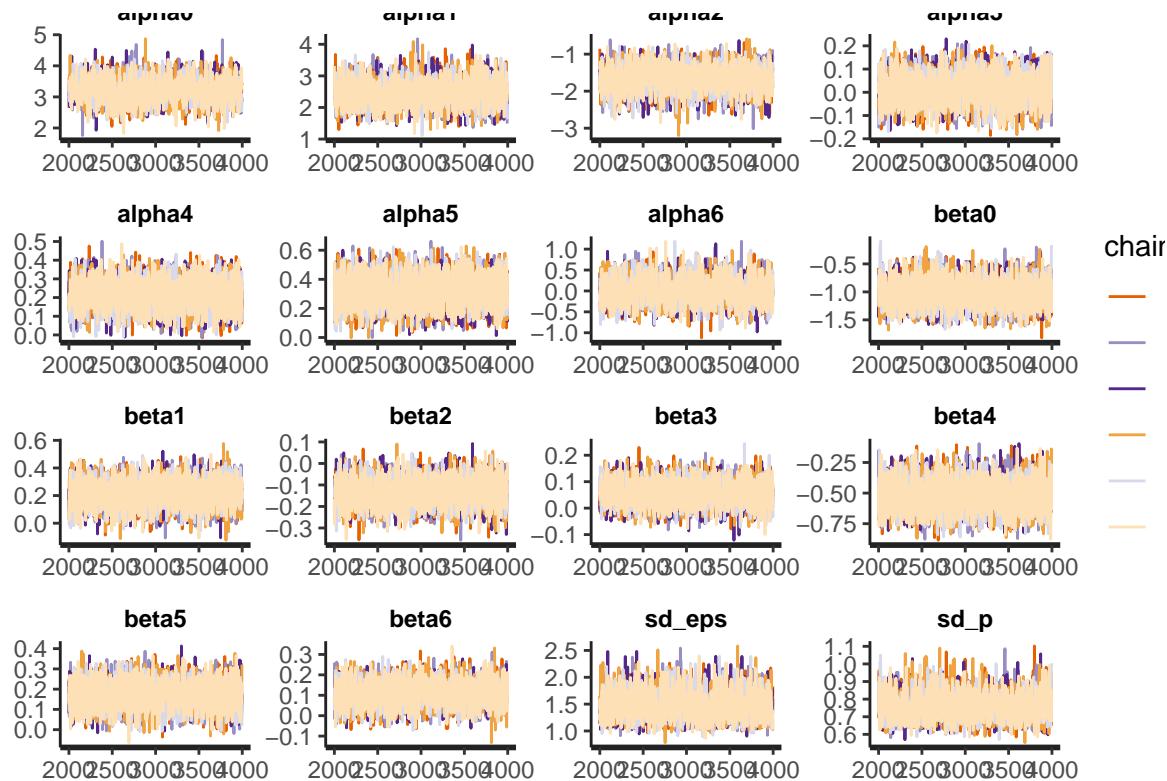


# HMC Diagnostics

Script for checking MCMC/HMC diagnostics - this might be better as an Rmd to just have one output for supplemental publication

