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Corrigendum

Correction to 'SIRT3 consolidates heterochromatin and counteracts senescence'

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The authors wish to introduce the following corrections to their article (1).

The human *SIRT3* DNA sequence was inaccurately noted in Figure 1B. The correction does not affect any result, conclusion, or discussion of this study. A new Figure 1 is provided below.

In Figures 2H and 3J on $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hMSCs at early and late passages, the same representative blot for β-Tubulin was inadvertently used, while multiple different blots had been generated from independent experiments. In the early versions of figures, Figures 2H and 3J were displayed together and therefore only one blot for β-Tubulin was presented. When the two figure panels were finally split, the authors neglected to add a second representative blot for β-Tubulin, which had already been generated. The corrected blots for β-Tubulin in Figure 2H from the same set of experiments support the original result in this study. A new Figure 2 is provided below.

The n values of the data in Supplementary Figure S2G were not clearly stated. Revised Supplementary Data are available at NAR Online.

Revised caption:

(G) Transmission electron microscopy analysis of mitochondrial number and area in $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hMSCs at EP (P4) and LP (P9). White arrow indicates mitochondrion. Scale bar, 400 nm. Data are presented as the means ± SEM. $n \geq 290$ mitochondria for mitochondrial area measurement and $n > 40$ cells for the determination of the number of mitochondria per cell. ***, $P < 0.001$.

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†The authors wish it to be known that, in their opinion, the first four authors should be regarded as Joint First Authors.

The published article has been updated. None of the corrections affect the results, conclusions, or discussion of this study.

REFERENCES

1. Diao,Z., Ji,Q., Wu,Z., Zhang,W., Cai,Y., Wang,Z., Hu,J., Liu,Z., Wang,Q., Bi,S. *et al.* (2021) SIRT3 consolidates heterochromatin and counteracts senescence. *Nucleic Acids Res.*, **49**, 4203–4219.

