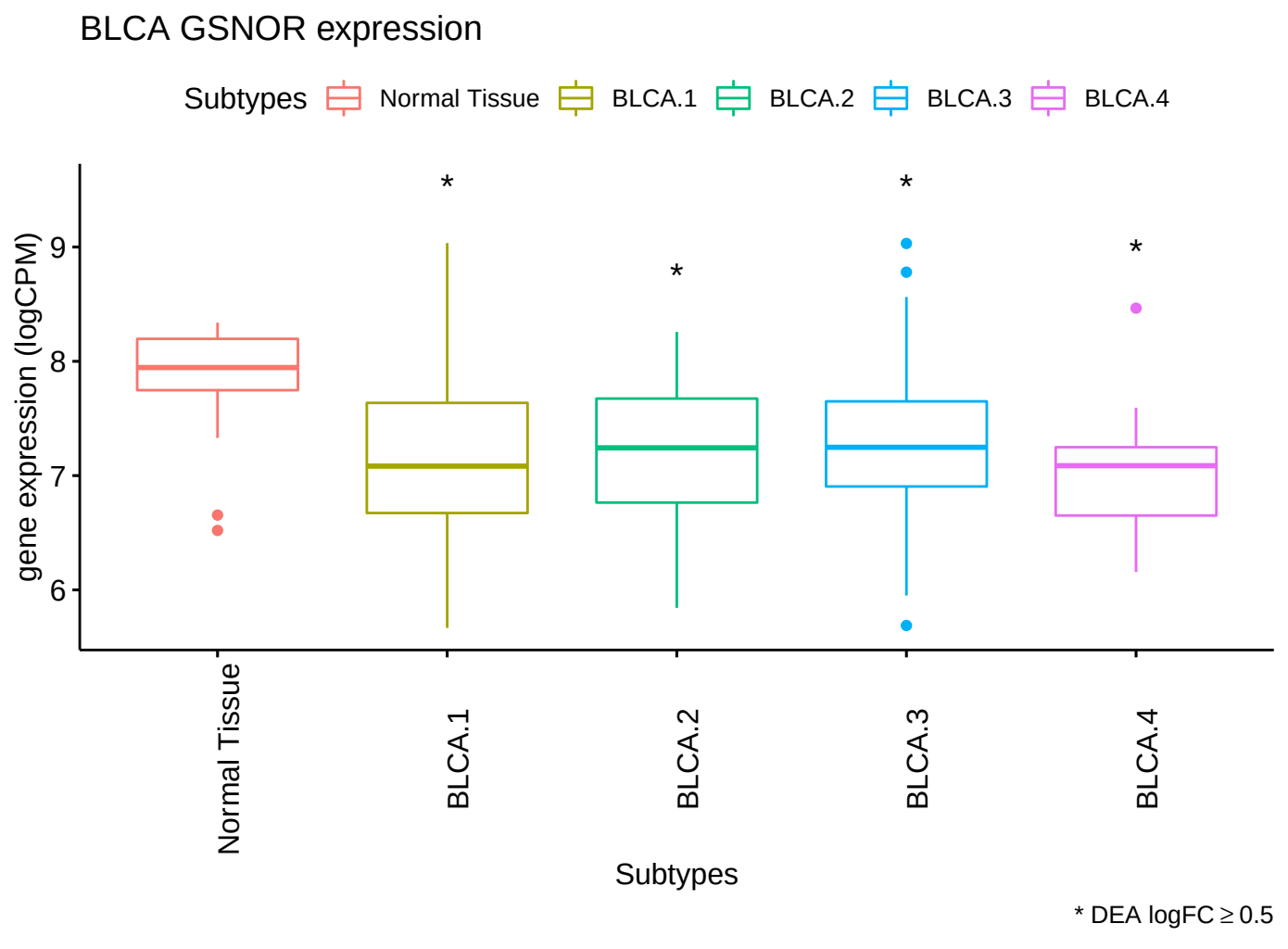
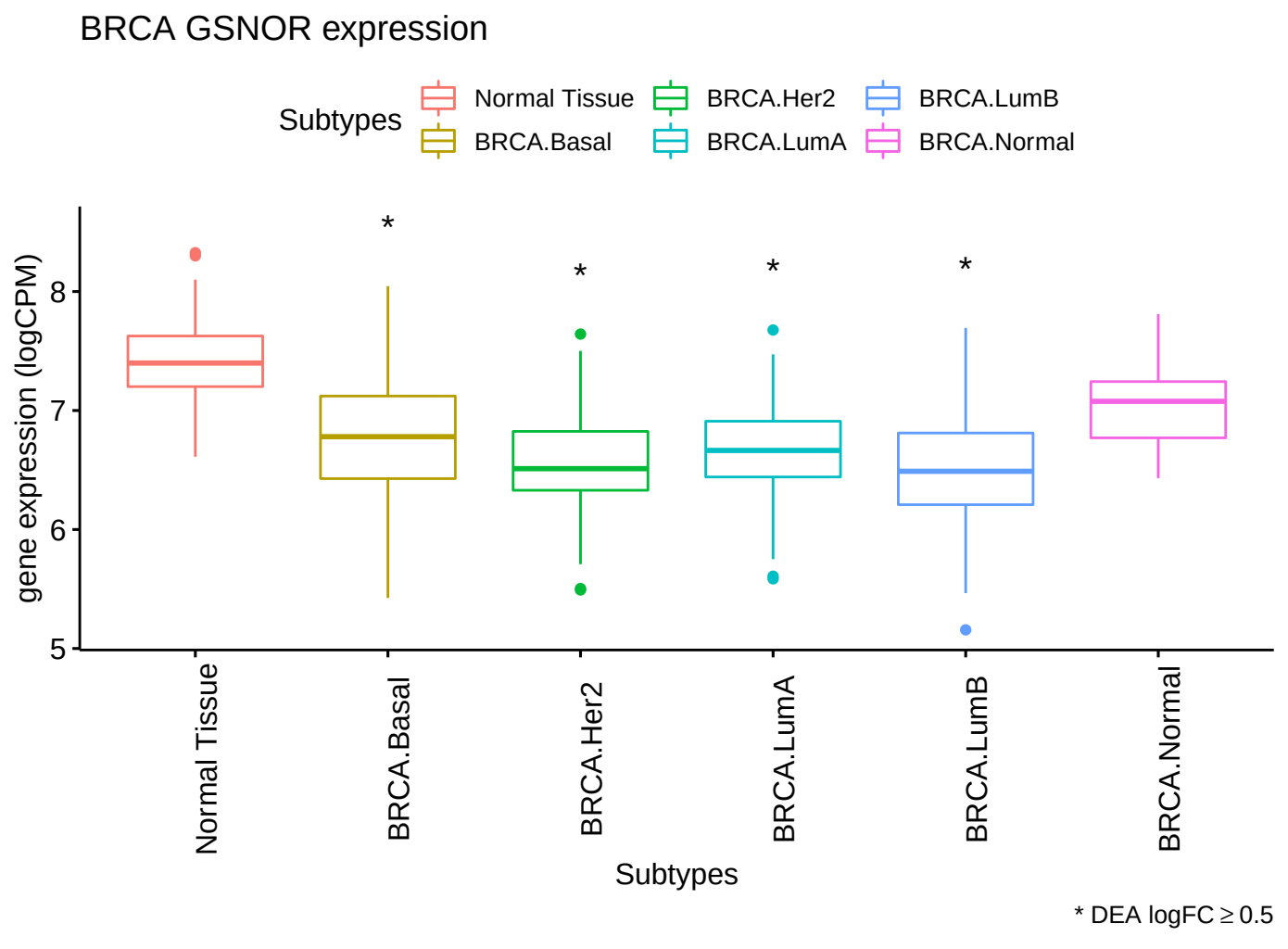
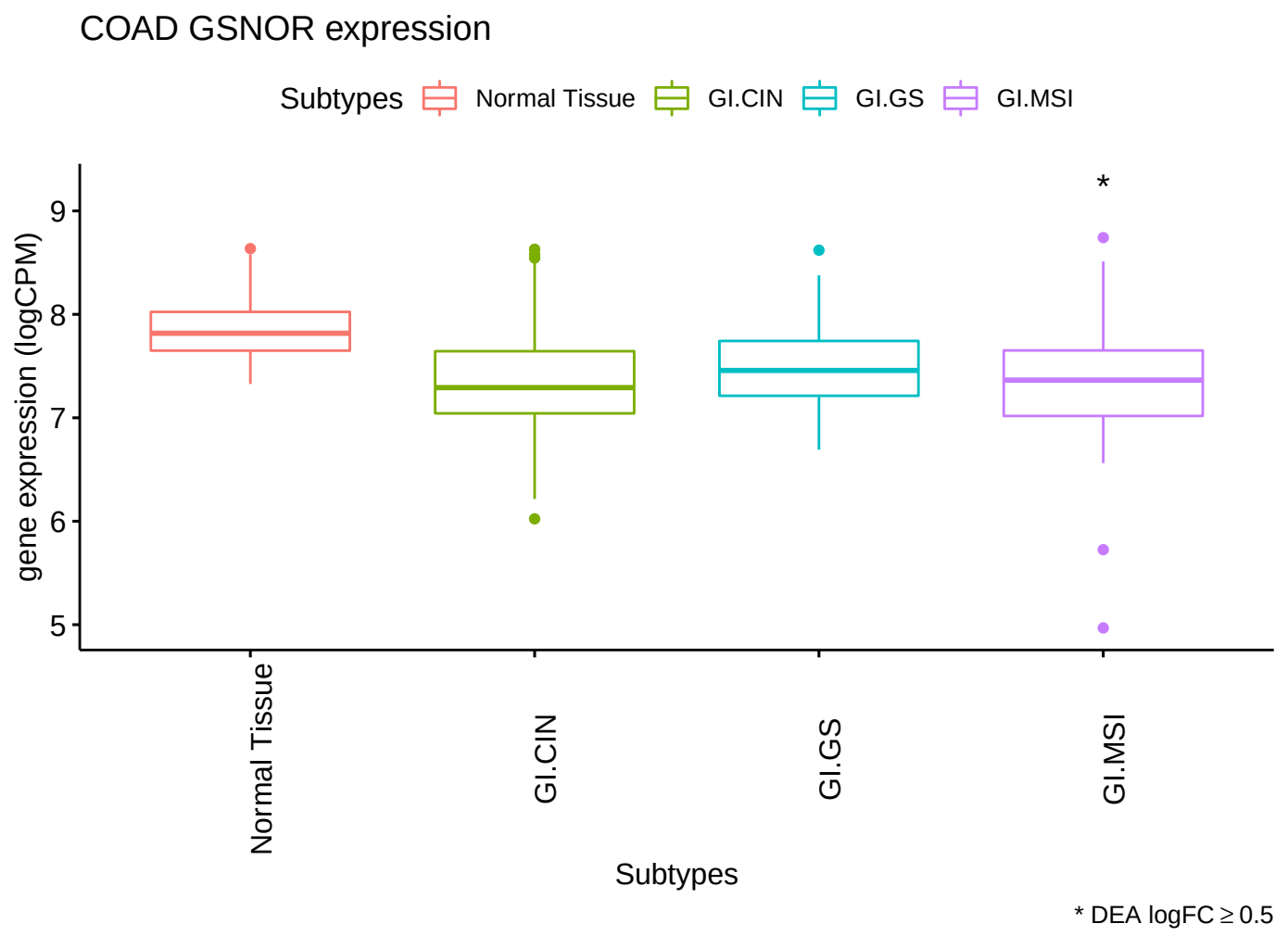
