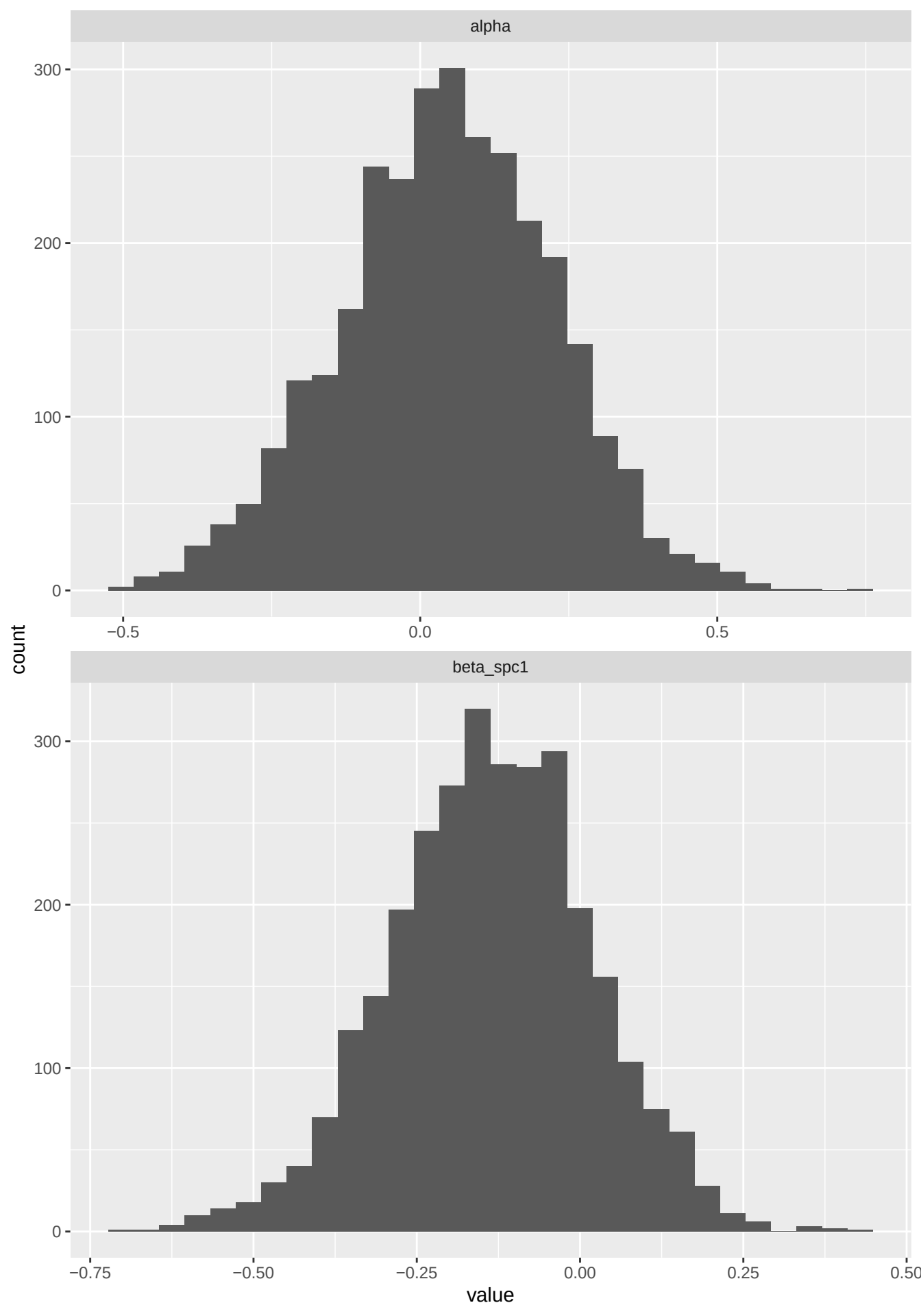
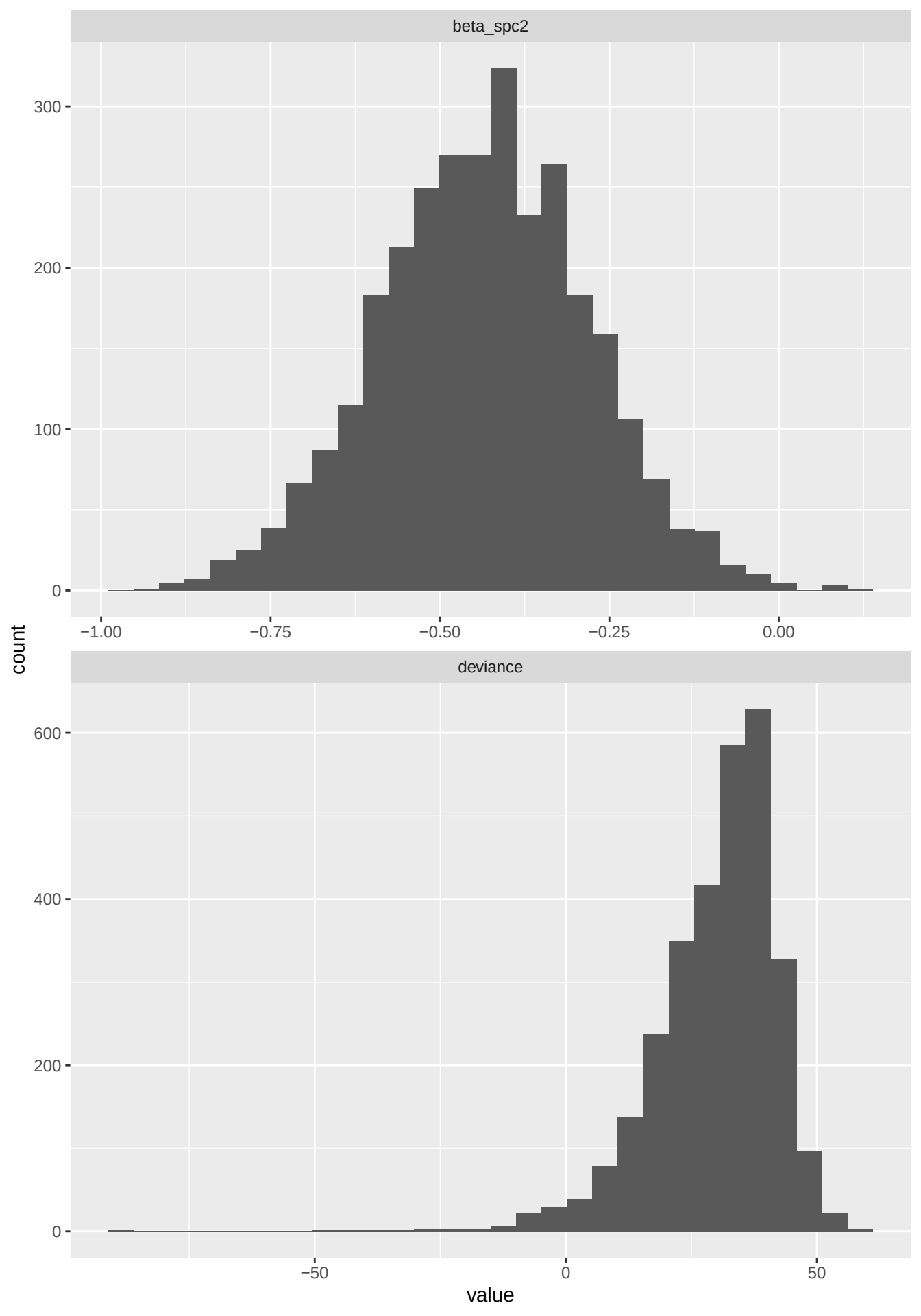
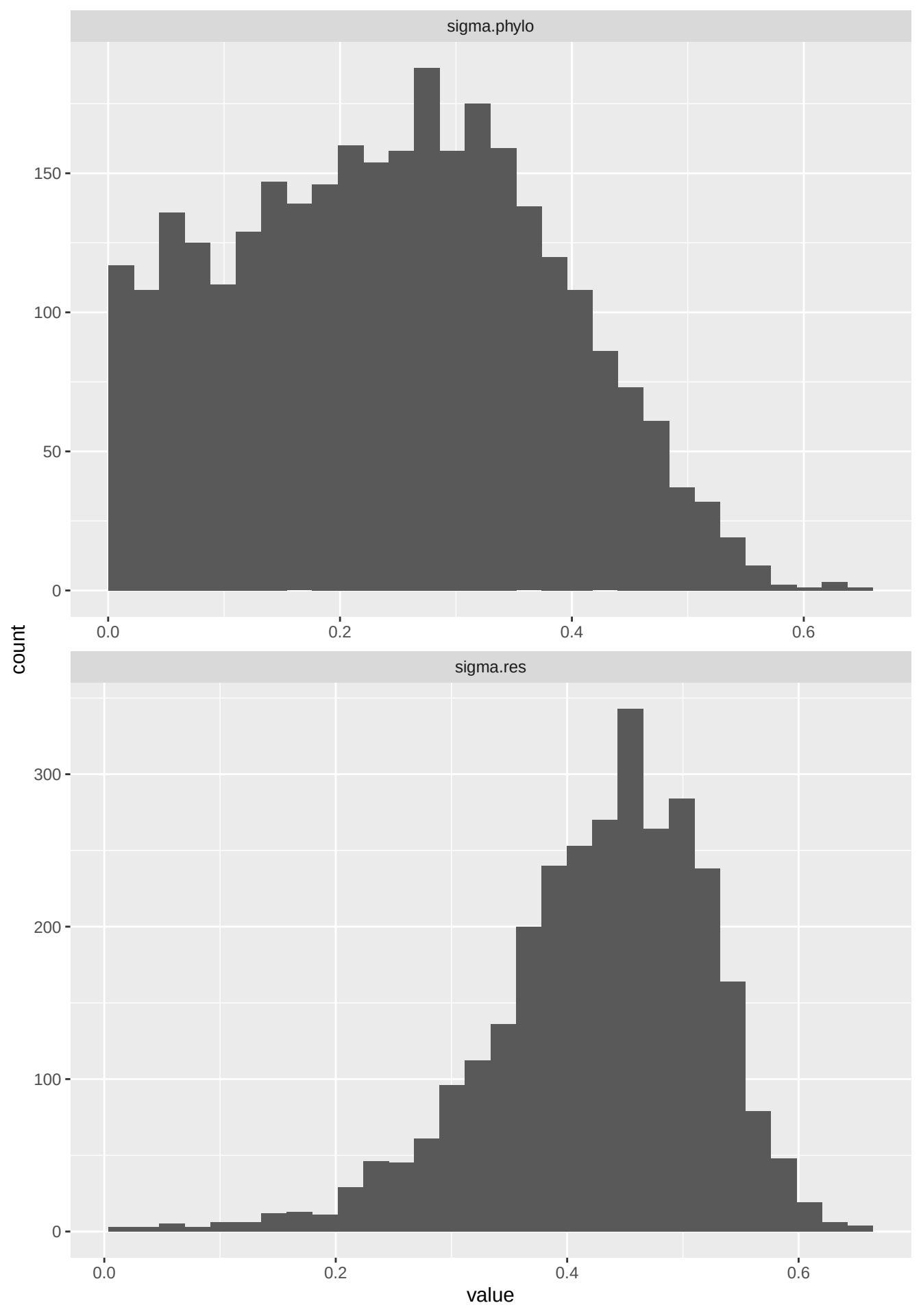
