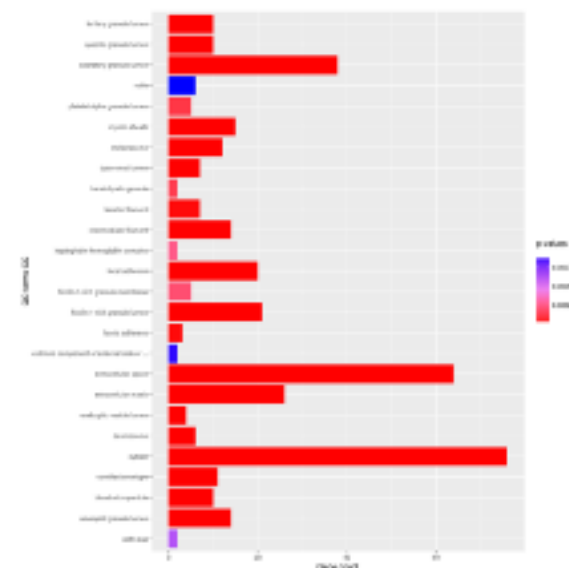
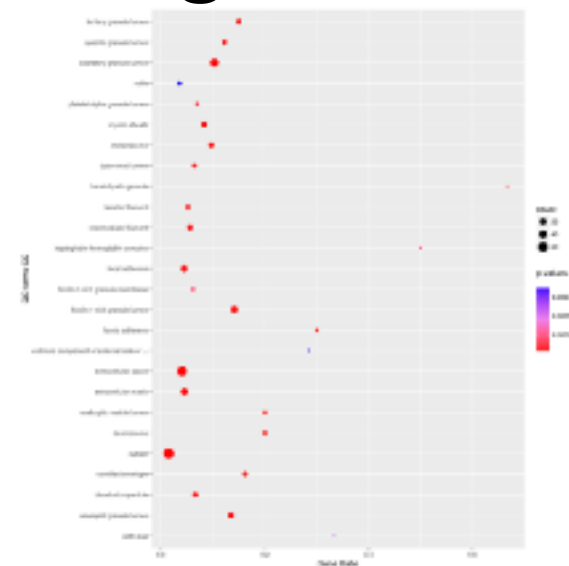


topGO enrichment analysis

- Results: bar plot, dot plot and textual output for each GO categories chosen



1	2	3	4	5	6
GO.ID	Term	Annotated	Significant	Expected	pvalues
GO:0045296	cadherin binding	328	21	2.29	3.9e-12
GO:0004869	cysteine-type endopeptidase inhibitor ac...	61	10	0.43	1.3e-11
GO:0004867	serine-type endopeptidase inhibitor acti...	103	10	0.72	2.7e-09
GO:0005200	structural constituent of cytoskeleton	120	10	0.84	1.2e-08
GO:0005198	structural molecule activity	778	27	5.44	4.9e-06
GO:0002020	protease binding	140	8	0.98	6.3e-06
GO:0001948	glycoprotein binding	108	7	0.76	1.1e-05
GO:0004197	cysteine-type endopeptidase activity	86	6	0.6	3.1e-05
GO:0004332	fructose-bisphosphate aldolase activity	3	2	0.02	0.00014
GO:0008426	protein kinase C inhibitor activity	3	2	0.02	0.00014
GO:0005509	calcium ion binding	751	15	5.25	0.00024
GO:0098641	cadherin binding involved in cell-cell a...	18	3	0.13	0.00025
GO:0019834	phospholipase A2 inhibitor activity	4	2	0.03	0.00029
GO:0004601	peroxidase activity	46	4	0.32	0.00030
GO:0016209	antioxidant activity	94	8	0.66	0.00031
GO:0051082	unfolded protein binding	132	6	0.92	0.00033
GO:0030492	hemoglobin binding	5	2	0.03	0.00048
GO:0003779	actin binding	433	13	3.03	0.00061
GO:0086083	cell adhesive protein binding involved i...	6	2	0.04	0.00071
GO:0042802	identical protein binding	1494	26	10.45	0.00076
GO:0003723	RNA binding	1776	28	12.42	0.00091
GO:0048306	calcium-dependent protein binding	62	4	0.43	0.00093

This tool uses R/Bioconductor package topGO - Alexa A and Rahnenfuhrer J (2016). topGO: Enrichment Analysis for Gene Ontology. R package version 2.30.0.

Get annotation from RNAseq/Ab-based experiments

- Purpose: get expression information (RNAseq- or antibody-based experiments) from the Human Protein Atlas (HPA) database
- Input: a list of Ensembl Gene IDs

Get annotation from RNAseq/Ab-based experiments (Human species) (Galaxy Version 0.1.0) Options

Enter your list of Ensembl gene ID

Input file containing your IDs

Choose your file

This file must import the case.

Please specify the file name

c1

Does your file have a header?

Yes

RNAseq/Ab-based

Choose the information to display

Select/Unselect

☒ Gene name

☐ Gene description

☐ Evidence (at protein level, at transcript level or no evidence)

☐ Antibody reference

☐ RNA tissue category

☐ IH detection level

☐ IF detection level

☐ Subcellular location

☐ RNA tissue specificity abundance in 'Transcript Per Million'

☐ RNA non-specific tissue abundance in 'Transcript Per Million'

31: Text output for topGO analysis MF category

28: Text output for topGO analysis CC category

25: Text output for topGO analysis BP category

15: GO Profile text output

13: Venn diagram text output

12: Venn diagram

11: Mucilli.txt

10: Bredberg.txt

History

Rechercher des données

23/01/18

20 shown, 10 deleted, 3 hidden

2.19 MB

33: Dotplot output for topGO analysis MF category

32: Barplot output for topGO analysis MF category

31: Text output for topGO analysis MF category

30: Dotplot output for topGO analysis CC category

29: Barplot output for topGO analysis CC category

28: Text output for topGO analysis CC category

27: Dotplot output for topGO analysis BP category