

Supplementary Table S3. 83-gene panel sequencing data. (Attached)

Supplementary Table S4. Limma and GOSTats analysis for differentially expressed genes and enriched biological pathways induced by treatment. (Attached)

The 1st spreadsheet provides the analysis of individual genes including the test statistics, the raw P-value and the FDR adjusted P-value (qvalue) on an overall F-test testing for any significance among the three comparisons (C1D1 vs. C0D1, C1D15 vs. C1D1, Surgery vs. C1D15) and the t tests for each comparison between two time points. Yellow highlighted are selected ER regulated genes that were significantly reduced at C1D1 compared to C0D1. The 2nd spreadsheet gives the gene ontology (GO) analysis result on enriched GO terms for genes significantly differentially expressed (DE) between C1D1 versus C0D1 (i.e., anastrozole effect genes). The 3rd spreadsheet gives the gene ontology (GO) analysis result on enriched GO terms for genes significantly differentially expressed (DE) between Surgery vs. C1D15 (i.e., palbociclib effect genes).