Supplementary Material

Visualization and characterization of RNA-protein interactions in living cells

Ningjun Duan^{1,4,*}, Maria Arroyo³, Wen Deng^{1,2}, M. Cristina Cardoso³ and Heinrich Leonhardt^{1,*}

1 Department of Biology II, Ludwig Maximilians University Munich, Großhaderner Str. 2, **82152 Planegg--Martinsried, Germany**

2 College of Veterinary Medicine, Northwest A&F University, Yangling, Shaanxi, 712100, **China**

3 Department of Biology, Technical University of Darmstadt, Schnittspahnstr. 10, 64287 Darmstadt, Germany

4 Department of Oncology, The First Affiliated Hospital of Nanjing Medical University, Nanjing **210029, China**

*** Corresponding author: Ningjun_official@outlook.com, h.leonhardt@lmu.de**

Supplementary Table 1

Source and catalog information of fragments used in plasmid construction.

RNA Traps

Supplementary Figure 1

Summary of the main functional elements of the constructs for the RNA trap, RNA and proteins.

Image analysis pipeline to obtain the fluorescence intensities in cells. The DAPI channel is used to segment the area of the nucleus, then the mean fluorescence intensities of the *lac*O spots and entire nucleus were measured in the EGFP channel and the mCherry channel, respectively.

(A) Detection of RNA trapped at *lac*O sites by FISH. Cy5 labeled anti-pp7 oligonucleotide probes were applied to detect pp7 RNA, and pp7 enrichment was observed specifically at the *lac*O sites, which confirms the successful trapping of ROI at the *lac*O site by the MCP RNA trap. (B) rF3H detection of pp7-PCP interaction by immunofluorescence. HA tagged POI (HA-PCP) was used instead of the mCherry-PCP for the assay, and the enrichment of POI was detected by antibody binding to HA tag (Alexa Fluor 594). For all the images, *lac*O sites are marked with arrowheads (filled arrowheads: signal enrichment; open arrowheads: no signal enrichment). Scale bars stand for 10 μ m.

The amount of RNA trap or test protein influences interaction assay (A) rF3H images with different amounts of RNA trap used for the assay (0.8 ng, 0.4 ng, 0.2 ng). rF3H performed without RNA (-RNA) serves as control for signal from background binding. (B) Image quantification shows an enhanced relative signal at the *lac*O spot along with the increase of RNA trap used, but also with increased background binding in the absence of RNA, resulting similar signal to background binding ratio for all the three groups (data are presented as mean \pm S.D., for the groups shown from left to right, $n = 25$, 30, 28, 28, 25, 28, respectively). (C) rF3H images with different amounts of PCP protein (0.8 ng, 0.4 ng, 0.2 ng). rF3H performed without RNA (-RNA) serves as control for signal from background binding. (D) Image quantification showed that 0.2 ng and 0.4 ng groups both resulted in higher relative signals and lower background at the *lac*O spot than the 0.8 ng group (data are presented as mean \pm S.D., for the groups shown from left to right, $n = 27$, 28, 26, 28, 26, 27). For all images, scale bars represent 10 μ m.

Enhancement of rF3H performance by doubling the RNA trapping unit in the RNA trap. (A) Representative rF3H images from RNA traps with single (MCP RNA trap) and double (2MCP RNA trap) RNA binding units for detecting the interaction between pp7 and PCP protein (scale bars represent 10 µm). (B) Quantification of relative PCP signals at *lac*O spots showed an increased PCP recruitment by the 2MCP RNA trap (2MCP). Data are presented as mean \pm S.D., for the groups shown from left to right, $n =$ 22, 27, 23, 29, $*$ $P < 0.05$.

Tests of different fluorescence protein tags for rF3H assay. (A) rF3H images of pp7-PCP interaction with mCherry or mScarlet-I tagged PCP proteins. Enrichment of PCP tagged by both fluorescent proteins could be observed (filled arrowheads), but not in controls without pp7 RNA (empty arrowheads). Scales bars represent 10 μ m. **(B)** Quantitative analyses of the fluorescence signals detected for PCP tagged with mCherry and mScarlet-I. Image quantification showed that mScarlet-I, which is brighter than mCherry, resulted higher relative signals at the *lac*O spot both with and without binding RNAs, but the readout ratio (ratio between +RNA and -RNA) is almost identical to the mCherry tagged group, indicating fluorescent protein itself does not affect the rF3H results (data are presented as mean \pm S.D., for the groups shown, from left to right, $n = 28$, 29, 27, 28. ** $P < 0.01$).

