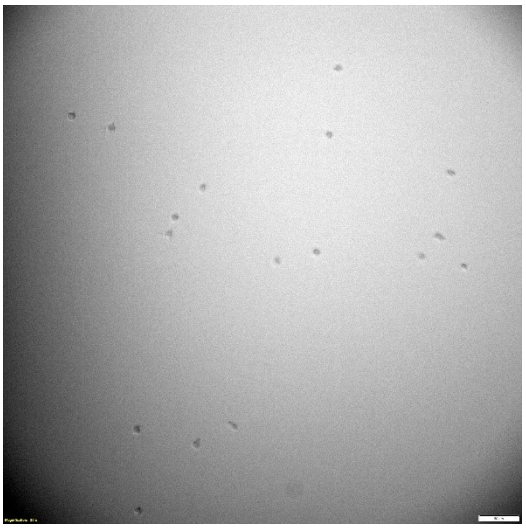
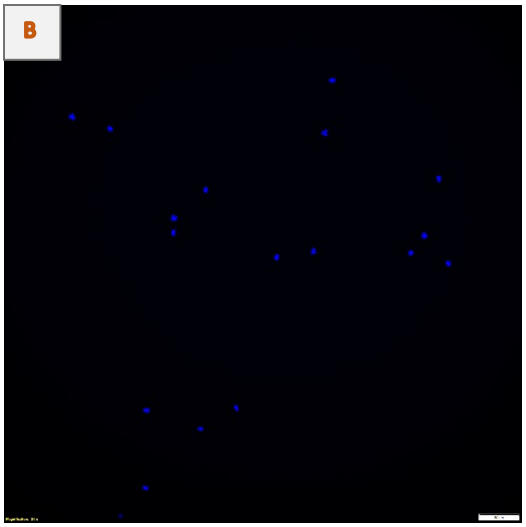
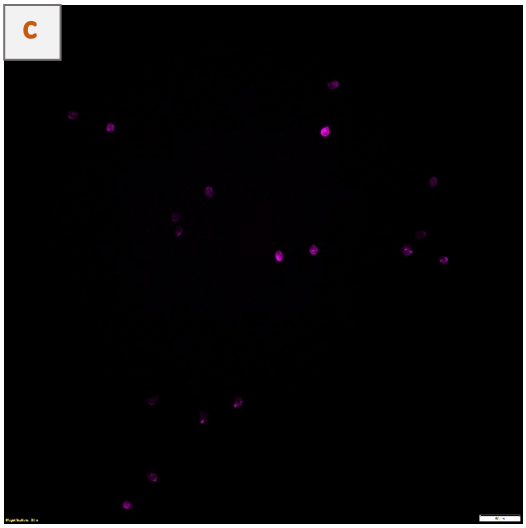
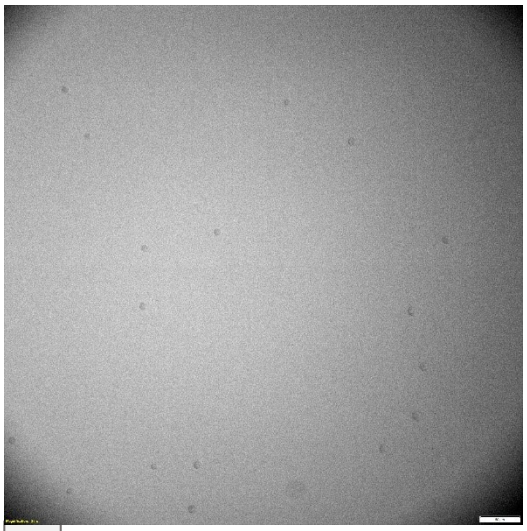
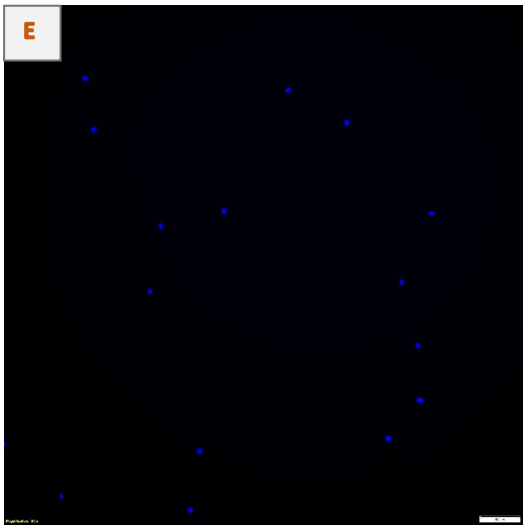
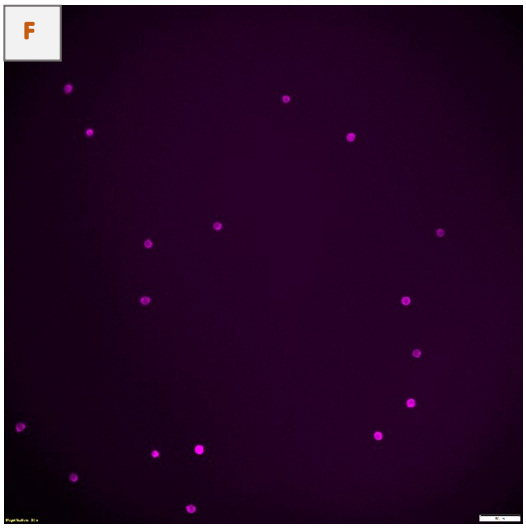




