Supplementary figures

Figures S1-S9. REVIGO treemaps of gene ontology processes that are significantly enriched (false discovery rate [FDR] < 0.05) one figure for tissue and species; figure for giant mole-rat skin is missing because the number of enriched terms was too small for summarizing).

Figure S10. Expression levels of examined genes.

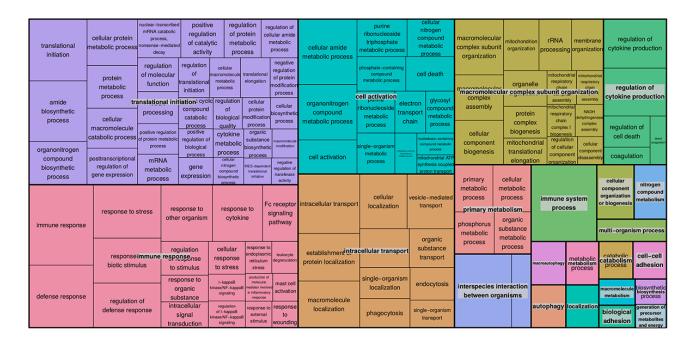


Figure S1. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in rat blood. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

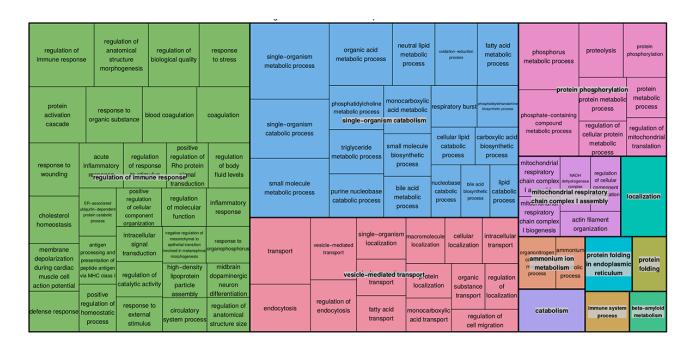


Figure S2. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in rat heart. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

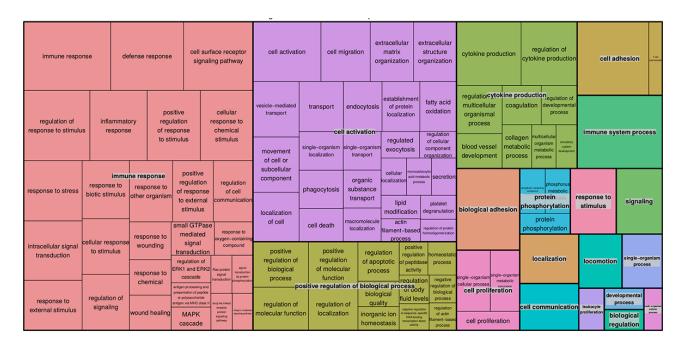


Figure S3. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in rat kidney. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms

response to external stimulus	respons purine-cor compoi	ntaining	response to chemical	response to cytokine		platelet degranulation	transport	vesicle-mediated transport cell death		th cel	l activation	coagulation	negative regulation of multicellular organismal process -coagulation	regulation of endodermal cell differentiation	muscle adaptation	
response to	response t	to	regulation of response to		response	cell migration	secretion platele	endocytosis	regulation of phagocytosis		egulation of icle-mediated transport	energy homeostasi	blood regula	negative regulation of developmenta process	regulation of multicellular organismal process	
organic substance	organophosph	ext	ernal stimulus				localization of cell	lamellipodium assembly	single-org transpo		fatty acid transport	single-organism	lipid meta	holic	protein	
protein activation cascade response to stress		response to response wounding other organ to external stimulus				secretion by cell	actin filament-based process	actin cytoskeletor	single-org		mellipodium rganization	metabolic process	proces	s	protein maturation protein	
					cellular	positive regulation			regulation		cell volume	lipid me monocarboxylic acid metabolic process	tabolism single-orga catabolic pi	anism	maturation	
immune response	response to endogenous stimulus	of respor to stimul	se hyperosm	se me	sponse to echanical stimulus	of heterotypic cell-cell adhesio	hydrolase activit	regulation of y hormone levels			eii voiume emeostasis	movement of cell single-org or subcellular biosynth component proce		etic	mune system process	
wound healing	response to oxygen-containing compound	response mechanic stimulus	al carbohydra	to reg	cositive gulation of and ERK2 ascade	regulation o	regulation of esitive regulation of apoptotic proces	heterotypic cell s homeostasis	negative -cell adhes ATPase ac	sion ho	lipid meostasis	localization	response to	reactive oxygen species	leukocyte	
response to metal ion	response to biotic stimulus	response low-dens lipoprotei particle	ty inflammatory response	response to netformin	positive regulation of response to external stimulus	regulation of biological quality	positive regulation of steroid biosynthetic process	steroid metabolic process	regulation of reactive oxygen species metabolic process	regulation of localization	motabolic	locomotion	biological adhesion	FasL bi	FasL osynthesis	

