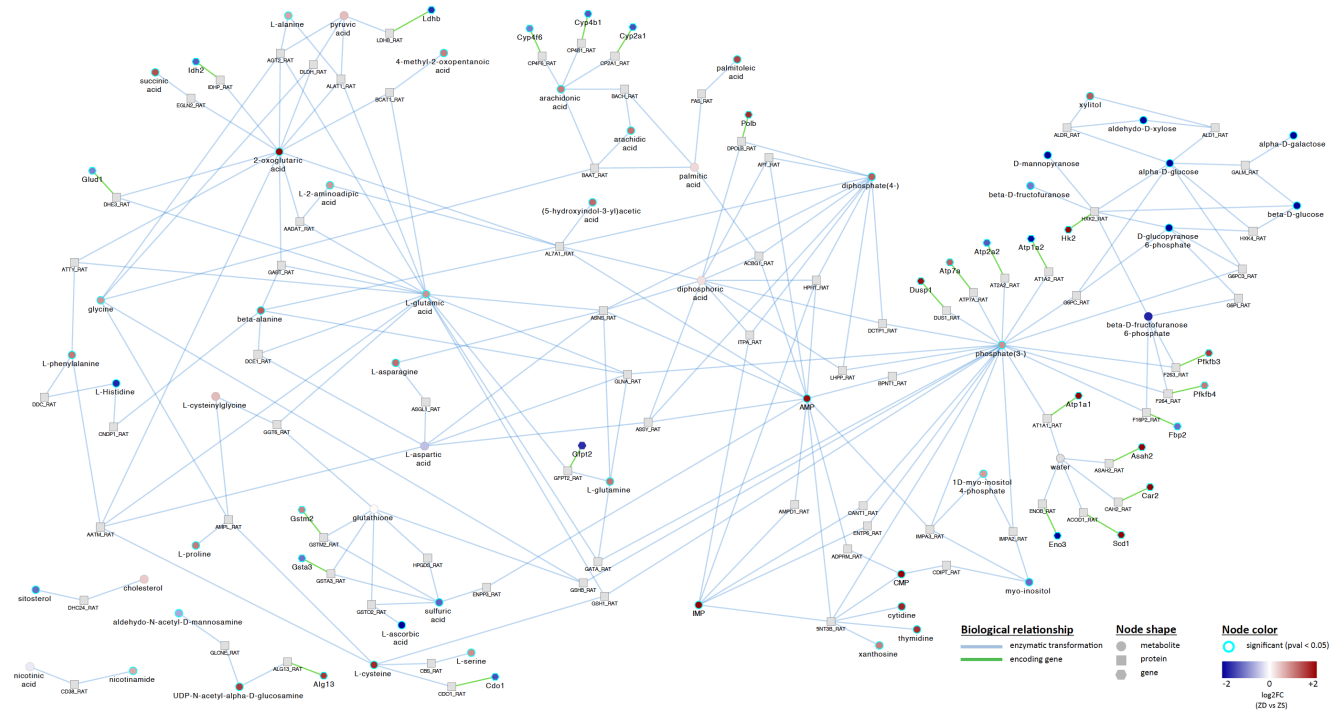


Integration of metabolomics, transcriptomics, and microRNA expression profiling reveals a miR-143-HK2-glucose network underlying zinc-deficiency-associated esophageal neoplasia

Supplementary Material



Supplementary Figure 1: A gene-metabolite integration network in ZD vs ZS esophagus calculated by queries from the 2,305 deregulated genes (reference #16) and 71 significantly deregulated metabolites (Table 1)