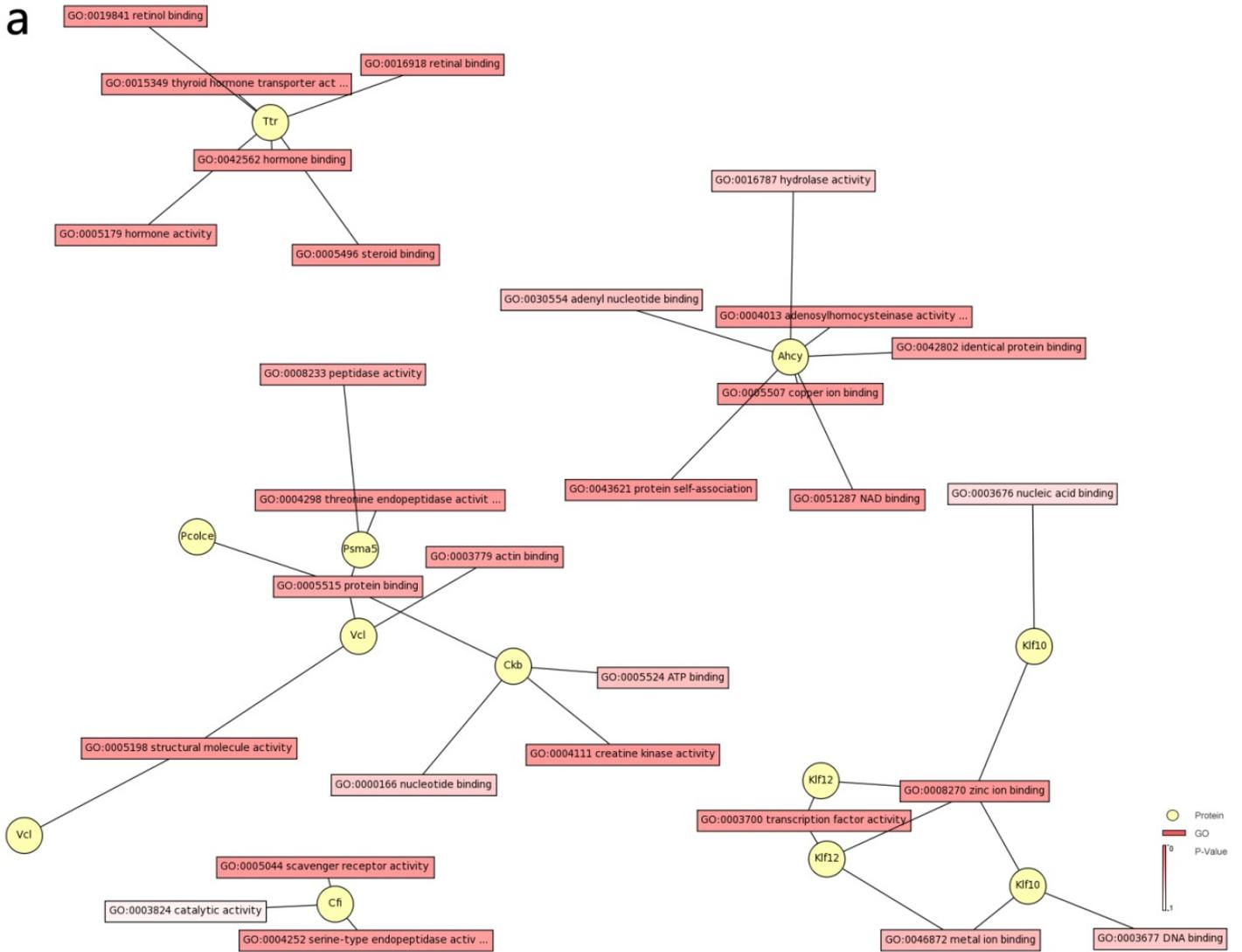
