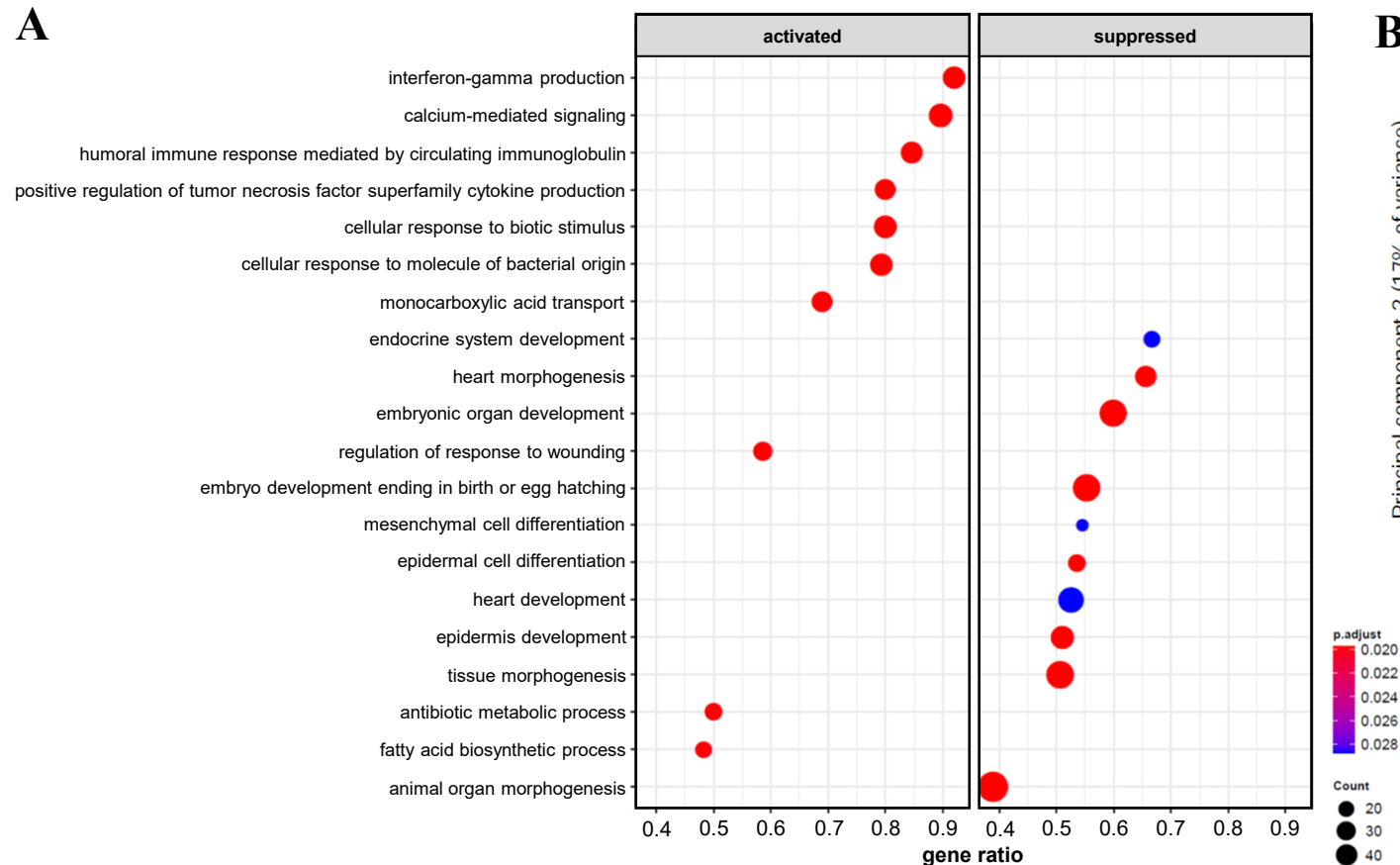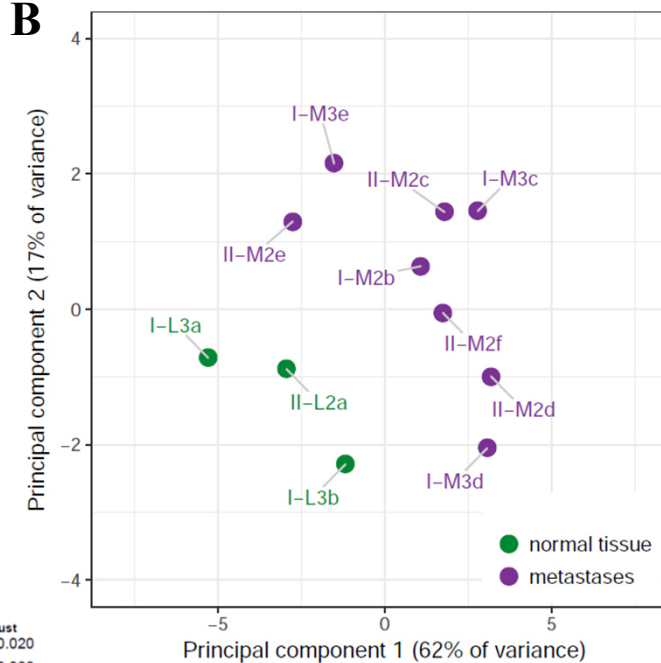**Figure S4: *A,*** GSEA plot depicting the enrichment of the top 10 up-/downregulated gene sets (≥20 genes) associated with the GO category biological process (BP) for genes differentially expressed in patient I and II. ***B,*** Principal component analysis of normal liver and metastatic tissue of patients I and II based on protein measurements. Clustering of normal tissue samples is less distinct than of CRLM compared with gene expression data.