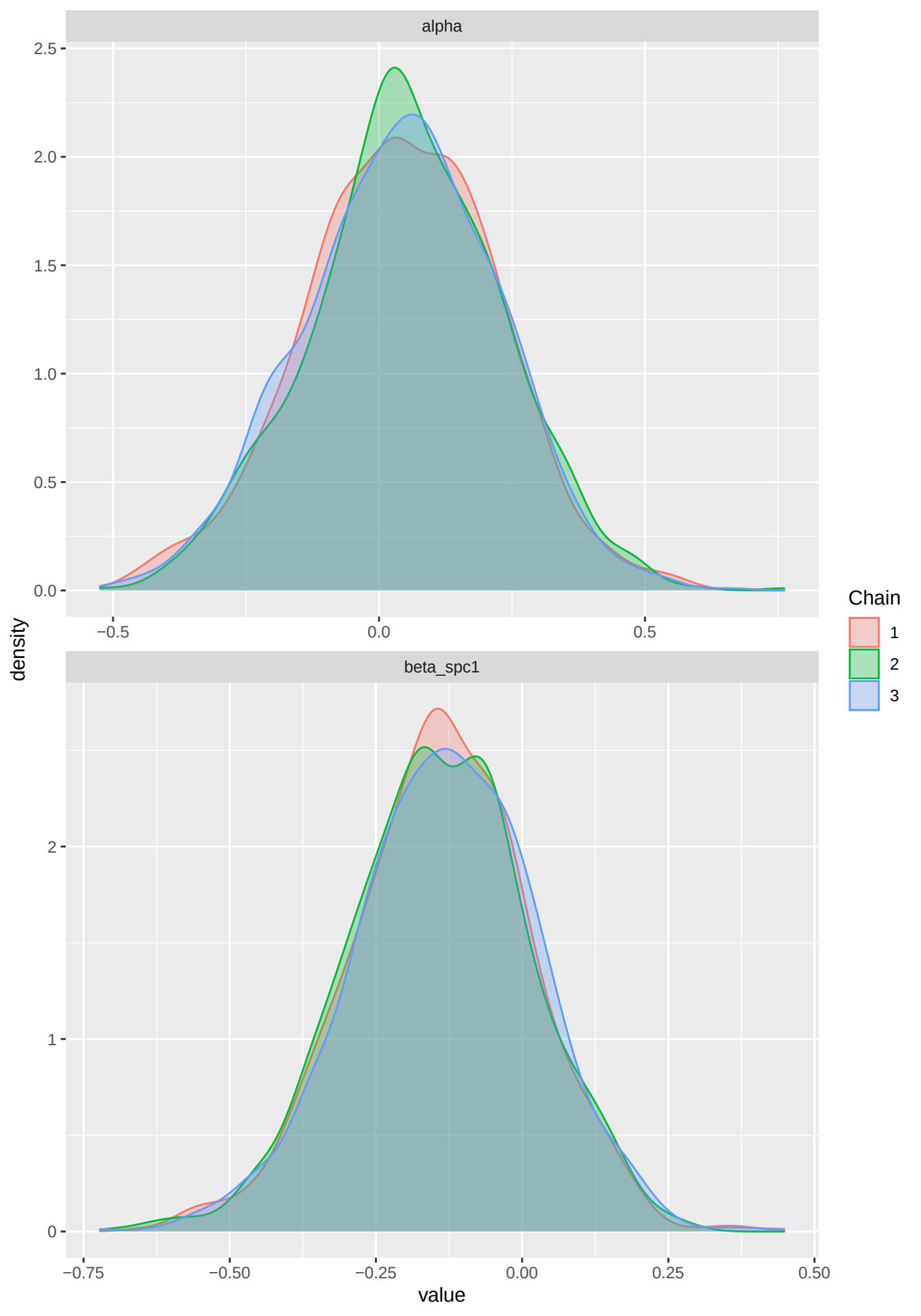
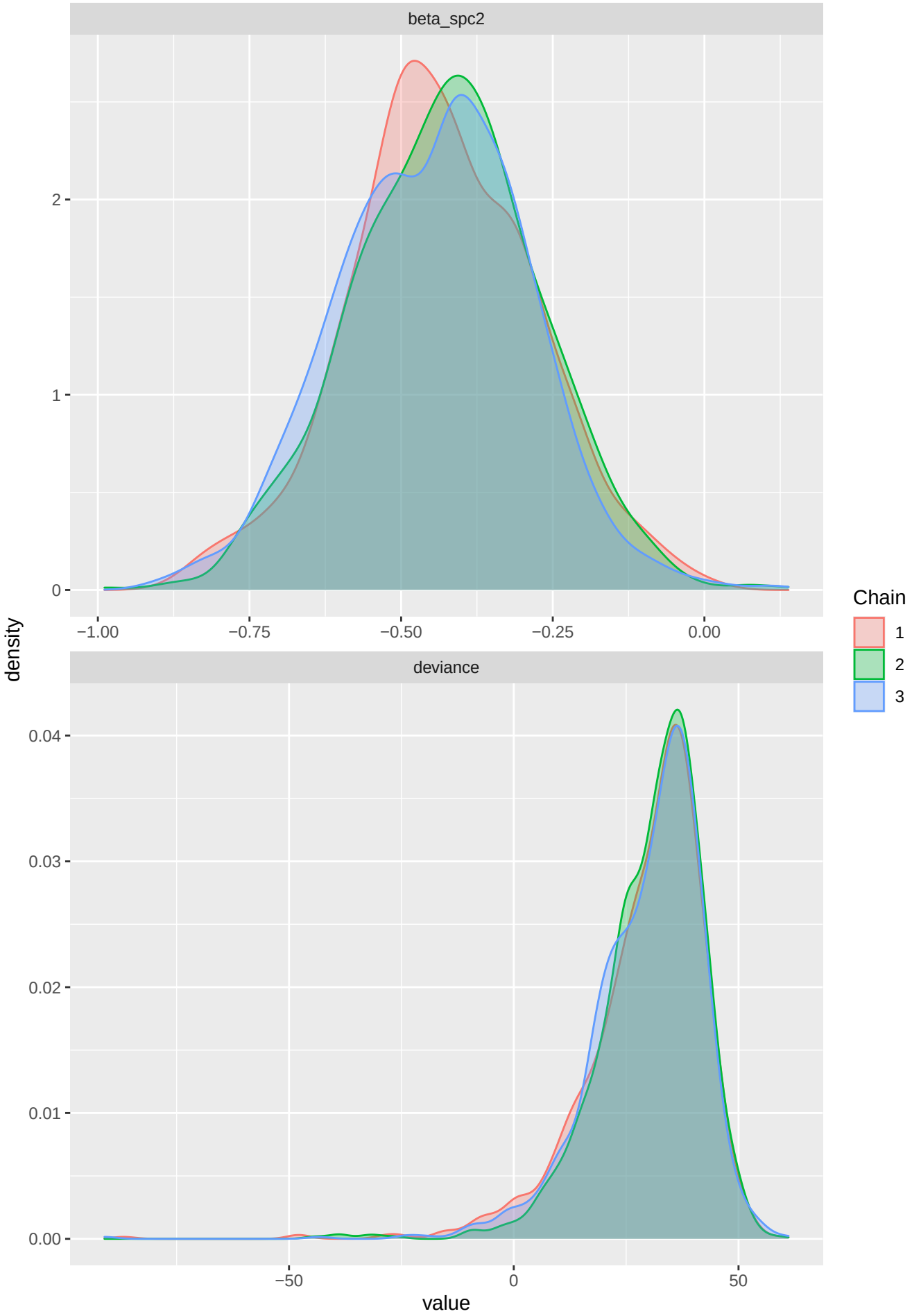
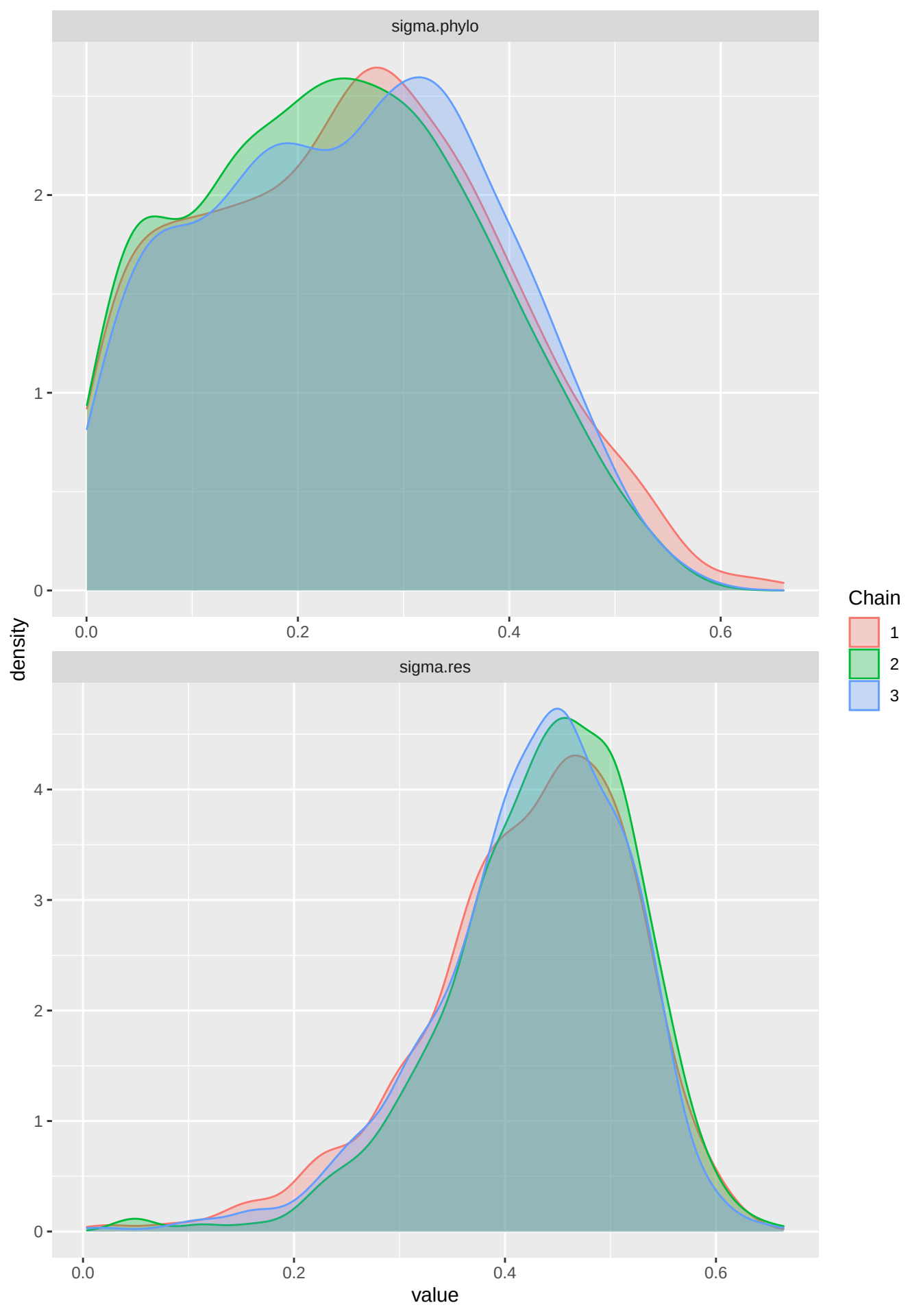

