

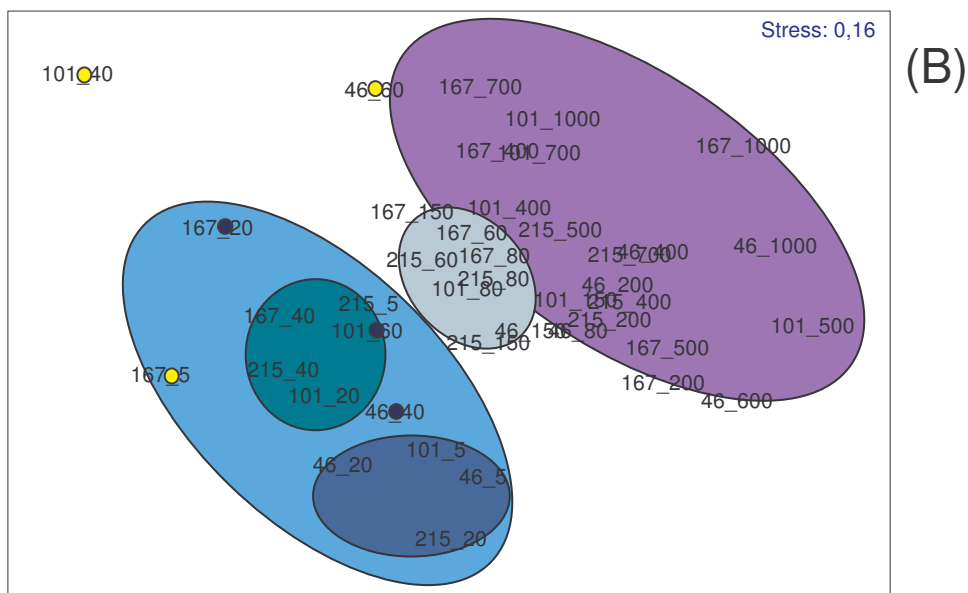
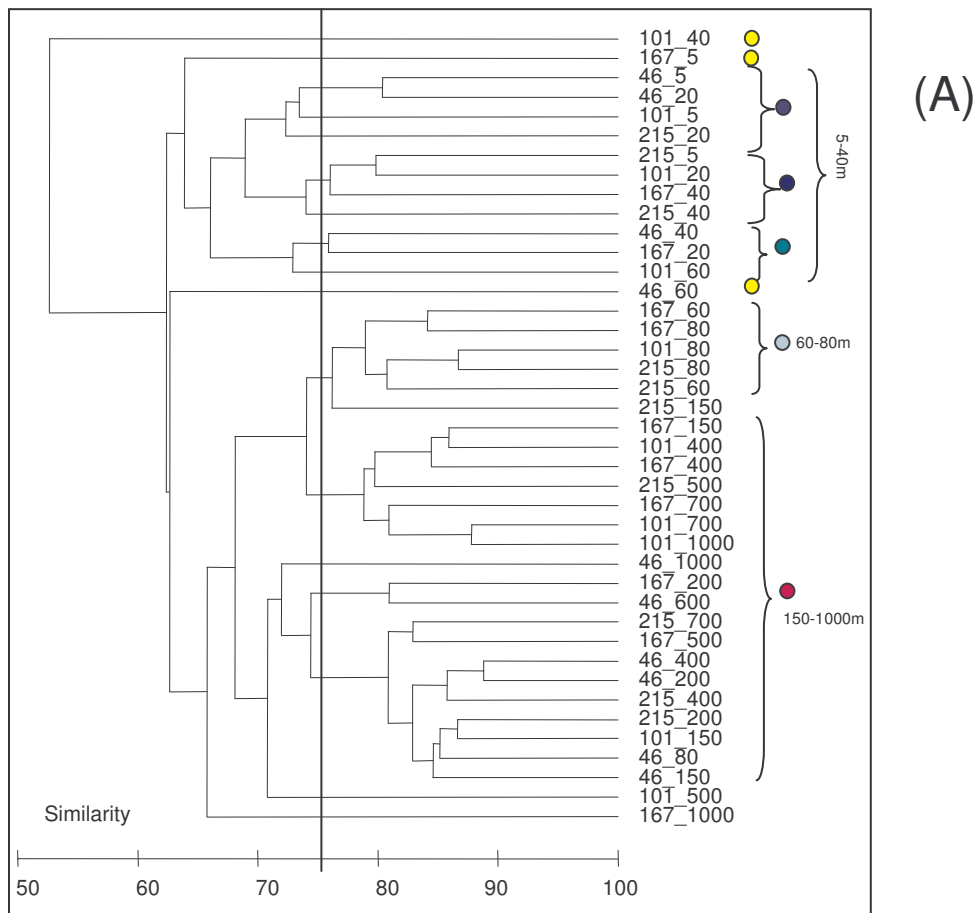


Figure legend. Depth organisation of bacterial community structure during the DYFAMED II cruise analysed by (A) UPGMA dendrogram or by (B) multidimensional scaling (MDS) generated from the CE-SSCP patterns based on 16S rDNA. Each sample is depicted by the CTD number and sampling depth.