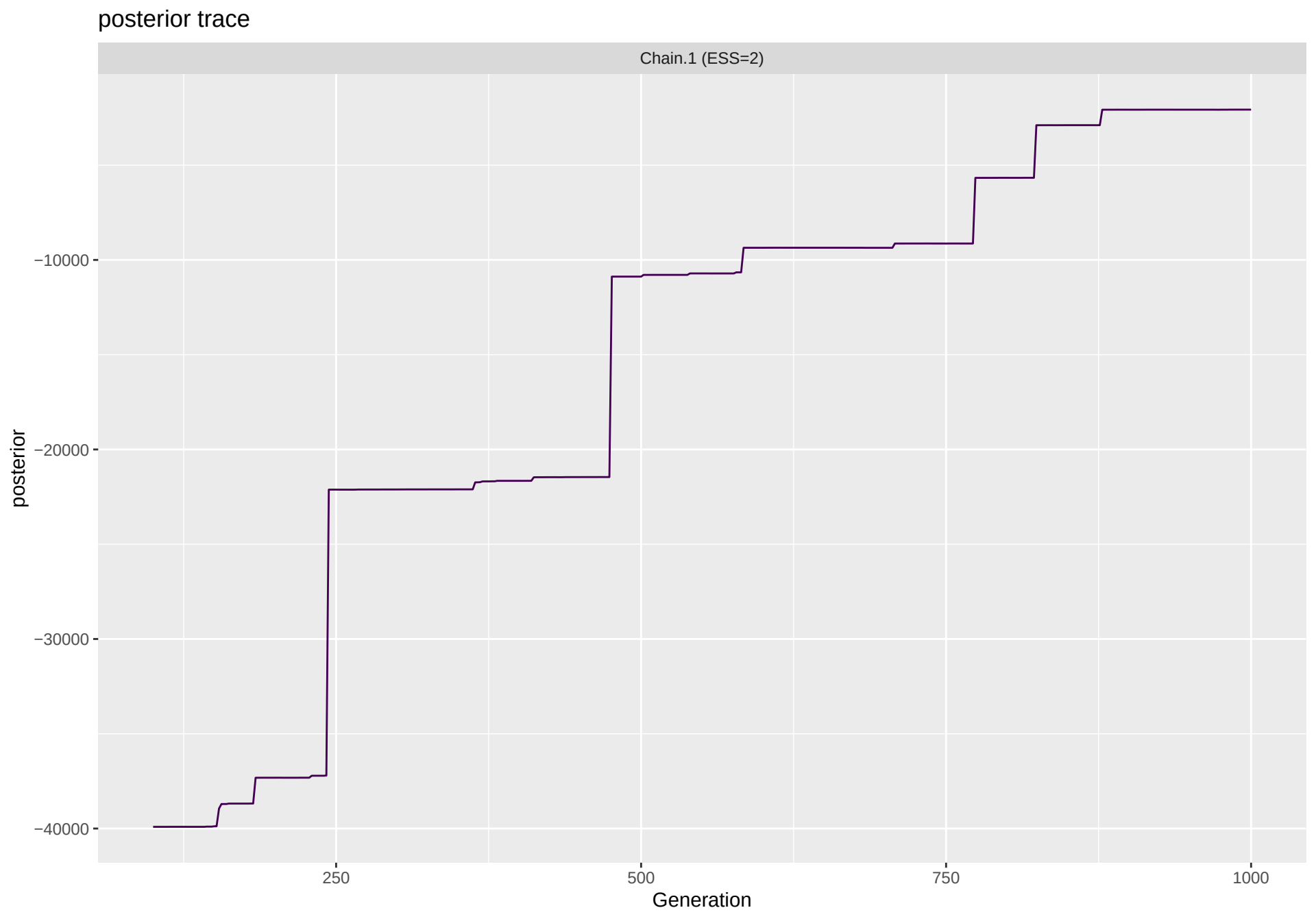
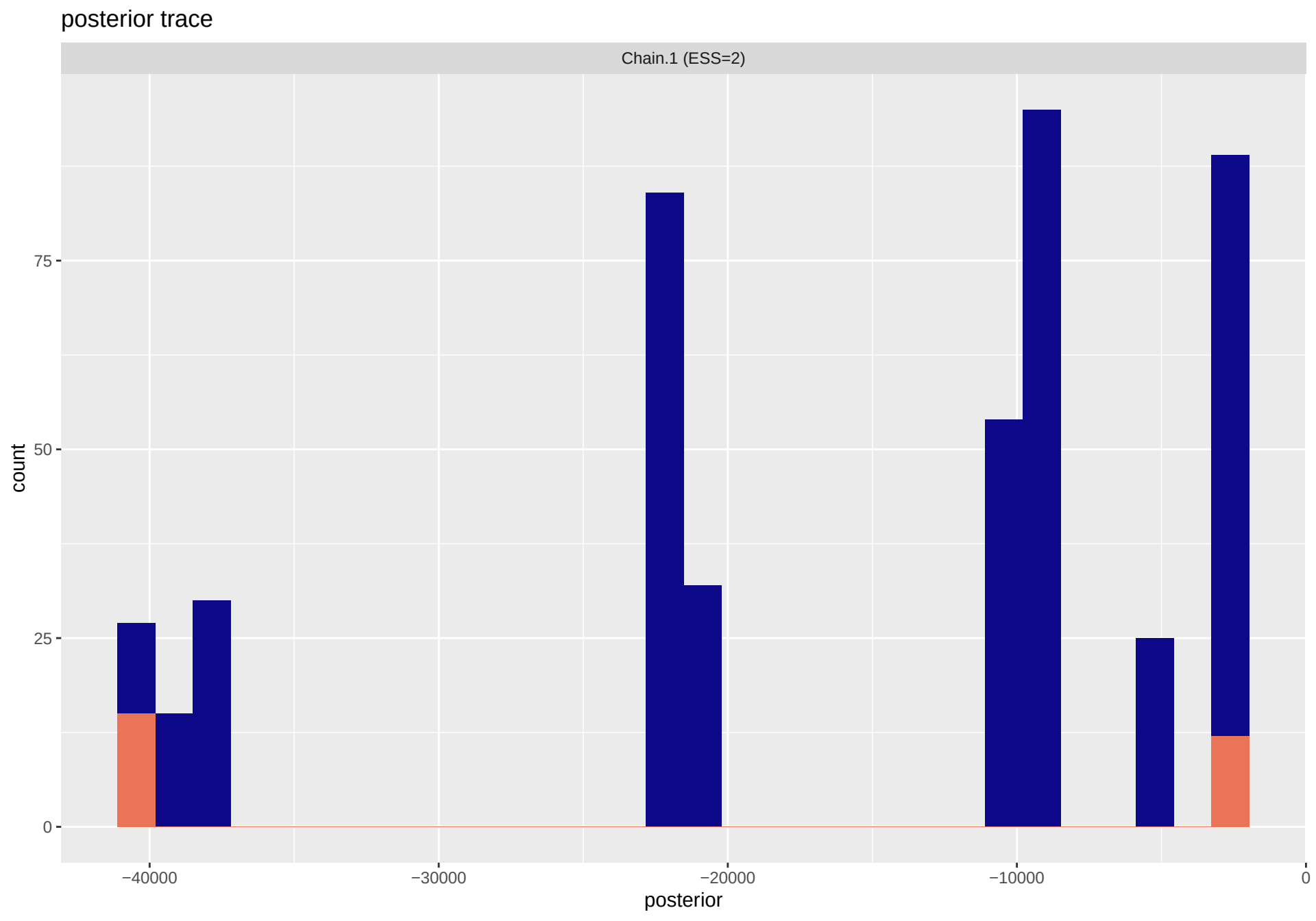
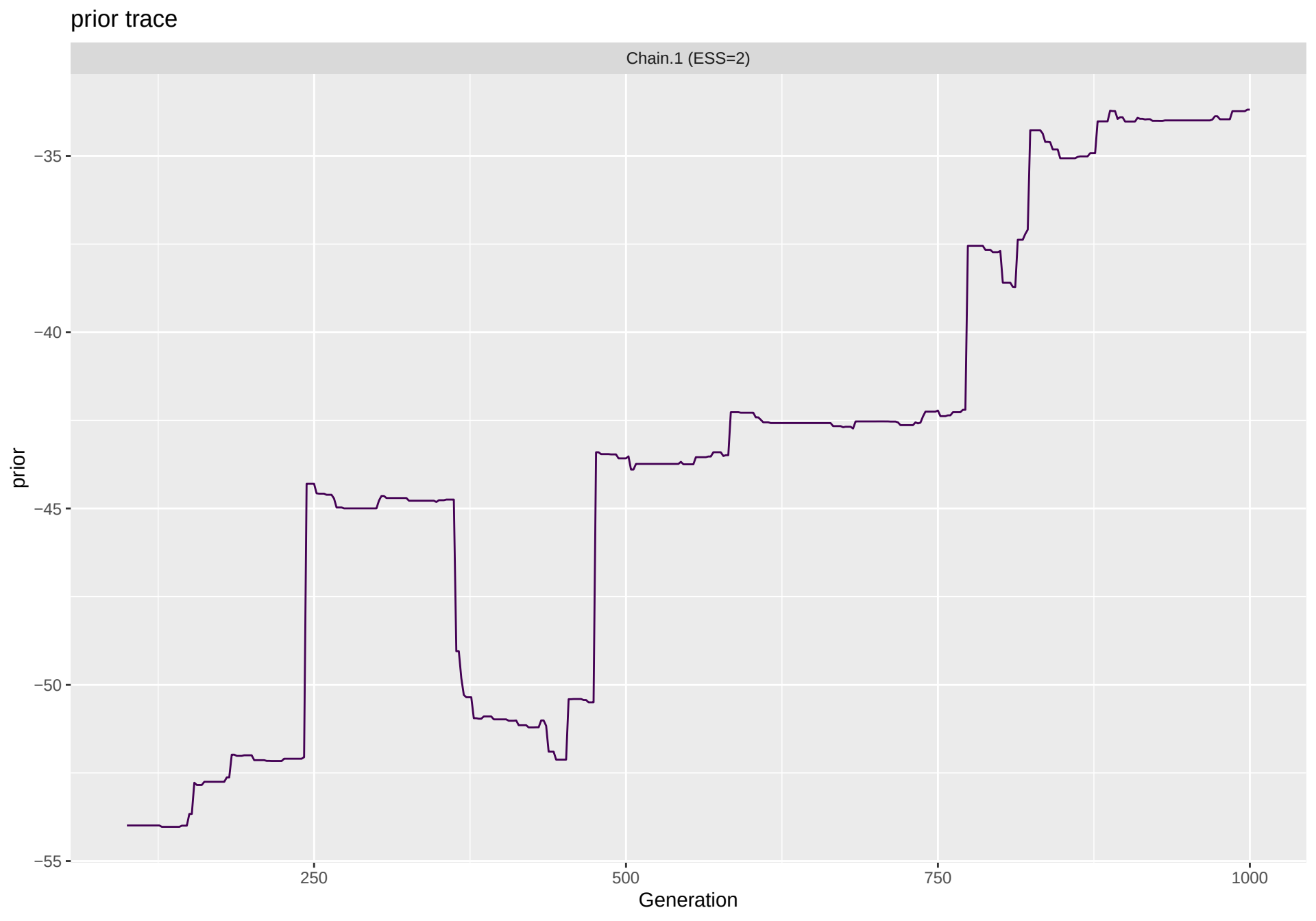
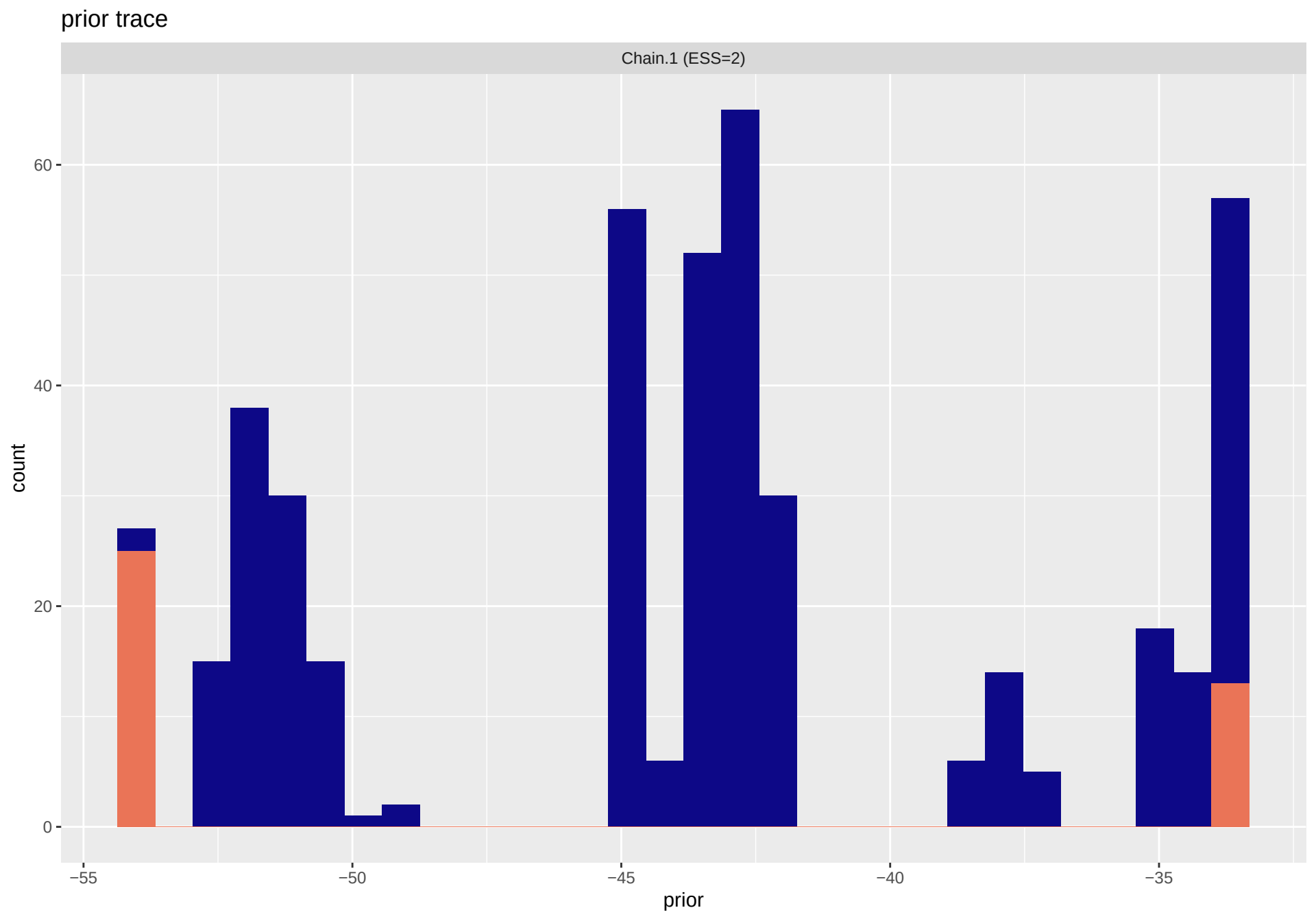
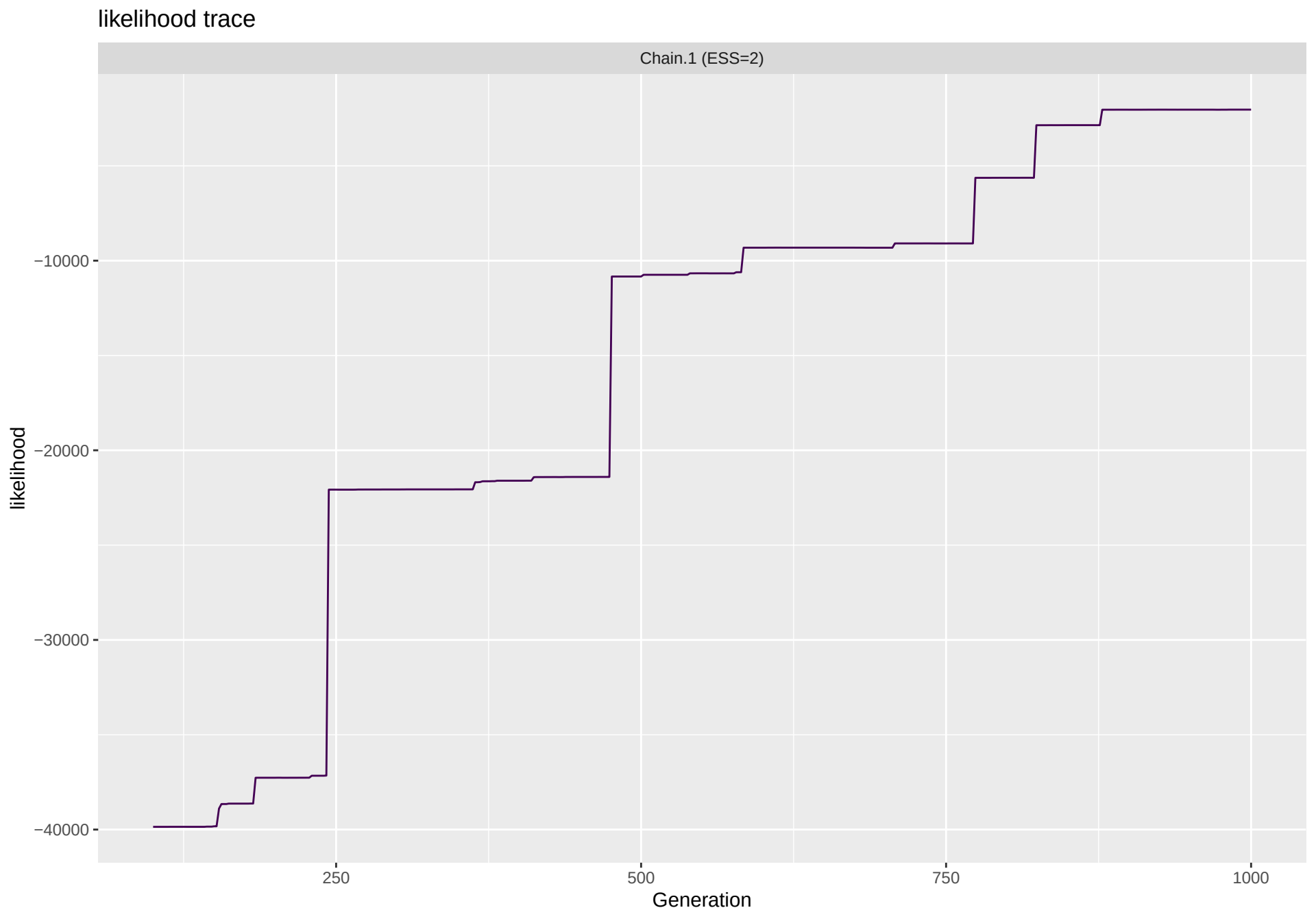
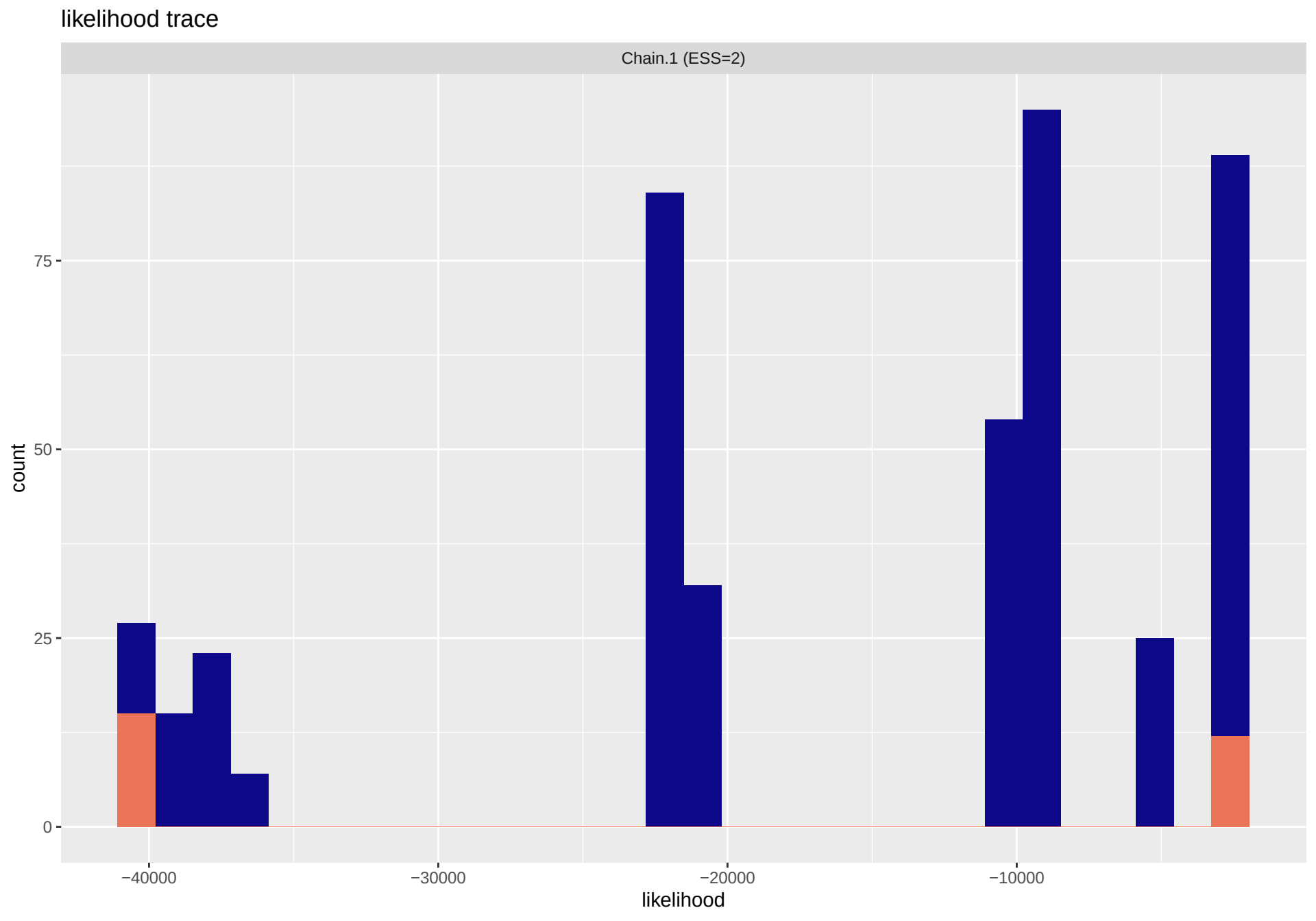

posterior trace
Chain.1 (ESS=2)
−10000
−20000
−30000
−40000
posterior
250
500
750
1000
Generation

