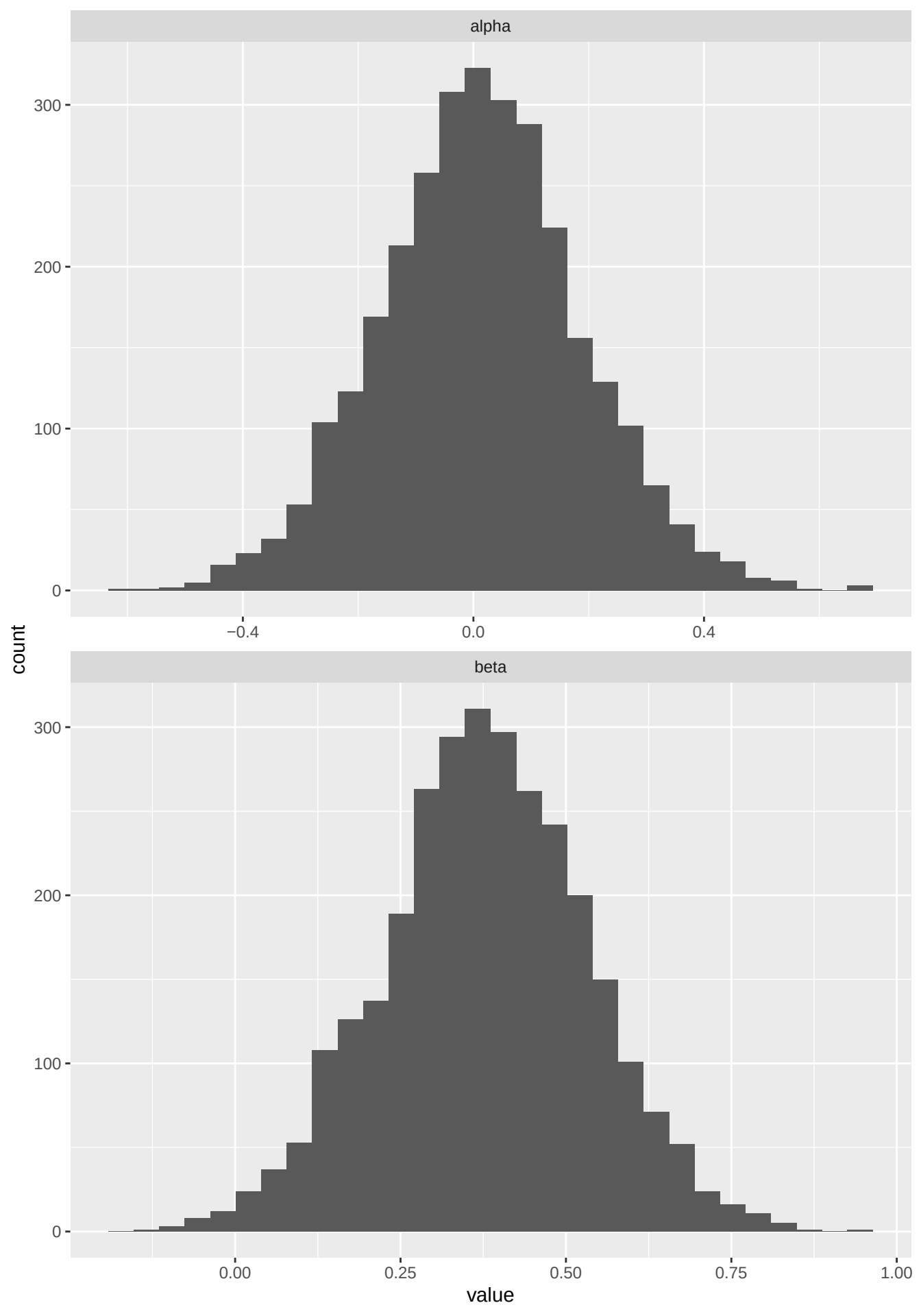
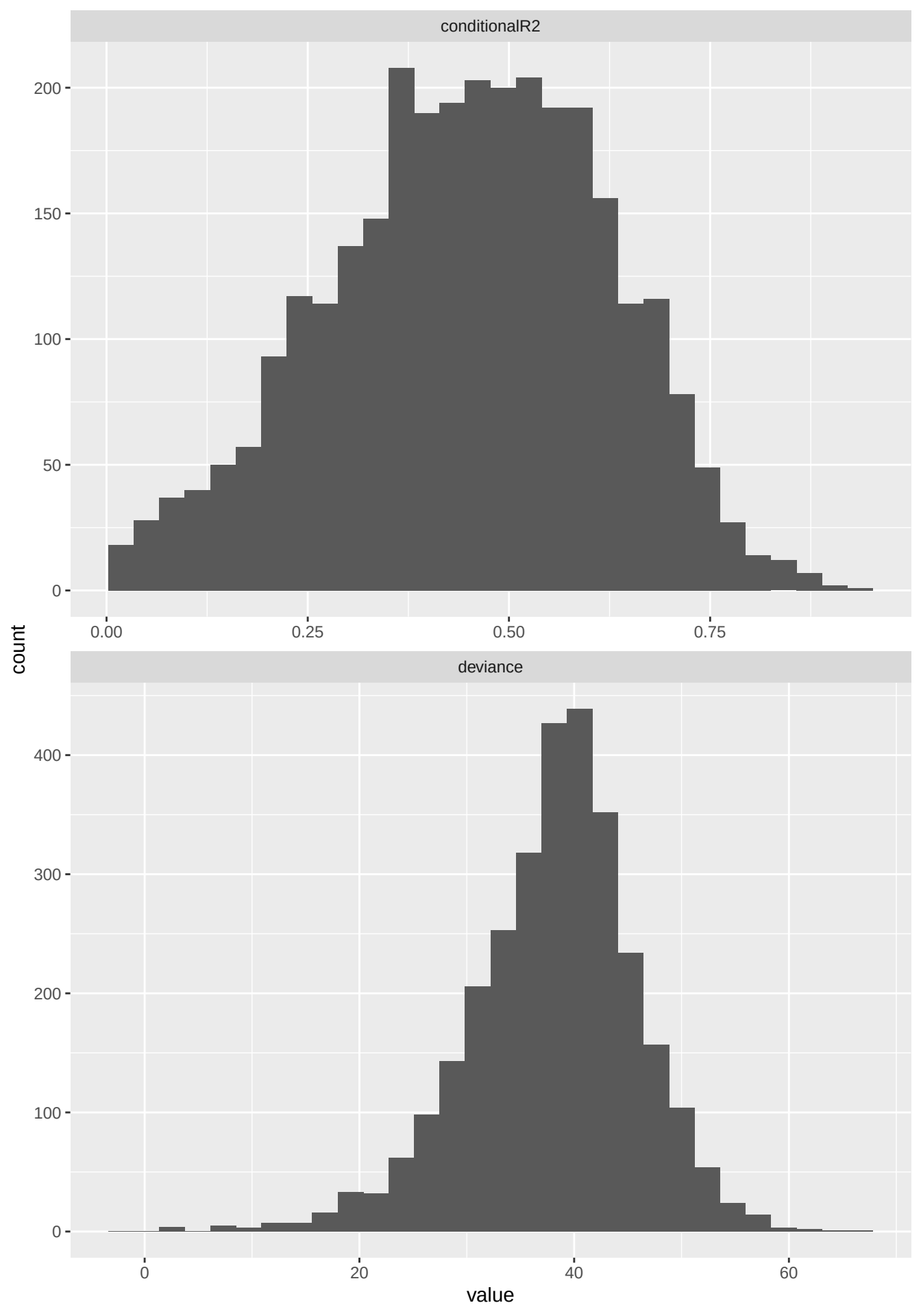
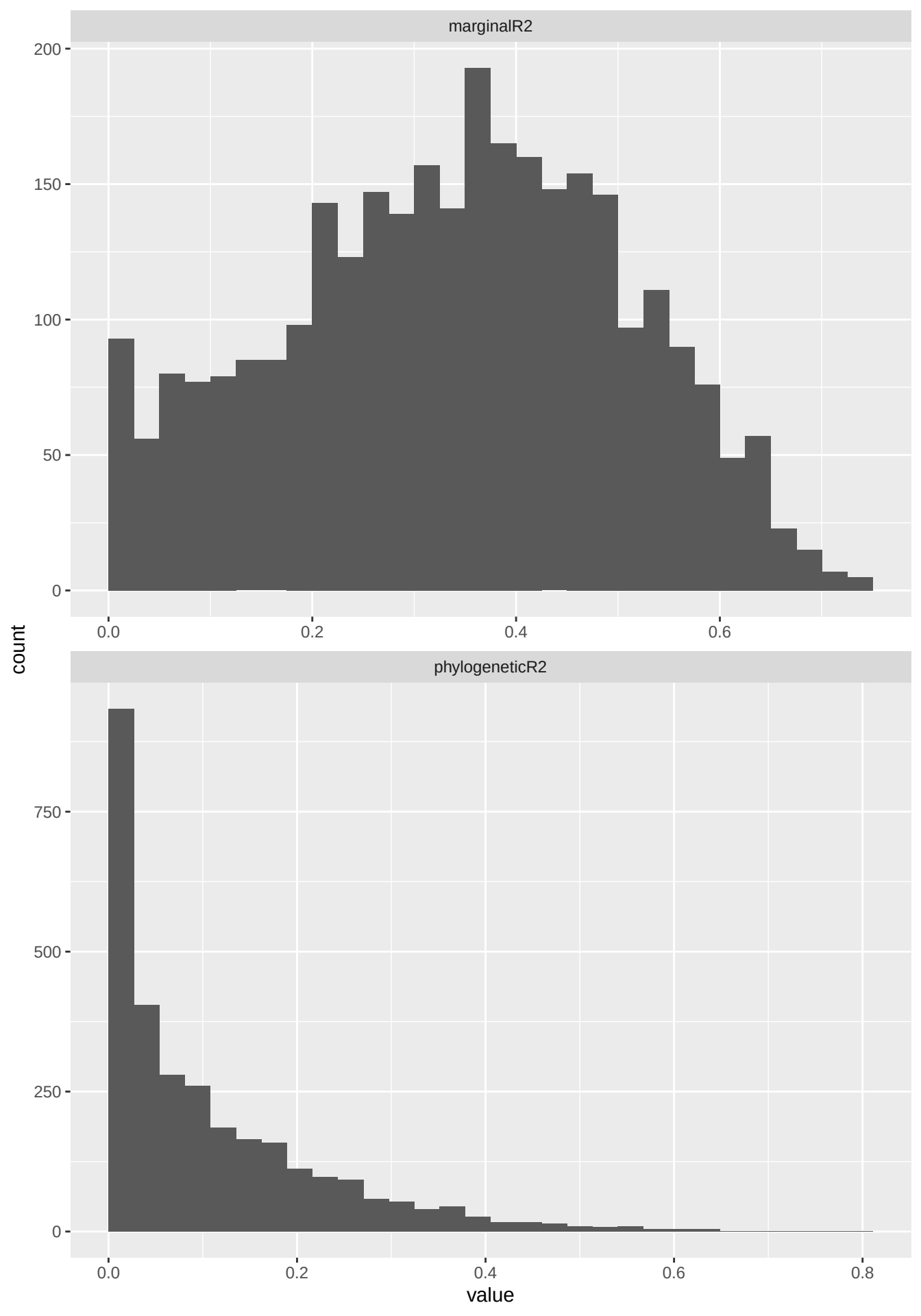
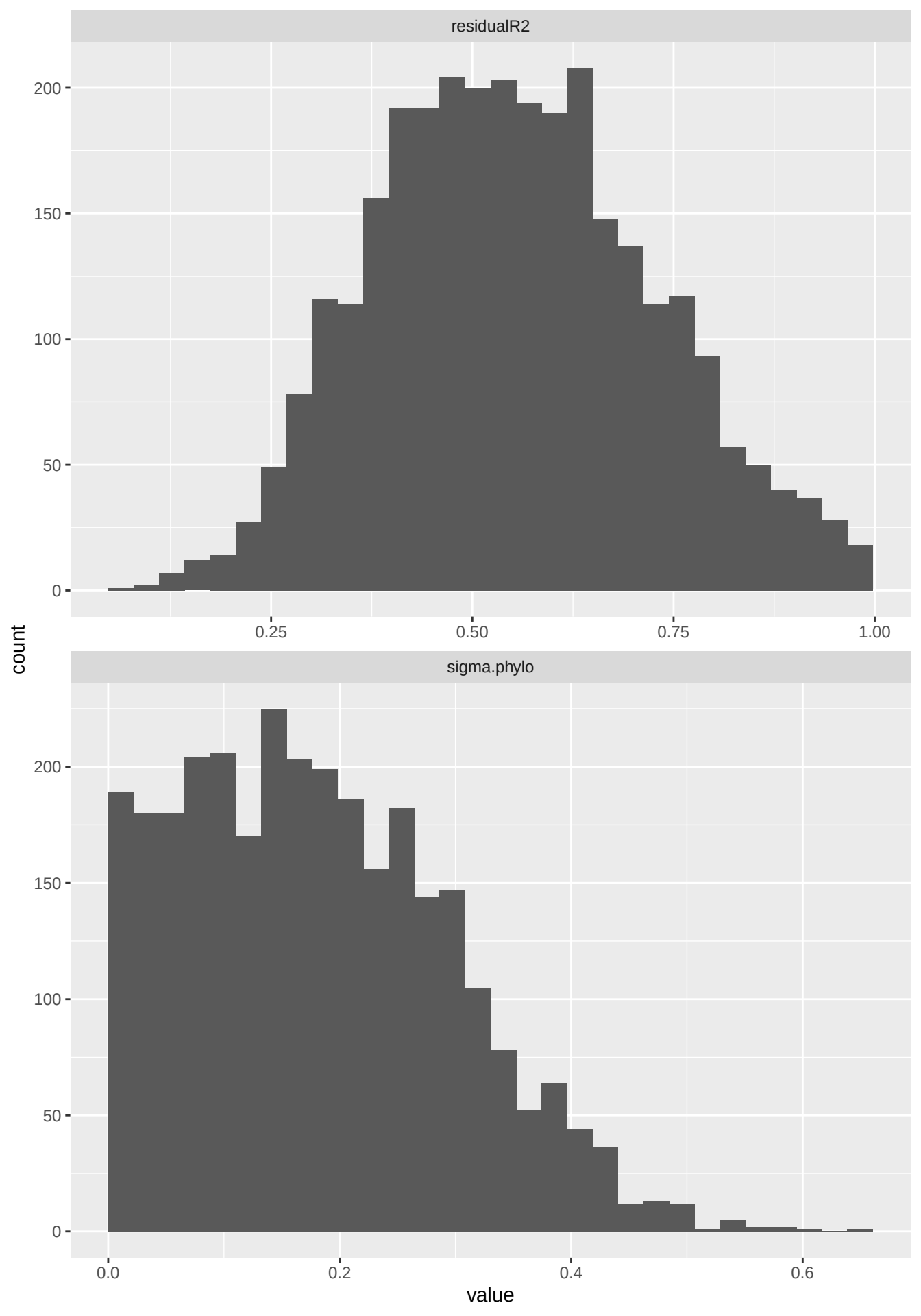
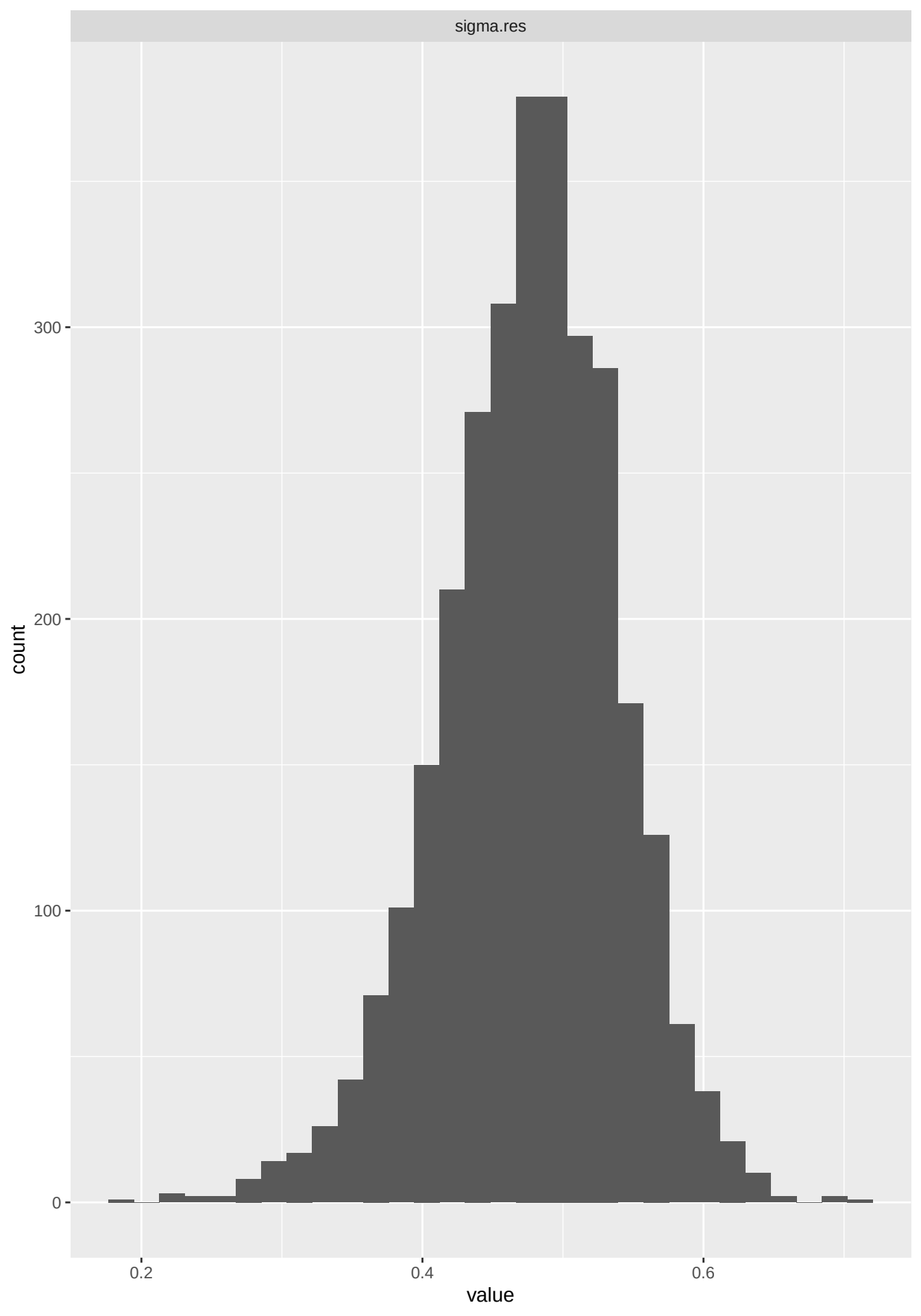
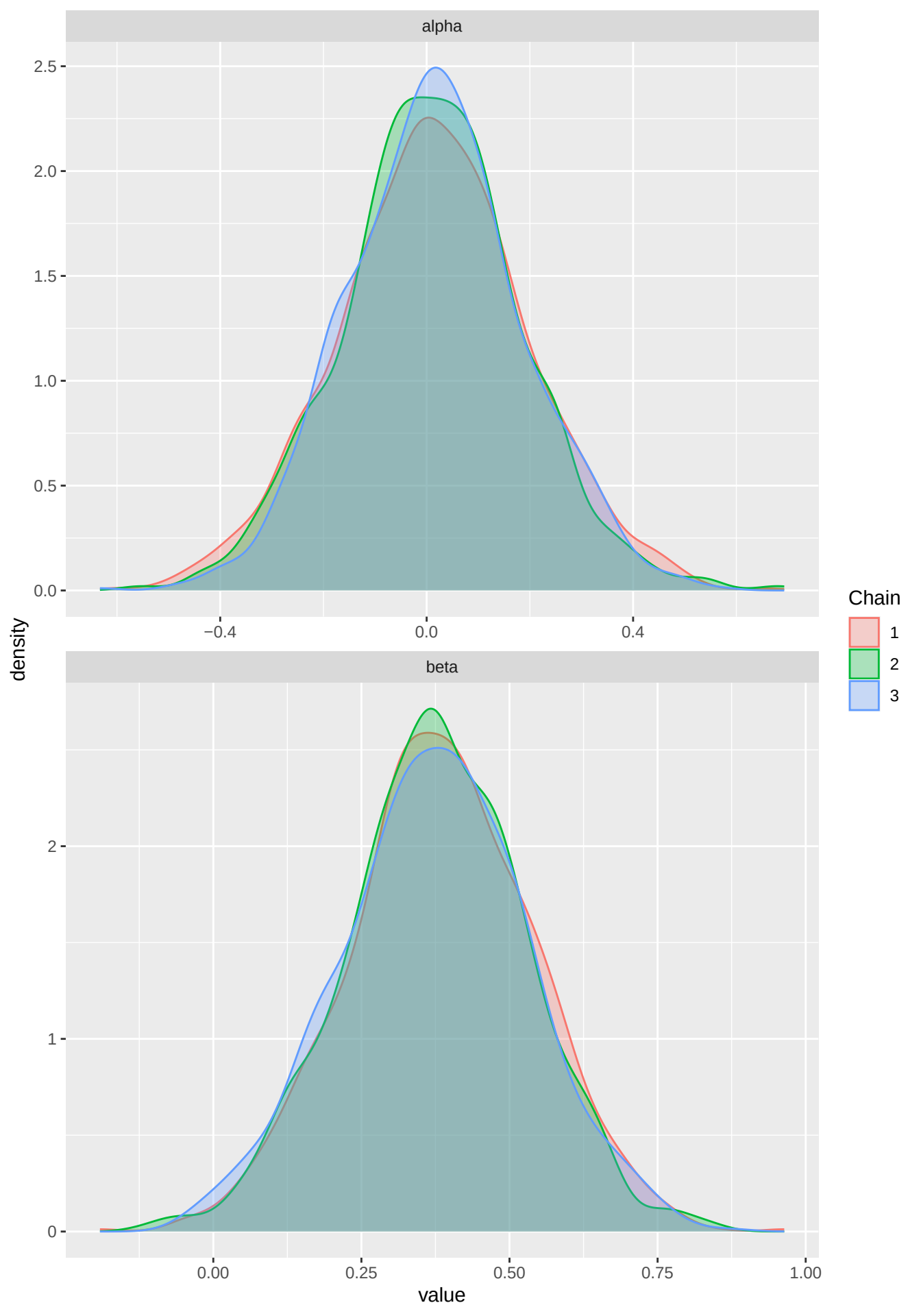

