

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)	40	536	5	50	3	40	6	33	257	1098	189	1149
# contigs (>= 5000 bp)	0	26	0	17	0	21	0	15	1	54	0	64
# contigs (>= 10000 bp)	0	16	0	9	0	12	0	6	0	24	0	14
# contigs (>= 25000 bp)	0	8	0	2	0	9	0	3	0	15	0	7
# contigs (>= 50000 bp)	0	5	0	1	0	8	0	1	0	8	0	3
Total length (>= 1000 bp)	50044	159365	6348	354708	3419	1593644	8174	360062	345468	4036596	242361	3273332
Total length (>= 5000 bp)	0	826620	0	277972	0	1552531	0	313743	7097	2014335	0	1166823
Total length (>= 10000 bp)	0	756284	0	226220	0	1488784	0	249923	0	1821840	0	855410
Total length (>= 25000 bp)	0	608355	0	121563	0	1432671	0	193444	0	1667565	0	739472
Total length (>= 50000 bp)	0	519815	0	95422	0	1383745	0	120673	0	1435118	0	619122
# contigs	2410	3095	285	854	205	614	35	84	3822	2702	3715	2629
Largest contig	1815	200099	1930	95422	1204	524098	1700	120673	7097	571027	2655	382744
Total length	1119475	2978418	114225	698991	80147	1831669	22502	387541	2124693	4973902	1984618	4121680
Reference length	3576081	3576081	3576081	3576081	3576081	3576081	3576081	3576081	3576081	3576081	3576081	3576081
GC (%)	51.92	48.72	50.99	46.74	50.90	39.17	47.53	43.98	51.76	50.53	51.83	50.93
Reference GC (%)	51.82	51.82	51.82	51.82	51.82	51.82	51.82	51.82	51.82	51.82	51.82	51.82
N50	458	1099	377	1221	375	402984	815	24104	575	3117	547	2310
NG50	-	856	-	-	-	331	-	-	372	16570	340	2887
N75	369	606	334	424	327	53296	416	7192	419	1272	411	1147
NG75	-	420	-	-	-	-	-	-	-	2650	-	1565
L50	884	435	114	46	84	2	10	4	1235	178	1251	343
LG50	-	747	-	-	-	476	-	-	2817	22	3100	237
L75	1566	1374	195	355	141	8	19	11	2325	828	2300	980
LG75	-	2262	-	-	-	-	-	-	-	246	-	673
# misassemblies	3	13	1	3	1	0	0	0	5	18	6	21
# misassembled contigs	3	13	1	3	1	0	0	0	5	18	6	21
Misassembled contigs length	1221	13999	446	1304	434	0	0	0	4074	34454	3869	61627
# local misassemblies	0	9	0	0	0	2	0	0	1	8	3	13
# 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	19	0	8	2	9	2	5	2	17	3	11
# unaligned contigs	7 + 16 part	17 + 127 part	2 + 9 part	8 + 60 part	3 + 6 part	6 + 45 part	1 + 11 part	8 + 42 part	6 + 24 part	11 + 155 part	7 + 15 part	16 + 140 part
Unaligned length	17588	988504	9551	361603	6010	1595141	12079	368429	29307	2084032	16105	1105018
Genome fraction (%)	28.943	52.574	2.508	8.559	1.787	5.995	0.099	0.182	53.800	75.562	51.032	78.280
Duplication ratio	1.065	1.058	1.167	1.102	1.160	1.103	2.953	2.941	1.089	1.069	1.079	1.078
# 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	2018.67	2241.66	1979.24	2028.95	2152.00	2196.09	3966.01	3508.77	2053.66	2319.34	2009.69	2327.87
# indels per 100 kbp	14.40	16.70	12.27	14.05	9.39	11.20	0.00	61.56	12.06	18.84	11.45	18.86
Largest alignment	1720	5104	704	1021	659	1325	310	417	2721	8916	2646	8390
Total aligned length	1042694	1918985	90862	312982	64606	220820	5000	10440	1965614	2813855	1857703	2942237
NA50	428	461	328	-	323	-	-	-	522	534	506	1041
NGA50	-	333	-	-	-	-	-	-	316	1112	290	1299
NA75	334	-	244	-	211	-	-	-	363	-	362	-
NGA75	-	-	-	-	-	-	-	-	-	382	-	496
LA50	947	1790	145	-	104	-	-	-	1328	1746	1329	975
LGA50	-	2545	-	-	-	-	-	-	3128	852	3409	741
LA75	1689	-	240	-	171	-	-	-	2553	-	2490	-
LGA75	-	-	-	-	-	-	-	-	-	2177	-	1823

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

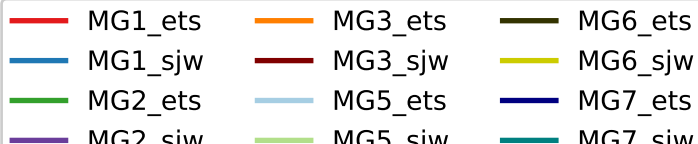
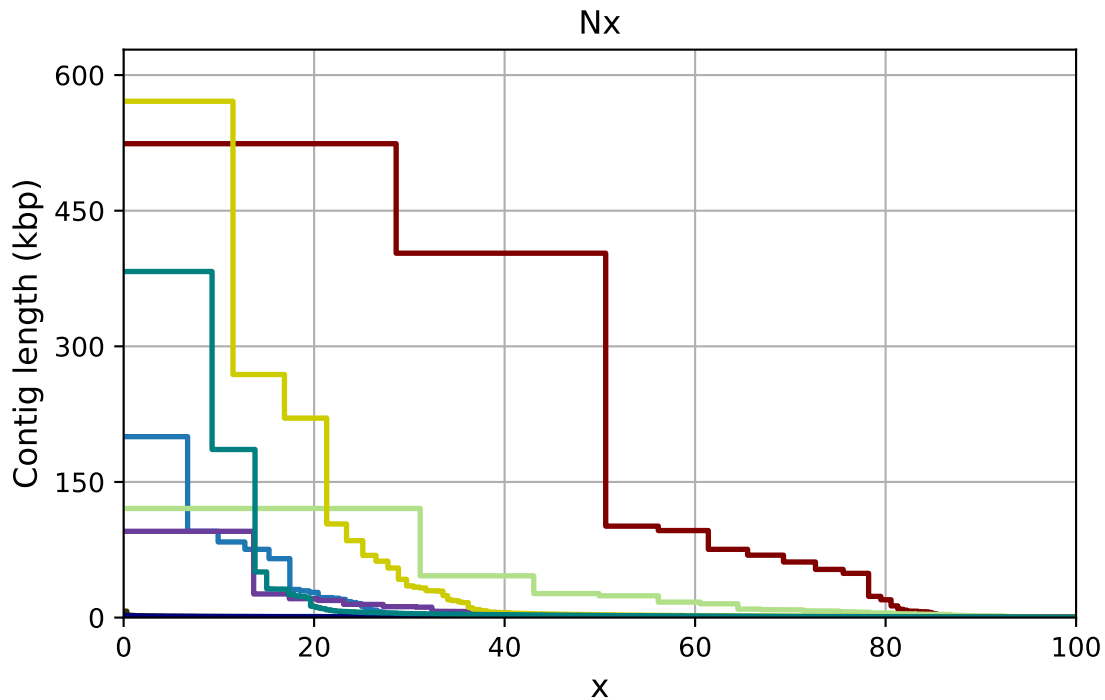
	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# misassemblies	3	13	1	3	1	0	0	0	5	18	6	21
# contig misassemblies	3	13	1	3	1	0	0	0	5	18	6	21
# c. relocations	2	2	1	2	1	0	0	0	2	10	2	8
# c. translocations	0	7	0	1	0	0	0	0	2	7	2	11
# c. inversions	1	4	0	0	0	0	0	0	1	1	2	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	3	13	1	3	1	0	0	0	5	18	6	21
Misassembled contigs length	1221	13999	446	1304	434	0	0	0	4074	34454	3869	61627
# possibly misassembled contigs	16	108	10	57	5	39	10	41	22	135	16	132
# possible misassemblies	16	131	10	72	5	55	10	52	23	165	16	164
# local misassemblies	0	9	0	0	0	2	0	0	1	8	3	13
# 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	19	0	8	2	9	2	5	2	17	3	11
# mismatches	20894	42145	1775	6210	1375	4708	140	228	39511	62672	36676	65165
# indels	149	314	11	43	6	24	0	4	232	509	209	528
# indels (<= 5 bp)	135	289	9	40	4	24	0	4	206	450	183	467
# indels (> 5 bp)	14	25	2	3	2	0	0	0	26	59	26	61
Indels length	303	633	24	73	26	33	0	4	599	1473	532	1476

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).