Figure S4. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in rat liver. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

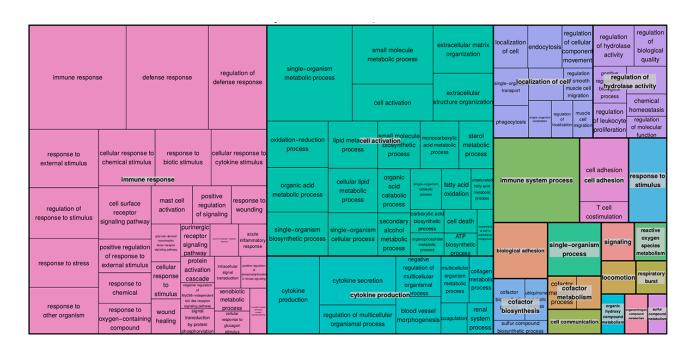


Figure S5. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in rat skin. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

				·						_			
immune response			positive respons		cytokine production		regulation of catalytic activity		regulation of protein metabolic process				
		defense response					positive regulation of NF-kappaB transcription	regulation	nomeostatic of bo		immune system process		response to
			cellular response to stimulus		regulation of regul cytokine production		factor activity	biological process	process fluid le				- Similarus
							lation of cytokin coagulation	of I	n negat naintenance of location of cell proce	ion ılar			
regulation of response to stimulus	response to biotic stimulus	cell surface receptor signaling pathway	regulation signaling		regulation of molecular function	positive regulation of	regulation of autophagy	protein phosphorylation	1 phosphorylation single-on localiza	anism	munication	signaling	
	im	regulation of I-kappaB	regulation	of small GTPase		biological process	regulation of biological quality		phosphorus		- Composition of the Composition		3.5.1411119
	response to stre	ss kinase/NF-kappaB signaling	cellular proc	mediated signa transduction					localizat			cell prol cell tion	biological
intracellular signal transduction		Fc receptor signaling	response to xygen-containing	cellular transmembrar sponse to receptor prote tyrosine kinas chemical	in	ctivation	cell death	phagocyt	osis of cel	1001	ocyte adhesion	proliferatio cellular proces	
	response to external stimulu	pathway		stimulus signaling pathway response	cell activat		tion	pha endocytosis	cytosolic gocytosis ion trans			locomotio	n multi-organism process
response to other organism		response to cytokine	response to chemical	to macrophag activation				endocytosis	панърон		biological	cytokine	THE RESIDENCE AND ADDRESS OF THE PERSON NAMED IN
	I-kappaB kinase/NF-kappa signaling	aB wound healing	response to	response to response to reptidoglycan by protein	apoptotic p	process	novement of cell or nucleoside salvage omponent	regulation of vesicle-mediated transport	secretion trans	proliferatio	n regulation		localization

Figure S6 REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in giant mole-rat blood. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

