

# Supplemental Figures

## **Nephronophthisis gene products display RNA-binding properties and are recruited to stress granules**

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<sup>2</sup>Faculty of Biology, University of Freiburg

<sup>3</sup>Max Planck Institute of Immunobiology and Epigenetics, Freiburg, Germany

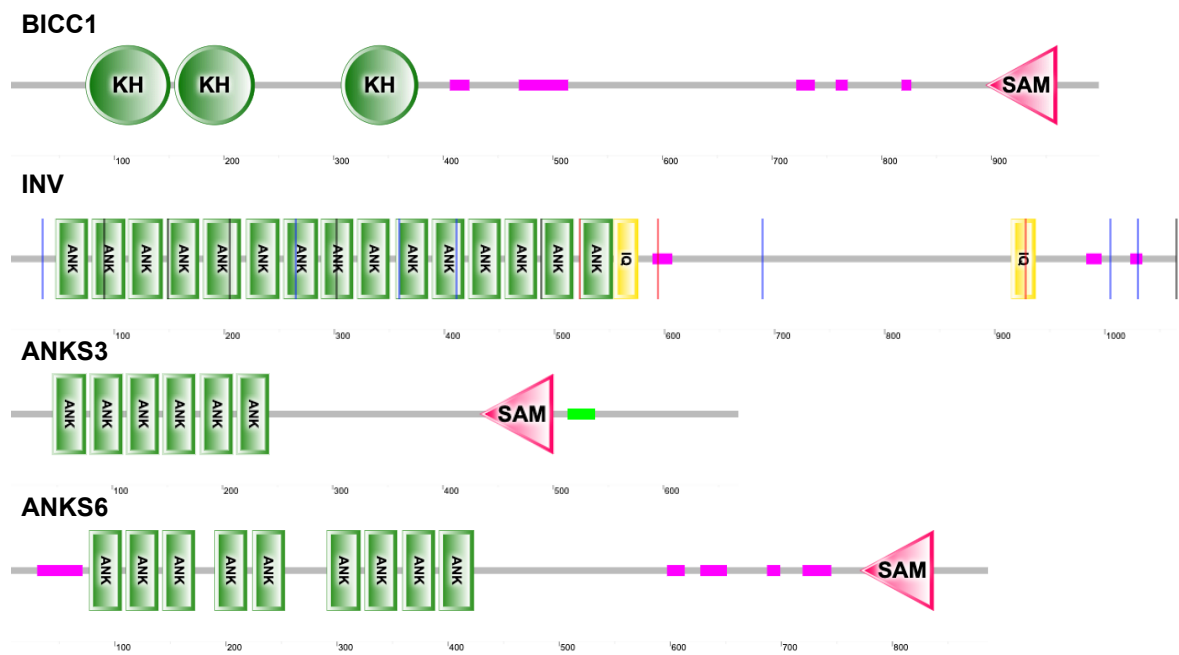
<sup>4</sup>Institute for Informatics, Albert-Ludwigs-University, Freiburg, Germany

<sup>5</sup>Department of Dermatology, Medical Center, and Freiburg Institute for Advanced Studies, University of Freiburg, Germany

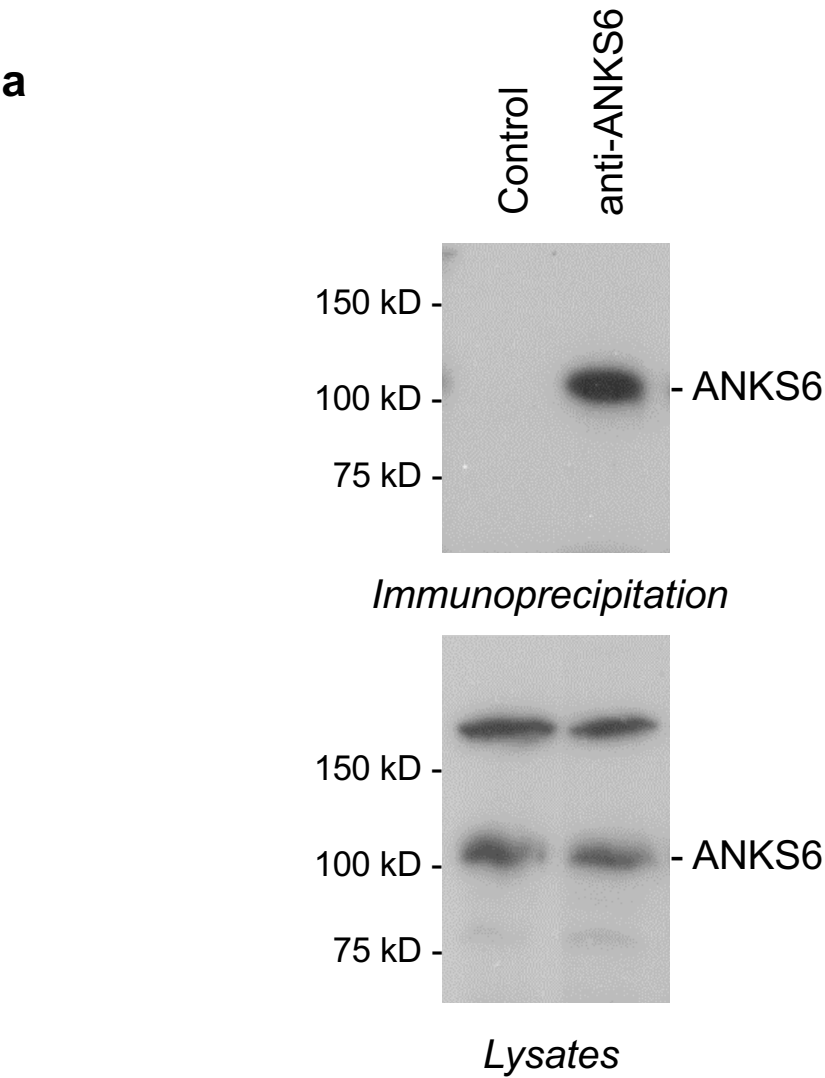
<sup>6</sup>CIBSS - Centre for Integrative Biological Signalling Studies, University of Freiburg

