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## Automated Deep Learning-Based System to Identify Endothelial Cells Derived from Induced Pluripotent Stem Cells

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## SUMMARY

Deep learning technology is rapidly advancing and is now used to solve complex problems. Here, we used deep learning in convolutional neural networks to establish an automated method to identify endothelial cells derived from induced pluripotent stem cells (iPSCs), without the need for immunostaining or lineage tracing. Networks were trained to predict whether phase-contrast images contain endothelial cells based on morphology only. Predictions were validated by comparison to immunofluorescence staining for CD31, a marker of endothelial cells. Method parameters were then automatically and iteratively optimized to increase prediction accuracy. We found that prediction accuracy was correlated with network depth and pixel size of images to be analyzed. Finally, K-fold cross-validation confirmed that optimized convolutional neural networks can identify endothelial cells with high performance, based only on morphology.

## INTRODUCTION

Machine learning consists of automated algorithms that enable learning from large datasets to resolve complex problems, including those encountered in medical science [\(Gorodeski et al., 2011; Heylman et al., 2015; Hsich et al.,](#page-7-0) [2011\)](#page-7-0). In deep learning, a form of machine learning, patterns from several types of data are automatically extracted [\(Lecun et al., 2015](#page-7-1)) to accomplish complex tasks such as image classification, which in conventional machine learning requires feature extraction by a human expert. Deep learning eliminates this requirement by identifying the most informative features using multiple layers in neural networks, i.e., deep neural networks [\(Hatipoglu and Bil](#page-7-2)[gin, 2014\)](#page-7-2), which were first conceived in the 1940s to mimic human neural circuits [\(McCulloch and Pitts,](#page-7-3) [1943\)](#page-7-3). In such neural networks, each neuron receives weighted data from upstream neurons, which are then processed and transmitted to downstream neurons. Ultimately, terminal neurons calculate a predicted value based on processed data, and weights are then iteratively optimized to increase the agreement between predicted and observed values. This technique is rapidly advancing due to innovative algorithms and improved computing power [\(Bengio et al., 2006; Hinton et al., 2006\)](#page-7-4). For example, convolutional neural networks have now achieved almost the same accuracy as a clinical specialist in diagnosing diabetic retinopathy and skin cancer [\(Esteva et al., 2017; Gulshan](#page-7-5) [et al., 2016\)](#page-7-5). Convolutional neural networks have also proved useful in cell biology such as morphological classification of hematopoietic cells, C2C12 myoblasts, and

## induced pluripotent stem cells (iPSCs) ([Buggenthin et al.,](#page-7-6) [2017; Niioka et al., 2018; Yuan-Hsiang et al., 2017](#page-7-6)).

iPSCs, which can be established from somatic cells by expression of defined genes [\(Takahashi and Yamanaka,](#page-8-0) [2006\)](#page-8-0), hold great promise in regenerative medicine ([Yuasa](#page-8-1) [and Fukuda, 2008\)](#page-8-1), disease modeling [\(Tanaka et al., 2014\)](#page-8-2), drug screening ([Avior et al., 2016](#page-7-7)), and precision medicine [\(Chen et al., 2016](#page-7-8)). iPSCs can differentiate into numerous cell types, although differentiation efficiencies vary among cell lines and are sensitive to experimental conditions ([Hu](#page-7-9) [et al., 2010; Osafune et al., 2008\)](#page-7-9). In addition, differentiated cell types are difficult to identify without molecular techniques such as immunostaining and lineage tracing. We hypothesized that phase-contrast images contain discriminative morphological information that can be used by a convolutional neural network to identify endothelial cells. Accordingly, we investigated whether deep learning techniques can be used to identify iPSC-derived endothelial cells automatically based only on morphology.

## RESULTS

## Development of an Automated System to Identify Endothelial Cells

We differentiated iPSCs as previously described ([Patsch](#page-7-10) [et al., 2015\)](#page-7-10), obtaining mesodermal cells at around day 3 and specialized endothelial cells at around day 5 (Figure S1A). At day 6, structures that resemble vascular tubes were formed (Figure S1B). CD31 staining confirmed that endothelial cells were obtained at an

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efficiency of 20%–35%, as assessed by flow cytometry. Differentiation efficiency was strongly variable (Figure S1C), highlighting the need for an automated cell identification system to assess iPSC differentiation or to identify and quantify the cell types formed.

The basic strategy to identify endothelial cells by convolutional neural networks is shown in [Figure 1](#page-2-0)A. In brief, differentiated iPSCs were imaged by phase contrast and by immunofluorescence staining for CD31, a marker of endothelial cells. The latter were then binarized into white and black pixels corresponding to raw pixels above and below a threshold value, respectively. Subsequently, input blocks were extracted randomly from phase-contrast images, and matching target blocks equivalent to or within input blocks were extracted from both phase-contrast and binarized immunofluorescence images. Binarized target blocks were then classified as unstained (0) or stained (1) depending on the ratio of white pixels to black, to generate answers. Finally, input blocks were analyzed in LeNet, a small network [\(Lecun et al., 1998\)](#page-7-11), and AlexNet, a large network ([Krizhevsky et al., 2012](#page-7-12)), to predict phase-contrast target blocks as unstained or stained. Predictions were compared with answers obtained from binarized target blocks, and weights were automatically and iteratively optimized to train the neural networks and thereby increase accuracy [\(Figure 1A](#page-2-0)).

Networks were then optimized according to [Figure 1B](#page-2-0). Number of blocks, input block size, and target block size were first optimized using the small network, along with staining threshold, the ratio of white pixels to black for a target block to be classified as stained. To improve performance, as assessed by F1 score and accuracy, the small network was compared with the large network, observed errors were analyzed, and binarized target blocks were rebinarized by visual comparison of raw fluorescent images with phase-contrast images. Finally, the optimized network was validated by K-fold cross-validation ([Figure 1](#page-2-0)B). To this end, we obtained 200 images from each of four independent experiments, of which 640 were used for training and 160 for validation to collect data shown in [Figures 2](#page-3-0) and [3](#page-4-0). From each image, 200 blocks were randomly extracted, and 500–128,000 of the blocks were used for training while 32,000 blocks were used for validation ([Figure 1C](#page-2-0)).

