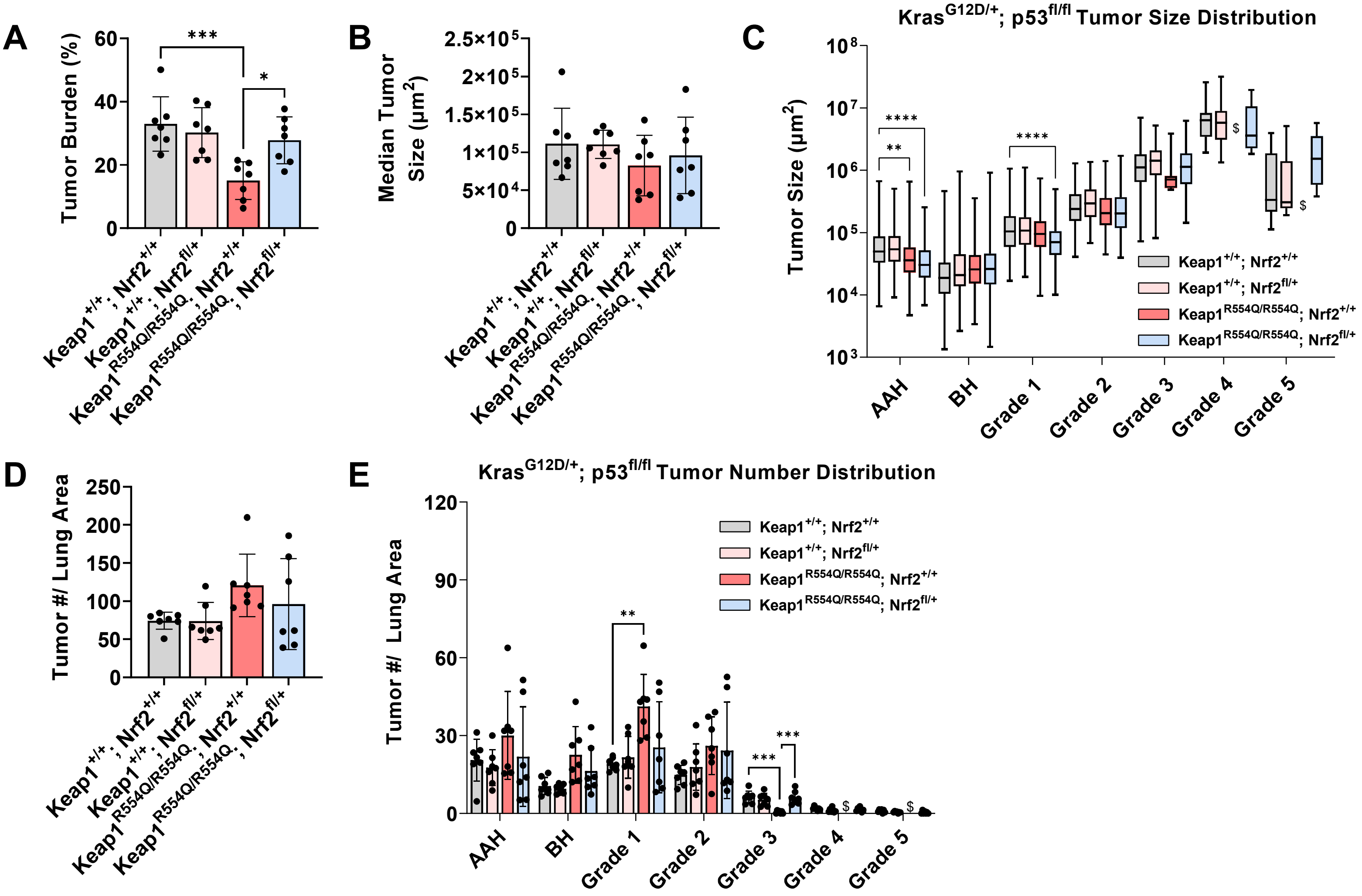
Fig. S5



A
Tumor Burden (%)
60
40
20
0
***
*
Keap1+/+; Nrf2+/+
Keap1+/+; Nrf2fl/+
Keap1R554Q/R554Q; Nrf2+/+
Keap1R554Q/R554Q; Nrf2fl/+
B
Median Tumor Size (μm2)
2.5×10^5
2×10^5
1.5×10^5
1×10^5
5×10^4
0
Keap1+/+; Nrf2+/+
Keap1+/+; Nrf2fl/+
Keap1R554Q/R554Q; Nrf2+/+
Keap1R554Q/R554Q; Nrf2fl/+
C
KrasG12D/+; p53fl/fl Tumor Size Distribution
Tumor Size (μm2)
10^8
10^7
10^6
10^5
10^4
10^3
****
**
****
$
$
Keap1+/+; Nrf2+/+
Keap1+/+; Nrf2fl/+
Keap1R554Q/R554Q; Nrf2+/+
Keap1R554Q/R554Q; Nrf2fl/+
AAH
BH
Grade 1
Grade 2
Grade 3
Grade 4
Grade 5
D
Tumor #/ Lung Area
250
200
150
100
50
0
Keap1+/+; Nrf2+/+
Keap1+/+; Nrf2fl/+
Keap1R554Q/R554Q; Nrf2+/+
Keap1R554Q/R554Q; Nrf2fl/+
E
KrasG12D/+; p53fl/fl Tumor Number Distribution
Tumor #/ Lung Area
120
90
60
30
0
Keap1+/+; Nrf2+/+
Keap1+/+; Nrf2fl/+
Keap1R554Q/R554Q; Nrf2+/+
Keap1R554Q/R554Q; Nrf2fl/+
**
***
***
$
$
AAH
BH
Grade 1
Grade 2
Grade 3
Grade 4
Grade 5

Figure S5. Lung tumor burden, size, and number quantification in the Kras$^{G12D/+}$; p53$^{fl/fl}$ model with single copy Nrf2 deletion. (A) Overall tumor burden (%) calculated by dividing the total area of lung tumor by the total area of the lung. **(B)** Median tumor size per mouse for each genotype. For **(A, B)**, $^{*}p<0.05$ (one-way ANOVA). **(C)** Tumor size across all mice per genotype. N=7 mice and $\geq$1,000 tumors per genotype. $^{*}p<0.05$ (Kruskal-Wallis test with Dunn's multiple comparisons test). $ = fewer than 3 tumors detected across all mice. **(D)** Tumor number per mouse normalized to lung area. $^{*}p<0.05$ (one-way ANOVA). **(E)** Distribution of tumor number by grade across Keap1/Nrf2 mutant models. N=7 mice per genotype, $^{*}p<0.05$ (unpaired t test with Holm-Sidak's multiple comparisons test). $ = fewer than 3 tumors detected across all mice. For **(C)** and **(E)**, only one grade 4 and two grade 5 tumors were found in the Keap1$^{R554Q/R554Q}$; Nrf2$^{+/+}$ cohort, and therefore were excluded from these analyses.