

miRNA pathway views for Alzheimer's Disease







Description of miRNApath algorithm



- The algorithm attempts to identify pathways where the genes predicted to be affected by miRNA changes are present much more so than one would expect by random chance alone.
- The slides below detail the observations seen for some pathways of interest
- The counts represent the number of miRNAs and genes affected in a pathway, with emphasis on the consistent directionality of the changes.
 - In large part, most pathways predicted to be significantly affected by the miRNA changes are affected by miRNAs which are all consistently up-regulated, or all consistently down-regulated.
 - In some cases, there are some miRNA changes in an opposing direction from the majority, which either reflects that pathways are often defined with some positive- and negative-effectors, or that the miRNA changes are not in complete agreement. In these cases, the section “Both” is used to show any differences from “Up” or “Down.”
- Note the library size, which is defined as the total set of miRNAs measured and detected, which therefore varies for each tissue and Braaks stage.
 - The library size is used to define the random background, a uniquely challenging estimate based upon the overall set of genes predicted to be affected by the “measured and detected” miRNAs.
 - From this background, the “measured, detected, and statistically-significantly-differentially expressed miRNAs” are compared, using only their set of genes predicted to be affected.

Understanding the miRNApath views

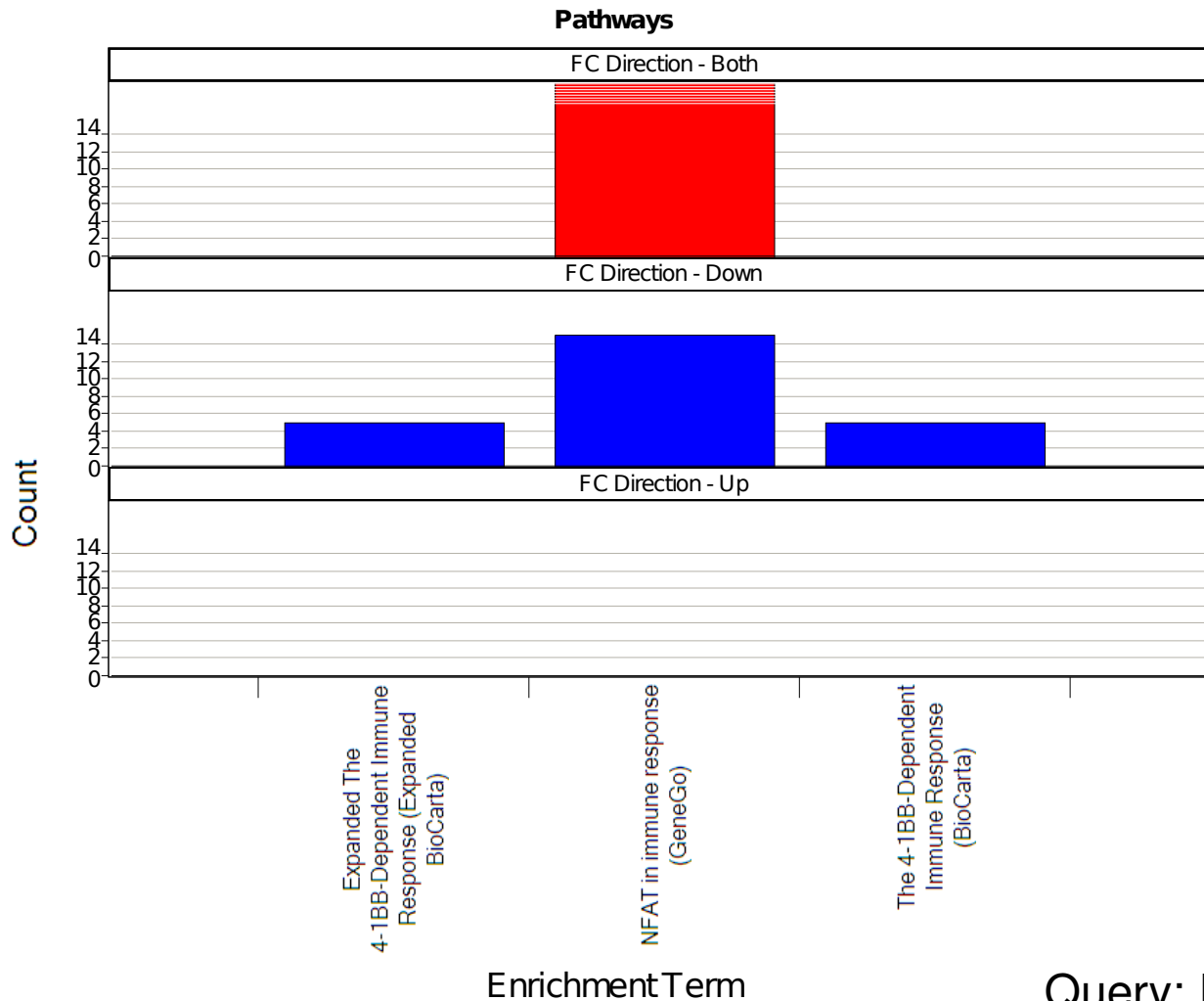
- The pathway views show the direction of the miRNAs regardless of the view (first is pathways, second is miRNAs, and third is targets)
- In the pathway and gene views, assume the genes and pathways are being modulated opposite to the direction of the miRNAs

