



Figure S4. Phylogenetic relationships of the whole genome sequenced strains of *P. dorei*, *B. uniformis* and *P. distasonis* based on 30 genes. The dendrogram was constructed using the UPGMA method. Numbers at nodes indicate the percentage bootstrap values of 1000 replicates. The sequences of the genes of the strains of *P. dorei* DSM 17855, CL03T12C01, CL02T12C06, CL02T00C15, HS1 L3 B 079, HS2 L2 B045b, HS1 L1B010, *B. uniformis* ATCC 8492 and *P. distasonis* ATCC 8503 were used as reference.