

Co-expression network analysis of asthma samples



Brian Barron

The Data Set

ORIGINAL ARTICLE

Noninvasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma

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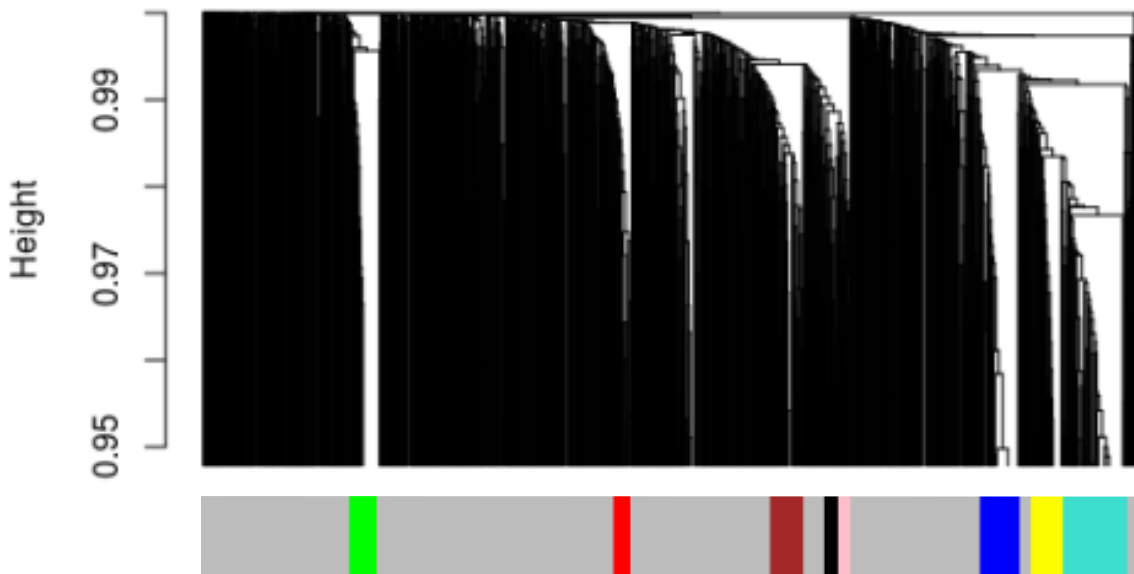
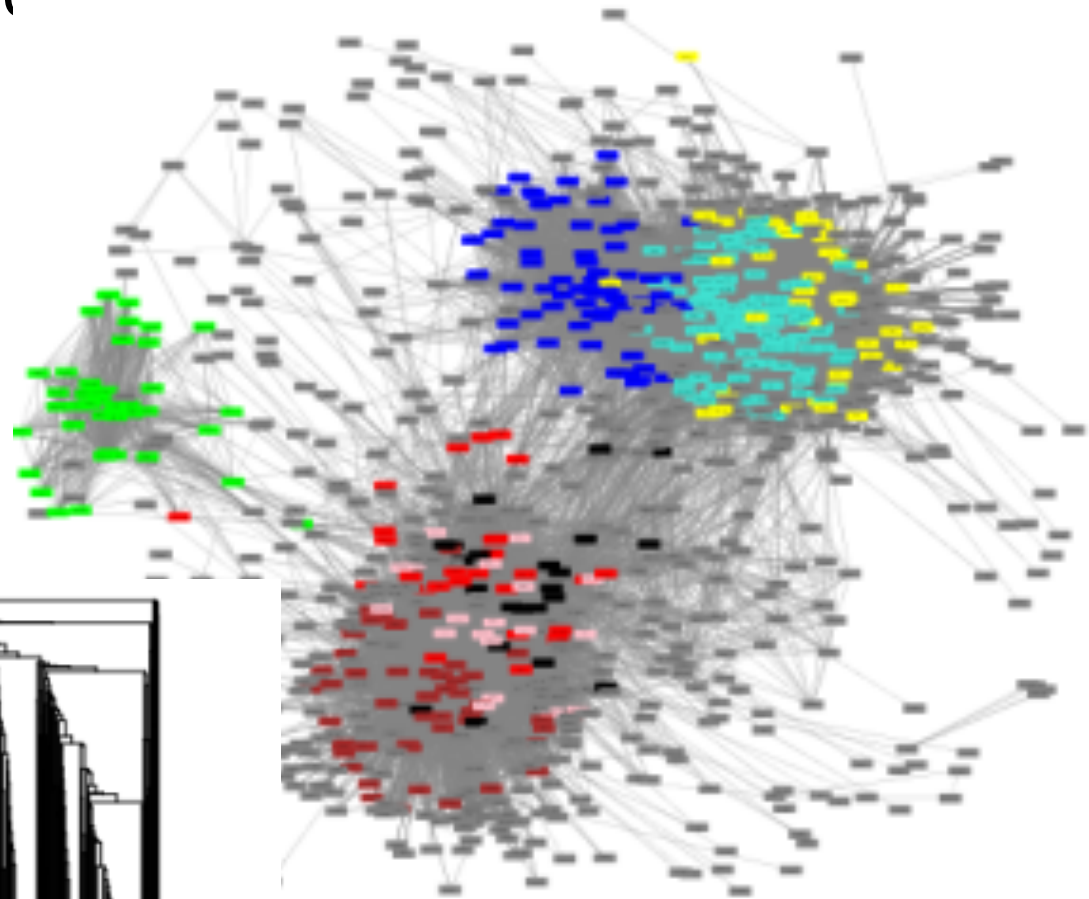
- 112 microarray samples (100 asthma, 12 control)
- 18,309 genes total on Affymetrix 1.0 ST gene array
- Clinical information for each sample
- 3 separate “TEA clusters” (transcriptional profiles) were present in the asthma samples.

