

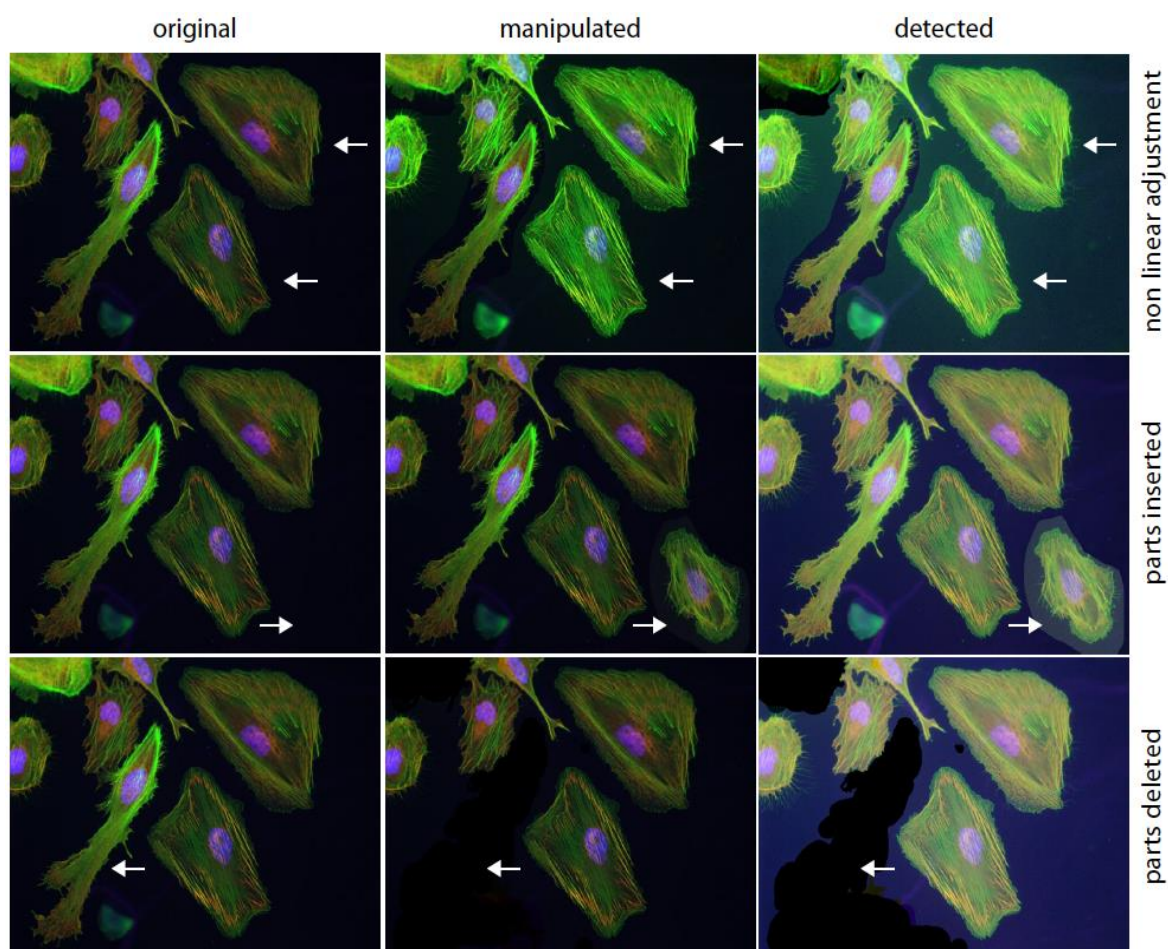
Disease Models & Mechanisms

Best Practices: gels, blots and images in DMM figures

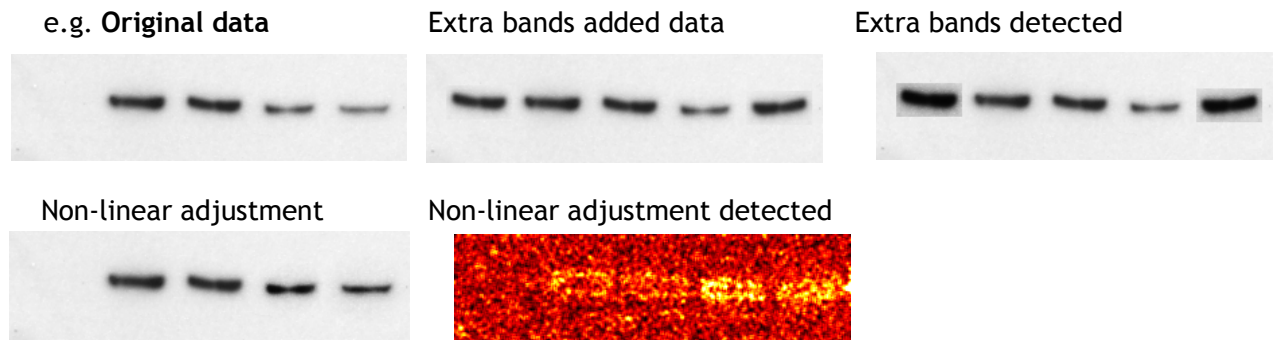
Disease Models & Mechanisms is committed to maintaining the integrity of the scientific record. We therefore screen all digital images in accepted manuscripts for signs of inappropriate manipulation.

Any article that does not meet the following requirements will be delayed in the publication process; your paper may be rejected on the basis of non-compliance with these guidelines.

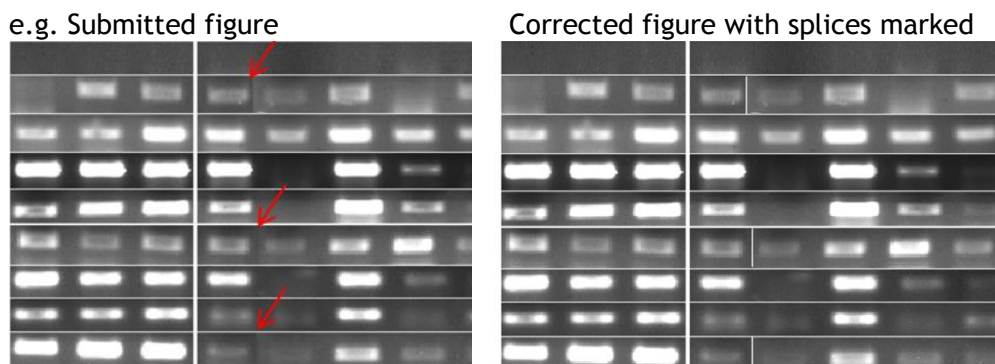
- Do not add to, alter, enhance, obscure, move or remove a specific feature of an image - the focus should be on the data rather than its presentation (e.g. do not 'clean up' backgrounds or remove/obscure imperfections and non-specific bands)



- Adjustments should be applied to the whole image so no specific feature of the original data, including background, is obscured, eliminated or misrepresented as a consequence. Any alterations, such as non-linear adjustments (e.g. changes to gamma settings), must be disclosed in the appropriate figure legends and in the Materials and Methods section.



- The splicing of multiple images to suggest they come from a single micrograph or gel is not allowed.
- Any grouping or consolidation of data (e.g. removal of lanes from gels and blots or cropping of images) must be made apparent (i.e. with dividing lines or white spaces) and should be explicitly indicated in the figure legends.



