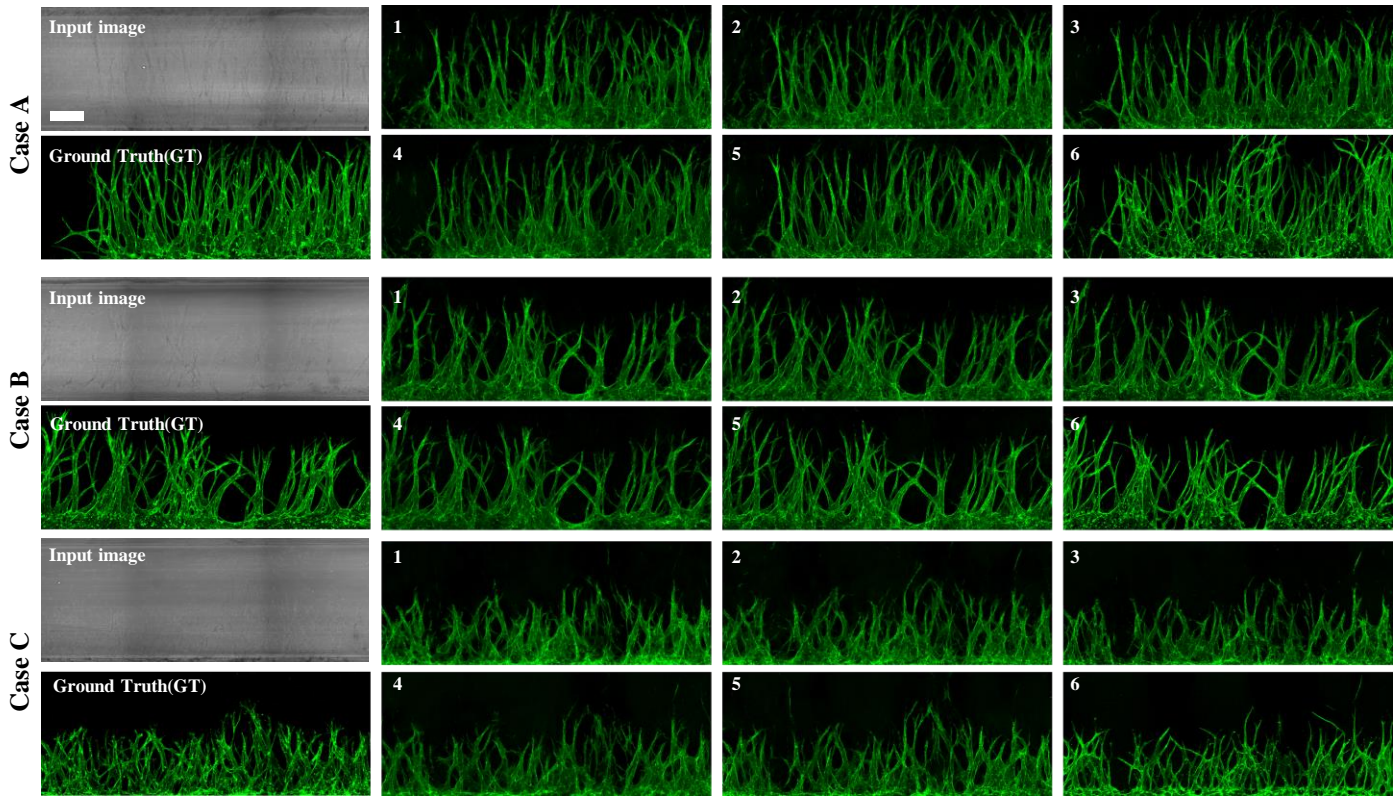
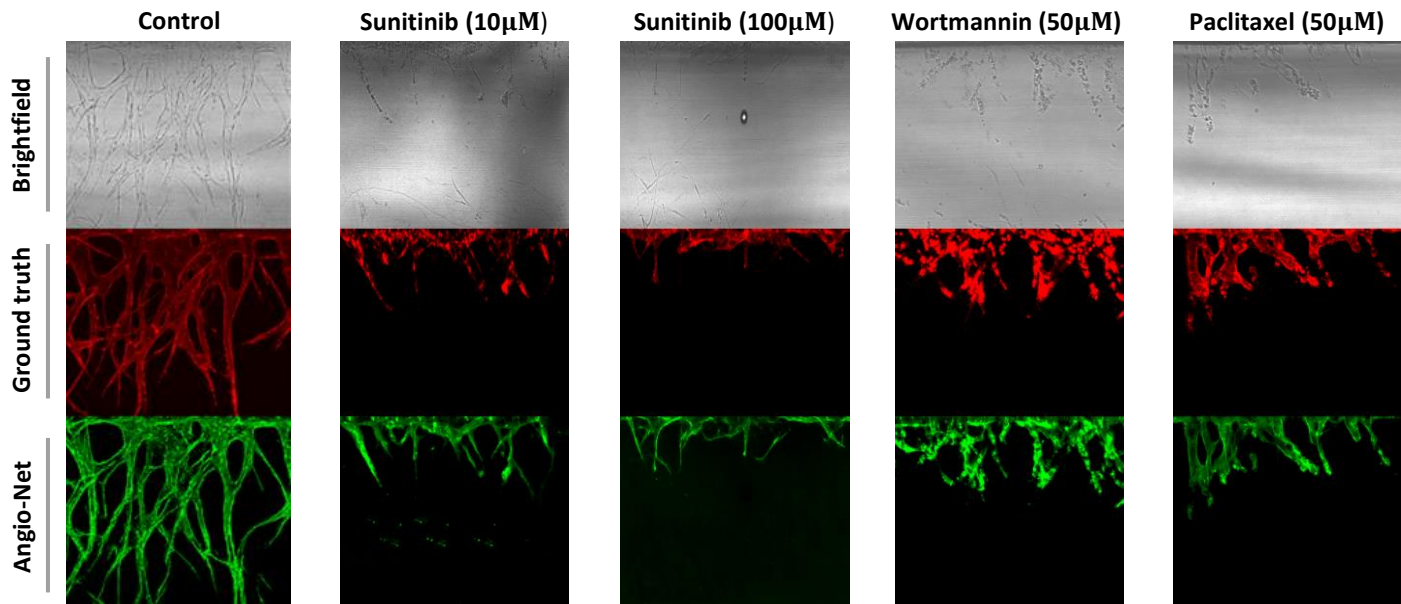


