

Supplementary material

GitHub material: https://github.com/Janek21/BDBI_TFG_MaizeCoexpression/tree/main/all_figures

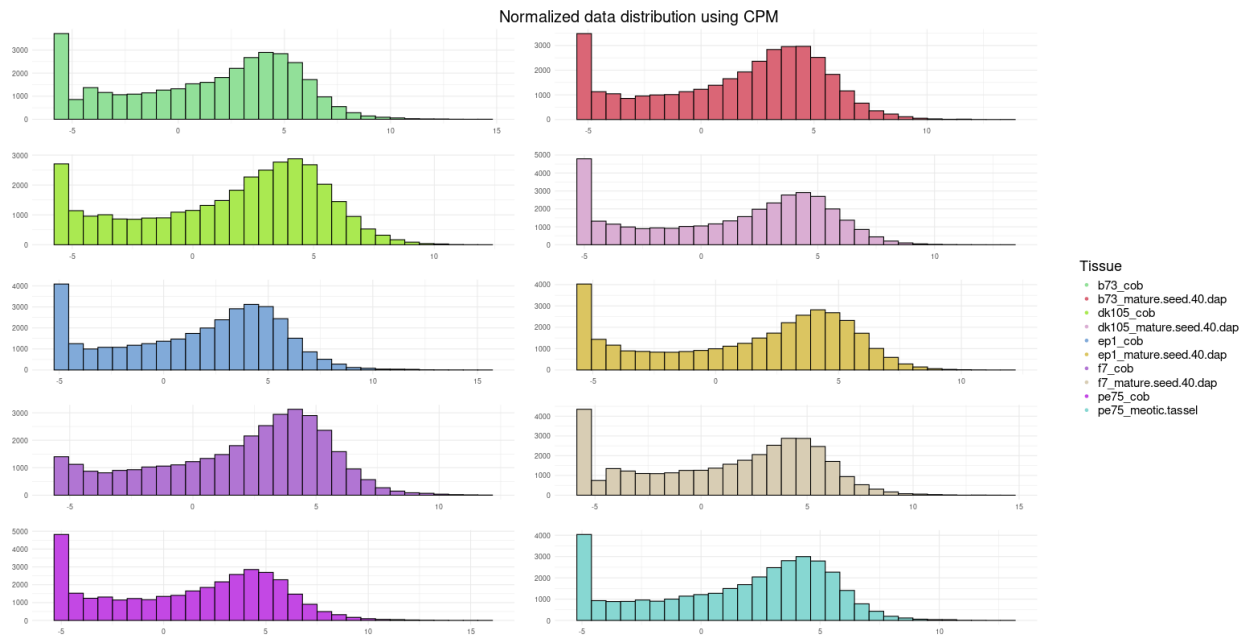


Figure 1: CPM distribution for 2 tissues of each line, the distribution shows overrepresentation in lowly expressed genes, even after filtering.

