

**Supplementary Material to “Coexpression network analysis of gastric adenocarcinoma identifies hub genes as biomarker candidates and their tumor microenvironment associations”**

**Table S3** - Ontology. Results of Gene Ontology enrichment analysis for selected gene sets. Each row corresponds to an enriched GO term and includes statistical parameters such as adjusted p-values (p.adjust), enrichment scores and associated gene lists. These annotations help infer biological processes overrepresented in the dataset.