Supplementary Figures

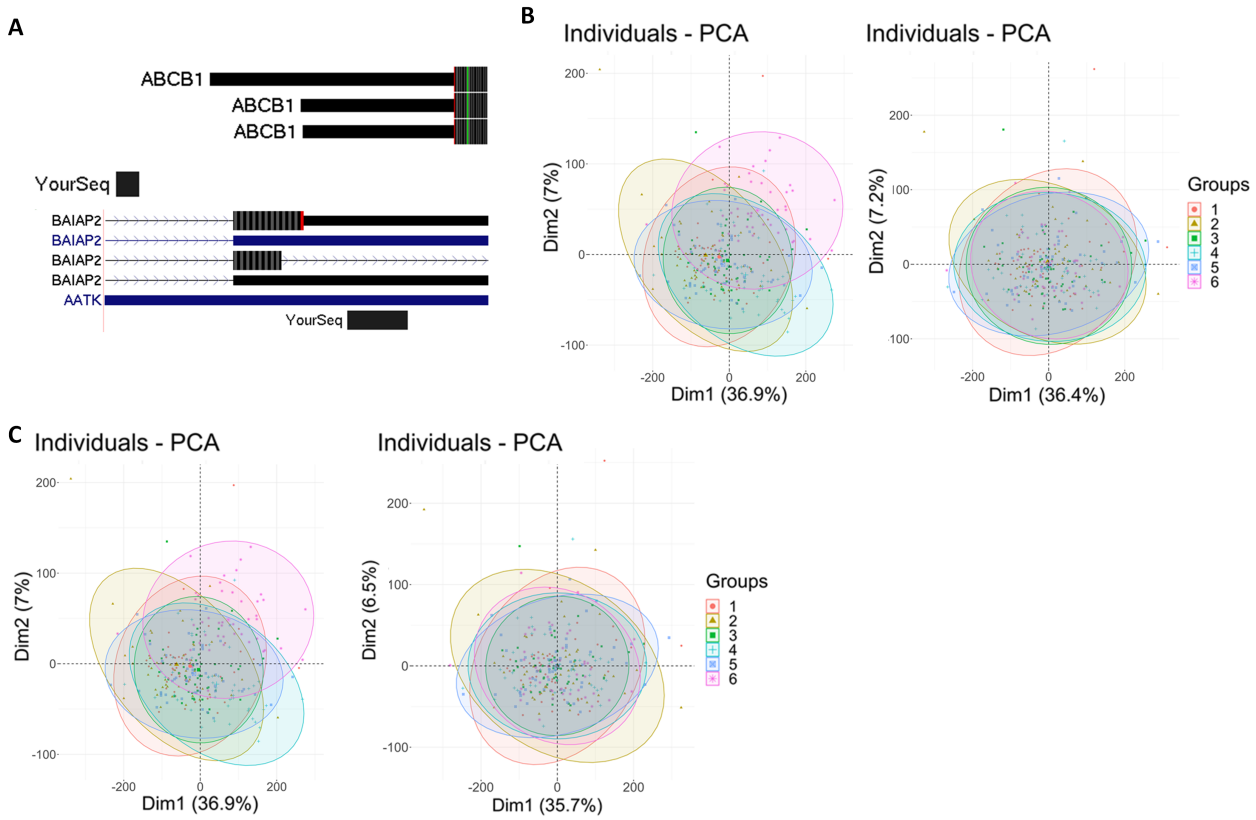


Figure S1. Annotation discrepancies and cluster analysis. Examples of false-positive and multiple mapping, top and bottom respectively (**A**). Here, instances are shown of incorrection annotation in the Rosetta probe set. PCA analysis of the microarray expression dataset pre-batch effect correction and pos-batch effect correction, left and right respectively, utilizing ComBat (**B**) and KS-weighted mean (**C**) Batch correction methods. Here, we show that before batch effect correction, variation exists between groups. Utilizing ComBat and KS-weighted mean correction provides similar results.

