

Expanded View Figures

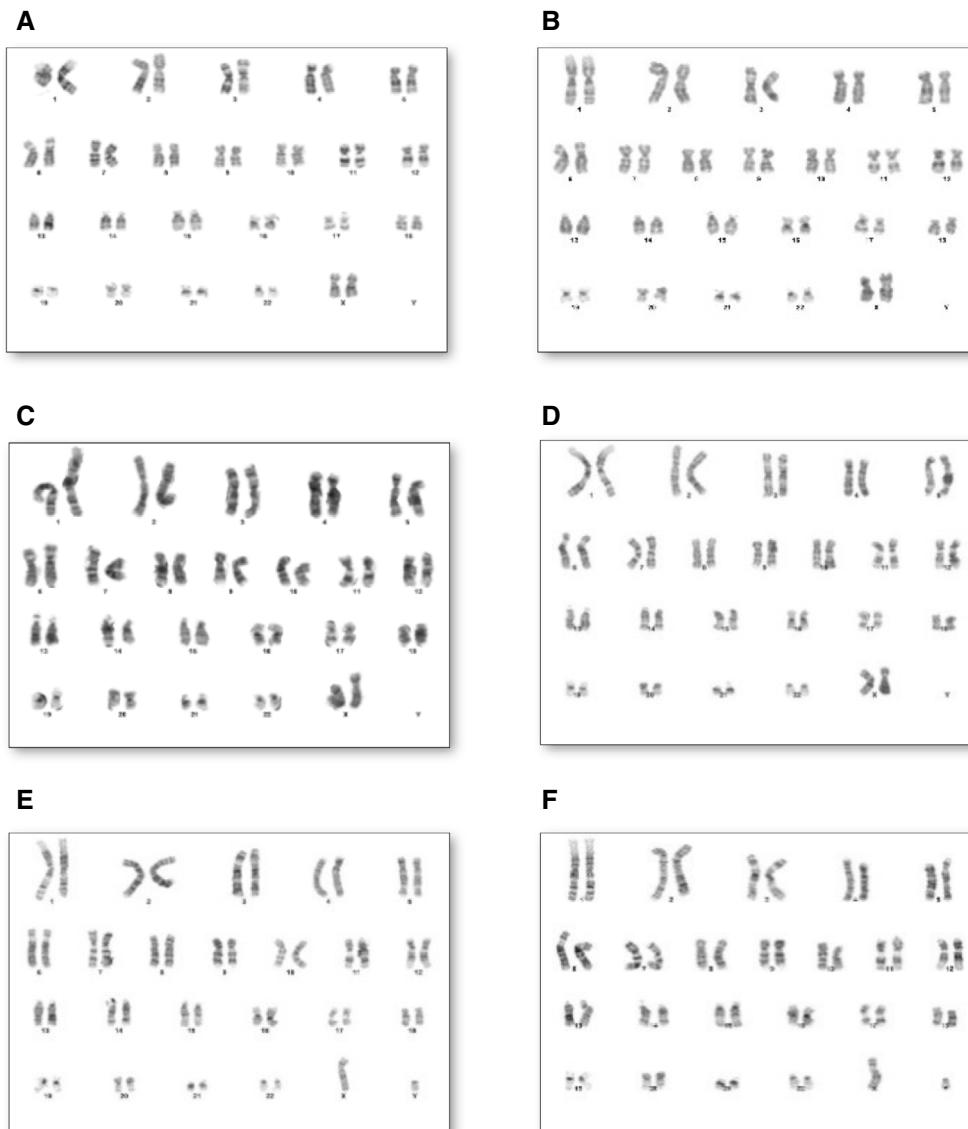


Figure EV1. Karyotype analysis for parental fibroblasts and reprogrammed iPSC lines.

A, C, E Representative karyotypes for Detroit 551 control fibroblasts (A) and WSSA and CP2A POLG fibroblasts (C, E).

B, D, F Representative karyotypes for control iPSC line (B) and POLG iPSC lines (D, F).

Figure EV2. Flow cytometric analysis of expression level of pluripotency markers TRA-1-60, TRA-1-81 and NANOG in iPSC lines.

