Zm Expanded, No DEG in Zm, All C3 Upregulated, BP, ReviGO 0.5, # HOGs 204 Total Sig. GO-Terms 13

			ин Ехра	nded, No D	EG III ZIII	, All C3 (pregula	ieu, br, r	revido	0.5, #	nogs.	204 101	ai Sig. (
lipid metabolic process		phospho	rylation	protein ubiquitination		lipid cat	l pro	tein folding	response to salt stress)	defense response to virus		ene–activated aling pathway intracellular signal	protein transport		 	vesicle-mediated transport	
		biosynthetic process	primary metaboli	process	gamma-aminobutyric acid catabolic process	glycerol metabolic process	Group II intron splicing	heterocycle biosynthetic process	C/tidativ	nse to r e stress	respor esponse sucr	nse to to salt s ose	itress response to anoxia	transduction response to chemical		protein transpor		rt.	
mRNA processing		 	translate aromatic amino	heterocycle lationnetabolic process	Hadioai	nucleoside monophosphate	organic cyclic compound biosynthetic process	organic cyclic compound metabolic process	response to salt	arsonoacetate metabolic process	alcium-mediated signaling	response to endoplasmic reticulum stress	response to wounding	monoatomic ion	proton transmembrane	outer mer	from plasmodesmata-mediated intercellular transport		
		metabolic process	arriirio	homogentisate catabolic process	organonitrogen compound biosynthetic process	plastid translation	polyadenylation-dependent snoRNA 3"-end processing	protein autophosphorylatior			cellular res	ponse to	response transport to silver virus in	transport of virus in host, cell to cell	transport	transport		he transmembrane	
translation		cellulose biosynthetic	cannabinoid nitro biosynthetic comp process biosyn	gen catabolic	oxalate catabolic process	protein glutathionylation	transcription elongation by RNA polymerase II	STON vedéla basa 5-mellonyesinayineky-2-fasadishilatan	chromatin orga						polarity specification of of odoxiol/aboxiol dilation		biological_proces	s cell cycle	
		electron transport chain	prod	intrachromosomal DNA recombination	peptidyl-arginine methylation, to asymmetrical-dimethyl arginine	protein repair	tyrosine catabolic process	very long-chain fatty acid biosynthetic process			inization	cell wall organization	flower	evelopment		meristem			
			rRNA processing diaden tetrapho biosyn proc	hate miRNA	phosphatidic acid metabolic process	sulfur compound biosynthetic process	ubiquinone biosynthetic process	I Vitamin				_		flower d	muscie	pollen	chromosome segregation	circadian rhythm	
positive regulation of DNA-templated	of DNA	e regulation -templated scription	regulation of stomatal closure	nitric oxide of sa	regulation alicylic acid ted signaling arthway regulat	ion regulation of cyclin-dependent	regulation of gluconeogenes	regulation of meristem structural organization	chromatin o		ron–sulfu organiza assembly	tion filamen	y pollen o	development	development sepa	rmination al giant cell erentiation ot system	rhythmic	apoptotic process	
transcription		positive regula	ation of DN	positive regulation A-templated 1	regulati	3	regulation o response to salt stress	I of response	COP9 signalosome assembly	lipid drople		protein homotetramerization			transport shoot syste developmen		process	carbohydrate homeostasis	
regulation of translation	regulation embryoni developme	u u	polar of defen ansport response bacteriu	m positive regulation	prolifera Julation regulat auxin of	ion regulation of respons	regulation of apical meris	shoot tem nt regulation of	ER body	nucleus n organization	I of cell		metab	olic process	methylation		cell divisio	response to stimulus	
แลกรเสนบท		,	negative regulation of DNA endoreduplicatio	of response bios	synthetic ocess rhythr		regulation shoot syst morphogen	em movement									photorespiration	toxin metabolic process	