Identify modules

Weighted Gene Co-expression Network Analysis (WGCNA)

Langfelder BMC Bioinformatics 2008

- Top 1,500 differentially expressed genes (DEGs) between asthma and control.



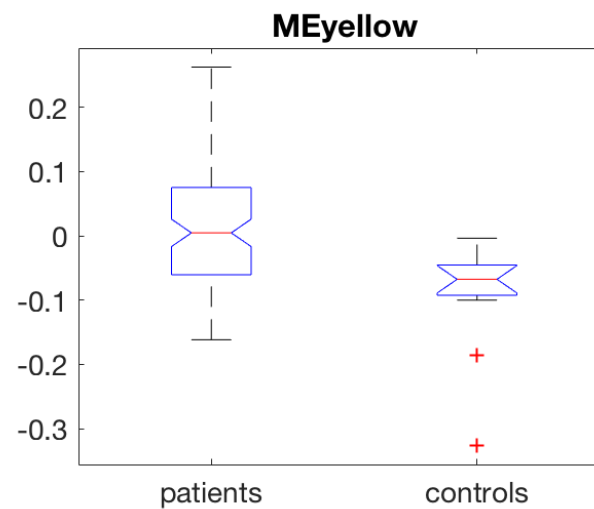
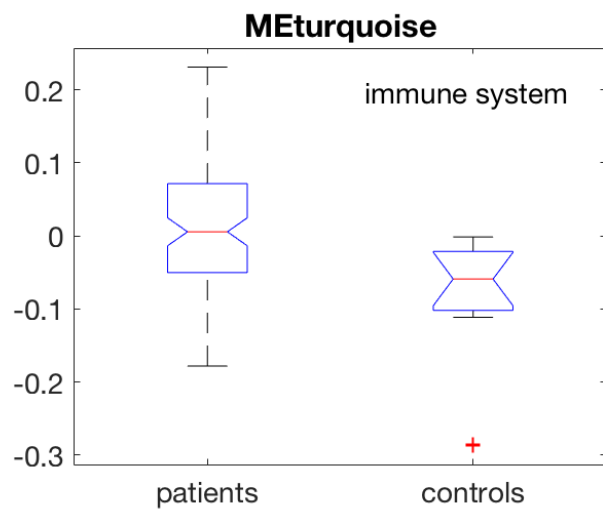
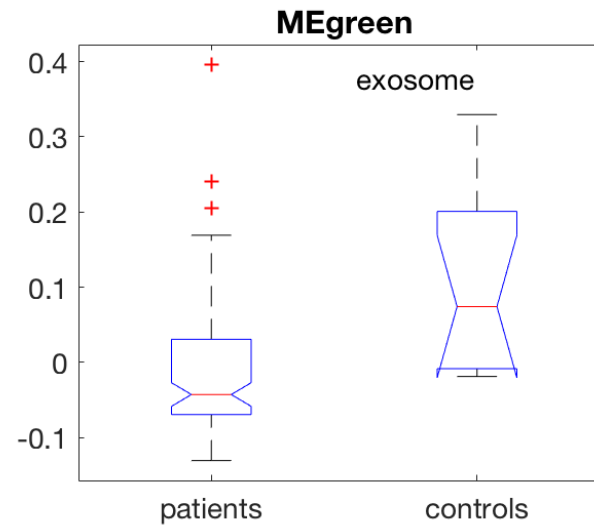
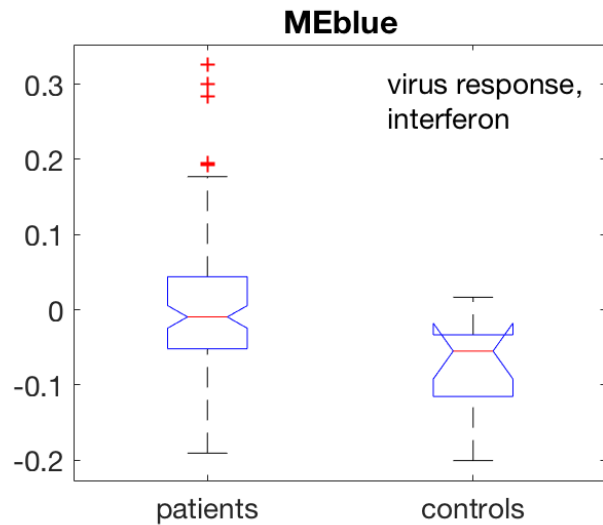
Identify modules

