Table S2. Notation for various symbols used in the main text and supplementary information

	Symbol	Name
Free Energies of different configurations	G_i^C	Closed chromatin conformation of enhancer *i*: (*i = s* (*Scl+19), g (Gata2-3), f (Fli1+12))*
	G_i^{Gata2}	Gata2 bound to enhancer *i*: (*i = s* (*Scl+19), g (Gata2-3), f (Fli1+12))*
	G_i^{Fli1}	Fli1 bound to enhancer *i*: (*i = s* (*Scl+19), g (Gata2-3), f (Fli1+12))*
	$G_i^{Fli1Gata2}$	Gata2& Fli1 bound to enhancer *i*: (*i = s* (*Scl+19), g (Gata2-3), f (Fli1+12))*
	$G_i^{SclGata2Fli1}$	Scl&Gata2&Fli1 bound to enhancer *i*: (*i = g (Gata2-3), f (Fli1+12))*
	G^N	Notch bound to promoter
	G^B	Bmp4 bound to promoter
	G^P	Polymerase bound to promoter
Free energies of interaction	G^{BP}	Bmp4 and RNA polymerase interaction energy
	G^{NP}	Notch and RNA polymerase interaction energy
Chromatin Equilibrium Constants	K_i	Chromatin equilibrium constant for enhancer *i*: (*i = s* (*Scl+19), g (Gata2-3), f (Fli1+12))* $K_i = e^{-G_i^C}$
Concentrations	*[SCL]*	Intracellular Scl concentration
	[GAT]	Intracellular Gata2 concentration
	[FLI]	Intracellular Fli1 concentration
	[Gata1]	Intracellular Gata1 concentration
	[N]	Intracellular Notch concentration
	[B]	Intracellular Bmp4 concentration
	$[R_p]$	Intracellular RNA polymerase concentration
Steady State Concentrations	$\overline{[SCL]}$	Scl concentration in high steady state
	$\overline{[GAT]}$	Gata2 concentration in high steady state
	$\overline{[FLI]}$	Fli1 concentration in high steady state

Dimensionless Concentrations	$[scl]$	Concentration of Scl relative to concentration in high steady state. $[scl]=[SCL]/\overline{[SCL]}$
	$[gat]$	Concentration of Gata2 relative to concentration in high steady state. $[gat]=[GAT]/\overline{[GAT]}$
	$[fli]$	Concentration of Fli1 relative to concentration in high steady state. $[fli]=[FLI]/\overline{[FLI]}$
	$[n]$	Concentration of Notch relative to dissociation constant of binding to the promoter. $[n]=[N]/e^{G^N}$
	$[b]$	Concentration of Scl relative to concentration in high steady state. $[b]=[B]/e^{G^B}$
Other symbols used	p_o^i	Probability of open chromatin conformation for enhancer *i*: (*i = s (Scl+19), g (Gata2-3), f (Fli1+12))*
	$p^i(R_p)$	Probability of RNA polymerase being bound to promoter for enhancer-reporter construct with enhancer *i*: (*i = s (Scl+19), g (Gata2-3), f (Fli1+12)).* $p^i(R_p)=[R_p]e^{-G^P}p_o^i$
	I_o^i	Maximum rate of transcription from SV promoter. $I_o=kR_pe^{-G^P}$
	I^i	Rate of transcription from SV promoter-enhancer construct for enhancer *i*: (*i = s (Scl+19), g (Gata2-3), f (Fli1+12))* $I^i=I_o p_o^i$
	I_1	Maximum rate of protein production from SV promoter. $I_1=k_1I_o$
	k	Rate of isomerization of SV promoter bound RNA polymerase to open conformation
	k_1	Number of proteins produced per lifetime of mRNA
	$\mathbf{Z_i}$	Partition function for enhancer *i*: (*i = s (Scl+19), g (Gata2-3), f (Fli1+12))*
	Z_i^E	Sum of Boltzmann weights for all open chromatin state enhancer configurations of enhancer *i*. (*i=s* (*Scl+19*), *g* (*Gata2-3*), *f* (*Fli1+12*)).
	k_d^i	Degradation rate for TR *i*: (*i=s* (Scl), *g* (Gata2), *f* (Fli1)).