

Article

Morphological Changes in Astrocytes by Self-Oxidation of Dopamine to Polydopamine and Quantification of Dopamine through Multivariate Regression Analysis of Polydopamine Images

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Supplementary:

1. Formula Proofs

1.1. Proof of (2)

If Y_i ($i = 1, \dots, n$) are functions of m regressor variables $X = [x_{i1}, \dots, x_{im}]$ with $n > m$, the multiple linear regression model $Y_i = A \cdot X_i$ can be used to linearly approximate the relationship between Y (DA concentrations) and X (RGB color intensities) [30]. In our application here, $m = 3$ (three colors) and $n = 6$ (six DA concentrations; one of which is for $C = 0$). Also, we had three different trials ($K = 3$) per experiment and the question was how to also incorporate their data in the formulation of the model. Let's denote by $X_i^{(k)}$ ($k = 1, \dots, K$) the observation/data point of the i^{th} intensity with the i^{th} concentration from the k^{th} trial. Then the best fitted model over the K trials can be found by minimizing the least squares errors of the trials in some optimal combination that we show below.

We now have a set of multiple linear regression models $Y = A \cdot X^{(k)}$. Then, the matrix format of the least squares error function can be expressed as:

$$L = \sum_{k=1}^K (Y - AX^{(k)})(Y - AX^{(k)})^T \quad (\text{S-1})$$

where A is a $(1 \times m)$ matrix containing the model coefficients (in this particular application, the intercepts of the model are assumed to be zero, that is, concentration $C = 0$ if RGB intensities = 0), Y and $X^{(k)}$ are matrices with dimensions $(1 \times n)$ and $(m \times n)$, respectively. The least squares estimates of the model coefficients must then satisfy:

$$\frac{\partial L}{\partial A} = \sum_{k=1}^K 2(AX^{(k)}\{X^{(k)}\}^T - Y\{X^{(k)}\}^T) = 0 \quad (\text{S-2})$$

which results in:

$$A \sum_{k=1}^K \mathbf{X}^{(k)} \{\mathbf{X}^{(k)}\}^T = \mathbf{Y} \sum_{k=1}^K \{\mathbf{X}^{(k)}\}^T \quad (\text{S-3})$$

$$\mathbf{Y} = A \left(\sum_{k=1}^K \mathbf{X}^{(k)} \{\mathbf{X}^{(k)}\}^T \right) \left(\sum_{k=1}^K \{\mathbf{X}^{(k)}\}^T \right)^+ \quad (\text{S-4})$$

Hence, the set of the multiple linear regression models over K trials is reduced to one general regression model of the form $\mathbf{Y} = A\bar{\mathbf{X}}$, where $\bar{\mathbf{X}} = \left(\sum_{k=1}^K \mathbf{X}^{(k)} \{\mathbf{X}^{(k)}\}^T \right) \left(\sum_{k=1}^K \{\mathbf{X}^{(k)}\}^T \right)^+$ with the superscript $(+)$ denoting the Moore-Penrose pseudo-inverse of a matrix [29].

1.2. Proof of (4)

In this case, we consider \mathbf{X} (the RGB intensities) as a function of \mathbf{Y} (the DA concentrations) because we are called to estimate \mathbf{X} if \mathbf{Y} is known. Then, the simple linear regression model $X_i = B \cdot Y_i$ is used to linearly approximate the relationship between \mathbf{X} and \mathbf{Y} . But we still here have data from multiple trials per experiment to fit the model on.

To fit a simple linear regression model to the data over K trials $\mathbf{X}^{(k)} = B \cdot \mathbf{Y}$ ($k = 1, \dots, K$), we have to minimize the least squares errors from each trial. Here, since RGB intensities could be non-zero even if DA concentration is zero, we consider the most general case where the intercept of the fitted line may not be zero. Then, \mathbf{Y} is a $(2 \times n)$ matrix where all its first-row elements are ones, and B is a (1×2) regression coefficient matrix containing the interception and the slope of the fitted line. Then, by defining the squared error function L as:

$$L = \sum_{k=1}^K (\mathbf{X}^{(k)} - B\mathbf{Y})(\mathbf{X}^{(k)} - B\mathbf{Y})^T \quad (\text{S-5})$$

