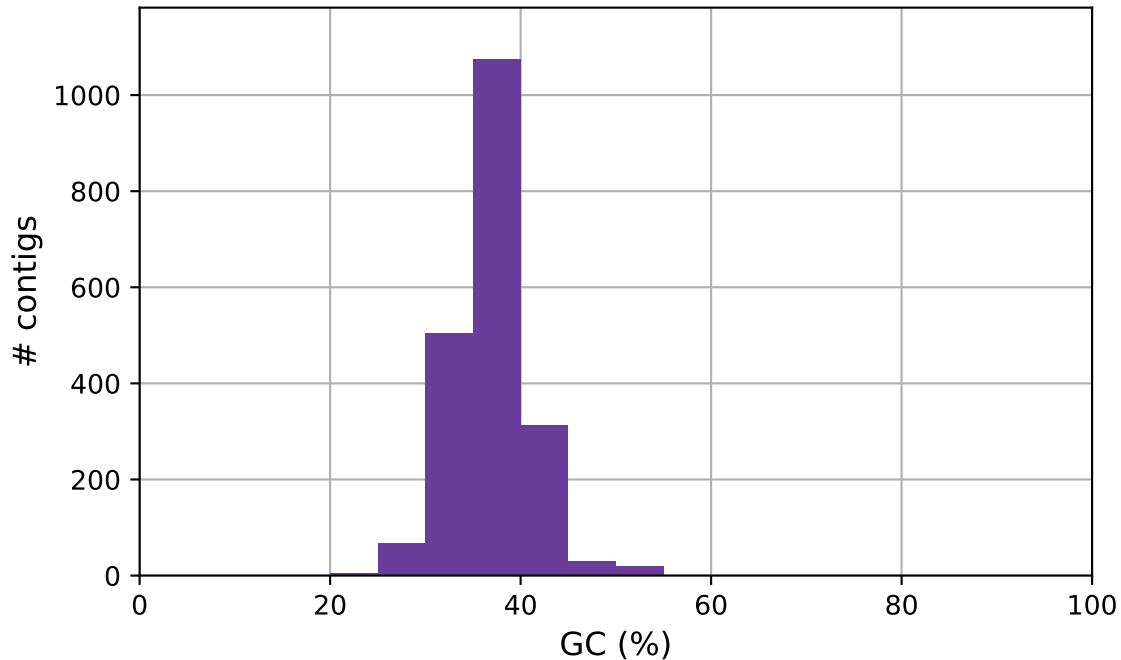
MG1_sjw

MG2_ets GC content



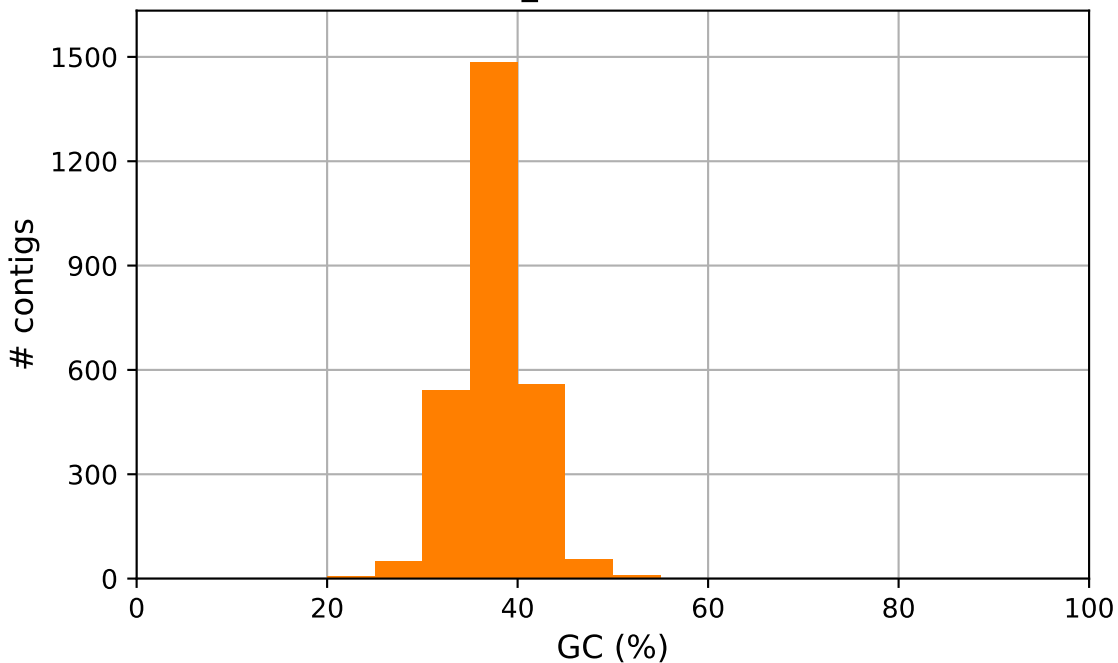
MG2_ets

MG2_sjw GC content



