

Figure 3: Conditional influences at GREs within canonical and non-canonical promoters differentially regulate multiple transcript isoforms from the same operon

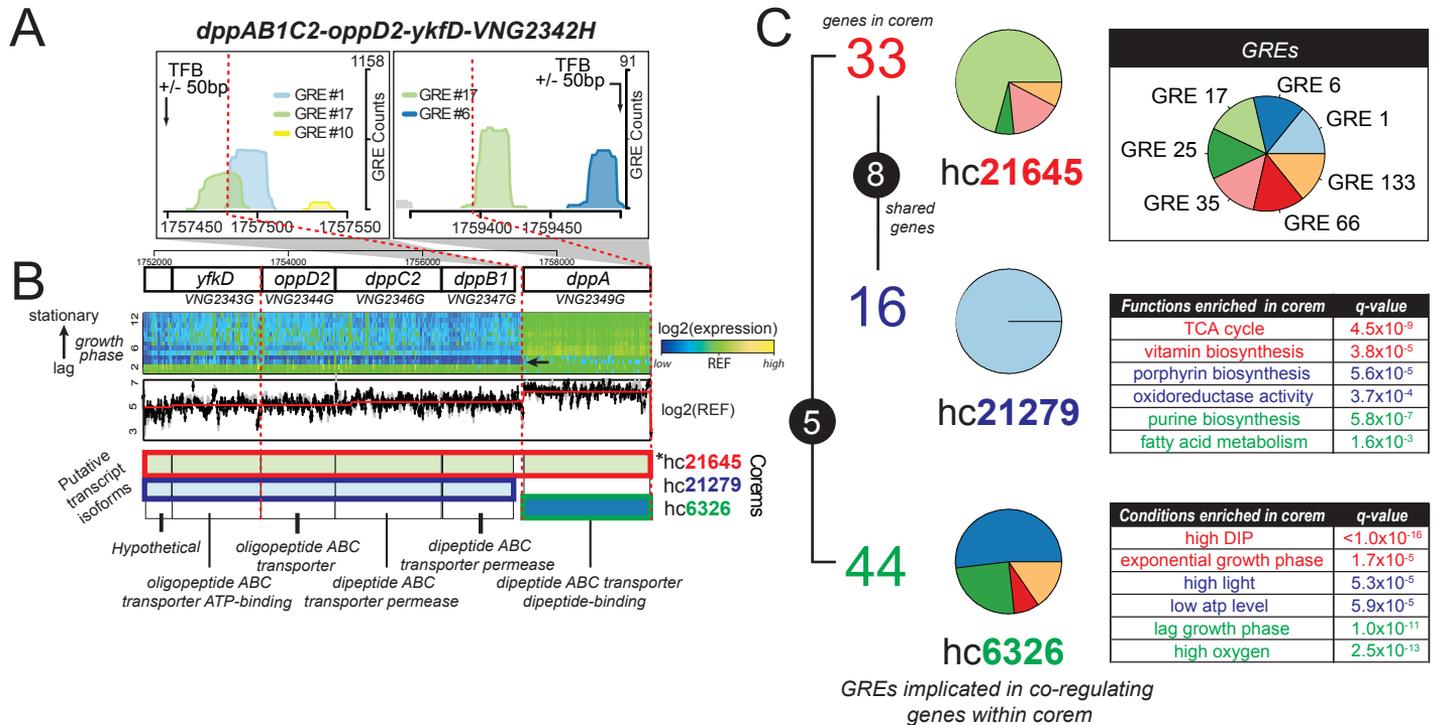


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(A) (Top) Predicted GREs located within (left) and upstream of (right) the *H. salinarum* *dpp* operon. Locations of experimentally mapped TFB binding sites (vertical arrows; 24), and experimentally mapped transcription break sites (vertical red dashed lines, see (B); 14) are indicated. (Bottom) Locations of predicted GREs relative to coding segments of the *dpp* operon.

(B) (Top) Expression changes during growth in the genomic region covering the *dpp* operon measured by high-resolution tiling microarray. (Middle) Raw RNA hybridization signal from mid-log growth phase. (Bottom) Three predicted transcripts from the *dpp* operon. Internal colors correspond to the GREs (as in (A)) putatively responsible for regulating each transcript (derived from core membership in (C)). Boxed colors indicate core membership for each transcript (described in (C)). Red dashed lines indicate experimentally measured transcription break sites. Transcriptional break at lag phase highlighted by an arrow. Functional annotation for each gene located at bottom.

(C) (Left) Three corems model differential regulation of *dpp* operon isoforms: (1) the entire operon (hc21645 –“*dpp* corem”; top); (2) five tail genes, excluding *dppA* (hc21279 –“*permease* corem”; center); and (3) the leader gene, *dppA* (hc6326 –“*leader* corem”; bottom). Colored numbers denote quantity of genes in each core; numbers in black shaded circles indicate the number of genes shared between corems. Pie charts represent average predicted influence of GREs on regulation of genes in each core (see Figure S3B for detail). (Top-Right) Pie chart key indicates GRE identity. (Bottom-Right) Tables list enriched gene functions (40) and environmental conditions for each of the corems (computed using the environmental ontology; see Methods and Supplementary Methods). See also Figure S3.