

Tissue-specific Co-expression of Long Non-coding and Coding RNAs Associated with Breast Cancer

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Supplementary Notes

Supplementary Figures Legends

Supplementary Figure S1. Unsupervised principal components analysis (PCA) of expressed transcripts in tumors and normal breast tissue. Tumor from breast cancer patients was indicated in red and normal breast tissue from healthy women was indicated in green. Scatter plots of principal components (PCs) for a) lncRNAs; and b) mRNAs; respectively.

Supplementary Figure S2. Volcano plots of the differential expression analysis in tumor and normal breast tissue. a) lncRNAs; and b) mRNAs. Vertical dotted lines denote fold change = ± 2 horizontal dotted line denote the FDR P -value = 0.01.

Supplementary Figure S3. Summary results for lncRNA *RP11-118E18.2* from TCGA BRCA dataset in TANRIC. a) Correlation analysis of the lncRNA expression level and ER status; b) correlation analysis of the lncRNA expression level and PR status; c) correlation analysis of the lncRNA expression level and PAM50; d) correlation

analysis of the lncRNA expression level and breast cancer therapy based molecular signatures; e) correlation analysis of the lncRNA expression level and *P53* mutation status.

Supplementary Figure S4: Functional enrichment for the mRNAs identified from differential expression analysis in our data.

Supplementary Figure S5: Ingenuity pathway analysis (IPA) of mRNAs that were differentially co-expressed with lncRNA *AC145110.1*. Green color represents down-regulated genes in breast tumor tissue, red color represents up-regulated genes in breast tumor tissue in our study.

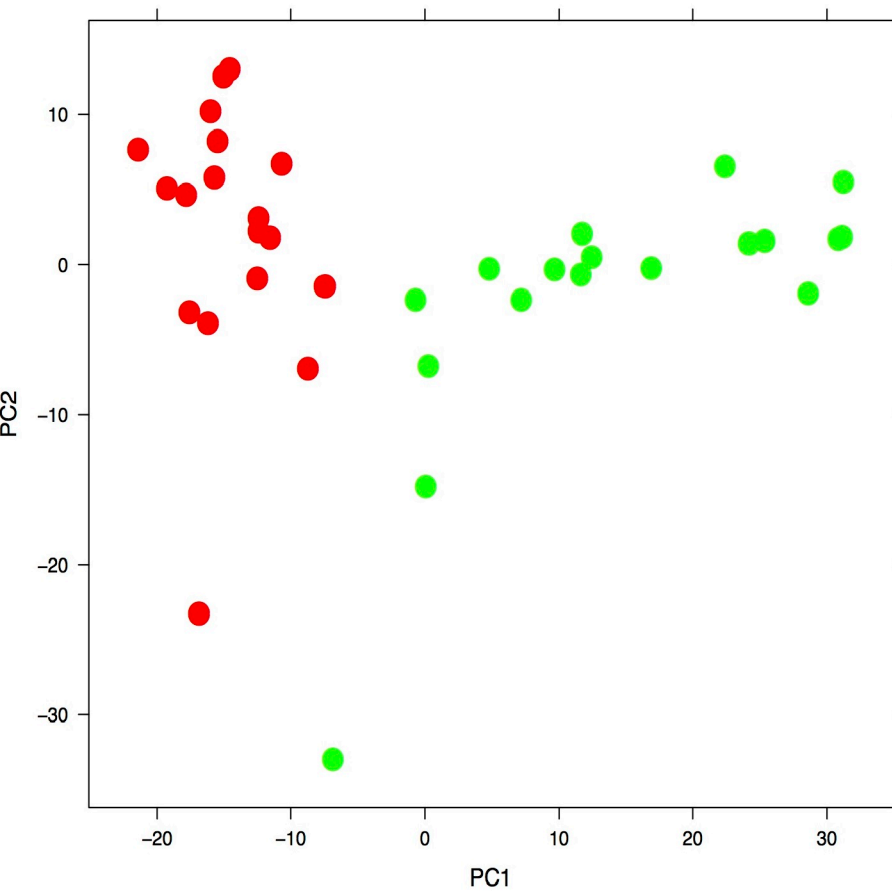
Supplementary Figure S6: Summary results for lncRNA *AC145110.1* from TCGA BRCA dataset in TANRIC. a) Correlation analysis of the lncRNA expression level and disease stage; b) correlation analysis of the lncRNA expression level and ER status; c) correlation analysis of the lncRNA expression level and HER2 status; d) correlation analysis of the lncRNA expression level and PAM50; e) correlation analysis of the lncRNA expression level and breast cancer therapy based molecular signatures; f) correlation analysis of the lncRNA expression level and *XIRP2* mutation status.

Supplementary Figure S7: Venn Diagram of lncRNAs overlaps among differential expression, differential co-expression, and dose-response co-expression analyses.