*Plethodon jordani*

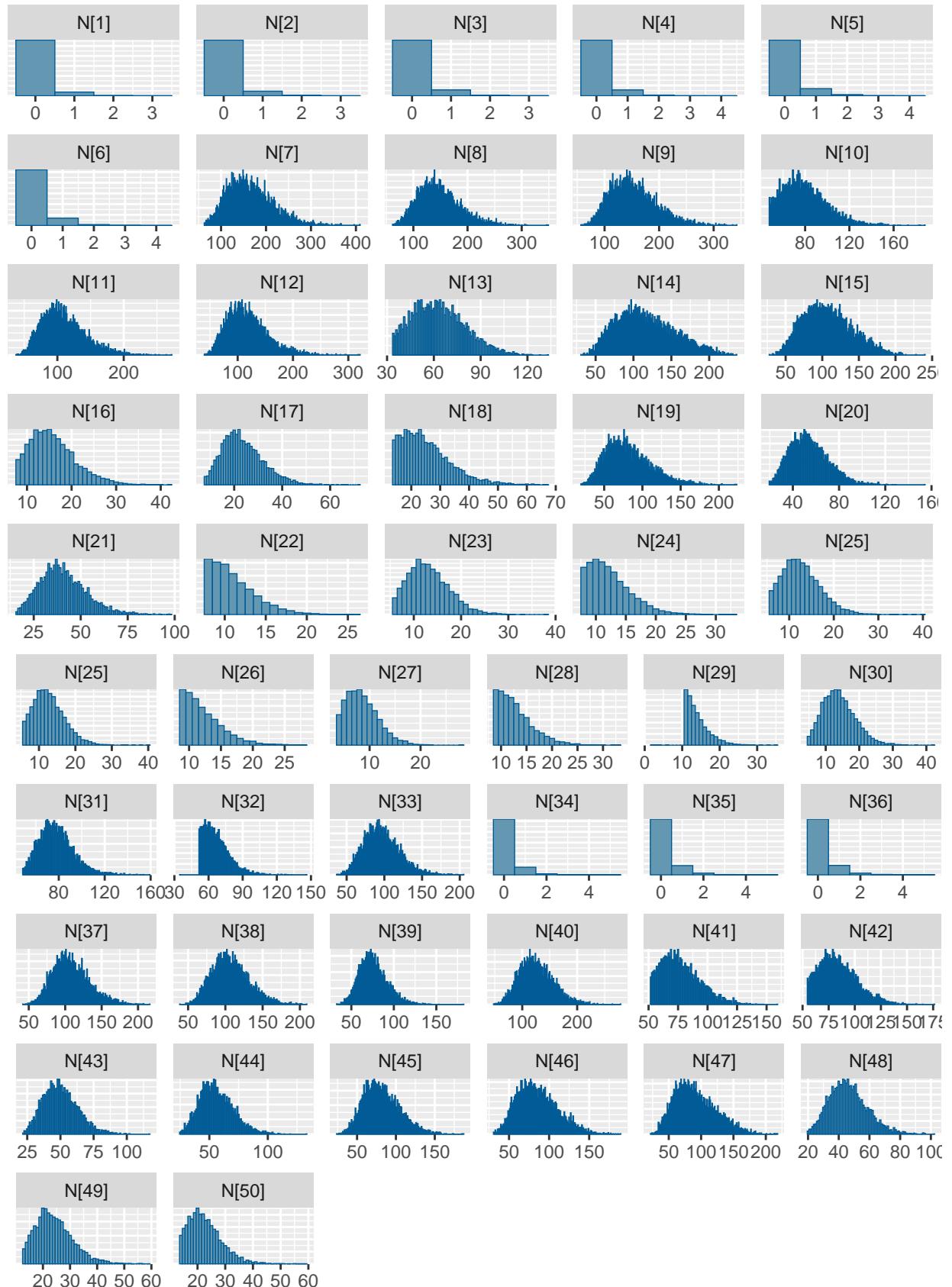
View Traceplots

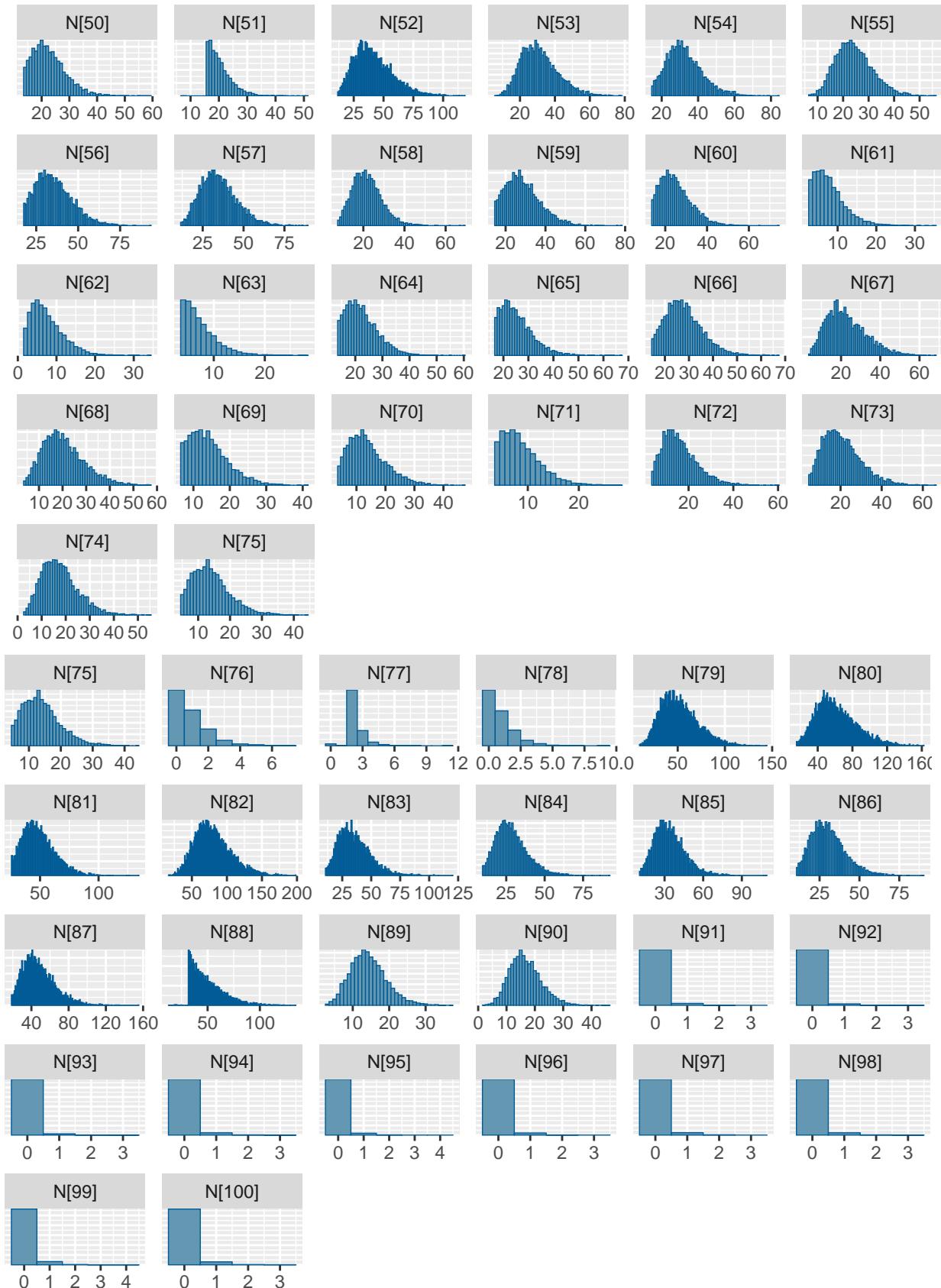


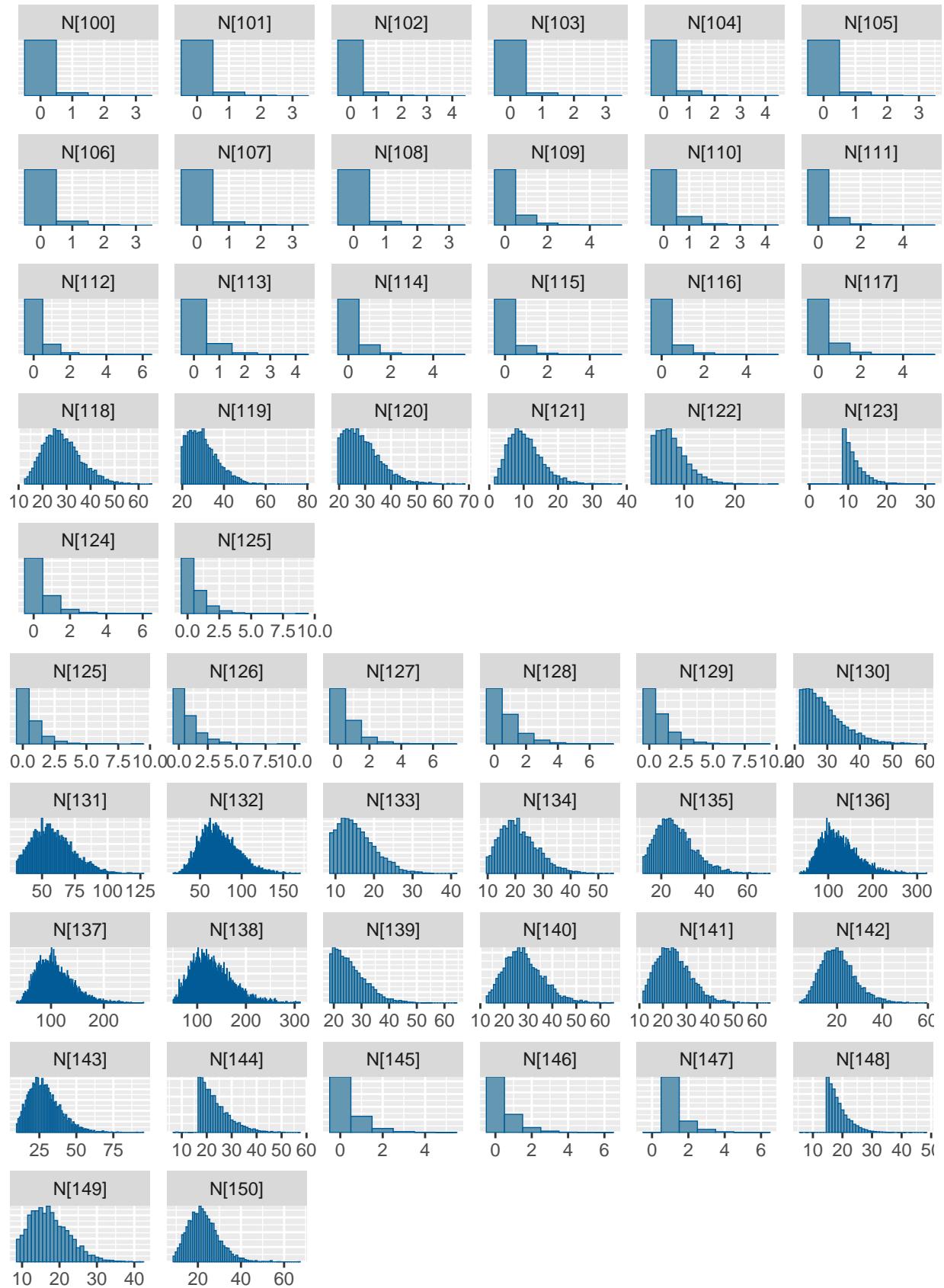
Check Domain Specific Expectations

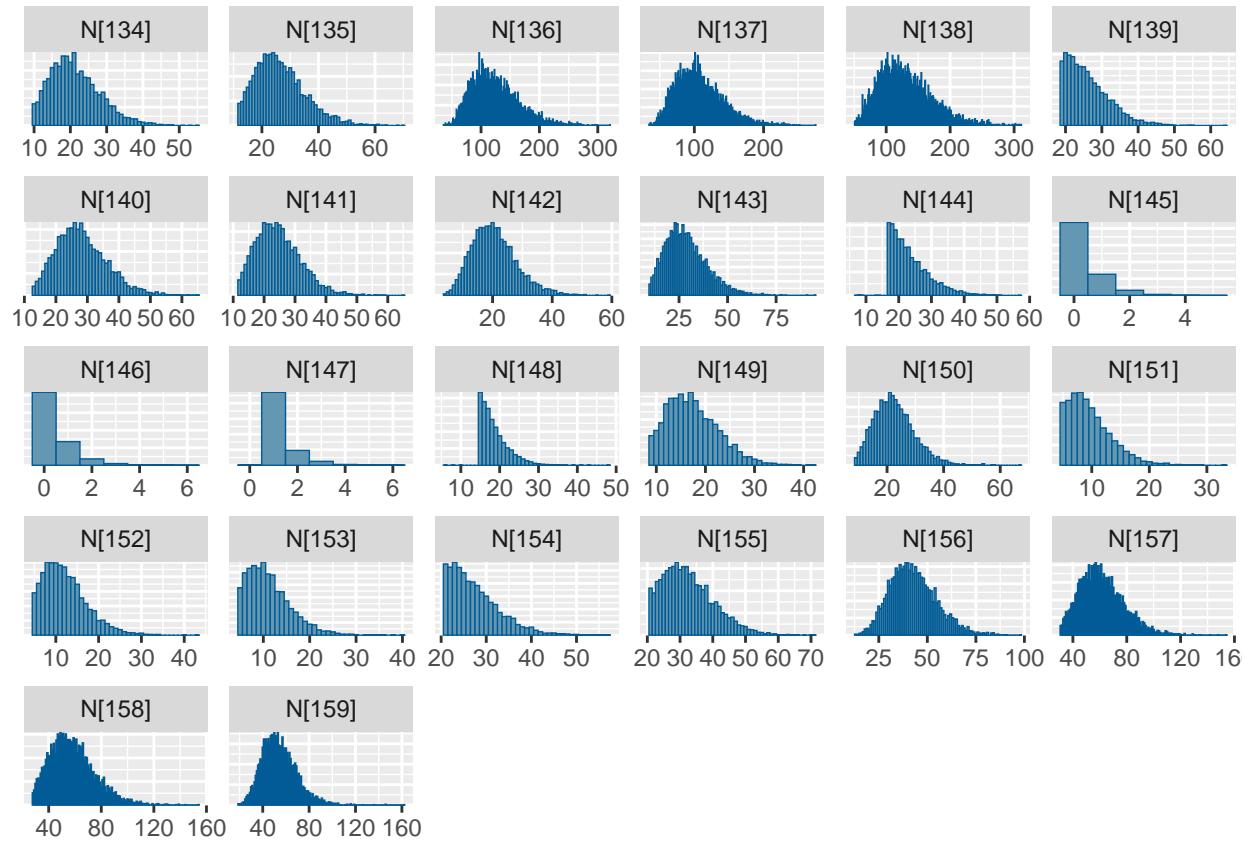
Check N for Truncation

The augmentation to marginalize N out as a latent discrete requires setting an upper bound, K, to loop through. If K is too small the posterior will be truncated. Need to check for every N.