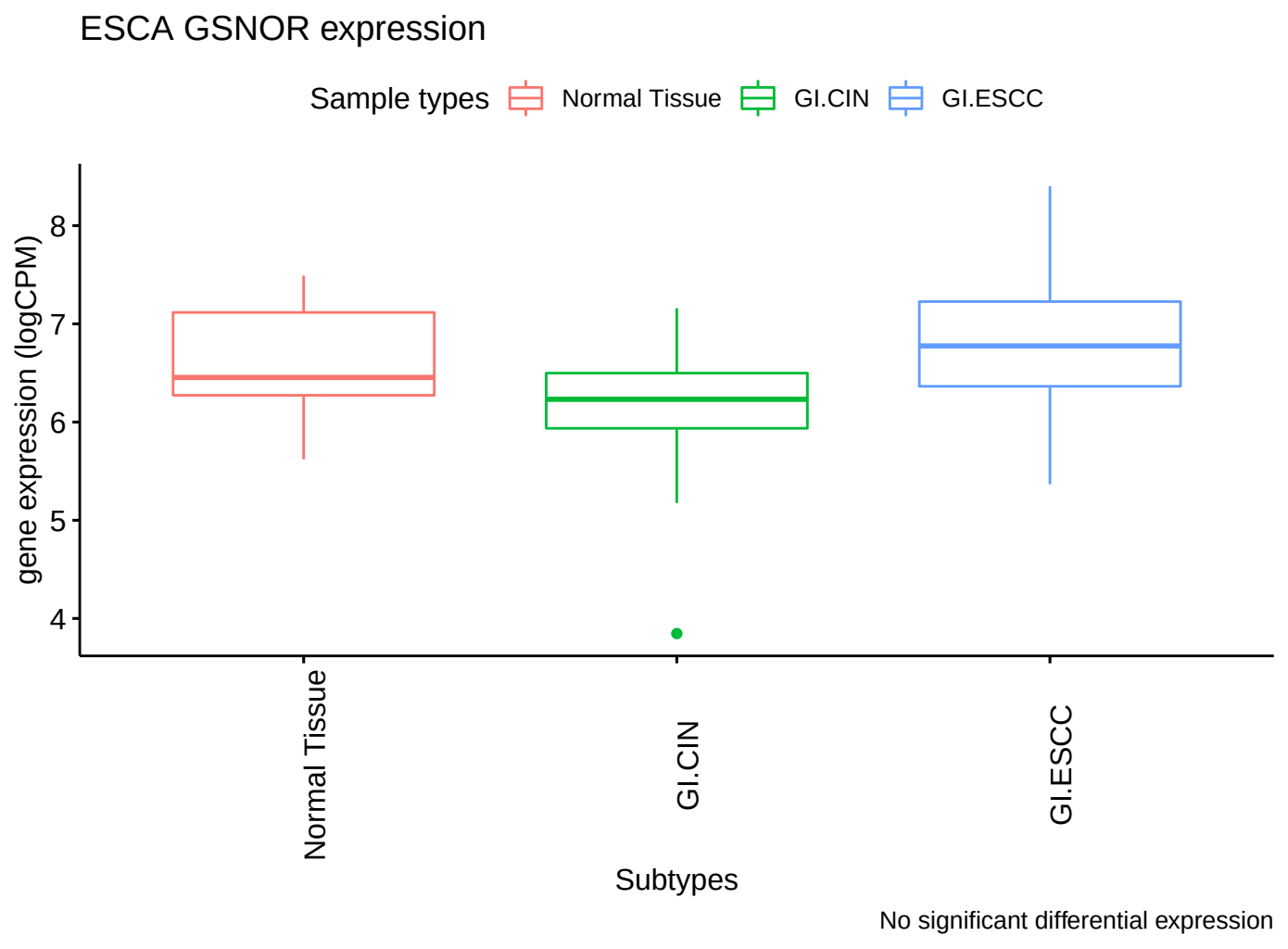
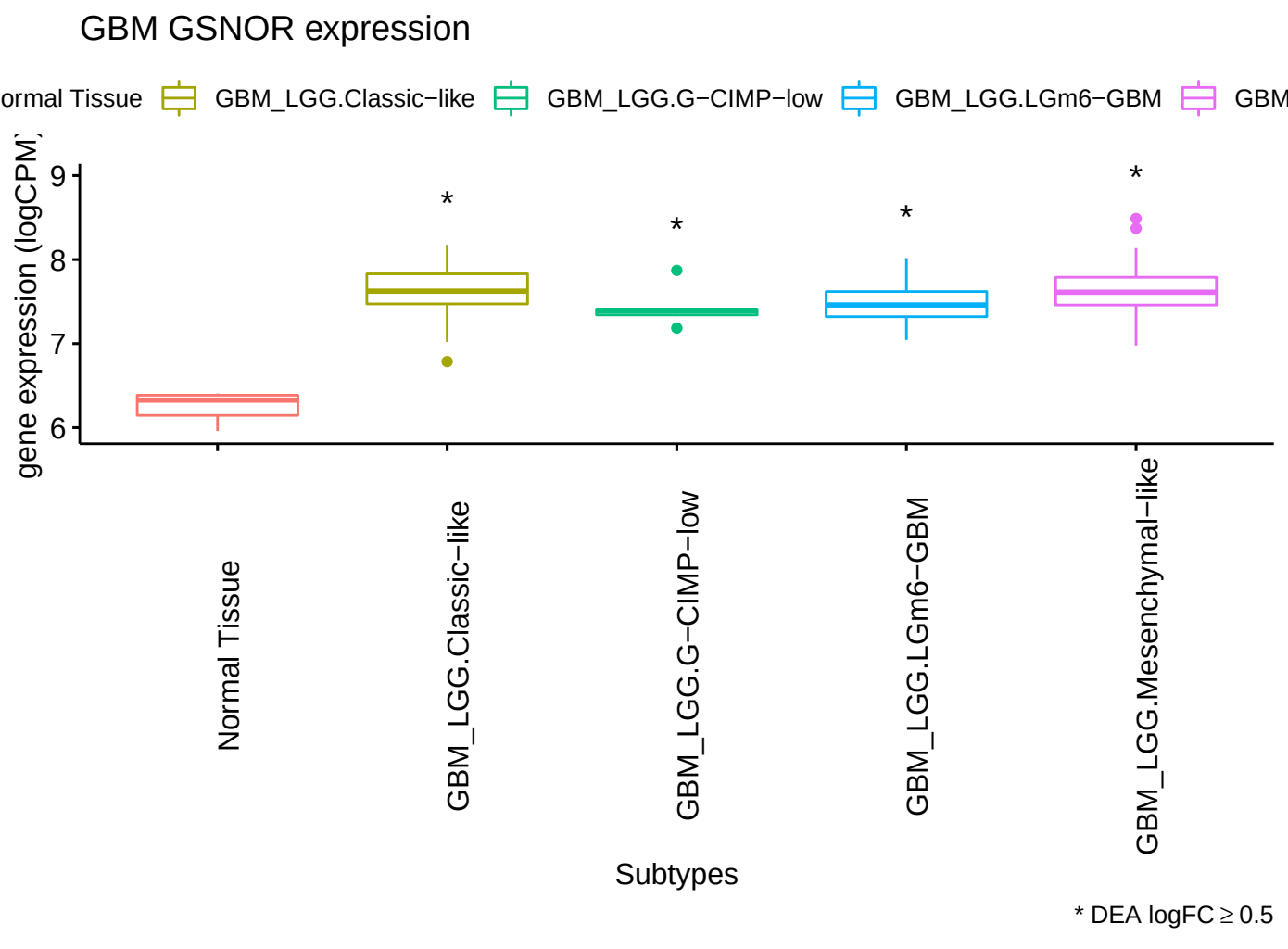
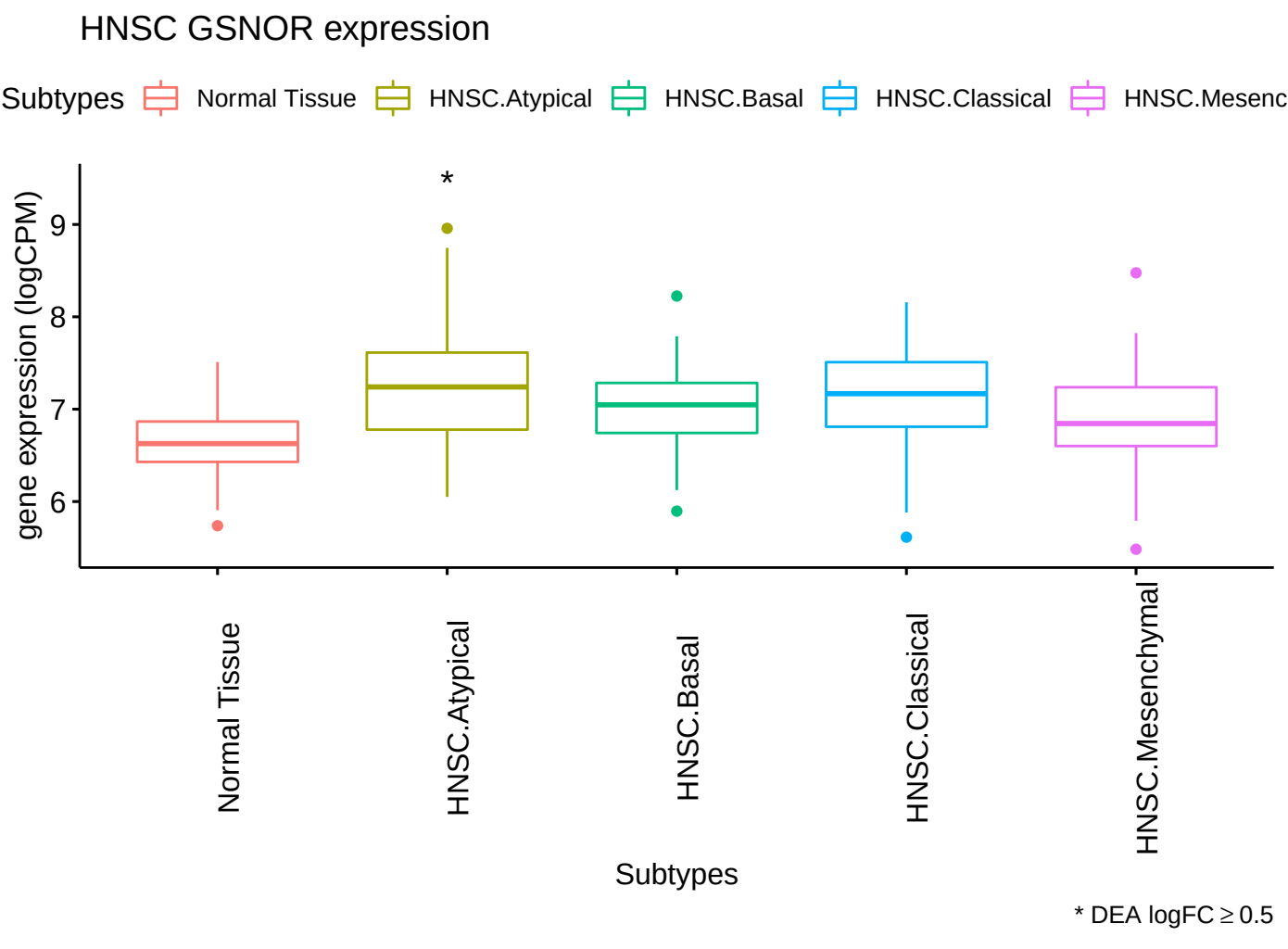

