**Supplementary Material 2: Chinook survival model figures** 

"Identification of infectious agents in early marine Chinook and Coho salmon

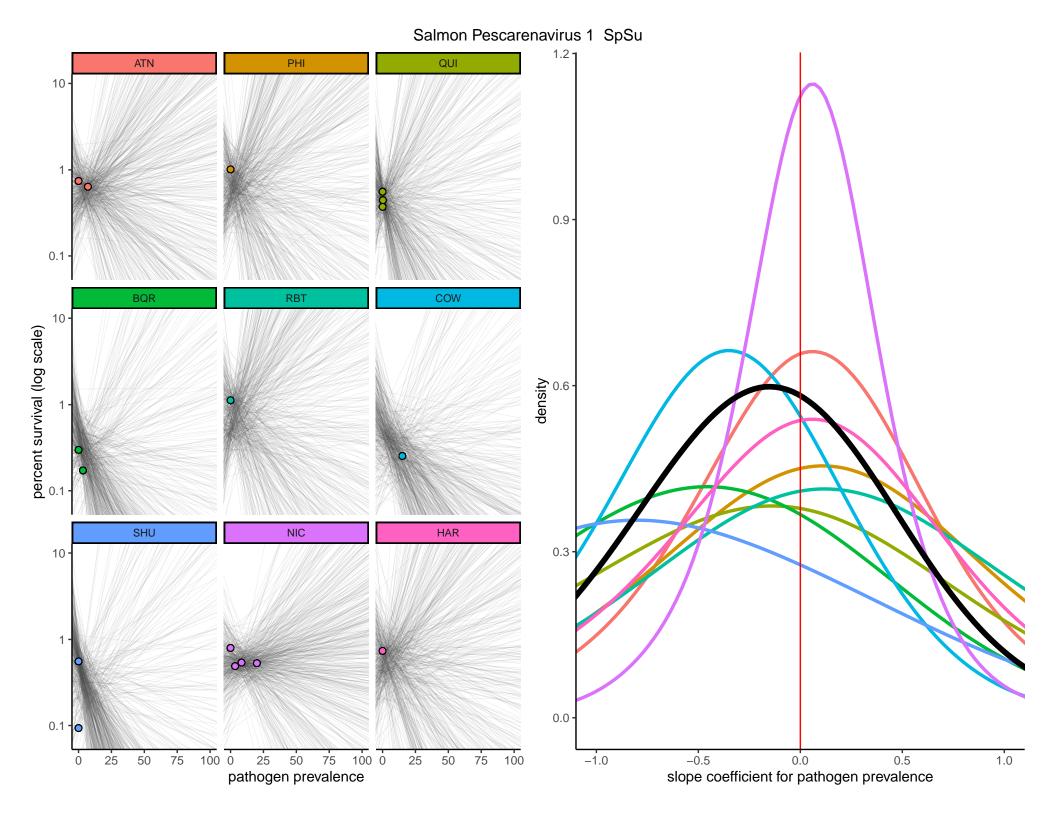
associated with cohort survival"

Arthur L. Bass, Andrew W. Bateman, Brendan M. Connors, Benjamin A. Staton, Eric B.

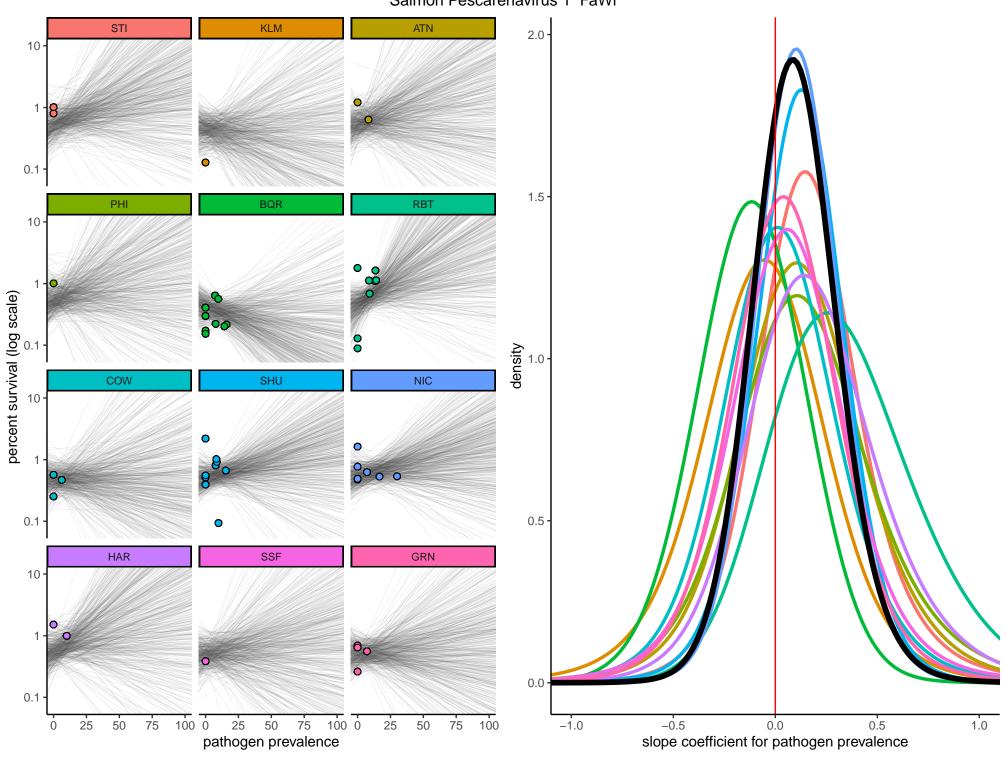
Rondeau, Gideon J. Mordecai, Amy K. Teffer, Karia H. Kaukinen, Shaorong Li, Amy M.

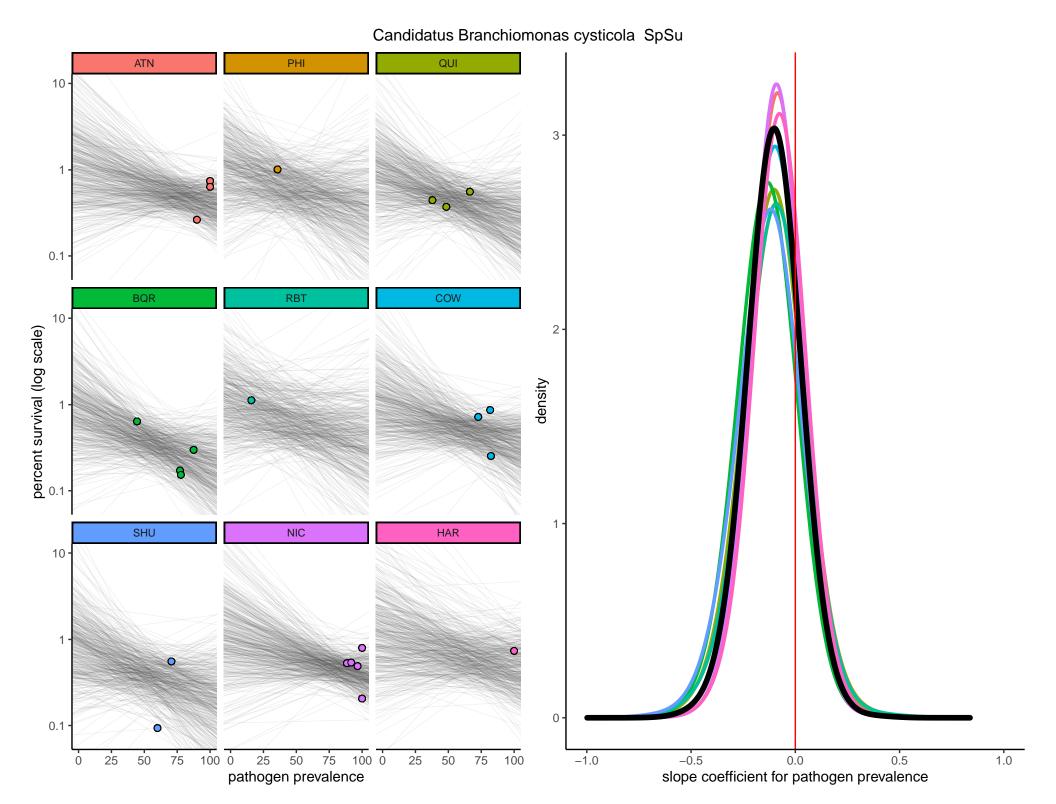
Tabata, David A. Patterson, Scott G. Hinch, Kristina M. Miller

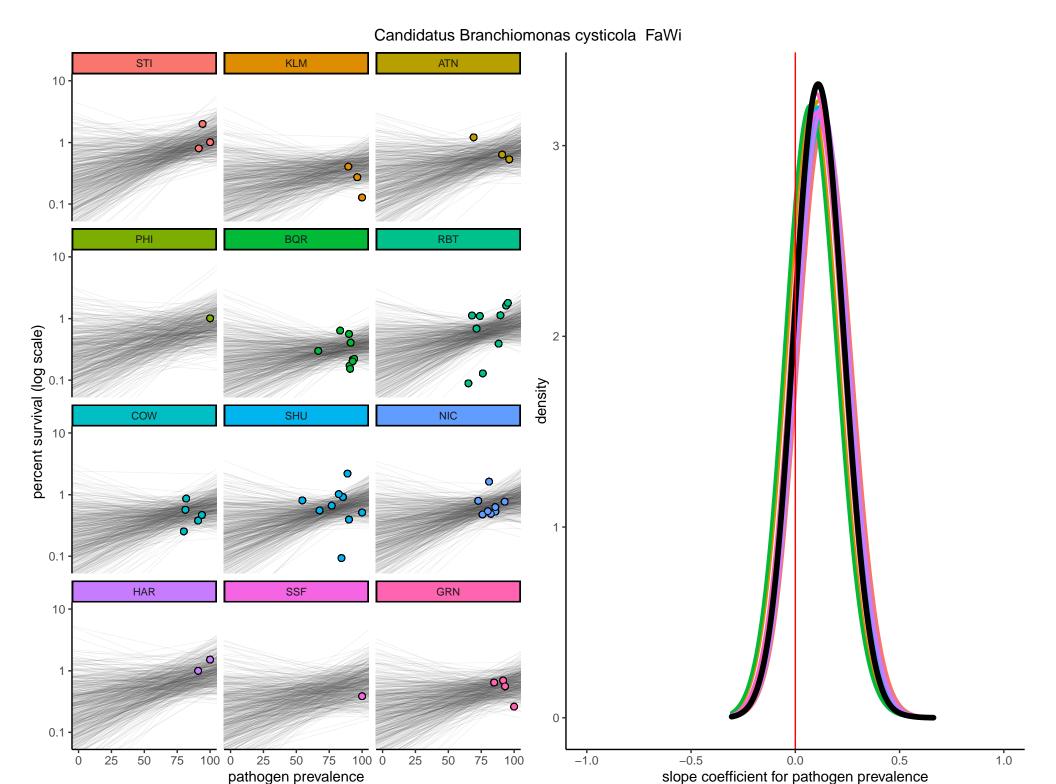
**Description:** Bayesian multi-level model results from Chinook survival models. Raw data (points) are presented in left panels and model results are presented in right panels (heavy black line indicates the posterior distribution of the hyperdistribution mean). Lines in left panels represent 1000 random draws from the posterior distributions of the stock-specific intercepts and slopes. Slope coefficient for the right panel is relative to a 10% increase in pathogen prevalence.

