

# **SUPPLEMENTAL MATERIAL**

**Table S1. Number of samples and cell batches used for functional assessment.**

<b>A</b>						
Experiment	Control 1	Control 2	Control 3	PAIVS 1	PAIVS 2	PAIVS 3
Day 7 contractility	37 (12)	40 (11)	24 (3)	42 (13)	47 (13)	7 (5)
Day 11 contractility	26 (10)	32 (9)	24 (3)	32 (11)	39 (11)	4 (4)
Day 14 contractility	20 (10)	23 (6)	23 (3)	28 (10)	38 (11)	3 (3)
Contractile kinetics	4 (4)	4 (4)	3 (3)	4 (4)	4 (4)	2 (2)
Calcium sensitivity	5 (5)	4 (4)	3 (3)	6 (4)	6 (5)	2 (2)

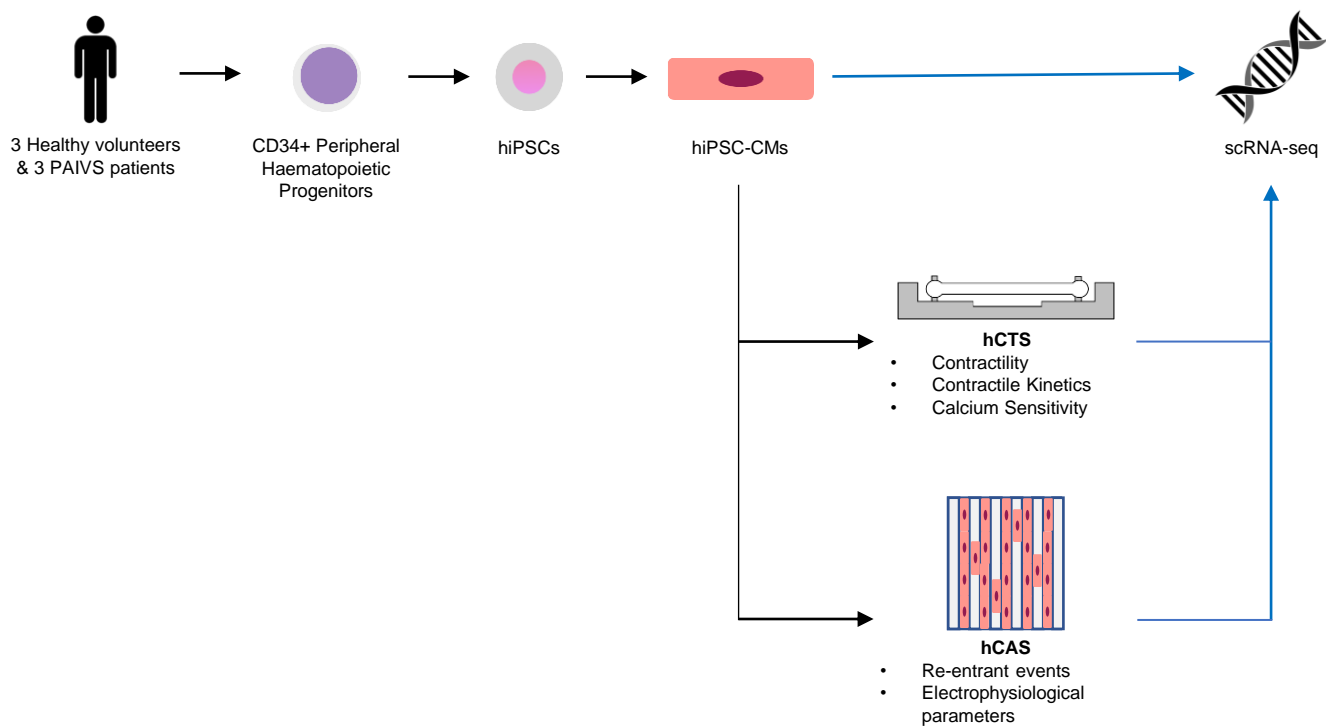
<b>B</b>						
Experiment	Control 1	Control 2	Control 3	PAIVS 1	PAIVS 2	PAIVS 3
Electrophysiological Parameters	4	4	3	3	5	3

(A) Table showing number of samples (number of cell batches) used for each experiment for hCTS. (B) Table showing number of samples used for each experiment for hCAS.