## Improvement of F1 Score and Accuracy by **Optimization**

To train the networks we optimized several experimental conditions, including number of input blocks, target block size, and input block size. Performance was evaluated based on F1 scores, which aggregates recall and precision, and on accuracy, which is the fraction of correct predictions. As noted, we first used 500–128,000 blocks for training ([Fig-](#page-2-0)

[ure 1](#page-2-0)C) to determine the number of blocks required to achieved convergence (Table S1). Inflection points in F1 scores and accuracy were observed at 16,000 blocks, and convergence was achieved at 32,000 blocks for an input and target block size of  $128 \times 128$  pixels, as well as for an input block size of  $512 \times 512$  pixels and a target block size of  $32 \times 32$  pixels ([Figure 2A](#page-3-0)). Hence, 32,000 blocks were used for training in subsequent experiments. Next, the optimal combination of block size and staining threshold was determined by input blocks of  $32 \times 32$ , 64  $\times$  64, 128  $\times$  128, 256  $\times$  256, and 512  $\times$  512 pixels. We note that  $32 \times 32$ -pixel blocks contained only single cells, while  $512 \times 512$ -pixel blocks contained entire colonies and surrounding areas (Figure S2A). Based on F1 scores, performance was best from an input block size of  $512 \times 512$  pixels combined with a staining threshold of 0.3 [\(Figures 2](#page-3-0)B and 2C; Table S2). Both F1 score and accuracy increased with input block size ([Figures 2D](#page-3-0), S2B, and S2C), indicating that areas surrounding cells should be included to increase accuracy. In contrast, target block size did not affect predictive power ([Figure 2E](#page-3-0)) or the correlation between input block size and F1 scores and accuracy (Figure S2D and Table S3).

#### Effect of Network Size on Predictive Power

As network architecture is critical to performance, we compared the predictive power of the small network LeNet ([Lecun et al., 1998](#page-7-11)) after training on 128,000 blocks with that of the large network AlexNet ([Krizhevsky et al.,](#page-7-12) [2012](#page-7-12)) ([Figure 3A](#page-4-0)). F1 scores and accuracy from the latter were higher [\(Figures 3B](#page-4-0) and S3A), suggesting that extraction of complex features by a large network improves cell identification by morphology. Performance was further enhanced by analyzing true positives, true negatives, false positives, and false negatives [\(Figures 3C](#page-4-0) and S3B). We found that true positives and true negatives were typically obtained in areas with uniformly distributed cells. In contrast, areas with heterogeneous appearance, such as at the border between abundantly and sparsely colonized surfaces, often led to false positives or false negatives. To examine whether F1 scores are influenced by heterogeneous appearance (Figure S4A), we scored the complexity of all 32,000 512  $\times$  512-pixel validation blocks as the average difference between adjacent pixels, normalized to the dynamic range ([Saha and Vemuri, 2000](#page-7-13)). Blocks with complexity of <0.04 were considered sparsely colonized, while blocks with complexity of 0.04 to 0.08 typically contained uniformly distributed cells with clear boundaries. All other images had complexity >0.08 and contained dense colonies with indistinct cell borders. In both the small and large networks (Figures S4B, S4C, and S4D), F1 scores were highest for blocks with complexity of 0.04 to 0.08 (typically 0.06), implying that variations in cell



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## Figure 1. Analysis of Induced Pluripotent Stem Cell-Derived Endothelial Cells Using Convolutional Neural Networks

(A) Training protocol. Input blocks were extracted from phase-contrast images and predicted by networks to be unstained (0) or stained (1) for CD31. Target blocks containing single cells were extracted from immunofluorescent images of the same field, binarized based on CD31 staining, and classified as stained or unstained based on the ratio of white pixels to black. Network weights were then automatically and iteratively adjusted to maximize agreement between predicted and observed classification. Scale bars, 400  $\mu$ m (upper panels), 5  $\mu$ m (middle panels), and 80  $\mu$ m (bottom panels).

(B) Optimization of experimental parameters to maximize F1 score and accuracy.

(C) Two hundred images each were obtained from four independent experiments. Images were randomized at 80:20 ratio into training and evaluation sets, and 200 blocks were randomly extracted from each image.



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#### Figure 2. Dataset Adjustment

(A) F1 score and accuracy as a function of number of input blocks. Left: network performance using  $128 \times 128$ -pixel (px) input blocks and 128  $\times$  128-px target blocks. Right: performance using 512  $\times$  512-px input blocks and 32  $\times$  32-px target blocks.

(B and C) F1 score as a function of input block size and staining threshold. The optimal threshold is boxed in red and the optimal input block size is boxed in blue.

(D) Average F1 score for different input block sizes.

(E) F1 score for different target block sizes.

See also Figure S2 and Tables S1–S3.

density and morphology affect network performance, in line with incorrect predictions as shown in [Figures 3](#page-4-0)C and S3B. In light of this result, we speculated that weak

staining, non-specific fluorescence, and autofluorescence in dense colonies may also degrade performance. Accordingly, we rebinarized target blocks by visual comparison



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(legend on next page)



with raw fluorescent images [\(Figure 3D](#page-4-0)). Following this step, 26,861 of 128,000 blocks (21%) were classified as stained, while fully automated binarization scored 40,852 of 128,000 blocks (32%) as stained (Table S4A). Notably, the F1 score and accuracy rose above 0.9 and 0.95, respectively, in the large network [\(Figure 3](#page-4-0)E and Table S4A).

### K-Fold Cross-Validation

Finally, we assessed network performance and generalization by K-fold cross-validation, in which  $k$  subsets of data are divided into  $k-1$  training datasets and one validation dataset. Training and validation are then performed k times using different combinations of training and validation datasets. In our case, 800 images were collected in four independent experiments, of which various combinations of 600 images from three experiments were used for training and 200 images from one experiment were used for validation ([Figure 4A](#page-6-0)). The F1 score and accuracy were approximately 0.7 and higher than 0.7 for the small network with automatically binarized target blocks, but over 0.75 and over 0.9, respectively, for the large network with rebinarized target blocks [\(Figures 4B](#page-6-0) and 4C; Table S4B).