alpha
beta
count
value
300
200
100
0
−0.4
0.0
0.4
0.00
0.25
0.50
0.75
1.00

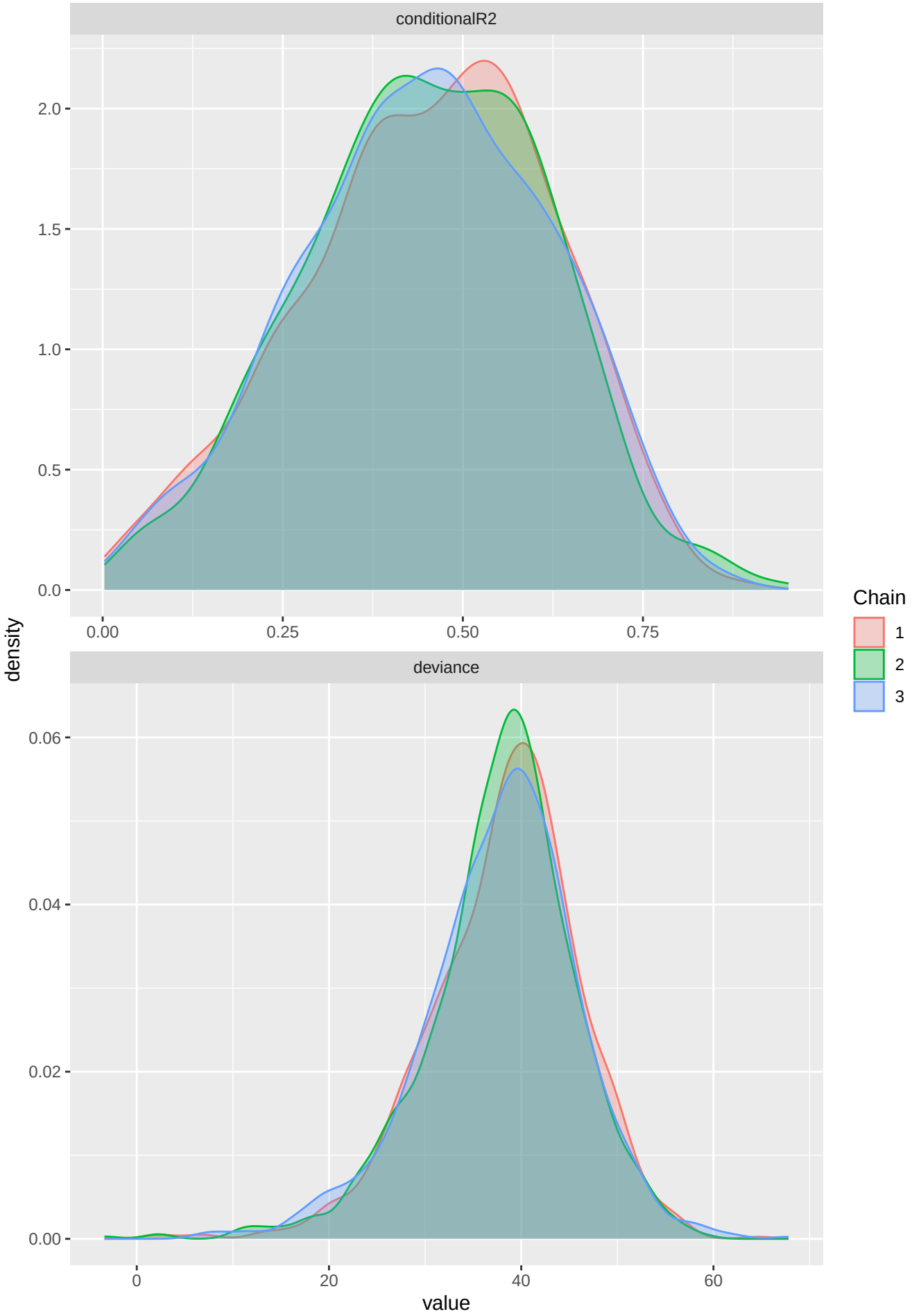

conditionalR2
deviance
count
value
0
50
100
150
200
0.00
0.25
0.50
0.75
0
100
200
300
400
0
20
40
60

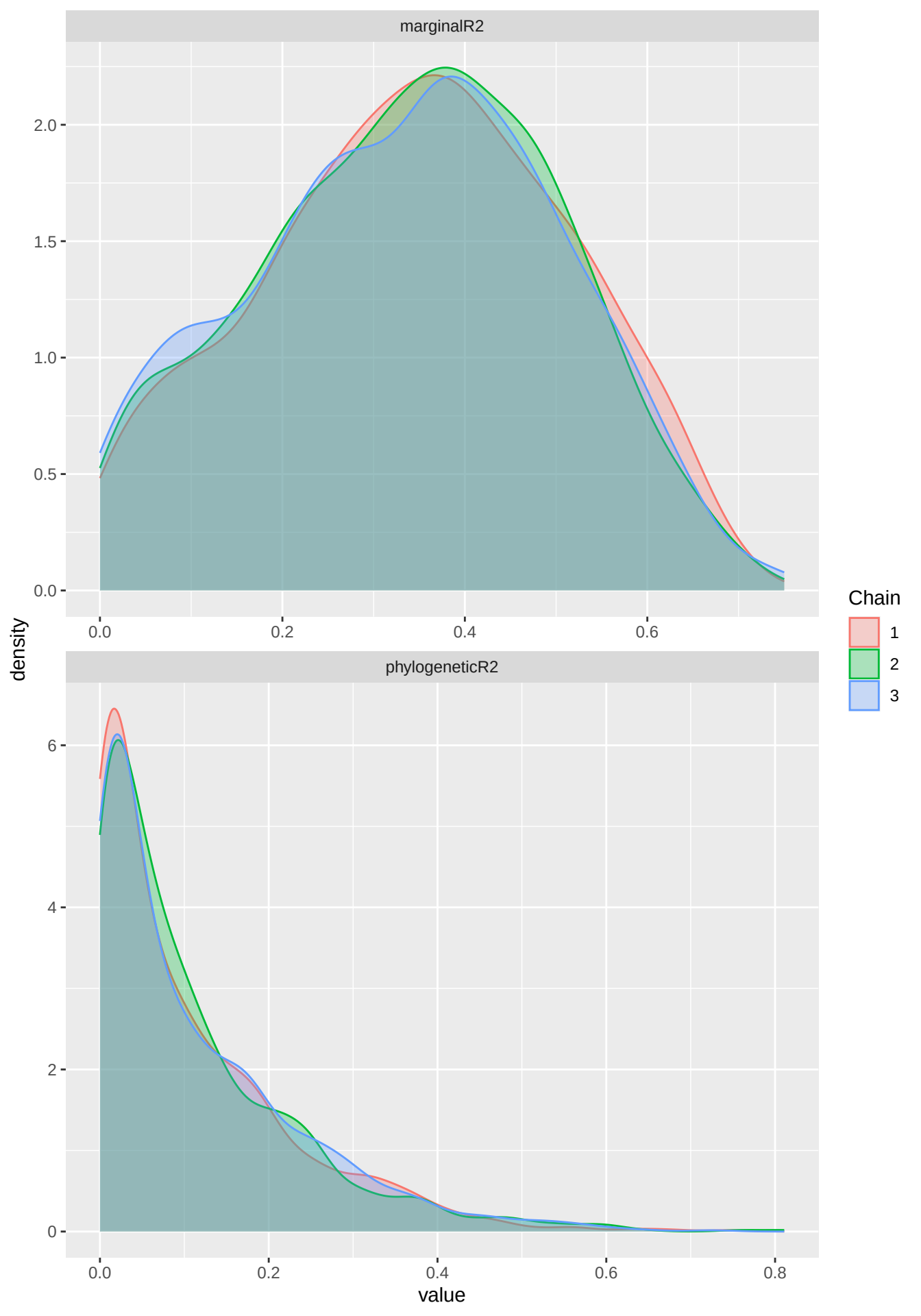

marginalR2
phylogeneticR2
count
value
200
150
100
50
0
750
500
250
0.0
0.2
0.4
0.6
0.8

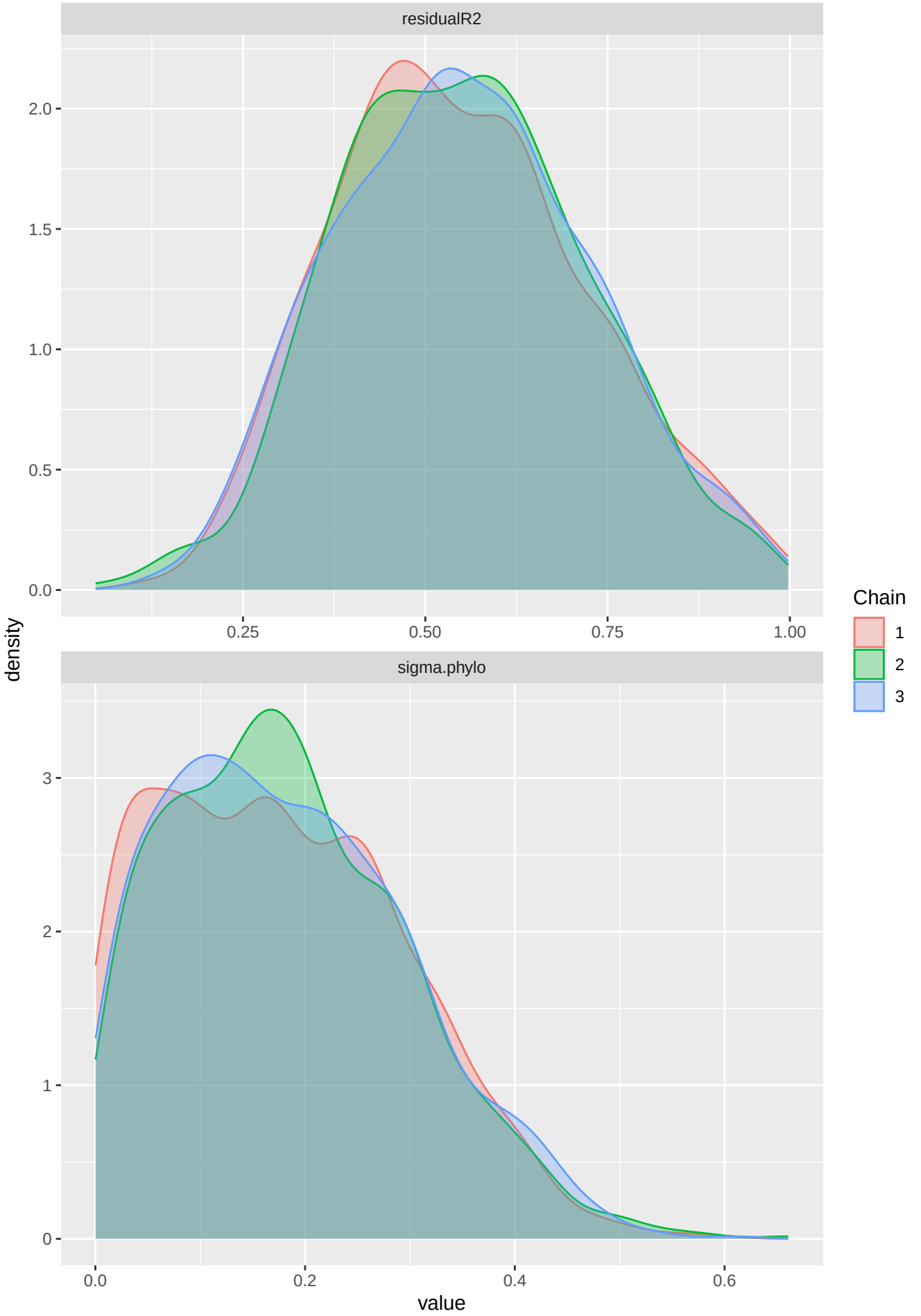

residualR2
sigma.phylo
count
value
0
50
100
150
200
0.25
0.50
0.75
1.00
0.0
0.2
0.4
0.6