representative genes in a module

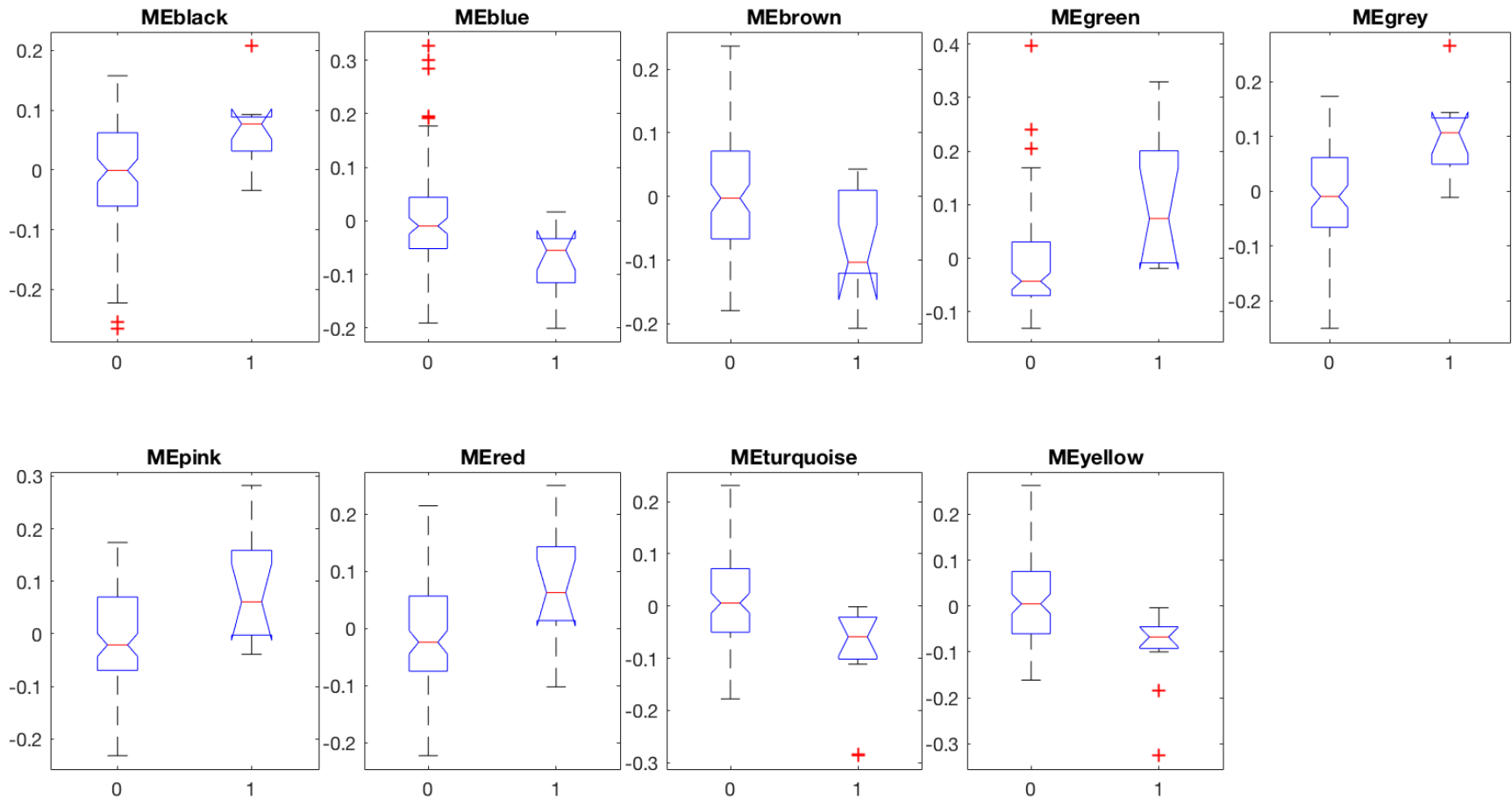
Module	GO enrichment	Eigengene gene
Blue	<i>virus response, interferon</i>	<i>RNF213 (Ubiquitin Ligase)</i>
Yellow		<i>NBPF14</i>
Turquoise	<i>Immune system</i>	<i>LCP2 (T-cell receptor signaling)</i>
Green	<i>Exosome</i>	<i>ECM1 (extracellular matrix prot)</i>
Red		<i>YDJC (deacetylates)</i>
Brown		<i>OSBPL7 (Oxysterol binding)</i>
Black		<i>HNMT (histamine degradation)</i>
Plink		<i>NHLRC2</i>