BLCA GSNOR expression
Subtypes
Normal Tissue
BLCA.1
BLCA.2
BLCA.3
BLCA.4
gene expression (logCPM)
9
8
7
6
*
*
*
*
Normal Tissue
BLCA.1
BLCA.2
BLCA.3
BLCA.4
Subtypes
* DEA logFC ≥ 0.5

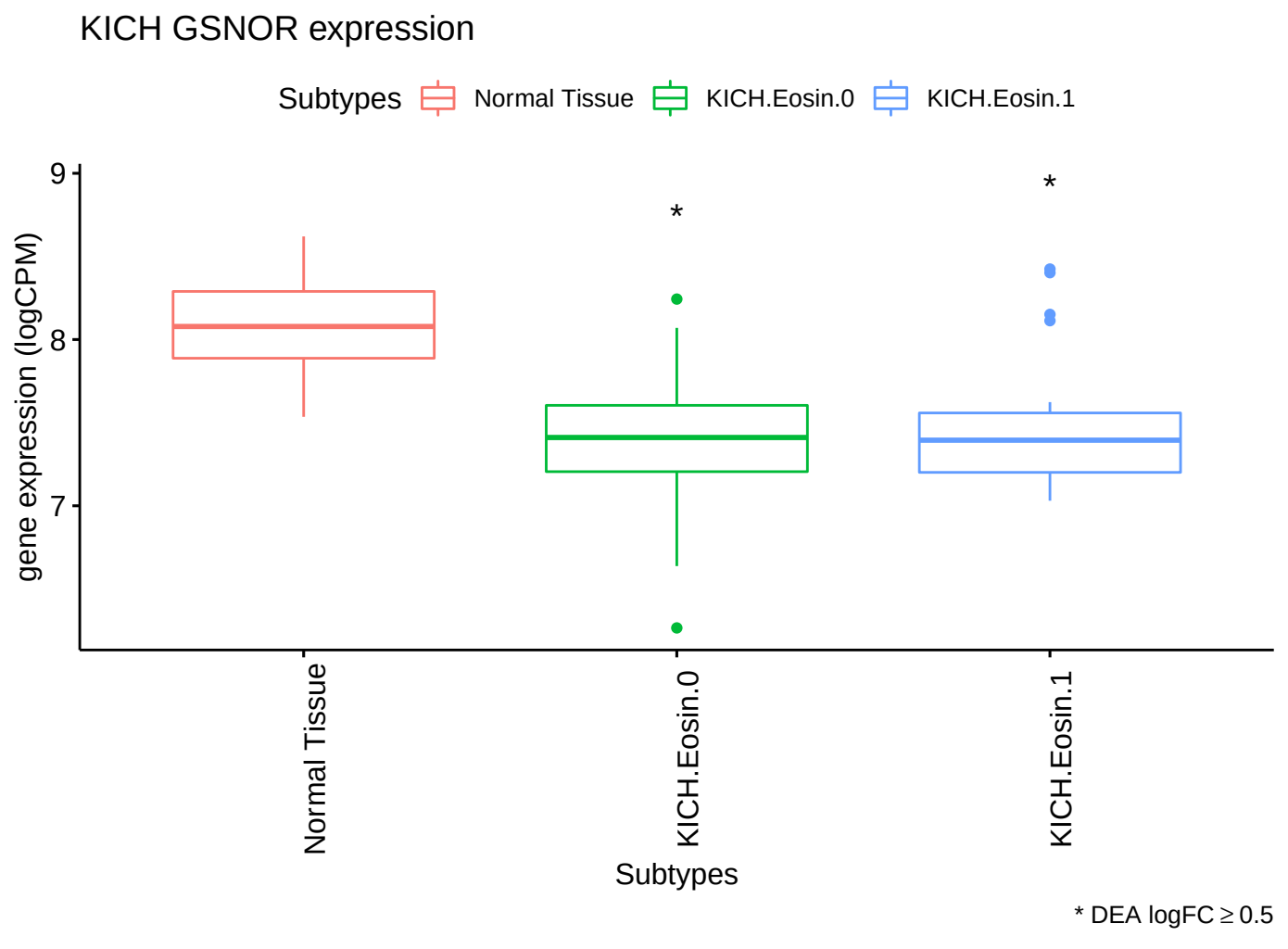

BRCA GSNOR expression
Subtypes
Normal Tissue
BRCA.Basal
BRCA.Her2
BRCA.LumA
BRCA.LumB
BRCA.Normal
gene expression (logCPM)
8
7
6
5
*
*
*
*
Normal Tissue
BRCA.Basal
BRCA.Her2
BRCA.LumA
BRCA.LumB
BRCA.Normal
Subtypes
* DEA logFC ≥ 0.5

