## REVIGO Gene Ontology treemap

							O Ocho Ontolog							
regulation of cardiac muscle cell proliferation	stem cell developmen	trabe nt forma		gonadal mesoderm development	negative regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation	preantral ovarian follicle growth	glycerol metabolic process		aspartate family amino acid biosynthetic process	oxidation-red process	cellular carbohydrate metabolic process	glycosyl compound biosynthetic process	response to methotrexate	response to organic cyclic compound
regulation of											nurine_containir	·	eteroid hermone	nethotrexate <sub>O</sub> toxic substance
cardiac vascular smooth muscle cell differentiation	umbilical cord			stem cell ifferentiation	trabecula morphogenesis	tricuspid valve development	small molecule metabolic process		aspartate family amino acid metabolic proglycerol r	carbohydra biosyntheti process netabolism	c biosynthetic process	cellular ketone metabolic process	response to follicle–stimulating hormone	response to lipid
arterial endothelial cell differentiation	Mullerian duct	muscular septum norphogenesis	positi regulat of alka	on ne agin	cardiac left yentricle morphogenes	hypertrophy	respiratory electron		-	amino acid	organonitrogen compound biosynthetic process	dicarboxylic acid metabolic process	generation of prec <b>reactive</b>	, ,
AV node cell to bundle of	positive regulation	germ cell	activity activation anator		Notch signaling	to stress synaptic	transport cha	n process		mitochondrial	nucleoside monophosphate metabolic process	transcription from mitochondrial promoter	melspecies me and energy	etabolism reactive oxygen species metabolic process
His cell communication	of synapregul maturation	ation of card	diac muso	e cell prolife		transmission, cholinergic	gluconeogenesis		fumarate metabolic process	transport,	glutamate catabolic process	mitochondrion	to a second a contract of	mitochondrion organization
dorsal aorta morphogenesis	l metaholic l	muscle cell proliferation	regulati of p38M/ cascad	PK regulatio	I phosphorylation	Loocoodo		energy cou	upled proton transmembrane	alpha-ketoglu	I DNA-template	negative regulation of transcription by transcription factor	phomeostasis epitreial structure of bone	mitochondrion organization actin
oogenesis stage	cardiocyte differentiation	sensory perception	sensory perceptior mechanic	al  biosyntheti		intracellular steroid hormone receptor signaling pathway	hydrogen ion transmembrane transport	transport, ag	gainst electrochemical gradient	transpor	initiation	localization	resorption maintena	cytoskeleton organization
regulation of		of sound intestinal	stimulus regulation	regulation f of nervous		sex determination		<b>hy</b> o	drogen ion trans ogen transport	mitochondria membrane t	purine I nucleobase ransport <sub>sport</sub>	regulation of cardiac muscle cell apoptotic process	cell activation neutrophil activation superoxide	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules  single-organism cellular process
receptor cell differentiation	organ growth	epithelial cell differentiation		system developmer	trophectodermal	acrosome reaction	ATP hydrolysis coupled proton				nucleobase transport	regulation of DNA-templated transcription,		
endocardial cushion to mesenchymal transition	coronary vasculature development	negative regulation of transcription regulatory region DNA binding	synapso maturatio	i oxidative	cellular	negative regulation of protein tyrosine kinase activity	transport	synt	chondrial ATP thesis coupled oton transport	negative regulation of mitochondrial outer membrane permeabilizati involved in apoptotic signaling pathway	transepithelial transport	initiation  actin filament-based process		