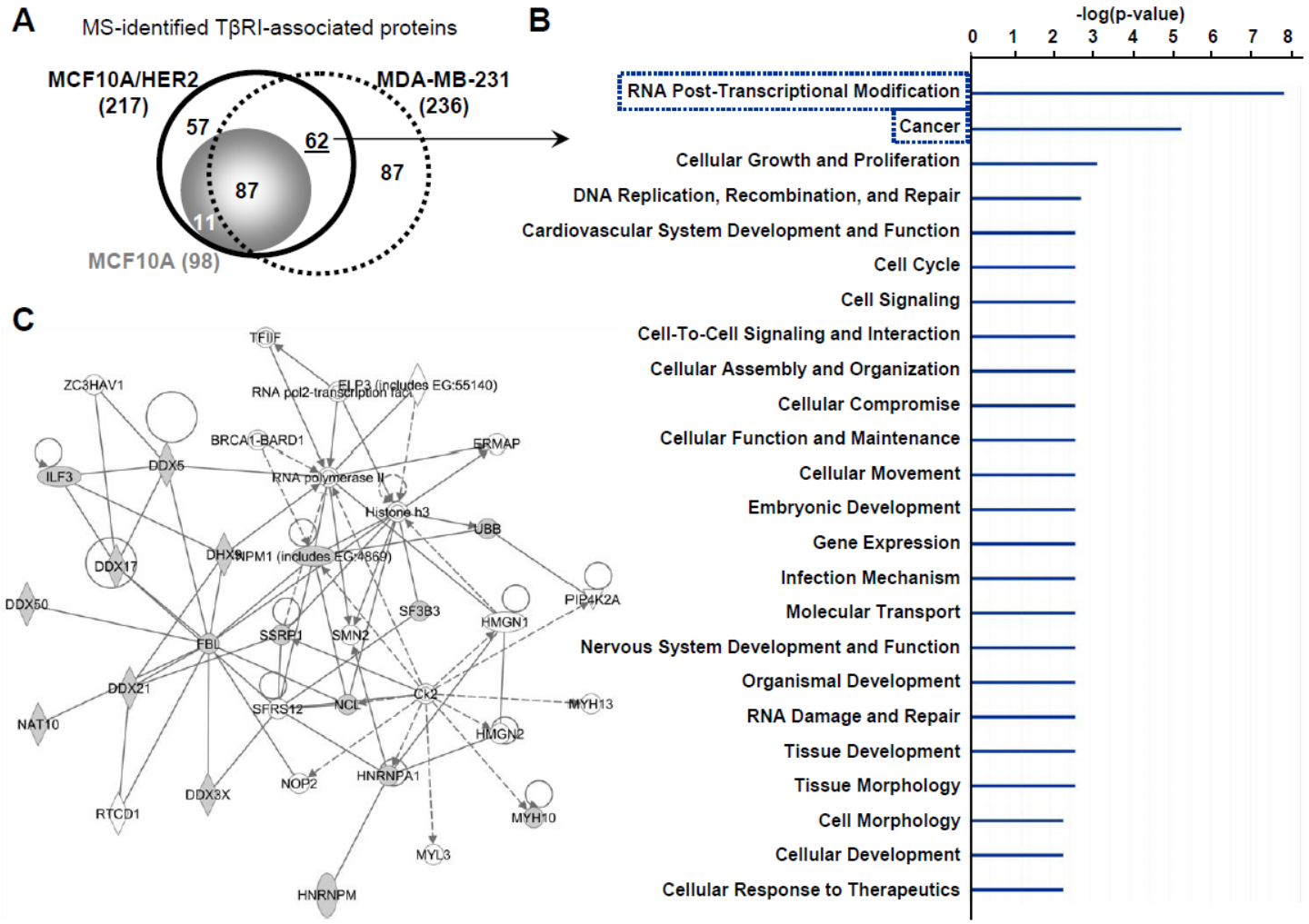
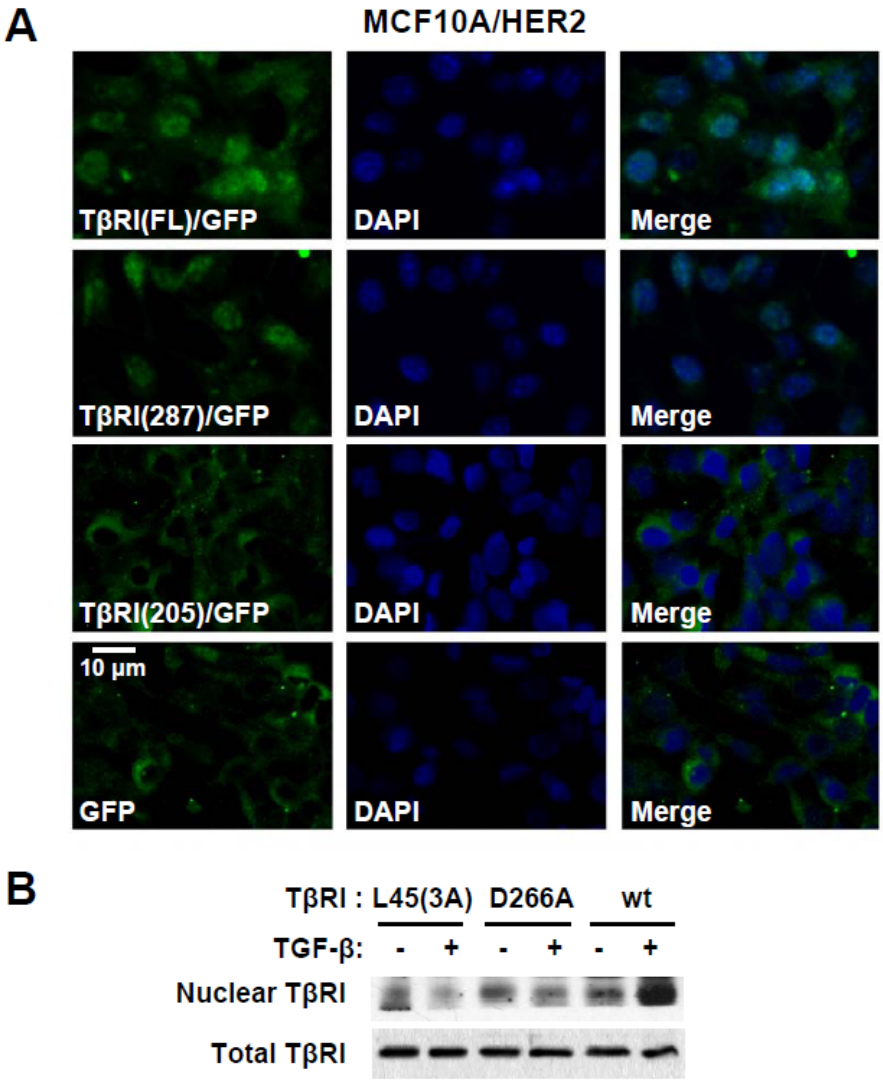
Supplemental Figure 1