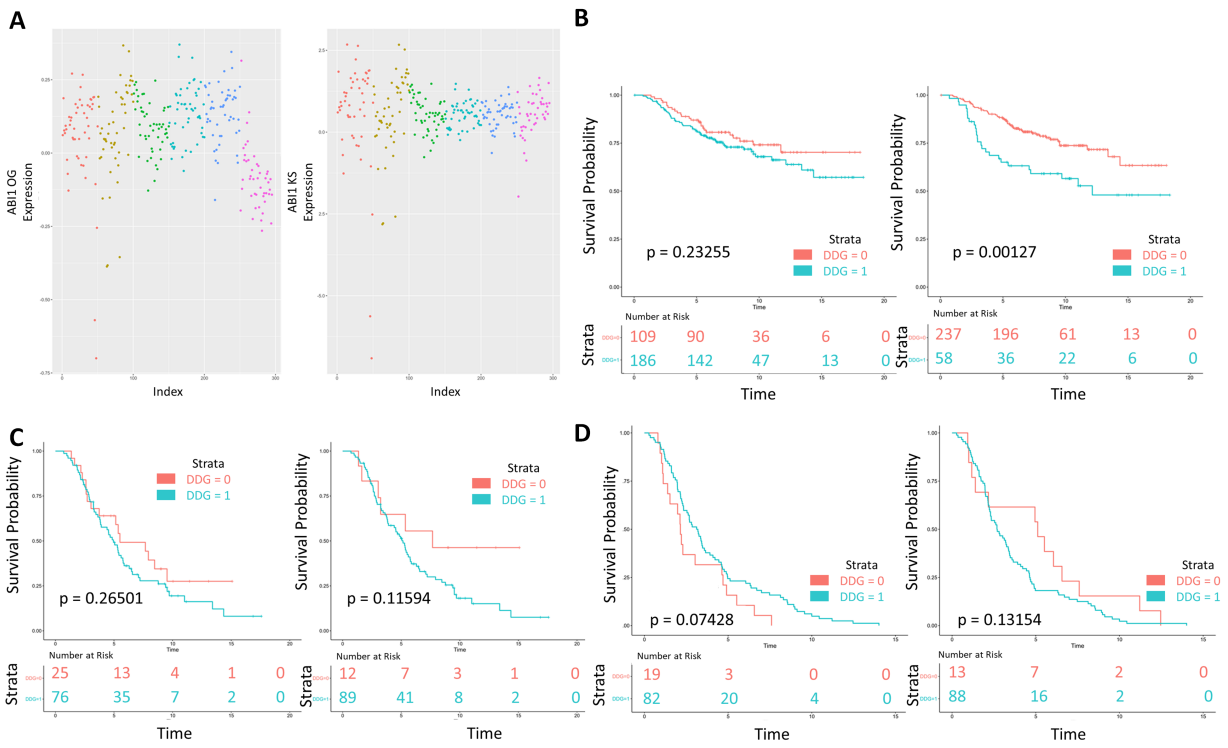
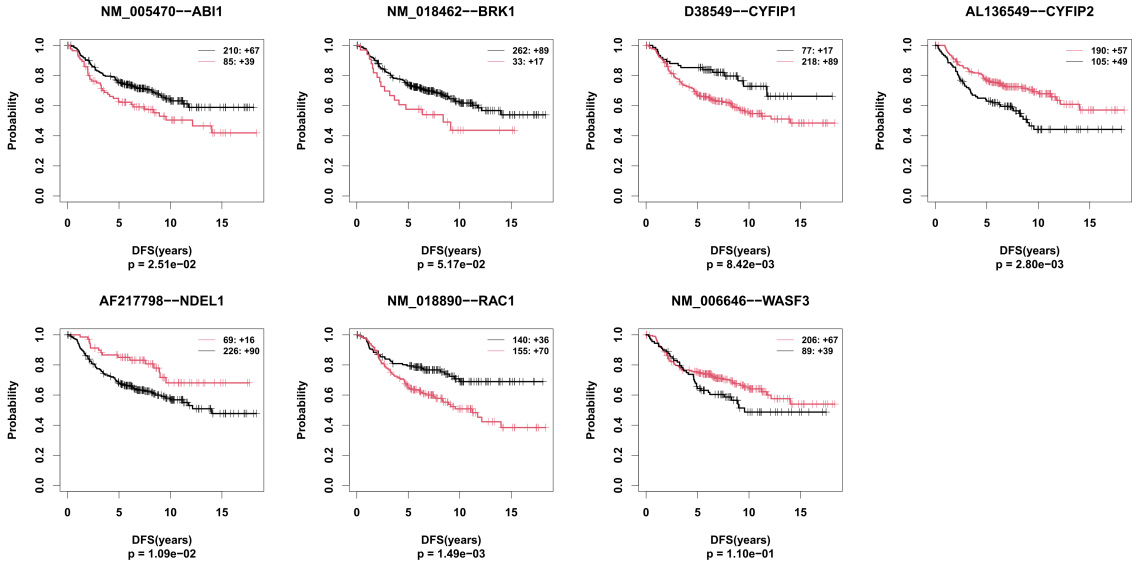


