Neural network and kinetic modelling of human genome replication reveal replication origin locations and strengths

Jean-Michel Arbona[1*], **Hadi Kabalane** [2,‡], **Arach Goldar**[3], **Olivier Hyrien**[4*], **Benjamin Audit**[2*]

[1]Laboratoire de Biologie et Modélisation de la Cellule, ENS de Lyon, Lyon, France; [2]ENS de Lyon, CNRS, Laboratoire de Physique, F-69342 Lyon, France; [3] Ibitec-S, CEA, France; [4]Institut de Biologie de l'Ecole Normale Supérieure (IBENS), Ecole Normale Supérieure, CNRS, INSERM, Université PSL, 46 rue d'Ulm, F-75005, Paris, France

***For correspondence:** jeanmichel.arbona@ens-lyon.fr (JMA); olivier.hyrien@bio.ens.psl.eu (OH); benjamin.audit@ens-lyon.fr (BA)

Present address: ‡Centre de Recherches en Cancérologie de Toulouse, Inserm, Université Paul Sabatier, CNRS, Toulouse, France.

Abstract

In human and other metazoans, the determinants of replication origin location and strength are still elusive. Origins are licensed in G1 phase and fired in S phase of the cell cycle, respectively. It is debated which of these two temporally separate steps determines origin efficiency. Experiments can independently profile mean replication timing (MRT) and replication fork directionality (RFD) genome-wide. Such profiles contain information on multiple origins' properties and on fork speed. Due to possible origin inactivation by passive replication, however, observed and intrinsic origin efficiencies can markedly differ. Thus, there is a need for methods to infer intrinsic from observed origin efficiency, which is context-dependent. Here, we show that MRT and RFD data are highly consistent with each other but contain information at different spatial frequencies. Using neural networks, we infer an origin licensing landscape that, when inserted in an appropriate simulation framework, jointly predicts MRT and RFD data with unprecedented precision. We furthermore uncover an analytical formula that predicts intrinsic from observed origin efficiency combined with MRT data. Comparison of inferred intrinsic origin efficiencies with experimental profiles of licensed origins (ORC, MCM) and actual initiation events (Bubble-seq, SNS-seq, OK-seq) show that intrinsic origin efficiency is not solely determined by licensing efficiency. Thus, human replication origin efficiency is set at both the origin licensing and firing steps.

Introduction

In eukaryotes, chromosome replication starts at multiple sites referred to as replication origins (***DePamphilis and Bell, 2010***). Origins are licensed for replication during the G1 phase of the cell cycle, when the origin recognition complex (ORC) loads the MCM2-7 replicative helicase in an inactive, double hexameric ring form (MCM DH), around origin DNA (***Evrin et al., 2009***; ***Remus et al., 2009***; ***Miller et al., 2019***; ***Schmidt and Bleichert, 2020***). This symmetric configuration prepares the helicases to initiate bidirectional replication upon activation. Origin activation (or firing) can take place at different times through S phase, by binding of multiple firing factors that trigger origin DNA unwinding and convert the inactive MCM DH into two active Cdc45/MCM/GINS helicases that

each encircles and translocates 3′-to-5′ along a single DNA strand (***Douglas et al., 2018***). Only a fraction of MCM DHs lead to productive initiation events, while the rest is inactivated by passing replication forks originating from other origins. This origin passivation mechanism (***Arbona et al., 2018***) cooperates with MCM2-7 loading restriction to G1 phase to prevent rereplication in a single cell cycle (***Siddiqui et al., 2013***).

Several experimental techniques allow to monitor origin licensing and firing as well as replication progression during S phase. Origin licensing can be monitored by experimental detection of ORC and MCM proteins, whose profiles are highly though not perfectly concordant (***Kirstein et al., 2021***; ***Miotto et al., 2016***; ***Foss et al., 2021***) . In contrast to these potential origin profiles, actual initiation events can be monitored by sequencing purified replication initiation intermediates, such as short nascent DNA strands (SNS-Seq; ***Picard et al.*** (***2014***)) or bubble-containing restriction fragments (Bubble-Seq; ***Mesner et al.*** (***2013***)). These two methods are only weakly concordant (***Hyrien, 2015***; ***Hulke et al., 2020***). Other methods monitor replication progression along the genome. Mean replication timing (MRT) profiles have been computed by sequencing newly replicated DNA from sorted cells at different stages of S phase (Repli-seq; ***Chen et al.*** (***2010***); ***Hansen et al.*** (***2010***); ***Zhao et al.*** (***2020***)) or by determining DNA copy number from proliferating cells (***Koren et al., 2014***). Peaks of early MRT must contain origins, but low resolution (50-100 kb; ***Chen et al.*** (***2010***); ***Hansen et al.*** (***2010***)) has long precluded precise origin mapping from human MRT profiles. Replication fork directionality (RFD) profiles, obtained by strand-oriented sequencing of purified Okazaki fragments (OK-seq) were more resolutive (< 5 kb) (***Petryk et al., 2016***; ***Wu et al., 2018***). RFD profiles revealed that: (i) each cell line contains 5,000 - 10,000 broad (10-100 kb) initiation zones (IZs), characterised by a left-to-right shift in RFD; (ii) IZs often but not always flank active genes; (iii) termination events occur in broad zones (TZs), characterized by a right-to-left RFD shift; (iv) TZs can directly follow IZs or can be separated from IZs by extended regions of unidirectional replication that lack initiation and termination events; (v) large randomly replicating regions, characterized by extended segments of null RFD, are observed in silent heterochromatin. OK-seq IZs were confirmed genome-wide by EdUseq-HU (***Tubbs et al., 2018***), high-resolution Repli-Seq (***Zhao et al., 2020***) and Optical Replication Mapping (***Wang et al., 2021***). Importantly, initiation events may additionally occur outside IZs, but in a too dispersed manner to be directly detected in cell population profiles. Recent single-molecule and OK-seq analyses of the yeast genome (***Müller et al., 2019***; ***Hennion et al., 2020***) and of two model chicken loci (***Blin et al., 2021***) provided direct evidence for dispersed initiation between efficient IZs in these two systems.

IZs can be shared between cell types or specific to a cell type, suggesting epigenetic regulation. They are enriched in DNAse I hypersensitive sites (HSSs) and histone modifications or variants such as H3K4me1, H3K27ac and H2A.Z, that usually mark active transcriptional regulatory elements (***Petryk et al., 2016***; ***Wu et al., 2018***; ***Petryk et al., 2018***). H2A.Z was proposed to facilitate origin licensing and firing by recruiting SUV420H1, which promotes H4K20me2 deposition, in turn facilitating ORC binding (***Long et al., 2020***). Furthermore, binding sites for the firing factor MTBP were found to colocalize with H3K4me1, H3K27ac, H2A.Z, and other active chromatin marks (***Kumagai and Dunphy, 2020***).

What mechanisms could regulate origin firing? Modeling studies showed that a probabilistic interaction of potential origins with rate-limiting firing factors, engaged with forks and recycled at termination events, can predict the time-dependent profiles of origin firing rate and fork density universally observed in eukaryotes (***Arbona et al., 2018***; ***Goldar et al., 2008***, ***2009***). Experimental studies indeed suggested that rate-limiting activators regulate replication kinetics in yeast (***Mantiero et al., 2011***; ***Tanaka et al., 2011***) and metazoans (***Wong et al., 2011***; ***Collart et al., 2013***). Thus, a simple model for replication regulation is that potential origins fire at different mean times because of their different affinities for limiting factors (***Douglas and Diffley, 2012***). Alternatively, potential origins may all have the same affinity for firing factors but their variable density along the genome may determine MRT (***Yang et al., 2010***; ***Das et al., 2015***). We refer to these two distinct models as the origin affinity model and the origin density model, respectively.

Modelling studies indicate that the reproducible spatial structure of genomic replication profiles can emerge from stochastic firing of individual origins (***Bechhoefer and Rhind, 2012***; ***Gindin et al., 2014***). The latter built a kinetic model in which the time-dependent probability of initiation at a yet unreplicated site was the product of the time-dependent availability of a limiting factor by the time-independent, local value of a genomic "initiation probability landscape" (IPLS). Of the various genomic and epigenomic profiles used as estimates of IPLS, DNase I HSS profiles produced the best match with experimental MRT profiles (Pearson correlation between simulated and experimental MRT of 0.865). Importantly, the same IPLSs did not produce realistic MRT profiles in models that did not include competition for limiting fork-associating factors (***Gindin et al., 2014***). Since this model did not explicitly separate origin licensing and firing, however, it remained unclear whether the IPLS reflected potential origin density, or affinity, or both.

Current experimental evidence has not yet clearly distinguished between the origin affinity and origin density models. ORC and MCM abundance profiles, which presumably reflect potential origin density, are well correlated with DNase I HSS and early MRT (***Miotto et al., 2016***; ***Foss et al., 2021***; ***Kirstein et al., 2021***). Furthermore, ORC- or MCM-based IPLSs produced realistic MRT profiles in Gindin-like simulations (***Miotto et al., 2016***; ***Foss et al., 2021***), which supports the origin density model. However, our comparison of ORC, MCM and RFD profiles of the Raji cell line showed that when confounding parameters such as MRT and transcription status are controlled, ORC and MCM densities are not predictive of IZs (***Kirstein et al., 2021***). This suggested that potential origins may be more widespread than initiation sites but have different firing efficiencies, perhaps due to specific MCM or histone modifications affecting their affinities for firing factors, in line with the origin affinity model.

In the present work, we harness our previous kinetic model of DNA replication (***Arbona et al., 2018***) to predict MRT and RFD profiles. Discrete, localized potential origins (MCM DHs), chosen from an arbitrary potential origin density landscape (PODLS), are activated in a stochastic manner by interaction with limiting firing factors that engage with forks and are released at termination (Fig. 1). As each potential origin is given the same probability to fire, the non-uniformity of the obtained replication profiles only comes from the non-uniformity of the PODLS (origin density model).

Our aim being to extract the PODLS that best predicts available MRT and RFD data, we first compare their information contents. We show a remarkable conformity of MRT and RFD data to a simple mathematical equation that links both profiles. Extending the work by Gindin et al. (***Gindin et al., 2014***), we then ask whether the correlation of DNase I HSS with origin activation seen at MRT resolution (50-100 kb) still holds true at RFD resolution (< 5 kb). We demonstrate that MRT and RFD data provide distinct information at different scales.

We then train a neural network on simulated MRT and RFD profiles to infer a PODLS that jointly predicts experimental MRT and RFD almost exactly, surpassing any PODLS based on DNase I HSS, ORC, MCM, Bubble-seq or SNS-seq profiles. In our model, each potential origin has the same intrinsic probability of activation per unit time.The optimized PODLS, which reflects intrinsic origin efficiencies, can be directly compared with ORC and MCM profiles. To compare the PODLS to actual initiation events as monitored by SNS-seq, bubble-seq or OK-seq, we establish a novel mathematical expression that relates observed and intrinsic origin efficiencies to MRT and therefore allows us to take origin passivation effects into account. The results show that the firing probability of potential origins is not uniform in time and space. Our results therefore support a combined origin density and affinity model and provide a basis to investigate the distinct genetic and epigenetic determinants of origin licensing and firing.

Results

Information complementarity between MRT and RFD profiles

Previous modelling works (***Gindin et al., 2014***; ***Löb et al., 2016***) compared simulated and experimental human MRT profiles to constrain their parameter values. RFD profiles have now been

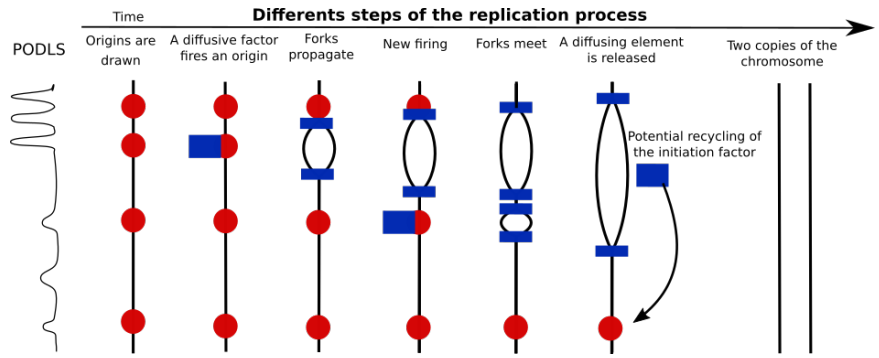

Figure 1. Modeling DNA replication. Given a PODLS derived from a specific genomic feature (e.g. a DNase I HSS profile), a fixed number of localized potential origins is drawn (red circles). Limiting firing factors (blue rectangles) activate origins in a probabilistic manner and engage with each pair of newly created forks, which propagate at velocity *v*. Engaged factors can no longer activate origins. Unfired origins are passivated when they are reached by a passing fork. Merging of two forks emanating from adjacent origins results in a replication termination event and the release of one firing factor which becomes available again for origin activation. MRT and RFD are then computed from the average of 200 simulations. See Materials and Methods.

established for many human cell lines (***Petryk et al., 2016***; ***Wu et al., 2018***), providing us with an alternative comparison point. It is thus of interest to compare the information content of RFD and MRT profiles. Within the hypothesis of a constant fork speed v, MRT and RFD profiles are equivalent as they are analytically related to one another by (***Guilbaud et al., 2011***; ***Baker et al., 2012***; ***Audit et al., 2012***):

$$RFD(x) = v\frac{d}{dx}MRT(x). \tag{1}$$

Here $MRT(x)$ is the mean replication time after entry in S-phase of bin x and is expressed in time units. Note that $MRT(x)$ as measured by Repli-seq experiments is the average global replicated fraction at the moments locus x is replicated, and thus has a value between 0 and 1. Assuming a linear relation between replication fraction and S phase duration, Repli-seq experiment can be converted into time by multiplication by an estimate of S-phase duration T_S. Equation (1) can be checked using experimental data. However, the derivative of a noisy profile is ill-defined and numerically unstable to compute. To avoid computing the MRT derivative, Eq. (1) can be integrated at point x over a length l leading to:

$$\Delta_l MRT(x) = MRT(x+l) - MRT(x) = \frac{1}{v}\int_x^{x+l} RFD(y)\,dy = \frac{l}{v}\langle RFD\rangle_x^{x+l}\,, \tag{2}$$

where $\langle\cdot\rangle_x^{x+l}$ stands for the average value over $[x, x+l]$. Equation (2) predicts that the MRT change across an interval is proportional to the average RFD over that interval. Using reported Repli-seq MRT (***Hansen et al., 2010***) and OK-seq RFD (***Wu et al., 2018***) profiles for the K562 cell line, Eq. (2) was very convincingly verified over scales ranging from 10 kb to 5 Mb, with a genome-wide correlation coefficient up to 0.94 at scale 1.5 Mb, and a proportionality coefficient ranging from $v = 1.2$ kb.min^{-1} to $v = 1.6$ kb.min^{-1}, assuming $T_S = 12$ hours (***Weis, 2012***). This is illustrated on Fig. 2 for scale 50 kb and Fig. S1 for other scales. Therefore, although OK-seq and Repli-seq experiments are complex and have been performed by different laboratories, they are highly consistent with each other, on a wide range of scales, within the hypothesis of a constant fork speed.