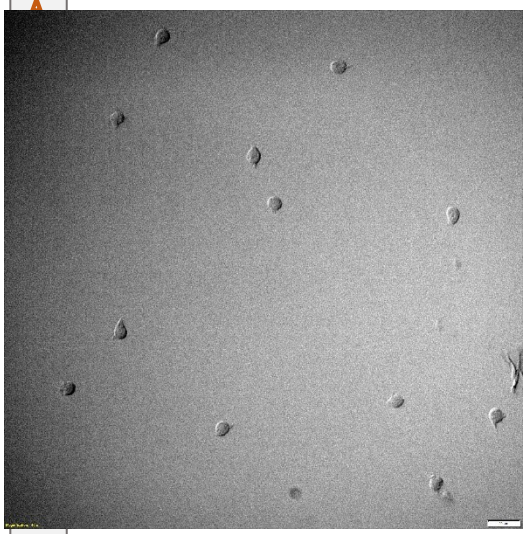


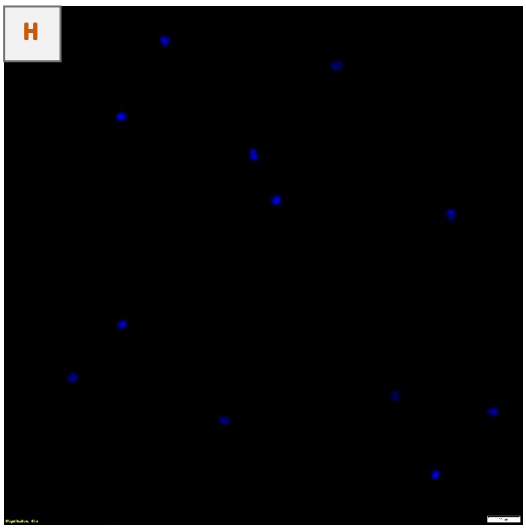