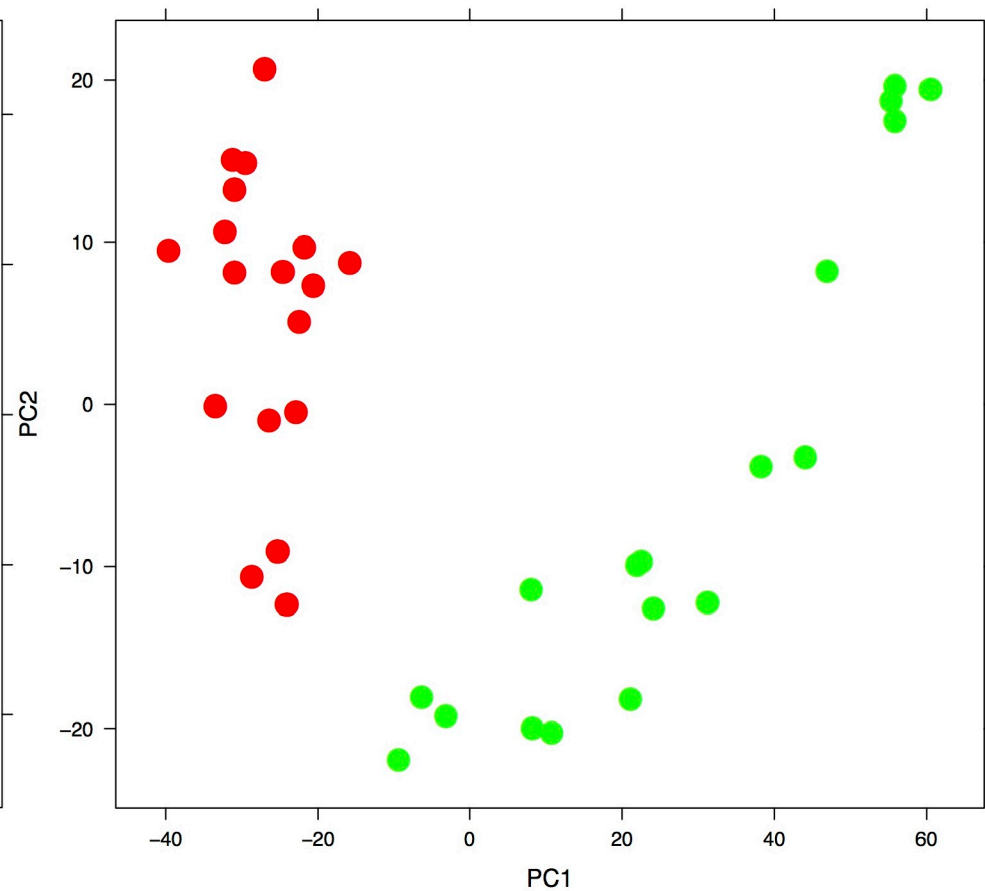
Supplementary Tables (please refer to the separate excel documents).