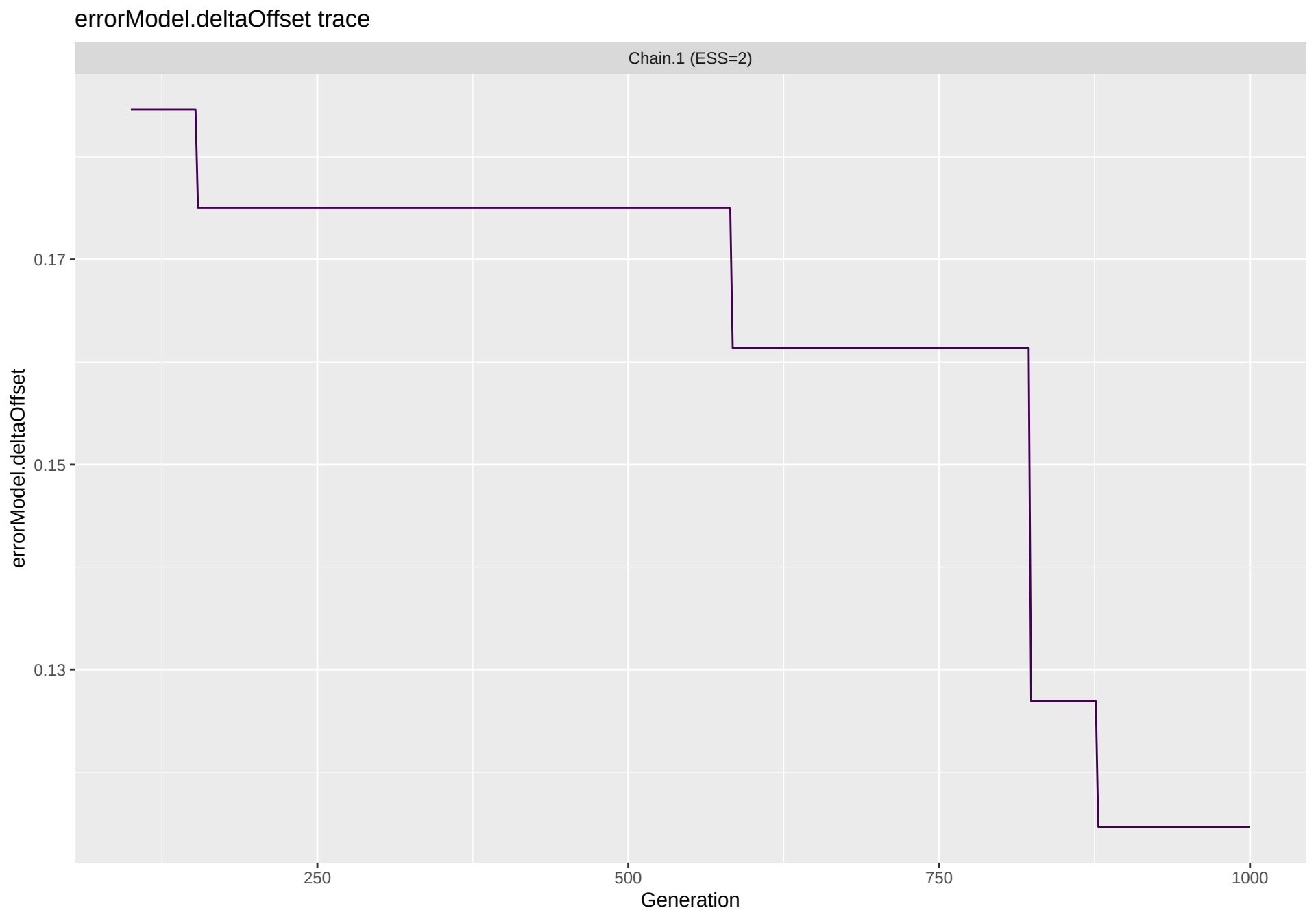

posterior trace
Chain.1 (ESS=2)
count
75
50
25
0
−40000
−30000
−20000
−10000
0
posterior

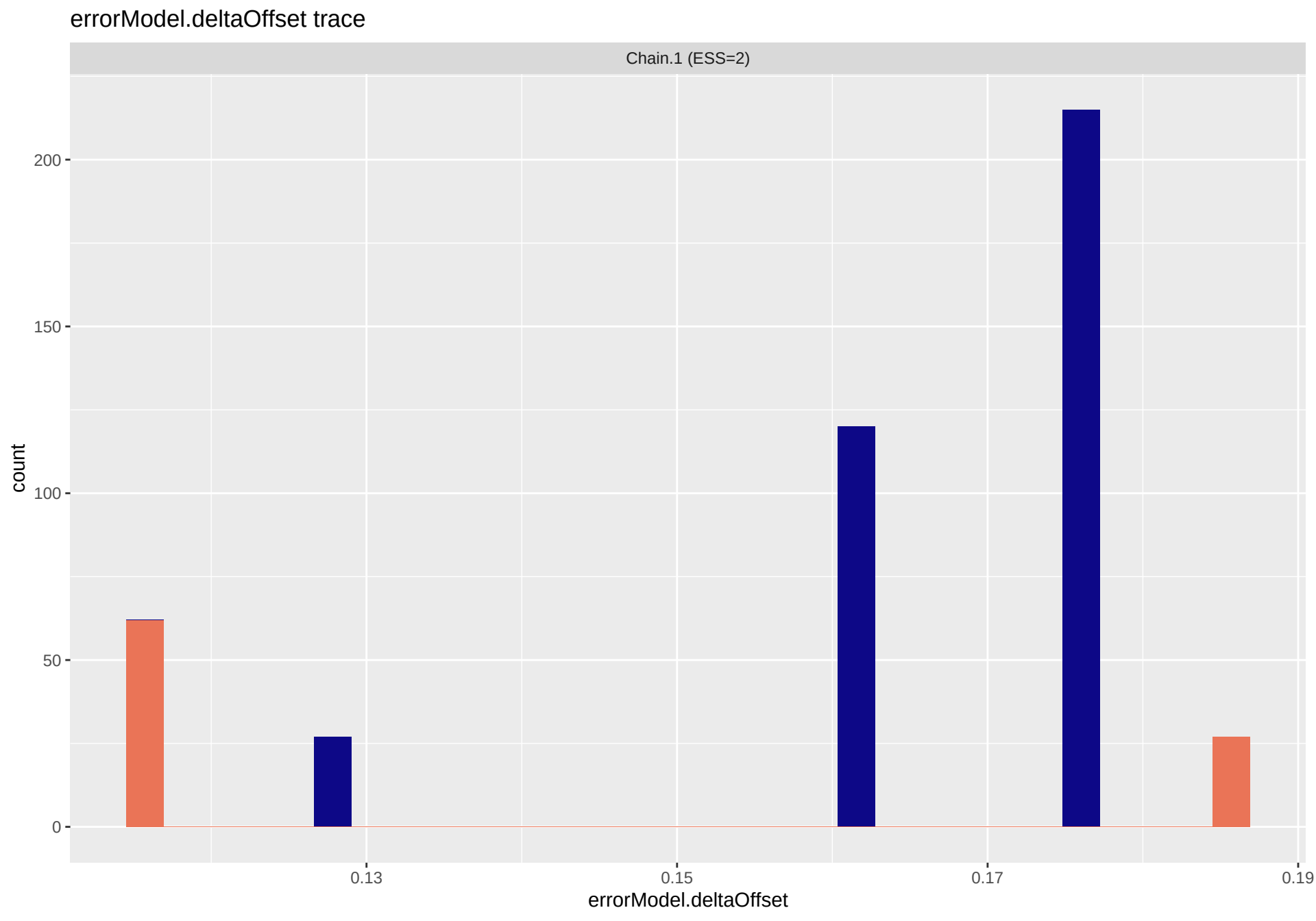

prior trace
Chain.1 (ESS=2)
prior
−35
−40
−45
−50
−55
250
500
750
1000
Generation

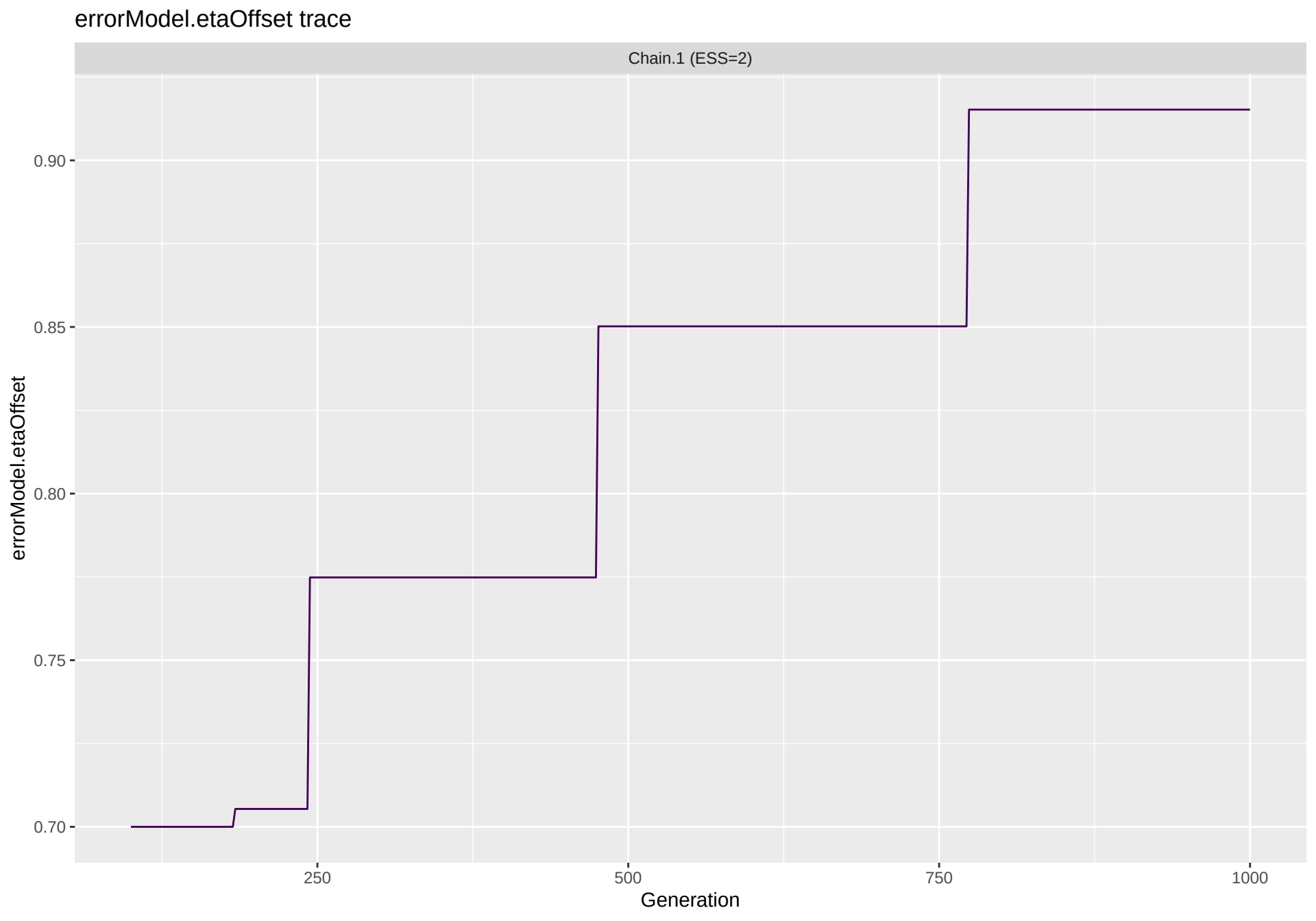

prior trace
Chain.1 (ESS=2)
count
60
40
20
0
−55
−50
−45
−40
−35
prior

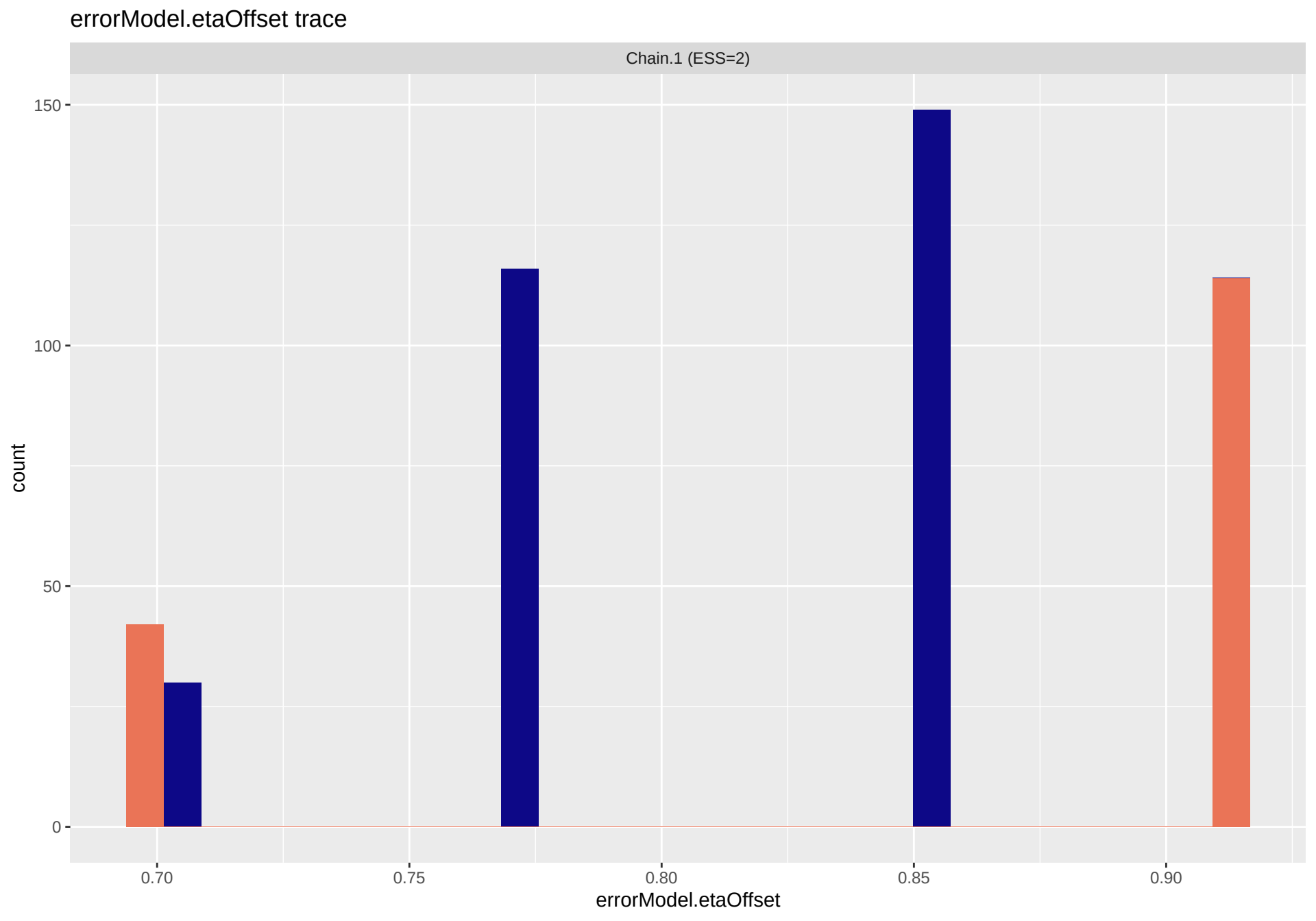

likelihood trace
Chain.1 (ESS=2)
−10000
−20000
−30000
−40000
likelihood
250
500
750
1000
Generation

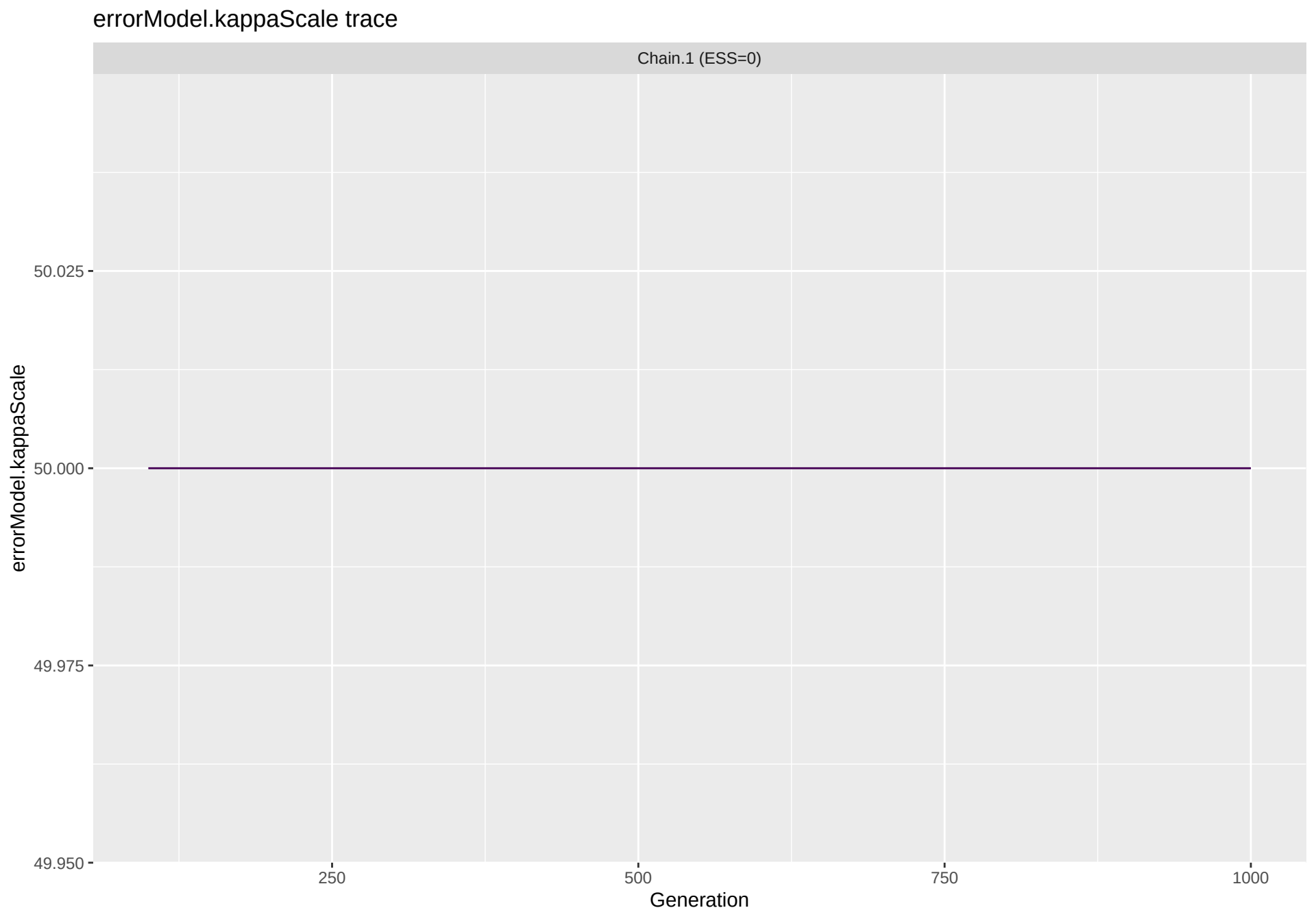

likelihood trace
Chain.1 (ESS=2)
count
75
50
25
0
−40000
−30000
−20000
−10000
likelihood

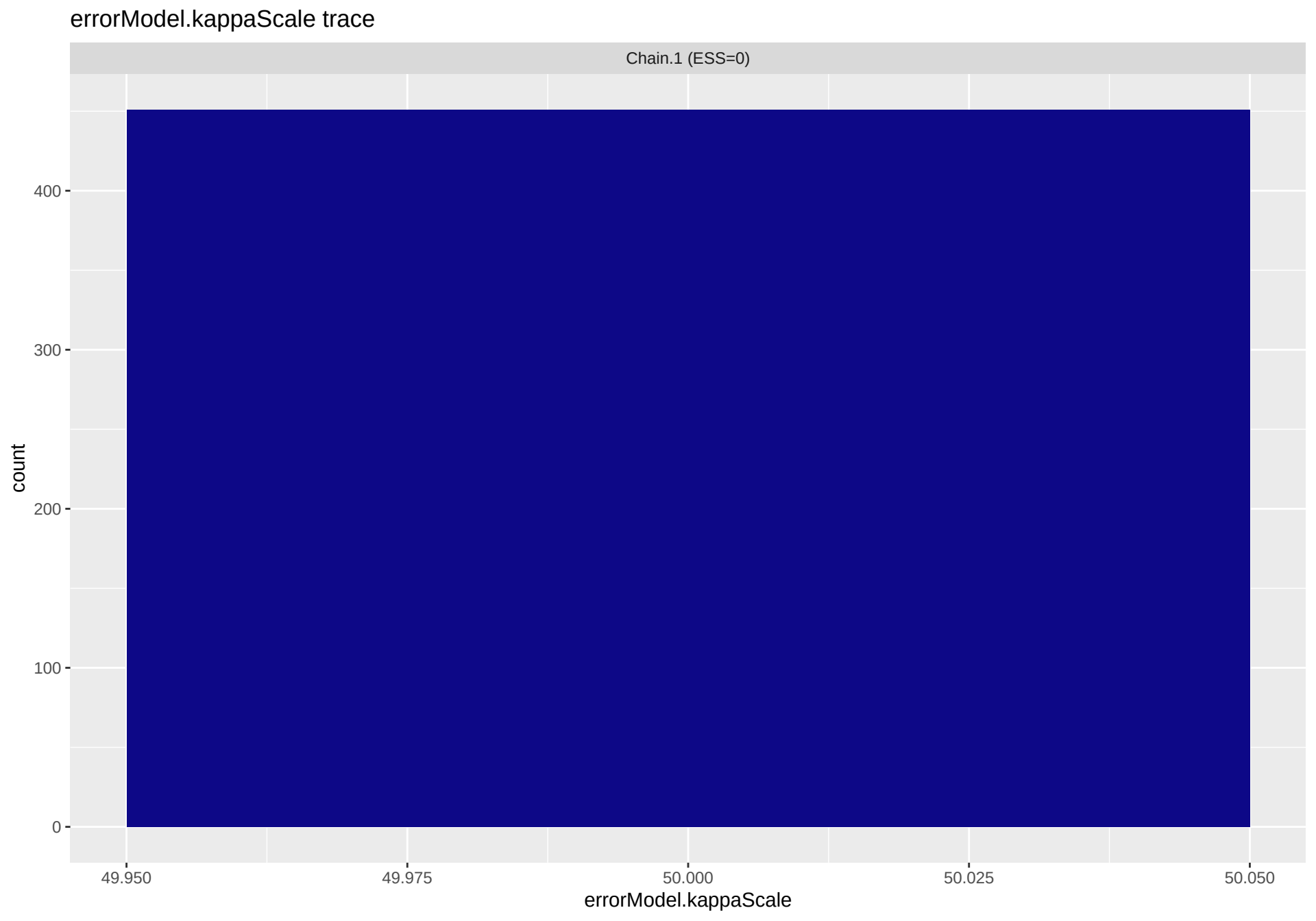

errorModel.deltaOffset trace
Chain.1 (ESS=2)
0.17
0.15
0.13
errorModel.deltaOffset
250
500
750
1000
Generation