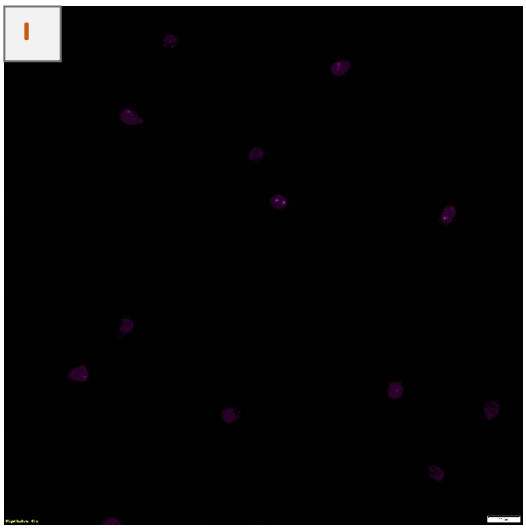




A







D

G

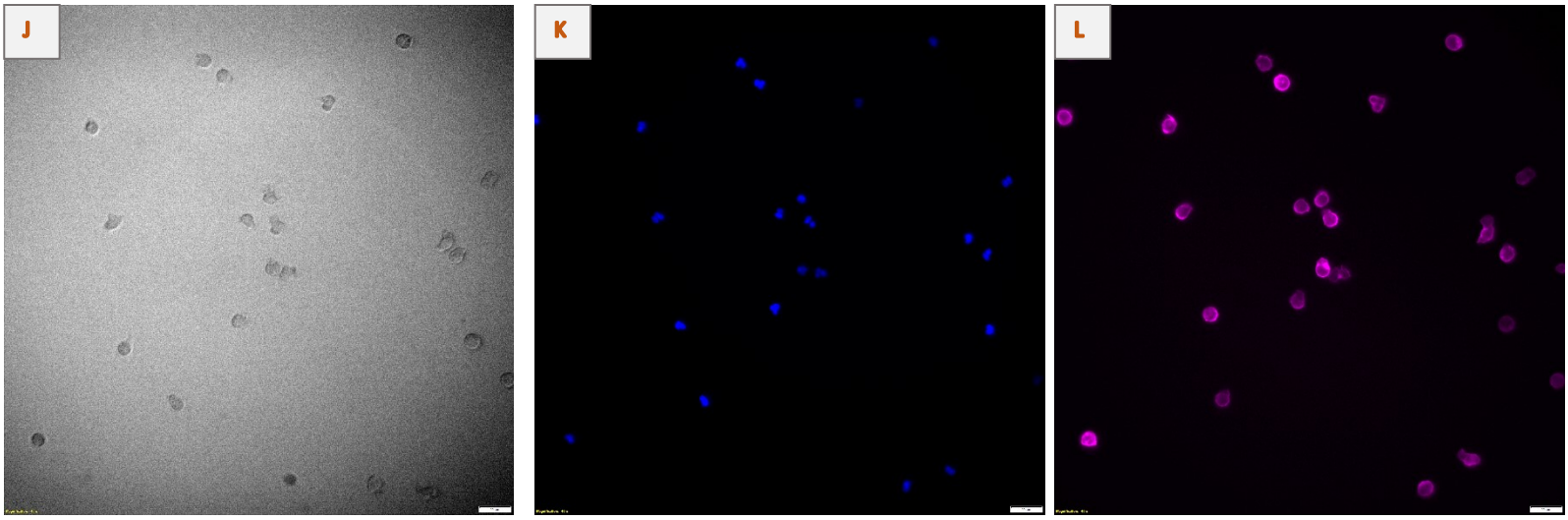
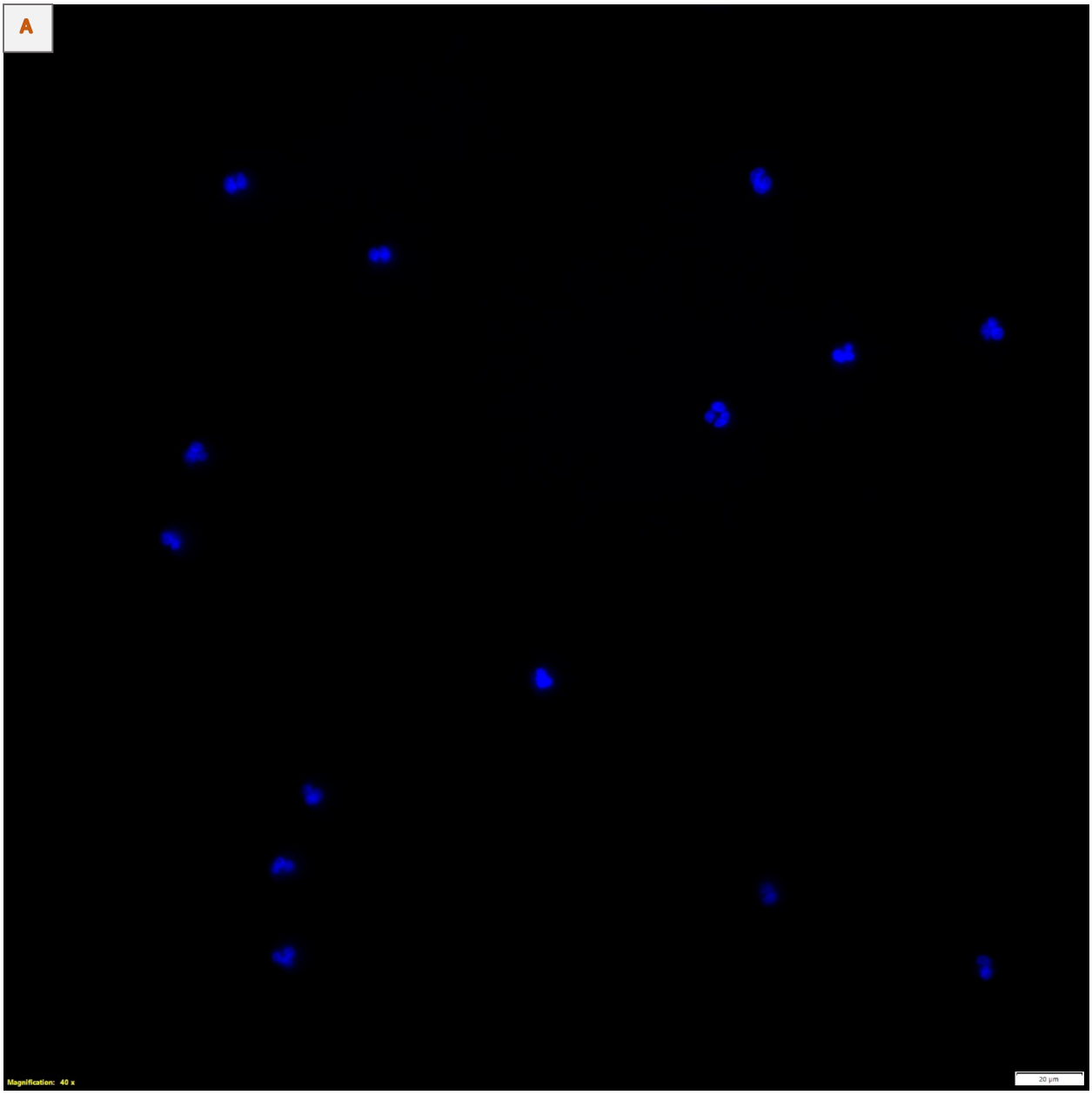
