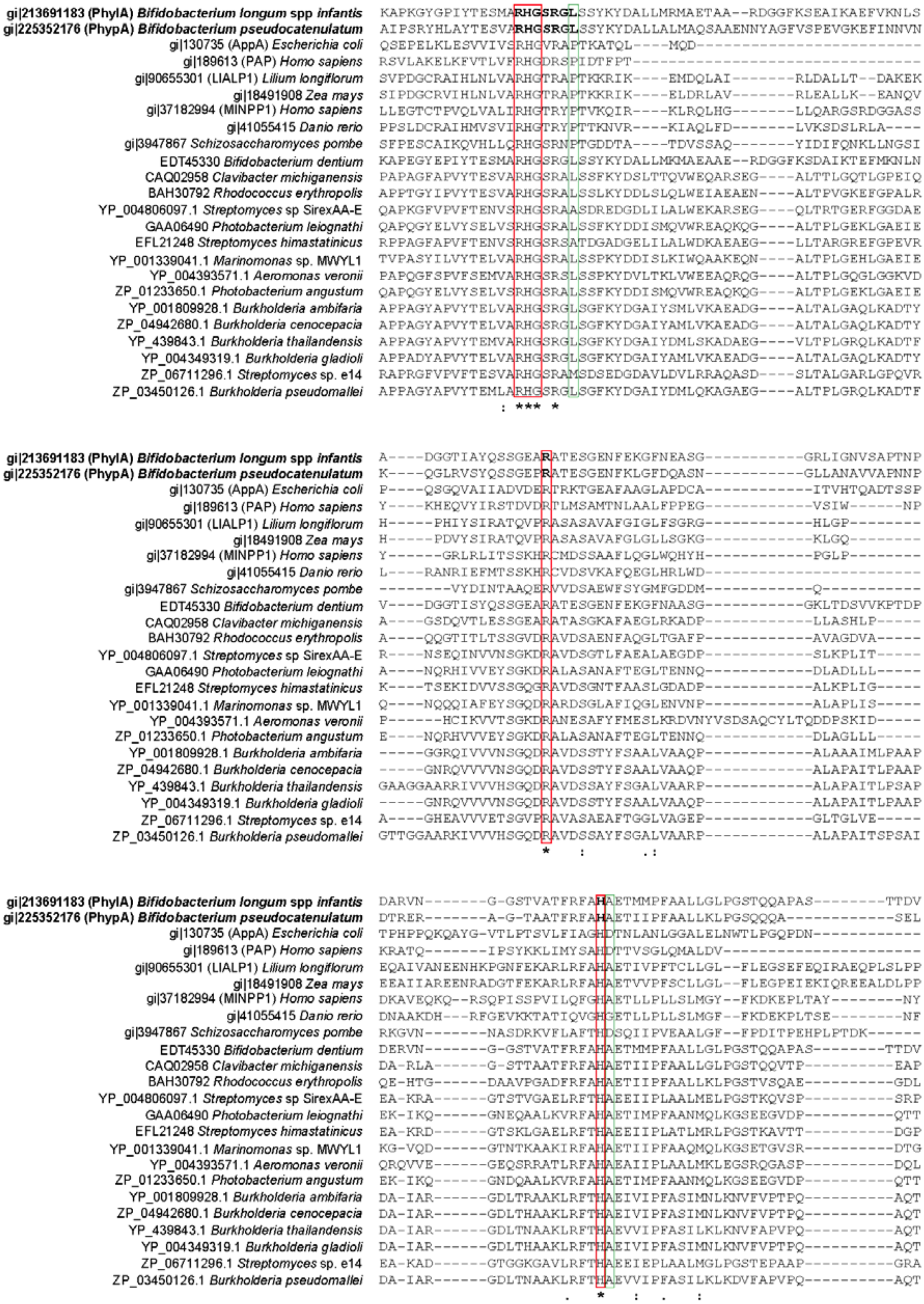

FIG. S1 Refined multiple sequence alignment of PhypA from *B. pseudocatenulatum* ATCC 27919, PhylA from *B. longum*spp *Infantis* ATCC 15697 and different phosphatases from the HAP family. Non-homologous regions were eliminated with GBlocks. Invariant conserved sequences in all members of the family and conserved sequences that differ between members are boxed.

