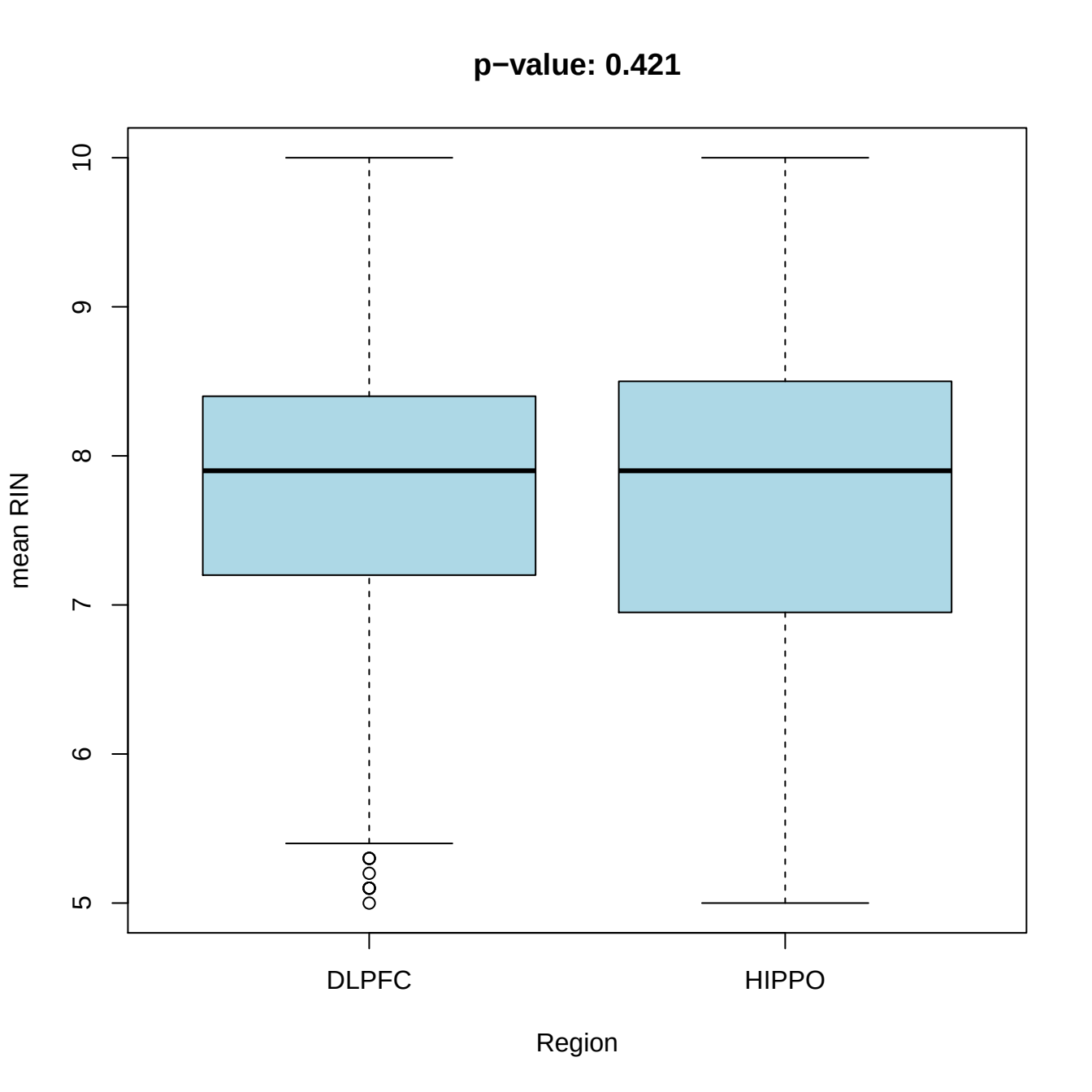
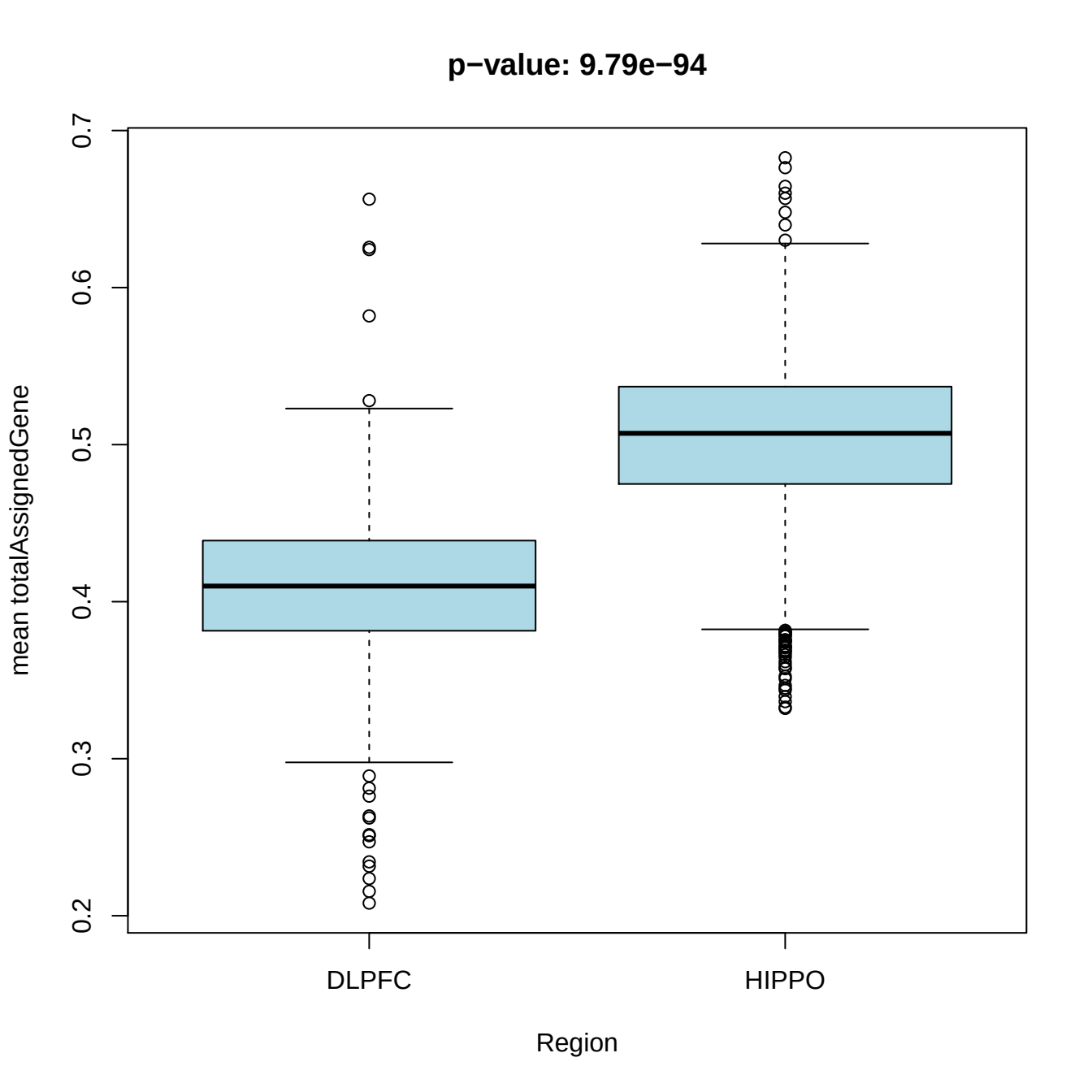
