Supplementary Material 3. Enrichments Proteomics. Treemaps showing enriched GO terms (BP: Biological Processes, MF: Molecular Functions, CC: Cellular Components) in proteins detected in ONUN and SMED. Additionally, the enrichment of HOGs including proteins detected in ONUN, proteins detected in SMED, and proteins detencted in both species

TreeMap_Enrichm_ONUN_prot_BP

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positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation involved in immune response	homeostasis	regula	tion informatory response	behavior activation of positive	or compound c	negative regulation	n positive regulation	catabolic	process pro	ocess process	process	ocess process	cellular	lipid mitochon	Irial	p	process	process	process	sarcomere	barbad and	folding	
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actin filament binding	unfolded protein binding SH3 domain	dynein light intermediate chain binding	cysteine-typ	methyl ndole–3–acetate esterase activity	ate	dehydrogenase (ubiquinone) activity oxidoreductase activity, acting on the CH–NH group of donors, NAD or NADP as acceptor	sarbonyl eductase NADPH) activity superoxide dismutase activity activity aldebyde dehydrogenase (NAD+) activity superior donor nADP as activity activity activity superior donor nADP as activity superior dehydrogenase superior donor nADP as activity dehydrogenase superior donor nADP as activity dehydrogenase superior activity superior donor nADP as activity superior nADP acti	g on row transfer activity acting activity acting activity, acting	transaminase dipho ki activity ac	hione acetyl-CoA erase C-acetyltransferase Ct activity	nucleobase-containing compound kinase activity biquitin-like protein protein onjugating enzyme activity enzyme activity pyruvate pyruvate pyruvate pyruvate pyruvate pyruvate pyruvate pyruvate pyruvate pyruvate
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binding phosphatidylinositol-4,5-bisphosphate magnesi	Steroi derivativ	binding bindin	amolecular act loreductase activity, acid	ivity ligase activity, forming carbon-carbon bonds -thiol activity activity activity activity	amidine-lyase activity transposing C=C bonds carbon-nitrogen ligase activity, with glutamine as amido-N-donor	ATPase	motor activity activity GTPase motor activity	motor activity motor activity long-chain fatty fatty acid-CoA ligase activity activity activity motor activity fatty fatty diphosphalase activity	- 4114	ATPase inhibitor activity	ein-macromolecule adaptor activity gnaling receptor blex adaptor activity

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myosin filame	ent I	dherens unction	path	nogen-containing vacuole	myosin com	plex con	nplex	cytos sm riboso subu	_{all} lipid ^{omal} drople	et dynein arm	lysosc	ome	rans–Golgi network	endoplasmic reticulum exit site	endoplasmic reticulum-Golg intermediate compartment	Z disc	P granul	striated muscle e dense body	mitochondria		endoplasmic reticulum lumen
