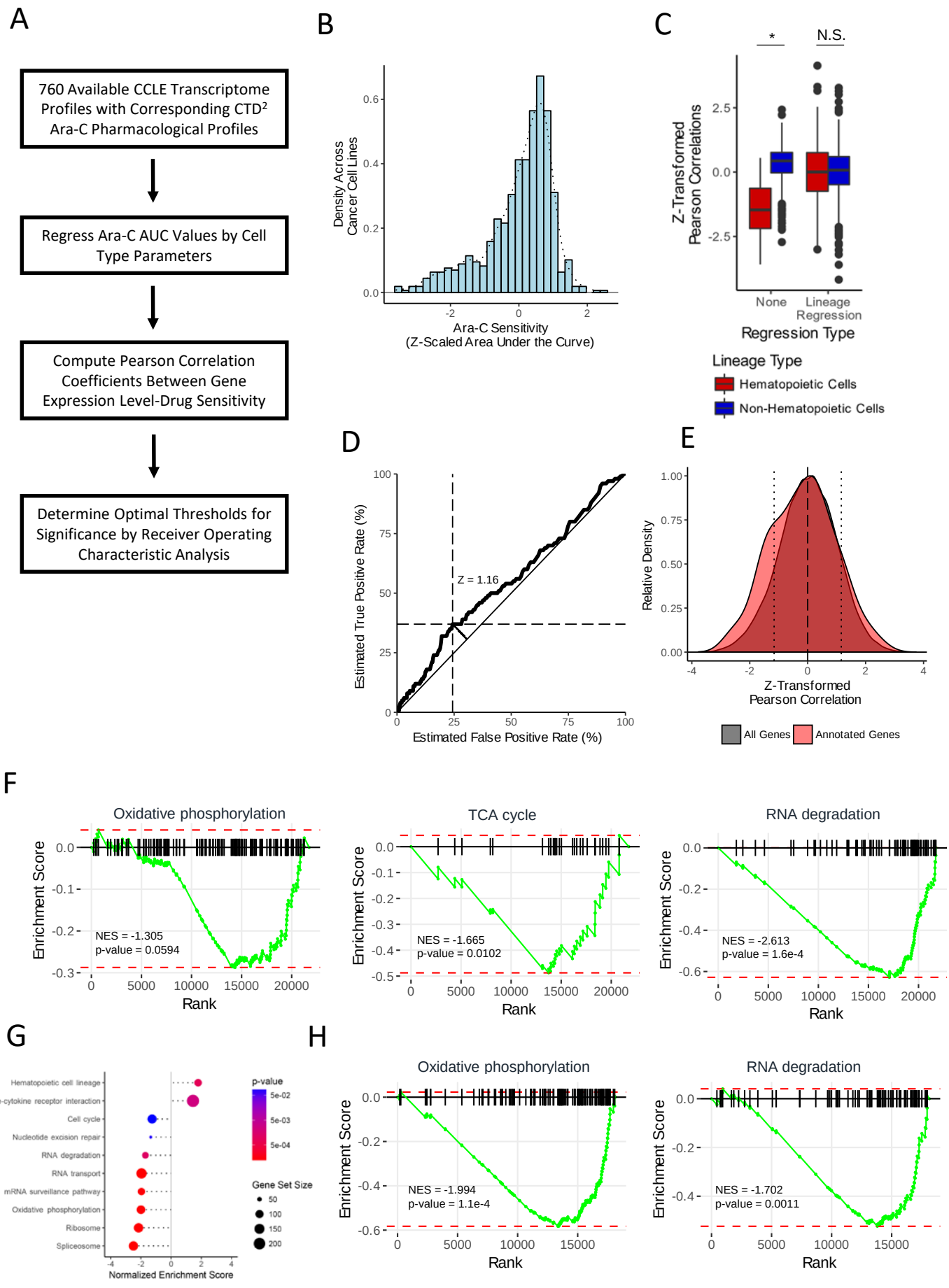
Figure S1.


A
760 Available CCLE Transcriptome Profiles with Corresponding CTD² Ara-C Pharmacological Profiles
Regress Ara-C AUC Values by Cell Type Parameters
Compute Pearson Correlation Coefficients Between Gene Expression Level-Drug Sensitivity
Determine Optimal Thresholds for Significance by Receiver Operating Characteristic Analysis
B
Density Across Cancer Cell Lines
Ara-C Sensitivity (Z-Scaled Area Under the Curve)
C
*
N.S.
Z-Transformed Pearson Correlations
None
Lineage Regression
Regression Type
Lineage Type
Hematopoietic Cells
Non-Hematopoietic Cells
D
Z = 1.16
Estimated True Positive Rate (%)
Estimated False Positive Rate (%)
E
Relative Density
Z-Transformed Pearson Correlation
All Genes
Annotated Genes
F
Oxidative phosphorylation
NES = -1.305
p-value = 0.0594
TCA cycle
NES = -1.665
p-value = 0.0102
RNA degradation
NES = -2.613
p-value = 1.6e-4
Enrichment Score
Rank
G
Hematopoietic cell lineage
Cytokine-cytokine receptor interaction
Cell cycle
Nucleotide excision repair
RNA degradation
RNA transport
mRNA surveillance pathway
Oxidative phosphorylation
Ribosome
Spliceosome
Significant KEGG Pathways
Normalized Enrichment Score
p-value
Gene Set Size
H
Oxidative phosphorylation
NES = -1.994
p-value = 1.1e-4
RNA degradation
NES = -1.702
p-value = 0.0011