

# Bin F. et al: Circadian Enhancers Coordinate Multiple Phases of Rhythmic Gene Transcription In Vivo

Lou Shaoke

Department of Molecular Biophysics and Biochemistry

*[loushaoke@gmail.com](mailto:loushaoke@gmail.com)*

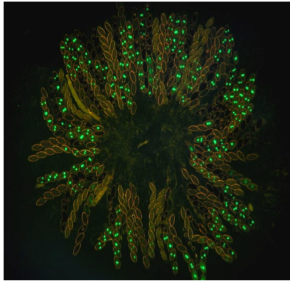
March 31, 2015

- 1 Background
- 2 Results
- 3 Conclusion
- 4 Related Works

# Circadian Rhythms

Circadian: about 1 day (24hour)

Most organisms from Bacterial to Human have circadian rhythms.



Neurospora

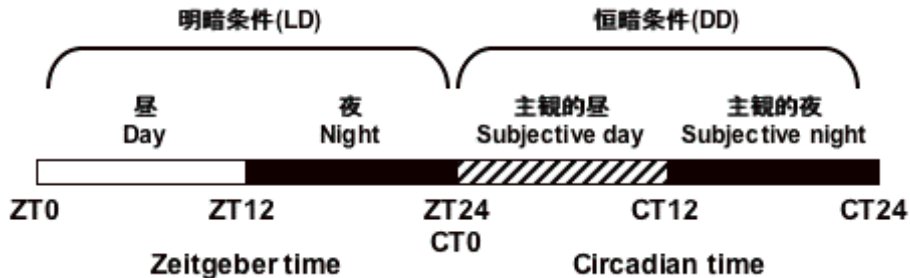


Mouse



Human

**Circadian hour** n. The unit of time corresponding to 1/24 of the duration of a circadian cycle.

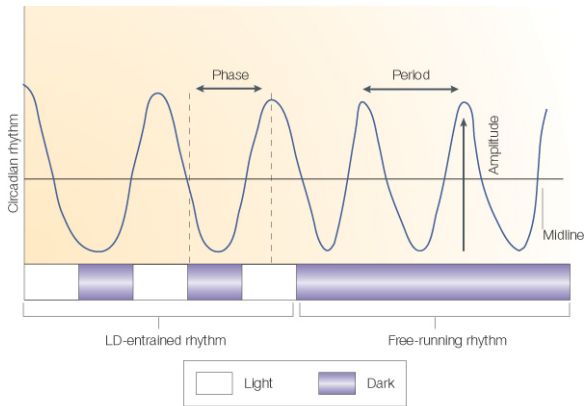


**Circadian time** n. A standard of time based on the free-running period of a rhythm (oscillation). Note: By convention, the onset of activity of diurnal organisms defines circadian time zero (**CT 0**). The onset of activity of nocturnal organisms defines circadian time twelve (**CT 12**).

**Zeitgeber time** n. A standard of time based on the period of a zeitgeber. Note: Under standard light-dark cycles, the time of lights on usually defines zeitgeber time zero (**ZT 0**) for diurnal organisms and the time of lights off defines zeitgeber time twelve (**ZT 12**) for nocturnal animals.



# Basic concepts



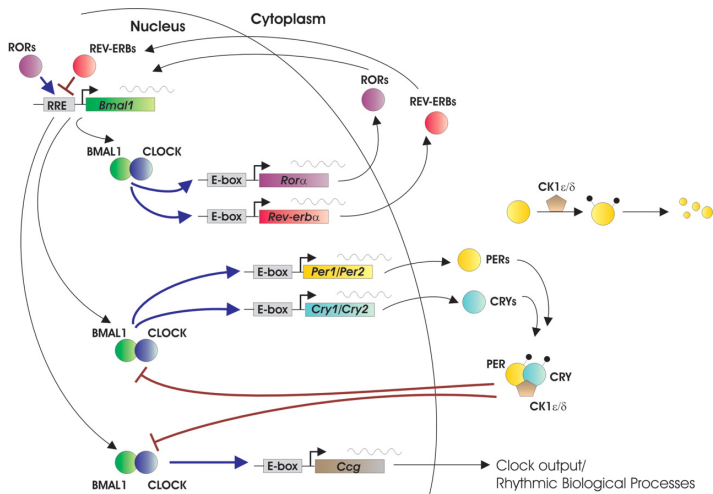
Copyright © 2005 Nature Publishing Group  
**Nature Reviews | Genetics**

**In-phase:** The same/similar phase

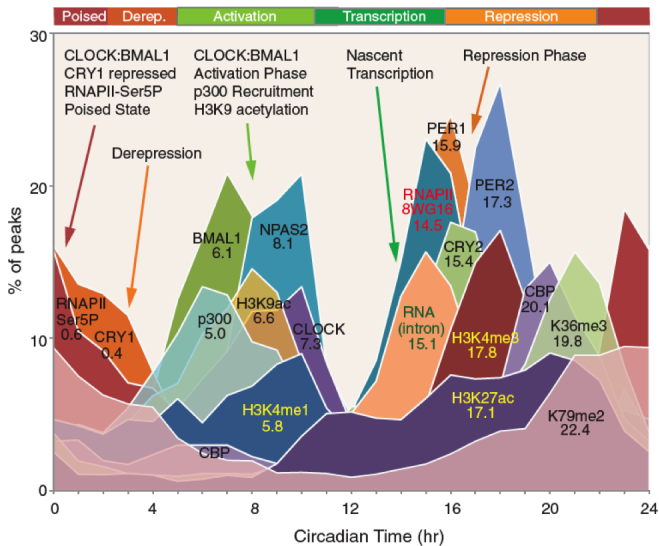
**Antiphase:** A phase shows 12 hour or half of circadian cycle difference.

