

Aix et al., <http://www.jcb.org/cgi/content/full/jcb.201510091/DC1>

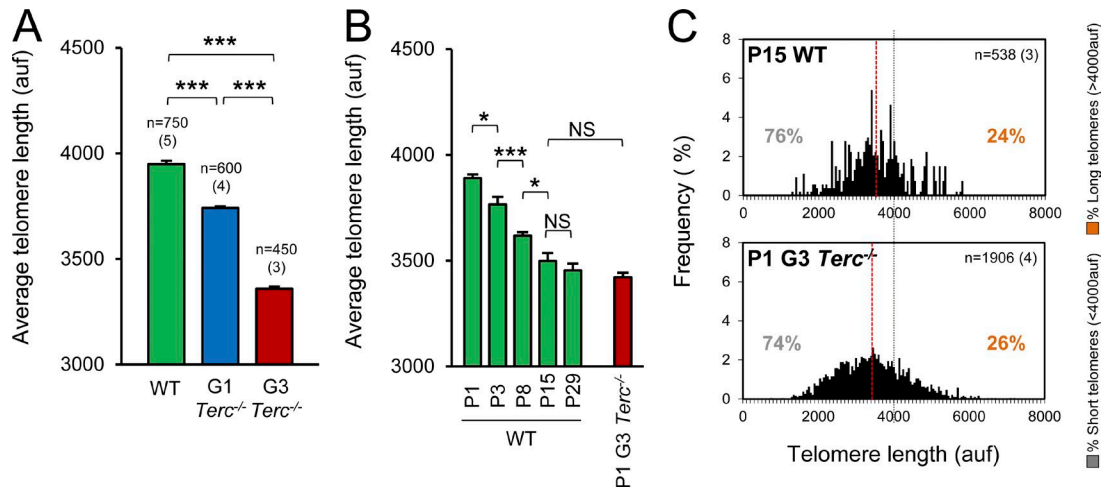


Figure S1. **P1 G3 *Terc*^{-/-} neonates present CMs with telomere shortening.** (A) Mean CM telomere length in WT, G1 *Terc*^{-/-}, and G3 *Terc*^{-/-} neonatal mice at P1. n indicates the number of CMs analyzed. Numbers in brackets indicate the animals analyzed per group. (B) Comparison between mean CM telomere length in G3 *Terc*^{-/-} neonatal mice at P1 and WT animals at different ages. (C) CM telomere length distribution and percentage of relatively short telomeres (<4,000 auf) and long telomeres (>4,000 auf) in WT mice at P15 and G3 *Terc*^{-/-} mice at P1. Gray lines at 4,000 auf facilitate comparisons of telomere size distribution between conditions. Red lines indicate mean telomere length. n indicates the number of CMs analyzed. Numbers in brackets indicate the animals analyzed per group. Data are mean ± SEM. *, P < 0.05; ***, P < 0.001; NS, nonsignificant.

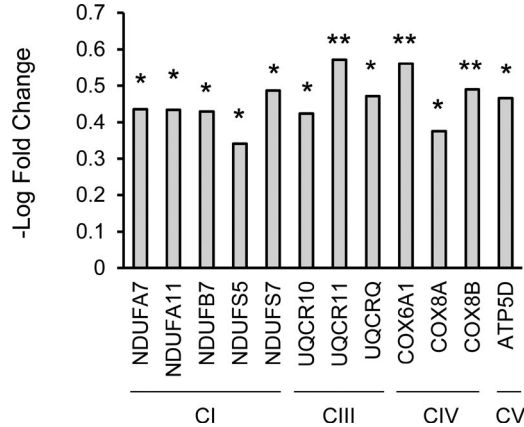


Figure S2. **G3 *Terc*^{-/-} P1 neonates present a hypertrophic response after cryoinjury.** Up-regulation of oxidative phosphorylation genes in G3 *Terc*^{-/-} cryo-injured hearts relative to WT hearts in RNA-sequencing analysis. n = 6 animals per group. *, P < 0.05; **, P < 0.01.

