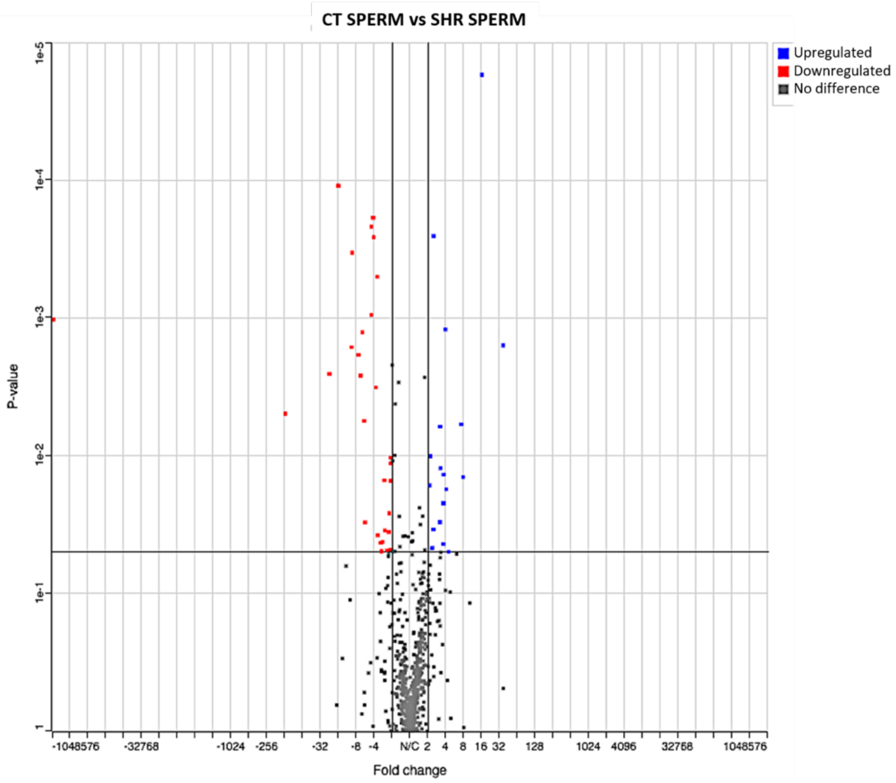
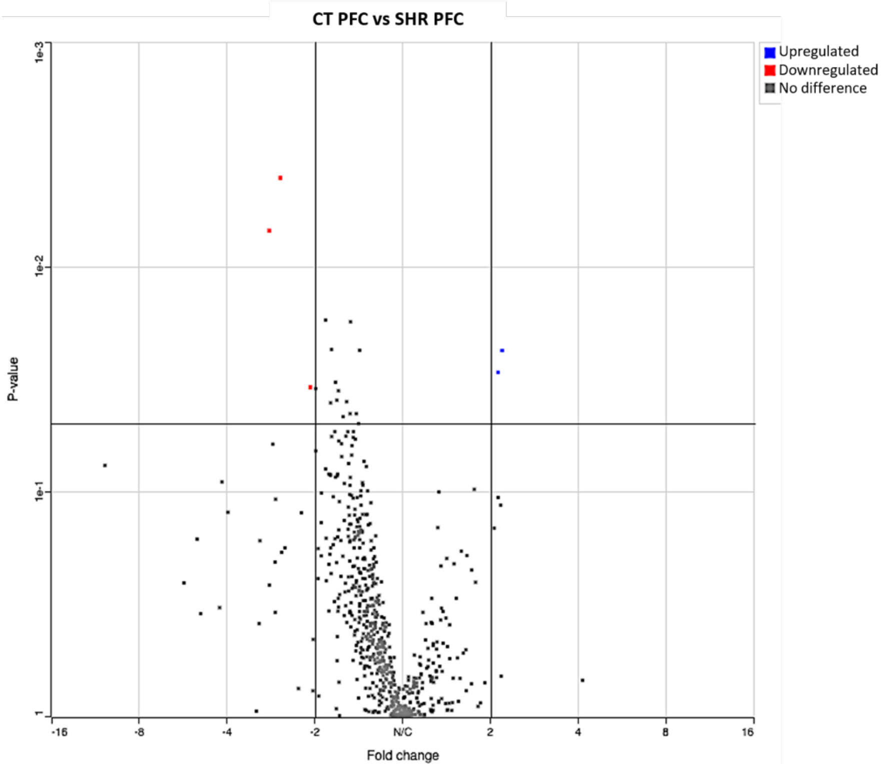
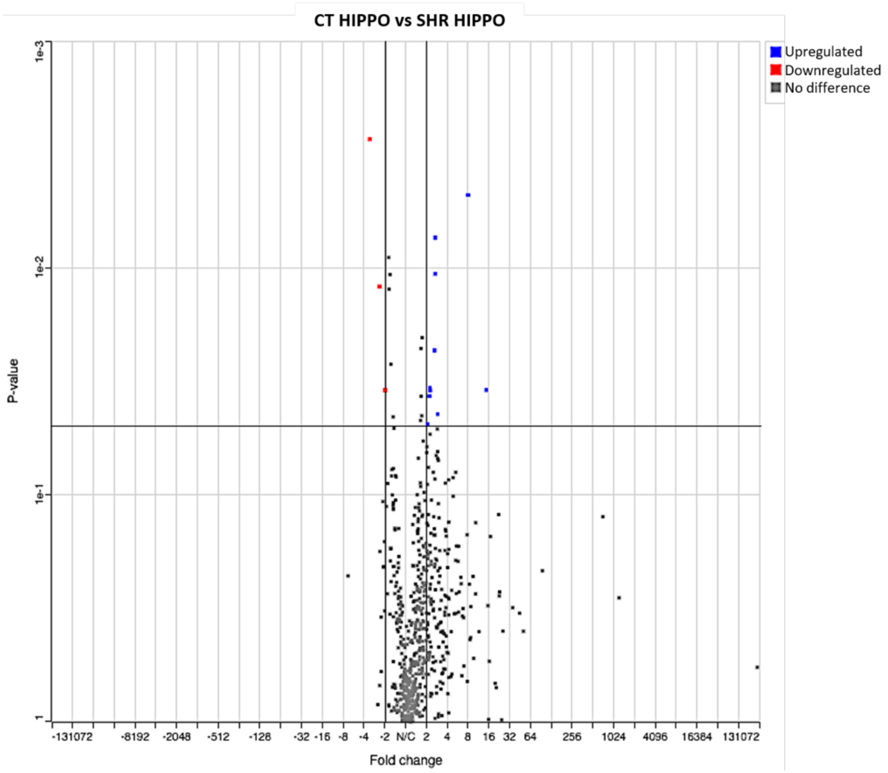
SUPPLEMENTARY MATERIAL



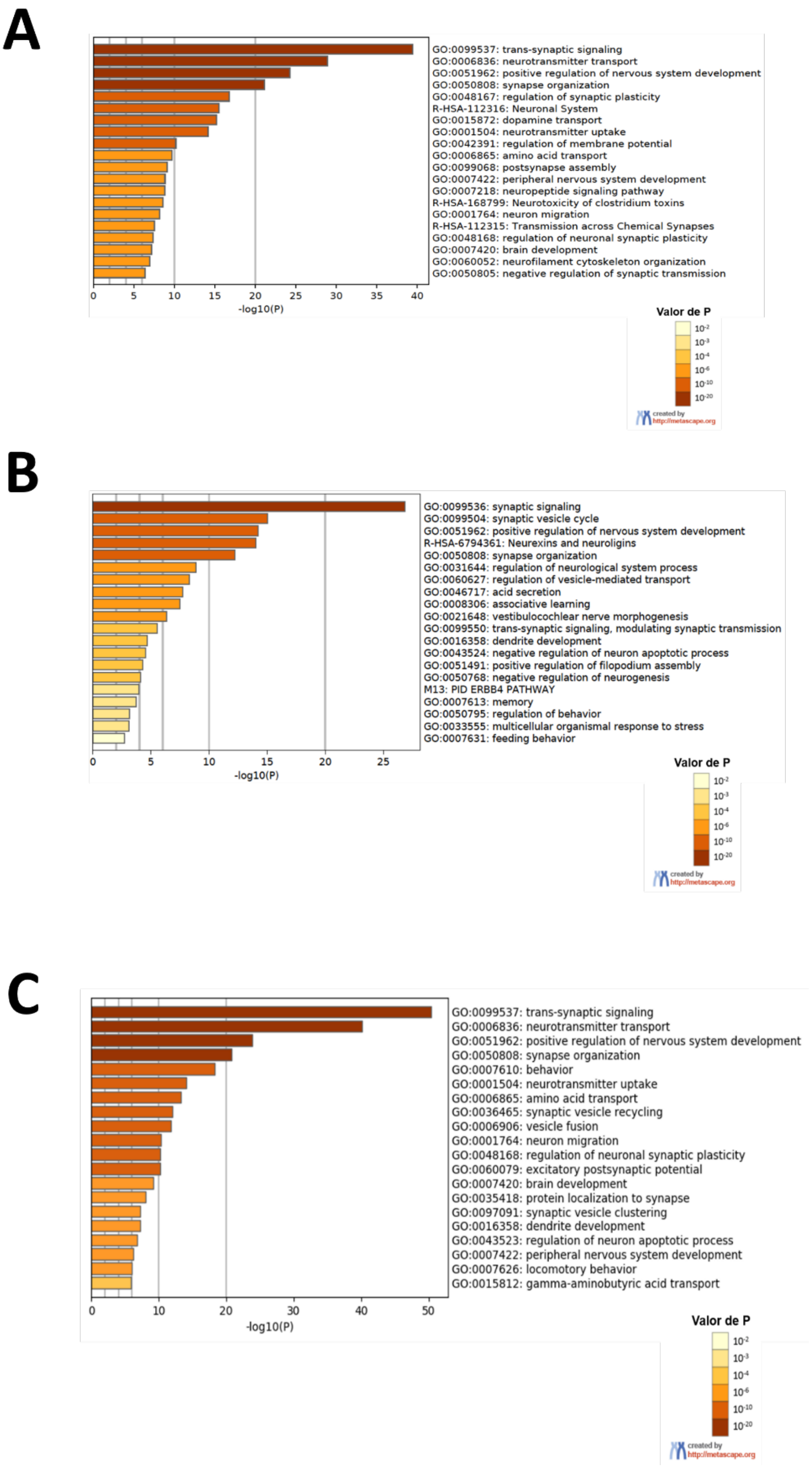
Suppl. Fig. 1: Volcano Plot: miRNAs expression in SPERM. Dots above the black horizontal line indicate the miRNAs whose expression analysis showed a value of p <0.05. Gray dots represent miRNAs that showed no significant difference in expression between the two groups. The red and blue dots represent hypoexpressed and hyperexpressed miRNAs, respectively. Vertical lines: Fold change of ± 2.