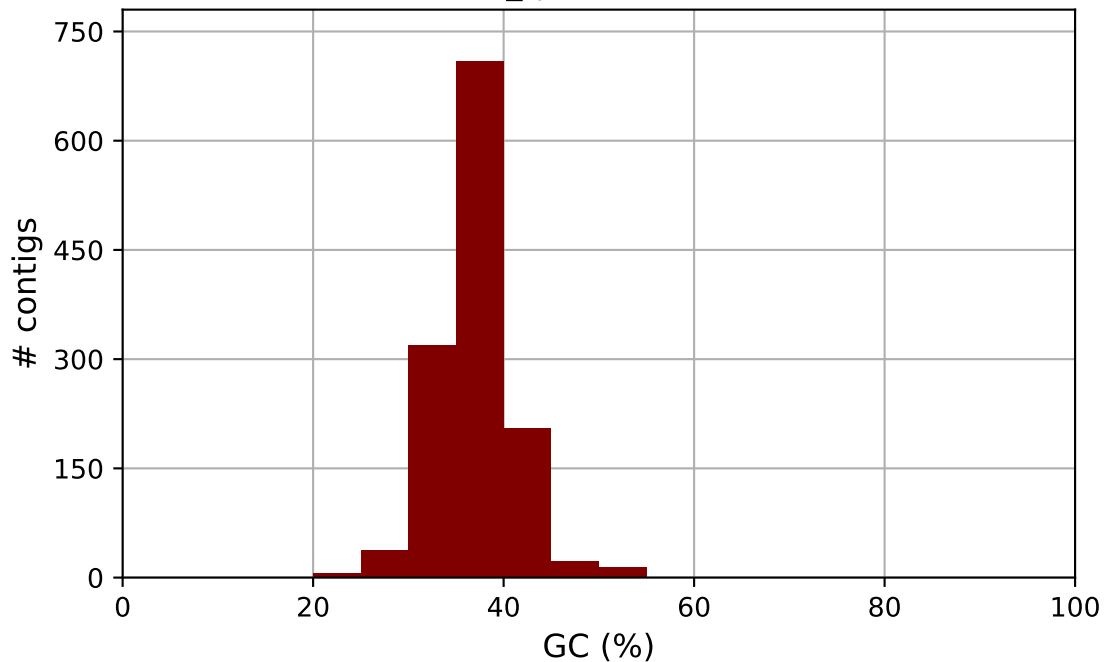
MG2_sjw

MG3_ets GC content



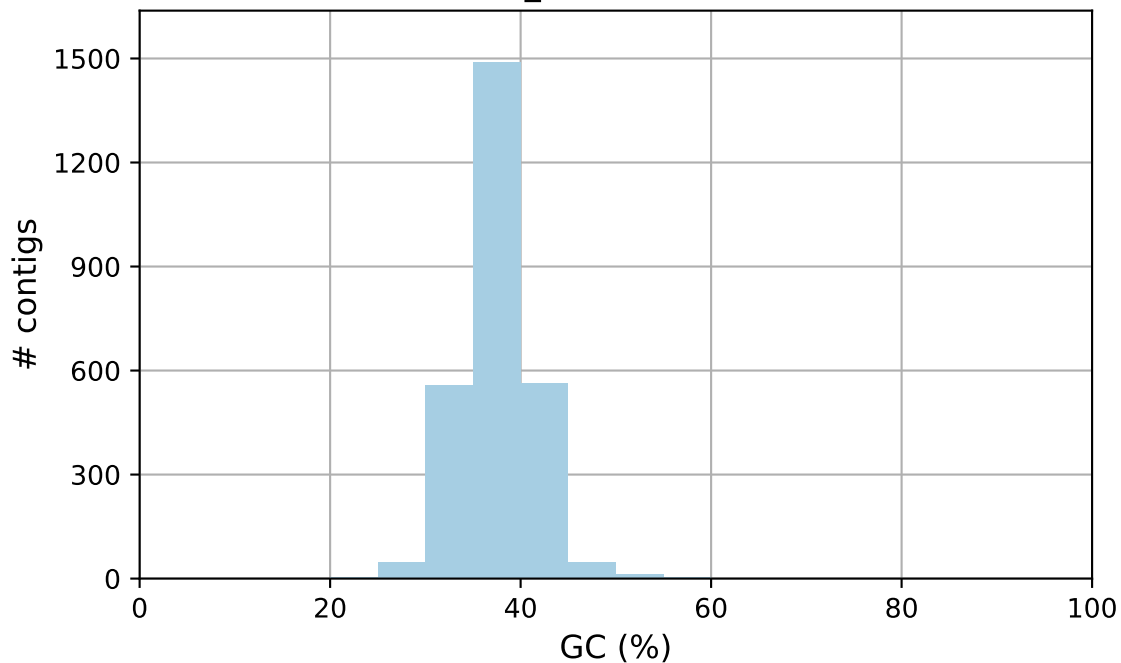
MG3_ets

