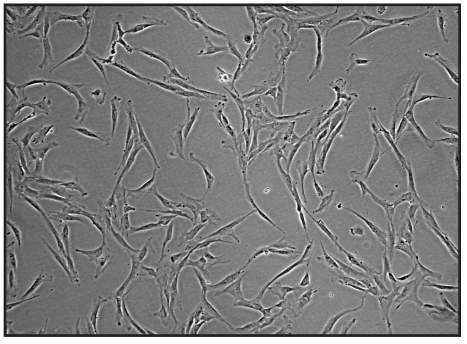
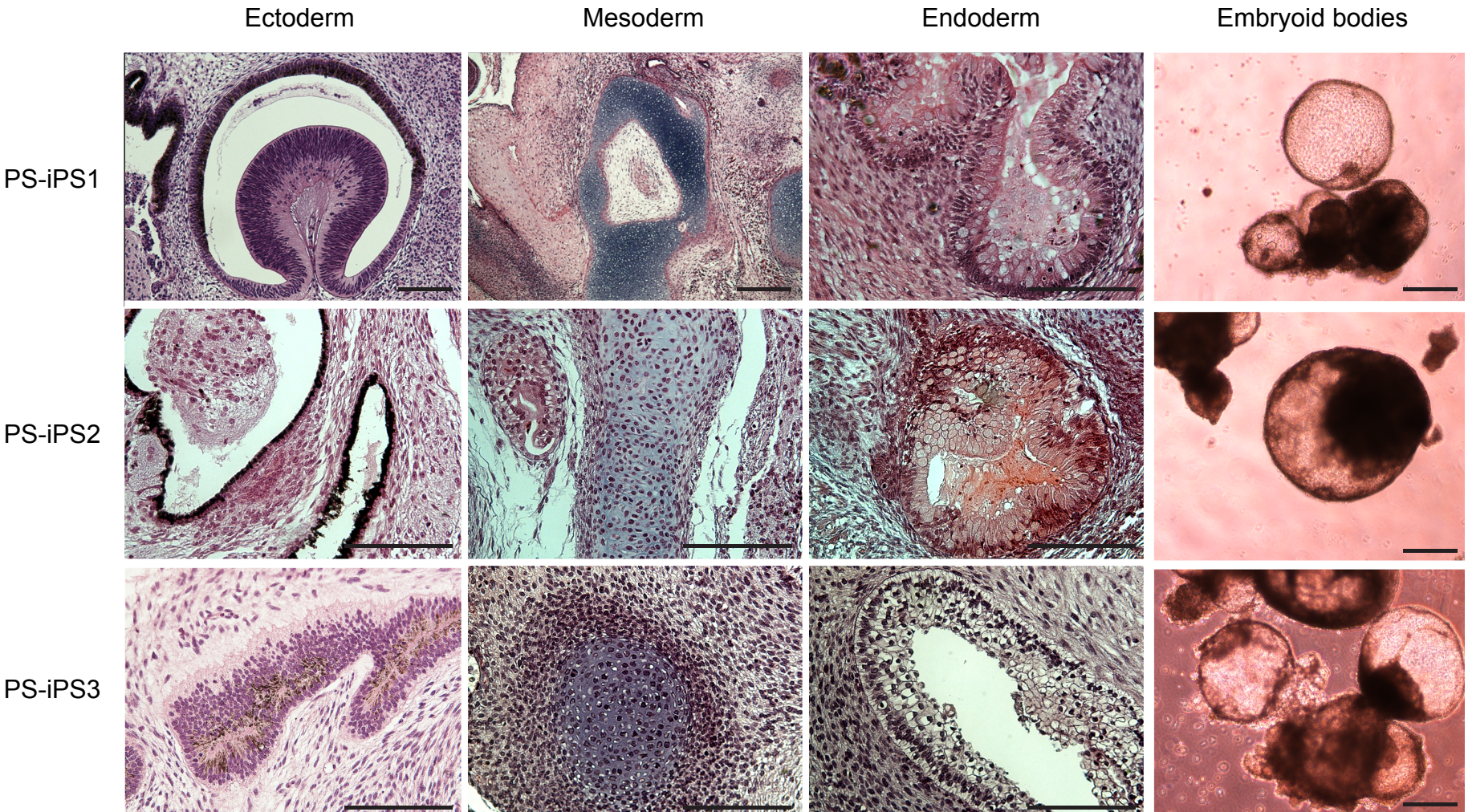
Supplementary Figure 1: Identification of Pearson syndrome patient mutation



