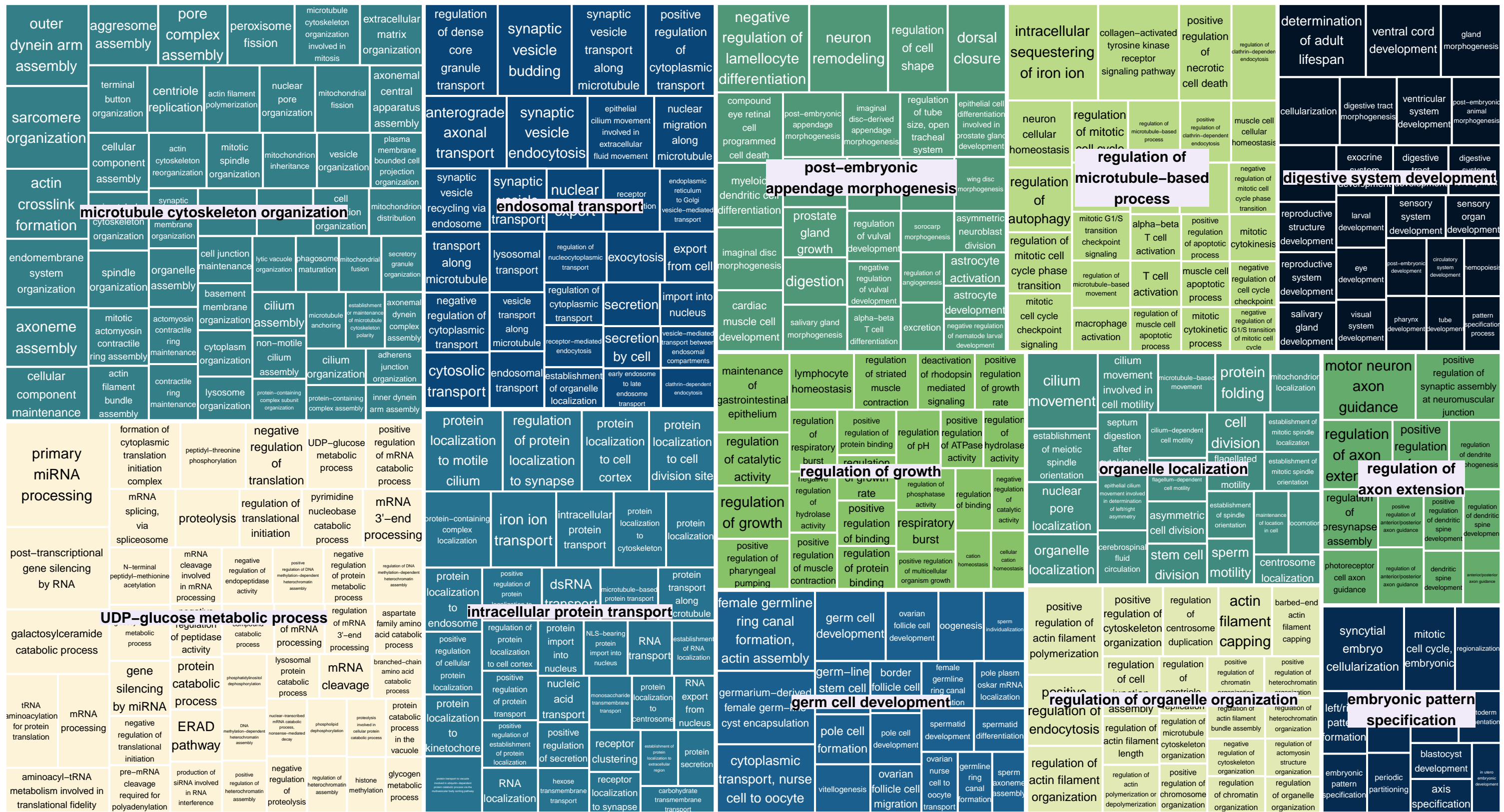


Supplementary Material 7. Functional characterization of Differentially Expressed Genes detected by proteomics (DGEs-prot) in *Obama nungara* (ONUN) and *Schmidtea mediterranea* (SMED). Treemaps showing enriched GO terms related to Biological Processes (BP). Extract of Reactome report for genes annotated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

TreeMap_Enrichm_Validated_DGE_prot_ONUN_BP



Most significant pathways DGEs-prot ONUN

link to full report: [poner link en github](#)

