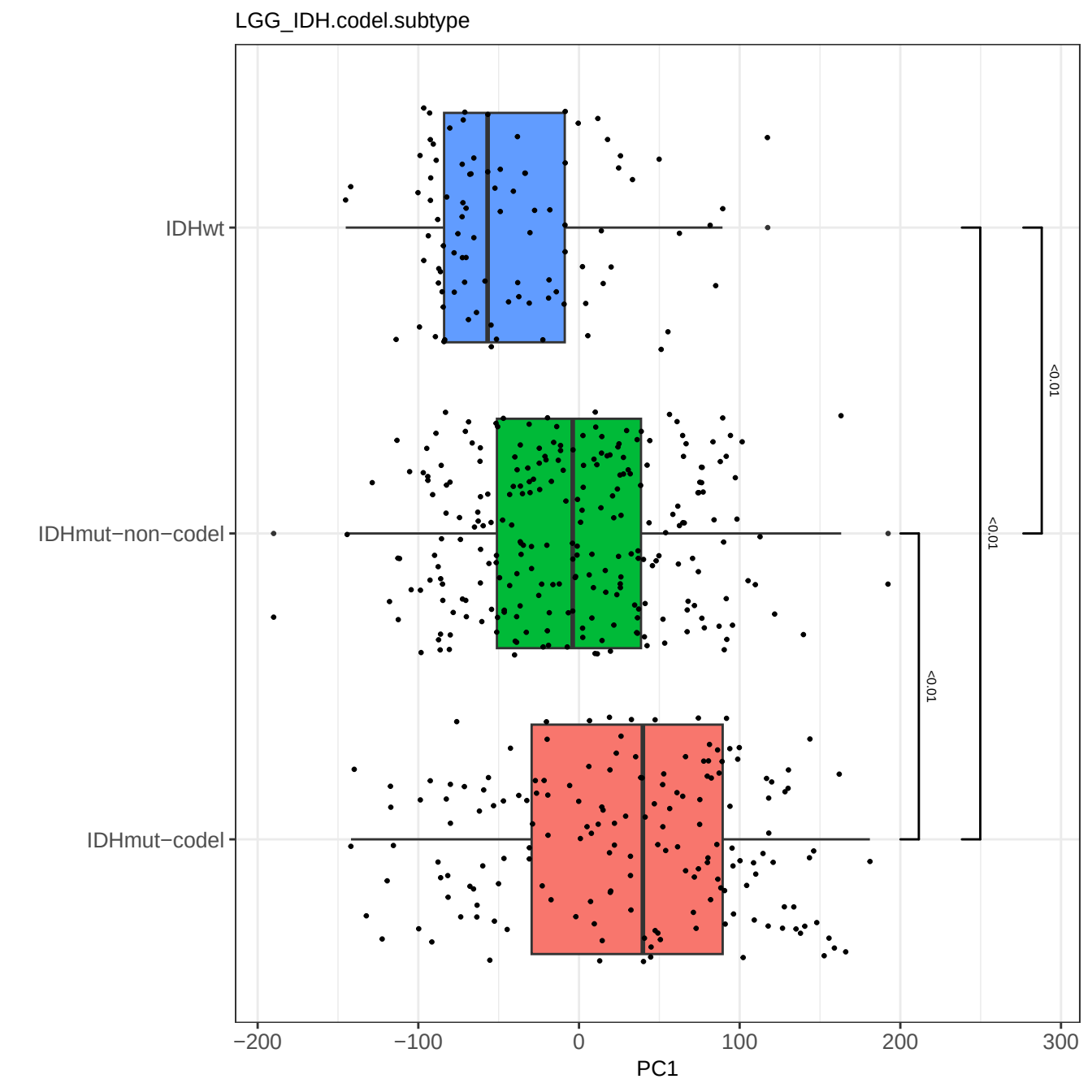
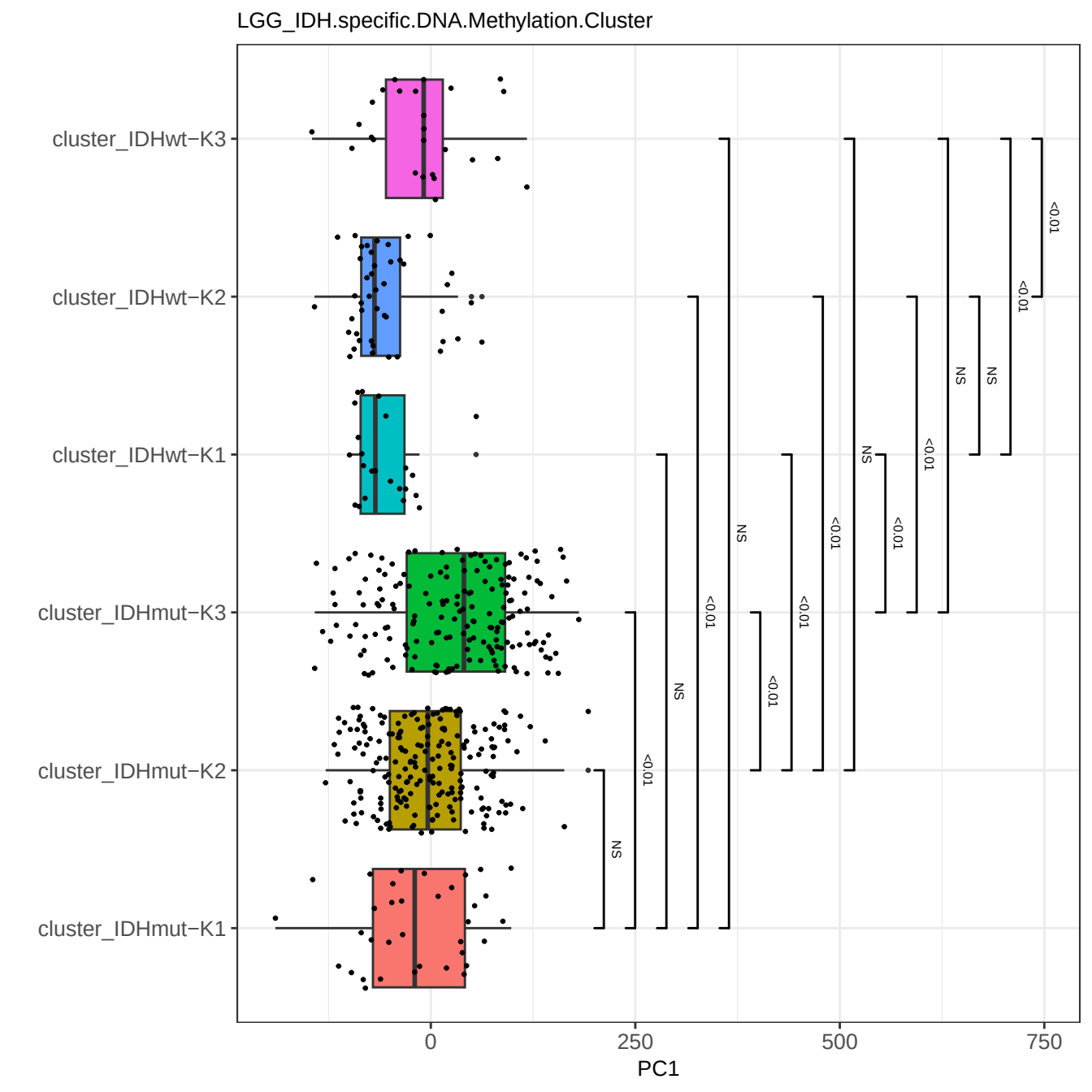
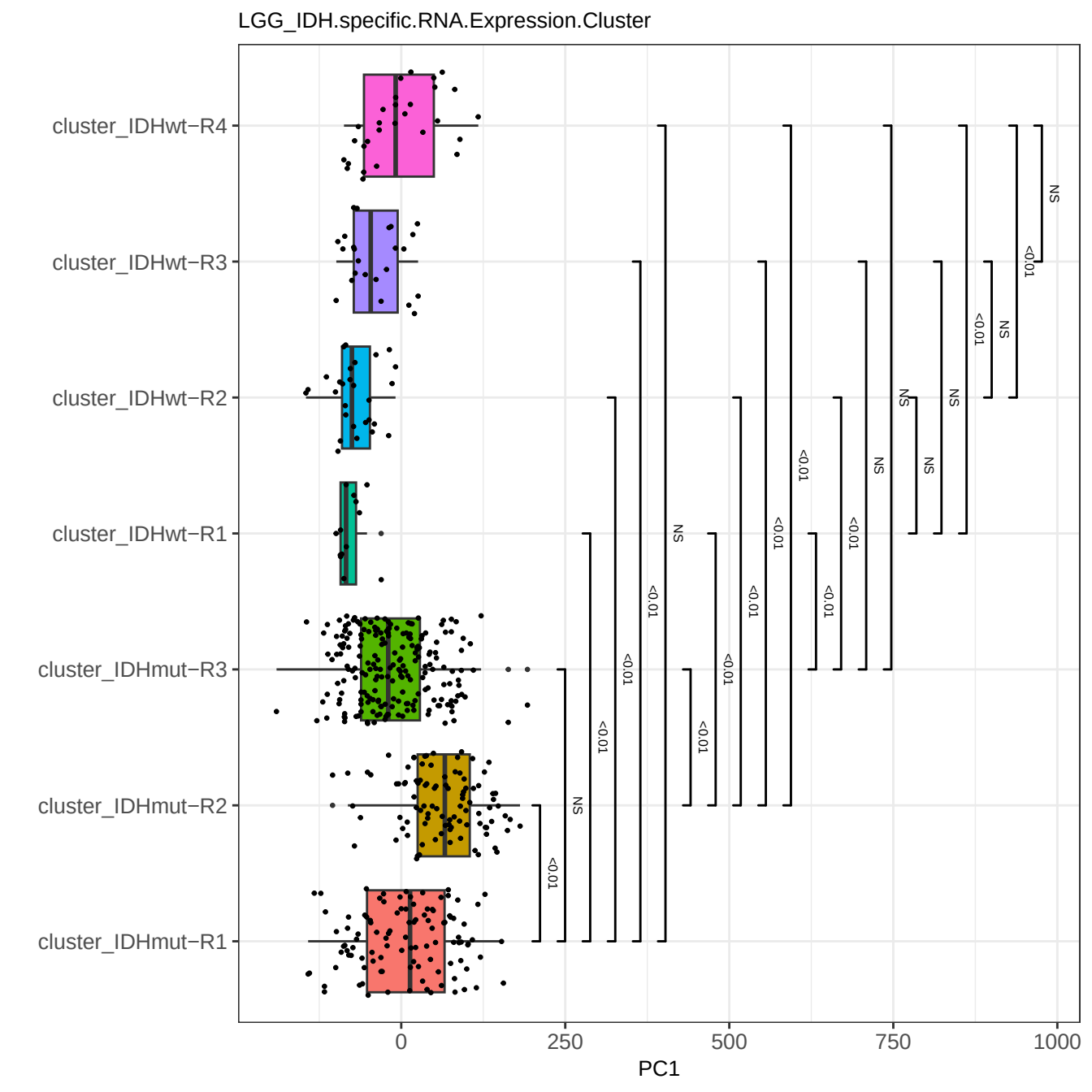
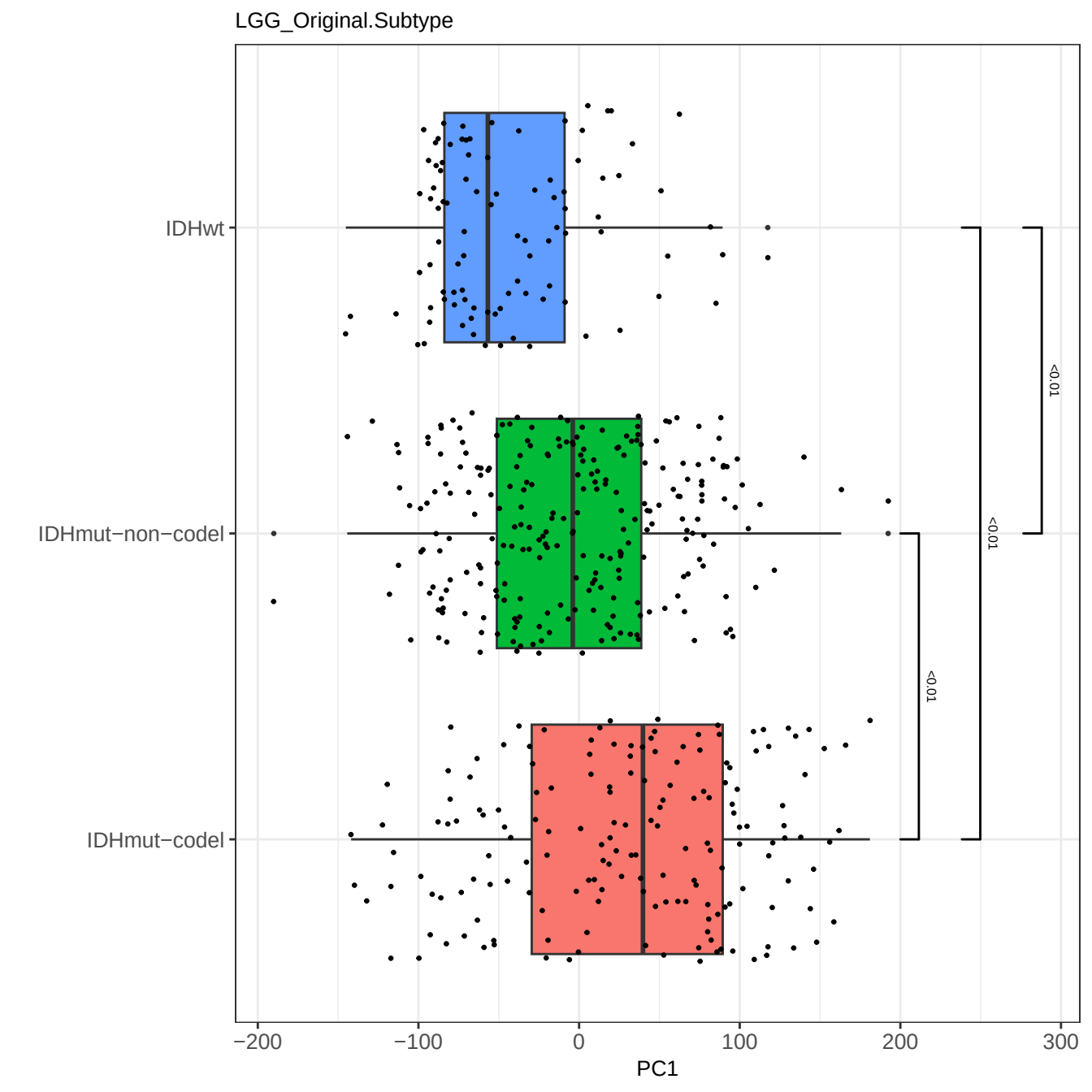
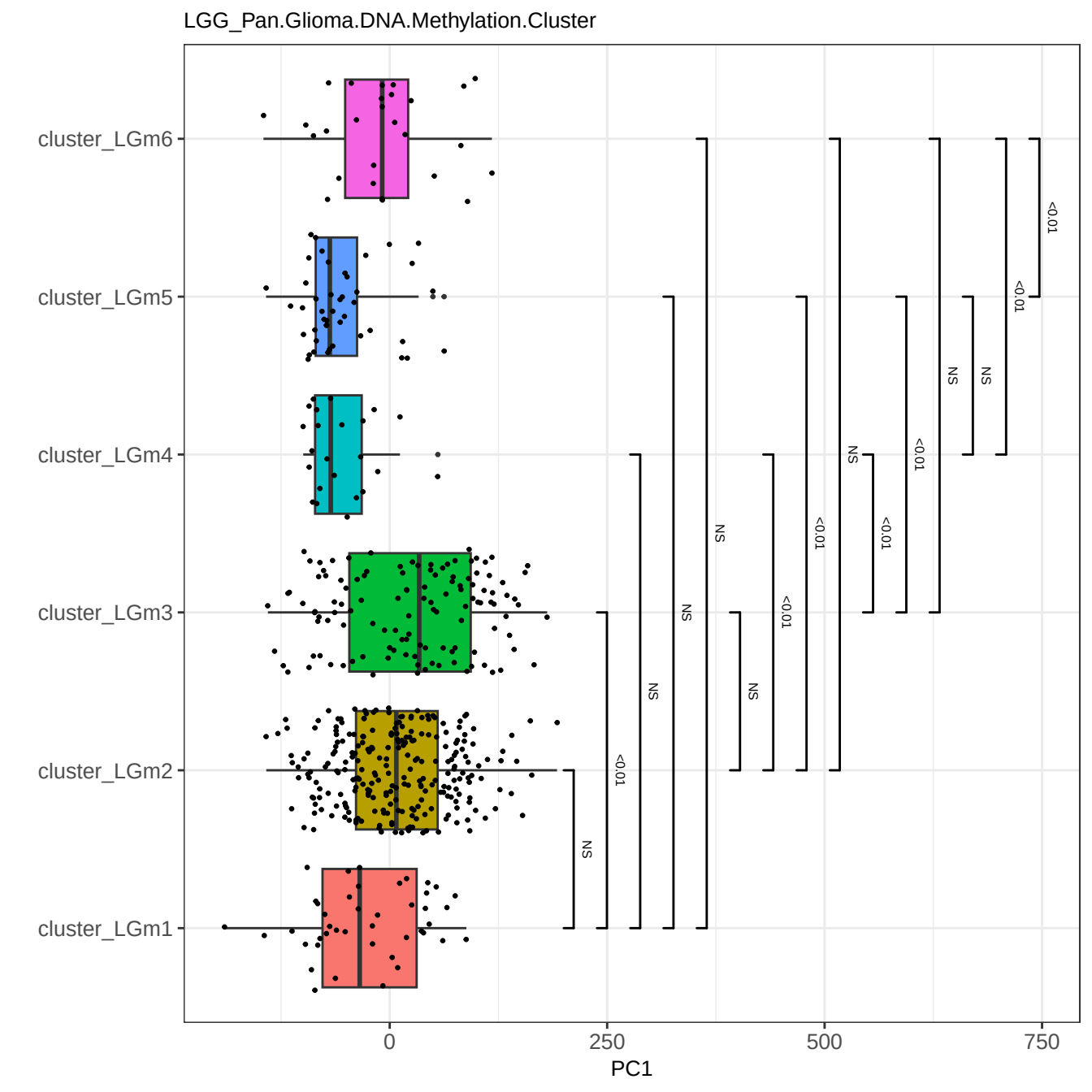
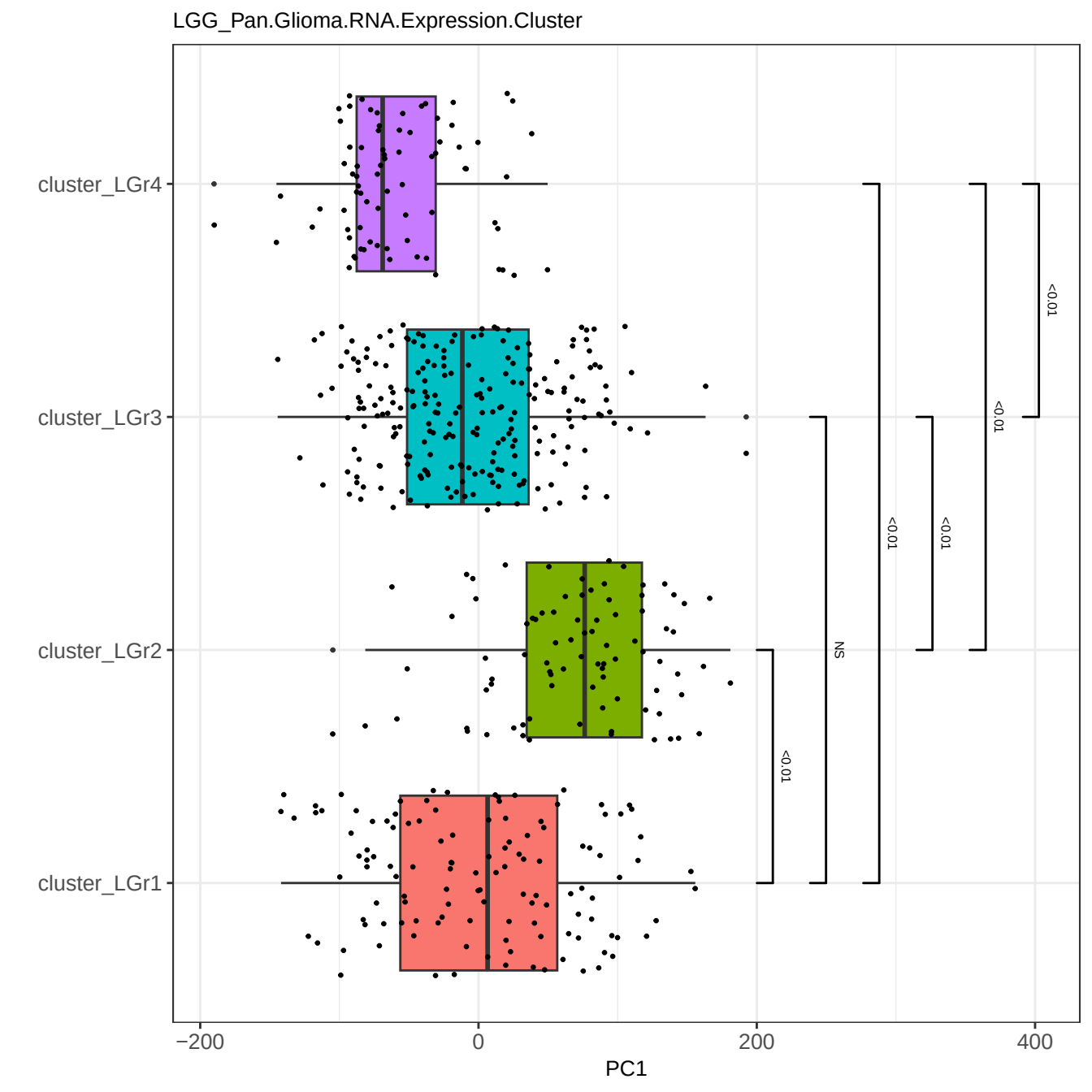

