Supplementary Material

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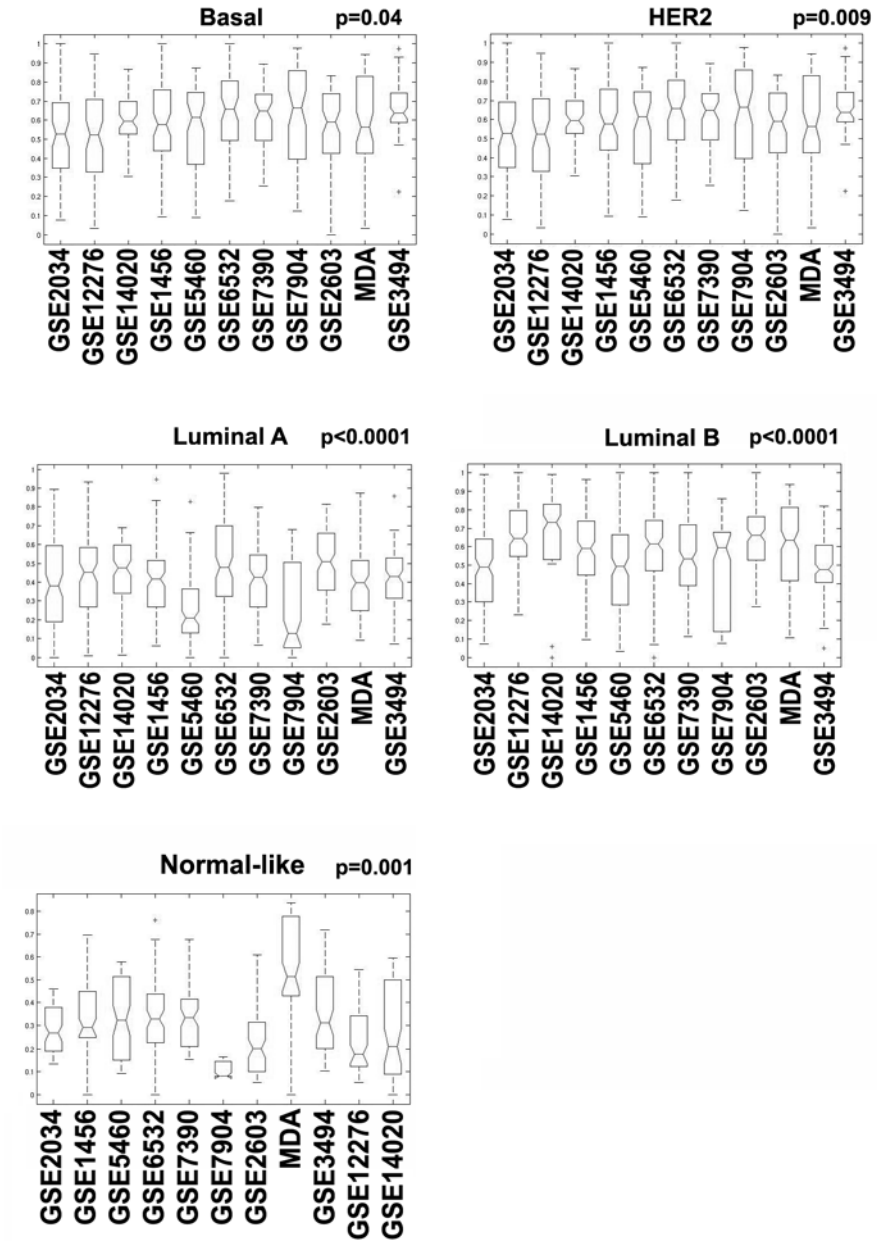
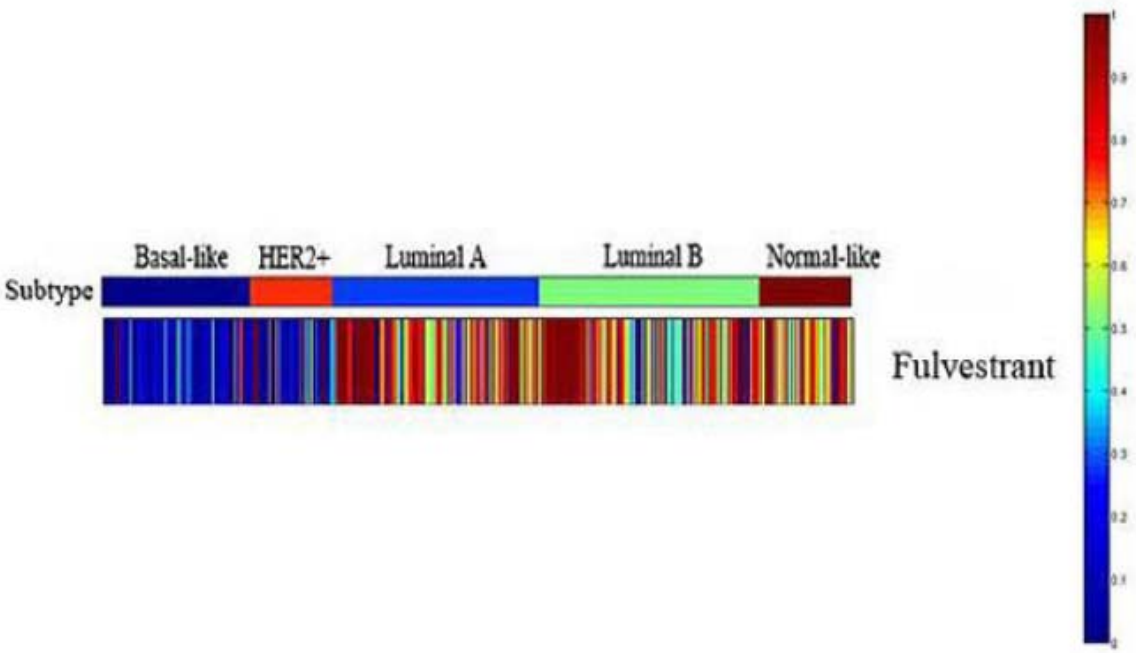
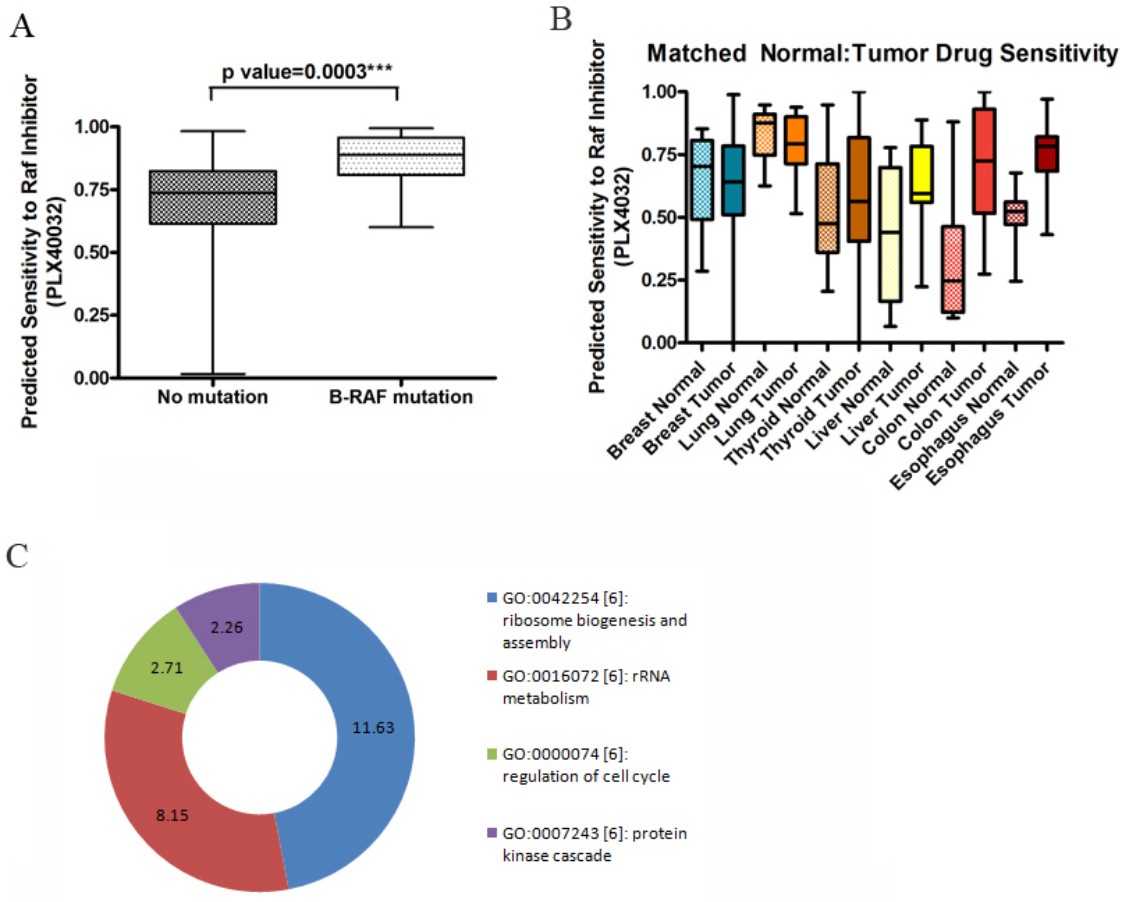


