

**Table S1. Phases and Relative Amplitudes of Bioluminescence Rhythm Driven by Clock-Controlled Elements, Related to Figures 1, 2, 3, 4, and 6**

Related to	Reporter construct	Phase (hours)		Relative amplitude		
		(n = 3, if not stated)		(n = 3, if not stated)		
		Mean	SD	Mean	SD	
<b>Figure 1A</b>						
	P( <i>Cry1</i> )	9.60	0.11	---	---	
	E'-box-P(SV40)	3.53	0.04	---	---	
	D-box-P(SV40)	10.42	0.16	---	---	
<b>Figure 1D</b>						
	Cry1proD-P(SV40)	12.37	0.05	---	---	
	E'-box-P(SV40)	3.41	0.14	---	---	
	D-box-P(SV40)	10.38	0.09	---	---	
<b>Figure 2B</b>						
	P( <i>Cry1</i> )	10.51	0.30	---	---	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 1.03k	14.62	0.20	---	---	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336	14.32	0.23	---	---	
	P( <i>Cry1</i> )- <i>Cry1</i> intron $\Delta$ 336	10.37	0.24	---	---	
<b>Figure 2C</b>						
	no <i>Cry1</i> intron	10.04	0.13	---	---	
	upstream of P( <i>Cry1</i> )	12.22	0.05	---	---	
	downstream of P( <i>Cry1</i> )	14.94	0.34	---	---	
	inside of the coding sequence	13.91	0.04	---	---	
	downstream of the coding sequence	12.61	0.39	---	---	
<b>Figure 3C</b>						
	P(SV40)	---	---	0.05	0.00	n=2
	P(SV40)- <i>Cry1</i> intron 336	17.58	0.52	0.29	0.00	
	P(SV40)- <i>Cry1</i> intron 336 R1deletion	17.28	---	0.15	0.05	n=2
	P(SV40)- <i>Cry1</i> intron 336 R2 deletion	17.77	0.17	0.12	0.04	n=2
	P(SV40)- <i>Cry1</i> intron 336 R1,2 deletion	---	---	0.05	0.00	
	P(SV40)- <i>Cry1</i> intron 336 R1 mutation	17.14	0.29	0.14	0.00	
	P(SV40)- <i>Cry1</i> intron 336 R2 mutation	---	---	0.05	0.00	
	P(SV40)- <i>Cry1</i> intron 336 R1,2 mutation	---	---	0.05	0.01	
	P(SV40)- <i>Cry1</i> intron 336 R1 inversion	17.30	0.30	0.27	0.02	
	P(SV40)- <i>Cry1</i> intron 336 R2 inversion	17.62	0.74	0.12	0.00	
	P(SV40)- <i>Cry1</i> intron 336 R1,2 inversion	17.74	0.13	0.11	0.03	n=2

**Table S1 (continued)**

Related to	Reporter construct	Phase (hours)		Relative amplitude		
		(n = 3, if not stated)		(n = 3, if not stated)		
<b>Figure 3E</b>		<b>Mean</b>	<b>SD</b>	<b>Mean</b>	<b>SD</b>	
	P( <i>Cry1</i> )	10.63	0.18	0.17	0.01	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336	14.03	0.45	0.21	0.08	n=2
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1deletion	11.70	0.51	0.19	0.02	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 deletion	11.65	0.22	0.23	0.01	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 deletion	10.36	0.58	0.24	0.01	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1 mutation	12.49	0.11	0.20	0.01	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 mutation	11.18	0.07	0.25	0.00	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 mutation	9.61	0.45	0.24	0.02	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1 inversion	13.43	0.53	0.21	0.06	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 inversion	10.48	0.85	0.21	0.01	
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 inversion	10.96	0.82	0.21	0.00	
<b>Figure 4A</b>						
	E'-box-P(SV40)	3.27	0.18	0.63	0.04	
	E'-box-P(SV40)- <i>Cry1</i> intron 336	2.13	1.79	0.10	0.00	
	D-box-P(SV40)	9.31	0.16	0.21	0.01	
	D-box-P(SV40)- <i>Cry1</i> intron 336	14.48	0.21	0.33	0.01	
	RRE-P(SV40)	17.04	0.12	0.37	0.01	
	RRE-P(SV40)- <i>Cry1</i> intron 336	16.32	0.04	0.64	0.01	
<b>Figure 6A</b>						
	3xE'-box-P(SV40)	3.37	0.11	0.40	0.03	
	3xRRE-P(SV40)	18.55	0.13	0.26	0.01	
	P( <i>Cry1</i> )	9.61	0.13	0.18	0.01	
	3xD-box-P(SV40)	9.84	0.50	0.14	0.02	
	2xD-box-P(SV40)	11.48	0.21	0.08	0.01	
	1xD-box-P(SV40)	---	---	0.06	0.00	
	3xCry1proD-P(SV40)	13.43	0.17	0.15	0.00	
	2xCry1proD-P(SV40)	12.70	0.32	0.18	0.01	
	1xCry1proD-P(SV40)	12.00	0.20	0.11	0.05	
	P(SV40)	---	---	0.06	0.00	

