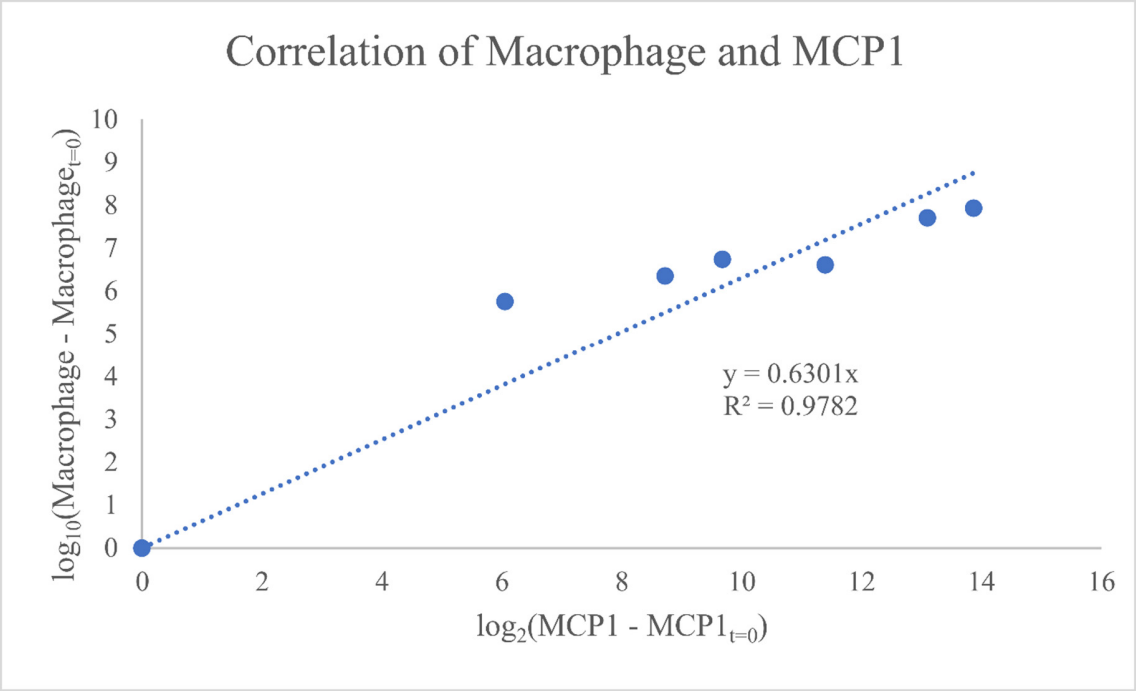


Figure S1. Macrophage and MCP1 correlation. Log_{10} of macrophage cell count in the lung is highly correlated with the log_2 of MCP1 gene expression. This regression is used to translate between MCP1 and Macrophage states.

