Figure S6

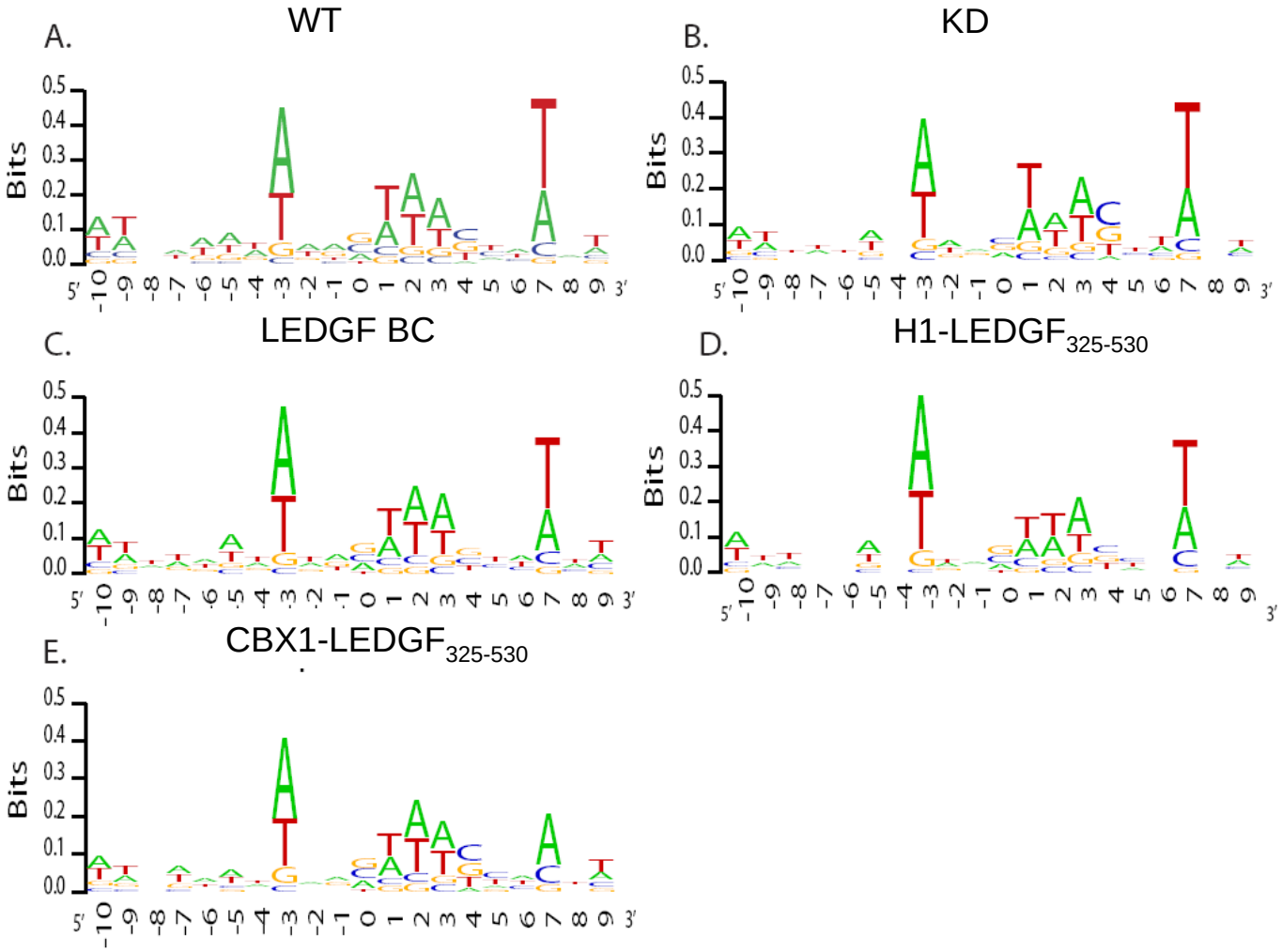

Figure S6. EIAV integration site consensus is not affected by LEDGF hybrids. Following alignment of 20 bp surrounding EIAV integration sites from each cell type, a consensus sequence was generated using the WebLogo program (weblogo.berkeley.edu/logo/cgi). Consensus sequence for integration sites from (**a**) WT cells, (**b**) KD cells, (**c**) cells complemented with LEDGF BC, (**d**) cells stably expressing H1-LEDGF$_{325\text{-}530}$, and (**e**) cells stably expressing CBX1-LEDGF$_{325\text{-}530}$. The x-axis shows the position relative to the integration site (between position -1 and 0). The y-axis shows bits of information at each position (perfect conservation at a position would score 2 bits).