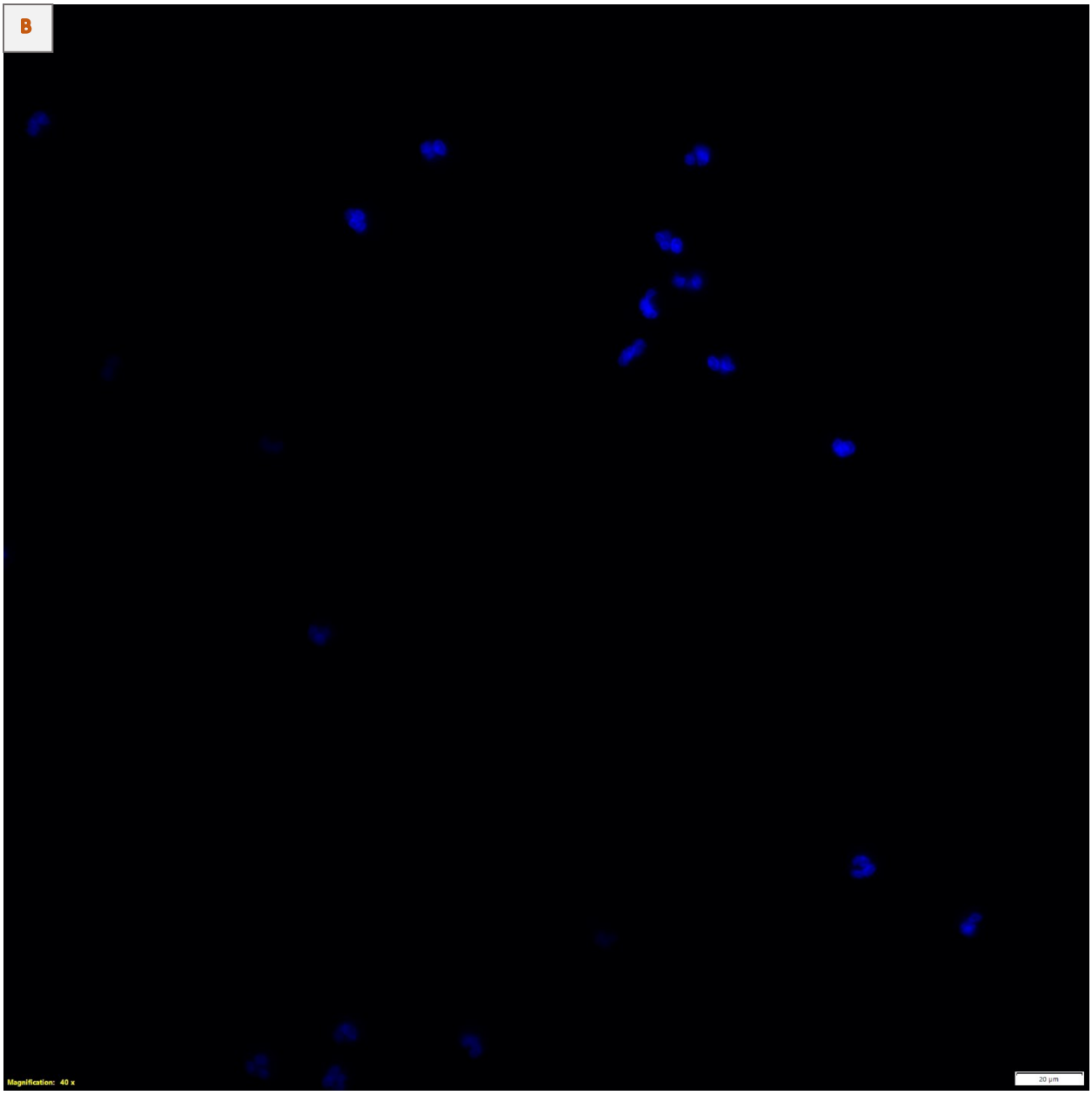
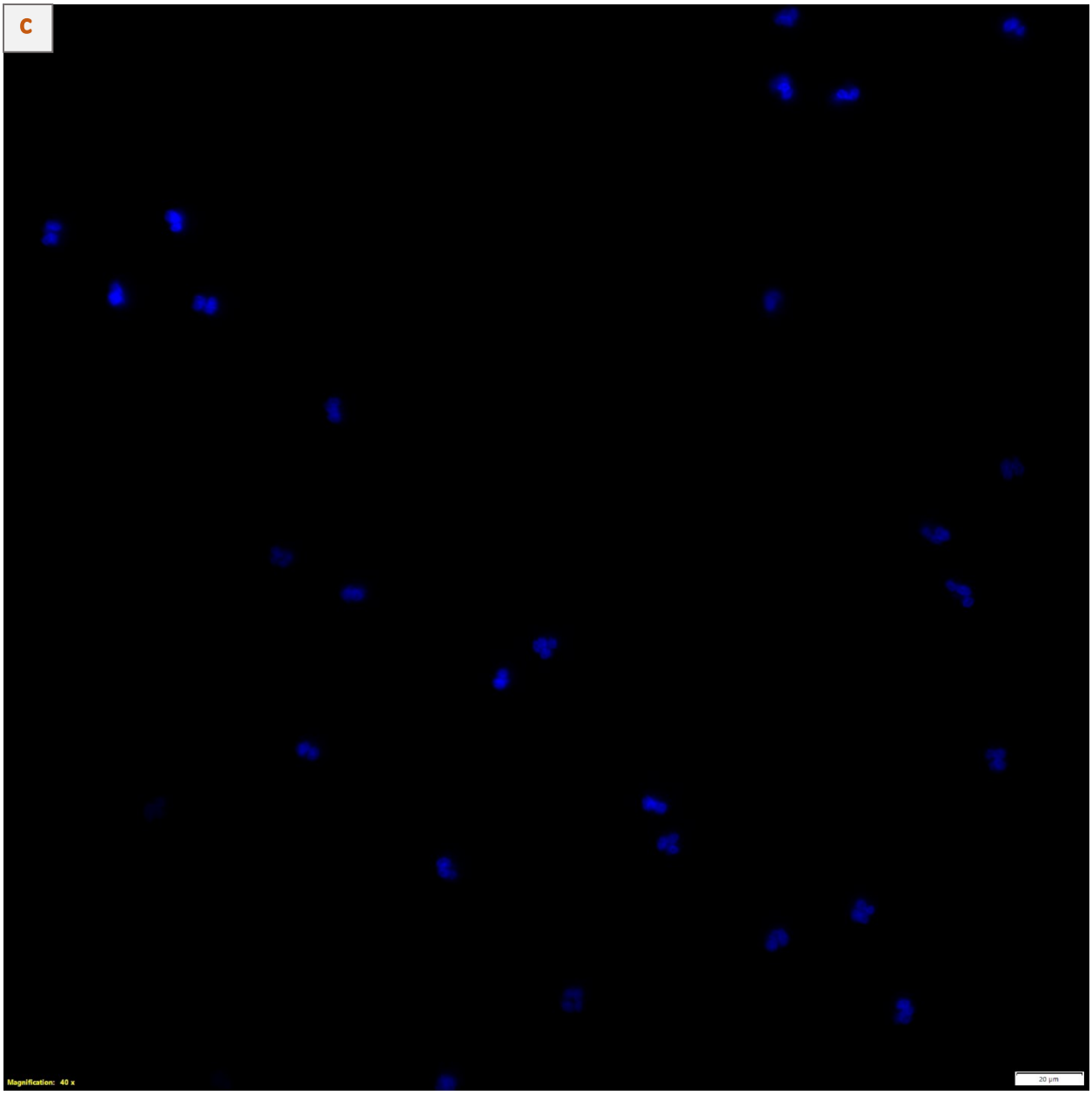


