Supplementary Material 6. Enrichments Differentially Expressed Genes (DEGs) under selection. Treemaps showing enriched GO terms (BP: Biological Processes, MF: Molecular Functions, CC: Cellular Components) in DGEs arisen in Tricladida (node 65), Continenticola (node64), Geoplanoidea (node 63), and Geoplaniidae (node 62) with shift selection signal

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node65\_BP

DNA restriction–modification system	protein peptidyl-prolyl isomerization striated muscle cell	proliferation	Or	peptidyl–amino acid modification	cardiac muscle cell apoptotic process	regulation of cell prolife	ration	positive regulation of mitotic cell cycle	canonical Wnt signaling pathway	regulation of G protein-coupled receptor signaling pathway		ation loca	protein calization to cell cortex	nuclear migration	mesoderm cell fate determinat	al <sub>in</sub> ii on <sup>disc-</sup>	elongation volved in naginal derived wing shogenesis	imaginal disc-derived wing morphogenesis
gamete generation	apoptotic process	peptidyl-proline modification	sodium ion transmembrane transport negative	of sodium ion transmembrane transporter activity	of protein deneddylation	positive regulation	negative regulation	_	regulation of cell	regulation of	vacuolar Ic	protein ocalization	protein localization	late endosome	regulation	al <sub>wii</sub>	maginal c–derived ng margin	developmental process involved in reproduction
cognition	phosphatidylinositcl-3-phosphate biosynthetic process	feeding reproduct	regulation of sodium ion	reproduction	growth	of cell cycle phase regul transition		icrotubule-		mitotic cell cycle phase essansition	transmembrane tran <mark>cellular m</mark>	to cell macromole synaptic vesicle	localization	synantic	cell fate specifica!	euron di	oid NA gerr	on root hair cell
regulation of gluconeogenesis	positive regulation of gluconeogenesis		activation of GTPase activity	invasive growth in response to glucose limitation	response to salt	cell cycle checkpoint signaling	positive regulation stem cel proliferation	of of cellu localizat	positive regulation of E endoreduplica		localization	budding ynaptic vesicl recycling via		endosomal processing	of a polarize epitheliur	1	zation develo	root hair cell
positive regulation of GTPase activity	phosphatidylinositol phosphate biosynthetic process	cellular response to ecdysone	base conversion of substitution editing	cell cycle	regulation of growth of unicellular organism as a thread of attached cells	cellular process involved in reproduction in multicellular	s mitotic	regulation of mitotic cell cycles	C regulation of V signaling path involved in dorsal/yeatr	pathway involved in dorsal/ventral axis	nuclear migration	endosome protein localization	localization of e	phosphatidylserine exposure on apoptotic cell surface	morphogen establishmenimaginal disc-de	of rived	ngation euron rentiation	differentiation trichoblast maturation
filamentous growth	ecdysone receptor-mediated signaling pathway	protein destabilization	invasive filamentous growth	protein maturation by iron–sulfur cluster transfer	stress response to copper ion		signaling				mitotic actom	myosin	mitotic actomyosir		tion of regu	ation of	positive egulation of anscription	n DNA-templated
chitin-based	gona	d dau	uer entry	nematode larval	negative regulation	peroxisor fission		heritance	membrane fission	mitochondrial fission	contractile assembl		contractile ring maintenanc	actin fil polyme	depoly	nerization	by RNA lymerase	elongation
larval cuticle pattern formation	developr	ment	d	levelopment	of vulval development	supramolecular fiber	filopodiun assembly	structure	r cellular component	cell–cell junction maintenance	mitotic spindle	le mi	itotic	actil	bed-end action ment cappir		DNA-to	ation of emplated cription,
segment polarity	digest <mark>iar</mark> morphoge	val develo	ermination of adult pment	vulval development	regulation of vulval development	organization cytoplasmic	cellular co organizing center	mponent or	ganization n regulation of cellular	nuclear		pindle org	midbo anization nization		ein <b>filar</b>	nent ping **	p O	gation ositive regulation f DNA-templated transcription,
determination		mai oʻ	ntenance f dauer	heart development	9	microtubule organization	organization microtubul cytoskeleto	e actin	organization	organization n of	establishment meiotic spindl orientation	chromo	osome of mitoti ment centrosol	actin fila	on of actin f	ament	e	elongation  ulation of transcription longation from RNA lymerase II promoter
salivary gland morphogenesis	spirac morphoge open trac syster	nesis, cheal	larval elopment	negative regulation of	development embryo development	cytoskeleton organization	organization microtubule-base process	on organization or	componen axonem	t size nucleus al organization	establishment mitotic spindle localization	le of mi	ation regulation of spino	on amino a transmer <mark>a</mark> transpo	cid carboxylic a mino acid tr rt transport	id organic a <b>nsmem</b> transp	<u>brane tra</u>	nsport acid smembrane