## **DISCUSSION**

In this study, we demonstrated that deep learning techniques are effective in identifying iPSC-derived endothelial cells. Following optimization of parameters such as number of input blocks, target block size, input block size, staining threshold, and network size, we achieved satisfactory F1 scores and accuracy. Notably, we found that a larger input block increases prediction accuracy, indicating that the environment surrounding cells is an essential feature, as was also observed for differentiated C2C12 myoblasts [\(Niioka et al.,](#page-7-14) [2018](#page-7-14)). We note that the immediate microenvironment is also an essential determinant of differentiation [\(Adams](#page-7-15) [and Alitalo, 2007; Lindblom et al., 2003; Takakura et al.,](#page-7-15) [2000](#page-7-15)), and that the positive correlation between input block size and F1 score or accuracymay prove helpful in future strategies to identify differentiated cells by morphology.

In comparison with other machine learning techniques, deep learning is straightforward and achieves high accuracies. Indeed, deep learning algorithms have won the ImageNet Large-Scale Visual Recognition Challenge since 2012 ([He et al., 2015; Krizhevsky et al., 2012; Szegedy](#page-7-16) [et al., 2014; Zeng et al., 2016](#page-7-16)), and have also proved useful in cell biology ([Buggenthin et al., 2017; Niioka et al., 2018;](#page-7-6) [Van Valen et al., 2016; Yuan-Hsiang et al., 2017](#page-7-6)). Although we used the older-generation networks LeNet and AlexNet, newer networks achieve even better accuracy in image classification ([Esteva et al., 2017; Gulshan et al., 2016](#page-7-5)). Several techniques, such as increasing network depth ([Simonyan](#page-8-3) [and Zisserman, 2014\)](#page-8-3), residual learning ([He et al., 2015](#page-7-16)), and batch normalization [\(Ioffe and Szegedy, 2015\)](#page-7-17), may also enhance performance, although these were not implemented in this study, since results were already satisfactory.

Inspection revealed some issues in binarizing heterogeneous areas in images with weak staining, non-specific fluorescence, and autofluorescence. To lower the number of false positives and improve performance, we rebinarized these images by comparing raw fluorescent images with phase-contrast images. In addition, cell density significantly affected F1 scores, implying that cells should be cultured carefully to a suitable density, or that networks should be trained to distinguish between true and false positives, especially when images are heterogeneous. Finally, K-fold cross-validation showed that iPSC-derived endothelial cells were identified with accuracy approximately 0.9 and F1 score 0.75, in line with similar attempts [\(Buggen](#page-7-6)[thin et al., 2017; Niioka et al., 2018; Yuan-Hsiang et al.,](#page-7-6) [2017](#page-7-6)).

Importantly, the data show that iPSC-derived endothelial cells can be identified based on morphology alone, requiring only 100 µs per block in a small network and 275  $\mu$ s per block in a large network (Figure S4E). As morphology-based identification does not depend on labeling, genetic manipulation, or immunostaining, it can be used for various applications requiring native, living cells. Thus, this system may enable analysis of large datasets and advance cardiovascular research and medicine.

## EXPERIMENTAL PROCEDURES

## iPSC Culture

iPSCs were maintained in mTeSR with 0.5% penicillin/streptomycin on culture dishes coated with growth factor-reduced

## Figure 3. Network Optimization

(A) Comparison of LeNet and AlexNet, which are small and large deep neural networks.

(C) Representative true positive, false positive, true negative, and false negative images. Scale bars, 80  $\mu$ m.

(E) F1 score and accuracy were compared following training of the small and large network on automatically binarized or rebinarized target blocks.

See also Figures S3 and S4; Table S4.

<sup>(</sup>B) F1 score learning curves from the small and large network.

<sup>(</sup>D) Immunofluorescent images were binarized automatically, or rebinarized by manual comparison of raw fluorescent images to phasecontrast images. Scale bars,  $100 \mu m$ .



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#### Figure 4. K-Fold Cross-Validation

(A) K-fold cross-validation based on four independent datasets, of which three were used for training and one was used for validation, in all possible combinations.

(B) K-fold cross-validation was performed using the small network trained on automatically binarized target blocks, and using the large network trained on rebinarized target blocks. Data are macro averaged F1 score and accuracy.

(C) Detailed K-fold cross-validation data. See also Table S4.

Matrigel, and routinely passaged every week. Media were changed every other day. Detailed protocols are described in Supplemental Experimental Procedures.

## Endothelial Cell Differentiation

iPSCs cultured on Matrigel-coated 6-well plates were enzymatically detached on day 7, and differentiated into endothelial cells as described in Supplemental Experimental Procedures.

### Flow Cytometry

At day 6 of differentiation, cells were dissociated, stained with APC-conjugated anti-CD31, and sorted on BD FACSAria III. As a negative control, we used unstained cells. Detailed protocols are described in Supplemental Experimental Procedures.

#### Immunocytochemistry

At day 6 of differentiation, cells were fixed with 4% paraformaldehyde, blocked with ImmunoBlock, probed with primary antibodies to CD31, and labeled with secondary antibodies as described in Supplemental Experimental Procedures.

## Preparation of Datasets

All phase-contrast and immunofluorescent images were acquired at day 6 of differentiation. Two hundred images were automatically obtained from each of four independent experiments. Of these, 640 were used for training and 160 were used for validation in [Figures 2](#page-3-0) and [3.](#page-4-0) For K-fold validation in [Figure 4](#page-6-0), 600 images from three experiments were used for training and 200 images from one experiment were used for validation, in all possible combinations. Datasets were constructed by randomly extracting 200 input blocks from each phase-contrast image. On the other hand, target blocks were extracted from binarized immunofluorescent images. Detailed procedures are described in Supplemental Experimental Procedures.

#### Deep Neural Networks

We used LeNet, a small network that contains two convolution layers, two max pooling layers, and two fully connected layers, as well as AlexNet, a large network that contains five convolution layers, three max pooling layers, and three fully connected layers. Network structures are shown in [Figure 3](#page-4-0)A and Supplemental Experimental Procedures.

#### Performance Evaluation

Performance was evaluated based on F1 scores, an aggregate of recall and precision, and on accuracy, the fraction of correct predictions. Detailed information is provided in Supplemental Experimental Procedures.

## SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, four figures, and four tables and can be found with this article online at [https://doi.org/10.1016/j.stemcr.2018.04.](https://doi.org/10.1016/j.stemcr.2018.04.007) [007.](https://doi.org/10.1016/j.stemcr.2018.04.007)

#### AUTHOR CONTRIBUTIONS

D.K., T. Kunihiro, and S.Y. designed experiments. D.K., M.L., T. Kunihiro, S.Y., Y.K., M.K., T. Katsuki, S.I., T.S., and K.F. collected data.



D.K., M.L., and T. Kunihiro analyzed data. K.F. supervised the research. D.K. and S.Y. wrote the article.

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#### <span id="page-7-15"></span>**REFERENCES**

[Adams, R.H., and Alitalo, K. \(2007\). Molecular regulation of](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref1) [angiogenesis and lymphangiogenesis. Nat. Rev. Mol. Cell Biol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref1) 8, [464–478](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref1).

<span id="page-7-7"></span>[Avior, Y., Sagi, I., and Benvenisty, N. \(2016\). Pluripotent stem cells](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref2) [in disease modelling and drug discovery. Nat. Rev. Mol. Cell Biol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref2) 17[, 170–182.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref2)

<span id="page-7-4"></span>[Bengio, Y., Lamblin, P., Popovici, D., and Larochelle, H. \(2006\).](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref3) [Greedy layer-wise training of deep networks. In Proceedings of](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref3) [the 19th International Conference on Neural Information Process](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref3)ing Systems, B. Schölkopf, J.C. Platt, and T. Hoffman, eds. (MIT [Press\), pp. 153–160](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref3).

<span id="page-7-6"></span>[Buggenthin, F., Buettner, F., Hoppe, P.S., Endele, M., Kroiss, M.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref4) [Strasser, M., Schwarzfischer, M., Loeffler, D., Kokkaliaris, K.D., Hil](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref4)[senbeck, O., et al. \(2017\). Prospective identification of hematopoi](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref4)[etic lineage choice by deep learning. Nat. Methods](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref4) 14, 403–406.

<span id="page-7-8"></span>[Chen, I.Y., Matsa, E., and Wu, J.C. \(2016\). Induced pluripotent](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref5) [stem cells: at the heart of cardiovascular precision medicine. Nat.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref5) [Rev. Cardiol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref5) 13, 333–349.

<span id="page-7-5"></span>[Esteva, A., Kuprel, B., Novoa, R.A., Ko, J., Swetter, S.M., Blau, H.M.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref6) [and Thrun, S. \(2017\). Dermatologist-level classification of skin can](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref6)[cer with deep neural networks. Nature](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref6) 542, 115–118.

<span id="page-7-0"></span>[Gorodeski, E.Z., Ishwaran, H., Kogalur, U.B., Blackstone, E.H.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7) [Hsich, E., Zhang, Z.M., Vitolins, M.Z., Manson, J.E., Curb, J.D.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7) [Martin, L.W., et al. \(2011\). Use of hundreds of electrocardiographic](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7) [biomarkers for prediction of mortality in postmenopausal women:](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7) [the Women's Health Initiative. Circ. Cardiovasc. Qual. Outcomes](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7) 4[, 521–532](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref7).

[Gulshan, V., Peng, L., Coram, M., Stumpe, M.C., Wu, D., Nar](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref8)[ayanaswamy, A., Venugopalan, S., Widner, K., Madams, T., Cua](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref8)[dros, J., et al. \(2016\). Development and validation of a deep](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref8) [learning algorithm for detection of diabetic retinopathy in](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref8) [retinal fundus photographs. JAMA](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref8) 316, 2402–2410.

<span id="page-7-2"></span>Hatipoglu, N., and Bilgin, G. (2014). Classification of histopathological images using convolutional neural network. Paper presented at: 2014 4th International Conference on Image Processing Theory, Tools and Applications (IPTA).

<span id="page-7-16"></span>He, K., Zhang, X., Ren, S., and Sun, J. (2015). Deep residual learning for image recognition. <https://doi.org/10.1109/CVPR.2016.90>.

[Heylman, C., Datta, R., Sobrino, A., George, S., and Gratton, E.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref11) [\(2015\). Supervised machine learning for classification of the elec](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref11)[trophysiological effects of chronotropic drugs on human induced](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref11) [pluripotent stem cell-derived cardiomyocytes. PLoS One](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref11) 10, [e0144572.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref11)

[Hinton, G.E., Osindero, S., and Teh, Y.W. \(2006\). A fast learning al](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref12)[gorithm for deep belief nets. Neural Comput.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref12) 18, 1527–1554.

[Hsich, E., Gorodeski, E.Z., Blackstone, E.H., Ishwaran, H., and La](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref13)[uer, M.S. \(2011\). Identifying important risk factors for survival in](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref13) [patient with systolic heart failure using random survival forests.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref13) [Circ. Cardiovasc. Qual. Outcomes](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref13) 4, 39–45.

<span id="page-7-9"></span>[Hu, B.Y., Weick, J.P., Yu, J., Ma, L.X., Zhang, X.Q., Thomson, J.A.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref14) [and Zhang, S.C. \(2010\). Neural differentiation of human induced](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref14) [pluripotent stem cells follows developmental principles but with](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref14) [variable potency. Proc. Natl. Acad. Sci. USA](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref14) 107, 4335–4340.

<span id="page-7-17"></span>Ioffe, S., and Szegedy, C. (2015). Batch normalization: accelerating deep network training by reducing internal covariate shift. ArXiv. <https://arxiv.org/pdf/1502.03167.pdf>.

<span id="page-7-12"></span>[Krizhevsky, A., Sutskever, I., and Hinton, G.E. \(2012\). ImageNet](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref16) [classification with deep convolutional neural networks. In Pro](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref16)[ceedings of the 25th International Conference on Neural Informa](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref16)[tion Processing Systems, F. Pereira, C.J.C. Burges, L. Bottou, and](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref16) [K.Q. Weinberger, eds. \(Curran Associates Inc.\), pp. 1097–1105.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref16)

<span id="page-7-1"></span>[Lecun, Y., Bengio, Y., and Hinton, G. \(2015\). Deep learning. Nature](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref17) 521[, 436–444](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref17).

