

Supplementary Table S3:

Fraction of DNA in fungal genomes corresponding to transposable elements

Organism	DNA with similarity to transposons ^a
<i>U. maydis</i>	1.1 %
<i>M. grisea</i>	7.3 % ¹
<i>C. neoformans</i>	5.0 % ²
<i>S. pombe</i>	1.1 % ³
<i>S. cerevisiae</i>	3.1 % ⁴
<i>N. crassa</i>	4.6 % ⁵

^a active and inactive transposons, pseudogenes and terminal repeats

¹ Dean, R. A. et al. The genome sequence of the rice blast fungus *Magnaporthe grisea*. Nature 434, 980-6 (2005).

² Loftus, B. J. et al. The genome of the basidiomycetous yeast and human pathogen *Cryptococcus neoformans*. Science 307, 1321-4 (2005).

³ Bowen, N. J., Jordan, I. K., Epstein, J. A., Wood, V. & Levin, H. L. Retrotransposons and their recognition of pol II promoters: a comprehensive survey of the transposable elements from the complete genome sequence of *Schizosaccharomyces pombe*. Genome Res 13, 1984-97 (2003).

⁴ Kim, J. M., Vanguri, S., Boeke, J. D., Gabriel, A. & Voytas, D. F. Transposable elements and genome organization: a comprehensive survey of retrotransposons revealed by the complete *Saccharomyces cerevisiae* genome sequence. Genome Res 8, 464-78 (1998).

⁵ Galagan, J. E. et al. The genome sequence of the filamentous fungus *Neurospora crassa*. Nature 422, 859-68 (2003).