

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)	542	663	397	488	401	322	292	319	534	769	415	655
# contigs (>= 5000 bp)	11	83	0	84	0	83	0	83	4	65	1	81
# contigs (>= 10000 bp)	0	27	0	24	0	33	0	33	0	17	0	23
# contigs (>= 25000 bp)	0	2	0	6	0	9	0	6	0	4	0	2
# contigs (>= 50000 bp)	0	0	0	2	0	3	0	1	0	1	0	0
Total length (>= 1000 bp)	996201	2038357	582463	1877646	585212	2171055	413764	1604295	905583	2131711	652097	1959462
Total length (>= 5000 bp)	67759	811937	0	990003	0	1621622	0	1063076	25153	674804	5030	787585
Total length (>= 10000 bp)	0	442994	0	570997	0	1251120	0	702299	0	371764	0	390531
Total length (>= 25000 bp)	0	78286	0	306988	0	888053	0	298067	0	184026	0	63722
Total length (>= 50000 bp)	0	0	0	180988	0	687555	0	94911	0	84933	0	0
# contigs	2333	2520	2321	1647	2136	1055	2111	751	2535	3131	2328	2276
Largest contig	7853	43497	4361	122265	4052	516683	3373	94911	7733	84933	5030	37343
Total length	1918817	2927725	1608131	2451480	1541528	2521786	1395509	1806777	1939046	3207999	1665161	2731850
Reference length	1967776	1967776	1967776	1967776	1967776	1967776	1967776	1967776	1967776	1967776	1967776	1967776
GC (%)	37.02	37.38	37.43	38.14	37.40	42.49	37.36	38.25	37.15	37.41	37.17	37.34
Reference GC (%)	36.69	36.69	36.69	36.69	36.69	36.69	36.69	36.69	36.69	36.69	36.69	36.69
N50	1045	2219	789	3448	819	9999	729	7172	935	1880	825	2243
NG50	1018	4253	653	5013	661	19348	534	6024	915	3592	698	3781
N75	567	781	509	1118	534	2642	493	2495	534	675	516	881
NG75	537	2190	358	2430	342	7263	-	1774	521	2157	381	1969
L50	507	280	650	142	607	34	629	57	601	381	615	258
LG50	530	121	900	83	898	14	1090	69	616	139	814	126
L75	1130	844	1287	452	1187	156	1212	166	1296	1107	1257	751
LG75	1197	286	1917	229	1930	60	-	223	1336	318	1770	310
# misassemblies	4	14	1	10	3	7	6	5	5	16	4	11
# misassembled contigs	4	13	1	9	3	7	6	5	5	15	4	10
Misassembled contigs length	3754	57483	1048	34673	2521	100984	5845	49958	5259	20836	2291	34007
# local misassemblies	3	15	1	7	2	6	0	4	1	6	0	10
# 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	0	13	0	8	0	9	0	4	1	17	1	9
# unaligned contigs	2 + 27 part	10 + 123 part	1 + 14 part	10 + 73 part	1 + 6 part	5 + 47 part	1 + 7 part	3 + 41 part	4 + 19 part	16 + 136 part	3 + 8 part	19 + 112 part
Unaligned length	31100	406846	10671	420470	8868	811923	8009	353208	20727	505896	8896	354860
Genome fraction (%)	76.343	81.881	69.521	75.525	68.751	70.922	63.062	65.537	74.981	81.829	71.020	80.245
Duplication ratio	1.257	1.565	1.168	1.367	1.133	1.225	1.118	1.127	1.300	1.678	1.185	1.506
# 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	1697.26	2399.33	1473.92	2182.80	1479.94	2028.35	1400.58	1840.24	1698.52	2569.66	1558.52	2318.98
# indels per 100 kbp	15.38	22.59	13.09	22.81	11.83	18.78	10.56	17.76	13.69	25.96	12.67	22.04
Largest alignment	7851	21617	4290	25499	4025	37889	3373	41962	7657	27640	4881	22331
Total aligned length	1828972	2493877	1507198	2015384	1455243	1697426	1304918	1440402	1832704	2671641	1575131	2352570
NA50	965	1330	717	1823	759	1586	665	3470	855	999	762	1493
NGA50	948	2646	579	2923	600	3828	458	2732	840	2251	634	2597
NA75	490	395	435	402	469	-	424	418	454	344	448	417
NGA75	459	1309	278	961	-	569	-	-	440	1194	323	1211
LA50	534	444	691	269	643	225	671	113	634	658	643	378
LGA50	559	187	969	165	959	109	1186	140	651	241	860	181
LA75	1230	1535	1410	1078	1285	-	1328	474	1420	2158	1358	1291
LGA75	1307	453	2179	460	-	464	-	-	1468	541	1959	460

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

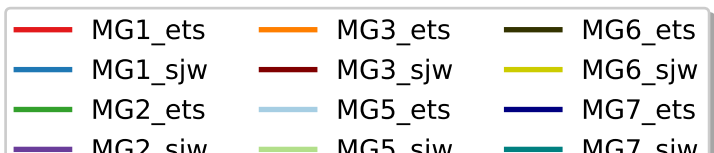
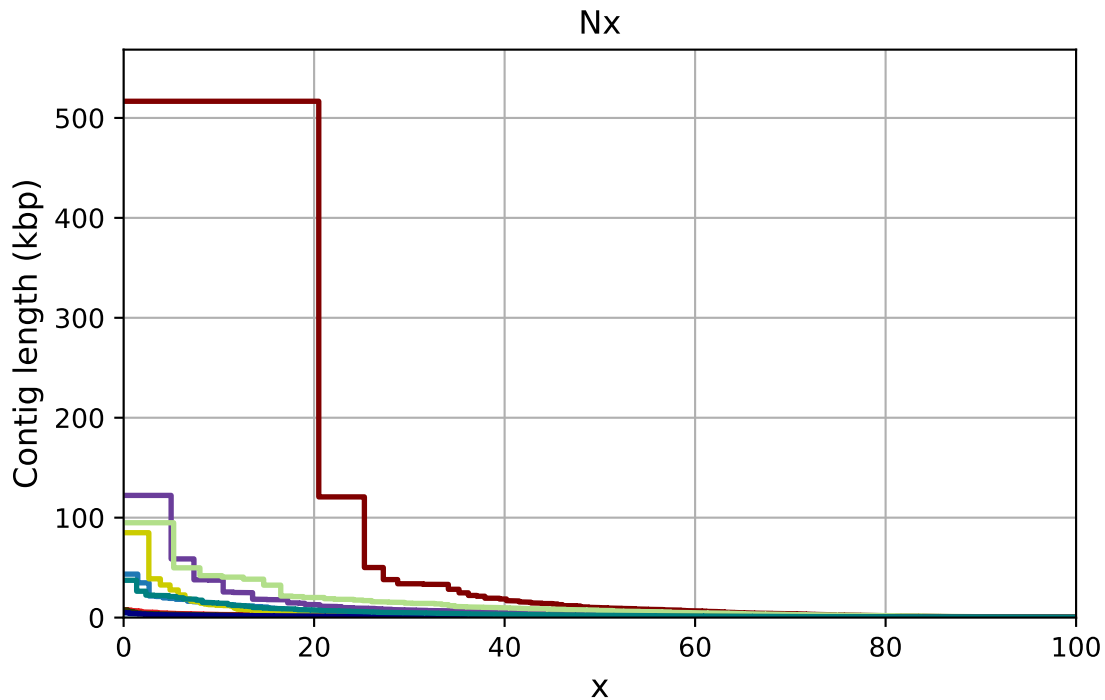
	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# misassemblies	4	14	1	10	3	7	6	5	5	16	4	11
# contig misassemblies	4	14	1	10	3	7	6	5	5	16	4	11
# c. relocations	1	7	0	5	1	4	0	2	4	8	1	5
# c. translocations	2	5	1	3	1	1	1	2	1	3	1	3
# c. inversions	1	2	0	2	1	2	5	1	0	5	2	3
# 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	4	13	1	9	3	7	6	5	5	15	4	10
Misassembled contigs length	3754	57483	1048	34673	2521	100984	5845	49958	5259	20836	2291	34007
# possibly misassembled contigs	22	74	8	49	4	28	3	26	11	89	8	66
# possible misassemblies	23	84	9	54	5	36	3	31	11	92	8	78
# local misassemblies	3	15	1	7	2	6	0	4	1	6	0	10
# 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	0	13	0	8	0	9	0	4	1	17	1	9
# mismatches	25494	38654	20161	32436	20019	28304	17378	23729	25058	41372	21778	36613
# indels	231	364	179	339	160	262	131	229	202	418	177	348
# indels (<= 5 bp)	226	343	175	313	154	250	126	217	194	392	165	326
# indels (> 5 bp)	5	21	4	26	6	12	5	12	8	26	12	22
Indels length	321	736	261	802	274	518	233	497	345	1031	386	726