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node65\_MF

p53 binding		dynein complex bind	ing chromatin bind	ling	protein tyrosine kinase activity	protein serine/threonine/tyrosine kinase activity	N–me	lysine ethyltransferase activity	purine ribor triphospha	
microtubule binding	protein binding transcription coregulator		protein binding histone binding		protein–lysine N–methyltransferase activity SUN	peptidyl–prolyl cis–trans isomerase activity IO transferase activity	isomerase activity		purine ribonucl	
		receptor serine/threonine kinase binding	protein binding		SUMO transferase activity	polynucleotide 5'–hydroxyl–kinase activity		histone methyltransferase	ATP binding	adenyl ribonucleotide binding
transcription corepressor binding		tubulin binding	transcription factor binding		phosphotransferase activity, alcohol group as acceptor	kinase activity		activity (H3–K36 specific)	adenyl nucled	otide binding

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node65\_CC

kinetochore microtubule	microtub	ule	mitotic s	spindle pole body	beta-catenin-TCF complex		COP9 s			e ferase ex	extrinsic component of endoplasmic reticulum membrane	medial co	ortex		mitotic actomyosin contractile ring	
chromatin	mitotic spindle midzone		spir	ndle midzone	MLL1/2 comple		extrinsic OP9 signalosome component of endosome membrane		CHD-type complex		I NURD COMDIEX I		cortical cytoskel <mark>cell co</mark>		o <mark>rtex</mark> CAR complex	
polytene chromosome	<mark>aster</mark> euchromatin	aster		kinesin complex	extrinsic component of organelle membrane		trans facto	olymerase scription or SL1 mplex	fungal–type vacuole lumen		endoplasmic reticulum palmitoyltransferase complex	actomyosin contractile ring	cell co	ortex	apical cortex	
mitotic spindle	pericentric heterochromatin	I chromosome		radial spoke	contractile ring	body meml	neuronal cell body membrane site of polariz		g on tip		odium tip g projection	host cell cytoplasm part		er m	nost cell ndosome embrane	
astral microtubule	tral microtubule rDNA mitotic spindle heterochromatin astral microtube			chromosomal region	site of polarized growth	cell boo membra		female germ		ne		host cell cytonic host cell Golgi membrane			part ell endosome	

# TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node64\_BP

regulation of mitotic cell cycle, embryor	i d	egulation of embryonic levelopment	digestive tract development	salivary gland morphogenesis d	salivary gland evelopment	syncytium formation	exocrine system development	neuron cel homeosta	cell Isis	ular c	pore omplex ssembly	stem cell proliferation	positive regulation of mitotic cell cycle	positive regulation of cell cycle process positive	cycle phase transition	G2/MI ransition f meiotic of	of meiosis I
positive regulati of multicellula organism grow	tion la	chitin-based arval cuticle pattern formation	segment polarity determination pseudocle	regulation of anatomical structure morphogenesi	S germ-line	first cell cycle tic pseudocleavag	midgut e development	engulfment of apoptotic cell	vacuolar transport vacuol	asymn cell div ar transfic	vision	cristae formation	meiotic cell cycle	regulation of meiotic tive regulation o positive regulation of G2/MI transition of meiotic cell	regulation of meiotic f meiotic cell positive regulatio of G2/M transition of mitotic cell	cycle ycle phase transition	regulation of cell cycle G2/M phase transition
embryo development ending in birth or egg hatchin	t h disa	ell elongation involved in imaginal c-derived wing orphogenesis	regulation of mesodermal cell fate specification	morphogenesi gland morphogenesi	germ-line determine positiv regulatio	pole c ation formati e n of		endosome transport via multivesicular body sorting pathway	phagocytosis, engulfment apoptotic cell	engulfme apoptotic plasma membran	nt of Ce	n of	positive regulation of reproductive process	cycle regulation of G2/MI transition of meiotic cell cycle	regulation of meiosis I	positive regulation of cell cycle phase transition	positive regulation of fertilization
mesodermal ce	eell mo	spiracle orphogenesis, pen tracheal system	ovulation	photoreceptor cell morphogenesi	developn Sex	pole ce developm	pseudocleavage ent	multivesicular body sorting pathway	negative regulation of apoptotic cell clearance	membran invaginatio	engulfmente ne reg	osis,	positive regulation of transforming growth factor beta receptor signaling	regulation of Notch signaling	proteir localizati to centrose	on loc	blishment protein alization vacuole
protein sumoylation	regulation of telomo	ere nucleobase-co	of ntaining stabolic gene silenci by RNA	regulation of macromolecule biosynthetic process	leucine catabolic process	positive regulation of RNA interference	positive regulation of RNA metabolic process	septin ri organiza	ng tion	ctomyosin ontractile g assembly	s	spindle anization	re signal tran	pathway egative sduction in DNA damage	regulation protein localization	tai vacu nment of p	
ubiquitin–dependent protein catabolic process via the multivesicular body	polysaccha biosynthe proces:	transles aride etic synthes	ion regulation of cellul biosynthe proces	on telomere maintenar	metaboli	regulation of translation	of autophagy	mitotic cytokinesis		ore cytosk organ ion involve mit	ization ved in osis	cytokinetic process	proliferation d ch DNA damage checkpoint t	amage eckpoint signal ransduction	regulation of nucleobase-containing compound transport	targeting targeting to vacuole	protein localization to nucleus
negative regulation of macromolecule biosynthetic	lipopolysacch metabolic pro	naride gene	proces positiv regulatio	etic of glu- ss biosynt e proce	hetic pess nuclei	etabolic rocess ar-transcribed NA catabolic ol	regulation of olysaccharide biosynthetic process igosaccharide biosynthetic	microtubule organizing center	centrosome duplication		centriole-centrio	regulation of microtubule nucleation	DNA integrity stre	DNA damage ess-activated rotein kinase signaling cascade	ATP	ATP transport	locomotor rhythm
regulation of transcription by RNA polymerase II	regulati of DN/ biosynth proces	A positiv regulatio gene siler	proces e positive n of regulation ncing posttranscrip	metabolic negat n of regulational cellular a	process exc ive pro on of miRN, amide gene	nucleolytic, 3'–5' duction of As involved in silencing by	biosynthetic process  positive regulation of transcription, DNA-templated	regulation of spindle assembly	a a II a vala	centrosome	regulation of spindle organization	e organization	mechanical "wowed in sen	of detection of detection of stimulus involved in sensory	detection stimulus red in sensor sensory perceptio	sensory y percept of touch	ion sponse to multiple multip multiple multiple multiple multiple multiple multiple multiple