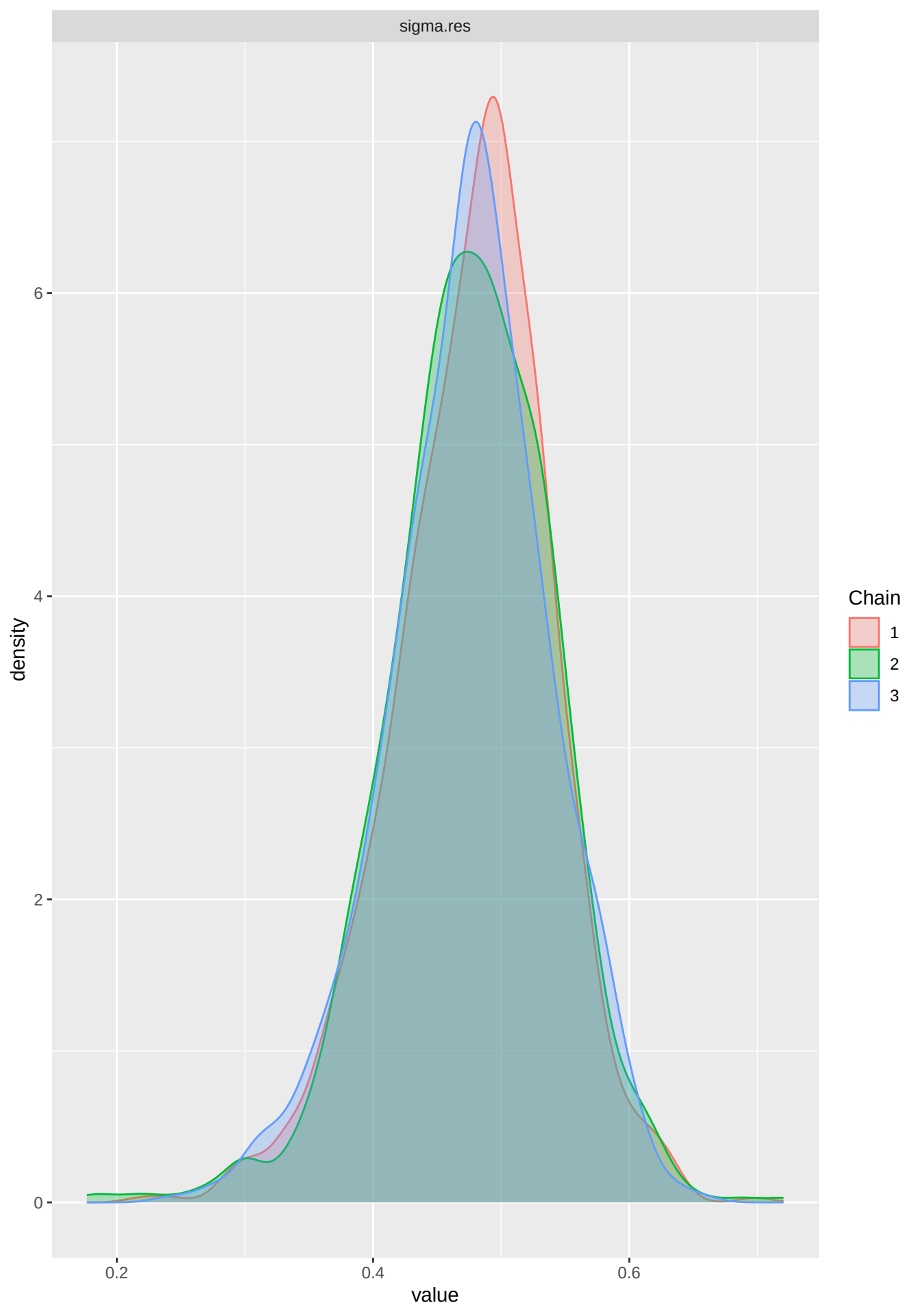

sigma.res
count
300
200
100
0
0.2
0.4
0.6
value

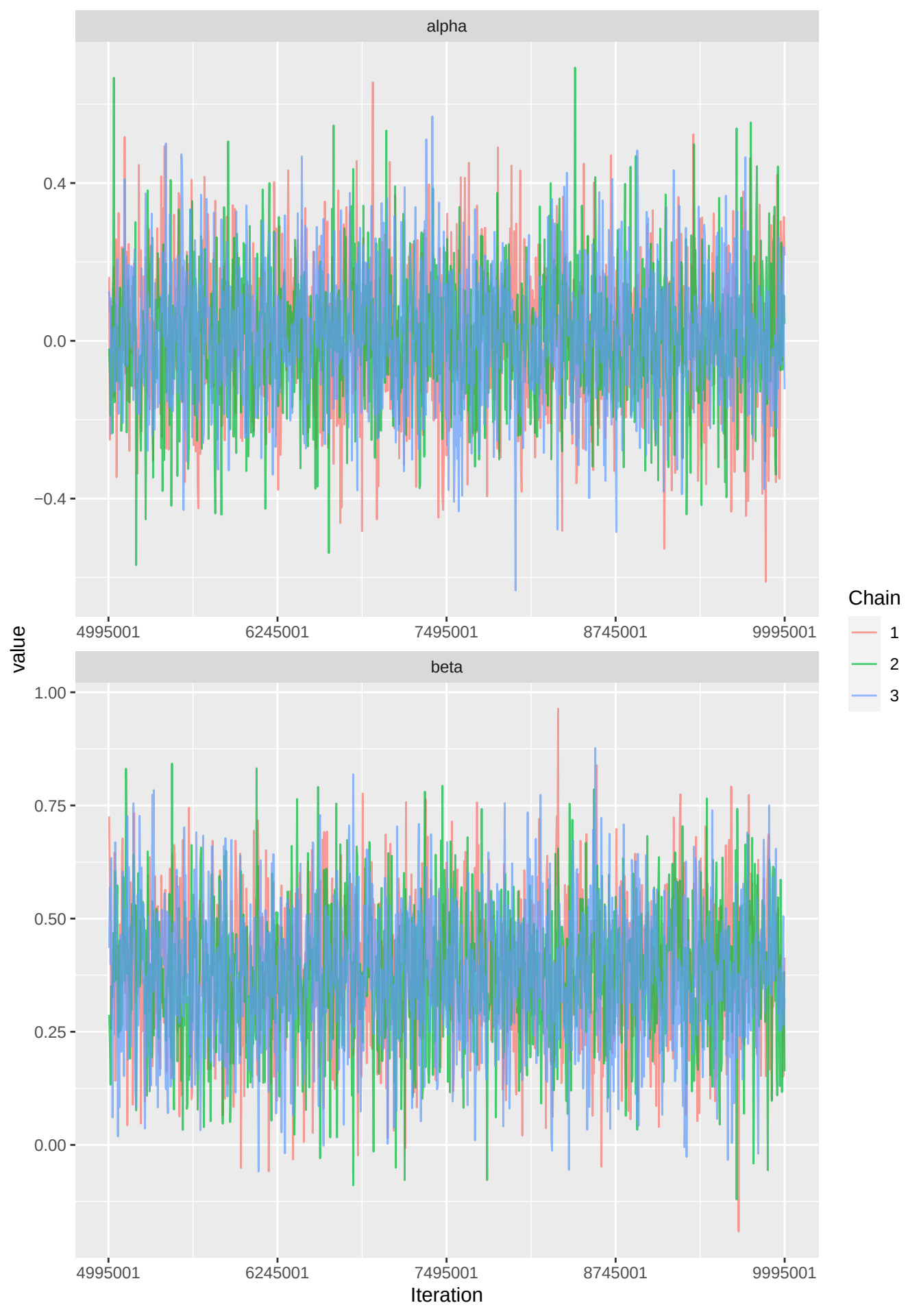

alpha
beta
density
value
Chain
1
2
3
2.5
2.0
1.5
1.0
0.5
0.0
−0.4
0.0
0.4
2
1
0
0.00
0.25
0.50
0.75
1.00

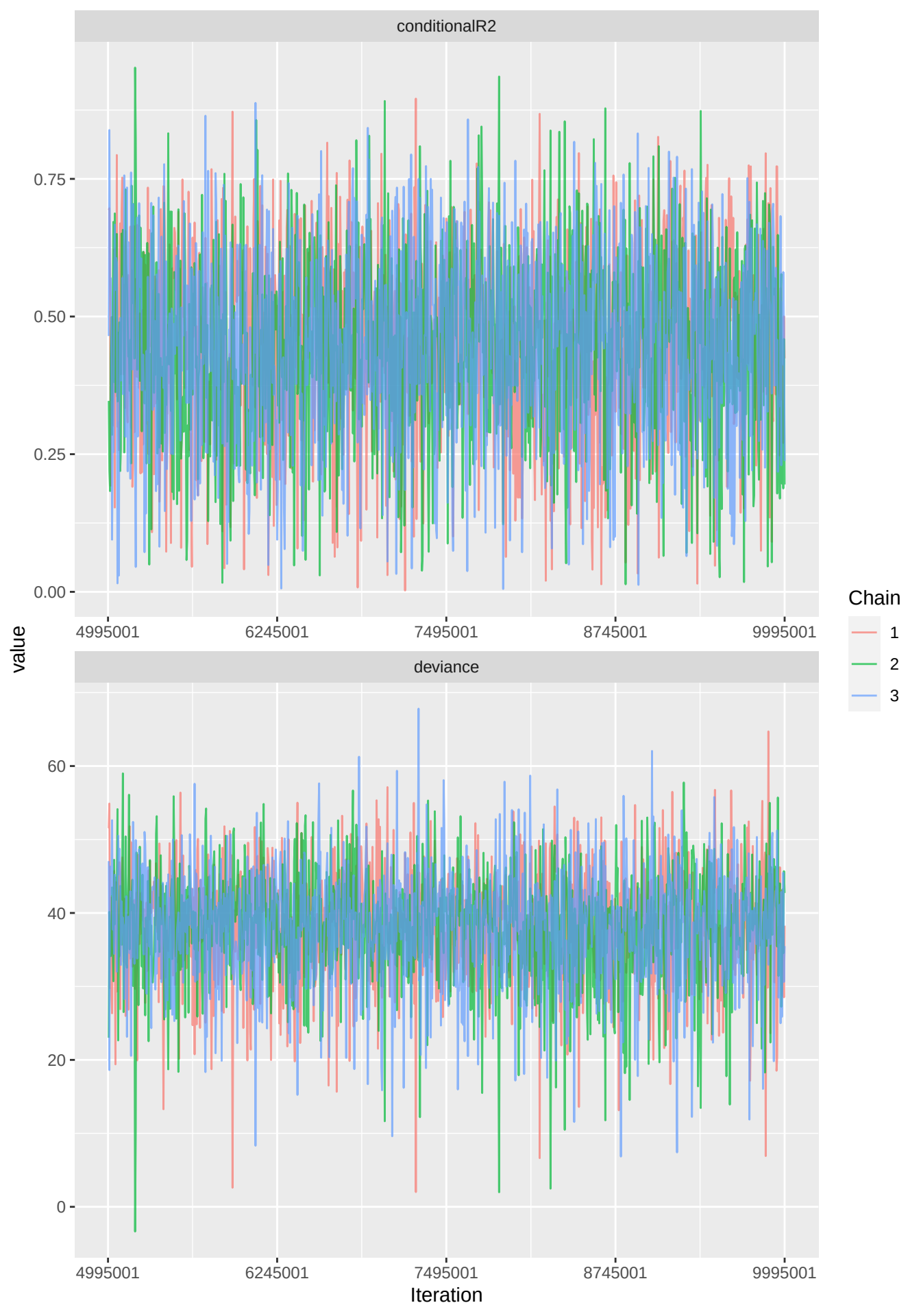

conditionalR2
deviance
density
value
Chain
1
2
3
0.0
0.5
1.0
1.5
2.0
0.00
0.25
0.50
0.75
0.00
0.02
0.04
0.06
0
20
40
60

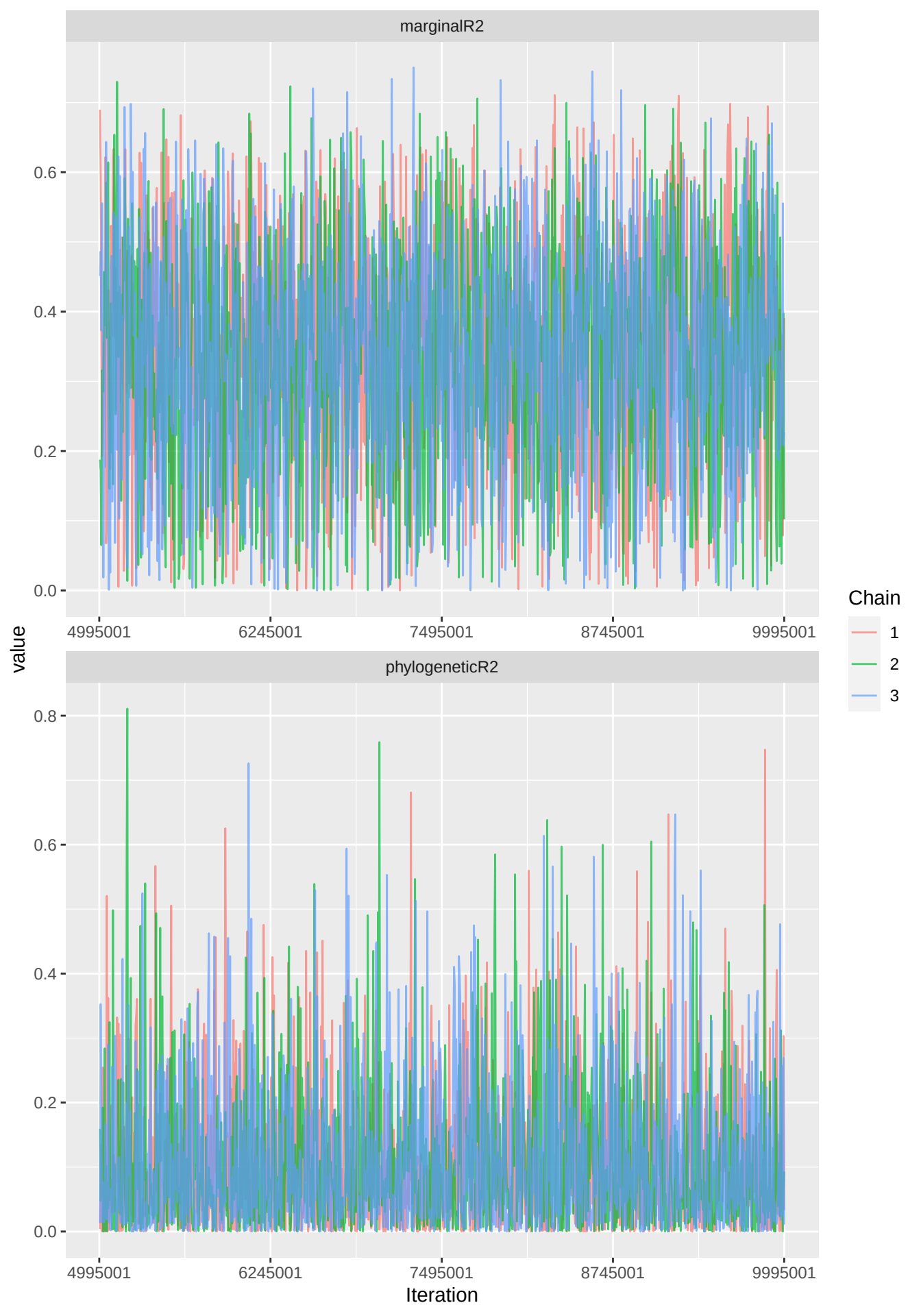

marginalR2
phylogeneticR2
density
value
Chain
1
2
3
0.0
0.5
1.0
1.5
2.0
0
2
4
6
0.0
0.2
0.4
0.6
0.8

