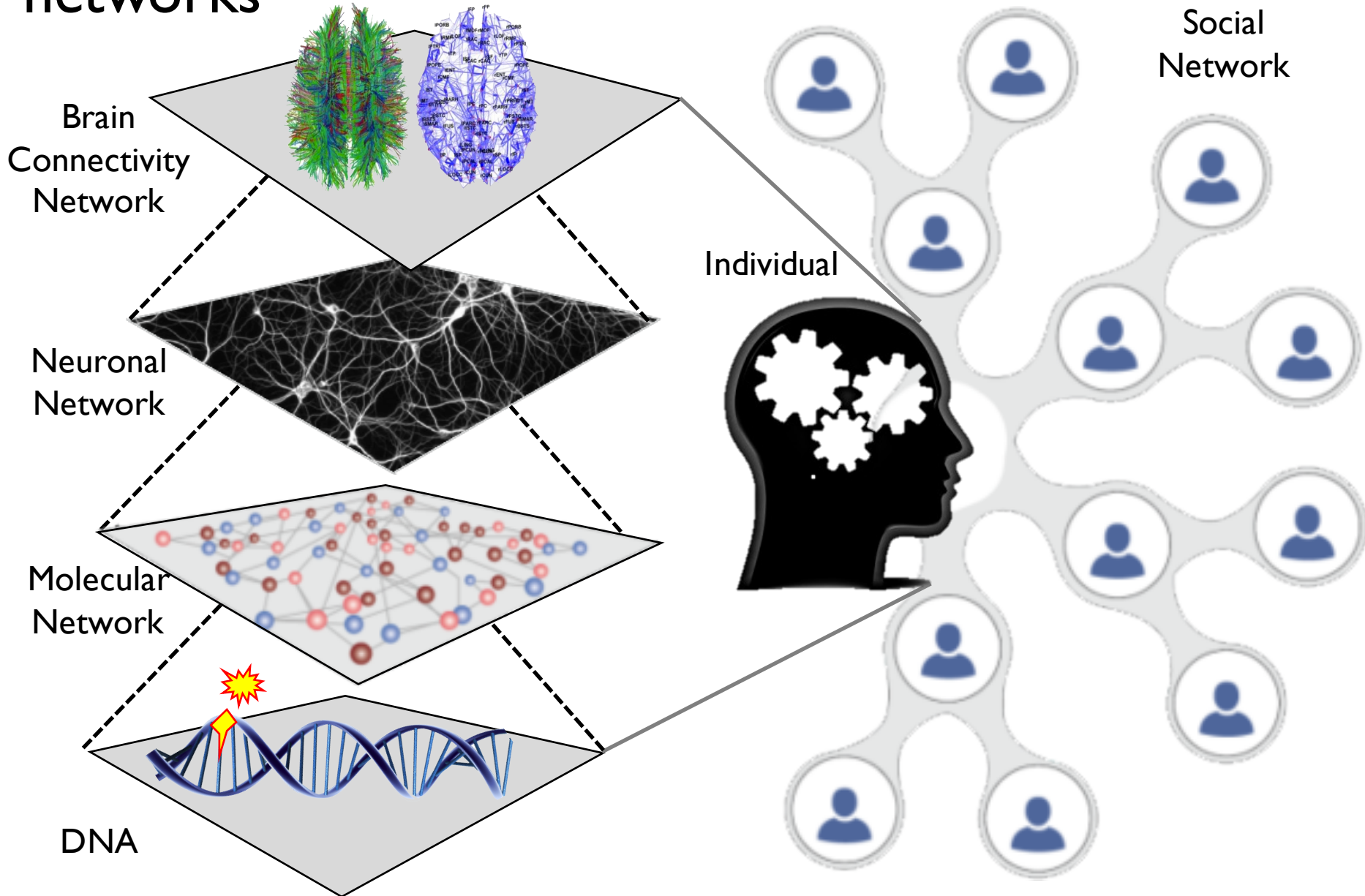




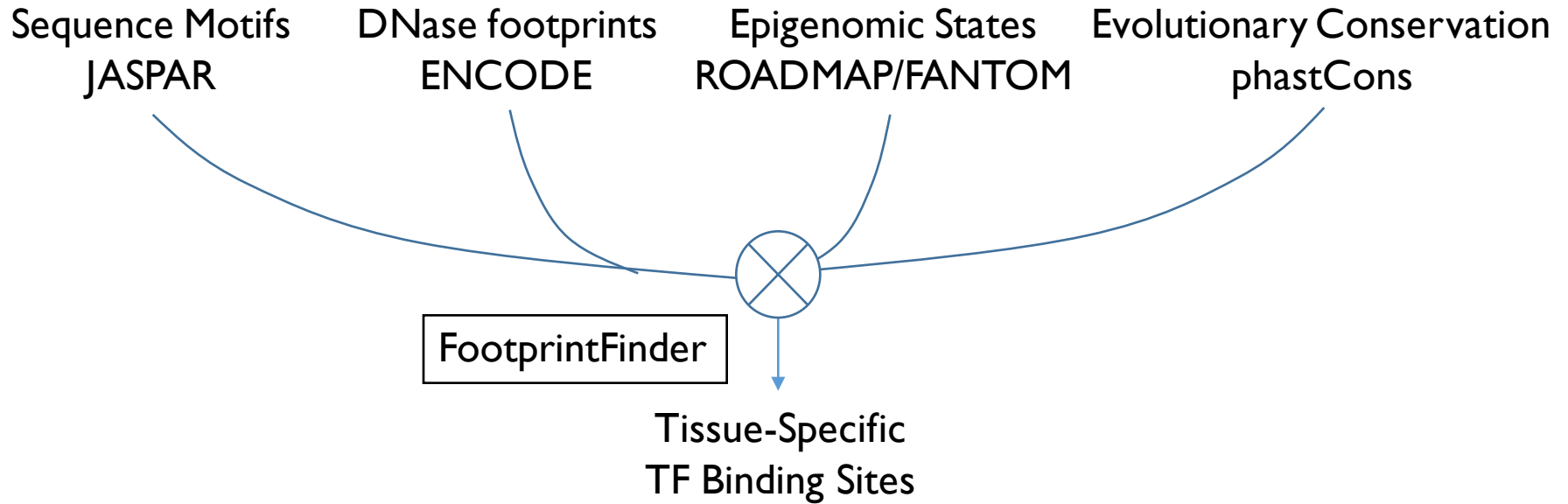
Reconstruction and Analysis of Transcriptional Regulatory Networks with TReNA

