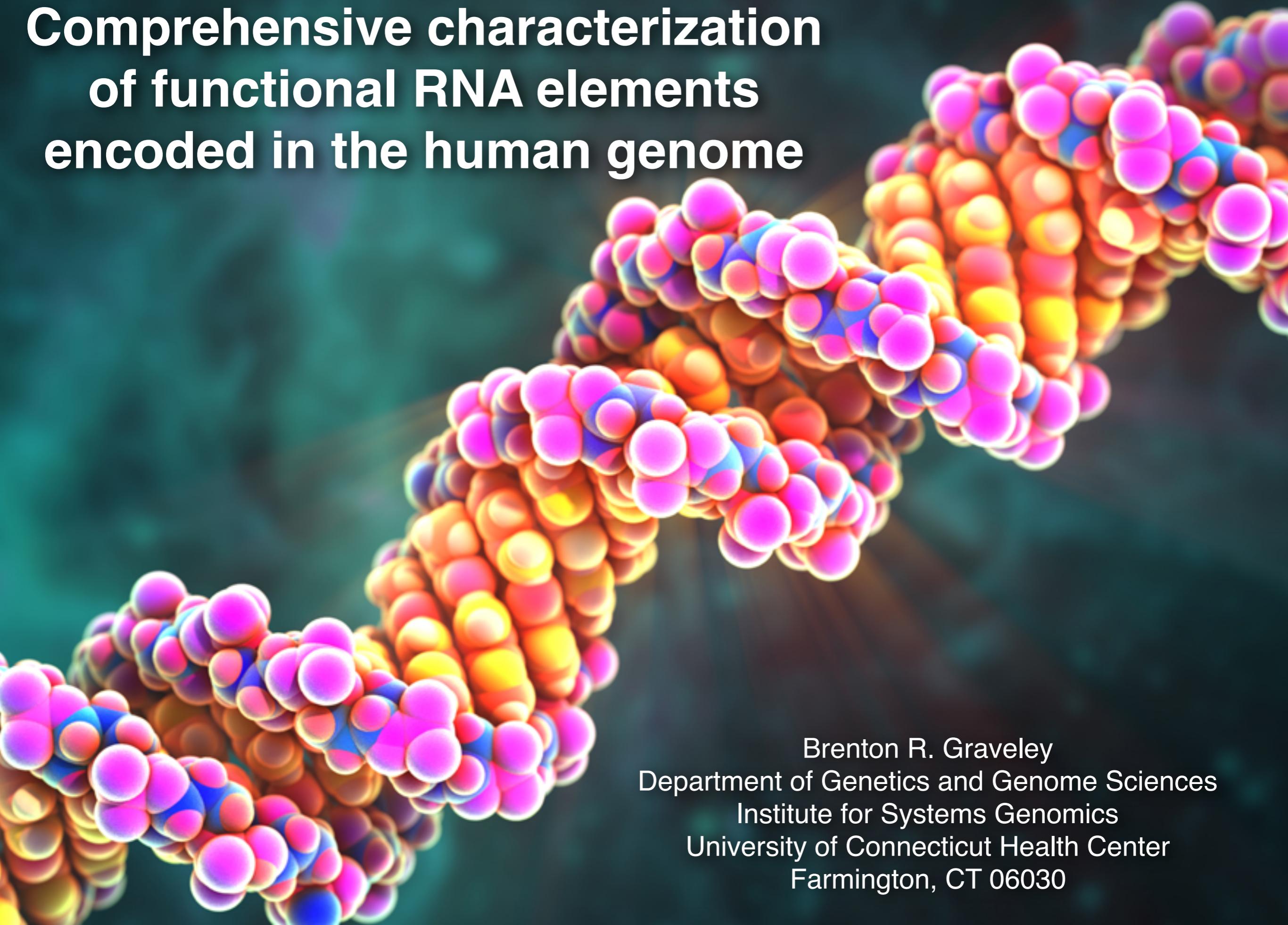


# Comprehensive characterization of functional RNA elements encoded in the human genome



Brenton R. Graveley

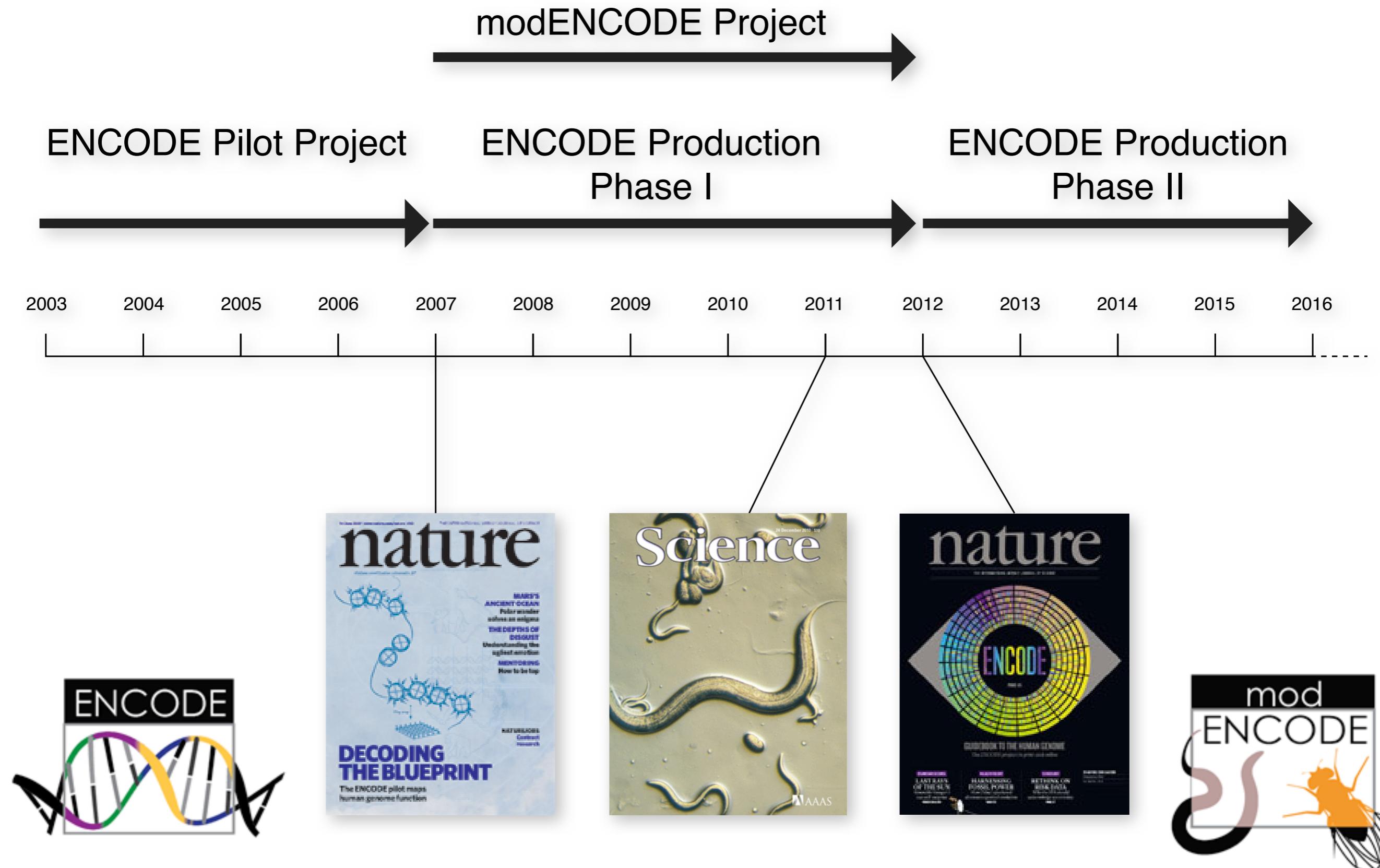
Department of Genetics and Genome Sciences

Institute for Systems Genomics

University of Connecticut Health Center

Farmington, CT 06030

# The ENCODE and modENCODE Projects



# MAKING A GENOME MANUAL

Scientists in the Encyclopedia of DNA Elements Consortium have applied 24 experiment types (across) to more than 150 cell lines (down) to assign functions to as many DNA regions as possible — but the project is still far from complete.

## EXPERIMENTAL TARGETS

**DNA methylation:** regions layered with chemical methyl groups, which regulate gene expression.

**Open chromatin:** areas in which the DNA and proteins that make up chromatin are accessible to regulatory proteins.

**RNA binding:** positions where regulatory proteins attach to RNA.

**RNA sequences:** regions that are transcribed into RNA.

**ChIP-seq:** technique that reveals where proteins bind to DNA.

**Modified histones:** histone proteins, which package DNA into chromosomes, modified by chemical marks.

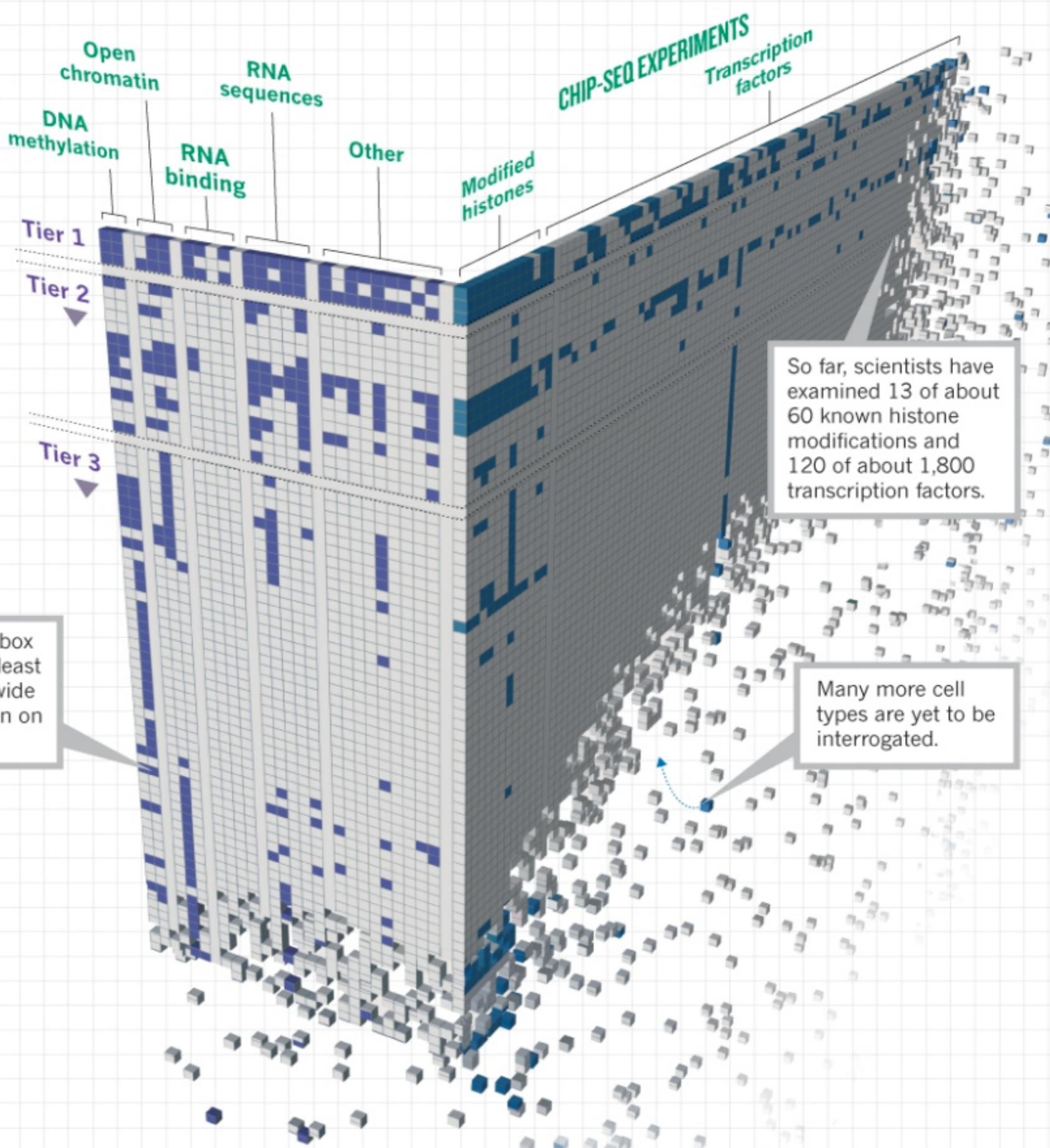
**Transcription factors:** proteins that bind to DNA and regulate transcription.

## CELL LINES

**Tiers 1 and 2:** widely used cell lines that were given priority.

**Tier 3:** all other cell types.

Every shaded box represents at least one genome-wide experiment run on a cell type.



**SHARE****REPORT**

14



## RNA splicing is a primary link between genetic variation and disease

Yang I. Li<sup>1</sup>, Bryce van de Geijn<sup>2</sup>, Anil Raj<sup>1</sup>, David A. Knowles<sup>3,4</sup>, Allegra A. Petti<sup>5</sup>, David Golan<sup>1</sup>, Yoav Gilad<sup>2,\*</sup>, Jonathan K. Pritchard<sup>1,6,7,\*</sup>

+ Author Affiliations

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Science 29 Apr 2016:  
Vol. 352, Issue 6285, pp. 600-604  
DOI: 10.1126/science.aad9417

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### RNA splicing links genetics to disease

Many genetic variants associated with disease have no apparent effect on any specific protein coding sequence. Li *et al.* systematically analyzed the effects of DNA variants on the main steps of gene regulation, from the chromatin state through protein function. One-third of expression quantitative trait loci (QTLs) are mediated through transcriptional processes, not chromatin. Splice QTLs and expression QTLs are about comparable in their complex disease risk. Posttranscriptional mechanisms therefore play a large role in translating genotype to phenotype.

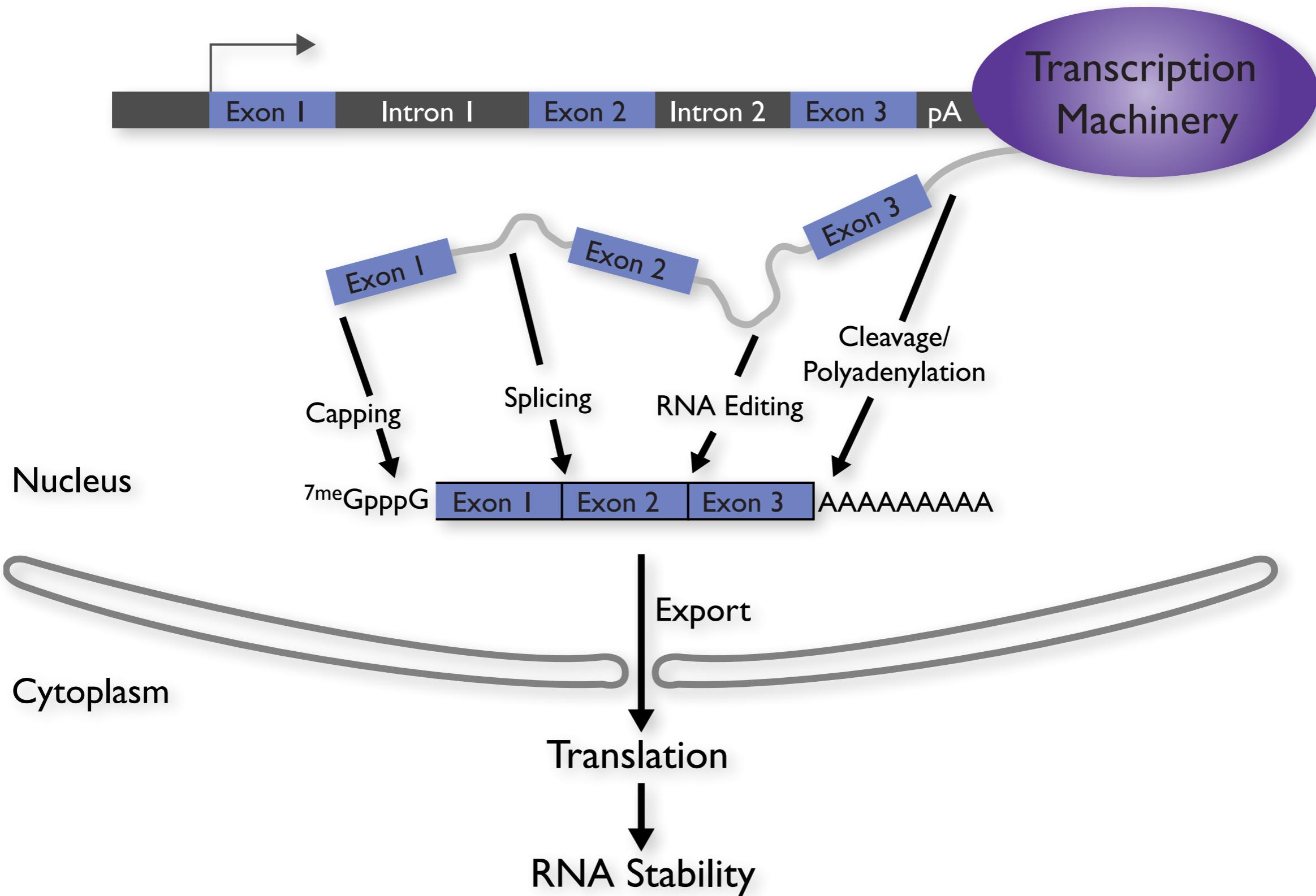
**Science**Vol 352, Issue 6285  
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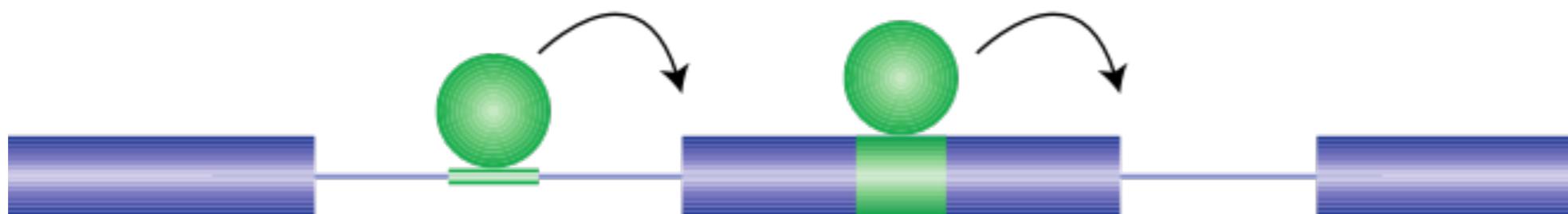
Howard Hughes Medical Institute,  
the Bill & Melinda Gates Foundation,  
the Wellcome Trust, and the  
Calouste Gulbenkian Foundation  
announce the International Research  
Scholars Program which aims to