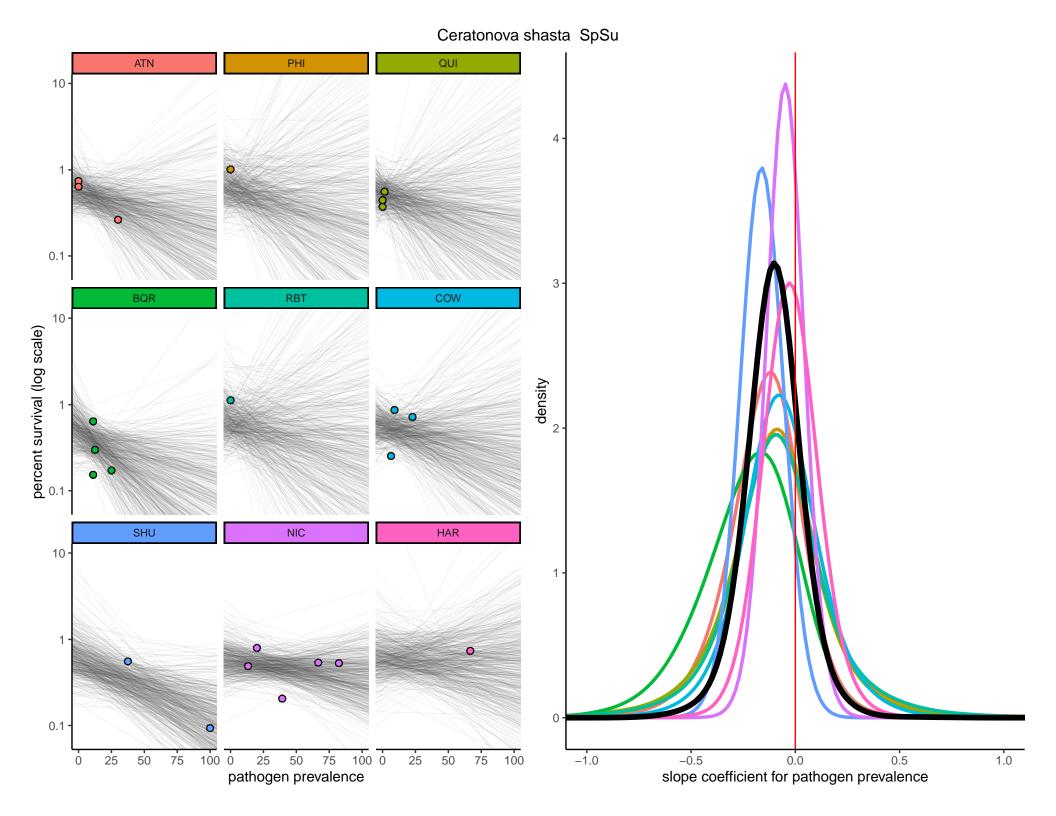


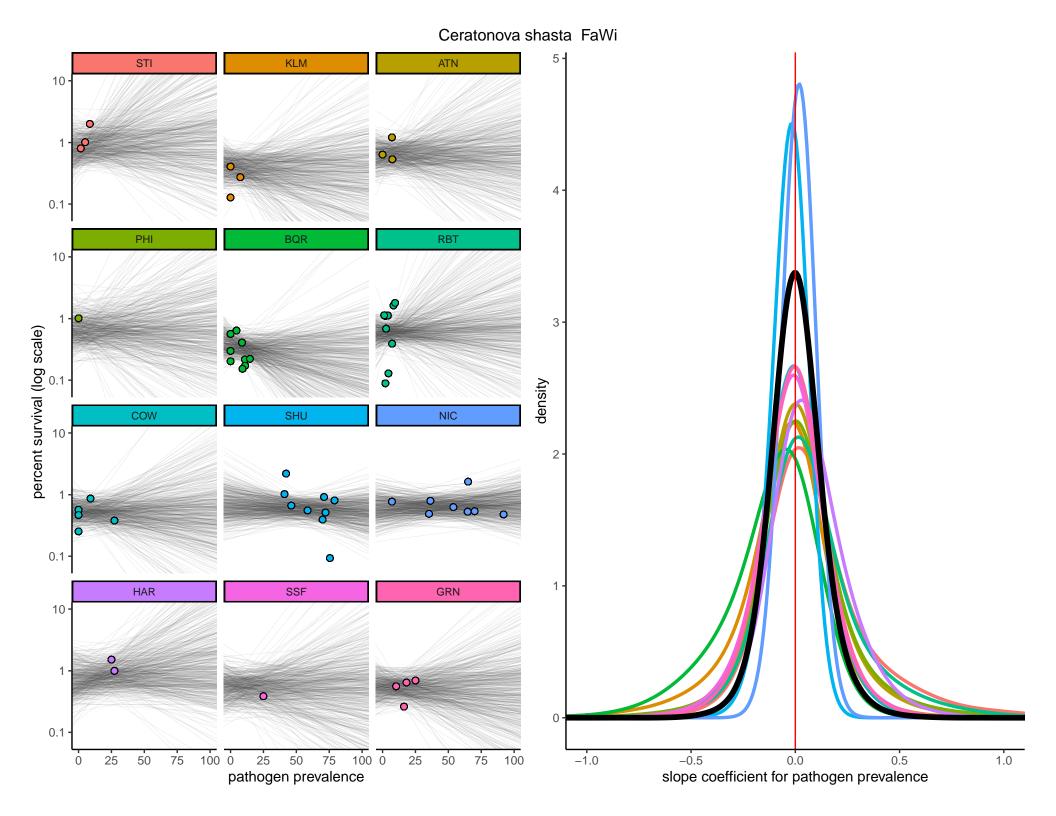
Salmon Pescarenavirus 1 FaWi

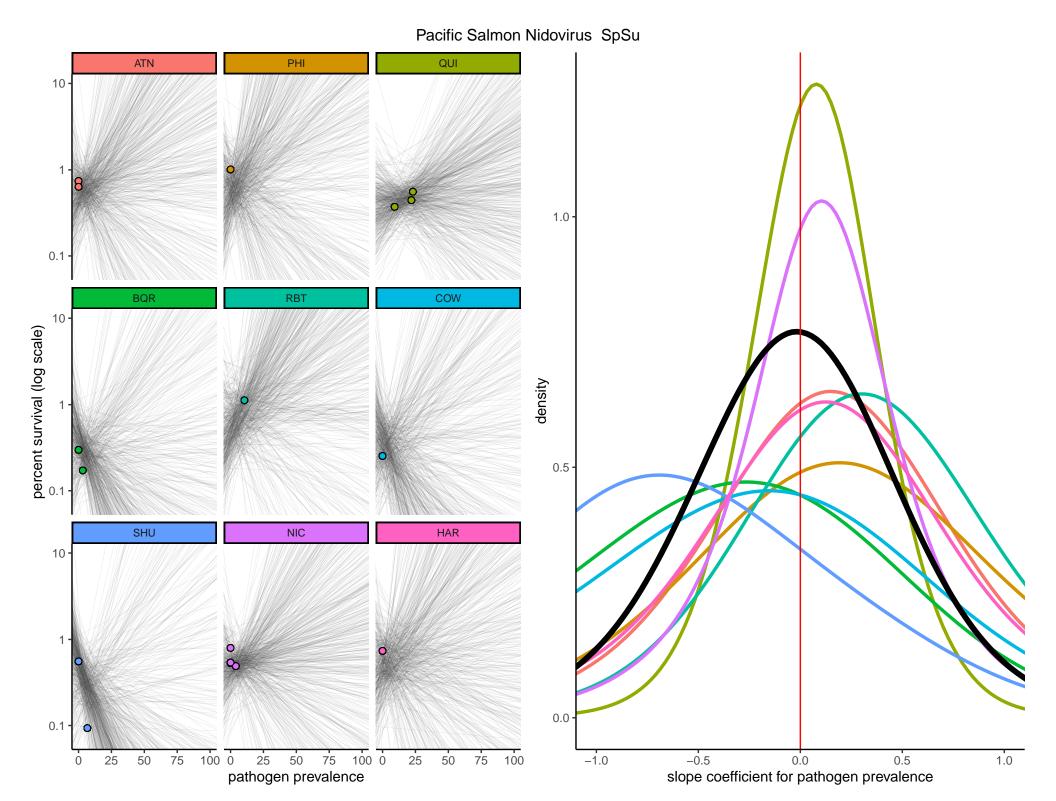


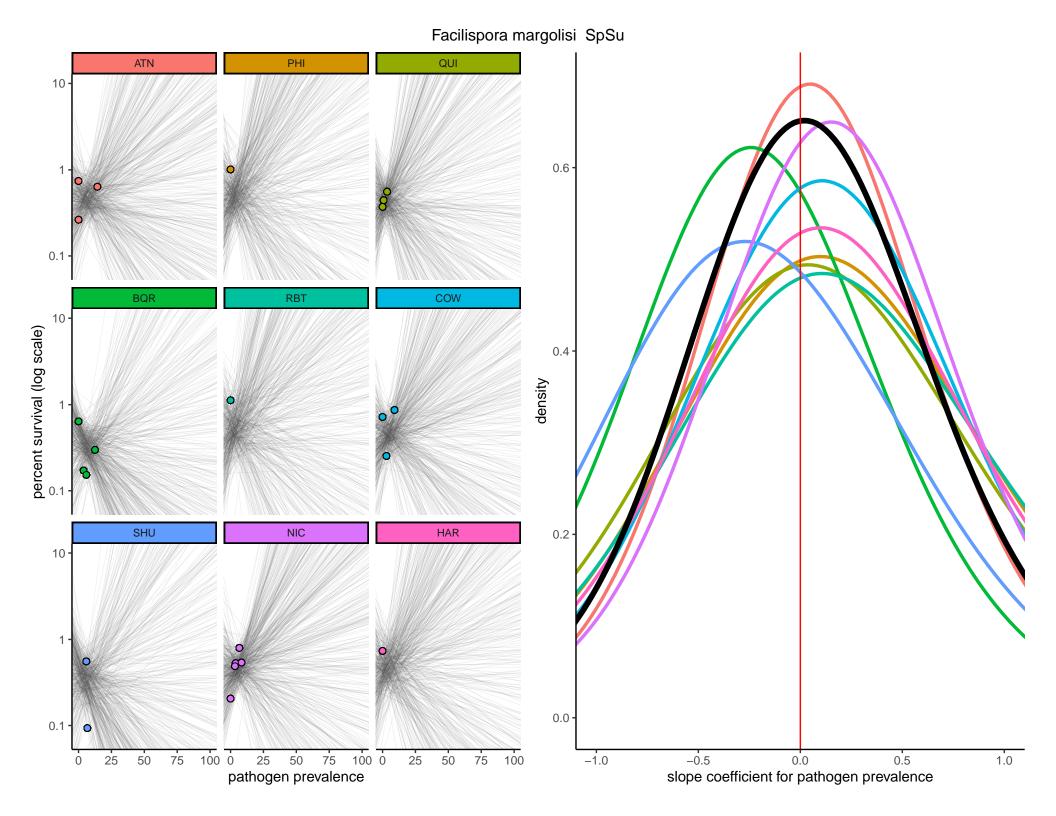


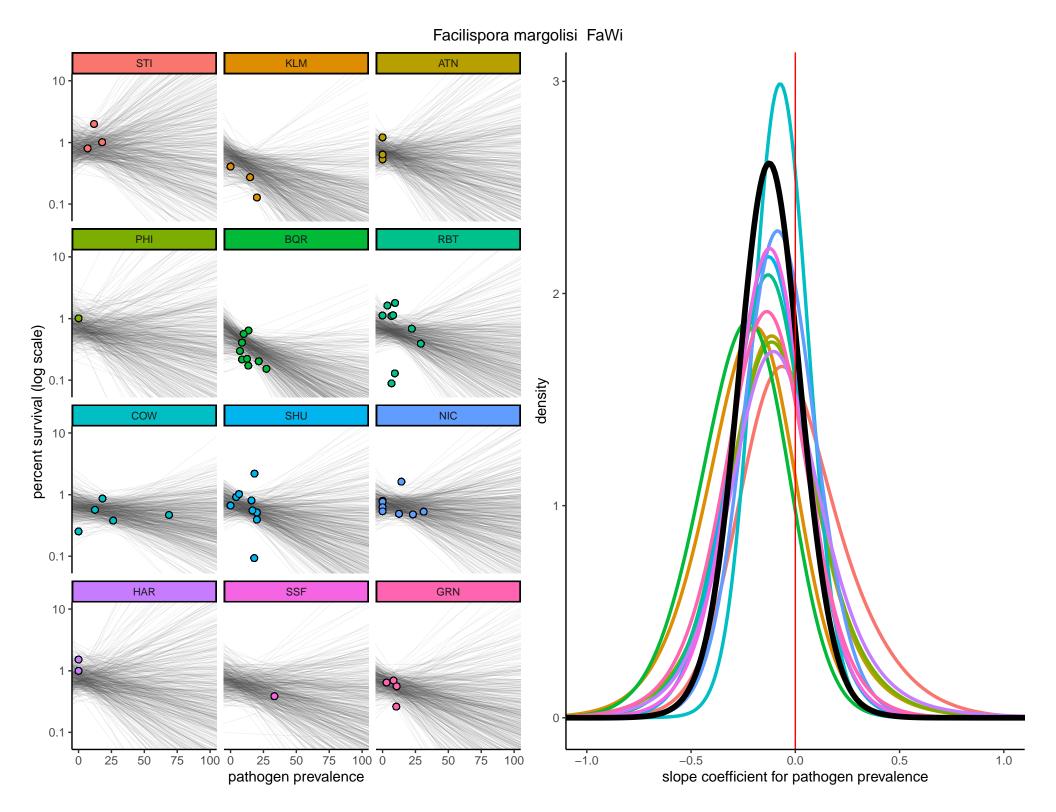


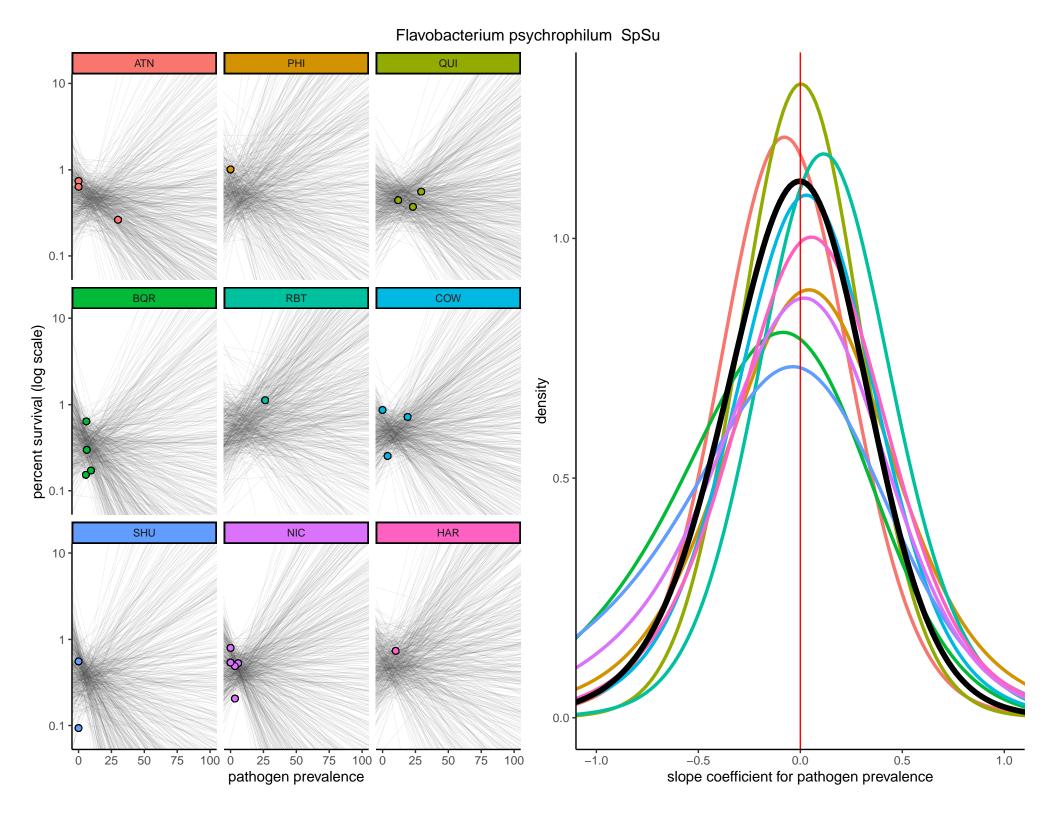


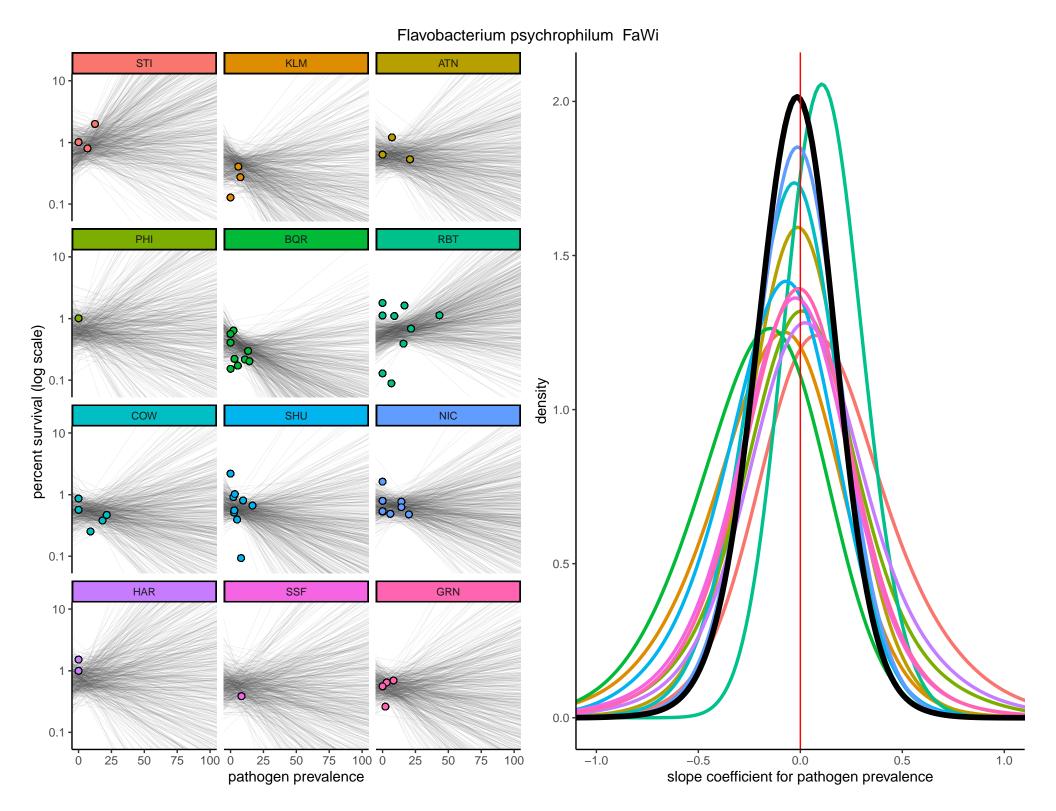


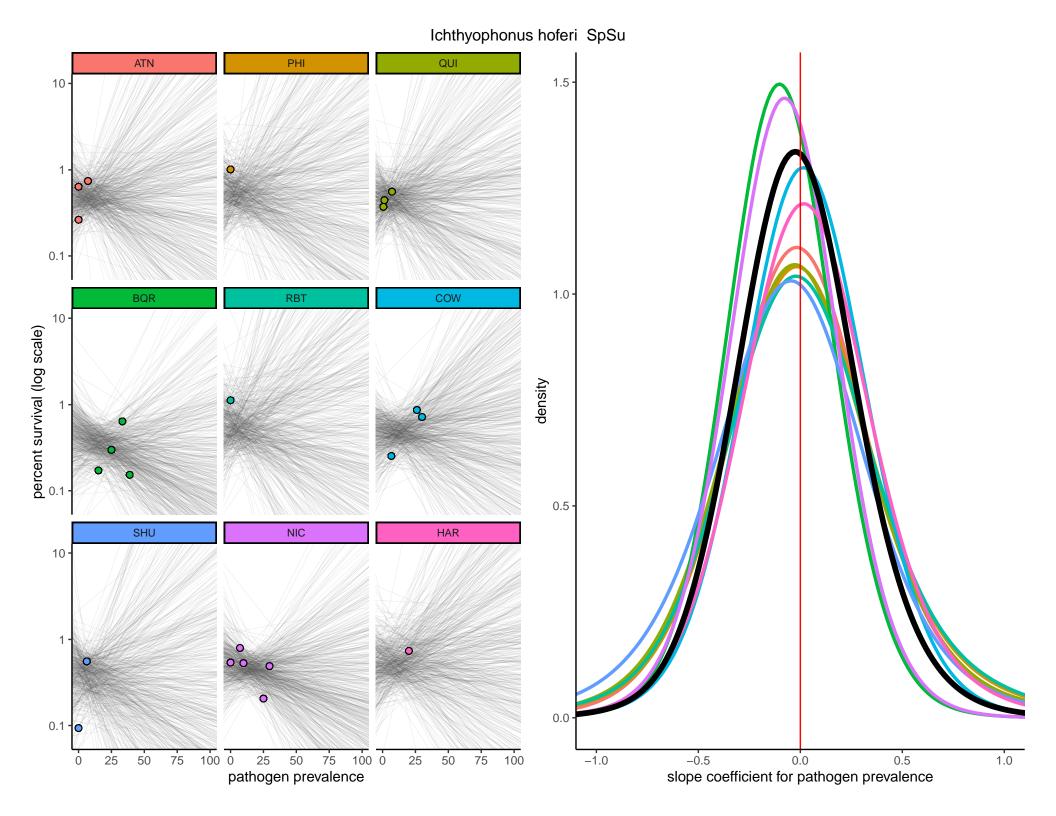