# Known circadian TFs and Pathway

A network of transcriptional-translational feedback loops constitutes the mammalian circadian clock

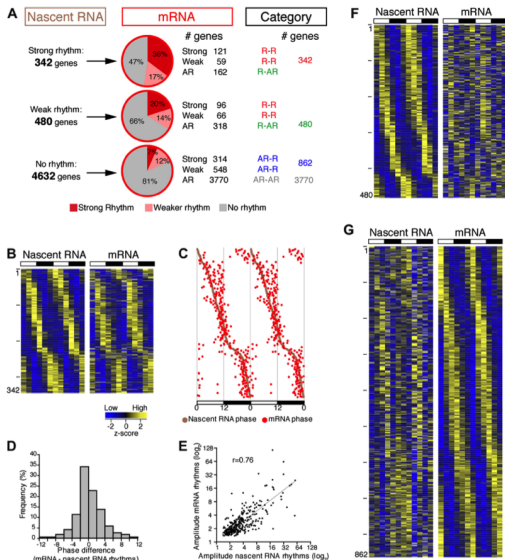


(Caroline 2006)



Circadian landscape of the cistrome and epigenome of the liver (Koike etc, Science 2012), RNA-Seq data



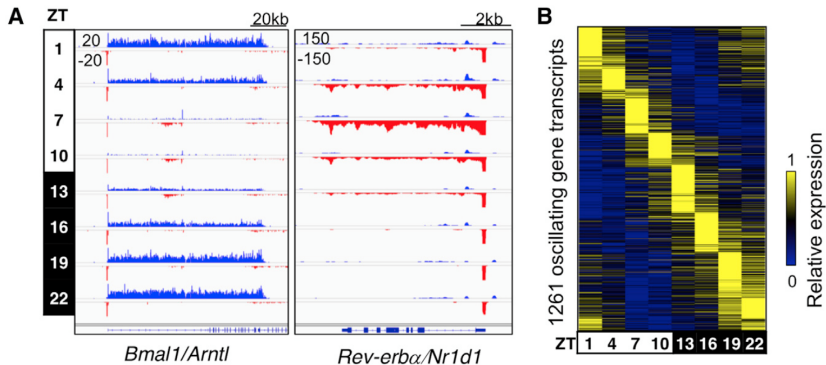


Post-transcriptional events account for a significant fraction of rhythmic gene expression in the mouse liver, RNA-Seq data

- Phases of targeting gene do not correlate with circadian TF's binding phase
- A substaintial portion of circadian TF binding far from TSS
- High degree of overlap between core clock TF with competing effect, such as BMAL1 and Rev-erb $\alpha$
- Delayed phase relative to BAML1/CLOCK

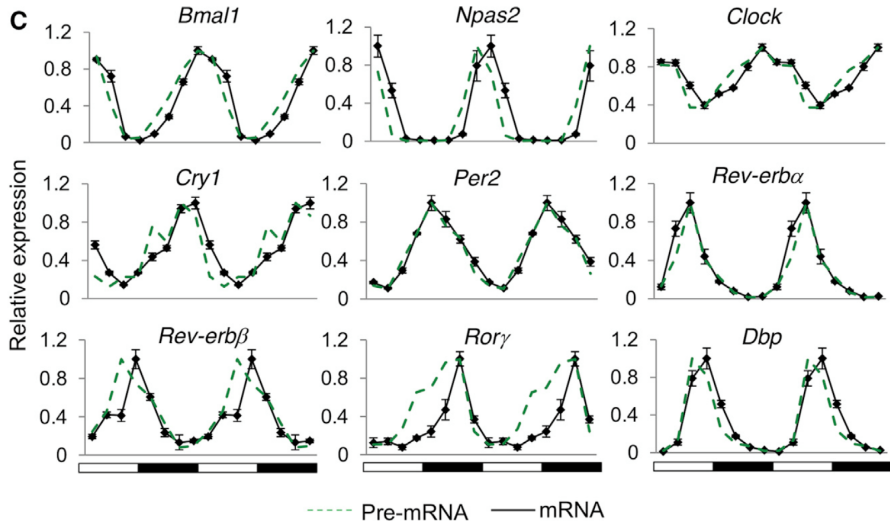
How the interaction of multiple regulators at the genome, particularly at distal enhancer elements, produces distinct phases of circadian transcriptional activity.

# Circadian Transcription in Mouse Liver



Three-hour interval GRO-seq, show robust oscillation patterns, BMAL1 and Rev-ERBa; total 1261 circadian genes sorted by the phase

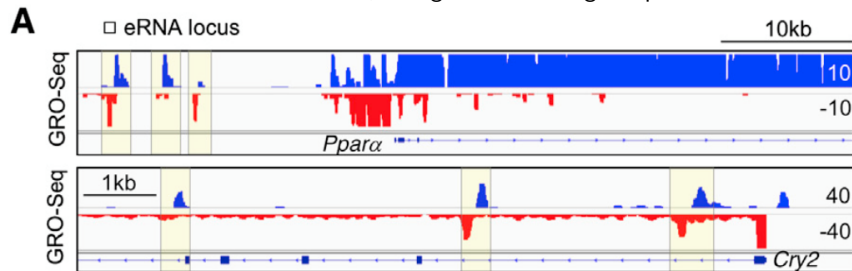
# Circadian Transcription in Mouse Liver