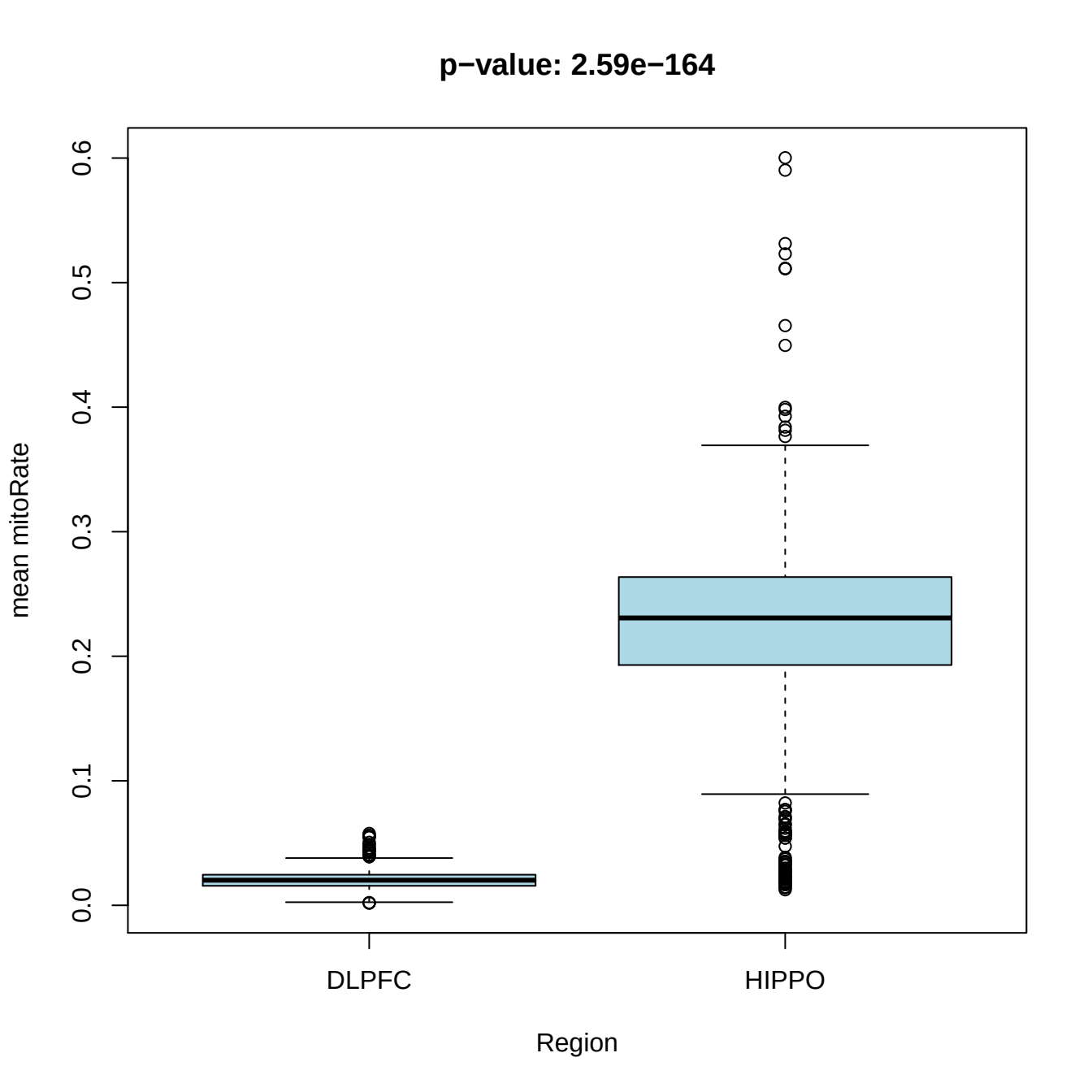
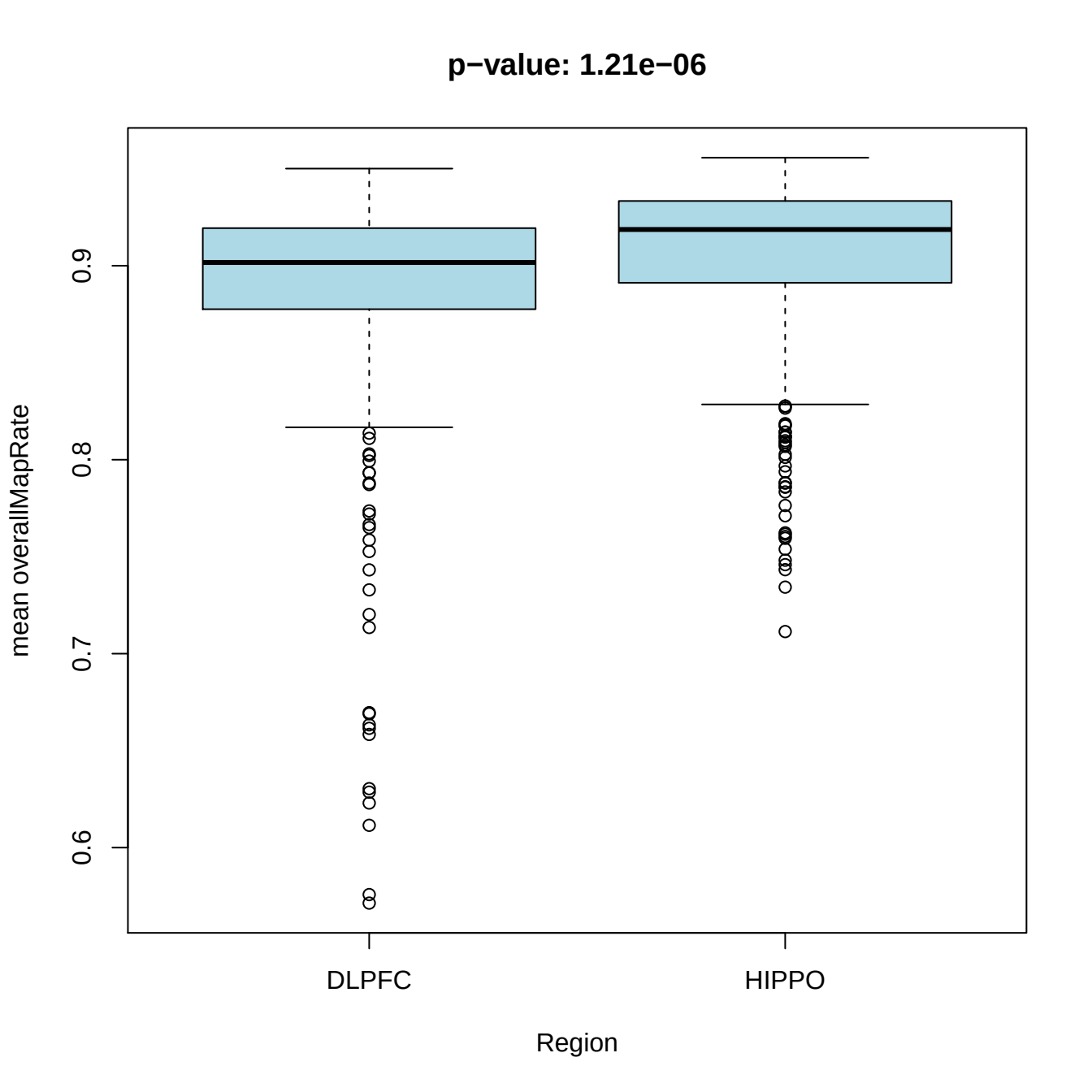