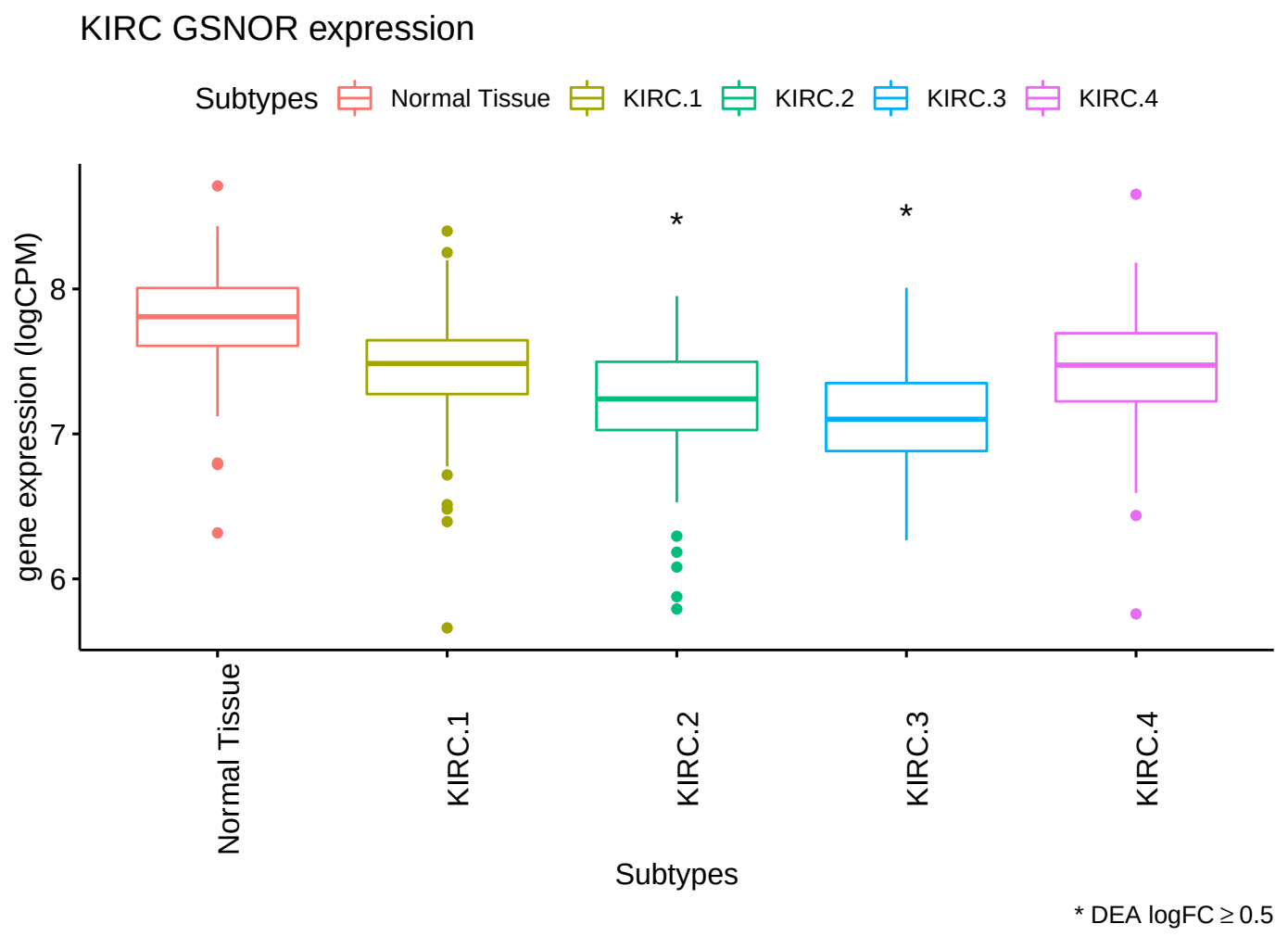

COAD GSNOR expression
Subtypes
Normal Tissue
GI.CIN
GI.GS
GI.MSI
gene expression (logCPM)
9
8
7
6
5
*
Normal Tissue
GI.CIN
GI.GS
GI.MSI
Subtypes
* DEA logFC ≥ 0.5

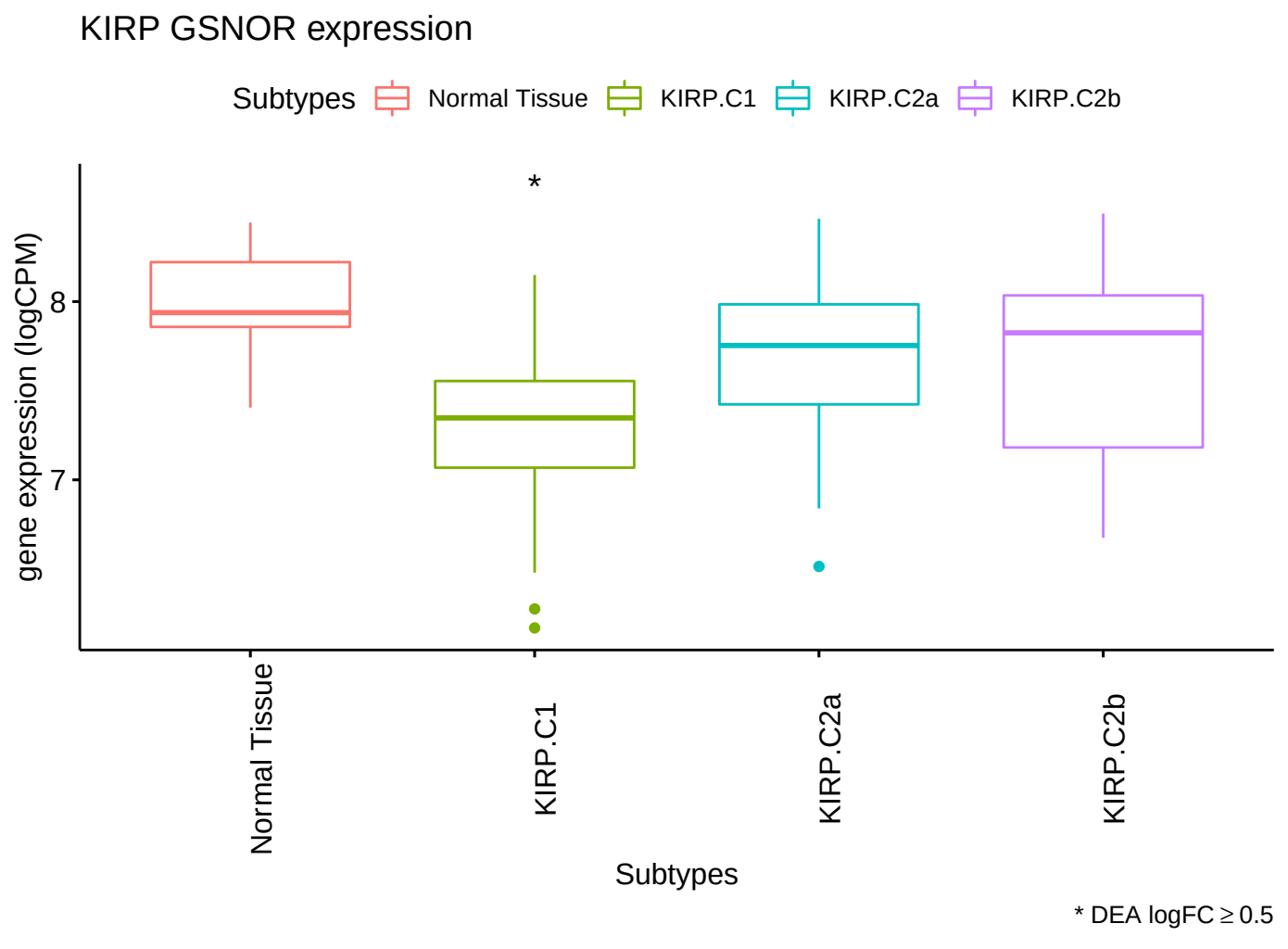

ESCA GSNOR expression
Sample types
Normal Tissue
GI.CIN
GI.ESCC
gene expression (logCPM)
8
7
6
5
4
Normal Tissue
GI.CIN
GI.ESCC
Subtypes
No significant differential expression

