

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)	606	547	89	562	6	41	1	15	557	516	254	840
# contigs (>= 5000 bp)	0	188	0	3	0	4	0	2	0	176	0	91
# contigs (>= 10000 bp)	0	59	0	1	0	1	0	1	0	63	0	19
# contigs (>= 25000 bp)	0	4	0	0	0	0	0	1	0	7	0	0
# contigs (>= 50000 bp)	0	0	0	0	0	0	0	0	0	0	0	0
Total length (>= 1000 bp)	861319	2632954	110660	916221	8079	84427	1641	63290	774643	2683652	327033	2347566
Total length (>= 5000 bp)	0	1786893	0	32648	0	36063	0	41916	0	1884960	0	705371
Total length (>= 10000 bp)	0	914195	0	19838	0	16729	0	34851	0	1092124	0	235749
Total length (>= 25000 bp)	0	114446	0	0	0	0	0	34851	0	232814	0	0
Total length (>= 50000 bp)	0	0	0	0	0	0	0	0	0	0	0	0
# contigs	3583	1108	2536	2521	815	1553	360	829	3773	1141	3397	1536
Largest contig	3728	29599	2384	19838	1663	16729	1641	34851	3345	40693	3200	18275
Total length	2476303	2913030	1269399	2013580	340712	807253	137630	411523	2521743	2990394	1928493	2744376
Reference length	3288122	3288122	3288122	3288122	3288122	3288122	3288122	3288122	3288122	3288122	3288122	3288122
GC (%)	54.84	54.33	54.93	54.62	54.89	54.25	54.52	52.90	54.68	54.47	54.93	54.15
Reference GC (%)	53.64	53.64	53.64	53.64	53.64	53.64	53.64	53.64	53.64	53.64	53.64	53.64
N50	776	6315	503	914	402	515	364	460	742	7245	595	2878
NG50	593	5449	-	510	-	-	-	-	591	6191	378	2334
N75	512	2981	391	585	348	395	329	359	499	3060	431	1485
NG75	303	1573	-	-	-	-	-	-	318	1878	-	797
L50	1039	129	895	658	324	518	152	259	1124	111	1107	272
LG50	1639	161	-	1591	-	-	-	-	1703	133	2554	377
L75	2026	287	1612	1345	553	965	251	515	2157	268	2063	602
LG75	3550	416	-	-	-	-	-	-	3593	361	-	972
# misassemblies	14	22	4	12	2	6	0	1	10	26	5	20
# misassembled contigs	14	22	4	11	2	6	0	1	9	26	5	19
Misassembled contigs length	12326	150519	2639	10841	943	3361	0	435	6219	143804	2899	54846
# local misassemblies	9	28	2	4	2	2	0	2	8	23	7	12
# 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	5	0	0	0	0	0	0	1	4	0	5
# unaligned contigs	11 + 15 part	18 + 89 part	6 + 4 part	13 + 30 part	2 + 4 part	8 + 14 part	2 + 2 part	6 + 16 part	14 + 21 part	18 + 88 part	8 + 10 part	12 + 87 part
Unaligned length	22221	180144	5561	73493	6670	55401	3022	65488	23963	193752	11279	193127
Genome fraction (%)	67.717	77.085	36.143	56.662	9.388	21.753	3.764	10.034	67.689	77.739	53.946	73.988
Duplication ratio	1.102	1.078	1.063	1.041	1.082	1.051	1.088	1.049	1.122	1.094	1.081	1.049
# 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	1721.43	1906.57	1609.60	1773.80	1714.94	1797.90	1555.47	1591.21	1668.60	1849.58	1692.36	1817.88
# indels per 100 kbp	12.66	21.90	12.29	14.92	12.96	15.52	9.70	10.61	13.66	18.07	9.64	16.57
Largest alignment	3728	29599	2356	5824	1208	1554	689	1104	3339	40667	3155	18273
Total aligned length	2323404	2688911	1198992	1893840	309572	720371	124047	330569	2331645	2746350	1817072	2509451
NA50	707	5727	473	849	373	461	345	370	668	6403	556	2515
NGA50	521	5061	-	438	-	-	-	-	508	5465	325	1929
NA75	444	2182	357	517	315	342	304	305	416	2251	384	1115
NGA75	-	877	-	-	-	-	-	-	-	1006	-	337
LA50	1102	138	941	724	357	634	166	415	1198	123	1167	305
LGA50	1769	173	-	1766	-	-	-	-	1856	149	2774	427
LA75	2213	325	1719	1485	605	1143	272	723	2392	314	2217	711
LGA75	-	527	-	-	-	-	-	-	-	460	-	1343

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	14	22	4	12	2	6	0	1	10	26	5	20
# contig misassemblies	14	22	4	12	2	6	0	1	10	26	5	20
# c. relocations	13	22	4	11	1	4	0	1	10	25	4	19
# c. translocations	0	0	0	0	0	0	0	0	0	0	0	0
# c. inversions	1	0	0	1	1	2	0	0	0	1	1	1
# 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	14	22	4	11	2	6	0	1	9	26	5	19
Misassembled contigs length	12326	150519	2639	10841	943	3361	0	435	6219	143804	2899	54846
# possibly misassembled contigs	16	83	4	33	5	16	2	15	20	87	10	81
# possible misassemblies	16	98	4	37	6	18	2	16	20	99	10	91
# local misassemblies	9	28	2	4	2	2	0	2	8	23	7	12
# 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	5	0	0	0	0	0	0	1	4	0	5
# mismatches	38330	48325	19129	33048	5294	12860	1925	5250	37138	47278	30019	44226
# indels	282	555	146	278	40	111	12	35	304	462	171	403
# indels (<= 5 bp)	253	491	130	249	36	103	11	29	274	415	158	359
# indels (> 5 bp)	29	64	16	29	4	8	1	6	30	47	13	44
Indels length	673	1815	303	794	92	227	23	110	752	1339	397	1234

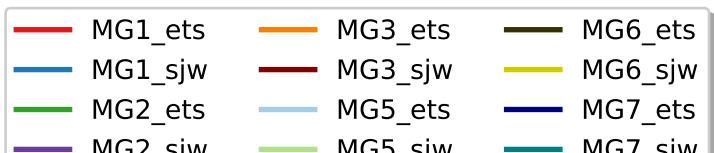
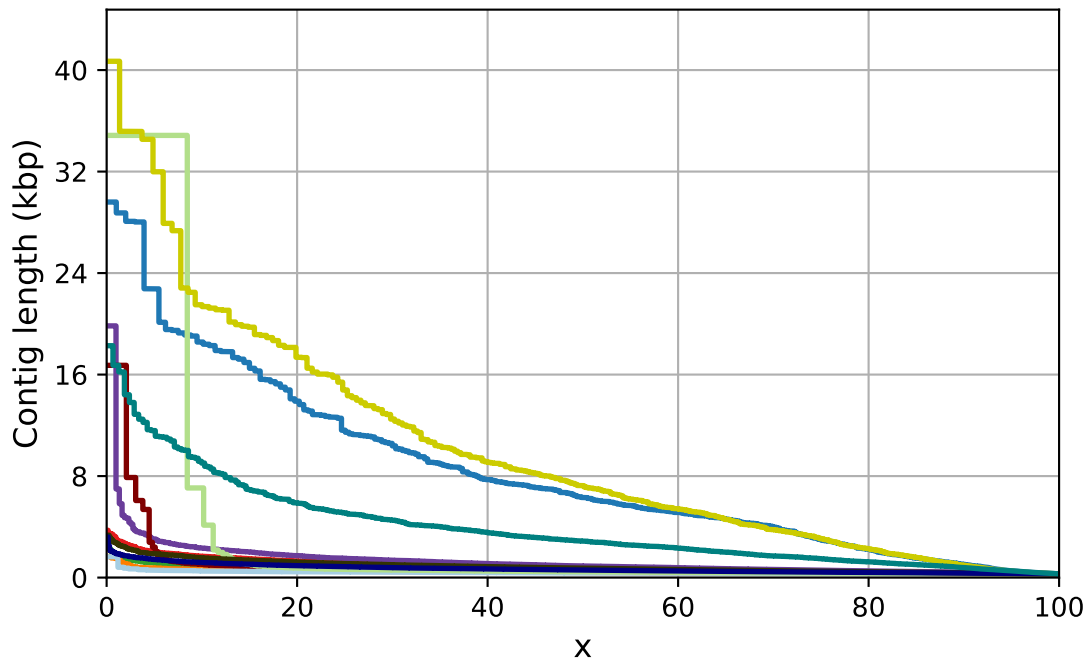
All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

