File S4

Supporting Figures

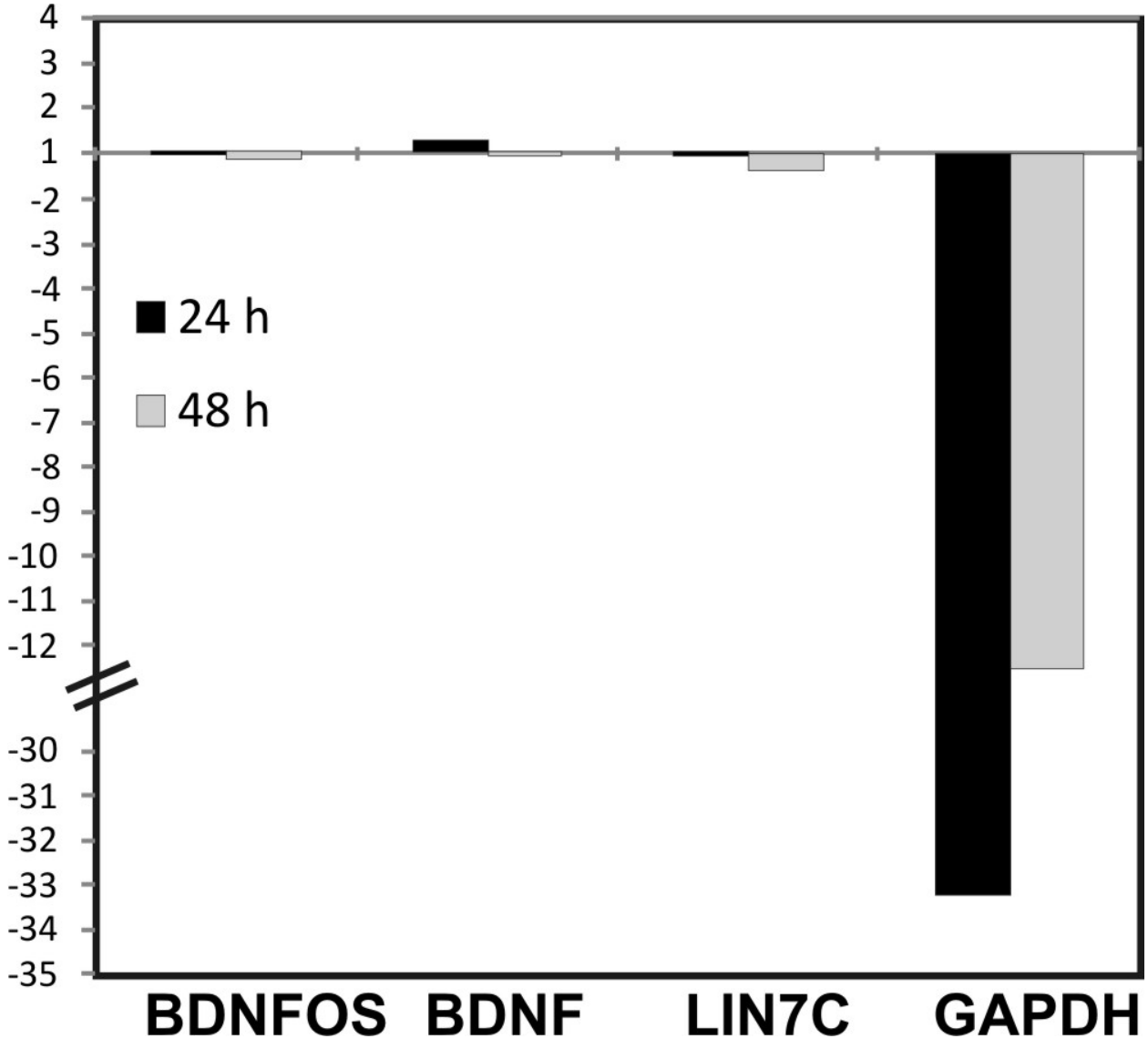

Figure S1 Control experiment to rule out non-specific effects of siRNA conditions. An siRNA against GAPDH was used on SY5Y cells in order to be certain that non-specific or off-target effects are not responsible for the results shown in Figure 2 of the manuscript. While GAPDH was significantly knocked down at 24 and 48 hours, there was no effect on BDNFOS, BDNF, or Lin7C. Results shown were each done in triplicate real-time qPCR with duplicates at 24 hours and a single sample at 48 hours.