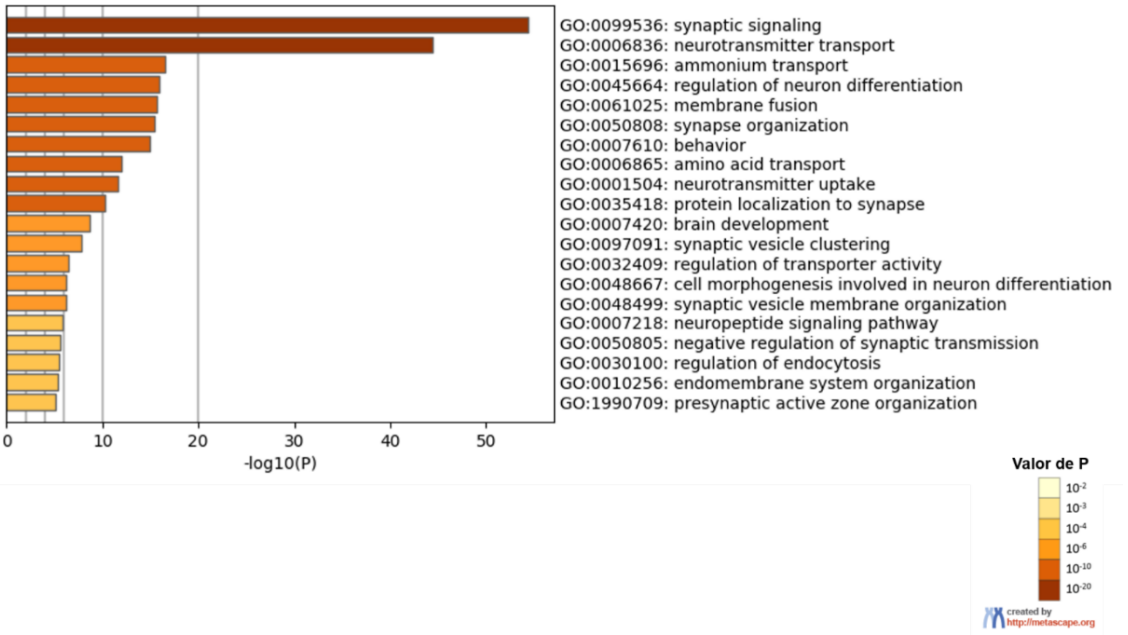
Suppl. Fig. 2: Volcano Plot: miRNAs expression for CPF. Dots located above the black horizontal line indicate the miRNAs whose expression analysis showed a value of p <0.05. The gray dots represent miRNAs that showed no significant difference in expression between the two groups. The red and blue dots represent hypoexpressed and hyperexpressed miRNAs, respectively. Vertical lines: Vertical lines: Fold change of ± 2.



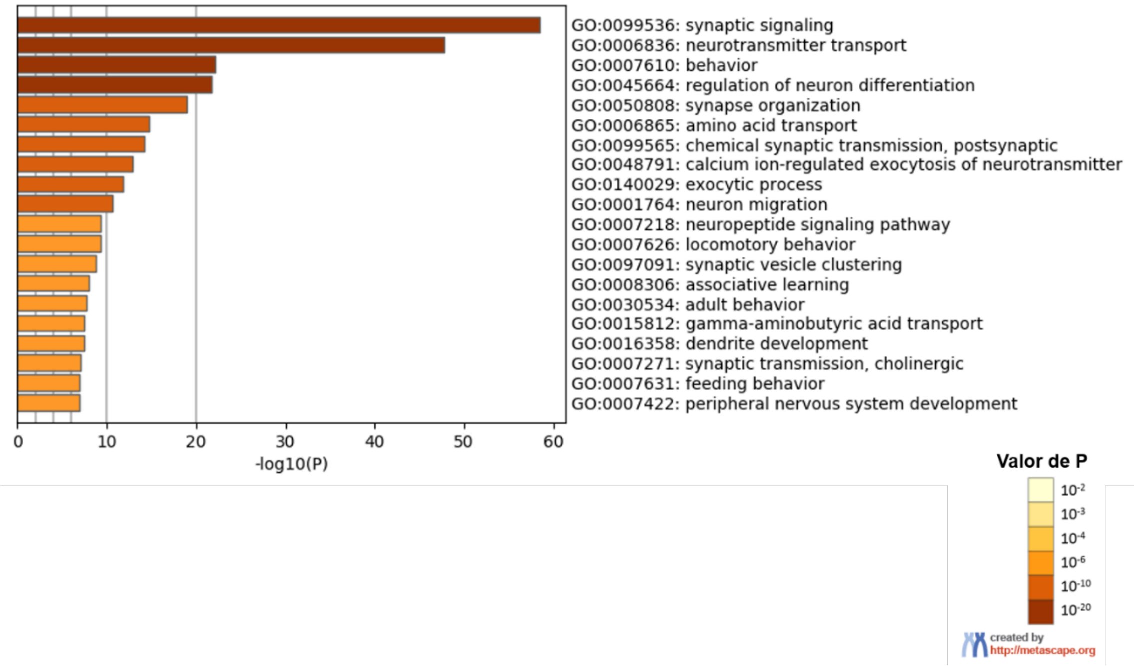
Suppl. Fig. 3: Volcano Plot: miRNAs expression in HIPO. Dots located above the black horizontal line indicate the miRNAs whose expression analysis showed a value of p <0.05. Gray dots represent miRNAs that showed no significant difference in expression between the two groups. The red and blue dots represent hypoexpressed and hyperexpressed miRNAs, respectively. Vertical lines: Vertical lines: Fold change of ± 2.