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).

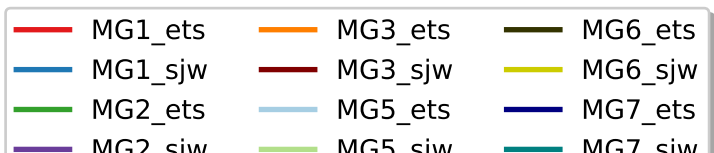
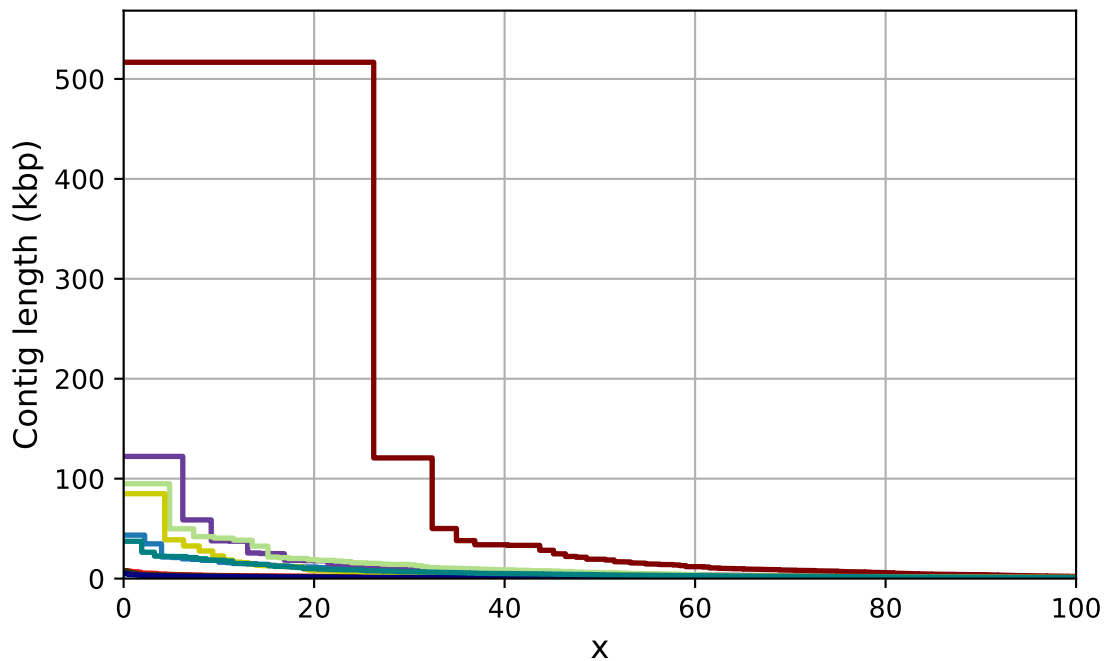
Unaligned report

	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	2	10	1	10	1	5	1	3	4	16	3	19
Fully unaligned length	1071	12117	411	26056	403	519427	437	19365	1559	24798	2265	23262
# partially unaligned contigs	27	123	14	73	6	47	7	41	19	136	8	112
Partially unaligned length	30029	394729	10260	394414	8465	292496	7572	333843	19168	481098	6631	331598
# N's	0	0	0	0	0	0	0	0	0	0	0	0

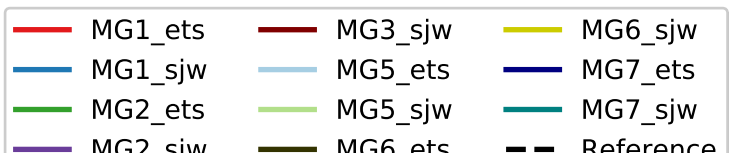
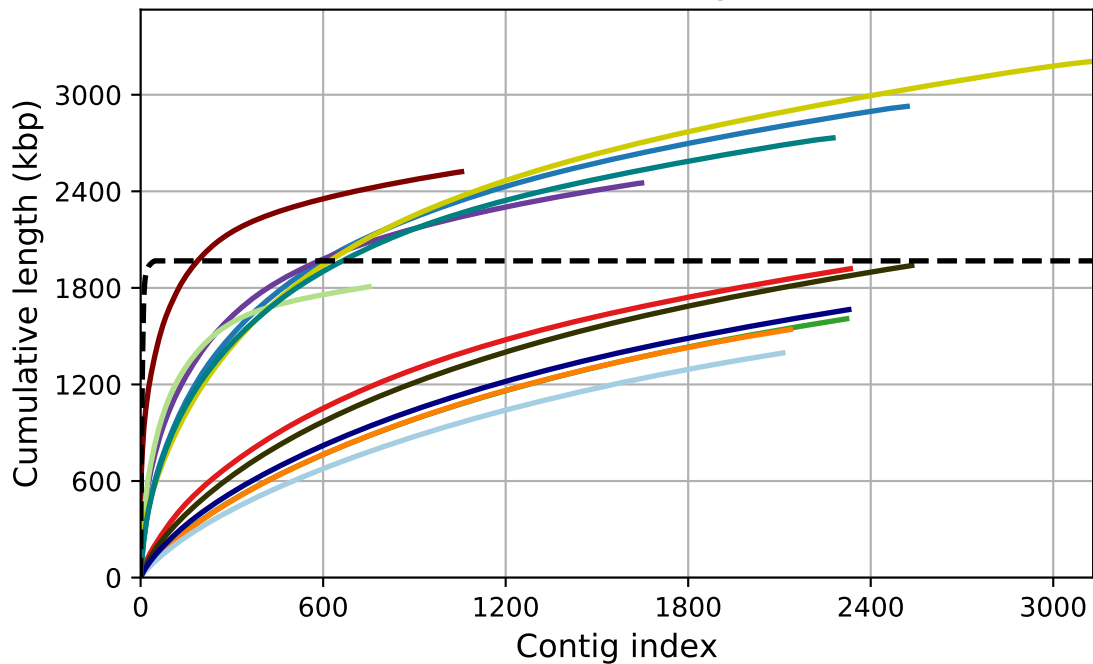
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