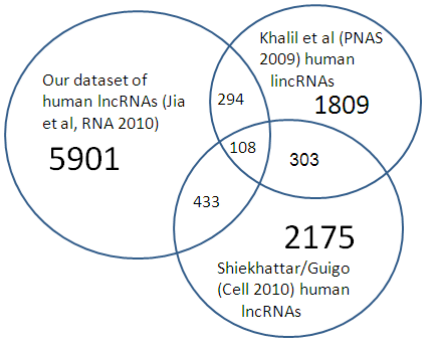

Figure S2 The majority of lncRNAs in our dataset are nonredundant by genomic position relative to lincRNAs and long ncRNAs published by two other groups.

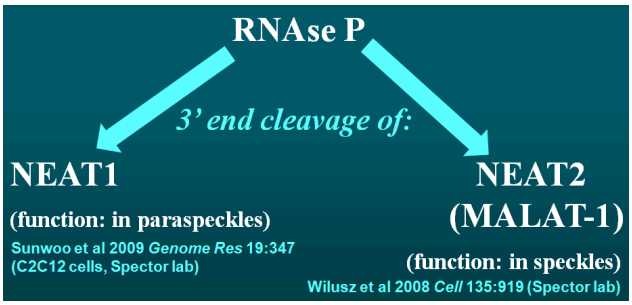

Figure S3 Three nuclear lncRNAs whose levels are increased in more electrophysiologically active areas of the human neocortex form a network: RNAse P is essential for maturation of both NEAT1 and NEAT2 (MALAT1).

