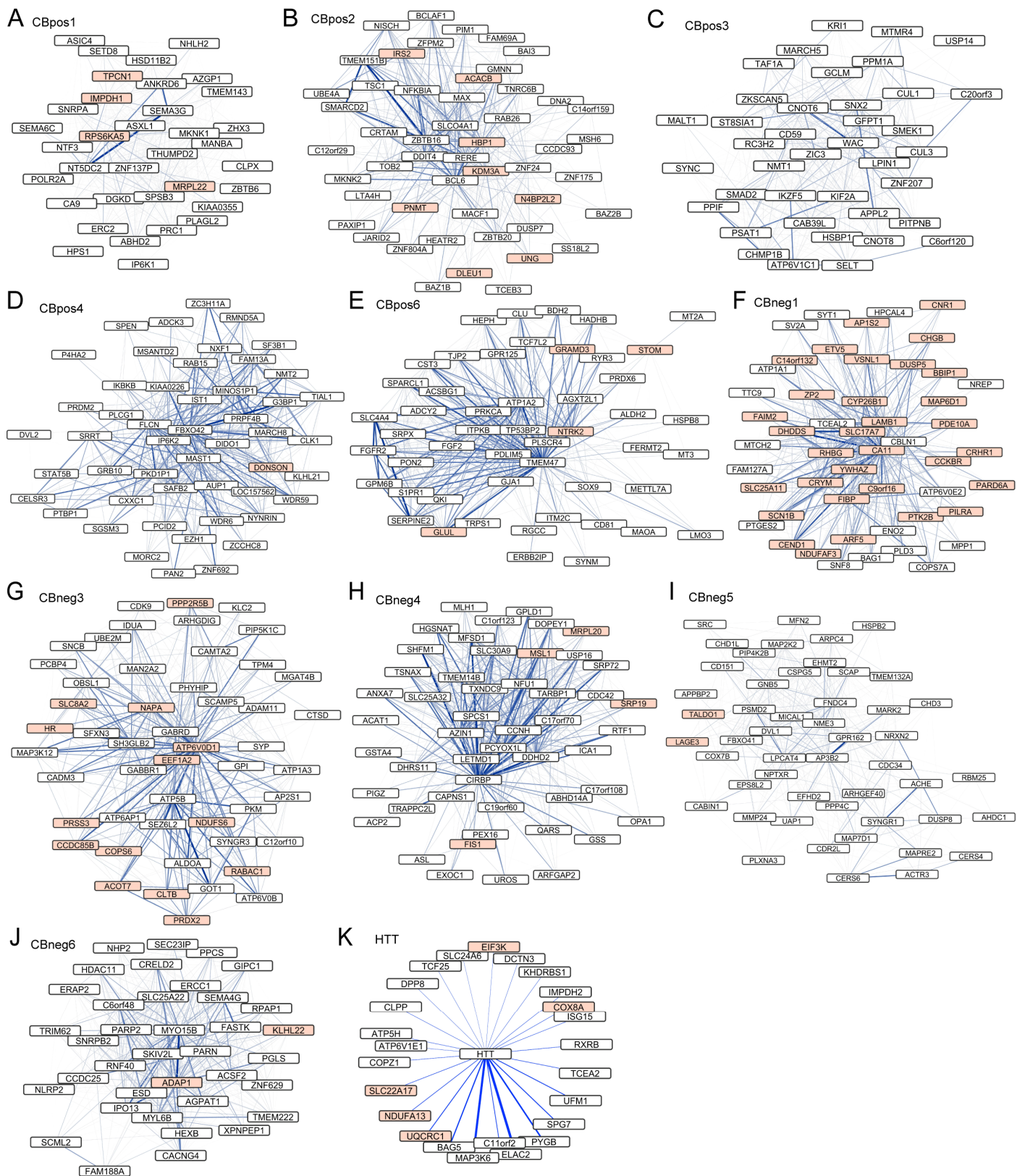




Additional data file 2. Visualization of hub genes in cerebellum network modules. **(A - K)** The 50 most connected genes (nodes) and the 500 strongest gene-gene interactions (edges) in each module are shown. The width and the color saturation of the lines (edges) correspond to the weight of the interactions. The orange highlighted nodes correspond to genes that were also statistically significantly dysregulated [27]. The hub genes for the positively correlated modules **A** to **E** and for the negatively correlated modules **F** to **J** are shown. **HTT** is a member of the **CBneg2** module in the cerebellum network. Its 25 strongest interactions are shown in **K**.