

## **Supplementary Materials**

*for*

### **Requirements for mammalian promoters to decode transcription factor dynamics**

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## Supplementary Text

### ***Mathematical model of gene expression in response to different synTF dynamics***

We model the process of gene expression using a deterministic, two-compartment model, with eleven variables. The two compartments represent the cytosol and the nucleus, and the ten variables represent the following molecular species:

TF: cytosolic synTF

NTF: nuclear synTF

P<sub>u</sub>: unbound promoter

P<sub>a</sub>: active promoter

P<sub>r</sub>: refractory promoter

PIC: pre-initiation complex

nRNA: nascent RNA

mRNA: mature mRNA

rbz: bound ribosome

iP: immature protein

mP: mature protein

We opted for a deterministic, instead of a stochastic model of gene expression, because our experimental setup is based on transient transfection of plasmid DNA, therefore, on average, there are more than two copies of the promoter of interest per cell; moreover, synTF is also expressed from the plasmid under the strong CMV promoter. We conclude that our species are present in medium copy and we can follow the average concentration of the species using ordinary differential equations (ODEs).

For each variable, we wrote an ODE that describes the change over time of its concentration.

The model consists of the following eleven ODEs describing cytosolic synTF [1], nuclear synTF [2], unbound promoter [3], active promoter [4], refractory promoter [5], PIC formation or stabilization [6], nascent RNA production [7], RNA maturation [8], bound ribosome [9], mRNA translation to immature protein [10], protein maturation [11], plus one equation that describes DNA looping efficiency [12].

The first two equations describe the change over time in the concentration of synTF in the cytoplasm and the nucleus:

$$\frac{dTF}{dt} = K_{TF} + darkrev(t) - lightAct(t) - d_{TF} * [TF] \quad [1]$$

$$\frac{dNTF}{dt} = lightAct(t) - darkrev(t) - d_{NTF} * [NTF] \quad [2]$$

$K_{TF}$ ,  $d_{TF}$  and  $d_{NTF}$  are constants that describe the *de novo* production rate and degradation rates of synTF in the cytosol and nucleus, respectively. Production occurs only in the cytoplasm, while degradation occurs in both compartments.

darkrev(t) and lightAct(t) are two functions that describe the export and import of synTF from/into the nucleus, respectively.

The lightAct(t) function is dependent on time (t), duration of activating blue light (tOn), duration of recovery phase in the dark (tOff), rates of synTF nuclear import during light activation (iOn) and dark recovery phase (iOff). We added this latter nuclear import in the dark to take into account the fact that the LOV domain is in equilibrium between its dark state, in which the C-terminal J $\alpha$  helix is folded and bound to the core domain, therefore shielding the NLS from the import machinery, and its lit state, characterized by an unfolded J $\alpha$  helix, which is further away from the core domain, letting the NLS be recognized (1). The duration of the light activation (lightdur) is defined in minutes. The function lightAct(t) is defined in python as shown below and returns synTF import rate (imp):

```
def lightAct(t,tOn,tOff,iOn,iOff):
    if (t <= lightdur):
        if (t%(tOn + tOff) < tOn):
            imp = iOn
        elif (t%(tOn + tOff) >= tOn):
            imp = iOff
        else:
            imp = iOff
    return(imp)
```

The darkrev(t) function is dependent on time (t), duration of activating blue light on (tOn), duration of recovery phase in the dark (tOff), rates of synTF export out of the nucleus during light activation (rOn) and dark phase (rOff). The function darkrev(t) is defined in python as shown below and returns synNTF export rate (exp):

```
def darkrev(t,tOn,tOff,rOn,rOff):
    if (t <= lightdur):
        if (t%(tOn + tOff) < tOn):
            exp = rOn
        elif (t%(tOn + tOff) >= tOn):
            exp = rOff
        else:
            exp = rOff
```

*return(exp)*

The next three equations describe the change over time in the promoter state. The promoter can assume three states: unbound ( $P_u$ ), active ( $P_a$ ) and refractory ( $P_r$ ). It is only in the active state that the promoter is able to trigger transcription pre-initiation complex (PIC) assembly (described by equation 6). A three-state promoter model that includes a refractory state was necessary to account for the refractory behaviour seen in the nascent RNA data of some promoters. All promoter states are reversible.

Equation 3 describes the species  $P_u$ .  $P_u$  becomes  $P_a$  when bound by NTF. NTF binding to  $P_u$  is modelled as cooperative using a Hill function of NTF concentration multiplied by the constant  $K_{on}$ , where  $m$  is the Hill coefficient and  $kD_1$  is the affinity of synTF for the RE. The change over time of  $P_u$  concentration also depends of the rate at which  $P_a$  and  $P_r$  revert back to the unbound state  $P_u$  ( $K_{off}$  and  $d1_{rf}$ , respectively):

$$\frac{dP_u}{dt} = K_{off} * P_a + d1_{rf} * P_r - K_{on} * \left( \frac{NTF^m}{kD_1^m + NTF^m} \right) * P_u \quad [3]$$

Equation 4 describes the species  $P_a$ .  $P_a$  is formed when  $P_u$  is bound by NTF. As mentioned above, NTF binding to  $P_u$  is modelled as cooperative using a Hill function of NTF concentration multiplied by the constant  $K_{on}$ , where  $m$  is the Hill coefficient and  $kD_1$  is the affinity of synTF for the RE.  $P_a$  is additionally gained back when  $P_r$  spontaneously reverts back from refractory to active with rate  $d2_{rf}$ .  $P_a$  can switch to either  $P_u$  or  $P_r$  with rates  $K_{off}$  and  $K_{rf}$ , respectively:

$$\frac{dP_a}{dt} = K_{on} * \left( \frac{NTF^m}{kD_1^m + NTF^m} \right) * P_u + d2_{rf} * P_r - (K_{off} + K_{rf}) * P_a \quad [4]$$

Equation 5 describes the species  $P_r$ . Only species  $P_a$  can become  $P_r$  with rate  $K_{rf}$ , while  $P_r$  can revert back to either  $P_u$  or  $P_a$  with rates  $d1_{rf}$  and  $d2_{rf}$ , respectively:

$$\frac{dP_r}{dt} = K_{rf} * P_a - (d1_{rf} + d2_{rf}) * P_r \quad [5]$$

The sum of  $P_u$ ,  $P_a$  and  $P_r$  was modelled as a constant throughout the simulation. For a promoter with 4 REs, for example, the total was 4 multiplied by a factor 2, a scaling factor that was found to be needed to fit the data.

Equation 6 describes the assembly of the PIC. This occurs when the promoter is in the active state  $P_a$ . The rate of PIC assembly depends on NTF binding to one or more REs, as well as on the looping

efficiency ( $j_m^{-1}$ ) of the DNA sequence between the REs and the TATA box. The PIC can additionally disassemble with rate  $d_{pic}$ :

$$\frac{dPIC}{dt} = \frac{K_{pic}}{j_m} * \left( \frac{NTF^m}{kD_1^m + NTF^m} \right) * P_a - d_{pic} * PIC \quad [6]$$

Equation 7 describes RNA transcription of the target gene, that is, formation of nascent RNA (nRNA). We model this process as a Hill function of the PIC concentration, where  $n$  is the Hill coefficient and  $kD_2$  is the dissociation constant of the PIC components from the core promoter, multiplied by the rate constant  $K_{nrna}$ . We use a Hill function to model the cooperative binding of the general transcription factors that form the PIC. Additionally, the nRNA is released from the DNA template at rate  $d_{nRNA}$ :

$$\frac{dnRNA}{dt} = K_{nrna} * \left( \frac{[PIC]^n}{kD_2^n + [PIC]^n} \right) - d_{nRNA} * nRNA \quad [7]$$

