

Functional analysis
of RNA-seq data :
answers to questions

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Question 1

- Use “Functional Annotation Chart” tool

Annotation Summary Results [Help and Tool Manual](#)

Current Gene List:
siMitfvssiLuc_upgenes_lfc1_padj005

Current Background: Homo sapiens

507 DAVID IDs

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

Question 1

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

728 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamin
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		64	12,6	2,8E-16	8,2E-13
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		64	12,6	3,0E-16	4,1E-13
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		191	37,7	1,0E-15	4,2E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		181	35,8	4,8E-14	8,3E-11
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		42	8,3	3,7E-13	7,9E-11
<input type="checkbox"/>	SP_PIR_KEYWORDS	signal	RT		149	29,4	6,1E-13	8,6E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		149	29,4	1,0E-12	8,8E-10
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix	RT		32	6,3	8,7E-9	2,9E-6
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region part	RT		59	11,7	1,4E-8	2,3E-6
<input type="checkbox"/>	GOTERM_CC_FAT	proteinaceous extracellular matrix	RT		30	5,9	2,2E-8	2,4E-6

- To view these genes click on :

64 record(s)

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OFFICIAL_GENE_SYMBOL	GENE NAME	Related Genes	Species
ADAM23	ADAM metalloproteinase domain 23	RG	Homo sapiens
CD24	CD24 molecule; CD24 molecule-like 4	RG	Homo sapiens
CASS4	Cas scaffolding protein family member 4	RG	Homo sapiens

Question 2

- Use “Functional Annotation Clustering” tool

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Combined View for Selected Annotation

-
-
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Question 2

- First identified cluster :

209 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 14.5				Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT			64	2.8E-16	8.2E-13
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT			64	3.0E-16	4.1E-13
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT			42	3.7E-13	7.9E-11

- Click here to visualize members of this cluster 

Question 2

sorbin and SH3 domain containing 1
syntaxin binding protein 1
polycystic kidney and hepatic disease 1 (autosomal recessive)
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
neuropilin 1
roporin, rhophilin associated protein 1B
Rho family GTPase 3
collagen, type IX, alpha 1
heparan sulfate proteoglycan 2
neuropilin 2
roundabout, axon guidance receptor, homolog 2 (Drosophila)
CD24 molecule; CD24 molecule-like 4
lysyl oxidase-like 2
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2
claudin 15
chemokine (C-C motif) ligand 2
polycystic kidney disease 2 (autosomal dominant)
deleted in liver cancer 1
alpha-2-glycoprotein 1, zinc-binding pseudogene 1; alpha-2-glycoprotein 1, zinc-binding
PTPRF interacting protein, binding protein 1 (liprin beta 1)
scavenger receptor class B, member 2
collagen, type XIV, alpha 1
laminin, alpha 4
protocadherin 1
laminin, beta 2 (laminin 5)
protocadherin gamma subfamily A, 6
ADAM metallopeptidase domain 23
vitronectin
catenin (cadherin-associated protein), alpha 2
collagen, type XIX, alpha 1
collagen, type XVIII, alpha 1
collagen, type XVI, alpha 1
contactin 6
cell adhesion molecule 4
laminin, gamma 1 (formerly LAMB2)
fibronectin leucine rich transmembrane protein 3
KIT ligand
selectin F ligand
protocadherin 15
laminin, beta 1
limbic system-associated membrane protein
integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
EGF-like repeats and discoidin I-like domains 3
collagen, type VI, alpha 1
basal cell adhesion molecule (Lutheran blood group)
amyloid beta (A4) precursor-like protein 1
tumor necrosis factor, alpha-induced protein 6
cadherin 7, type 2
neuroigin 3
cysteine-rich, angiogenic inducer, 61
protocadherin 18
FAT tumor suppressor homolog 4 (Drosophila)
catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
cadherin 19, type 2
FRAS1 related extracellular matrix protein 2
collagen, type VI, alpha 3
Cas scaffolding protein family member 4
connective tissue growth factor
integrin, alpha 1
dachous 2 (Drosophila)
neuroigin 1
oligodendrocyte myelin glycoprotein
cadherin 12, type 2 (N-cadherin 2)

cell adhesion
GO:0007155-cell adhesion
GO:0022610-biological adhesion

Question 3

- Use “Functional Annotation Table” tool

Annotation Summary Results [Help and Tool Manual](#)