LGG_IDH.codel.subtype
IDHwt
IDHmut−non−codel
IDHmut−codel
<0.01
<0.01
<0.01
−200
−100
0
100
200
300
PC1

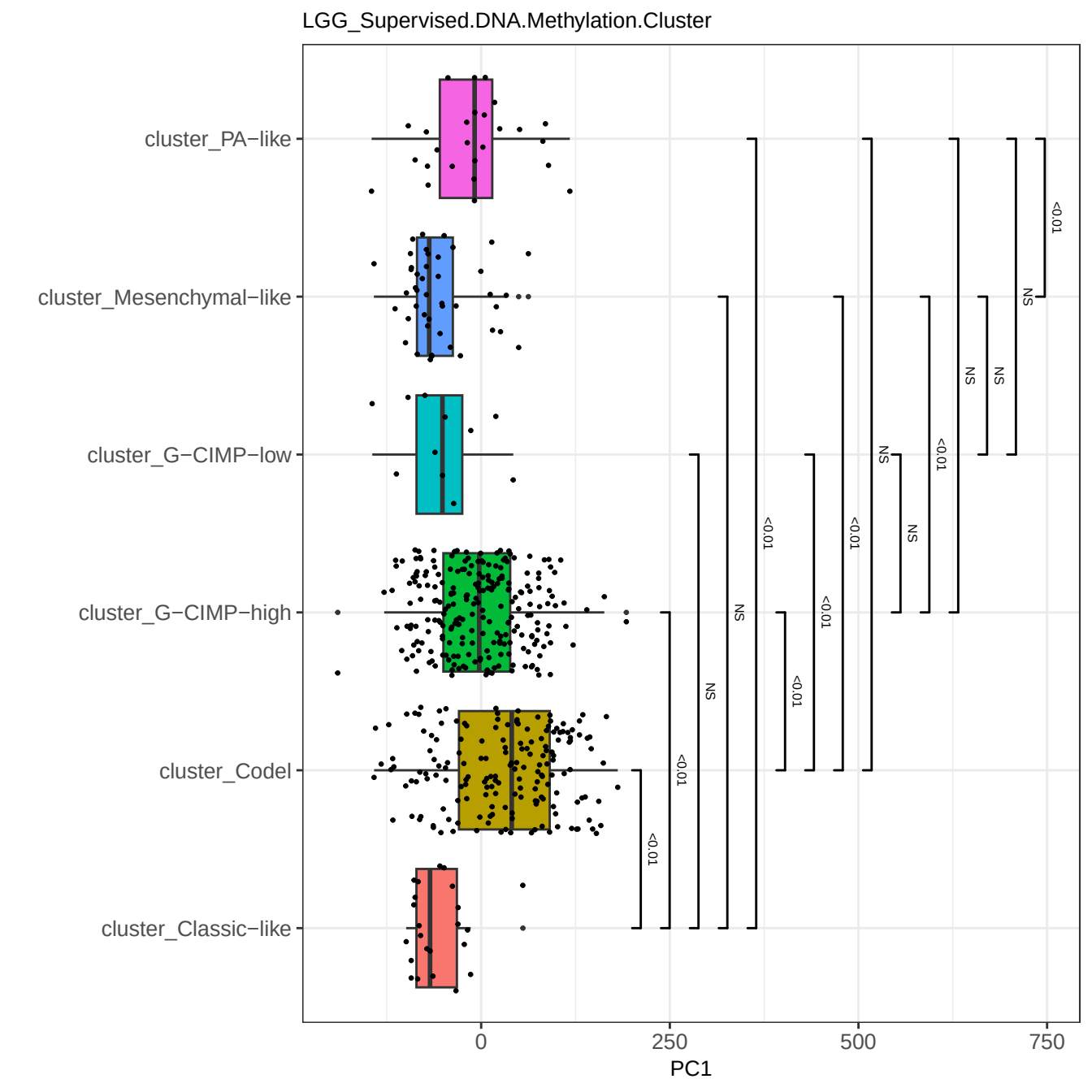

LGG_IDH.specific.DNA.Methylation.Cluster
cluster_IDHwt−K3
cluster_IDHwt−K2
cluster_IDHwt−K1
cluster_IDHmut−K3
cluster_IDHmut−K2
cluster_IDHmut−K1
0
250
500
750
PC1
NS
<0.01

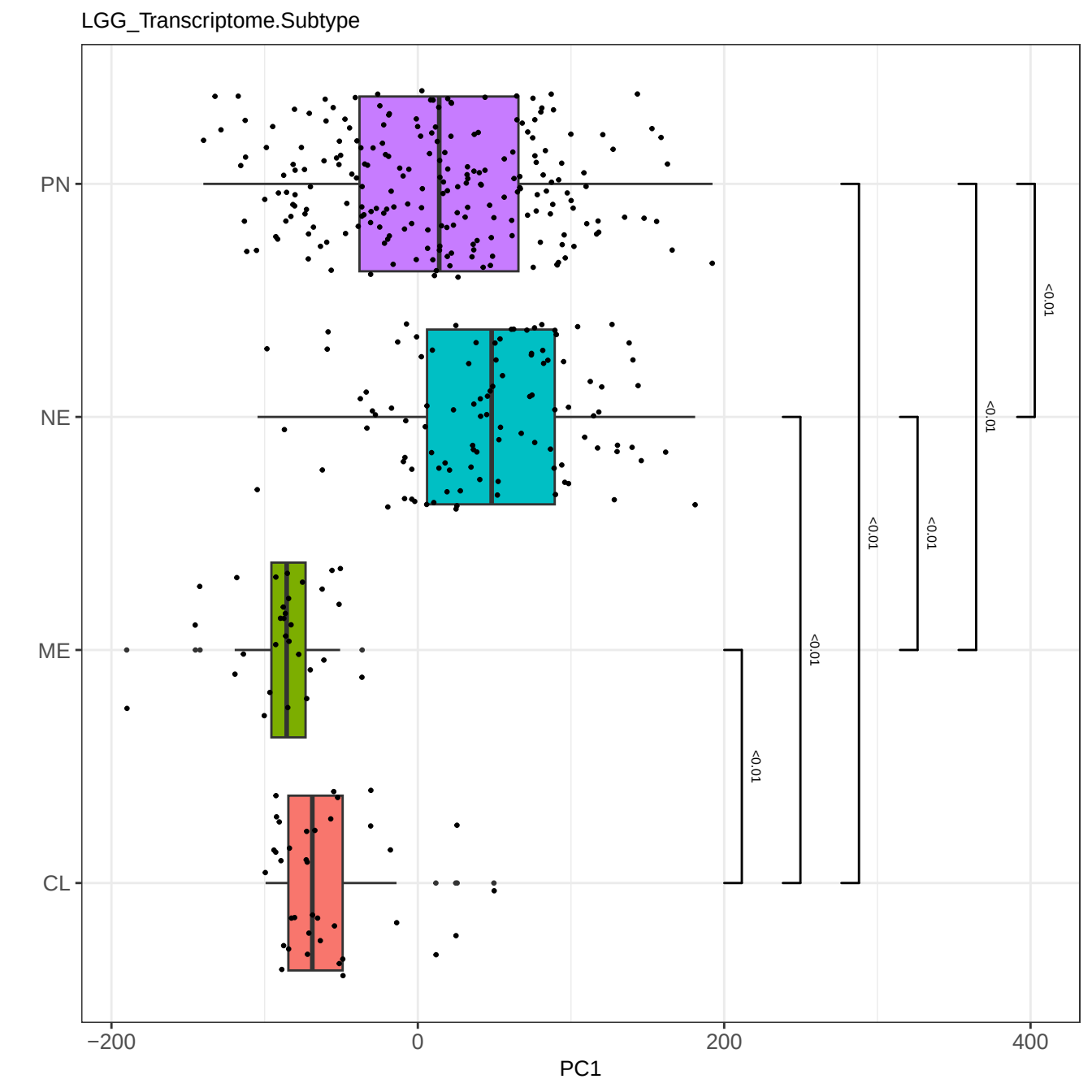

LGG_IDH.specific.RNA.Expression.Cluster
cluster_IDHwt−R4
cluster_IDHwt−R3
cluster_IDHwt−R2
cluster_IDHwt−R1
cluster_IDHmut−R3
cluster_IDHmut−R2
cluster_IDHmut−R1
0
250
500
750
1000
PC1
NS
<0.01

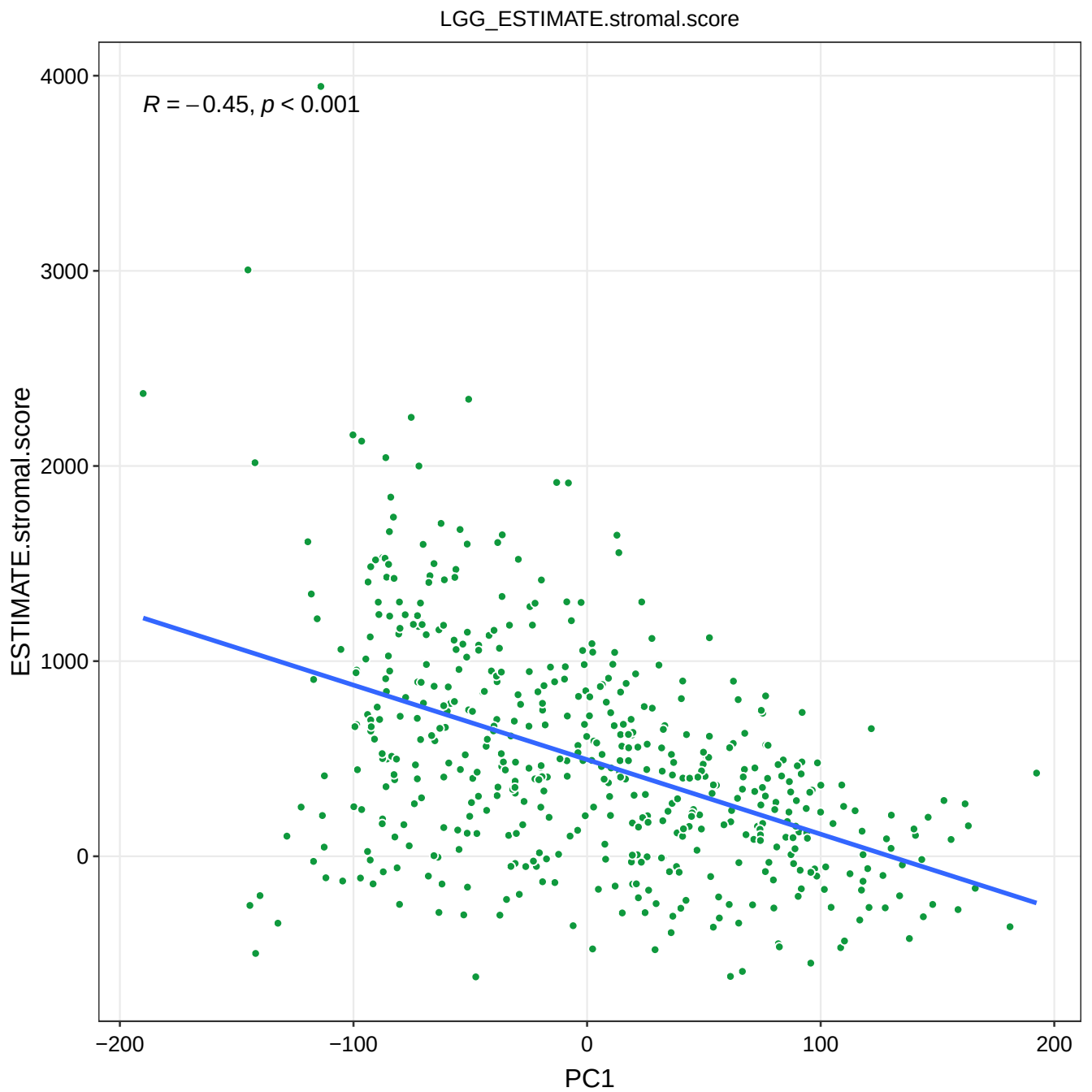

LGG_Original.Subtype
IDHwt
IDHmut−non−codel
IDHmut−codel
<0.01
<0.01
<0.01
−200
−100
0
100
200
300
PC1

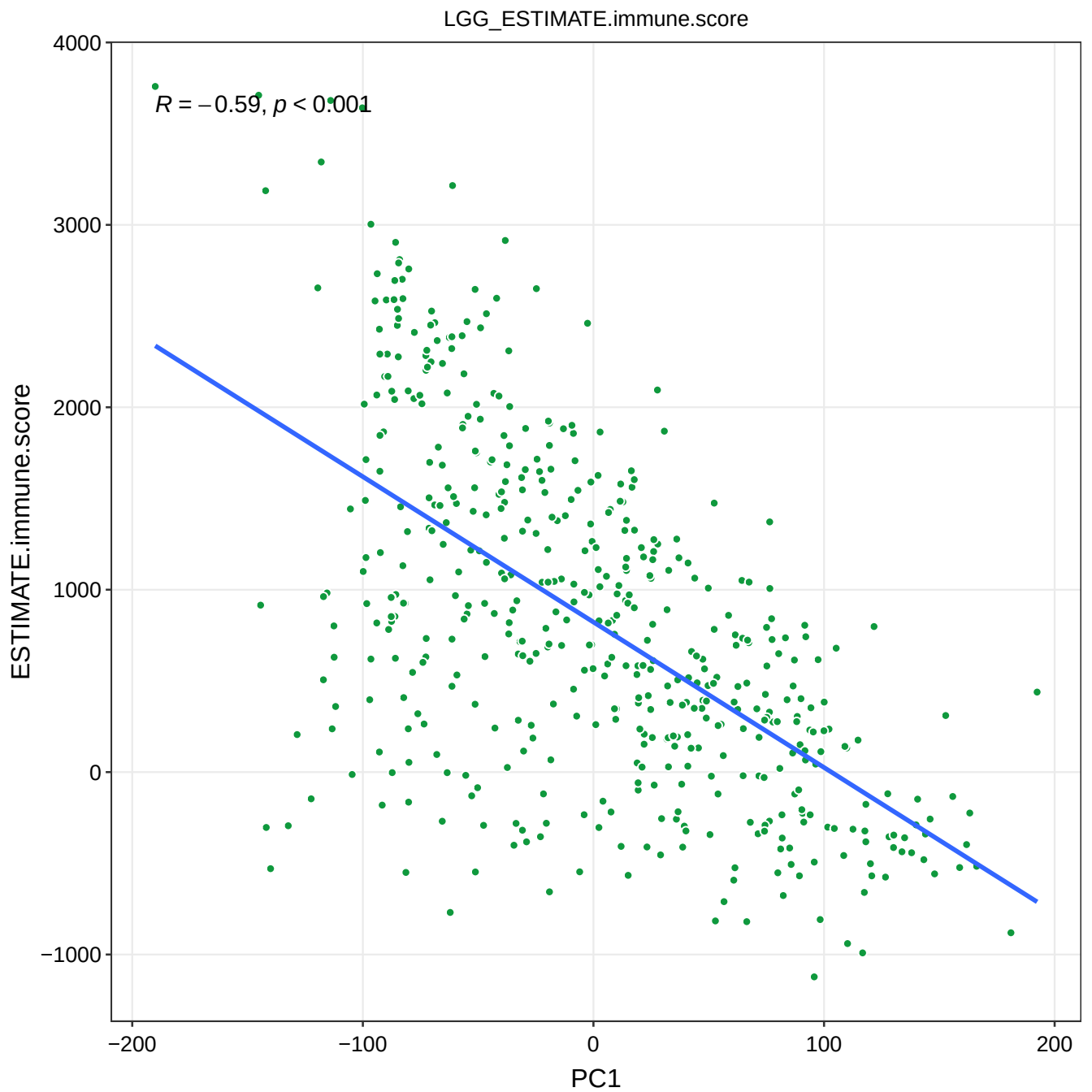

LGG_Pan.Glioma.DNA.Methylation.Cluster
cluster_LGm6
cluster_LGm5
cluster_LGm4
cluster_LGm3
cluster_LGm2
cluster_LGm1
NS
<0.01
0
250
500
750
PC1

