



**Figure 5: Predictive outcome of machine learning.** A, B. Density curves of pathogen colonization with global minima used for splitting into “protected” (positive) and “not-protected” (negative) classes presented as vertical dashed lines. C, D. Performances of classification algorithms compared to a random classification (*i.e.*, “No Model”) based on presence/absence of Mini5SynCom members. E, F. Root mean square errors (RMSE) of the regression algorithms with dashed lines corresponding to predictions based on the global average of pathogen colonization (“No Model”) based on presence/absence of Mini5SynCom members or absolute abundance of Mini5SynCom members (“colonization”). A, C, E. Results derived from algorithms trained on the median of pathogen colonization for each treatment. B, D, F. Results derived from algorithms trained on pathogen colonization of individual plants.