Genes expressed in cotton (*Gossypium hirsutum*) buds isolated with a subtractive library

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ABSTRACT. A subtractive cDNA library from cotton buds was constructed to prospect for differentially expressed genes related to early bud development. A library was constructed and 768 cDNA sequences were obtained, comprising 168 clusters, with 126 contigs and 42 singlets. Both the *Gossypium* as well as *Arabidopsis* databases were utilized for the *in silico* analysis, since some genes identified in cotton have not yet been studied for functionality, although they have homology with genes from other species. The transcriptome revealed a large number of transcripts, some of them with unknown function, and others related to pollen development, pollen tubes, ovules, and fibers at different stages. The most populated contig was identified as fiber

from 0-10 days after anthesis, with 12 reads. The success and novelty rates generated from the library were 67 and 51%, respectively. The information obtained here will provide a framework for research on functional cotton genomics.

Key words: Fiber; Ovule; Genes; Sequencing