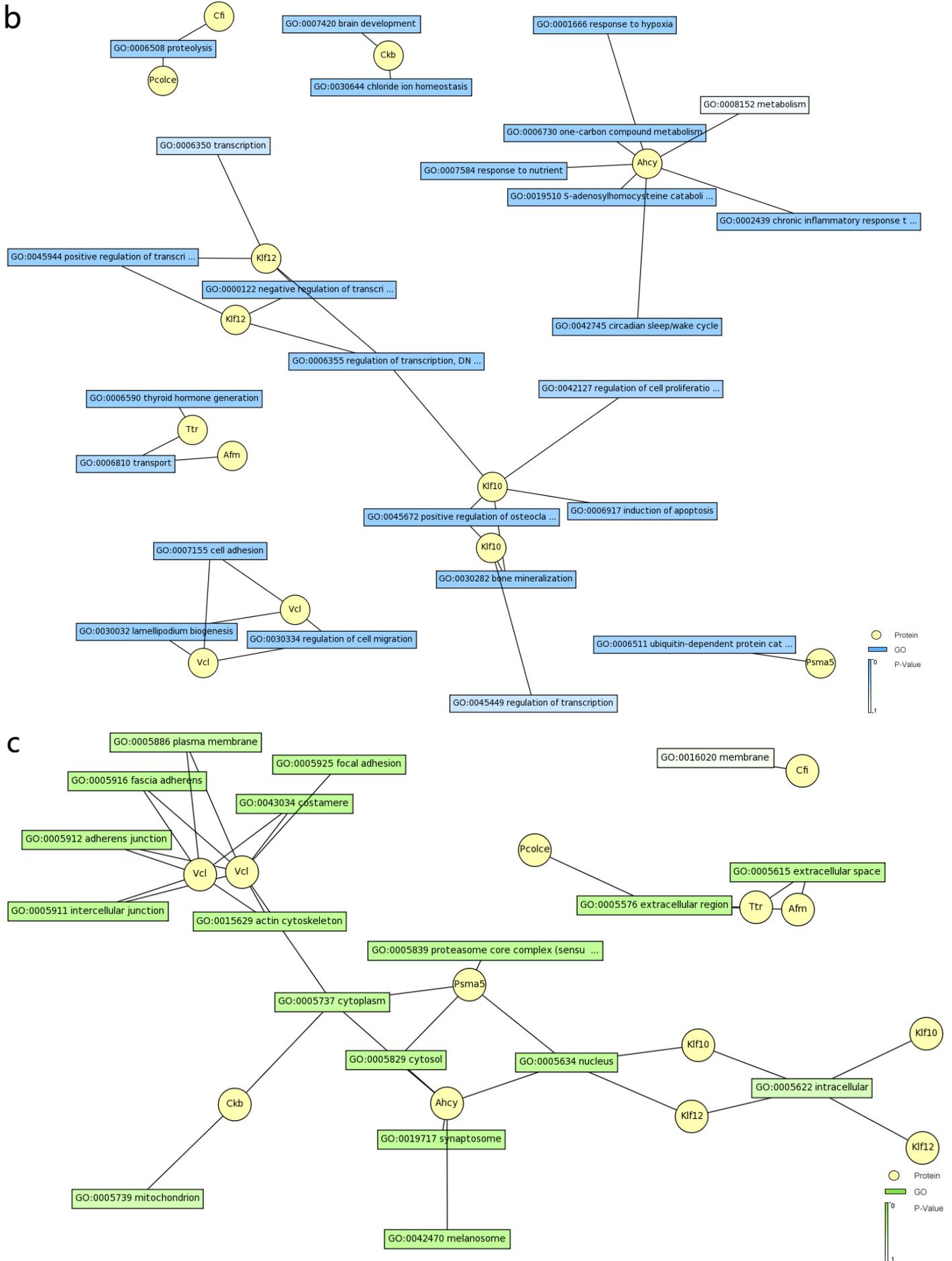


