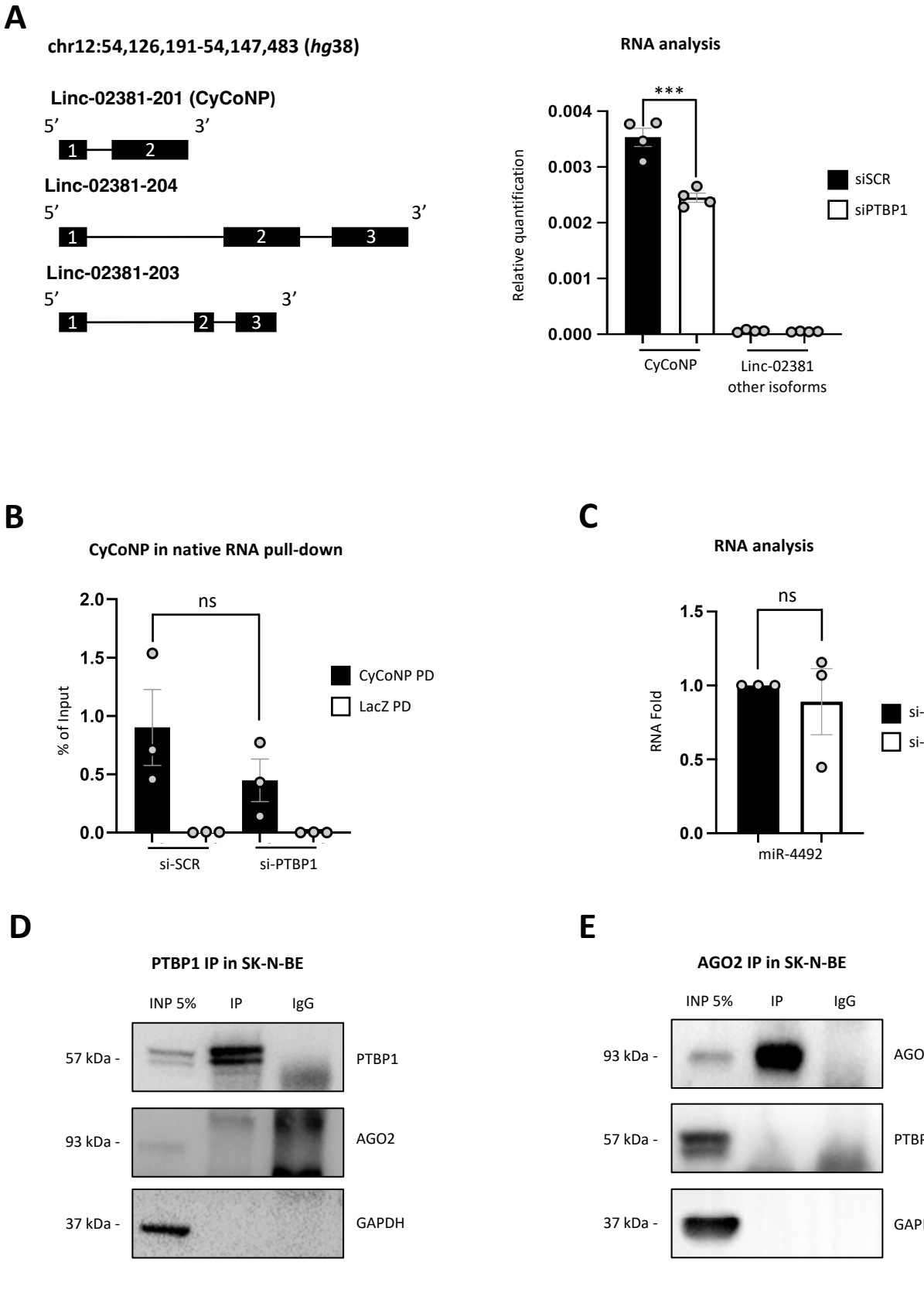
Supplemental Figure 2



Supplemental Figure 2

A) Left: schematic representation of Linc-02381 locus structure according to the *hg38* version of the human genome. Exons are numbered and represented as bold lines. Right: RT-qPCR quantification of linc-02381-201 (CyCoNP) and linc-02381 other isoforms transcripts in SK-N-BE cells (D 1.5) treated with si-SCR or siPTBP1. Data were normalized to GAPDH transcript and represent means ± SEM of four biological replicates.

B) RT-qPCR quantification of CyCoNP transcript in the specific pull-down (CyCoNP PD) and in the control (LacZ PD) performed on SK-N-BE cells (D 1.5) treated with si-SCR or si-PTBP1. Values are expressed as percentage (%) of Input and represent means ± SEM of three biological replicates.

C) RT-qPCR quantification of miR-4492 transcript in SK-N-BE cells (D 1.5) treated with si-SCR or si-PTBP1. Data were normalized to miR-93-3p transcript (a cytoplasmic microRNA expressed at a comparable level of miR-4492) and represent means ± SEM of three biological replicates.

D) Western blot analysis of the retrieved protein fractions in PTBP1 IP and IgG samples. GAPDH protein serves as a loading control. Input (Inp) sample represents 5% of the total protein extract.

E) Western blot analysis of the retrieved protein fractions in AGO2 IP and IgG samples. GAPDH protein serves as a loading control. Input (Inp) sample represents 5% of the total protein extract.

Data information: ns (non-significant) $p > 0.05$, ***$p < 0.001$, unpaired Student's t test.