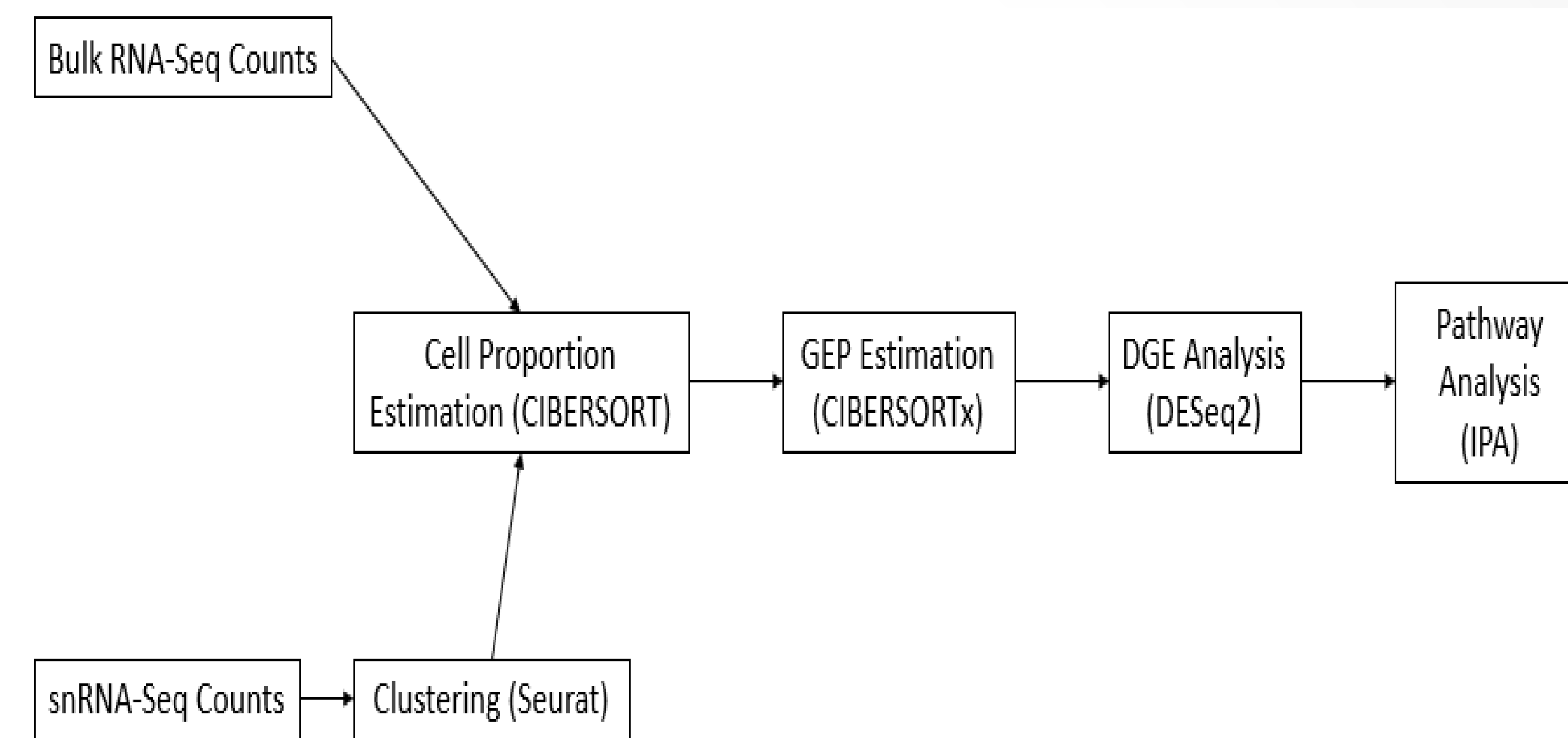


## Background

- Spinal Cord Injuries (SCI) are very dangerous to the body.
- Axons can get cut off during an SCI, which can lead to an impairment in the way the body can communicate with itself.
- Elucidation of the molecular changes that occur during a SCI could lead to treatment for SCI
- If there are specific genes that are upregulated or downregulated after SCI, knowledge of the genes can be used to help treat injuries.
- One method that has been used to analyze the molecular changes is via RNA sequencing.
- A method that is used to reveal what genes are expressed in specific areas
- A view of molecular changes at the cellular level allows for a more targeted treatment
- Deconvolution analysis on bulk RNA-seq to identify cell type-specific gene activities in various types of spinal cord injuries.