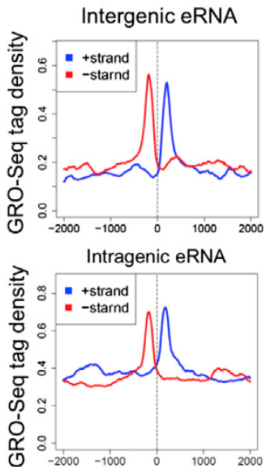
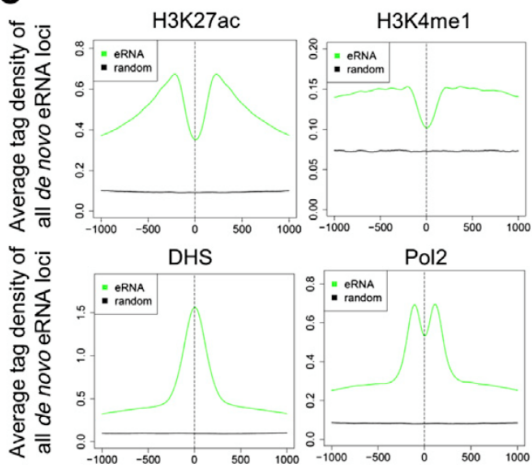
# De Novo Identification of Circadian Liver Enhancer RNAs

Both bidirectional and unidirectional, intergenic and intragenic peaks are considered



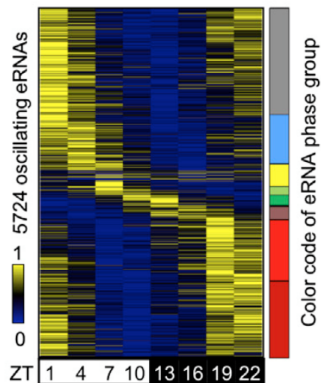
Example of eRNA locus, from 19086 high confidence loci

# De Novo Identification of Circadian Liver Enhancer RNAs

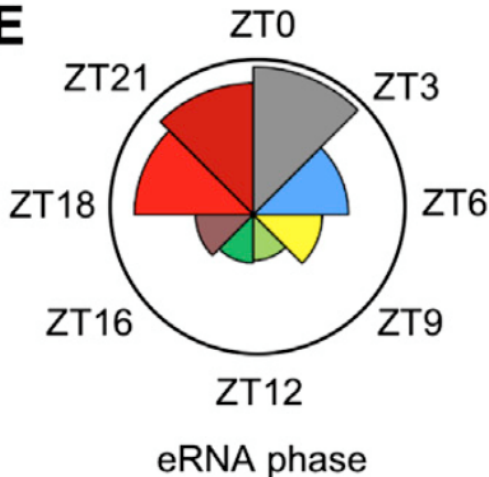
**B****C**

Bimodal profile and enrichment of epigenomic features

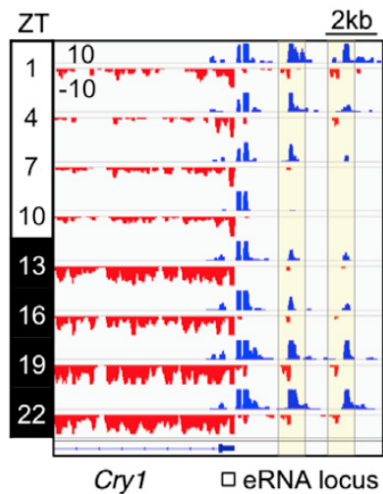
**D**



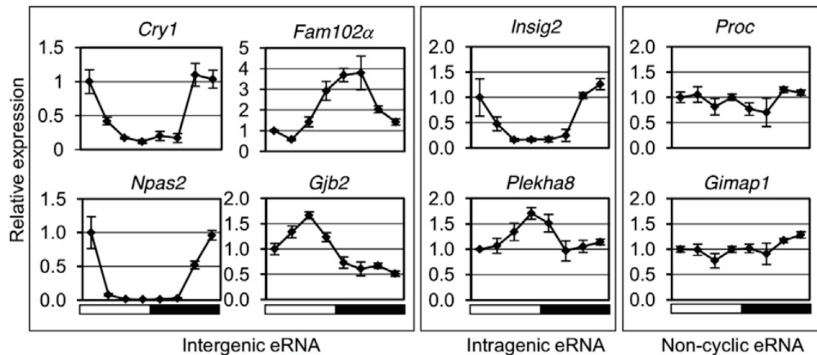
**E**



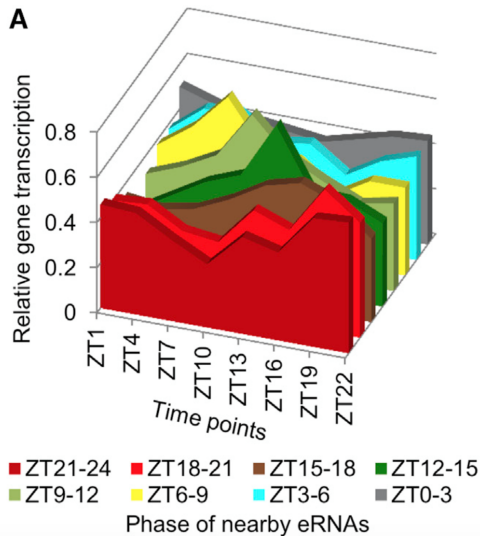
5724(30%) circadian. Define 8 group phases; 71% with a phase between ZT18 and ZT3, 29% in other phases

**F**ZT22 *Cry1* and RT-qPCR

# De Novo Identification of Circadian Liver Enhancer RNAs



# Phase-Specific Transcription Factors at Circadian Enhancers

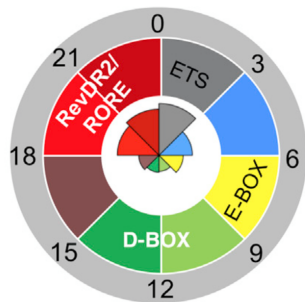


gene expr vs closest oscillating eRNA (within 200kb from TSS) (3a), show patterns in phase