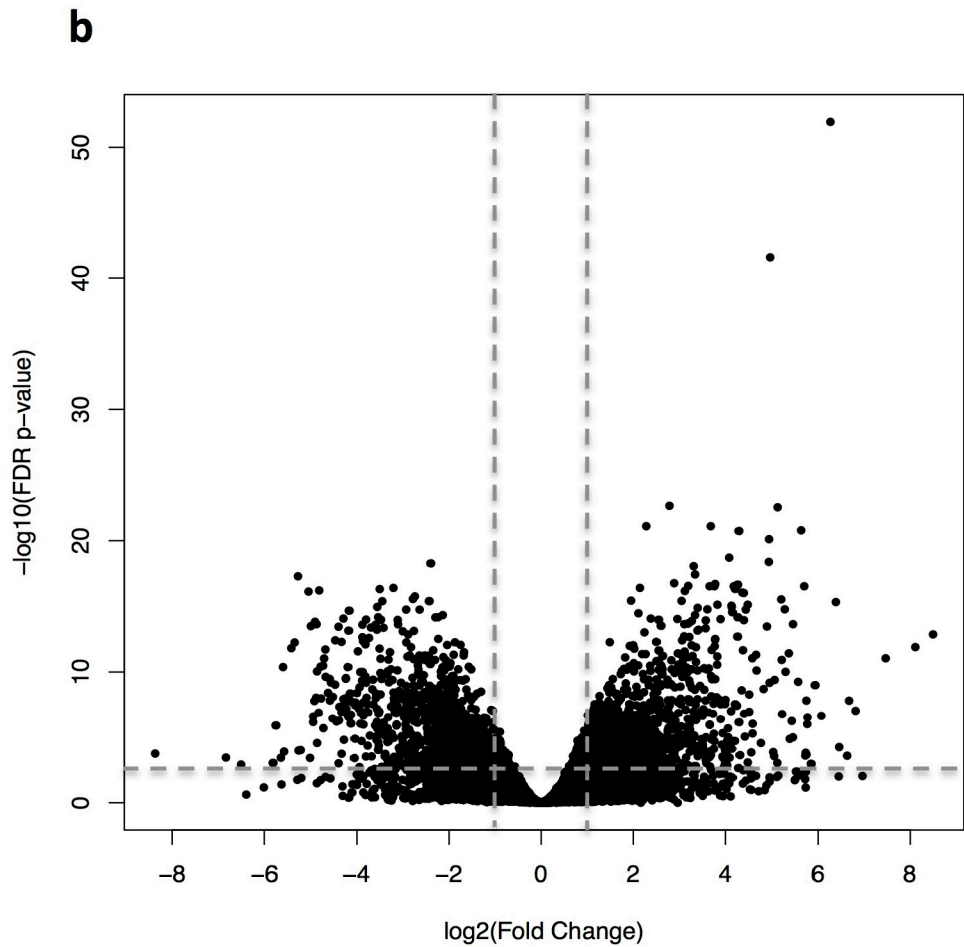
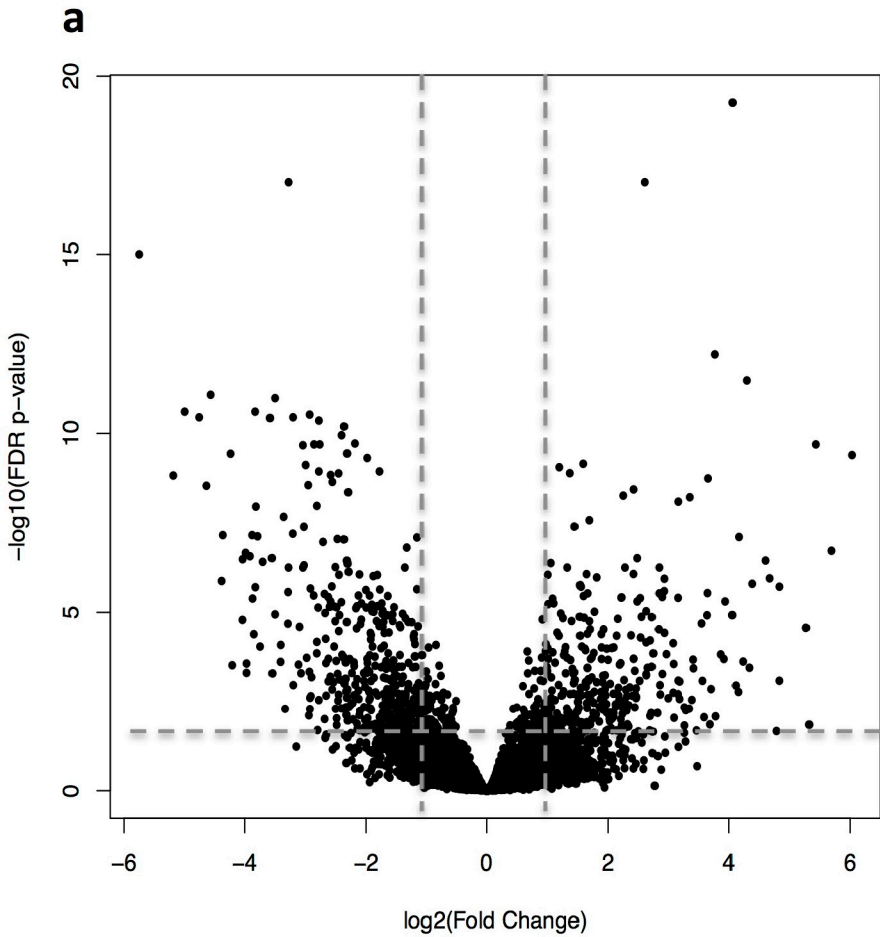
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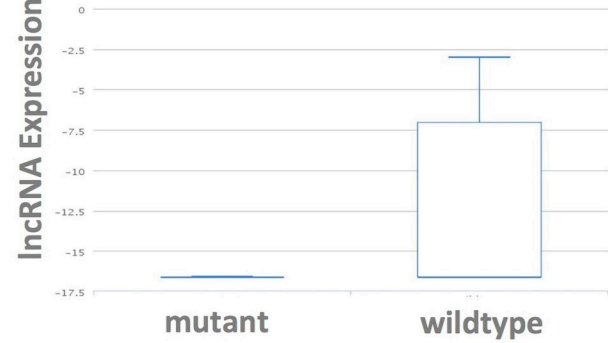
