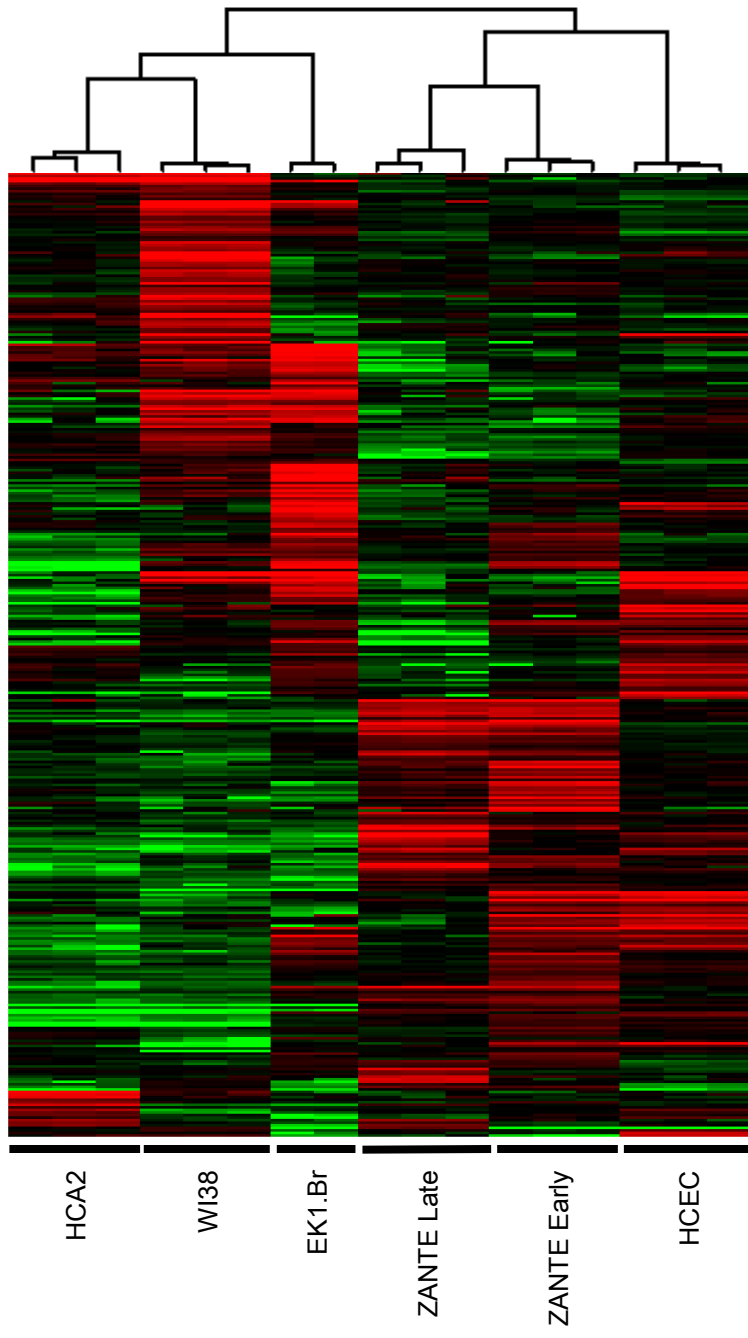


a



b

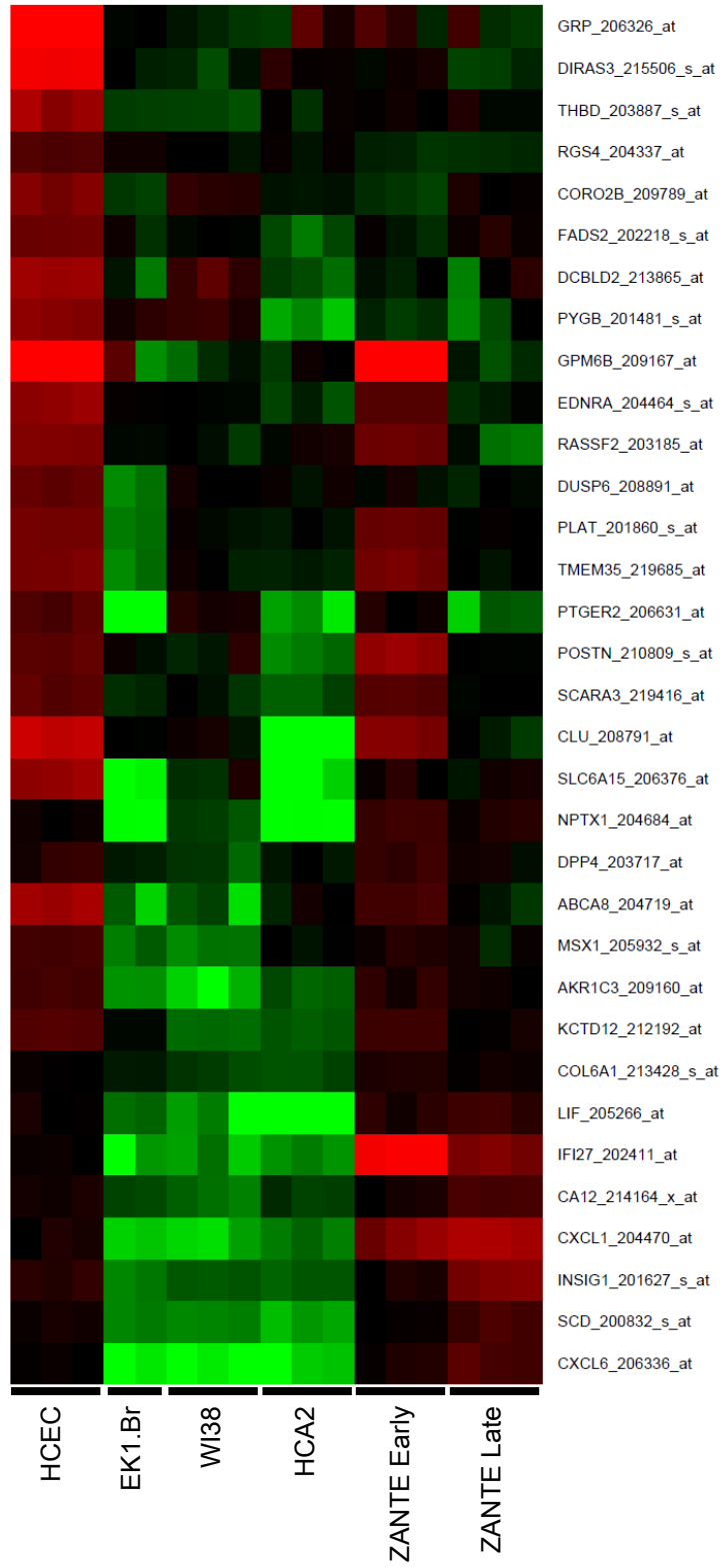


Figure S6 Legend

a) Immortalised HCEC-CDK4-TERT (Zante) cells preserve a similar transcriptional profile to parent primary HCEC cultures

Gene expression profiles were compared from early passage proliferating cultures of primary HCEC, corneal keratocytes (EK1.Br), two strains of human diploid fibroblasts (HCA2 and WI38), and HCEC-CDK4-TERT at PD52 (Zante Early) and PD193 (Zante Late). Differentially expressed genes were discovered by ANOVA. The heatmap shows hierarchical clustering of the top 377 significantly differentially expressed probesets ($FDR < 1 \times 10^{-6}$). The colour scheme indicates expression in \log_2 -space for each probeset relative to the experiment-wide (i.e. row) median. Red indicates upregulation relative to the row median and green indicates lower expression relative to the median.

b) Expression of HCEC-specific transcripts is largely retained in the immortalised HCEC-CDK4-TERT (Zante) cell line

Thirty-three genes had previously been identified (Kipling *et al*, 2009, *Exp Eye Res* 88 277-285) that exhibited high expression levels in primary HCEC cultures compared with corneal keratocytes (strain EK1.Br) and two human diploid fibroblast strains (WI38 and HCA2), and are listed in Table S2. This 33-gene HCEC signature was used to heatmap visual data from HCEC, fibroblasts, keratocytes, and Zante at early and late stages. The colour scheme indicates expression in \log_2 -space for each probeset relative to the experiment-wide (i.e. row) median. Red indicates upregulation relative to the row median and green indicates lower expression relative to the median.