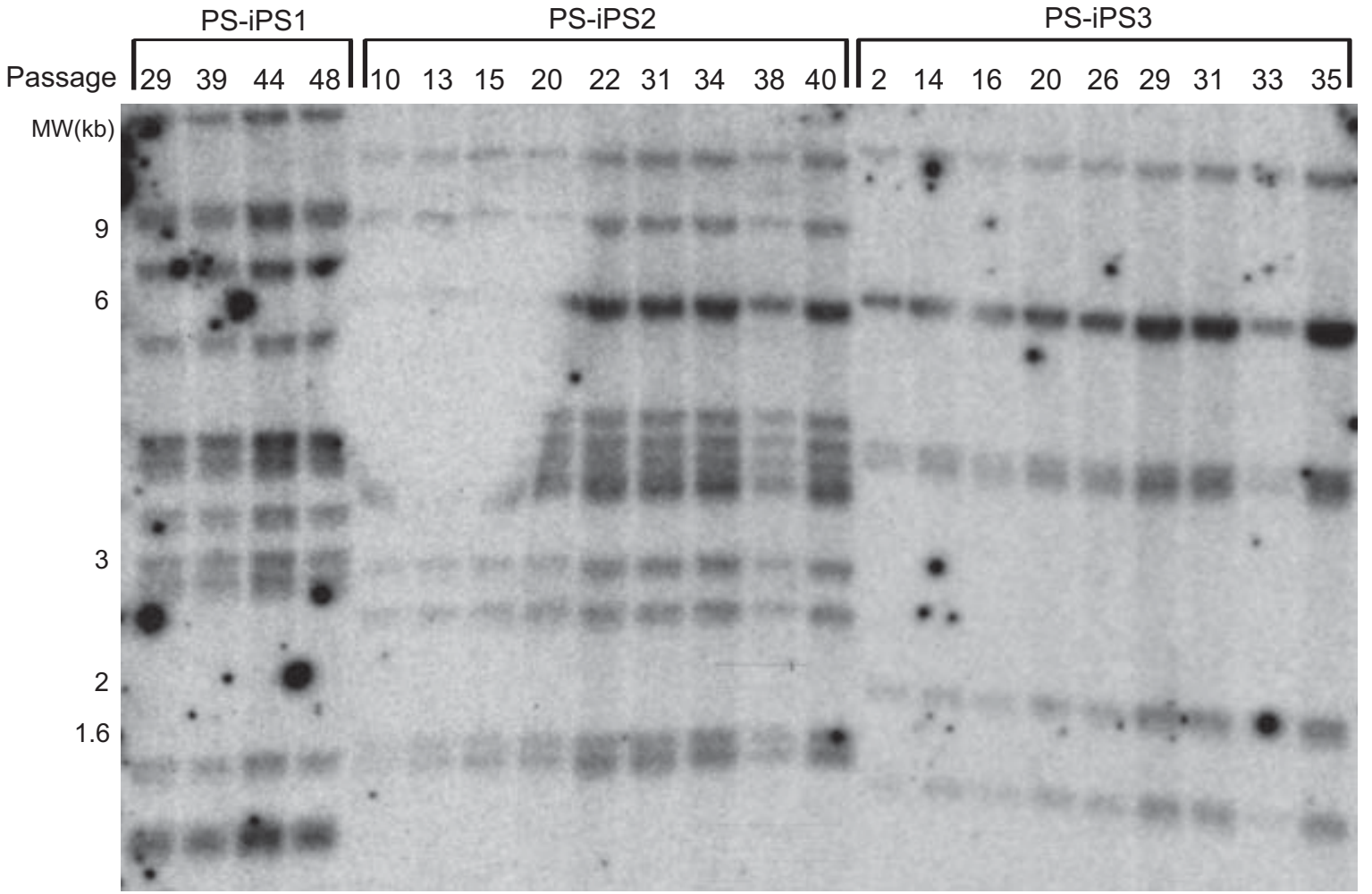
Supplementary Figure 1: Identification of Pearson syndrome patient mutation. (**A**): PS-Fib, the patient bone marrow-derived fibroblast line that was reprogrammed to create the PS-iPS cells (40x). (**B**): Schematic of the mitochondrial genome and the location of the patient's 2501 base pair (BP) deletion. The mitochondrial genome is numbered counterclockwise from base pair 1/16569, located at 12 o'clock in the diagram. (**C**): Sequencing results confirm the deletion encompassing two Complex I genes and three tRNAs. The deletion brings together two distant regions of the mitochondrial genome, illustrated in red and blue, creating a novel junction sequence. (**D**): Protein quantification by sandwich ELISA. Complex I activity is measured by a nitrotetrazolium blue-based assay, Complex IV activity is measured by a cytochrome c and di-amino benzidinetetrachloride (DAB) assay.