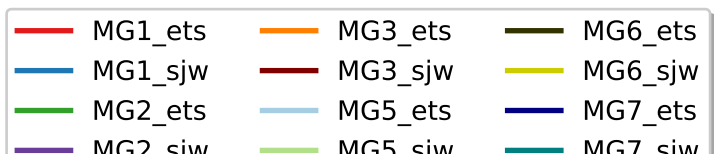
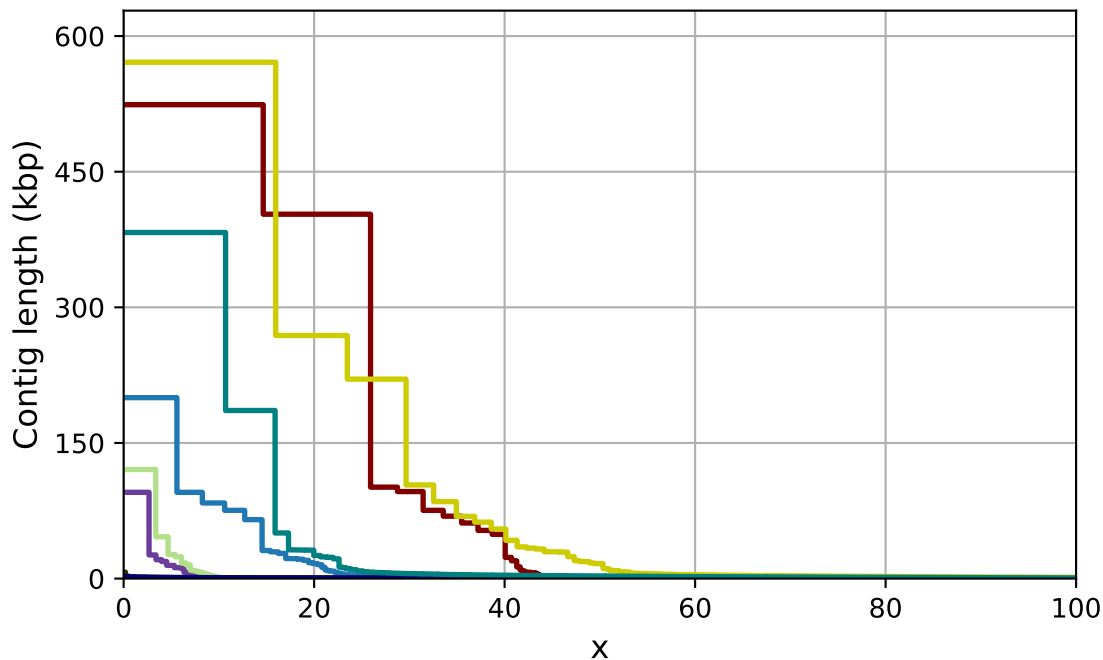
Unaligned report

	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	7	17	2	8	3	6	1	8	6	11	7	16
Fully unaligned length	3870	17891	1438	12357	1149	11071	616	22650	3136	63706	3985	26465
# partially unaligned contigs	16	127	9	60	6	45	11	42	24	155	15	140
Partially unaligned length	13718	970613	8113	349246	4861	1584070	11463	345779	26171	2020326	12120	1078553
# N's	0	0	0	0	0	0	0	0	0	0	0	0

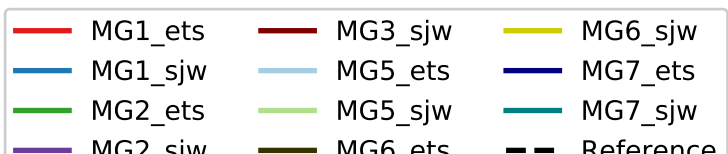
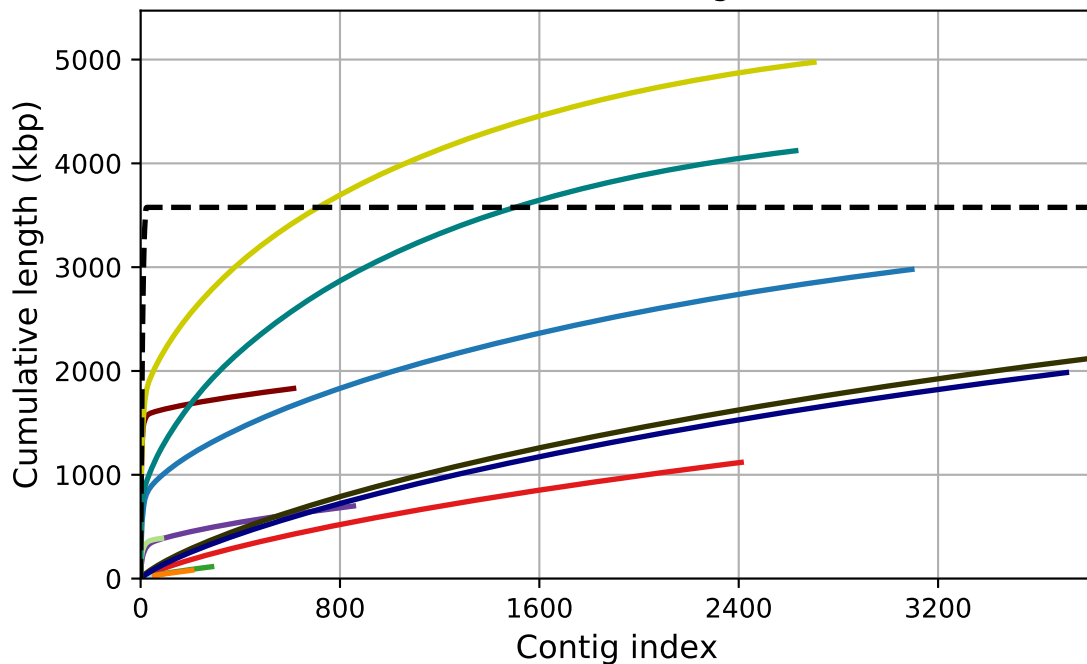
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



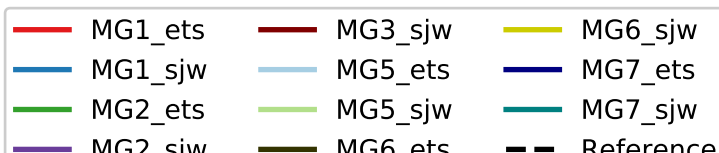
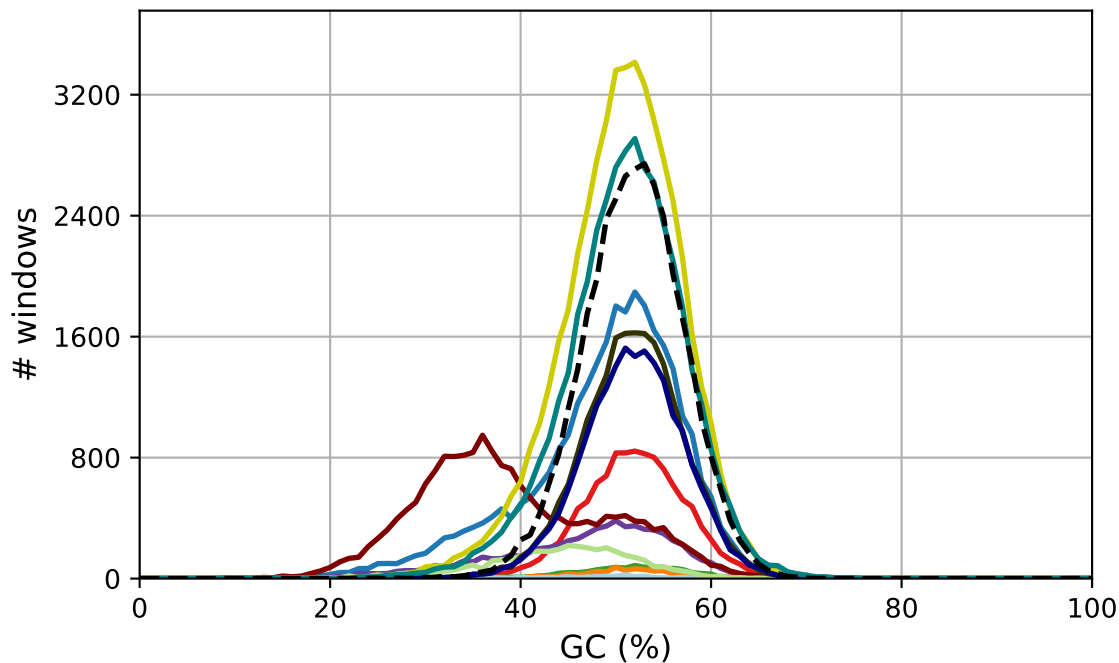
NGx



