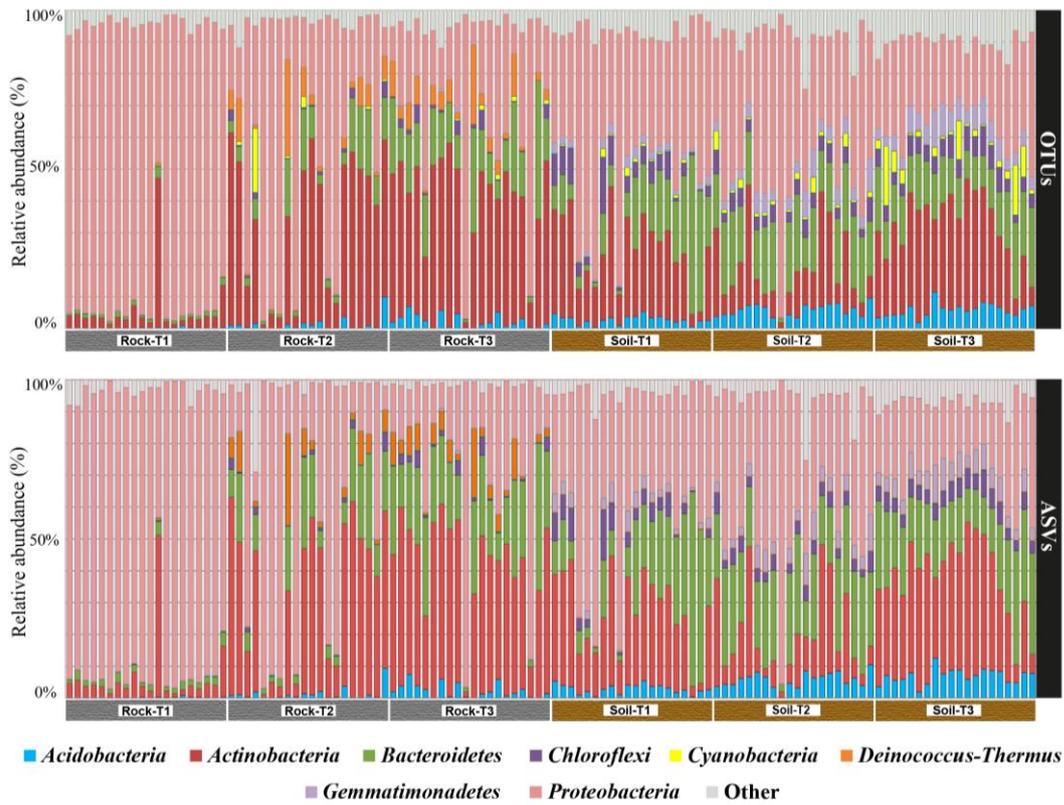
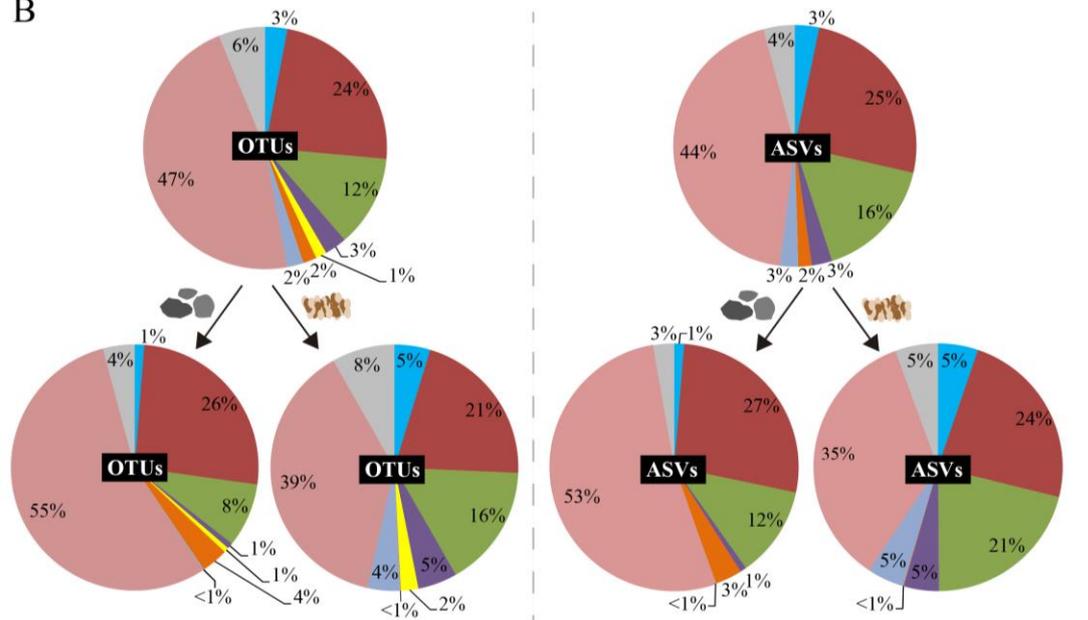


A



B



**Supplementary Figure S3.** Relative abundance of bacterial phyla per sample calculated with OTU and ASV data and arranged by substrate type (rocks, soil) and successional stage (A). Proportion of each bacterial phylum based on OTUs and ASVs

for the entire chronosequence, and considering the two substrate types independently

(B).