For minimization of L , the least squares estimators should satisfy:

$$\frac{\partial L}{\partial B} = \sum_{k=1}^K 2(B\mathbf{Y}\mathbf{Y}^T - \mathbf{X}^{(k)}\mathbf{Y}^T) = 0 \quad (\text{S-6})$$

$$B\mathbf{Y}\mathbf{Y}^T = \left(\sum_{k=1}^K \mathbf{X}^{(k)} \right) \mathbf{Y}^T \quad (\text{S-7})$$

$$\left(\sum_{k=1}^K \mathbf{X}^{(k)} \right) = B\mathbf{Y} \quad (\text{S-8})$$

Hence, the simple linear regression model over K trials is reduced to a simple regression model of the form $\bar{\mathbf{X}} = B\mathbf{Y}$, where $\bar{\mathbf{X}}$ is to be taken as the average of \mathbf{X} over the K trials.

2. Figures

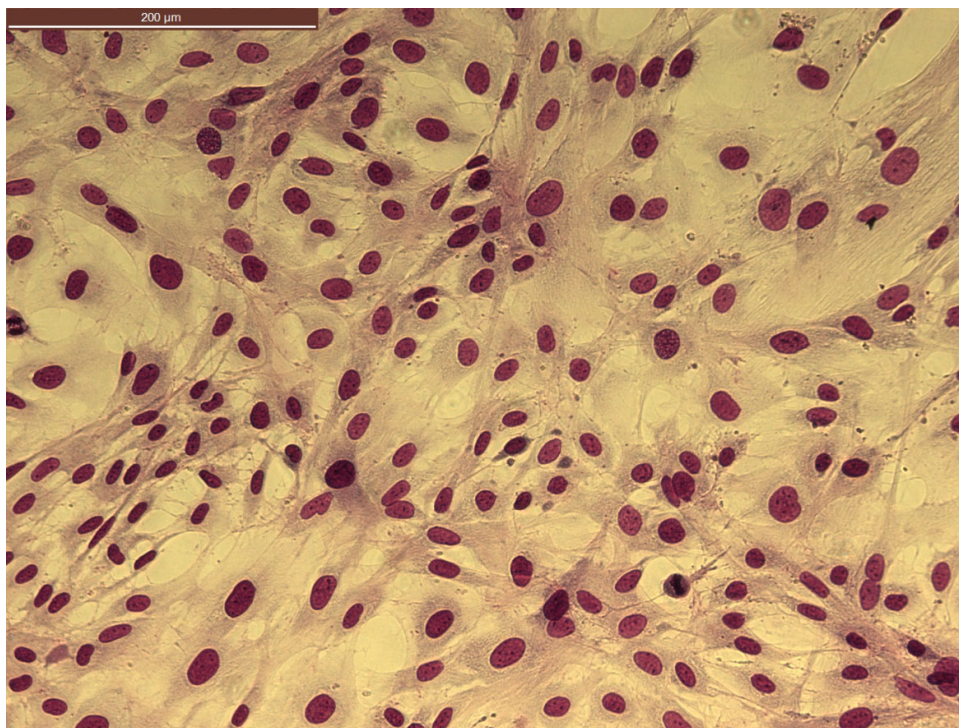


Figure S1: Treatment of 5000 astrocytes/well with no dopamine added (control). Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