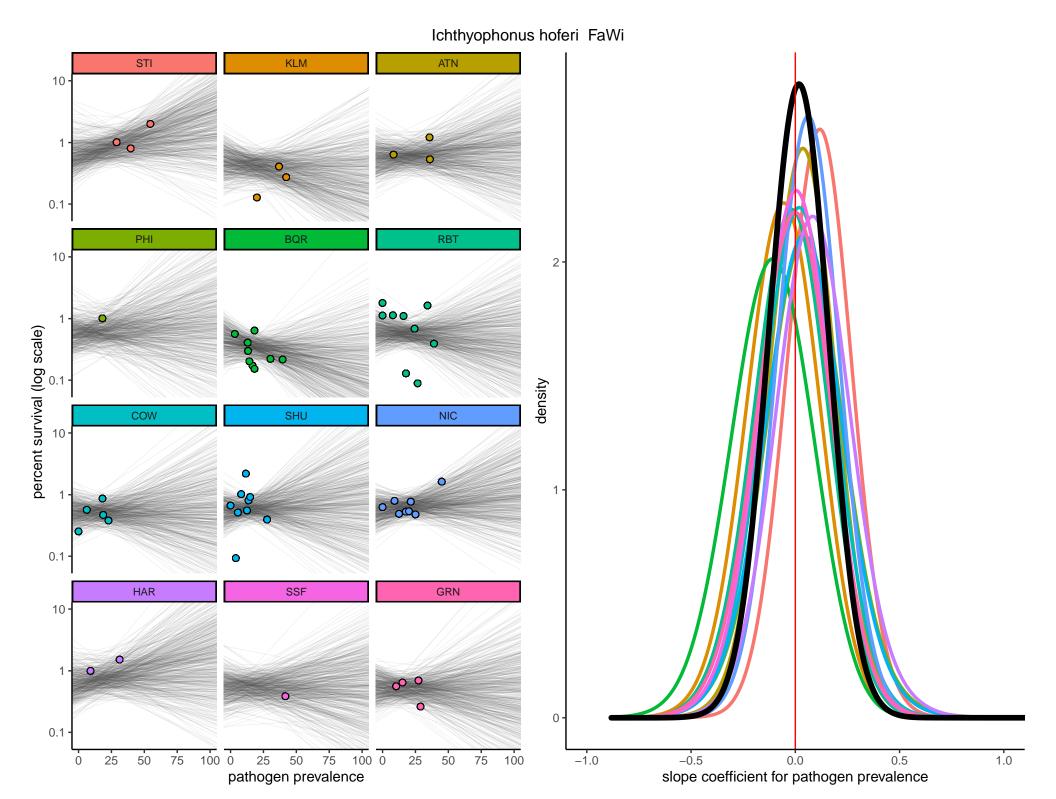


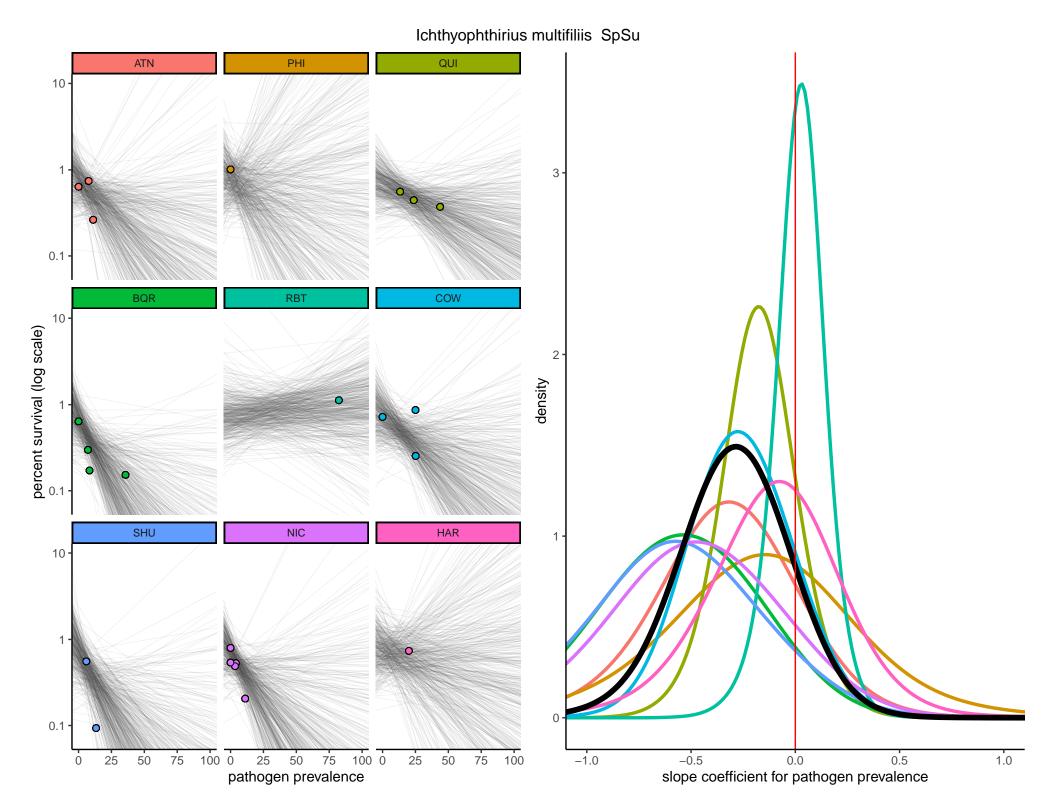


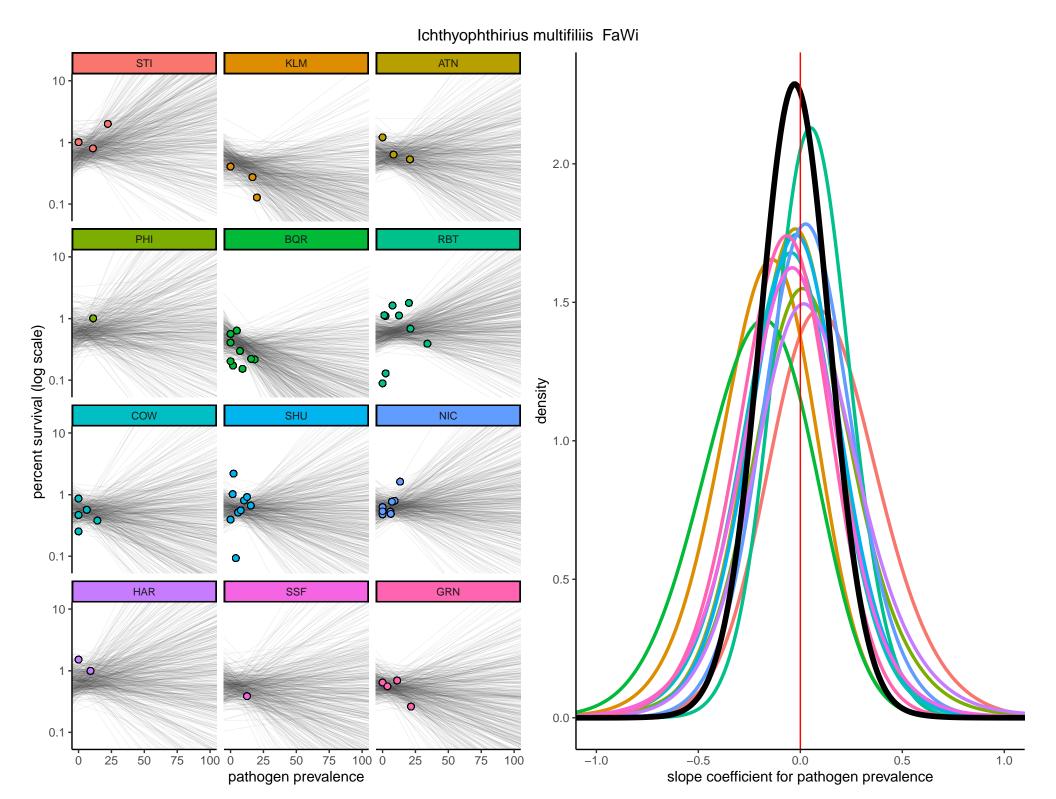


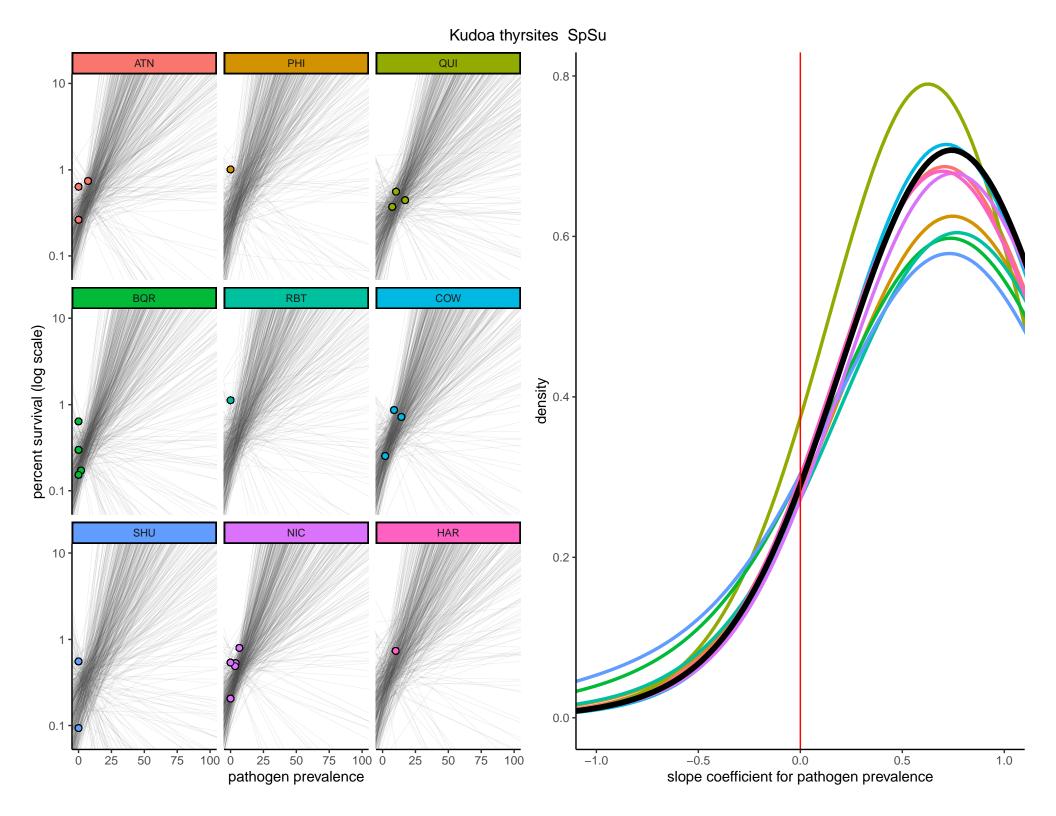


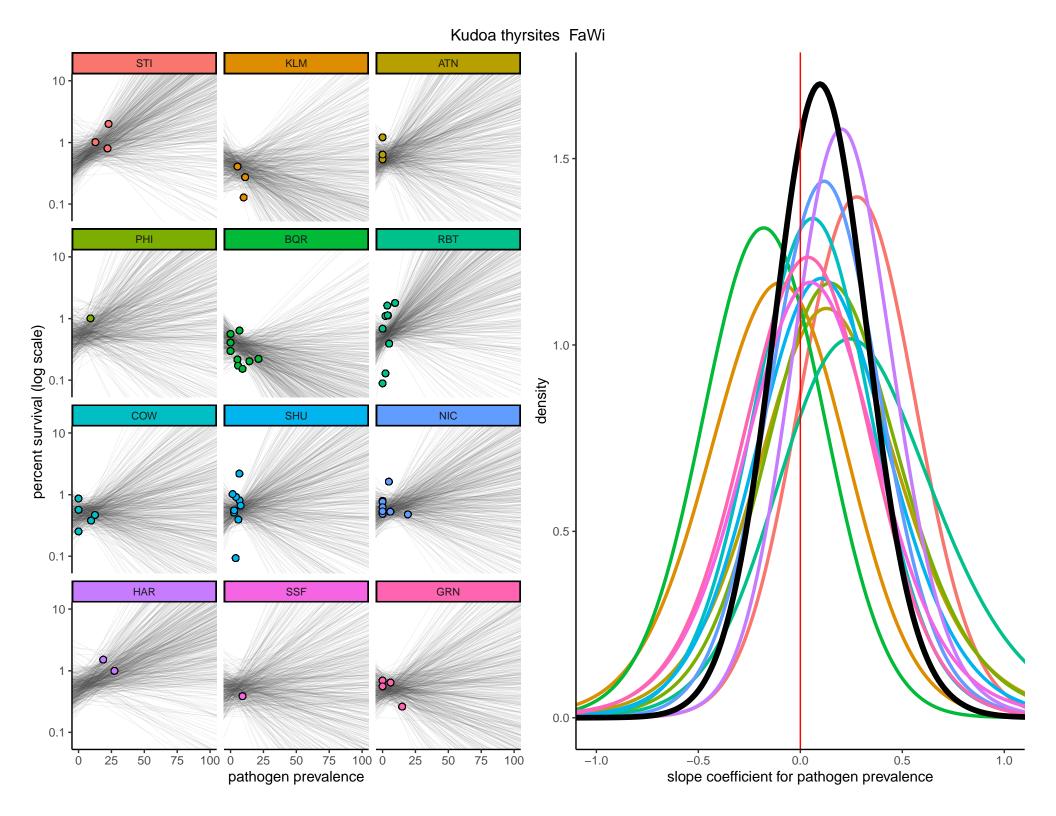


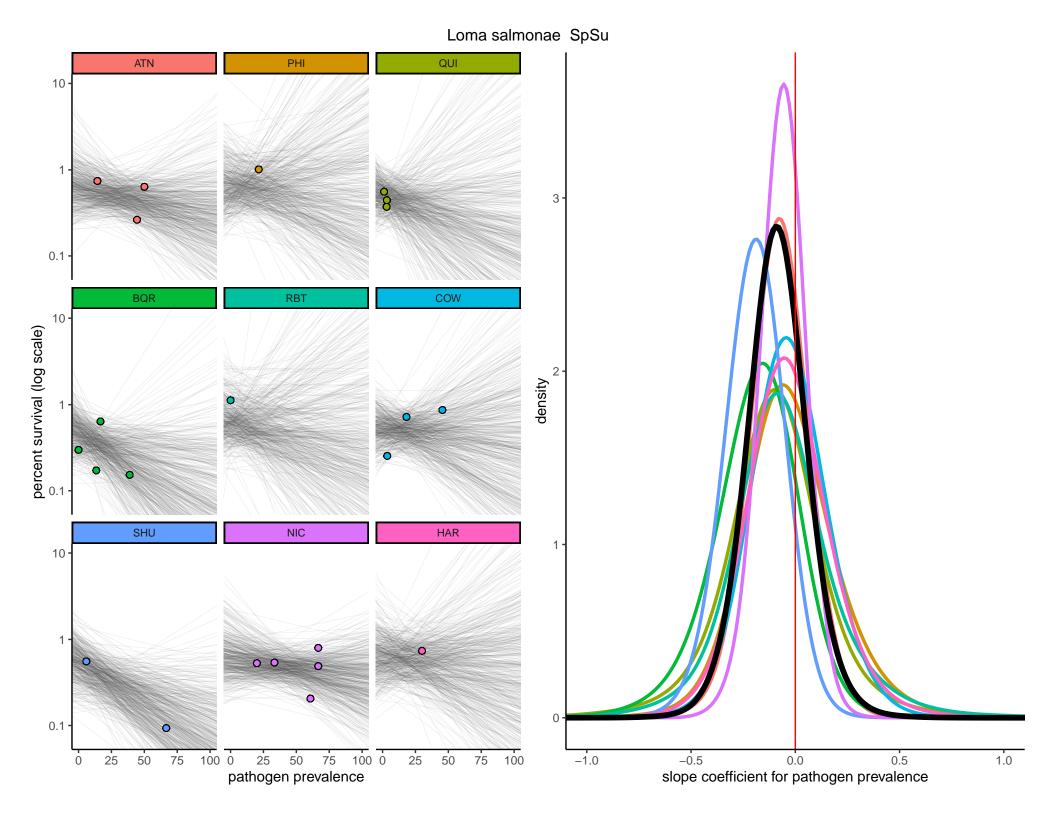


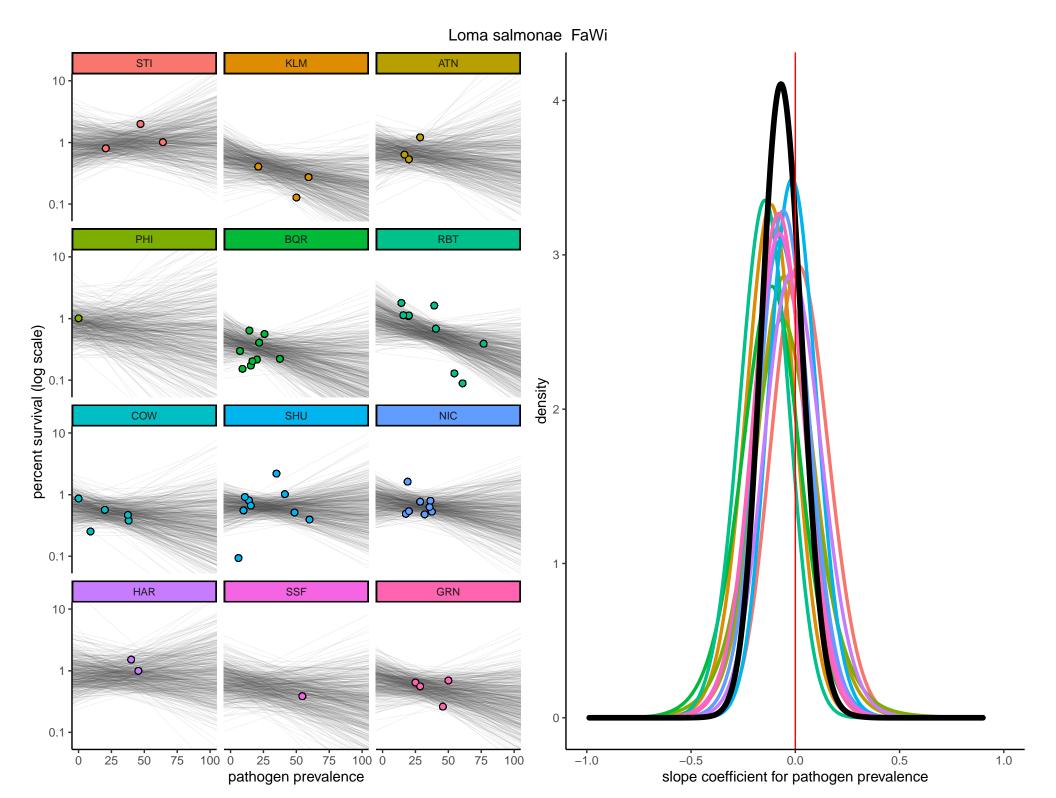


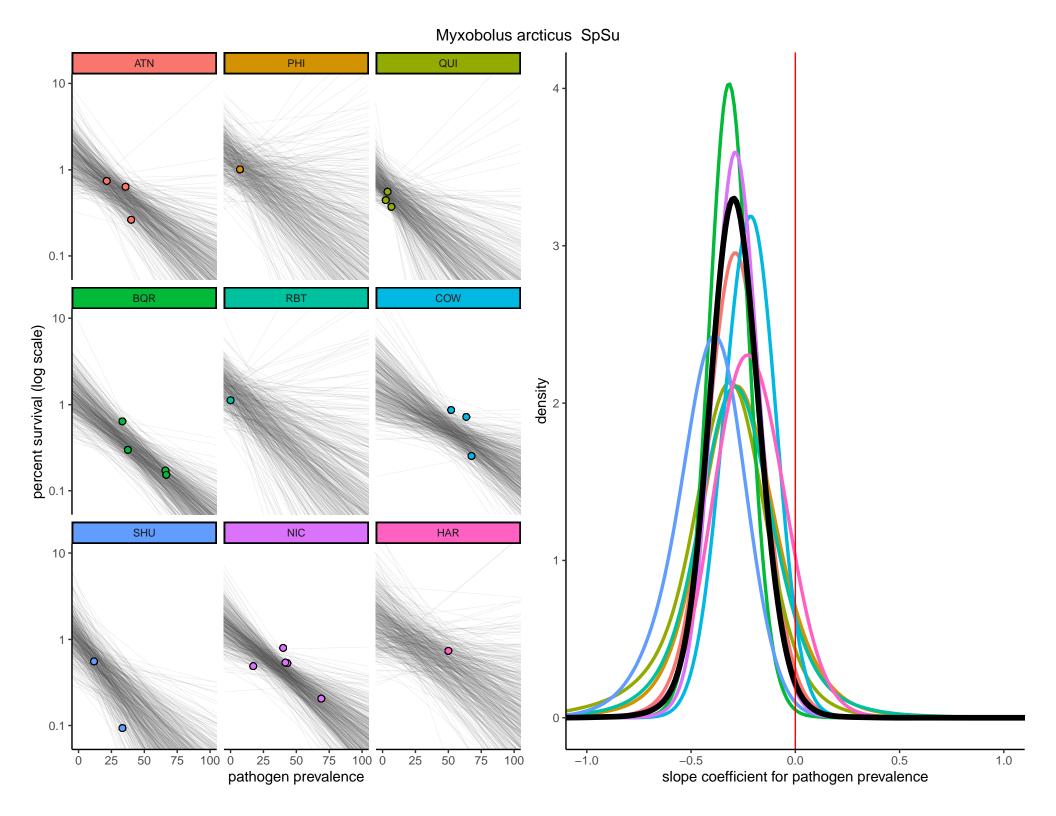


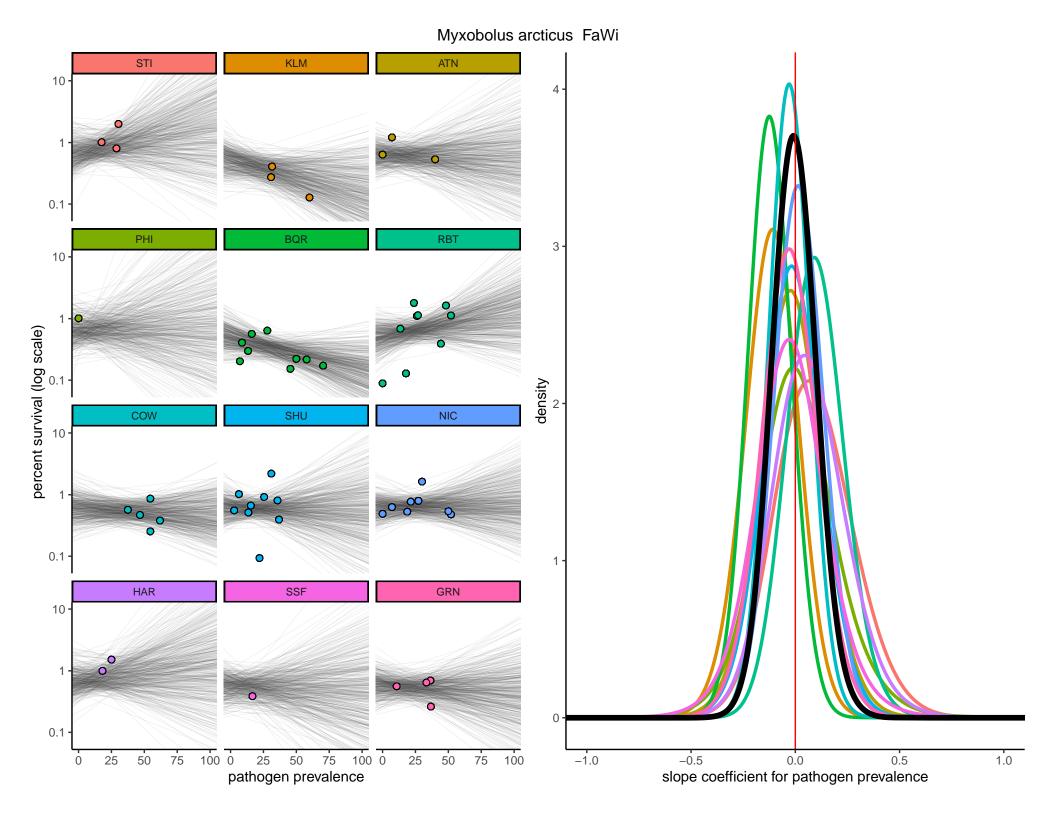