Comparison of the RNA transcription cassettes for rF3H assay. (A) The structure of CMV and U6 cassettes for RNA transcription. In the CMV cassette, the ms2-pp7 RNA transcription is under the control of a CMV promoter and $poly(A)$ sequences are added to the 3' mediated by an SV40 $poly(A)$ signal sequence, while in the U6 cassette, U6 promoter and Oligo(A) sequence regulate the expression of the ms2-pp7 RNA. **(B)** Images of mCherry tagged PCP protein recruitment at the *lac*O array by ms2-pp7 RNA that was produced from U6 or CMV cassettes. Scale bars stand for 10 μ m. (C) Quantification of the PCP protein signal at *lac*O spots showed that the RNA products from the U6 cassette led to a higher enrichment of the PCP protein than that from the CMV cassette products. Data are presented as mean \pm S.D., for control, U6 and CMV groups, $n = 23$, 27 and 26, respectively. ** $P < 0.01$. (D and E) Comparison of test RNA generated by CMV and U6 promoter in different cellular parts by qPCR. The amounts of ms2-pp7 RNA generated from the CMV and U6 cassettes were almost the same, as quantified in **D**, but the U6 cassette products showed a one-fold higher concentration in the nucleus than the CMV products (in E), which may explain the better rF3H performance with RNAs from the U6 cassette. (Each group

contains three biological repeats, and the standard deviation was shown as an error bar. ns: not significant, $*** P < 0.001$)

Supplementary Figure 8

(A) rF3H detection of the interaction between an mRNA mimic and PABPC1. The polyadenylated ms2 mRNA mimics recruits and colocalizes with PABPC1 protein at the *lac*O spot (marked as filled arrowheads), but not in the control groups without RNA or without polyadenylation (marked as empty arrowheads). (B) Images of PABPC1-mCherry mRNA and PABPC1 interaction assay with control group, as supplementary for Fig. 2E. (C) Complete images of the NORAD ncRNA and PUM2 interaction assay, as supplementary for Fig. 2H. Scale bars stand for 10 μ m.

(A) rF3H images of the interaction between H300 RNA and EZH2 protein fragments. Both the N- and Cterminal parts of EZH2 are recruited to *lac*O spots by the H300 RNA, but not in absence of the RNA. (B) Detection of the interaction between H300 and the EZH2 phosphorylation mimics. A phosphorylation mimic (EZH2 T350D) and an unphosphorylation mimic (EZH2 T350A) were tested, both of which showed interactions with the H300 RNA, but with different binding affinities. Image quantification is shown in Fig. 3G. Scale bars stand for 10 µm, and *lac*O spots are marked by arrowheads (filled arrowheads: enrichment of fluorescence; empty arrowheads: no enrichment of fluorescence). (C) The interaction between EZH2 and H300 RNA is promoted by EED protein, which can be further enhanced by T350 phosphorylation, shown here as supplementary for Fig. 3H (filled arrowheads: enrichment of fluorescence; empty arrowheads: no enrichment of fluorescence).

(A and **B)** Detection of RNA-protein interaction with PUF RNA trap. ms2 RNA are anchored to nuclear *lac*O spots by PUF RNA trap recognizing a 9 nt RNA sequence, and recruitments of MCP to the same loci are observed (lower panel) but not in control group (upper panel) in (A). rF3H images of the interaction between S47R mutant and ms2 RNA is shown in (B), as a supplementary for Fig. 6D. (C) Complete images of ms2 RNA and MCP interaction assay with the dCas13a RNA trap. Scale bars stand for 10 μ m.

Detection of pp7- PCP interaction in living cells. (A) Live cell imaging was performed to detect pp7- PCP interaction, and recruitments of PCP-mCherry to *lac*O spots could be observed in the presence of pp7 RNAs, providing the possibility for analyzing dynamical RNA-protein interactions. *lac*O spots are marked with arrowheads. Scale bars represent 10 μm. (B) Image quantification reveals a significant enrichment of mCherry labeled PCP proteins at the *lac*O array with the ms2 tagged pp7 RNA, showing a similar detection sensitivity with the fixed samples (data are presented as mean \pm S.D., for control and +ms2pp7 RNA groups, *n* = 20 and 22, respectively. ** *P* < 0.01).

Supplementary References

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