Supplementary Figure 1. Schematic representation of experiments to determine the role of macrophages and endothelial cells in the βVEGF-A mouse model. (a) Clodronate liposomes were used to suppress macrophage (MΦ) infiltration, followed by administration of doxycycline (Dox) to overexpress VEGF-A in β cells. (b–c) To modulate endothelial cells (ECs), an inducible EC-specific VEGFR2 knockout mouse model Cd5-CreER; VEGFR2<sup><i>fl/fl</i></sup> (VEGFR2<sup><i>ΔEC</i></sup>)<sup>26</sup> was bred into the βVEGF-A line. Tamoxifen (Tm) was used to inactivate VEGFR2 in ECs either prior to (b) or after (c) VEGF-A induction to discern the role of proliferative and quiescent ECs, respectively in the β cell loss and recovery. (d) ECs, MΦs, and β cells were isolated from βVEGF-A mice at three time points; introduction of the MIP-GFP transgene facilitated β cell sorting. For additional details, see Methods.
Supplementary Figure 2. Experimental design for clodronate-mediated macrophage depletion. (a) Gating strategy for flow cytometry analysis of circulating monocytes. Peripheral blood (50-100 μl) was collected from the retro-orbital sinus of βVEGF-A mice to assess monocyte depletion following clodronate treatment. Cell debris were excluded by forward scatter (FSC) and side scatter (SSC), single cells were identified by voltage pulse geometry, and non-viable cells were excluded using propidium iodide. From remaining white blood cells, CD45 was used as a pan-leukocyte marker and monocytes were identified by a CD11b+ Ly6G– profile. Approximately 10,000 white blood cells were analyzed and quantified per each animal. See also Figure 2b. (b) Representative images showing islet macrophage (MΦ) infiltration during VEGF-A induction (1 wk Dox). These cells express Iba1 (green), which colocalizes with canonical MΦ markers CD11b and F4/80 (red). Scale bar, 50 μm. See also Figure 2c.
Supplementary Figure 3. Acute ablation of VEGFR2 in endothelial cells does not alter islet vascular homeostasis or β cell proliferation. (a) To inactivate VEGFR2 in endothelial cells (ECs), Cdh5-CreERT2; VEGFR2<sup>ΔEC</sup> (<em>VEGFR2<sup>ΔEC</sup></em>) mice received treatments (Tx) of corn oil (vehicle) or tamoxifen (Tm; 4mg s.c.) every other day for 5 days. (b) Representative images of islet ECs (CD31<sup>+</sup>) and β cells (Insulin<sup>+</sup>) in vehicle- and Tm-treated VEGFR2<sup>ΔEC</sup> mice. VEGFR2 expression (red) is virtually undetectable in ECs at 8 or 15 days (d) after initial Tx. Scale bar, 50 μm. (c) VEGF-A expression (red) is maintained in β cells (blue) after VEGFR2 inactivation. Scale bar, 50 μm. (d) Quantification (mean ± s.e.m.) of islet architecture in VEGFR2<sup>ΔEC</sup> mice at 8d post-Tx; each circle represents one animal. Islet capillary density and area per islet capillary determined by CD31<sup>+</sup> and Insulin<sup>+</sup> stain; 138 ± 15 x 10<sup>5</sup> μm<sup>2</sup> total islet area analyzed per animal. (e) In both vehicle- and Tm-treated mice, the number of islet capillaries increases proportionately with islet size. Note both axes have a base 2 logarithmic scale. (f) Basal β cell proliferation rate; 1,892 ± 259 cells counted per animal. Statistics shown in panels d and f reflect unpaired two-tailed t-tests.