# Eukaryotic mRNA Synthesis

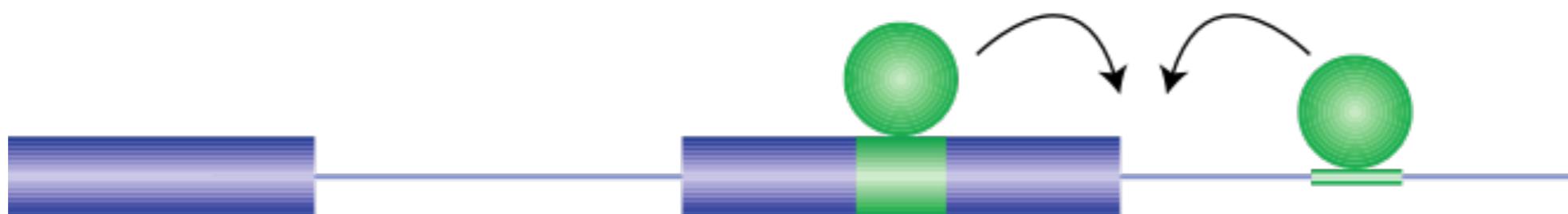


# Functionally Important RNA Elements

Splicing



Polyadenylation



Translation, Localization, or Stability

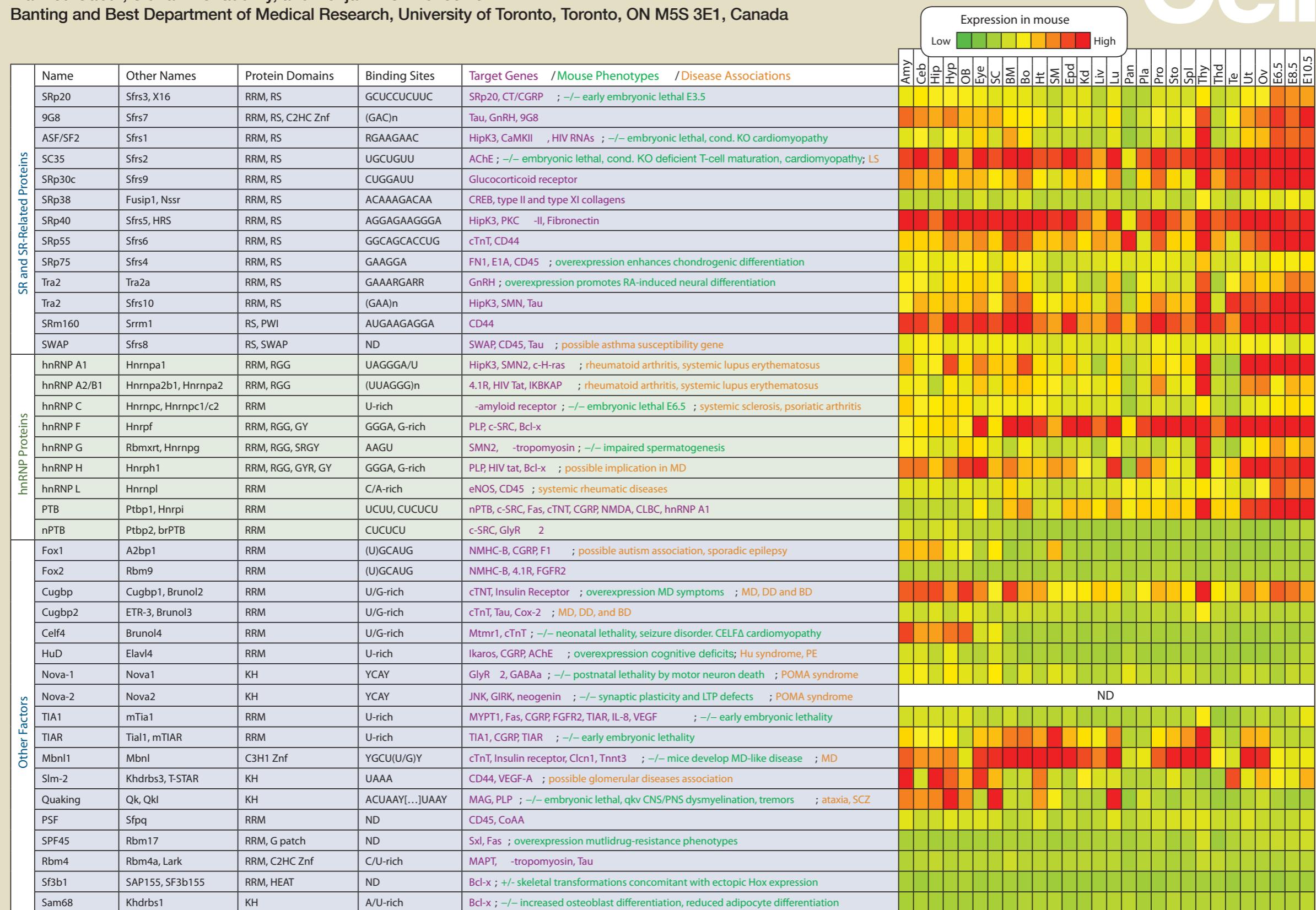


# SnapShot: The Splicing Regulatory Machinery

Mathieu Gabut, Sidharth Chaudhry, and Benjamin J. Blencowe

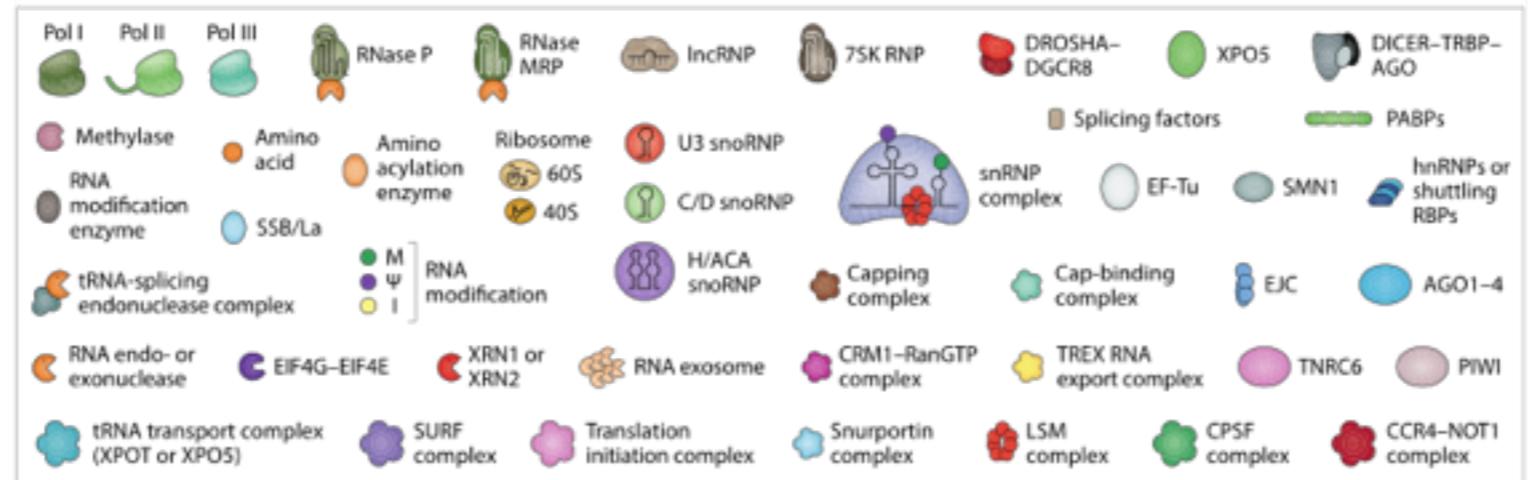
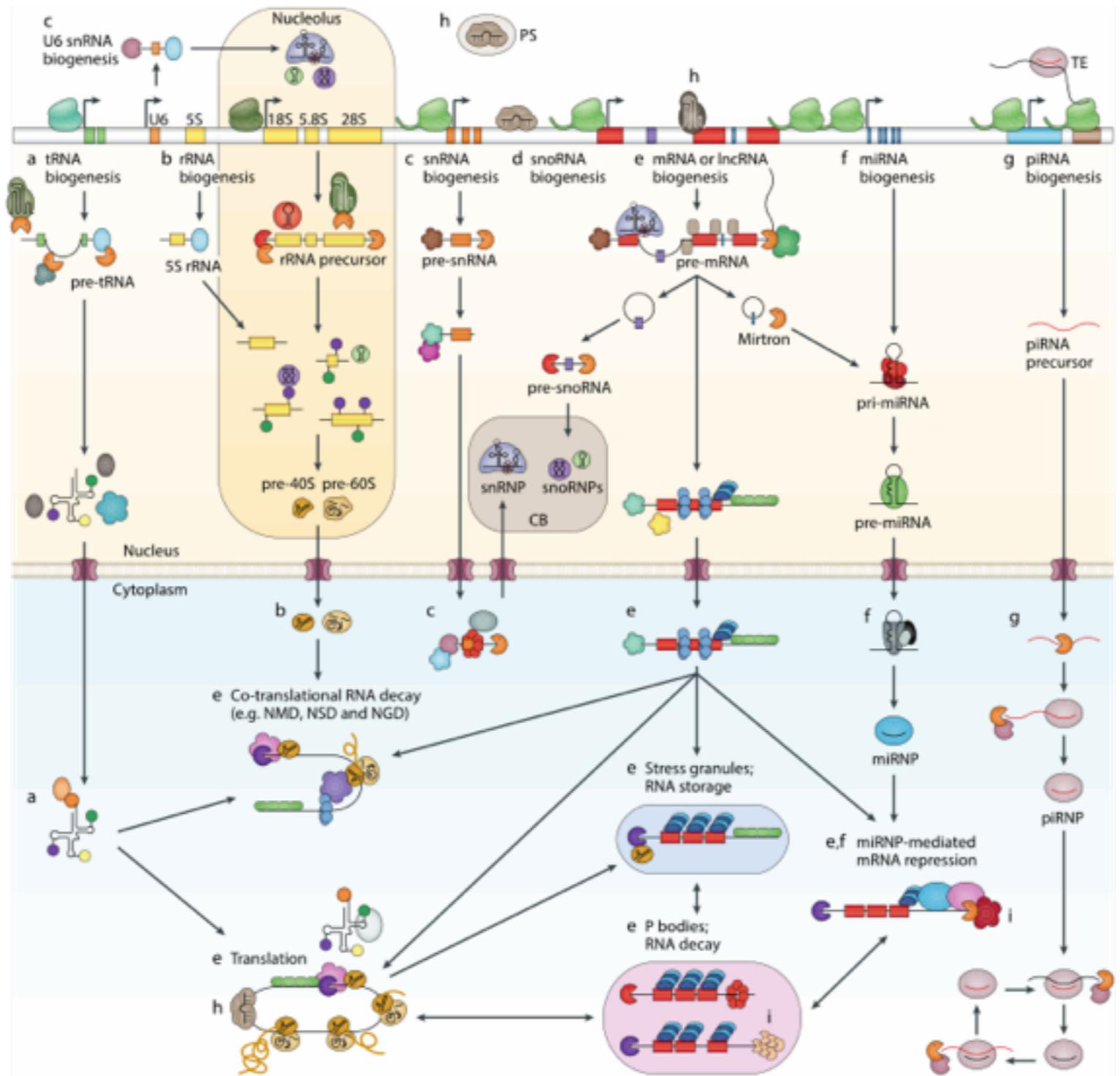
Banting and Best Department of Medical Research, University of Toronto, Toronto, ON M5S 3E1, Canada

Cell



# 1072 “RNA binding proteins”

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 BTF3 BZW1 BMS1 DAZ2 DDX1 DUT ENO1 EEF2 FCF1 H1F0 KTN1 IFI16MILL3 NFX3PLEC PKM2 PURB RBM7 RPL3 RPS6 RRP9 RPL8 SND1 TBL2 TNS1 XRN2 XPO1  
 AIMP1 BAT4 CLK3 CSTB DAZ3 DDX5 EIF4B FIP1L1 EIF4H HFM1 LLPH LYAR PARN NPM3 NSA2 PWP2 RBM11 RIMS1 RPL17 RPS11 RPS5 STIP1 TBL3  
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 AARS CELF1 CISD2 DDX31 DDX42 DDX47 DHX16 ESRP1 LSM7 HSPE1 MKI67 MFAP1 KRHNONOPDIA3 RBM14 RBM15 RPL17 RPL28 RPL29 RPS15 STK31 TFB1M UBFD1  
 CCT4 CANX CSR1 CSDE1 DDX42 DDX47 DHX16 ESRP1 LSM7 HSPE1 LSM10 NAT10 NOL10 MSI2 PPRC1 RC3H1 RPL36 RPL35 RPP25 RTN4 SREK1 SSBP1  
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 ASCC1 ANXA2 CHERP CDC40 DSPEIF2C2 EIF2C4 DHX58 ESRP2 HDLBP LARP6 MAZMYEF2 PAPD5 PHF5A RBM22 RBM47 SART1 SF3A2 SRSF9 SRSF8  
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 ZNF326 ZRANB2 YTHDF3  
 AC010724.1 APOBEC4 C30RF77 DROSHA EIF4G2 GLRX3 HNRNPH3 HNRNPC METAP2 MRPL39 PABPC1 PNLD C1NCL RBMY1J RPS15A SETD1A  
 TIA1 SUPT5H UBAP2L ZC3H10  
 AC018450.1 C17ORF42 BX511012.1 DNAJC21 DNAJC17 EIF4G3 GNB2L1 HNRNPA3 HNRNPA1NVL MRPS28 MRPL28 PNO1 R3HDM1 RBMY1E  
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 SRSF6 ZC3H4 ZC3H8  
 BYSL BCCIP CELF3 CPSF7 DDX25 DDX52 DHX29 DMT1L HSPD1 NAA15 NOSIP PUF60 PTBP2 RBM19 RPLP0 RPS26 RPL32 UBA1 SSRP1  
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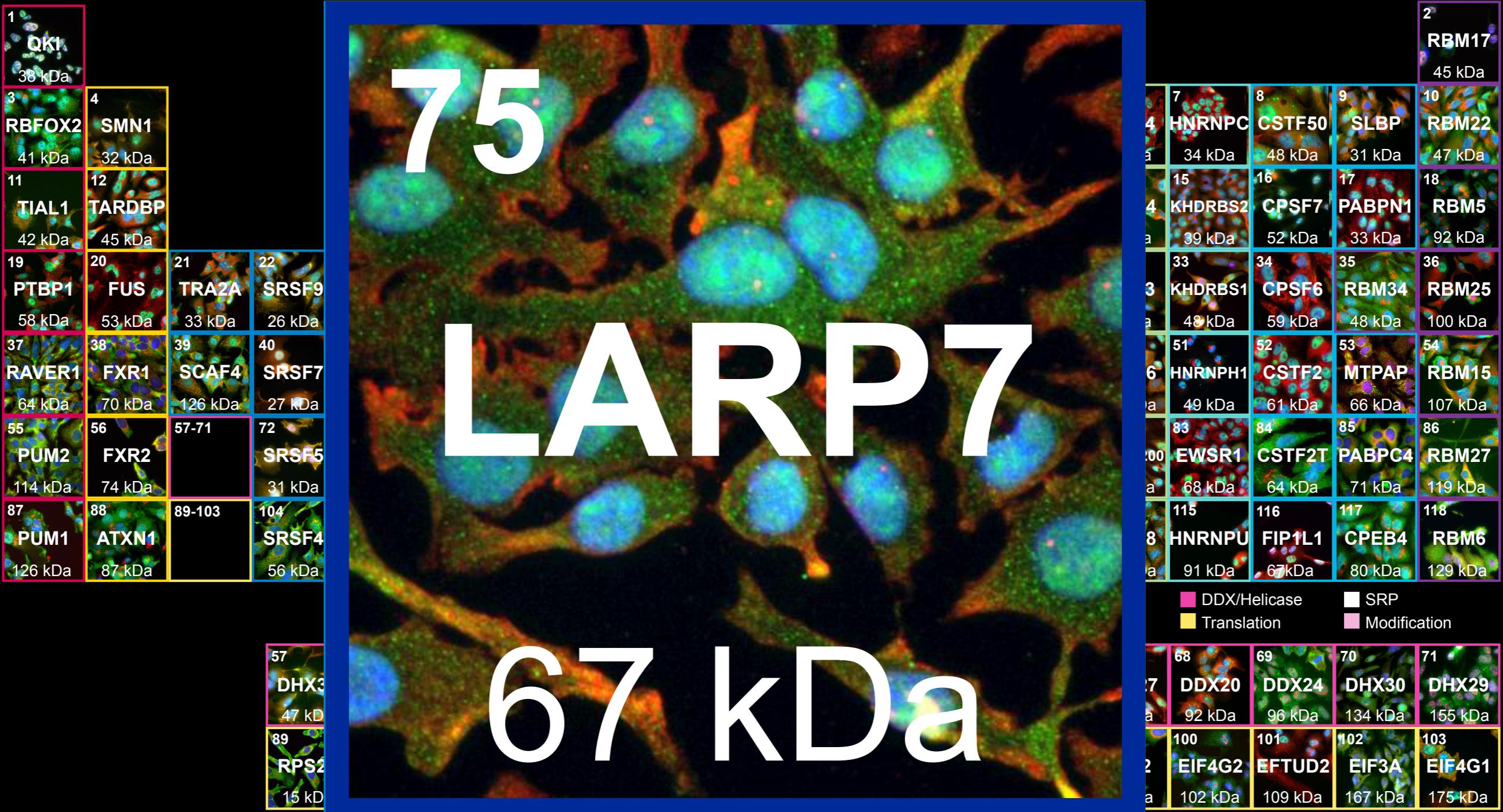
# Comprehensive Identification of Functional RNA Elements in the Human Genome

- Identify RNA Elements Recognized by 250 (All) Human RNA Binding Proteins *in vivo*
- Characterize the Binding Affinity of each RNA Binding Protein to all possible RNA Sequences
- Determine the functions of the Protein-RNA Interactions



