Lab Report 1

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75%

A couple oversights but overall, good job. You wrote a good background and abstract and just missed a few things at cursory glance. Same goes for the analysis, you were able to handle the dataset and generate dose-response curves from images with small mistakes.

- Inhibitors
    - ZM33 is an inhibitor of c-Raf *in vitro* but has been seen to cause Raf activation in cells. Any ideas why or how?
    - GM6001 is a general MMP inhibitor and should not prevent EGFR activation, but rather inhibit the production of EGFR ligands as well as many other cleavage products
    - BMS is similar to GM6001 but is specific to TACE and therefore TGF-α production in this system
- FRET does not create a third, distinct wavelength but rather allows for excitation of the donor to generate emission from the acceptor. In other words low FRET would be adding violet light and getting cyan out, high FRET would be adding violet light and getting yellow out, too (even though the YFP isn't excited by violet).
- I don't think it's very useful to show the location of wells on a 96 well plate in the lab report unless you hope to make some claim about location being important for the data obtained. This felt more convenient than practical.
- Using the 99% quartile to determine what values to set to 0 is simply intensity-based segmentation and a harsh one at that. Background subtraction is an actual subtraction from the image to correct for it's inevitable addition in the experiment.
- Dynamic range of sensor is hidden when the plots are this normalized, hiding the actual reason the 10% FBS plot looks so noisy. This would have

helped in determining what serum does to the pathway more than comparing EC_{50} or R^2 values.

- It looks like you used the EGF concentrations for the inhibitor concentrations
- It's worth taking a closer look at the data to determine why something looks the way it does in your final graph:
    - The large error in the 10% FBS graph due to a squashed dynamic range where all of the values are very similar
    - The last point in your no serum graph is due to a crazy outlier in one of the wells, in which you are no longer quantifying cells and should probably remove it from the dataset.

Critiques

- Clear, concise abstract
- Good discussion on why the error was so big
- Maybe include error when reporting IC_{50} and EC_{50} (+/-)
- Good organization and presentation of results
- Don't include the details of results in conclusion section
- Great job exploring alternative methods to address shortcomings in the study