

1 **Supplemental File 2**

2 **for**

3
4 **Identification of Novel Activators of the Metal Responsive Transcription Factor (MTF-1)**

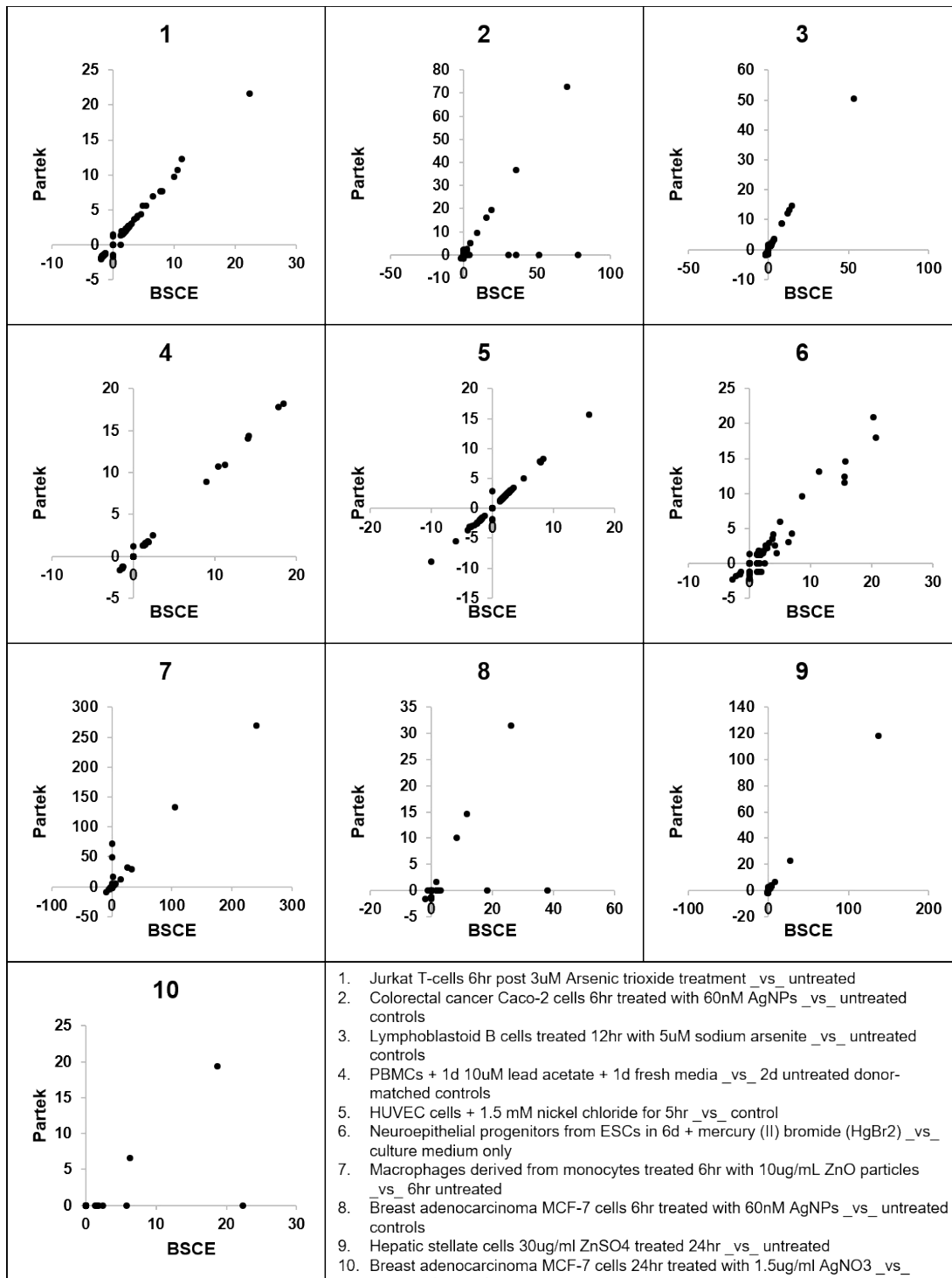
5 **Using a Gene Expression Biomarker in a Microarray Compendium**