In their modeling work, Gindin et al (***Gindin et al., 2014***) found that of all epigenetic features tested, IPLSs based on DNase I HSS profiles produced the best match between simulated and experimental MRT profiles (Pearson correlation coefficient, PCC = 0.865). We performed similar simulations, using our model (Fig. 1) as detailed in Materials and Methods. Using a PODLS based on the K562 DNase I HSS profile, we drew a fixed number of potential origins and simulated a bimolecular reaction with firing factors, whose number increased from the start of S phase and

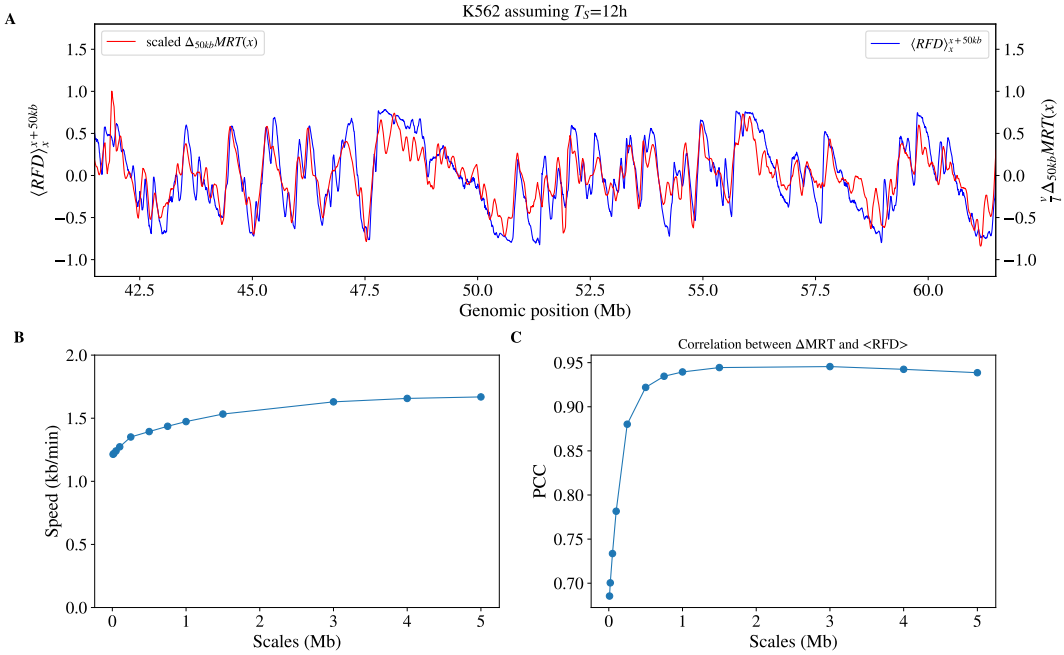

Figure 2. (A) Comparison, for a 20 Mb region of chromosome 1, of the K562 RFD profile averaged over 50 kb windows (blue; $\langle RFD \rangle_x^{x+50kb}$) with K562 MRT changes across 50 kb intervals ($\Delta_{50kb} MRT(x)$), following Eq. (2) with $v = 1.24$ kb.min^{-1} assuming $T_S = 12$ hour. (B) Replication speed v derived from the proportionality coefficient (Eq. (2)) and (C) Pearson correlation coefficient (PCC) between the $\Delta_l MRT(x)$ and $\langle RFD \rangle_x^{x+l}$ profiles at the indicated scales l.

plateaued after ≈ 1 h (***Arbona et al., 2018***; ***Löb et al., 2016***). Productive initiation events trap the factors at the forks and termination events release them, making them available for new initiation events. After grid search optimisation of the number of potential origins and the number of firing factors, we observed a high correlation (PCC = 0.88), similar to Gindin et al (***Gindin et al.*** (***2014***); 0.865), between simulated and experimental MRT profiles, and a lower correlation between simulated and experimental RFD profiles (PCC = 0.70) (Fig. 3). Reasoning that addition of dispersed, random initiation to the PODLS (see Methods) might improve the results, we extended the grid search for this parameter and obtained an optimal correlation for RFD at PCC = 0.75 for 5% of random initiation events, while maintaining the same correlation with MRT (PCC = 0.88) (Fig. 3). These observations confirm that MRT and RFD data are consistent with each other and suggest that RFD data are furthermore informative about random initiation.

Despite the theoretical equivalence of MRT and RFD profiles (Eqs. (1) and (2)), their correlation (Fig. 2) decreased at small scales, due to the low (100 kb) resolution of MRT profiles. It also decreased, to a lower extent, at large scales, because integrating RFD sums up its experimental noise. In fact, RFD provides better origin position information, while MRT better reflects integrated origin activity over broad regions. This is illustrated by the following numerical experiments.

When the positions of DNase I HSS were resampled within each 200 kb window prior to constructing the PODLS, the simulated MRT profile retained a high correlation with the experimental MRT (PCC = 0.87; Fig. 4A, green curve), while the correlation between simulated and experimental RFD profiles dropped (PCC = 0.61; Fig. 4B, green curve). The exact positions of DNase I HSS were critical to reproduce RFD profiles upward jump positions, in line with the observed enrichment of OK-seq IZs with DNase I HSS (***Petryk et al., 2016***). On the other hand, the tolerance of MRT profiles to DNase I HSS resampling suggested that MRT is not sensitive to precise origin positions within a sampling window.

Although MRT can be computed by integrating RFD (Eq. (2)), this cumulates the experimen-

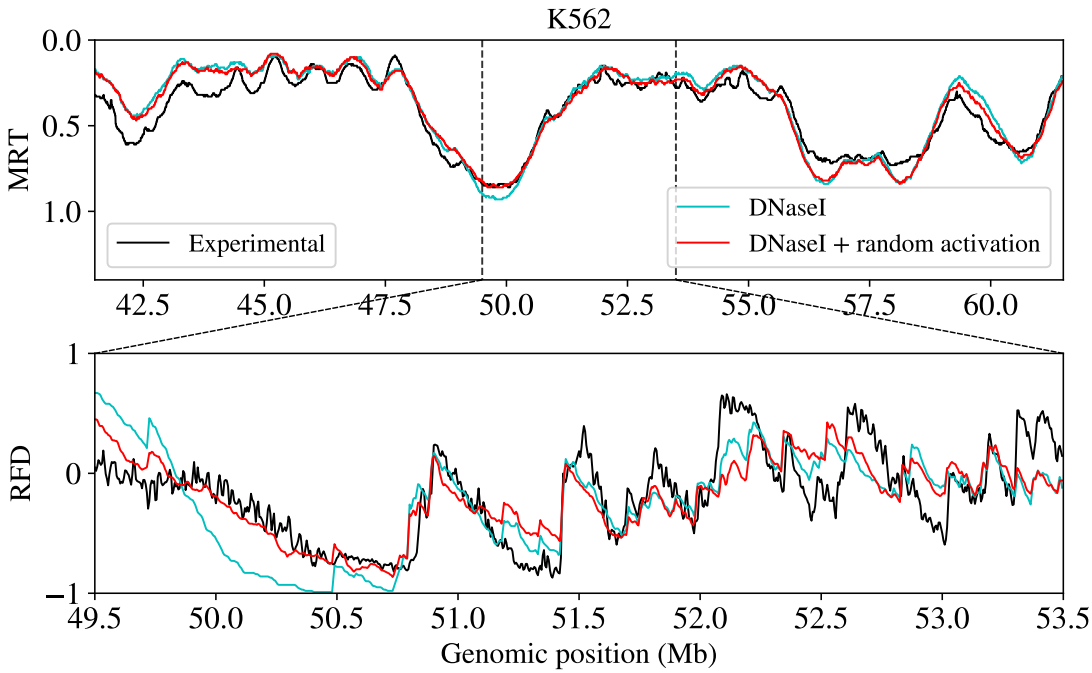

Figure 3. Comparison of experimental (black) and simulated (red, light blue) MRT profiles for a ≈ 20 Mb region of chromosome 1 (top) and RFD profiles for a 4 Mb region centered in the middle of the 20 Mb region (bottom) using a PODLS based on DNAse I HSS, with (red) or without (light blue) the addition of 5% of random initiation events. All the parameters of the replication model except the percent of random initiation are the same.

tal noise, blurring large scale features that MRT data more directly capture. The lesser sensitivity of RFD than MRT to large scale patterns was revealed in a second numerical experiment where we modulated the DNase I HSS signal amplitude with a slow varying function of large period ($P = 25$ Mb) before constructing the PODLS. In that setting, the correlation between simulated and experimental profiles decreased markedly for MRT (PCC = 0.72) but only slightly for RFD (PCC = 0.72) (Fig. 4AC, blue curves). Therefore, MRT is constrained by the collective action of multiple origins, so that the sum of neighbouring DNase I HSS signals is critical, while their exact positions per 200 kb windows are not (Fig. 4A). RFD is instead sensitive to the location rather than the magnitude of these signals. The influence of a single origin on RFD rapidly decreases with distance, due to the influence of intervening origins.

To summarize, incorporating RFD as a target for simulations likely allows to test origin positioning at much higher resolution than was achieved with MRT (***Gindin et al., 2014***; ***Löb et al., 2016***). Deriving RFD profile from MRT data (Eq. (1)) by numerical derivative would produce low resolution RFD profiles with amplified noise, while determining MRT profile from the summation of RFD data (Eq. (2)) would produce MRT profiles with unreliable MRT changes over large distances. Experimental MRT and RFD profiles thus provide complementary information. We use both in the following analyses.

Learning a PODLS that accurately predicts both experimental MRT and RFD data.

Having shown that experimental MRT and RFD profiles are consistent with each other over a wide range of scales at constant fork speed, we assessed to which extent they could be jointly explained by a single PODLS in our replication model. At 5 kb resolution, the PODLS correspond to ~ 575000 parameters which must be optimised. To achieve this, we designed an iterative method that progressively improves the PODLS (Fig. 5). It uses model simulations to train a neural network to predict the PODLS given the MRT and RFD profiles, i.e., to invert our replication model. We initialised the method by setting non zero values of the PODLS in regions with the highest RFD derivative (See Materials and Methods) i.e. in the strongly ascending segments of the RFD profile corresponding

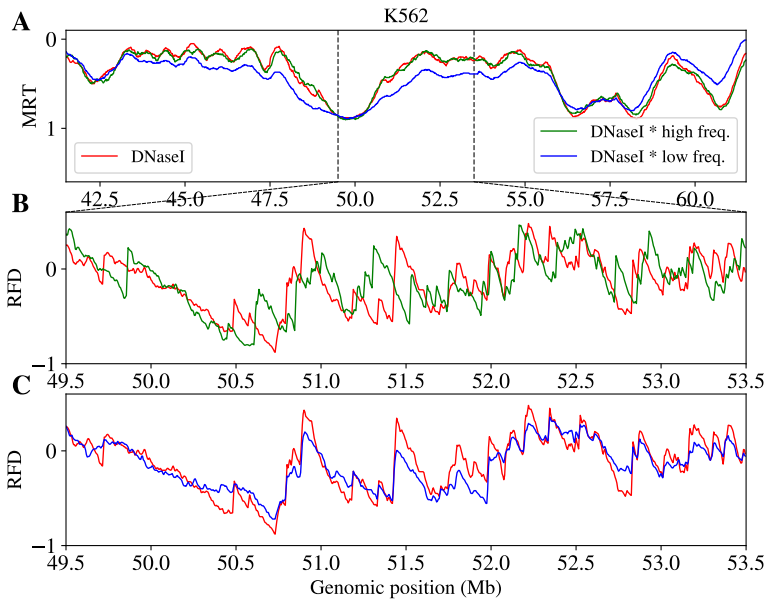

Figure 4. Comparison of simulated MRT (A) and RFD (B,C) profiles corresponding to different PODLS profiles all other model parameters being kept constant. PODLS were derived from (i) experimental DNase I HSS data (red), (ii) the DNase I HSS data after random shuffling of HS sites position within all 200 kb non-overlapping windows (green), and (iii) DNase I HSS data after modulating their amplitude over a period $P = 25$ Mb (we divided the amplitude signal by $1.1 + \cos(2x/P)$) (blue). DNase I HS site position shuffling in 200 kb windows does not influence simulated MRT profiles but alters RFD profiles significantly, as both red and green signals overlap in (A) but present clear differences in (B). Low-frequency modulation of HS site amplitude changes the relative strength of replication timing domains thus altering the MRT profiles, but do not influence the main features of the RFD profile as red and blue signal overlap in (C) but present clear differences in (A).