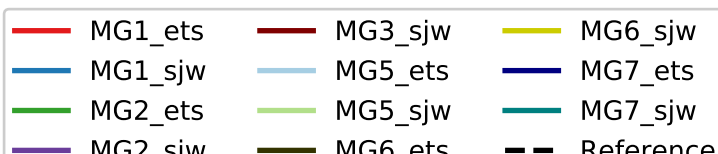
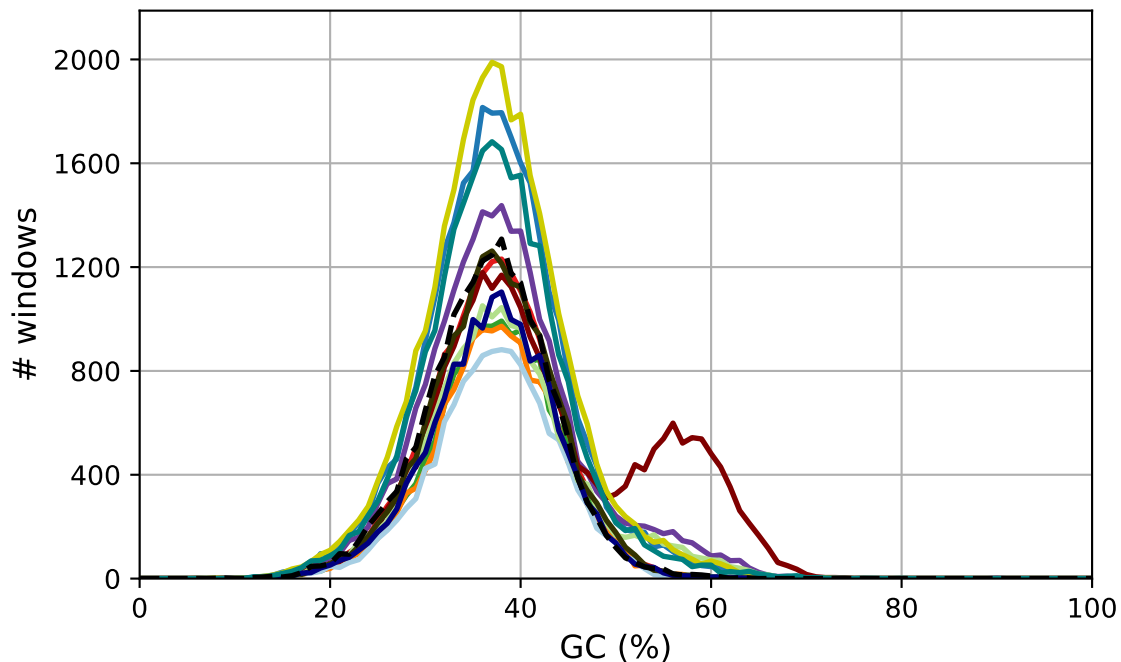
NGx



