## REVIGO Gene Ontology treemap

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	RNA processing	cellular aromati compound metab process	•	ion, co	anic cyclic ompound oolic process	macromolecule metabolic process		mRNA metabolic process		RNA localizatio	n mRN	A transport	nucleobase–containing compound transport	ribonucleoprotein complex biogenesis		ribosome biogenesis
		cellular nitrogen compound metabolic	protein folding	nucleic acio metabolic process	nitrog compo metab proce	ound polic r	primary metabolic process		gene xpression	nuclear export	establishn of prote localizatio	n to mitocho ransport	tion to regulation of neutrophil degranulation	rilribonucleoprotein co		mitochondrial mitochondrial respiratory complex biogenesis chain
	ncRNA metabolic process	RNA metabolic process	regulation of viral transcription	peptidyl-arginine omega-N-methylation	translation	7-methylguanos RNA capping		oing	mRNA 3'-end processing	cytoplasmic transport	nucleopla transpo UDP-galac	ucleolus to ucleoplasm transport  DP-galactose  vesi trans alor microte organi substan	fibroblast migration  ubule maintenance of proteir localization in	n	endoplasmi reticulum organization	establishment of protein localization to mitrochondrial
	ncRNA processing	regulation of nuclease activity	DNA-terRNA protection, elongation	transcription elongation  A processing polymerase on, Il promoter	positive regulation of protein kinase activity anscription	histone arginine methylation	ine N-linked glycosylation via asparagin		ne erol	negative regulation of fibroblast migration	nitroge compou transpo	n early endoson to late	transport  ER to Golgi vesicle-mediated transport		lamellipodiui organization	assembly
	cellular macromolecule	cellular metabolic	chaperone-mediated protein folding	catabolic process	rom RNA nolymerase cle	eavage me	etabolic process	ether netabol process pyrimidine ponucleosid	metabolic process	response to unfolded prote	n topo	conse to ologically ect protein	chorion development cerebral	structure regression	cell cerentiation	ER-nucleus signaling pER+nucleus signaling pathway
	metabolic process  nucleobase–containing	process	RNA modification	histone do	regulation of lene expression Pi di Olichol–linked ligosaccharide hinsynthetic	etabolic corocess de novo' rrimidine cleobase path	change bookenesis	riphosphate biosynthetic process  btidyl-prolin nodification	negative regulation	negative regulation	sponse to doplasmic	of protein nal	regionalization_ labyrinthine	ligodendrocyte dev	velopmental	regulation of epidermal growth factor receptor signaling pathway
(	compound metabolic process	of RNA polymerase II transcription organic	purine ribonucleoside triphosphate catabolic process	methylation  negative regulation of receptor catabolic	process p  ptidyl-arginine	lipid	idyl-aminomac acid me dification	romolecu ethylation	splicing carbohydrate le derivative	cellular response	esponse to heat	CRD-mediated mRNA stabilization	antigen processing and pantigen proces	presentation of exogenous sing and presentation		cellular zinc ion homeostasis
	heterocycle metabolic process	substance metabolic process	histone mRNA	macromolecule c biosynthetic r	compound reg metabolic of r	gulation receptor tran	of a	ranscri	dulation of pyrimidine nucleoside piption in other triphosphate mitrohead it rinteraction metabolic process	renair	ise–excision repair, gap–filling	detection of mechanical stimulus involved in sensory perception of sound	processing and presentation of exogenous	presentation of presentation of great		metabolic metabolism process