REVIGO Gene Ontology treemap

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ncRNA metabolic process		ncRNA processing		RNA processing		ncRNA catabolic process	positive regulation of phosphatidylinositol 3-kinase activity	positive regulation oxidoreduct activity	of tyrosine kinas	n response to	androgen receptor signaling pathway	nucleobase–contai compound transp	ining	port	nitrogen compound transport	cell mig	ion of Imuscle gration	positive regulation of isotype switching zinc ion
							regulation	regulation of apoptotic process	1 '	response to	process	<mark>nu</mark> RNA localizati	cleobase on of	dative difference disport	ferentiation	self anti	gen isport	cytosolic calcium
folic acid-containing compound metabolic	RNA modification	pseudouridir synthesis		ene	polyamine metabolic process	methionine biosynthetic process	positive regular cell adhesion	senic-containing substance Si		cellular	vitamin A ase activity process regulation of MAP kinase	RNA transpo	rt regu	of re	nigration negative gulation o assium io ransport	i anion	regi	transport ulation of
CUT catabolic process	heterocycle metabolic process	cellular aromatic compound metabolic	nucleobase- compound i	metabolic	cellular nitrogen compound metabolic	mitochondrial RNA processing	of MAPKKK cascade by fibroblast growth factor receptor signaling pathway	activation of hospholipase — D activity	negative	eptide hormone stimulus peptidyl–tyrosine ephosphorylation	activity IMP	ribonucleoprotein complex biogenesis		positive regulation cell gro	wth cel	Il junction ganization	home	ygen ostasis ation of
CUT metabolic process	histone mRNA metabolic process	compound	nitrogen compound metabolic process	l''	I Drotair	RNA metabolic	regulation of cell–matrix adhesion	-protein coupled glutamate receptor ignaling pathway	regulation of	regulation of exidoreductase activity	positive regulation of hydrolase activity	ribonucle	-	extracel matri assem	x s	snoRNP ssembly esis	ox	gen ostasis ostasis
polyadenylation-dependent RNA catabolic process	activation of plasma proteins involved in acute inflammatory response	mRNA metabolic process	N-terminal protein amino acid acetylation	7-methylguand mRNA cappi		Inhosphodieste		cortex neuron differentiation		lens fiber cell differentiation	crest cell development	protein heterooligomerization CO	cellular emponent ogenesis		regulation	hexamerization on	nomeostasi	stability
	guanine metabolic process	nucleic acid metabolic p	ermination of RNA rolymerase II anscription	positive regulation of nflammator response	metabolic process	protein peptidyl-prolyl isomerization	in mammary gland duct morphogenesis	structure	endoderm mechanic mechanic involved	epithelia cell fate commitme	process controlling posture sympathetic	adherens ju organizat		small nucleolar ribonucleoproteii complex assembly	regulation of histone ubiquitinatio	sympathetic neuron projection extension	gas nomeostas	regulation
RNA metabolic process	isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine	lhoto amulaid	one-carbon me	Iding requiring	break processing meta	rating RNA ctor 5'-end abolic processing cess	multicellular	involved in rendocardial value cushion formation	nervous system vasculogenesis d	ganglion evelopment ube lumen	projection guidance body fluid	stem cell proliferation stem cell	regulation oligodendro progenito proliferati	ocyte precu or ce	rsor r	e–entry in totic cell c	volo	stem cell division
pteridine–containing compound metabolic process	cellular macromolecule metabolic process	connective tissue replacement involved in inflammatory response wound healing	organic ubstance p netabolic process	lasminogen _{pr} activation	modification	NA primary metabolic process	movement	negative regulation of chondrocyte	semaphorin-plexin signaling pathway involved in neuron projection guidance	dendritic spine evelopment	secretion gland development	oligodendrocyte progenitor	regulation	n of chondr	ooyto	amino sug piosynthes		death