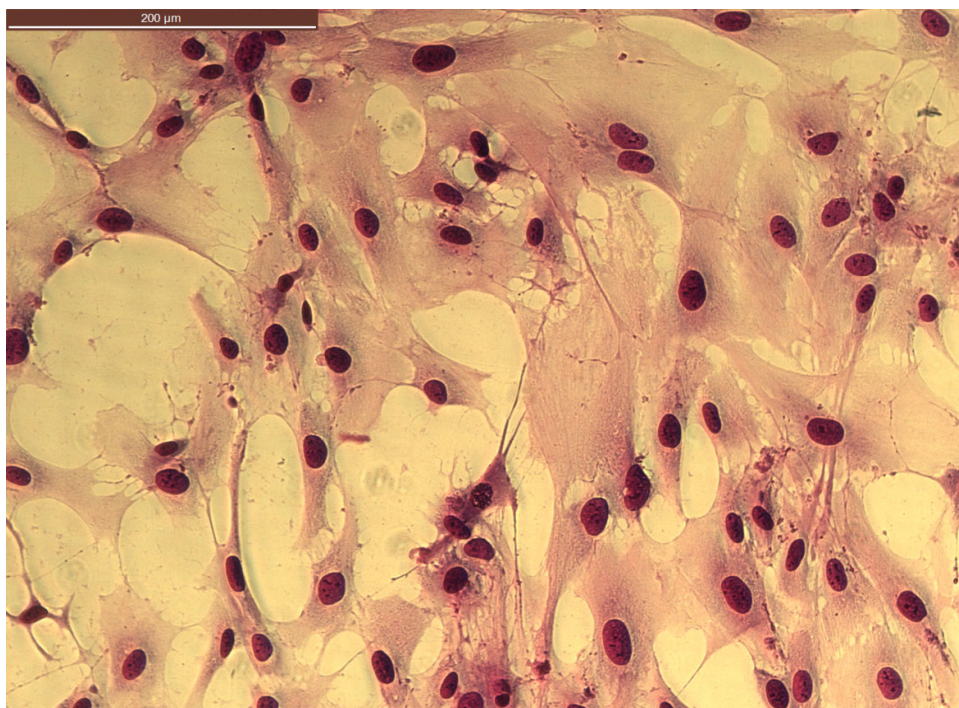


Figure S2: Treatment of 5000 astrocytes/well with 25 μM dopamine. Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

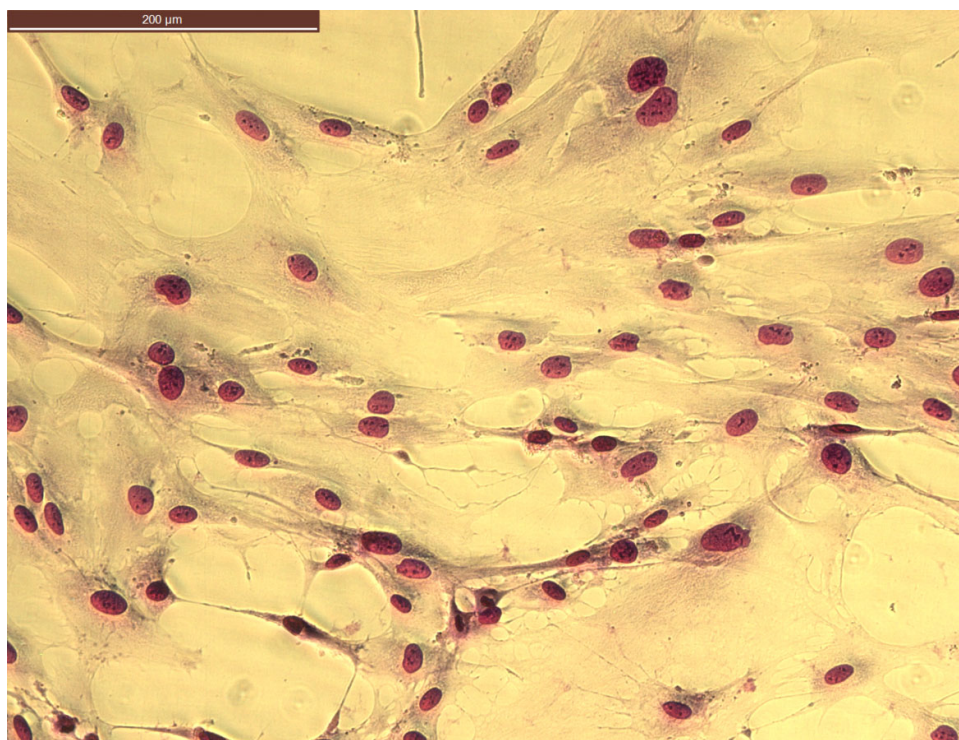


Figure S3: Treatment of 5000 astrocytes/well with 50 μ M dopamine. Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