MG3_sjw GC content



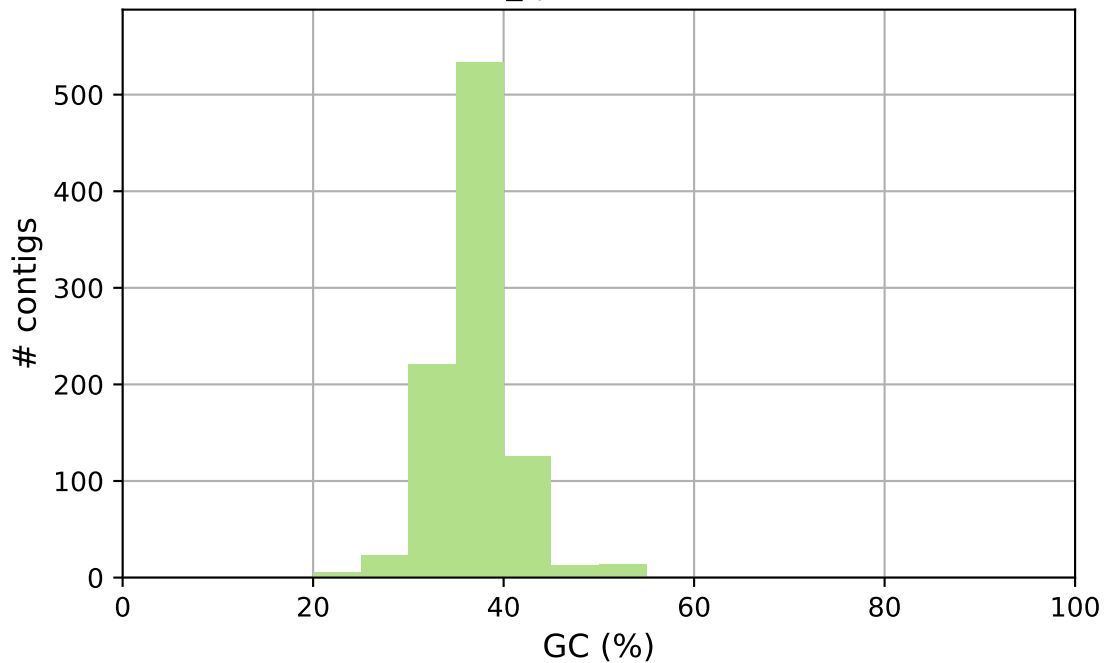
MG3_sjw

MG5_ets GC content



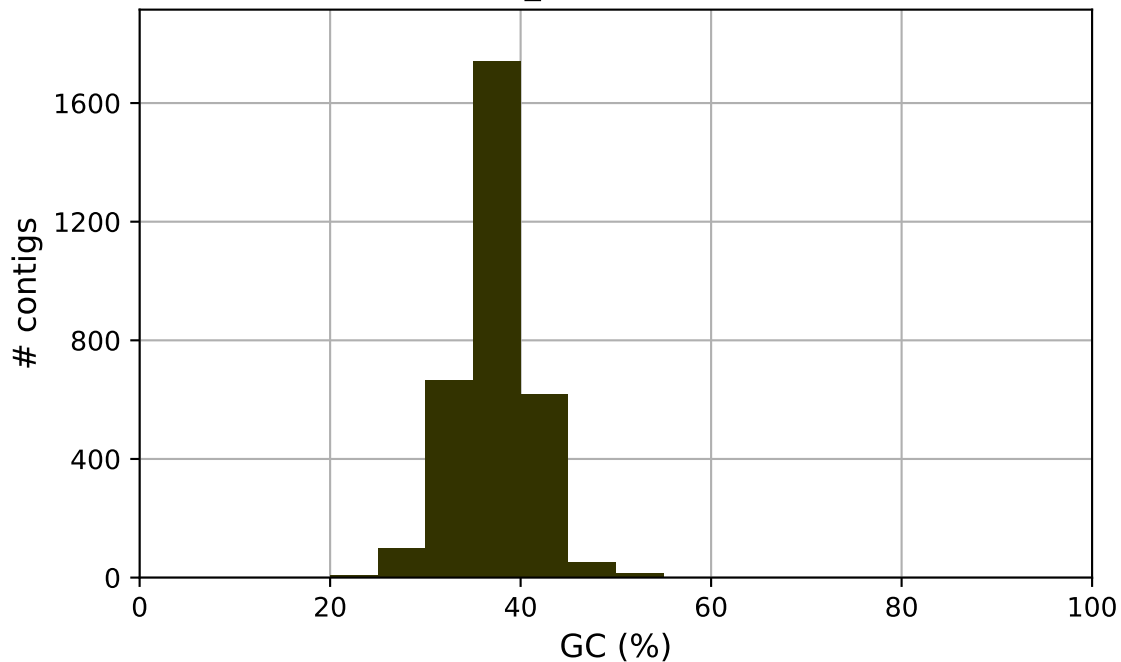