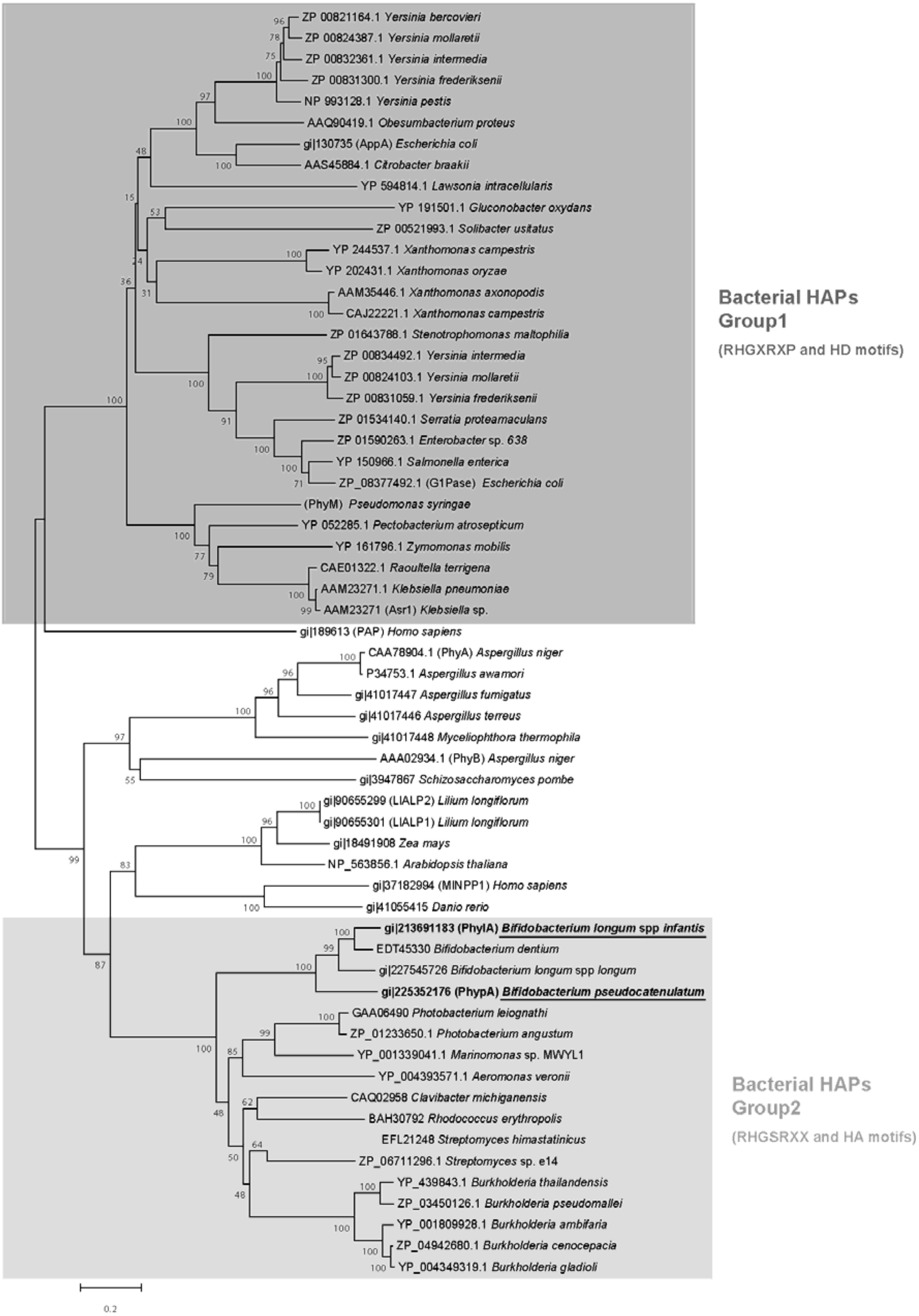

FIG. S2 Phylogenetic analysis of phosphatases from different origins belonging to the branch 2 HAP group, including PhylA and PhypA from bifidobacteria. Amino acid sequences were aligned with the EBI ClustalW2 tool and sequence trimming was done with GBlocks. The phylogenetic trees were constructed with MEGA4 (Poisson correction model, pairwise deletion and 1000 replicates).