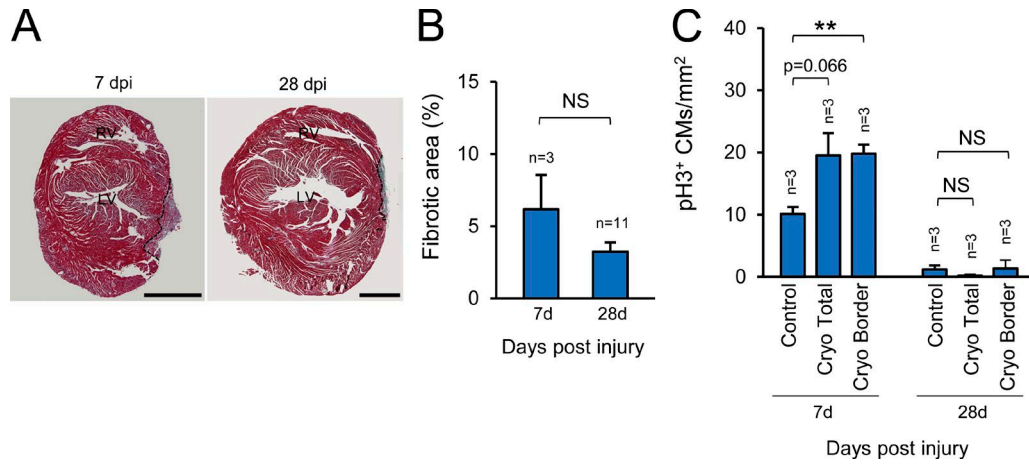


Figure S3. **Cardiac response to cryoinjury in G1 *Terc*^{-/-} P1 neonates.** (A) Masson's trichrome staining in G1 *Terc*^{-/-} hearts after cryoinjury at P1. LV, left ventricle; RV, right ventricle. Bars, 1 mm. (B) Quantification of the fibrotic area. n indicates the number of animals analyzed. (C) Quantification of CM mitosis in G1 *Terc*^{-/-} mice after cardiac cryoinjury at P1. n indicates the number of animals analyzed. Data are means \pm SEM. **, $P < 0.01$; NS, nonsignificant.

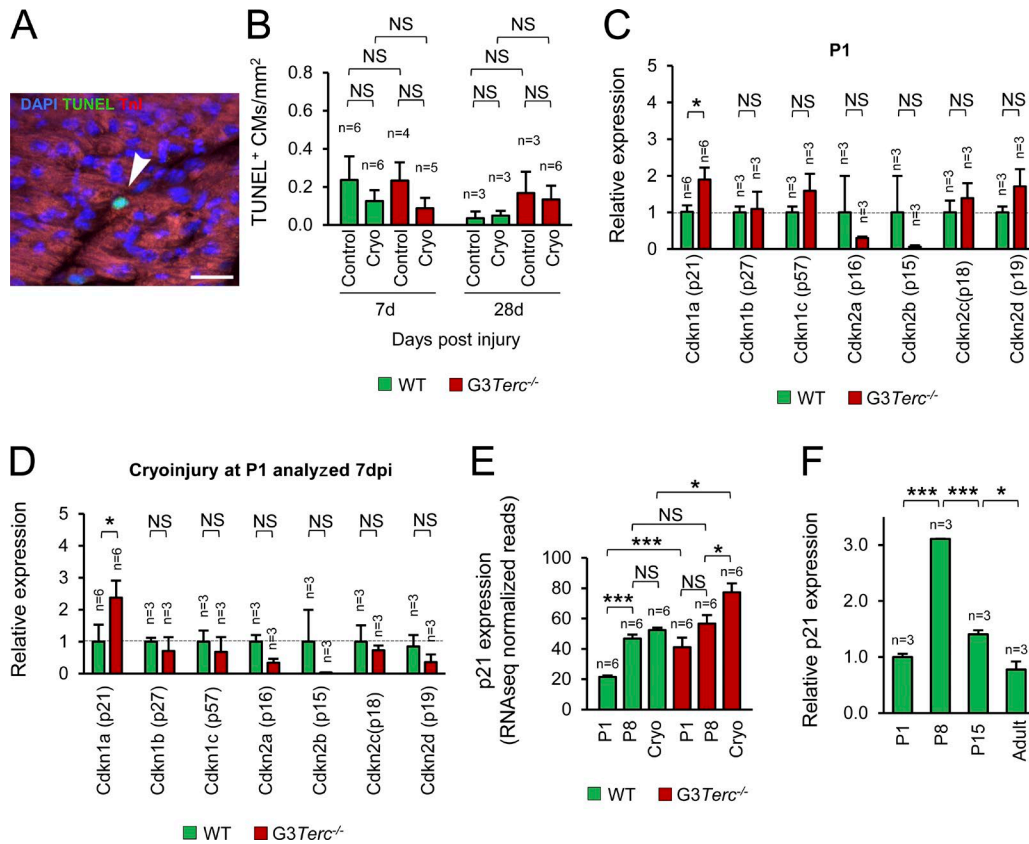


Figure S4. **TUNEL and CDKIs expression in WT and G3 *Terc*^{-/-} neonates.** (A) Detail of TUNEL and Tnl immunofluorescence. The arrowhead indicates a TUNEL-positive CM. Bar, 20 μ m. (B) Quantification of TUNEL-positive CMs. Controls are age-matched uninjured animals. n indicates the number of animals analyzed. (C) Relative CDKIs expression at P1 measured by quantitative PCR. n indicates the number of animals analyzed. (D) Comparison of CDKIs expression in WT and G3 *Terc*^{-/-} cryoinjured hearts (7 dpi) measured by quantitative PCR. n indicates the number of animals analyzed. (E) *p21* expression measured by RNA sequencing in uninjured P1 and P8 hearts and cryoinjured P1 hearts (analyzed 7 dpi). n indicates the number of animals analyzed. (F) Relative *p21* expression in WT hearts at different ages measured by quantitative PCR. Adult animals were 2 mo old. n indicates the number of animals analyzed. Data are mean \pm SEM. *, $P < 0.05$; ***, $P < 0.001$; NS, nonsignificant.