focal adhesion	terminal bouton	lamellip	oodium	axon	actin cytoskelete	ribose sub on mite sep	omal unit cytoskele otin spino	ton lie comple	actin Arp2/3 protein	complex actin filament bundle	endoplasmic reticulum	endoplass reticulur protein-cont endo mitochono protein-cont comple	reticulum membrane plasmic reti rial aining organelle	endoplasmic reticulum chaperone iculum chloroplast thylakoid	peroxisome plastid thylakoid	cytoplasmi <mark>co</mark> stress	ntractile fib	er A band	mitochondrial simitocho ribosomal subunit	cc	chondrial mitochondria atrix industribusional omplex ribosomal subunit
rhabdomere	type lb lamellip terminal bouton	spine	c speri flagell	um	dynein com	olex tropo com	onin spol	podosom ribosom	associated	organellar ribosome spindle midzone	Golgi stack Nebenkern	microne	endoplasmic reticulum subcompartment	plastid sthylakoid Golgi	membrane arcoplasmic reticulum smooth endoplasmic reticulum	granule muscle myosin	myofibril	cytoplasmic cytosolic microtubule ribosome	dehydrogenase complex mitochondrial	nuclear periphery vacuolar lumen nuclear	mitochondrial nuclear lamina Golgi mitochondria tricarboxylic
neuronal cell body	junction basement membrane	density	growing	neuron to	axoneme	ро	le centri	subunit	large , ribosomal subunit	ericentriolar dynein dynein complex	mitocho respira	envelo ondrial		membrane		complex	P-body actin cortic	contractile fiber	endosome	matrix COPII vesicle	lumen add cycle enzyme complex
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positive myosin actin vacuole filament filament inheritance organization of myosin II filament organization organization organization organization	short-term epithelial structure maintenance management of lipid maintenance epithelial structure epithelial epitheli	mitochondrial cytoplasmic mitochondrial proteolysis protein translation translation	protoporphyrinogen retabolic metabolic metabolic process fatty-acyl-CoA metabolic reduction retabolic metabolic metabolic metabolic reduction retabolic metabolic reduction retabolic reduction reduction reduction of synaptic assembly regulation of synaptic assembly regulation of synaptic assembly regulation of synaptic assembly reduction reduc
sarcomere assembly capping actin regulation of actin contractile actin planet of actin	memory storage cycle, sleep receptor levels appetite post-mating positive regulation positive of ATPace of	translation processing processing received recei	IX biosynthetic process
mitochondrial organization orga	regulation of epithelial synaptic ransmission, of stabilization of stabilization entered for the control of the	maturation isomerization biosynthetic process process tRNA protein protein N-linked protein process	mitochondrial ATP synthesis coupled prote process Purine nucleotide biosynthetic process proce
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cellular amino valine valine valine metabolic process rocess long-chain fatty acid glutamine histidine metabolic metabolic metabolic process	open tracheal cell cycle, embryonic differentiation of development	nitrile nitrile process pyrimidine-containing compound catabolic process metabolic process process process peptide amino-acid metabolic process peptide peptide metabolic process process process	folding cell-substrate adhesion plasmatocyte differentiation confidence activation activation protein