Color coding for Spotfire files

	B3,4	B5,6
Hippocampus		
Medial Frontal Gyrus		
Cerebellum		

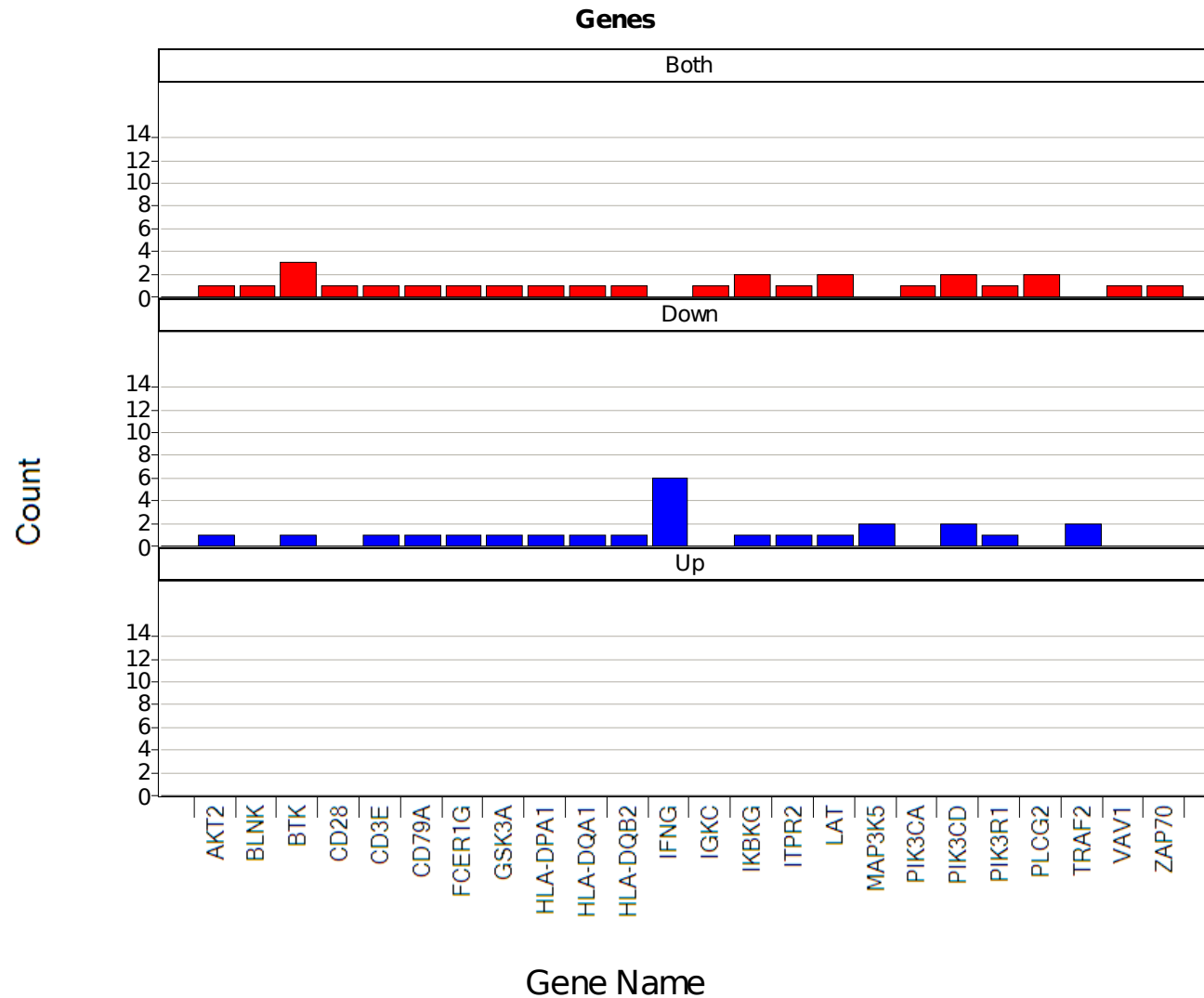
	Up	Down
CSF		

AD CSF: miRNAs in T cell signaling pathways

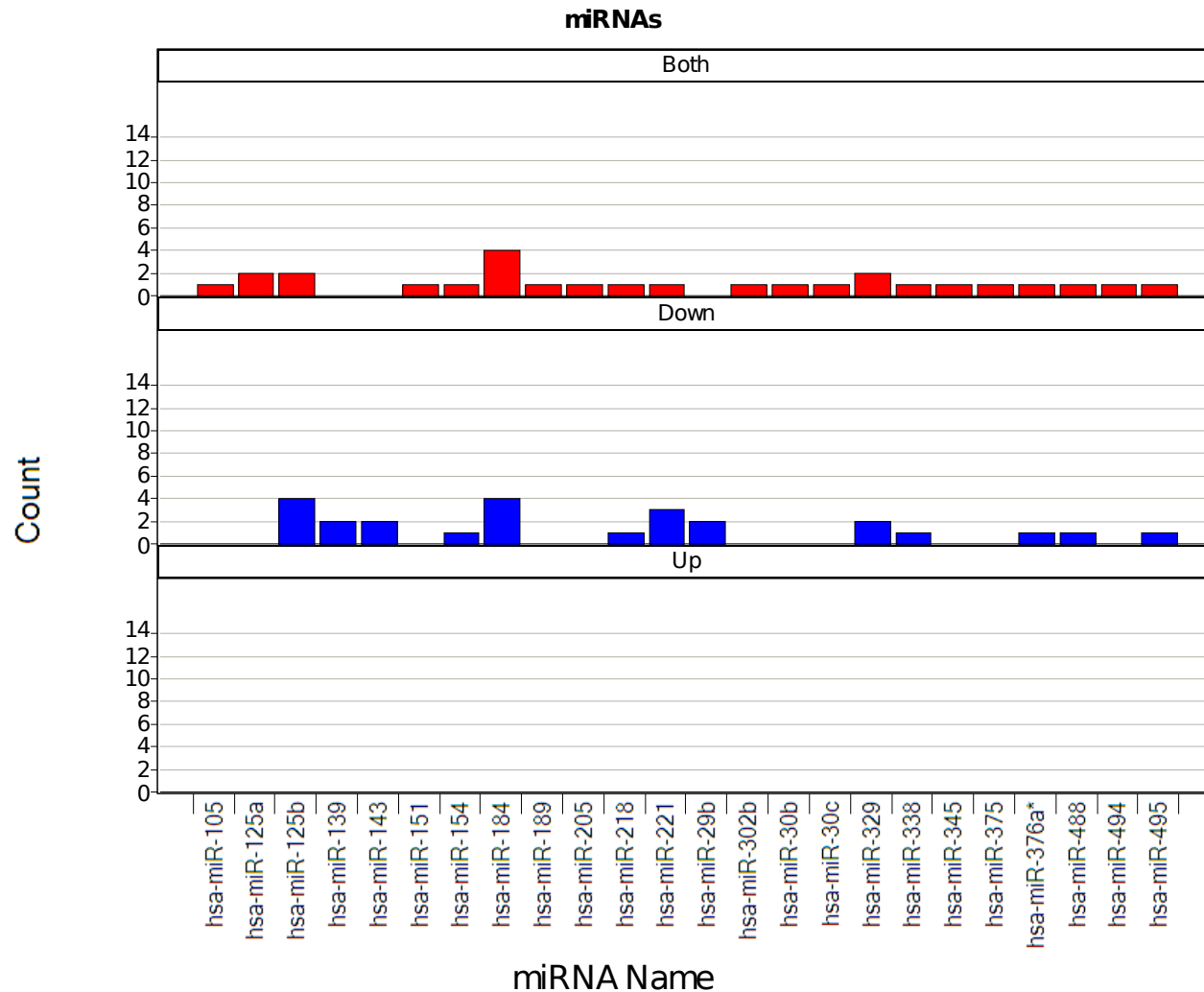


Query: Immune
P-value: 0.05

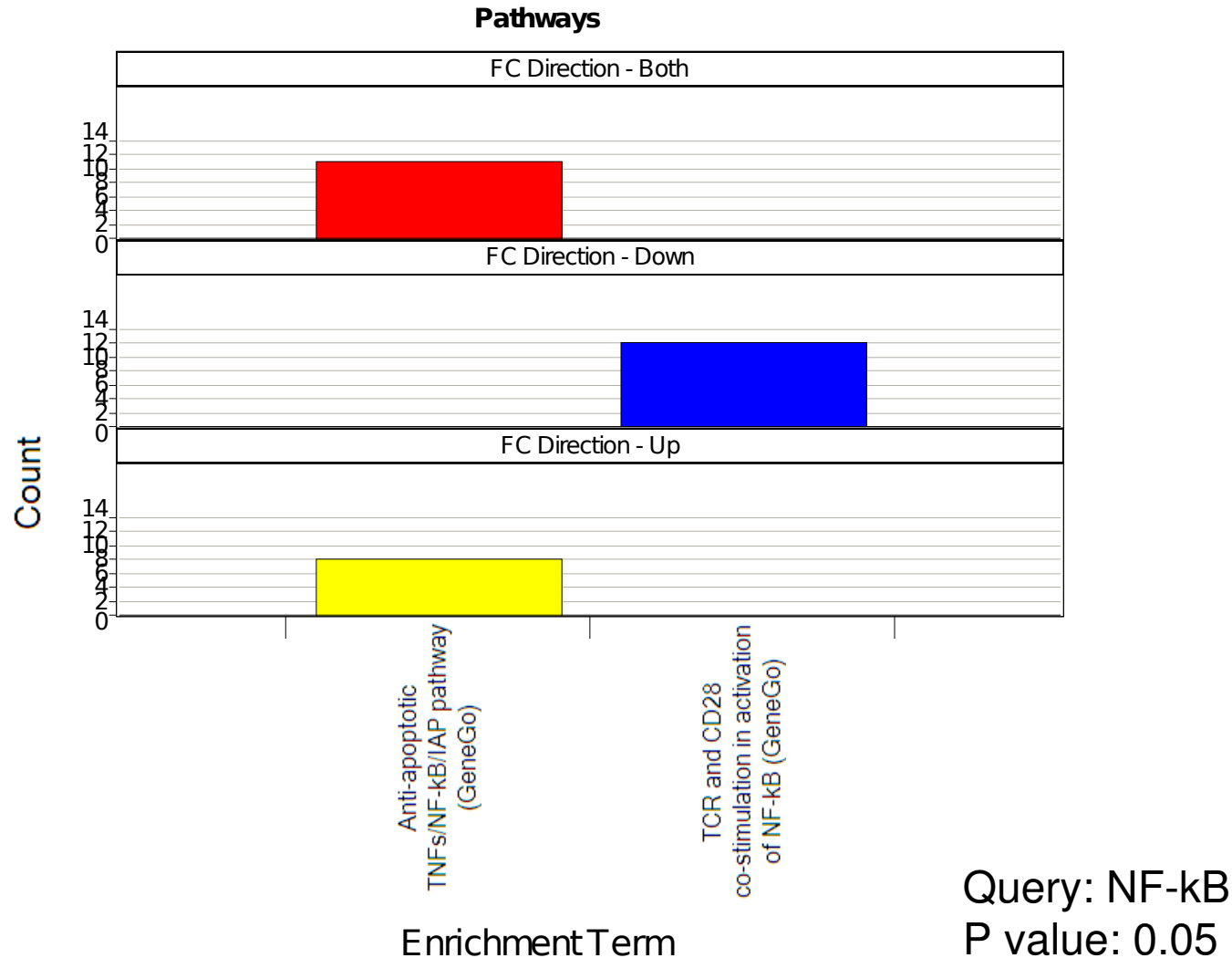
AD CSF: miRNAs in T cell signaling pathways