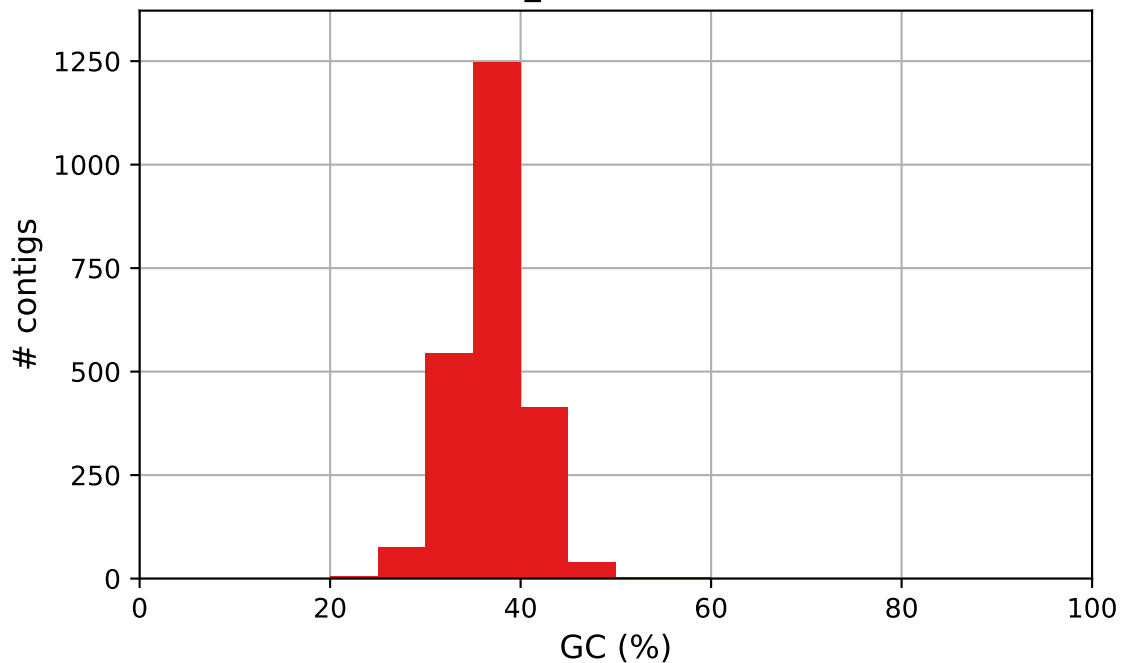
Cumulative length



GC content

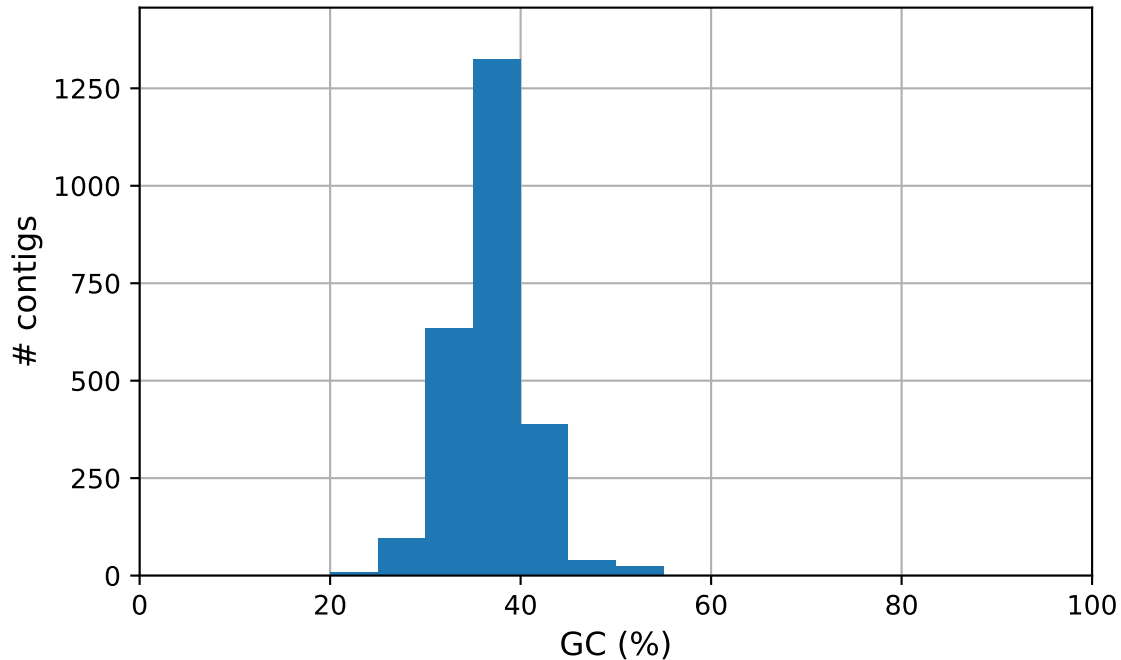


MG1_ets GC content



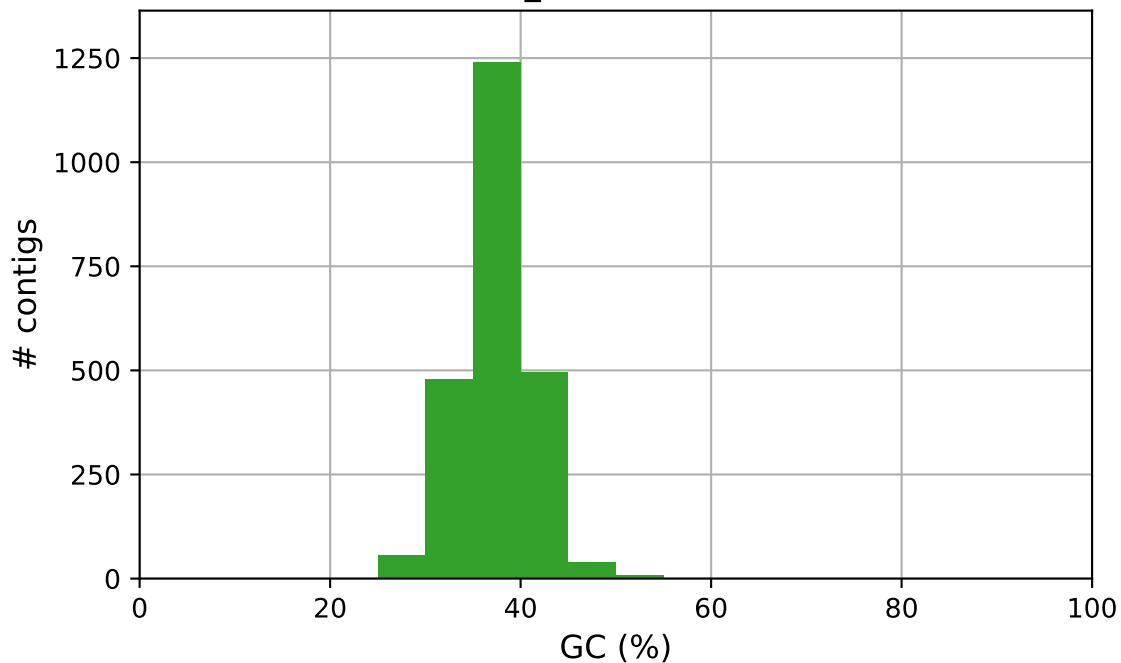
MG1_ets

MG1_sjw GC content



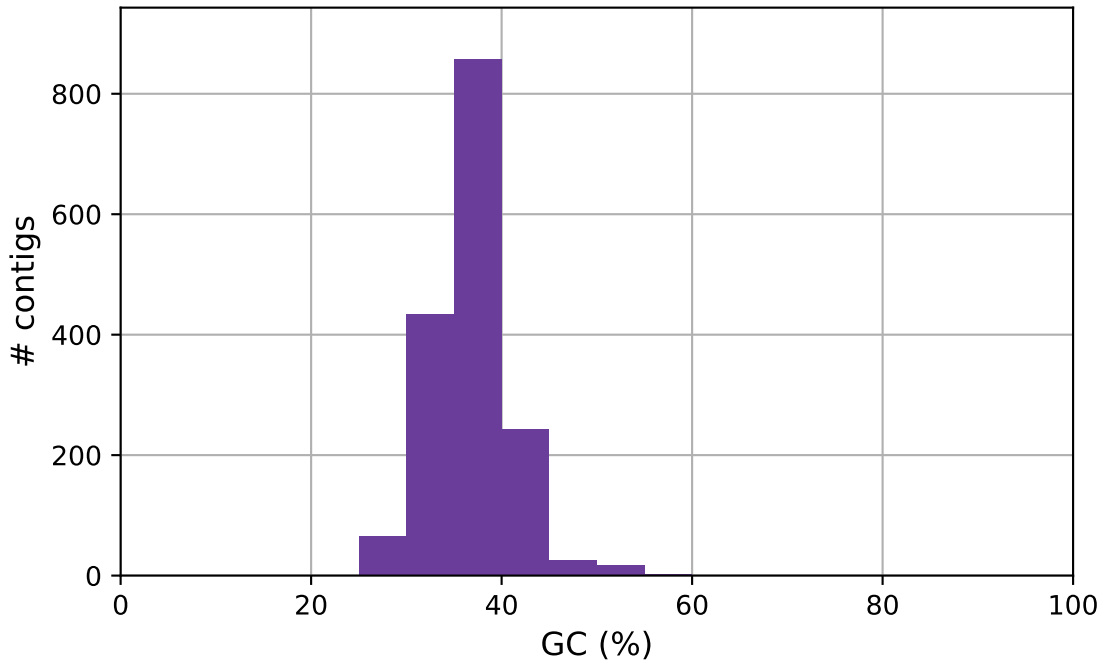
