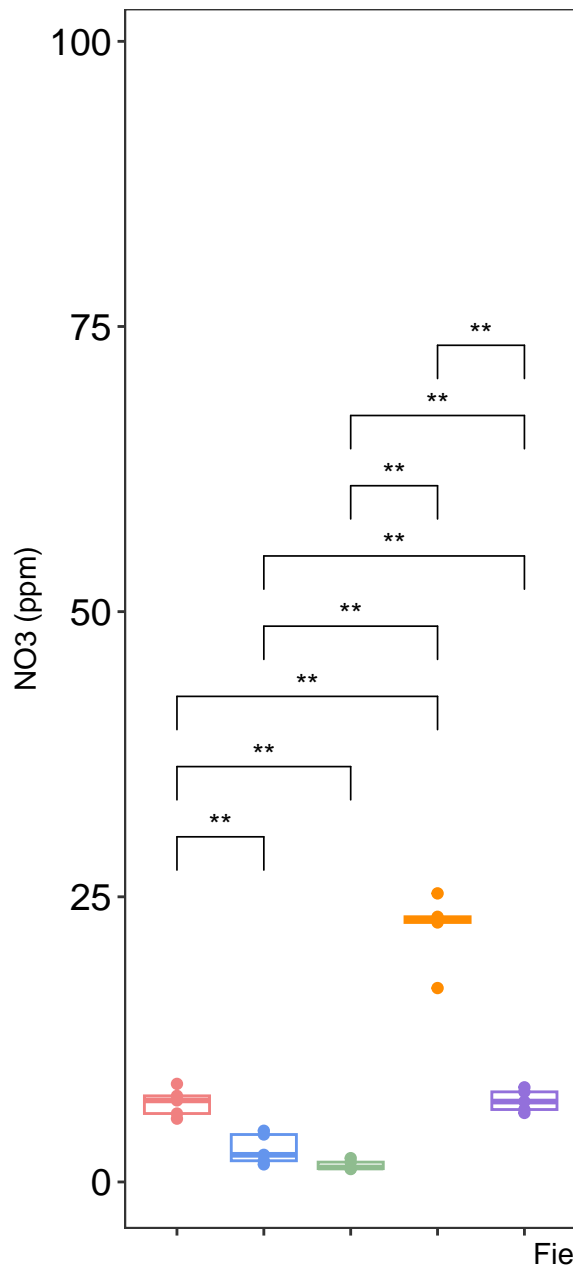
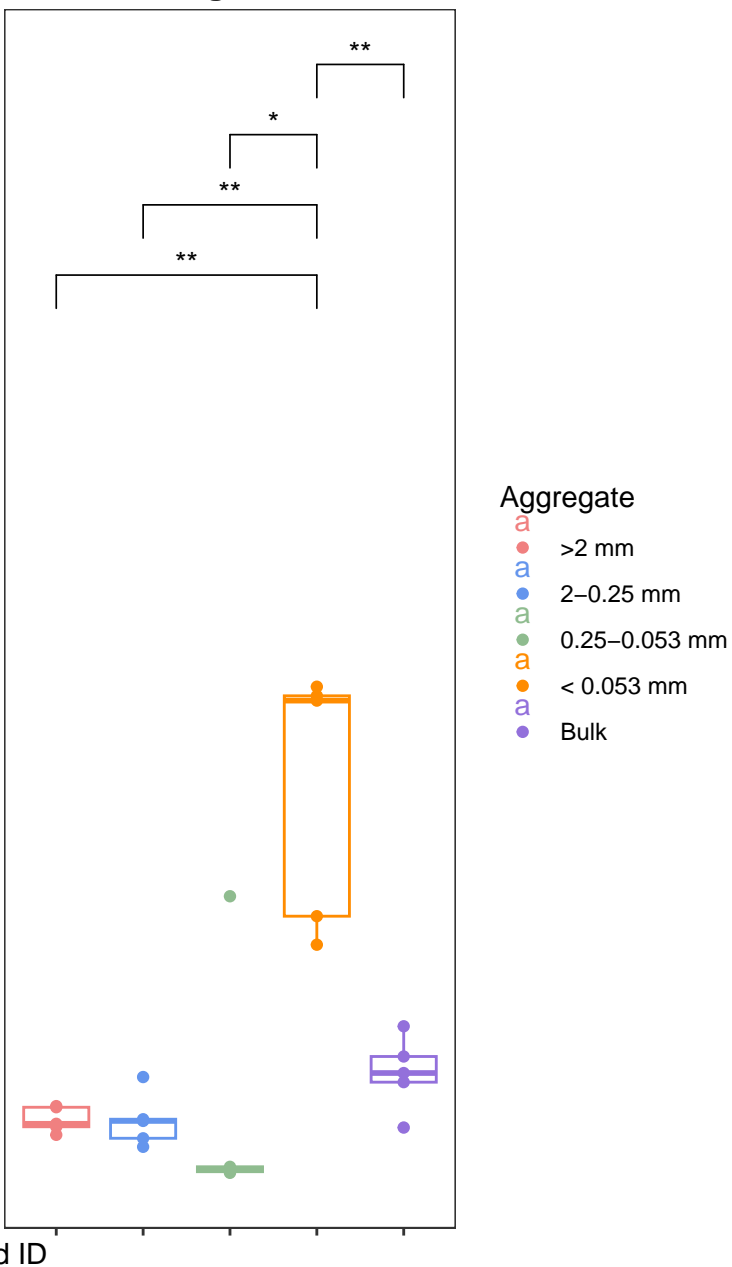


