**Supplementary Table 1, collected public data**

**a,** Metadata of collected public Origin data.

**b,** Sample number of each cell type.

**c,** Metadata ofcollected public ORC ChIP-seq data.

**d**, Metadata of collected public MCM ChIP-seq data.

**e,** Metadata of collected public ORC and MCM ChIP-seq data in yeast.

**Supplementary Table 2, parameters of model**

Parameters of exponential model for NS-seq origins.

**Supplementary Table 3, union and shared ORC binding sites**

**a,** Union ORC ChIP-seq peaks, with coordinates and occupancy scores.

**b,** Shared ORC binding sites (defined as union ORC ChIP-seq peaks with an occupancy score >=2).

**Supplementary Table 4, highest confidence origins**

**a,** Coordinates ofunion ORC ChIP-seq binding sites with shared origins in 1kb region.

**b,** Coordinates ofshared origins with shared ORC binding sites in 1kb region.

**c,** Coordinates ofshared origins with union ORC binding sites in 1kb region.

**Supplementary Table 5, 74 most confident origins**

Coordinates of 74 origins that were reproducibly identified by multiple methods (shared origins, near shared ORC binding sites, overlapping with MCM3-7 binding sites and MCM2 binding sites).