alpha
300
200
100
0
−0.5
0.0
0.5
count
beta_spc1
300
200
100
0
−0.75
−0.50
−0.25
0.00
0.25
0.50
value

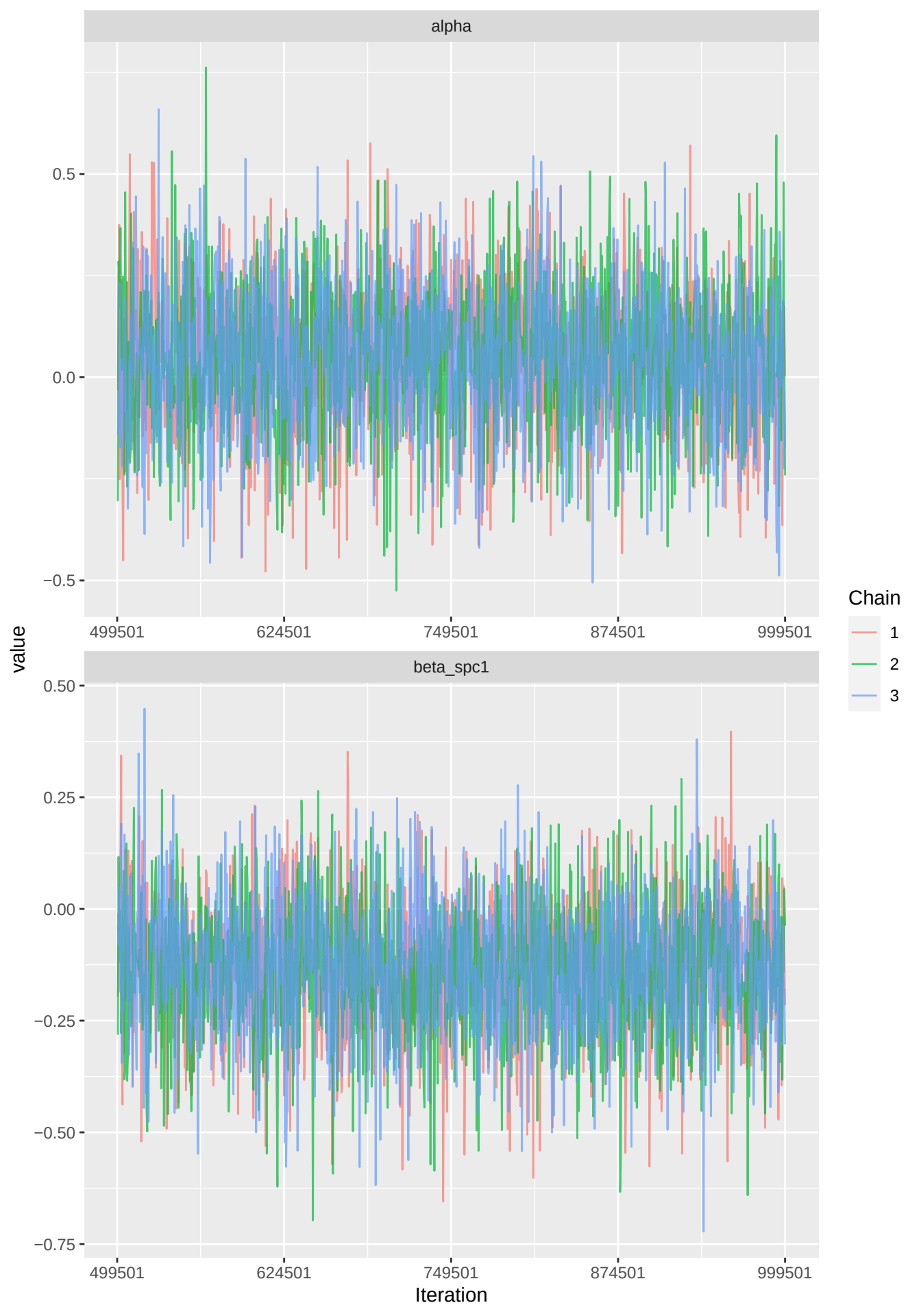

beta_spc2
deviance
count
value
300
200
100
0
600
400
200
0
−1.00
−0.75
−0.50
−0.25
0.00
−50
0
50

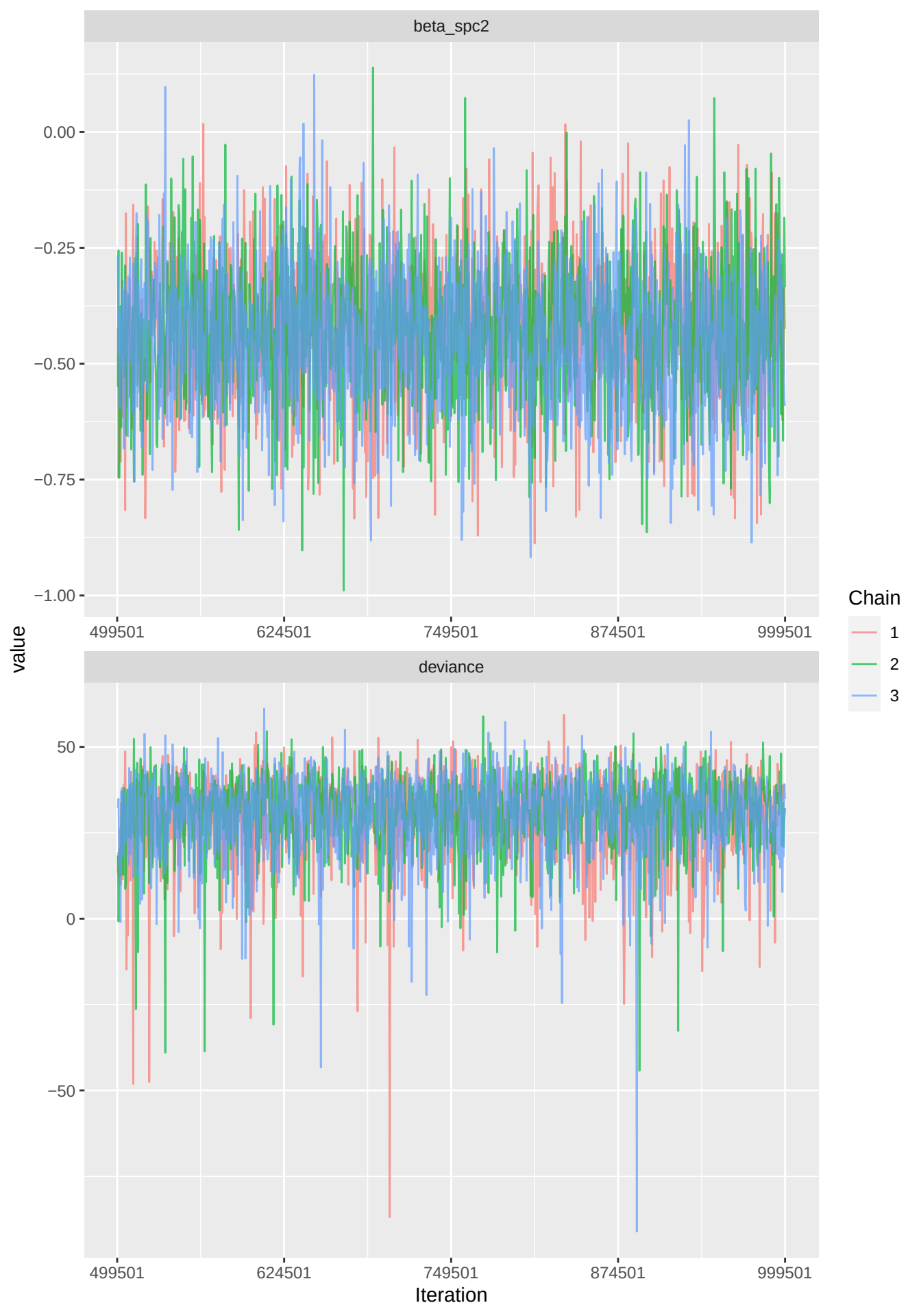

sigma.phylo
150
100
50
0
0.0
0.2
0.4
0.6
count
sigma.res
300
200
100
0
0.0
0.2
0.4
0.6
value

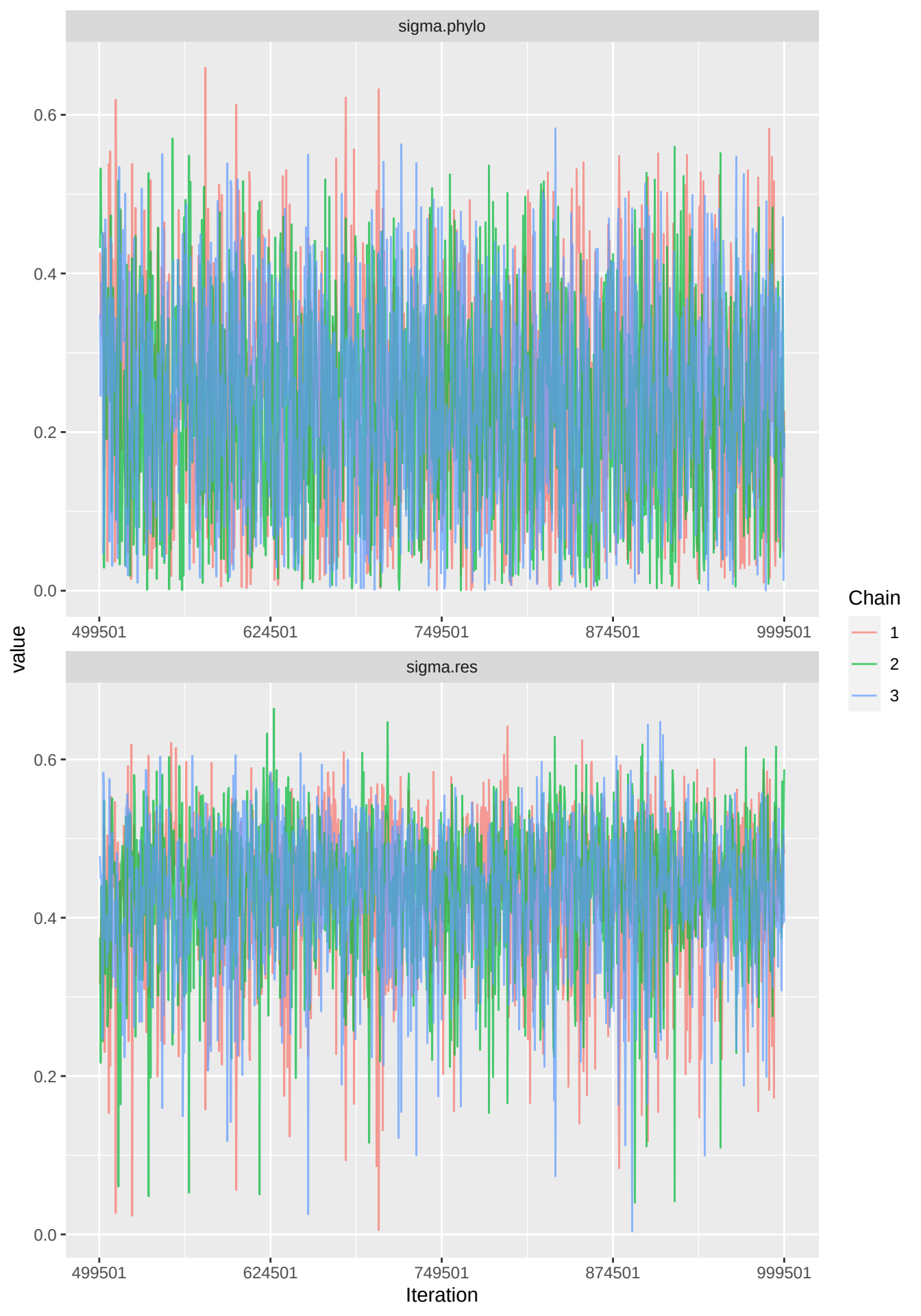

alpha
beta_spc1
density
value
Chain
1
2
3
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
0.0
0.5
2
1
0
−0.75
−0.50
−0.25
0.00
0.25
0.50

