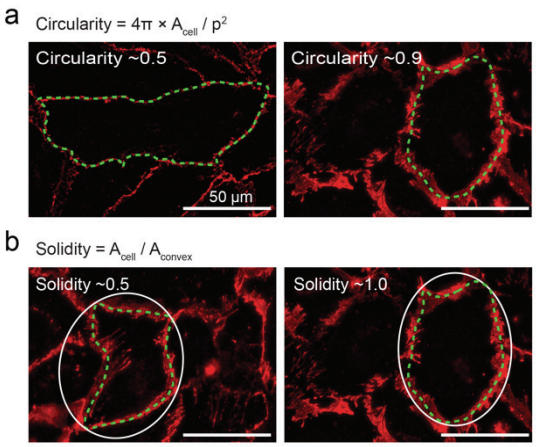
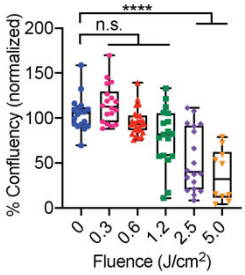
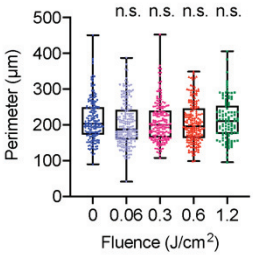


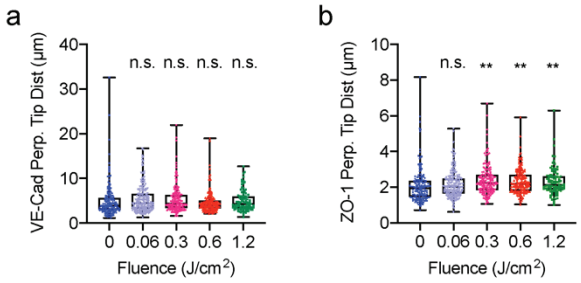
Supplementary Fig. 1. Cell shape factors. Equations and schematics represent how (a) circularity and (b) solidity are calculated. Cells are stained for VE-cadherin (red). Green dashes represent waypoints that trace the cell perimeter (p), showing the area of a cell (A_{cell}). White circles represent the area of the cell convex (A_{convex}). All scale bars are 50 µm.



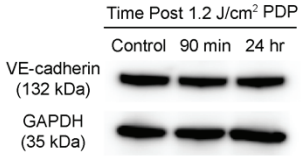
Supplementary Fig. 2. Low dose PDP does not impact cell confluency. HBMECs were incubated with BPD (0.25 µM) for 24 hours followed by light activation (690 nm, 0–5 J/cm^2, 6 mW/cm^2). The confluence of HBMECs was determined from Live/Dead® imaging at 24- post-PDP. The number of cells stained with Calcein AM (green channel) per frame was normalized to the control group. A One-Way ANOVA with multiple comparisons was used to calculate significant differences, where n.s. indicates not significant ($p > 0.05$), * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, and **** $p < 0.0001$. $N > 10$, where N equals the number of images captured over 3 trials. Box plots show the mean and the likely range of variation. Error bars show the maximum and minimum values.



Supplementary Fig. 3. PDP does not alter cell perimeter. 90-minutes post priming (0-1.2 J/cm^2, 6 mW/cm^2), cells were fixed and stained for VE-cadherin and ZO-1. The cell perimeter was traced via 'way pointing' within the Junction Analyzer Program. The Kruskal-Wallis test with a Dunn's multiple comparison test was used to calculate significant differences, where n.s. indicates not significant ($p > 0.05$). The significance between the experiment group and the control is presented. $N > 105$, where N is the number of cells, from 3 different trials. Box plots show the mean and the likely range of variation. Error bars show the maximum and minimum values.



Supplementary Fig. 4. PDP did not alter the (a) protrusion length (i.e., tip-to-tip distance) of VE-cadherin perpendicular junctions, (b) but modulated the protrusion length of ZO-1 perpendicular junctions. At 90 minutes post-priming (0-1.2 J/cm^2, 6 mW/cm^2), cells were fixed and stained. The Junction Analyzer Program calculated the protrusion length of the perpendicular junctions after cells were way pointed. The Kruskal-Wallis test with a Dunn's multiple comparison test was used to calculate significant differences, where n.s. indicates not significant ($p > 0.05$). The significance between the experiment group and the control is presented. $N > 105$, where N is the number of cells, from 3 different trials. Box plots show the mean and the likely range of variation. Error bars show the maximum and minimum values.



Supplementary Fig. 5. PDP does not alter total junction protein expression. HBMECs were grown to confluency, incubated with BPD (0.25 µM) for 24 hours, and primed (690 nm, 1.2 J/cm^2, 6 mW/cm^2). Representative immunoblotting of VE-cadherin confirms protein expression was unchanged at 90 minutes and 24 hours post-priming. GAPDH was used as the loading control. N=4, where N is the number of gels ran over 2 lysates.

Supplementary Table 1. Physical parameters of rhodamine-liposomes.

Liposome Characteristics	
Hydrodynamic diameter (nm)	104.08 ± 3.39
Polydispersity Index (PdI)	0.06 ± 0.02