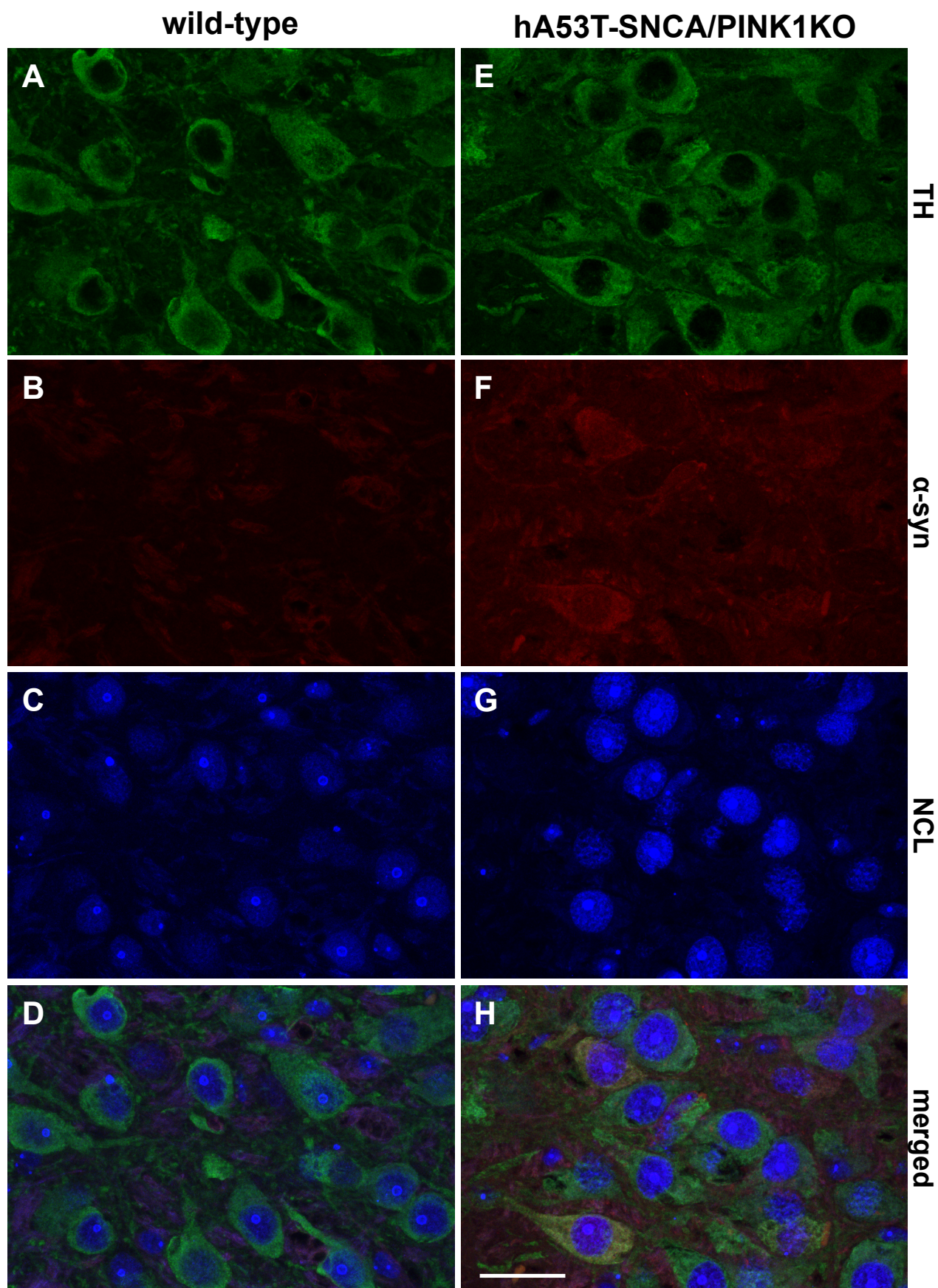


Supplementary information

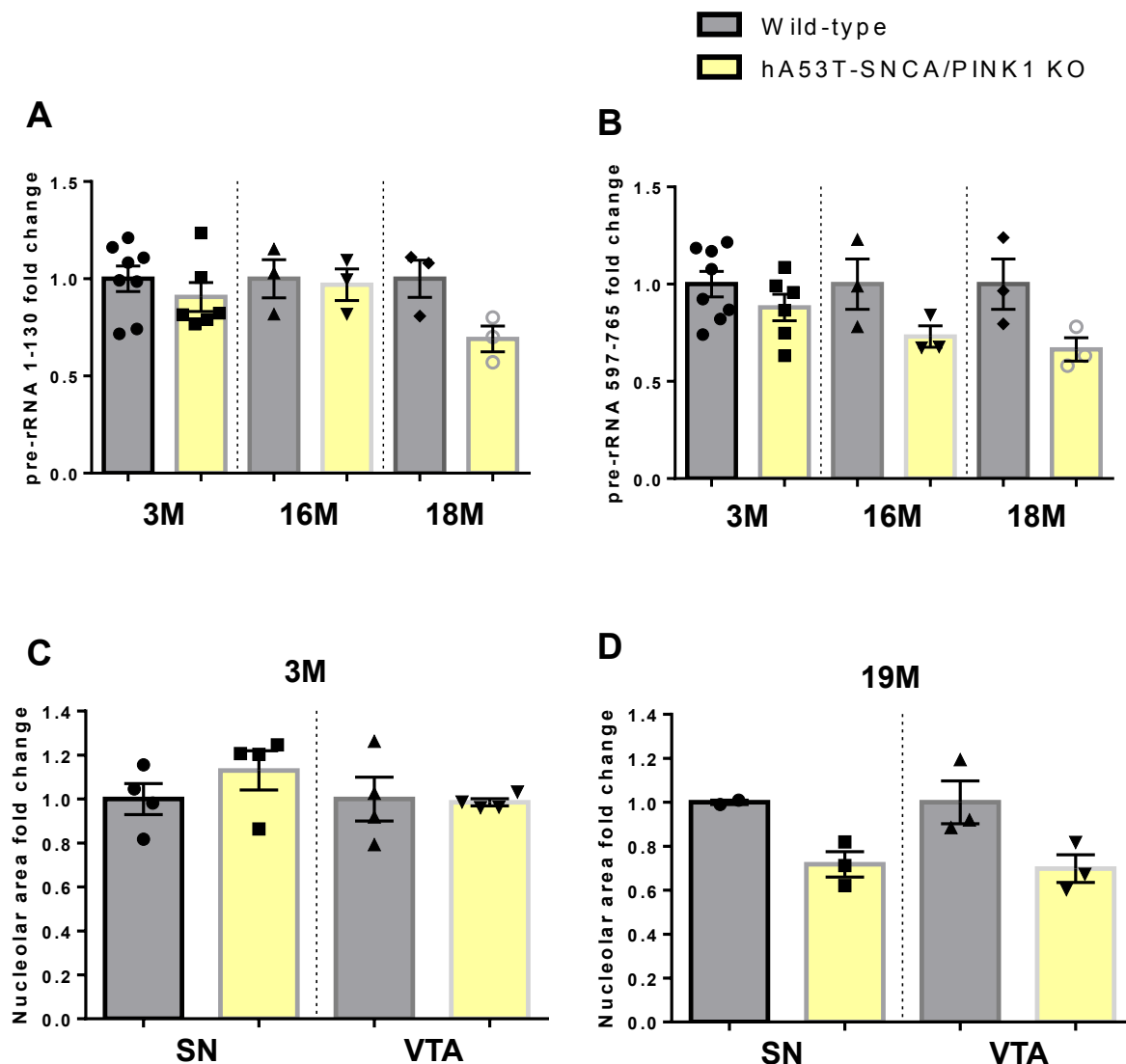


Suppl. Fig. 1

Suppl. Figure 1

hA53T-SNCA is expressed in DA neurons in the cytoplasm and in the nucleolus.

