

# Antibody dynamics for Dengue

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## Background

- Data provided by Dr. Supawat Chatchen from Mahidol University in Thailand.
- A large serosurvey for Dengue conducted from 2007-2010 among children aged 4-14 in Muang Ratchaburi, Ratchaburi Province, Thailand.
  - 4 different time periods
    - \* Visit 1: Jan-Sep 2007
    - \* Visit 2: Jan-Apr 2008
    - \* Visit 3: Jul-Nov 2008
    - \* Visit 4: May-Oct 2009
  - Data on incident cases gathered from clinic, therefore we know onset date for all positive dengue cases.

Table 1

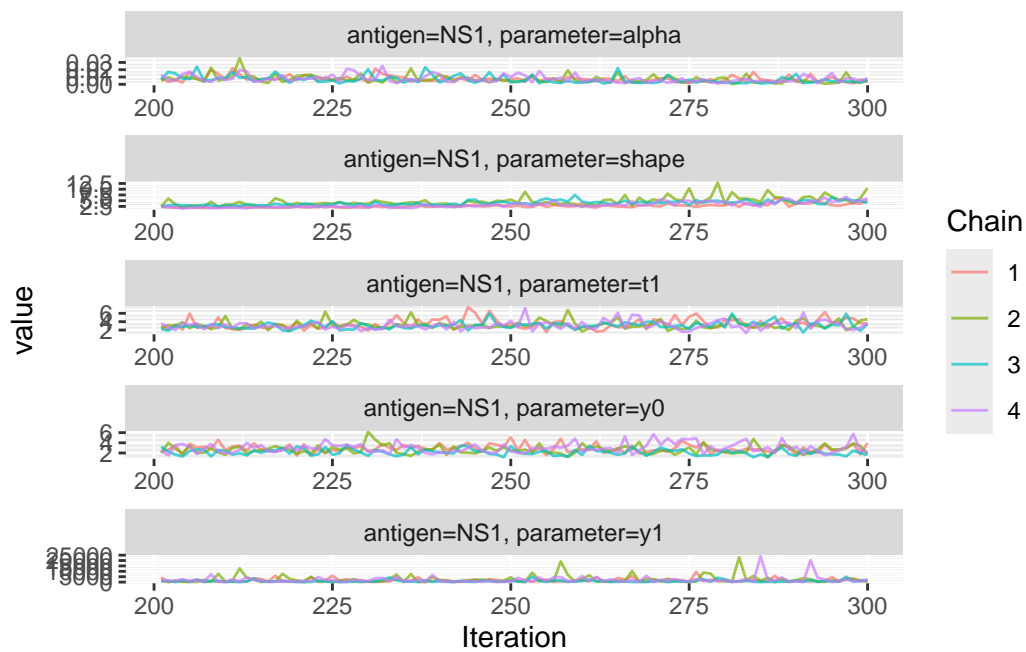
	DHF	No DHF	Overall
	(N=70)	(N=497)	(N=567)
Age_cat			
10orolder	44 (62.9%)	250 (50.3%)	294 (51.9%)
Lessthan10	26 (37.1%)	247 (49.7%)	273 (48.1%)
Laboratory_diagnosis			
Acute Primary Infection	2 (2.9%)	60 (12.1%)	62 (10.9%)
Acute Secondary Infection	68 (97.1%)	437 (87.9%)	505 (89.1%)
PCR_Result			
DEN1	28 (40.0%)	226 (45.5%)	254 (44.8%)
DEN2	18 (25.7%)	134 (27.0%)	152 (26.8%)
DEN3	18 (25.7%)	85 (17.1%)	103 (18.2%)

	DHF	No DHF	Overall
DEN4	6 (8.6%)	52 (10.5%)	58 (10.2%)

