Supplementary Information

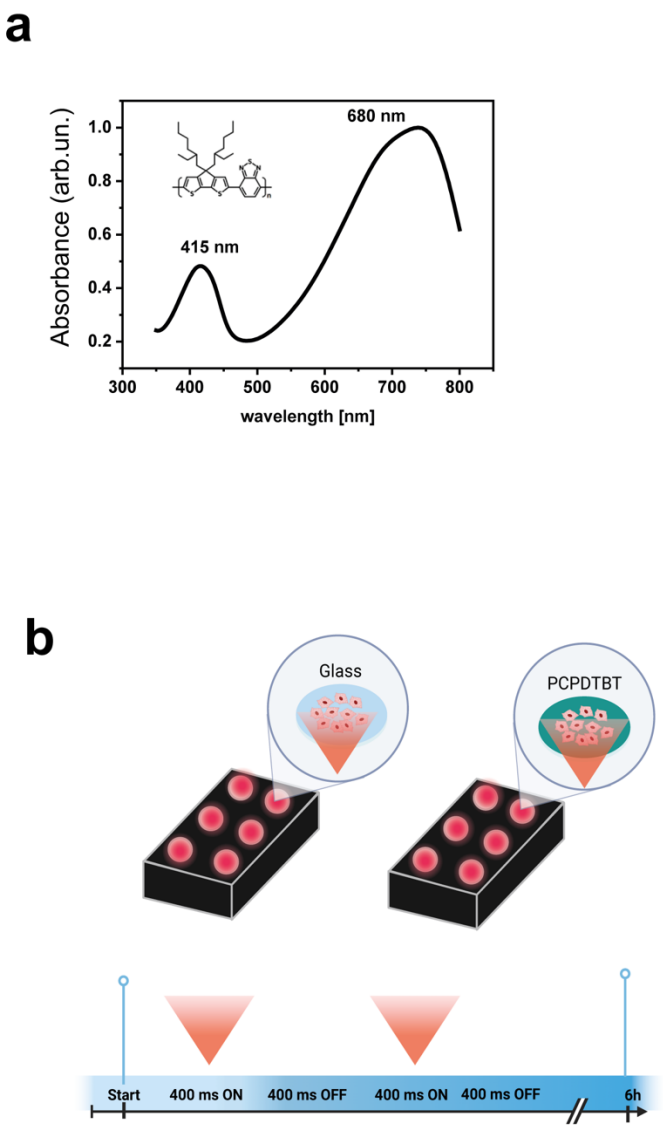

Figure S1. Experimental set up and biocompatibility assessment. a) Chemical structure and normalized optical absorption spectrum of the PCPDTBT polymer. **b)** Schematic representation of the experimental setup and protocol used for PCPDTBT optical stimulation. PCPDTBT thin films were deposited by spin coating from a solution in organic solvent. Subsequently, polymer films were thermally sterilized, adhesion protein layer was deposited on top of the polymer surface and hPSC-CMs were seeded on top of the fibronectin-coated polymer for the illumination.