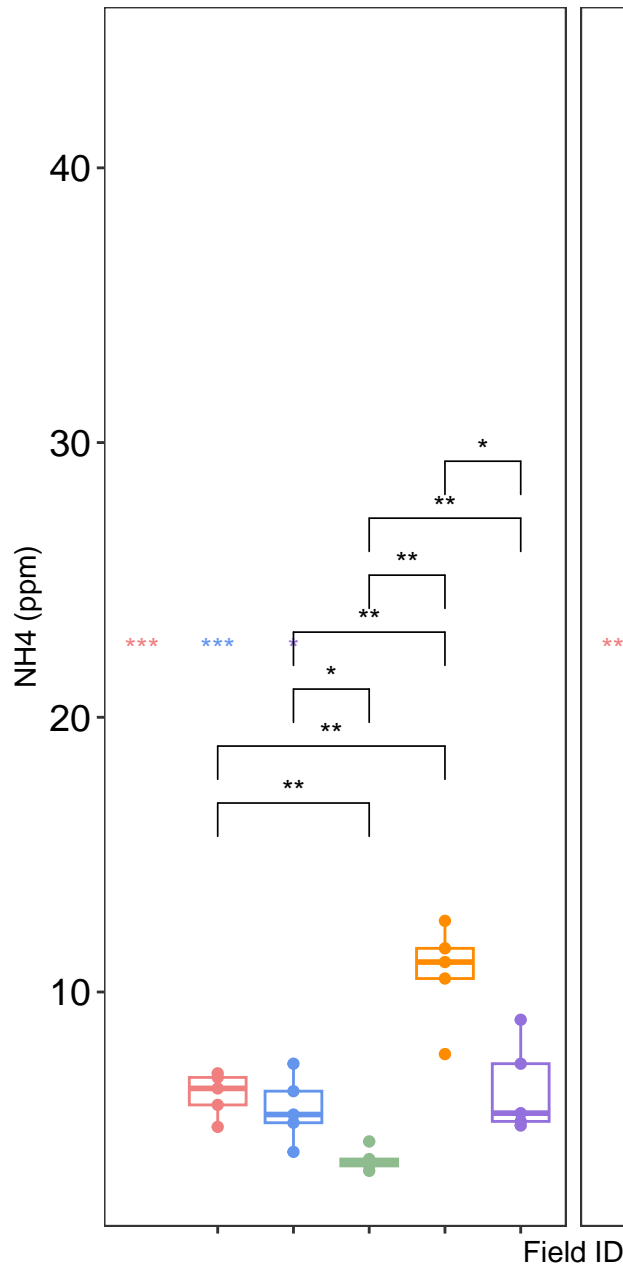
## Conventional



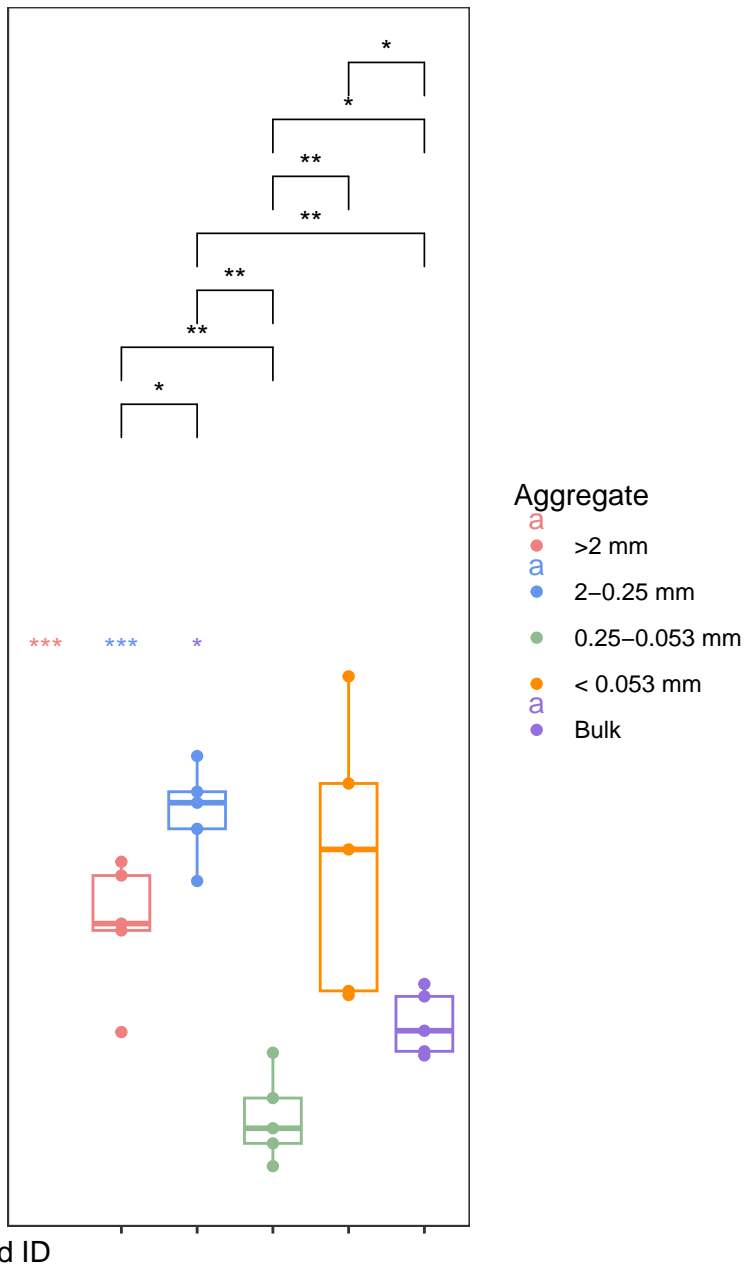
## Organic



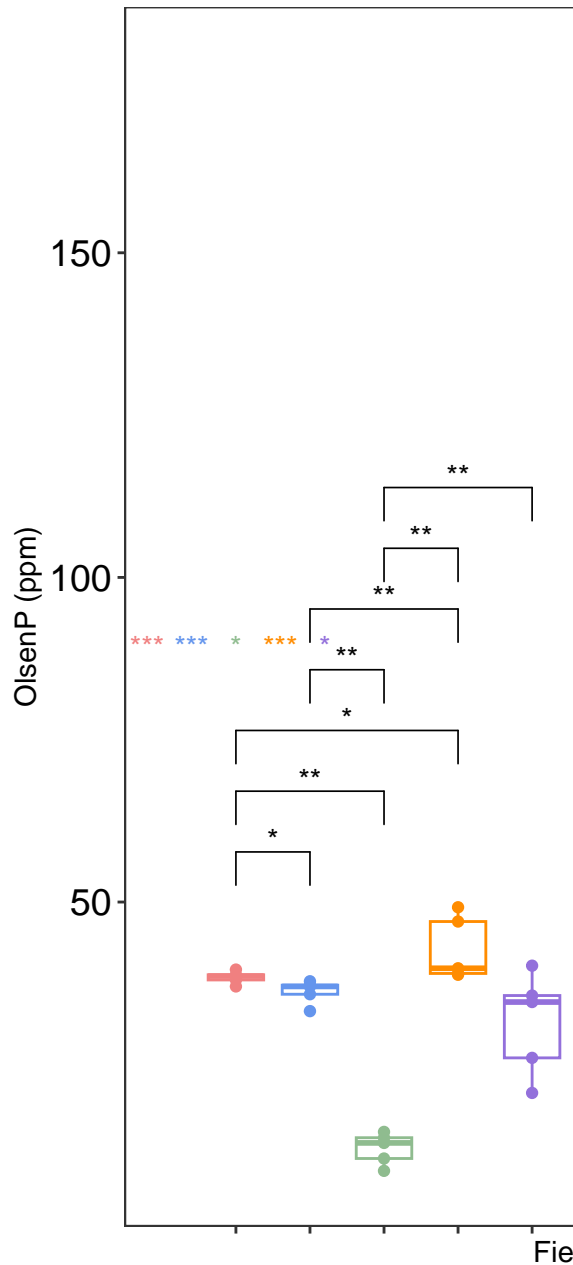
## Conventional



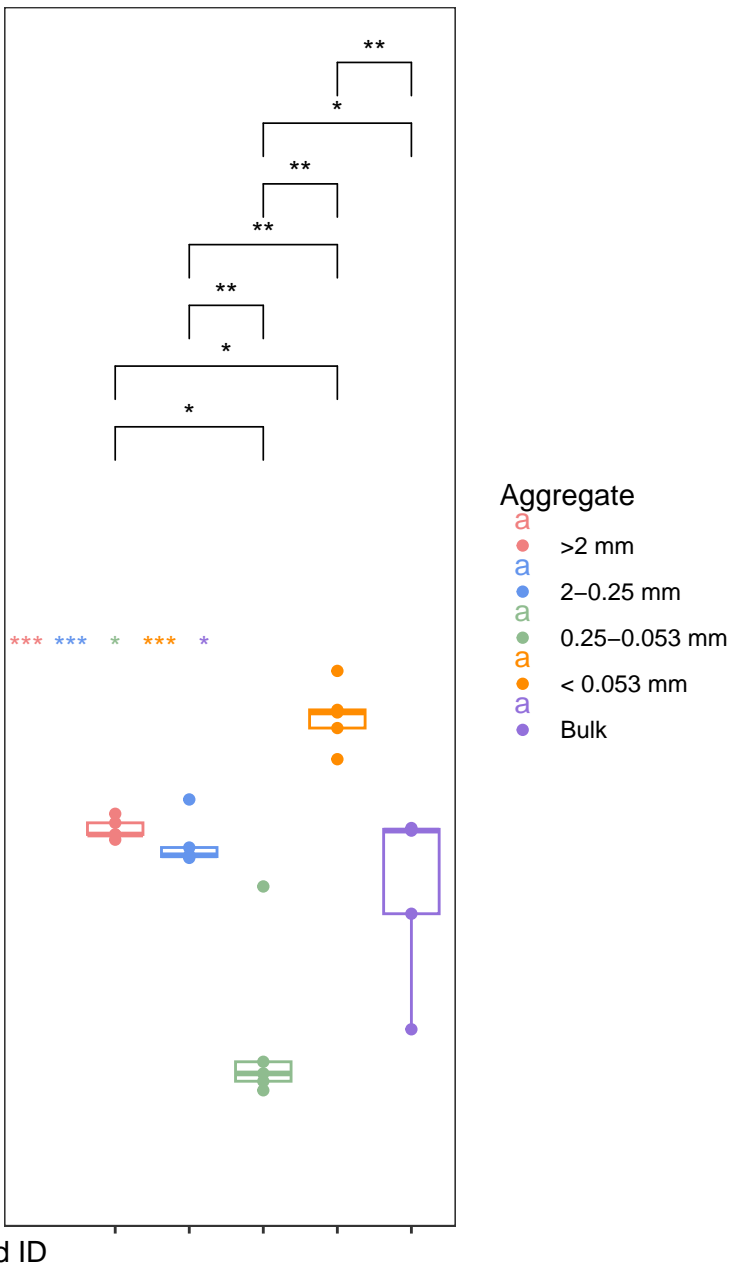
## Organic



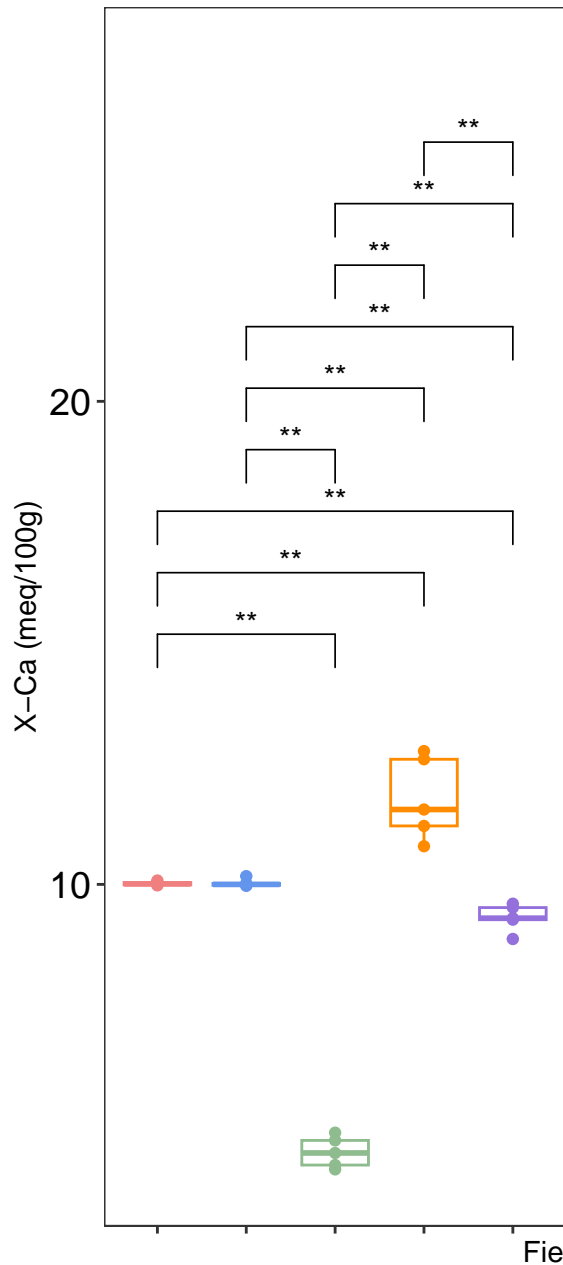
## Conventional



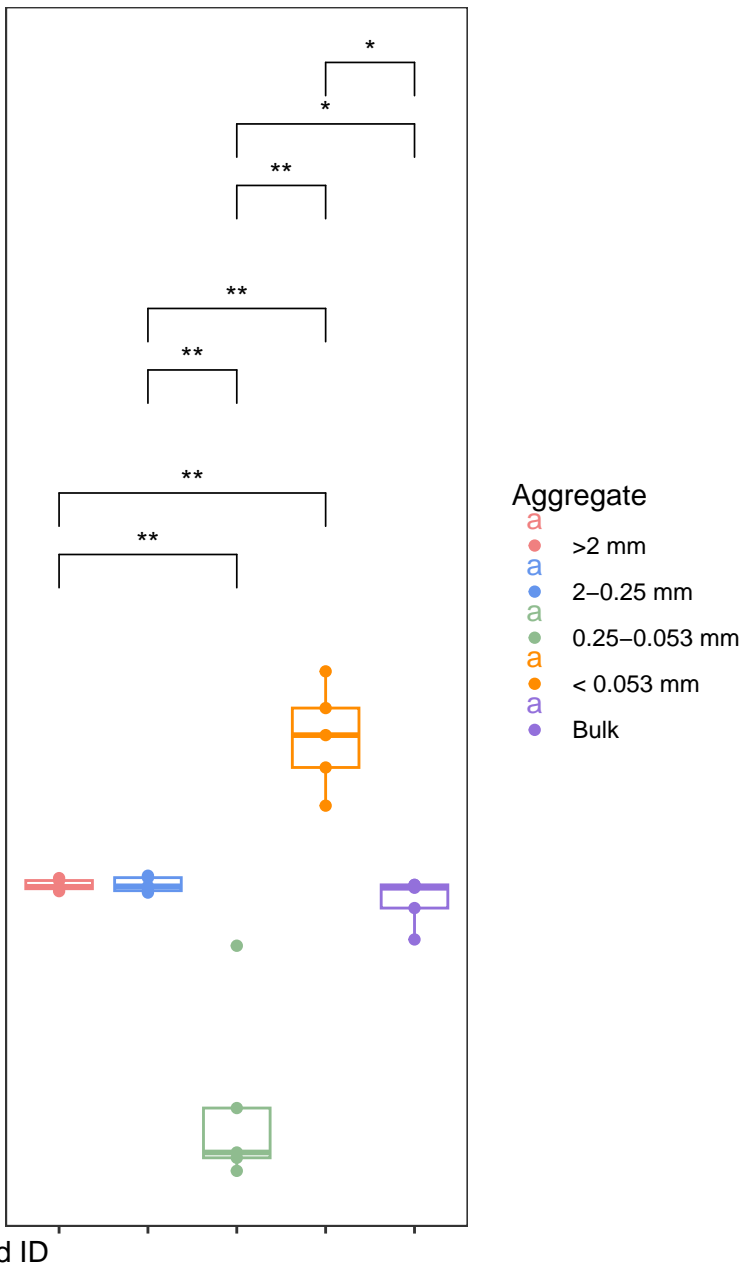
## Organic



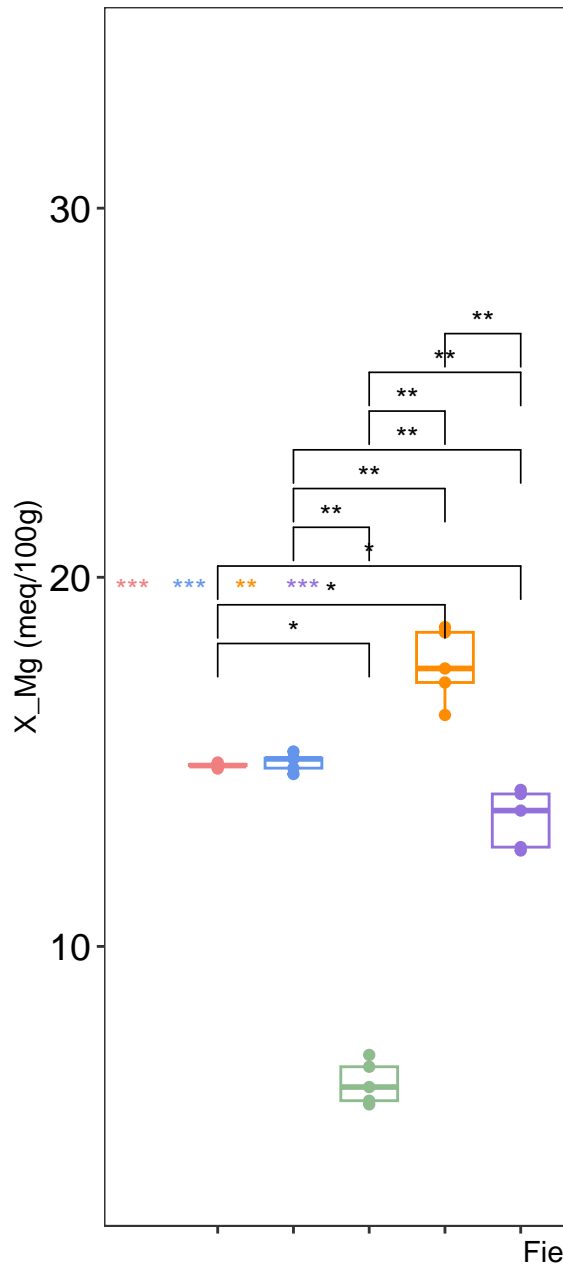
## Conventional



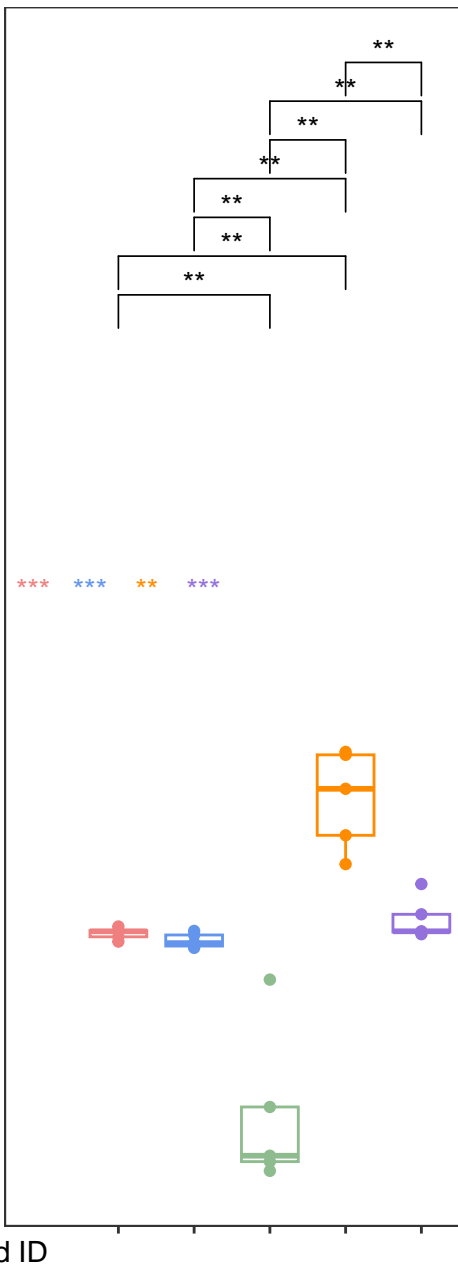
## Organic



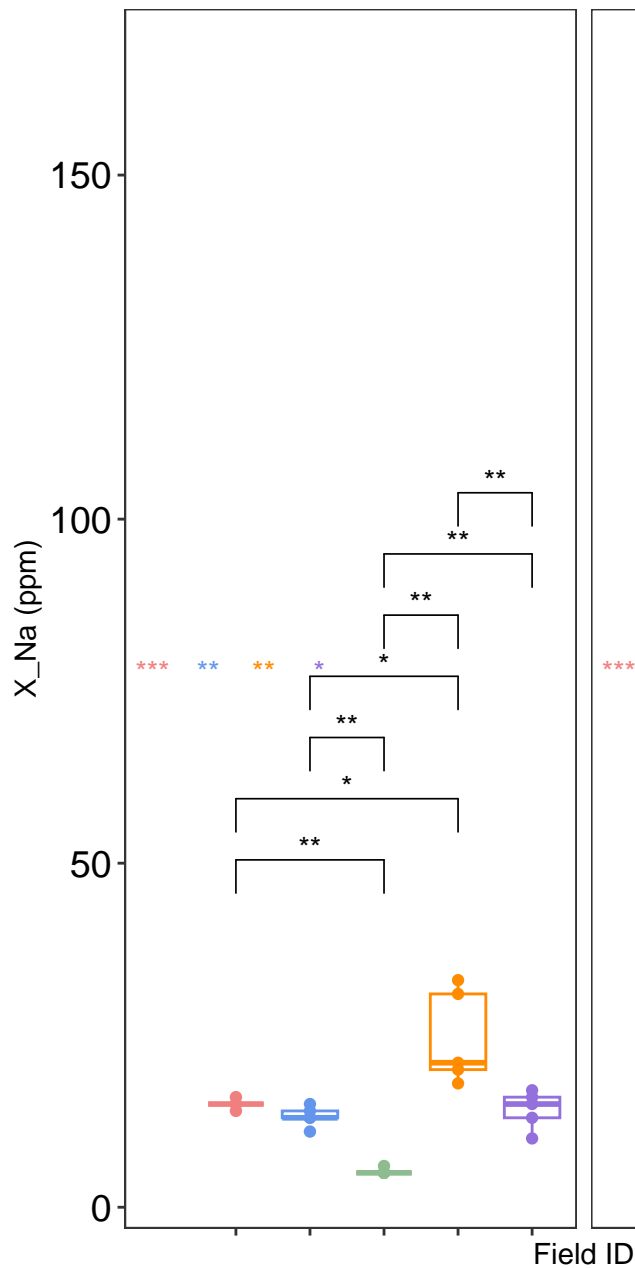
## Conventional



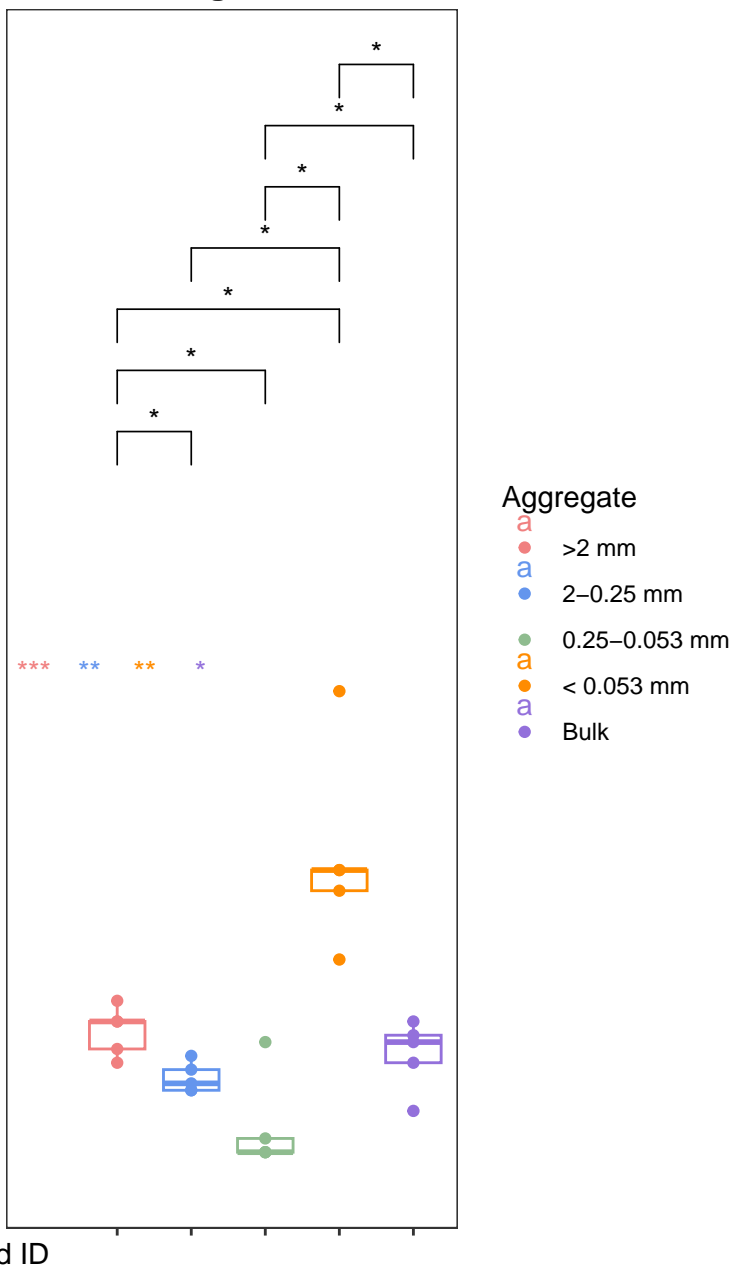
## Organic



Conventional

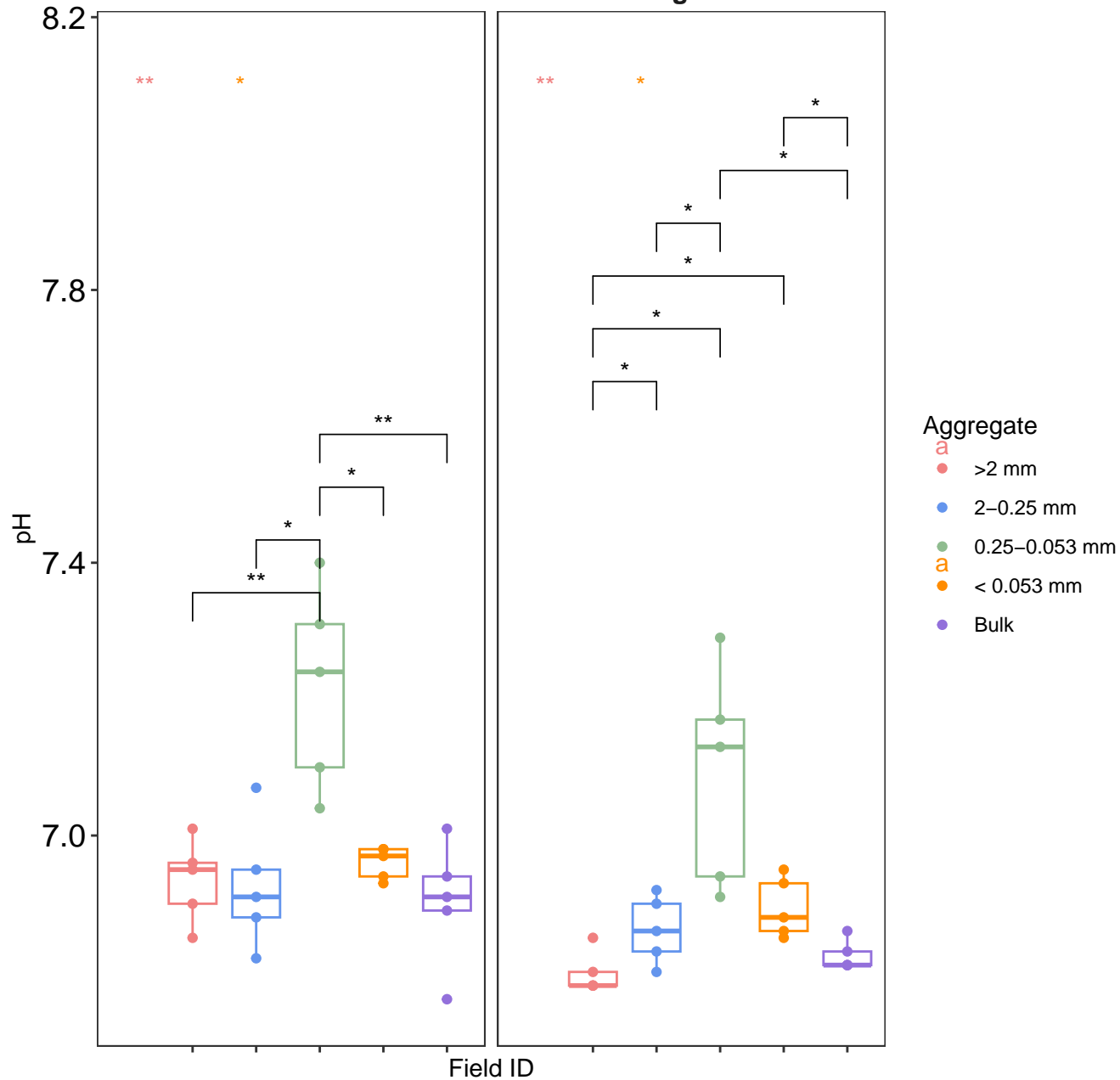


Organic

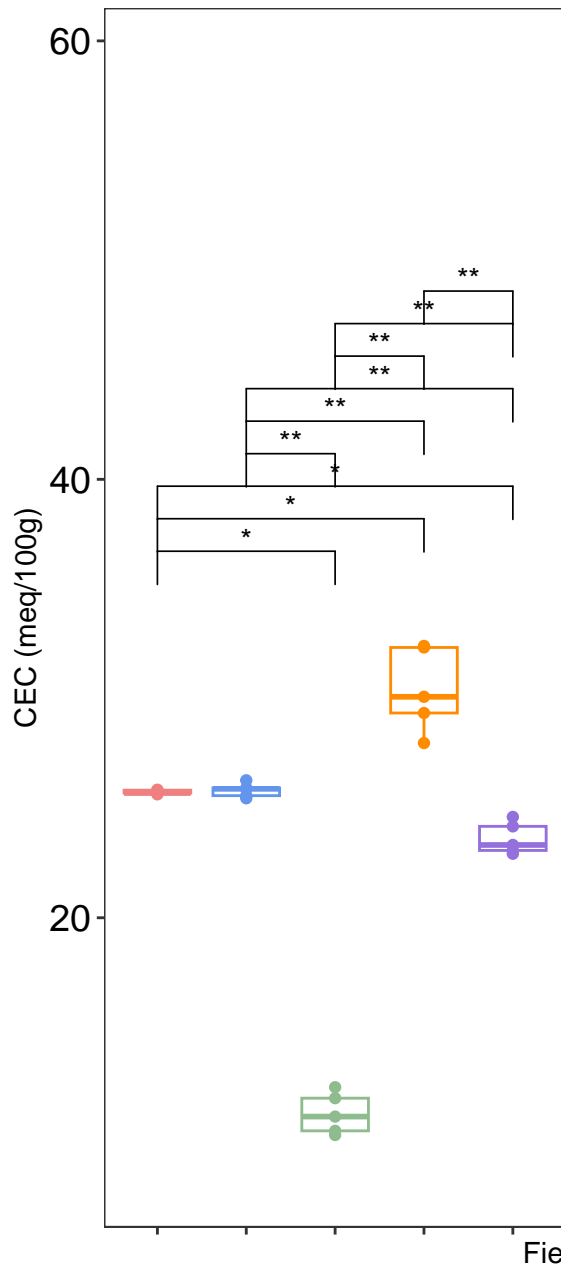


## Conventional

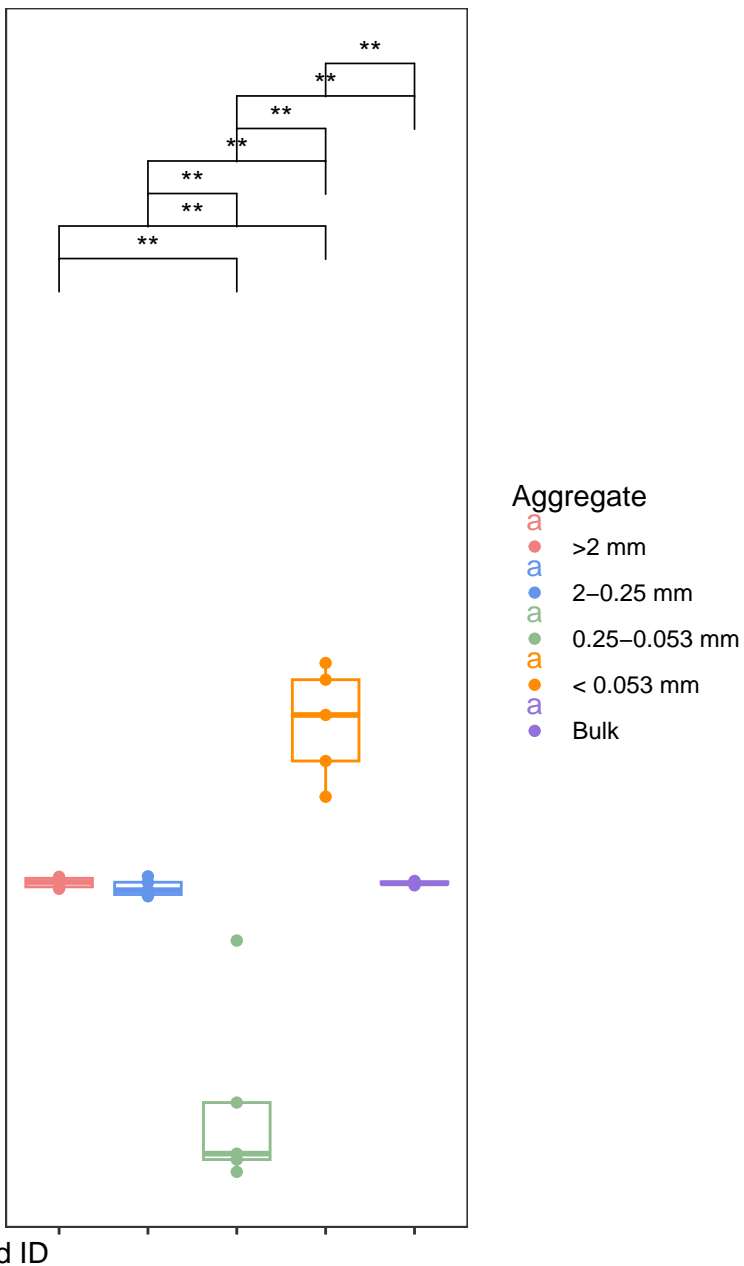
## Organic



## Conventional

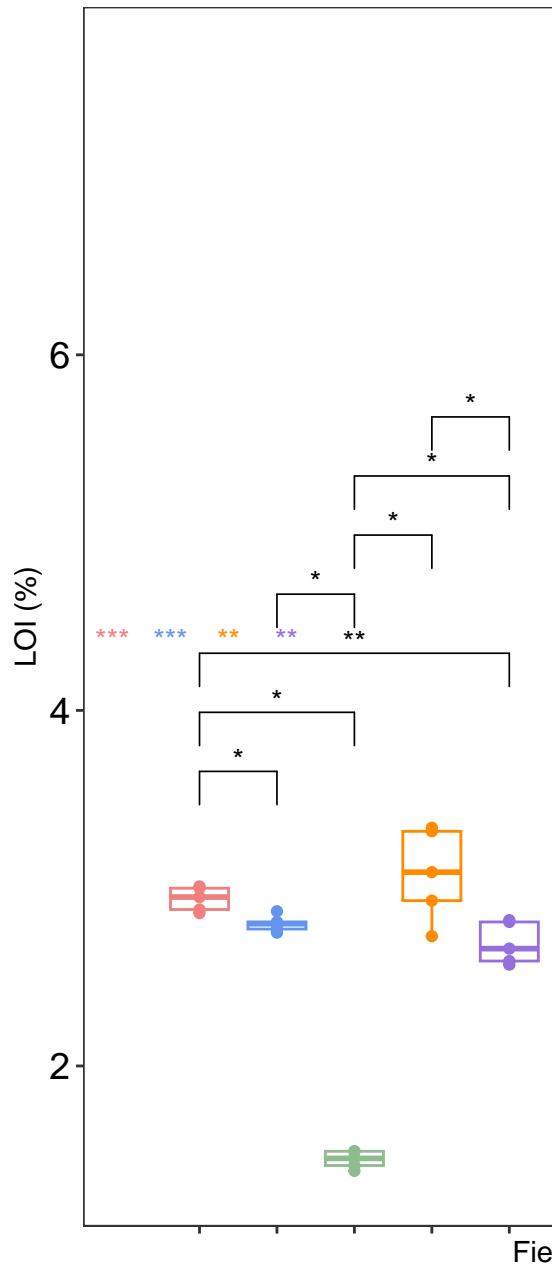


## Organic

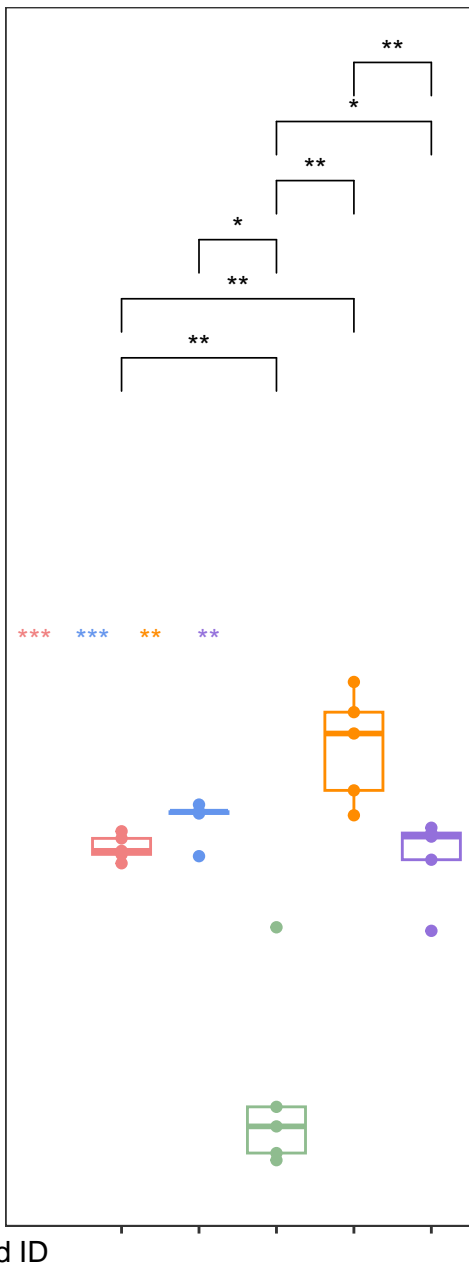




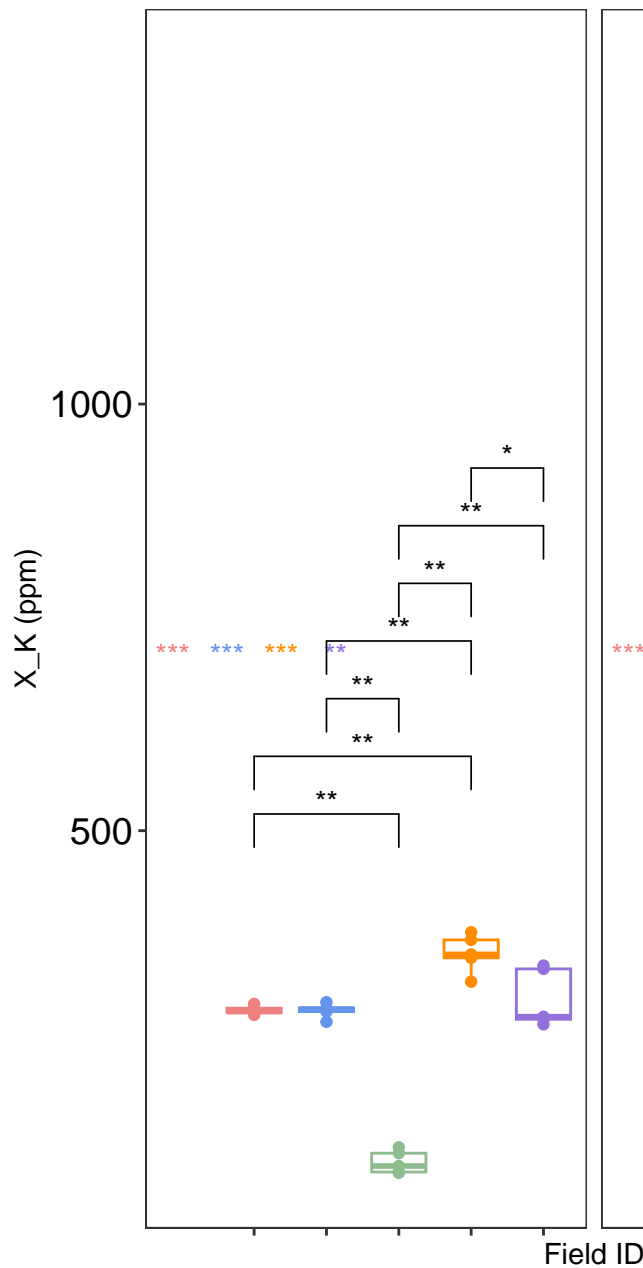
## Conventional



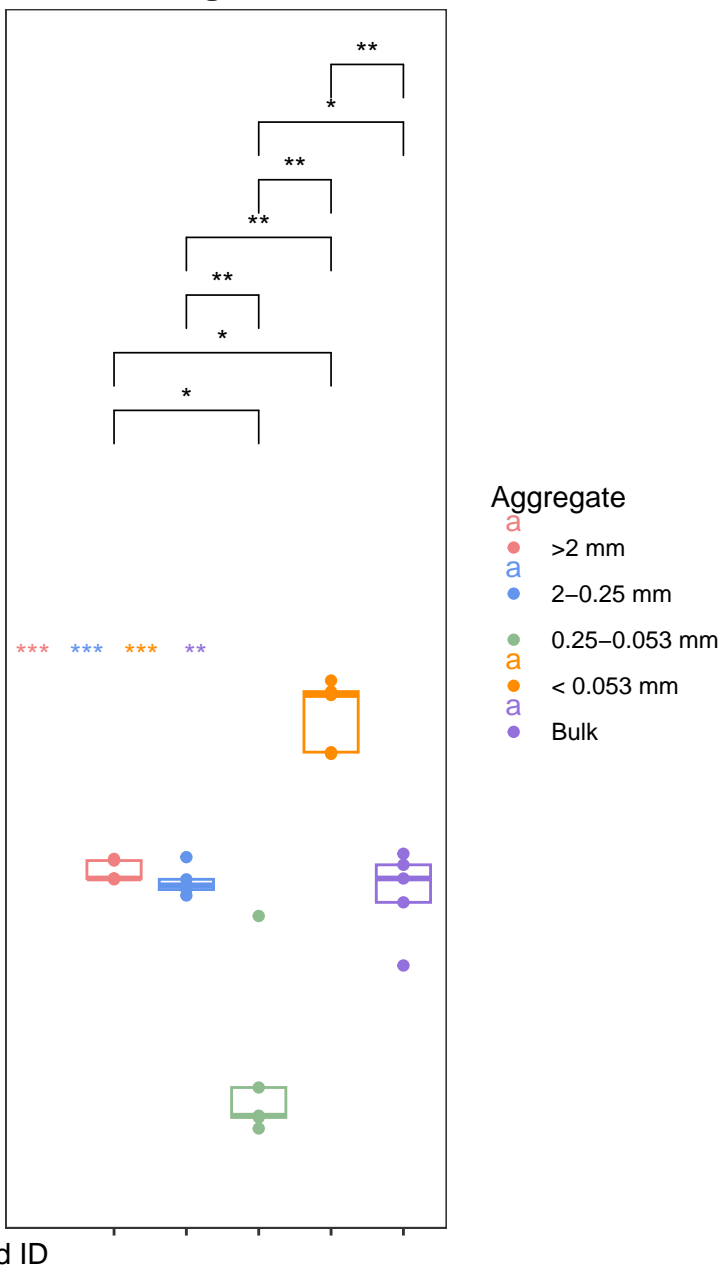
## Organic



## Conventional



## Organic



## Conventional

## Organic

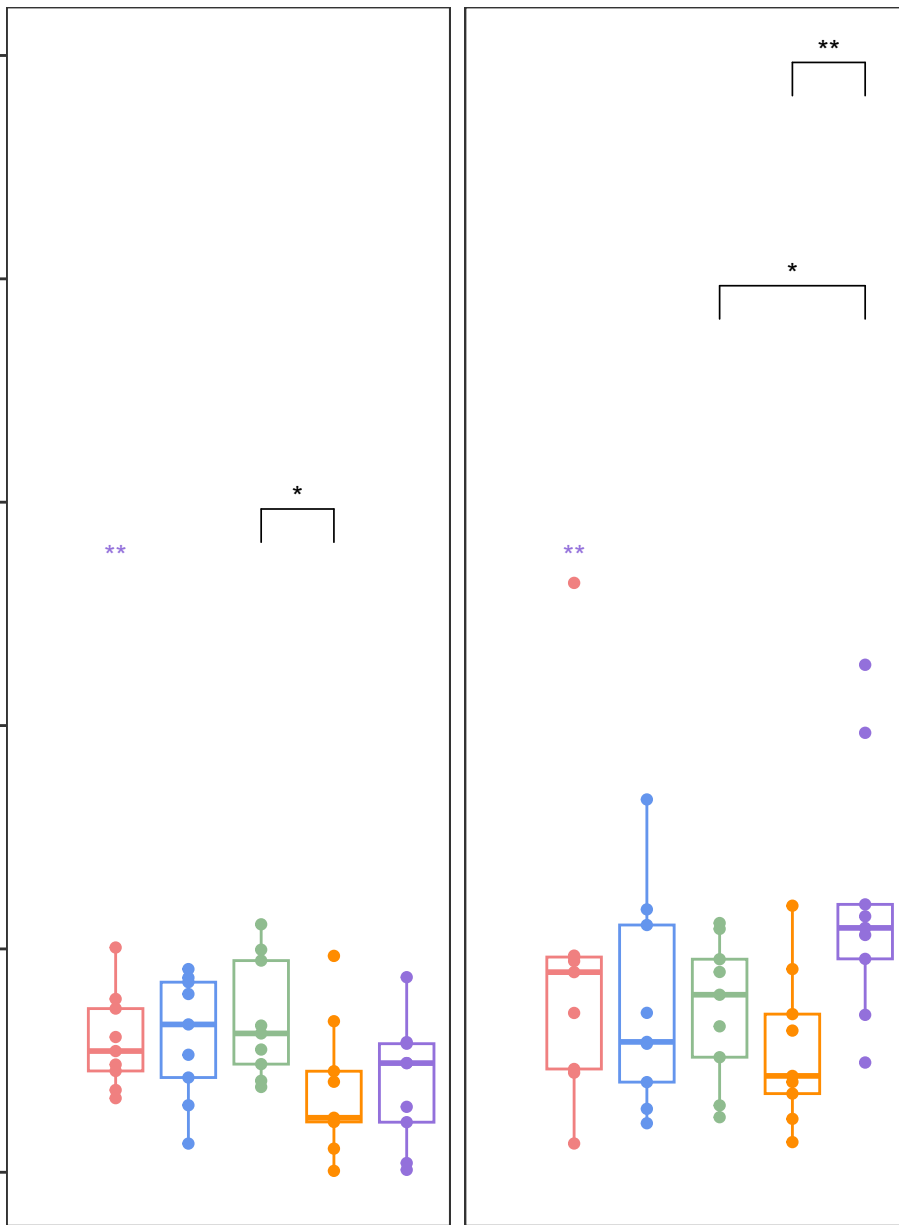
MBC ( $\mu\text{g C g}^{-1}$  dry aggregate)

500  
400  
300  
200  
100  
0

Field ID

Aggregate

- >2 mm
- 2–0.25 mm
- 0.25–0.053 mm
- < 0.053 mm
- Bulk



## Conventional

## Organic

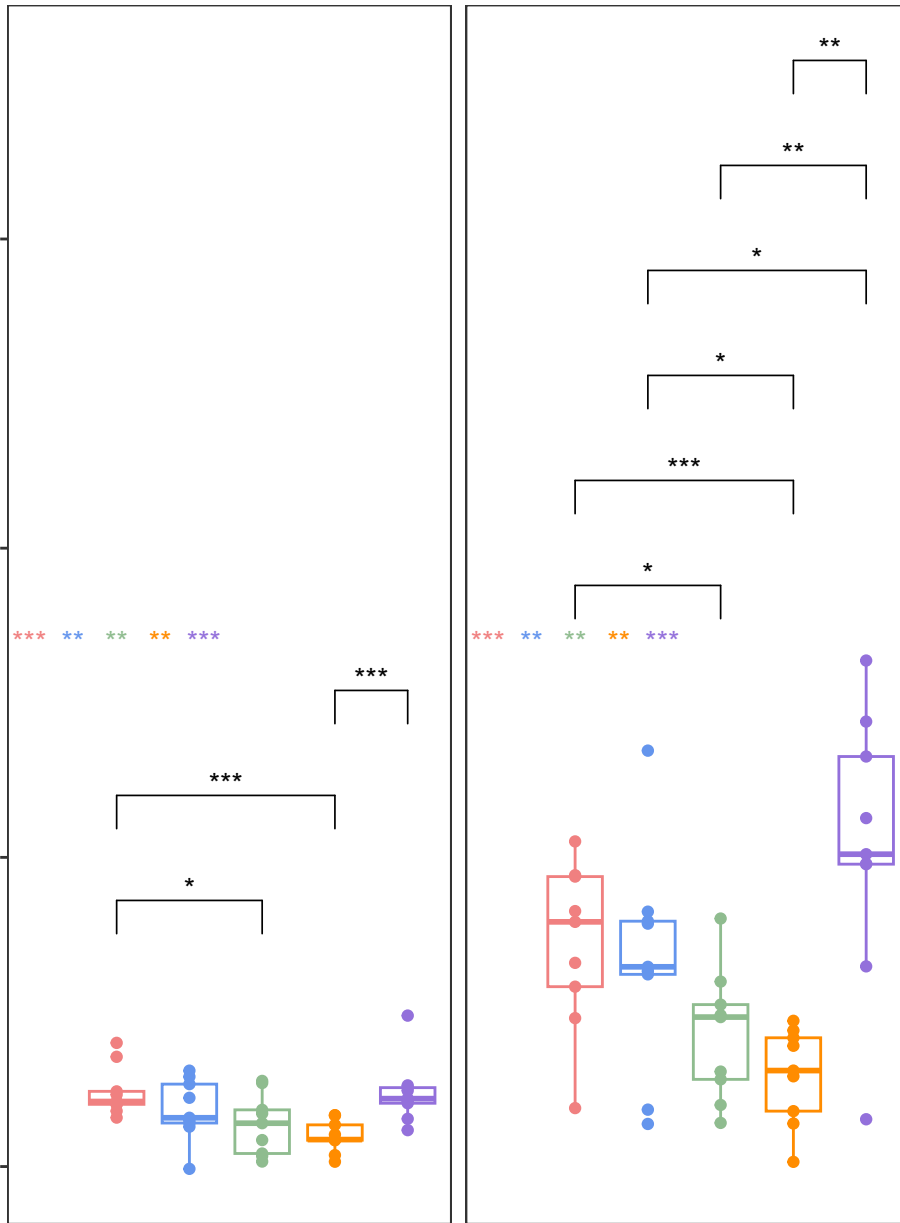
MBN ( $\mu\text{g N g}^{-1}$  dry aggregate)