## Materials and Methods



## Results

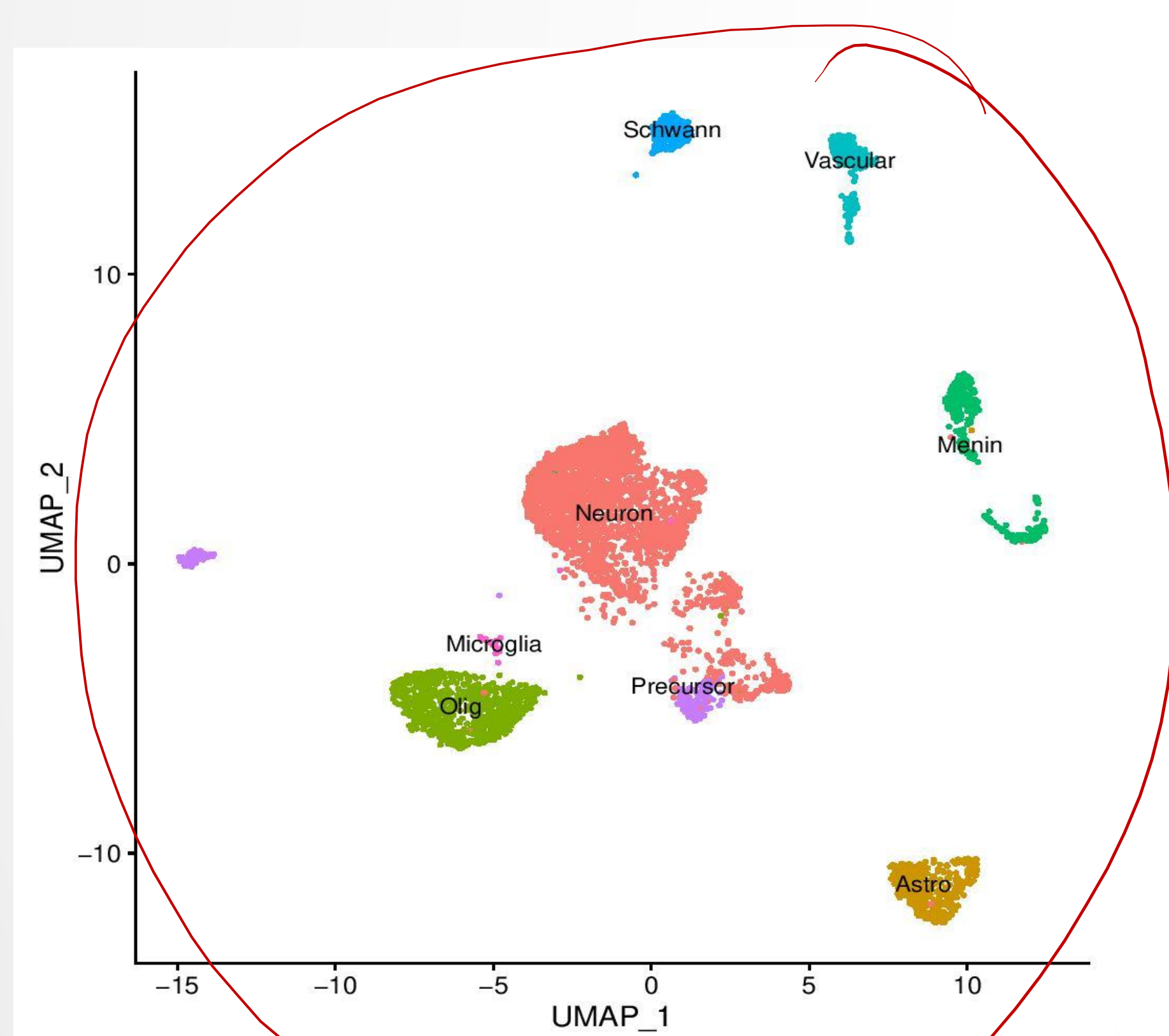


Figure 1: Cluster Plot for Spinal Cord Cells