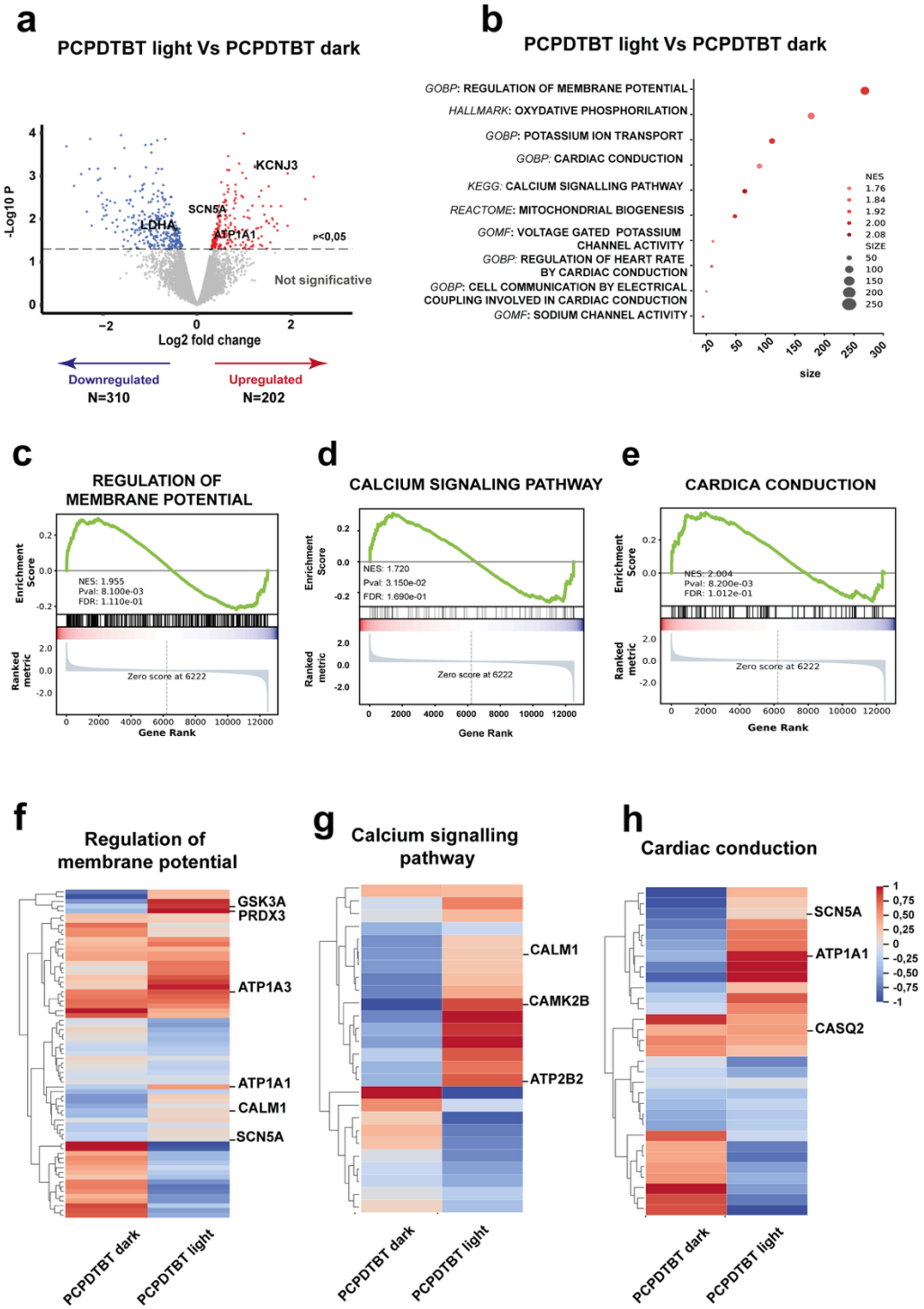

Figure S2. Effect of polymer-mediated photostimulation on hPSC-CM transcriptional profile. (a) Volcano plot showing differentially expressed genes between PCPDTBT light and PCPDTBT dark conditions. Significantly upregulated and downregulated genes (FDR < 0.05) are highlighted in red and blue respectively; non-significant genes are shown in grey. Some of the key genes indicative of hPSC-CM maturation are shown in bold. (b) Dot plot of the most significantly enriched pathways (both up- and downregulated) in the PCPDTBT light vs PCPDTBT dark comparison, with relevance to cardiomyocyte maturation and functionality (c, d, e) Representative GSEA enrichment plots of

selected pathways. (f, g, h) Heatmaps displaying expression of leading-edge genes from significantly upregulated pathways. Some relevant genes are shown in bold. RNA-sequencing was performed on n = 3 independent hPSC-CM batches.

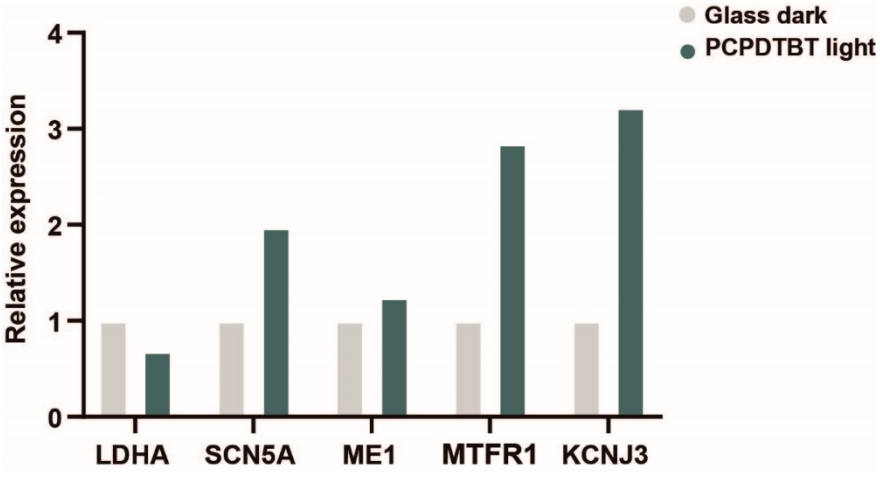

Figure S3. RNA-sequencing validation. Relative expression of *LDHA, SCN5A, ME1, MTFR1* and *KCNJ3* genes, measured via Rt-qPCR and normalized to18S gene analysed in hPSC-CMs under two experimental conditions (glass dark and PCPDTBT light). Data are represented relative to the glass dark condition.