Seth A. Ament
Institute for Systems Biology
Seattle, Washington

Genes influence phenotypes through a network of networks



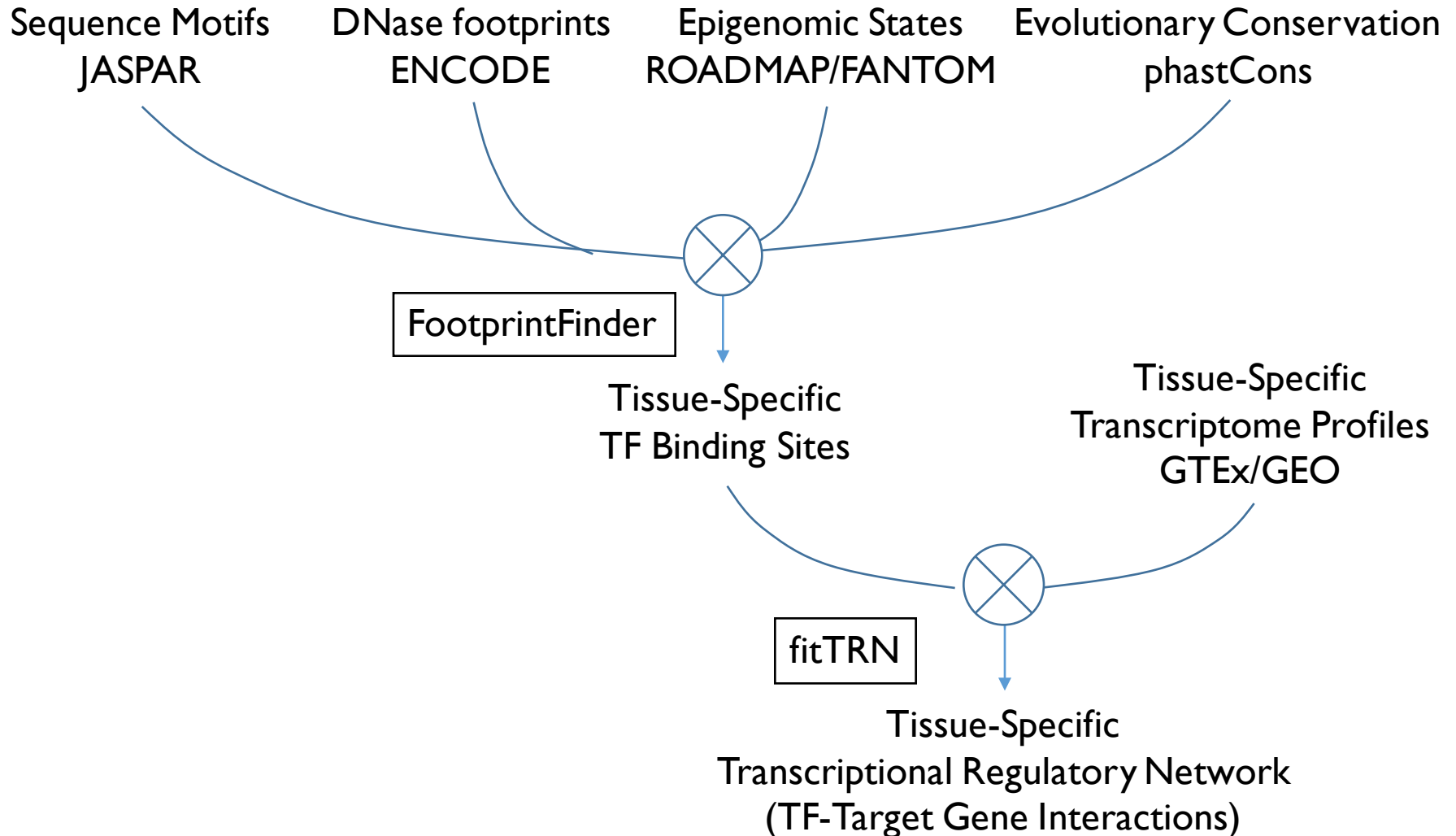