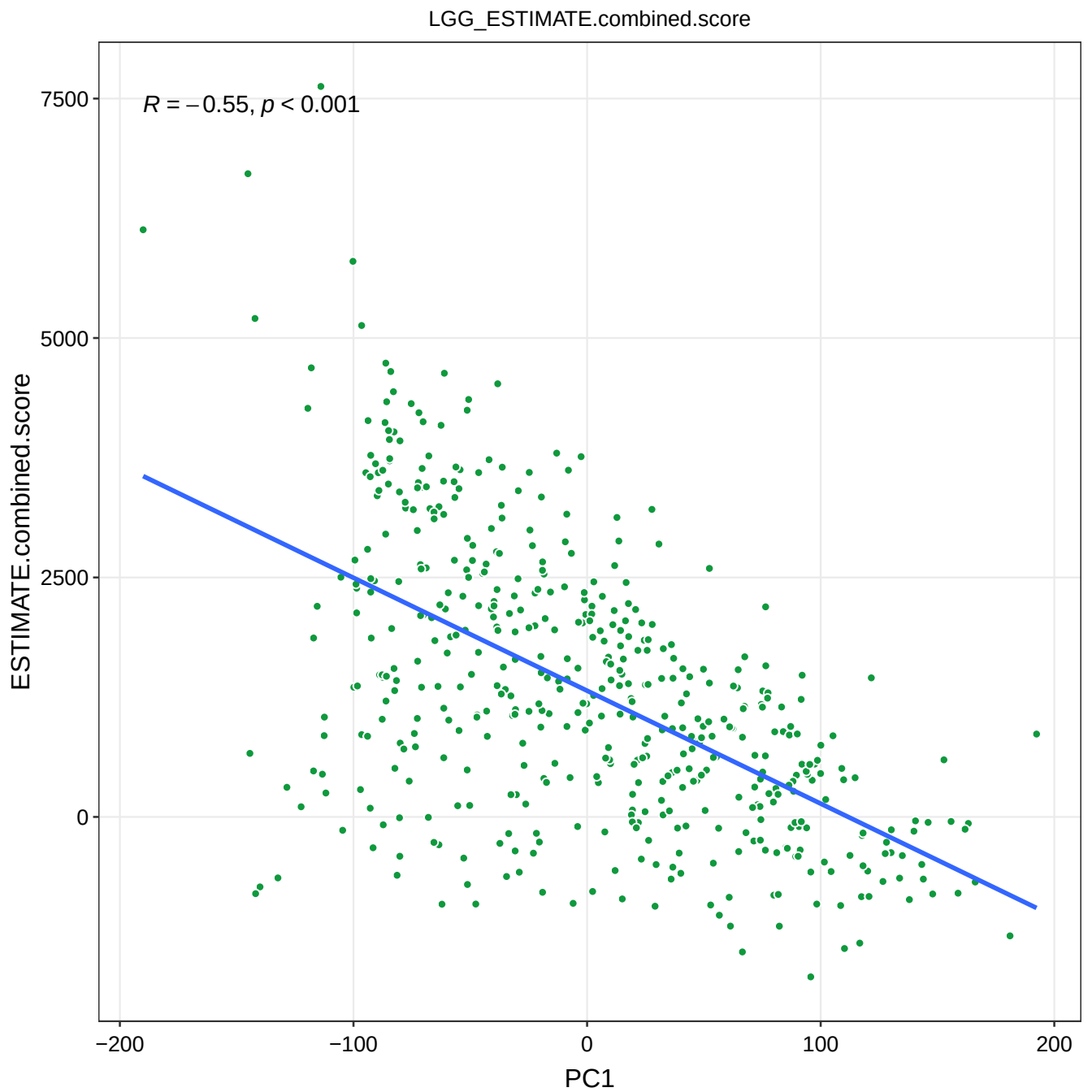

LGG_Pan.Glioma.RNA.Expression.Cluster
cluster_LGr4
cluster_LGr3
cluster_LGr2
cluster_LGr1
<0.01
<0.01
<0.01
NS
<0.01
−200
0
200
400
PC1

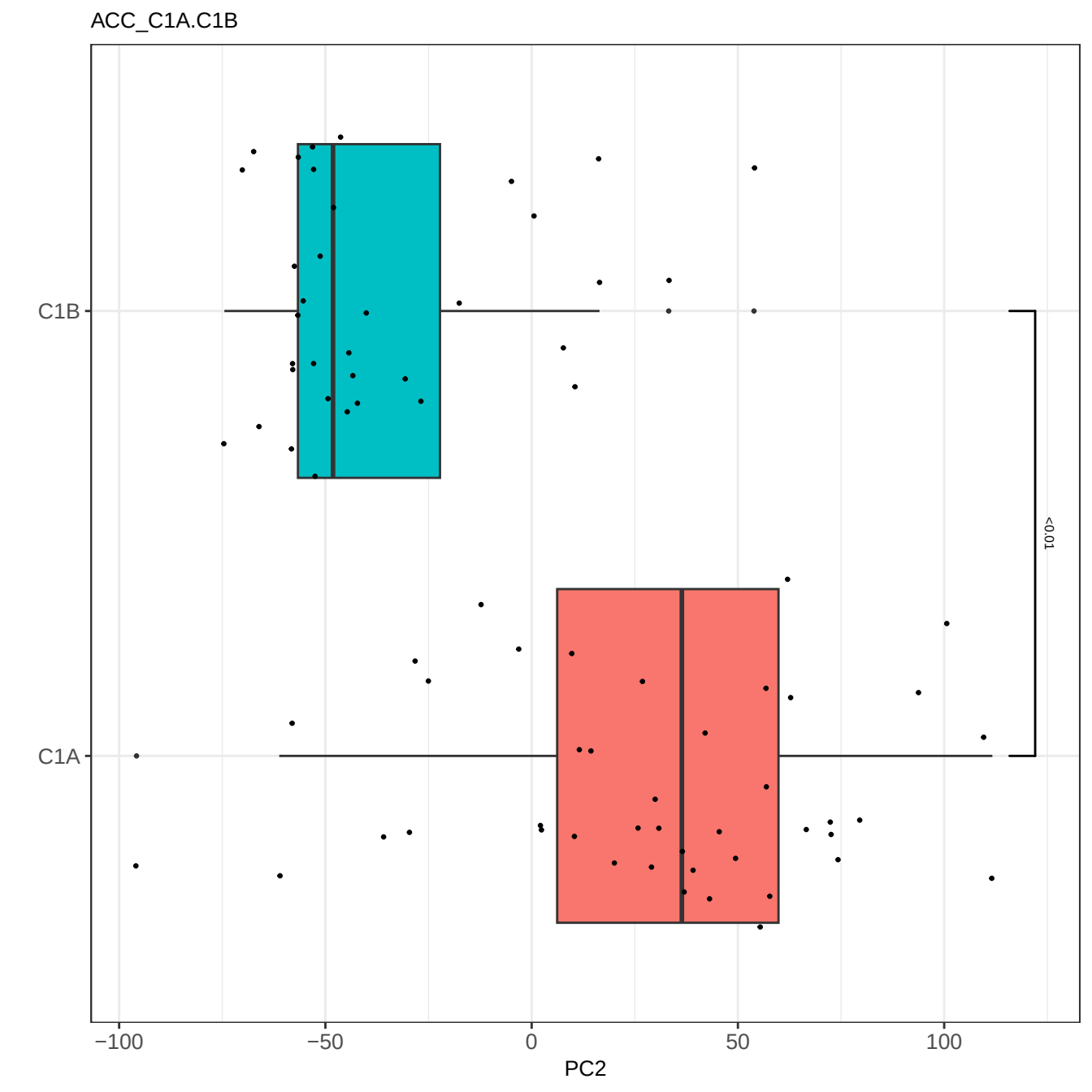

LGG_Supervised.DNA.Methylation.Cluster
cluster_PA−like
cluster_Mesenchymal−like
cluster_G−CIMP−low
cluster_G−CIMP−high
cluster_Codel
cluster_Classic−like
<0.01
NS
0
250
500
750
PC1

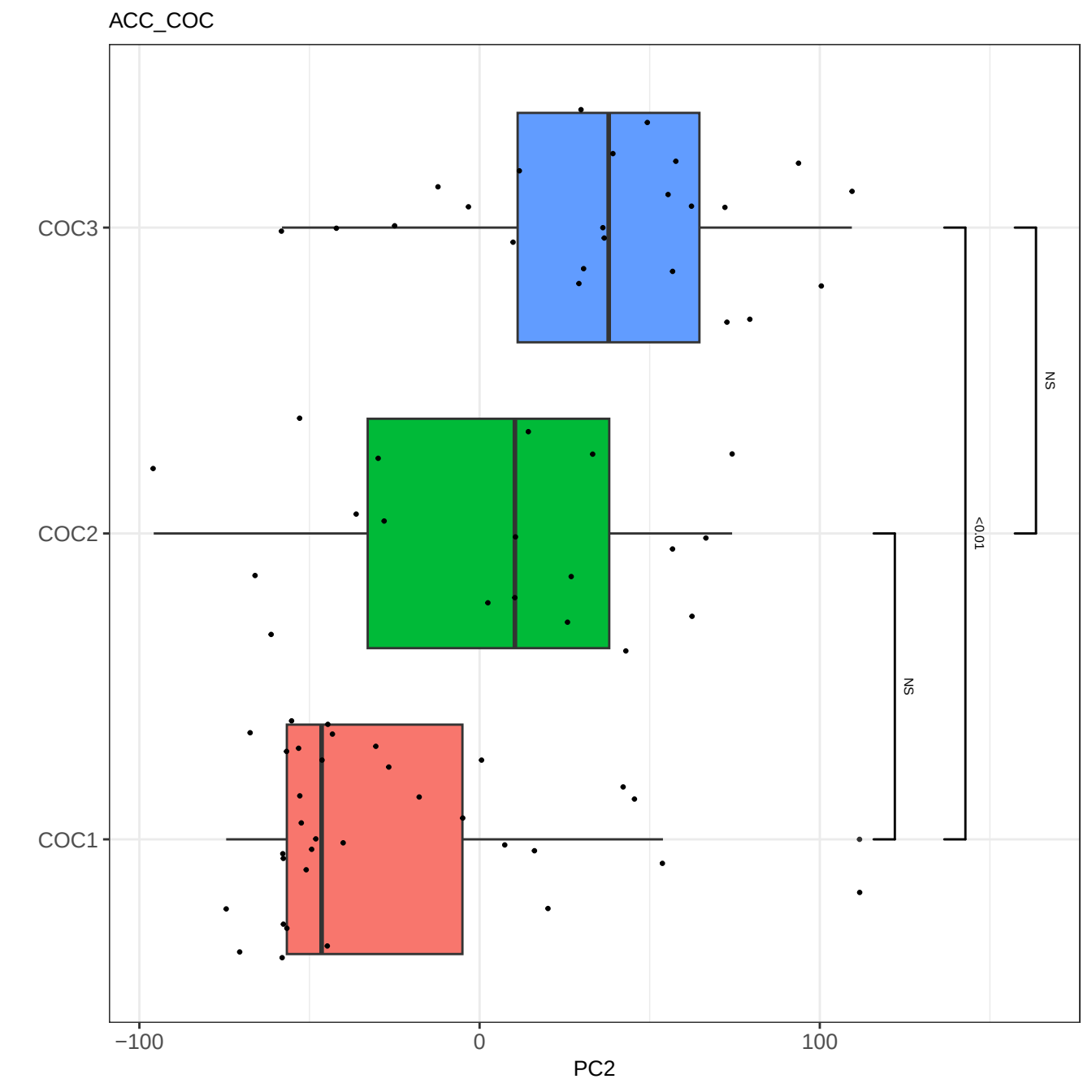

LGG_Transcriptome.Subtype
PN
NE
ME
CL
<0.01
<0.01
<0.01
<0.01
<0.01
−200
0
200
400
PC1

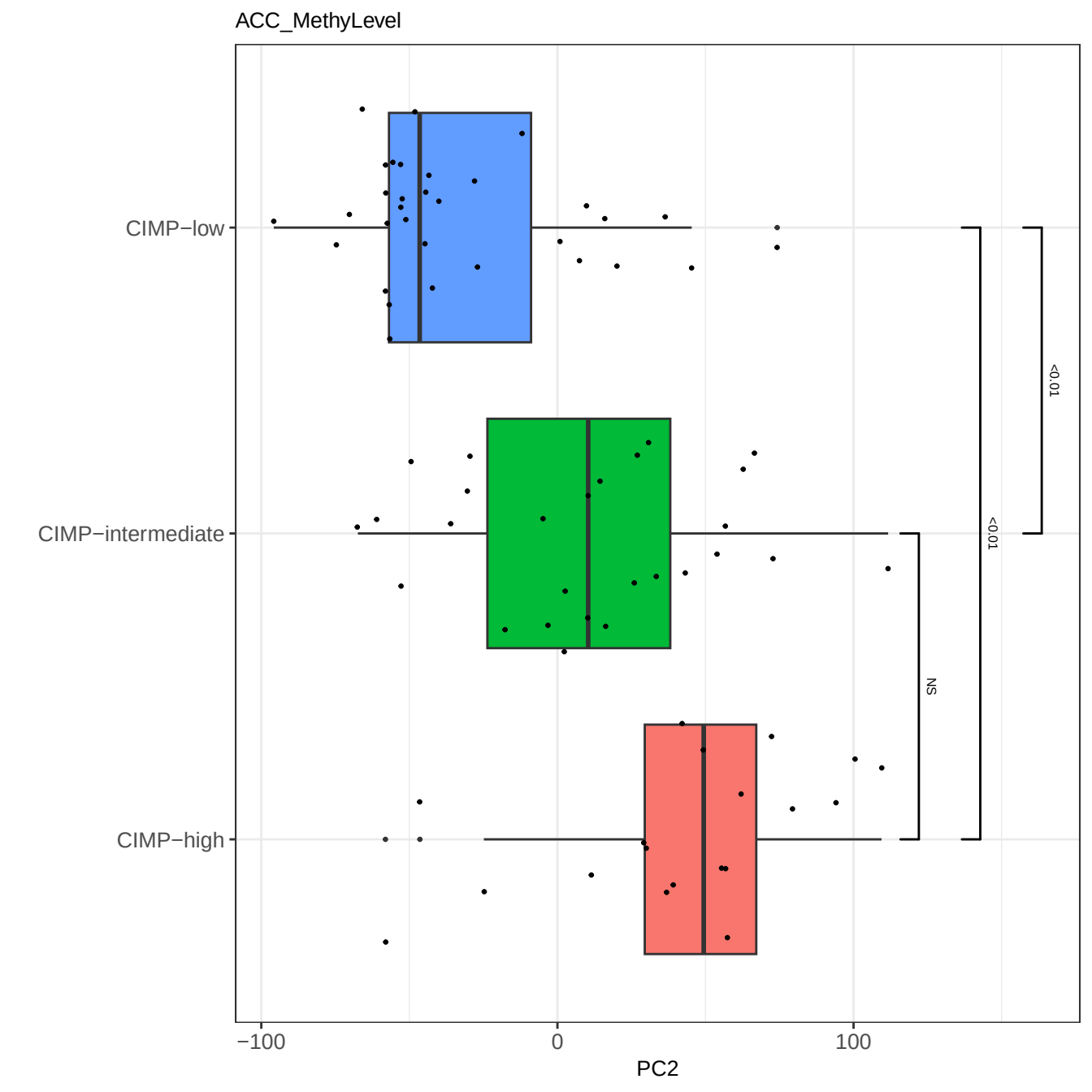

LGG_ESTIMATE.stromal.score
R = −0.45, p < 0.001
ESTIMATE.stromal.score
4000
3000
2000
1000
0
−200
−100
0
100
200
PC1

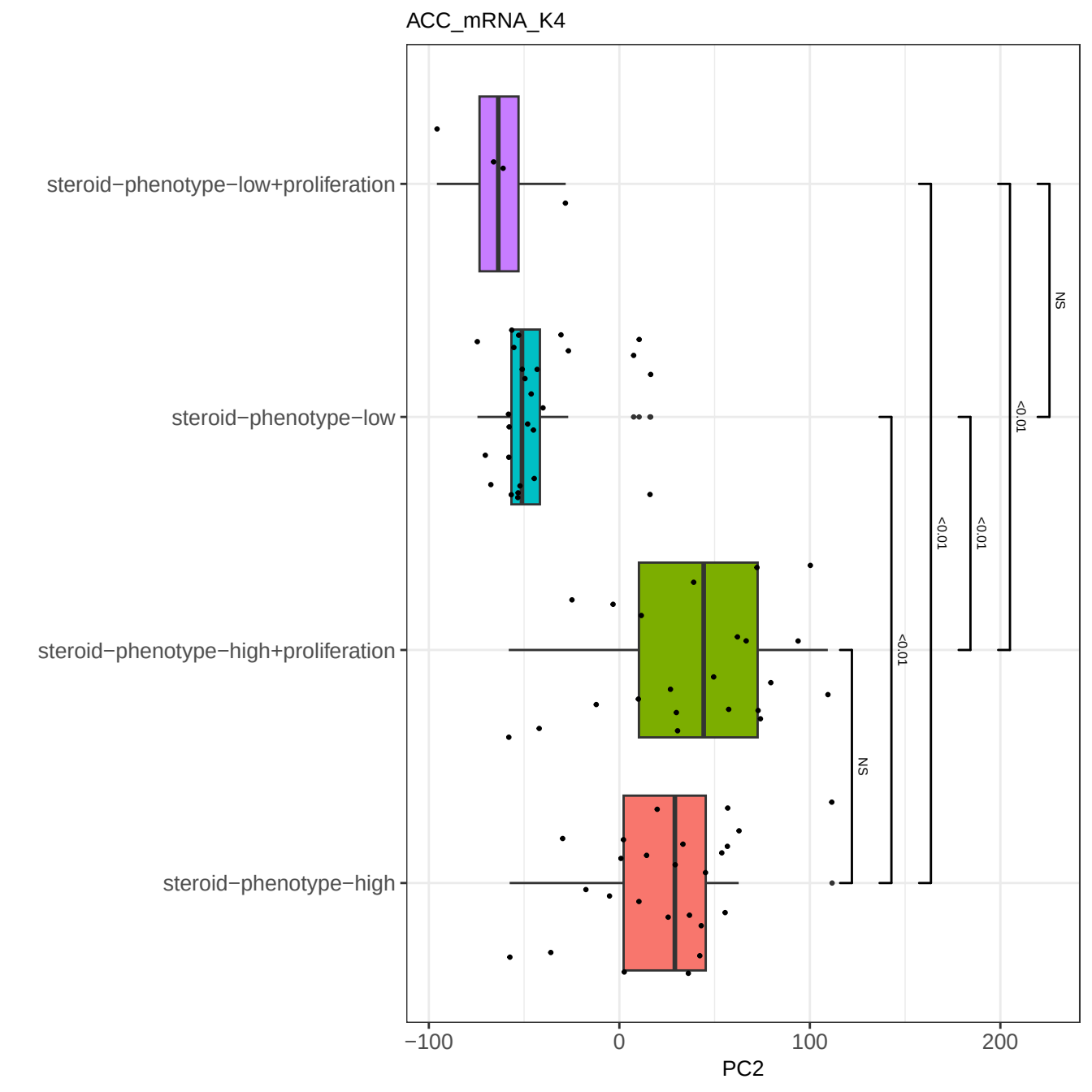

LGG_ESTIMATE.immune.score
R = −0.59, p < 0.001
ESTIMATE.immune.score
PC1
4000
3000
2000
1000
0
−1000
−200
−100
0
100
200