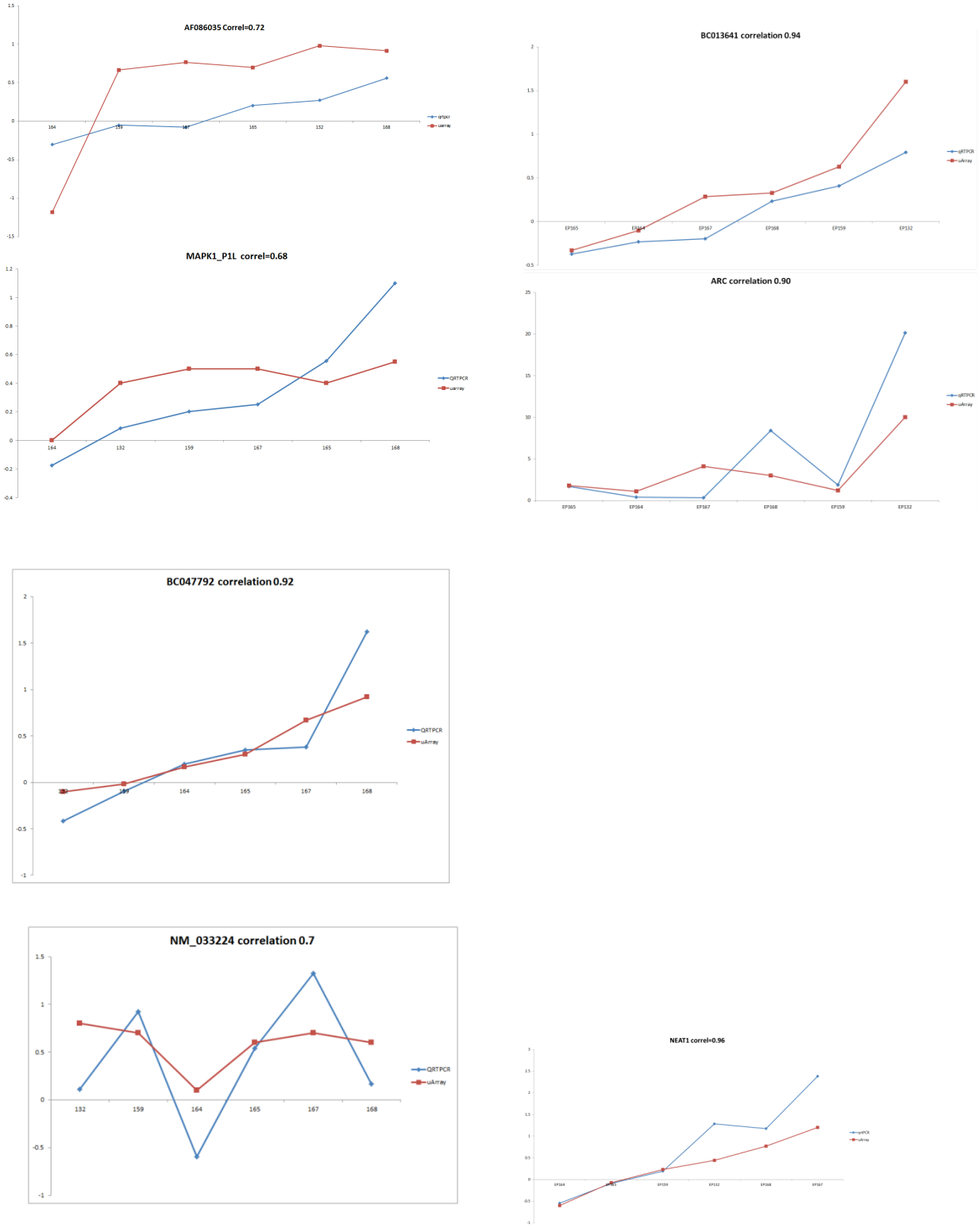

Figure S4 Taqman qRTPCR results closely parallel microarray results for lncRNA and mRNA differential expression at lncRNA-mRNA cis-pairs across the within-patient sample pairs of high- and low-activity neocortical regions.
MALAT-1 is not shown because of the discrepancy between its microarray probeset coverage and its Taqman amplicons coverage.

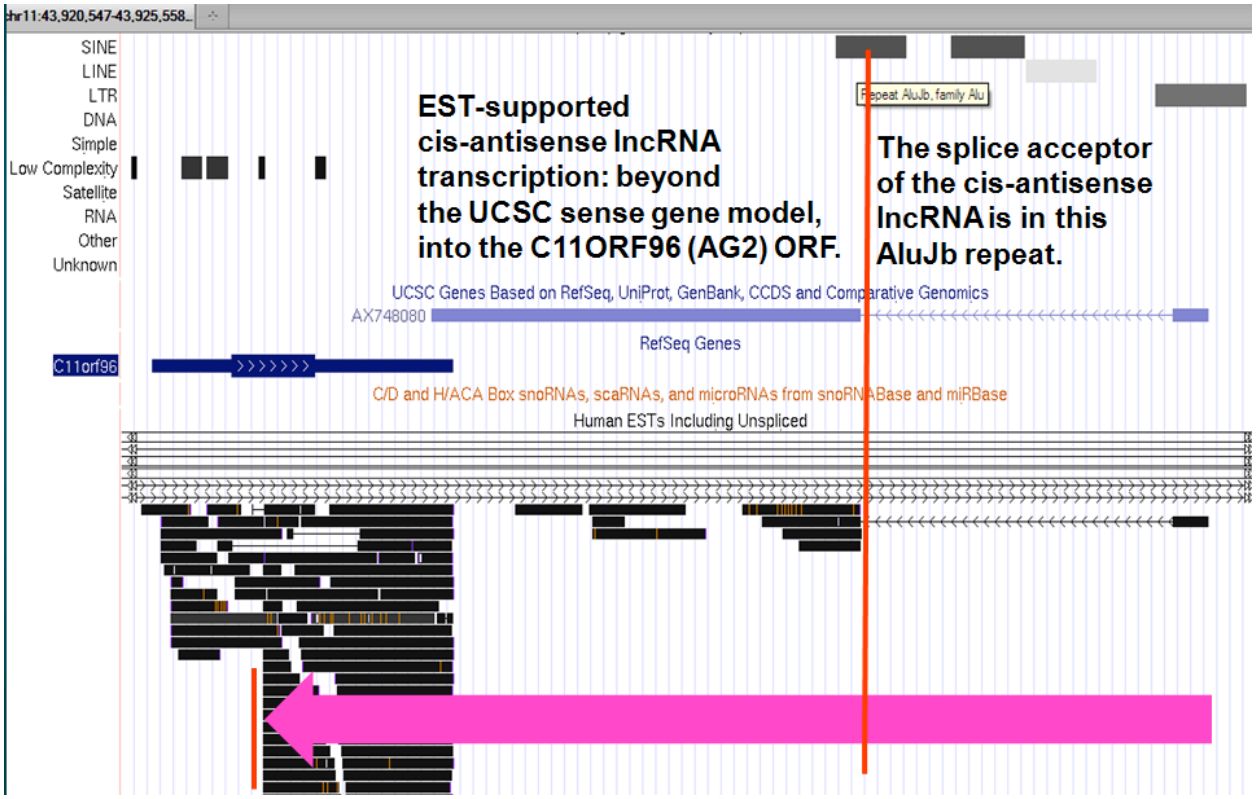

Figure S5 Genomic complexity of the human AK093366-AG2 lncRNA-mRNA cis-antisense pair which is co-differentially-expressed in human neocortical epilepsy. Red vertical line: lncRNA splice acceptor within an Alu repeat. Magenta arrow: extent of EST-supported cis-antisense lncRNA transcription overlapping the AG2 protein-coding gene. Genomic diagram was generated using the UCSC Genome Browser (Kent 2002).