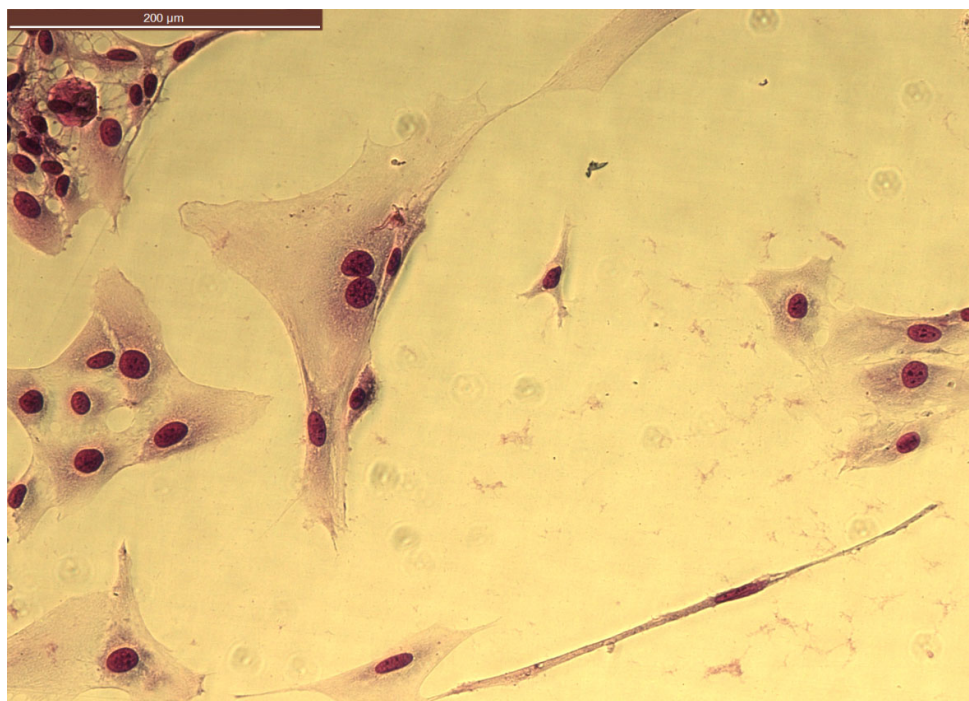


Figure S4: Treatment of 5000 astrocytes/well with 75 μ M dopamine. Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

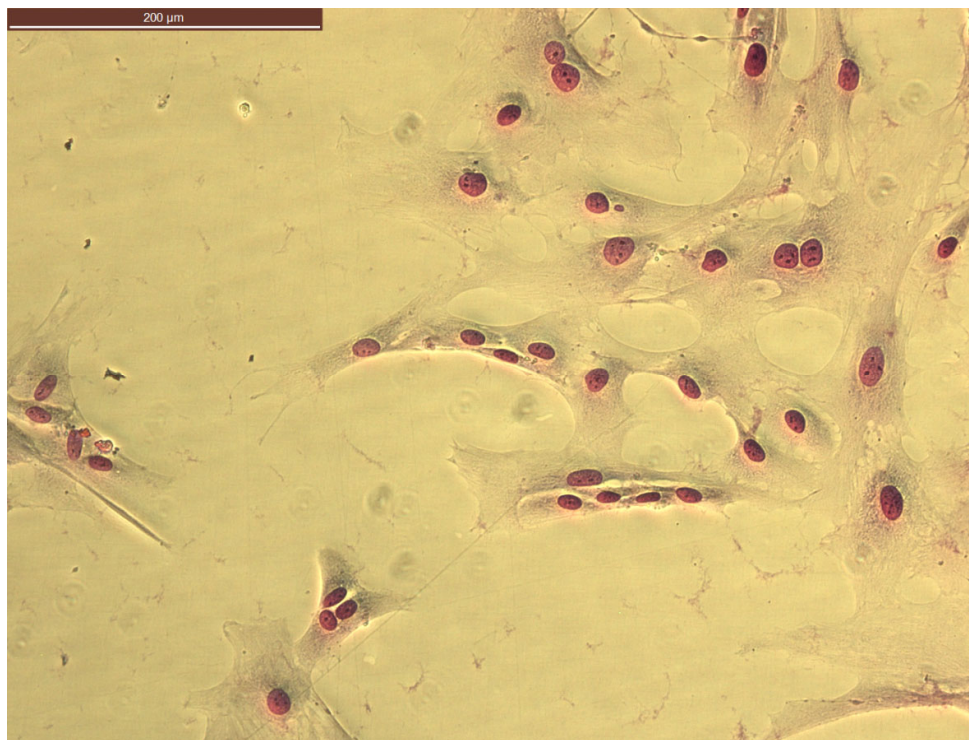


Figure S5: Treatment of 5000 astrocytes/well with 100 μ M dopamine. Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