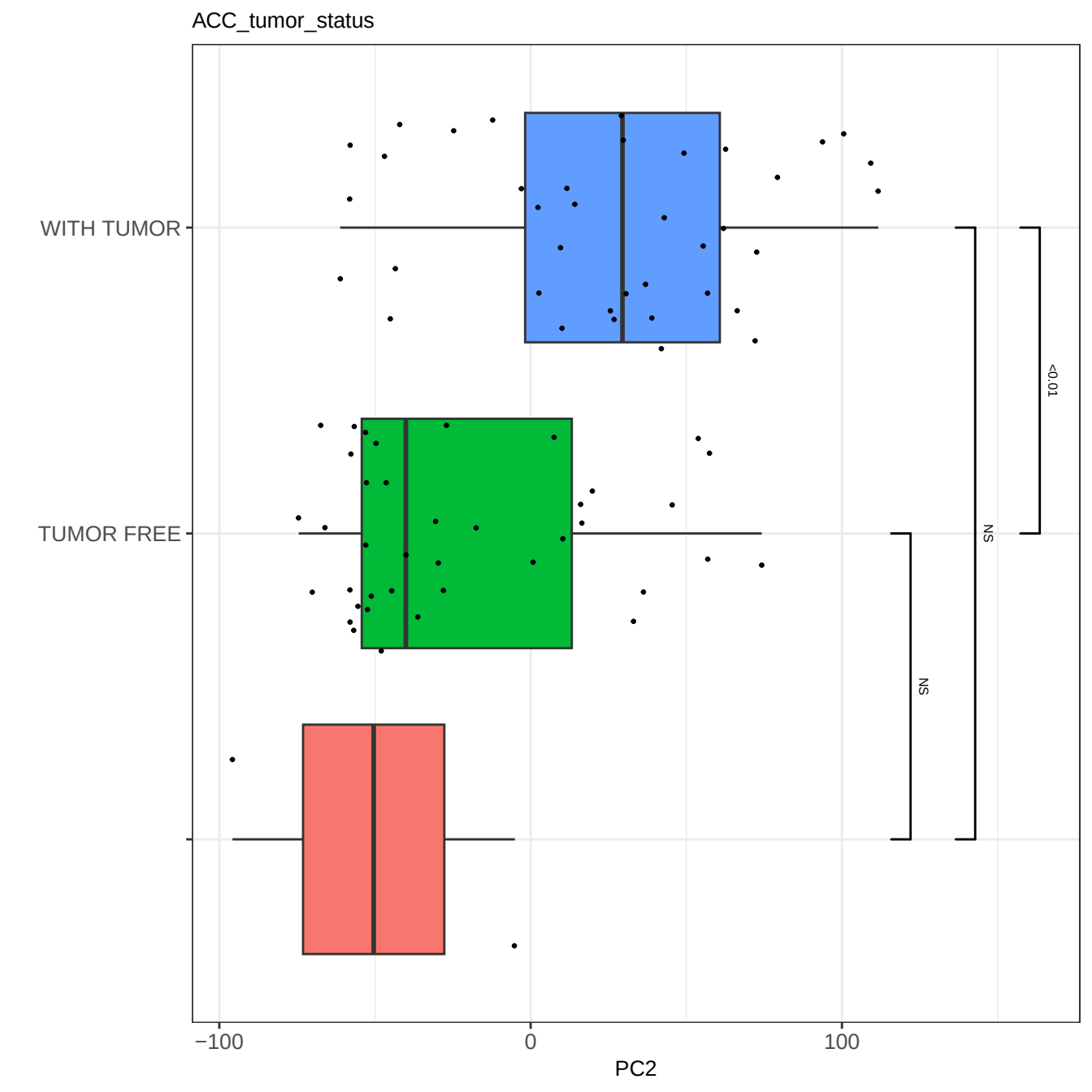

LGG_ESTIMATE.combined.score
R = −0.55, p < 0.001
7500
5000
2500
0
ESTIMATE.combined.score
−200
−100
0
100
200
PC1

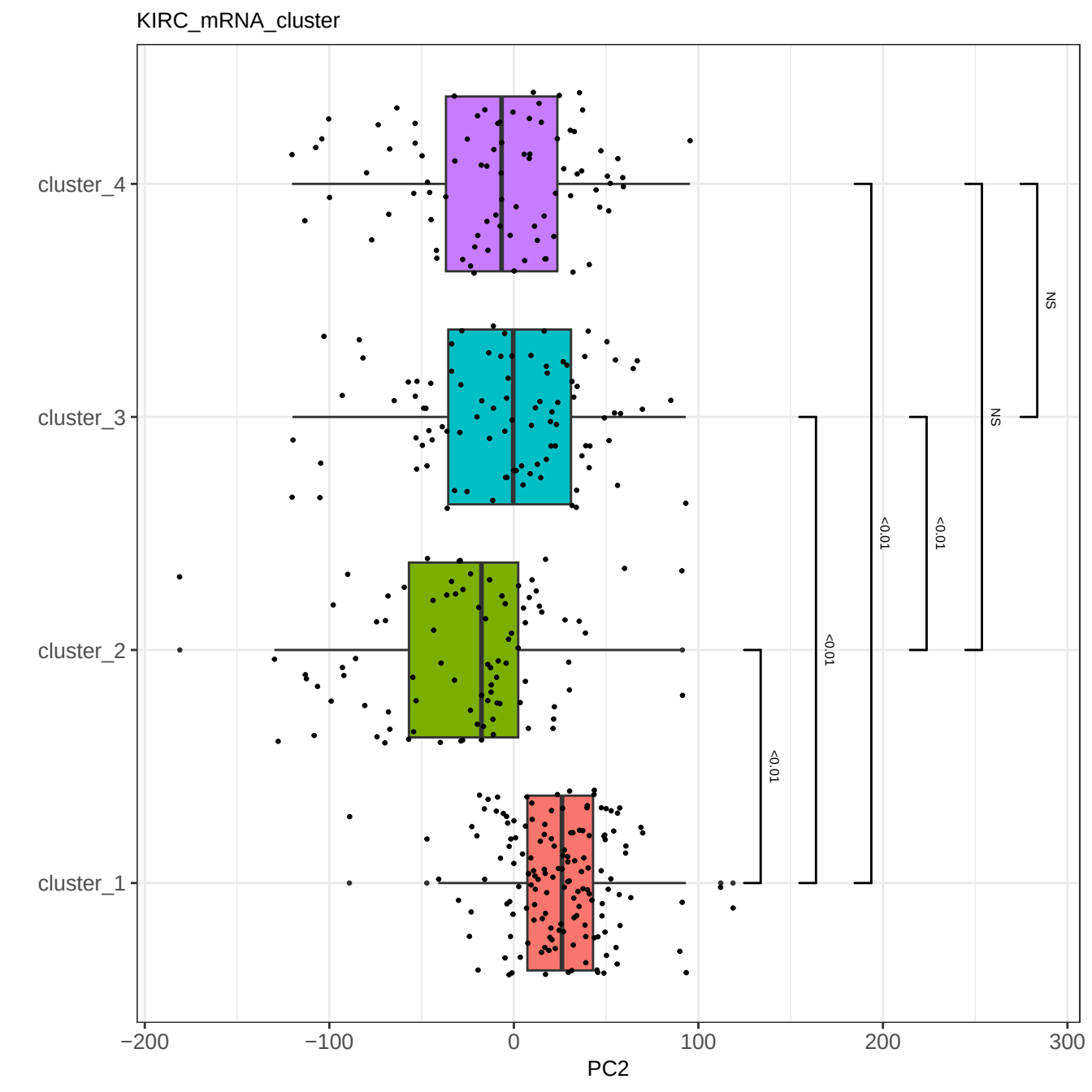

ACC_C1A.C1B
C1B
C1A
<0.01
−100
−50
0
50
100
PC2

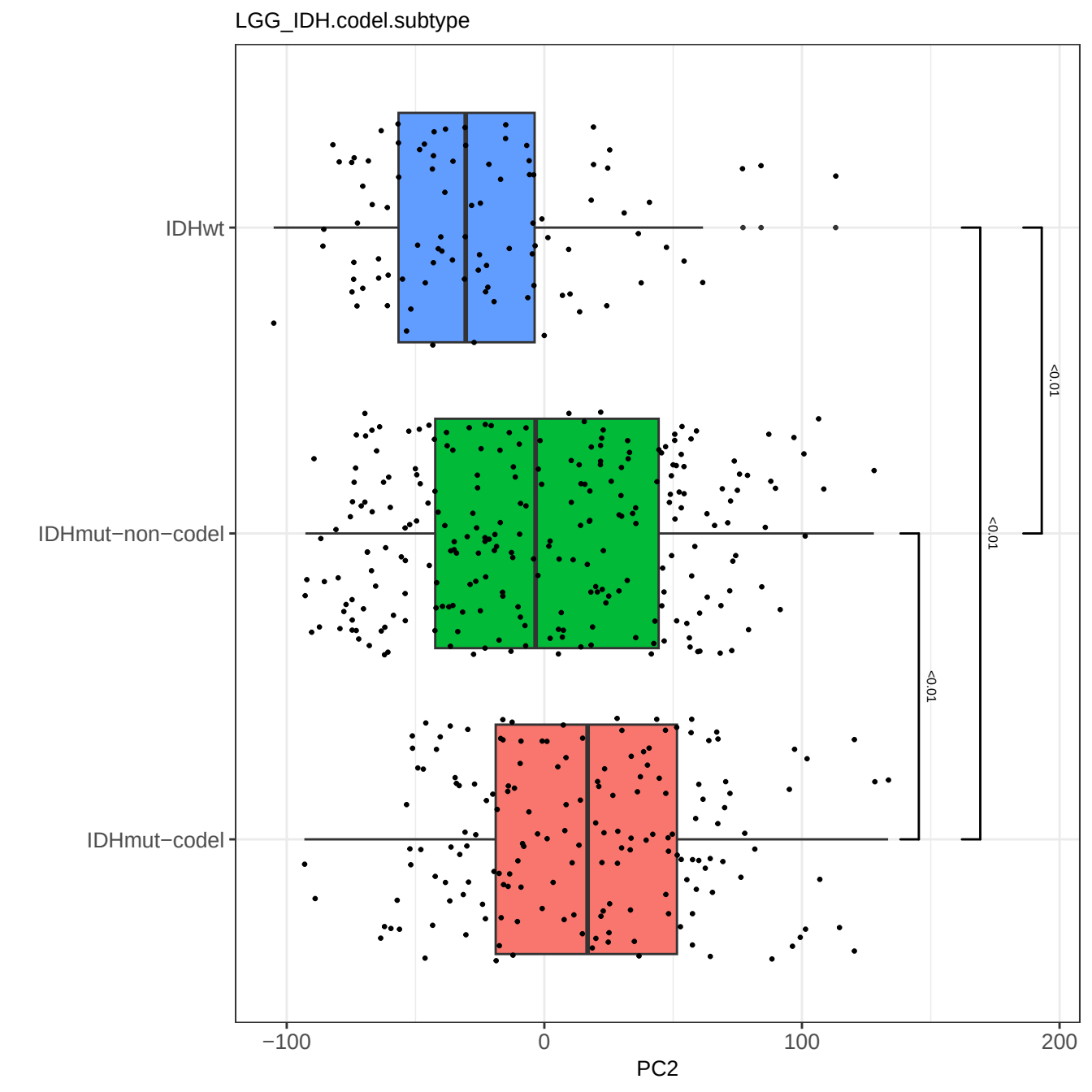

ACC_COC
COC3
COC2
COC1
NS
<0.01
NS
−100
0
100
PC2

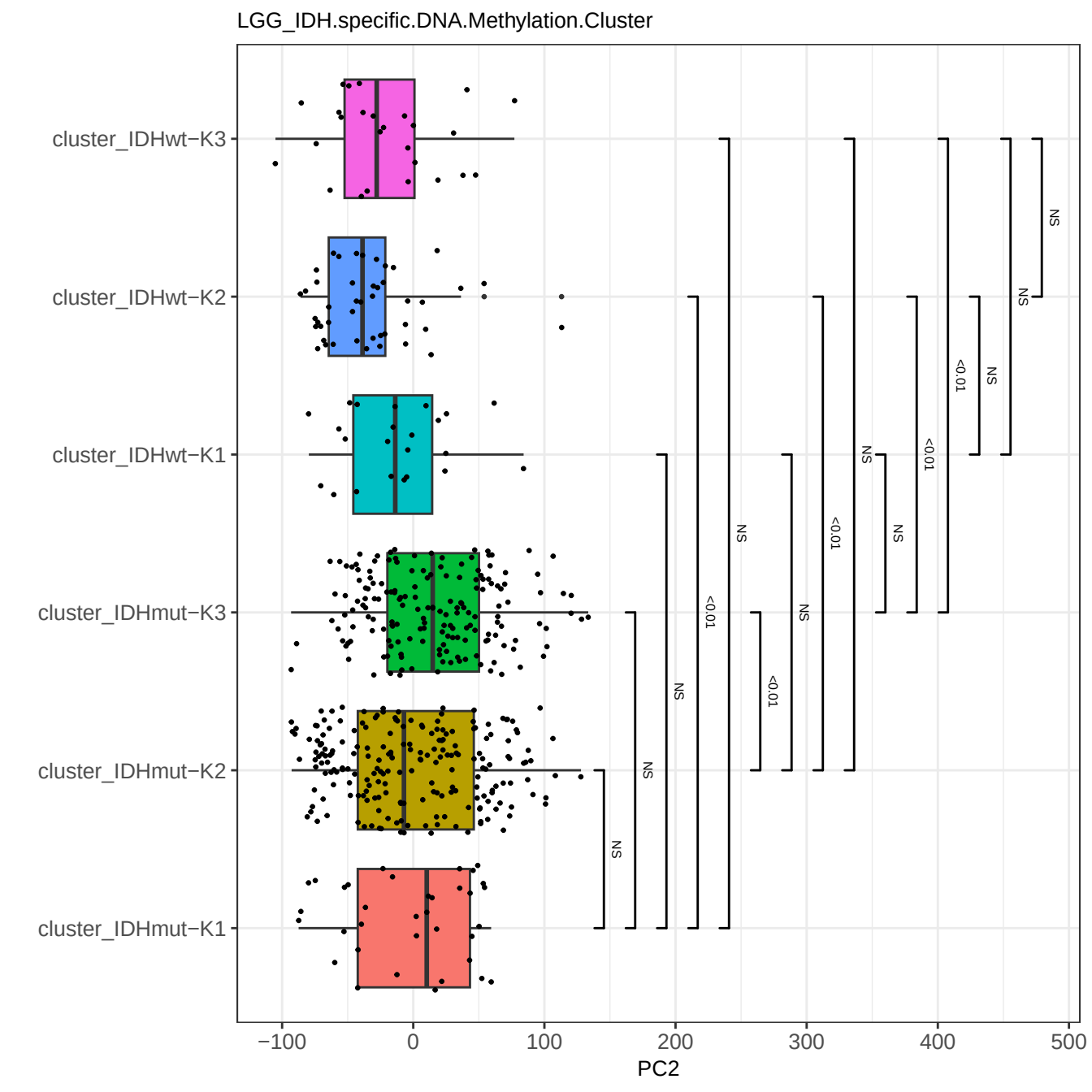

ACC_MethyLevel
CIMP−low
CIMP−intermediate
CIMP−high
<0.01
<0.01
NS
−100
0
100
PC2

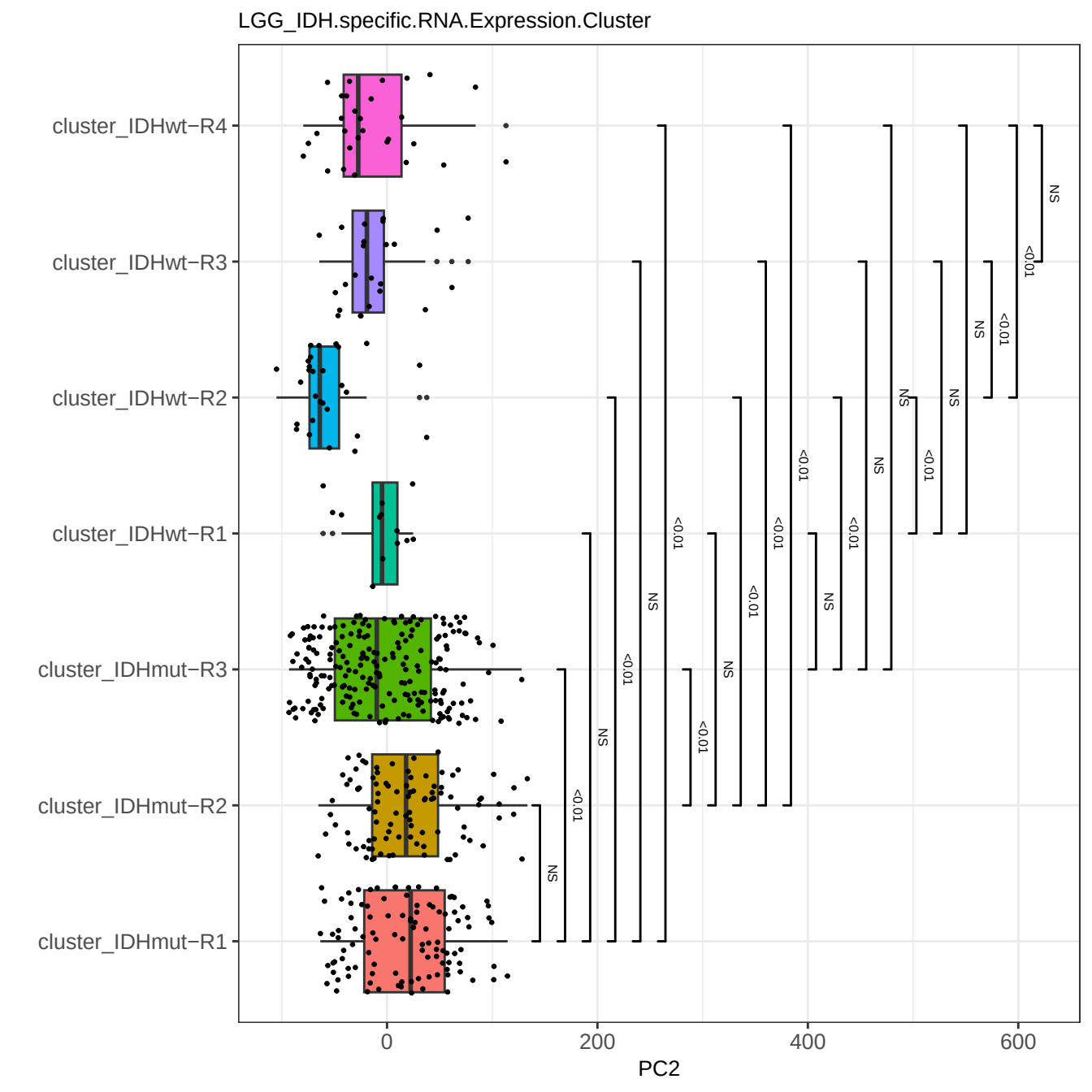

ACC_mRNA_K4
steroid−phenotype−low+proliferation
steroid−phenotype−low
steroid−phenotype−high+proliferation
steroid−phenotype−high
NS
<0.01
<0.01
<0.01
NS
−100
0
100
200
PC2

