

Fig. S1

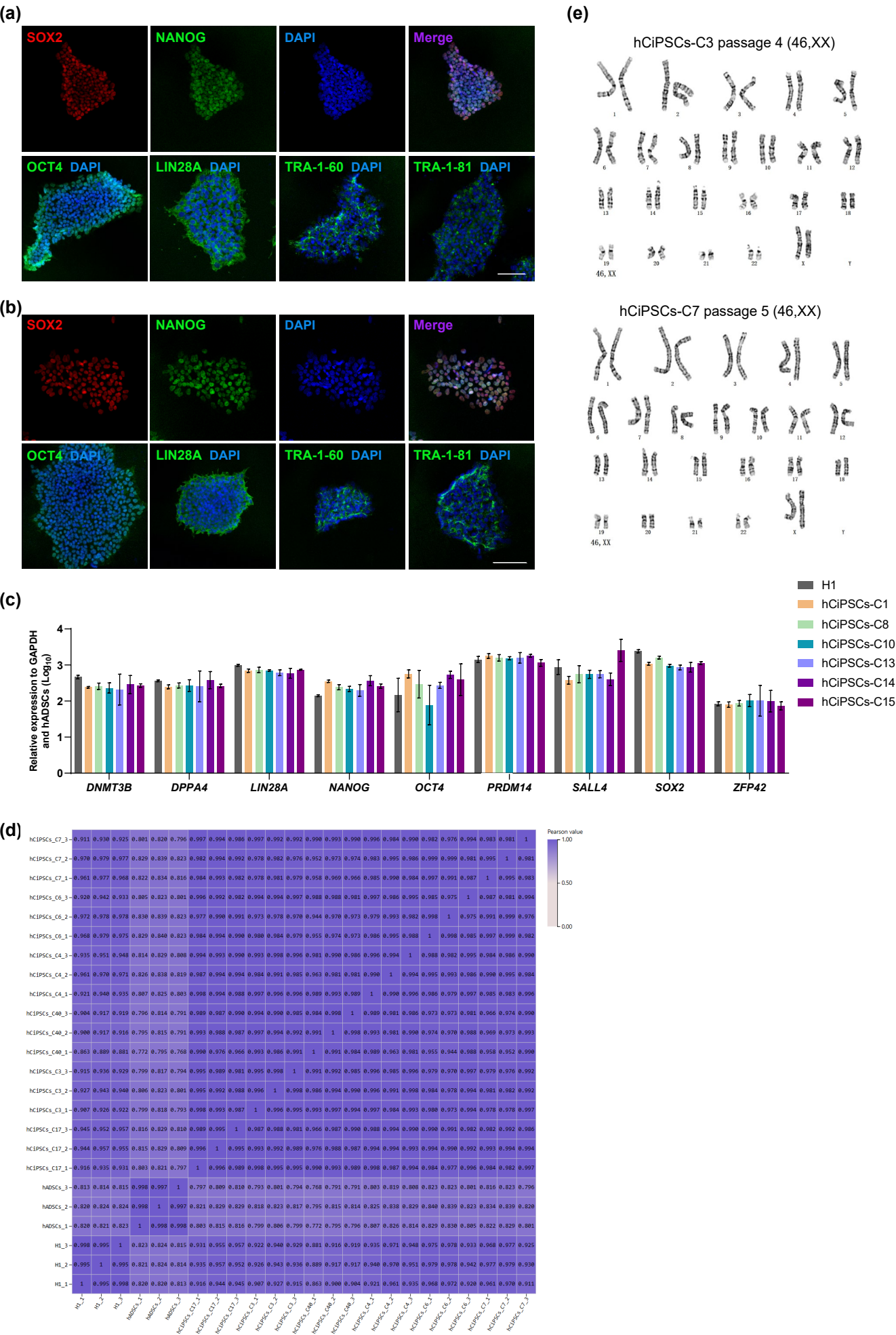


Fig. S1. Characterization of hADSC-derived hCiPSCs. (a-b) Immunofluorescence staining for pluripotency markers in hCiPSCs-C3 (a) and hCiPSCs-C7 (b). Scale bar, 100 μ m. (c) Relative expression levels of pluripotency marker genes in hESCs (H1) and hADSC-derived hCiPSCs, as determined by RT-qPCR. Data are presented as means $\pm$ SDs; $n = 3$. (d) Correlation analysis of the global transcriptomes of H1, hADSCs, and hADSC-derived hCiPSCs. (e) Karyotype analysis showing hADSC-derived hCiPSCs-C3 and hCiPSCs-C7 with normal diploid chromosomal content.