150  
100  
50  
0

Field ID

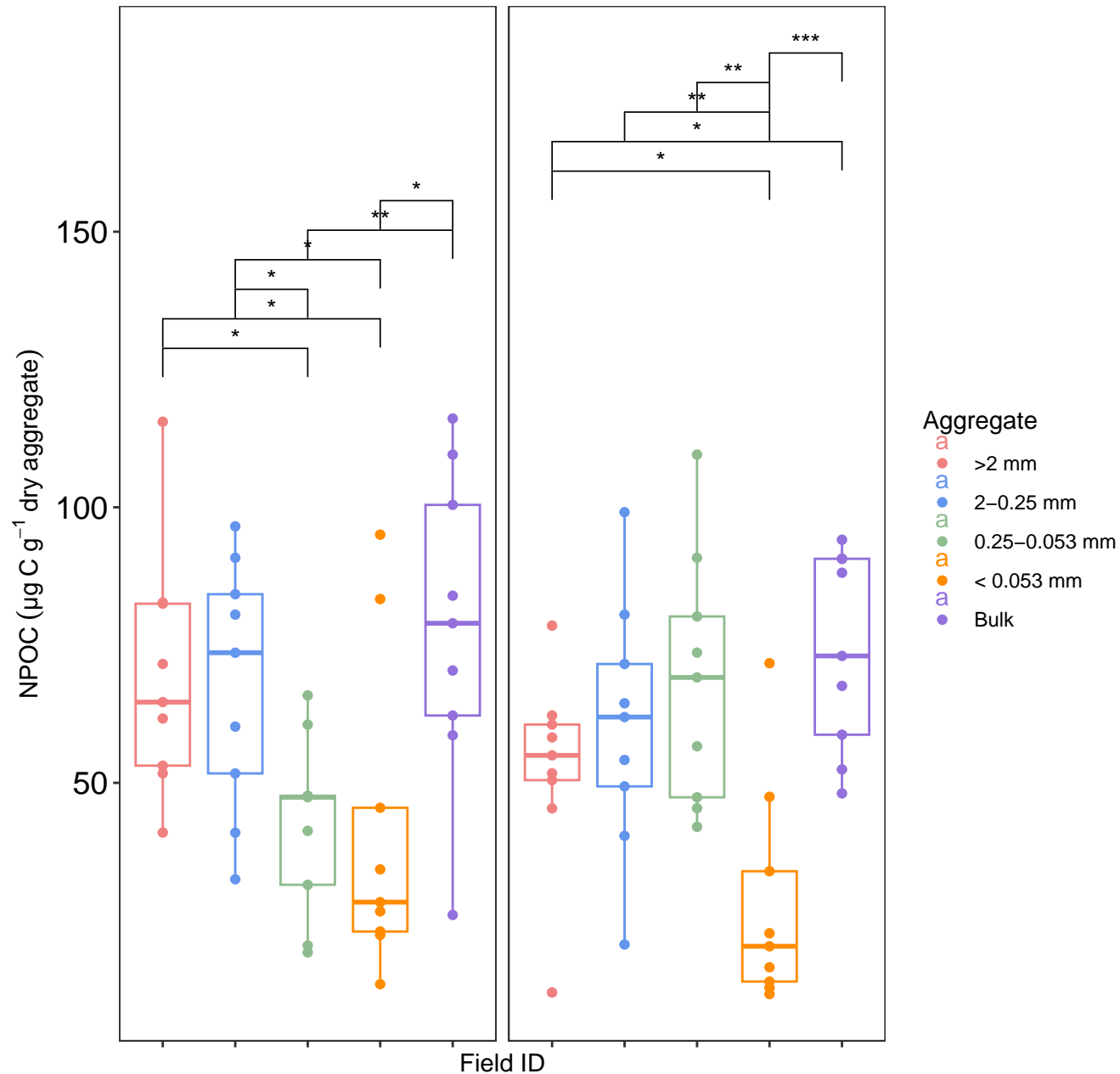
Aggregate

- >2 mm
- 2–0.25 mm
- 0.25–0.053 mm
- < 0.053 mm
- Bulk



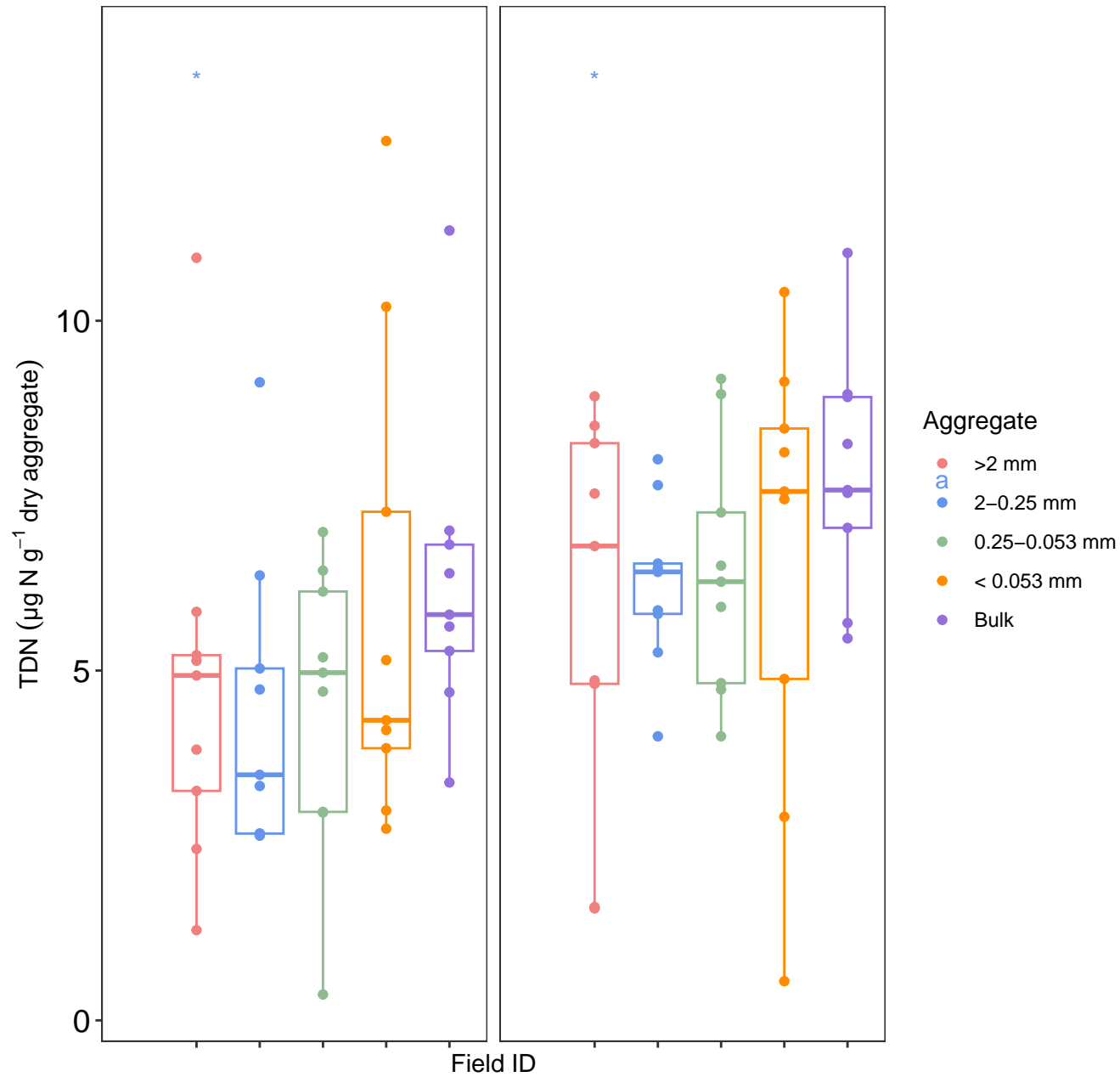
## Conventional

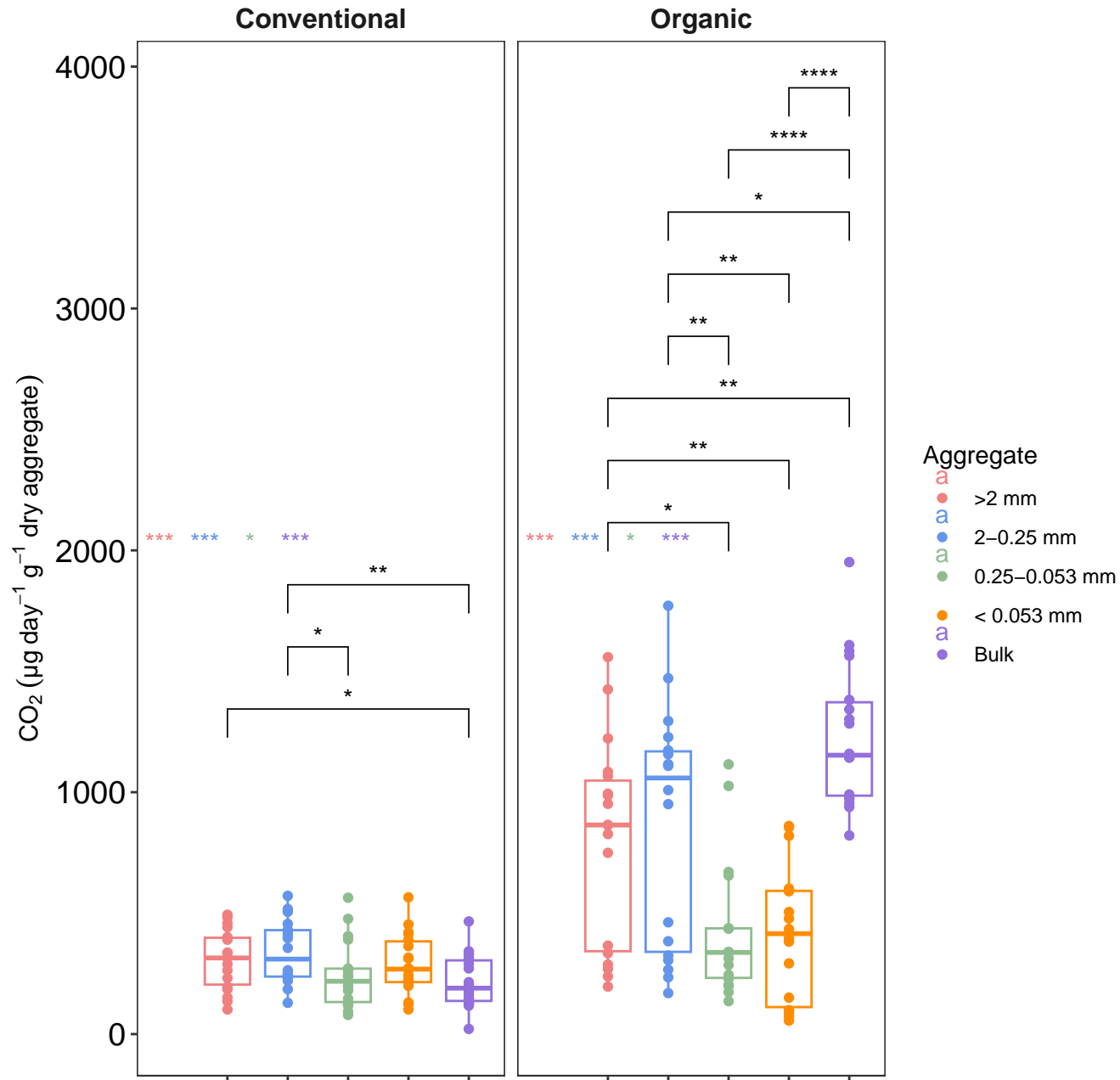
## Organic

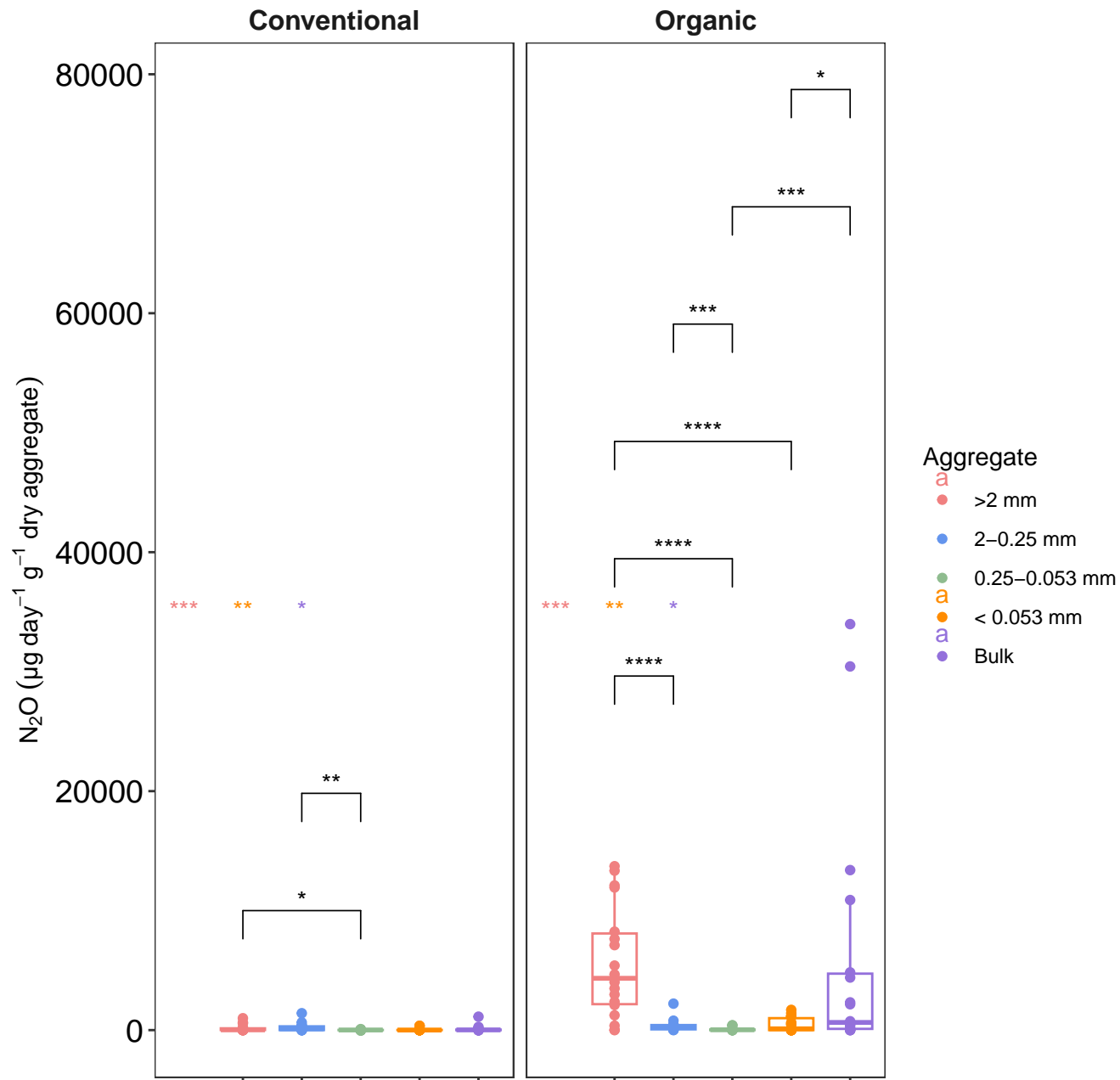


Conventional

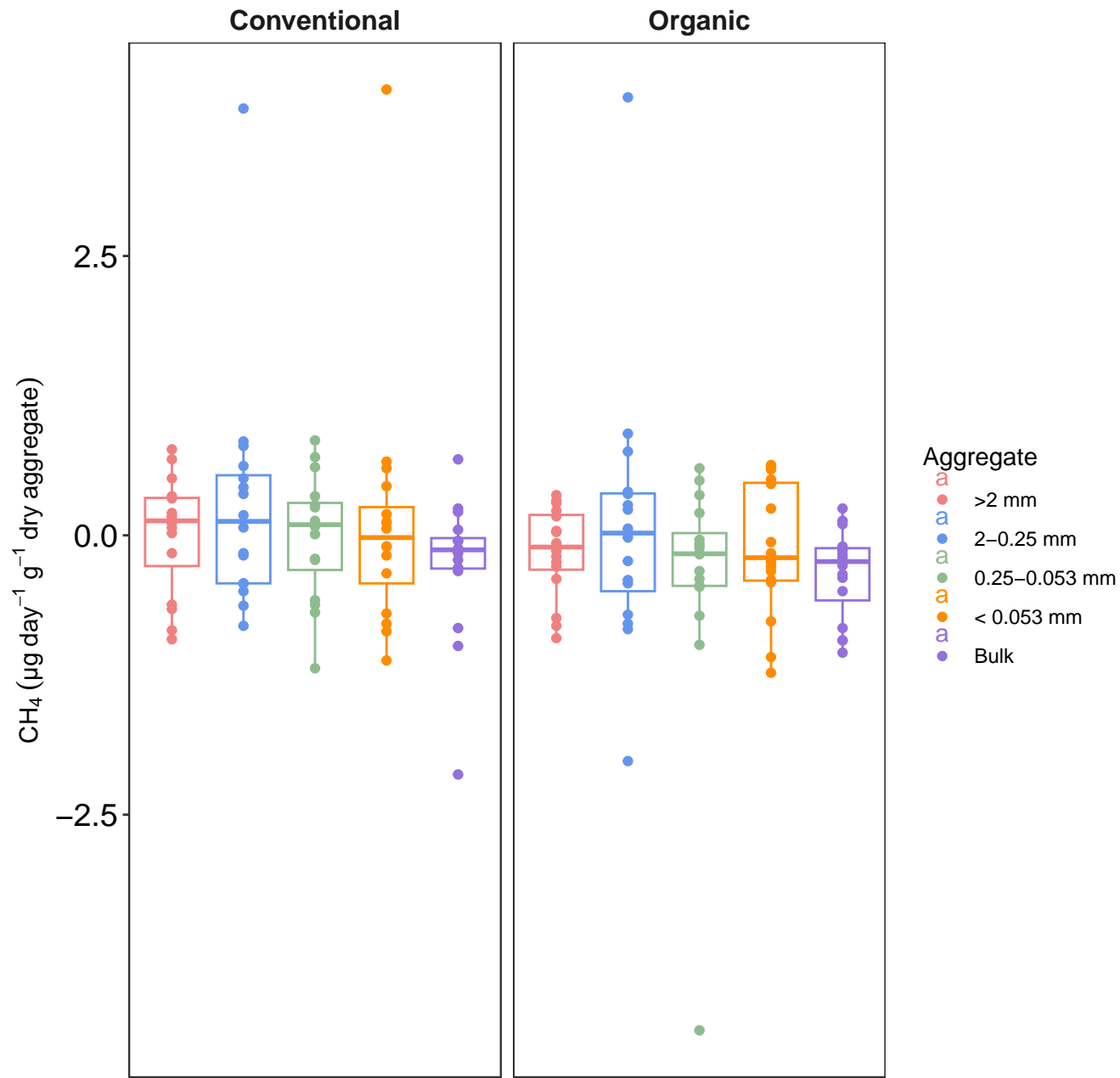
Organic

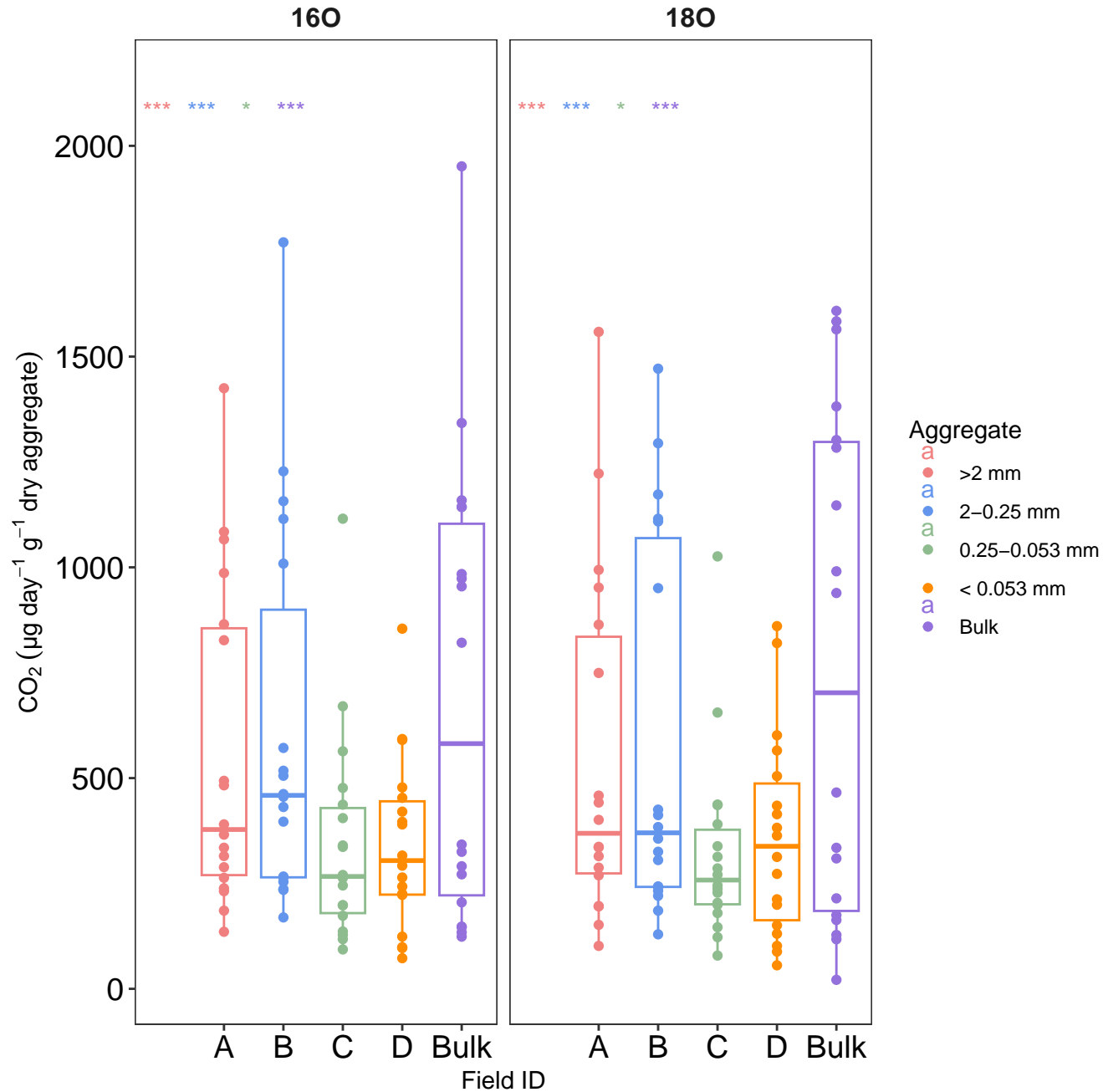


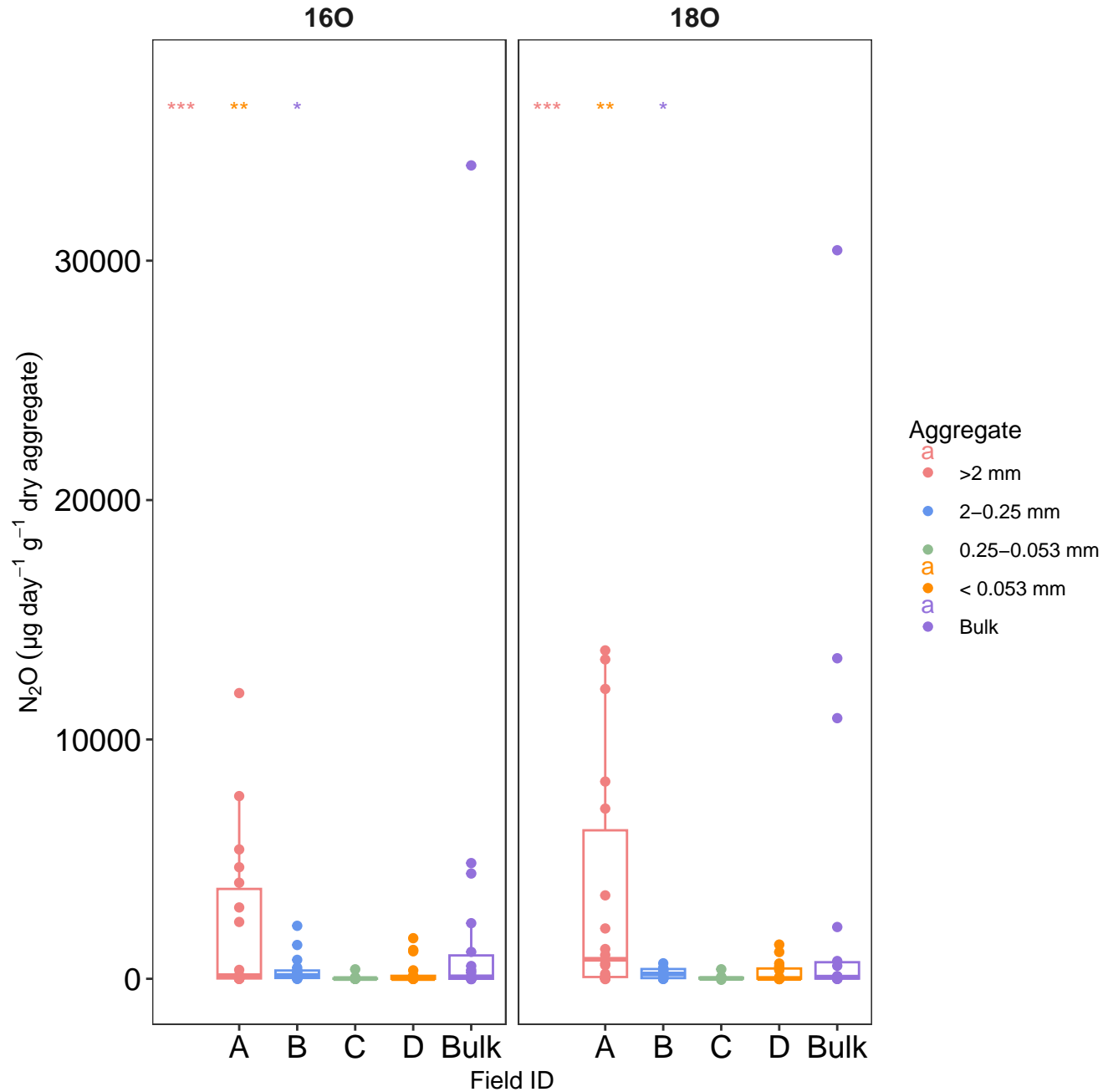


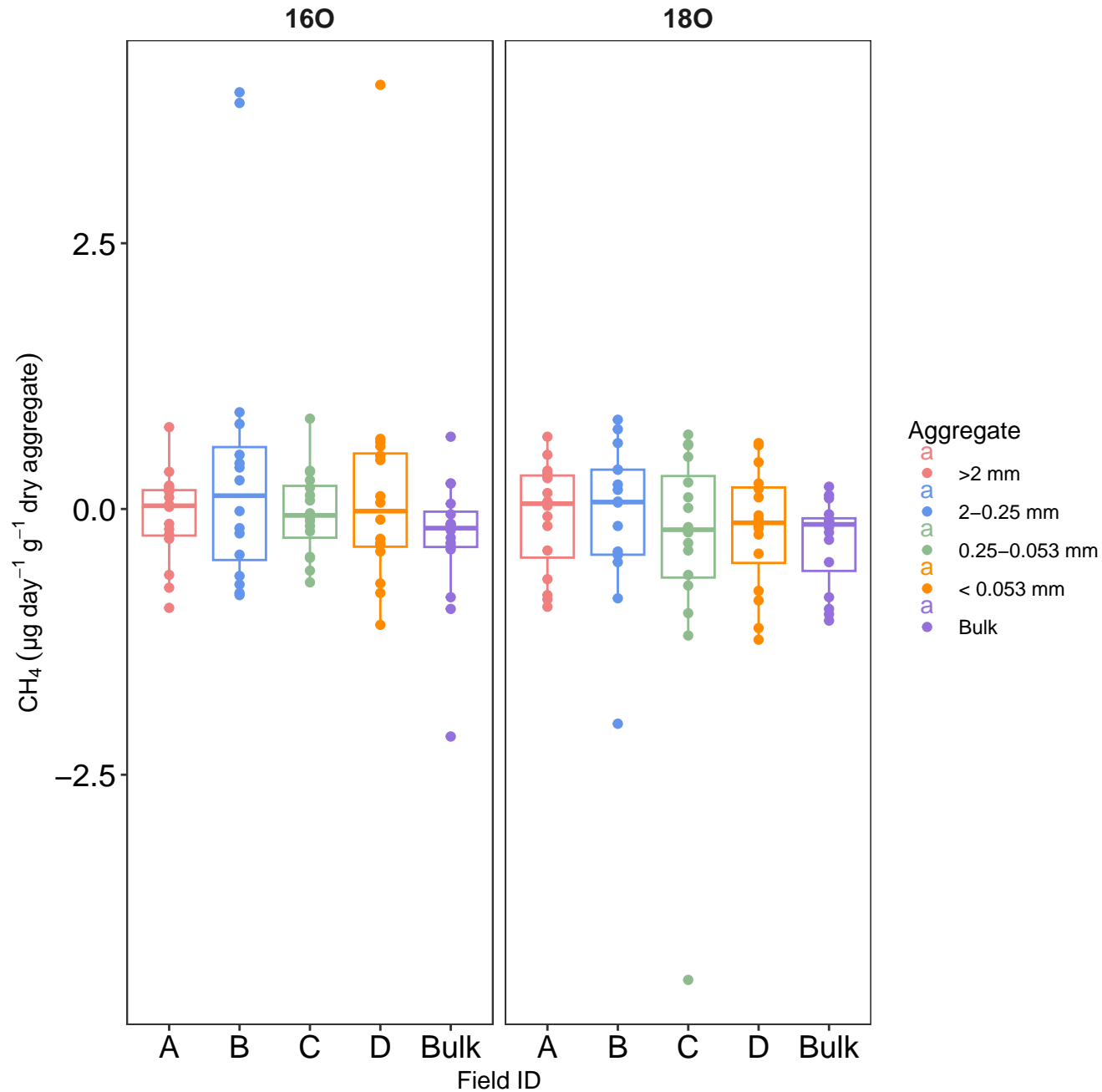


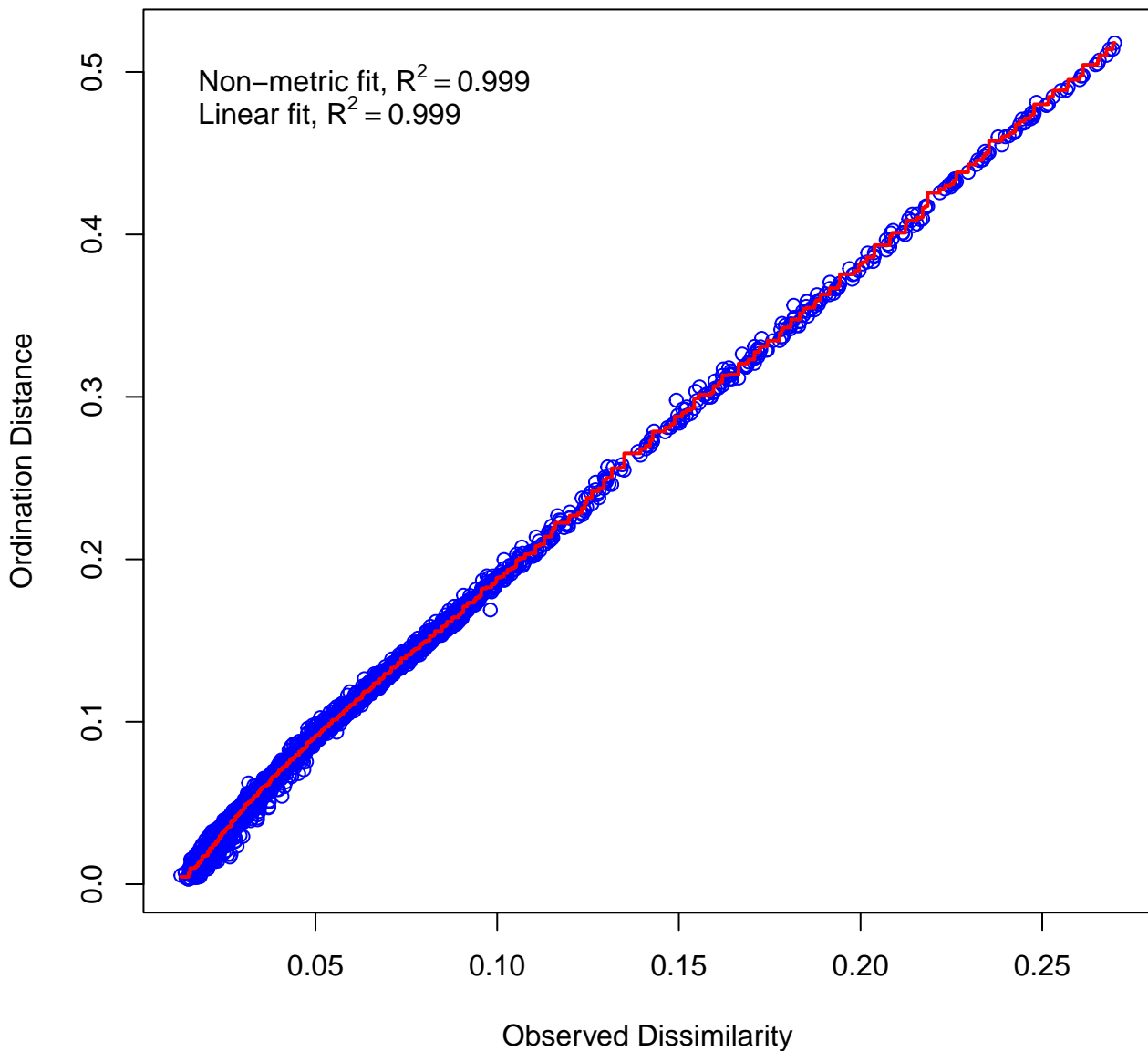




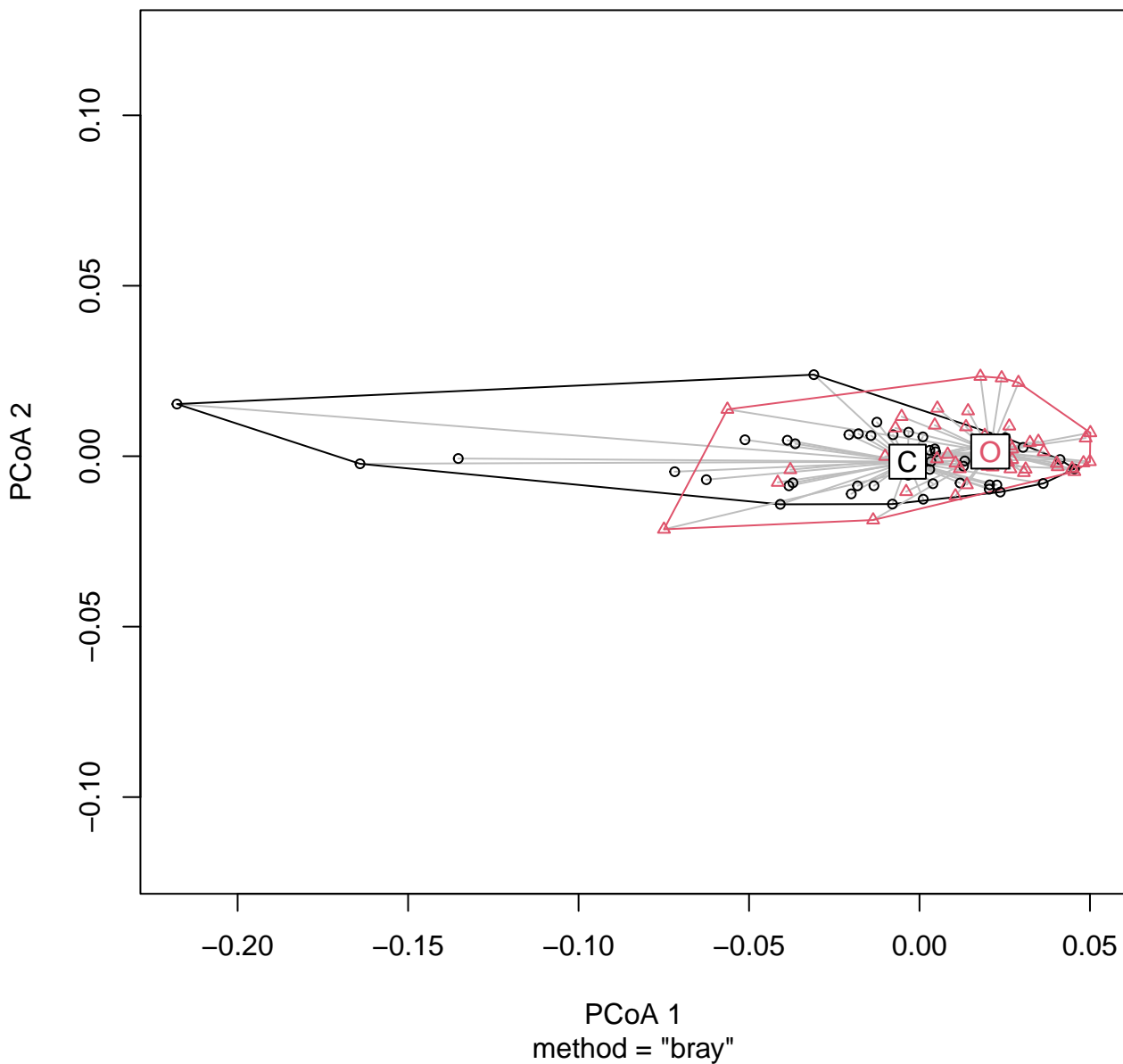


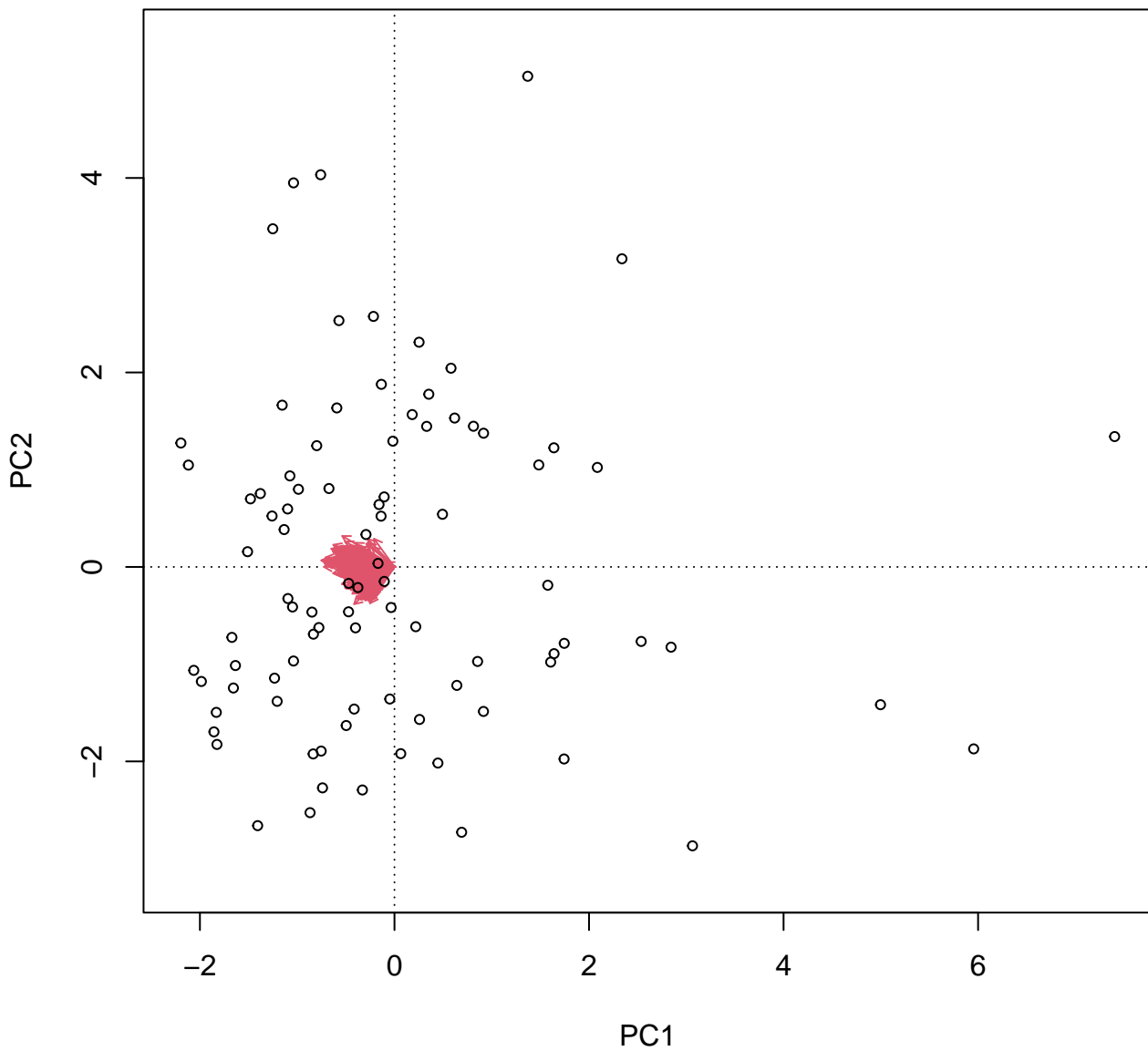


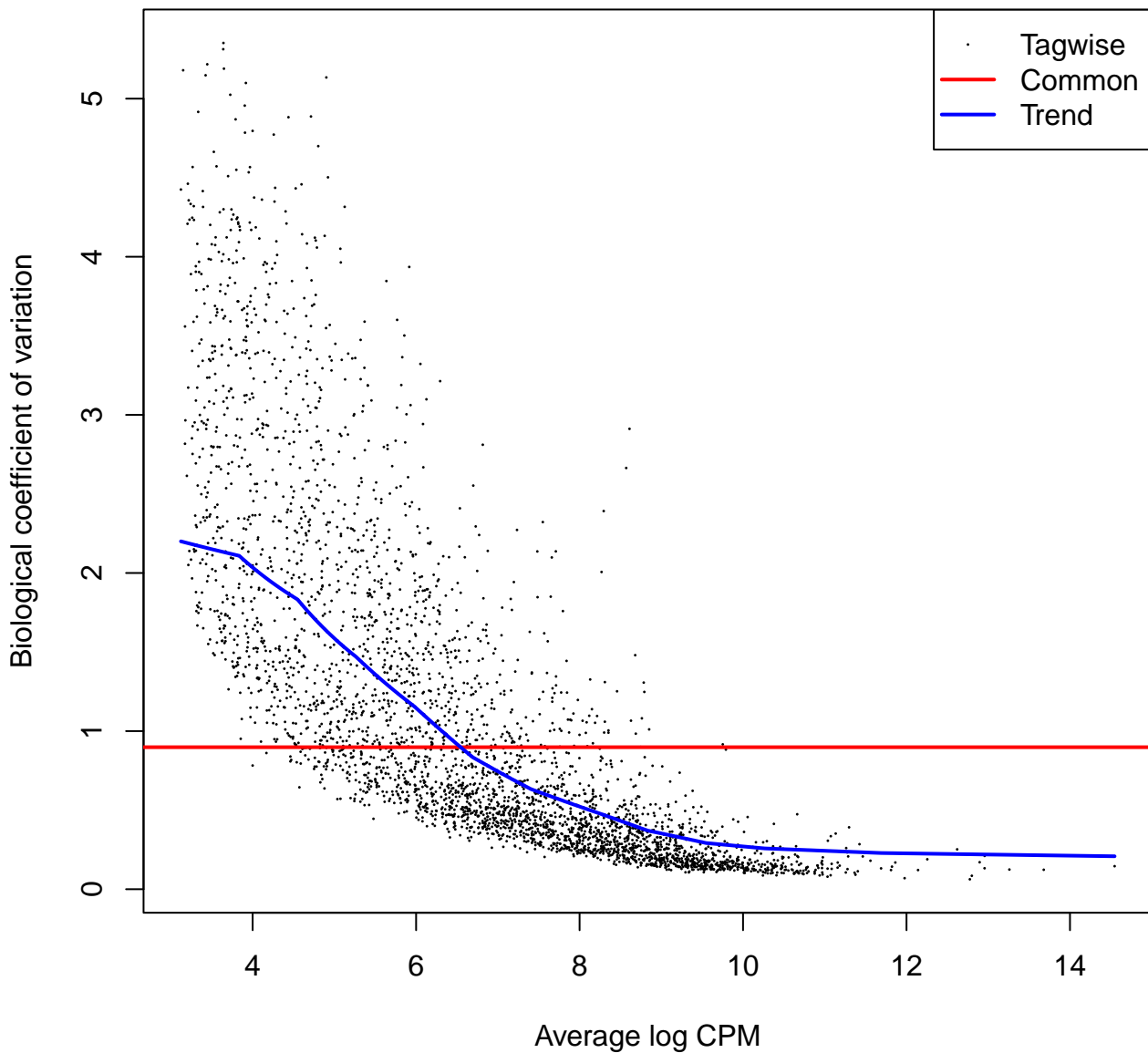




ps.disper

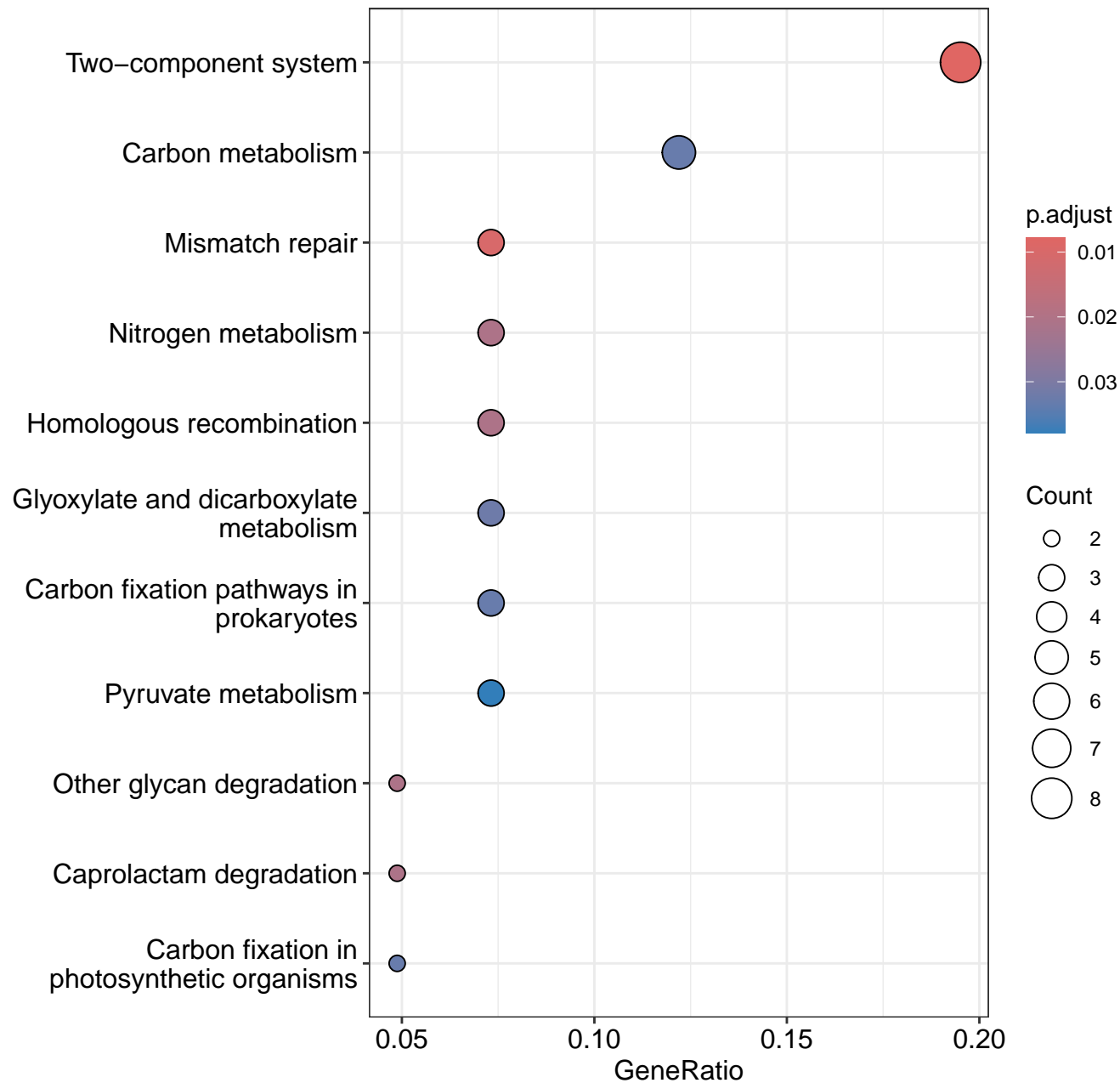




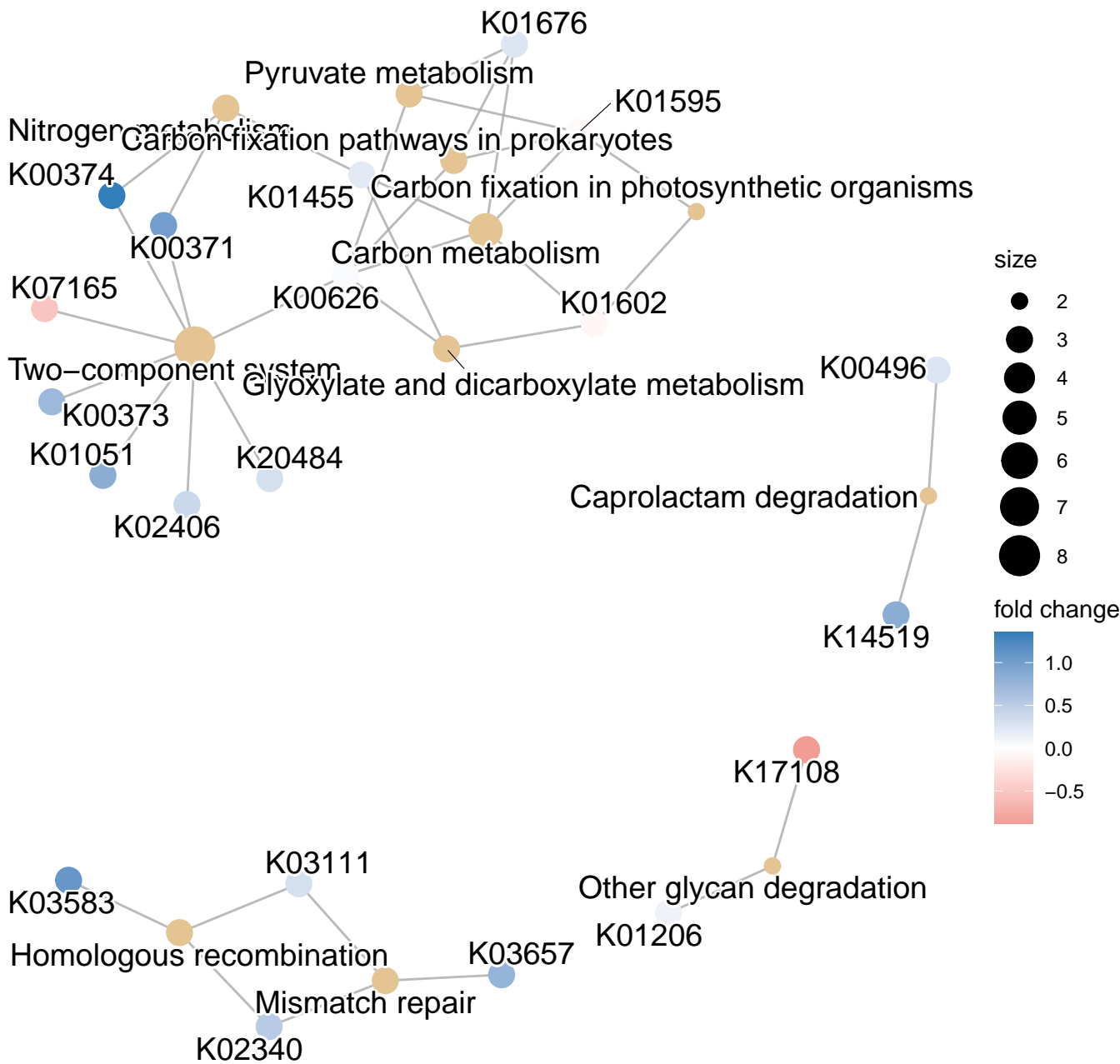




