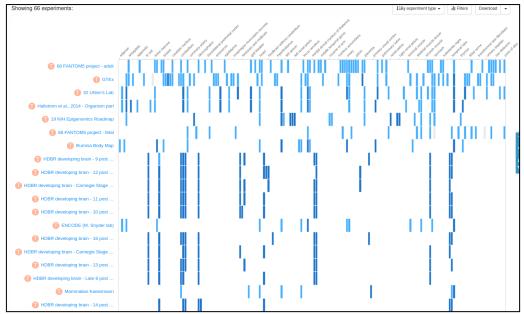
TOPIC 6 - PRACTICAL ASSESSMENT

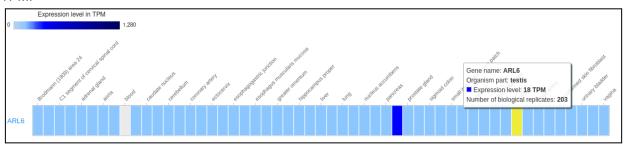
As a first step, we can study the ARL6 gene focusing on Homo sapiens. We can learn some information about this gene using the **ENCODE database**, such as the GeneID, the official gene name, and its location.

Entrez GeneID: 84100 🗗 Gene symbol: ARL6 Official gene name: ADP ribosylation factor like GTPase 6 BBS3 Synonyms: RP55 Gene locations: GRCh38 chr3:97764758-97801229, hg19 chr3:97483602-97520073 RefSeq:NR_136595.2 🗗 External resources: HGNC:13210 ☑ MIM:608845 2 Vega:OTTHUMG00000159189 ☑ UniProtKB:Q9H0F7 2 ENSEMBL:ENSG00000113966 ☑ RefSeq:NR_103511.2 2

Secondly, when we know some things about it, we can do the basal expression in the database **Expression Atlas.** There have been 66 experiments on this gene in total.



Additionally, if we check the GTEx, we would find that ARL6 is much more expressed in the pituitary gland and the testis. Among them, the first is expressed at a level of 12 TPM, while the second is expressed at a level of 18 TPM.

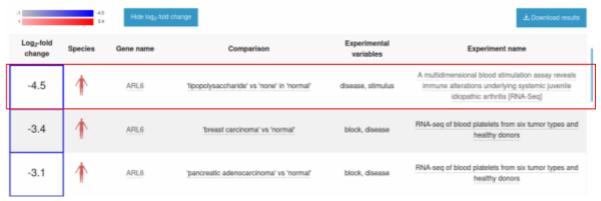


The pituitary gland is located in the brain, and the testis is located in the reproductive system.

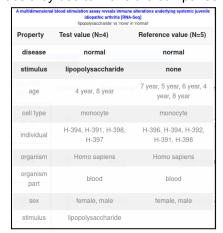
Furthermore, this gene has a "differential expression" in which it can be upregulated or downregulated. There are two experimental types that would be considered: "Microarray 1-colour mRNA differential" and "RNA-seq mRNA differential".

In the case of downregulated, we can find the comparison of 'lipopolysaccharide' vs 'none' in 'normal' that is -4.5, so we can say it is the most downregulated. The experiment name is "A multidimensional blood stimulation assay reveals immune alterations underlying systemic juvenile idiopathic arthritis [RNA-Seq]".

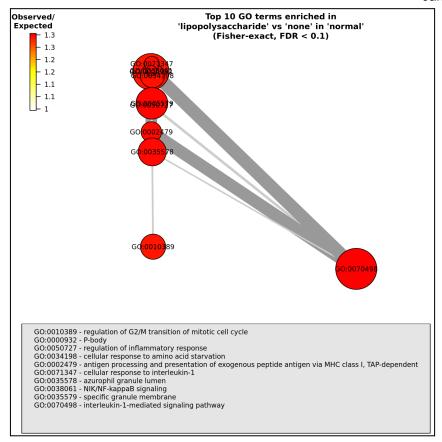
Also, we can know that the experimental variables are disease and stimulus.



This image shows the different properties they use to make the comparison.

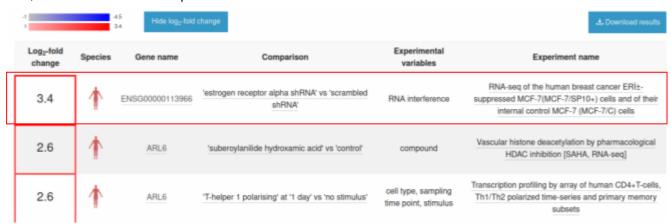


Taking into consideration the experiment, we can find this plot in the comparison. Among differentially expressed genes, "interleukin-1-mediated signaling pathway" is the predominant GO function.



In the case of upregulated, we can find the comparison of 'estrogen receptor alpha shRNA' vs 'scrambled shRNA' that is 3.4, so we can figure out which is higher upregulated. The experiment name is "RNA-seq of the human breast cancer ERα-suppressed MCF-7(MCF-7/SP10+) cells and of their internal control MCF-7 (MCF-7/C) cells".

Also, we can know that the experimental variable is RNA interference.



This image shows the different properties they use to make the comparison.

Jana Moreno Ruestes

RNA-seq of the human breast cancer ERIs-suppressed MCF-7(MCF-7/RP10+) cells and of their internal control MCF-7 (MCF-7/C) cells 'estrogen receptor alpha shRNA' vs 'scrambled shRNA'		
Property	Test value (N=3)	Reference value (N=3)
RNA interference	estrogen receptor alpha shRNA	scrambled shRNA
cell line	MCF-7	MCF-7
cell type	epithelial cell	epithelial cell
disease	breast adenocarcinoma	breast adenocarcinoma
organism	Homo sapiens	Homo sapiens
phenotype	estrogen receptor alpha negative	estrogen receptor alpha positive

This experiment does not produce a plot of the comparison like the previous experiment did.