Fig. S2

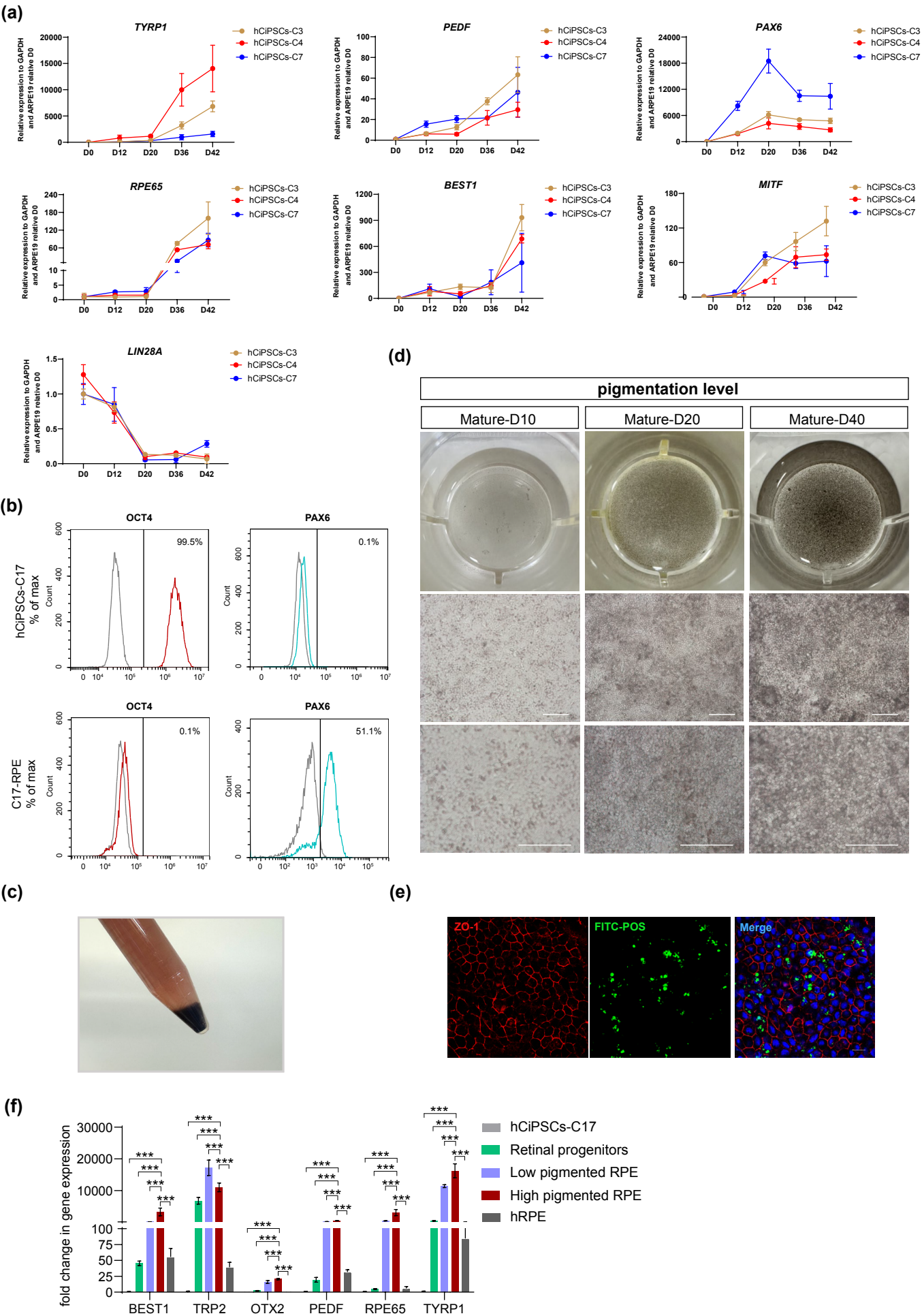


Fig. S2. Characterization of RPE cells derived from other hCiPSCs. (a) RT-qPCR analysis of RPE marker genes and pluripotency-related genes throughout the differentiation process of hCiPSCs (C3/C4/C7). Values are presented as means $\pm$ SDs; $n = 3$. (b) Flow cytometry analysis of C17-RPE cells at day 20 for the positive markers (PAX6) and pluripotency marker (OCT4). (c) Cell pellets after collection and dissociation of hCiPSC-derived RPE cells. (d) Changes of macroscopic photographs and microscopic morphology of hCiPSCs-derived RPE cells on day 10, 20, and 40 after enrichment. Scale bar, 100 μ m. (e) Phagocytosis activity measurement of C17-RPE using FITC-labeled POS by immunofluorescence microscopy. Immunostaining of ZO-1 to define the cell boundary. The cell nuclei were stained with DAPI. Scale bar, 10 μ m. (f) RT-qPCR shows the mature RPE marker gene expression level relative to undifferentiated hCiPSCs -C17 in retinal progenitors ($\sim$ day 20), low pigmentation RPE cells ($\sim$ day 50), high pigmentation RPE cells ($\sim$ day 75), and hRPE cells.