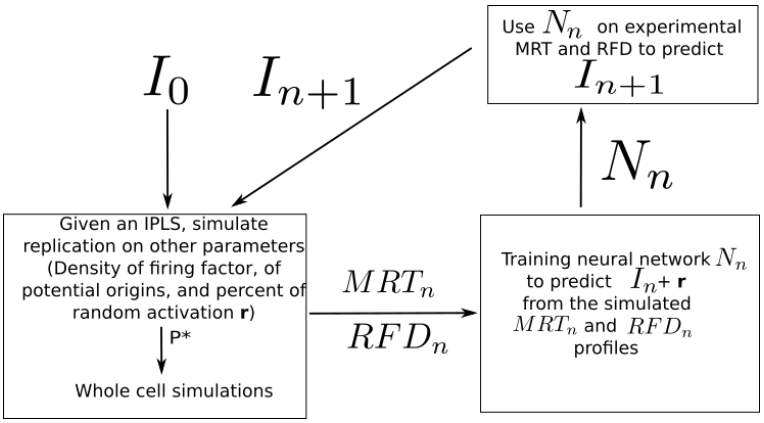

Figure 5. Schema of the iterative optimization procedure of the PODLS for simultaneous prediction of experimental MRT and RFD data. The starting PODLS I_0 may be a crude approximation of the target PODLS such as given by the peaks of RFD derivative, or the DNAse HSS profile, but not a random profile. We observed that the procedure does not improve the prediction quality after a small number of iterations (maximum of 4 in *S. cerevisiae*, Supplementary Table S1).

to the main initiation zones previously described (***Petryk et al., 2016***). This crude approximation of the PODLS is named I_0. Then a grid search optimisation on the other parameters $P = (\rho_F, d_{PO}, r)$ of the replication model (See Material and methods) was performed. To limit computation time, this optimisation was performed over chromosome 2 only and resulted in a set of optimal parameters P_0 that maximized the sum of the Pearson correlation coefficients between experimental and simulated MRT and RFD profiles. Then we simulated whole genome replication using I_0 and P_0 to generate MRT_0 and RFD_0 and trained a neural network (See Materials and Methods) to predict

$I_0 + r_0$ from MRT_0 and RFD_0, where r_0 is the optimal fraction of random initiation events given I_0. We then used this network to predict I_1 from experimental MRT and RFD, reasoning that I_1 should produce a more accurate prediction of MRT and RFD than I_0. Another grid search optimisation on P, given I_1, was performed to obtain P_1 and given P_1 and I_1 we simulated MRT_1 and RFD_1. Then a new neural network was trained to predict $I_1 + r_1$ and was then applied to experimental MRT and RFD to obtain I_2. These steps were iterated four times, because the correlations between experimental MRT and RFD profiles and their simulated estimates never improved with further iterations.

We first applied the procedure to K562 data. The sequences of joint correlations between experimental MRT and RFD and simulated profiles $(MRT_0, \cdot, MRT_4)$ and $(RFD_0, \cdot, RFD_4)$ were (0.81, 0.93 ,0.98 ,0.98, 0.98) and (0.79, 0.89, 0.91, 0.92, 0.92), respectively. The highest joint correlation was practically reached at the third iteration and we refer to the maximum initiation potential as I_M. We ran a grid search on the whole genome given I_M, this yielded unchanged correlation for both MRT and RFD, suggesting that parameter optimization on chromosome 2 only was not a limitation. We also tried using K562 DNase I HSS as the I_0 of the method. The I_0 profiles obtained from DNase I HSS or RFD derivative peaks presented some differences (PCC=0.76), but led to very similar I_M profiles (PCC=0.94; Supplementary Figure S2) and produced identical high correlations between simulated and experimental MRT (0.98) and RFD (0.91) profiles. In contrast, we were unable to ameliorate the PODLS starting from a random I_0 (MRT and RFD correlations were 0.67 and 0.84, respectively, using I_2, but decreased at step 3). Therefore, our optimization method required some initial information about the PODLS, but converged to nearly the same optimized PODLS from heterogeneous starting points. This is not a constraint as an adequate initialisation can be obtained from experimental RFD data.

To test the robustness of this inversion procedure, it was applied to replication profiles of GM06990 and HeLa human cell lines and yeast *Saccharomyces cerevisiae*. It systematically resulted in high PCC between experimental and simulated profiles at the third or forth iteration: for MRT 0.99 with GM06990; 0.99 with HeLa and 0.96 with *S. cerevisiae*; for RFD 0.91 with GM ; 0.84 with HeLa RFD and 0.91 with *S. cerevisiae* (see Supplementary Table S1 for the results of the different iterations). Figure 6 illustrates the striking consistency between simulation and experiments obtained for the three different human cell lines. Correlation for HeLa RFD profile was less than for other cell lines. Indeed HeLa is more challenging as it has about twice as many IZs as K562 and GM06990 (***Petryk et al., 2016***; ***Wu et al., 2018***), but regions of poor RFD prediction also showed inconsistencies between experimental MRT and RFD probably due to the use of different Hela cell lines in different laboratories (Fig. 6).

Sensitivity of MRT and RFD with respect to model parameters.

For K562, we performed simulations of whole genome replication to assess the sensitivity of MRT and RFD and S-phase duration to: (i) the density of firing factors ρ_F (number per Mb); (ii) the mean distance between potential origins d_{PO}; (iii) the proportion of random initiation r; and (iv) fork speed v. Working around the reference set of parameters ($\rho_F = \rho_F^* = 0.56$ Mb^{-1}; $r = r^* = 0\%$, $d_{PO} = 20$ kb, $v = 1.5$ kb.min^{-1}), we let one of the parameter vary (Fig. 7). ρ_F^* and r^* are the optimal values obtained at the end of the iterative procedure, without the final grid search exploration on the whole genome as it did not improve the correlations; the values for d_{PO} and v are reasonable choices justified below.

The correlations of simulated with experimental MRT and RFD profiles showed a clear maximum at $\rho_F = \rho_F^* = 0.56$ Mb^{-1}, more pronounced for RFD (Fig. 7A,B). This number implied that the maximum density of forks was ~ 1 fork per Mb, or $\sim 6,000$ forks per diploid nucleus, at any time in S phase. This was in reasonable agreement with upper estimates of the maximal density of limiting factor Cdc45 (3.5 molecules per Mb) in mammalian cells (***Wong et al., 2011***), considering that 2 molecules of Cdc45, but only one limiting factor in our model, are required to activate two diverging forks.

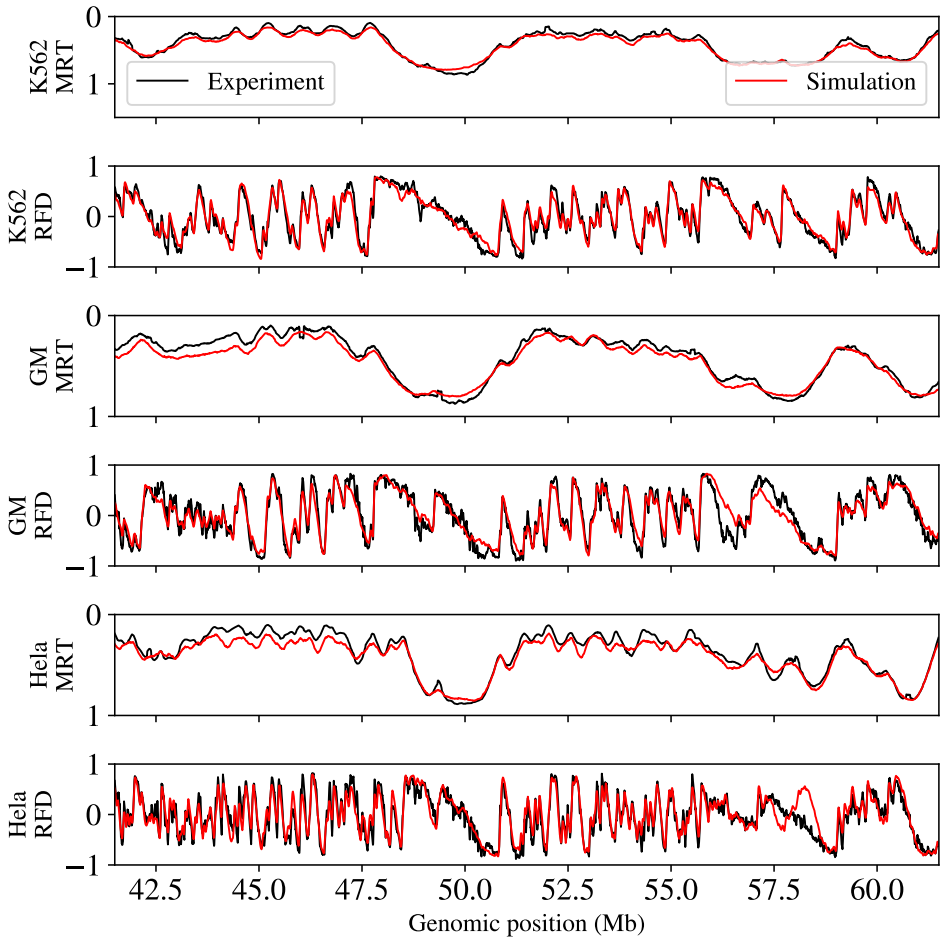

Figure 6. Comparison for the three indicated cell lines of experimental MRT and RFD (black) and simulated MRT_M and RFD_M profiles (red). A representative 20 Mb segment of chromosome 1 is shown. Note that the HeLa region of strong discrepancy between experimental and simulated profiles (between 57.7 and 58 Mb) correspond to a region where experimental MRT and RFD are not coherent: there is no increasing RFD region corresponding to the early timing peak at position 57.6 Mb.

The optimal value for the random initiation r^* = 0% was confirmed as increasing r up to 20% slightly decreased both MRT and RFD correlations (Fig. 7G,H). The value r = 0% means that random initiation was correctly learned by the iterative method and did not require further external addition. In order to further apprehend the requirement of a minimal amount of random initiation, we performed the following experiments: (i) the random initiation was treated as an external parameter in the iterative PODLS optimisation procedure i.e., it was excluded from the training, the neural network was trained to output I_n instead of $I_n + r$; in that case the correlation with MRT and RFD was maximal for 5% of added random initiation (Fig. 7G,H); (ii) setting to zero the lowest I_M bin values totalling 5% of potential origins (≈ 53% of the bins), significantly decreased the correlation with RFD data to PCC = 0.82 : without these random initiations, the simulations failed to capture the RFD in large late replicating regions whose replication time was also clearly delayed (Supplementary Figure S5). The extended null RFD segments observed in these regions are indeed consistent with random initiation.

Varying d_{PO} and v over a large range of values only weakly changed the correlation of experimental and simulated MRT and RFD (Fig. 7D,E,J,K), which justifies why they were left out of the parameter optimization procedure. We decided to set v to 1.5 kb.min^{-1} and d_{PO} to 20 kb, for the

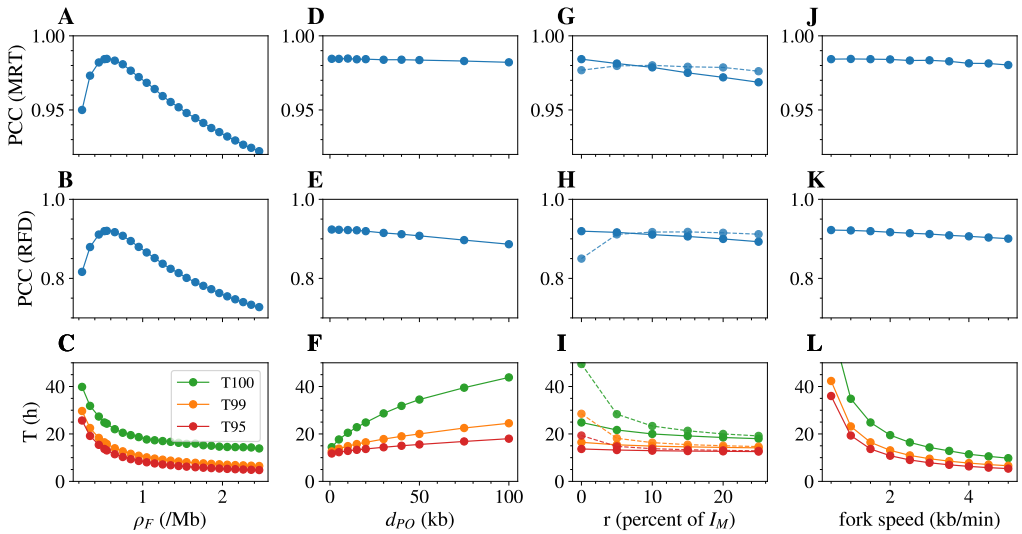

Figure 7. Effect of single parameter variation on measurable targets in K562, other parameters being kept as their value in the reference parameter set. Effect of the density of firing factors ρ_F (A,B,C); the average distance between potential origins d_{PO} (D,E,F); the proportion of random initiation r (G,H,I); the fork speed v (J,K,L), on the Pearson Correlation Coefficient (PCC) between simulated and experimental MRT (A,D,G,J) and RFD (B,E,H,K) profiles, and on the median of T95 (red), T99 (orange) and T100 (green), the times required to replicate 95% 99% and 100% of the genome (C,F,I,L). In (G,H,I) dots joined by dashed lines correspond to the effect of the additional random activation r when using the PODLS profile determined using a neural network where r is treated as an outside parameter (the network is trained on I_n and not on $I_n + r$), see main text.

following reasons. First, single molecule studies of DNA replication in human cells have repeatedly reported replication fork speeds of 1-3 kb min^{-1} and distances between activated origins of 50-200 kb (***Conti et al., 2007***; ***Técher et al., 2013***). Second, MCM depletion experiments indicated a 5-10 fold excess of loaded MCM DHs over actual initiation events (***Ibarra et al., 2008***). Third, biochemical quantitation suggested that chromatin is loaded with 1 MCM DH per 20-40 kb at S phase entry (***Burkhart et al., 1995***; ***Wong et al., 2011***). Taken together, these figures are reasonably consistent with each other and with a d_{PO} of 20 kb. Similar results were robustly observed using GM06990 and Hela replication data, with maximum PCC values observed for ρ_F^* of 0.56 and 0.91 Mb^{-1}, respectively (Supplementary Figures S6 and S7).

