

# MCMC Convergence Report

## Condition 002

Simulation Parameters:

T=500 | A1=-9 | A2=9 | Cop=Clayton | Tau=0.4

VAR Coefficients: phi11=0.50, phi12=0.30, phi21=0.30, phi22=0.50

Interpretation Guide:

- \* Divergences: Should be 0 (numerical issues if present)
  - \* E-FMI: Should be > 0.3 for efficient sampling
- \* R-hat: Should be < 1.05 for reliable chain convergence
  - \* N\_eff: Should be > 400 for key parameters
- \* Accept Stat: Should be near adapt\_delta (often 0.99)

## **Convergence Summary & Parameter Diagnostics**

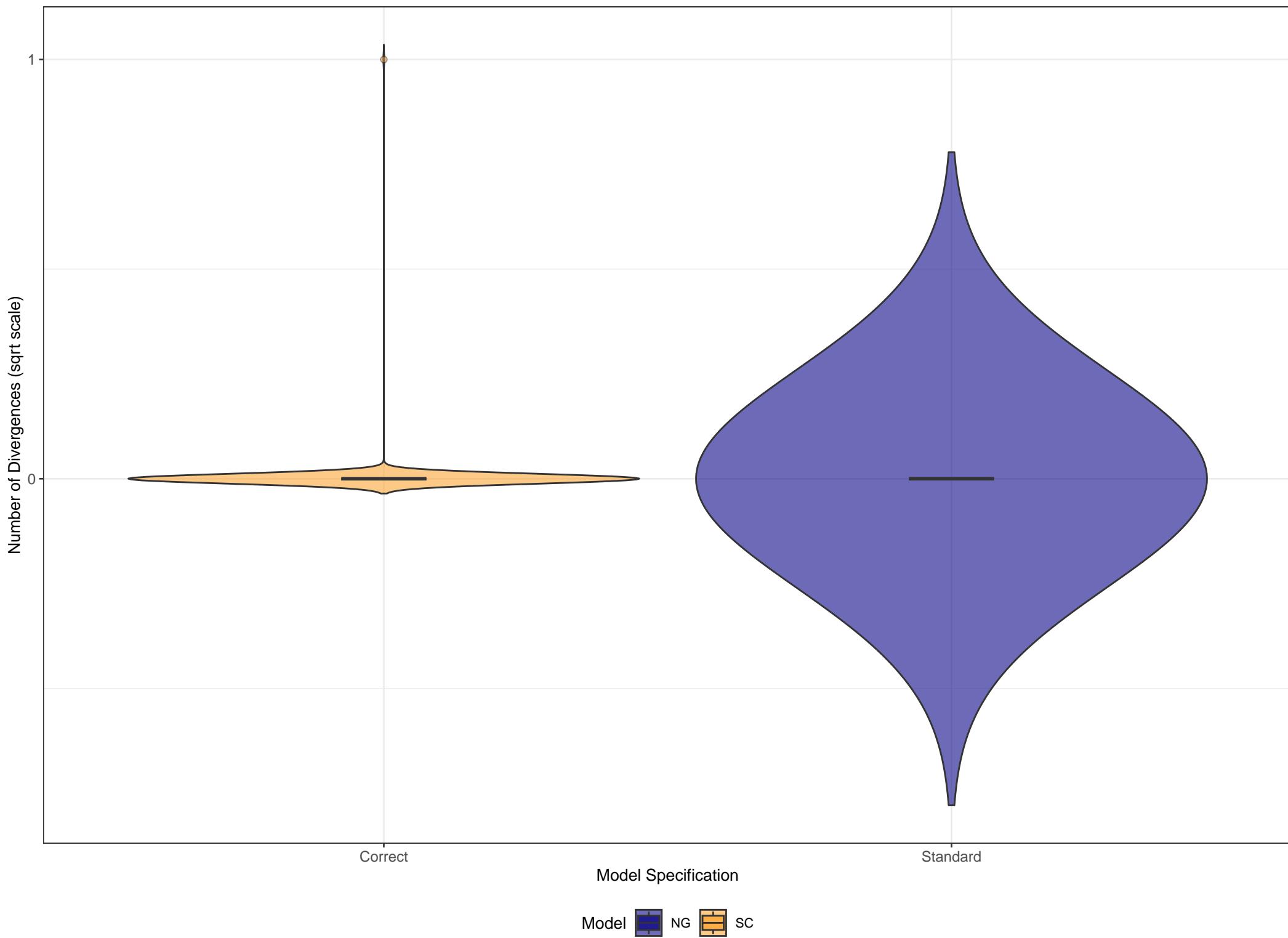
<b>Model</b>	<b>Divergences</b>	<b>% with Divergences</b>	<b>E-FMI</b>	<b>Min E-FMI</b>	<b>Avg R-hat</b>	<b>Max R-hat</b>	<b>Median N_eff</b>	<b>Accept Stat</b>
1 NG (Standard)	N/A	0.0% [GOOD]	0.500 [GOOD]	0.485 [GOOD]	1.000 [GOOD]	1.003 [GOOD]	4386	0.989 [GOOD]
2 SC (Correct)	1 [WARNING]	0.2% [WARNING]	0.498 [GOOD]	0.487 [GOOD]	1.000 [GOOD]	1.017 [WARNING]	4812	0.989 [GOOD]

