

Supplement Table S1. Primer sequences used quantitative real-time PCR

Gene	Forward primer (5'→3')	Reverse primer (5'→3')	Products size (bp)	Accession No.
<i>GAPDH</i>	GTCTCCTCTGACTTCAACAGCG	ACCACCCTGTTGCTGTAGCCAA	131	NM_001256799.3
<i>OCT</i>	CCTGAAGCAGAAGAGGATCACC	AAAGCGGCAGATGGTCGTTTGG	106	AB971680.1
<i>SOX2</i>	GCTACAGCATGATGCAGGACCA	TCTGCGAGCTGGTCATGGAGTT	135	OP680447.1
<i>NANOG</i>	CTCCAACATCCTGAACCTCAGC	CGTCACACCATGCTATTCTTCG	115	JX104835.1
<i>PAX6</i>	CTGAGGAATCAGAGAAGACAGGC	ATGGAGCCAGATGTGAAGGAGG	131	NM_001604.6
<i>Nestin</i>	TCAAGATGTCCCTCAGCCTGGA	AAGCTGAGGGAAGTCTTGGAGC	106	NM_006617.2
<i>p16 (CDKN2A)</i>	CTCGTGCTGATGCTACTGAGGA	GGTCGGCGCAGTTGGGCTCC	134	NM_058195.4
<i>p21 (CDKN1A)</i>	AGGTGGACCTGGAGACTCTCAG	TCCTCTTGGAGAAGATCAGCCG	95	NM_000389.5

