SUPPLEMENTARY FILE LEGENDS

Additional File 1. Brain samples informations

Clinicopathological information of the LOAD and control brain samples utilized for RNAseq and qRT-PCR in the study.

Additional File 2. Gene expression profile of LOAD and control hippocampi

RNAseq data showing the expression of protein-coding genes (PCGs), long intergenic ncRNAs (lincRNAs) and antisense RNAs in the hippocampi of 4 LOAD patients and 4 controls.

Additional File 3. Genes differentially expressed in LOAD hippocampus

Differentially expressed protein-coding genes (PCGs), long intergenic ncRNAs (lincRNAs) and antisense RNAs in the hippocampi of 4 LOAD patients and 4 controls

Additional File 4. RNAseq and qRT-PCR correlation analysis.

Pearson correlation analysis of log2 fold change differences from RNAseq and qRT-PCR data for 6 different protein coding genes, 6 lincRNAs and 6 AS RNA transcripts.

Additional File 5. Gene expression changes showing in vitro differentiation of human NSCs into a mixed population of neural cells.

qRT-PCR analysis of the expression of the neural stem cells marker Nestin and different neuronal markers (NFH, DCX, bIII-Tub) in RNA isolated from human NSCs differentiated for 21 days. On the Y axe is depicted the expression of the analyzed gene relative to the housekeeping gene β-ACTIN. Gene expression is normalized to hNSCs.

Additional File 6. Expression of genes nearby LOAD-dysregulated lncRNAs upon KCl-induced depolarization of human neural cells.

qRT-PCR analysis showing expression changes 1h post KCl stimulation of genes located nearby LOAD-dysregulated lncRNAs. EBF3, MGMT and Linc00959 are located nearby EBF3-AS. OGFRL1 is located nearby AD-linc2. On the Y axe is depicted the expression of the analyzed gene relative to the housekeeping gene β-ACTIN. Gene expression is normalized to non-treated cells. Error bars are S.D.

Additional File 7. qPCR Primers sequence.