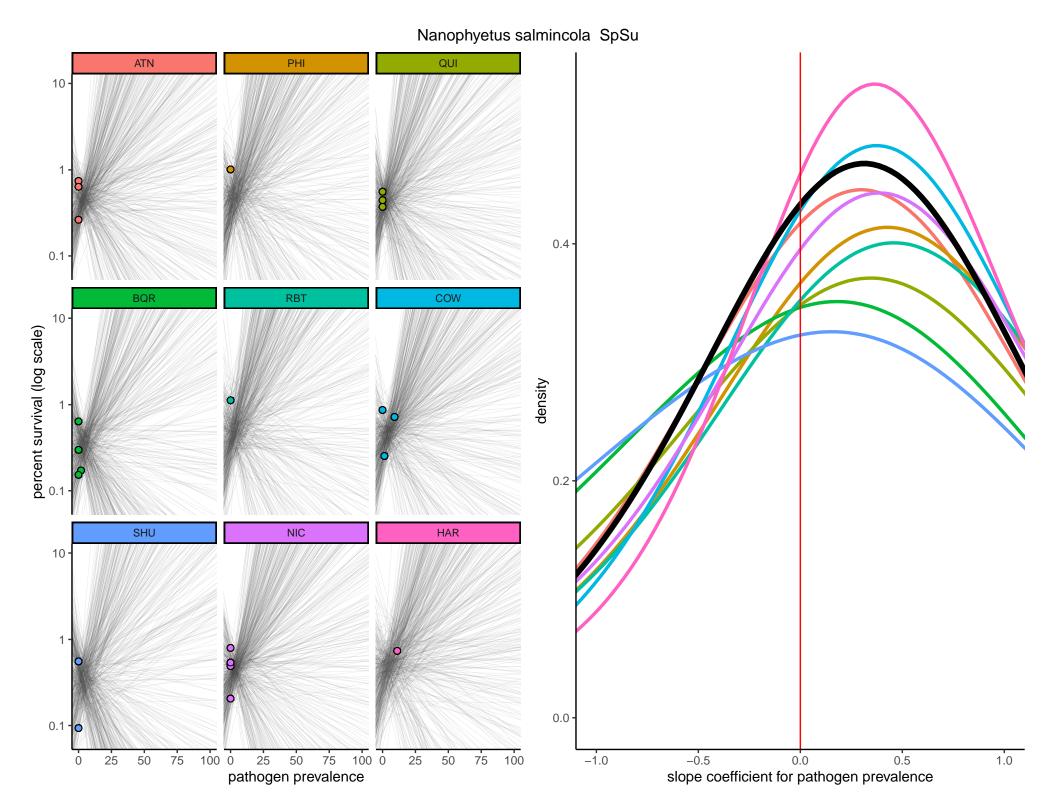




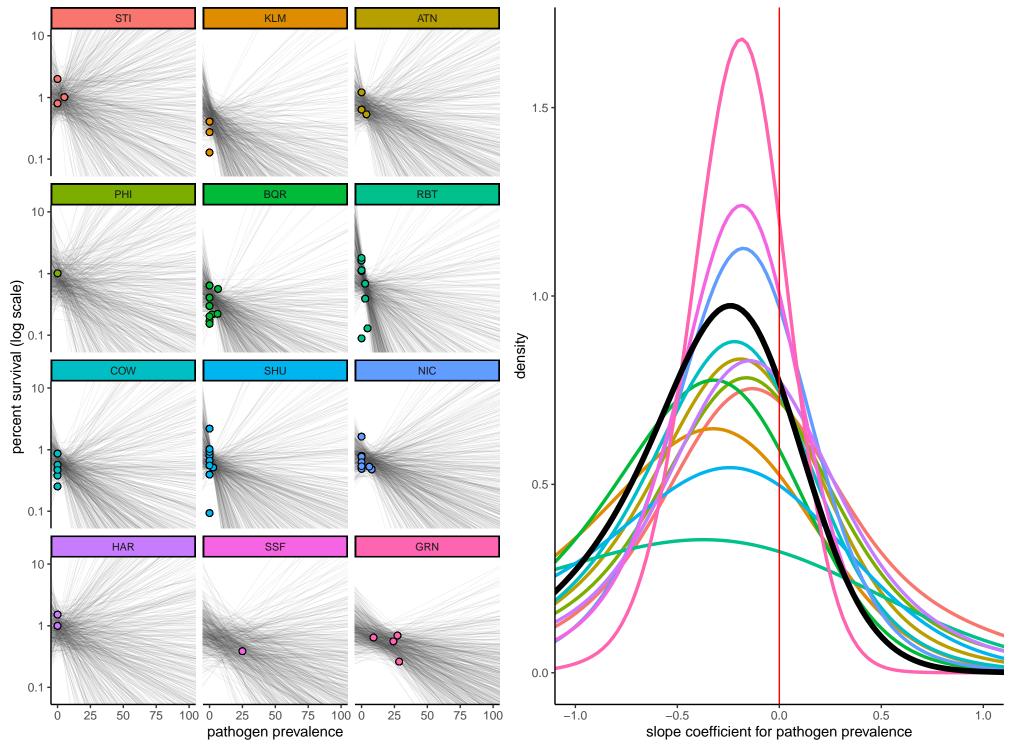


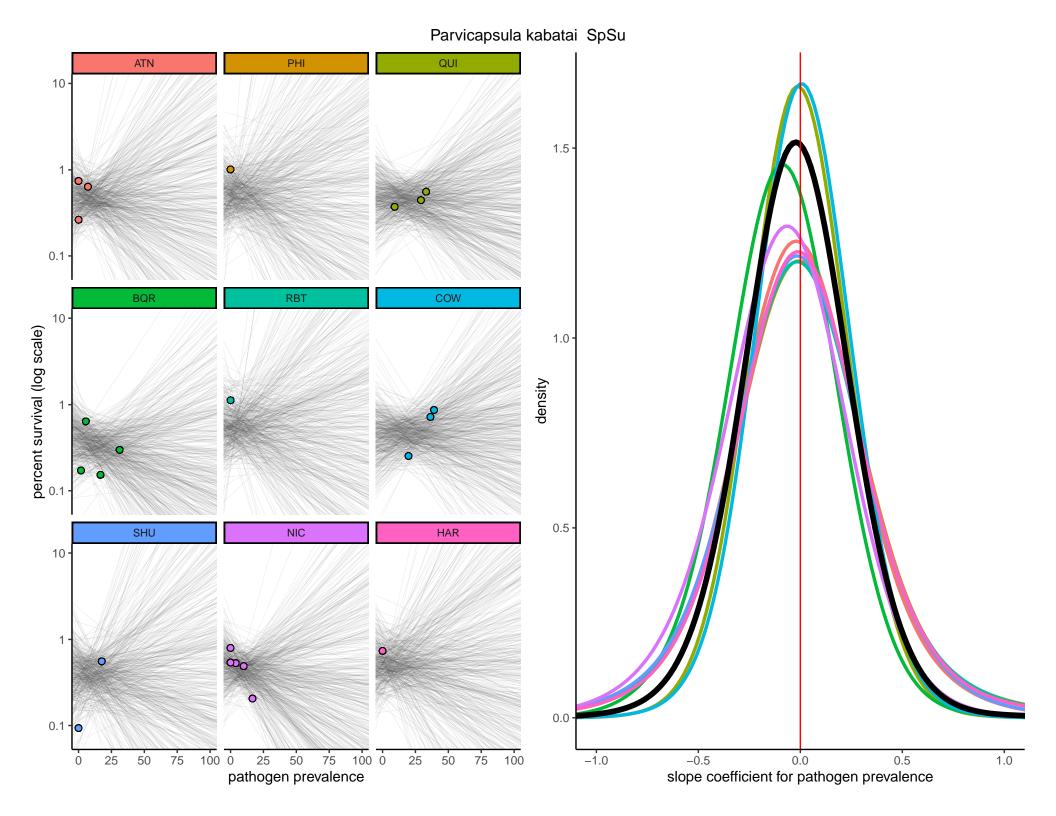


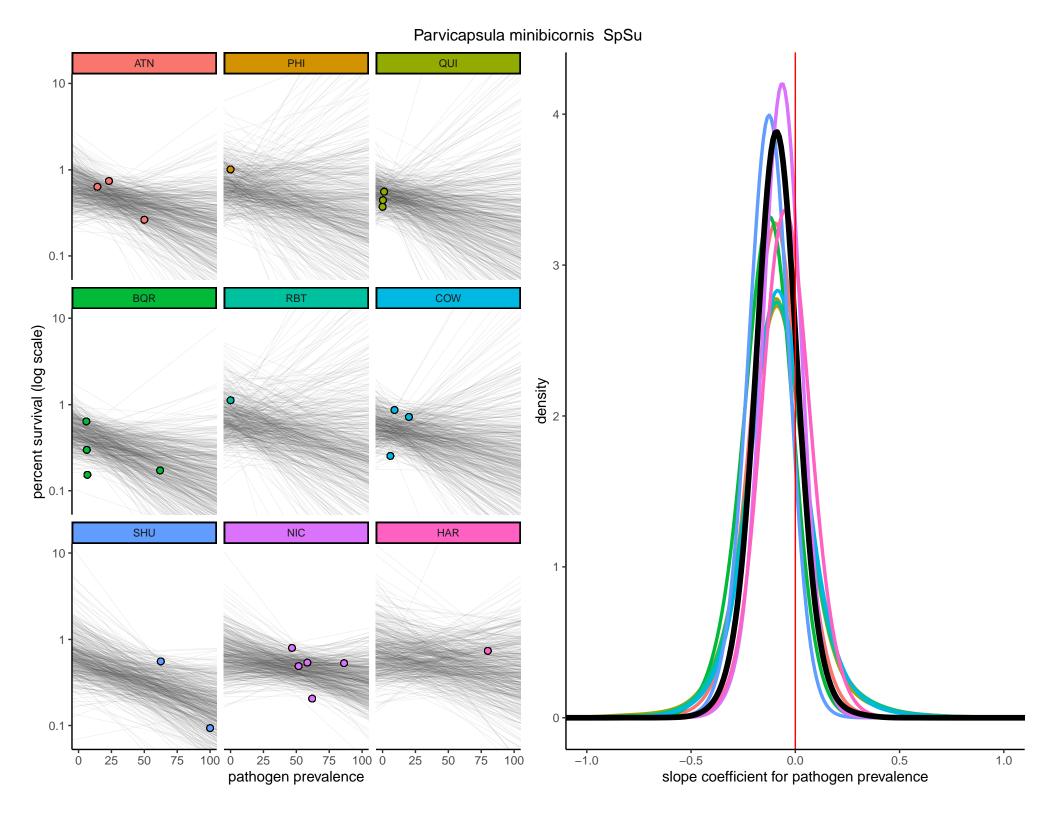


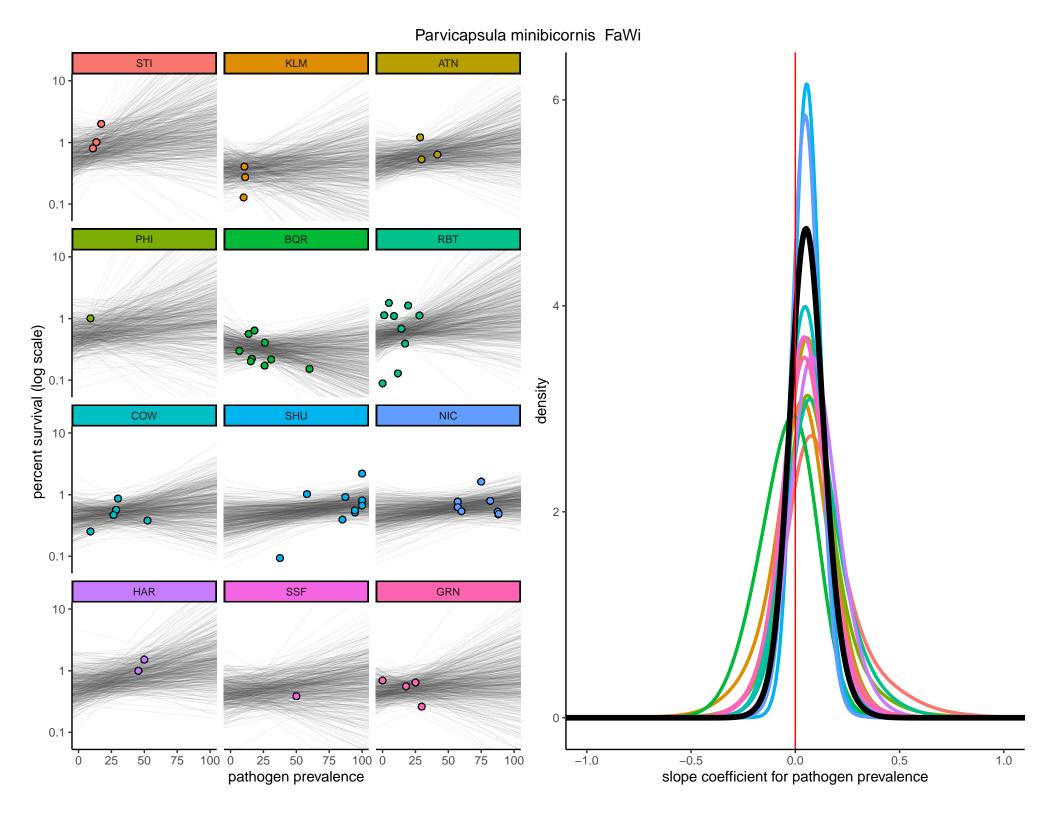


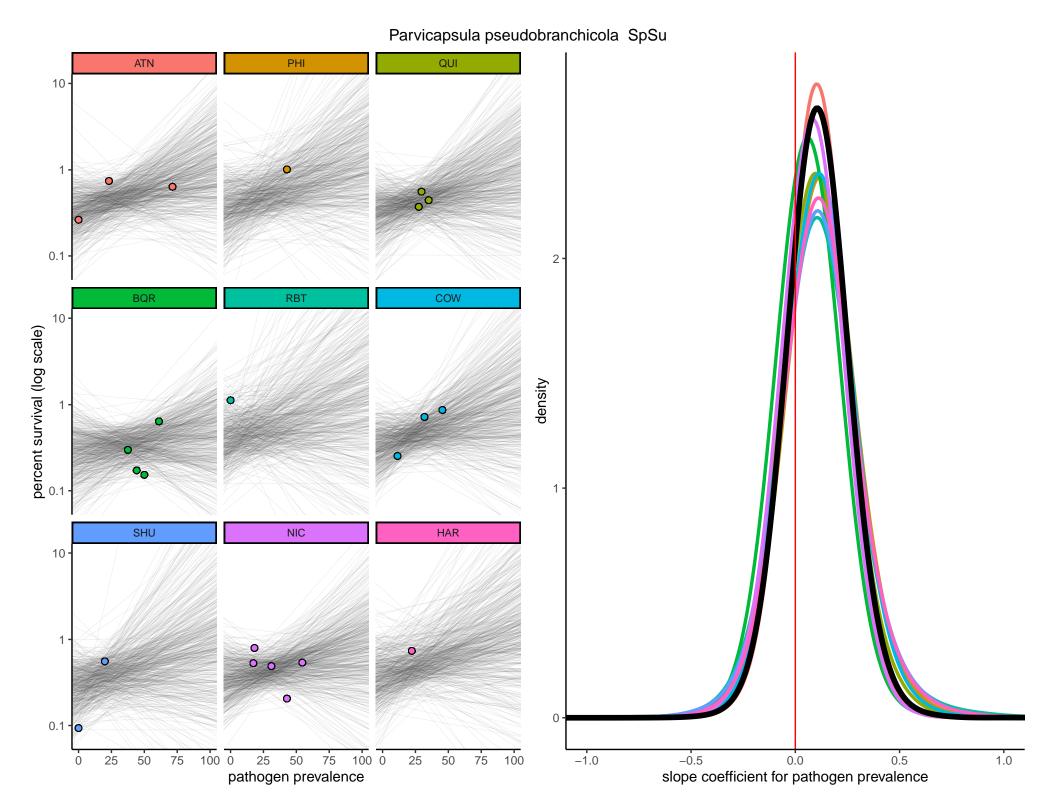
Nanophyetus salmincola FaWi

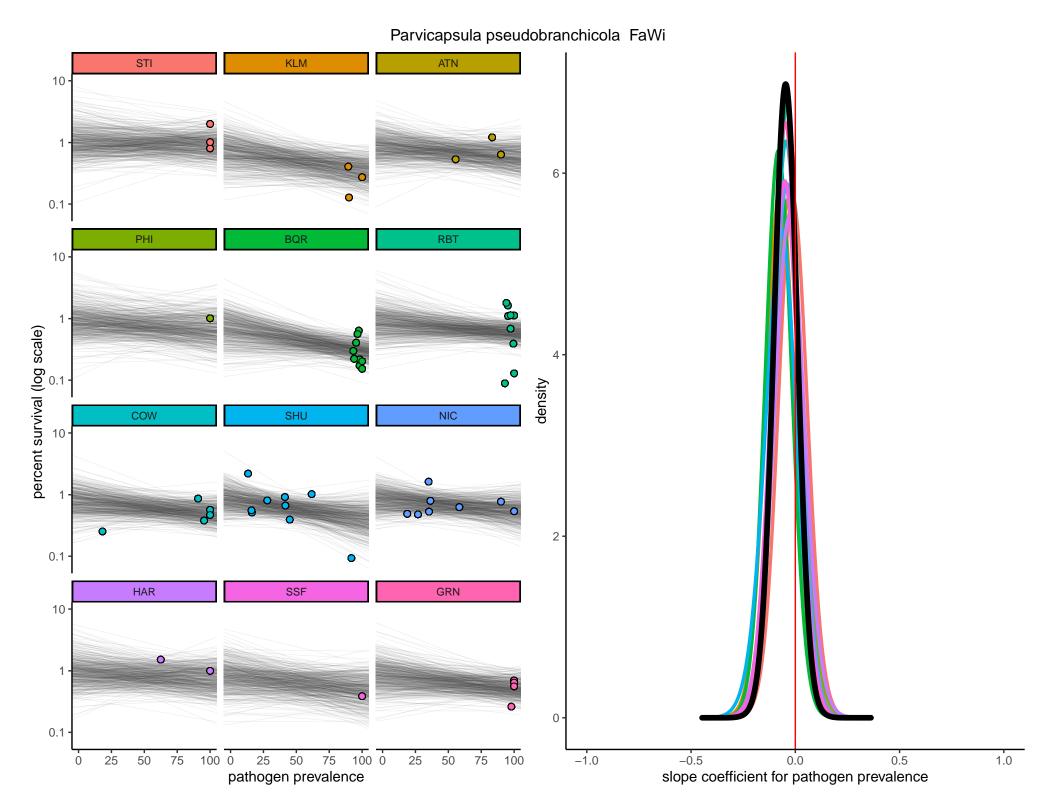


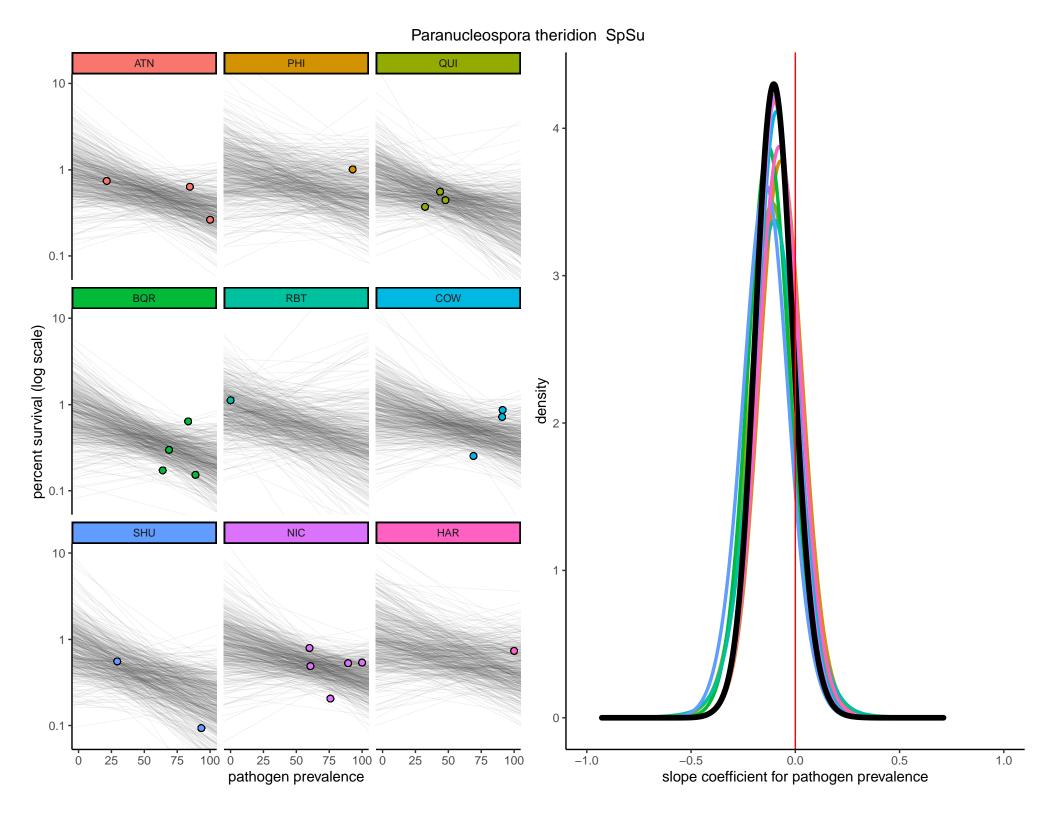