Figure S2. Example of KS-weighted means batch effect correction and its effect on survival analysis. Distributions of ABI1 expression values for each group pre-batch effect correction and post-batch effect correction, left and right respectively **(A)**. Here, we show increased consistency of ABI1 expression values between groups. Survival analysis of survival time and event death of original dataset and KS-corrected dataset including all patients left and right respectively **(B)**. Survival analysis of survival time and event death of original dataset and KS-corrected dataset in only patients with metastasis left and right respectively **(C).** Survival analysis of metastasis time and metastasis event of the original dataset and KS-corrected dataset in only patients with metastasis, left and right respectively **(D).** In the case of (**B)** and (**C)**, KS-weighted means batch effect correction results in better significance. For D, KS-weighted means batch effect correction provides results that adhered to findings in the literature while the original dataset did not.

A



B

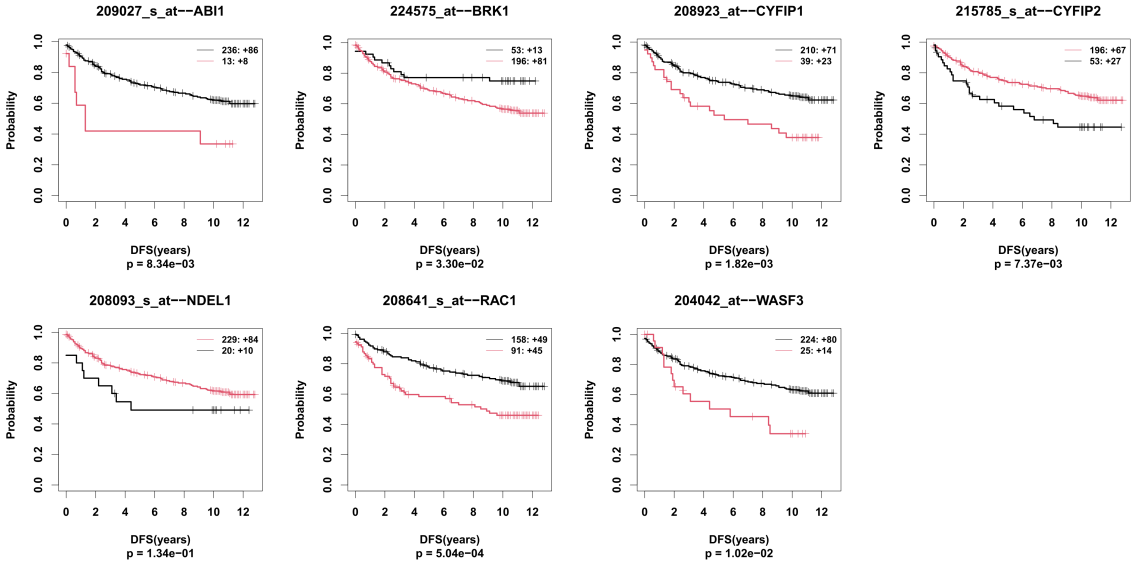
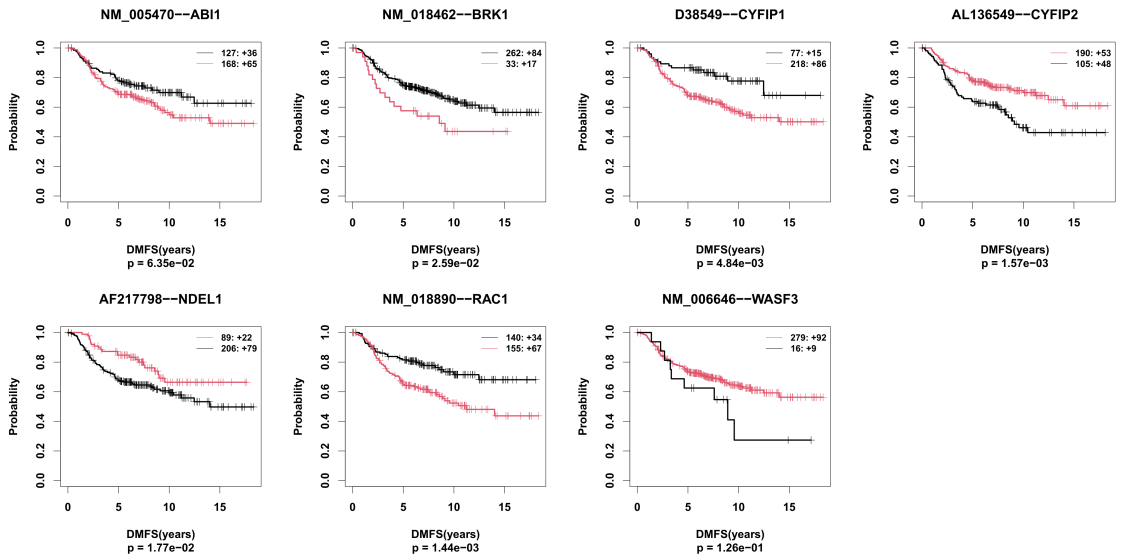