Equation 8 describes the formation of mature RNA (mRNA). This is a function of the nascent RNA after it dissociates from the DNA template, and gets processed and translocated to the cytosol giving rise to the matured mRNA (mRNA) with rate  $K_{prosRNA}$ . To compensate for the fact that the nRNA visualization method we use gives only a rough estimate of the total transcribed RNA (that is, we can visualize only a focus when several nRNAs are present), we add a scaling factor  $f$ . We call the product of these two constants  $K_{mRNA}$ . We also assume that the mRNA gets degraded at a constant rate  $d_{mRNA}$ :

$$\frac{dmRNA}{dt} = K_{mRNA} * nRNA - d_{mRNA} * mRNA \quad [8]$$

Equation 9 describes ribosome loading on properly processed mRNA. This is modelled as a mass action function with rate  $K_{rbz}$  multiplied by the amount of translated mRNA. We assumed that not all mRNAs are translation-competent, hence a constant  $rt$  is subtracted from the mRNA amount. This term was deemed necessary because the model does not fit the 5'UTR constructs without it. mRNA-bound ribosomes can also dissociate at a fixed rate  $d_{rbz}$ :

$$\frac{drbz}{dt} = K_{rbz} * (mRNA - rt) - d_{rbz} * rbz \quad [9]$$

Equation 10 describes mRNA translation to an immature protein iP. We model this process as a function of the bound ribosomes multiplied by the constant  $K_{p1}$ . iP becomes mature protein mP at rate  $R_p$  and is degraded at rate  $d_p$ :

$$\frac{diP}{dt} = K_{p1} * rbz - (R_p + d_p) * iP \quad [10]$$

Finally, equation 11 describes the maturation of the fluorescent protein mP. mP gets degraded at rate  $d_{mp}$ :

$$\frac{dmP}{dt} = R_p * iP - d_{mP} * mP \quad [11]$$

The experimentally measured iRFP670 protein corresponds to the species mP.

Equation 12 describes how we calculate the factor  $j_m$ , and is based on previous work (2). L represents the distance between the TATA box and the last RE (that is, the RE closest to the TATA box) in bp, while P is the length of the DNA in nm. To calculate the length we use a previous estimate (2, 3):

$$j_m = \left( \frac{1.25e^5}{P^3} \right) * \left( \frac{4*P}{L*10^4} \right)^{\frac{3}{2}} * e^{-(510*P^2)/(6.25*L^2+50*P^2)} \quad [12]$$

The ODEs were written in python v3.8.3.final.0 using the Anaconda v2020.07 distribution. Numerical simulations were performed using the odeint function in SciPy v1.5.0 `scipy.integrate` module, which is used as a wrapper for the LSODA ordinary differential equation solver for stiff or non-stiff systems from the FORTRAN library `odepack`.

Initial conditions were set according to experimental observations or were fitted. Variables of interest were plotted using `matplotlib` plotting library.

## Parameters

The model entails a total of 22 parameters if we consider the promoter-specific parameters. Except for  $kD_1$ ,  $kD_2$ ,  $d_{mRNA}$  and  $R_p$ , all parameters were first fitted together using experimental data obtained with promoter p2 under sustained dynamics, namely nascent RNA and reporter protein kinetics, as well as reporter protein expression at the end of the experiment under different NTF levels (Supplementary Figure S4). The parameter  $d_{mRNA}$  was experimentally calculated for different mRNAs (Supplementary Figure S5). Parameter fitting was done using both adaptive memory programming for global optimization (`ampgo`) and basinhopping global optimization algorithms in the `Imfit.minimize` package in python. The parameter set that successfully predicted the nascent RNA and protein data for the remaining pulsatile dynamics (high- and low-frequency) was used for the other promoters. The values of  $m$ ,  $K_{pic}$ ,  $d_{pic}$ ,  $K_{nrna}$ ,  $d_{nrna}$ ,  $d_{rbz}$ ,  $K_{p1}$ ,  $dp$ , and  $d_{mp}$  were fixed for all promoters.  $K_{mRNA}$  was, instead, fitted for all constructs (due to the fact that the scaling factor  $f$  might differ across constructs).

In the instances of modified 5' UTR,  $rt$  was re-estimated from experimental data, and  $K_{on}$ ,  $K_{off}$ ,  $K_{rf}$ ,  $d1rf$ ,  $d2rf$ ,  $K_{mRNA}$ , and  $K_{rbz}$  were allowed to change, since we reasoned that changing 5' UTR affects the loading of ribosomes and the proportion of mRNA that is translated.

## **Parameter fitting**

All parameter fittings were done with data from the sustained dynamics. Parameters were first fitted with the least square function (leastsq) from the lmfit.minimize python module. The resulting parameters were then used as the initial parameter guesses for global parameter fit using the adaptive memory programming for global optimization method (ampgo) or basinhopping algorithm implemented in lmfit.minimize python module. To improve on the global parameter values, the ampgo fitted output was used as initial guesses for another round of leastsq function fitting to find the local minima of the global parameters.

## **A promoter that responds more strongly to pulses than to sustained signal exists: theoretical analysis**

From our data and previous studies (2, 4, 5), we can conclude that, whenever a promoter is activated by pulsatile dynamics, it is also activated by a sustained TF signal. In other words, from the building blocks that make a promoter (mostly the RE and the TATA box), it is not possible to obtain a variant that specifically filters sustained signals out, while responding to pulsatile ones. Wilson and colleagues showed, for the Ras/Erk pathway, that negative feedback can promote a band-pass filtering behaviour allowing target genes to be most efficiently activated by Erk pulses of specific frequencies (5). We asked ourselves if there could exist an alternative mechanism, involving no other molecule than the TF itself, which could allow a promoter to be better activated by pulsatile than sustained TF dynamics.

Recently, phase separation around genomic loci has been shown to play a regulatory role in gene expression (6–8). These studies relate condensate formation with enhanced activity of the transcriptional activators that localize in them. Theoretically, however, formation of condensates could have an inhibitory function as well: too high local TF concentrations could lead to a strong refractory response of the promoter, which could eventually enter into an inactive state. As a reminder, the refractory state is defined as the state of the promoter for which the PIC cannot be assembled despite the TF being bound at the RE(s), due to lack of GTFs locally available at the promoter to nucleate the PIC. Recent work by Chong and colleagues supports this notion (9). Here, the endogenous TF EWS::FLI1 is brought into condensates of different sizes by differentially overexpressing the EWS low complexity domain. Depending on the size of the condensates, the TF either activates or represses the reporter genes (9).

We sought to explore *in silico* whether this mechanism could make a promoter respond better to pulsatile than sustained TF dynamics. We modified the original mathematical model to include a fourth promoter state: inactive. We assume that the inactive state is reachable from the refractory state and that, from this inactive state, the promoter can go back to being in the unbound state (Supplementary Figure S9A). The rate at which the promoter switches from the inactive to the unbound state is a nonlinear inverse hill function of synTF concentration multiplied by the parameter  $D_{in}$ , which is a scaling factor that depends on how fast the TF dissociates from the promoter. With this modified model we scanned the values for  $D_{in}$  and the interval between pulses that would lead to higher reporter protein

levels at the end of the experiment (630 min) for pulses than sustained synTF signal (special case when the time between pulses = 0). We found several combinations of  $D_{in}$  and pulse frequencies that would lead to higher reporter protein levels in this case (Supplementary Figure S9B). We then took one such combination and simulated two dynamics for synTF: sustained and pulses of the selected frequency specified by the arrow in Figure 6B (55 min light activation followed by 25 min dark phase;  $D_{in}=0.0031$ ). Importantly, also in these simulations, we kept synTF cumulative levels constant, as done in the experiments. Therefore, the activation of synTF in the case of the pulsatile dynamics goes on for a longer time than for the sustained dynamics. We calculated the simulated mean nascent RNA levels over time for both dynamics. The model predicts that, while transcription rapidly decreases and eventually ceases for the sustained synTF signal, transcription goes on for the pulsatile synTF signal until there is no nuclear synTF (Supplementary Figure S9C). The predicted cumulative nascent RNA levels are, therefore, higher for the pulsatile than the sustained dynamics (Supplementary Figure S9D). The simulations show that a sustained synTF signal would lead to much lower reporter protein levels than the pulses (Supplementary Figure S9E). Taken together, the mathematical model indicates that it is possible for a promoter to be more efficiently activated by a pulsatile than a sustained TF signal, provided the TF inhibits PIC assembly when above a certain threshold.