- At least several band widths should be retained above and below cropped bands
- A positive and a negative control and a set of molecular weight markers must be indicated on all images of gels and blots.
- High-contrast gels and blots are unacceptable (i.e. no white backgrounds) - grey backgrounds are expected unless otherwise justified

Not acceptable

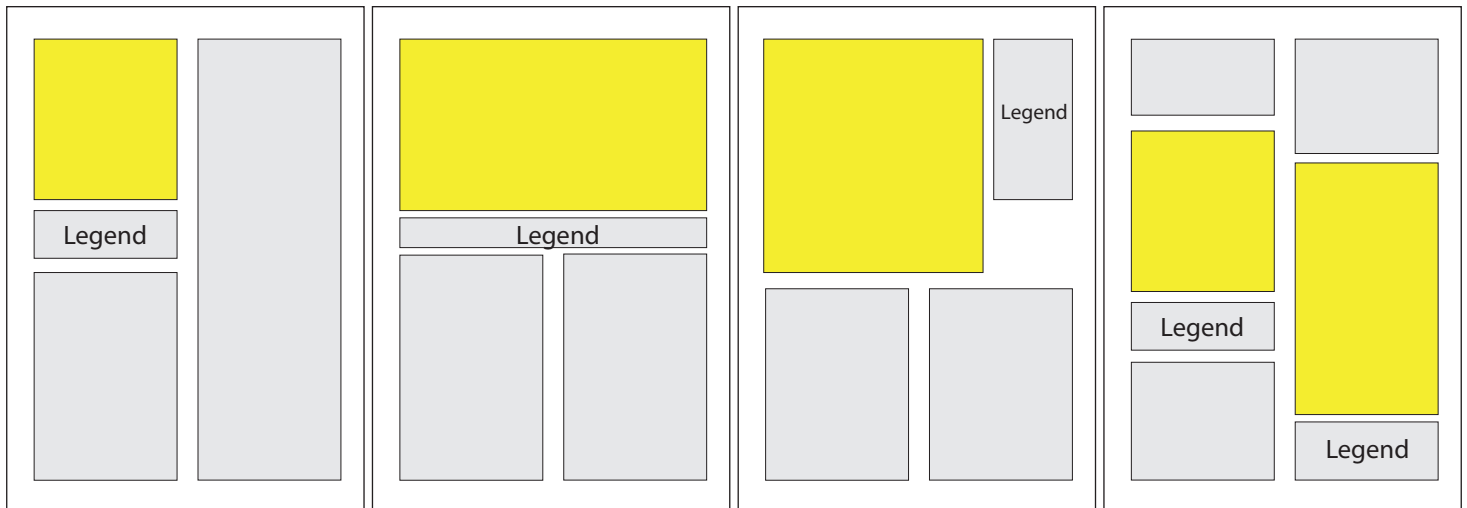


Acceptable



- The same data in whole or part should not be presented in multiple figures (e.g. loading controls; different exposures of the same gel), unless explicitly stated and justified
- Previously published data in whole or in part (e.g. loading controls) should not be presented

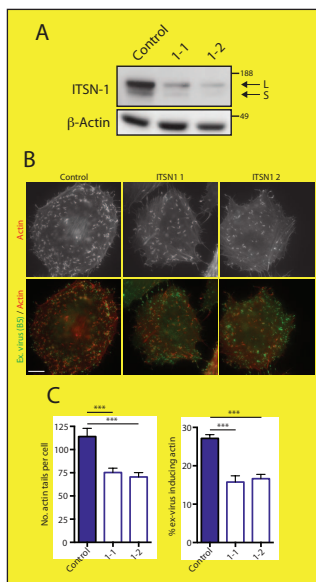
Better figure layout can help reviewers and readers to appreciate your science



DMM text is spread over two columns (grey boxes) into which figures fit (yellow boxes)

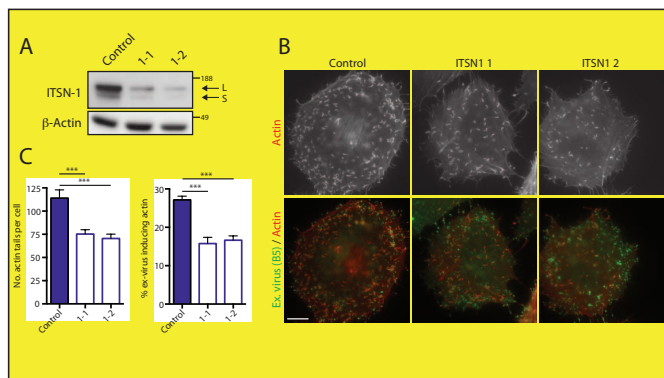
1. Consider figure layout in the context of single or double columns (the yellow boxes above).
2. Within the figure (yellow box) maximise information (data) and minimise background.
3. Consider that different data work on different scales. Images of cells and western blots should be large enough to see the relevant features. Information in graphs can often be read when smaller (see page 2).

