Supplementary Materials for:

Nascent transcription and the associated cis-regulatory landscape in rice

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Figures S1 to S13
Figure S1. Distribution of genome-wide dREG scores (top) and dREG peak size (bottom).

Median dREG score is 0.591 and median dREG peak size is 390 bp.
Figure S2. dREG scores for $d\text{REG}_\text{proximal}$ and $d\text{REG}_\text{distal}$ peaks.
Figure S3. Epigenetic marks for dREG$_{pro	ext{ximal}}$ and dREG$_{distal}$ peaks. The dREG$_{pro	ext{ximal}}$ and dREG$_{distal}$ peaks were also divided on whether it overlapped an ATAC peak region.
Figure S4. Epigenetic marks for coding and repetitive sequences in the rice genome. (a) Transcriptionally active genes binned by gene expression levels. (b) Class I retrotransposons and (c) class II DNA transposons.
Figure S5. (a) DNA methylation levels for dREG\textsubscript{proximal} and dREG\textsubscript{distal} peaks. (b) Scatter plot for dREG peak regions’ dREG score and DNA methylation level.
Figure S6. Scatter plot for dREG peak regions’ score and evolutionary conservation scores. (a) plot for dREG_{proximal} and dREG_{distal} peaks with phyloP scores and (b) plot for dREG_{proximal} and dREG_{distal} peaks with fitcons scores.
**Figure S7.** Evolutionary scores (a) phyloP and (b) fitCons for dREG\textsubscript{proximal} and dREG\textsubscript{distal} peaks. dREG peaks are divided by its repeat class. *** indicates significant differences after a Mann-Whitney test (p-value < 0.0001).
Figure S8. Chromatin profiles of dREG\textsubscript{Proximal} peaks that are binned by dREG scores.
Figure S9. Epigenetic marks surrounding TAD boundaries.
Figure S10. Distribution of loops detected by Pore-C for dREG\textsubscript{distal} peaks. (a) Total number of noncoding-gene loops where the noncoding anchor contains either an ATAC peak, a dREG peak, both an ATAC and a dREG peak, or none. (b) Across the noncoding-gene loops the number of noncoding anchor contacts per gene (left) and the distance between the gene and noncoding anchor (right).
Figure S11. Distribution of dREG scores for the dREG peaks contacting a gene.
Figure S12. Enrichment of eQTLs within dREG\textsubscript{distal} peaks identified in Figure 5D
Figure S13. Enrichment of eQTLs within ATAC peaks.