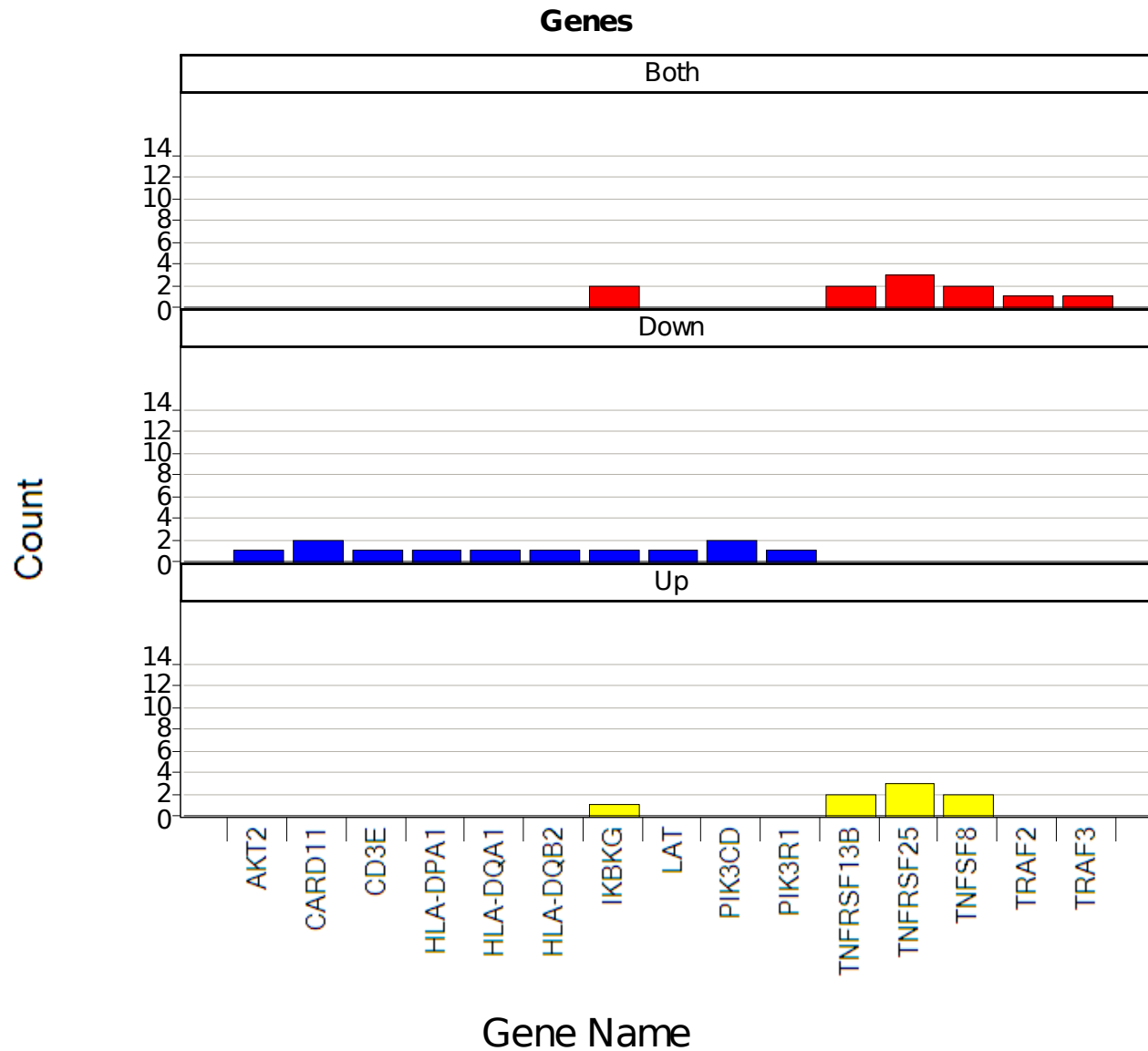
AD CSF: miRNAs in T cell signaling pathways