Transcriptional Regulatory Network Analysis (TReNA)



Software Availability:

<https://github.com/PriceLab/TReNA>

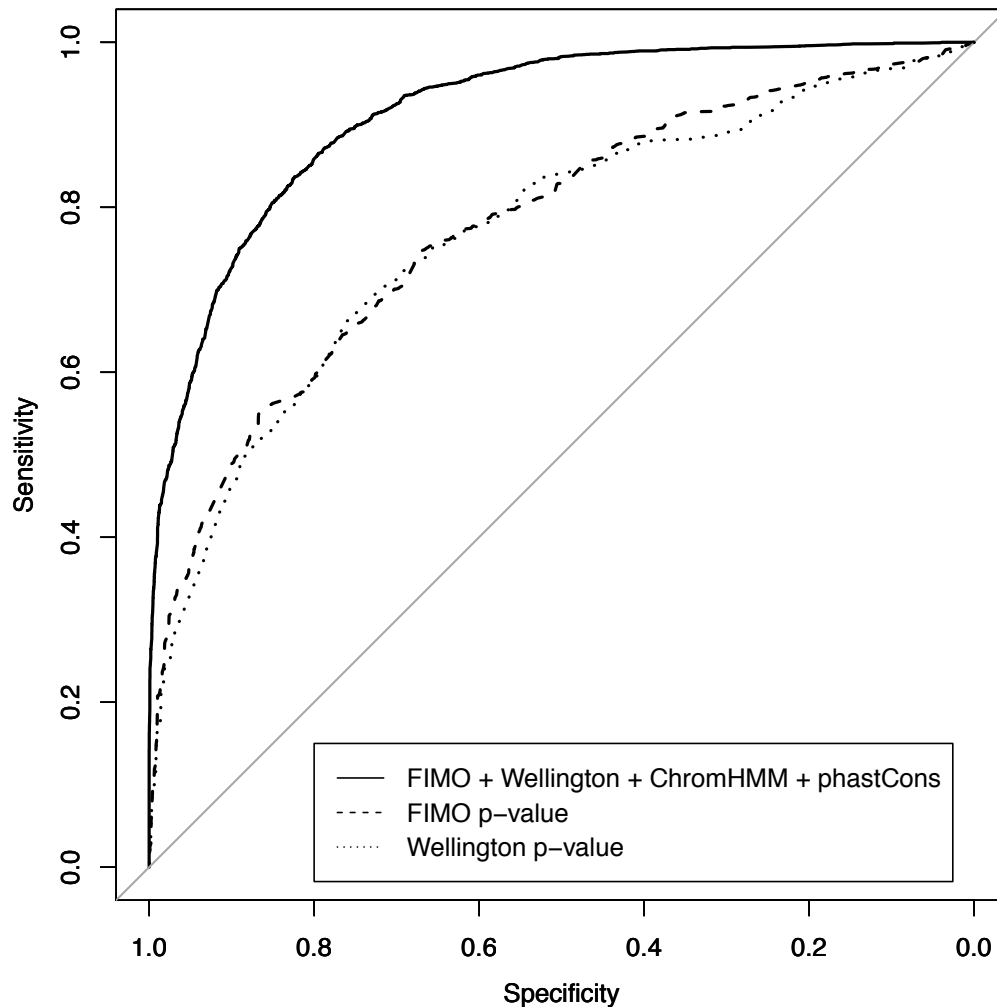
Transcriptional Regulatory Network Analysis (TReNA)