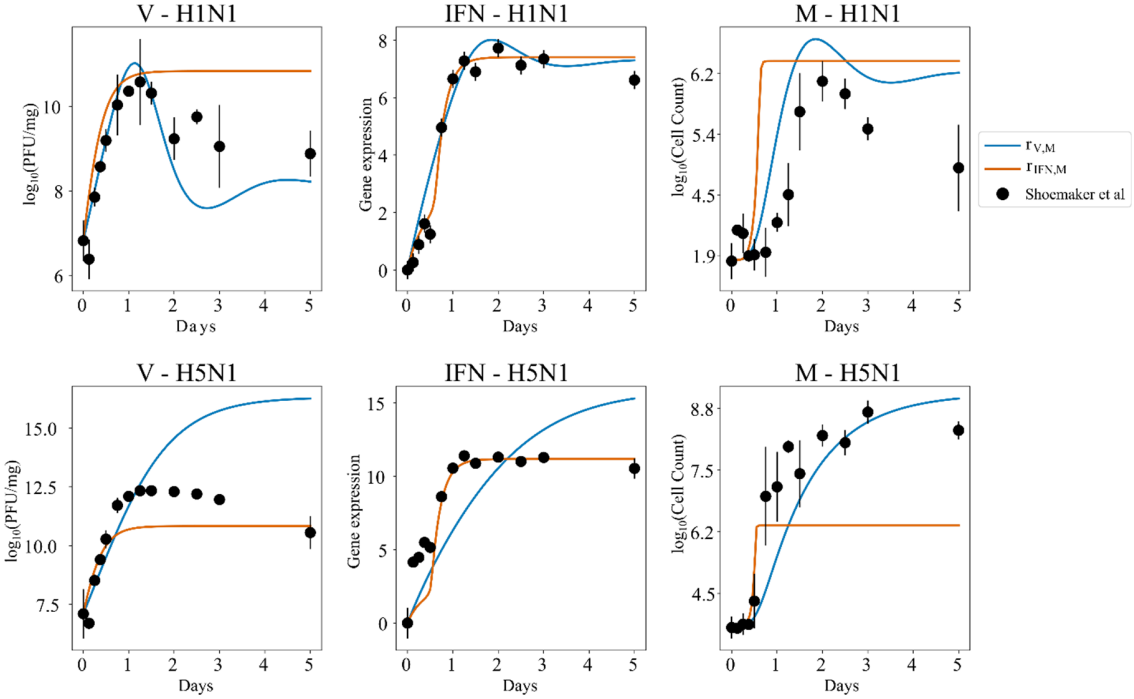


Figure S2. Models 2 and 3 predictions**.** Macrophage-dependent feedback mechanisms (Models 2 and 3 NSSD) exhibit worse fits than a model structure without these mechanisms (Model 4). Macrophage-based clearance of Virus ($r_{V,M}$, blue line) fits

H5N1 data poorly. Data from Shoemaker et al [1] are shown with the standard error associated with triplicate data points per timepoint.