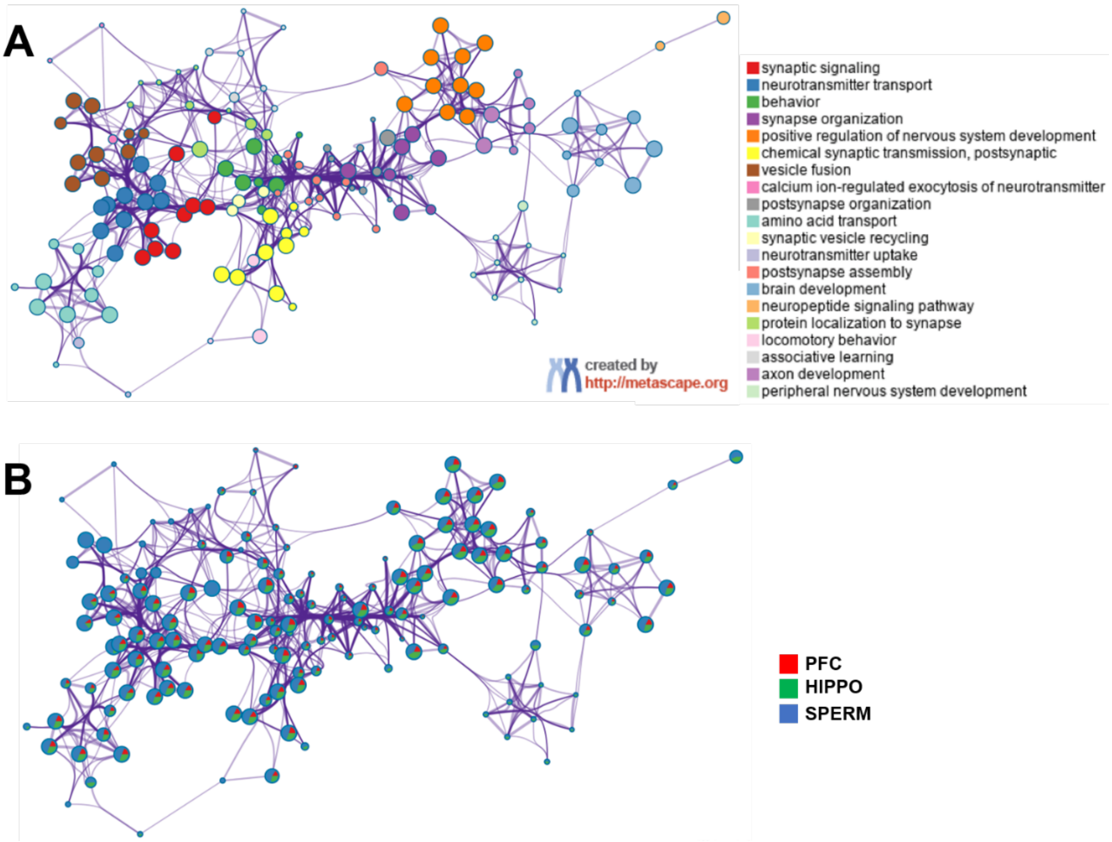
Suppl. Fig. 4: Representation of the biological phenomena in which the DE miRNA in SPERM are involved. The colors of the bars indicate the values of P; the darker the colors, the lower the P value. Analysis was performed using the human database. **A**: Part 1; **B**: Part 2; **C**: Part 3.