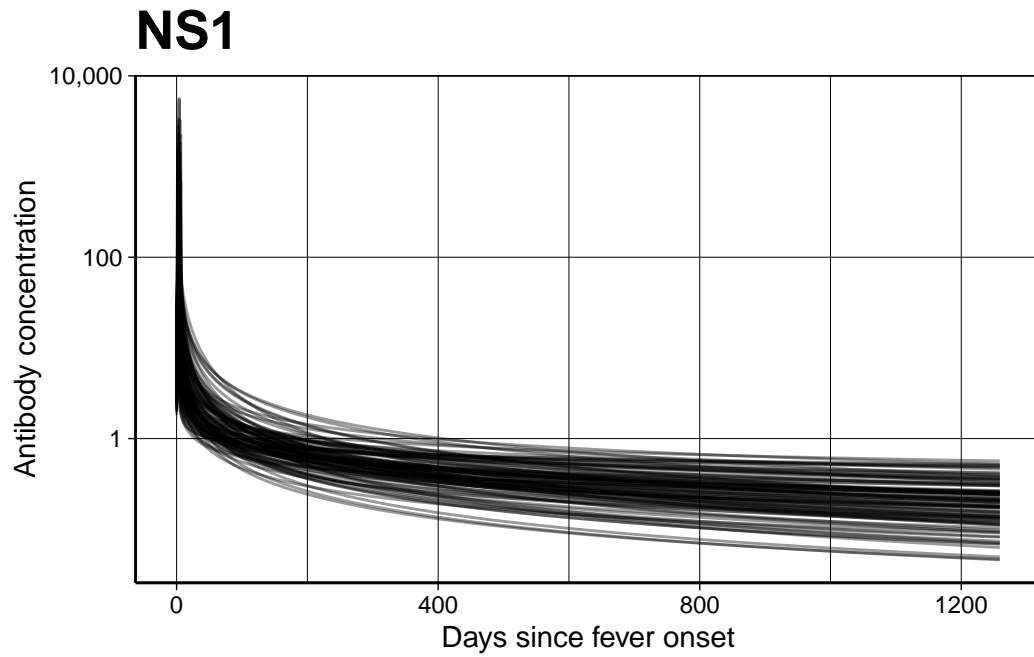
Methods: Dengue data was run through jags simulation using the following settings: inputs for jags model: nchains <- 4; # nr of MC chains to run simultaneously nadapt <- 4000; # nr of iterations for adaptation nburnin <- 100; # nr of iterations to use for burn-in nmc <- 100; # nr of samples in posterior chains niter <- 10000; # nr of iterations for posterior sample nthin <- round(niter/nmc); # thinning needed to produce nmc from niter

Data from the “New person” were subset and used for the following figures.

