OMTN, Volume *22*

Supplemental Information

Preeclampsia-Associated lncRNA *INHBA-AS1* Regulates the Proliferation, Invasion, and Migration of Placental Trophoblast Cells

Sijia Jiang, Qian Chen, Haihua Liu, Yue Gao, Xiaoxue Yang, Zhonglu Ren, Yunfei Gao, Lu Xiao, Mei Zhong, Yanhong Yu, and Xinping Yang

SUPPLEMENTAL INFORMATION

Contents

Supplemental figures

Supplemental tables

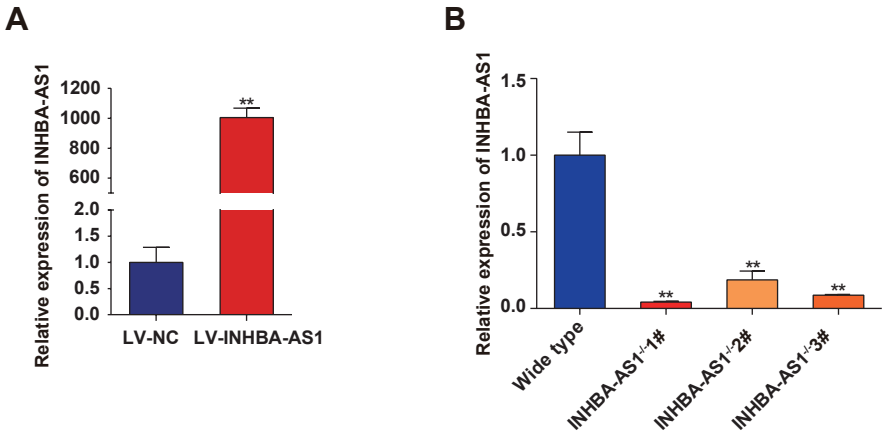

Figure S1. Overexpression and knockout of INHBA-AS1. (Refers to Figure2,3)

（A）INHBA-AS1 expression in HTR-8/SVneo cells, detected by qRT-PCR: Red bar: cells transfected with full-length human INHBA -AS1; blue bar: cells transfected with empty vector. （B）INHBA-AS1 expression in HTR-8/SVneo cells, detected by qRT-PCR. Red bars: INHBA-AS1 knockout by CRISPR/Cas9; blue bar: without knockout.

LV represents Lentivirus, NC represents normal control. The values are shown as the mean ± SD of three independent experiments; **P<0.01.

