

Fig. S3

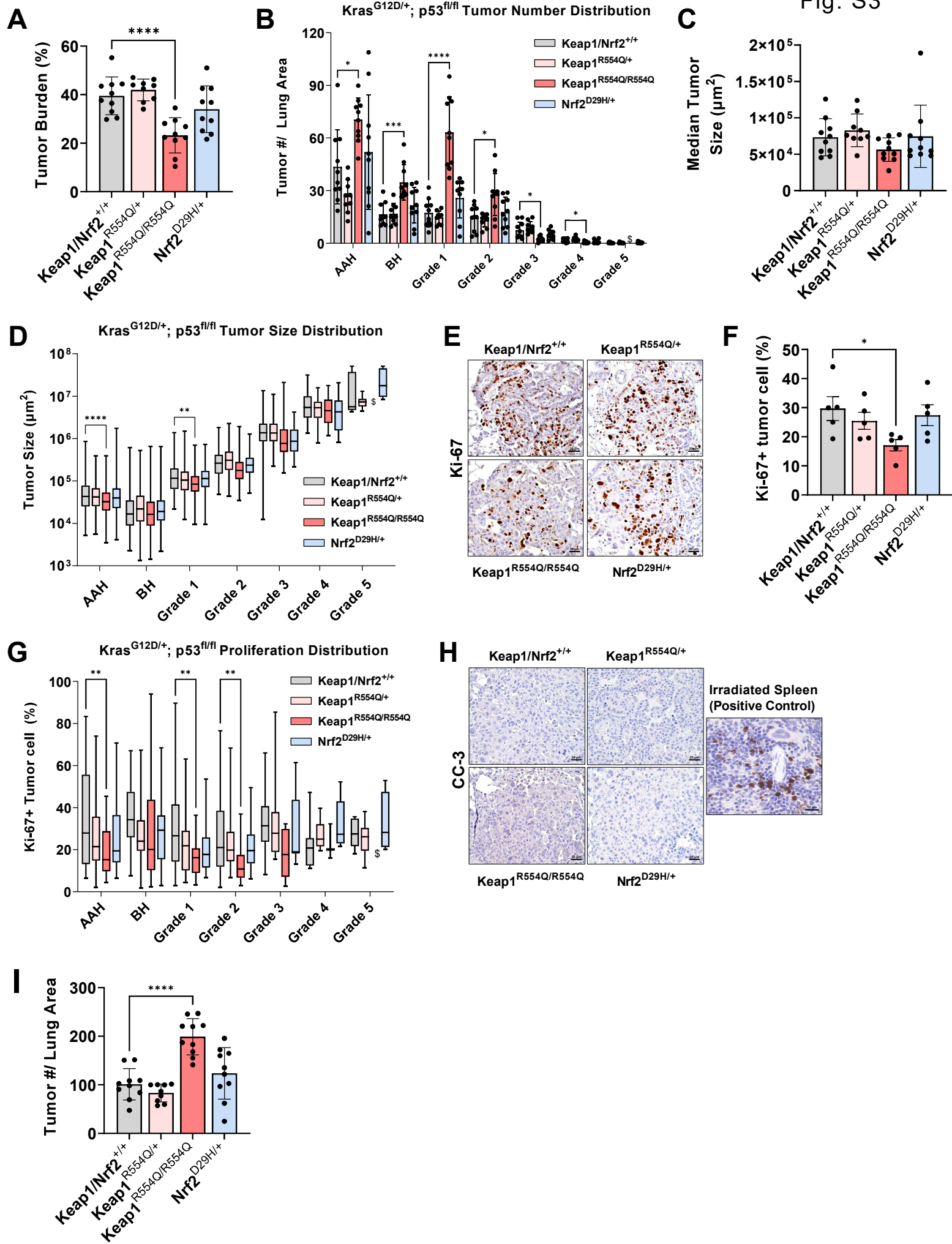


Figure S3. Lung tumor analysis and tumor cell proliferation/ death in the *Kras*^{G12D/+}; *p53*^{fl/fl} model with *Keap1/Nrf2* mutation. (A) Overall tumor burden (%) calculated by dividing the total area of lung tumor by the total area of the lung. **p*<0.05 (one-way ANOVA). (B) Distribution of tumor number by grade across *Keap1/Nrf2* mutant models. *N*≥9 mice per genotype, **p*<0.05 (unpaired t test with Holm-Sidak's multiple comparisons test). \$ = fewer than 3 tumors detected across all mice. (C) Median tumor size per mouse for each genotype. **p*<0.05 (one-way ANOVA). (D) Tumor size by grade across all mice per genotype. *N*≥9 mice and ≥1,900 tumors per genotype. **p*<0.05 (Kruskal-Wallis test with Dunn's multiple comparisons test). \$ = fewer than 3 tumors detected across all mice. (E) Representative immunohistochemical (HC) staining of Ki-67 (scale bars = 20 μM). (F) Proportion of tumor cells positive for Ki-67 per mouse. **p*<0.05 (one-way ANOVA). (G) Percentage of Ki-67 positive tumor cells in each tumor grade per genotype. *N*=5 mice per genotype, >20,000 tumor cells per mouse. **p*<0.05 (unpaired t test with Holm-Sidak's multiple comparisons test). \$ = fewer than 3 tumors detected across all mice. For (B), (D), and (G), only one grade 5 tumor was found in the *Keap1*^{R554Q/R554Q} cohort, and therefore was excluded from these analyses. (H) Representative immunohistochemical (IHC) staining of cleaved caspase-3 (CC-3) (scale bars = 20 μM). *N*=5 mice per genotype. Positive control is BL6 mouse spleen 1 hour after irradiation with 7.5 Gy (scale bar = 10 μM). (I) Tumor number per mouse in *Keap1/Nrf2* mutant models normalized to lung area. **p*<0.05 (one-way ANOVA).