A–C Flow cytometric analysis of expression level of pluripotency markers TRA-1-60 (A, $n = 3$, technical replicates per line/clone), TRA-1-81 (B, $n = 3$, technical replicates per line/clone), and NANOG (C, $n = 9$, technical replicates per line/clone for ESCs, control, and WSSA iPSCs; $n = 6$, technical replicates per clone for CP2A iPSCs) in ESC and iPSC lines. Data are demonstrated as individual clones (left panel, a) and combination as a group for ESCs, CTRL iPSCs, and WSSA and CP2A patient lines (right panel, b).

Data information: The data points in A–C represent 2 ESC lines, 2 different control clones from Detroit 551 iPSCs, 3 different iPSC clones from WSSA patient, and 2 different clones from CP2A patient iPSCs. Data are presented as mean \pm SEM for the number of samples. Mann–Whitney U -test was used for the data presented in B, b. Two-sided Student's t -test was used for the data presented in A, b and C, b. Significance is denoted for P values of less than 0.05. * $P < 0.05$; ** $P < 0.01$. Source data are available online for this figure.

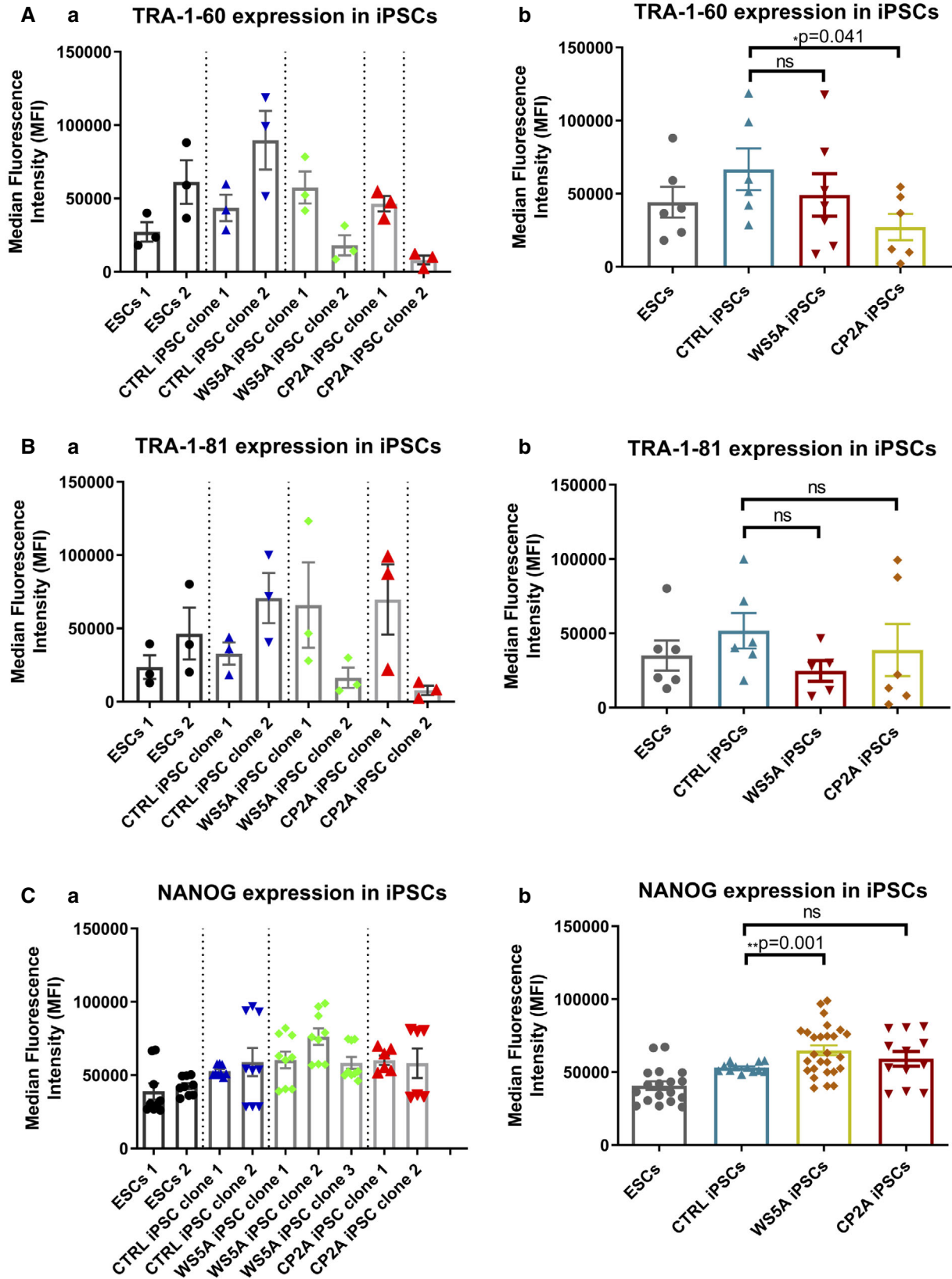


Figure EV2.

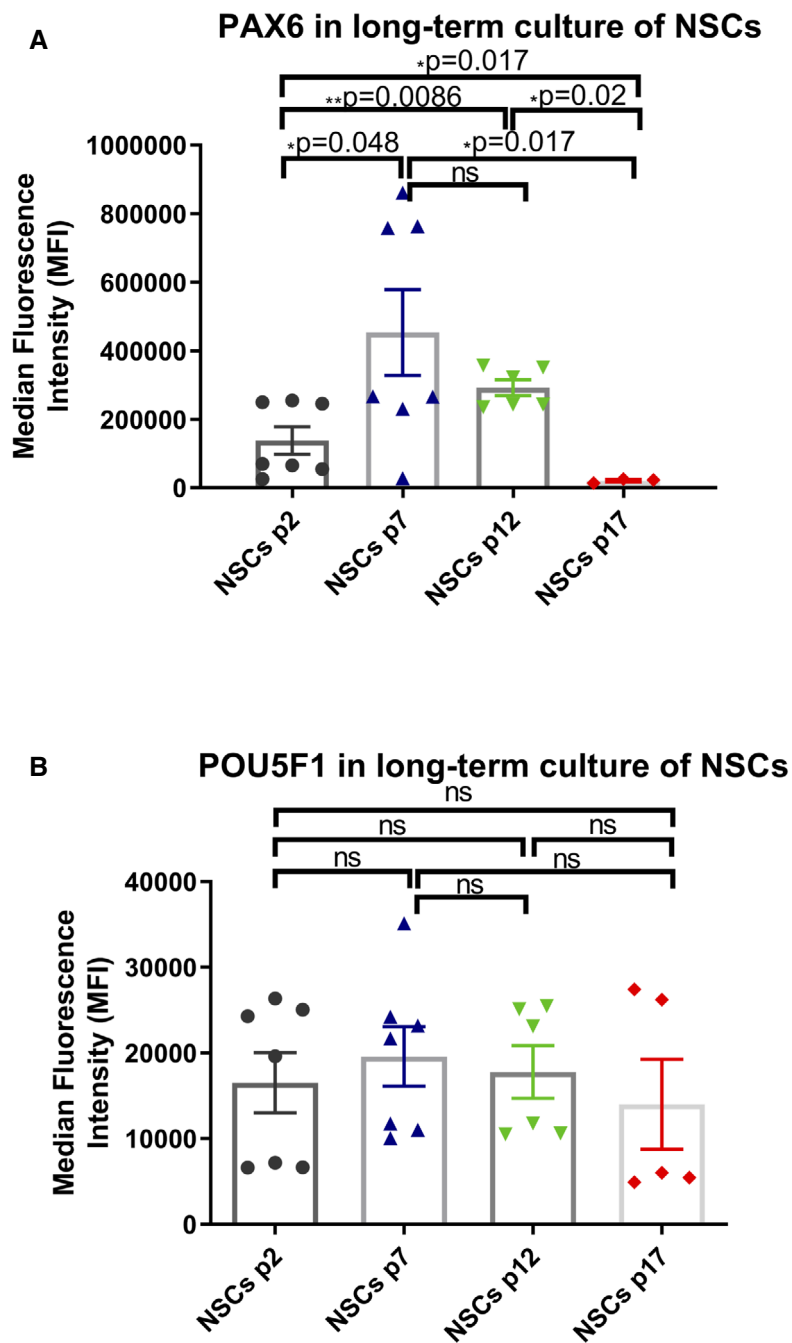


Figure EV3. Flow cytometric analysis of NSC marker PAX6 and pluripotency marker POU5F1 expression in long-term NSC culture.

