Experimental design

1. Sample size
   Describe how sample size was determined.
   Thirty eight monkeys were screened by spontaneous movement calculated with the PrimateScan image analysis system (CleverSys Inc., Virginia, USA), which can calculate animal movement from analog video. Eleven monkeys with spontaneous movements of 100–400 m/hr were used in this study.

2. Data exclusions
   Describe any data exclusions.
   One monkey (#10) unexpectedly weakened at eight months due to acute gas accumulation in the intestines and was euthanized. We omitted this monkey from the behavioral analyses.

3. Replication
   Describe whether the experimental findings were reliably reproduced.
   In all experiments, we used multiple samples and the sample numbers are presented. For example, we grafted dopaminergic progenitors derived from eight different iPS cell lines and all of them survived in the brains of eight monkeys.

4. Randomization
   Describe how samples/organisms/participants were allocated into experimental groups.
   The 11 PD model monkeys were assigned into three groups (healthy, PD and vehicle group) without randomization so that the average monkey PD scores in each group was similar.

5. Blinding
   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.
   A blinded observer evaluated PD symptoms of the monkeys.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.
6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

<table>
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<td>√</td>
<td>The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)</td>
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<td>A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly</td>
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<td>A statement indicating how many times each experiment was replicated</td>
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<td>The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)</td>
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<td>A description of any assumptions or corrections, such as an adjustment for multiple comparisons</td>
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<td>The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted</td>
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<td>A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)</td>
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<td>Clearly defined error bars</td>
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See the web collection on statistics for biologists for further resources and guidance.

7. Software

Describe the software used to analyze the data in this study.

The microarray data were analyzed with GeneSpring software (Agilent Technologies). TH fiber extension was evaluated with Adobe Photoshop CC software (Adobe Systems). The statistical analyses were performed using a commercially available software package (GraphPad Prism, GraphPad Software Inc.) To calculate the graft volumes from MRI, we used Functional Magnetic Resonance Images of Brain (FMRIB) software libraries. An analysis of PET data was performed using PMOD software (PMOD Technologies LLC, Zurich, Switzerland). The video data was analyzed with MATLAB software (The MathWorks Inc.).

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). Nature Methods guidance for providing algorithms and software for publication provides further information on this topic.

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

N117-11 cells can be available from the corresponding author, and all iPSC cell lines from PD patients will be available from RIKEN BioResource Center.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

The primary antibodies used are as follows: STEM121 (cellartis, Y40410, 1:500), Ki67 (Novo CASTRA, NCL-Ki67p, 1:1000), TH (Millipore, AB152, 1:400), GIRK2 (Alomone Labs, APC-006, 1:200), MHC class II (Dako, MO775, 1:1000), CD45 (Dako, MO701, 1:1000), Monkey IgG (Nordic-MUbio BV, GAMON/IGG(H+L)/BIO, 1:2000), FOXA2 (R&D, AF2400, 1:500), NURR1 (Gift from KAN Research Institute, 1:1000), PAX6 (BD bioscience, 561462, 1:1000), MONK IgG (Nordic-MUbio BV, GAMON/IGG(H+L)/BIO, 1:2000), FOA2 (R&D, AF2400, 1:500), NURR1 (Gift from KAN Research Institute, 1:1000), PAX6 (BD bioscience, 561462, 1:200), SOX1 (R&D, AF3369, 1:200), SEROTONIN (Millipore, MAB352, 1:200), GABA (SIGMA, A-1052, 1:10000), VGLUT1 (Synaptic Systems, 135303, 1:1000), CHAT (Millipore, AB144p, 1:1000), GFAP (DAKO, Z0334, 1:400), and TUJ1 (Covance, MMS-435P, 1:600).
10. Eukaryotic cell lines
   a. State the source of each eukaryotic cell line used. The origin of cell line are as follows: N117-11 (healthy person #1, 74-year-old male, dermal fibroblasts), 1147F1 (healthy person #2, 50-year-old male, peripheral blood cells), 83683 (HDF1388, dermal fibroblast from 36-year-old female), 1231A3 (healthy person #3, 29-year-old female, dermal peripheral blood cells), PD12-1 (PD patient #12, 52-year-old male, dermal fibroblasts), 783E2 (PD patient #12, 52-year-old male, peripheral blood cells), 1275A3 (PD patient #15, 71-year-old male, peripheral blood cells) and 1263A18 (PD patient #2, 82-year-old male, peripheral blood cells).
   b. Describe the method of cell line authentication used. Cells that had normal karyotypes (46, XX or 46, XY) and no mycoplasma contamination were used for the experiments.
   c. Report whether the cell lines were tested for mycoplasma contamination. The cell lines were tested for mycoplasma.
   d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use. No cell line is listed in the ICLAC database.

- Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals
   Provide details on animals and/or animal-derived materials used in the study. Adult (2–3 years old) male cynomolgus monkeys (Macaca fascicularis) were obtained from Shin Nippon Biomedical Laboratories (Kagoshima, Japan) and used for this study.

Policy information about studies involving human research participants

12. Description of human research participants
   Describe the covariate-relevant population characteristics of the human research participants. Three PD patients, PD2 (82-year-old male, PD onset at 70 years old, Hoehn & Yahr Scale II), PD12 (52-year-old male, PD onset at 38 years old, Hoehn & Yahr Scale III), and PD15 (71-year-old male, PD onset at 68 years old, Hoehn & Yahr Scale III) without familial history of PD are included in this study.
MRI Studies Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Experimental design

1. Describe the experimental design. Repeated MRI scanning for partial volume correction of PET

2. Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials. Not applicable

3. Describe how behavioral performance was measured. Not applicable

Acquisition

4. Imaging
   a. Specify the type(s) of imaging. Structural imaging
   b. Specify the field strength (in Tesla). 3-Tesla
   c. Provide the essential sequence imaging parameters.
      #1 T1-weighted image, a magnetization prepared rapid gradient echo (MPRAGE) sequence (TR=2300 ms, TE=3.13 ms, TI=900 ms, FA=7 degree, matrix=128x128, field of view=102 mm, slice thickness=0.8 mm)
      #2 T2-weighted image, T2 SPACE sequence (TR=2500 ms, TE=301 ms, base resolution=128, FOV=102 mm, Slice thickness=0.8 mm, Turbo factor=77, Slice turbo factor=2)
      #3 T1- and T2-weighted images, a FLAIR (fluid-attenuated-inversion recovery) image (TR=11500 ms, TR=81 ms, TI=2670.4 ms, base resolution=128, flip angle=150 deg, FOV=102 mm, slice thickness=0.8 mm)
   d. For diffusion MRI, provide full details of imaging parameters. Not applicable

5. State area of acquisition. A whole brain scan

Preprocessing

6. Describe the software used for preprocessing. Functional Magnetic Resonance Images of Brain (FMRIB) software libraries for measurement of the graft volumes

7. Normalization
   a. If data were normalized/standardized, describe the approach(es). Normalized with structurally to the standardized MNI space of macaca fascicularis
   b. Describe the template used for normalization/ transformation. The standardized MNI space of macaca fascicularis

8. Describe your procedure for artifact and structured noise removal. Not applicable
9. Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

**Statistical modeling & inference**

10. Define your model type and settings.

11. Specify the precise effect tested.

12. Analysis
   a. Specify whether analysis is whole brain or ROI-based.
   b. If ROI-based, describe how anatomical locations were determined.

13. State the statistic type for inference. (See Eklund et al. 2016.)

14. Describe the type of correction and how it is obtained for multiple comparisons.

15. Connectivity
   a. For functional and/or effective connectivity, report the measures of dependence used and the model details.
   b. For graph analysis, report the dependent variable and functional connectivity measure.

16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.

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