Expanded View Figures

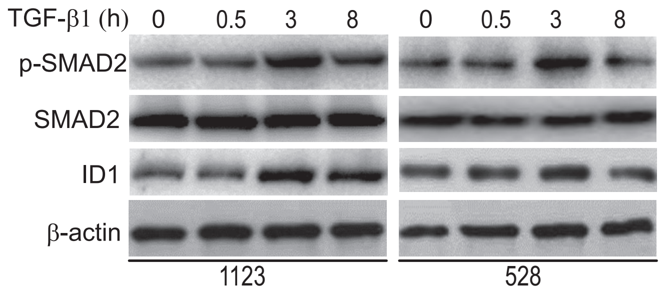

Figure EV1. TGF-β activated SMAD2 phosphorylation and ID1 expression in GSCs.

Western blotting of TGF-β-activated SMAD2 phosphorylation and ID1 expression in GSCs. 1123 and 528 GSCs were pre-cultured for 16 h in DMEM/F12 medium with EGF (2 ng/ml) and bFGF (2 ng/ml) and then followed by co-culturing with or without 20-μg/ml TGF-β1 for the indicated times. Data are representative of three independent experiments.

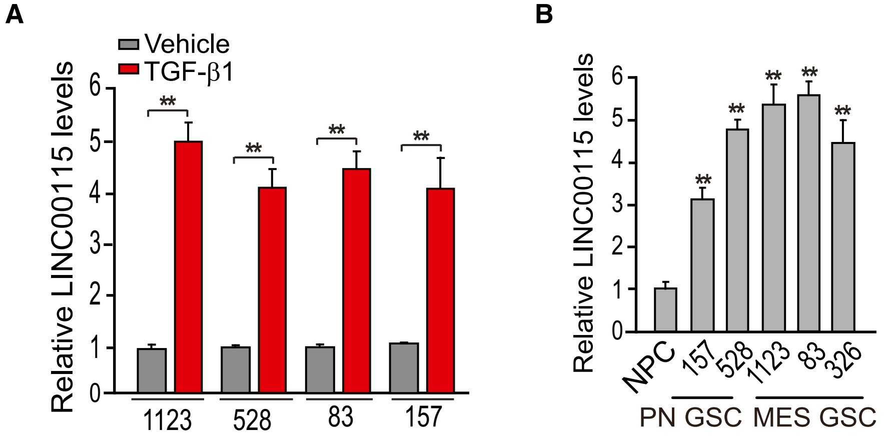

Figure EV2. qRT–PCR analysis of LINC00115 expression in GSCs.

- A qRT–PCR analysis of LINC00115 expression in 1123, 528, 83, and 157 GSCs stimulated with or without TGF-β for 3 h.
- B qRT–PCR analysis of LINC00115 expression in NPCs, PN, and MES GSCs.

Data information: In (A and B), data are representative of three independent experiments. Error bars, ± SD. $^{**}P < 0.01$, by two-tailed *t*-test.

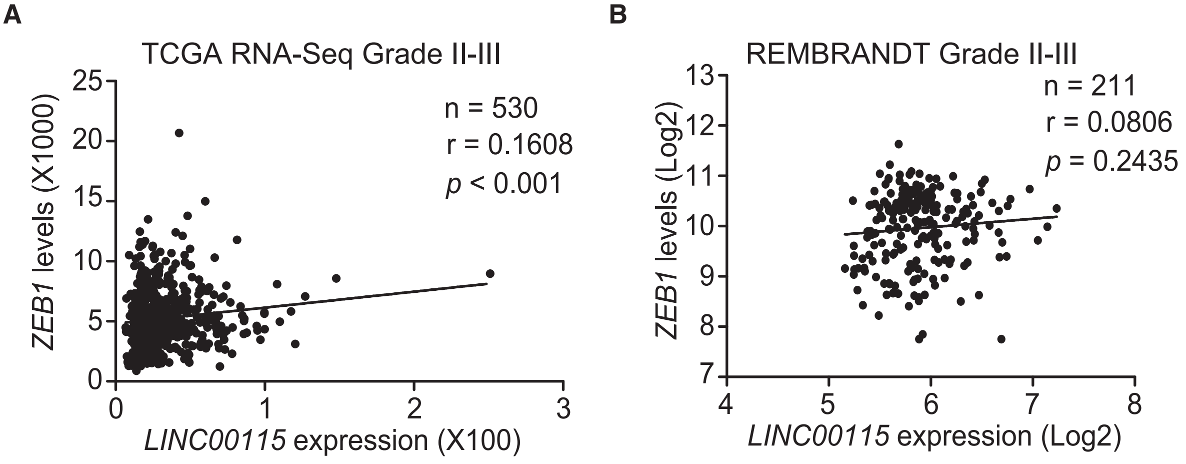

Figure EV3. Correlation of expression between *LINC00115* and *ZEB1* in grade II-III glioma specimens.

