



## Transcriptome Analysis of Rat's Hippocampal Cell Layers

João Paulo D. Machado\*, Alexandre H. Matos, Iscia Lopes-Cendes, André S. Vieira.

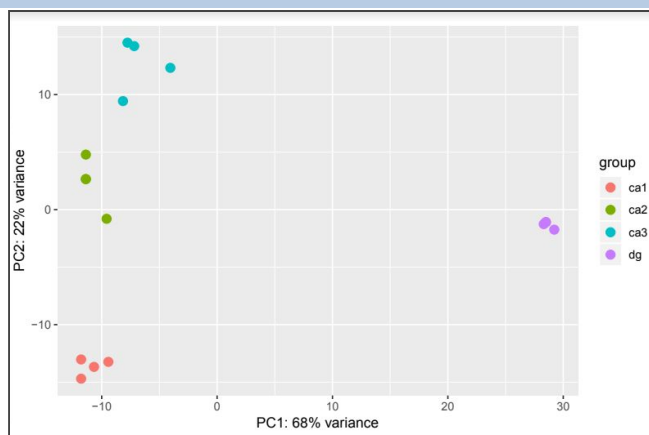
**Abstract:** Hippocampus is a brain region mainly composed by neuron layers described as Dentate Gyrus(DG) and Ammon's horn(CA). This study explores the differential transcripts datasets of hippocampal layers (CA1, CA2, CA3, DG) for elucidating their distinctions. All layers were bilaterally collected from hippocampus of each rat, total RNA was extracted, and libraries for RNA-Seq in Illumina Hiseq platform were prepared according to manufacturer instructions. Sequences were aligned and quantified with the STAR Aligner/DESeq2 pipeline. Gene Ontologies were analyzed with the DAVID software. In results, CA1 neurons are expressing more genes related to circadian rhythms, postsynaptic membrane receptors that are important for maintenance of excitability, learning and memory. In CA2 and CA3 were found transcripts associated to higher metabolic pathways demand and endocytosis recycling. Dentate gyrus neurons expression was related to ribosome, spliceosome, essential for protein synthesis that supports dendritic growth and maintenance of long-term potentiation. These findings yield new information into specific molecular alterations in hippocampus layers which contribute to understanding the singularity of hippocampal formation.

**Key Words:** Hippocampus, transcriptome, RNA-Seq.

### Introduction

Differences between the granule cells presents in Dentate Gyrus (DG) layer and the pyramidal cells in Ammon's horn (CA) layers are described in anatomical and genetic rat's hippocampus studies<sup>1</sup>. RNA-Seq precisely generate a extensive gene expression profiles capable to explore the large heterogeneity of molecular mechanisms in different regions<sup>2</sup>. Thus, the present study explores the differential transcripts datasets of hippocampal layers (CA1, CA2, CA3, DG) for elucidating their distinctions. Dentate gyrus transcripts presents.

### Results and Discussion



**Figure 1:** PCA graphic for hippocampal gene expression data.

The PCA analysis display a evident clustering of samples on the different regions of hippocampus. It's clear the difference among all pyramidal neurons layers(CA) and dentate gyrus neurons(DG)(Figure 1).

Over thousands of differentially expressed genes comparing the layers(Table 1). There are enrichment genes related to zinc-fingers and postsynaptic membrane receptors when comparing transcriptome data of smaller pyramidal neurons(CA1) to largests pyramidal neurons(CA2, CA3). Furthermore, CA2 and CA3 has different expressed genes in metabolic pathways demand and endocytosis recycling.

### Pyramidal Neurons Comparison

(A) Differentially Expressed Genes in CA1 x CA3		(B) Differentially Expressed Genes in CA1 x CA2		(C) Differentially Expressed Genes in CA2 x CA3	
Total	4527	Total	3505	Total	2063
Upregulated	2273	Upregulated	1704	Upregulated	954
Downregulated	2254	Downregulated	1801	Downregulated	1109

### Dentate gyrus cells to Pyramidal neurons comparison

(D) Differentially Expressed Genes in CA1 x DG		(E) Differentially Expressed Genes in CA2x DG		(F) Differentially Expressed Genes in CA3 x DG	
Total	5676	Total	7331	Total	7401
Upregulated	2766	Upregulated	3724	Upregulated	3726
Downregulated	2910	Downregulated	3607	Downregulated	3675

**Table 1:**(A, B, C, D, F, G) Representation of the number differentially expressed genes comparing pyramidal cells and granule cells( $p < 0,05$ ).

On the other hand, granular neurons(DG) have upregulated genes associated to ribosome, spliceosome and intracellular signaling when comparing to all pyramidal layers. However, genes connected to oxidative phosphorylation and energetic metabolism are downregulated in DG.

### Conclusion

In this study, analysis of transcriptome profile shows in detail the complex heterogeneity in biological process and pathways of rat hippocampal layers.

### Acknowledgement

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