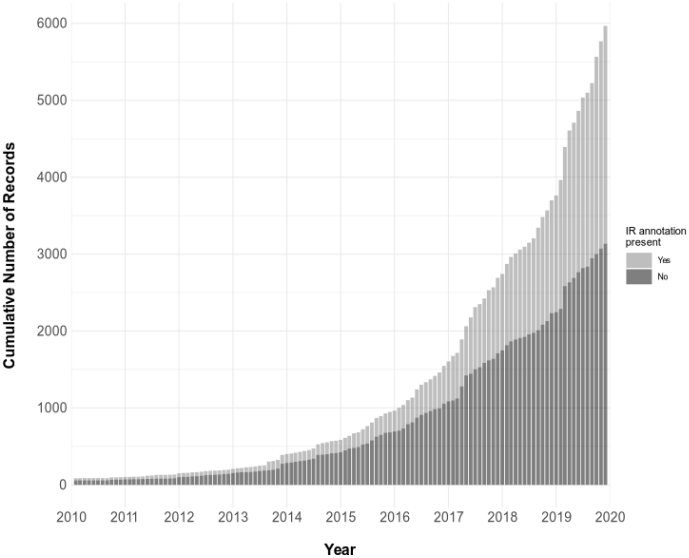


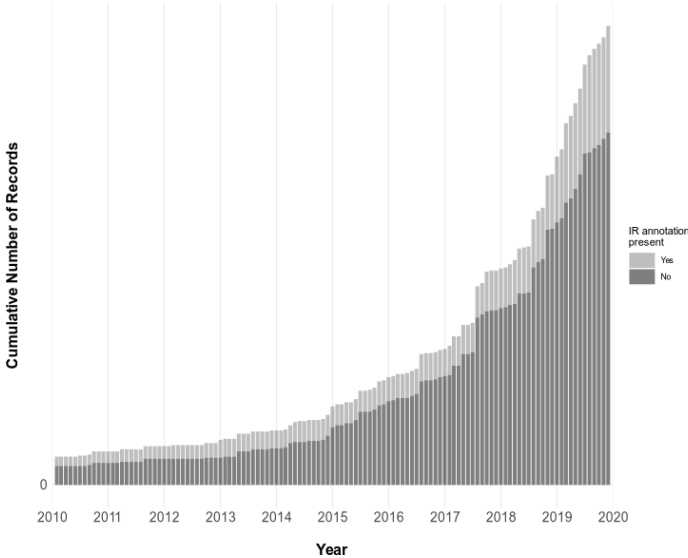
Figure 2

(a) Cumulative number of complete plastid genomes on NCBI GenBank per year, separated by presence of IR annotation  
*Note: Only data after 2009 is displayed.*

