Using genetic variability in whole transcriptome expression in the hippocampus and temporal cortex to understand the pathogenesis of Alzheimer’s disease

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Using genetic variability in whole transcriptome expression in the hippocampus and temporal cortex to understand the pathogenesis of Alzheimer's disease

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3

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Research Abstract
In the past two decades scientists have shown that some individuals have common changes in their DNA (the instruction manual for all the building blocks needed to make the body) that put them at higher risk of developing Alzheimer’s disease (AD). Some of these genetic risk factors

might cause disease by changing how much or the way particular genes are expressed in the brain. We will check this by measuring the genetic variation an individual carries and linking this information to the genes expressed in the brain. We will use a technology called “RNA-seq” to measure all kinds of gene product from specific brain regions and pure collections of cells. We will focus on brain regions and cell types most affected in AD, such as the hippocampus and temporal cortex, in neurologically normal individuals and people who suffered from AD during their life. We already have the RNA and DNA data we need on normal individuals, which means that the new information we generate will be quickly and cost-effectively analysed so that we can make progress faster. All the data we generate on the human brain will be made publicly available so that other scientists can use this information too.

Further information available at:

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