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process dephosphorylation target metabolic catabolic process p	endoplasmic sodium ion establishment transport membrane orientation plasma prioritation transport membrane orientation orientation orientation space transport transpo	endoplasmic reticulum regulation of regulation of regulation of regulation of signaling astway regulation of regul	Vesicle budding from membrane regulation of vesicle budding from membrane regulation of apparatus regulation of secretion by cell process

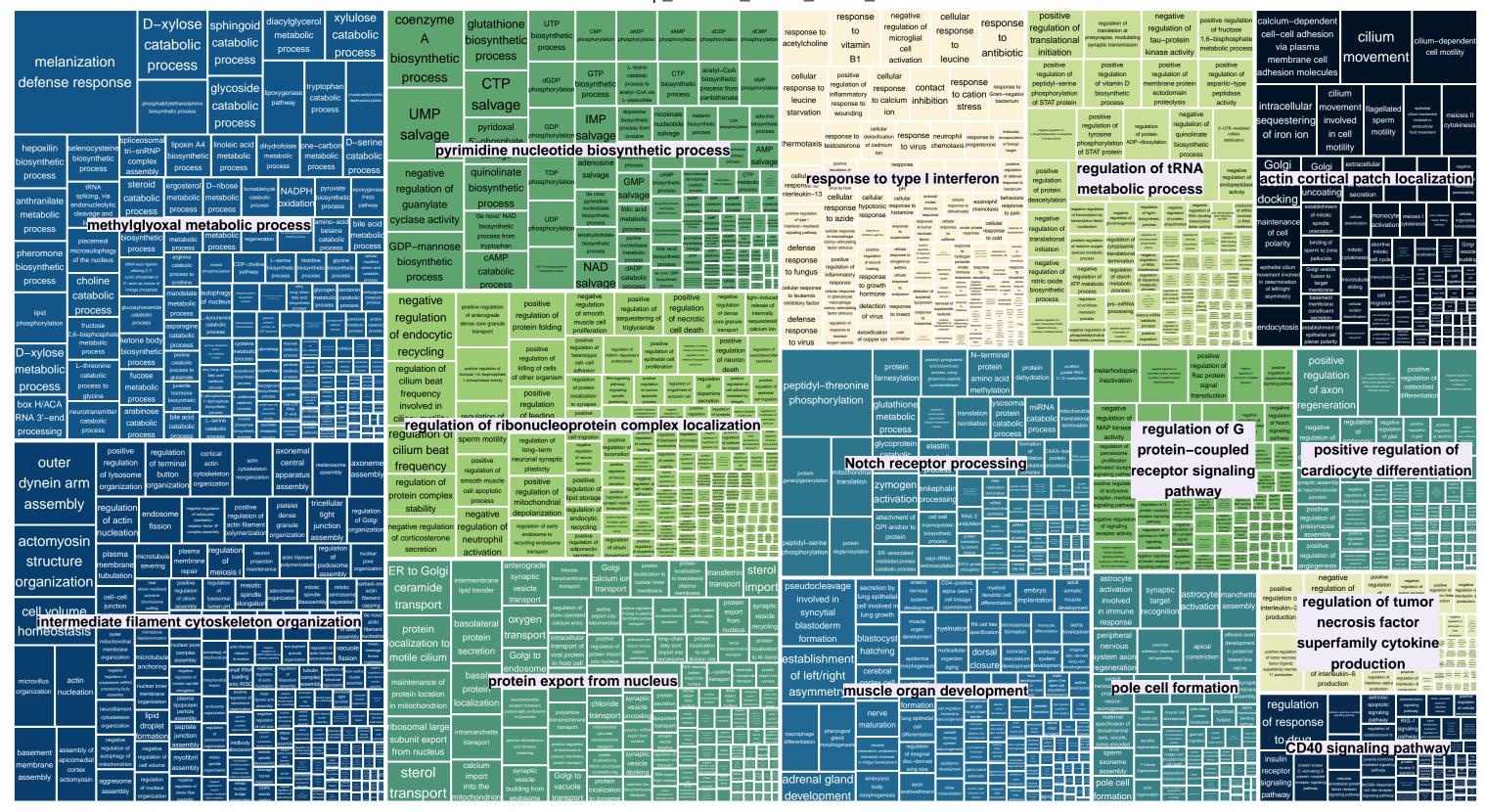
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structural constituent	metalloendopeptidase activity	toxin activity	proton-transpo ATP synthas activity, rotational mechanisn	cis-traisome isome activ	ans a	antioxida activity	ant a for carbo	ligase activity, orming on–carbon bonds	NADH dehydrogenase (ubiquinone) activity	acyl-CoA dehydrogenas activity oxidoreductase activity.	aldeh Se dehydrog (NAD+) :	jenase re	in-disulfide ductase	xidoreductase activity, acting on the CH–NH2 group of donors	GTP bir	nding	pyrido: phosph bindir	nate
of ribosome	aminoacyl-tRNA	endopeptidase activity	ATPase	fatty acid–CoA ligase activity	carboxy–ly activity	yase y rec		utamate-ammonia ligase activity	oxidoreductase	acting on a sulfur group of donors	activity, acting on he aldehyde or oxo group of donors, isulfide as acceptor	oxidoreductas activity	peroxidas activity	ferroxidase				
	ligase activity		ligase activity	deaminase activity	biquitin–like modifier activating enzyme activity	calcium-dependent protein serine/threonine phosphatase activity	hydrolase activity acting on carbon-nitrogen (l not peptide) bond in cyclic amidine		activity, acting on the CH–OH group of donors, NAD or NADP as acceptor	oxidoreductase ac oxidoredu a sultur group of donors, disulfide as acceptor	activity	tivity ehydrogenase activity	oxidoreductase activity, acting on CH–OH group of donors	steroid dehydrogenase activity	flavin aden NAD binding	ine dinucleot dinucleotide	de bind FAD b	
GTPase activity	protein disulfide	carbon-nitrogen	metallocarboxypeptidase activity	IINACA	carbonate ehydratase ⁹ activity	galactosylceramidase activity	intramolecular transferase activity, phosphotransferases	hydrolase activity, hydrolyzing O-glycosyl compounds	oxidoreductase activity, acting on the CH–CH	isomerase activity	oxidoreductase activity, acting on the aldehyde or oxo troup of donors, NAD or NADP as acceptor	oxidoreductase activity, acting on the CH–NH group of onors, NAD or NADP as acceptor	oxidoreductase activity, acting on the CH–NH group of donors oxidoreductase	peroxidase activity		binding	<u> </u>	
	isomerase activity	hydrolase activity, acting on	protein folding	yrophosphatase activity	arboxypeptidase a activity	amidine-lyase activity	hydrolase activity, acting on glycosyl bonds	CoA-ligase activity	group of donors electron transfer	oxidoreductase activity, acting on single donors with incorporation of molecular	rotein-disulfide reductase (NAD(P))	disulfide exidoreductase activity erroxiredoxin	activity, acting on peroxide as acceptor oxidoreductase activity, acting on	oxidoreductase strikly, scing activity, acting a sulfur group on the CH-NH2 group of donors, as acceptor	ATP binding	GDP binding	binding	AMP g binding