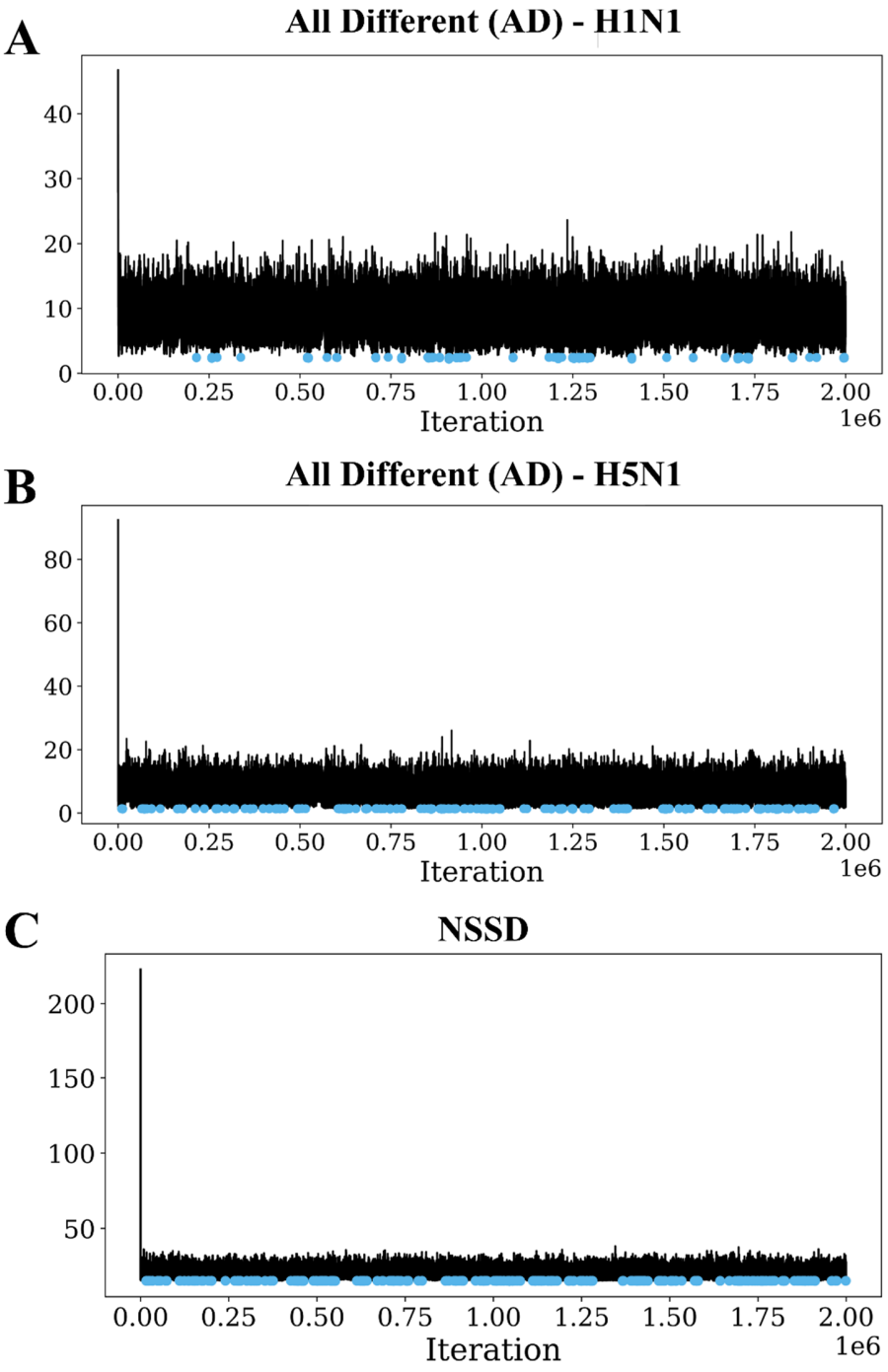
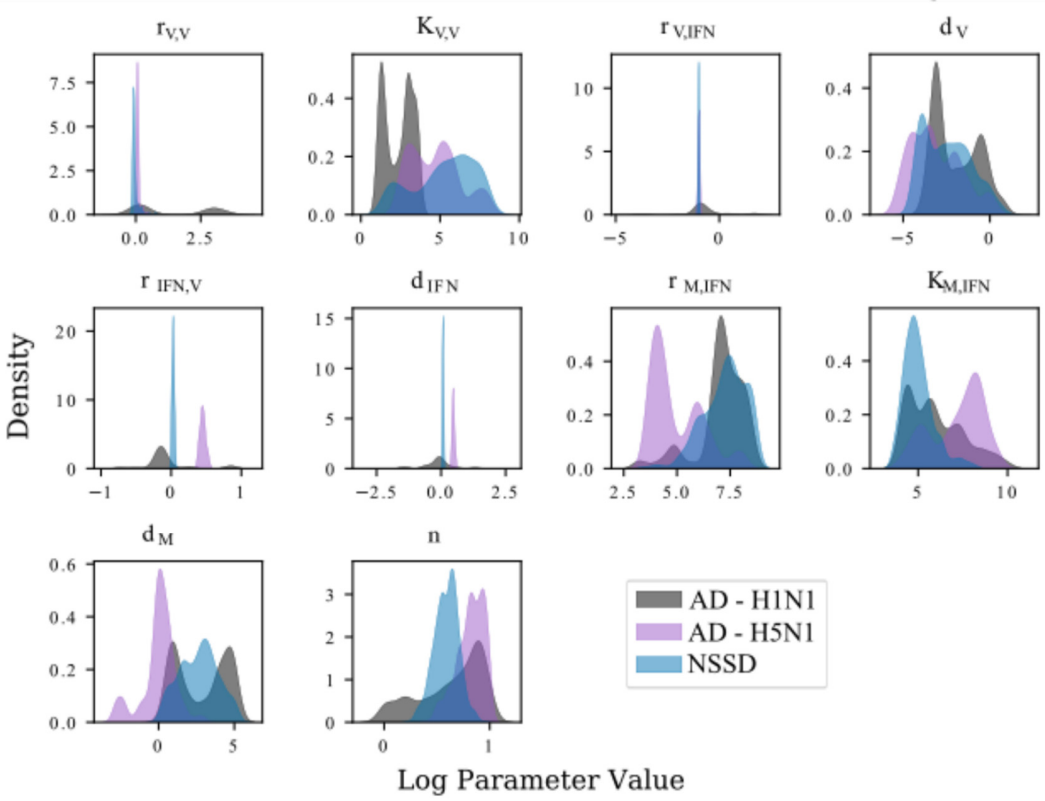
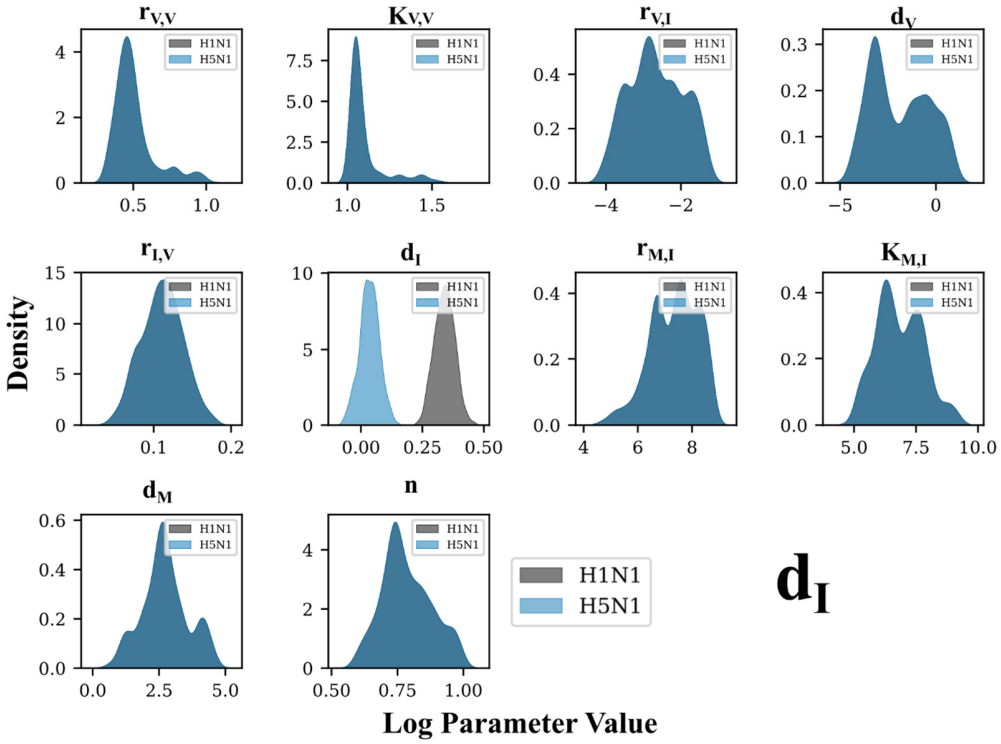
