REVIGO Gene Ontology treemap

						Sono Ontolog	,					
protein glycosylation in Golgi	fatty acid beta-oxidation	protein lipidat	telom mainter via telo lengthe	nance reg mere glyco	gative ulation orotein osylation Golgi	prenylcysteine atabolic process	cellular response to laminar fluid shear stress	T-helper 17 cell differentiation	negative regulation of defense response to virus	necroptotic signaling pathway	negative regulation of thymocyte apoptotic process	regulation of response to reactive oxygen species
regulation of	meiotic cell cycle	lipoprotein bio		NA-dependent m	neiotic nuclea	cardiolipin r metabolic	negative regulation of peroxisome proliferator	Cellular res	cilium organization	signaling pathwa	y response to	defense response to protozoan
chromatin assembly	-	process	process D	NA replication	division	process	activated receptor signaling pathway	-	regulation of bone mineralization	endopeptidase activity	response t	o cold
regulation of heat generation	branched-chain amino acid metabolic process	glycerol metabolic process	nuclear-transcribed mRNA poly(A) tail shortening	protein monoubiquitination	lipid catabolic process	regulation of chromosome organization	negative regulation of fat cell differentiation	interleukin–6–mediated signaling pathway	adiponectin–activated signaling pathway	cellular response to exogenous dsRNA	smoothe signaling pa	
protein auto-ADP-ribosylation	negative regulation of DNA endoreduplication	organelle fission	sylation in Golg	- itatia	temperatui homeostas	I small protein	fat pad development	left/right pattern formation	prostate gland	heart looping ir	regulation of branching volved in lung orphogenesis	regulation of intracellular protein transport regulation of
redulation of mitotic i	positive regulation of mRNA splicing, via spliceosome	positive regulation of chromosome organization	regulation of	_		Temovai			development			intracellular protein transport negative
			cholesterol homeostasis	melanosome organization	regulation of pro	diphosphate	soft palate development	adipose ti fat pa development	dorsal/ventral pattern formation d development	embryonic heart tube development	pattern specification process	regulation of lipid storage
small molecule catabolic process	regulation of chromatin assembly or	chromosome organization	selenocysteine incorporation	DNIA manatahadi	ic multice				salivary gland epithelia	glomerular visc		T-helper 17 type immune
	disassembly			process	organis		regulation of	regulation of		epithelial ce developmen		T_helper 17 _type immune_
tubulin deacetylation	selenocysteinyl–tRNA(Sec) biosynthetic process	peroxisome organization	translational readthrough	protein K63-linked deubiquitinatio	4111110	acid	interferon-beta production	chemokine biosynthetic process	negative regulation of multicellular organismal metabolic process	type I interfero	vessel	response neutrophii mediated immunity