**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:

$$f_T = \int_{t=0}^{T} \frac{1}{T} n(t).$$  \hspace{1cm} (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:

$$CV_P = \frac{\delta f_T}{\langle f_T \rangle} = \sqrt{\frac{\langle f_T^2 \rangle - \langle f_T \rangle^2}{\langle f_T \rangle^2}},$$  \hspace{1cm} (15)

in which $\langle f_T \rangle=0.5$ and $\langle f_T^2 \rangle$ are respectively the first and second moments of the readout at the pattern’s boundary ($X=X_0$). Let us define a vector $s_{\text{fire}}$ where $s_{\text{fire, i}} = a_i s_i$. $\langle f_T^2 \rangle$ is calculated numerically from the transition matrix $U$ [9]:

$$\langle f_T \rangle = \frac{2a^T}{T} \left[ \int_0^T dt (T-t) e^{Ut} \right] s_{\text{fire}},$$  \hspace{1cm} (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 ($k_{i} = i.k.N/N$).