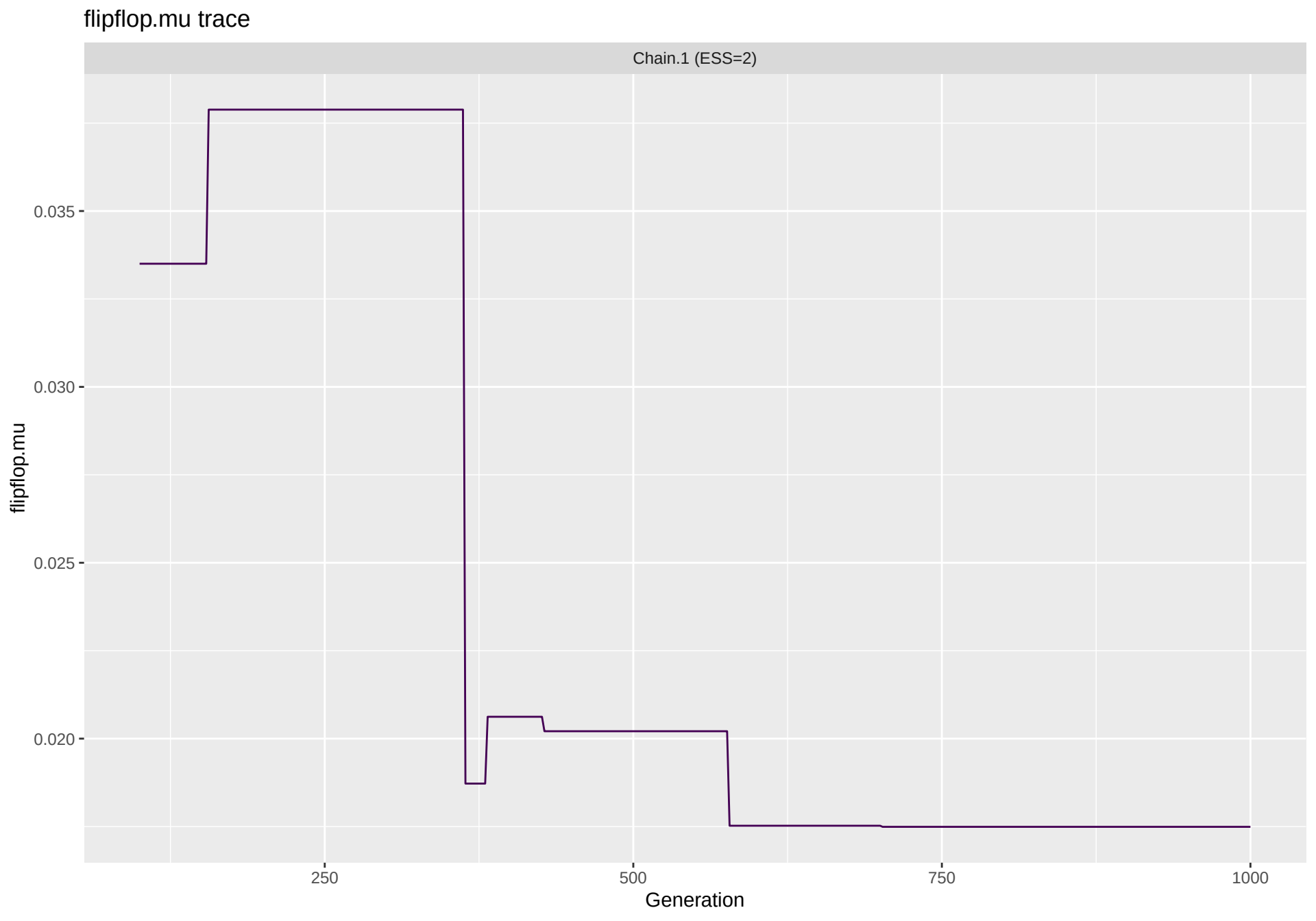

errorModel.deltaOffset trace
Chain.1 (ESS=2)
count
200
150
100
50
0
0.13
0.15
0.17
0.19
errorModel.deltaOffset

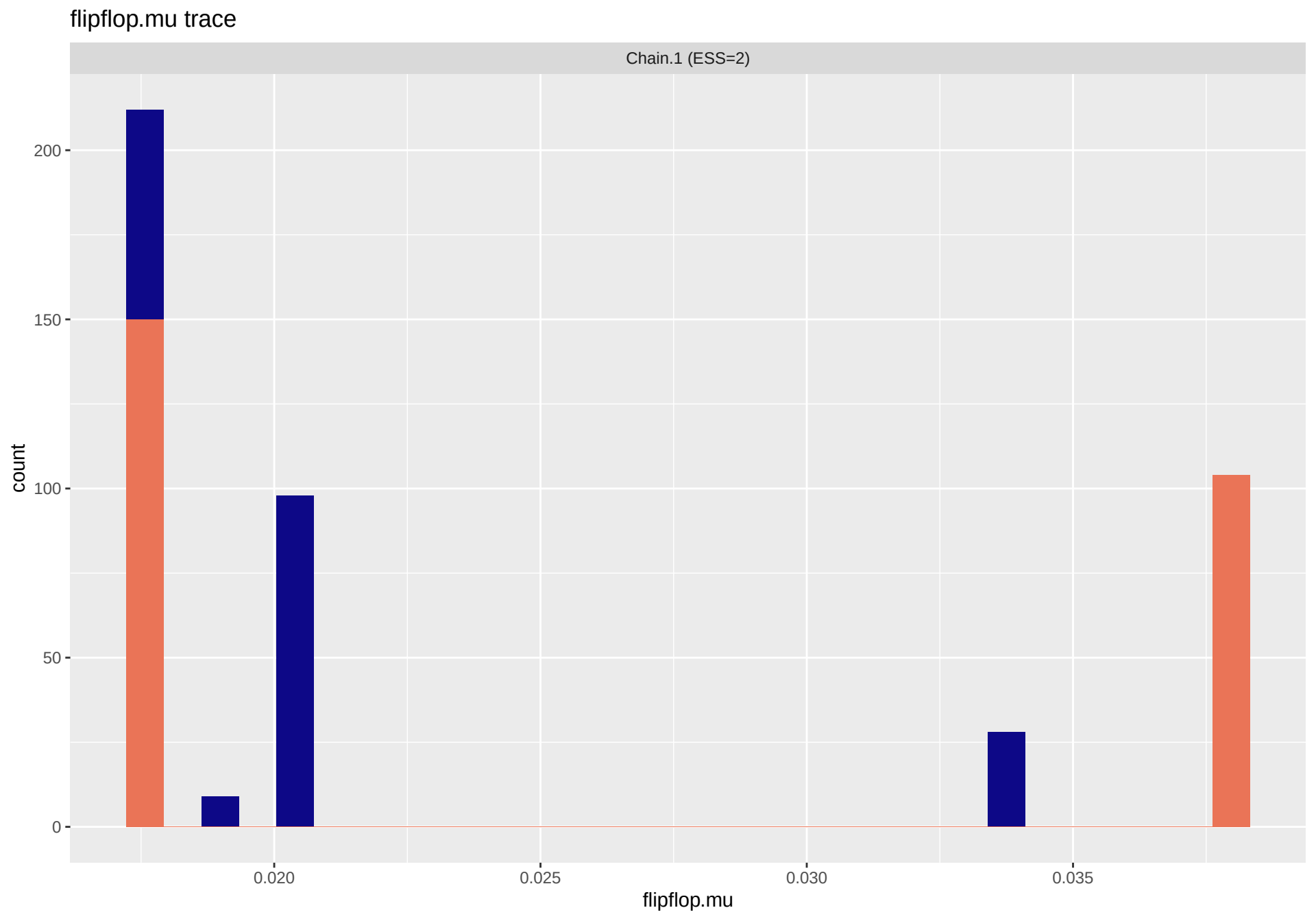

errorModel.etaOffset trace
Chain.1 (ESS=2)
errorModel.etaOffset
0.90
0.85
0.80
0.75
0.70
250
500
750
1000
Generation

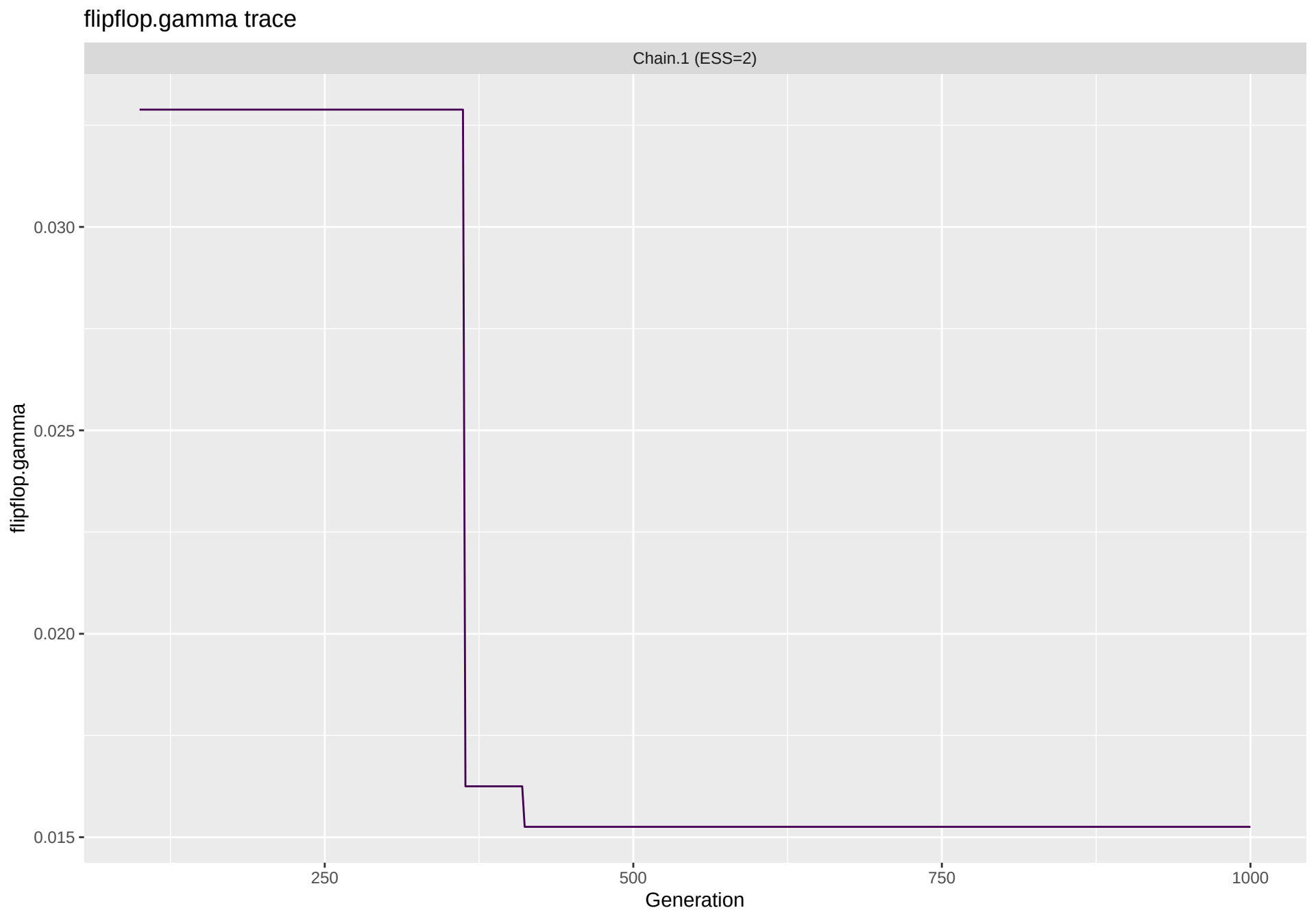

errorModel.etaOffset trace
Chain.1 (ESS=2)
150
100
50
0
count
0.70
0.75
0.80
0.85
0.90
errorModel.etaOffset

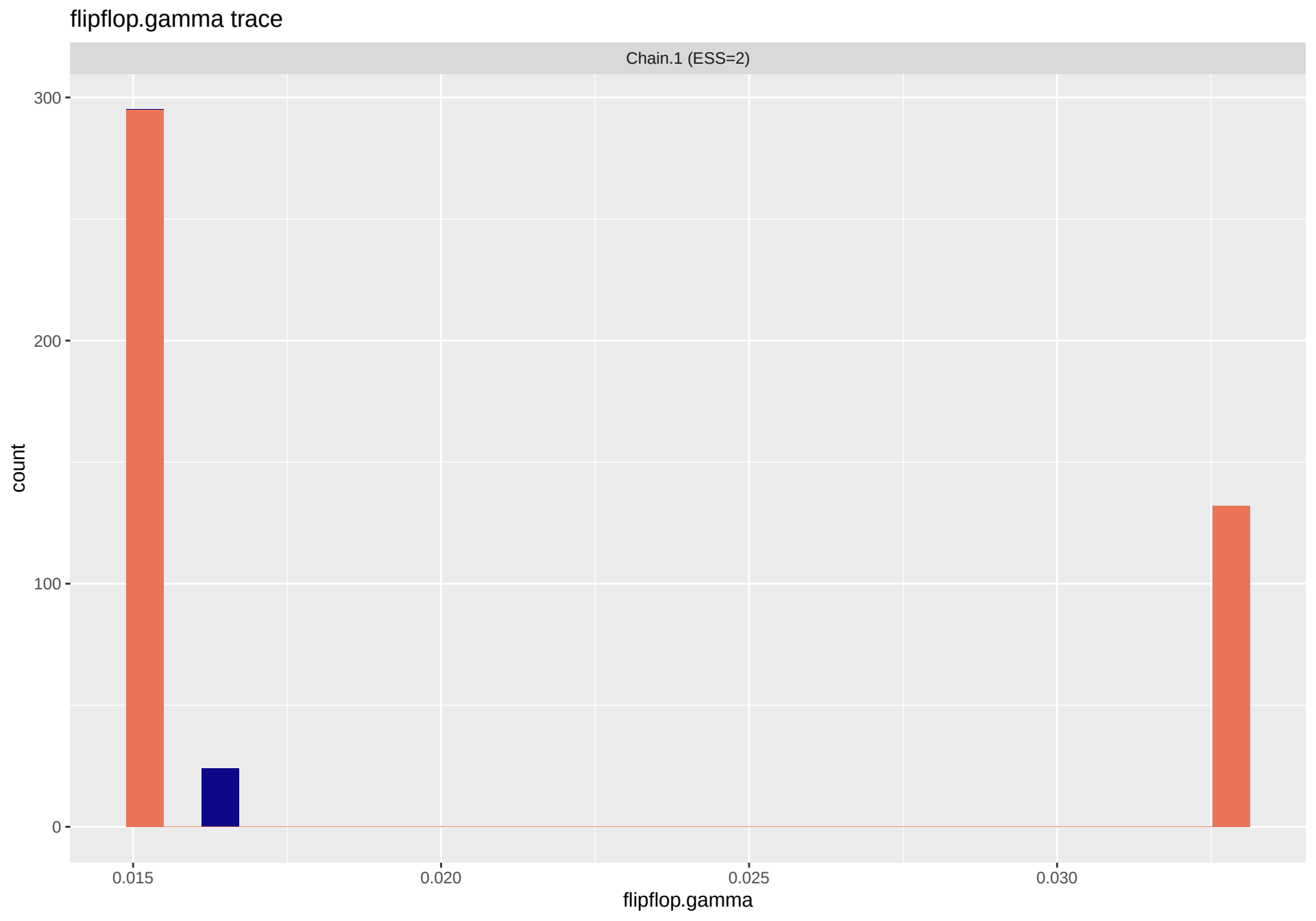

errorModel.kappaScale trace
Chain.1 (ESS=0)
50.025
50.000
49.975
49.950
errorModel.kappaScale
250
500
750
1000
Generation

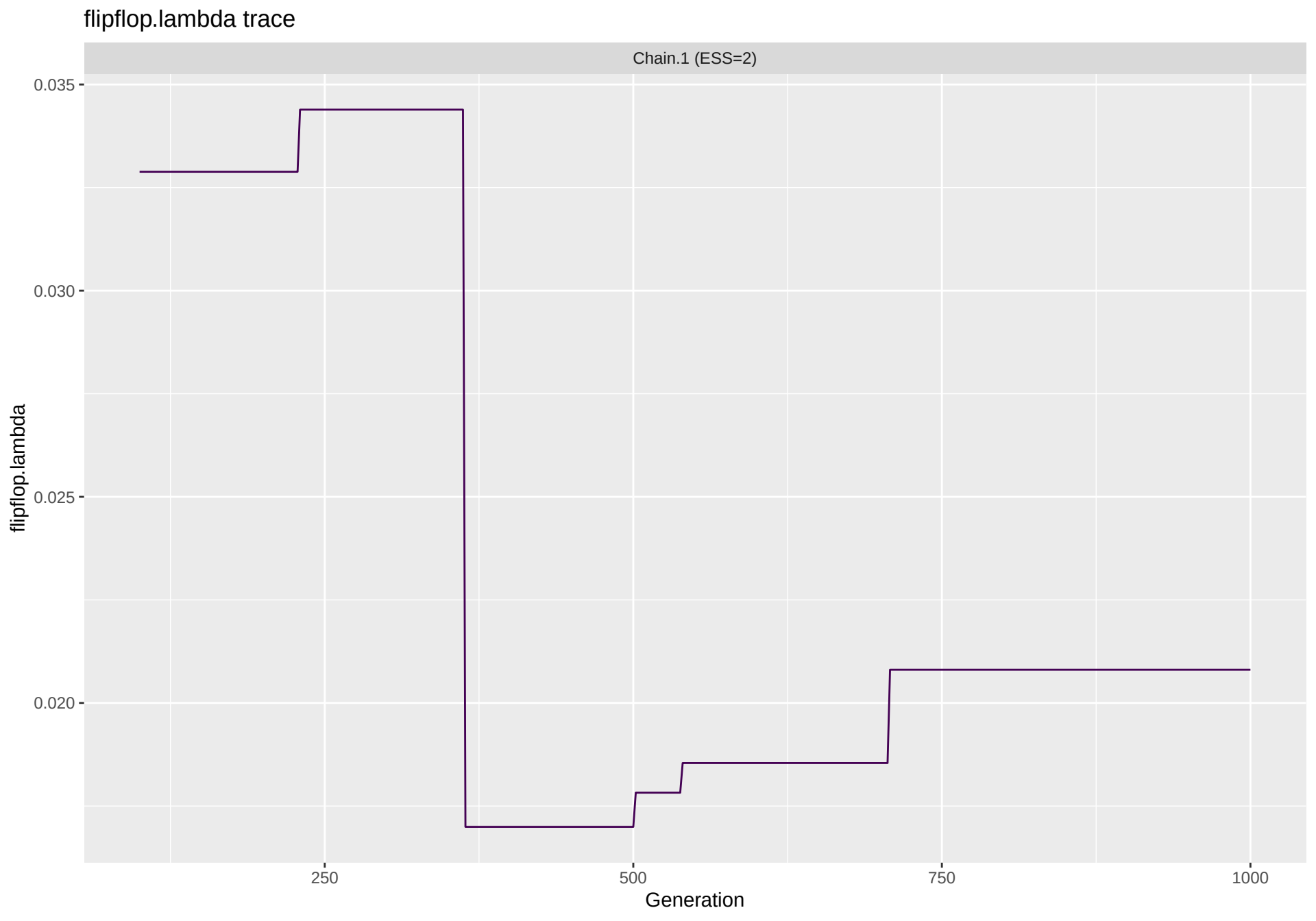

errorModel.kappaScale trace
Chain.1 (ESS=0)
count
400
300
200
100
0
49.950
49.975
50.000
50.025
50.050
errorModel.kappaScale

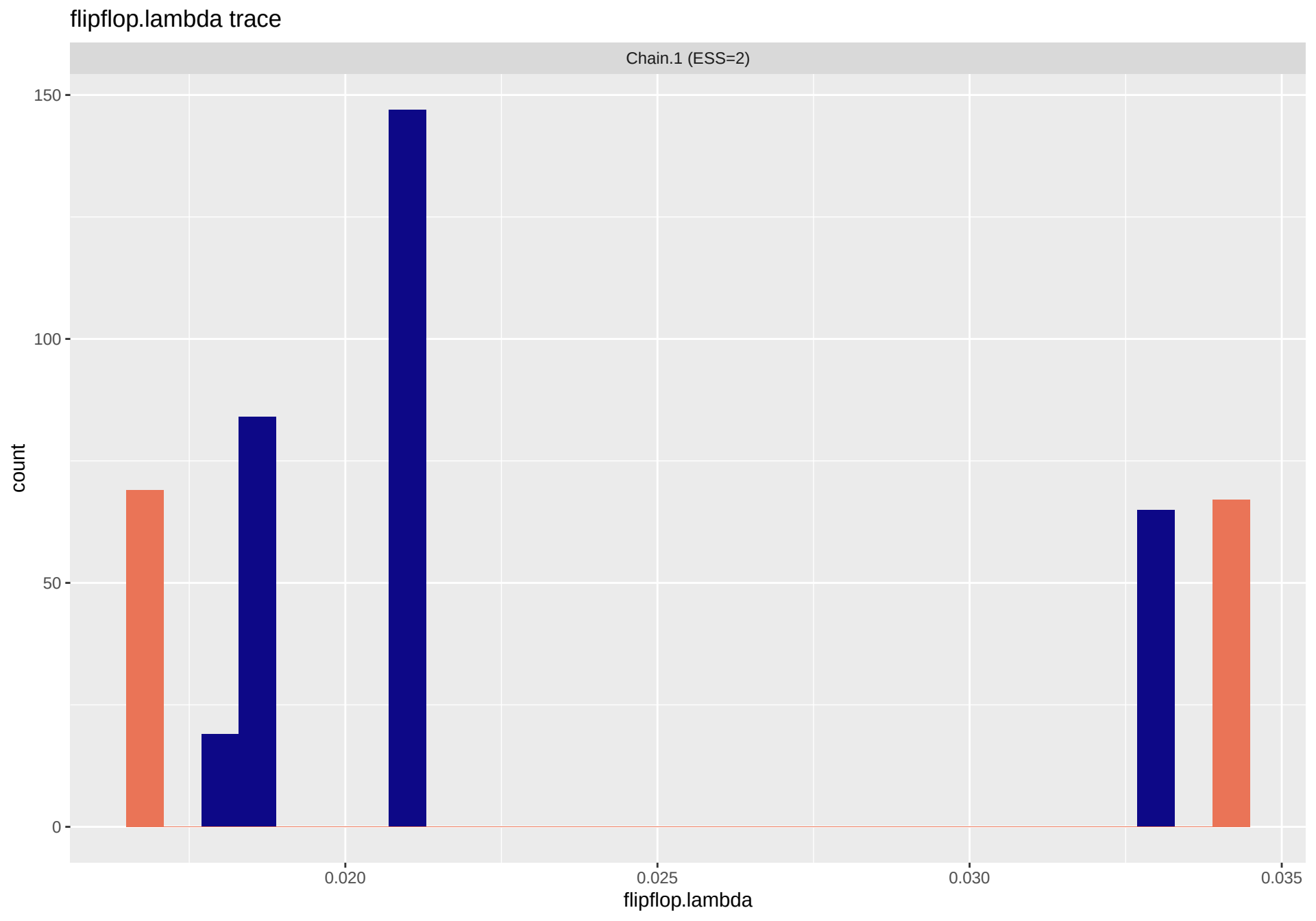

flipflop.mu trace
Chain.1 (ESS=2)
0.035
0.030
0.025
0.020
flipflop.mu
250
500
750
1000
Generation