<sup>7</sup>Signalling Research Centres BIOSS and CIBSS, University of Freiburg

Supplemental Figure 1



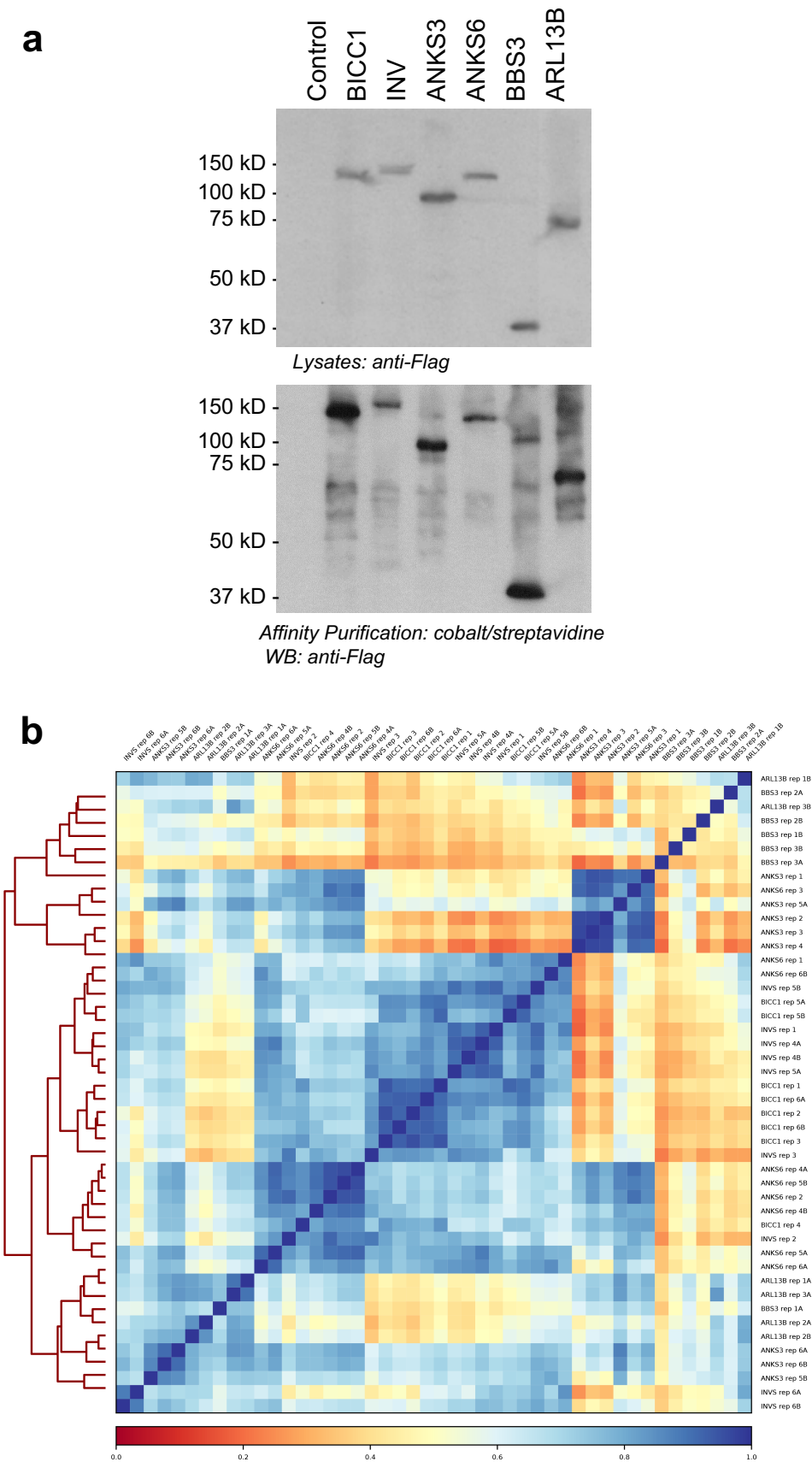
Supplemental Figure 2



**b**

GO-Term	Term Description	Observed Gene Count	Background Gene Count	FDR
<b>Biological Process</b>				
GO:0043604	amide biosynthetic process	66	414	1.01e-60
GO:0006412	translation	61	313	1.43e-60
GO:0006518	peptide metabolic process	63	440	1.45e-55
GO:0043603	cellular amide metabolic process	68	644	1.46e-52
GO:1901566	organonitrogen compound biosynthetic process	73	1122	2.74e-43
<b>Molecular Function</b>				
GO:0003735	structural constituent of ribosome	58	153	3.78e-72
GO:0005198	structural molecule activity	70	546	5.04e-60
GO:0003723	RNA binding	66	986	1.40e-39
GO:1901363	heterocyclic compound binding	106	4748	3.66e-26
GO:0097159	organic cyclic compound binding	106	4818	1.03e-25
<b>Cellular Component</b>				
GO:0022626	cytosolic ribosome	58	107	1.69e-79
GO:0044391	ribosomal subunit	60	181	2.82e-72
GO:0005840	ribosome	61	215	3.04e-70
GO:0044445	cytosolic part	59	228	7.80e-66
GO:1990904	ribonucleoprotein complex	78	765	2.34e-61
<b>KEGG</b>				
mmu03010	Ribosome	55	128	3.76e-71
mmu01200	Carbon metabolism	8	118	0.00052
mmu05322	Systemic lupus erythematosus	7	92	0.00064
mmu00020	Citrate cycle (TCA cycle)	4	32	0.0063
mmu00010	Glycolysis / Gluconeogenesis	5	65	0.0065

