Figure 1-Source Data 3

ORF1-all\_called\_spots-NORM\_CYT.csv

* Output data matrix from the spot detection algorithm run on the ORF1-Halo and reporter L1 RNA FISH colocalization data, with intensity information for the detected cytoplasmic Halo+ spots, including intensities in the Halo channel and the RNA channel, with the following columns:
  + plane (z): Z plane of the detected spot
  + row (y): y coordinate of the detected spot
  + col (x): x coordinate of the detected spot
  + radius: radius of the detected spot
  + roi: image name or ROI name in which the spot was detected
  + nuclei\_ch\_intensity: DAPI intensity at the detected spot
  + Halo\_intensity: raw Halo-JF549 intensity at the detected spot
  + RNA\_intensity: raw 640-nm RNA intensity at the detected spot
  + location: cytoplasmic localization determined by nuclear stain intensity at the spot as described in the Methods
  + file\_name: source image name
  + Halo\_intensity-norm: normalized Halo intensity at the detected spot, calculated by dividing the raw intensity by the corresponding normalization factor (median Halo intensity at the random spots within the given ROI)
  + RNA\_intensity-norm: normalized RNA intensity at the detected spot (as above)

ORF1-all\_random\_spots-NORM-CYT.csv

* Output data matrix from the spot detection algorithm run on the ORF1-Halo and reporter L1 RNA FISH colocalization data, with intensity information for the randomly assigned cytoplasmic “Halo” spots, with the same columns as above

RNA-all\_spots-NORM\_CYT.csv

* Output data matrix from the spot detection algorithm run on the ORF1-Halo and reporter L1 RNA FISH colocalization data, with intensity information for the detected cytoplasmic RNA spots, with the same columns as above. This data was used to determine a threshold for calling RNA-positive detected Halo spots.

RNA-all\_random\_spots-NORM-CYT.csv

* Output data matrix from the spot detection algorithm run on the ORF1-Halo and reporter L1 RNA FISH colocalization data, with intensity information for the randomized cytoplasmic “RNA” spots, with the same columns as above. This data was used to determine a threshold for calling RNA-positive detected Halo spots.