Screening of differentially expressed genes in pathological scar tissues using expression microarray

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ABSTRACT. Pathological scar tissues and normal skin tissues were differentiated by screening for differentially expressed genes in pathologic scar tissues via gene expression microarray. The differentially expressed gene data was analyzed by gene ontology and pathway analyses. There were 5001 up- or down-regulated genes in 2-fold differentially expressed genes, 956 up- or down-regulated genes in 5-fold differentially expressed genes, and 114 up- or down-regulated genes in 20-fold differentially expressed genes. Therefore, significant differences were observed in the gene expression in pathological scar tissues and normal foreskin tissues. The development of pathological scar tissues has been correlated to changes in multiple genes and pathways, which are believed to form a dynamic network connection.

Key words: Pathological scar tissue; Differentially expressed gene; Gene chip