# The Periodic Table of Human RNA Binding Proteins

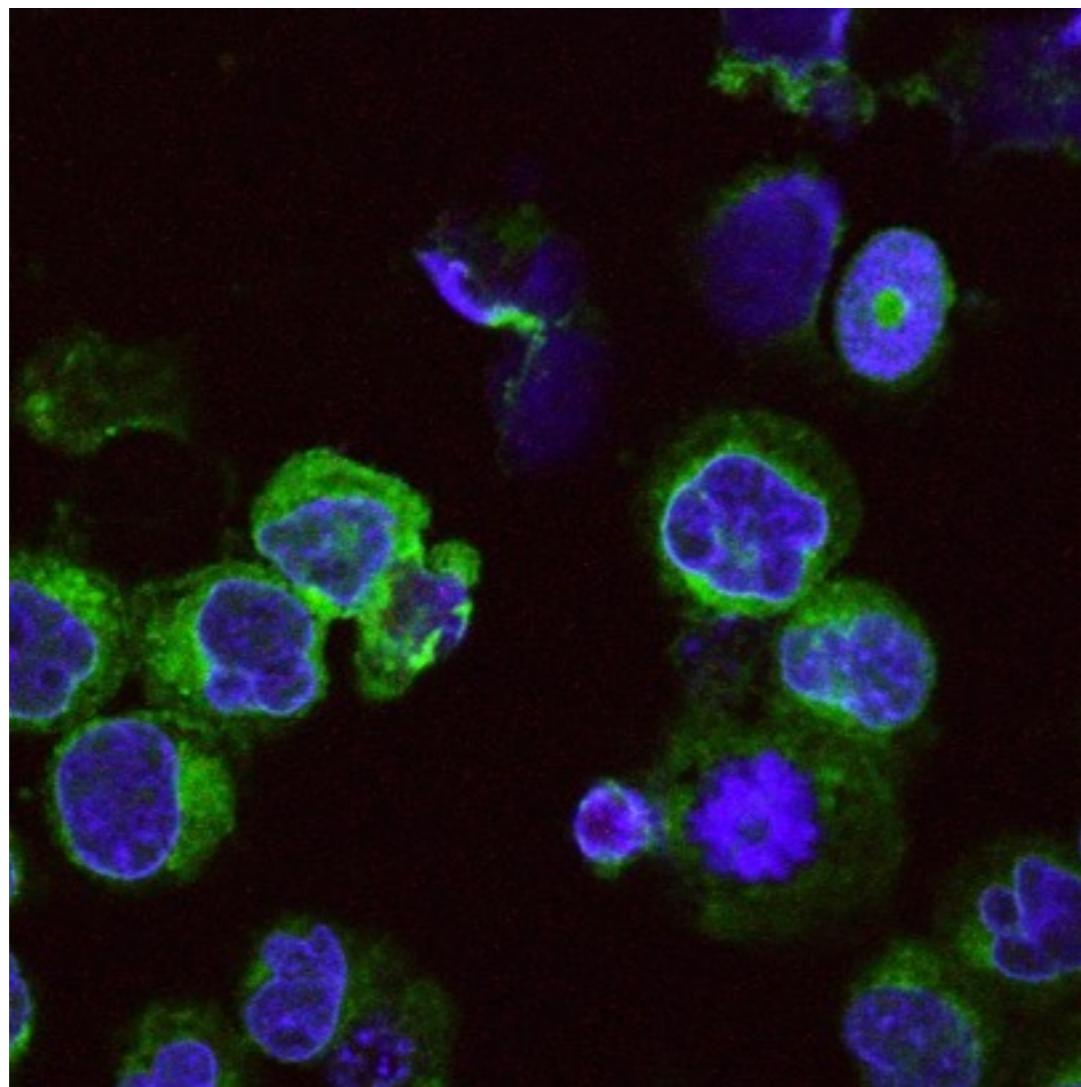
## RIBOSOME LOCALIZATION



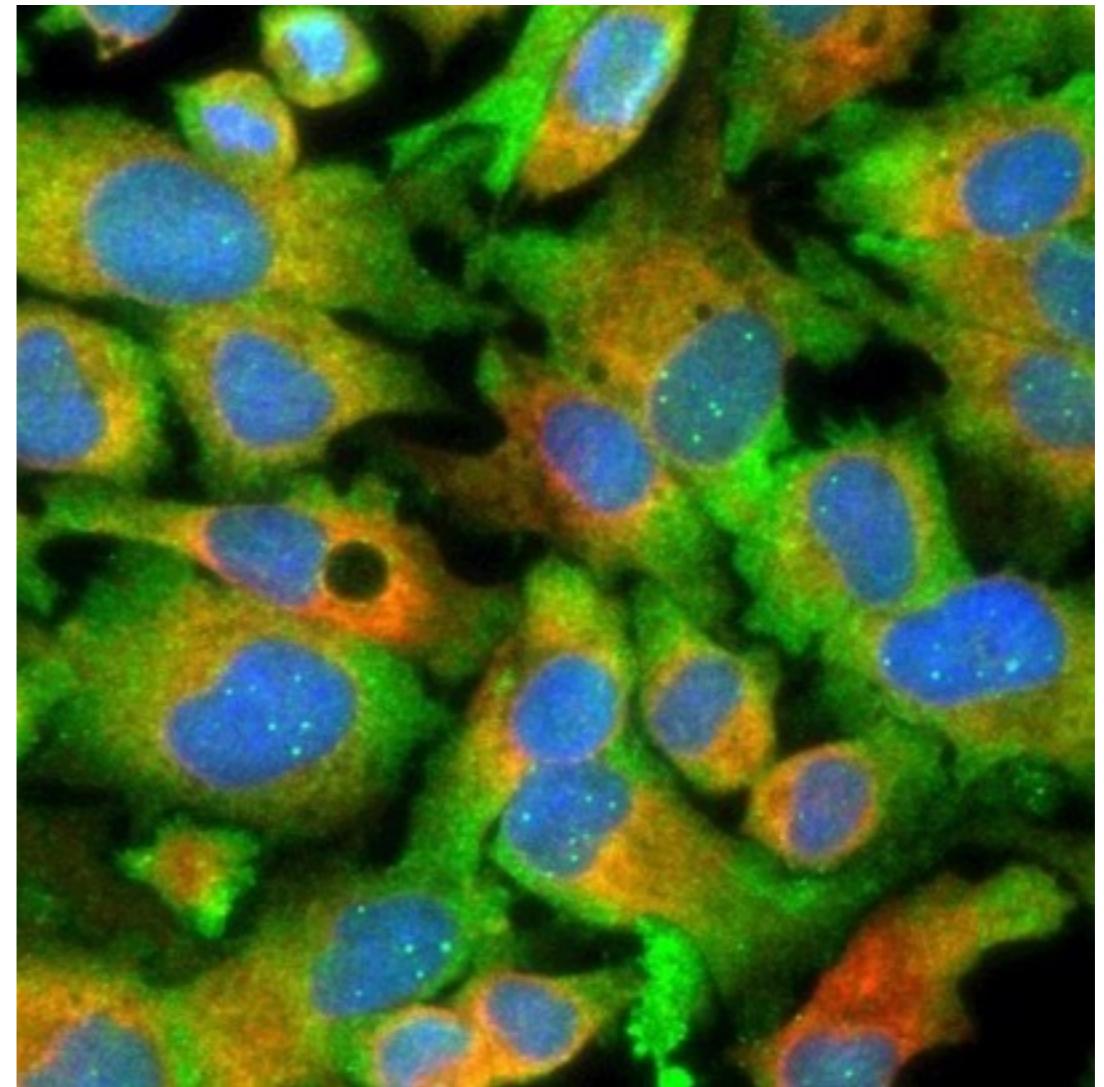
# What can be done with these data?

- Identify binding sites for all RBPs
- Determine the function of RBP binding sites
  - Determine RNP composition
  - Predict how mutations will impact RNA processing
  - New insights into RNA biology

# Cell lines being studied



K562 (bone marrow)  
chronic myelogenous leukemia (CML)  
53 year old female



HepG2 (Liver)  
Hepatocellular carcinoma  
15 year old male

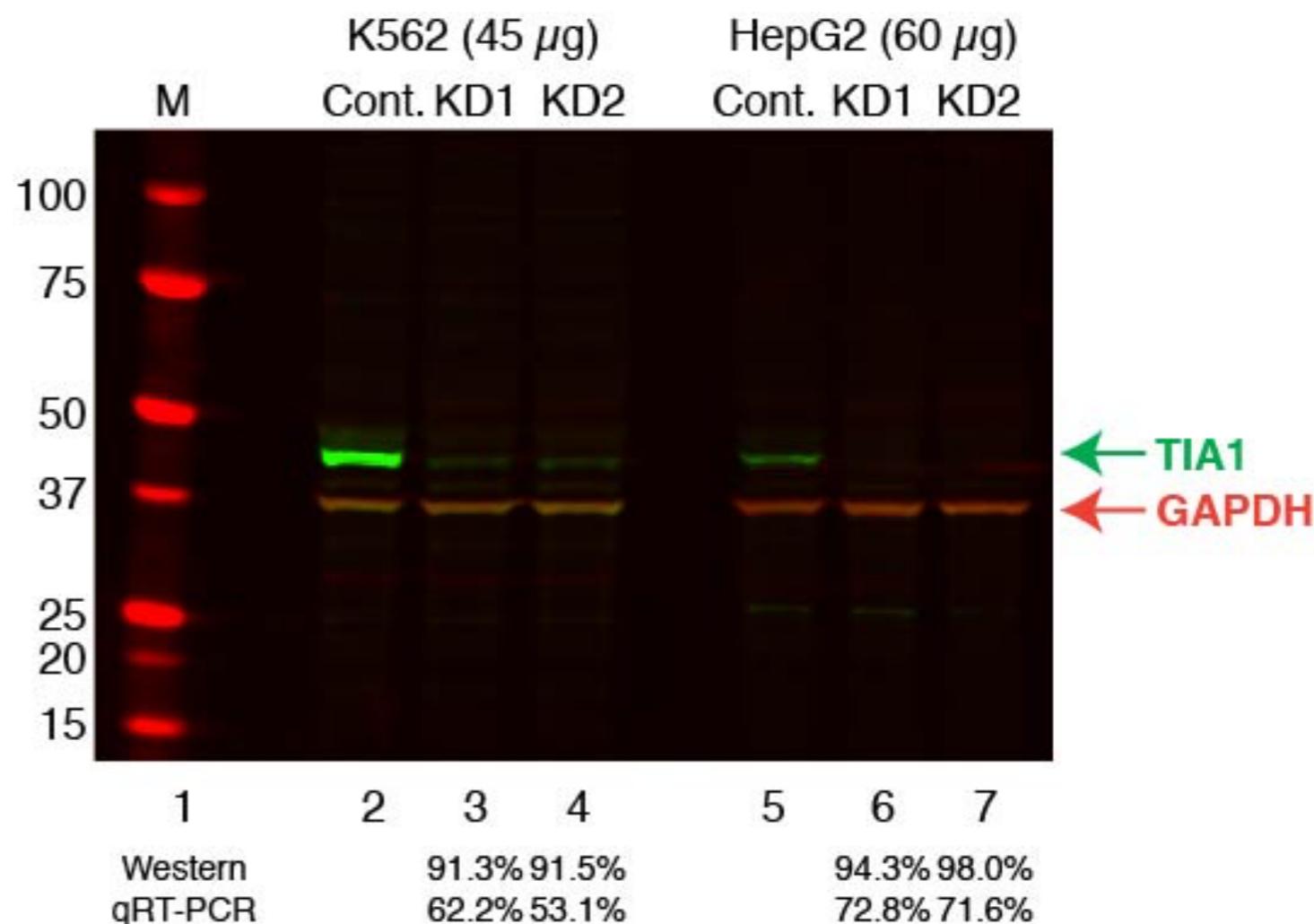
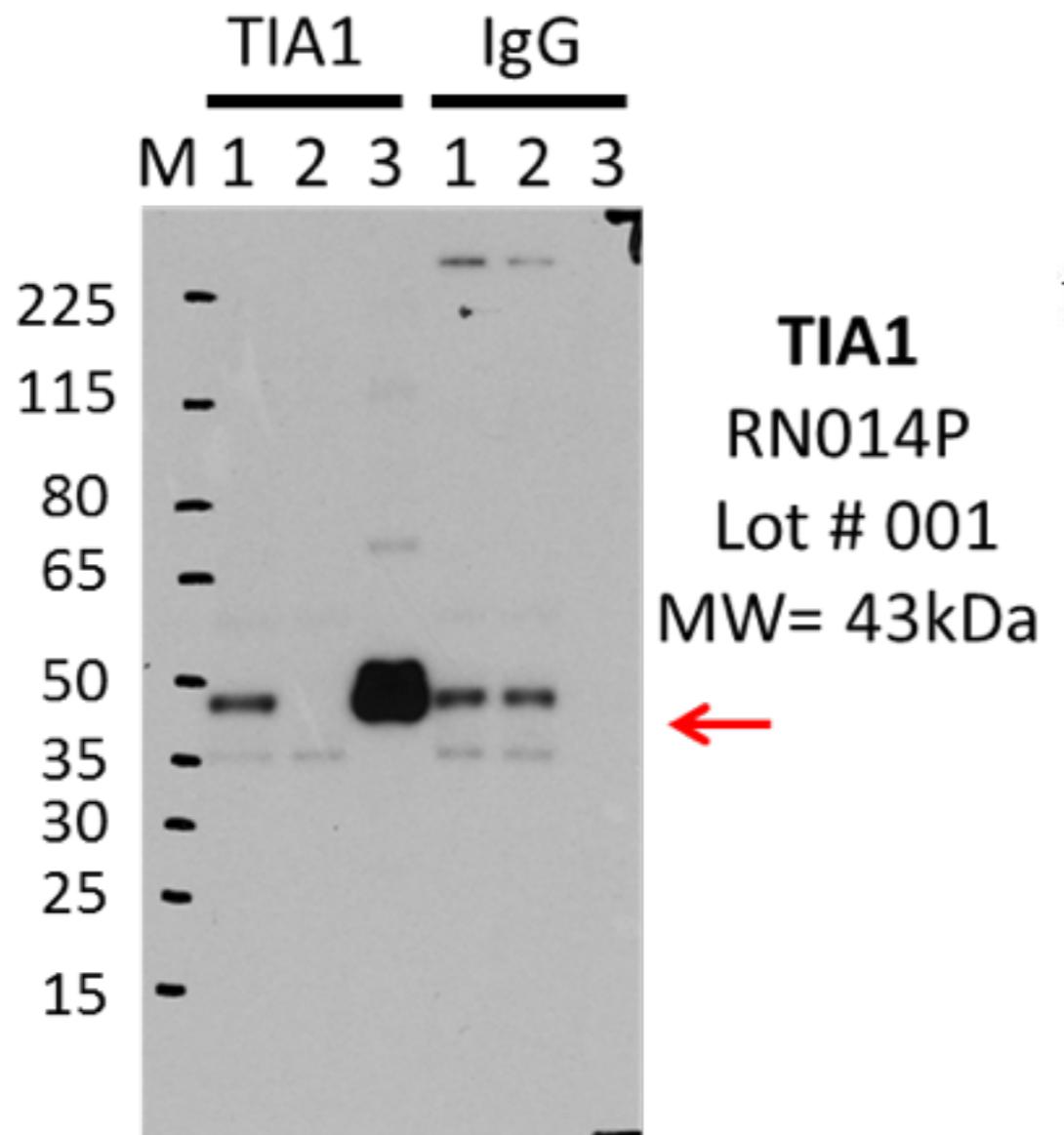
# 1,072 “RNA binding proteins”



# Antibody Validations

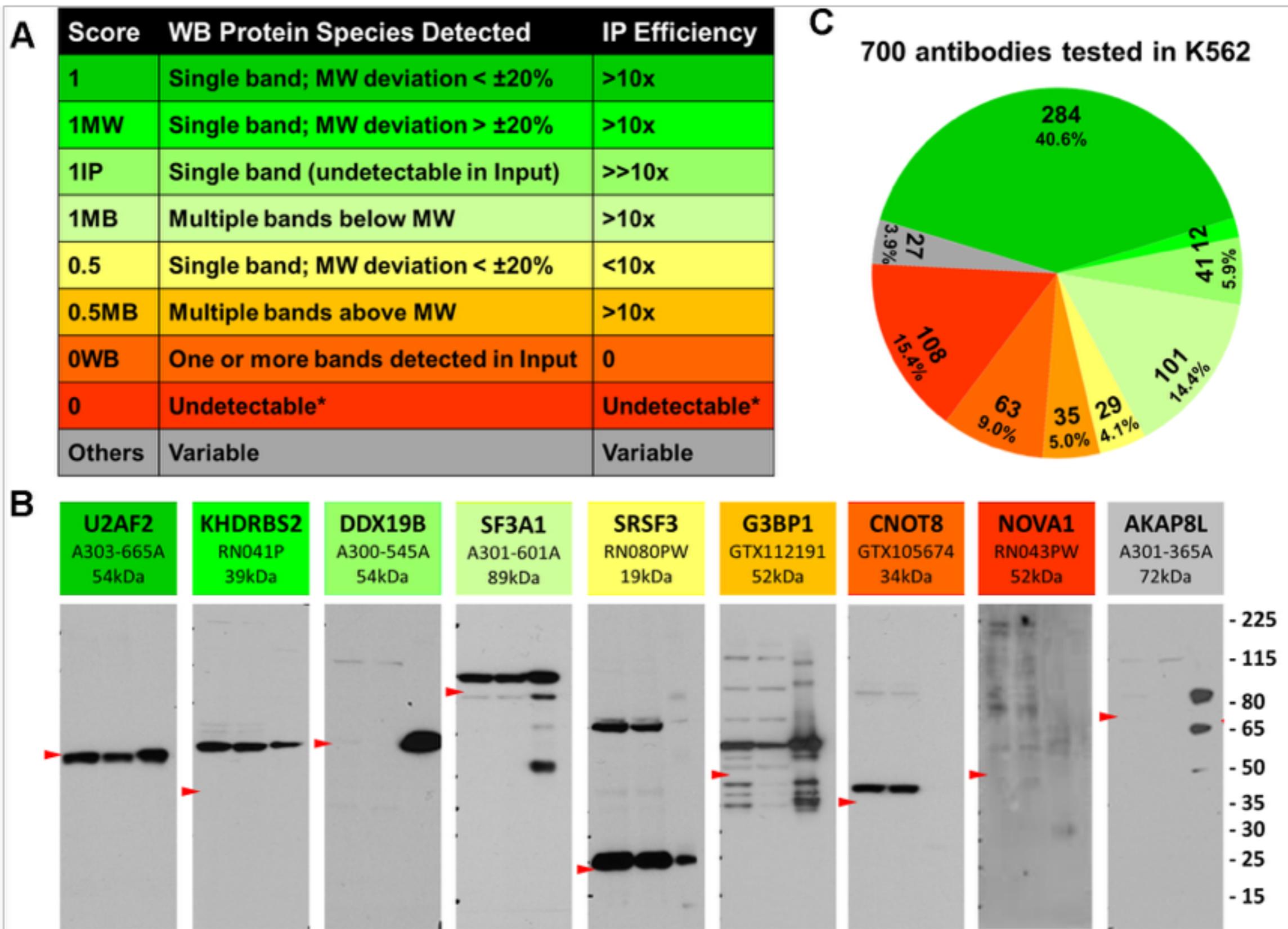
Acquired 852 antibodies and >1,000 shRNAs

Tested 701 antibodies against 538 unique RBPs



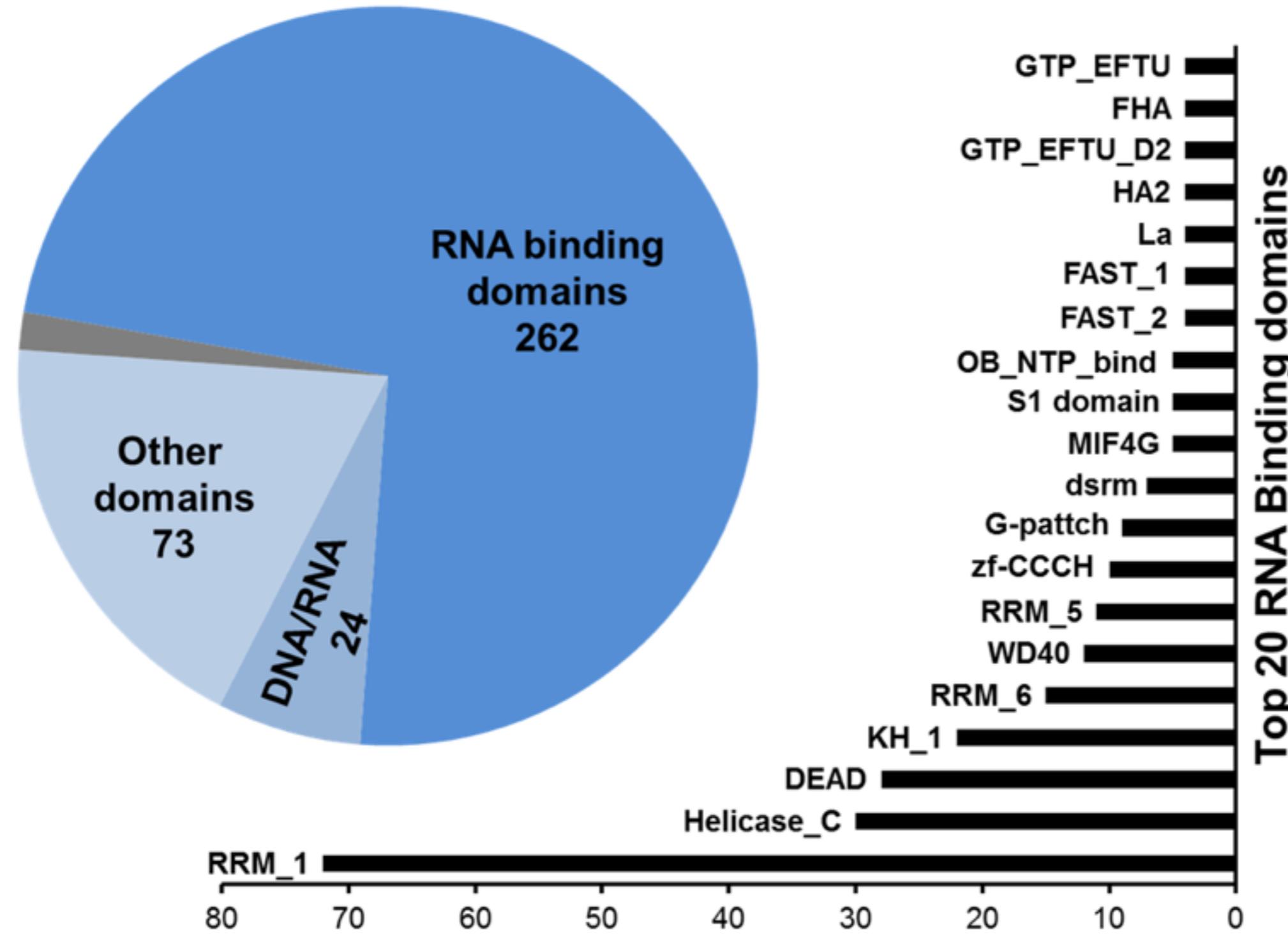
438 antibodies against 385 RBPs  
362 shRNAs against 276 RBPs

# Antibody Validations



# Antibody Validations

## Domain analysis of RBPs with IP-grade antibodies



# Antibody Resource

The screenshot shows the ENCODE Antibody Resource interface. At the top is a dark blue header bar with the ENCODE logo and navigation links: Data, Methods, About ENCODE, Help, Search ENCODE, and Sign in. A red box highlights the Search ENCODE input field. Below the header is a table of antibody entries. On the left, there are four filter panels: Eligibility status, Target Organism, Target of antibody, and Characterization method, each with a 'See more...' link. A large black box labeled 'Filters' covers the middle section of the table. A red box highlights the 'Search box' at the top right of the table area. A black box labeled 'Dropdown menus' covers the top right corner of the table area. Arrows point from the 'Filters' box to the 'Search box', 'Dropdown menus', and the 'Target of antibody' and 'Characterization method' filters.