A, B Representative bar graphs of NSC marker PAX6 (A, $n = 7$, technical replicates for p2; $n = 6$, technical replicates for p7, 12; $n = 3$, technical replicates for p17) and pluripotency marker POU5F1 (B, $n = 7$, technical replicates for p2; $n = 6$, technical replicates for p7, 12; $n = 3$, technical replicates for p17) in different passages during long-term NSC culture using flow cytometric analysis.

Data information: The data points in A and B represent NSCs generated from one Detroit 551 control iPSC line. Data are presented as mean \pm SEM for the number of samples. Mann–Whitney U -test was used for the data presented in A and B. Significance is denoted for P values of less than 0.05. * $P < 0.05$; ** $P < 0.01$.

Source data are available online for this figure.

Figure EV4. Intracellular and mitochondrial ROS production in Detroit 551 control, WSSA, and CP2A fibroblasts, iPSCs, and NSCs.

- A, B Intracellular ROS production measurements of the total ROS (DFCDA) level (A, $n = 7$, technical replicates per clone for control; $n = 5$, technical replicates per clone for WSSA; $n = 8$, technical replicates per clone for CP2A) and specific ROS level (B, $n = 7$, technical replicates per clone for control; $n = 5$, technical replicates per clone for WSSA; $n = 8$, technical replicates per clone for CP2A) calculated by total DCFDA/MTDR in iPSCs.
- C, D Total intracellular ROS (C, $n = 6$, technical replicates for control; $n = 4$, technical replicates for WSSA; $n = 5$, technical replicates for CP2A) and specific ROS (D, $n = 6$, technical replicates for control; $n = 4$, technical replicates for WSSA; $n = 5$, technical replicates for CP2A) production measurements in fibroblasts.
- E, F Intracellular ROS production measurements of the total ROS level (E, $n = 6$, technical replicates per clone for control; $n = 5$, technical replicates per clone for WSSA; $n = 4$, technical replicates per clone for CP2A) and mitochondrial ROS level (F, $n = 6$, technical replicates per clone for control; $n = 5$, technical replicates per clone for WSSA; $n = 4$, technical replicates per clone for CP2A) in NSCs.

Data information: The data points in A, B and F represent iPSCs and NSCs generated from 3 different control clones including 2 different clones from Detroit 551 control, 3 different clones from WSSA patient, and 2 different clones from CP2A patient. The data points in E represent NSCs generated from 4 clones from Detroit 551 control and one clone from control AG05836, 3 clones from WSSA patient, and 2 clones from CP2A patient. Data are presented as mean \pm SEM for the number of samples. Mann-Whitney U -test was used for the data presented in A–C and E. Two-sided Student's t -test was used for the data presented in D and F. Significance is denoted for P values of less than 0.05. * $P < 0.05$; ** $P < 0.01$; **** $P < 0.0001$.

Source data are available online for this figure.