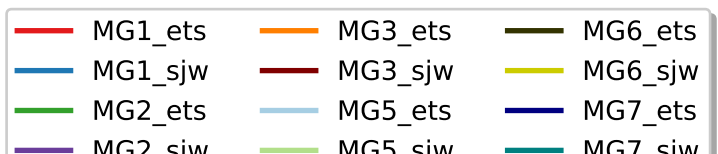
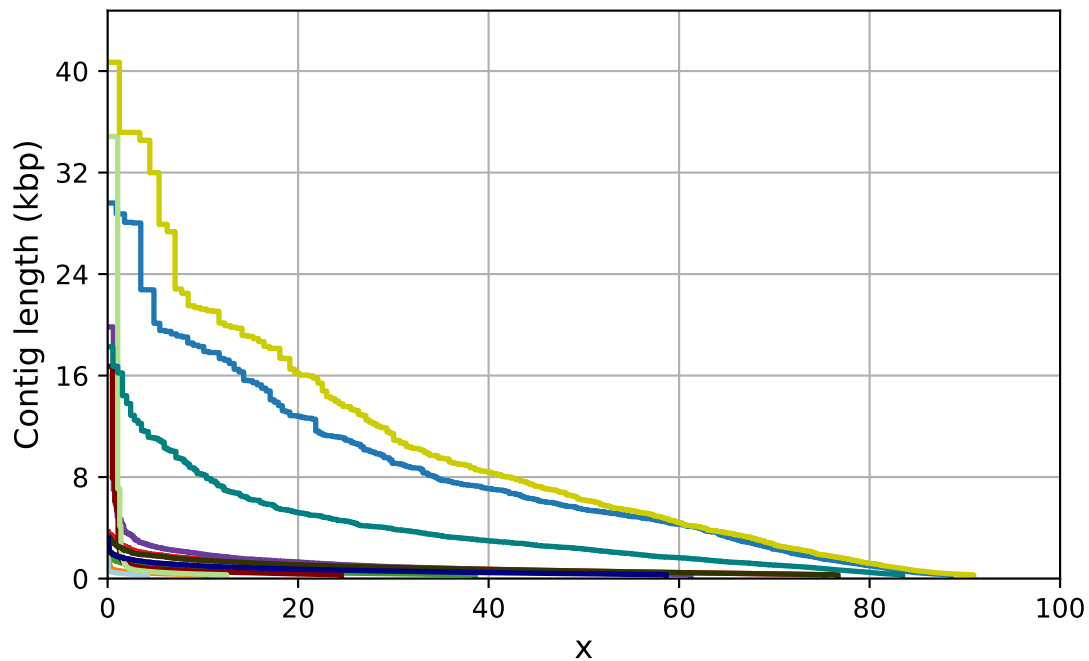
	MG1_ets	MG1_sjw	MG2_ets	MG2_sjw	MG3_ets	MG3_sjw	MG5_ets	MG5_sjw	MG6_ets	MG6_sjw	MG7_ets	MG7_sjw
# fully unaligned contigs	11	18	6	13	2	8	2	6	14	18	8	12
Fully unaligned length	6987	11826	2980	11578	2106	35854	888	10509	8874	50030	4303	18567
# partially unaligned contigs	15	89	4	30	4	14	2	16	21	88	10	87
Partially unaligned length	15234	168318	2581	61915	4564	19547	2134	54979	15089	143722	6976	174560
# 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).

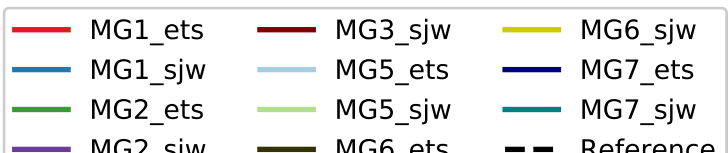
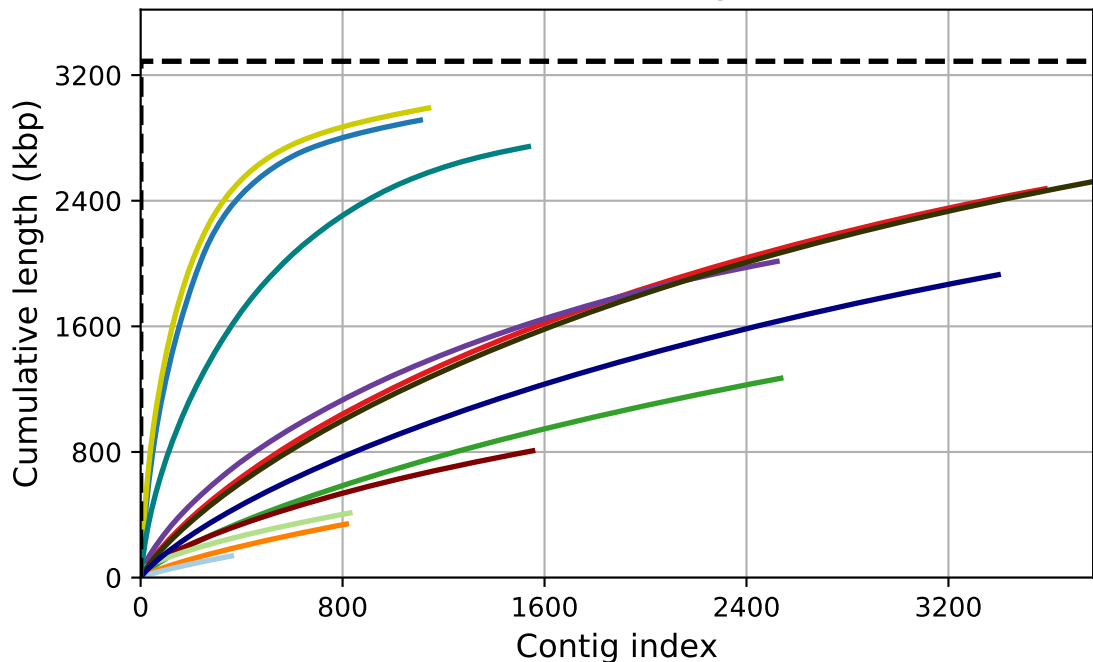
Nx