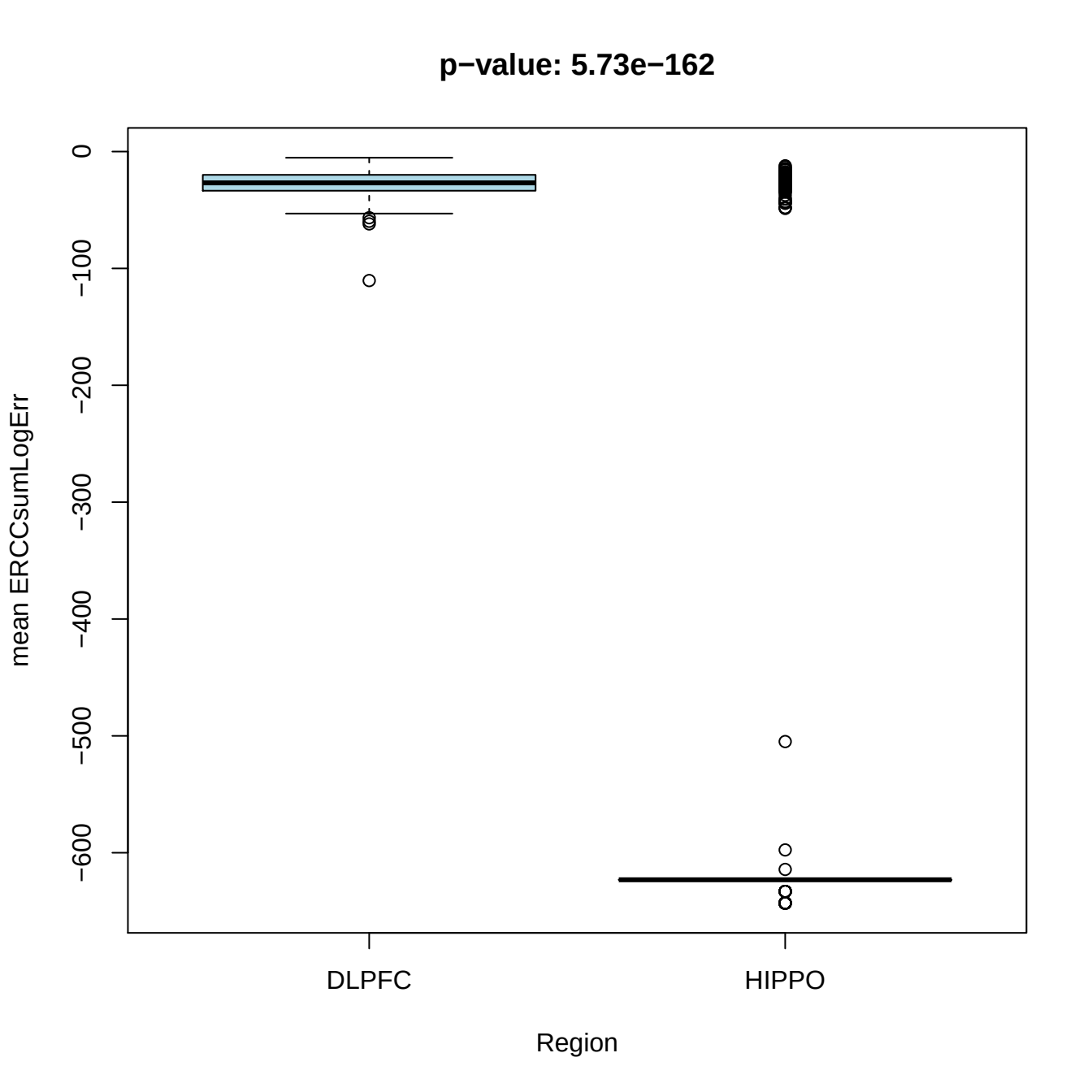
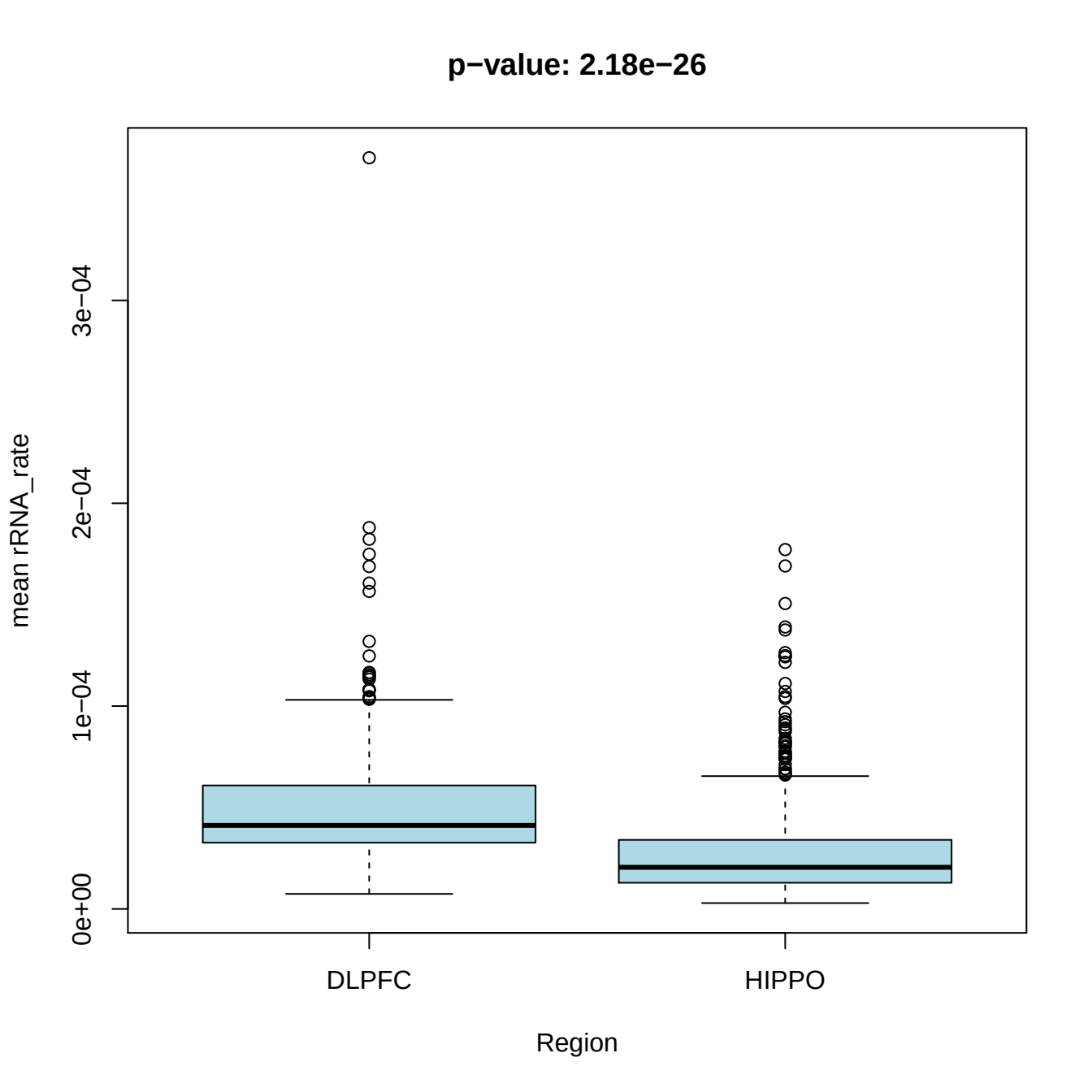

