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Genetic clustering of depressed patients and normal controls based on single-nucleotide variant proportion

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Abstract

Background

Genetic components play important roles in the susceptibility to major depressive disorder (MDD). The rapid development of sequencing technologies is allowing scientists to contribute new ideas for personalized medicine; thus, it is essential to design non-invasive genetic tests on sequencing data, which can help physicians diagnose and differentiate depressed patients and healthy individuals.

Methods

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