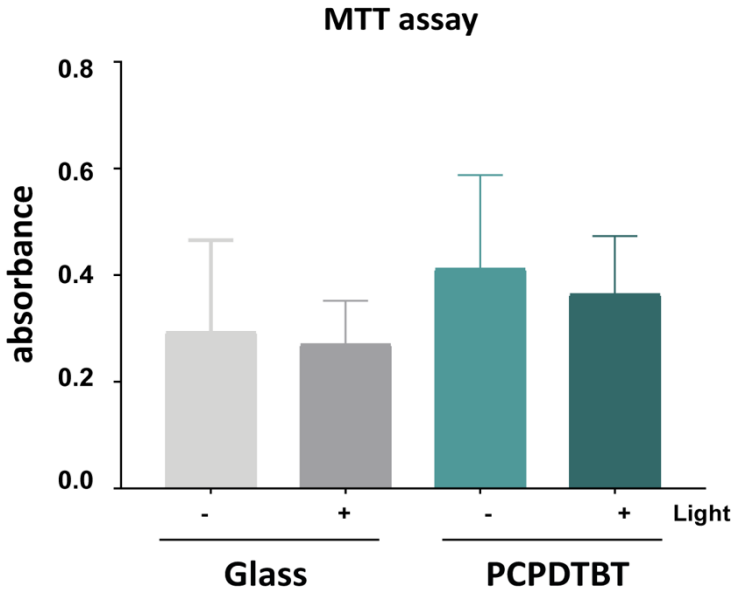

Figure S4. MTT assay. MTT assay performed of hPSC-CMs seeded on control glass and PCPDTBT thin film in dark condition and following light stimulation protocol. N=3. Not significative (Unpaired t-test).

