

Gene expression in superior temporal cortex of schizophrenia patients

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We investigated gene expression pattern obtained from microarray data of 10 schizophrenia patients and 10 control subjects. Brain tissue samples were obtained postmortem; thus, the different ages of the patients at death also allowed a study of the dynamic behavior of the expression patterns over a time frame of many years. We used statistical tests and dimensionality reduction methods to characterize the subset of genes differentially expressed in the two groups. A set of 10 genes were significantly downregulated, and a larger set of 40 genes were upregulated in the schizophrenia patients. Interestingly, the set of upregulated genes includes a large number of genes associated with gene transcription (zinc finger proteins and histone methylation) and apoptosis. We furthermore identified genes with a significant trend correlating with age in the control (MLL3) or the schizophrenia group (SOX5, CTRL). Assessments of correlations of other genes with the disorder

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