Figure S3. Risk-predicting ability of individual members of the ABI1-WAVE signature in disease-free survival (DFS). Kaplan-Meier survival curves depict the survival associated with patients stratified into low-risk and high-risk groups according to the ABI1-WAVE signature in the Rosetta (**A**) and MetaData (**B**) datasets. In all plots, black color is associated with low-risk and red color is associated with high-risk.

A



B

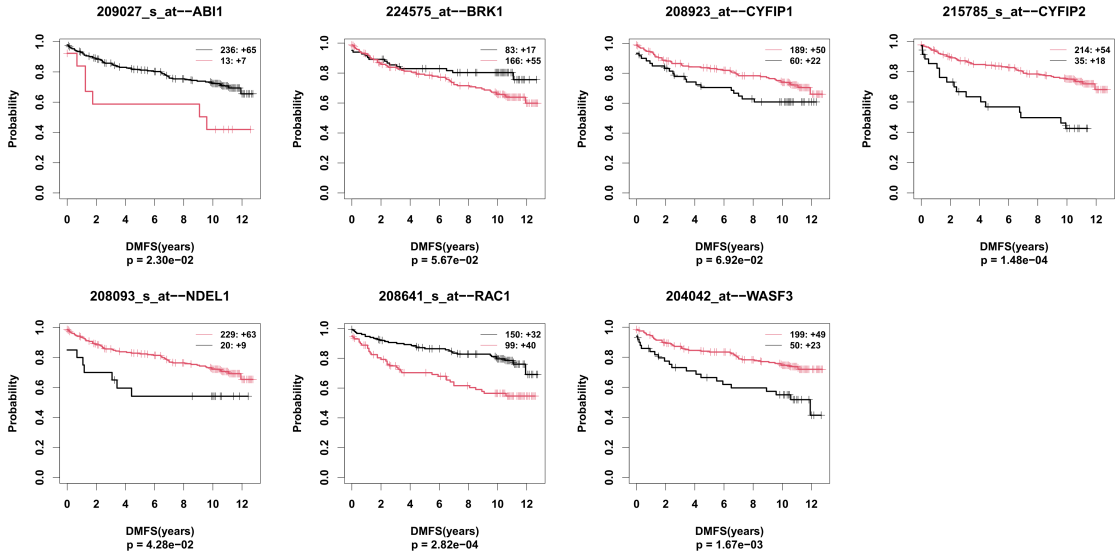


Figure S4. Risk-predicting ability of individual members of the ABI1-WAVE signature in distant-metastasis free survival (DMFS). Kaplan-Meier survival curves depict the survival associated with patients stratified into low-risk and high-risk groups according to the ABI1-WAVE signature in the Rosetta (**A**) and MetaData (**B**) datasets. In all plots, black color is associated with low-risk and red color is associated with high-risk.