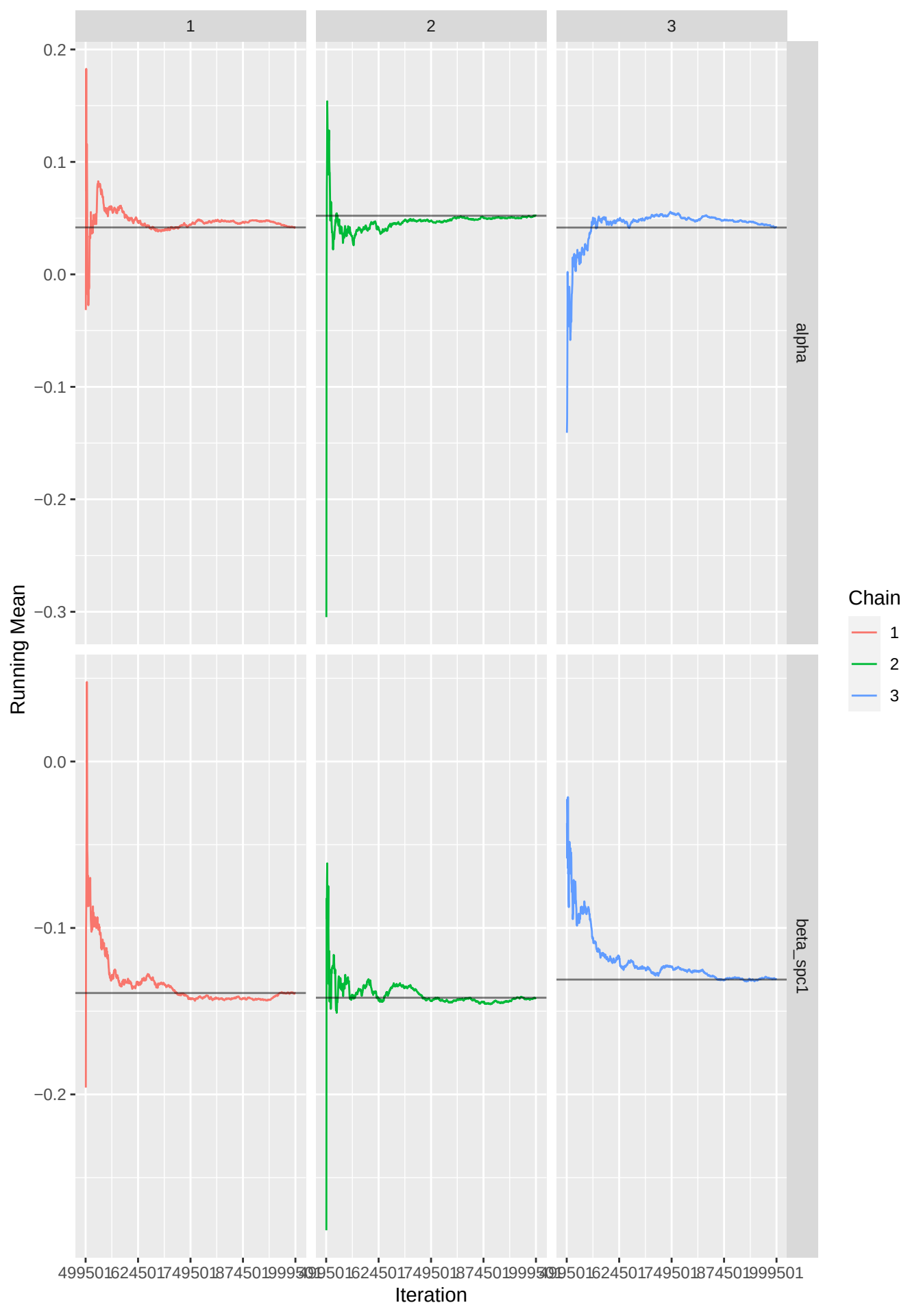

beta_spc2
deviance
density
value
Chain
1
2
3
0
1
2
−1.00
−0.75
−0.50
−0.25
0.00
0.04
0.03
0.02
0.01
0.00
−50
0
50

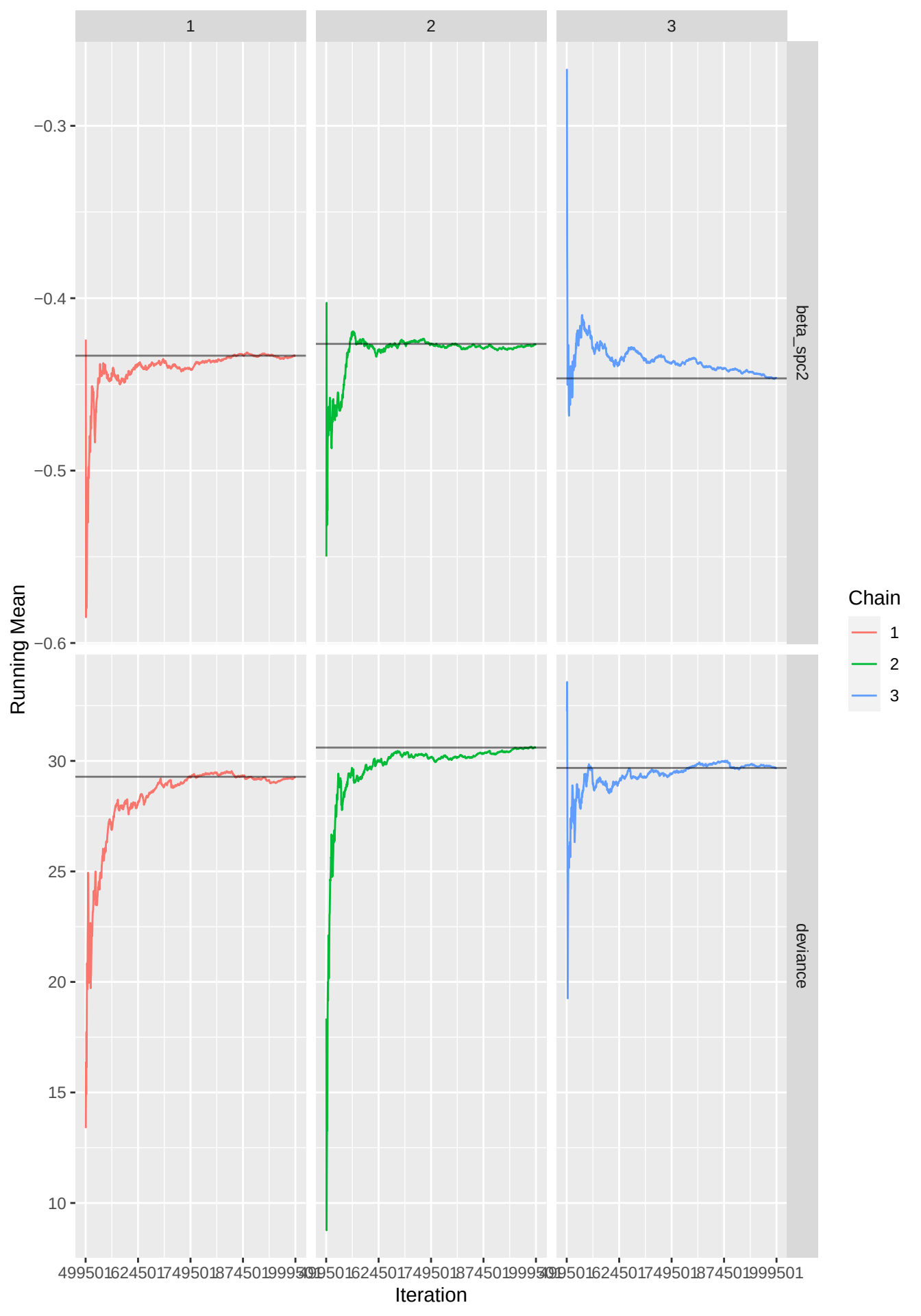

sigma.phylo
sigma.res
density
value
0
1
2
3
4
0.0
0.2
0.4
0.6
Chain
1
2
3

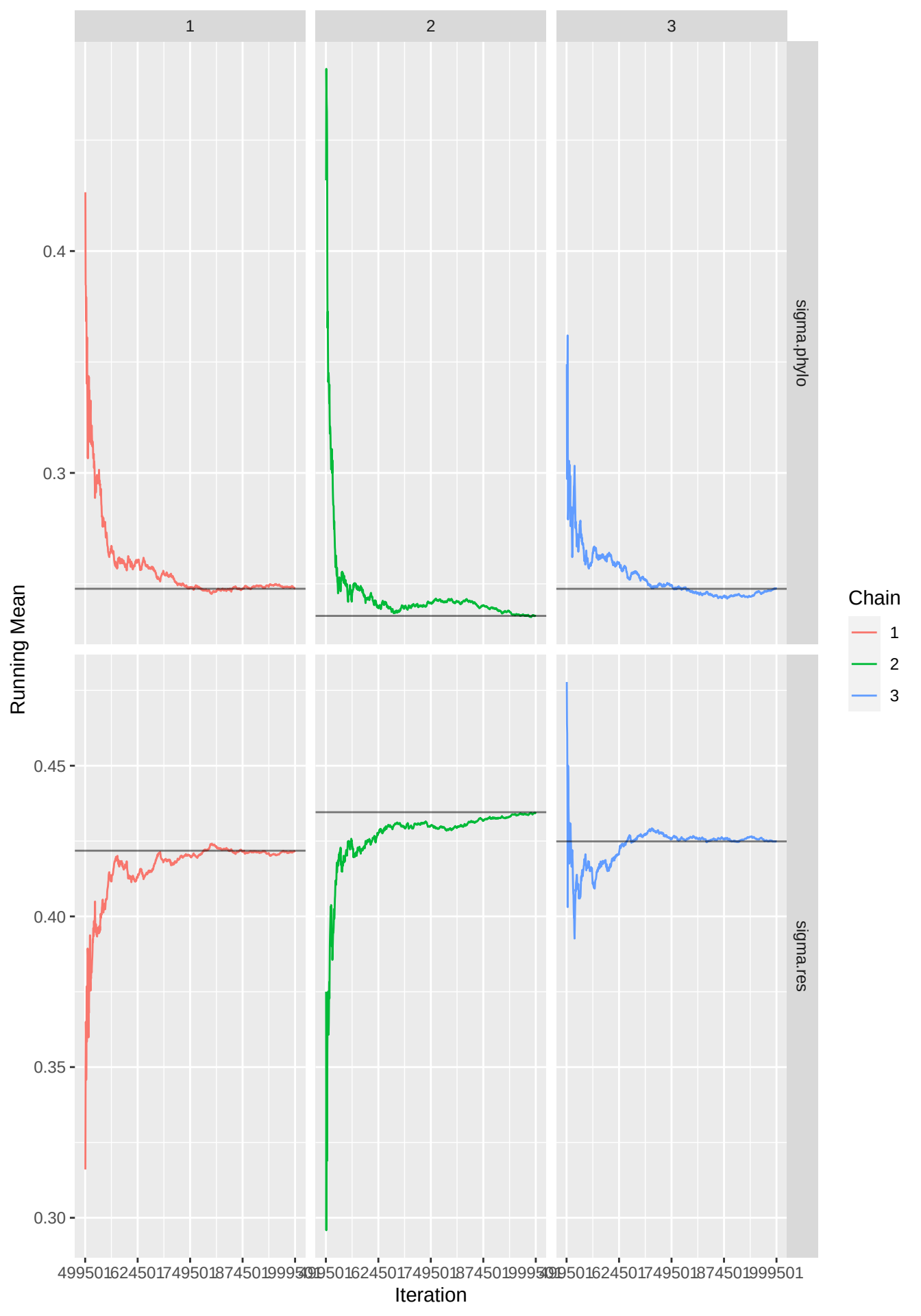

alpha
beta_spc1
0.5
0.0
−0.5
0.50
0.25
0.00
−0.25
−0.50
−0.75
499501
624501
749501
874501
999501
value
Iteration
Chain
1
2
3

