

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

GO:0071677, positive regulation of mononuclear cell migration

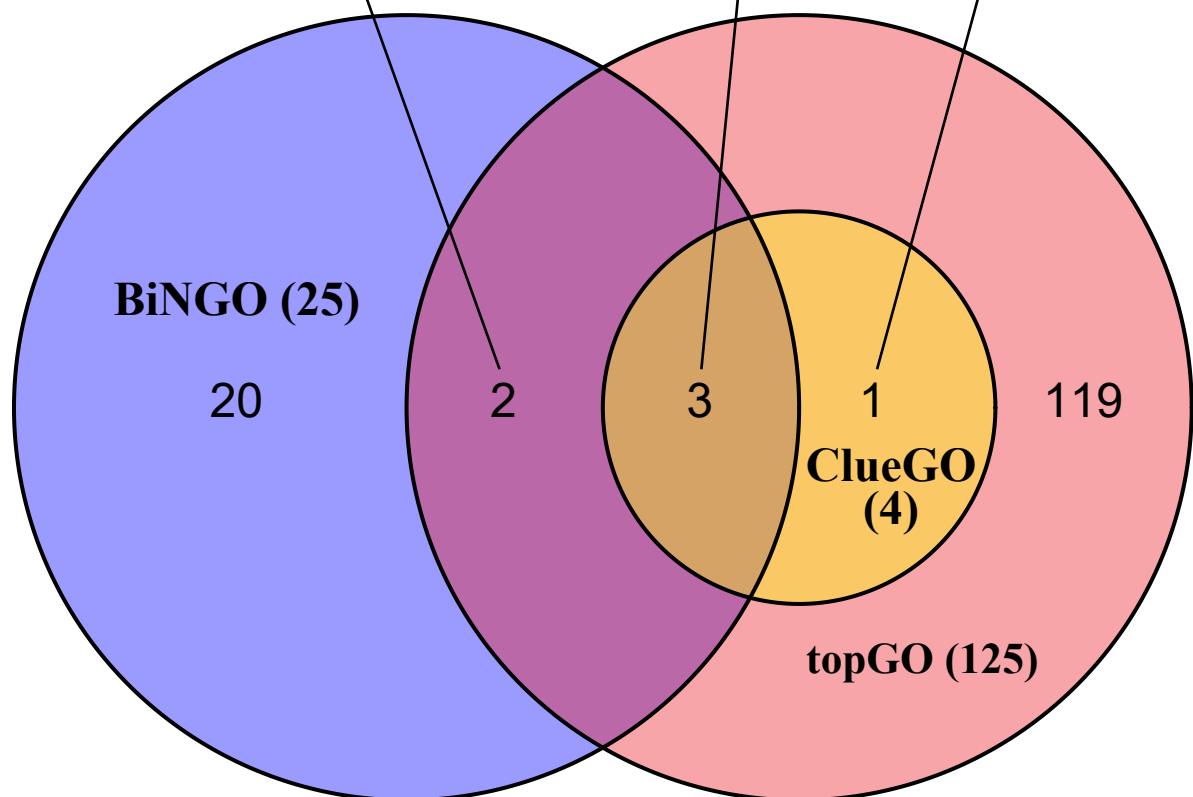
GO:0090025, regulation of monocyte chemotaxis

GO:0090026, positive regulation of monocyte chemotaxis

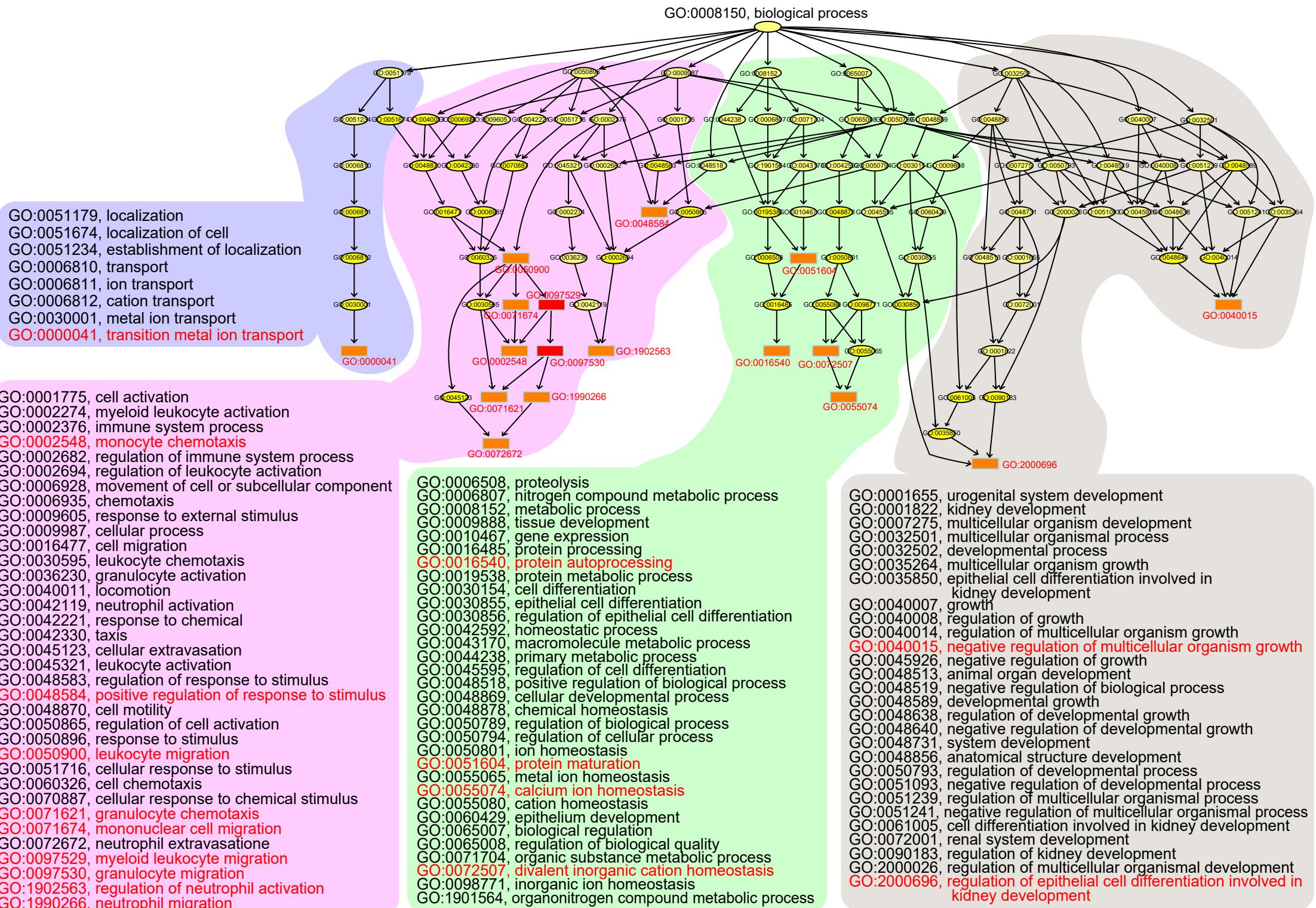
GO:0071624, positive regulation of granulocyte chemotaxis

GO:0032594, protein transport within lipid bilayer

GO:0071622, regulation of granulocyte chemotaxis



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



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