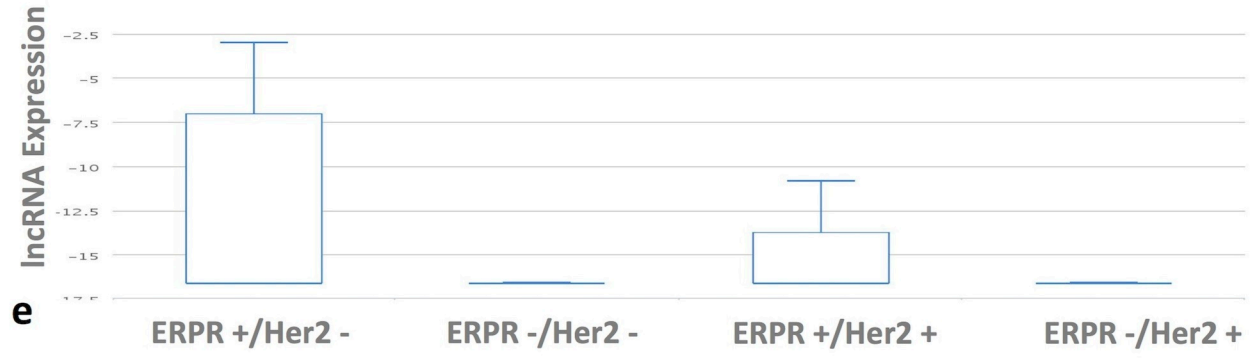
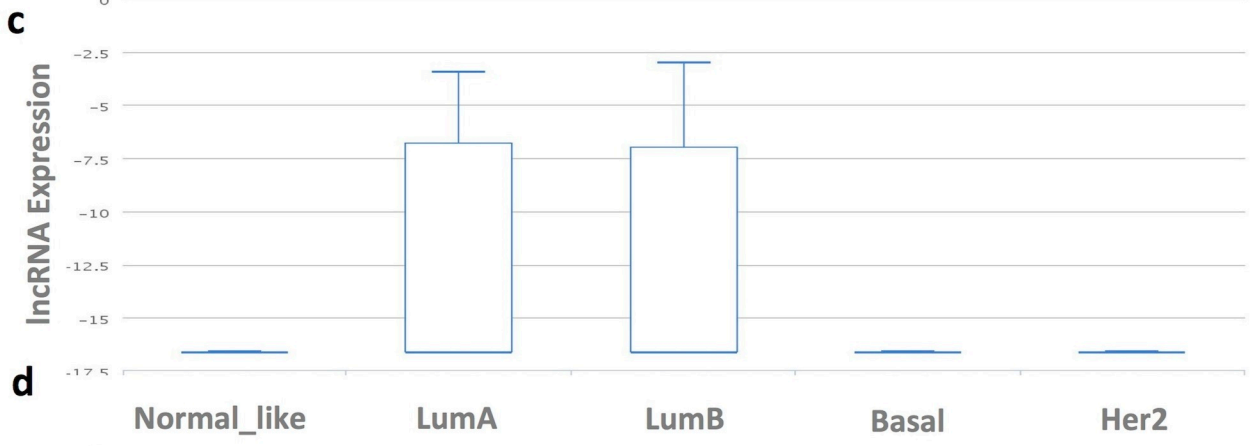
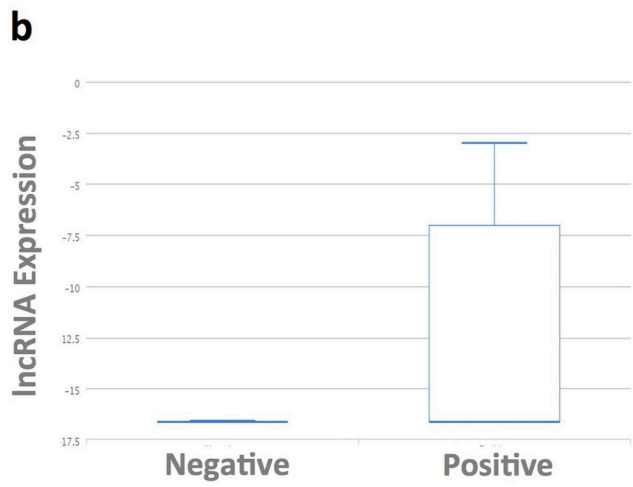
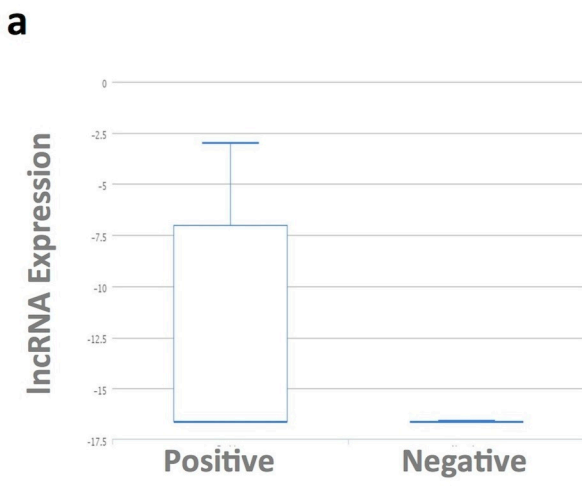
Normal
Tumor

