Supplementary files

Transcriptome- and proteome-oriented identification of dysregulated eIF4G, STAT3, and Hippo pathways altered by *PIK3CA*^{H1047R} in HER2/ER-positive breast cancer

Feixiong Cheng,[1,†,#] Junfei Zhao,[1,2,#] Ariella B. Hanker,[3] Monica Red Brewer,[3]
Carlos L. Arteaga,[3,4,5,*] Zhongming Zhao[1,2,4,5*]

[1]Department of Biomedical Informatics, Vanderbilt University Medical Center, Nashville, TN 37203

[2]Center for Precision Health, School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX 77030, USA

[3]Department of Medicine, Vanderbilt-Ingram Cancer Center, Vanderbilt University, Nashville, TN 37232

[4]Department of Cancer Biology, Vanderbilt-Ingram Cancer Center, Vanderbilt University, Nashville, TN 37232

[5]Breast Cancer Research Program, Vanderbilt-Ingram Cancer Center, Vanderbilt University, Nashville, TN 37232

[†]Present Address: Center for Cancer Systems Biology (CCSB), Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA 02215, USA, and Center for Complex Networks Research, Northeastern University, Boston, MA 02115, USA.

#These authors contributed equally to this work.

*Address correspondence to: carlos.arteaga@vanderbilt.edu (C.L.A), Department of Medicine and Cancer Biology, Vanderbilt-Ingram Cancer Center, Vanderbilt University, Nashville, TN 37232, Phone: (615) 936-1919, Fax: (615) 343-7602;

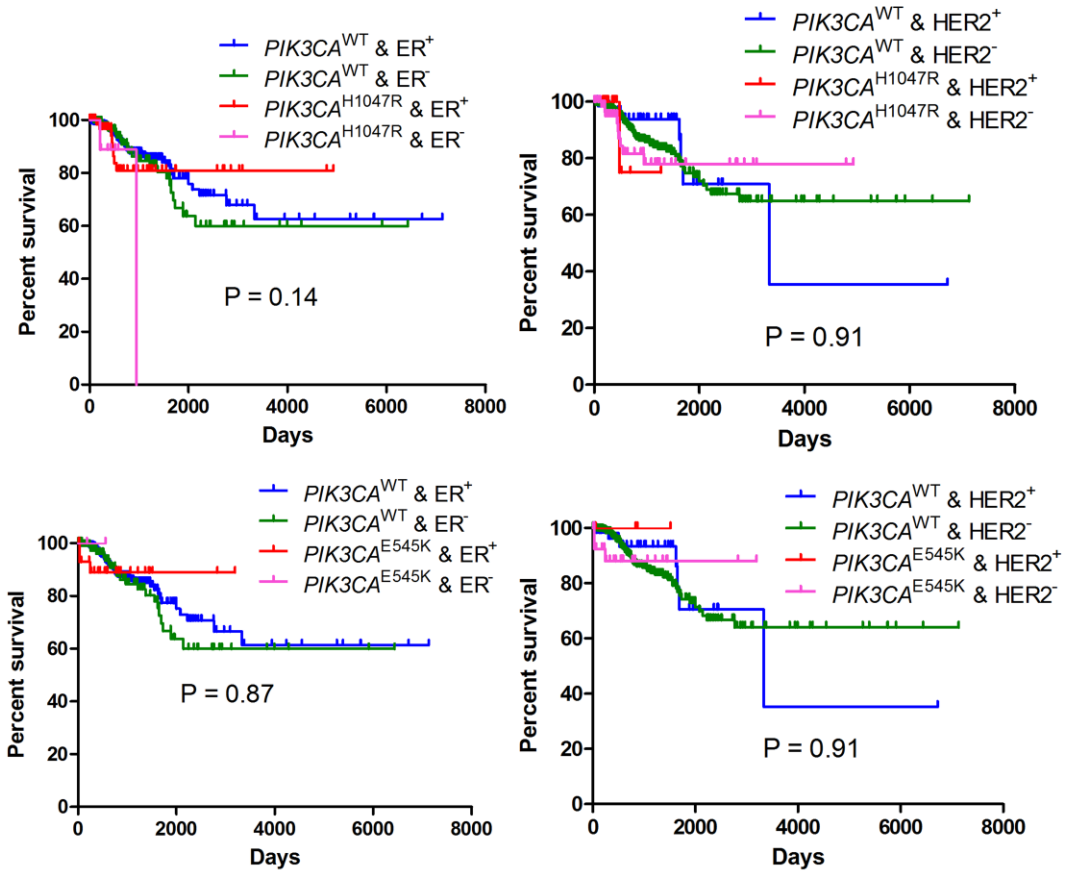
zhongming.zhao@vanderbilt.edu (Z.Z), Department of Biomedical Informatics, Vanderbilt University Medical Center, Nashville, TN 37203, Phone: (615) 343-9158, Fax: (615) 936-8545