Below we illustrate points 1 to 3 using data from Fig. 5, Humphries et al., *Journal of Cell Science* (2014), 127, 673–685.



Single column / half-page width

- Data fits nicely in area
- Background minimised
- Western and graph size ok
- Cell images too small

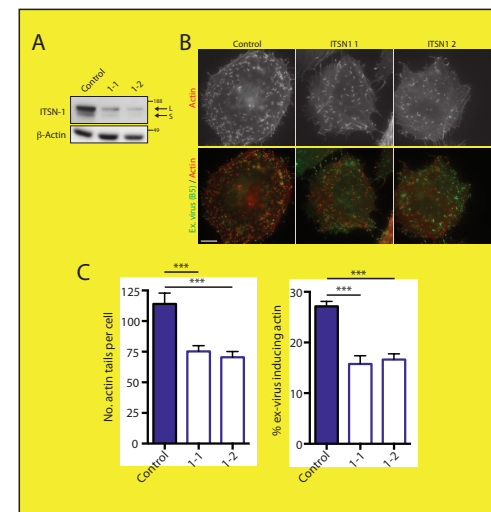


Double column / full-page width

- Data fits nicely in area
- Background minimised
- Relevant features in images and graphs are visible

We prefer single or double column width layouts

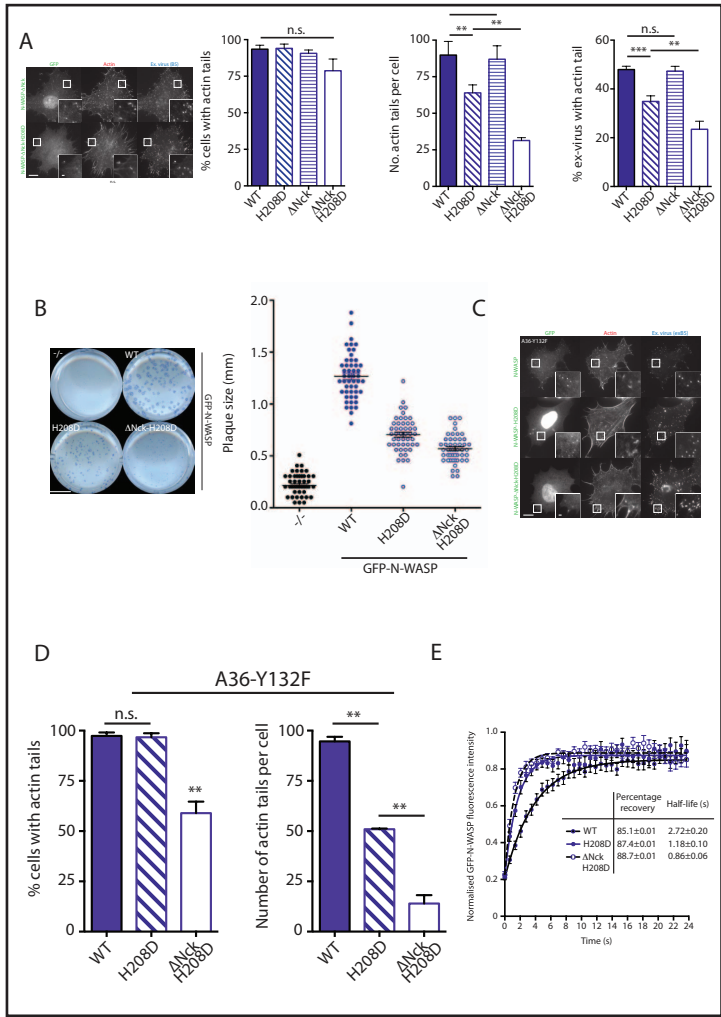
See page two for more layout examples and tips