MG5_ets

MG5_sjw GC content



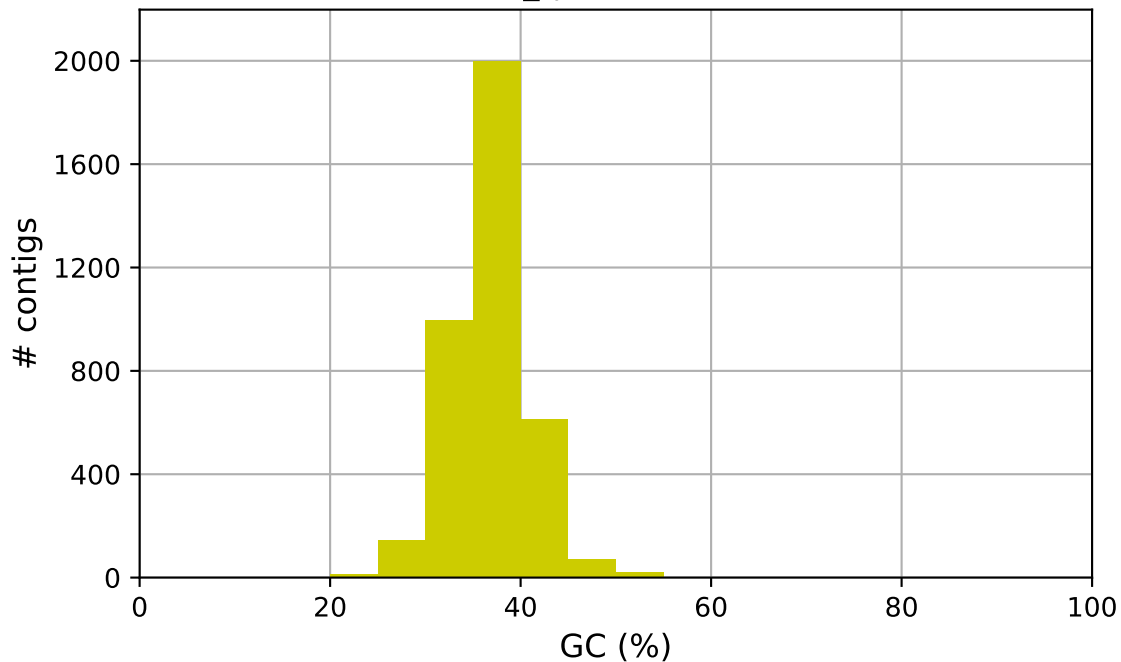
MG5_sjw

MG6_ets GC content



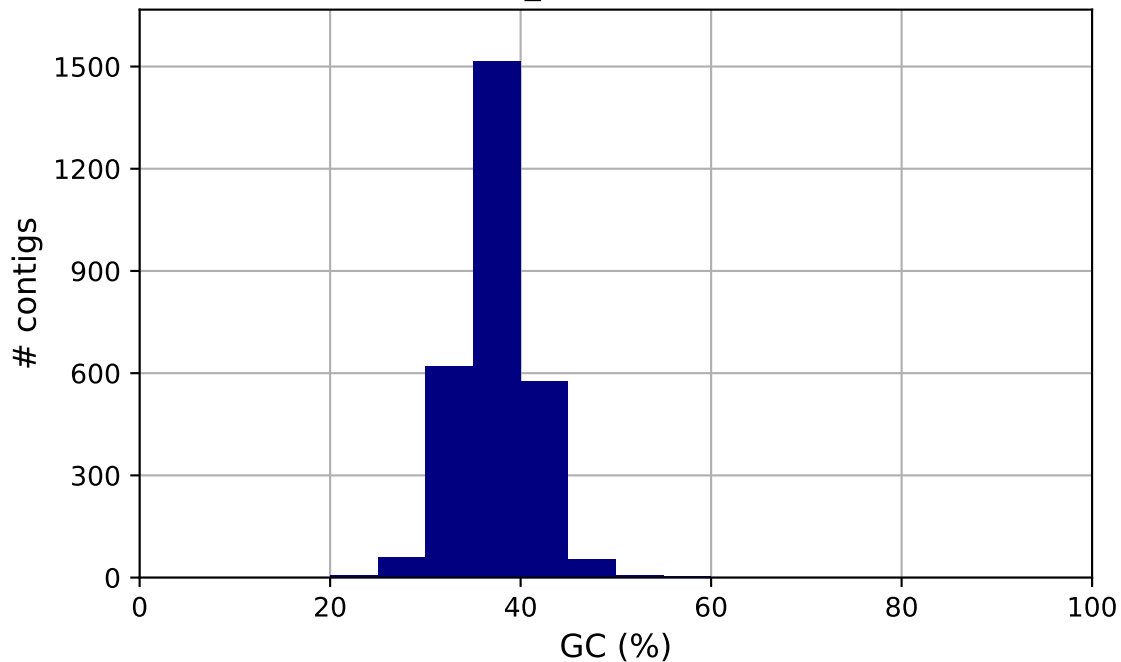