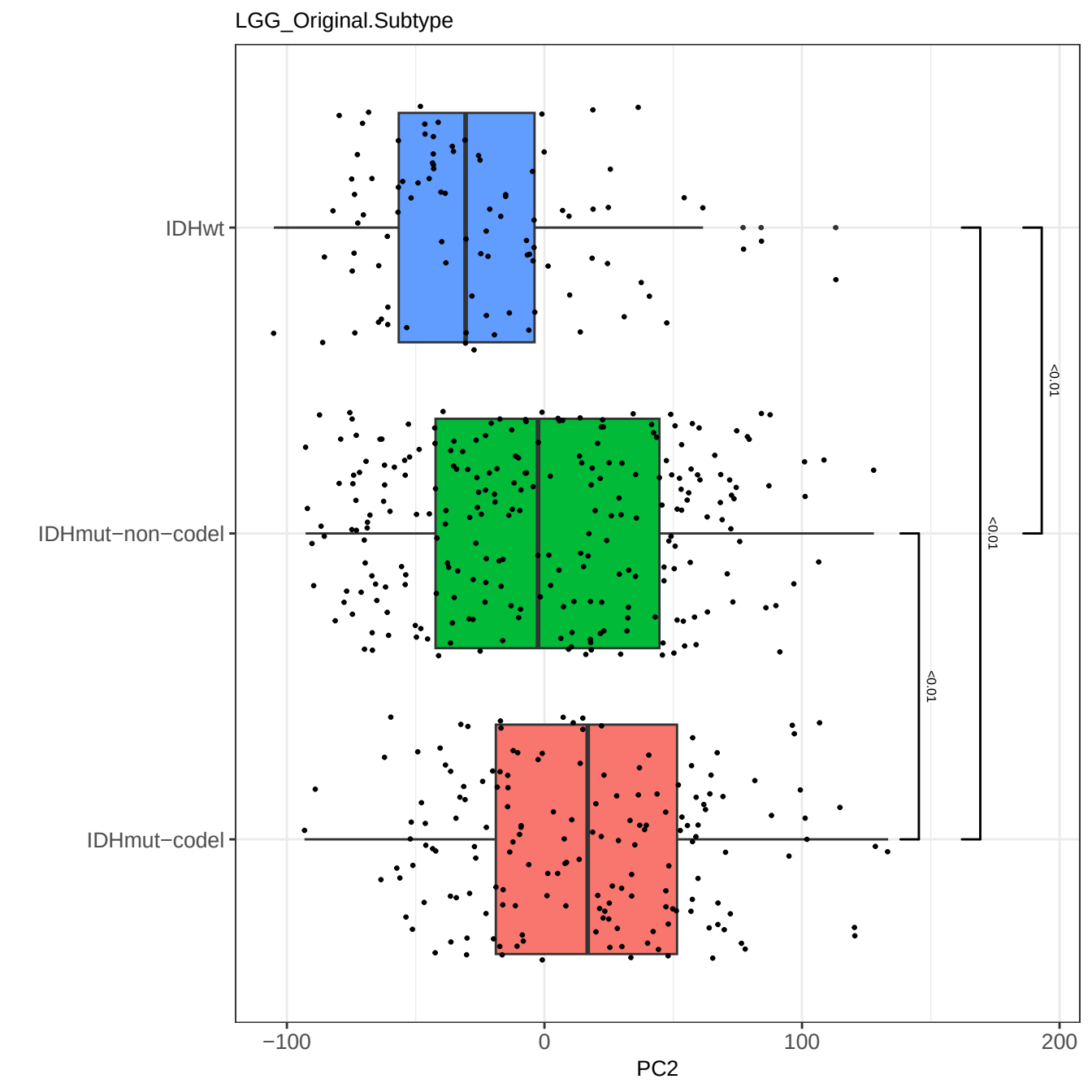

ACC_tumor_status
WITH TUMOR
TUMOR FREE
<0.01
NS
NS
−100
0
100
PC2

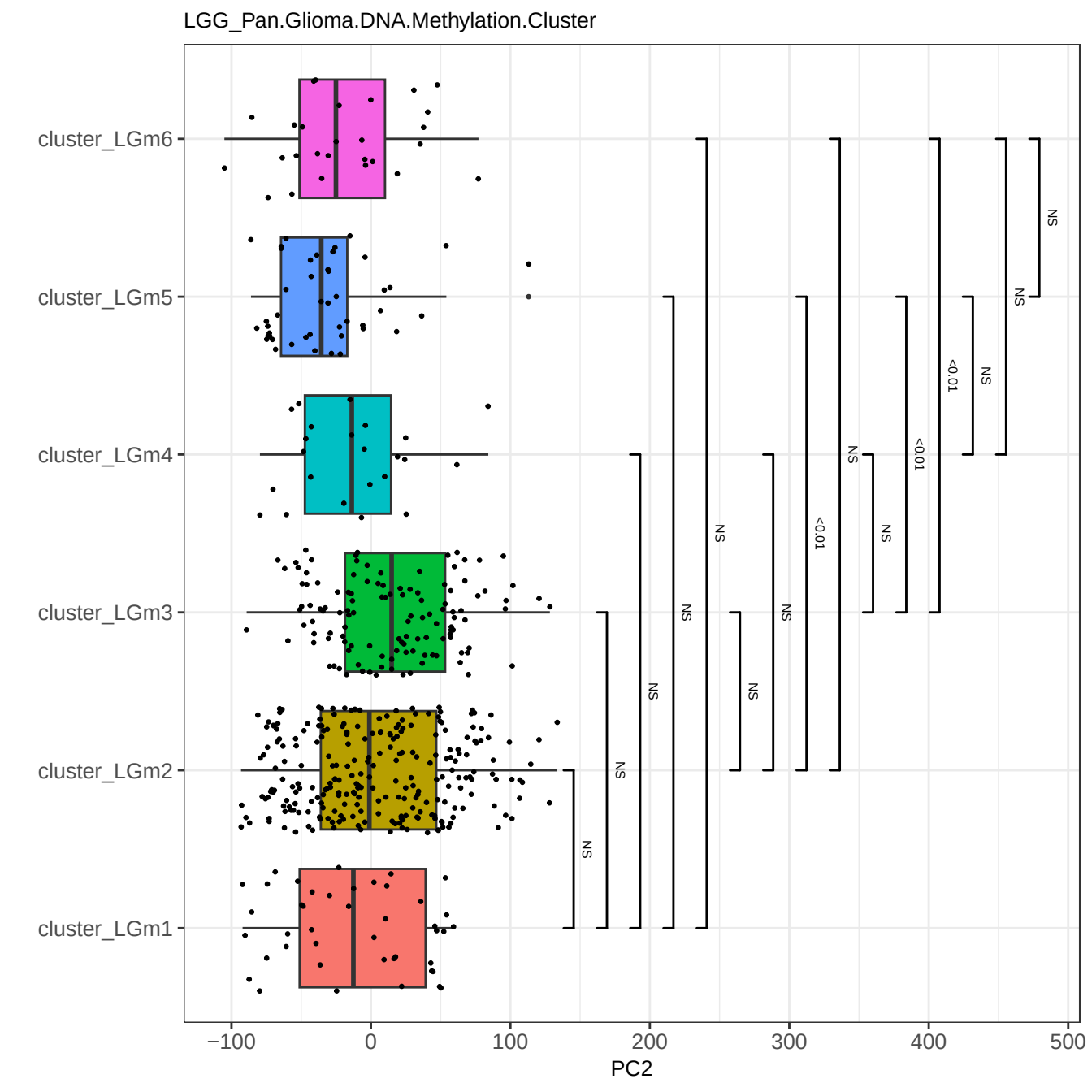

KIRC_mRNA_cluster
cluster_4
cluster_3
cluster_2
cluster_1
−200
−100
0
100
200
300
PC2
<0.01
<0.01
<0.01
NS
NS

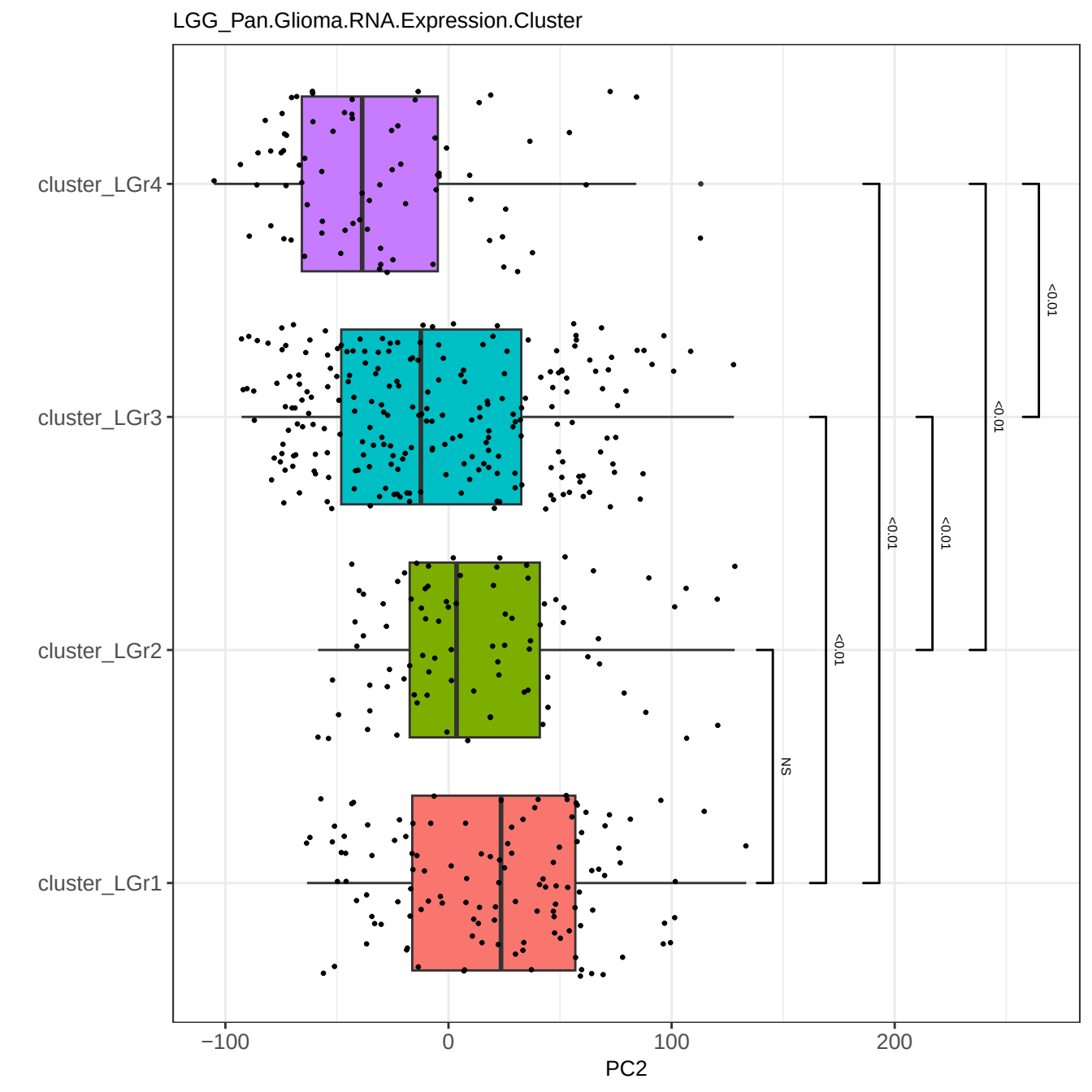

LGG_IDH.codel.subtype
IDHwt
IDHmut−non−codel
IDHmut−codel
<0.01
<0.01
<0.01
−100
0
100
200
PC2

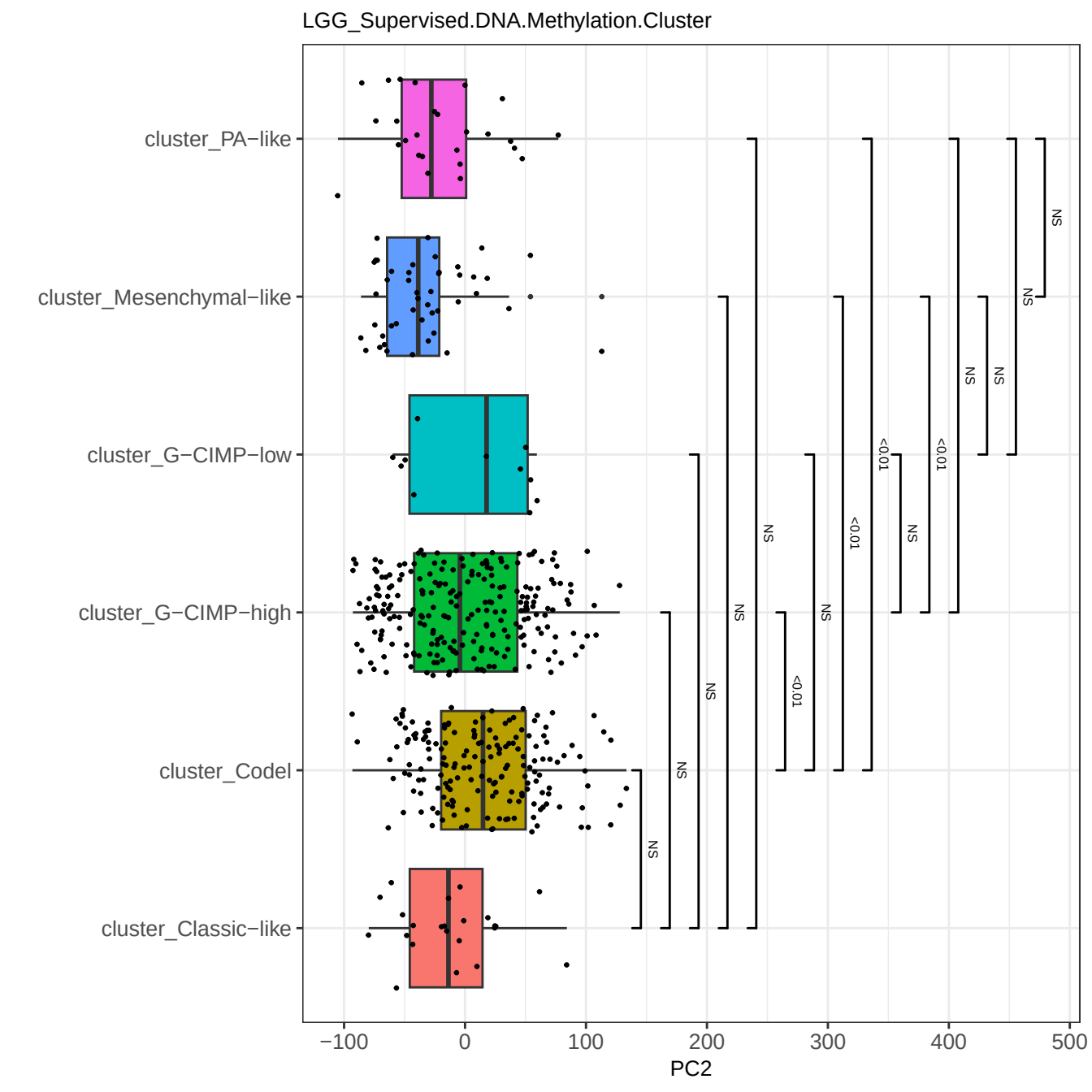

LGG_IDH.specific.DNA.Methylation.Cluster
cluster_IDHwt−K3
cluster_IDHwt−K2
cluster_IDHwt−K1
cluster_IDHmut−K3
cluster_IDHmut−K2
cluster_IDHmut−K1
NS
<0.01
−100
0
100
200
300
400
500
PC2

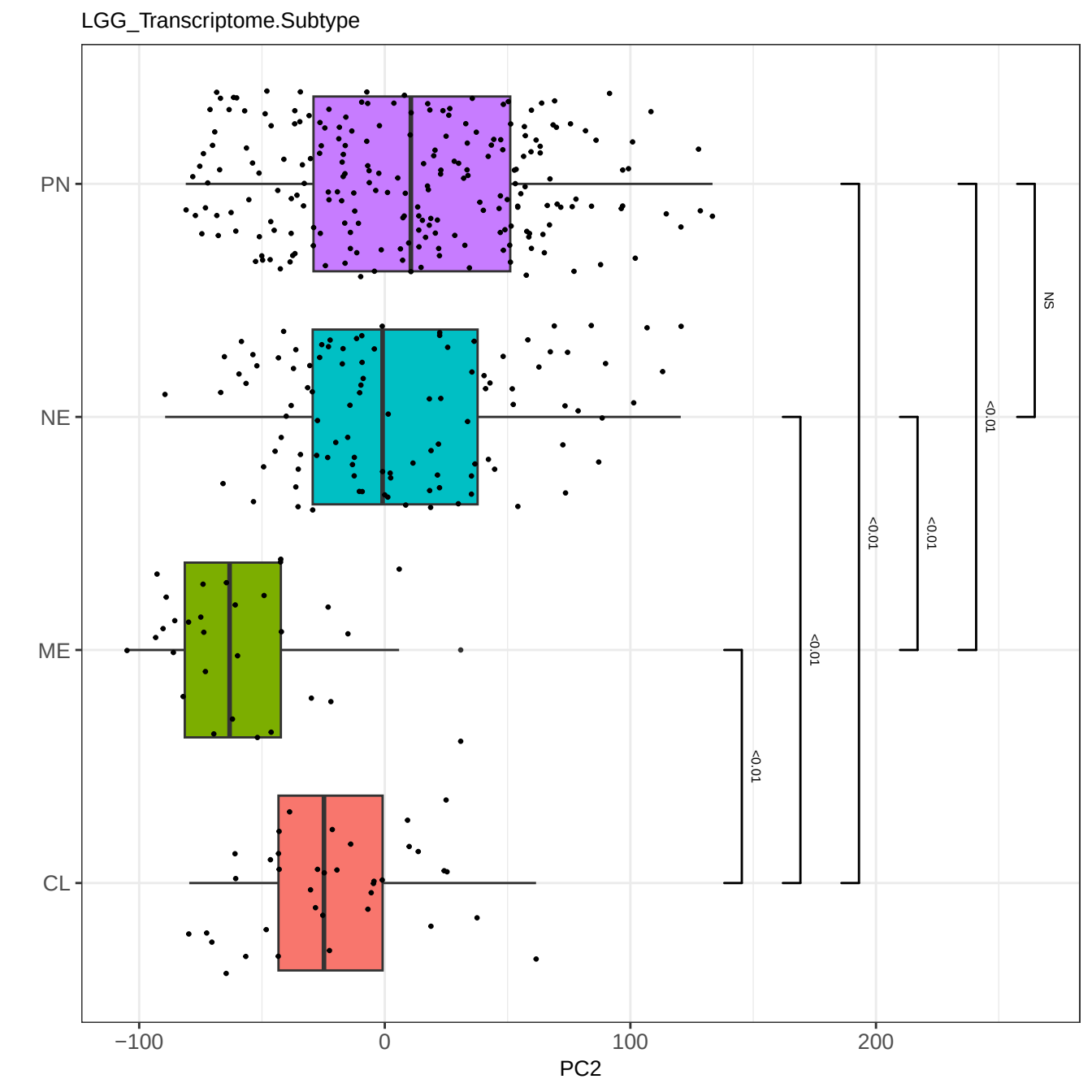

LGG_IDH.specific.RNA.Expression.Cluster
cluster_IDHwt−R4
cluster_IDHwt−R3
cluster_IDHwt−R2
cluster_IDHwt−R1
cluster_IDHmut−R3
cluster_IDHmut−R2
cluster_IDHmut−R1
0
200
400
600
PC2
NS
<0.01