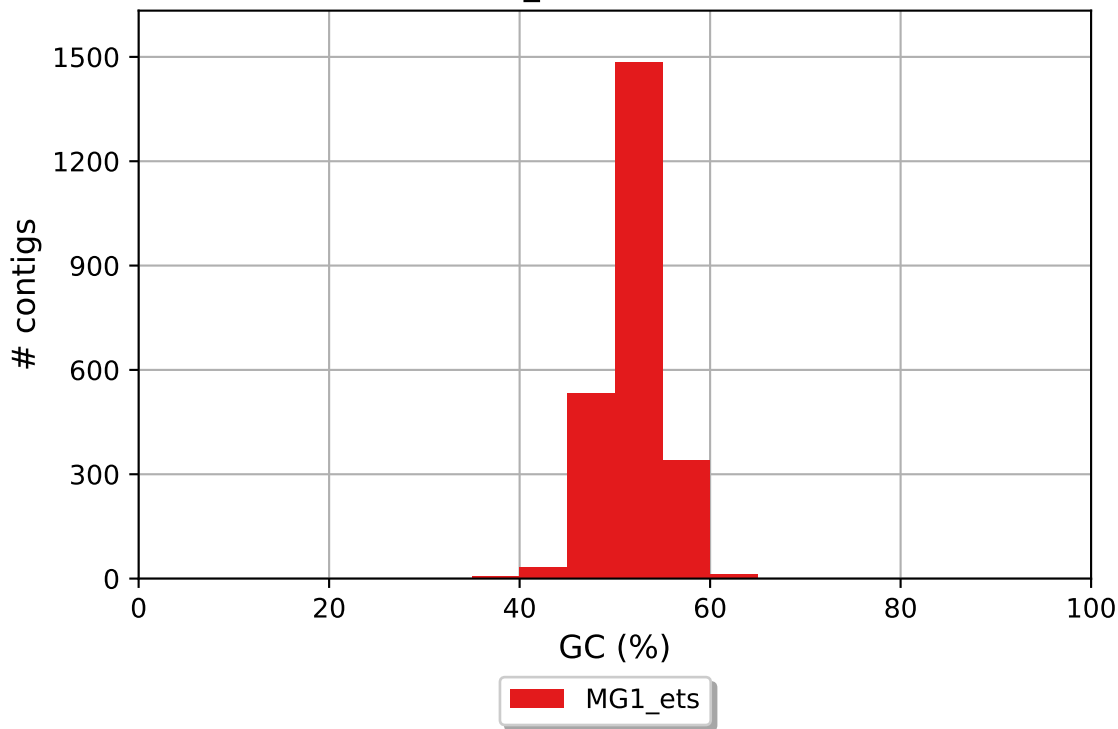
Cumulative length



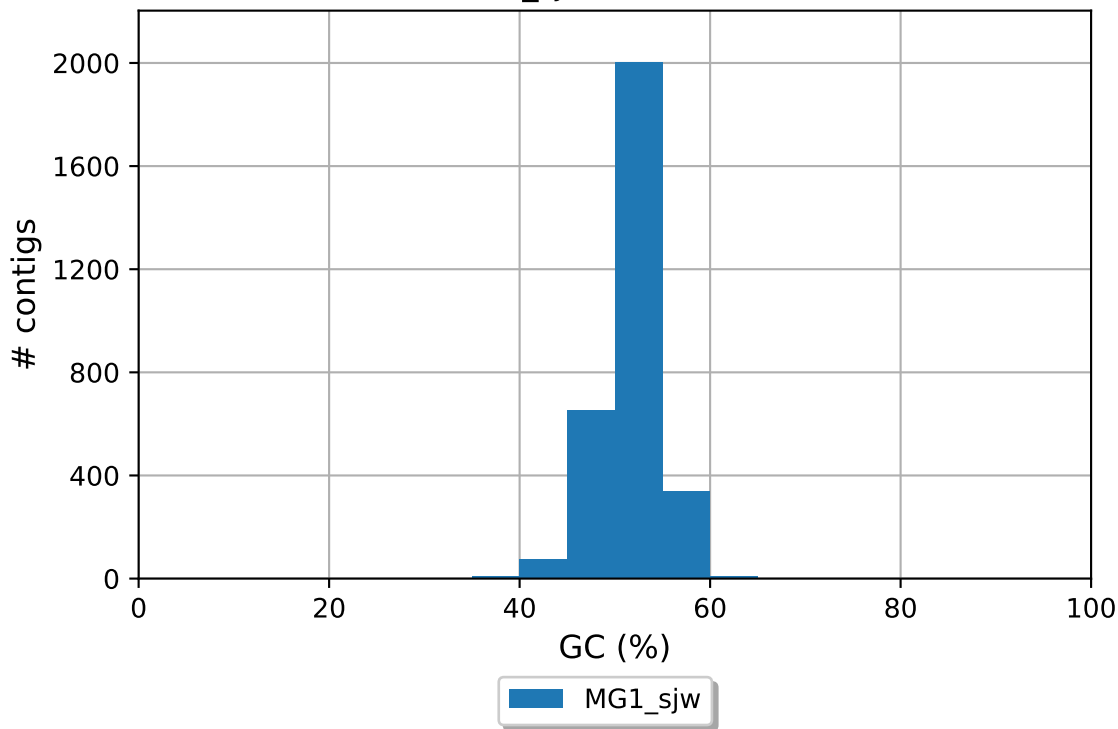
GC content



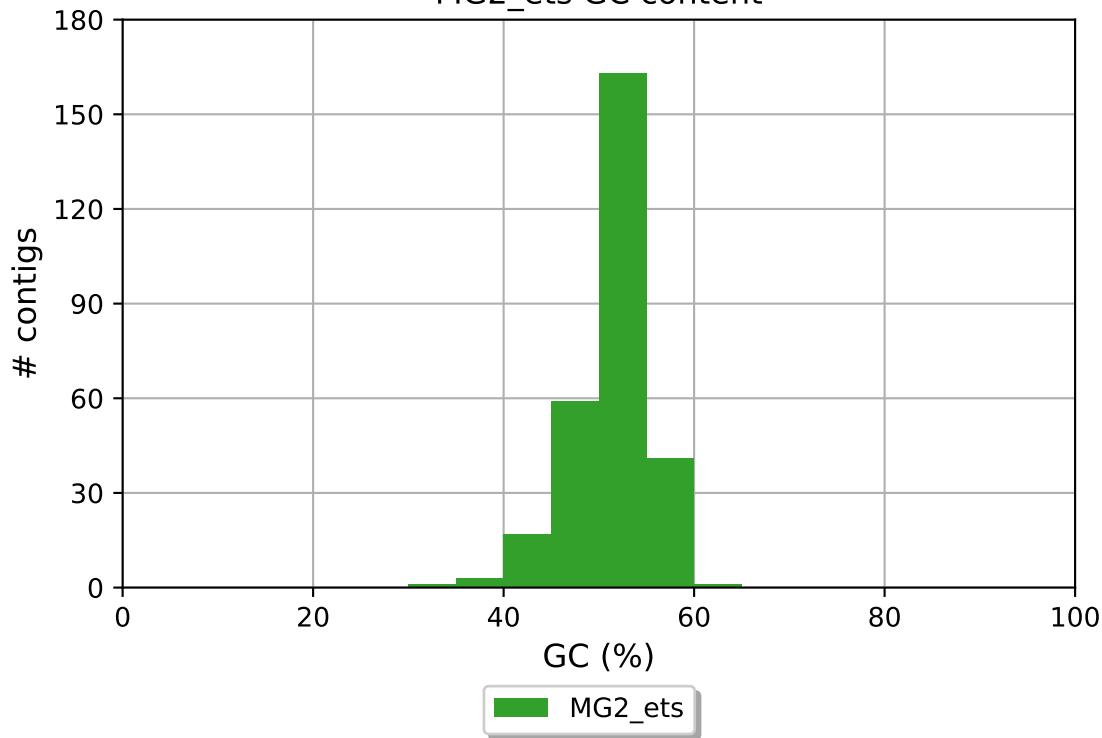
MG1_ets GC content



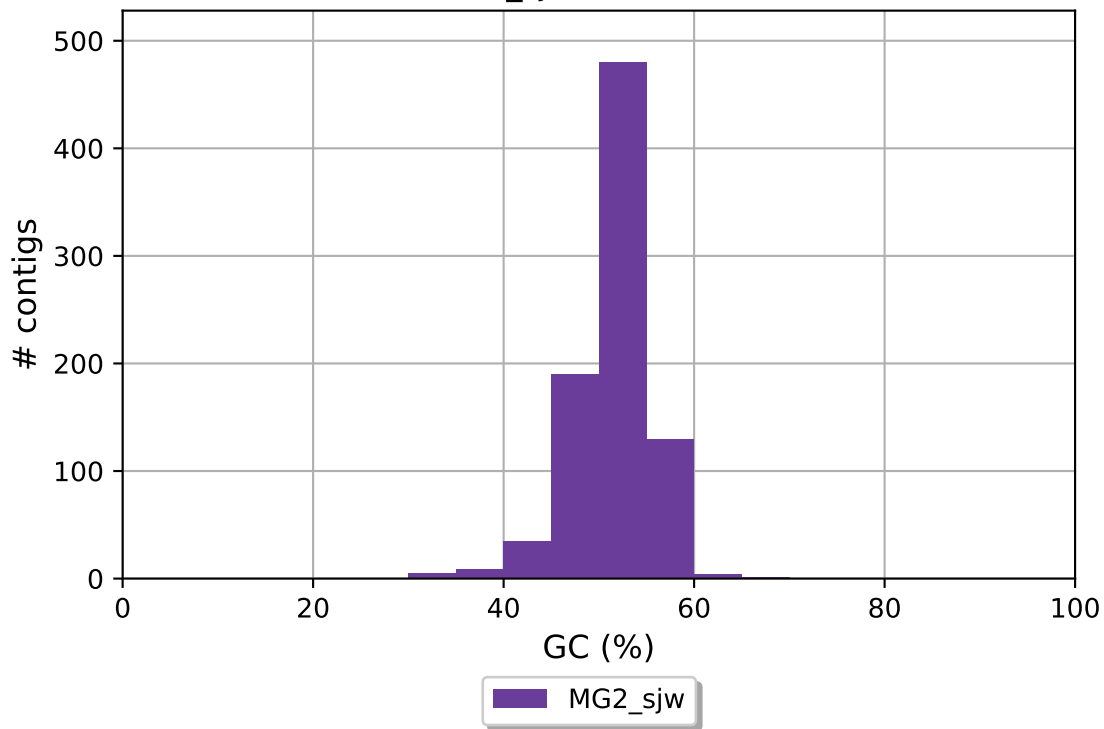
