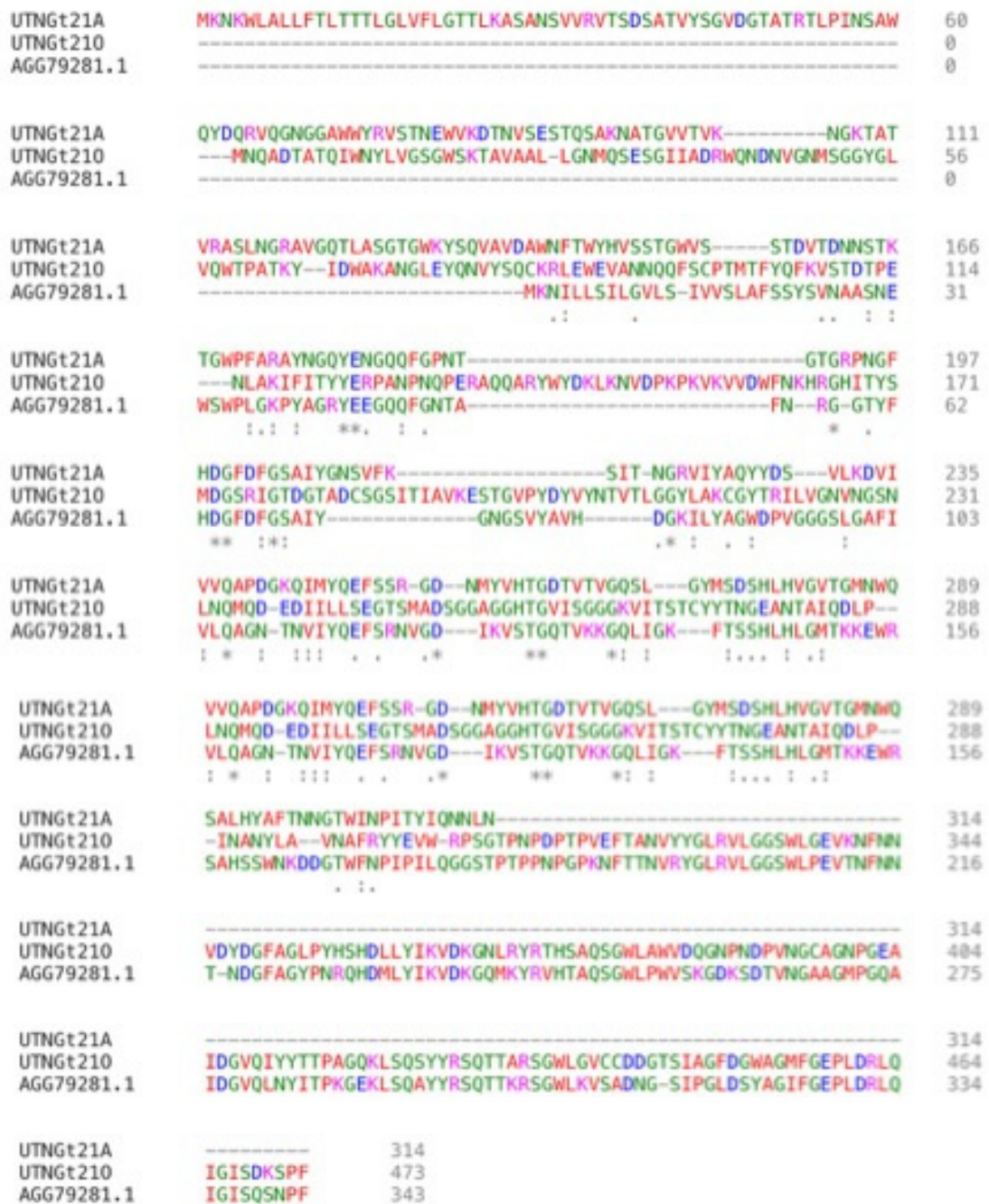


Figure S3. A). Protein sequence pairwise alignment of putative bacteriocin from UTNGT21A and enterolysin_A from UTNGt21O and *Enterococcus faecalis* (NCBI accession no. AGG79281.1) with Clustal WS (v.2.0) retrieved from Jalview. *: indicate the similar amino acids. B). Average distance calculated based on percentage of similarity between sequences. The number on branch is the bootstrap value that indicates the extent of relatedness between two subjects.



A.