# Phase-Specific Transcription Factors at Circadian Enhancers

Hypothesis: Specific cTF responsible for the different phase of gene expr by driving the transcription of diversly phased eRNA

**B**

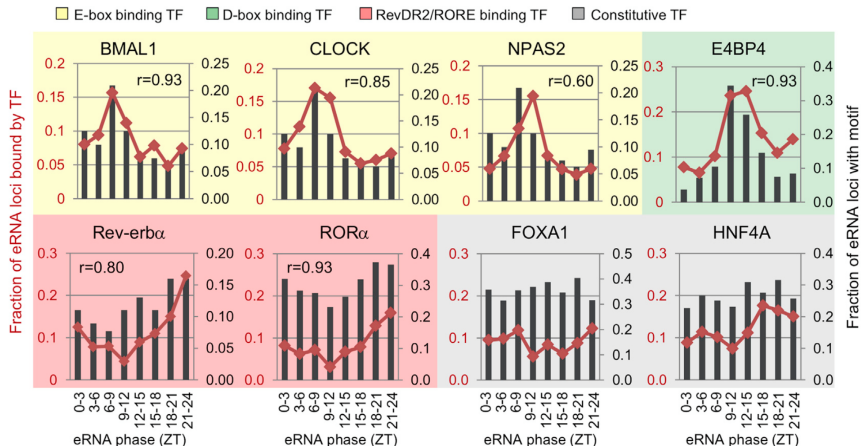


Phase specific motifs in enhancer groups

Phase-specific	Annotated motif	P-value*
RevDR2		6e-7
RORE		2e-8
E-box		5e-10
D-box		4e-16
ETS		1e-9
Constitutive	Annotated motif	P-value**
Forkhead		1e-13
HNF4		1e-60

\* Hypergeometric test, in-phase eRNAs vs. out-of-phase eRNAs. \*\* Highest enrichment in phased eRNAs vs. matched genomic control.

# Phase-Specific Transcription Factors at Circadian Enhancers

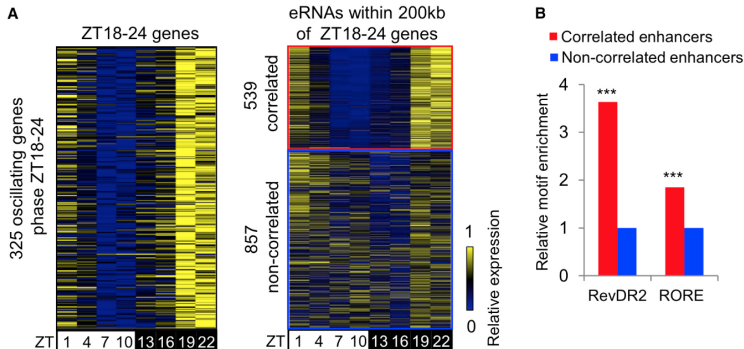


Correlation of motif occurrence and TF binding (Question: Fraction of both Tf bound and with motif?)



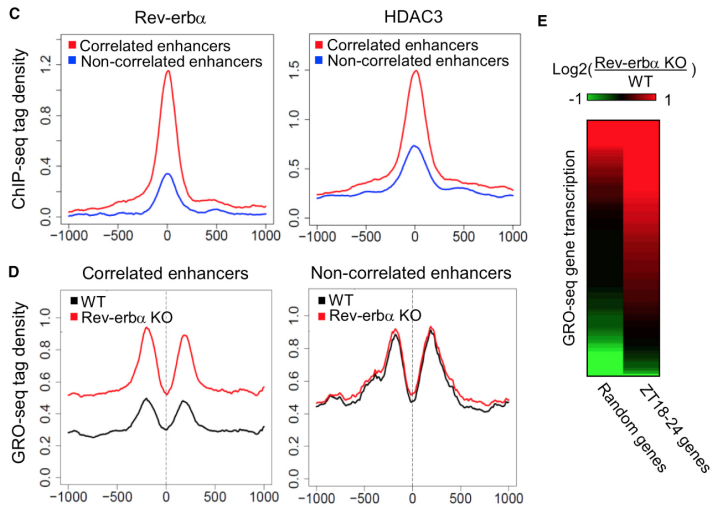
# Phase Correlation between eRNA and Gene Body Transcription Marks Functional Enhancers of Circadian Genes

Whether specific TF found to bind at circadian enhancers were driving transcription of nearby in-phase gene:



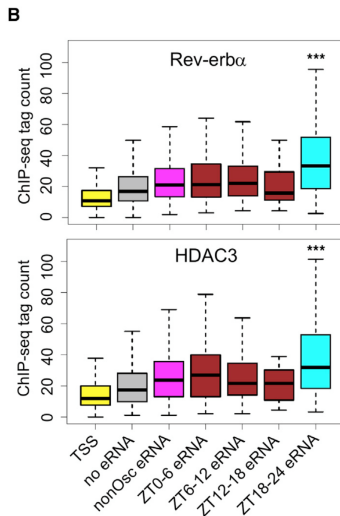
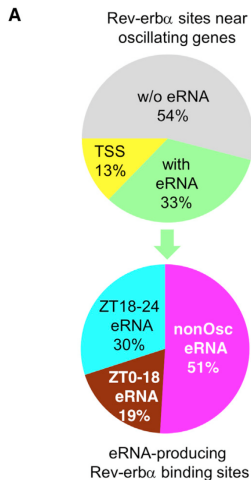
ZT18-24: 325 circGene with 539 neighboring eRNA correlated, while 857 not correlated