Supplementary Figure 4. Effective VEGFR2 inactivation in endothelial cells prevents islet capillary expansion by acute elevation of VEGF-A in the islet microenvironment. (a) To inactivate VEGFR2 in endothelial cells (ECs), βVEGF-A; R2ΔEC mice and βVEGF-A; R2fl/fl controls were treated with Tamoxifen (Tm; 4mg s.c.) prior to VEGF-A induction. (b) Left panel: induction of VEGFA expression at 3d Dox compared to baseline (No Dox) in βVEGF-A; R2ΔEC mice and controls; VEGF-A (red); β cells (Insulin*, blue). Boxes indicate regions enlarged in insets. Right panel: inactivation of VEGFR2 expression in ECs at baseline and 3d Dox; VEGFR2 (red), ECs (CD31*, green); β cells (Insulin*, blue). Scale bars, 50 μm; inset, 10 μm.
**Supplemental Figure 5. Effects of VEGF-A induction and VEGFR2 inactivation during β cell recovery.** (a) To inactivate VEGFR2 in endothelial cells (ECs) during β cell recovery, control (βVEGF-A; VEGFR2^fl/fl^) and VEGFR2^iΔEC^ (βVEGF-A; VEGFR2^iΔEC^) mice received Tamoxifen (Tm; 4mg s.c.) after 7 days (d) of Dox withdrawal (WD). (b–c) Expression of VEGF-A in β cells (b) and VEGFR2 in ECs (c) at 7d WD and 9d WD. Boxes show regions enlarged in insets; arrowheads point to extracellular VEGF-A staining. (d) Intra-islet M2-like macrophages (MΦs, CD206^+^ Iba1^+^) were present in both control and VEGFR2^iΔEC^ mice before and after Tm treatment. Approximate islet area is outlined; boxes show regions enlarged in insets with insulin channel (blue) removed. Scale bars in b–d are 50 μm; insets, 10 μm.
Supplemental Figure 6. Transcriptome analysis demonstrates unique gene expression profiles in β cells, endothelial cells and macrophages purified from islets during the period of β cell loss and recovery. (a–b) Dispersed islet cells from βVEGF-A; MIP-GFP mice were immunolabeled with fluorophore-conjugated anti-CD31 and anti-CD11b antibodies to separate endothelial cell (EC) and macrophage (MΦ) populations, respectively. GFP+ β cells were sorted from the CD31- CD11b- population. Initial gating is shown in first four plots. (c) Principal component analysis (PCA) plot shows the clustering of samples from sorted β cells (blue), ECs (green), and MΦs (red) at No Dox, 1wk Dox, and 1wk WD; n=3-5 biological replicates per time point as listed in Key. Islets from multiple mice were pooled to obtain adequate cells for each sample. (d) Pairwise correlation between all samples at all time points based on the Spearman correlation coefficient, which ranks and quantifies the degree of similarity between each pair of samples (perfect correlation=1; green). (e) Total number of genes for each cell type significantly up- or down-regulated (FC ≥2 or ≤-2) when comparing time points (dashed outlines): 1wk Dox vs. No Dox, 1wk WD vs. 1wk Dox, and 1wk WD vs. No Dox.

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Supplemental Figure 7. Temporal changes in gene expression profiles of islet cell subpopulations by RNA-sequencing. (a) Normalized expression of selected genes in isolated β cell (blue), EC (green), and MΦ (red) samples; n=3-5 biological replicates per cell type per time point. ECM, extracellular matrix. Numbers listed on heat map in 1wk Dox and 1wk WD columns represent fold-change ≥2 or ≤-2 (p<0.05) as compared to No Dox. Color scales beneath each column correspond to normalized expression values ranging from 0 (white) to ≥15,000 (dark blue, green, or red for β cells, ECs, or MΦs, respectively). (b) Ingenuity Pathway Analysis (IPA) was applied to fold-change data (1wk Dox vs. No Dox, 1wk WD vs. 1wk Dox, and 1wk WD vs. No Dox) for β cell, EC, and MΦ populations. Pathways showing significant regulation (z-score ≥2 or ≤-2, p<0.05) in at least two cell types are shown; a full list is provided in Supplementary Table 1. Z-scores of relevant comparisons are listed on heat map. Color scales represent positive or negative regulation of pathways (z-score); β cell pathways are upregulated only (blue), while pathways enriched in ECs and MΦs include those positively regulated (green and pink, respectively) and those downregulated (magenta and teal, respectively).