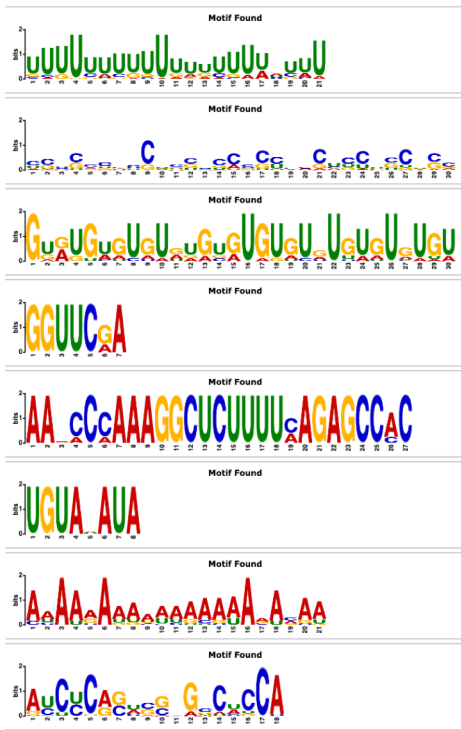
Supplemental Figure 3



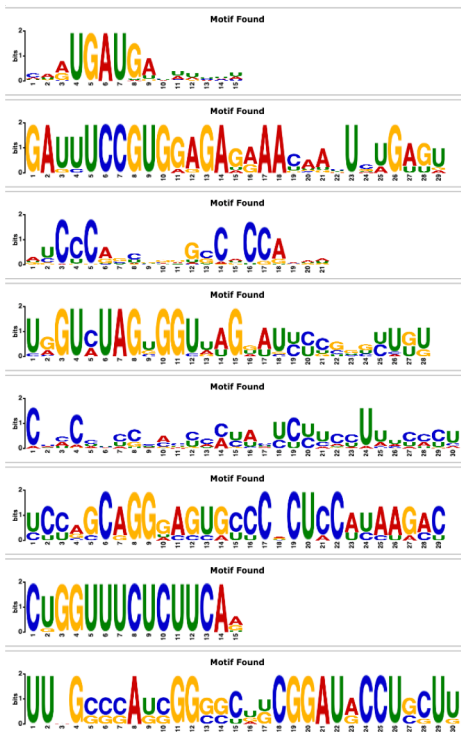


## Supplemental Figure 4

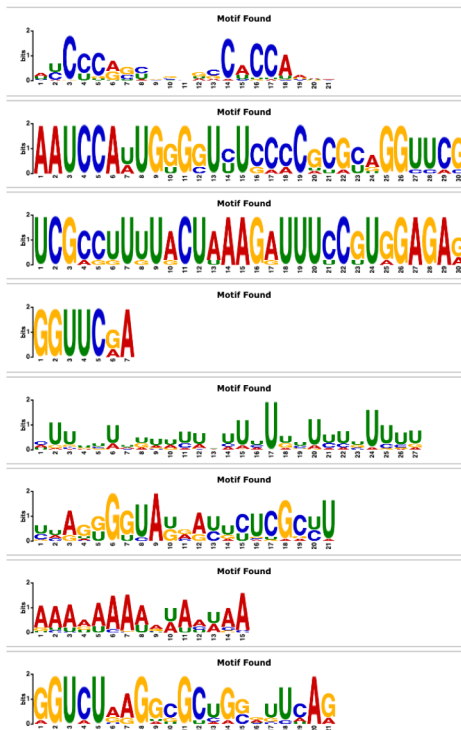
# BICC1



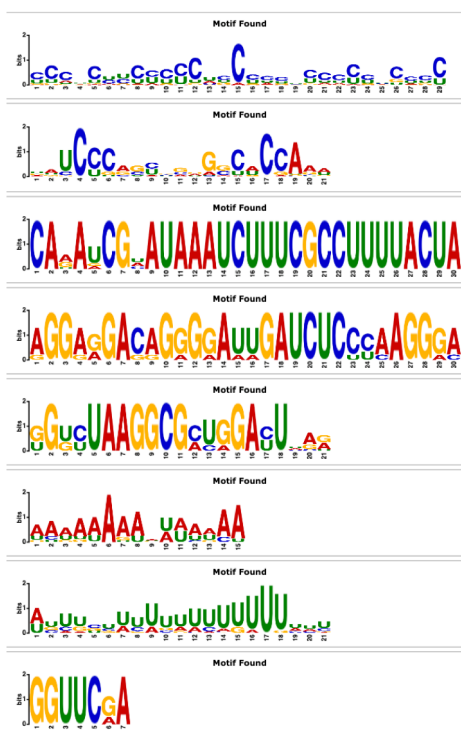
# ANKS3



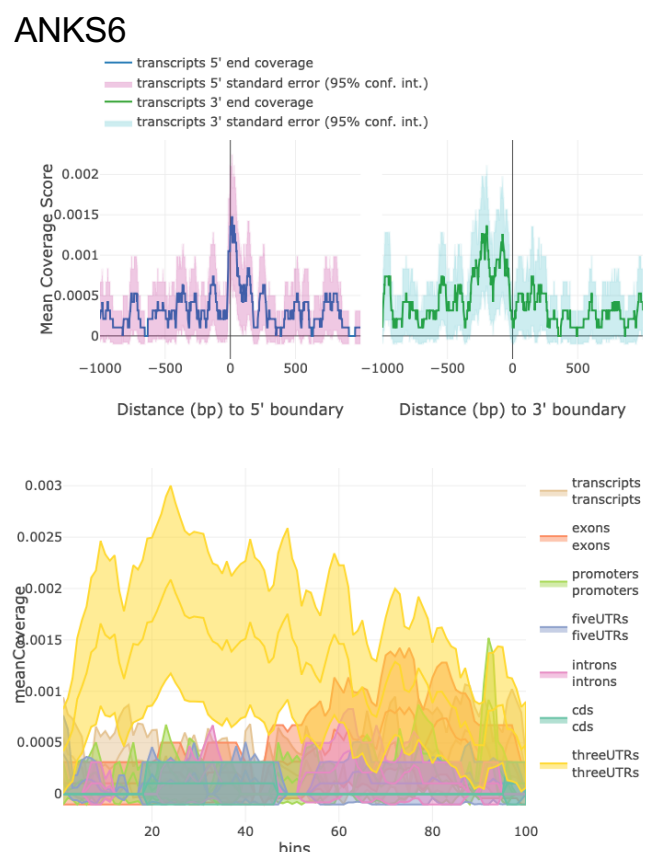
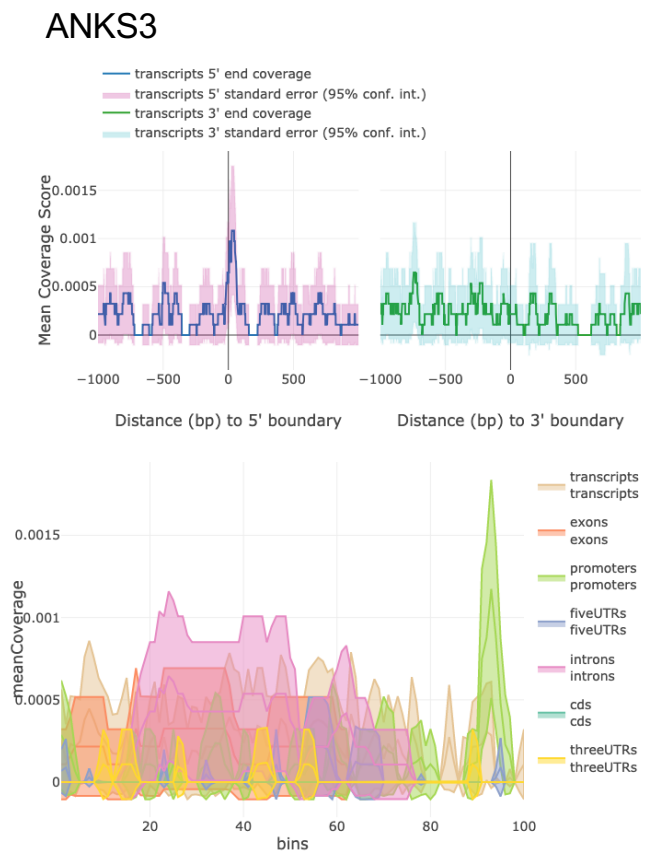
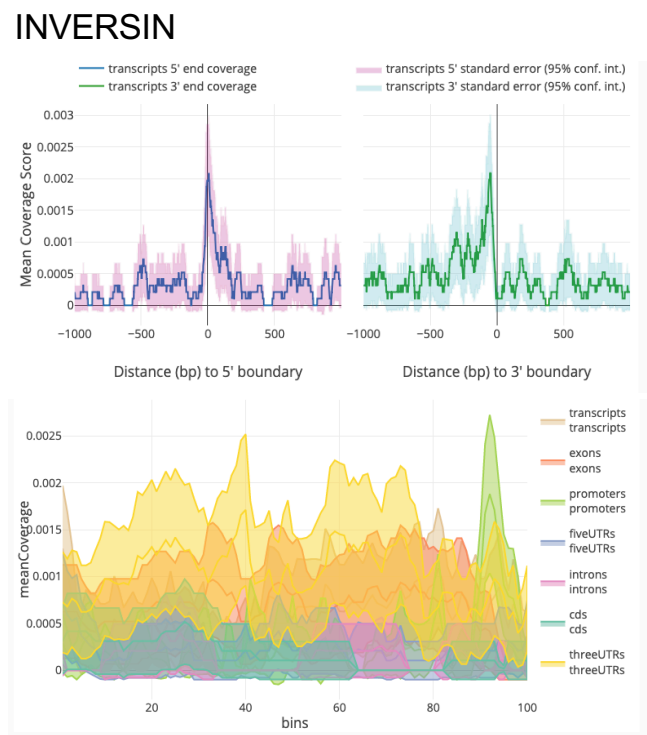
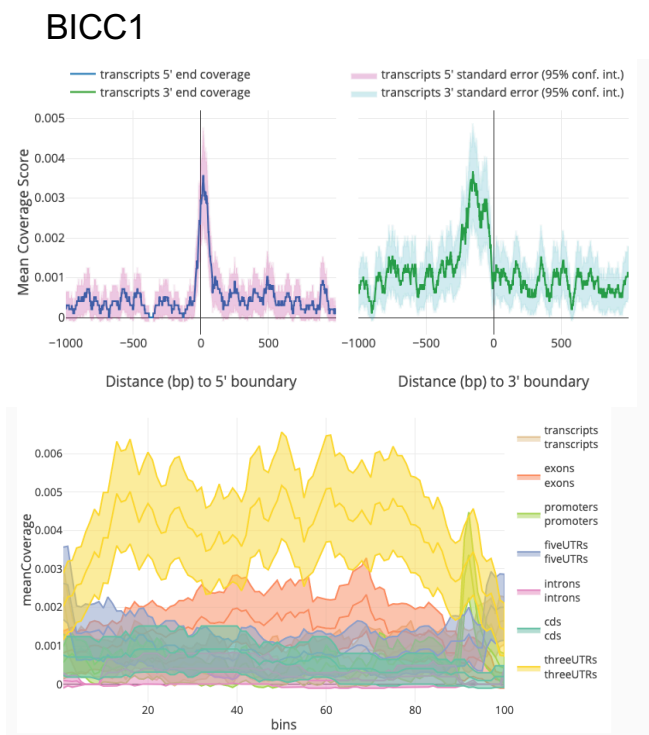
## INVER SIN