Supplementary Table S1. The significantly up-regulated genes for 10 subgroups characterized by *PIK3CA*^{H1047R} or *PIK3CA*^{E545K} in HER2^{+}/ER^{+} breast cancer patients.

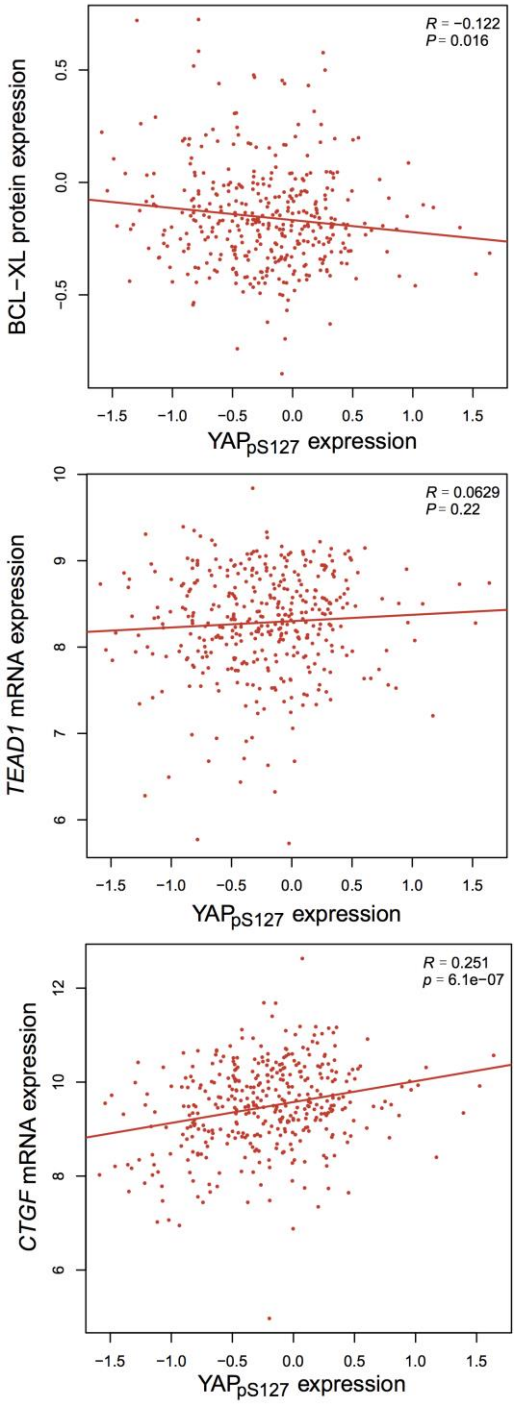
Supplementary Table S2. The 52 well-annotated gene signatures and their enrichment analysis results.

Supplementary Table S3. Lists of up-/down-regulated proteins in four groups: HER2^{+}*PIK3CA*^{H1047R} versus HER2^{+}*PIK3CA*^{WT}, HER2^{+}*PIK3CA*^{E545K} versus HER2^{+}*PIK3CA*^{WT}, ER^{+}*PIK3CA*^{H1047R} versus ER^{+}*PIK3CA*^{WT}, and ER^{+}*PIK3CA*^{E545K} versus ER^{+}*PIK3CA*^{WT}.