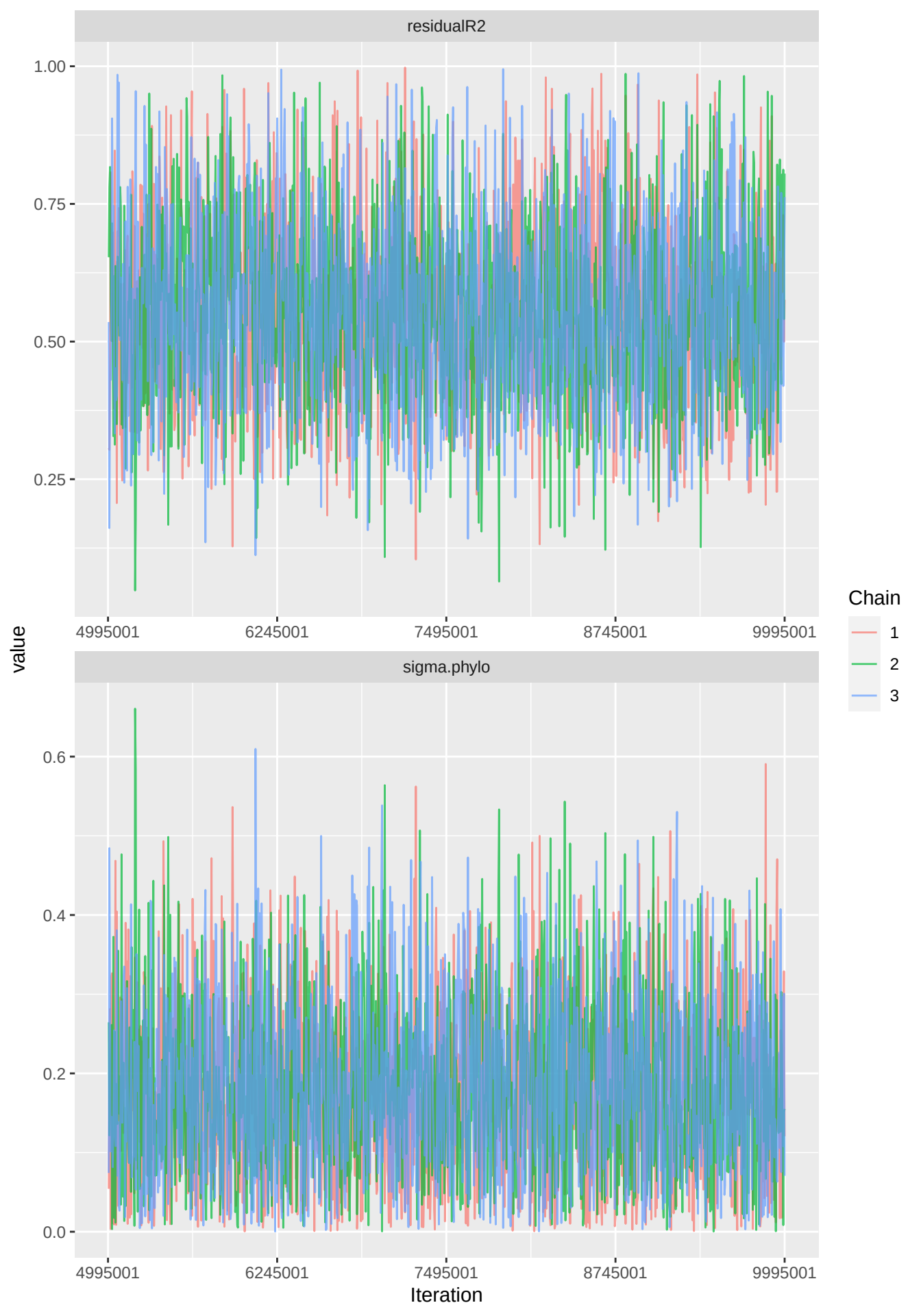

residualR2
sigma.phylo
density
value
Chain
1
2
3
0.0
0.5
1.0
1.5
2.0
0.25
0.50
0.75
1.00
0
1
2
3
0.0
0.2
0.4
0.6

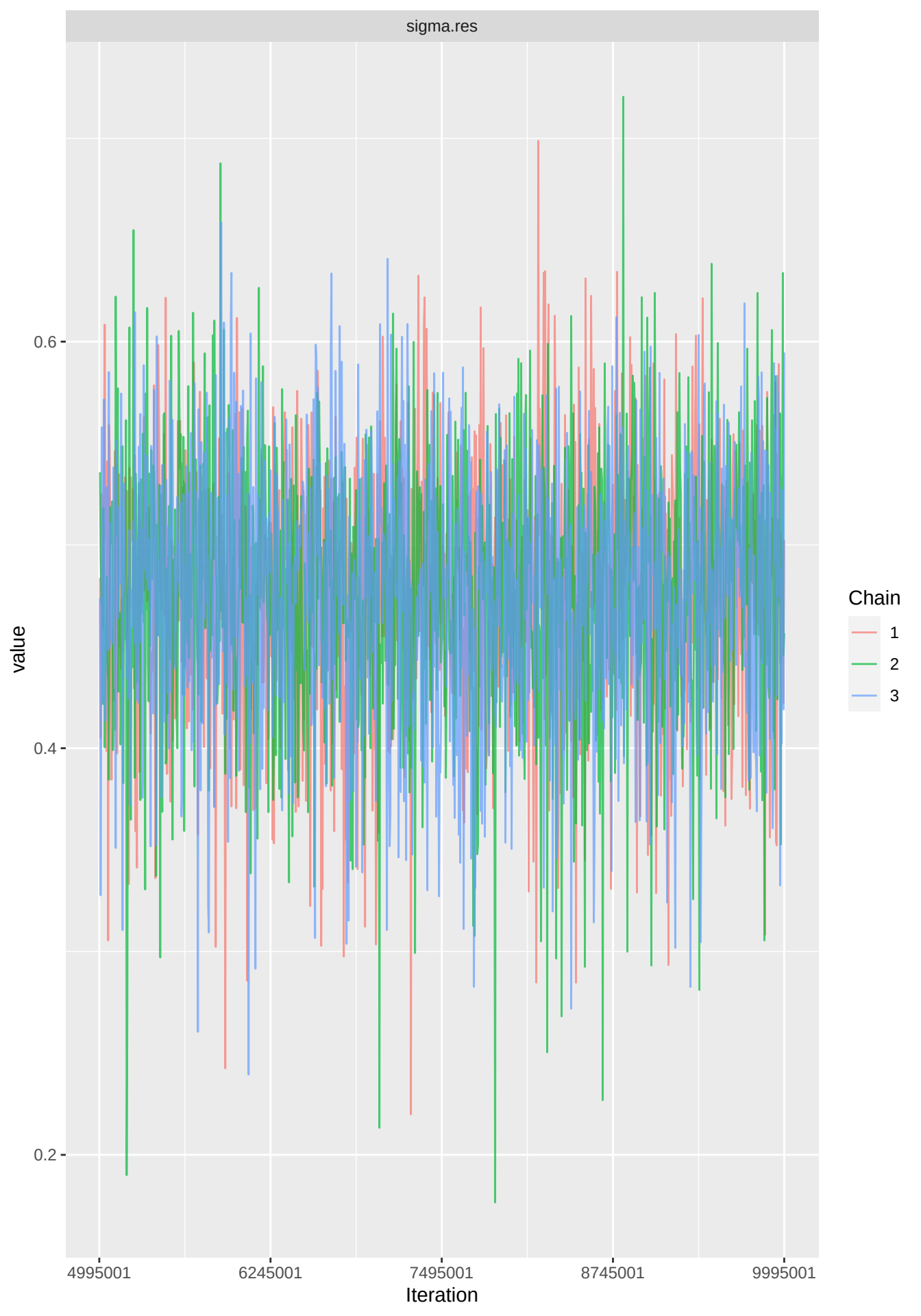

sigma.res
density
6
4
2
0
0.2
0.4
0.6
value
Chain
1
2
3

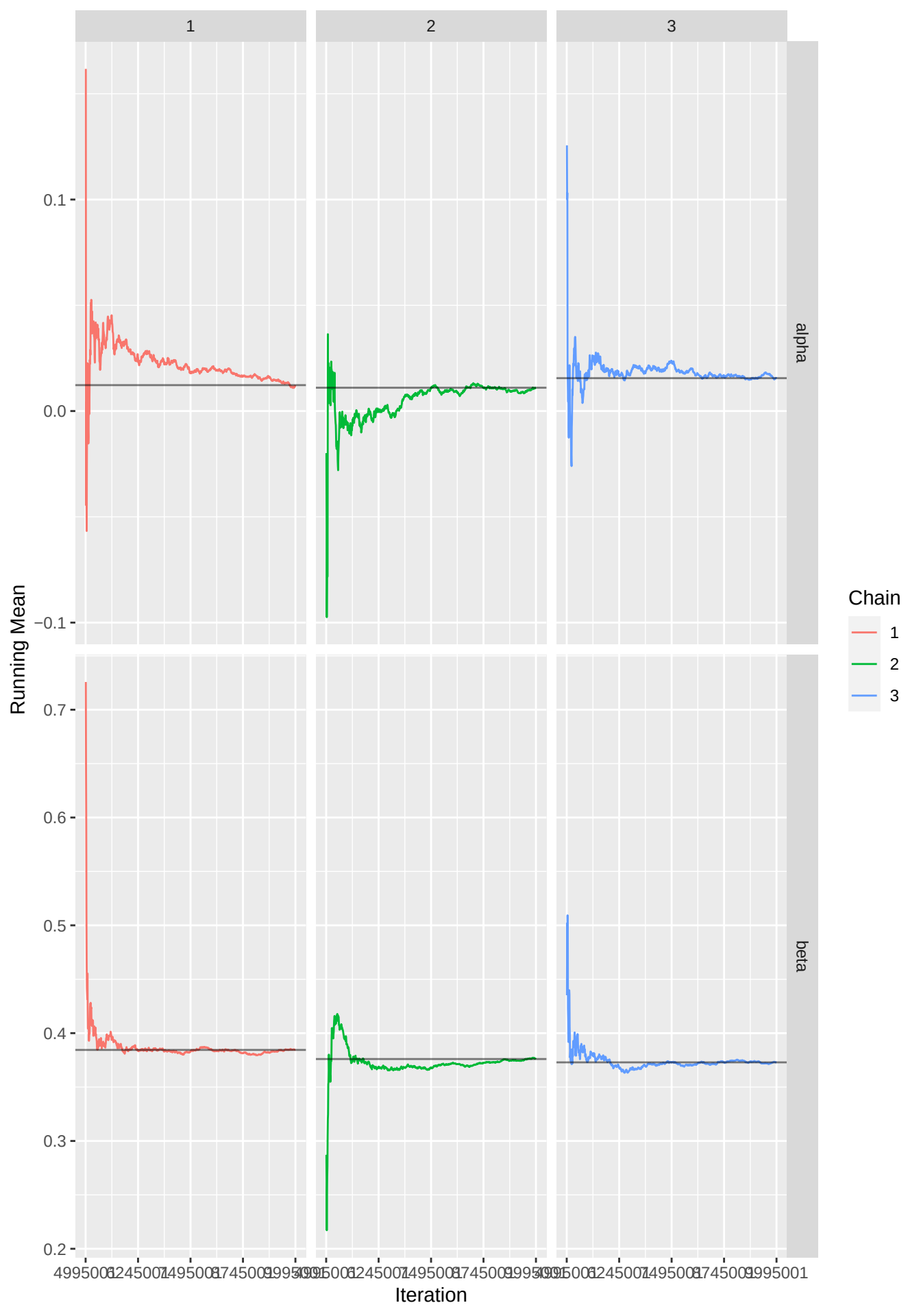

alpha
beta
0.4
0.0
−0.4
1.00
0.75
0.50
0.25
0.00
4995001
6245001
7495001
8745001
9995001
value
Iteration
Chain
1
2
3

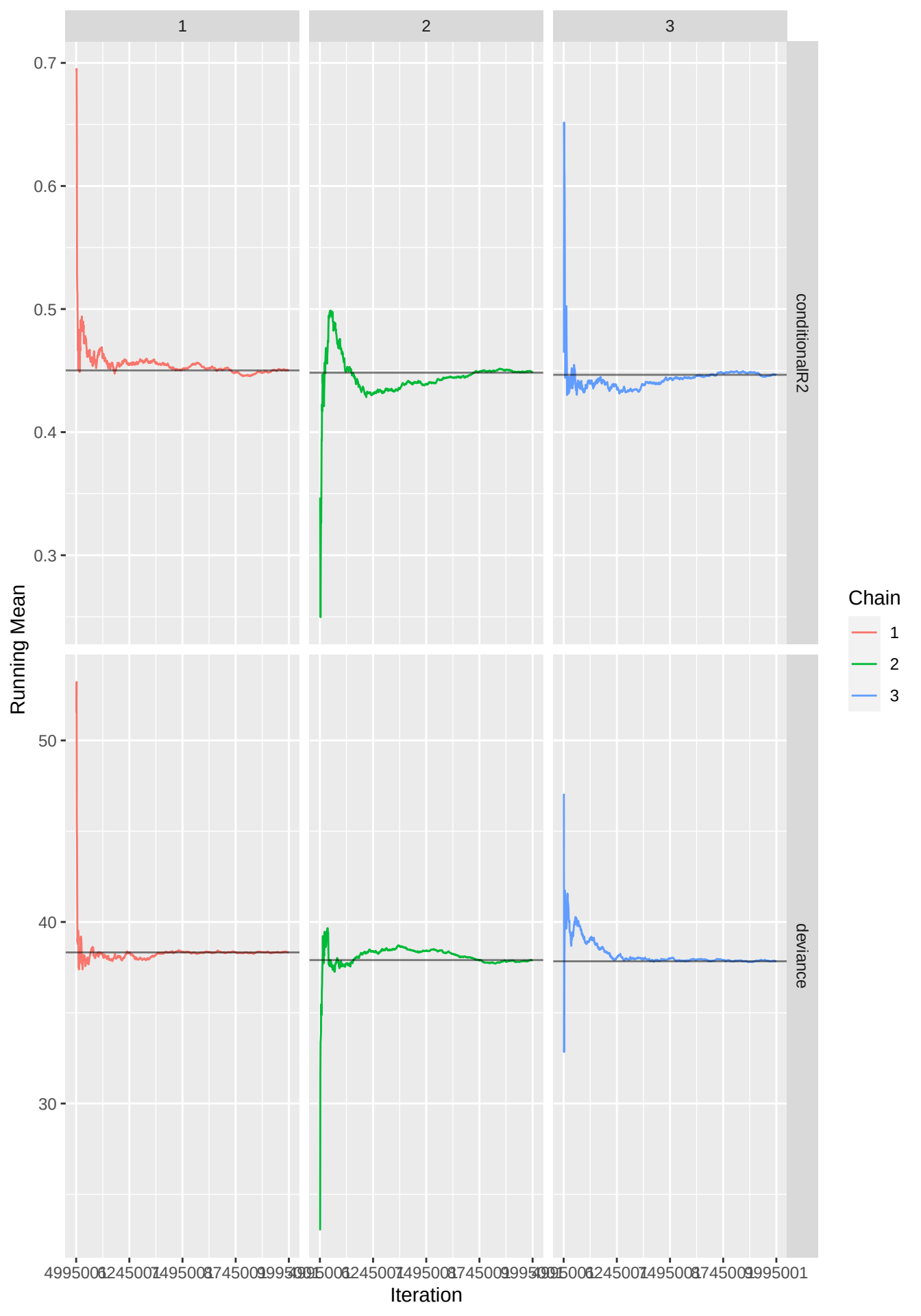

conditionalR2
0.75
0.50
0.25
0.00
4995001
6245001
7495001
8745001
9995001
deviance
60
40
20
0
4995001
6245001
7495001
8745001
9995001
value
Iteration
Chain
1
2
3

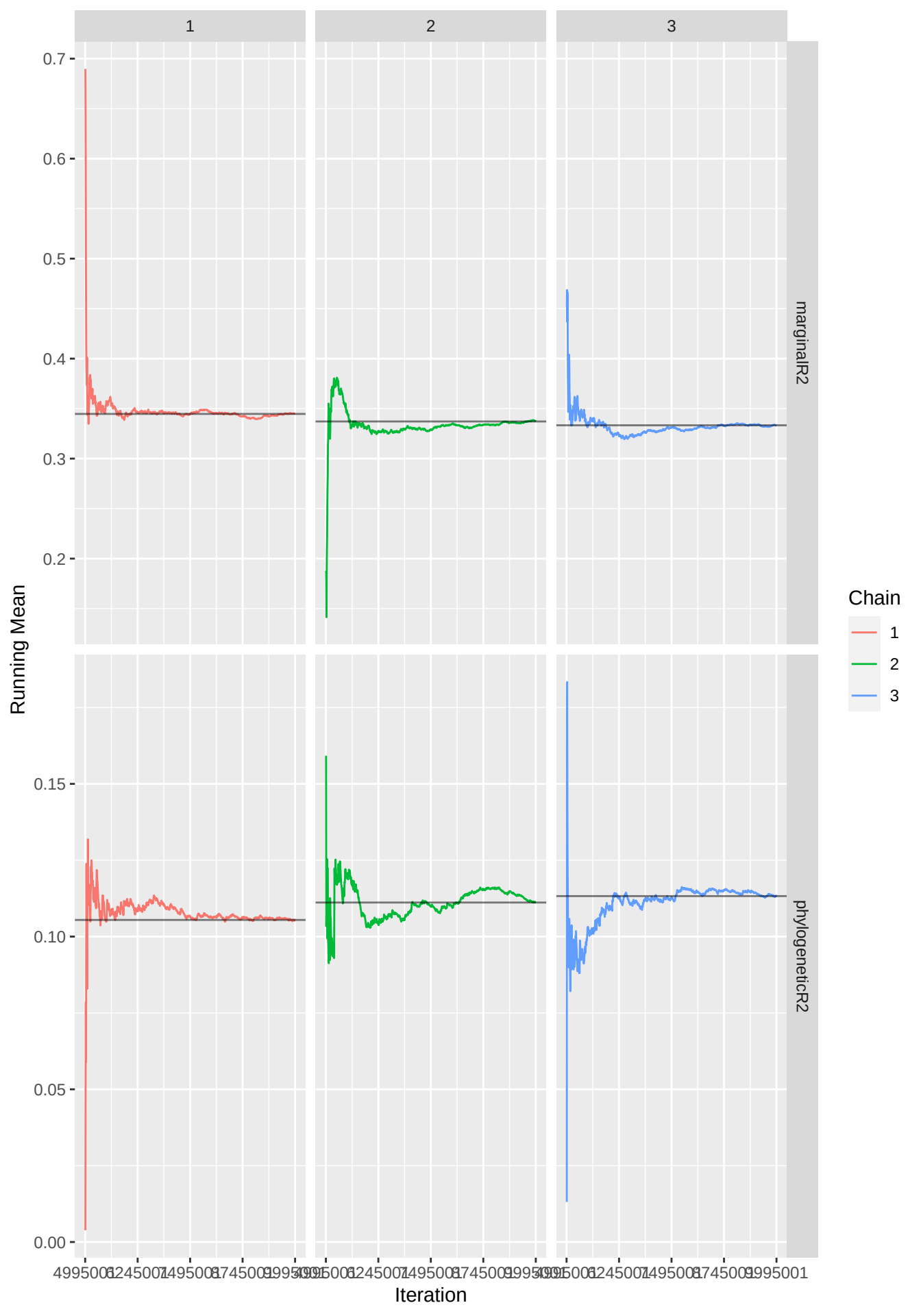

marginalR2
phylogeneticR2
value
Iteration
0.0
0.2
0.4
0.6
0.8
4995001
6245001
7495001
8745001
9995001
Chain
1
2
3

