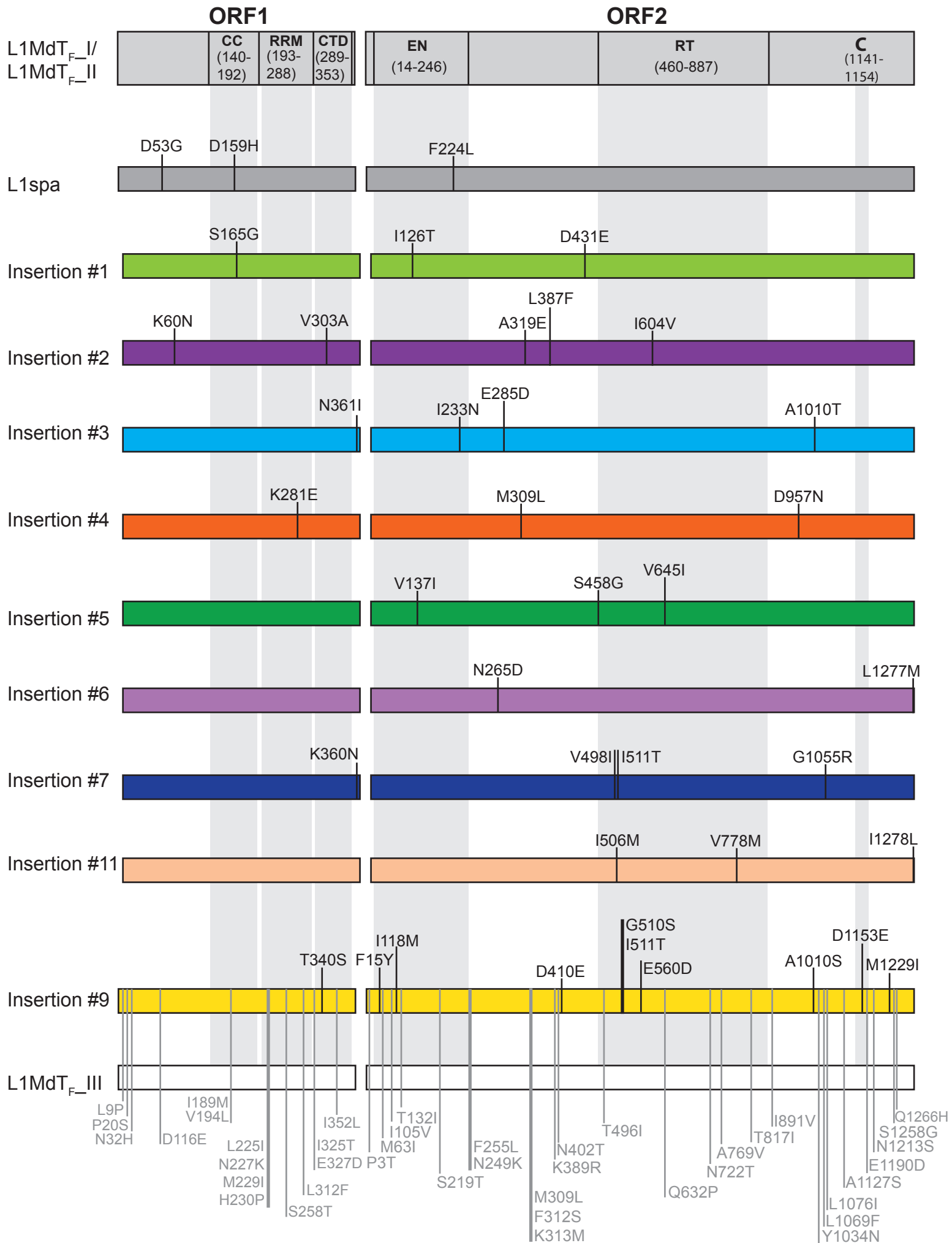


Supplemental Figure 2



Supplemental Figure S2. Sequence comparison of *de novo* L1 insertions

Amino acid substitutions in ORF1 and ORF2 of L1_{spa} and 9 fully sequenced *de novo* L1 insertions from this study, compared to the amino acid sequence of the L1MdT_{F_I} and L1MdT_{F_II} consensus sequences (Sookdeo et al. 2013). The amino acid sequences of L1MdT_{F_I} and L1MdT_{F_II} are identical to one another. The locations of functional domains in ORF1 and ORF2 are shown: CC = coiled-coil, RRM = RNA recognition motif, CTD = C-terminal domain, EN = endonuclease, RT = reverse transcriptase, C = cysteine-rich motif. Insertion #9 closely resembles the L1MdT_{F_III} consensus. Amino acid substitutions relative to L1MdT_{F_I}/L1MdT_{F_II} that are shared by insertion #9 and the L1MdT_{F_III} consensus are indicated below the L1MdT_{F_III} schematic, in grey. Amino acid substitutions unique to insertion #9 are shown above the insertion #9 schematic in black.