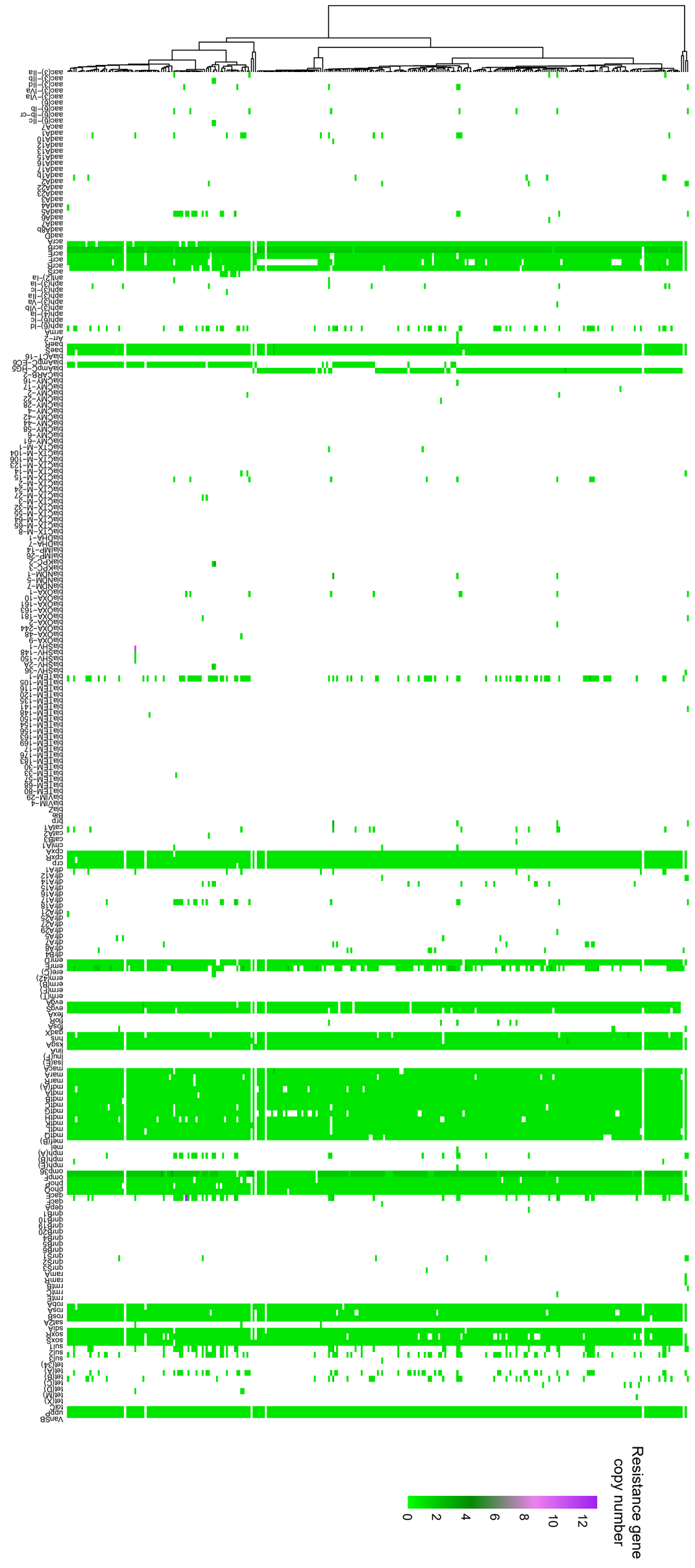Hierarchical clustering of the genomes based on complete k-mer content