



**Figure S3 – Ty3 Family**

ML phylogeny using a nucleotide alignment of 177 Ty3 LTR sequences analysed at 361 sites. Strong or maximally supported ( $\geq 70\%$  mlBP) branches are indicated by \* where space allows (tree is available as File S2 in Supplementary Material). Scale bar indicates number of substitutions per site. SGRP (Liti et al. 2009) *S. cerevisiae* sequences in red allow NZ strain LTR sequences (yellow) to be identified. SGRP *S. paradoxus* LTR sequences (brown) form their own distinct clade. The tree is rooted with *S. kudriavzevii* Ty3 (orange) sequences.