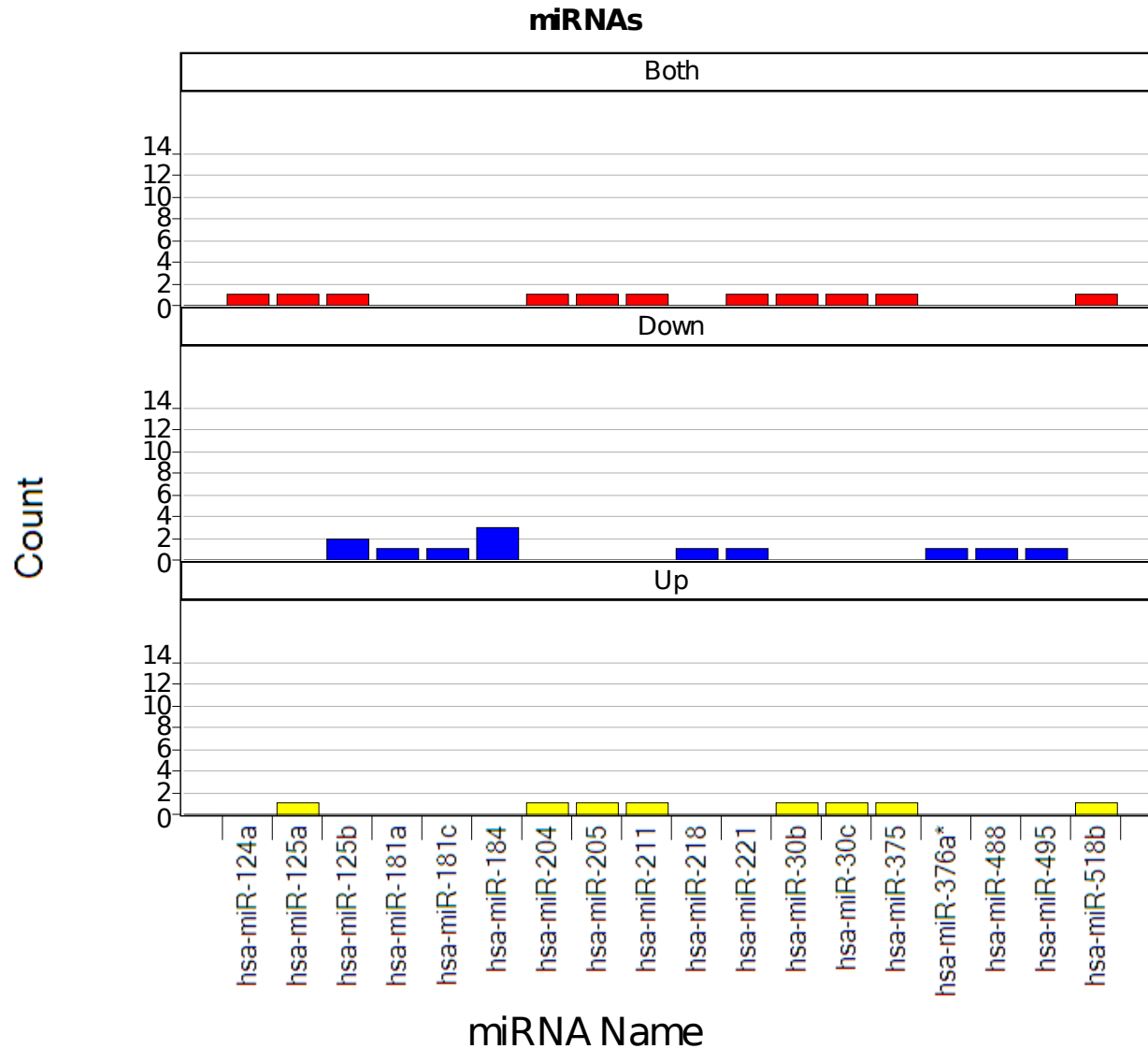
AD CSF: miRNAs in NF-kB pathway



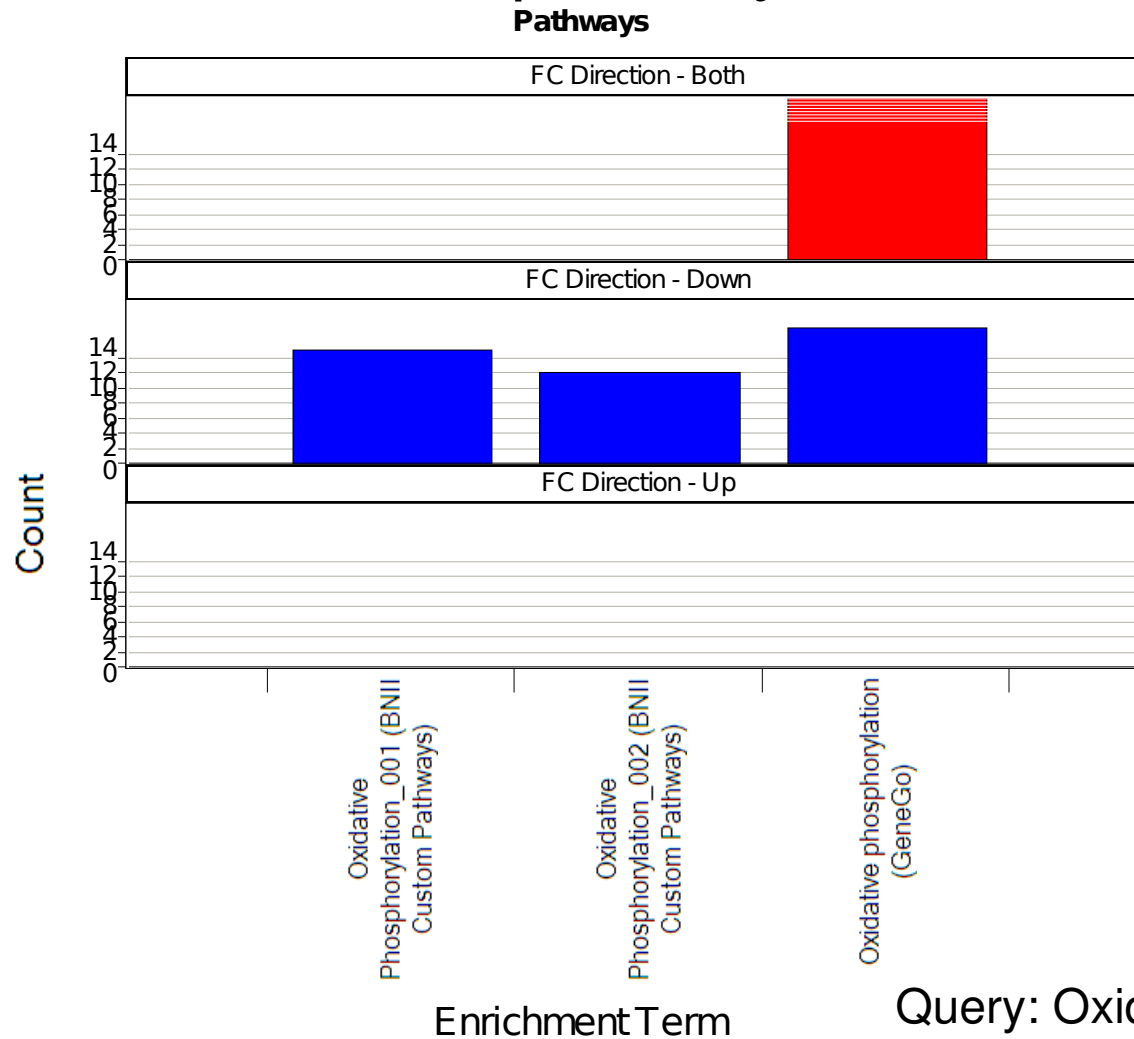
AD CSF: miRNAs in NF-kB pathway



AD CSF: miRNAs in NF-kB pathway

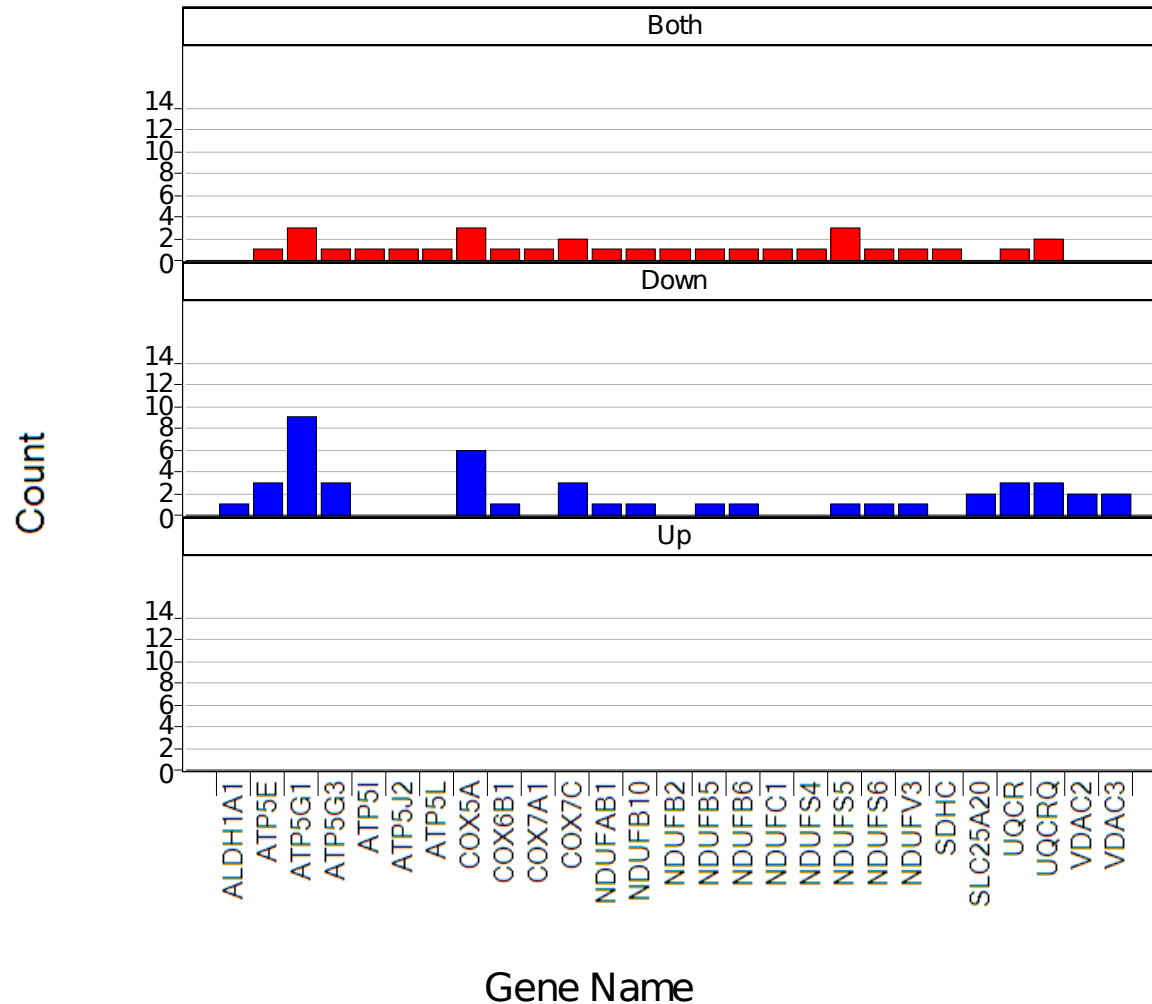


AD CSF: miRNAs in Oxidative phosphorylation pathways

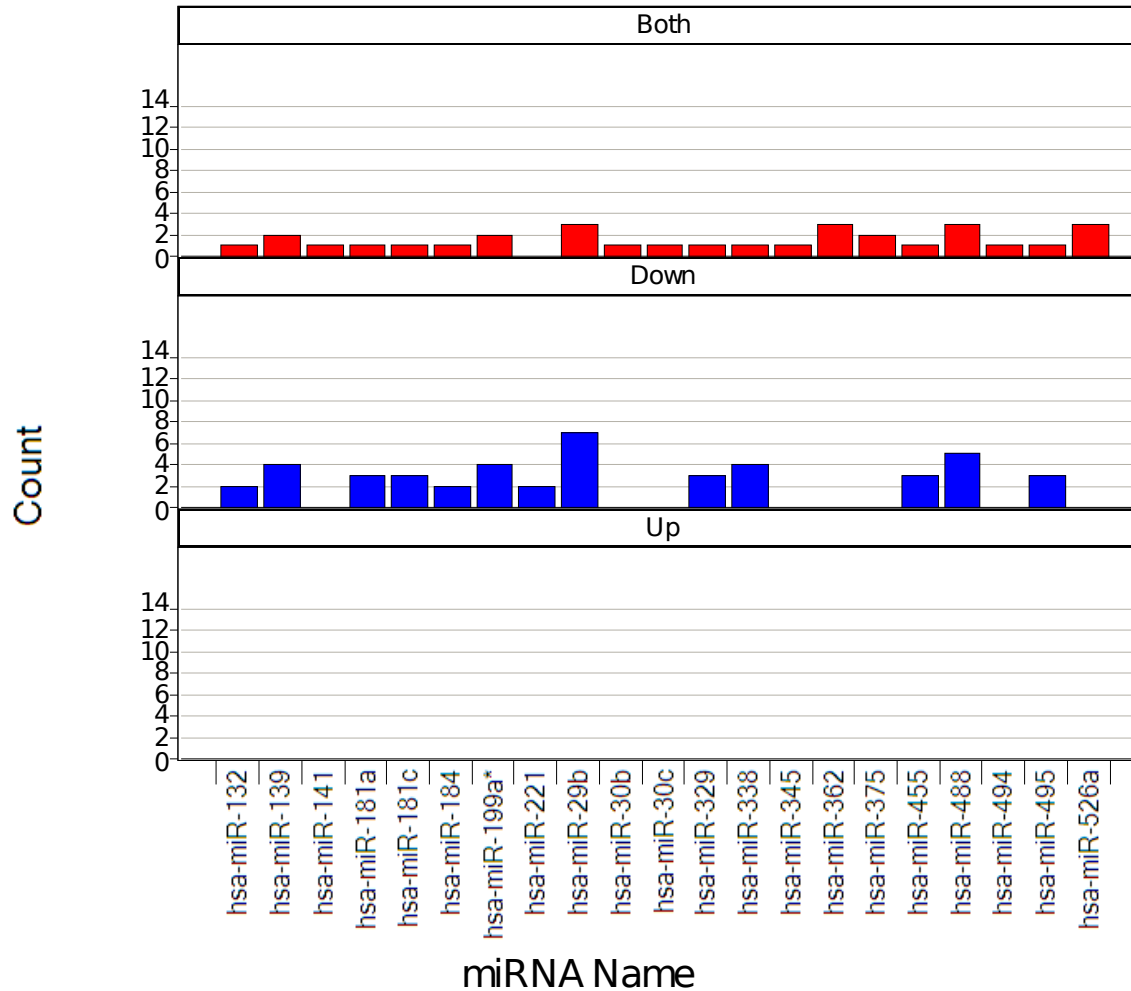