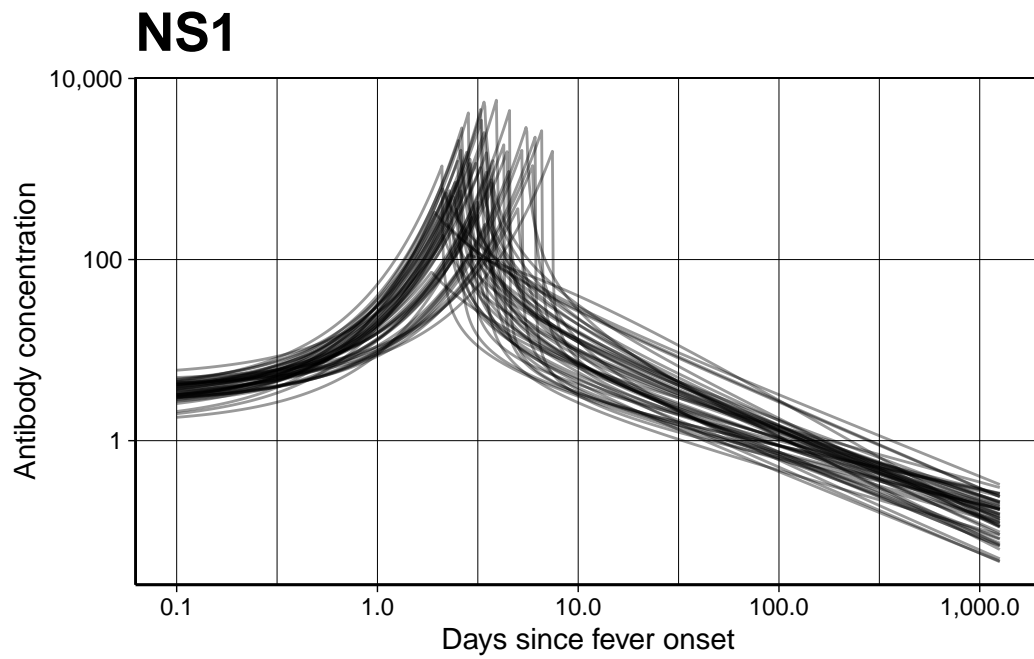
Traceplot of parameters for NS1 antigen



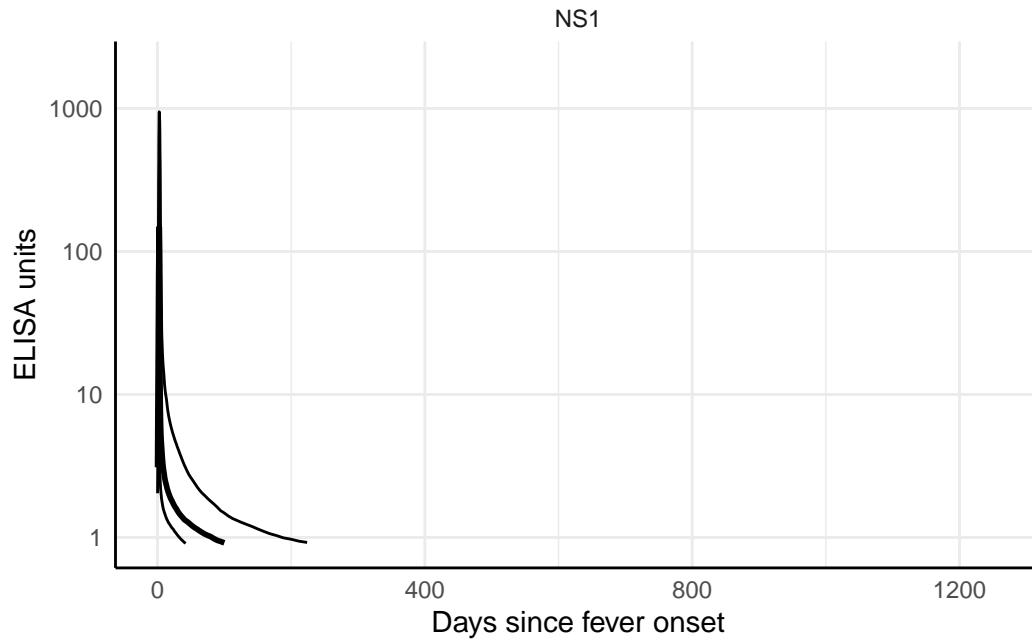
Antibody dynamic curve for Dengue data



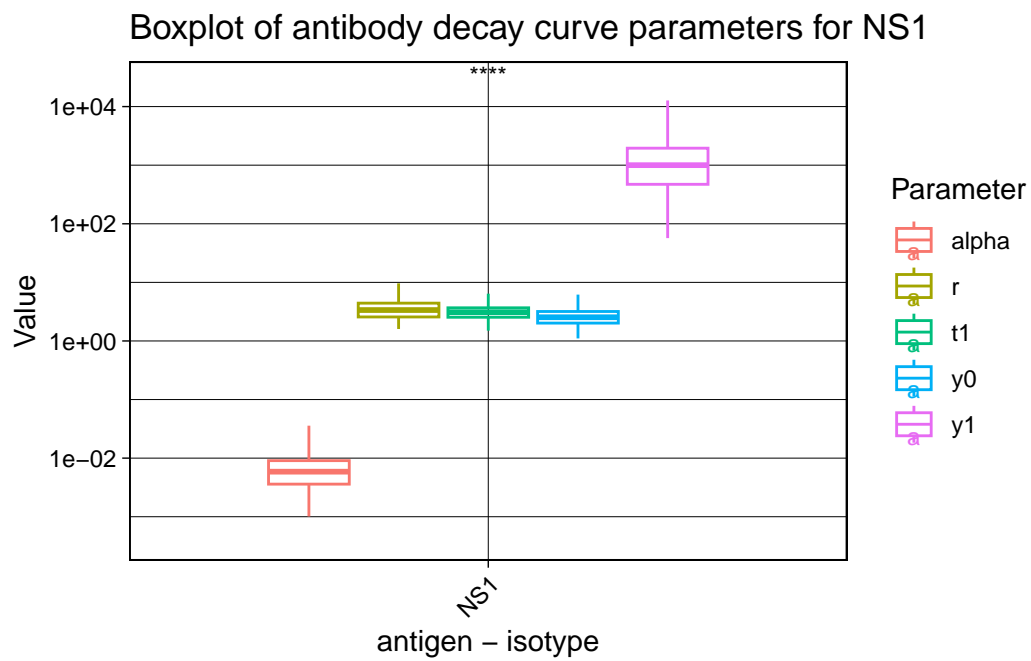
Antibody dynamic curve plotted on the log scale



