

SUPPLEMENTARY FIGURES

Sample	Type	Code	Biopsy	Sex	Age	Mutated gene	Mutation	Karyotype
Ax0083	Healthy	Ctrl1	Skin	F	Commercial	-	-	Normal
38530A	Healthy	Ctrl2	Skin	M	55	-	-	Normal
PD33879	PD	PD1	Skin	F	66	LRRK2	G2019S	Normal
FH1509	PD	PD2	Skin	M	58	LRRK2	G2019S	Normal

Table S1. Description of healthy and PD donors. Ax0083 was commercially derived and didn't show the age donor. All kariotype were normal, as evidenced in Fig S4

Primary Antibody	Reactivity	Reference	Dilution
GFAP	Rat, Human	Abcam (ab53554)	1:1000
S100b	Human	Dako	1:400
EAAT2	Human	Santa Cruz	1:1000
CD49f	Human	Biologend	1:750
SOX2	Human	Santa Cruz (17320)	1:300
Oct4	Human	Santa Cruz (sc-5279)	1:100
Nanog	Human	Abcam (ab21624)	1:1000
MAP2	Human	Abcam	1:500
NG2	Human	Abcam (ab50009)	1:300
β III tubulin (Tuj I)	Human	Thermo Fisher (A25538)	1:500
Smooth muscle actin, SMA IgG2a	Human	Thermo Fisher (A25538)	1:200
α -fetoprotein, AFP IgG1	Human	Thermo Fisher (A25538)	1:500

Table S2. Primary antibodies used in the paper, with reference and working dilution

