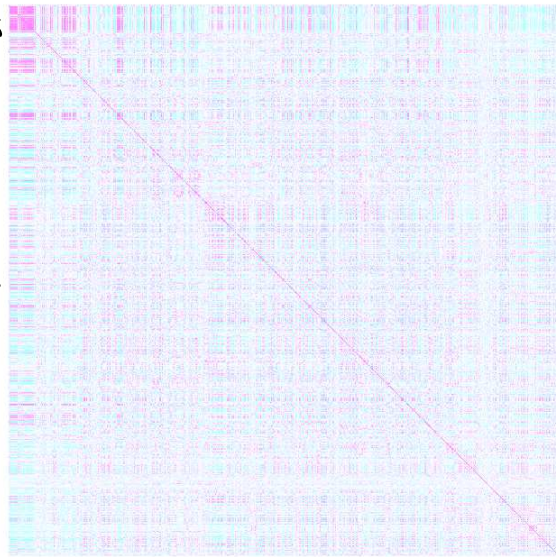


Supplemental Figure S1: The distribution of the expression matrix (A) and correlation coefficients (B) for the 3 organs are based on 9k genes calculated using the RMA algorithm.

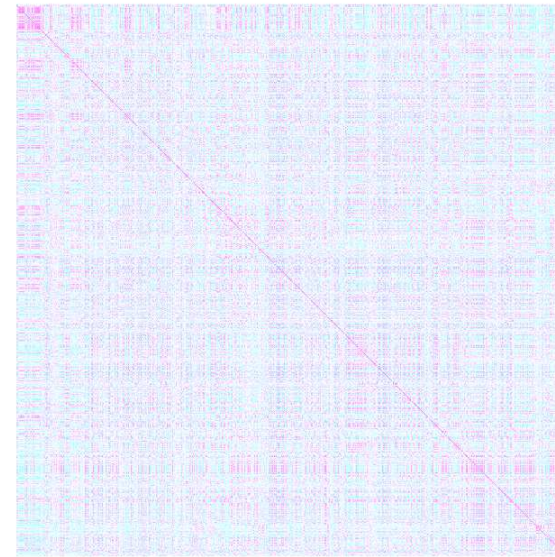
MapMan functional categories

photosynthesis
light reaction
major CHO metabolism
minor CHO metabolism
Glucoseoneogenesis
glycolysis
fermentation
xylose cycle
TCA / org. transformation
Mitochondrial electron transport / ATP synthesis

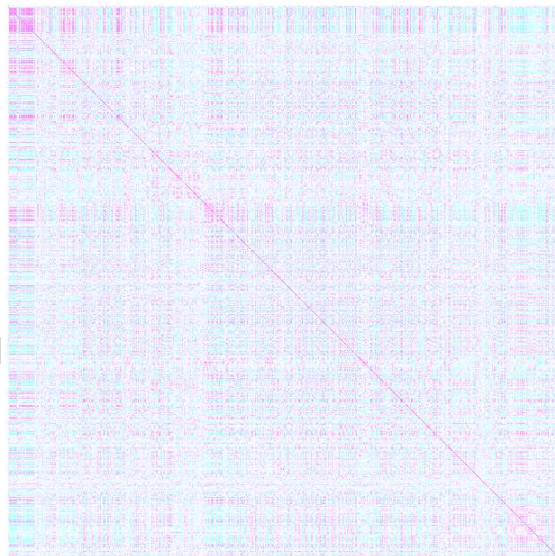
Correlation Matrix of all dataset



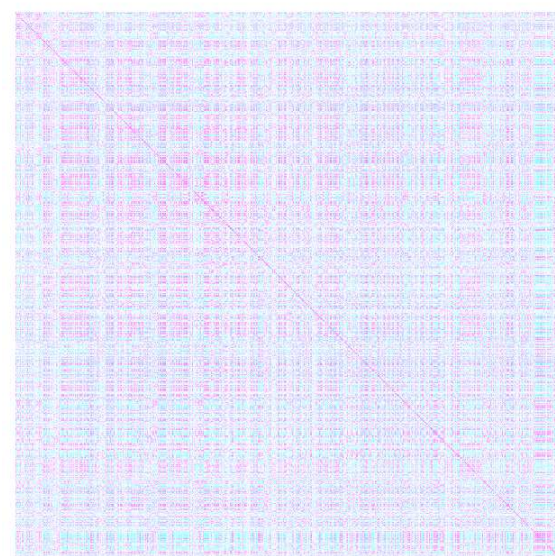
Correlation Matrix of leaves



Correlation Matrix of fruits



Correlation Matrix of roots



Supplemental Figure S2:
Correlation heatmaps for 4 datasets, "all data", "leaves", "fruits", and "roots". The values represent Pearson's correlation coefficients.

Supplemental Figure S3: Correlation of expression values measured by quantitative real-time PCR (qRT-PCR) and microarray. r , Pearson's correlation coefficient.