# Phase Correlation between eRNA and Gene Body Transcription Marks Functional Enhancers of Circadian Genes



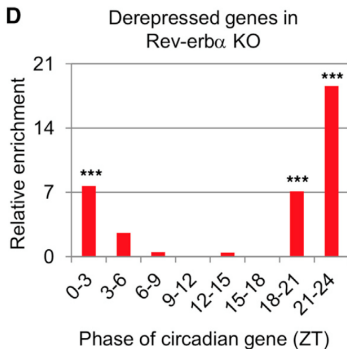
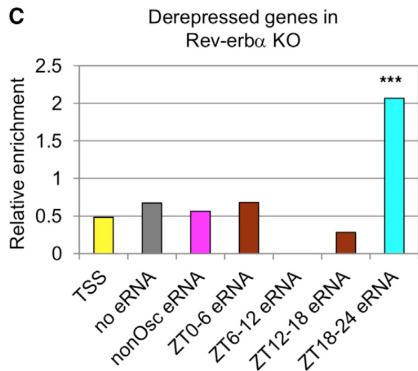
WT and KO(Rev-erb $\alpha$  ZT10). However, in KO mice, there are also down-regulated genes identified

# Circadian eRNAs Reveal the Functional Rev-erb Cistrome at Oscillating Genes



High ChIP-seq signal of Rev-erb $\alpha$  and HDAC3, resulting in the descreasing of H3K9ac

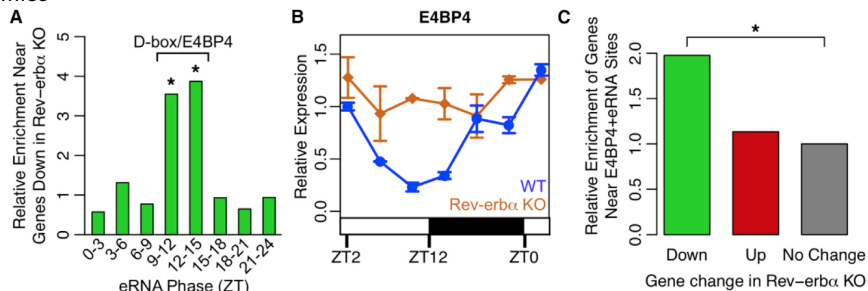
# Circadian eRNAs Reveal the Functional Rev-erb Cistrome at Oscillating Genes



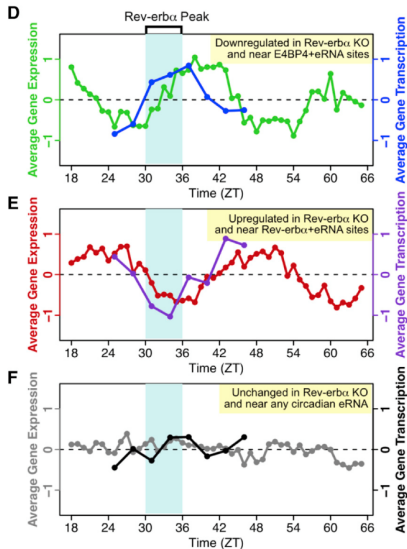
Enrichment of de-repressed circ Gene in KO mice  $\approx$  3fold near site producing ZT18-24 ; de-repressed gene also highly in ZT18-24

# eRNA Analysis Identifies E4BP4 as a Key Mediator of Gene Activation by Rev-erb

There is a substantial set of genes paradoxically down-regulated at ZT10 in Rev-erb $\alpha$  KO mice

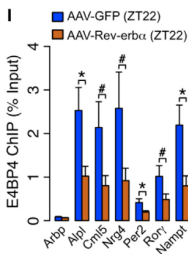
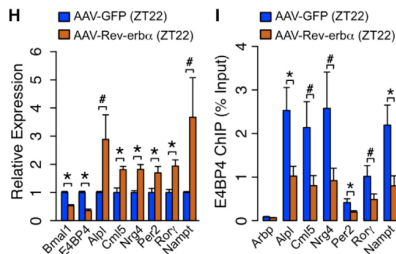
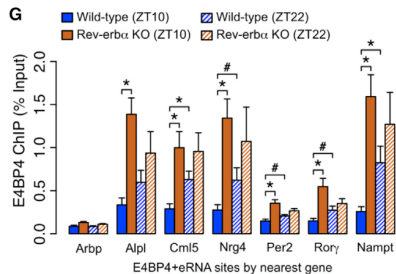


# eRNA Analysis Identifies E4BP4 as a Key Mediator of Gene Activation by Rev-erb



E4BP4+eRNA (E4BP4 putative target genes) were generally circadian with peak and trough expression in phase with Rev-erb $\alpha$  (D). antiphase with the gene repressed by Rev-erb $\alpha$

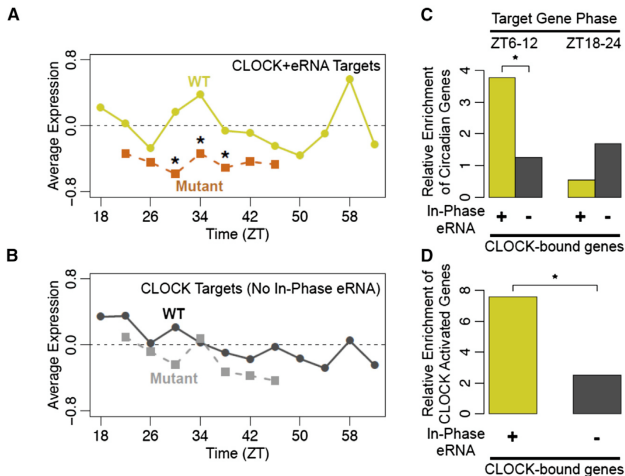
# eRNA Analysis Identifies E4BP4 as a Key Mediator of Gene Activation by Rev-erb



ChIP-qPCR of E4BP4 binding at genes downregulated in KO livers at ZT10; mRNA expression for the overexpression of Rev-erb $\alpha$