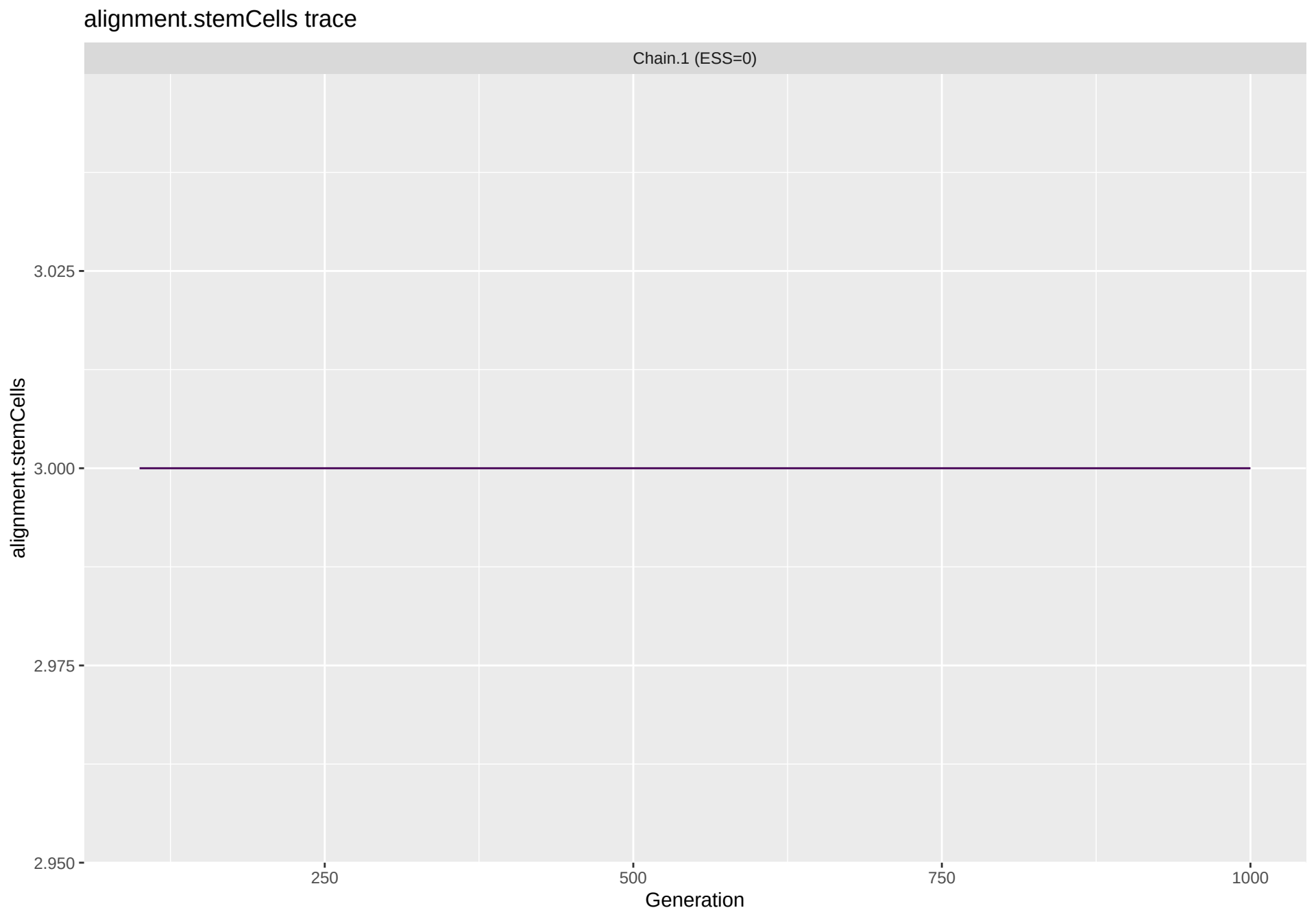

flipflop.mu trace
Chain.1 (ESS=2)
count
200
150
100
50
0
0.020
0.025
0.030
0.035
flipflop.mu

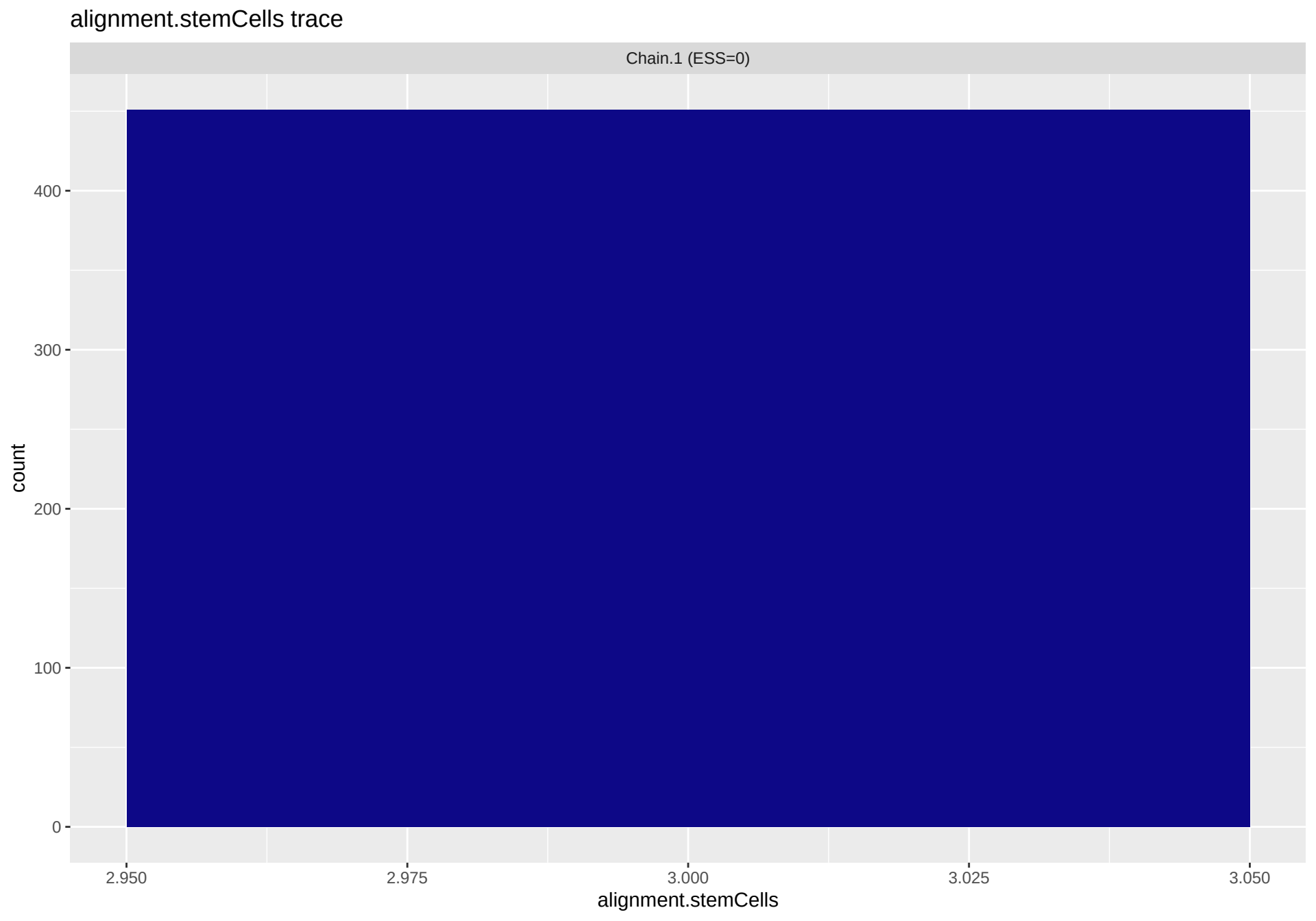

flipflop.gamma trace
Chain.1 (ESS=2)
0.030
0.025
0.020
0.015
flipflop.gamma
250
500
750
1000
Generation

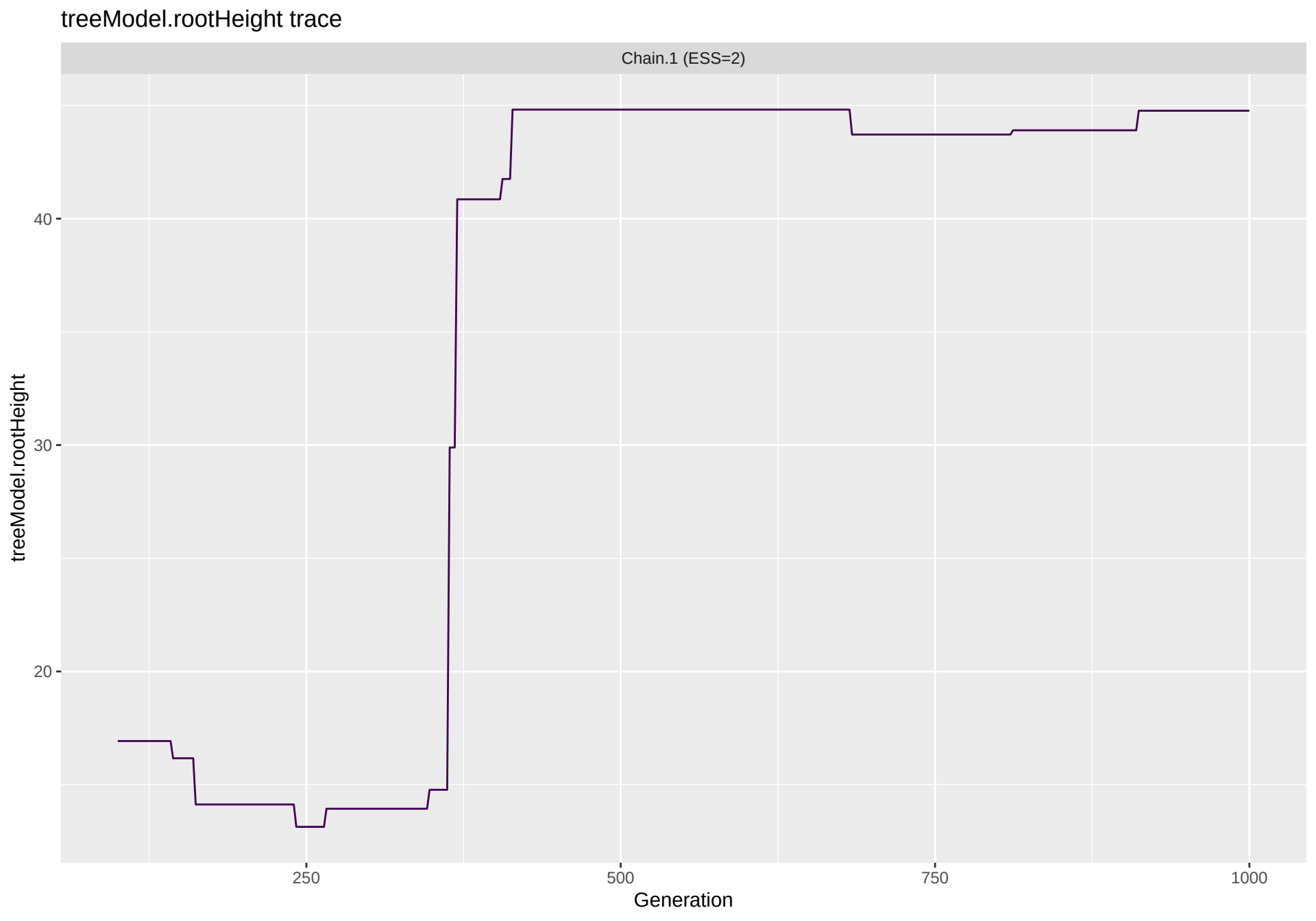

flipflop.gamma trace
Chain.1 (ESS=2)
300
200
100
0
count
0.015
0.020
0.025
0.030
flipflop.gamma

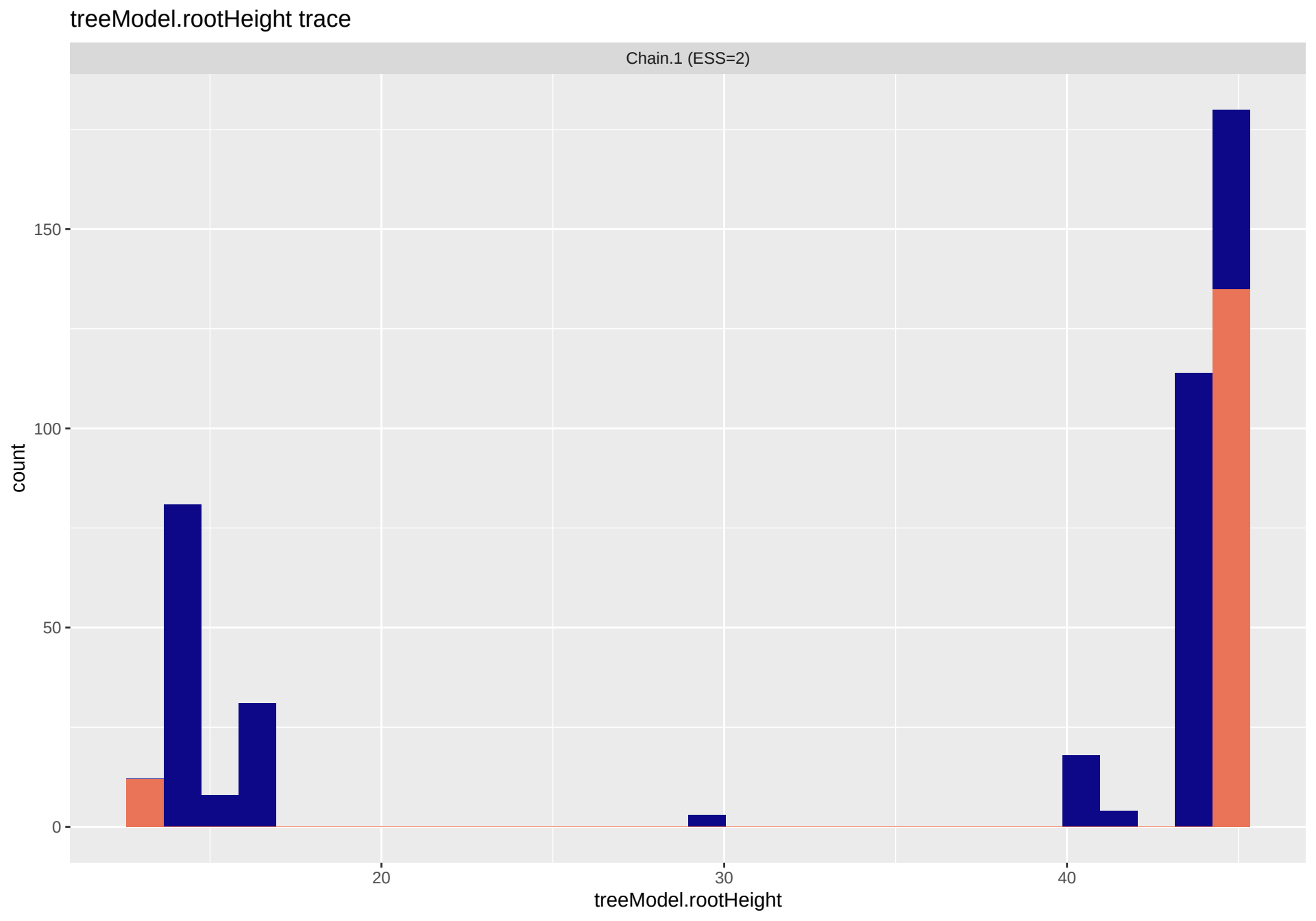

flipflop.lambda trace
Chain.1 (ESS=2)
0.035
0.030
0.025
0.020
flipflop.lambda
250
500
750
1000
Generation

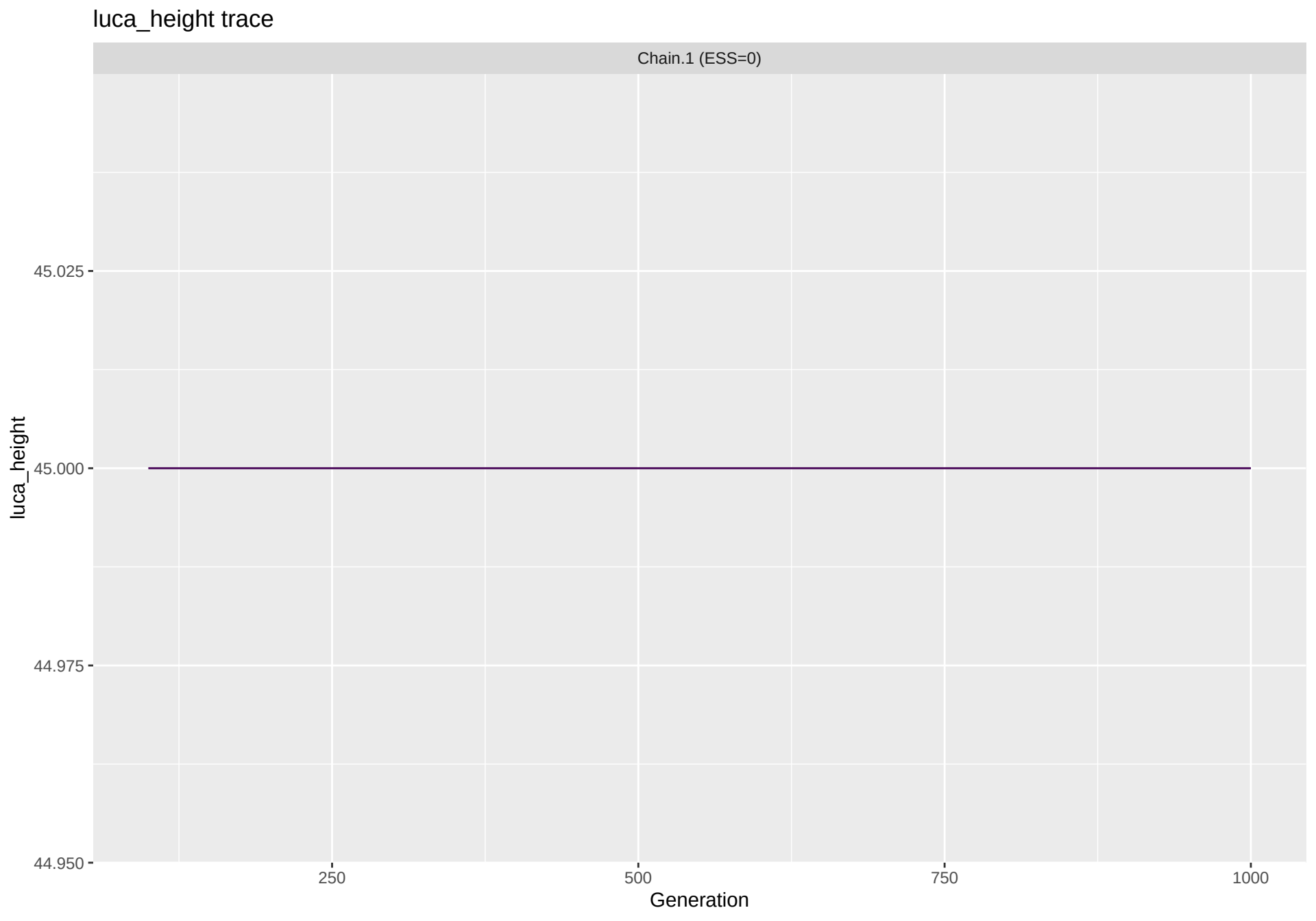

flipflop.lambda trace
Chain.1 (ESS=2)
150
100
50
0
count
0.020
0.025
0.030
0.035
flipflop.lambda

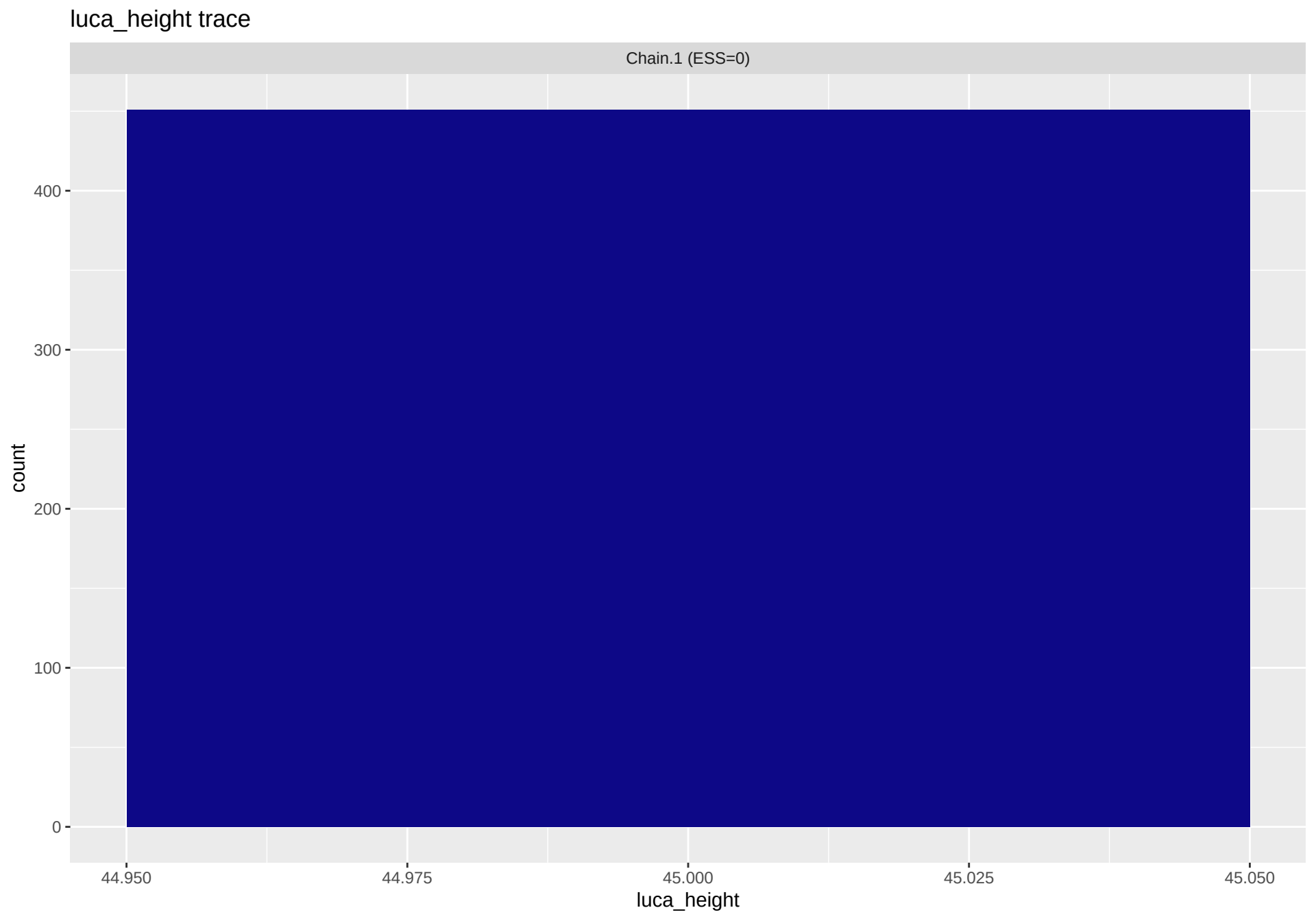

alignment.stemCells trace
Chain.1 (ESS=0)
alignment.stemCells
3.025
3.000
2.975
2.950
250
500
750
1000
Generation