MG1_sjw

MG2_ets GC content



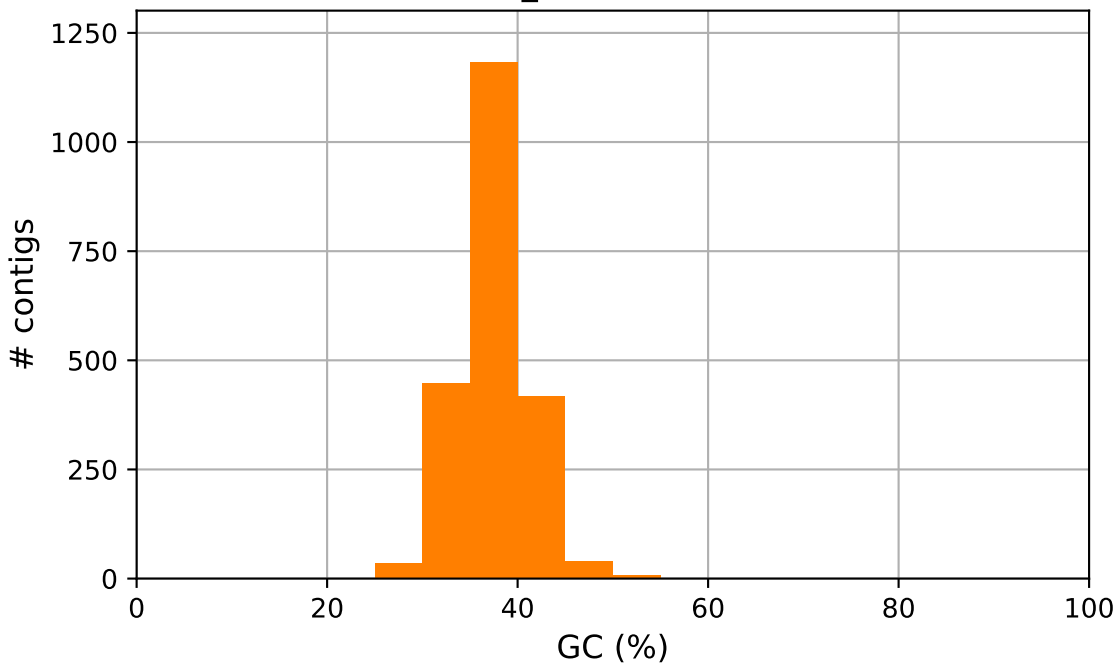
MG2_ets

MG2_sjw GC content



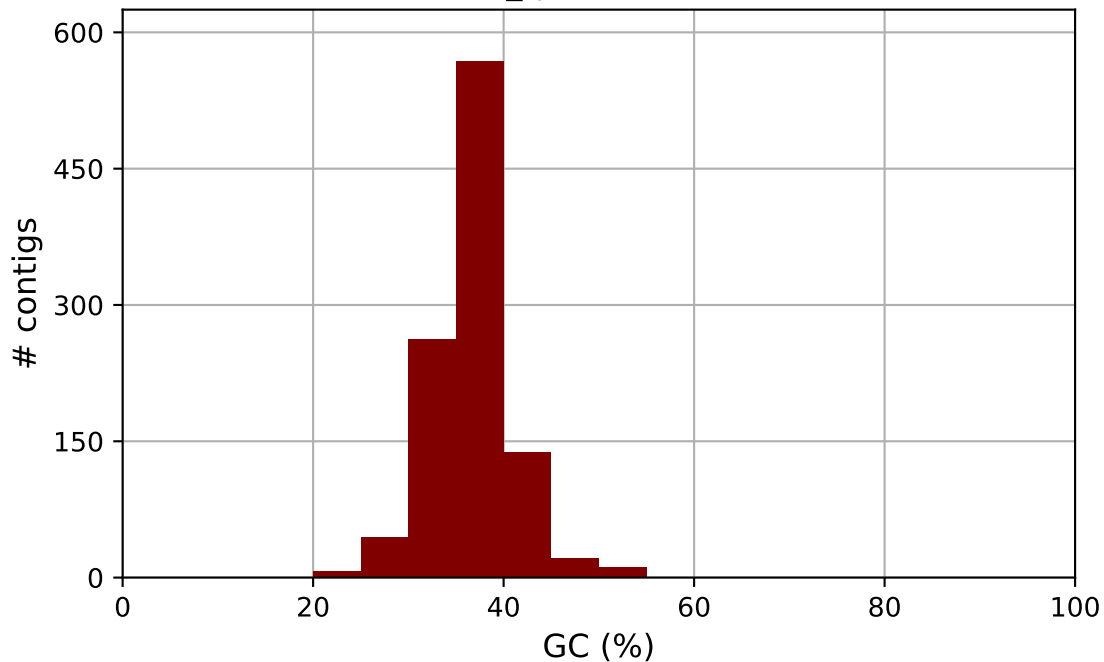
MG2_sjw

MG3_ets GC content



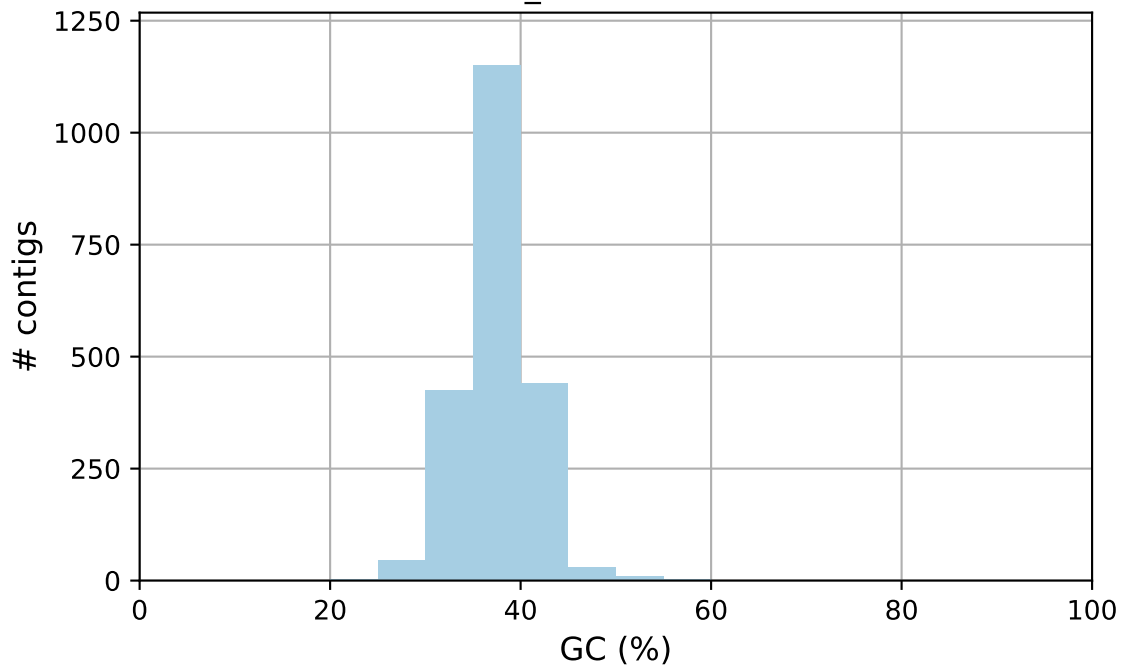
MG3_ets

MG3_sjw GC content



