Newmark COBA project

**Background**

ovaries folder: pHH3\_nanos\_klf4 dataset. 26 z-stack images.

The goal is to count all the nanos+ (magenta) cells and all the klf4+ (green) cells. Then, to quantify the % of nanos+ cells that are also klf4+ and vice versa. Each of these files contains a single ovary. They are easily recognized as rounded lobes that have nanos+ cells around the periphery and mature oocytes (big cells) in the middle and they have a "streak" of nanos- and klf4-expressing cells projecting anteriorly from each ovary. Is it possible to delineate a boundary between the "anterior streak" and the round ovary and to make separate coutns? Another marker in these files in the mitotic marker phosphohistone H3 (pH3, cyan). A final goal would be to get a mitotic index (number of nanos+ or klf4+ cells that are also pH3 positive).

4 channels present: channel 1: (Ch2-T1) cyan (these are pH3+ mitotic cells), channel 2: (ChS2-T2) magenta (these are nanos+ cells), channel 3: (ChS1-T3) green, (these are klf4+ cells), channel 4: (Ch1-T4) gray (this is DAPI; all nuclei). 8 Bit. 1024x1024 pixels. 1 um z step.

There are no differences in these images, they all show different examples of the same thing.