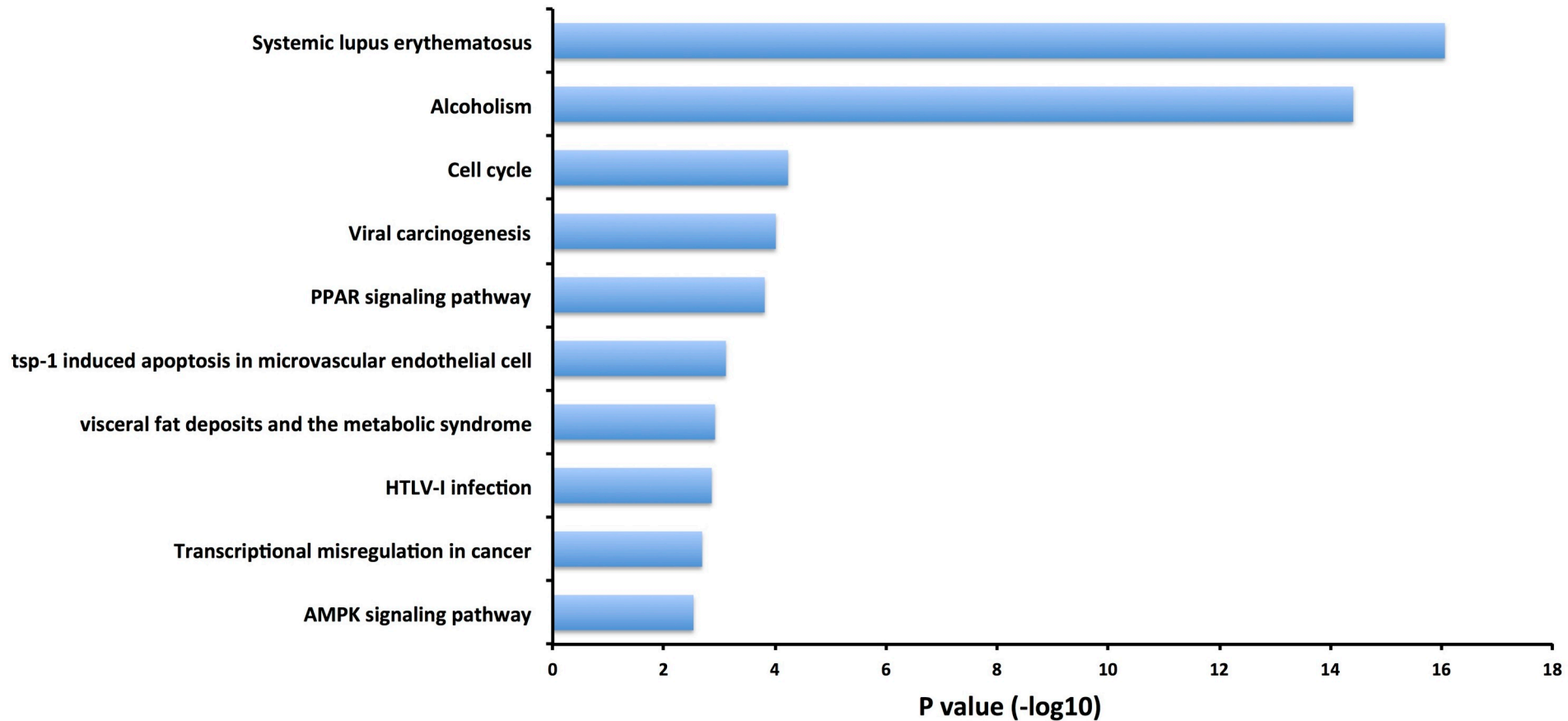
**b**

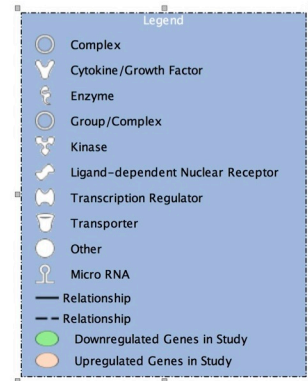