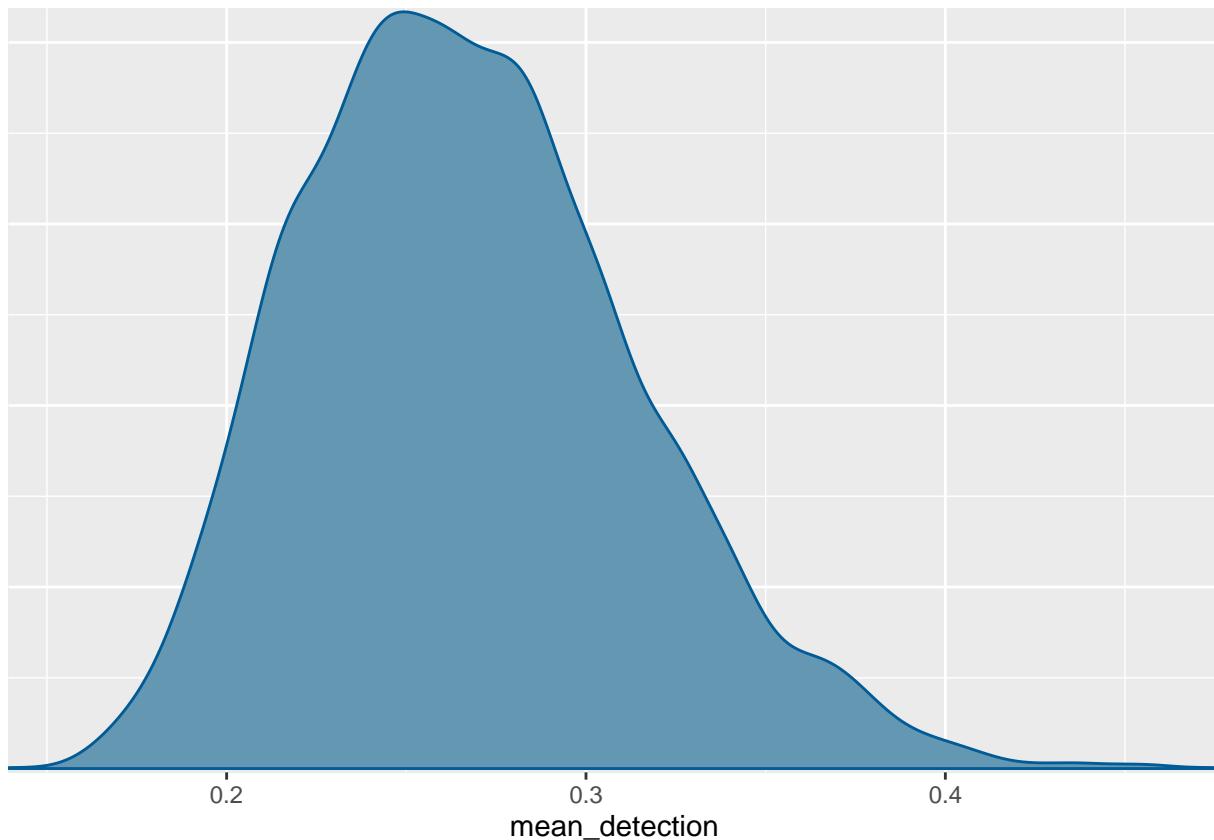




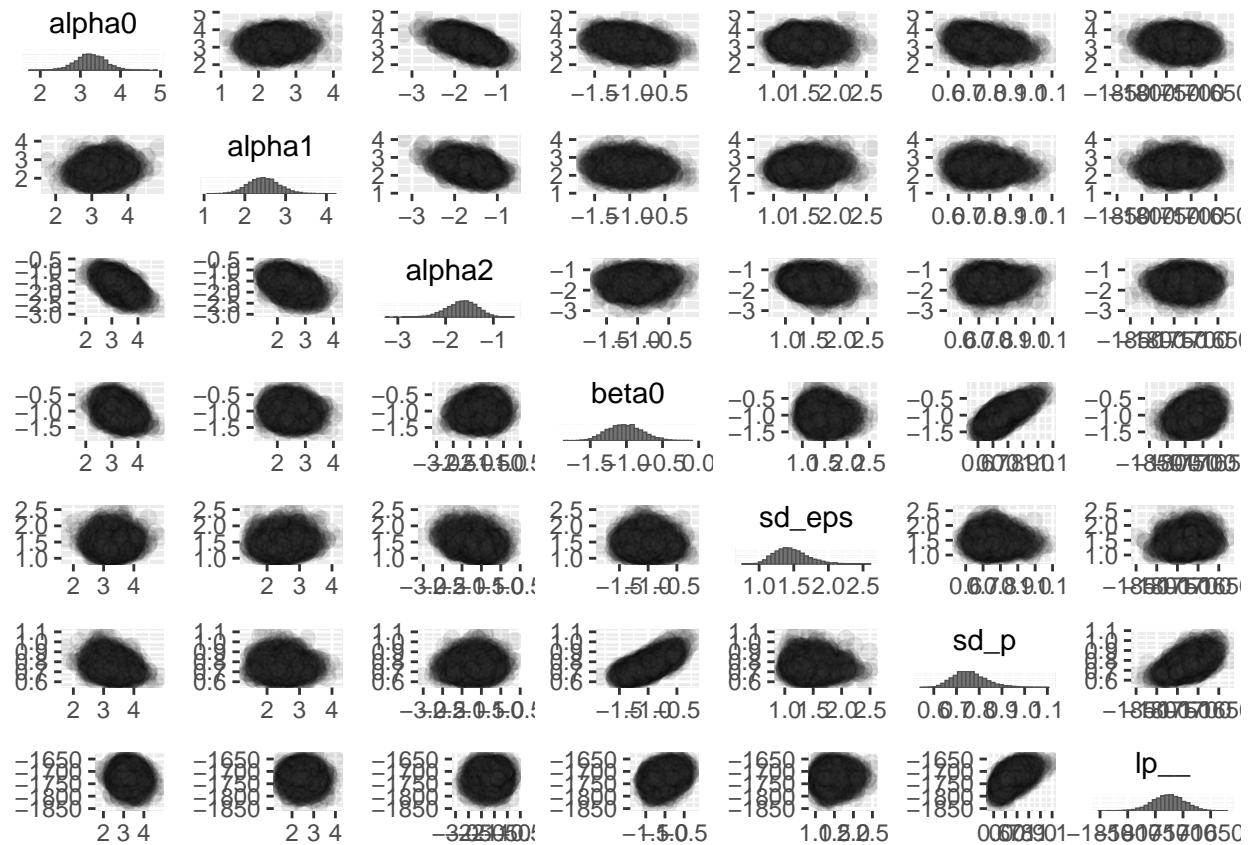
```
## null device
##           1
```

Check detection

In simulations abundance estimates are unreliable when detection gets below 20%



## Check Divergences and Pairwise Correlations



## Check Energy and Treedepth

### Summarize Samples Sizes and Mixing

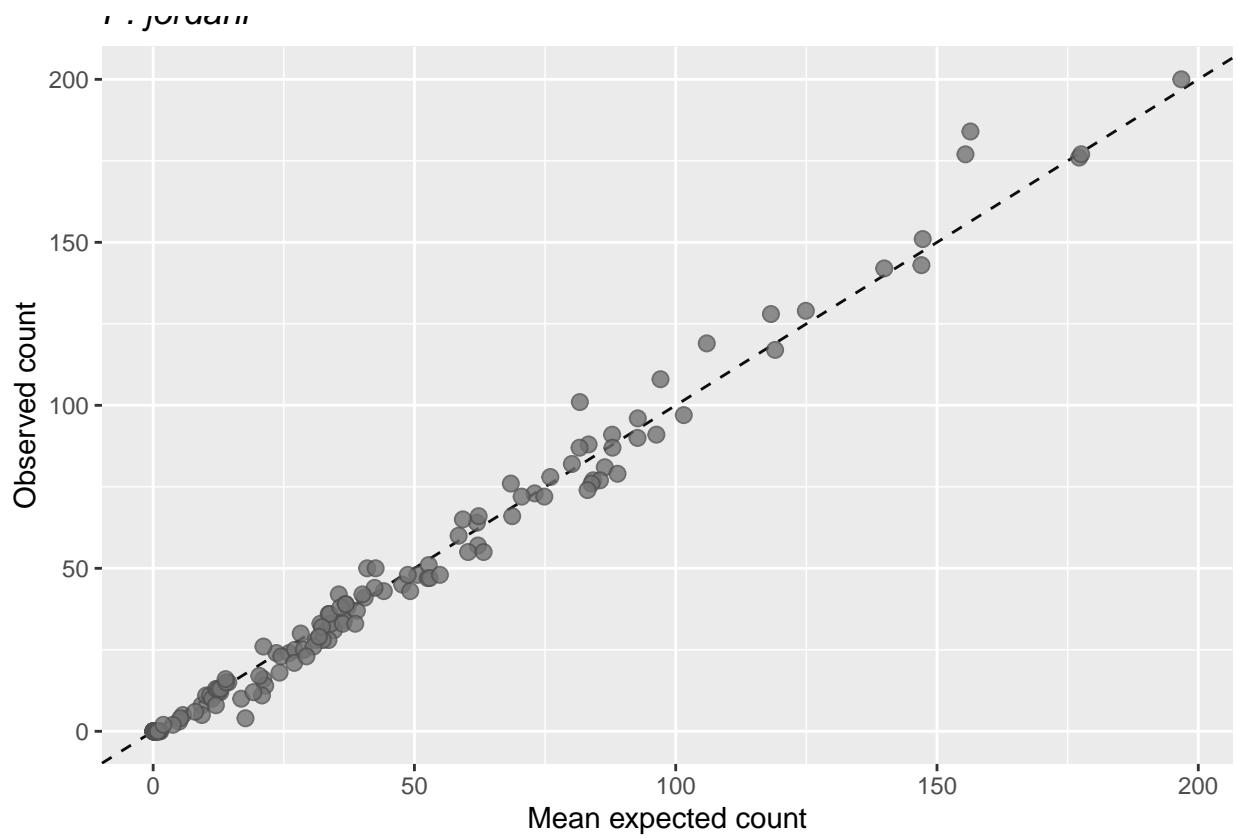
Effective samples sizes using rstan::monitor following Hoffman and Gelman (2014) to be more reliable and accurate (as in Monnahan et al. 2017) - UPDATE - now follow Vehtari et al. 2019.

effective sample sizes (should be > 100) - Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2019). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC. arXiv preprint arXiv:1903.08008.

```
## [1] 1.003609
## [1] 1675
## [1] 2564
```

## Posterior Predictive Checks

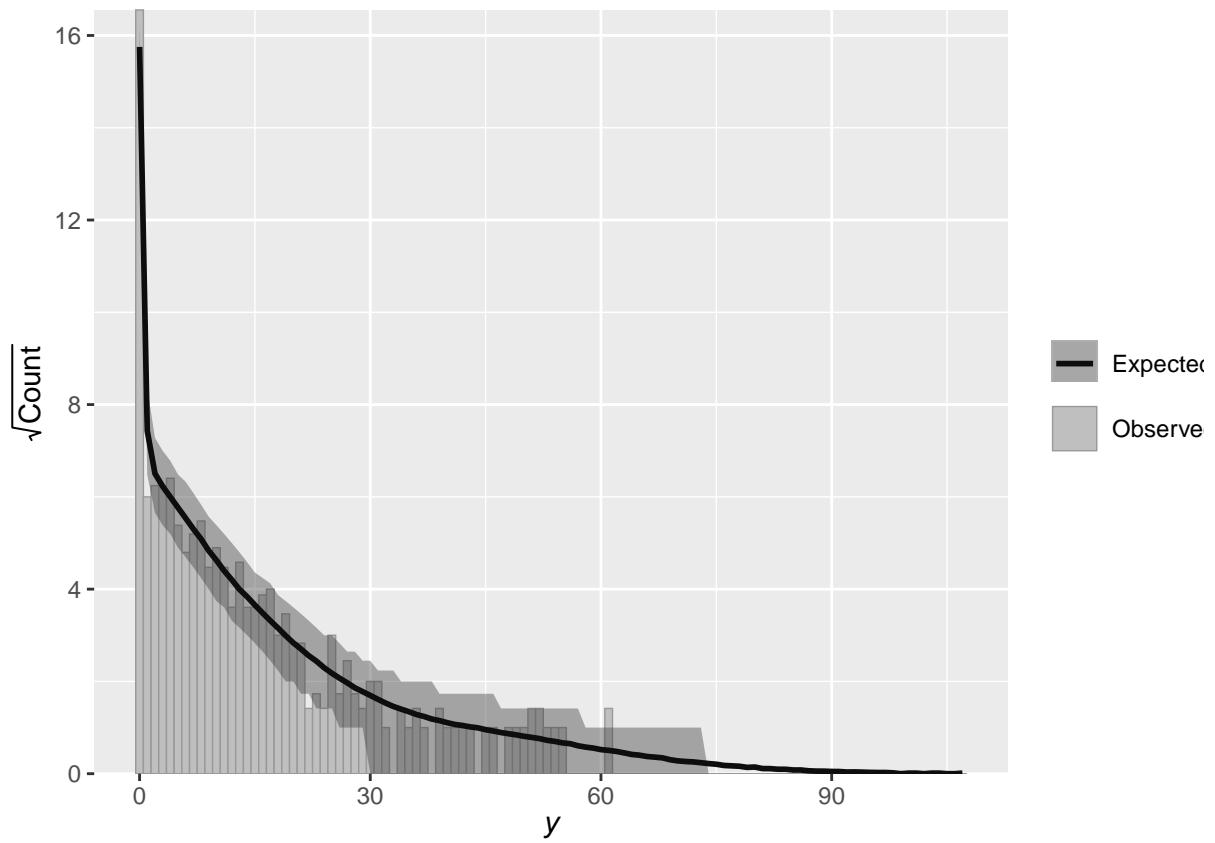
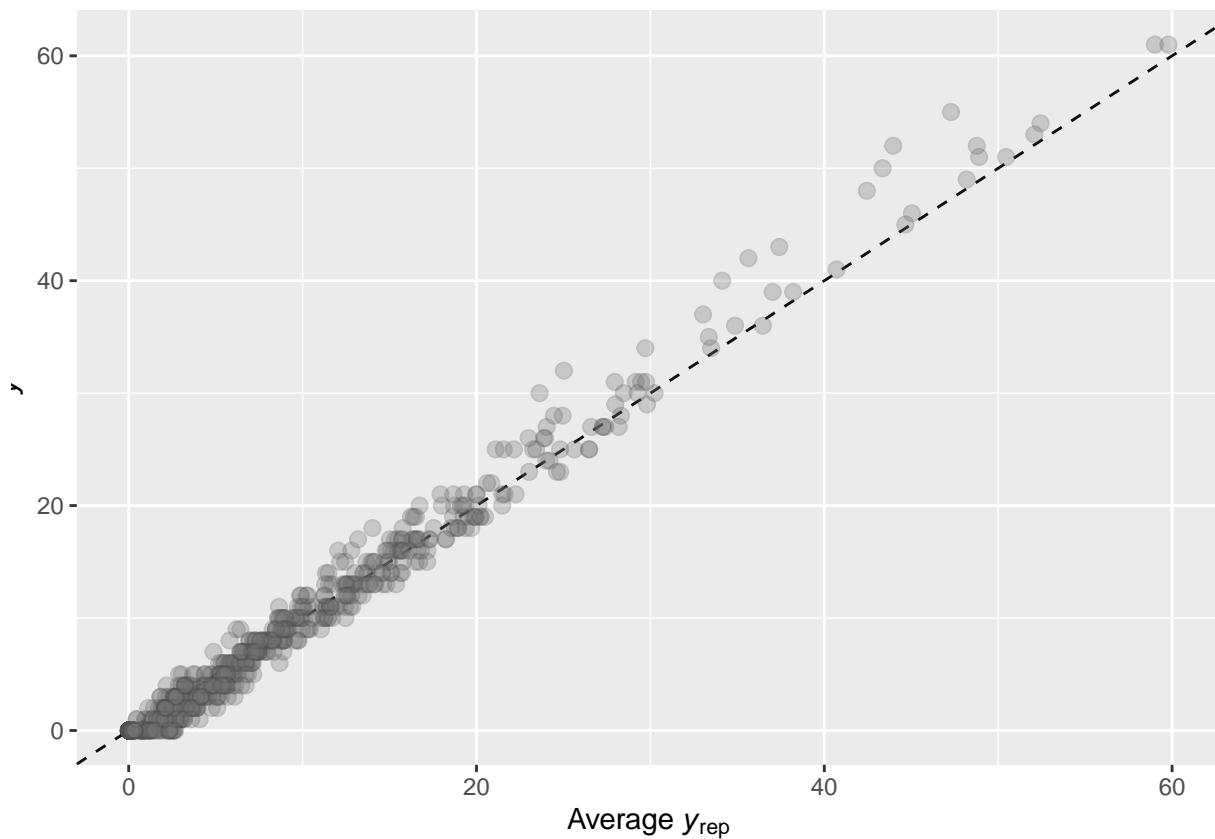
Examine posterior predictions of total counts across all 5 visits