ChIP-qPCR of E4BP4 binding for over-expression of Rev-erb $\alpha$

# Circadian eRNAs Define Functional Cistromes that Distinguish CLOCK and Rev-erb Target Genes

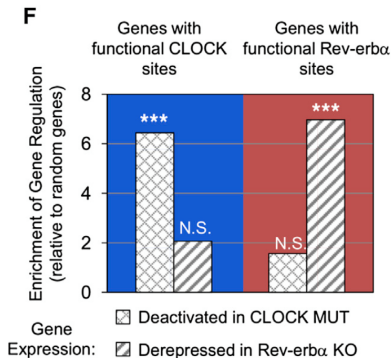
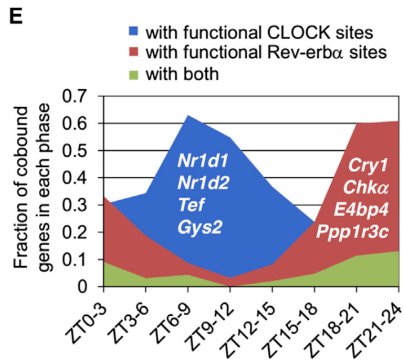


Rev-erb and Clock maximal binding to genome the same time window ZT8-10

CLOCK with in-phase eRNA, stronger reduction in mutant vs WT, than binding site with non-phase eRNA. ZT6-10

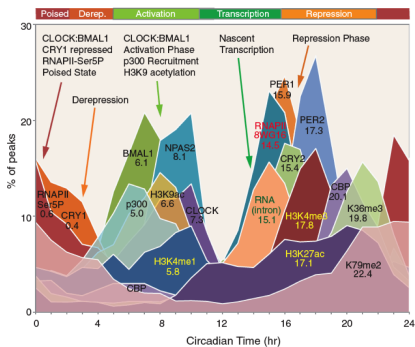
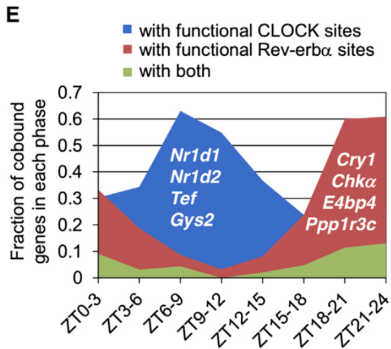


# Circadian eRNAs Define Functional Cistromes that Distinguish CLOCK and Rev-erb Target Genes



Target circ Gene for Clock and Rev-erb shows enrichment in ZT6-9 and ZT18-24 respectively.

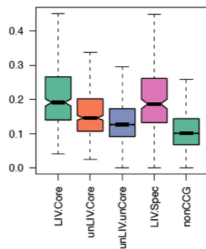
# Circadian eRNAs Define Functional Cistromes that Distinguish CLOCK and Rev-erb Target Genes



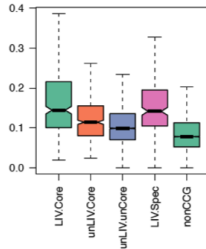
(Koike et al. 2012)

- Identified oscillating enhancers with varying peak activity times
- Specific phases of oscillation are associated with distinct regulatory motifs and TF binding patterns
- eRNA oscillations are highly predictive of the rhythmicity and phase of transcription at nearby genes
- Circadian eRNA can both identify the TF coordinating specific phases of gene transcription and distinguish the functional binding sites within a circadian cistrome

