Table 1 Kinetic parameters and calculations derived from the model solutions

Description	Symbol	Value[a]	Method or equation for determination
Initiation constant	$k_{ini}^{Pol\ II}$	0.0216 s^{-1}	Model solution
Promoter dissociation constant	$k_{off}^{Pol\ II}$	0.145 s^{-1}	Model solution
Promoter escape constant	$k_{escape}^{Pol\ II}$	0.00159 s^{-1}	Model solution
Abortive initiation constant	$k_{abor}^{Pol\ II}$	0.0170 s^{-1}	Model solution
Termination constant	$k_{term}^{Pol\ II}$	0.0016 <>	Model solution
		0.0024 s^{-1}	
mRNA release constant	k_{out}^{MS2}	0.0302 s^{-1}	Model solution
mRNA pausing constant	k_{p}^{MS2}	0.00131 s^{-1}	Model solution
mRNA pause-releasing constant	k_{-p}^{MS2}	0.00326 <>	Model solution
		0.00489 s^{-1}	
Number of nascent mRNAs in the array	n_{mRNA}	200–400	FISH (this study)
Number of genes in the array	n_{genes}	200	Southern blot[b]
Number of active genes in the array	n_{acts}	200	Assumption[c]
Partition of elongating versus pausing MS2-labeled polymerases	P_{elong}	0.76	Model solution
Ratio: MS2-labeled polymerases/total engaged polymerases	R_{MS2}	0.7	Assumption[d]
Number of elongating Pol II making MS2-labeled mRNA	$n_{MS2\ elong}$	106–213	$P_{elong} \cdot R_{MS2} \cdot n_{mRNA}$
Number of paused Pol II making MS2-labeled mRNA	$n_{MS2\ paused}$	33–66	$(1 - P_{elong}) \cdot R_{MS2} \cdot n_{mRNA}$
Initiation efficiency		13%	$k_{ini}^{Pol\ II} / (k_{ini}^{Pol\ II} + k_{off}^{Pol\ II})$
Promoter release efficiency		8.6%	$k_{escape}^{Pol\ II} / (k_{escape}^{Pol\ II} + k_{abor}^{Pol\ II})$
Pausing probability		4.2%	$k_{p}^{MS2} / (k_{p}^{MS2} + k_{out}^{MS2})$
Promoter residence time	$t_{promoter}$	6 s	$(k_{off}^{Pol\ II} + k_{ini}^{Pol\ II})^{-1}$
Initiation residence time	$t_{initiation}$	54 s	$(k_{escape}^{Pol\ II} + k_{abort}^{Pol\ II})^{-1}$
Engaged residence time	$t_{engaged}$	517 ± 103 s	$(k_{term}^{Pol\ II})^{-1}$
Elongation residence time	$t_{elongation}$	32 s	$(k_{p}^{MS2} + k_{out}^{MS2})^{-1}$
Pause residence time	t_{pause}	204 <>	$(k_{-p}^{MS2})^{-1}$
		307 s	
Average frequency of mRNA production in the gene array	f_{array}	3.2–6.4 s^{-1}	$k_{out}^{MS2} \cdot n_{MS2\ elong}$
Average frequency of mRNA production per gene (promoter escape frequency)	f_{gene}	0.016–0.032 s^{-1}	f_{array} / n_{acts}

Rate constants obtained from least-squares fits of the experimental data are shown, as well as values calculated from these rates. Rate constants derived from the YFP–Pol II FRAP data have Pol II superscript; rate constants derived from the GFP-MS2 FRAP data have MS2 superscript.

[a]The symbol <> represents lower and upper bounds of determined value. [b]Southern data provided in ref. 17. [c]To calculate the frequency of engaged polymerases, we assumed that all 200 genes were activated. [d]Polymerases transcribe 1 kb of nonfluorescent pre-mRNA before entering the MS2 repeat region and then transcribe 2.3 kb of pre-mRNA where they are labeled by fluorescent MS2 proteins linked to the polymerase through the nascent RNA (**Fig. 1a**). Because we experimentally determined the number of nascent mRNAs present at the transcription site, we assumed that polymerases were evenly distributed on the gene to estimate the number of polymerases loaded on the transcription unit upstream of the MS2-binding repeats (using the ratio 2.3 kb / 3.3 kb). Models were created with ProcessDB and solutions were obtained by exporting these models to Berkeley Madonna.