

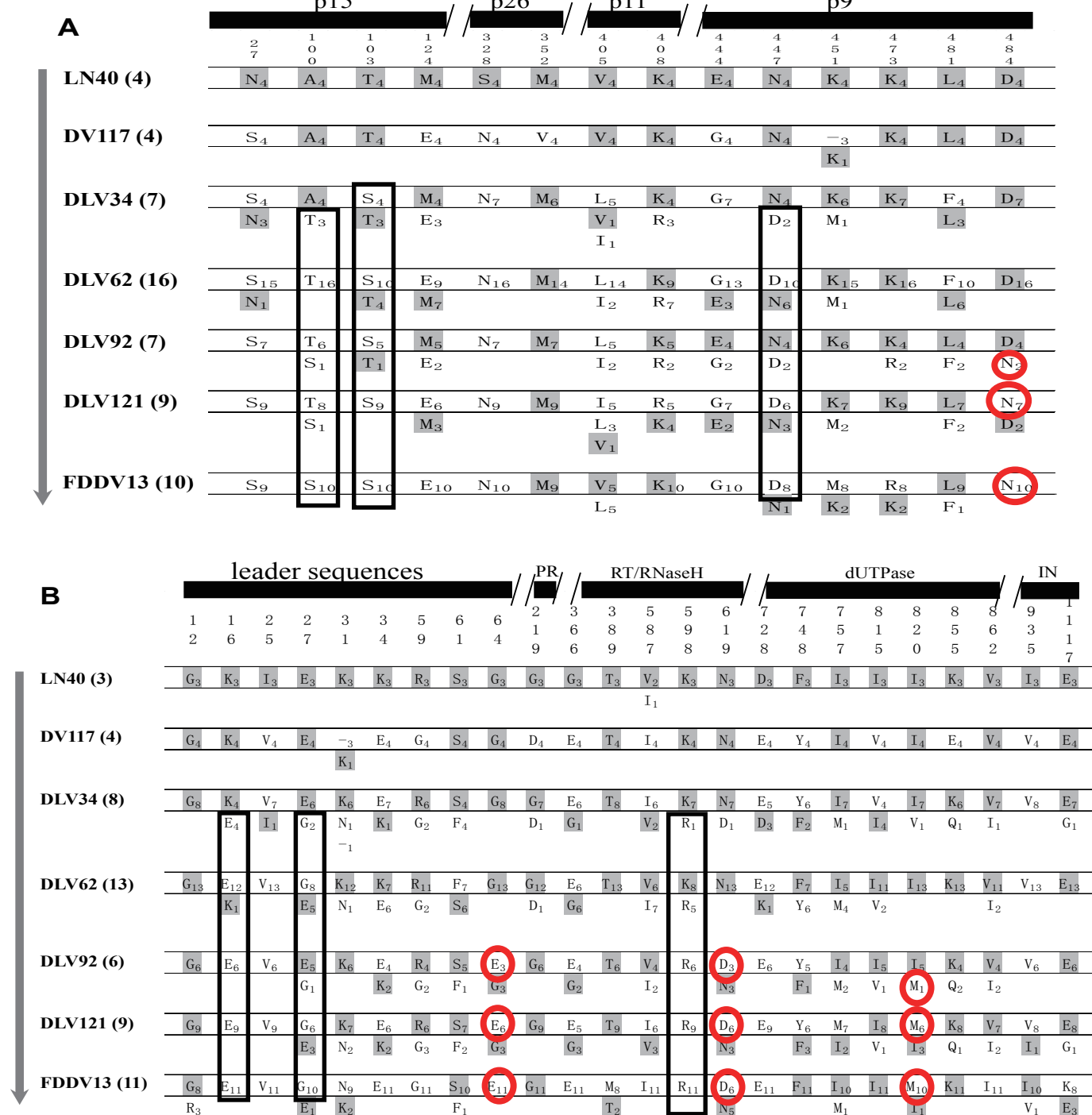
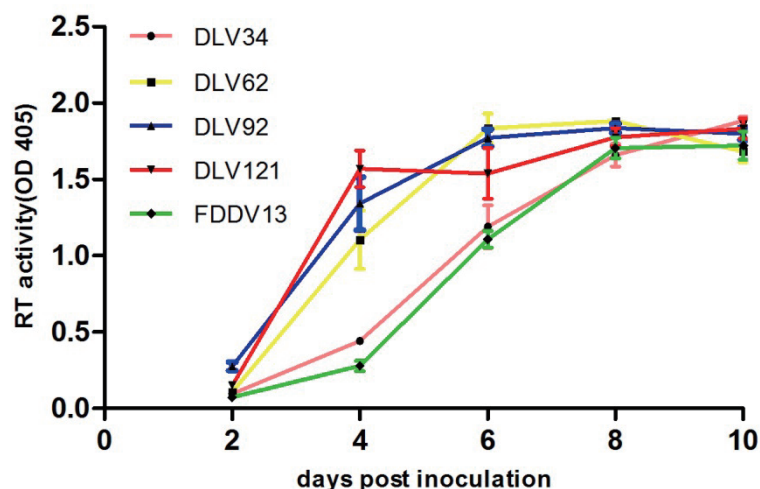
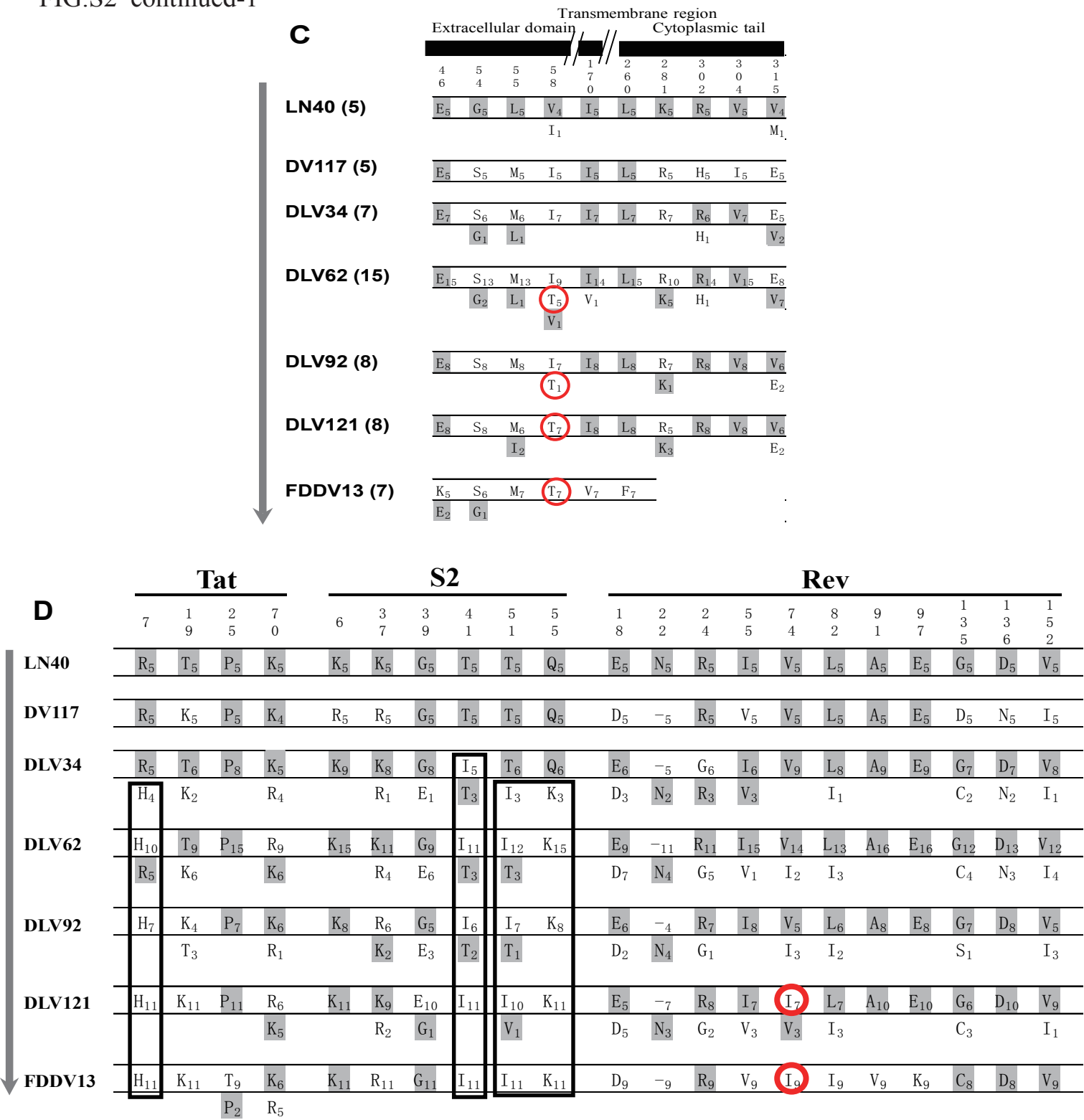


FIG.S2 continued-1



Supplementary Figure 2. Stable mutations in Gag (A), Pol (B), gp45 (C), Tat, S2 and Rev (D) generated during different vaccine development stages. The amino acid sequences were deduced from the gene sequences originating from either the proviral genomes or from the directly cloned PCR products after removing sequences containing premature stop codons. The sequences of each gene were aligned to the reference sequence EIAV_{LN40}. The shadowed residues and white background residues are identical to or different from the reference sequence, respectively. Stable mutation sites detected primarily in virus strains adapted to cultivated cells are boxed, whereas those limited in the attenuated strains are marked with red circles. The numbers on the top of the graphs show the positions of stable mutation sites, and those at the left side indicate the sequences applied for the analysis. The downward arrows indicate the direction of the vaccine development process.