Software Availability:

<https://github.com/PriceLab/TReNA>

Combining diverse annotations improves prediction of TF binding sites



TRUE/FALSE classes:

USFI DNase footprints
with/without *USFI* ChIP-seq
peaks

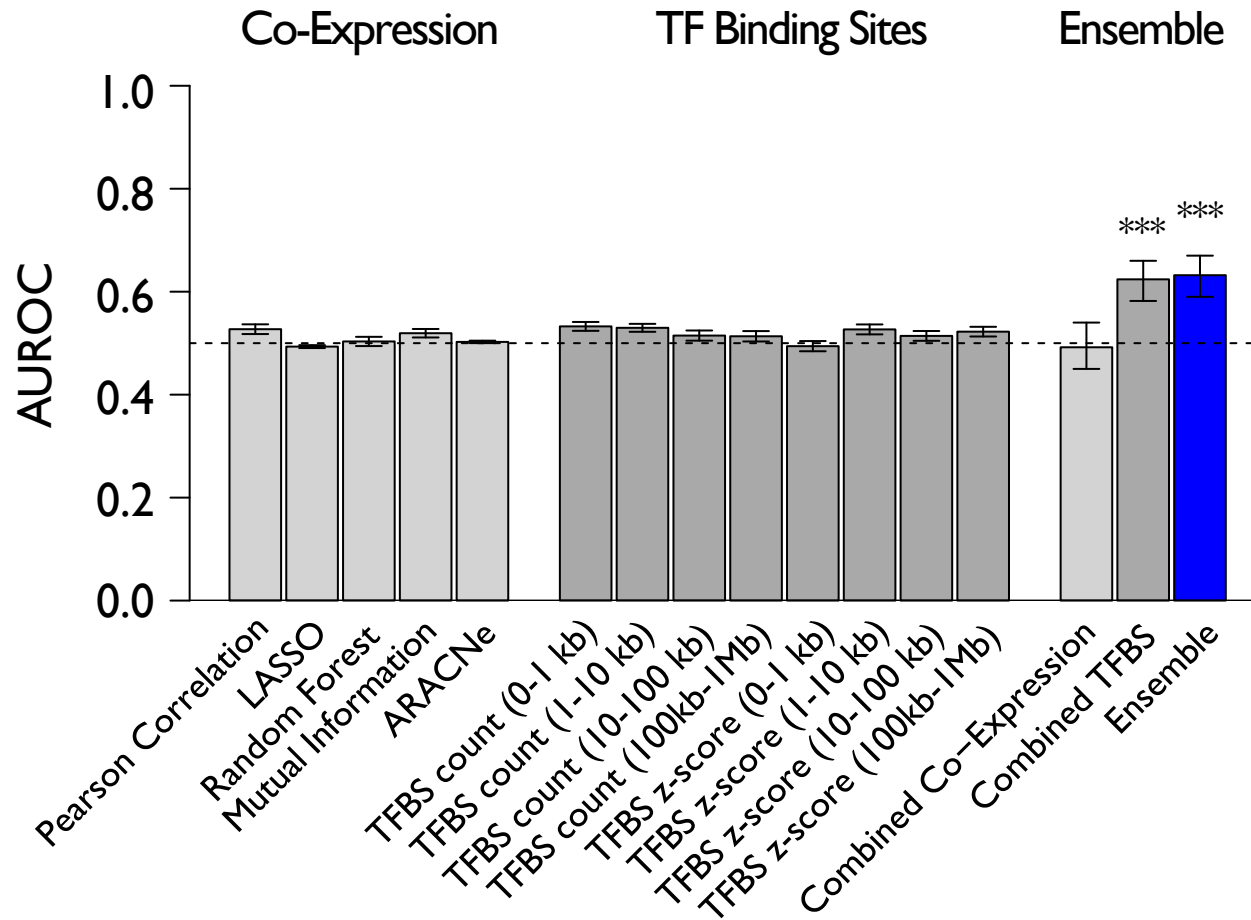
All *USFI* footprints:

