Supplementary Figure 1: Sequence tree produced by Bayesian inference, based on the amino acid sequences of the reverse transcriptase domain. The matrix was composed of the sequences of *X. tropicalis* and *X. laevis* DIRS elements obtained from the Rebpase database, the copies retrieved from both genomes and diagnostic sequences from each DIRS superfamily. The posteriorprobability values are indicated at the branches.

Supplementary Figure 2: Proportion of all *X. laevis DIRS-like* families in the subgenomes S and L.