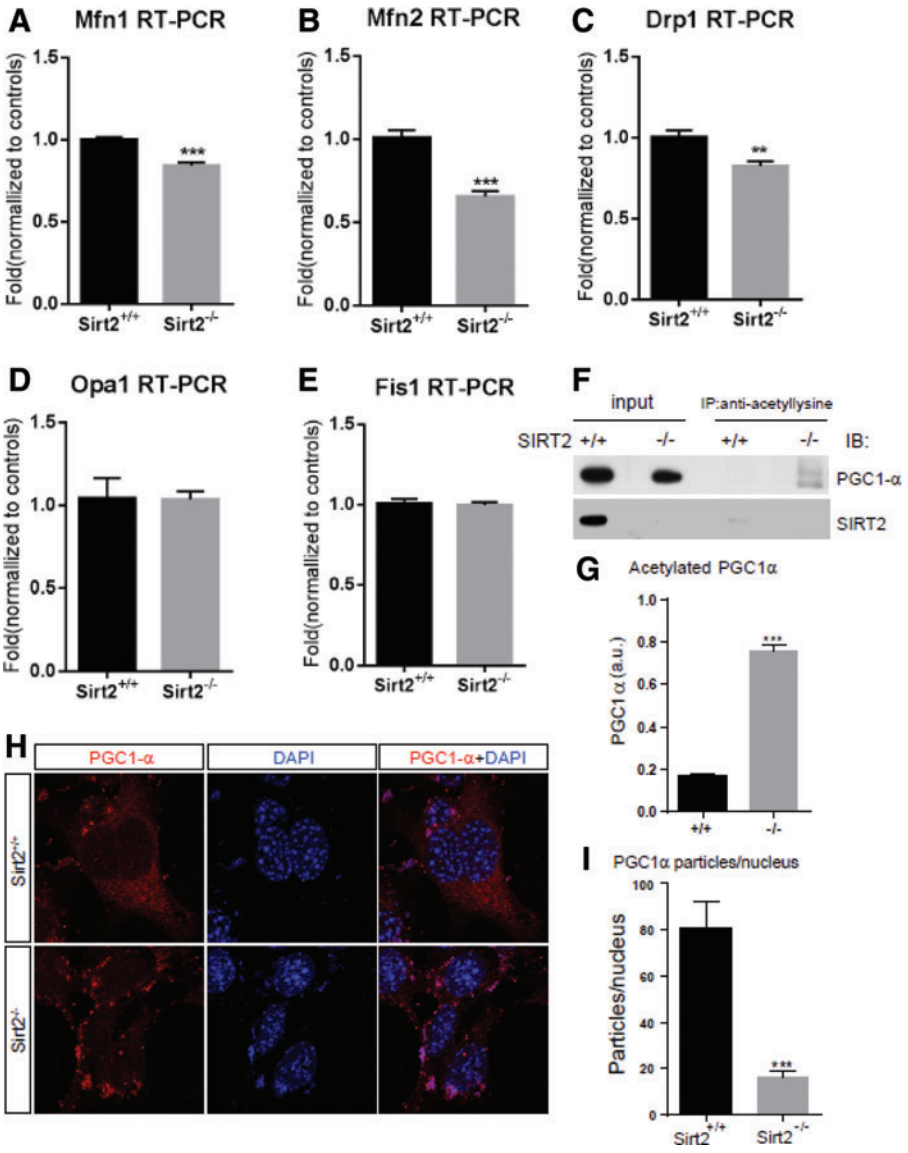

SUPPLEMENTARY FIG. S4. Loss of Sirt2 increases PGC1α acetylation level and inhibits PGC1α transcription activity. (A–E) Real-time reverse transcription polymerase chain reaction analysis of Mfn1, Mfn2, Drp1, Opa1, and Fis1 expression in $Sirt2^{+/+}$ and $Sirt2^{-/-}$ mice (three per genotype). Data are presented as the mean ± SEM ($n = 5$). $^{**}p < 0.01$, $^{***}p < 0.001$. Lysates from brain tissues of $Sirt2^{+/+}$ and $Sirt2^{-/-}$ mice were harvested, IPed with an anti-acetyllysine antibody, and, subsequently, immunoblotted with antibodies against PGC1α. Quantification of acetylated PGC1α. $N = 3$ mice per genotype. Data are presented as the mean ± SEM. $^{***}p < 0.001$. MEFs cells were stained with anti-PGC1α antibody and 4′,6-diamidino-2-phenylindole, and representative immunofluorescent images are shown. Particles in the nucleus were counted with ImageJ. Error bars represent one standard deviation from the mean. $^{***}p < 0.001$. **(F)** Lysates from brain tissues of $Sirt2^{+/+}$ and $Sirt2^{-/-}$ mice were harvested, (IP)ed with an anti-acetyllysine antibody, and subsequently immunoblotted with antibodies against PGC1α. **(G)** Quantification of acetylated PGC1α. N = 3 mice per genotype. Data are presented as the mean ± SEM. $^{***}p < 0.001$. **(H)** MEFs cells were stained with anti-PGC1α antibody and DAPI, and representative immunofluorescent (IFC) images are shown. **(I)** Particles in nucleus were counted with ImageJ. Error bars represent one standard deviation from the mean. $^{***}p < 0.001$.