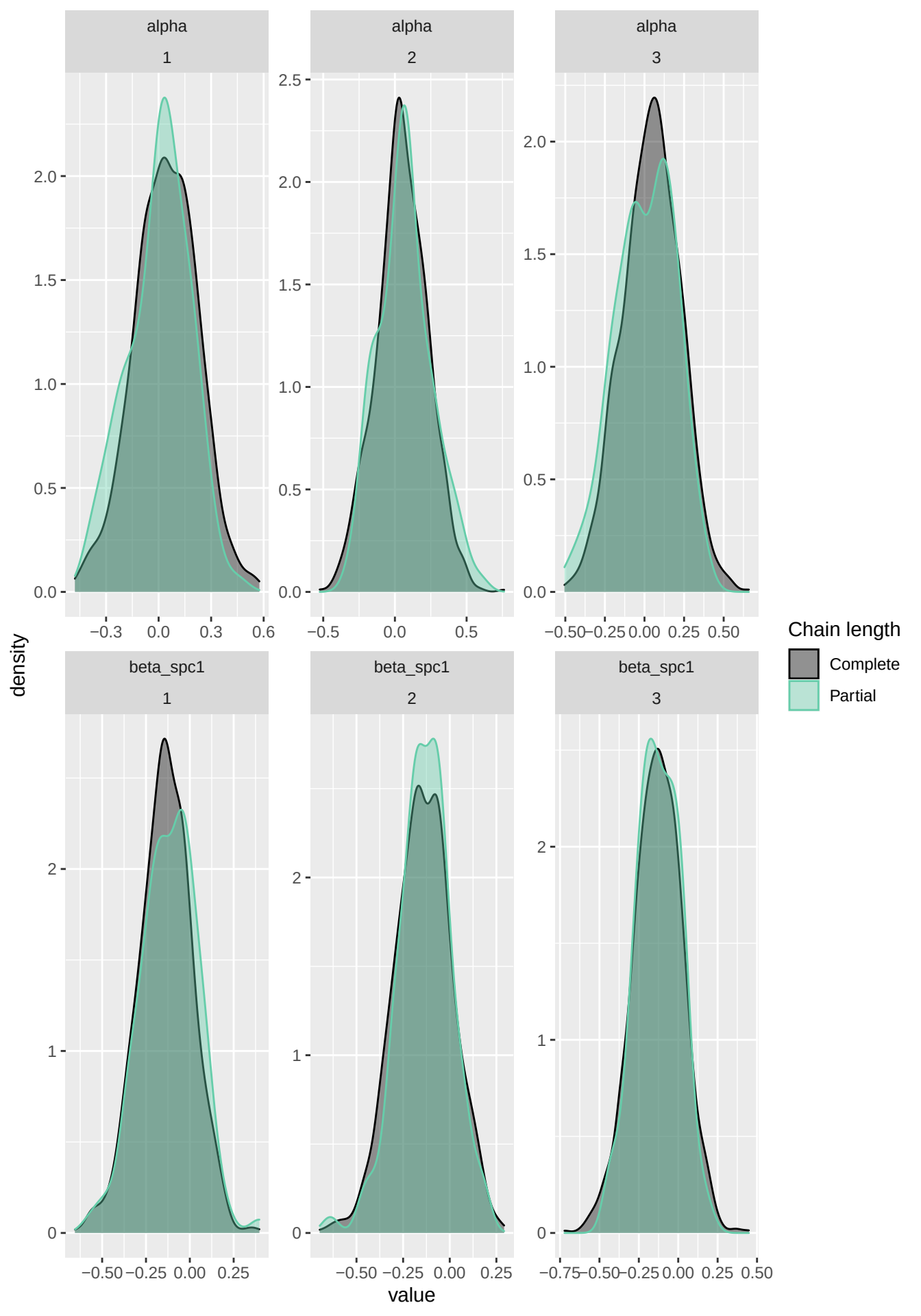

beta_spc2
0.00
−0.25
−0.50
−0.75
−1.00
499501
624501
749501
874501
999501
deviance
50
0
−50
499501
624501
749501
874501
999501
Iteration
value
Chain
1
2
3

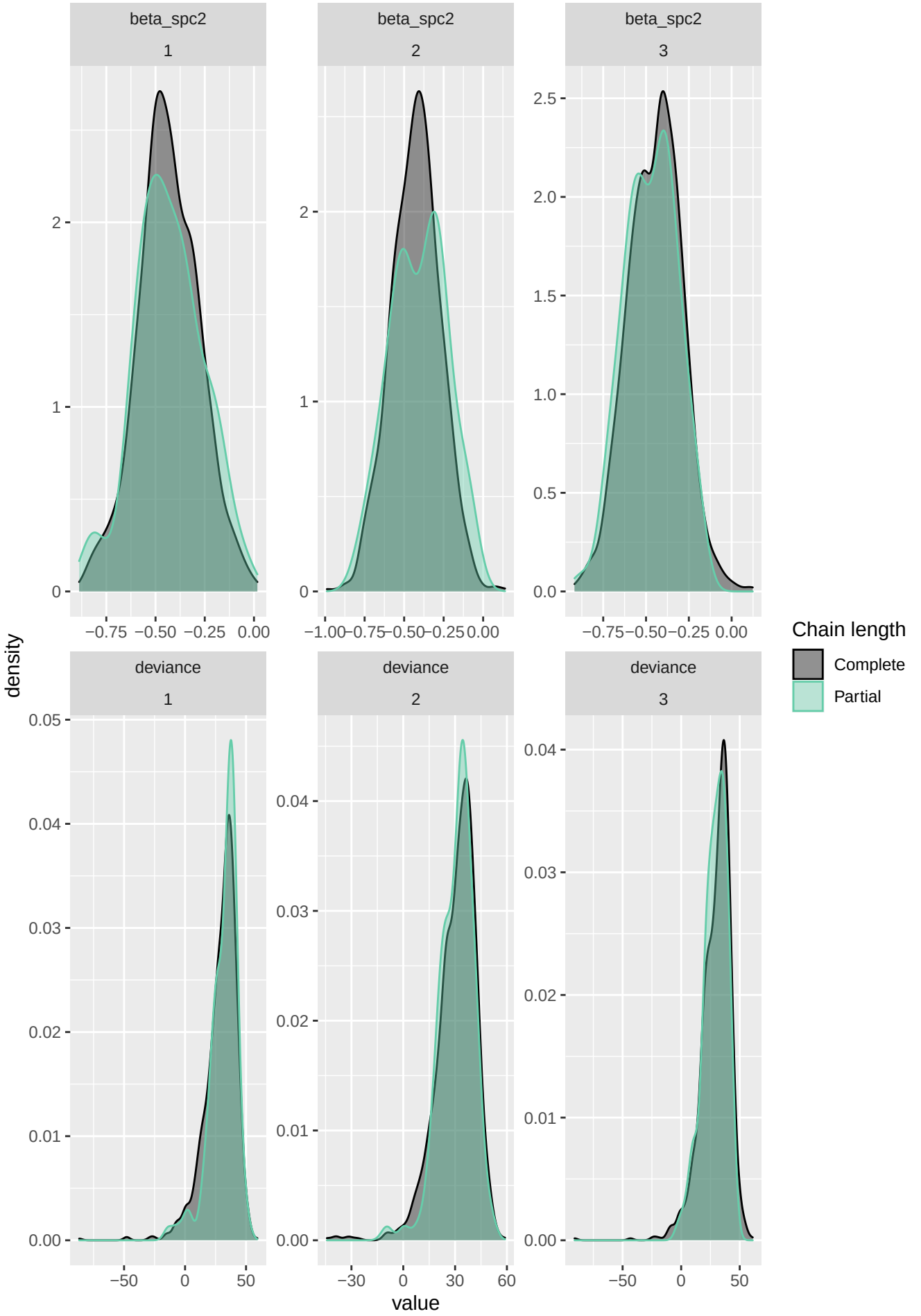

sigma.phylo
sigma.res
value
0.0
0.2
0.4
0.6
499501
624501
749501
874501
999501
Iteration
Chain
1
2
3

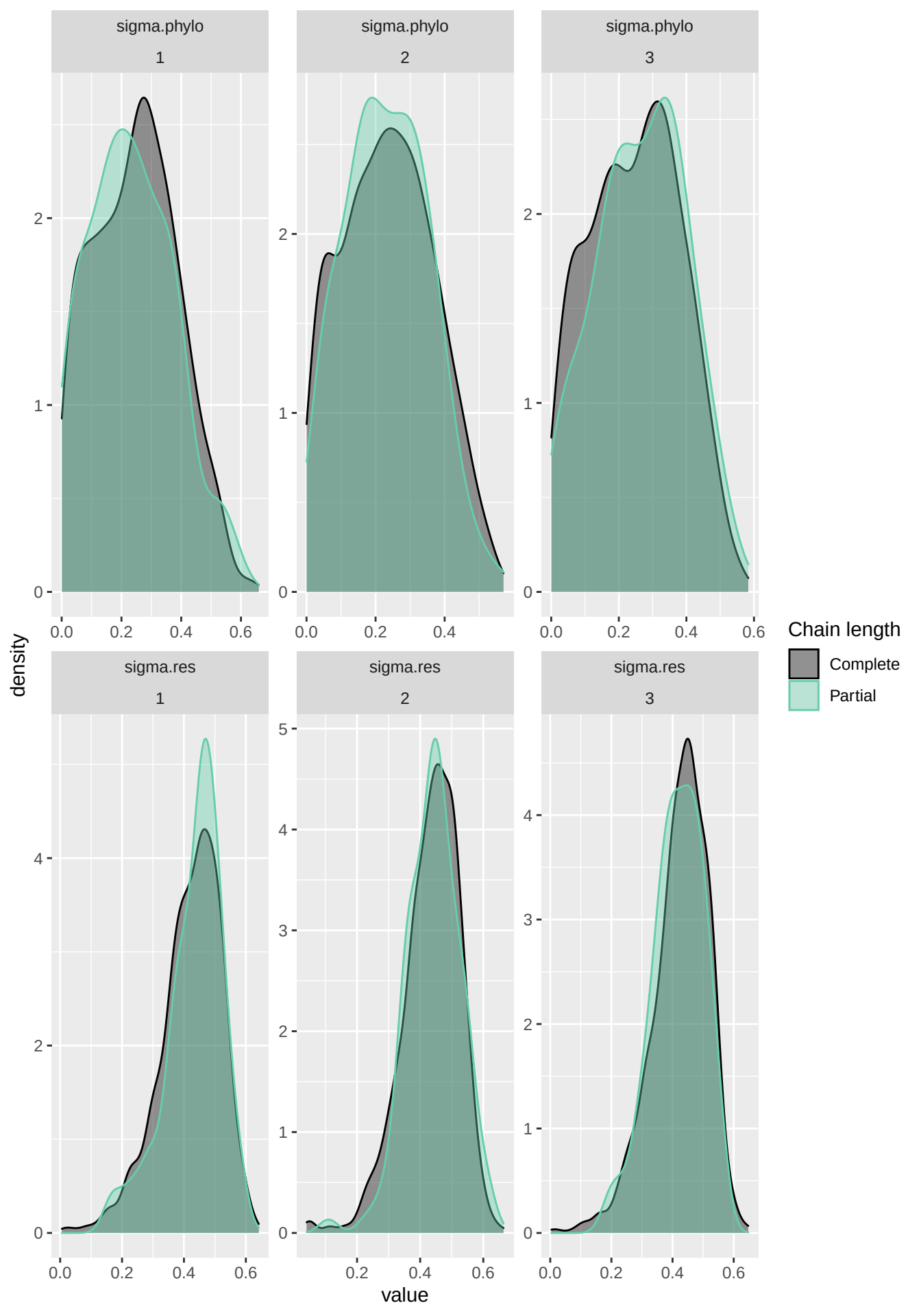

1
2
3
alpha
beta_spc1
Running Mean
Iteration
Chain
1
2
3
0.2
0.1
0.0
−0.1
−0.2
−0.3
499501
1624501
1749501
1874501
1999501