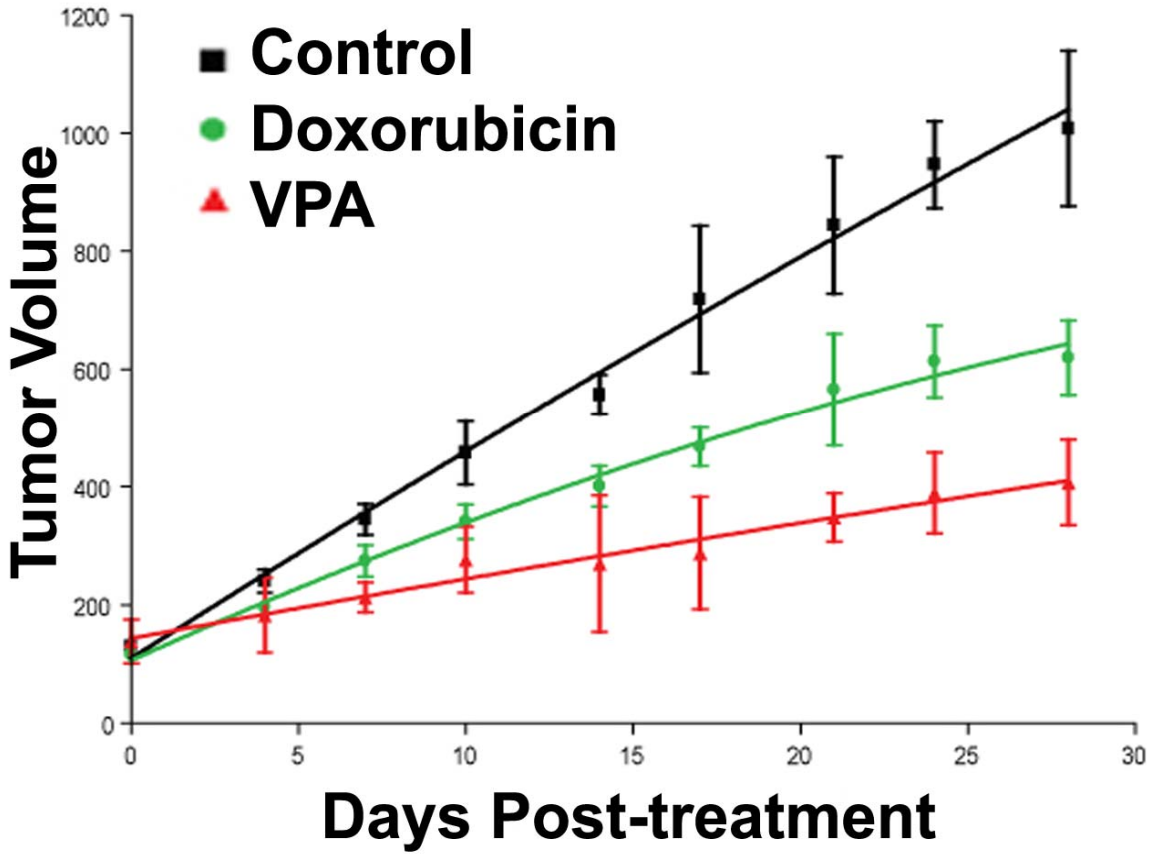
Supplemental Figure 1. **Box and whisker analysis of datasets**, Each graph represents one of the five subtypes of breast cancer. The x-axis gives the eleven datasets used in the meta-analysis. The y-axis is the predicted sentsitivity to VPA. The horizontal line indicates the median for each dataset. The box ranges from the 25th to the 75th percentile. The whiskers show the maximum and minimum value for each dataset, excluding outliers, which are indicated by plus signs. P-values from ANOVA are given below the graphs.



