## REVIGO Gene Ontology treemap

NEVIOO Ocho Ontology treemap													
glycine decarboxylation via glycine cleavage system		respiratory elec transport cha	etron species	reactive nitrogen species metabolic process		ular nitrogen ound catabolic process	hydrogen ion transmembrane transport		hydrogen transport		positive regulation of hydrogen peroxic metabolic process  positive regulation	de regulation of	regulation of phosphatase activity
nitrate catabolic process		ATP catabolic pro	compleme catabolism ernati	ent activation ve pathway		otide-excision , DNA incision	extracellular aming hydrogen ion acid transport		nsmembrane transport <sup>acellular</sup> transport		positive regulation of steroid hormone biosynthetic proces	regulation of ligase activity	negative regulation of hydrolase activity
nitric oxide catabolic process		nucleoside monophospha catabolic proce	ate	anaphase-promoting complex-dependent protessional ubequire-dependent protes calabolic process		carnitine metabolic process	early endosome Golgi transport	to n	ositive regulation of mitochondrial outer obtained by the control of the control	neutral amino acid transport	free ubiquitin chain polymerization		
						axon ensheathment in central ervous system	,		nvolved in apoptotic signaling pathway	dold transport	free ubiquitin o	hain polymerization methylation	cellular organofluorine metabolism
central nervous system myelin formation	m myelin		bone mineralization	in uter embryo developn	nic e		protein K27–linked ubiquitination	chaperone cofactor-dependent protein refolding		protein lyglutamylation	histone H4–R3 methylation	peptidyl–arginine N–methylation	
growth plate cartilage chondrocyte proliferation	hen <b>gro</b> v cell	wth plate cartilage differentiation	e chondrocyte pro negative regula hematopoietic pr cell differentia	ogenitor	hematopoietic stem cell differentiation		prote	protein	n transf	tion ve regulation quitin–protein erase activity	cellular	cellular response to follicle-stimulating hormone stimulus	g
	embryonic cleavage		erythrocyte mat	uration	biomineral tissue development		protein K29-linked ubiquitination	K6–linked ubiquitination	ation pepti	dyl-arginine odification	organohalogen metabolism	flavonoid metabolisr	protection