Query: Oxidative Phosphorylation
P-value: <0.05

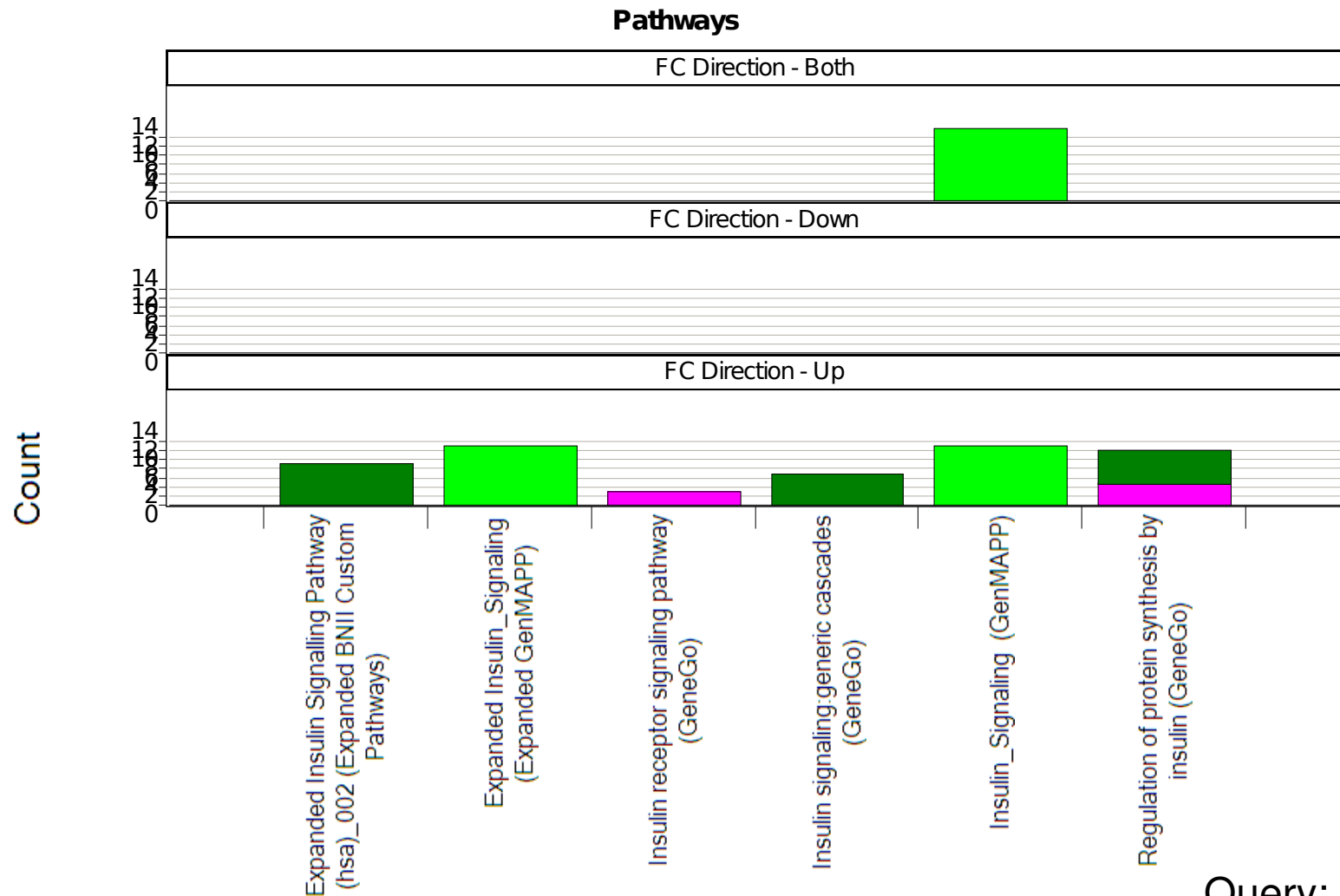
AD CSF: miRNAs in Oxidative phosphorylation pathways



AD CSF: miRNAs in Oxidative phosphorylation pathways



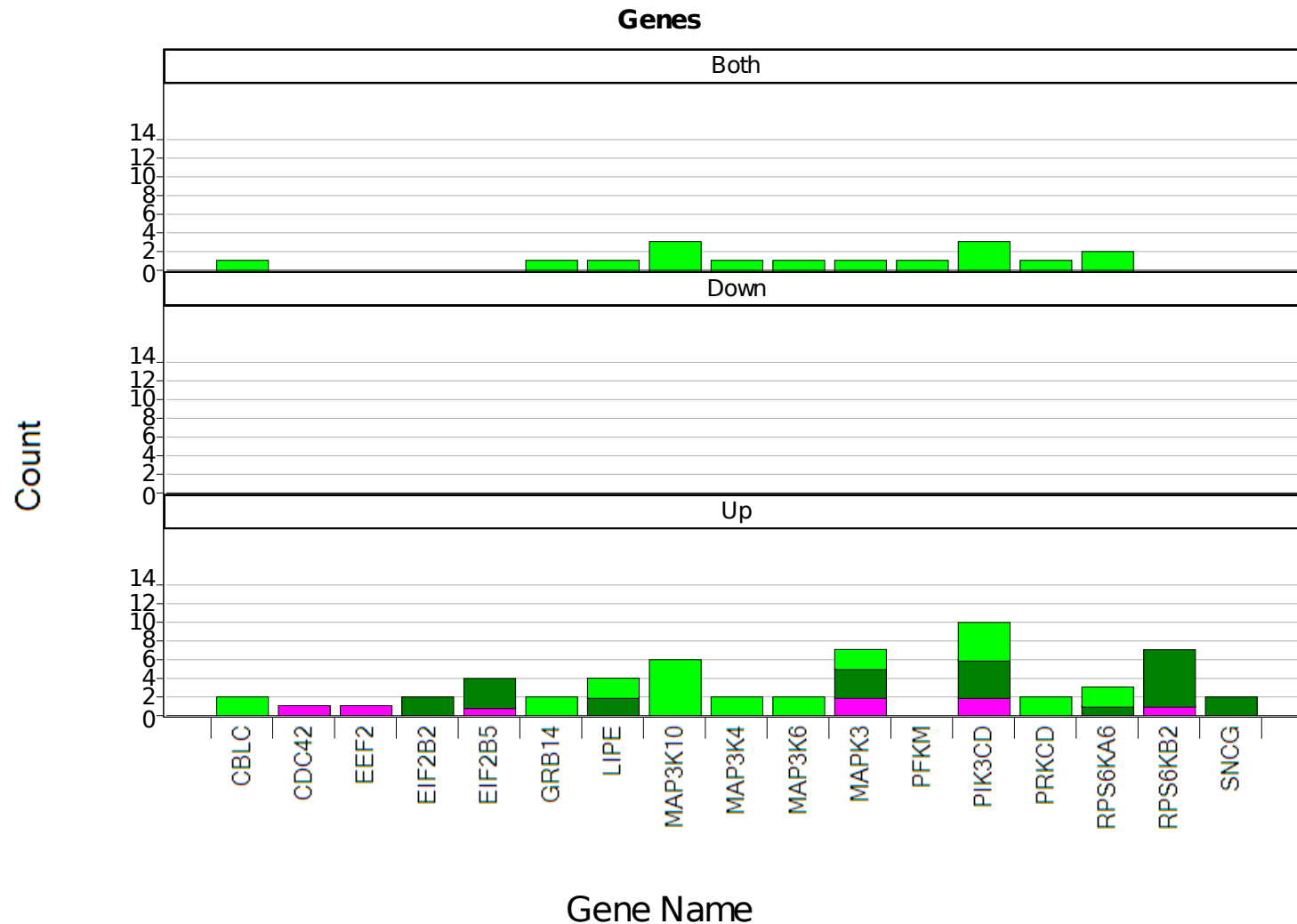
AD Brain: miRNAs in Insulin Signaling Pathways



