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## Directed Differentiation of Hemogenic Endothelial Cells from Human Pluripotent Stem Cells

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**TITLE:**

Directed Differentiation of Hemogenic Endothelial Cells from Human Pluripotent Stem Cells

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**KEYWORDS:**

pluripotent human stem cells, human endothelial cells, hemogenic endothelial cells, arterial endothelial cells, cell culture protocol, directed differentiation

**SUMMARY:**

Presented here is a simple protocol for the directed differentiation of hemogenic endothelial cells from human pluripotent stem cells in approximately 1 week.

**ABSTRACT:**

Blood vessels are ubiquitously distributed within all tissues of the body and perform diverse functions. Thus, derivation of mature vascular endothelial cells, which line blood vessel lumens, from human pluripotent stem cells is crucial for a multitude of tissue engineering and regeneration applications. In vivo, primordial endothelial cells are derived from the mesodermal lineage and are specified toward specific subtypes, including arterial, venous, capillary, hemogenic, and lymphatic. Hemogenic endothelial cells are of particular interest because, during development, they give rise to hematopoietic stem and progenitor cells, which then generate all blood lineages throughout life. Thus, creating a system to generate hemogenic endothelial cells in vitro would provide an opportunity to study endothelial-to-hematopoietic transition, and may lead to ex vivo production of human blood products and reduced reliance on human donors. While several protocols exist for the derivation of progenitor and primordial endothelial cells, generation of well-characterized hemogenic endothelial cells from human stem cells has not been described. Here, a method for the derivation of hemogenic endothelial cells from human embryonic stem cells in approximately 1 week is presented: a differentiation protocol with

primitive streak cells formed in response to GSK3 $\beta$  inhibitor (CHIR99021), then mesoderm lineage induction mediated by bFGF, followed by primordial endothelial cell development promoted by BMP4 and VEGF-A, and finally hemogenic endothelial cell specification induced by retinoic acid. This protocol yields a well-defined population of hemogenic endothelial cells that can be used to further understand their molecular regulation and endothelial-to-hematopoietic transition, which has the potential to be applied to downstream therapeutic applications.

## INTRODUCTION:

Endothelial cells (ECs) are a heterogeneous population of cells that perform multiple functions throughout the human body and in engineered tissues. In addition to supporting and regulating other cell types (i.e., cardiomyocytes<sup>1</sup>, osteoblastic cells<sup>2</sup>), these functions include forming a selective barrier between blood and tissues and assisting in tissue formation<sup>3</sup>. Differentiation of mature ECs during normal development requires diverse signaling pathways. Primordial ECs are derived from mesoderm progenitors, and are then specified toward mature arterial, venous, capillary and lymphatic phenotypes<sup>4</sup>. Additionally, a small subset of ECs in the extraembryonic yolk sac and embryonic Aorta-Gonad-Mesonephros (AGM) region are also specified to become hemogenic ECs, which give rise to hematopoietic stem and progenitor cells (HSPCs) that migrate to the fetal liver and fetal bone marrow, where they remain postnatally and generate all blood cell types throughout life<sup>4</sup>. The diverse range of EC phenotypes is essential for all tissue development and maintenance.

Thus, ECs and their derivatives are critical components of studies aimed at modeling, and elucidating mechanisms of, human development and/or disease, as well as regenerative medicine and tissue engineering applications<sup>5-8</sup>. However, the main limitation for these types of studies is the lack of availability of primary human ECs in the quantity required. It has been estimated that a minimum of  $3 \times 10^8$  ECs would be required for the majority of therapeutic applications<sup>6</sup>. To solve this problem, the use of human embryonic stem cells (hESCs) and human induced pluripotent stem cells (hiPSCs) has been proposed due to their diverse lineage potential and their ability to generate large numbers of progeny<sup>6,9</sup>.

Indeed, the usefulness of cells derived from hESCs or hiPSCs has been demonstrated in multiple studies focused on disease modeling and drug screening<sup>10-12</sup>. Organ-on-a-Chip (OOC) technology has been used to more faithfully recapitulate the physiology of the human body by integrating cells and tissues into three-dimensional scaffolds. Furthermore, connection of multiple individual OOCs (a so-called body- or human-on-a-chip, BOC/HOC) can be accomplished via microfluidics to allow for crosstalk between the organs of interest<sup>13-15</sup>. Supporting tissues, such as the vasculature, are critical components of OOCs and BOC/HOCs; incorporating vasculature allows for the transport of nutrients, oxygen, and paracrine factors throughout the tissues, thereby promoting the requisite tissue-specific microenvironment<sup>3,12</sup>. Thus, methods for deriving mature human ECs, such as arterial, venous, lymphatic, and hemogenic ECs, are crucial to advancing these tissue engineering approaches.

Multiple protocols have been published detailing steps for the derivation of human primordial or progenitor ECs from hESCs or hiPSCs<sup>5,16-26</sup>. Many of these protocols rely on embryoid body (EB)

formation or co-culture of ESCs/iPSCs with a murine feeder layer of stromal cells. These strategies tend to be difficult and time consuming, with low EC yields and/or contamination of human ECs with murine cells. Protocols that rely strictly on 2D culture without the use of stromal cells often require long inductions, utilize complex combinations of growth factors and/or inhibitors for induction, have extended expansion periods following cell separation, or a combination of these factors. Advancing knowledge of signaling pathways and factors involved in the derivation of mature EC types in vivo provides the groundwork for a straightforward and robust in vitro differentiation protocol.

Previously, key roles for Notch and Retinoic Acid (RA) signaling pathways in the specification of murine arterial and hemogenic ECs, respectively, during development were identified. The Notch signaling pathway plays multiple roles in the specification and maintenance of the arterial EC phenotype. Work using the murine retinal vascularization model identified a pathway in which fluid shear stress induces a Notch-Cx37-p27 signaling axis, promoting G1 cell cycle arrest, which enables arterial EC specification<sup>27</sup>. Cell cycle states have been hypothesized to play a role in cell fate decisions by providing distinct windows of opportunity in which cells are receptive to certain signals that can induce gene expression and phenotypic changes<sup>28</sup>. This Notch-mediated G1 arrest enabled the expression of genes enriched in arterial ECs, including ephrinB2, Cx40, DLL4, Notch1, and Notch 4 (reviewed in<sup>29,30</sup>). It has also been shown that hemogenic EC specification is promoted in vivo via RA signaling<sup>31,32</sup>. Additional studies identified that, downstream of RA signaling, expression of c-Kit and Notch upregulate p27, which enables hemogenic specification in the murine yolk sac and AGM<sup>33</sup>. Murine hemogenic ECs can be minimally identified by expression of both endothelial (i.e., CD31, KDR) and hematopoietic (i.e., c-Kit, CD34) markers<sup>4</sup>. Finally, hemogenic ECs undergo an endothelial-to-hematopoietic transition (EHT) to form HSPCs, which can give rise to all blood cell types<sup>4,34,35</sup>.

Recent work tested whether this same signaling hierarchy can promote human hemogenic EC specification. To do so, a serum- and feeder-free 2D culture protocol to derive hemogenic ECs from hESCs was developed, and these hemogenic ECs were characterized on a single cell level as CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup>. This study also took advantage of the Fluorescent Ubiquitination Cell Cycle Indicator (FUCCI) reporter, which identifies different cell cycle states, using H9-hESCs that express the FUCCI reporter construct (H9-FUCCI-hESC)<sup>36</sup>. In studies with these cells, it was demonstrated that RA promotes early G1 cell cycle arrest in ECs, and early G1 state enables hemogenic specification in vitro<sup>37</sup>. Herein, a detailed protocol for the differentiation of these human hemogenic endothelial cells and assays confirming their identity are provided. This straightforward method provides a useful means of generating this specialized subset of ECs for future studies of mechanisms of human blood cell development.

## **PROTOCOL:**

### **1. Reagents and reagent preparation**

NOTE: A list of reagents is provided in **Table of Materials**.

1.1. Obtain the human pluripotent stem cell lines: H1-hESC, H9-Fucci-hESC.

NOTE: The generation of hemogenic ECs may be more efficient in the H1 cell line.

1.2. Prepare matrix protein stocks: Aliquot the matrix protein into pre-chilled 1.5 mL tubes (on ice) so that each tube contains 1 mg of matrix protein. 1 mg of matrix protein is enough to coat all wells of two 6-well plates (12 wells total). Store the aliquots at -20 °C until use.

NOTE: Perform all the steps involving matrix protein on ice or at 4 °C. Thaw the frozen stock vial of matrix protein on ice at 4 °C overnight. Once thawed, swirl the vial to ensure the contents are mixed. Prechill 1.5 mL microcentrifuge tubes for at least 1 h at -20 °C and transfer to ice immediately prior to aliquoting.

1.3. Prepare matrix protein-coated plates: Thaw matrix protein aliquots on ice at 4 °C. Add 12.5 mL of ice-cold DMEM:F12 to a prechilled conical tube on ice. Utilizing pre-chilled pipette tips, transfer one aliquot (1 mg) of matrix protein to the conical tube and mix well by pipetting up and down. Aliquot 1 mL of the diluted matrix protein to each well of pre-chilled 6-well plates (on ice) using a pre-chilled serologic pipette. Swirl and rock the plates so that the entire well is coated evenly. Incubate the plates for a minimum of 30 min at room temperature to allow the matrix protein to solidify. Wrap the plates with parafilm and store at 4 °C until use. Use matrix protein-coated plates within 2 weeks of preparation.

NOTE: Use the matrix protein-coated 6-well plates for routine passaging of cells and differentiation to primordial and hemogenic endothelial cells. Perform all the steps on ice. Pre-chill 6-well plates, pipette tips, serologic pipettes, and conical tubes prior to use for at least 1 h at -20 °C. Transfer these items to ice when ready to use.