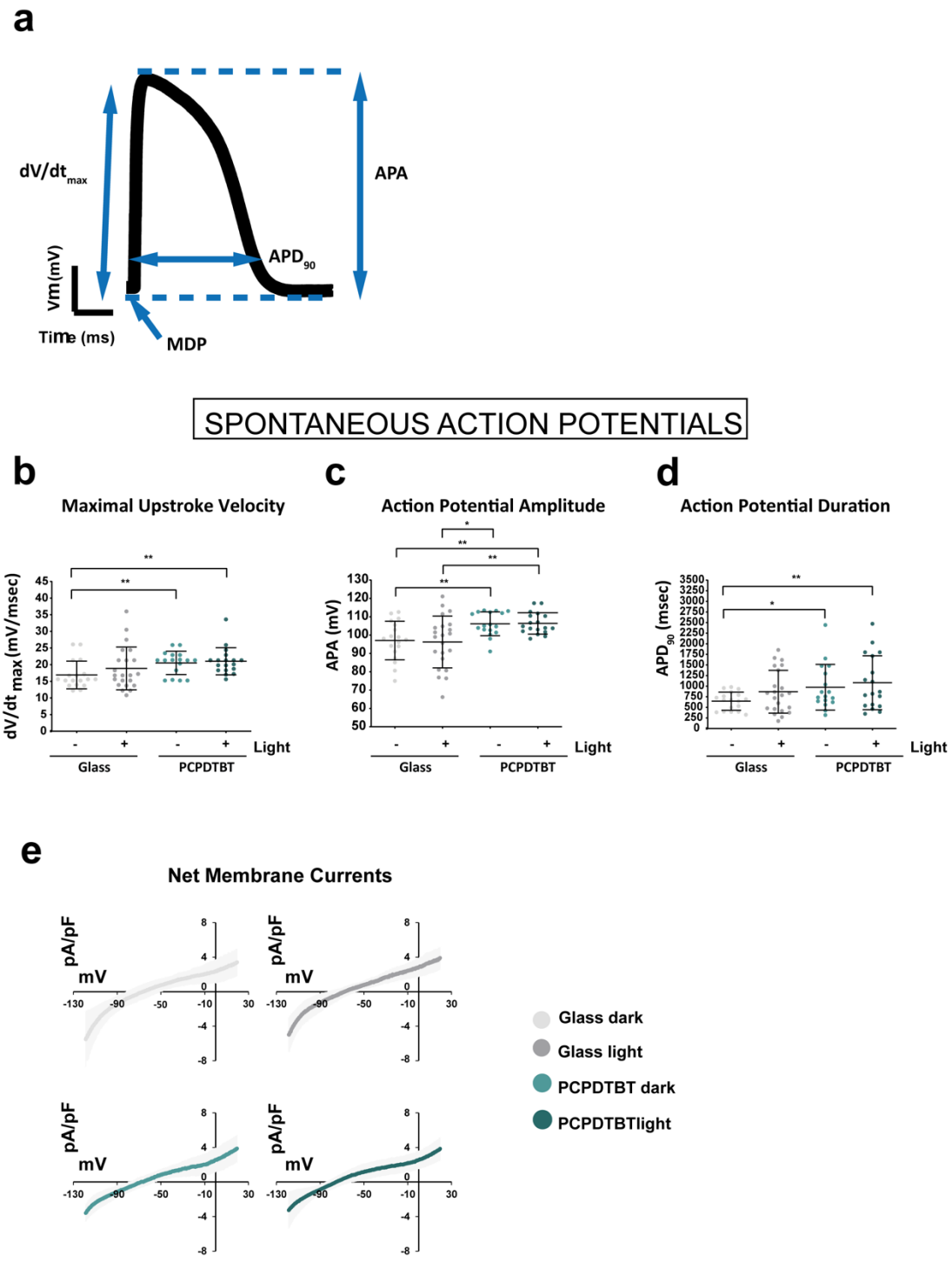

Figure S5. (a) Schematic representation of key action potential parameters analysed in hPSC-CMs: maximal diastolic potential (MDP), action potential amplitude (APA), maximal upstroke velocity (dV/dt_{max}) and action potential duration at 90% repolarization (APD_{90}). **(b-d)** Quantification of spontaneous action potential parameters in hPSC-CMs cultured on glass or PCPDTBT substrates, with or without chronic red-light stimulation: (a) maximal upstroke velocity (dV/dt_{max}), (b) action potential amplitude (APA), and (c) action potential duration at 90% repolarization (APD_{90}). Glass dark n= 18, Glass light n= 22, PCPDTBT dark n= 17, PCPDTBT light n= 18. **(d)** Net membrane current

(NMC) recordings obtained using a voltage ramp protocol in hPSC-CMs grown on the indicated substrates and under the specified conditions. Currents are normalized to cell capacitance (pA/pF); shaded areas indicate SD.

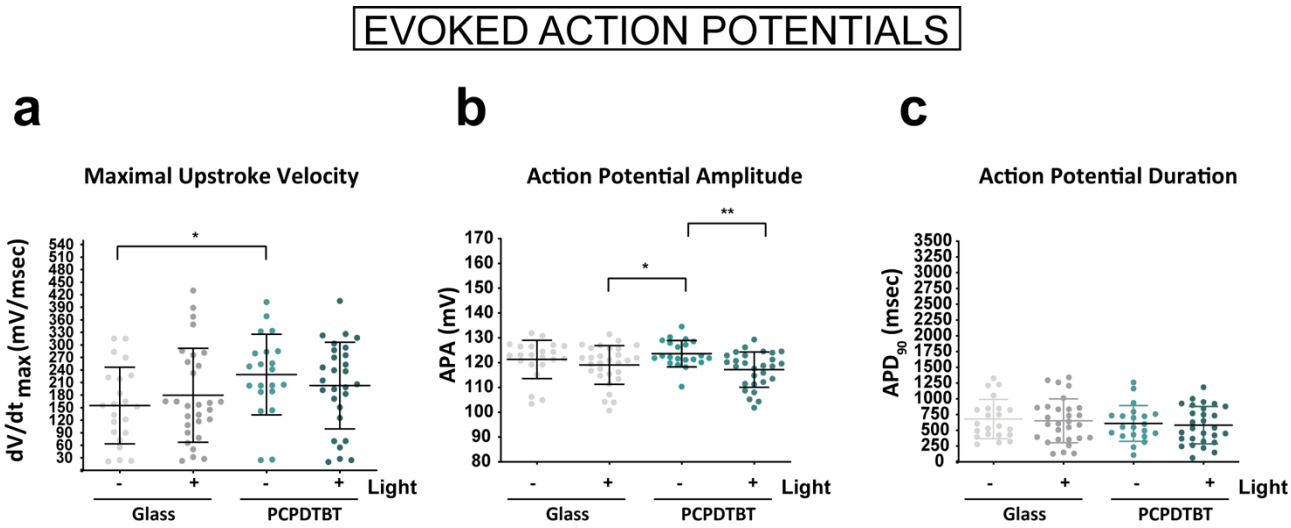

Figure S6. AP parameters measurements in evoked hPSC-CM action potentials. 1 (a–c) Quantification of evoked action potential parameters in hPSC-CMs cultured on glass or PCPDTBT substrates, with or without chronic red-light stimulation: (a) maximal upstroke velocity (dV/dt_{max}), (b) action potential amplitude (APA), and (c) action potential duration at 90% repolarization (APD_{90}). Data are presented as mean ± SD; $p^* < 0.05$, $p^{**} < 0.005$ (unpaired t-test). Glass dark n= 22, Glass light n= 29, PCPDTBT dark n=21, PCPDTBT light n=28**.**