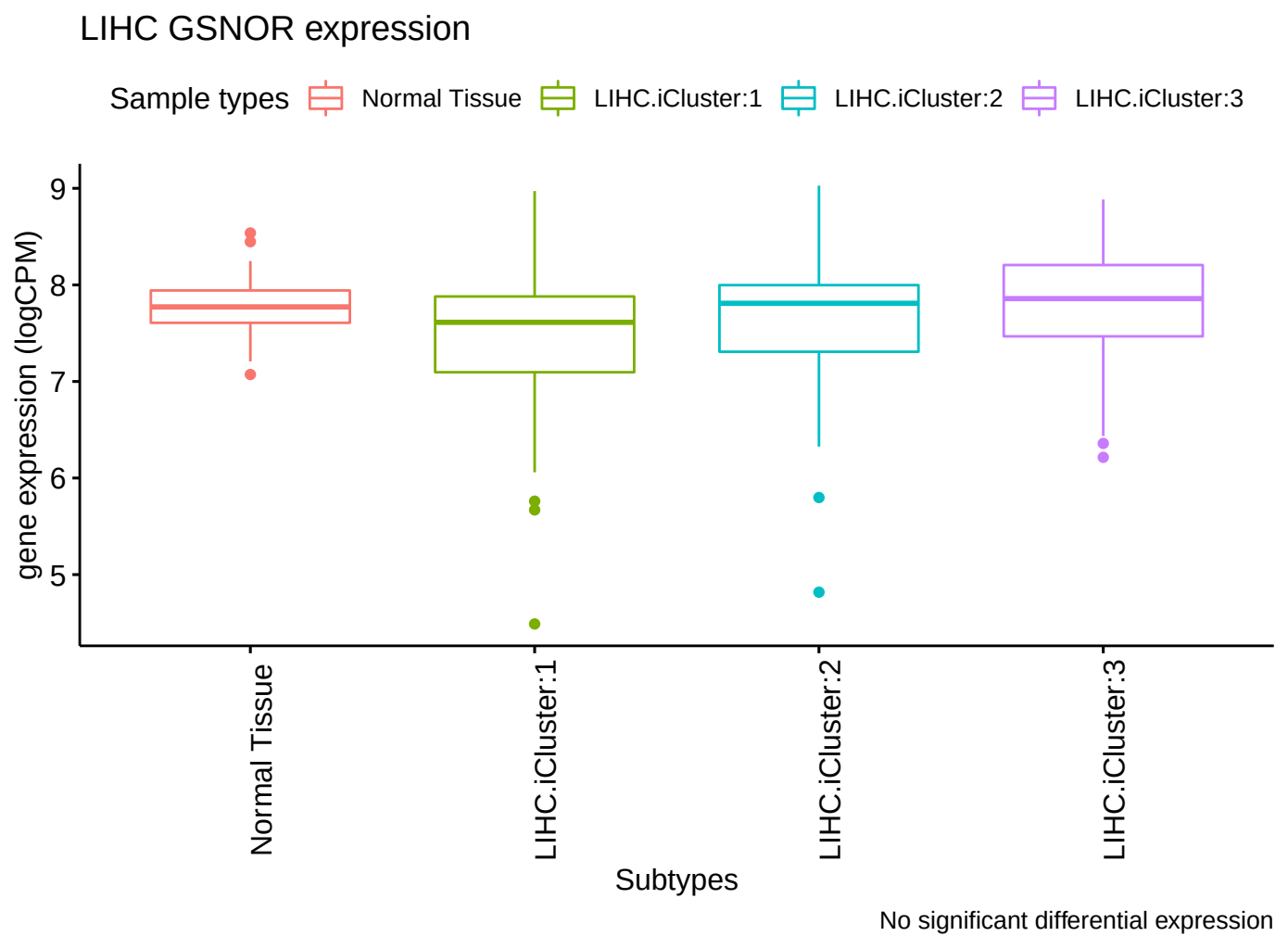

GBM GSNOR expression
ormal Tissue
GBM_LGG.Classic−like
GBM_LGG.G−CIMP−low
GBM_LGG.LGm6−GBM
GBM
gene expression (logCPM)
9
8
7
6
*
*
*
*
Normal Tissue
GBM_LGG.Classic−like
GBM_LGG.G−CIMP−low
GBM_LGG.LGm6−GBM
GBM_LGG.Mesenchymal−like
Subtypes
* DEA logFC ≥ 0.5

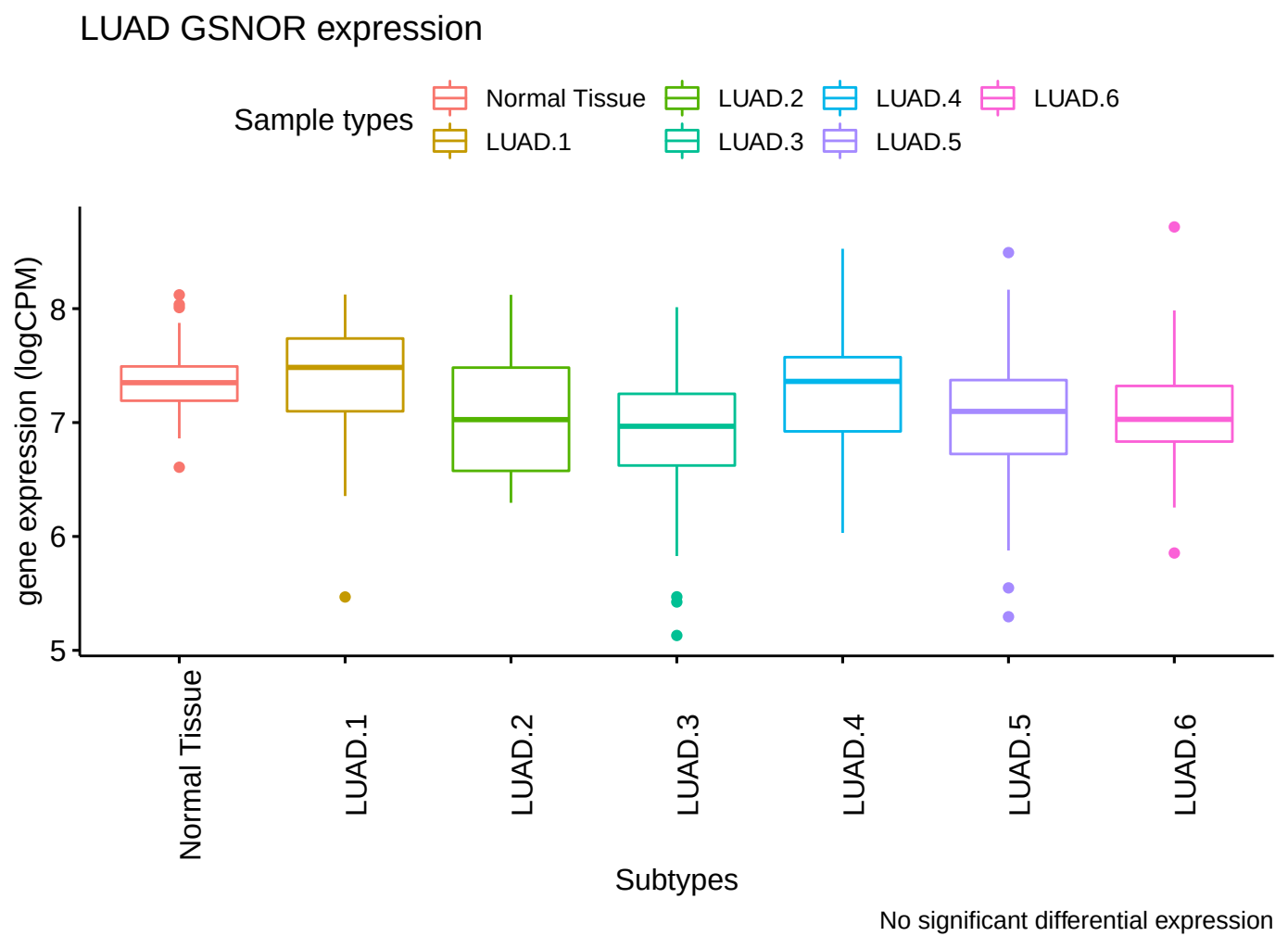

HNSC GSNOR expression
Subtypes
Normal Tissue
HNSC.Atypical
HNSC.Basal
HNSC.Classical
HNSC.Mesenc
gene expression (logCPM)
9
8
7
6
*
Normal Tissue
HNSC.Atypical
HNSC.Basal
HNSC.Classical
HNSC.Mesenchymal
Subtypes
* DEA logFC ≥ 0.5

