Supplementary Tables

Table S1: Gene ontology results. Gene ontology output for caffeine downregulated genes (A), caffeine upregulated genes (B), dexamethasone downregulated genes (C), dexamethasone upregulated genes (D), retinoic acid downregulated genes (E), and selenium downregulated genes(F). Note that retinoic acid and selenium had no significantly enriched gene ontology terms for upregulated genes.

A) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1A`
B) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1B`
C) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1C`
D) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1D`
E) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1E`
F) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S1F`

Table S2: 1000 Genomes SNP annotations. We have annotated 1000 Genomes SNPs on the basis of whether they are within (1) or not within (0) a response factor footprint for each treatment. Column 1 is the SNP ID including chromosome and position, column 2 - 6 are annotations for dexamethasone, caffeine, selenium, retinoic acid, and the combined controls, respectively.

`http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S2.txt.gz`

Table S3: Enrichment of footprints in opening DARs. For retinoic acid (A), dexamethasone (B), and caffeine (C), we have included the motif enrichment in DARs in opening chromatin. Columns 1-11 are: 1) Motif ID, 2) Odds ratio from Fisher's exact test for opening DARs, 3) Lower bound of 95% confidence interval of odds ratio for opening DARs, 4) Upper bound of 95% confidence interval of odds ratio for opening DARs, 5) P-value from Fisher's exact test for opening DARs, 6) Number of footprints in opening DARs, 7) Number of footprints in regions tested for differential accessibility that are not opening DARs, 8) Number of opening DARs without footprint, 9) Number of regions tested for differential accessibility without opening DARs and without footprint, 10) Benjamini-Hochberg adjusted p-value, 11) Transcription factor name.

A) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S3A.tab`
B) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S3B.tab`
C) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S3C.tab`

Table S4: Enrichment of footprints in closing DARs. For caffeine (A) and selenium (B), we have included the motif enrichment in DARs in closing chromatin. Columns 1-11 are: 1) Motif ID, 2) Odds ratio from Fisher's exact test for closing DARs, 3) Lower bound of 95% confidence interval of odds ratio for closing DARs, 4) Upper bound of 95% confidence interval of odds ratio for closing DARs, 5) P-value from Fisher's exact test for closing DARs, 6) Number of footprints in closing DARs, 7) Number of footprints in regions tested for differential accessibility that are not closing DARs, 8) Number of closing DARs without footprint, 9) Number of regions tested for differential accessibility without closing DARs and without footprint, 10) Benjamini-Hochberg adjusted p-value, 11) Transcription factor name.

A) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S4A.tab`
B) `http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S4B.tab`

Table S5: Colocalization results.This file includes the output from the colocalization with enloc. Columns 1-9 are: 1) eQTL signal ID 2) eQTL posterior inclusion probability (PIP) 3) GWAS PIP 4) number of SNPs in the group 5) original enloc regional colocalization probability (RCP) 6) experimental enloc PIP 7) lead SNP in the signal group 8) SNP-level colocalization probability for the lead SNP 9) tissue.

`http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S5.txt`

Table S6: Colocalization reQTLs.This file includes reQTLs with permutation p<0.05. Columns 1-6 are: 1) rsID of reQTL, 2) gene ID, 3) treatment (sel = selenium, dex = dexamethasone, ret = retinoic acid, caf = caffeine), 4) reQTL effect size, 5) permutation p-value, 6) zvalue from coronary artery disease (CAD) GWAS.

`http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S6.txt`

Table S7: Active factor enrichment.This file includes the enrichment of footprints of each motif in each condition in highly active chromatin. Columns 1-20 are: 1) Motif ID, 2) Transcription factor name, 3) Odds ratio of enrichment of footprints in dexamethasone in highly accessible regions, 4) P-value of enrichment of footprints in dexamethasone in highly accessible regions, 5) Benjamini-Hochberg adjusted p-value of enrichment of footprints in dexamethasone in highly accessible regions, 6) Odds ratio of enrichment of footprints in caffeine in highly accessible regions, 7) P-value of enrichment of footprints in caffeine in highly accessible regions, 8) Benjamini-Hochberg adjusted p-value of enrichment of footprints in caffeine in highly accessible regions, 9) Odds ratio of enrichment of footprints in selenium in highly accessible regions, 10) P-value of enrichment of footprints in selenium in highly accessible regions, 11) Benjamini-Hochberg adjusted p-value of enrichment of footprints in selenium in highly accessible regions, 12) Odds ratio of enrichment of footprints in retinoic acid in highly accessible regions, 13) P-value of enrichment of footprints in retinoic acid in highly accessible regions, 14) Benjamini-Hochberg adjusted p-value of enrichment of footprints in retinoic acid in highly accessible regions, 15) Odds ratio of enrichment of footprints in water control in highly accessible regions, 16) P-value of enrichment of footprints in water control in highly accessible regions, 17) Benjamini-Hochberg adjusted p-value of enrichment of footprints in water control in highly accessible regions. 18) Odds ratio of enrichment of footprints in ethanol control in highly accessible regions, 19) P-value of enrichment of footprints in ethanol control in highly accessible regions, 20) Benjamini-Hochberg adjusted p-value of enrichment of footprints in ethanol control in highly accessible regions.

`http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S7.txt`

Table S8: TWAS results.This file includes the significant TWAS genes (p-value $< 10^{-5}$ which are differentially expressed in at least one condition. Columns 1-9 are: 1) Chromosome 2) Locus 3) Ensembl gene ID 4) Gene name 5) Tissue 6) Number of SNPs in locus 7) TWAS test statistic 8) TWAS p-value 9) Treatment in which gene is differentially expressed

`http://genome.grid.wayne.edu/FUNGEI/data_tables/Table_S8.txt`

Supplementary Figures

Figure S1: Differential gene expression near DARs QQ-plot of p-values from DESeq2 analysis of gene expression for dexamethasone (**A**), caffeine (**B**), and selenium (**C**). The colored dots represent genes within 50kb of a DAR, while the gray dots represent genes not within 50kb of a DAR.