Showing 25 of 1144 antibodies		
<b>IGF2BP3 (<i>Homo sapiens</i>) ●</b>		
Source: MBLI		
Product ID / Lot ID: RN009 / 002		
<b>EZH2 (<i>Homo sapiens</i>) ●</b>		
Source: Cell Signaling		
Source: Millipore		
Product ID / Lot ID: 07-449 / 2120130		
<b>CHD4 (<i>Homo sapiens</i>) ●</b>		
Source: Abcam		
Product ID / Lot ID: ab70469 / GR104037-5		
<b>IGF2BP2 (<i>Homo sapiens</i>) ●</b>		
Source: MBLI		
Product ID / Lot ID: RN008P / 002		
<b>H3K36me3 (<i>Mus musculus</i>) ●</b>		
Source: Abcam		

# Antibody Resource

ENCODE Data Methods About ENCODE Help Search ENCODE Sign in

ENCAB934MDN → Accession ID

Antibody against *Homo sapiens* IGF2BP3

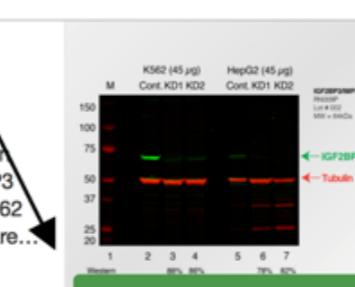
Homo sapiens K562 Antibody status → Eligible for new data

Source (vendor): MBLI ↗  
Product ID: RN009) ↗  
Lot ID: 002  
Targets: IGF2BP3 (*Homo sapiens*)  
Host: Rabbit  
Clonality: Polyclonal  
Isotype: IgA  
Antigen description: KLH-conjugated synthetic peptide HQQQKALQSGP

Meta data

Characterization status

IGF2BP3 (*Homo sapiens*) Method: immunoprecipitation  
Caption excerpt: IP-Western Blot analysis of HepG2 whole cell lysate using IGF2BP3 specific antibody. Lane 1 is 1% of twenty million whole cell lysate input and lane 2 is 25% of IP enrichment using rabbit normal IgG...  
  
compliant

IGF2BP3 (*Homo sapiens*) Method: knockdown or knockout  
Caption excerpt: Western blot following shRNA against IGF2BP3 in K562 and HepG2 whole cell lysate using IGF2BP3 specific antibody. Lane 1 is a ladder, lane 2 is K562 non-targeting control knockdown, lane 3 and 4 are...  
  
compliant

Experiments using antibody ENCAB934MDN

Links to CLIP experiments

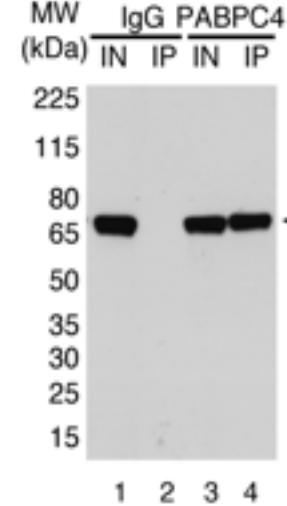
Accession	Assay	Biosample term name	Target	Description	Lab
ENCSR077KVG	eCLIP	HepG2	IGF2BP3 eCLIP mock input	eCLIP control experiment on HepG2 against IGF2BP3	Gene Yeo, UCSD
ENCSR993OLA	eCLIP	HepG2	IGF2BP3	eCLIP experiment on HepG2 against IGF2BP3	Gene Yeo, UCSD
ENCSR096IJV	iCLIP	K562	IGF2BP3		Gene Yeo, UCSD

# Antibody and shRNA Resources

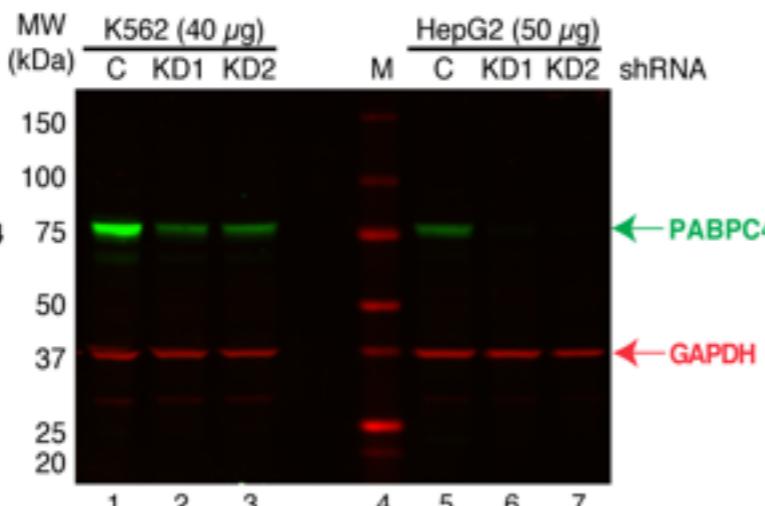
A

PABPC4 (A301-466A) 71 kDa

IP Western



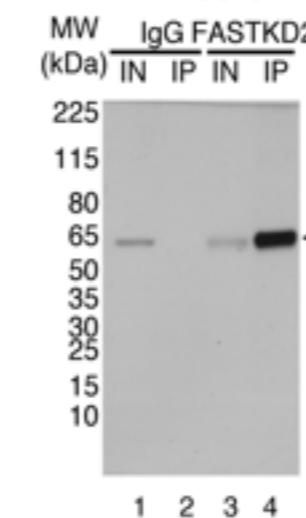
Knockdown Western



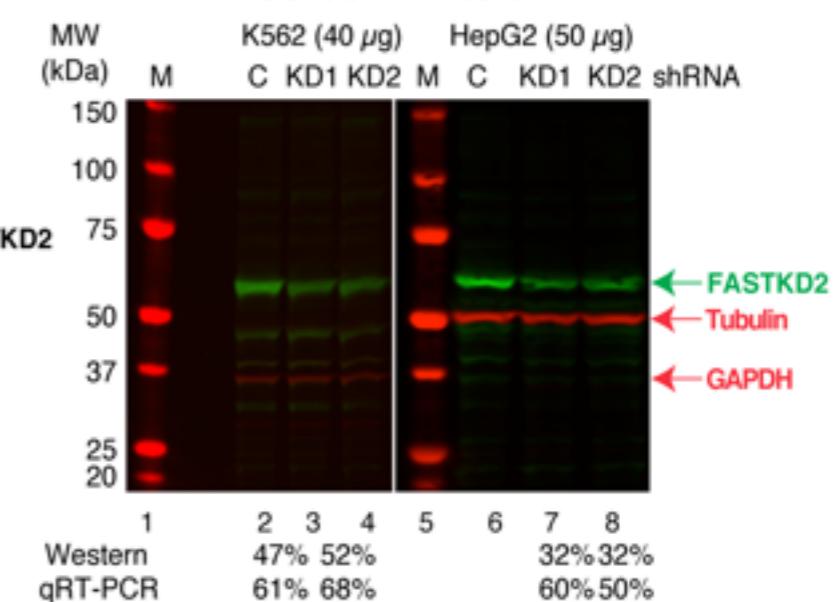
C

FASTKD2 (A303-788A) 81 kDa

IP Western



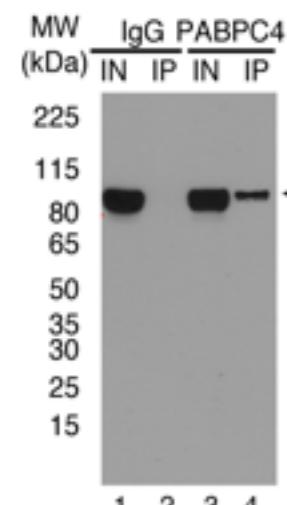
Knockdown Western



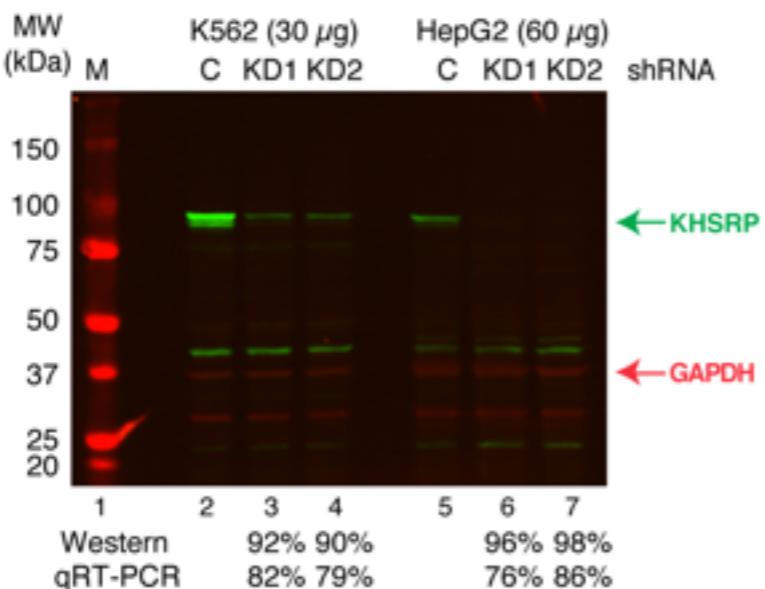
B

KHSRP (RN065PW) 73 kDa

IP Western



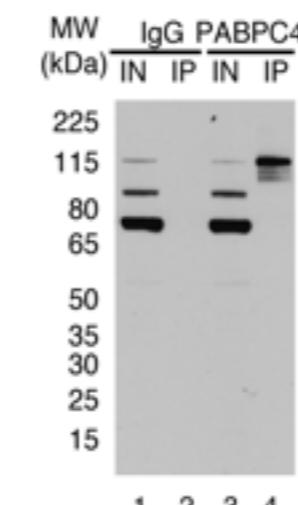
Knockdown Western



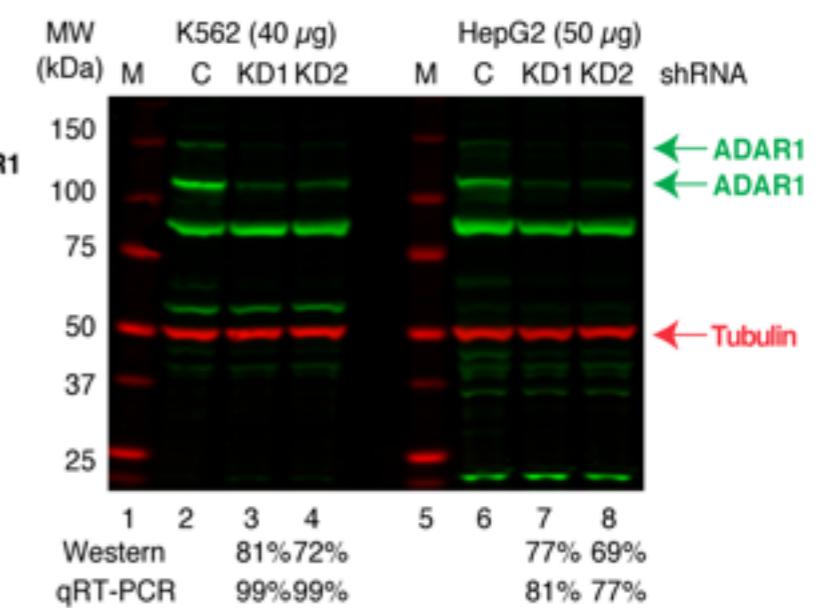
D

ADAR1 (A303-883A) 136 kDa

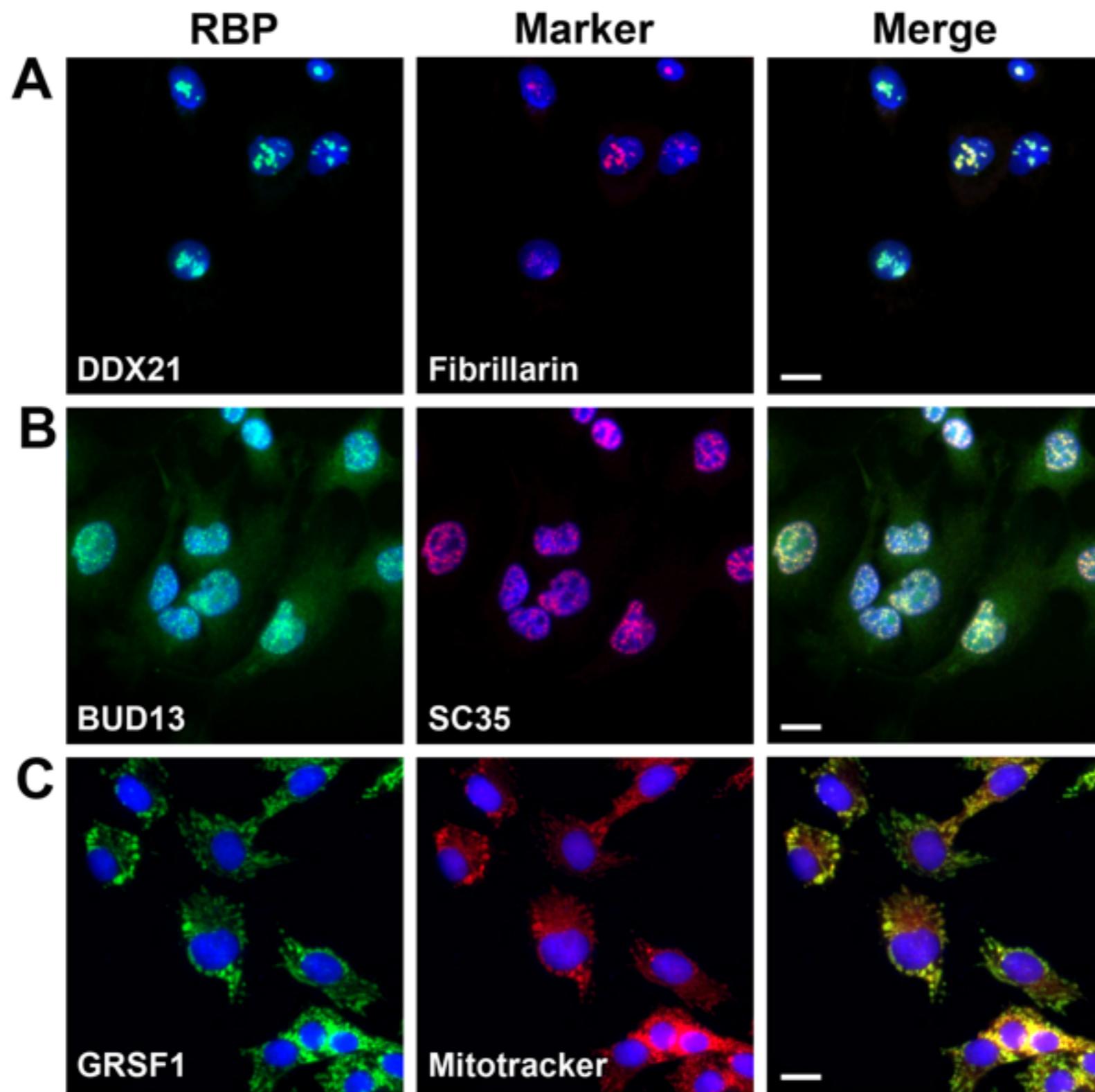
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Knockdown Western

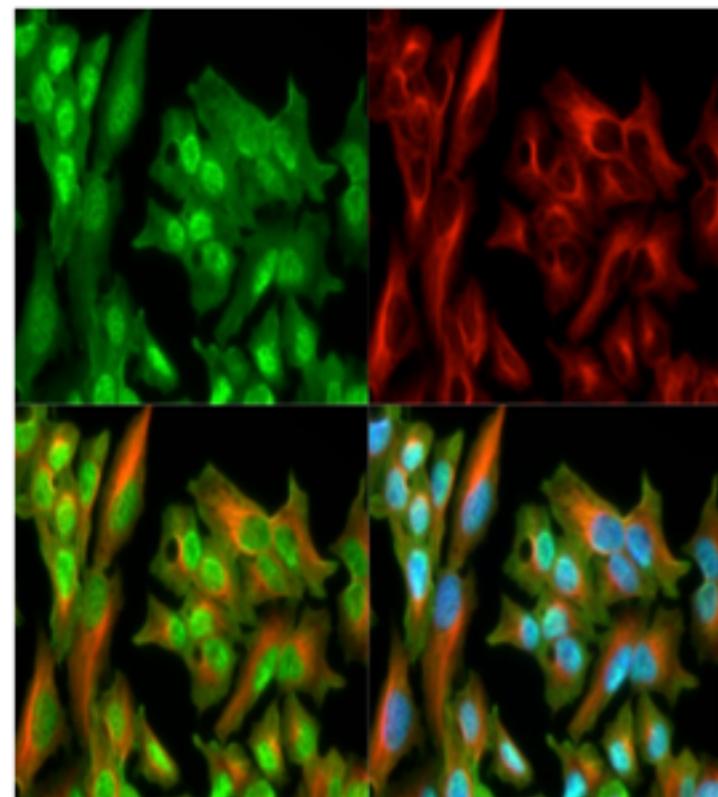


# Protein Localization Studies



# Accessing ENCODE RBP Data

## RBP Image Database



## About the database

This microscopy image database documents the results of immuno-fluorescence (IF) experiments to characterize the subcellular localization properties of human RNA binding proteins (RBPs) studied in the context of the ENCODE team grant entitled "Comprehensive analysis of function RNA elements encoded in the human genome", led by Dr. Brenton Graveley at the UConn Health Center. These studies are being conducted using several human model cell lines prioritized by the ENCODE consortium (e.g. HepG2, MCF7 and HeLa) and validated commercial antibodies targeting over 250 distinct RBPs. The database displays images resulting from co-labeling experiments of individual RBPs in conjunction with a panel of cellular markers for various organelles and subcellular structures. The data can be accessed via different search options, either by searching for individual RBPs or in batch display formats. Antibody validation was performed in the lab of Dr. Gene Yeo at UCSD, while all IF experiments and analyses are being conducted in the laboratory of Dr. Eric Lécuyer at the IRCM in Montreal.