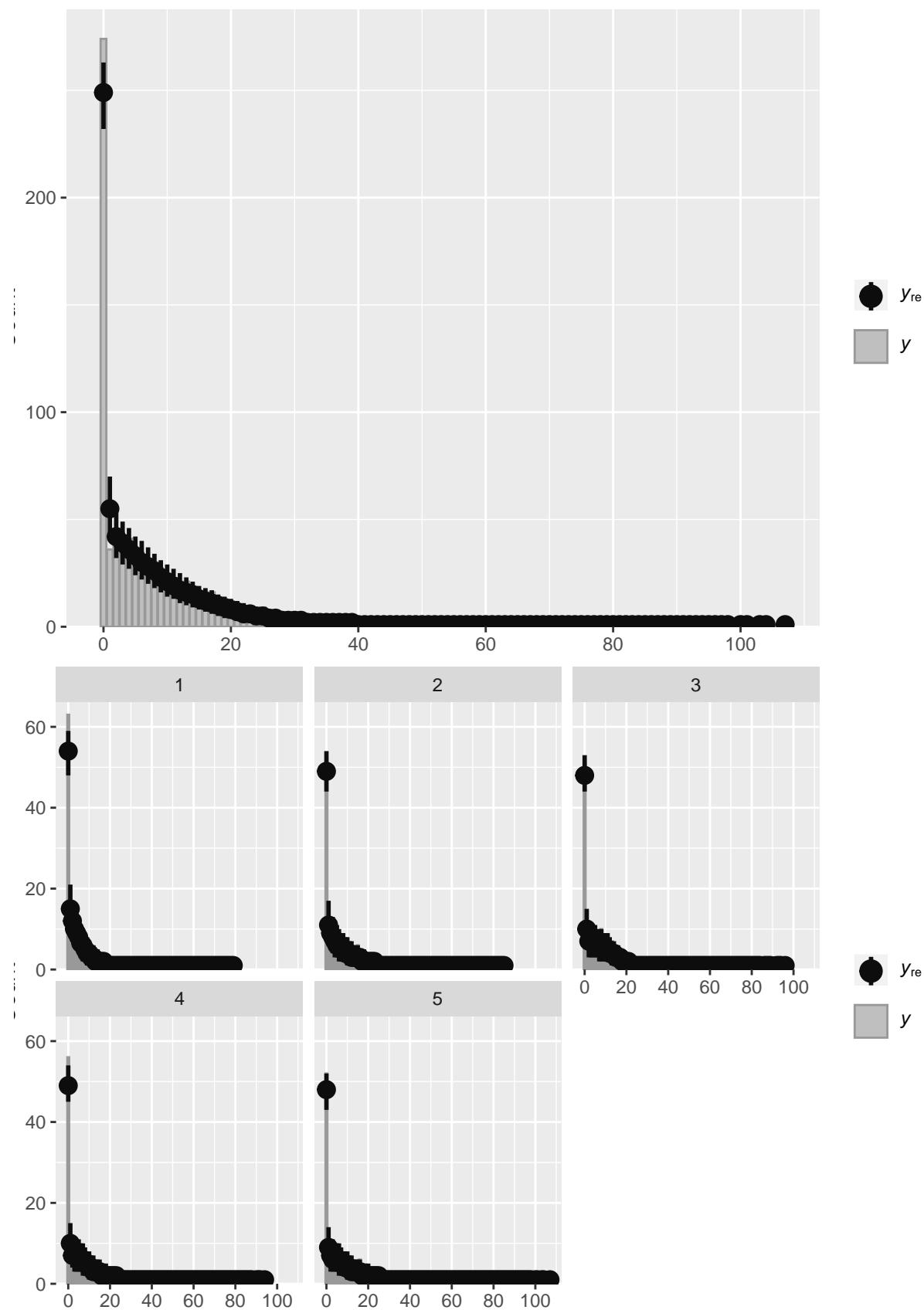


RMSE of posterior predictive

```
## [1] 5.070722
```

Posterior predictive check for each visit





RMSE of posterior predictive for observations per visit

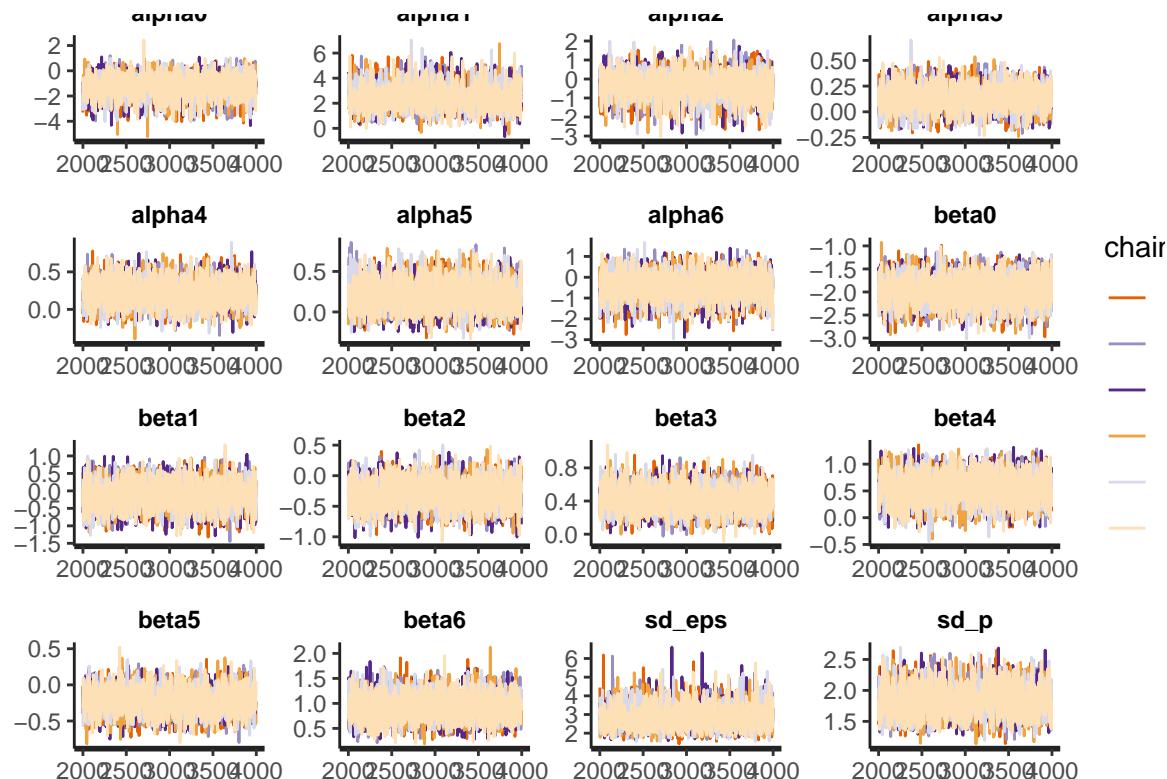
```
## [1] 2.956443
```

RMSE of posterior predictive

```
## [1] 1.322162
```

### *Desmognathus wrighti*

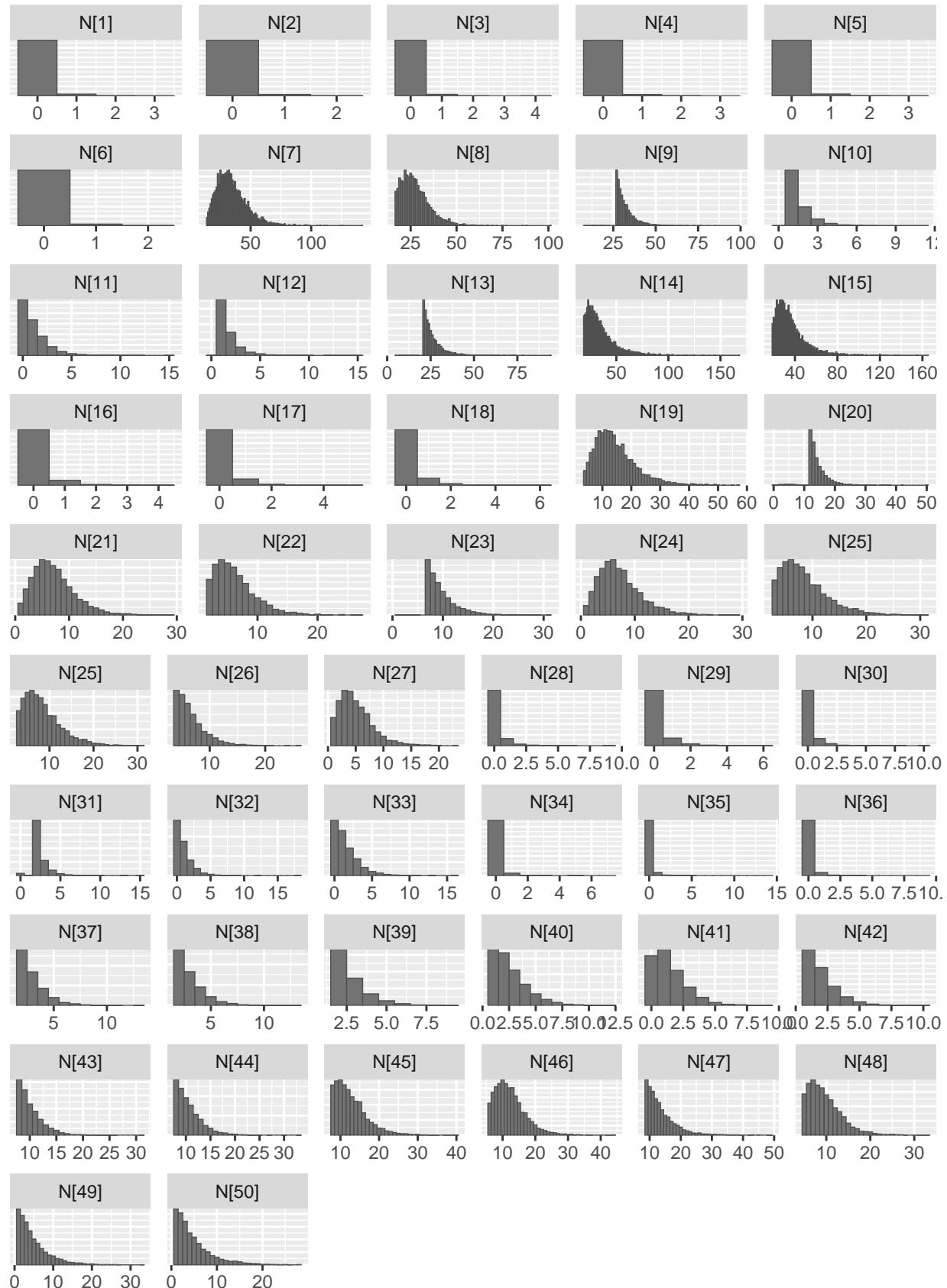