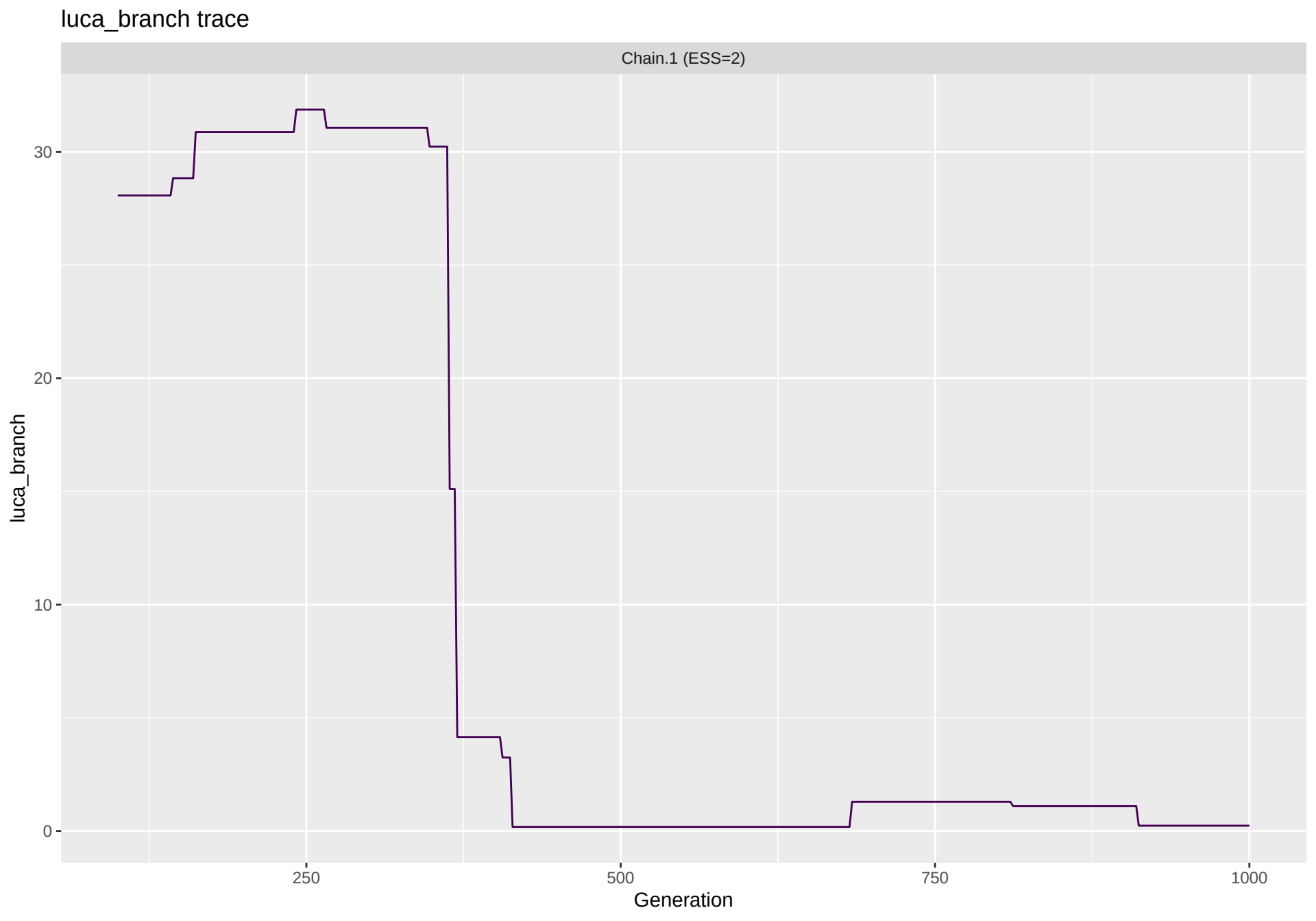

alignment.stemCells trace
Chain.1 (ESS=0)
count
400
300
200
100
0
2.950
2.975
3.000
3.025
3.050
alignment.stemCells

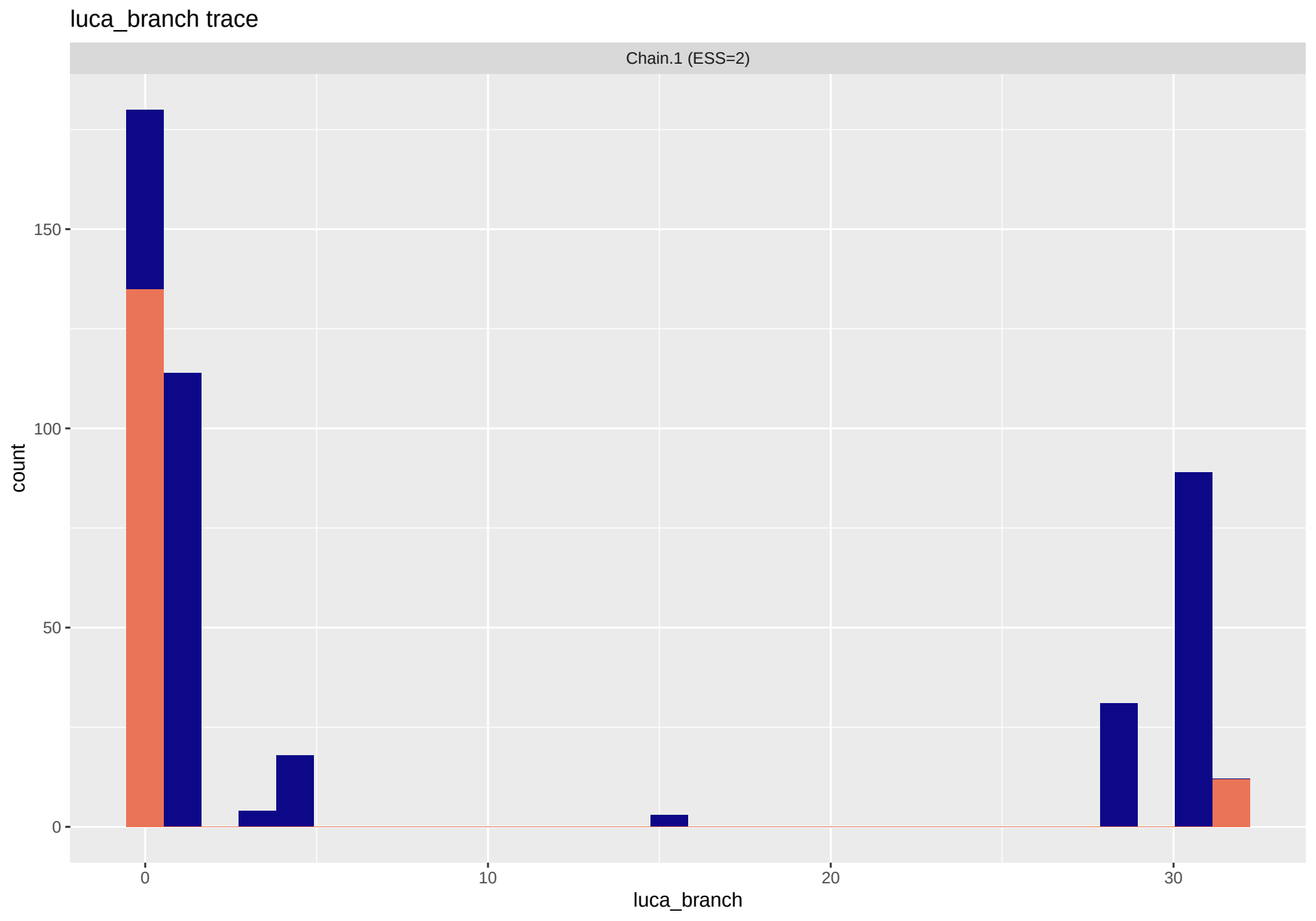

treeModel.rootHeight trace
Chain.1 (ESS=2)
treeModel.rootHeight
40
30
20
250
500
750
1000
Generation

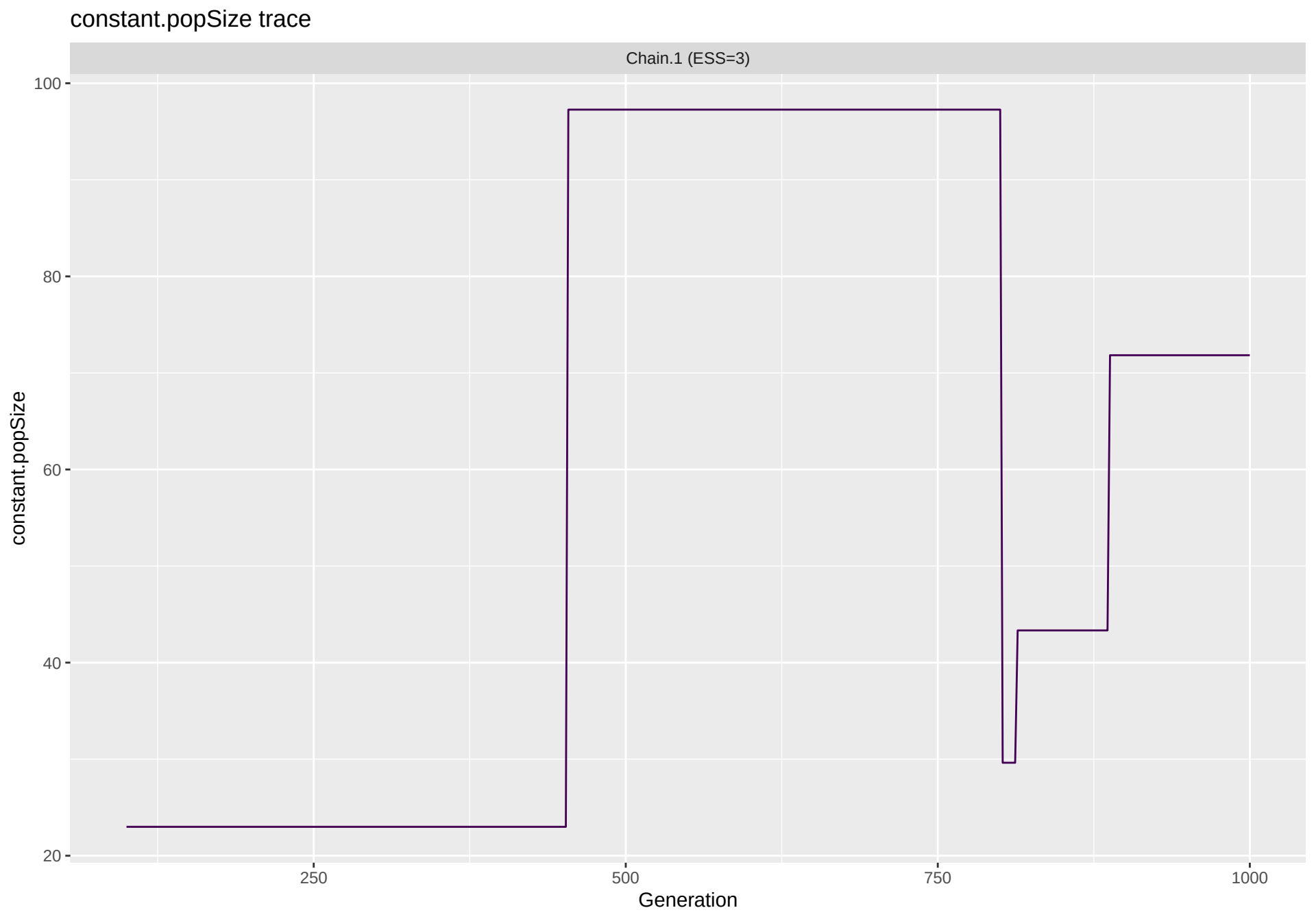

treeModel.rootHeight trace
Chain.1 (ESS=2)
count
150
100
50
0
20
30
40
treeModel.rootHeight

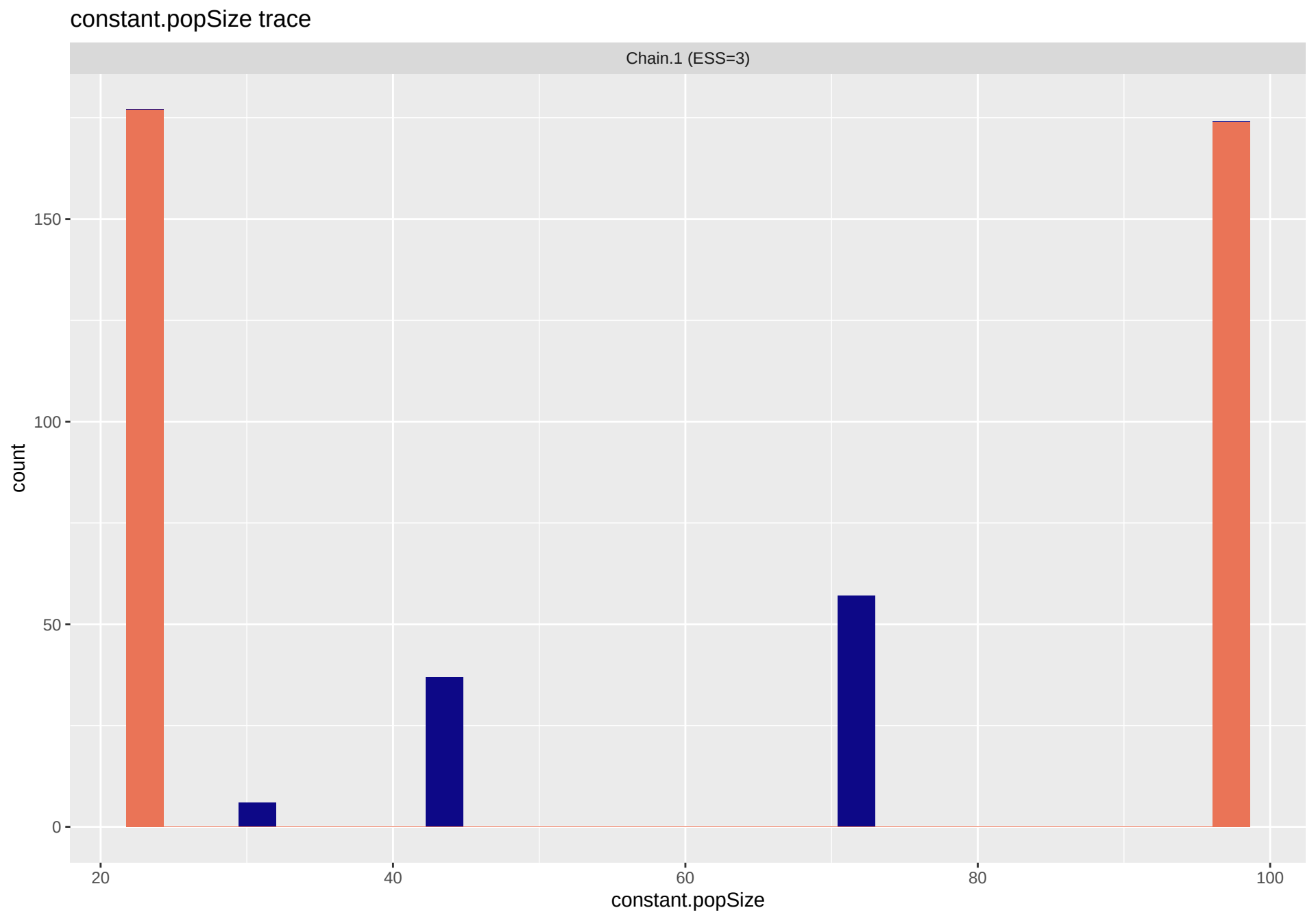

luca_height trace
Chain.1 (ESS=0)
45.025
45.000
44.975
44.950
luca_height
250
500
750
1000
Generation

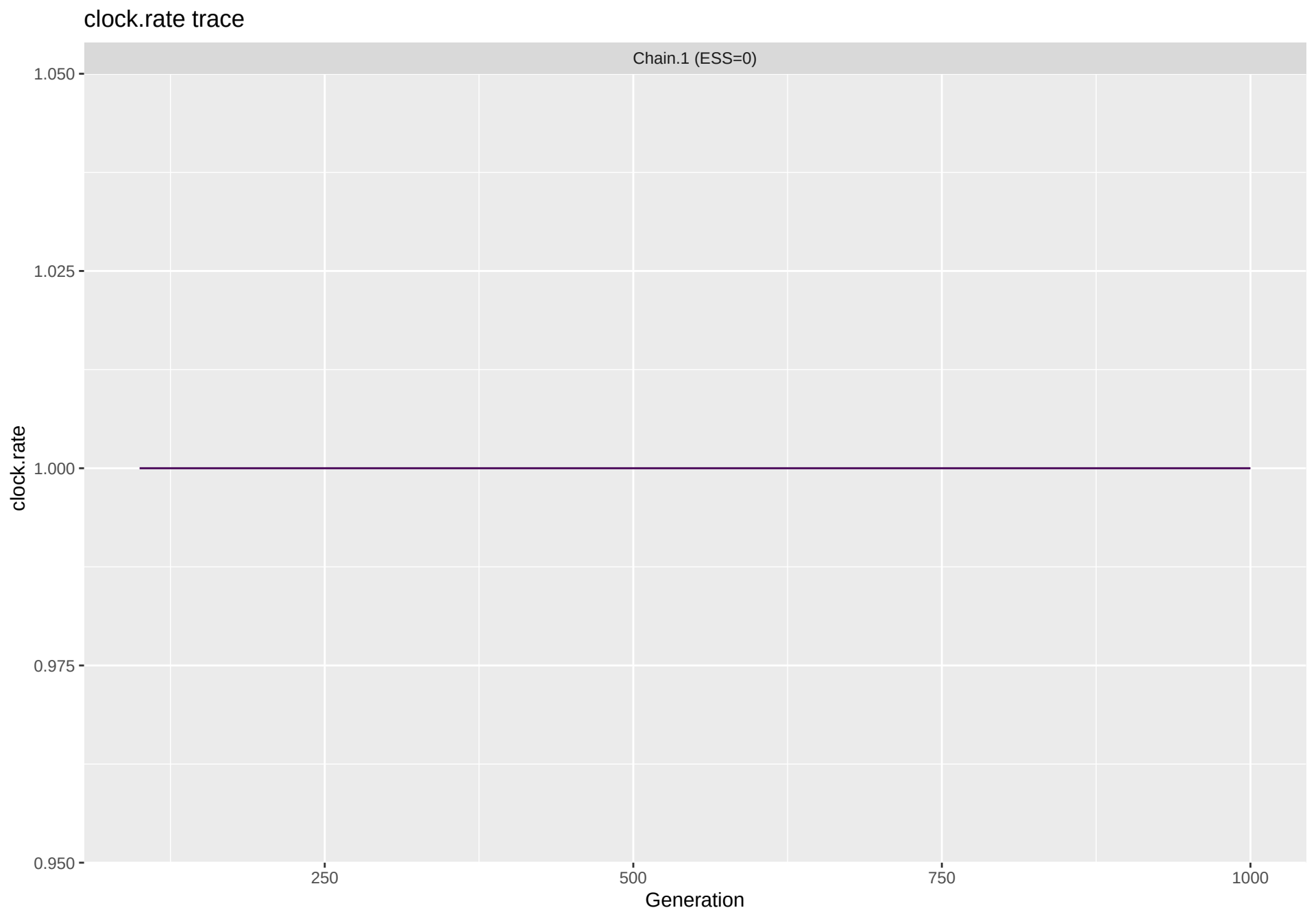

luca_height trace
Chain.1 (ESS=0)
count
400
300
200
100
0
44.950
44.975
45.000
45.025
45.050
luca_height

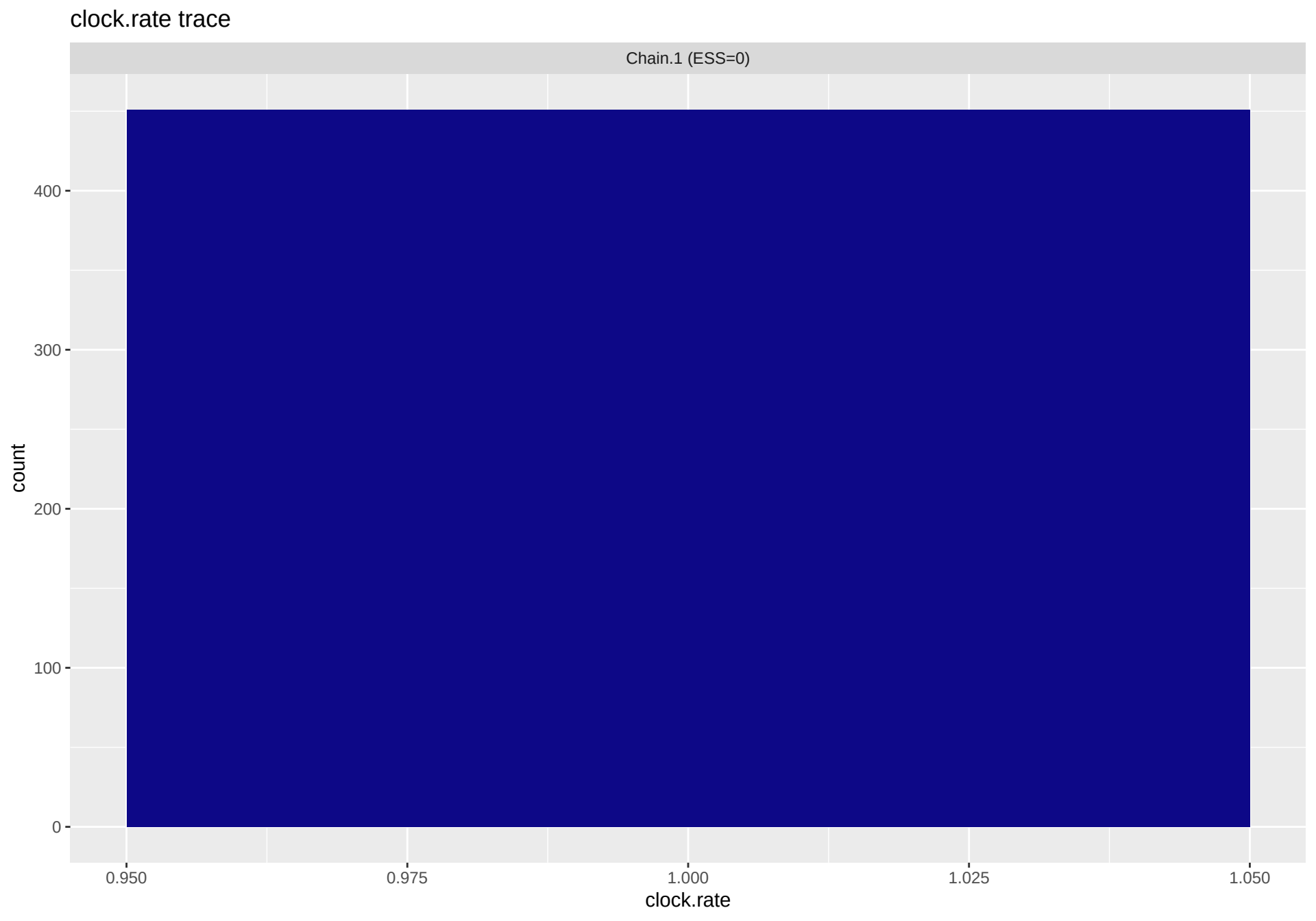

luca_branch trace
Chain.1 (ESS=2)
30
20
10
0
luca_branch
250
500
750
1000
Generation