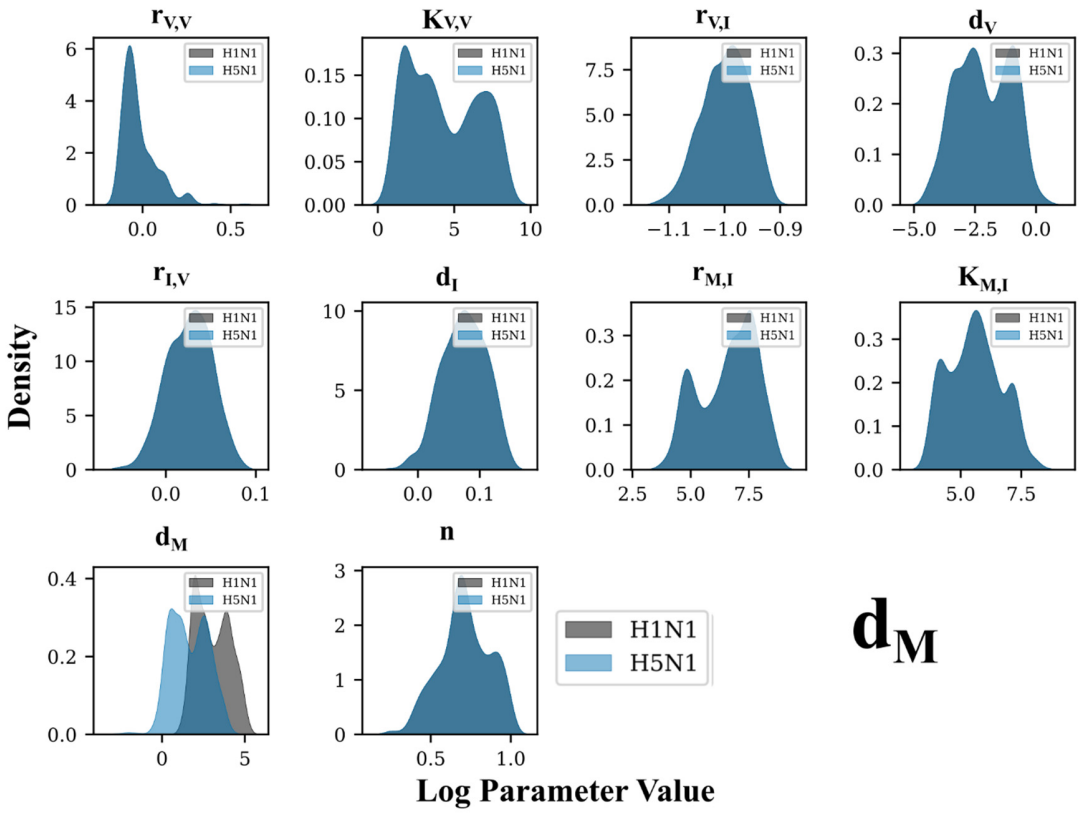
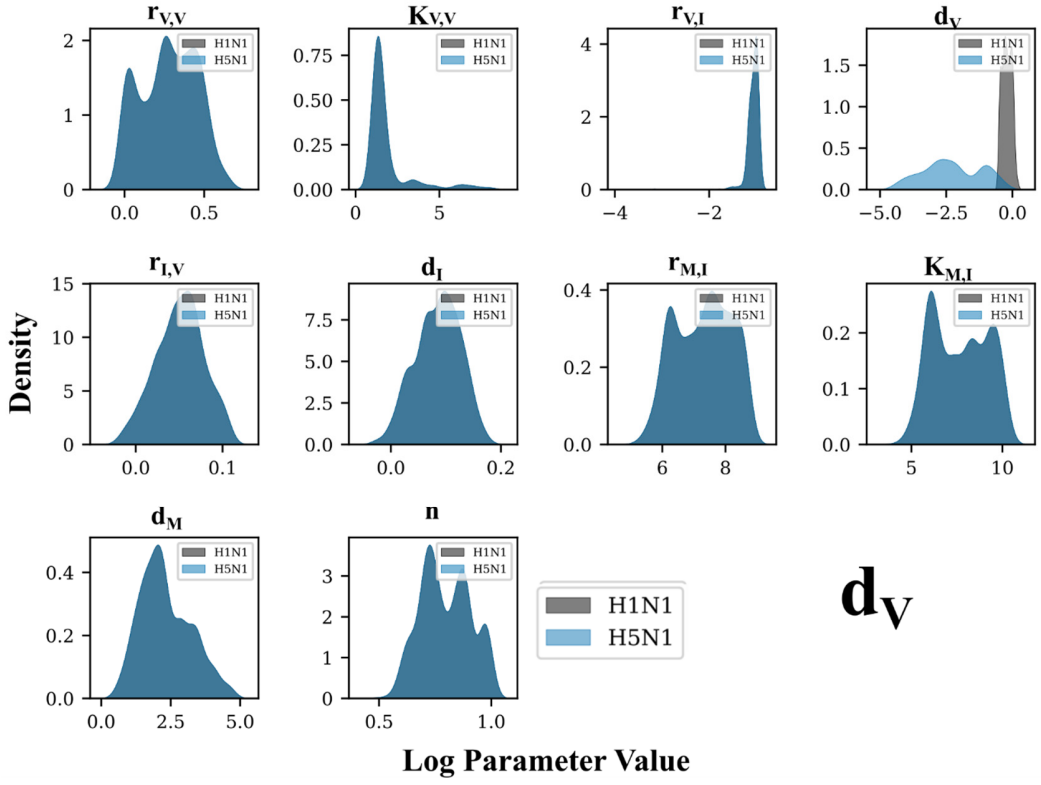