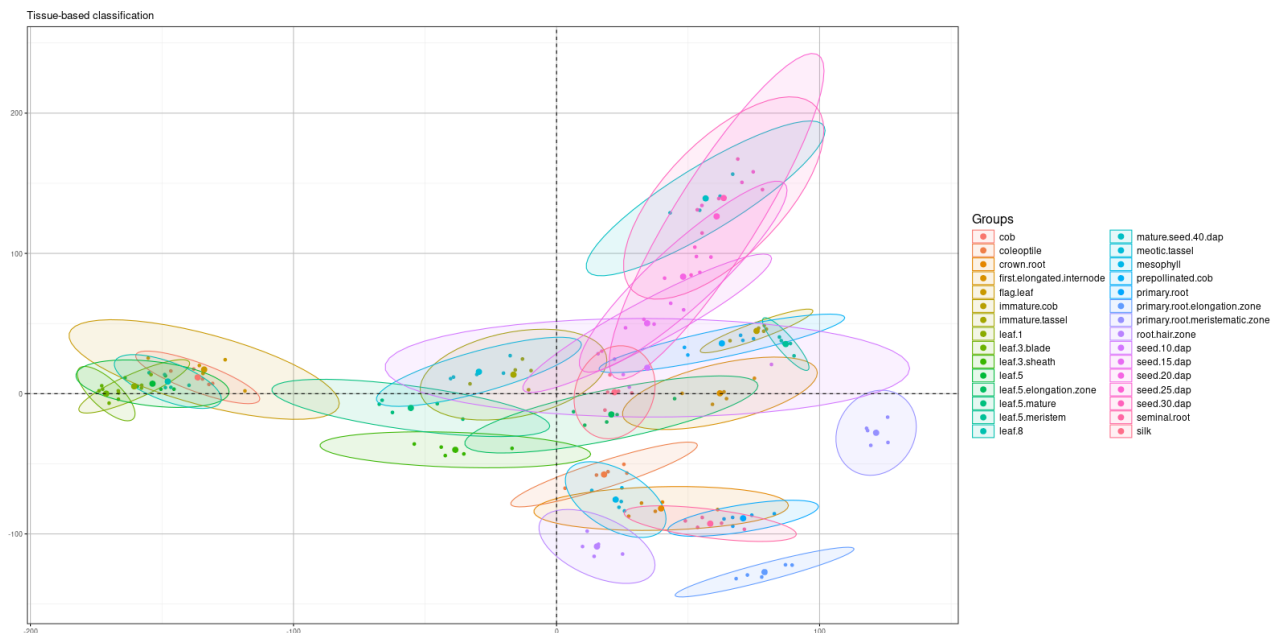


Figure 2: Representations of gene expression colored according to tissue. The representation is a PCA where clusters by expression similarity can be observed.

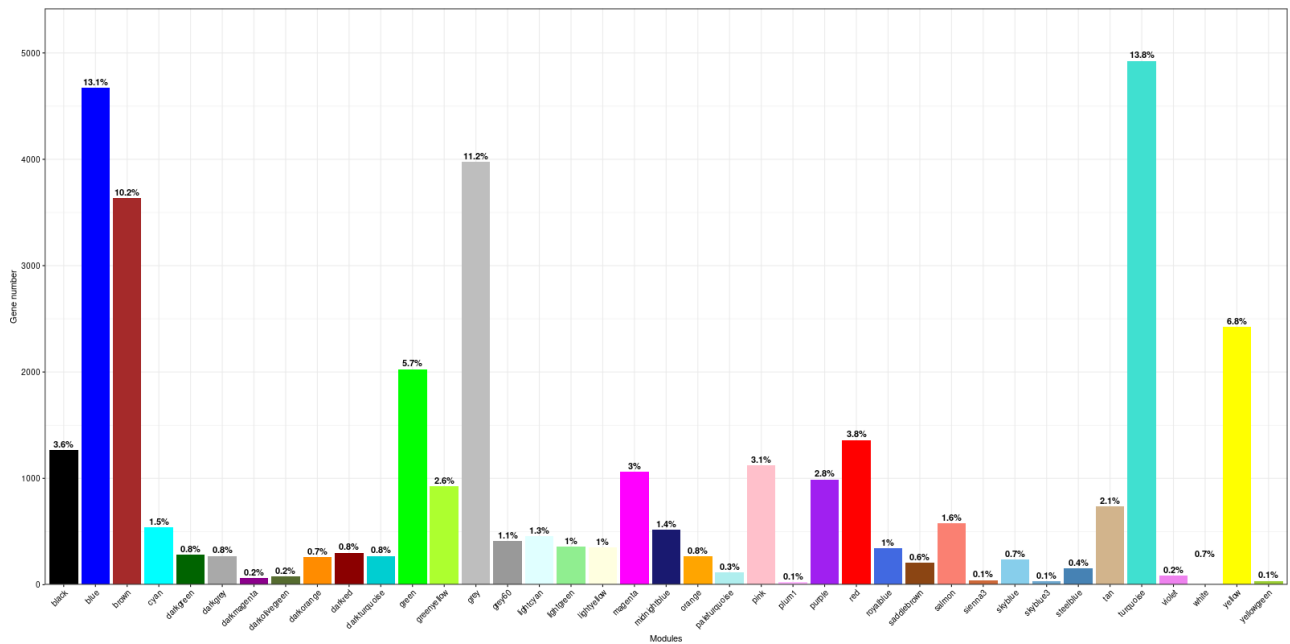


Figure 3: Classification of genes per module according to the network construction. The size of a module can also reflect its significance, since highly correlated genes tend to be involved in similar biological processes. This suggests that the function they perform is essential, as it is carried out by many different genes. (Kitano, 2004)