#### View Traceplots

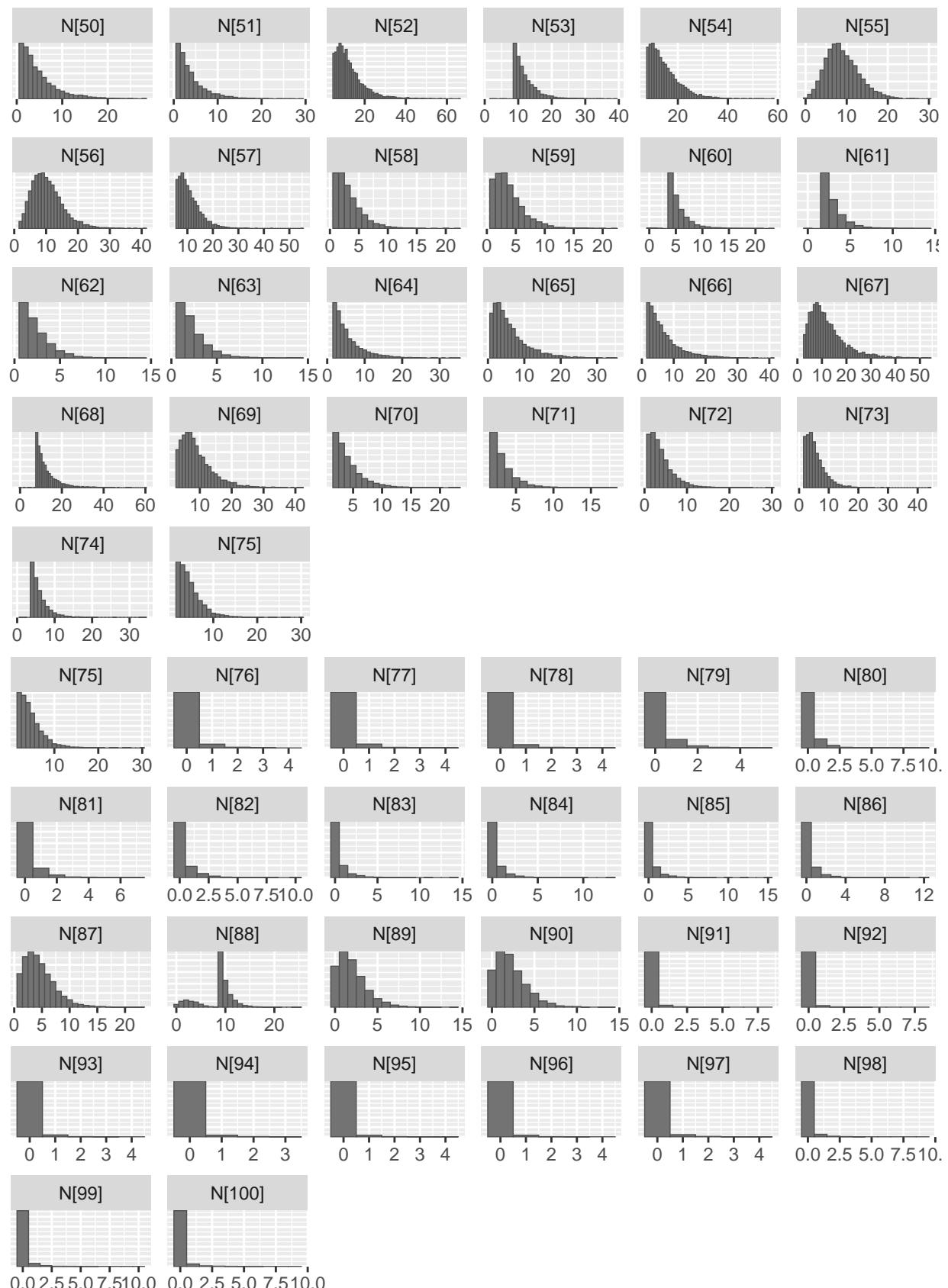


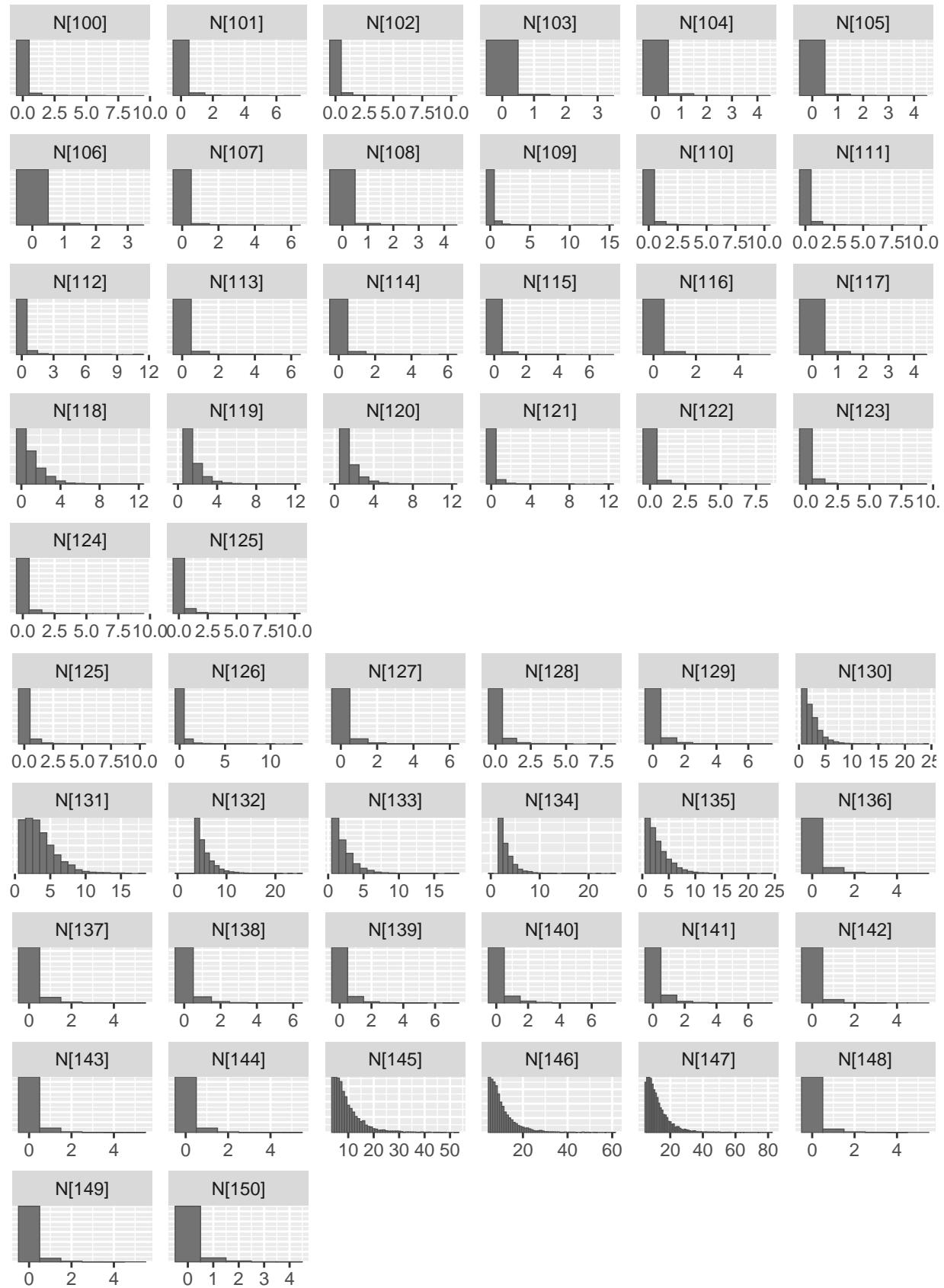
#### Check Domain Specific Expectations

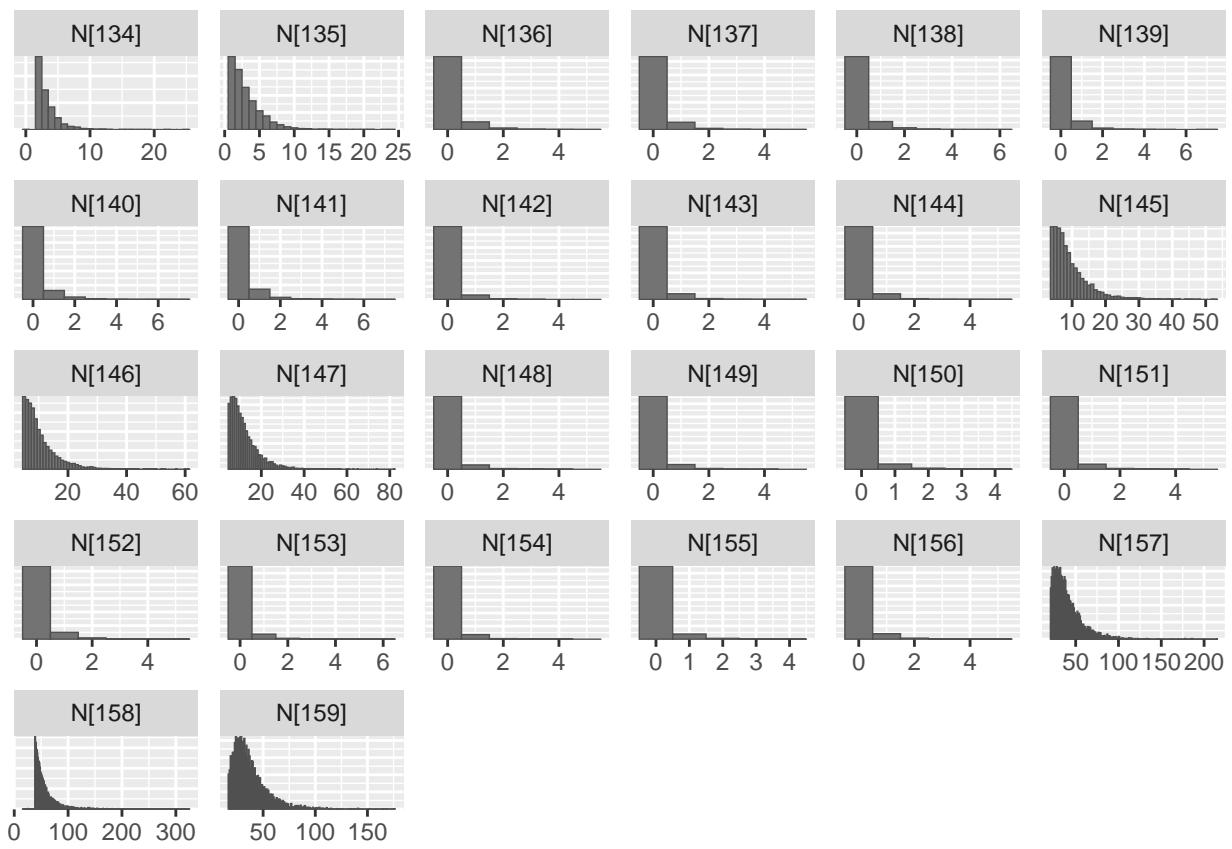
##### Check N for Truncation

The augmentation to marginalize N out as a latent discrete requires setting an upper bound, K, to loop through. If K is too small the posterior will be truncated. Need to check for every N.