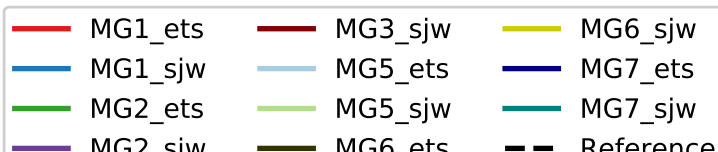
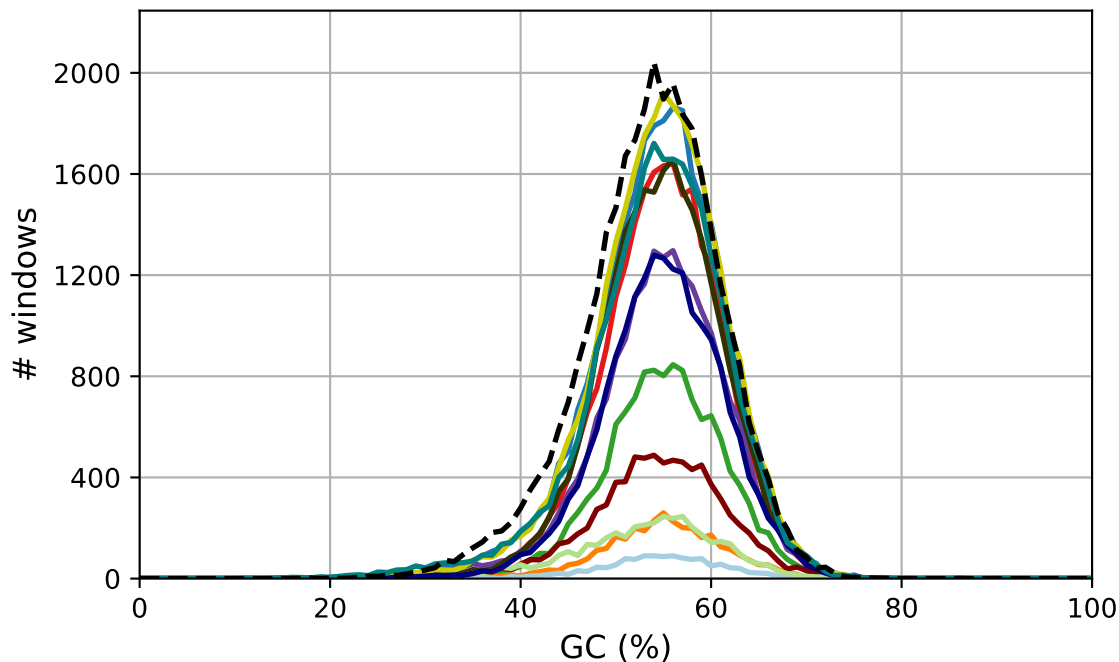
NGx