MG1_sjw GC content



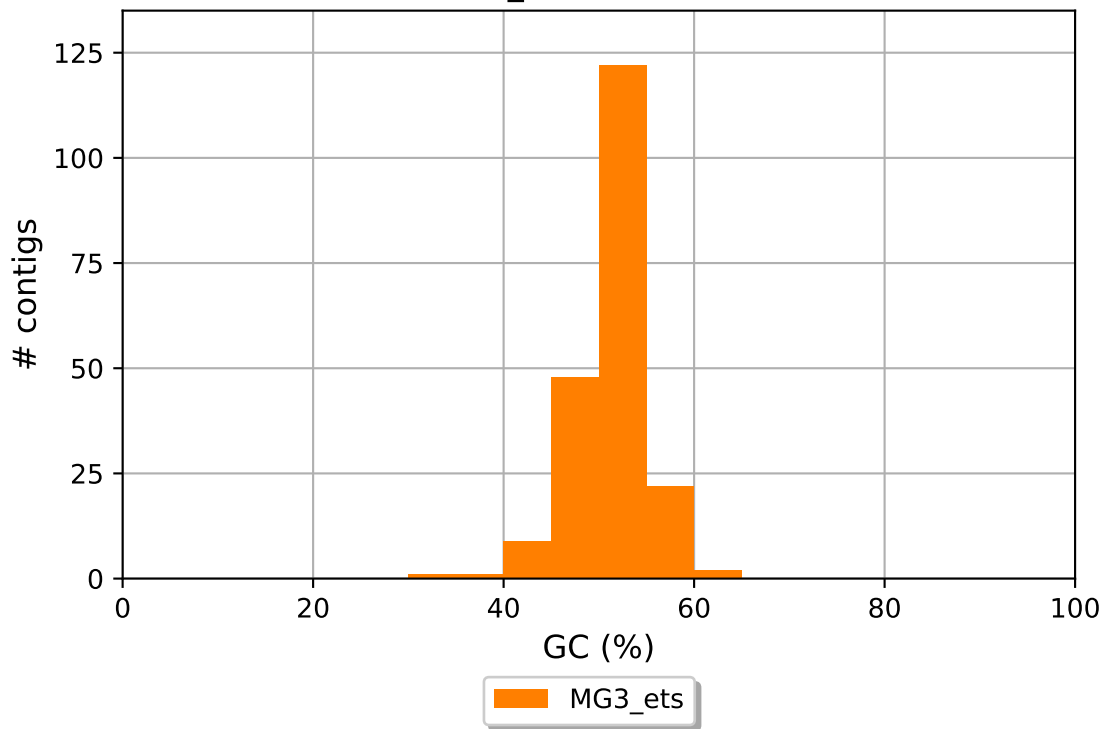
MG2_ets GC content



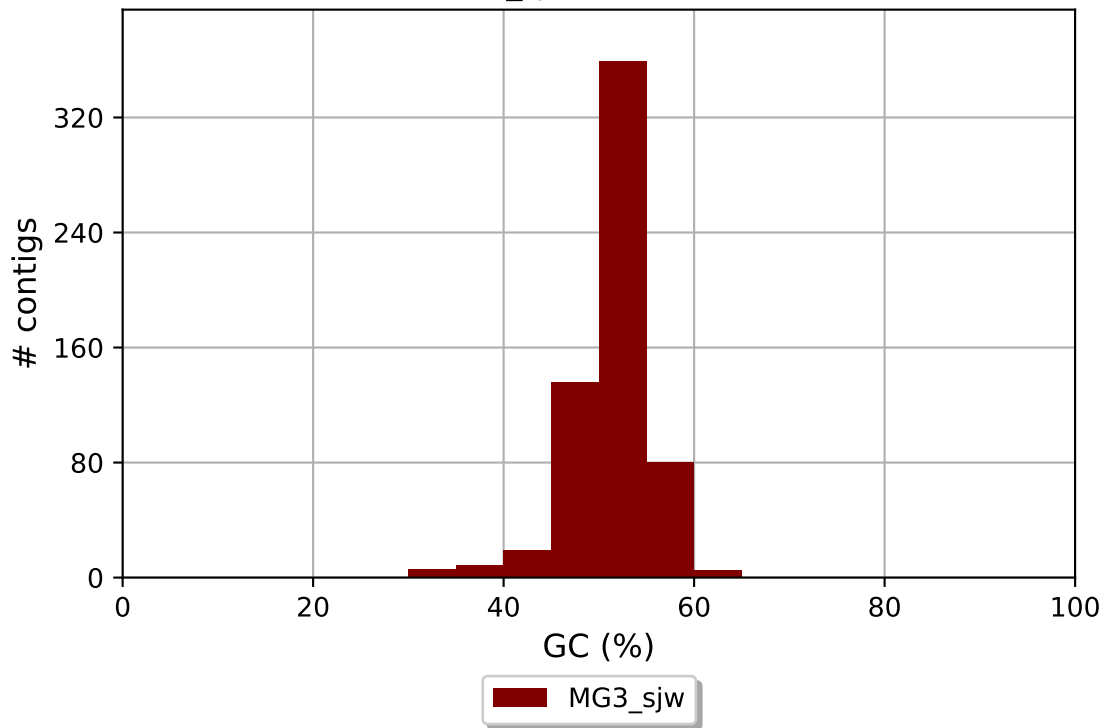
MG2_sjw GC content



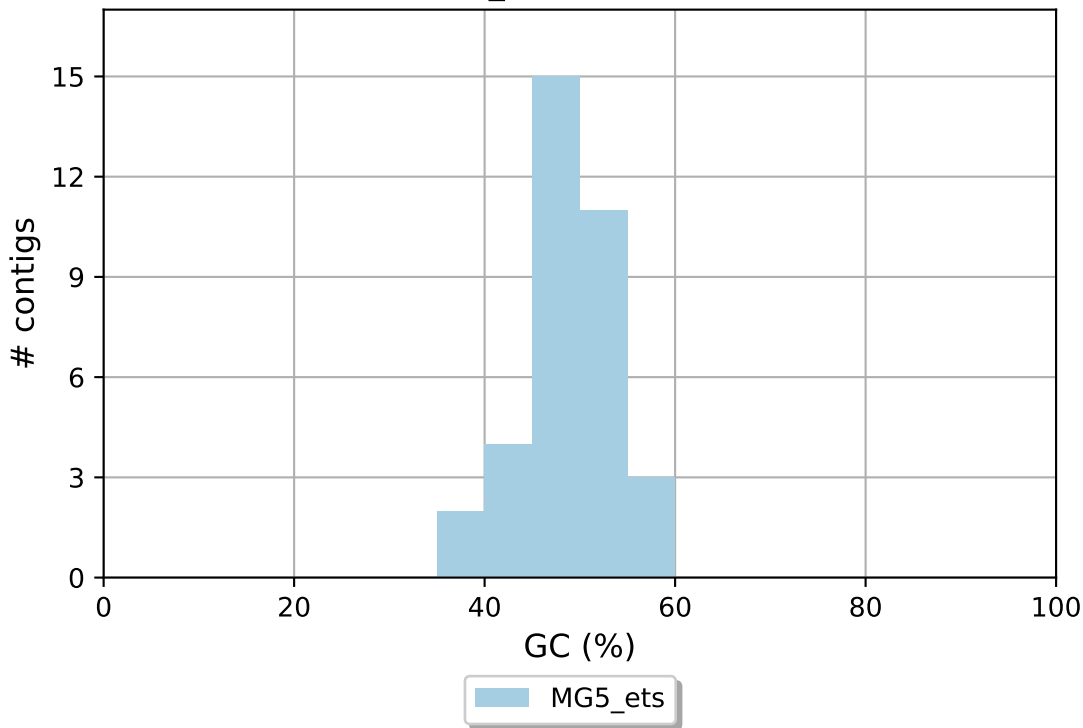