79% sensitivity
31% specificity

***USFI* footprints with modeled probability > 50%:**

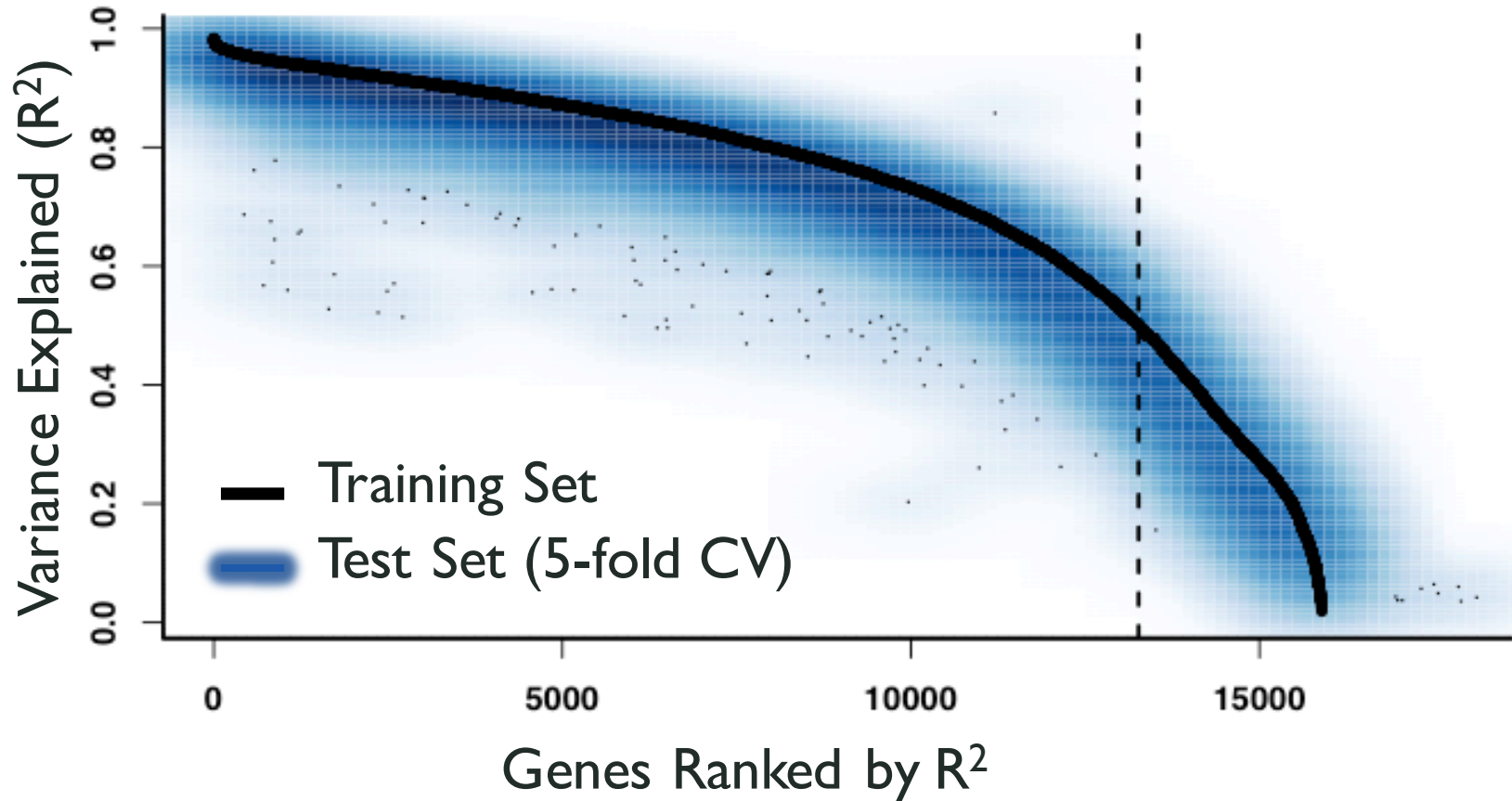
55% sensitivity
70% specificity

Combining TF binding sites and gene co-expression improves prediction of TFs' functional target genes



