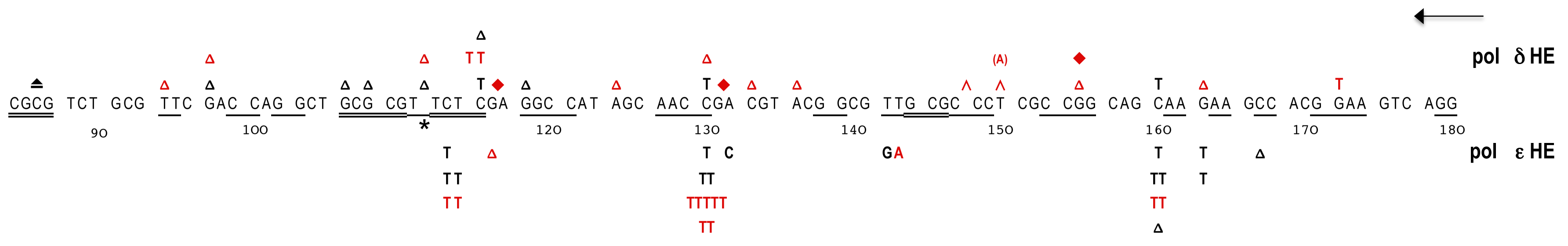
Supplemental Figure 1. Distribution of Pol δ and Pol ε errors within the HSV-tk coding region. Top panel corresponds to the HSV-tk sense strand template sequence (pSStu2 GD); bottom panel corresponds to the antisense strand template sequence (pSAStu2 GD). The middle line of each panel is the wild-type sequence of the MluI-StuI single-stranded gap. The direction of DNA synthesis (5' to 3') is indicated by arrows. The microsatellite sequence insertion point (111-112) is indicated by an asterisk. Individual monitor loci of one or two base tandem repeats are indicated by underlines. Independent mutants produced by the DNA polymerases are indicated by symbols above (Pol δ) and below (Pol ε) the wild-type sequence. Errors produced by the exonuclease-deficient forms of each polymerase are shown in red. Each symbol represents one independent mutant. Base substitution mutations are indicated with text, and misalignment-mediated errors are indicated by the following symbols: Δ, one base deletion; ◆, two base deletion; ∧, one base insertion; ⏏, two base insertion.

HSV-*tk* Sense Strand (pSStu 2)



HSV-*tk* Antisense Strand (pSAStu2)