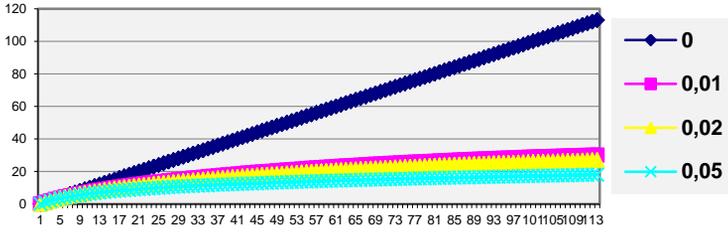


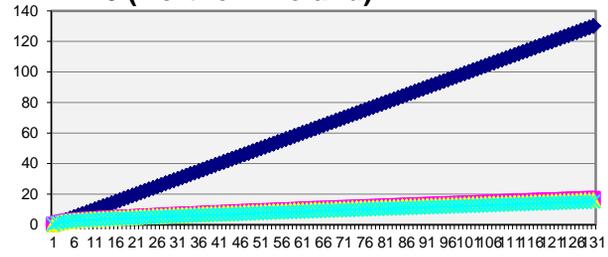
Bacteria

Eukaryotes

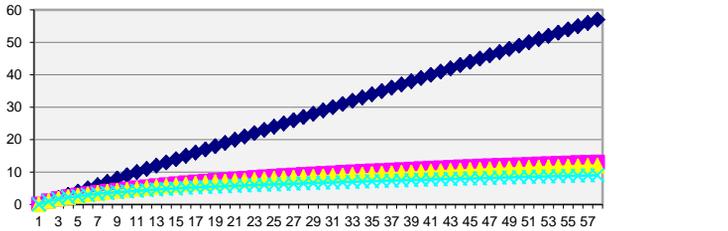
B1.6 (Northern Ireland)



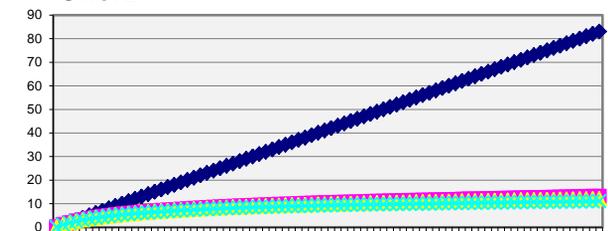
B1.6 (Northern Ireland)



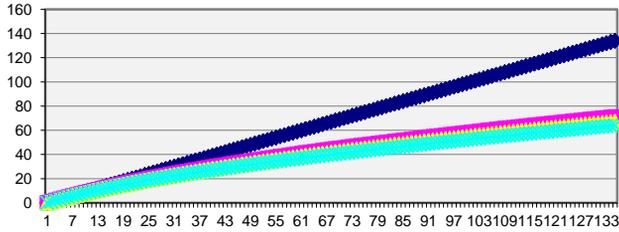
Cher2



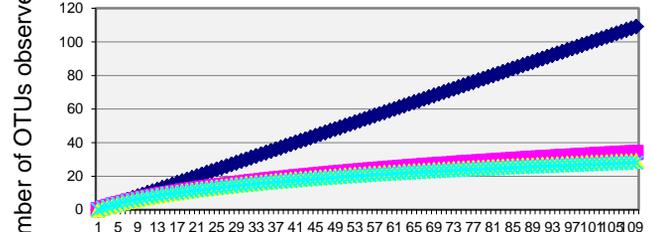
Cher2



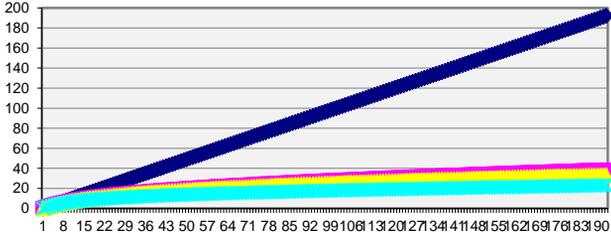
Cher4



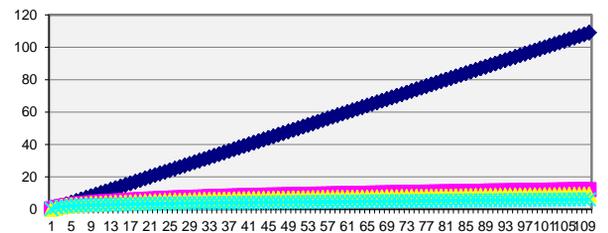
Cher4



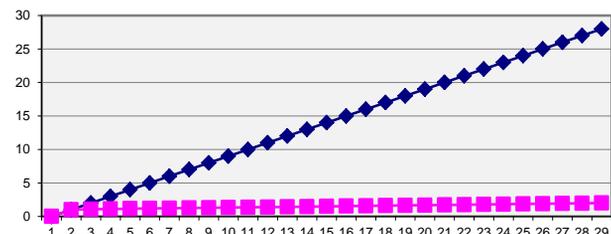
Cher6



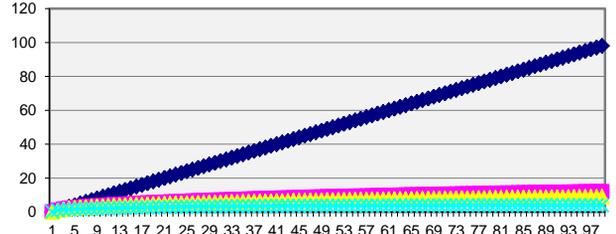
Cher6



Cher8



Cher8



Number of sequences sampled

Number of sequences analyzed

Figure S1. Accumulation curves for SSU rDNA libraries of biofilm samples in Chernobyl (Cher) and North Ireland. In all cases, the number of different sequences observed is plotted against the number of sequences analyzed. The different curves in each plot indicate the various cut-off values considered (grey box) from 0 to 5% divergence. Generally, 97-98% identity are used to define OTU levels representing the species level.