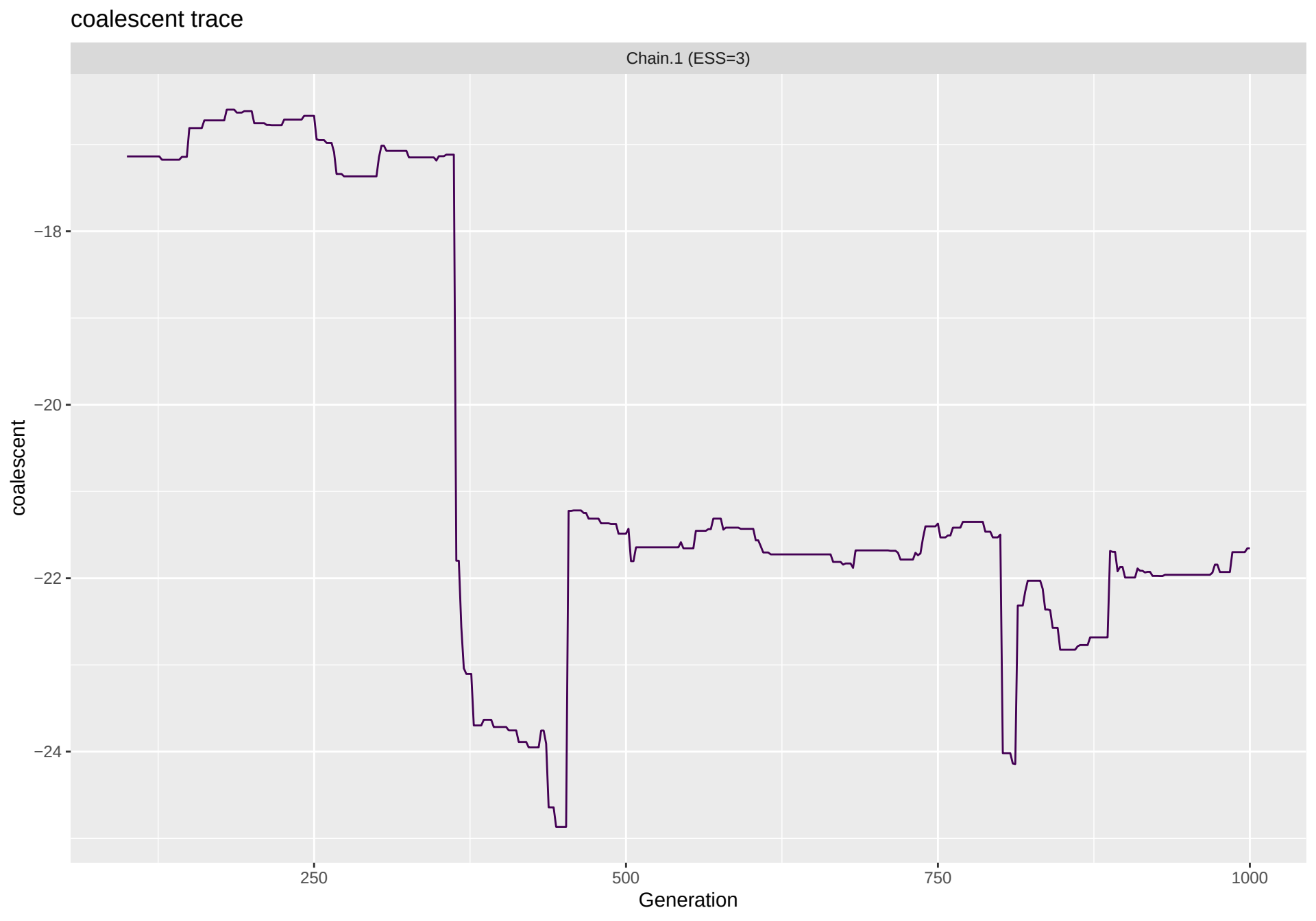

luca_branch trace
Chain.1 (ESS=2)
count
150
100
50
0
0
10
20
30
luca_branch

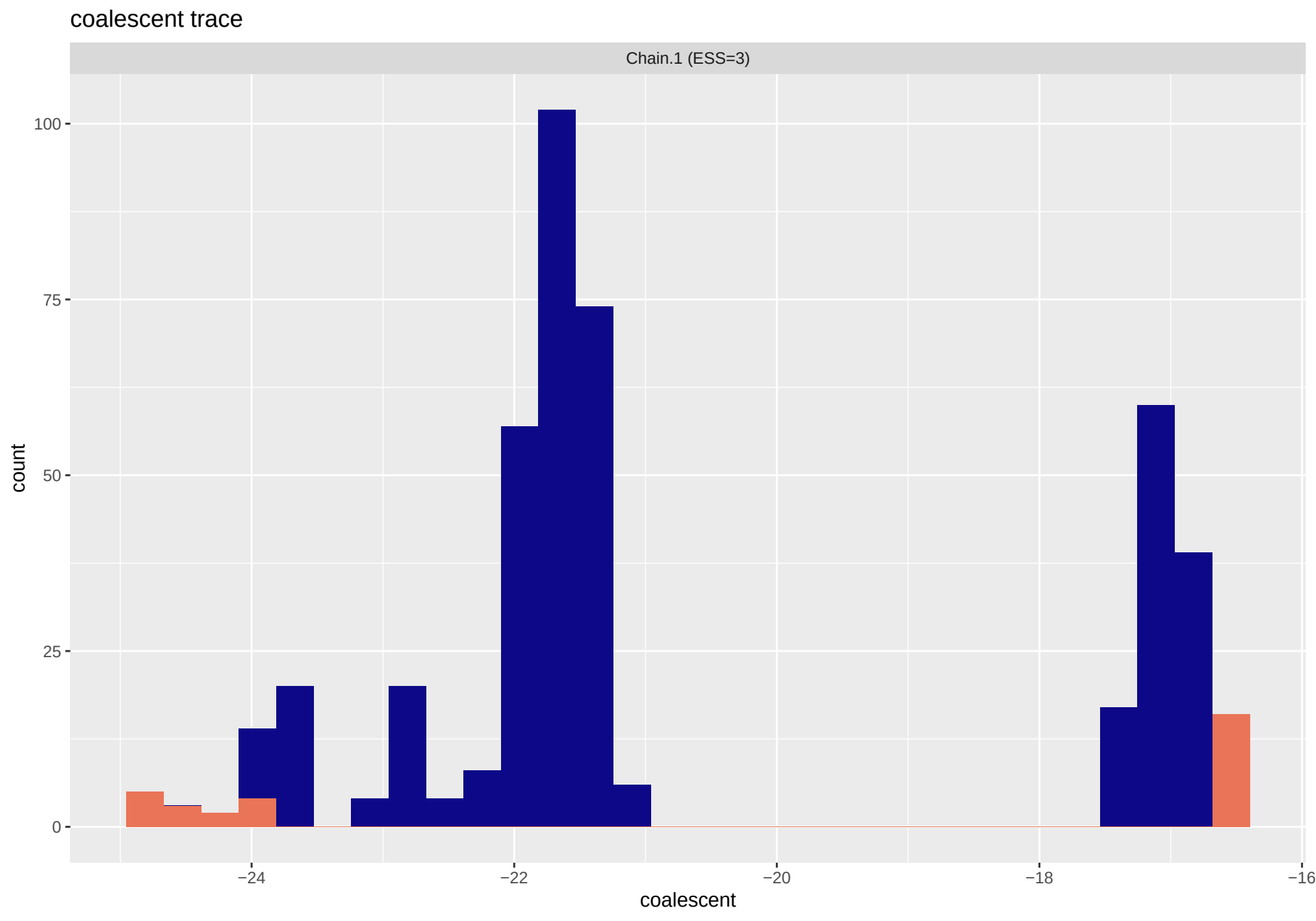

constant.popSize trace
Chain.1 (ESS=3)
100
80
60
40
20
constant.popSize
250
500
750
1000
Generation

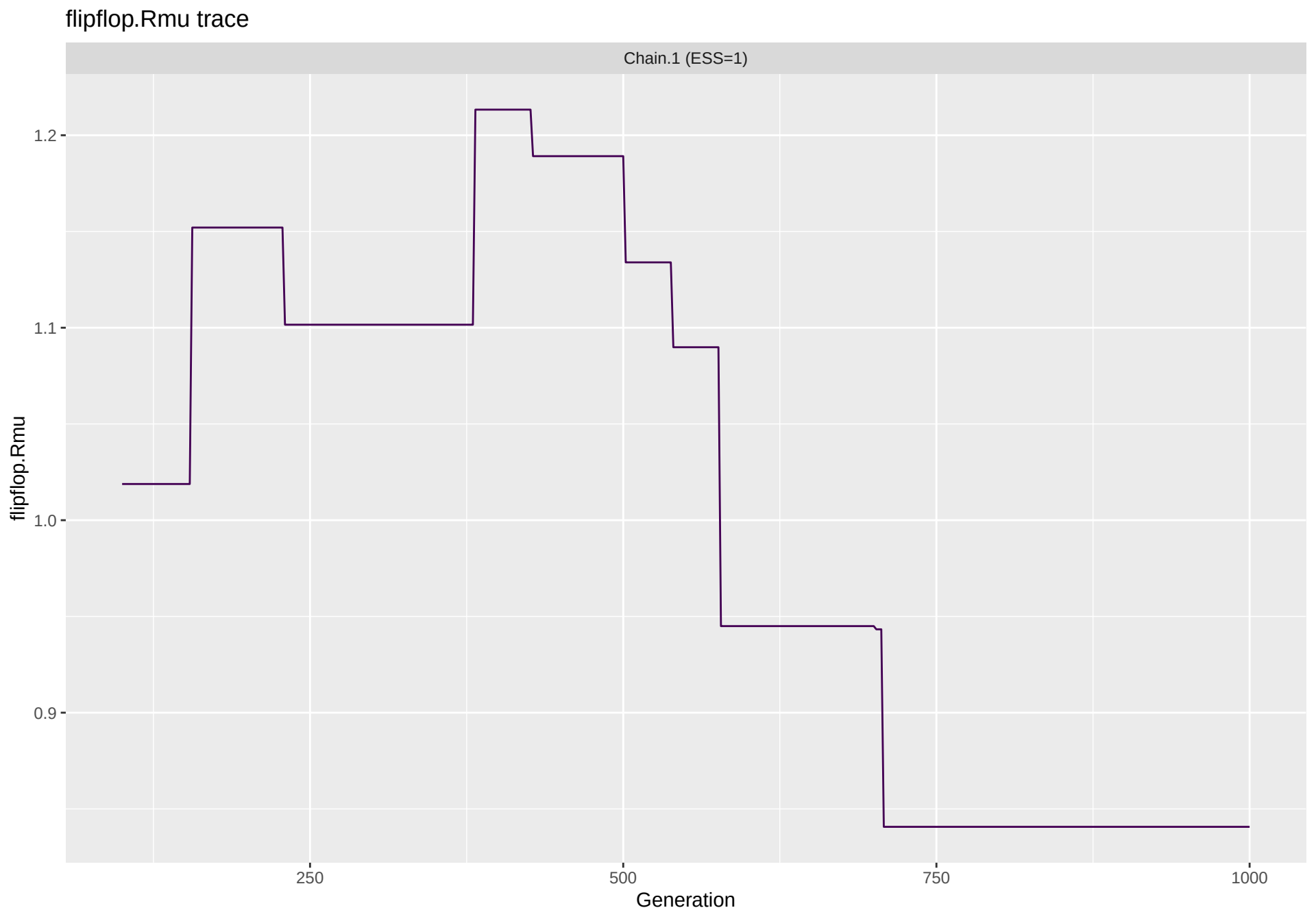

constant.popSize trace
Chain.1 (ESS=3)
count
150
100
50
0
20
40
60
80
100
constant.popSize

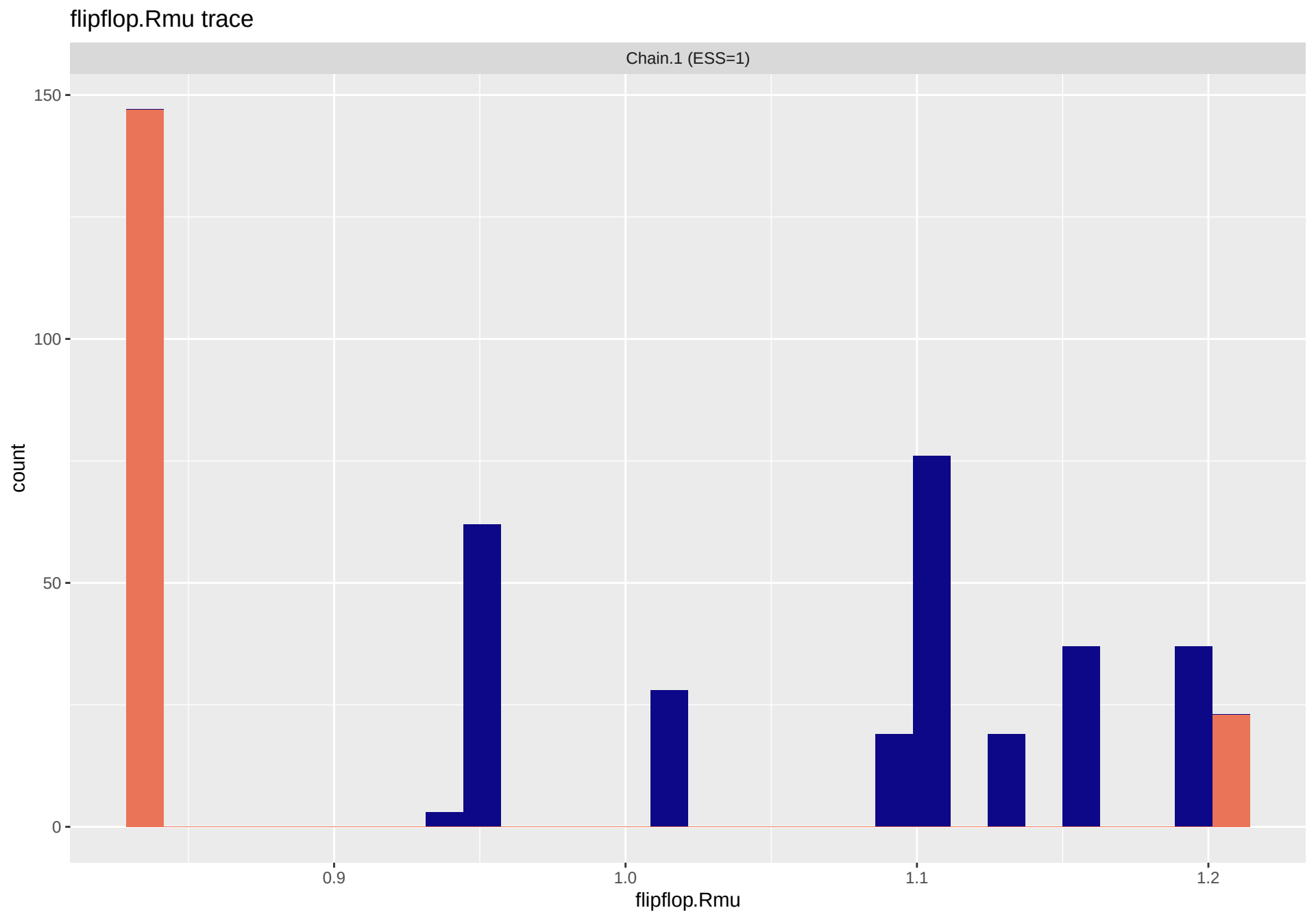

clock.rate trace
Chain.1 (ESS=0)
1.050
1.025
1.000
0.975
0.950
clock.rate
250
500
750
1000
Generation

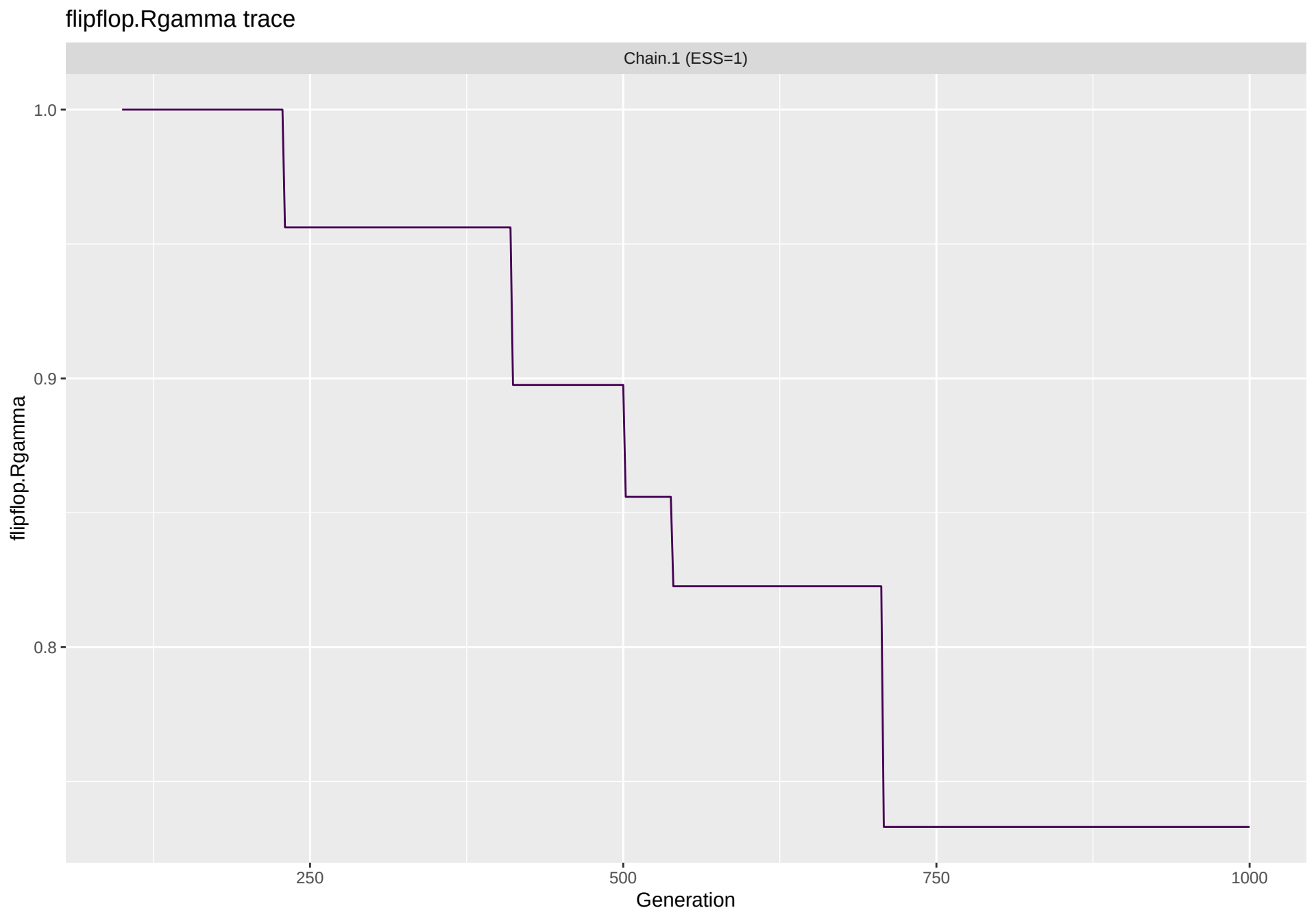

clock.rate trace
Chain.1 (ESS=0)
count
400
300
200
100
0
0.950
0.975
1.000
1.025
1.050
clock.rate

