

CORRECTION

Correction: Discovering Functional Modules across Diverse Maize Transcriptomes Using COB, the Co-Expression Browser

The *PLOS ONE* Staff

The link and image for [Fig. 4](#) are not correct. Please view the correct [Fig. 4](#) here.



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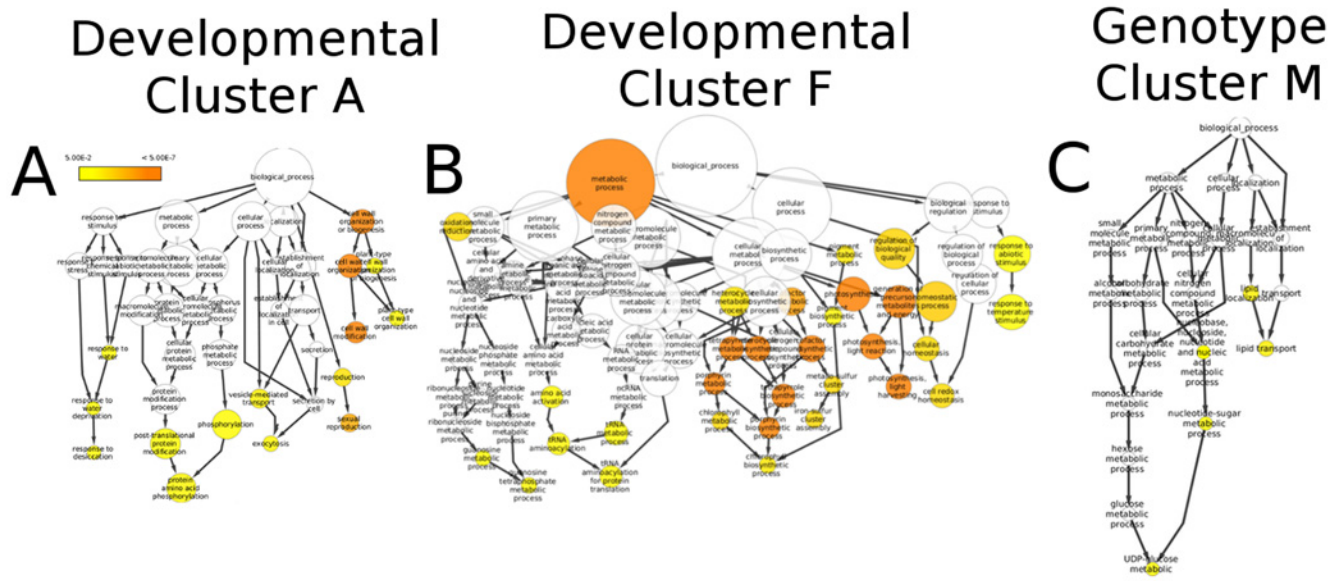


Fig 4. GO enrichment analysis of co-expression clusters. Gene clusters identified in Figure 2 were examined for enrichment of Gene Ontology terms. (A) Developmental cluster A, which exhibited a strong signal for expression in the anthers (see Figure 3), is enriched for GO terms related to sexual reproduction, response to desiccation, and cell wall biogenesis/modification. (B) Developmental cluster F, highlighted by patterns of expression in the leaves, is notably enriched for terms annotated for photosynthesis, response to temperature stimulus, and chlorophyll metabolism. (C) Genotype cluster M exhibits drastic under-expression in the P39 genotype, a sweet corn line, and shows significant GO enrichment in terms related to UDP-glucose as well as nucleotide-sugar metabolism and lipid transport

doi:10.1371/journal.pone.0120222.g001

Reference

1. Schaefer RJ, Briskine R, Springer NM, Myers CL (2014) Discovering Functional Modules across Diverse Maize Transcriptomes Using COB, the Co-Expression Browser. PLoS ONE 9(6): e99193. doi: [10.1371/journal.pone.0099193](https://doi.org/10.1371/journal.pone.0099193) PMID: [24922320](https://pubmed.ncbi.nlm.nih.gov/24922320/)