1.4. Prepare the base differentiation medium by adding 5 mL of PFHM to 100 mL of pluripotent stem cell differentiation medium. Store at 4 °C.

1.5. Prepare 0.1% BSA-PBS by dissolving 0.1 g BSA in 100 mL PBS. Filter sterilize BSA-PBS by passing through a 0.22 µm filter and store at 4 °C.

1.6. Prepare 5 mM HCl by diluting stock HCl (12 M) 1:2400 with water. Adjust the pH to 3.0 utilizing NaOH. Filter sterilize the solution by passing through a 0.22 µm filter and store at 4 °C.

1.7. Prepare bFGF, BMP4, VEGF-A, Retinoic Acid (RA), and DLL4 stocks.

1.7.1. bFGF: Reconstitute the lyophilized powder to 100 µg/mL in 0.1% BSA-PBS. Aliquot and store at -20 °C. Use bFGF stocks within 3 months of preparation. Thaw the aliquots immediately prior to use.

1.7.2. BMP4: Reconstitute the lyophilized powder to 1 mg/mL in 5mM HCl, pH 3.0. Further dilute to 50 µg/mL in 0.1% BSA-PBS. Aliquot and store at -20 °C. Use the BMP4 stocks within 3 months of preparation. Thaw the aliquots immediately prior to use.

1.7.3. VEGF-A: Reconstitute the lyophilized powder to 1 mg/mL in dH<sub>2</sub>O. Further dilute to 100 µg/mL in 0.1% BSA-PBS. Aliquot and store at -20 °C. Use the VEGF-A stocks within 3 months of preparation. Thaw the aliquots immediately prior to use.

1.7.4. RA: Reconstitute the lyophilized powder to 100 mM in DMSO. Aliquot and store at -80 °C. Use the RA stocks within 1 month of preparation. Thaw the aliquots immediately prior to use.

NOTE: Protect RA stocks from light.

1.7.5. DLL4: Reconstitute the lyophilized powder to 1 mg/mL in PBS. Aliquot and store at -20 °C. Use the DLL4 stocks within 12 months of preparation. Thaw the aliquots immediately prior to use.

1.8. Prepare the endothelial cell differentiation medium immediately prior to use by diluting VEGF-A and BMP4 in base differentiation medium (step 1.4) so that the final concentrations are 25 ng/mL and 50 ng/mL, respectively.

1.9. Prepare the working RA immediately prior to use by diluting 100 mM stock 1:1,000 in DMSO to 100 µM.

NOTE: Protect working RA from light.

1.10. Prepare the hemogenic endothelial cell differentiation medium immediately prior to use by diluting VEGF-A, BMP4, and working RA in base differentiation medium (step 1.4) so that the final concentrations are 25 ng/mL, 50 ng/mL, and 0.5 µM, respectively.

1.11. Prepare the antibody staining buffer by making HBSS containing 10% FBS and supplement with 1:500 diluted antimicrobial reagent. Sterile filter the buffer and use immediately.

1.12. Prepare the cell sorting buffer by making HBSS containing 1% FBS and supplement with 1:500 diluted antimicrobial reagent. Sterile filter the buffer and use immediately.

1.13. Prepare 1 mg/mL fibronectin stocks by adding 5 mL of sterile water to 5 mg lyophilized fibronectin. Aliquot and store at -20 °C. Use the fibronectin stocks prior to the expiry date on the lyophilized product label. Thaw the aliquots immediately prior to use.

1.14. Prepare the fibronectin-coated 35 mm dishes. Dilute the fibronectin stocks (1 mg/mL) to 4 µg/mL in sterile water. Add 1 mL of this fibronectin coating solution to each dish and incubate at 37 °C for 30 min to 1 h. Use the dishes immediately following coating.

1.15. Prepare 3 or 4 mL aliquots of methylcellulose-based medium following the manufacturer's instructions. Store the aliquots at -20 °C until use. Use the methylcellulose-based medium aliquots prior to the expiry date indicated on the stock product label. Thaw the aliquots immediately prior to use.

1.16. Prepare the DLL4 coating solution by diluting recombinant human DLL4 stock to a final concentration of 10 µg/mL in PBS.

1.17. Prepare and store the endothelial cell growth medium according to the manufacturer's instructions.

1.18. Prepare the flow cytometry analysis buffer by making PBS containing 0.1% BSA. Sterile filter the buffer and store at 4 °C until use.

## **2. Cell culture and passaging of hESCs**

2.1. Allow the matrix protein-coated plates, stem cell growth medium, and DMEM:F12 to warm to room temperature.

2.2. Grow the hESC cell lines in stem cell growth medium (2 mL/well) on matrix protein-coated 6-well plates in a 37 °C, 5% CO<sub>2</sub> incubator.

2.3. Check the cells daily and remove the differentiated cells as necessary by gently scraping them off the plate using a p200 pipette tip.

NOTE: Differentiated cells will appear on the periphery of colonies. Refer to the stem cell growth medium product manual for examples of differentiated cells in culture.

2.4. Passage the cells once they reach 70%–80% confluency. To passage cells, perform the following steps.

NOTE: Cells should be split prior to reaching 70%–80% confluency if increased differentiation occurs.

2.4.1. Remove the medium above the cells and gently wash with 1 mL DMEM:F12 per well.

2.4.2. Add 1 mL of DMEM:F12 per well.

2.4.3. Add 160 µL/mL of Dispase per well and incubate the cells at 37 °C in a 5% CO<sub>2</sub> incubator for 45 min.

2.4.4. Following Dispase incubation, add an additional 1 mL of DMEM:F12 per well and gently pipette to lift the cells.

NOTE: Avoid dissociating the cells into a single-cell suspension. Passage the cells as small clumps.

2.4.5. Transfer the cells to a conical tube containing 12 mL of DMEM:F12 and allow the cells to settle by gravity (~5–10 min).

2.4.6. Remove the supernatant and gently resuspend the pellet in 0.5 mL of stem cell growth medium per well of lifted cells to obtain small clumps of cells.

NOTE: Avoid dissociating the cells into a single-cell suspension. Passage the cells as small clumps.

2.4.7. Aspirate the matrix protein coating solution from the wells of the prepared matrix protein-coated plate and add 1.5 mL of the stem cell growth medium per well.

2.4.8. Add the desired volume of resuspended cells (step 2.4.6) to each well of the prepared matrix protein-coated plate.

2.4.9. Incubate the plate in a 37 °C, 5% CO<sub>2</sub> incubator. Change the medium every 24 h to fresh stem cell growth medium.

### **3. Differentiation of hESCs to primordial endothelial cells**

3.1. Day -1: Culture and passage the cells as described above in section 2. Seed the cells (step 2.4.6) in small clumps (~50 µm) at a density of approximately 2 clumps per square centimeter<sup>38</sup>.

NOTE: Evaluate the seed density and refine empirically if necessary.

3.2. Day 0: 24 h after seeding the cells, aspirate the medium from each well and gently wash the cells with 1 mL DMEM:F12 per well. Add 1 mL of the base differentiation medium containing 5 µM GSK3i (CHIR99021, added fresh) to each well and incubate for 24 h (37 °C, 5% CO<sub>2</sub>).

NOTE: For all the wash steps, slowly add the indicated wash media to the plate by pipetting against the wall of the plate well. Gently swirl the plate so that the entire surface of the well is covered by wash media. Slightly tilt the plate so that the wash media pools at the six o'clock position and carefully aspirate the wash media.

3.3. Day 1: Aspirate the medium from each well and gently wash the cells with 1 mL DMEM:F12 per well. Add 1 mL of the base differentiation medium containing 50 ng/mL bFGF (added fresh, 1:2,000 from frozen stock) to each well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).

3.4. Day 2: Aspirate the medium from each well and gently wash the cells with 1 mL of DMEM:F12 per well. Add 1 mL of the endothelial cell differentiation medium to each well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).



306 3.5. Day 3: Replace the medium above the cells with 1 mL of freshly prepared endothelial cell  
307 differentiation medium per well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).  
308

309 3.6. Day 4: Replace the medium above the cells with 1 mL of freshly prepared endothelial cell  
310 differentiation medium per well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).  
311

312 3.7. Day 5: FACS purify the cells to assess EC phenotype (sections 4–5) or keep in culture and  
313 differentiate towards hemogenic endothelial cells (section 6).  
314

#### 315 **4. FACS purification of primordial endothelial cells**

316  
317 4.1. Aspirate the medium above the cells and gently wash once with 1 mL of DMEM:F12 per  
318 well.  
319

320 4.2. Add 1 mL of cell detachment solution per well and incubate the cells for 12 min in a 37 °C,  
321 5% CO<sub>2</sub> incubator, or until cells have dissociated.  
322

323 4.3. Transfer the dissociated cells to a conical tube containing 12 mL of DMEM:F12 and pellet  
324 by centrifugation for 5 min, 1,000 x *g*.  
325

326 4.4. Remove the supernatant and resuspend the pellet in 12 mL of DMEM:F12 to wash.  
327

328 4.5. Pellet the cells by centrifugation for 5 min, 1,000 x *g*.  
329

330 4.6. Remove the supernatant and resuspend the cell pellet in ice-cold antibody staining buffer  
331 and count the cells. Adjust the concentration using ice-cold antibody staining buffer to 1 x 10<sup>5</sup>  
332 cells/mL.  
333

334 4.7. Divide the cells evenly into microcentrifuge tubes on ice, each containing a minimum of  
335 600 µL cells at 1 x 10<sup>5</sup> cells/mL, for antibody staining.  
336

337 NOTE: Four tubes of cells are required for staining of primordial ECs: unstained control, CD31  
338 single antibody control, CD45 single antibody control, and sample containing both CD31 and  
339 CD45 antibodies. Information about antibodies is provided in **Table of Materials**.  
340

341 4.8. Add antibodies to the tubes containing cells, as appropriate, and incubate on ice and  
342 protected from light for 30 min.  
343

344 4.8.1. Unstained control: Do not add any antibody.  
345

346 4.8.2. CD31 single antibody control: Add only CD31 antibody.  
347

348 4.8.3. CD45 single antibody control: Add only CD45 antibody.  
349

4.8.4. Sample: Add both CD31 and CD45 antibodies.

NOTE: The final antibody concentration in the sample, as well as the fluorescent conjugates, should be optimized based on the specific antibodies and cell sorter used.