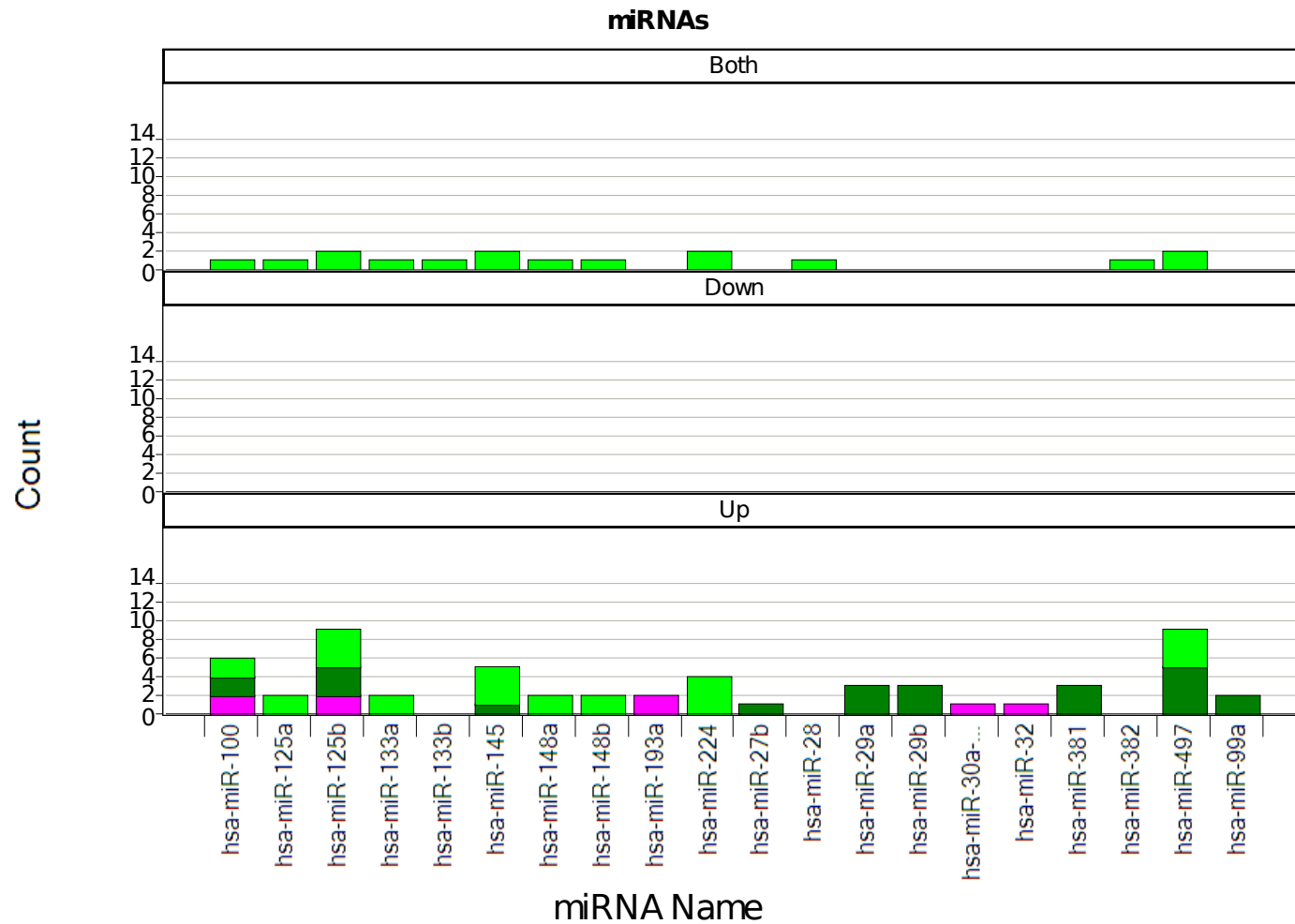
Enrichment Term

Query: Insulin
P value: 0.05

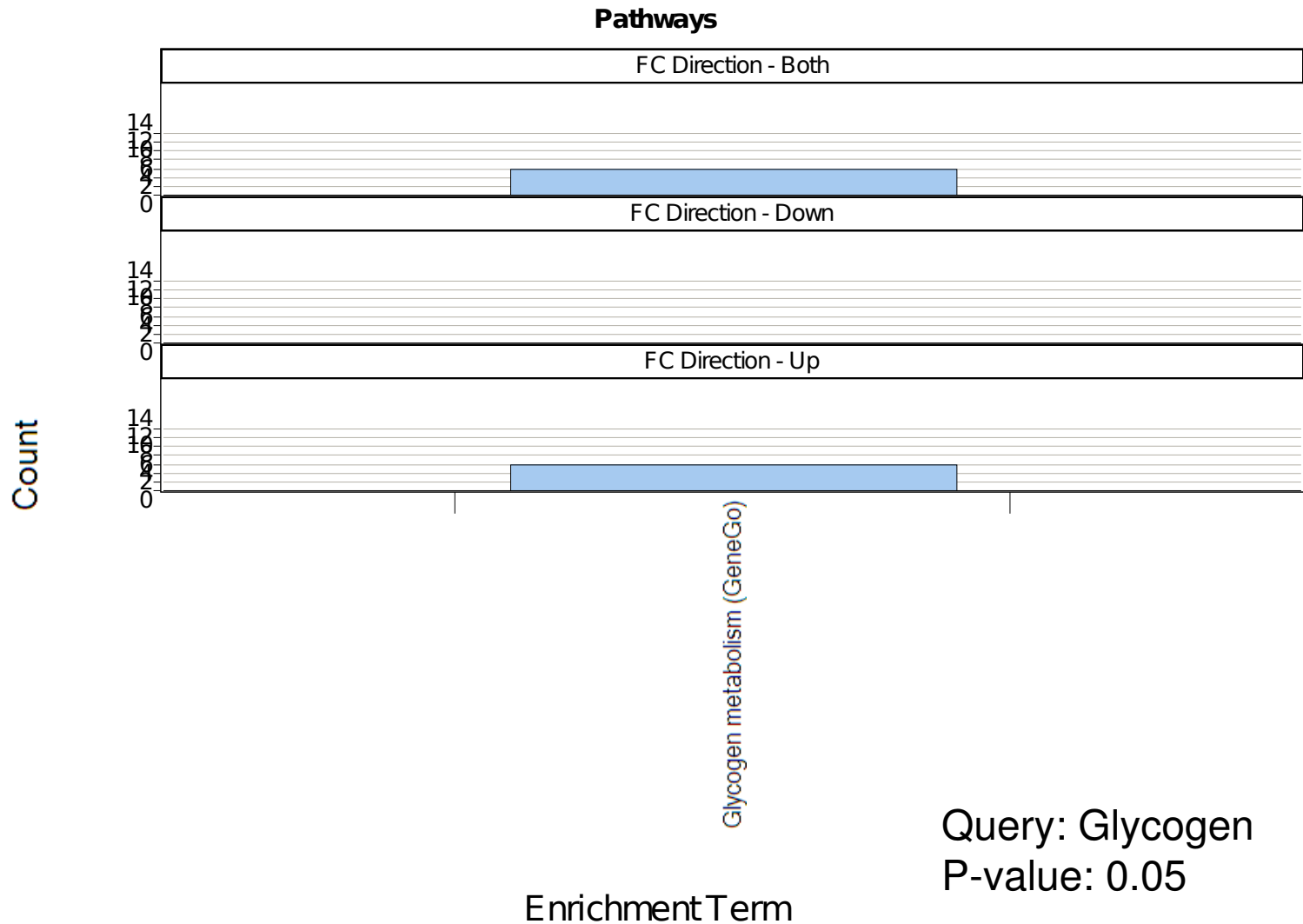
AD Brain: miRNAs in Insulin Signaling Pathways