<span id="page-7-11"></span>[Lecun, Y., Bottou, L., Bengio, Y., and Haffner, P. \(1998\). Gradient](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref18)[based learning applied to document recognition. Proc. IEEE](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref18) 86, [2278–2324](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref18).

[Lindblom, P., Gerhardt, H., Liebner, S., Abramsson, A., Enge, M.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref19) [Hellstrom, M., Backstrom, G., Fredriksson, S., Landegren, U., Ny](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref19)[strom, H.C., et al. \(2003\). Endothelial PDGF-B retention is required](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref19) [for proper investment of pericytes in the microvessel wall. Genes](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref19) Dev. 17[, 1835–1840](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref19).

<span id="page-7-3"></span>[McCulloch, W.S., and Pitts, W. \(1943\). A logical calculus of the](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref20) [ideas immanent in nervous activity. Bull. Math. Biol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref20) 5, 115–133.

<span id="page-7-14"></span>[Niioka, H., Asatani, S., Yoshimura, A., Ohigashi, H., Tagawa, S., and](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref21) [Miyake, J. \(2018\). Classification of C2C12 cells at differentiation by](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref21) [convolutional neural network of deep learning using phase](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref21) [contrast images. Hum. Cell](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref21) 31, 87–93.

[Osafune, K., Caron, L., Borowiak, M., Martinez, R.J., Fitz-Gerald,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref22) [C.S., Sato, Y., Cowan, C.A., Chien, K.R., and Melton, D.A. \(2008\).](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref22) [Marked differences in differentiation propensity among human](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref22) [embryonic stem cell lines. Nat. Biotechnol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref22) 26, 313–315.

<span id="page-7-10"></span>[Patsch, C., Challet-Meylan, L., Thoma, E.C., Urich, E., Heckel, T.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref23) [O'Sullivan, J.F., Grainger, S.J., Kapp, F.G., Sun, L., Christensen, K.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref23) [et al. \(2015\). Generation of vascular endothelial and smooth mus](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref23)[cle cells from human pluripotent stem cells. Nat. Cell Biol.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref23) 17, 994– [1003](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref23).

<span id="page-7-13"></span>Saha, S., and Vemuri, R. (2000). An analysis on the effect of image activity on lossy coding performance. Paper presented at: 2000 IEEE International Symposium on Circuits and Systems Emerging Technologies for the 21st Century Proceedings (IEEE Cat No 00CH36353).



<span id="page-8-3"></span>Simonyan, K., and Zisserman, A. (2014). Very deep convolutional networks for large-scale image recognition. ArXiv. [https://arxiv.](https://arxiv.org/pdf/1409.1556.pdf) [org/pdf/1409.1556.pdf](https://arxiv.org/pdf/1409.1556.pdf).

Szegedy, C., Liu, W., Jia, Y., Sermanet, P., Reed, S., Anguelov, D., Erhan, D., Vanhoucke, V., and Rabinovich, A. (2014). Going deeper with convolutions. ArXiv. [https://arxiv.org/pdf/1409.4842.pdf.](https://arxiv.org/pdf/1409.4842.pdf)

<span id="page-8-0"></span>[Takahashi, K., and Yamanaka, S. \(2006\). Induction of pluripotent](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref27) [stem cells from mouse embryonic and adult fibroblast cultures](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref27) [by defined factors. Cell](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref27) 126, 663–676.

[Takakura, N., Watanabe, T., Suenobu, S., Yamada, Y., Noda, T., Ito,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref28) [Y., Satake, M., and Suda, T. \(2000\). A role for hematopoietic stem](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref28) [cells in promoting angiogenesis. Cell](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref28) 102, 199–209.

<span id="page-8-2"></span>[Tanaka, A., Yuasa, S., Mearini, G., Egashira, T., Seki, T., Kodaira, M.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref29) [Kusumoto, D., Kuroda, Y., Okata, S., Suzuki, T., et al. \(2014\). Endo](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref29)[thelin-1 induces myofibrillar disarray and contractile vector vari](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref29)[ability in hypertrophic cardiomyopathy-induced pluripotent](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref29) [stem cell-derived cardiomyocytes. J. Am. Heart Assoc.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref29) 3, e001263. [Van Valen, D.A., Kudo, T., Lane, K.M., Macklin, D.N., Quach, N.T.,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref30) [DeFelice, M.M., Maayan, I., Tanouchi, Y., Ashley, E.A., and Covert,](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref30) [M.W. \(2016\). Deep learning automates the quantitative analysis of](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref30) [individual cells in live-cell imaging experiments. PLoS Comput.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref30) Biol. 12[, e1005177](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref30).

Yuan-Hsiang, C., Abe, K., Yokota, H., Sudo, K., Nakamura, Y., Cheng-Yu, L., and Ming-Dar, T. (2017). Human induced pluripotent stem cell region recognition in microscopy images using convolutional neural networks. Annual International Conference of the IEEE Engineering in Medicine and Biology Society 2017, 4058–4061.

<span id="page-8-1"></span>[Yuasa, S., and Fukuda, K. \(2008\). Cardiac regenerative medicine.](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref32) Circ. J. 72 (Suppl A[\), A49–A55](http://refhub.elsevier.com/S2213-6711(18)30175-9/sref32).

Zeng, X., Ouyang, W., Yan, J., Li, H., Xiao, T., Wang, K., Liu, Y., Zhou, Y., Yang, B., Wang, Z., et al. (2016). Crafting GBD-Net for object detection. ArXiv. [https://arxiv.org/pdf/1610.02579.pdf.](https://arxiv.org/pdf/1610.02579.pdf)

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## Supplemental Information

## Automated Deep Learning-Based System to Identify Endothelial Cells

## Derived from Induced Pluripotent Stem Cells

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## **Supplemental Figure Legends**

## **Figure S1. Generation of iPSC-derived Endothelial Cells**

(A) Differentiation of endothelial cells. iPSCs were seeded onto Matrigel-coated dishes, cultured in indicated conditions, and examined at day 6.