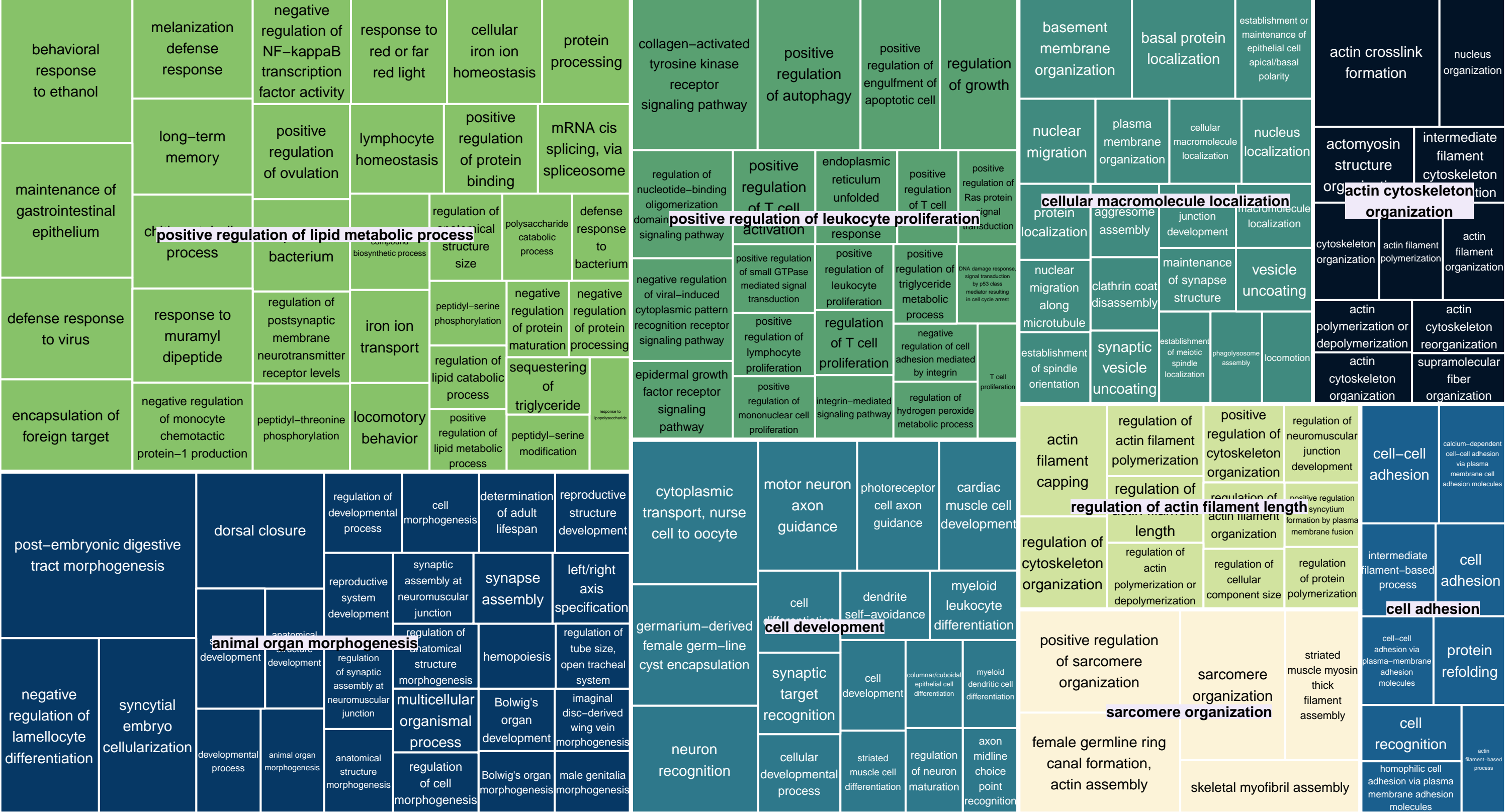
The following table shows the 25 most relevant pathways sorted by p-value.

Pathway name	Entities				Reactions	
	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

Pathway name	Entities				Reactions	
	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

TreeMap_Enrichm_Validated_DGE_prot_SMED_BP



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.

Pathway name	Entities				Reactions	
	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

Pathway name	Entities				Reactions	
	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

link to Blast results ONUN: poner link en github

link to Blast results SMED: poner link en github