MG3_ets GC content



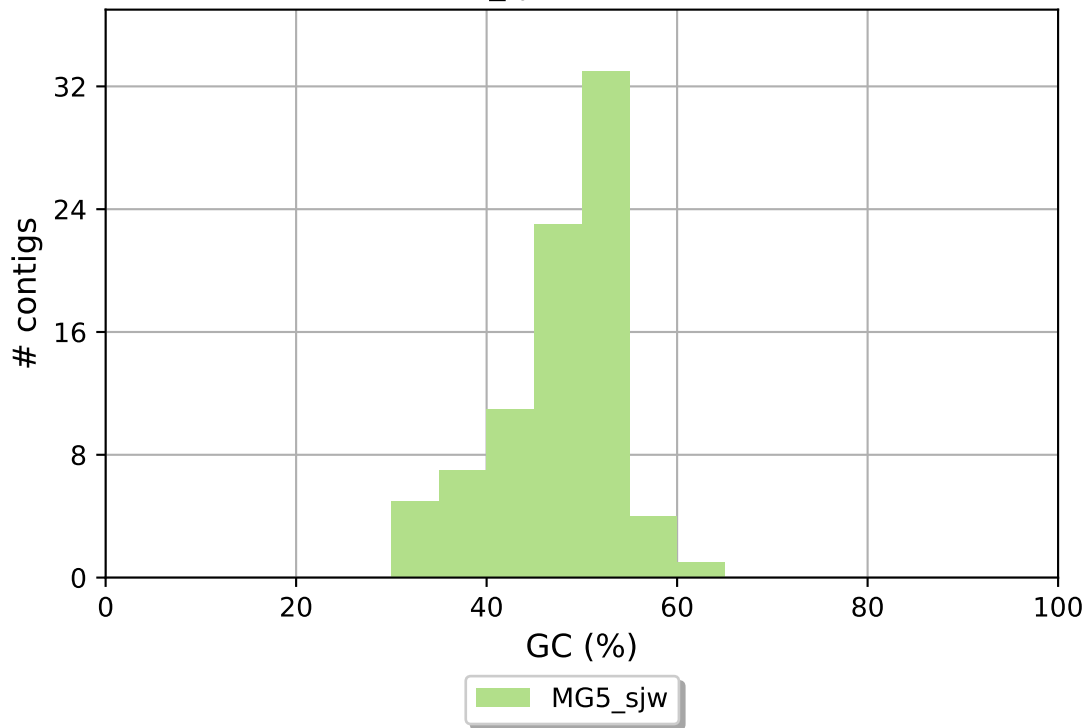
MG3_sjw GC content



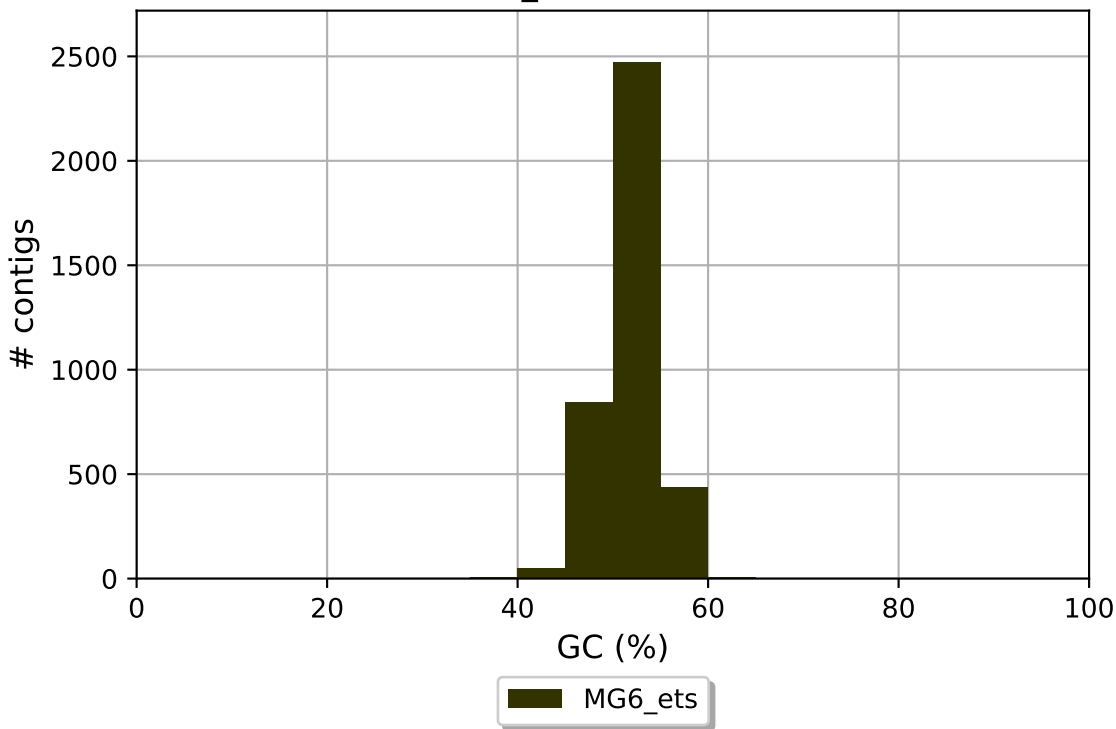
MG5_ets GC content



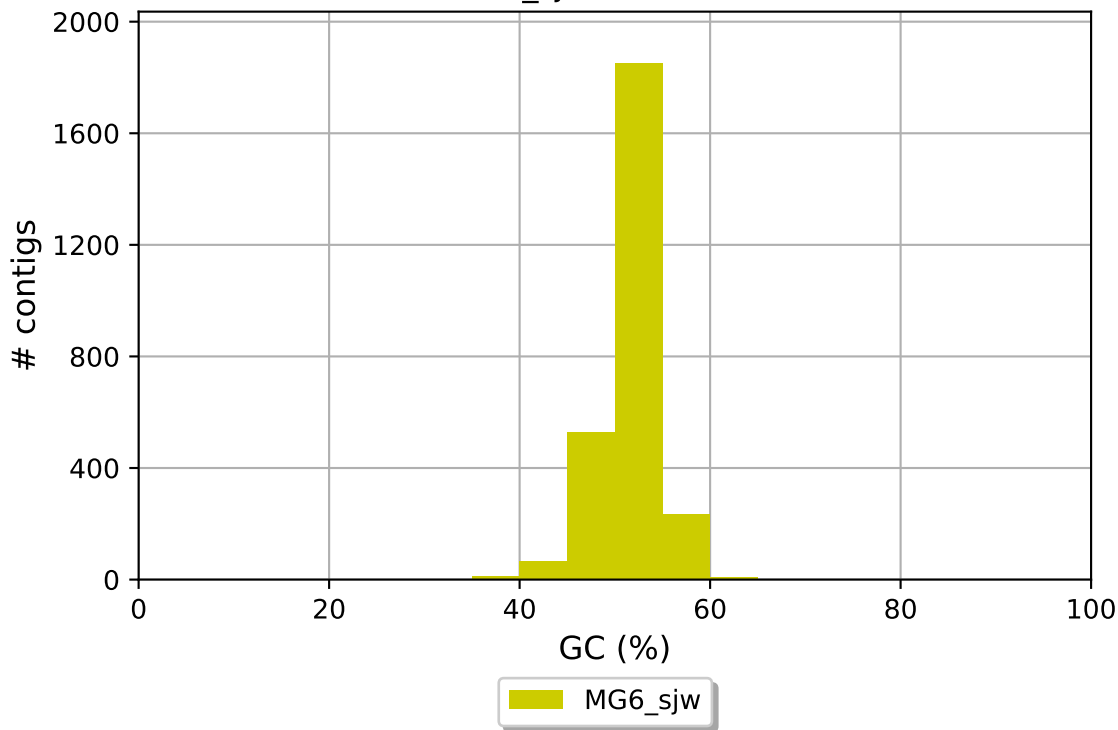