4.9. Pellet the cells by centrifugation in a 4 °C tabletop microcentrifuge for 5 min at 1,000 x *g*.

4.10. Remove the supernatant and resuspend the cell pellets in 600 µL of ice-cold sorting buffer.

4.11. Strain the samples through the mesh filter caps of 5 mL FACS tubes and store the cells on ice, protected from light, for immediate FACS.

4.12. Obtain primordial endothelial cells (CD31<sup>+</sup> CD45<sup>-</sup>), by performing the following steps.

4.12.1. Identify the CD45-negative cell population and gate (CD45<sup>-</sup>).

4.12.2. Within (CD45<sup>-</sup>), identify the CD31-positive (CD31<sup>+</sup>) cell population and sort cells into 6 mL ice-cold cell sorting buffer. Use these cells for downstream applications (see section 5).

## **5. Assay to confirm primordial endothelial cell phenotype**

5.1. Coat three wells of a 6-well plate with 1 mL/well DLL4 coating solution for 30 min in a 37 °C, 5% CO<sub>2</sub> incubator. As a control, mock-coat the other three wells of the plate with 1 mL/well PBS.

5.2. Aspirate the DLL4 coating solution and PBS, and plate 25,000 sorted primordial endothelial cells (see step 4.12) in 2 mL of endothelial cell growth medium per well.

5.3. Incubate the cells for 24 h in a 37 °C, 5% CO<sub>2</sub> incubator.

5.4. Aspirate the medium above the cells and wash once with 2 mL/well PBS. Analyze the cells by qPCR or flow cytometry (for cells expressing the Fucci construct).

5.4.1. To analyze the cells by qPCR, perform the following steps.

5.4.1.1. Aspirate the liquid above the cells and isolate the RNA in the cells using an RNA extraction kit according to the manufacturer's protocol.

5.4.1.2. Perform reverse transcription reactions with a reverse transcription master mix according to the manufacturer's protocol.

5.4.1.3. Perform qPCR reactions with a SYBR Green master mix according to the manufacturer's protocol.

NOTE: Primers utilized (EFNB2, GJA5, GJA4, NR2F2, EPHB4, HEY2) are listed in **Table 1**.

5.4.2. To analyze cells expressing the Fucci construct by flow cytometry, perform the following steps.

5.4.2.1. Aspirate the liquid above the cells and add 500  $\mu$ L/well 0.25% trypsin-EDTA.

5.4.2.2. Incubate the cells at 37 °C in a 5% CO<sub>2</sub> incubator until lifted, ~5 min.

5.4.2.3. Transfer the cells to a microcentrifuge tube and pellet the cells in a 4 °C microcentrifuge for 5 min at 1,000 x *g*.

5.4.2.4. Aspirate the supernatant and resuspend the pellet in 500  $\mu$ L of ice-cold flow cytometry analysis buffer.

5.4.2.5. Strain the samples through the mesh filter cap of a 5 mL FACS tube and store the cells on ice, protected from light, for immediate flow cytometry analysis.

5.4.2.6. Analyze the percentage of cells plated on DLL4 vs. PBS control in early G1 (no color), late G1 (mCherry<sup>+</sup>/mVenus<sup>-</sup>), G1/S (mCherry<sup>+</sup>/mVenus<sup>+</sup>), and S/G2/M (mCherry<sup>-</sup>/mVenus<sup>+</sup>).

## **6. Differentiation of hESCs to hemogenic endothelial cells**

NOTE: Differentiate the cells to day 4 primordial ECs, as described above in sections 3.1–3.6.

6.1. Day 5: Aspirate the medium above the cells and gently wash the cells with 1 mL of DMEM:F12 per well. Add 1 mL of freshly prepared hemogenic endothelial cell differentiation medium per well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).

6.2. Day 6: Replace the medium above the cells with 1 mL of freshly prepared hemogenic endothelial cell differentiation medium per well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).

6.3. Day 7: Replace the medium above the cells with 1 mL of freshly prepared hemogenic endothelial cell differentiation medium per well and incubate 24 h (37 °C, 5% CO<sub>2</sub>).

6.4. Day 8: FACS isolate hemogenic endothelial cells (see section 7).

## **7. FACS-isolation of hemogenic endothelial cells**

7.1. Lift and wash the cells as described above in sections 4.1–4.6.

7.2. Divide the cells evenly into microcentrifuge tubes on ice, each containing a minimum of 600  $\mu$ L cells at  $1 \times 10^5$  cells/mL, for antibody staining.

NOTE: Eight tubes of cells are required for antibody staining of hemogenic ECs: unstained control, CD31 single antibody control, CD45 single antibody control, KDR single antibody control, c-Kit single antibody control, CD34 single antibody control, VE-cadherin single antibody control, and sample containing all six antibodies.

NOTE: Antibody information is provided in **Table of Materials**.

7.3. Add antibodies to the tubes containing cells, as appropriate, and incubate on ice and protected from light for 30 min.

7.3.1. Unstained control: Do not add antibody.

7.3.2. CD31 single antibody control: Add only CD31 antibody.

7.3.3. CD45 single antibody control: Add only CD45 antibody.

7.3.4. KDR single antibody control: Add only KDR antibody.

7.3.5. c-Kit single antibody control: Add only c-Kit.

7.3.6. CD34 single antibody control: Add only CD34 antibody.

7.3.7. VE-cadherin single antibody control: Add only VE-cadherin antibody.

7.3.8. Sample: Add CD31, CD45, KDR, c-Kit, CD34, and VE-cadherin antibodies.

NOTE: The final antibody concentration in the sample, as well as the fluorescent conjugates, should be optimized based on the specific antibodies and cell sorter used.

7.4. Pellet the cells by centrifugation in a  $4^\circ\text{C}$  microcentrifuge for 5 min at  $1,000 \times g$ .

7.5. Remove the supernatant and resuspend the pellets in 600  $\mu$ L of ice-cold sorting buffer.

7.6. Strain the samples through the mesh filter cap of 5 mL FACS tubes and store cells on ice, protected from light, for immediate FACS.

7.7. To obtain hemogenic endothelial cells ( $\text{CD31}^+ \text{KDR}^+ \text{c-Kit}^+ \text{CD34}^+ \text{VE-Cadherin}^- \text{CD45}^-$ ), perform the following steps.

7.7.1. Identify the  $\text{CD45}^-$  cell population and gate ( $\text{CD45}^-$ ).

7.7.2. Within (CD45<sup>-</sup>), identify the CD31<sup>+</sup> cell population and gate (CD31<sup>+</sup>).

7.7.3. Within (CD31<sup>+</sup>), identify the VE-Cadherin<sup>-</sup> cell population and gate (CDH5<sup>-</sup>).

7.7.4. Within (CDH5<sup>-</sup>), identify the c-Kit<sup>+</sup> cell population and gate (KIT<sup>+</sup>).

7.7.5. Within (KIT<sup>+</sup>), identify the CD34<sup>+</sup> cell population and gate (CD34<sup>+</sup>).

7.7.6. Within (CD34<sup>+</sup>), identify and sort the KDR<sup>+</sup> cells into 6 mL ice-cold cell sorting buffer. Use these cells in downstream applications (see section 8).

## 8. Colony forming unit assay

8.1. Thaw the aliquots of methylcellulose-based medium following the manufacturer's instructions.

NOTE: One 3 mL aliquot is sufficient for two samples and one 4 mL aliquot is sufficient for three samples.

8.2. Count the sorted hemogenic endothelial cells obtained in step 7.7.

8.3. Following the manufacturer's instructions, calculate the volume of sorted cells to add to each methylcellulose-based medium aliquot so that each sample will contain a minimum of 1,000 hemogenic endothelial cells.

NOTE: The number of cells can be adjusted as necessary.

8.4. Add the calculated volume of cells to the methylcellulose-based medium aliquot and vortex thoroughly. Allow the methylcellulose-based medium cultures to sit at room temperature for 10 min, or until the bubbles dissipate.

8.5. Aspirate the fibronectin coating solution from the prepared 35 mm dishes. Following the manufacturer's instructions, dispense 1 mL of methylcellulose-based medium culture per 35 mm dish. Gently rotate the dish to evenly distribute the culture.

8.6. Place these 35 mm dishes, as well as two additional 35 mm dishes filled with sterile water, within a 15 cm tissue culture dish.

8.7. Incubate the cultures in a 37 °C, 5% CO<sub>2</sub> incubator, and observe the cultures on days 8 and 14.

8.7.1. On day 8, count the CFU-E and BFU-E colonies.

8.7.2. On day 14, count the CFU-GM and CFU-GEMM colonies.

NOTE: Refer to the methylcellulose-based medium manual for morphological identification of colony types.

