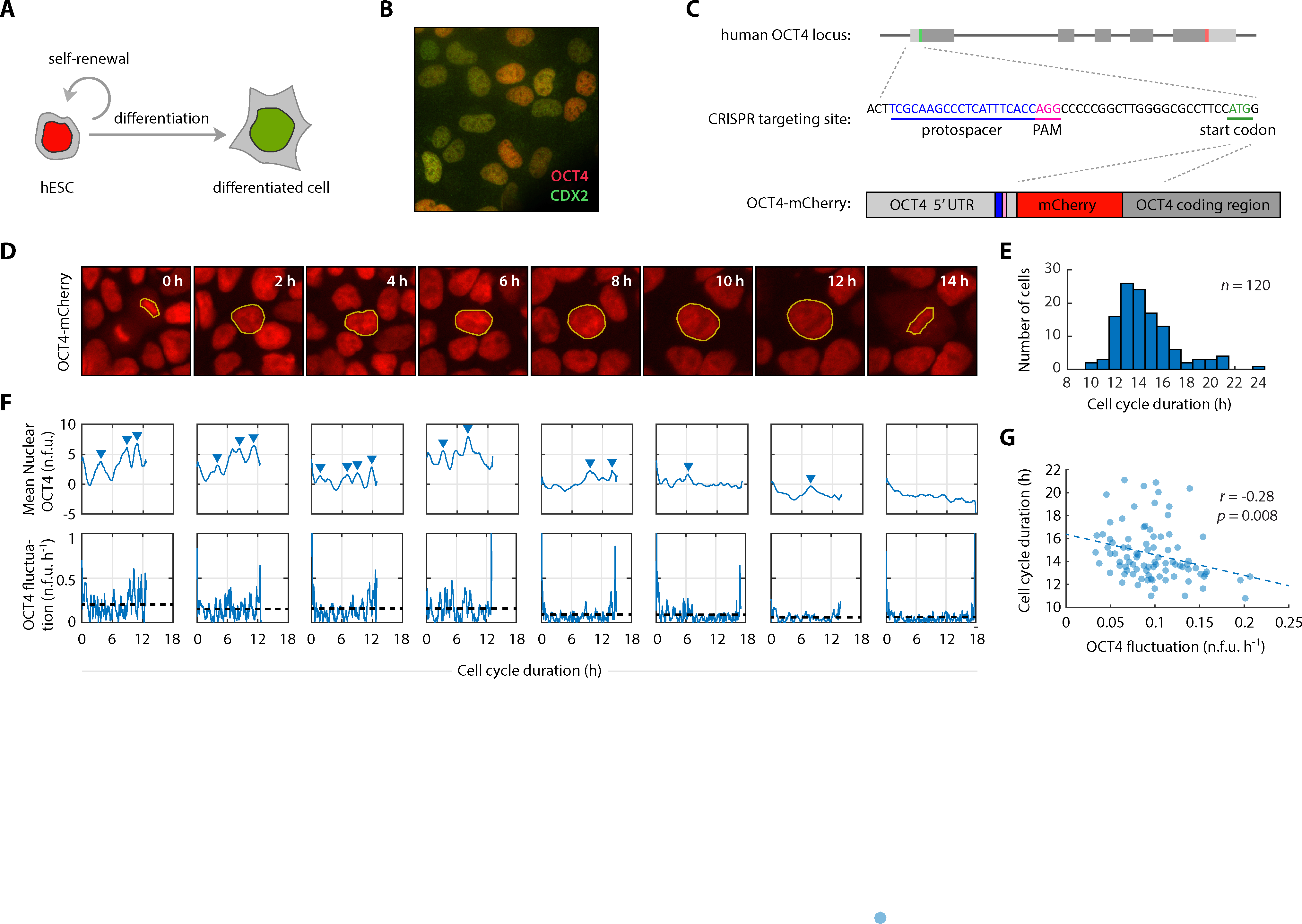
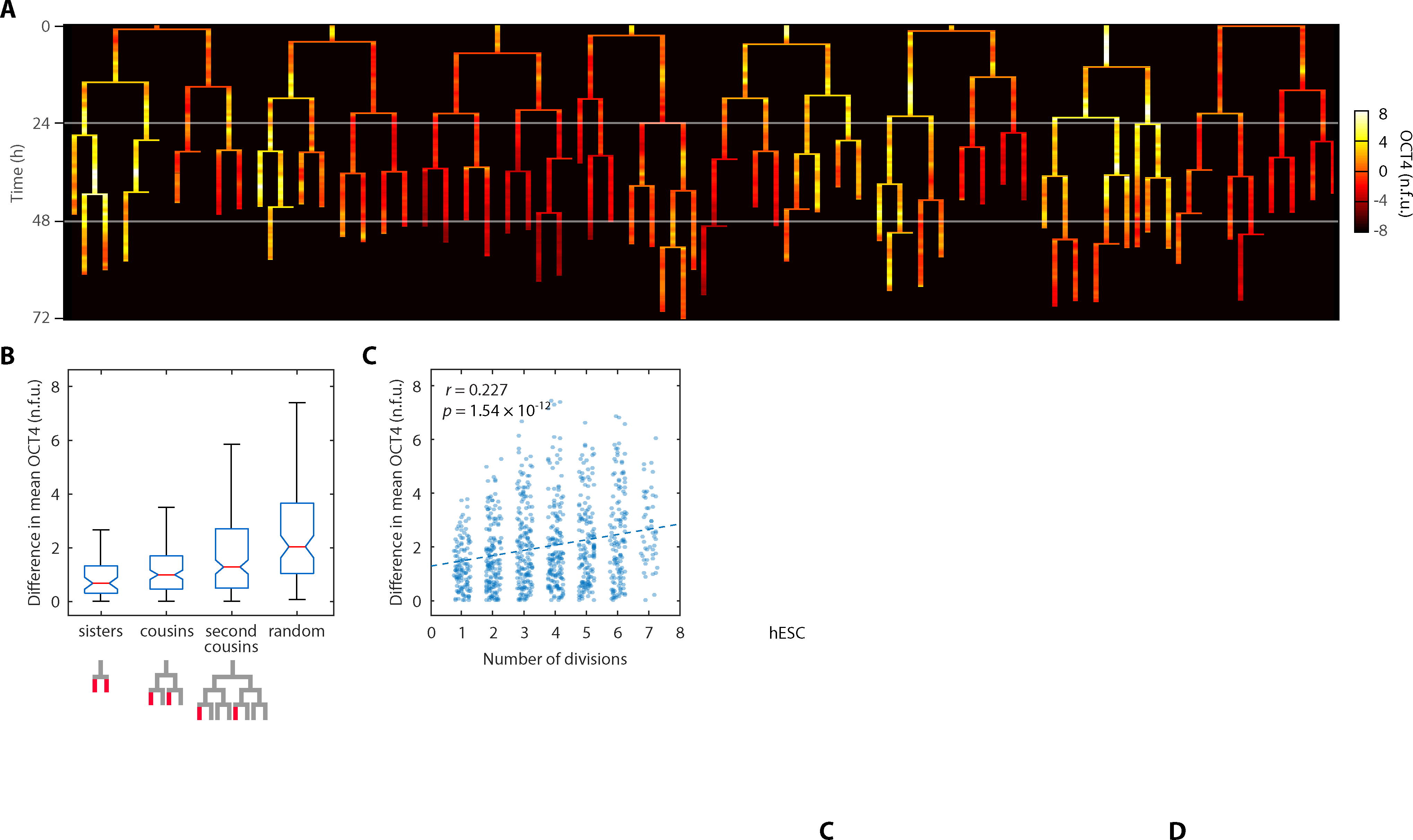
Pedigree Analysis of Human Embryonic Stem Cells

PI: Jeremy Purvis

We are looking for a creative team of BD2K trainees to develop a novel algorithm to identify, and quantify, “cell cycle segments” from live-imaging data of human stem cells. Understanding the biology of human stem cells is critical for studies of human development, tissue regeneration, and disease. To this end, we have developed experimental tools that allow us to follow the real-time behavior of thousands of human embryonic stem cells as they interact in time and space:



We are gaining tremendous insights from these live-, single-cell imaging experiments but currently suffering from the fact that each movie—and each cell—has to be carefully tracked and annotated by hand. Although various tracking algorithms exist, none of them can adequately track human stem cells and demarcate the time at which cell division events occur. To solve this problem, our approach will be to identify image objects in the full 3-dimensional image data (2D Space x Time), rather than in each time frame separately. The goal will be to extract a series of 3D segments that represent the path of an individual stem cell from birth (division of its mother cell) to death (its own division event). We have a “gold standard” data set that was tracked by hand that will be useful for evaluating the performance of the algorithm and implementing machine learning approaches:



The final product of the project will be a brief publication entitled “Pedigree Analysis of Human Embryonic Stem Cells” in which we describe the method used to extract cell cycle segments and characterize various high level features of the data, such as the distribution of cell cycle lengths and growth characteristics of the population.