	<b>Parameter Group</b>	<b>Model</b>	<b>Avg R-hat</b>	<b>% R-hat &gt; 1.05</b>	<b>Median N_eff</b>	<b>Min N_eff</b>
1	Copula Params	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6187	4435
2	Copula Params	SC (Correct)	1.000 [GOOD]	0.0% [GOOD]	5296	4150
3	Intercepts	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6129	4526
4	Intercepts	SC (Correct)	1.000 [GOOD]	0.0% [GOOD]	4713	3246
5	Other	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	4007	2633
6	Other	SC (Correct)	1.000 [GOOD]	0.0% [GOOD]	4748	1648
7	Residual Params	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6482	4672
8	Residual Params	SC (Correct)	1.000 [GOOD]	0.0% [GOOD]	4695	179
9	VAR Coeffs	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	4141	2869
10	VAR Coeffs	SC (Correct)	1.000 [GOOD]	0.0% [GOOD]	4863	3044



## Divergent Transitions by Model Type

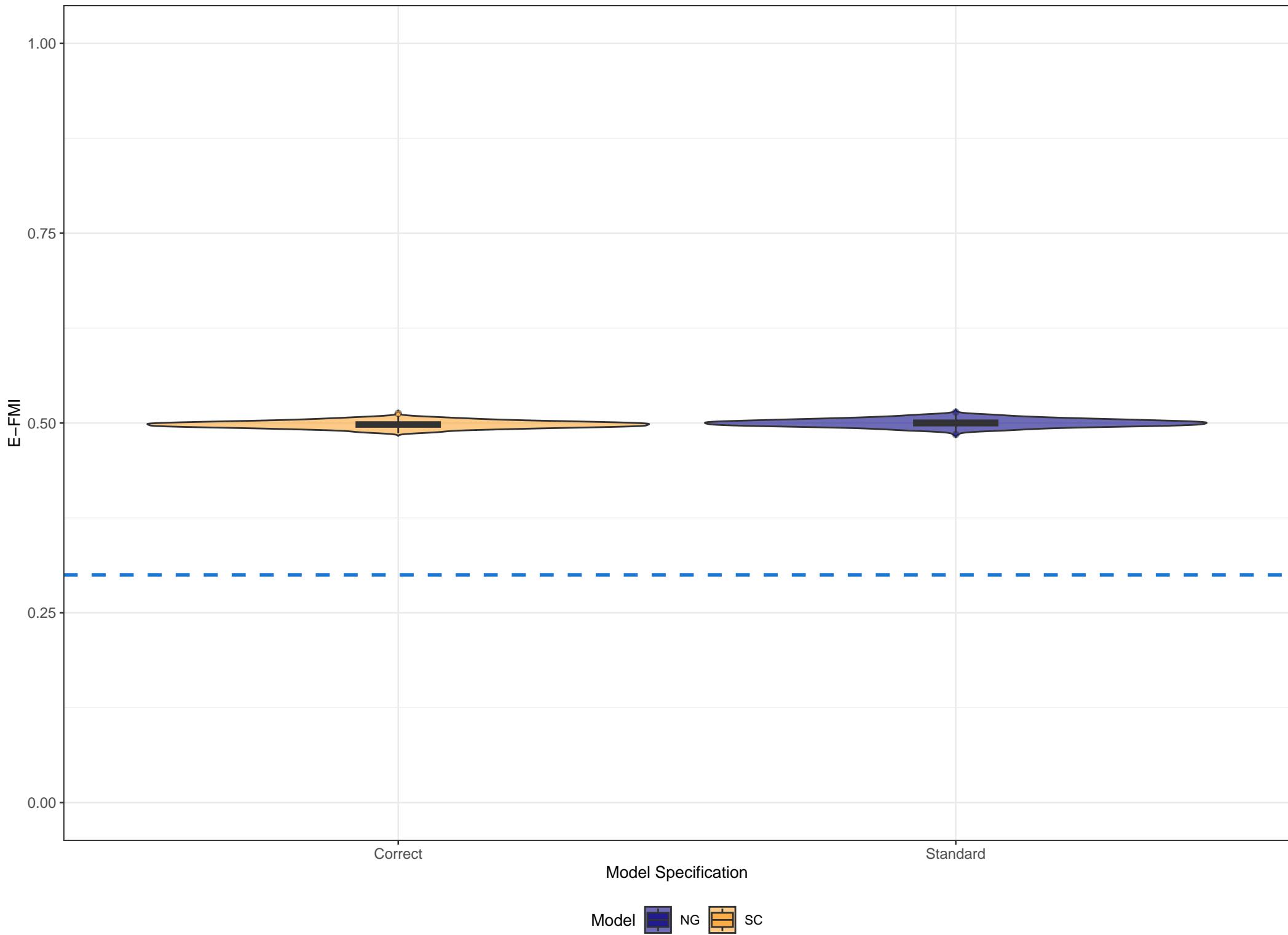
Lower is better (ideally zero). Distribution across replications (violin).