Supplemental Figure 8. Biological processes enriched in islet macrophages, endothelial cells, and β cells of βVEGF-A mice during β cell loss and recovery. Venn diagrams showing profiles of β cells (a), endothelial cells (ECs) (b), and macrophages (MΦs) (c) as determined by Gene Ontology (GO) term analysis; n=3-5 biological replicates per cell type per time point. Processes are organized by pairwise comparisons between time points (1wk Dox vs. No Dox, 1wk WD vs. 1wk Dox, and 1wk WD vs. No Dox), with location of text in Venn diagram accounting for processes that are represented in multiple time point comparisons. (d) Unique and shared processes of β cells, ECs, and MΦs during β cell recovery (1wk WD vs. 1wk Dox and/or 1wk WD vs. No Dox). All terms diagrammed in (a–d) appeared in top 20 hits (highest statistical significance) for the indicated population(s); those omitted due to space constraints are provided in Supplementary Table 2.
## Supplementary Table 1: GO Terms for sorted cell populations

| Term                                                                 | Process                              | p value:         | β cells | 
|---------------------------------------------------------------------|--------------------------------------|------------------|---------| 
| GO:0000087 M phase of mitotic cell cycle                            |                                      | 5.31E-09 G1vG0   | 1.13E-06 | 
| GO:0000278 Mitotic cell cycle                                       |                                      | 3.29E-06 G2vG0   | 3.37E-10 | 
| GO:0000279 M phase                                                  |                                      | 8.80E-11 G2vG1   | 3.58E-07 | 
| GO:0000280 Nuclear division                                         |                                      | 3.28E-06 G1vG0   | 1.05E-09 | 
| GO:0000902 Cell morphogenesis                                       |                                      | 6.64E-05 G2vG0   | 2.70E-09 | 
| GO:0000904 Cell morphogenesis involved in differentiation            |                                      | 1.59E-06 G2vG1   | 3.62E-04 | 
| GO:0001501 Skeletal system development                              |                                      | 2.97E-08         |         | 
| GO:0001503 Ossification                                             |                                      | 3.53E-04         | 0.002241 | 
| GO:0001525 Angiogenesis                                             |                                      | 7.92E-13         | 6.32E-05 | 
| GO:0001568 Blood vessel development                                 |                                      | 3.64E-21         | 9.44E-13 | 
| GO:0001775 Cell activation                                         |                                      | 1.79E-15         | 1.55E-12 | 
| GO:0001817 Regulation of cytokine production                        |                                      | 1.57E-10         |         | 
| GO:0001944 Vasculature development                                  |                                      | 3.10E-22         | 1.52E-13 | 
| GO:0002504 Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II |                                      | 5.63E-10         |         | 
| GO:0002526 Acute inflammatory response                              |                                      |                 | 6.27E-05 | 
| GO:0002684 Positive regulation of immune system process             |                                      | 1.63E-13         | 2.60E-13 | 
| GO:0002694 Regulation of leukocyte activation                       |                                      | 4.06E-09         |         | 
| GO:0006323 DNA packaging                                            |                                      |                 | 2.18E-04 | 
