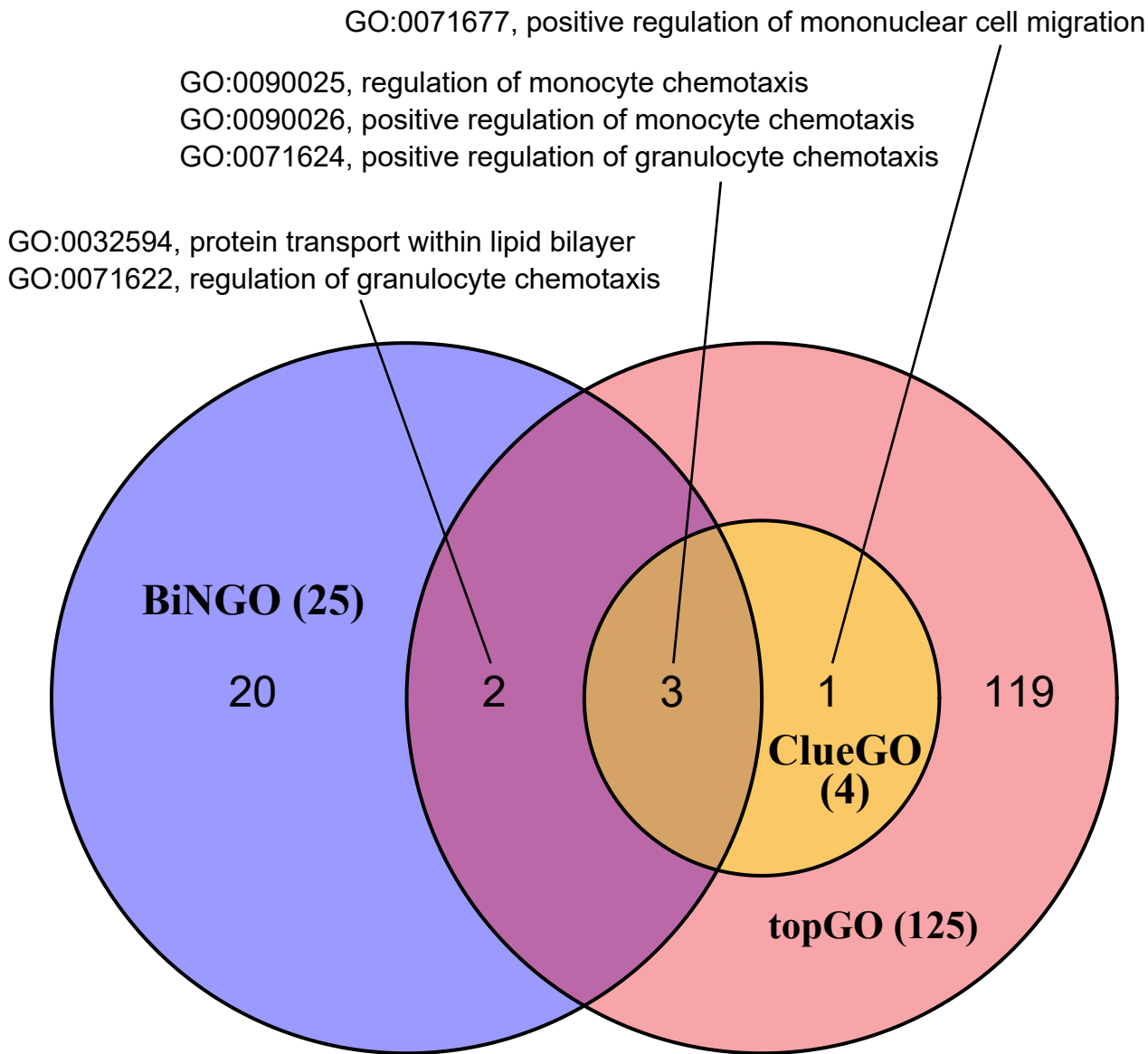
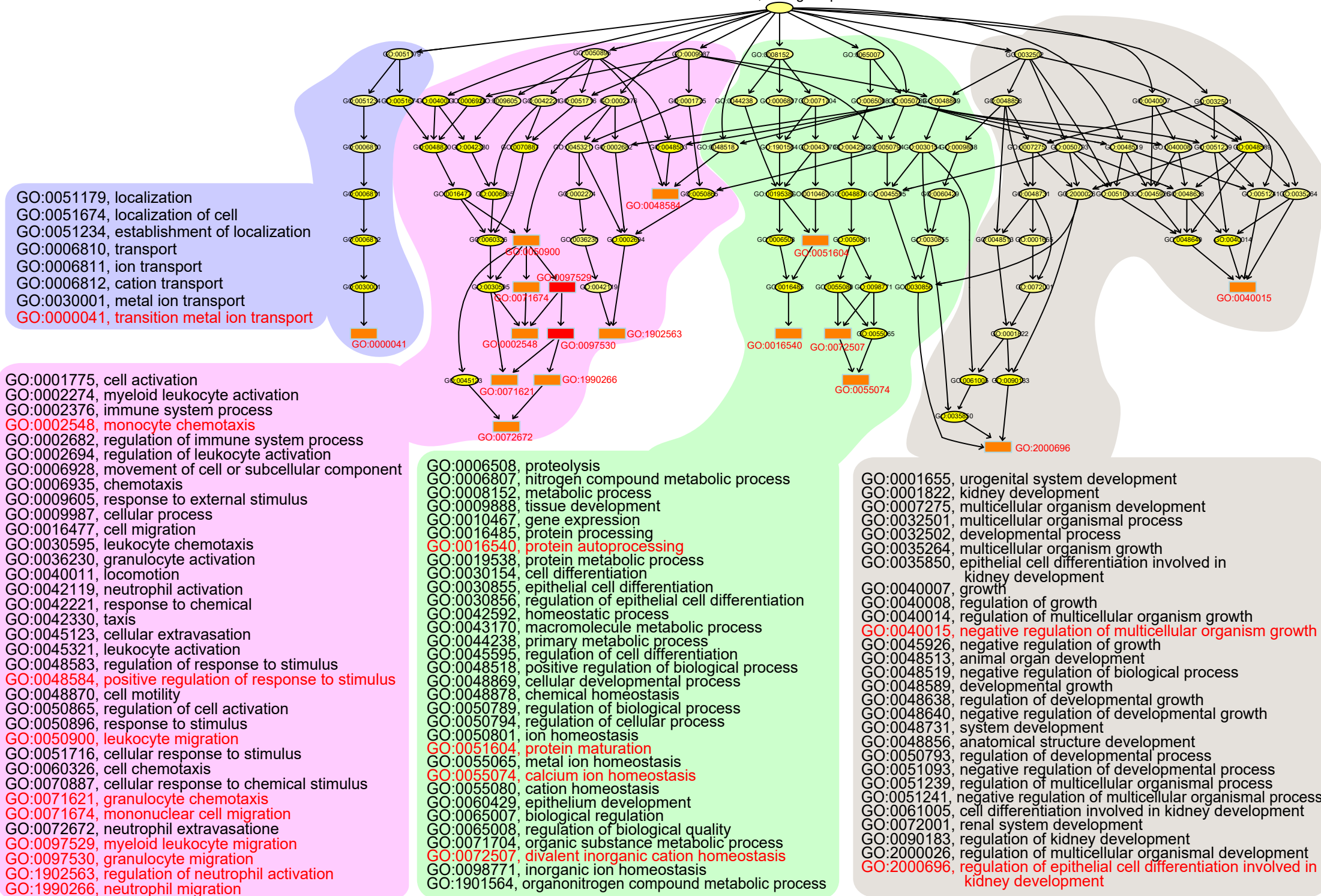


Supplementary Figure S1. Expression levels of the nine differentially expressed genes with $|LFC|$ of > 7 , identified by the edgeR program, in each of the study subjects. Read counts represent the estimated expression abundance at the gene level.



Supplementary Figure S2. Venn diagram of Gene Ontology terms estimated from 30 differentially expressed genes using three enrichment analysis methods.

GO:0008150, biological process



Supplementary Figure S3. Hierarchical tree of the overrepresented Gene Ontology terms (shown in red characters) estimated from 30 differentially expressed genes.