**Table S1 (continued)**

Related to	Reporter construct	Phase (hours)		Relative amplitude	
		(n = 3, if not stated)		(n = 3, if not stated)	
Figure 6B		Mean	SD	Mean	SD
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336	14.61	0.14	0.19	0.01
	3xD-box-P(SV40)- <i>Cry1</i> intron 336	15.46	0.30	0.21	0.02
	2xD-box-P(SV40)- <i>Cry1</i> intron 336	16.60	0.20	0.26	0.01
	1xD-box-P(SV40)- <i>Cry1</i> intron 336	17.35	0.10	0.29	0.02
	3xCry1proD-P(SV40)- <i>Cry1</i> intron 336	16.64	0.11	0.26	0.01
	2xCry1proD-P(SV40)- <i>Cry1</i> intron 336	16.56	0.15	0.27	0.02
	1xCry1proD-P(SV40)- <i>Cry1</i> intron 336	16.61	0.16	0.21	0.03
	P(SV40)- <i>Cry1</i> intron 336	17.39	0.12	0.34	0.02

**Table S2. Relative Amplitudes of Rescued Rhythms, Related to Figure 5**

Related to	Rescue construct	Relative amplitude (n = 3)	
		Mean	SD
Figure 5A	without <i>Cry1</i>	0.14	0.02
	P( <i>Cry1</i> )	0.23	0.00
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336	0.81	0.01
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1deletion	0.41	0.00
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 deletion	0.48	0.02
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 deletion	0.32	0.01
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1 mutation	0.41	0.01
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 mutation	0.36	0.03
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 mutation	0.30	0.01
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1 inversion	0.79	0.03
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R2 inversion	0.60	0.01
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 inversion	0.54	0.02

**Table S3. Periods of Rescued Rhythms, Related to Figures 6, 7, S5, and S6**

Related to	Rescue construct	Period (hours)	
		(n = 3)	
		Mean	SD
<b>Figure 6D</b>			
	P(SV40)- <i>Cry1</i> intron 336	30.89	0.13
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336	27.03	0.15
	3xD-box-P(SV40)- <i>Cry1</i> intron 336	29.42	1.33
	2xD-box-P(SV40)- <i>Cry1</i> intron 336	29.45	0.12
	1xD-box-P(SV40)- <i>Cry1</i> intron 336	30.27	0.09
	3xCry1proD-P(SV40)- <i>Cry1</i> intron 336	28.80	0.01
	2xCry1proD-P(SV40)- <i>Cry1</i> intron 336	28.90	0.12
	1xCry1proD-P(SV40)- <i>Cry1</i> intron 336	29.75	0.10
<b>Figure 7A</b>			
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336- <i>Cry1</i>	26.77	0.12
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336 R1,2 mutation- <i>Cry1</i>	---	---
	P(SV40)- <i>Cry1</i> intron 336- <i>Cry1</i>	32.00	0.58
	P(SV40)- <i>Cry1</i> intron 336 R1,2 mutation- <i>Cry1</i>	---	---
<b>Figure S5E</b>			
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336- <i>Cry1</i>	26.24	0.27
	P(SV40)- <i>Cry2</i>	---	---
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336- <i>Cry1</i> and P(SV40)- <i>Cry2</i>	25.38	0.06
<b>Figure S6D</b>			
	P( <i>Cry1</i> )- <i>Cry1</i>	---	---
	P( <i>Cry1</i> )- <i>Cry1</i> intron 336- <i>Cry1</i>	27.02	0.01
	P(SV40)- <i>Cry1</i>	---	---
	P(SV40)- <i>Cry1</i> intron 336- <i>Cry1</i>	30.99	0.26
	P(TKms)- <i>Cry1</i>	---	---
	P(TKms)- <i>Cry1</i> intron 336- <i>Cry1</i>	30.65	0.21

**Table S4. Phases of Transcription Factors and Outputs Produced by Those Factors, Related to Figure S7A**

Related to	Reporter construct	Phase (hours)		Relative amplitude		Note
		(n = 3)		(n = 3)		
Figure S7A		Mean	SD	Mean	SD	
	3xE'-box-P(SV40)	4	0.29	1.105	0.016	morning-time activator/night-time repressor
	3xRRE-P(SV40)	17.10	0.37	0.857	0.006	
	UAS-P(CMVmini)	7.70	0.85	0.287	0.019	
	3xD-box-P(SV40)	8.90	0.28	0.338	0.000	day-time activator/morning-time repressor
	3xE'-P(SV40)	3.90	0.14	0.888	0.022	
	UAS-P(CMVmini)	16.60	1.04	0.270	0.023	
	3xRRE-box-P(SV40)	16.90	0.55	0.721	0.028	night-time activator/day-time repressor
	3xD-box-P(SV40)	9.00	1.29	0.357	0.012	
	UAS-P(CMVmini)	22.20	0.70	0.530	0.032	
	3xRRE-P(SV40)	16.90	0.55	0.721	0.028	morning-time repressor/night-time activator
	3xE'-box-P(SV40)	3.90	0.30	0.934	0.027	
	UAS-P(CMVmini)	20.60	0.91	0.705	0.048	
	3xE'-box-P(SV40)	3.90	0.98	1.095	0.132	day-time repressor/morning-time activator
	3xD-box-P(SV40)	7.40	0.14	0.452	0.001	
	UAS-P(CMVmini)	4.70	0.40	0.286	0.004	
	3xD-box-P(SV40)	9.70	0.81	0.438	0.026	night-time repressor/day-time activator
	3xRRE-P(SV40)	18.40	0.34	0.711	0.035	
	UAS-P(CMVmini)	11.00	0.79	0.204	0.041	