



Figure S4 – Ty4 Family

ML phylogeny using a nucleotide alignment of 136 Ty4 LTR sequences analysed at 374 sites. Strong or maximally supported ($\geq 70\%$ mlBP) branches are indicated by * where space allows (tree is available as File S3 in Supplementary Material). Scale bar indicates number of substitutions per site. / indicates this branch has been arbitrarily shortened for figure clarity. SGRP (Liti et al. 2009) *S. cerevisiae* sequences in red allow identification of NZ strain LTR sequences (yellow) unique to this population. SGRP *S. paradoxus* Ty4 LTR sequences (brown) are grouped in the basal position with older, long-branched NZ sequences. The tree is rooted with *S. kudriavzevii* Ty4 (orange) sequences.