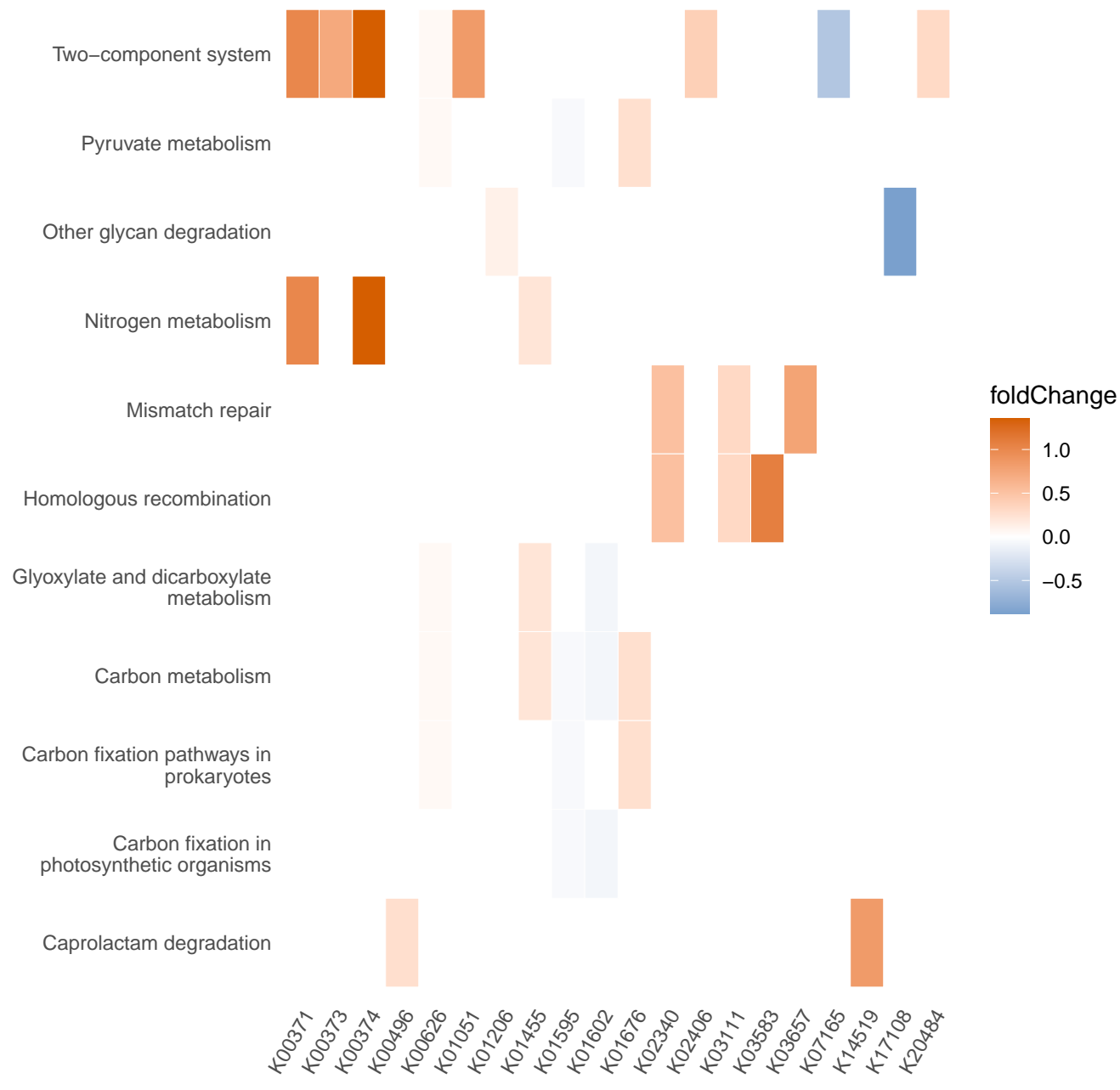
Site geom\_path



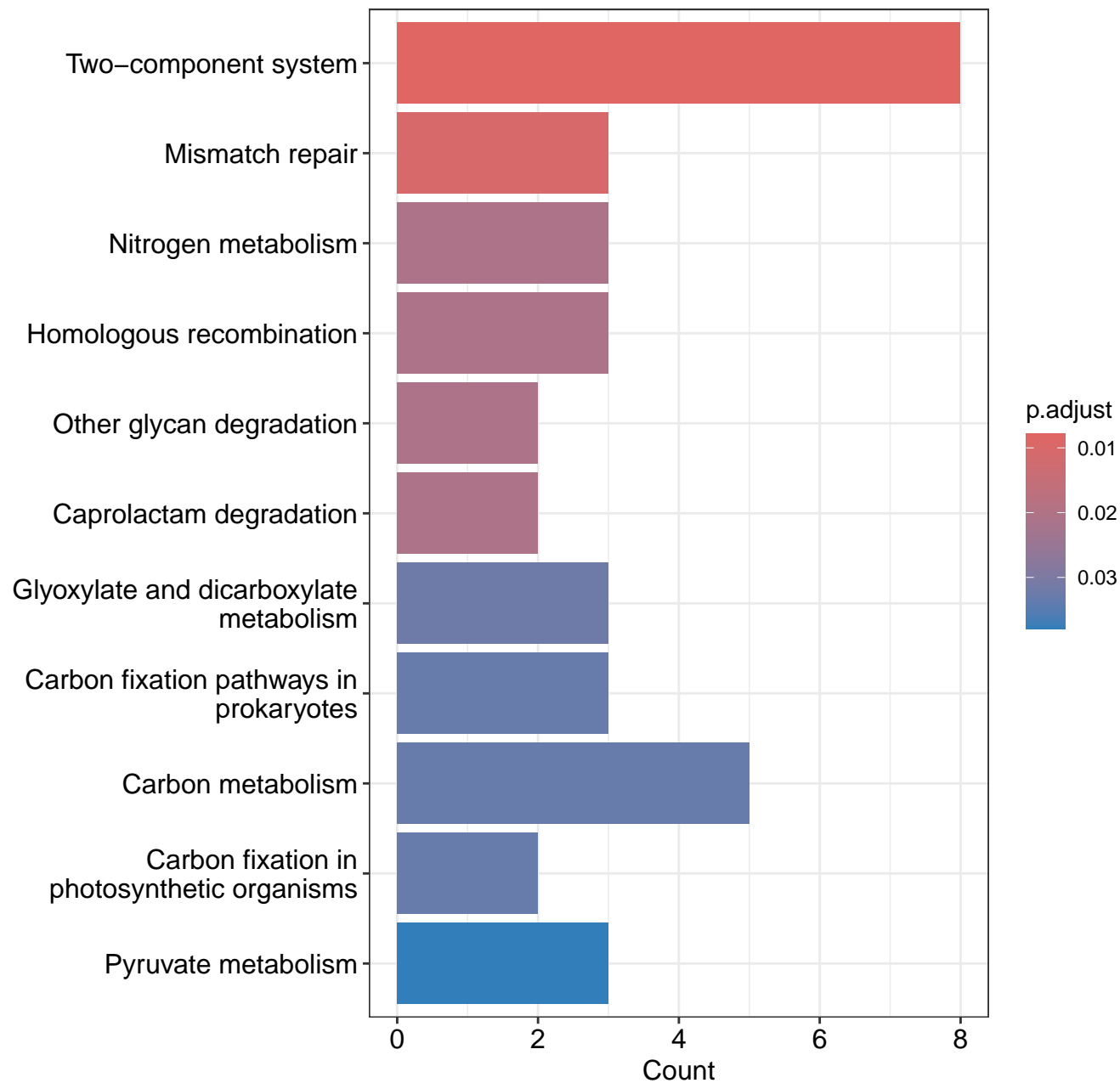
Site geom\_path



## Site geom\_path







Site gsea\_path

Flagellar assembly

p.adjust

0.005364302

Count

21

0.60

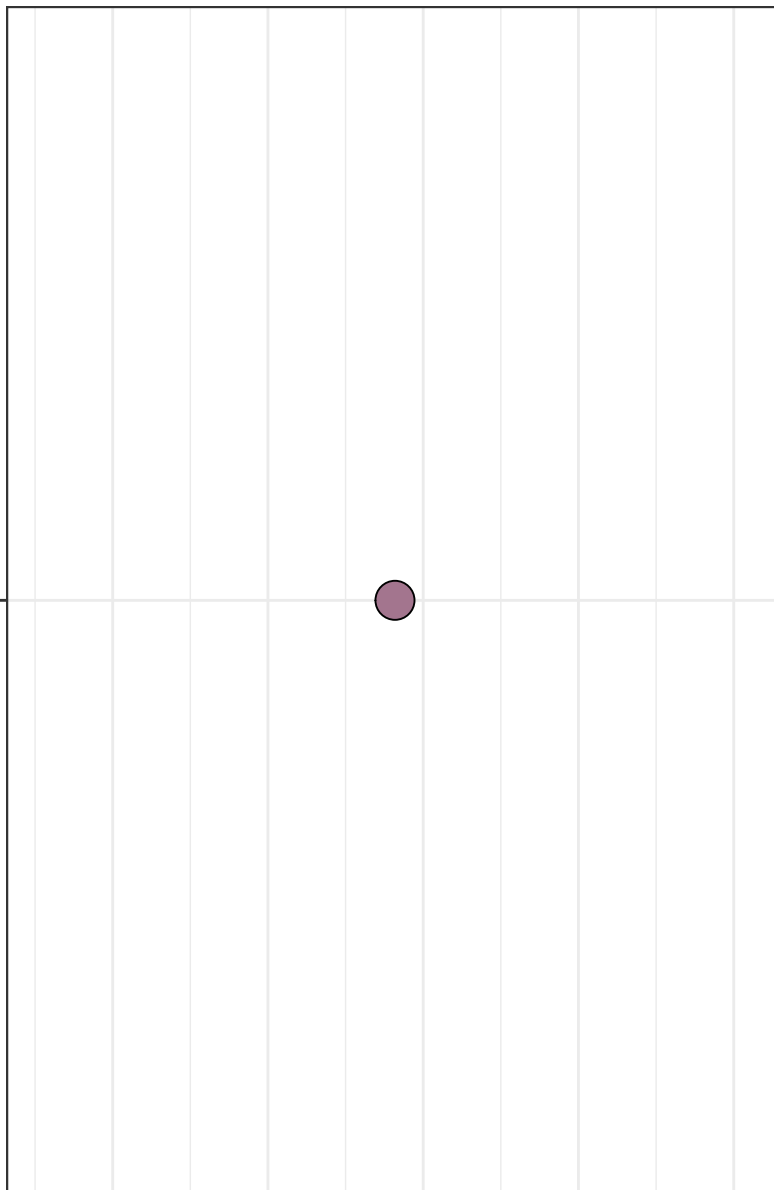
0.62

0.64

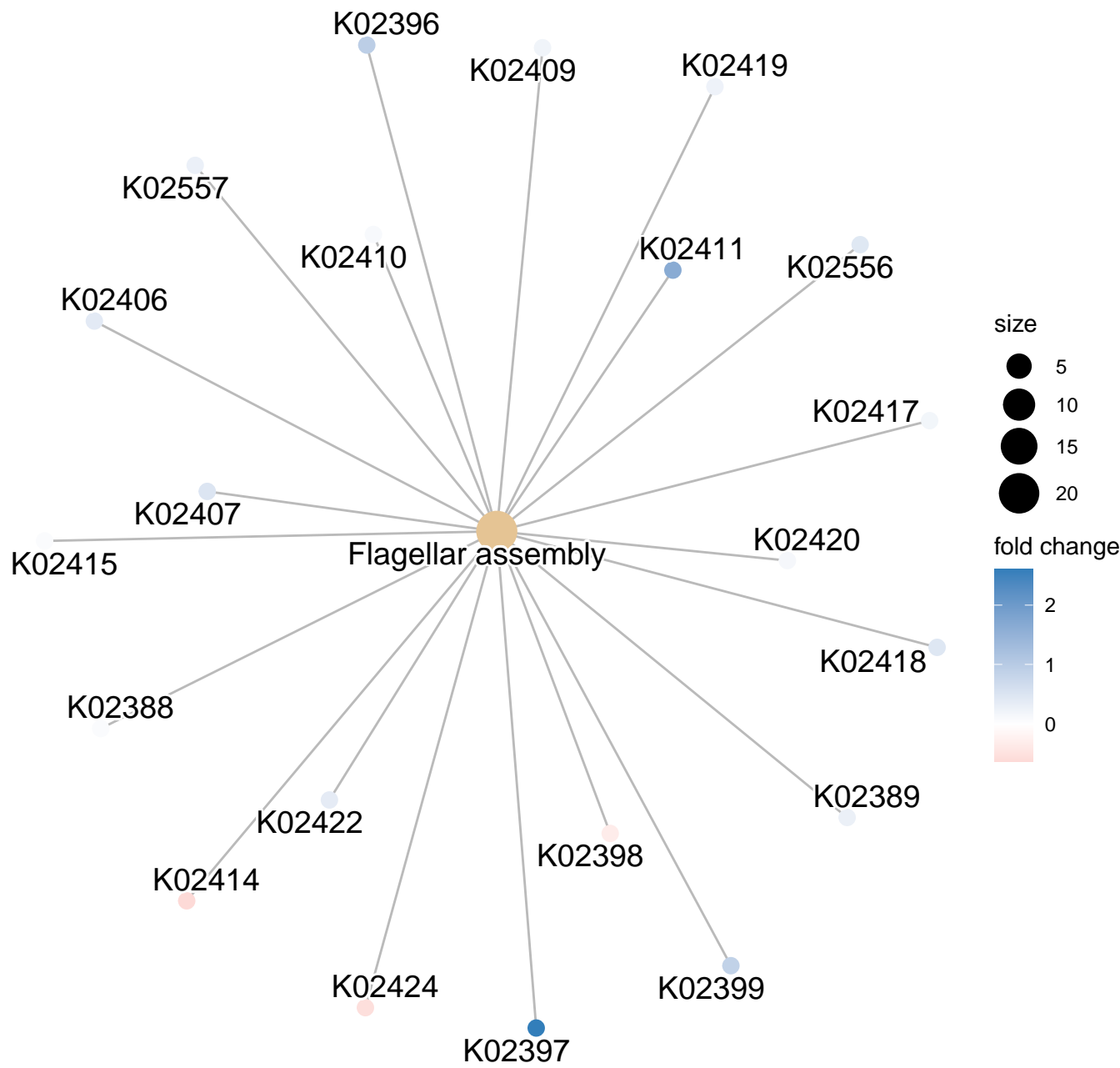
0.66

0.68

GeneRatio



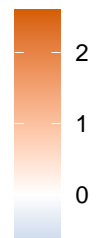
Site gsea\_path



# Site gsea\_path

Flagellar assembly

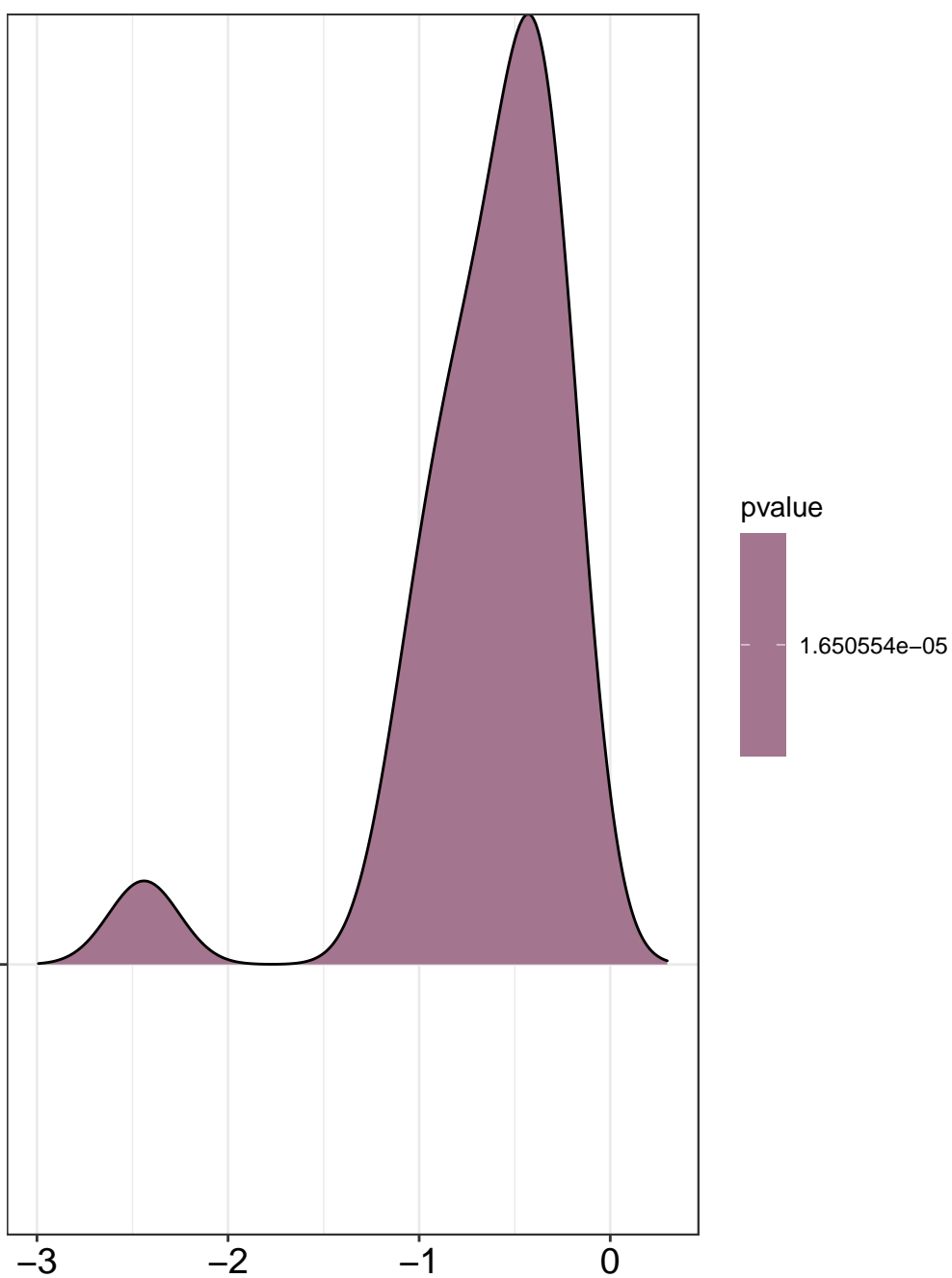
foldChange



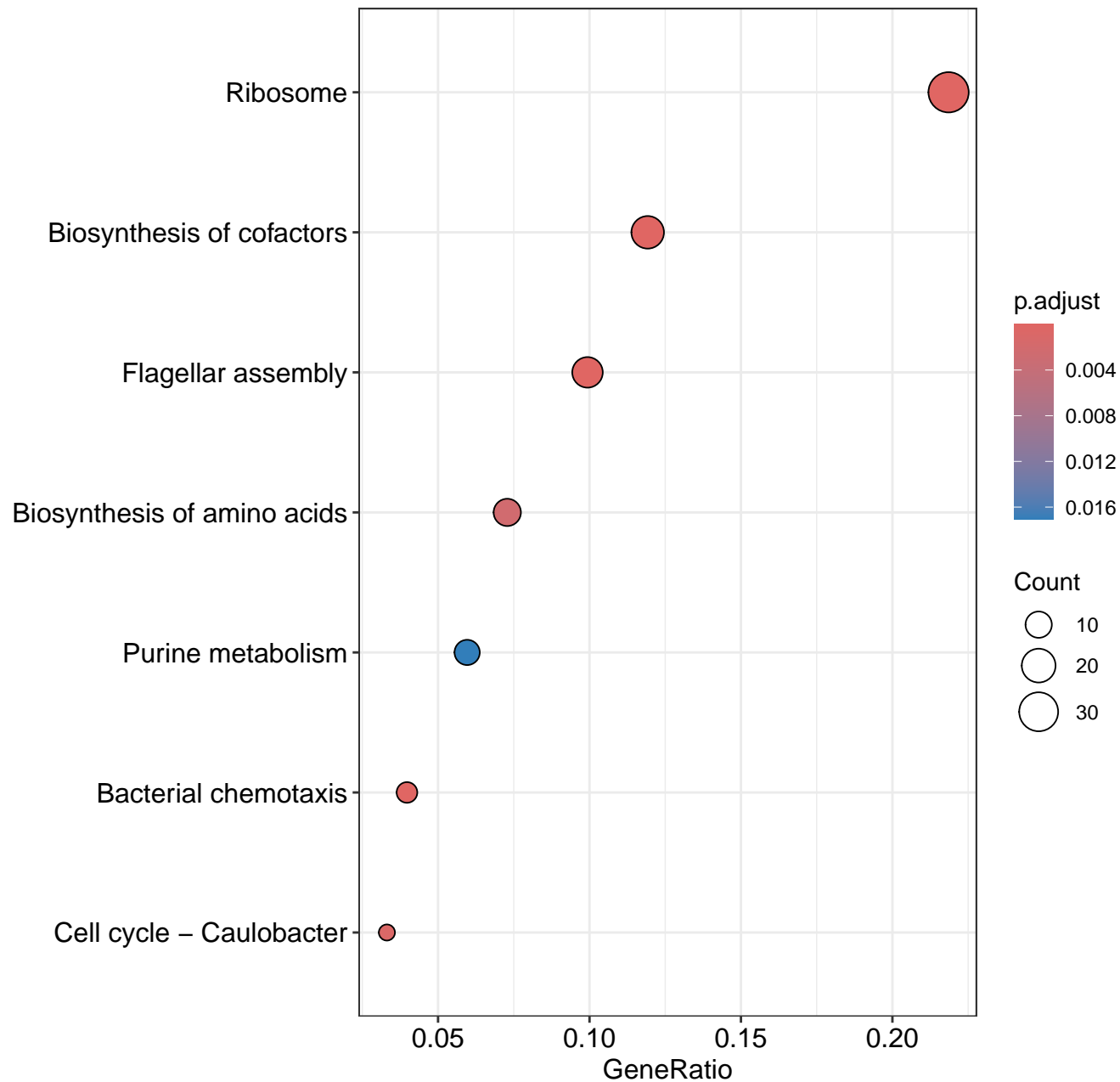
K02388  
K02389  
K02396  
K02397  
K02398  
K02399  
K02406  
K02407  
K02409  
K02410  
K02411  
K02414  
K02415  
K02417  
K02418  
K02419  
K02420  
K02422  
K02424  
K02556  
K02557



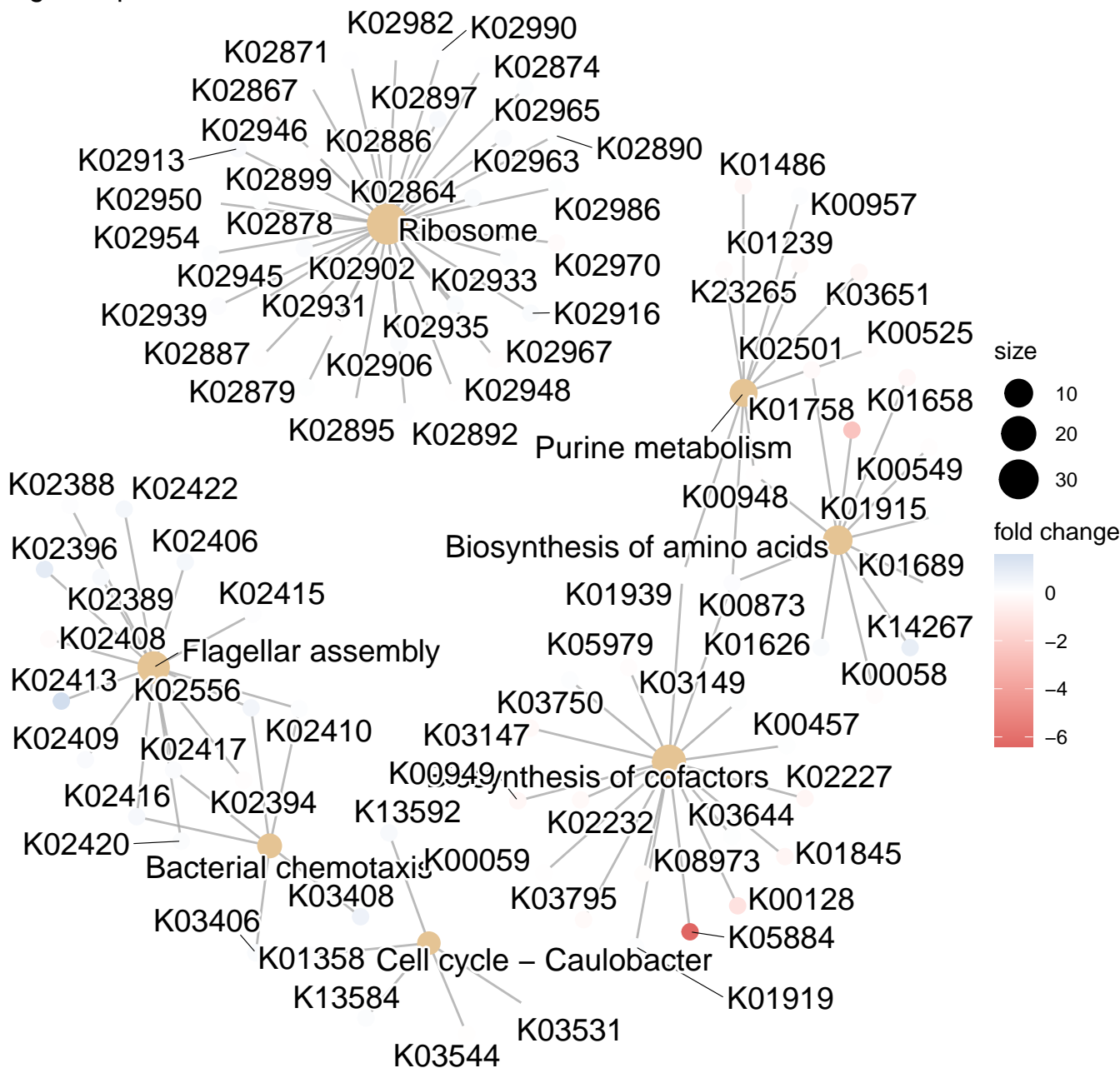
Flagellar assembly



