

A compendium of RNA-binding motifs for decoding gene regulation

Ray D., et al. Nature, 2013, vol. 499, pp. 172-177

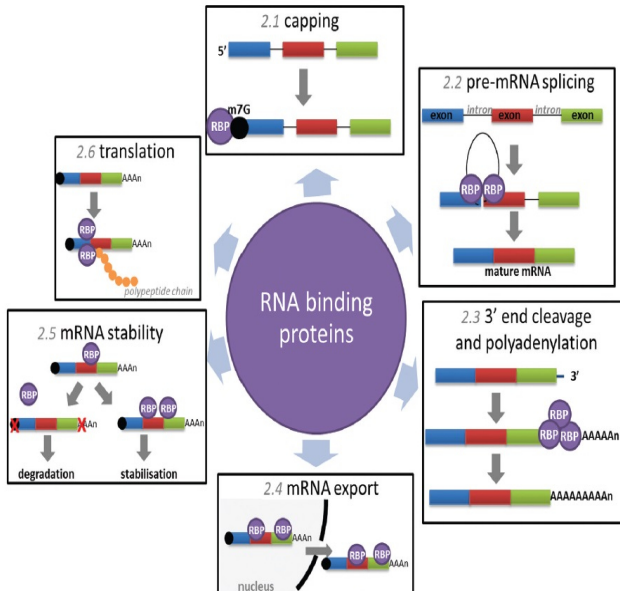
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Introduction

RNA-binding proteins (RBPs)

- Are proteins binding to double or single stranded RNA in cells.
- Regulate numerous aspect of co- and post-transcriptional gene expression
 - RNA splicing, capping, polyadenylation, mRNA export, etc.

RNA-binding proteins (RBPs)



RNA-binding domains (RBDs)

Functions

- Recognize RNA: bind short, single-stranded RNA sequences, or structured RNAs.

Types

- RNA recognition motif, hnRNP K-homology (KH), zinc finger domains, etc.

Motivation: study of post-transcriptional regulation

Post-transcriptional regulation contributes substantially to gene expression across human tissues. However,

- Lack of motifs for the vast majority of RBPs across all branches of eukaryotes.
 - Due to higher flexibility of the RNA-protein interface for major types of RBPs;
 - Example: only 15% of human RBD-containing proteins have known RNA-binding motifs.

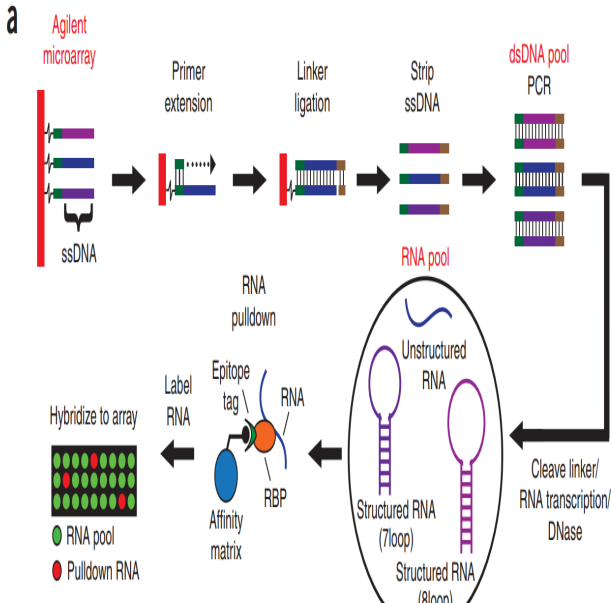
This paper: identifies binding motifs for a broad range of RBPs

Methods

RNAcompete **experiments**

- An *in vitro*, high-throughput method for the analysis of RNA binding preferences of hundreds of RBD-containing RBPs, from diverse eukaryotes.
- Rely on binding reaction between RBD and RNA-binding motifs.
 - An RBP is incubated in a complex pool of RNAs by affinity selection.
 - The pool contains ~240,000 short RNAs, divided into two halves for internal cross-validation purpose.
- The associated RNAs are interrogated by microarray and computational analyses.

