



Article

Multiplex Patient-Based Drug Response Assay in Pancreatic Ductal Adenocarcinoma

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Supplementary materials

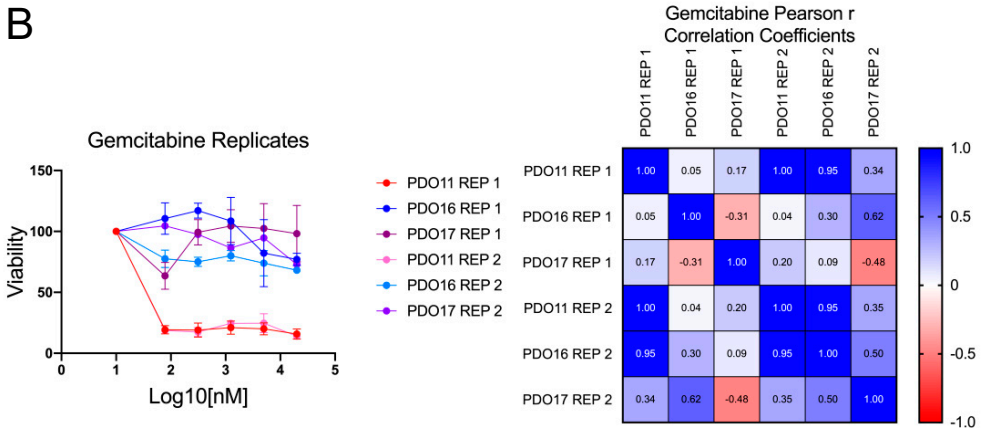
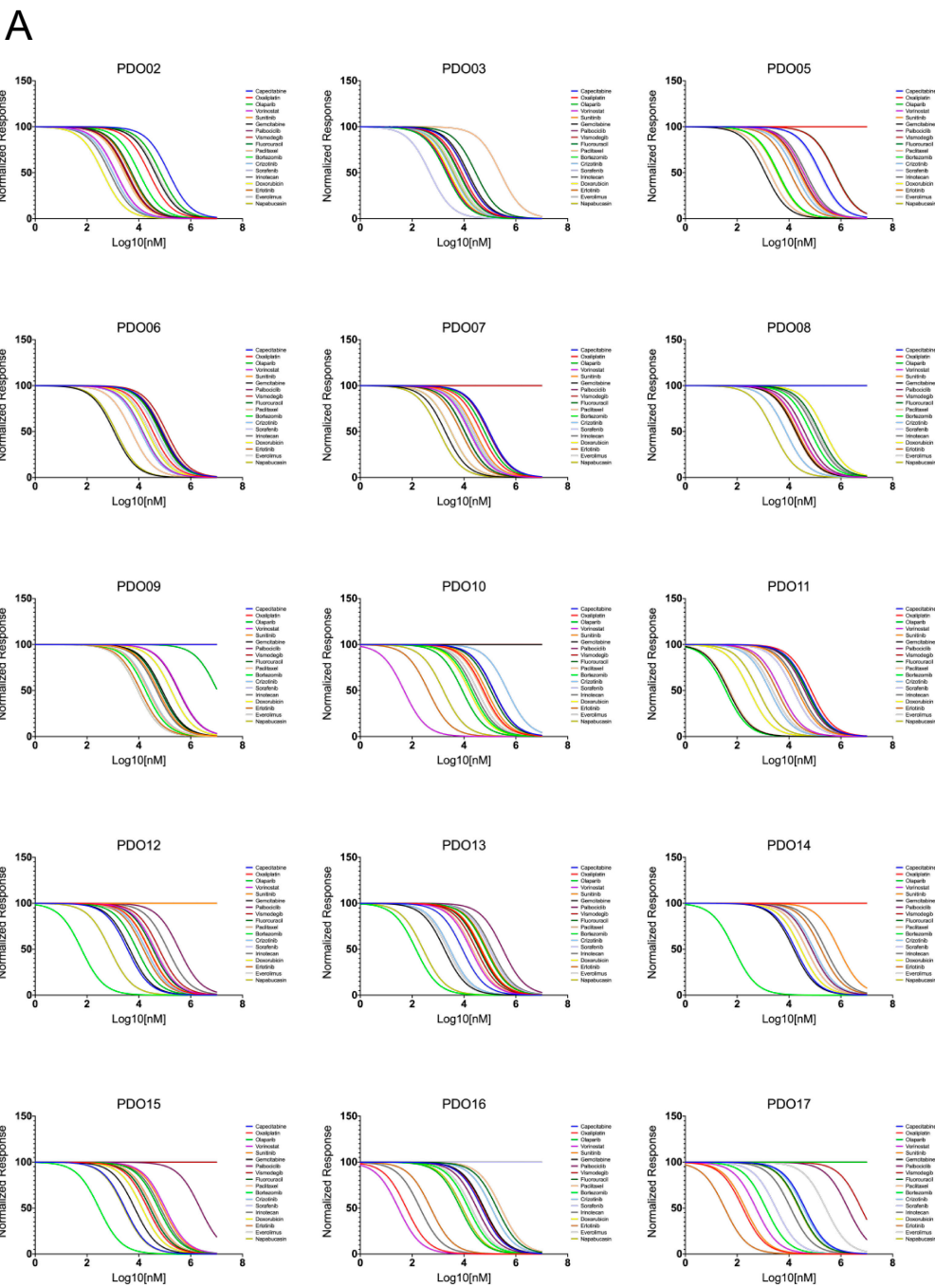