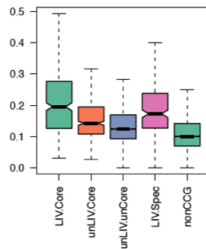
**CLOCK\_CT0**



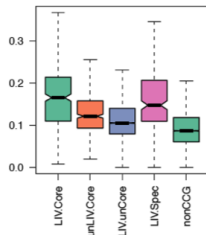
**CLOCK\_CT4**



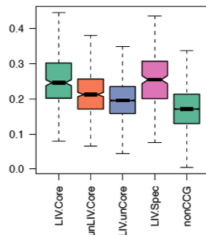
**CLOCK\_CT8**



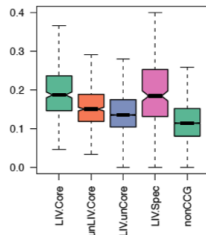
**CLOCK\_CT12**



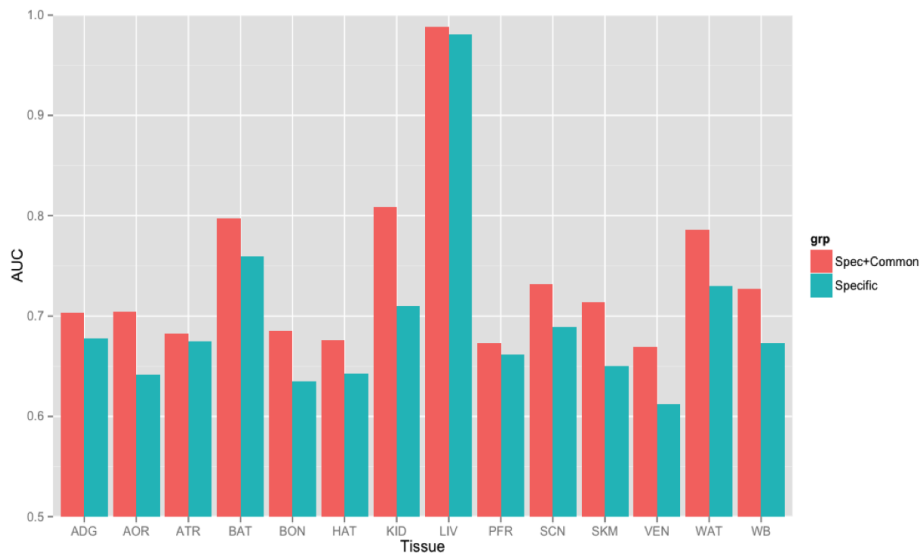
**CLOCK\_CT16**



**CLOCK\_CT20**



## Related work



### Ploscb CT vs unCT

		Ploscb CT vs unCT					
		0.86	0.87	0.84	0.84	0.85	0.81
eCT16		0.70	0.69	0.66	0.71	0.69	0.68
		0.72	0.75	0.76	0.73	0.75	0.72
eCT8		0.86	0.86	0.87	0.87	0.87	0.85
		0.65	0.67	0.65	0.67	0.73	0.65
eCT0		0.62	0.62	0.61	0.62	0.61	0.66
		#CT0	#CT8	#CT16			

### Ploscb CCG vs unCCG

		Ploscb CCG vs unCCG					
		0.91	0.91	0.92	0.90	0.91	0.92
eCT16		0.89	0.91	0.90	0.91	0.89	0.90
		0.88	0.89	0.89	0.89	0.88	0.88
eCT8		0.94	0.93	0.93	0.95	0.94	0.94
		0.86	0.86	0.86	0.84	0.84	0.86
eCT0		0.83	0.85	0.83	0.83	0.82	0.83
		#CT0	#CT8	#CT16			

### Exon CT vs unCT

		Exon CT vs unCT					
		0.75	0.79	0.77	0.81	0.76	0.80
eCT16		0.51	0.49	0.51	0.53	0.48	0.51
		0.54	0.52	0.52	0.53	0.55	0.50
eCT8		0.49	0.53	0.54	0.50	0.57	0.49
		0.54	0.52	0.51	0.53	0.52	0.58
eCT0		0.53	0.52	0.51	0.53	0.52	0.58
		#CT0	#CT8	#CT16			

### Exon CCG vs unCCG

		Exon CCG vs unCCG					
		0.89	0.91	0.90	0.90	0.90	0.90
eCT16		0.77	0.76	0.78	0.79	0.78	0.76
		0.76	0.80	0.76	0.78	0.75	0.76
eCT8		0.74	0.78	0.75	0.74	0.77	0.74
		0.79	0.78	0.77	0.78	0.80	0.78
eCT0		0.81	0.82	0.78	0.82	0.79	0.79
		#CT0	#CT8	#CT16			

### Intron CT vs unCT

		Intron CT vs unCT					
		0.48	0.51	0.51	0.48	0.53	0.51
eCT16		0.57	0.52	0.56	0.54	0.57	0.50
		0.47	0.52	0.54	0.50	0.54	0.48
eCT8		0.83	0.88	0.85	0.81	0.84	0.85
		0.92	0.90	0.91	0.90	0.88	0.89
eCT0		0.86	0.87	0.82	0.83	0.85	0.86
		#CT0	#CT8	#CT16			

### Intron ctCCG vs unCCG

		Intron ctCCG vs unCCG					
		0.71	0.76	0.77	0.72	0.76	0.76
eCT16		0.73	0.70	0.71	0.77	0.75	0.74
		0.79	0.77	0.75	0.75	0.73	0.73
eCT8		0.93	0.90	0.90	0.90	0.91	0.92
		0.96	0.95	0.95	0.93	0.93	0.94
eCT0		0.92	0.95	0.91	0.93	0.91	0.91
		#CT0	#CT8	#CT16			

**Elife.Post CT vs unCT**

	0.62	0.68	0.70	0.66	0.60	0.60
eCT16	0.91	0.91	0.90	0.91	0.93	0.89
	0.65	0.60	0.64	0.66	0.58	0.59
eCT8	0.62	0.67	0.66	0.64	0.67	0.64
	0.92	0.87	0.88	0.89	0.88	0.92
eCT0	0.61	0.63	0.64	0.62	0.61	0.67
	#CT0	#CT4	#CT8	#CT12		#CT20

**Elife.Post CCG vs unCCG**

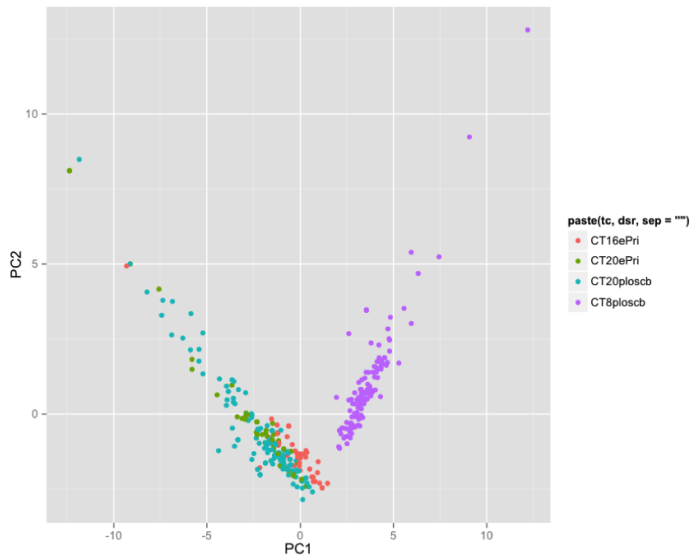
	0.86	0.86	0.86	0.86	0.86	0.85
eCT16	0.96	0.96	0.93	0.95	0.96	0.94
	0.84	0.90	0.88	0.87	0.89	0.85
eCT8	0.87	0.90	0.88	0.86	0.88	0.87
	0.94	0.94	0.92	0.92	0.92	0.92
eCT0	0.86	0.85	0.85	0.84	0.83	0.86
	#CT0	#CT4	#CT8	#CT12		#CT20