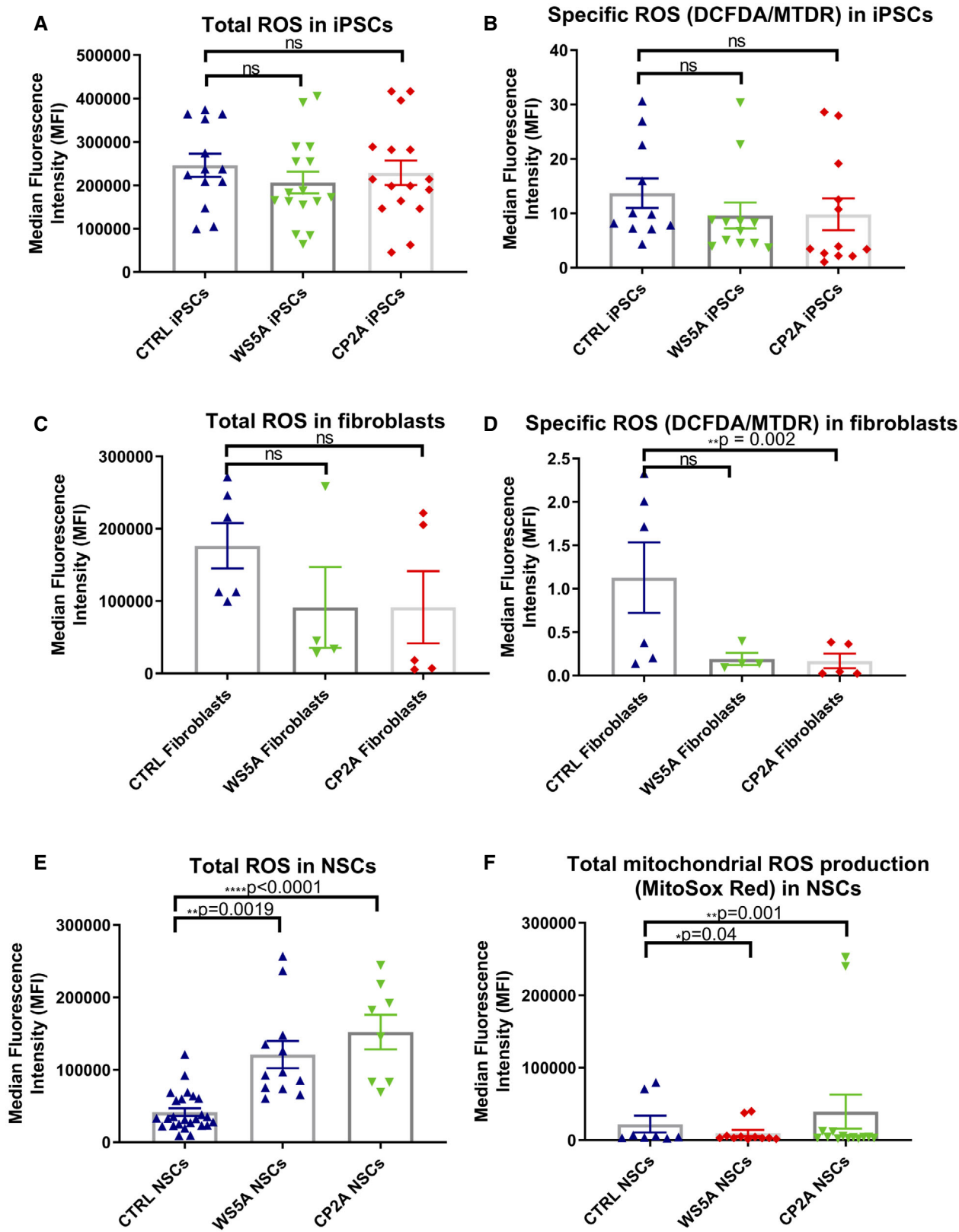


Figure EV4.

Cellular senescence marker p16INK4a in NSCs

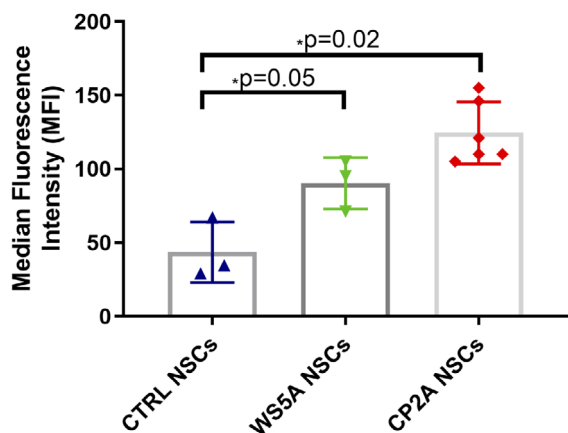


Figure EV5. Flow cytometric analysis of the expression level of cellular senescence marker p16INK4a in NSCs.

The data points represent NSCs generated from one clone from Detroit 551 control, one clone from WS5A patient, and 2 different clones from CP2A patient. Data are presented as mean \pm SEM for the number of samples ($n = 3$, technical replicates per clone). Mann–Whitney U -test was used for the data presented. Significance is denoted for P values of less than 0.05. * $P < 0.05$. Source data are available online for this figure.