



Analysis of RNA-seq data answers to questions

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Question 1

- Use “Functional Annotation Chart” tool

Annotation Summary Results

Current Gene List: List_1

668 DAVID IDs

Current Background: Homo sapiens

Check Defaults

- Disease (1 selected)
- Functional_Categories (3 selected)
- Gene_Ontology (3 selected)
- General_Annotations (0 selected)
- Literature (0 selected)
- Main_Accessions (0 selected)
- Pathways (3 selected)
- Protein_Domains (3 selected)
- Protein_Interactions (0 selected)
- Tissue_Expression (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Functional Annotation Clustering

Functional Annotation Chart






Functional Annotation Table

Question 1

- 5 most significantly enriched functional annotation terms among the over-expressed genes annotations
- Number of genes annotated with each of these terms

790 chart records

 [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		258	38,6	1,6E-23	7,5E-21
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		249	37,3	1,2E-22	2,3E-19
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		82	12,3	5,0E-21	1,2E-17
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		81	12,1	1,8E-20	2,2E-17
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		59	8,8	5,5E-20	1,3E-17

- To view these genes click on :

258 record(s)

 [Download File](#)

OFFICIAL_GENE_SYMBOL	GENE NAME	Related Genes	Species
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	RG	Homo sapiens
ADAM23	ADAM metalloproteinase domain 23	RG	Homo sapiens
ADAMTS18	ADAM metalloproteinase with thrombospondin type 1 motif, 18	RG	Homo sapiens
ADAMTS6	ADAM metalloproteinase with thrombospondin type 1 motif, 6	RG	Homo sapiens

Question 2

- Use “Functional Annotation Clustering” tool

Annotation Summary Results

Current Gene List: List_1

668 DAVID IDs

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Check Defaults

- Disease (1 selected)
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- Gene_Ontology (3 selected)
- General_Annotations (0 selected)
- Literature (0 selected)
- Main_Accessions (0 selected)
- Pathways (3 selected)
- Protein_Domains (3 selected)
- Protein_Interactions (0 selected)
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Functional Annotation Clustering

Functional Annotation Chart

Functional Annotation Table

Question 2

- First identified cluster :

Annotation Cluster 1		Enrichment Score: 16.59		G			Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT			82	5.0E-21	1.2E-17	
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT			81	1.8E-20	2.2E-17	
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT			59	5.5E-20	1.3E-17	
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell adhesion	RT			31	9.2E-8	7.7E-5	

- Click on  to visualize members of this cluster :

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cell growth regulator with E1-ncad domain 1
alpha-2-macroglobulin
schlemmer receptor class B, member 2
E-cadherin (FACIT-4) and desmosomal hemagglutinin 1
angiotensinogen (serpin peptidase inhibitor, class A, member B)
integrin beta 1
collagen, type V, alpha 1
collagen, type XI, alpha 1
fibrinogen
fibrinogen and fibrinogen receptor beta 1 (alpha 1)
fibrinogen and fibrinogen receptor beta 2 (alpha 1)
fibrinogen and fibrinogen receptor beta 3 (alpha 1)
fibrinogen and fibrinogen receptor beta 4 (alpha 1)
fibrinogen and fibrinogen receptor beta 5 (alpha 1)
fibrinogen and fibrinogen receptor beta 6 (alpha 1)
fibrinogen and fibrinogen receptor beta 7 (alpha 1)
fibrinogen and fibrinogen receptor beta 8 (alpha 1)
fibrinogen and fibrinogen receptor beta 9 (alpha 1)
fibrinogen and fibrinogen receptor beta 10 (alpha 1)
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fibrinogen and fibrinogen receptor beta 95 (alpha 1)
fibrinogen and fibrinogen receptor beta 96 (alpha 1)
fibrinogen and fibrinogen receptor beta 97 (alpha 1)
fibrinogen and fibrinogen receptor beta 98 (alpha 1)
fibrinogen and fibrinogen receptor beta 99 (alpha 1)
fibrinogen and fibrinogen receptor beta 100 (alpha 1)

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Question 3

- Use “Functional Annotation Table” tool

Annotation Summary Results

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Question 3

- Search for claudin 15 in the page to see all associated annotations :

