



Figure S1. DGGE fingerprints and UPGMA cluster analyses based on *alp* gene fragments **(A)** and *nifH* gene fragments **(B)** of phosphate mineralizing and nitrogen fixing bacterial communities, respectively, present in the rhizosphere of the tuberous roots (replicates 1 – 5 in parenthesis) from three different sweet potato genotypes (IPB-149, IPB-137 and IPB-052) sampled three (t1, _3M - black squares) and six (t2, _6M - grey squares) months after planting.