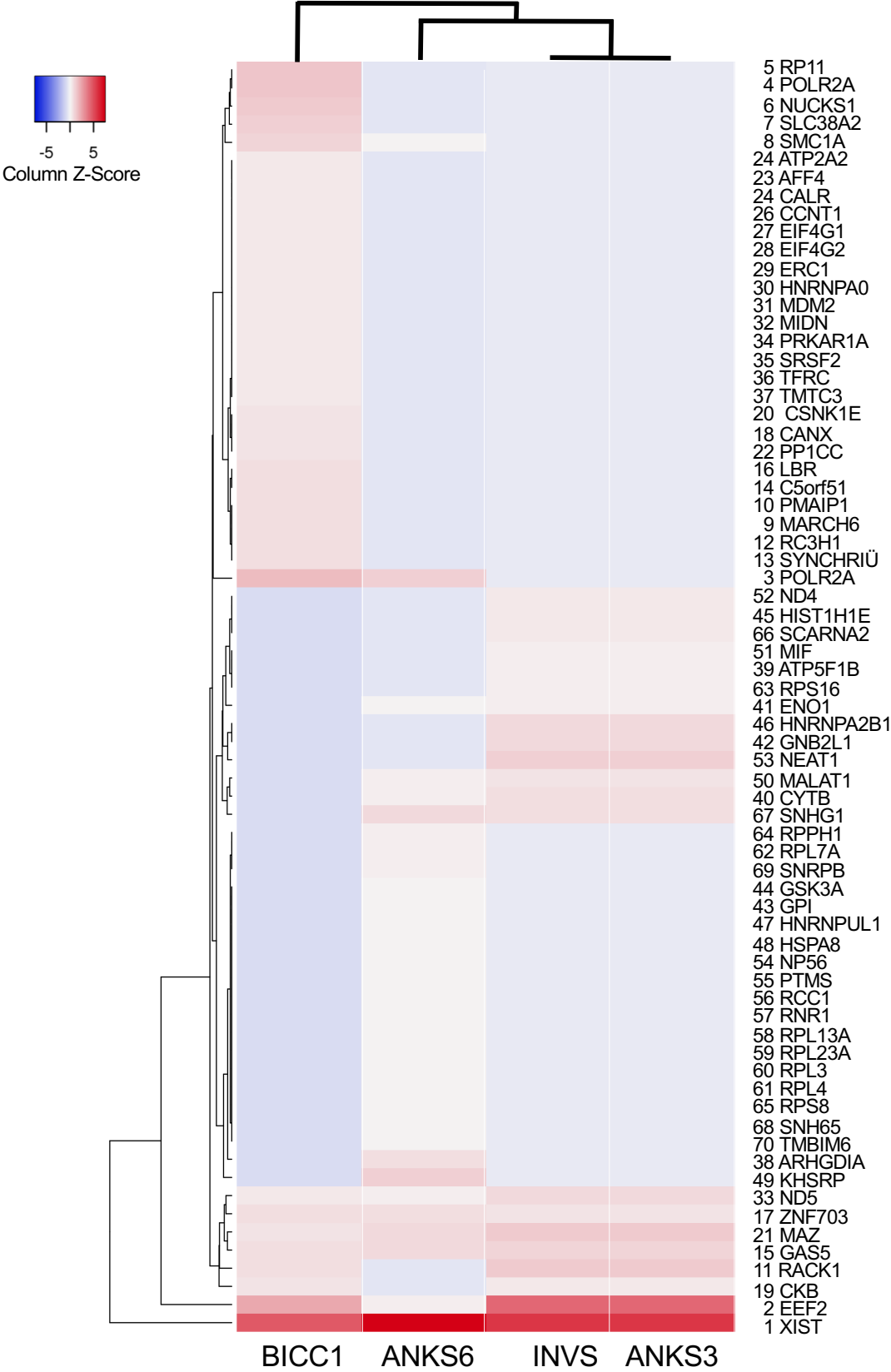
## ANKS6



# Supplemental Figure 5



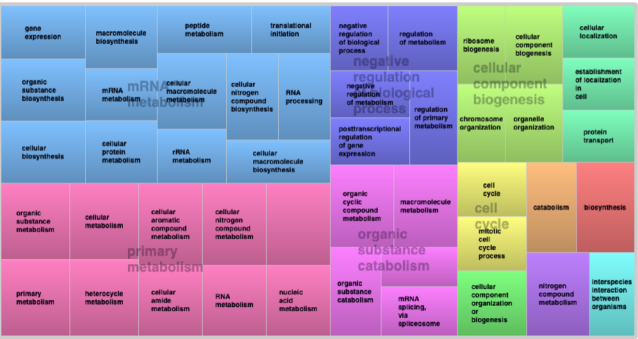
Supplemental Figure 6



# Supplemental Figure 7

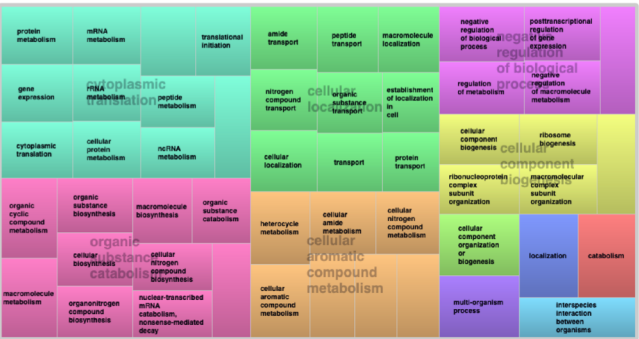
## a BICC1

mRNA metabolism



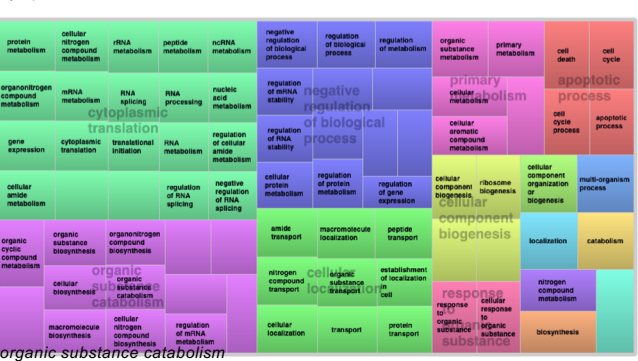
## INVERIN

cytoplasmic translation



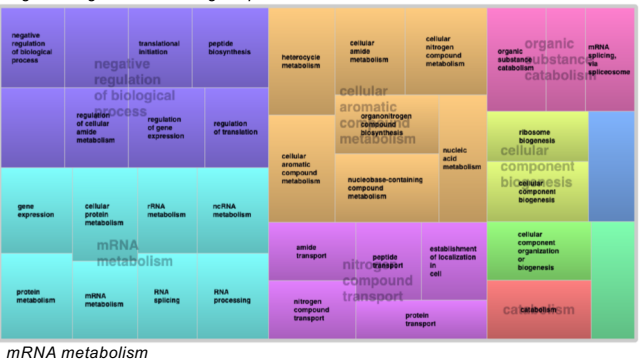
## ANKS3

cytoplasmic translation



## ANKS6

negative regulation of biological process