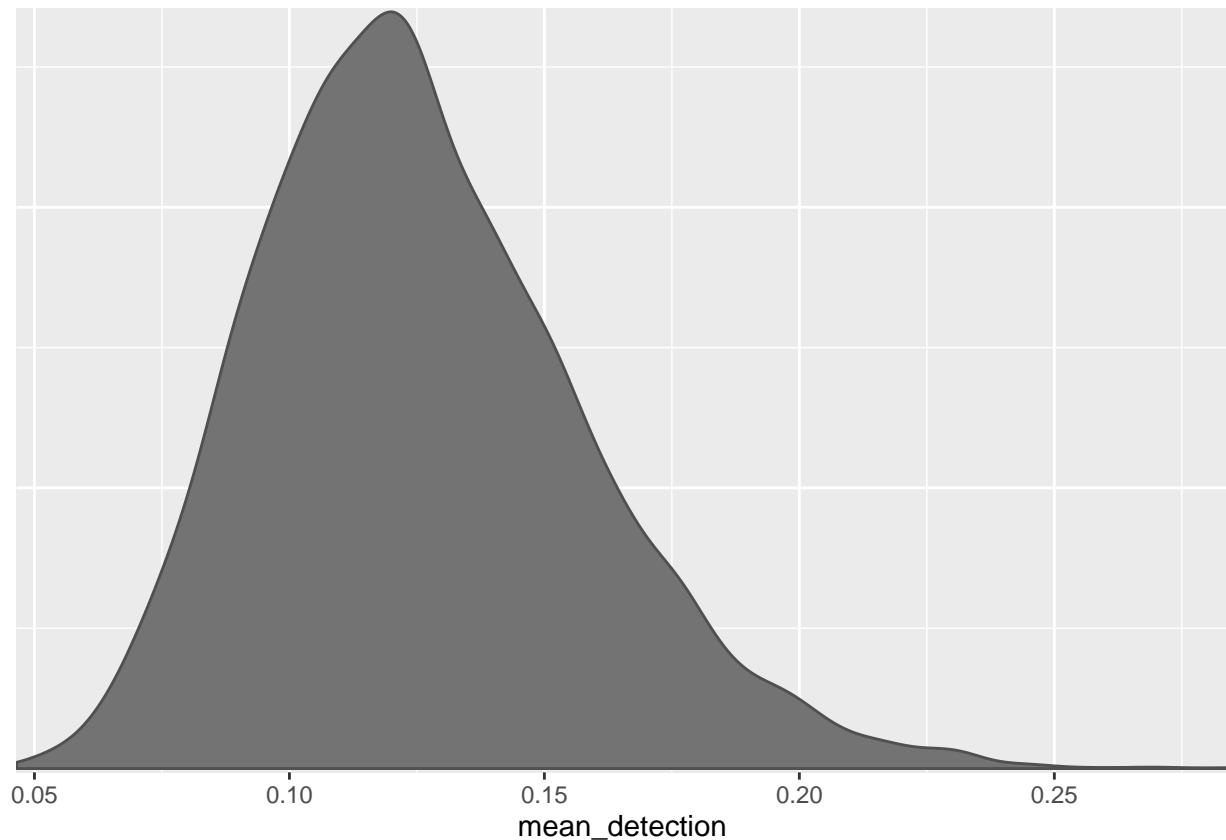




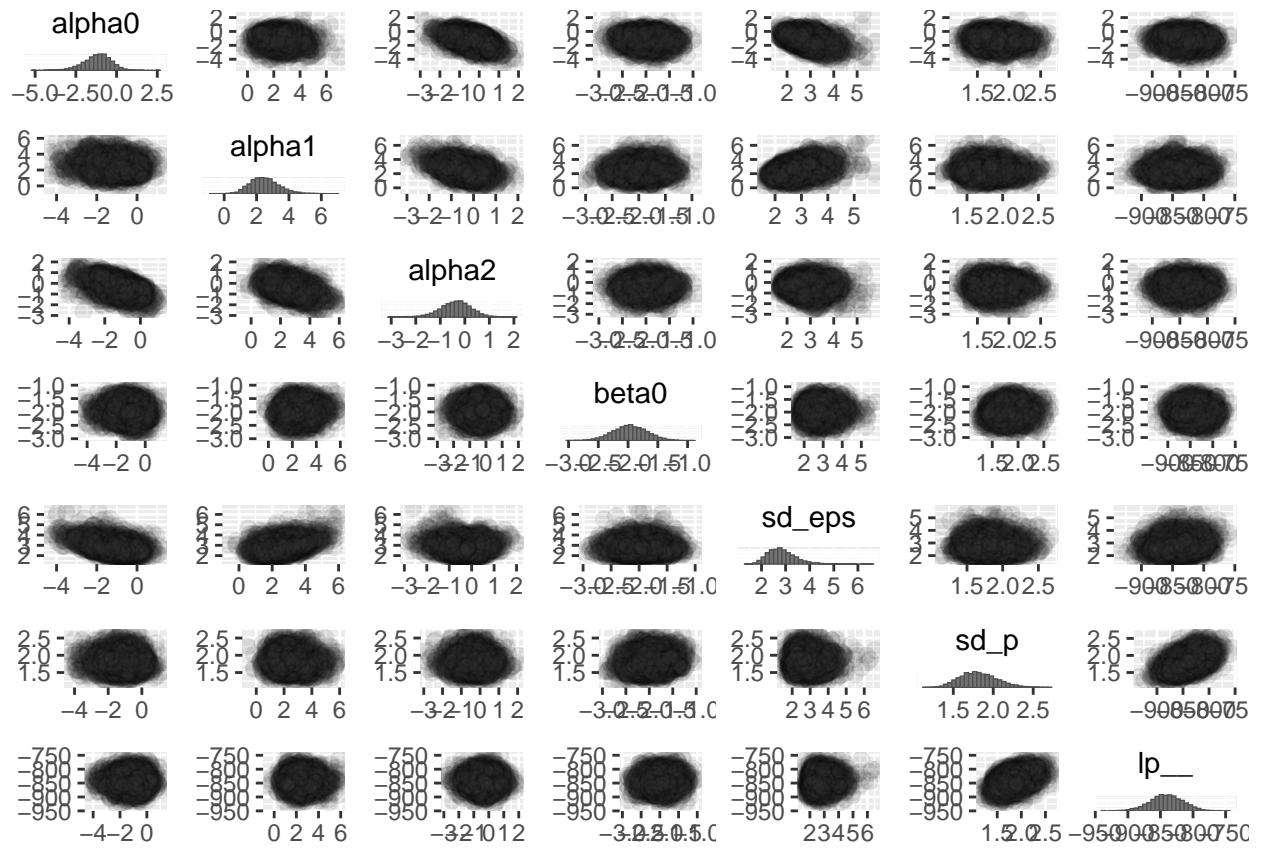
```
## null device
##          1
```

Check detection

In simulations abundance estimates are unreliable when detection gets below 20%



## Check Divergences and Pairwise Correlations



## Check Energy and Treedepth

### Summarize Samples Sizes and Mixing

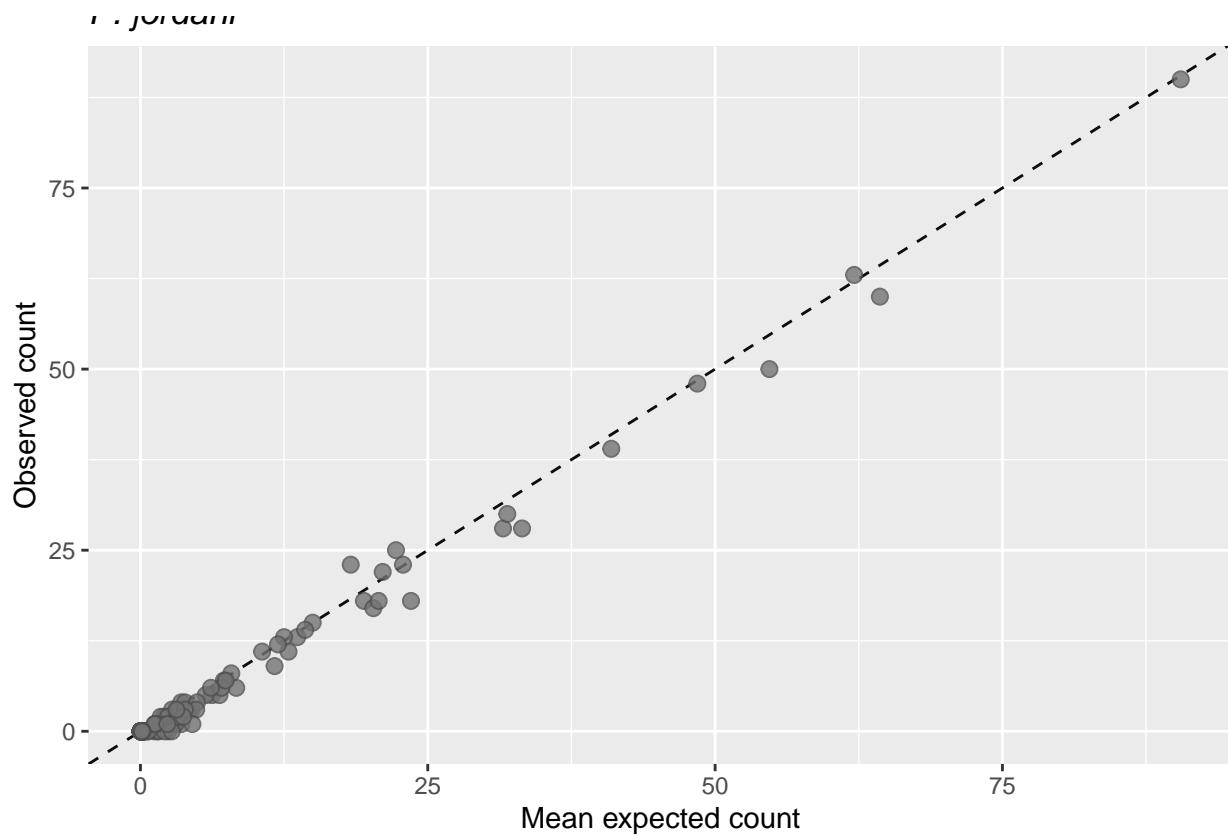
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effective sample sizes (should be > 100) - Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2019). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC. arXiv preprint arXiv:1903.08008.

```
## [1] 1.00399
## [1] 2346
## [1] 2987
```

## Posterior Predictive Checks

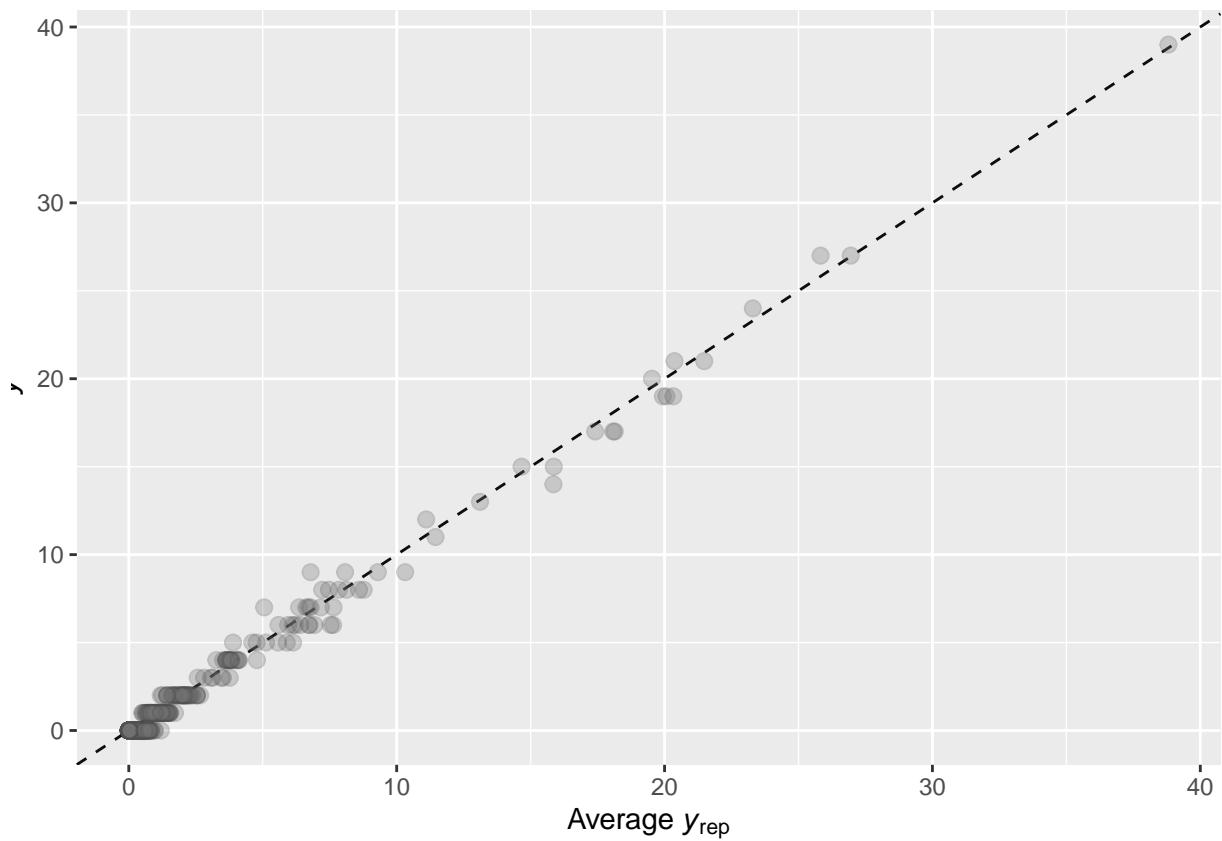
Examine posterior predictions of total counts across all 5 visits