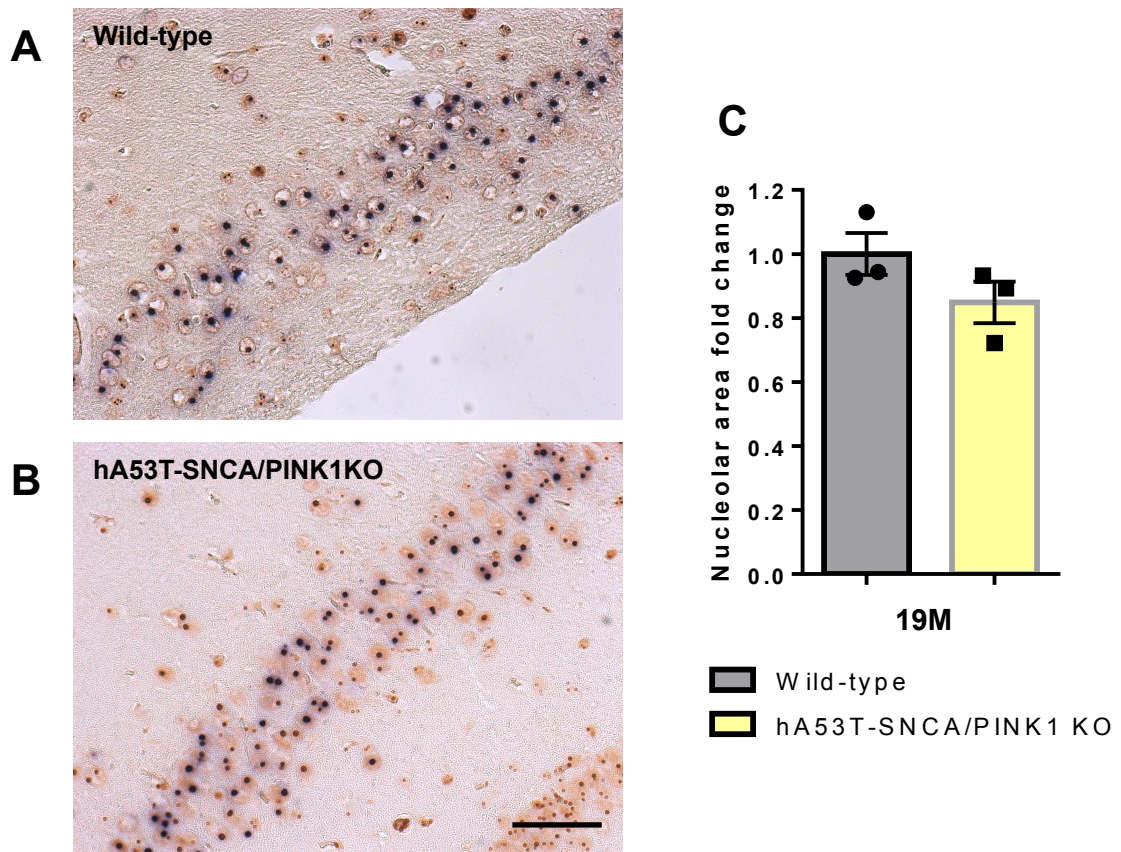
Representative confocal microscopy images of paraffin sections immunostained with TH (green), human alpha-synuclein (red) and NCL (blue) specific antibodies from 3 month-old wild-type (**A-D**) and hA53T-SNCA overexpressing transgenic mice in a PINK1 KO background (hA53T-SNCA/PINK1KO) (**E-H**). Scale bar: 25 μ m.