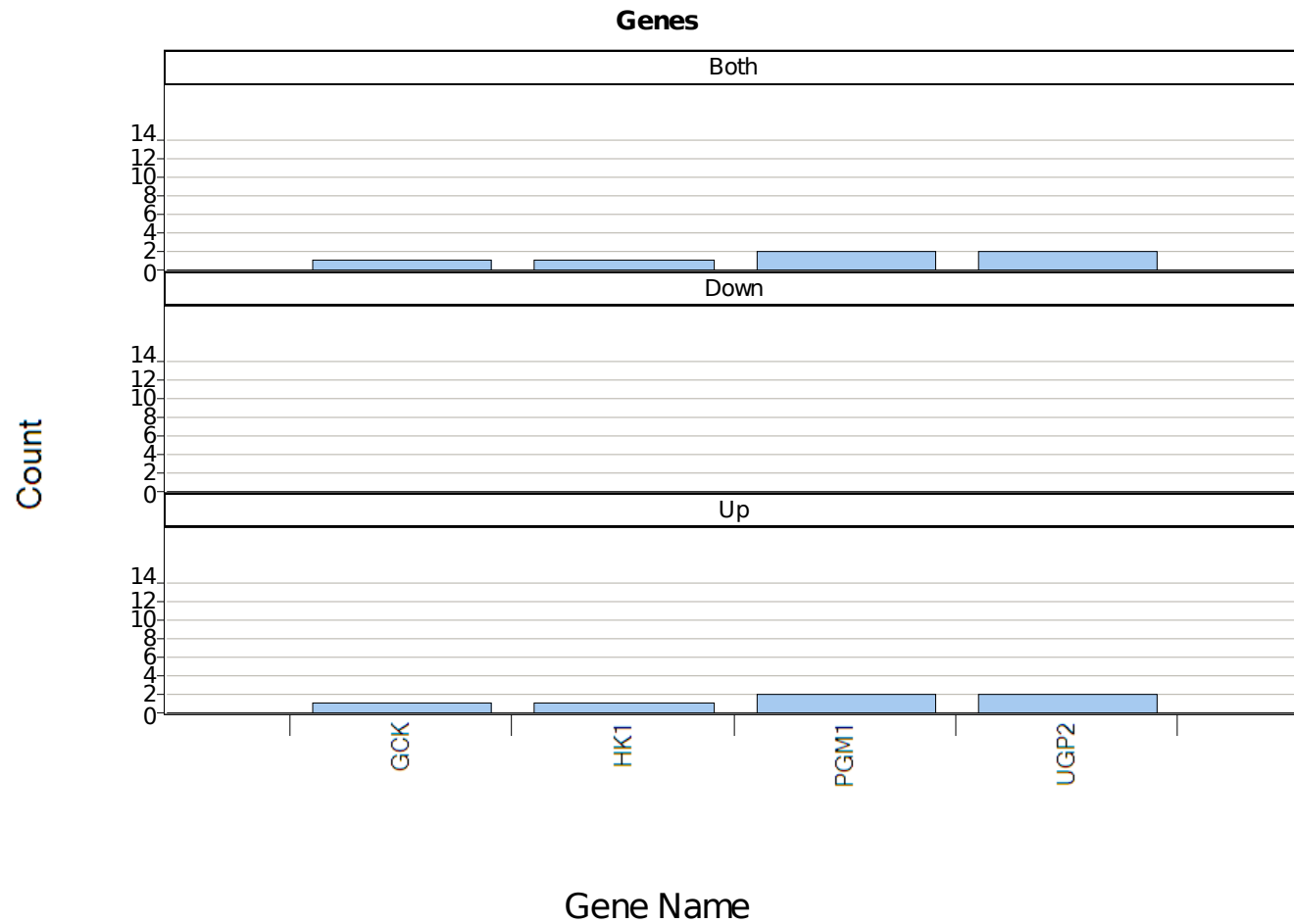
AD Brain: miRNAs in Insulin Signaling Pathways