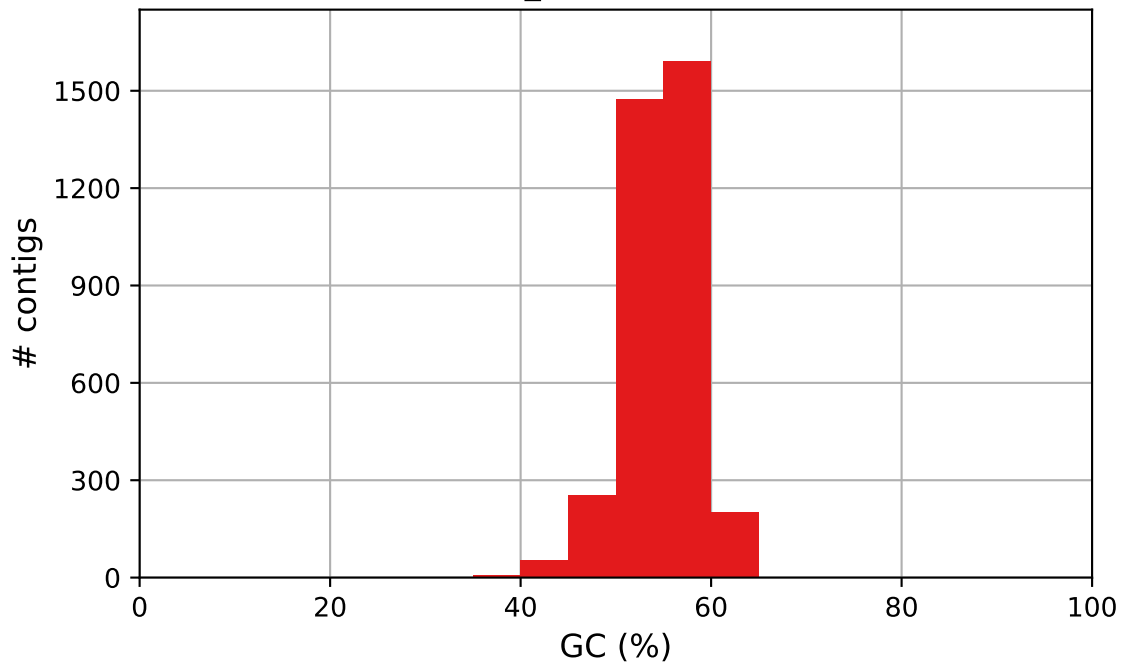
Cumulative length



GC content

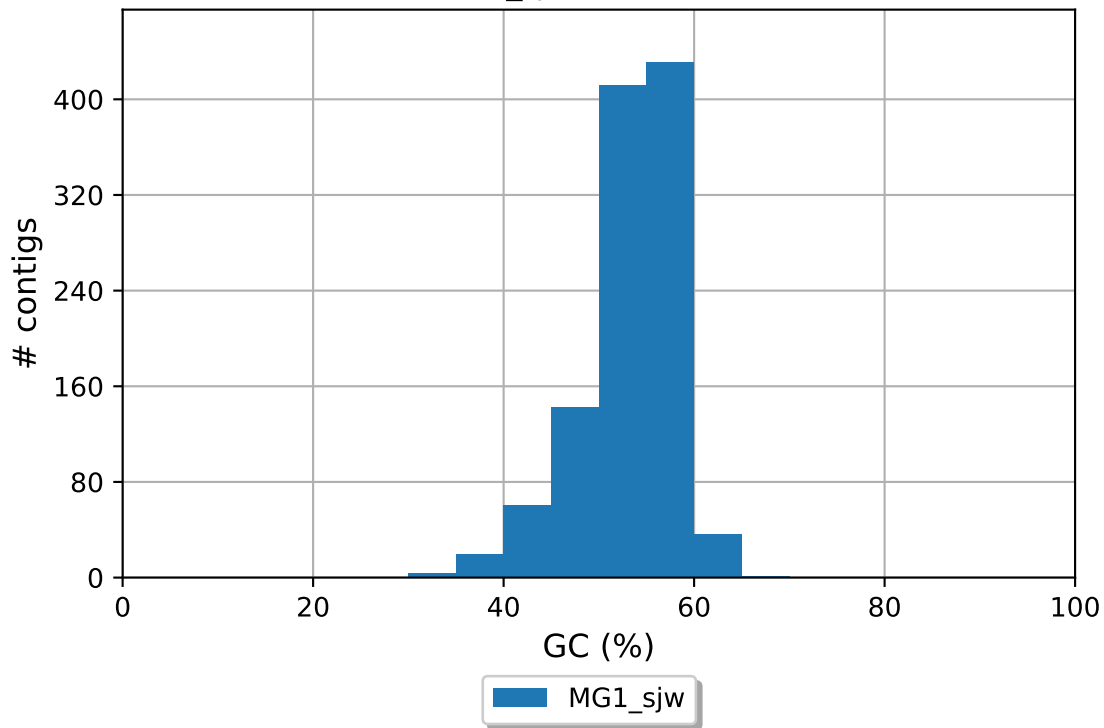


MG1_ets GC content

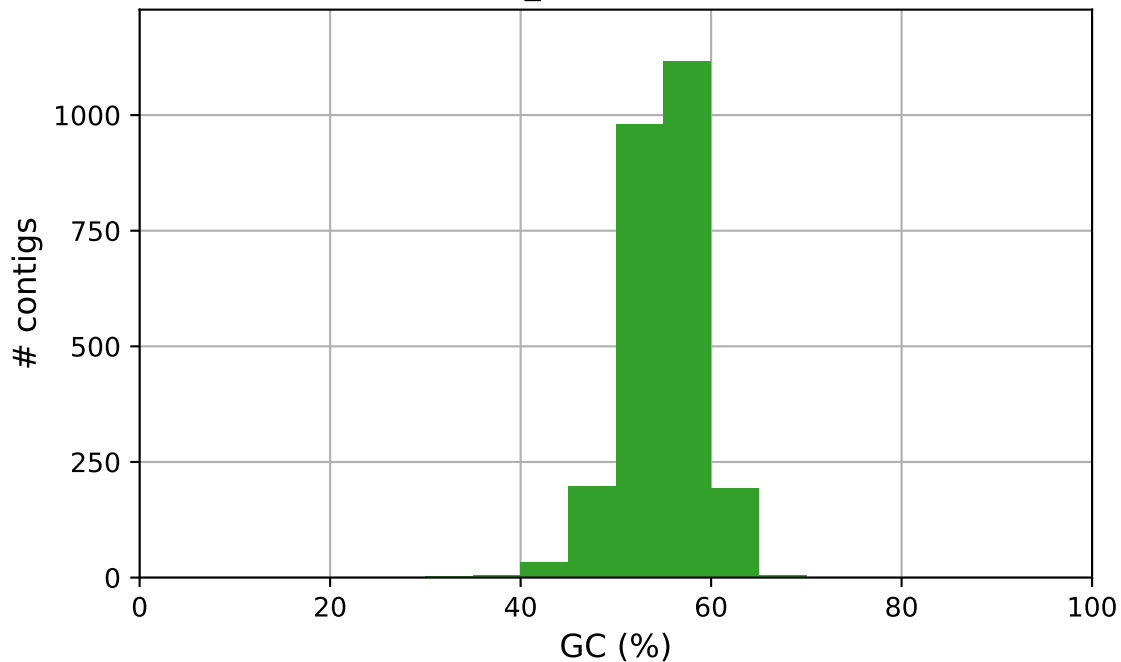


MG1_ets

MG1_sjw GC content

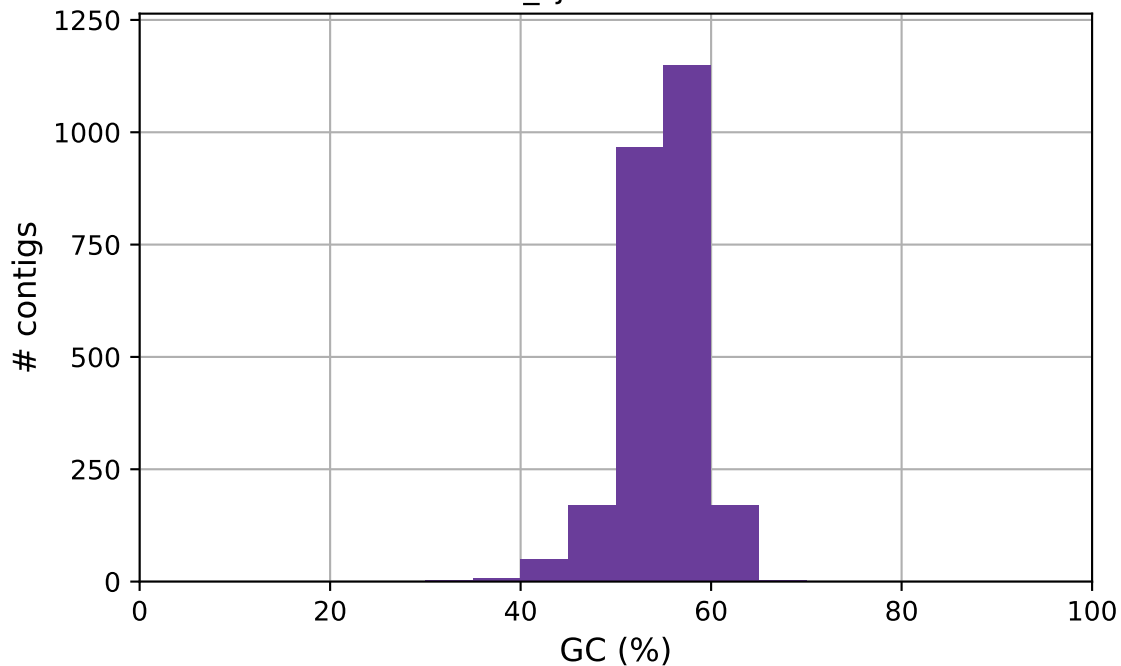


