

Table S3. ncRNA candidates for study from the RNA-Seq project.

Region	Strand	Nearest Gene	Description	Expression	Enhancer
chr2:20,890,433-20,892,100	+	Gm13375	transcription of enhancer, single strand	NP _{Nuc} ,NP _{Cyt}	NP
chr2:84,573,971-84,585,570	-	Ypel4, mir130a	bidirectional transcription of enhancer	Un _{Nuc} ,NP _{Nuc}	mESC, NP
chr2:165,618,601-165,668,700	+	Zmynd8	bidirectional transcription of enhancer	Un _{Nuc} ,Un _{Cyt}	mESC
chr3:89,018,478-89,033,164	+	THBS3, mir92b	bidirectional transcription of enhancer; intronic	NP _{Nuc}	NP, forebrain
chr4:22,406,798-22,425,777	+	Oct3	transcription of enhancer, single strand	NP _{Nuc} ,NP _{Cyt}	NP
chr4:99,319,831-99,326,069	-	Foxd3	bidirectional transcription at homeobox gene	Un _{Nuc}	none
chr4:123,340,299-123,362,182	+	Macf1	bidirectional transcription of enhancer; lincRNA	NP _{Nuc}	mESC, NP
chr5:123,583,162-123,592,735	-	Setd1b	transcription of enhancer, single strand; lincRNA	Un _{Nuc} ,NP _{Nuc}	mESC, NP
chr6:124,806,079-124,814,476	+	Gpr162	bidirectional transcription of enhancer	NP _{Nuc}	mESC, NP
chr7:80,564,273-80,569,279	+	Rgma	transcription of enhancer, single strand	NP _{Nuc} ,NP _{Cyt}	NP
chr8:91,564,336-91,582,454	-	Sall1	transcription of enhancer, single strand	Un _{Nuc} ,Un _{Cyt}	mESC
chr9:39,982,808-40,052,077	-	Zfp202	transcription of enhancer, single strand	Un _{Nuc}	mESC, NP
chr10:80,869,755-80,882,086	+	Nfic	bidirectional transcription of enhancer	Un _{Nuc} ,Un _{Cyt}	mESC, NP
chr13:83,878,326-83,881,072	+	C130071C03Rik	transcription of enhancer, single strand	NP _{Nuc} ,NP _{Cyt}	forebrain, NP
chr15:88,538,699-88,541,837	+	Brd1	bidirectional transcription of enhancer	Un _{Nuc} ,Un _{Cyt}	mESC
chr16:35,472,958-35,491,824	+	Pdia5	bidirectional transcription of enhancer	NP _{Nuc}	NP
chr17:37,103,007-37,109,588	-	RT1-M6-2 (rat)	transcription of enhancer, single strand	Un _{Nuc} ,Un _{Cyt}	mESC
chr19:57,676,283-57,778,594	-	Atrnl1	bidirectional transcription of enhancer	Un _{Nuc} ,NP _{Nuc}	mESC

Columns indicate the following information: Region, genomic coordinates for area of novel transcription on the UCSC Genome Browser mouse assembly mm9; Strand, strand of novel transcription; Nearest Gene, nearest known gene; Description, properties of novel transcription; Expression, RNA-Seq libraries containing the novel transcription; Enhancer, cell types with enhancer activity in this area, with enhancers defined from previous literature as stated in the text of this section. Two identified regions correspond to lincRNAs first reported by Guttman et al [64]. NP, neural precursors.