Module eigengenes separate patients and controls

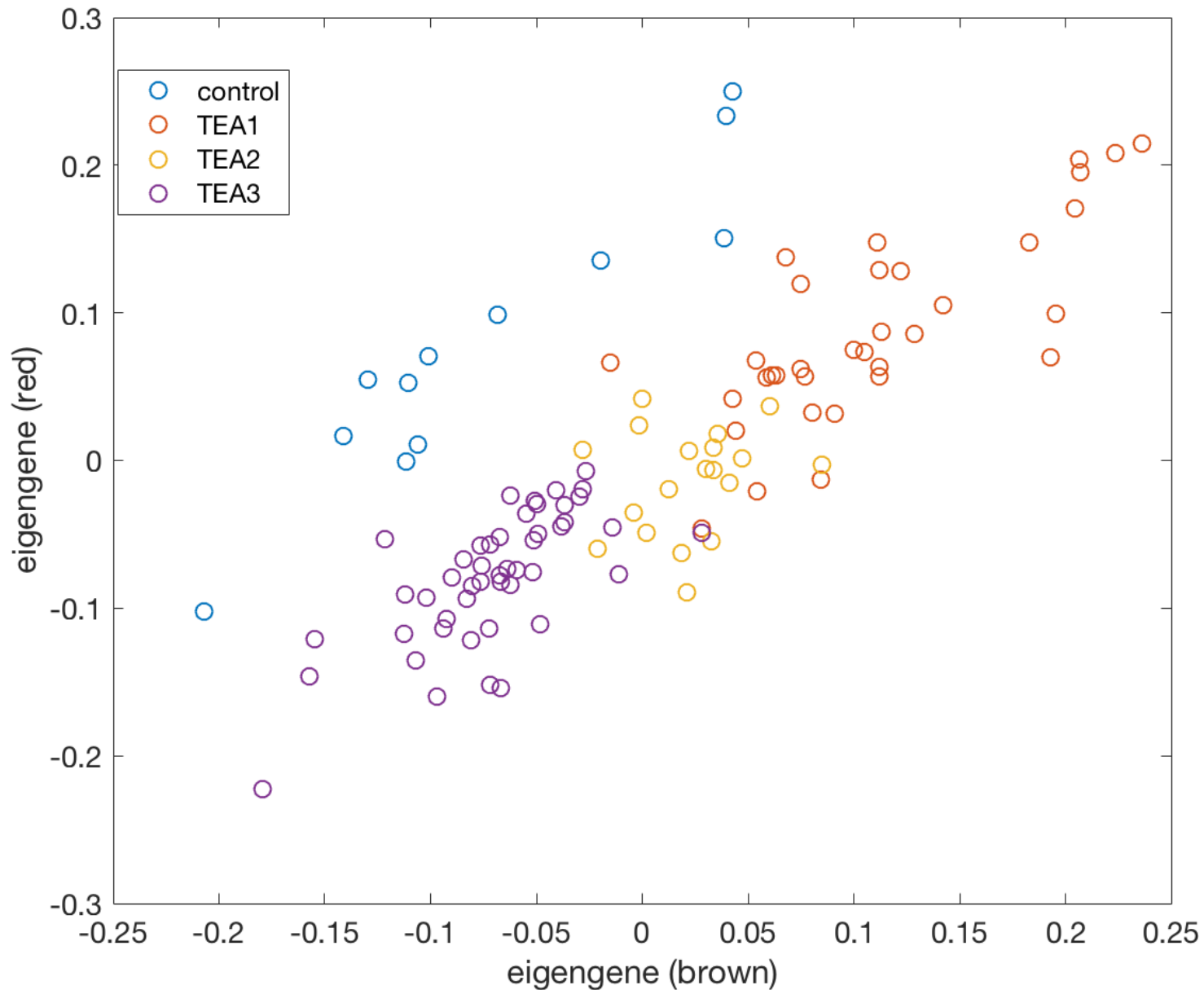


