

Figure 1: A complex network diagram showing the enrichment of biological processes in the top 100 differentially expressed genes. The diagram is a dense web of interconnected nodes, each representing a biological process. Nodes are colored in shades of blue, green, and orange, indicating different levels of enrichment or significance. The network is organized into several clusters, with some nodes acting as hubs. Key clusters include 'response to hypoxia' (top left), 'positive regulation of transcription' (top right), 'response to hypoxia' (middle left), 'response to hypoxia' (middle right), 'response to hypoxia' (bottom left), and 'response to hypoxia' (bottom right). The diagram illustrates the complex interplay of various biological processes in response to hypoxia.

Figure S1-Network with annotations. The GO (Gene Ontology) annotation of each node of the network in Figure 5A is presented. Red dots-nodes in network; Blue lines-edges in network; labels-GO annotation terms.