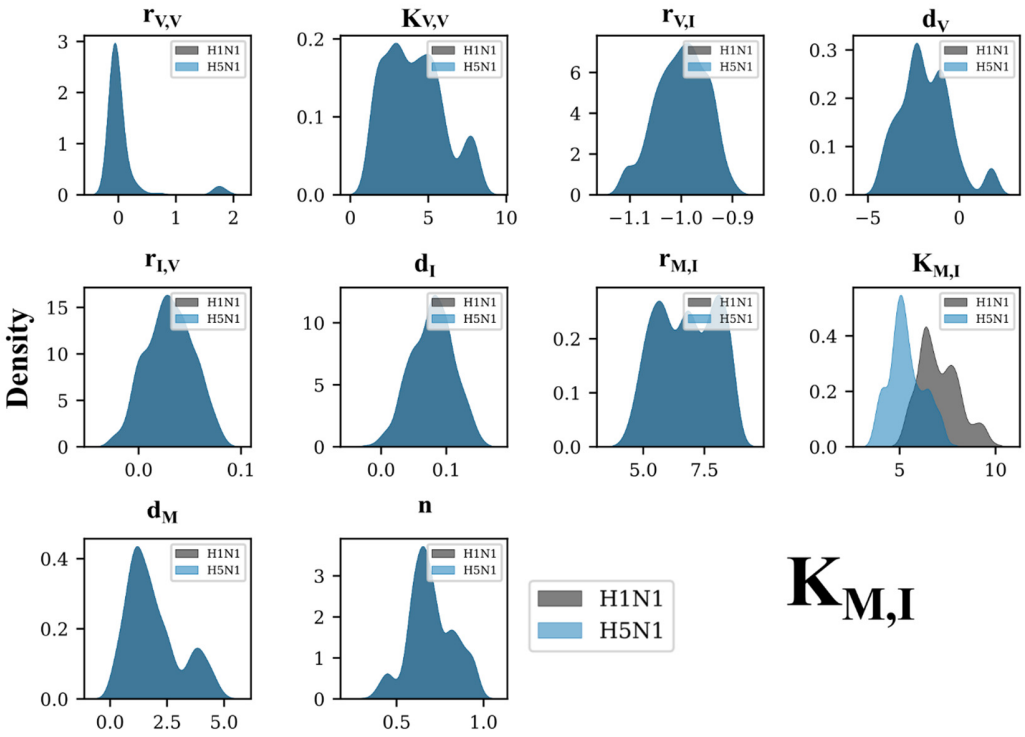
Figure S3. AD and NSSD model 4 energy plots. MCMC quickly completes burn-in and thoroughly explored parameter space for all three scenarios.

