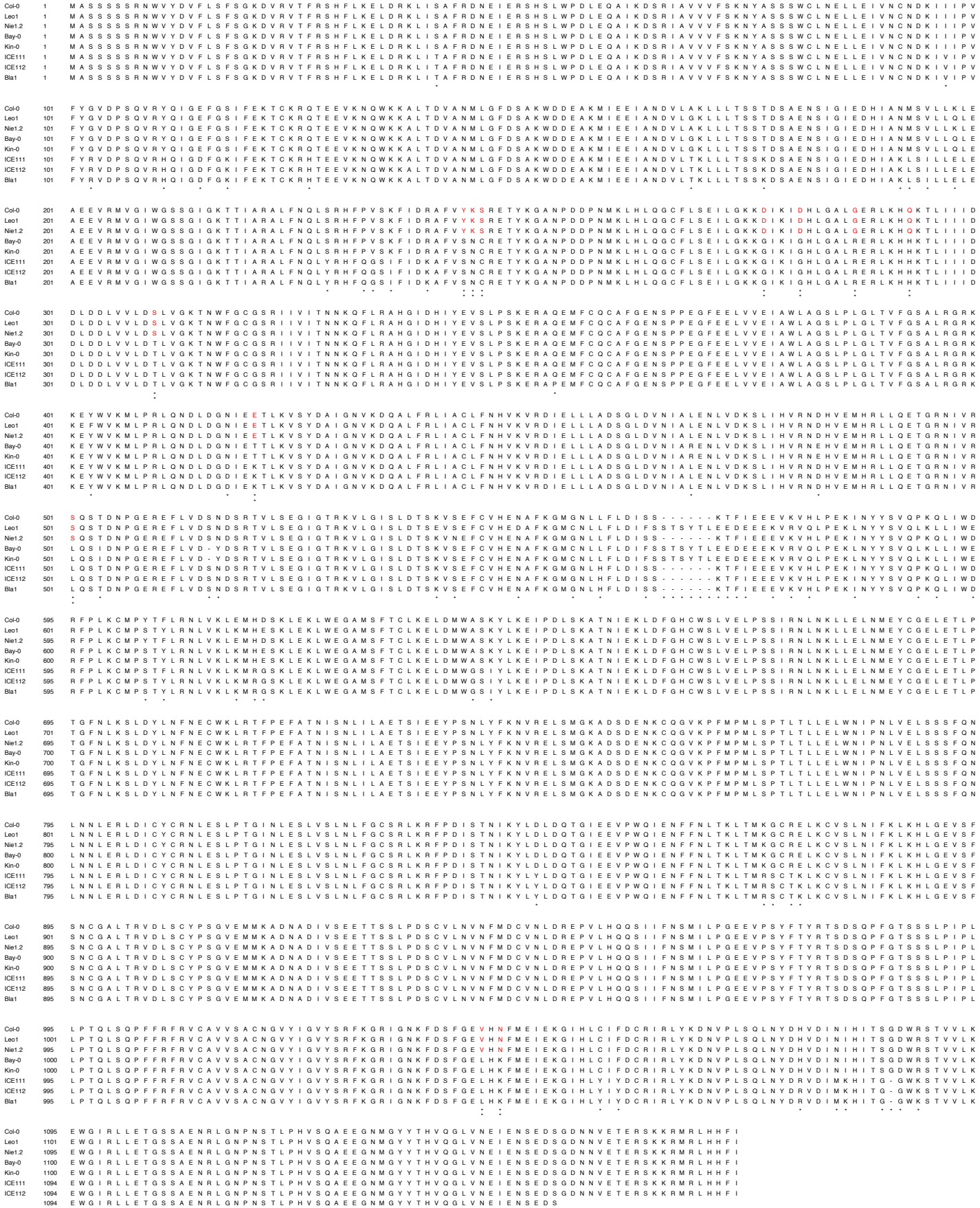

Figure S2. Sequence comparison of *VICTR* alleles from 8 different Arabidopsis accessions.
Each amino acid sequence was deduced by sequencing of full-length *VICTR* genomic DNAs from eight different Arabidopsis accessions. The sequence alignment was generated using Clustal Omega. Amino acid polymorphisms of *VICTR* specifically found in DFPM-sensitive accessions are marked by asterisks.