MG6_ets

MG6_sjw GC content



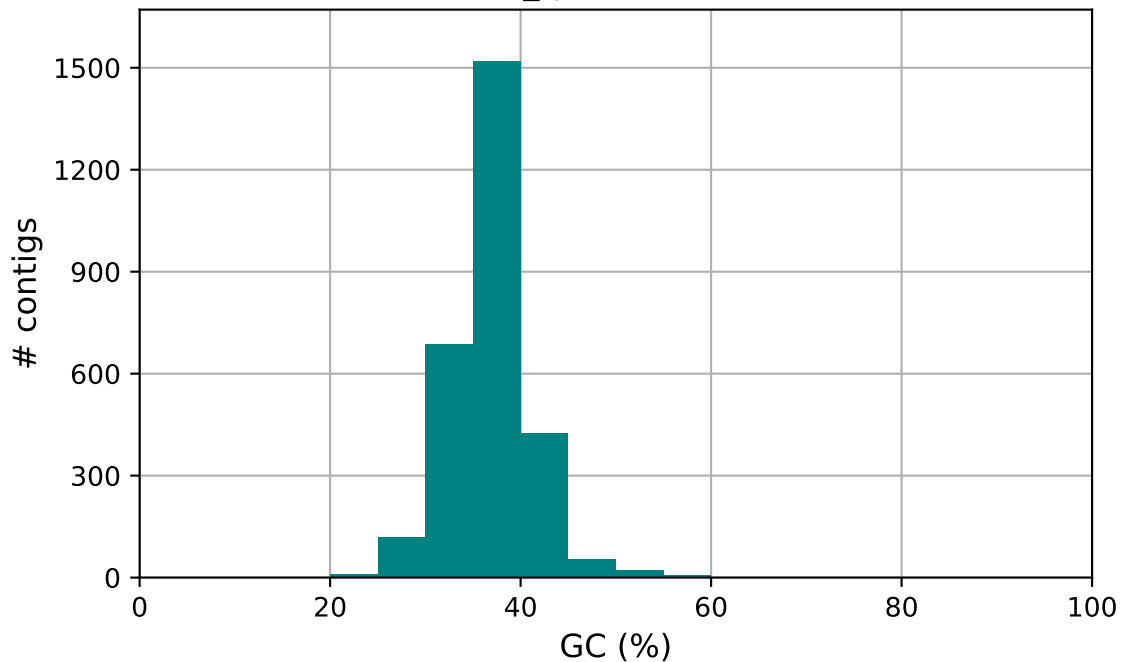
MG6_sjw

MG7_ets GC content



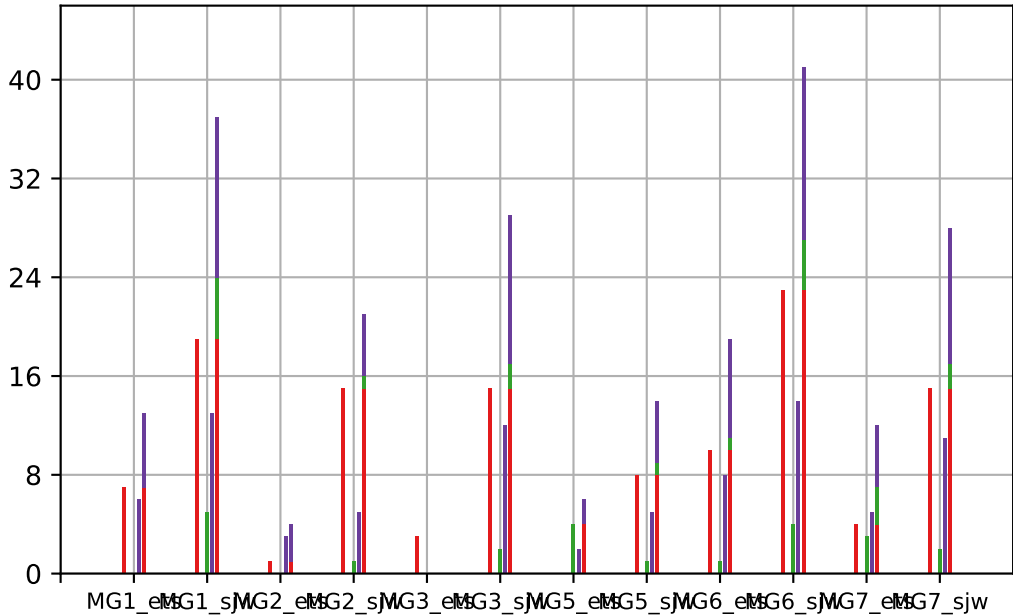