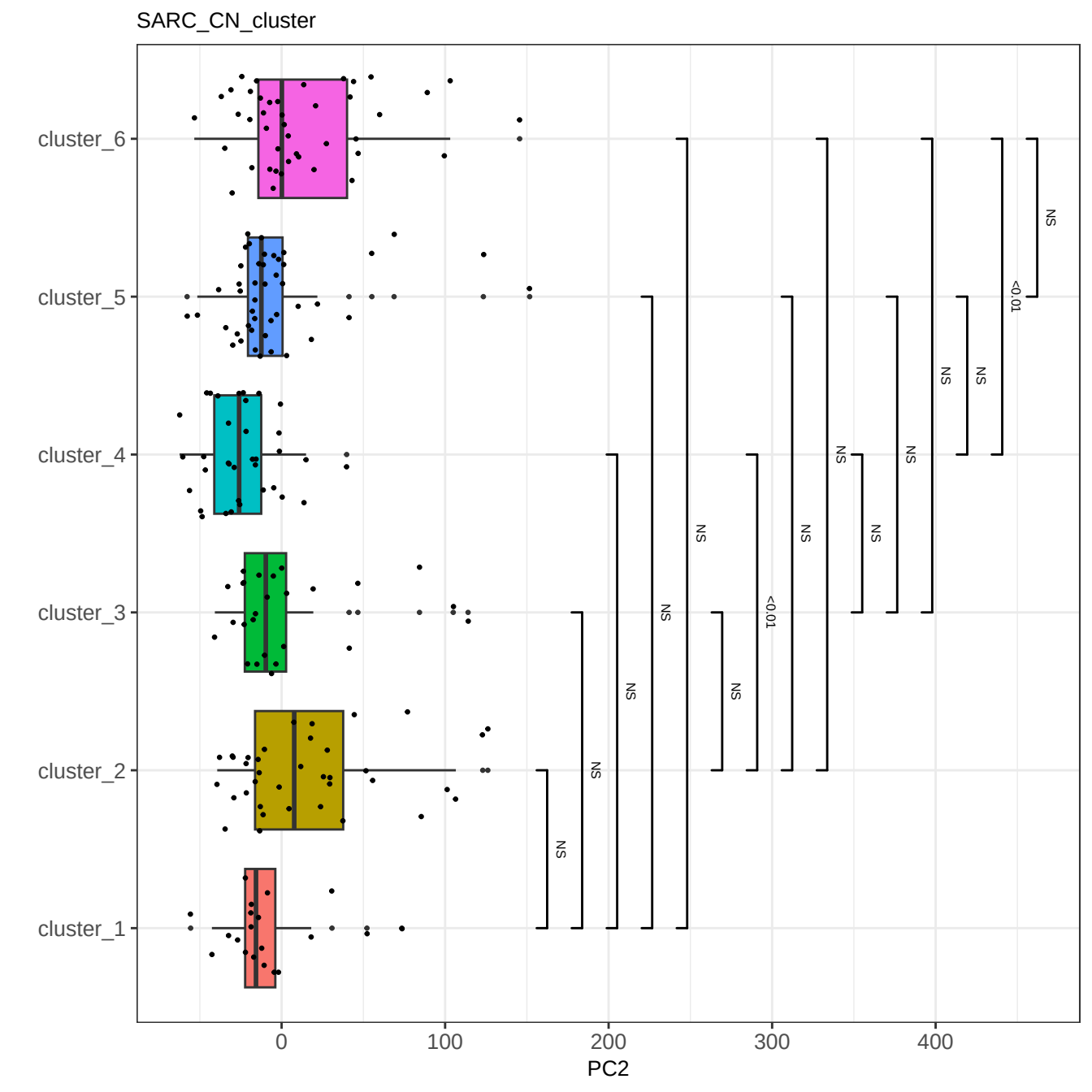

LGG_Original.Subtype
IDHwt
IDHmut−non−codel
IDHmut−codel
<0.01
<0.01
<0.01
−100
0
100
200
PC2

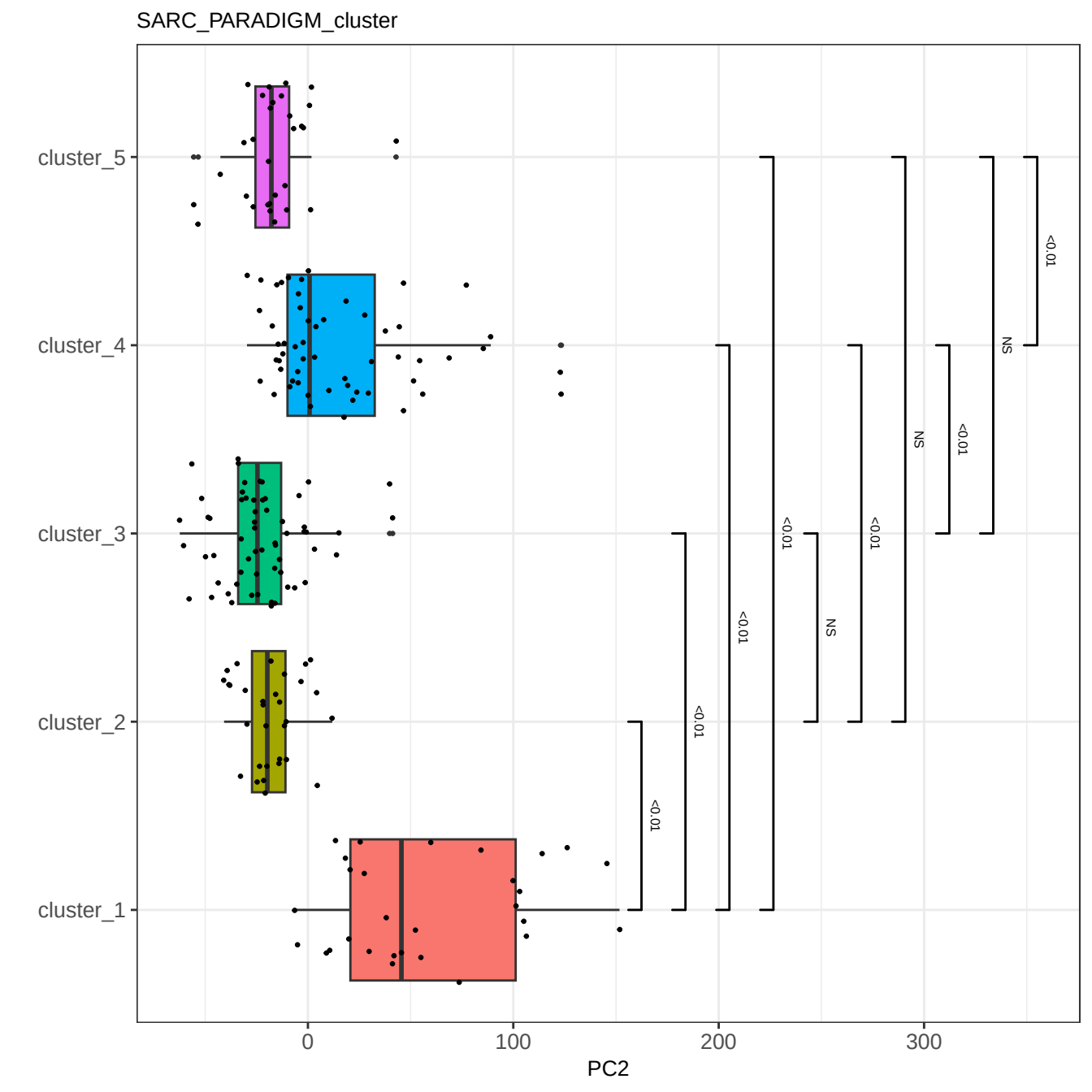

LGG_Pan.Glioma.DNA.Methylation.Cluster
cluster_LGm6
cluster_LGm5
cluster_LGm4
cluster_LGm3
cluster_LGm2
cluster_LGm1
NS
<0.01
−100
0
100
200
300
400
500
PC2

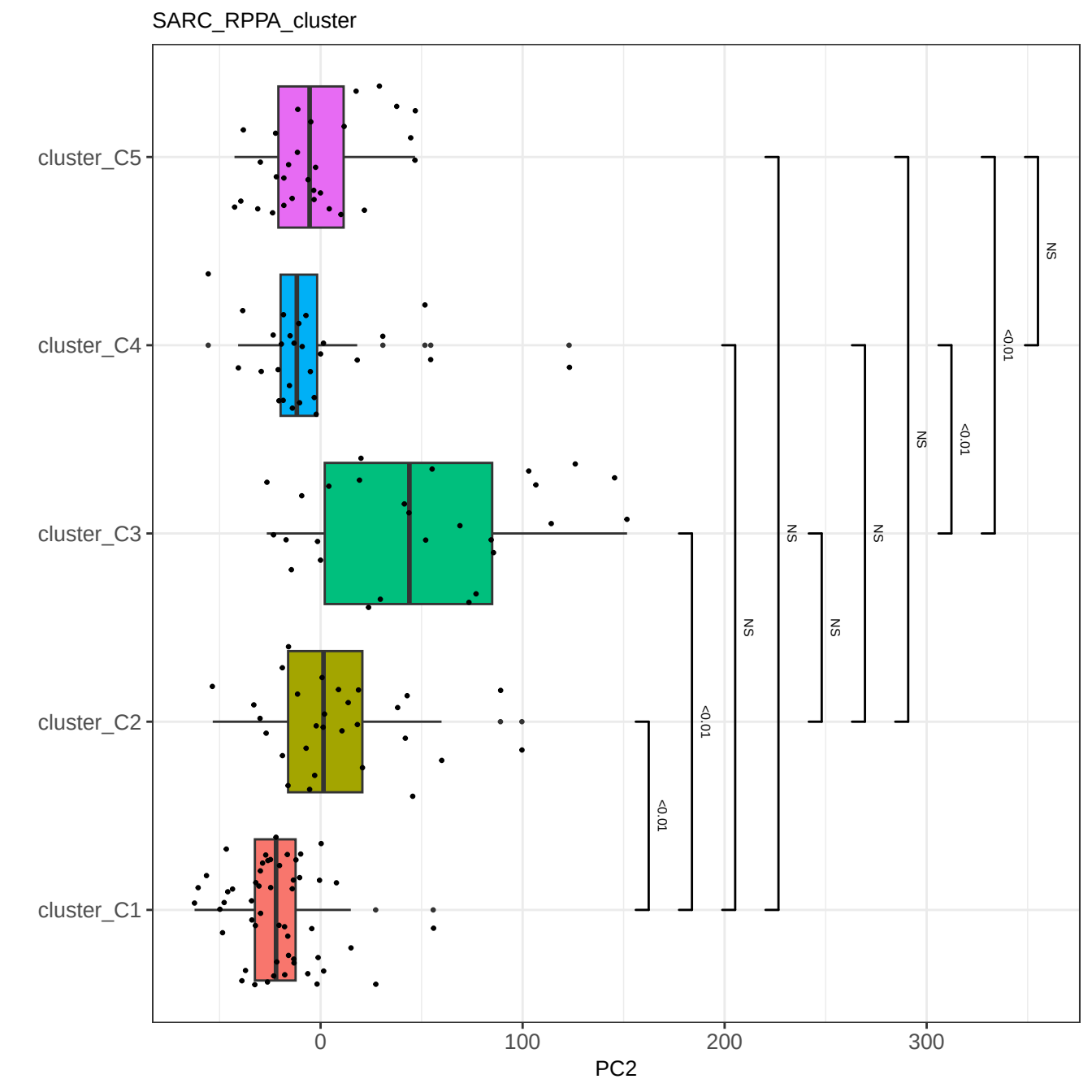

LGG_Pan.Glioma.RNA.Expression.Cluster
cluster_LGr4
cluster_LGr3
cluster_LGr2
cluster_LGr1
<0.01
<0.01
<0.01
<0.01
NS
−100
0
100
200
PC2

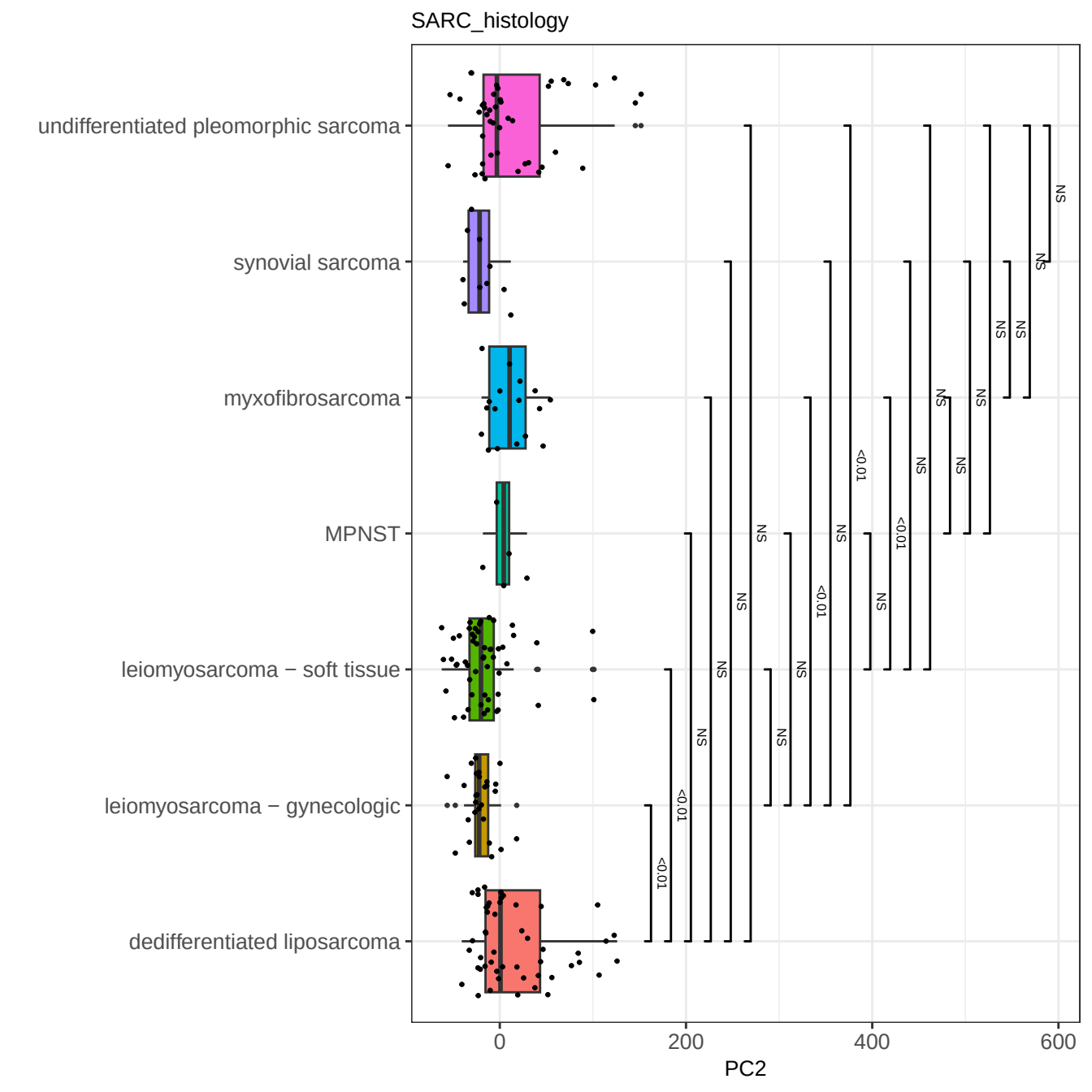

LGG_Supervised.DNA.Methylation.Cluster
cluster_PA−like
cluster_Mesenchymal−like
cluster_G−CIMP−low
cluster_G−CIMP−high
cluster_Codel
cluster_Classic−like
NS
<0.01
−100
0
100
200
300
400
500
PC2