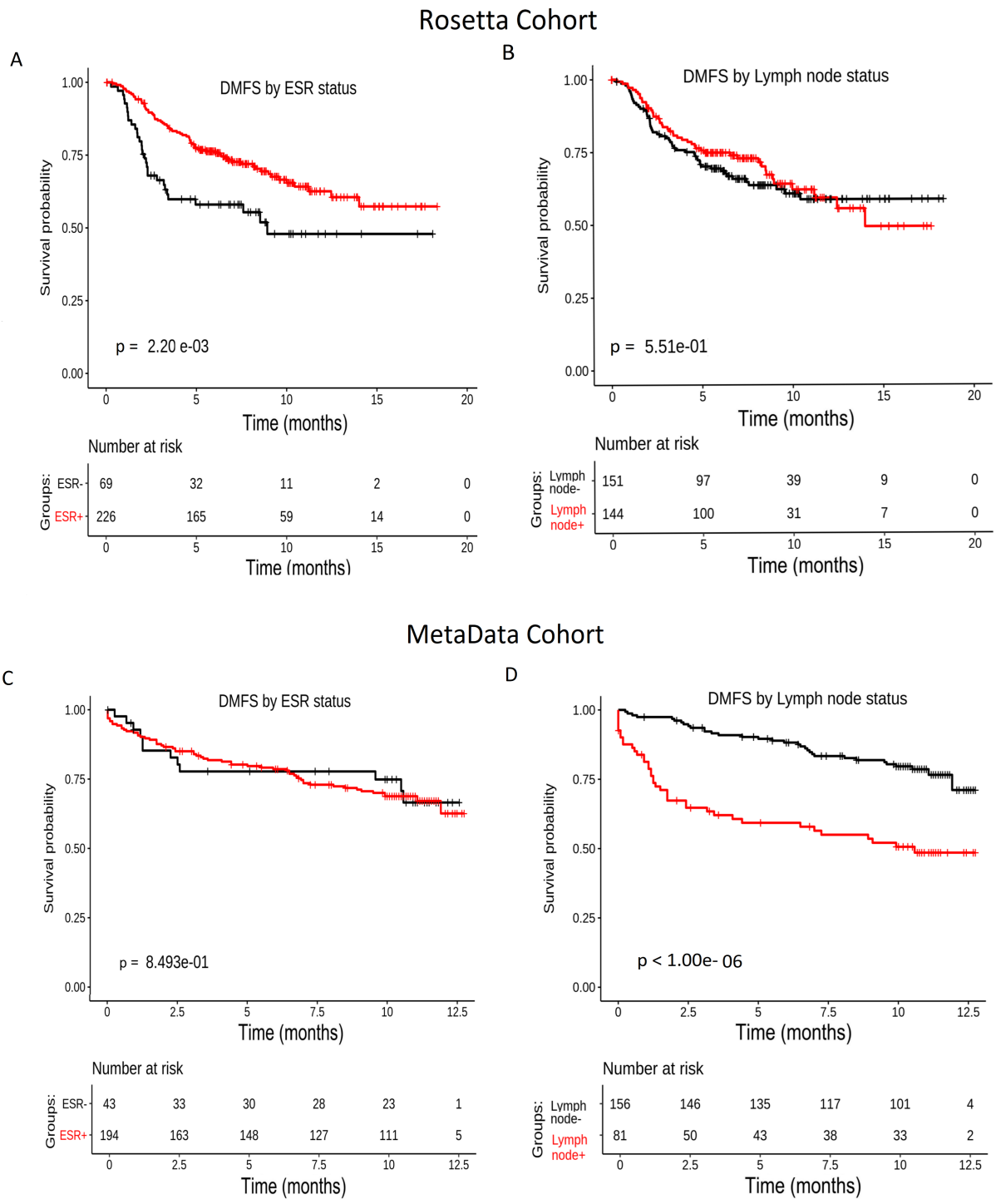


Figure S5. Commonly used clinical variables are insufficient for robust patient risk stratification. Kaplan-Meier survival curves for the Rosetta dataset were stratified based on (a) estrogen receptor (ESR) status (red: positive vs. black: negative; Log-rank p=0.0022) and (b) lymph node status (red: positive vs. black: negative; Log-rank p=0.52). Kaplan-Meier survival curves for the Rosetta dataset were stratified based on

(c) estrogen receptor (ESR) status (red: positive vs. black: negative; Log-rank p=0.0.85) and (d) lymph node status (red: positive vs. black: negative; Log-rank p < 0.001).

