Figure S1. *Bioinformatics analysis of CGA* expression. (A) CGA expression in different cancer types. Different tumors showed inconsistent expression, with some upregulated and some downregulated. Data analysis was performed using cBioPortal (https://www.cbioportal.org/) (+ indicates data on gene CNA is present in this database). (B) CGA expression in seven different breast cancer high-throughput sequencing datasets. The expression rate is nearly 1%. Data analysis was performed using cBioPortal (https://www.cbioportal.org/). (C) Overall survival in CGA-upregulated breast cancer (P=0.365). Data analysis was performed at cBioPortal (https://www.cbioportal.org/). (D) CGA interaction-related protein prediction. Data analysis was performed at GENEMANIA (http://genemania.org). (E) Downregulation of PTPN12 expression was found following upregulation of CGA at the mRNA level in T-4D cells. ****P<0.001. CGA, glycoprotein hormone α-subunit; PTPN12, protein tyrosine phosphatase non-receptor type 12; CNA, copy number alteration.