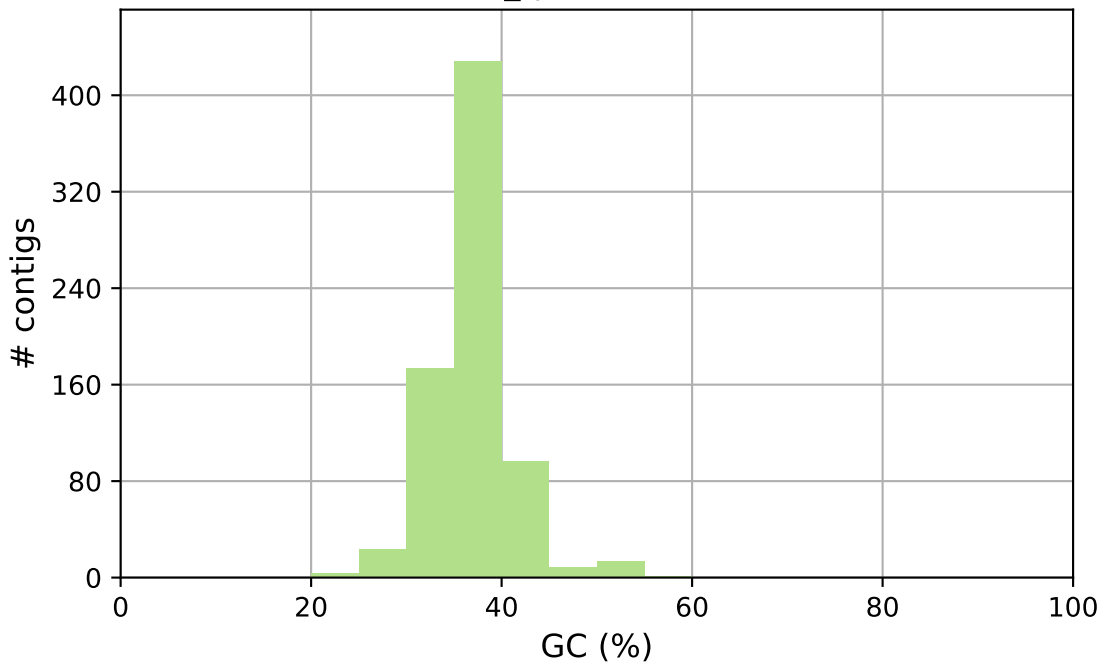
MG3_sjw

MG5_ets GC content



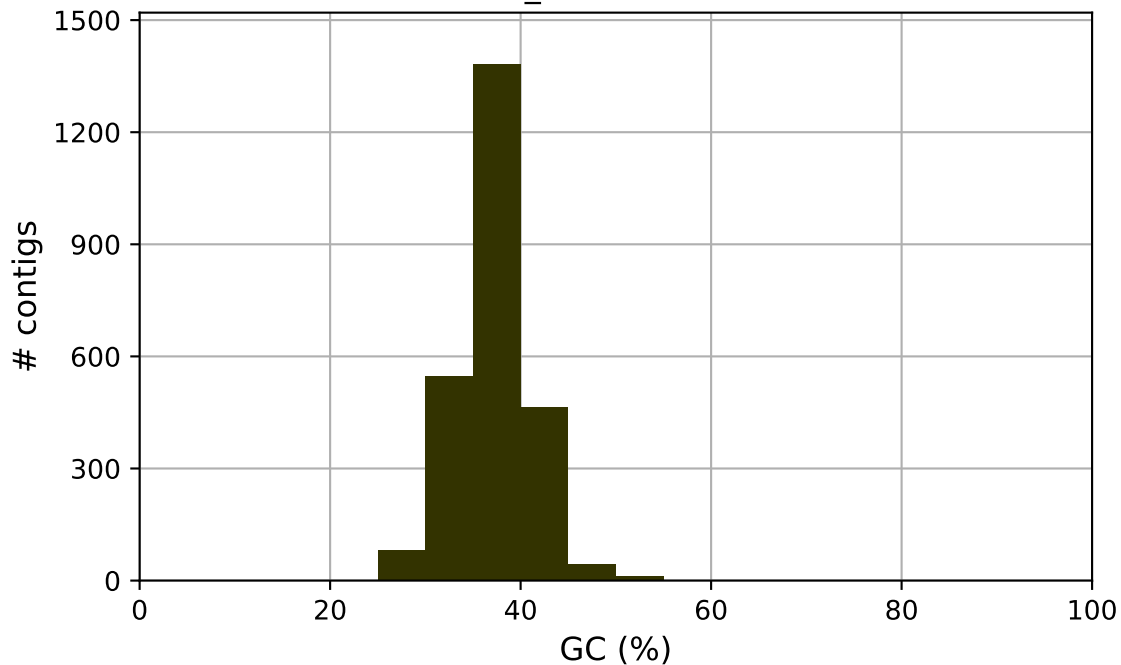
MG5_ets

MG5_sjw GC content



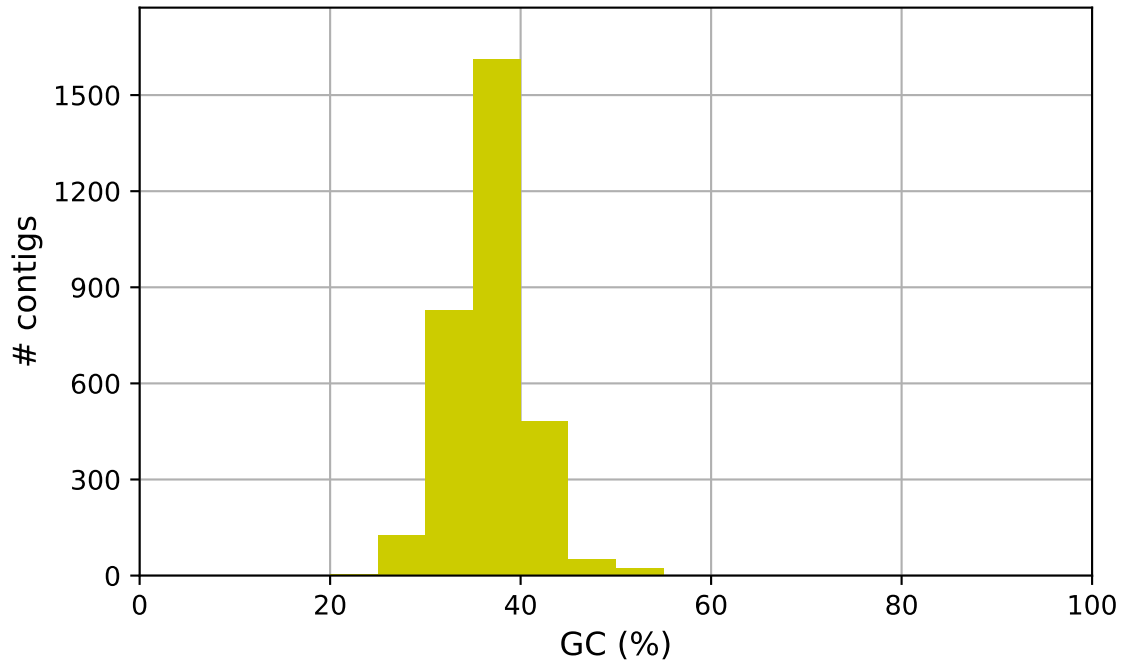
MG5_sjw

MG6_ets GC content



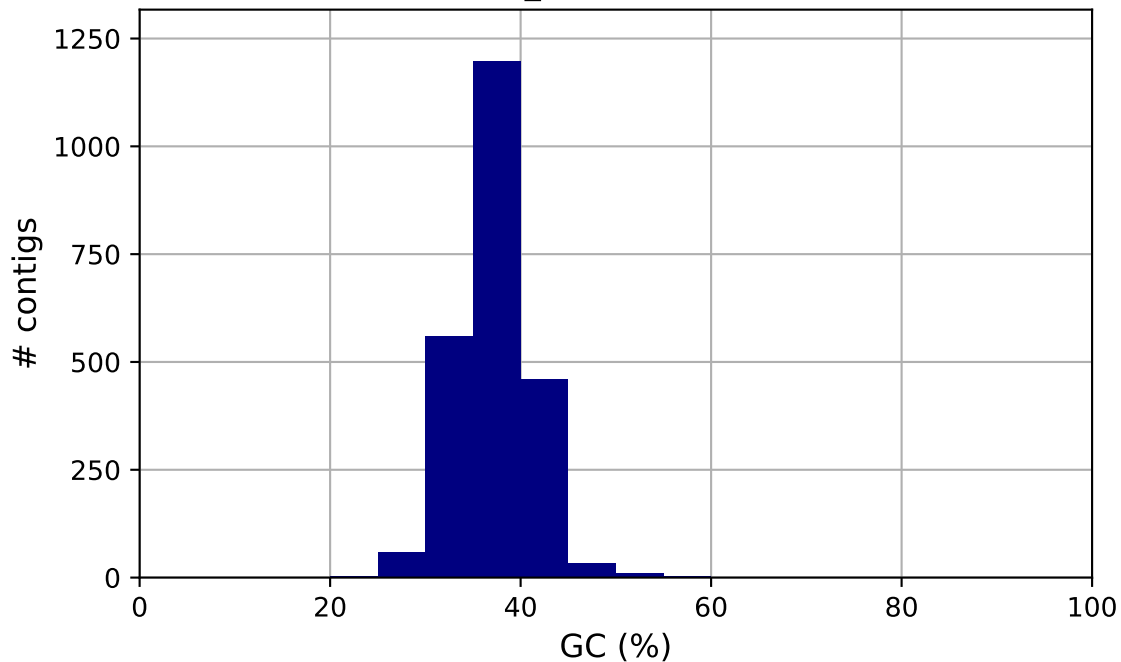
MG6_ets