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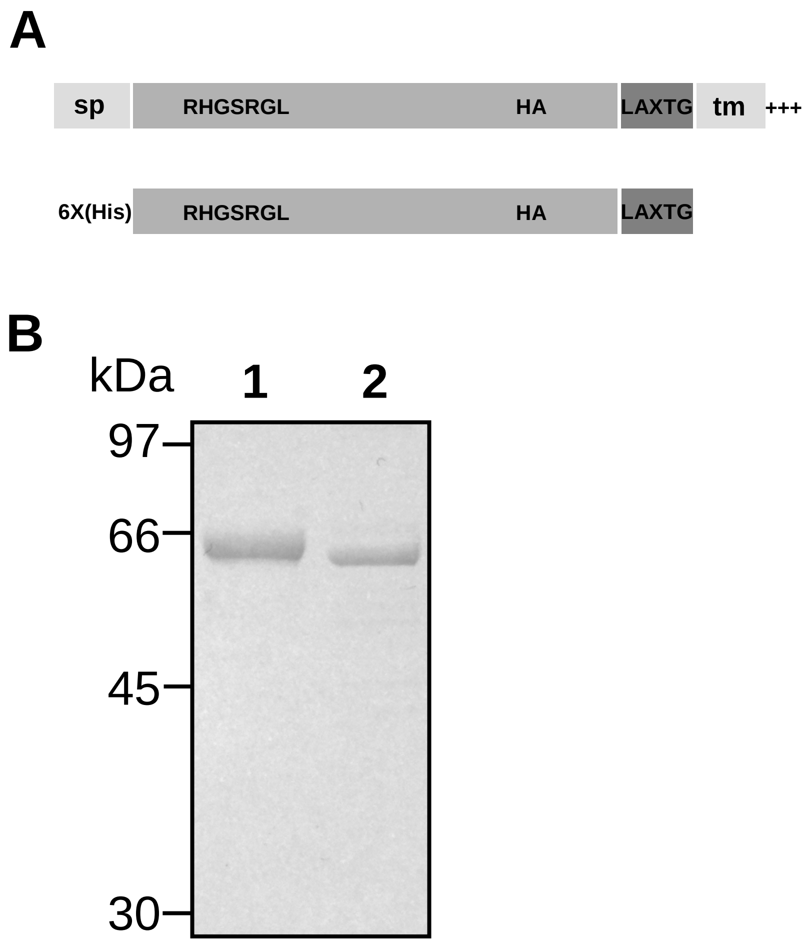

FIG. S3 (A) Schematic representation of the PhylA and PhypA phytases and the truncated 6X(His)-tagged version lacking the signal peptide (sp) and the hydrophobic C-terminal region (tm). The (+) symbol at the C-terminal part represent positively charged amino acids. Signature sequences of the different conserved motifs are also shown (HAPs RHGSRGL and HA domains and the C-terminal cell-wall anchoring domains (LAXTG)); (B) SDS-PAGE analysis of purified 6X(His) truncated phytases. Lane 1, 6x(His)^{49}PhypA^{612} from *B. pseudocatenulatum*; lane 2, 6x(His)^{32}PhylA^{599} from *B. longum* spp *infantis.* The calculated molecular weight of the truncated enzymes is 61.8 and 62.2 kDa, respectively. Attempts to express in *E. coli* the N-terminal deleted proteins carrying the C-terminal hydrophobic helices (6x(His)^{49}PhypA^{639} and 6x(His)^{32}PhylA^{623}) which form part of the sortase-dependent cell wall anchoring motif, always rendered insoluble inclusion bodies.