In summary, MRT and RFD data, being highly consistent with each other, are jointly and precisely explained by a simple model featuring a unique PODLS input and values for d_{PO}, v and ρ_F in agreement with the current knowledge. A small amount $\sim 5\%$ of random initiation was necessary to fully account for experimental data, suggesting that most if not all of the genome has a minimal replication initiation potential.

Dependence of replication kinetics on model parameters.

We first analyzed K562 S-phase duration T_S using the median of the times to replicate 95%, 99% and 100% of the genome, T95, T99 and T100 respectively. As expected, each of these three times decreased with the density of firing factors ρ_F and the fork speed v (Fig. 7C,L) as we are in a regime of strong affinity between firing factors and potential origins (large k_{on}) so that $T_S \approx \frac{1}{2*v*\rho_F}$ (***Arbona et al., 2018***). The model predicted much larger differences between T100 and T99, than between T99 and T95, consistent with the latest replicated regions being the most devoid of potential origins. Indeed, for a genome-averaged distance $d_{PO} = 20$ kb, the predicted distance between potential origins increased from a short 2 kb value in MRT < 0.15 regions to 380 kb in MRT > 0.85 regions (Supplementary Figure S3). This observation also explained that (i) the cell-to-cell variability of T95 or T99 (~ 10 min) was much smaller than that of T100 (hours) (Supplementary Figure S4); (ii) increasing d_{PO} increased T100 to a much greater extent than T95 or T99 (Fig. 7F); and (iii) adding

random initiation decreased T100 to a much greater extent than T99 or T95 (Fig. 7I). The latter effect was maximal when random initiation was an outside parameter, and decreased with increasing r, consistent with the latest replicated regions being fully devoid of origins when r = 0 (Fig. 7I). Consistenly, many late replicating regions show flat MRT and null RFD profiles revealing random initiation (***Petryk et al., 2016***), but the even later-replicating, common chromosomal fragile sites (CFSs), show an origin paucity that explains their fragility (***Letessier et al., 2011***).

Experimentally reported S phase lengths were closer to T95 than T100. Using the reference set of parameters ($\rho_F = \rho_F^*$; $r = r^* = 0\%$, $d_{PO} = 20$ kb, $v = 1.5$ kb.min^{-1}), the predicted T95 was 8.6 h for HeLa (experimental estimate 8.8 h; ***Hahn et al.*** (***2009***)), 13 h in K562 (experimental estimate 12 h; ***Weis*** (***2012***)) and, taking account a fork speed of $v = 2.0$ kb.min^{-1} in the closely related JEFF cell line (***Técher et al., 2013***), 10.7 h for GM06990 (experimental estimate 10 h; ***Guilbaud et al.*** (***2011***)). One probable explanation is that experimental detection of S phase markers misses the earliest and latest S phase cells, when the replication rate is the lowest. Indeed, very late replication of specific sequences was reported to linger during what is termed the G2 phase of the cell cycle (***Widrow et al., 1998***), and S phase length variations around the mean ranged from minutes to hours depending on cell lines and detection methods (***Pereira et al., 2017***; ***Weber et al., 2014***). Within the parameter range we explored, T95 variations (~10 min) were smaller than for T100 (hours) (Fig. S4). Experiments may therefore have underestimated the exact duration of S phase. Another possibility is that we underestimated *r* or *v*, since increasing either parameter above its reference value efficiently reduced T100 without much compromising the correlations of simulated and experimental MRT and RFD (Fig. 7GHI, Fig. S6, Fig. S7). In our simulations, the faster replication of HeLa cells was explained by a larger number of firing factors than in GM06990 (2.0-fold) and K562 (1.9-fold). Thus, the optimisation procedure selected a density of firing factors ρ_F that gave relative S phase durations consistent with experimental measurements using sensible values for d_{PO} and v.

The origin firing rate per length of unreplicated DNA, $I(t)$, was previously reported to follow a universal bell-shaped curve in eukaryotes (***Goldar et al., 2009***; ***Arbona et al., 2018***) . As expected from the choice of the k_{on} value, the simulations produced the expected shape for the three cell lines with a maximum of $I(t)$, I_{max} between 0.01 and 0.02 Mb^{-1}.min^{-1}, in reasonable agreement with a crude estimate of 0.03-0.3 Mb^{-1}.min^{-1} from low-resolution MRT data (Supplementary Figure S8) (***Goldar et al., 2009***). Finally, we measured in K562 the dispersion of replication times (RT) of each locus as a function of its MRT. A recent high-resolution Repli-Seq study (***Zhao et al., 2020***) reported that RT variability, estimated as the width between the first and the third quartiles of RT distribution, increased from early to mid S phase and decreased thereafter. For most regions the RT variability was in the 1.25–2.5 h range. Our simulations in K562 produced a similar behavior of RT variability but over a wider range, from ~ 0.5 h in early or late S phase to 3 h in mid S phase (Supplementary Figure S10).

In summary, the kinetic parameters of S phase predicted by our stochastic model were (i) consistent with the reported time-dependencies of the firing rate $I(t)$ and the RT variability and (ii) predictive of relative S phase durations. However, RT variablity was broader than reported, suggesting lower stochasticity of *in vivo* replication kinetics than in our model, in which origins fire strictly independently of each other.

Direct estimation of the PODLS from experimental data

Origin firing can be prevented by context-dependent passivation from nearby origins. An important concept in DNA replication modeling is therefore the distinction between observed origin efficiency (OE) and intrinsic origin efficiency (IE). OE is the fraction of origin copies that fire in a population, whereas IE is the efficiency that would be observed, in the absence of passivation, over the entire length of S phase.

In our model, potential origins are MCM DHs which all have the same elementary probability of firing. For one bin x with $n(x)$ MCM DHs, given the reaction rate k_{on} and the number of free firing

factor $F_{free}(t)$, the probability for firing to take place during an elementary time dt is:

$$k_{on} n(x) F_{free}(t) dt \ . \tag{3}$$

If we consider that $F_{free}(t)$ is constant and equal to $\left[F_{free}\right]$ for a large part of the S phase (Supplementary Figure S11), the probability $A_x(t)$ for bin x to have been activated at time t without considering passivation is given by:

$$A_x(t) = 1 - e^{-k_{on} n(x) [F_{free}] t} \ . \tag{4}$$

Hence, with an infinite time to fire, $A_x(t)$ converges to one unless the locus is devoid of any potential origins ($n(x) = 0$). The observed firing efficiency OE is smaller than one due to passivation. Reasoning that replication of a small bin occurs much more often by passivation from nearby origins than by internal initiation (for 5 kb bins, $\Delta RFD/2$ which is an approximation of OE as discussed later has a maximum value of 0.17), we can consider than the average passivation time of a bin is not very different from its MRT and thus $OE(x) = A_x(MRT(x))$ which leads to:

$$OE(x) = 1 - \mathrm{e}^{-k_{on} n(x) [F_{free}] MRT(x)} \ . \tag{5}$$

We first assessed the validity of this relationship in the set of 200 S-phase simulations using the optimized PODLS I_M and the reference set of model parameters in K562. $OE(x)$ and $MRT(x)$ were the averages of origin firing status and RT recorded in each simulation. The total number of MCM DHs over the genome being L/d_{PO} and as the I_M profile is normalised to 1, the average MCM DH density profile is $n(x) = I_M(x) * L/d_{PO}$ (MCM DH/5kb). Finally we used $\left[F_{free}\right] = 52$, the almost constant value observed for $MRT < 0.5$ in K562 simulations (Supplementary Figure S11). The two terms of Eq. (5) were computed. They showed a genome-wide Pearson correlation coefficient of 0.83 and a proportionality coefficient of 0.96. When focusing on the local maxima of ΔRFD ($\sim 10,000$ peaks in K562, Materials and methods), which correspond to IZs, the PCC raised to 0.9, and the proportionality coefficient to 0.98 (Supplementary Figure S12). These results indicate that our hypothesis that $OE(x) = A_x(MRT(x))$ is globally valid but applies even more precisely at IZs determined as ΔRFD local maxima. However, when exploring different values for k_{on} and d_{PO}, we noted that the PCC was stable, but the proportionality coefficient varied from 0.6 to 1.7, even if we replaced the assumed constant $[F_{free}]$ by its time-dependent value $F_{free}(t)$. This indicates that, for unclear reasons, the validity of Eq (5) is sensitive to the precise combination of origin density and reactivity parameters.

Generally speaking, the ΔRFD across a genomic segment is twice the difference between the density of initiation and termination events in the segment (***Audit et al., 2012***). Mammalian IZs are broad and may contain multiple MCM DHs. Termination events are nevertheless rare or absent within IZs (***Petryk et al., 2016***; ***Hamlin et al., 2010***; ***Blin et al., 2021***). Therefore, forks emanating from the first activated MCM DH must rapidly passivate nearby MCM DHs and one can estimate $OE(x) = \Delta RFD(x)/2$ in these loci. For example, the RFD will shift from -1 to +1 across a 100% efficient IZ, creating a jump of $\Delta RFD = 2$. We indeed found a PCC of 0.96 with a proportionality coefficient of 0.92 between $OE(x)$ and $\Delta RFD(x)/2$ at the 10,000 local maxima of ΔRFD in our K562 simulations (Fig S13). As a consequence, Eq. (5) linking $OE(x)$, $n(x)$ and $MRT(x)$ provides a link between $RFD(x)$, $n(x)$ and $MRT(x)$ in IZs suggesting a simple and direct way to estimate the PODLS ($\propto n(x)$) from MRT and RFD profiles:

$$n_e(x) = \frac{-\ln(1 - \Delta RFD(x)/2)}{k_{on} \left[F_{free}\right] MRT(x)} \ , \tag{6}$$

where $n_e(x)$ is the $n(x)$ profile estimated from the measurable parameters ΔRFD and MRT. Note that for small value $\Delta RFD(x)$ (for 5 kb bins, the maximum value of $\Delta RFD/2$ is 0.17), one can use a Taylor extension of $\ln$ to simplify Eq. (6) yielding:

$$n_e(x) \approx \frac{\Delta RFD(x)}{2k_{on} \left[F_{free}\right] MRT(x)} \ . \tag{7}$$

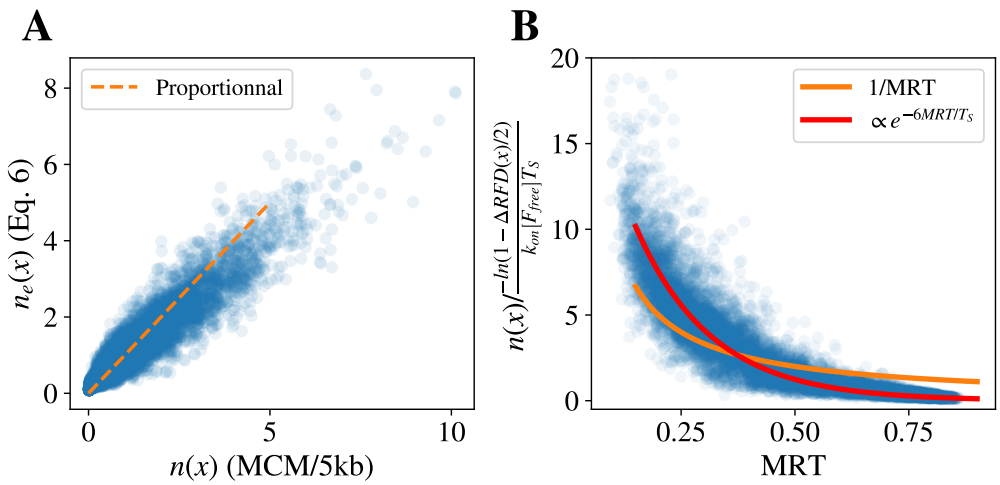

Figure 8. (A) Comparison of the average number $n(x)$ of MCM per 5kb bin used in the simulations, and the predicted number of MCM $n_e(x)$ using Eq. (6) at the 10,000 ΔRFD peaks in K562. (B) Scaled $n(x) \times k_{on}[F_{free}]T_S/(-\ln(1-\Delta RFD(x)/2)$ as a function of Repli-seq MRT at the 11,000 ΔRFD peaks (blue circles) in K562 simulations; it is compared with $1/MRT$ (orange) and proportionality to exp^{-6MRT/T_S} (red).

We then compared $n_e(x)$ estimated using simulated MRT and RFD with $n(x)$, the input of the simulation (Fig. 8 A). The Pearson correlation was 0.95 and the coefficient of proportionality was 0.78 at the 10,000 ΔRFD local maxima. Similarly to Eq. (5), when exploring different values for k_{on} and d_{PO}, the PCC remained stable but the proportionality coefficient varied from 0.4 to 1.2.

We observed from further empirical exploration that the dependency of $n(x)$ on $MRT(x)$ (Fig. 8 B) was even better captured (PCC = 0.97) by the exponential dependency on MRT of Eq. (8) than by the inverse linear dependency of Eqs. (6) :

$$n_e^{exp}(x) \propto \Delta RFD(x)e^{-6MRT(x)/T_s} \tag{8}$$

We hypothesise that Eq. (8) accounts for the actual variations of $F_{free}(t)$ (Supplementary Figure S11) boosting potential origin firing efficiency in late S phase, so that a smaller number of MCM DHs are required to produce the same OEs.

We then wondered if it would be possible to simulate replication using a PODLS directly derived from experimental data using Eqs. (6) or (8) (note that since the PODLS is normalized the ignorance on the prefactors in Eq. (8) is not an issue). For this we selected the 15% highest experimental $\Delta RFD(x)$ (Materials and Methods) and used Eq. (6) to predict the PODLS that we used in our model. The resulting simulated MRT and RFD profiles were highly correlated with experimental profiles (Table 1), for example PCC=0.94 between MRT and 0.88 between RFD profiles in K562. Interestingly, this formula for PODLS prediction robustly applied also in *S. cerevisae* with Pearson correlations of 0.93 for MRT and 0.90 for RFD. The PODLS derived from Eq. (8) led to even higher correlations between simulated and experimental MRT (PCC=0.97) and RFD (PCC=0.91), very close to the correlation coefficients obtained using I_M profiles (Table 1). We also confirmed this result in *S. cerevisae* with PCC=0.96 for MRT and PCC=0.9 for RFD. These results show that combining OEs, estimated by local RFD upshifts, with MRT data, suffices to produce a near optimal PODLS.

