

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

550 DAVID IDs

Current Background: Homo sapiens

Check Defaults



Clear All

- 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

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

604 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamin
<input type="checkbox"/>	UP_KEYWORDS	Glycoprotein	RT		200	36,4	6,8E-17	4,1E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		187	34,0	3,6E-15	6,4E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT		154	28,0	1,5E-13	1,3E-10
<input type="checkbox"/>	UP_KEYWORDS	Cell adhesion	RT		43	7,8	4,0E-12	7,3E-10
<input type="checkbox"/>	UP_KEYWORDS	Signal	RT		173	31,5	7,9E-12	9,7E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell adhesion	RT		40	7,3	4,7E-10	1,2E-6
<input type="checkbox"/>	UP_KEYWORDS	Secreted	RT		92	16,7	1,7E-8	1,6E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		123	22,4	2,6E-8	1,5E-5
<input type="checkbox"/>	UP_KEYWORDS	Disulfide bond	RT		138	25,1	2,8E-8	2,1E-6
<input type="checkbox"/>	INTERPRO	Immunoglobulin I-set	RT		18	3,3	2,2E-7	2,1E-4

- To view these genes click on :

200 record(s)

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OFFICIAL_GENE_SYMBOL	GENE NAME	Related Genes	Species
HTR2B	5-hydroxytryptamine receptor 2B(HTR2B)	RG	Homo sapiens
ADAM23	ADAM metalloproteinase domain 23(ADAM23)	RG	Homo sapiens
ADAMTS18	ADAM metalloproteinase with thrombospondin type 1 motif 18(ADAMTS18)	RG	Homo sapiens
ART3	ADP-ribosyltransferase 3(ART3)	RG	Homo sapiens
ALG9	ALG9, alpha-1,2-mannosyltransferase(ALG9)	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









-
-
-

Question 2

- First identified cluster :

89 Cluster(s)

 [Download File](#)

Annotation Cluster 1		Enrichment Score: 11.06		G		Count	P_Value	Benjamini
<input type="checkbox"/>	UP_KEYWORDS	Glycoprotein	RT			200	6.8E-17	4.1E-14
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT			187	3.6E-15	6.4E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	signal peptide	RT			154	1.5E-13	1.3E-10
<input type="checkbox"/>	UP_KEYWORDS	Signal	RT			173	7.9E-12	9.7E-10
<input type="checkbox"/>	UP_KEYWORDS	Secreted	RT			92	1.7E-8	1.6E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT			123	2.6E-8	1.5E-5
<input type="checkbox"/>	UP_KEYWORDS	Disulfide bond	RT			138	2.8E-8	2.1E-6

- [Click here to visualize members of this cluster](#)

Question 2

■ corresponding gene-term association positively reported ■ corresponding gene-term association not reported yet

	complement factor H(CFH)
	proline and arginine rich end leucine rich repeat protein(PRELP)
	vitronectin(VTN)
	semaphorin 3D(SEMA3D)
	matrilin 2(MATN2)
	latent transforming growth factor beta binding protein 1(LTBP1)
	latent transforming growth factor beta binding protein 2(LTBP2)
	hemicentin 1(HMCN1)
	apolipoprotein D(APOD)
	lysyl oxidase like 2(LOXL2)
	collagen type VI alpha 3 chain(COL6A3)
	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)
	semaphorin 3B(SEMA3B)
	C-C motif chemokine ligand 2(CCL2)
	connective tissue growth factor(CTGF)
	leptin receptor(LEPR)
	laminin subunit gamma 1(LAMC1)
	laminin subunit beta 1(LAMB1)
	laminin subunit beta 2(LAMB2)
	laminin subunit alpha 4(LAMA4)
	heparan sulfate proteoglycan 2(HSPG2)
	matrix metalloproteinase 17(MMP17)
	sclerostin domain containing 1(SOSTDC1)

GENE:KIT ligand(KITLG)