MG2_ets GC content



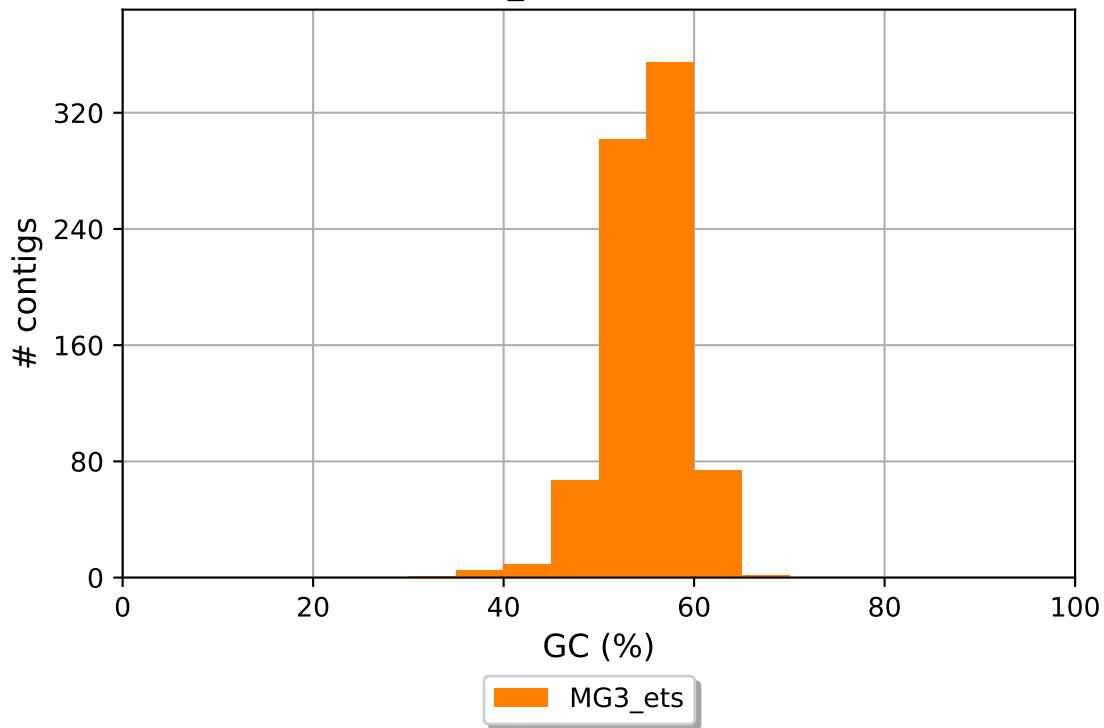
MG2_ets

MG2_sjw GC content

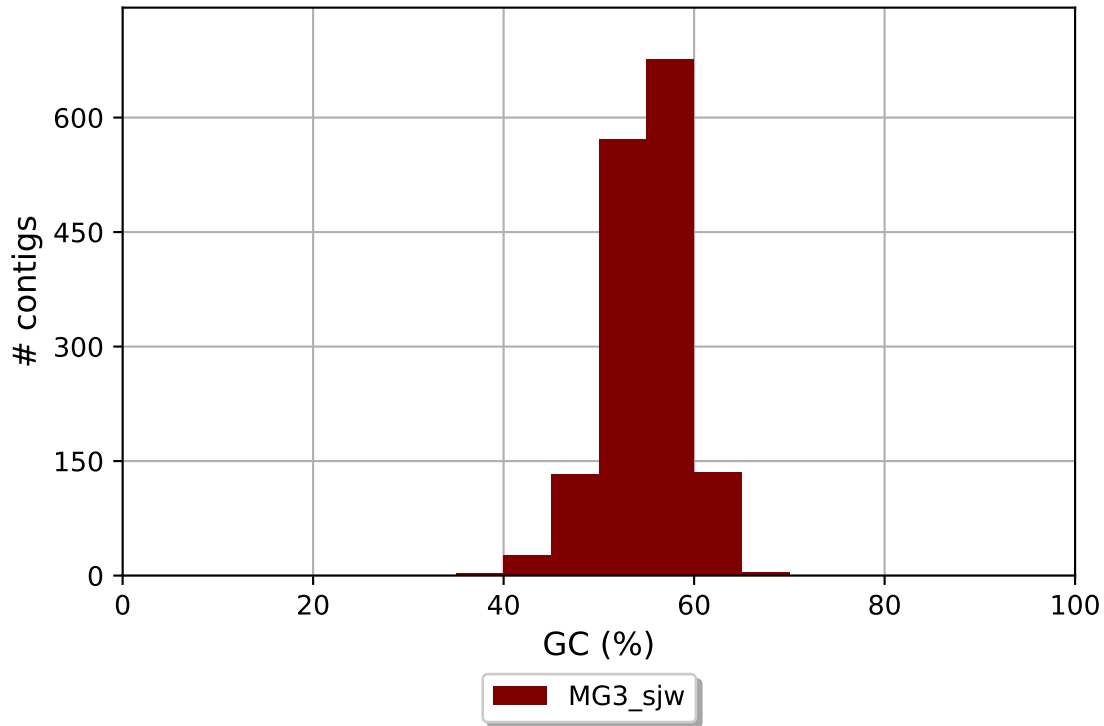


MG2_sjw

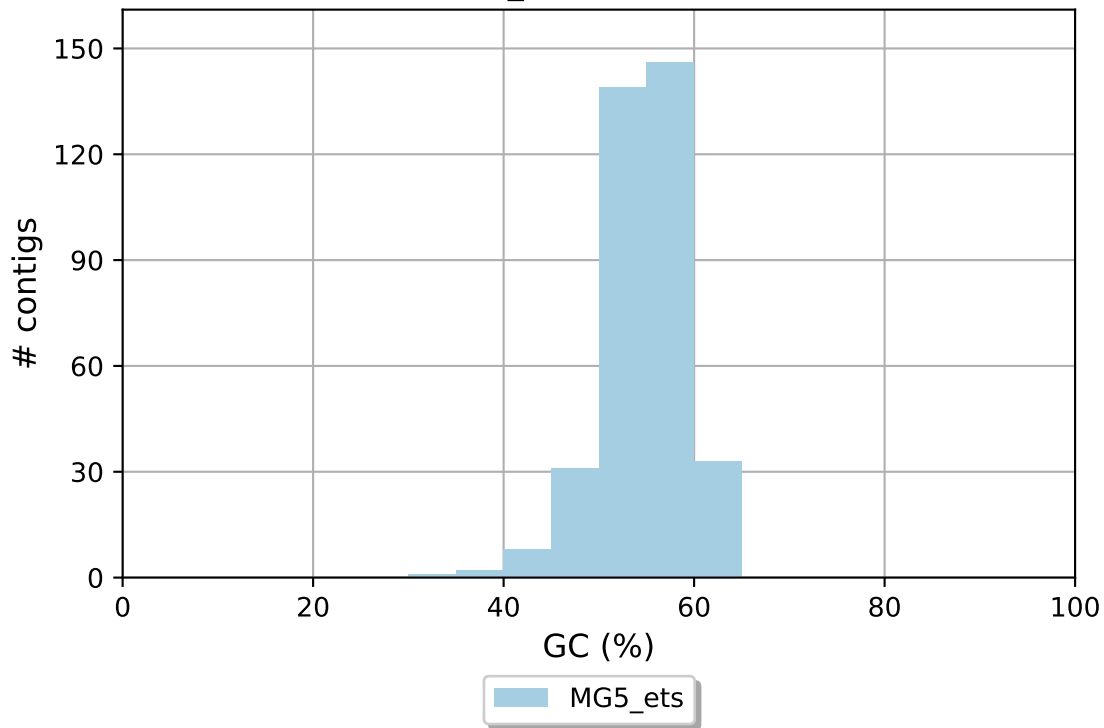
MG3_ets GC content



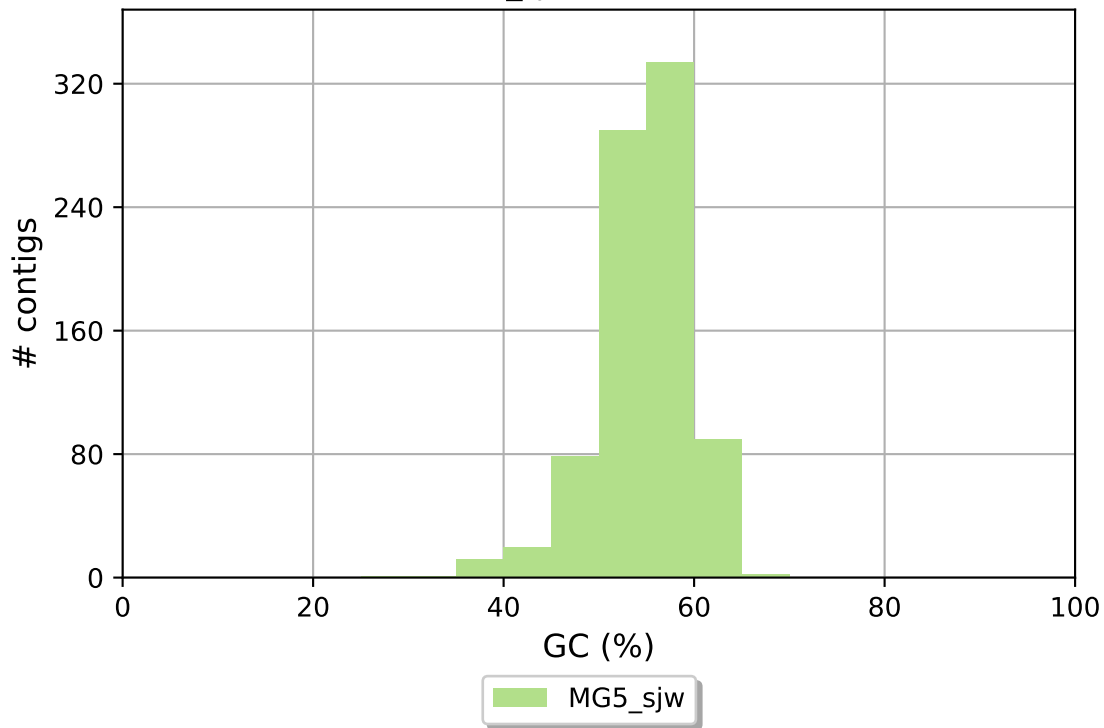