metalloaminopeptidase	hydro–lyase	carbon-nitrogen (but not peptide) bonds, in linear amides intramolecular	chaperone	structural constituent	scavenger receptor activity	dipeptidyl-peptidase activity	cis-trans isomerase activity	p. o.o	activity	oxygen, incorporation of two atoms of oxygen hydroxymethyl– formyl– and	pyruvate	activity	the CH-CH group of donors, NAD or NADP as acceptor	L-malate dehydrogenase activity		NADP bindin	FIMIN	binding
activity	activity	oxidoreductase activity	nucleotidase activity	structural constituent of chromatin	exopeptidase activity	ligase activity, forming carbon-nitrogen bonds	phosphoemologravasis phosphi carbooyksass carb (GTP) archity z	oenobyvuste bydridase activity, controlly activity activi	transaminase activity	related transferase activity	kinase activity	activity	ase activity, transferring alk or aryl (other the methyl) groups	calciu			G	glioside GM1 nding
	interferon-gamma receptor binding	cyclosporin A binding	proteasome binding	clathrin binding	ribosor bindin		IARE g	alactoside binding		ase activity, to		roups	nucleoside monophosphate kinase activity	bind	ding ion bin	gangliosi	de gang	llioside
actin filament binding	receptor billuling	translation	quaternary ammonium	cell-cell adhesion mediator activity	protein-conta complex bind	aining ding pro	shock otein ho	protein modimerization activity	adenylate glutathic kinase transfera activity	_{ase} carbohydrate y kinase	UDP-glucosyltransferase activity	MAP kinase kinase activity	phosphotransferase activity, phosphate group as acceptor	met	al ion binding magnesium ca ion binding bin	ition bin GM	glioside 1 bindin	e ing ing
	carbohydrate binding	initiation (factor oskeletal prot	group binding	scaffold protein	MHC protein	cytoskelet protein	tal integri	a kinase	adarray	activity	poly(U	compound kinase activity	kinase activity translation		ferric iron m	etal GP1c b		fatty
	misfolded	2 iron, 2 sulfur	binding 4 iron, 4	modified amino acid	Hsp90 protein	signal sequenc	protein kinas A catalytic subunit	binding	mRNA binding	pre-mRNA binding	N RNA binding	binding	elongation factor activity	potassiur ion binding	binding bir alkali metal ar	nion gangli	Joide	acid binding
unfolded protein binding	protein binding	cluster binding myosin	sulfur cluster binding	binding actin monomer	binding actin binding	_	e _{monosacchar}	Arp2/3 complex	sing translation	le-stranded binding	RNA bin bindin		rRNA binding	3	G	BPI anchor pho		phosphatidylserine binding
	protease binding	heavy chain binding	clathrin adaptor activity	binding vitamin binding	kinase	enzym	e dynacti	binding n ubiquitin g binding	initiation factor activity	single-strande RNA binding	7 - mounyiguanic		hinding		phosphatidy	ylinositol bind tidylinositol-3,4,5-trisphosphate pho binding	phatidylcholine ^{ph}	phosphatidylinositol bisphosphate binding

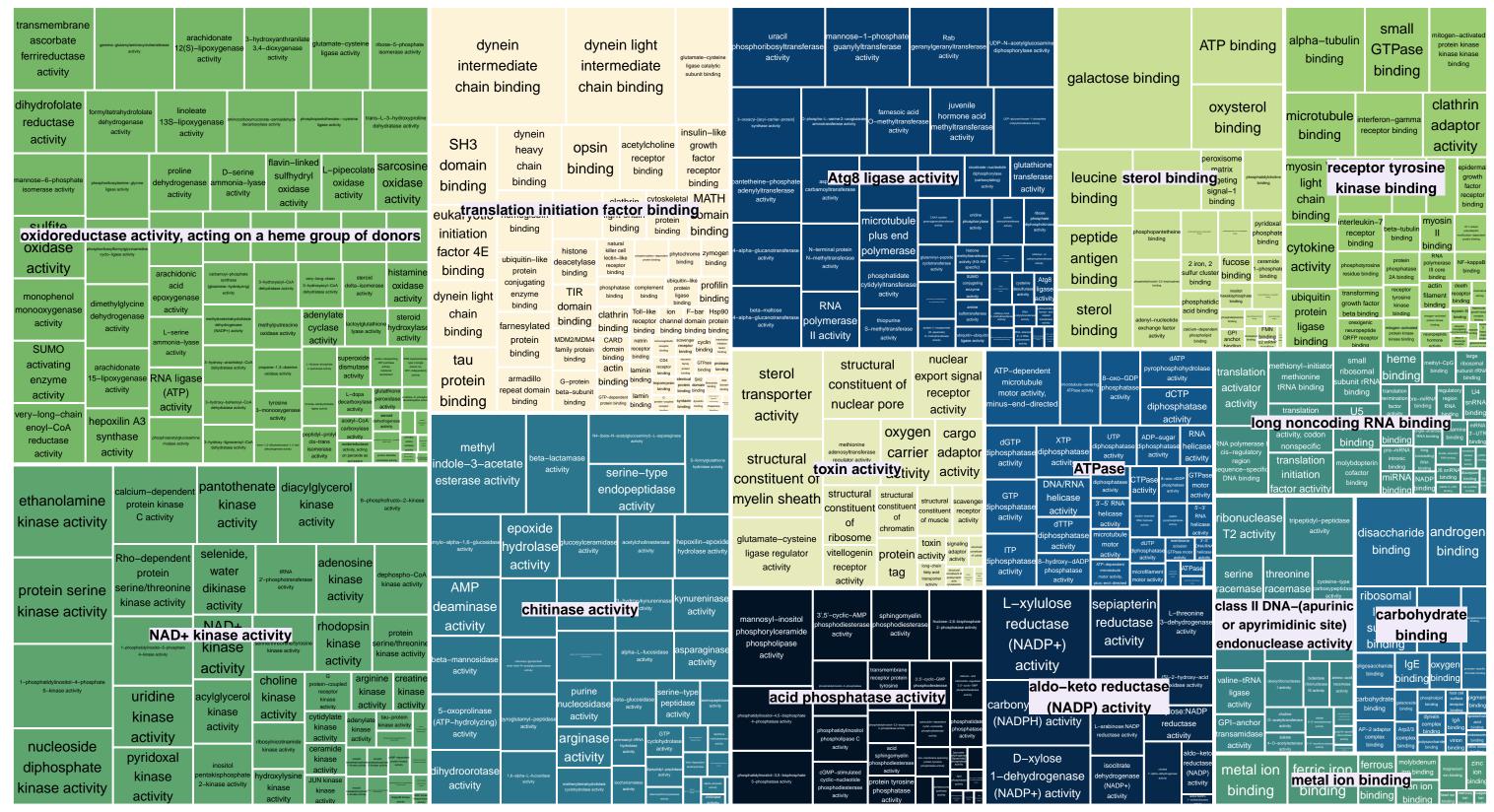
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	cytoplasm	SNA	ARE com	plex	eukaryotic 43S preinitiation			multivesio body	ph	agolysosome	extracellular s		extracellu matrix	lar apic		ırin–coated pit	oxidoreductase complex	proteasome complex	alpha-subunit complex	t complex