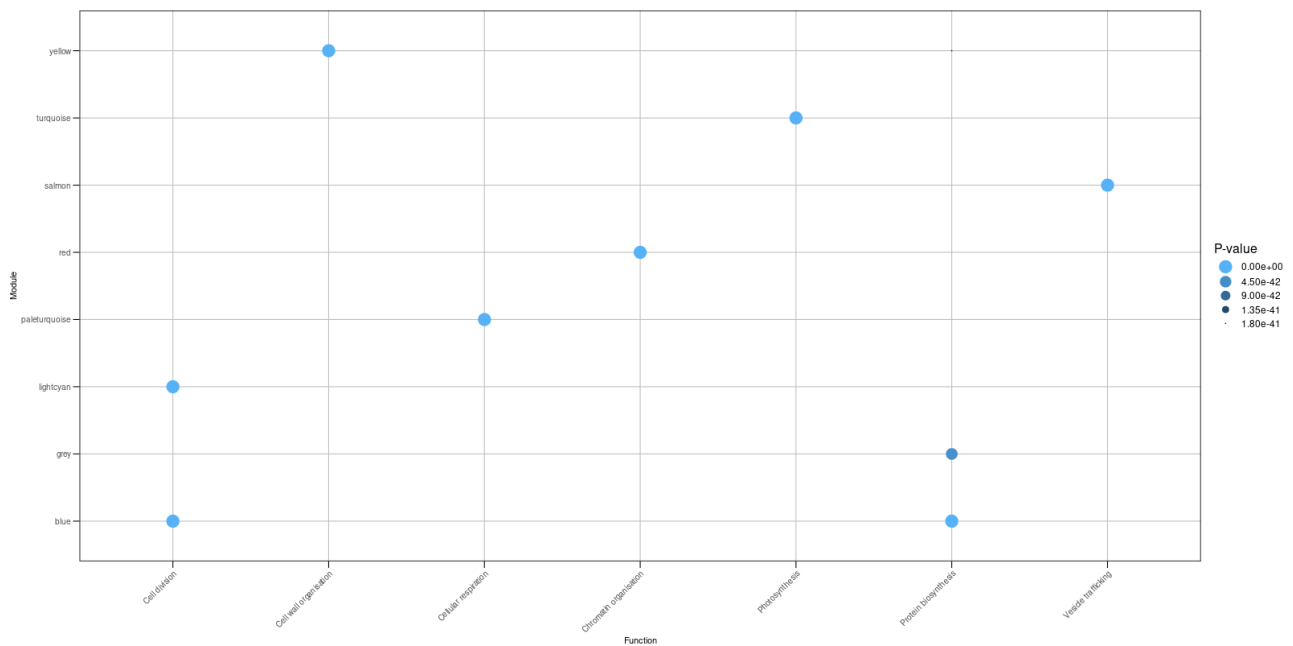


Figure 4: 10 most significant functions for all modules.

