DNA replication begins at specific locations called replication origins, where helicase and polymerase act in concert to unwind and process the single DNA filaments. The sites of active DNA synthesis site are called replication forks. The density of initiation events is low when replication forks travel fast, and is high when forks travel slowly. Despite the potential involvement of epigenetic factors, transcriptional regulation and nucleotide availability, the causes of differences in replication times during DNA synthesis have not been established satisfactorily yet. Here we aimed at quantifying to which extent sequence properties contribute to the DNA replication time in budding yeast. We interpreted the movement of the replication machinery along the DNA template as a directed random walk, decomposing influences on DNA replication time into sequence-specific and sequence-independent components. Specifically, within the first element, we highlighted that, it is rather the sequence length than the sequence composition that influences the replication time. Furthermore, we show that the replication rate in budding yeast can be best approximated using only a single parameter, as we have recently proposed. Finally, we provide a spatial map of regions with sequence-independent alterations in replication rates within the genomic landscape of budding yeast.