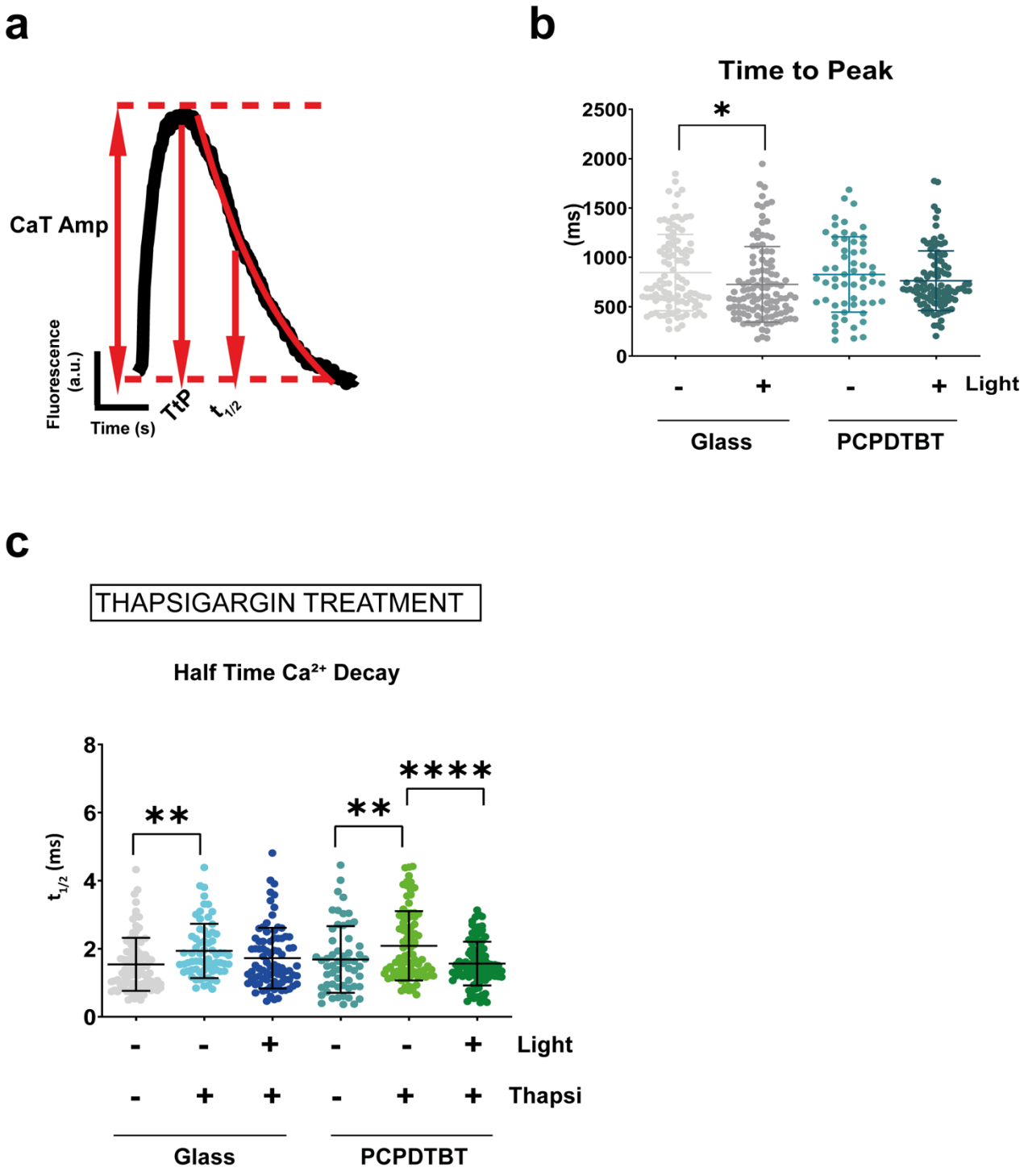

Figure S7. Ca^{2+} dynamics. **(a)** Schematic representation of the different Ca^{2+} parameters measured. **(b)** Time to Peak (TtP) of hPSC-CMs seeded on control glass and PCPDTBT in dark or light conditions **(c)** Half Time Ca^{2+} decay of hPSC-CMs seeded on control glasses and PCPDTBT in dark or light conditions and treated with Thapsigargin (Thapsi). Glass dark n= 99, glass light + Thapsi n= 75, Glass light + Thapsi n= 86; PCPDTBT dark n=58, PCPDTBT dark + Thapsi=95, PCPDTBT light + Thapsi=96. Data are presented as dot plot with mean ± SD; $p^* < 0.05$, $p^{**} < 0.005$, $p^{****} < 0.0001$ (unpaired t-test).