cytop	olasm				complex	phagod	cytic vesicle	clathrir	n	COPII		ex	contractile tracellula	r region	thylakoid membrane	apoplast	protein phosphatas _{pe} type 2A	calcineurir eptidase co	cytochrome cmplex	box C/D RNP complex
	cyt	eukar oplasm 48	yotic tr	ukaryot anslatio			endo	vesicle c		vesicle coat	autor a lluda a		germline ring	membrane raft membrane	nucleoid apical	apical	complex	polysome	regulatory particle, lid subcomplex peptidase	small-subunit processome
		preinit	iation olex	nitiation factor 3 comple	3	ESCRT III complex	transport _{EI} vesicle _t	R to Golgi	dosome	COPI vesicle coat	extracellular re	egion	canal respirasome	microdomair aggresome	cortex blood microparticle	part of cell external encapsulating structure	core complex, beta-subunit complex	proteasome regulatory particle	complex nuclear cap binding	ribonucleoprotein complex ubiquitin conjugating enzyme complex
cyto	osol	cell corte	chaperonin-c T-com	cytopl ontaining ubiq lex liga	lasmic quitin WASH ase complex aplex	synaptic vesicle	endosome	lanosome me	ndocytic vesicle embrane cycling	endosome membrane	presynapse		rminal	adherens	pore comple	ada	hrin ptor complex	pathogen-	complex -containing) myosin
		tricarbox acid cy enzym comple	cle region	of mult	ti-eIF inclusion nplex body	early endosome	synaptic m vesicle	embrane early end	docytic	omplex transport vesicle membrane phagocytic vesicle membrane		bo	outon	junction	proton-transporti	V-type ATPase,	clathrin coat of proton-transporting two-sector on sporting		cuole 	filament
cytosolic large ribosomal subunit	striated muscle dense body	P granule	myosi comp		actin filament		momorane pa	lysosoma lumen	mit al l	tochondrial pyruvate nydrogenase complex		presyr neuromuse junction	cular presynap	piasinouesina	_	ctor ATF		collagen type IV trimer	side of apical plasma membrane	seudopodium
cortical actin	actin cortical	Arp2/3 protein	mito actom contra	osin C	cytoplasmic stress	mitochor	ndrial matrix	mitochondrial large ribosomal subunit	mitochondr small ribosoma subunit	rial trans-Golgi network membrane	cell-substrate	foca adhesi	(ose inal	respirator chain complex	complex	proton-transporting / V-type ATPase complex death-inducing signaling complex	growth	projection tip	filopodium
cytoskeleton		complex toskeleto	n _{eptin}	er	granule			contractile tra		vacuolar proton-transporting V-type ATPase complex	mitochondr	·ial	inner mitochondrial membrane	mitochondrial proton–transporting ATP synthase	U2 sr	ıRNP	precatalytic spliceosome	endoplas reticulu chapero	reticul	oplasmic lum–Golgi rmediate partment
cytosolic small ribosomal subunit	ribosome medial	A band filamentous	P-body	mitotic	n troponin	endoplasm reticulum lur	Ivsosome	vacuole _{interm}	chondrial nembrane autoph mer space	hagosome mbrane vacuolar membrane		ex I r mito	chondrial	ochondrial -transporting v synthase	Mei2 I	catal ster nuclear spliced	ytic commitment		ndoplasmic asmic retio	endoplasmic reticulum
lipid droplet	cortex septin ring actin	actin	M band	actomyosir	myofilament kinesin I complex	Coloi kura	endoplasmic	membrane va		Golgi fungal-type mbrane vacuole	mitochondr	ial	nitochoodial respiratory chain	factor F(o)	post-mRN release	U2-ty	CHD true MIIRI)	plant-type	reticulum	endoplasmic reticulum exit site
