

Figure S1. Sample clustering dendrogram and phenotype heatmap for the GSE31210 dataset. Hierarchical clustering was performed using average linkage and Euclidean distance. The lower color bar represents clinical phenotype classification (purple, LUAD; blue, normal tissue). The dendrogram and heatmap confirm consistency between sample grouping and phenotype labels and indicate no obvious outliers. This visualization supports the reliability of subsequent module-trait correlation analyses. LUAD, lung adenocarcinoma.

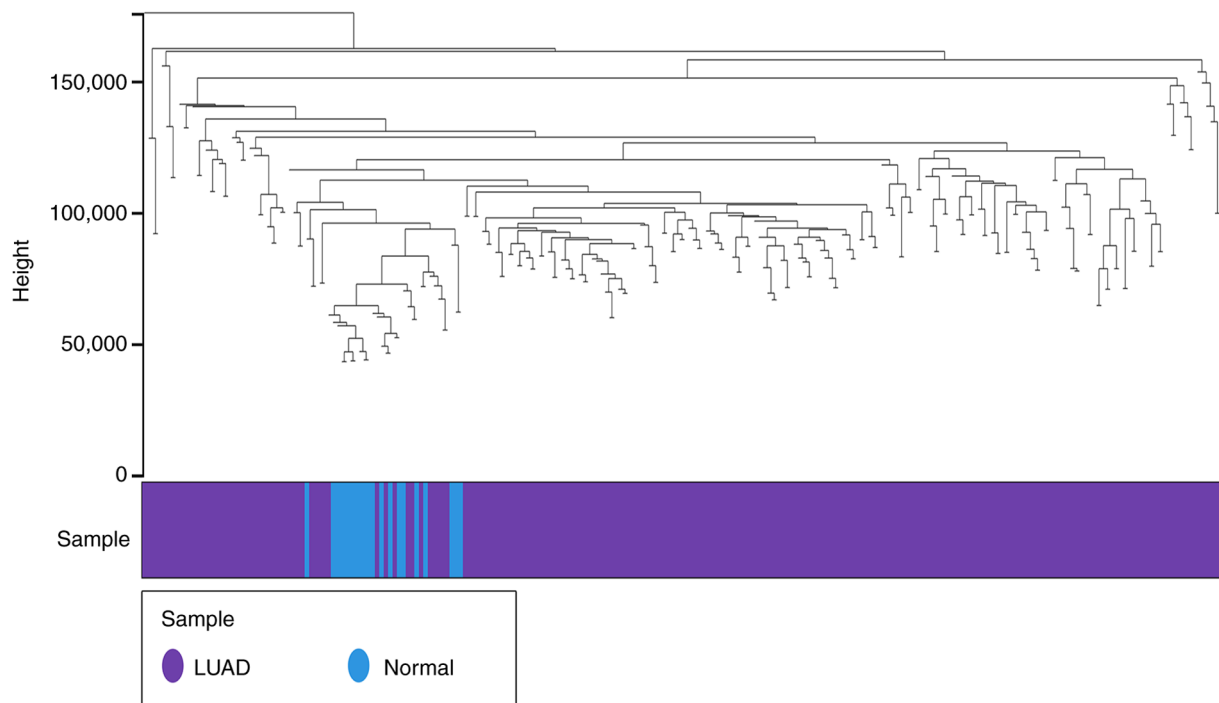


Figure S2. CDH5 mRNA expression in patients with lung adenocarcinoma from the GSE68465 dataset, stratified by lymph node metastasis status (N stage). CDH5 expression was significantly higher in N0-stage samples compared with that in N1 ( $P < 0.001$ ) and a significant difference was also observed between N1 and N2 ( $P < 0.05$ ). \* $P < 0.05$  and \*\*\* $P < 0.001$ . CDH5, cadherin 5.