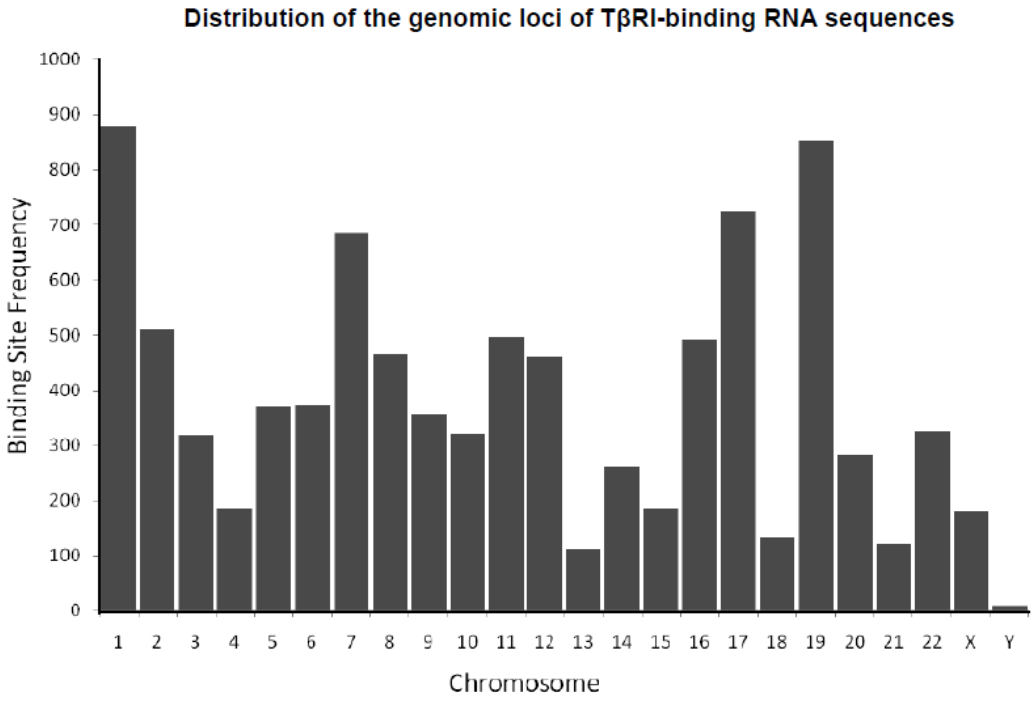
Supplemental Figure 1. Identification of TβRI-associated proteins in different cellular contexts. **A:** A summary of the numbers of TβRI-associated proteins identified in MCF10A, MCF10A/HER2, and MDA-MB-231 cells. **B:** Potential functions of identified TβRI-associated proteins as analyzed by Ingenuity Pathways Analysis (IPA). **C:** Proteins involved in the IPA-determined top functional network of RNA post-transcriptional modification. Proteins in grey indicate those identified in transformed cells by mass spectrometry.