Fig. 1 Transmigrated neutrophils in the bottom chamber. (A–C) 20×: DIC (A), NucBlue/DAPI nuclei (B), CD66b–AF647 (Cy5) primary marker (C). (D–F) 20×: DIC (D), NucBlue/DAPI (E), CD16b–AF647 (Cy5) backup marker (F). (G–I) 40×: DIC (G), NucBlue/DAPI (H), CD66b–AF647 (Cy5) (I). (J–L) 40×: DIC (J), NucBlue/DAPI (K), CD16b–AF647 (Cy5) (L). Bi-/multilobed nuclear morphology and Cy5 labeling confirm neutrophil identity.


A
Magnification: 40 x
20 µm


B
Magnification: 40 x
20 µm


C
Magnification: 40 x
20 µm

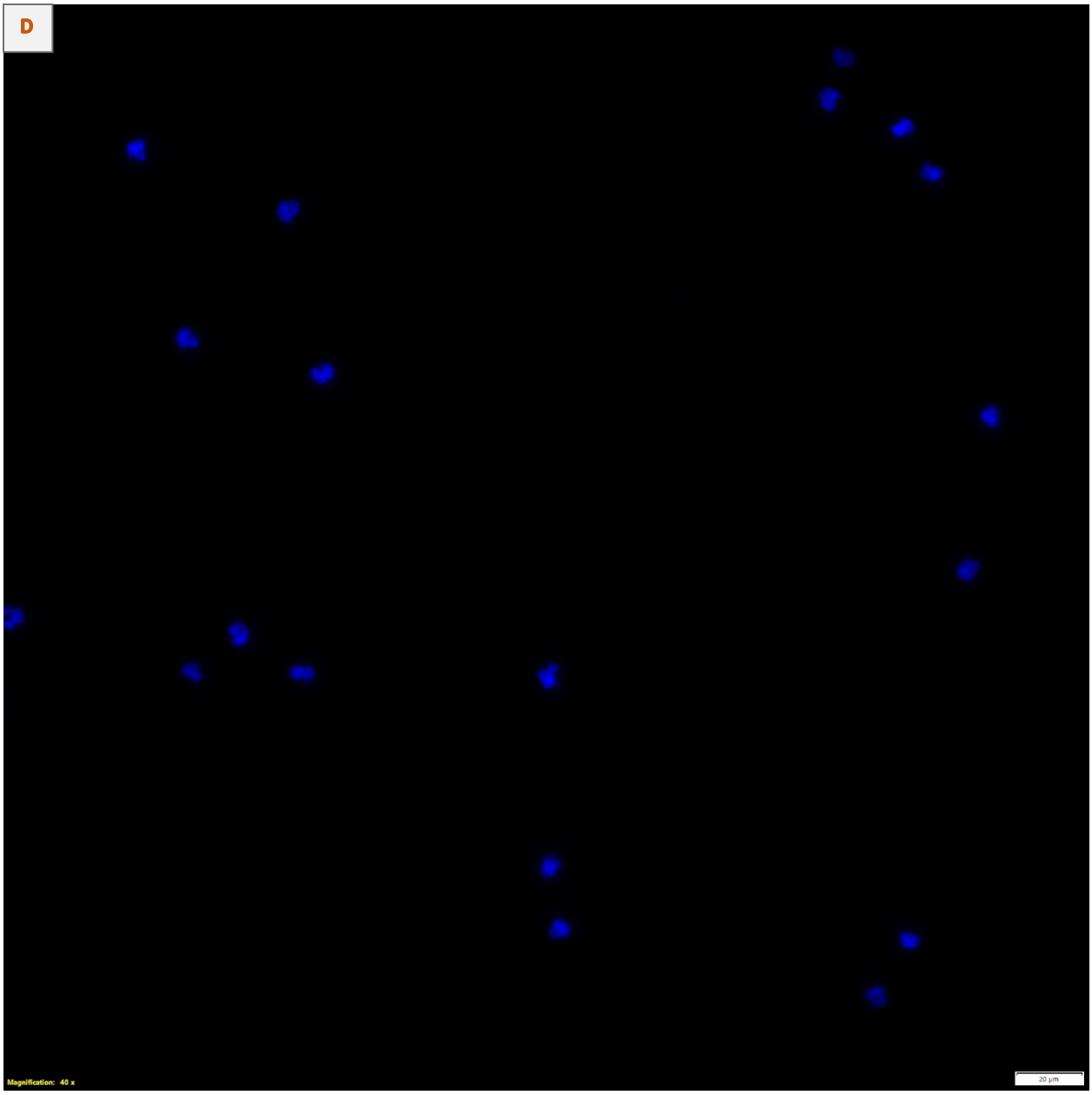


Fig. 2 Transmigrated neutrophils in the bottom chamber. (A-D) 40X image of NucBlue-stained neutrophils (DAPI). Clearer views of neutrophils with bi- or multilobed nuclei.

