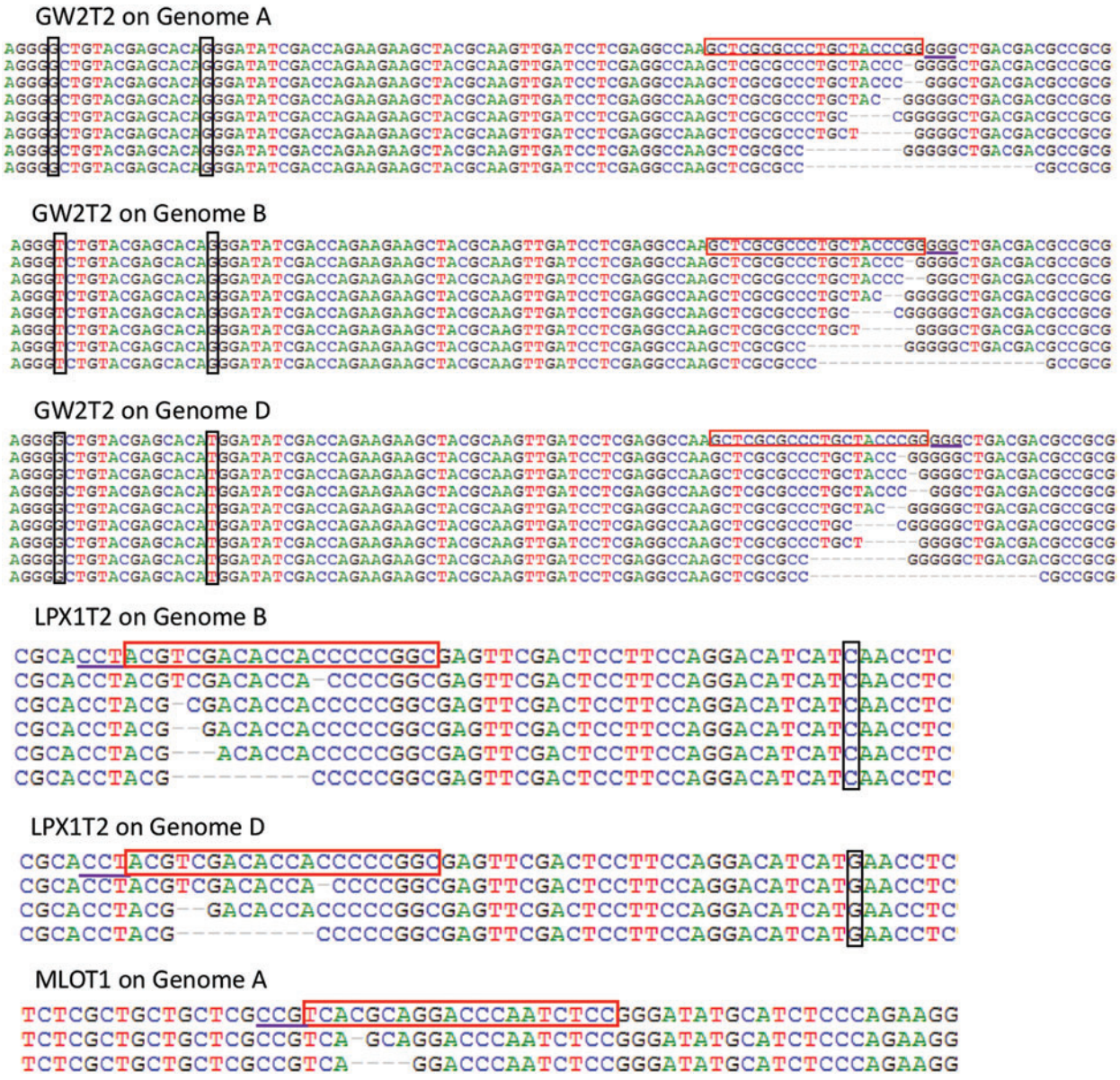

SUPPLEMENTARY FIG. S5. Comparison of the gene editing efficiency of single and multiplex gene editing CRISPR-Cas9 constructs using the protoplast transient expression assay. The mutations were detected by the NGS of the PCR amplicon libraries generated from the protoplast DNA. Representative reads with mutations in the target sites GW2T2, LPX1T1, and LPX1T2 induced by the MGE construct pBUN421-GLM are shown. The first rows correspond to the wild-type genomic sequences from the A, B, or D genomes. The targeted regions are shown within the red rectangles; the PAM sequences are underlined. The genome specific nucleotide bases are shown within the black rectangles.