Kindly note that this website is still under active construction. Not all functions are implemented or yet fully functional. Thank you for your comprehension.

**Search by gene symbols**

Select a Cell Line

Select a Target

Search

**Search by Annotation**

Under construction

Search

**Browse by cell lines**

HepG2 253 genes

MCF7 22 genes

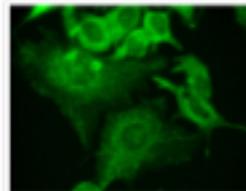
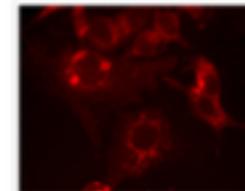
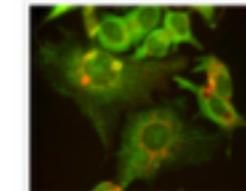
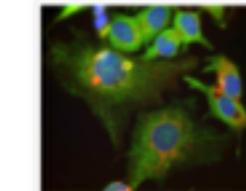
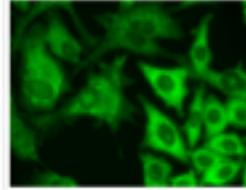
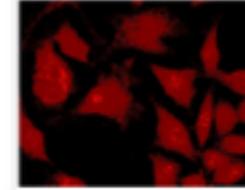
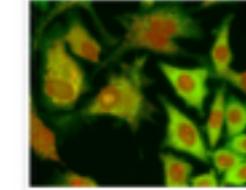
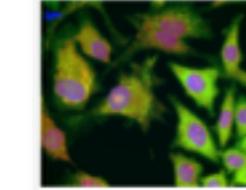
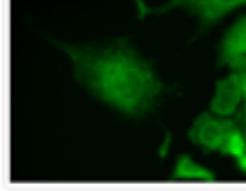
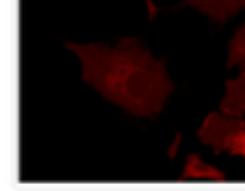
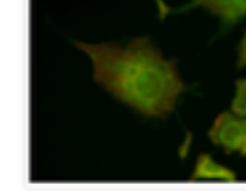
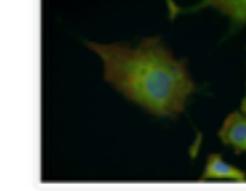
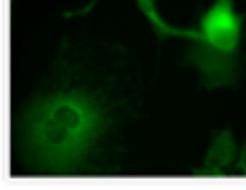
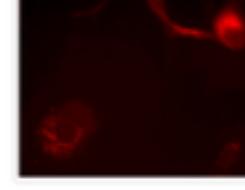
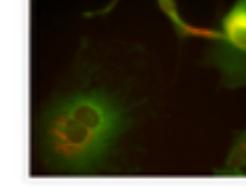
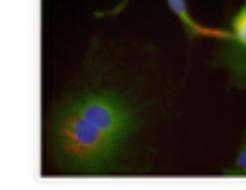
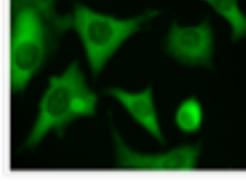
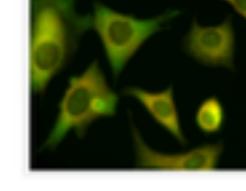
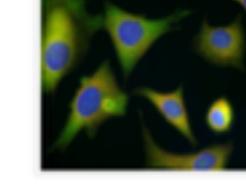
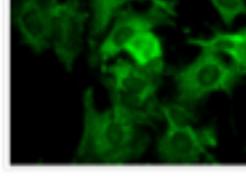
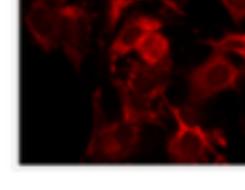
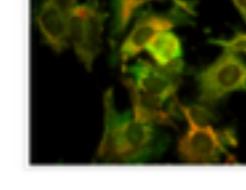
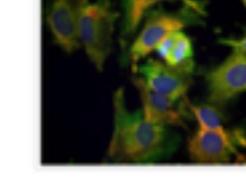
Browse

This database was developed and is maintained by the Lécuyer Lab. Please [email](#) us for any comments, suggestions or bug reports.

<http://rnabiology.ircm.qc.ca/RBPIimage/>

# Accessing ENCODE RBP Data

## Gene sets

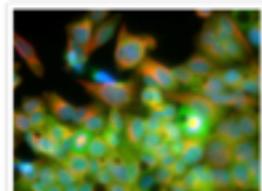
	AARS	Marker	Co-labelled	Co-labelled with DAPI	Comments	Annotation
Endosomal Network (anti-CD63)						Quality: Good Exposure time: Molecular weight: Product: Catalogue: Notes : HepG2 Marker Co-Localized Nuclei Nucleolus Cytoplasm Compartment/Organelle Mitochondria Cytosolic Unidentified Cytoplasm (UN) Cyto Foci (UN) Nuclei (UN) Nucl Foci (UN) Additional comments: Mainly cytosolic; though not always as prominent in the mitochondria and nucleoli, it is consistently observed in all the images. .
Cajal Bodies (anti-Collin)						
P-Bodies (anti-DCP1a)						
Golgi Apparatus (anti-GM130)						
Endoplasmic Reticulum (anti-KDEL)						
Mitochondria (Mitotracker)						

<http://rnabiology ircm qc ca/RBPIimage/>

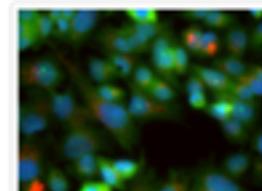
# Accessing ENCODE RBP Data

## ACO1

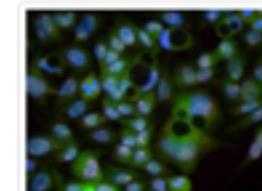
Microtubules  
(anti- $\alpha$ Tubulin)



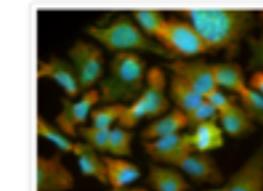
Endosomal Network  
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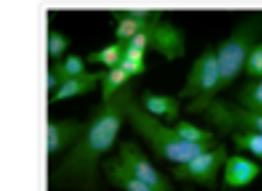
Cajal Bodies  
(anti-Collin)



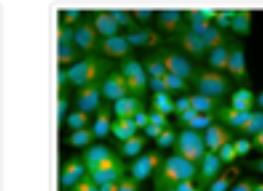
P-Bodies  
(anti-DCP1a)



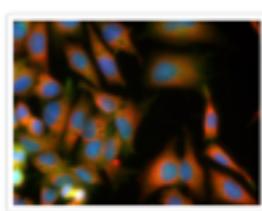
Nucleoli  
(anti-Fibrillarin)



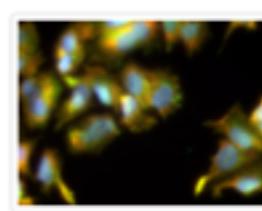
Golgi Apparatus  
(anti-GM130)



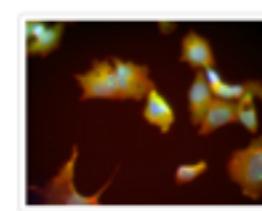
Endoplasmic Reticulum  
(anti-KDEL)



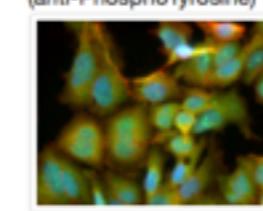
Mitochondria  
(Mitotracker)



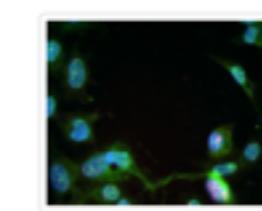
Filamentous Actin  
(Phalloidin)



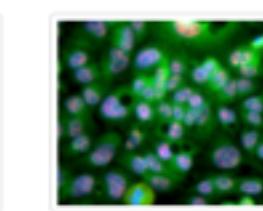
Cell Cortex and Focal  
Adhesions  
(anti-PhosphoTyrosine)



PML Nuclear Bodies  
(anti-PML)

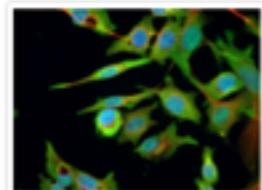


Nuclear Speckles  
(anti-SC35)

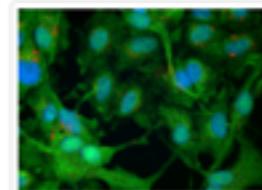


## ADAR

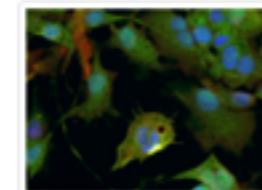
Microtubules  
(anti- $\alpha$ Tubulin)



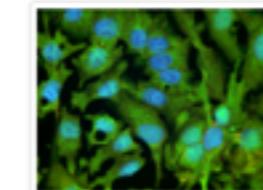
Endosomal Network  
(anti-CD63)



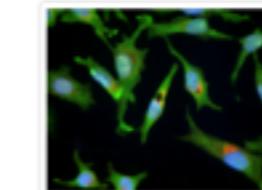
Cajal Bodies  
(anti-Collin)



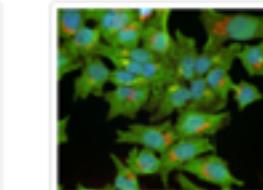
P-Bodies  
(anti-DCP1a)



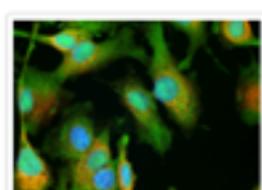
Nucleoli  
(anti-Fibrillarin)



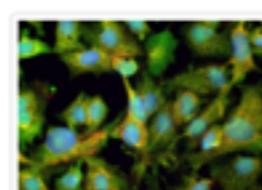
Golgi Apparatus  
(anti-GM130)



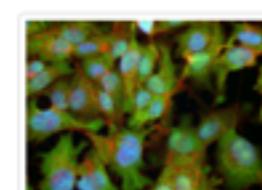
Endoplasmic Reticulum  
(anti-KDEL)



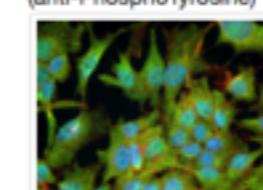
Mitochondria  
(Mitotracker)



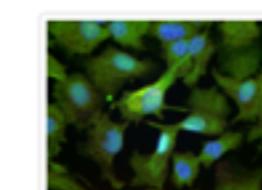
Filamentous Actin  
(Phalloidin)



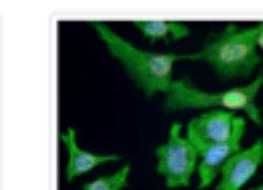
Cell Cortex and Focal  
Adhesions  
(anti-PhosphoTyrosine)



PML Nuclear Bodies  
(anti-PML)



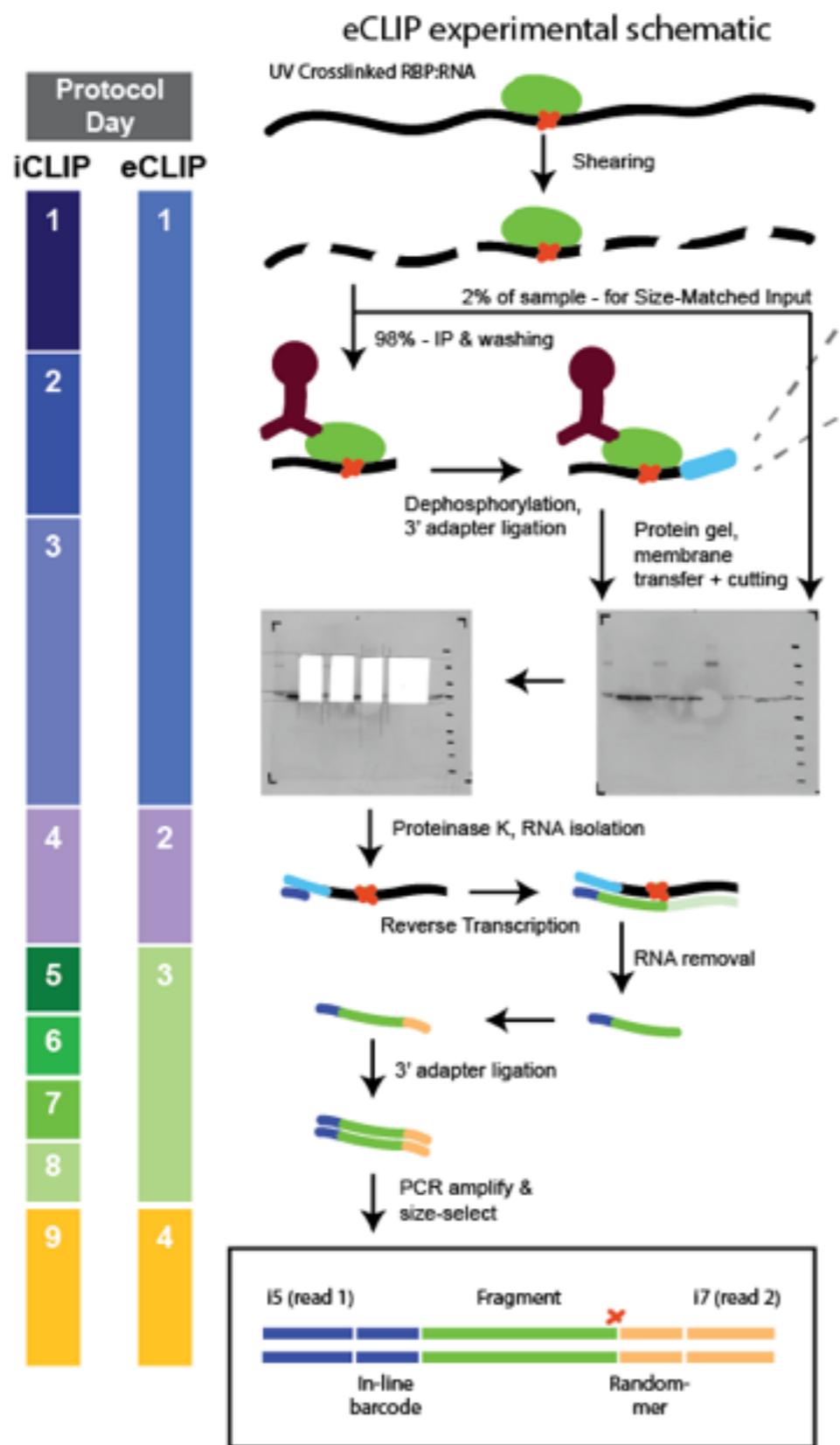
Nuclear Speckles  
(anti-SC35)



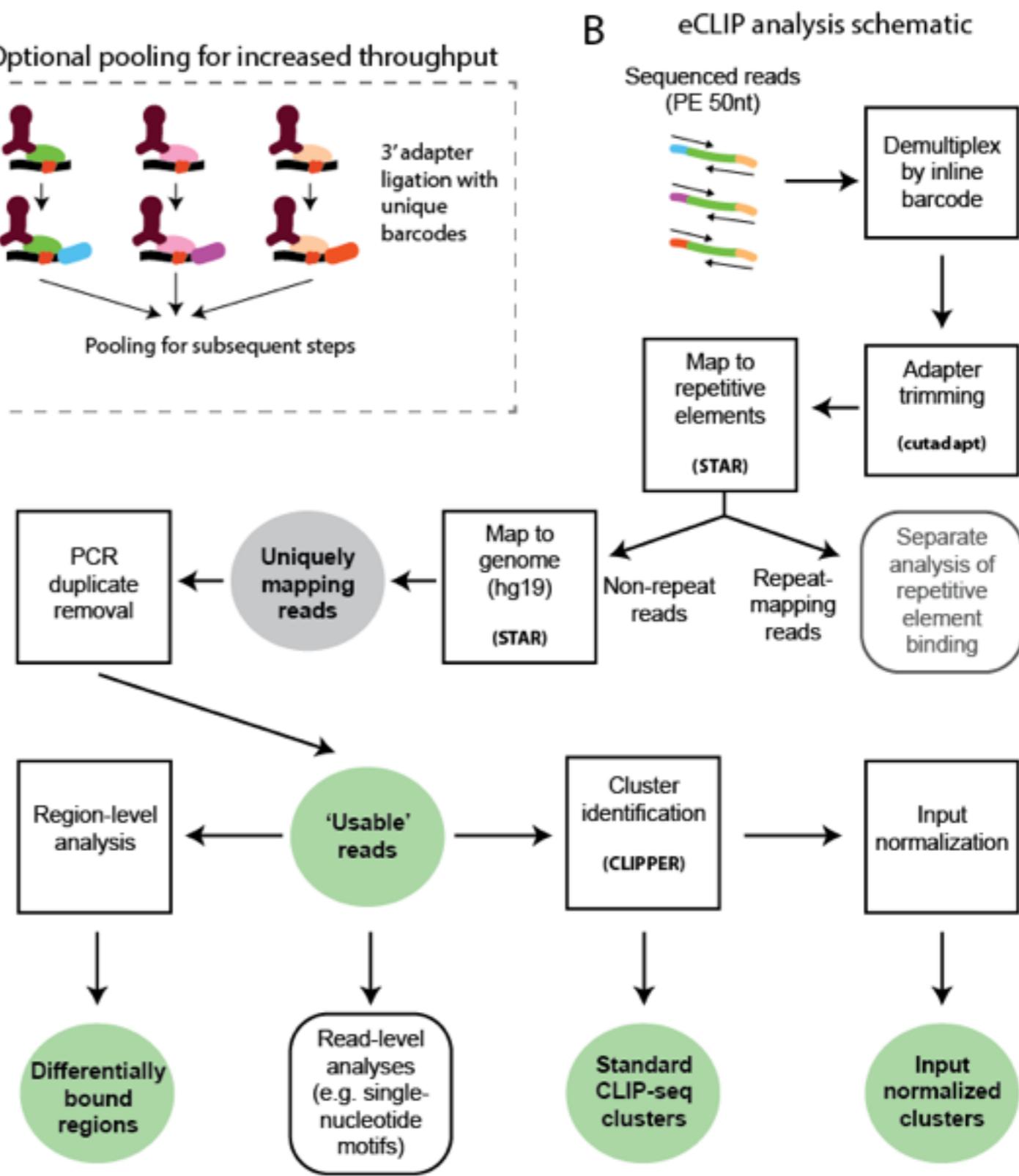
<http://rnabiology ircm qc ca/RBPIimage/>