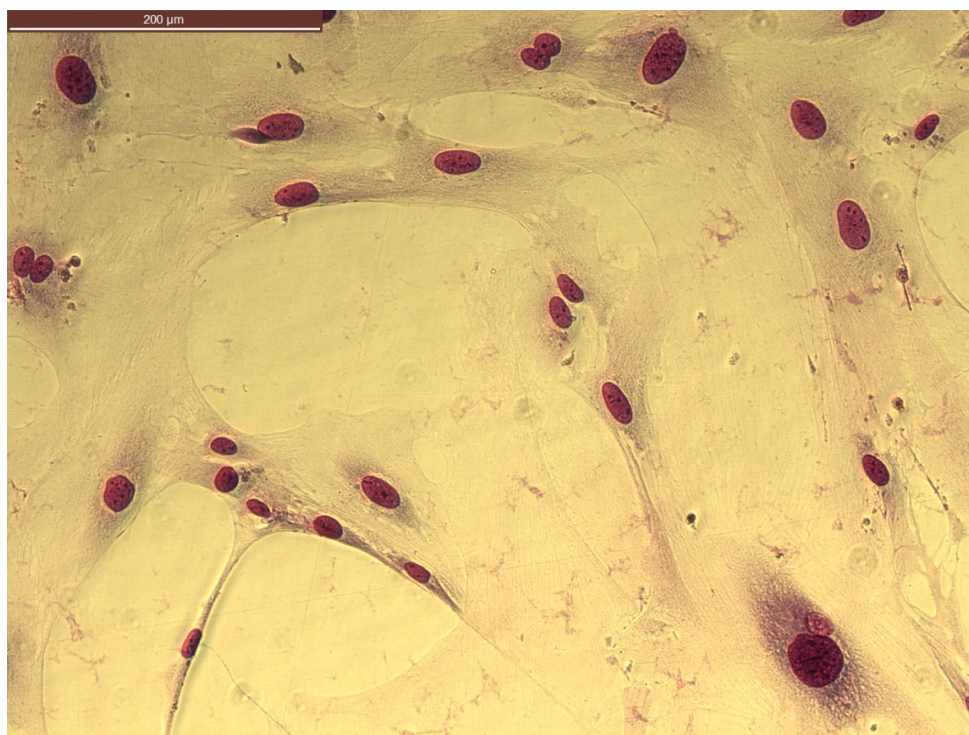


Figure S6: Treatment of 5000 astrocytes/well with 125 μ M dopamine. Diff-Quik stained astrocytes, 48 h post treatment; scale bar indicates 200 microns.

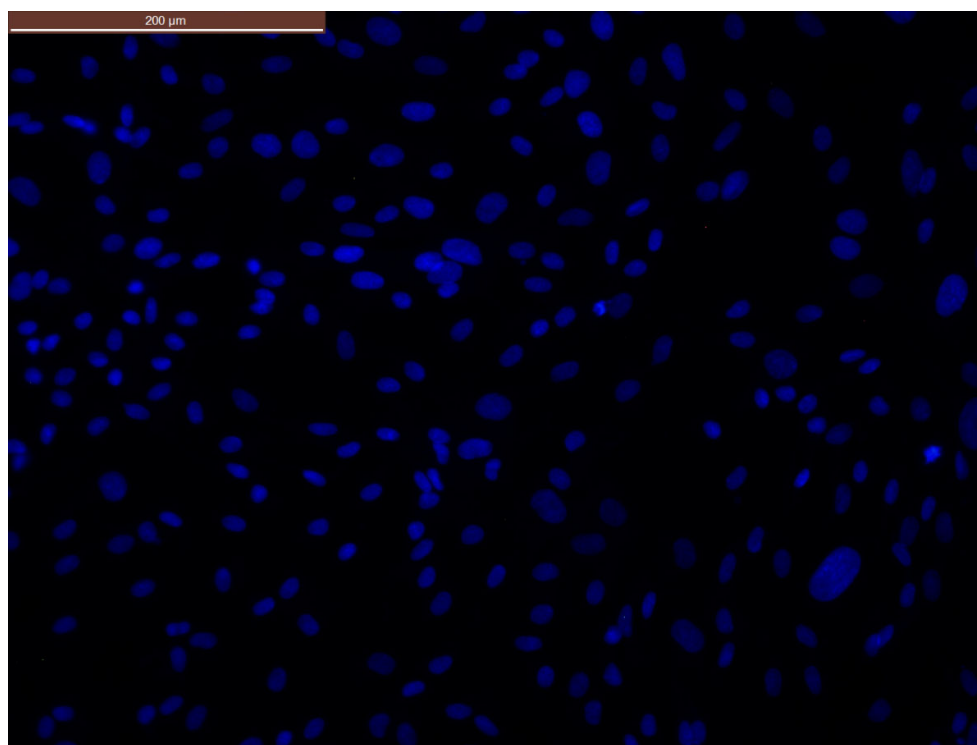


Figure S7: DAPI stained astrocytes (untreated control); scale bar indicates 200 microns.

