

Protocol S4. Fits Based on the Combined Network Structure

The regulatory relationships in the Combined model are sufficient to fit the expression data using either the gene circuit formalism (RMS error 14.01) or the logical formalism (RMS error 14.91) for representing the production rate functions. Figure 1 shows the parameters from the best-scoring fits. The simulated expression resulting from these models is shown in Figure 2B,C.

Combined-GC

Gene	Max prod. rate (R^a)	regulatory weights (T^{ab})							Bias (h^a)	Decay (λ^a)	Diff. (D^a)
		Bcd	Cad	Hb	Kr	Gt	Kni	Tll			
Hb	32.5274	0.1090	.	0.0332	-0.0220	.	-0.0303	0.0179	-3.5	0.1377	1.997
Kr	17.0549	0.4517	.	-0.2671	0.2506	-0.0413	-0.2549	-0.0001	-3.5	0.0647	0.918
Gt	22.6812	0.0691	0.0180	-0.0023	-0.0235	0.0185	.	-0.0055	-3.5	0.1125	0.148
Kni	13.0381	0.6958	0.0204	-1.1855	.	-0.0049	.	-0.3178	-3.5	0.0381	0.269

Combined-Logic

Gene	Max prod. rate (R^a)	Production Rule	Decay (λ^a)	Diff. (D^a)
Hb	30.6	$(Bcd \geq 23 \text{ or } Hb \geq 54 \text{ or } Tll \geq 126) \text{ and } Kr \leq 148 \text{ and } Kni \leq 3$	0.146	1.48
Kr	15.5	$(Bcd \geq 9 \text{ or } Kr \geq 147) \text{ and } Hb \leq 147 \text{ and } Gt \leq 7 \text{ and } Kni \leq 123 \text{ and } Tll \leq 4$	0.065	0.61
Gt	16	$(Bcd \geq 38 \text{ or } Cad \geq 132 \text{ or } Gt \geq 91) \text{ and } Hb \leq 208 \text{ and } Kr \leq 17 \text{ and } Tll \leq 94$	0.076	0.64
Kni	16.7	$(Bcd \geq 5 \text{ or } Cad \geq 175) \text{ and } Hb \leq 3 \text{ and } Gt \leq 80 \text{ and } Tll \leq 8$	0.07	0.74

Figure 1: Parameters for best-scoring models using the Combined regulatory relationships, with gene circuit and logical formalisms for production rate functions.

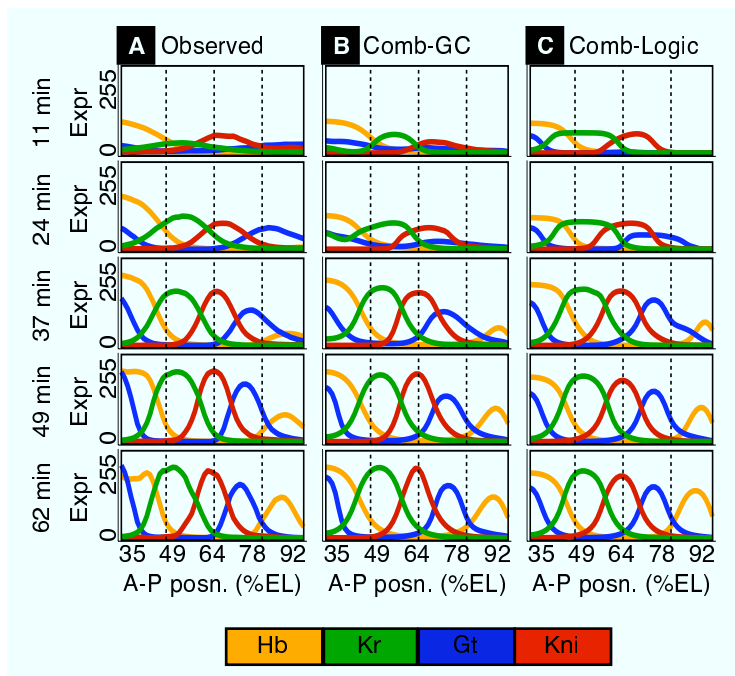


Figure 2: Observed gap expression and simulated expression from the Combined models.