Supplementary Material 7. Functional characterization of Differentially Expressed Genes detected by proteomics (DGEs-prot) in *Obama nungara* (ONUN) and *Schmidtea mediterranea* (SMED). Treemaps showing enriched GO terms related to Biological Processes (BP). Extract of Reactome report for genes annotated with eggnog-mapper. The full Reactome reports and the Blast output are available at (see links below)

TreeMap_Enrichm_Validated_DGE_prot_ONUN_BP

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Most significant pathways DGEs-prot ONUN

link to full report: poner link en github

The following table shows the 25 most relevant pathways sorted by p-value.

D. II		Ent	Reactions			
Pathway name	found	ratio	p-value	FDR*	found	ratio
MHC class II antigen presentation	19 / 199	0.009	1.50e-06	0.002	15 / 26	0.002
Cytosolic tRNA aminoacylation	7 / 63	0.003	9.58e-05	0.071	13 / 21	0.001
mRNA Splicing - Minor Pathway	10 / 139	0.006	5.59e-04	0.275	5/5	3.36e-04
RHO GTPases activate KTN1	3 / 12	5.22e-04	0.001	0.398	1/2	1.34e-04
Clathrin-mediated endocytosis	13 / 234	0.01	0.002	0.562	27 / 35	0.002
Golgi-to-ER retrograde transport	11 / 248	0.011	0.003	0.712	9 / 18	0.001
Formation of annular gap junctions	3 / 18	7.83e-04	0.003	0.712	2/2	1.34e-04
Scavenging by Class A Receptors	4 / 49	0.002	0.009	0.875	6 / 10	6.72e-04
Gap junction degradation	3 / 26	0.001	0.009	0.875	4 / 4	2.69e-04
Retrograde neurotrophin signalling	6 / 50	0.002	0.01	0.875	3/3	2.02e-04
COPI-mediated anterograde transport	9 / 215	0.009	0.01	0.875	10 / 12	8.06e-04
Formation of a pool of free 40S subunits	6 / 111	0.005	0.011	0.875	2/2	1.34e-04
Prefoldin mediated transfer of substrate to CCT/TriC	3 / 29	0.001	0.012	0.875	1/2	1.34e-04
Formation of the ternary complex, and subsequently, the 43S complex	4 / 54	0.002	0.013	0.875	1/3	2.02e-04
Neutrophil degranulation	15 / 478	0.021	0.013	0.875	6 / 10	6.72e-04
Formation of tubulin folding intermediates by CCT/TriC	3 / 30	0.001	0.014	0.875	2/2	1.34e-04
Defective SFTPA2 causes IPF	1/1	4.35e-05	0.016	0.875	1/1	6.72e-05
ALK mutants bind TKIs	2 / 12	5.22e-04	0.017	0.875	1/1	6.72e-05
Interaction between L1 and Ankyrins	3 / 33	0.001	0.017	0.875	4 / 4	2.69e-04
L13a-mediated translational silencing of Ceruloplasmin expression	6 / 126	0.005	0.019	0.875	2/3	2.02e-04
Rev-mediated nuclear export of HIV RNA	7 / 92	0.004	0.019	0.875	9 / 10	6.72e-04
Glycogen metabolism	4 / 61	0.003	0.019	0.875	10 / 37	0.002
WNT5A-dependent internalization of FZD2, FZD5 and ROR2	2 / 13	5.65e-04	0.02	0.875	1/2	1.34e-04
Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	3 / 36	0.002	0.022	0.875	1/1	6.72e-05

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Dothway name		Ent	Reactions			
Pathway name	found	ratio	p-value	FDR*	found	ratio
Depolymerization of the Nuclear Lamina	3 / 36	0.002	0.022	0.875	3/6	4.03e-04

^{*} False Discovery Rate

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TreeMap_Enrichm_Validated_DGE_prot_SMED_BP

