Construction and analysis of a suppression subtractive hybridization library of regeneration-related genes in soybean

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ABSTRACT. The development of a genetic transformation system is needed to address the problem of the low efficiency associated with soybean regeneration. To contribute to the enhancement of the soybean regenerative capacity, we explored the developmental mechanisms of soybean regeneration at the molecular level using a suppression subtractive hybridization cDNA library constructed from cotyledonary nodes of soybean cultivar DN50. A total of 918 positive clones were identified and screened, with most inserted fragments ranging from 100 to 750 bp. Of these, 411 differentially expressed functional expressed sequence tags were identified and annotated based on their similarity to orthologs and paralogs detected in GenBank using the nucleotide and translated nucleotide Basic Local Alignment Search Tools. Functional analysis revealed that the associated genes were involved in signal

transduction, synthesis, and metabolism of macromolecules, glucose and protein synthesis and metabolism, light and leaf morphogenesis, regulation of apoptosis, cell defense, cell wall differentiation, and a variety of hormone and cytokinin-mediated signaling pathways. The information uncovered in our study should serve as a foundation for the establishment of an efficient and stable genetic transformation system for soybean regeneration.