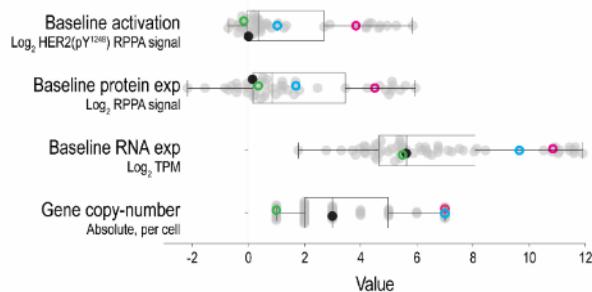




Supplementary Materials:

HER2



HER3

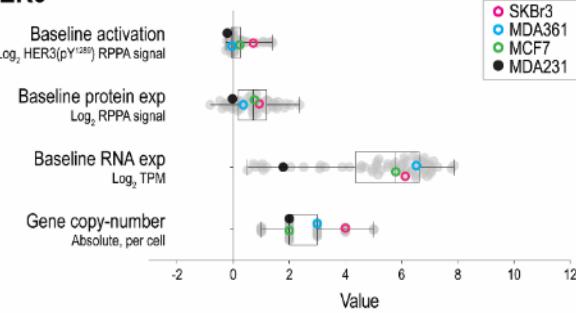


Figure S1. Cell line selection. Plots show cancer Cell Line Encyclopaedia gene copy number, RNAseq and reverse-phase protein array (RPPA) data for breast cancer cell lines, highlighting those selected for this study.

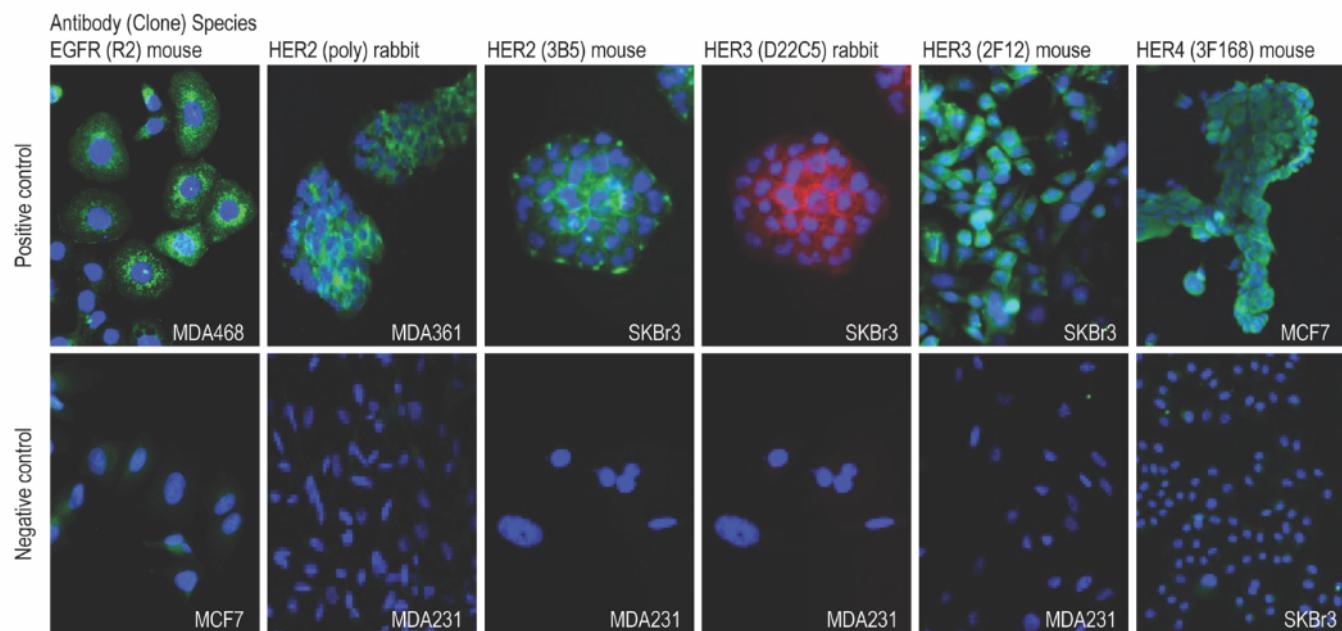


Figure S2. Validation of PLA immuno-detection conditions using immunofluorescence and fluorescent microscopy (images taken at 20x magnification). Positive and negative control cell lines were selected based on known HER family expression status.