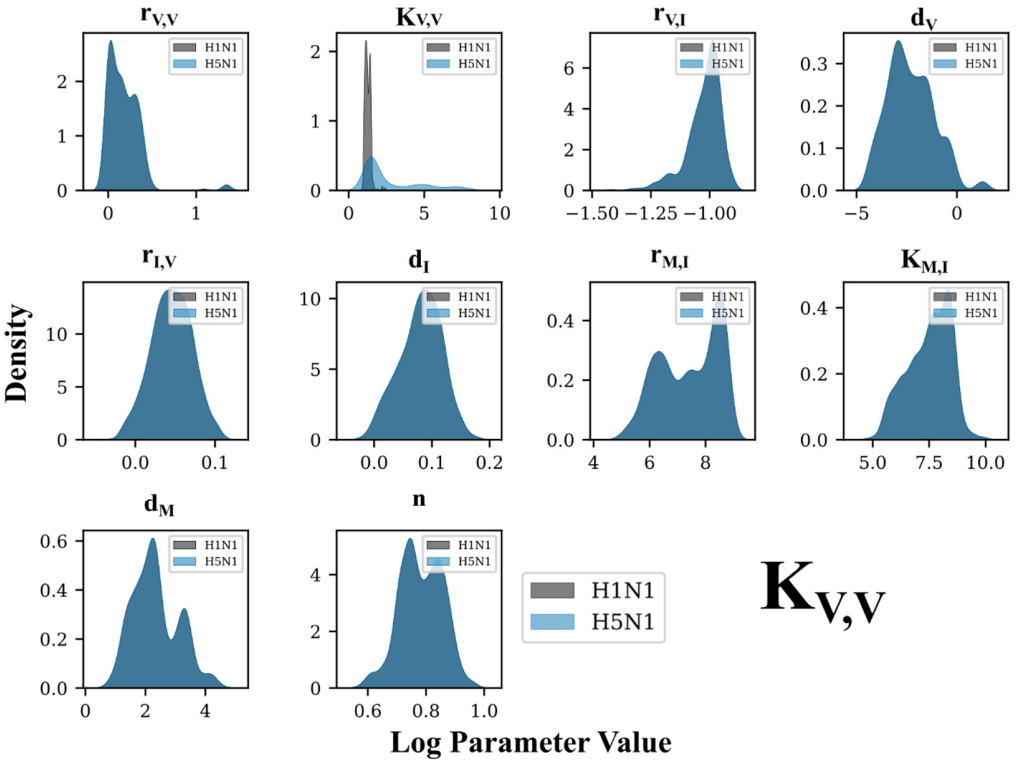

$r_{V,V}$
$K_{V,V}$
$r_{V,IFN}$
d_V
$r_{IFN,V}$
d_{IFN}
$r_{M,IFN}$
$K_{M,IFN}$
d_M
n
Density
AD - H1N1
AD - H5N1
NSSD
Log Parameter Value