Supplemental Figure 2. Predicted response to fulvestrant across breast cancer subtypes. Heatmap of predicted sensitivity to fulvestrant, an estrogen antagonist. Each vertical line is a sample. Red indicates more sensitive and blue indicates less sensitive.



Supplemental Figure 3. PLX4032 Signature and Validation. (A) Box-whisker plot of predicted PLX4032 sensitivtiy across the GSK cell lines stratified by the presence of a B-RAF mutation as listed in the Sanger database. (B) Box-whisker plot for PLX4032 sensitivity across cancer types in GSE5364. Boxes for normal adjacent tissue are checkered. Median is indicated by a horizontal line. The box gives the interquartile range, and the error bars indicate the total range. (C) Doughnut plot of the level 6 Gene Ontology terms for the genes in the PLX4032 signature with Bayes factor greater than 2. Bayes factor for each term is given on the doughnut



Supplemental Figure 4. In vivo response to VPA and doxorubicin in a VPA-sensitive xenograft. Ten mice are in each sample.

GEO GSE	Basal-like	Her2+	Luminal A	Luminal B	Normal-like	Total
GSE2034	66	36	86	85	13	**286**
GSE2603	30	13	22	25	9	**99**
GSE3494	16	16	38	27	23	**120**
GSE1456	28	12	41	49	29	**159**
GSE5460	38	20	39	27	3	**127**
GSE6532	45	35	111	148	73	**412**
GSE7390	42	14	41	49	12	**158**
MDA	28	24	31	30	13	**126**
GSE7904	20	8	8	11	3	**50**
GSE12276	60	35	50	49	10	**204**
GSE14020	19	12	13	12	6	**62**
Total	**392**	**225**	**480**	**512**	**194**	**1803**

Supplemental Table 1. Subtype breakdown for the eleven independent breast cancer datasets. Duplicate samples from overlapping datasets have been removed.