#### REPRESENTATIVE RESULTS:

A schematic outlining the specification of primordial ECs and hemogenic ECs from hESCs, and a representative image of cells 24 h after plating are shown in **Figure 1**. Following specification, primordial ECs and hemogenic ECs are FACS purified on days 5 and 8, respectively. Primordial ECs are defined as CD31<sup>+</sup> CD45<sup>-</sup> and hemogenic ECs are defined as CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup>. A representative flow cytometric gating strategy for primordial ECs and hemogenic EC purification is shown in **Figure 2**. Cells are initially gated based on the negative expression of CD45 and positive expression of CD31 to obtain purified primordial ECs (**Figure 2A**). To obtain purified hemogenic ECs, cells are initially gated as in **Figure 2A** and are then further purified based on positive or negative expression of (in order) VE-Cadherin (CDH5), c-Kit (KIT), CD34, and KDR (**Figure 2B**).

To assess the potential of H9-Fucci-hES-derived primordial CD31<sup>+</sup> CD45<sup>-</sup> endothelial cells, isolated via FACS at day 5 of differentiation (protocol section 4), to give rise to endothelial subtypes, the purified cells are seeded onto plates coated with either the Notch ligand DLL4 to induce arterial specification, or PBS (control), and incubated for 24 h in a 37 °C, 5% CO<sub>2</sub> incubator. The cells are then lysed with RNA lysis buffer, the RNA extracted, and reverse transcribed to cDNA, and qPCR is performed to compare gene expression levels in the DLL4-treated vs. control cells. As expected, endothelial cells grown on DLL4 have increased expression of the Notch-responsive gene HEY2, as well as the arterial-associated genes EFNB2, GJA5, and GJA4. Additionally, these cells also have decreased expression of the venous transcription factor NR2F2 (**Figure 3A**). Alternatively, to determine the effect of DLL4 treatment on cell cycle state, the FACS purified CD31<sup>+</sup> CD45<sup>-</sup> cells are incubated on plates coated with either DLL4 or PBS for 24 h, lifted, and analyzed based on the expression of hCdt1(30/120)-mCherry (late G1) and hGem(1/110)-mVenus (S/G2/M). Consistent with the findings that Notch signaling promotes late G1 cell cycle arrest<sup>27</sup>, a greater percentage of primordial ECs are arrested in late G1 after growth in the presence of DLL4, compared to control cells (**Figure 3B,C**).

To verify the hematopoietic potential of hemogenic endothelial cells, the CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup> endothelial cells isolated through FACS (methods in section 7) are seeded in a methylcellulose-based medium formulated for growth of hematopoietic progenitor cells in colony-forming unit (CFU) assays and are allowed to grow for 14 days. CFU-E erythroid colonies and blast-forming unit (BFU)-E erythroid colonies are counted on day 8 (**Figure 4A,B**), and CFU-GM granulocyte/macrophage and GFU-GEMM (granulocyte, erythroid, macrophage, and megakaryocyte) multipotent hematopoietic progenitor colonies are counted on day 14 (**Figure 4C and D**). Per 1,000 hemogenic ECs plated, approximately 20 CFU are generated (**Figure 4F**). Cells with endothelial cell morphology can also be seen in the cultures (**Figure 4E**); these are the hemogenic endothelial cells that give rise to multi-lineage hematopoietic progenitors on a single cell level<sup>37</sup>.

## FIGURE AND TABLE LEGENDS:

**Figure 1: Protocol for the specification of primordial and hemogenic ECs.** (A) Schematic diagram of the differentiation protocol. Embryonic stem cells are plated on Day -1 on matrix protein-coated plates and are allowed to attach overnight. The cells are then treated on Days 0 and 1 with GSK3i inhibitor (CHIR99021) and bFGF, respectively, to induce primitive streak and mesoderm specification, respectively. Beginning on Day 2, the cells are treated with a combination of BMP4 and VEGF-A to promote primordial EC development. Primordial ECs (red circle) are FACS purified on Day 5. Alternatively, to generate hemogenic ECs, the medium above the primordial ECs is exchanged on Day 5 to fresh hemogenic differentiation medium containing BMP4, VEGF-A, and RA. This medium is replaced daily until Day 8, when hemogenic ECs (red star) are FACS purified. (B) Colonies on Day 0 of differentiation, scale bar= 100  $\mu$ m. Panel A has been modified from Qiu et al.<sup>37</sup> with permission from Elsevier.

**Figure 2: FACS analysis of hemogenic ECs derived from hESCs.** Representative flow cytometric gating strategy for the purification of (A) primordial ECs and (B) hemogenic ECs. Note that since hemogenic ECs are derived from primordial ECs, the flow cytometry gating strategy for CD45 and CD31 is identical for both cell populations. Shown in the top row of each panel (sample) are cells that were differentiated to hemogenic ECs as described in protocol section 6 and stained with antibodies as described in protocol section 7.3.8. Shown in the bottom row of each panel (control) are unstained cells that were differentiated for 8 days without RA treatment.

**Figure 3: DLL4-induction of H9-Fucci CD31<sup>+</sup> CD45<sup>-</sup> primordial endothelial cells results in late G1 arrest and increased arterial gene expression.** (A) DLL4 treatment of CD31<sup>+</sup> CD45<sup>-</sup> H9-hESC-derived primordial endothelial cells expressing the Fucci construct purified at day 5 of differentiation results in increased expression of arterial genes (i–iii) and the Notch responsive gene Hey2 (v), which is accompanied by a concomitant decrease in the expression of the venous gene NR2F2 (iv). (B) Representative FACS plots showing the cell cycle state distribution of 5,000 H9-Fucci-derived CD31<sup>+</sup> CD45<sup>-</sup> grown on PBS (control) or DLL4 for 24 h. (C) DLL4 induction results in a 15% increase in cells in the late G1 phase compared to control. Data is the average of triplicate samples from the same experiment shown in panel (B). Error bars indicate standard deviation.

**Figure 4: Analysis of hematopoietic potential of hemogenic ECs derived from hESCs.** Representative images showing morphology of H1-hESC derived (A) CFU-E erythroid colony (scale bar = 35  $\mu$ m), (B) BFU-E erythroid colony (scale bar = 75  $\mu$ m), (C) CFU-GM granulocyte/macrophage colony, (D) CFU-GEMM multipotent hematopoietic progenitor colony, and (E) CFU-GM granulocyte/macrophage colony with underlying endothelial cells (ECs) (red arrows). (F) number and distribution of CFUs formed per 1,000 plated hemogenic endothelial cells. Scale bar = 100  $\mu$ m in (C–E). Additional images of CFUs differentiated using this protocol can be found in Qiu et al.<sup>37</sup>. Panel F has been modified from Qiu et al.<sup>37</sup> with permission from Elsevier.

## Table 1: qPCR primer information

## DISCUSSION:

Herein, the steps for producing hemogenic endothelial cells from human embryonic stem cells in approximately 1 week using a murine feeder- and serum-free 2D culture system (**Figure 1**) are outlined. This protocol expands on a method described by Sriram et al. (2015) to obtain primordial ECs<sup>38</sup>. The primordial nature and specification potential of the CD31<sup>+</sup> CD45<sup>-</sup> ECs is demonstrated by culturing these cells on DLL4-coated plates and observing gene expression changes consistent with arterial specification (**Figure 3**). Additionally, the gain of arterial identity is associated with late G1 cell cycle arrest (**Figure 3**), which is consistent with previous studies<sup>27</sup>. After culturing primordial ECs for an additional 3 days in the presence of 0.5  $\mu$ M RA, 25 ng/mL BMP4, and 50 ng/mL VEGF-A, it was possible to generate and FACS-isolate hemogenic ECs (**Figure 2**) that are capable of giving rise to CFU-erythroid, BFU-erythroid, CFU-granulocyte/macrophage, and CFU-granulocyte, erythrocyte, macrophage, and megakaryocyte colonies (**Figure 4**). Using this method in a recently published study, gene expression changes over an 8-day time period consistent with loss of pluripotency, primitive streak, and mesoderm induction, acquisition of endothelial cell identity, and finally hematopoietic identity were observed<sup>37</sup>. Furthermore, RA treatment induced early G1 cell cycle arrest to enable hemogenic EC specification<sup>37</sup>.

Recently, Ohta et al. (2019) described a protocol for the differentiation of hemogenic ECs from hPSCs<sup>39</sup>. However, the protocol described above offers significant advantages: 1) this method does not require the formation of spheroids; 2) this protocol utilizes a standard 37 °C, 5% CO<sub>2</sub> incubator rather than a hypoxic incubator, eliminating the need for dedicated specialty equipment; and 3) this protocol utilizes only one medium (pluripotent stem cell differentiation medium supplemented with PFHM), a cost-saving advantage, whereas the Ohta protocol requires mediums for induction. Another recently published study by Galat et al. (2017) described a protocol in which CHIR99021 induction was utilized to generate a population of CD34<sup>+</sup> hemogenic endothelial cells<sup>40</sup>. These cells also expressed CD31 and were capable of giving rise to endothelial cells when cultured under monolayer conditions or cells expressing myeloid and lymphoid markers after co-culturing with OP9 or OP9-DLL4 cells, respectively, in the presence of additional cytokines. The requirement for additional co-culture could lead to potential contamination of desired cell populations with murine cells. Additionally, although Ohta et al. and Galat et al. utilized a hemogenic induction period that was shorter than the one described here (4 days and 5 days, respectively vs. 8 days), both defined hemogenic ECs as CD34<sup>+</sup>, whereas this protocol utilized a more stringent definition: CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup>. While CD34 is recognized as a marker of hematopoietic cells, it is also expressed by other non-hematopoietic cell types, such as mesenchymal stromal cells and endothelial cells<sup>41</sup>. The definition of hemogenic ECs in this protocol (CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup>) is therefore more rigorous and represents a more defined population.