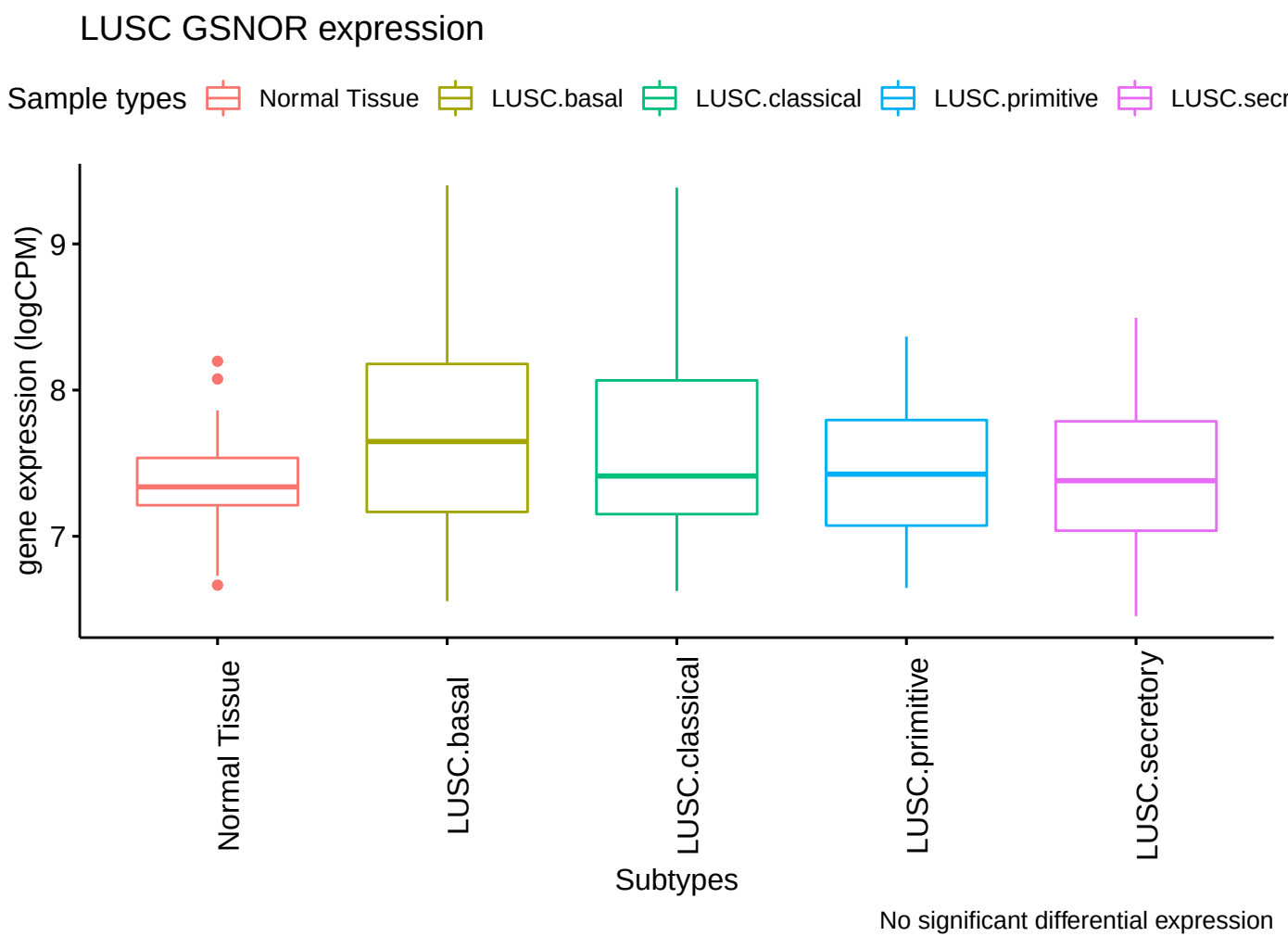

KICH GSNOR expression
Subtypes
Normal Tissue
KICH.Eosin.0
KICH.Eosin.1
gene expression (logCPM)
9
8
7
*
*
Normal Tissue
KICH.Eosin.0
KICH.Eosin.1
Subtypes
* DEA logFC ≥ 0.5

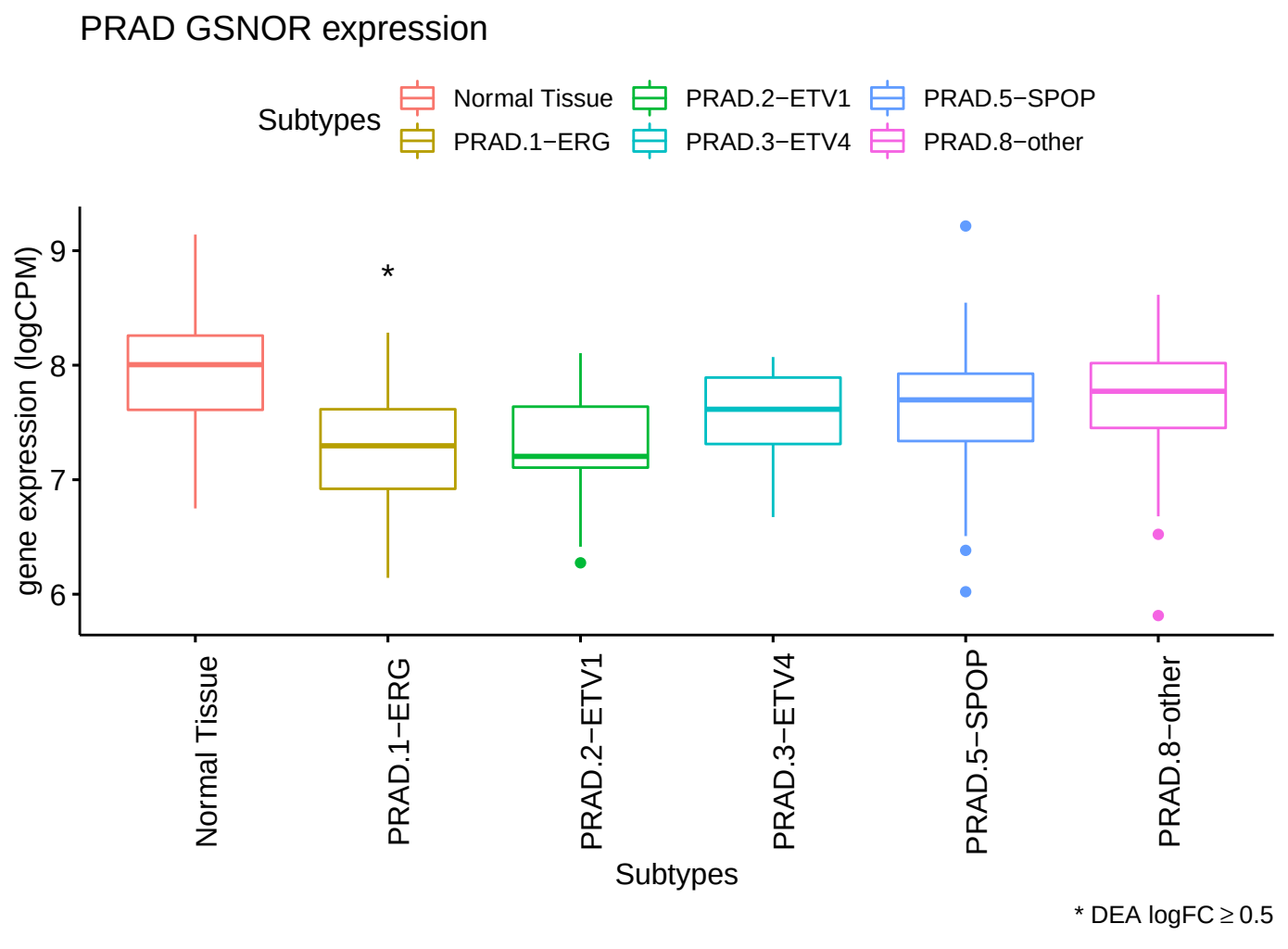

KIRC GSNOR expression
Subtypes
Normal Tissue
KIRC.1
KIRC.2
KIRC.3
KIRC.4
gene expression (logCPM)
8
7
6
*
*
Normal Tissue
KIRC.1
KIRC.2
KIRC.3
KIRC.4
Subtypes
* DEA logFC ≥ 0.5