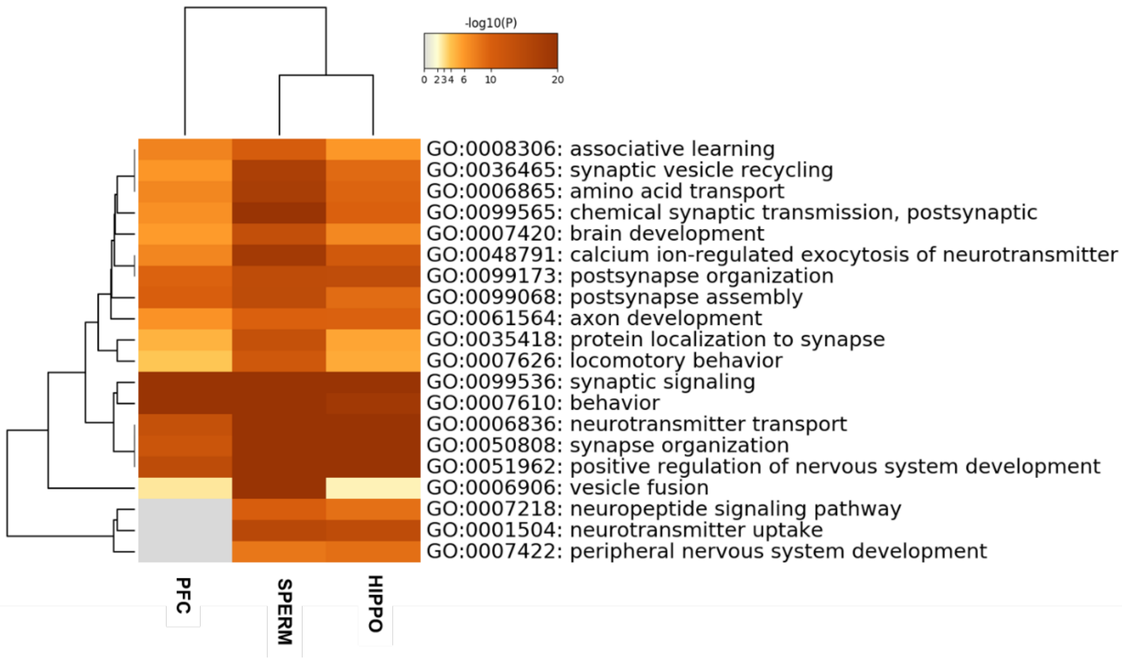
Suppl. Fig. 5: Representation of the biological phenomena in which the DE miRNA in PFC are involved. The colors of the bars indicate the values of P; the darker the colors, the lower the P value. Analysis was performed using the human database.



