

8,954 nasal swabs (NS)  
18,026 tracheal swabs (TS)  
6,532 pig sera (PS)

174 H3 SIVs isolated  
from NS and TS

6,532 sets of paired  
NS and PS samples

Molecular epidemiology  
analysis

Only samples collected from  
Guangdong province

Only samples collected from  
major source farms†

4,226 paired NS and  
PS samples

5,832 paired NS and  
PS samples

Force of Infection estimation  
for H3 infection in farms and  
during transport

Logistic Regression analysis on  
multiple potential risk factors to  
58 H3 infections

† Major source farm is defined as farms providing  $\geq 20$  samples