Supplemental files for “Inferences of individual drug responses across diverse cancer types using a novel competing endogenous RNA network”

Identification of ceRNAs across various cancer types

Human mature miRNA sequences were downloaded from the miRBase database (release 19) [1], and lncRNA sequences were obtained from the GENCODE database (v19) [2]. Previous studies indicated that lncRNAs could compete with mRNAs to bind miRNAs, which could then be detected using traditional miRNA target prediction algorithms [3-5]. The miRNA–lncRNA interactions were predicted using TargetScan (v.6.0) [6], PITA (March 2007 version) [7], miRanda (November 2010 version) [8] and RNAhybrid (v.2.1.1) [9] using the default parameters. To decrease the false positive rate of traditional prediction methods, miRNA–lncRNA interactions were filtered using AGO-CLIP-seq data [10], and then the experimentally validated miRNA–lncRNA interactions derived from DIANA-LncBase [10] and starBase v2.0 [11] were integrated. The miRNA–mRNA interactions were collected from TarBase (v6.0) [12] and mirTarBase (release 4.5) [13], which store manually curated collections of experimentally supported miRNA targets. For each cancer, the ceRNAs were identified by the following relationships. 1) miRNA–lncRNA and miRNA–mRNA interactions with a significant negative correlation of expression (Pearson correlation coefficient [PCC] < -0.3, $p < 0.05$) were retained [14, 15]. 2) The ceRNA triplet consisted of miRNA–lncRNA and miRNA–mRNA interactions sharing at least one miRNA [16]. 3) Expression of the lncRNA and mRNA in the ceRNA triplet were positively correlated (PCC > 0.3, $p < 0.05$) [17].