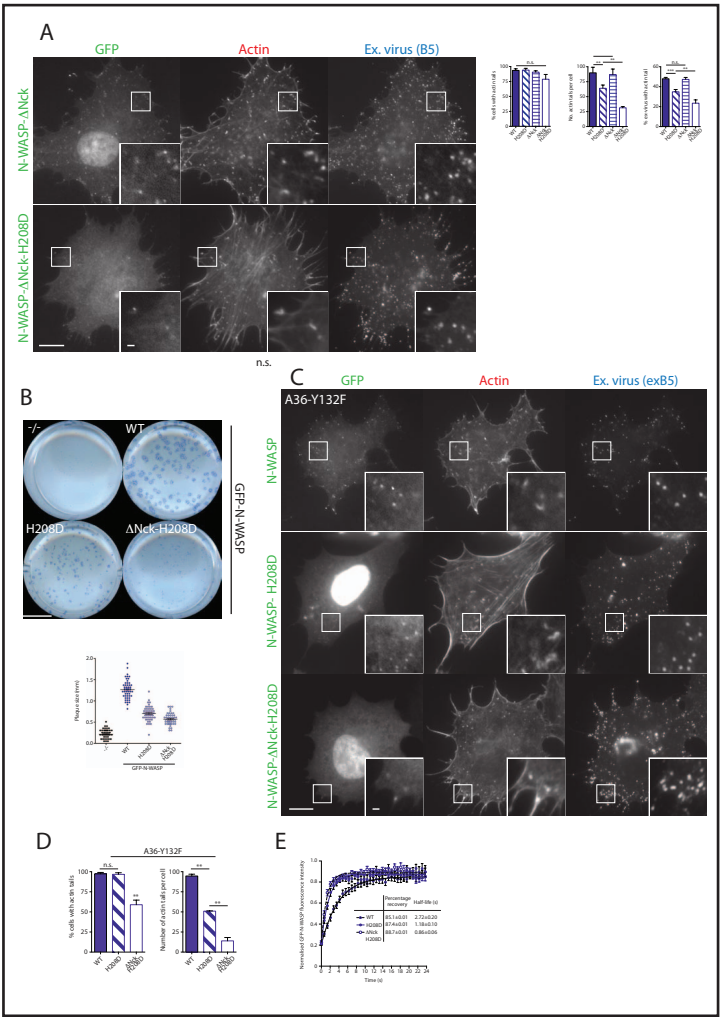
1.5 columns / box format

- Data layout not optimal
- Background content not minimised
- Western blot and cell images too small
- Graphs bigger than they need to be

