

Supplementary Tables

Table S1. Summary of RNA sequencing data cleaning for four *Capsicum* species at flowering, small fruit, and middle fruit stages.

Table S2. Precursor sequences of novel miRNAs.

Table S3. Seed sequence of novel miRNAs.

Table S4. Annotation of known and novel miRNA target genes in *Capsicum annuum*.

Table S5. List of primers used for stem-loop RT-qPCR validation.

Table S6. RT-qPCR primer sequences of selected targets of known and novel miRNAs.

Supplementary Figures

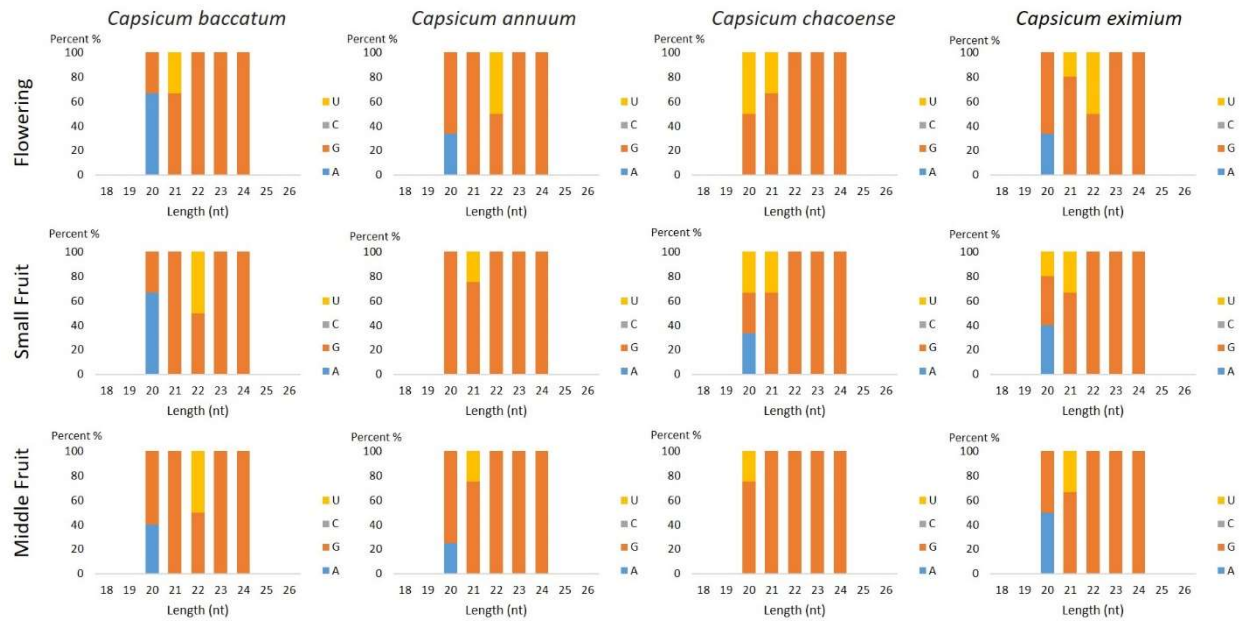


Figure S1. First nucleotide bias for different lengths of 20 to 24 nt for miRNAs from all *Capsicum* species at flowering, small fruit and middle fruit stages. The horizontal coordinates are each position of sRNA reads and the vertical coordinates are percentage of AUCG at each base.