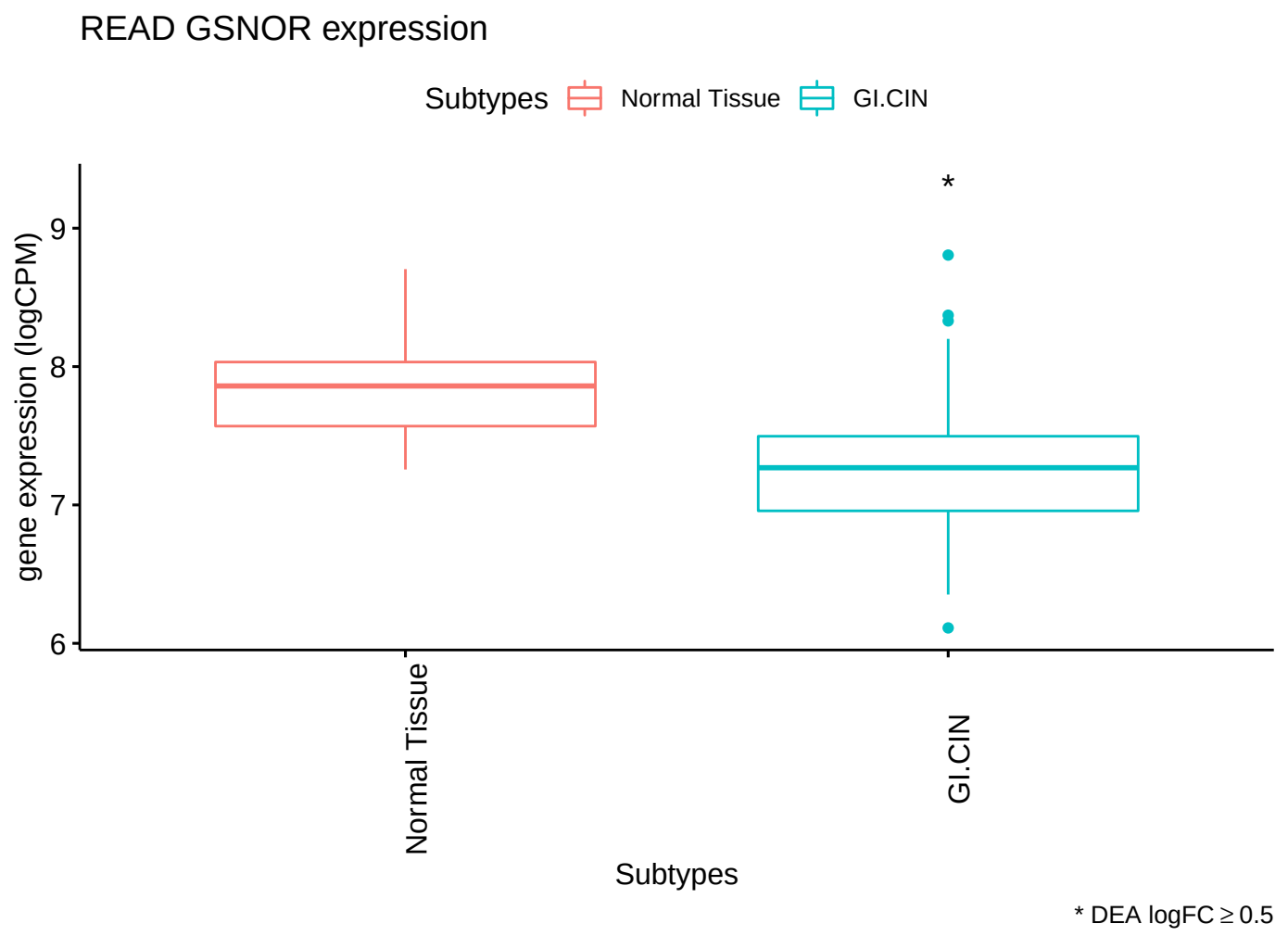

KIRP GSNOR expression
Subtypes
Normal Tissue
KIRP.C1
KIRP.C2a
KIRP.C2b
gene expression (logCPM)
8
7
*
Normal Tissue
KIRP.C1
KIRP.C2a
KIRP.C2b
Subtypes
* DEA logFC ≥ 0.5

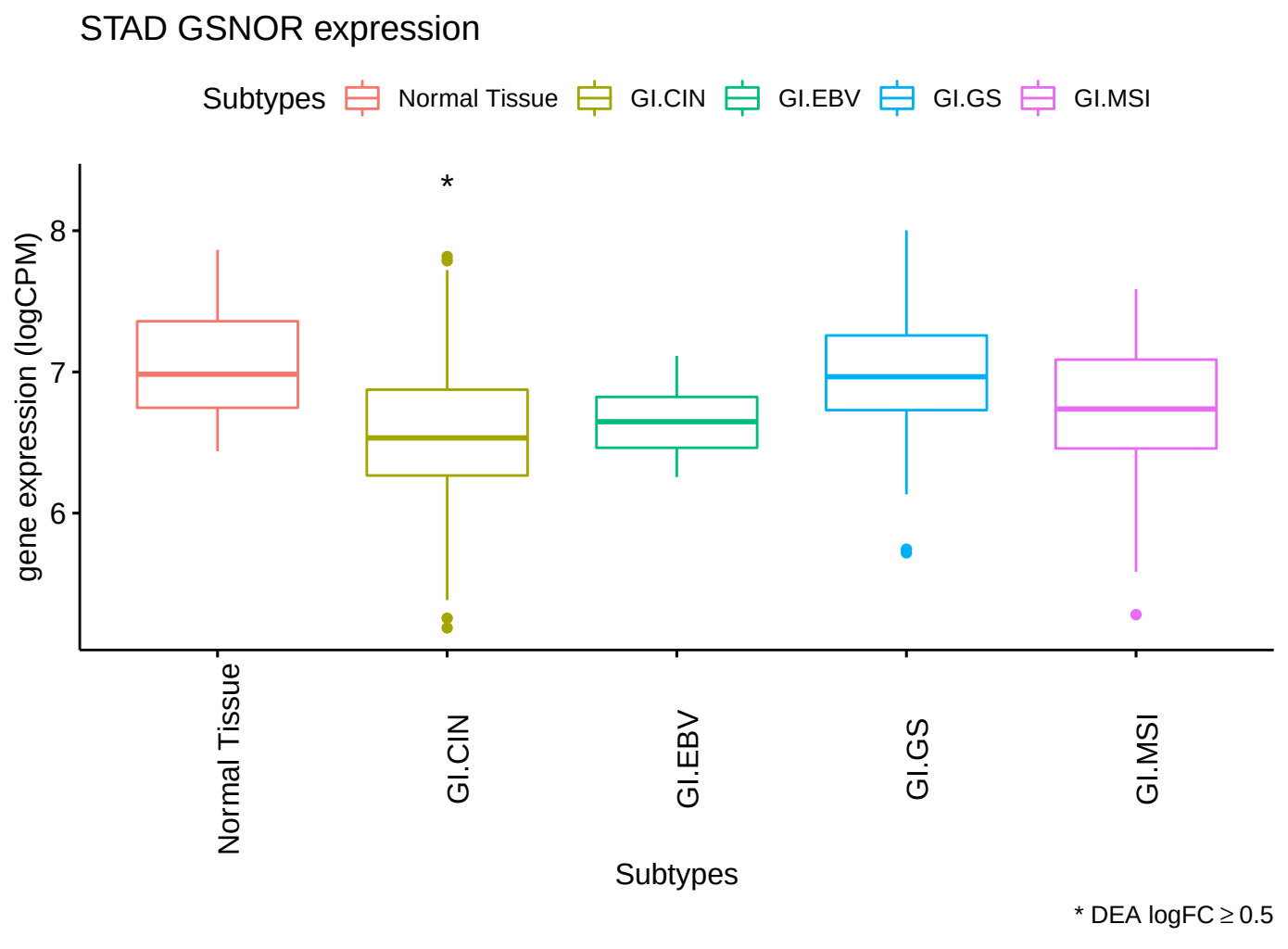

LIHC GSNOR expression
Sample types
Normal Tissue
LIHC.iCluster:1
LIHC.iCluster:2
LIHC.iCluster:3
gene expression (logCPM)
9
8
7
6
5
Normal Tissue
LIHC.iCluster:1
LIHC.iCluster:2
LIHC.iCluster:3
Subtypes
No significant differential expression