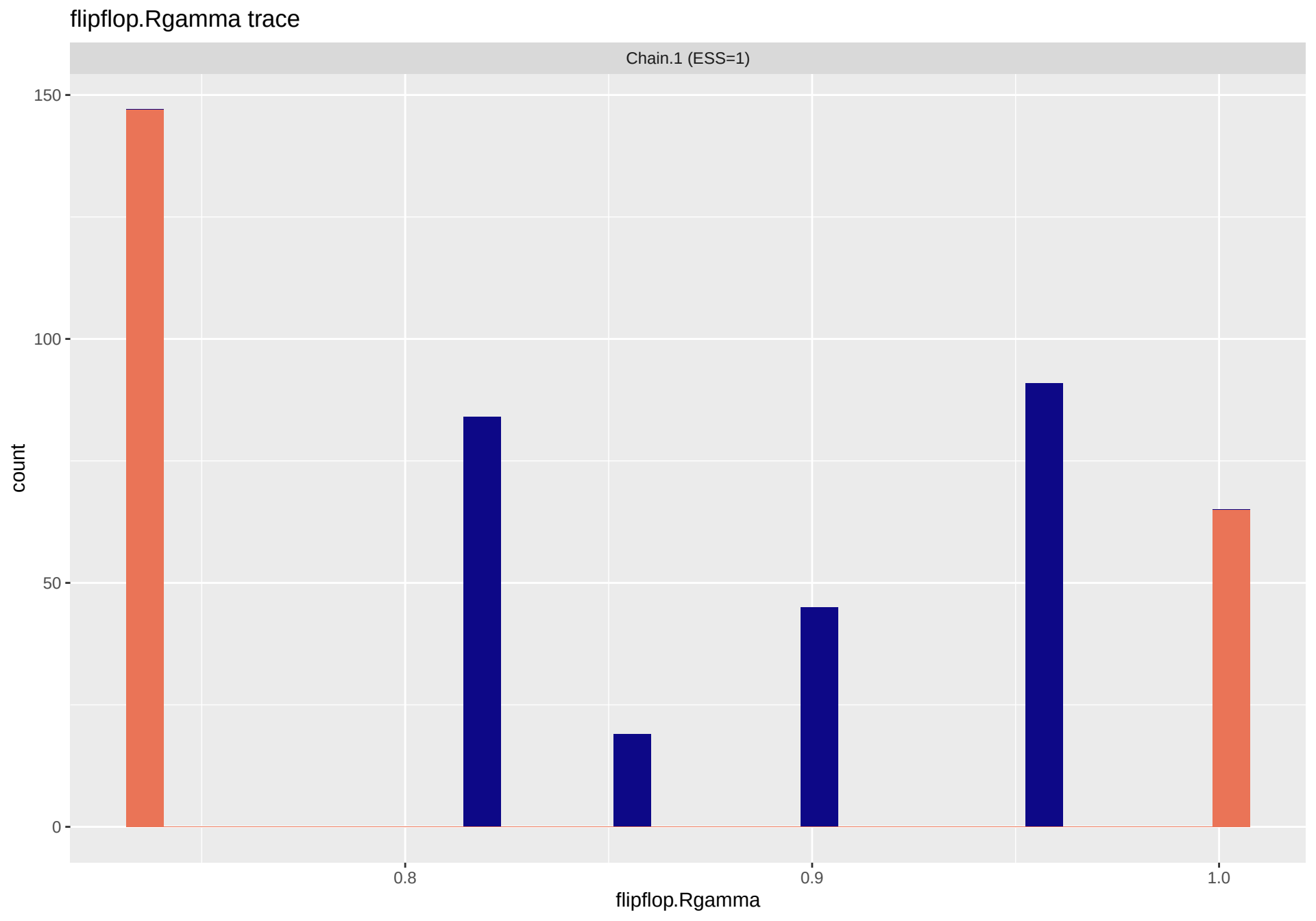

coalescent trace
Chain.1 (ESS=3)
coalescent
−18
−20
−22
−24
250
500
750
1000
Generation

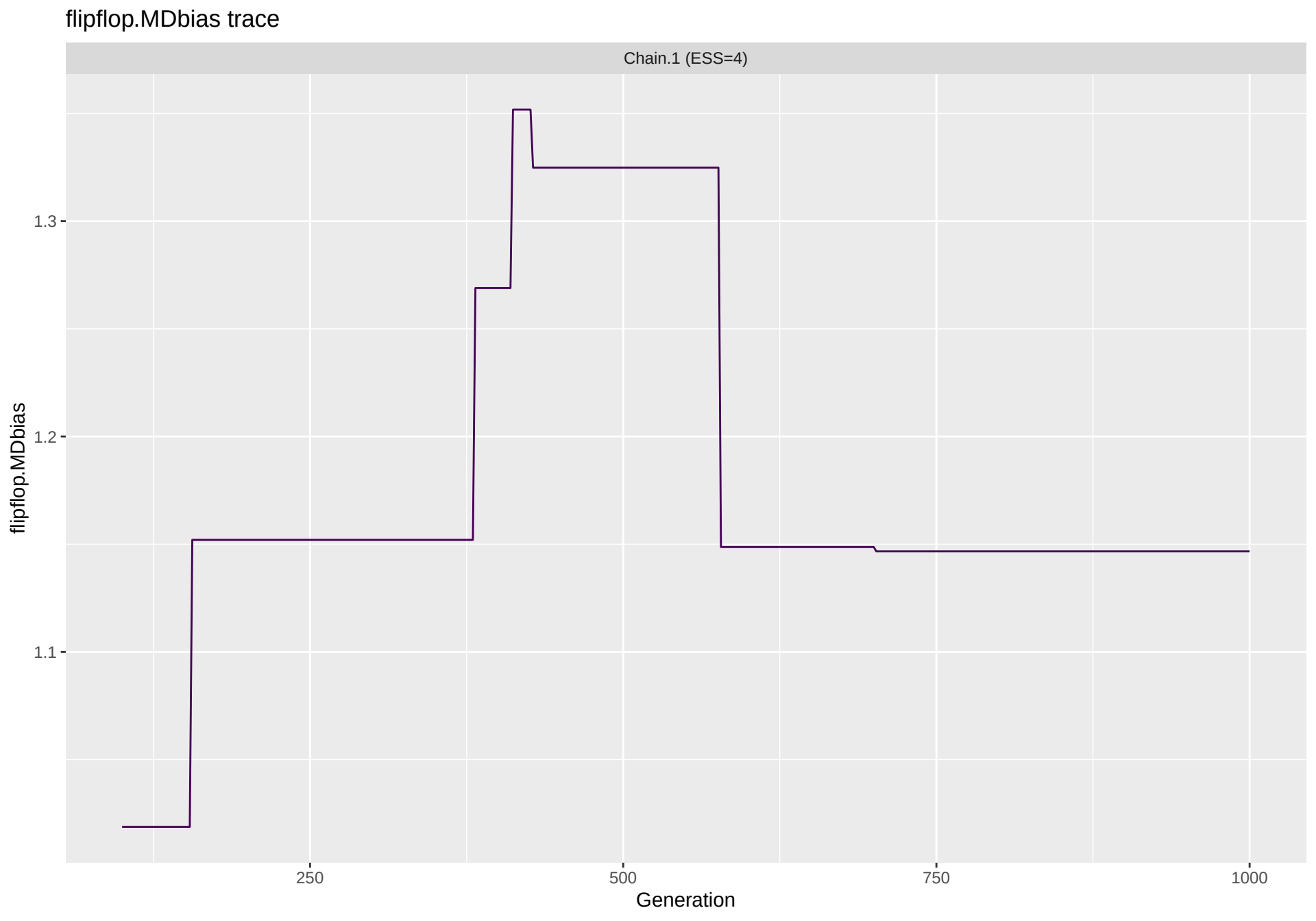

coalescent trace
Chain.1 (ESS=3)
100
75
50
25
0
count
−24
−22
−20
−18
−16
coalescent

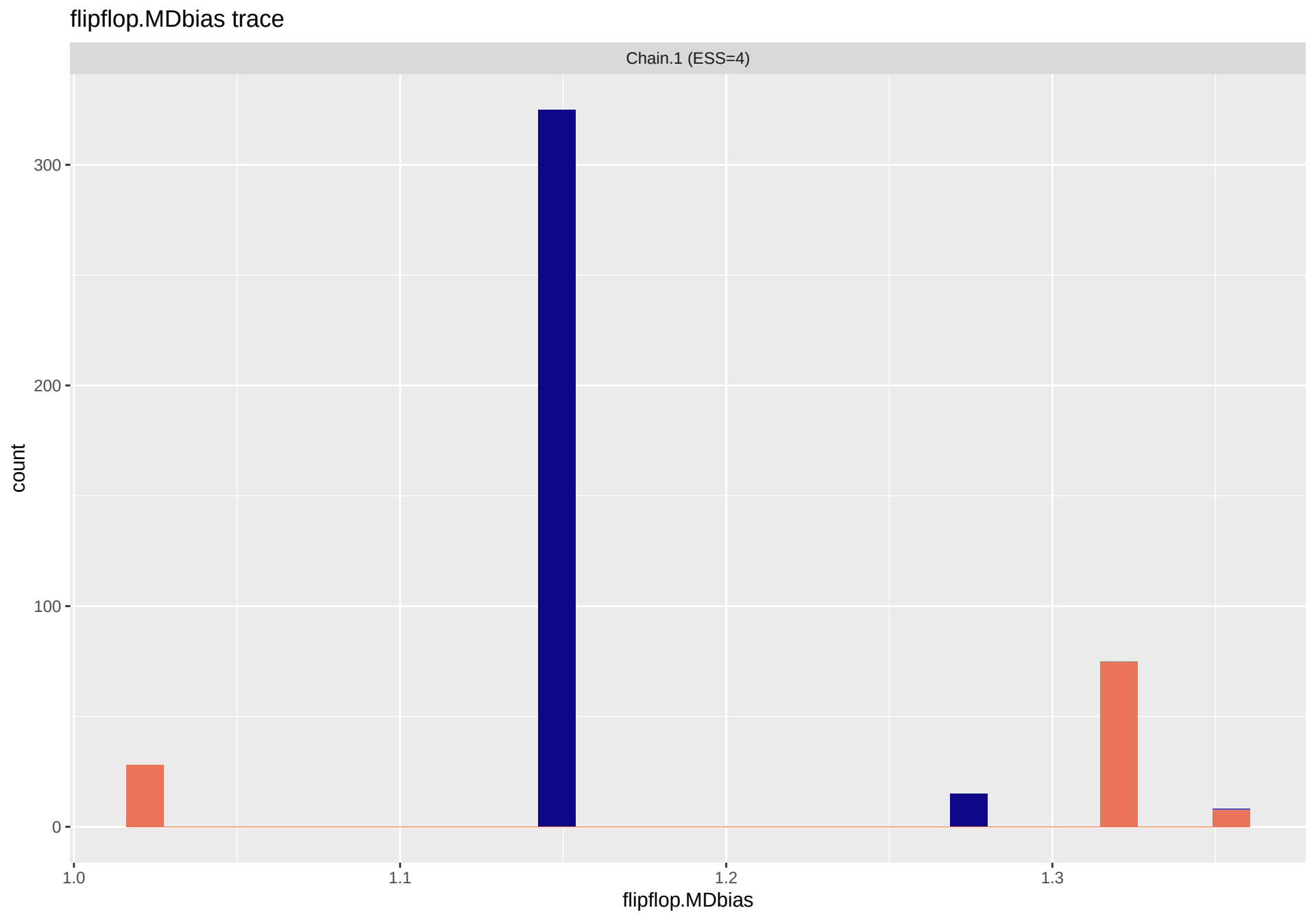

flipflop.Rmu trace
Chain.1 (ESS=1)
1.2
1.1
1.0
0.9
flipflop.Rmu
250
500
750
1000
Generation

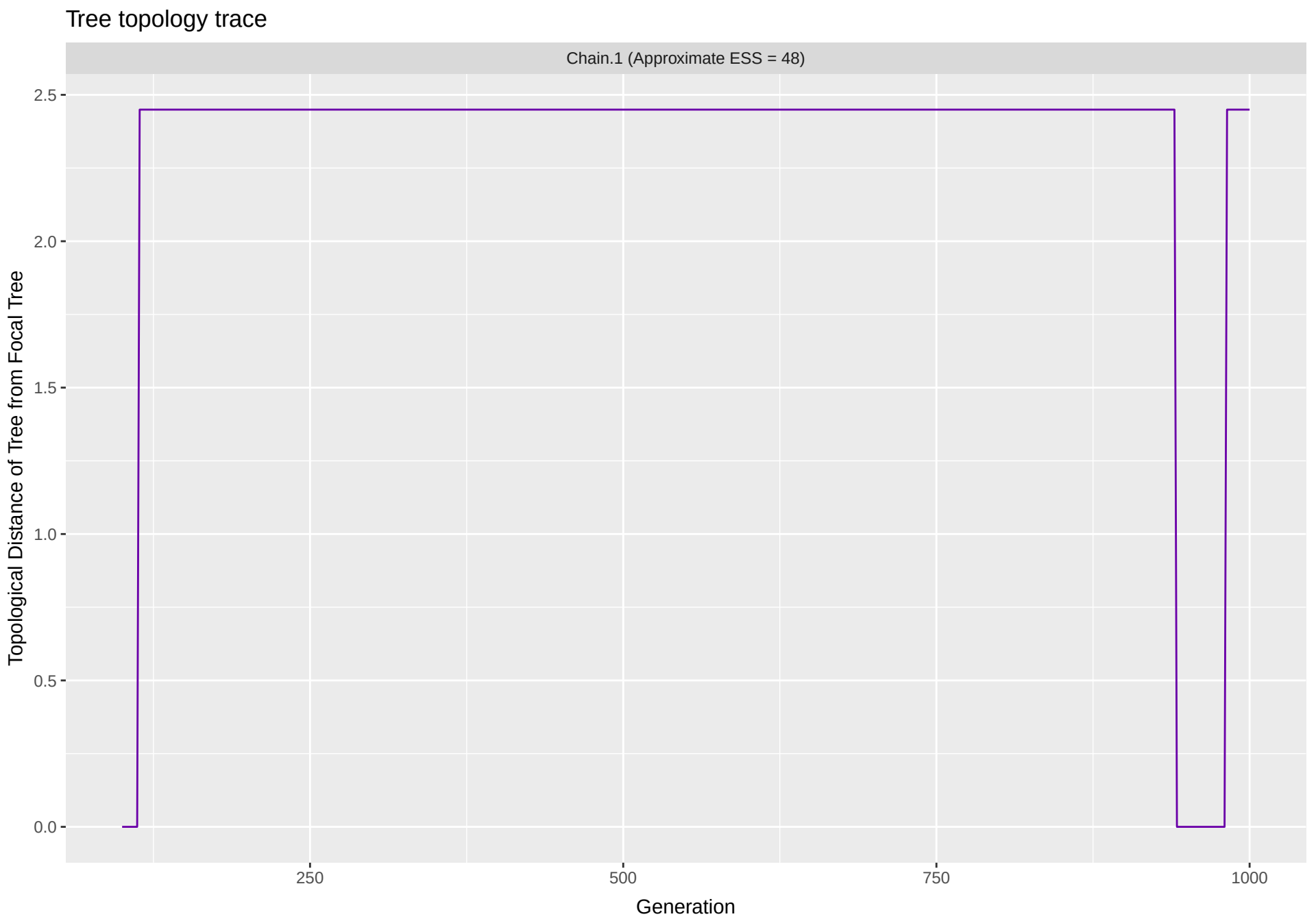

flipflop.Rmu trace
Chain.1 (ESS=1)
150
100
50
0
count
0.9
1.0
1.1
1.2
flipflop.Rmu

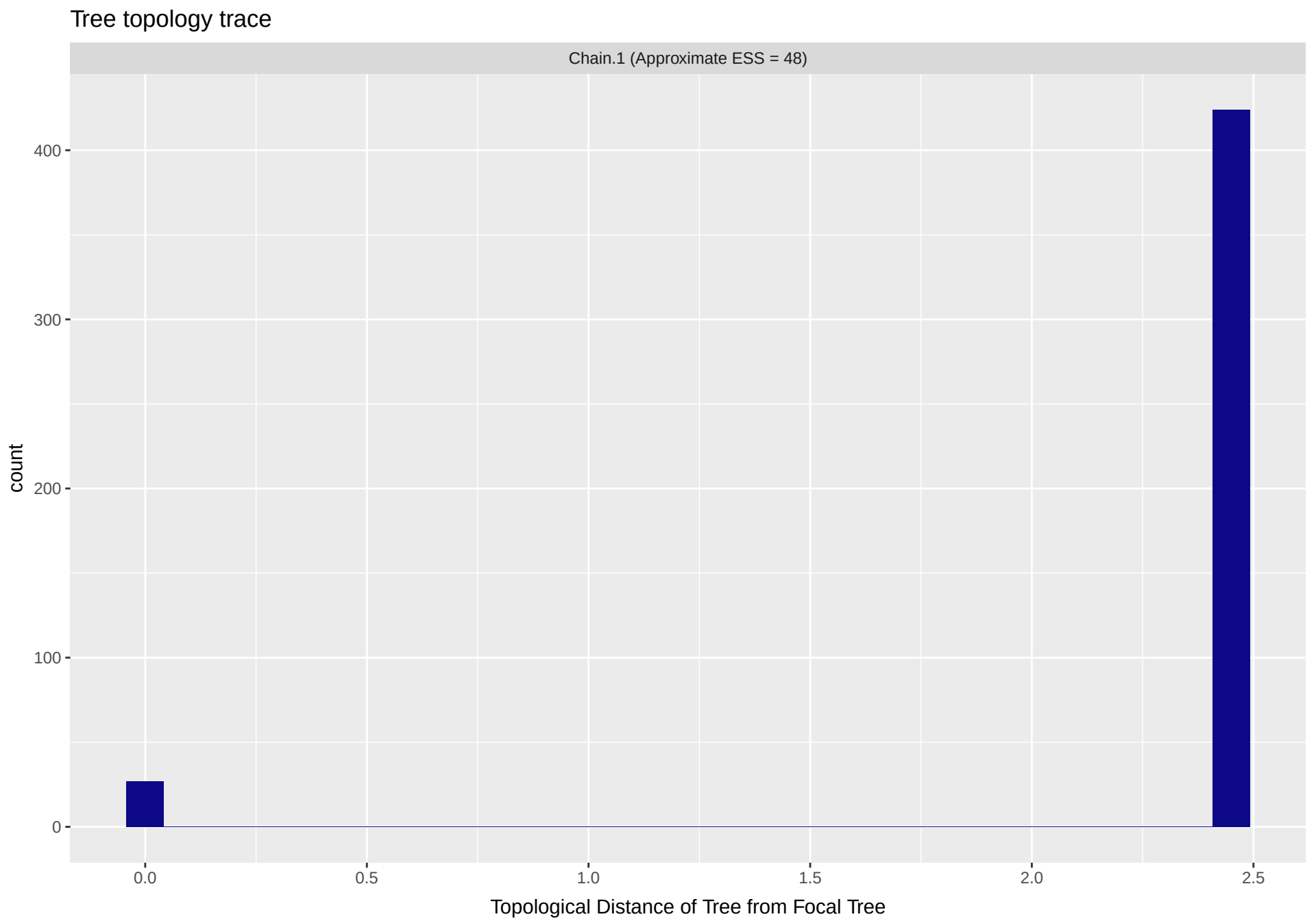

flipflop.Rgamma trace
Chain.1 (ESS=1)
1.0
0.9
0.8
flipflop.Rgamma
250
500
750
1000
Generation

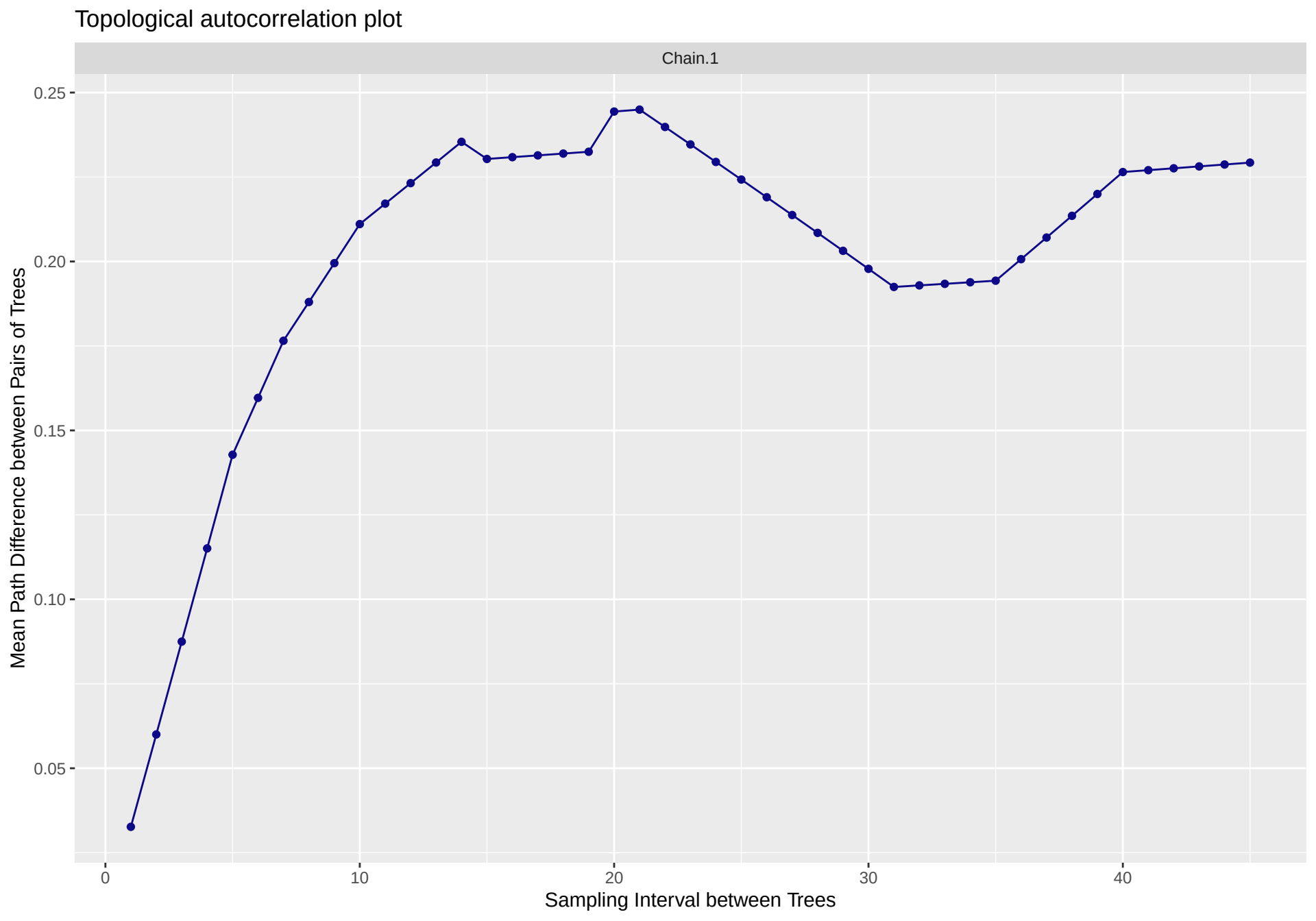

flipflop.Rgamma trace
Chain.1 (ESS=1)
150
100
50
0
count
0.8
0.9
1.0
flipflop.Rgamma