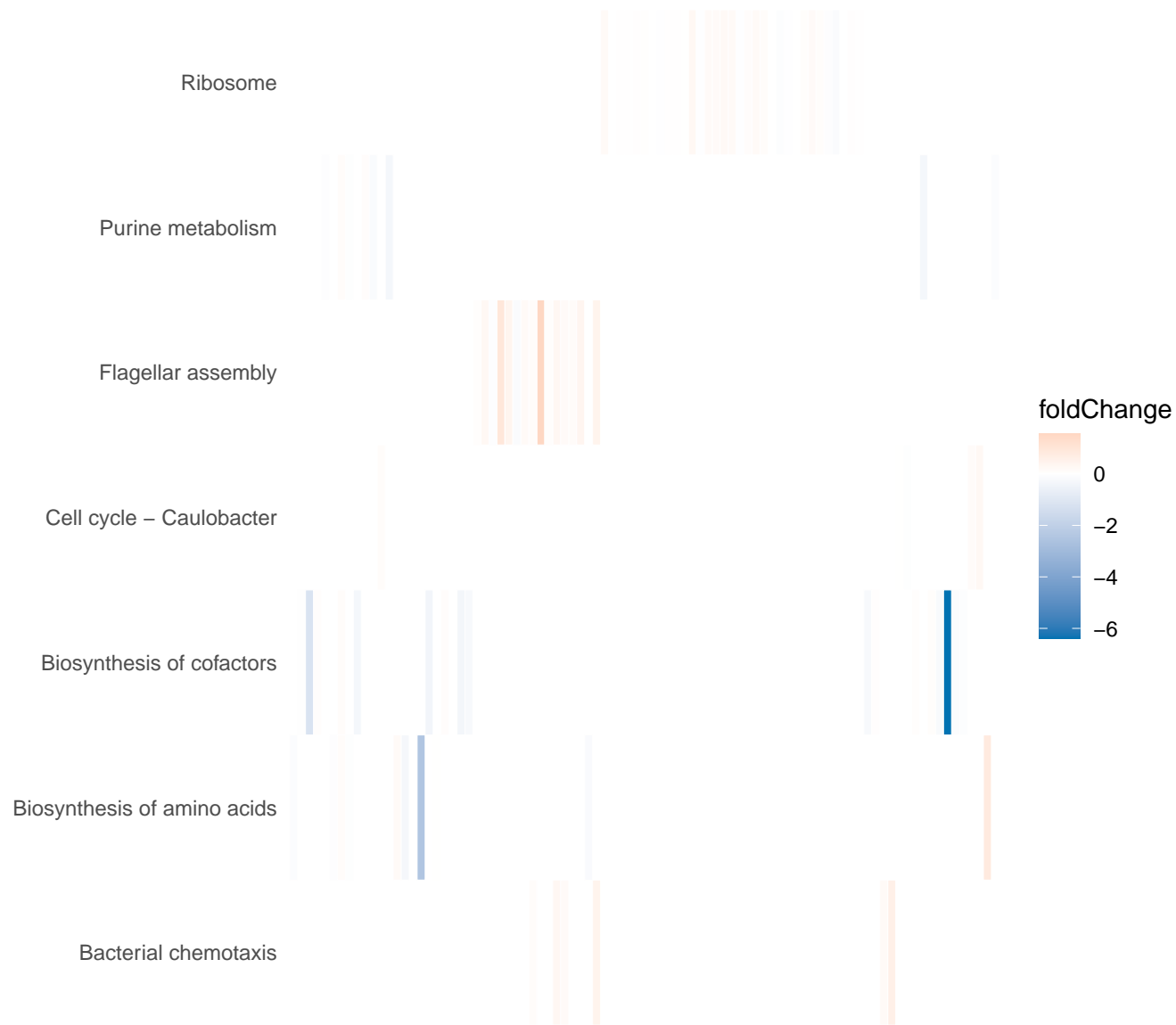
C geom\_path

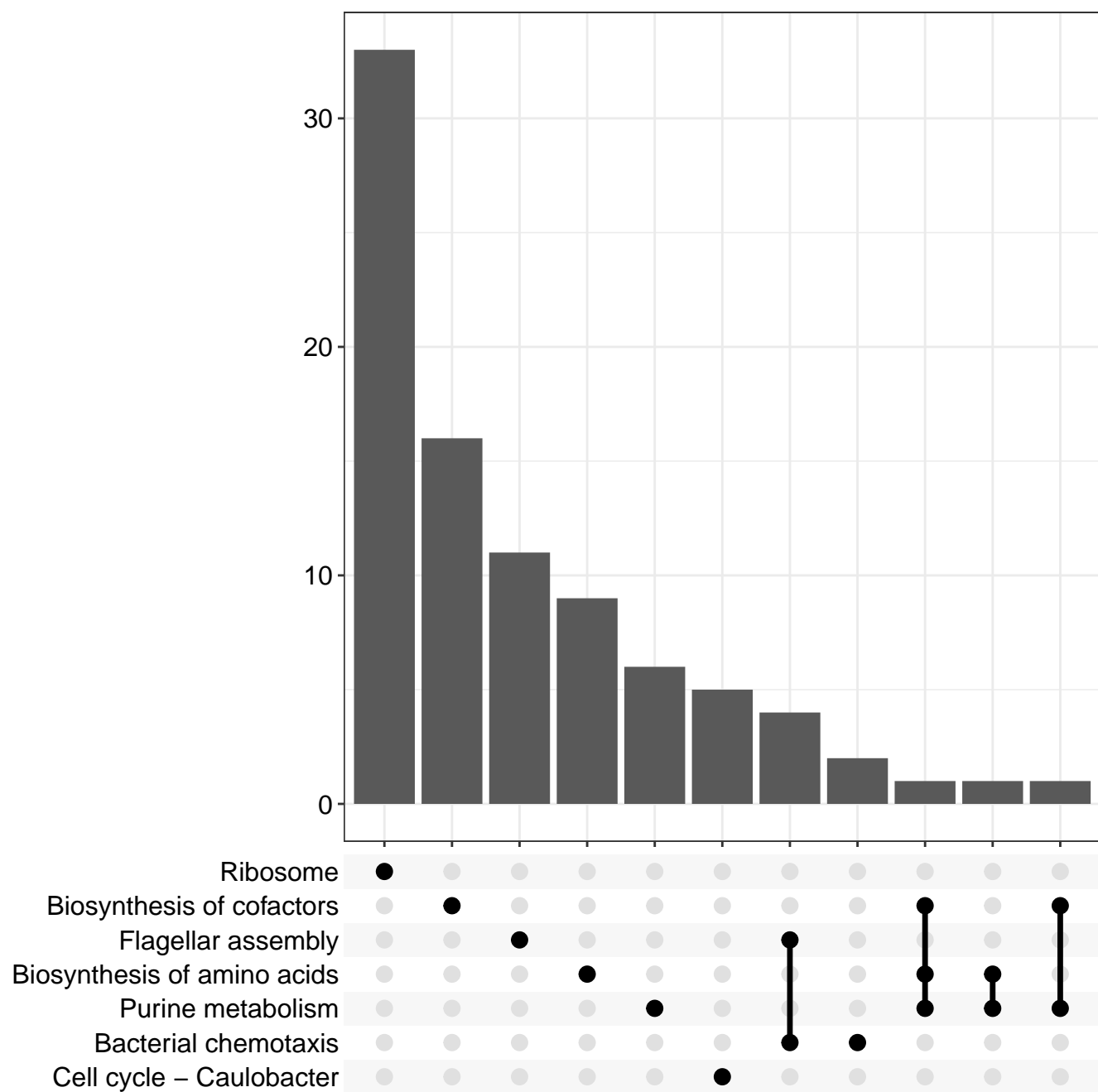


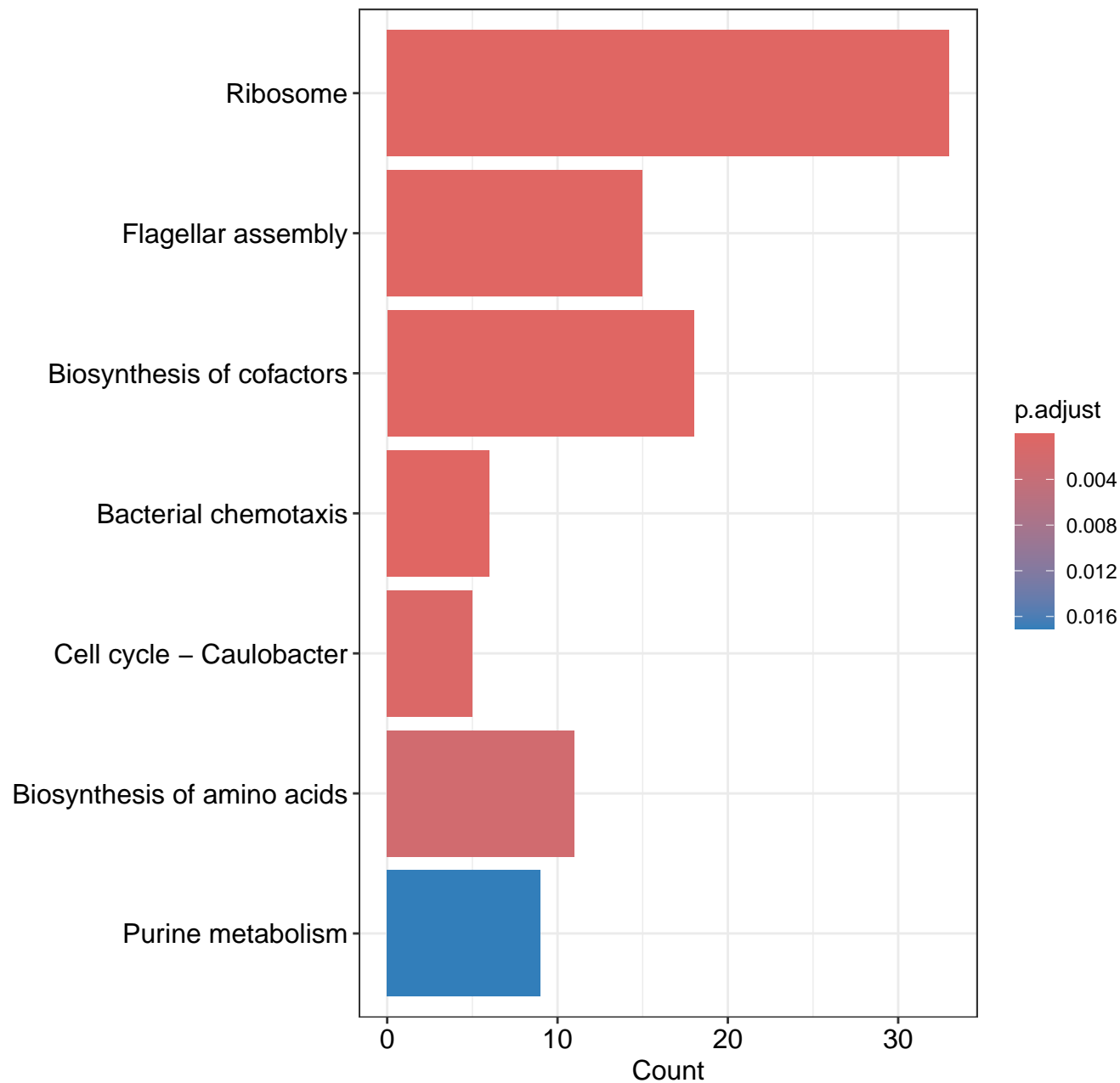
## C geom\_path



*[Illegible scribbled-out text]*







C gsea\_path

Flagellar assembly

p.adjust

3.25e-08

Count

29

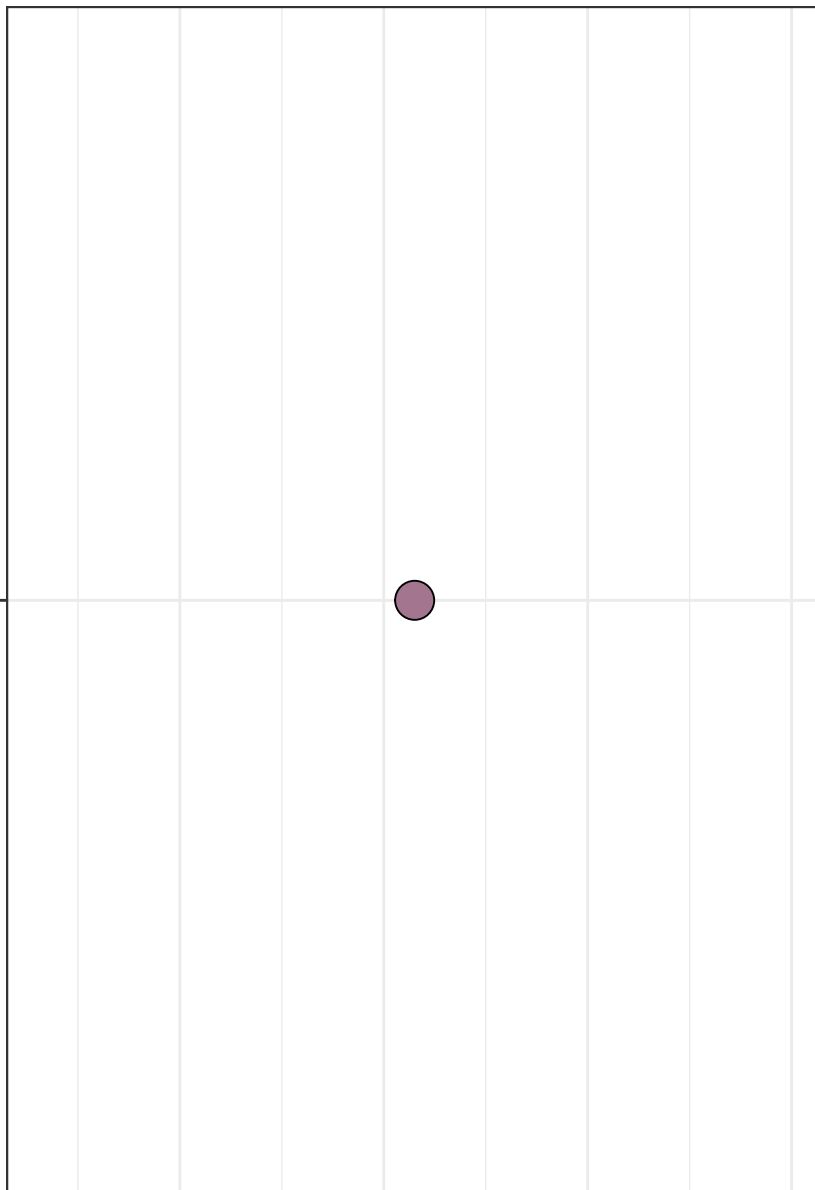
0.850

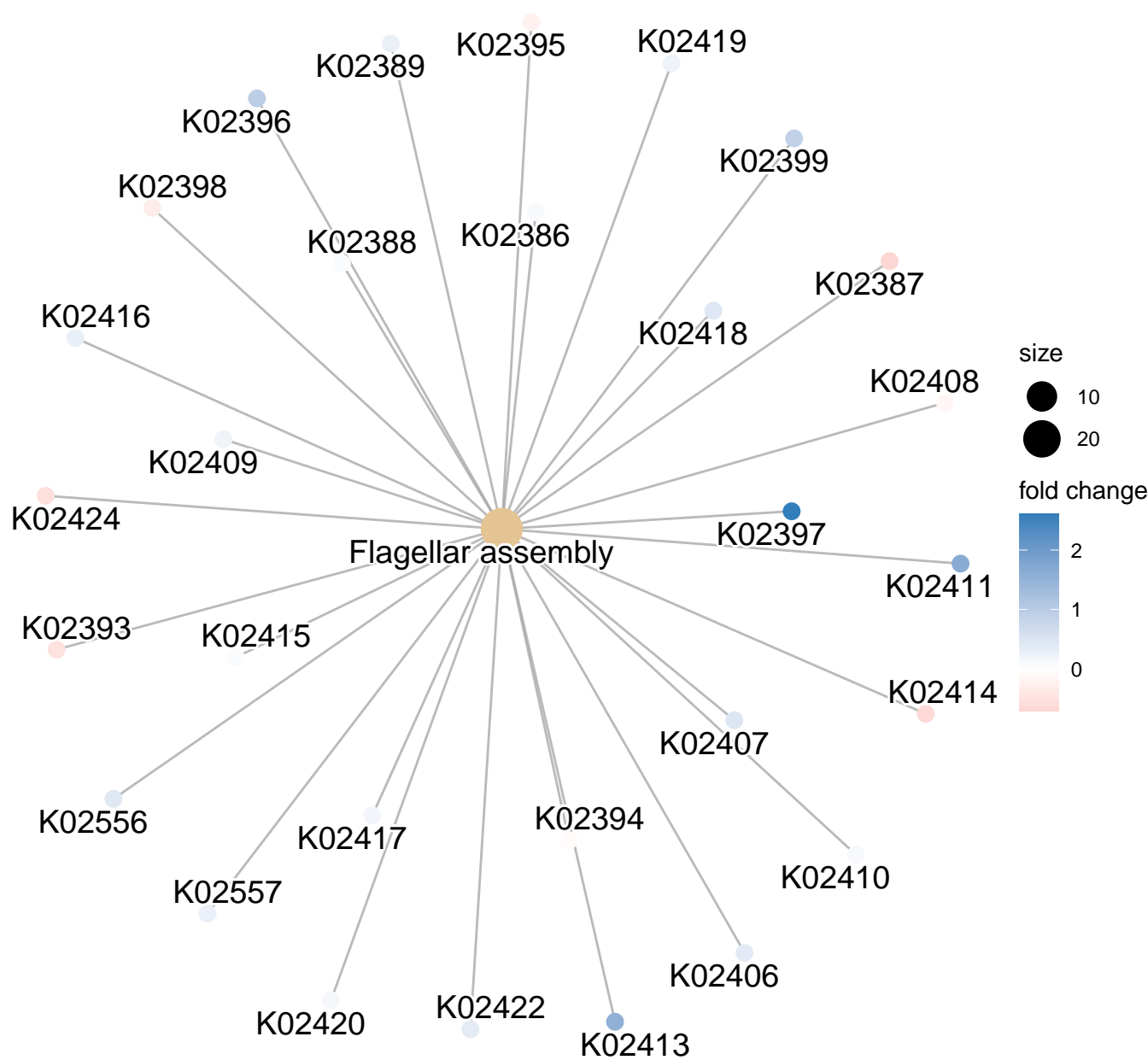
0.875

0.900

0.925

GeneRatio



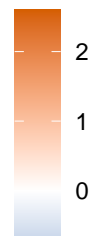




C gsea\_path

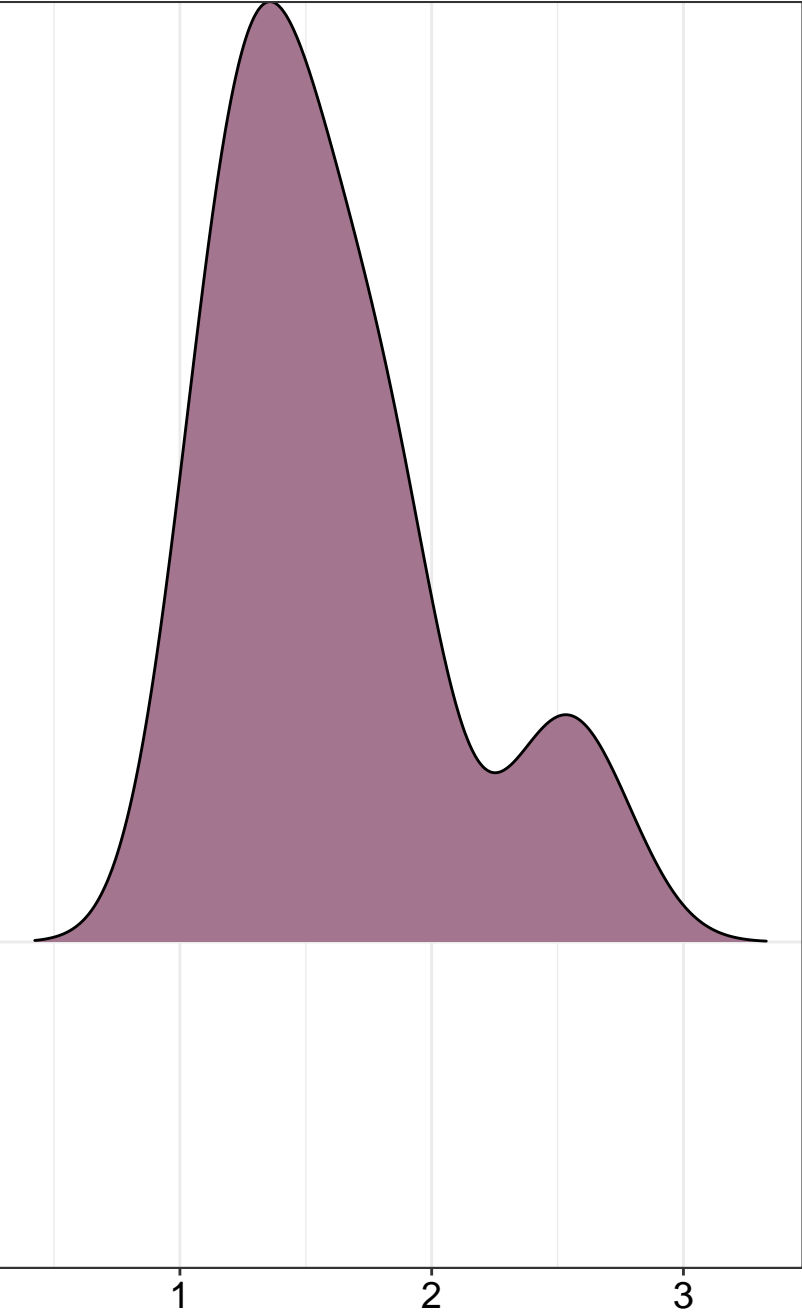
Flagellar assembly

foldChange



K02386  
K02387  
K02388  
K02389  
K02393  
K02394  
K02395  
K02396  
K02397  
K02398  
K02399  
K02406  
K02407  
K02408  
K02409  
K02410  
K02411  
K02413  
K02414  
K02415  
K02416  
K02417  
K02418  
K02419  
K02420  
K02422  
K02424  
K02556  
K02557

