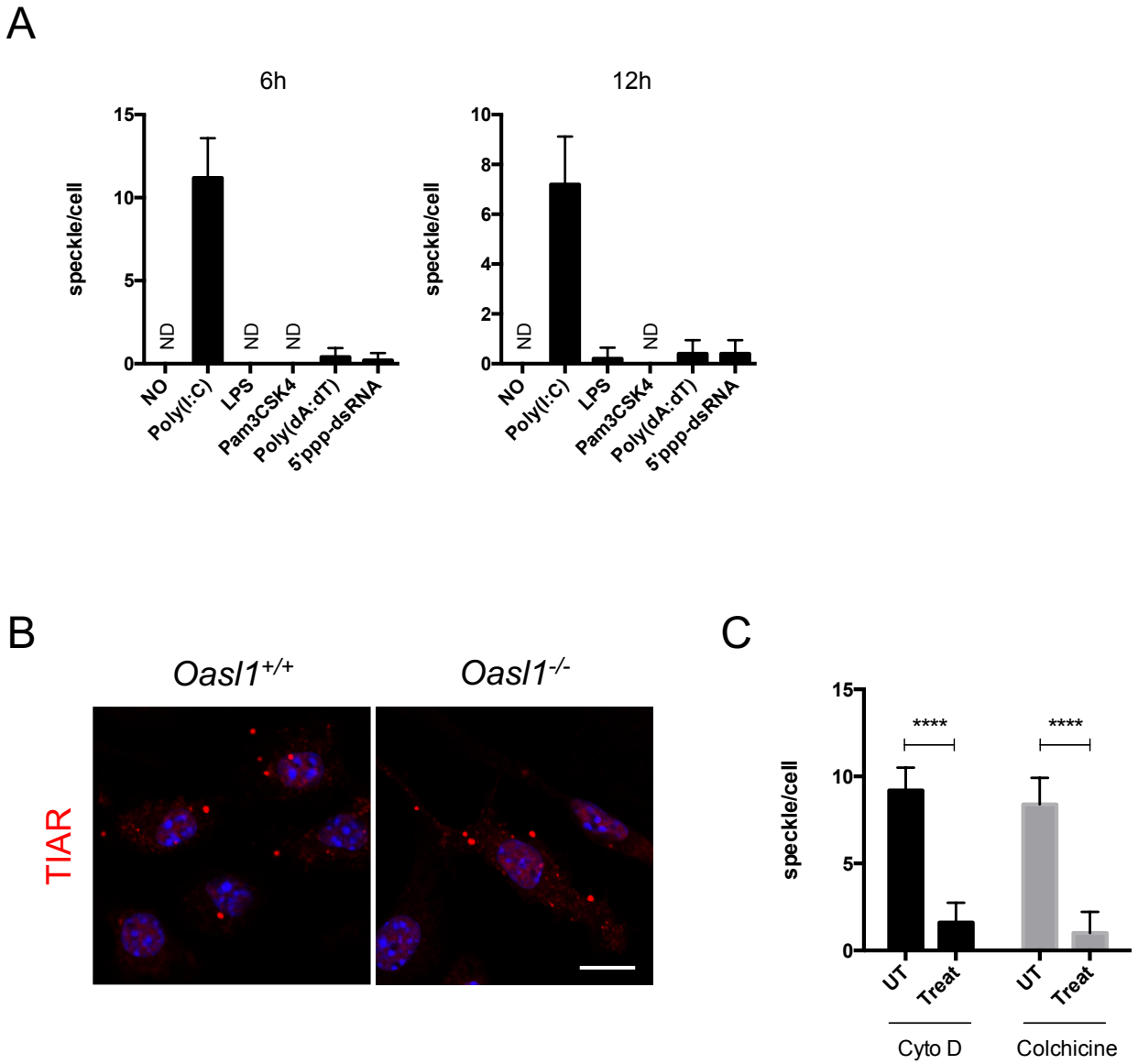
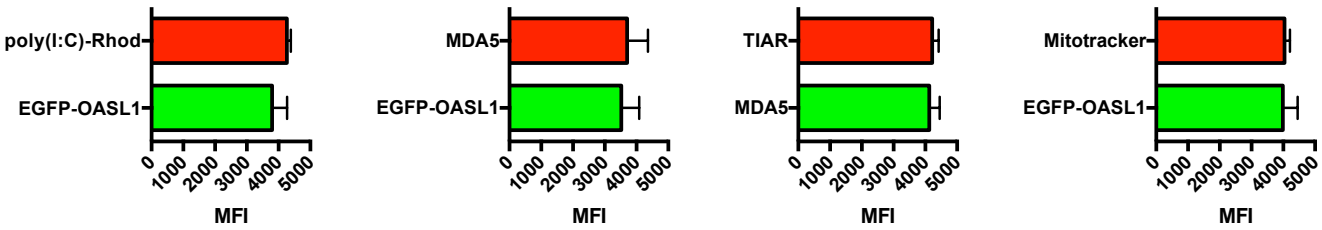
