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Supplementary Figure Legends

Figure S1. Immunocytochemical analysis of pluripotency status of hESCs cultured over Matrigel.

Phase contrast photomicrographs show the compact, well defined morphology of hESC colonies upon culture in mTeSR1 over Matrigel. Immunofluorescence micrographs show the expression of pluripotency markers OCT4, SSEA4, TRA-1-60, TRA-1-81 and alkaline phosphatase (AP) by H1 hESCs **(a)** and H9-hESCs **(b)**. Scale bars: 500µm.

Figure S2. Immunocytochemical analysis of pluripotency status of hESCs cultured over fibronectin.

Phase contrast photomicrographs show the compact, well defined morphology of H1-hESCs **(a)** and H9-hESCs **(d)** colonies upon culture in mTeSR1 over fibronectin for 24 hours. Real time RT-PCR comparison of expression of pluripotency genes (*OCT4, SOX2, NANOG*) by the H1-hESCs **(b)** and H9-hESCs **(e)** cultured over Matrigel and fibronectin. The plots show no significant difference in the gene expression between the cells grown on Matrigel and fibronectin. For gene expression plots, the levels of expression were normalized to corresponding *β-ACTIN* values and are shown as relative to that of respective undifferentiated hESCs cultured over Matrigel. Immunofluorescence micrographs show the expression of pluripotency markers OCT4, SSEA4, TRA-1-60, TRA-1-81and alkaline phosphatase (AP) by H1-hESCs **(c)** and H9-hESCs **(f)**. Scale bars: 200µm.

Figure S3. Time course analysis of early differentiation of hESCs towards mesodermal lineage.

(a) Schematic representation of differentiation of hESCs towards mesoderm using bFGF (Gi.F.F) after 24 hours of treatment with CHIR99021 (+GSKi). Condition without bFGF (Gi.-.-) and the one with bFGF+FGF receptor inhibitor PD173074 (Gi.FFi.FFi) were used as controls. **(b)** Representative photomicrographs display the change in the morphology of the hESC colonies under different differentiation conditions after 2 and 3 days of differentiation. The cells can be seen spreading and migrating away from the center of the colony similar to early migratory events observed in early embryonic development. **(c)** mRNA expression kinetics of markers associated with PS

(mesendoderm), anterior PS/ endoderm, mesodermal subsets and epithelial-mesenchymal transition (EMT) after differentiation of hESCs under the three different conditions. For all gene expression plots, the levels of expression were log normalized to corresponding *β-ACTIN* values and are shown as relative to that of undifferentiated hESCs. Scale bars: 500µm. Error bars: s.d. (n≥3). *p<0.05.**p<0.01.p values represent the levels of significance in relation to (Gi.-.-).

Figure S4. Time course analysis of early differentiation of hESCs towards endodermal lineage.

(a) Schematic representation of differentiation of hESCs towards endoderm using Activin A (Gi.A.A) after 24 hours of treatment with CHIR99021 (+GSKi). Condition without Activin A (Gi.-.-) and the one with Activin+TGFβ inhibitor SB431542 (Gi.ASb.ASb) were used as controls. **(b)** Representative photomicrographs display the change in the morphology of the hESC colonies under different differentiation conditions after 2 and 3 days of differentiation. The cells can be seen spreading and migrating away from the center of the colony similar to early migratory events observed in early embryonic development. **(c)** mRNA expression kinetics of markers associated with PS (PS/mesendoderm), anterior PS / endoderm, mesodermal subsets and epithelial-mesenchymal transition (EMT) after differentiation of hESCs under the three different conditions. For all gene expression plots, the levels of expression were log normalized to corresponding *β-ACTIN* values and are shown as relative to that of undifferentiated hESCs. Scale bars: 500µm. Error bars: s.d. (n≥3). *p<0.05.**p<0.01.p values represent the levels of significance in relation to (Gi.-.-).

Figure S5. Differentiation of H9-hESCs towards endothelial lineage.

Representative flow cytometry overlays display the kinetics of co-expression of VEGFR2 and CD34 **(a)**, CD31 and CD34 **(b)** upon induction of H9-hESCs with BMP4 (Gi.F.B), VEGF (Gi.F.V) and BMP4+VEGF (Gi.F.BV) over a differentiation period of 5 days.

Figure S6. Effect of VEGF on hESC-derived endothelial cells under serum-free conditions.

(a) Representative photomicrographs of endothelial cells after 24 hour exposure to increasing concentrations of VEGF reveal the apoptosis of cells at higher VEGF concentrations. (b) Representative flow cytometry plots displaying the Annexin V/ PI staining to quantify the apoptotic cell death with increasing concentrations of VEGF. Scale bar: 500µm.

Figure S7. Plasticity of hESC-derived arterial and venous ECs.