MG7_ets

MG7_sjw GC content



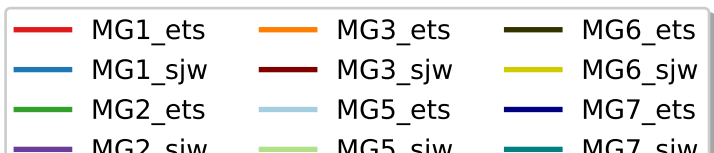
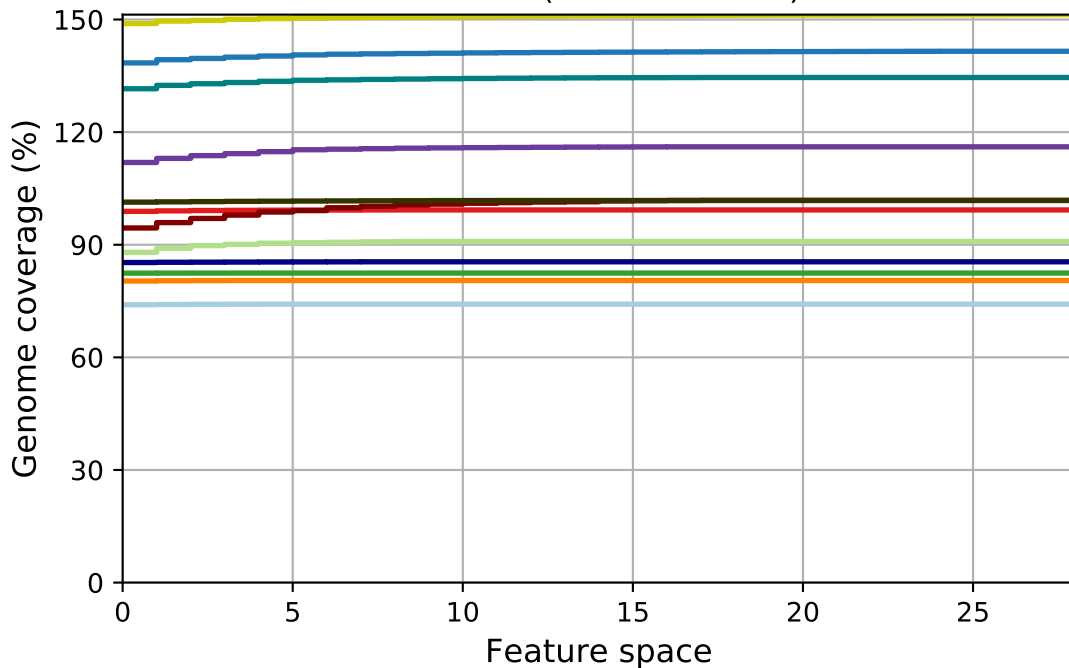
MG7_sjw