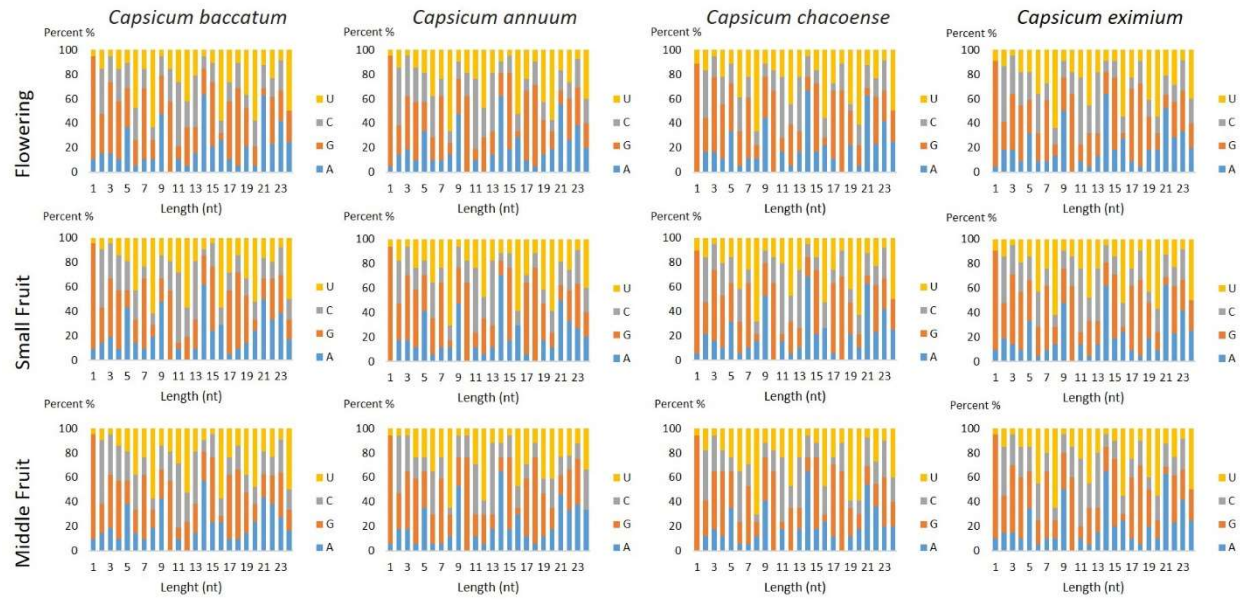


Figure S2. Nucleotide bias at each position of miRNAs from all *Capsicum* species analyzed at flowering, small fruit, and middle fruit stages. The horizontal coordinates are each position of sRNA reads and the vertical coordinates are the percentage of AUCG at each base.

miRNA-Target Functional Category

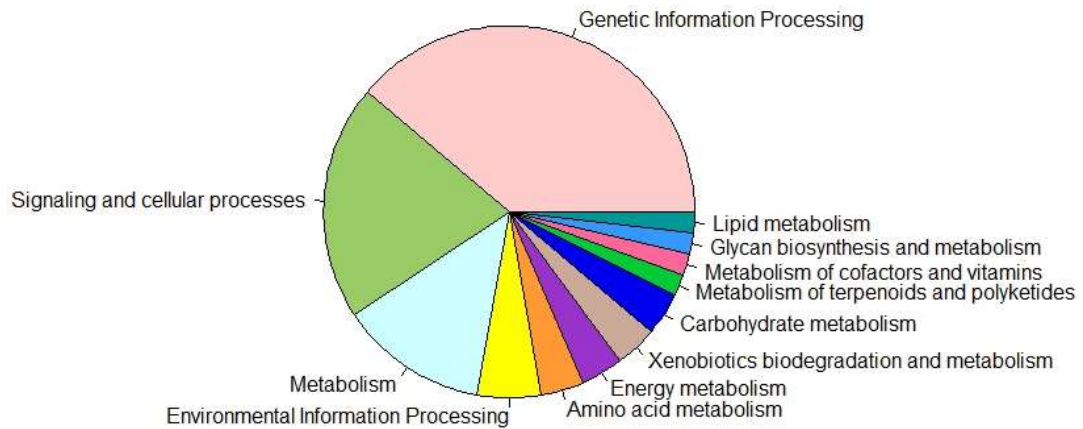


Figure S3. Functional characterization of miRNA targets with the BLASTKOALA sequence similarity tool. The chart illustrates different KEGG pathway groups: most of the miRNAs target genetic information processing (21), signaling and cellular processes (11), metabolism (7), environmental information processing (3), amino acid metabolism (2), energy metabolism (2), xenobiotics biodegradation and metabolism (2), carbohydrate metabolism (2), lipid metabolism (1), metabolism of terpenoids and polyketides (1), metabolism of cofactors and vitamins (1) and glycan biosynthesis and metabolism (1).