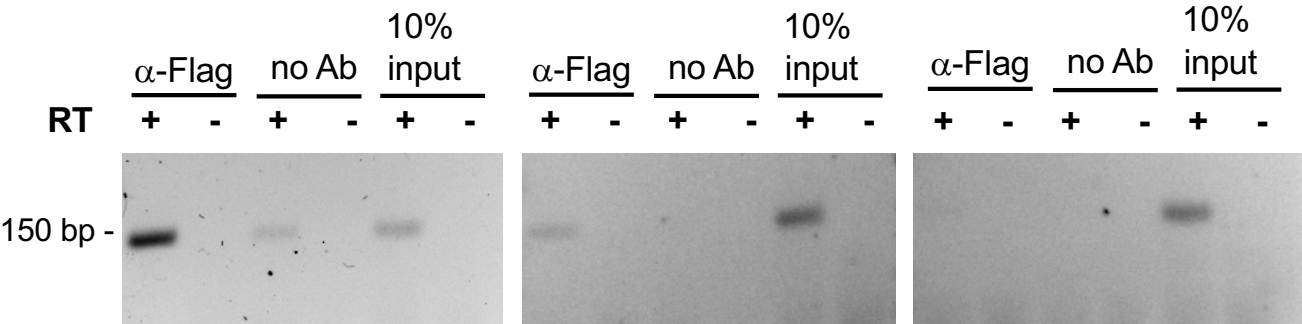


## b

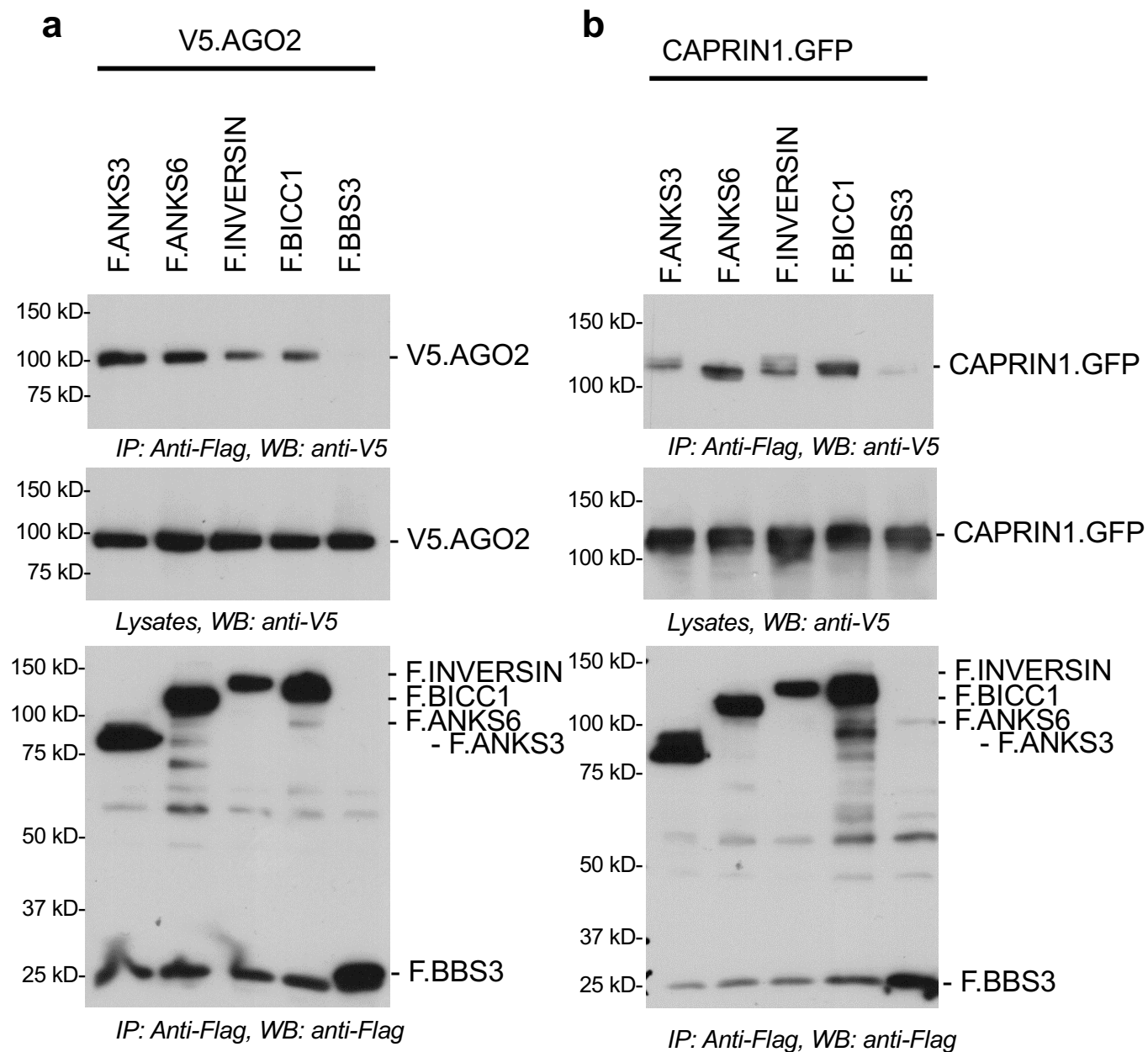
### ANKS6

### ANKS3

### INVERIN

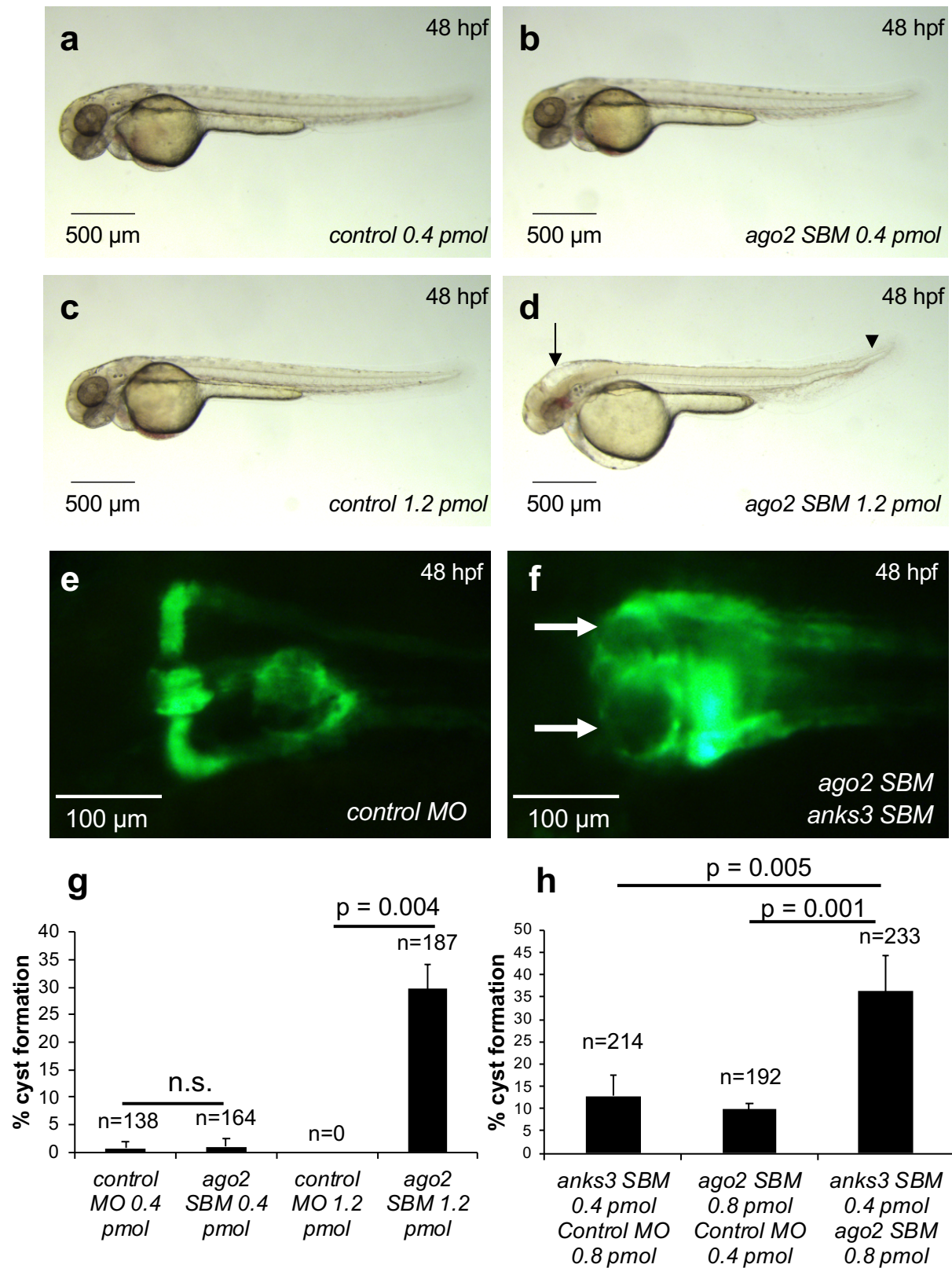


## Supplemental Figure 8

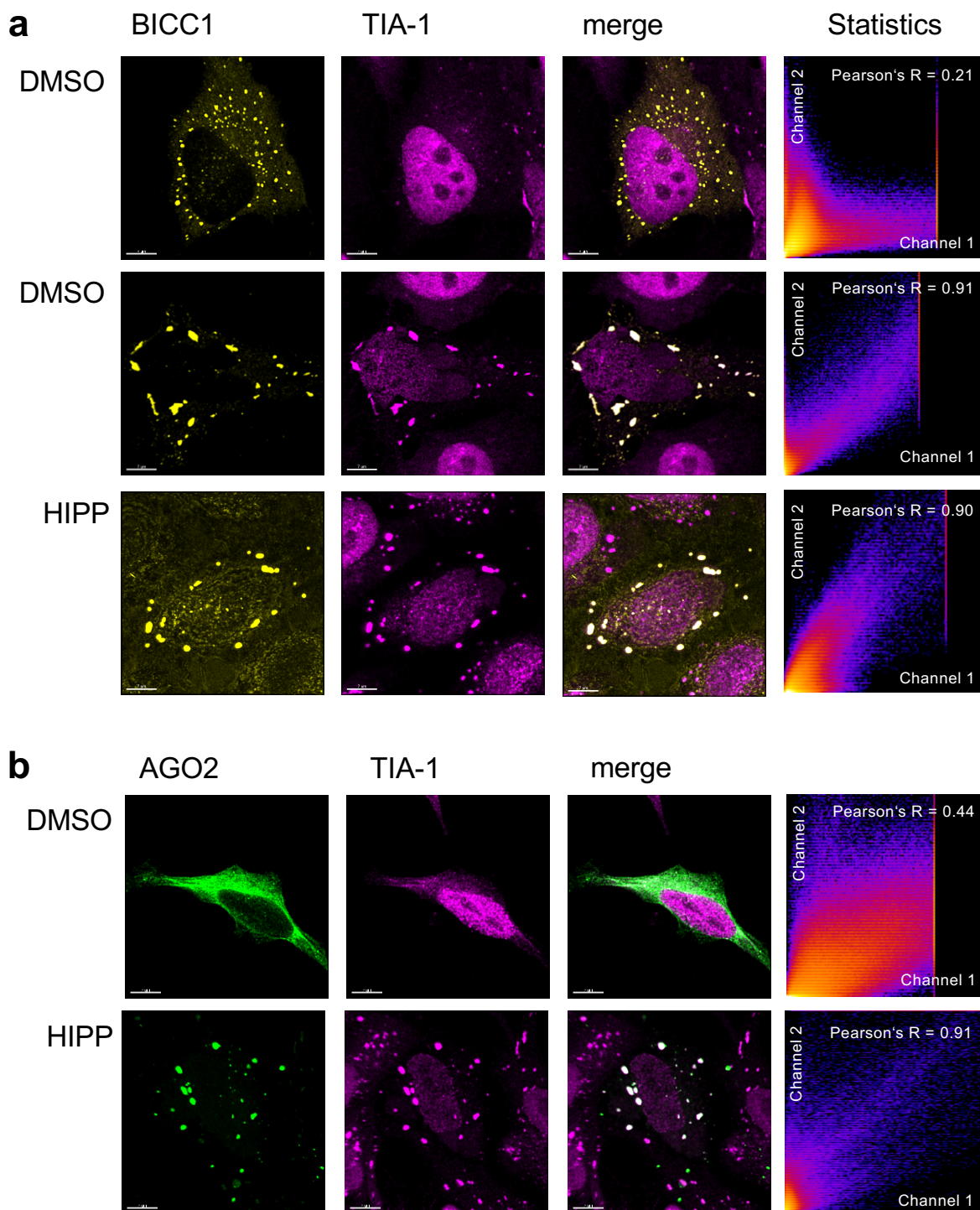




## Supplemental Figure 9



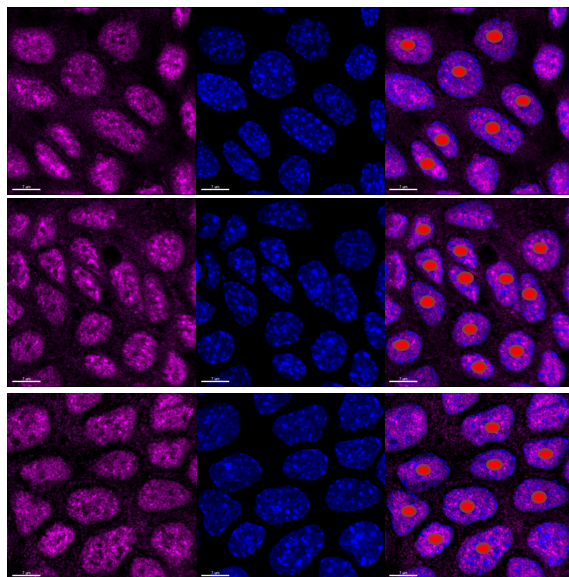
## Supplemental Figure 10



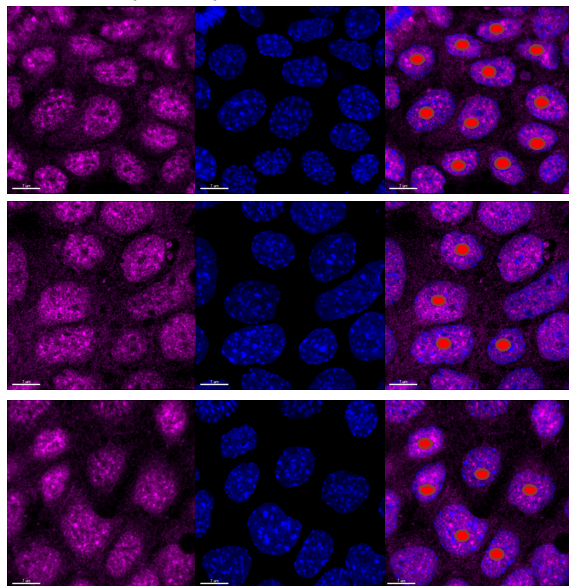


# Supplemental Figure 11

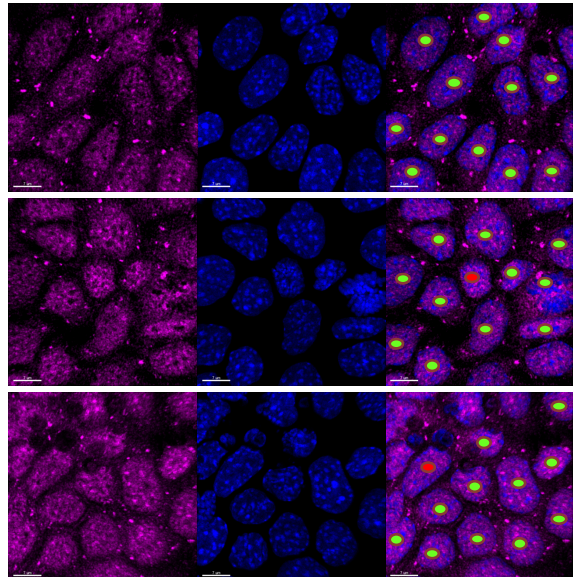
**a** IMCD3 (Control)