**Supplementary Table S1** Sequences and affinities of promoter elements used to design reporter constructs tested in this study

<i>Element</i>	<i>Sequence</i>	<i>K<sub>d</sub> (nM)</i>
<i>strong RE</i>	CTGTATATAAAACCAGTGGTTATATGTACAGACTAGA	1.61
<i>weak RE</i>	CTGTAAAAAAAAAACAGTGGTTATATGTACAGACTAGA	5.64
<i>strong TATA</i>	AGACGCTATAAAAGGGATCC	2
<i>weak TATA</i>	AGAGGGTATATAATGGATCC	4
<i>seq1</i>	CTGTATATAAAACCAGTGGTTATATGTACAGACTAGACTCTG GACTCCTCCCCGGGTGTCGCTCCTTCATCTGACAATATGCA GCCGCTACCACCATCGATTAATAACAACGAACGGTGATGTTG TCATAGATTGCGCACATTTCCCTTGAGGTGTGAAATCACTT AGCTTCGCGCCGAAGTCTTATGAGTCCGAGCGGAGACTCT AGAGGGTATATAAT	-
<i>seq2</i>	CTGTATATAAAACCAGTGGTTATATGTACAGACTAGACTCTG GAGAATCCCGGTCTGCAGGCCGCTCAATTGGTCGTAGACA GCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCG CGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCA CGTGTCAGATATATACATCCTGATGAGTCCGAGCGGAGACT CTAGAGGGTATATAA	-
<i>UTR1</i>	AGAGGGTATATAATCGGCTATGCACGAAGCAACTCTTGCCA CCATGGCGCGTAAGGT	-
<i>UTR2</i>	AGAGGGTATATAATCGGCTATGCACGAAGCAACTCTAACCA CCATGGCGCGTAAGGT	-
<i>UTR3</i>	AGAGGGTATATAATCGGCTATGCACGAAGCAACTCTTGAGT GTATGGCGCGTAAGGT	-
<i>UTR4</i>	AGAGGGTATATAATGGATCCCCGGGTACCGAGCTCGAATTC CAATGGCGC	-
<i>UTR5</i>	AGAGGGTATATAATCGGCTATGCACGAAGCAACTCTAACCA CCATGGCGC	-
<i>UTR6</i>	AGACGCTATAAAAGGGCGGTACTGTTGGTAAATAGGCGCC ACCATGGCGC	-
<i>Stronger RE</i>	CTGTATATATATACAGTGGTTATATGTACAGACTAGA	0.8
<i>INR</i>	AGACTCTTACATCTACTGTT	-

The red coloured nucleotides indicate the sequence of the elements.

**Supplementary Table S2** Complete list of reporter constructs tested in this study

<i>Promoter</i>	<i>#RE</i>	<i>LexA affinity for RE (kD<sub>1</sub>) (nM)</i>	<i>λ (bp)</i>	<i>TBP affinity for TATA box kD<sub>2</sub> (nM)</i>	<i>δ (bp)</i>	<i>REF</i>
<i>p1</i>	4	1.61	49	2 <sup>*</sup>	69	(10, 11)
<i>p2</i>	4	1.61	49	4 <sup>*</sup>	69	(10, 11)
<i>p3</i>	4	5.64	49	2	69	(11, 12)
<i>p4</i>	4	5.64	49	4	69	(11, 12)
<i>p5</i>	4	1.61	196 <sup>a</sup>	2	69	(10, 11)
<i>p6</i>	4	1.61	196 <sup>a</sup>	4	69	(10, 11)
<i>p7</i>	4	1.61	196 <sup>b</sup>	4	69	(10, 11)
<i>p8</i>	2	1.61	49	4	69	(10, 11)
<i>p9</i>	2	1.61	49	2	69	(10, 11)
<i>p10</i>	4	0.80	49 bp	2	69	(11, 12)
<i>p11</i>	4	0.80	49bp	4	69	(11, 12)
<i>p12</i>	2	0.80	49bp	4	69	(11, 12)
<i>p13</i>	4	1.61	343 <sup>c</sup>	4	69	(10, 11)
<i>p14</i>	4	1.61	343 <sup>c</sup>	2	69	(10, 11)
<i>p15</i>	4	0.80	343 <sup>c</sup>	2	31	(11, 12)
<i>p16</i>	8	1.61	343 <sup>c</sup>	4	69	(10, 11)
<i>p17</i>	4	1.61	343 <sup>d</sup>	4	69	(10, 11)
<i>p18</i>	2	1.61	196 <sup>a</sup>	4	69	(10, 11)
<i>p19<sup>e</sup></i>	4	1.61	49	N/A	69	(10, 11)
<i>p20<sup>f</sup></i>	4	1.61	49	N/A	31	(10, 11)
<i>p21<sup>g</sup></i>	4	1.61	49	N/A	69	(10, 11)
<i>5UTR1</i>	4	1.61	49	4	31 <sup>h</sup>	(10, 11)
<i>5UTR2</i>	4	1.61	49	4	31 <sup>i</sup>	(10, 11)
<i>5UTR3</i>	4	1.61	49	4	31 <sup>j</sup>	(10, 11)
<i>5UTR4</i>	4	1.61	49	4	31 <sup>k</sup>	(10, 11)
<i>5UTR5</i>	4	1.61	49	4	31 <sup>l</sup>	(10, 11)
<i>5UTR6</i>	4	1.61	49	2	31 <sup>m</sup>	(10, 11)
<i>5UTR7</i>	4	5.64	49	2	31 <sup>n</sup>	(11, 12)
<i>5UTR8</i>	4	1.61	49	N/A	31 <sup>o</sup>	(10, 11)

<sup>\*</sup> We have used values derived from experimental studies in yeast (11). Experimental data obtained using human TBP appear to lie in a similar range (13). <sup>a</sup> Insertion of seq1 between REs and TATA box.

<sup>b</sup> Insertion of seq2 between REs and TATA box. <sup>c</sup> Insertion of 2x seq1 between REs and TATA box. <sup>d</sup> Insertion of 2x seq1 flanked by the CTCF binding sequence on both 5' and 3' ends. <sup>e</sup> Promoter with initiator sequence in place of TATA box combined by downstream promoter element. <sup>f</sup> Promoter with

2x initiator sequence (Inr) in place of the TATA box. <sup>g</sup> Promoter with 2x initiator sequence in place of the TATA-box. <sup>h</sup> Promoter p2 combined with optimal Kozak sequence. <sup>i</sup> Promoter p2 combined with suboptimal Kozak sequence. <sup>j</sup> Promoter p2 combined with a random sequence in place of the Kozak sequence. <sup>k</sup> Promoter p2 with 62% GC content between the TATA box and the start codon without Kozak sequence. <sup>l</sup> Promoter p2 with 55% GC content between the TATA box and the start codon combined with the suboptimal Kozak sequence. <sup>m</sup> Promoter p1 with 59% GC content between the TATA box and the start codon, and optimal Kozak sequence. <sup>n</sup> Promoter p4 with 59% GC content between the TATA box and the start codon, and optimal Kozak sequence. <sup>o</sup> Promoter p1 with the start codon, and optimal Kozak sequence without the TATA box.