behavioral response to ethanol	melanization defense response	negative regulation NF-kappa transcription	of response t aB red or far on red light	o cellular iron ion homeostas	processing	collagen–activated tyrosine kinase receptor signaling pathway	positive regulation of autophagy	positive regulation of engulfment of apoptotic cell	regulation of growth	basemer membrar organizati	e basal p	epitheli	ance of al cell actil	n crosslink rmation	nucleus organization
	long-term memory	positive regulatio of ovulatio	n homeostasi	•	splicing, via	regulation of	reti	plasmic positiv	regulation of	nuclear migration		cellular cromolecule ocalization localiz	zation acto stru	icture	ntermediate filament ytoskeleton
maintenance of gastrointestinal epithelium	c [†] positive regu process	llation of lip bacteriur	compound -	regulation of cocessical structure	defense response to bacterium	oligomerization domain positive reg signaling pathway posi	of T cell ulation of leuk ctivation	ponse sitive positive ation of regulatio	Ras protein ignal ignal iransduction re n of DNA damage respons- signal transduction	protein a localization nuclear	ggresome ju assembly deve	ule localization nction localization localiz	ation cytoskel	organizat eton actin filame	actin
defense response to virus	response to muramyl dipeptide	regulation of postsynapt membrane neurotransmi receptor lev	ic iron ion transport	peptidyl-serine phosphorylation of ma	negative negative regulation regulation of protein aturation processing requestering	of viral-induced cytoplasmic pattern recognition receptor signaling pathway	positive regulation of ymphocyte	triglycer metabout metabout proces regulation r cell regulation adhesion by interpretation	in cell cycle arrest at the cycle arrest at th	along di microtubule	allilli Coal	phagolysosome dle assembly loc	polyme depolynomotion	nerization re	actin cytoskeleton corganization pramolecular
encapsulation of foreign target	negative regulation of monocyte chemotactic protein–1 production	peptidyl-threor		process to positive regulation of pe	of riglyceride eptidyl-serine modification	factor receptor signaling nothway	-	-mediated g pathway metabolio	proliferation tion of peroxide	actin	regulation of actin filament polymerization	regulation o	orgal regulation of neuromuscula junction		rganization calcium-dependent cell-cell adhesion via plasma
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negative	<mark>≉anim</mark> developm yncytial	anatomical al organ mo	regulation of synaptic assembly at	ation of omical ordered ogenesis cellular Bolw	regulation of tube size, open tracheal system imaginal	germarium-derived female germ-line cyst encapsulation	synaptic target	cell columnari epitheli differen	differentiation	positive roof sard	omere zation	sarcomere organization	striated muscle myosir thick filament	cell-cell adhesion via plasma-membrane	protein refolding
regulation of e	embryo ularization _{developmer} process	morphogenesis	anatomical regulator	nismal orga develop ulation Bolwig's	an disc-derived wing vein	neuron recognition	acvolopinontal	striated regula muscle cell of nei lifferentiation matur	uron choice	female ger canal for actin as	mline ring mation,	organization skeletal myofib	assembly aril assembly	recogniti homophilic c adhesion via pl membrane adh molecules	filament-based process asma esion

Most significant pathways DGEs-prot SMED

link to full report: poner link en github

The following table shows the 25 most relevant pathways sorted by p-value.

- 4		Ent	Reactions			
Pathway name	found	ratio	p-value	FDR*	found	ratio
Surfactant metabolism	6 / 95	0.004	4.50e-06	0.004	11 / 29	0.002
Formation of a pool of free 40S subunits	5 / 111	0.005	1.41e-04	0.059	2/2	1.34e-04
SRP-dependent cotranslational protein targeting to membrane	5 / 119	0.005	1.95e-04	0.059	5/5	3.36e-04
L13a-mediated translational silencing of Ceruloplasmin expression	5 / 126	0.005	2.53e-04	0.059	2/3	2.02e-04
Interaction between L1 and Ankyrins	3 / 33	0.001	4.43e-04	0.072	4 / 4	2.69e-04
FLT3 signaling by CBL mutants	2/7	3.04e-04	4.59e-04	0.072	1/1	6.72e-05
Modulation by Mtb of host immune system	3 / 36	0.002	5.70e-04	0.076	2/6	4.03e-04
Defective CSF2RB causes SMDP5	3 / 40	0.002	7.72e-04	0.08	1/1	6.72e-05
Defective CSF2RA causes SMDP4	3 / 40	0.002	7.72e-04	0.08	1/1	6.72e-05
GTP hydrolysis and joining of the 60S ribosomal subunit	7 / 170	0.007	9.71e-04	0.083	3/3	2.02e-04
Signal regulatory protein family interactions	3 / 45	0.002	0.001	0.083	1/10	6.72e-04
Myoclonic epilepsy of Lafora	2 / 11	4.78e-04	0.001	0.083	1/2	1.34e-04
Peptide chain elongation	4 / 105	0.005	0.001	0.083	4/5	3.36e-04
Diseases associated with surfactant metabolism	3 / 48	0.002	0.001	0.083	3/7	4.70e-04
Scavenging by Class A Receptors	3 / 49	0.002	0.001	0.083	6 / 10	6.72e-04
Eukaryotic Translation Termination	4 / 109	0.005	0.001	0.083	3/5	3.36e-04
Selenoamino acid metabolism	5 / 191	0.008	0.002	0.089	3 / 33	0.002
Selenocysteine synthesis	4 / 115	0.005	0.002	0.09	2/7	4.70e-04
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	4 / 123	0.005	0.002	0.108	1/1	6.72e-05
Maturation of protein E	2 / 18	7.83e-04	0.003	0.131	1/5	3.36e-04
Regulation of TLR by endogenous ligand	3 / 65	0.003	0.003	0.131	2 / 13	8.73e-04
Viral mRNA Translation	4 / 136	0.006	0.003	0.131	2/2	1.34e-04
Cap-dependent Translation Initiation	7 / 225	0.01	0.003	0.131	12 / 18	0.001
Eukaryotic Translation Initiation	7 / 228	0.01	0.003	0.135	14 / 21	0.001

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Dathway nama		Ent	Reactions			
Pathway name	found	ratio	p-value	FDR*	found	ratio
Translesion synthesis by POLI	2 / 22	9.57e-04	0.004	0.149	3/3	2.02e-04

^{*} False Discovery Rate

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link to Blast results ONUN: poner link en github

link to Blast results SMED: poner link en github