We propose to compare complete genomes using a new evolutionary distance defined from maximum unique matches (MUMs). We first evaluate the minimum length of a MUM to be significant before to compute, with a linear time algorithm, MUMs shared by two genomes. Then, simulating sets of sequences evolving according to a given tree topology, we prove that this distance varies monotonously with the amount of evolutionary events, and using the NJ method we get phylogenetic trees very close to the initial ones. Finally, we apply this very fast method to compare bacterial genomes among the Gammaproteobacteria family.