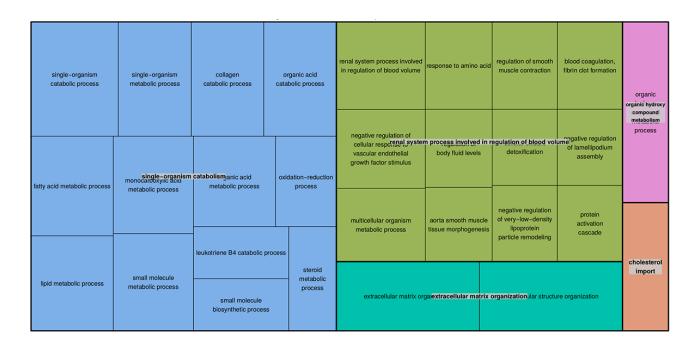


Figure S7. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in giant mole-rat heart. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

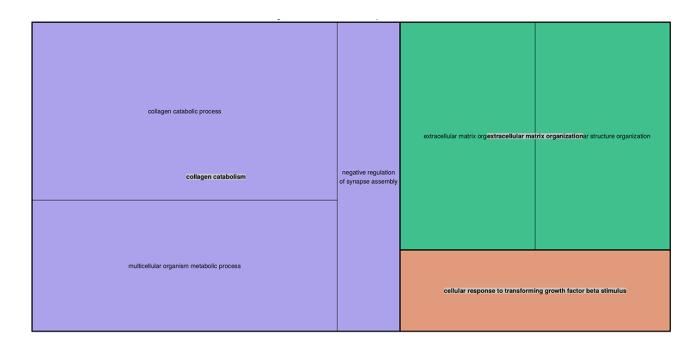


Figure S8. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in giant mole-rat kidney. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

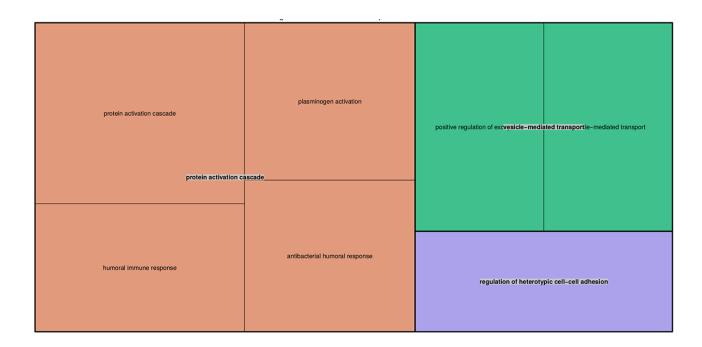


Figure S9. REVIGO treemap of gene ontology processes that are significantly enriched (FDR<0.05) for gene ontology processes in giant mole-rat liver. Each rectangle is a single cluster representative. The representatives are joined into superclusters of loosely related terms, visualized with different colors. The size of the rectangles reflects the enrichment p-values of the covered GO-terms.

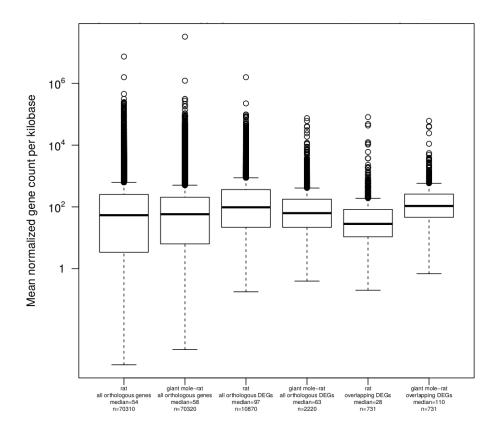


Figure S10. Expression levels of examined genes. Gene counts were first normalized for overall read number per sample. Then, separately for each tissue, across samples of, both, young and old animals, mean gene counts per kilobase transcript length were determined. Whiskers extend to the most extreme datum within 1.5 times inter quartile range. DEGs - differentially expressed genes. Overlapping DEGs - DEGs found, both, in rat and giant mole-rat.