Supplementary Figure 2: PS-iPS cell differentiation



Supplementary Figure 2: PS-iPS cell differentiation. Left panels, histology from teratomas generated using each PS-iPS line. The teratomas from each line contained tissues from all three germ layers (scale bars are 200 μm). Right panels, embryoid bodies derived *in vitro* from each of the PS-iPS line (scale bars are 500 μm).

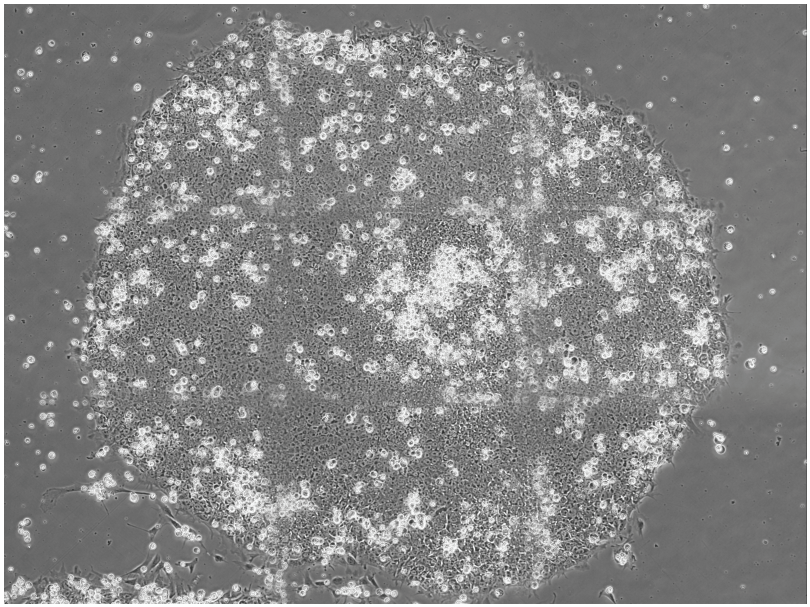
Supplementary Figure 3: Proviral integration pattern by Southern blot of iPS lines



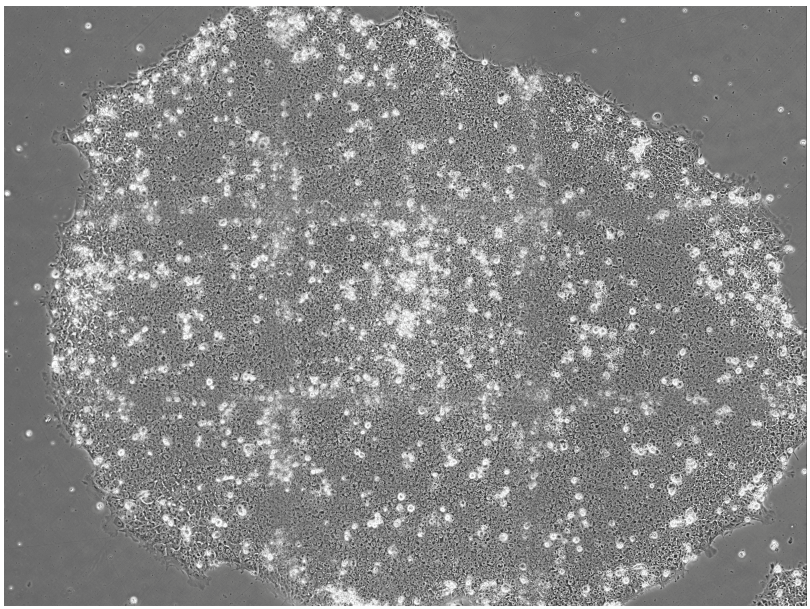
Supplementary Figure 3: Proviral integration pattern by Southern blot of iPS lines. Genomic DNA from PS-iPS cells digested with NcoI and probed with a GFP probe to demonstrate the integration pattern of retroviruses encoding reprogramming factors. Passage number is indicated.