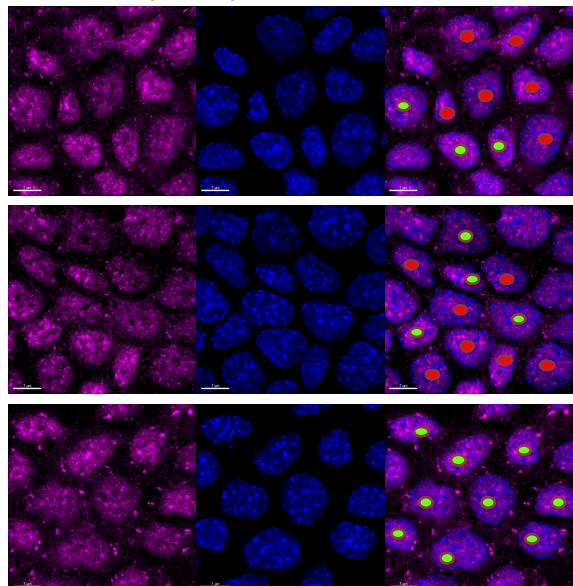
IMCD3 (+ Tet) *Anks6* kd



IMCD3 + Hippu



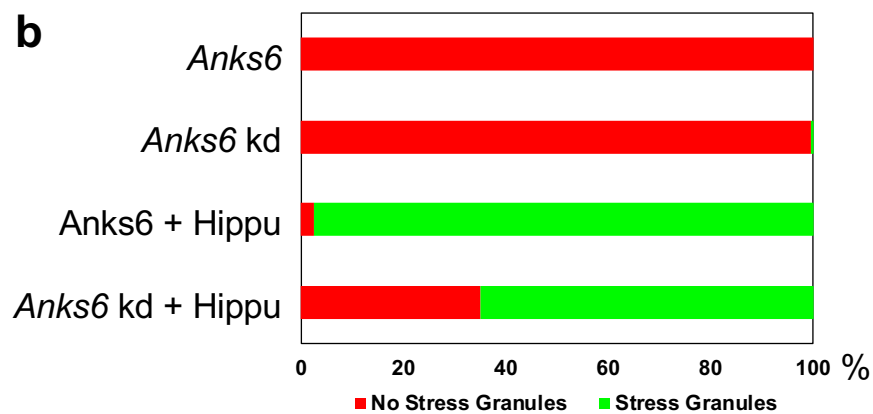
IMCD3 (+ Tet) *Anks6* kd + Hippu



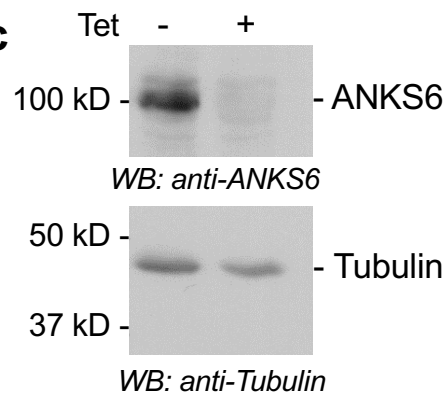
● No Stress Granules

● Stress Granules