## Energy Fraction of Missing Information (E-FMI)

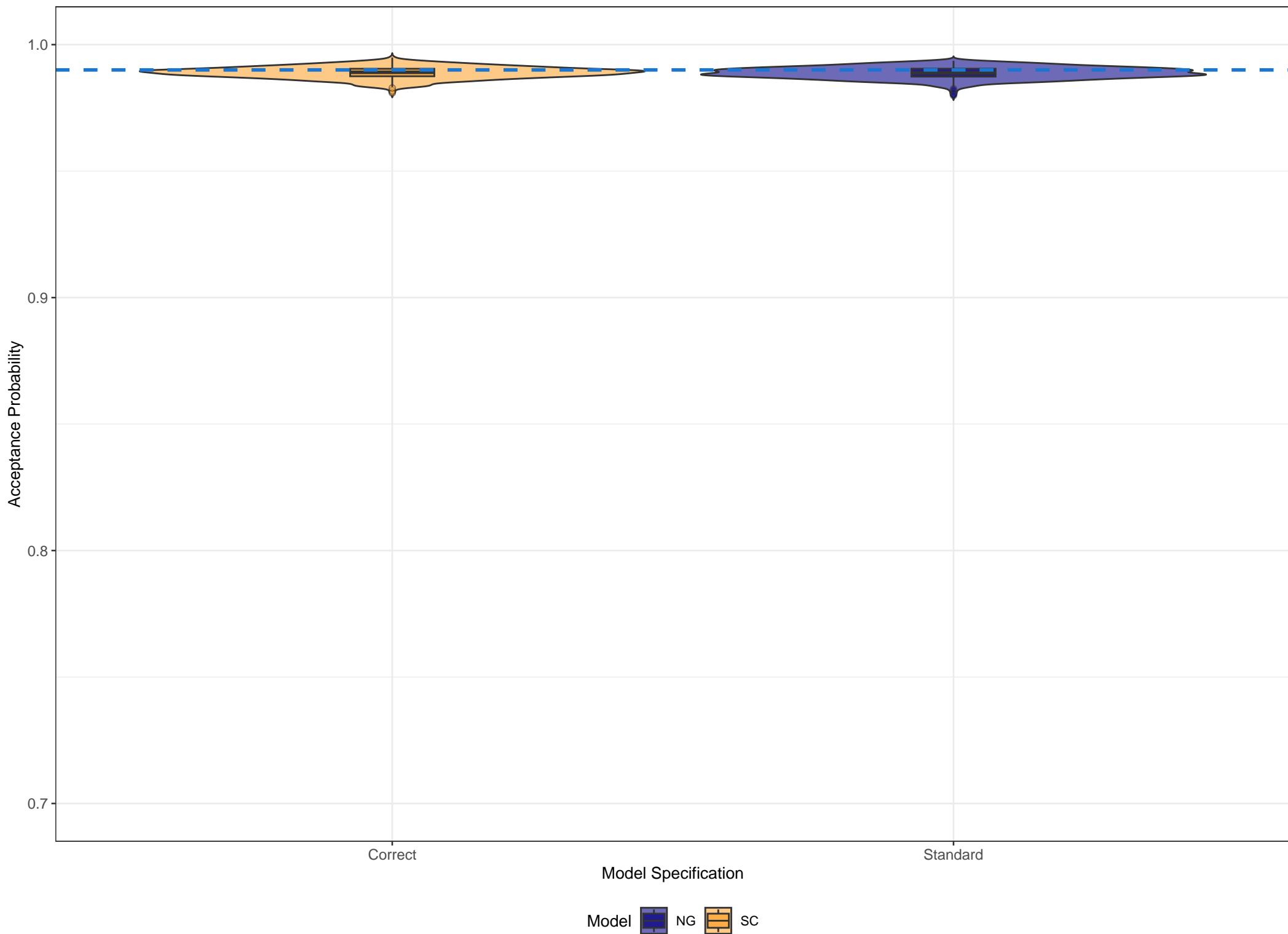
Should be above 0.3 (blue line) for efficient exploration.