(B) Phase-contrast images at day 1 to 6. Scale bars, 500 µm.

(C) Phase-contrast images (upper panels), immunofluorescent staining for CD31 (middle panels), and FACS analysis (bottom panels) showed variability in differentiation at day 6 in various experiments. Left, middle, and right panels show experiments with high, intermediate, and low differentiation efficiency. Scale bars,  $200 \mu m$ .

## **Figure S2. Network Performance Depending on Input Block Size, Staining Threshold and Target Block Size, Related to Figure 2, Tables S1 and S2.**

(A) Phase-contrast and binarized fluorescent images of  $512 \times 512$  px,  $256 \times 256$  px,  $128 \times 128$  px,  $64 \times 64$  px, and 32  $\times$  32 px blocks. Scale bars, 80 µm, 40 µm, 20 µm, 10 µm, and 5 µm, respectively.

(B) and (C) Accuracy obtained from networks trained on  $32 \times 32$  px,  $64 \times 64$  px,  $128 \times 128$  px,  $256 \times 256$  px, and  $512 \times 512$  px input blocks, using 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, and 0.9 as staining threshold, *i.e.*, the ratio of white pixels to black for a binarized image to be classified as stained..

(D) F1 score and accuracy obtained from networks trained on input and target blocks of various sizes.

### **Figure S3. Optimization of Network Performance, Related to Figure 3.**

(A) Learning curve of the small and large network, as assessed by accuracy.

(B) Representative images of true positives and true negatives (blue) and of false positives and false negatives (red). Yellow areas are CD31-stained. Scale bars, 200  $\mu$ m.

#### **Figure S4. Correlation Between Image Complexity and F1 score, Related to Figure 3.**

(A) Representative phase-contrast images with complexity 0.00-0.04 (group 1), 0.04-0.08 (group 2), and over 0.08 (group 3). Scale bars,  $80 \mu m$ .

(B) F1 score in each group using the small and large network (left), and relationship between F1 score and image complexity (right).

(C) and (D) Performance statistics from each group (C) and over increasing complexity (D). True positive: TP, True negative: TN, False positive: FP, and False negative: FN

(E) Time required to classify each block.

## **Supplemental Table Legends**

## **Table S1. Number of Blocks Required for Learning, Related to Figure 2.**

Networks were trained on 500, 1,000, 2,000, 4,000, 8,000, 16,000, 32,000, 64,000, and 128,000 blocks. Accuracy, recall, precision, and F1 score were assessed using  $128 \times 128$  px input blocks and  $128 \times 128$  px target blocks (left), or using  $512 \times 512$  px input blocks and  $32 \times 32$  px target blocks (right).

## **Table S2. Network Performance Depending on Input Block Size and Staining Threshold, Related to Figures 2 and S2.**

Networks were trained using  $32 \times 32$  px,  $64 \times 64$  px,  $128 \times 128$  px,  $256 \times 256$  px, and  $512 \times 512$  px input blocks, using 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, and 0.9 as staining threshold, *i.e.*, the ratio of white pixels to black for a binarized image to be classified as stained. Accuracy, recall, precision, and F1 score were calculated.

## **Table S3. Network Performance Depending on Target Block Size, Related to Figures 2 and S2.**

F1 score, accuracy and other indices obtained from networks trained on input and target blocks of various sizes.

## **Table S4. Network Performance, Related to Figures 3 and 4.**

(A) Network performance was compared following training on automatically binarized or rebinarized fluorescent images.

(B) K-fold cross validation of the small network trained on automatically binarized fluorescent images (left), and of the large network trained on rebinarized fluorescent images (right). Independent training and validation were performed according to Figure 4.

## **Supplemental Experimental Procedures**

## **iPSC Culture**

iPSCs were maintained in mTeSR1 (Stem Cell Technologies, Vancouver, BC, Canada) media with 0.5 % penicillin/streptomycin (Thermo Fisher Scientific, Waltham, MA, USA) on culture dishes coated with growth factorreduced Matrigel (BD Biosciences, San Jose, CA, USA). iPSCs were routinely passaged every week by washing in PBS, incubating in TrypLE Select (Thermo Fisher Scientific) for 3 min at 37 °C, detaching with a cell scraper, harvesting, and reseeding at a split ratio of 1:5 to 1:8 in mTeSR1 with 0.5 % penicillin/streptomycin and 10 µM ROCK inhibitor Y-27632 (Wako, Osaka, Japan). Media were changed every other day.

## **Endothelial Cell Differentiation**

iPSCs cultured on Matrigel-coated 6-well plates were detached using TrypLE Select on day 7, and clumps with diameter 100-200 µm were reseeded on Matrigel-coated dishes and incubated for 24 hours in mTeSR1 media with 10 µM ROCK inhibitor Y-27632. On day 1, mesoderm was induced in N2B27 media (1:1 mixture of DMEM/F12 and Neurobasal media containing N2 and B27, all reagents from Thermo Fisher Scientific) supplemented with βmercaptoethanol, 8 µM CHIR-99021 (Cayman Chemical, Ann Arbor, MI, USA), and 25 ng/mL BMP4 (R&D Systems, Minneapolis, MN, USA). At day 3 and 4, media were replaced with StemPro-34 SFM (Thermo Fisher Scientific) containing 200 ng/mL VEGF (Wako) and 2 µM forskolin (Abcam, Cambridge, UK) to induce endothelial cell specification (Patsch et al., 2015). Endothelial cell clusters were reliably obtained on day 6. After sorting by flow cytometry, cells expressing CD31 were cultured for another four days in StemPro-34 SFM containing 50 ng/mL VEGF.

## **Flow Cytometry**

At day 6 of differentiation, cells were dissociated into singe cells using Accutase (Innovative Cell Technologies, San Diego, CA, USA), suspended in PBS with 0.5 % BSA, and stained with a 1:50 dilution of APC-conjugated anti-CD31 (Miltenyi Biotec, Bergisch Gladbach, NRW, Germany, catalog no. 130-092-652) according to the manufacturer's instructions. As a negative control, we used unstained cells. Cells were then sorted on a BD FACS Aria III (Becton Dickinson, Franklin Lakes, NJ, USA), and data were collected from at least 10,000 events.