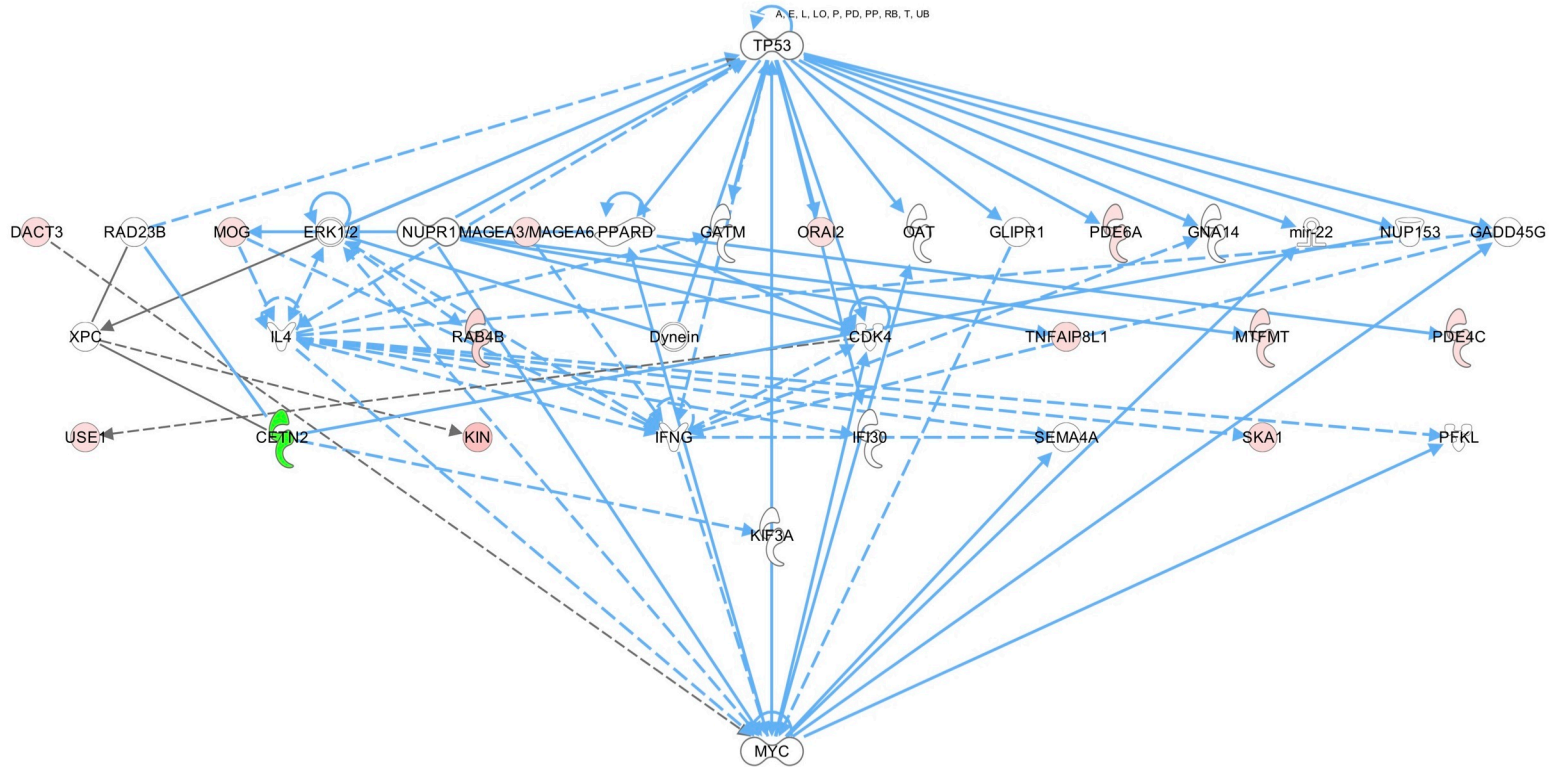
Normal
Tumor