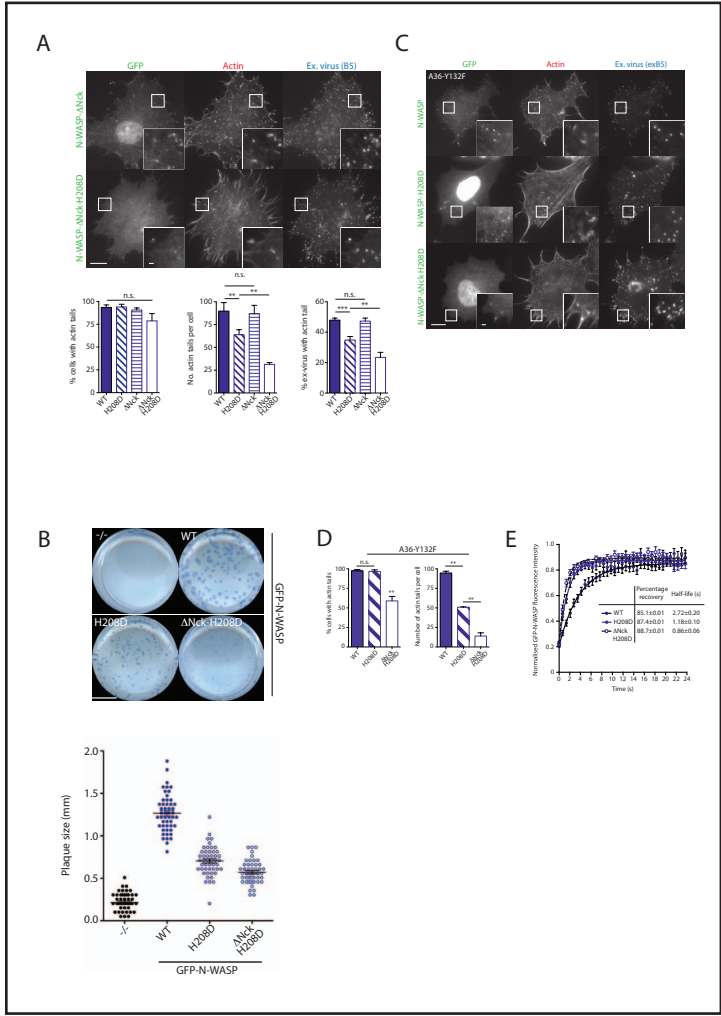
Small images, overly big graphs and white gaps between rows.



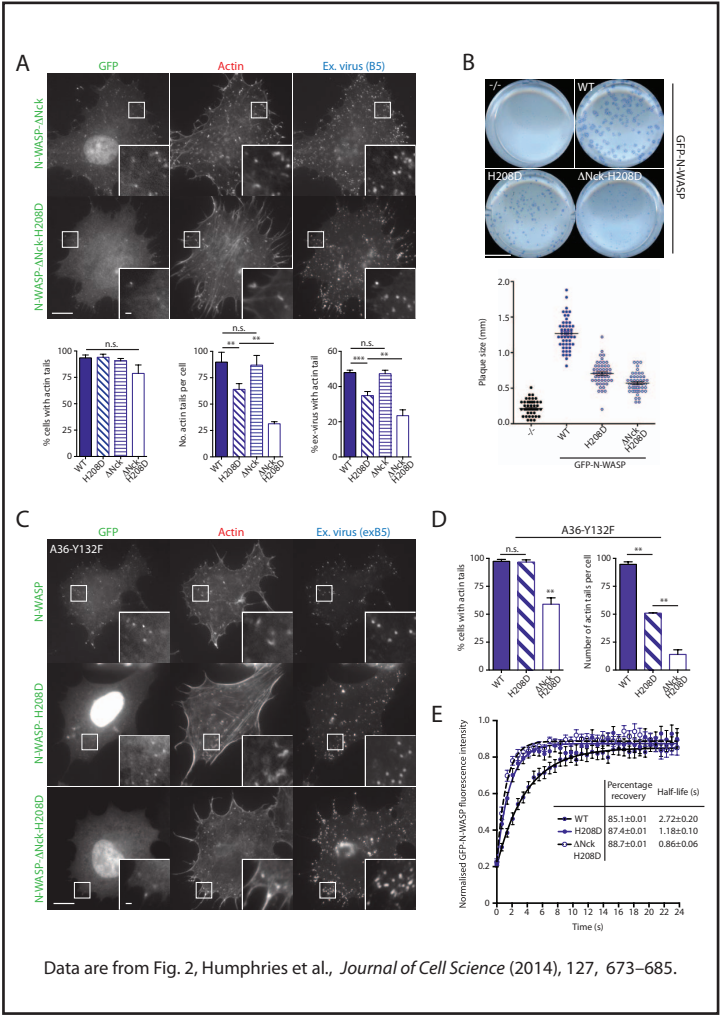
Images too big, graphs too small and odd white gaps.



Odd ordering , large white gaps and ineffective use of space.



Layout as published maximises information in available space.



Data are from Fig. 2, Humphries et al., *Journal of Cell Science* (2014), 127, 673–685.