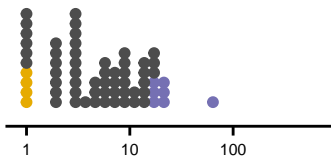


Dinis et al., 2016

total samples: 68

samples analyzed: 57

region sequenced: HA only

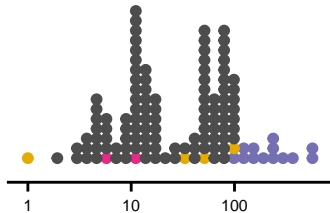


Debbink et al., 2017

total samples: 123

samples analyzed: 104

region sequenced: full genome

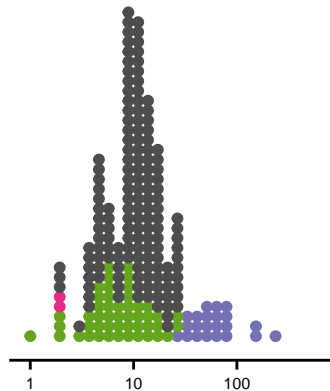


McCrone et al., 2018

total samples: 220

samples analyzed: 147

region sequenced: full genome



Reason for  
sample exclusion

- Top 10% of samples,  
total number of variants
- Low sequencing  
coverage
- Longitudinal pair,  
first timepoint
- Plasmid control
- None

Number of mutations