**Supplementary Table S3** List of plasmids used in this study

<i>Name</i>	<i>Backbone</i>	<i>Insert</i>	<i>Promoter</i>	<i>Source</i>
<i>pDN98</i>	pmCherry-N1	LexA DNA binding /VP48 /IkBa NES/mCherry/LINuS (biNLS10)	CMV	(14)
<i>pDN100</i>	pFR-Luc	Firefly luciferase	4x LexA operator based promoter	(14)
<i>pEA00</i>	pDN98	Full length LexA	CMV	This study
<i>pEAXX</i>	pDN100	iRFP670-CAAX	4x LexA operator based promoter	This study
<i>pEA01</i>	pEA00	4x-LexA0/iRFP670-CAAX/BGH terminator	p2	This study
<i>pEA02</i>	pEA00	Reversed 4x-LexA0/iRFP670-CAAX/BGH terminator	p2	This study
<i>pEA03</i>	pEA01	Reversed CMV-full length LexA /VP48 /IkBa NES/mCherry/LINuS (biNLS10)/ SV40 terminator	p2	This study
<i>pEA04</i>	pEA01	Promoter p1	-	This study
<i>pEA05</i>	pEA04	Promoter p3	-	This study
<i>pEA06</i>	pEA05	Promoter p4	-	This study
<i>pEA07</i>	pEA04	Promoter p5	-	This study
<i>pEA08</i>	pEA01	Promoter p6	-	This study
<i>pEA09</i>	pEA01	Promoter p7	-	This study
<i>pEA10</i>	pEA04	Promoter p8	-	This study
<i>pEA11</i>	pEA01	Promoter p9	-	This study
<i>pEA12</i>	pEA01	Promoter p10	-	This study
<i>pEA13</i>	pEA12	Promoter p11	-	This study
<i>pEA14</i>	pEA12	Promoter p12	-	This study
<i>pEA15</i>	pEA01	Promoter p13	-	This study
<i>pEA16</i>	pEA04	Promoter p14	-	This study
<i>pEA17</i>	pEA12	Promoter p15	-	This study
<i>pEA18</i>	pEA15	Promoter p16	-	This study

**Supplementary Table S3** continued

<i>pEA19</i>	<i>pEA15</i>	<i>Promoter p17</i>	-	<i>This study</i>
<i>pEA20</i>	pEA08	Promoter p18	-	This study
<i>pEA21</i>	pEA01	Promoter p19	-	This study
<i>pEA22</i>	pEA01	Promoter p20	-	This study
<i>pEA23</i>	pEA04	Promoter p21	-	This study
<i>pEA24</i>	pEA01	Promoter p2 5UTR1	-	This study
<i>pEA25</i>	pEA01	Promoter p2 5UTR2	-	This study
<i>pEA26</i>	pEA01	Promoter p2 5UTR3	-	This study
<i>pEA27</i>	pEA01	Promoter p2 5UTR4	-	This study
<i>pEA28</i>	pEA01	Promoter p2 5UTR5	-	This study
<i>pEA29</i>	pEA04	Promoter p2 5UTR6	-	This study
<i>pEA30</i>	pEA06	Promoter p2 5UTR7	-	This study
<i>pEA31</i>	pEA01	Promoter p2 5UTR8	-	This study
<i>pEAm</i>	pEA01	IRES-SV40/NLS-MCP	-	This study
<i>pEAm00</i>	pEAm	12xMBS-PBS	-	This study
<i>pEAm01</i>	pEAm00	Minus BGH terminator	-	This study
<i>pEAm02</i>	pEAm01	Promoter p1	-	This study
<i>pEAm03</i>	pEAm01	Promoter p3	-	This study
<i>pEAm04</i>	pEAm01	Promoter p4	-	
<i>pEAm05</i>	pEAm01	Promoter p5	-	This study
<i>pEAm06</i>	pEAm01	Promoter p6	-	This study
<i>pEAm07</i>	pEAm01	Promoter p7	-	This study
<i>pEAm08</i>	pEAm01	Promoter p8	-	This study
<i>pEAm09</i>	pEAm01	Promoter p9	-	This study
<i>pEAm10</i>	pEAm01	Promoter p12	-	This study

**Supplementary Table S4** List of primers

#	Primer sequence 5'-3'
1	tcgtgtggctgccggtgaaccacttctggcgcaacagcat
2	gtcggccggcccgccgcttctgtaattaagctggtccgctaccaccagccagtcgccgttgcg
3	gaaagcggcgggcccggcc
4	tggttcaccggcagccac
5	aaaagaagaaaaagaagtcaaagacaaagtgtgaattatgtaggcggccgctcgagcatg
6	ggtggcgctatttaccac
7	gttggtaaataggcgccaccatggcgcgtaaggctgatc
8	ttgtctttgacttcttttcttttacccttatagcgttggtggtggcgccg
9	atagtaataattacggggcattagttc
10	taataactaatgcatggcggaatac
11	ccgccatgcattagtattacagacggatcgggagatc
12	accccgtaattgattactatgctggcaagtgtagcggtc
13	atccccgggtaccgagctcgaattccagcttgga
14	gctcggtagccgggatccctttatagcgtctagagtctccgctcggactcg
15	tgatcagacatgtatatggactgtaaaaaaaaacagtggttatatgtacagactagactgtaaaaaaaaacagt ggttatatgtacagactagactcgagtccgag
16	tccaatatacatgtctgatcactgtttttttacagtctagtctgtacatataaccactgtttttttacagtctagatgcgg ccgcgaa ttaatacaacgaacggtgatgtgtcatagattcggcacatttccctgtagggtgtgaaatcacttagcttcgcgccg
17	aagtcttatgagtcggagcggagactc
18	tgacaacatcaccgttcgttgattaatcgatggtgtagcggctgcattgtcagatgaaggagcgacaccgg ggaggagtccagagtctagtctgtacata
19	cgtacgcgctgtcccccgcttttaaccgccaaggggattactccctagtctccaggcacgtgtcagatatatacat cctgatgagtcggagcggagactcta
20	cgcgggggacagcgcgtacgtgcgtttaagcgggtgctagagctgtctacgaccaattgagcggcctgcagacc gggattctccagagtctagtctgtacatata
21	aattcgcggccgcatctagactgtatataaaaccagtgtacagacatgtatattggactgtatataaaaccagtgg tatatgtacagactagactcgagtccgagcg
22	tctagatgcggccgcgaattcggta
23	tatatacagtgatcagacatgtatattggactgtatatatatacagtgggttatatgtacagactagactgtatatata cagtgggttatatgtacagactagactcgagtccg
24	tccaatatacatgtctgatcactgtatatatatacagtctagtctgtacatataaccactgtatatatatacagtctagat gcggccgcgaattcgg
25	gcgtagctgcgcataagcaaatgacaattaaccactgtgtactcgttataacatctggcagttaaagtcgggaga ataggagccgagtcggagcggagactc
26	ttgcttatgcgcagctacgccatcgcgaggccggtccggcggggaagcatataaaagaagctcgtcacatcc acatagttgtataagacttcggcgcgaa