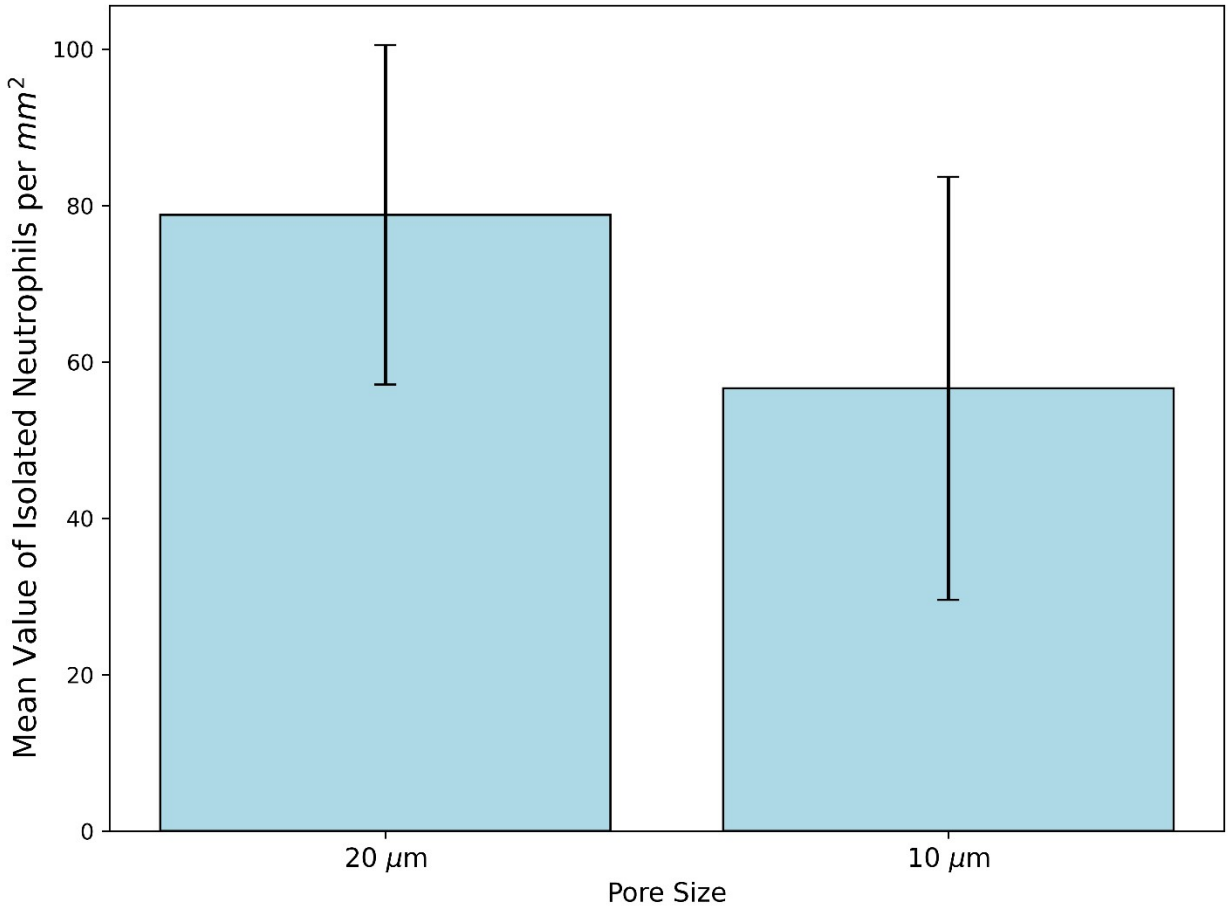


Fig. 3 Membrane pore size impact on the quantity of neutrophils migrated. Devices were manufactured with 10 and 20 um polycarbonate filters and experiments were performed with whole blood at top, 2 mg/ml ECM collagen concentration and 150 nM fMLP concentration. After 2 hours, the number of neutrophils in the transmigration chamber were counted. Data indicates the four individual (n=4) measurements for each pore size. The p-value of 0.2480 indicates that there was no serious influence on the average value of the isolated neutrophiles between the two groups of data.