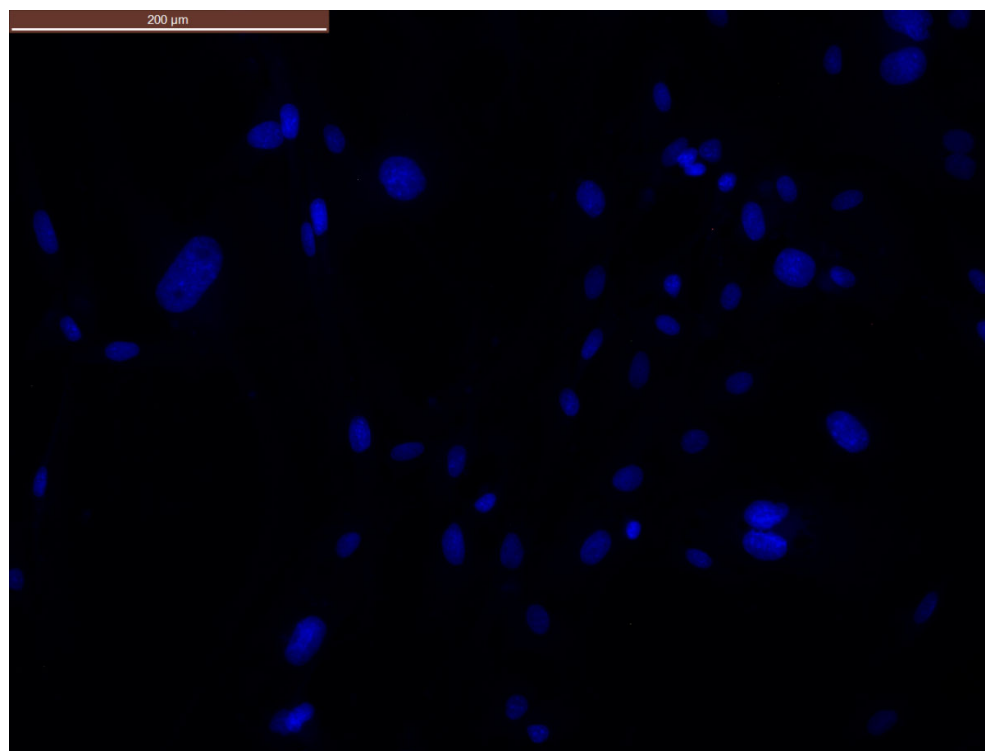


Figure S8: DAPI stained astrocytes (treated with 25 μM dopamine); scale bar indicates 200 microns.