Flagellar assembly

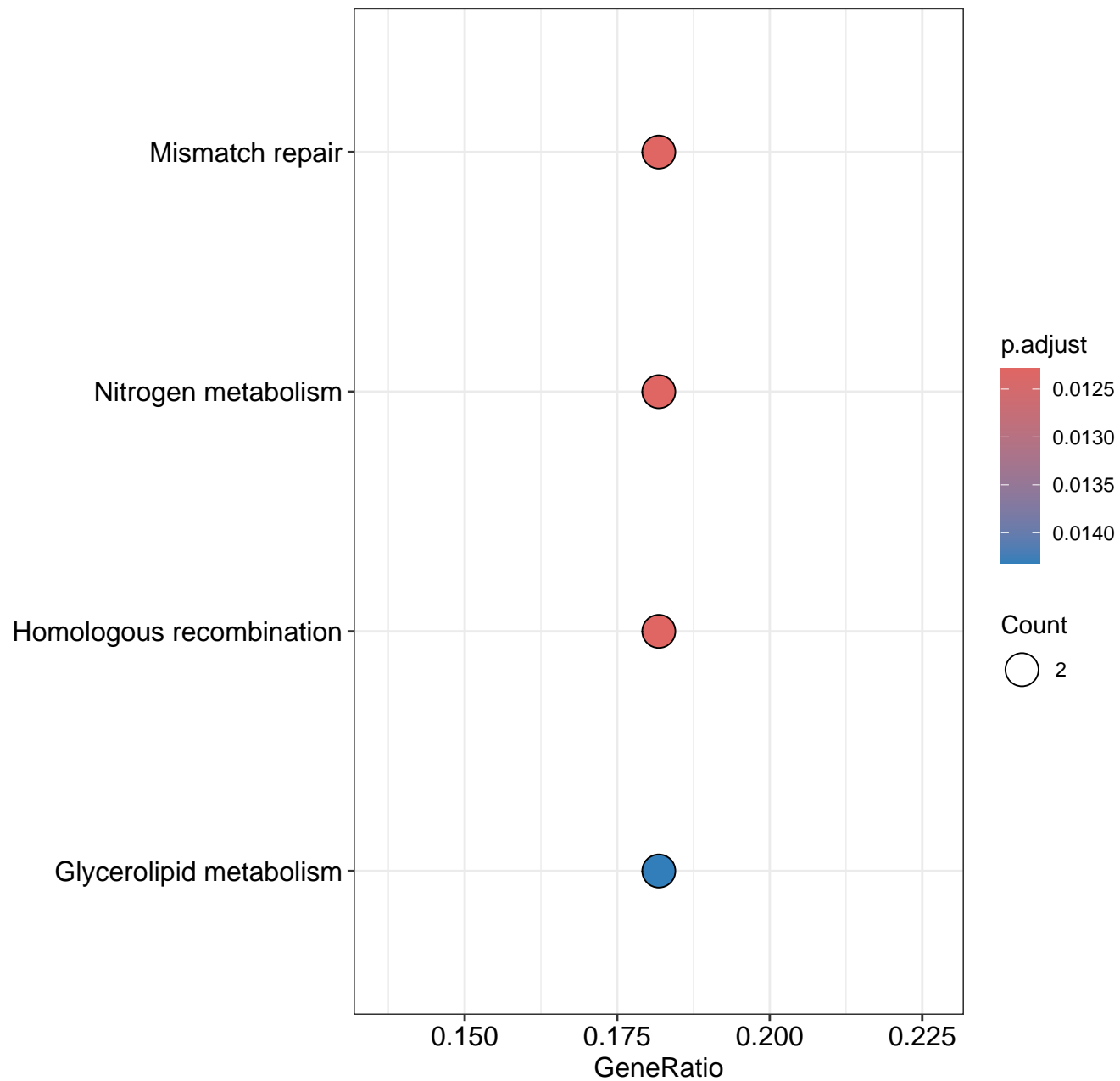


pvalue

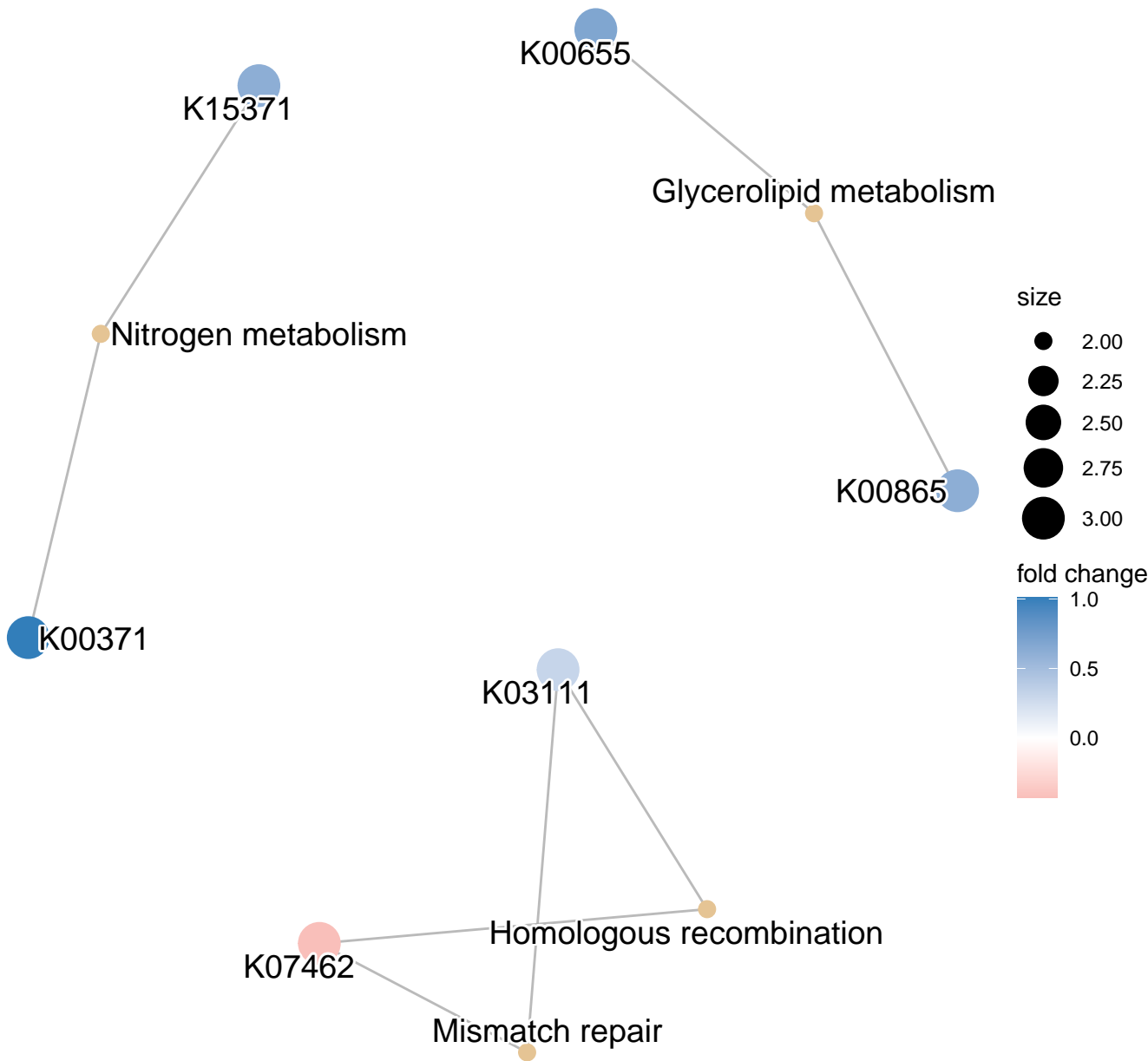


1e-10

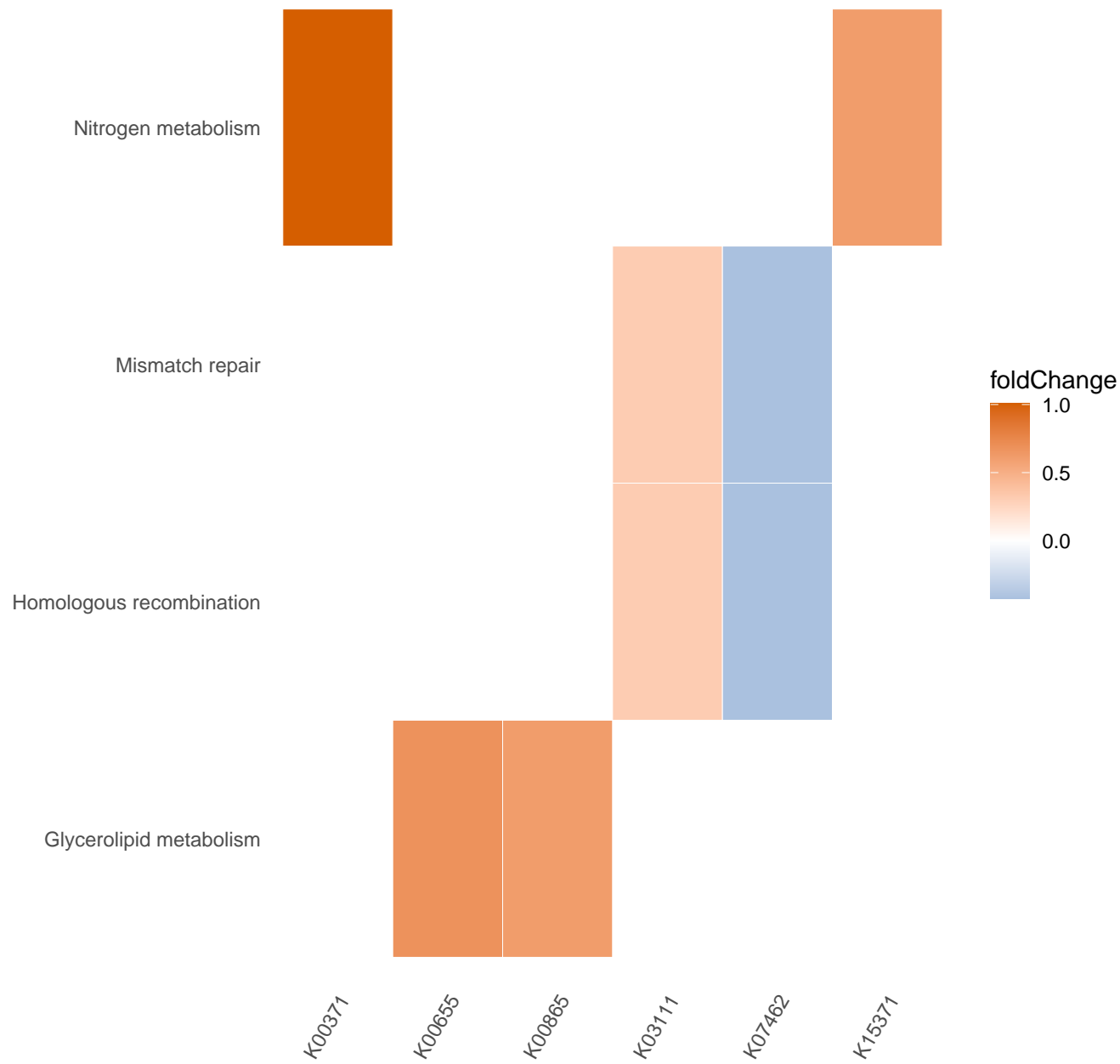
D geom\_path

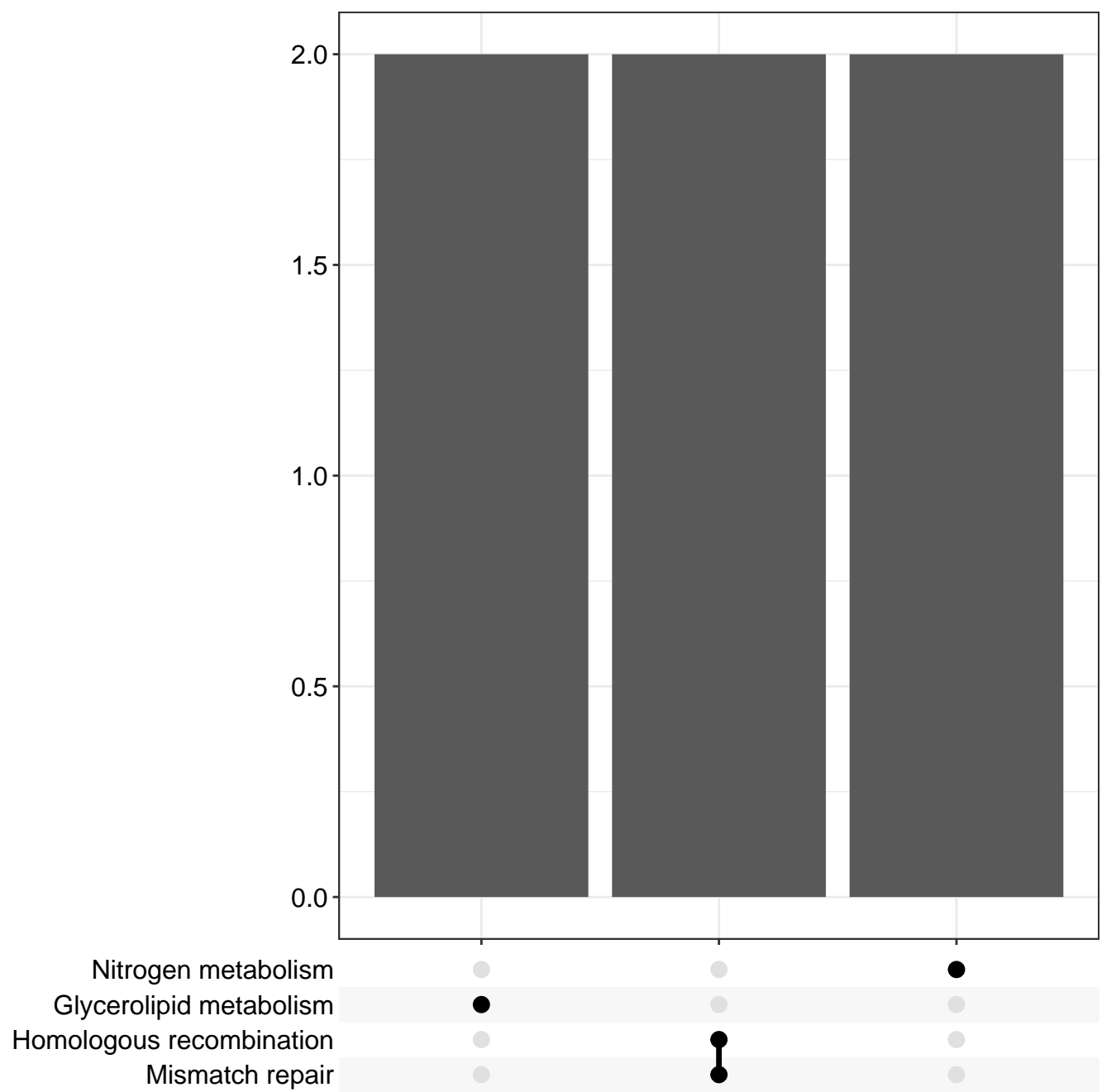


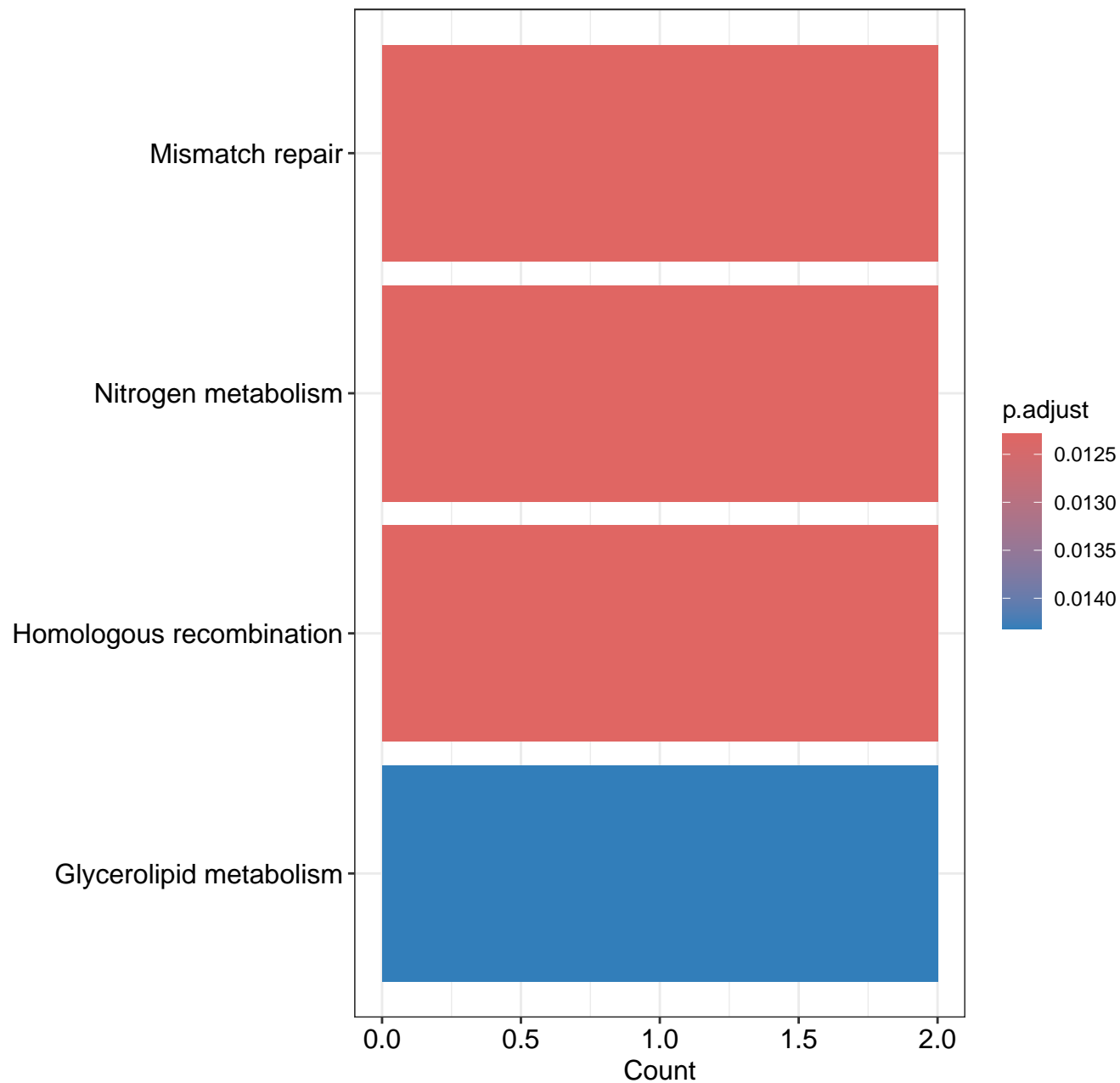
D geom\_path



D geom\_path







D gsea\_path

Coronavirus disease – COVID-19

Ribosome

p.adjust

0.02470505

Count



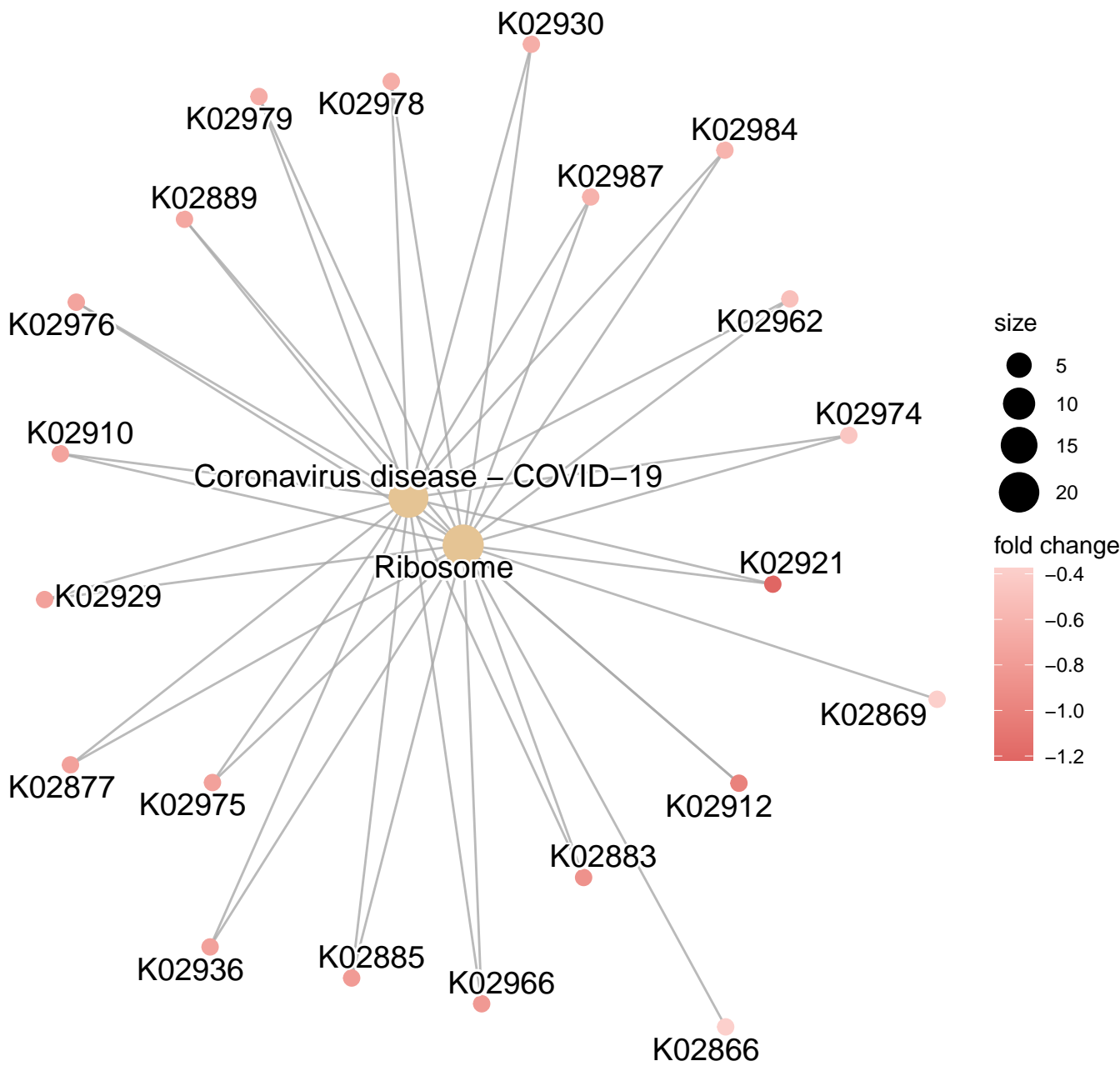
0.4

0.6

0.8

GeneRatio

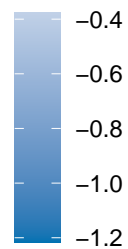




D gsea\_path

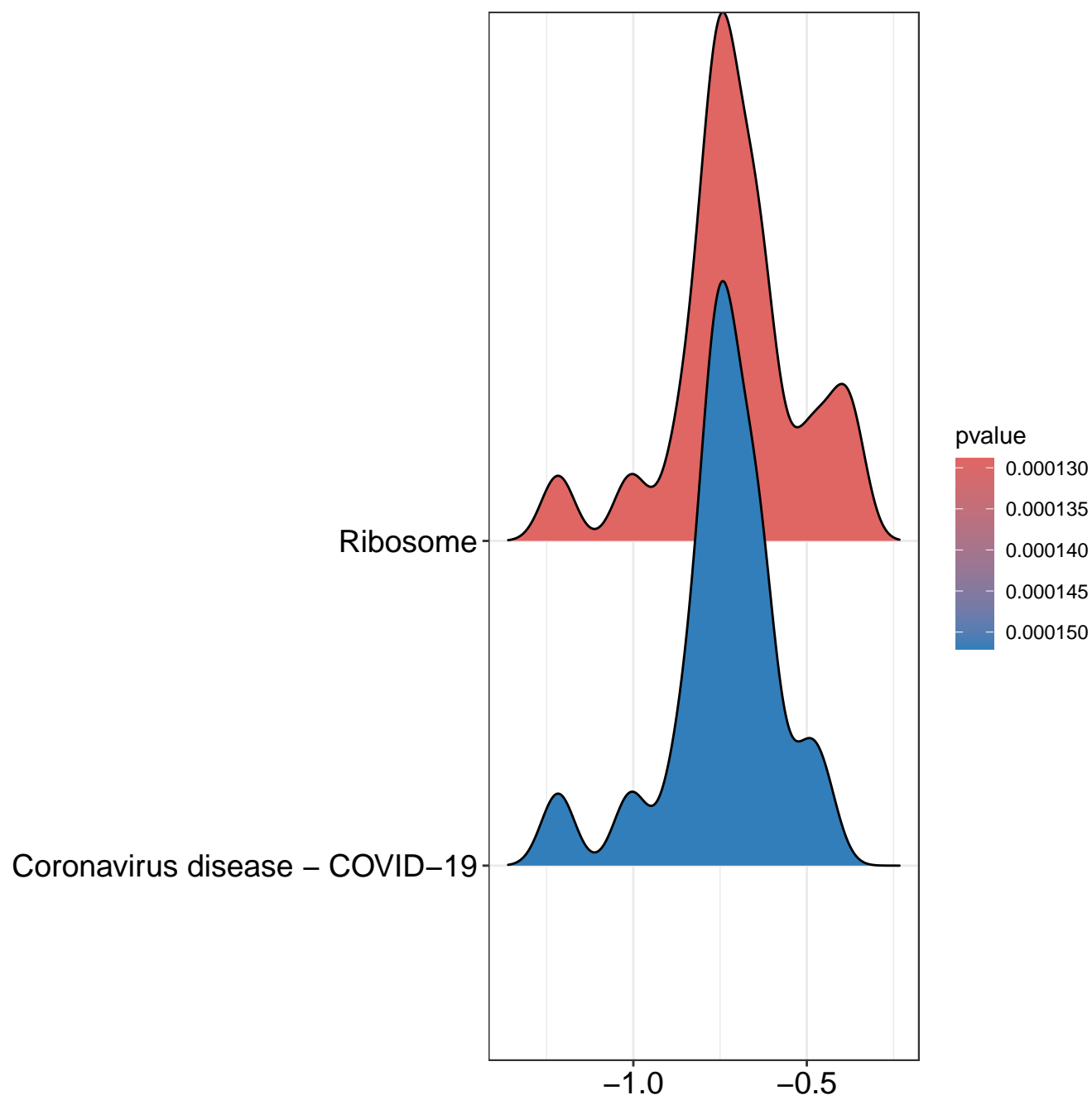
Ribosome

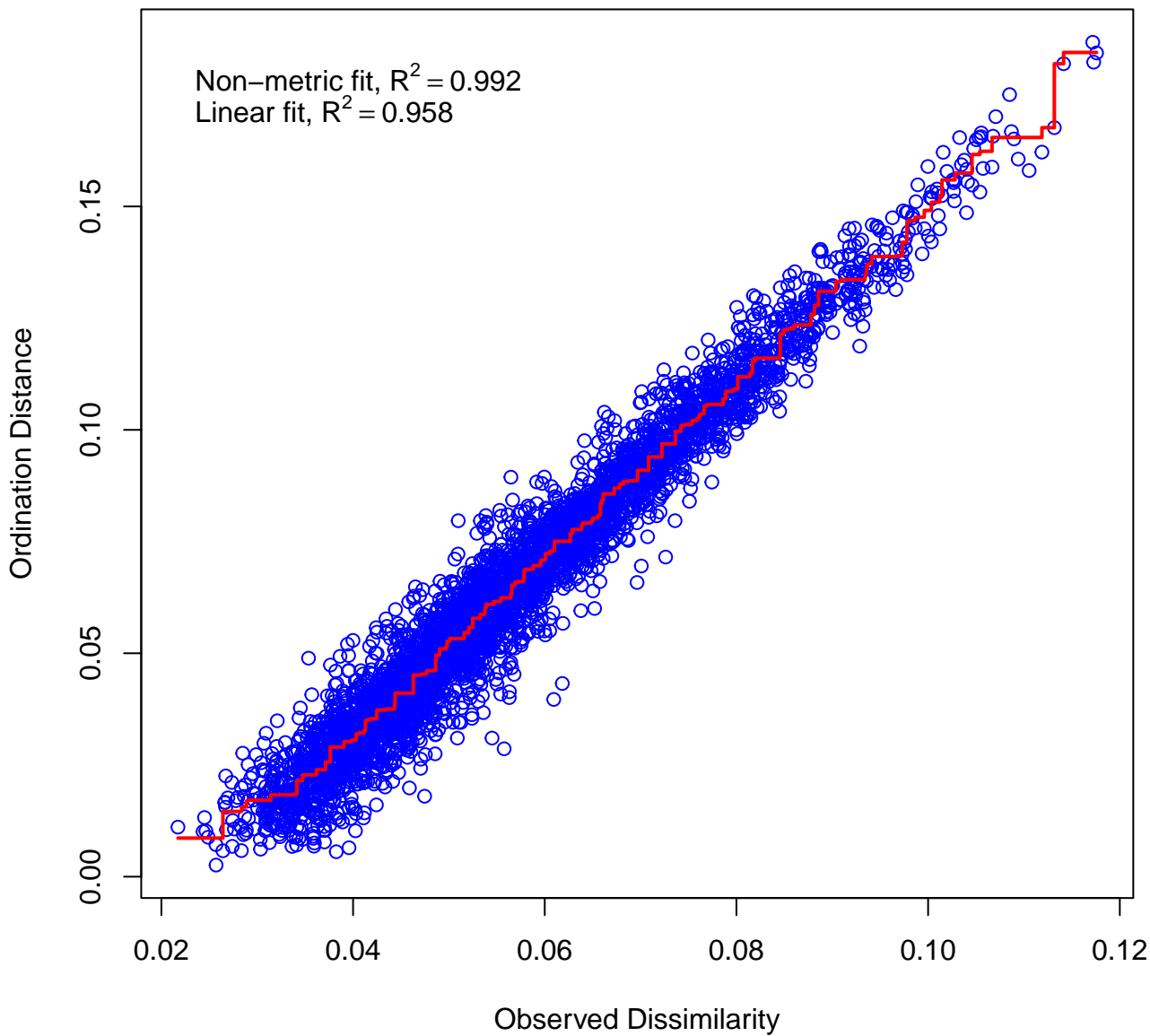
foldChange



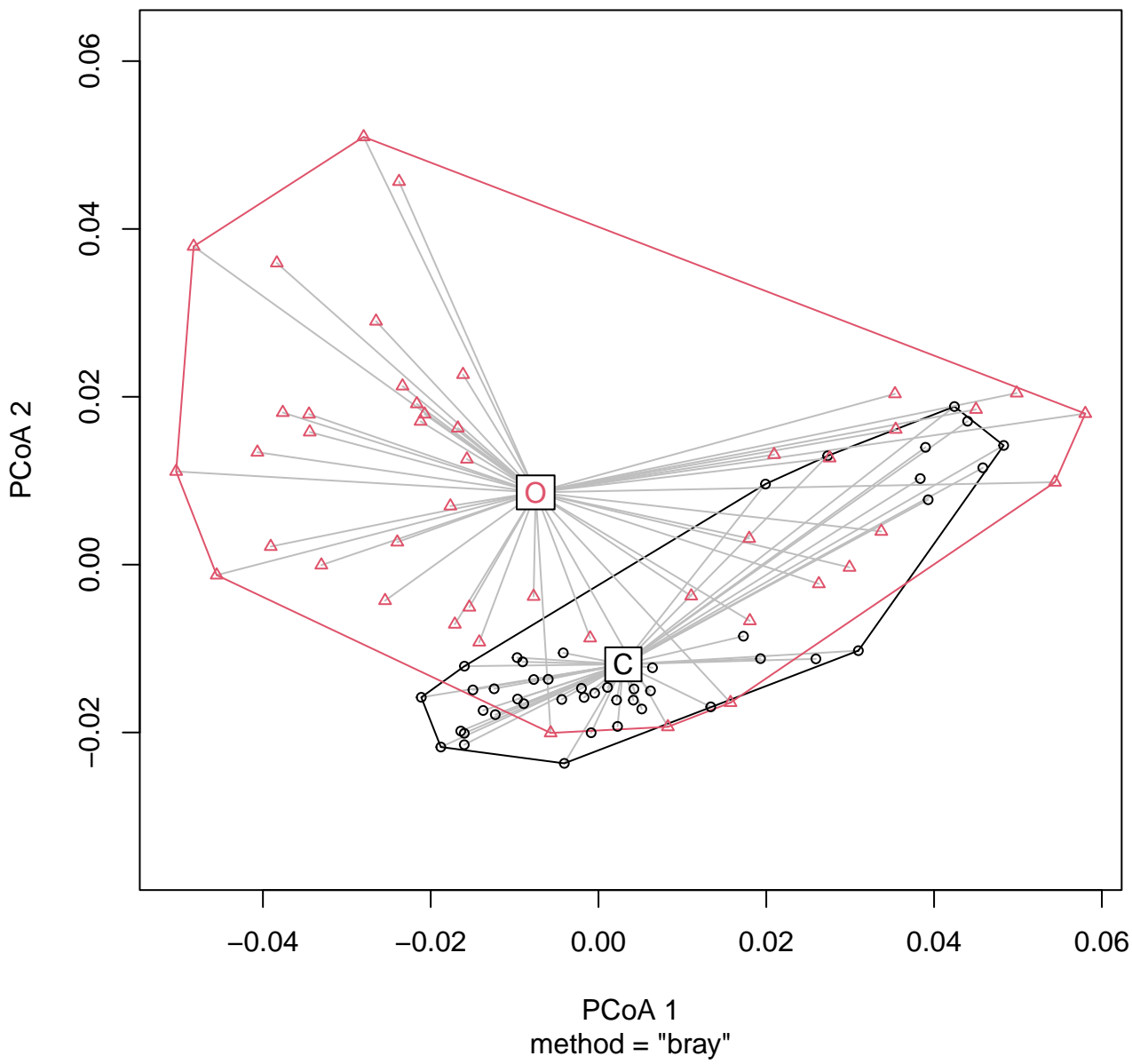
K02866  
K02869  
K02877  
K02883  
K02885  
K02889  
K02910  
K02912  
K02921  
K02929  
K02930  
K02936  
K02962  
K02966  
K02974  
K02975  
K02976  
K02978  
K02979  
K02984  
K02987