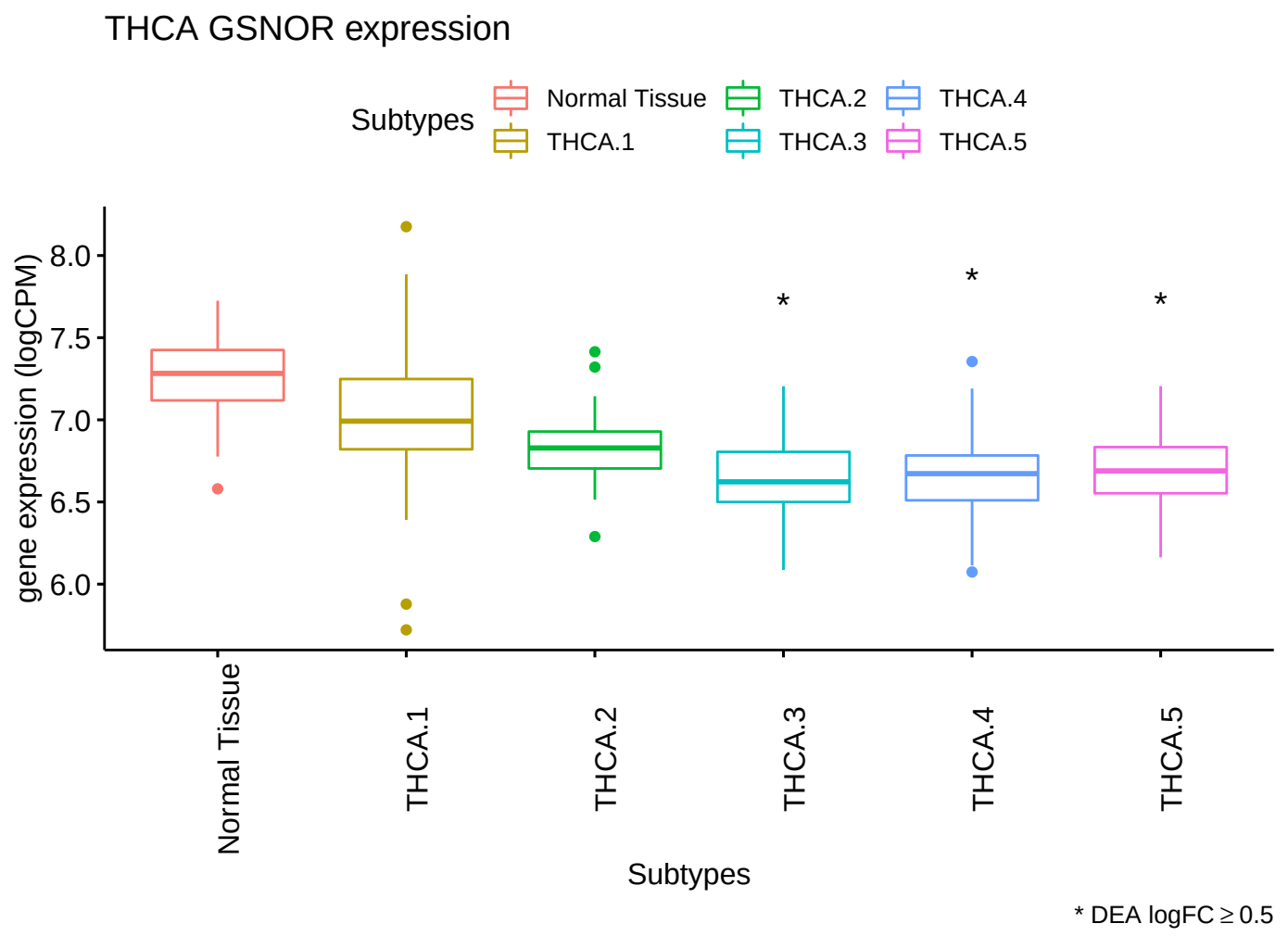

LUAD GSNOR expression
Sample types
Normal Tissue
LUAD.1
LUAD.2
LUAD.3
LUAD.4
LUAD.5
LUAD.6
gene expression (logCPM)
8
7
6
5
Normal Tissue
LUAD.1
LUAD.2
LUAD.3
LUAD.4
LUAD.5
LUAD.6
Subtypes
No significant differential expression

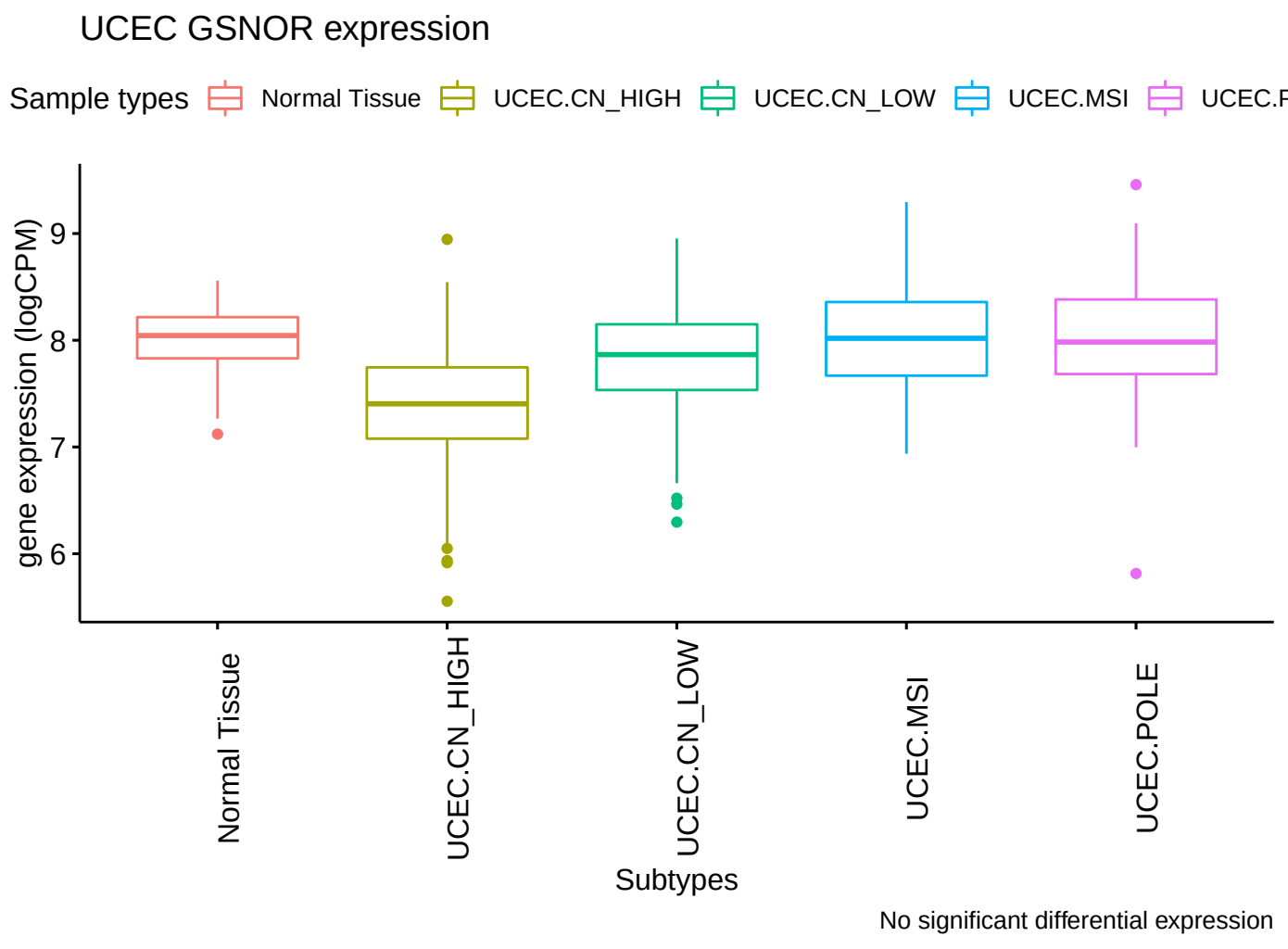

LUSC GSNOR expression
Sample types
Normal Tissue
LUSC.basal
LUSC.classical
LUSC.primitive
LUSC.secr
gene expression (logCPM)
9
8
7
Normal Tissue
LUSC.basal
LUSC.classical
LUSC.primitive
LUSC.secretory
Subtypes
No significant differential expression


PRAD GSNOR expression
Subtypes
Normal Tissue
PRAD.1−ERG
PRAD.2−ETV1
PRAD.3−ETV4
PRAD.5−SPOP
PRAD.8−other
gene expression (logCPM)
9
8
7
6
*
Normal Tissue
PRAD.1−ERG
PRAD.2−ETV1
PRAD.3−ETV4
PRAD.5−SPOP
PRAD.8−other
Subtypes
* DEA logFC ≥ 0.5


READ GSNOR expression
Subtypes
Normal Tissue
GI.CIN
gene expression (logCPM)
9
8
7
6
*
Normal Tissue
GI.CIN
Subtypes
* DEA logFC ≥ 0.5


STAD GSNOR expression
Subtypes
Normal Tissue
GI.CIN
GI.EBV
GI.GS
GI.MSI
gene expression (logCPM)
8
7
6
*
Normal Tissue
GI.CIN
GI.EBV
GI.GS
GI.MSI
Subtypes
* DEA logFC ≥ 0.5


THCA GSNOR expression
Subtypes
Normal Tissue
THCA.1
THCA.2
THCA.3
THCA.4
THCA.5
gene expression (logCPM)
8.0
7.5
7.0
6.5
6.0
*
*
*
Normal Tissue
THCA.1
THCA.2
THCA.3
THCA.4
THCA.5
Subtypes
* DEA logFC ≥ 0.5


UCEC GSNOR expression
Sample types
Normal Tissue
UCEC.CN_HIGH
UCEC.CN_LOW
UCEC.MSI
UCEC.P
gene expression (logCPM)
9
8
7
6
Normal Tissue
UCEC.CN_HIGH
UCEC.CN_LOW
UCEC.MSI
UCEC.POLE
Subtypes
No significant differential expression