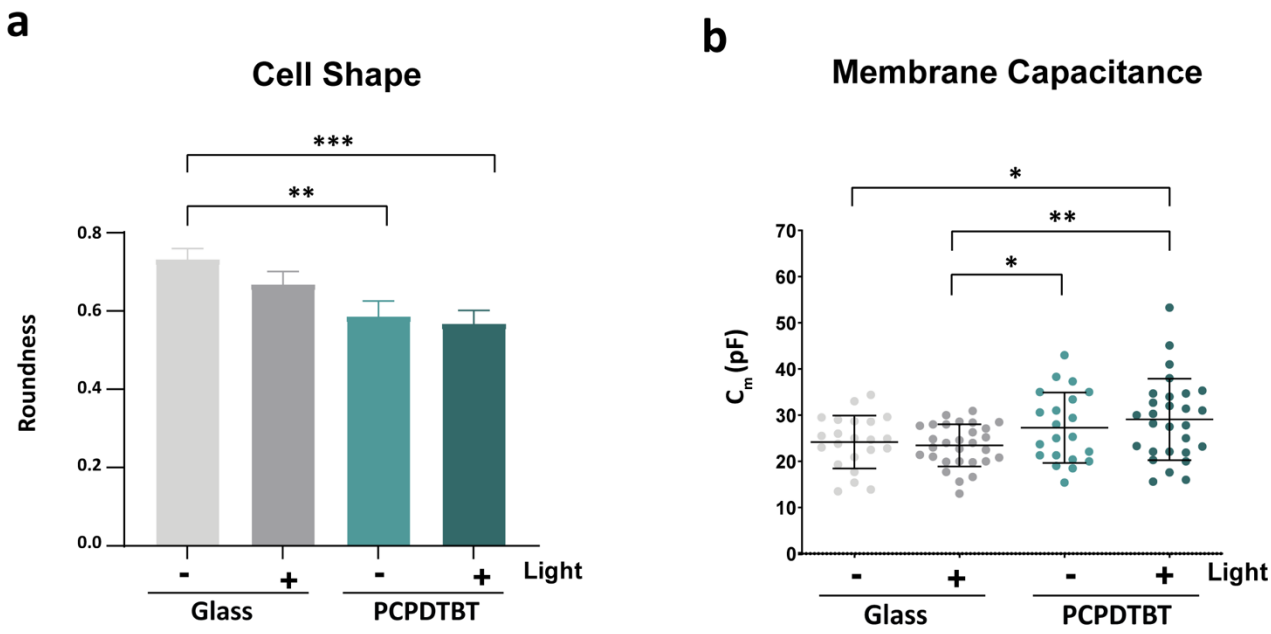

Figure S8. PCPDTBT photostimulation effects of hPSC-CMs structure. a) Cell roundness quantification. b) Dot plot with membrane capacitance (mC) data recorded from hPSC-CMs seeded on control glasses and PCPDTBT in dark or light conditions. glass dark n=43, glass light n=29, PCPDTBT dark n=32, PCPDTBT light n=38). *p<0,05, ****p<0,0001 (Unpaired t-test).