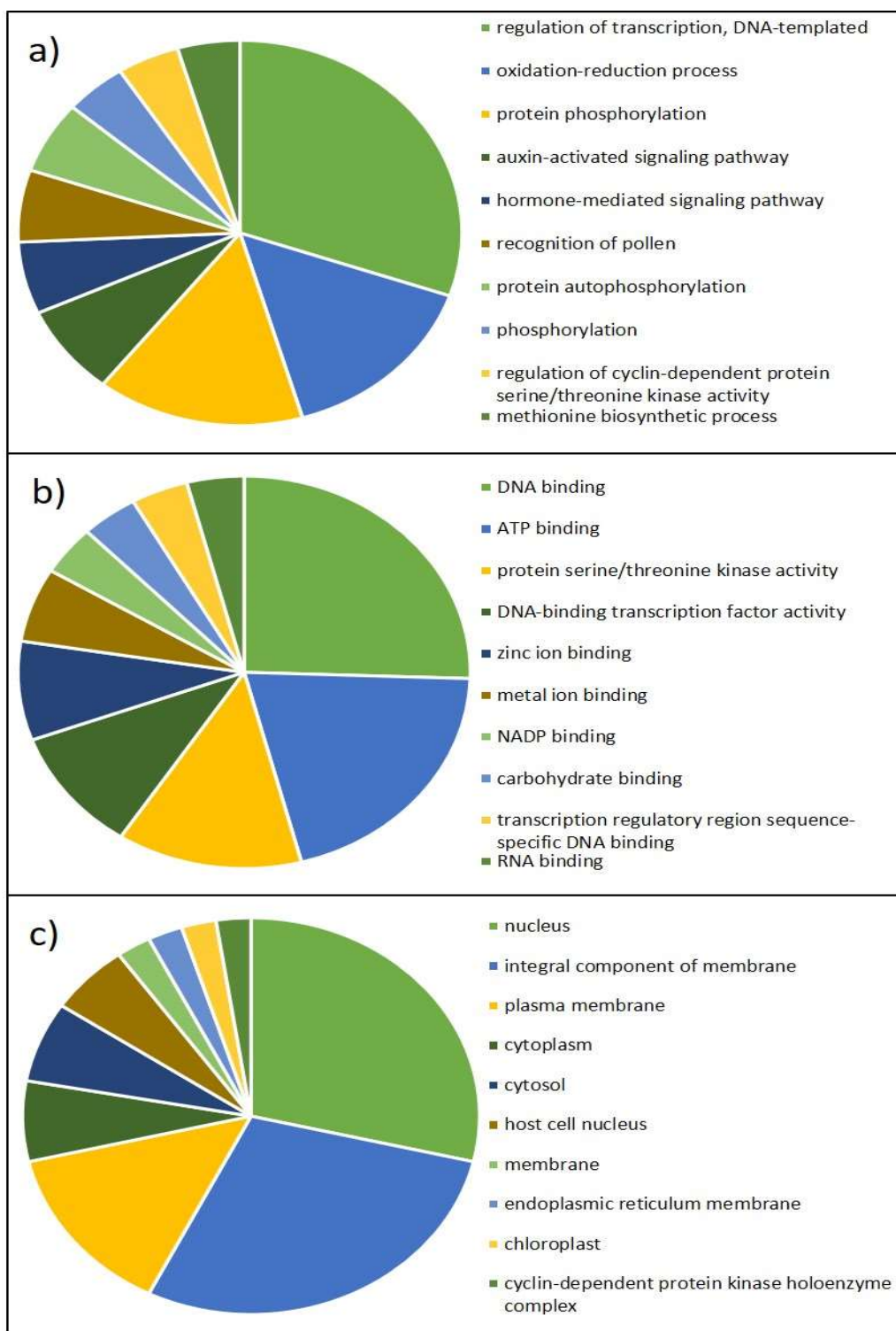


Figure S4. Gene ontology (GO) classification of the predicted target genes. The figure shows partial GO enrichment for the genes in three categories: a) biological process, b) molecular function and c) cellular component.

