## REVIGO Gene Ontology treemap

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mRNA splicing, via spliceosome	DNA repair	r regulation cell cycle a	n of   met	erocycle tabolic ocess	regulation ligase acti	of co	cellular romatic empound etabolic process	regulation of cellular amino acid metabolic process	chromosome organization	ribonucleoproteir complex assembl	I complex subunit I	cellular macromolecular complex assembly	localization within membrane	receptor internalization
	nucleic acid metabolic process	DNA strand elongation	protein polyubiquitinati	metab	polic nucleob	pase–containing bund metabolic process	nitrogen compound metabolic process	organic cyclic compound metabolic process	nucleosome organization	macromolecular complex subunit organization	TP-dependent actomy chromatin structure remodeling organiza	ire histone deubiquitination	Golgi vesicle transport	protein insertion into membrane tail-anchored
mRNA metabolic process	negative regulation of cell cycle	peptidyl-serine dephosphorylation	positive regulation of ligand-depender nuclear receptor transcription coactivator activity	positive regularity of transcription RNA poly	ulation ption proteir ymerase lir	n-cofactor nkage	cell cycle DNA replication	nuclear cell cycle DNA replication	protein–DNA comple		system organ	nelle lipid particle nbly organization	localize within me	protein
RNA processing	peptidyl–cysteine S–nitrosylation	polymerase ii	mitotic porr combination bios	compound	DNA-dependent		activation of cysteine-type endopeptidase activation involved in apop signaling pathw	ctivity metabolic	subunit organization organelle	pre-catalytic	dense membrane granule organization positive regulation histone	complex biogenesis endoplasmic reticulum organization	metal ion transport	transport
	protein	mRNA spl DNA e packaging	avtracellular l	otidyl-cysteine		organizat	protein modification small prote removal	catabolic	interspecies	of histone modification multi-organ	of actin cytoskeleton eorganization	mitochondrion morphogenesis antigen rocessing and wa	x biosynthetic	glycolytic
DNA metabolic process	nitrosylation macromolecule	hyperosmotic m	otic metabolic t	gulation of ranslation amine	regulation of telomerase activity	proces cellular	gene eynres	substance of sion metabolic process	multi-organi modulatio	process	exogenous peptide antigen via MHC class  TAP dependent antigen proce  presentation of peptide antige	exogenous n via MHC	process process  wax biosynthesis carbohydrate catabolic process	
negative regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle cell cycle	catabolic process  DNA strand	telomere of g maintenance	gene expression involved in racellular matrix organization	process cytokinetic m		motalloonzyr	tabolic proces sitive ation of proces	s peptidyl-hypusine sphingoid metabolic		proviral latend	processing and processing	processing processing and presentation	cell cy	
	elongation involved in DNA replication cellular	RNA 3'-end nuclear receptor	and-dependent uclear receptor transcription activator activity	socitrate metabolic process	nucleotide-excision repair, DNA gap filling	positive regulation translation	cellular of response	DNA-templated transcription, elongation	keratinization muscle	regulation of Lightstonia	catabolic catabolism process	toxin metabolism		hromosome segregation signal transduction
cellular macromolecule catabolic process	macromolecule metabolic process	double-strand break repair via nonhomologous end joining	n-recombinational repair	aintenance of DNA ethylation	primary metabolic process	regulation of metalloenzyr activity	regulation of gene		regulation of determination of dorsal identity Refact determination of dorsal/vent asymmetr	regulation regulation of heart beta	metabolism	multi-organism process	N-acetylglucosamine metabolism	by p53 class mediator ellular component organization or biogenesis