Eukaryotic genomes replicate in defined patterns, with some loci replicating early in S phase and others replicating later. Replication timing correlates with transcription, chromatin modification, sub-nuclear localization and genome evolution, suggesting an intimate association between replication timing and other important aspects of chromosome metabolism. We have shown that origin timing is regulated by the number of MCM helicase complexes loaded at an origin, with origins that have more MCMs loaded having a higher probability of firing and thus an earlier average replication time. This model explains how stochastic origin firing can produce defined replication patterns, how replication timing patterns can arise without a hierarchical timing mechanism and why replication completion is robust, even in the absence of efficient origin firing or a replication completion checkpoint.