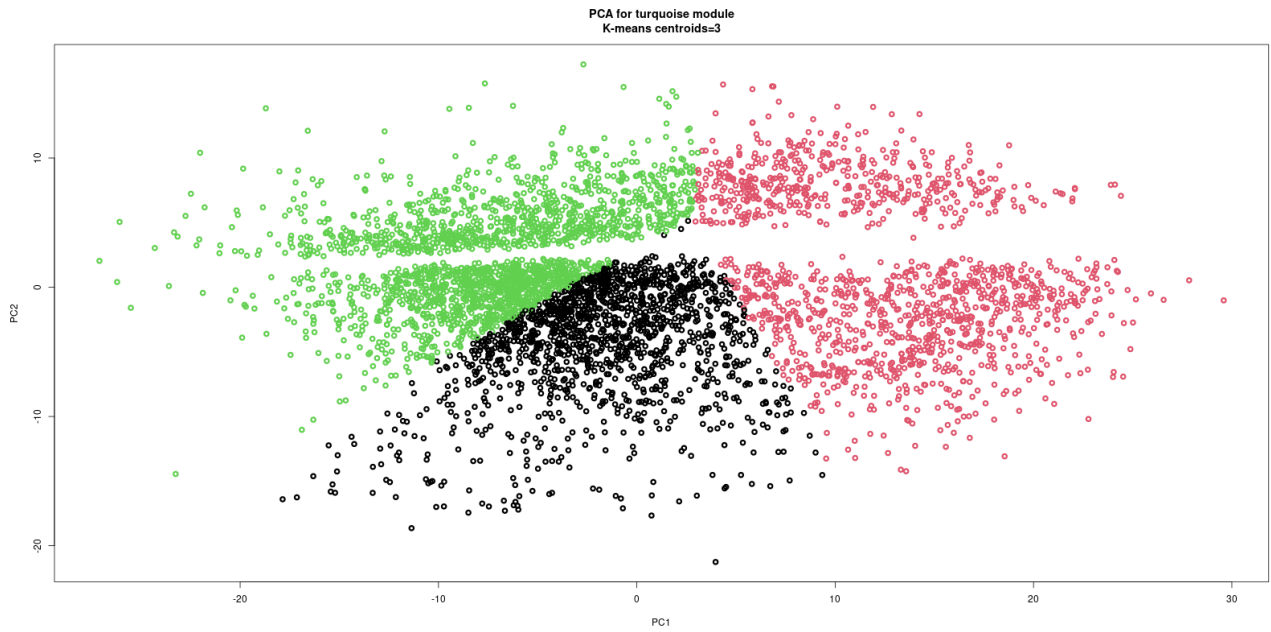


Figure 5: PCA of the gene co-expression in the turquoise module, colored by the 3 clusters determined by K-means

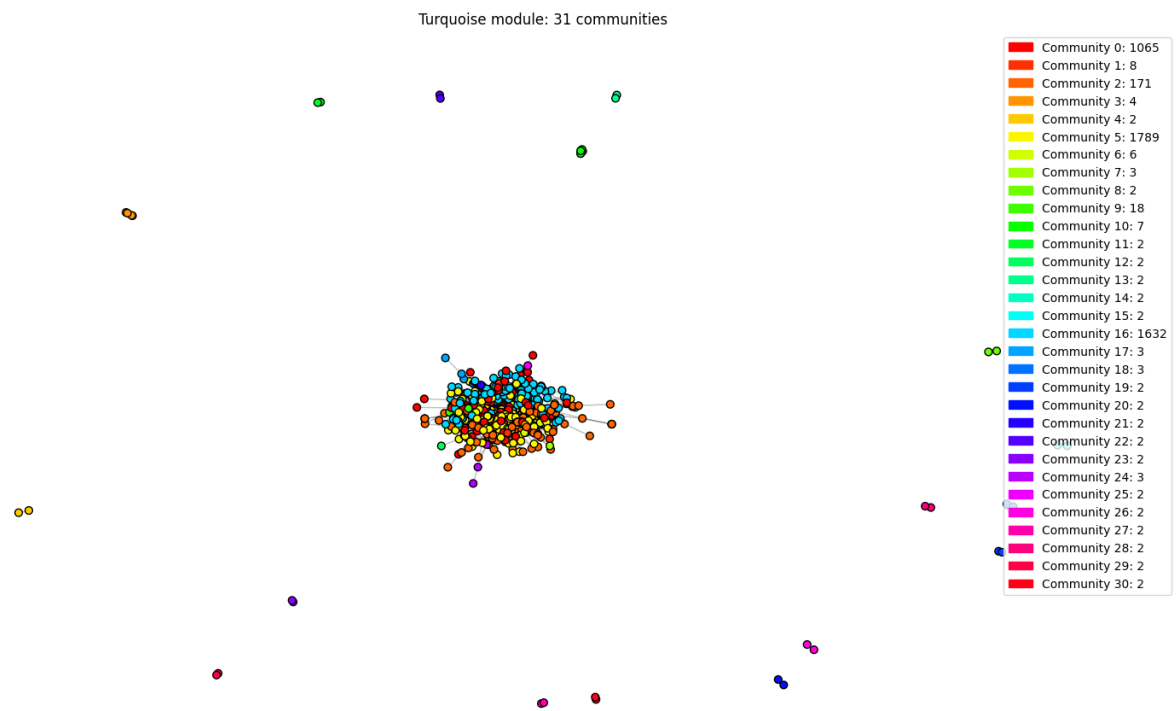


Figure 6: Complete visualization of the turquoise module colored according to communities.

