Exploration of transcriptome landscapes

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/ IIDIALY (NUALCHUEL) > dim(Data\$OV\$GE\$Agilent) [1] 17813 589 > m0 <- Data\$OV\$GE\$Agilent[,sample(colnames(Data\$OV\$GE\$Agilent), 5)];</pre> > ov1 <- samples2ags(m0, method="top", Ntop=30);</pre> > print.ags.list(ov1, File = "OV.5groups.txt");

Next, we submit the obtained text file with N=30 genes per sample using the first tab.

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Project ov			Org	anism:	huma
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Graph	Ta ble				
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Graph legend

Rounded rectangles: AGS Circles: FGS

Double-headed arrows: summarized AGS-FGS connections (both directed and undirected) Arrow thickness and label: no. of individual gene-gene links between AGS and FGS genes Arrow transparency: confidence of enrichment (each one is confident at the FDR level set in the tab "Check and submit") Found problems? Send us email

AGS/FGS size: node size, i.e. no. of genes that have any links in the global network. AGS/FGS color: overall "network activity" of the node, i.e. total no. of links in the global network.





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1259 219	CHECKLIST: Selected AGS: tcga-09-1670-01 & tcga-13-1411-01 & tcga-23-1119-01 & tcga-30-1860-01 & tcga-36-1577-01
1529 42	Selected network: FunCoup LE
6032 825	Selected FGS: KEGG pathways, signaling
5115 233	
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1878 133	Filter AGS (your groups) by mask:
lore how do the unique features of each	Filter FGS (pathways) by mask:
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ee details in tutorial "How to begin?").	Sublint and calculate Restore latest allalysis
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email	
	As was explained in tutorial "How to begin?", we
	overview the selected parameters and click "Submit".
	overview the selected parameters and ener submit.

\$	#links AGS ∲	FGS	#genes FGS ∲	#links FGS	#linksAGS2FGS 🔶	Score	FDR
	721	GO_0002347_RESPONSE_TO_TUMOR_CELL	3	328	2	26.88	4.1969
	721	GO_0006915_APOPTOSIS	510	54172	36	9.80	1.1179
	721	GO_0017134_FGF_BINDING	12	1144	3	14.29	1.3483
95						Previous	1

https://www.evinet.org

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