RMSE of posterior predictive

```
## [1] 1.315241
```

Posterior predictive check for each visit



RMSE of posterior predictive for observations per visit

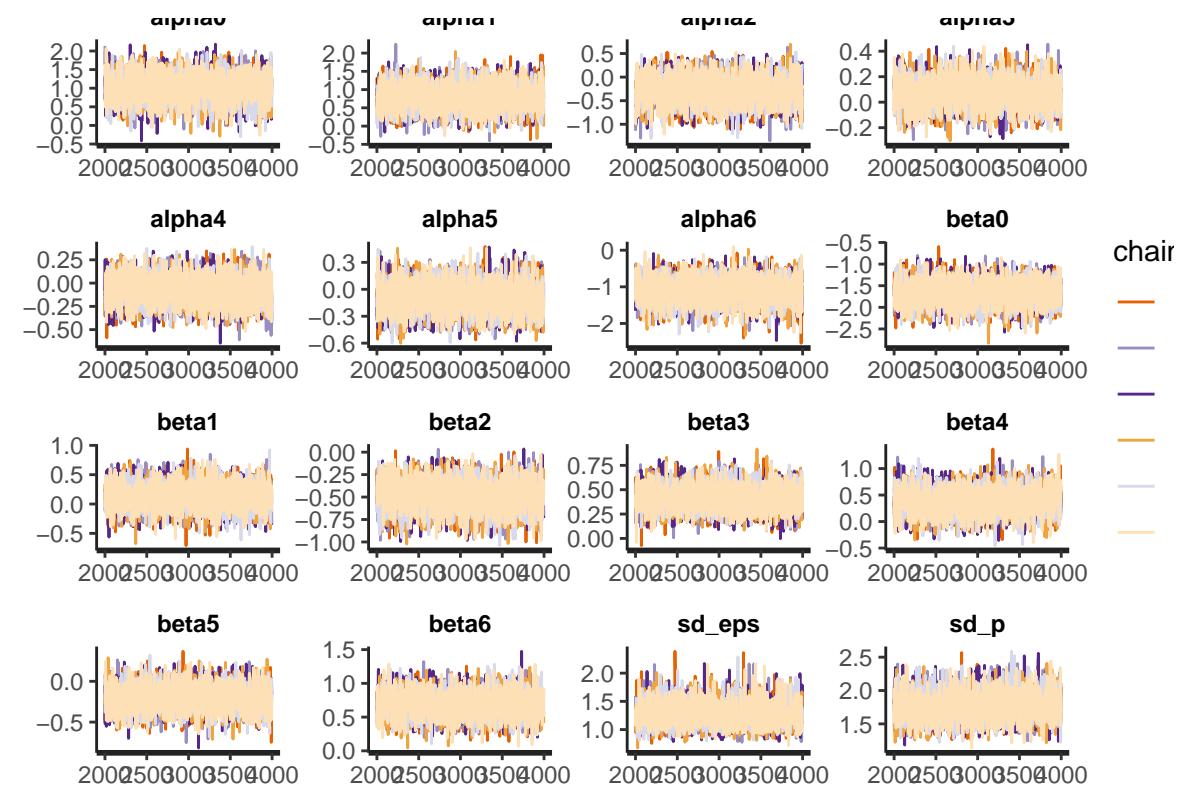
```
## [1] 0.7504749
```

RMSE of posterior predictive

```
## [1] 0.3356226
```

## *Eurycea wilderae*

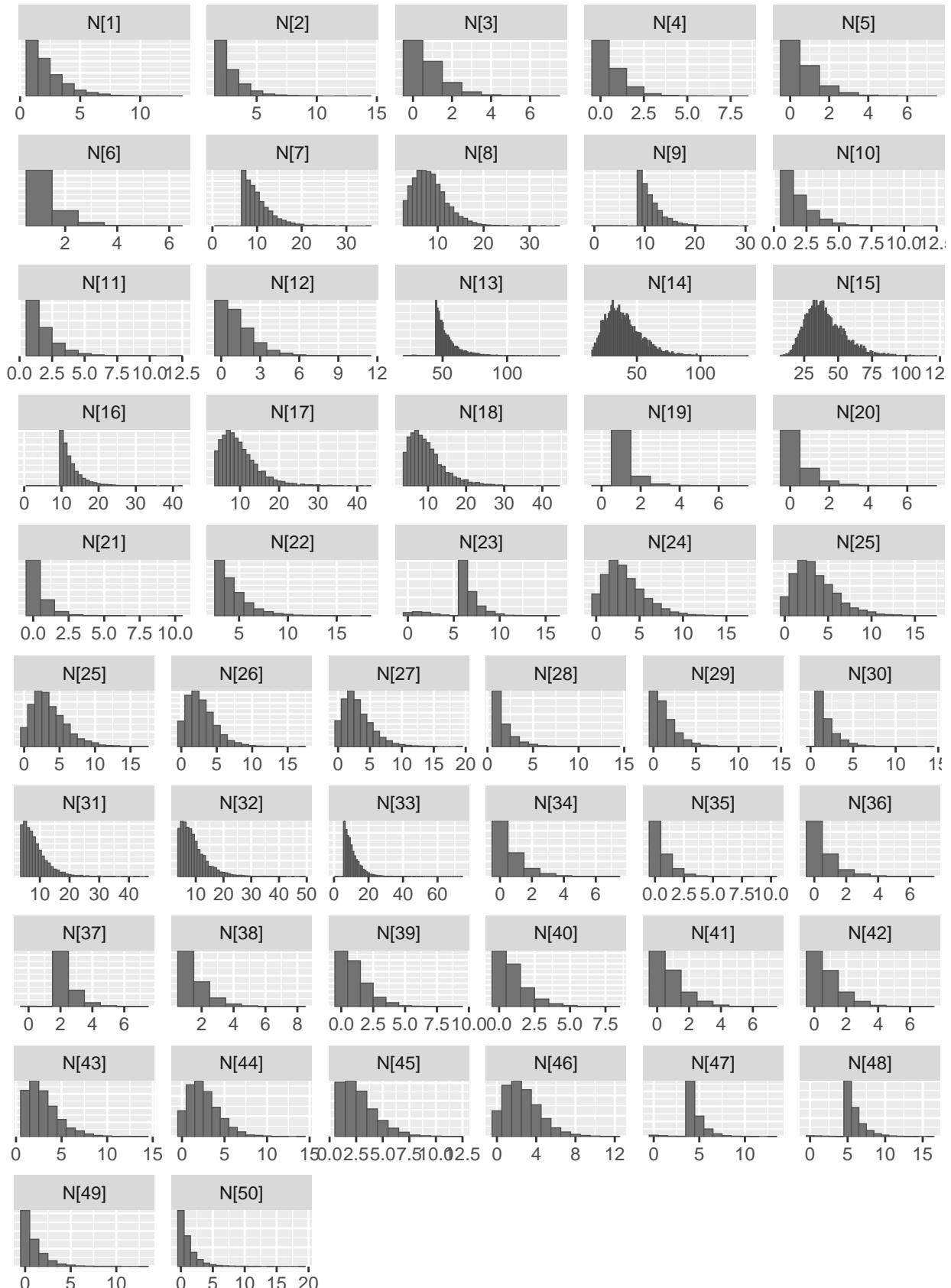
### View Traceplots

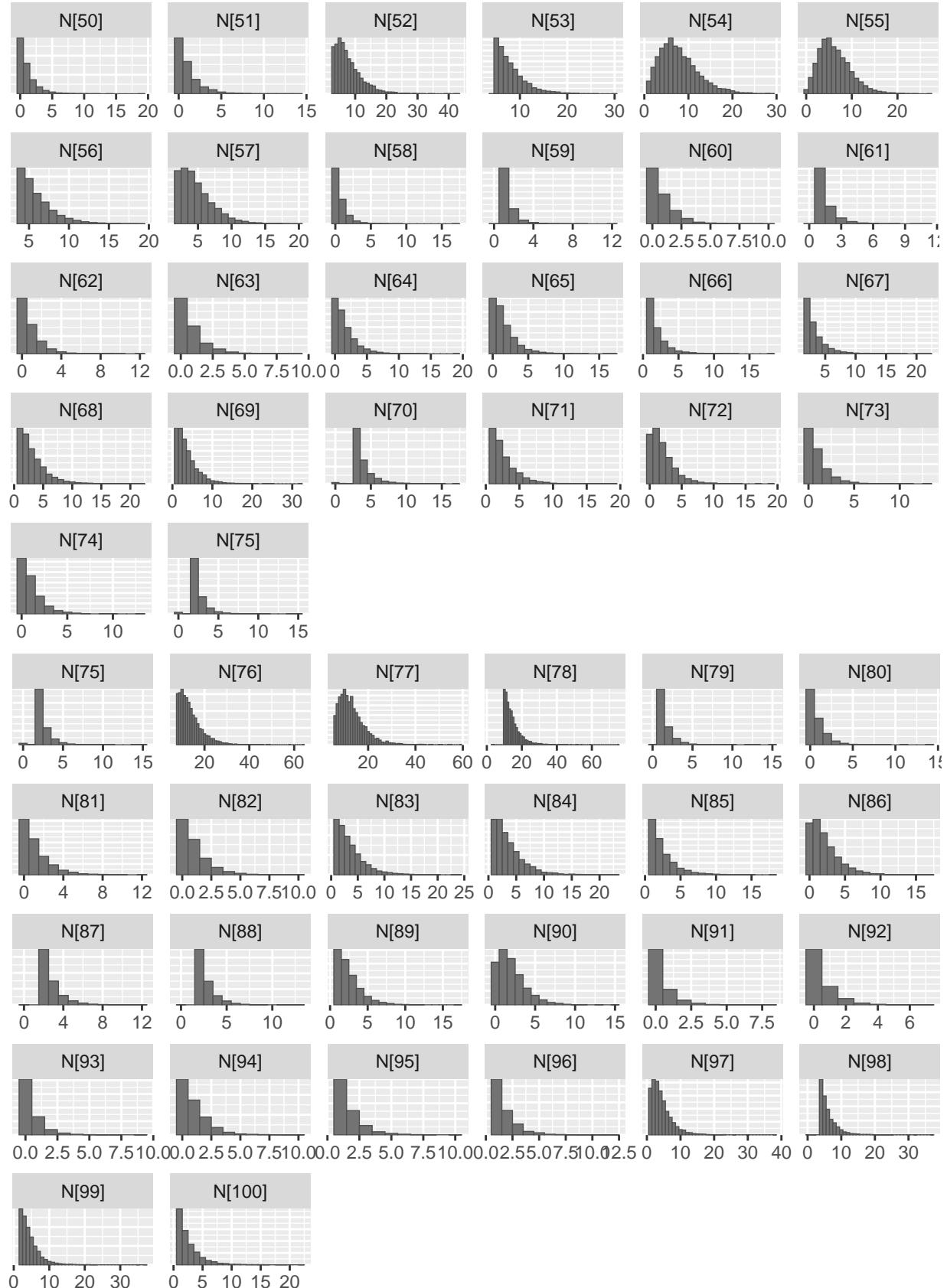


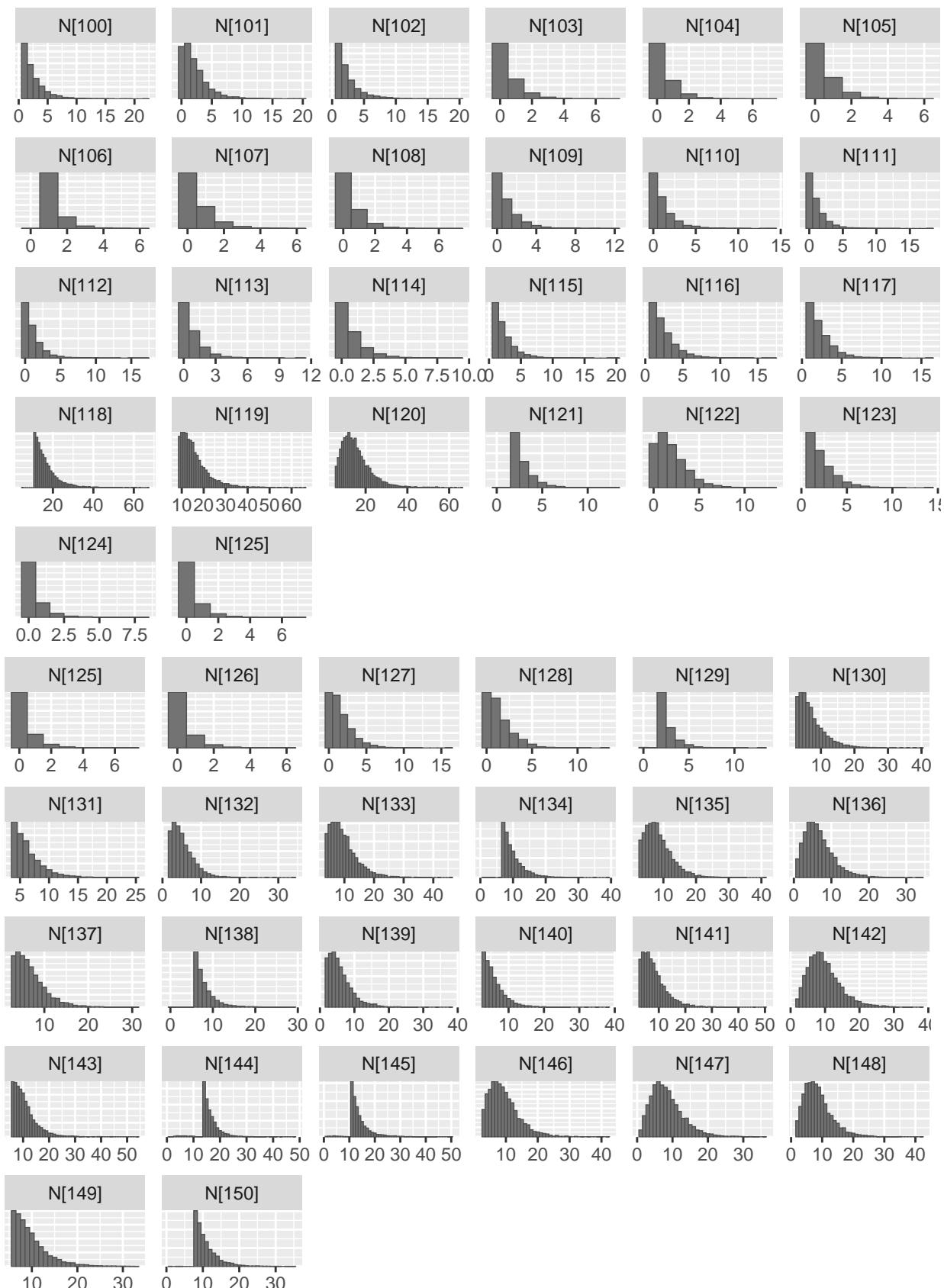
### Check Domain Specific Expectations

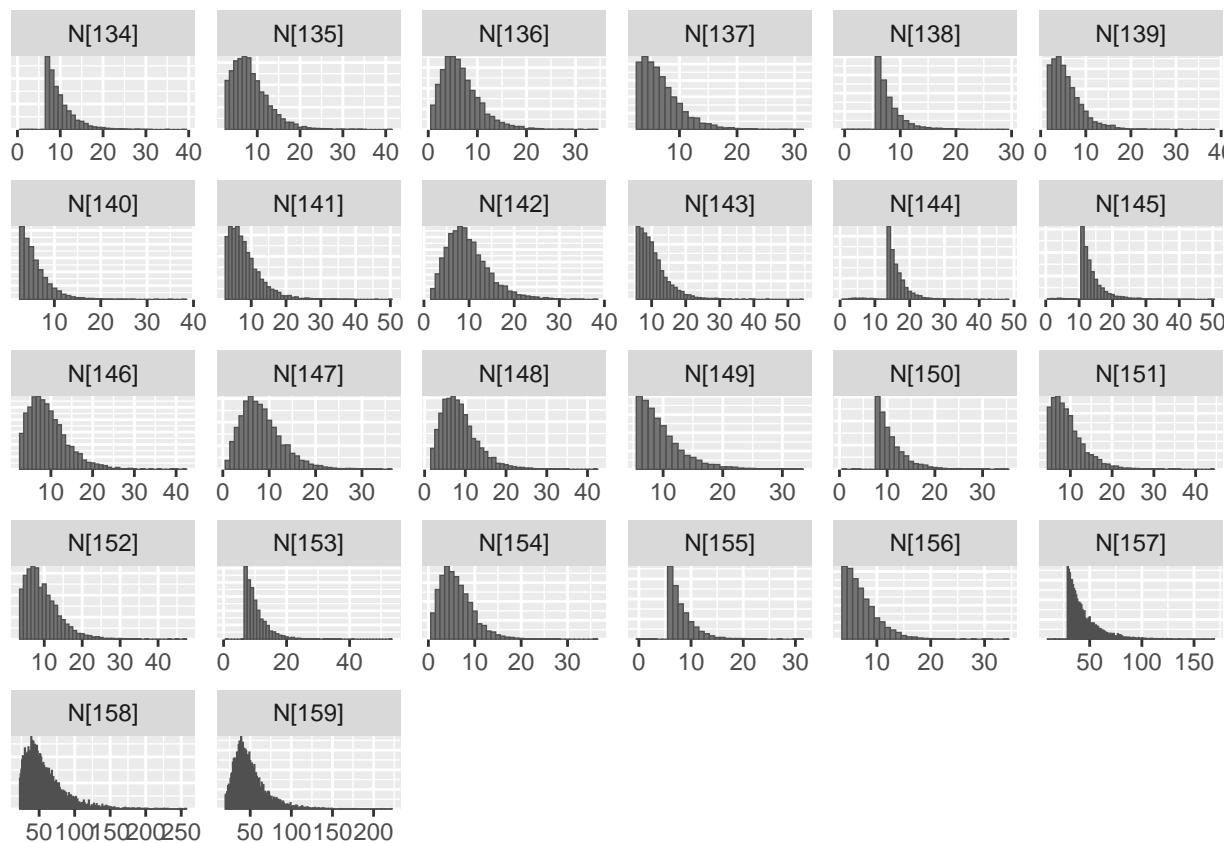
#### Check N for Truncation

The augmentation to marginalize N out as a latent discrete requires setting an upper bound, K, to loop through. If K is too small the posterior will be truncated. Need to check for every N.