	cytoskeleton	Z disc	filament bundle	polysoma ribosome	striated muscle	Golgi lumer	n reticulum membrane	envelope mitod		peroxisomal matrix	inner membr	ane	mitochondral respiratory chain complex II, succinate dehydrogenase complex (ubiquinone) men	respiratory uter chain nbrane complex IV	spliceoson complex	al COF signalos	iviei∠ nuclear		Golgi vad apparatus	orage mitochondrial protein-containing complex

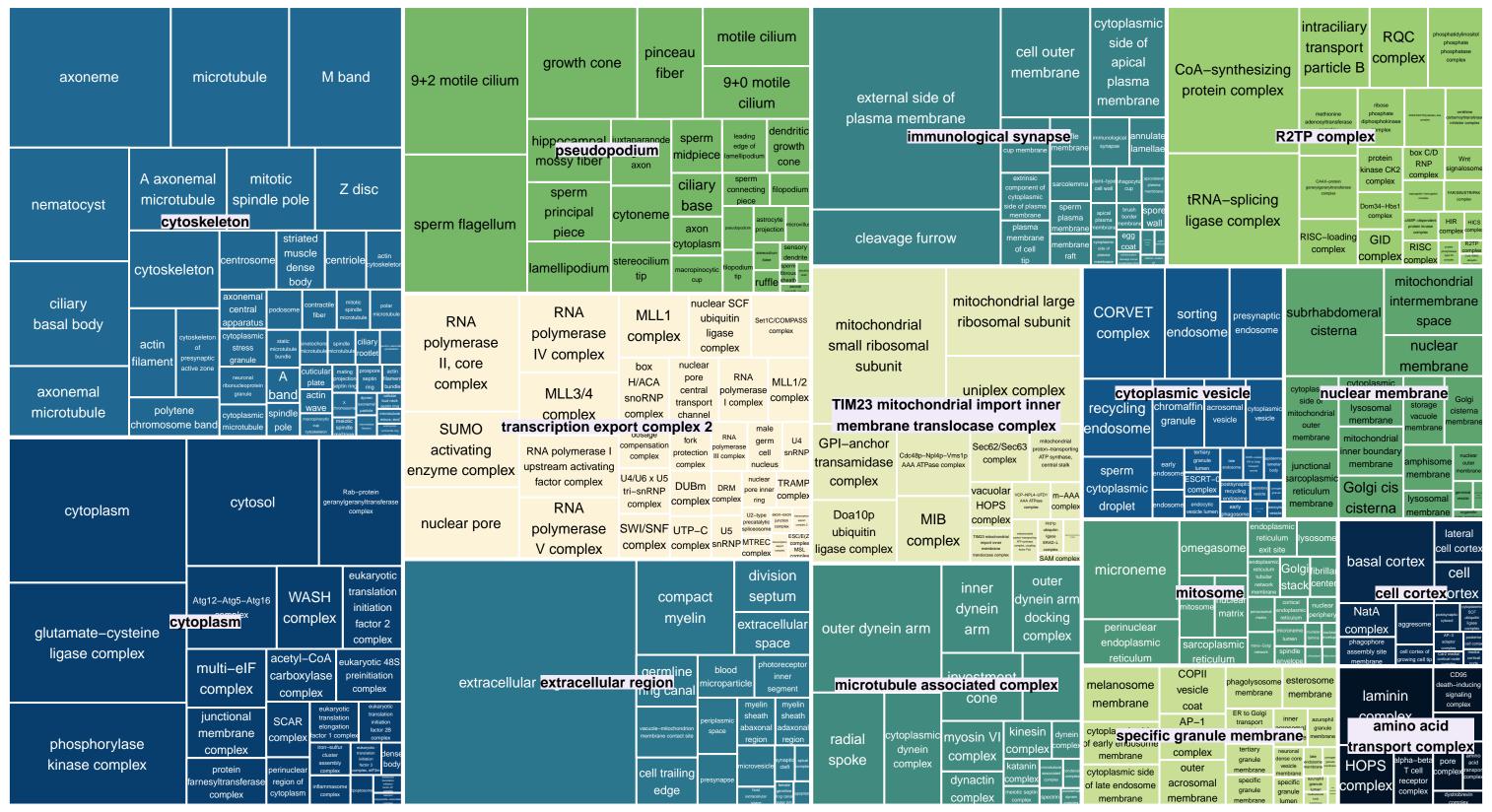
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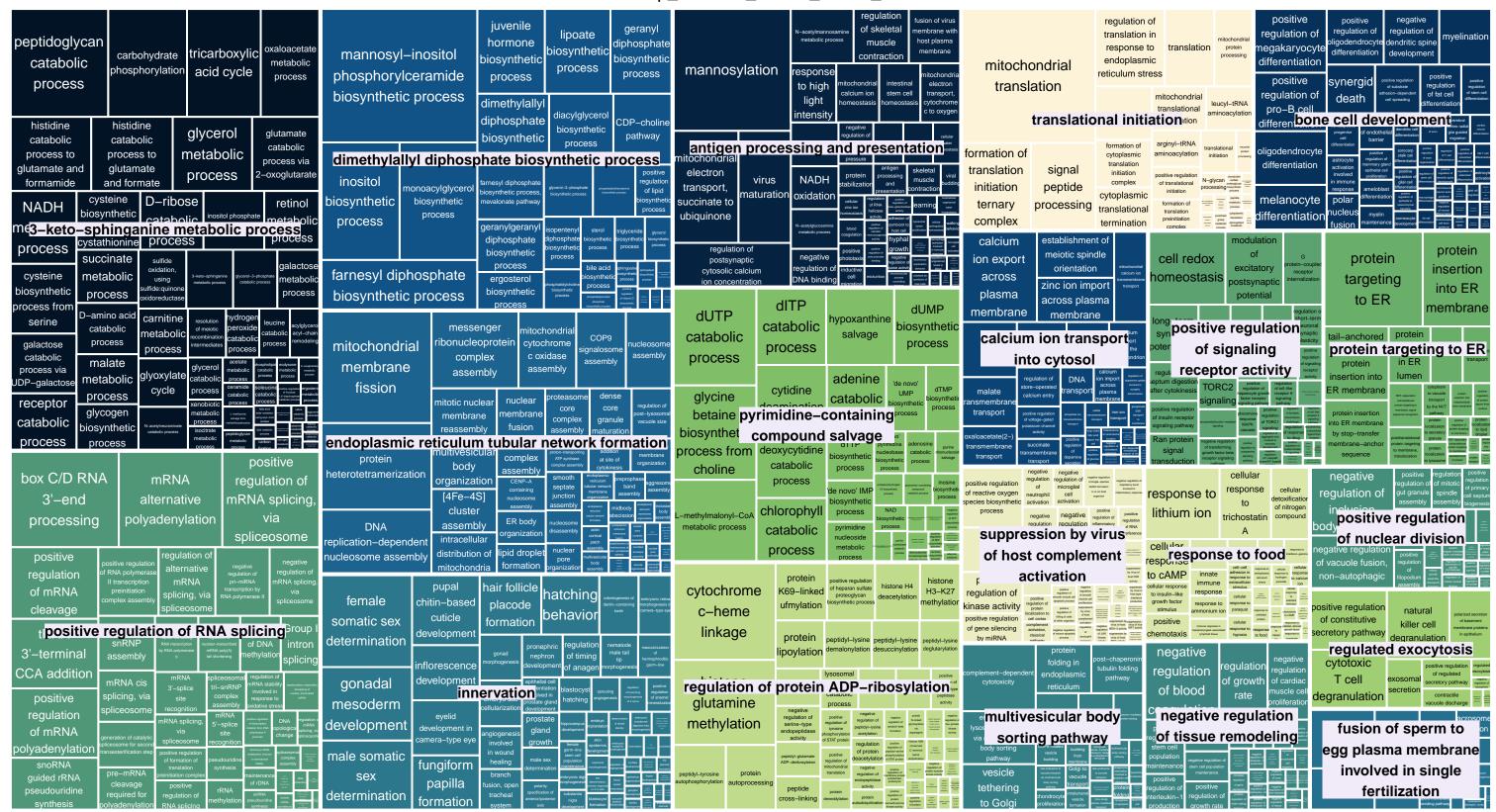
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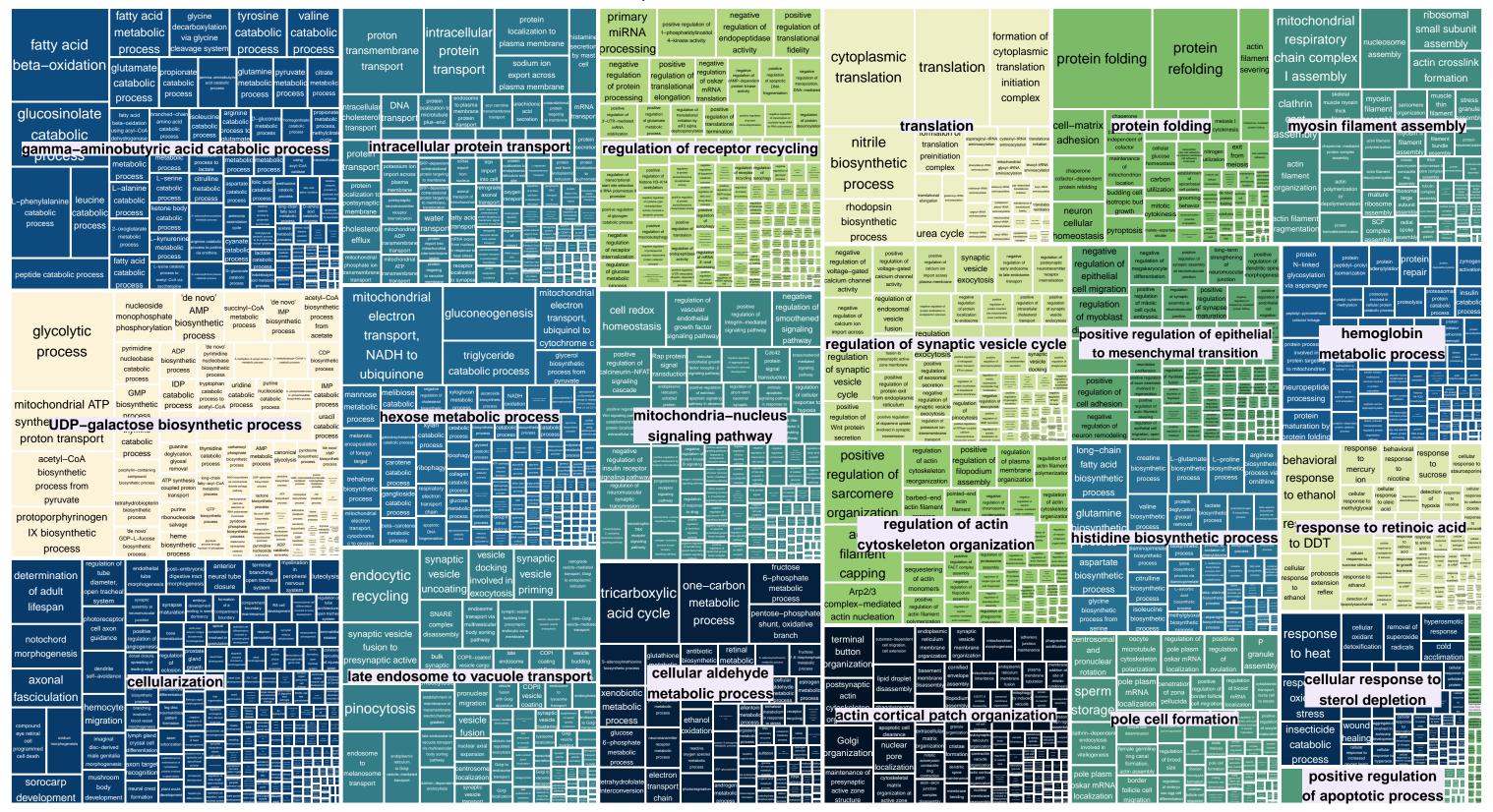
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phosphatidylserine decarboxylase activity	methylmalonyl–CoA epimerase activity	cystathioning beta-synthas activity	terroxidas	dehydr	ogenase prof	gen-dependent toporphyrinogen xidase activity	inositol monophosphate 1–phosphatase activity		hate mond ase 4-ph	nositol pphosphate nosphatase activity	N-acetylmuramoyl-L-alanine amidase activity	IMP cyclohydro activity cytidine deaminas	deoxycytidine deaminase activity	mannose bind	ing peptidoglycan binding
holocytochrome-c synthase activity	thioredoxin peroxidase activity protein	hydroxyacid-oxoacid transhydrogenase activity sphingolipid		oseudouridylate synthase activity	cytochrome–c oxidase activity	peptidylamidoglycolate lyase activity	diphosphatase activity	inositol nexakisphosphato 2–phosphatase activity	activity	activity	NAD-dependent protein deacetylase activity	activity ceram tylase activ		4 sulfur clus <mark>carbohyd</mark> binding reti	nost cell surface galactoside ecceptor binding comer ribosomal small recognition
		doglycan mu desaturase activity	D-amino-acid Iralytic activit activity	IP-independent) activity	choline dehydrogenase activity etinol protein-dist	hydratase activity		3–O–acetylesterase activity	rG(5')pppN nosphatase activity	oligosaccharide -marrosidase cirivity ADP-ribosylglutamas hydrolase activity	adenine deaminase activity	cinyllysine protein-glutaryllysins e activity deglutarylase activity	e tomindoylguamase N-acylsphingosini amiddhydrolase activity activity	ubiquinone bir binding lipid a	subunit particle binding particle binding binding particle binding binding binding binding binding cromain binding control binding binding control binding con
farnesol dehydrogenase activity	aspartate dehydrogenase activity	isopentenyl-diphosphate delta-isomerase activity	L-maiate	activity a dehy	merase reductas activity socitrate ydrogenase NADP+) activity	Basin of Baseprotein as one doors, and horoprossion of one atom of oxygen and horoprossion of one atom of oxygen.		activity aminoacyl-tRNA inc	dependent plidase cutivity poly/ADP-ribose) glycohydrolase sphatase cutivity	arylesterase acid phosphatase activity activity arminoacyl-tRNA editing activity DNA/RNA	2–iminobutanoate deaminase activity activ	nase activity	activity NAD-dependent histone deaceh/ase activity activity activity activity activity activity activity activity	bindina 4 iro	Alose carbohydrate binding