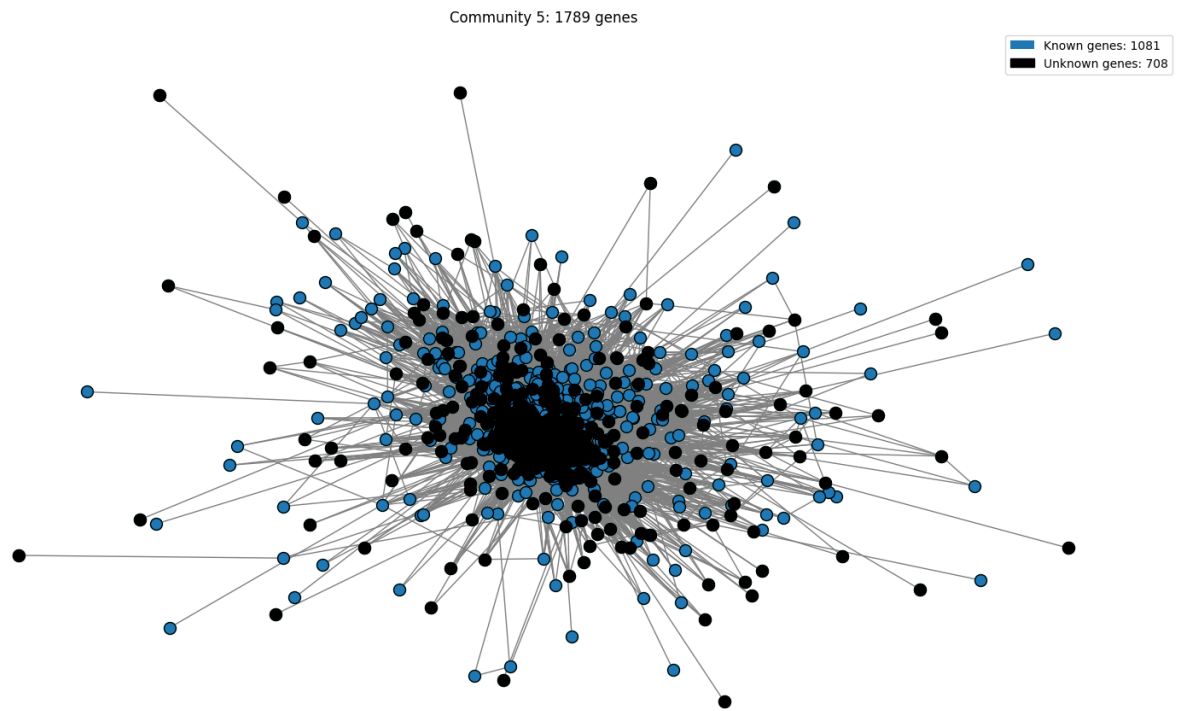


Figure 7: This figure represents a community of the turquoise module, the unknown genes are marked in black while the known genes are blue. It can be observed that there is a very high proportion of unknown genes, which translates into a low confidence level in the significant functions.