One limitation to the use of hESCs or hiPSCs in therapeutic applications is the large number of cells required, and standard 2D derivation methods are primarily restricted to small-scale differentiations. Utilizing hiPSC lines, Olmer et al. (2018) demonstrated the feasibility of scaling up production of functional CD31<sup>+</sup> ECs that expressed both arterial (DLL4) and venous (EPHB4) cell markers utilizing either suspension culture or a stirred-tank bioreactor<sup>6</sup>. Importantly, they



showed that they were able to obtain  $1.18 \times 10^7$  CD31<sup>+</sup> ECs that co-express CD34 and KDR from a single flask containing 20 mL suspension culture. In order to obtain the requisite  $3 \times 10^8$  ECs necessary for the majority of therapeutic applications, just over two 500 mL flasks would be required<sup>6</sup>. Future experiments should explore the application of scaling techniques to the protocol presented here for large-scale production of hemogenic ECs.

#### ACKNOWLEDGMENTS:

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#### DISCLOSURES:

The author has nothing to disclose.

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Figure 1

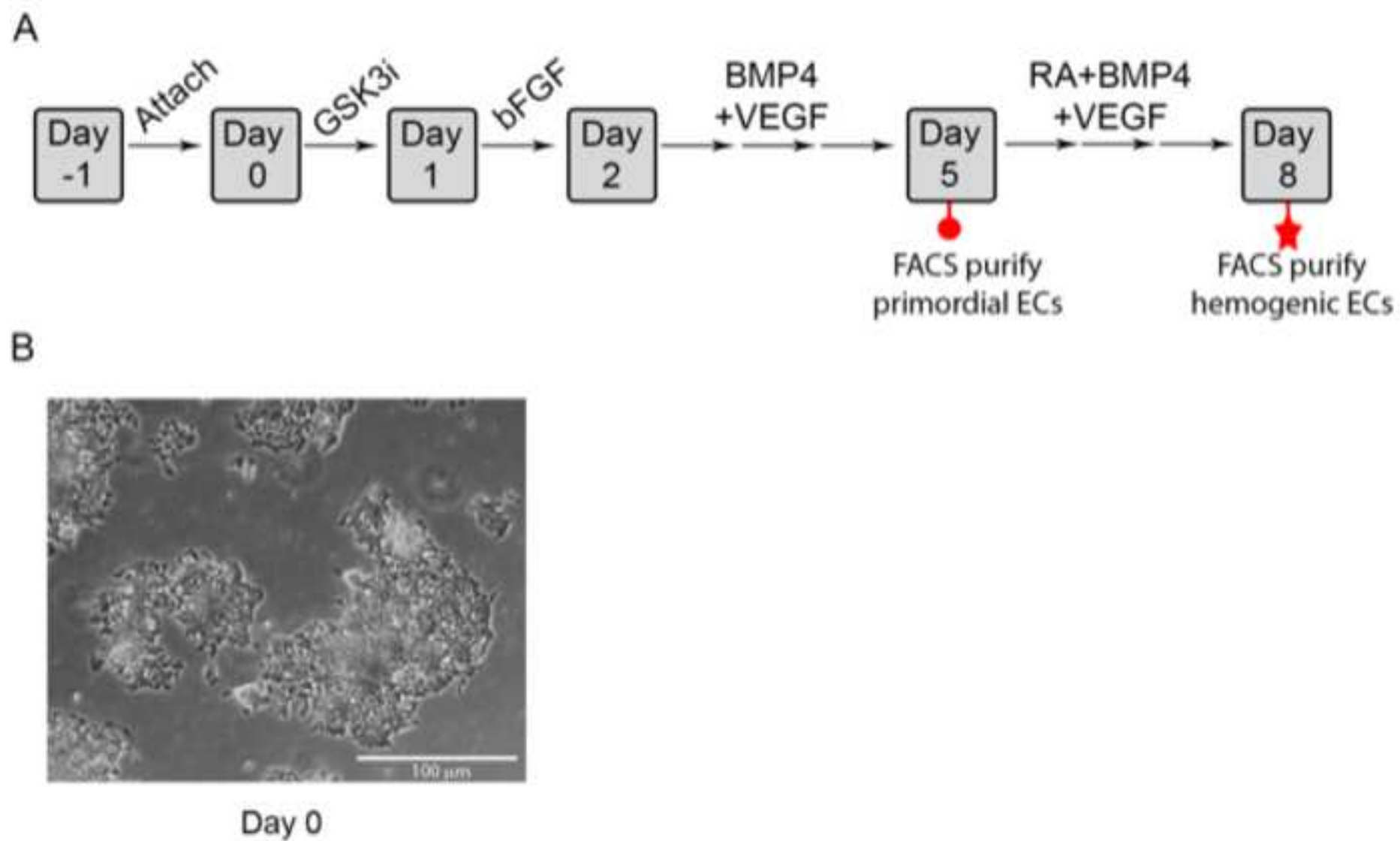


Figure 2

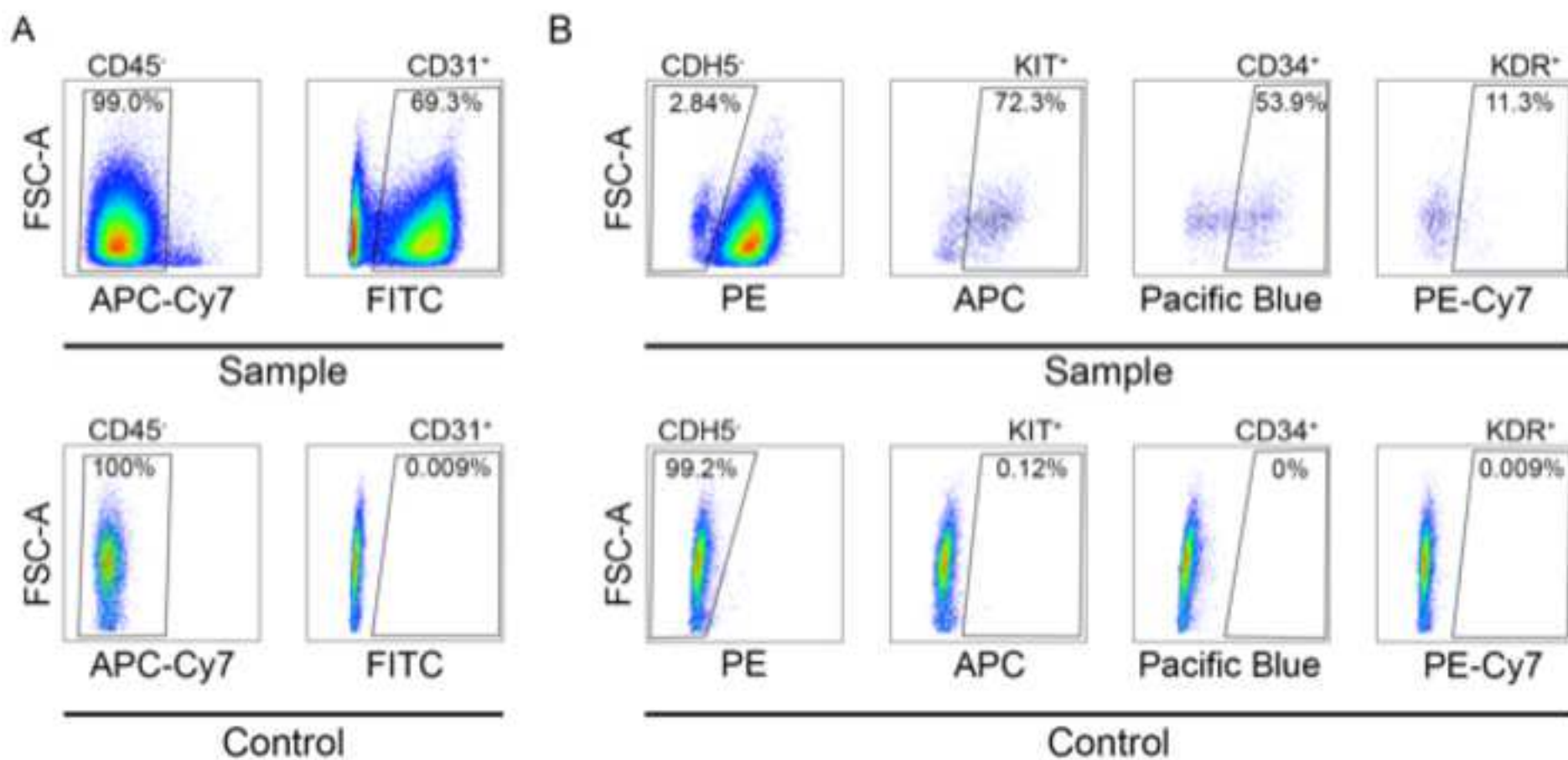


Figure 3

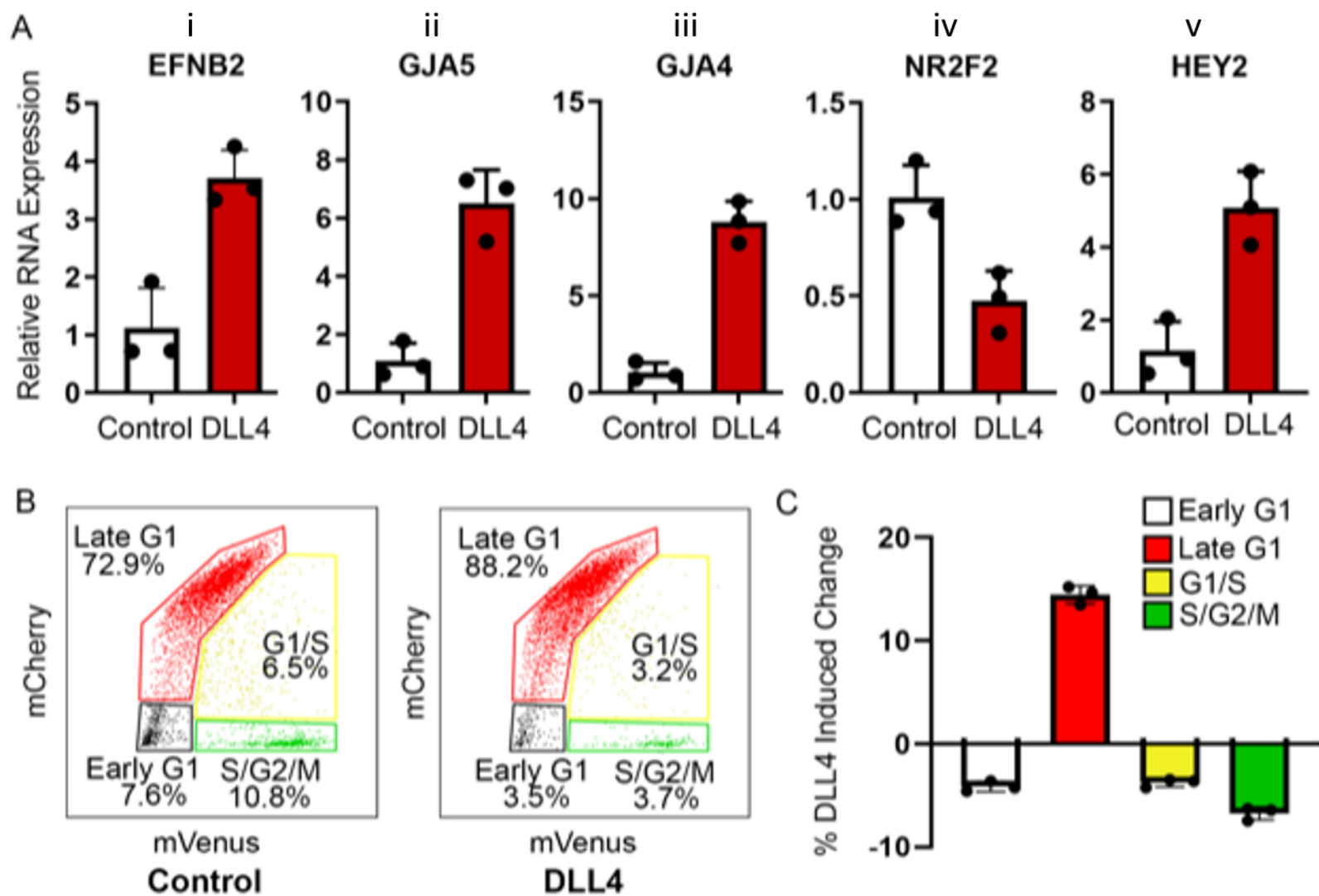
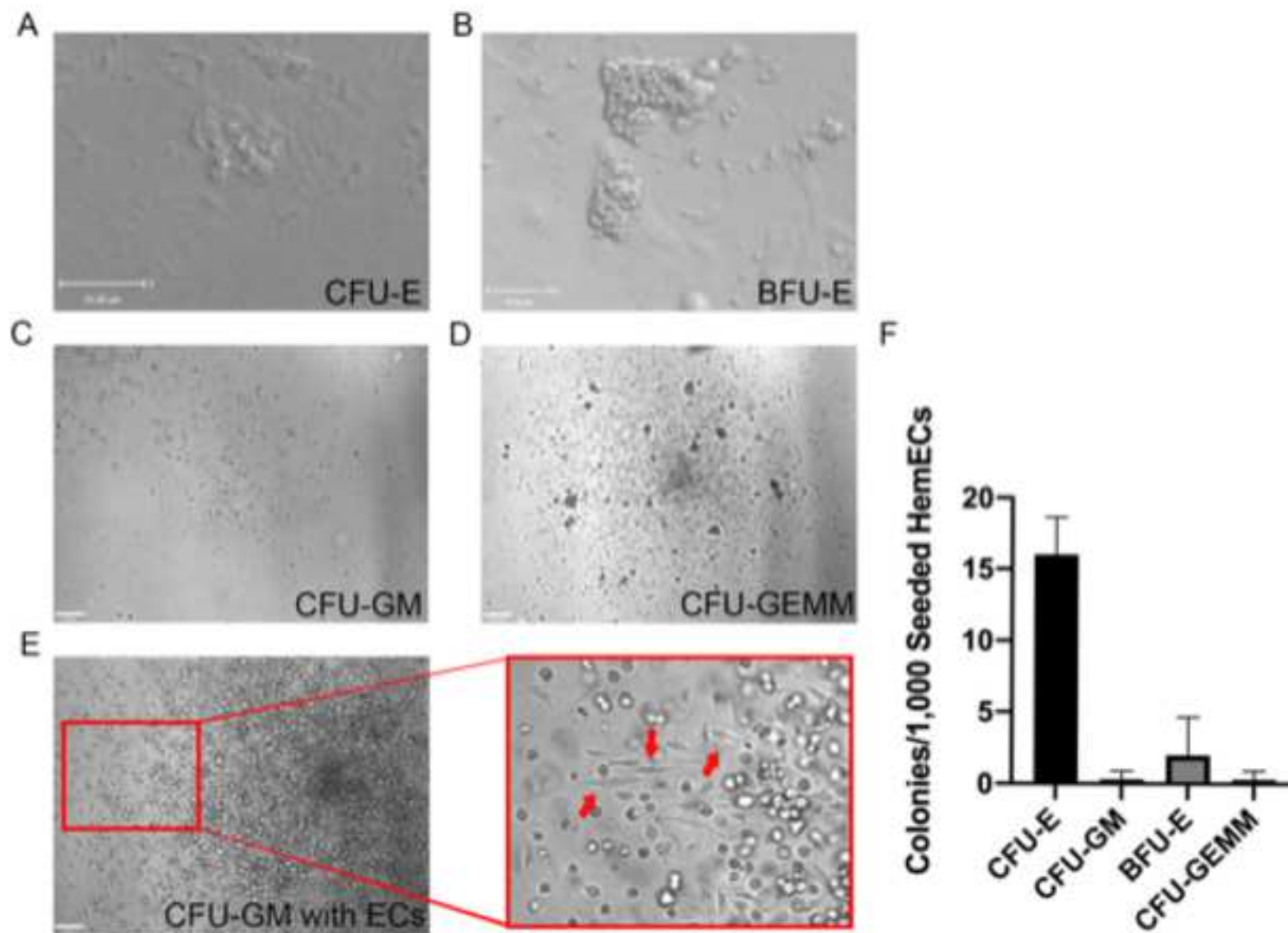
[Click here to access/download;Figure;Figure 3.pdf](#)

Figure 4



Name	Forward	Reverse
EFNB2	TATGCAGAACTGCGATTTCCAA	TGGGTATAGTACCAAGTCCTTGTC
EPHB4	CGCACCTACGAAGTGTGTGA	GTCCGCATCGCTCTCATAGTA
GJA5	CCGTGGTAGGCAAGGTCTG	ATCACACCGGAAATCAGCCTG
GJA4	ACACCCACCCTGGTCTAC	CACTGGCGACATAGGTGCC
HEY2	GCCCGCCCTTGTCAGTATC	CCAGGGTCGGTAAGGTTTATTG
NR2F2	GGACCACATACGGATCTTCCAA	ACATCAGACAGACCACAGGCAT



Name of Material/ Equipment	Brand Name	Company	Catalog Number