Figure S1

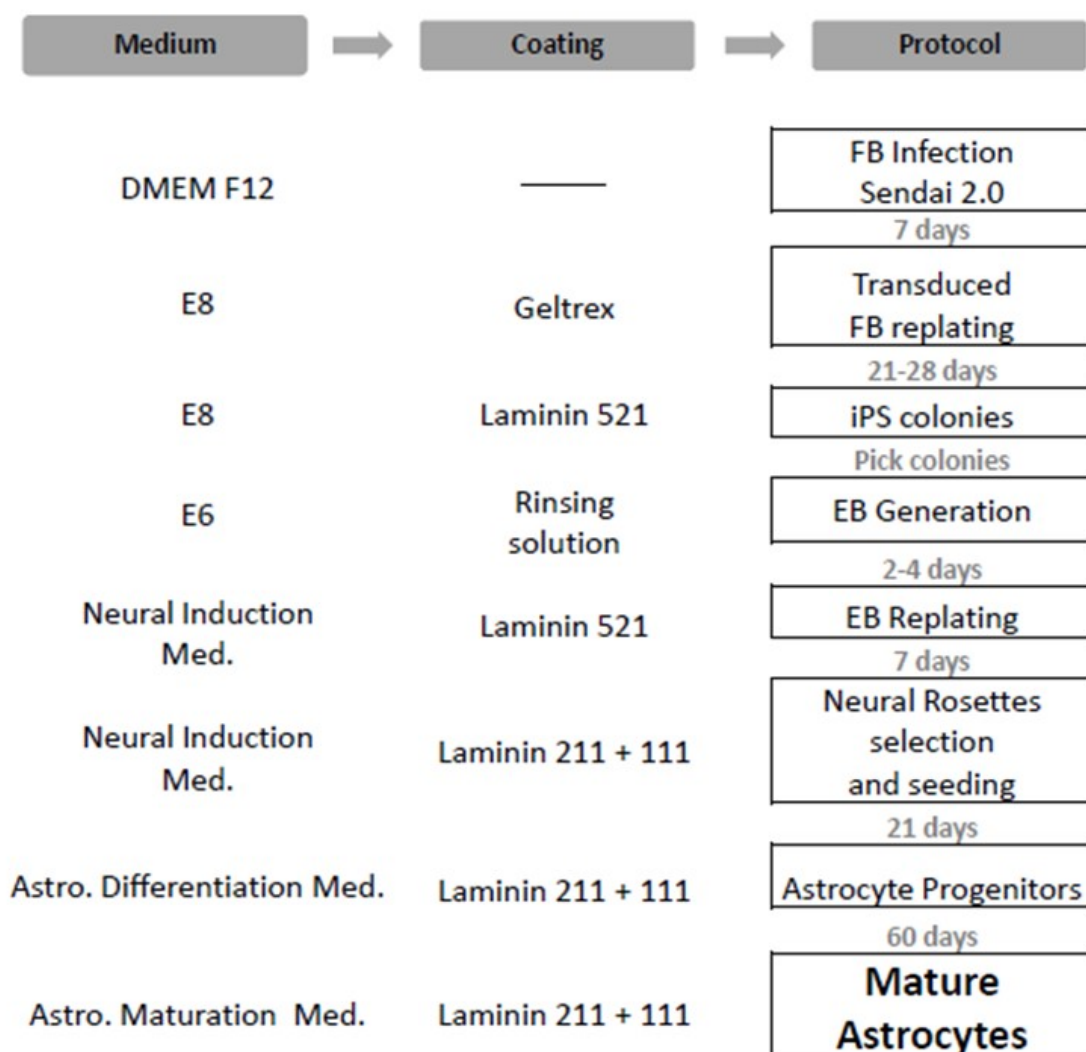


Figure S2

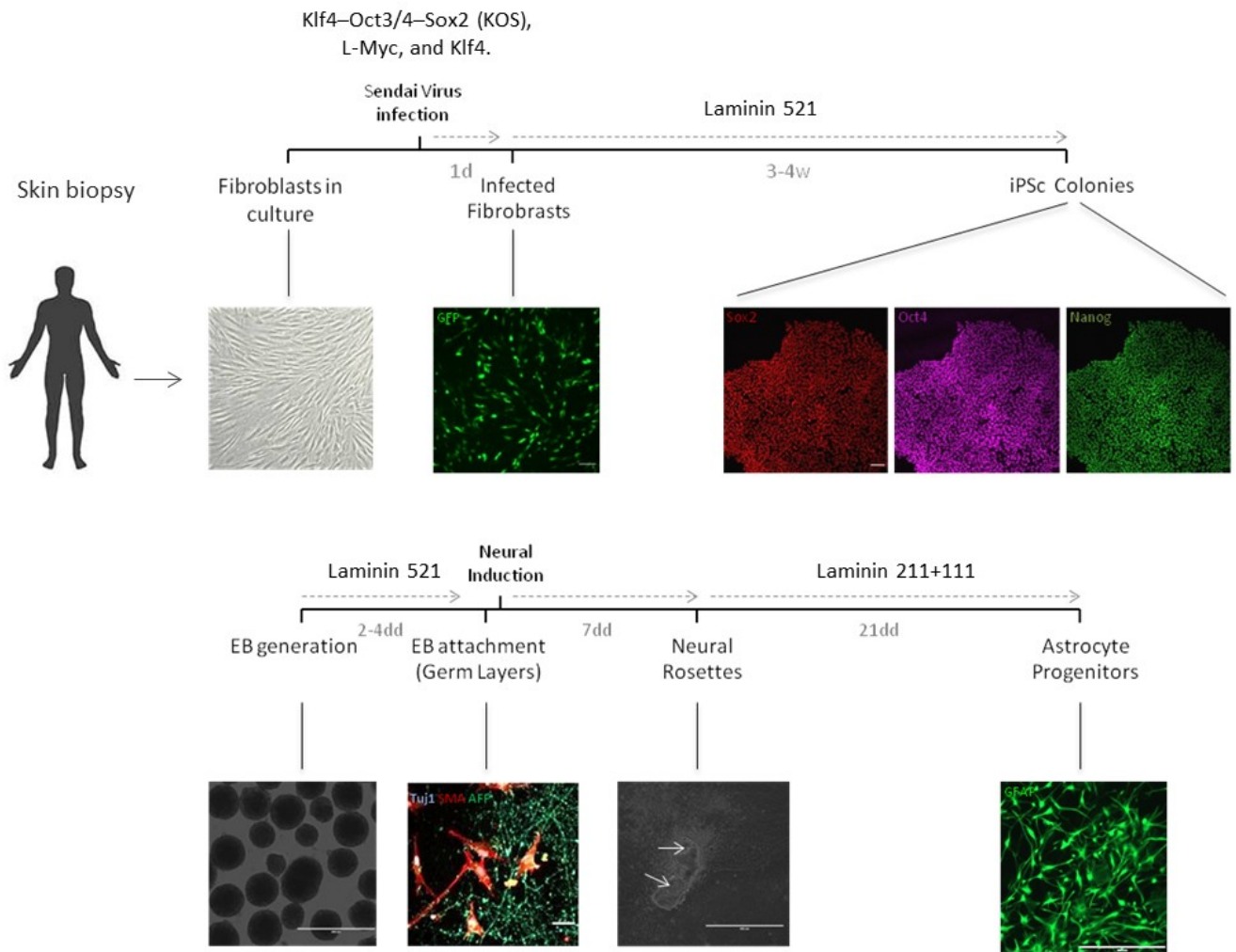


Figure S3

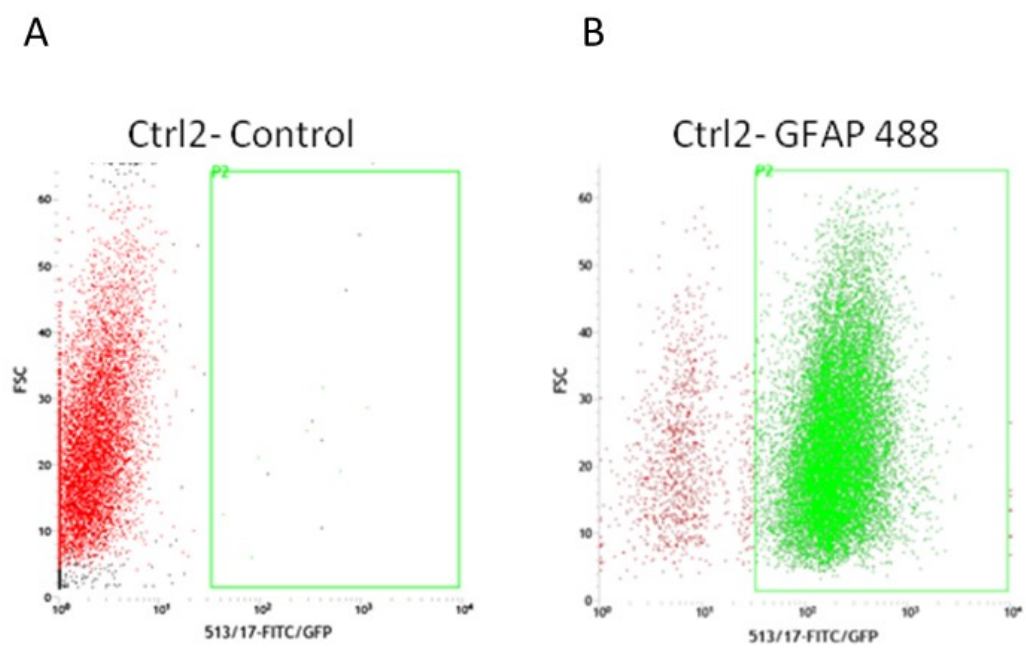


Figure S4

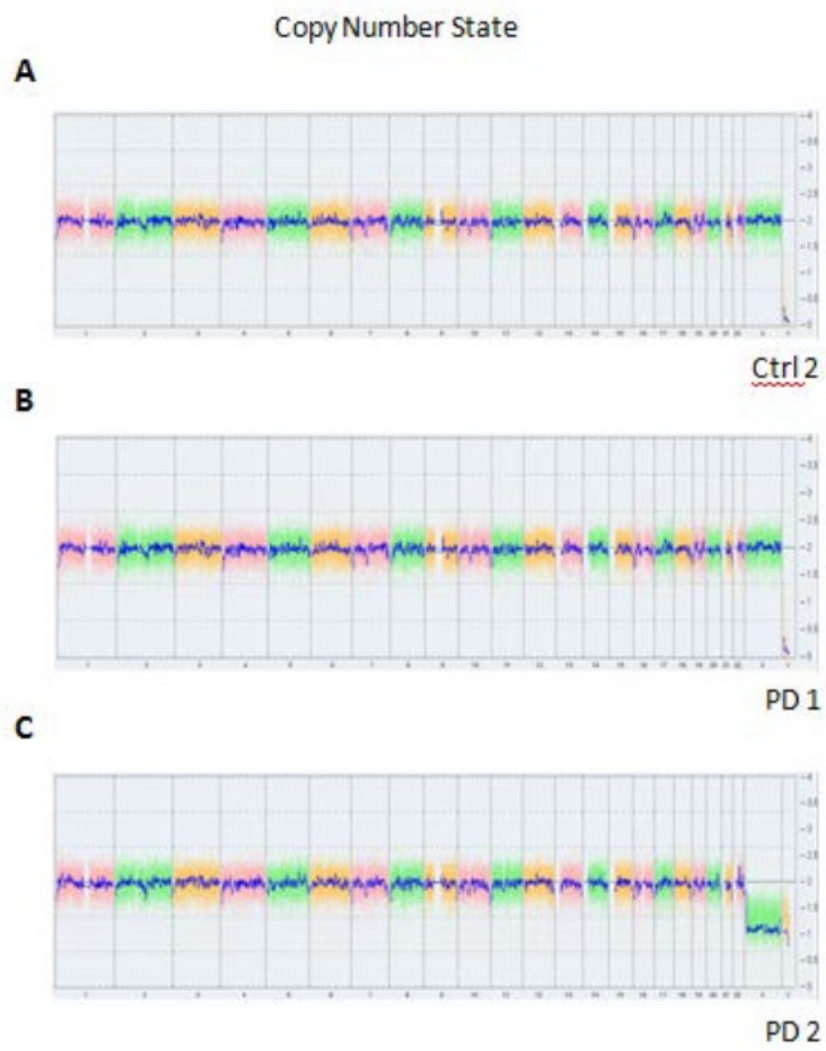


Figure S5

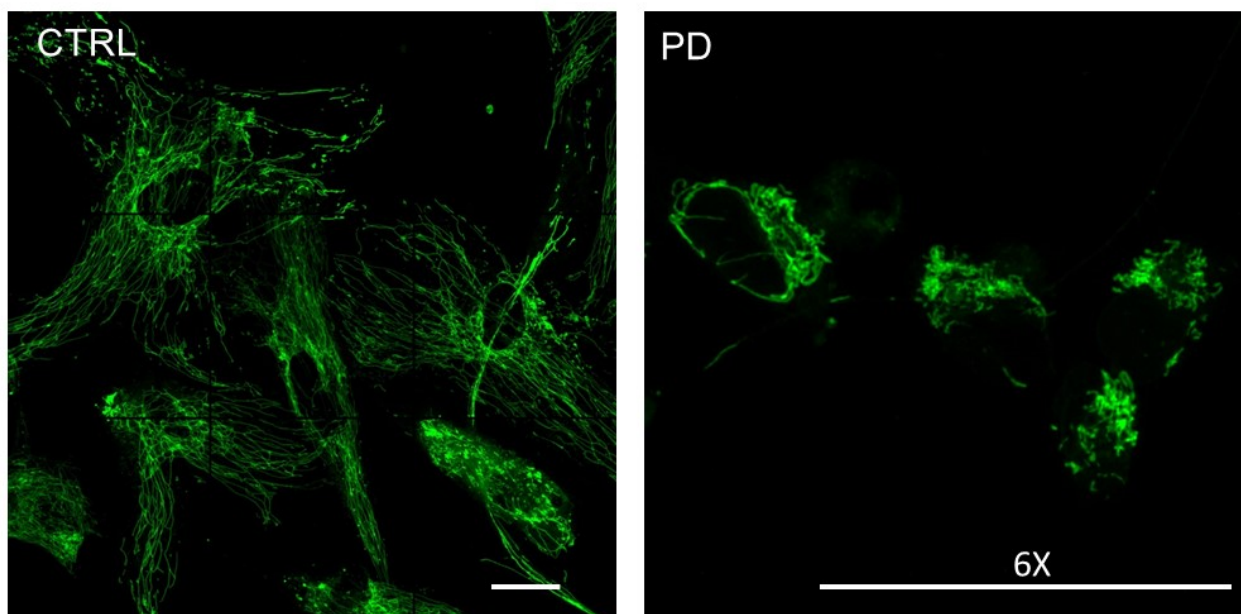


Figure S1. Schematic view of the protocol used to reprogram and differentiate human fibroblasts to hiA.

Figure S2. Protocol and cell characterisation at different culture steps. Fibroblasts infection was evidenced by the co-infection with eGFP protein. iPSC colonies were positive for the pluripotent markers Sox2 (red), Oct4 (purple) and Nanog (green). Embryoid bodies (EB) spontaneously differentiated to the 3 germ layers as evidenced by Tuj1 (in blue for endoderm), SMA 8in red for mesoderm) and AFP (in green for ectoderm). Astrocyte progenitors were positive for GFAP immunostaining (green).

Figure S3. Astrocytes differentiation efficiency. Representative cytofluorimetry assay of healthy donors. hiA were matured for 60 days in vitro, fixed with 4% PFA (as described in Material and Methods) and stained with anti-GFAP. Unstained cells are visualised in A whereas specific stained cells are gated in B.

Figure S4. Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios that depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalised probe signal which is used to identify copy number and aberrations (if any). A, B and C correspond to Ctrl 2, PD 1 and PD 2 respectively, and do not show any alteration. Ctrl 1 were not analyzed because of commercial derivation and already tested by Axol.

Figure S5. Mitotracker staining. Healthy (Ctrl) and patient (PD)-derived astrocytes were seeded in laminin 111/211 coated 35mm glass transparent wells. After 30 day of maturation, astrocytes were loaded in vivo with 100nM Mitotracker green probe for 30 minutes, washed and analysed by confocal microscopy. Scale bar represents 20µm.