

Table S9. References used to determine locations of genomic elements.¹

Genomic elements	Data source
Ty element	SGD; YeastMine
Solo LTR	SGD; YeastMine
Centromeres	SGD; YeastMine
Intron-containing genes	SGD; YeastMine
ARS elements	SGD; YeastMine
tRNA genes	SGD; YeastMine
Long genes	SGD; YeastMine
Regions of high transcription	SGD; YeastMine
Regions of low transcription	SGD; YeastMine
ORFs with high GC content	SGD; YeastMine
High G content on the non-transcribed strand	SGD; YeastMine
Sites of Rbp3 accumulation in S phase	Fachinetti <i>et al.</i> 2010
TER sites	Fachinetti <i>et al.</i> 2010
TER sites related to high transcription	Fachinetti <i>et al.</i> 2010
Sites of Rrm3 accumulation	Azvolinsky <i>et al.</i> 2009
Palindromic sequences	Lisnic <i>et al.</i> 2005
Sites of G4 quadruplex formation (predicted by sequence context <i>in silico</i>)	Capra <i>et al.</i> 2010
Sites of differential transcription in response to NMM ²	Hershman <i>et al.</i> 2008
Regions of transcription-transcription conflicts resolved by Elc1p ³	Hobson <i>et al.</i> 2012
Tracts of poly A or poly T \geq 25 bp	SGD
Sites of RNA/DNA hybrid accumulation in <i>rh1 rh201</i>	Chan <i>et al.</i> 2014

¹Most of the genomic elements were identified in Saccharomyces Genome Database (SGD) using the YeastMine tool (described: <http://www.yeastgenome.org/help/video-tutorials/yeastmine>). The criteria used to determine the number each elements in the genome are described in File S1. We chose to identify tracts of poly A or poly T > 25 bp based on a personal communication from Doug Koshland (University of California, Berkeley) who found an association between such tracts and the locations of R-loops.

²NMM is an abbreviation for N-methyl mesoporphyrin IX, a drug that binds G4 quadruplex structures.

³Elc1p is a protein required to remove stalled RNA polymerase II complexes (Hobson *et al.*, 2012).