**Supplementary Table S4** continued

27	<b><i>tgatcagacatgtatattggactgtatataaaaccagtggttatgtacagactagactgtatataaaacc agtgattcgcggccgcacatctagactgt</i></b>
28	tccaatatacatgtctgatcactggttttatatacagctagctgtacatataaaccactggttttatatacagtcggtac ccggtcacagcttgtctg
29	gactcttactccctagctcttgatccccgggtaccg
30	aagactagggagtaagagtctccgctcggactc
31	gactcttactccctagctcttccggtactgttgtaaataagg
32	atggcgcgtaaggtcgatctcacctcctgcgatcgcgagccg
33	atcgaccttacgcgccatggtggcaagagtgtctcgtgcatagccgattatataccctc
34	atcgaccttacgcgccatggtggttagagttgcttcgtgcatagccgattatataccctc
35	atcgaccttacgcgccatacactcaagagtgtctcgtgcatagccgattatataccctc
36	atggatccccgggtaccgagctcgaattccaatggcgcgtaaggtcgatc
37	tggaattcgagctcggtagcccggggatccattatataccctctagagtctccgctc
38	atcgaccttacgcgccatggtggttcgagttgattcgtgcatagccgattatataccctctagagtctccgctcggac tcg
39	tggcgcctatttaccacagtagccgccctttatagcgtctagagtctccgctcggactc
40	ggtggcgcctatttaccacagtagccggaatcgcgcgccctctagagtctccgc
41	tcgctcgtccagtagttccaggtcatcagagcatgcacatagagggcc
42	tgctttcttggaataagtagcgtaggatcactagtacttccacctgaacctccctacataattacacactttgtcttg ac
43	acctaaatgctagagctcgtgatcagcctatagtaataattacggggtc
44	aggctgatcagcgagctc
45	agaagaaaaagctggactagatcgatggatccctcccccc
46	ccattttaacggtagcatgccaactttcttttcttttgggcccatcctgcaggctg
47	atgctagccgttaaaatggcttctaac
48	atcccgtctagaatccgcgtag
49	ttctagacgggatccaccggtcgccaccatggtgagcaagggcgaggag
50	gattatgatctagagtgcggccgctcgagttactgtacagctcgtc

### Supplementary Table S5 Model parameters

[illegible]



**Supplementary Table S5** continued

<i>Parameter</i>	<i>p8</i>	<i>p9</i>	<i>5UTR1</i>	<i>5UTR2</i>	<i>5UTR3</i>
<i>iOn</i>	0.0514	0.0514	0.0514	0.0514	0.0514
<i>iOff</i>	0.0059	0.0059	0.0059	0.0059	0.0059
<i>rOn</i>	0.1948	0.1948	0.1948	0.1948	0.1948
<i>rOff</i>	0.0817	0.0817	0.0817	0.0817	0.0817
<i>KTF</i>	52.1835	52.1835	52.1835	52.1835	52.1835
<i>dTF</i>	0.0297	0.0297	0.0297	0.0297	0.0297
<i>dNTF</i>	0.0081	0.0081	0.0081	0.0081	0.0081
<i>m</i>	2.8445	2.8445	2.8445	2.8445	2.8445
<i>kD1</i>	161.18	161.18	161.18	161.18	161.18
<i>n</i>	2.33	1.60	1.71	1.71	1.71
<i>kD2</i>	400	200	400	400	400
<i>Kon</i>	0.0410	0.0484	0.0999	0.0999	0.0999
<i>Koff</i>	0.0300	0.0119	0.0941	0.0941	0.0941
<i>Krf</i>	0.0213	0.4924	0.1594	0.1594	0.1594
<i>d1rf</i>	3.11E-05	2.94E-02	1.41E-02	1.41E-02	1.41E-02
<i>d2rf</i>	0.0000	0.0037	0.0061	0.0061	0.0061
<i>Kpic</i>	8.48E-06	8.48E-06	8.48E-06	8.48E-06	8.48E-06
<i>dpic</i>	0.5560	0.5560	0.5560	0.5560	0.5560
<i>Knrna</i>	19.5869	19.5869	19.5869	19.5869	19.5869
<i>dnRNA</i>	0.0474	0.0474	0.0474	0.0474	0.0474
<i>KmRNA</i>	17.7182	19.3246	26.5994	26.5994	17.7182
<i>dmRNA</i>	0.2340	0.2340	0.2090	0.2090	0.2340
<i>rt</i>	0	0	170	165	415
<i>Krbz</i>	0.0057	0.0057	0.0166	0.0115	0.0100
<i>drbz</i>	0.3600	0.3600	0.3600	0.3600	0.3600
<i>Kp1</i>	2.5381	2.5381	2.5381	2.5381	2.5381
<i>dp</i>	1.87E-03	1.87E-03	1.87E-03	1.87E-03	1.87E-03
<i>dmp</i>	1.41E-04	1.41E-04	1.41E-04	1.41E-04	1.41E-04
<i>Rp</i>	2.31E-03	2.31E-03	2.31E-03	2.31E-03	2.31E-03

**Supplementary Table S6** List of NF- $\kappa$ B target genes and the corresponding binding sites in the promoter region.

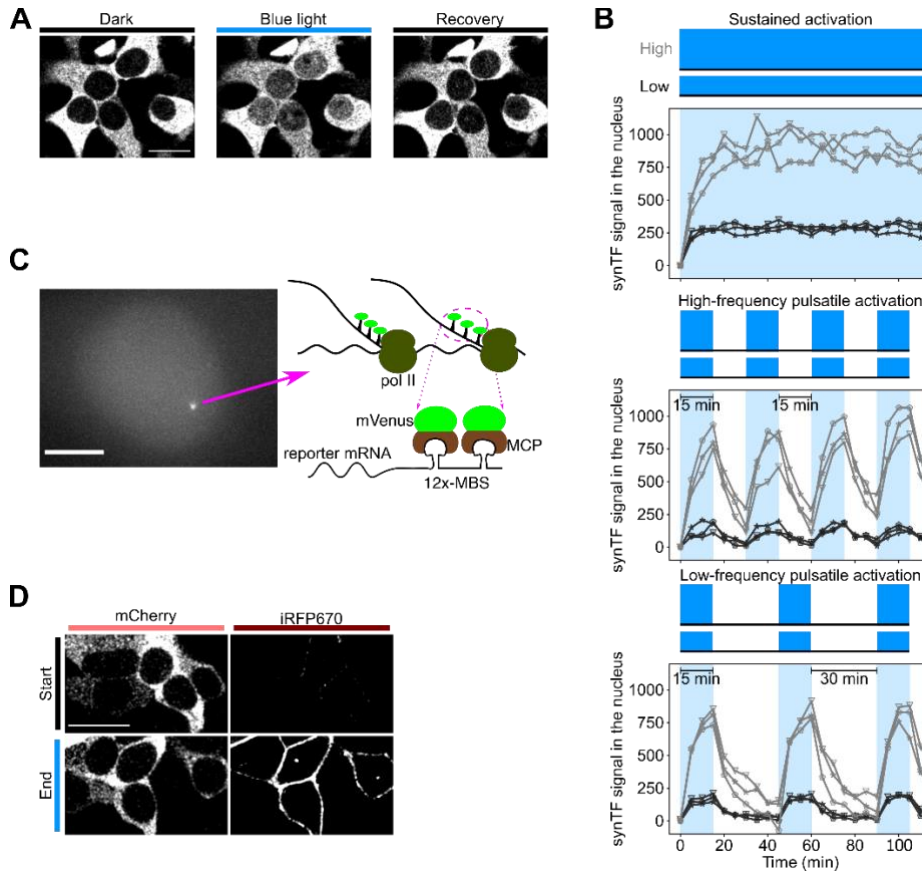
<i>Gene</i>	<i>NF-<math>\kappa</math>B binding site</i>	<i>Reference</i>
<i>IL1A</i>	ctacaggggcatgccatcac gaggaggggctcccctcaca	(15)
<i>IL1B</i>	aacgtgggaaaatccagtat	(16)
<i>TNF</i>	ccccggggctgtcccaggct tgtgaggggtatccttgatg ctcatgggtttctccaccaa	(17–19)
<i>CXCL10</i>	gcagagggaattccgtaac	(20)
<i>CXCL1</i>	actccgggaattccctggc	(21)
<i>CSF2</i>	gttcaggtagtcccccgcc	(22)
<i>CXCL8</i>	tcgtggaattcctctgaca	(23)
<i>IL6</i>	aatgtgggattttccatga	(24, 25)
<i>NFKBIA</i>	tcggaaggactttccagcca ggcttgaaattccccgagc	(26)
<i>TRAF1</i>	accctggggatttccaccag aaccaggggaactctcactg acaaagggttaattcctgctc	(27)
<i>IFNG</i>	cgtctggaactccccctggg	(28)