Suppl. Fig. 2

Suppl. Figure 2: Individual data plots from Figure 2

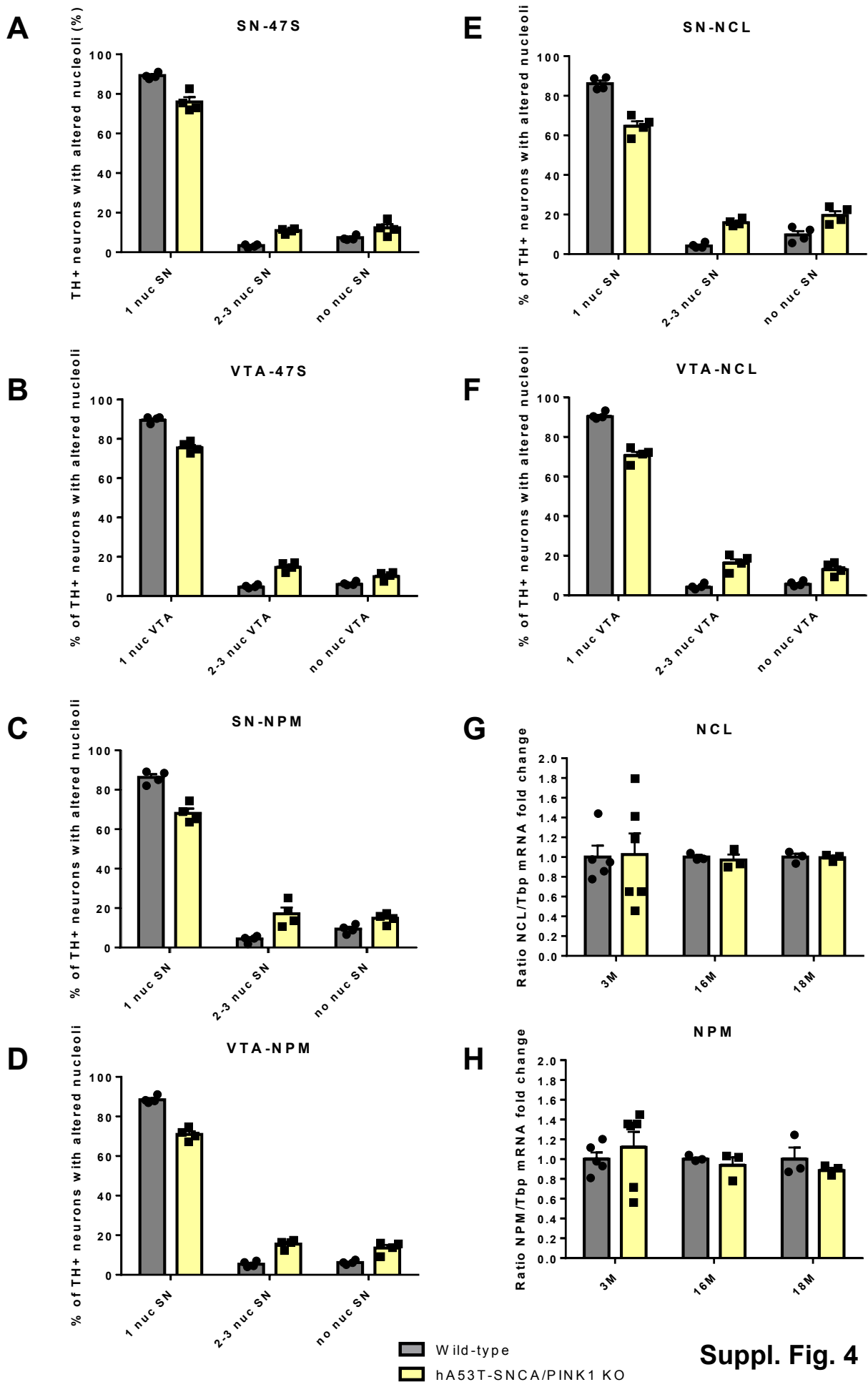
A, B: Analysis of pre-rRNA (1-130) and pre-rRNA (597-765) by qRT-PCR at 3, 16 and 18 months in the ventral midbrain of wild-type (N=8,3,3) and hA53T-SNCA/PINK1KO mice (N=6,3,3) expressed as fold change to respective controls and normalized by GAPDH. **C, D:** Quantification of the area occupied by the 47S staining in hA53T-SNCA/PINK1KO expressed as fold change relative to respective controls in SN and VTA at 3 and 19 months (N=4 and 3). Data are mean ± SEM.



