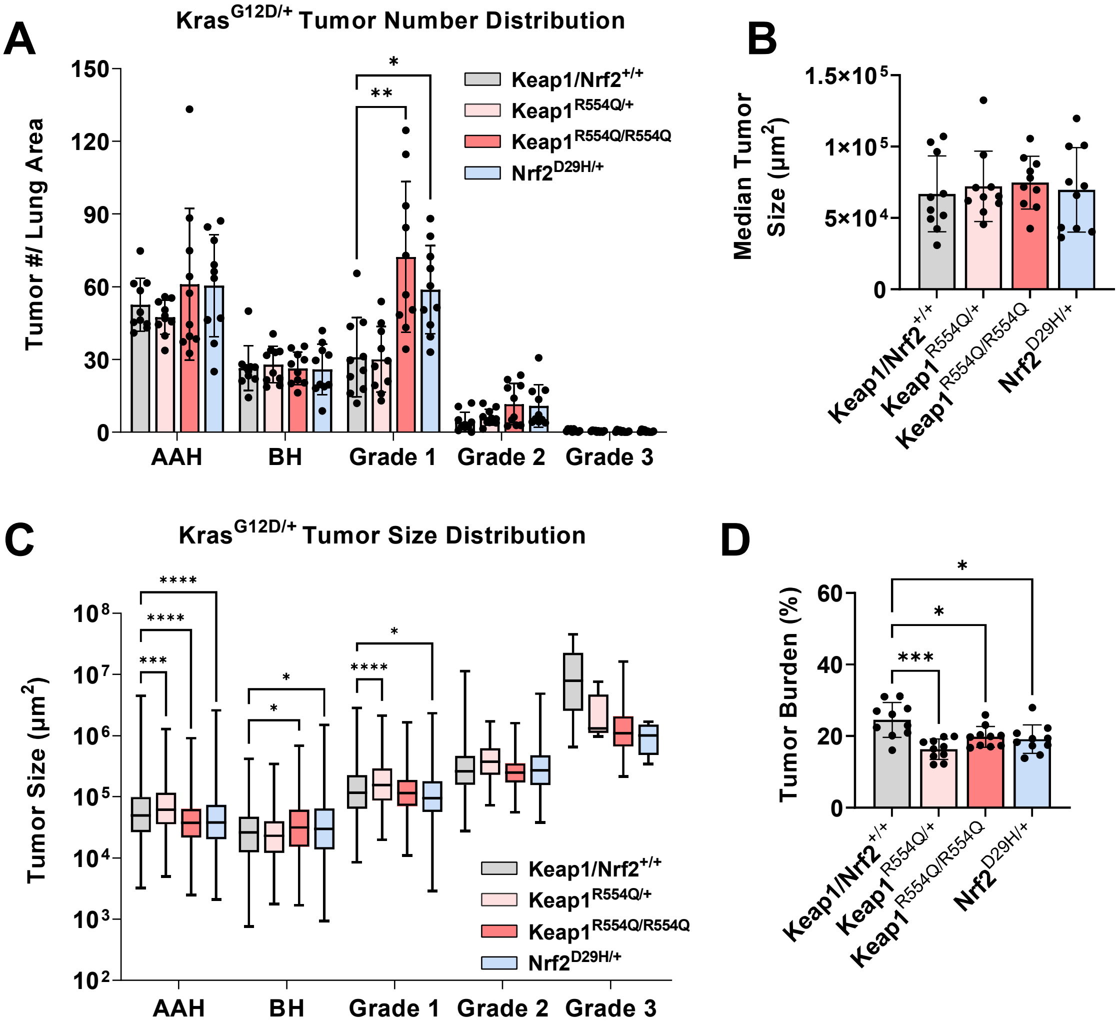
Fig. S2



A
KrasG12D/+ Tumor Number Distribution
Tumor #/ Lung Area
150
120
90
60
30
0
AAH
BH
Grade 1
Grade 2
Grade 3
*
**
Keap1/Nrf2+/+
Keap1R554Q/+
Keap1R554Q/R554Q
Nrf2D29H/+
B
Median Tumor Size (μm2)
1.5×10^5
1×10^5
5×10^4
0
Keap1/Nrf2+/+
Keap1R554Q/+
Keap1R554Q/R554Q
Nrf2D29H/+
C
KrasG12D/+ Tumor Size Distribution
Tumor Size (μm2)
10^8
10^7
10^6
10^5
10^4
10^3
10^2
****
****
***
*
*
****
*
AAH
BH
Grade 1
Grade 2
Grade 3
Keap1/Nrf2+/+
Keap1R554Q/+
Keap1R554Q/R554Q
Nrf2D29H/+
D
Tumor Burden (%)
60
40
20
0
*
*
***
Keap1/Nrf2+/+
Keap1R554Q/+
Keap1R554Q/R554Q
Nrf2D29H/+

Figure S2. Lung tumor burden, size, and number quantification in the Kras$^{G12D/+}$ model with Keap1/Nrf2 mutation. (A) Distribution of tumor number by grade across Keap1/Nrf2 mutant models. N=10 mice per genotype, *p<0.05 (unpaired t test with Holm-Sidak's multiple comparisons test). **(B)** Median tumor size per mouse for each genotype. *p<0.05 (one-way ANOVA). **(C)** Tumor size by grade across all mice per genotype. N=10 mice and $\geq$2,300 tumors per genotype, *p<0.05 (Kruskal-Wallis test with Dunn's multiple comparisons test). **(D)** 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).