



**Figure S1. Weighted Gene Co-expression Network Analysis (WGCNA) and Gene variation analysis (GSVA) based on cuproptosis clusters. (A-C)** All genes were categorized into six gene sets based on different clusters of cuproptosis. **(D)** Degree of correlation between cuproptosis gene sets and keloids. **(E-G)** All genes were partitioned into ten gene sets to compare the differences between the normal and keloid groups. **(H)** Degree of correlation between gene sets and keloid. **(I)** GSVA analysis was performed on keloid samples to assess gene set variation.