p−value: 0.421
mean RIN
10
9
8
7
6
5
DLPFC
HIPPO
Region

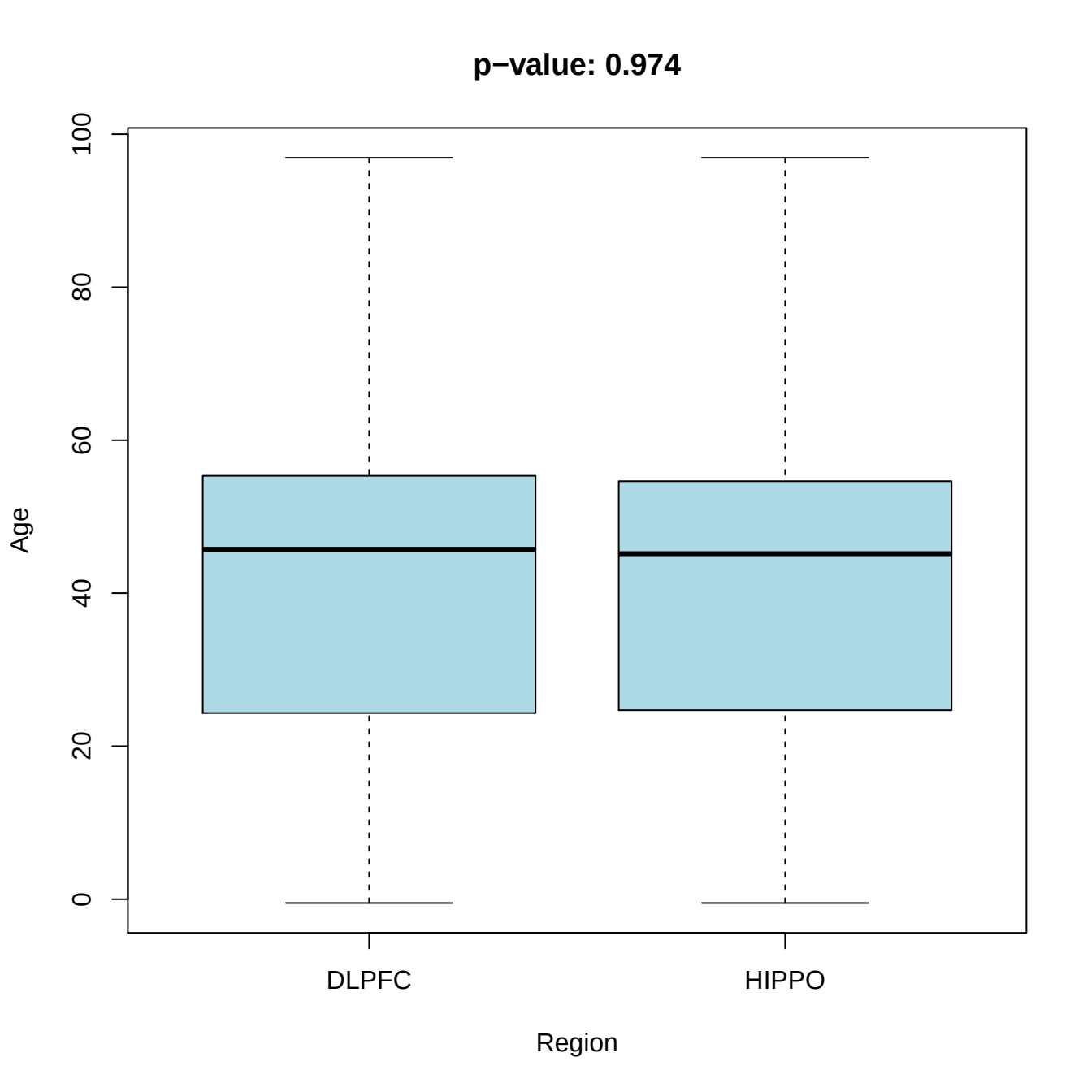

p−value: 9.79e−94
mean totalAssignedGene
0.2
0.3
0.4
0.5
0.6
0.7
DLPFC
HIPPO
Region

