Figure A3. Distribution of time course correlations between the 60 putative lncRNAs and their neighboring coding genes (teal) versus correlations between coding genes and their neighboring coding genes (red). The set of 60 putative lncRNAs is enriched for transcripts that are highly correlated to nearby genes, suggesting that some are spliced or un-annotated untranslated regions (UTRs) to genes. The arrow marks the correlation of lncRNA-TARE-4L to its neighbor.