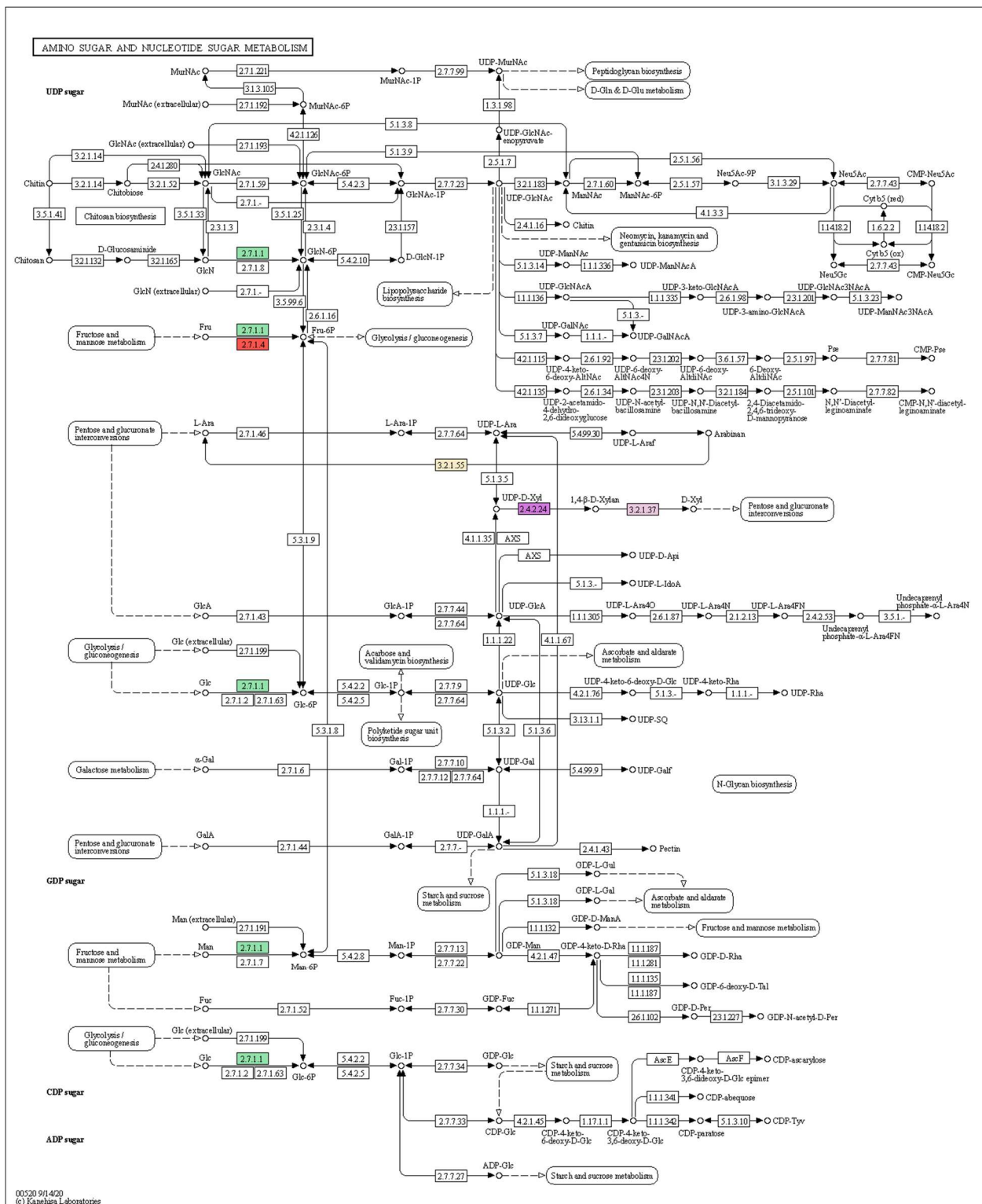


Figure S5. Principal KEGG pathway showing participation of miRNA target genes in amino sugar and nucleotide sugar metabolism.