Supplemental Figure 2



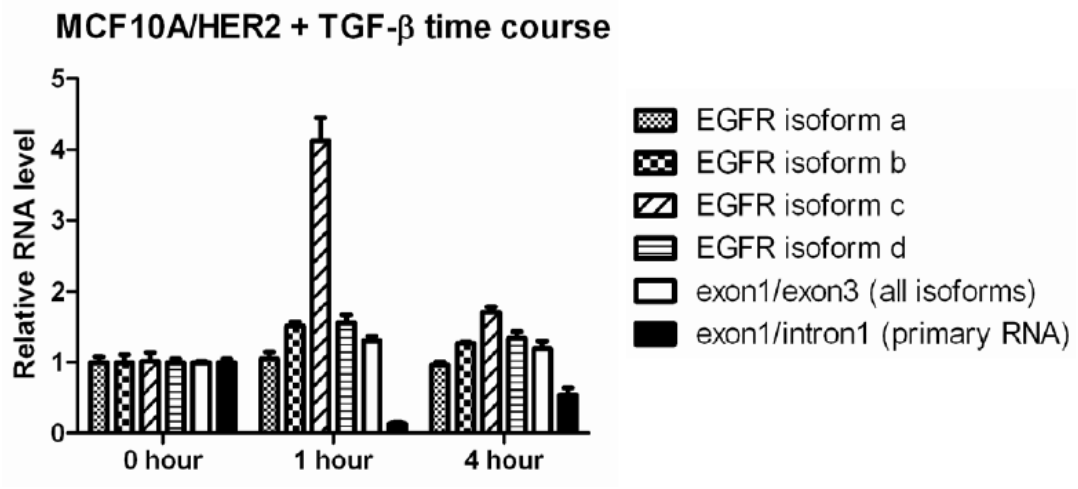
Supplemental Figure 2. Nuclear transport of TβRI mutants in MCF10A/HER2 cells. **A:** IFA images of TGF-β-treated MCF10A/HER2 cells expressing the GFP-fused TβRI constructs. **B:** MCF10A/HER2 cells transfected with HA-tagged wild-type TβRI, L45(3A) mutant or D266A mutant were treated with TGF-β for 0.5 h or left untreated, and the HA-tagged TβRI levels were analyzed in the nuclear fraction and whole cell lysates by Western blot.

Supplemental Figure 3



Supplemental Figure 3. Chromosomal distribution of identified TβRI-binding RNA sequences.

Supplemental Figure 4



Supplemental Figure 4. Time course of the TGF-β-induced splicing of EGFR isoform c. Quantitative RT-PCR of various EGFR-derived RNAs was performed using total RNA isolated from MCF10A/HER2 cells that were treated with TGF-β for 0, 1 or 4 h. Data was normalized to the level of GAPDH, and then compared to that in untreated cells (the first set of bars). Each data point represents the mean ± S.D. of 3 wells.