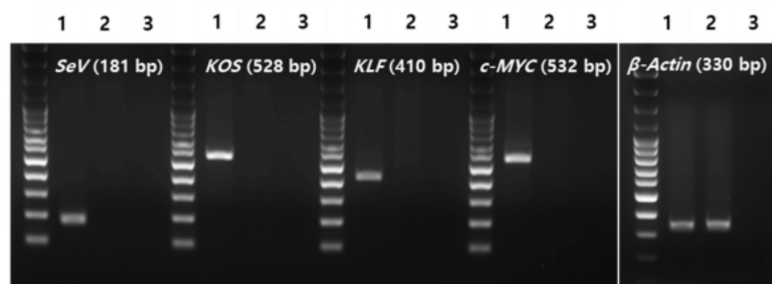
A STR analysis of both iPSCs and PBMCs

Sample No. 1

Match Analysis

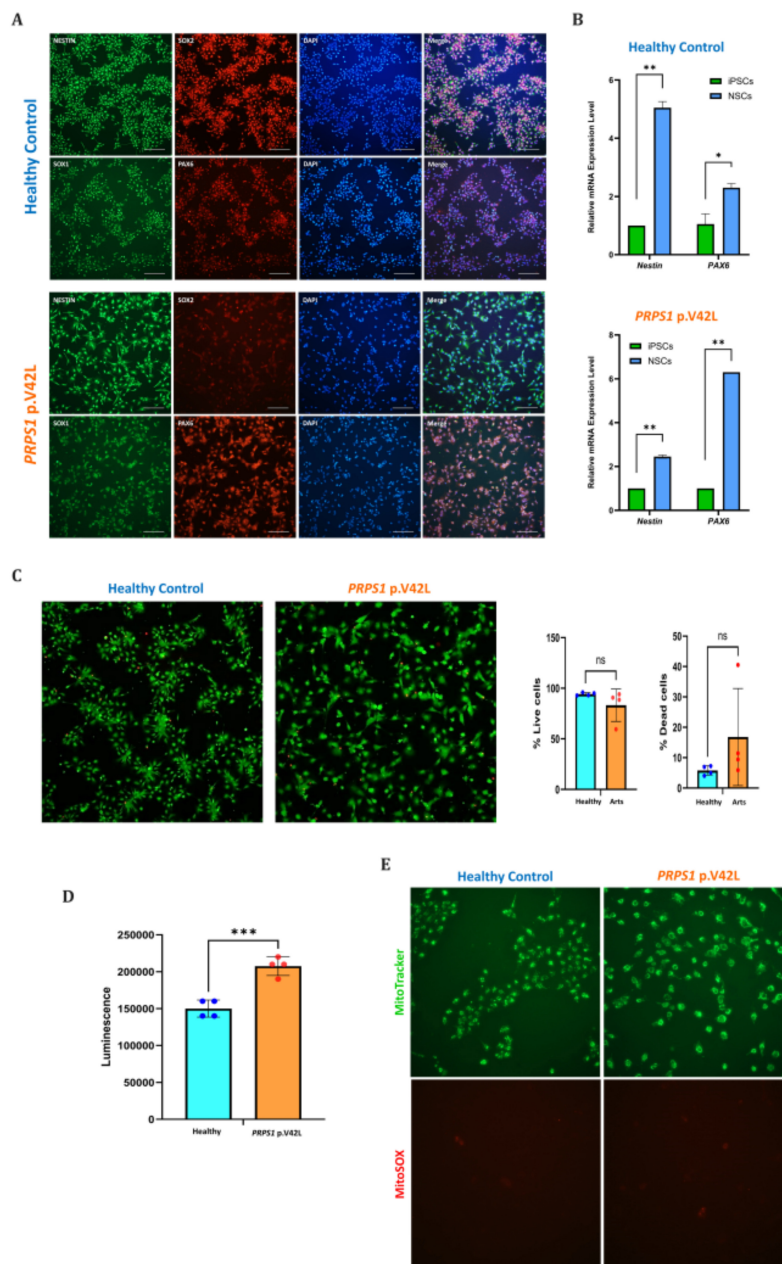
Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : P1_PBMC		Sample Name : P1_IPSC		
D5S818	9	12	9	12	2
D13S317	11	12	11	12	2
D7S820	10	11	10	11	2
D16S539	10	11	10	11	2
vWA	18	20	18	20	2
TH01	6	9	6	9	2
TPOX	9	11	9	11	2
CSF1PO	10	13	10	13	2
AMEL	X	Y	X	Y	2
D3S1358	15	16	15	16	2
D21S11	30	32	30	32	2
D18S51	13	14	13	14	2
D8S1179	12	13	12	13	2
FGA	22		22		1
D2S1338	18	22	18	22	2
D19S433	13	14.2	13	14.2	2
Penta D	9	13	9	13	2
Penta E	5	17	5	17	2
Number of shared alleles					35
Total number of alleles in the reference database profile					35
% match					100.0%
Result interpretation					Related

B Detecting the Sendai reprogramming vector



- 1, Positive Control (Day18)
2, iPSCs (p10)
3, No Template Control (H₂O)

Supplementary Fig. S1. Authentication and pluripotency confirmation of induced pluripotent stem cells (iPSCs) lines. (A) STR profiling confirms genetic identity between peripheral blood mononuclear cells (PBMCs) and established iPSCs. (B) PCR analysis confirms clearance of Sendai virus vectors in late-passage iPSCs.



Supplementary Fig. S2. Characterization and comparable viability and metabolic activity in patient-derived neural stem cells (NSCs). (A) Immunofluorescence images confirming successful differentiation of induced pluripotent stem cells (iPSCs) into NSCs, characterized by the co-expression of neural progenitor markers (SOX2, Nestin, SOX1, PAX6). (B) Quantitative real-time PCR quantification of NSC markers (Nestin, PAX6) expression compared to iPSCs. Data are normalized to GAPDH. Data are presented as mean $\pm$ standard error of the mean (SEM). Statistical significance was determined using an unpaired two-tailed Student's t-test. $n=3$ independent biological replicates. (C) Live/dead staining and quantitative analysis of cell viability show no significant difference (ns) between healthy control and *PRPS1*-mutant (p.V42L) NSCs. Data are presented as mean $\pm$ SEM. Statistical significance was determined using an unpaired two-tailed Student's t-test. $n=3$ independent biological replicates. ns, not significant. (D) Quantification of intracellular adenosine triphosphate (ATP) content in NSCs derived from healthy control and *PRPS1* p.V42L-patient iPSCs. *PRPS1*-mutant NSCs exhibit significantly elevated ATP levels, suggesting altered energy metabolism. Data are presented as mean $\pm$ SEM. Statistical significance was determined using an unpaired two-tailed Student's t-test. $n=3$ independent biological replicates. (E) Mitochondrial morphology (MitoTracker) and mitochondrial reactive oxygen species levels (MitoSOX) are similar between control and *PRPS1*-mutant NSCs. Scale bar = 200 μ m, 10 $\times$ magnification. * $p<0.05$, ** $p<0.01$, *** $p<0.001$.