

Description of Additional Supplementary Files

Supplementary Data 1: CELF2 CLIP-seq peak sequences and statistical information.

Mouse CELF2 CLIP-seq was performed using stable Neuro2A cell line expressing biotin-tagged CELF2. After the reads were trimmed and cleaned, they were aligned to mouse genome (mm9) with STAR 2.5.2b. ChIPseeker was used to annotate and associate the peaks. CLIP-seq peaks from whole cell lysate, cytoplasmic fraction and nucleus fraction are listed. Fold enrichment, $-\log_{10}(\text{p-value})$ and adjusted P value $[-\log_{10}(\text{q-value})]$ are listed for each peak.