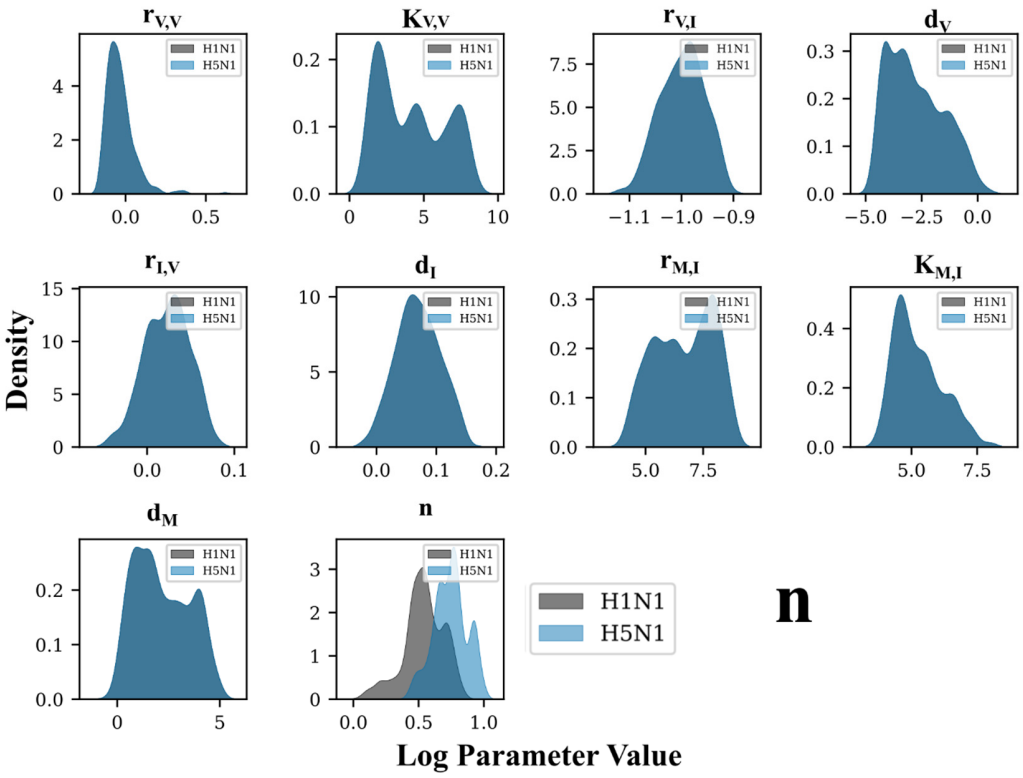

$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
d_I

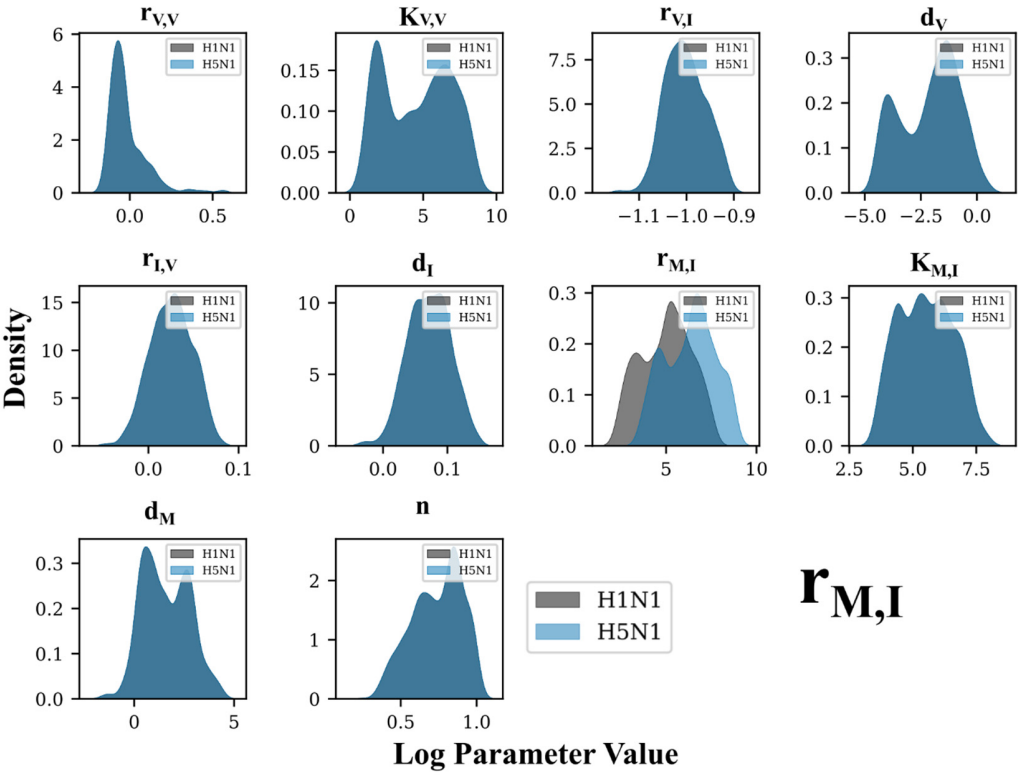

$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
d_M


$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
d_V


$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
$K_{M,I}$


$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
$K_{V,V}$


$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
n


$r_{V,V}$
$K_{V,V}$
$r_{V,I}$
d_V
$r_{I,V}$
d_I
$r_{M,I}$
$K_{M,I}$
d_M
n
H1N1
H5N1
Density
Log Parameter Value
$r_{M,I}$