Figure S1. (A) Viability curves of patient derived organoids for each drug. Lines represent non-linear regression curve fit based on viability data. Curves were set to a range of 0-7. (B) Co(rrelations curves depicting replicate drug screening assays for three individual PDOs. Replicate drug screens were repeated at least 2 weeks apart.

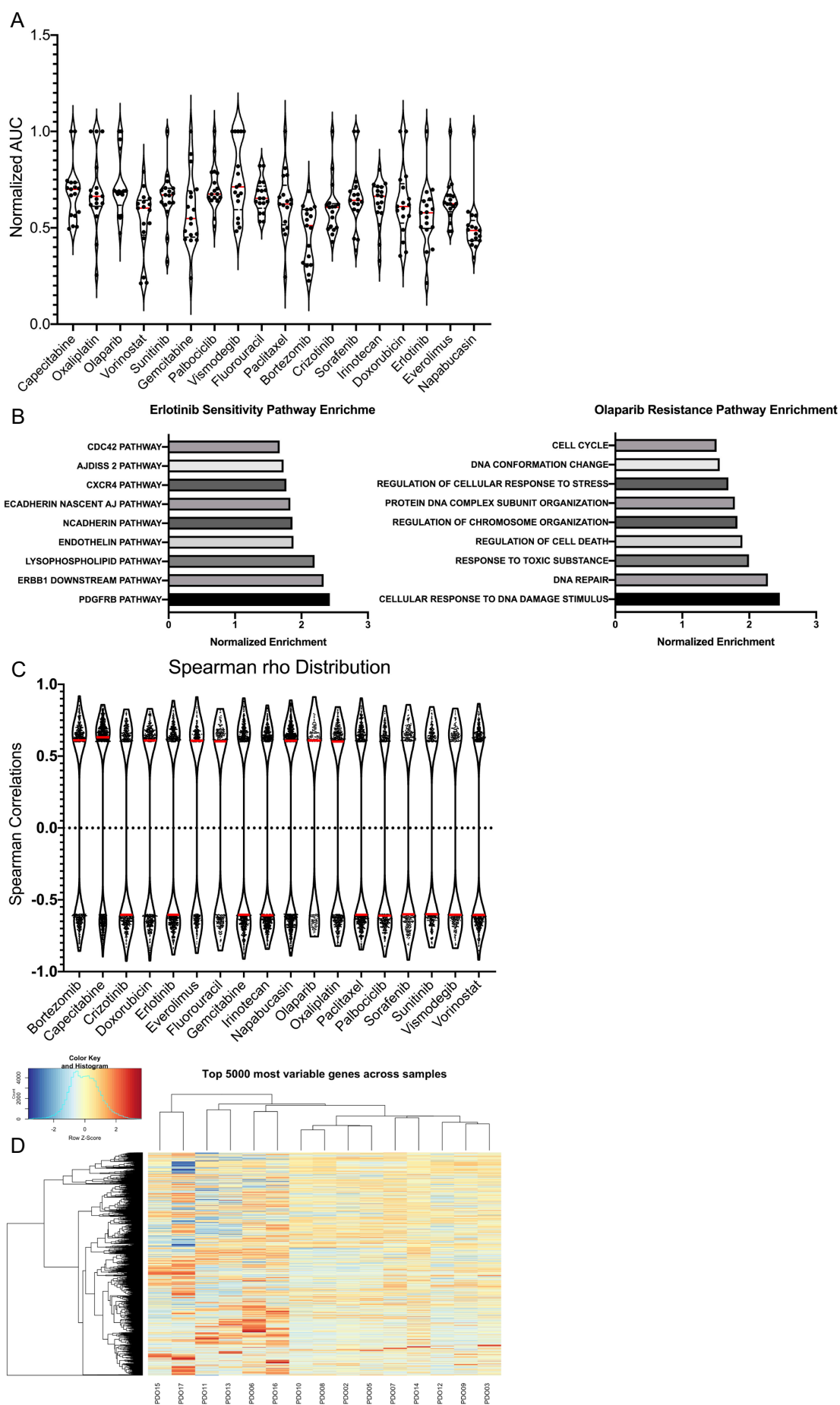


Figure S2. (A) The distribution of normalized AUC values for all drugs. (Mean; red line, quartiles; dashed gray lines) (B) Gene set enrichment analysis of drug specific gene profiles reveals pathways correlated with erlotinib and olaparib sensitivity. Pathways are plotted using normalized enrichment scores and all pathways are significant and FDR $Q < 0.25$. (C) The distribution of Spearman correlation coefficient for each drug. Using gene expression and treatment response for all PDOs, the spearman rank correlation of gene expression to normalized AUC were calculated for each gene. (D) Heatmap and histogram of the top 5000 most variably expressed genes among all PDOs.

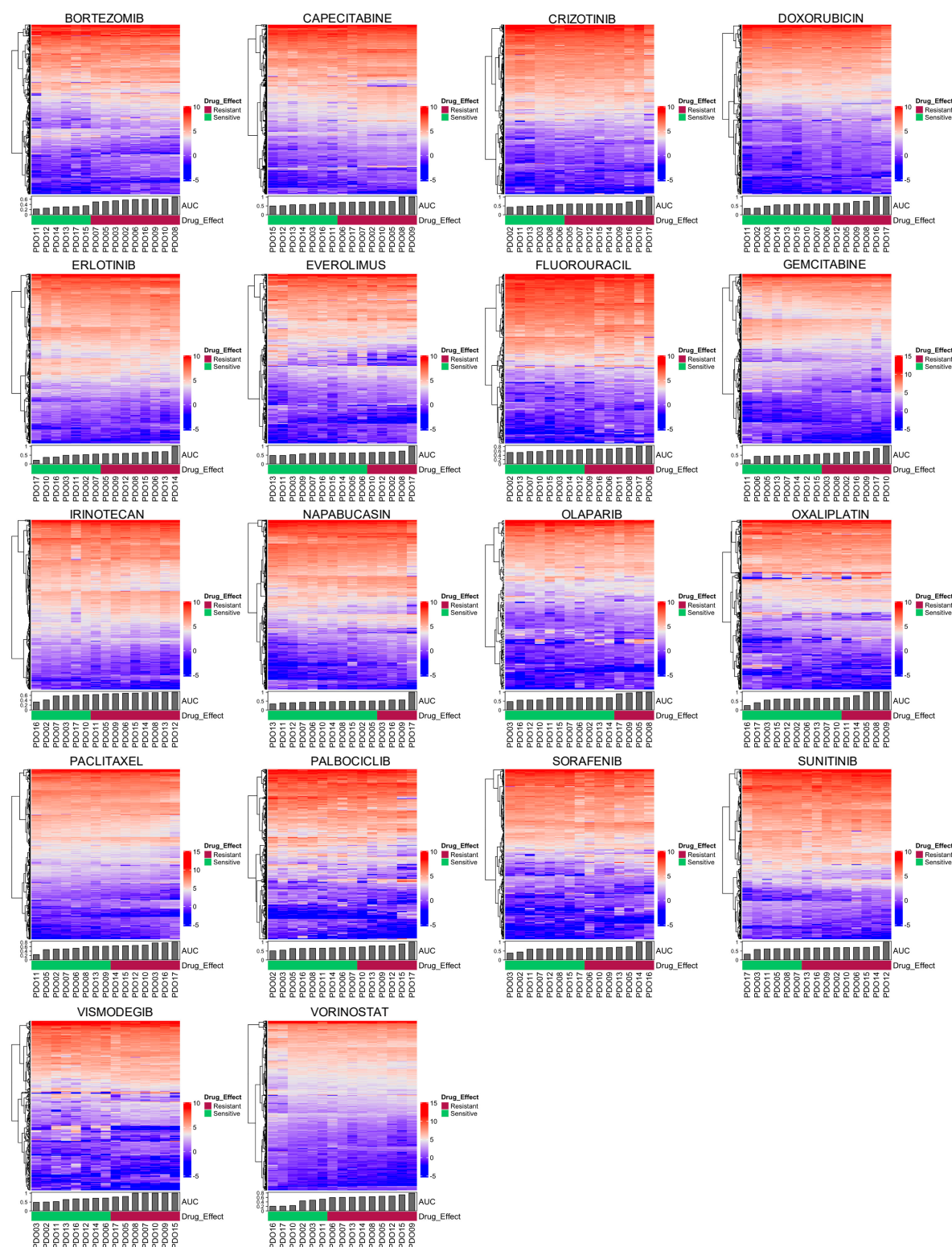


Figure S3. Heatmaps of log 2 cpm gene expression for genes that are highly correlated with drug sensitivity. Bar plots indicate normalized AUC for each PDO. Normalized AUC values were transformed to z-scores and PDOs with negative z-scores were specified as resistant to drug treatment (Green-sensitive, Maroon-resistant). Highly correlated genes- $\rho > 10.61$.