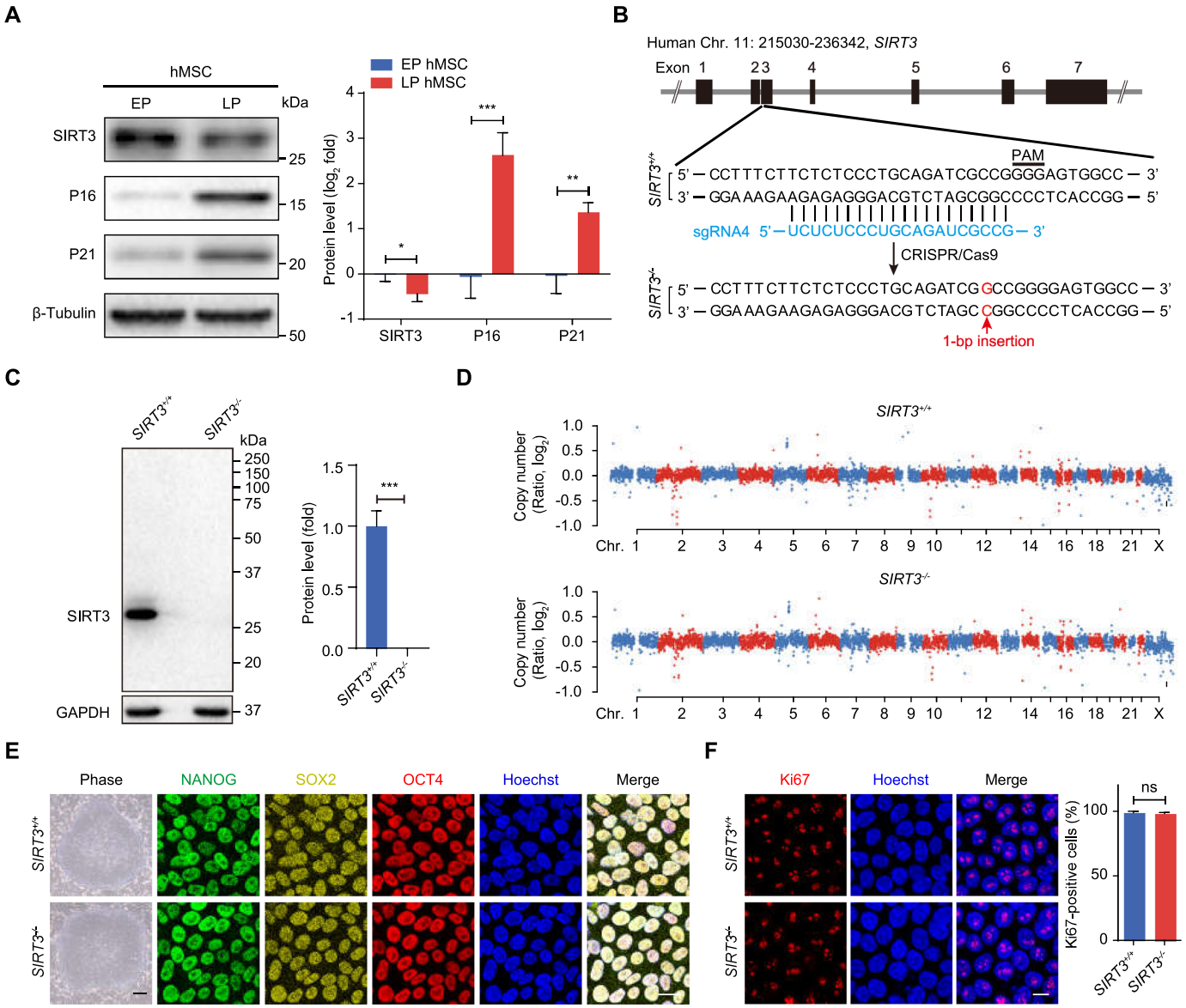

Figure 1. Downregulation of SIRT3 in senescent hMSCs and generation of SIRT3-deficient hESCs. (**A**) Western blot analysis of SIRT3, P16 and P21 expression in replicative senescent hMSCs. Early passage (EP), passage 4 (P4); late passage (LP), P14. β-Tubulin was used as loading control. Data are presented as the means ± SEM. $n = 3$. $^{*}P < 0.05$; $^{**}P < 0.01$; $^{***}P < 0.001$. (**B**) Schematic diagram of *SIRT3* gene editing strategy using CRISPR/Cas9-mediated non-homologous end-joining (NHEJ) in hESCs. The *SIRT3* sgRNA is shown in blue. 1-bp insertion (shown in red) was identified by DNA sequencing. (**C**) Western blot analysis of SIRT3 in $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hESCs. GAPDH was used as a loading control. Data are presented as the means ± SEM. $n = 3$. $^{***}P < 0.001$. (**D**) Copy number variation (CNV) analysis of $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hESCs by whole genome sequencing. (**E**) Immunofluorescent (IF) images of pluripotency markers NANOG, SOX2 and OCT4 and phase-contrast images for $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hESCs. Scale bar, 25 μm (IF images) and 250 μm (phase-contrast images). (**F**) Immunofluorescence analysis of Ki67 in $SIRT3^{+/+}$ and $SIRT3^{-/-}$ hESCs. Scale bar, 10 μm. The statistical analysis of Ki67-positive cells is shown on the right. Data are presented as the means ± SEM. $n = 3$. ns, not significant.