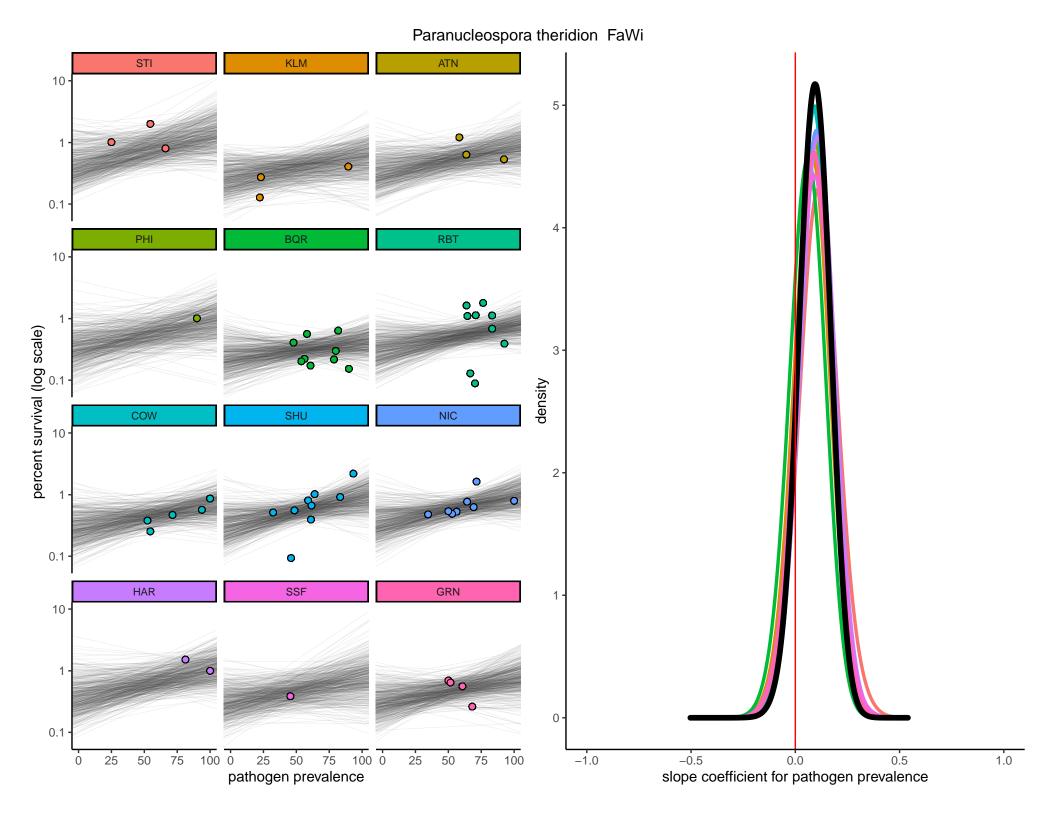


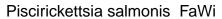


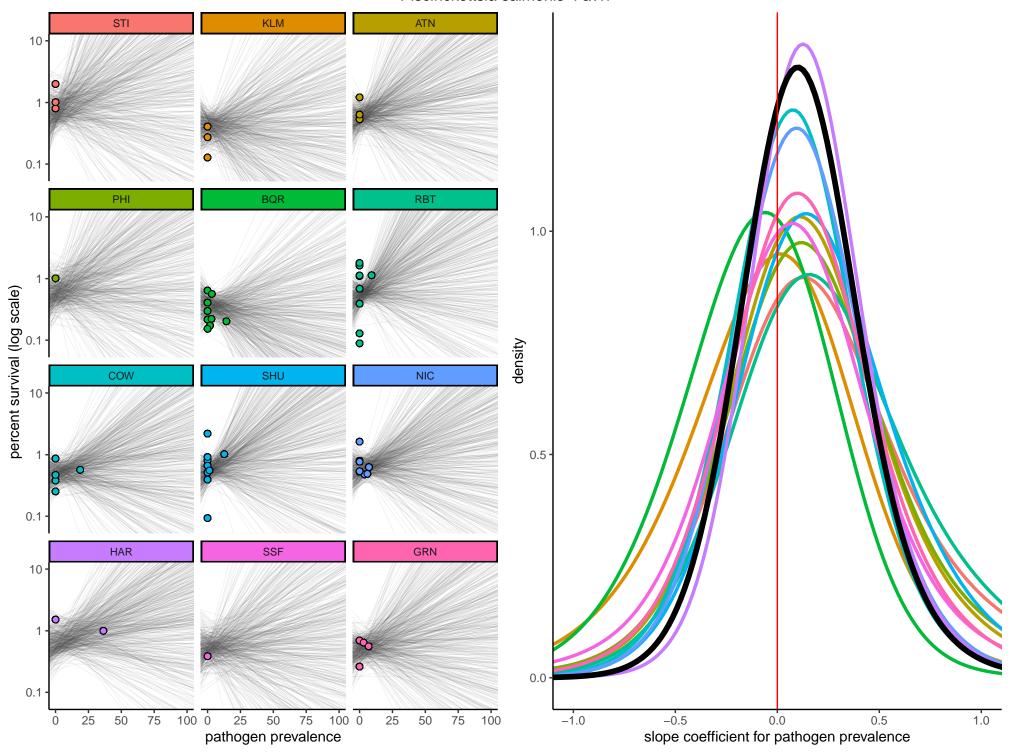


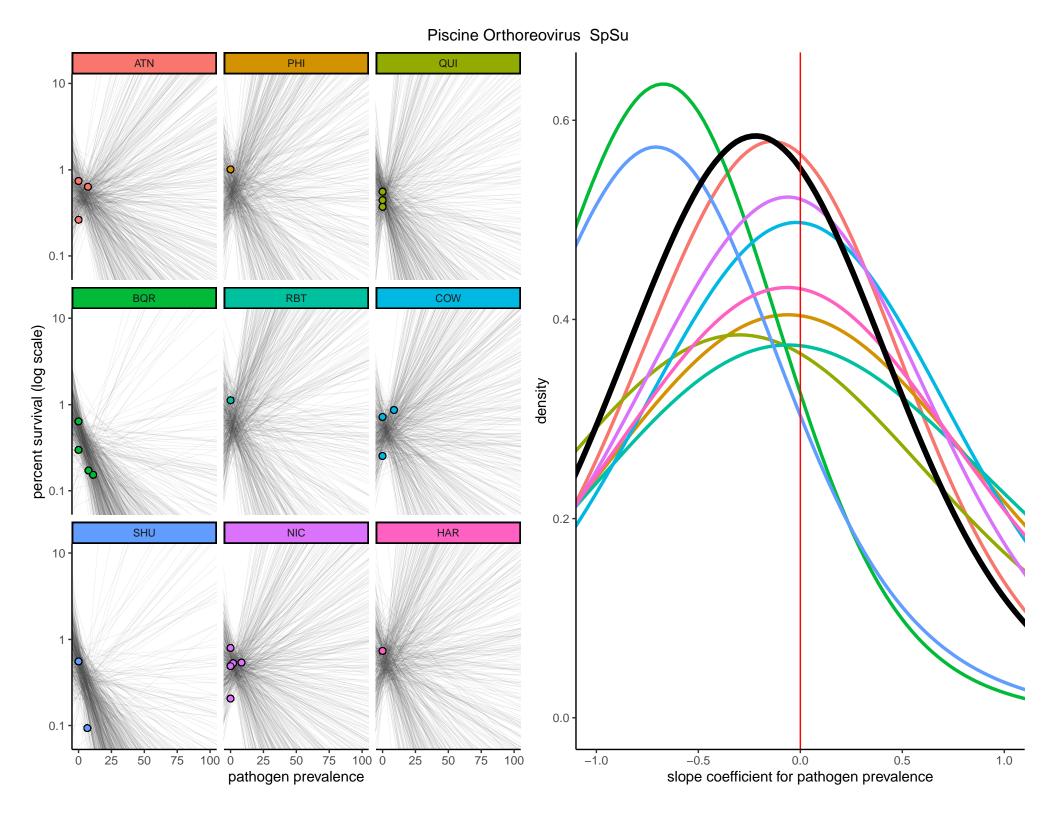


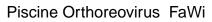


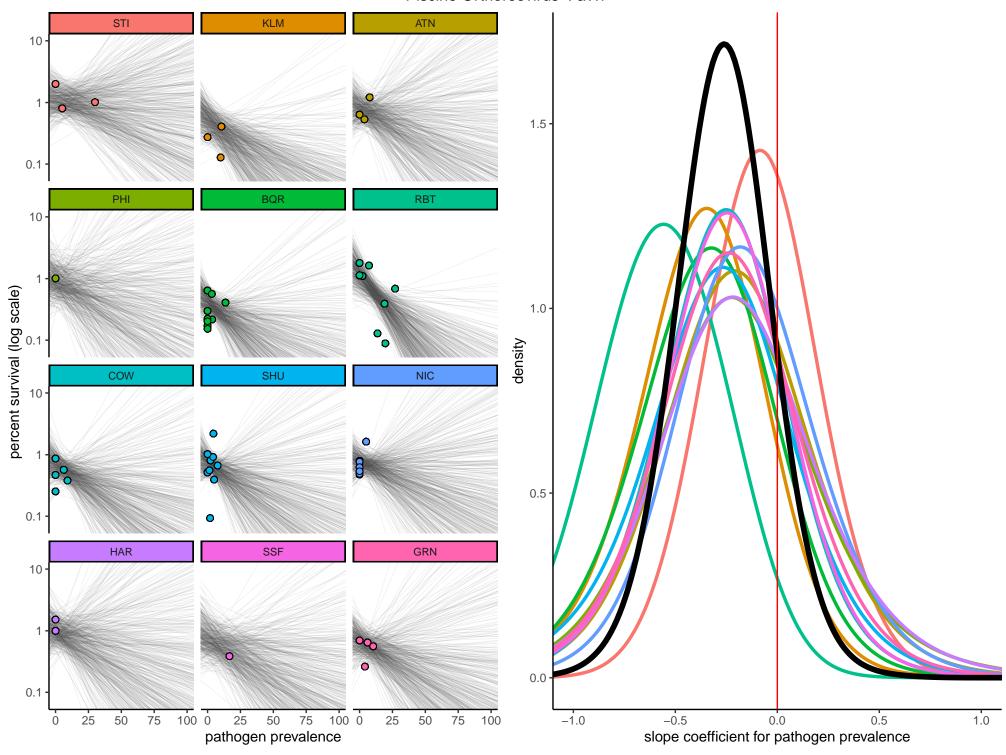


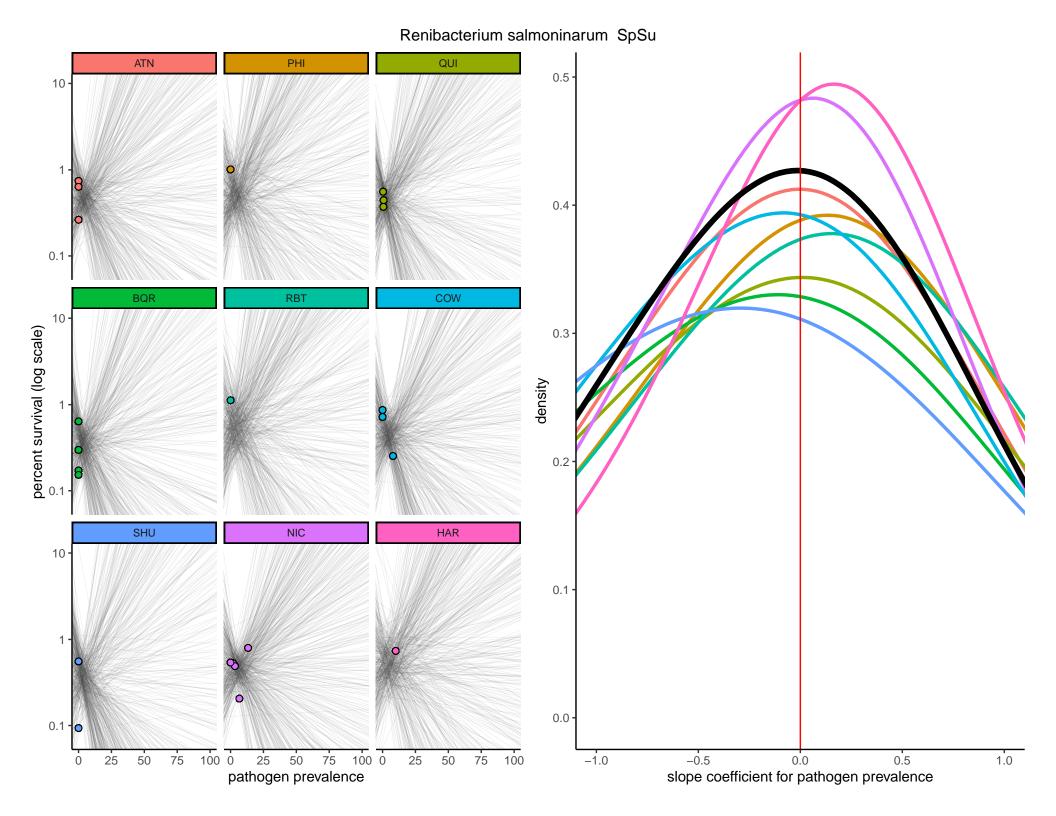


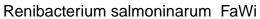


