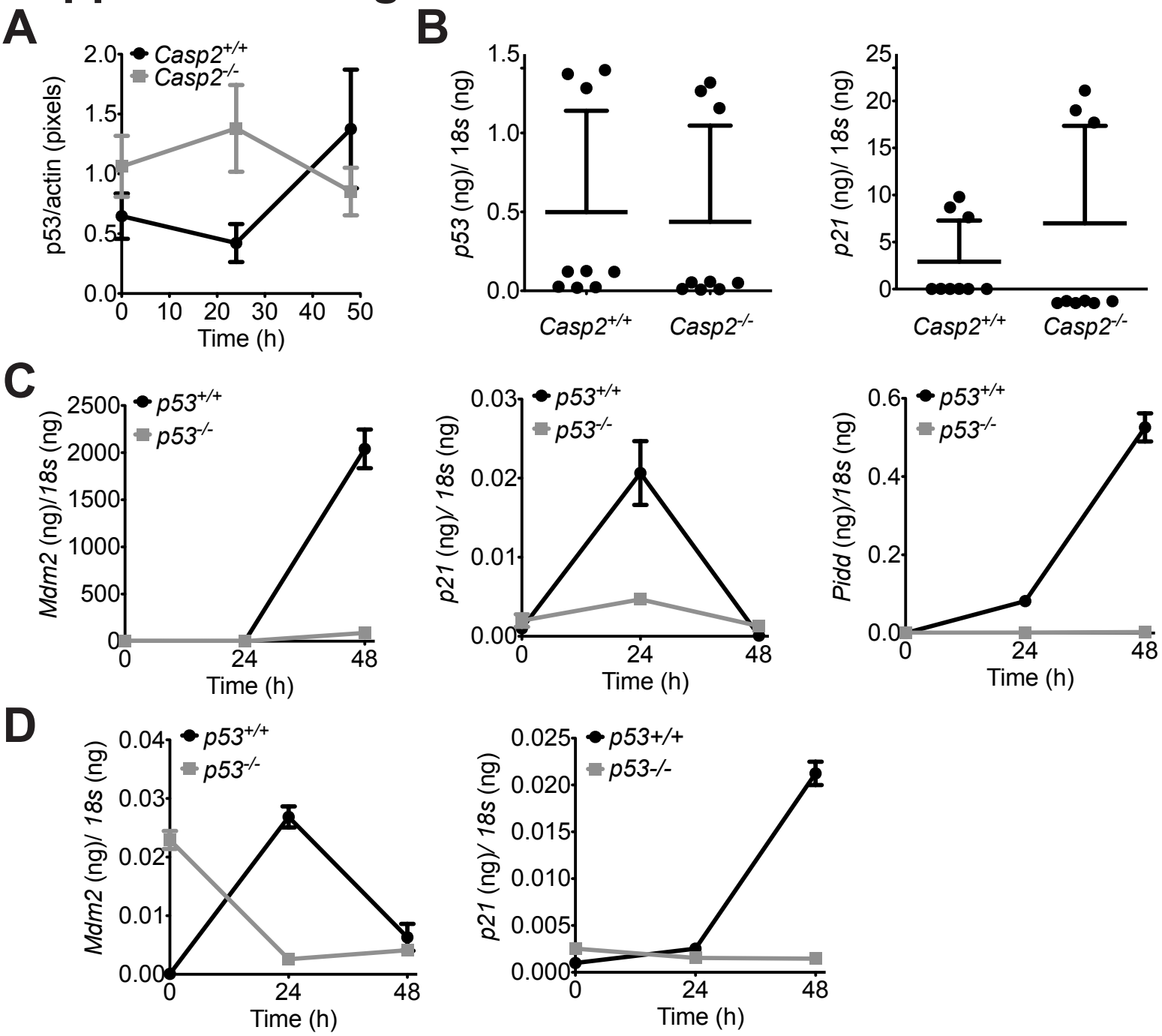
Supplemental Figure 5



Supplemental Figure 5. The p53 response to PALA and etoposide treatment is abrogated in *p53*$^{-/-}$ MEFs. *A*, Littermatched E1A/Ras-transformed *Casp2*$^{+/+}$ and *Casp2*$^{-/-}$ MEFs were treated with 100 μM PALA for the indicated times, at which point total protein was harvested and p53 and actin levels were analyzed by western blot analysis. Shown are the average levels of p53 protein as determined by densitometry analysis (p53/actin) of seven separate experiments. Error bars represent the SEM. *B*, Total RNA was isolated from *Casp2*$^{+/+}$ and *Casp2*$^{-/-}$ MEFs, reverse transcribed as described in the Materials and Methods, and analyzed by quantitative real-time PCR analysis for the indicated genes. All samples were normalized to 18s as a control. Shown are the average amounts of *p53* and *p21* mRNA (ng gene/ ng 18s) of nine independent determinations. *C* and *D*, Littermatched E1A/Ras *p53*$^{+/+}$ and *p53*$^{-/-}$ MEFs were treated with 100 μM PALA (*C*) or 10 μM etoposide (*D*) for the indicated times, as which point total RNA was isolated, reverse transcribed and analyzed by quantitative real-time PCR as described in the Materials and Methods. Shown are the levels of the indiated genes at each timepiont normalized to 18s as a control. Error bars represent the standard deviation of triplicate determinations.