Ability of hESC-derived ECs to maintain the arterial and venous endothelial phenotypes was investigated by cross culturing hESC-derived arterial ECs in venous media conditions (i.e., in the absence of VEGF) and hESC-derived venous ECs in arterial media conditions by supplementing the medium with VEGF. **(a**) Representative flow cytometry overlays display the expression of arterial and venous markers among H1-Art-ECs, H1-Art-ECs cultured in the absence of VEGF [H1-Art-ECs (Venous)], H1-Ven-ECs and H1-Ven-ECs cultured in the presence of VEGF [H1-Ven-ECs (Arterial)]. **(b)** Bar charts show the percentage of H1-hESC-derived ECs (top panel) and H9-hESC-derived ECs (bottom panel) expressing arterial and venous markers upon culture in different culture conditions. The different culture conditions are represented as A (Art-ECs in arterial media), A to V (Art-ECs cultured in venous media), V (Ven-ECs in venous media) and V to A (Ven-ECs in arterial media). Error bars: s.d. ($n \ge 3$). $\text{*}p < 0.05$ (paired Student t test).

Figure S8. Survey of angiocrine secretory profile of arterial and venous ECs using angiogenesis antibody array.

Graphical representation of the relative amounts of 55 angiocrine factors secreted by H1-hESC derived Ven-ECs and Art-ECs analyzed using angiogenesis antibody array. The bars represent relative amounts of factors secreted based on densitometric analysis of relative pixel density of the blots. Error bars: s.d. of 2 independent experiments. *p<0.05.**p<0.01.

Table S1: Legend of coordinates for the human angiogenesis array.

Table S2: Sequences of primers used for real time RT-PCR.

Table S3: List of antibodies used for flow cytometry.

Table S4: List of antibodies used for immunocytochemistry.

Figure S1

Figure S3

Figure S4

Annexin V-AF488

SUPPLEMENTARY TABLES

Table S1: Legend of coordinates for the human angiogenesis array.

The location of controls and captured antibodies in the Human Angiogenesis Array is listed below. The picture shows the coordinates of each control/ captured antibody in the array.

Table S2: Sequences of primers used for real time RT-PCR.

Table S3: List of antibodies used for flow cytometry.

SUPPLEMENTARY METHODS

Culture of primary endothelial cells

Human umbilical vein endothelial cells (HUVECs, Lonza) (kind gift from Koon Gee Neoh, National University of Singapore) were cultured in Clonetics™ EGM™-2 media (endothelial growth media with 2% serum and other growth factor supplements) as per manufacturer's instructions. Human coronary artery endothelial cells (HCAECs) (Promocell) were cultured in Promocell™ ECGM-2 media (endothelial cell growth media with 2% serum and other growth factor supplements) as per manufacturer's instructions. Passage 3-5 of HUVECs and HCAECs were used for the experiments.

RNA extraction and real-time PCR

Total cellular RNA was isolated from harvested cells using RNeasyPlus Mini kit (Qiagen) and reverse transcribed using iScript™ cDNA synthesis kit (BioRad) according to manufacturer's instructions. Real-time PCR was performed in triplicates using Fast SYBR Green PCR master mix (Applied Biosystems) and Stepone Plus real-time PCR system (Applied Biosystems) as per manufacturer's instructions. Real-time PCR reaction mixtures were denatured at 94° C for 20s and cycled for 40 cylces at 95° C for 3s, 60° C for 30s, followed by melt curve stage. The expression levels of specific genes were quantified by normalization against corresponding internal control gene *β-ACTIN* and expressed as the fold change relative to control sample (undifferentiated hESCs). Details of related primer sequences used in this study are presented in **Supporting Information, Table S2**. The results are presented as mean \pm standard deviations of atleast three independent experiments.

Flow Cytomerty analysis and sorting

hESCs and differentiated cells were harvested using accutase, resuspended in FACS buffer (1xPBS/ 0.5% BSA) and incubated with FcR blocking agent (1:10; MiltenyiBiotec) for 10 minutes at 4° C to block non-specific binding of antibodies. For labeling of cell surface antigens, the cells were incubated with the antibodies for 10 minutes at 4°C. The list of antibodies used is presented in **Supporting Information, Table S3**. After labeling with appropriate antibodies, the cells were washed thrice with FACS buffer to remove unbound antibodies and resuspended in FACS buffer for analysis and/or sorting. The labeled cells were analyzed for surface-marker expression using Dako Cytomation CyAn ADP and sorted using a Dako Cytomation MoFlo high speed flow cytometer. The flow cytometry data was further analyzed using FlowJo v7.6.5 (TreeStar).

Immunocytochemistry

hESCs and differentiated cells were fixed with 4% paraformaldehyde (Sigma) for 20 minutes at room temperature. The fixed cells were permeabilized using PBS/ 0.1% Triton X-100 (Sigma) for 10 minutes, washed thrice with PBS/0.05% Tween-20 (Sigma) and blocked with PBS/5% goat serum for 60 minutes to block non-specific binding. Subsequently, the cells were labeled with appropriate primary antibodies (listed in **Supporting Information, Table S4**) at 4°C overnight and fluorescently labeled using appropriate secondary antibodies (listed in **Supporting Information, Table S4**) for 60 minutes. For nuclear labeling, the cells were washed and labeled with 4`,6-diamidino-2-phenylindole (DAPI; Sigma) for 3 minutes. After washing thrice, the cells were observed using fluorescence microscope (Olympus IX70). The images in Figure 1 were obtained using laser scanning confocal microscope, while all other fluorescent images were obtained using epifluorescence microscope.

