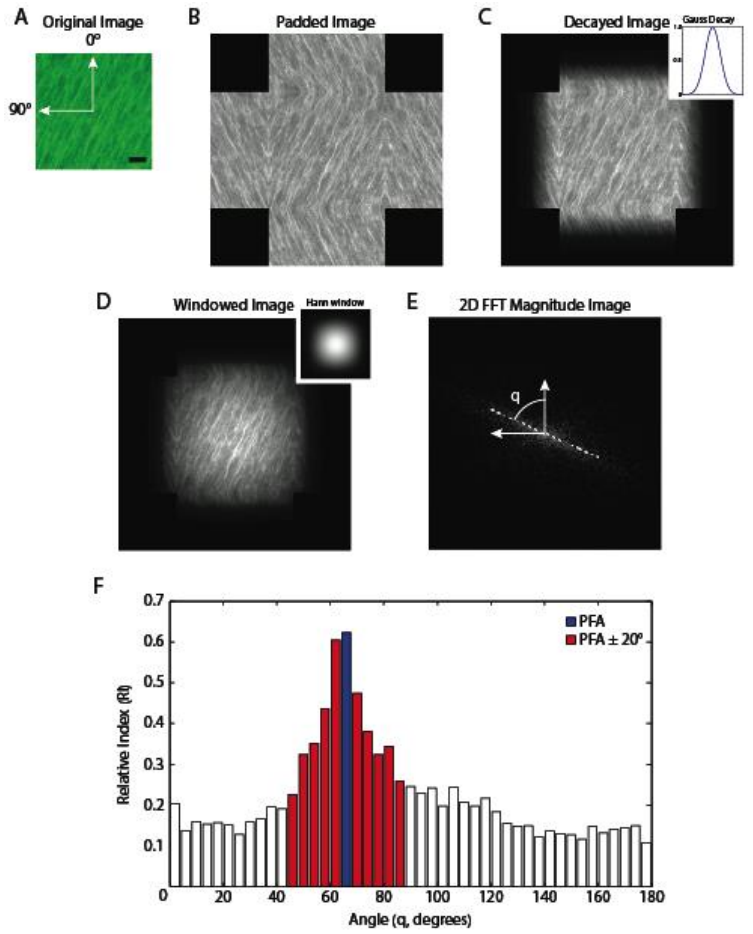
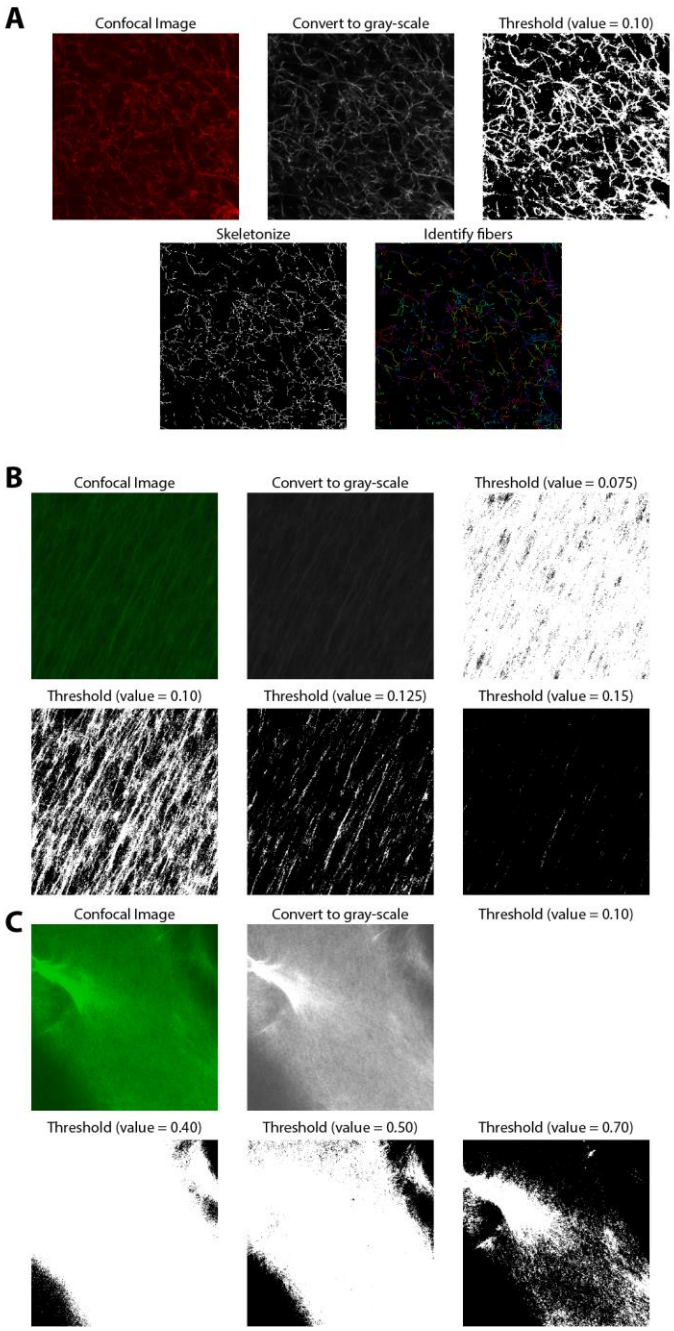


Supplemental Figure 1: Quantification of clot fiber alignment. The original confocal microscopy image (A) was preprocessed – padded (B), application of a Gaussian decay (C), application of 2D Hann window (D) – prior to application of a 2D fast Fourier transform to determine the power spectrum (E). Preferred fiber angle (PFA; blue bar) and alignment index [AI; PFA ± 20°(red bars)/random fiber distribution] were determined to assess fiber alignment. Scale bar = 20 μm



Supplemental Figure 2: Quantification of clot morphologic characteristics. The original confocal images were processed, which included conversion to grayscale, normalization, application of a threshold filter, and skeletonization to identify individual fibers. Application of these steps on the adult clot (A) allowed for evaluation of clot structural features. However, due to the nearly uniform pixel values in the neonate clots (B, C), these features could not be identified. Note the lack of identifiable fibers in the thresholded neonate clots, regardless of the chosen threshold value, as compared to the adult clot. Representative images are presented. (A) 2.5 mg/ml adult fibrinogen, 5 μg/ml thrombin; (B) 2.5 mg/ml neonatal fibrinogen 5 μg/ml thrombin; (C) 3.5 mg/ml neonatal fibrinogen 20 μg/ml thrombin