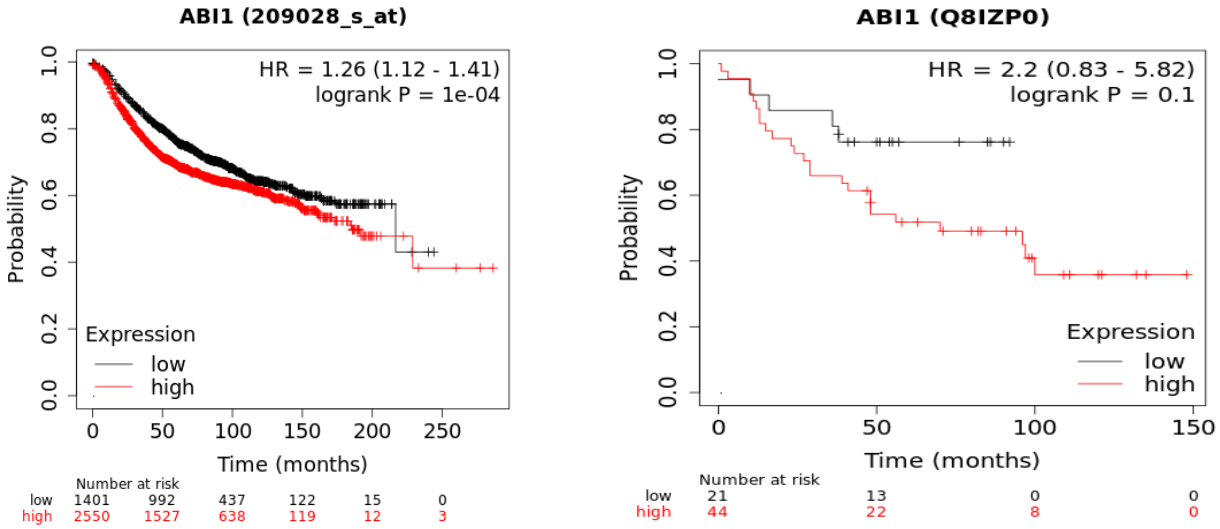


Figure S6. Survival predictive analysis (RFS time) at transcription and protein level suggests a pro-oncogenic role of ABI1 in BC progression and outcome. (**A**) Microarray mRNA expression dataset of the 3951 BC patients suggests a pro-oncogenic role of ABI1 in BC progression and outcome. p=0.0001, Log rank test; FDR=5%, Median survival time (months): low expression: 216.7; high expression: 185.2. Expression cut-off value: 746, expression range: 121 - 4621. Dataset source and method:https://kmplot.com/analysis/index.php?p=service&cancer=breast. (**B**) Protein level analysis support ABI1 as a survival prognostic marker in BC patient samples. Survival prediction analysis (Data: GEO/NCBI GSE39004) (2): http://kmplot.com/analysis/index.php?p=service&cancer=breast_protein