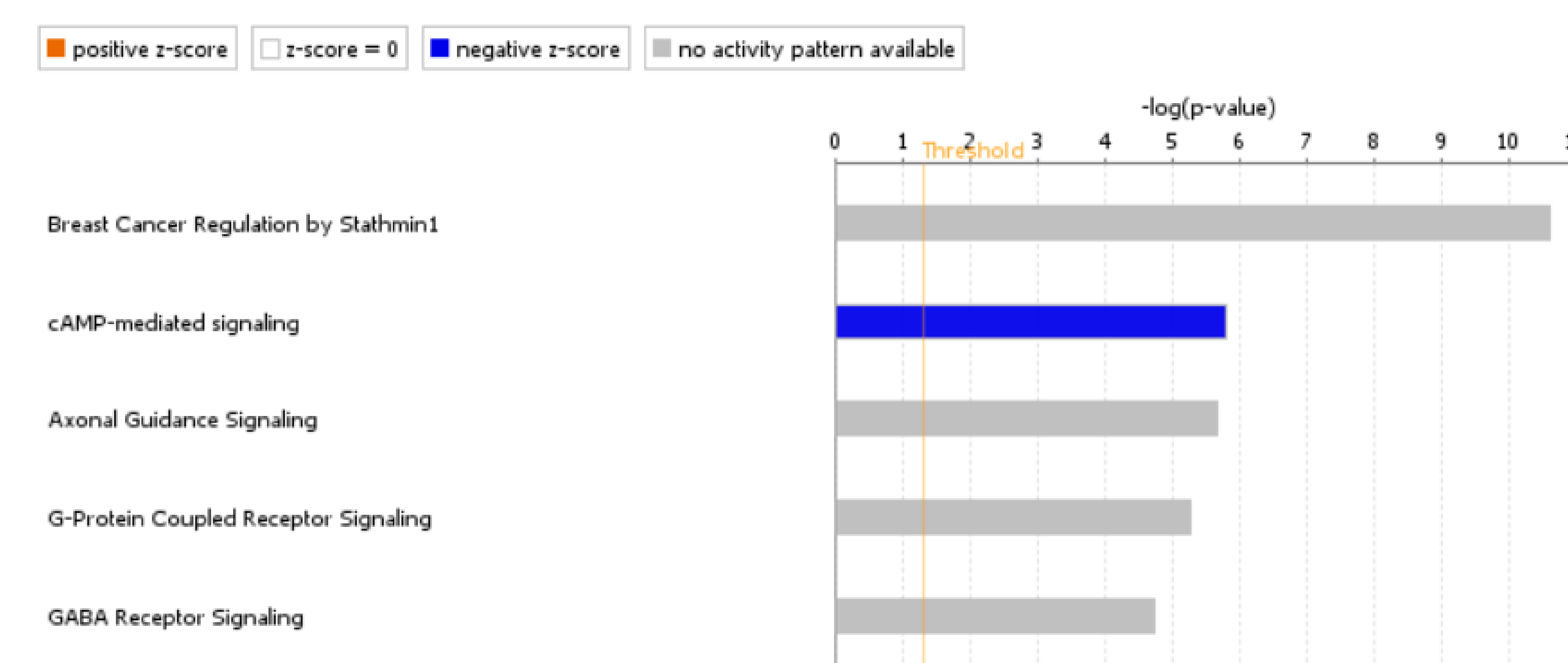


Figure 2: Common Pathways of the Genes that are present in a Contusion after 7 Days

