

Step4: Differential Analysis

Group-Specific Correlation Networks

Reveal spatial co-expression relationships between top differential features:

- Constructs separate networks for each group
- Computes Spearman correlations using group-specific pixels
- Multiple testing correction: Applies Bonferroni adjustment to p-values
- Filters: $|r| > 0.6$ & adjusted p-value ≤ 0.01

By default, top 20 differential features per modality (by p-value) are included.

Correlation threshold ($|r|$):

0.5

adjusted p-value threshold:

0.05

Features per modality:

10

Network layout:

Kamada-Kawai (kk)

Display node labels:

yes

Node size:

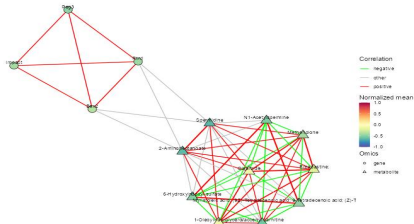
6

Label size:

3

Treatment Group Network

- Edges: Red: positive correlation, Green: negative correlation
- Nodes shapes: Triangles: metabolites, Circles: genes
- Node Colors: Feature abundance gradient (blue-low to red-high)

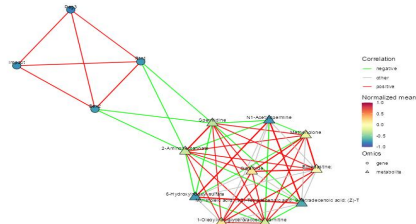


Download image

Export network

Control Group Network

- Identical node layout for direct comparison
- Edge differences indicate altered regulatory relationships
- Node color differences reflect abundance changes



Download image

Export network