Supplementary materials

Supplementary Figure





Supplementary Figure. Significantly enriched pathway terms of 13 common elements between RM-induced AKI and normal renal tissue. Signaling pathway enrichment were conducted using KEGG PATHWAY(a), BioCyc(b) and GenMAPP(c).

Supplementary Table

Input Symbol	Count	Molecular Function	Biological Process	Cellular Component
Afm	3		GO:0006810 transport	GO:0005576 extracellular region;GO:0005615 extracellular
Cfi	5	GO:0003824 catalytic activity;GO:0004252 serine-type endopeptidase activity;GO:0005044 scavenger receptor activity	GO:0006508 proteolysis	GO:0016020 membrane
Ttr	10	GO:0005179 hormone activity;GO:0005496 steroid binding;GO:0015349 thyroid hormone transporter activity;GO:0016918 retinal binding;GO:0019841 retinol binding;GO:0042562 hormone binding	GO:0006590 thyroid hormone generation;GO:0006810 transport	GO:0005576 extracellular region;GO:0005615 extracellular space
Ahcy	19	GO:0004013 adenosylhomocysteinase activity;GO:0005507 copper ion binding;GO:0016787 hydrolase activity;GO:0030554 adenylyl nucleotide binding;GO:0042802 identical protein binding;GO:0043621 protein self-association;GO:0051287 NAD binding	GO:0001666 response to hypoxia;GO:0002439 chronic inflammatory response to antigenic stimulus;GO:0006730 one-carbon compound metabolism;GO:0007584 response to nutrient;GO:0008152 metabolism;GO:0019510 S-adenosylhomocysteine catabolism;GO:0042745 circadian sleep/wake cycle	GO:0005634 nucleus;GO:0005737 cytoplasm;GO:0005829 cytosol;GO:0019717 synaptosome;GO:0042470 melanosome
Ckb	8	GO:0000166 nucleotide binding;GO:0004111 creatine kinase activity;GO:0005515 protein binding;GO:0005524	GO:0007420 brain development;GO:0030644 chloride ion homeostasis	GO:0005737 cytoplasm;GO:0005739 mitochondrion
Pcolce	3	GO:0005515 protein binding	GO:0006508 proteolysis	GO:0005576 extracellular region
Klf12	9	GO:0003700 transcription factor activity;GO:0008270 zinc ion binding;GO:0046872 metal ion binding	GO:0000122 negative regulation of transcription from RNA polymerase II promoter;GO:0006350 transcription;GO:0006355 regulation of transcription, DNA-dependent;GO:0045944 positive regulation of transcription from RNA	GO:0005622 intracellular;GO:0005634 nucleus
Psm5	8	GO:0004298 threonine endopeptidase activity;GO:0005515 protein binding;GO:0008233 peptidase activity	GO:0006511 ubiquitin-dependent protein catabolism	GO:0005634 nucleus;GO:0005737 cytoplasm;GO:0005829 cytosol;GO:0005839 proteasome core complex (sensu Eukaryota)
Vcl	14	GO:0005198 structural molecule activity;GO:0003779 actin binding;GO:0005198 structural molecule activity;GO:0005515 protein binding	GO:0007155 cell adhesion;GO:0030032 lamellipodium biogenesis;GO:0030334 regulation of cell migration	GO:0005737 cytoplasm;GO:0005886 plasma membrane;GO:0005911 intercellular junction;GO:0005912 adherens junction;GO:0005916 fascia adherens;GO:0005925 focal adhesion;GO:0015629 actin cytoskeleton;GO:0043034 costamere
Klf10	10	GO:0003677 DNA binding;GO:0008270 zinc ion binding;GO:0046872 metal ion binding	GO:0006355 regulation of transcription, DNA-dependent;GO:0006917 induction of apoptosis;GO:0030282 bone mineralization;GO:0042127 regulation of cell proliferation;GO:0045672 positive regulation of osteoclast differentiation	GO:0005622 intracellular;GO:0005634 nucleus
S100a8	3	GO:0005509 calcium ion binding;GO:0005515 protein binding	GO:0006935 chemotaxis	
Serpina3n	5	GO:0004867 serine-type endopeptidase inhibitor activity	GO:0006953 acute-phase response;GO:0043434 response to peptide hormone stimulus;GO:0034097 response to cytokine stimulus	GO:0005576 extracellular region
Psm3	8	GO:0004298 threonine endopeptidase activity;GO:0008233 peptidase activity	GO:0006511 ubiquitin-dependent protein catabolism;GO:0030163 protein catabolism	GO:0005839 proteasome core complex (sensu Eukaryota);GO:0005634 nucleus;GO:0005737 cytoplasm;GO:0005829 cytosol;GO:0005839 proteasome core complex (sensu Eukaryota)
Klf5	11	GO:0003700 transcription factor activity;GO:0005515 protein binding;GO:0008270 zinc ion binding;GO:0046872 metal ion binding	GO:0001525 angiogenesis;GO:0006355 regulation of transcription, DNA-dependent;GO:0008284 positive regulation of cell proliferation;GO:0030033 microvillus biogenesis;GO:0045941 positive regulation of transcription	GO:0005622 intracellular;GO:0005634 nucleus
Krt8	10	GO:0005198 structural molecule activity;GO:0005515 protein binding	GO:0000904 cellular morphogenesis during differentiation;GO:0006915 apoptosis;GO:0007275 development;GO:0051707 response to other organism;GO:0033209 tumor necrosis factor-mediated signaling	GO:0030018 Z disc;GO:0042383 sarcolemma;GO:0045095 keratin filament
Klf6	6	GO:0003676 nucleic acid binding;GO:0008270 zinc ion binding	GO:0019221 cytokine and chemokine mediated signaling pathway	GO:0005622 intracellular;GO:0005634 nucleus;GO:0005737 cytoplasm
Hp	5	GO:0003824 catalytic activity;GO:0004252 serine-type endopeptidase activity;GO:0030492 hemoglobin binding	GO:0006508 proteolysis	GO:0005576 extracellular region

Supplementary Table. The gene ontology enrichment analysis of 17 common elements with DAVID v6.7 Functional Annotation Clustering tools.