



Supplementary figure 1. (A) VIRIDIC plot of intergenomic sequence similarity, aligned genome fraction and genome length ratio for 105 isolated *P. syringae* phages. **(B)** Left, phylogenetic tree of all 13 phylogroups within *P. syringae*. Middle, bar chart indicating the number of phages infecting each isolate. Right, overview of the broadest covering phage combination. **(C)** Bioassay using a six-phage cocktail demonstrates significant reduction in the amount of bacterial specks caused by *P. syringae* pv. *tomato* 14 days post infection (p-value= 5.2×10^{-8} , Wilcoxon test). **Unpublished data.**