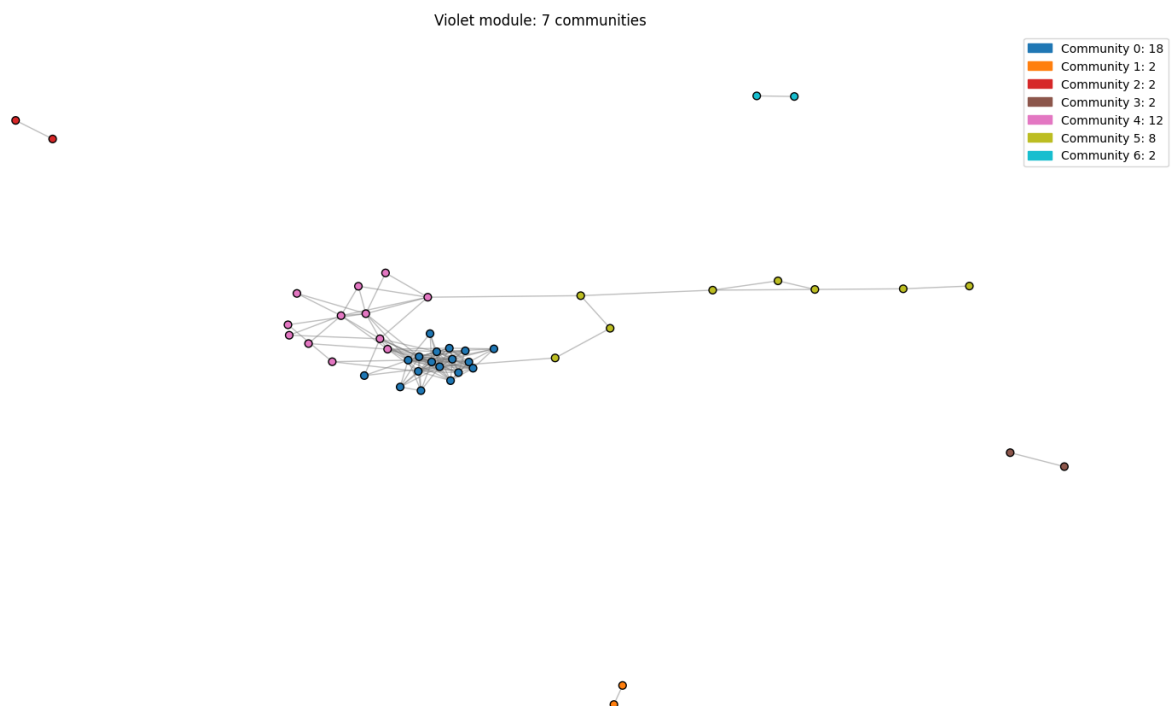


Figure 8: Complete visualization of the violet module colored according to communities.

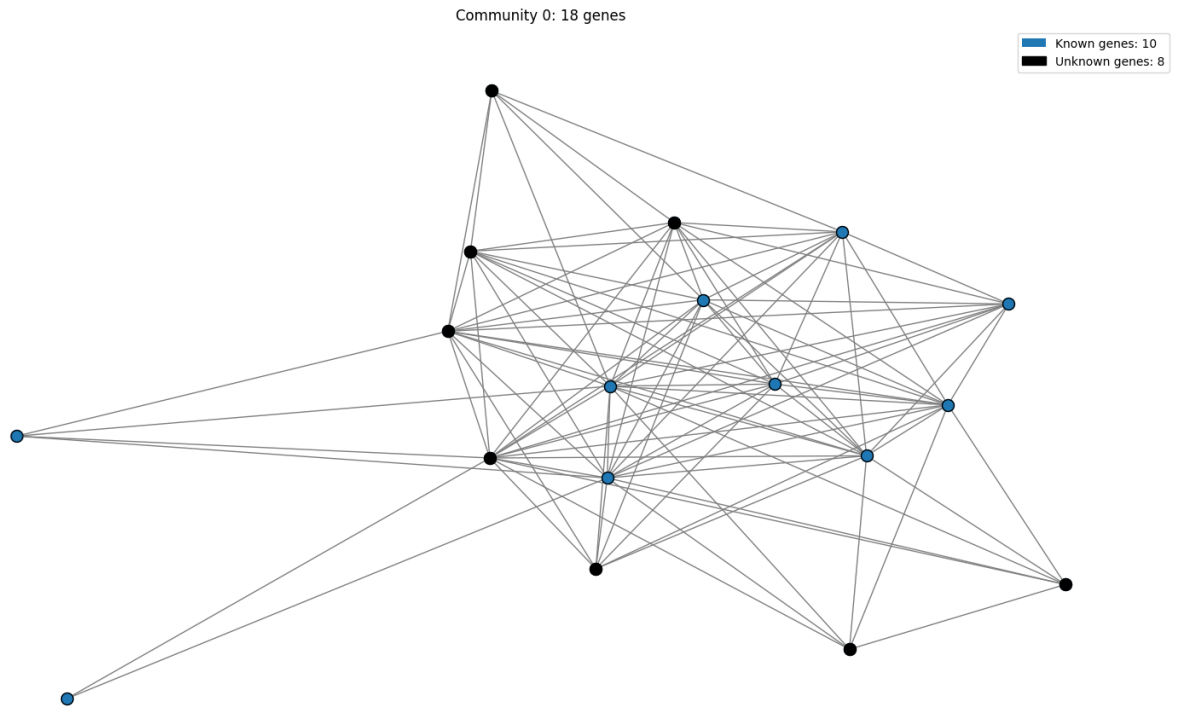


Figure 9: Visualization of a violet community.

Community	Known	Unknown
C0	537	528
C1	952	714
C2	94	98
C3	2	4
C5	1081	708
C6	5	1
C7	3	0
C9	0	18
C16	939	693
C24	3	0

Table 1: Communities in the turquoise module, with the known and unknown genes for each