Comparing the noise in positional readout between models

With the fitted parameters (S2 Table), we compare the precision of gene expression readout f_T between the case N=6, N=9 at the boundary position (X=X_0). Here, the readout is defined as the mean duration the *hb* gene is activated at steady-state:

$$f_T = \int_{t=0}^{T} \frac{1}{T} n(t). \tag{14}$$

with $n(t)$ being the trajectory of the gene activity state over time. $n(t)$ is 1 when the gene is activated and 0 otherwise. The relative noise in the readout CV_P is defined as follow:

$$CV_P = \frac{\delta fT}{\langle f_T \rangle} = \sqrt{\frac{\langle f_T^2 \rangle - \langle f_T \rangle^2}{\langle f_T \rangle^2}}, \tag{15}$$

in which $<f_T>$=0.5 and $<f_T^2>$ are respectively the first and second moments of the readout at the pattern's boundary (X=$X0$). Let us define a vector s_{fire} where $s_{fire,i}=\alpha_i.s_i$. $<f_T^2>$ is calculated numerically from the transition matrix U [9]:

$$\langle f_T \rangle = \frac{2\alpha^{\mathrm{T}}}{T}\left[\int_0^T dt(T-t)e^{Ut}\right] s_{fire}, \tag{15}$$

The precision of gene expression readout between the model with N=6 and N=9 are shown in S12 Fig. Also shown is precision from the "no cooperativity" case, where interactions of TF with the binding sites are independent ($k_{-i} = i.k_{-N}/N$)**.**