

Supplemental Table 1. Transcription factors with discrete expression within the mouse SCN at P0.

Gene	Entrez Gene ID	Family	SCN	Potentially in SCN	Boundary	In Situ Verified	Source	ABA E18 Expression Confirmation	ABA Adult Expression Confirmation
Sox2	20674	HMG	X					X	X
Sox5	20678	HMG	X						
Zfhx3	11906	Homeobox	X					X	X
Hmx3	15373	Homeobox	X						
Lhx1	16869	Homeobox	X			X		X	X
Six3	20473	Homeobox	X			X		X	
Six6*	20476	Homeobox	X			X	Jean et al., 1999		
Vax1	22326	Homeobox	X						X
Rora	19883	Nucrec	X			X		X	X
Rorb*	225998	Nucrec	X			X	Schaeren-Wiemers et al., 1997	X	X
Nr4a1	15370	Nucrec	X					X	X
Pou2f2*	18987	Pou	X			X	Rivkees et al., 1992	X	
Peg3	18616	ZN C2H2	X						
Tcf12	21406	bHLH		X					
Olig2	50913	bHLH		X					
Sox14	20669	HMG		X					
Dlx2	13392	Homeobox		X				X	X
Dlx5	13395	Homeobox		X					
Lhx9	16876	Homeobox		X					
Sox4	20677	HMG			X			X	
Dlx1	13390	Homeobox			X			X	
Isl1	16392	Homeobox			X			X	X
Lhx2*	16870	Homeobox				X	Menger et al., 2005	X	
Lhx5	16873	Homeobox			X			X	
Lhx8	16875	Homeobox			X			X	
Otp	18420	Homeobox			X	X		X	
Pbx3	18516	Homeobox			X			X	
Nr2f2	11819	Nucrec			X			X	

List of 28 transcription factors identified as within, potentially within, or directly adjacent to the postnatal mouse SCN obtained from re-examination of a genome-scale transcription factor expression database (Gray et al., 2004) and other published work (*Rivkees et al., 1992; Schaeren-Wiemers et al., 1997; Jean et al., 1999; Menger et al., 2005). Genes highlighted in grey were further assessed for precise expression within the SCN region. The last two columns represent those genes whose expression was further confirmed in the Allen Brain Atlas either E18 (ABA E18) or Adult (ABA Adult) (Lein et al., 2007). bHLH – basic helix-loop-helix, HMG – high mobility group, Nucrec – nuclear receptor, ZN-Zinc finger type C2H2.

Supplemental Table 2. Transcription factors with discrete mRNA expression within the mouse anterior hypothalamus at E13.5.

Gene	Entrez Gene ID	Family	Anterior Hypothalamus	Boundary	In Situ Verified	Source	Database Expression Confirmation
Npas1	18142	bHLH	X				
Olig2	50913	bHLH	X				X
Baz2a	116848	Bromo	X				X
Baz2b	227940	Bromo	X				
Smarcc1	20588	Bromo	X				
Smarcd3	66993	Bromo	X				
FoxD3	15221	Forkhead	X				
FoxO1	56458	Forkhead	X				
Foxp4	74123	Forkhead	X				X
Hmgb1	15289	HMG	X				X
Hmgb2	97165	HMG	X				X
Sox21	223227	HMG	X				X
Sox4	20677	HMG	X				
Sox5	20678	HMG	X				X
Tcf7l2	21416	HMG	X				X
Atbf1	11906	Homeobox	X				X
Dlx1	13390	Homeobox	X				X
Dlx2	13392	Homeobox	X		X		X
Dlx5	13395	Homeobox	X				X
Hes1	15205	Homeobox	X				X
Hmx2*	15372	Homeobox	X			Wang and Lufkin, 2000	X
Hmx3	15373	Homeobox	X				
HoxD3	15434	Homeobox	X				
Lhx1	16869	Homeobox	X		X		X
Lhx2	16870	Homeobox	X				X
Lhx4	16872	Homeobox	X				
Nkx2.1	21869	Homeobox	X				X
Six3	20473	Homeobox	X		X		X
Six6*	20476	Homeobox	X		X	Jean et al., 1999	X

Supplemental Table 2 (Con't). Transcription factors with discrete mRNA expression within the mouse anterior hypothalamus at E13.5.

Gene	Entrez Gene ID	Family	Anterior Hypothalamus	Boundary	In Situ Verified	Source	Database Expression Confirmation
Tef2	21410	Homeobox	X				
Vax1	22326	Homeobox	X				X
Crip2	68337	LIM	X				X
Csrp2	13008	LIM	X				
Lmo4	16911	LIM	X				X
Zyx	22793	LIM	X				
Nr1h2	22260	Nucrec	X				X
Rxra	20181	Nucrec	X				
Nr2e1	21907	Nucrec	X				X
Pou2f2	18987	Pou	X		X		X
Rfx3	19726	RFX	X				X
Peg3	18616	ZN C2H2	X				X
Zic3	22773	ZN C2H2	X				X
Zic4	22774	ZN C2H2	X				
Chd4	107932	ZN PHD	X				
Sim1	20464	bHLH		X			
Baz1b	22385	Bromo		X			X
Cited1	12705	Cited		X			X
Dlx6	13396	Homeobox		X			X
Isl1	16392	Homeobox		X			X
Lhx5	16873	Homeobox		X			X
Otp	18420	Homeobox		X	X		X
Lmo1	109594	LIM		X			X
Rxrg	20183	Nucrec		X			
Nr2f2	11819	Nucrec		X			X
Pou3f1	18991	Pou		X			X
Pou3f2	18992	Pou		X			
Stat5A	20850	Stat		X			
Zdhhc2	70546	ZN DHHC		X			X

List of 58 transcription factors identified as within or directly adjacent to the SCN obtained from re-examination of a genome-scale transcription factor expression database (Gray et al., 2004) and other published work (*Jean et al., 1999; Wang and Lufkin, 2000). Genes highlighted in grey were further assessed for precise expression within the SCN region. The last column represents those genes whose expression was further confirmed using either Genepaint (Visel et al., 2004) or Eurexpress (Diez-Roux et al., 2011). bHLH – basic helix-loop-helix, Bromo - Bromodomain, CITED – CREB-binding protein/p300-interacting transactivator with ED-rich tail HMG – high mobility group, Forkhead – Forkhead box, Nucrec – nuclear receptor, RFX – Regulatory factor X, STAT – signal transducer and activator of transcription, ZN C2H2 – Zinc finger type C2H2, ZN DHHC – Zinc finger DHHC domain-containing.

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