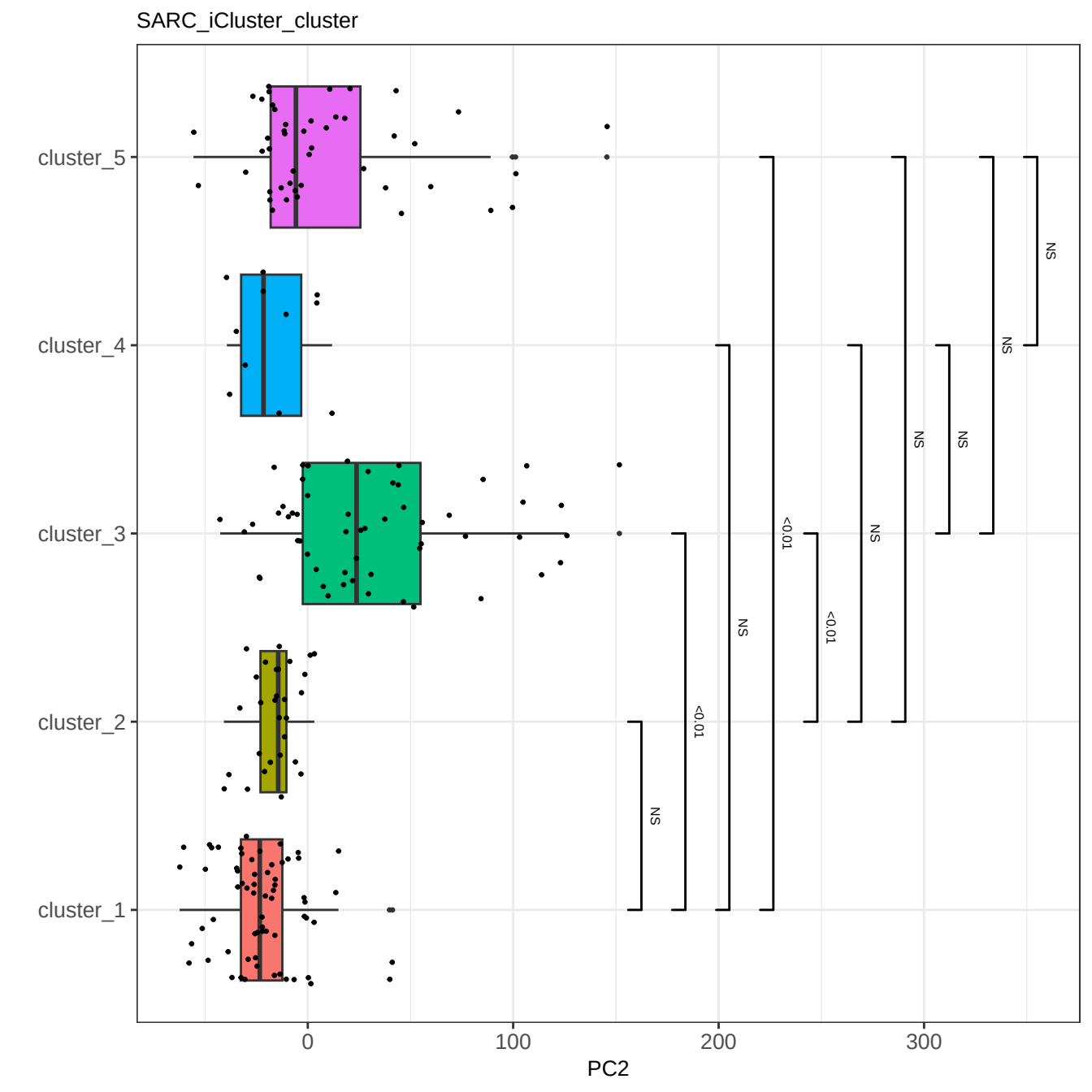

LGG_Transcriptome.Subtype
PN
NE
ME
CL
−100
0
100
200
PC2
NS
<0.01
<0.01
<0.01
<0.01
<0.01

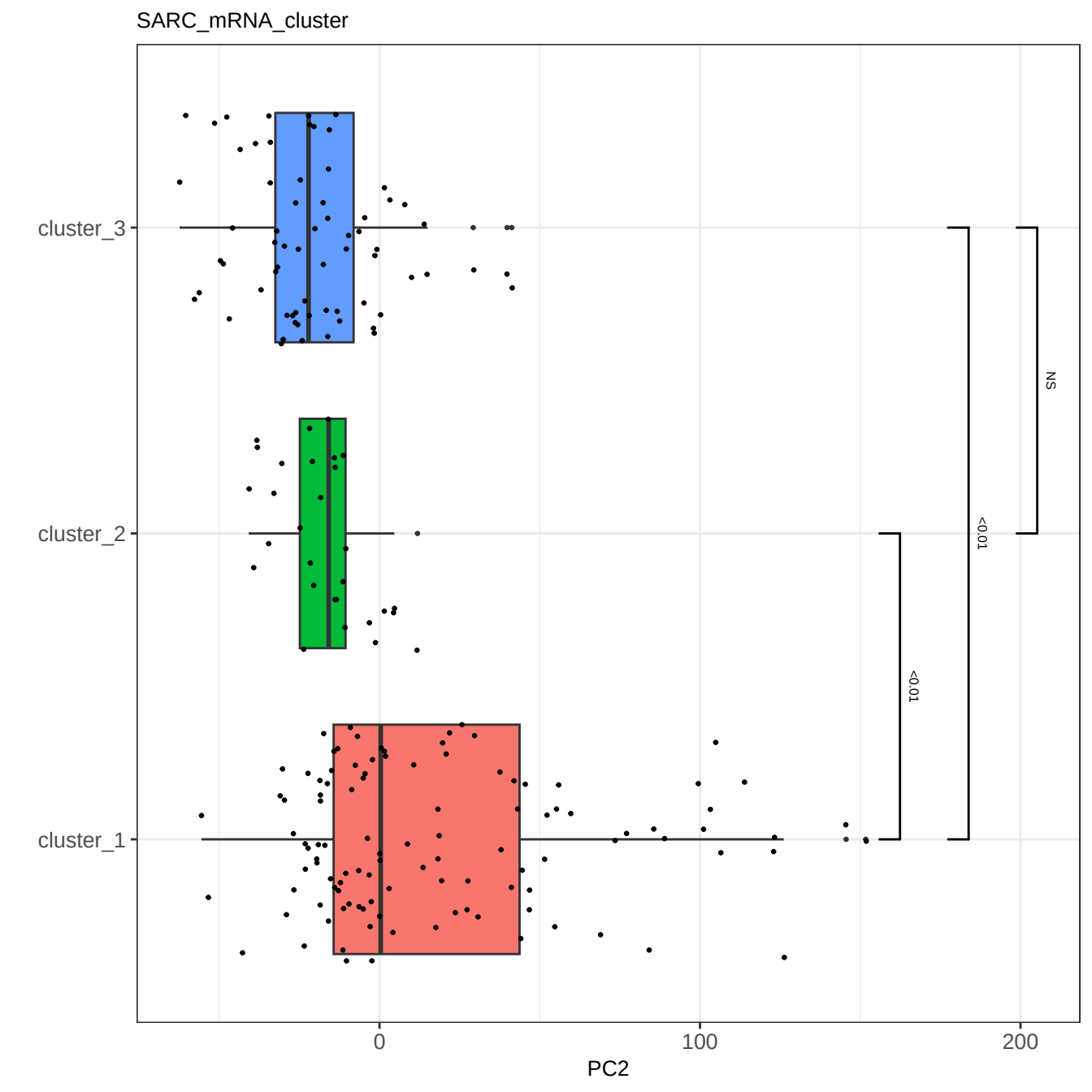

SARC_CN_cluster
cluster_6
cluster_5
cluster_4
cluster_3
cluster_2
cluster_1
0
100
200
300
400
PC2
NS
<0.01

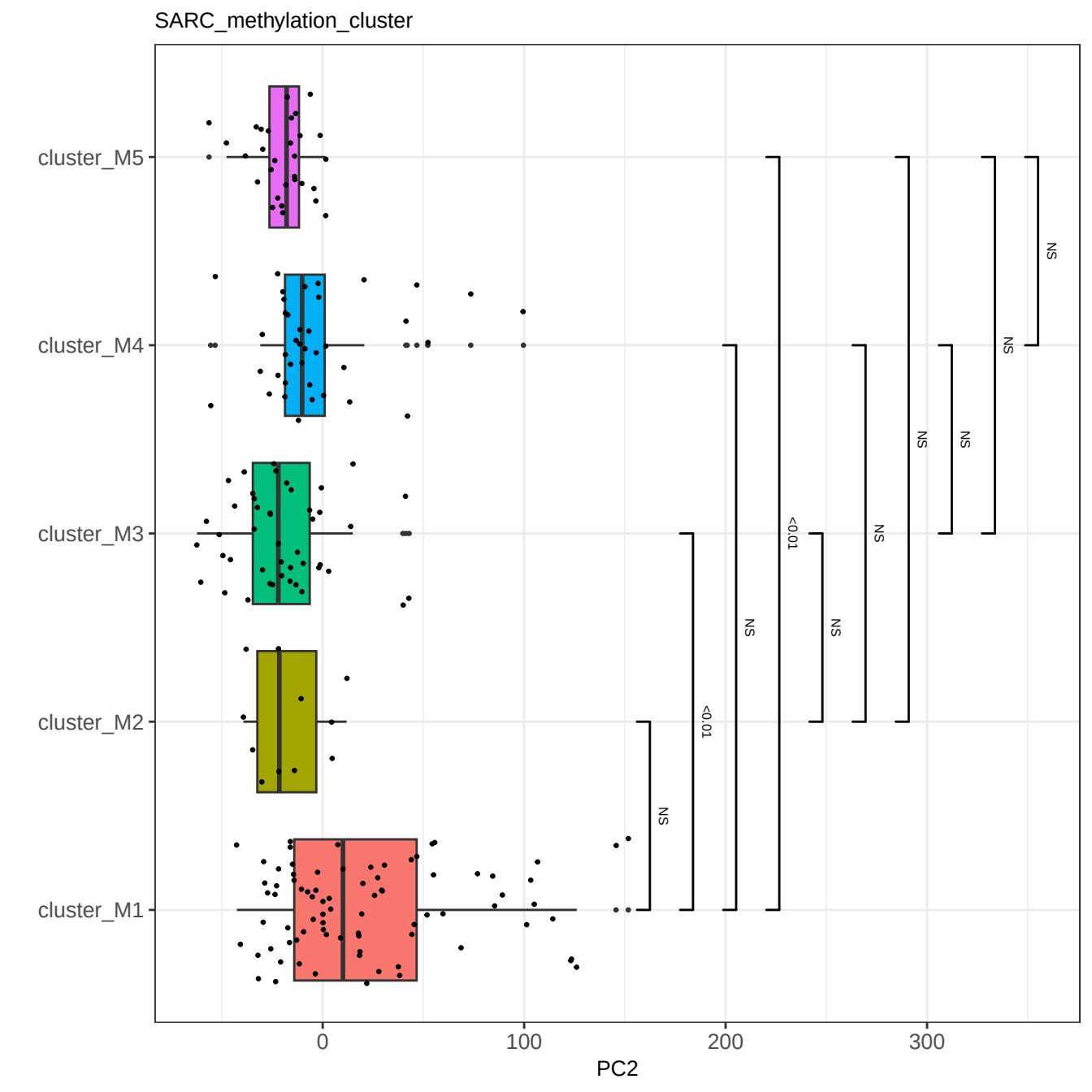

SARC_PARADIGM_cluster
cluster_5
cluster_4
cluster_3
cluster_2
cluster_1
0
100
200
300
PC2
<0.01
NS
<0.01
<0.01
<0.01
NS
<0.01
NS
<0.01
<0.01

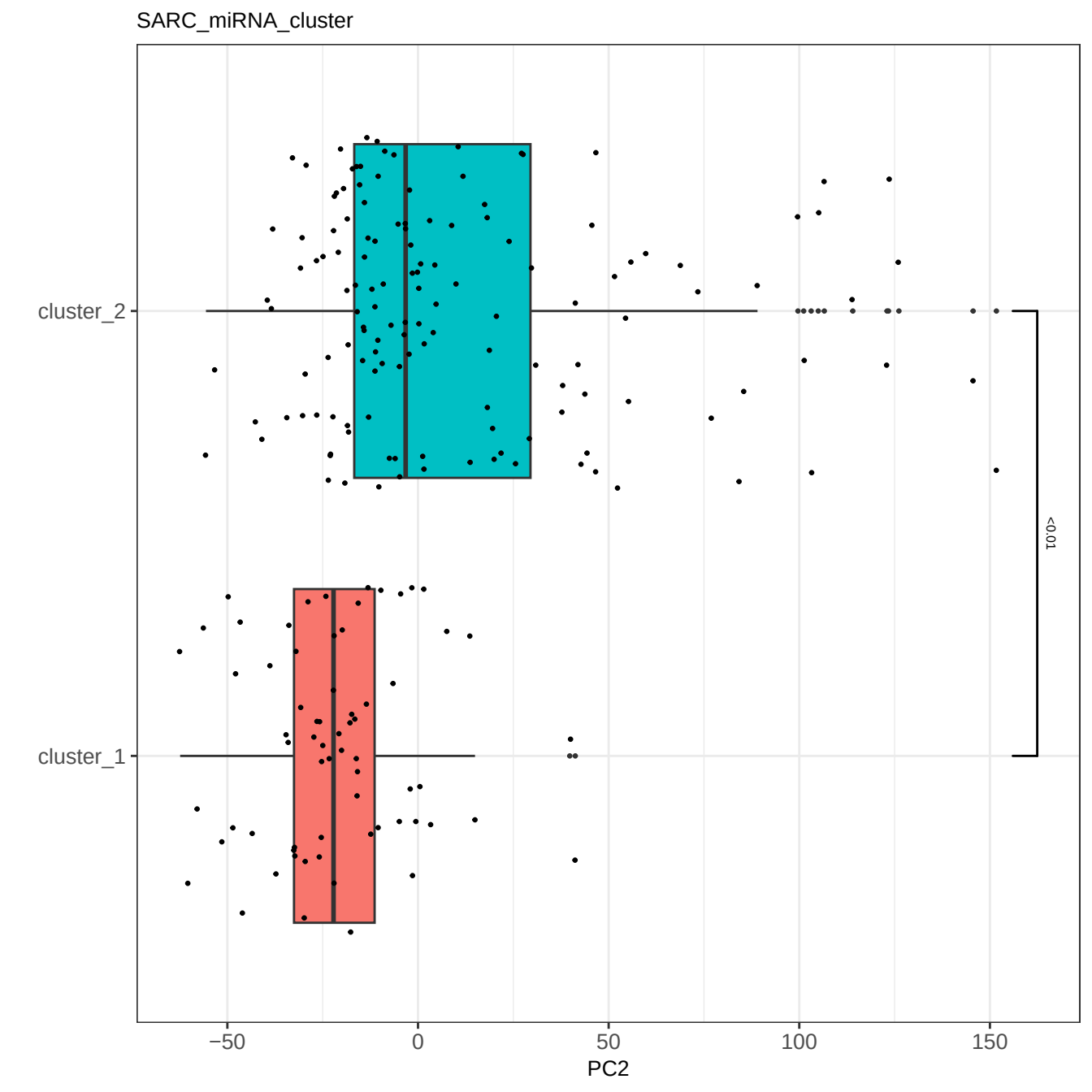

SARC_RPPA_cluster
cluster_C5
cluster_C4
cluster_C3
cluster_C2
cluster_C1
NS
<0.01
NS
<0.01
NS
NS
NS
<0.01
<0.01
0
100
200
300
PC2

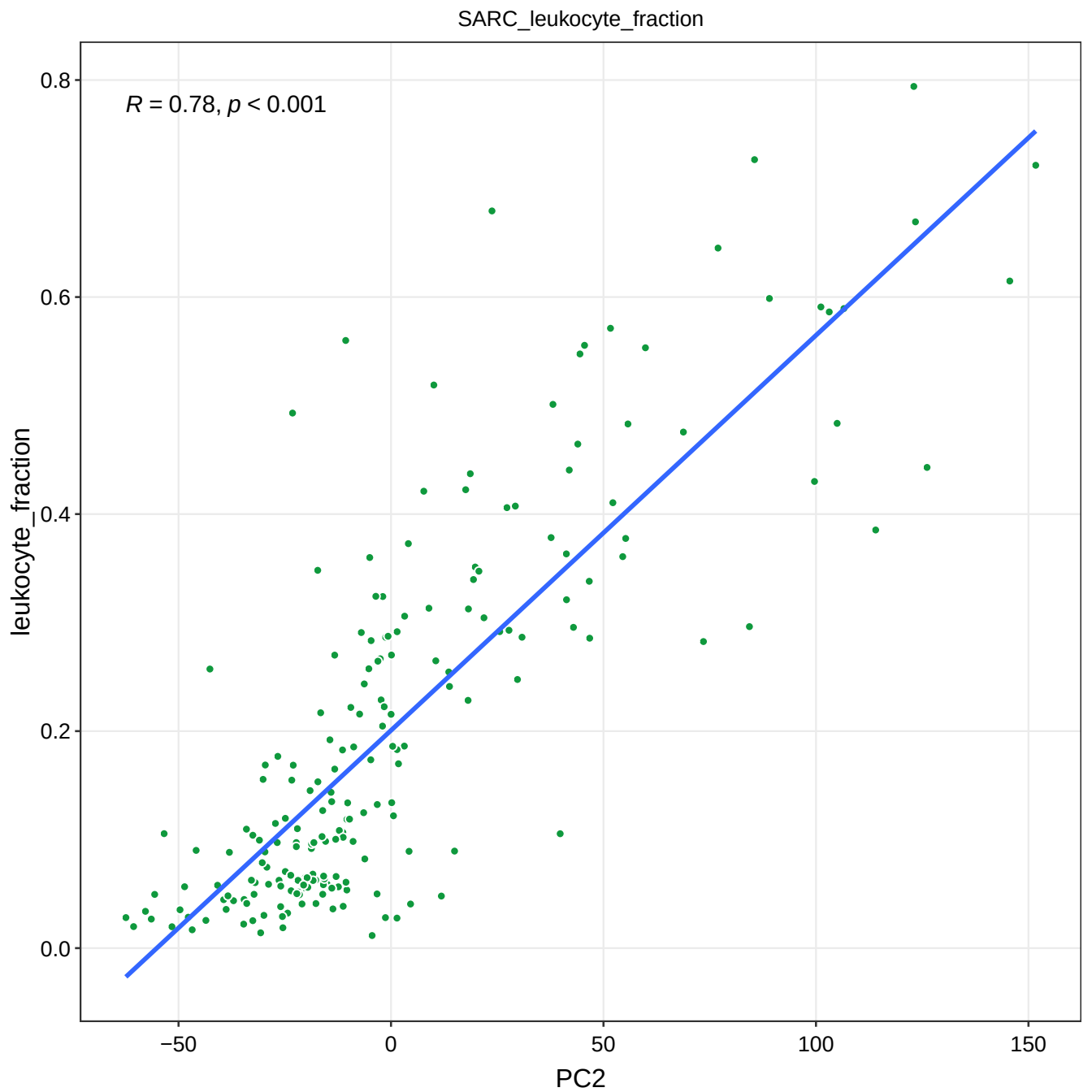

SARC_histology
undifferentiated pleomorphic sarcoma
synovial sarcoma
myxofibrosarcoma
MPNST
leiomyosarcoma − soft tissue
leiomyosarcoma − gynecologic
dedifferentiated liposarcoma
NS
<0.01
0
200
400
600
PC2