Corresponding to Fig 4A and B. Correlation of expression between *LINC00115* and *ZEB1* in grade II-III glioma specimens from TCGA RNA-Seq (A) and REMBRANDT array dataset (B). Statistical analysis was performed by two-tailed *t*-test.

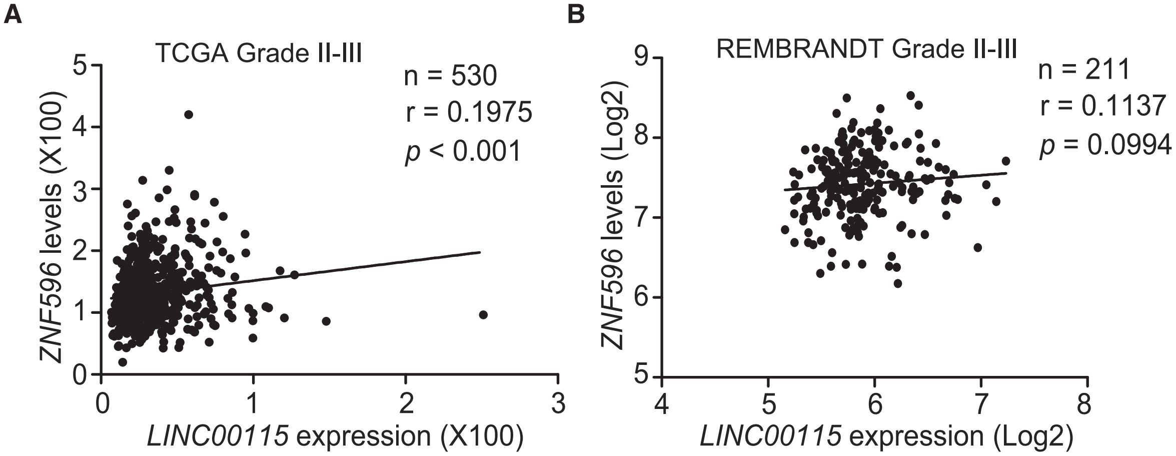

Figure EV4. Correlation of expression between *LINC00115* and *ZNF596* in grade II-III glioma specimens.

Corresponding to Fig 5J and K. Correlation of expression between *LINC00115* and *ZNF596* in grade II-III glioma specimens from TCGA RNA-Seq (A) and REMBRANDT array dataset (B). Statistical analysis was performed by two-tailed *t*-test.

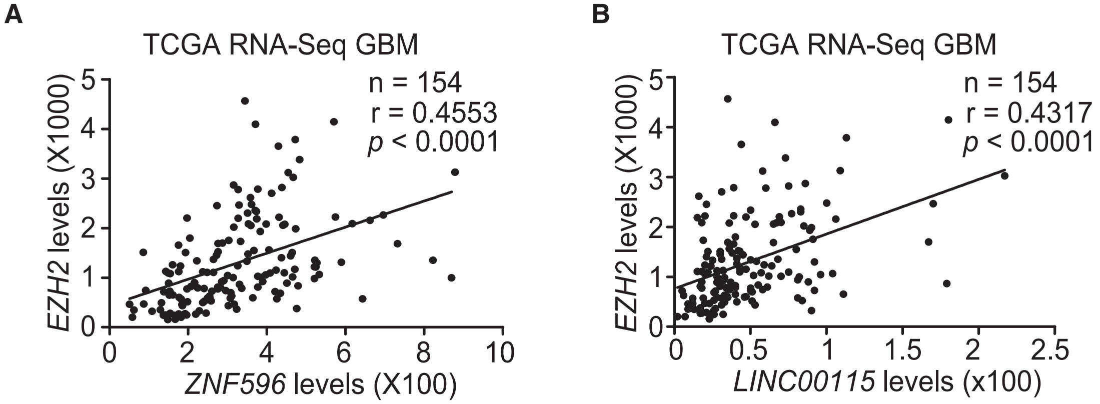

Figure EV5. Correlation of expression between *EZH2* and *ZNF596* or *LINC00115* in GBM specimens.

Correlation of expression between *EZH2* and *ZNF596* (A) or *LINC00115* (B) in GBM specimens from TCGA RNA-Seq dataset. Statistical analysis was performed by two-tailed *t*-test.