MG5_sjw GC content



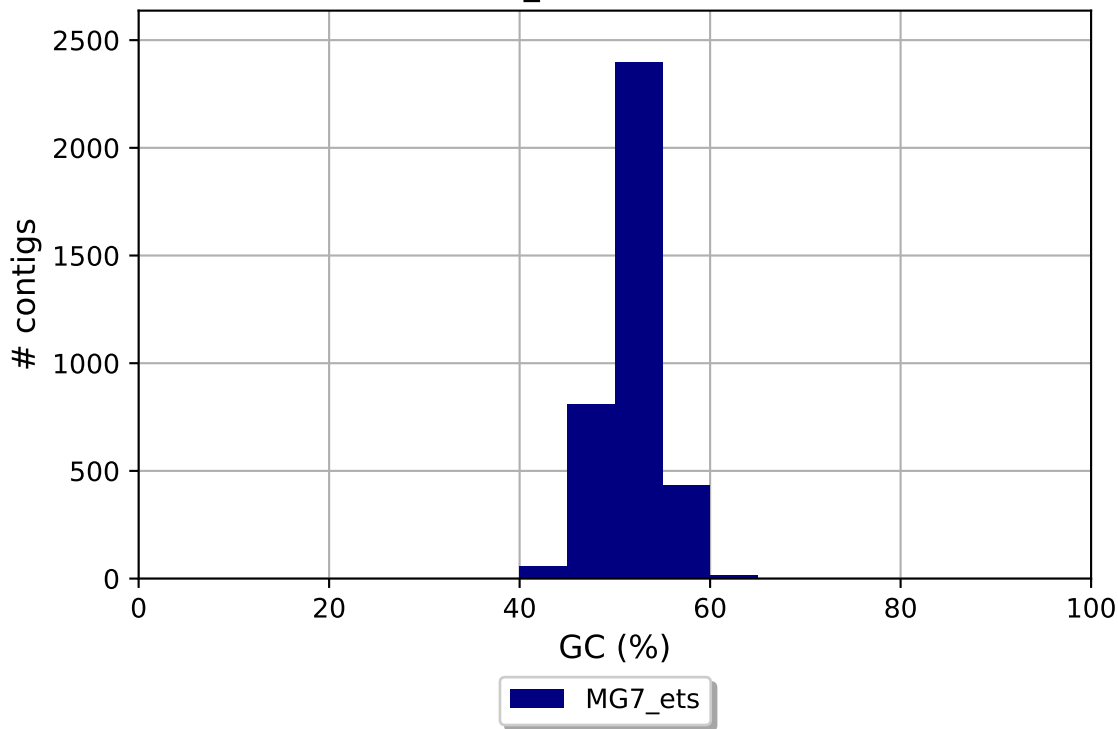
MG6_ets GC content



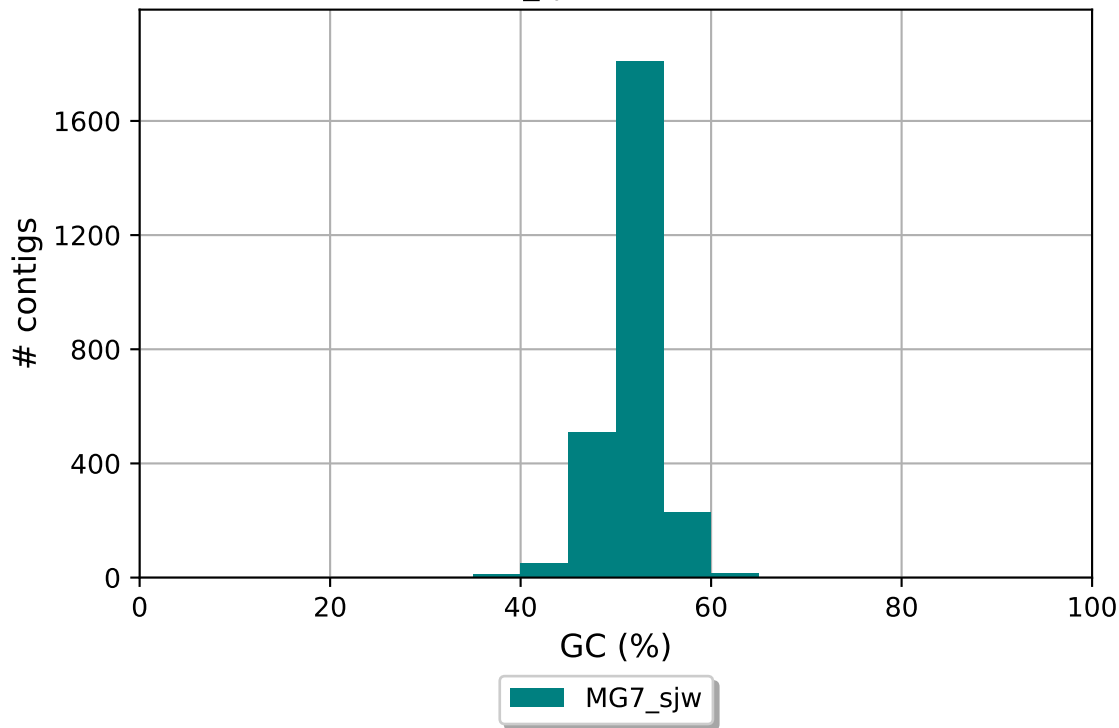
MG6_sjw GC content



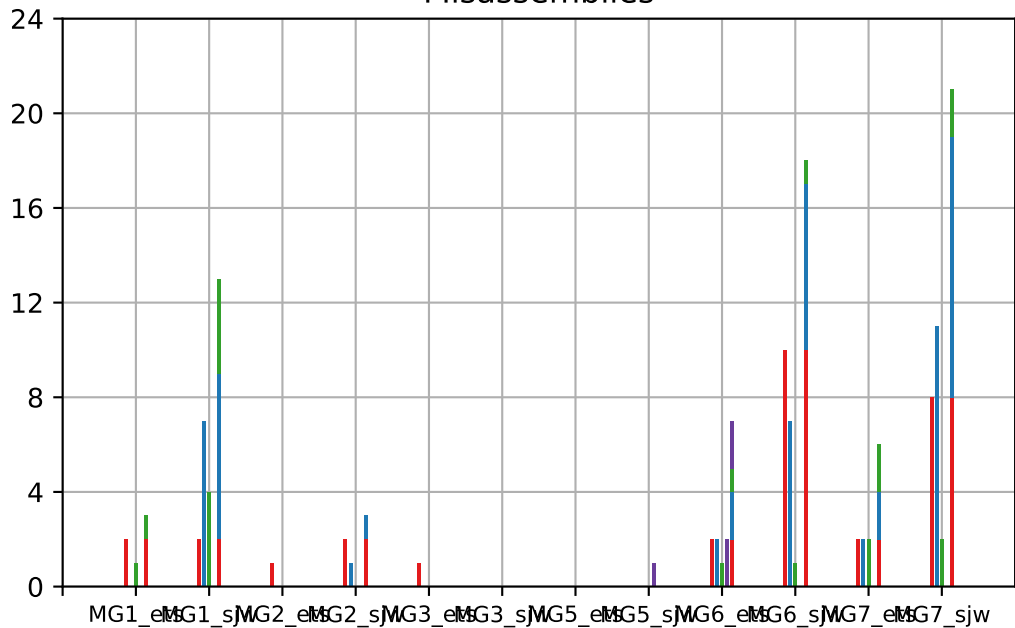
MG7_ets GC content