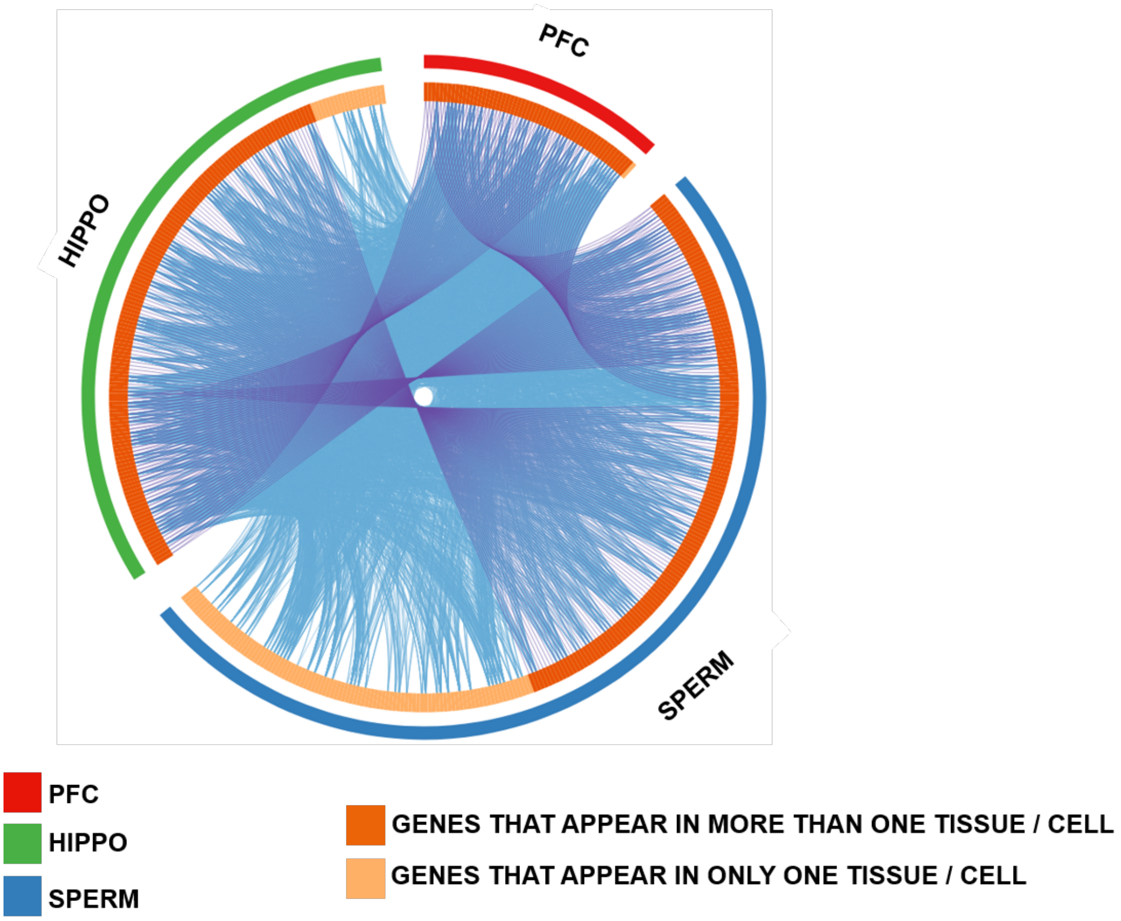
Suppl. Fig. 6: Representation of the biological phenomena in which the DE miRNA in HIPPO are involved. The colors of the bars indicate the values of P; the darker the colors, the lower the P value. Analysis was performed using the human database.



Suppl. Fig. 7: Enrichment network (Gene Ontology Enrichment) in which the nodes represent the hits involved in each biological process. In **A**, each process is represented by a color. The size of the nodes indicates the amounts of genes involved in the hits and the purple lines between the nodes represent their interactions. Analysis was performed using the human database. In **B** the nodes are represented as pie charts. Each portion of the pie represents a type of sample, and the size of each portion represents the proportion of each hit in each type of sample. Each hit includes the genes involved in biological processes, which are identified by the colors in **A**.



Suppl. Fig. 8: Hierarchical heatmap illustrating the relationship between the identified biological processes and between three type of samples. The colors of the rectangles indicate the P values; the darker the colors, the lower the value of P. It is observed that there is considerable similarity between the hippocampus and sperm. Behavior, synaptic organization and synaptic signaling appear as processes that could be significantly affected in the three types of sample. Analysis was performed using the human database.



Suppl. Fig. 9: Circus Plot illustrates how differently expressed miRNA target genes coincide between the three types of sample. The outermost arches, represented in blue, red and green, indicate sperm, prefrontal cortex and hippocampus, respectively. The internal arcs, represented in dark orange and light orange, represent the genes that appear in more than one type of sample or in a single type of sample, respectively. The purple lines indicate genes that appear in more than one type of sample. The blue lines link genes that are in the same "gene ontology term" in different types of sample. Analysis was performed using human database.