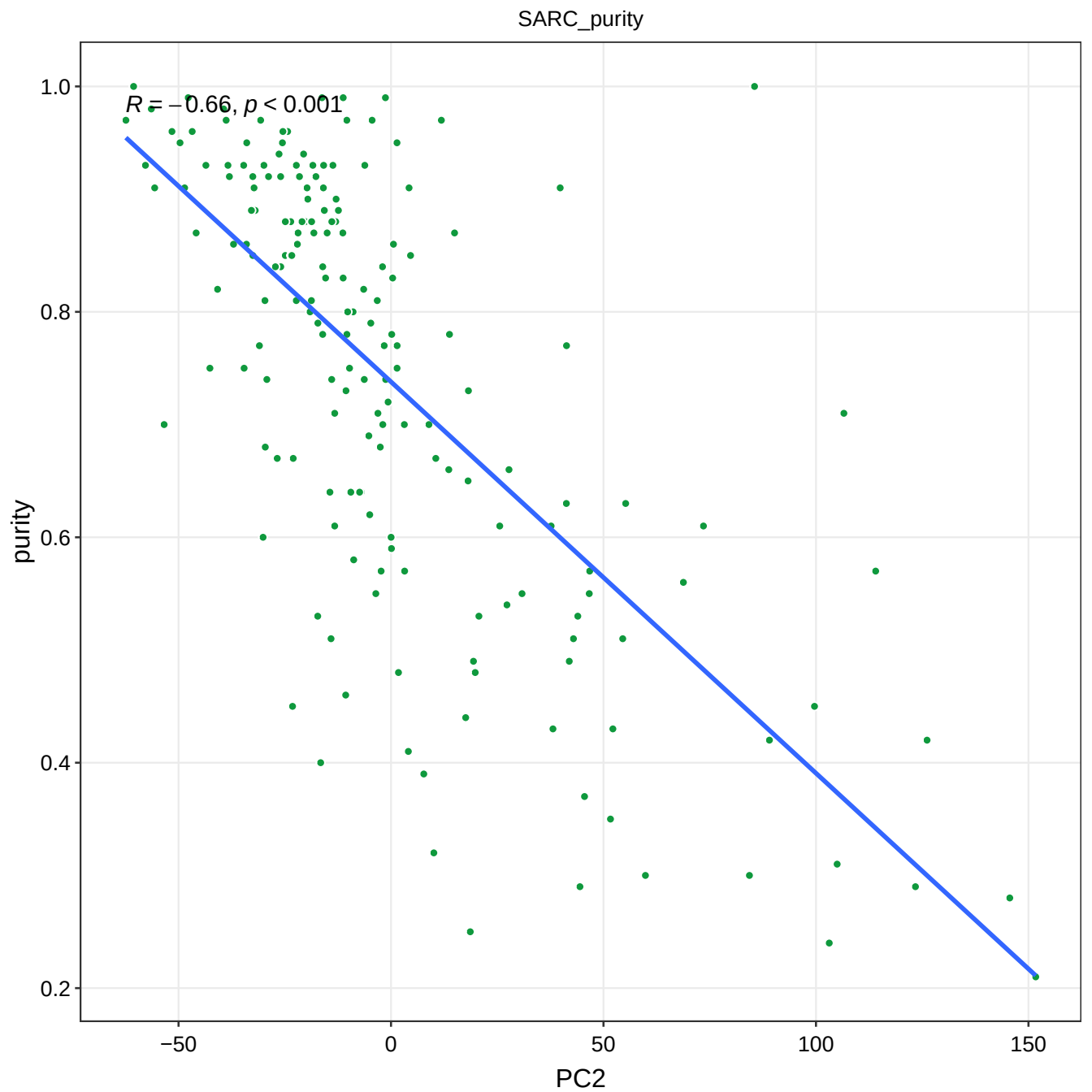

SARC_iCluster_cluster
cluster_5
cluster_4
cluster_3
cluster_2
cluster_1
0
100
200
300
PC2
NS
<0.01
NS
<0.01
<0.01
NS
NS
NS
NS
NS

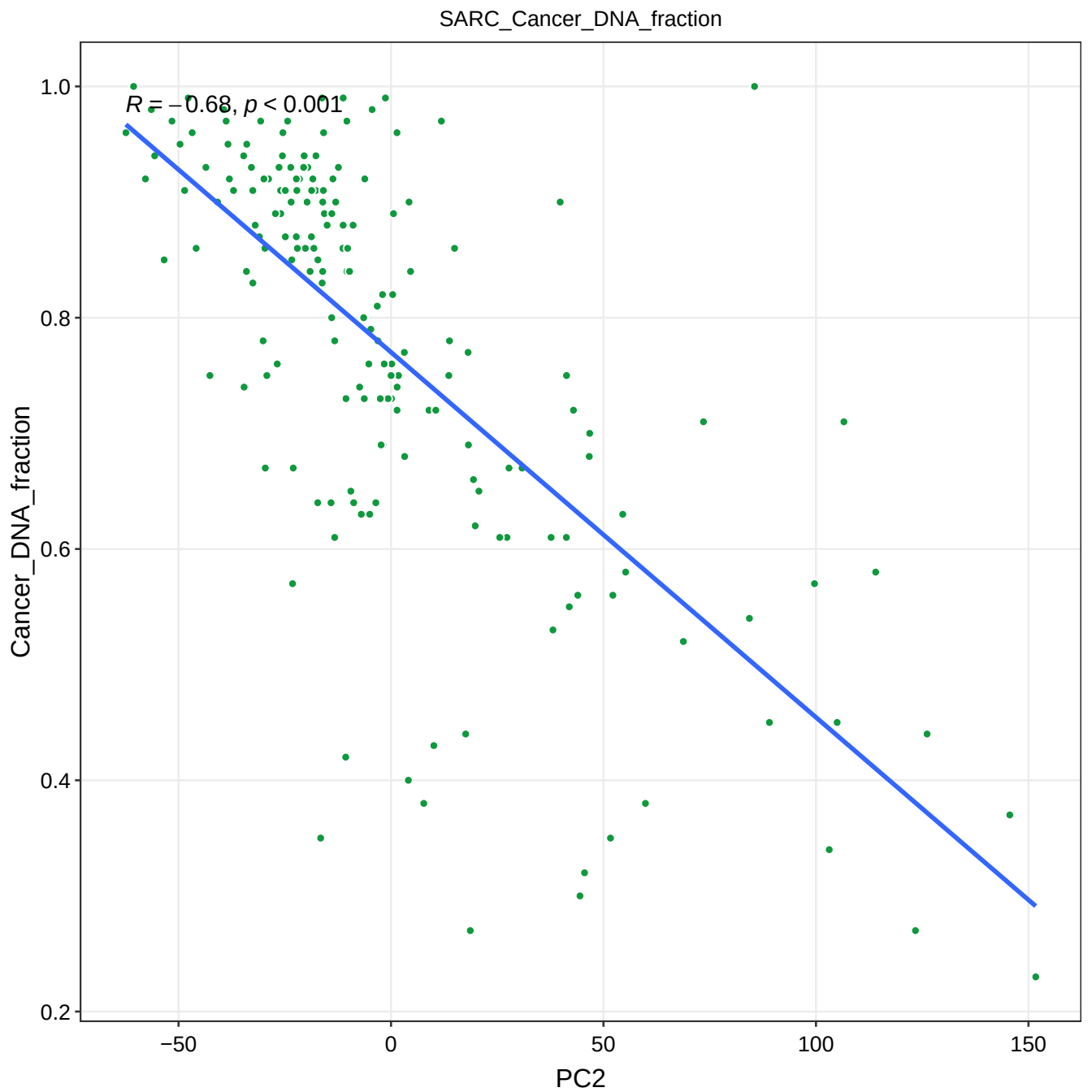

SARC_mRNA_cluster
cluster_3
cluster_2
cluster_1
NS
<0.01
<0.01
0
100
200
PC2

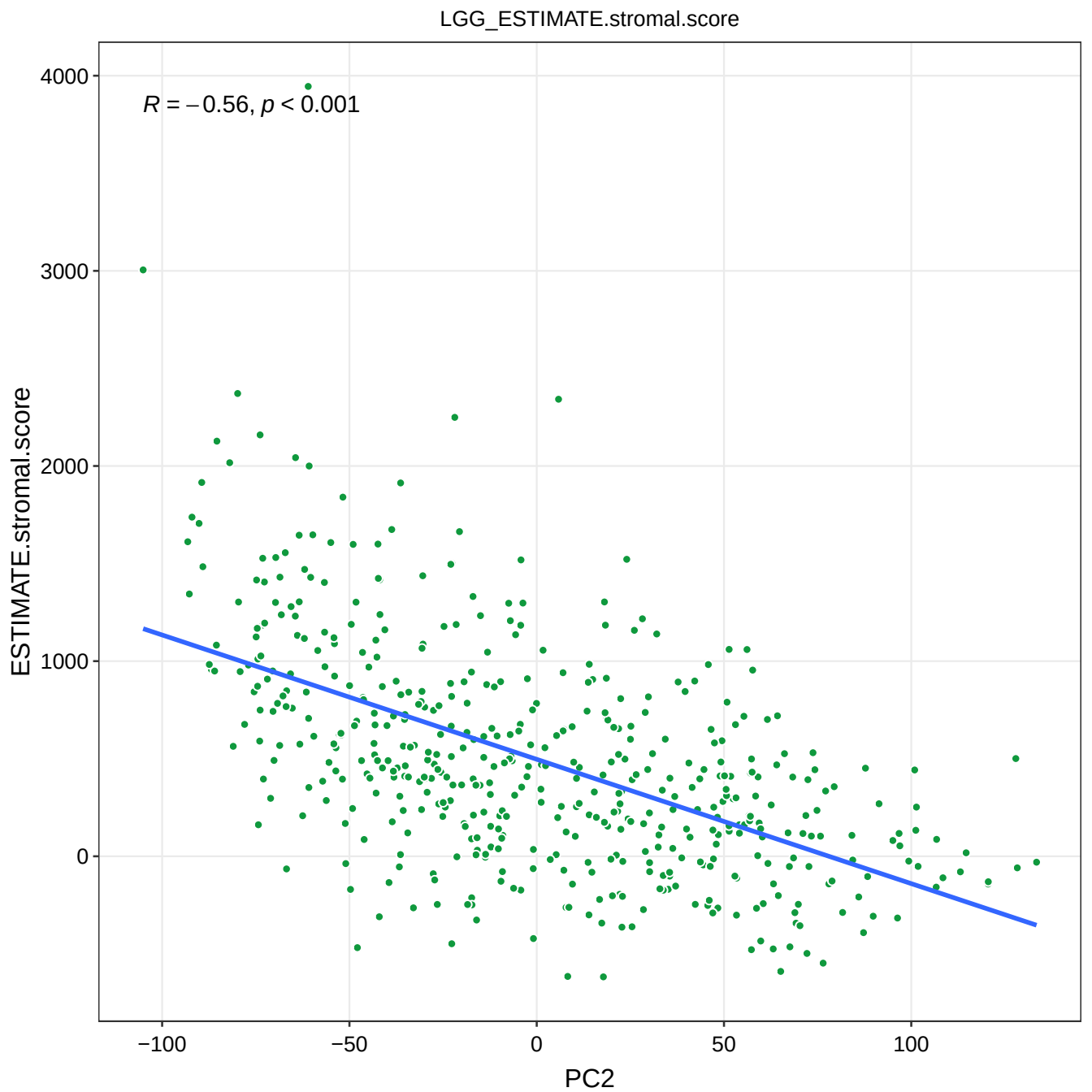

SARC_methylation_cluster
cluster_M5
cluster_M4
cluster_M3
cluster_M2
cluster_M1
0
100
200
300
PC2
NS
NS
NS
<0.01
NS
NS
NS
NS
NS
<0.01
NS

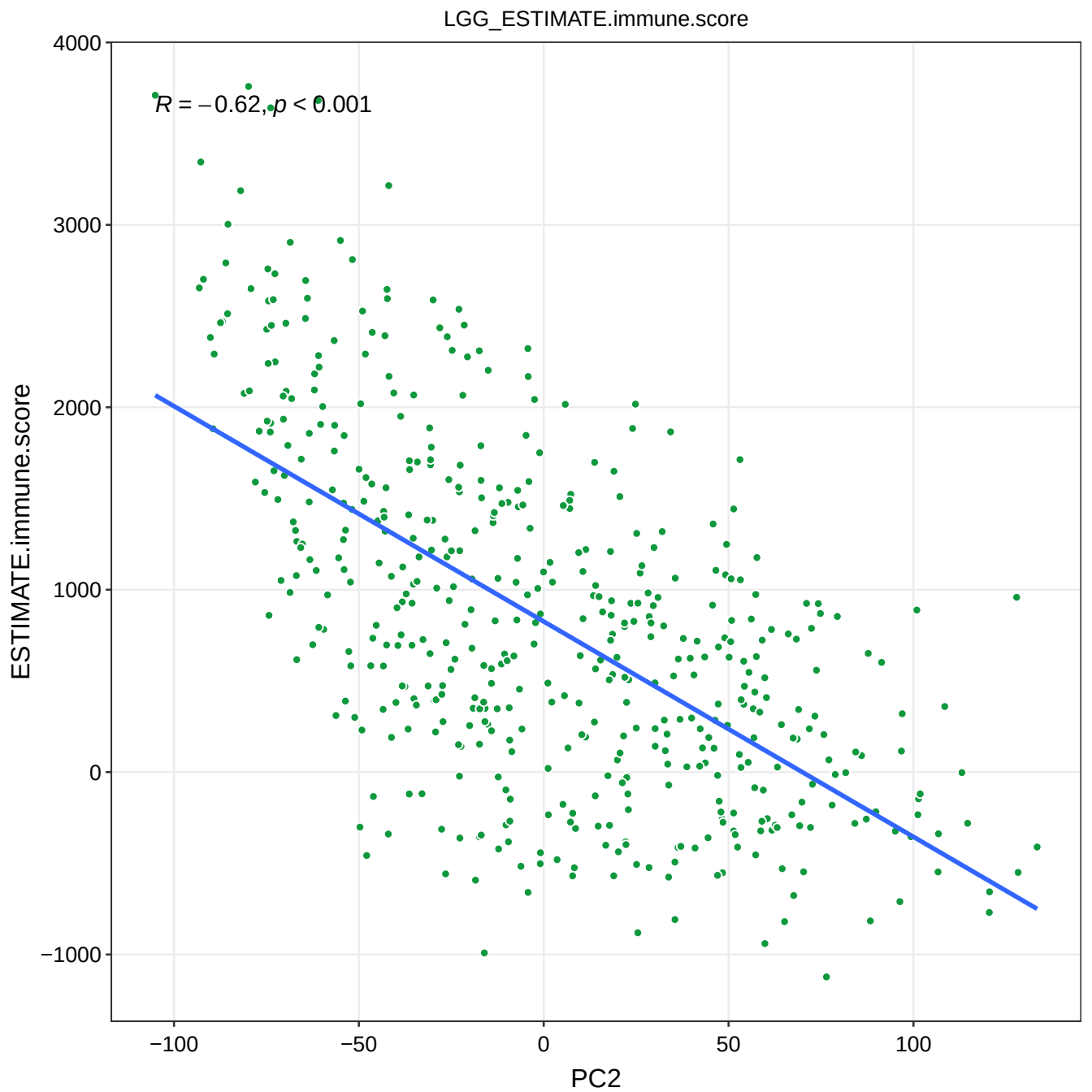

SARC_miRNA_cluster
cluster_2
cluster_1
<0.01
−50
0
50
100
150
PC2

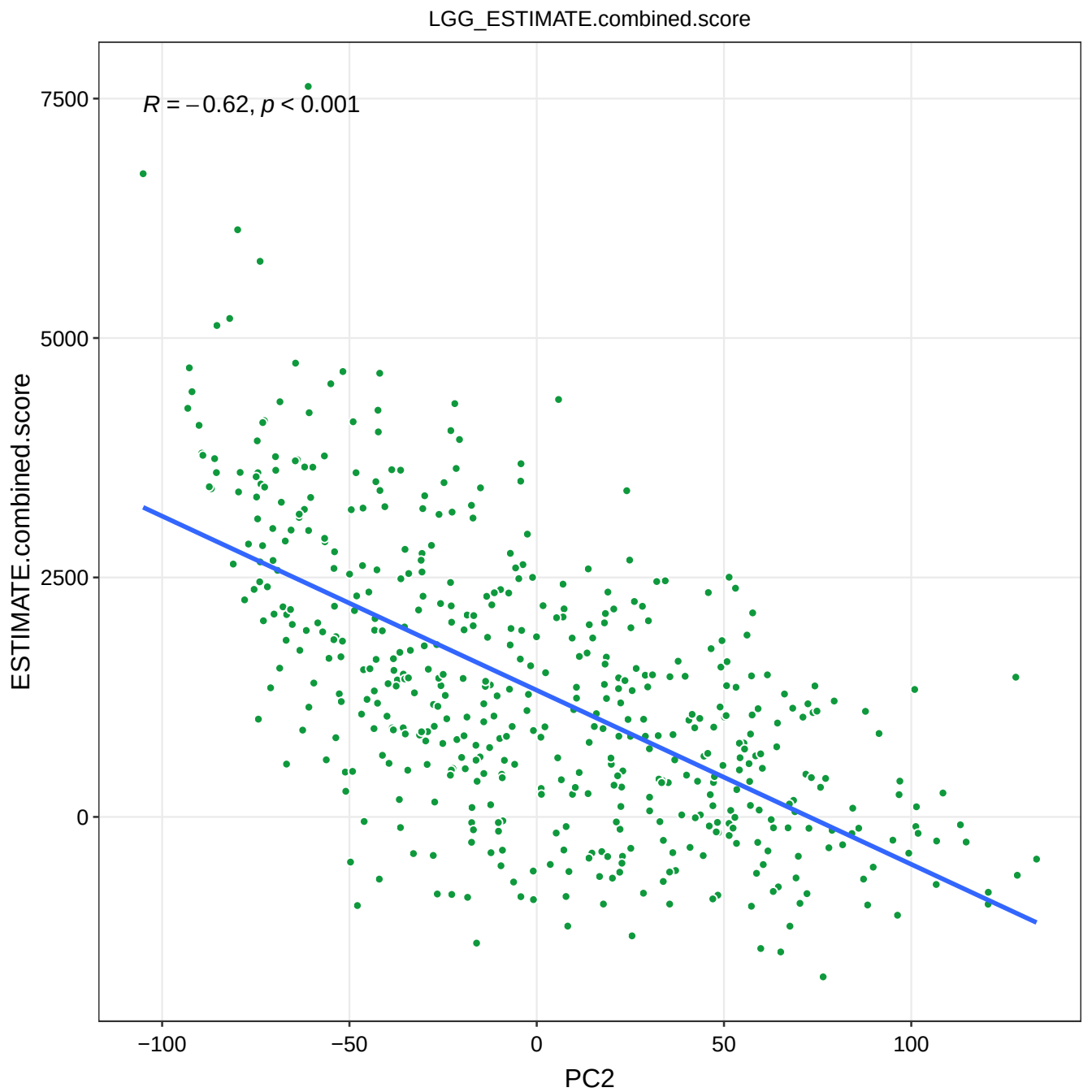

SARC_leukocyte_fraction
R = 0.78, p < 0.001
leukocyte_fraction
0.8
0.6
0.4
0.2
0.0
−50
0
50
100
150
PC2


SARC_purity
R = −0.66, p < 0.001
purity
PC2
1.0
0.8
0.6
0.4
0.2
−50
0
50
100
150


SARC_Cancer_DNA_fraction
R = −0.68, p < 0.001
Cancer_DNA_fraction
1.0
0.8
0.6
0.4
0.2
−50
0
50
100
150
PC2


LGG_ESTIMATE.stromal.score
R = −0.56, p < 0.001
ESTIMATE.stromal.score
4000
3000
2000
1000
0
−100
−50
0
50
100
PC2


LGG_ESTIMATE.immune.score
R = −0.62, p < 0.001
ESTIMATE.immune.score
PC2
4000
3000
2000
1000
0
−1000
−100
−50
0
50
100


LGG_ESTIMATE.combined.score
R = −0.62, p < 0.001
7500
5000
2500
0
ESTIMATE.combined.score
−100
−50
0
50
100
PC2