Detecting Transcription Factor Binding Sites

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OVERVIEW:

- Setup
- AIM
- Results

RECALL

Given:

- Candidate lists of genes (based on literature)

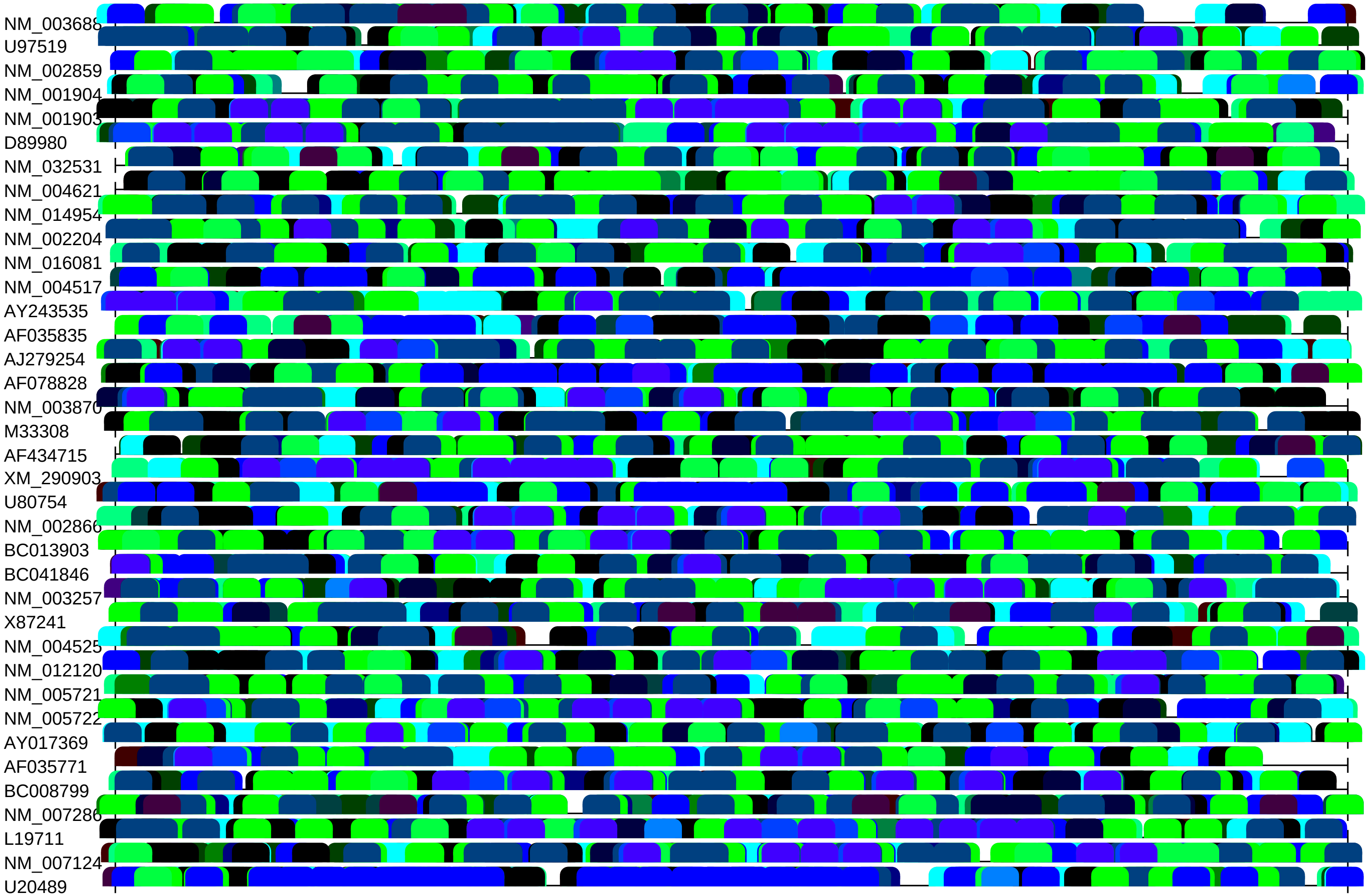
Assumption:

- Subset of genes are simultaneously expressed (which are (de-)activated by the same transcription factors).

Method:

- Find common TFBS on DNA
  ↳ shared motifs in promoter regions of these genes.

Results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U97519
NM_002859
NM_001904
NM_001903
D89980
NM_032531
NM_004621
NM_014954
NM_002204
NM_016081
NM_004517
AY243535
AF035835
AJ279254
AF078828
NM_003870
M33308
AF434715
XM_290903
U80754
NM_002866
BC013903
BC041846
NM_003257
X87241
NM_004525
NM_012120
NM_005721
NM_005722
AY017369
AF035771
BC008799
NM_007286
L19711
NM_007124
U20489

Develop Integrated approach:

Matinspector, Transfac, Weeder, cis-module, cluster-buster show promising approaches, but lack in one respect or the other.

Approach should combine all available information:

- known binding sites (transfac)
- over-expressed motifs
- conservation information
- modules

Further information needed !

⇒ focus on motifs that appear in Nephrin
⇒ longer modules