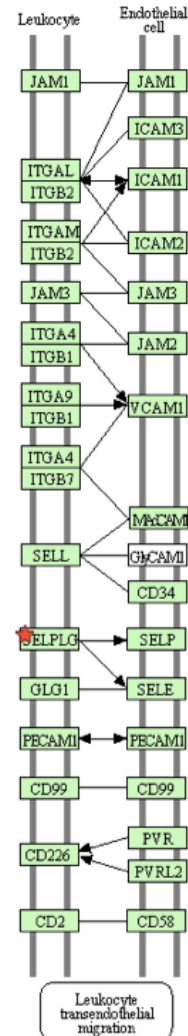
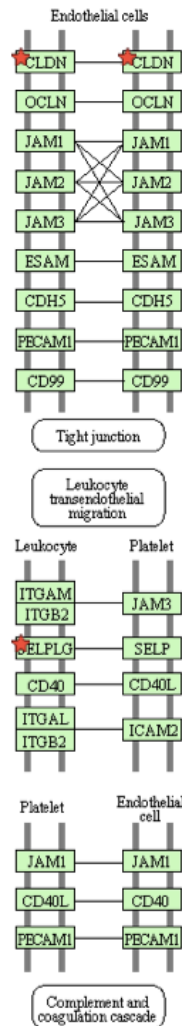
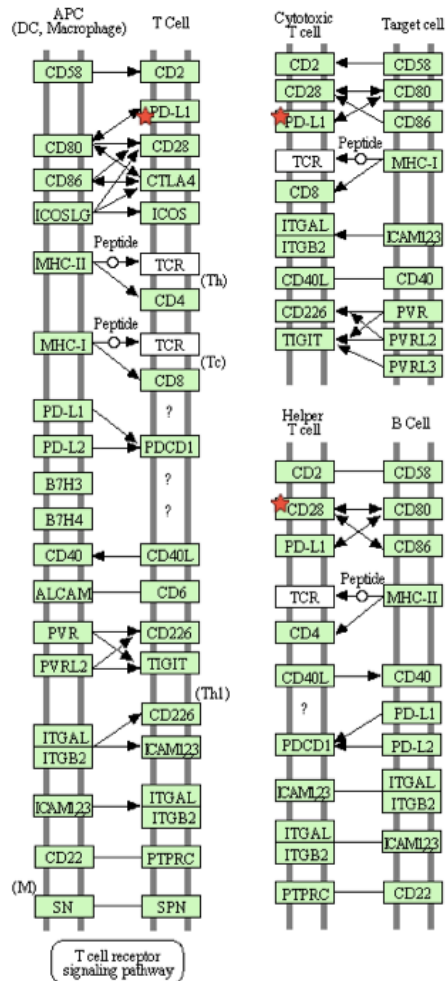
CLDN15	claudin 15	Related Genes	Homo sapiens
GOTERM_BP_FAT	cell adhesion , cell-cell adhesion , calcium-independent cell-cell adhesion , biological adhesion ,		
GOTERM_CC_FAT	plasma membrane , cell-cell junction , tight junction , integral to membrane , apicolateral plasma membrane , cell junction , intrinsic to membrane , apical junction complex , plasma membrane part , occluding junction ,		
GOTERM_MF_FAT	structural molecule activity , identical protein binding ,		
INTERPRO	PMP-22/EMP/MP20/Claudin , Claudin , Claudin-15 , Claudin , conserved site ,		
KEGG_PATHWAY	Cell adhesion molecules (CAMs) , tight junction , Leukocyte transendothelial migration ,		
SP_PIR_KEYWORDS	cell junction , cell membrane , complete proteome , membrane , phosphoprotein , Tight junction , transmembrane ,		
UP_SEQ_FEATURE	chain:Claudin-15, modified residue, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region,		

- Click on [Cell adhesion molecules \(CAMs\)](#) to see all genes from the list annotated with this pathway

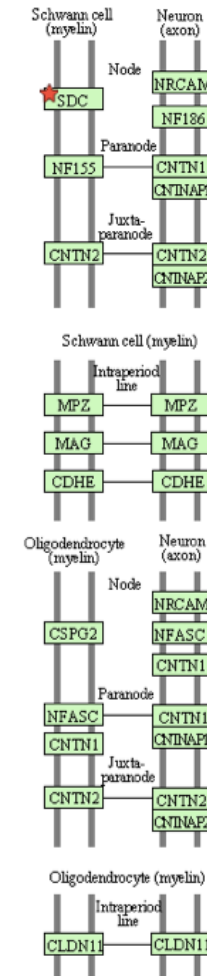
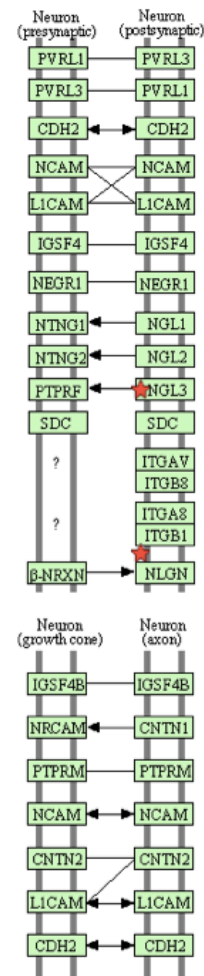
Question 3

CELL ADHESION MOLECULES

IMMUNE SYSTEM



NEURAL SYSTEM



OTHER SYSTEMS