**Elife.Pri CT vs unCT**

	0.92	0.91	0.95	0.94	0.94	0.95
eCT16	0.97	0.97	0.94	0.95	0.95	0.95
	0.67	0.64	0.65	0.73	0.65	0.64
eCT8	0.68	0.74	0.74	0.71	0.62	0.68
	0.64	0.69	0.65	0.69	0.68	0.69
eCT0	0.69	0.72	0.68	0.68	0.61	0.70
	#CT0	#CT4	#CT8	#CT12		#CT20

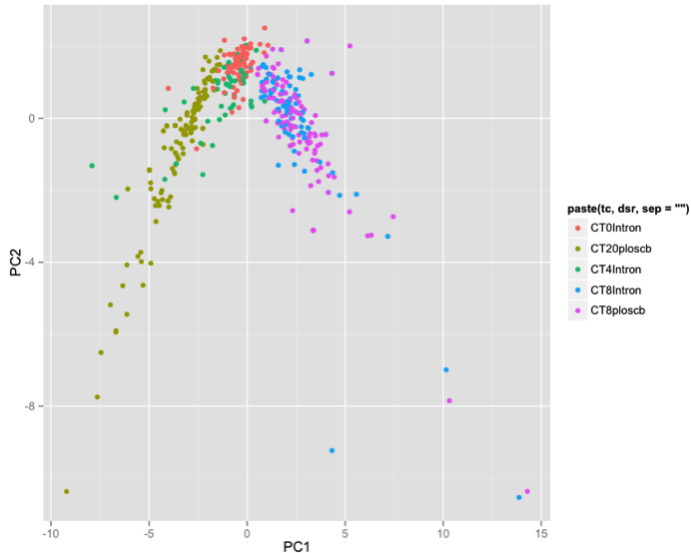
**Elife.Pri cCCG vs unCCG**

	0.96	0.95	0.97	0.96	0.96	0.97
eCT16	0.96	0.96	0.98	0.98	0.98	0.97
	0.85	0.87	0.88	0.89	0.88	0.87
eCT8	0.89	0.90	0.90	0.90	0.87	0.89
	0.83	0.86	0.86	0.86	0.87	0.85
eCT0	0.84	0.86	0.84	0.84	0.84	0.82
	#CT0	#CT4	#CT8	#CT12		#CT20



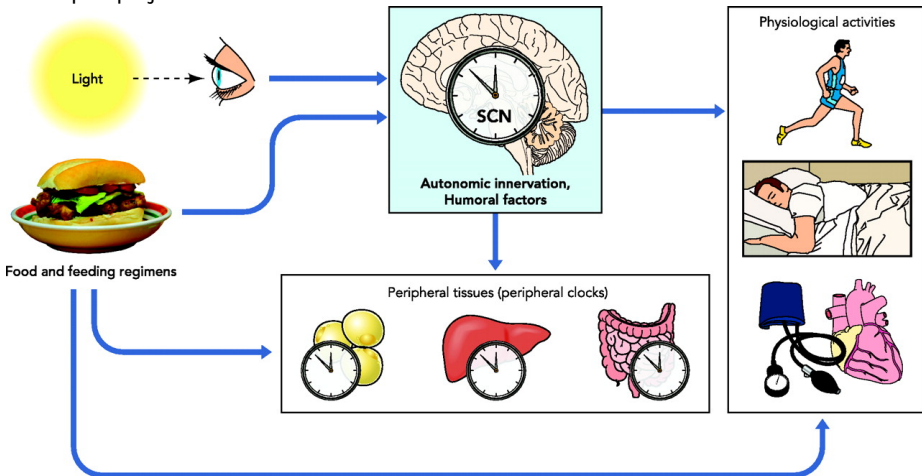


## Related work



# Brain circadian

The circadian rhythmic regulation in brain, so consider this effect when analyzing Brainspan project?



The circadian rhythmic regulation in brain, so consider this effect when analyzing  
Brainspan project?

# Circadian patterns of gene expression in the human brain and disruption in major depressive disorder

Jun Z. Li<sup>a,1</sup>, Blynn G. Bunney<sup>b</sup>, Fan Meng<sup>c</sup>, Megan H. Hagenauer<sup>c</sup>, David M. Walsh<sup>b</sup>, Marquis P. Vawter<sup>b</sup>,  
Simon J. Evans<sup>c</sup>, Prabhakara V. Choudary<sup>d</sup>, Preston Cartagena<sup>b</sup>, Jack D. Barchas<sup>e</sup>, Alan F. Schatzberg<sup>f</sup>,  
Edward G. Jones<sup>d,2</sup>, Richard M. Myers<sup>g</sup>, Stanley J. Watson, Jr.<sup>c</sup>, Huda Akil<sup>c,1</sup>, and William E. Bunney<sup>b</sup>

<sup>a</sup>Department of Human Genetics and <sup>c</sup>Molecular and Behavioral Neuroscience Institute, University of Michigan, Ann Arbor, MI 48109; <sup>b</sup>Department of Psychiatry and Human Behavior, University of California, Irvine, CA 92697; <sup>d</sup>Center for Neuroscience, University of California, Davis, CA 95616; <sup>e</sup>Department of Psychiatry, Weill Cornell Medical College, New York, NY 10017; <sup>f</sup>Department of Psychiatry, Stanford University, Palo Alto, CA 94305; and <sup>g</sup>HudsonAlpha Institute for Biotechnology, Huntsville, AL 35806

The phasing of known circadian genes was consistent with data derived from other diurnal mammals. Cyclic patterns were much weaker in the brains of patients with MDD due to shifted peak timing and potentially disrupted phase relationships between individual circadian genes