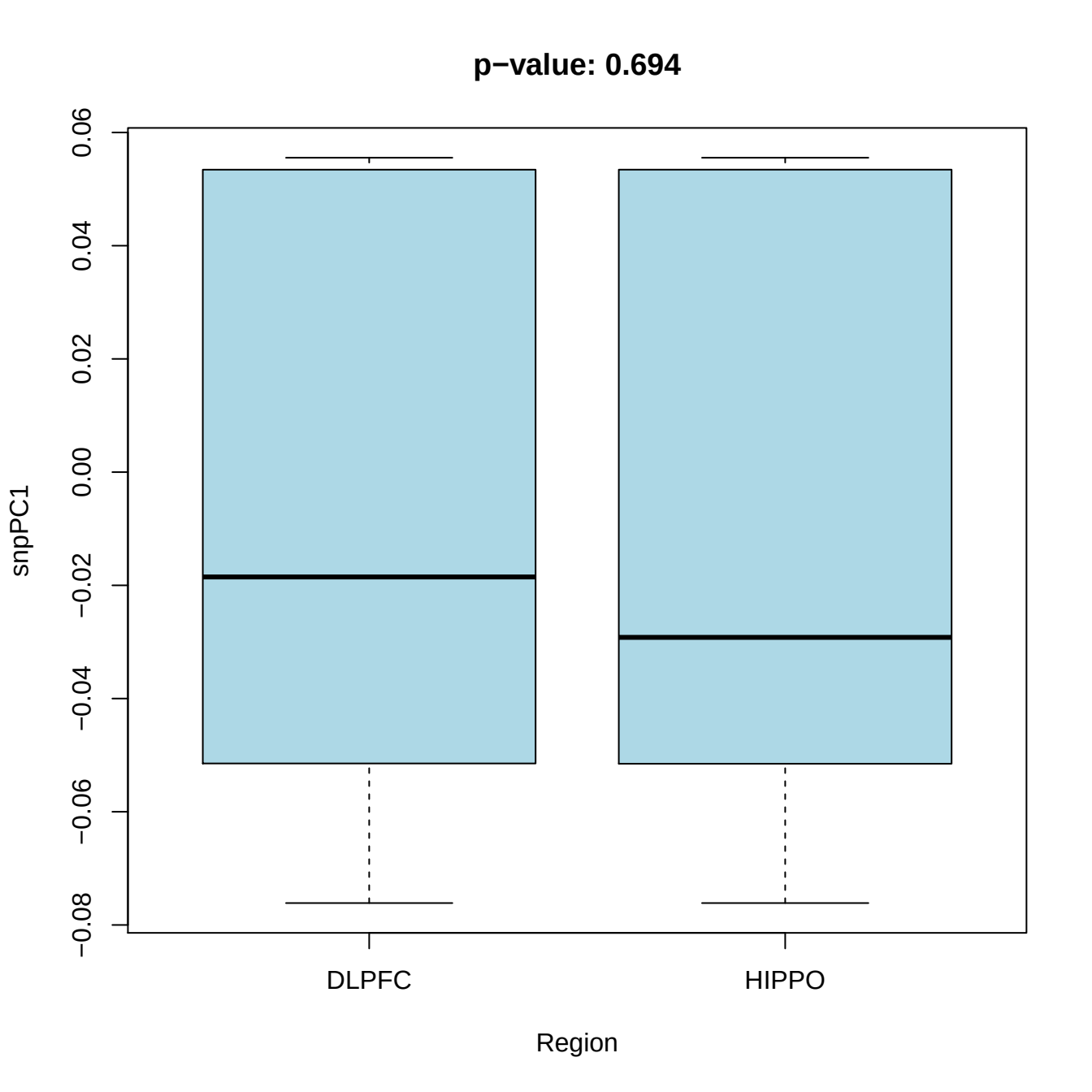

p−value: 2.59e−164
mean mitoRate
0.0
0.1
0.2
0.3
0.4
0.5
0.6
DLPFC
HIPPO
Region

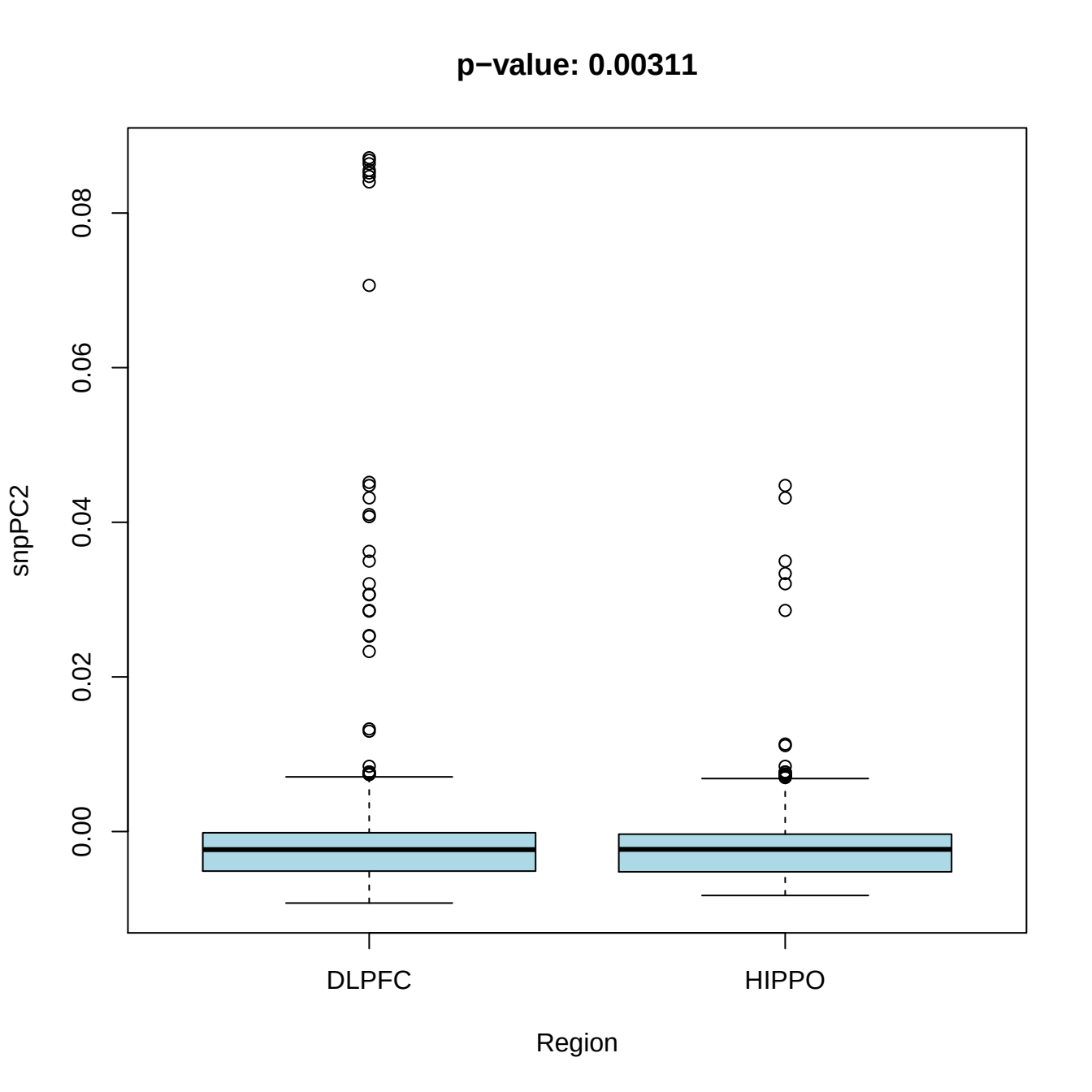

p−value: 1.21e−06
mean overallMapRate
0.6
0.7
0.8
0.9
DLPFC
HIPPO
Region

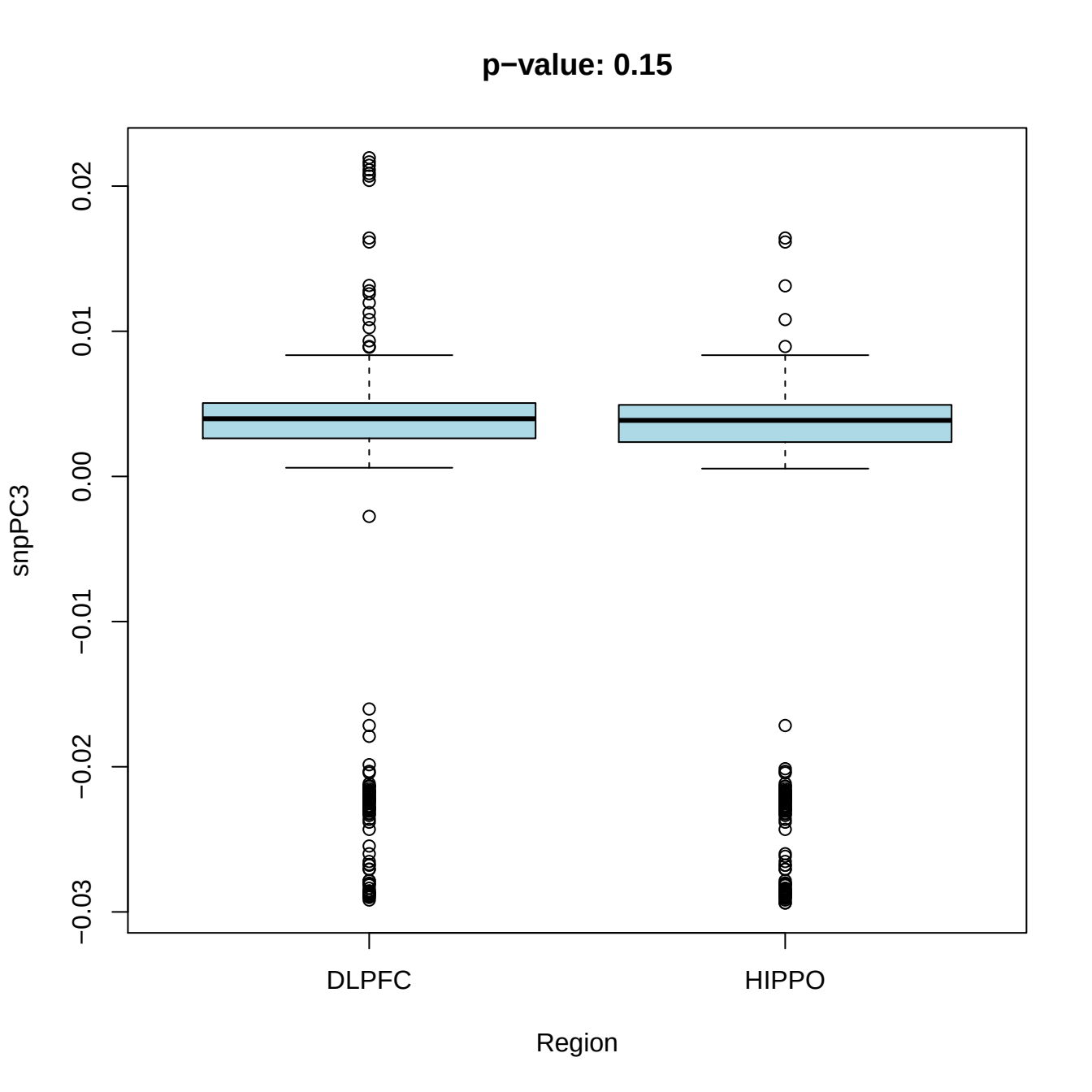

p−value: 5.73e−162
mean ERCCsumLogErr
0
−100
−200
−300
−400
−500
−600
DLPFC
HIPPO
Region