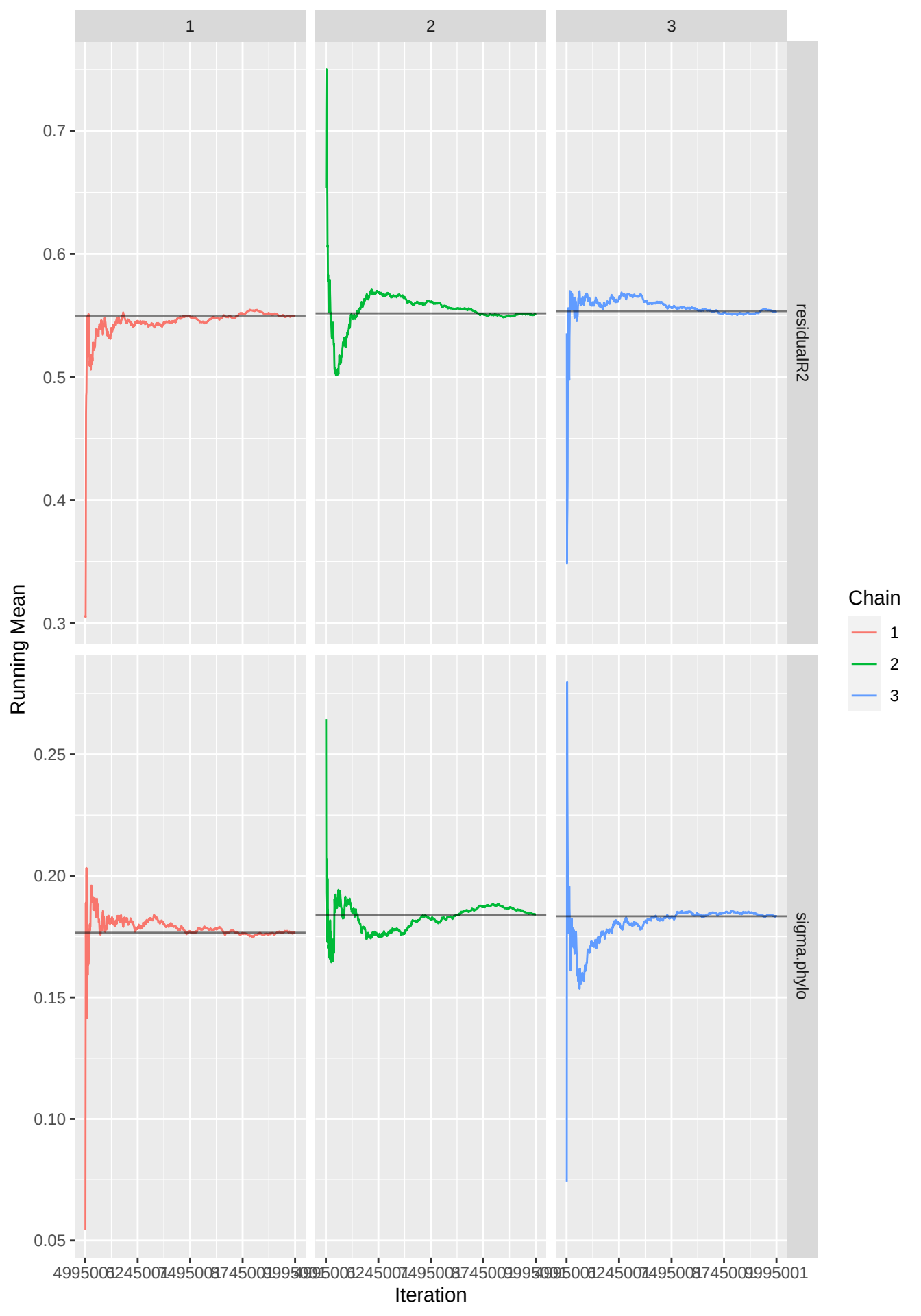

residualR2
1.00
0.75
0.50
0.25
4995001
6245001
7495001
8745001
9995001
sigma.phylo
0.6
0.4
0.2
0.0
4995001
6245001
7495001
8745001
9995001
value
Iteration
Chain
1
2
3

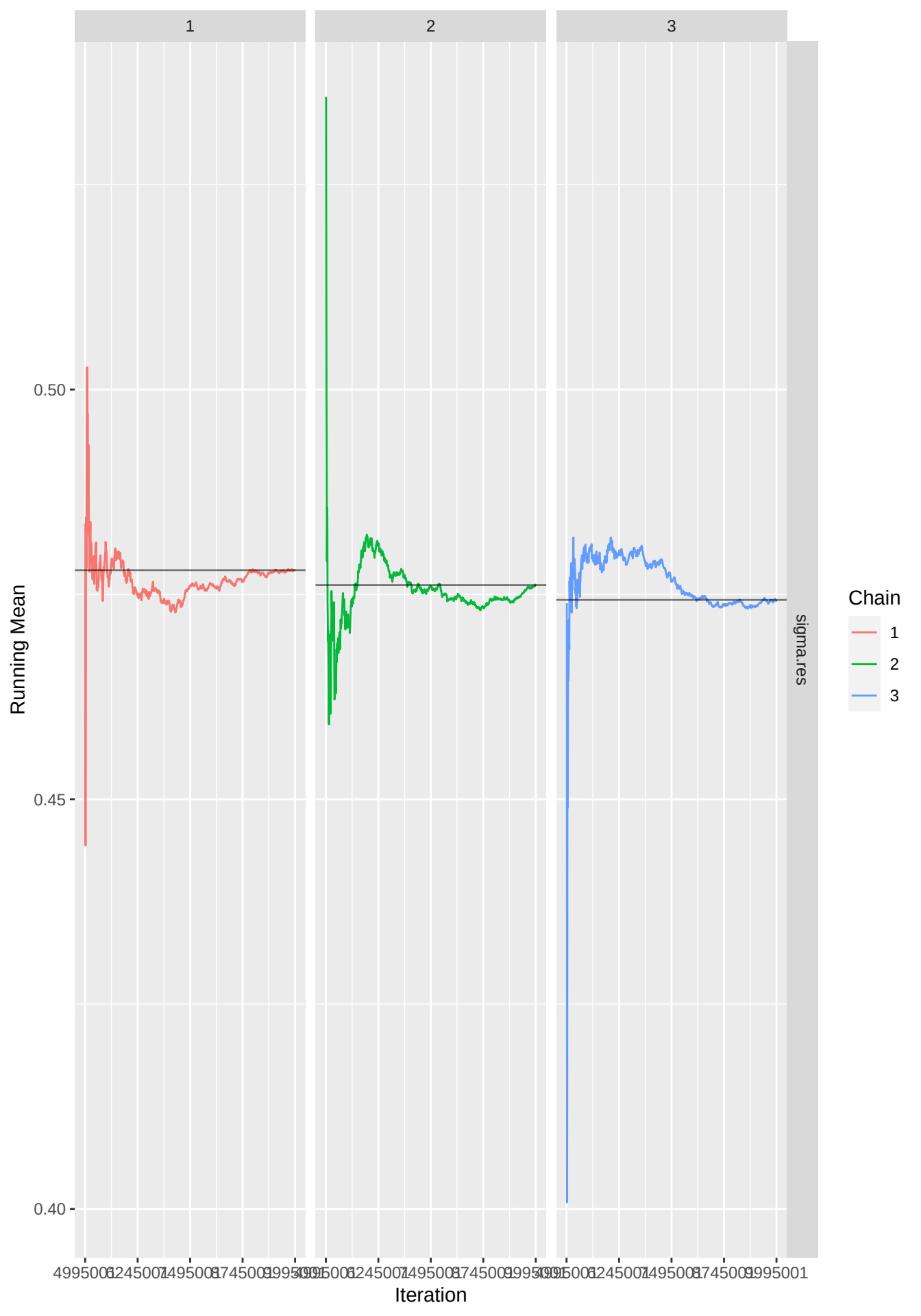

sigma.res
value
0.6
0.4
0.2
4995001
6245001
7495001
8745001
9995001
Iteration
Chain
1
2
3

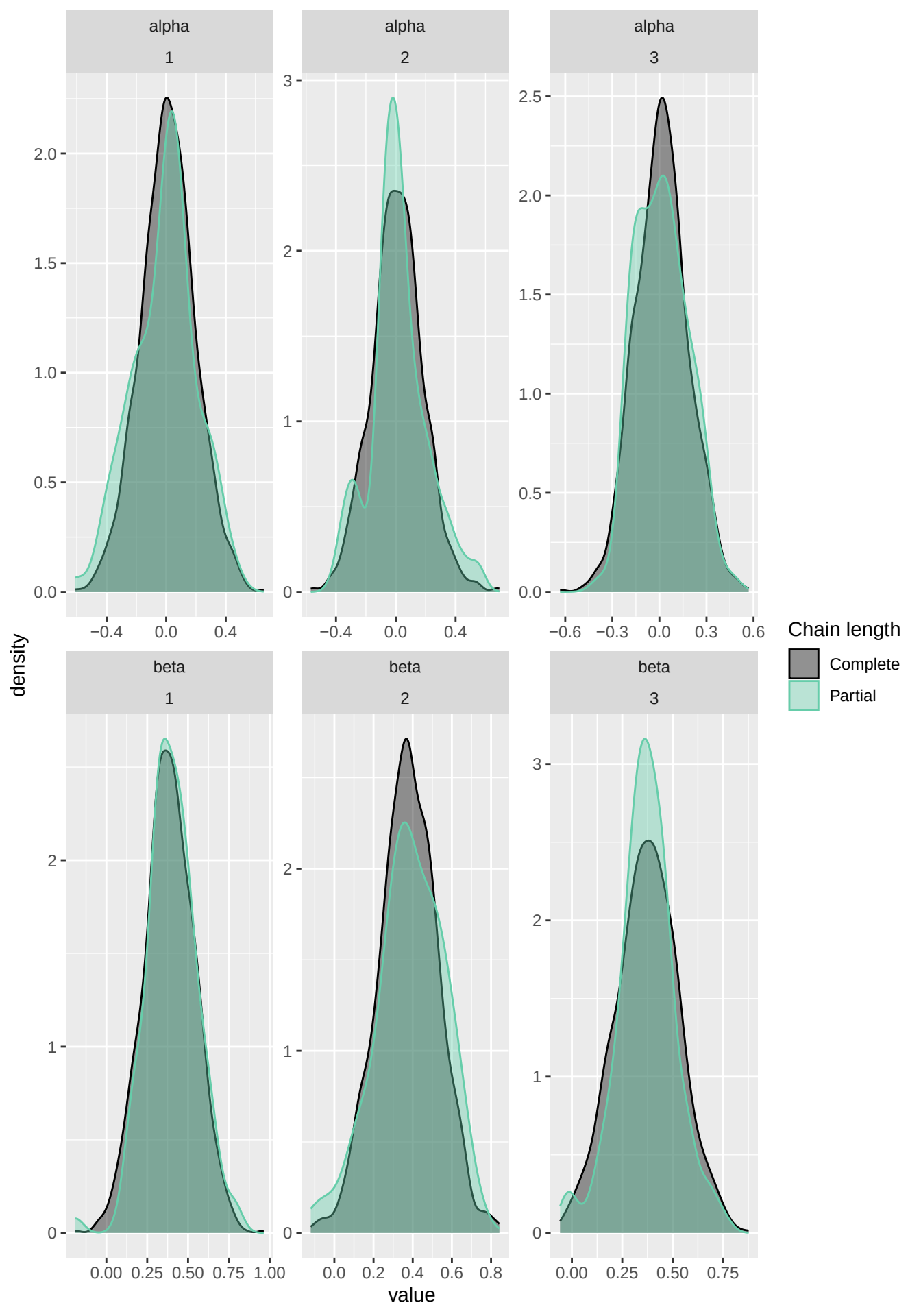

1
2
3
alpha
beta
Running Mean
Iteration
Chain
1
2
3
0.1
0.0
−0.1
0.7
0.6
0.5
0.4
0.3
0.2
4995001
6245001
7495001
8745001
9995001

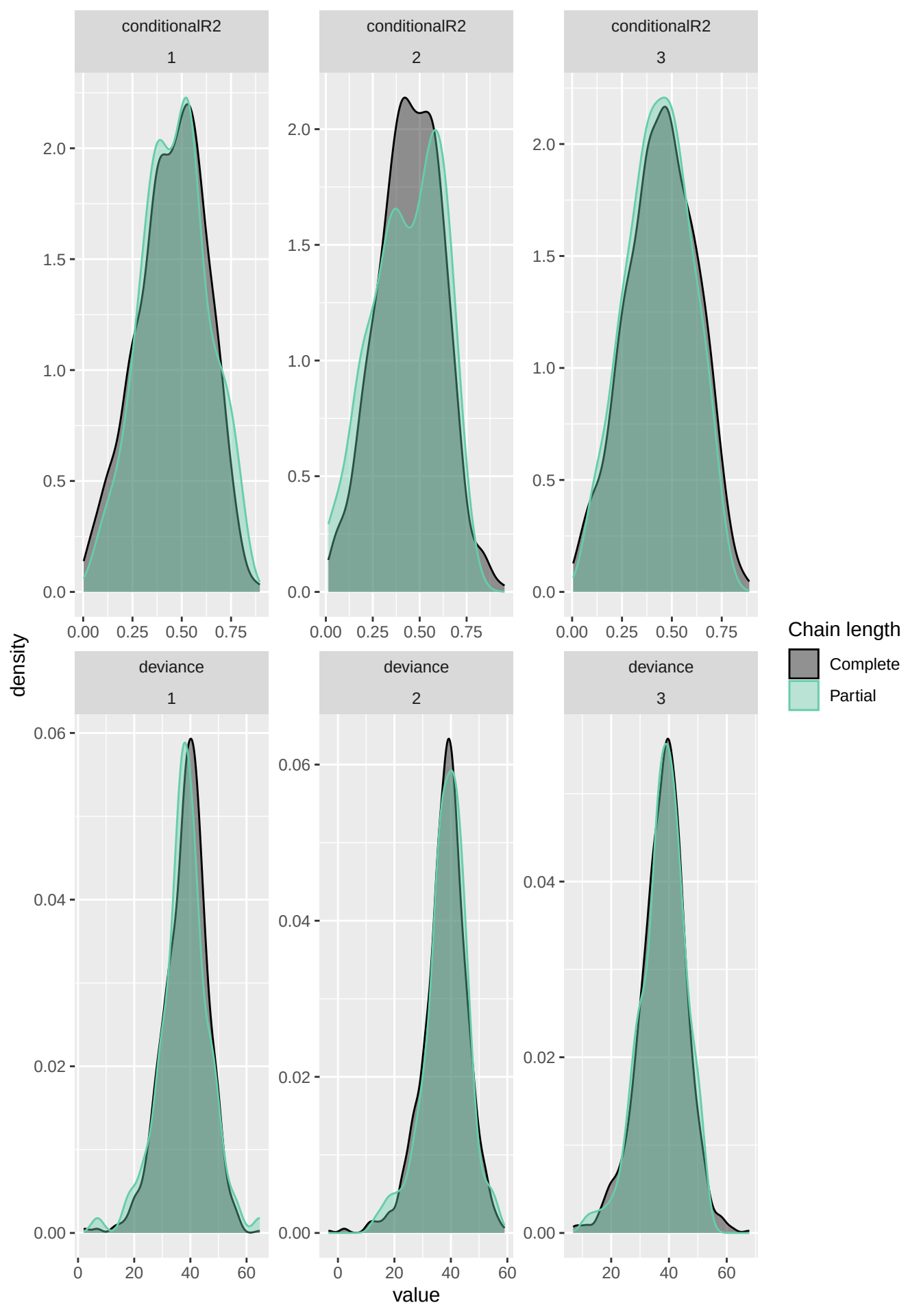

1
2
3
conditionalR2
deviance
0.7
0.6
0.5
0.4
0.3
50
40
30
Running Mean
4995001
6245001
7495001
8745001
9995001
Iteration
Chain
1
2
3