# The eCLIP Protocol and Analysis Pipeline

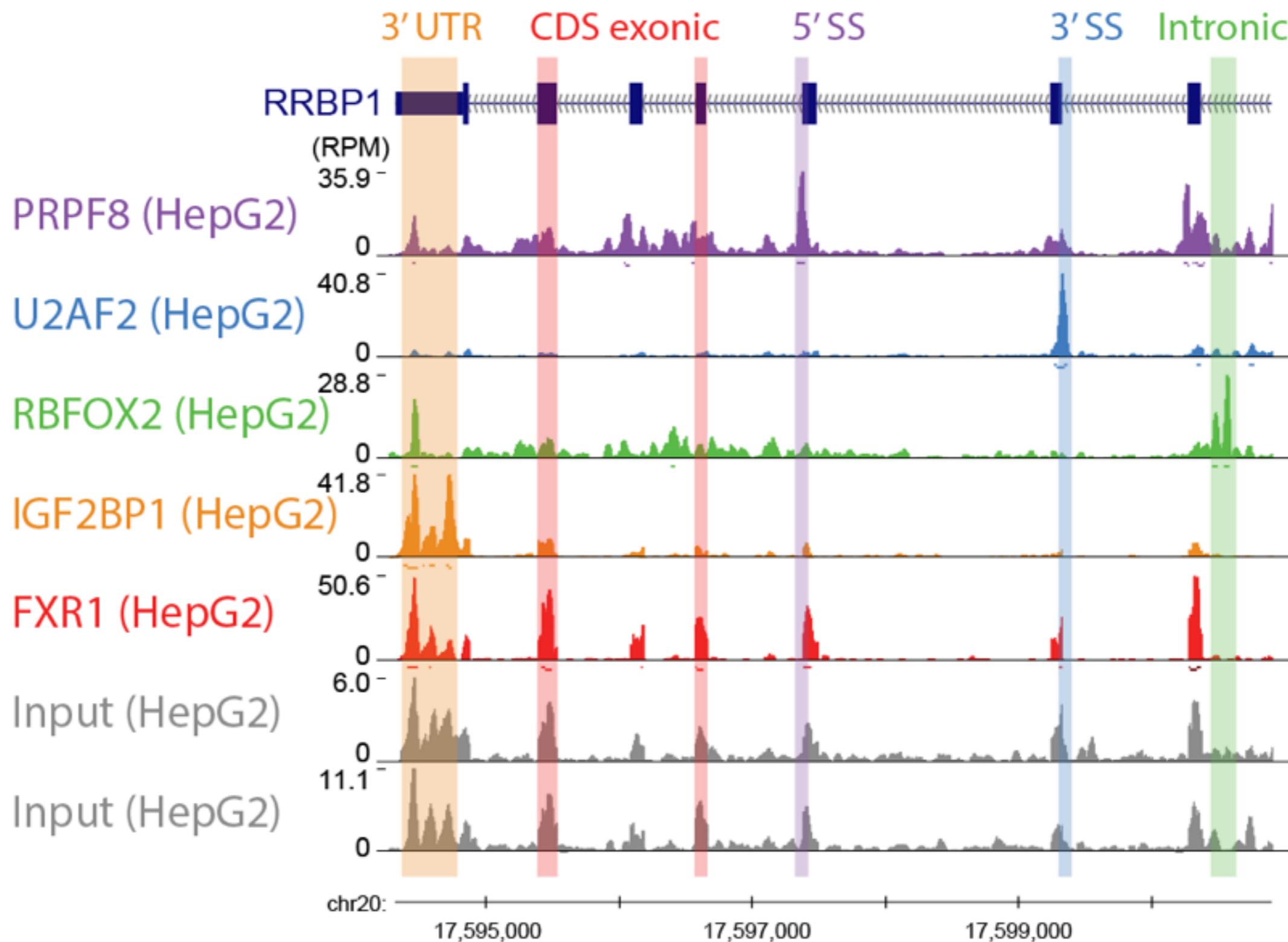
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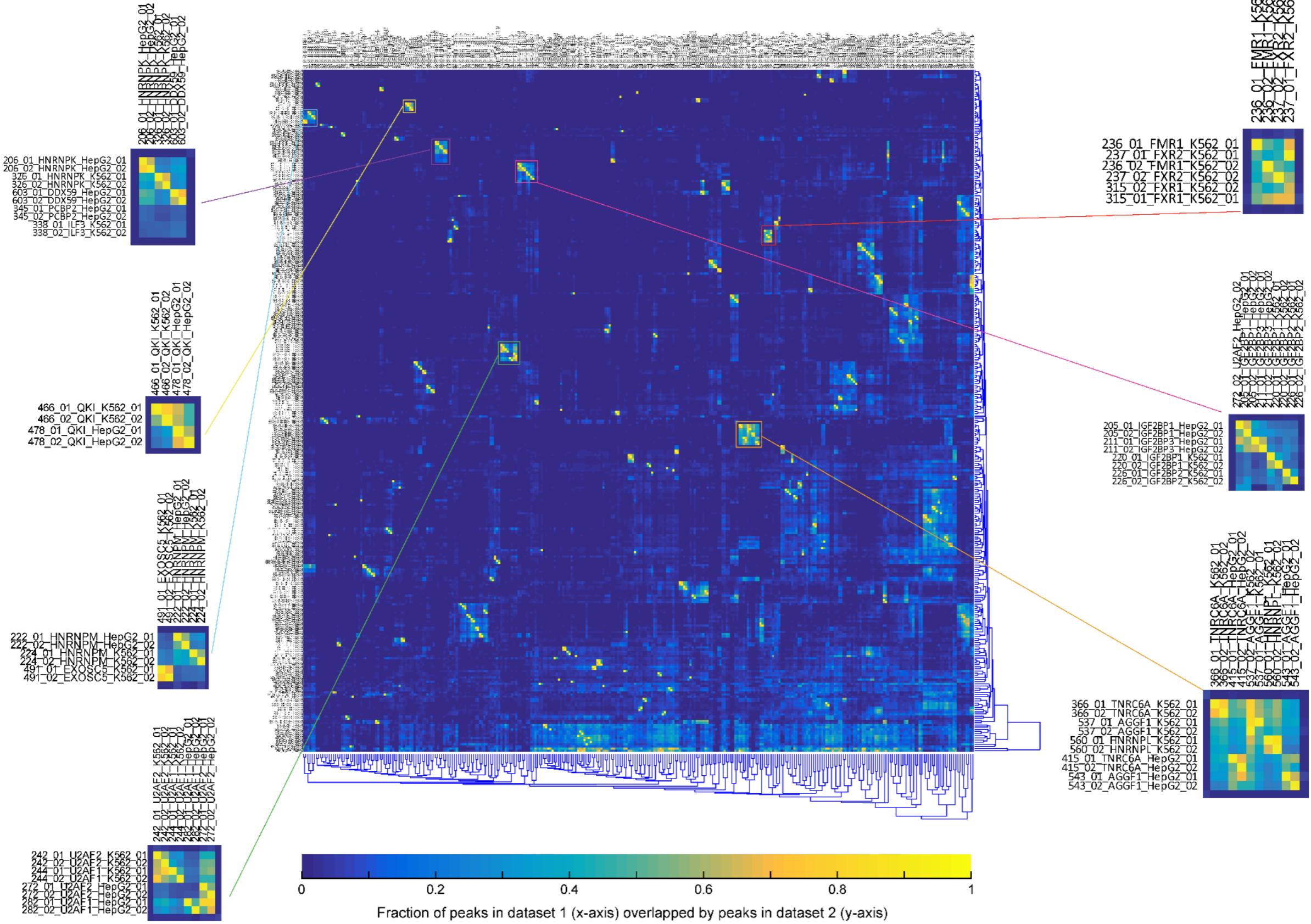
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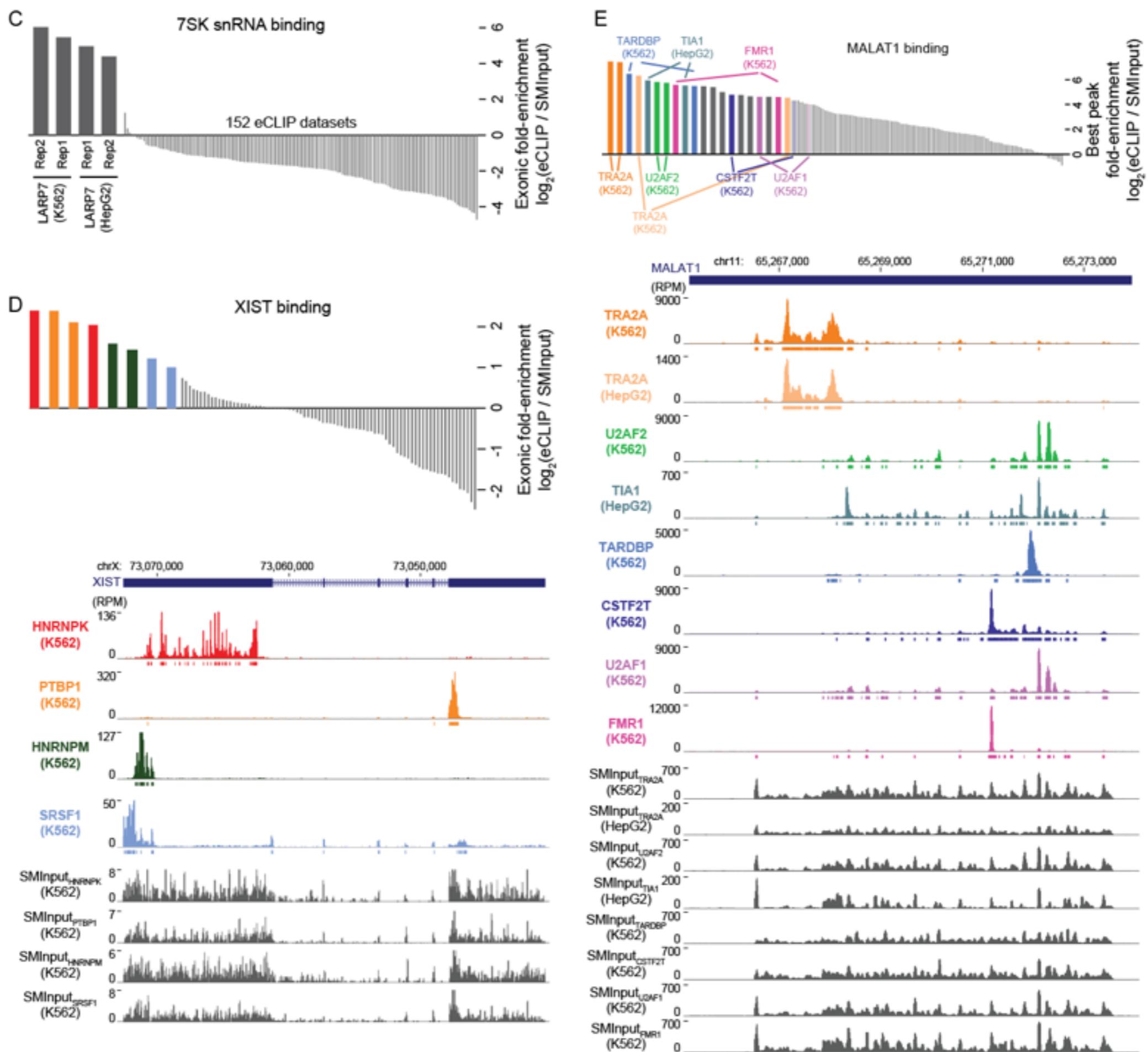
# eCLIP-seq reveals RBP-specific binding profiles



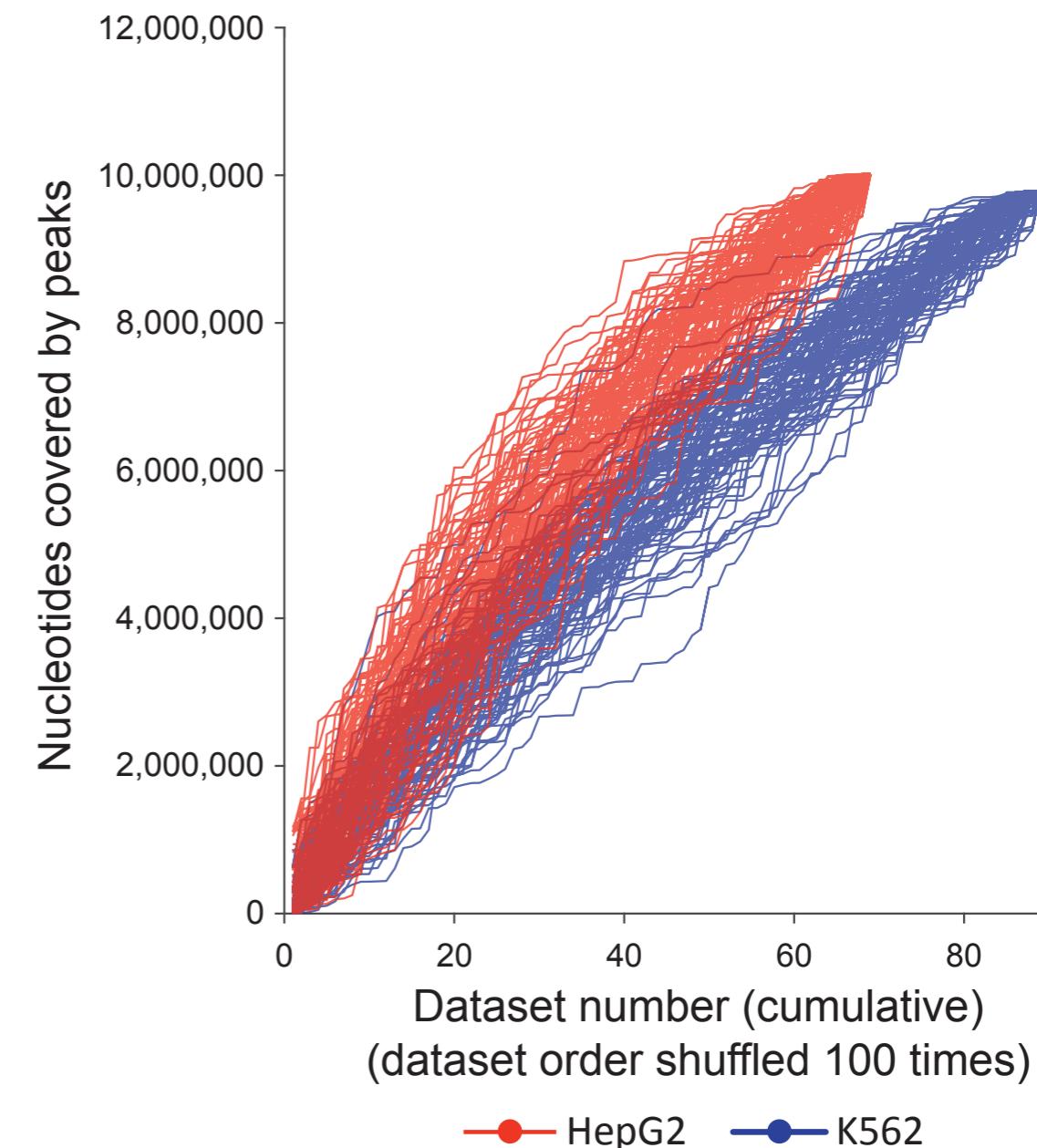
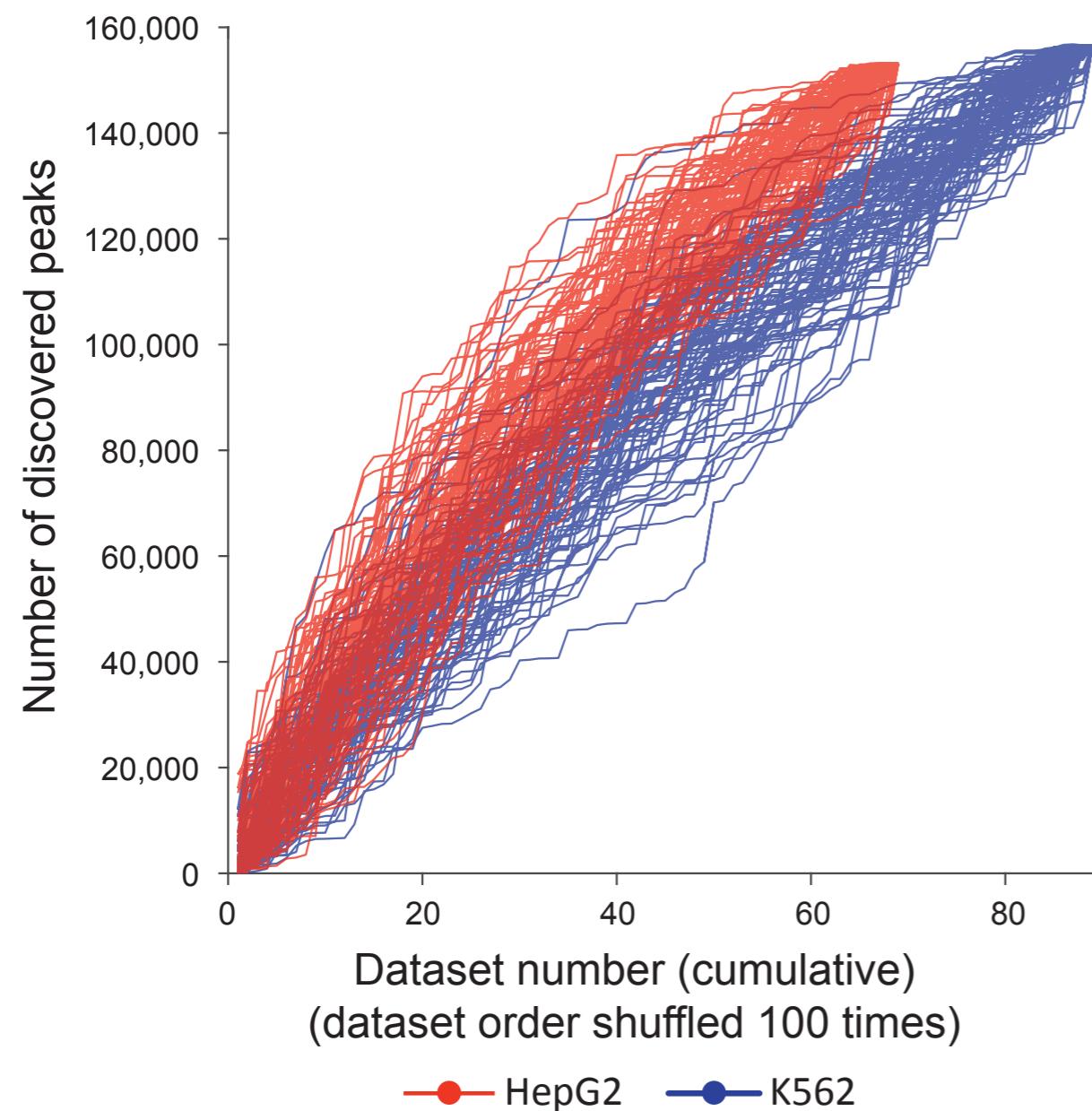
# eCLIP-seq Identifies Co-Associated Proteins