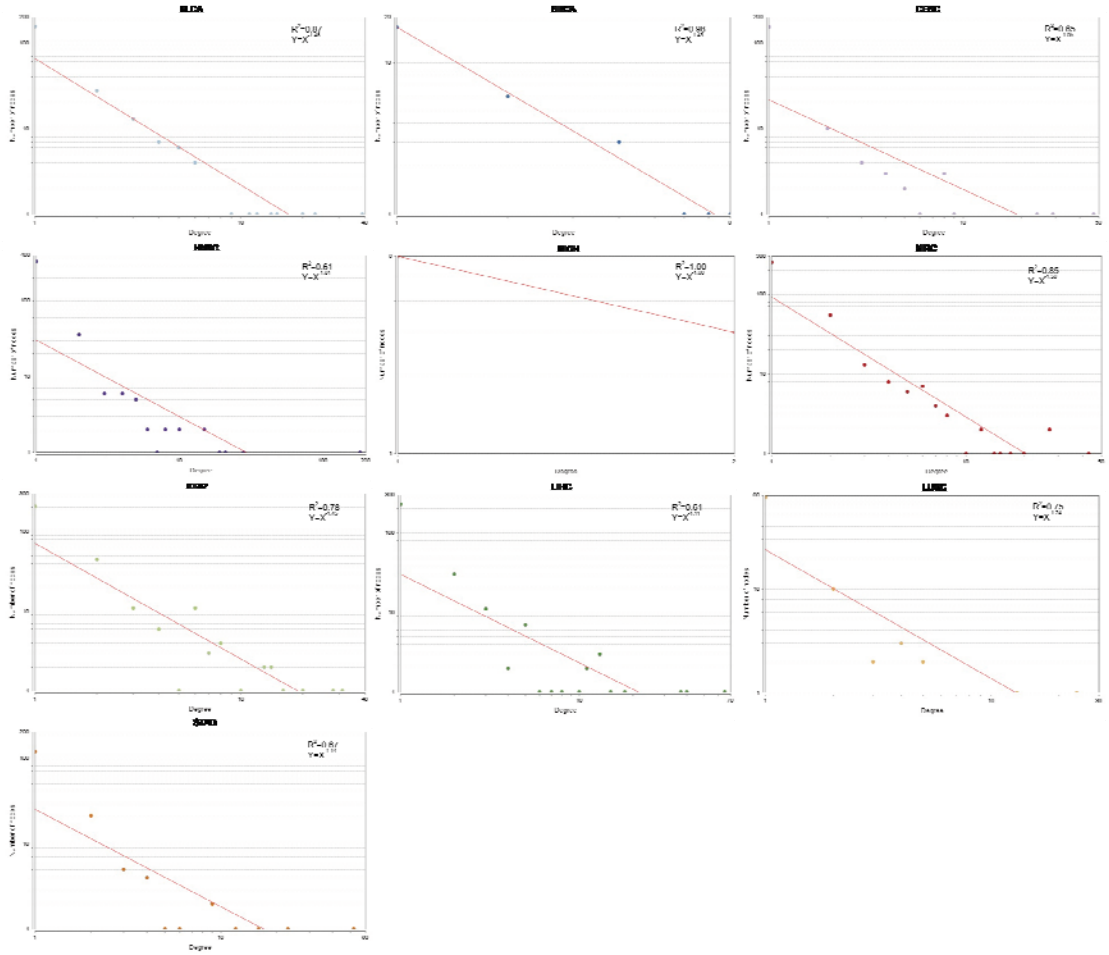

Figure S1. Degree distribution of the DRCE networks across 10 types of cancer. The x-axis is the ranked degree and the y-axis is the number of nodes at this rank. Most nodes are lowly connected and only a few are relatively highly connected. The examination of the degree distribution reveals a scale-free power-law distribution.

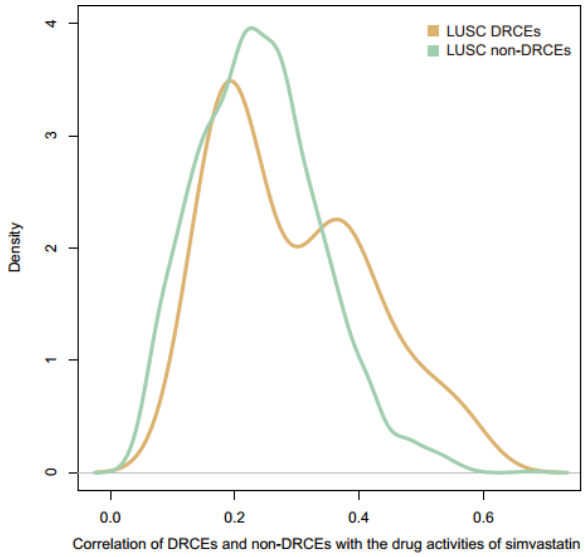

Figure S2. Correlation-density curves of LUSC DRCEs and non-DRCEs.

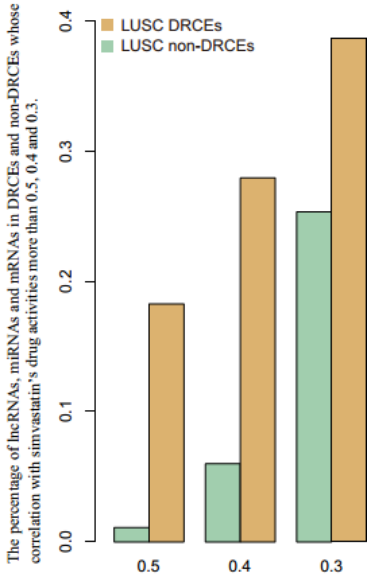

Figure S3. The percentage of lncRNAs, miRNAs and mRNAs in DRCEs and non-DRCEs whose correlation with simvastatin's drug activities more than 0.5, 0.4 and 0.3.

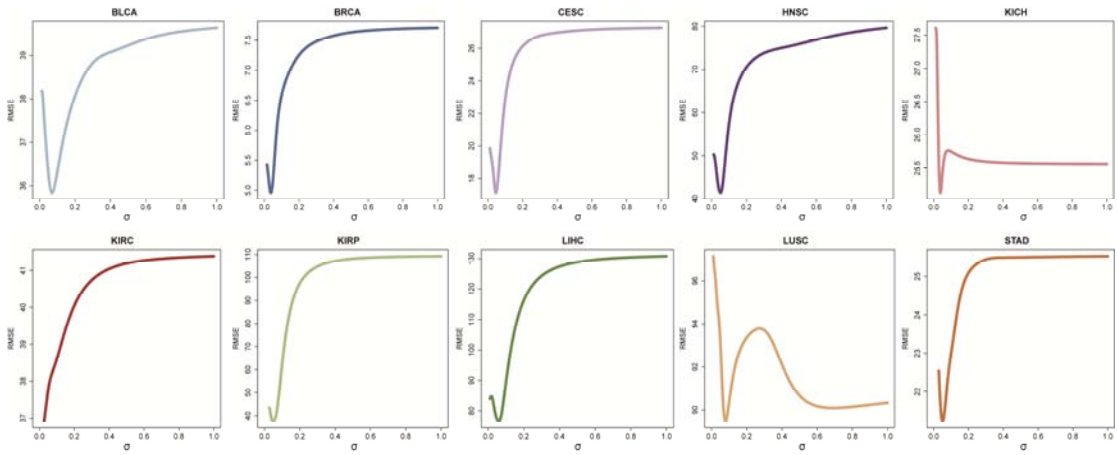

Figure S4. Parameter optimization of the patient-drug two-layer integrated network model. The RMSE range with a change in σ in 10 cancer types.

