FIGURE S1.—Consensus phylogenetic tree showing the relationship of amino acid transposase sequences, between 50 selected full-length hAT elements based on Bayesian inference (50% majority rule consensus). Numbers next to most nodes show Bayesian posterior probability values produced by the program MRBayes. Nodal support inside the SPIN, MiBuster2 clade is not shown for purposes of clarity. The scale bar represents a phylogenetic distance of 1 amino acid substitutions per site.