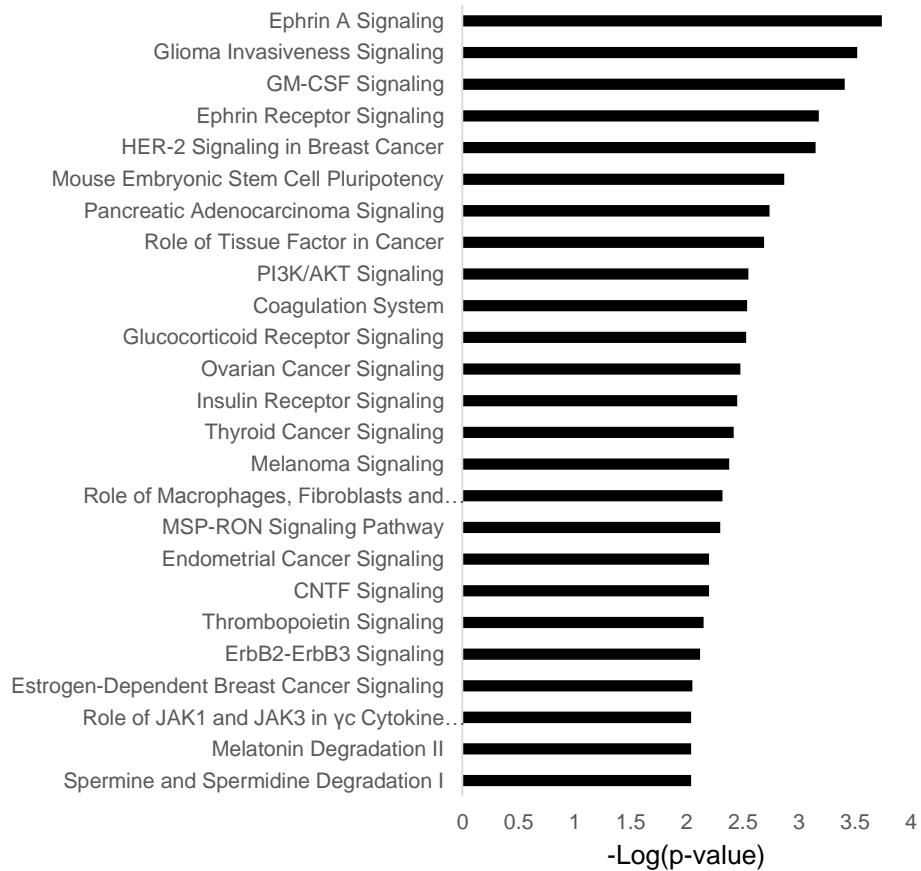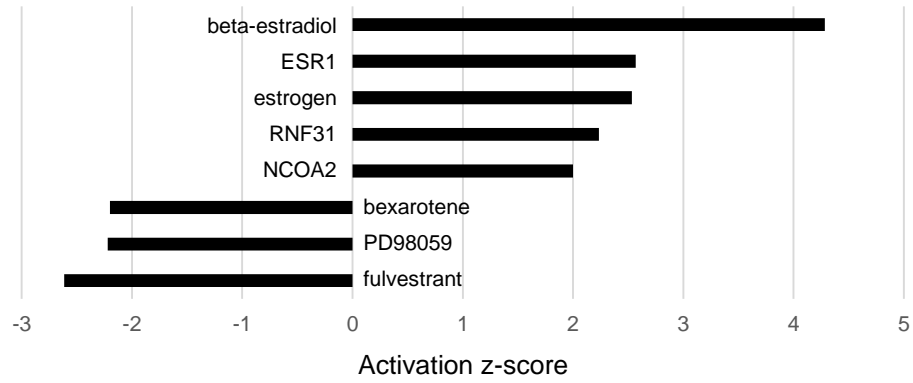Supplemental Figures for

Moving Toward Integrating Gene Expression Profiling into High-throughput Testing: A Gene Expression Biomarker Accurately Predicts Estrogen Receptor α Modulation in a Microarray Compendium

by Ryan *et al*.

Supplemental Figure 1. IPA Canonical Pathways. Top 25 canonical pathways represented by the genes in the ERα biomarker, as indicated by Ingenuity Pathways Analysis.

Supplemental Figure 2. IPA Upstream Regulators. Transcription factors (TFs) and chemicals predicted to act as upstream regulators of ERα biomarker genes, as determined by Ingenuity Pathways Analysis. Only TFs or chemicals with activation z-scores ≥ 2 are shown.
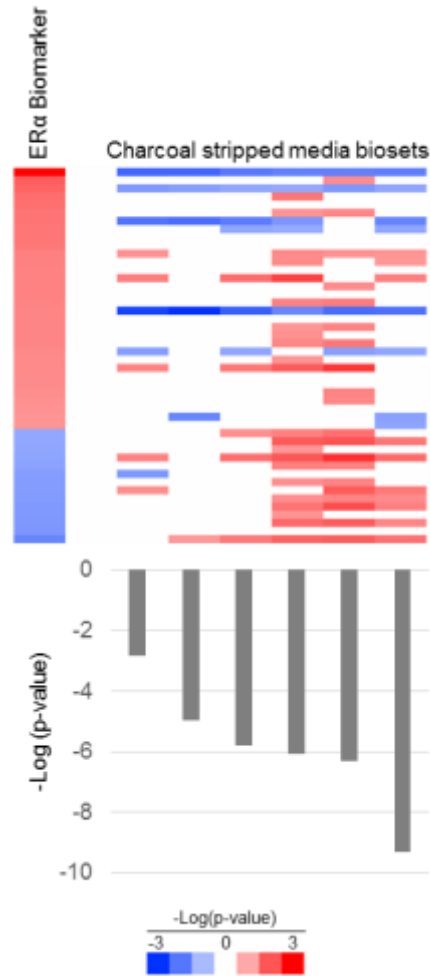
Supplemental Figure 3. Stripping media of steroids results in suppression of ERα. (Top) Heat map showing expression behavior of 6 biosets from GSE51448 in which MCF-7 cells were grown in charcoal stripped media (CSM) vs. unstripped media. Note that culture medium with 10% fetal bovine serum contains approximately 20 pM E2. While many of the positive biomarker genes were suppressed, most of the negative biomarker genes exhibited increased expression. (Bottom) –log(p-values) from predictions using the ERα biomarker. Of the 6 biosets, 5 exhibited significant suppression of ERα.