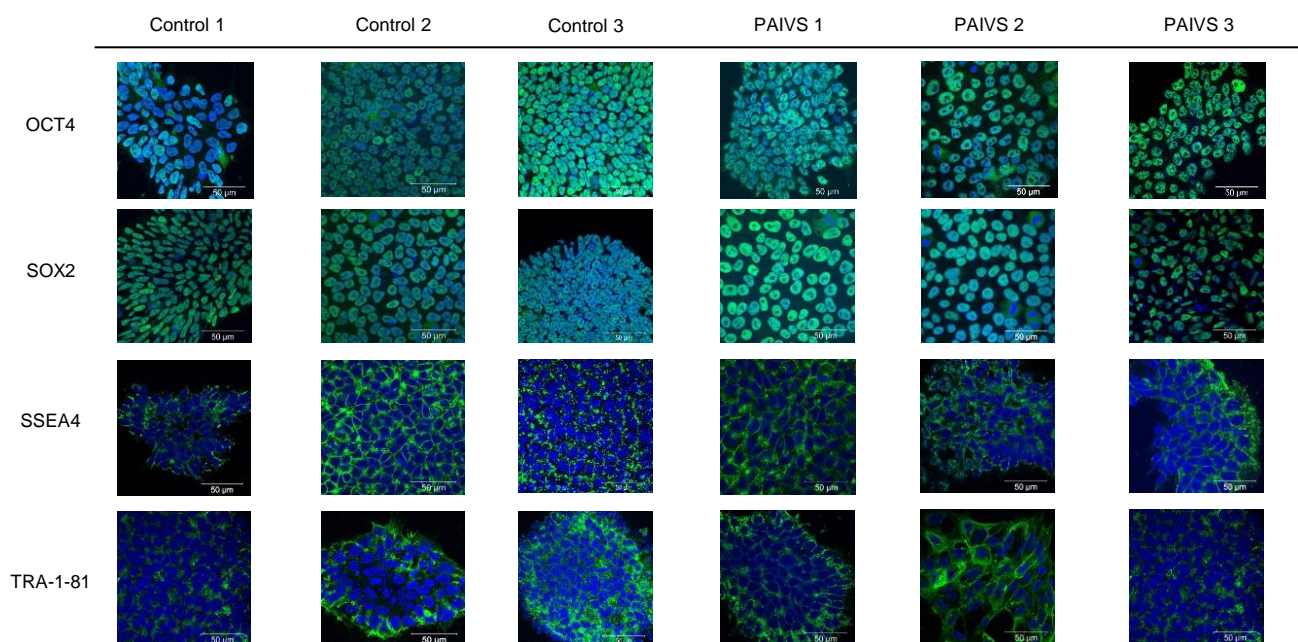
**Table S2. List of forward and reverse primers used in RT-qPCR.**

Gene	Forward Sequence	Reverse Sequence
<i>ACTN2</i>	GTACGTCTCTTGCTTCTACCAC	CTCCATCAGCCTCTCATTCTC
<i>CSRP3</i>	GAAGTTTGGAGAGTCCGAGAAG	ATGGCACAGCGAAACA
<i>FHL2</i>	GTGGCAGTAGTCTGTGGAATAA	GTCACTGATGCTCCATTCTAA
<i>HOPX</i>	GCAGATCCGTCACAGACTAAG	GTTAAGCGGAGGAGAGAAACA
<i>MYH6</i>	CAGCACAGAGCTCTTCAAGC	GTCCGAGATTTCTCTGAA
<i>MYH7</i>	GAGACTGTGCTGGGCTTGTA	CTTCTCAATAGCGCATCAG
<i>MYL2</i>	CAGAACAGGGATGGCTTCAT	CGGAGCCTCCTTGATCATT
<i>NPPA</i>	ATGAGCTCCTTCTCCACCAC	TCCAGCAAATCTTGAAATCC
<i>NPPB</i>	TCCTGCTCTTCTTGCATCTG	GTAACCCGGACGTTTCCAA
<i>PDLIM3</i>	TGCGCAGGACAGGATTAAG	GGGCTTTCCCATCTTCAGATAC
<i>SORBS2</i>	GAGCTGTGACGATCTCCTAAAC	CTTGGAGTCTCCTCACATAAC
<i>SYNPO2L</i>	CTCTTCCGTCTAAGGCATGAAT	TCCCAAAGTGCTGGGATTAC
<i>TCAP</i>	GGGCAGAATGGAAGGATCTG	TGGTGGTAGGTCTCATGTCT
<i>TMSB4X</i>	GAAGAAGACAGAGACGCAAGAG	GAAGGCAATGCTTGTGGAATG
<i>TNNT2</i>	AAGAGGCAGACTGAGCGGAAA	AGATGCTCTGCCACAGCTCCT
<i>TPM1</i>	TGCTTCACTTCTCCCAAGAC	GCAGGATGCTAAGAGAGAGAAC

**Figure S1. An illustrated overview of this study.**

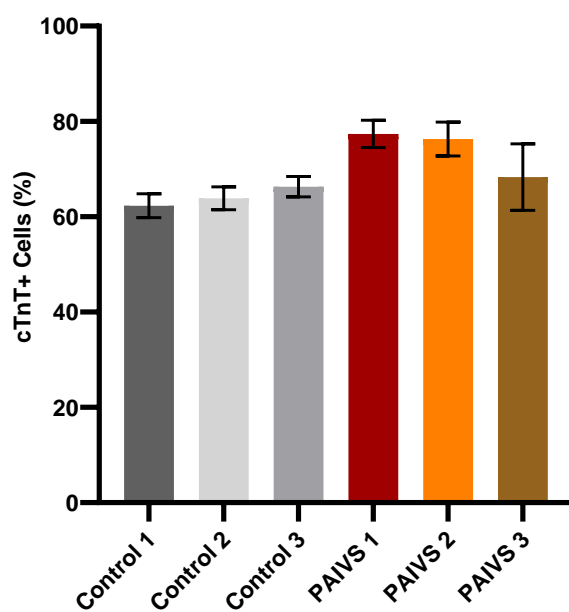


**Figure S2. Validation of hiPSCs with immunostaining of pluripotency markers.**



Immunostaining showing the expression of pluripotency protein markers (OCT4, SOX2, SSEA4, TRA-1-81) for putative hiPSC clones reprogrammed from blood samples of three healthy controls and three PAIVS patients.

**Figure S3. Average percentage of cTnT+ cells at day 14 post-differentiation for all control and PAIVS cell lines.**



*n* = 13 for Control 1, *n* = 12 for Control 2, *n* = 6 for Control 3, *n* = 13 for PAIVS 1, *n* = 13 for PAIVS 2, *n* = 6 for PAIVS 3. Error bars represented as mean  $\pm$  SEM.