Antibody dynamic curve plotted with median an 95%



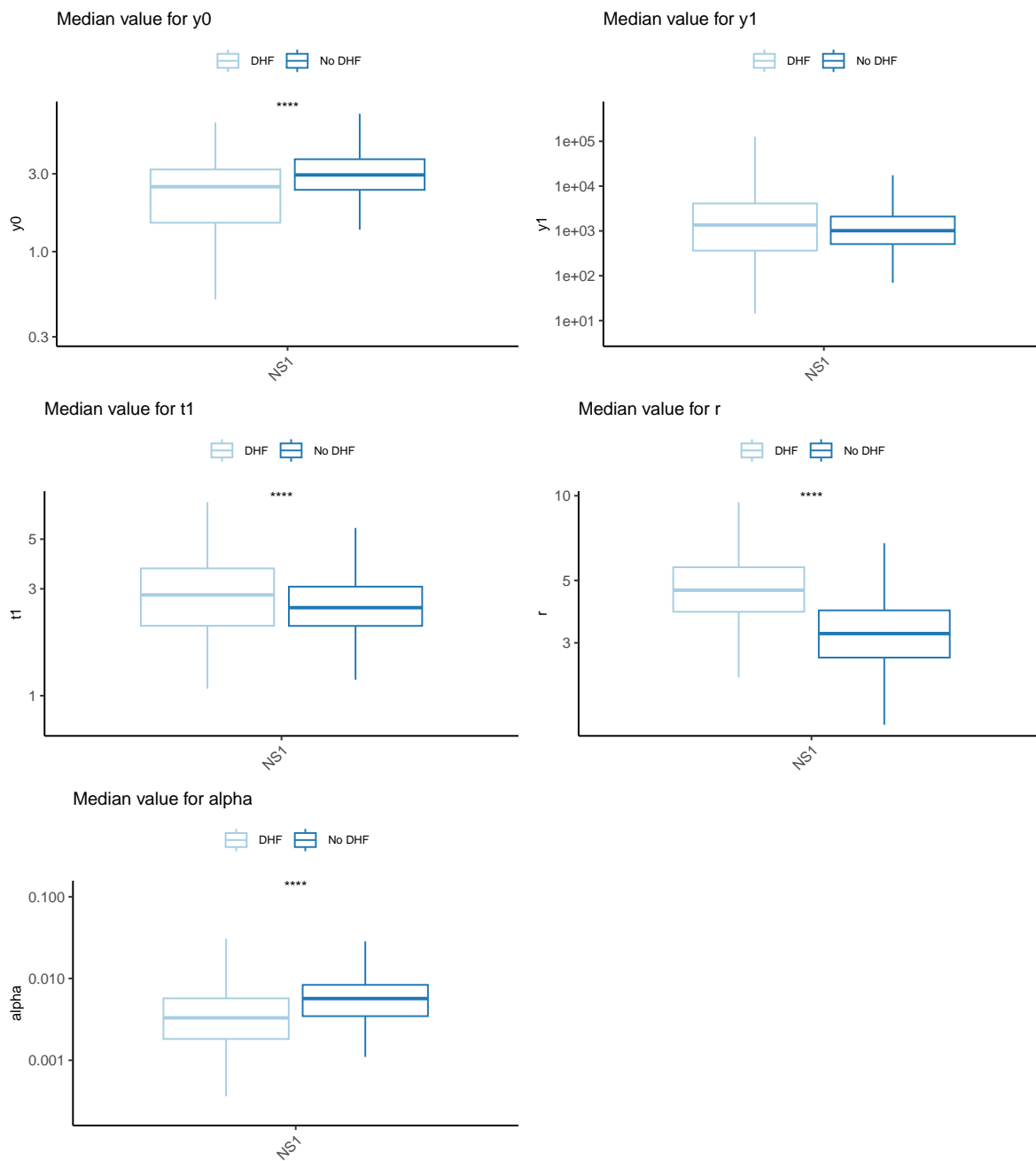
Parameter Values for Dengue antibody dynamic curve