Supplementary Figure 4: Colony morphology in growth experiment

A 30% mutant mtDNA - day 5-6

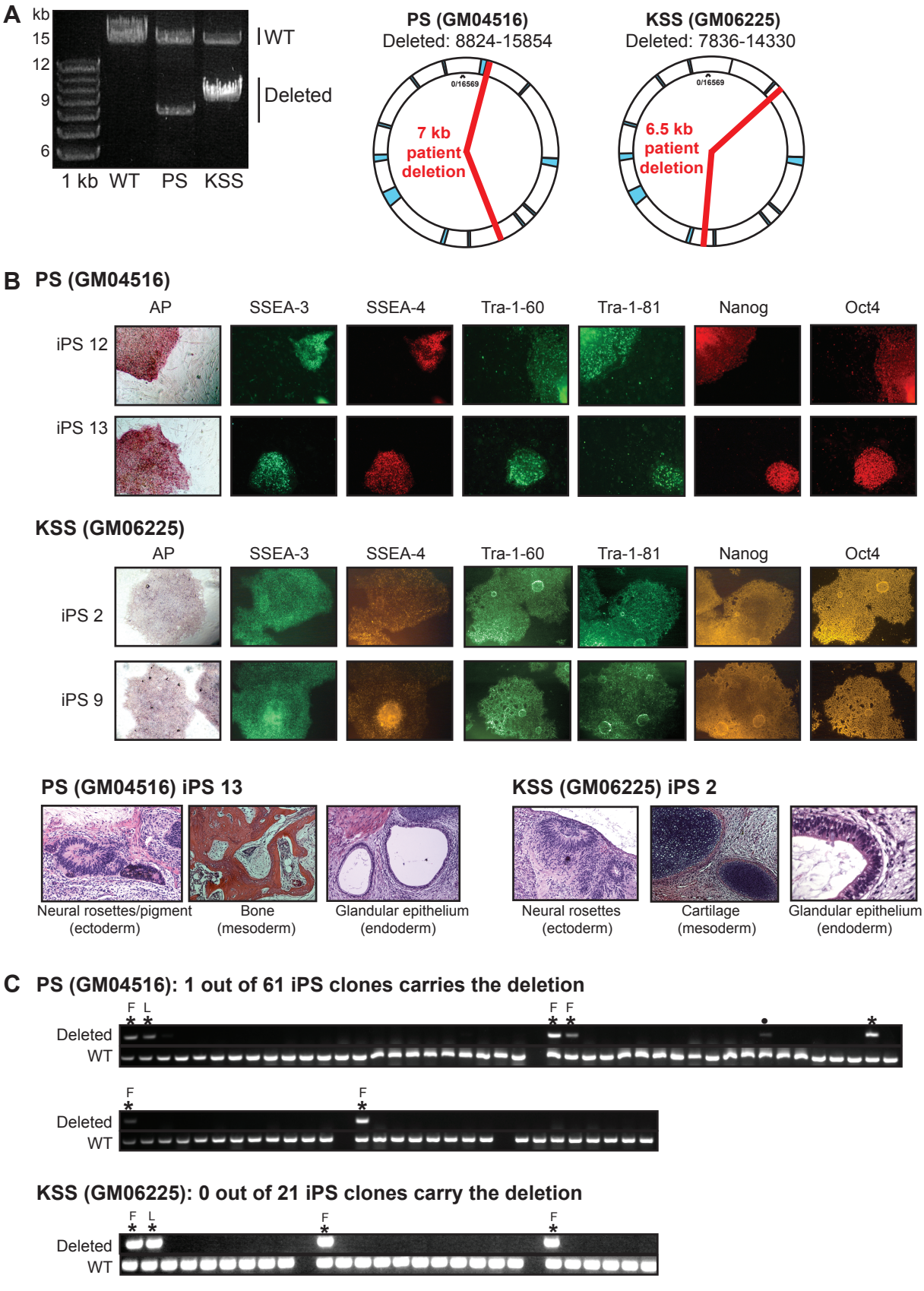


B 0% mutant mtDNA - day 5-6



Supplementary Figure 4: Colony morphology in growth experiment (Reference Figure 4A). (A) A colony representative of PS-iPS1 with 30% heteroplasmy (200x). **(B)** A colony representative of PS-iPS1 with 0% heteroplasmy (200x).

Supplementary Figure 5: iPS lines from other patients with mtDNA deletions



Supplementary Figure 5: iPS lines from other patients with mtDNA deletions. (**A**): Detection of mutant mtDNA in cells from a Pearson syndrome patient (PS; GM04516) and a Kearns-Sayre syndrome patient (KSS; GM06225) by long range PCR. The location of each mutation is illustrated in the schematic. (**B**): Demonstration of pluripotency in iPS cell lines derived from PS (GM04516) and KSS (GM06225) by immunofluorescence and teratoma analysis (40-100x). (**C**): PCR evaluation of iPS clones for the presence of the mutant species of DNA. "Deleted" primers covered the deletion junction for each patient (Supplemental Table 1). Patient fibroblasts (F) and lymphocytes (L) are included as positive controls, all other lanes are individual iPS clones. Asterisk (*) denotes true positive, filled circle (•) denotes false positive, determined on subsequent testing. 61 independent iPS cell clones were analyzed for PS (GM04516) and 21 independent iPS cell clones for KSS (GM06225).