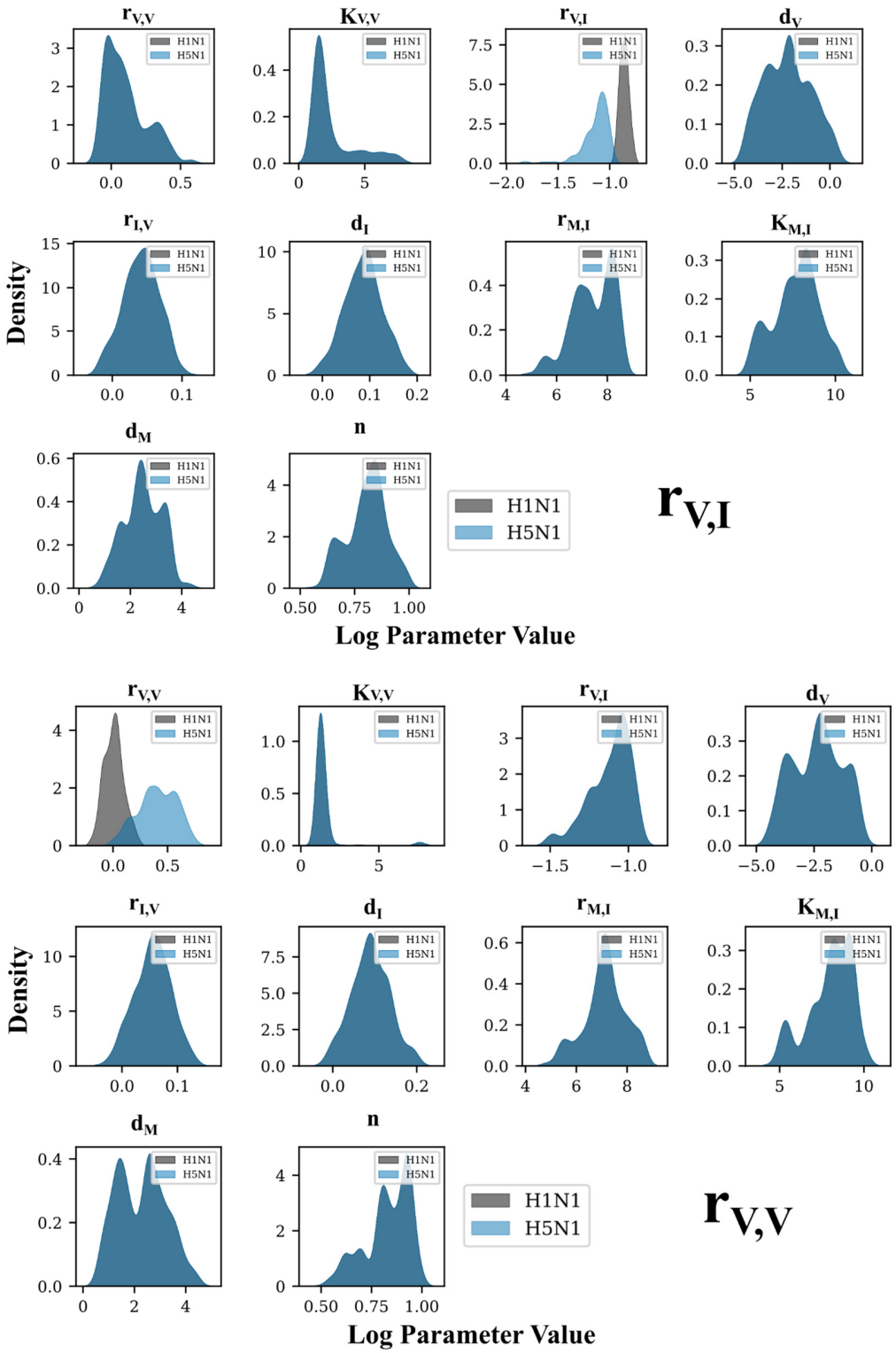


Figure S4. AD, NSSD, and OSSD model 4 parameter posterior density distributions. Overlapping distributions with an OSSD parameter ($r_{M,I}$, etc.) likely indicate non strain-specific mechanisms are likely, while distinct distributions (d_I, etc.) likely indicate strain-specific differences exist.