
Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: The Cancer Genome Atlas (TCGA) patient cohorts and cohort groups used in this study

File name: Supplementary Data 2

Description: Primary and metastatic samples of the MSK-IMPACT cohort used in this study

File name: Supplementary Data 3

Description: CAA transition probabilities in the TCGA-BRCA dataset

File name: Supplementary Data 4

Description: Single and co-occurring CAAs that predict good or poor overall survival

File name: Supplementary Data 5

Description: Single and co-occurring CAAs that predict good or poor disease-free survival

File name: Supplementary Data 6

Description: Co-occurring CAAs across 31 cancer types

File name: Supplementary Data 7

Description: Summary table of single and co-occurring CAAs that predict good or poor patient survival

File name: Supplementary Data 8

Description: Correlation between CAA burden and predicted pCR to preoperative T/FAC chemotherapy

File name: Supplementary Data 9

Description: Members of the TFAC pharmaco-genomic gene expression predictor

File name: Supplementary Data 10

Description: Pan-cancer features predicting increased drug resistance or sensitivity using the expanded GDSC dataset

File name: Supplementary Data 11

Description: Identification of potential synthetic lethal and synergistic resistance pharmacogenomic interactions

File name: Supplementary Data 12

Description: Pharmacogenomic interactions of co-lost and co-gained focal copy number alterations on the same chromosome arm

File name: Supplementary Data 13

Description: CAA and CFE model performance per drug

File name: Supplementary Data 14

Description: Centromere regions excluded from CAA analyses
