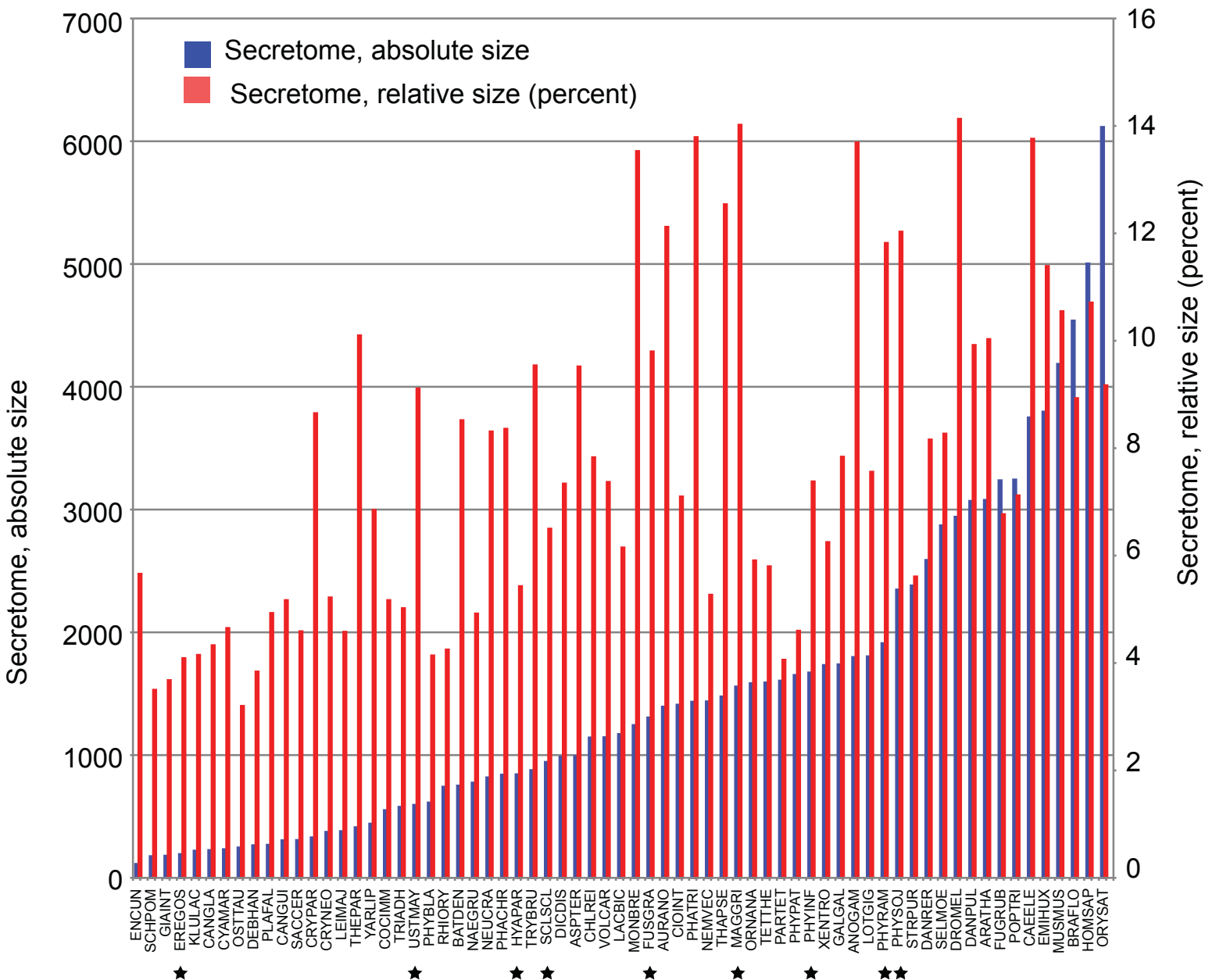
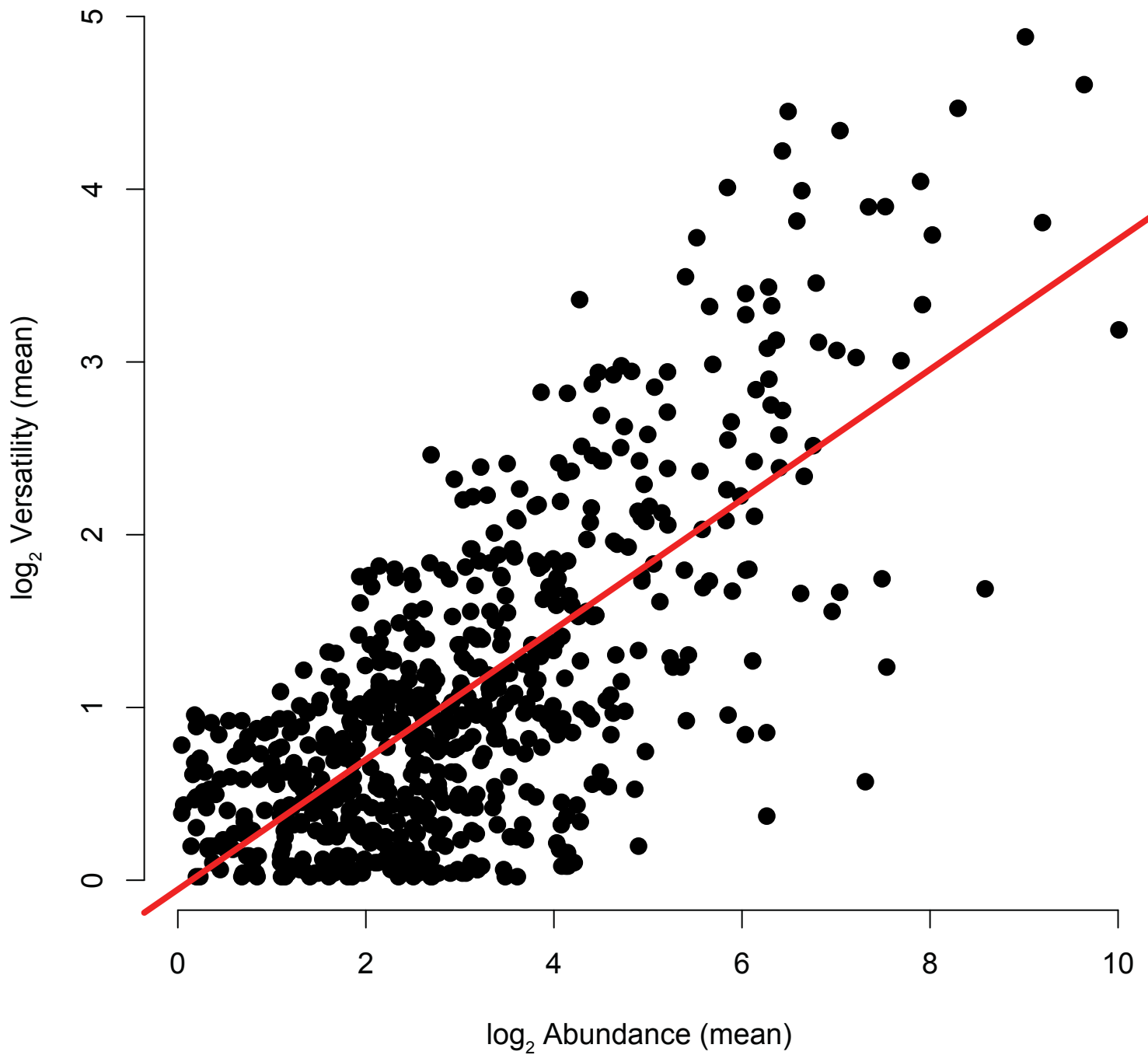


Supplementary Figure 1 – (a) Dependence of the number of domain and bigram types excluding singletons observed in the species analyzed. (b) Relationship between the proteome size and the number of distinct domain types as well as (c) the number of bigram types. The species names corresponding to the abbreviations can be found in Supplementary Table 1.



Supplementary Figure 2 – The predicted secretome of the 67 analyzed eukaryotic species. The absolute size as well as the percentage of the predicted secretome is displayed. The analyzed plant pathogens are indicated with a star and species abbreviations are shown in Supplementary Table 1.



Supplementary Figure 3 - The average abundance and versatility of all observed domains in a log₂-log₂ plot. The graph displays a linear positive correlation between the abundance and versatility of different domains (regression line in red). Domains that are highly abundant and do not have a high number of different N- or C-terminal partners are shown in the lower right sector of the plot. Domains that show an uneven distribution of versatility in the examined species might have a low average versatility, even if they have many different partners in some species.