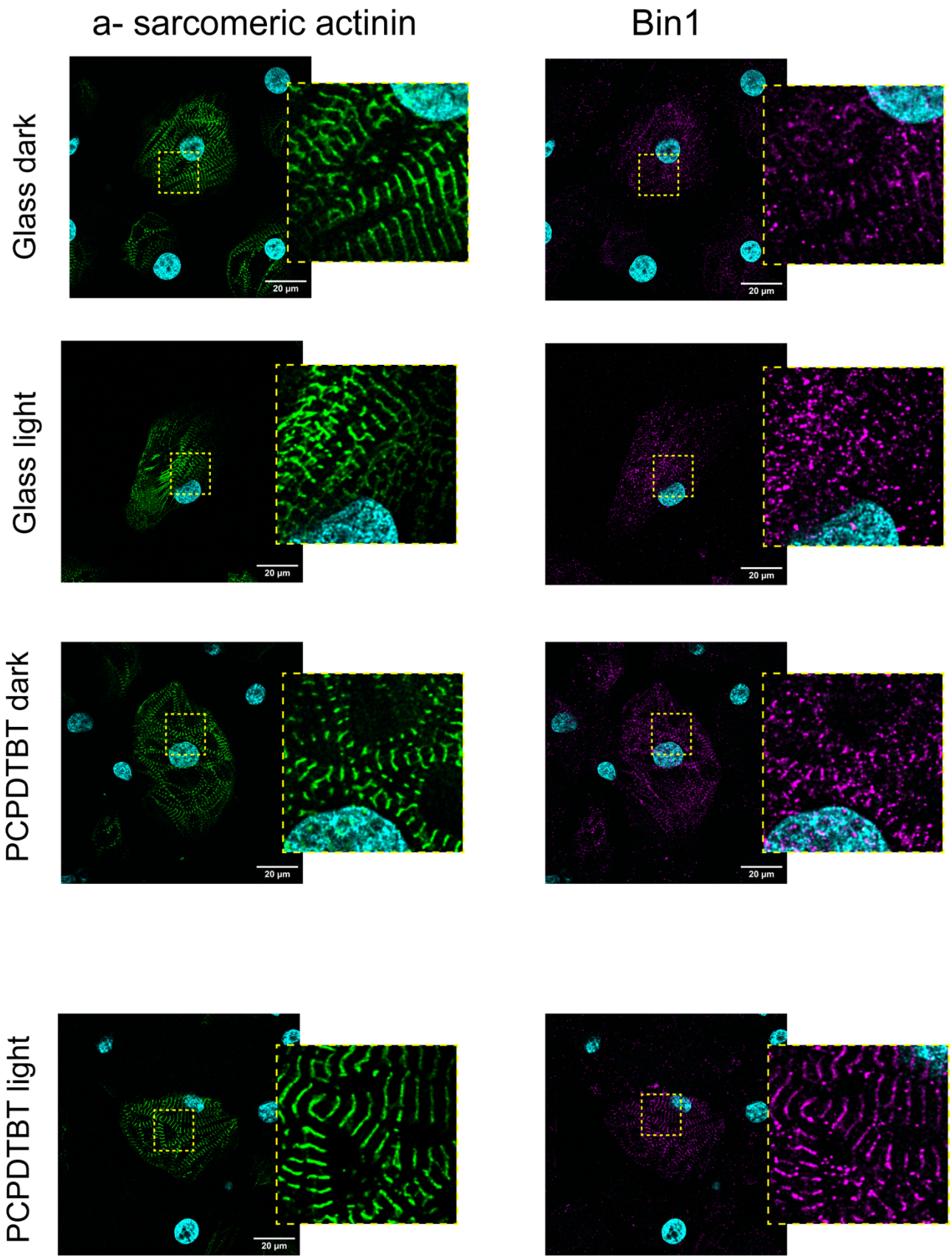

Figure S9. Effect of PCPDTBT photostimulation of Bin-1 expression in hPSC-CM. **(a-d)** Representative immunofluoresce images for α-sarcomeric actinin (green) and Bin1 (magenta) of

hPSC-CMs seeded on control glass and PCPDTBT both in dark and light conditions. Nuclei were marked with DAPI (cyan).