Suppl. Fig. 3

Suppl. Figure 3: 47S pre-rRNA localization and nucleolar area in hippocampal neurons of hA53T-SNCA/PINK1KO mice.

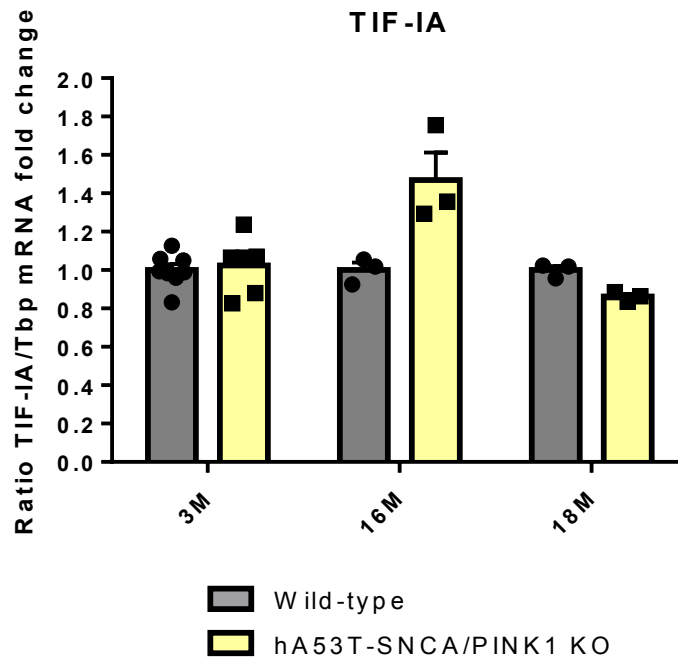
A, B: Representative images of ISH with 47S specific riboprobe (blue) and counterstained with Nuclear Fast Red at 19 months in CA1 of wild-type and hA53T-SNCA/PINK1KO mice. **C:** Quantification of the area occupied by the 47S staining in hA53T-SNCA/PINK1KO expressed as fold change relative to wild-type control at 19 months (N=3). Data are mean \pm SEM.