15 cm dishes	Normocin	Corning	430599
35 mm dishes		Corning	430165
6-well plates		Corning	3516
Antimicrobial reagent		Invitrogen	ant-nr-1
bFGF		R&D systems	233-FB-025
BMP4		BioLegend	595202
Bovine Serum Albumin (BSA)	Accutase	Fisher	BP1600-1
		Scientific	
Cell Detachment Solution		Stemcell	7920
Dimethyl Sulfoxide (DMSO)		Technologies	
		Sigma Aldrich	D2650-100mL
		Stemcell	7913
Dispase	EGM-2 Endothelial Cell Growth Medium-2 BulletKit (EGM-2)	Technologies	
DLL4		R&D systems	1506-D4/CF
DMEM:F12		Gibco	11320-033
Dulbecco's Phosphate Buffered Saline (PBS)		Gibco	14190144
Endothelial cell growth medium		Lonza	CC-3162
FACS tubes		Corning	352235
Fetal Bovine Serum (FBS)		Gemini Bio	100-106
		ThermoFisher	33016015
Fibronectin		Scientific	
GSK3i/CHIR99021		Stemgent	04-0004-02
Hanks Balanced Salt Solution (HBSS)		Gibco	14175-095

Hydrochloric Acid (HCl)		Fisher Scientific	A144S-500
Matrix protein	Matrigel	Corning Stemcell	356230
Methylcellulose-based medium	MethoCult H4435 Enriched	Technologies	4435
Pluripotent stem cell differentiation medium	STEMdiff APEL 2	Stemcell Technologies	5270
Pluripotent stem cells: H1, H9, H9-FUCCI		WiCell	WA09 (H9), WA01 (H1)
Protein-Free Hybridoma Medium (PFMH)		Gibco	12040077
Retinoic Acid		Sigma Aldrich	R2625-50mg
	iScript Reverse Transcription		
Reverse transcription master mix	Supermix	BioRad	1708840
RNA extraction kit	RNeasy Mini Kit	Qiagen	74104
		Fisher Scientific	SS255-1
Sodium Hydroxide (NaOH)		Stemcell Technologies	
Stem cell growth medium	mTeSR1		85850
	iTaq Universal SYBR Green		
SYBR Green master mix	Master Mix	BioRad	1725121
Trypsin-EDTA		Gibco	25299956
VEGF <sub>165</sub> (VEGF-A)		PeproTech	100-20
$\alpha$ -CD31-FITC		BioLegend	303104
$\alpha$ -CD34-Pacific Blue		BioLegend	343512
$\alpha$ -CD45-APC/Cy7		BioLegend	304014
$\alpha$ -c-Kit-APC		BioLegend	313206