| GO:0006412 Translation                                              |                                      | 1.06E-04         | 6.97E-06 | 
| GO:0006811 Ion transport                                            |                                      | 2.18E-04         | 5.92E-04 | 
| GO:0006812 Cation transport                                         |                                      | 1.07E-04         | 4.04E-04 | 
| GO:0006813 Potassium ion transport                                  |                                      | 2.24E-04         | 3.99E-04 | 
| GO:0006836 Neurotransmitter transport                              |                                      |                 | 5.17E-04 | 
| GO:0006928 Cell motion                                             |                                      | 1.71E-10         |         | 
| GO:0006935 Chemotaxis                                              |                                      | 1.78E-11         |         | 
| GO:0006952 Defense response                                         |                                      | 1.51E-14         | 1.18E-04 | 
| GO:0006954 Inflammatory response                                   |                                      | 2.18E-15         | 3.41E-06 |
**Supplementary Table 1: GO Terms for sorted cell populations**

| Term | Process | p value: | \( \beta \) cells | ECs | Macrophages |
|------|---------|----------|-------------------|-----|-------------|
| GO:0006955 | Immune response | | G1vG0: 1.35E-10 G2vG0: 4.67E-22 G2vG1: 6.57E-12 | G1vG0: 4.58E-06 G2vG0: 8.85E-06 G2vG1: 1.61E-05 | G1vG0: 1.12E-10 G2vG0: 4.43E-10 G2vG1: 9.81E-11 |
| GO:0007017 | Microtubule-based process | | | | |
| GO:0007018 | Microtubule-based movement | | | | |
| GO:0007049 | Cell cycle | G2vG0: 4.50E-09 G2vG1: 8.81E-07 G2vG0: 4.02E-13 | | |
| GO:0007059 | Chromosome segregation | | | | |
| GO:0007067 | Mitosis | G2vG0: 1.42E-05 G2vG1: 8.85E-06 | | |
| GO:0007126 | Meiosis | | | | |
| GO:0007155 | Cell adhesion | G2vG0: 1.06E-28 G2vG1: 4.21E-36 | G2vG0: 2.29E-06 G2vG1: 6.68E-10 | G2vG0: 4.43E-10 G2vG1: 5.82E-14 G2vG1: 9.81E-11 |
| GO:0007156 | Homophilic cell adhesion | | | | |
| GO:0007167 | Enzyme linked receptor protein signaling | | | | |
| GO:0007169 | Transmembrane receptor protein tyrosine kinase signaling pathway | | | | |
| GO:0007229 | Integrin-mediated signaling pathway | | | | |
| GO:0007267 | Cell-cell signaling | | | | |
| GO:0007409 | Axonogenesis | | | | |
| GO:0007411 | Axon guidance | | | | |
| GO:0008284 | Positive regulation of cell proliferation | | | | |
| GO:0009611 | Response to wounding | G2vG0: 6.84E-09 G2vG1: 8.15E-18 | G2vG0: 5.42E-04 G2vG1: 2.09E-07 G2vG1: 3.20E-09 | | |
| GO:0015672 | Monovalent inorganic cation transport | | | | |
| GO:0016337 | Cell-cell adhesion | | | | |
| GO:0016477 | Cell migration | G2vG0: 1.65E-08 | | | |
| GO:0016485 | Protein processing | | | | |
| GO:0019886 | Antigen processing and presentation of exogenous peptide antigen via MHC class II | | | | |
| GO:0022402 | Cell cycle process | | | | |
| GO:0022403 | Cell cycle phase | G2vG0: 2.53E-09 G2vG1: 1.90E-07 | G2vG0: 5.16E-15 | | |
| GO:0022610 | Biological adhesion | G2vG0: 1.32E-28 G2vG1: 5.59E-36 | G2vG0: 2.52E-06 G2vG1: 7.21E-10 | G2vG0: 4.92E-10 G2vG1: 6.46E-14 G2vG1: 1.07E-10 | | |
| GO:0030001 | Metal ion transport | | | | |

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**Supplementary Table 1:** GO Terms for sorted cell populations

| Term                                      | Process                              | β cells       | ECs           | Macrophages  |
|-------------------------------------------|--------------------------------------|---------------|---------------|--------------|