aldose 1–epimerase activity	dihydroorotate dehydrogenase activity	succinate dehydrogenase (ubiquinone) activity	peptidylglycine monooxygenase activity (N	hydrogenase lAD+) activity argi liga liga liga liga lacine–tRNA lase activity deh)	electror transfer activity steroid ydrogenase activity steroid sactivity	activity, oxidase activity	3–phosphatase activity r	III activity	serine-type carboxypepidase activity sin-dependent phosphatase activity adenyty/sulfatase activity	helicase activity helicase activity activity loss a 3-5 DNA activity solutions activity helicase activity	lithium ion binding	dinucleotid binding g NAD+	binding GPI FAD	N–acetylglucosamine kinase activity	ribokinase activity ^{activity}
glycogenin glucosyltransfera activity	diacylglyce se O–acyltransfe activity	cytidylyltr		nethylglutaryl–CoA hase activity	UFM1 ligase activity	dimethylallyltranstransferase activity	translation release factor activity, codon specific	mRNA binding	translation initiation factor activity	adenine/cytosine mispair binding	sulfa manganese ion binding	binding bate binding phosphatidylcholine binding ga	binding binding singlioside ganglioside GM2 GM3 binding binding singlioside ganglioside GP1c GT1b binding binding	pseudouridine kinase activity	receptor protein tyrosine kinase activity glycerol kinase activity activity
, i	retinal	formyltransf	erase activity		tobiosyldiphosphodolichol eta-mannosyltransferase activity	carnitine O–acetyltransferase activity	cytosine/cytosine the mispair binding n	alamain binalina	J1 snRNA binding RNA bindir	U6 snRNA binding ng	ferric iron binding	ion binding ganglioside	GDP retinol copper binding binding sulfate since or binding bi	Crueppel-associated box domain binding bind	
JDP-alpha-D-glucose:glucosyl-gl alpha-D-glucosyltransferase ac	octivity	synt	hase synt	idylate hase s-nestyl-5-sto phosphorylase ivity		ase farnesyltranstransferase activity	cytosine/thymine mispair binding	U-rich region binding bin	SK H/AC snoR bindi	CA rRNA INA binding	structura	al ceptor activ	activity structural nutrient reservoir	binding binding cyto cyto protein kinase	protein NF-kappaB NF-kappa
histone–glutamir methyltransferas activity		cytidylyltr	tRNA ansferase ATP-3-condition ivity	e-cysidine-IRNA O-acyltran sdensse activity activi	sferase	methyltanarierase catoliny molybdopterin synthase activity molybdopterin colatorate activity molybdopterin colatorativity molybdopte	single cytosine — insertion sec	cap binding site	binding DNA	rRNA binding activity binding RNA strand-exchange activity NAD binding	of riboson		chromatin activity cargo receptor activity structural constituent of cooth enamel activity cargo toxin activity structural constituent of receptor activity activity	translation protein doma specific	ain hemoglobin binding protein binding protein binding binding binding protein binding

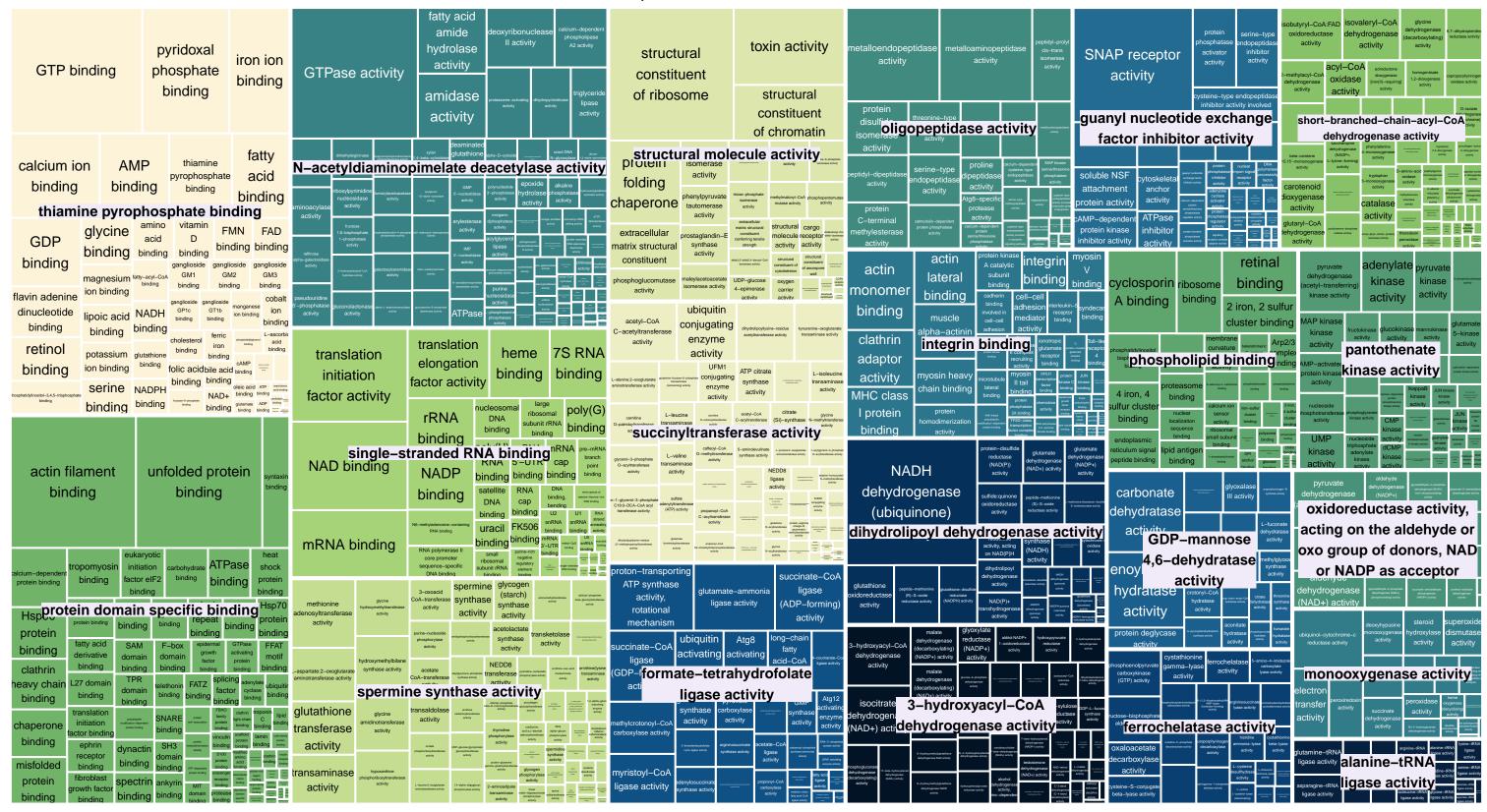
TreeMap_Enrichm_SMED_HOGs_CC

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cis–Golgi network membrane	trans–Golgi network membrane	perinuclear endoplasmic reticulum membrane	EMC complex	U1 snRNP	catalytic 2 spliceo	•	NuRD omplex	precatalytic spliceosome	extracellular region	extracellular exosome	eukaryotic translation initiation factor 2B complex	translation release factor complex