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7 Abigail C. Jackson^{1,2}, Jerry Liu¹, Beena Vallanat¹, Carlton Jones¹, Mark D. Nelms^{1,3}, Grace
8 Patlewicz¹ and J. Christopher Corton^{1*}

9
10 ¹Center for Computational Toxicology and Exposure, US Environmental Protection Agency,
11 Research Triangle Park, NC 27711

12 ²Department of Chemistry, Duke University, Durham, NC 27708

13 ³Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA.



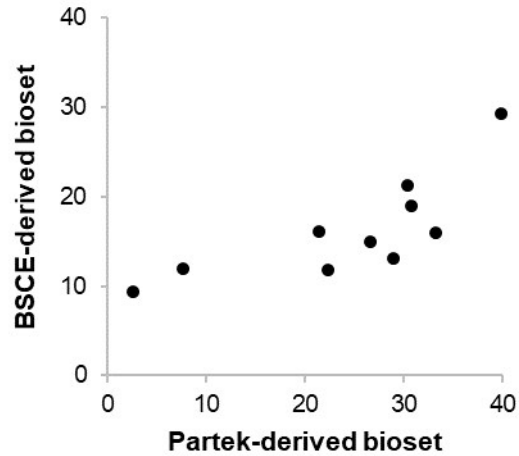
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15 **Figure S1. Comparison of gene lists from BSCE and those generated in Partek Genomics**
 16 **Suite for the ten biosets used in the biomarker.**

17 Only genes which are present in the biomarker are shown. A minor number of the genes present
 18 in BSCE gene lists were found to be insignificant using the Partek method indicating that the

19 statistical filters used in the Partek analysis were slightly more stringent than those used by
20 BSCE.

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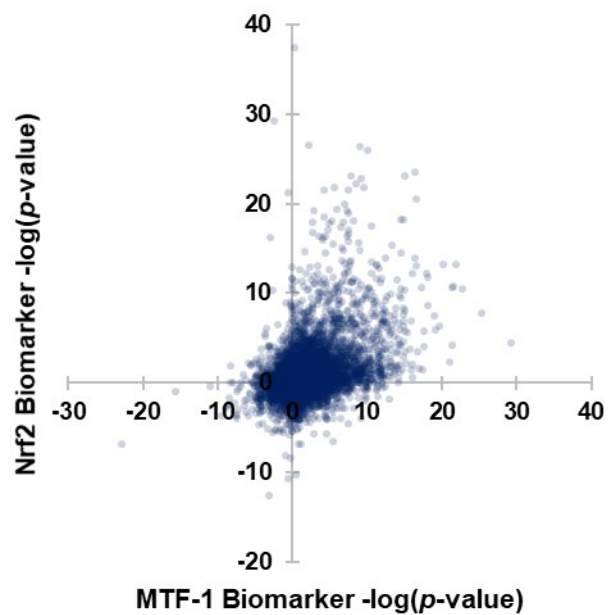
23 **Figure S2. Comparison of the $-\log(p\text{-value})$ s from the Partek-derived vs. the BSCE-derived**
24 **lists.**

25 A regression analysis indicated an R^2 value of 0.600 ($p\text{-value} = 0.0085$) indicating that the
26 biomarker correlations were similar independent of the method used to derive the bioset.