**b**

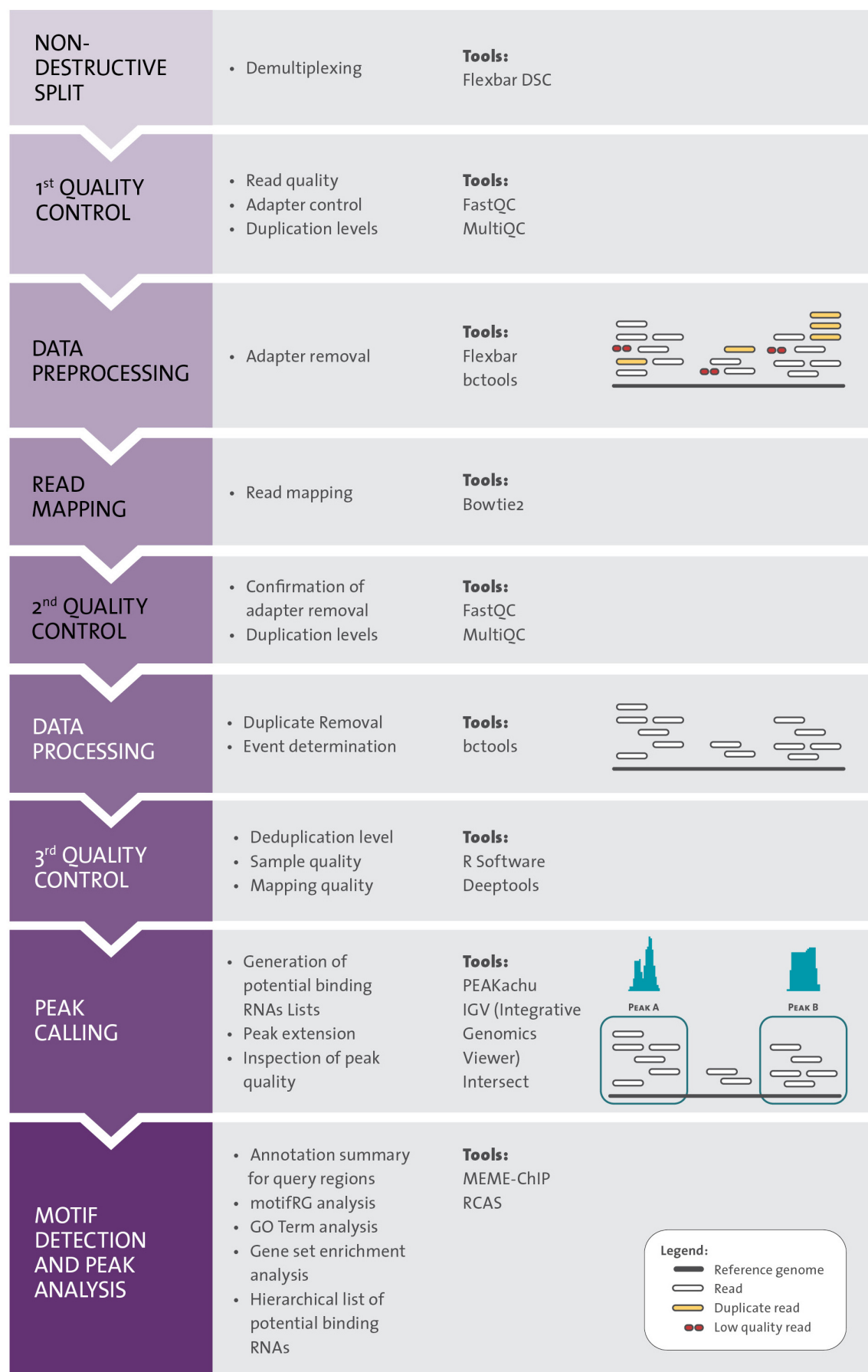


**c**

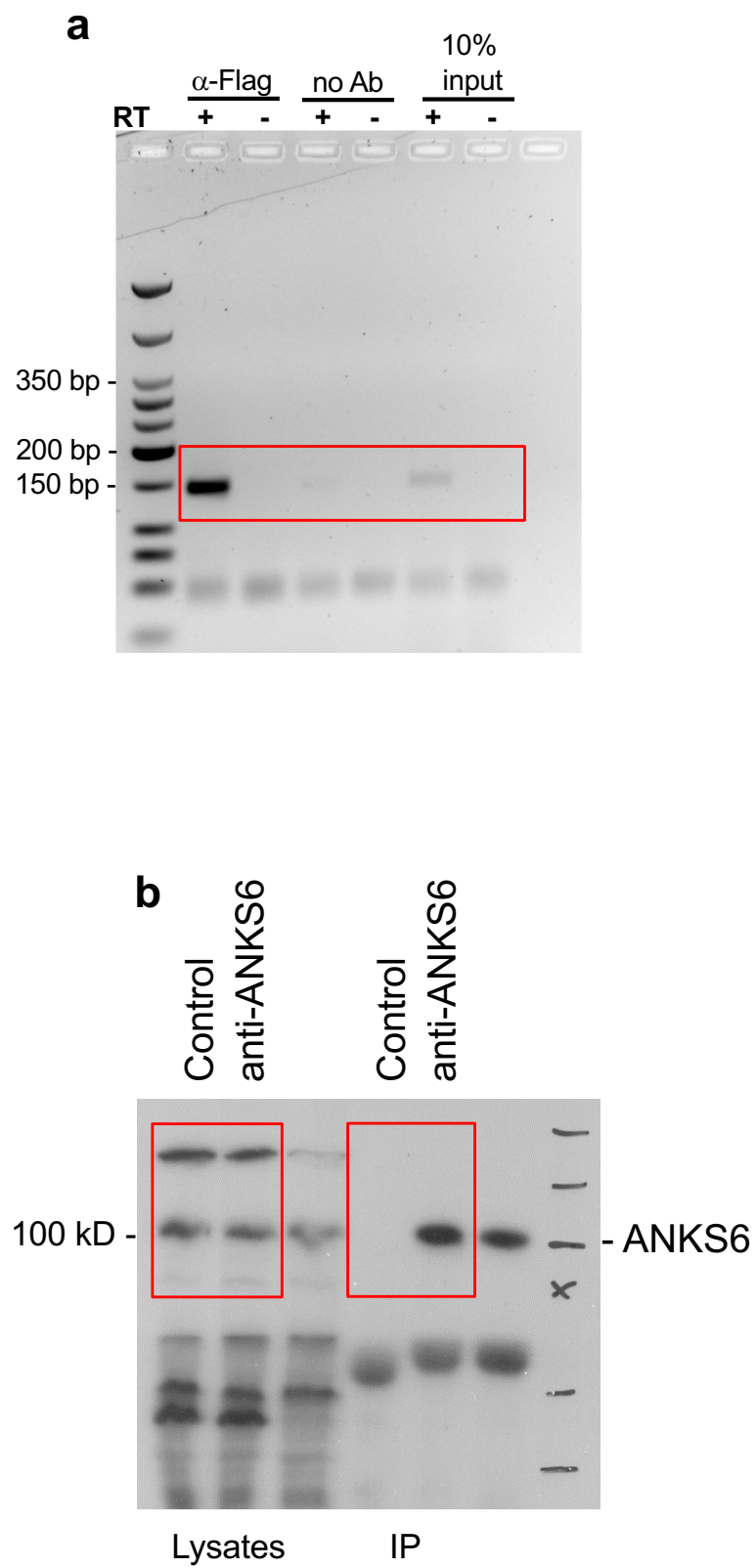




# Supplemental Figure 12

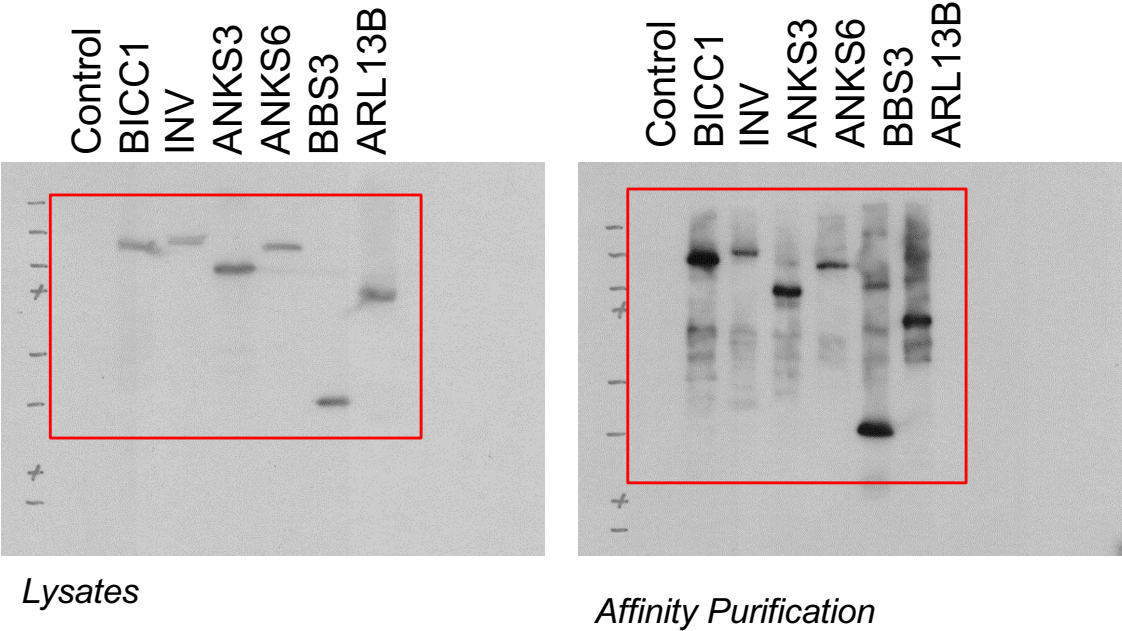


## Supplemental Figure 13

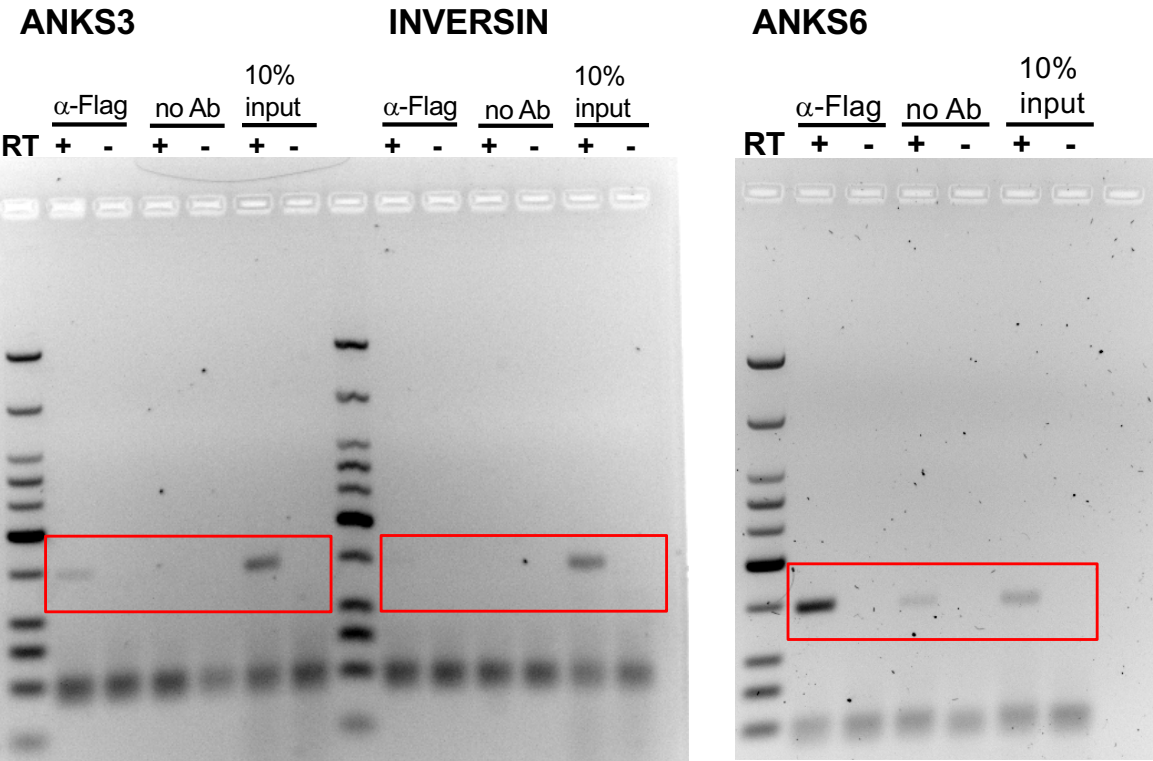


Supplemental Figure 13 (cont.)

