

**Additional file 1****Supplementary Table 1**

Pluripotent stem cells used in the study

<b>PSC line</b>	<b>PSC series</b>	<b>Type</b>	<b>HTT polyQ-length</b>	<b>Origin</b>
30 <sup>Q</sup>	IsoHD	ESC	30/19	Courtesy of M. Pouladi, Agency for Science, Technology and Research and National University of Singapore, Singapore
45 <sup>Q</sup>			45/19	
81 <sup>Q</sup>			81/19	
QS1	HD family	iPSC	58/22	UCL Queen Square Institute of Neurology
QS2			20/22	
QS3			69/22	
QS4			75/22	
QS5	-	iPSC	125/22	UCL Queen Square Institute of Neurology
15 <sup>Q</sup>	-	iPSC	15/15	Courtesy of H. Houlden, UCL Queen Square Institute of Neurology

**Supplementary Table 2**

Oligonucleotide primers used for qPCR

<b>Gene target</b>	<b>Forward primer sequence</b>	<b>Reverse primer sequence</b>
<i>CIQA</i>	GTGACACATGCTCTAAGAAG	GACTCTTAAGCACTGGATTG
<i>GAS6</i>	CGAAGAACTCAAGAAGCAG	AGACCTTGATCTCCATTAGG
<i>GPR34</i>	GAAGACAATGAGAAGTCATACC	TGTTGCTGAGAAGTTTTGTG
<i>PROS1</i>	AAAGATGTGGATGAATGCTC	TCACATTCAAAATCTCCTGG
<i>MERTK</i>	AGGACTTCCTCACTTTACTAAG	TGAACCCAGAAAATGTTGAC
<i>P2RY12</i>	AAGAGCACTCAAGACTTTAC	GGGTTTGAATGTATCCAGTAAG
<i>TMEM119</i>	AGTCCTGTACGCCAAGGAAC	GCAGCAACAGAAGGATGAGG
<i>TREM2</i>	TCTGAGAGCTTCGAGGATGC	GGGGATTCTCCTTCAAGA
<i>CD93</i>	CAGAATGCGGCAGACAGTTA	TTCAGCAGTCTGTCCCAGGT
<i>CX3CR1</i>	GGCAGACTTGGATTTTCAGGA	GGGAACTGATCCATGGTGAA
<i>CD14</i>	ATTTGGTGGCAGGAGATCAA	GGCTTCCAGGCTTCACACT
<i>HTT</i>	AGTGATTGTTGCTATGGAGCGG	GCTGCTGGTTGGACAGAACTC
<i>GAPDH</i>	AACAGCGACACCCACTCCT	CATACCAGGAAATGAGCTTGACAA
<i>ACTB</i>	AAGGCCAACCGTGAAAAGAT	GTGGTACGACCAGAGGCATAC

<i>NANOG</i>	AACTCTCCAACATCCTGAACCT	GGCATCCCTGCGTCACA
<i>POU5F1</i>	CTTCAGGAGATATGCAAAGCAGAA	CTGGGCGATGTGGCTGAT
<i>SOX2</i>	GAAATGGGAGGGGTGCAAAA	TACCGGGTTTTCTCCATGCT
<i>ZFP42</i>	CTCCCTTGGGAATTCAGACCTA	TCCAGCCTCAGTACATTTGTTTC

**Supplementary Table 3**

Antibodies used for immunofluorescence measures.

<b>Antibody</b>	<b>Species</b>	<b>Dilution</b>	<b>Supplier</b>
Anti-IF1/IBA1 (cat. NB100-1028)	Goat polyclonal	1:500	Novus Biologicals
Anti-PU.1 (cat. 2266)	Rabbit polyclonal	1:100	Cell Signaling Technology
Anti-TREM2 (cat. AF1828)	Goat polyclonal	1:50	R&D Systems
Anti-TMEM119 (cat. HPA052650)	Rabbit polyclonal	1:200	Atlas Antibodies
Anti-CTIP2 (25B6)	Rat monoclonal	1:300	Abcam
Anti-cleaved caspase 3 (5A1E)	Rabbit monoclonal	1:400	Cell Signaling Technology
Anti-DARPP32 (H-62)	Rabbit polyclonal	1:200	Santa Cruz Biotechnology
Anti- $\beta$ III-tubulin (cat. ab18207)	Rabbit polyclonal	1:500	Abcam
Anti-nestin (10C2)	Mouse monoclonal	1:600	Merck Millipore
Anti-gamma H2A.X (cat. ab11174)	Rabbit polyclonal	1:200	Abcam