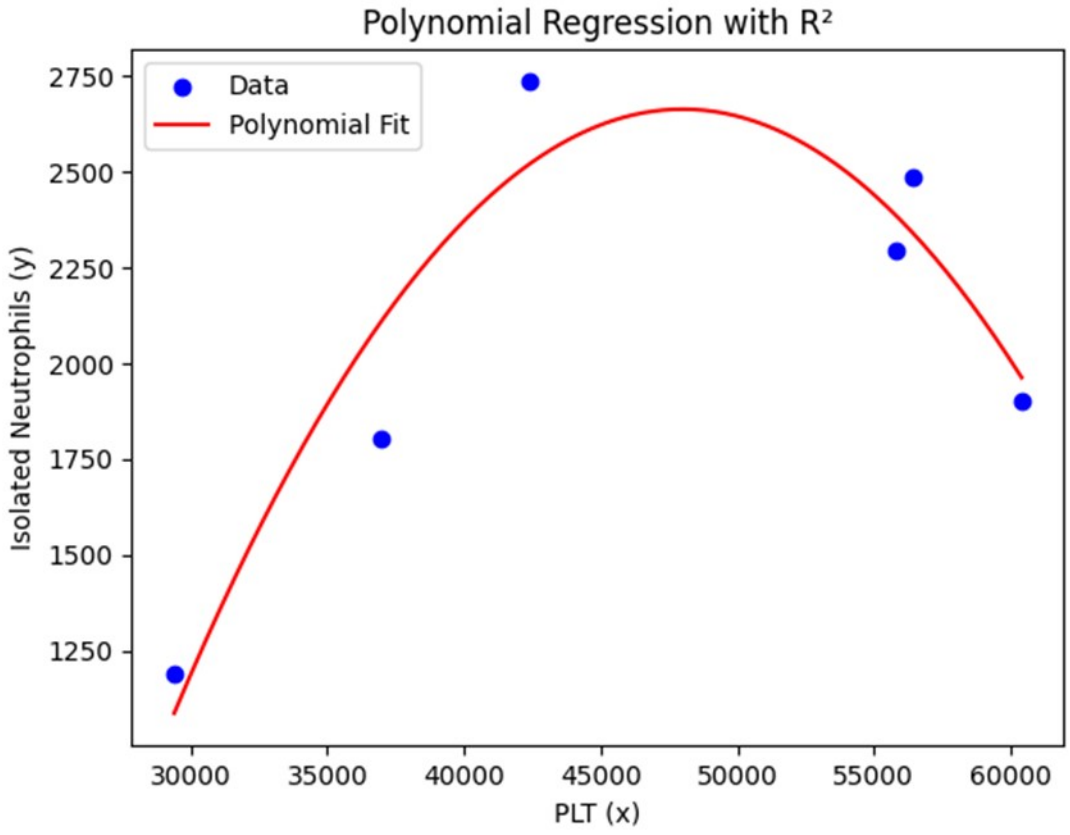


Fig. 4 Polynomial regression curve fitting the relationship between platelet count (PLT) and the number of isolated neutrophils. The blue dots represent the experimental data points (n = 6), while the red curve illustrates the polynomial fit. The coefficient of determination ($R^2 = 0.88$) indicates a strong correlation between platelet count and neutrophil isolation, suggesting a non-linear relationship between these variables.