



Figure 2. The seeds AGCAGC and GAGGUA are very represented in the miRNAs potentially regulating the selected pathway.

are typically neuronal), and the predicted involved miRNAs are shown in Fig. 1. The abundance of each seed sequence represented in the miRNAs highlighted from our research are shown in Fig. 2.

Discussion

All the predicted miRNA-mRNA interactions need an experimental validation, and the zebrafish model can be used for some experimental approach [6]. Among the miRNAs we identified the miR-194b, that could act on GLUD1, GS2 and CAT-4; two different miRNAs (miR-738 and miR-132*) could regulate both NOS-1 and the glutamate NMDA receptor, two molecules that are functionally linked [7]. In this perspective, single miRNA reveals potentially able to mediate more points of the same metabolic pathway.

Some cues indicate also a relationship between a pathway and some seed sequences, and this would deserve further investigation. The use of integrated computational protocols allow for planning an experimental validation on a limited number of target reducing time and costs of pilot validation.

References

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