Misassemblies

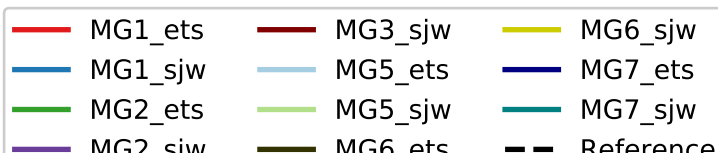
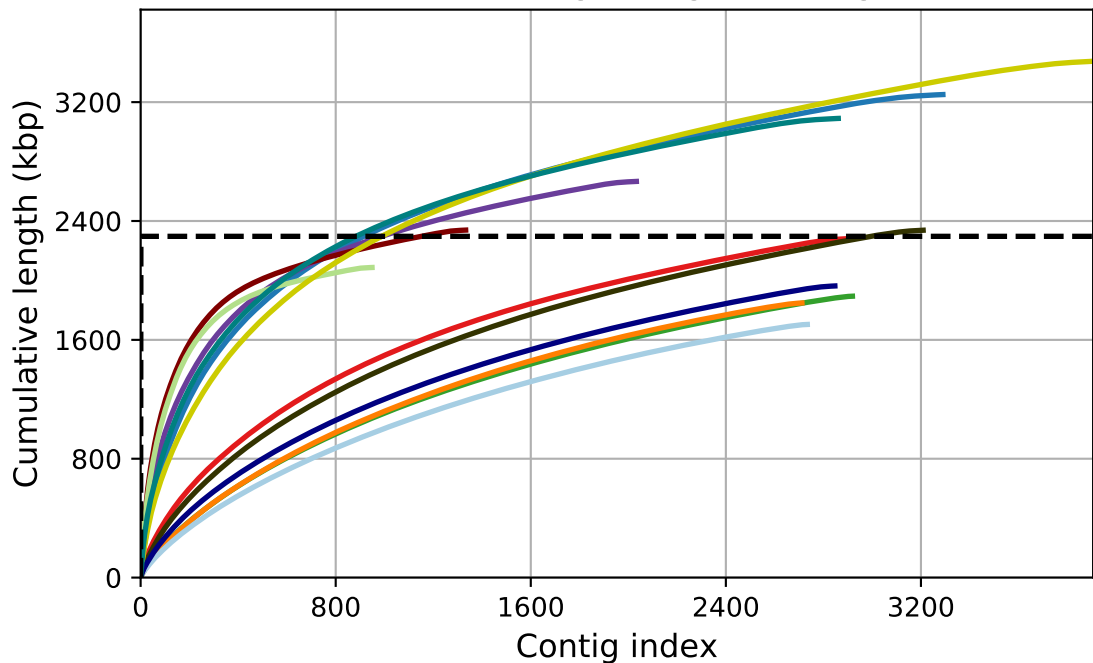