SNS-seq or Bubble-seq signals also provide in principle a direct estimate of OEs, up to a proportionality coefficient. Using such OE estimates (K562 and HeLa SNS-seq, GM 06998 Bubble-seq) directly as PODLS resulted in poor correlations between simulated and experimental profiles (MRT, PCC=0.54 , 0.43 and 0.30 and RFD, PCC=0.16 , 0.23 and 0.12, respectively). Combining the same data with MRT data to infer the PODLS using Eq. (8) improved the correlations (MRT, 0.81 , 0.87 and 0.83 and RFD 0.48 , 0.59 and 0.53, respectively) (Table 1 1), but combining the same MRT information with a flat OE profile produced even better correlations (MRT, 0.97 , 0.98 and 0.98 and RFD

0.71 , 0.62 and 0.71, respectively), suggesting that SNS and Bubble-seq data do not synergize with MRT as favorably as RFD data.

We also analysed experimental data on potential origin positioning (Table 1). Using PODLS computed from K562 ORC2 (***Miotto et al., 2016***), HeLa MCM7 (***Sugimoto et al., 2018***) and HeLa MCM2 (***Foss et al., 2021***) resulted in PCCs between simulated and experimental profiles of 0.87, 0.46 and 0.54 for MRT and 0.74, 0.28 and 0.43 for RFD, respectively. Finally, we computed the correlation of SNS-seq, Bubble-seq and ORC/MCM signals with the optimized PODLS I_M in the corresponding cell line at 5 kb and 50 kb resolution. For K562 SNS, Hela SNS and GM Bubbles, the correlations at 5 kb and 50 kb were 0.05 and 0.16, 0.19 and 0.32, and 0.06 and 0.15, respectively. For K562 ORC2, Hela MCM7 and HeLa MCM2, the correlations were 0.30 and 0.54, 0.19 and 0.32, and 0.27 and 0.42, at 5 kb and 50 kb resolution, respectively. Therefore, in contrast to to RFD upshifts, none of these experimental datasets were convincing predictors of the PODLS I_M, for reasons that remain to be elucidated. The fact that ORC location better predicted the PODLS than MCM is unexpected if the multiple MCM DHs loaded by ORC are equally competent to trigger initiation (***Harvey and Newport, 2003***; ***Edwards et al., 2002***). Assuming this discrepancy does not stem from experimental limitations, it suggests that ORC-proximal MCM DHs are more likely to fire than ORC-distal ones.

In our model, all origins have the same k_{on}, and the spatial dependency is encoded in the non uniform density of potential origins. Since the effective reactivity of a potential origin is proportional to $k_{on}F_{free}$, the observed differences between the experimental MCM density and the inferred PODLS (I_M) may be explained by spatial or temporal non-uniformity, i.e. locus-dependent k_{on} or time-dependent F_{free}, with the $k_{on}F_{free}$ landscape given by the I_M/MCM ratio. We found that the normalized I_M/MCM ratio computed in 50 kb windows in HeLa cells (excluding null MCM windows; Fig. S14) decreased with MRT but was broadly dispersed even at constant MRT. The global trend could be explained if firing factor abundance decreased during S phase, as recently reported (***Wittig et al., 2021***), but the broad dispersion also implied that even at similar MRT, all MCM DHs are not equally reactive to firing factors, possibly due to MCM DH modifications or to chromatin environment. Finally, we cannot exclude that experimental noise or differential MCM loading dynamics during G1 (***Mei et al., 2021***) prevent an accurate picture of MCM distribution at S phase entry. Interestingly, the I_M/ORC ratio (computed in K562) did not vary with MRT but was still broadly dispersed at constant MRT Fig. S14). This suggests that more MCM DHs are loaded per ORC in late than in early replicating regions, but that the resulting equalization of MCM loading is counteracted by above-discussed mechanisms, possibly including an increased firing propensity of ORC-proximal MCM DHs.

According to Eq. (6), the faster passivation of early than late IZs means that early IZs require several-fold more MCM DHs than late IZs to achieve a similar OE. In our simulation with optimized k_{on} , F_{free} and d_{PO}, the maximum RFD upshift per 5kb bin was 0.17, an OE that would require as much as ~ 20 MCM DHs per 5 kb if an early MRT of 1h is to be achieved. Given that MCM DHs occupy 60 bp each and are only found in internucleosome linkers ***Foss et al.*** (***2021***), a 5 kb chromatin segment may not accomodate more than 25 MCM DHs. This steric limit is almost reached (see also Fig S3), suggesting that additional regulatory mechanisms that increase k_{on} or F_{free} in early S phase may be required to boost the intrinsic firing efficiency of some MCM DHs, consistent with Fig. S14.

To summarize, we checked that OEs can be accurately measured from RFD upshifts and we could predict from these OEs and MRT the number of potential origins (MCM DHs) per 5 kb bin in IZs assuming the specific value for d_{PO} used in our model, where all MCM DHs have the same locus- and time-independent probability of firing per unit time. However, the observed discrepancies between predicted and observed MCM DH densities, and the steric MCM loading constraint discussed above, support a mixed, potential origin density and affinity model where MCM DHs may have different affinities for firing factors. Future investigations of the I_M/MCM and I_M/ORC ratios should help reveal the licensing and post-licensing mechanisms that regulate origin firing probability.

PODLS	K562 MRT	K562 RFD	GM MRT	GM RFD	Hela MRT	Hela RFD
I_M	0.98	0.92	0.99	0.91	0.99	0.84
n_e^{exp} Eq. (8)	0.97	0.91	0.97	0.88	0.96	0.83
n_e Eq. (6)	0.94	0.88	0.91	0.82	0.92	0.80
e^{-6MRT/T_S}	0.97	0.71	0.98	0.71	0.98	0.62
ORC2	0.87	0.75	–	–	–	–
SNS e^{-6MRT/T_S}	0.81	0.48	–	–	0.87	0.59
Bubble e^{-6MRT/T_S}	–	–	0.83	0.53	–	–
MCM2	–	–	–	–	0.54	0.43
MCM7	–	–	–	–	0.46	0.28
SNS	0.54	0.16	–	–	0.43	0.23
Bubble	–	–	0.30	0.12	–	–

Table 1. Best joint correlation between simulated and experimental MRT and RFD data in K562, GM and Hela cell lines, marginalising over the other parameters of the simulation for different choices of PODLS.

Discussion

Without noise, MRT and RFD profiles in a constant fork speed hypothesis account for the same information. Here we have shown that it is possible to compare MRT increments with the integral of RFD with only one free parameter, the fork speed. The narrow range of values obtained by fitting the fork speed (from ≈ 1.2 to ≈ 1.6 kb/min) over the large range of scales explored (5 kb to 5 Mb), and the high correlations obtained (from 0.68 to 0.95), suggest that both experiments are compatible, even at lower resolutions than expected (MRT resolution $\approx$ 100kb) and that the hypothesis of a constant fork speed at resolutions down to 5 kb is robust. We have also shown by randomly resampling DNaseI HSSs that RFD profiles contain higher resolution information than MRT profiles. However MRT profiles contain information about integrated initiation strengths of large domains, that is lost when integrating noisy RFD profiles. We therefore used both profiles in our inversion method.

Mathematical models have been developed to estimate intrinsic origin efficiencies from MRT (***de Moura et al., 2010***; ***Baker and Bechhoefer, 2014***), and RFD (***Bazarova et al., 2019***). The models assign either a discrete number of origins (***de Moura et al., 2010***; ***Bazarova et al., 2019***), each having a time-dependent probability of firing, or a continuous spatiotemporal initiation density (***Baker and Bechhoefer, 2014***). In principle our inversion method could be applied to these models, but their hypotheses are more complex than ours. As the probability to activate an origin changes with time, it is more difficult to test whether firing efficiency is set at the end of licensing. Furthermore, these methods either require a non trivial optimisation that may be feasible with the yeast but not the human genome, given its size, or a Bayesian analysis that so far was limited to sets of 3 origins ***Bazarova et al.*** (***2019***). In contrast, our approach is very flexible, can easily accommodate new datasets and is fast even with the human genome. Furthermore it outputs a 1D profile of potential origin density in human cells, which can be directly compared to experimental origin licensing profiles, as first achieved in yeast (***Das et al., 2015***).

We found that the PODLS could be segmented in peaks and flat areas of random initiation. However the level of random activation found here (5 %) was much lower than inferred in Miotto (***Miotto et al., 2016***) (60%). Our estimate is more consistent with recent single molecule analyses reporting 10-20% of random initiation events in yeast (***Müller et al., 2019***; ***Hennion et al., 2020***). Nevertheless, the correlations between simulated and experimental MRT and RFD data were not much affected by increasing the percentage of initiation and we cannot exclude that our estimate is conservative. The inferred PODLS allowed us to generate simulated MRT and RFD profiles ex-

tremely similar to experimental ones in three different cell lines. The correlations were 0.98 for MRT and 0.86-0.91 for RFD. Therefore, a remarkably simple stochastic model featuring a constant fork speed, an almost constant number of limiting firing factors and a time-independent initiation strength profile suffices to jointly account for MRT and RFD data nearly exactly. Importantly, the correlations obtained using experimental ORC or MCM-based PODLSs were lower than with the optimal PODLS I_M inferred by neural networks, by 0.11-0.16 for ORC and by 0.4-0.5 for MCM. This suggests either that ORC and, more strikingly, MCM datasets do not accurately reflect the true distribution of these proteins at S phase entry, or that their abundance is not the sole factor determining initiation strength.

Reasoning that an origin's passivation typically occurs at its MRT, we derived a novel mathematical relationship (Eq. (5)) that, assuming a constant availability of firing factors through S phase, predicts an origin's intrinsic efficiency (IE) from its observed efficiency (OE) and its MRT. OEs can be estimated by RFD upshifts. Knowing d_{PO}, predicted IEs can be converted into absolute MCM DH densities proportional to the RFD upshift and to $1/MRT$ (Eq. (6)). This was fairly well verified in simulated datasets, but we empirically found that an $1/e^{6MRT}$ dependency (Eq. (8)) gave even better predictions, probably because the recycling of firing factors by termination events increases in late S phase. Strikingly, the PODLS inferred from experimental RFD and MRT data using Eq. (8) generated almost as good simulated profiles as the PODLS inferred using neural networks. We however caution that this procedure is sensitive to smoothing and thresholding parameters and is therefore less robust that neural networks.

Eq. (5) to (8) imply that early IZs require several-fold more MCM DHs than late IZs to achieve a similar OE, which may potentially explain why SNS-seq and Bubble-seq profiles were poorly correlated to the optimal PODLS. We therefore used Eq. (8) to exploit the MRT information and convert these OE measurements into IEs. The resulting PODLS was improved but gave poorer results than a PODLS inferred from a flat OE profile. We conclude that SNS-seq and Bubble-seq data are not accurately consistent with MRT and RFD data.

Although our model allowed us to infer a PODLS that jointly predicts RFD and MRT almost exactly, this PODLS was not perfectly correlated with experimental ORC and MCM profiles. Assuming that these profiles are not biased, this imposes to relax the assumption that all MCM DHs are equally reactive to firing factors, or the assumption that the concentration of firing factors is constant. Examination of the I_M/ORC and I_M/MCM ratios suggests that, while more MCMs per ORC are loaded in late- than in early-replicating DNA, MCM DH activation probability is higher in early-replicating DNA and next to ORC, and varies along the genome even at constant MRT. Mechanisms that increase I_M/MCM may allow early IZs to reach a high IE without increasing MCM DH density beyond steric constraints. Understanding the genetic and epigenetic determinants of MCM DH density and reactivity to firing factors is a goal for future studies.

Materials and Methods

Model and simulation

Model and parameters

We model the replication initiation process by a bimolecular reaction between free firing factors F_{Free} and potential origins PO on the genome of size L with a reaction rate k_{on}. This rate is the probability per unit of time that a firing factor and a PO meet and that an initiation follows. Once an initiation event has occurred, two forks propagate in opposite direction at speed v and a firing factor is trapped. The number N_F of firing factor is fixed and parametrised as $N_F = \rho_F L$ with ρ_F the density of firing factors. A potential origin density landscape I is used to position $\frac{L}{d_{PO}}$ origin prior to each S phase entry along the genome, with d_{PO} the genome average distance between potential origins. We also decompose the initiation probability landscape I in two terms: it is the sum of an inhomegeneous profile I_e, for example derived from an epigenetic landscape, and a uniform contribution which correspond to a proportion r of the initial profile I_e. In all the simulations we

fixed v = 1.5 kb/min and $k_{on} = 3e^{-6}$ min^{-1}. A typical simulation therefore has 4 free parameters (ρ_F,ρ_{PO},I_e,r).

Simulation implementation

The modeled genome is always considered at 5 kb resolution. The input spatial profile $I_e + r$ is normalised so that the sum is one. We draw from this normalised profile $N_{PO}(t=0) = \frac{L}{d_{PO}}$ origins, with replacement, meaning that several origins can be drawn in the same 5 kb window. During the simulation we introduce $\rho_F L$ firing factors following an exponential characteristic law $\rho_F L(1-e^{-t/\tau})$ with τ a characteristic time taken to 1 h to simulate progressive activation of firing factor upon S-phase entry. We use a Gillespie algorithm (***Gillespie, 1976***) to simulate an initiation reaction with reaction rate $k_{on}N_{PO}(t)N_F(t)$ with $N_F(t)$ the number of free firing factor at time t. The Gillespie algorithm considers that the the next reaction between an origin and a firing factor will take place after a time δt_A drawn from an exponential distribution of parameter $\frac{1}{k_{on}N_{PO}(t)N_F(t)}$. Then δt_A is compared to δt_E, the smallest time of encounter for two forks on the genome. The system then evolve for an increment of time $\delta t = min(\delta t_E, \delta t_A)$, meaning that all the forks on the genome moves of $v\delta t$. If $\delta t_A < \delta t_E$ then one origin is activated at random, a firing factor is trapped ($N_F(t+\delta t) = N_F(t) - 1$), and two forks propagate on opposite directions at a velocity v from the origin. Otherwise the termination event releases a factor so that $N_F(t+\delta t) = N_F(t) + 1$ and a new time step begin. If a fork replicates a position with unfired origins, then these origins are passivated and remove from the list of potential origins.

