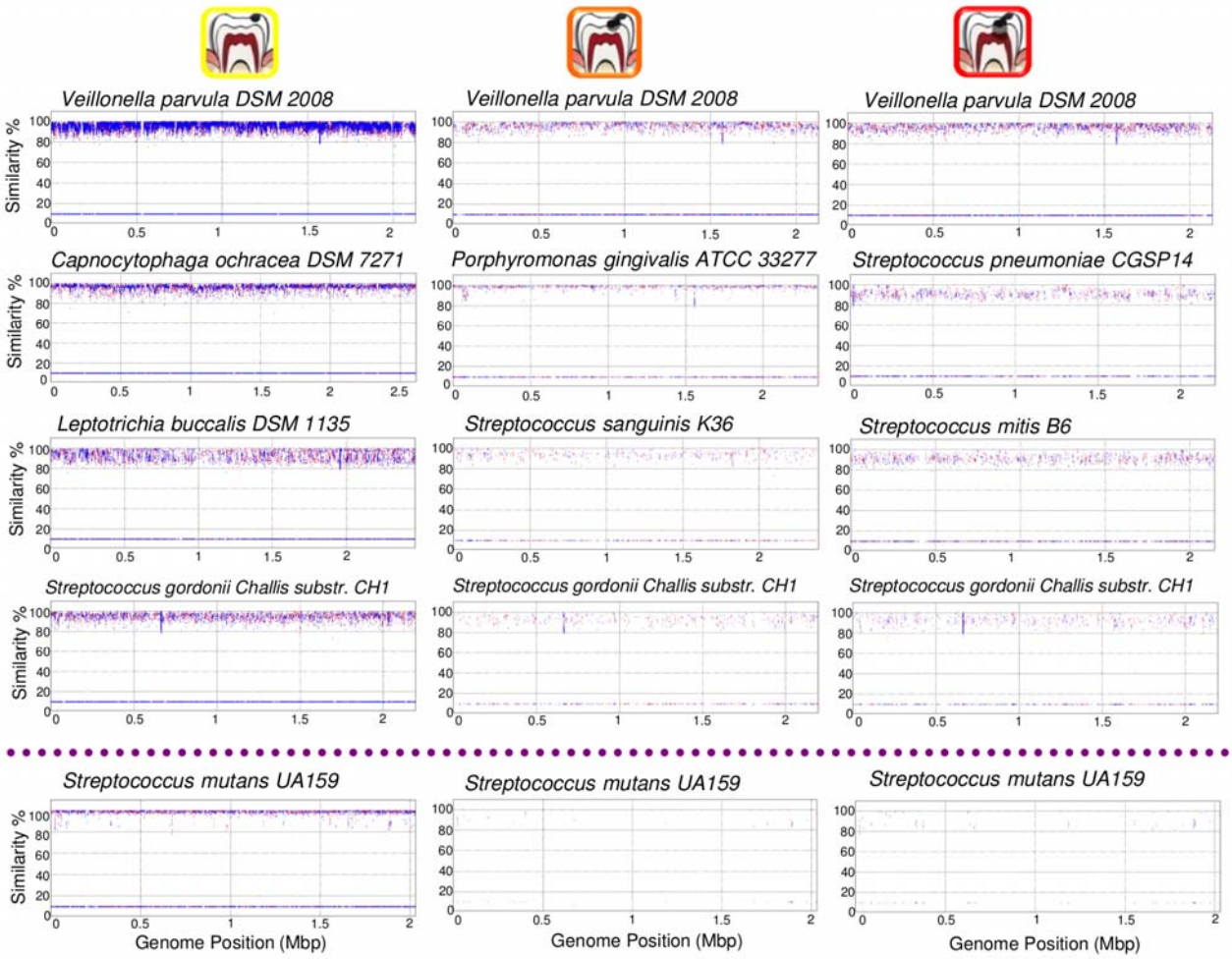


**Supplementary Figure S1. Most common species in enamel, dentin and deep dentin caries samples.** Graphs are metagenomic recruitment plots in which each metagenomic read was compared against the genomes of all sequenced bacterial species available. Values on the Y axis indicate the sequence identity between each pyrosequence and the genome sequence of the 4 species with highest coverage, as well as for the species *Streptococcus mutans*. The coverage level is related to the proportion of DNA of that species in the sample and it is not subject to PCR amplification biases. The classic cariogenic species *S. mutans* is only detected in enamel caries lesions.