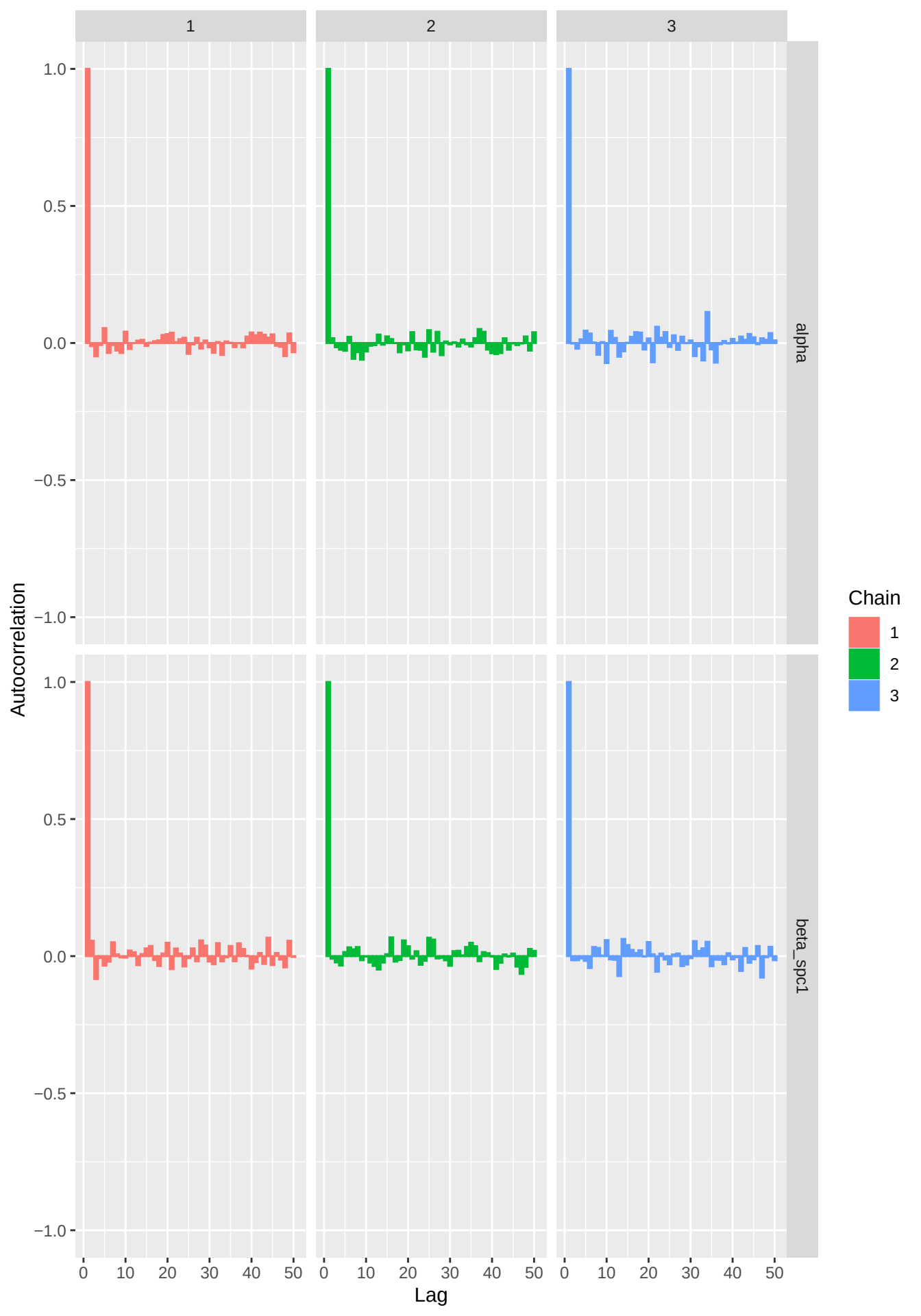

1
2
3
beta_spc2
deviance
Running Mean
−0.3
−0.4
−0.5
−0.6
30
25
20
15
10
Iteration
Chain
1
2
3

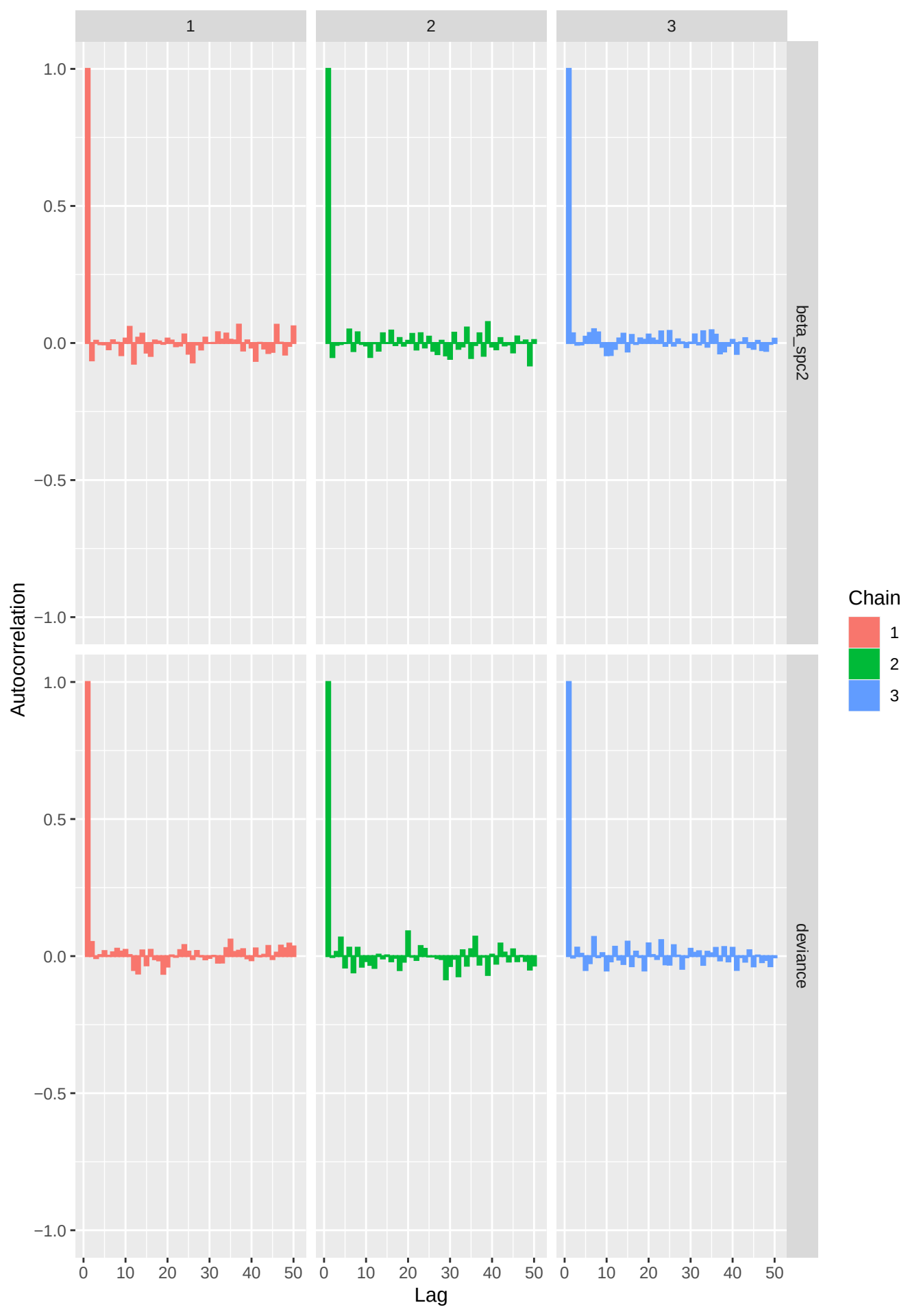

1
2
3
sigma.phylo
sigma.res
Running Mean
0.4
0.3
0.45
0.40
0.35
0.30
Iteration
Chain
1
2
3

