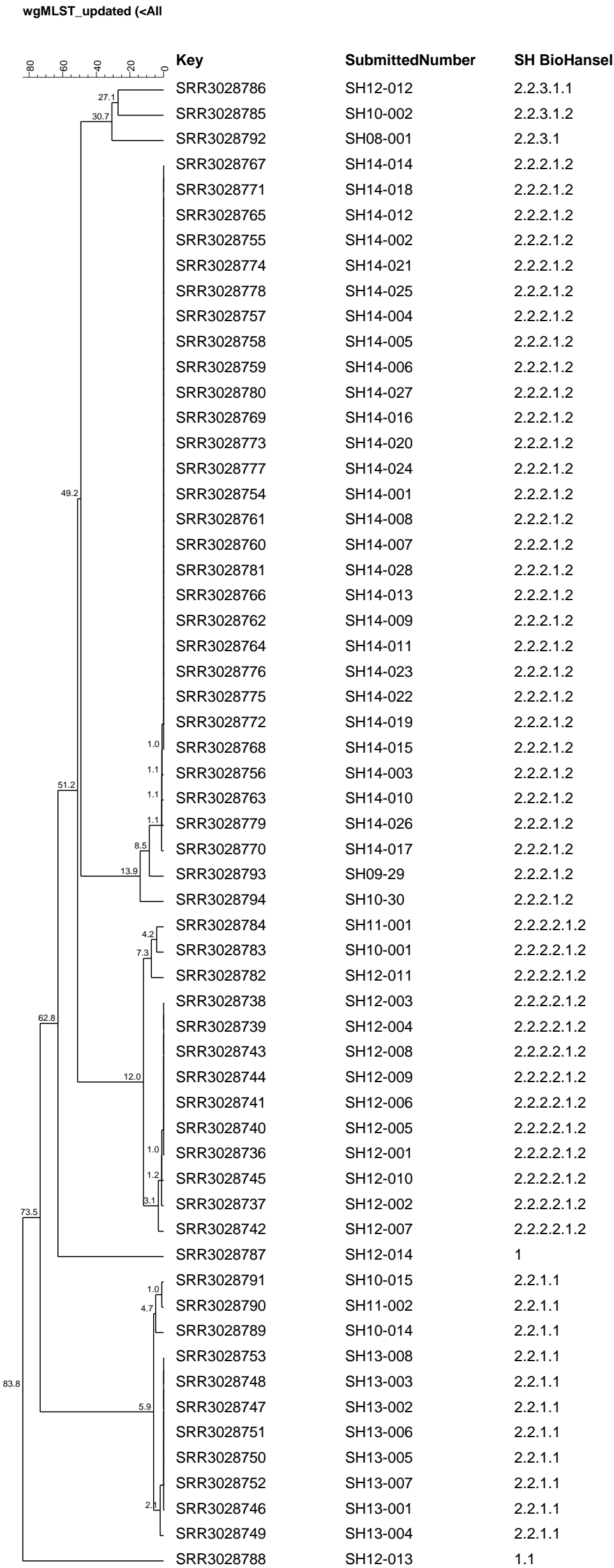


wgMLST for Salmonella Heidelberg dataset with Biohansel genotypes



Comparison generated using BioNumerics v 7.6.3 on 4396 alleles. The wgMLST allele differences indicated at the nodes were calculated using UPGMA and therefore, are not whole numbers. To determine the nearest whole number value, round up if the digit following the decimal is 5 or greater; round down if the digit following the decimal is less than 5.