■ # relocations ■ # inversions ■ # interspecies translocations

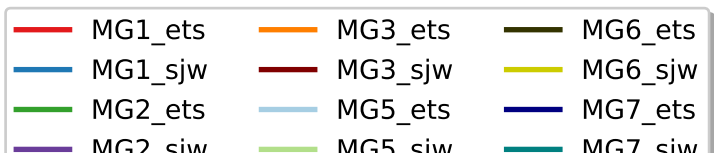
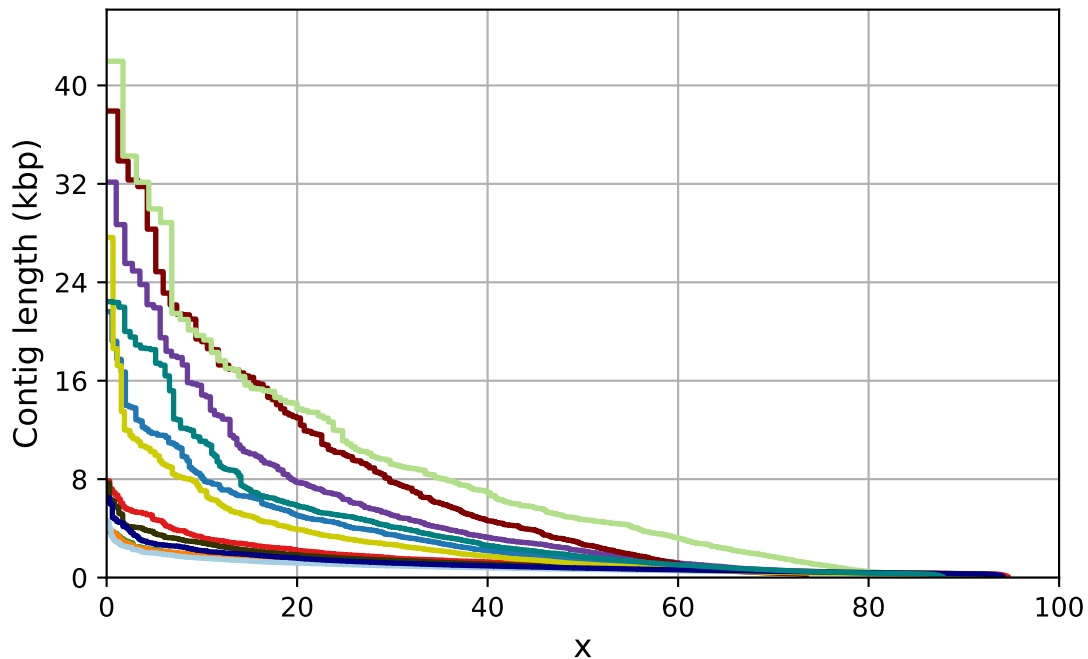
FRCurve (misassemblies)



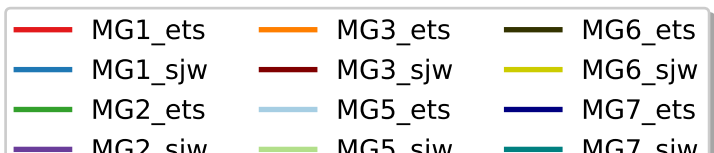
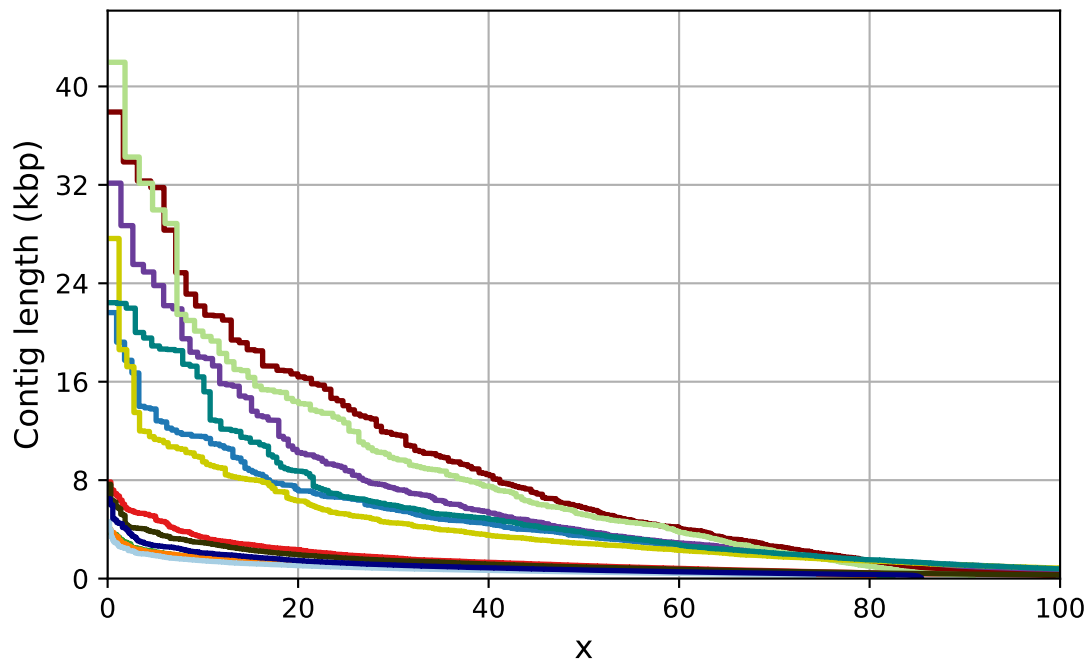
Cumulative length (aligned contigs)



NAX



NGAx



Genome fraction, %