## Average Acceptance Statistic

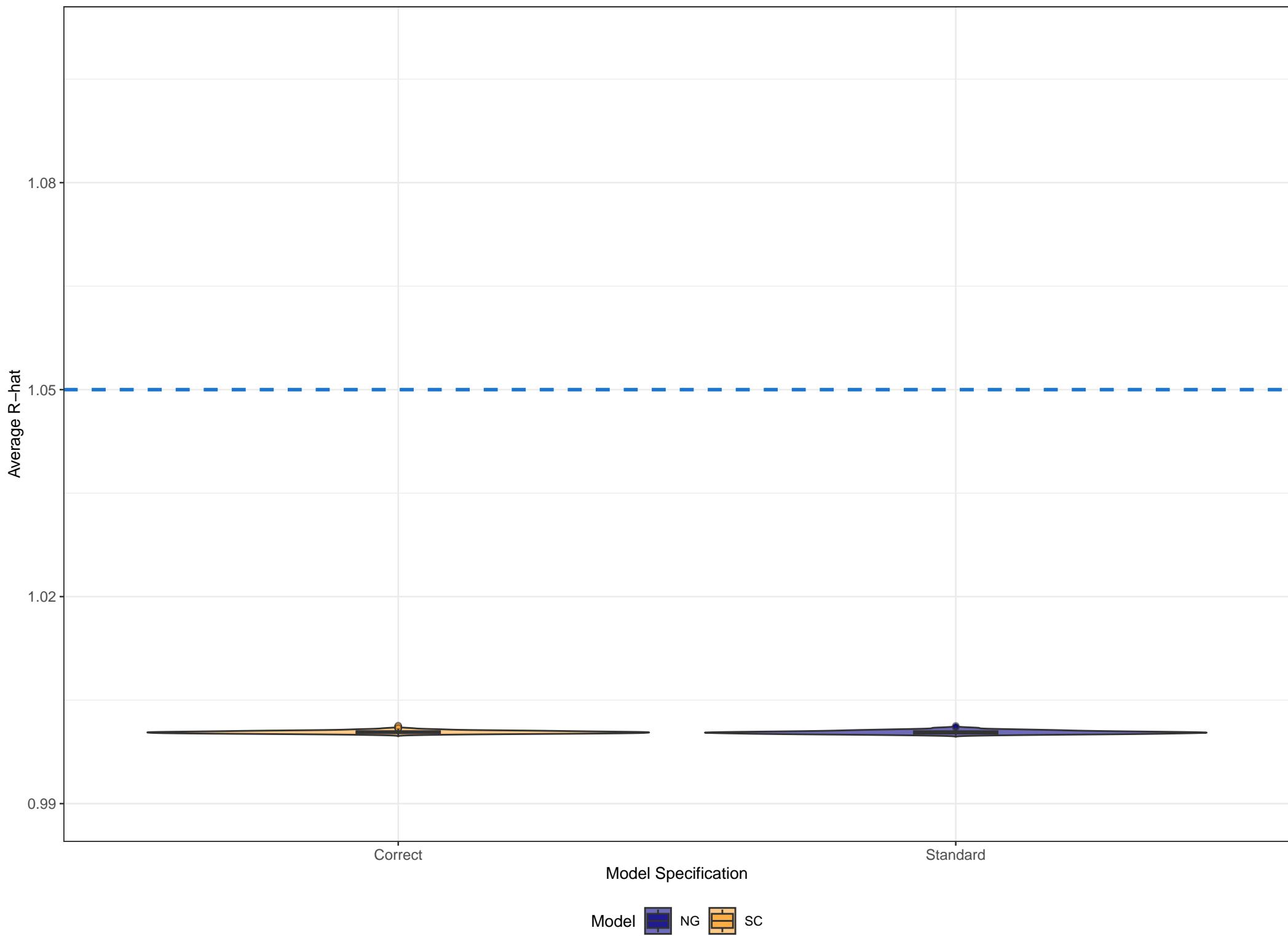
Target near 0.99 (blue line). Higher is generally better.