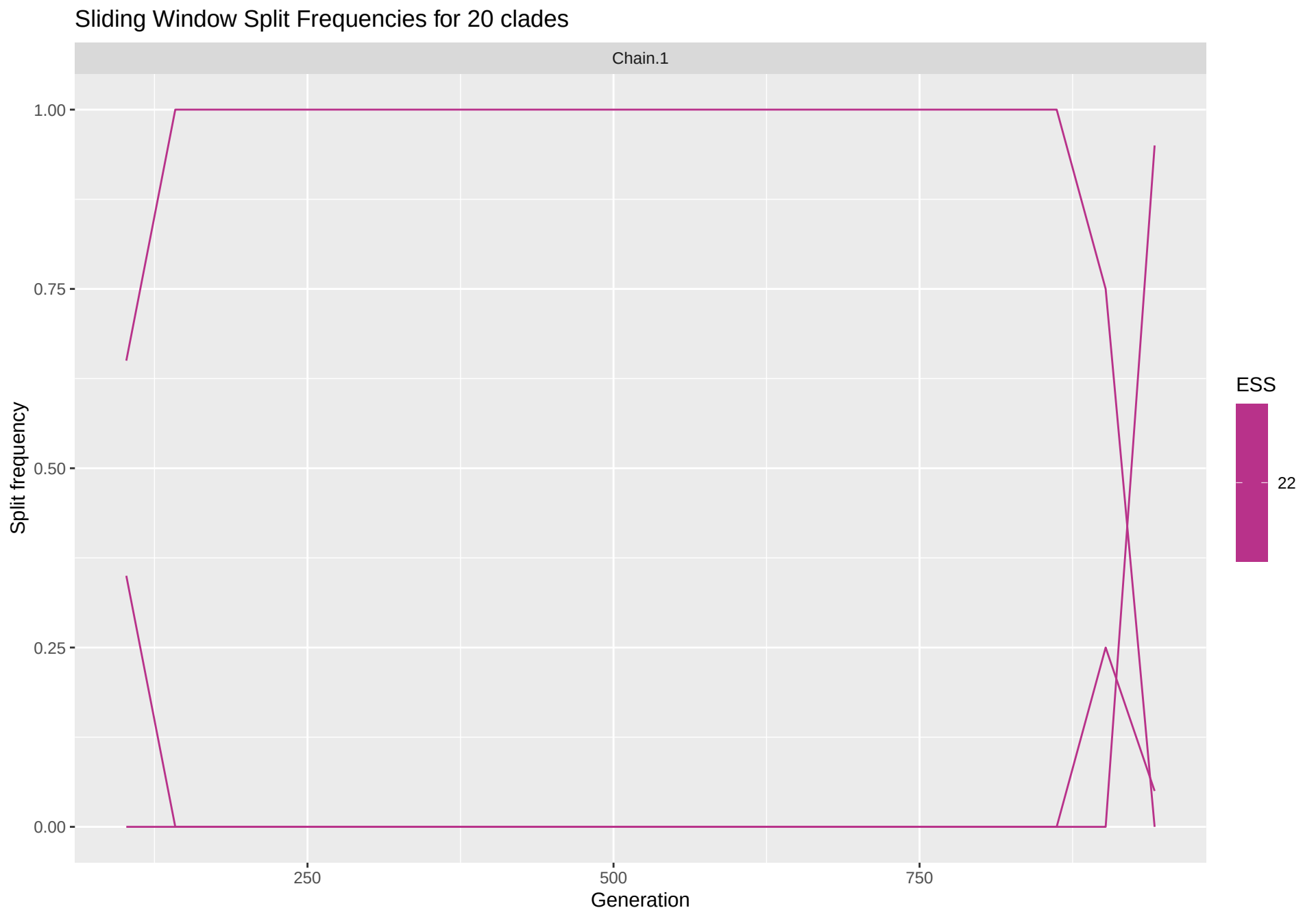

flipflop.MDbias trace
Chain.1 (ESS=4)
flipflop.MDbias
1.3
1.2
1.1
250
500
750
1000
Generation

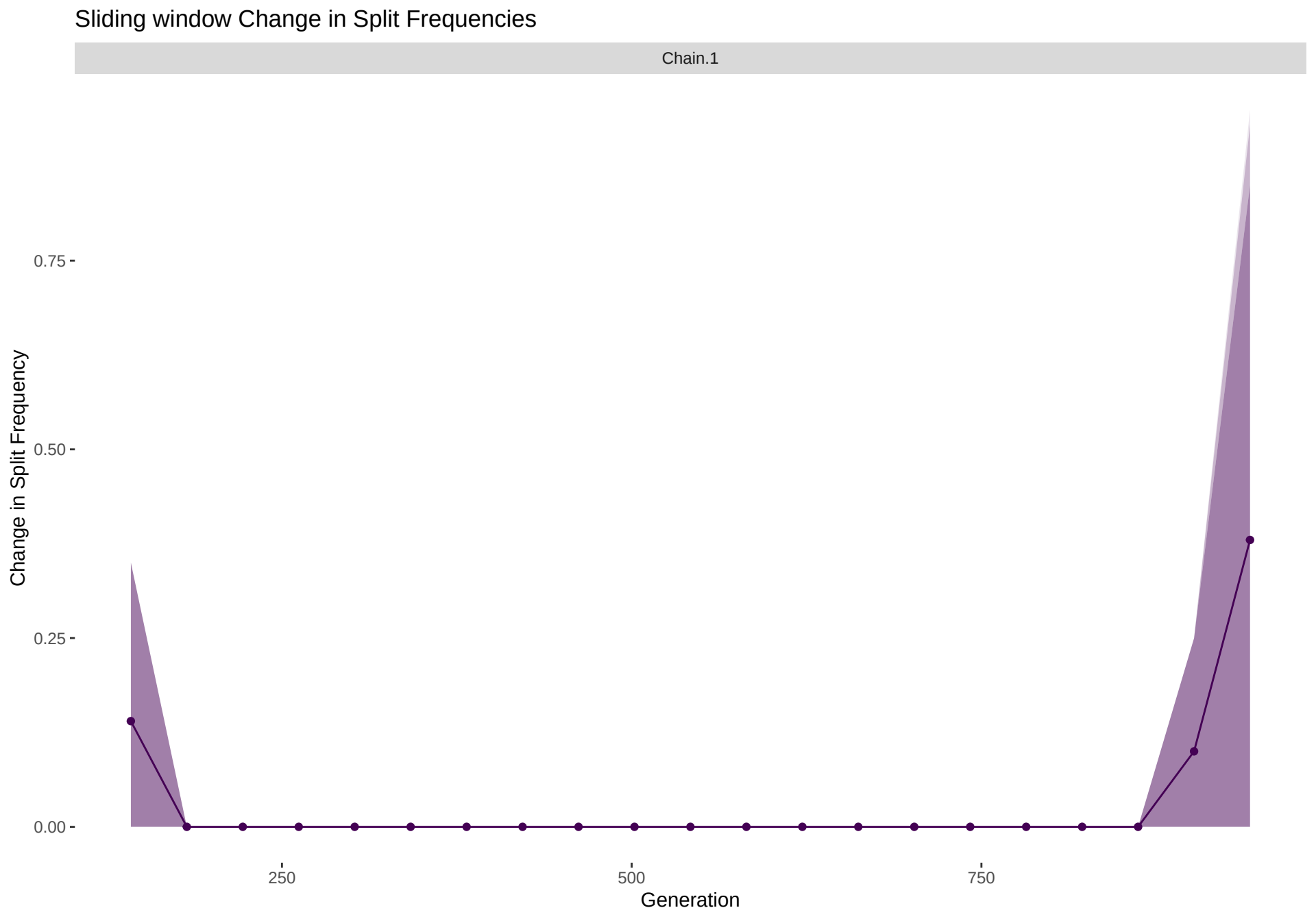

flipflop.MDbias trace
Chain.1 (ESS=4)
count
300
200
100
0
1.0
1.1
1.2
1.3
flipflop.MDbias

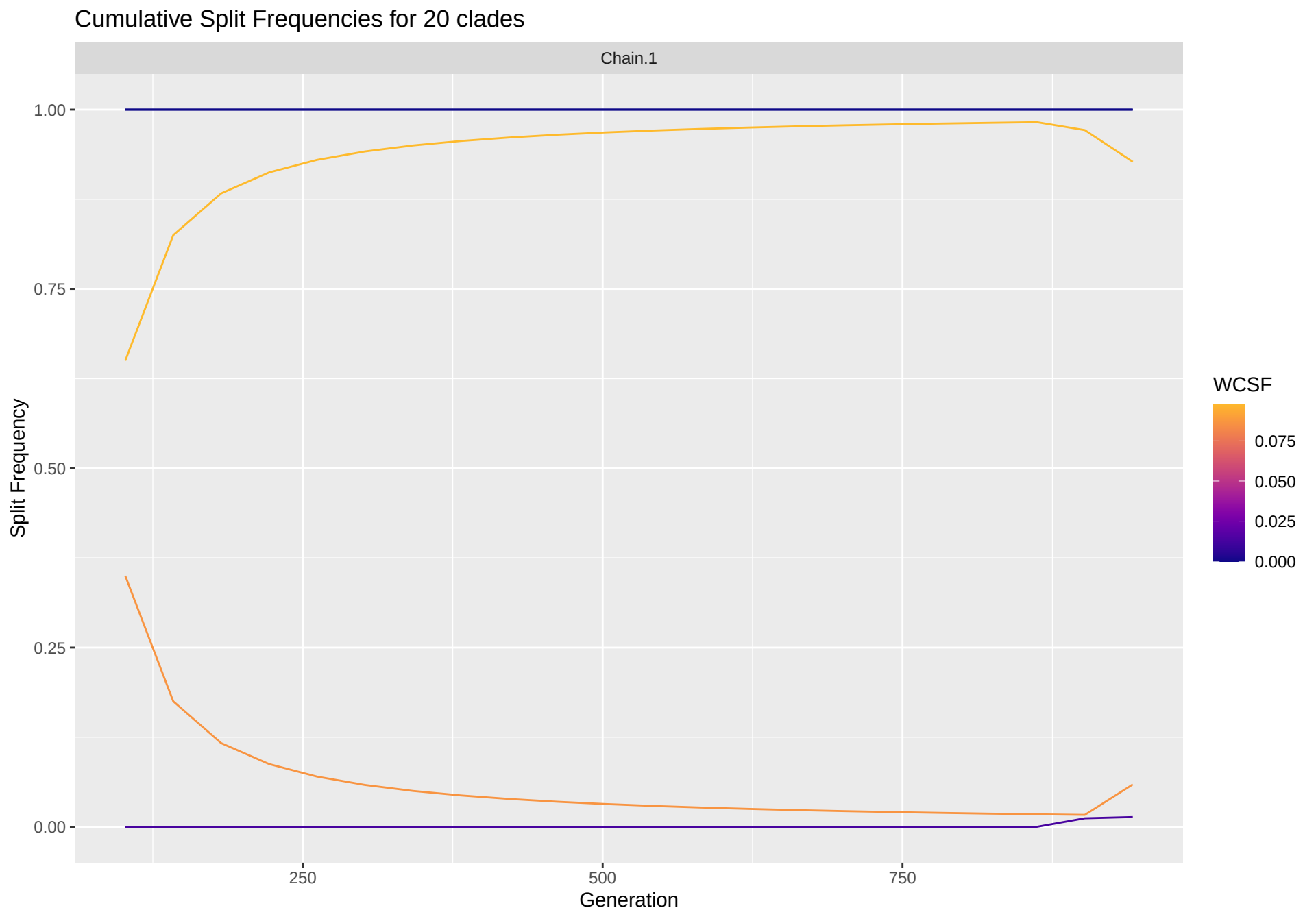

Tree topology trace
Chain.1 (Approximate ESS = 48)
Topological Distance of Tree from Focal Tree
2.5
2.0
1.5
1.0
0.5
0.0
250
500
750
1000
Generation

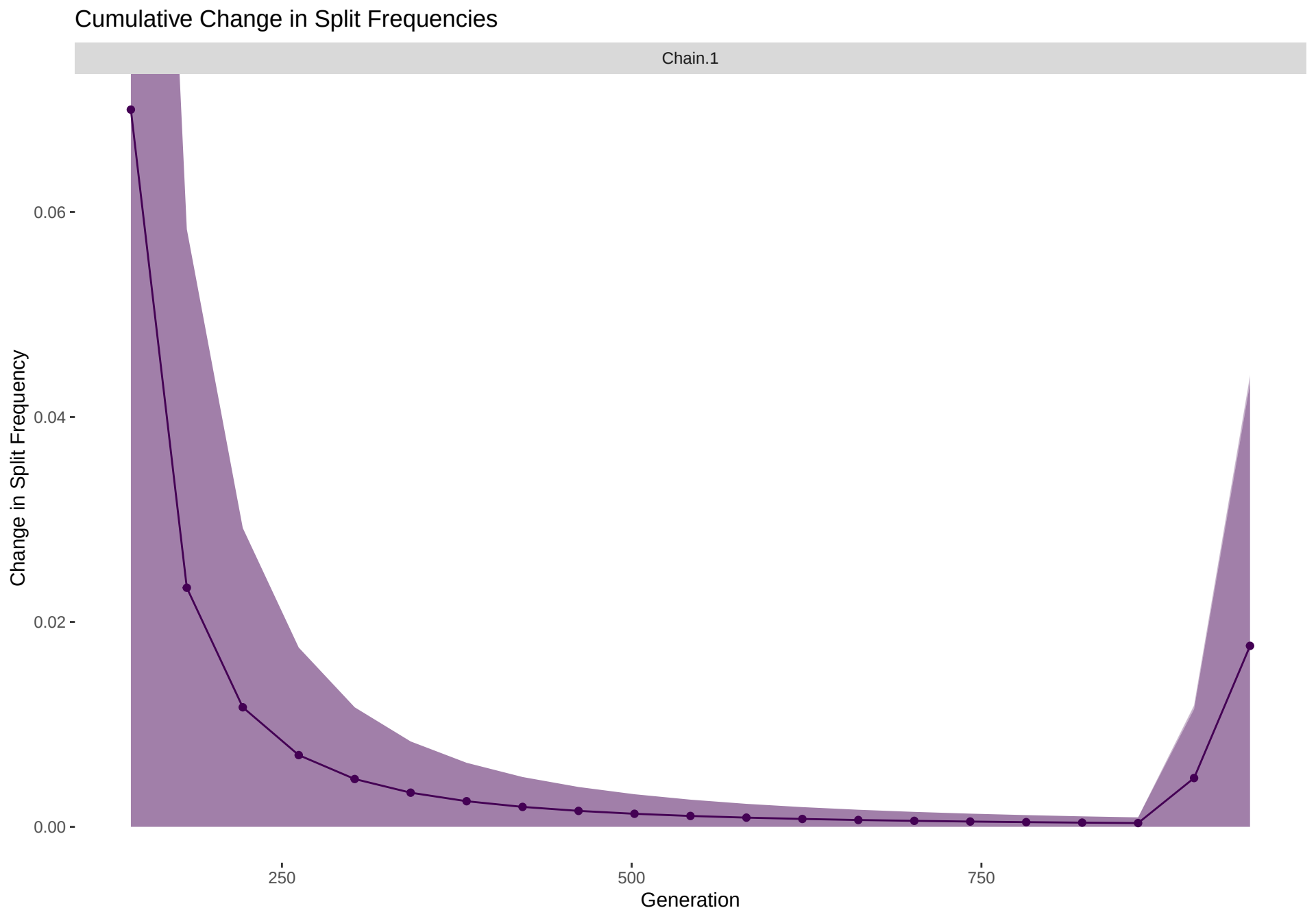

Tree topology trace
Chain.1 (Approximate ESS = 48)
count
400
300
200
100
0
0.0
0.5
1.0
1.5
2.0
2.5
Topological Distance of Tree from Focal Tree

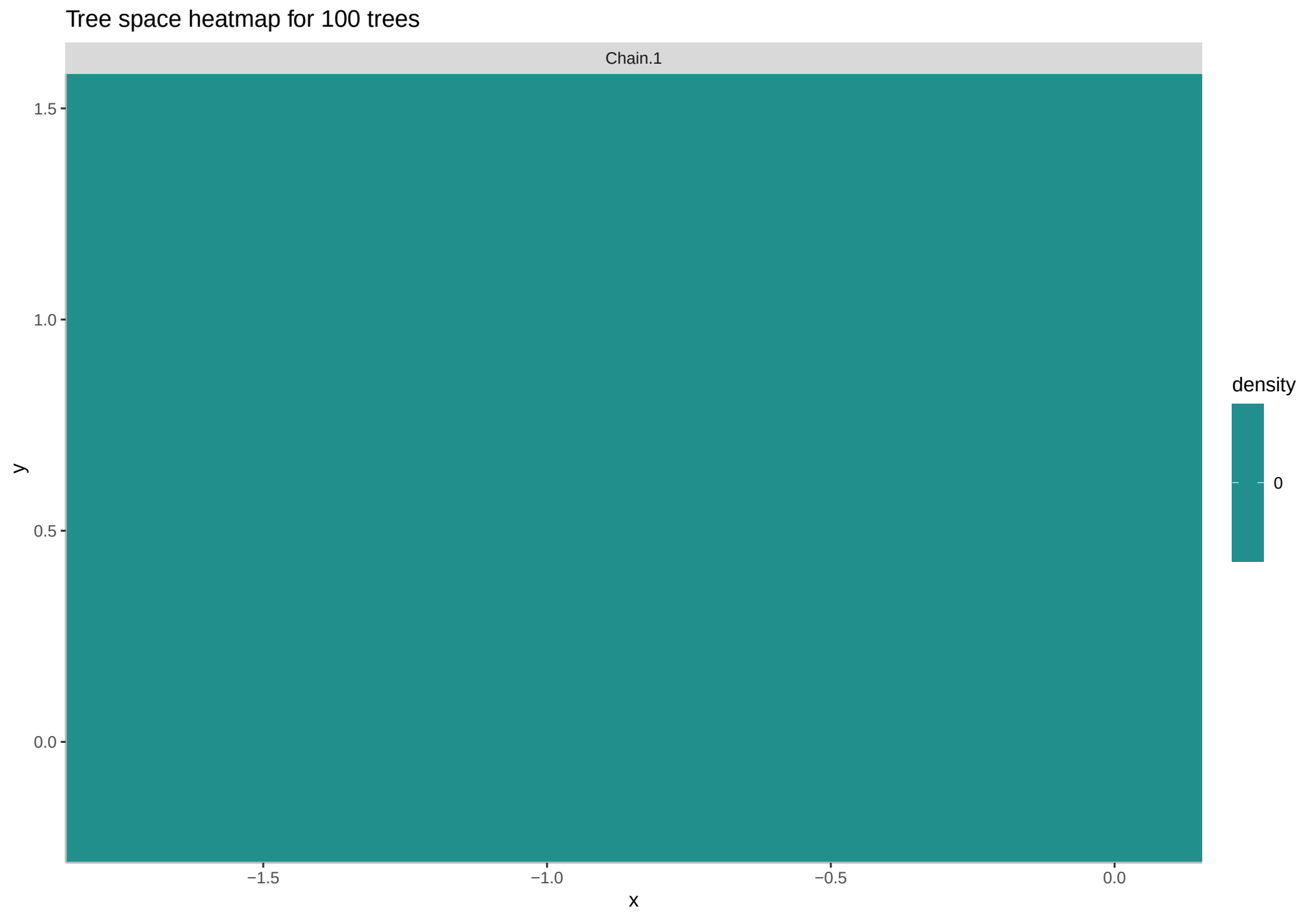

Topological autocorrelation plot
Chain.1
Mean Path Difference between Pairs of Trees
0.25
0.20
0.15
0.10
0.05
0
10
20
30
40
Sampling Interval between Trees

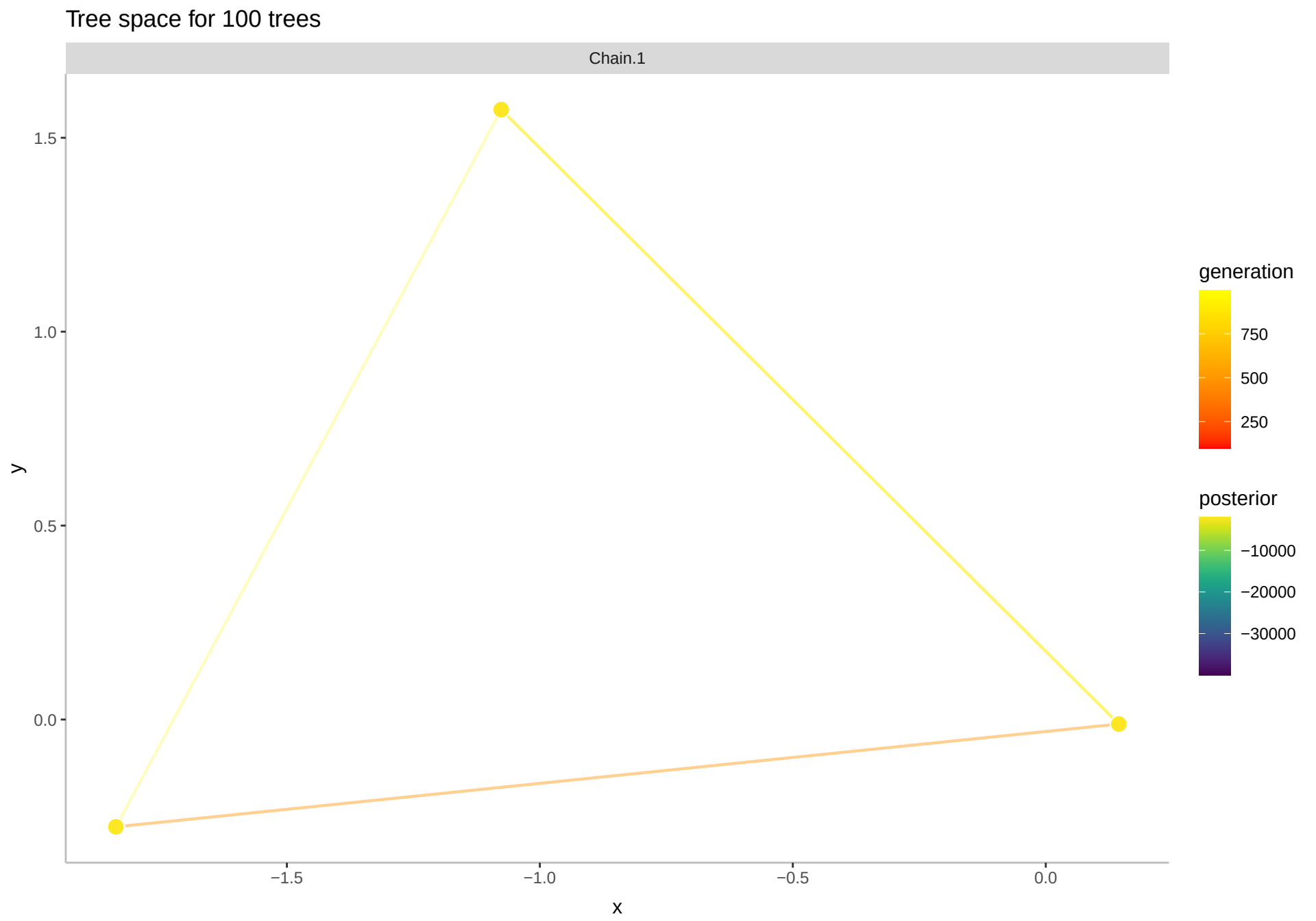

Sliding Window Split Frequencies for 20 clades
Chain.1
1.00
0.75
0.50
0.25
0.00
Split frequency
250
500
750
Generation
ESS
22


Sliding window Change in Split Frequencies
Chain.1
0.75
0.50
0.25
0.00
Change in Split Frequency
250
500
750
Generation


Cumulative Split Frequencies for 20 clades
Chain.1
1.00
0.75
0.50
0.25
0.00
Split Frequency
250
500
750
Generation
WCSF
0.075
0.050
0.025
0.000


Cumulative Change in Split Frequencies
Chain.1
Change in Split Frequency
0.06
0.04
0.02
0.00
250
500
750
Generation


Tree space heatmap for 100 trees
Chain.1
1.5
1.0
0.5
0.0
y
−1.5
−1.0
−0.5
0.0
x
density
0


Tree space for 100 trees
Chain.1
1.5
1.0
0.5
0.0
y
−1.5
−1.0
−0.5
0.0
x
generation
750
500
250
posterior
−10000
−20000
−30000