MG6_sjw GC content



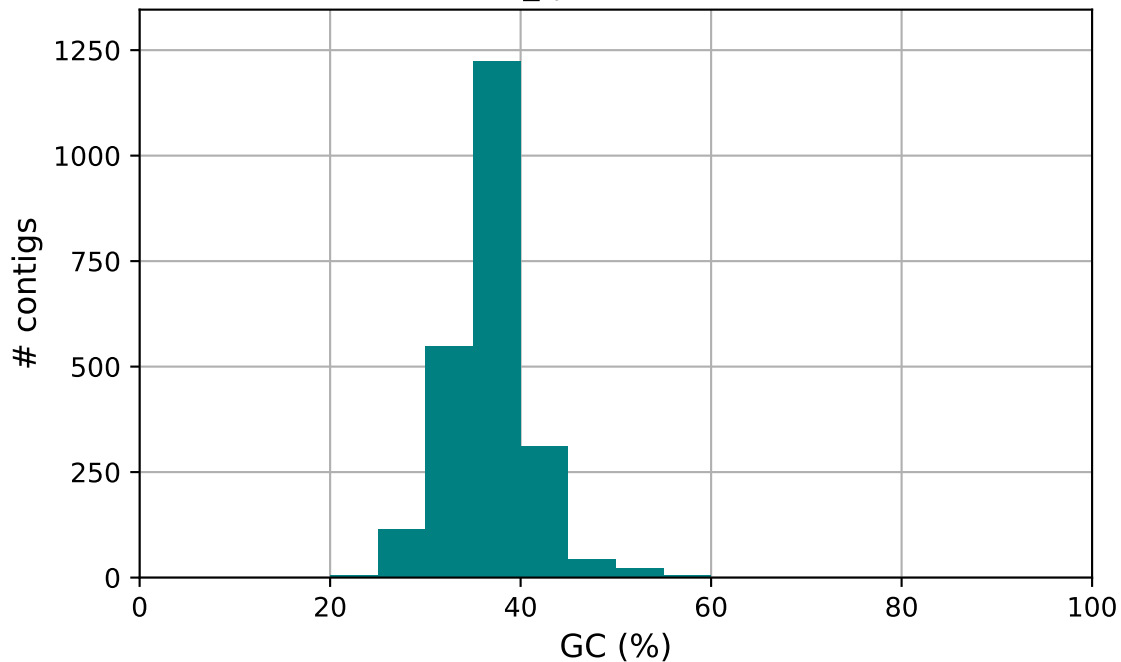
MG6_sjw

MG7_ets GC content



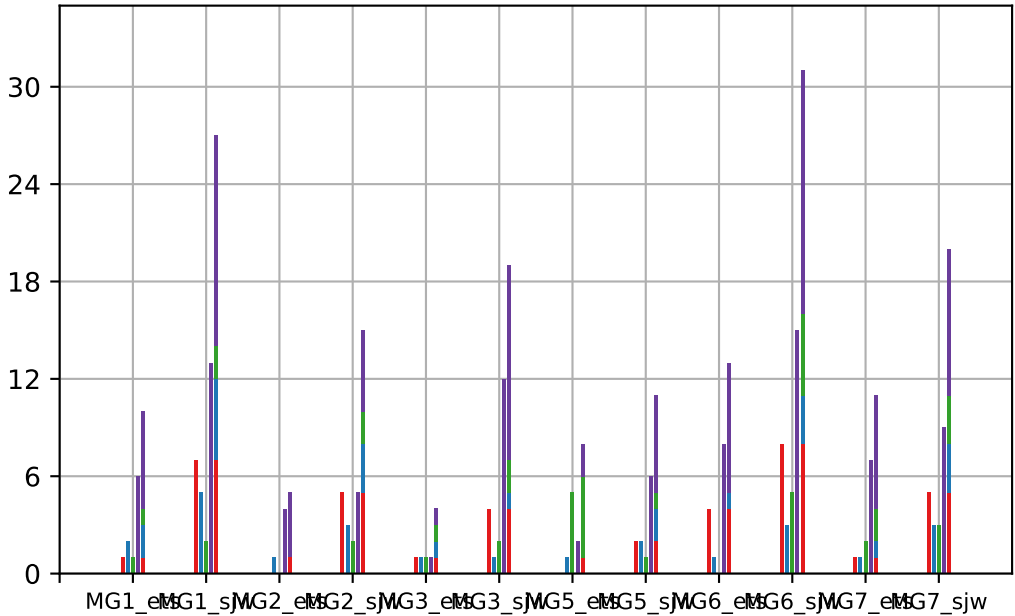
MG7_ets

MG7_sjw GC content



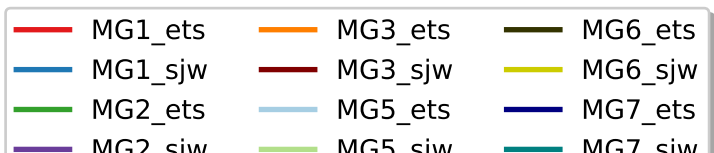
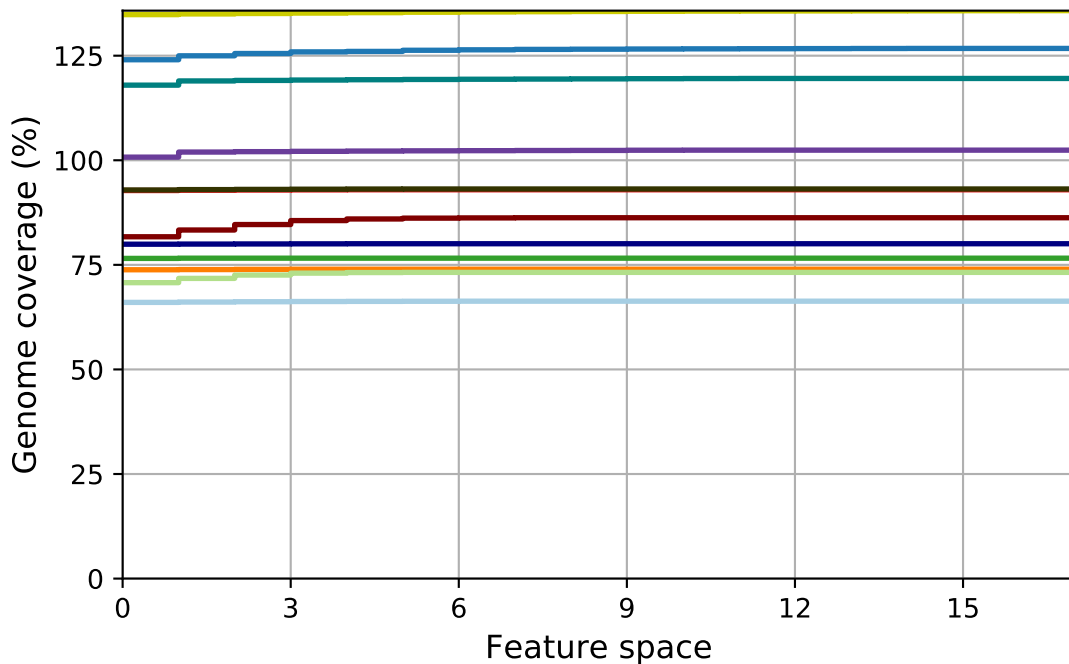
MG7_sjw