TERM:Glycoprotein

ASSOCIATION:1

Genes

Annotations

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

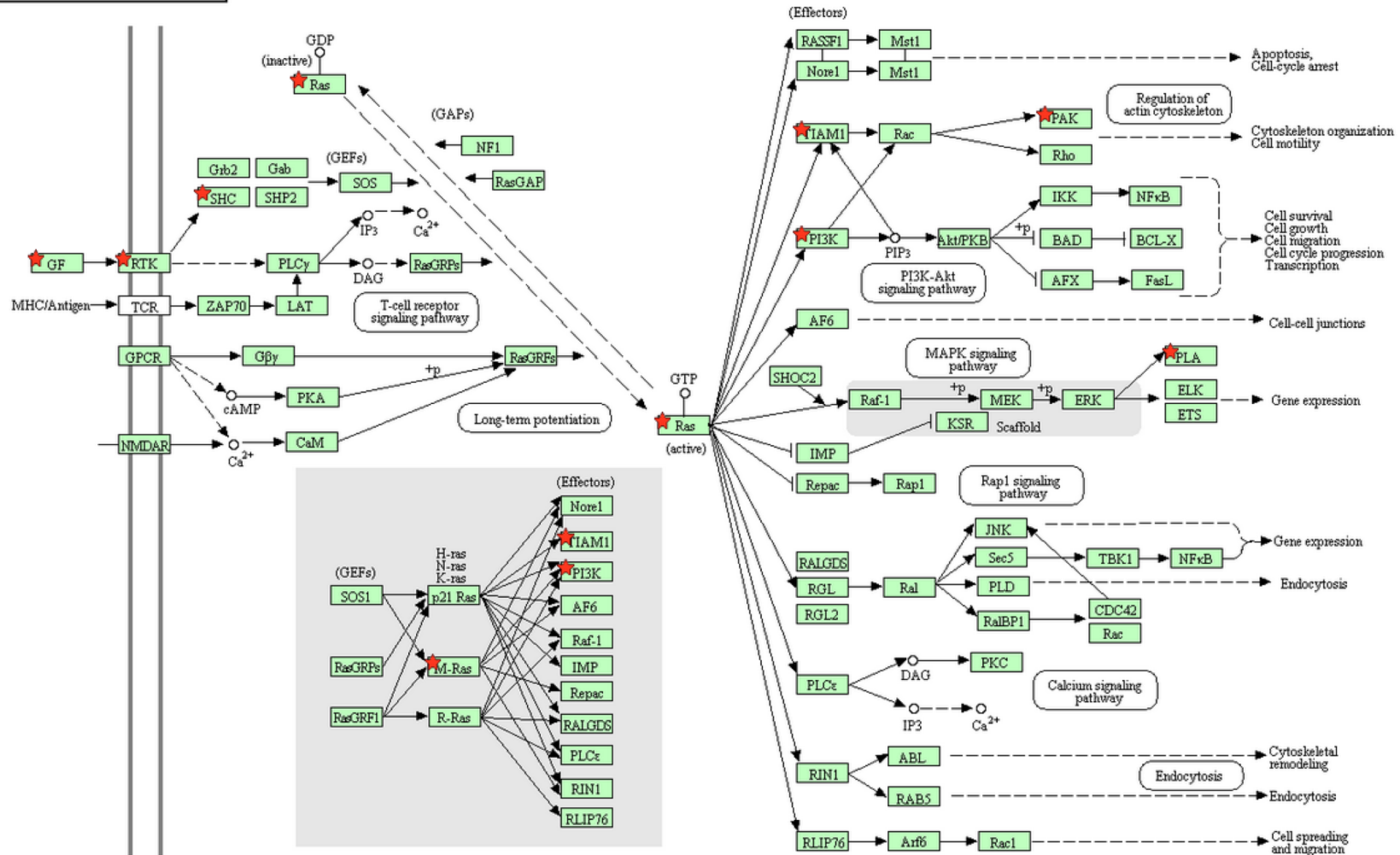
- Search for *KITLG* in the page to see all associated annotations

KITLG	KIT ligand(KITLG)	Related Genes	Homo sapiens
BBID	124.GH-IGF1 thymopoiesis ,		
BIOCARTA	Regulation of BAD phosphorylation , Erythrocyte Differentiation Pathway , IL 17 Signaling Pathway , CDK Regulation of DNA Replication , Melanocyte Development and Pigmentation Pathway ,		
GOTERM_BP_DIRECT	MAPK cascade , ovarian follicle development , neural crest cell migration , positive regulation of leukocyte migration , positive regulation of myeloid leukocyte differentiation , cell adhesion , signal transduction , cell proliferation , male gonad development , regulation of phosphatidylinositol 3-kinase signaling , negative regulation of mast cell apoptotic process , embryonic hemopoiesis , ectopic germ cell programmed cell death , positive regulation of MAP kinase activity , positive regulation of GTPase activity , positive regulation of melanocyte differentiation , positive regulation of DNA replication , positive regulation of Ras protein signal transduction , phosphatidylinositol phosphorylation , phosphatidylinositol-mediated signaling , positive regulation of peptidyl-tyrosine phosphorylation , positive regulation of mast cell proliferation , extrinsic apoptotic signaling pathway in absence of ligand , positive regulation of hematopoietic stem cell proliferation ,		
GOTERM_CC_DIRECT	extracellular region , extracellular space , cytoplasm , cytoskeleton , plasma membrane , membrane , integral component of membrane , lamellipodium , filopodium ,		
GOTERM_MF_DIRECT	Ras guanyl-nucleotide exchange factor activity , cytokine activity , stem cell factor receptor binding , protein binding , growth factor activity , phosphatidylinositol-4,5-bisphosphate 3-kinase activity ,		
INTERPRO	Stem cell factor , Four-helical cytokine-like_core , Four-helical cytokine_core ,		
KEGG_PATHWAY	Ras signaling pathway , Rap1 signaling pathway , PI3K-Akt signaling pathway , Hematopoietic cell lineage , Melanogenesis , Pathways in cancer ,		
OMIM_DISEASE	Hyperpigmentation with or without hypopigmentation , Skin/hair/eye pigmentation 7 , blond/brown hair , Deafness, congenital, unilateral or asymmetric ,		
PIR_SUPERFAMILY	Kit ligand precursor , stem cell factor ,		
UP_KEYWORDS	3D-structure , Alternative splicing , Cell adhesion , Cell membrane , Cell projection , Complete proteome , Cytoplasm , Cytoskeleton , Deafness , Direct protein sequencing , Disease mutation , Disulfide bond , Glycoprotein , Growth factor , Membrane , Non-syndromic deafness , Polymorphism , Proteomics identification , Reference proteome , Secreted , Signal , Transmembrane , Transmembrane helix ,		
UP_SEQ_FEATURE	chain:Kit ligand, disulfide bond, glycosylation site:N-linked (GlcNAc...), glycosylation site:N-linked (GlcNAc...); partial, glycosylation site:O-linked (GalNAc...), helix, sequence conflict, sequence variant, signal peptide, site:Not glycosylated, splice variant, strand, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region, turn,		

- Click on “Ras signalling pathway” to see all genes from this pathway

Question 3

RAS SIGNALING PATHWAY



Genes from your list are highlighted with a red star