$\alpha$ -Flk-1-PE/Cy7	BioLegend	359911
$\alpha$ -VE-Cadherin-PE	BioLegend	348506

\* Antibody fluorescent conjugates should be optimized based on the cell sorter used. Presented here are the

### Comments/Description

tissue culture treated  
tissue culture treated  
tissue culture treated

use at 50 ng/mL  
use at 25 ng/mL

recombinant human; use at 10 µg/mL

polystyrene round bottom with filter cap

use at 4 µg/cm<sup>2</sup>  
10 mM stock; use at 5 µM

Growth factor reduced. Refer to the Certificate of Analysis for the lot to determine the protein (Matrigel) concentration. This concentration is required to calculate the volume of Matrigel that contains 1 mg of protein.

human; H9-FUCCI were obtained from Dr. Ludovic Vallier's lab at Cambridge Stem Cell Institute

use at 0.5  $\mu$ M

0.25%

use at 50 ng/mL

2  $\mu$ g/mL\*

2  $\mu$ g/mL\*

2  $\mu$ g/mL\*

2  $\mu$ g/mL\*

2 µg/mL\*

2 µg/mL\*

final concentrations utilized in this study.

We thank the reviewers and editorial staff for their suggestions, and summarize below the changes that we have made to address all concerns. We appreciate your input, which helped to significantly improve our manuscript, and hope that it will now be acceptable for publication in *JoVE*.

**Editorial comments:**

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

[We checked through the manuscript and corrected all errors.](#)

2. Please revise the text to avoid the use of any personal pronouns (e.g., "we", "you", "our" etc.).

[Personal pronouns have been removed.](#)

3. JoVE cannot publish manuscripts containing commercial language. Please remove all commercial language from your manuscript and use generic terms instead. All commercial products should be sufficiently referenced in the Table of Materials: e.g., Matrigel, Normocin, MethoCult, Qiagen, Bio-Rad, Stemcell Technologies), etc. We must maintain our scientific integrity and prevent the subsequent video from becoming a commercial advertisement.

[The commercial language has been removed.](#)

4. Please use standard abbreviations for time units preceded by a numeral. Examples: 5 h, 10 min, 100 s, 8 days, 10 weeks (Line: 140, 278, 288, 299, 306, 310, etc.).

[The abbreviations have been changed to follow the suggested style.](#)

5. Line 145: Please ensure that the term "tritulating" used is appropriate in the context of this protocol.

[Tritulating has been replaced with "pipetting up and down".](#)

6. Line 449-463: Please ensure that all text in the protocol section is written in the imperative tense as if telling someone how to do the technique (e.g., "Add this," "Ensure that," etc.).

[The text has been edited to the imperative tense.](#)

7. Please highlight up to 3 pages of the Protocol (including headings and spacing) that identifies the essential steps of the protocol for the video, i.e., the steps that should be visualized to tell the most cohesive story of the Protocol. Remember that non-highlighted Protocol steps will remain in the manuscript, and therefore will still be available to the reader.

[We have reduced the highlighted essential sections of the protocol to 3 pages.](#)

## **Reviewers' comments:**

### **Reviewer #1:**

**Manuscript Summary:** The manuscript from Nelson et al. established an easy-to-follow protocol to generate hemogenic endothelium from human pluripotent stem cells. As described in the discussion section, I agree with the significant advantage of this protocol over previously published one from Ohta et al. No requirement of spheroid formation, standard 37C 5% CO<sub>2</sub> incubator, and one media (STEMdiff Ape1 2) make this protocol more affordable for users than Ohta et al. To improve the visibility of the protocol, I would recommend the authors address the following points.

### **Major Concerns:**

1. Morphological changes of colonies. Would help readers to grasp the idea of density and size of colonies if they see the representative pics lined with figure 1. E.g. days 0, 2, 5, and 8. In my experience, the density and size of colonies influenced the yield of hemogenic endothelium.

Thank you for this suggestion. Due to the importance of proper seeding density in order to obtain efficient differentiation, a representative image of the density and size of the colonies at day 1 of differentiation has been added to **revised Figure 1 (panel B)**. Additional images on subsequent days are shown in our recently published paper (Qiu et al. *Cell Reports* 2020)<sup>1</sup> that we refer the readers to.

2. Can the authors generate mature blood cells? The awaited application of this protocol includes the production of functional blood cells. As T-cells and B-cells take too long (>8 weeks) and require feeder cells (e.g. OP9-DLL4, MS5) in a healthy condition, I would be more satisfied to see the generation of mature myeloid cells as a bottom line. May the authors keep the culture after day 8 and see the expression of CD14, CD16, and CD33. Might take additional >14 days and constant media change though. SCF might be required for EHT. Both IL-3 and M-CSF might be required for monocyte differentiation. Still worth trying.

In related studies by our lab<sup>1</sup> utilizing the differentiation protocol described here, we used flow cytometry (Figures 1E, S1, and S2) to show that multi-lineage blood cells expressing lymphoid markers (CD20, CD3), myeloid markers (CD14, CD66b, CD41, CD235ab) and leukocyte markers (CD11b, CD45) are generated by day 8 of differentiation. However, as the focus of the protocol presented here is to describe a straight-forward method to generate hemogenic endothelial cells and study their molecular regulation, we did not try to optimize their further differentiation into mature blood cells because that was beyond the scope of our studies.

3. The yield of hemogenic endothelium. Could the authors explicit how many hemogenic endothelial cells can be isolated from 1 well of 6 well plates? Any difference between H1 and H9? Though both are good blood producer lines, just wanted to know the protocol works in independent lines.

The protocol works well in both H1 and H9 cell lines, but the H1 cell line generates hemogenic endothelial cells more efficiently compared to the H9 line. A note has been added after Protocol section 1.1. We have not measured the exact number of hemogenic endothelial cells that can be isolated from 1 well of a 6-well plate, but the expected yield would be 1.2% of total cells, based on our studies, to date.

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<sup>1</sup> Qiu, J., Nordling, S., Vasavada, H.H., Butcher, E.C., Hirschi, K.K. Retinoic Acid Promotes Endothelial Cell Cycle Early G1 State to Enable Human Hemogenic Endothelial Cell Specification. *Cell Reports*. **33** (9) (2020).



4. The yield of CFU. Could the authors explicit the input cell number (FACS-sorted hemogenic endothelium?) and output the CFU number? Perhaps having a bar graph representation of each type of CFU per 1K HE cells would help visualization.

Thank you for this suggestion. We have incorporated a panel into **revised Figure 4 (panel F)** that displays the number of CFU obtained per 1000 plated hemogenic endothelial cells. This is also addressed in text in line 553.

5. Could the author comment on the application of MACS? Although FACS isolation of precise markers defines HE better, a routine harvest of HE cannot be capped by the availability and cost of a sorter. Especially for readers in a small institute... I would appreciate it if the authors comment on the hematopoietic capacity of CD34+ MACS isolated cells on day 8. They could adhere to fibronectin and undergo EHT eventually? Generate CFU-GEMM?

In this protocol, we describe a novel method for the identification and purification of hemogenic endothelial cells, a population of cells that expresses both endothelial and hematopoietic markers. Due to their complex phenotype, FACS isolation is required to purify hemogenic endothelial cells, and for this reason we have chosen not to discuss MACS sorting. We discuss in lines 649-651 that while CD34 is recognized as a hematopoietic marker, it is also expressed by other non-hematopoietic cell types<sup>2</sup>. Thus, while it is possible to sort cells at day 8 based on CD34<sup>+</sup> expression alone using MACS, a mixed population of cells would be obtained. Therefore, we expect that not all CD34<sup>+</sup> cells sorted using MACS would be capable of undergoing EHT and generating CFU-GEMM.

6. Semantic issue. What would the authors call this protocol? Elefany & Stanley called hematopoietic organoids. Crooks called artificial thymic organoids. Even with some differences in protocols, both start from PSC aggregates go through primitive streak to hemogenic endothelium. The highlighted feature in both protocols is the invagination of primitive streak cells self-form certain 3D structures, thus called organoids. The same thing occurs in hematopoietic induction of PSC colonies, usually forming a sack-like structure. Probably occurs in the case of Nelson et al. too. It is up to authors, but having a memorable name would increase the visibility of this protocol to readers.

We have considered this interesting suggestion, and have chosen to keep the name of our protocol "Directed Differentiation of Hemogenic Endothelial Cells from Human Pluripotent Stem Cells." Our focus was generating a serum- and murine feeder-free culture method for the differentiation of primordial and hemogenic endothelial cells from human pluripotent stem cells grown in a 2D monolayer. This method does not require or rely on the formation of embryoid bodies, and we did not observe the formation of organoids. Thus, we are not comfortable adding such information to our title.

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<sup>2</sup> Sidney, L.E., Branch, M.J., Dunphy, S.E., Dua, H.S., Hopkinson, A. Concise Review: Evidence for CD34 as a Common Marker for Diverse Progenitors: CD34 as a Common Marker for Diverse Progenitors. *STEM CELLS*. **32** (6), 1380–1389 (2014).

**Reviewer #2:**

**Manuscript Summary:** This manuscript by Nelson and colleagues describes a detailed, useful and timely protocol for the directed differentiation of hemogenic endothelial cells from human PSC.

**Major Concerns:**

None.

**Minor Concerns:**

1. Title page: affiliation 4 seems to be missing

This information has been added.