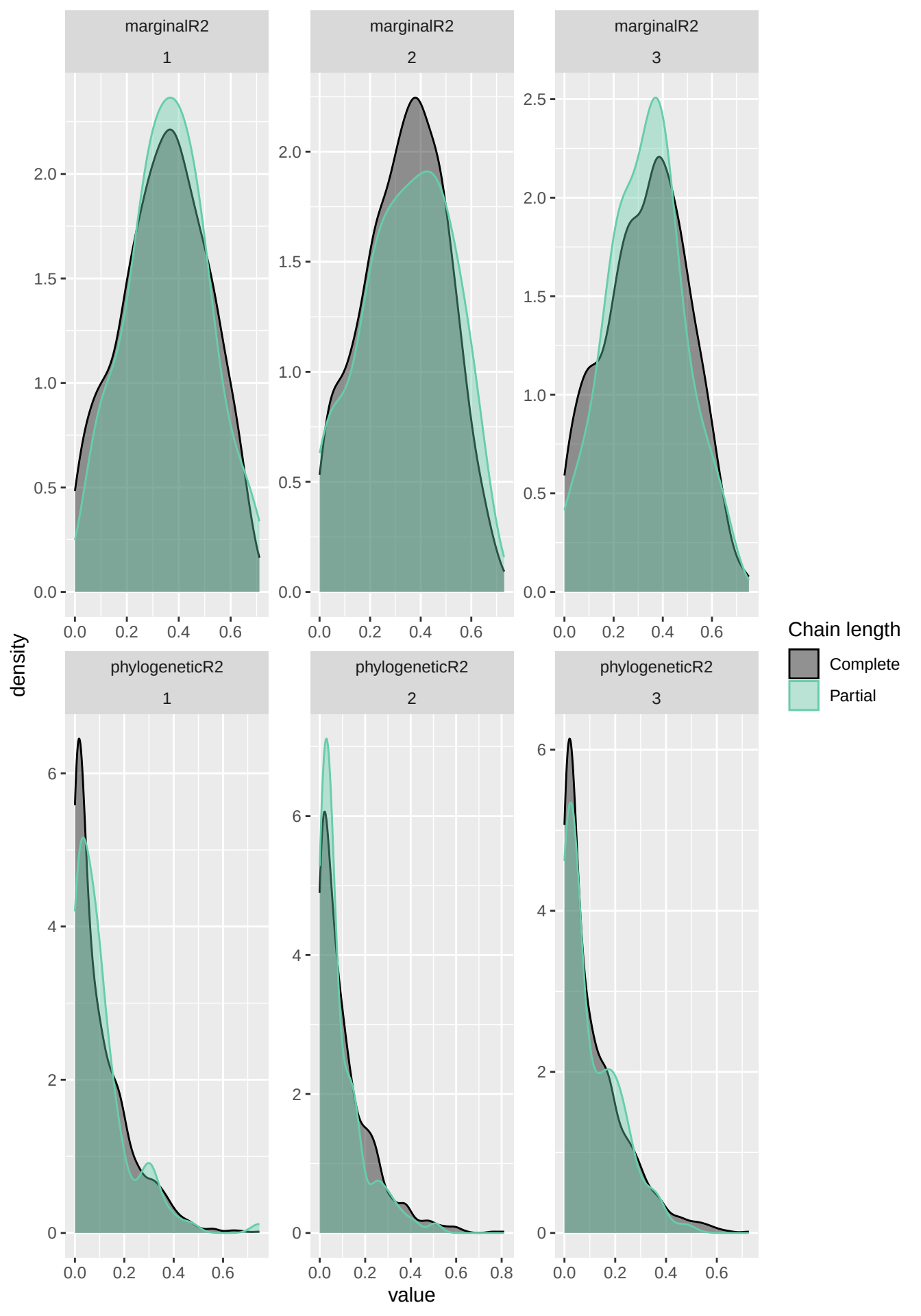

1
2
3
marginalR2
phylogeneticR2
Running Mean
Iteration
Chain
1
2
3
0.7
0.6
0.5
0.4
0.3
0.2
0.15
0.10
0.05
0.00
4995001
6245001
7495001
8745001
9995001

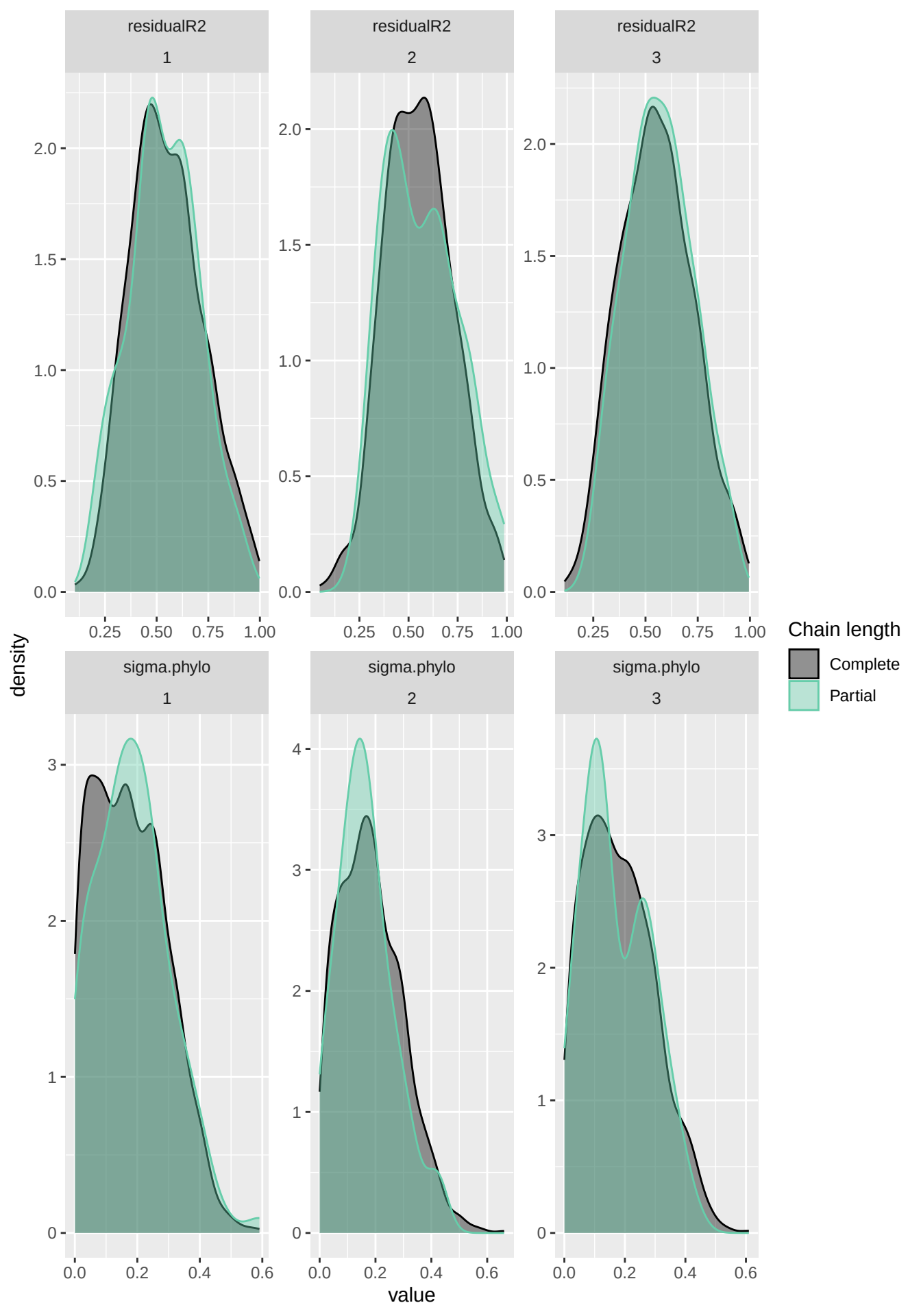

1
2
3
residualR2
sigma.phylo
Running Mean
0.7
0.6
0.5
0.4
0.3
0.25
0.20
0.15
0.10
0.05
4995001
1245001
1495001
1745001
1995001
Iteration
Chain
1
2
3

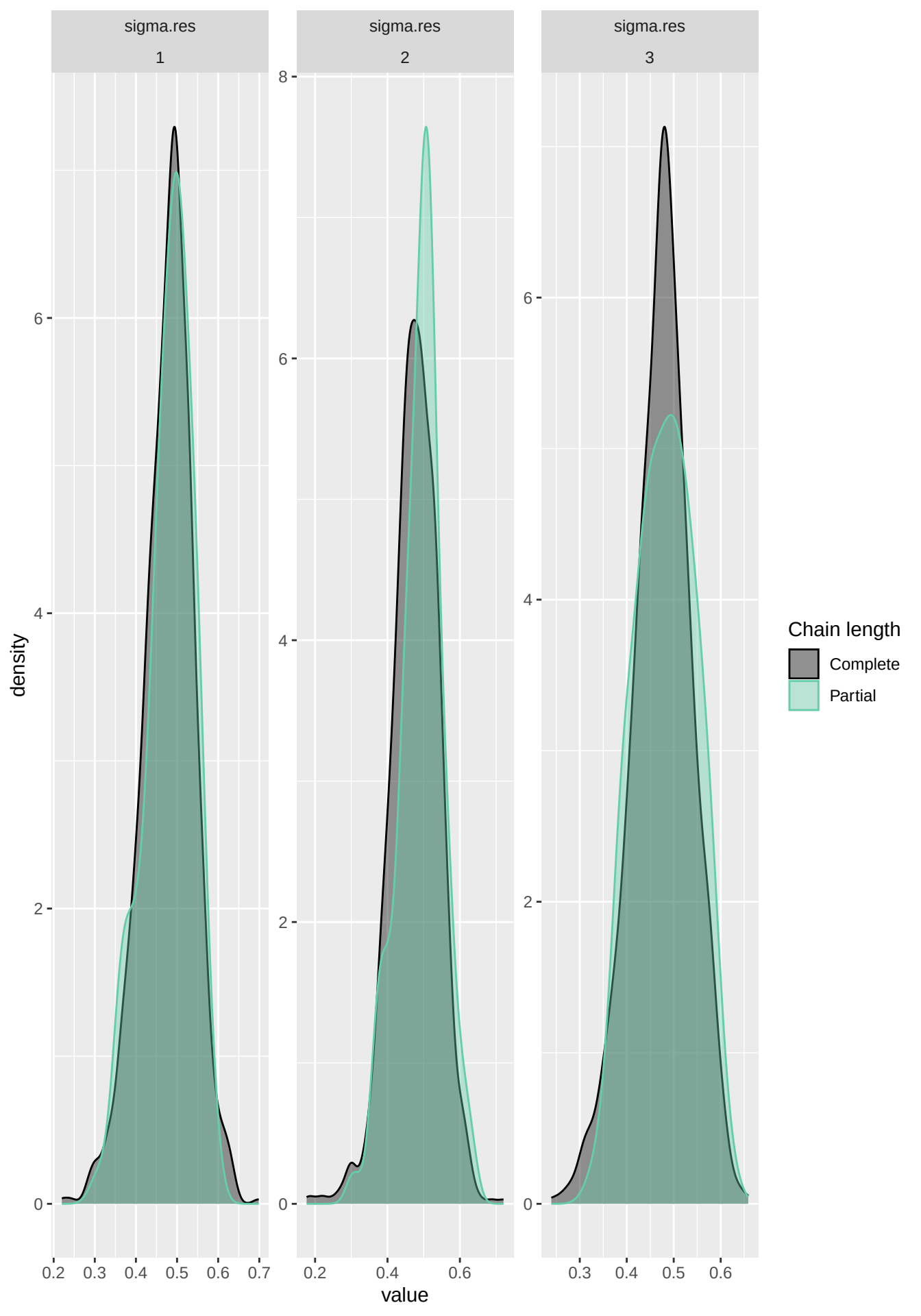

1
2
3
0.50
0.45
0.40
Running Mean
Iteration
sigma.res
Chain
1
2
3

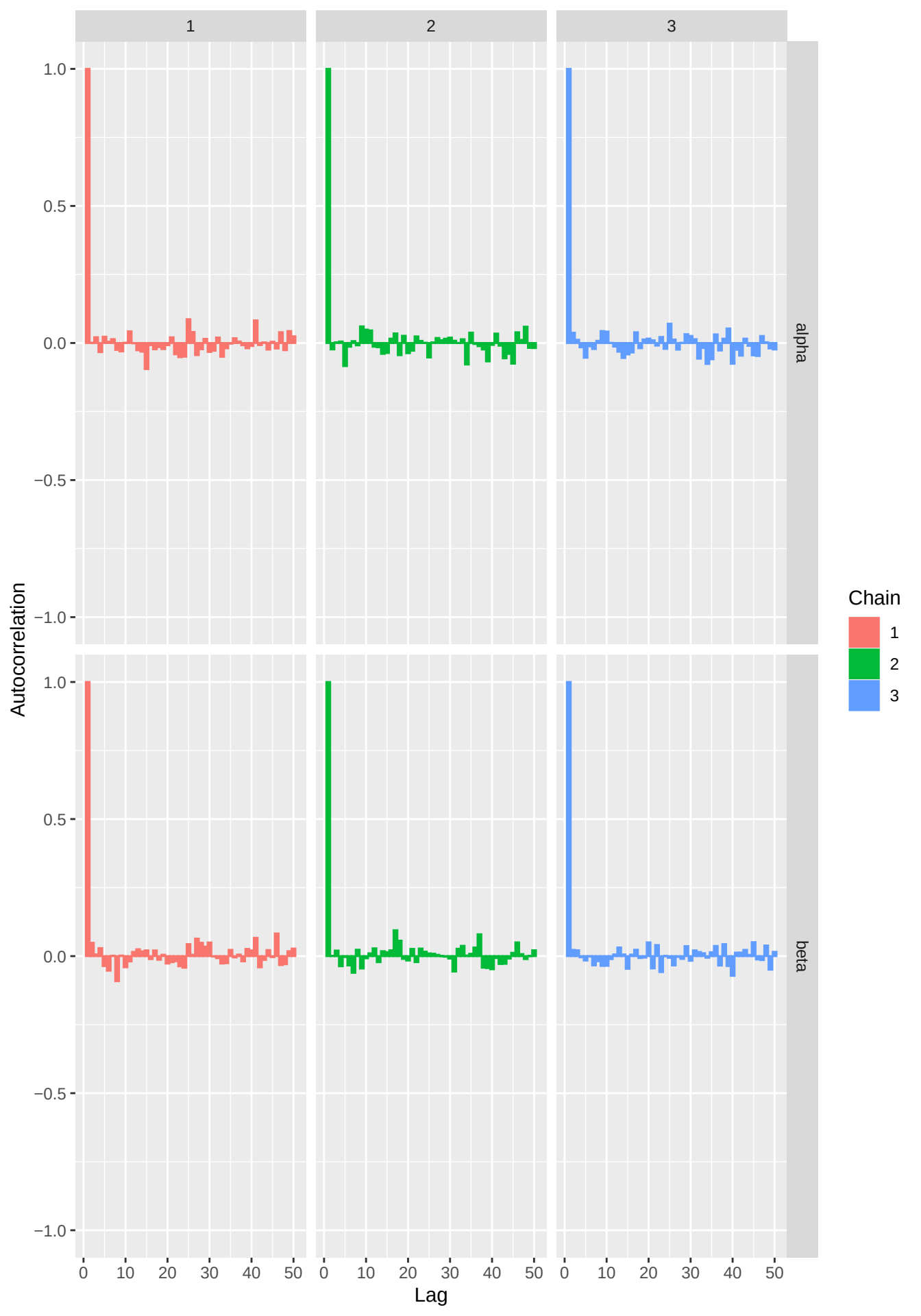

alpha
1
alpha
2
alpha
3
beta
1
beta
2
beta
3
density
value
Chain length
Complete
Partial

