Supplementary Figure 5: Positional distribution and underlying mutational processes of SAVs.
(A) Visualization of mutational patterns for five representative mutation signatures identified by pmsignature software. These patterns are defined by substitution type, strand bias, and sequence context of 2 bp within the substituted bases (Shiraishi et al. 2015). **(B)** Fraction of estimated SAVs relative to estimated total variants

attributed to each mutational signature in each cancer type. Red dashed lines represent the overall fraction of SAVs relative to total variants for each cancer. **(C-E)** Scatter plot showing the relationship between SAV and total variant counts **(C)**, and box plots showing the number of SAVs **(D)** and the SAV fraction **(E)** according to smoking history in LUAD and LUSC. **(F-H)** Scatter plot showing the relationship between SAV and total variant counts **(F)**, and box plots showing the number of SAVs **(G)** and the SAV fraction **(H)** according to POLE mutation status in COAD and LUSC.