MG3_sjw GC content



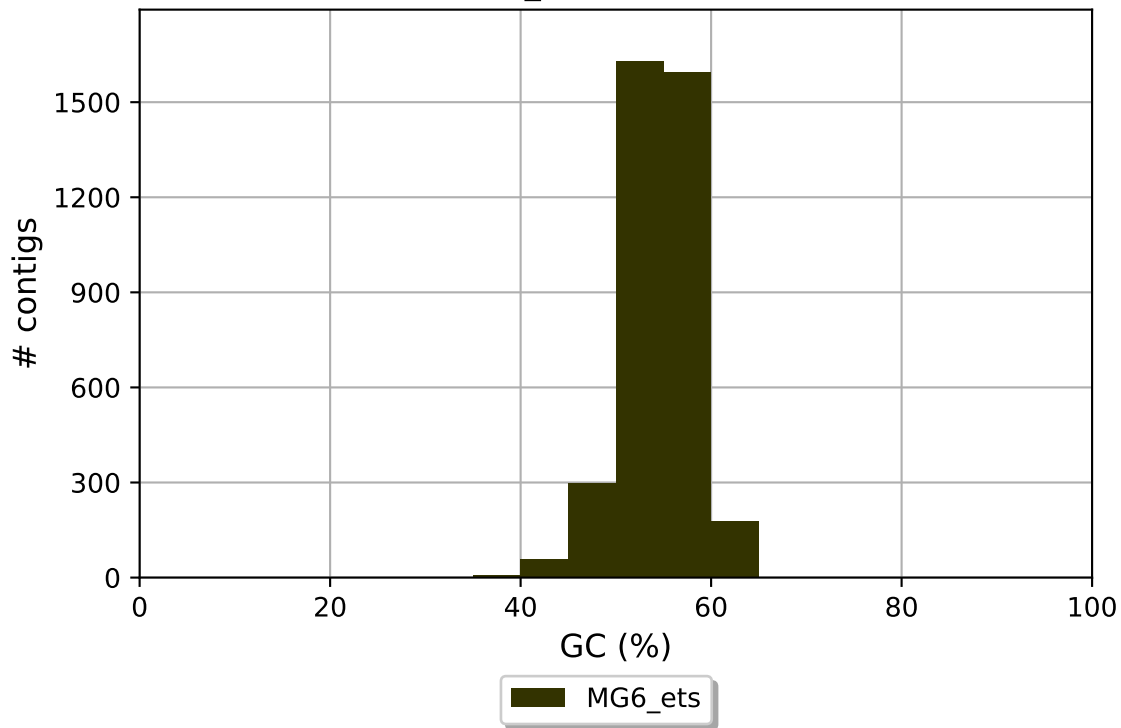
MG5_ets GC content



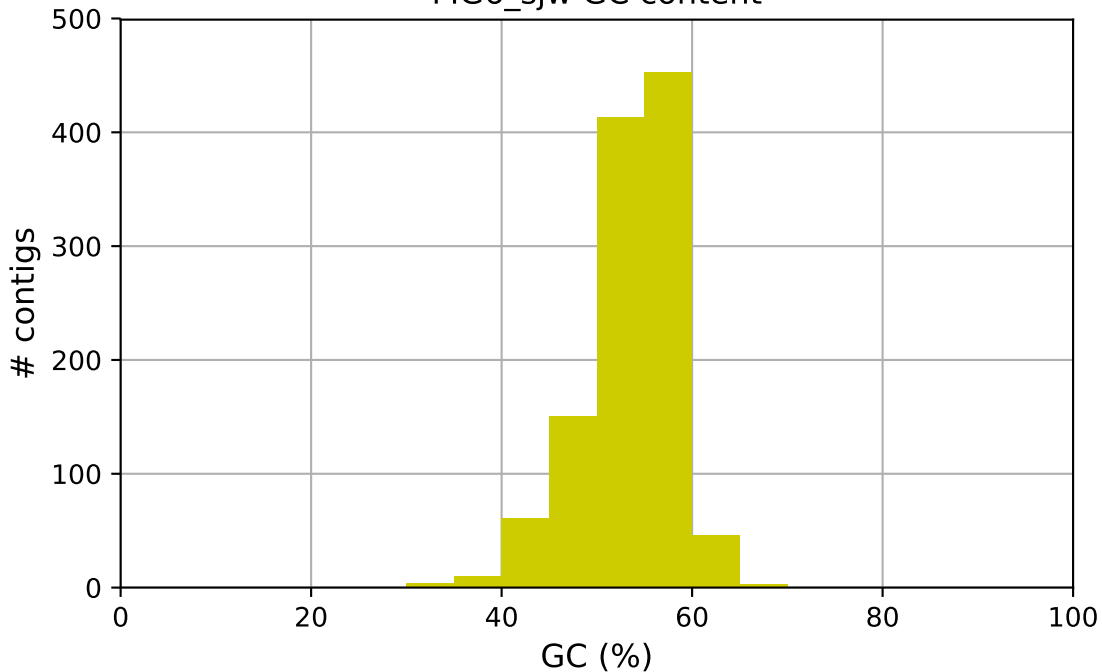
MG5_sjw GC content



MG6_ets GC content

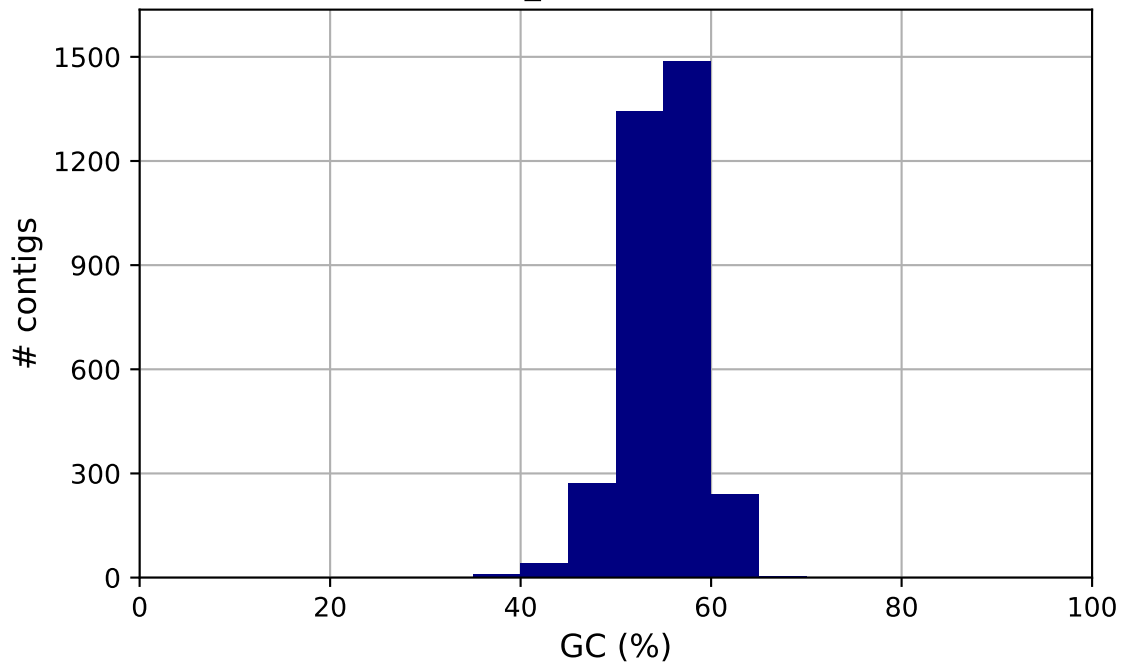


MG6_sjw GC content