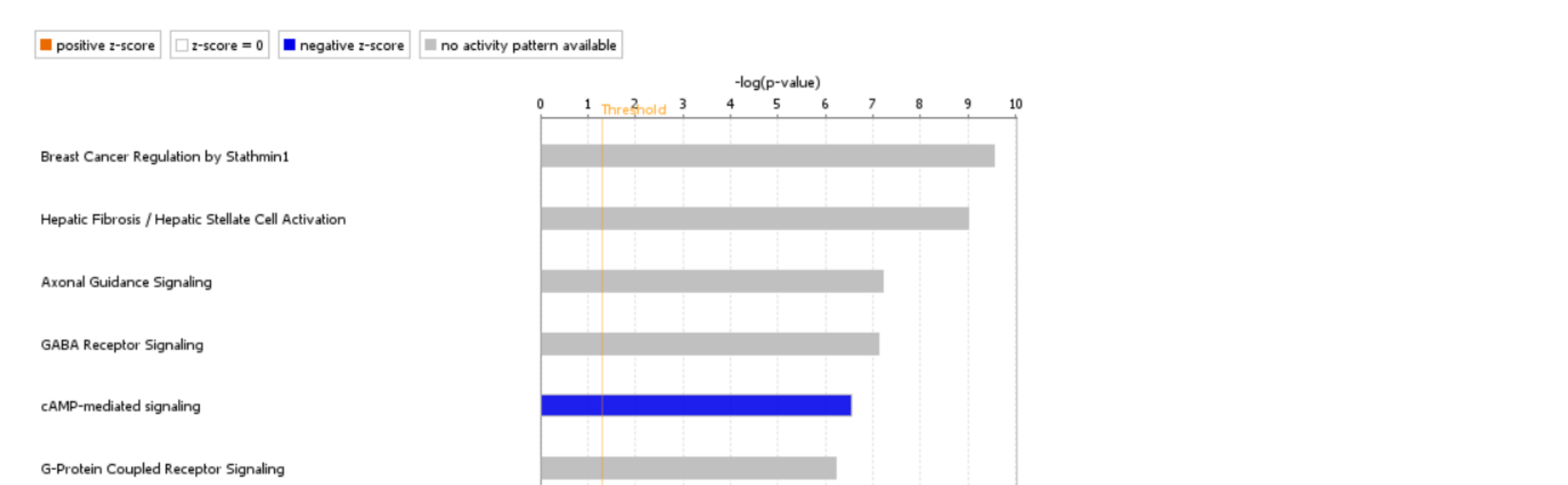


Figure 3: Common Pathways of the Genes that are present in a Full transection after 7 Days

## Gene Expression Comparison Tables

Table 3: Highest Expressed Genes in Contusion after 3 days

CT3d vs Control			FT3d vs Control		
Gene ID	log2Fold Change	P-value	Gene ID	log2Fold Change	P-value
Ctsz	18.49	1.37e-89	Ctsz	19.59	1.37e-89
Plin2	17.33	1.92e-28	Plin2	17.70	1.92e-28
Cybb	16.70	8.20e-27	Cybb	16.91	8.20e-27
CD44	16.59	2.59e-32	Gm4149	16.80	2.59e-32
Anxa4	16.05	1.80e-13	E230029 C05Rik	16.78	5.93e-16

Table 4: Highest Expressed Genes in Full Transection after 3 days

## Conclusion and Future Work

During a spinal cord injury, many of the genes that are upregulated in different types of injuries are present (Ctsz, Plin2, and Cd44). Although many of the expressed genes are similar in the different types of injuries, these genes are very different. All of the genes were predominantly found in meningeal cells. This makes sense as during a SCI, the meninges are one of the first things to be affected.

Future work includes the study of potential of these genes for the treatments to damaged spinal cords by manipulating them in the injured spinal cord.

## Acknowledgments and References

This work was supported by the NSF REU in Cellular Bioengineering: From Biomaterials to Stem Cells (NSF EEC 1763005).

Newman et al., Robust enumeration of cell subsets from tissue expression profiles, Nature Methods 2015  
 Steen et al, Profiling cell type abundance and expression in bulk tissues with CIBERSORTx, Methods in Molecular Biology 2020

MCT3d	Similar	MCT7d
Respiratory Disease	Cancer	Reproductive Disease
Carbohydrate Metabolism	Cell Cycle	Molecular Transport
Embryonic Development	Organismal Development	Organ Morphology
Cardiac Dysfunction	Cardiac Fibrosis	Tachycardia

Table 1: Diseases and Functions related to the upregulation of genes after moderate Contusions

HS3d	Similar	HS14d
Hepatic Fibrosis	Histadine Degradation VI	Histadine Degradation III
Endocrine System Disorders	Cancer	Reproductive System Disease
Tissue Morphology	Organismal Development	Organ Morphology
Renal Necrosis	Renal Dysplasia	Glomerular Injury

Table 2: Diseases and Functions related to the upregulation of genes after Hemisections