| GO:0030030 Cell projection organization   |                                      |               |               |              |
| GO:003155 Regulation of cell adhesion     |                                      | 5.67E-10      |               |              |
| GO:003182 Neuron differentiation          |                                      |               |               | 3.32E-08     |
| GO:003198 Extracellular matrix organization| 1.11E-13 1.62E-11                     | 6.79E-04      |               | 9.99E-04     |
| GO:003218 Erythrocyte differentiation     |                                      |               |               | 9.14E-04     |
| GO:003175 Neuron projection development   |                                      |               |               | 1.48E-07     |
| GO:0032940 Secretion by cell              | 2.48E-04                              |               | 3.34E-08     |
| GO:0032989 Cellular component morphogenesis| 1.22E-04                             |               | 8.57E-04     |
| GO:0032990 Cell part morphogenesis        |                                      |               | 2.09E-07     |
| GO:0034101 Erythrocyte homeostasis        |                                      |               | 5.06E-04     |
| GO:0035295 Tube development               | 7.39E-09                              |               |              |
| GO:0042127 Regulation of cell proliferation| 1.27E-14 7.62E-13                     |               | 8.49E-07     |
| GO:0042330 Taxis                          | 1.78E-11                              |               | 0.001387     |
| GO:0043062 Extracellular structure organization| 2.74E-10 5.05E-11                   | 1.18E-04      | 0.001091     |
| GO:0044057 Regulation of system process   |                                      |               | 7.29E-04     |
| GO:0045321 Leukocyte activation           | 4.48E-15 3.83E-12                     |               |              |
| GO:0045597 Positive regulation of cell differentiation| 2.62E-08 | |              |
| GO:0045765 Regulation of angiogenesis     | 3.60E-08                              |               |              |
| GO:0045785 Positive regulation of cell adhesion| 1.37E-08 | |              |
| GO:004649 Lymphocyte activation           | 3.34E-12 3.00E-10                     |               |              |
| GO:0046903 Secretion                      | 7.69E-05                              |               |              |
| GO:0048285 Organelle fission              |                                      | 9.66E-06 3.91E-09 |              |
| GO:0048514 Blood vessel morphogenesis     | 7.41E-20 2.09E-12                     |               | 4.47E-05     |
| GO:0048666 Neuron development             |                                      |               | 8.58E-09     |
| GO:0048667 Cell morphogenesis involved in neuron differentiation | 5.62E-05 | | 1.10E-08 |
| GO:0048812 Neuron projection morphogenesis| 2.34E-04                              |               | 1.70E-07     |
| GO:0048858 Cell projection morphogenesis  |                                      |               | 5.79E-08 7.17E-04 |
### Supplementary Table 1: GO Terms for sorted cell populations

| Term                  | Process                                      | p value: | β cells | ECs  | Macrophages |
|-----------------------|----------------------------------------------|----------|---------|------|-------------|
| GO:0050863            | Regulation of T cell activation              |          | 6.50E-09|      |             |
| GO:0050865            | Regulation of cell activation                |          | 1.74E-09|      |             |
| GO:0050867            | Positive regulation of cell activation       |          | 4.69E-09|      |             |
| GO:0050870            | Positive regulation of T cell activation     |          | 4.71E-11|      |             |