Remark on rescaling the simulation for the simulation on chromosome 2 only.

In ***Arbona et al.*** (***2018***), we showed that to reproduce the shape of the experimental temporal rate of DNA replication origin firing, one has to be in a regime governed by the critical parameter $\rho_F^* = \frac{v}{k_{on}Ld_{PO}}$. In order to stay in this regime no matter the size of the genome, we in fact parameterized the simulations with $k_{on}^e = k_{on}L$ chosen constant. k_{on}^e = 8.625 kb min^{-1}, so that when we simulated the whole genome (in our case, the first 22 human chromosomes whose total size is 2 875 Mb), then $k_{on} = 3e^{-6}$ min^{-1}. This means that if we decrease the size of the system, the constant of reaction k_{on} increases, which is coherent as k_{on} encompass the efficiency of encounter between one potential origin and one firing factor and being in a smaller system their encounter rate is increased.

Missing data.

For all simulations if a gap larger than 1.5 Mb without data in either MRT or RFD experimental data was present, the region extended of 500 kb on both ends was removed. This mainly happen in telomeric and centromeric regions, and it means that a chromosome can be segmented in two or more pieces. Then when comparing e.g. simulated with experimental MRT, we also remove all gaps in MRT data that are smaller than 1.5 Mb extended of 500 kb on both ends. These two steps remove less than 10 % of the genome for either MRT or RFD in all considered cell lines. When computing replication time, we exclude all gaps present in either MRT or RFD data as well their surrounding 500 kb.

Computing experimental quantities, comparison with experimental data.

To compute RFD, we record for each 5 kb window in each simulation the fork direction as +1, -1 or 0 if an initiation or a termination occurred. The final RFD is the mean of 200 simulations. To compute the MRT as done in repli-seq experiments, we recorded for each simulation and each locus the actual replicated fraction of the genome at the time the locus is replicated. Then to simulate the six fractions of the repli-seq experiment, the continuous $[0..1]$ interval of replicated fraction of the genome is mapped to six bin of length 1/6. Then $MRT(x) = \sum p_i(x)i/6 + 1/12$ where $p_i(x)$ if the fraction of the simulations where the locus at position x has been replicated when the replicated fraction of the genome was between $[i/6, (i+1)/6]$ ($i \in \{0, \cdots, 5\}$).

For both MRT and RFD when comparing with experimental data, we masked the region removed as specified in the missing data paragraph. Pearson correlations were computed at 5 kb

resolution for RFD and 10 kb resolution for MRT. T_{100} was defined as the replication time of the latest replicated window. T99 (resp. T95) is defined as the time at which 99% (resp. 95%) of the genome was replicated.

Experimental data

DNaseI HS data were downloaded from the ENCODE project (***Hansen et al., 2010***; ***Thurman et al., 2007***): (K562 DNaseI HS Uniform Peaks from ENCODE/Analysis (table wgEncodeAwgDnaseUwduke-K562UniPk.narrowPeak).

ORC2 binding sites in K562 cells were obtained from ***Miotto et al.*** (***2016***) (supplementary material table S1 in the ***Miotto et al.*** (***2016***) article).

SNS-seq data were obtained for K562 from ***Picard et al.*** (***2014***) (GSE46189_Ori-Peak.bed) and for Hela from ***Besnard et al.*** (***2012***) (Hela_SNS_seq_Besnard_Tot.1kb.csv).

Bubble-Seq data were obtained from ***Mesner et al.*** (***2013***) (GSE38809_GM_combined_RD_bubbles-.bedgraph).

RFD profiles derived from OK-seq data were obtained for Hela from ***Petryk et al.*** (***2016***) and for GM06990 and K562 from ***Wu et al.*** (***2018***).

For mean replication timing data, GM12878, K562, HeLaS3, alignment files of Repli-seq libraries (BAM files) for six S-phase fractions were obtained from the ENCODE project (***Hansen et al., 2010***; ***Thurman et al., 2007***) at http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeUwRepliS

For yeast, RFD profiles derived from OK-seq data were obtained from ***Hennion et al.*** (***2018***) and MRT was obtained from ***Müller et al.*** (***2014***). We shifted MRT by 0.05 for numerical stability.

Grid search optimisation

When performing grid search optimisation on the four parameters ρ_F, d_{PO}, r ,υ we noticed, as explained in the main text, that both d_{PO} and υ had little effect on the MRT and RFD profiles. These two parameters where thus left out so that ρ_F and r optimisation was carried on a 2-dimensional grid. The optimum selected is the one of highest sum of Pearson correlation between simulated and experiment MRT and RFD. For the grid search optimisation carried on chromosome 2 (second Results' section), the explored r values were [0,0.02,0.05,0.1], and ρ_F values were [0.6, 0.7, 0.8, 0.9, 1. , 1.1, 1.2, 1.3, 1.4]×ρ_{start} where ρ_{start} was defined as the firing factor density needed to replicate the whole genome at a fork speed of 1.5 kb.min^{-1} in an S-phase duration T_S, if all the firing factors are active: $\rho_{start} = \frac{1}{2*\upsilon*T_S}$, with T_S = 8 h for Hela cell and 12 h for GM06990 and K562.

When performed genome-wide (Results reported in Table 1), we chose the same grid for all human cell lines. r varied from 0 to 20 % by increments of 5 %, and explored ρ_F values were [0.27 0.41 0.55 0.68 0.82 0.95 1.1] Mb^{-1}.

Iterative procedure used in learning the PODLS that best predicts both MRT and RFD data.

To define a starting initiation profile, we computed the RFD increments between 5 kb bins, smoothed the profile using a 50 kb average sliding window, kept values higher than the 80th percentile and set the rest to zero. Using this profile we ran a grid search optimisation (See previous paragraph) to obtain MRT_0 and RFD_0 that best fitted experimental data. Then a neural network N_1 was trained to predict the initiation profile $I_0 + r$ (r being the amount of random activation obtained from the grid search optimisation part) from the simulated MRT_0 and RFD_0 (See next paragraph for details on the neural network). N_1 was then applied on experimental MRT and RFD predicting the I_1 profile, which was then used in a simulation to obtain MRT_1 and RFD_1 and compute the correlation with experimental MRT and RFD. We reiterated the process twice using successively MRT_1 and RFD_1 as input and then the obtained MRT_2 and RFD_2 as input to produce MRT_3 and RFD_3. We reiterated the procedure once more and stopped as it did not improve the correlations. The code to reproduce these steps is available at (https://github.com/organic-chemistry/repli1D).

Neural network training

The input of the network was a window of size 2005 kb (401 bins of 5 kb) with both MRT and RFD, an the output was the initiation signal at the center of the window. The RFD was smoothed with a 50 kb rolling window. We used a three-layer convolutional neural network with kernel length 10 and filter size 15 and a relu activation. Each layer was followed by a dropout layer at a value of 1 %. The last convolutional layer was followed by a maxpooling of kernel size 2. The resulting vector went through a dense layer with sigmoid activation and output size 1, meaning that the 2005 kb window allowed to compute the probability of activation at its center. We used a binary cross entropy loss and the layer was trained with the adadelta algorithm. The procedure was implemented using keras. We used chromosome 3 to 23 for the training, chromosome 2 for validation and chromosome 1 for testing. To make the network more robust to experimental noise, we randomly added noise to the input RFD profile by assigning 1% of the bins a random value between -1 and 1.

Analytical extraction of n_e from ΔRFD and MRT data

Eq. (7) requires that ΔRFD be estimated. We smoothed human RFD data using a running average window of 15 kb (3 bins) then computed ΔRFD between consecutive 5kb windows. The 15% top values were selected and the other bins set to 0. The non-zero bins were divided by $1/MRT$ or by e^{-6MRT} .

Selecting ΔRFD peaks

We ran a peak detection algorithm over ΔRFD at a 5 kb resolution , using scipy routine find_peaks with parameters width=4 and height=0.02, thus selecting peaks ≥4x5kb in width and ≥ 0.02 ΔRFD/5kb in height. This yielded 9878 peaks for GM06990 , 13466 peaks for Hela and 10009 peaks for K562. The selected peaks as well as ΔRFD and I_M for comparison are shown on Fig. S15.

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Supporting information

PODLS	K562 MRT	K562 RFD	GM MRT	GM RFD	Hela MRT	Hela RFD	*S. cer.* MRT	*S. cer.* RFD
I_0	0.81	0.79	0.74	0.77	0.78	0.74	0.60	0.71
I_1	0.93	0.89	0.95	0.88	0.95	0.82	0.80	0.83
I_2	0.98	0.91	0.98	0.91	0.97	0.85	0.87	0.84
I_3	0.98	0.92	0.99	0.91	0.98	0.85	0.94	0.90
I_4	0.98	0.92	0.99	0.91	0.99	0.84	0.96	0.91

Table S1. Pearson correlation coefficients between experimental MRT and RFD profiles and their simulated MRT_n and RFD_n estimates obtained for the series of iteratively optimized PODLS I_n using RFD derivative for initialisation of I_0. Results are shown for K562, GM and Hela cell lines as well as *S. cerevisiae*. At the 5th iteration none of the PCC increased (not shown).

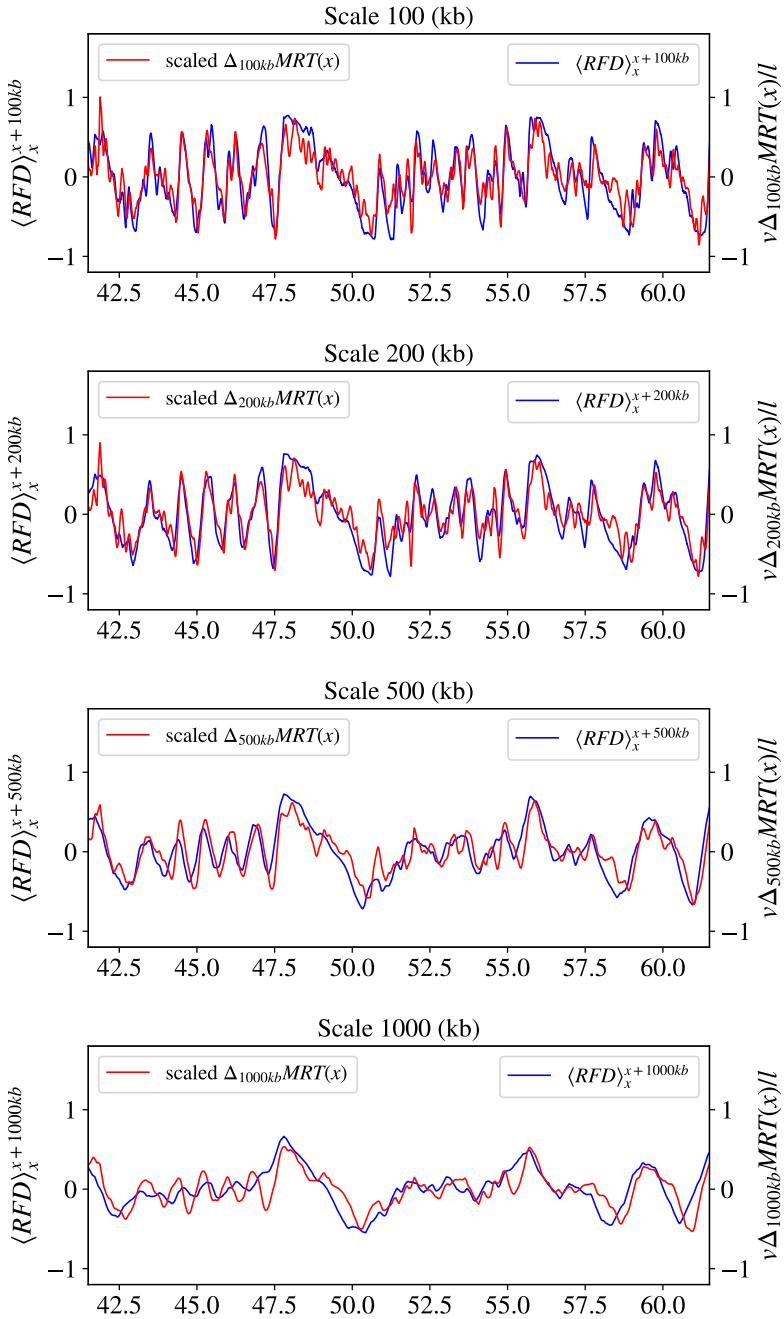

Figure S1. Comparison between $\langle RFD \rangle_x^{x+l}$ (blue) and $\frac{v}{l}\Delta_l MRT(x)$ (red) (Eq. (2)) assuming $T_S = 12$h at different scale l. From (top) to (bottom), $l = 100$ kb, 200 kb, 500 kb and 1000 kb and fork speed values v are taken from Fig. 2B. The same 20 Mb region of chromosome 1 as in Fig. 2A is shown.

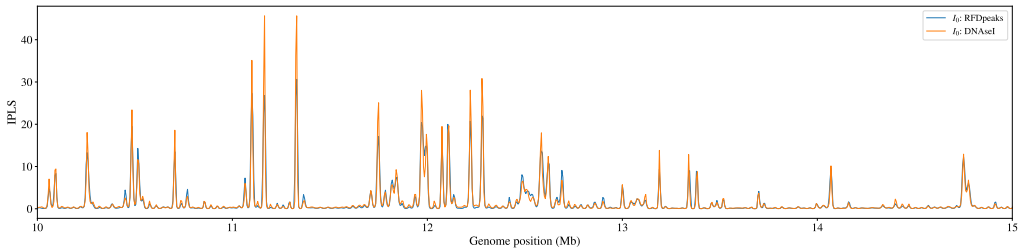

Figure S2. Comparison of K562 potential origin density landscapes optimized either from the PODLS derived from DNase I HS peaks (orange) or from the experimental ΔRFD peaks (blue). The obtained I_M are almost identical (PCC = 0.94).