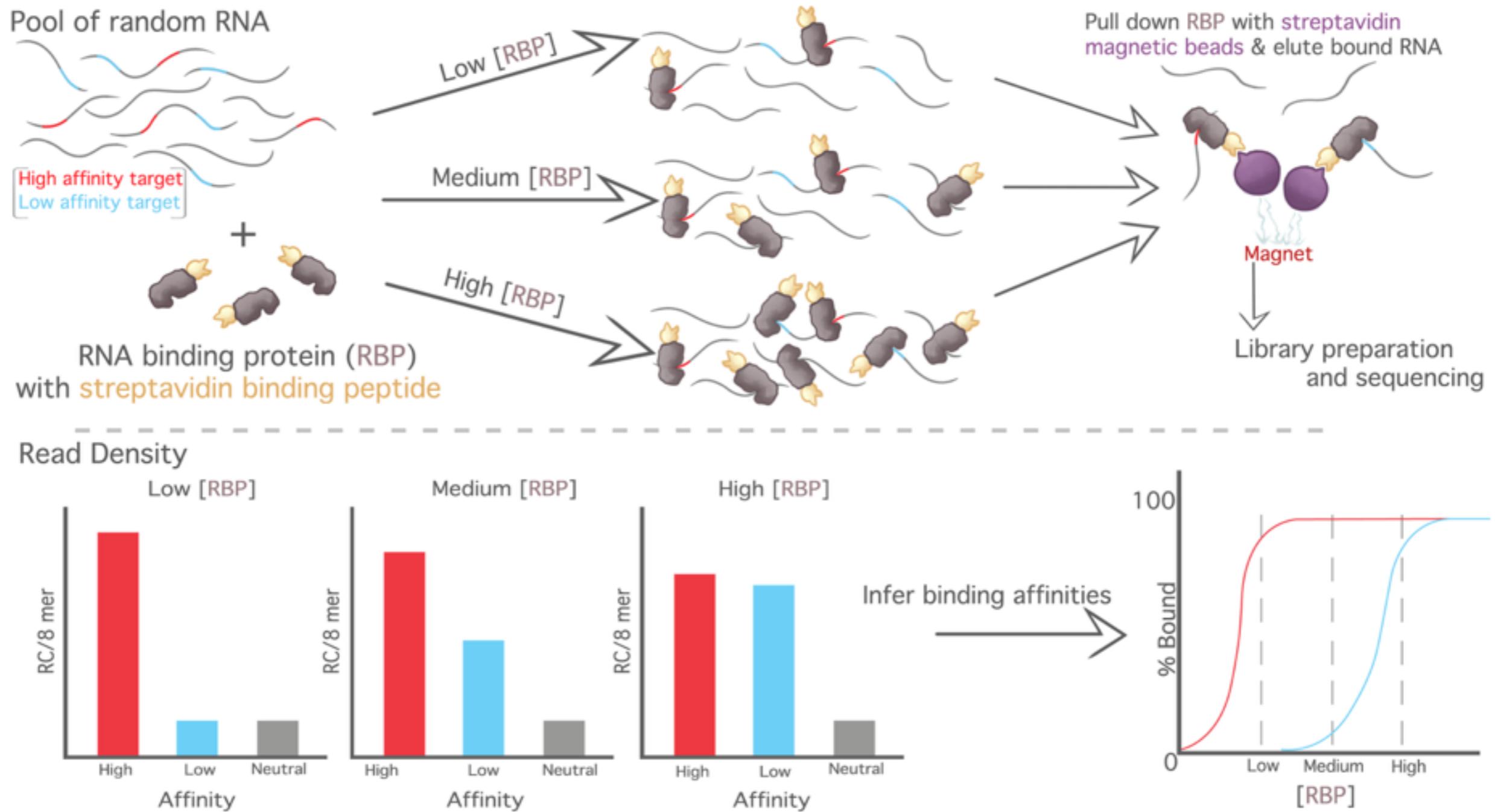
# An “RNA-centric” view of RBP-binding



# Discovery of RNA elements in the Human Genome

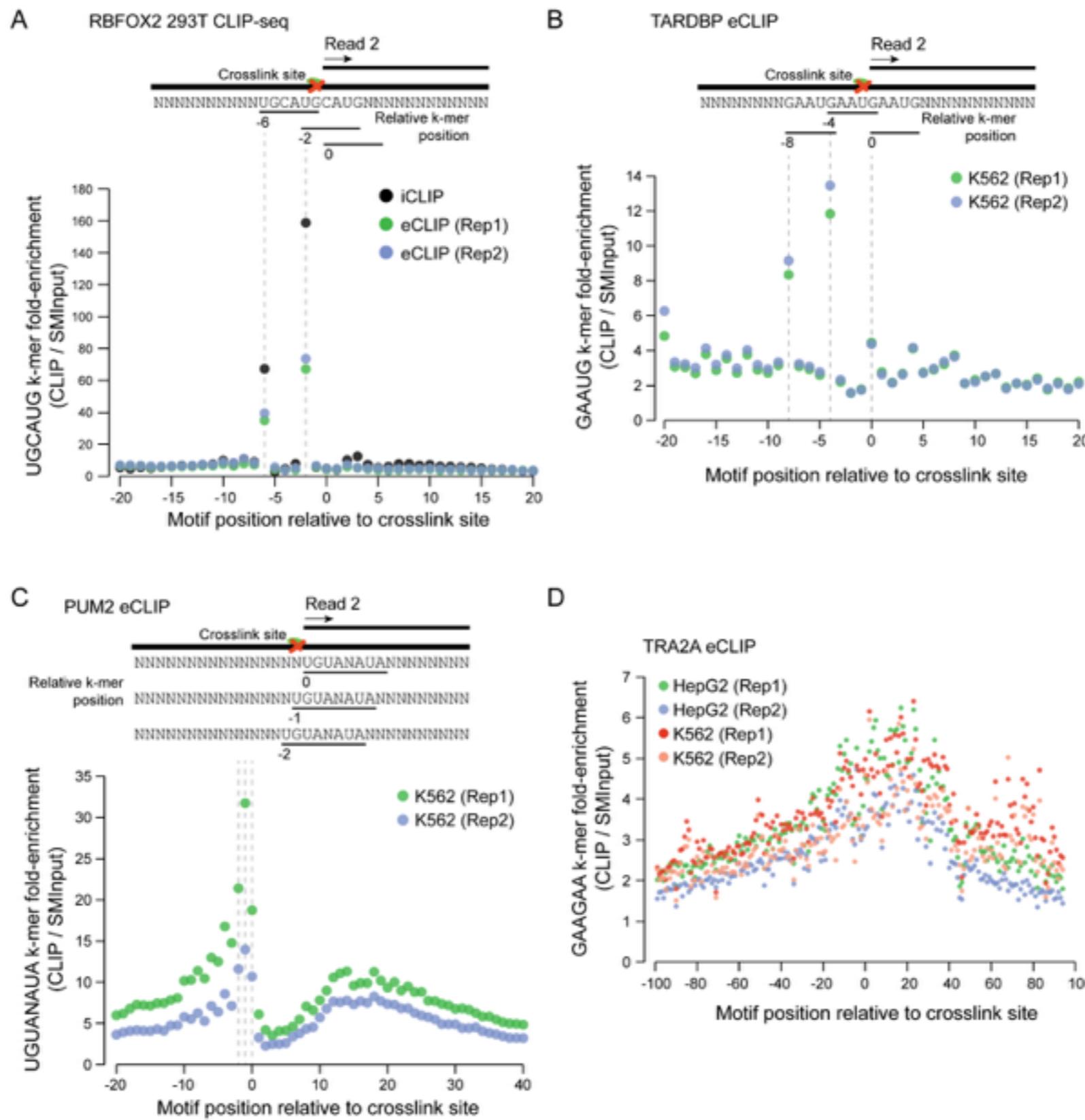


# RNA Bind-n-Seq (RBNS): A method to quantify protein/RNA interactions

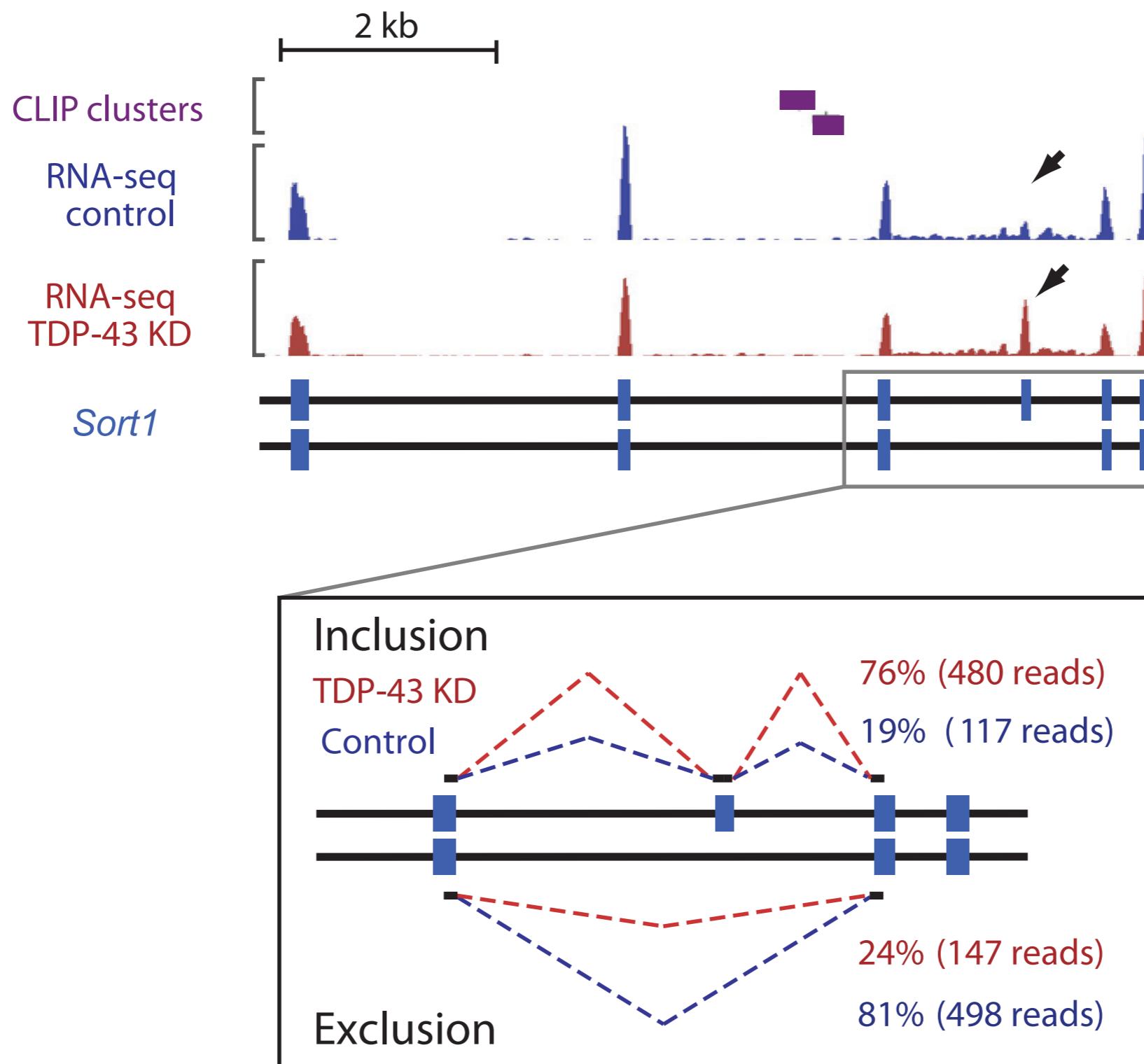


Lambert, N., et al. (2014). RNA Bind-n-Seq: Quantitative Assessment of the Sequence and Structural Binding Specificity of RNA Binding Proteins. *Mol Cell*.

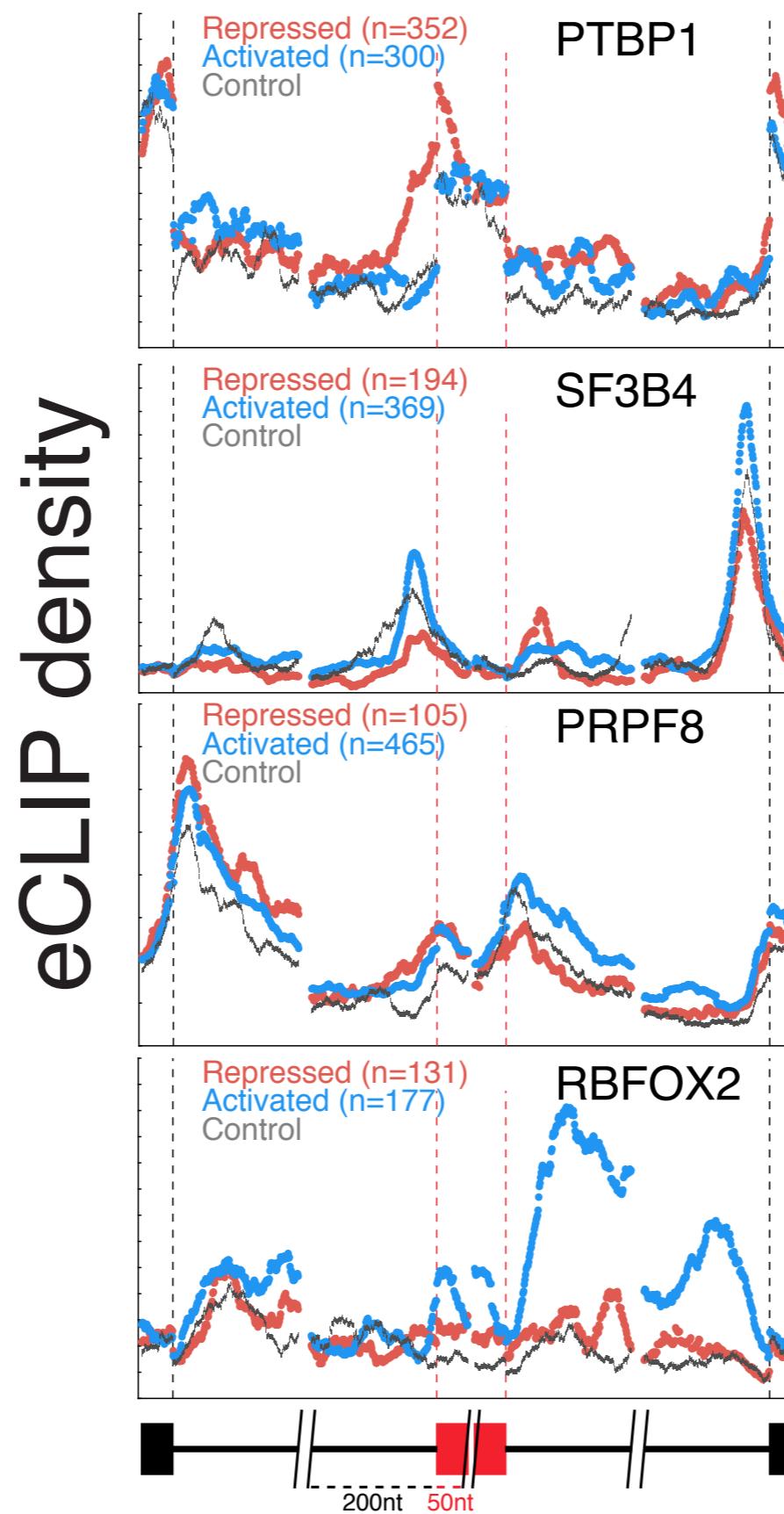
# eCLIP identifies motifs at crosslink-termination points