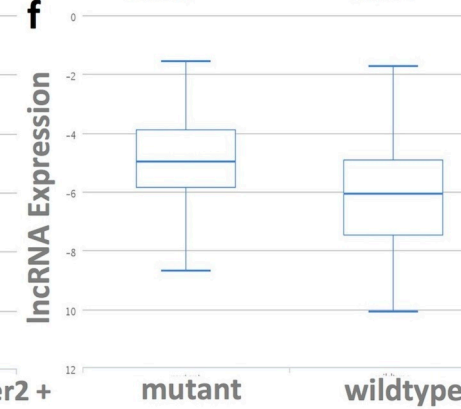
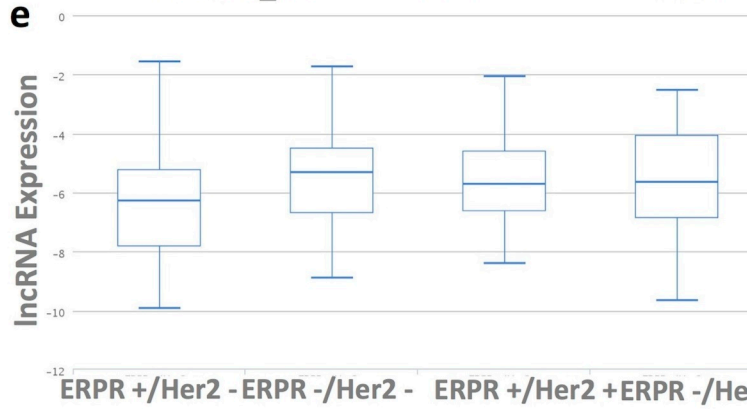
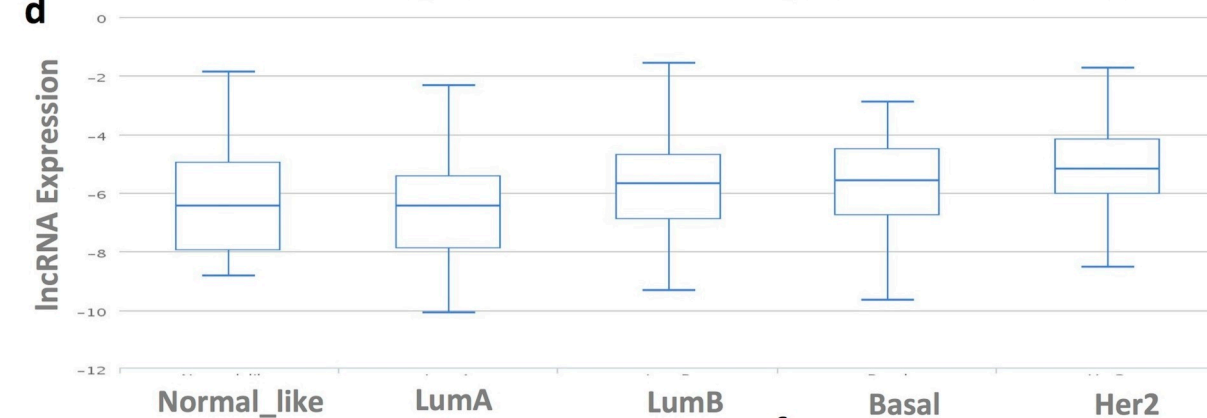
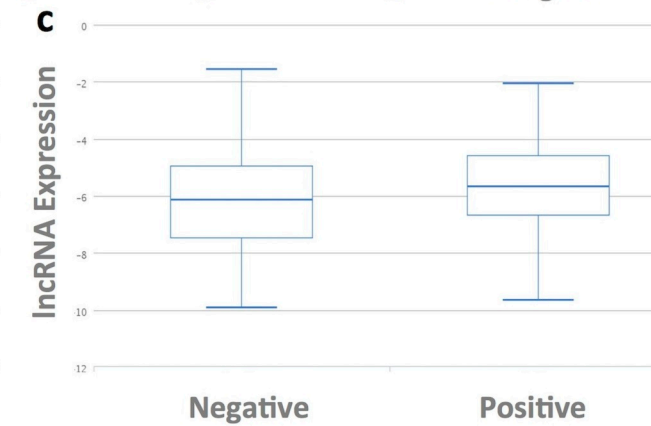
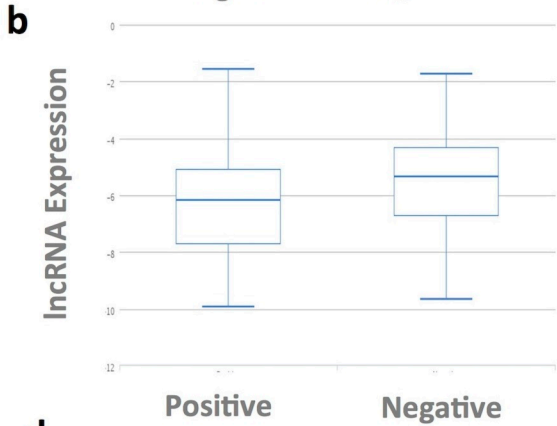
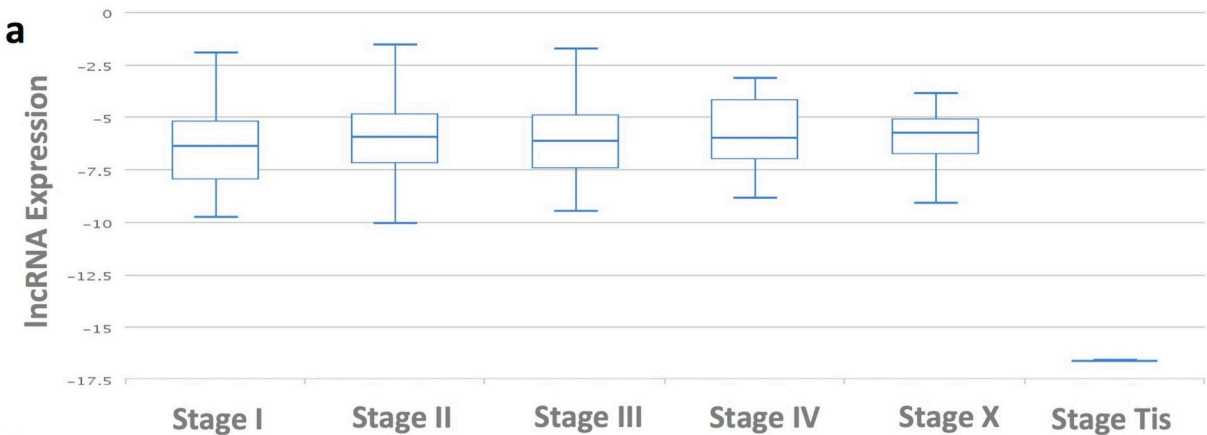