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node64\_MF

SUMO transferase activity	guanyl–nucleotide exchange factor activity	translation repressor activity	polynucleotide adenylyltransferase activator activity	sequence–specific double–stranded DNA binding	translation repressor activity, mRNA regulatory element binding	tran: regula sequen	olymerase II scription tory region ce-specific a binding	
				transcription r	egulatory region nucleic acid	d binding		
	SUMO binding	protein serine/threonine/tyrosine kinase activity	copper chaperone activity		cis-regulatory region binding		centromeric DNA binding	
GTPase regulator activity	metallochaperone activ	vity		sequence–specific mRNA binding		transcription regulatory region nucleic acid binding		
					region nucleic acid bil	iding		
transcription corepressor binding	poly(A)-specific ribonuclease activity	phosphatase activity	SUMO ligase activity	DNA-binding transcription fac activity, RNA polymerase II-spe	trancarintian			
				DNA-bin	ding transcription factor acti	vity	DNA-binding transcription activator activity, RNA polymerase II-specific	
kinase binding	sulfurtransferase activity	metallochaperone activity	ubiquitin–like protein binding	transcription regulator activit	/	DNA-binding transcription activator activity		

TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node64\_CC

eukaryotic translation initiation factor 4F complex	actomyosin contractile ring	MICOS complex	sperm connecting piece	phagophore assembly site membrane	phosphatase complex
Cvt complex	ESCRT complex Cvt compl	ex ESCRT-0 complex	mating-type region heterochromatin	pericentriolar material	RNA-directed RNA polymerase complex
beta-catenin-TCF complex	centriole	PML body	phagophore assembly site	shelterin complex	RNA-directed RNA polymerase complex