Suppl. Fig. 4

Suppl. Figure 4: Individual data plots from Figure 3

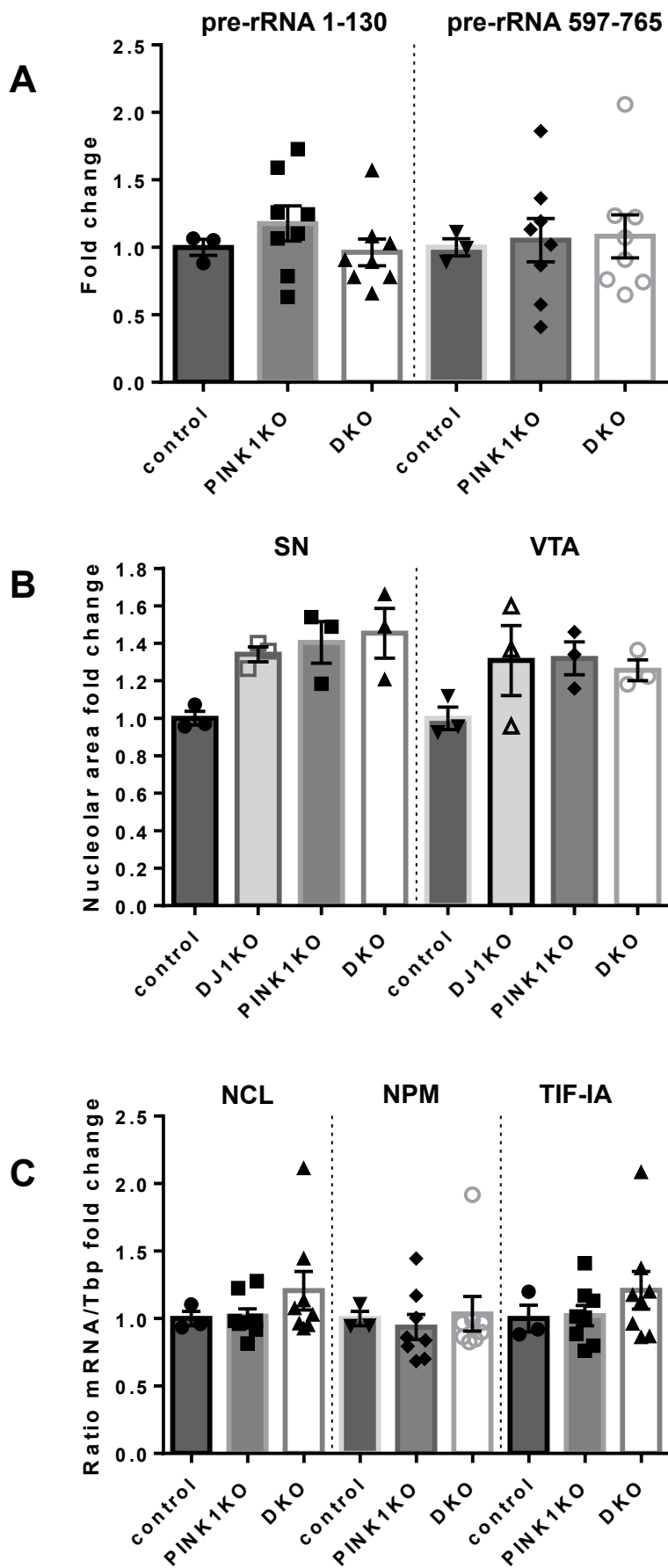
A, B: Quantification of the number of nucleoli detected by ISH with 47S specific riboprobe in TH positive neurons of 3 months old wild-type and hA53T-SNCA/PINK1KO mice (N=4) in SN (left) and VTA (right) expressed as percentage of TH positive neurons with 1, 2-3 or no nucleoli. Quantification of the number of nucleoli detected by NPM (**C, D**) and NCL (**E, F**) immunostaining in TH positive neurons of wild-type and hA53T-SNCA/PINK1KO mice (N=4) in SN and VTA expressed as percent of TH positive neurons with 1, 2-3 or no nucleoli. **G, H:** Analysis of NCL and NPM mRNA levels by qRT-PCR at 3, 16 and 18 months in wild type (N=5,3,3) and hA53T-SNCA/PINK1 KO mice (N=6,3,3) expressed as fold change to respective controls and normalized by Tbp. All data are mean \pm SEM; nuc: nucleolus.