**Supplementary Table S7** List of p53 target genes and the corresponding binding sites in the promoter region.

<i>Genes</i>	<i>p53 responsive element</i>	<i>Reference</i>
<i>MDM2</i>	ggtcaagtcagacacgttc agttaagtctgactgtct	(29, 30)
<i>CDKN1A</i>	gaacatgtcccaacatgtg agactgggcatgtctgggca	(31)
<i>BAX</i>	tcacaagttagagacaagcctgggcgtgggc	(32, 33)
<i>GADD45A</i>	gaacatgtctaagcatgctg	(34, 35)
<i>PML</i>	gcgctggcctggagccaggggcatgtcc	(36)
<i>YPEL3</i>	gggctcgggtgaaacaagtccaggcgctgcga	(37)
<i>APAF1</i>	agacatgtctggagaccctaggacgacaagccc aggcacgtccccagcgacagcaggctc	(38–40)
<i>BBC3</i>	ctgcaagtcctgactgtcc	(34)
<i>XPC</i>	gaatttgcccagacaagcaacatggct	(41)
<i>TP53AIP1</i>	tctctgcccgggctgtcg	(42)
<i>PPM1D</i>	ggcccagctctcgcggaagtc	(43)

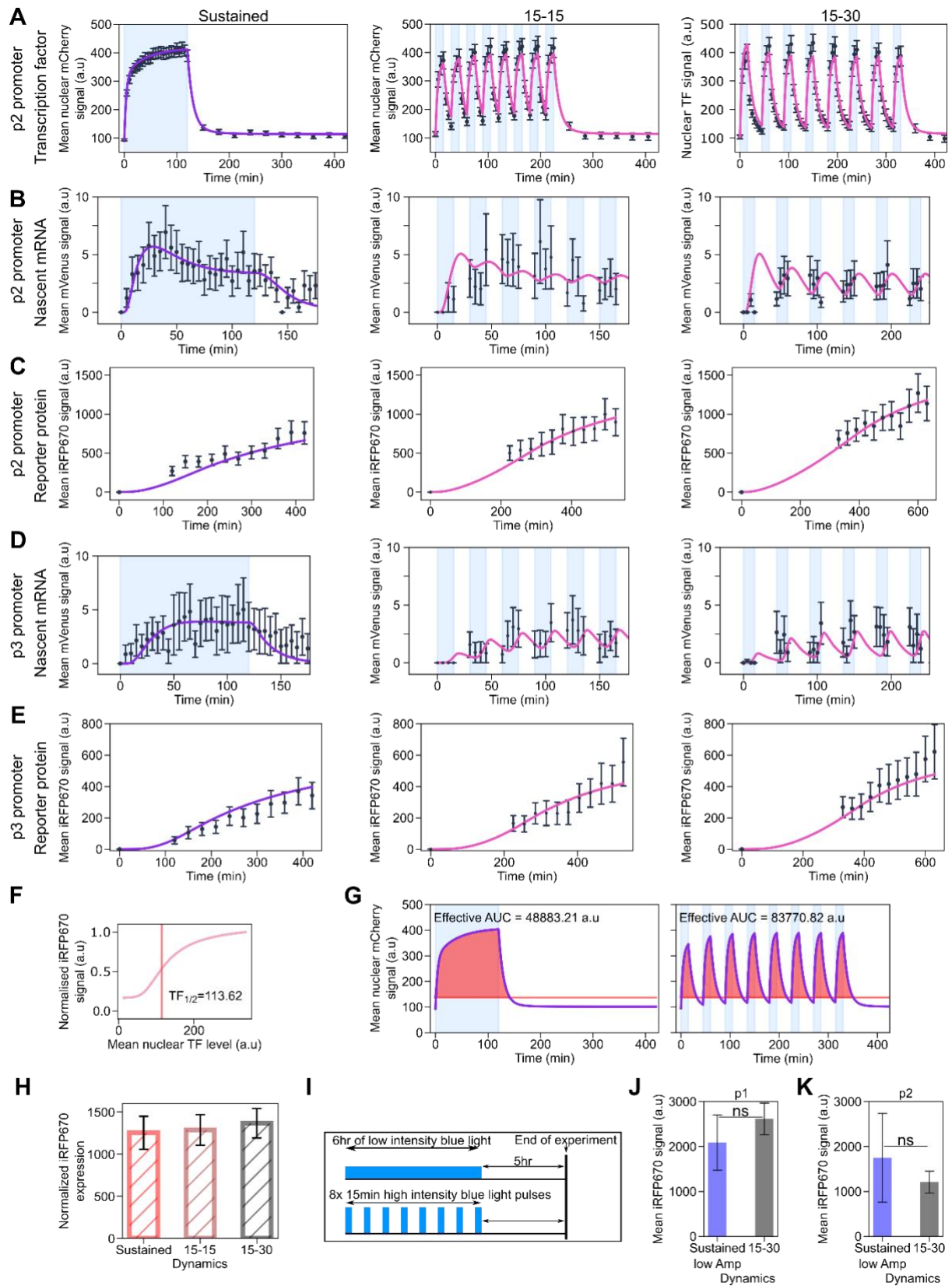
## Supplementary Figures

### Supplementary Figure S1



Experimental setup used in this study. **(A)** Representative fluorescence microscopy images showing accumulation of synTF in the nucleus of HEK293 cells upon blue light activation and recovery of cytoplasmic localization when the cells are kept in the dark. Illumination was performed shining  $6.44 \text{ Wm}^{-2}$  blue light for 125 msec every 45 sec for 15 min. Scale bar, 20  $\mu\text{m}$ . **(B)** Generation of different TF dynamics with synTF. Graphs showing the nuclear TF signal over time in three distinct cells. Grey curves, high amplitude signal. Black curves, low amplitude signal. The low amplitude signal was achieved by illuminating the cells every 90 sec instead of every 45 sec. **(C)** Setup for live cell imaging of nascent RNA (nRNA). To monitor nRNAs in living cells, we deployed the MS2/MCP system (44, 45), comprising the bacteriophage MS2 capsid protein (MCP), fluorescently labeled by means of a genetic fusion to an FP (mVenus in our case), and multiple repeats of sequence-specific RNA stem loops (twelve in our case), which are integrated in the reporter transcript at the 5' or 3' UTR (3' UTR in our case). The stem loops are specifically bound by MCP, rendering the transcripts visible under the microscope at the site of transcription. Left, representative fluorescence microscopy image showing a fluorescent focus indicating the presence of several nRNAs. Scale bar, 5  $\mu\text{m}$ . Right, schematic representation of the RNA visualization method used. MCP, MS2 coat protein. MBS, MCP binding site. MCP is expressed as a fusion to mVenus. **(D)** Representative fluorescence microscopy images of HEK293 cells showing synTF (mCherry) and reporter (iRFP670) levels before and after illumination with blue light. The reporter protein, iRFP670, is fused to the CAAX motif for plasma membrane localization. Scale bar, 20  $\mu\text{m}$ .