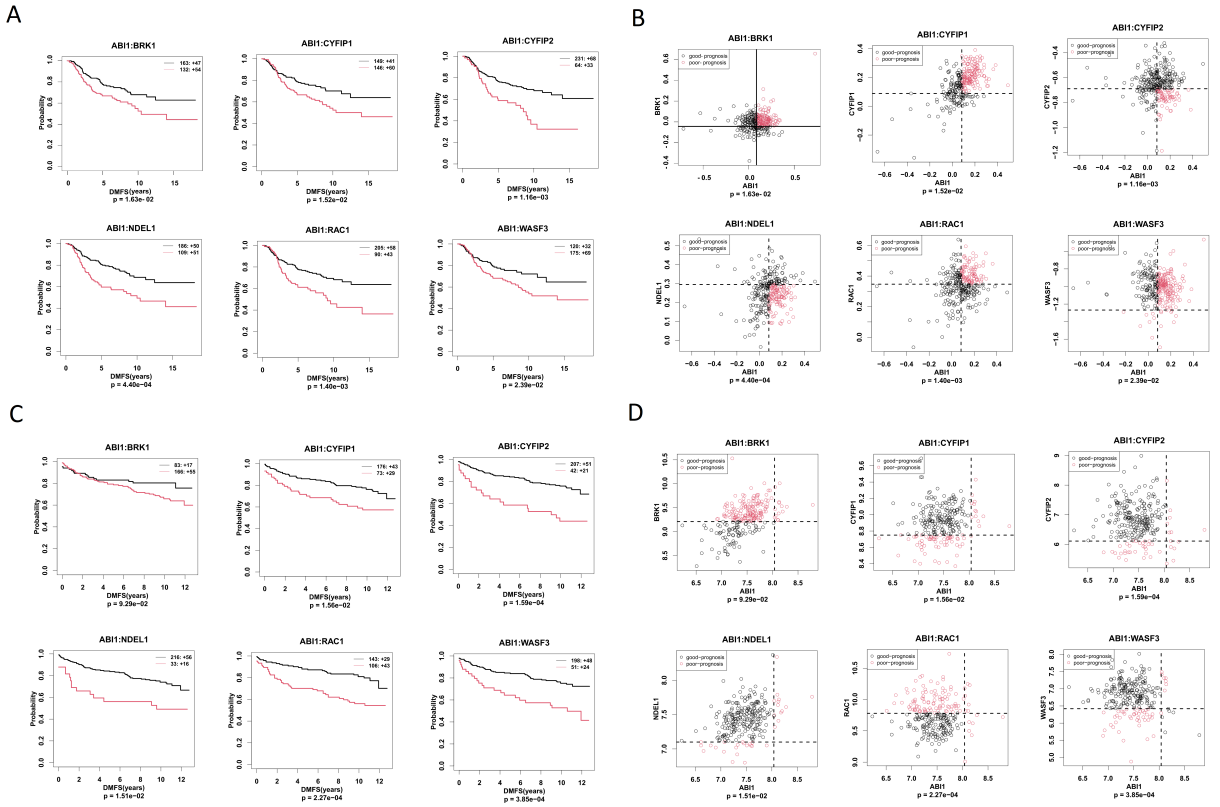


Figure S7. The implementation of 2D-DDg survival prediction to Rosetta data (DFS and DMFS). Panels (**A**) and (**C**) show the K-M function plots for low- and high-risk groups defined by *ABI1* expression paired with the expression of our other 6 genes (as potential interaction partners) for DFS and DMFS respectively. Panels (**B**) and (**D**) provide a visual presentation of bi-bivariate distributions of the expression data in the case of DFS and DMFS respectively. The scatter plots give a visual representation of the separation of patients according to the individual cut-off values associated with each gene in the synergistic gene pairs, for Rosetta (**B**) and MetaData (**D**) datasets. Each circle represents a tumor sample; circles with red outlines are associated with relatively high risk and circles with black outlines are associated with lower-risk survival outcome groups. In (**A**) and (**C**) the red color indicates the survival time of the high-risk group, while the color black indicated the survival function of the low-risk group. In panels (**B**) and (**D**), the points colored with red correspond to patients in the high-risk group, and the black points refer to patients in the low-risk group.

References:

1. Pereira B, Chin SF, Rueda OM, Vollan HK, Provenzano E, Bardwell HA*, et al.* The somatic mutation profiles of 2,433 breast cancers refines their genomic and transcriptomic landscapes. *Nat Commun* 2016;**7**:11479 doi 10.1038/ncomms11479.

2. Tang W, Zhou M, Dorsey TH, Prieto DA, Wang XW, Ruppin E*, et al.* Integrated proteo-transcriptomics of breast cancer reveals globally increased protein-mRNA concordance associated with subtypes and survival. *Genome Med* 2018;**10**(1):94 doi 10.1186/s13073-018-0602-x.