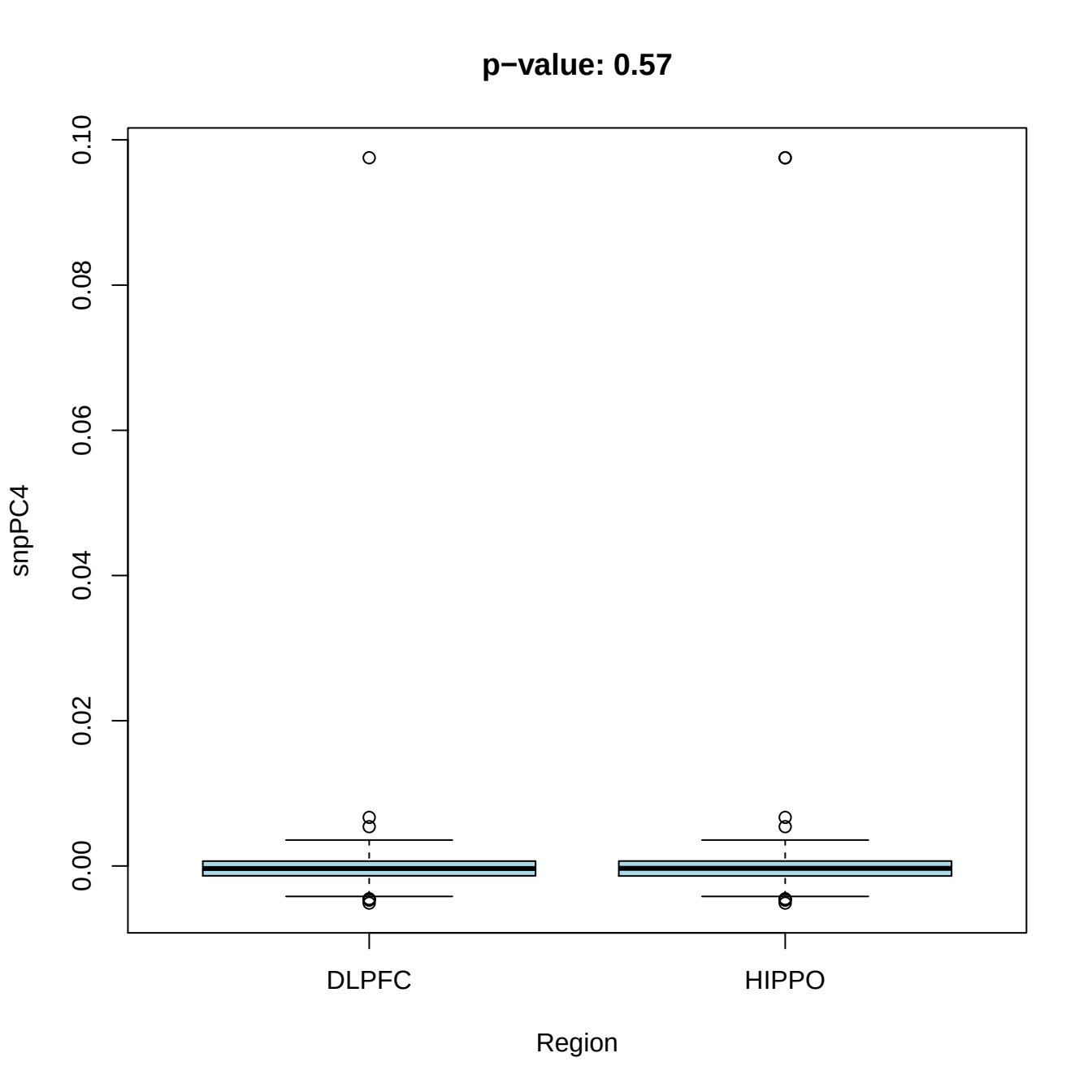

p−value: 2.18e−26
mean rRNA_rate
0e+00
1e−04
2e−04
3e−04
DLPFC
HIPPO
Region

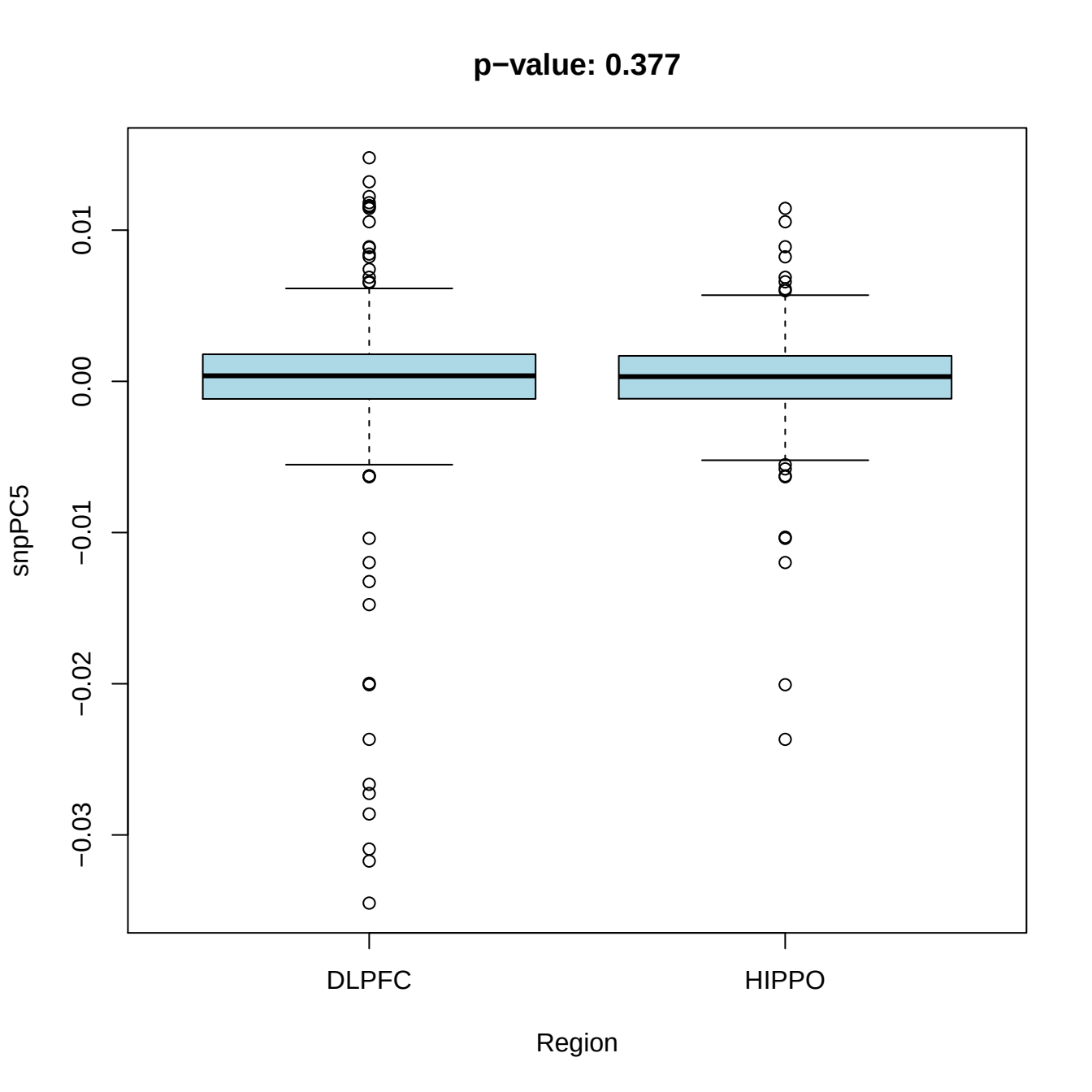

p−value: 0.974
Age
0
20
40
60
80
100
DLPFC
HIPPO
Region

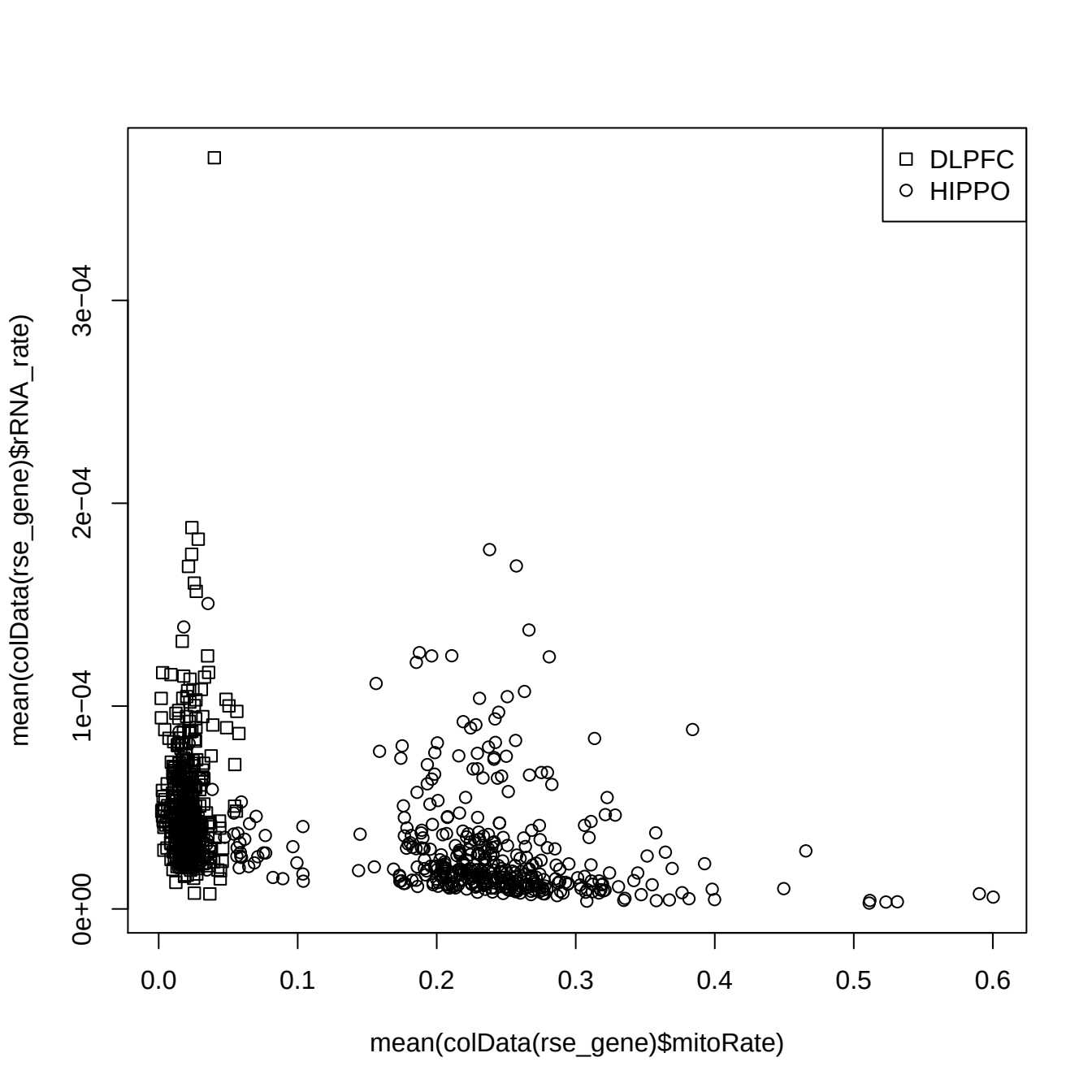

p−value: 0.694
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
−0.08
snpPC1
DLPFC
HIPPO
Region