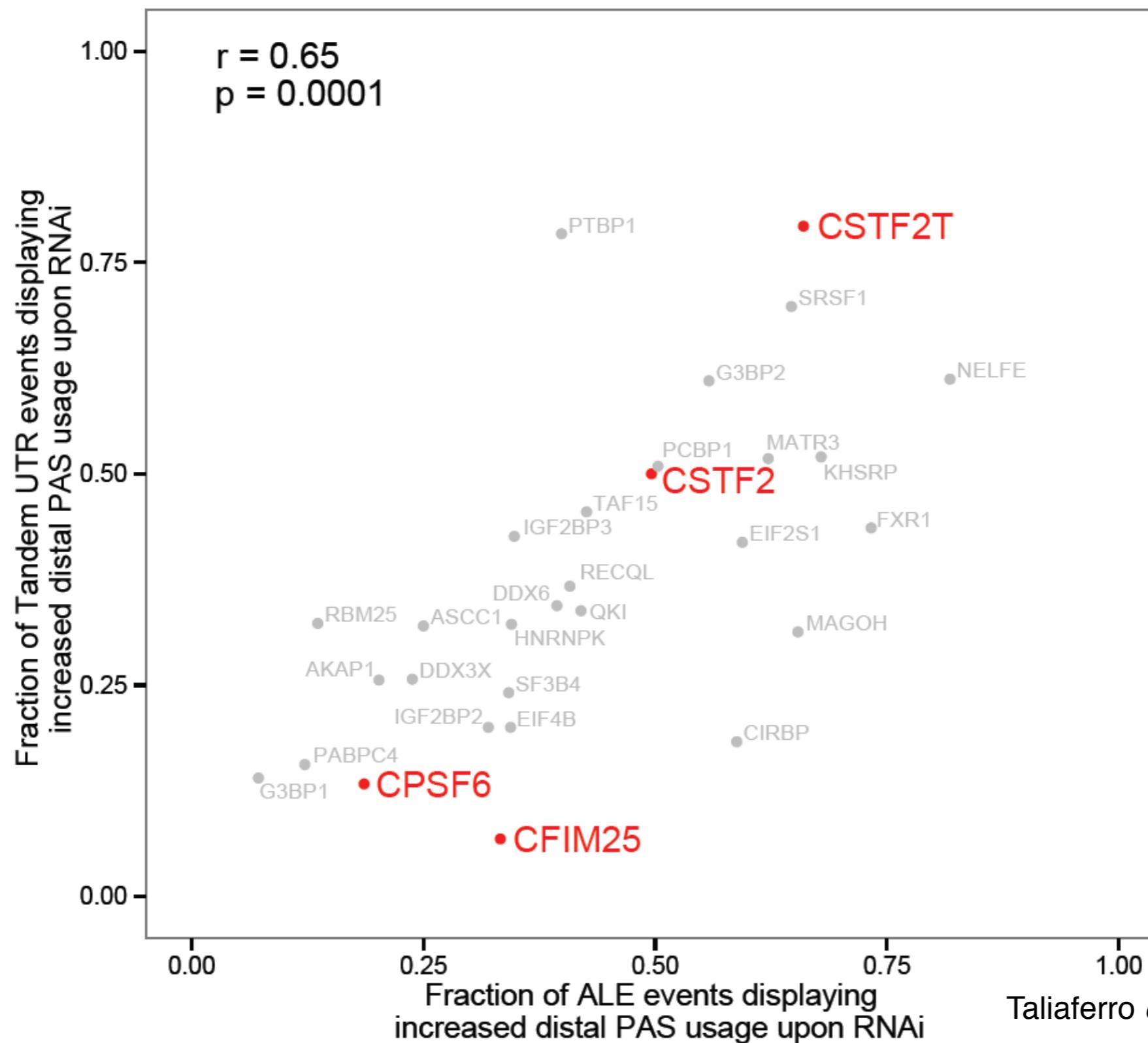
# Assigning Function to Binding Sites



# RNA Maps for RBPs

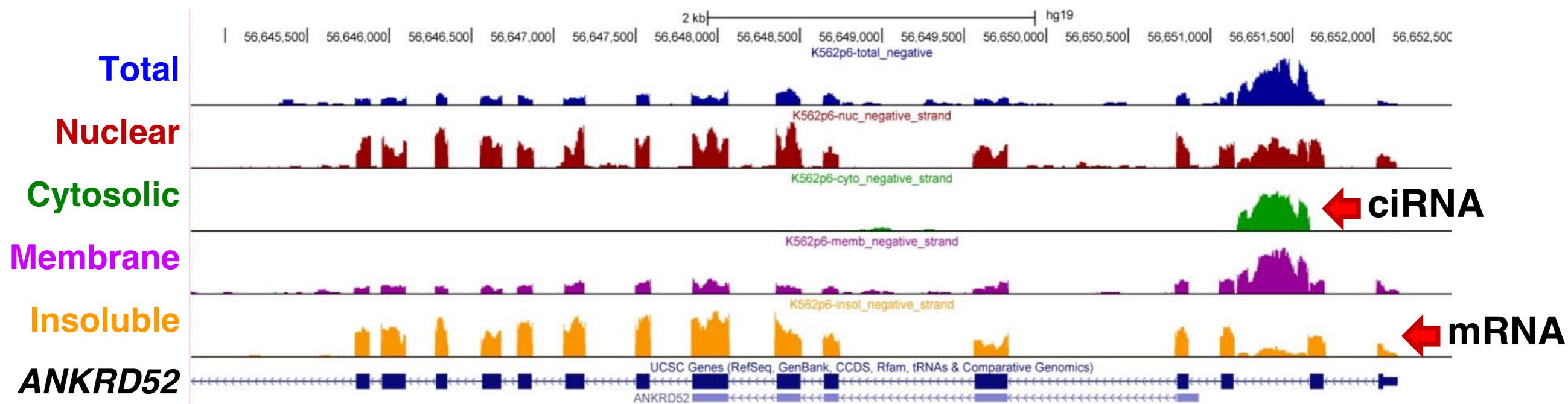


# Identification of RBPs that regulate proximal vs distal polyadenylation site usage

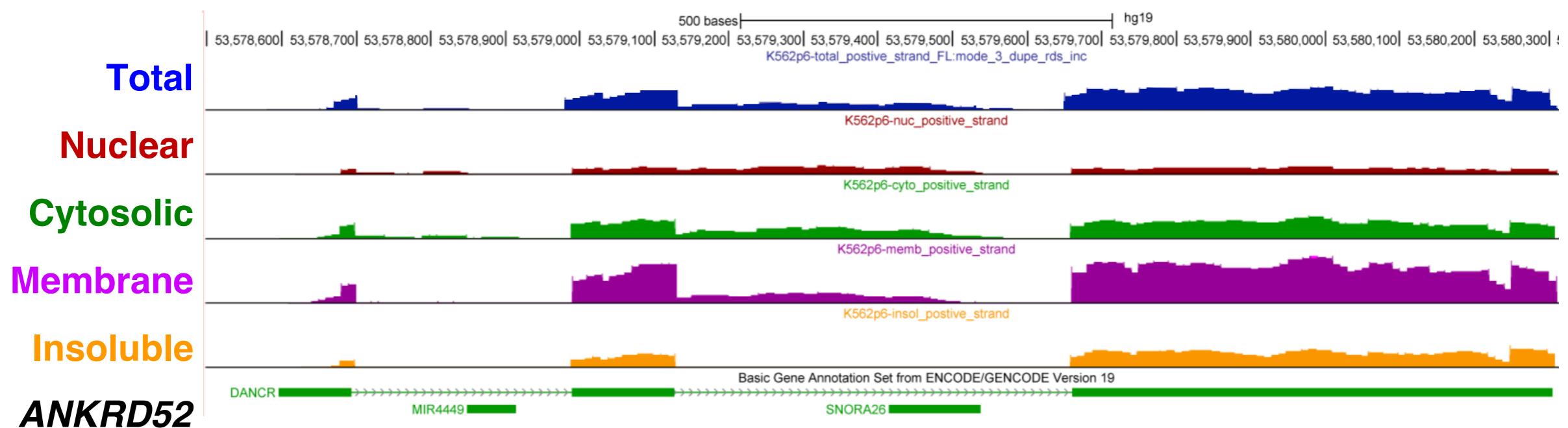


# RNA Localization (Frac-Seq)

## *ANKRD52* (*mRNA and ciRNA*)



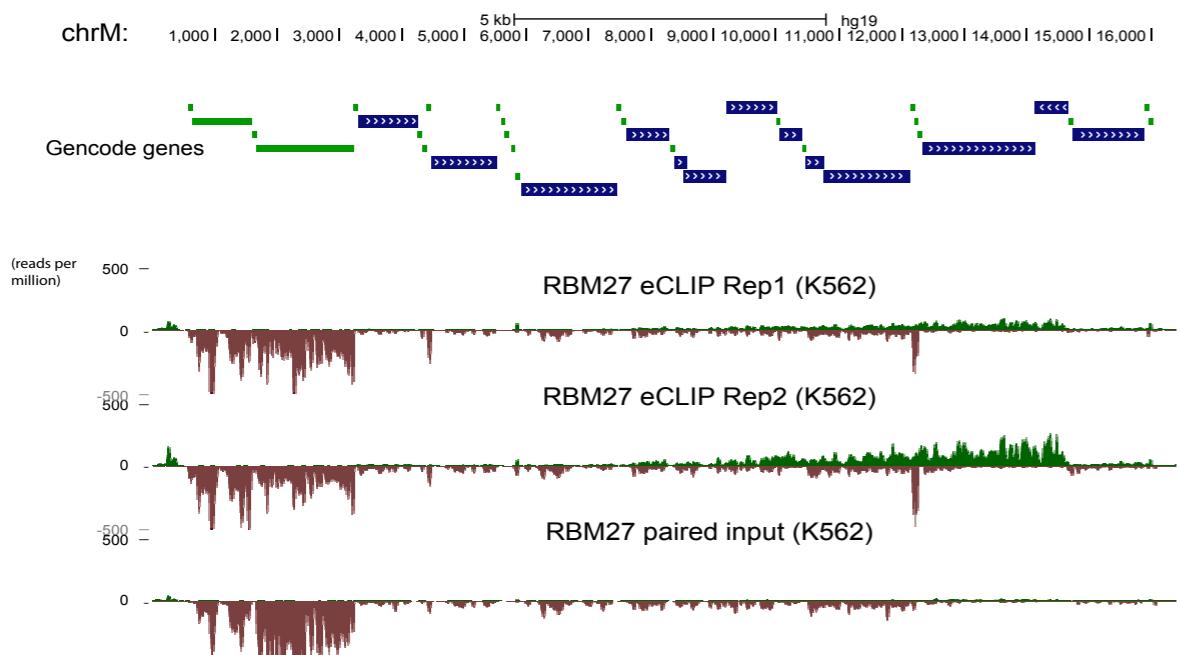
## *DANCR* (*lncRNA*)



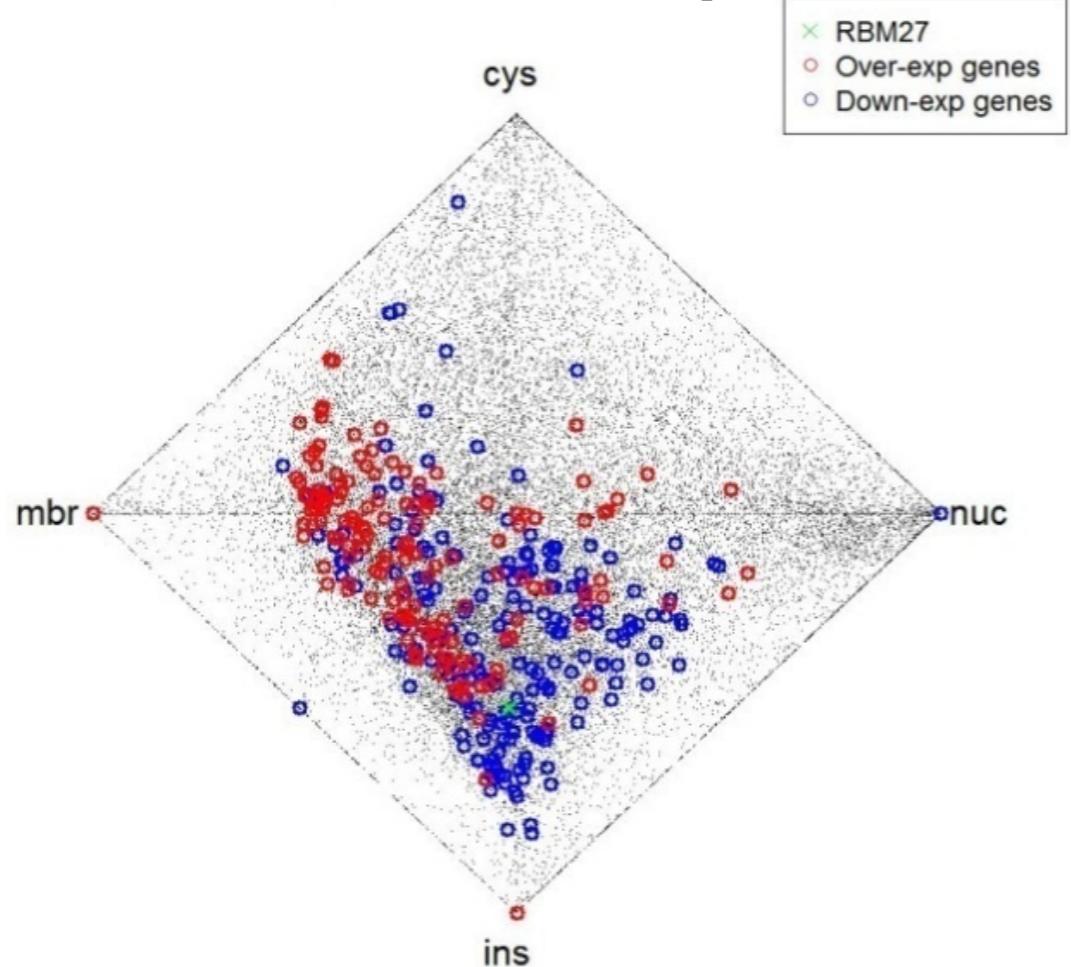
(Neal Cody)

# Integrative Analysis

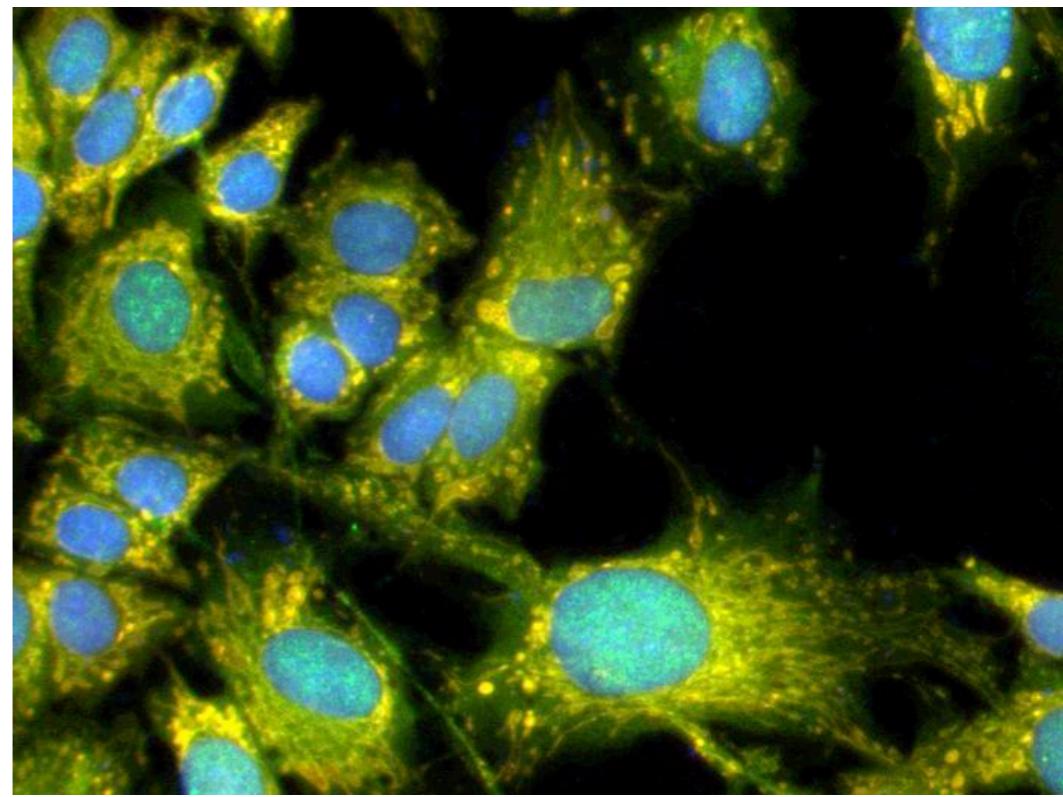
## eCLIP-Seq



## Frac-Seq

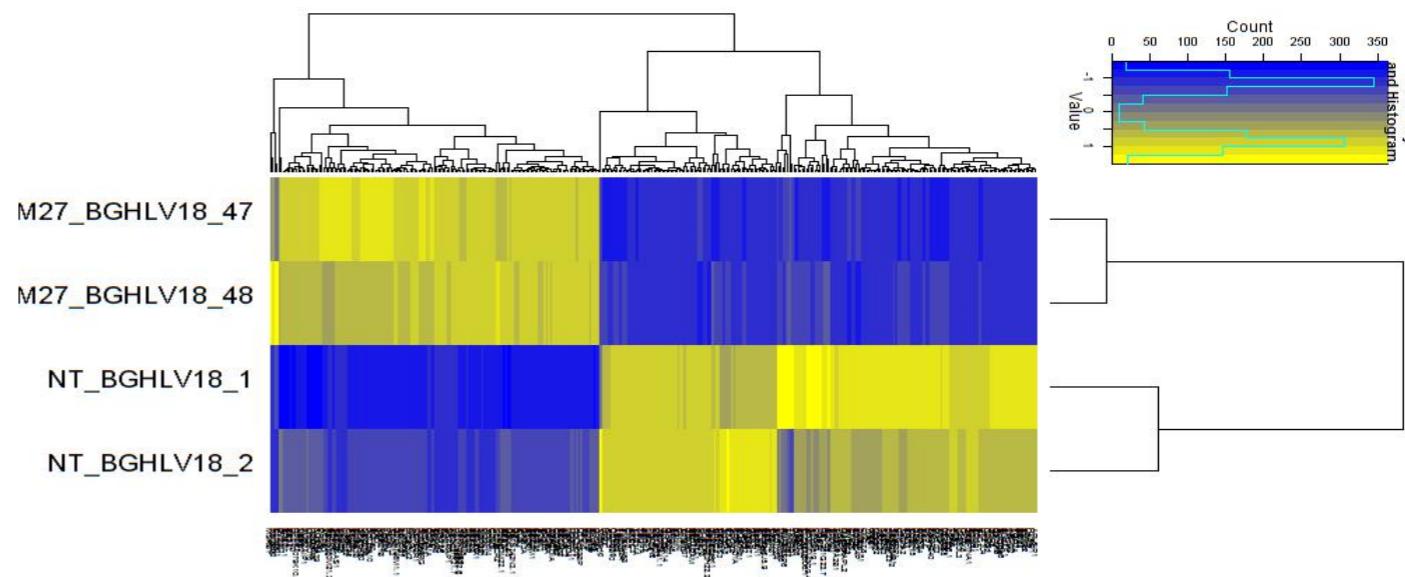


## Imaging



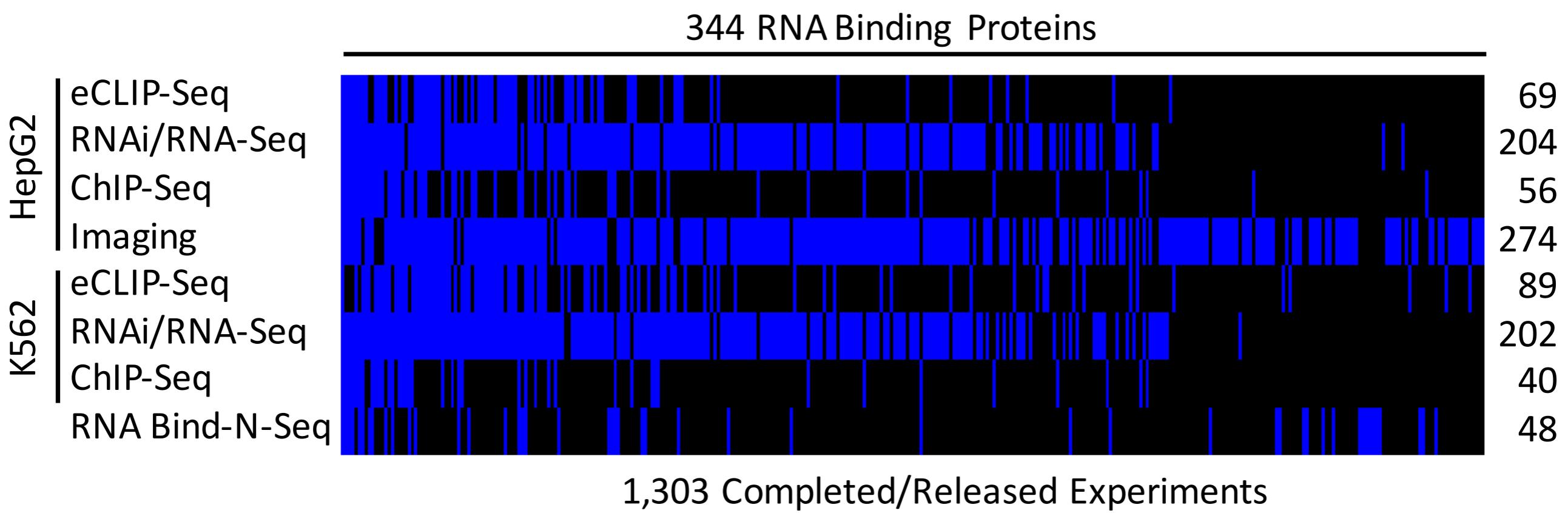
**RBM27    Mito    DNA**

## Gene Expression



# Data Production Status

(as of 06/06/16)



# The Periodic Table of Human RNA Binding Proteins



# Acknowledgments

## Brent Graveley – UConn

Michael Duff  
Sara Olson  
Xintao Wei  
Lijun Zhan

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Abigail Hochman

Mitch Guttman  
Alex Shishkin

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Eric van Nostrand  
Balaji Sundararaman  
Keri Elkins  
Rebecca Stanton  
Thai Nguyen  
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Rui Xiao

## Grace Xiao - UCLA

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Xiaofeng Wang  
Neal Cody  
Olivia Zhang  
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Jean Davidson  
Eurie Hong

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Mike Pazin  
Dan Gilchrist

**U54 HG007005**

**R21 HG008799**

R01 GM067842

R01 GM095296

R35 GM118140