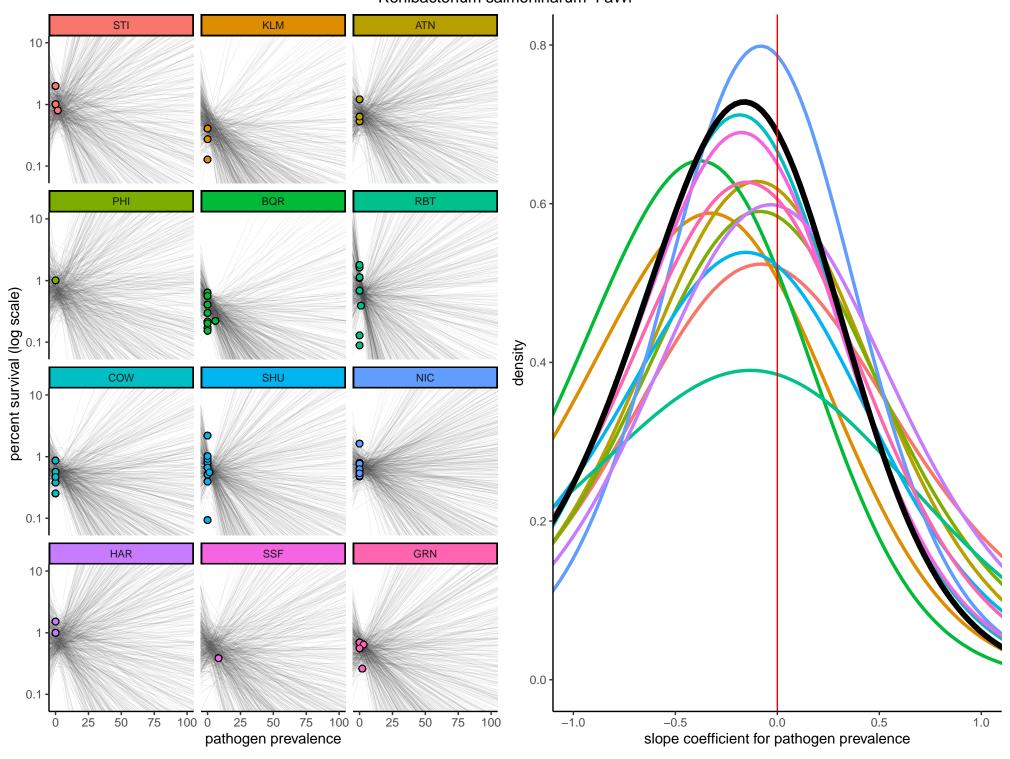


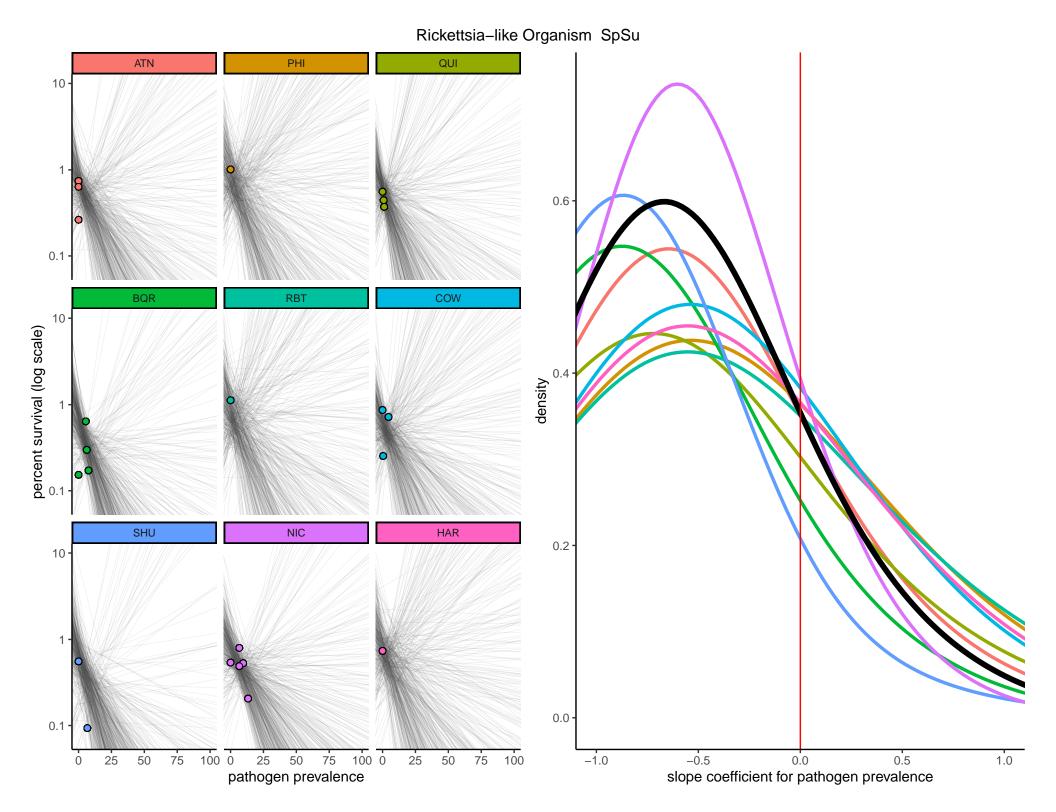


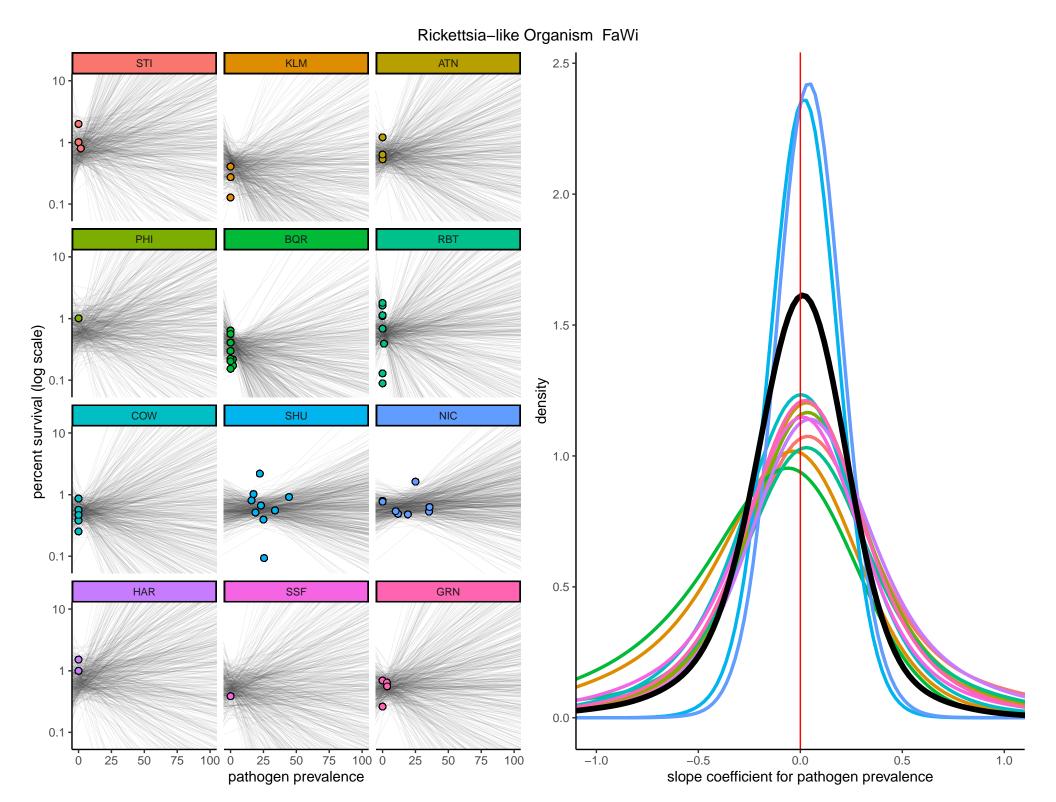


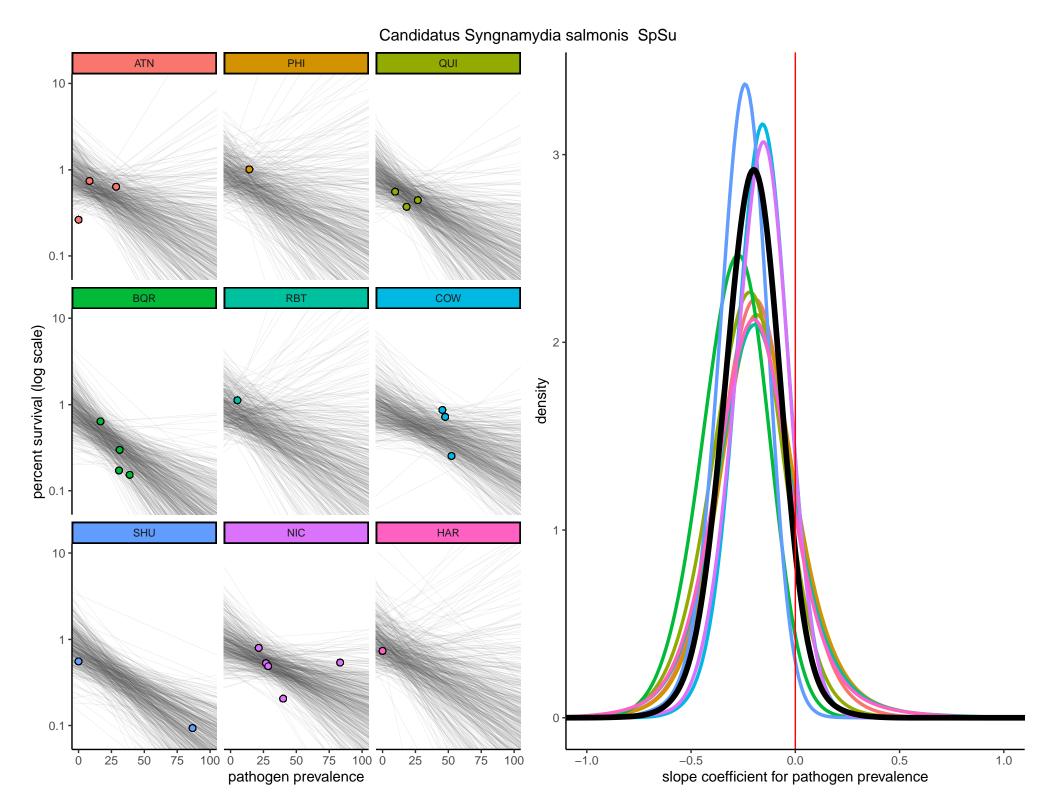


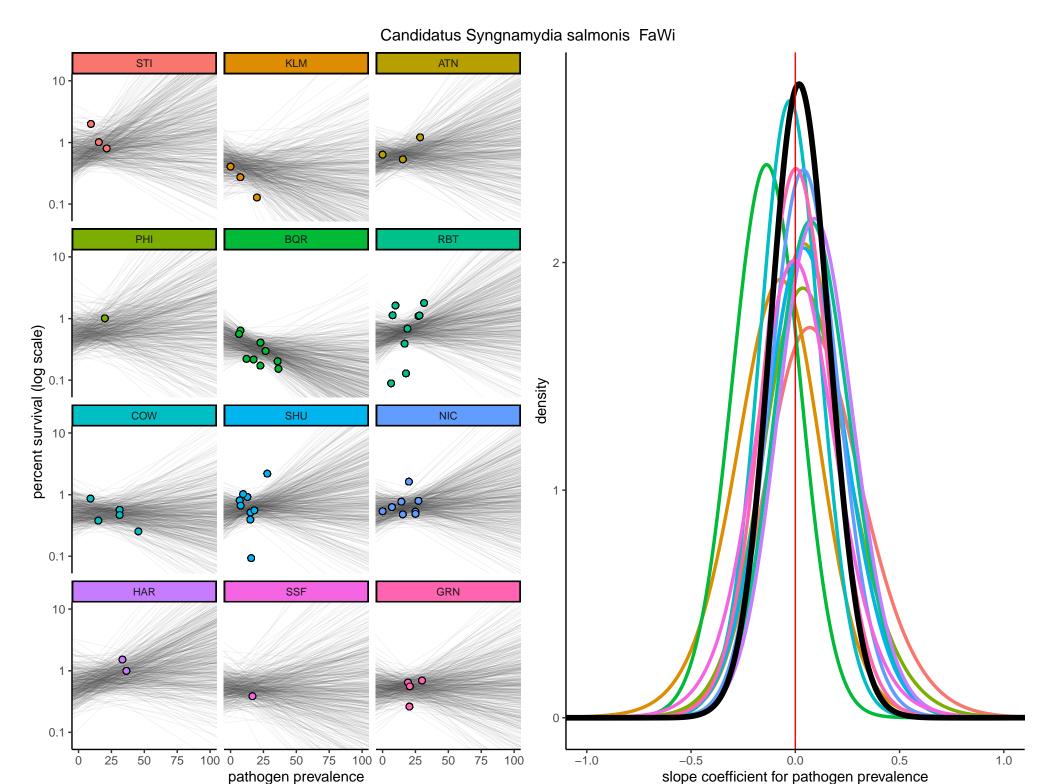


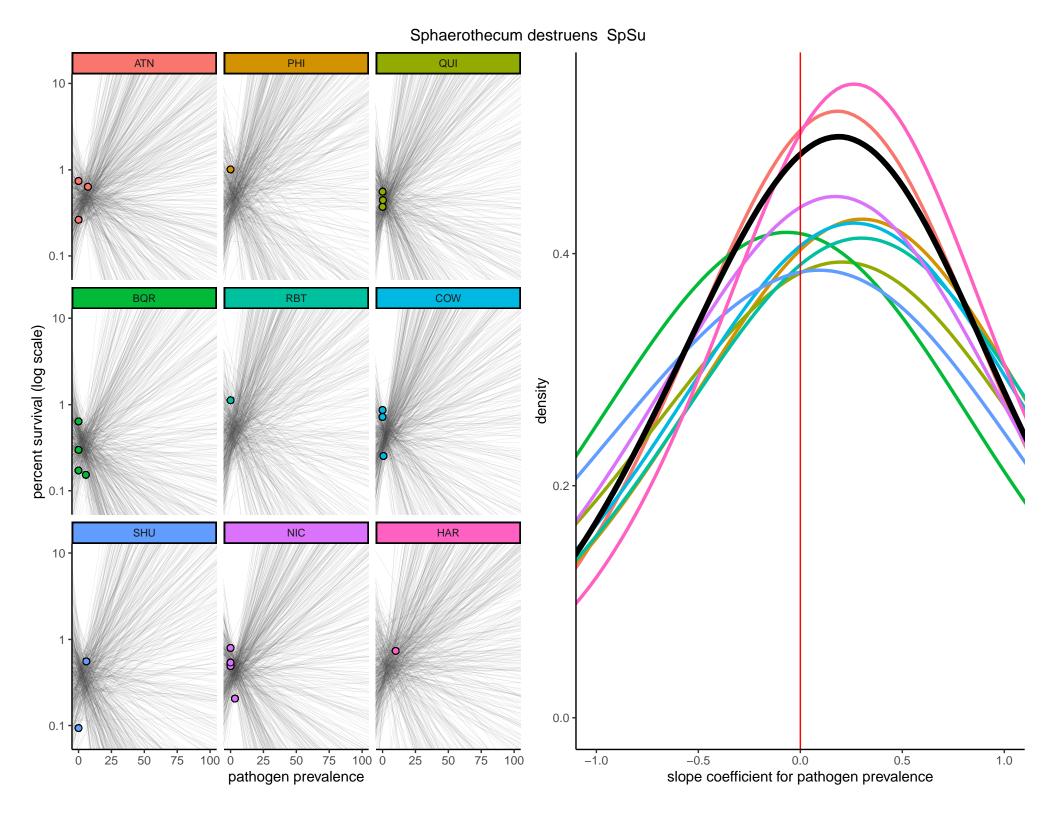


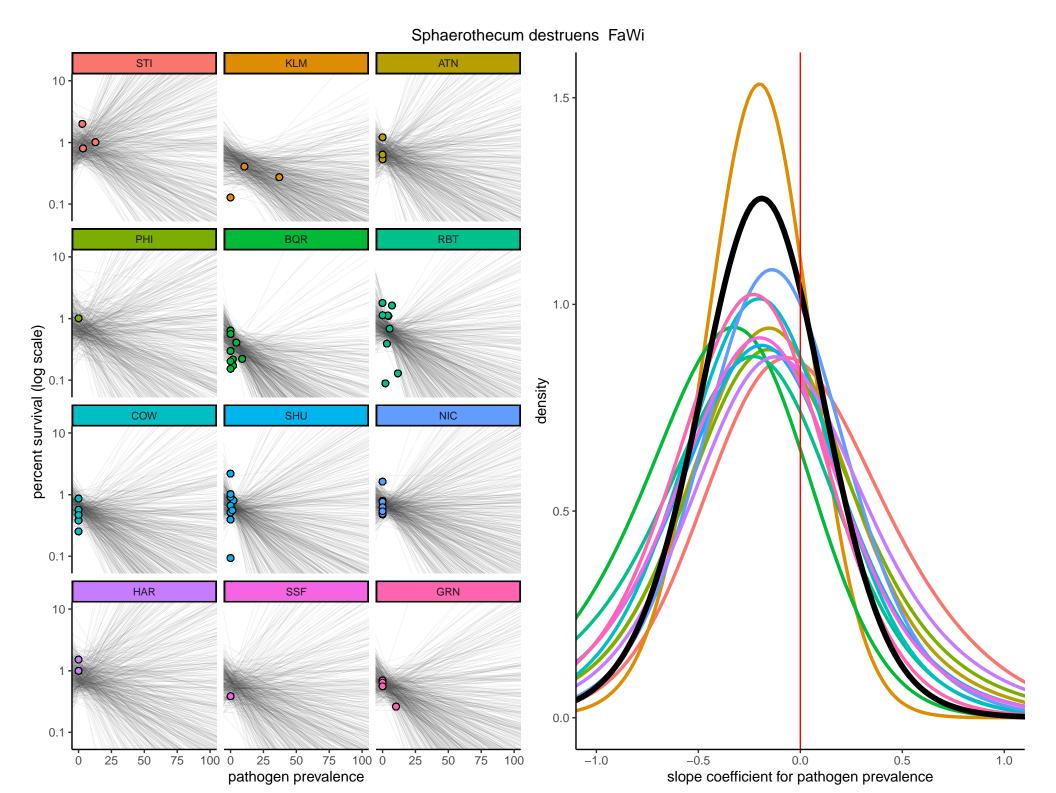


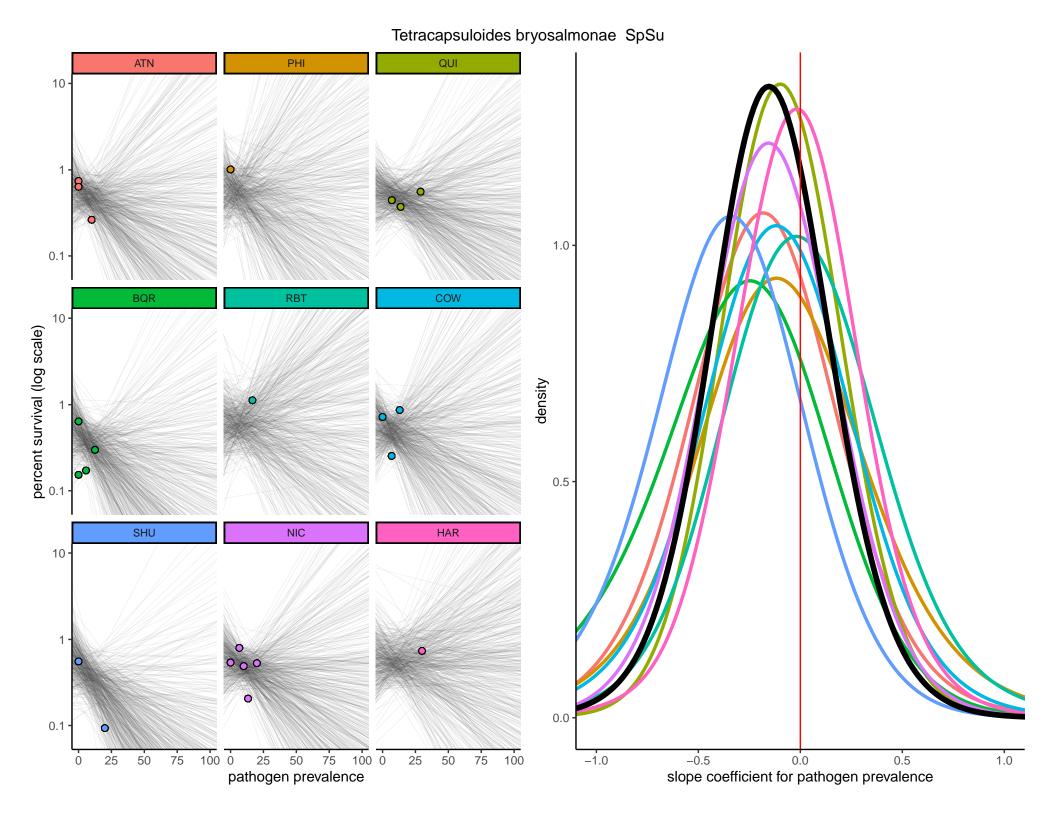


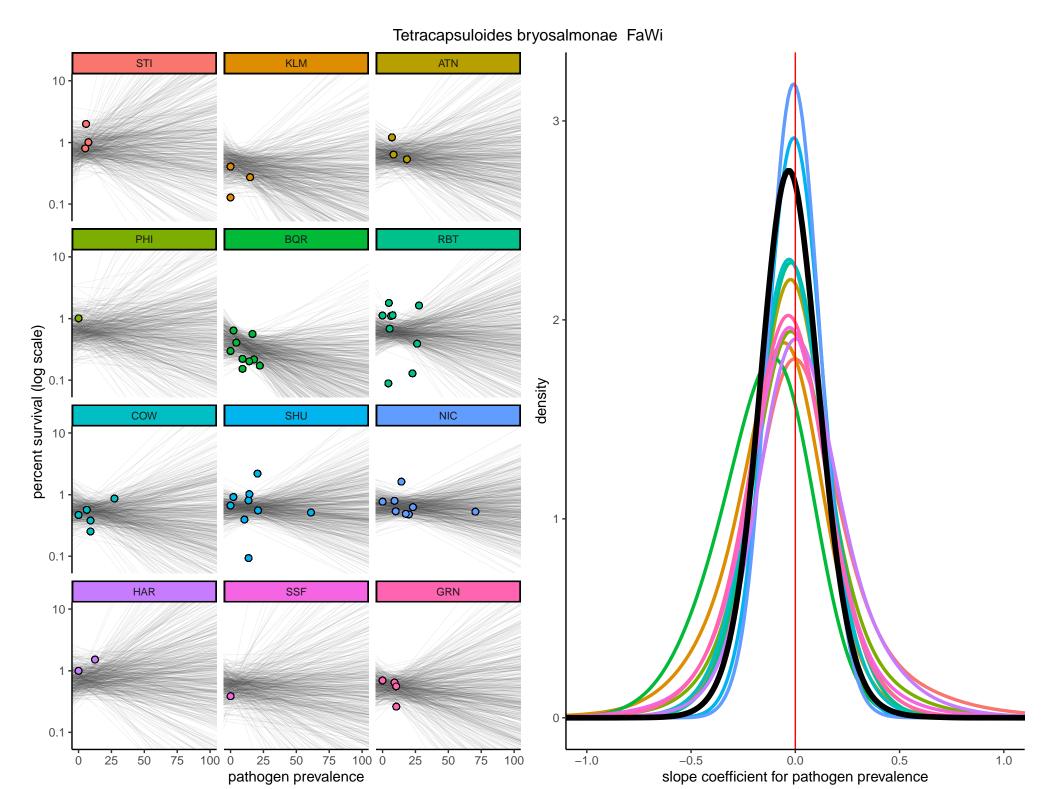