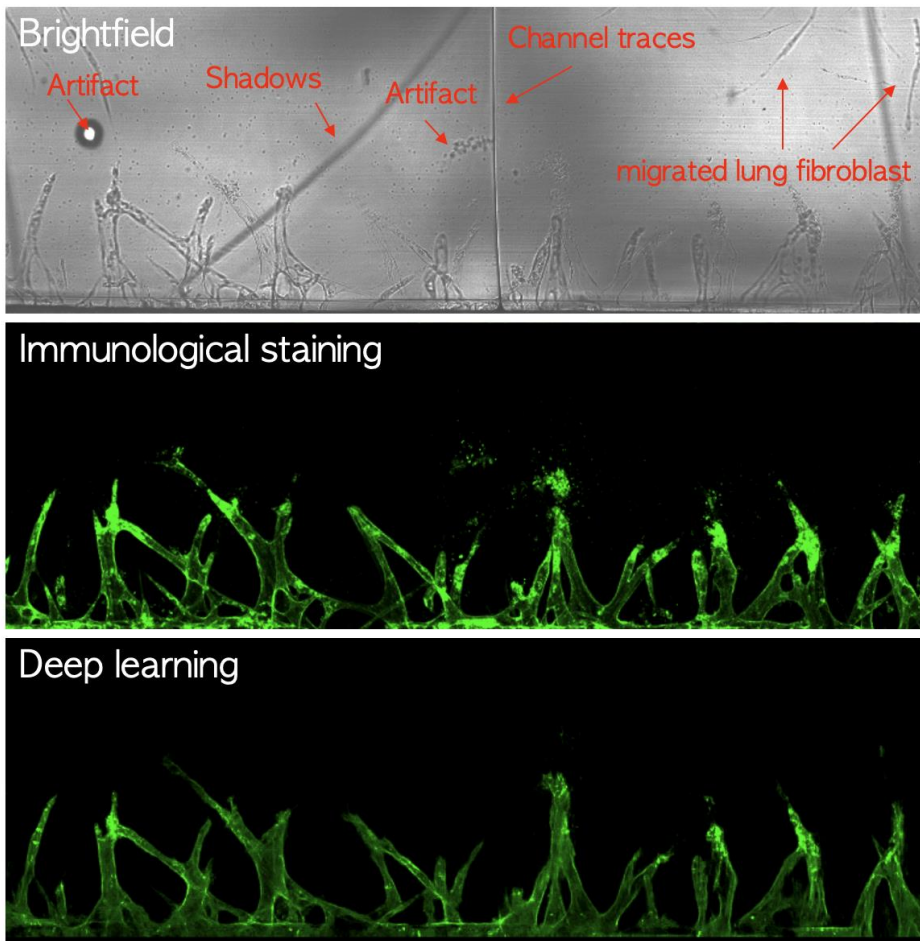
S. Figure 1. Angiogenesis quantification algorithm process. Start from preprocessing grayscale image by Gaussian Blur and Threshold binary to skeletonization network. Then skeletonization network is classified under three categories (sprout length, tip cell number, vascular area).



S. Figure 2. Input image, ground truth and six virtual immunostaining images from input images in case A, B and C with difference vessel growth height. (GT : Ground truth, 1 : L1 loss, 2 : L2 loss, 3 : L1 loss + GAN, 4 : L2 loss + GAN, 5 : SSIM + GAN, 6 : MSSSIM + GAN, $200\mu\text{m}$)



S. Figure 3. Virtual staining representation for high dose drug conditions: Control, Sunitinib 10 μ M and 100 μ M, Wortmannin 50 μ M, and Paclitaxel 50 μ M, representing brightfield, ground truth fluorescence (red image), and Angio-Net generated images (green image).



S. Figure 4. Brightfield image, immunologically stained image, and virtual stained image from one sample. The Brightfield image presents non-vascular elements, whereas the two stained images exhibit similarity, enabling specific identification of blood vessels.