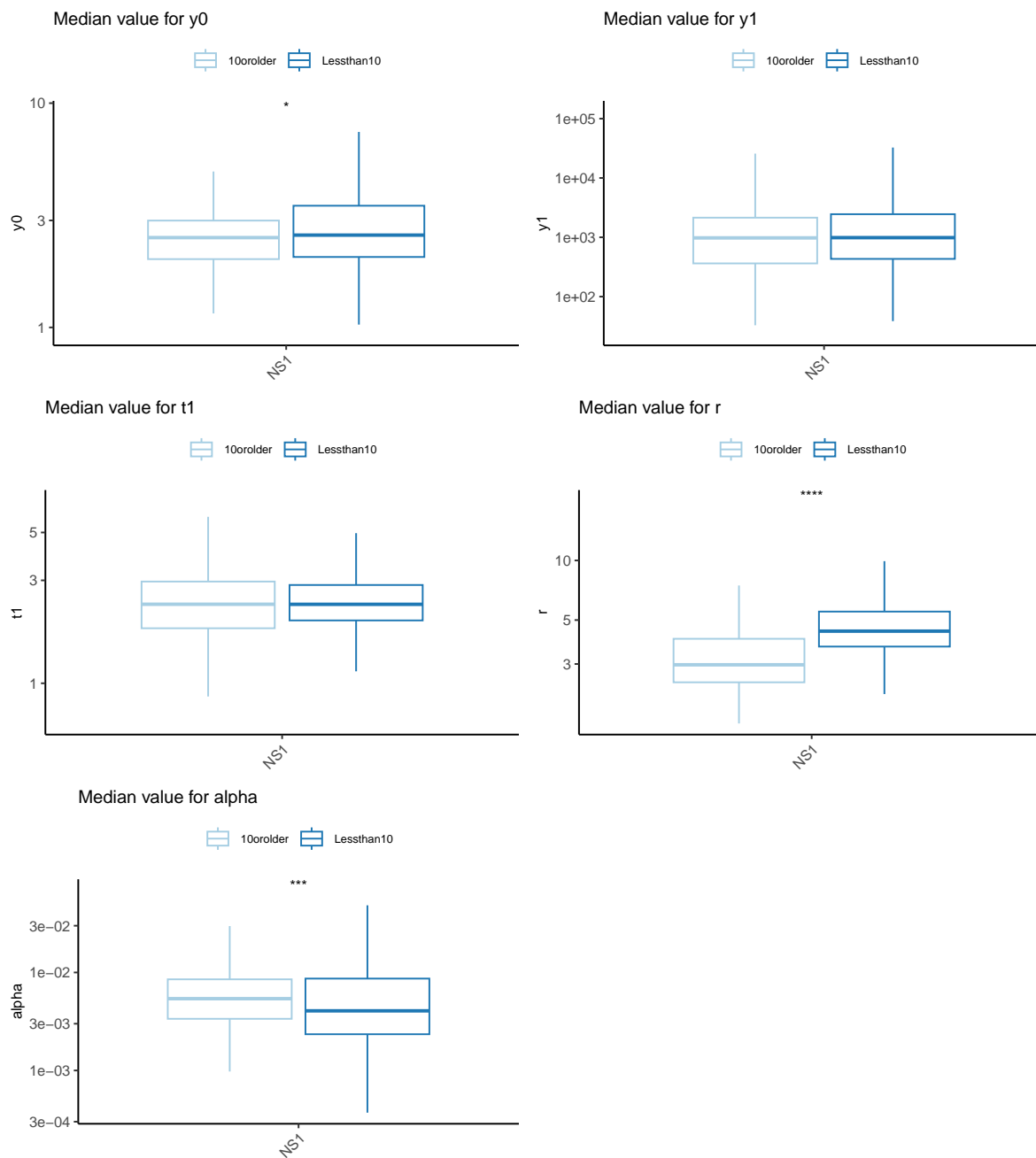
Methods: Dengue data set was stratified by DHF vs non-DHF case and  $<10$  years vs  $\geq 10$  years of age and run through jags simulation using the following inputs: inputs for jags model

```
nchains <- 4; # nr of MC chains to run simultaneously nadapt <- 4000; # nr of iterations
for adaptation nburnin <- 100; # nr of iterations to use for burn-in nmc <- 100; # nr of
samples in posterior chains niter <- 10000; # nr of iterations for posterior sample nthin <-
round(niter/nmc); # thinning needed to produce nmc from niter
```

