A) INTRODUCTION

✓ The authors in the introduction session should place the study in a broad context and highlight why it is important in comparison with published articles. I.e., the current state of the research field should be reviewed carefully, and all key publications cited.

✓ They should define the aim of the work and clearly explain the specific hypothesis being tested.

✓ It is fundamental to specify if the observation could be based on previous research by others or your own pilot study.

✓ It is essential to include a summary of findings from previous, relevant studies.

B) MATERIALS AND METHODS

New experimental procedures and protocols should be described in detail, while well-established methods can be briefly described but appropriately cited.

✓ The materials and analysis should provide robust information to allow replication of the study.

✓ Study design should be described in detail, and descriptions of reagents and equipment should facilitate replication.

✓ Plasmids, if not commercially available from a company, have to be described in detail. Also, antibodies have to be validated, and cell lines should be authenticated.

✓ DNA/RNA quantification methods must be well described in terms of calculation and references adopted to enable researchers' access to the raw data. The oligonucleotides sequence, as well as the PCR protocols, should be described in detail in the manuscript.

✓ DNA, RNA, and protein sequences used in the manuscript should be provided with an accession number. New sequence information must be deposited to the appropriate database (GenBank, EMBL, or DDBJ.) prior to submission of the manuscript.

✓ Statistical methods must be described with enough detail to enable a knowledgeable reader with access to the original data to verify the results.

C) RESEARCH DATA

This journal encourages and enables you to attach data that supports your research publication.

The author should share the algorithms, protocols, methods, and other useful materials related to the project. In specific all numerical anonymized raw data should be transposed in a common spreadsheet program (i.e., Excel, sigma plot, etc.) then attached with manuscript files during the submission process.

D) FIGURES

✓ Linear adjustment of contrast, brightness or color must be applied to an entire image or plate equally. Nonlinear adjustments must be specified in the figure legend. Selective enhancement or alteration of one part of an image is not acceptable. In addition, we ask authors of papers to provide additional documentation of their primary data as they are acquired to the computer or instrumentation in which they were analyzed. No photoshop or other modification program saved figures are accepted as original pictures.

✓ In the legend, it has to describe in detail what is represented in the figure in a way to better understand the results, not replying what has been written in the results.

✓ The values for *N*, *p*, and the specific statistical test performed for each experiment should be included in the appropriate figure legend or main text.

E) BLOT AND GEL

✓ Adjusting the intensity of a single band in a blot is not accepted. No specific feature within an image may be enhanced, obscured, moved, removed, or introduced. While it is acceptable practice to adjust the overall brightness and contrast of a whole image, such adjustments should not obscure or eliminate any information present in the original.

✓ Is not accepted to combine bands from different gels of proteins or nucleic acids. If the result is not what you would like, the experiment should be rerun all of the samples on the same gel, instead of over-adjusting digitally the brightness and contrast of the scanned image. Moreover, it is necessary to communicate the quantization method used to measure the intensity of the bands, and you need to show the images (for example, Image lab or ImageJ).

✓ Moreover, the legends of Histograms have to detail the units of measurement, and it has to attach also the original file where they are created.

F) MICROGRAPH

✓ It is crucially important to keep your original digital or analog data exactly as they were acquired and to record your instrument settings. It is acceptable to reduce the number of pixels in an image, which may be necessary if you have a large image at high resolution and want to create a small figure out of it without altering your original data. All the modifications should be disclosed in the figure legend explaining the reason why you did it.

✓ In the histological figures, you have to include a scale bar, and you have to send the original acquisition images from the instrument used.

✓ When the experiment needs to overlap some images (for example, DAPI with other fluorophores), you have to display all single images before the merge.

G) DISCUSSION

Do not simply restate the results but you have to explain your conclusions and interpretations of the results section.