Table S10. The majority of genes bound by circadian transcriptional regulators (CTR), co-activators and RNAPII are expressed. Only 1-5% of unexpressed genes are bound by CTRs. Cycling intron and cycling exon RNA rhythms are enriched for CTR occupancy. Non-cycling RNA genes are also bound by CTRs (this may be in part due to false negative scoring of cycling – i.e., the inability to detect cycling). Note the cycling and non-cycling classes do not include intermediate classes of weak cycling, and thus the sum total does not add up to 100%. From the UCSC canonical gene set of 28,661 genes, 13,197 genes are expressed at the RNA level, 15,464 genes are unexpressed, 1371 genes are intron cycling, 2037 genes are exon cycling, and 5839 genes are non-cycling.

Name	**No. of Genes Bound**	**Bound Genes that are Expressed**		**Unexpressed Genes that are Bound**		**Cycling Intron RNA Genes Bound**		**Cycling Exon RNA Genes Bound**		**Non-Cycling Genes Bound**	
BMAL1	3,175	2,824	89%	351	2%	442	32%	678	33%	1178	20%
CLOCK	2,459	2,209	90%	250	2%	346	25%	557	27%	901	15%
NPAS2	1,278	1,150	90%	128	1%	182	13%	329	16%	442	8%
PER1	2,585	2,298	89%	287	2%	340	25%	537	26%	975	17%
PER2	3,833	3,367	88%	466	3%	475	35%	767	38%	1432	25%
CRY1	6,384	5,592	88%	792	5%	758	55%	1212	59%	2456	42%
CRY2	4,667	4,143	89%	524	3%	583	43%	944	46%	1794	31%
CBP	5,097	4,534	89%	563	4%	584	43%	892	44%	2059	35%
p300	673	619	92%	54	0%	118	9%	173	8%	232	4%
RNAPII-8WG16	4,794	4,478	93%	316	2%	648	47%	992	49%	2113	36%
RNAPII-Ser5P	7,533	6,927	92%	606	4%	908	66%	1431	70%	3373	58%