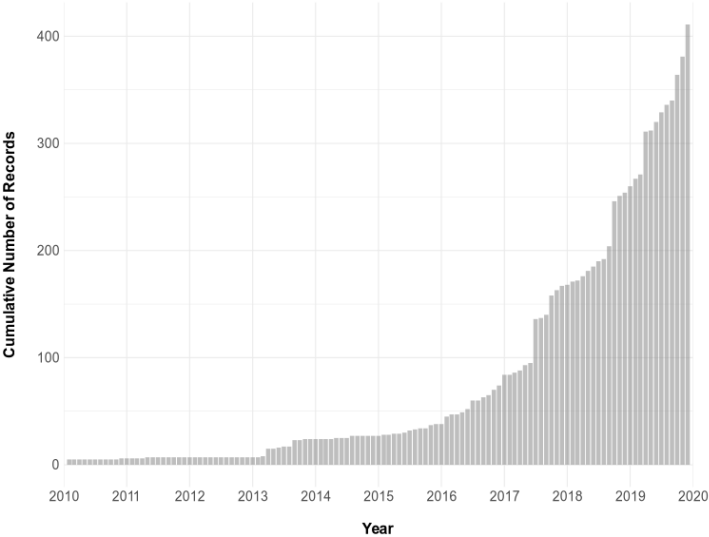


Foo bar  
baz

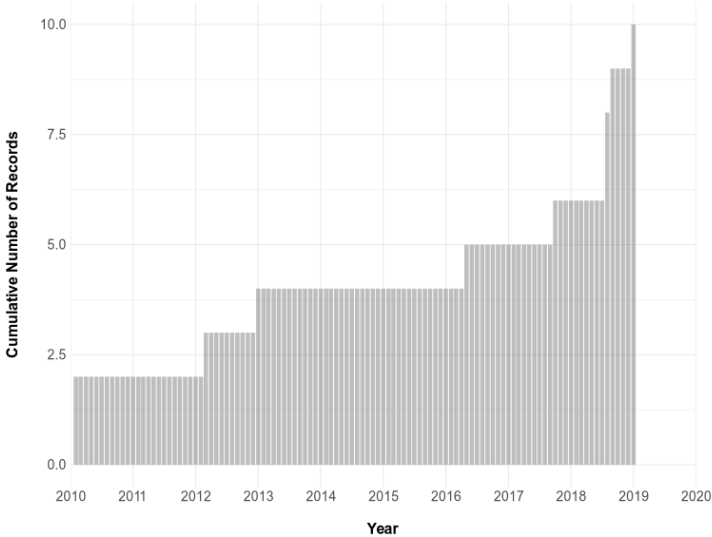
(b) Cumulative number of complete plastid genomes on NCBI GenBank per year, separated by presence of IR annotation  
*Note: Only data after 2009 is displayed.*



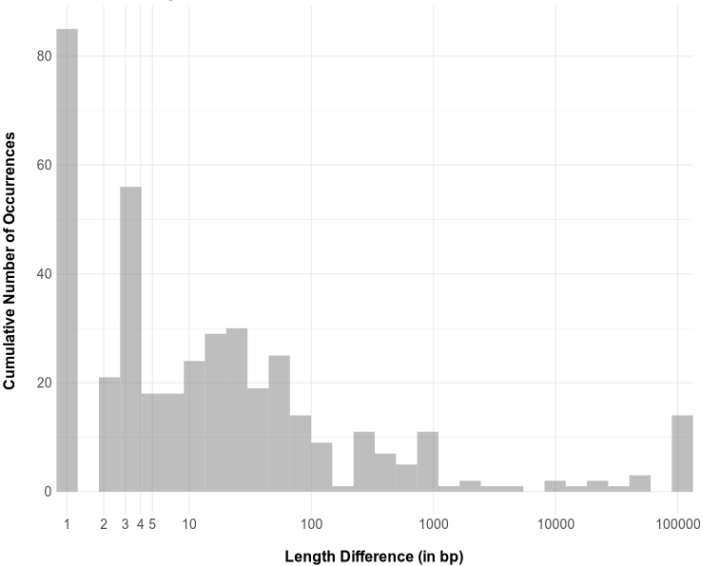
(c) Cumulative number of complete plastid genomes on NCBI GenBank per year, whose reported IR annotations have unequal lengths  
*Note: Only data after 2009 is displayed.*



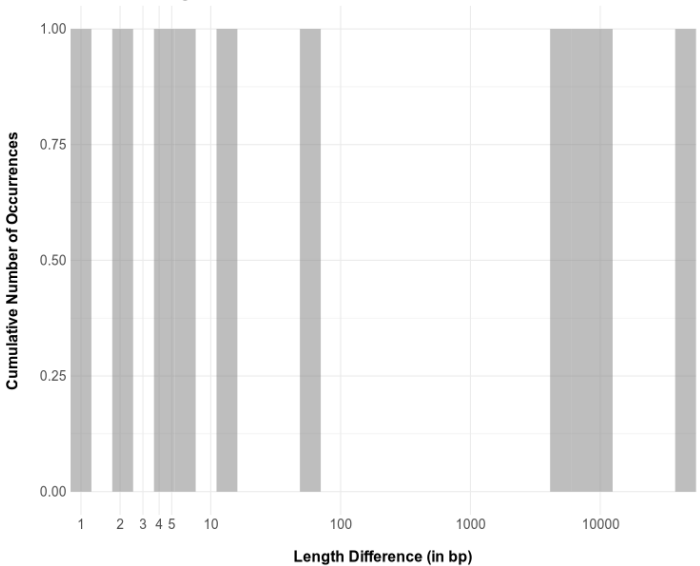
(d) Cumulative number of complete plastid genomes on NCBI GenBank per year, whose reported IR annotations have unequal lengths  
*Note: Only data after 2009 is displayed.*



(e) Distribution of the differences in length between the IRa and the IRb  
*Note: only data after 2010 is displayed; x-axis is set to logarithmic scale*



(f) Distribution of the differences in length between the IRa and the IRb  
*Note: only data after 2010 is displayed; x-axis is set to logarithmic scale*



**Figure 2:** Overview of the presence and length equality of IR annotations among all complete plastid genomes on GenBank. The plots of the upper row visualize the cumulative number of complete plastid genomes over the past 20 years that contain (light grey) or lack (dark grey) annotations for the IRs, separated by **(a)** angiosperms and **(b)** non-angiosperms. The plots in the center row visualize the cumulative number of complete plastid genomes over the past