Suppl. Fig. 5

Suppl. Figure 5: Individual data plot from Figure 4

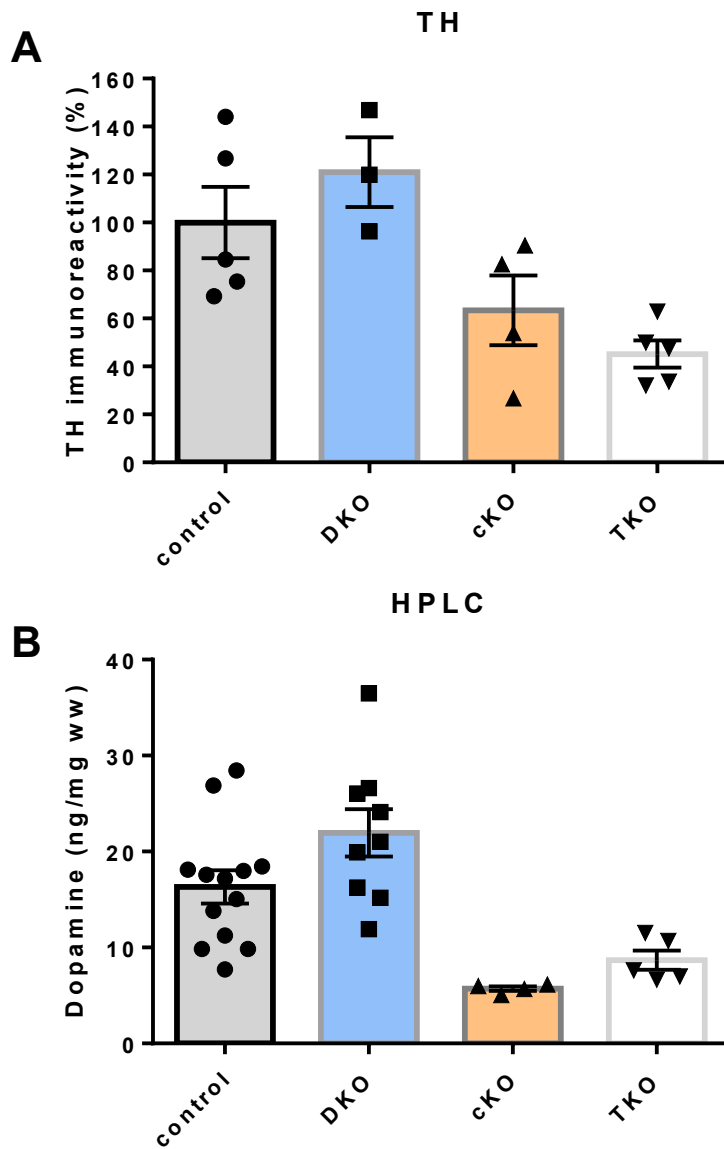
Analysis of TIF-IA expression by qRT-PCR in 3, 16 and 18 months old wild-type (N=8,3,3) and hA53T-SNCA/PINK1KO mice (N=6,3,3) expressed as fold change to respective controls normalized by Tbp. Data are mean \pm SEM.



Suppl. Fig. 6

Suppl. Figure 6: Individual data plots from Figure 5 including nucleolar area analysis for DJ-1 KO mice.

A: Analysis of pre-rRNA (1-130) and pre-rRNA (597-765) by qRT-PCR in controls (N=3), PINK1 KO (N=8) and DJ-1/PINK1 DKO mice (N=8) expressed as fold change to respective controls normalized by GAPDH. **B:** Quantification of the area occupied by the 47S staining in control, DJ-1 KO, PINK1 KO and DKO mice (N=3) expressed as fold change relative to respective controls in SN and VTA. **C:** Analysis of NCL, NPM and TIF-IA mRNA levels by qRT-PCR in wild-type (N=3), PINK1 KO (N=8) and DJ-1/PINK1 DKO (N=8) mice at 9 months expressed as fold change to respective controls normalized by Tbp. All data are mean \pm SEM.



Suppl. Fig. 7

Suppl. Figure 7: Individual data plots from Figure 6

A: Quantification of TH immunoreactivity in the striata of control (N=5), DKO (N=3), cKO (N=4) and TKO (N=5) mice. **B:** Analysis of dopamine content by HPLC-ED in the striata of control (N=13), DKO (N=9), cKO (N=4) and TKO (N=5) mice. Data are mean \pm SEM; ww: wet weight.