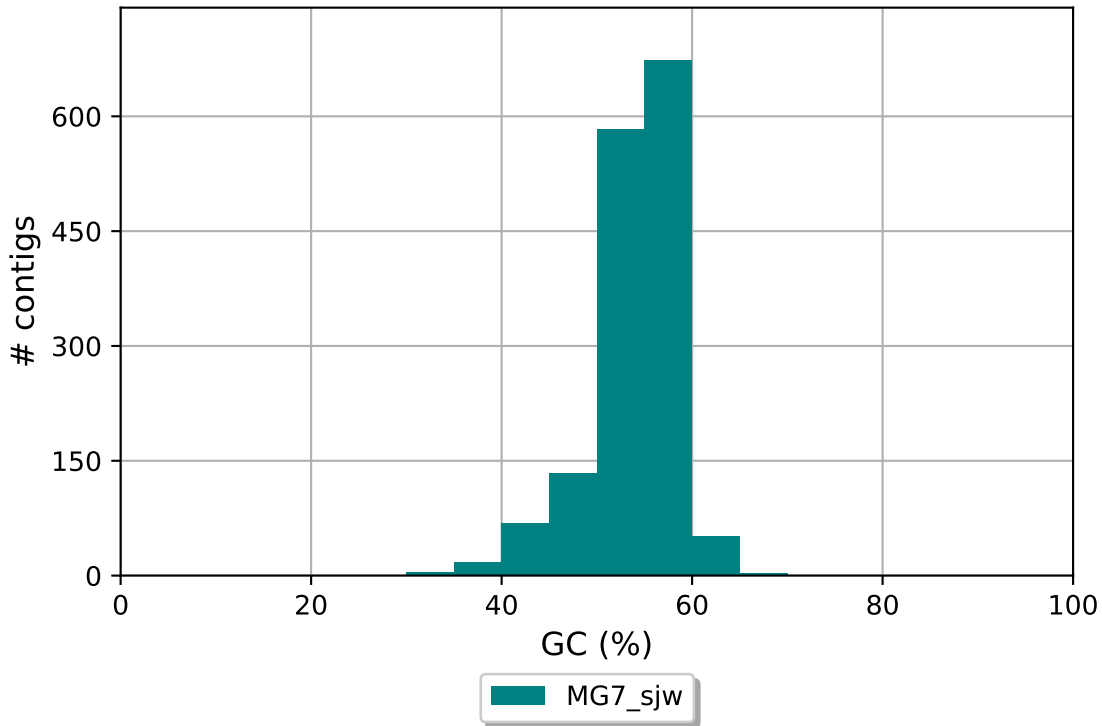
MG6_sjw

MG7_ets GC content

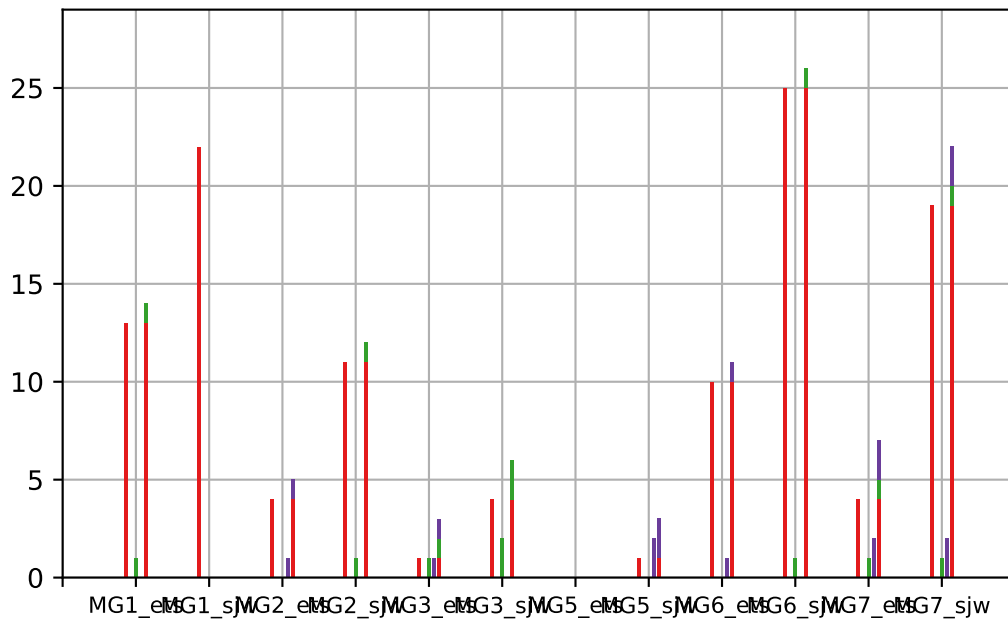


MG7_ets

MG7_sjw GC content



Misassemblies



relocations

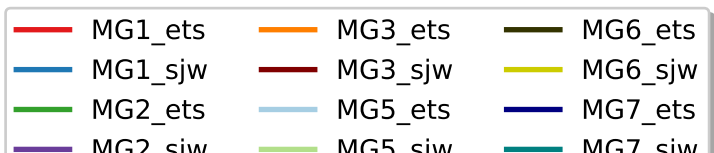
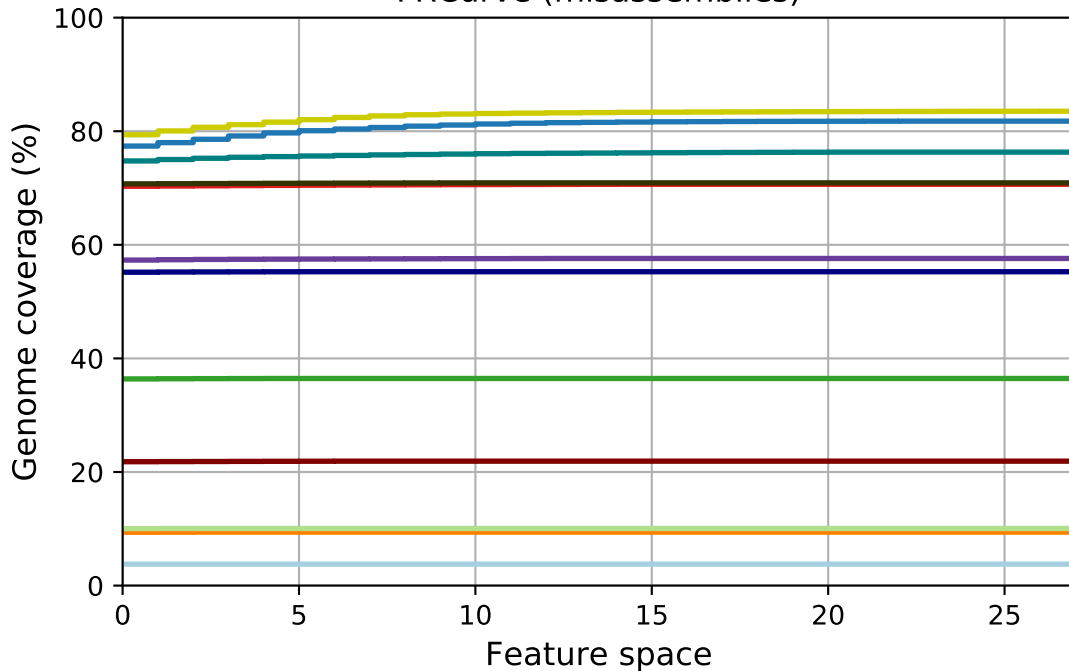