Misassemblies

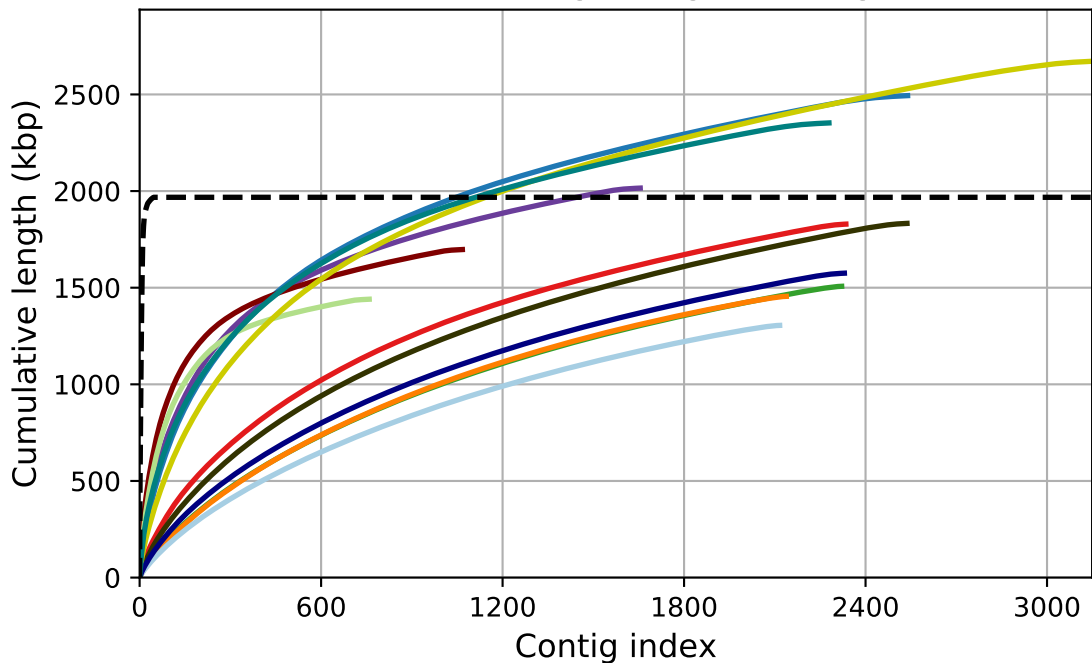


relocations **# inversions** **# interspecies translocations**
translocations

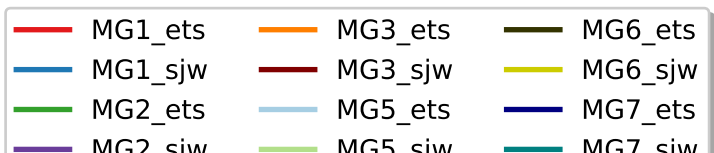
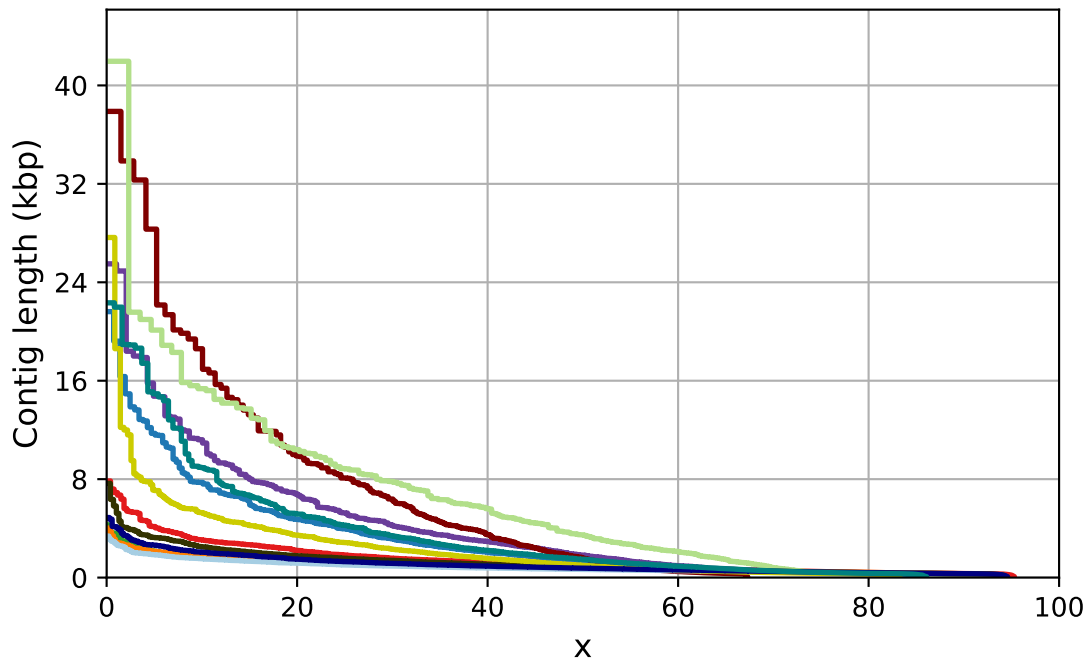
FRCurve (misassemblies)



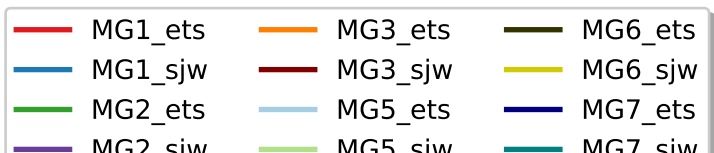
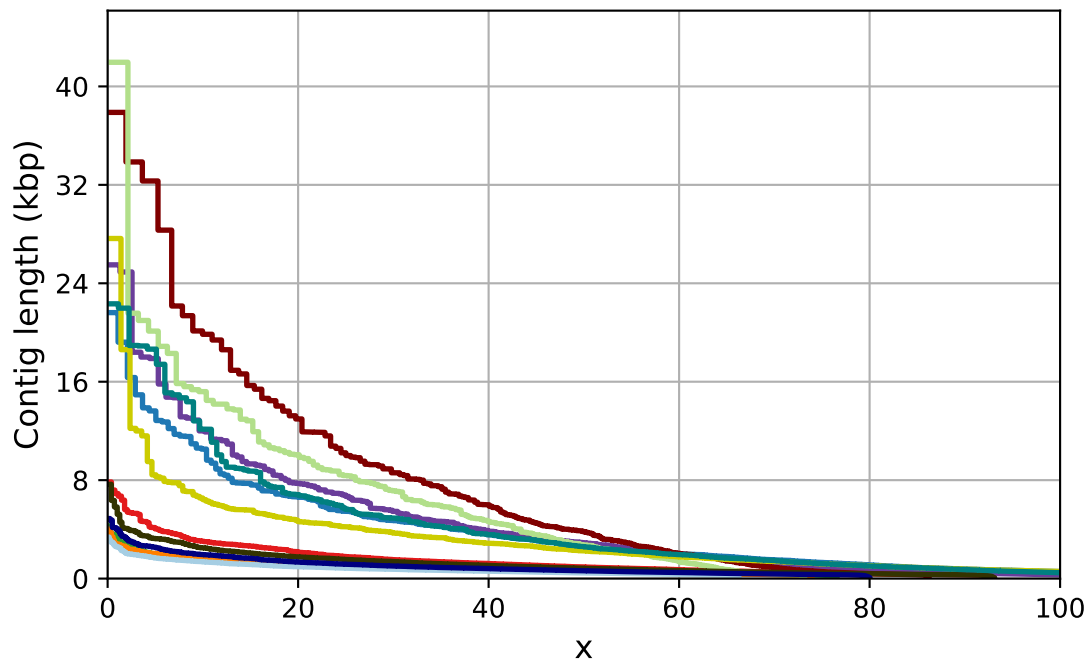
Cumulative length (aligned contigs)



NAX



NGAx



Genome fraction, %