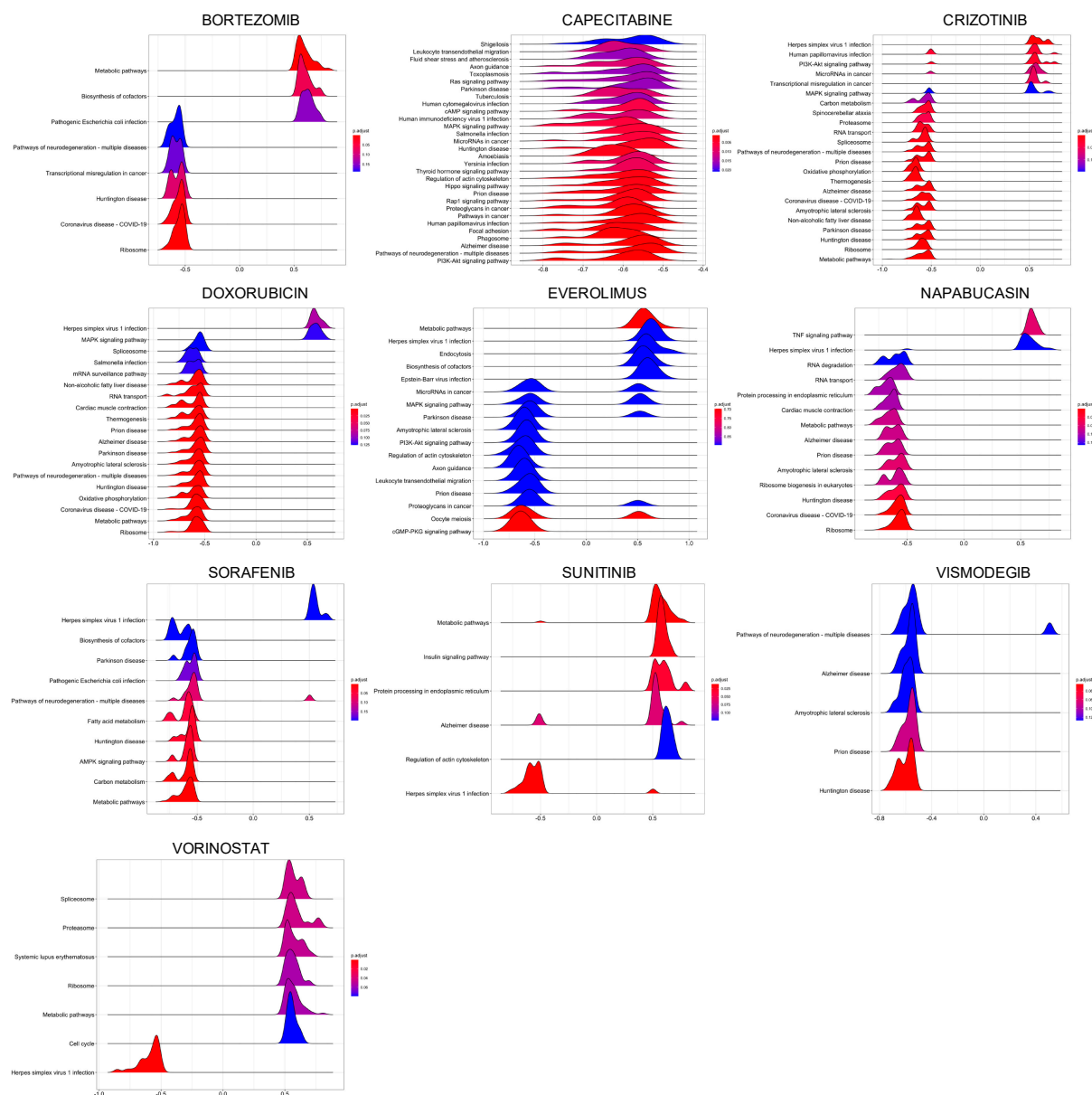


Figure S4. Ridge plot of KEGG pathways associated with response to individual drugs. Positively enriched pathways are associated with treatment sensitivity, and negatively enriched pathways are associated with treatment resistance. Pathway analysis was conducted using Gene Set Enrichment Analysis of KEGG pathways based on RNAseq gene expression.