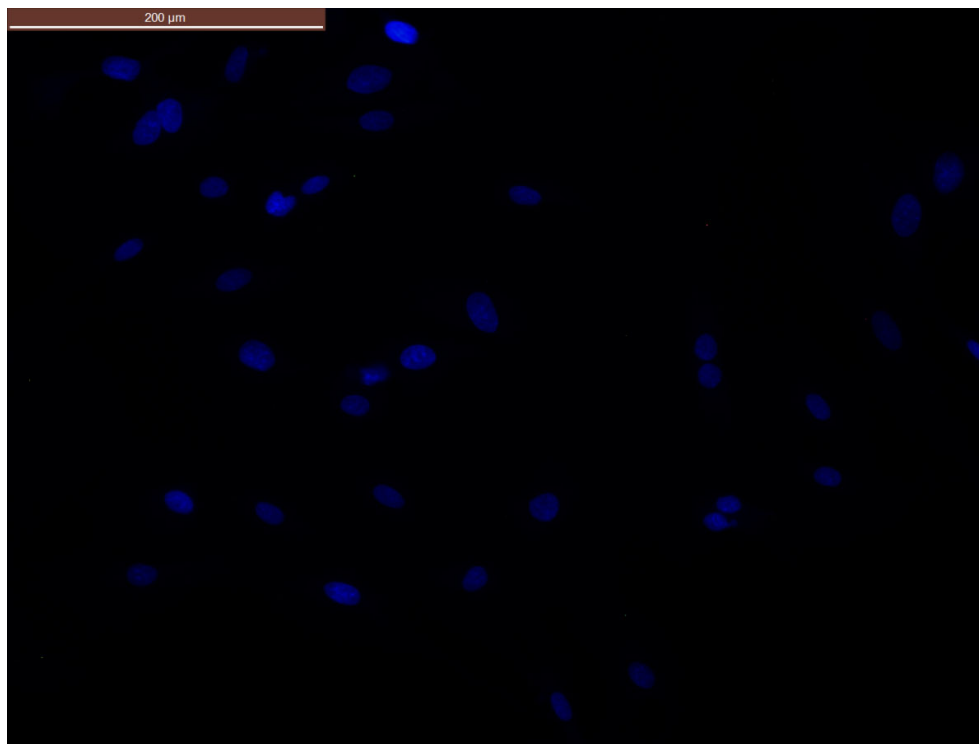


Figure S9: DAPI stained astrocytes (treated with 50 μ M dopamine); scale bar indicates 200 microns.

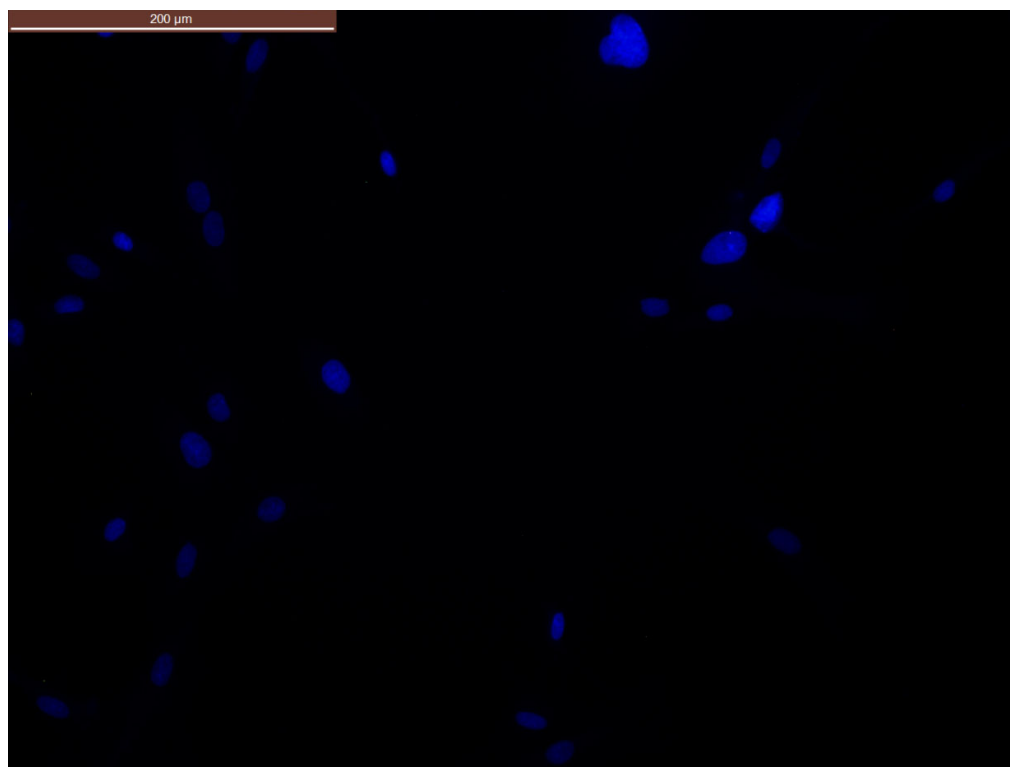


Figure S10: DAPI stained astrocytes (treated with 75 μ M dopamine); scale bar indicates 200 microns.