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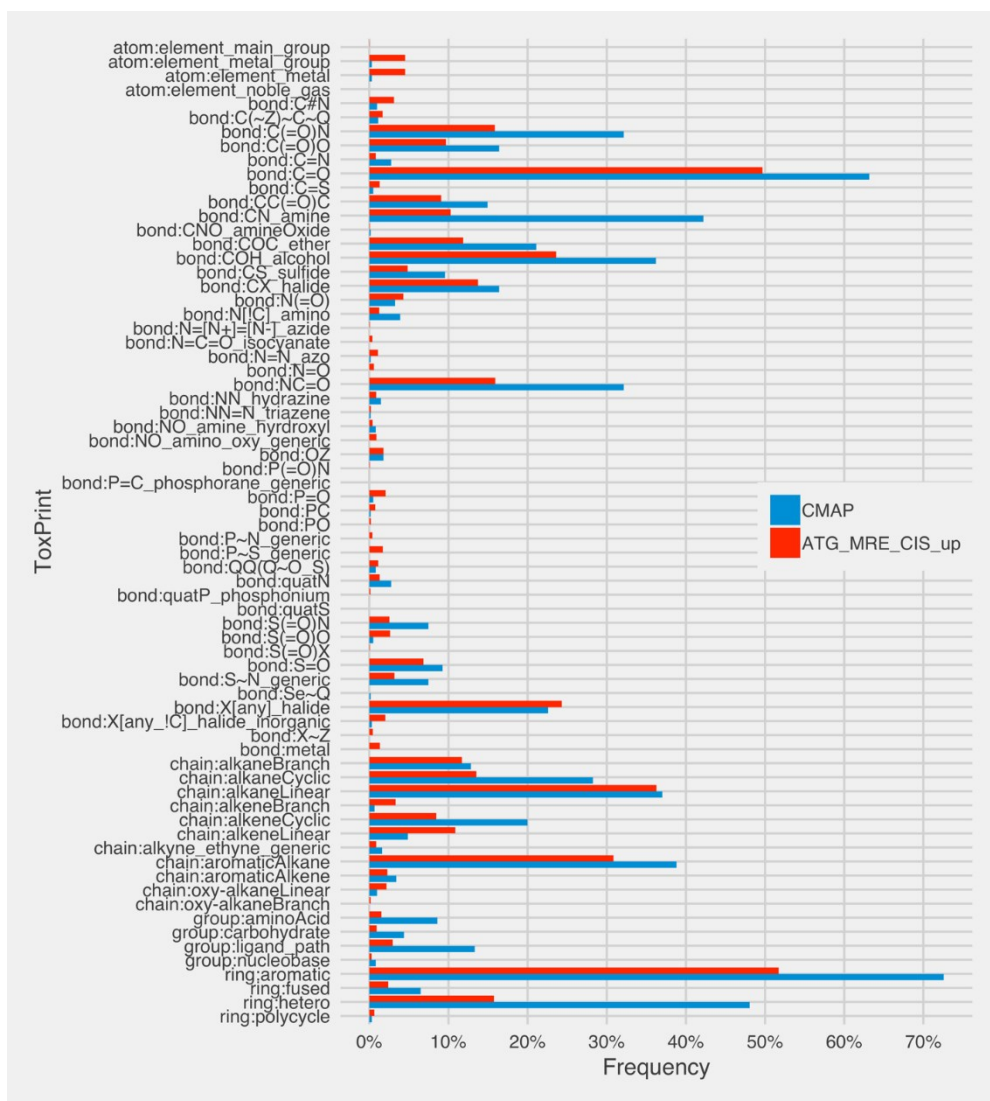
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31 **Figure S3. MTF-1 and Nrf2 are simultaneously activated by chemical exposure.**