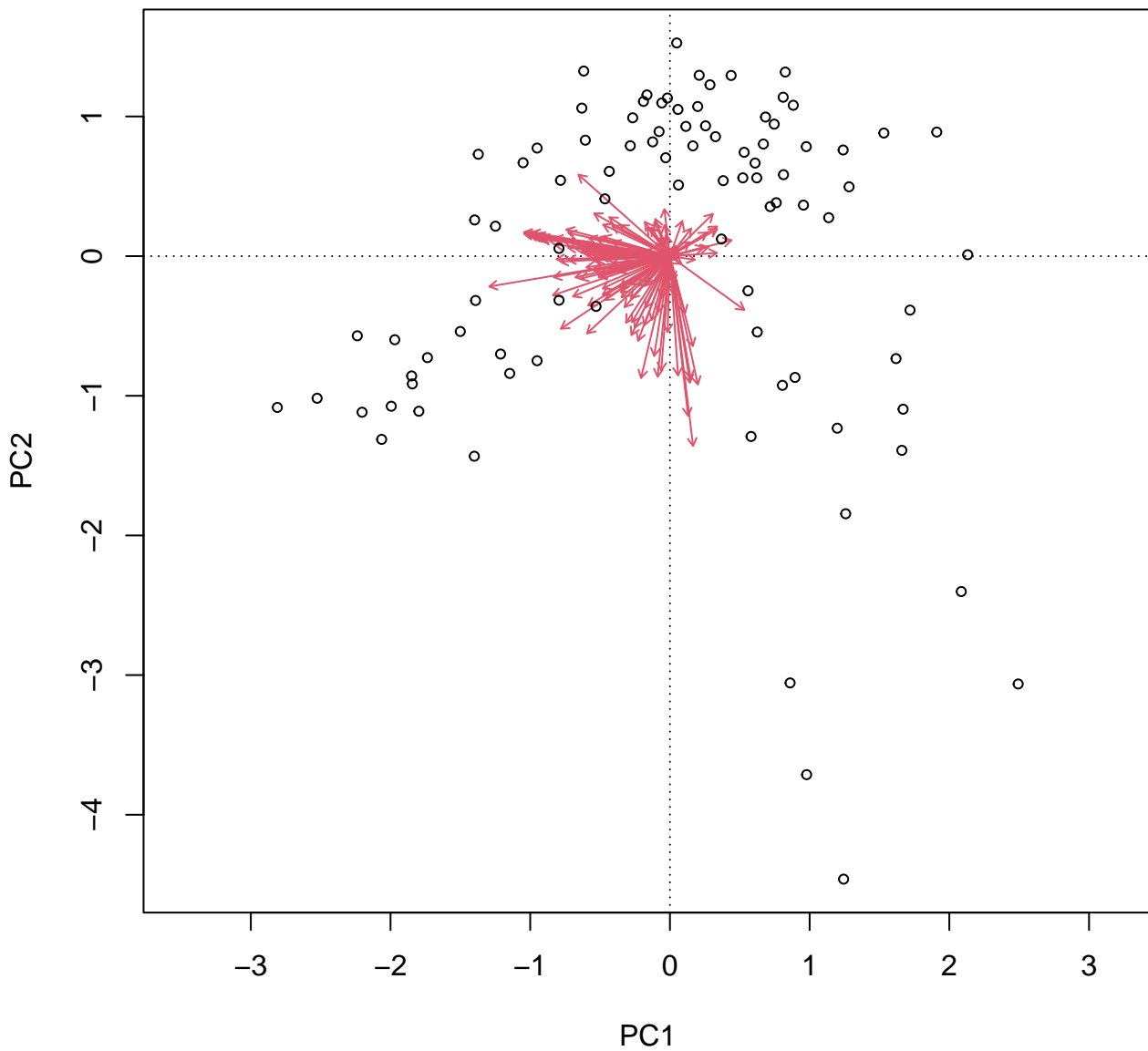
Coronavirus disease – COVID-19

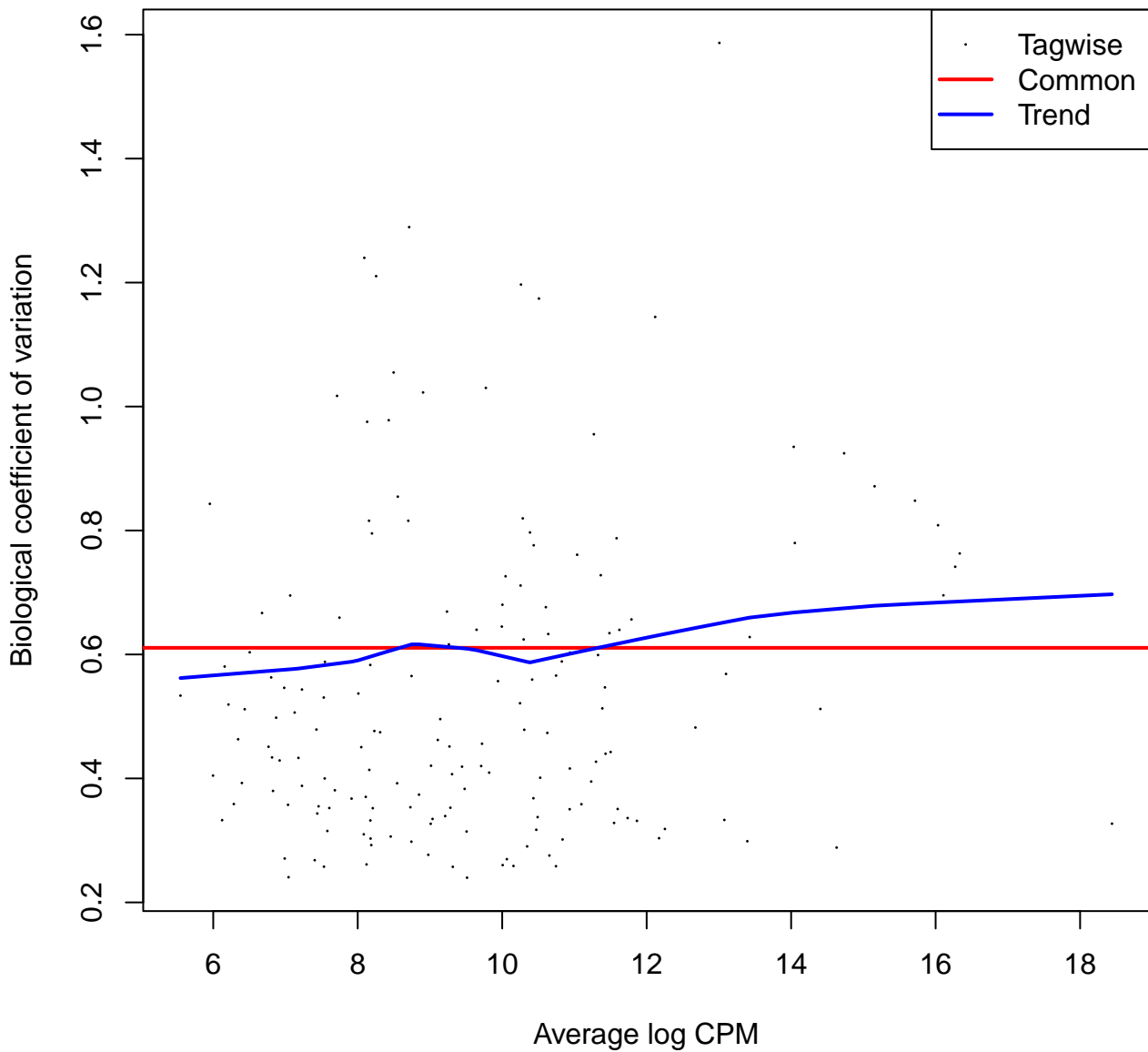




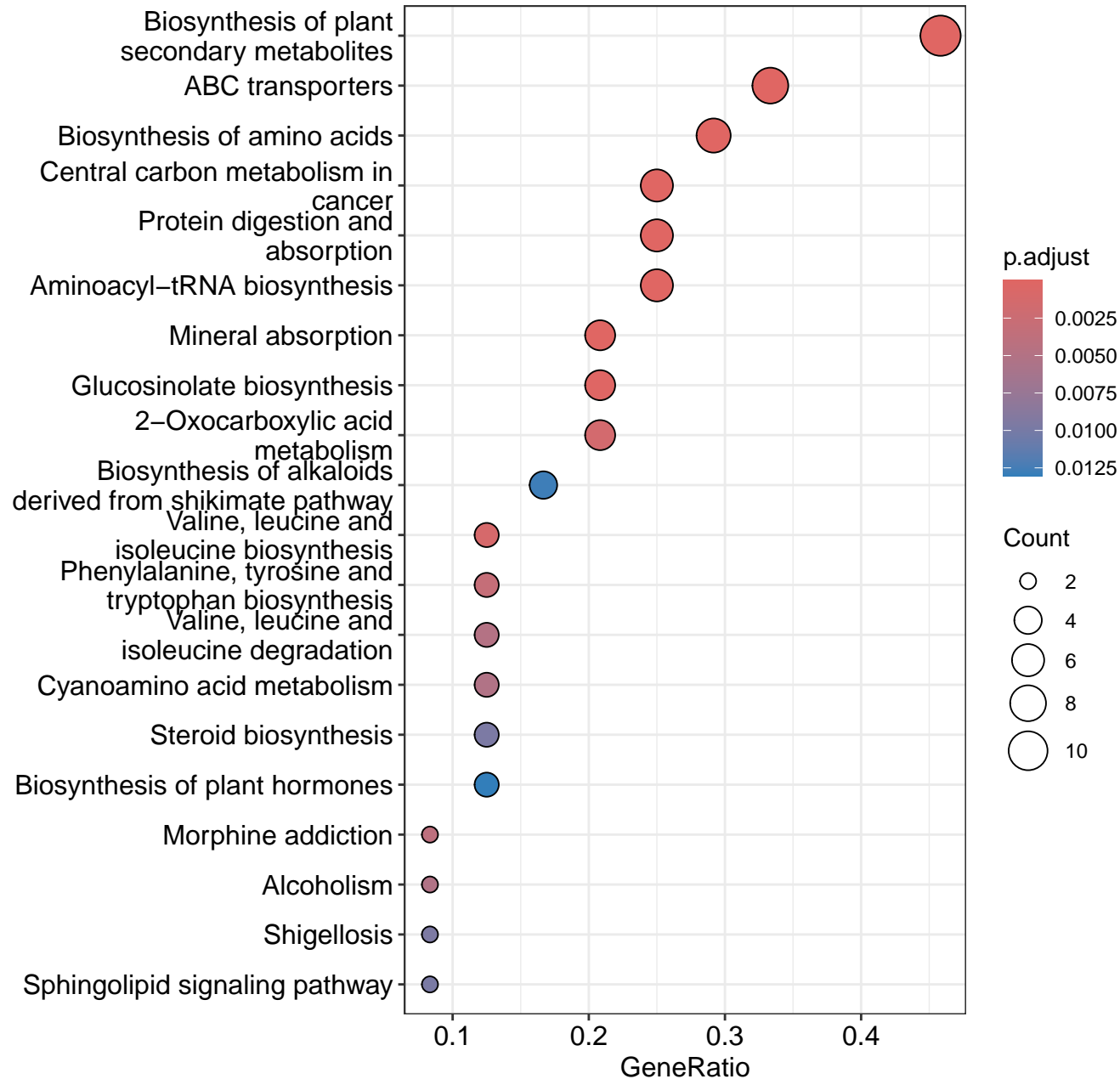
ps.disper





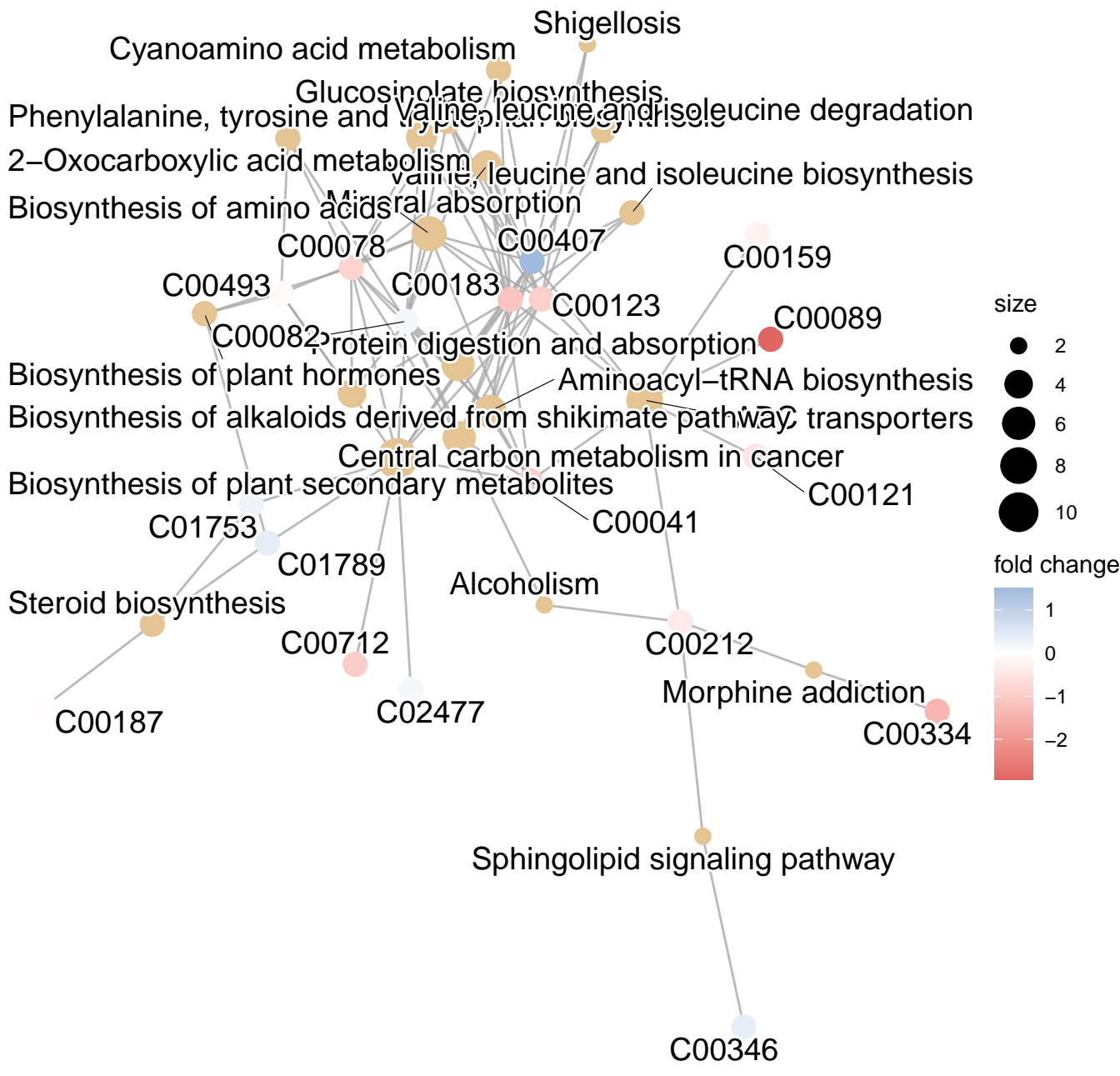


Site geom\_path



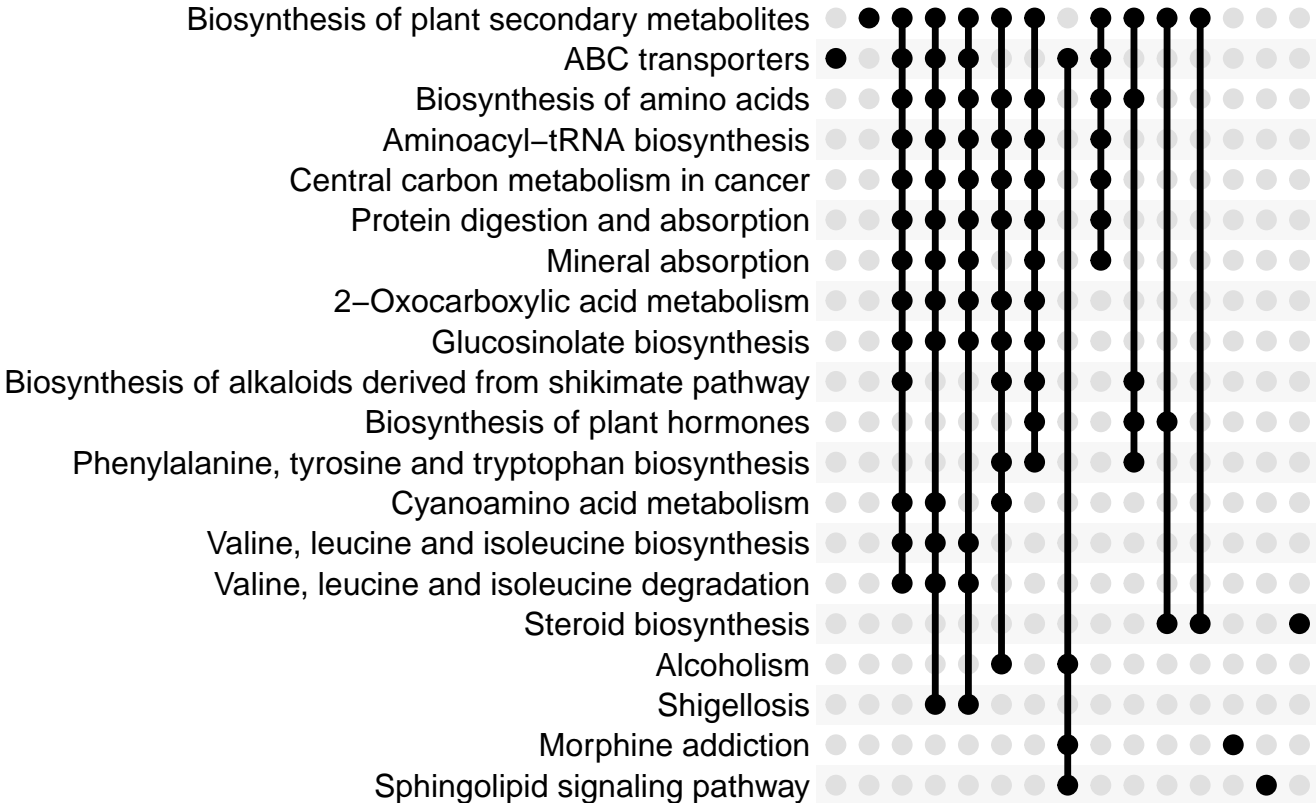
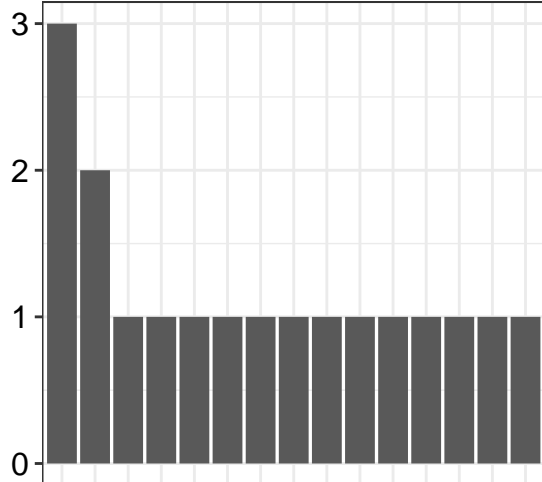


