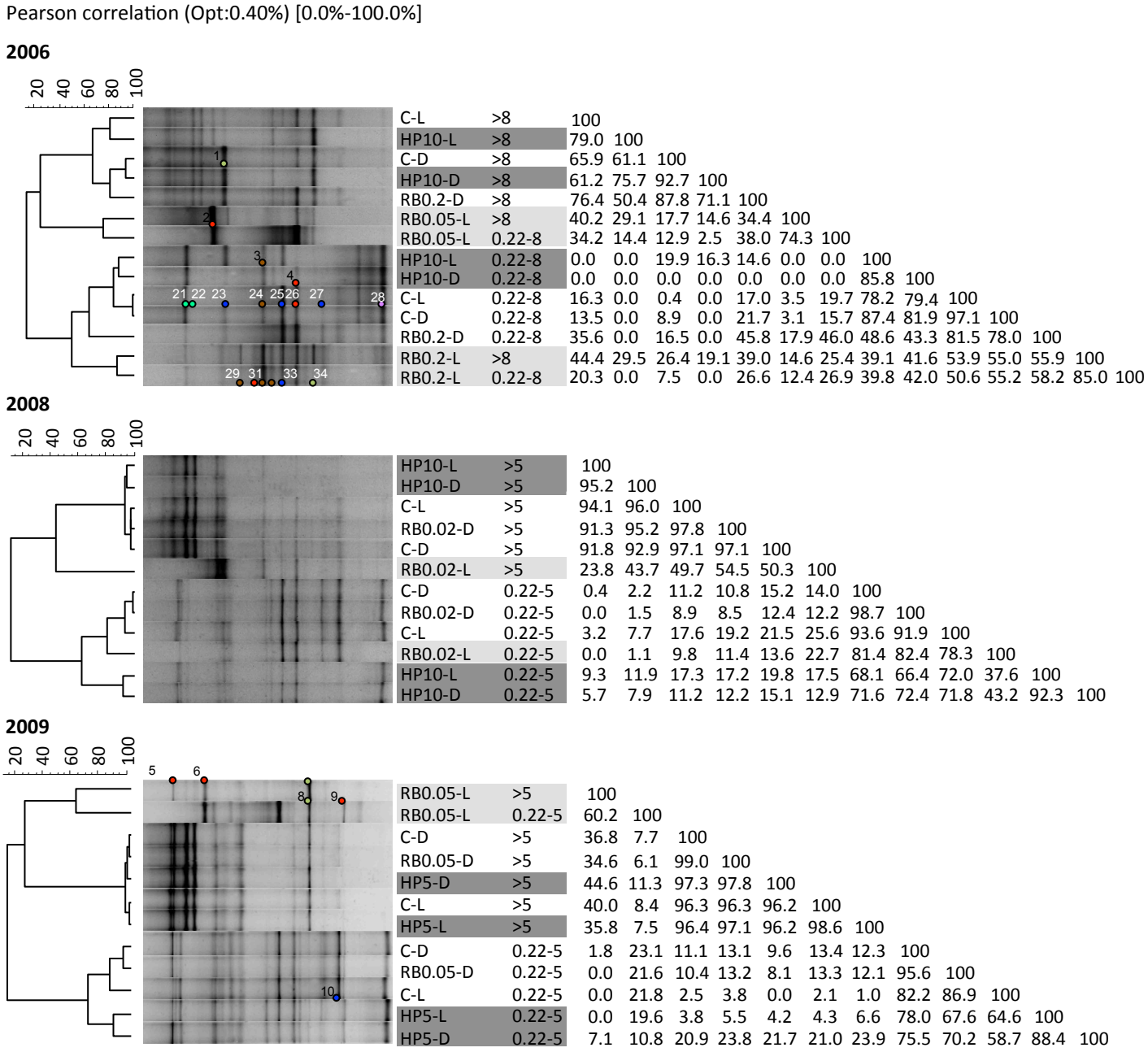

Figure S4

Distance matrices of Pearson correlation based UPGMA cluster analysis performed for *Bacteria* RT-PCR DGGE patterns of *in situ* experiments 2006, 2008, and 2009. Abbreviations are given in Figure S2. White numbers on DGGE bands correspond to DGGE band sequences determined in respective PCR-DGGE pattern of the same experiment published previously (Glaeser *et al*., 2010). Colours indicate the phylogenetic affiliation: *Actinobacteria* (purple), *Gammaproteobacteria* (brown), *Alphaproteobacteria* (red), and *Betaproteobacteria* (blue).