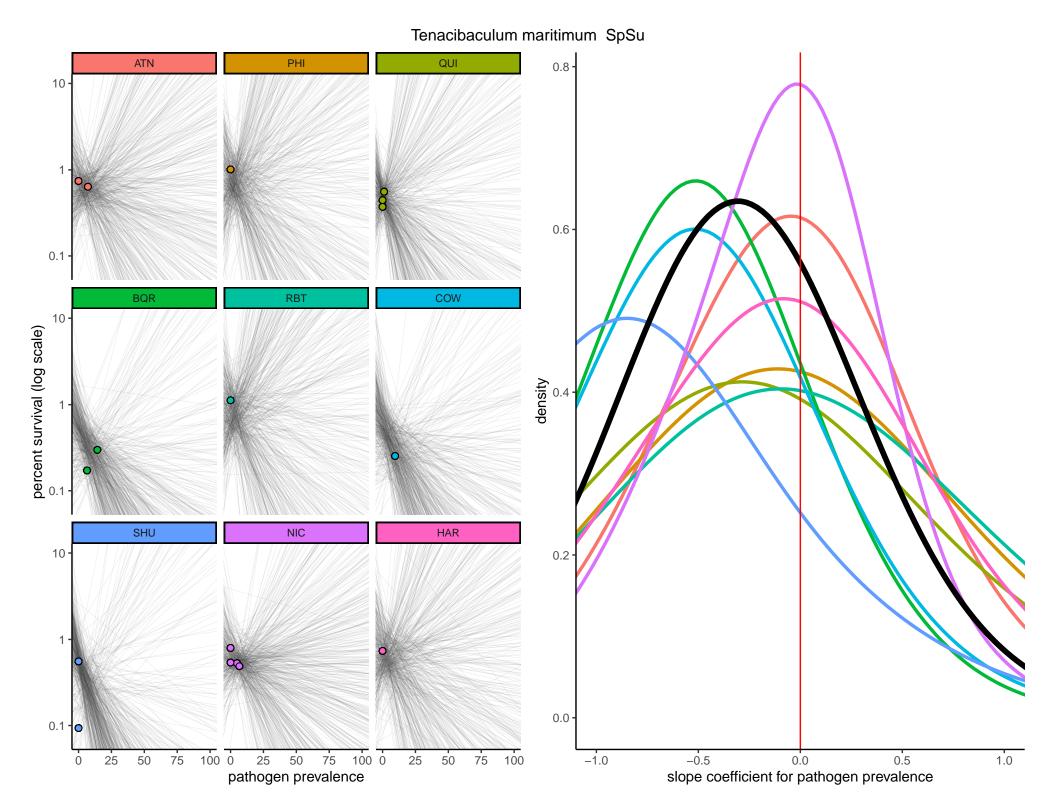


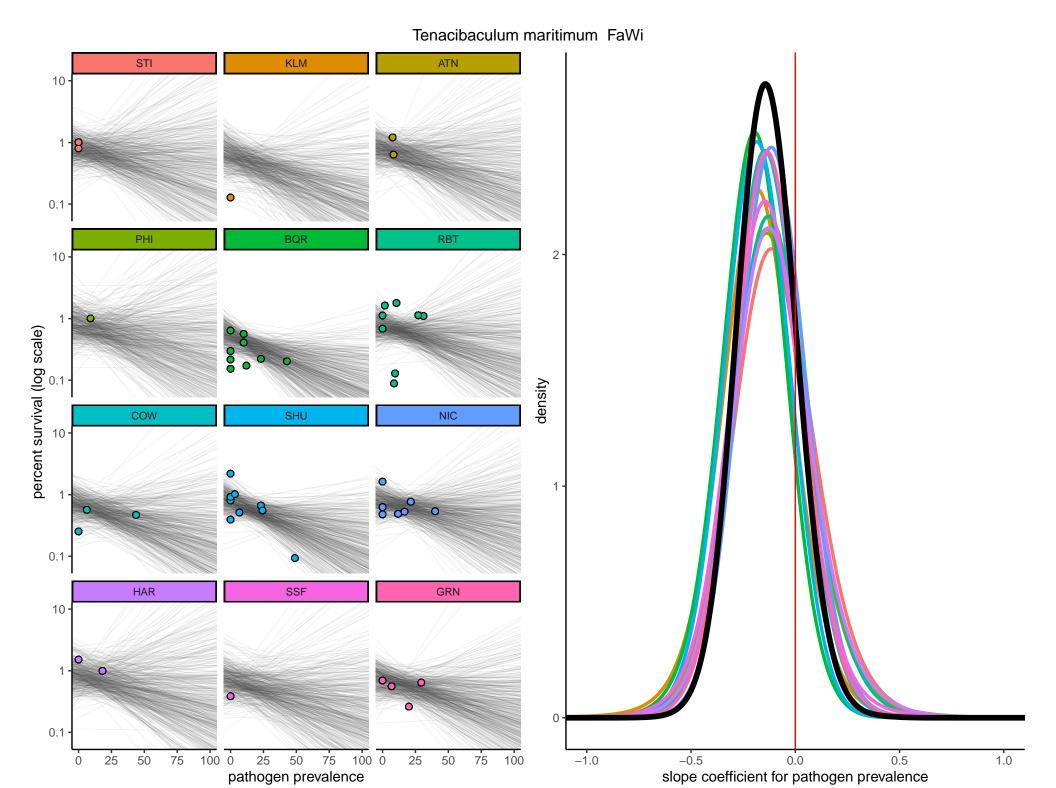


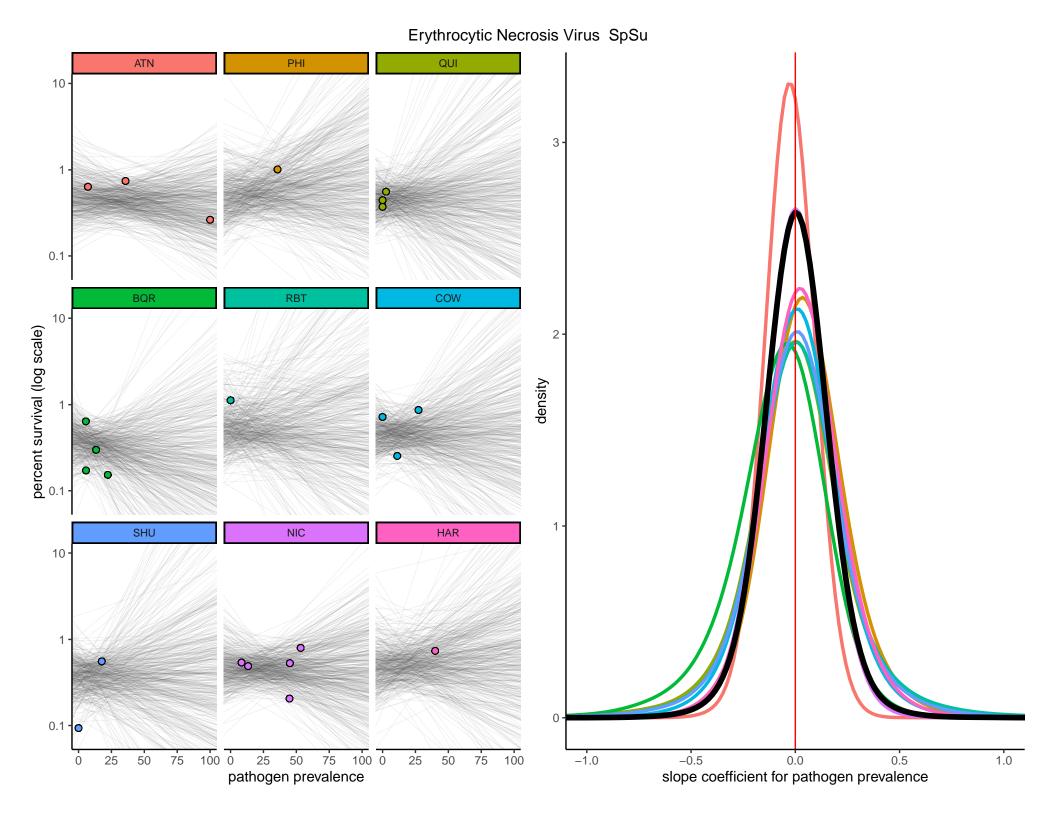


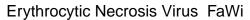


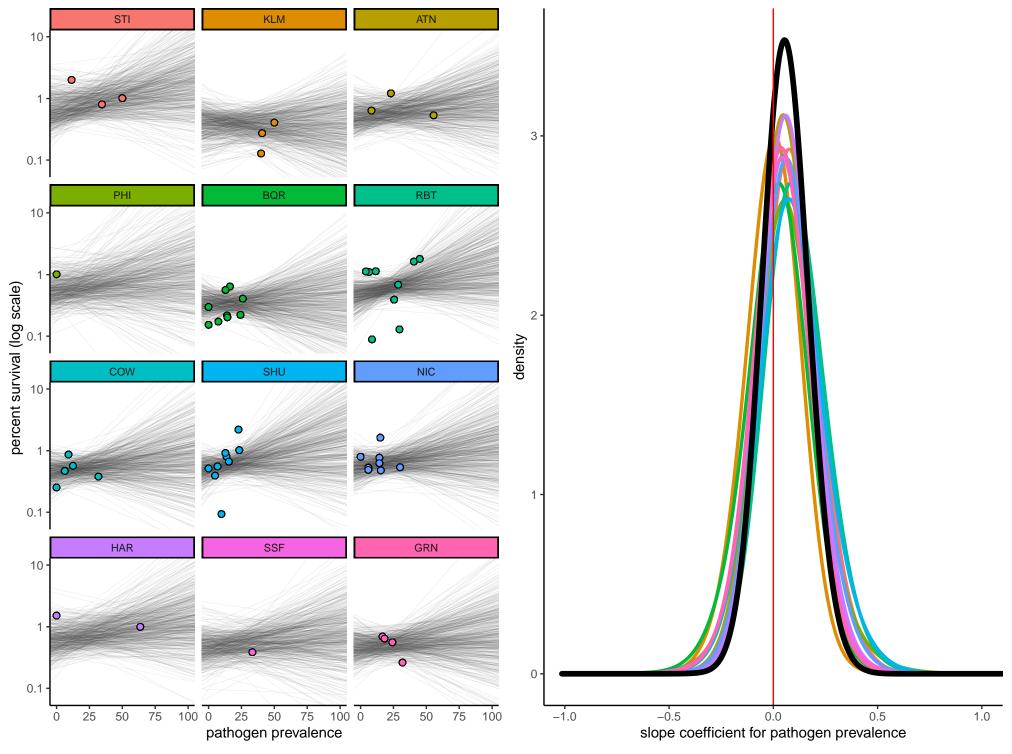












Total number of pathogen taxa SpSu PHI ATN QUI 2.5 10 -2.0 0.1 BQR COW RBT percent survival (log scale) 1.5 density 1.0 SHU NIC HAR 10 0.5 -0.1

-1.0

0

total number pathogen taxa

0.0

slope coefficient for total pathogen taxa

0.5

1.0

Total number of pathogen taxa FaWi KLM STI ATN 2.0 -10 1 0.1 1.5 PHI BQR RBT 10 percent survival (log scale) density of 1.0 COW SHU NIC 0.5 -0.1 HAR SSF GRN 10 0 0.0 0.1 -1.0 0.0 0.5 1.0 2 6 8 0 Ö 6 8

slope coefficient for total pathogen taxa

total number pathogen taxa