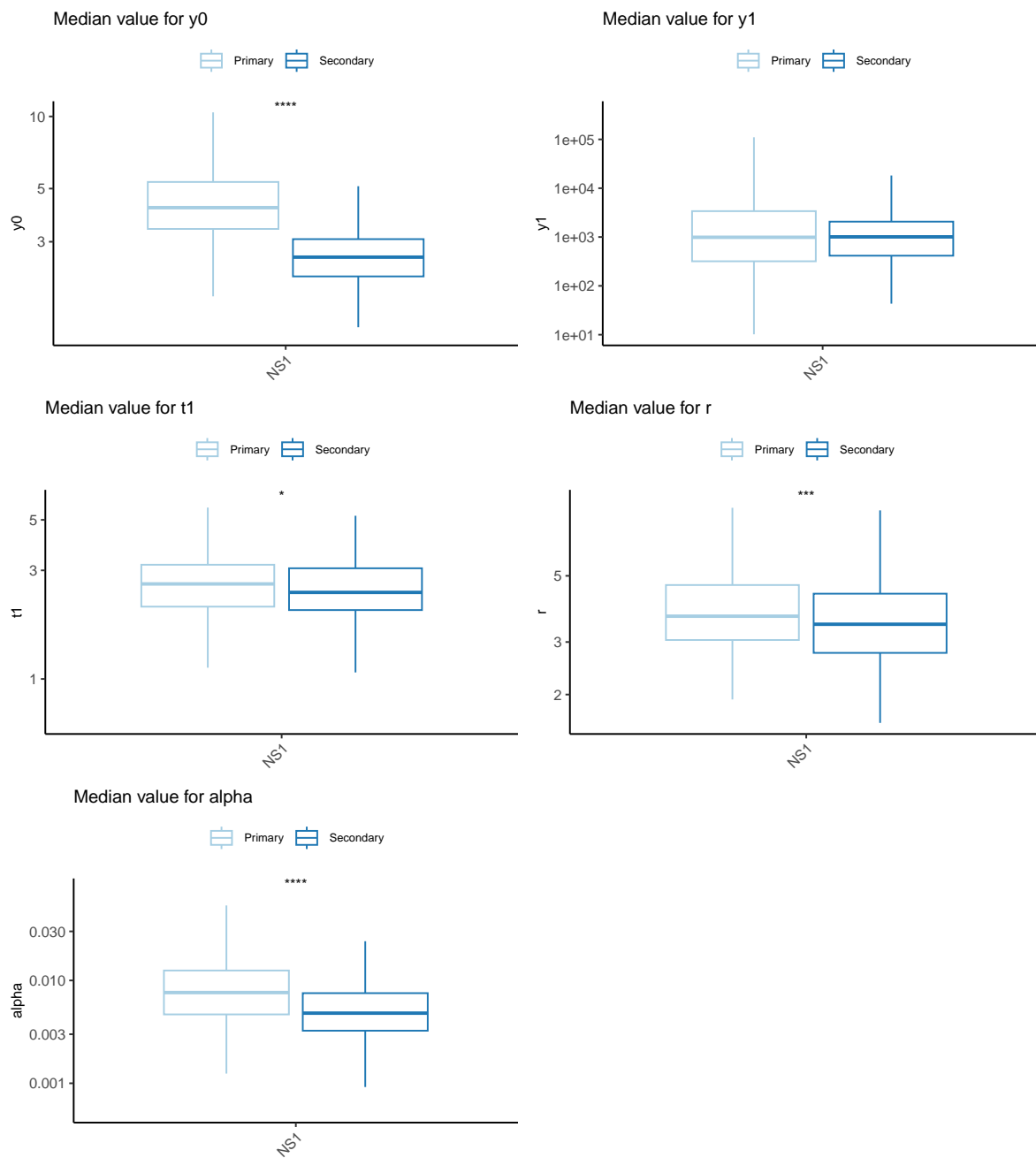
## Parameter boxplots and diagnostics stratified by DHF status



## Parameter boxplots stratified by age group (<10 years vs 10+ years)



## Parameter boxplots stratified by diagnosis, primary vs secondary infection





## Parameter boxplots stratified by diagnosis, primary vs secondary infection