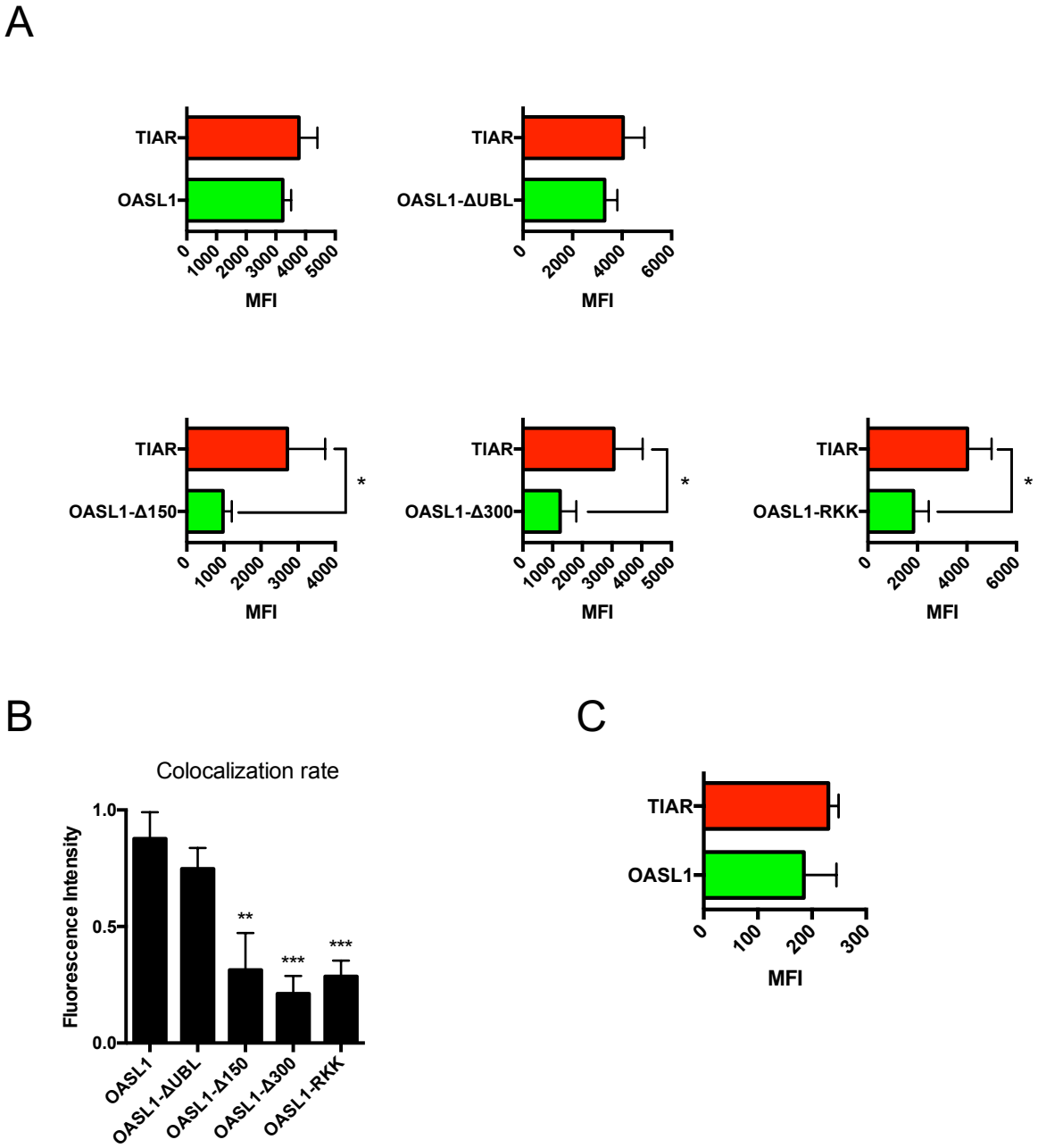