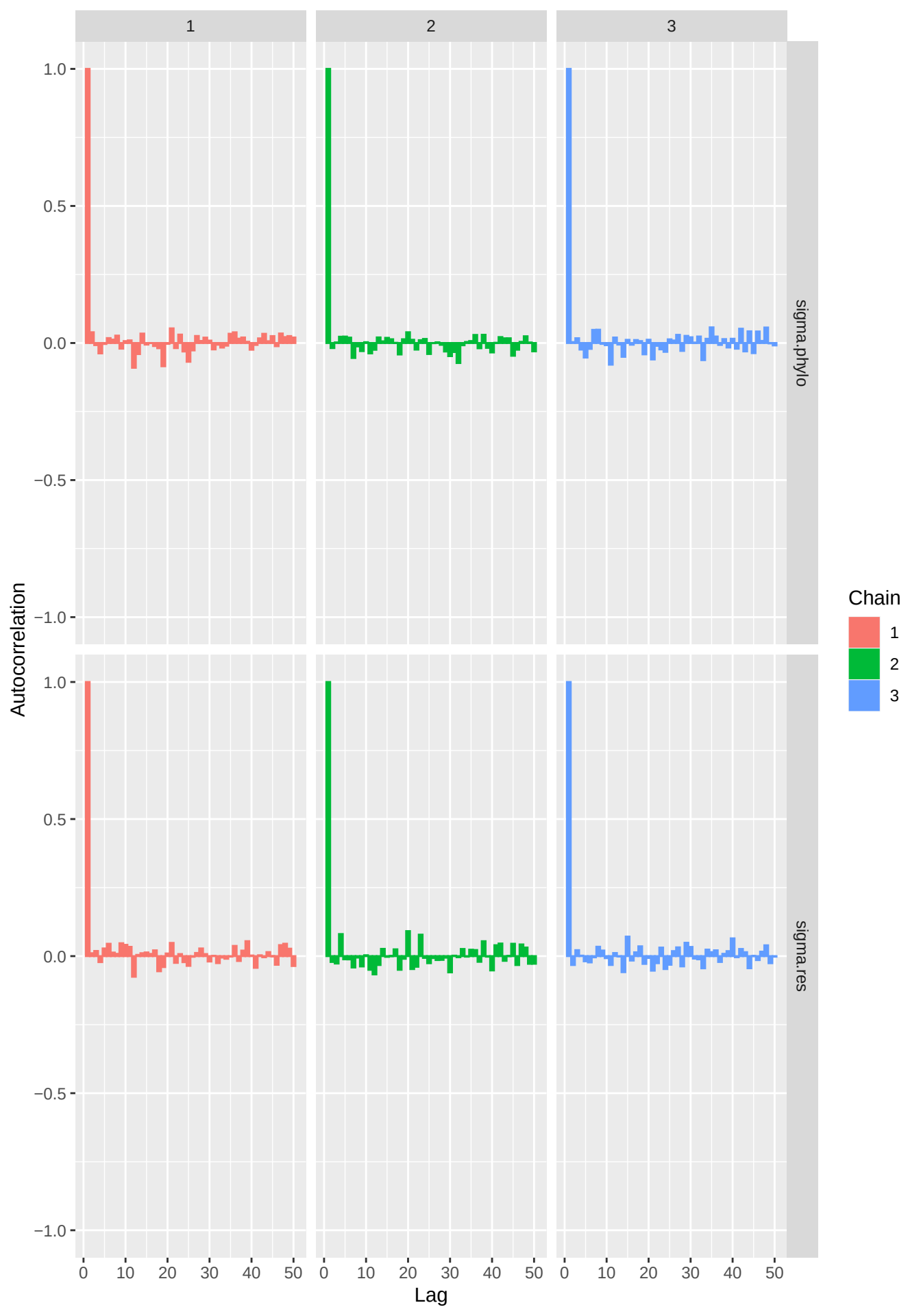

alpha
1
alpha
2
alpha
3
beta_spc1
1
beta_spc1
2
beta_spc1
3
density
value
Chain length
Complete
Partial

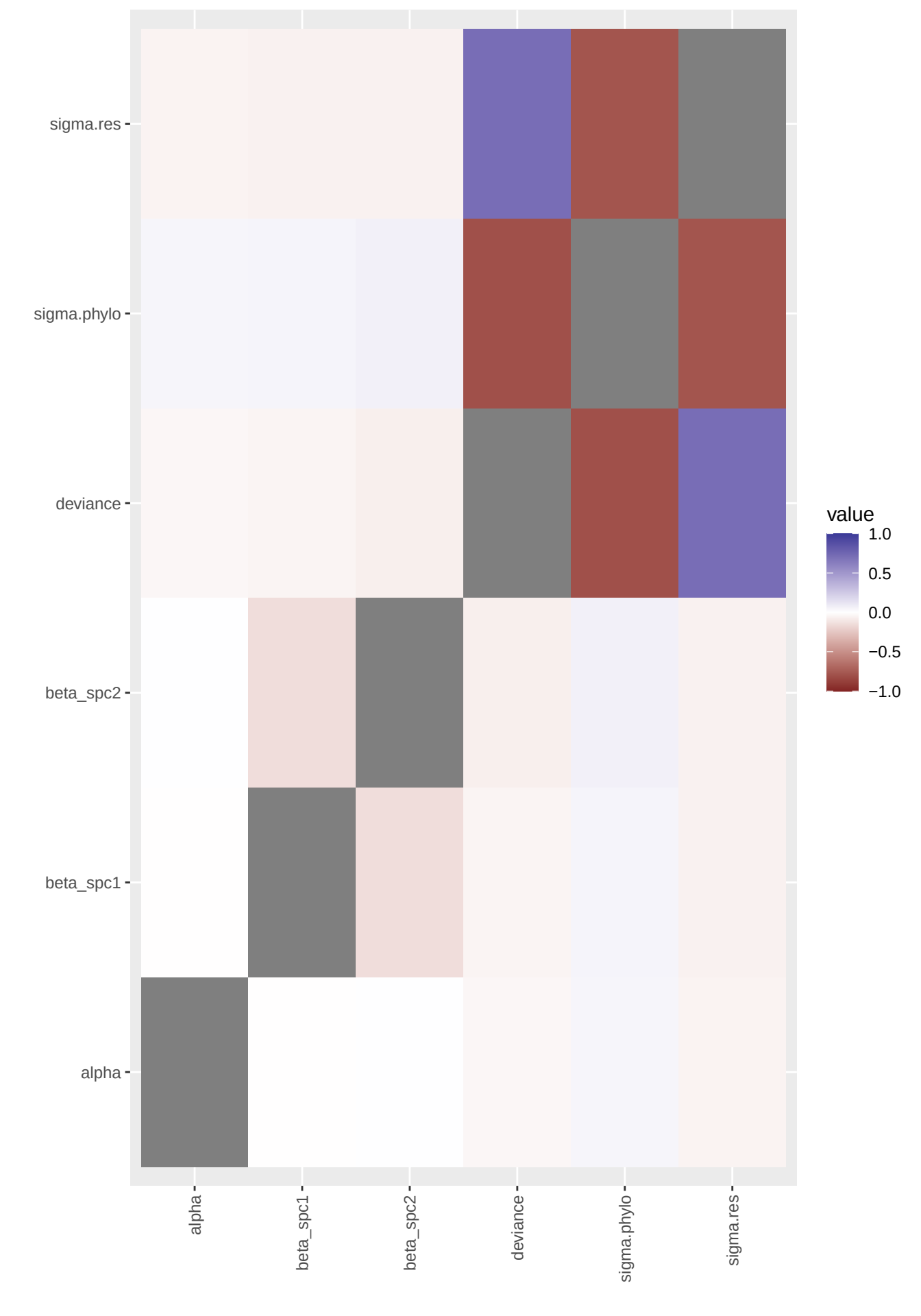

beta_spc2
1
beta_spc2
2
beta_spc2
3
deviance
1
deviance
2
deviance
3
density
value
Chain length
Complete
Partial

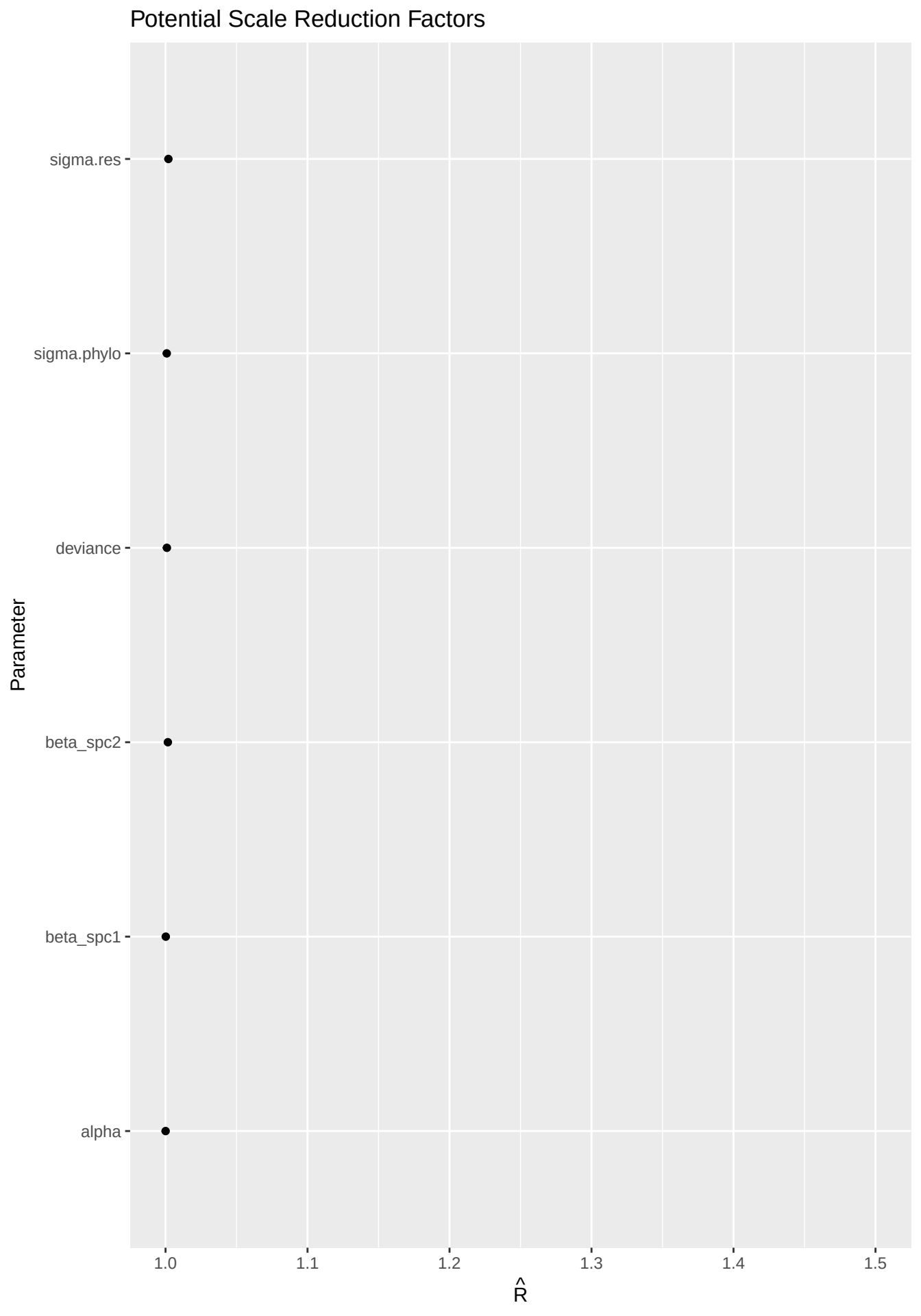

sigma.phylo
1
sigma.phylo
2
sigma.phylo
3
sigma.res
1
sigma.res
2
sigma.res
3
density
value
Chain length
Complete
Partial