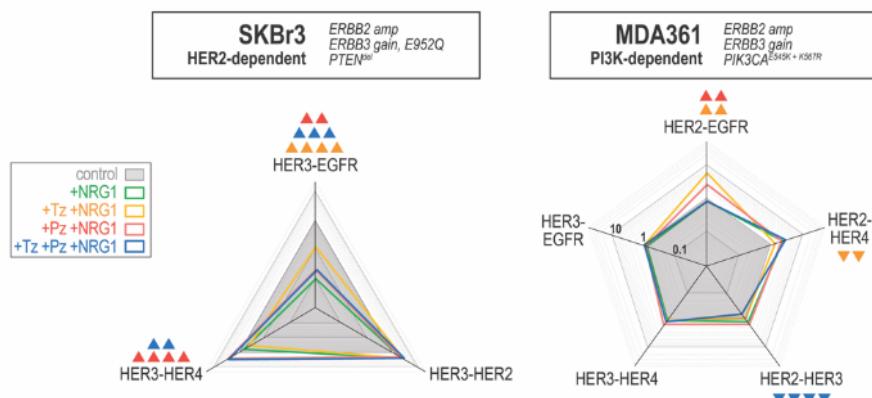


Figure S3. *In vitro* PLA data supporting Figure-4, second biological PLA replicate for the dimer complexes shown, in SKBr3 and MDA361 cells.

Supplementary Data: The following scripts can be run in Qupath ‘Script Editor’ as a batch.

| Qupath script | Description |
|---|--|
| <pre>setImageType('FLUORESCENCE'); createSelectAllObject(true); def path = buildFilePath(PROJECT_BASE_DIR, 'annotations') def annotations = getAnnotationObjects() new File(path).withObjectOutputStream { it.writeObject(annotations) } selectAnnotations();</pre> | 1. Annotate the image. |
| <pre>runPlugin('qupath.imagej.detect.nuclei.WatershedCellDetection', {'detectionImageFluorescence': 1, "requestedPixelSizeMicrons": 0.5, "backgroundRadiusMicrons": 0.0, "medianRadiusMicrons": 0.0, "sigmaMicrons": 3.0, "minAreaMicrons": 50.0, "maxAreaMicrons": 400.0, "threshold": 7000.0, "watershedPostProcess": true, "cellExpansionMicrons": 10.0, "includeNuclei": true, "smoothBoundaries": true, "makeMeasurements": true}); name = getProjectEntry().getImageName() cells = getCellObjects() println name + " " + (cells.size()) + "_cells")</pre> | 2. Select the whole image annotation and perform cell detection based on nuclear stain. |
| <pre>import qupath.imagej.plugins.ImageJMacroRunner import qupath.lib.plugins.parameters.ParameterList def params = new ImageJMacroRunner(getQuPath()).getParameterList() print ParameterList.getParameterListJSON(params, ' ') params.getParameters().get('downsampleFactor').setValue(4.0 as double) print ParameterList.getParameterListJSON(params, ' ') def macro = 'Stack.setChannel(3); run("Find Maxima...", "noise=1000 output=Count");' def imageData = getCurrentImageData() def annotations = getAnnotationObjects() for (annotation in annotations) { ImageJMacroRunner.runMacro(params, imageData, null, annotation, macro)}</pre> | 3. Print file name and cell count. Data is then copy into Excel sheet. |
| | 4. Exports the annotated image to ImageJ and execute ‘Find Maxima’ on the designated channel which counts the PLA signals. Data is then copy into Excel sheet. |