| GO:0051094            | Positive regulation of developmental process | 3.48E-09 |         |      |             |
| GO:0051249            | Regulation of lymphocyte activation          |          | 6.63E-09|      |             |
| GO:0051301            | Cell division                                |          | 5.30E-06| 8.55E-10|             |
| GO:0051321            | Meiotic cell cycle                           |          |         | 2.82E-04|             |
| GO:0051327            | M phase of meiotic cell cycle                |          | 2.02E-04|      |             |
| GO:0051604            | Protein maturation                           |          | 1.15E-04|      |             |
| GO:0051605            | Protein maturation by peptide bond cleavage  |          | 4.52E-06|      |             |
| GO:0060348            | Bone development                             |          |         | 0.001779|             |
Supplementary Table 2: Mouse strains utilized in experimental models

| Abbreviation | MGI Nomenclature or Strain Name | References |
|---------------|---------------------------------|------------|
| Cd5-CreER     | Tg(Cdh5-cre/ERT2)#Ykub          | Okabe et al., 2014<sup>24</sup> |
| MIP-GFP       | B6.Cg-Tg(Ins1-EGFP)1Hara/J      | Hara et al., 2003<sup>63</sup> |
| RIP-rtTA      | Tg(Ins2-rtTA)2Efr               | Milo-Landesman et al., 2001<sup>10</sup> |
| TetO-VEGF     | n/a                             | Efrat et al., 1995<sup>79</sup>; Ohno-Matsui et al., 2002<sup>91</sup> |
| VEGFR<sup>2<sub>fl/fl</sub></sup> | Kdr<sup>tm2Sato</sup>            | Hooper et al., 2009<sup>82</sup> |

Supplementary Table 3: Breeding scheme to generate βVEGF-A; VEGFR<sup>2ΔEC</sup> mice

| Cross | Male breeder | Female breeder | Desired Offspring | Frequency |
|-------|--------------|----------------|-------------------|-----------|
| A1    | Cd5-CreER<sup>tg/+</sup> | VEGFR2<sup>fl/fl</sup> | Cd5-CreER<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup> | 50%       |
| A2    | Cd5-CreER<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> | VEGFR2<sup>fl/fl</sup> | Cd5-CreER<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup> | 25%       |
| A3    | Cd5-CreER<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> ; RIP-rtTA<sup>tg/tg</sup> | VEGFR2<sup>fl/fl</sup> | Cd5-CreER<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup>; RIP-rtTA<sup>tg/+</sup> | 50%       |
| A4    | Cd5-CreER<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> ; RIP-rtTA<sup>tg/tg</sup> | VEGFR2<sup>fl/fl</sup> | Cd5-CreER<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup>; RIP-rtTA<sup>tg/+</sup> | 12.5%     |
| B1    | VEGFR2<sup>fl/fl</sup> | TetO-VEGFA<sup>tg/tg</sup> | TetO-VEGFA<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup> | 100%      |
| B2    | TetO-VEGFA<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> | TetO-VEGFA<sup>tg/tg</sup> | TetO-VEGFA<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup> | 50%       |
| B3    | TetO-VEGFA<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> ; VEGFR<sup>2ΔEC</sup> | TetO-VEGFA<sup>tg/tg</sup> ; VEGFR2<sup>fl/fl</sup> | TetO-VEGFA<sup>tg/+</sup>; VEGFR<sup>2ΔEC</sup> | 25%       |
| C1    | Cd5-CreER<sup>tg/+</sup> ; VEGFR2<sup>fl/+</sup> ; RIP-rtTA<sup>tg/tg</sup> | TetO-VEGFA<sup>tg/tg</sup> ; VEGFR2<sup>fl/fl</sup> | TetO-VEGFA<sup>tg/+</sup>; Cd5-CreER<sup>tg/+</sup>; VEGFR2<sup>fl/+</sup>; RIP-rtTA<sup>tg/+</sup> | 25%       |
| Genotype   | Primers                                                                 | PCR Conditions | Product(s)          |
|------------|-------------------------------------------------------------------------|----------------|---------------------|