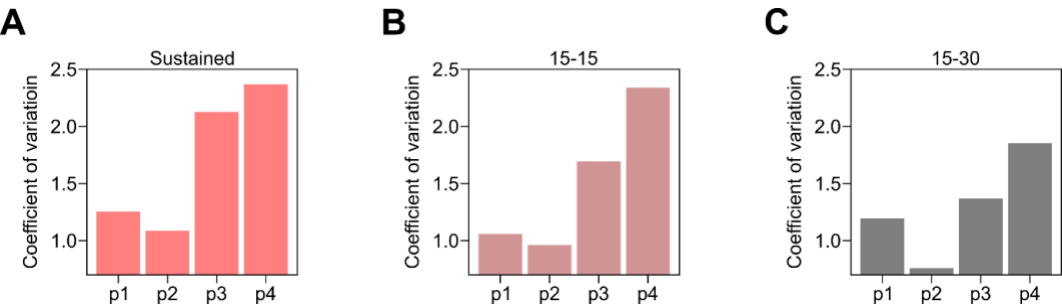
## Supplementary Figure S2



Characterization of promoters p1, p2 and p3. **(A)** Quantification of synTF nuclear translocation over time for the indicated TF dynamics. **(B,D)** Quantification of mean reporter nascent RNA over time for the indicated TF dynamics. **(C,E)** Quantification of mean reporter protein levels over time for the indicated TF dynamics. (A-C) The promoter

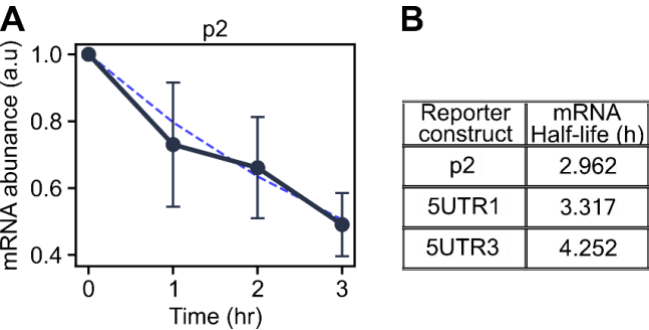
used in these experiment was p2. (D-E) The promoter used in these experiment was p3. (F) Prediction of synTF concentration above which the reporter protein is expressed above the half maximal value. (G) Calculation of the effective synTF cumulative levels using the threshold calculated in (F) for sustained (upper panel) and 15-30 pulsatile (lower panel) dynamics. (H) Quantification of mean reporter protein levels at the end of the experiment for the indicated synTF dynamics normalized using the effective cumulative synTF levels calculated in (G). (F-G) The promoter used was p1. (I) Schematic showing the experimental setup in which amplitude was varied to achieve similar cumulative synTF levels at fixed experimental time. (J,K) Quantification of mean reporter protein levels for the indicated TF dynamics for promoters p1 (J) and p2 (K). Light blue shadowing, blue light illumination phase. Together with the experimental data (black dots), fitted (violet line; for sustained dynamics) and simulated (pink line; for both pulsatile dynamics) values are shown. The mathematical model is shown in Figure 4 and the equations are described in the Supplementary Text. (A-E, H, J-K) Data represent mean  $\pm$  s.e.m. of at least n=20 individual cells, imaged on at least n=3 biologically independent experiments. P-values were calculated with the Welch's t-test. ns, non significant ( $P > 0.05$ ).

Supplementary Figure S3



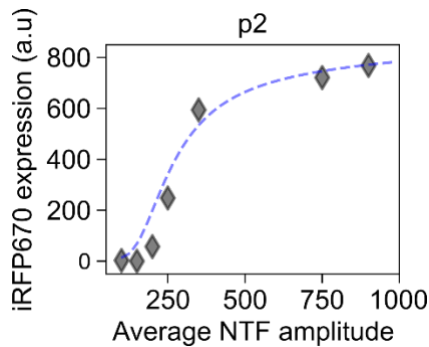
Promoters p3 and p4 are noisy. (A-C) Quantification of the coefficient of variation for the mean reporter protein levels at the end of the experiments for the indicated promoters under sustained (A), 15-15 (B) and 15-30 (C) pulsatile dynamics.

Supplementary Figure S4



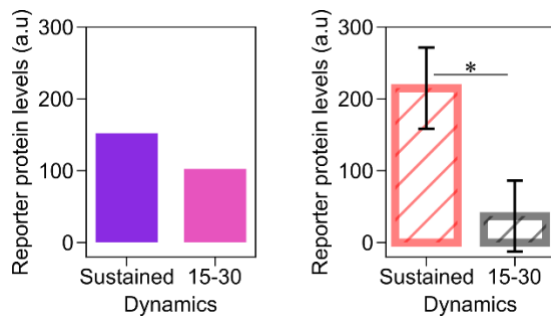
Experimental estimation of mRNA half-life. (A) Graph showing the mRNA levels measured via qPCR using the construct with the p2 promoter after addition of actinomycin D to the cells at time point t = 0. The experimental data are shown in black, the trend line in blue. Data represent the mean  $\pm$  s.d. of n=3 biologically independent experiments. (B) Estimated mRNA half-life for the three indicated reporter constructs.

### Supplementary Figure S5



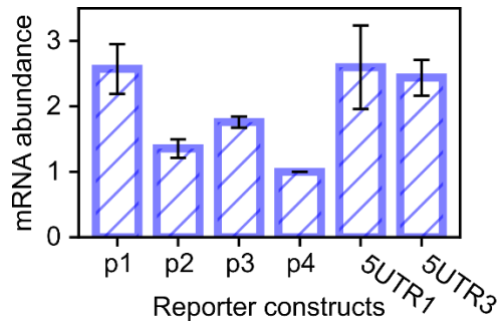
Reporter gene expression as a function of NTF concentration. Graph showing the amount of iRFP670 measured at the end of the experiment (5 h post sustained light activation, using promoter p2) in HEK293 cells expressing synTF in the nucleus at a certain concentration (indicated on the X-axis). Gray diamonds and blue dashed line represent experimental and fitted data, respectively. Data represent the mean of at least  $n=20$  individual cells, imaged on at least  $n=3$  biologically independent experiments.

