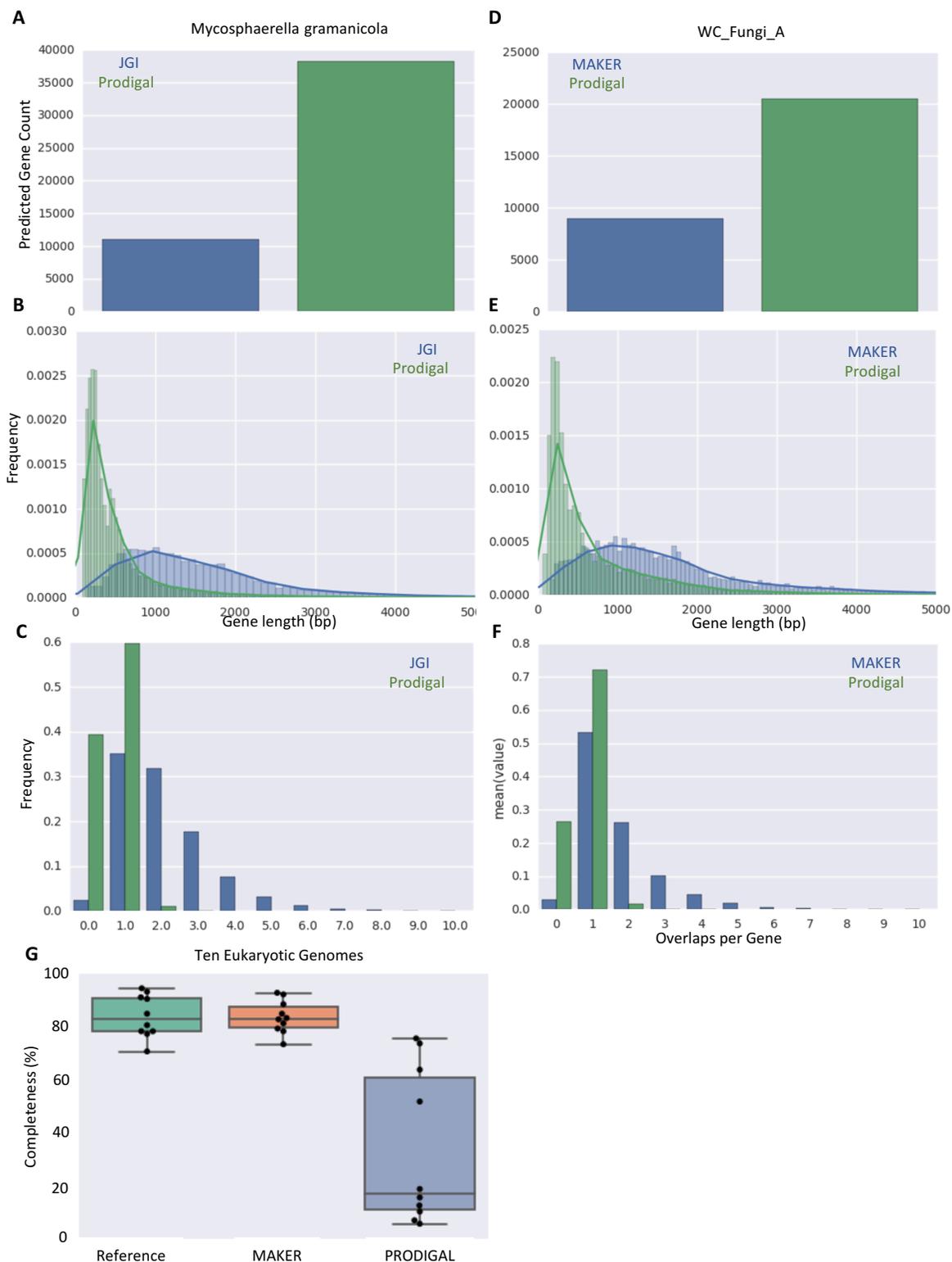


Supplemental Figure S2



**Supplemental Figure S2 Prodigal gene prediction results in poor quality gene models for eukaryotic genomes.**

(A-C) Prodigal predicted gene set as compared to the reference JGI annotation pipeline predicted gene set for the *Mycosphaerella graminicola* genome. (A) Total number of predicted genes in each set. (B) Histogram of predicted gene lengths for both gene sets. Overlaid lines are kernel density estimate plots. (C) Comparison of for a given gene from one gene set, how many genes in the other gene set it overlaps. 99% of Prodigal predicted genes overlap either zero or one genes from the JGI predicted gene set. An overlap is defined as sharing any length of the same genomic region. (D-F) Prodigal predicted gene set compared to MAKER2 predicted gene set (using GeneMark-ES and AUGUSTUS gene predictors) for the WC\_Fungi\_A genome binned from the CG\_WC sample. (G) BUSCO completeness estimates for protein sets derived from Prodigal, MAKER2 (using GeneMark-ES and AUGUSTUS gene predictors), and NCBI reference protein sets for the eukaryotic genomes listed in Figure 3A.