MG7_sjw GC content

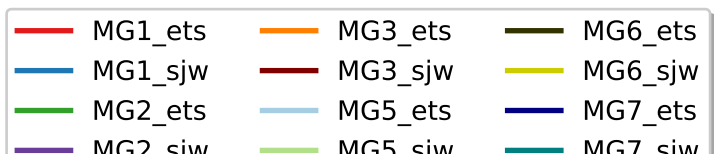
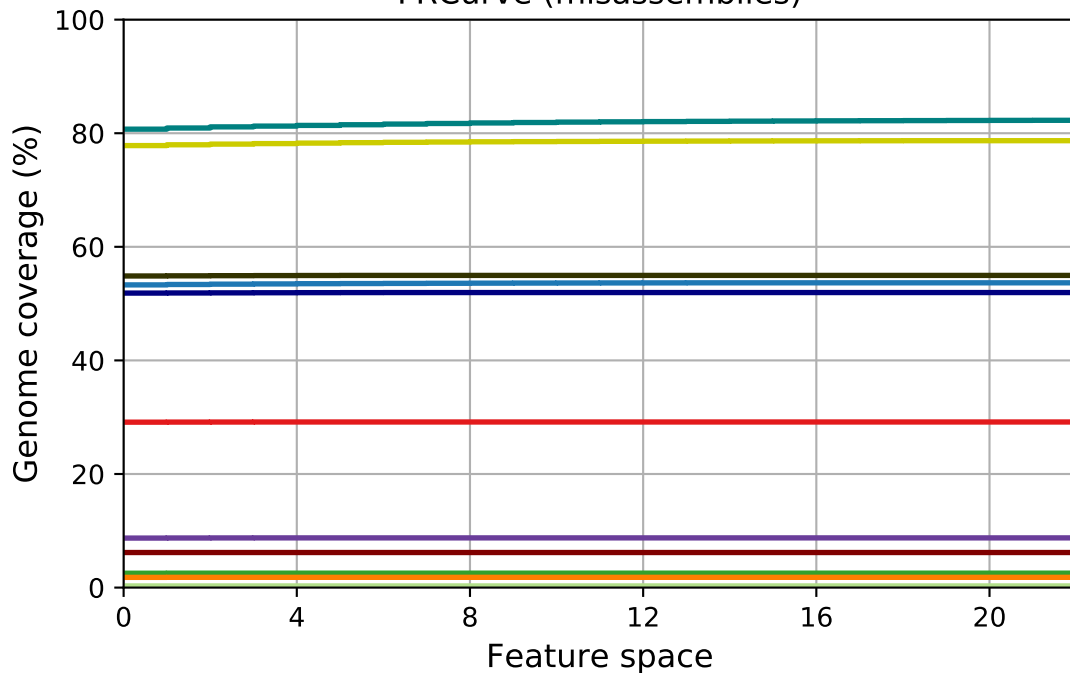


Misassemblies

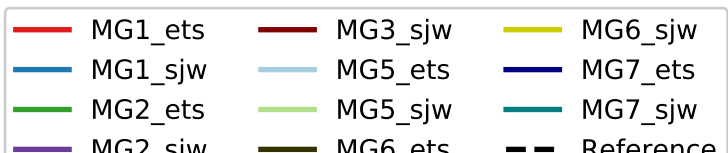
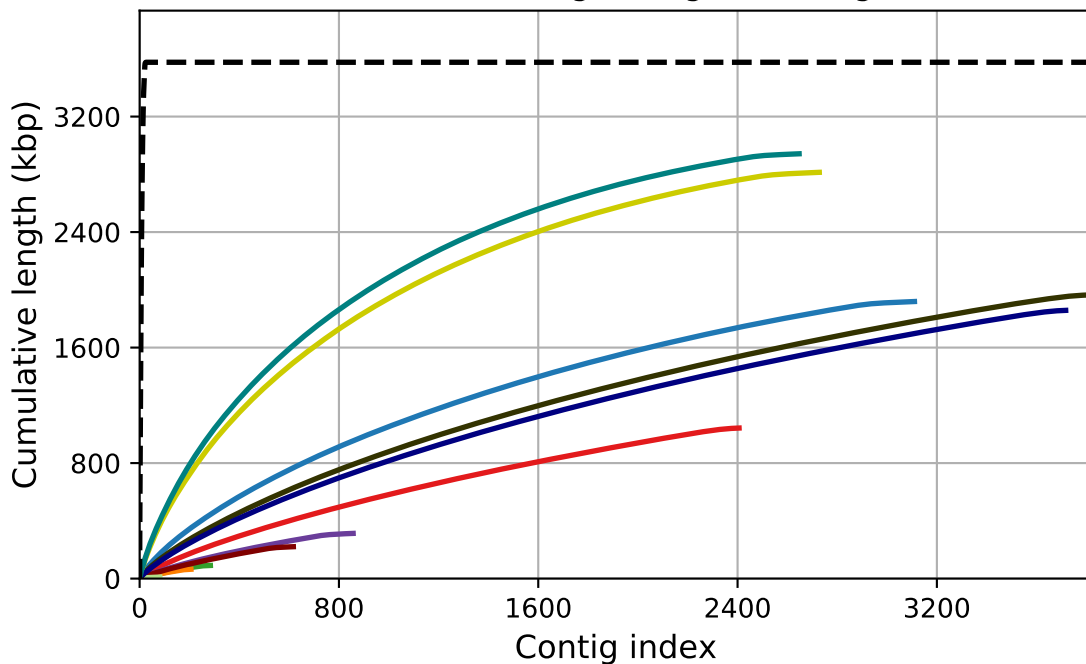


