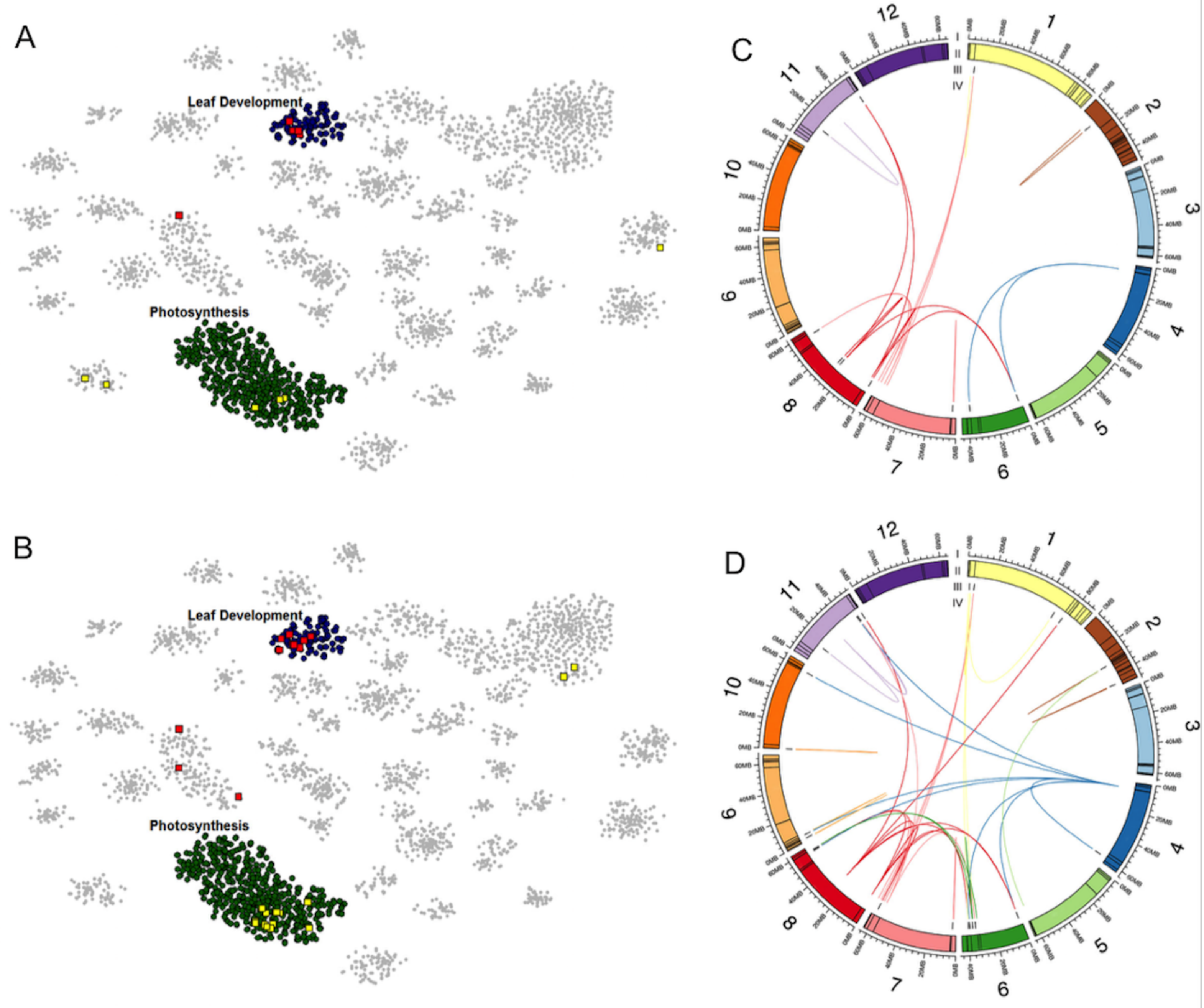

Supplemental Figure S9. eQTL regulation of transcript abundance patterns that correlate with leaf complexity.

A, B) Forty-two distinct modules identified by DBscan from the eQTL mapping generated by BH-SNE analysis. Modules enriched for genes with leaf development and photosynthesis GO terms are labeled in blue and green, respectively. Genes with transcript levels correlated with leaf complexity under simulated sun (A) and shade (B) are indicated by squares with positive correlations in red and negative correlations in yellow.

C, D) Genes with transcript levels correlated with leaf complexity under simulated sun (C) and shade (D) are shown connected to their respective eQTL with chords. I) The 12 tomato chromosomes in megabases. II) Colored boxes indicate the sizes of each bin. III) Black bars indicate the locations of the genes. IV) Chords connect eQTL to the genes whose transcript levels they regulate. Chords are colored by the chromosome location of the eQTL.