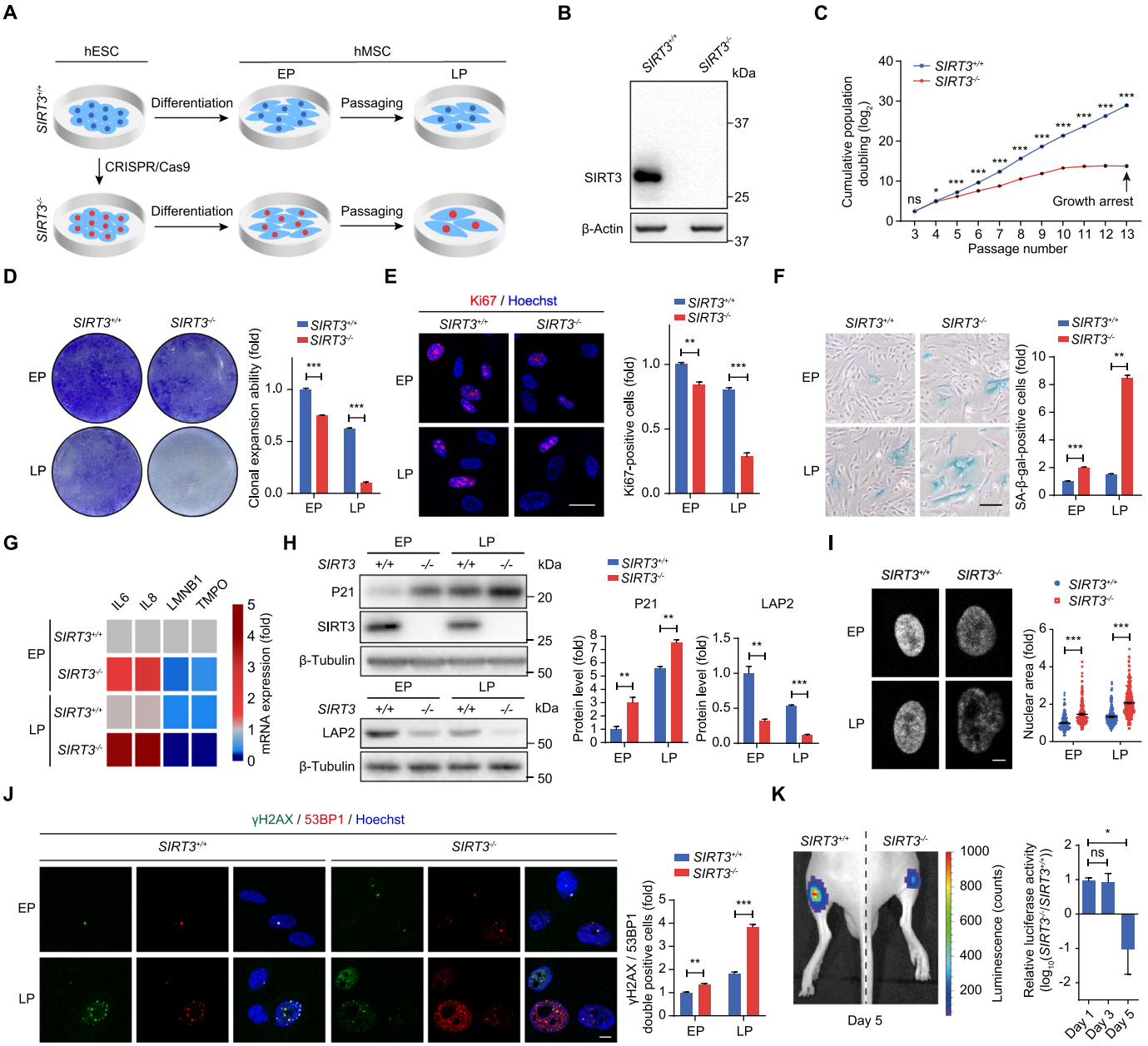

Figure 2. SIRT3 deficiency accelerates hMSC senescence and cellular dysfunction. (**A**) Schematic diagram showing the generation of *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs from hESCs. (**B**) Western blot analysis of SIRT3 in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4). β-Actin was used as a loading control. (**C**) Growth curve showing cumulative population doubling of *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs. Data are presented as the means ± SEM. $n = 3$. ns, not significant; $^{*}P < 0.05$; $^{***}P < 0.001$. (**D**) Clonal expansion analysis of *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Data are presented as the means ± SEM. $n = 3$. $^{***}P < 0.001$. (**E**) Immunofluorescence analysis of Ki67 in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Scale bar, 25 μm. The statistical analysis of Ki67-positive cells is shown on the right. Data are presented as the means ± SEM. $n = 3$. $^{**}P < 0.01$; $^{***}P < 0.001$. (**F**) SA-β-gal staining of *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Scale bar, 50 μm. Data are presented as the means ± SEM. $n = 3$. $^{**}P < 0.01$; $^{***}P < 0.001$. (**G**) RT-qPCR analysis for the expression of *IL6*, *IL8*, *LMNB1* (Lamin B1) and *TMPO* (LAP2) in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Data are representative of three independent experiments. (**H**) Western blot analysis of P21, LAP2 and SIRT3 in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). β-Tubulin was used as loading control. Data are presented as the means ± SEM. $n = 3$. $^{**}P < 0.01$; $^{***}P < 0.001$. (**I**) Nuclear area analysis in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Nuclei were stained with Hoechst 33342 and nuclear area was measured with ImageJ. Scale bar, 5 μm. Data are presented as the means ± SEM. $n \geq 150$. $^{***}P < 0.001$. (**J**) Immunofluorescence analysis of γH2AX and 53BP1 in *SIRT3*$^{+/+}$ and *SIRT3*$^{-/-}$ hMSCs at EP (P4) and LP (P9). Scale bar, 10 μm. The statistical analysis of γH2AX and 53BP1 double-positive cells is shown on the right. Data are presented as the means ± SEM. $n = 3$. $^{**}P < 0.01$; $^{***}P < 0.001$. (**K**) Photon flux from tibialis anterior (TA) muscles of nude mice transplanted with *SIRT3*$^{+/+}$ (left) or *SIRT3*$^{-/-}$ hMSCs (right) expressing luciferase. Luciferase activity in TA tissue was detected using an *in vivo* imaging system (IVIS). Data are presented as the means ± SEM. $n = 5$. ns, not significant; $^{*}P < 0.05$.