Module eigengenes separate patients and controls

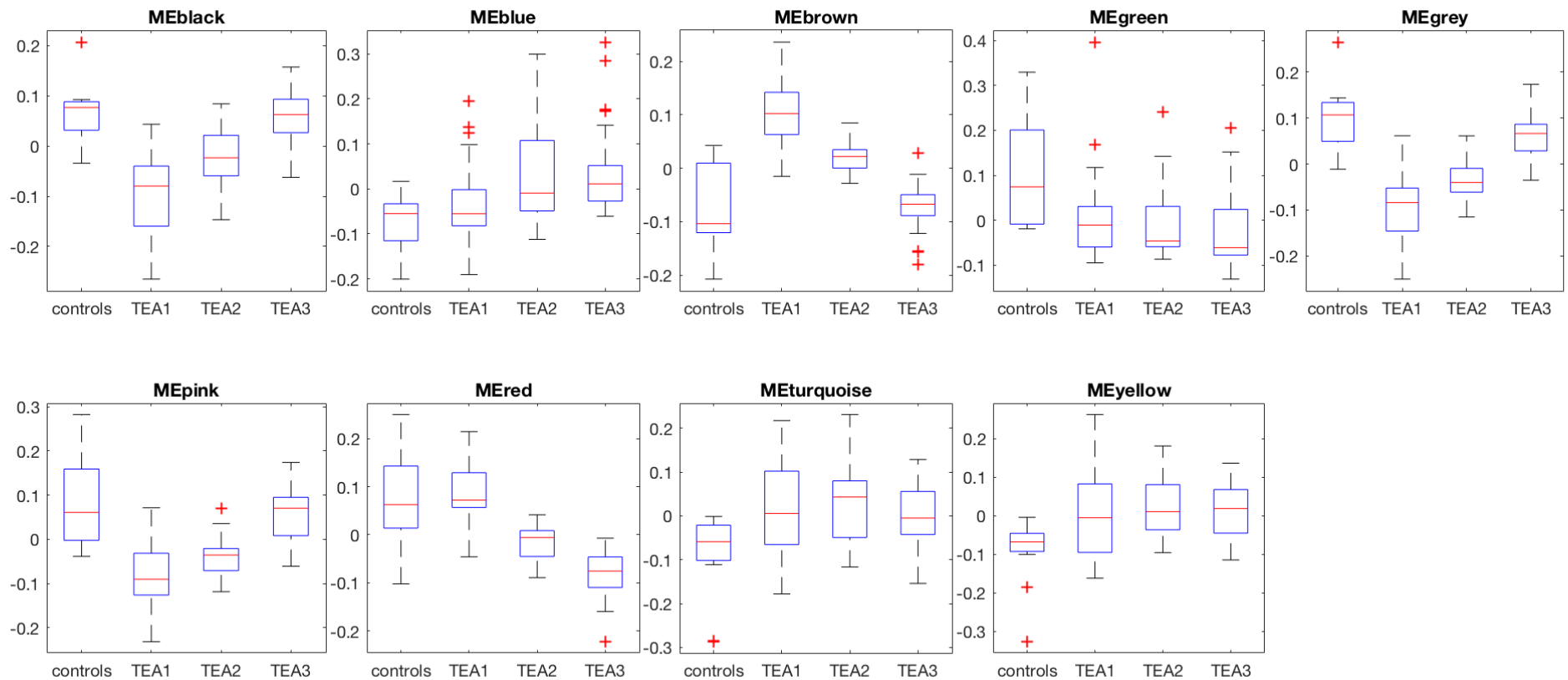


0: patient
1: control

