Supplementary Figure 1. Nucleotide sequence of fission yeast NUMTs. Nucleotide sequences of fission yeast NUMTs are compared to corresponding regions of mtDNA genome. BLAST scores are provided.

Supplementary Figure 2. Independent NUMT insertion sites from *S. pombe* (12) and *S. cerevisiae* (26) were classified according to their genomic localization: coding (blue) or non-coding (pink). NUMT distribution was compared to the expected frequency of coding (blue hatchings) or non-coding (pink hatchings) DNA sequences in both genomes.

Supplementary Figure 3. *Saccharomyces cerevisiae* NUMTs associated with ARS. The genomic loci of budding yeast NUMTs located next to ARS are described. ORFs are shown by white arrows, green boxes represent *Ty* transposons, tRNA-encoding genes are shown by blue arrows, ARS are represented by blue circles and NUMTs are in red.

Supplementary Figure 4. Orp1/Mcm6 binding profiles described by Hayashi *et al.* (2007) at the genomic loci tested in Figure 4.

Supplementary Figure 5. Control for ChIP experiments with a constitutively expressed gene. Lysates from *orp1::orp1-5flag* (AD552) and *orp1::orp1-5flag NUMT10/11Δ* (AD566) cells were subjected to ChIP analysis using anti-FLAG antibobies. Total chromatin (TOT) or DNA associated with immunoprecipitates (IP) was amplified using primer sets that amplify a ??-bp fragment of *cdc2* gene. Position of the PCR product (black box) is shown on *cdc2* ORF.

Supplementary Figure 6. MtDNA fragments captured at extrachromosomal DSBs can act as DNA replication origins in the nucleus. A. When introduced into yeast cells, PCR fragments comprising either *S. pombe ura4* or *S. cerevisiae LEU2* gene are circularized through NHEJ and mtDNA fragments are recovered at high frequency at repair junctions (Decottignies 2005). The *ura4* gene was PCR-amplified as described previously (Decottignies 2005). The 2.2 kb-*LEU2* fragment was amplified by PCR on pREP3 plasmid (Maundrell 1993) using primers 5'-ATACCTAATATTATTGCCTTAT and 5'-GACTTAAACTCCATCAAATG and *Taq* polymerase (Takara, Berkeley, CA). B. Yeast cells were transformed with 1.5 µg of either pREP3 circular plasmid (*ARS1*, *LEU2*), PCR-amplified *LEU2* gene, pREP4 circular plasmid (*ARS1*, *ura4*) or PCR-amplified *ura4* gene.

Yeast colonies recovered after transformation were counted. Results from two yeast transformations are shown. C. Maintenance of either leu$^+$ or ura$^+$ phenotype was tested after growing cells in non-selective medium for 5 days, with daily dilutions. The graph gives the percentage of colonies that retained the phenotype. D. The presence of mtDNA fragments in *ura4* episomes was detected by sequencing of PCR-amplified repair junctions as described previously (Decottignies 2005). MtDNA inserts at repair junctions of *LEU2* circles were amplified with 5'-TGAACAAGGAAGTACAGGAC and 5'-TGGCTCAACGTGATAAGGAA and sequenced with 5'-CATTAATATTGACAAGGAGG. E. Growth rate of three ura$^+$ and five leu$^+$ yeast colonies recovered after transformation with PCR-amplified DNA. Population doublings were measured for ura$^+$ colonies containing (ura/mtDNA) or not (ura/empty) mtDNA fragments in the *ura4* episomes and for leu$^+$ colonies with either mtDNA-containing *LEU2* episomes (LEU/mtDNA) or integrated *LEU2* gene (LEU/integrated). *LEU2* episomes without mtDNA insert were not recovered.

Supplementary Figure 7. Mcm6 binding profiles described by Hayashi *et al.* (2007) at the genomic loci tested in Figure 6.