shRNA-microarray profiling of 25 TFs in lymphoblasts

Expression patterns of TFs accurately predict the expression patterns of thousands of genes in each tissue



Prediction of brain gene expression with fitTRN

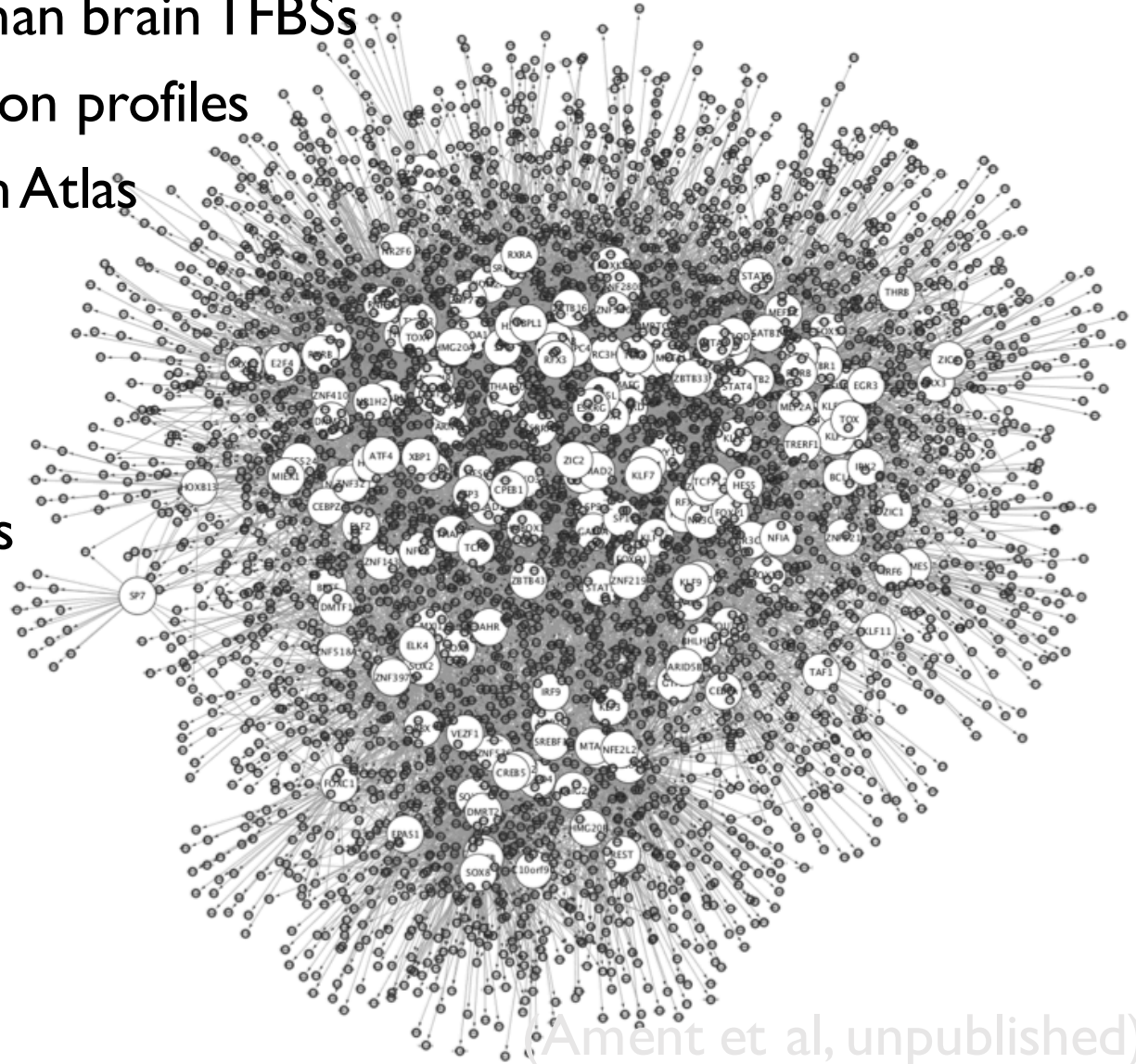
Genome-scale TRN model for the human brain