<b>Antibody</b>	<b>Supplier</b>
Goat anti-rat AlexaFluor 488	Thermo Fisher Scientific
Goat anti-rabbit AlexaFluor 488	Thermo Fisher Scientific
Goat ant-mouse AlexaFluor 568	Thermo Fisher Scientific
Goat anti-chicken AlexaFluor 647	Thermo Fisher Scientific
Donkey anti-goat AlexaFluor 488	Thermo Fisher Scientific
Donkey anti rabbit AlexaFluor 568	Thermo Fisher Scientific

**Supplementary Table 4**

Perkin Elmer Columbus software parameters used for the unbiased analysis of each immunofluorescence imaging metric in the study.

<b>Cell feature</b>	<b>Columbus building block</b>	<b>Specifics</b>	<b>Method</b>	<b>Output name</b>
<b>Nuclei</b>	Find Nuclei	Channel: HOECHST 33342 Region: None	Method: M Diameter: 15 $\mu$ m Splitting coefficient: 0.4 Common threshold: 0.1	Population: Nuclei
	Calculate Intensity Properties	Channel: HOECHST 33342 Population: Nuclei Region: Nucleus	Method: Standard, mean	Properties: Intensity nuclear HOECHST 33342
	Calculate Morphology Properties	Population: Nuclei Region: Nucleus	Method: Standard, area, roundness	Properties: Nucleus morphology
	Select Population	Population: Nuclei	Method: Filter by property Nucleus area [ $\mu$ m <sup>2</sup> ]: $\geq$ 40 Intensity nucleus HOECHST 33342 mean: $\leq$ 18512 Nucleus area [ $\mu$ m <sup>2</sup> ]: $\leq$ 200 Boolean operations: F1 and F2 and F3	Population: Viable nuclei
<b>Caspase 3 +ve neurons</b>	Find Cytoplasm	Channel: Alexa 488 Nuclei: Nuclei	Method: B Common threshold: 0.45 Individual threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 488 Population: Nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Caspase 3 cytoplasmic intensity in all cells

	Select Population	Population: Nuclei	Method: Filter by property Intensity cytoplasmic caspase 3 in all cells, mean: $\geq 1000$	Population: Cells with cytoplasmic caspase 3 over a threshold
<b>Caspase 3 +ve microglia</b>	Find Cytoplasm	Channel: Alexa 488 Nuclei: Nuclei	Method: B Common threshold: 0.45 Individual threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 568 Population: Nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Caspase 3 cytoplasmic intensity in all cells
	Select Population	Population: Nuclei	Method: Filter by Property Caspase 3 cytoplasmic intensity in all cells Mean: $\geq 335$	Population: Cells with Caspase 3 over a threshold
<b>Nestin+ cells</b>	Find Cells	Channel: Alexa 568 ROI: Viable nuclei ROI Region : Cell	Method: B Common threshold: 0.4 Area: $> 70 \mu\text{m}^2$ Split factor: 7 Individual threshold: 0.5 Contrast: $> 0.3$	Population: Nestin+ cells
	Find Cytoplasm	Channel: Alexa 568 Nuclei: Viable nuclei	Method: B Common threshold: 0.45 Individual threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 568 Population: Viable nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Intensity cytoplasm Alexa 568

	Select Population	Population : Viable nuclei	Method: Filter by Property Intensity cytoplasm Alexa 568, mean: $\geq 1500$	Population: Viable nuclei with cytoplasmic Nestin over a threshold
<b><math>\beta</math>III-tubulin+ neurons</b>	Find Cytoplasm	Channel: Alexa 647 Nuclei: Viable nuclei	Method: B Common threshold: 0.45 Individual threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 647 Population: Viable nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Intensity cytoplasm Alexa 647
	Select Population	Population: Viable nuclei	Method: Filter by Property Intensity cytoplasm Alexa 647, mean: $\geq 1200$	Population: Viable nuclei with cytoplasmic B3tubulin over a threshold
<b>CTIP2+ neurons</b>	Calculate Intensity Properties	Channel: Alexa 568 Population: Viable nuclei Region: Nucleus	Method: Standard, mean	Properties : Intensity nucleus Alexa 568
	Select Population	Population: Viable nuclei	Method: Filter by property Intensity nucleus Alexa 568 mean: $\geq 500$	Population: CTIP+ cells
<b>DARPP32+ neurons</b>	Find Cells	Channel: Alexa 488 Region: None	Method: B Common threshold: 0.4 Area: $> 70 \mu\text{m}^2$ Split Factor: 7 Individual threshold: 0.5 Contrast: $> 0.3$	Population: DARPP32+ cells (Find Cells)
	Calculate Intensity Properties	Channel: Alexa 488 Population: DARPP32+ cells (Find Cells)	Method: Standard, mean	Properties: Intensity of DARPP32+ cells

