Revigo TreeMap

							vigo irodivid										
regulation of (1->3)-beta-D-glucan biosynthetic process		inositol lipid-mediated signaling		regulation of vesicle–mediated transport		negative regulation of phosphorylation positive regulation of phosphatase activity		N–glycan processing		histidyl–tRNA aminoacylation		branched-chain amino acid biosynthetic process polyamine biosynthetic process		pollen exine formation		ıl axis ication	embryonic meristem development
														anther wall	protoin		maturation
			regulatio	egulation regulation of		negative		mitochondrial translation	base conversion or N-gl	catabolic	tetrapyrrole metabolic ssing		CUT catabolic process	tapetum cell differentiation poll	protein-containing complex assembly en exine formati		rRNA
hyperosmotic response	negative regulation of developmen	of homeostasis	of defens response to insect	e RNA polyr	nerase II tra	gulation of nscription by RNA ymerase II	response to light intensity	indole–containing compound metabolic	editing tRNA N2–guanine methylation	cytokinin catabolic process	D-gluc catab	protein deglycosylation protein phosphorylation		socket cell 'differentiation	nale–female gamete recognition during double fertilization orming a zygote and endosperm	embryo developme	Idehiscence
	growth	response to flooding	cellular response to UV-C	photoperiodism, flowering	positive regulation of cellular response to	regulation of cellular componen	r regulation of DNA-templated			=				plant-type - primary cell wall biogenesis	abscissio	reticului tubulai	doplasmic eticulum tubular network ganization seedling development
positive regulation of hydrogen peroxide metabolic process	cellular respo to nitroger regulat starvarion	n tion of (1->3)-beta- regulation of		osynthetic p	oxidative stress	regulation o	of regulation of		N-terminal protein myristoylation	fatty acid	i arou		nonocarboxylic acid biosynthetic process	abaxial cell fate	nuclear membranereassemble	organizat	
	positive regulation of catalytic activity	process regulation of	defense response by	development signal transduction	biosynthetic process double-strand break repair	response to zinc ion strand innate s-link immune	negative					acylg	glycerol	neutral amino acid transport	iro	n ion embrane	lignin metabolic
regulation of mitotic cell cycle	response to	metabolic process to regulation	callose deposition	response to toxic substance	interstrand cross-link repair		by RNA	phosphatidic acid biosynthetic process phosphatidic acid bios		galactolipid biosynthetic process synthetic process		tran	sport acy	/Iglycerol trans from nucleus	port ciatifin-coated vesicle cargo	urea transport	glyoxal
negative regulation of response to salt		response to hypoxia regulation of	signaling regulation	regulation of histone H3–K9 dimethylation	cellular	positive regulation of metabolic process	regulation of cell					ER to chloroplast			loading, AP–1–mediated		
stress	response to organonitrog compound	gen tryptophan metabolic	of response to osmotic stress	regulation of post–transcriptional gene silencing	regulation of cell		of ribosome	e phospholipid	lipio biosynt proce	hetic biosy	golipid nthetic cess	lipid tra	ansport	oxygen transport	tran	im ion sport	metabolic process
positive regulation of cell death	detection of brassinostero stimulus	roid response to sorbitol	positive regulation of phytol biosynthetic process	negative regulation of cytokinin–activated signaling pathway	regulation of lipid biosynthetic process	cellular chemica	biogenesis Ras protein signal sis transduction	catabolic process	pentose-ph shunt, oxi brand	dative 5-ph	-D-xylulose osphate etic process	regulatior		on of microtubule binding trans		lation of binding cription activity	viral genome replication