Input data

- 4.6M predicted human brain TFBSs
- 2,756 gene expression profiles from the Allen Brain Atlas

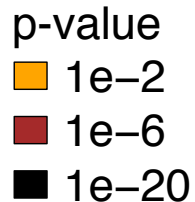
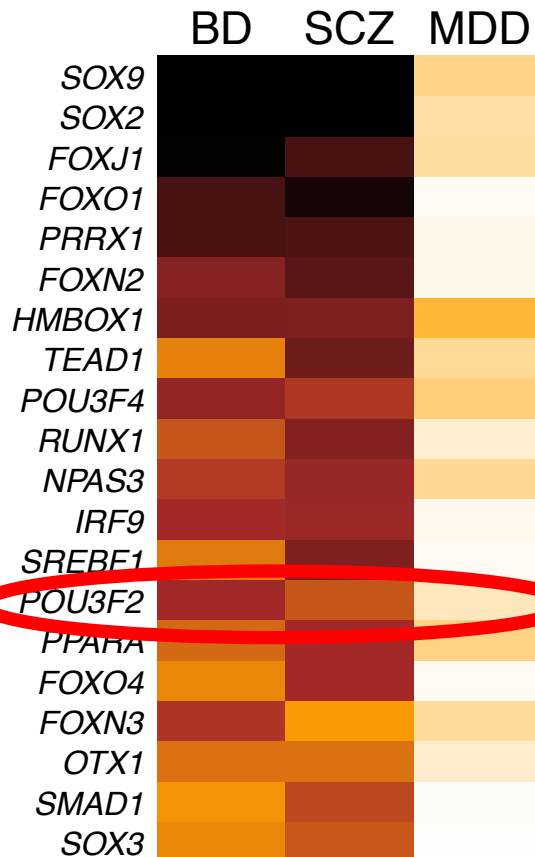
Summary Statistics

- 745 TFs
- 11,093 target genes
- 201,218 interactions

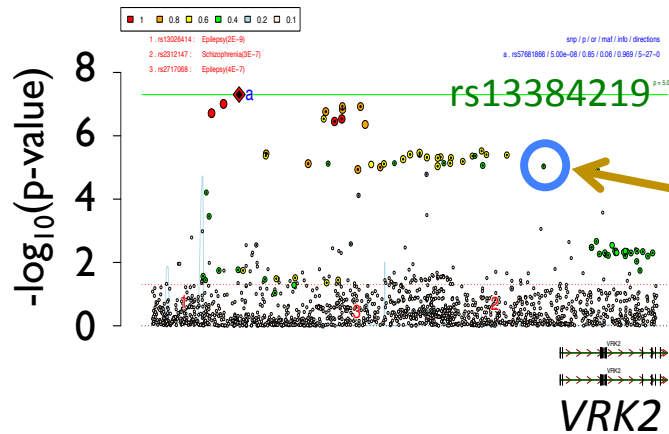


TReNA reveals master regulator TFs and regulatory genetic variants in psychiatric disorders

Master Regulator TFs



PGC2-BD GWAS (Stahl et al., in prep)



Risk-associated SNP in a predicted POU3F2 binding site



rs13384219 allele and POU3F2 expression influence the activity of the VRK2 promoter