RNAcompete experiments



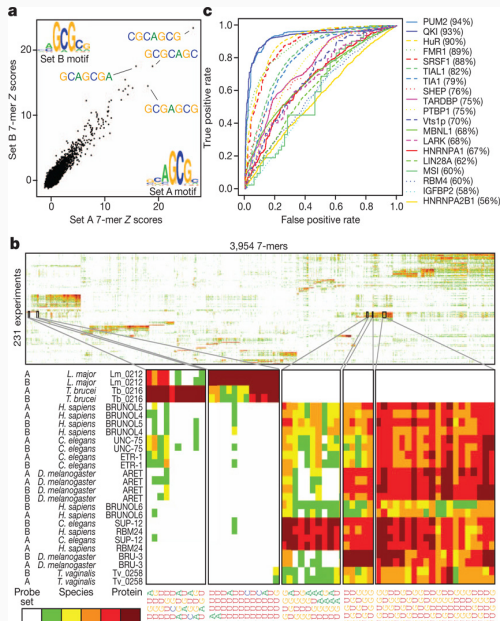
Results

Large-scale analysis of RBPs

Determined sequence preferences for 207 RBPs (from 193 unique RBP-encoding genes), 85 from human.

- Most RBDs fundamentally recognize and bind ssRNA, requires rarely on RNA second structure.
 - Fig. 1a: Z score and motifs for ZC3H10 (no previously known motif)
- Highlight specificity and diversity of RBP sequence preferences.
 - Fig. 1b: E score (enrichment score, Berger MF, et al., Nature Biotech 2006)
- The RNAcompete motif substantially outperforms the literature motif by AUROC analysis.
 - Fig. 1c: AUROC

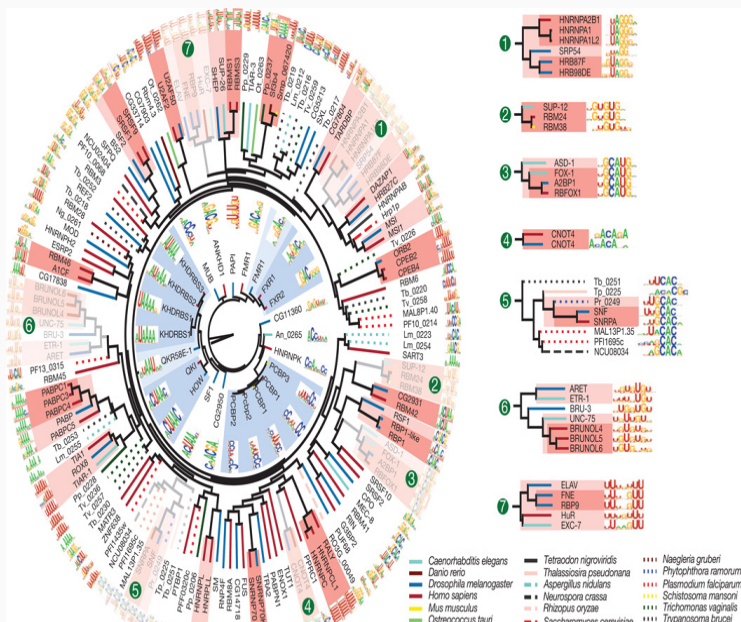
Large-scale analysis of RBPs



Conservation of ancient motifs

- Groups of ancient RBP families retain closely related sequence preferences.
 - A2BP1/RBFOX1, BRUNO/ARET
 - all RBPs in the SUP12RBM24RBM38 cluster prefer similar (G+U)-rich sequences.
- Subtle differences between more distantly related proteins are found.
 - family members from fungi, protists and algae maintained the presumed ancestral CAC core-recognition specificity, but differ in their preference for flanking nucleotides