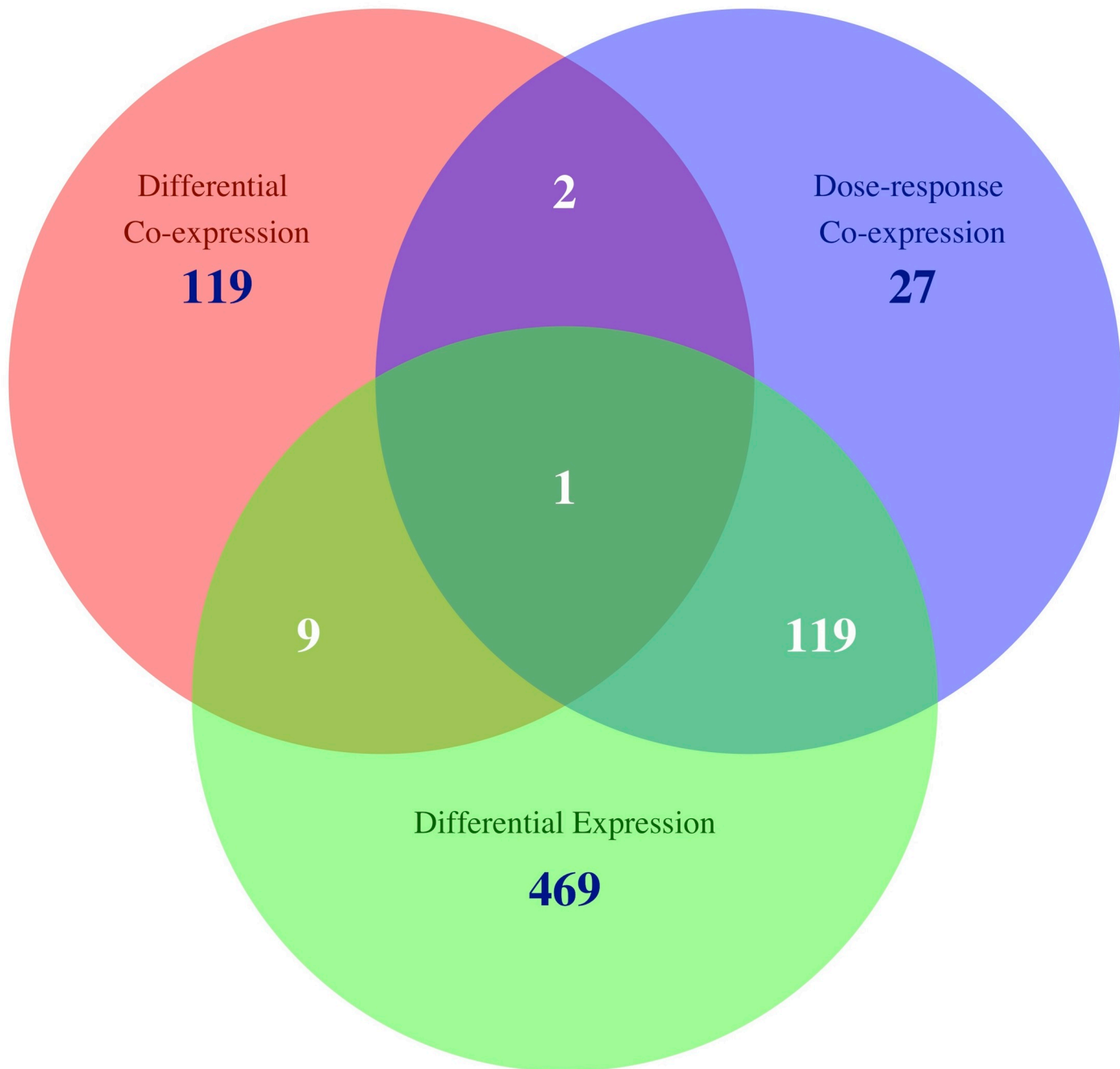












Differential
Co-expression

119

2

Dose-response
Co-expression

27

1

9

119

Differential Expression

469