## Potential Scale Reduction Factor (R-hat)

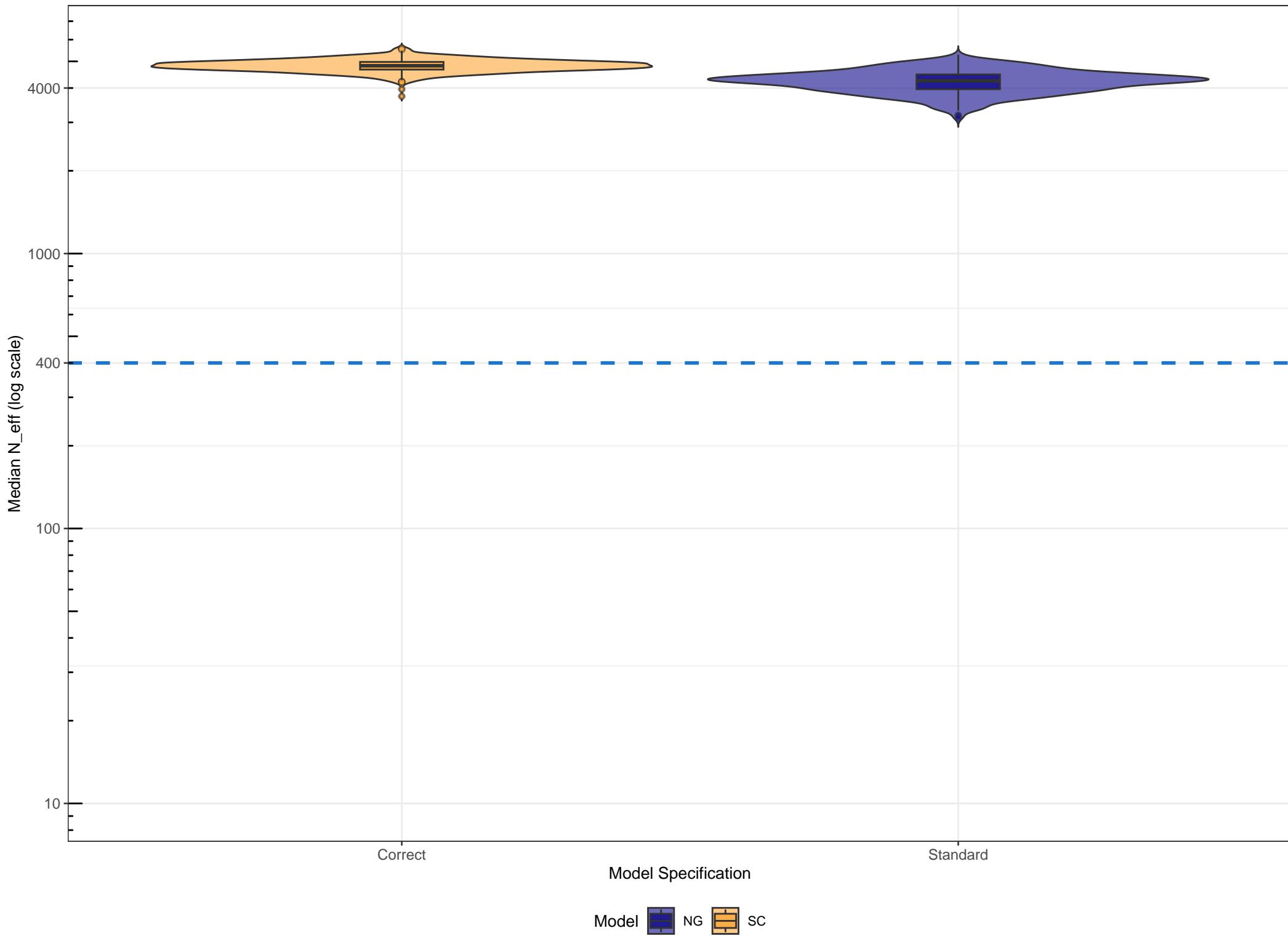
Should be  $< 1.05$  (blue line). Average R-hat across params per replication.