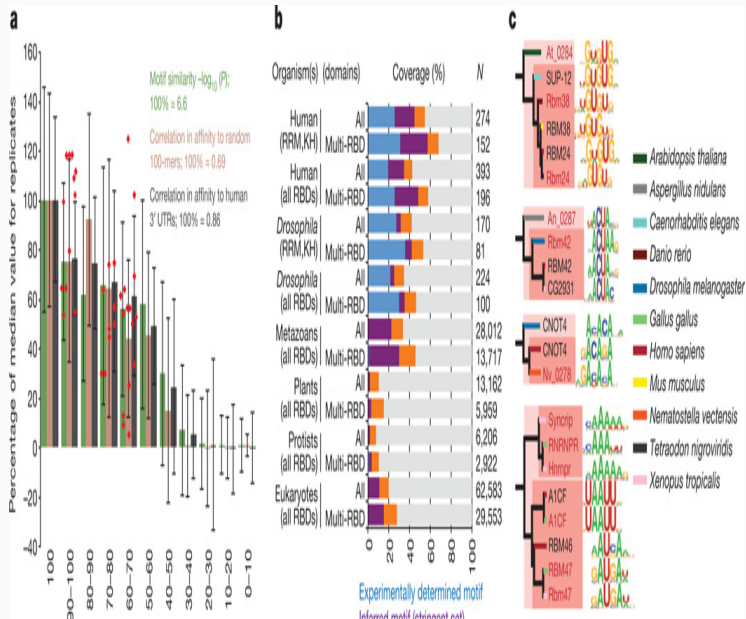
Conservation of ancient motifs



RBD based inference of RNA motifs

- Amino acid sequence identity higher than ~70% yields very similar motifs
- RNAcompete data captured 57% of all human RBPs contained multiple RBDs, assuming 70% sequence identity
- Validation of motifs predicted for proteins at 6196% amino acid identity

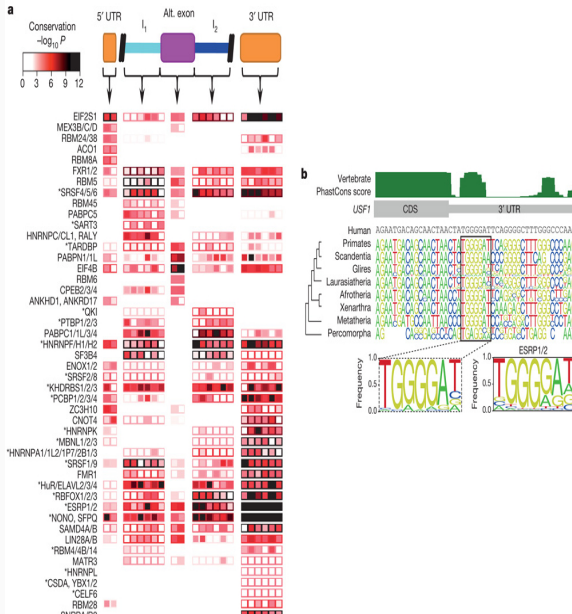
RBD based inference of RNA motifs



Sequence conservation of motif matches

- Motifs for most RBP families display significant conservation in one or more of the three regions examined.

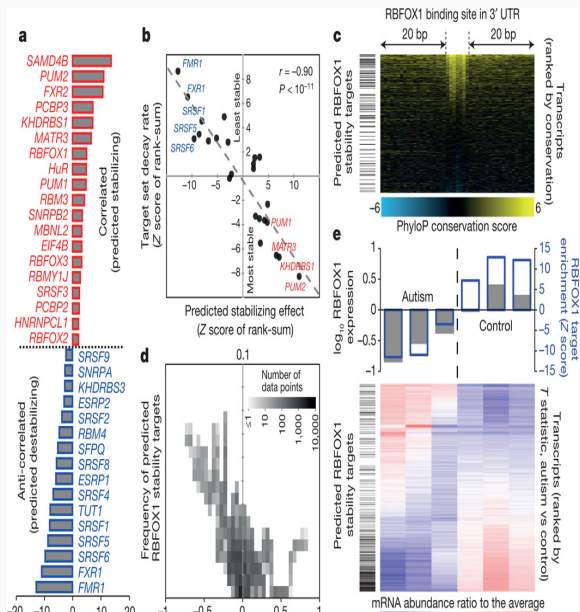
Sequence conservation of motif matches



Insights into RBP multi-functionality

- Role of RBPs in mRNA stability: positive/negative regulator
 - For example: RBFOX1 positively regulates mRNA stability/stabilizes its predicted mRNA targets
- Reduction of the stability of RBFOX1 targets may affect nervous-system-specific processes
 - Levels of RBFOX1 in the brains of individuals with autism is associated with changes in alternative splicing of exons

Insights into RBP multi-functionality



Discussion

Significance of identified motifs

- represent an unprecedented resource for the analysis of post-transcriptional regulation across eukaryotes;
- provide insight into the function and evolution of both RBPs and their binding sites;
- reveal broad linkages among different post-transcriptional regulation processes;
- uncover an unexpected role for a splicing factor in the control of transcript abundance that is mis-regulated in autism.