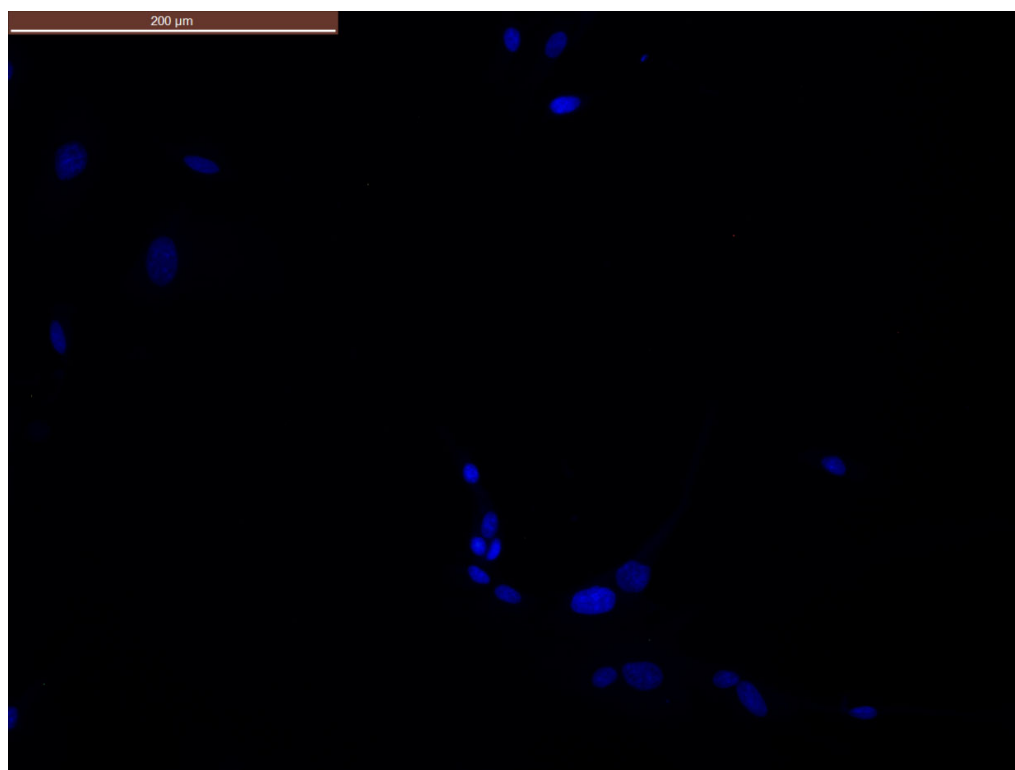


Figure S11: DAPI stained astrocytes (treated with 100 μ M dopamine); scale bar indicates 200 microns.

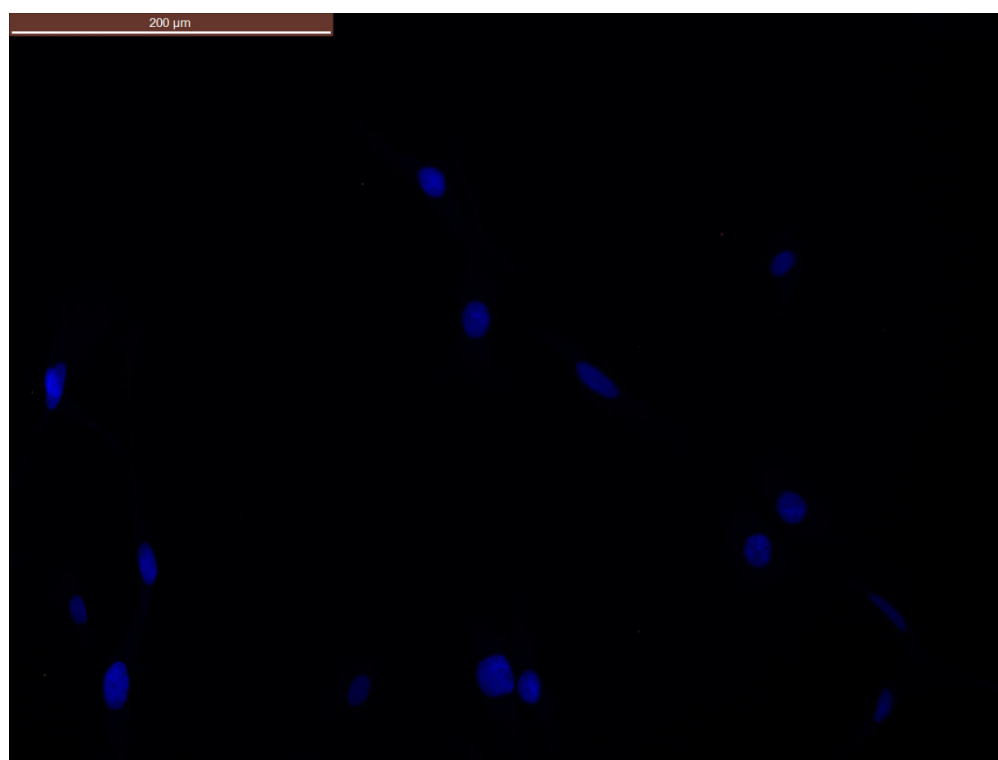


Figure S12: DAPI stained astrocytes (treated with 125 μ M dopamine); scale bar indicates 200 microns.