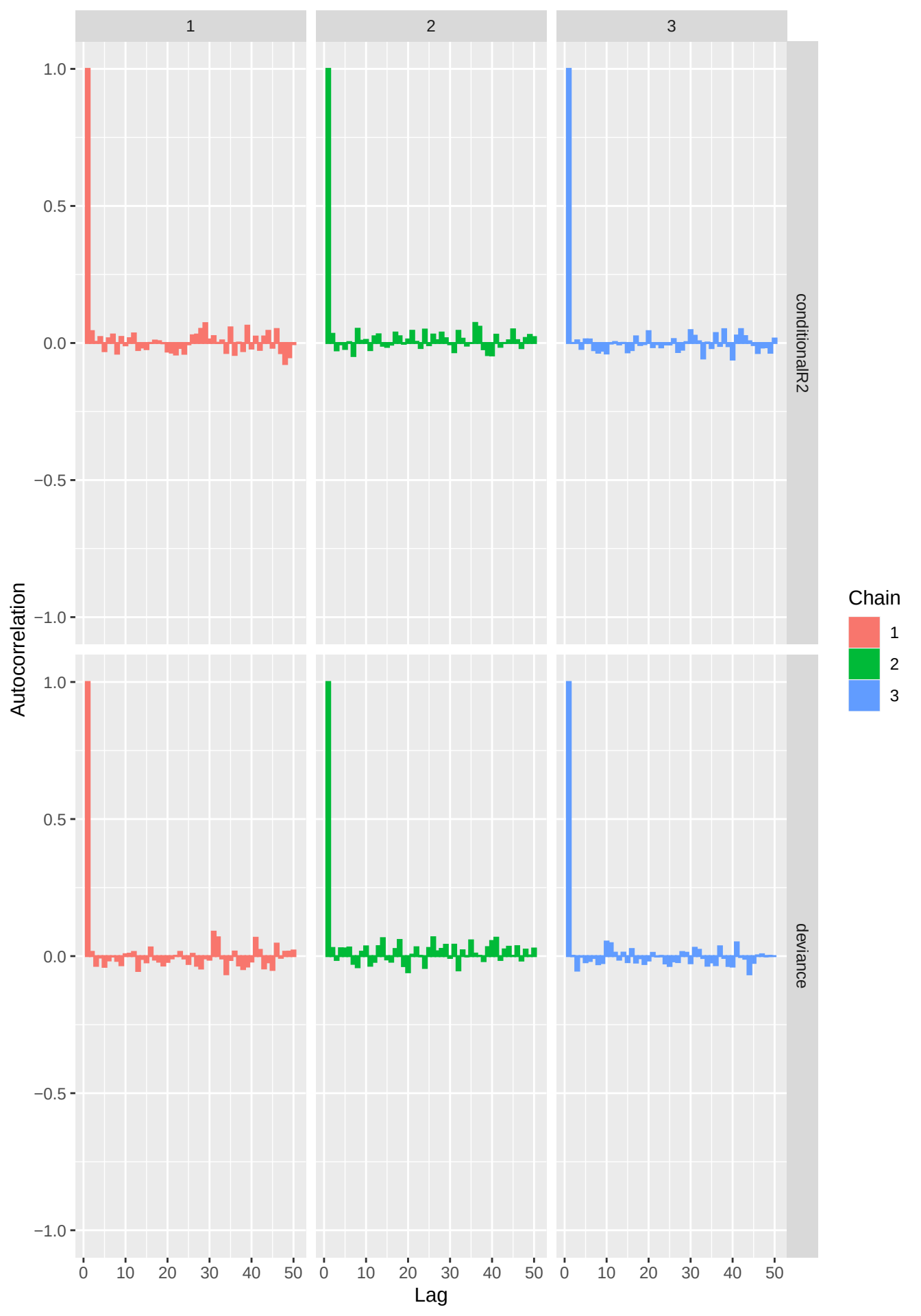

conditionalR2
1
conditionalR2
2
conditionalR2
3
deviance
1
deviance
2
deviance
3
density
value
Chain length
Complete
Partial

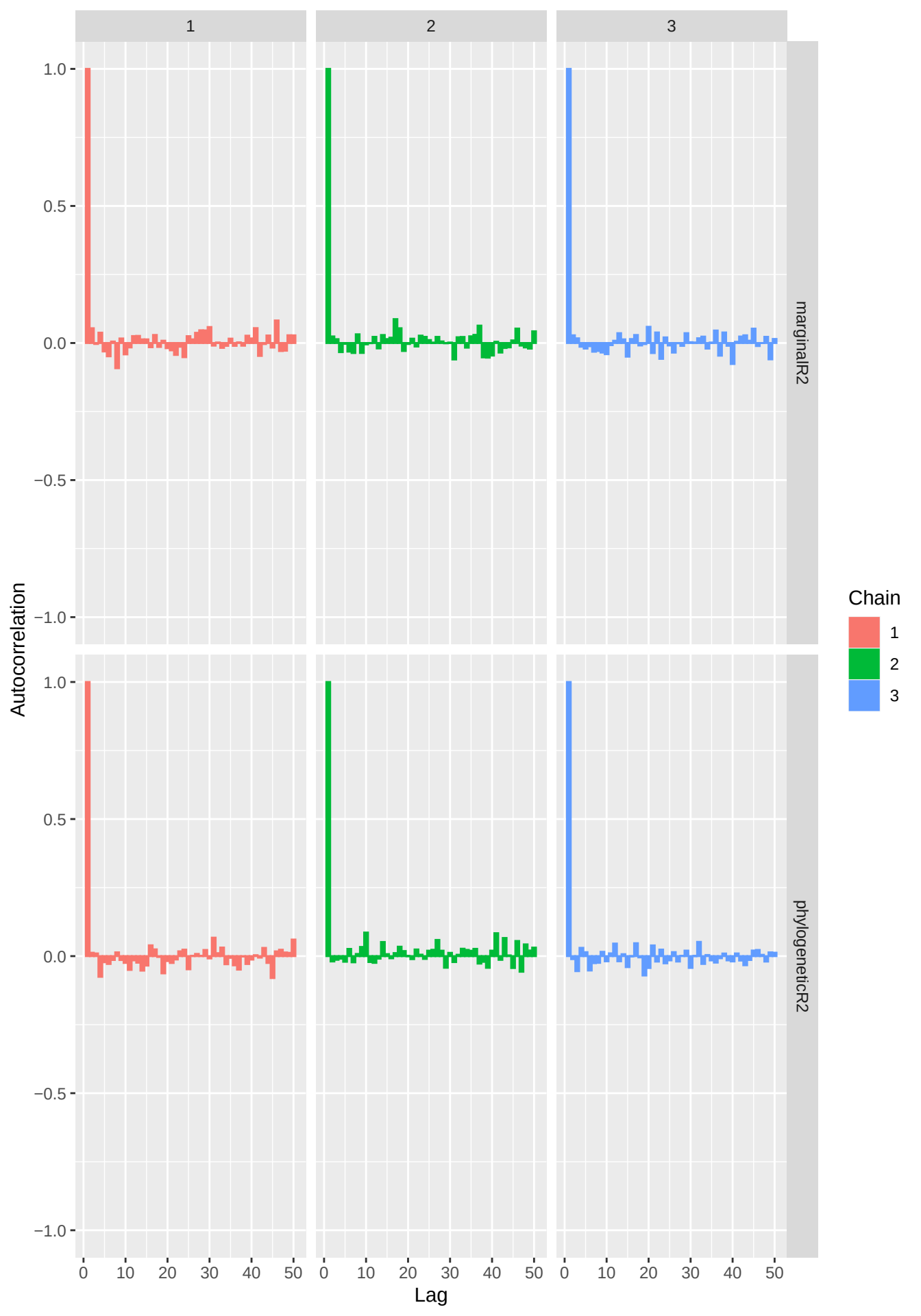

marginalR2
1
marginalR2
2
marginalR2
3
phylogeneticR2
1
phylogeneticR2
2
phylogeneticR2
3
density
value
Chain length
Complete
Partial

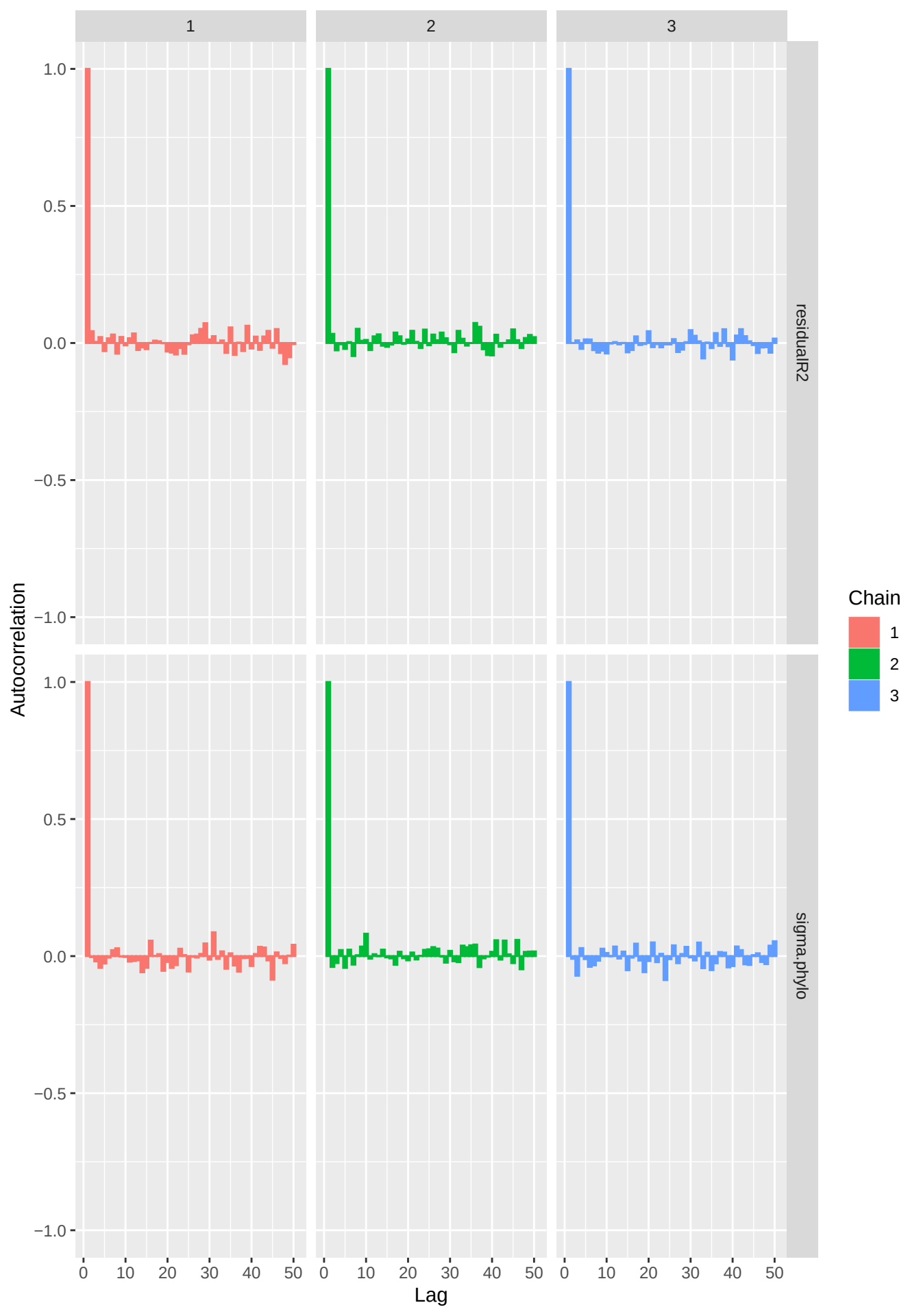

residualR2
1
residualR2
2
residualR2
3
sigma.phylo
1
sigma.phylo
2
sigma.phylo
3
density
value
Chain length
Complete
Partial

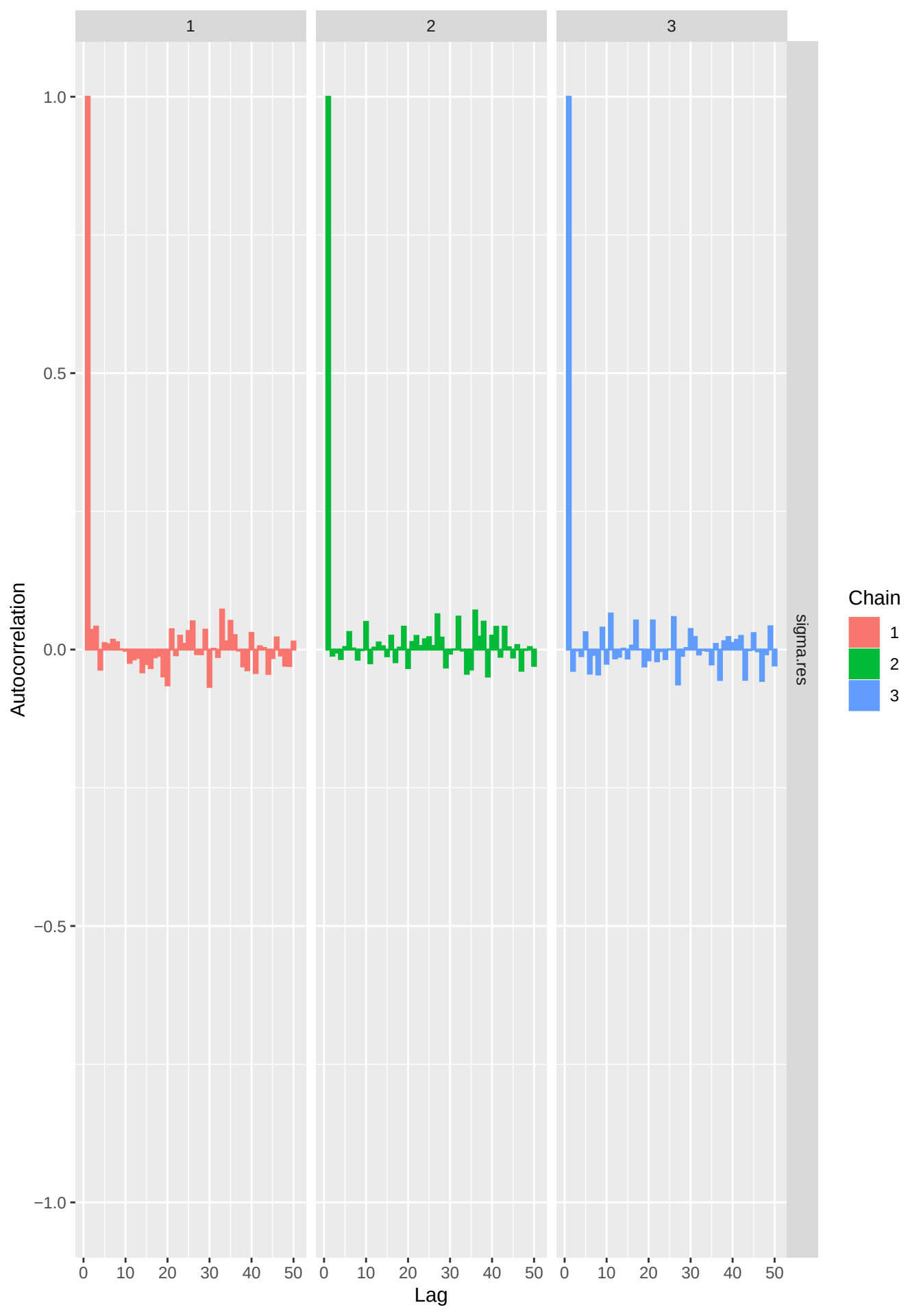

sigma.res
1
sigma.res
2
sigma.res
3
density
value
0
2
4
6
8
0.2
0.3
0.4
0.5
0.6
0.7
Chain length
Complete
Partial

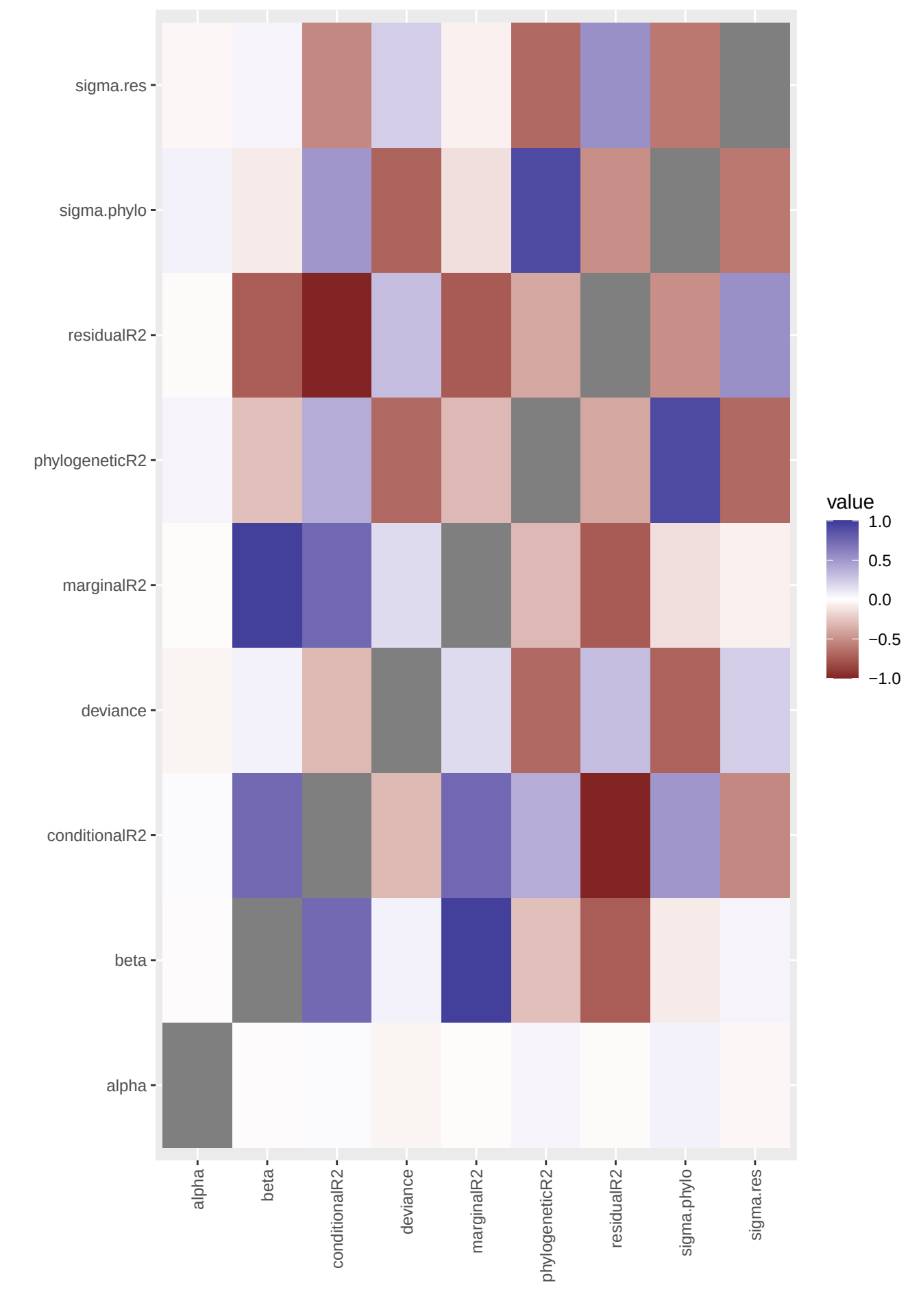

1
2
3
alpha
beta
1.0
0.5
0.0
−0.5
−1.0
Autocorrelation
0
10
20
30
40
50
Lag
Chain
1
2
3