		Region: Cell		
	Find Image Region	Channel: Alexa 488 Region: None	Method : Common threshold Threshold: 0.5 Area: > 10 $\mu\text{m}^2$	Population: DARPP32+ area Region: DARPP32+ total staining
	Calculate Morphology Properties	Population: DARPP32+ area Region: DARPP32+ total staining	Method: Standard, area, roundness	Properties: DARPP32+ total staining
	Calculate Intensity Properties	Channel: Alexa 488 Population: DARPP32+ area Region: DARPP32+ total staining	Method: Standard, sum	Properties: Intensity DARPP32+ total staining
	Find Cytoplasm	Channel: Alexa 488 Nuclei: Viable nuclei	Method: B Common threshold: 0.45 Individual threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 488 Population: Viable nuclei Region: Cell (2)	Method: Standard, mean	Properties: Intensity Cell Alexa 488
	Select Population	Population: Viable nuclei	Method: Filter by Property Intensity Cell Alexa 488 Mean: $\geq 1200$	Population: Viable nuclei with cytoplasmic DARPP32+ over a threshold
	Find Spots	Channel: Alexa 488 Region: Viable nuclei	Method: C Radius: < 5px Contrast: > 0.1 Uncorrected Spot to Region Intensity: > 1 Distance: > 3px Spot Peak Radius: 0 px	Population: H2AX+ spots in viable nuclei



<b>H2AX+ spots</b>			Calculate Spot Properties	
	Select Population	Population: Viable nuclei	Method: Filter by property Number of spots: > 4	Population: Viable nuclei with >4 H2AX+ spots
	Select Population	Population: Viable nuclei	Method: Filter by property Number of Spots: > 10	Population: Viable nuclei with >10 H2AX+ spots
<b>TMEM119+ cells</b>	Calculate Intensity Properties	Channel: Alexa 568 Population: Viable nuclei Region: Nucleus	Method: Standard, mean	Properties: Intensity Nucleus Alexa 568
	Select Population	Population: Viable nuclei	Method: Filter by property Intensity Nucleus Alexa 568 Mean: >= 380	Population: Tmem119+ viable cells (nuclear stain)
<b>IBA+ cells</b>	Find Cytoplasm	Channel: Alexa 488 Nuclei: Viable Nuclei	Method: B Common Threshold: 0.45 Individual Threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 488 Population: Viable Nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Intensity Cytoplasm Alexa 488
	Select Population	Population: Viable Nuclei	Method: Filter by Property Intensity Cytoplasmic Alexa 488 Mean: >= 300	Population: Viable nuclei with cytoplasmic IBA1 over a threshold

<b>PU.1+ cells</b>	Calculate Intensity Properties	Channel: Alexa 568 Population: Viable Nuclei Region: Nucleus	Method: Standard, mean	Properties: Intensity Nucleus Alexa 568
	Select Population	Population: Viable Nuclei	Method: Filter by Property Intensity Nucleus Alexa 568 Mean: $\geq 380$	Population: PU1+ viable nuclei
<b>TREM2+ cells</b>	Find Cytoplasm	Channel: Alexa 488 Nuclei: Viable nuclei	Method: B Common Threshold: 0.45 Individual Threshold: 0.15	
	Calculate Intensity Properties	Channel: Alexa 488, Population: Viable Nuclei Region: Cytoplasm	Method: Standard, mean	Properties: Intensity Cytoplasm Alexa 488
	Select Population	Population: Viable Nuclei	Method: Filter by Property Intensity Cytoplasm Alexa 488 Mean: $\geq 200$	Population: Viable nuclei with cytoplasmic Trem2+ over a threshold