inversions

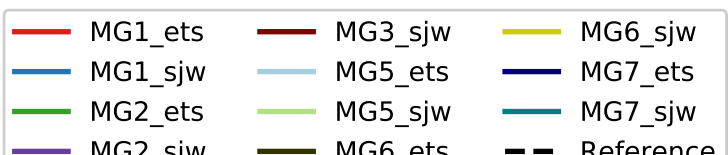
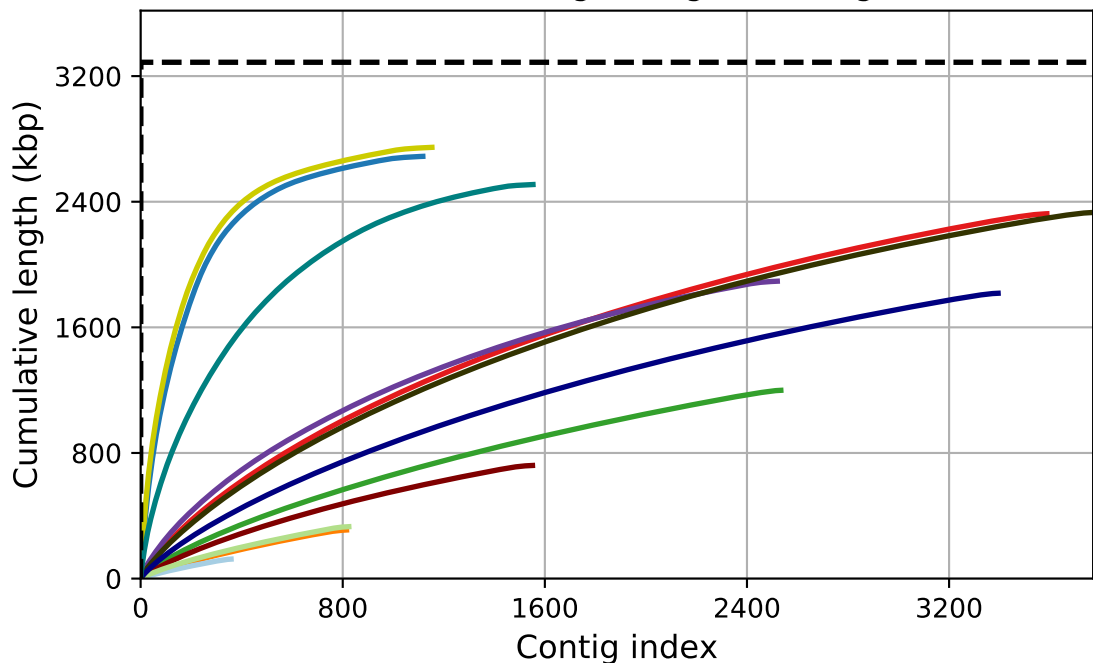


interspecies translocations

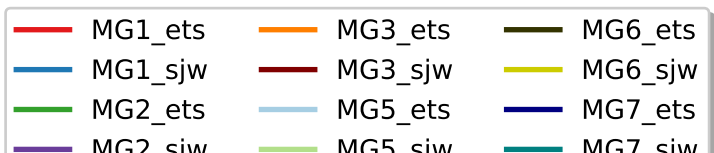
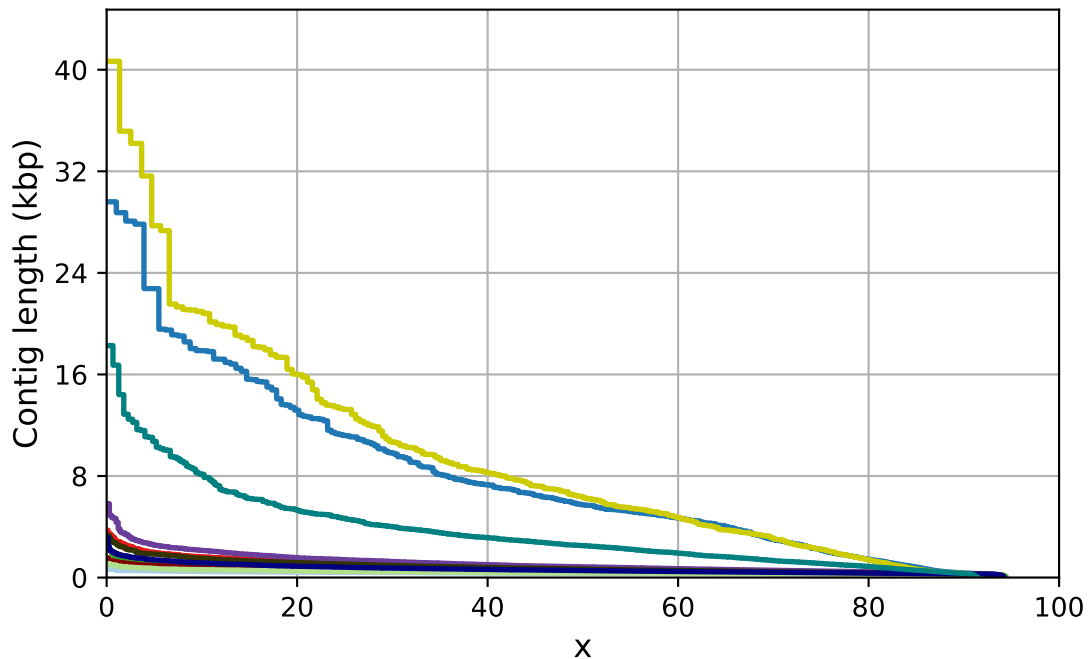
FRCurve (misassemblies)



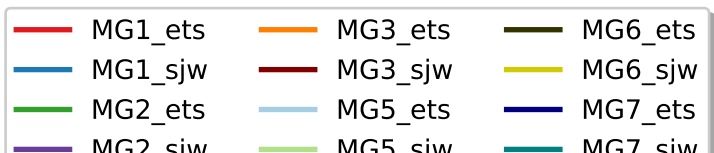
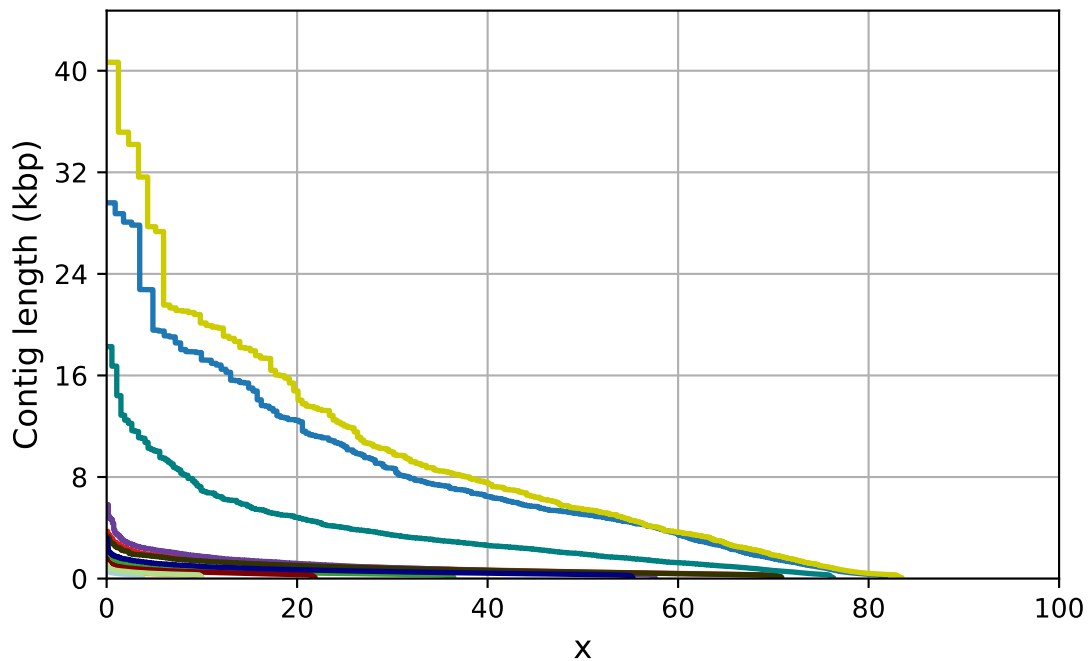
Cumulative length (aligned contigs)



NAX



NGAx



Genome fraction, %

