

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_ifc1_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

727 chart records [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamin
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		64	12,6	3,1E-16	8,2E-13
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		64	12,6	3,2E-16	4,1E-13
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		192	37,9	6,7E-16	2,8E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		182	35,9	2,8E-14	4,9E-11
<input type="checkbox"/>	SP_PIR_KEYWORDS	signal	RT		150	29,6	3,3E-13	7,1E-11
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		42	8,3	4,0E-13	5,7E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		150	29,6	5,6E-13	4,9E-10
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region part	RT		60	11,8	6,0E-9	2,0E-6
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular matrix	RT		32	6,3	9,4E-9	1,5E-6
<input type="checkbox"/>	GOTERM_CC_FAT	proteinaceous extracellular matrix	RT		30	5,9	2,4E-8	2,6E-6

- To view these genes click on :

64 record(s) [Download File](#)

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
EDIL3	EGF-like repeats and discoidin I-like domains 3	RG	Homo sapiens

Question 2

- Use “Functional Annotation Clustering” tool

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

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Combined View for Selected Annotation

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Question 2

- First identified cluster :

209 Cluster(s)

 [Download File](#)

Annotation Cluster 1		Enrichment Score: 12.06		G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT			64	3.1E-16	8.2E-13
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT			64	3.2E-16	4.1E-13
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT			42	4.0E-13	5.7E-11
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell adhesion	RT			23	1.5E-5	2.3E-3

- Click here to visualize members of this cluster

Question 2

sorbin and SH3 domain containing 1
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
neurophilin 1
Rho family GTPase 3
collagen, type IX, alpha 1
heparan sulfate proteoglycan 2
neurophilin 2
lysyl oxidase-like 2
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2
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
polycystic kidney and hepatic disease 1 (autosomal recessive)
roporin, rhophilin associated protein 1B
roundabout, axon guidance receptor, homolog 2 (Drosophila)
CD24 molecule; CD24 molecule-like 4
claudin 15
syntaxin binding protein 1
laminin, alpha 4
laminin, beta 2 (laminin 5)
ADAM metallopeptidase domain 23
vitronectin
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
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
neuroigin 1
cysteine-rich, angiogenic inducer, 63
collagen, type VI, alpha 3
Cas scaffolding protein family member 4
integrin, alpha 1
oligodendrocyte myelin glycoprotein
collagen, type XIV, alpha 1
protocadherin 1
protocadherin gamma subfamily A, 6
catenin (cadherin-associated protein), alpha 2
collagen, type XIX, alpha 1
selectin P ligand
protocadherin 15
cadherin 7, type 2
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
connective tissue growth factor
dachous 2 (Drosophila)
neuroigin 1
cadherin 12, type 2 (N-cadherin 2)

GO:004537-cell-cell adhesion
cell adhesion
GO:0007155-cell adhesion
GO:0022018-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

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Question 3

- Search for *Claudin 15* in the page to see all associated annotations

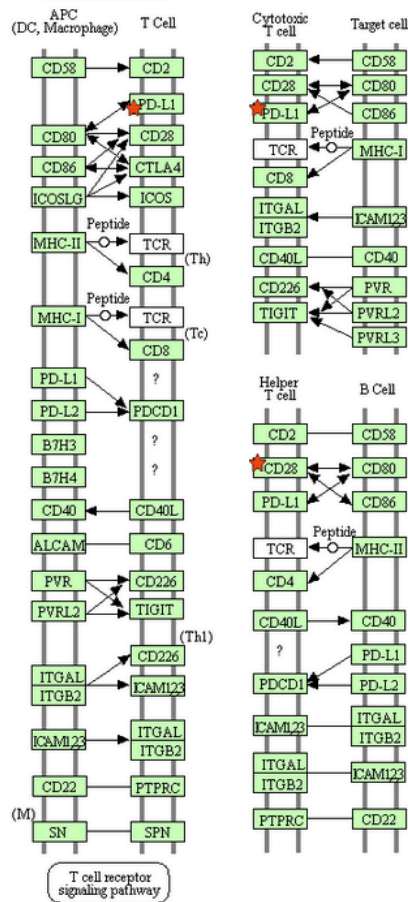
CLDN15	claudin 15	Related Genes	Homo sapiens
GOTERM_BP_FAT	cell adhesion , cell-cell adhesion , calcium-independent cell-cell adhesion , biological adhesion ,		
GOTERM_CC_FAT	plasma membrane , cell-cell junction , tight junction , integral to membrane , apicolateral plasma membrane , cell junction , 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 molecule (CAMs)” to see all genes from this pathway

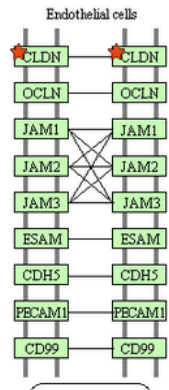
Question 3

CELL ADHESION MOLECULES

IMMUNE SYSTEM



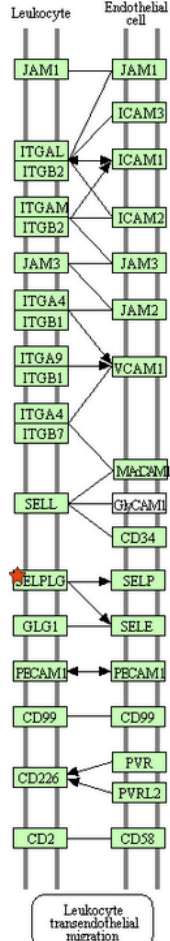
T cell receptor signaling pathway



Tight junction

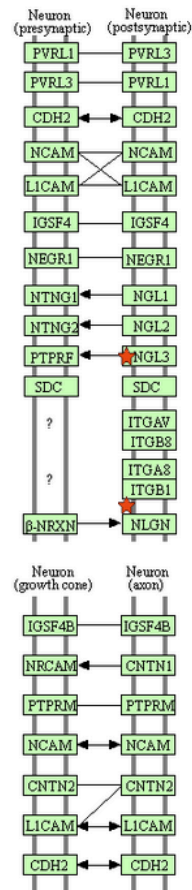
Leukocyte transendothelial migration

Complement and coagulation cascade

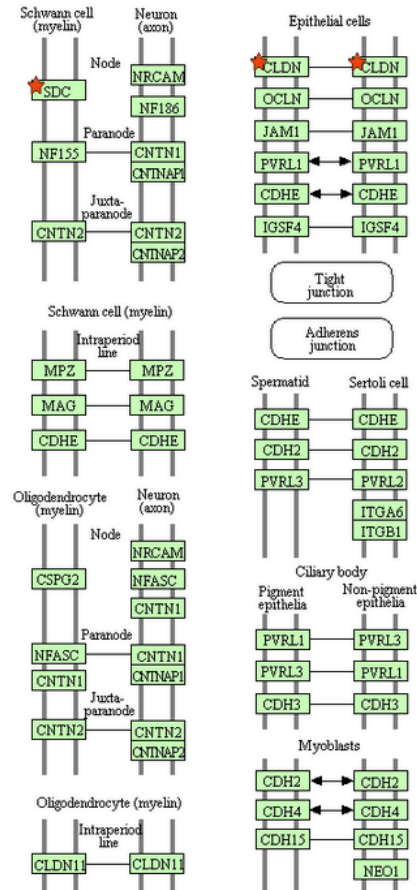


Leukocyte transendothelial migration

NEURAL SYSTEM



OTHER SYSTEMS



Tight junction

Adherens junction

Genes from your list are highlighted with a red star