REVIGO Gene Ontology treemap

									<u> </u>							
regulation of cellular process	_	lation of al process	regulation of cellular response to stress	regulation of metabolic process	regulation of cell differentiatio	signal transductio	intracellular signal transduction	macromolecule	II promoter	compound biosynthet	d he tic bio	terocycle synthetic rocess	macromo biosyntl proce	netic d	cellular nitrogen compound iosynthetic process	positive regulation of interleukin–2 production
toll–like receptor 3 signaling pathway	intrinsic apoptotic signaling pathway	regulation of I damage respo signal transdu by p53 clas mediator	regulation	of axial mesoderm	stress–activated protein kinase signaling cascade	regulation of signaling	regulation of cell communication	biosynthetic	positive regulation of macromolecule biosynthetic process	phosphorylation keratan	cellular protein modification process	biosynti	oid phos	phorylation negative	macromolecule modification nitrogen	cytokine production positive regulation of interleukin-2
cellular developmental process	regulation of response to stress	regulation of respons to stimulus	e response to	signaling	organismal	stem cell development		cellular macromolecule metabolic	histone H4 deacetylation	biosynthetic org process	anizationn		phosphorylation	regulation of RNA biosynthet process regulation	ic metabolic process	of cytokine production
regulation of intracellular signal	apoptotic signaling pathway		immune system on of cellular	,	fat cell to ar	Communi	I to growth	regulation of transcription from RNA	transo nucleic acid metabolic process	of vitamin org	unction ganization cellular aromatic	projection organization regulation of vitamin	process	of transferas activity organic	signal transduction by phosphorylation membrane protein	regulation of T cell cytokine production positive
regulation of developmental	activation o Rho GTPas activity	l signal	, of lymphocyte	endocytosis of i	sponse import	into receptor prof tyrosine kina signaling pathway	regulation ase of fat cell differentiation	polymerase II promoter	oositive regulation of NF-kappaB transcription factor activity	nucleobase–containing compound metabolic process pept	compound metabolic process tidyl-threonine nodification	metabolic process cellular nitrogen	microtubule organization dendrite norphogenesis	metabolic process neurofilamen	intracellular domain proteolysis retrograde axon cargo	regulation of interleukin–5 production
process positive regulation of	intracellular receptor	activation Ras GTPa activity	se immune response	nucleus organ	positi regula of imm respoi	tion lymphocy mediate immunit	d component	gene expression	biosynthetic process	peptidyl-serine he	terocycle	metabolic process regulation of cellular	cellular	chromosome organization	negative regulation of response	cell communication cell activation
cellular process positive regulation of	signaling pathway stem cell	NIK/NF-kappa signaling		receptor neur signaling communication pathway neur neur neur neur neur neur neur neur	developm gative positive	ar protein cell localization ent cytoskeleto Wnt	to receptor	macromolecule metabolic process	regulation of RNA splicing	regulation of metabolic	anic cyclic	component or organization alcohol biosynthetic process	histone	protein dealkylation	ellular phosphorus metabolic process	cell
	regulation of insulin-like	n axial mesoderr developme		response-regulating signaling pathway impo	lation of regulation of I-kappaB protein kinase/NF-kappal signaling ort into cleus	signaling tran	response to lipid		signaling	develo	orocess opmental ocess	death	resp	onse to	rhythmic process	L-fucose catabolism
regulation of JUN kinase activity	growth factor receptor signaling pathwa	spleen developme	immune nt response	molecule of	palate palate uration	l cho	ordate execution phase of apoptosis		Signailig	activation circadi	an rhythm	immune sys process		m cell	nulticellular organismal process	cellular component organization or biogenesis