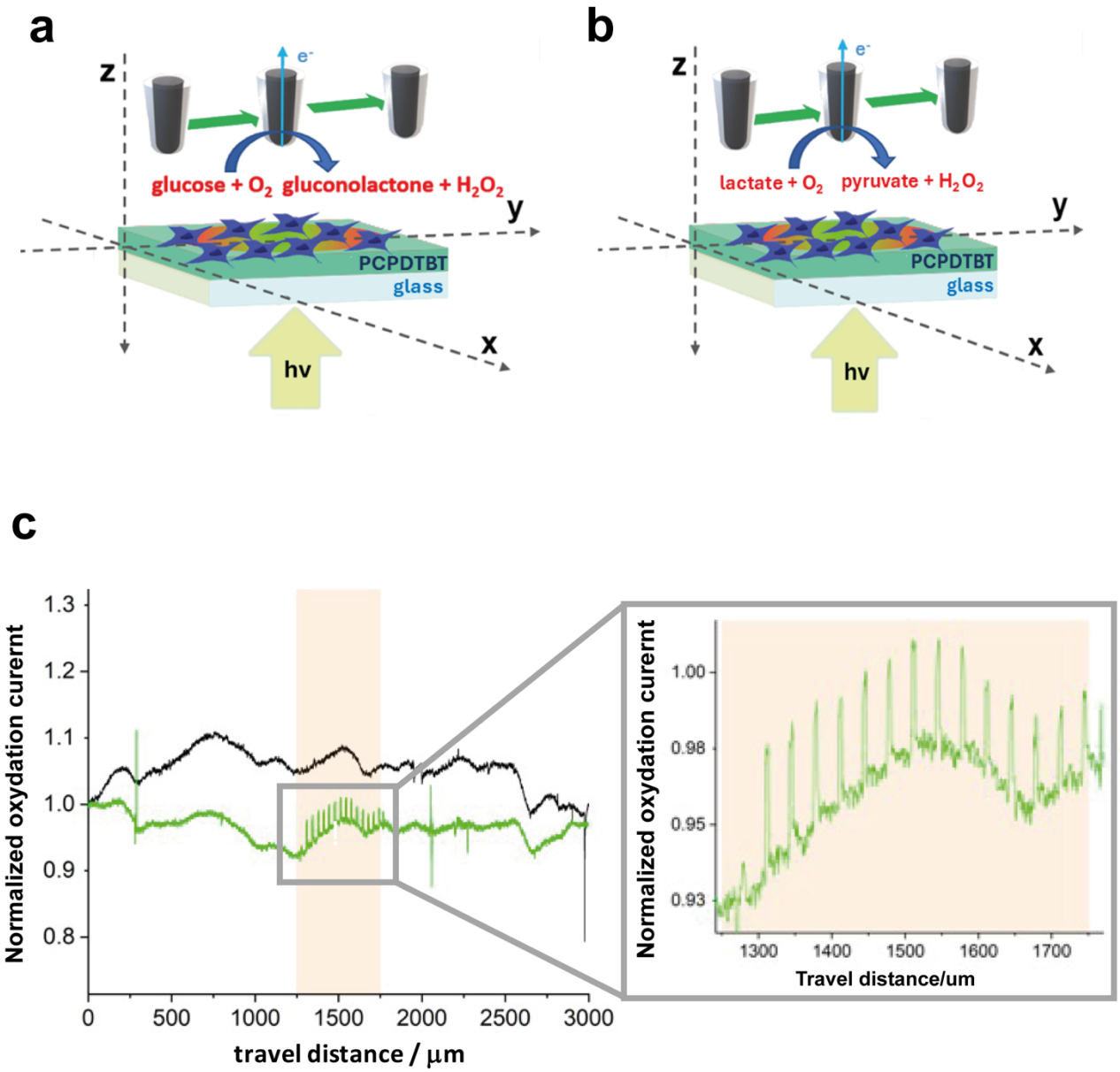

Figure S10 SECM apparatus and rationale of SECM measurements to quantify changes of glucose uptake and lactate release in hPSC-CMs upon chronic illumination of PCPDTBT films. (a-b) Schematic representations of SECM horizontal Probe-Scan Curves (PSCs) at fixed height from the surface of the PCPDTBT films. Scheme of the measurement strategy employing modified platinum microelectrodes for glucose detection **(a)** and lactate release **(b)**. **(c)** Representative horizontal PSCs, before (black trace) and during (green trace) illumination. In this region, spikes, which are due to transient local hydrogen peroxide production as a consequence of PCPDTBT film illumination, are visible.

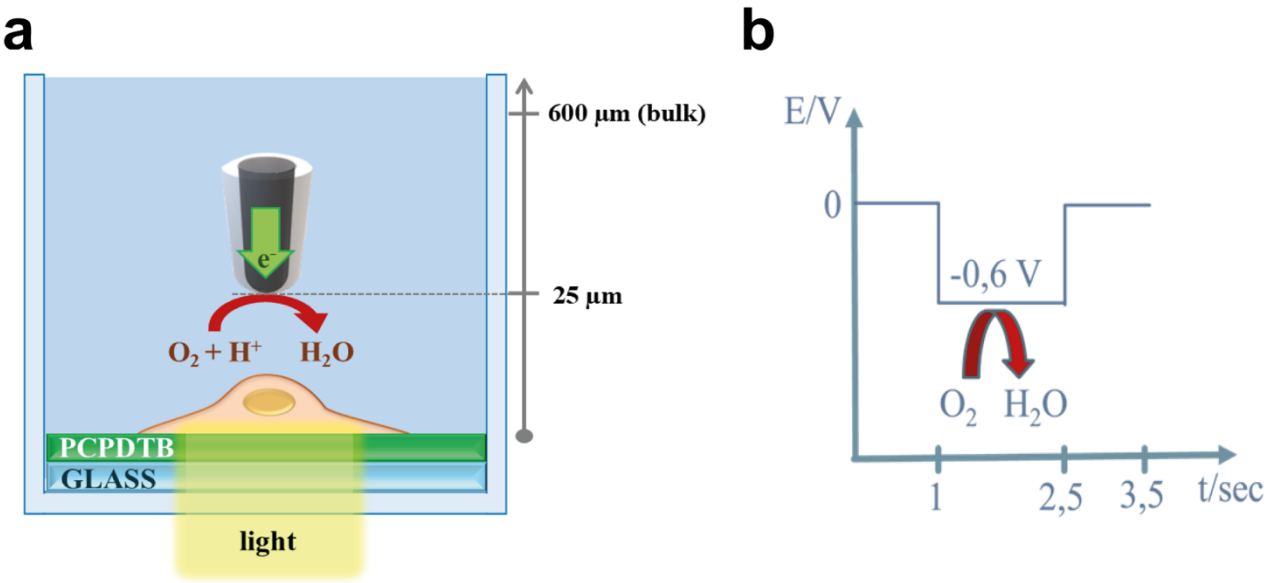

Figure S11 SECM apparatus and rationale of SECM measurements to quantify oxygen consumption changes in hPSC-CMs upon PCPDTBT chronic photostimulation

(a-b) Schematic representation of the analytical strategy for oxygen consumption determination with SECM. Potential scan pulses at -0.6 V vs Ag/AgCl (KCl 3 M) were programmed and performed as represented in panel **b** at two distances from PCPDTBT film surface, 25 and 600 µm, as showed in panel **c**. Potential pulses were performed at - 0.6 V vs Ag/AgCl (KCl 3M) for 0.5 s to measure oxygen reducing currents, which can be directly related to local oxygen concentration in the bulk, 600 µm, and in the cell proximity, 25 µm.

Primers	Sequences
LDHA FWD	5’ TTGTCTCTGGCAAAGTGGAT 3’
LDHA REV	5’ CTCCATGTTCCCCAAGGACC 3’
ME1 FWD	5’ TGTTTCGGAAGCCAAGAGGT 3’
ME1 REV	5’ CATCCCTCCGCAAGCTGTAT 3’
MTFR1 FWD	5’ GCGGCCGAGTGTGTTTT 3’
MTFR1 REV	5’ AGGCGCTTAATCCAGCCAA 3’
KCNJ3 FWD	5’ CAAGCTGCTCAAAGGATGACT 3’
KCNJ3 REV	5’ AAGGGGACGACATGAGAAGC 3’

Table S1. List of PCR primer sequences used for RNA-seq validation