## Effective Sample Size (N\_eff)

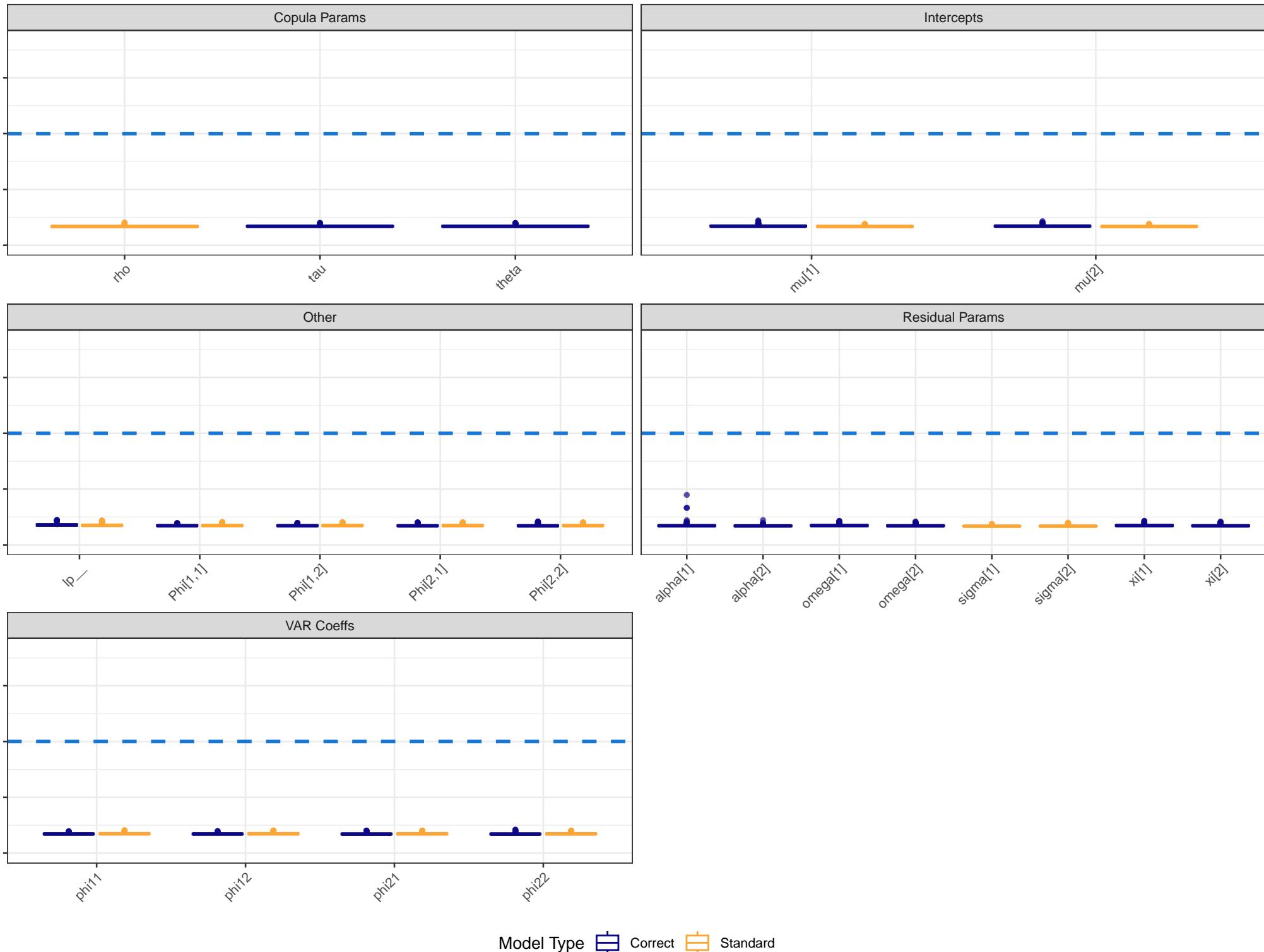
Higher is better; 400+ is a common guideline (blue line).