### Supplementary Figure S6



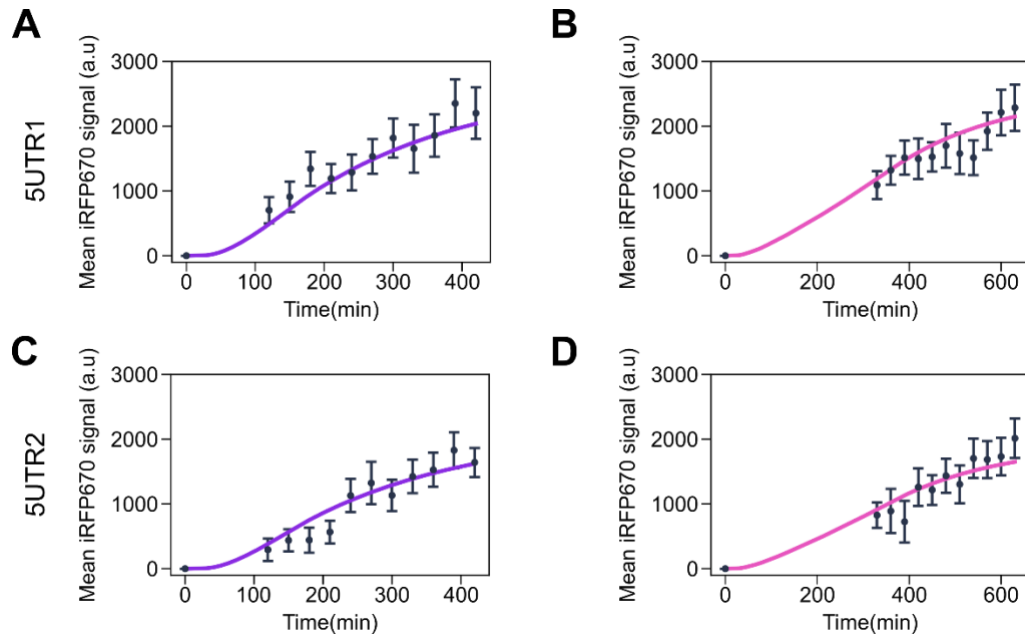
Promoter p2 with two instead of four REs senses dynamics also at the protein level. Model predictions (left panel; fitted (violet bar) and simulated (pink bar)), and experimental data (right panel) for the mean reporter protein levels at the end of the experiment for the indicated synTF dynamics in combination with promoter p9, which is a version of promoter p2 with two instead of four REs. Data represent mean  $\pm$  s.e.m. of at least  $n=20$  individual cells, imaged on at least  $n=3$  biologically independent experiments. P-values were calculated with the Welch's t-test. \*, P-value = 0.01545.

### Supplementary Figure S7



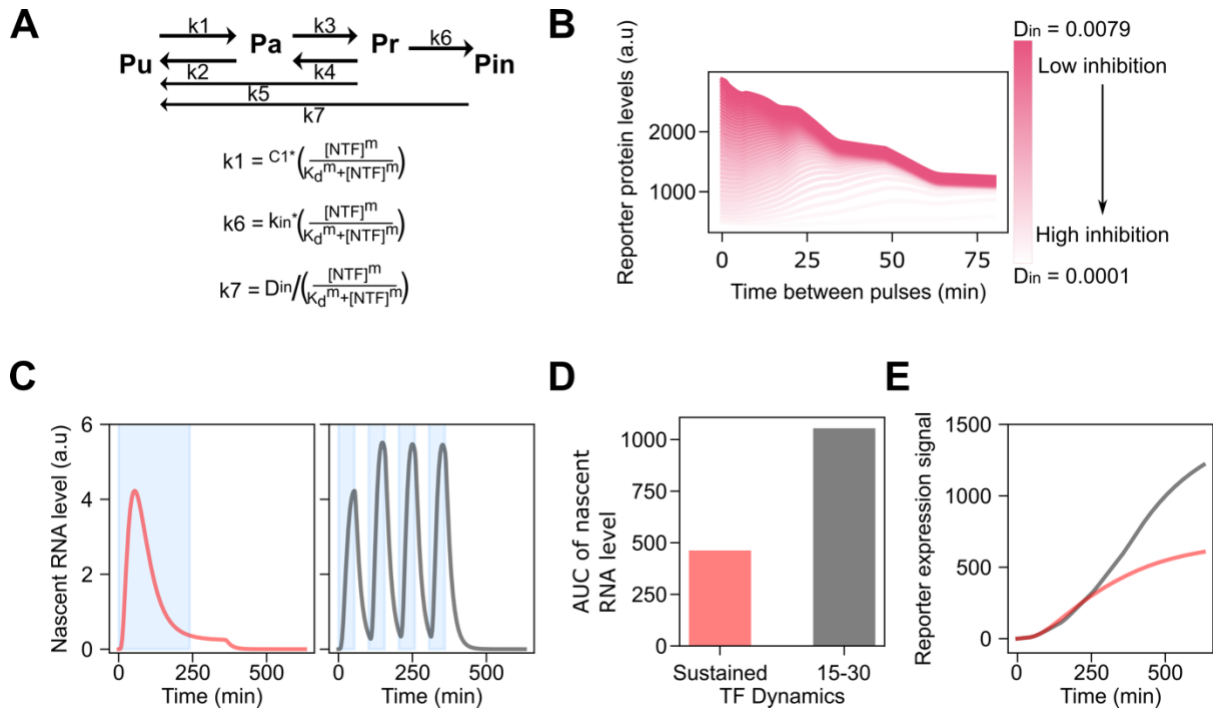
Relative mRNA abundance for different reporter constructs. Graph showing the mRNA levels measured by qPCR in HeLa cells transfected with the indicated constructs. Data represent mean  $\pm$  s.d. of  $n=3$  biologically independent experiments.

### Supplementary Figure S8



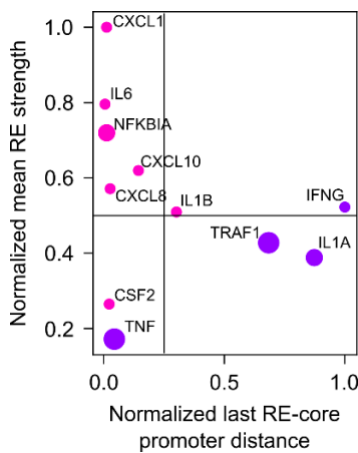
Measurements of mean reporter protein levels over time for constructs 5UTR1 and 5UTR2. **(A-D)** Quantification of mean reporter protein levels over time for sustained (A,C) and 15-30 pulsatile (B,D) dynamics for constructs 5UTR1 (A,B) and 5UTR2 (C,D). Data represent mean  $\pm$  s.e.m. of at least  $n=20$  individual cells, imaged on at least  $n=3$  biologically independent experiments. Lines represent simulations. Violet lines represent data fitting, while pink lines represent predictions.

**Supplementary Figure S9**



A promoter that filters out sustained signal, but is activated by pulses can theoretically exist. **(A)** Modified mathematical model that includes a fourth promoter state. Only the rates, which are different compared with the model without the fourth promoter state, are shown. **(B)** Simulated values of the reporter protein at the end of the experiment as a function of the interval between pulses for different values of the parameter  $D_{in}$ . When the time between pulses is zero the signal is sustained. Black arrow, selection of parameters used to simulate the system in (C-E).  $D_{in} = 0.0007$ . Time between pulses = 48 min. **(C)** Simulated nascent RNA levels for sustained (left panel) or pulsatile (right panel) dynamics using the model shown in (A) and the values for  $D_{in}$  and time between pulses selected in (B). Simulated area under the curve (AUC) for the nascent RNA for the indicated dynamics. **(E)** Simulated reporter protein levels over time for sustained (coral curve) or pulsatile (grey curve) TF dynamics.

**Supplementary Figure S10**



Promoter features allow the classification of NF- $\kappa$ B-responsive promoters into sensitive and insensitive to dynamics. Plot showing NF- $\kappa$ B-responsive promoters according to the distance between the last RE and the core promoter normalized to the longest distance (x-axis) and the mean RE strength normalized to the strongest RE (y-



axis). Each dot represents a promoter, color-coded to indicate activation by pulsatile (magenta) or sustained (violet) TF signal. The size of the dots increases with the number of REs.

### **Legend to Supplementary Video S1**

Nascent RNA visualization for promoter p1 under sustained synTF dynamics. HEK293 cells expressing NLS-MCP-mVenus for the visualization of the target RNA were transiently transfected with the plasmid encoding synTF and the reporter gene iRFP670 under promoter p1. synTF was subjected to sustained dynamics. Nascent RNA was visualized every 5 min for two hours.

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