**Supplementary material – Methods**

1. Data preprocessing
2. Survival Analysis
3. lmQCM
4. WGCNA
5. Eigengene Matrix
6. Gene ontology enrichment analysis
7. Functional Plot: circos plot

Supplementary material – Pipelines

1. Comprehensive gene co-expression and gene ontology enrichment analysis
2. Direct gene ontology enrichment analysis
3. Survival Analysis
4. Generate circos plot based on a group of genes.