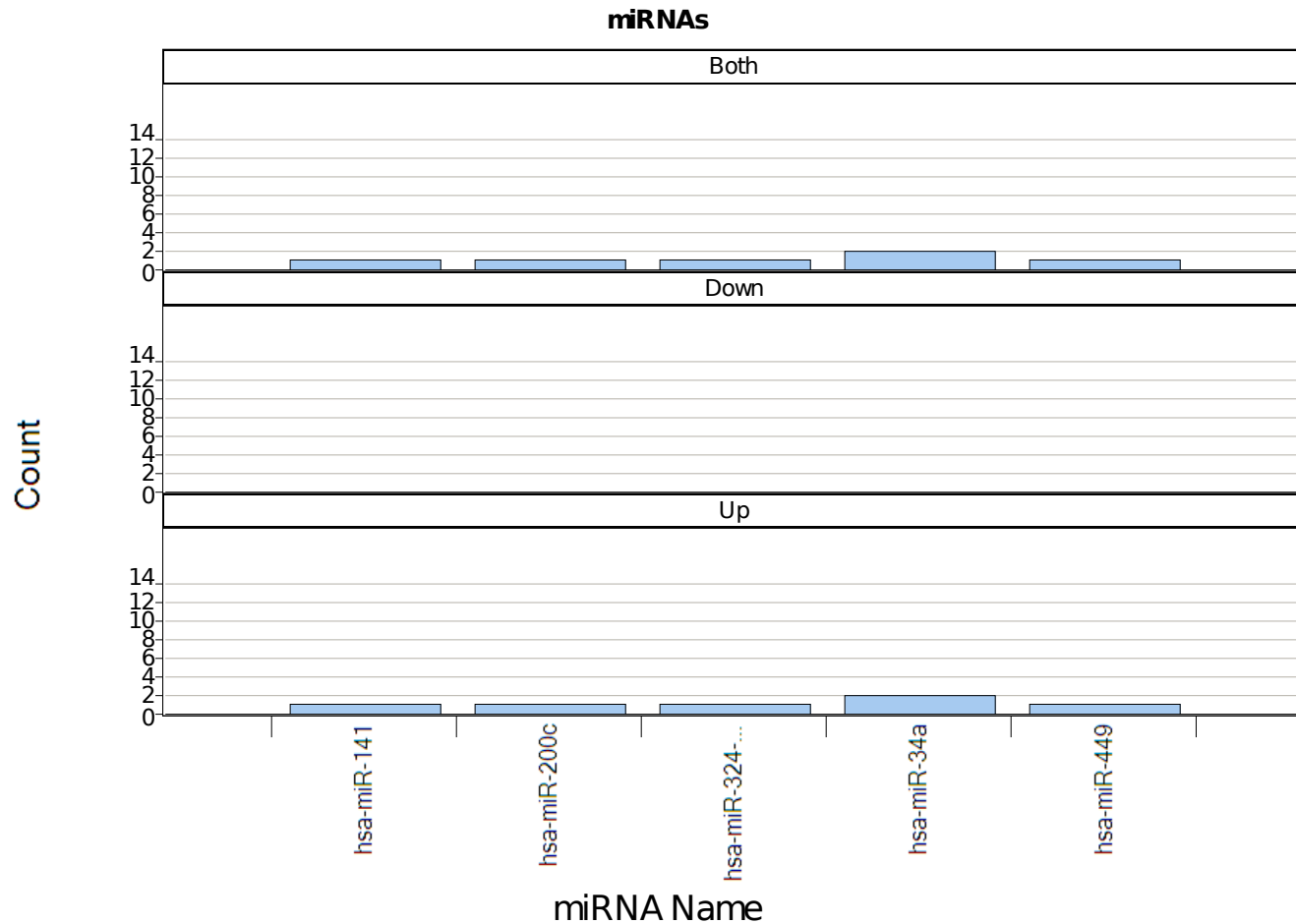
AD Brain: miRNAs in Glycogen Metabolism



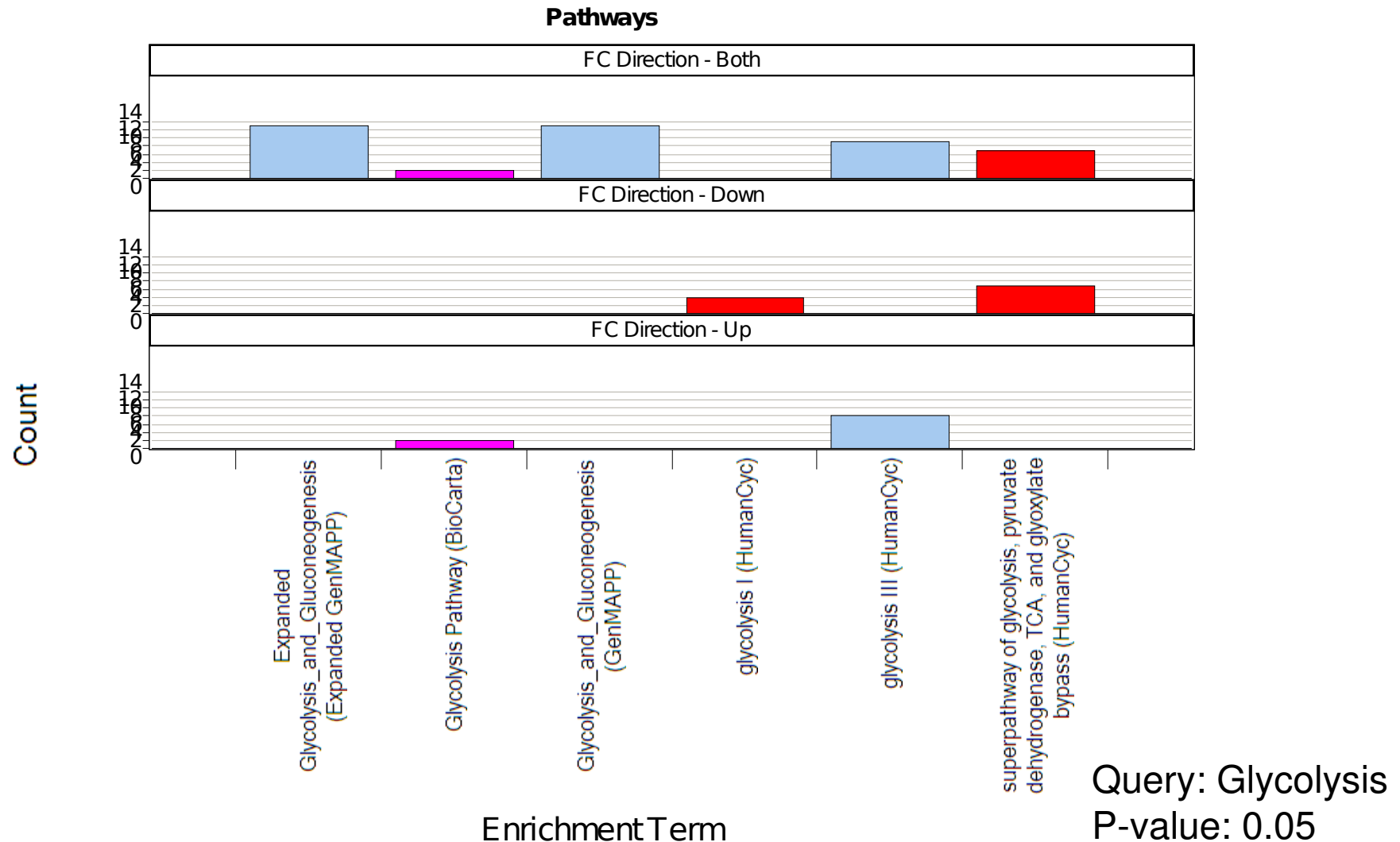
AD Brain: miRNAs in Glycogen Metabolism



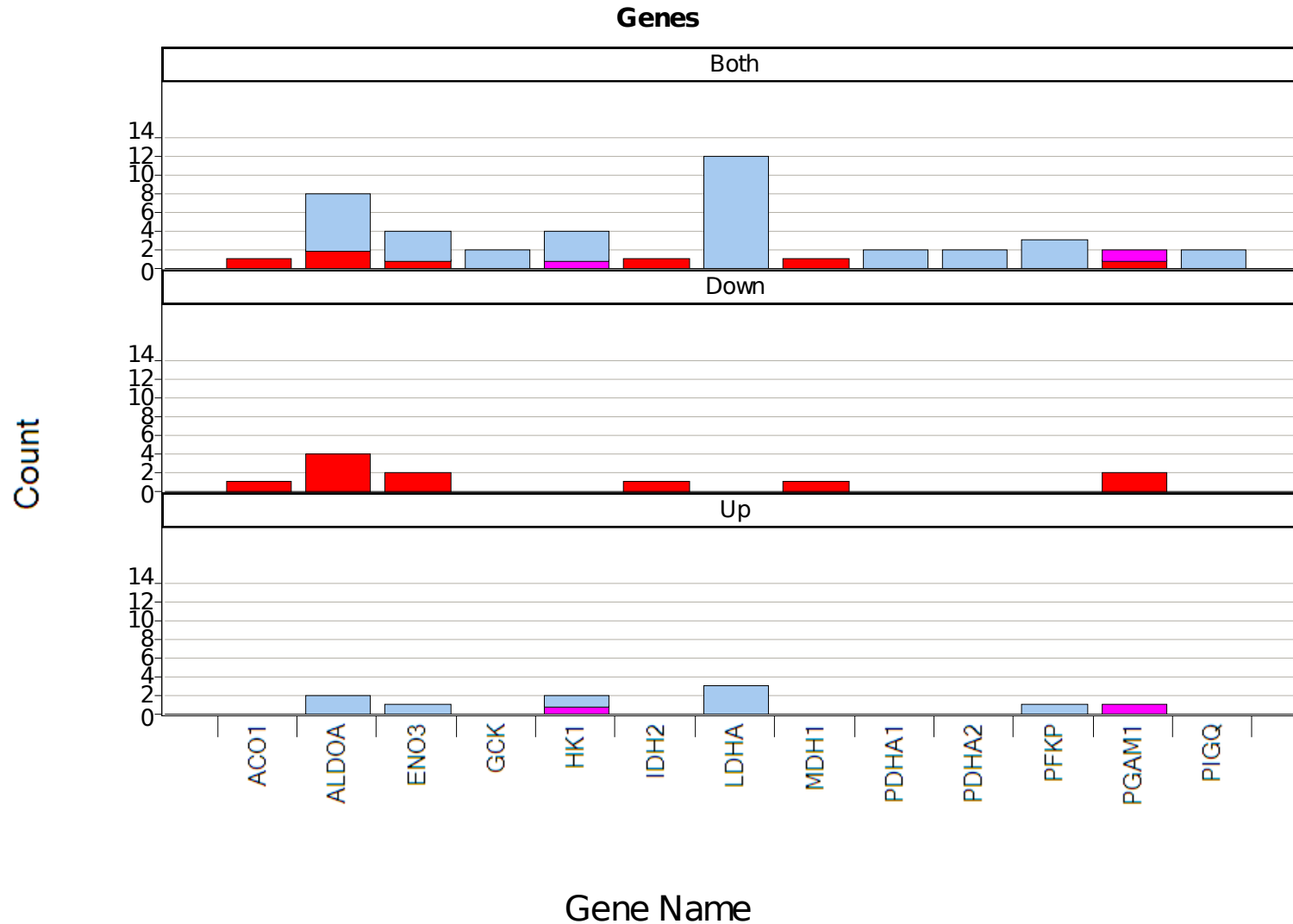
AD Brain: miRNAs in Glycogen Metabolism



AD Brain: miRNAs in Glycolysis Pathways



AD Brain: miRNAs in Glycolysis Pathways



AD Brain: miRNAs in Glycolysis Pathways