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Combined View for Selected Annotation

- Functional Annotation Clustering
- Functional Annotation Chart
- Functional Annotation Table**

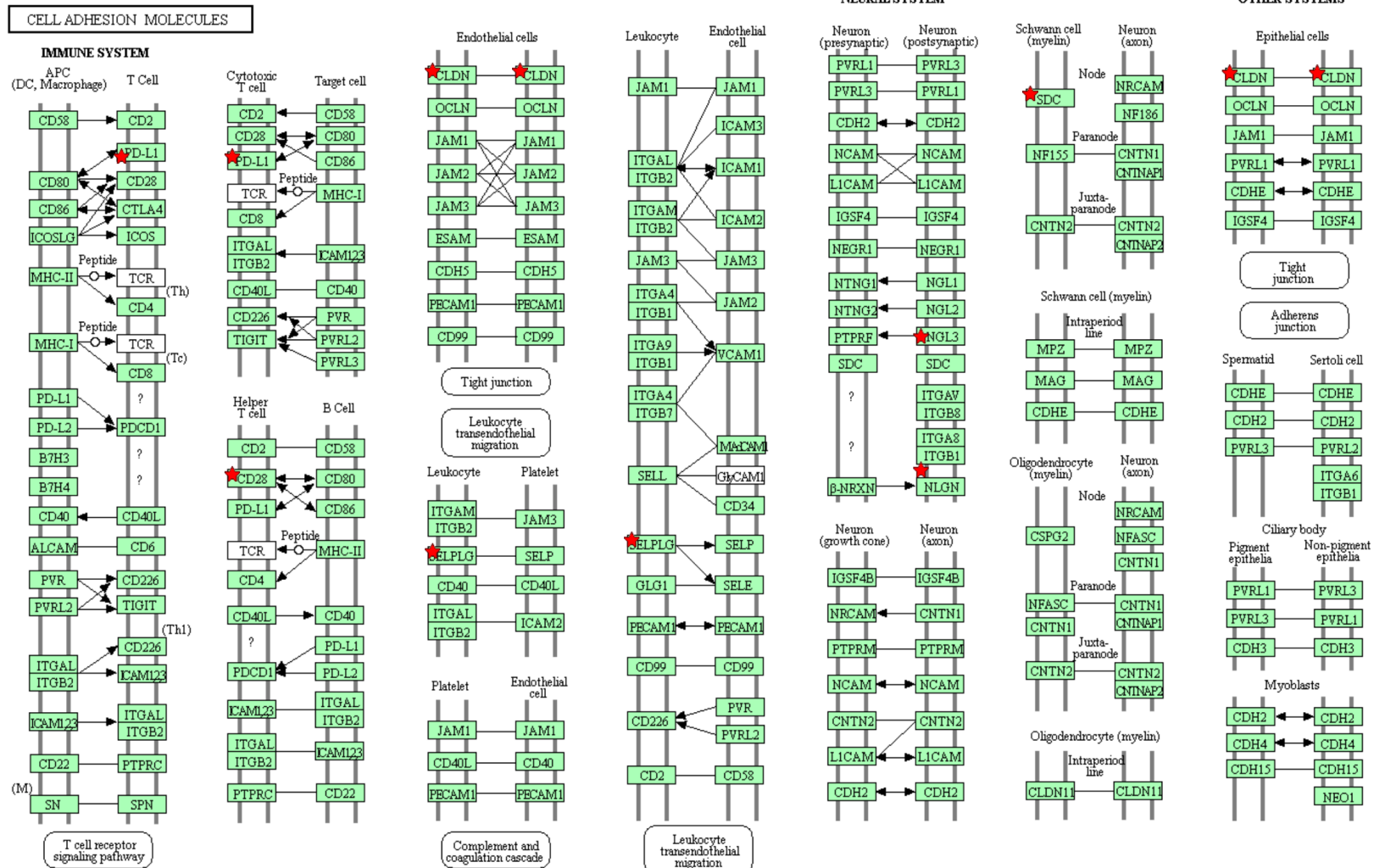
Question 3

- 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 molecule (CAMs)” to see all genes from this pathway

Question 3



Genes from your list are highlighted with a red star