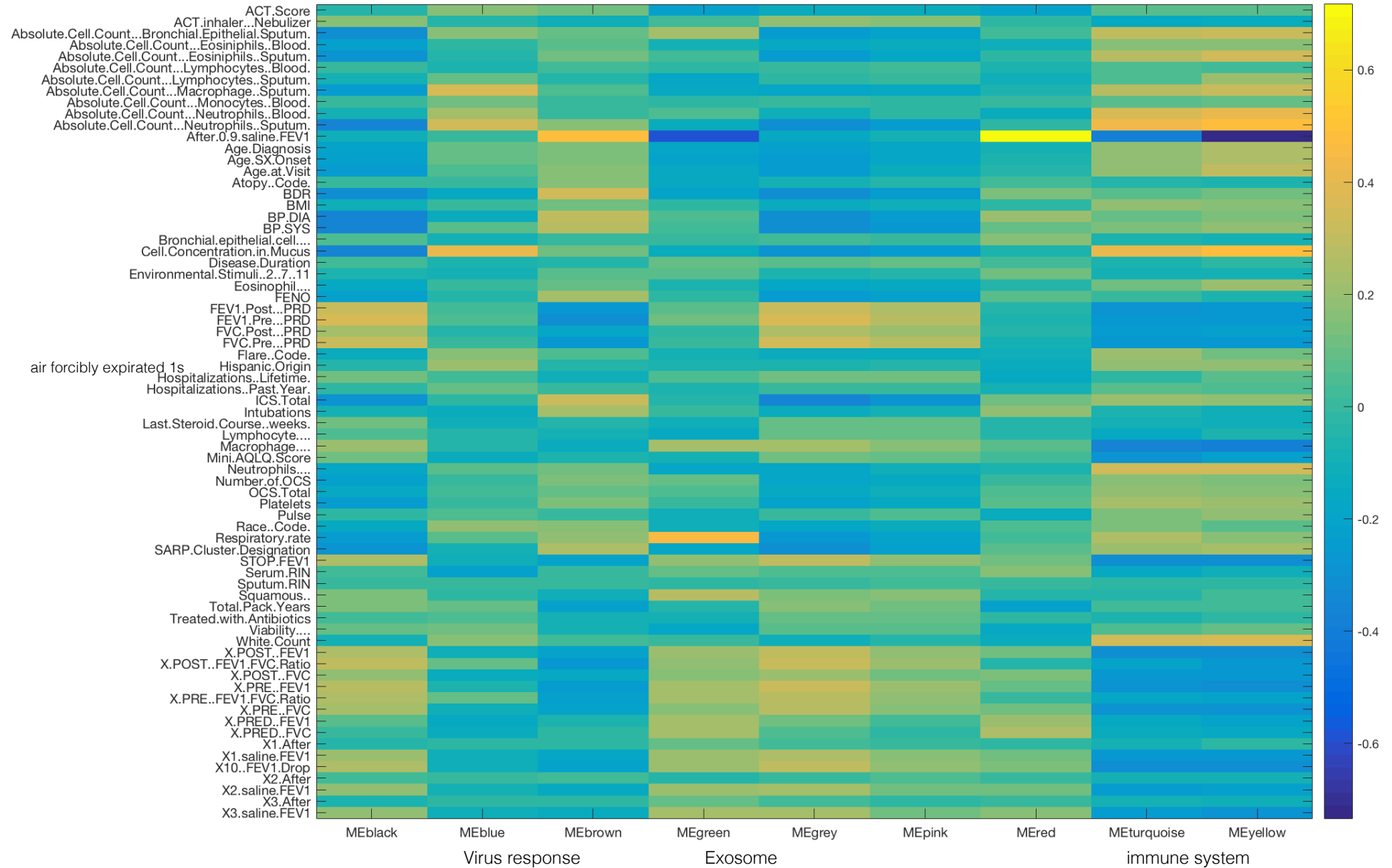
Module eigengenes can predict TEA clusters / redefine TEA clusters