c

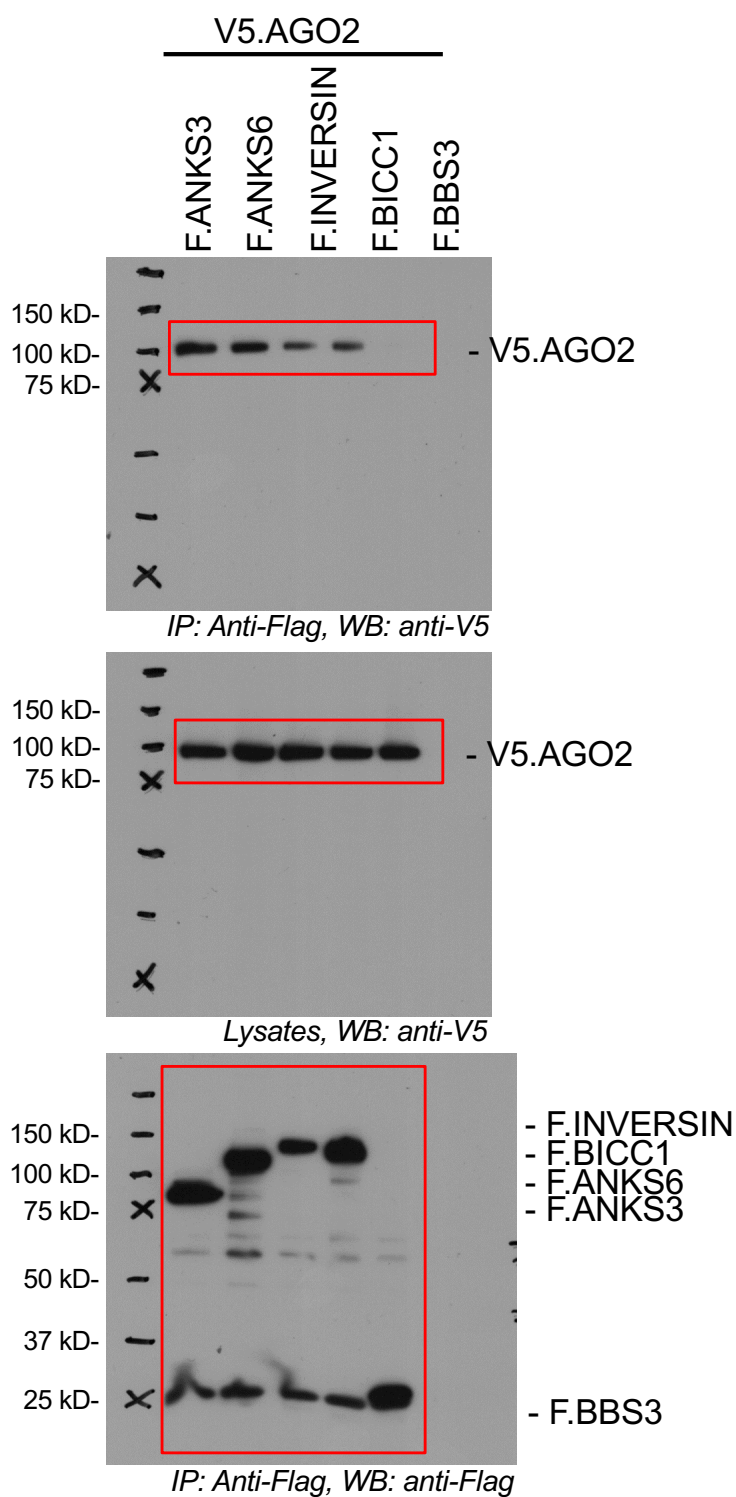


d

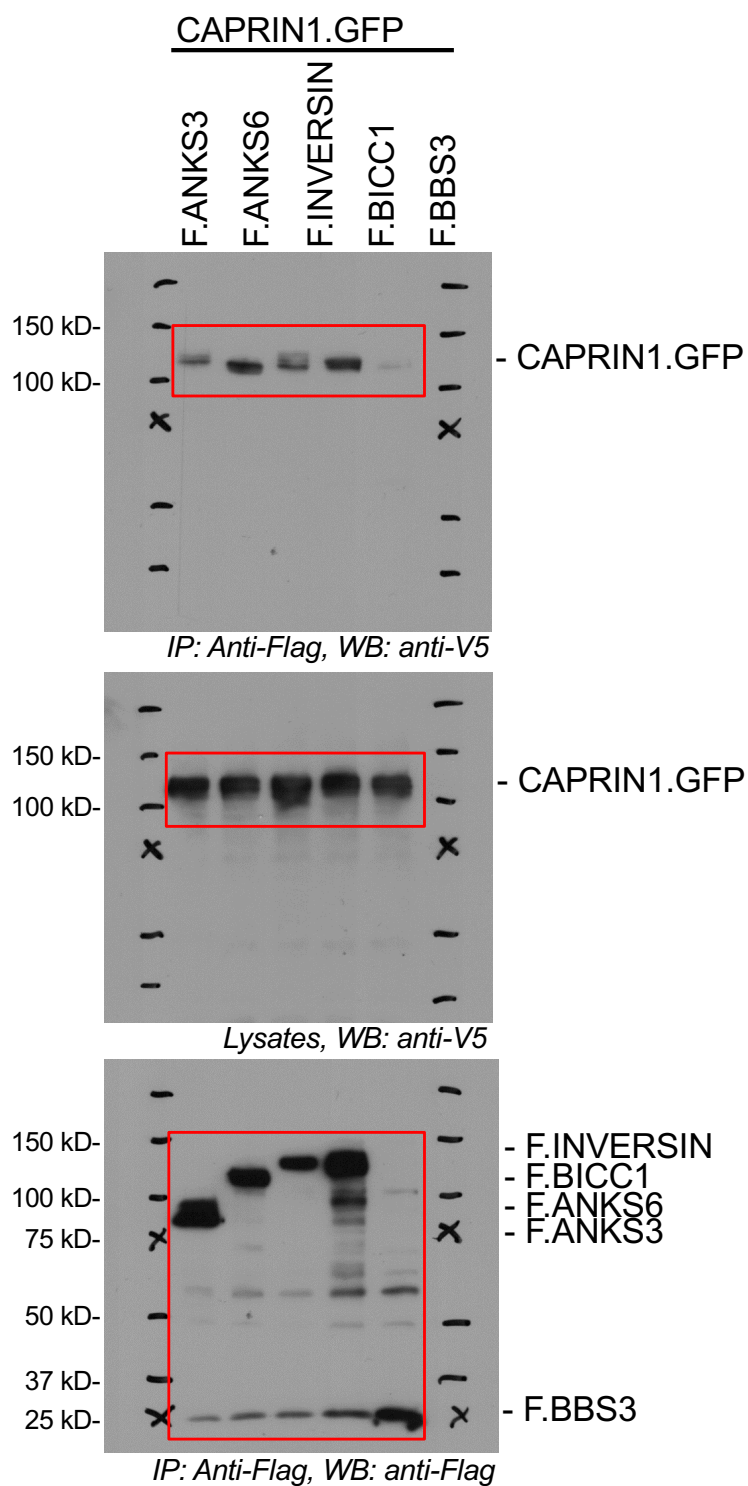


# Supplemental Figure 13 (cont.)

**e**

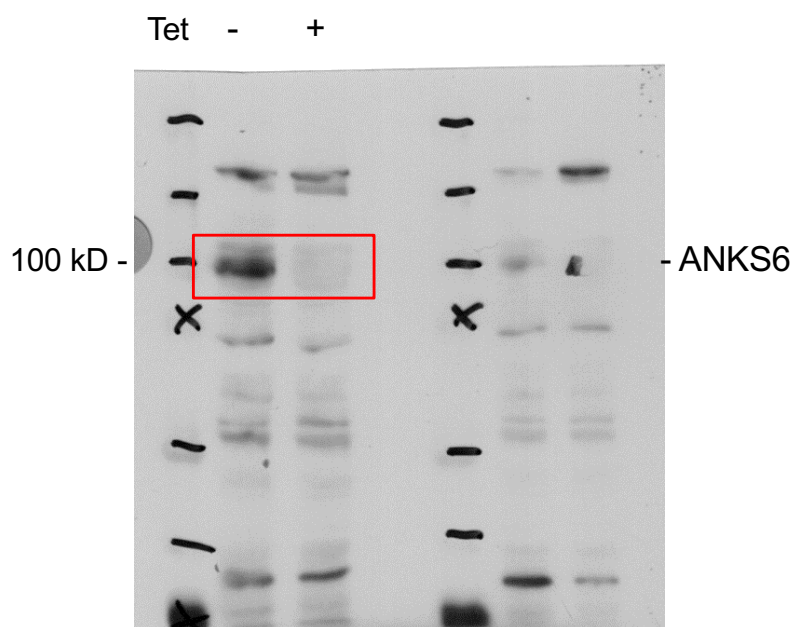


**f**

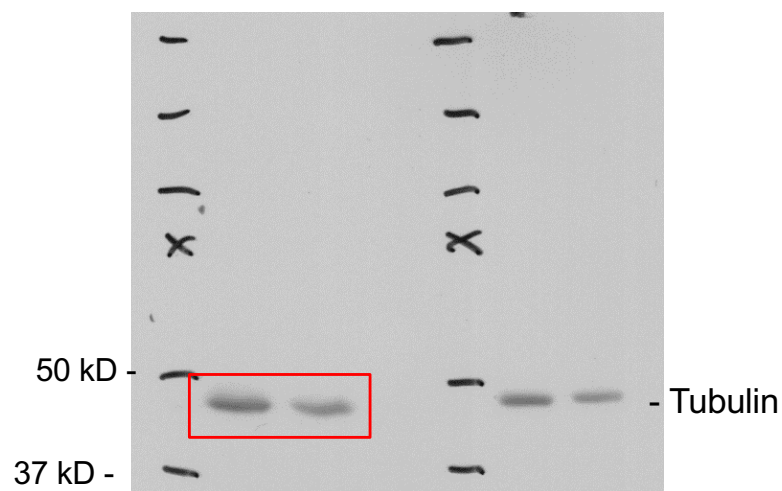


## Supplemental Figure 13 (cont.)

**g**



WB: anti-ANKS6



WB: anti-Tubulin