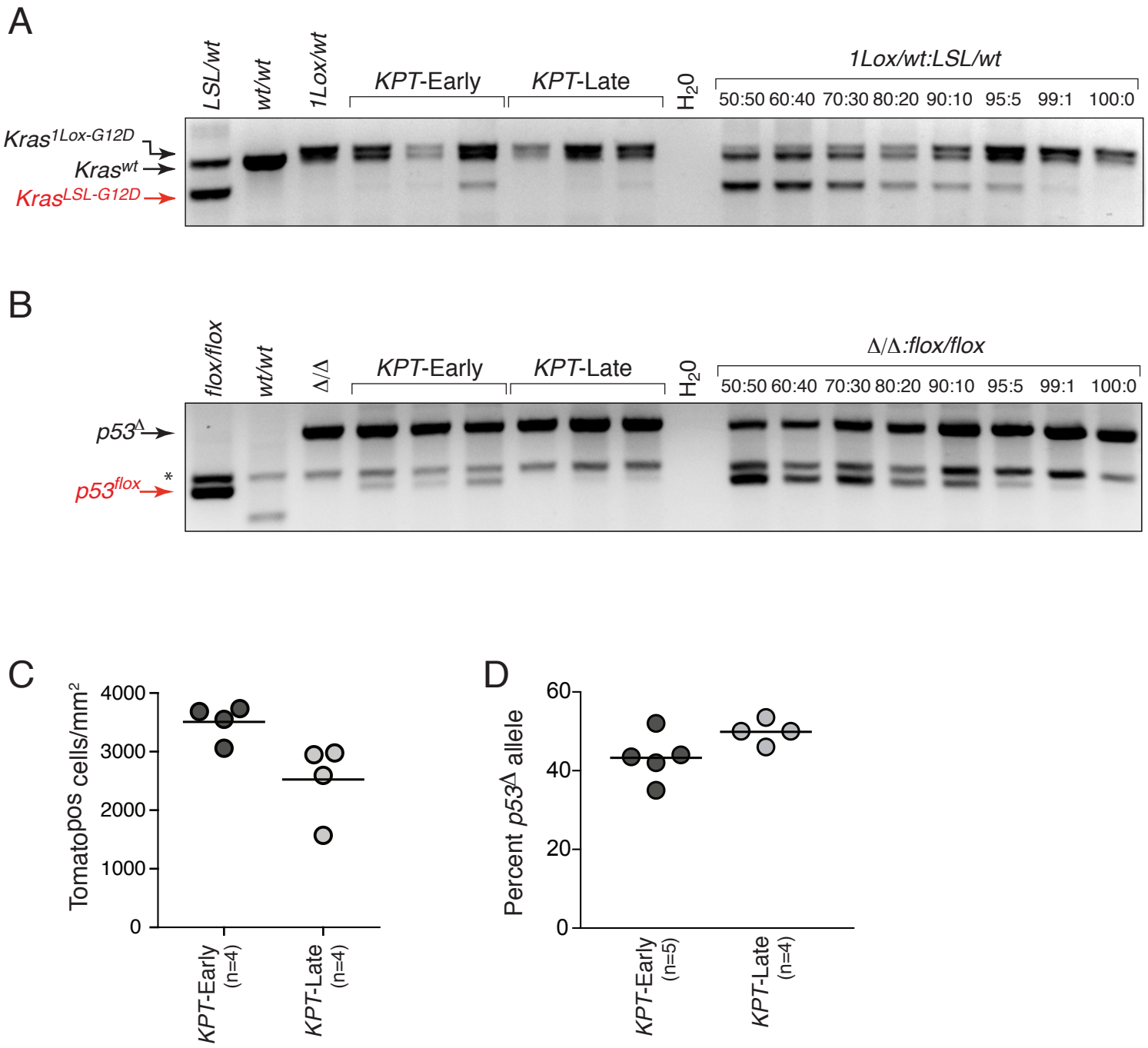
*Caswell et al, Supplemental Figure 2*




**Supplemental Figure 2. Similar total tumor burden and core genomic alterations in *KPT*-Early and *KPT*-Late mice**
**A., B.** Expanding Tomato$^{positive}$ cells from *KPT*-Early and *KPT*-Late mice have fully recombined $Kras^{LSL\text{-}G12D}$ and $p53^{floxed}$ alleles. Semi quantitative genomic PCR was used to assess the portion of $Kras^{LSL\text{-}G12D}$ alleles and $p53^{floxed}$ alleles that were recombined. Recombination in Tomato$^{positive}$ cells from *KPT*-Early and *KPT*-Late mice was compared to a standard titration of $p53^{floxed}$ to $p53^{\Delta}$ or $Kras^{LSL\text{-}G12D}$ to $Kras^{1lox\text{-}G12D}$ from tail and cell line DNA. Recombination efficiency was >95% for all samples. (*) Background band.
**C.** To determine the relative tumor burden between *KPT*-Early and *KPT*-Late mice, immunohistochemistry was used to stain and count Tomato$^{pos}$ cells. Each dot represents a mouse and the bar represents the mean.
**D.** To estimate the total cancer burden in *KPT*-Early and *KPT*-Late mice we used semi quantitative genomic PCR to assess the percent of the $p53^{floxed}$ alleles that were recombined into the $p53^{\Delta}$ form. *p53* recombination in *KPT*-Early and *KPT*-Late total lung DNA was compared to a standard titration of $p53^{floxed}$ to $p53^{\Delta}$ alleles to determine the tumor cell to normal cell ratio. Densitometry of the $p53^{floxed}$ and $p53^{\Delta}$ PCR bands for the standards and experimental samples allowed the percent recombined p53 to be interpolated for each mouse. Each dot represents a mouse and the bar represents the mean.