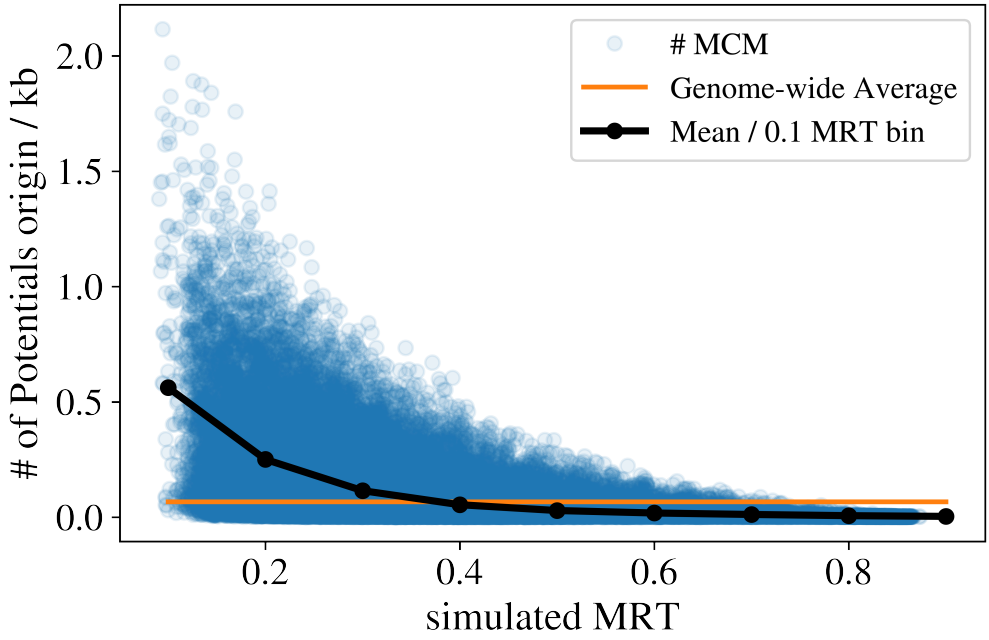

Figure S3. Predicted number of potential origins per kb, computed for each 5 kb bin, vs. MRT in K562 replication simulations.

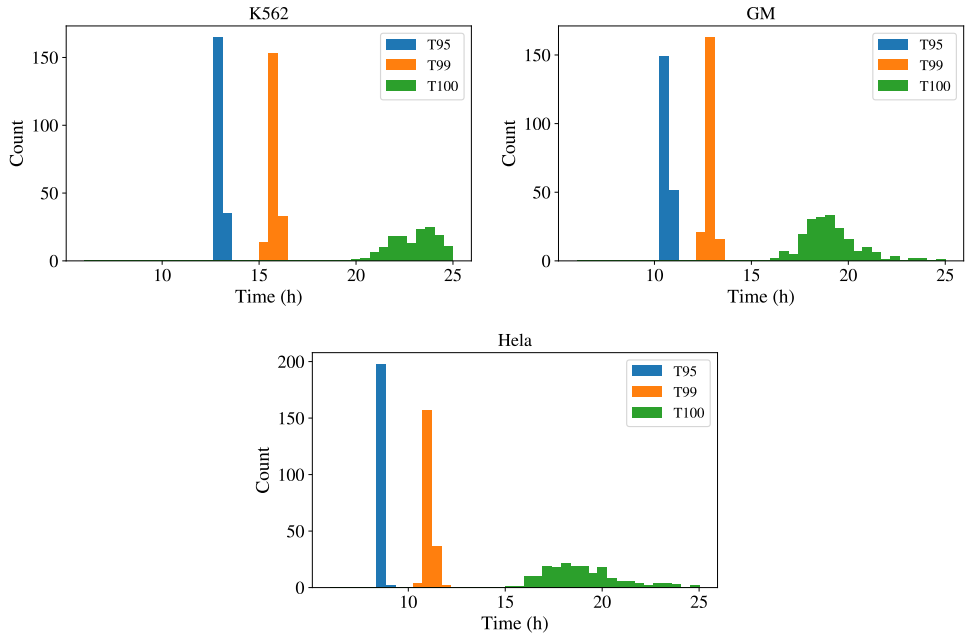

Figure S4. Distribution of T95 (blue),T99 (orange) and T100 (green) replication times as defined in the text for the three different cell lines.

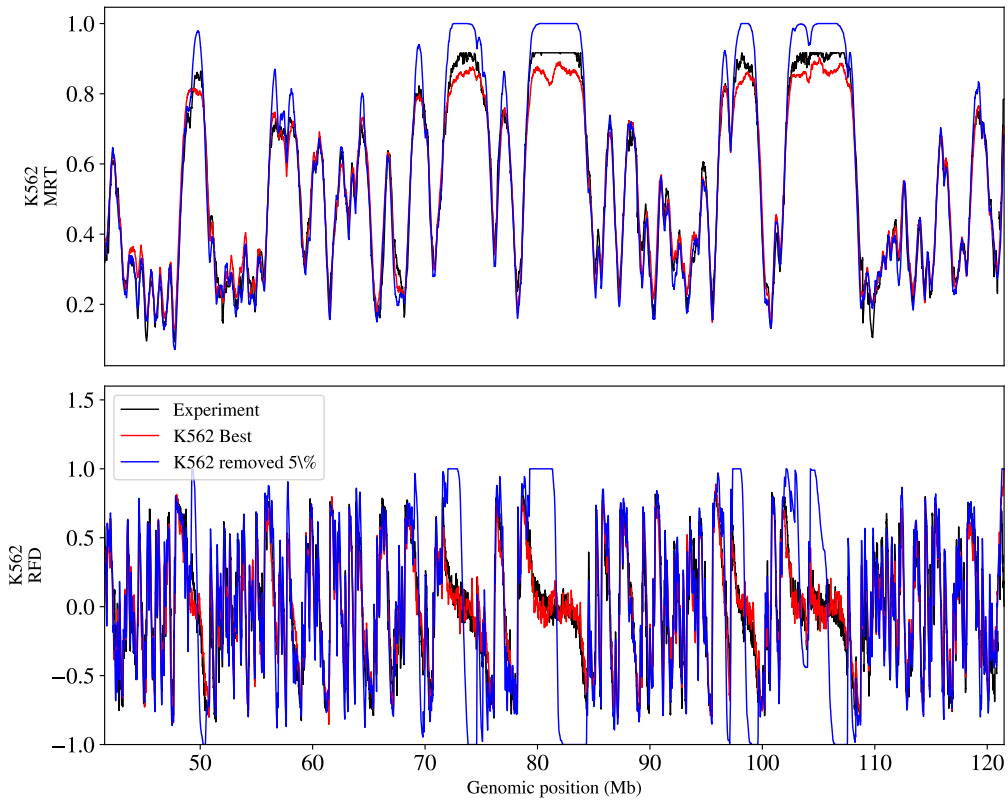

Figure S5. (Top) Comparison of experimental MRT with simulated MRT using the optimized PODLS I_M (red) and after setting to zero the bins with the lowest I_M values corresponding to 5% of the total origin firing events ($\approx$ 53% of the bins) (blue). (Bottom) Same comparison for the RFD profiles.

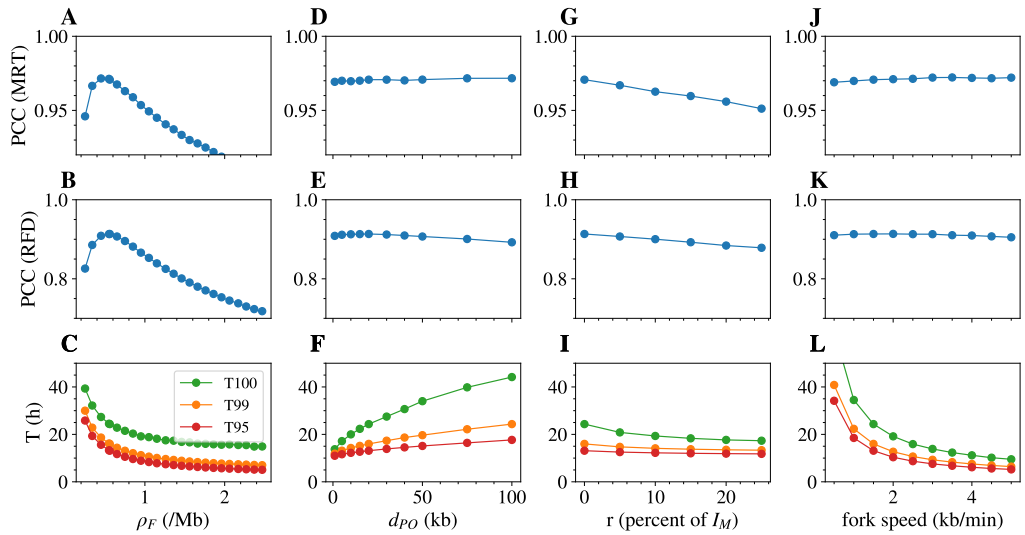

Figure S6. Effect of single parameter variation on measurable targets in GM06990. Effect of the density of firing factors ρ_F (A,B,C); the average distance between potential origins d_{PO} (D,E,F) ; the percent of random initiation r (G,H,I); the fork speed v (J,K,L), on the Pearson Correlation Coefficient (PCC) between simulated and experimental MRT (A,D,G,J) and RFD (B,E,H,K) profiles, and on T95 (red), T99 (orange) and T100 (green), the median times required to replicate 99% and 100% of the genome (C,F,I,L).

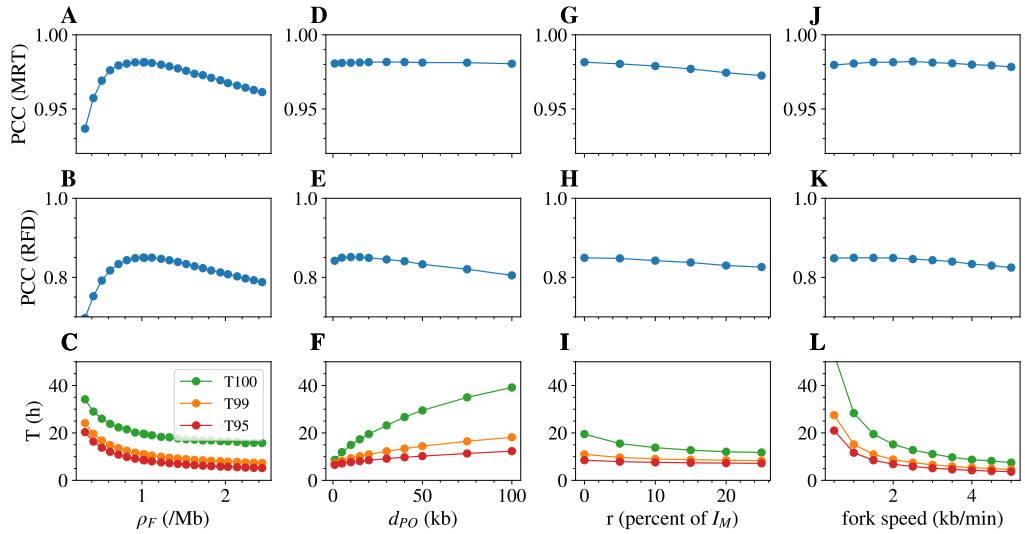

Figure S7. Effect of single parameter variation on measurable targets in Hela. Effect of the density of firing factors ρ_F (A,B,C); the average distance between potential origins d_{PO} (D,E,F) ; the percent of random initiation r (G,H,I); the fork speed v (J,K,L), on the Pearson Correlation Coefficient (PCC) between simulated and experimental MRT (A,D,G,J) and RFD (B,E,H,K) profiles, and on n T95 (red), T99 (orange) and T100 (green), the median times required to replicate 99% and 100% of the genome (C,F,I,L).