Acetylated-low density lipoprotein uptake assay

To demonstrate the ability of ECs to phagocytize low-density lipoprotein (LDL), hESC-derived arterial and venous ECs, were incubated with 10µg/ml of Dil-acetylated-LDL (Dil-Ac-LDL; Molecular Probes) for 4h. The cells were washed with PBS and the nuclei counterstained with Hoescht 33258 (Sigma) and observed using fluorescence microscope (Olympus IX70).

Matrigel tube formation assay

Ability of the endothelial cells to form vascular tube-like structures over Matrigel™ was analyzed as previously described [1]. Briefly, 7.5x10³ ECs were seeded onto each well of ibidi µ-angiogenesis slides that is coated with 10µl of Matrigel. After incubation for 18h, the vascular tube-like structures were labeled with 1µM Calcein-AM (Sigma) as per manufacturer's instructions and visualized using fluorescence microscope (Olympus IX70).

Annexin V-Propidium Iodide (PI) apoptosis assay

Analysis of live cells and apoptotic cells were performed using Alexa Fluor® 488 Annexin V/Dead Cell Apoptosis Kit (Molecular Probes). Briefly, the after 24 hour exposure to varying concentration of VEGF, the cells in the culture supernatant and culture plate were collected, washed and resuspended in 1x annexin-binding buffer. Then, the cells were incubated with Alexa Fluor® 488 annexin V and PI for 15 minutes at room temperature as per manufacturer's instructions. After the incubation period, the cells were analyzed immediately using DakoCytomationCyAn ADP and FlowJo v7.6.5.

Wound closure assay

Confluent monolayers of H1-Art-ECs, H1-Ven-ECs, H9-Art-ECs, H9-Ven-ECs, HUVECs and HCAECs were scraped with a 200µl pipette tip to create a "wound" as described previously [2]. Following the creation of the wound, the cells were washed with PBS to remove debris and floating cells. H1-Art-ECs, H1-Ven-ECs, H9-Art-ECs and H9-Ven-ECs were incubated for a period of 30 hours at 37^0C in endothelial serum-free media supplemented with EGF (10ng/ml) and bFGF (20ng/ml). The H1-Art-ECs and H9-Art-Ecs were not supplemented with VEGF to eliminate the bias that could be created otherwise. Similarly, HUVECs and HCAECs were incubated in respective serum containing endothelial media and necessary supplements except VEGF. Photomicrographs of the same field were acquired every 3 hours starting from 0 hours to 30 hours. The closure of the wound by migration of the cells was analyzed using T-Scratch program [3], available from www.cselab.ethz.ch/software.html. The results are tabulated as mean \pm standard deviations of three independent experiments.

Angiocrine secretome profiles of differentiated ECs

Human Angiogenesis Proteome Profiler™ antibody array (R&D Systems) was used to survey the levels of 55 different angiocrines secreted by H1-Art-ECs and H1-Ven-ECs using media conditioned by the respective cells. The ECs were seeded onto fibronectin-coated plates at a seeding density of 1.2x10 4 /cm² in their respective media. After 24 hours, the media for H1-Art-ECs and H1-Ven-ECs were changed to ESFM supplemented with EGF and bFGF only and incubated for 24 hours. After the incubation, the conditioned media were collected and stored at -80 $\mathrm{^0C}$. Total protein concentration within cell-free culture supernatants were quantified using Micro BCA™ Protein Assay Kit (Thermoscientific) as per manufacturer's instructions. Cell culture supernatant containing 200µg of protein was used for the antibody array as per manufacturer's instructions. The membranes were developed using 10 minute exposure to X-ray film. The array data was quantified by densitometry analysis using Image J (NIH, USA). The co-ordinates for the antibody arrays are presented in **Supporting Information, Table S1**.

Histological analysis

Formalin-fixed and paraffin-embedded tissues were appropriately processed and sections of 5µm were stained with haematoxylin and eosin. Immunohistochemical staining of the explants were performed using EnVision+/HRP kit (Dako) after antigen retrieval using heat treatment at 95°C for 20

minutes in Citrate buffer, pH6.0. The primary antibodies used were mouse anti-human CD31 (1:50; Clone: 9G11, R&D Systems), mouse anti-human Collagen-IV (1:50; Clone: COL-94, Sigma-Aldrich), rabbit anti-human Ephrin-B2 (1:200; polyclonal, GeneTex) and rabbit anti-human Eph-B4 (1:200; polyclonal, GeneTex).

Statistical analysis

To compare the difference between means among three groups as in Figures 1, 2, S3, and S4, the statistical significance was analyzed using one way ANOVA and Tukey's HSD posthoc analysis. Similarly, the difference in means between two groups as in Figures 5, 6, S2, S7 and S8 were analyzed using Student's t-test.

SUPPLEMENTARY REFERENCES

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