# R-hat by Parameter Category

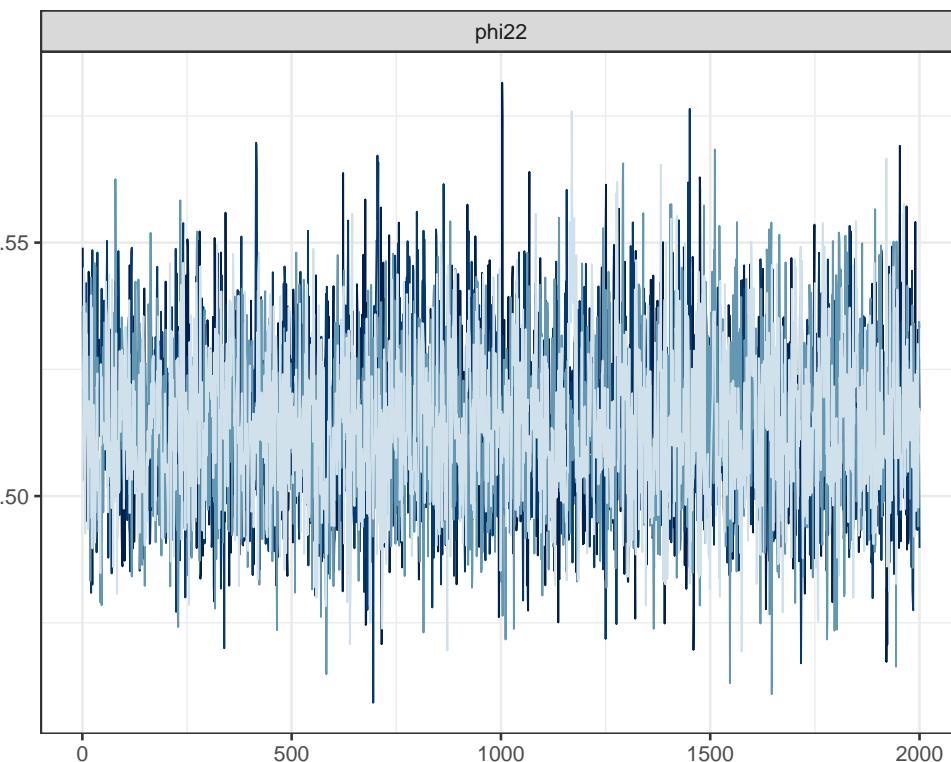
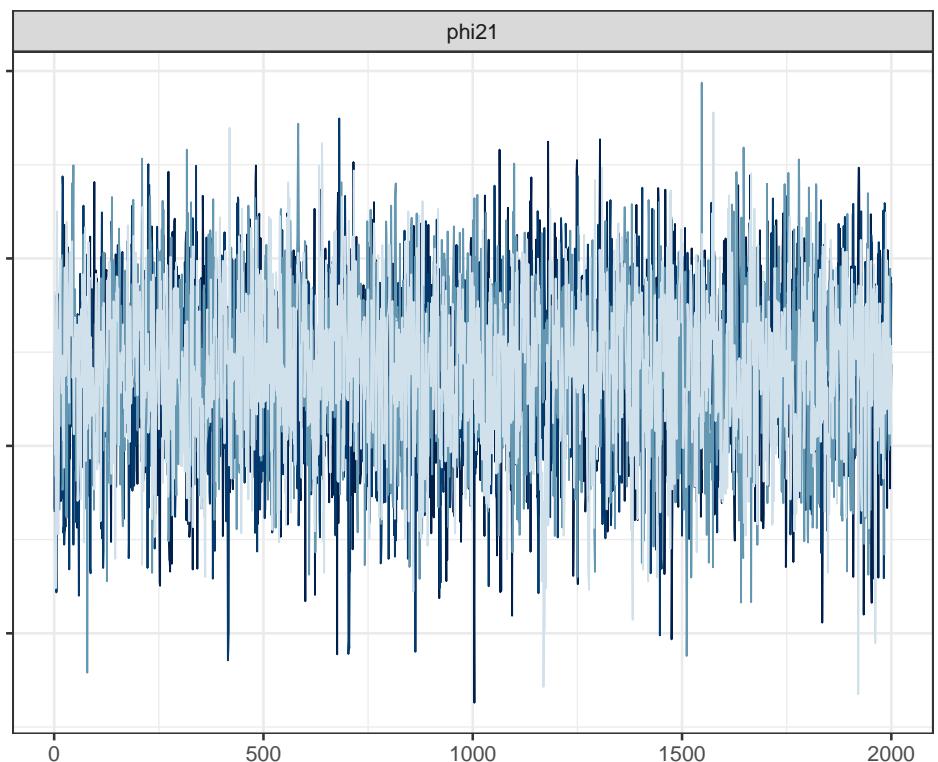
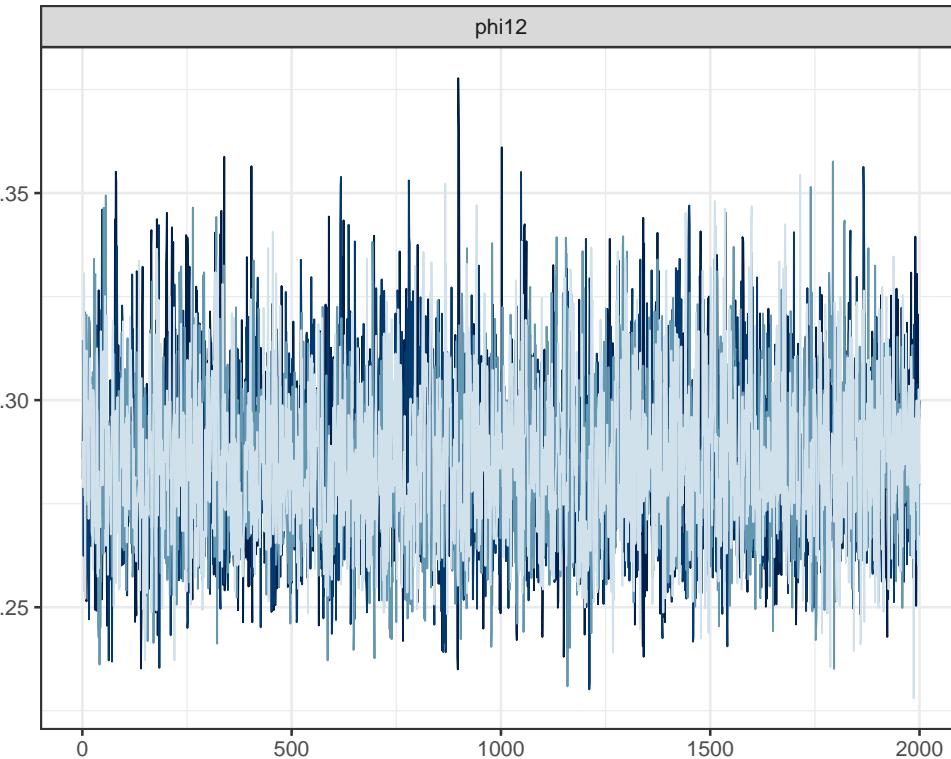
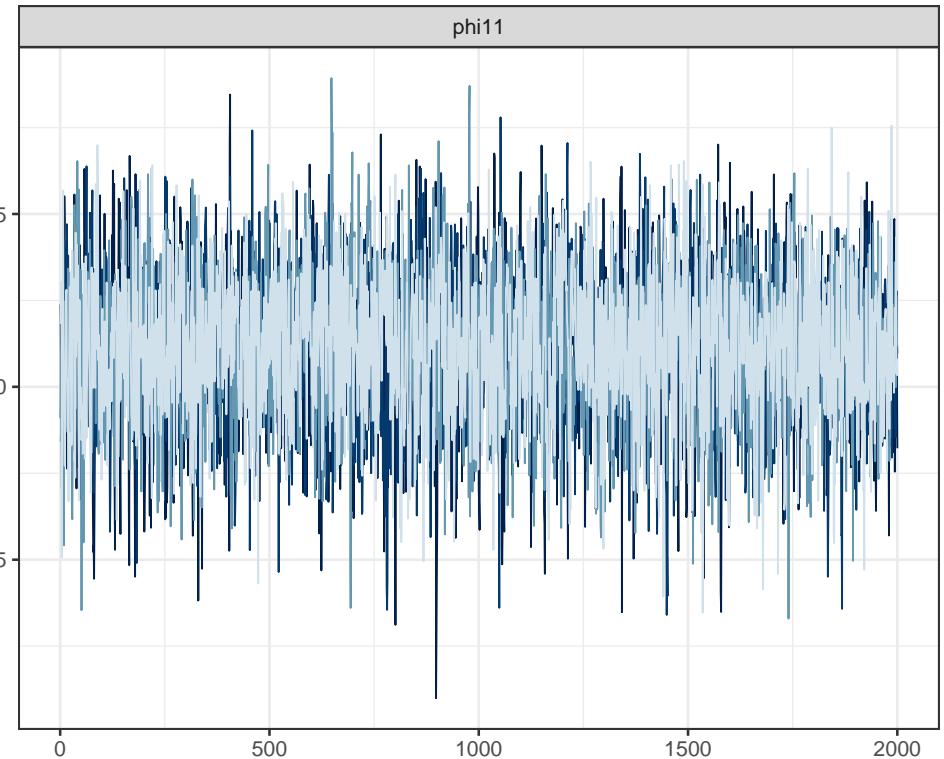
Boxplots across replications for each parameter. Helps spot tough parameters.





# Trace Plot: SC Model (Rep 48 with 1 divergences)

Looking for 'hairy caterpillar' appearance – good mixing across chains.



Chain

- 1
- 2
- 3
- 4