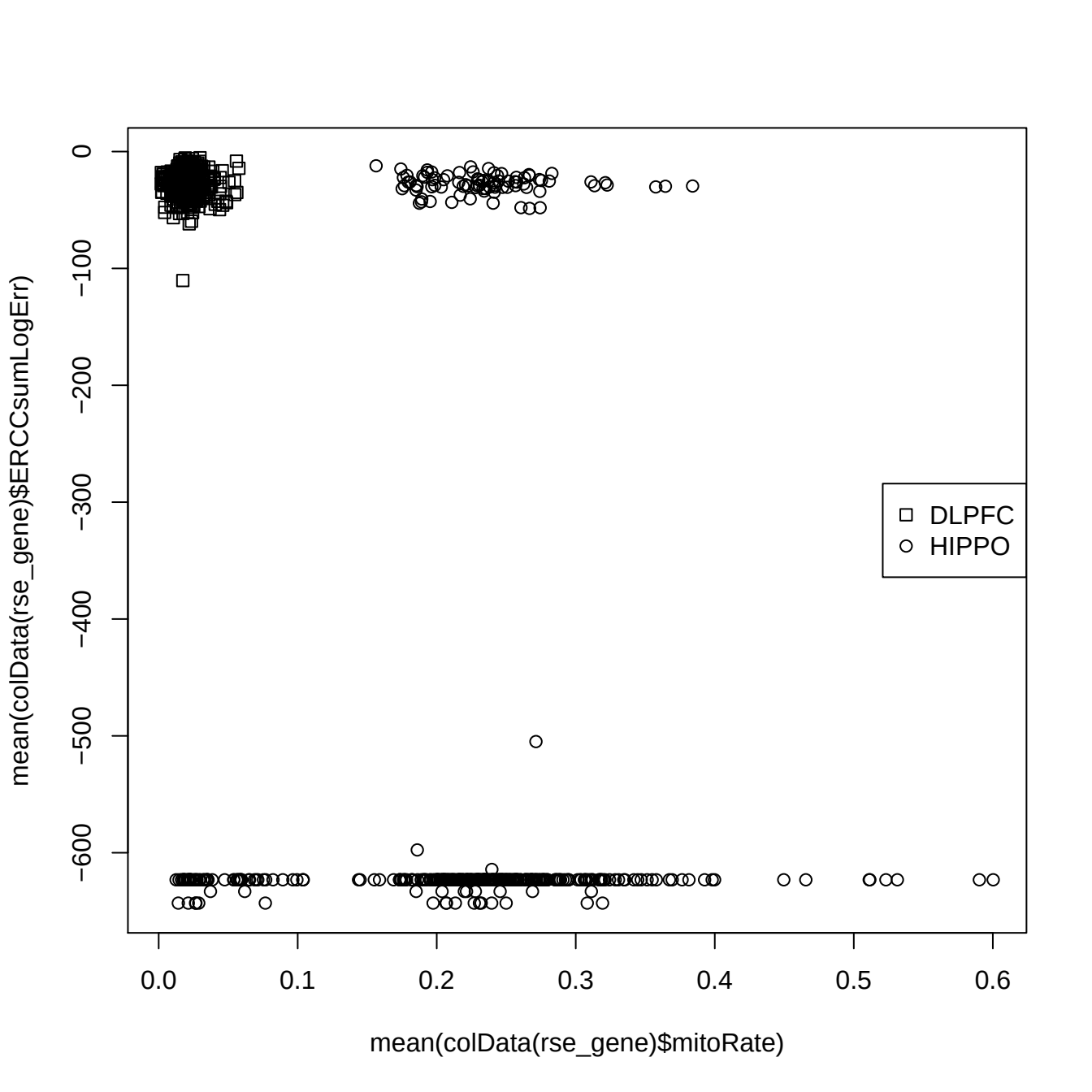

p−value: 0.00311
snpPC2
0.00
0.02
0.04
0.06
0.08
DLPFC
HIPPO
Region

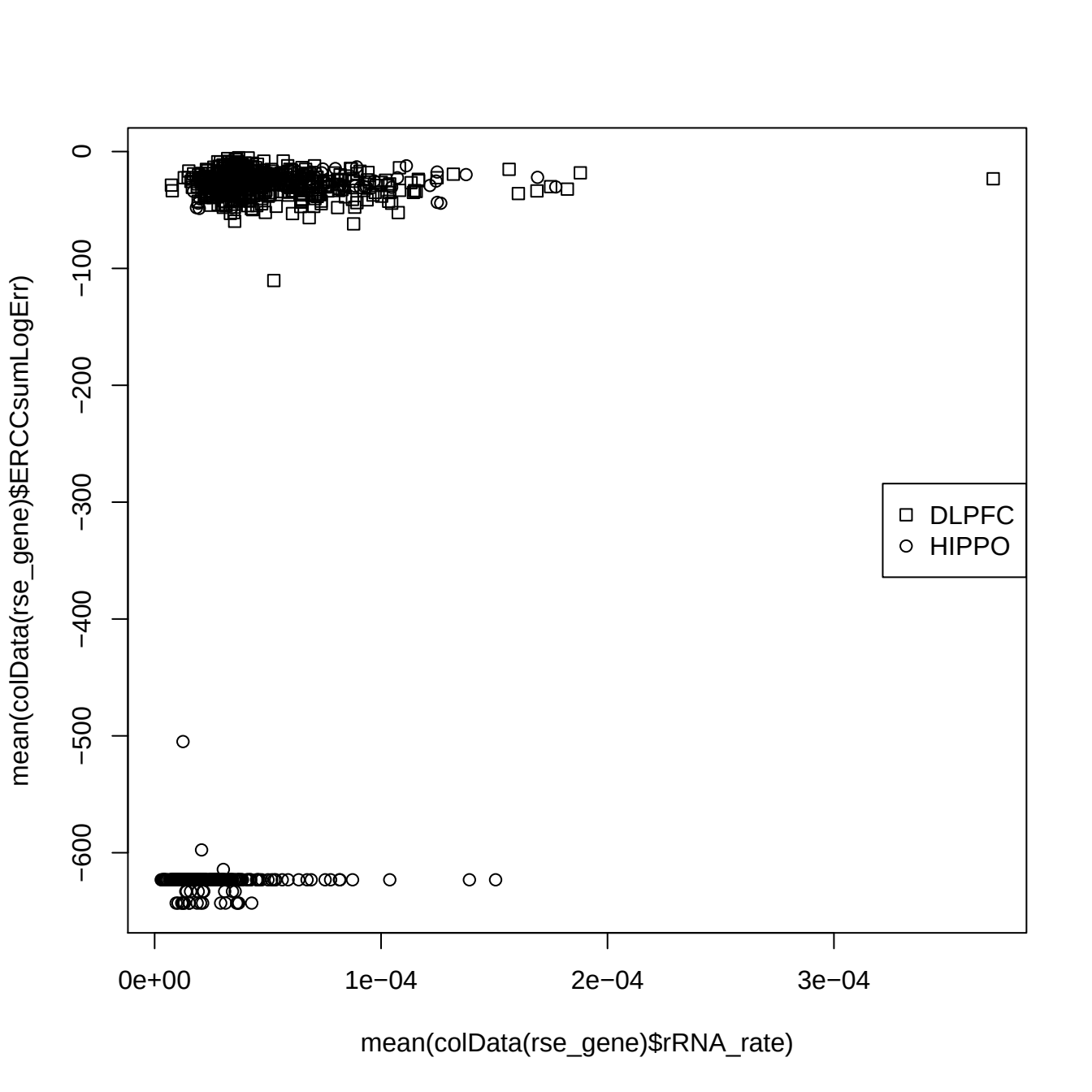

p−value: 0.15
snpPC3
0.02
0.01
0.00
−0.01
−0.02
−0.03
DLPFC
HIPPO
Region

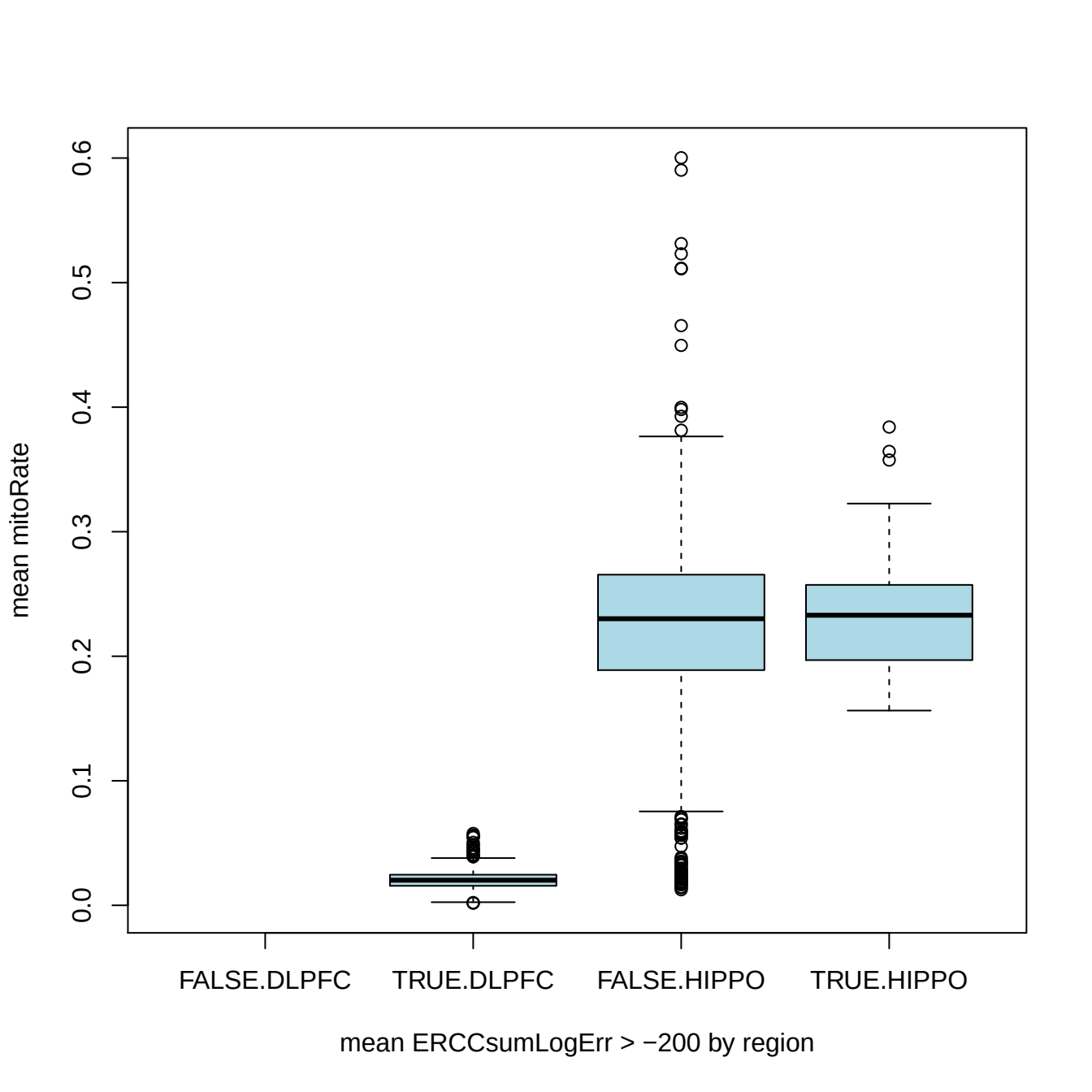

p−value: 0.57
snpPC4
0.00
0.02
0.04
0.06
0.08
0.10
DLPFC
HIPPO
Region

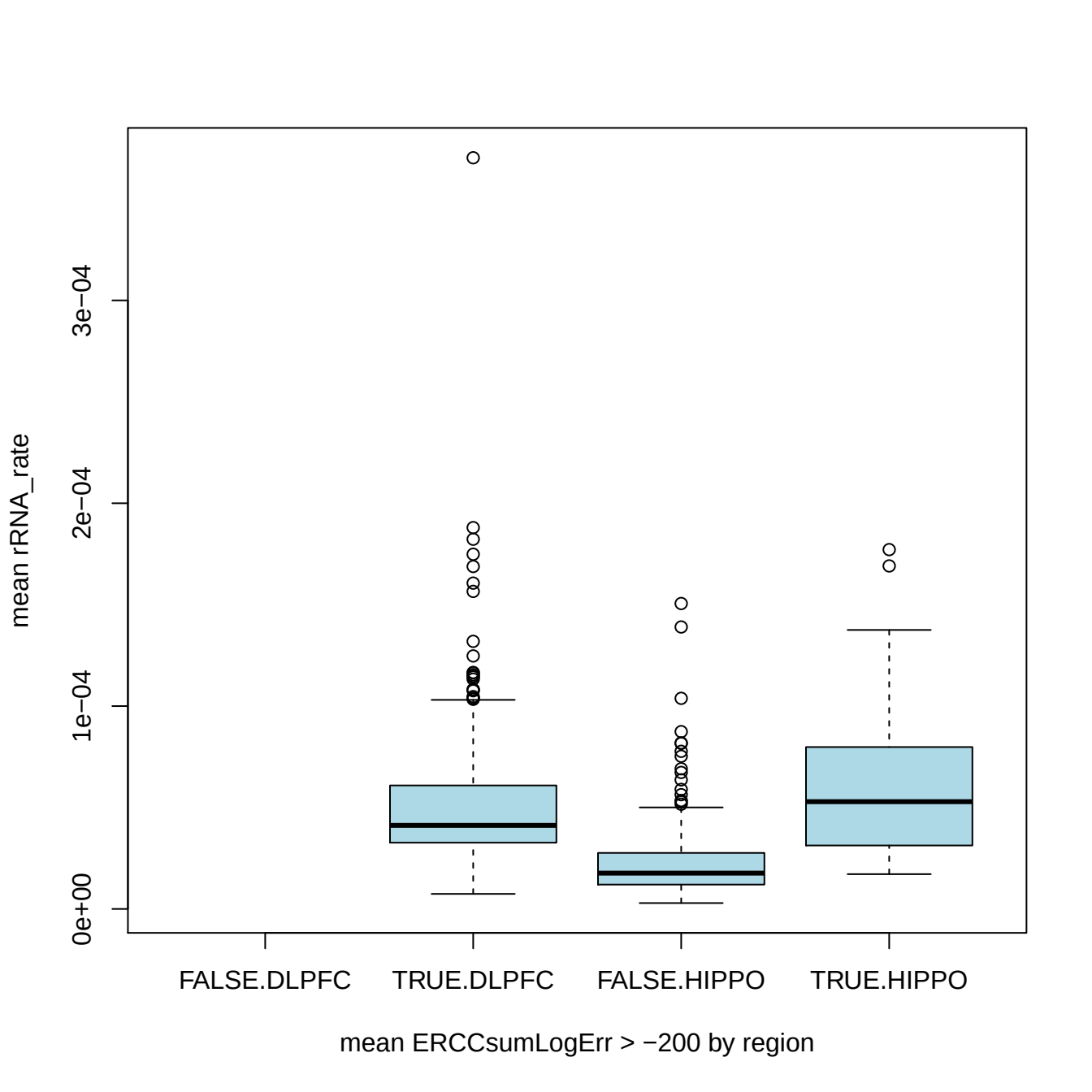

p−value: 0.377
0.01
0.00
−0.01
−0.02
−0.03
snpPC5
DLPFC
HIPPO
Region


DLPFC
HIPPO
mean(colData(rse_gene)$rRNA_rate)
0e+00
1e−04
2e−04
3e−04
0.0
0.1
0.2
0.3
0.4
0.5
0.6
mean(colData(rse_gene)$mitoRate)


mean(colData(rse_gene)$ERCCsumLogErr)
0
−100
−200
−300
−400
−500
−600
0.0
0.1
0.2
0.3
0.4
0.5
0.6
mean(colData(rse_gene)$mitoRate)
DLPFC
HIPPO


mean(colData(rse_gene)$ERCCsumLogErr)
0
−100
−200
−300
−400
−500
−600
0e+00
1e−04
2e−04
3e−04
mean(colData(rse_gene)$rRNA_rate)
DLPFC
HIPPO


mean mitoRate
0.0
0.1
0.2
0.3
0.4
0.5
0.6
FALSE.DLPFC
TRUE.DLPFC
FALSE.HIPPO
TRUE.HIPPO
mean ERCCsumLogErr > −200 by region


mean rRNA_rate
0e+00
1e−04
2e−04
3e−04
FALSE.DLPFC
TRUE.DLPFC
FALSE.HIPPO
TRUE.HIPPO
mean ERCCsumLogErr > −200 by region