



Serial analysis of gene expression in adenocarcinoma samples and normal colonic mucosa in a Chinese population

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ABSTRACT. The goal of this study was to identify the differences in gene expression between adenocarcinoma samples and colonic normal mucosa of a Chinese population. Gene expression libraries of adenocarcinoma and normal colonic mucosa were generated by serial analysis of gene expression (SAGE). Expression tags were obtained from sequencing results using the SAGE2000 software. Representative genes of tags were determined based on the SAGEmap from NCBI. Expressed genes were selected and their expression in different libraries was compared using the SPSS 17.0 software. The expression of 78 tags representing 88 types of genes showed significant differences. Compared with normal mucosa, 38 genes showed decreased expression in cancer, whereas the expression of the remaining 50 genes showed significant up-regulation. Expressed tags in SAGE libraries of normal and cancerous tissues were significantly different. Further studies examining these genes, which showed different

expression levels between the 2 tissues, may be used as tumor markers and offer clues for studying the etiopathogenesis of colon cancer.

Key words: Colon normal mucosa; Colonic adenocarcinoma; Difference; Serial analysis of gene expression