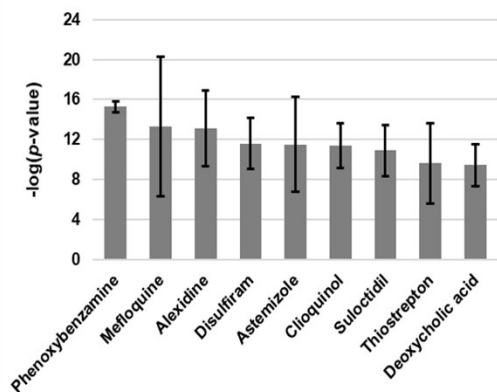
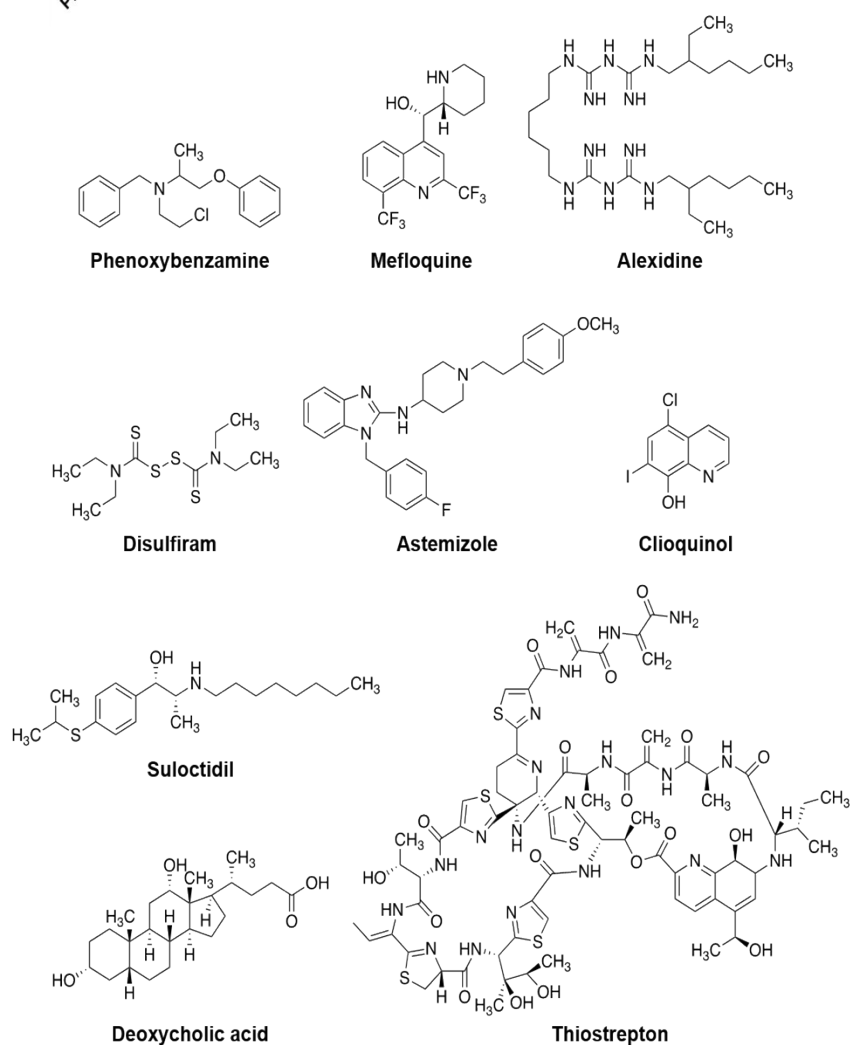
32 The -log(p-value)s for correlations of 11,735 biosets of chemical vs. control comparisons
33 between the Nrf2 and MTF-1 biomarkers are shown.



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35 **Figure S4.** Comparison of the frequency of the 70 “level 2” ToxPrints for the chemicals in the
 36 CMAP dataset (blue) and the chemicals tested in the ToxCast ATG_MRE_CIS_up assay (red).

37

A**B**

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39 **Figure S5. Analysis of nine putative MTF-1 activators.**

40 A. Average $-\log(p\text{-value})$ of the correlation across biosets for each chemical examined and the
 41 MTF-1 biomarker for 9 predicted MTF-1 activators. Error bars show standard deviation (n = 2–
 42 4.)

43 B. Structures of the nine chemicals.

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46 **Figure S6. Identification of genes that exhibit expression changes in the MTF-1-null cells.**

47 Control wild-type MCF-7 and control MTF-1-null cells were examined for expression changes
48 using TempO-Seq human 1500+ platform examining the expression changes in ~3000 genes.

49 Significant expression differences between *MTF1*-null vs. wild-type cells were identified as
50 described in the Methods. There were 44 genes that were differentially expressed in the *MTF1*-
51 null vs. wild-type comparison.

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