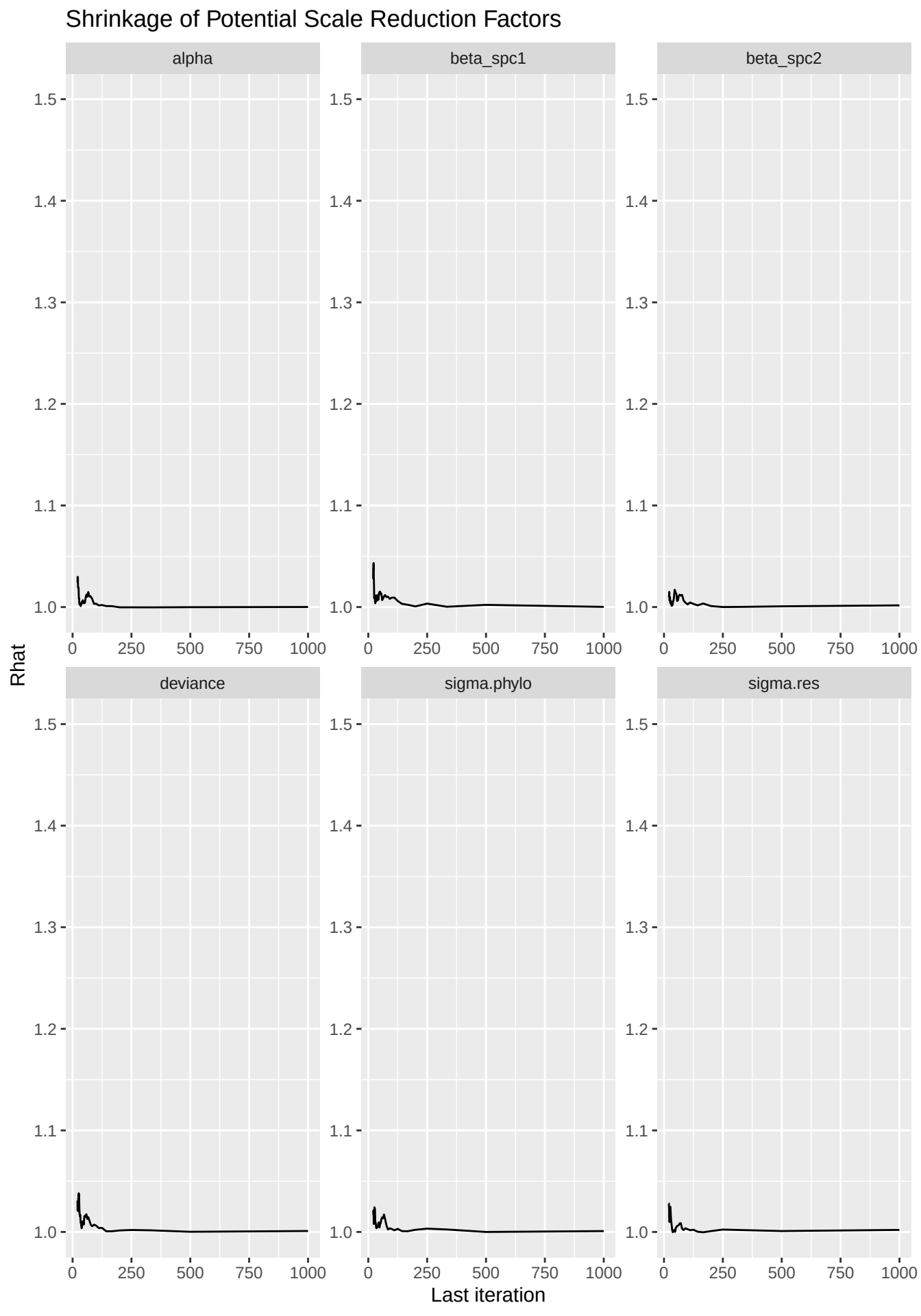

1
2
3
alpha
beta_spc1
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Lag
Chain
1
2
3

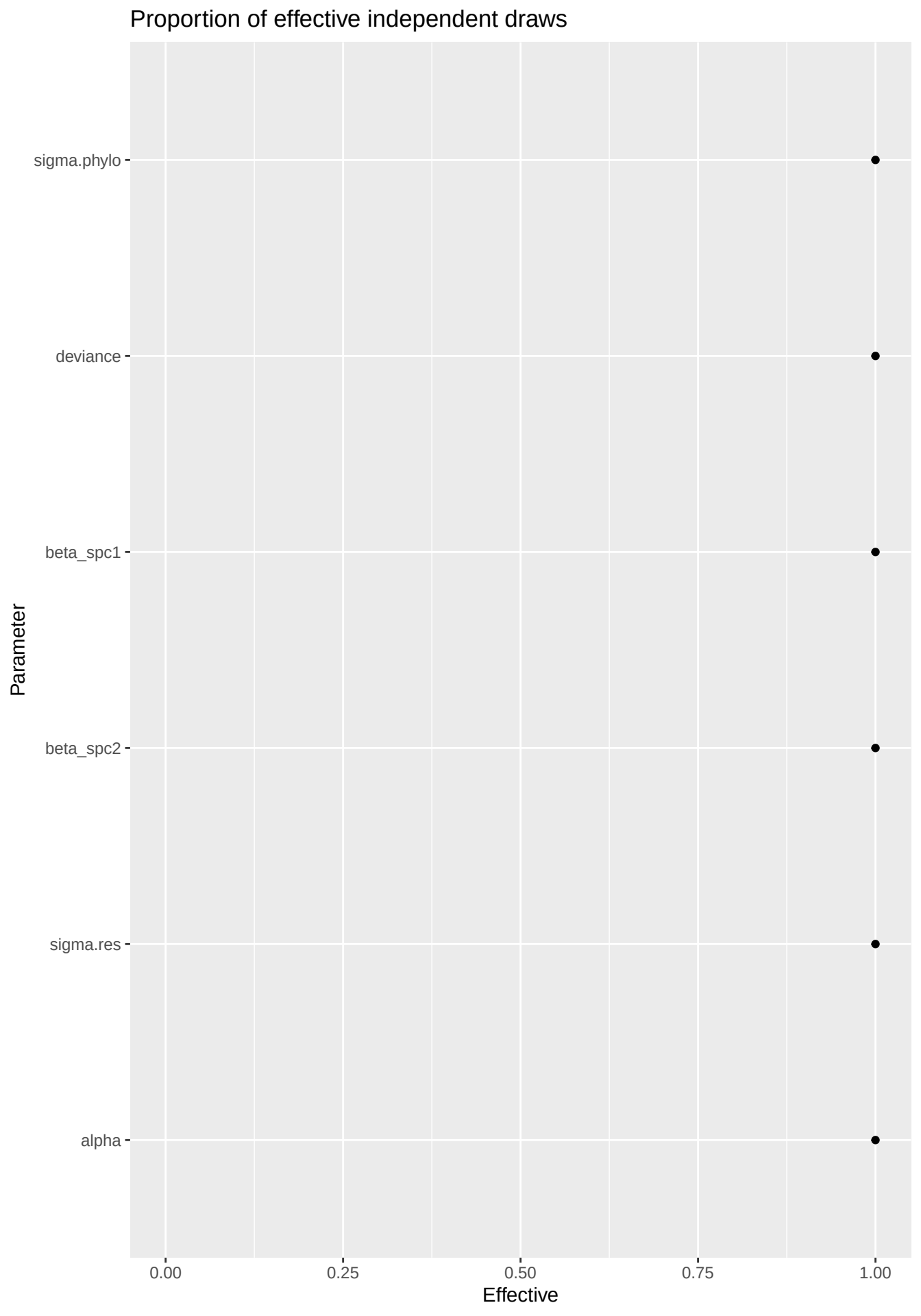

1
2
3
beta_spc2
deviance
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Lag
Chain
1
2
3

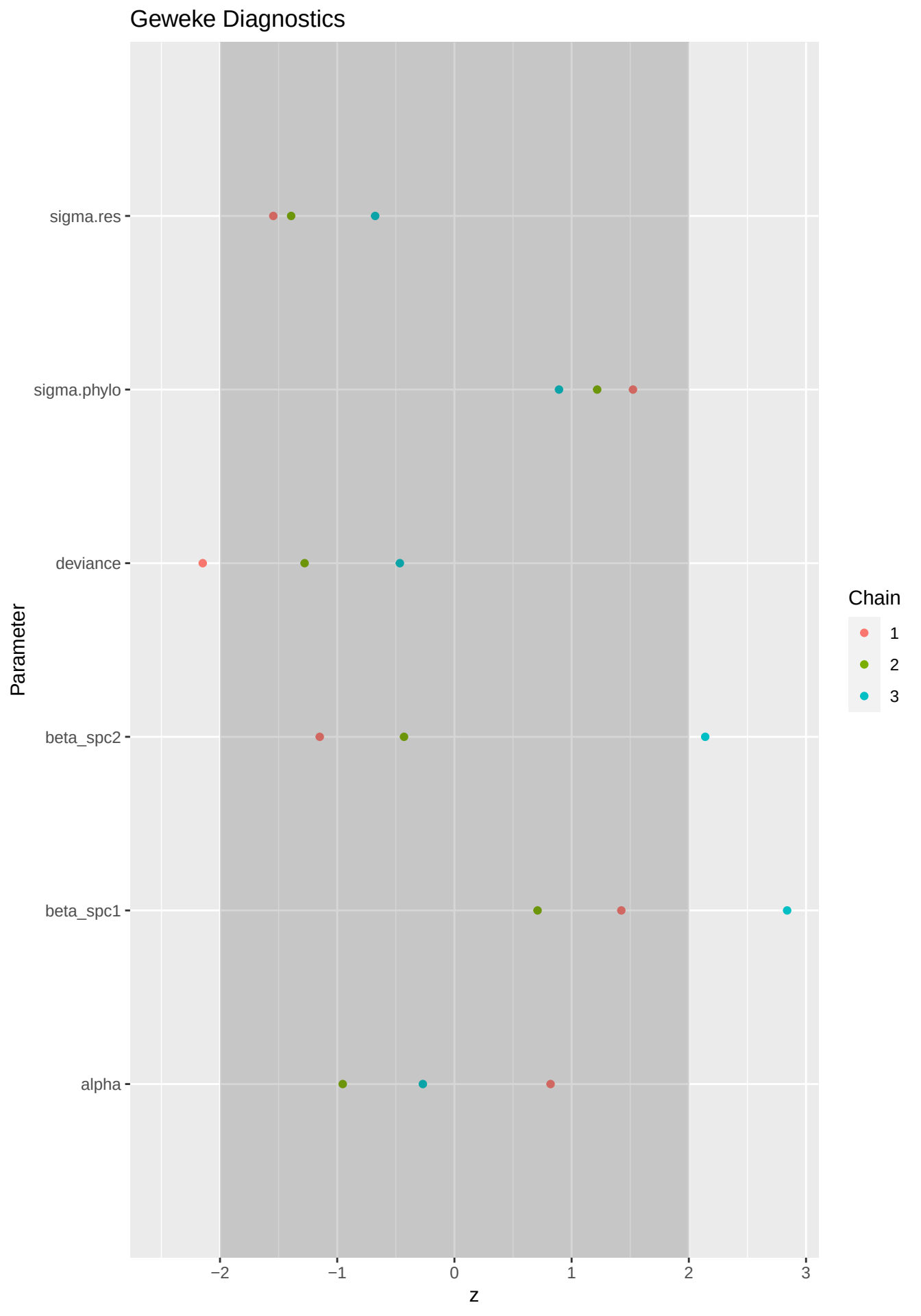

1
2
3
sigma.phylo
sigma.res
Autocorrelation
Lag
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Chain
1
2
3


sigma.res
sigma.phylo
deviance
beta_spc2
beta_spc1
alpha
alpha
beta_spc1
beta_spc2
deviance
sigma.phylo
sigma.res
value
1.0
0.5
0.0
−0.5
−1.0


Potential Scale Reduction Factors
sigma.res
sigma.phylo
deviance
beta_spc2
beta_spc1
alpha
Parameter
1.0
1.1
1.2
1.3
1.4
1.5
R̂


Shrinkage of Potential Scale Reduction Factors
alpha
beta_spc1
beta_spc2
deviance
sigma.phylo
sigma.res
Rhat
1.5
1.4
1.3
1.2
1.1
1.0
0
250
500
750
1000
Last iteration


Proportion of effective independent draws
sigma.phylo
deviance
beta_spc1
beta_spc2
sigma.res
alpha
Parameter
0.00
0.25
0.50
0.75
1.00
Effective


Geweke Diagnostics
sigma.res
sigma.phylo
deviance
beta_spc2
beta_spc1
alpha
Parameter
−2
−1
0
1
2
3
z
Chain
1
2
3