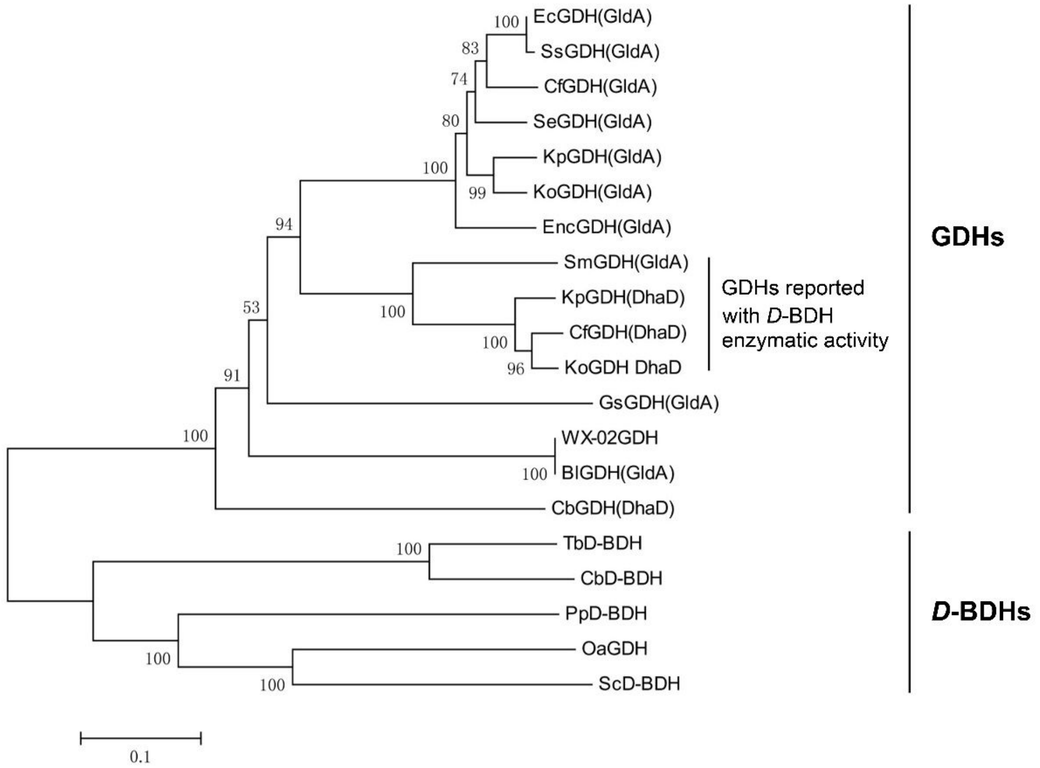

**Figure S2**. Phylogenetic analysis of amino acid sequences of GDHs and *D*-BDHs from different strains. The phylogenetic tree is constructed with the neighbor-joining method (1000 bootstraps) using the MEGA 5.1 program [29]. The sequences compared include GDHs mentioned in Fig. S4 and *D*-BDHs from *Thermoanaerobacter brockii* (TbD-BDH, CAA46053), *Clostridium beijerinckii* (CbD-BDH, AAA23199), *Paenibacillus polymyxa* (PpD-BDH, AEV53933.1), *Saccharomyces cerevisiae* (ScD-BDH NP_009341) and GDH from *Ogataea angusta* (OaGDH, BAD32688).