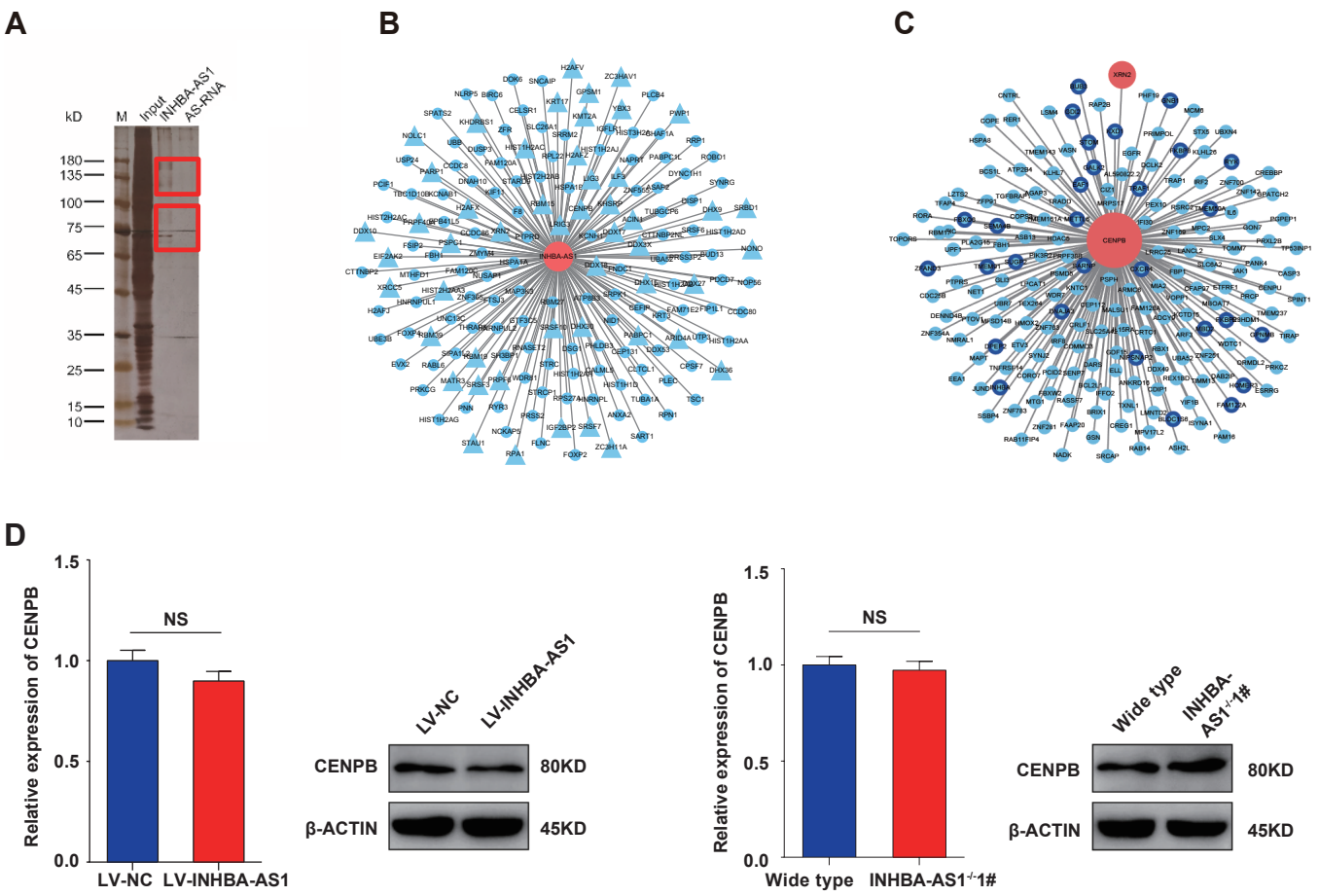

Figure S2. INHBA-AS1 binding proteins. (Refer to Figure4)

(A)The silvery staining of the proteins pulled down by INHBA-AS1 in polyacrilamide gel. (B) Network of INHBA-AS1 and its binding proteins detected by pulldown and mass spectrometry. (C) Network of transcription factor CENPB and its target genes. (D) Expression level of transcription factor CENPB in HTR-8/SVneo cells with INHBA-AS1 overexpression or knockout. Left panel: qRT-PCR results; right panel: western blotting results. LV represents Lentivirus, NC represents normal control. The values are shown as the mean ± SD of three independent experiments.

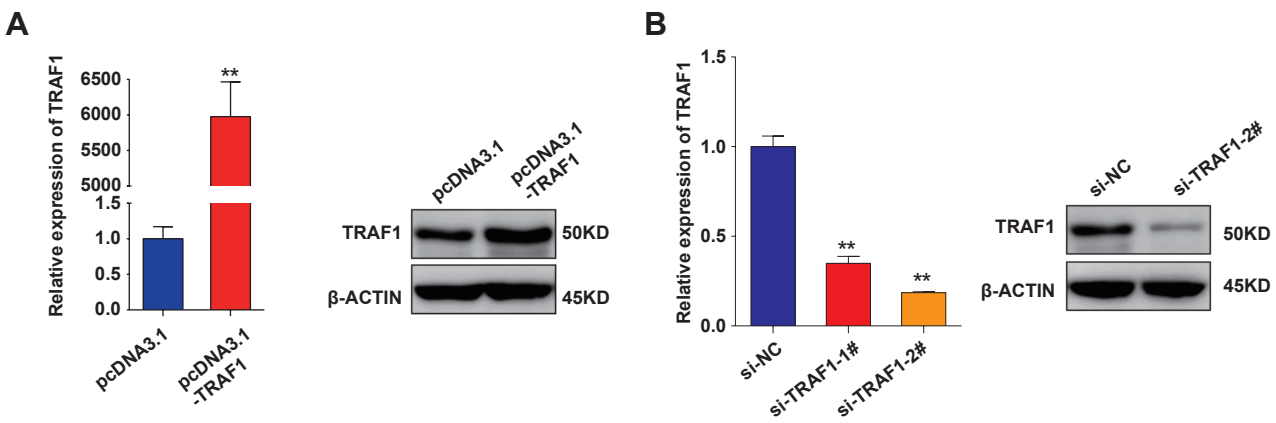

Figure S3. The Efficiency after overexpression or knockdown of TRAF1 in HTR-8/SVneo. (Refer to Figure6)
(A) The expression of TRAF1 in HTR8/SVneo cells with TRAF1 over-expression. Left panel: qRT-PCR results; right panel: western blotting results. (B) The expression of TRAF1 in HTR8/SVneo cells with TRAF1 knockdown. Left panel: qRT-PCR results; right panel: western blotting results. NC represents normal control. The values are shown as the mean ± SD of three independent experiments; **P<0.01.

Supplemental table legends

Tables S1-S5 are uploaded separately as excel files.

Table S1. INHBA-AS1-protein-interactions. (Refers to Figure1)

Sheet1. INHBA-AS1-protein-interactions collected from databases and predicted by catRAPID omics.

Sheet2. The enrichment pathways of DEG of INHBA-AS1-TF targeting genes.

Table S2. Mass spectrometry results of INHBA-AS1 pulldown. (Refers to Figure4)

Table S3. Targets of TFs interacting with INHBA-AS1. (Refers to Figure4)

Sheet1. All TFs interacted with INHBA-AS1 and corresponding target genes.

Sheet2. All TFs and corresponding target genes which differentially expressed in EOSPE.

Sheet3. Targets of transcription factor interacting with INHBA-AS1 enriched with DEGs in EOSPE.

Table S4. Top 20 TFs in “INHBA-AS1-TF-target” network based on the node betweenness centrality. (Refers to Figure4)

Table S5. Primer sequences. (Refers to Figure1,4,5,6)