## **Immunocytochemistry**

Cells were fixed in 4 % paraformaldehyde (MUTO Pure Chemicals, Tokyo, Japan) for 20 min at room temperature, washed with PBS, blocked with ImmunoBlock (DS Pharma Biomedical, Osaka, Japan) for 1 h, and probed at 4 °C overnight with 1:20 primary antibodies to CD31 (R&D Systems, catalog no. AF806). Specimens were then washed thrice in PBS, labeled for 1 h with 1:200 secondary anti-sheep IgG (Thermo Fisher Scientific, catalog no. A-11015), and imaged on an inverted fluorescence phase-contrast microscope.

## **Preparation of Datasets**

Phase-contrast and immunofluorescent images were acquired at day 6 of differentiation. Two hundred images were automatically acquired from each of four independent experiments. Phase contrast and fluorescent images were taken on an SI8000 Research Microscope (SONY, Tokyo, Japan) at  $10\times$  and 0.454  $\mu$ m/pixel. Each image was saved as a

 $2752 \times 2200$  px grayscale image in BMP format at 8 bits per pixel. To generate datasets for training and evaluation, 200 input blocks of  $32 \times 32$  px,  $64 \times 64$  px,  $128 \times 128$  px,  $256 \times 256$  px, and  $512 \times 512$  px were randomly extracted from each phase-contrast image. The  $256 \times 256$  px and  $512 \times 512$  px input blocks were resized to  $128 \times 128$  px as needed. Immunofluorescent images of CD31 were binarized using in-house software to distinguish specific signals from nonspecific signals. In particular, pixels were binarized to white if its value (0-255 in raw immunofluorescent images) is above a threshold value empirically determined based on the complete image. All other pixels were binarized to black. Finally,  $32 \times 32$  px and  $128 \times 128$  px target blocks were extracted, corresponding to the center of input blocks.

Data in Figure 2 and 3 were generated based on 640 training images and 160 validation images. In both experiments in Figure 2A, 500, 1,000, 2,000, 4,000, 8,000, 16,000, 32,000, 64,000, and 128,000 blocks were used for training, and 32,000 blocks were used for validation. In Figure 2B, 32,000 blocks were used for training, and 32,000 blocks were used for validation. In Figure 2C to 3E, all 128,000 blocks were used for training, and 32,000 blocks were used for validation. For K-fold validation in Figure 4, four independent data sets of 200 images each were obtained, of which three were used as training sets and one was used as validation set in all possible combinations, such that the number of folds is 4. To rebinarize target blocks, we compared raw fluorescent images to phase-contrast images in GNU Image Manipulation Program, and rebinarized weakly stained, dense colonies as black pixels. All 800 images were processed in this manner.

## **Deep Neural Networks**

We used LeNet, a small convolutional neural network with two convolution layers, two max pooling layers, and two fully-connected layers, as well as AlexNet, a large network with five convolution layers, three max pooling layers, and three fully-connected layers (Figure 3A). In both networks, each convolutional layer is connected to Rectified Linear Units for activation (Nair and Hinton, 2010). In the output layer, we used a sigmoid function, consistent with binary classification. We used mini-batch training with stochastic gradient descent, learning rate 0.01, cross-entropy error as loss function. Weights were initialized using the Xavier algorithm (Glorot and Bengio, 2010). To avoid overfitting, dropout techniques were used in the large network. Networks were trained using the TensorFlow/Keras framework (Cholle, 2015) on a computer with a Core i7-6700 CPU (Intel, Santa Clara, CA, USA), 16 GB memory, and GeForce GTX980Ti GPU (NVIDIA, Santa Clara, CA, USA).

## **Image Complexity**

We calculated image complexity (activity), which we used as an index of cell density, in all  $32,000\,512 \times 512$  px validation blocks used in the small and large network. This value was  $Activity = \frac{\sum_{i=0}^{m-2} \sum_{j=0}^{n-1} |I(i,j) - I(i+1,j)| + \sum_{i=0}^{m-1} \sum_{j=0}^{n-2} |I(i,j) - I(i,j+1)|}{(m-1)n + m(n-1) \cdot (m\alpha x(L) - m(n-1))}$ 



calculated according to

where m is the image width in pixels, n is the image height in pixels, *I* is the pixel value, and *(i, j)* are coordinates (xaxis, y-axis). Essentially, image complexity is the average difference between adjacent pixels normalized to the dynamic range (Saha and Vemuri, 2000). Thus, the numerator is the sum of differences in adjacent pixels on both x

 $\{(m-1)n + m(n-1)\}\$  {max(*l*) – min(*l*)}

and y axes, while the denominator is the product of image size and dynamic range, which is the difference between the maximum and minimum pixel value.

## **Evaluation of Prediction Performance**

Network performance was evaluated based on accuracy and F1 score, which combines recall (sensitivity) and precision (true positive rate). Accordingly, the F1 score is 1 for perfect predictions and 0.5 for random predictions. On the other hand, precision is the fraction of true positives among predicted positives, while recall is the fraction of true positives detected among all positives:

$$
F1 score = \frac{2Recall \times Precision}{Recall + Precision}, Precision = \frac{TP}{TP + FP}, Recall = \frac{TP}{TP + FN}
$$

Precision and recall for negative predictions were calculated in a similar manner:

$$
Precision \ (negative) = \frac{TN}{TN + FN}, Recall \ (negative) = \frac{TN}{TN + FP}
$$

Finally, accuracy is the ratio of correct predictions to all predictions:

$$
Accuracy = \frac{TP + TN}{TP + FP + TN + FP}
$$

## **Supplemental References**

Cholle, F. (2015). Keras [\(https://github.com/fchollet/keras:](https://github.com/fchollet/keras:) GitHub).

Glorot, X., and Bengio, Y. (2010). Understanding the difficulty of training deep feedforward neural networks. In Proceedings of the Thirteenth International Conference on Artificial Intelligence and Statistics, T. Yee Whye, and T. Mike, eds. (Proceedings of Machine Learning Research: PMLR), pp. 249--256.

