

A resource for investigating the impact of differences in gene expression levels on Gallus Reactome Pathways. This takes as input a two column list, first column is currently required to be Entrez Gene IDs and second is the $\log(2)$ of the ratio of gene expression determined for two different biological states (i.e. tumor vs. control). See sample list linked from this page. The results are first visualized as a table (Figure 1).

Pathway Statistic Analysis Result: [Click](#)
 Cytoscape Software Download: [Download](#)
 Tutorial for Results: [View](#)
 Cytoscape Style File: [Download](#) (prerequisite for cytoscape to visualize our result)

pathwayName	ratio	total	up	down	unchanged	crossTalk	rateLimit
Transcriptional Regulation of White Adipocyte Differentiation	0.0178571428571	56	0	1	0	1	0
Transmission across Chemical Synapses	0.00617283950617	162	0	1	0	1	0
Metabolism of amino acids and derivatives	0.00595238095238	168	0	1	0	0	0
Cytokine Signaling in Immune system	0.00442477876106	226	0	1	1	1	0
Metabolism of lipids and lipoproteins	0.00221238938053	452	0	1	0	1	0
Biological oxidations	0.0	104	0	0	0	0	0
Potassium Channels	0.0	81	0	0	0	0	0
Apoptotic execution phase	0.0	43	0	0	0	0	0
Signaling by NODAL	0.0	13	0	0	0	0	0
Amyloids	0.0	33	0	0	0	0	0
tRNA Aminoacylation	0.0	42	0	0	0	0	0

Figure 1: Sample data analyzed impact on Gallus Reactome pathways.

Explanation of Table

- PathwayName refers to the affected signaling or metabolic pathway.
- Ratio: the ratio of genes affected by differential expression to the total number of genes in the pathway.
- Total is the total number of genes in the pathway.
- Up is the number of genes up-regulated (positive log value).
- Down is the number of genes down-regulated (negative log value)
- Unchanged is the number of genes whose ratio of expression falls between the upper and lower cutoff chosen on the submission page.
- crossTalk gives the number of affected genes in the submitted list that are found in multiple pathways (they cross talk between pathways).
- rateLimit gives the number of genes in the submitted list that are rate limiting steps in the respective pathway.

Up, down, unchanged, crosstalk and rateLimit are active links and will display the respective gene products.

Obtaining Cytoscape Files-(first download **Tutorial for Results**)

Click on a specific pathwayName in the table to download a GML file that can be opened under File –Import –Network.

You will also need one copy of the Cytoscape Style File which can be reused with all pathways. Click on File – Import –Style. To view differentially regulated genes, you must chose the regulated Network style under the Style dropdown menu.