| Cd5-CreER  | 5′- GCG GTC TGG CAG TAA AAA CTA TC -3′ 3′- TT CAC TGT CGT TAC GAC AAA GTG -5′ | 93°C 3' 93°C 20' 60°C 20' 30 cycles 72°C 45' 72°C 5' 4°C hold | 100 bp |
| MIP-GFP    | 5′- AAG TTC ATC TGC ACC ACC G -3′ (GFP) 3′- GC GTG GTA GAA GAA GTT CCT -5′ (GFP) | 94°C 1.5' 94°C 30' 60°C 1' 35 cycles 72°C 1' 72°C 2' 4°C hold | 173 bp (GFP) 324 bp (IC) |
| RIP-rtTA   | 5′- GTG AAG TGG GTC CGC GTA CAG -3′ 3′- CTA CGG GAA CCT TAA CTG CTC ATG -5′ | 92°C 2' 94°C 30' 57°C 30' 30 cycles 72°C 30' 72°C 10' 4°C hold | 400 bp |
| TetO-VEGF  | 5′- TCG AGT AGG CGT GTA CGG -3′ 3′- GCT ACG CCC CCG ACG ACG -5′ | 95°C 4' 95°C 1' 57°C 30' 29 cycles 72°C 1' 72°C 10' 4°C hold | 420 bp |
| VEGFR2fl/fl| 5′ - CCA CAG AAC AAC TCA GGG CTA -3′ 3′- AA AGG TCT CTG AAA CGA GGG -5′ | 94°C 2' 94°C 20' 65°C 15' 10 cycles 68°C 10' 94°C 15' 60°C 15' 28 cycles 72°C 10' 72°C 1' 4°C hold | 179 bp (VEGFR2) 230 bp (VEGFR2loxP) |

GFP, green fluorescent protein; IC, internal control
Supplementary Table 5: Antibodies used for immunohistochemistry and flow cytometry

| Antigen/Conjugate | Species | Source               | Catalog #       | Application   | Dilution       |
|-------------------|---------|----------------------|-----------------|---------------|----------------|
| Caveolin-1        | Rabbit  | Abcam                | ab2910          | IHC (1º)      | 1:2000         |
| CD11b             | Rat     | Novus                | NB600-1327      | IHC (1º)      | 1:400          |
| CD11b – APC       | Rat     | BD Pharmingen        | 561690          | FC            | 1:100, 1:500   |
| CD206 (Mrc1)      | Rat     | BioLegend            | 141701          | IHC (1º)      | 1:500          |
| CD31              | Rat     | BD Pharmingen        | 553370          | IHC (1º)      | 1:100          |
| CD31 – PE         | Rat     | BD Pharmingen        | 561073          | FC            | 1:500          |
| CD45 – PE         | Rat     | BD Pharmingen        | 561087          | FC            | 1:500          |
| Col-IV            | Rabbit  | Abcam                | ab6586          | IHC (1º)      | 1:1000         |
| F4/80             | Rat     | ThermoFisher Scientific | 14-4801-82   | IHC (1º)      | 1:200          |
| Goat IgG – Cy3    | Donkey  | Jackson Immunoresearch | 705-165-147 | IHC (2º)      | 1:500          |
| Guinea pig IgG – Cy2 | Donkey  | Jackson Immunoresearch | 706-225-148 | IHC (2º)      | 1:500          |
| Guinea pig IgG – Cy5 | Donkey  | Jackson Immunoresearch | 706-175-148 | IHC (2º)      | 1:200          |
| Iba1              | Rabbit  | Wako                 | 019-19741       | IHC (1º)      | 1:500          |
| Iba1              | Rabbit  | Abcam                | ab221790        | IHC (1º)      | 1:1000         |
| Insulin           | Guinea pig | Dako              | A0564           | IHC (1º)      | 1:1000         |
| Insulin           | Guinea pig | Cell Marque         | 273A-15         | IHC (1º)      | 1:500          |
| Ki67              | Rabbit  | Abcam                | ab15580         | IHC (1º)      | 1:5000         |
| Ly6G-FITC         | Rat     | BD Pharmingen        | 551460          | FC            | 1:500          |
| pERK              | Rabbit  | Cell Signaling       | 4370            | IHC (1º)      | 1:200          |
| Rabbit IgG – Cy2  | Donkey  | Jackson Immunoresearch | 711-225-152 | IHC (2º)      | 1:500          |
| Rabbit IgG – Cy3  | Donkey  | Jackson Immunoresearch | 711-165-152 | IHC (2º)      | 1:500          |
| Rat IgG – Cy2     | Donkey  | Jackson Immunoresearch | 712-225-153 | IHC (2º)      | 1:500          |
| VEGF-A            | Goat    | R&D Systems          | AF564           | IHC (1º)      | 1:200          |
| VEGFR2            | Goat    | R&D Systems          | AF644           | IHC (1º)      | 1:2000         |

1º, primary antibody; 2º, secondary antibody; FC, flow cytometry; IHC, immunohistochemistry