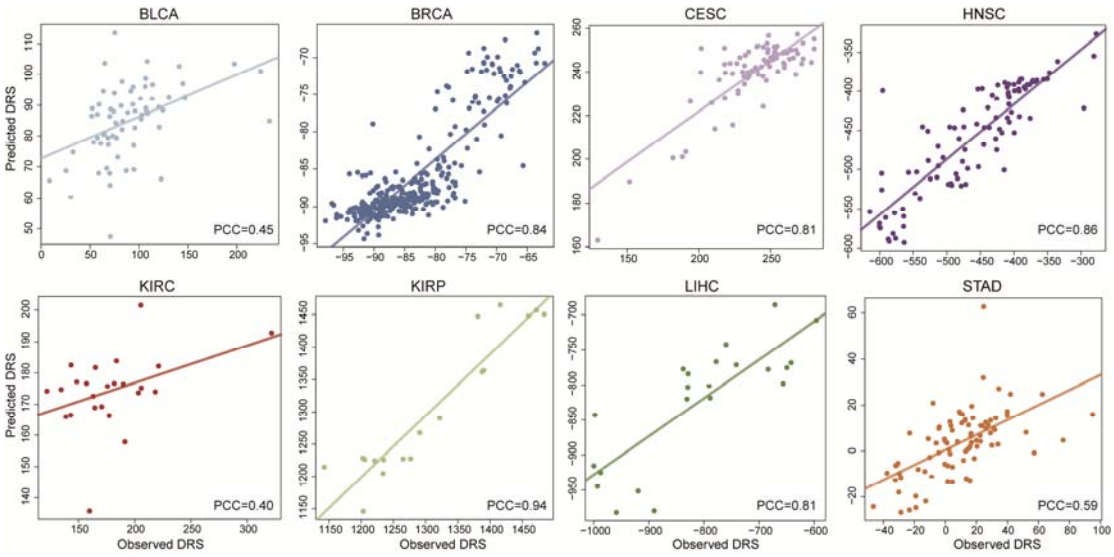

Figure S5. Scatter plots of observed and predicted DRS.

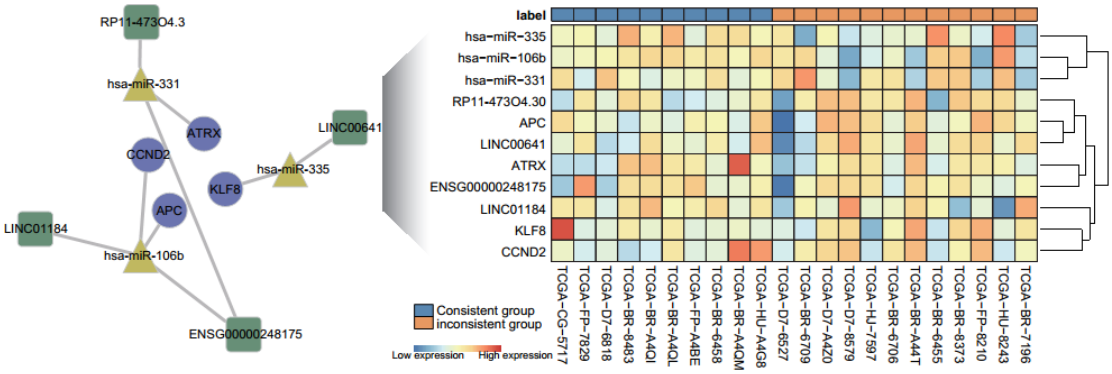

Figure S6. Expression of six STAD DRCEs (hsa-miR-335_KLF8_LINC00641, hsa-miR-106b_APC_ENSG00000248175, hsa-miR-106b_APC_LINC01184, hsa-miR-106b_CCND2_ENSG00000248175, hsa-miR-331_ATRX_ENSG00000248175 and hsa-miR-331_ATRX_RP11-473O4.3) in patients treated with 5-FU.

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