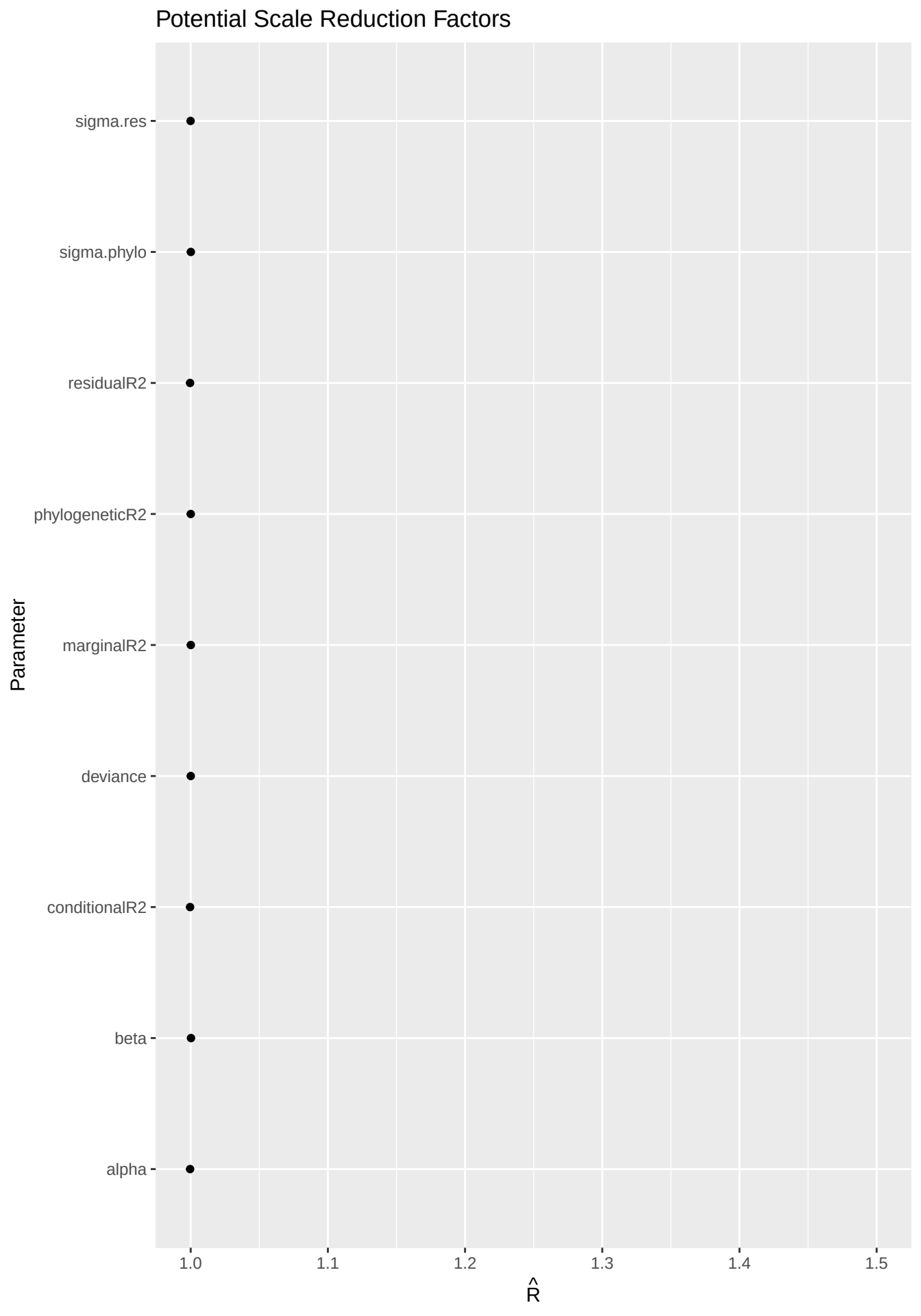

1
2
3
conditionalR2
deviance
Autocorrelation
Lag
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Chain
1
2
3

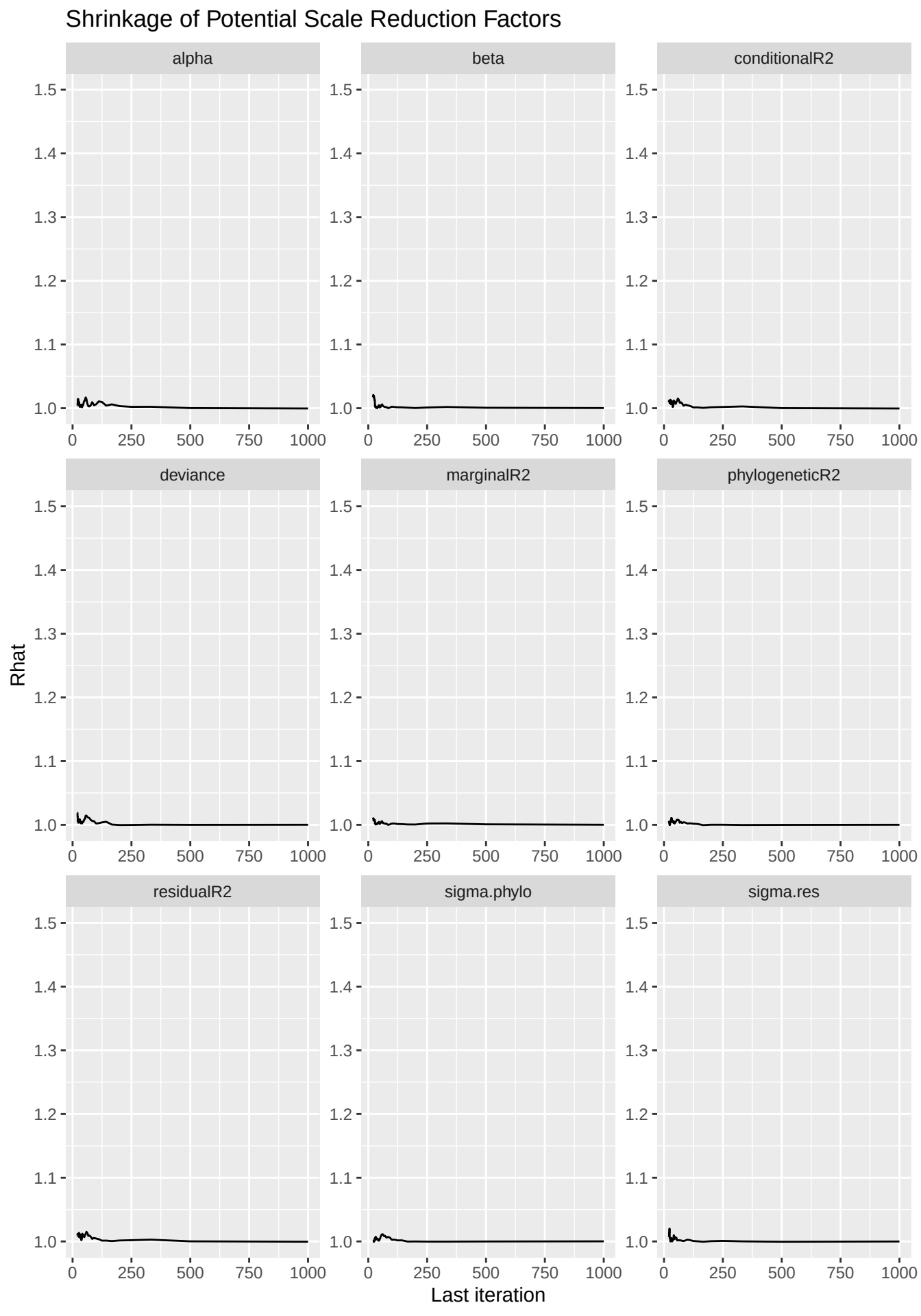

1
2
3
marginalR2
phylogeneticR2
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Lag
Chain
1
2
3

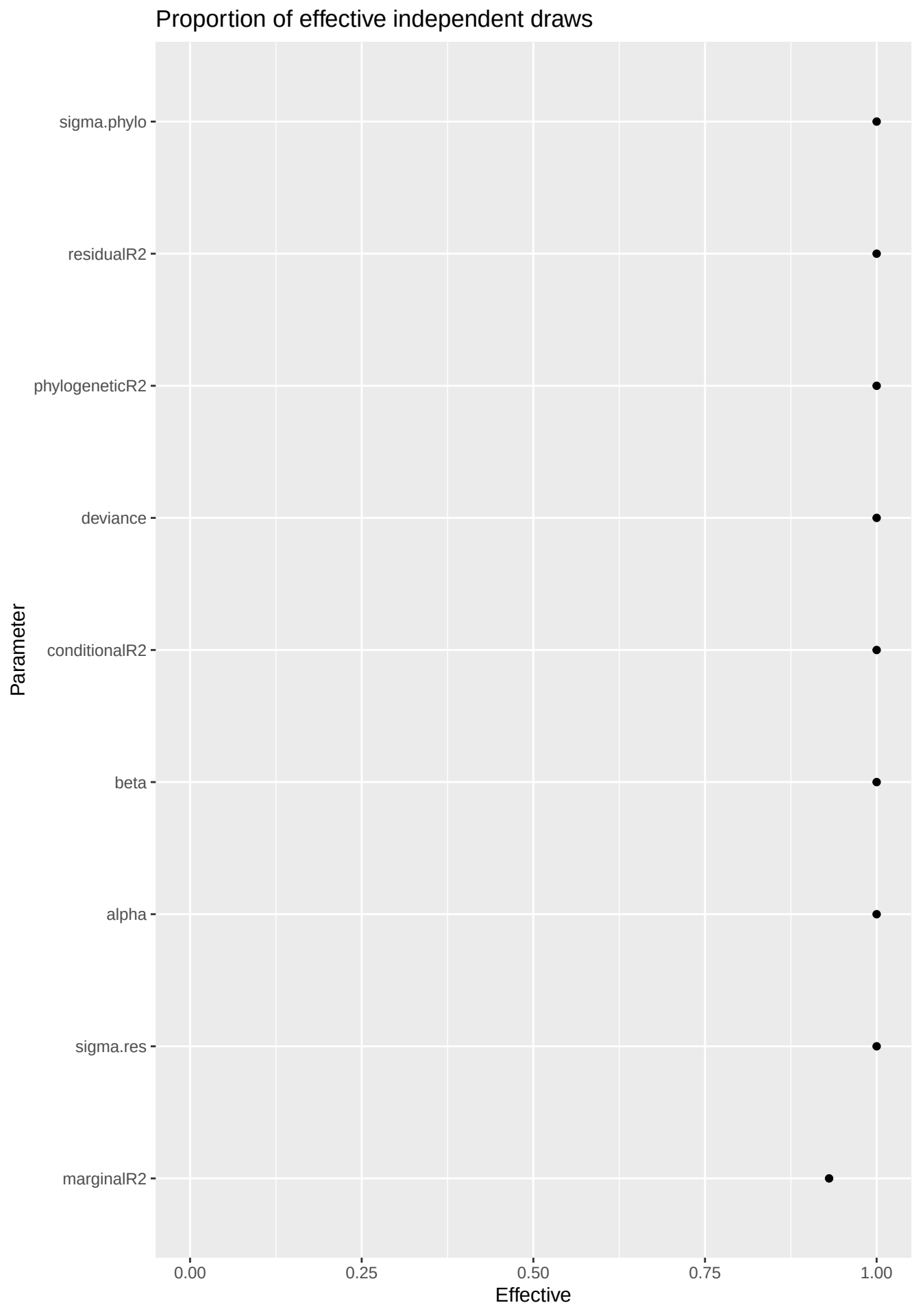

1
2
3
residualR2
sigma.phylo
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Lag
Chain
1
2
3

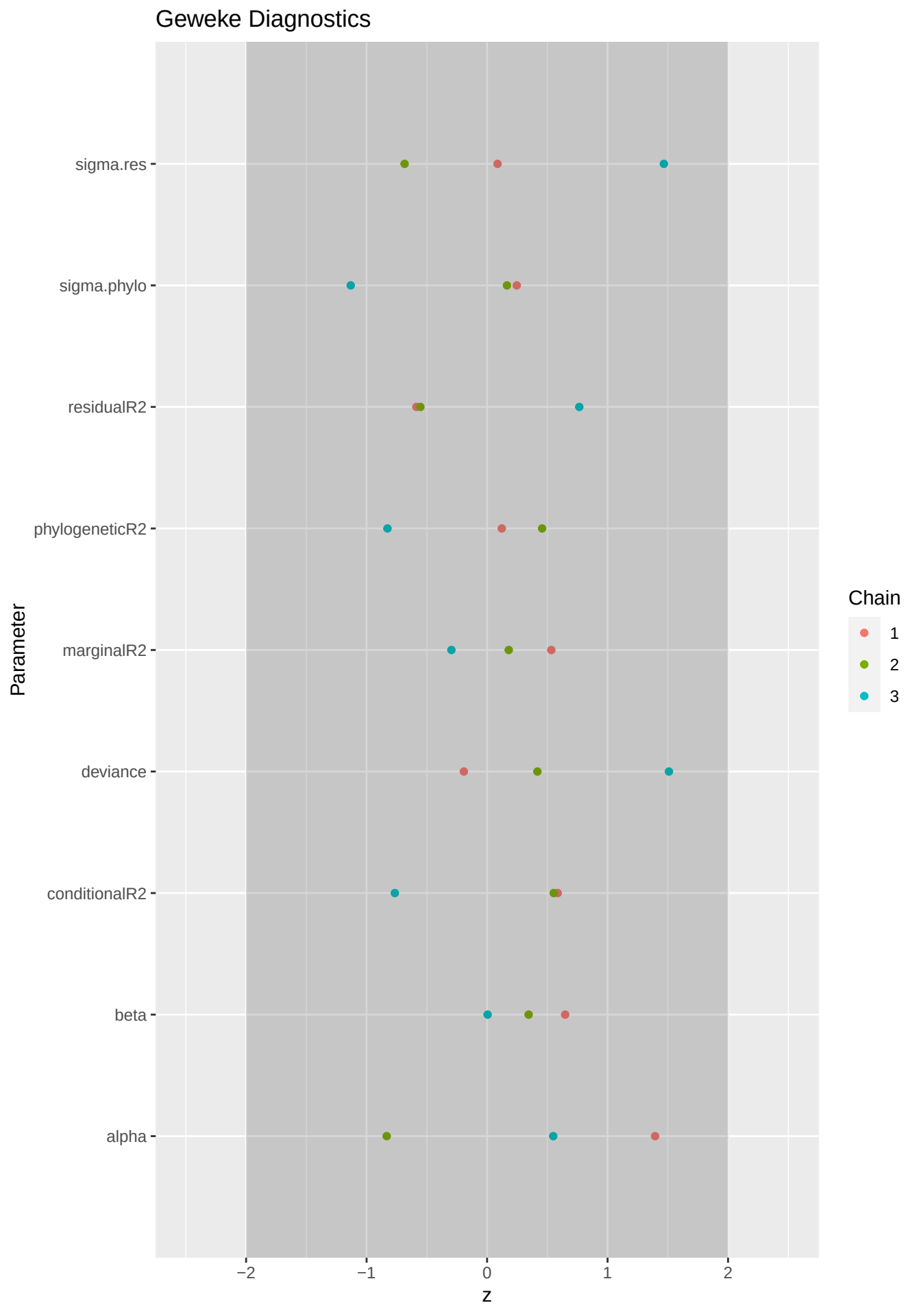

1
2
3
sigma.res
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
10
20
30
40
50
Lag
Chain
1
2
3


sigma.res
sigma.phylo
residualR2
phylogeneticR2
marginalR2
deviance
conditionalR2
beta
alpha
alpha
beta
conditionalR2
deviance
marginalR2
phylogeneticR2
residualR2
sigma.phylo
sigma.res
value
1.0
0.5
0.0
−0.5
−1.0


Potential Scale Reduction Factors
sigma.res
sigma.phylo
residualR2
phylogeneticR2
marginalR2
deviance
conditionalR2
beta
alpha
Parameter
1.0
1.1
1.2
1.3
1.4
1.5
R̂


Shrinkage of Potential Scale Reduction Factors
alpha
beta
conditionalR2
deviance
marginalR2
phylogeneticR2
residualR2
sigma.phylo
sigma.res
Rhat
Last iteration
1.5
1.4
1.3
1.2
1.1
1.0
0
250
500
750
1000


Proportion of effective independent draws
sigma.phylo
residualR2
phylogeneticR2
deviance
conditionalR2
beta
alpha
sigma.res
marginalR2
Parameter
0.00
0.25
0.50
0.75
1.00
Effective


Geweke Diagnostics
sigma.res
sigma.phylo
residualR2
phylogeneticR2
marginalR2
deviance
conditionalR2
beta
alpha
Parameter
−2
−1
0
1
2
z
Chain
1
2
3