2. The authors should indicate if they would expect their protocol to work equally well on induced pluripotent stem cells (iPSC).

We have initiated studies to determine whether this protocol can be used to generate hemogenic endothelial cells from human iPSCs. Results, to date, reveal that we are able to generate CD31<sup>+</sup> KDR<sup>+</sup> c-Kit<sup>+</sup> CD34<sup>+</sup> VE-Cad<sup>-</sup> CD45<sup>-</sup> cells from human iPS cells. However, as this work is ongoing and still preliminary, we prefer not to make any speculations in the manuscript.

3. Table 2: The sentence "Antibody fluorescent conjugates should be optimized based on cell sorter utilized. We used antibody at a final concentrations of 2 mg/mL" is given 6x. Maybe this is just a pdf formatting error, but if this refers to Table 2, consider adding an asterix referring to the individual antibodies and providing the sentence once.

Thank you for this suggestion; the change has been made.

4. Table of materials / Table 1: use at 5 0ng/mL --> there seems to be an extra space in between the number(s)

This typo had been edited.

**Reviewer #3:**

**Manuscript Summary:** The manuscript is well written with detailed explanation of the protocol. It would be a very useful protocol for scientists in the field. It is well presented.

**Major Concerns:**

1. The authors do not mention the volume of matrigel aliquoted into each tube.

The volume of the Matrigel aliquots will vary depending on the Matrigel lot. The researcher should refer to the certificate of analysis for the lot to identify the protein concentration. The volume containing 1mg of protein (Matrigel) can be calculated from this value. To clarify this point, a comment/description has been added to **revised Table 1** (List of reagents). In addition, to comply with publication guidelines, all direct references to Matrigel have been replaced with "matrix protein" in the manuscript text. The commercial product name can be found in **revised Table 1**.

2. The statement, "To passage cells:", should be on 2.4.1.

The statement "to passage cells" appears in Step 2.4, which is the parent heading for steps 2.4.1- 2.4.9. Steps 2.4.1- 2.4.9 are all steps necessary to passage cells; thus, we think this statement is more appropriately in Step 2.4.

3. What plate size are you using for differentiation?

Differentiation is performed in 6-well plates. A note has been added after Protocol Step 1.3 to clarify this point.

4. What coating is used for differentiation?

Differentiation is performed on Matrigel-coated plates. However, to comply with publication guidelines, all direct references to Matrigel in the main text have been replaced with "matrix protein." The commercial product name can be located in **revised Table 1**. A note has been added after Protocol Step 1.3 to clarify that matrix protein-coated plates should be used for differentiation.

5. An approximate cell density for seeding would be desirable as too many cells would hinder optimum endothelial differentiation.

Thank you for catching this inadvertent omission. Small clumps of cells were seeded at a density of approximately 2 colonies per square centimeter, as described in Sriram et al.<sup>3</sup> This information has been added to Protocol Step 3.1. It is still advisable that the seeding density be evaluated and refined empirically, as needed.

6. What is the composition of the HE differentiation medium? This should be mentioned in the text.

We agree and the composition of the HE differentiation medium is provided in Protocol Step 1.10.

7. in Line 8.4, Where are the methocult cultures placed for 10 mins, at RT or 37 water bath?

The Methocult cultures are left at room temperature for 10 min. This has been added to Protocol Step 8.4. To comply with publication guidelines, all direct references to Methocult in the main text have been replaced with "methylcellulose-based medium". The commercial product name can be located in **revised Table 1**.

8. Fig. 4C and 4D are not clear. include better pictures or at least show cytopins to show morphology of cells.

We agree that the images shown in Figs 4C and 4D are not ideal. However, our best higher quality images of CFU-GM and CFU-GEMM generated using this protocol have been recently published in a related manuscript<sup>1</sup> from our lab. We direct readers to this manuscript for additional CFU images in the **revised Figure 4 legend**.

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<sup>3</sup> Sriram, G., Tan, J.Y., Islam, I., Rufaihah, A.J., Cao, T. Efficient differentiation of human embryonic stem cells to arterial and venous endothelial cells under feeder- and serum-free conditions. *Stem Cell Research & Therapy*. **6** (1), 261 (2015).

**Reviewer #4:**

**Comments to Authors:** In this study, the authors provide a novel method for the derivation of hemogenic endothelial cells from human embryonic stem cells within approximately one week using a murine feeder- and serum-free 2D culture system. This protocol yields a well-defined population of hemogenic endothelial cells (CD31+Flk-1+c-Kit+CD34+VE-Cadherin-CD45-). This study provides useful methods in detail. Some details still need to be improved during the revise.

**Major comments:**

1. The author claimed that the increased generation of hemogenic endothelial cells by DLL4 is associated with late G1 cell cycle arrest. It will be better that the authors provide more evidence to validate this.

We apologize for the confusion. The purpose of the DLL4 induction experiment in the present study was to demonstrate that the FACS-purified H9-Fucci CD31<sup>+</sup>CD45<sup>-</sup> cells isolated at day 5 of differentiation are primordial in nature (able to be further specified to other endothelial cell types, such as arterial endothelial cells, as shown in Figure 3). This experiment was conducted independently of hemogenic specification. We have clarified this in the results section (lines 581-582) as well as in the **revised Figure 3 legend**.

2. In the Fig.2B, please provide flow cytometric gating strategy for CD45 and CD31, as shown in Fig.2A.

Since hemogenic endothelial cells are derived from primordial endothelial cells, the flow cytometric gating strategy for CD45 and CD31 in Fig 2B (representative flow cytometry gating strategy for hemogenic endothelial cells) is identical to that shown in Fig. 2A (representative flow cytometry gating strategy for primordial endothelial cells). A note has been added to **revised Figure 2 legend** to clarify this. This is also now mentioned in the text in lines 573-575.

3. Why CFU-E and BFU-E Fig.2B are not red?

We think the reviewer is referring to Figure 4, since Figure 2B illustrates representative flow cytometric gating for hemogenic endothelial cells. In the representative pictures of colony types in **revised Figure 4**, the cells are likely at an early stage of development and not yet hemoglobinized.

**Minor comments:**

1. In the step 3.1, please ensure how many or the numbers of small clumps were seed? Or provide more detail information how to evaluate the seeding density of small clumps.

Thank you for catching this inadvertent omission. Small clumps of cells were seeded at a density of approximately 2 colonies per square centimeter, as described in Sriram et al.<sup>3</sup>. This information has been added to Protocol Step 3.1. It is still advisable that the seed density be evaluated and refined empirically, as needed.

2. Please describe the differentiation protocol by using more accurate words, ie. don't use sentence like "If the media has become yellow" in the part of 3.5 and 3.6.

This phrasing has been removed from the protocol.

3. The "+" and "-" Fig.2 should be superscript.

This edit has been made.

**Reviewer #5:**

**Manuscript Summary:** The manuscript of Nelson et al, "Directed Differentiation of Hemogenic Endothelial Cells from Human Pluripotent Stem Cells" provides a detailed, step by step, description of the method.

**Major Concerns:**

1. Please discuss the reason for selection VE-Cadherin negative cells for hematopoietic differentiation: "To verify the hematopoietic potential of hemogenic endothelial cells, the CD31<sup>+</sup> Flk-1<sup>+</sup> c-Kit<sup>+</sup>554 CD34<sup>+</sup> VE-Cadherin<sup>-</sup> CD45<sup>-</sup> endothelial cells isolated through FACS". Some other authors believe that VE-Cadherin is an essential marker of hemogenic endothelium (VE-Cadherin<sup>+</sup>, CD31<sup>+</sup>, CD34<sup>+</sup>, CD73<sup>-</sup>, CD43<sup>-</sup>), see, for instance, the review in Blood "Hematopoietic specification from human pluripotent stem cells". 2013 12;122(25):4035-46. 10.1182/blood-2013-07-474825

We refer the reviewer to Figure 2D of our companion publication in *Cell Reports* (Qiu, J., Nordling, S., Vasavada, H.H., Butcher, E.C., Hirschi, K.K. Retinoic Acid Promotes Endothelial Cell Cycle Early G1 State to Enable Human Hemogenic Endothelial Cell Specification. *Cell Reports*. **33** (9) (2020)). In this study, although both CD31<sup>+</sup>CD45<sup>-</sup>VE-Cad<sup>+</sup> and CD31<sup>+</sup>CD45<sup>-</sup>VE-Cad<sup>-</sup> cells generated hematopoietic colonies, we found significantly greater hematopoietic potential among the CD31<sup>+</sup>CD45<sup>-</sup>VE-Cad<sup>-</sup> cells; thus, we used absence of VE-Cad to enrich for endothelial cells with blood-forming potential. Furthermore, it is important to note that hemogenic endothelial cells exist on a continuum of gene expression, and they must lose expression of the endothelial specific genes such as VE-Cadherin to generate hematopoietic cells.

**Minor Concerns:**

1. Please indicate if the lymphoid component was not attainable with described method or it was not tested?

In related studies by our lab<sup>1</sup> utilizing the differentiation protocol described here, we show (Figures 1E, S1, and S2) through flow cytometry that multi-lineage blood cells expressing lymphoid markers (CD20, CD3), myeloid markers (CD14, CD66b, CD41, CD235ab) and leukocyte markers (CD11b, CD45) are generated by day 8 of differentiation.

2. Please provide a reference to a closely related study on the differentiation of human pluripotent stem cells to hemogenic endothelium with GSK3 inhibitor (CHIR99021). Stem Cell Res Ther 2017 Mar 17;8(1):67 DOI: 10.1186/s13287-017-0519-0

Thank you for directing us to this reference. We have incorporated it into our **revised Discussion** (lines 639-648).

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