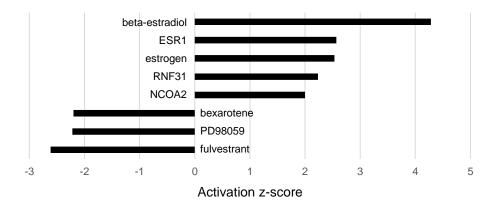
Supplemental Figures for

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

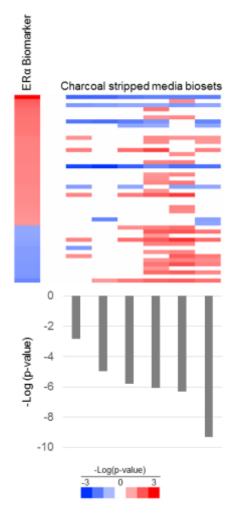
Ephrin A Signaling Glioma Invasiveness Signaling **GM-CSF** Signaling Ephrin Receptor Signaling HER-2 Signaling in Breast Cancer Mouse Embryonic Stem Cell Pluripotency Pancreatic Adenocarcinoma Signaling Role of Tissue Factor in Cancer PI3K/AKT Signaling **Coagulation System Glucocorticoid Receptor Signaling Ovarian Cancer Signaling** Insulin Receptor Signaling Thyroid Cancer Signaling Melanoma Signaling Role of Macrophages, Fibroblasts and. MSP-RON Signaling Pathway Endometrial Cancer Signaling **CNTF** Signaling Thrombopoietin Signaling ErbB2-ErbB3 Signaling Estrogen-Dependent Breast Cancer Signaling Role of JAK1 and JAK3 in vc Cytokine. Melatonin Degradation II Spermine and Spermidine Degradation I 0 0.5 1.5 2 2.5 1 3 3.5 4 -Log(p-value)

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Supplemental Figure 1. IPA Canonical Pathways. Top 25 canonical pathways represented by the genes in the ER α 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 ER α 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 ER α . (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 ER α biomarker. Of the 6 biosets, 5 exhibited significant suppression of ER α .