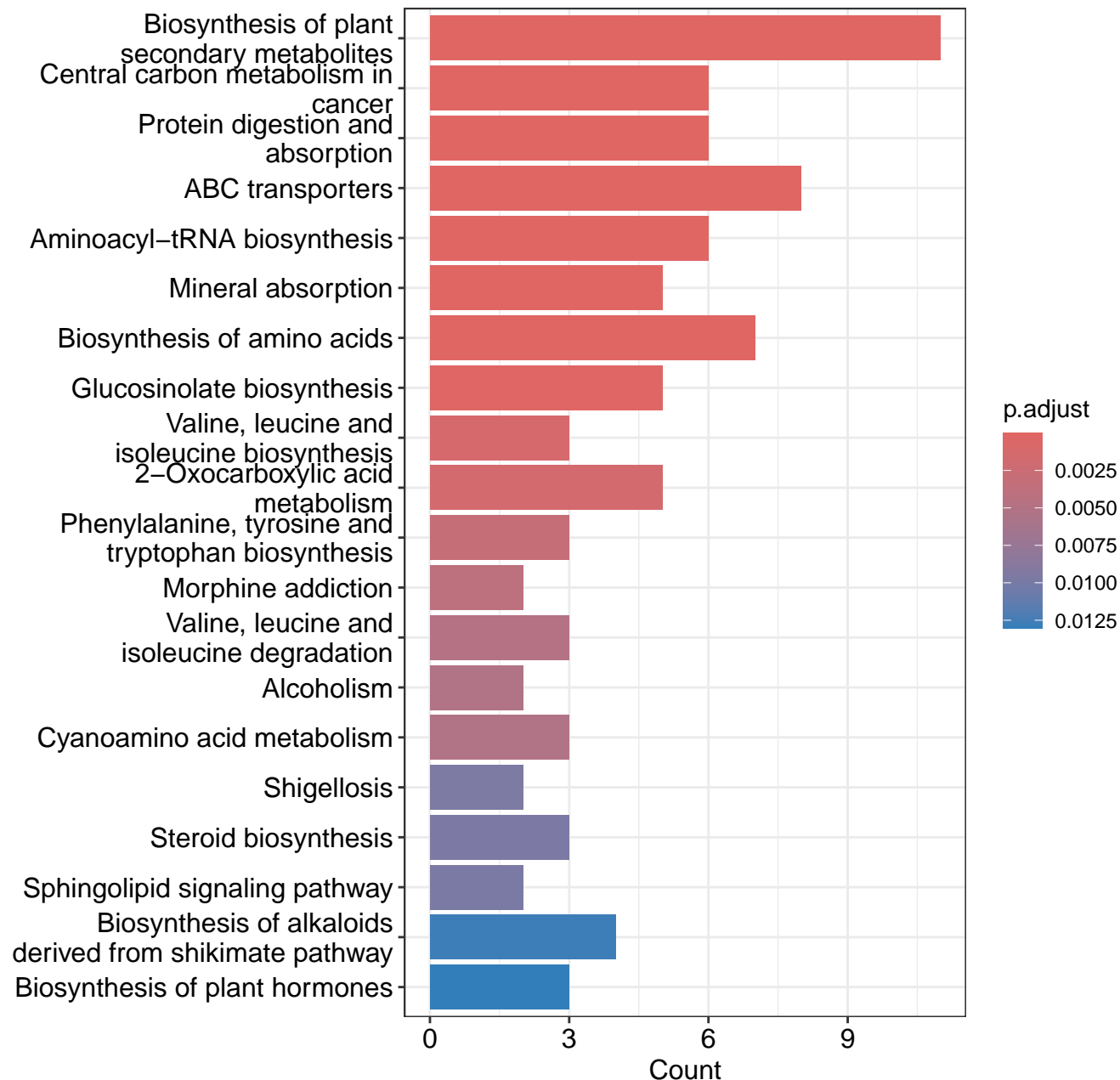
Site geom\_path



# Site geom\_path

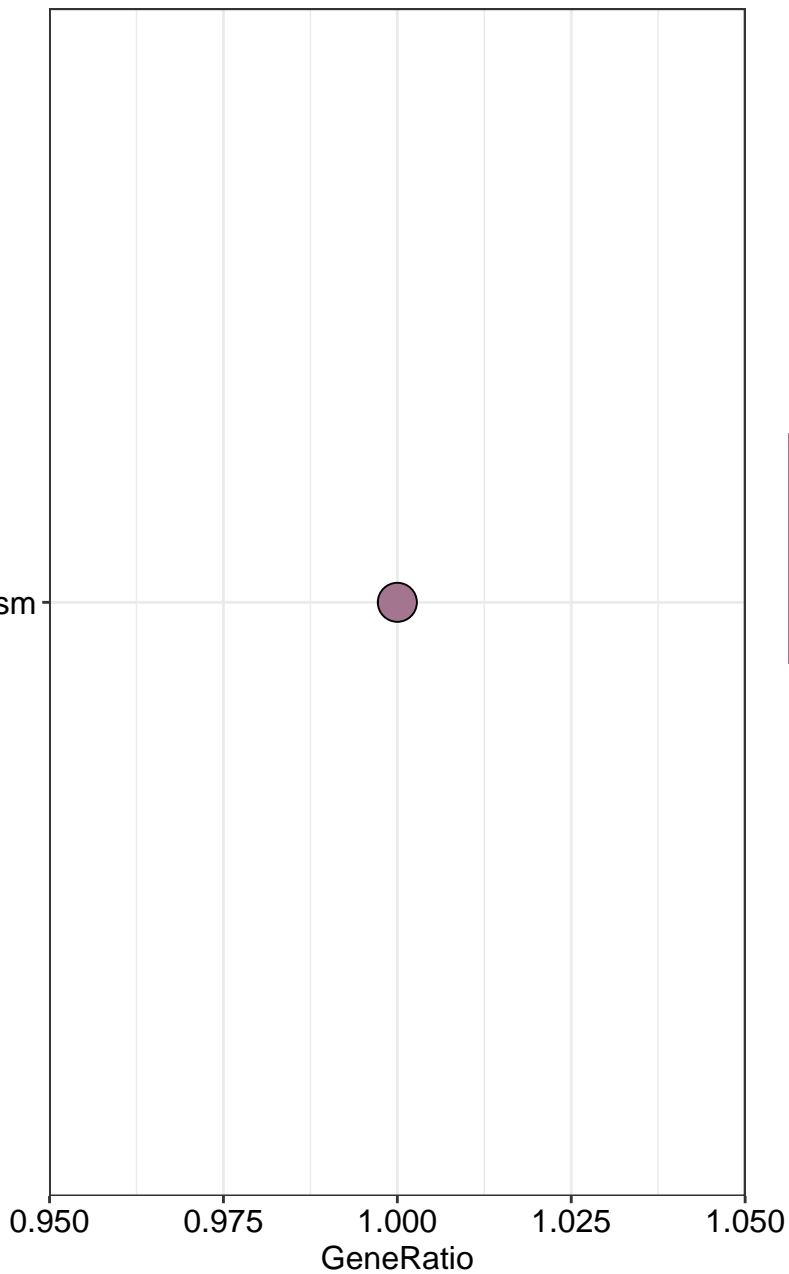






B geom\_path

Sphingolipid metabolism



p.adjust

0.004012197

Count

1

B geom\_path

C12144

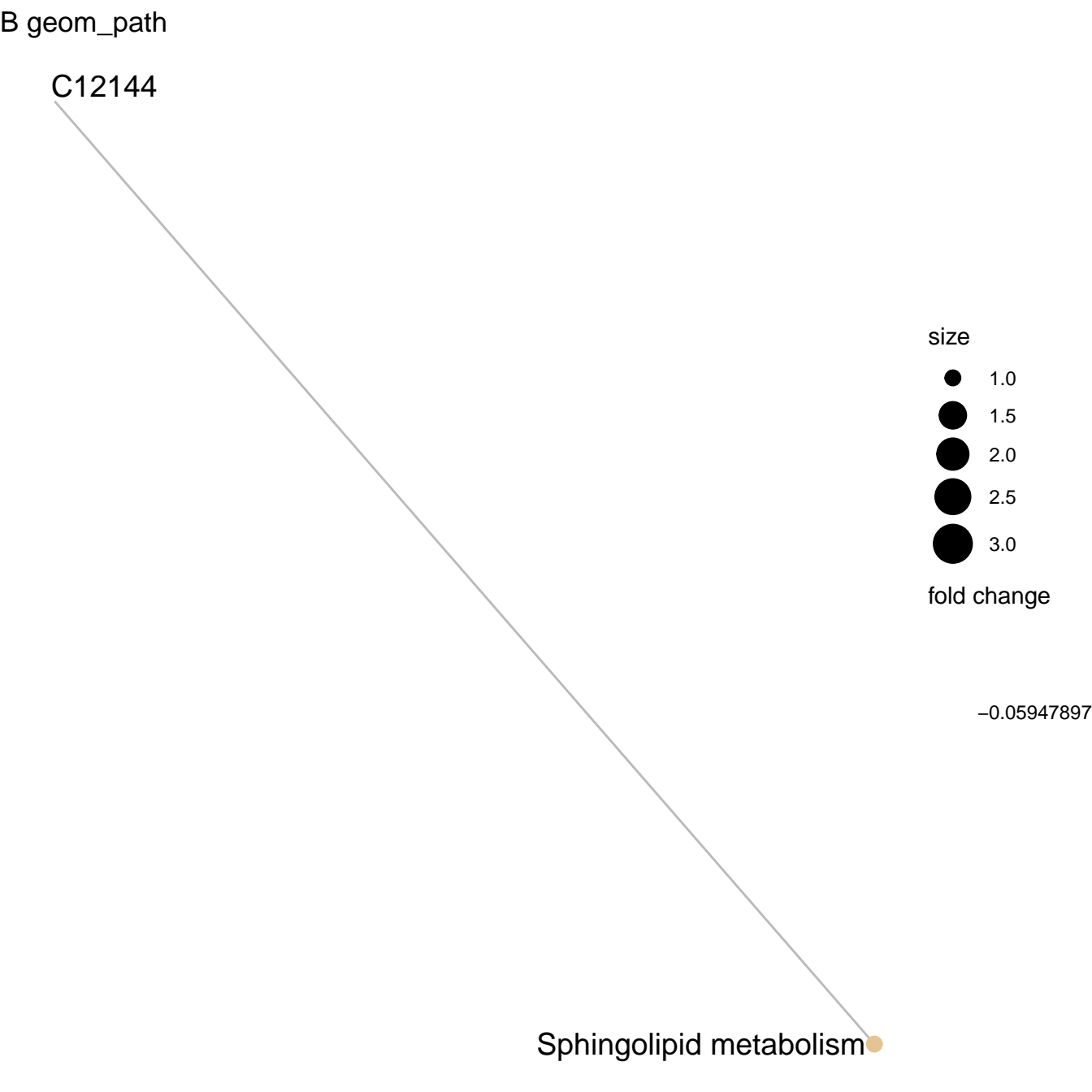
size



fold change

-0.05947897

Sphingolipid metabolism



B geom\_path

foldChange

Sphingolipid metabolism

-0.05947897

C12144

1.00  
0.75  
0.50  
0.25  
0.00

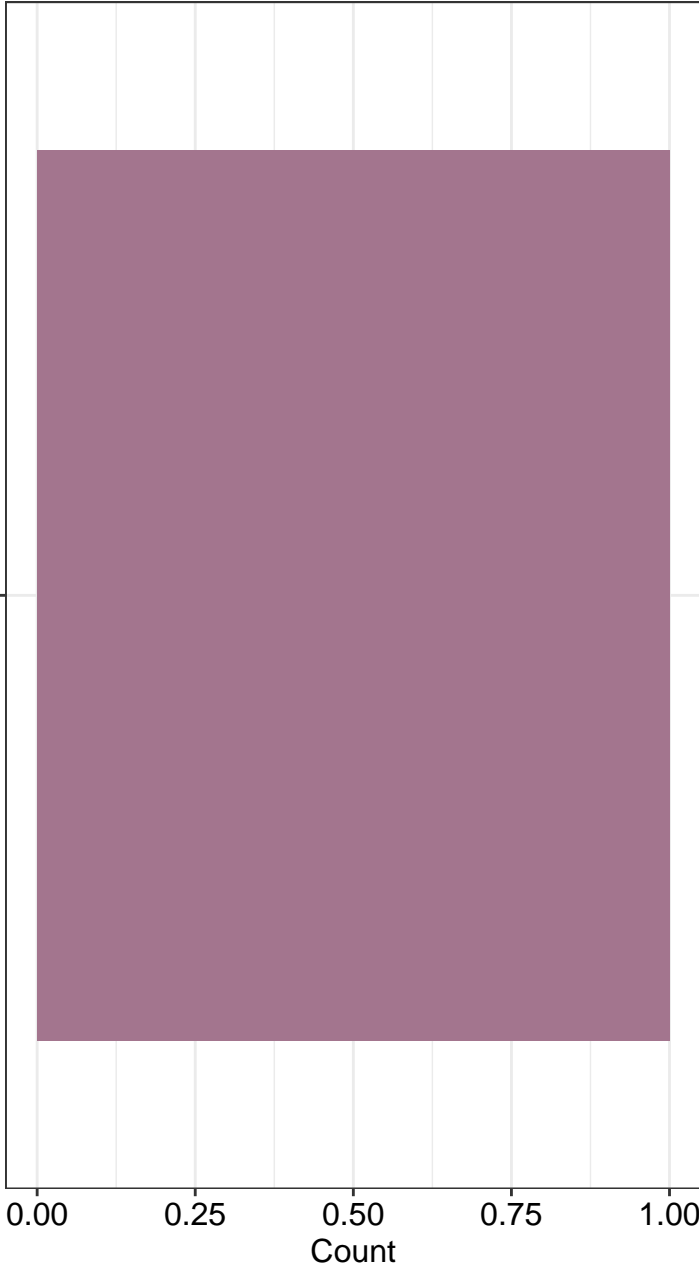


Sphingolipid metabolism

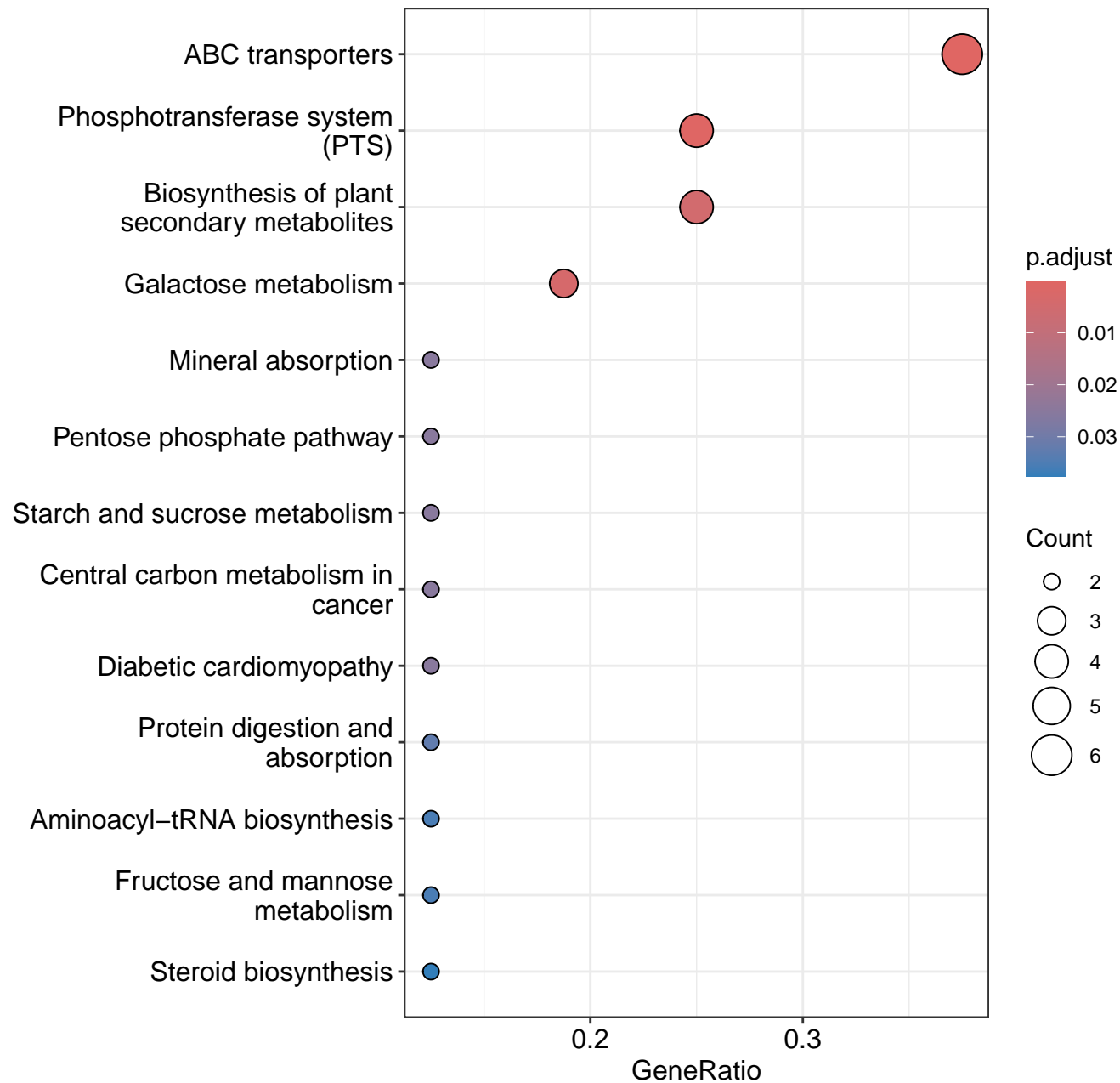




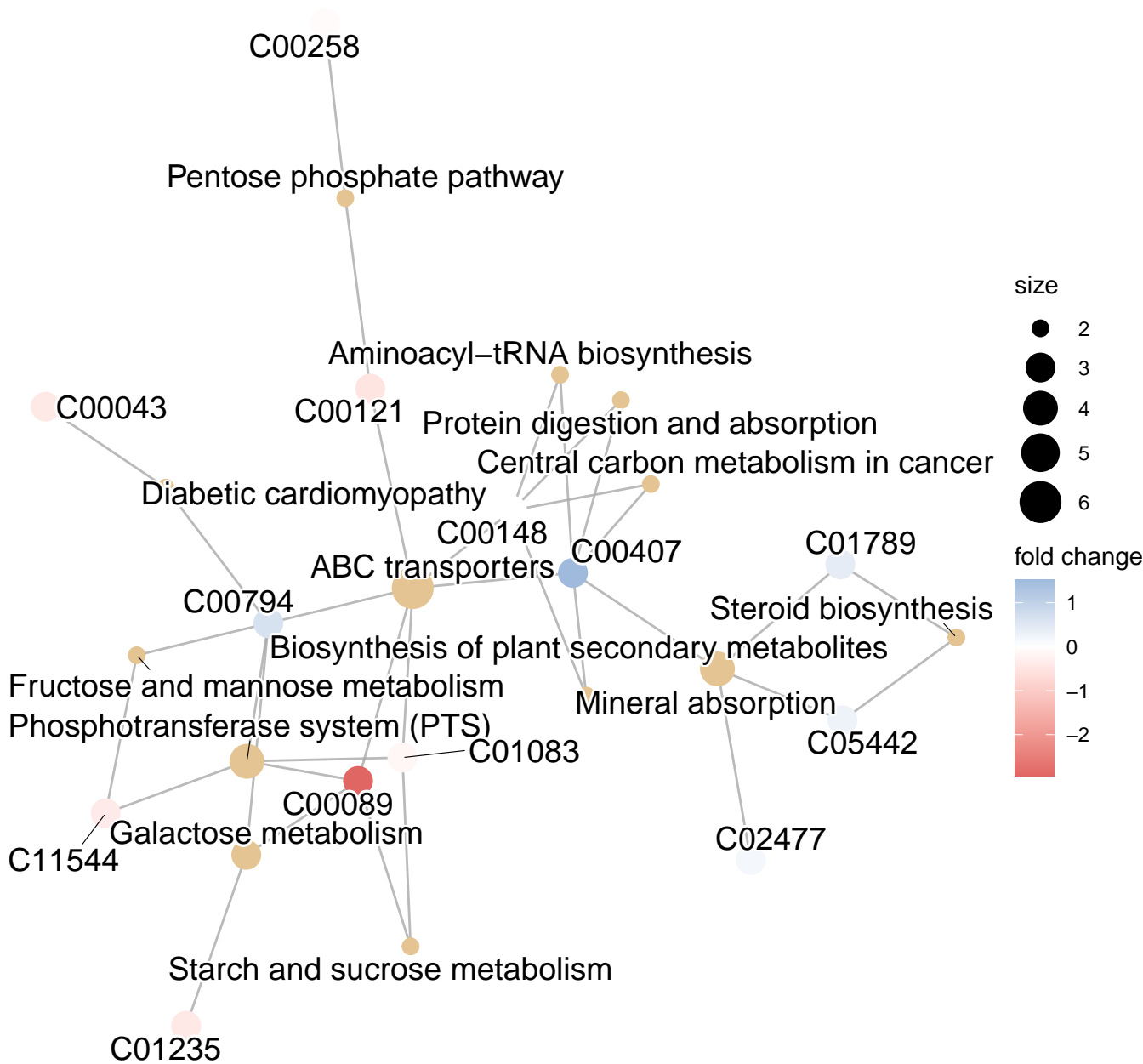
Sphingolipid metabolism



C geom\_path

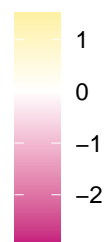


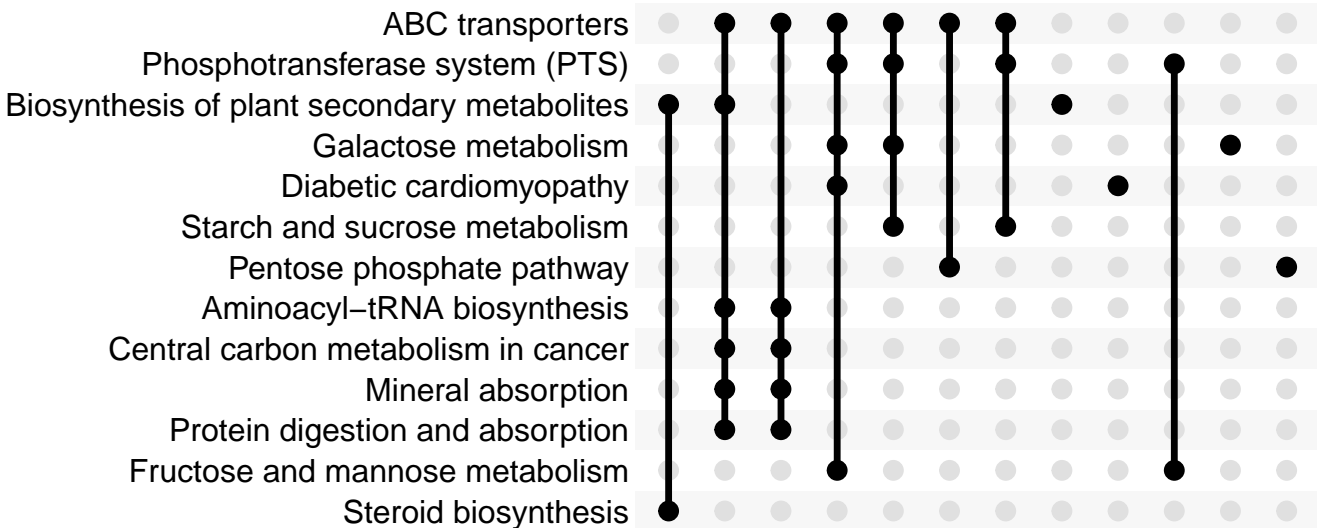
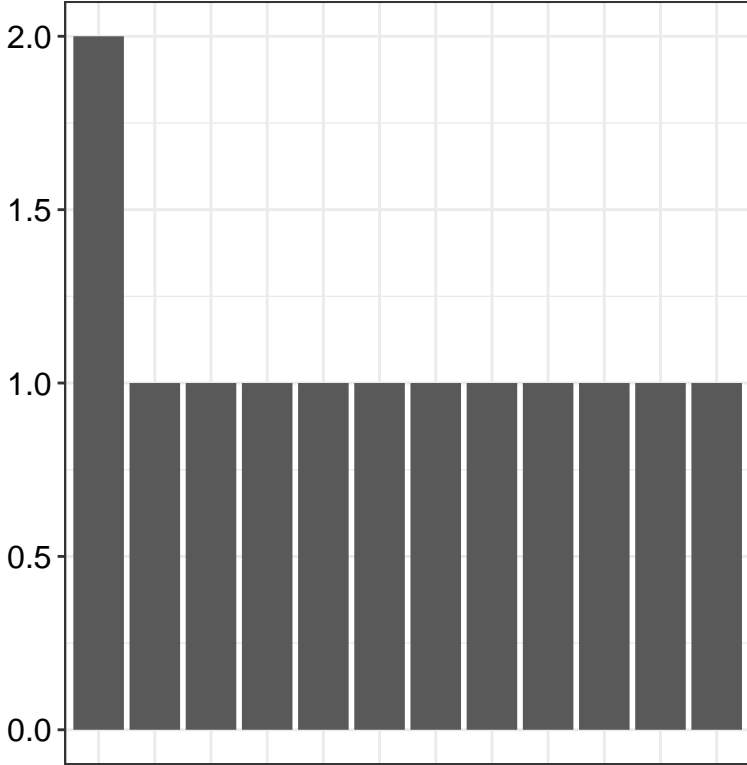
C geom\_path

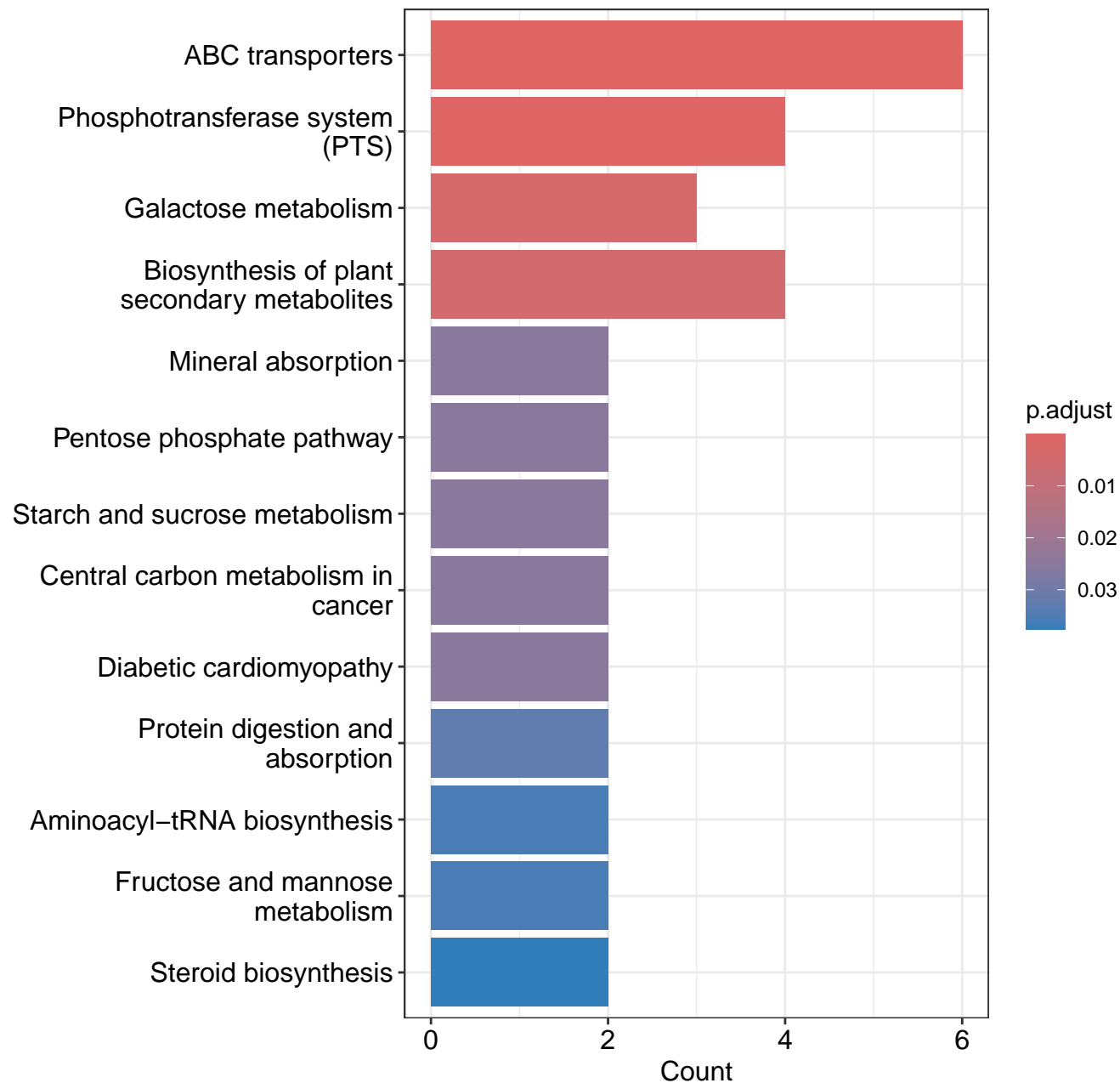


# C geom\_path

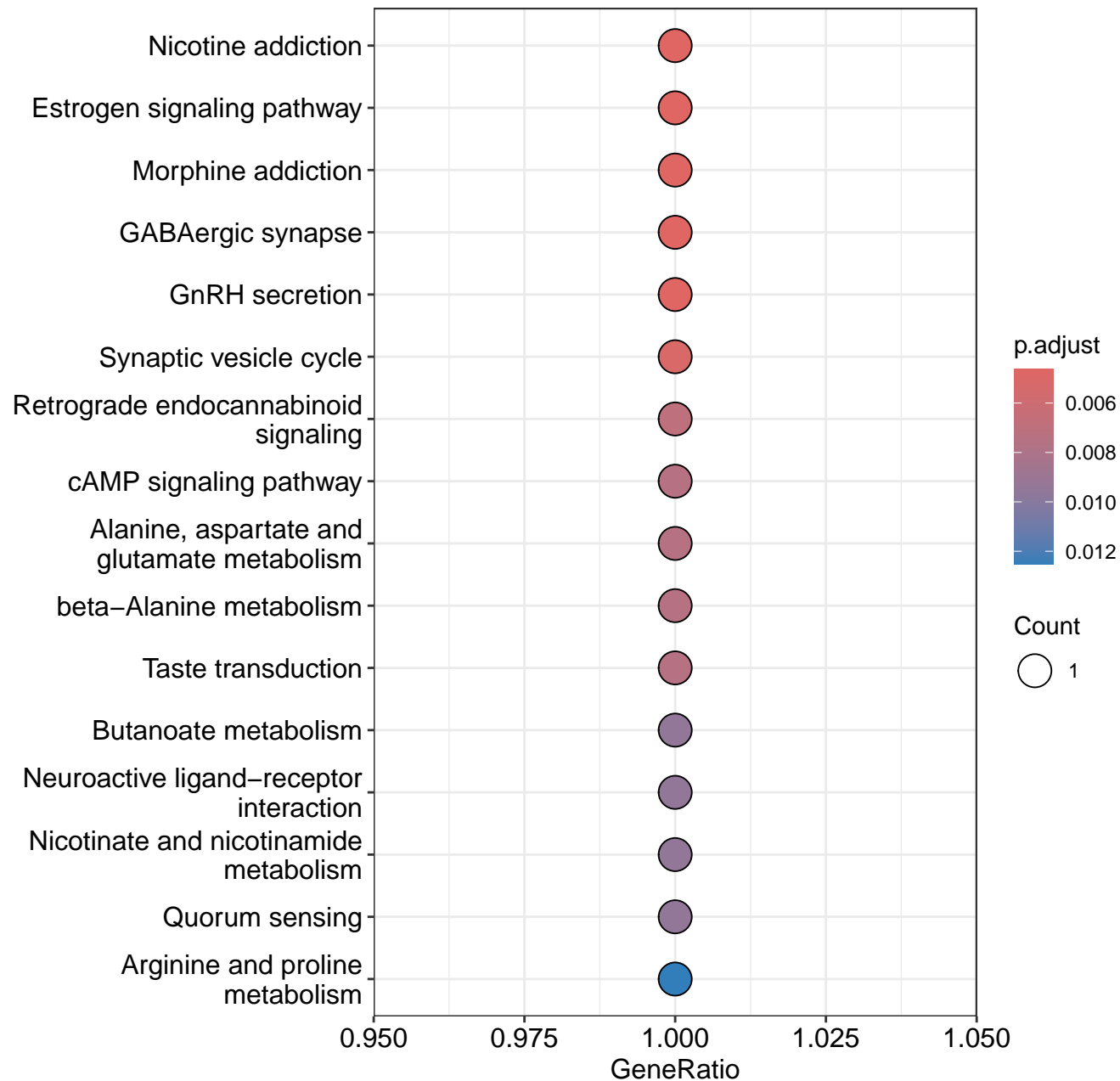
foldChange



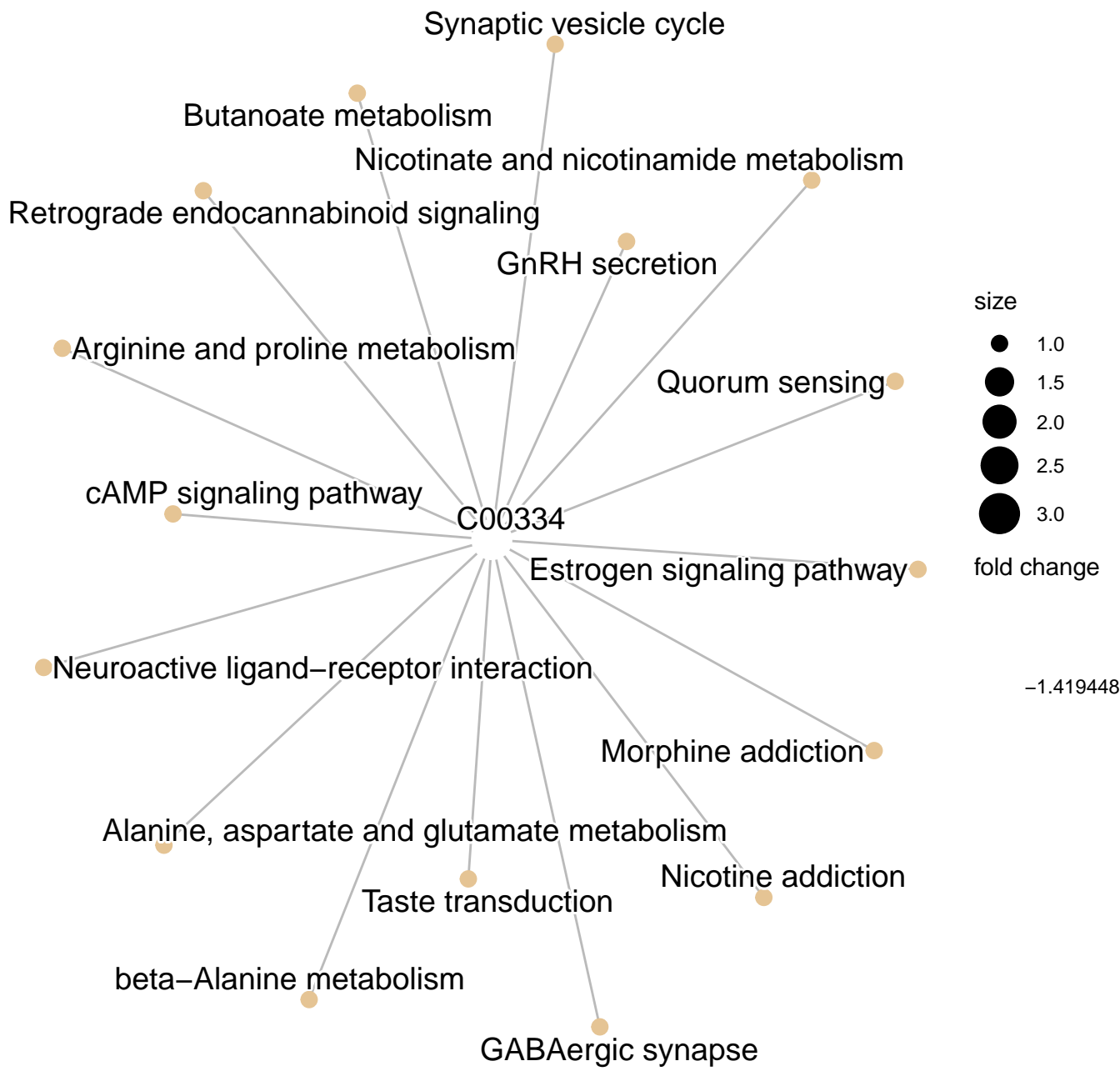




D geom\_path



D geom\_path





# D geom\_path

foldChange

−1.419448

C00334

Taste transduction

Synaptic vesicle cycle

Retrograde endocannabinoid  
signaling

Quorum sensing

Nicotine addiction

Nicotinate and nicotinamide  
metabolism

Neuroactive ligand–receptor  
interaction

Morphine addiction

GnRH secretion

GABAergic synapse

Estrogen signaling pathway

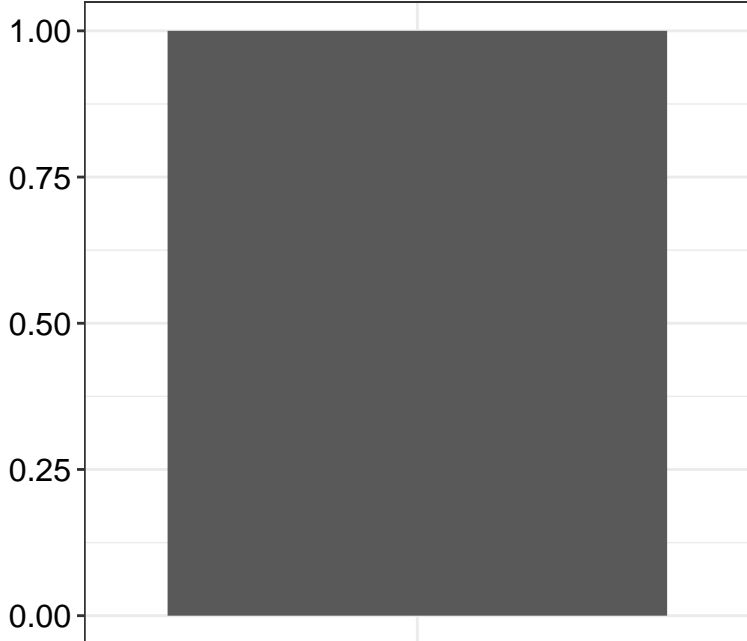
cAMP signaling pathway

Butanoate metabolism

beta–Alanine metabolism

Arginine and proline  
metabolism

Alanine, aspartate and  
glutamate metabolism



Alanine, aspartate and glutamate metabolism

Arginine and proline metabolism

beta-Alanine metabolism

Butanoate metabolism

cAMP signaling pathway

Estrogen signaling pathway

GABAergic synapse

GnRH secretion

Morphine addiction

Neuroactive ligand-receptor interaction

Nicotinate and nicotinamide metabolism

Nicotine addiction

Quorum sensing

Retrograde endocannabinoid signaling

Synaptic vesicle cycle

Taste transduction