Nair, V., and Hinton, G.E. (2010). Rectified linear units improve restricted Boltzmann machines. In Proceedings of the 27th International Conference on International Conference on Machine Learning (Haifa, Israel: Omnipress), pp. 807-814.

Patsch, C., Challet-Meylan, L., Thoma, E.C., Urich, E., Heckel, T., O'Sullivan, J.F., Grainger, S.J., Kapp, F.G., Sun, L., Christensen, K., et al. (2015). Generation of vascular endothelial and smooth muscle cells from human pluripotent stem cells. Nat Cell Biol 17, 994-1003.

Saha, S., and Vemuri, R. (2000). An analysis on the effect of image activity on lossy coding performance. Paper presented at: 2000 IEEE International Symposium on Circuits and Systems Emerging Technologies for the 21st Century Proceedings (IEEE Cat No00CH36353).

## Supplementary Figure 1





C

Differentiation efficiency





## Supplementary Figure 3



## Supplementary Figure 4



E Small network: 100 usec

Large network: 275 µsec

## Supplementary Table 1

500

1,000

2,000

4,000

8,000

Pred = "Prediction" ; Ans = "Answer" ; 0 = "unstained" ; 1 = "stained"

Input block size: 128 x 128 (px) Target block size:  $128 \times 128$  (px) Pred=0 Pred=1 Total Recall<br>
21,261 0 21,261 1<br>
10,739 0 10,739 0 Ans=0 | 21,261 | 0 | 21,261 | 1 | | Ans=0 | 21,148 | 0 | 21,148 | 1 Ans=1 | 10,739 | 0 | 10,739 | 0 | | Ans=1 | 10,852 | 0 | 10,852 | 0 Total 32,000 0 32,000 Total 32,000 0 32,000 Precision | 0.6644 | 0 | | | | | Precision | 0.6609 | 0 F1 score 0.7984 0 F1 score 0.7958 0 Accuracy 0.6644 Pred=0 | Pred=1 | Total | Recall | | | Pred=0 | Pred=1 | Total | Recall Ans=0 | 21,261 | 0 | 21,261 | 1 | | Ans=0 | 21,148 | 0 | 21,148 | 1 Ans=1 | 10,737 | 2 | 10,739 | 0.0002 | | Ans=1 | 10,852 | 0 | 10,852 | 0 Total | 31,998 | 2 | 32,000 | | | Total | 32,000 | 0 | 32,000 Precision 0.6644 1<br>F1 score 0.7984 0.0004 F1 score | 0.7984 | 0.0004 | | | F1 score | 0.7958 | 0 Accuracy 0.6645 Pred=0 | Pred=1 | Total | Recall | Pred=0 | Pred=1 | Total | Recall Ans=0 21,261 0 21,261 1 Ans=0 21,129 19 21,148 0.9991 Ans=1 | 10,738 | 1 | 10,739 | 0.0001 | | Ans=1 | 10,774 | 78 | 10,852 | 0.0072 Total 31,999 1 32,000 Total 31,903 97 32,000 Precision 0.6644 1<br>F1 score 0.7984 0.0002 F1 score | 0.7984 | 0.0002 | | | F1 score | 0.7966 | 0.0142  $Accuracy$  0.6644 Pred=0 Pred=1 Total Recall Pred=0 Pred=1 Total Recall Ans=0 | 20,913 | 348 | 21,261 | 0.9836 | | Ans=0 | 18,684 | 2,464 | 21,148 | 0.8835 Ans=1 | 9,901 | 838 | 10,739 | 0.078 | | Ans=1 | 8,276 | 2,576 | 10,852 | 0.2374 Total 30,814 1,186 32,000 Total 26,960 5,040 32,000 Precision | 0.6787 | 0.7066 | |Precision | 0.693 | 0.5111 F1 score 0.8032 0.1405 F1 score 0.7768 0.3242 Accuracy| 0.6797 | | | Accuracy| 0.6644 Pred=0 | Pred=1 | Total | Recall | | | Pred=0 | Pred=1 | Total | Recall Ans=0 | 18,933 | 2,328 | 21,261 | 0.8905 | | Ans=0 | 18,836 | 2,312 | 21,148 | 0.8907 Ans=1 6,646 4,093 10,739 0.3811 Ans=1 6,514 4,338 10,852 0.3997 Total 25,579 6,421 32,000 Total 25,350 6,650 32,000 Precision 0.7402 0.6374 Precision 0.743 0.6523 F1 score 0.8084 0.477<br>Accuracy 0.7196 Accuracy



32,000

16,00

Number of input blocks

Number of input blocks



64,000



128,000





## Pred = "Prediction" : 0 = "unstained" , 1 = "stained" Ans = "Answer" : 0 = "unstained" , 1 = "stained"

## Input block size (px)



F1 score 0.846 0.324 F1 score 0.8645 0.3405 F1 score 0.8763 0.4093 F1 score 0.8902 0.4089 F1 score 0.9032 0.4654 Accuracy 0.7491 Accuracy 0.7752 Accuracy 0.7954 Accuracy 0.8147 Accuracy 0.836

Pred = "Prediction" : 0 = "unstained" , 1 = "stained" Ans = "Answer" : 0 = "unstained" , 1 = "stained"

## Target block size: 32 x 32 (px) Target block size: 128 x 128 (px)

Pred=0 Pred=1 Total Recall

32 x 32



Ans=0 17,991 2,394 20,385 0.8826 Ans=1 | 5,533 | 6,082 | 11,615 | 0.5236 Total 23,524 8,476 32,000

Precision 0.7648 0.7176 F1 score 0.8195 0.6054

Accuracy 0.7523

64 x 64





256 x 256



512 x 512









## Supplementary Table 4

Rebinarized

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A

## Small network **Large network**









## B

Small network Automatically binarized Large network

	$Pred = 0$	$Pred = 1$	Total	Recall
Ans= $0$	17,764	12,928	30,692	0.5788
Ans=1	488	8,820	9,308	0.9476
Total	18,252	21,748	40,000	
Precision	0.9733	0.4056		
F1 score	0.7259	0.568		
Accuracy	0.6646			







# Large network<br>Rebinarized