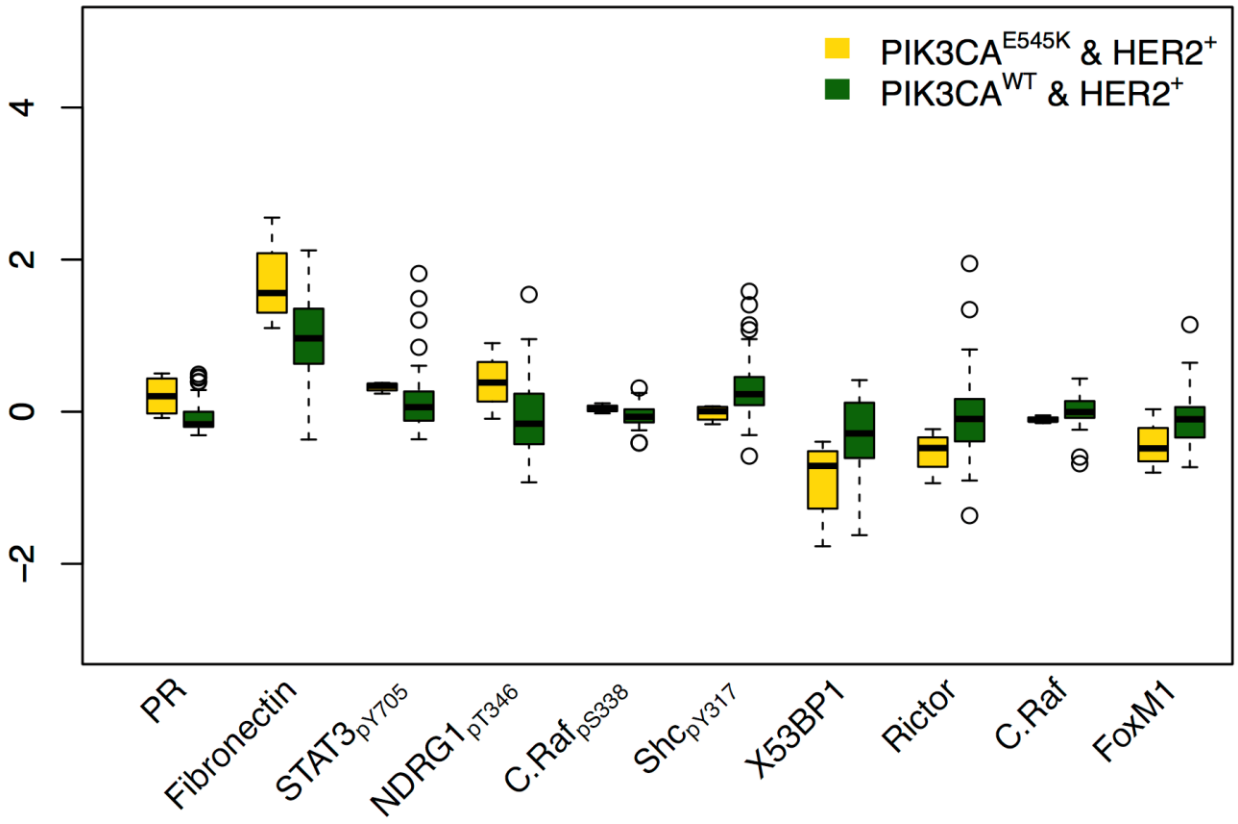
Supplementary Figure S1. Kaplan-Meier overall survival rates for HER2+ or ER+ breast cancer patients with or without two PIK3CA hotspot mutations (H1047R and E545K) using TCGA data. All P values of Kaplan-Meier survival analysis were performed using a log-rank test.



Supplementary Figure S2. Correlation analyses for the protein expression level of YAP_{pS127} with protein expression of BCL-XL and mRNA expression level of TEAD1 and CTGF in ER+/PIK3CA-H1047R breast cancer patients. R was calculated by Pearson correlation coefficient and P-value was calculated by F-statistics.



Supplementary Figure S3. Box plots showing the representative differential proteins/phosphoproteins in HER2^{+}*PIK3CA*^{E545K} versus HER2^{+}*PIK3CA*^{WT} subgroups. Top 5 up-regulated and down-regulated proteins in HER2^{+}*PIK3CA*^{E545K} patients versus HER2^{+}*PIK3CA*^{WT} subgroup were shown. The detailed data are provided in Supplementary Table S3.



Supplementary Figure S4. Box plots showing the representative differential proteins/phosphoproteins in ER$^+$*PIK3CA*^{E545K} versus ER$^+$*PIK3CA*^{WT} subgroups.

Top 5 up-regulated and down-regulated proteins in ER$^+$*PIK3CA*^{E545K} patients versus ER$^+$*PIK3CA*^{WT} subgroup were shown. The detailed data are provided in Supplementary Table S3.