Module eigengenes can predict TEA clusters / redefine TEA clusters

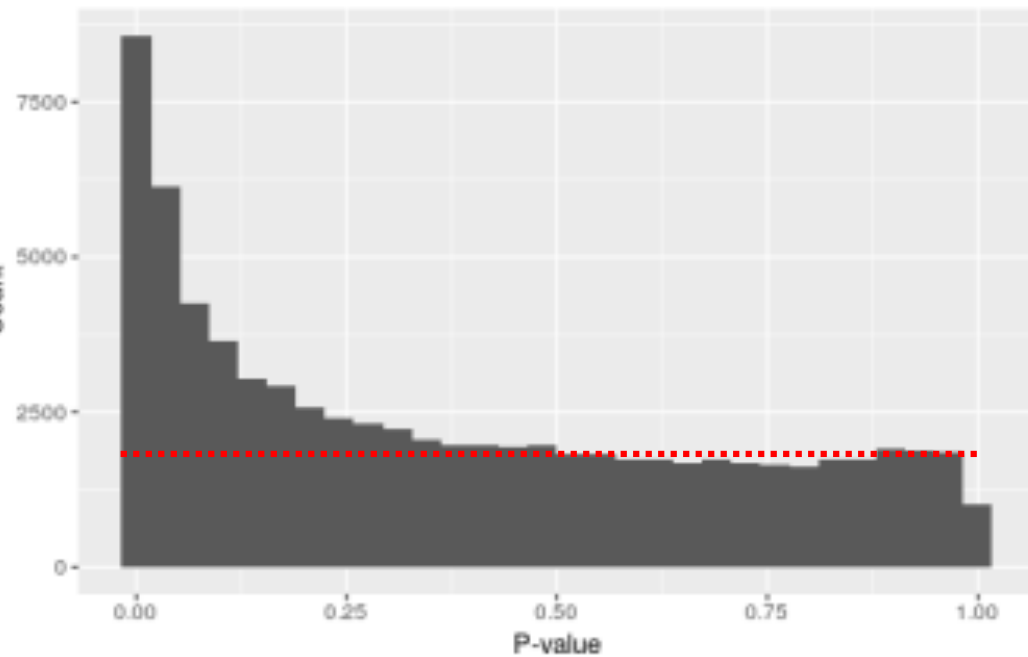


Eigengenes vs clinical features

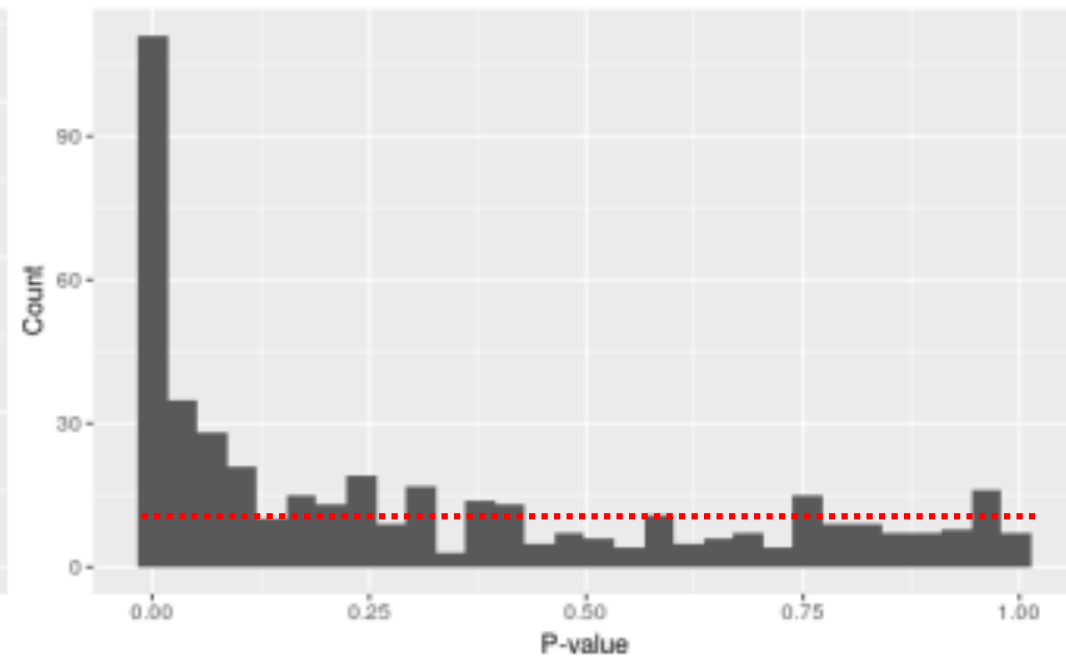


Modules are better biomarkers than individual genes

Gene-by-ClinicalVariable Correlation P-values

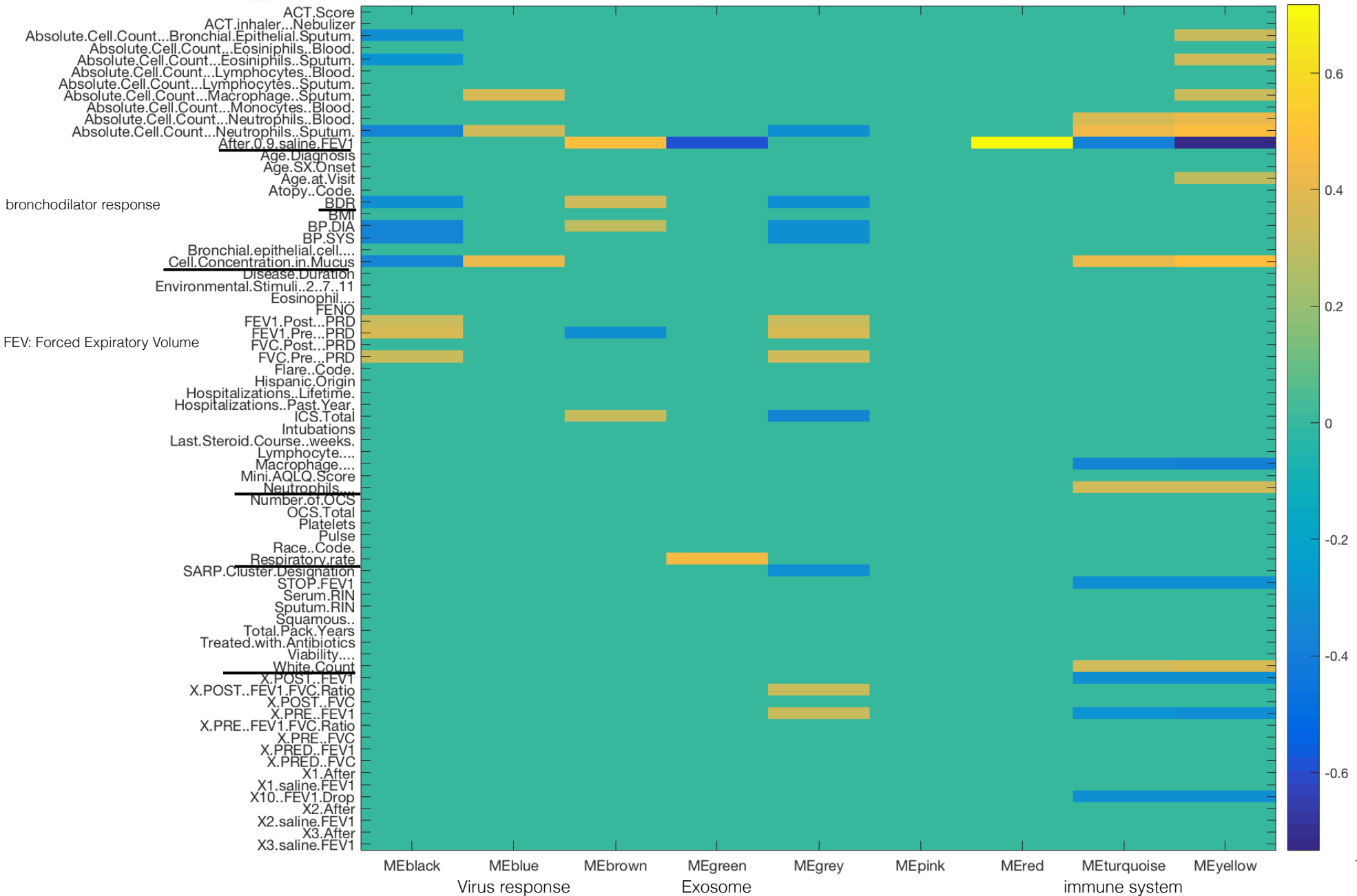


Module-by-ClinicalVariable Correlation P-values



Lower FDR

Eigengenes vs clinical features



Points worth highlighting

- Go from individual genes to network or modules
- Module eigengenes can be used to look at the heterogeneity of asthma patients
 - redefine the TEA clusters
 - correlate with clinical parameters
- Module eigengenes have potential to be biomarkers (lower FDR).
- The same analysis can be repeated based on the bulk RNA-Seq data