



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.