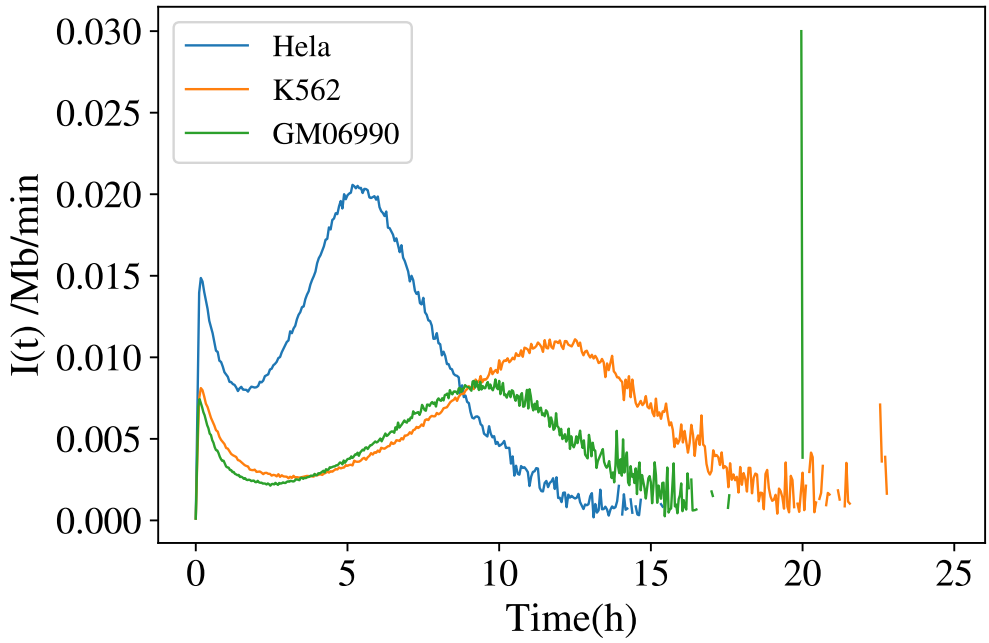

Figure S8. Probability of initiation per length of unreplicated DNA per minute for the three indicated cell lines

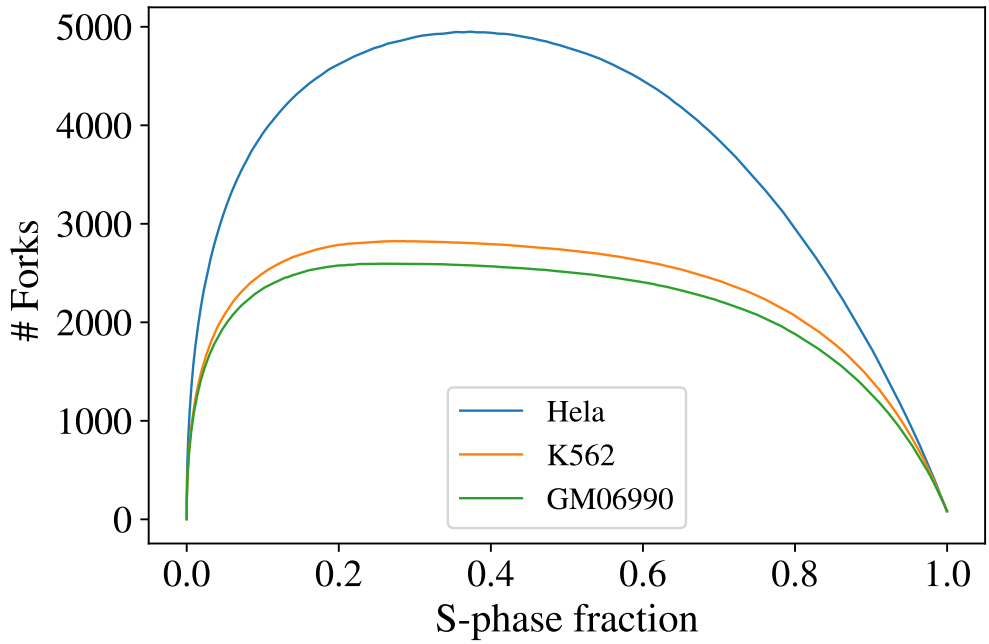

Figure S9. Active fork number as a function of S-phase fraction for the three indicated cell lines

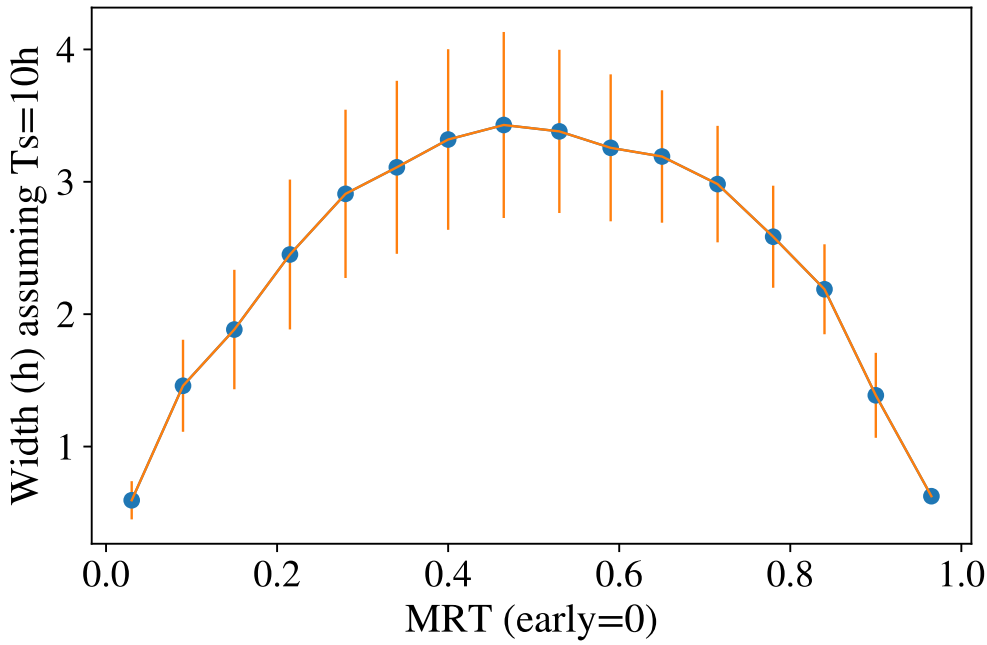

Figure S10. Replication time variability as a function of MRT in simulated K562 replication. Blue dots and orange bars indicate the genome-wide average and range of values, respectively of replication time variability.

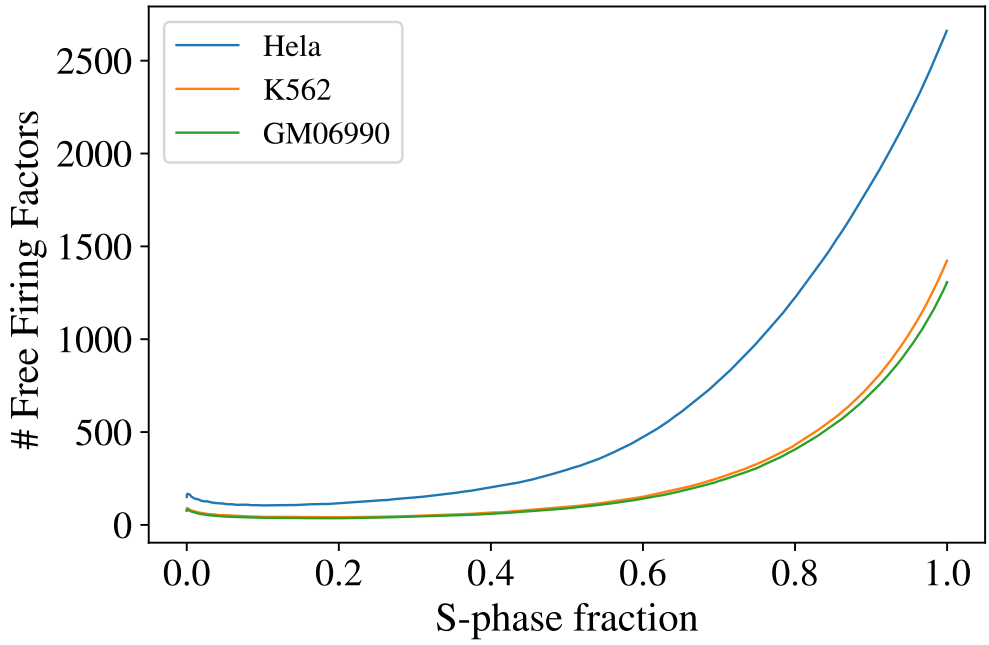

Figure S11. Number of Free firing factors as a function of the S-phase fraction for the three indicated cell lines

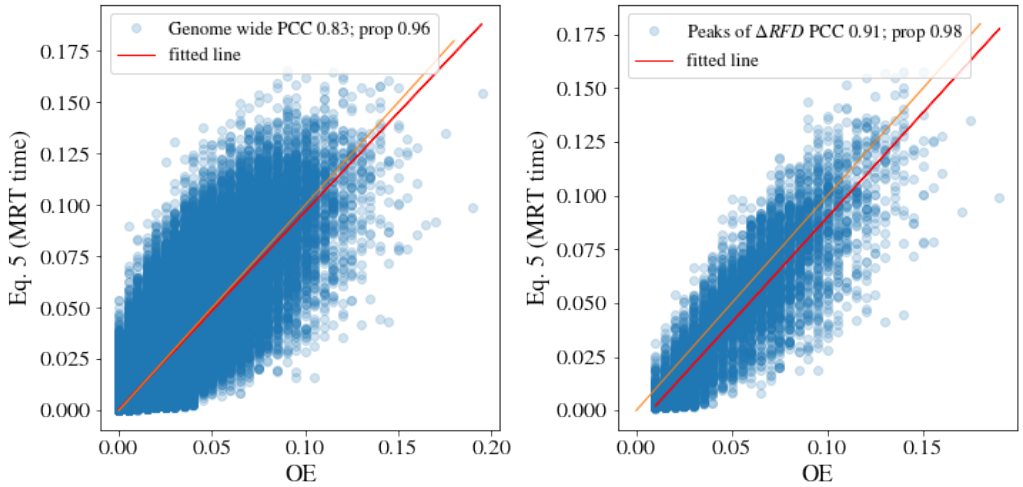

Figure S12. Comparison of observed origin efficiency in K562 replication simulation, directly counted as the fraction of simulations in which replication started in a bin (OE), or computed as the right-side term of Eq (5), genome wide (left) or restricted to the peaks of ΔRFD (right). Red line represents the linear fit and the orange line the first diagonal.

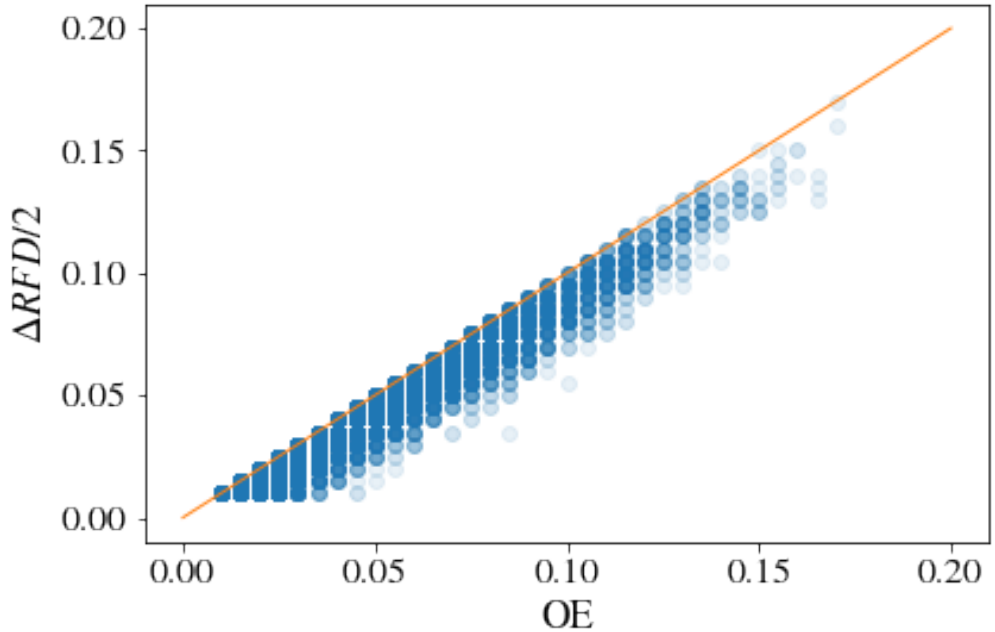

Figure S13. Comparison of OE, directly counted as the fraction of simulations in which replication started in a bin (OE), with its estimation by $\Delta RFD/2$ restricted to peaks of ΔRFD. The orange line is the first diagonal.

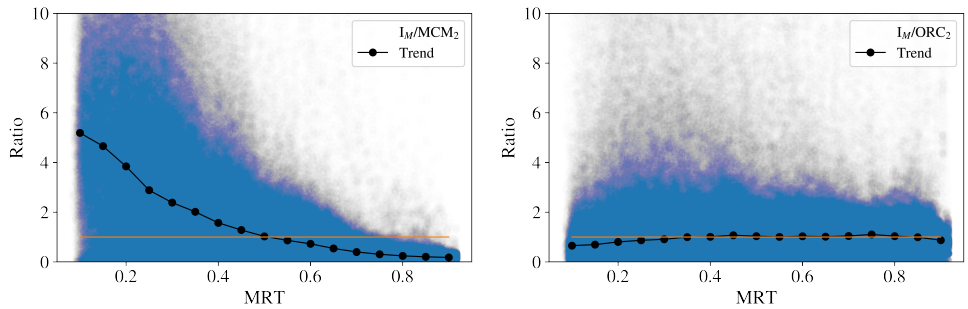

Figure S14. I_M/MCM_2 ratio in Hela (left). I_M/ORC_2 ratio in K562 (right). Both signals were smoothed with a 50 kb sliding window due to noise in MCM data and normalized so that the median value over all the genome was one (orange line). The black dotted lines indicate the median value of the ratios by 0.05 MRT steps.

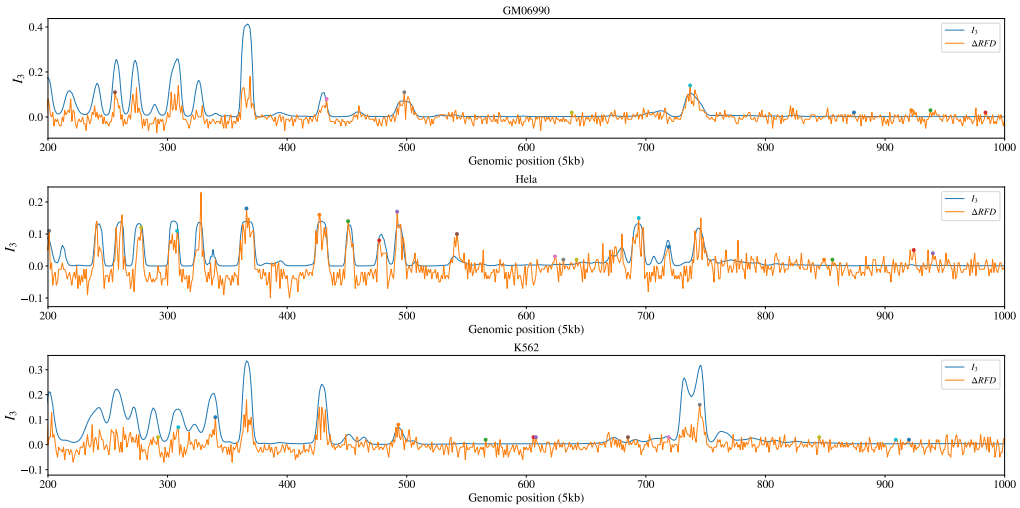

Figure S15. Peak detection of ΔRFD (dots on the top of the orange signal) overlayed with I_M (blue curves) for the three indicated cell lines