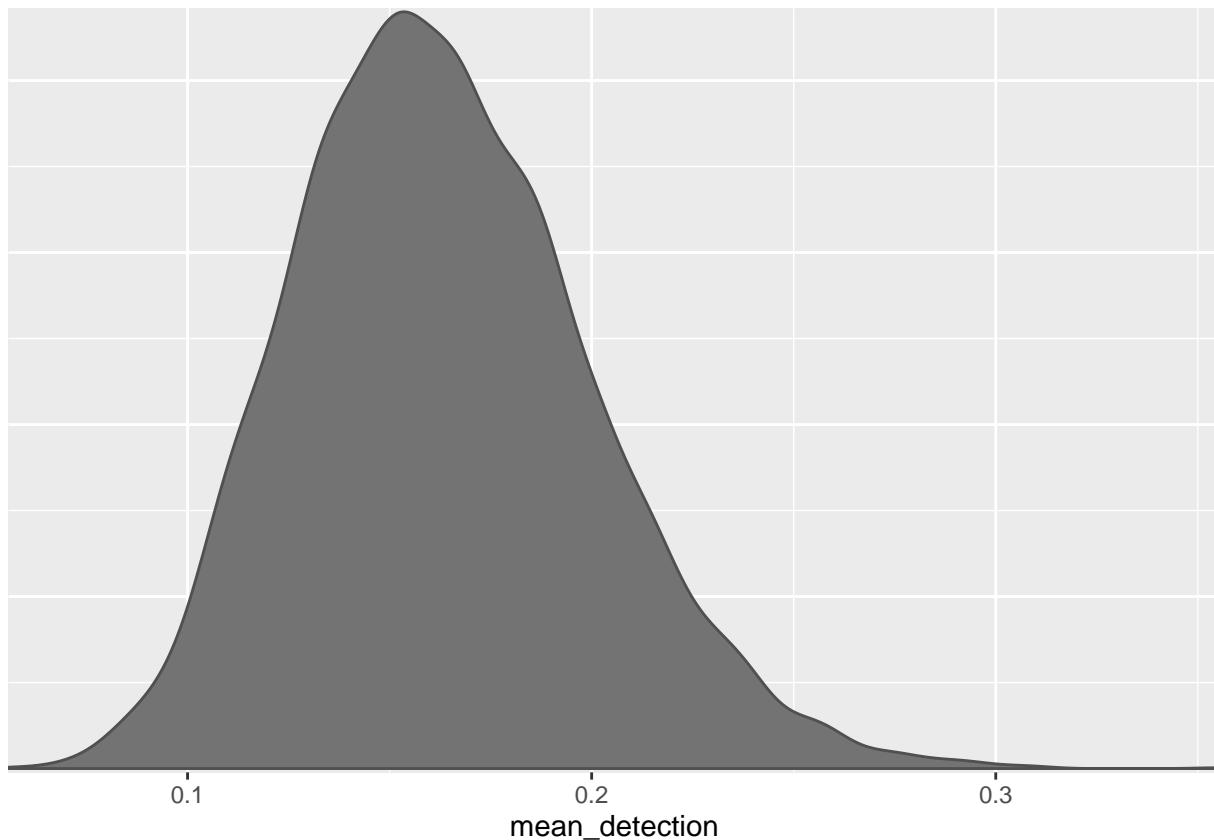




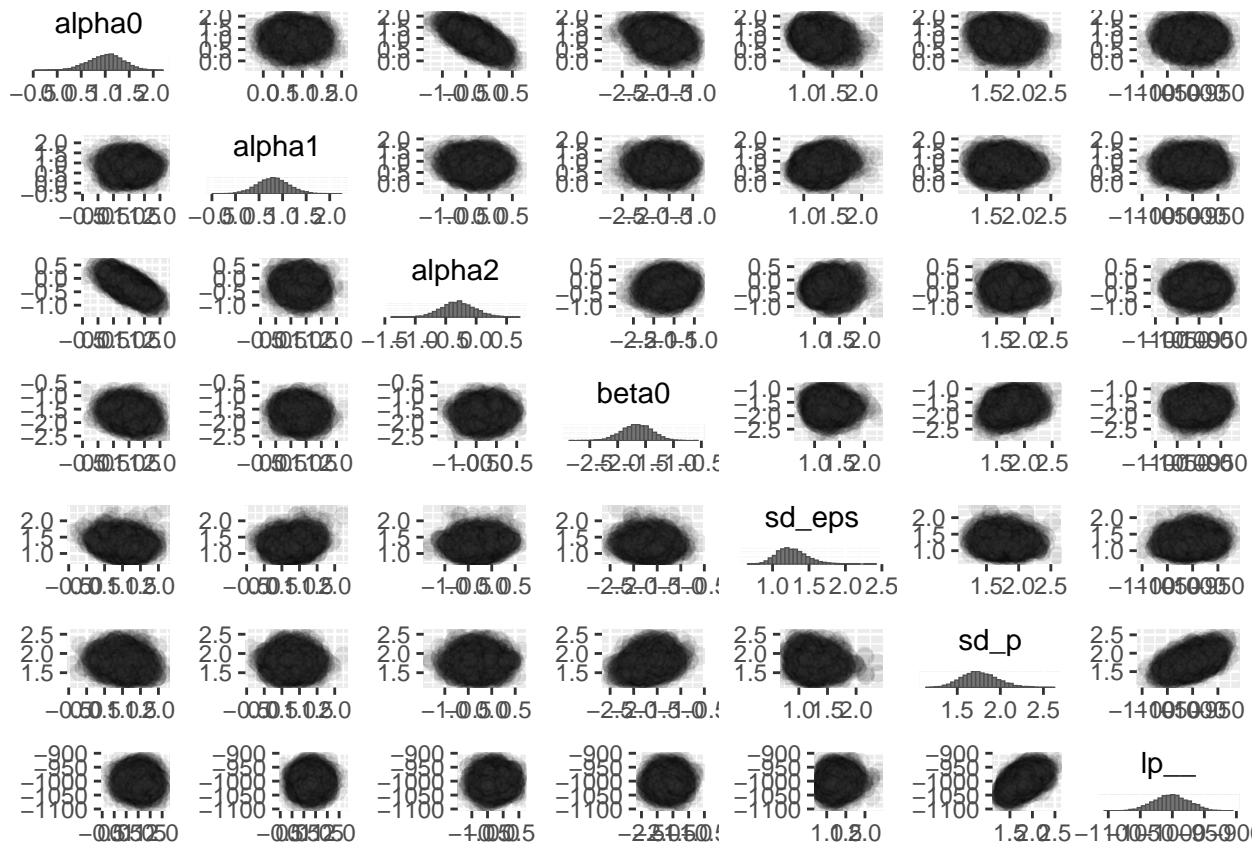
```
## null device
##          1
```

Check detection

In simulations abundance estimates are unreliable when detection gets below 20%



## Check Divergences and Pairwise Correlations



## Check Energy and Treedepth

### Summarize Samples Sizes and Mixing

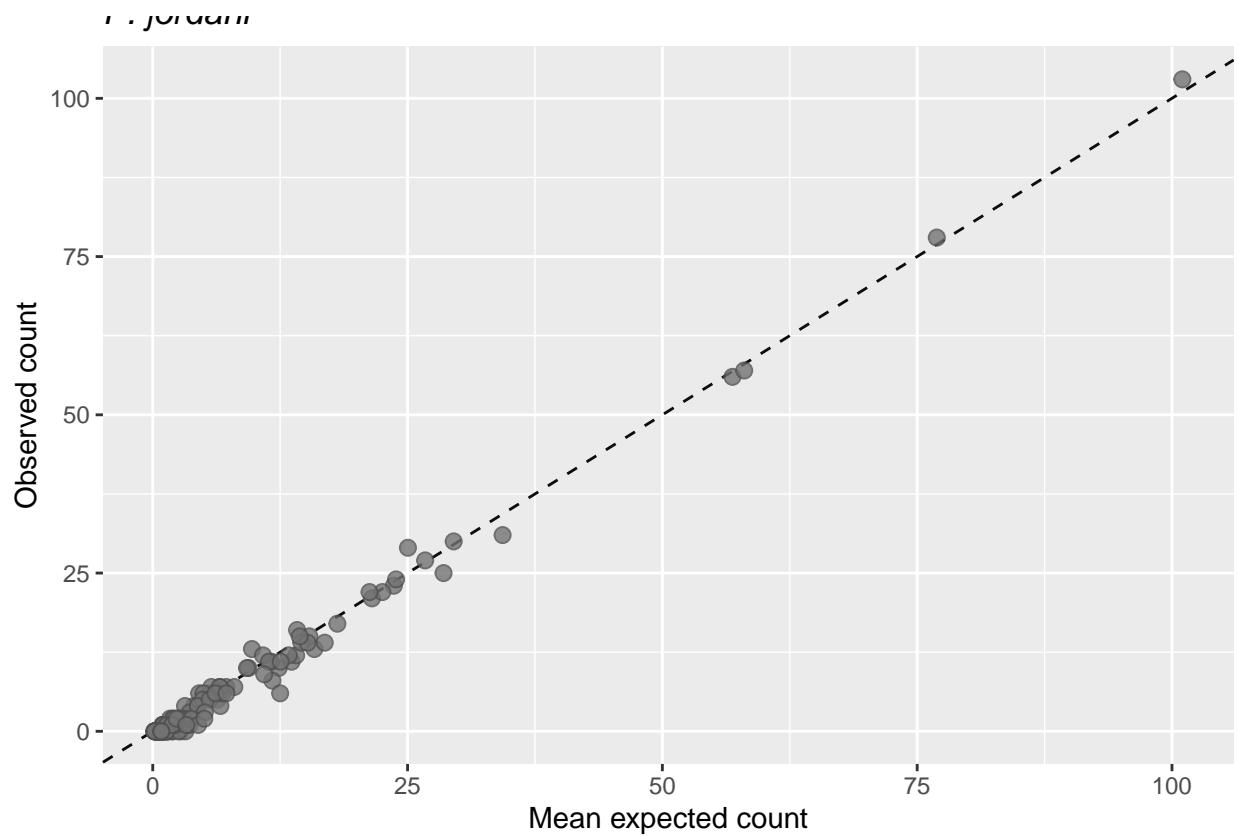
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```
## [1] 1.003496
## [1] 2495
## [1] 3415
```

## Posterior Predictive Checks

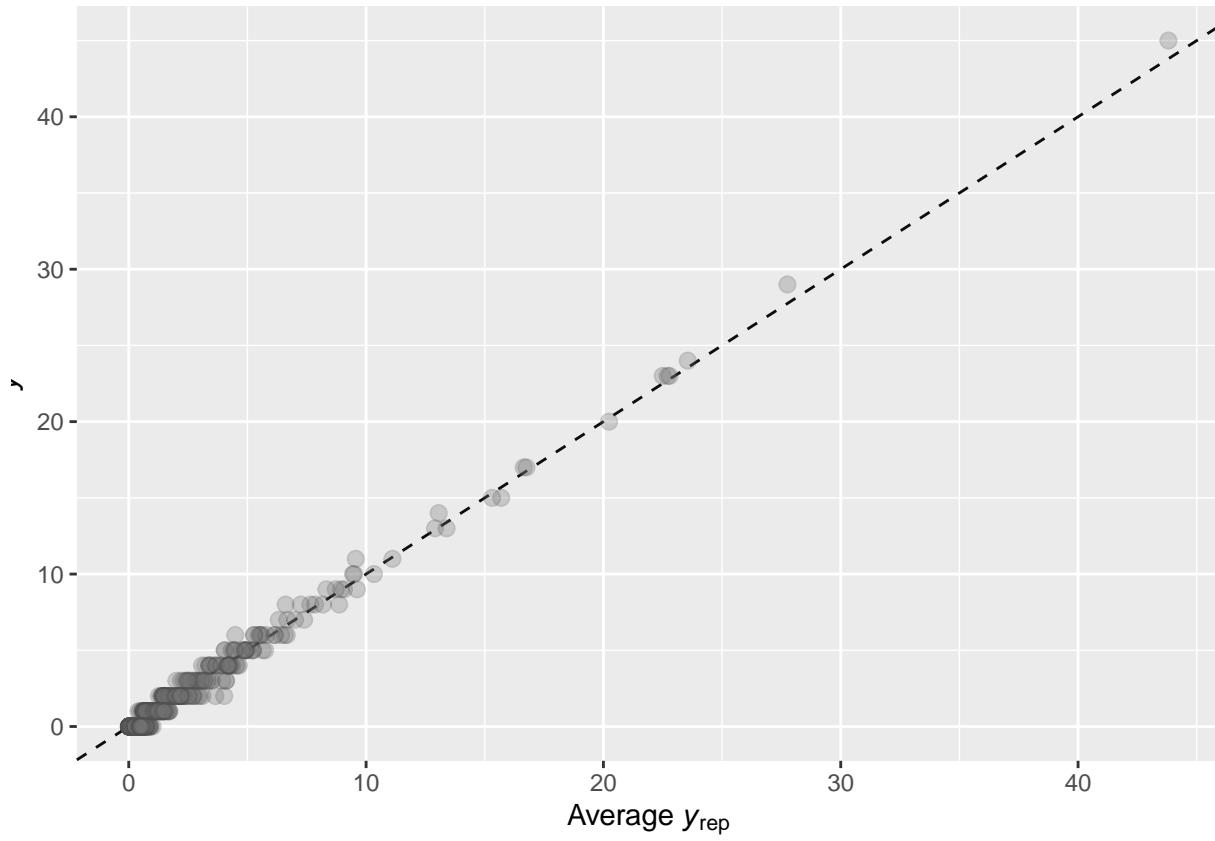
Examine posterior predictions of total counts across all 5 visits



RMSE of posterior predictive

```
## [1] 1.404227
```

Posterior predictive check for each visit



RMSE of posterior predictive for observations per visit

```
## [1] 0.8349771
```

RMSE of posterior predictive

```
## [1] 0.3734131
```