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# Single-cell RNA sequencing analysis of human Alzheimer's disease brain samples reveals neuronal and glial specific cells differential expression

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## Abstract

Alzheimer's disease is the most common neurological disease worldwide. Unfortunately, there are currently no effective treatment methods nor early detection methods. Furthermore, the disease underlying molecular mechanisms are poorly understood. Global bulk gene expression profiling suggested that the disease is governed by diverse transcriptional regulatory networks. Thus, to identify distinct transcriptional networks impacted into distinct neuronal populations in Alzheimer, we surveyed gene expression differences in over 25,000 single-nuclei collected from the brains of two Alzheimer's in disease patients in Braak stage I and II and age- and gender-matched controls hippocampal brain samples. APOE status was not measured for this study samples (as well as CERAD and THAL scores). Our bioinformatic analysis identified discrete glial, immune, neuronal and vascular cell populations spanning Alzheimer's disease and controls. Astrocytes and microglia displayed the greatest transcriptomic impacts, with the induction of both shared and distinct gene programs. © 2023 Soreq et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

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