■ # relocations
 ■ # inversions
 ■ # interspecies translocations
 ■ # translocations

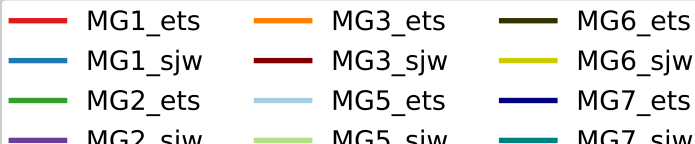
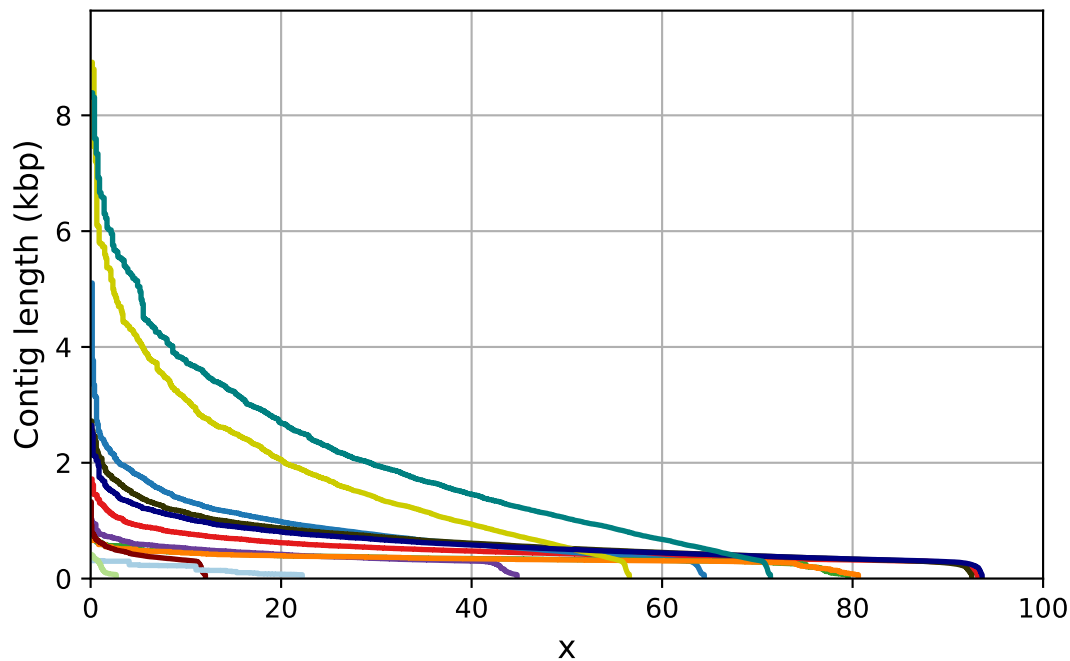
FRCurve (misassemblies)



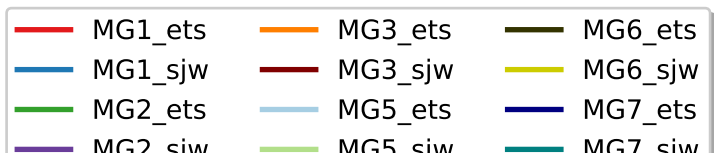
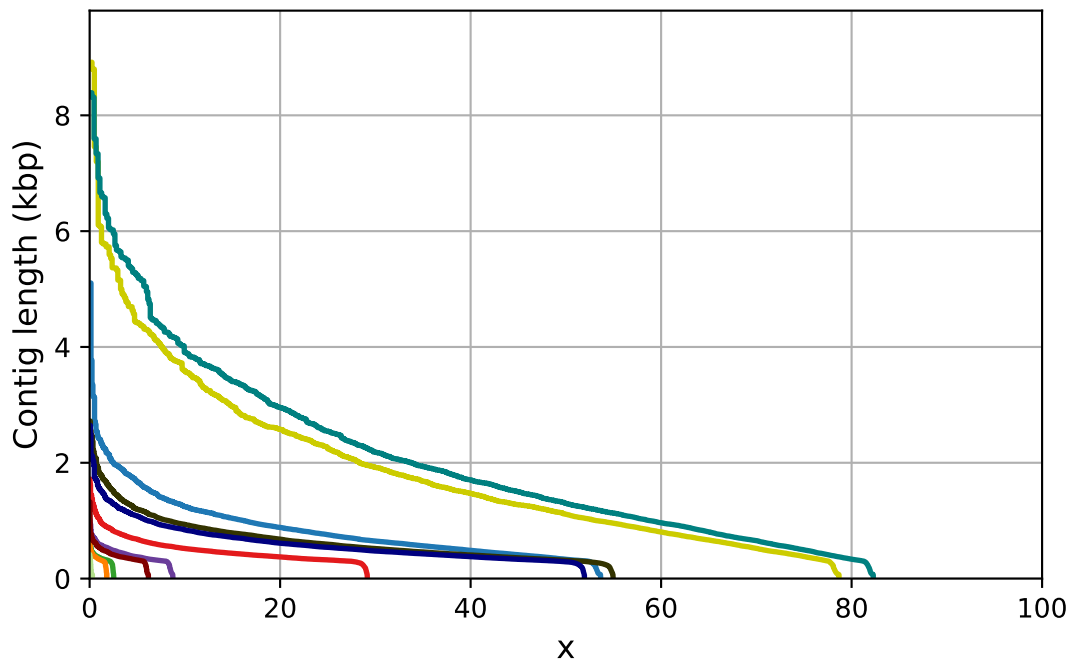
Cumulative length (aligned contigs)



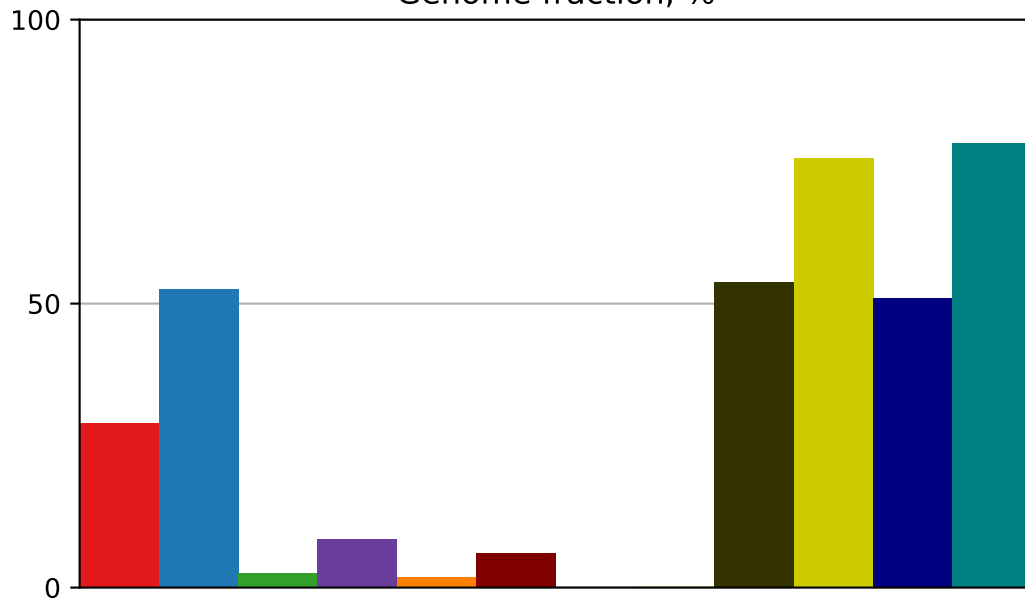
NAx



NGAx



Genome fraction, %



■ MG1_ets	■ MG3_ets	■ MG6_ets
■ MG1_sjw	■ MG3_sjw	■ MG6_sjw
■ MG2_ets	■ MG5_ets	■ MG7_ets
■ MG2_siw	■ MG5_siw	■ MG7_siw