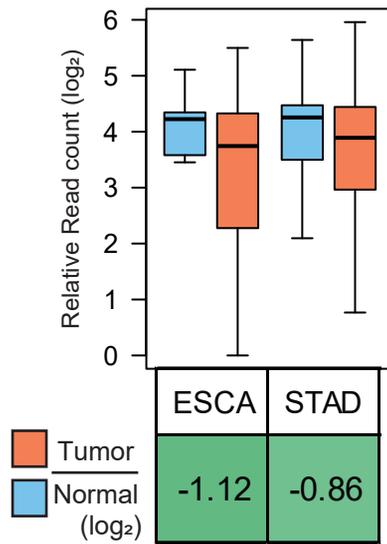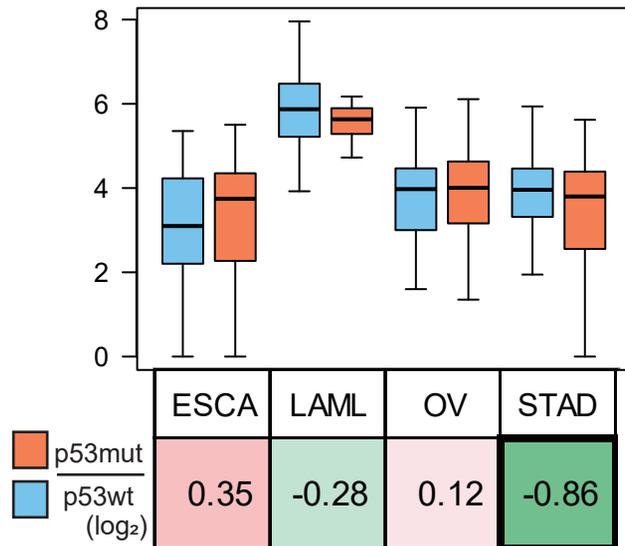**Supplementary Figure 2.**

Comparisons of long form NEAT1 (NEAT1_2) expression.

(A) RNA-seq data of normal and tumor tissues in TCGA database were analyzed, and NEAT1_2 expression is presented in the boxplot. Tumor/Normal ratios are indicated as log2 values in the box under the tissue labels.

(B) RNA-seq data of tumor tissues in TCGA database were divided into p53 wild-type (p53wt) and p53 mutant (p53mut) groups and then analyzed. NEAT1_2 expression is presented in the boxplot. p53mut/p53wt ratios are indicated as log2 values in the box under the tissue labels.

In (A) and (B), significant changes (p < 0.05 by two-sided Welch's t-test after the confirmation of normal distributions) are marked with a bold frame.