endopla	signal smic reticulum m	Hrd1p pembrane ubiquitin	chloroplast	nuclear pore transmembrane ring	U5 snRNP	U2-type prespliceosom	post-mRN release e spliceoson complex	spliceosomal mal complex	endoplasmi reticulum-plas		protein prot	eukaryotic 43S teasome preinitiation
signal peptidase complex	particle treceptor complex mit	complex complex tochondrial reticulum-Golgi intermediate	thylakoid membrane sarcoplasmic reticulum membrane reticulum reticulum	post–spliceosomal complex	spliceos U4 snRNP	omal complex		step 2	extracellular reg	on particle spore plant-type	cyto	complex proteasome core complex, dehydrogenase complex beta-subunit
mitochondrial respiratory chain complex II, succinate dehydrogenase	mitochondrial co	tochondrial membrane	doplasmic SAM component of motorane extrinsic extrinsic component of motorane extrinsic extrinsi	Sin3 complex	commitment complex U2-type	ring mRNA cleavage	complex mRNA	complex spliceosomal complex nuclear	female germline ring canal outer rim external side	wall cell wall alpha9-beta1 myelin sheath each adhean molecule-1 complex racellular cell outer mercellula space membrane bridge	eukaryotic 48S	complex cytosol sarcoplasm BLOC-1 complex
complex (ubiquinone)	m	nembrane membrane	ner membrane i-AAA membrane comple:	LI12-type	catalytic step 1 spliceosome nuclear pore nuclear	specificity factor complex	complex COP9 signalosome	complex	midbody of plasma membrane female germline ring canal inner rim cortex myelin sheath adaxonal region blood microparticle	cell virion virion de la composition della compo	cytoplasmic S ubiquitin ligase complex	eukaryotic translation initiation factor 3 complex BAT3 complex mating
	mitocho	ondrion paraspeckl	es autolysosome	complex	basket	snRNP tubulin fo		Myb ursing recomplex omplex Meiz nuclear dot complex protein phosphatase	ficolin–1–rich late granule lumen endoson	mitoti spind microtul	e protein complex co	yosin V aggregate center protein septin ring meiotic septin romplex spore kinetochore gamma-tubulin nematocyst comptor.
mitochondrial large ribosomal s	mitochondrion	Golgi lumen	ER fungal-type vacuole lumen	Prp19 cor	mplex	cofactor o	omplex	inhibitor complex	secretory	RecQ fam	illy RZZ	cytosolic large ribosoma subunit subun
	glycoso	endon!:	clear mitochondrial fibrillar	a	protein-	ASAP lipid comp	phosphatase	calcineurin calcineurin calcineurin calcineurin calcineurin complex respiratory t chain complex IV	secretory granulele lumen epidermal multivesicular body epidermal lamellar phagod vesic	HIGHIDI	nule ^{transport} ane vesicle	ESCRT IV ESCRT I complex
mitochondrial small ribosomal s	ubunit lysosor lume	microneme reticu cytol gran	ytic cure resource resource for the same complex will milliochondrial intermembers space space with the same complex will be restoration with the same complex will be restorated with the same complex w	box C/D RNP	complex	peptidase inhibitor complex	nuclear cap binding complex proteasome regulator, particle, base subcomplex	complex complex	COPII-coated ER to Golgi		le body membrane	

TreeMap_Enrichm_SHARED_HOGs_BP



TreeMap_Enrichm_SHARED_HOGs_MF



TreeMap_Enrichm_SHARED_HOGs_CC