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node63\_BP

error–pron translesior	n	positive protein phosphor regulation of DNA biosynthetic negative regula		nosphorylation	negative regulation of DNA	regulation of TORC1 signaling	regulation of sporulation	of regul	positive regulation of response to stimulus		mitotic	regulation of mitotic cell cycle phase transition		eiotic aphase blate ression	meiotic cell cycle			
synthesis		biosyn proc		of	re regulation cellular netic process	damage checkpoint	regulation of	positive regulation of mitotic	i regula	tion of	lymphocyte costimulatio	spindle m	spindle midzone		positive regulation	ma an dadian		
positive	prote	suppression  protein  moylation		rus of	regulation of transcription	regulation of establishment or	terminal button organization positive regulation	cell cycle				assen	nblv regu	spindle lation of ma sister chro		of chromatid		
regulation of DNA repair	pair sumoylation host RNA polymeras		nerase tivity	by RNA polymerase II	maintenance of bipolar cell polarity regulating cell shape	positive regulation of intracellular signal	T cell costimulation	regulation of growth rate	regulation of I–kappa kinase/NF–ka signaling	аВ кіnase/NF–kaр рраВ signaling	of mainter meiotic	of maintenance of meiotic sister		of tid karyos	tion			
suppression by virus of host transcrip <mark>modul</mark>	by sympioni		tion of acid	negative regulation of fatty acid otion:tabolic	mitotic DNA damage checkpoint signaling	transduction positive	positive regulation of I–kappaB	regulation of presynapse	positiv regulation	on regulation	meiotic	ince of sister	cohesion  chromosome organization involved in meiotic	reg	formation			
	lialistii	puon	proc	ocess process		checkpoint signaling	regulation of apoptotic process	kinase/NF-kappaB signaling	organization	ganization signalin		cohes		cell cycle	chro	matid cohesion		
regulation of DNA repair	negati regulatio macromol biosynth	on of lecule netic	posit regulati DNA-dep DNA rep	ion of pendent	peptidyl-lysine modification	RNA processing	RNA splicing, via transesterification	production small RNA involved in go	\ tRNA :	tRNA 5'-end sil		d positive	positive regulatio of cytokinesis		ary cell otum enesis	regulation of mitotic division septum assembly		
	proces	ss				ration processing	reactions	silencing by F			interference			•	sitive ation of	positive regulation of		
regulation	regulation of		positive regulation of	positive regulatio							ncRNA		T	cell s	eptum	division septum		
-	regulation DNA-dependent of gene DNA replication com		obase-containing bound metabolic process	of DNA replication	host gene	mRNA splicing, via spliceosome	tRNA 5'-leader removal	A processing processing		plicing	metabolic process	regulation of primary cell septul	of prima cell	positive	y cell sept regulation nitotic	assembly um biogenesis positive regulation		
mitochondrial	mitochondrial regulation	Of	gulation	modulati	on negative	RNA splicing, via			mRNA		sno(s)Rl	biogenesi		cytoking	tic process	of mitotic cytokinesis		
mitochondrial regulation of fatty acid biosynthetic process process		atty acid synthetic process of		fatty acid iosynthetic metabolic modular		by virus of host gene expression regulation of lipid biosynthetic		transesterification	mRNA processing	transcription by RNA polymerase	metabo proces	mRNA metabolic process		positive of se			ılation nitotic kinetic ocess	mitotic division septum assembly

### TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node63\_MF

proteasome binding		ATP binding		ATP binding		F	protein binding	SUMO ligase activity		serir	protein ne/threonine/tyrosine kinase activity	protein serin	e kinase activity	pre–mRNA binding
ribonuclease P activity	protein-macro ribonuclease P activity molecular adap		ty coregulator activity					1-phosphat	ine/threonine kinase tidylinositol–4–phosphate –kinase activity	activity  aspartic-type peptidase activity	myosin light chain kinase activity	pre-mRNA branch point binding  pre-mRNA binding		
RNA polymerase II–specific DNA–binding transcription factor binding		chaperone tivity			cyclin binding	protein serine/threonine kinase activity		aspartic-type endopeptidase activity		phosphatidylinosit	ol kinase activity	N6-methyladenosine-containing RNA binding		
			DNA 6	indina		P–type potassium:proton	_P_tvne	sodium	P–type	P–type potassium	P-type proton-exporting	DNA binding, bending		
copper chaperone activity	molecular adaptor activity		· tranccri		zinc ion binding	transporter activity	P-type transport	potassium ter activity	P-type transmembrane tran transporter activity	sporter activityne transporter activity	transporter activity	poly(A) binding		

## TreeMap\_Enrichm\_DGEs\_ONUN\_Sel\_node63\_CC

division septum	nucleolar ribonuclease P complex	mitotic spindle pole	t	A polymerase II transcription ressor complex	multimeric ribonuclease P complex	ribonud	clease MRP complex	Lst4–Lst7 complex
aggresome	cell tip  chromatin	central plaque of spindle pole body	mitotic	spindle midzone	sno(s)RNA ribonuclease P complex		ing ribonucleoprotein of enzyme activator complex	sno(s)RNA-containing ribonucleoprotein complex
	cell pole	Il pole endoplasmic reticulum			GTPase activator complex		RNAi effector complex	
fibrillar center	SAGA complex	mitochondrial respirat chain complex IV	ory	chromatin	host cell endoplasmic reticu <mark>host cell e</mark>		ndoplasmic reticulum e	ndoplasmic reticulum