Supplementary Figure 1. OASL1 forms speckles following intracellular poly(I:C) treatment. (A) The EGFP-OASL1 speckles of different stimuli treated for 6 h and 12 h were counted. (B) Confocal images for investigation of the level of SG formation in *Oasl1*$^{+/+}$ and *Oasl1*$^{-/-}$ BMMs. Nuclei were stained with DAPI (blue). Scale bars correspond to 10 mm. Images are representative of three independent experiments. (C) The EGFP-OASL1 speckles were counted after poly(I:C) transfection with or without cytoskeleton inhibitors pretreatment. The results are presented as means ± SD. Statistical significance was determined with the Student's *t*-test. ****$P < 0.0001$.

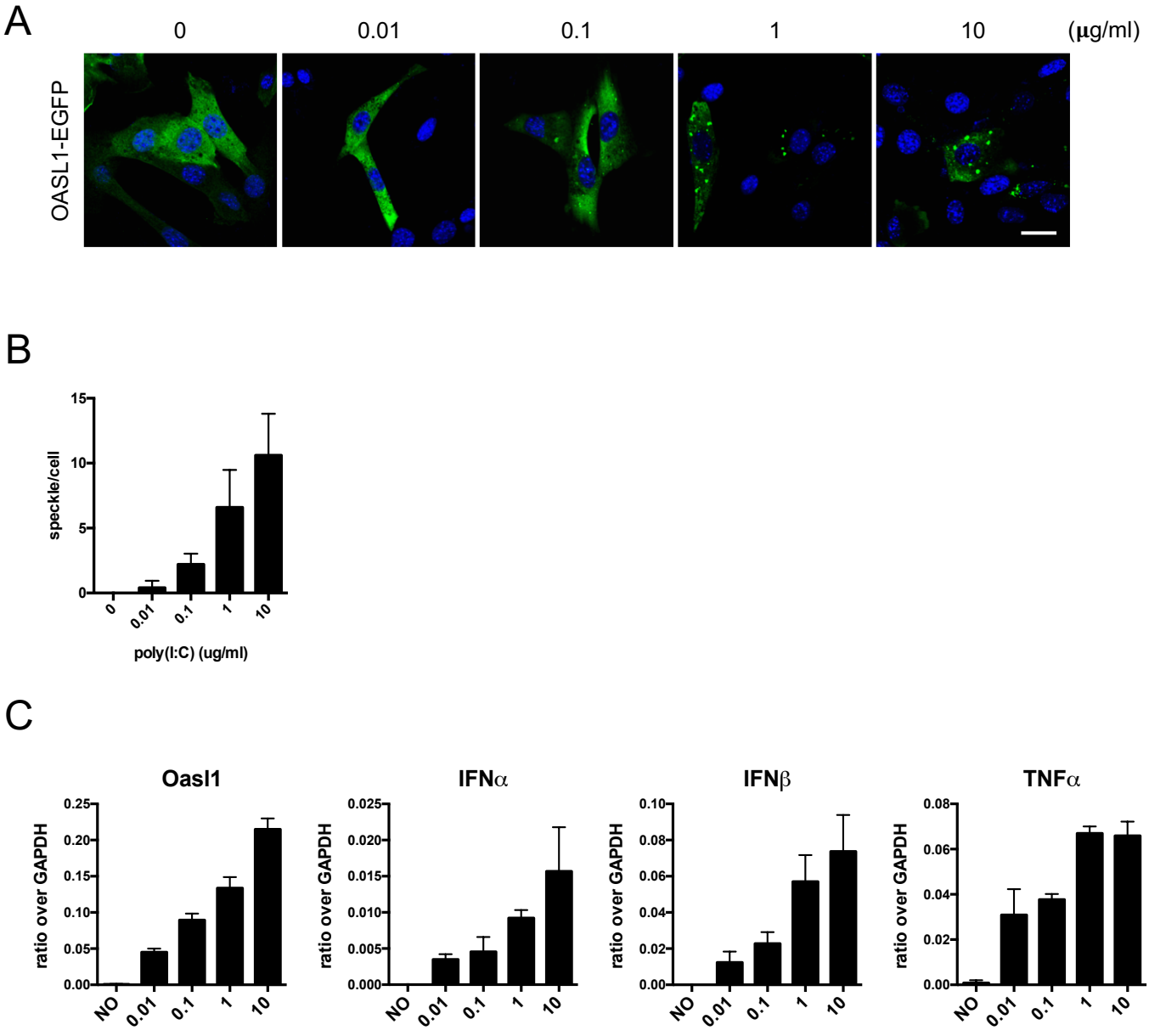


Supplementary Figure 2. OASL1 interacts with stress granule components.

The green and red fluorescence intensity graphs of individual panel in Fig. 3B. The mean of fluorescence intensities (MFI) were measured by ZEN 2.3 Software. More than 5 different fields were quantified for each sample.



Supplementary Figure 3. OAS domain and RNA-binding ability are required for proper translocating to SG. (A) The green and red fluorescence intensity graphs of individual panel in Fig. 3B. (B) The fluorescence intensities of confocal images comparing colocalization rate of each panel in Fig. 3B. (C) The green and red fluorescence intensity graph of Fig. 3C. The mean of fluorescence intensities (MFI) were measured by ZEN 2.3 software. More than 5 different fields were quantified for each sample. The results are presented as means ± SD. Statistical significance was determined with the Student's *t*-test. **P* < 0.05, ***P* < 0.01, ****P* < 0.001.



Supplementary Figure 4. Dose-dependent responses of OASL1 upon intracellular poly(I:C) stimulation. (A) EGFP-OASL1–expressing cells were transfected with gradually increasing doses of poly(I:C) (indicated at the top), and the OASL1 localization pattern was observed by confocal microscopy. Nuclei were stained with DAPI (blue). Scale bars correspond to 10 mm. (B) The speckle quantitation graph of Sup Fig. 4A. (C) Levels of *Oasl1*, *Ifna*, *Ifnb*, and *Tnfa* mRNA were analyzed with qRT-PCR in cells stimulated with increasing doses of poly(I:C) (indicated at the bottom). RNA levels were normalized against the level of *Gapdh* mRNA in the same sample. Data represent means ± SD. Each experiment was performed at least three times.