ALZHEIMER'S DISEASE from a genetics and transcriptomics perspective

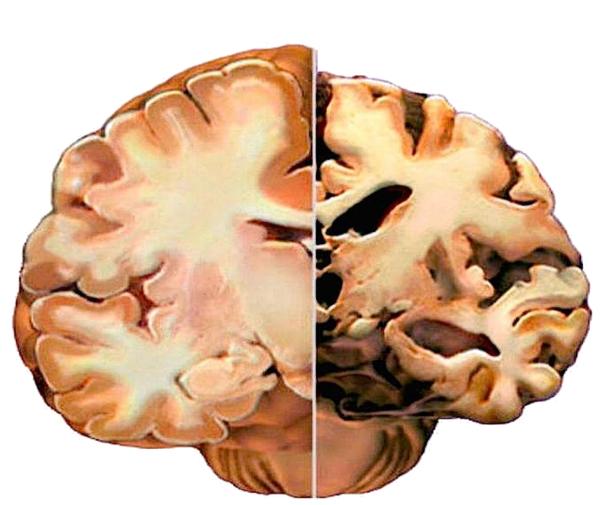




VIB -UAntwerp Center for Molecular Neurology Prof. Dr. Kristel Sleegers Contact: kristel.sleegers@uantwerpen.vib.be

SLEEGERS LAB

The Sleegers lab at the VIB-UAntwerpen Center for Molecular Neurology is committed to increase insight in the complex genetics of Alzheimer's disease and to investigate the translational potential of genetic discovery.







alzheimer's Sociation

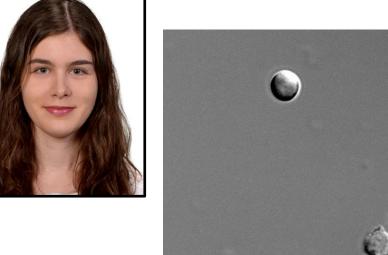


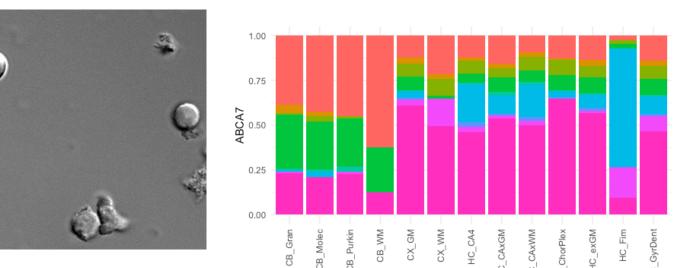


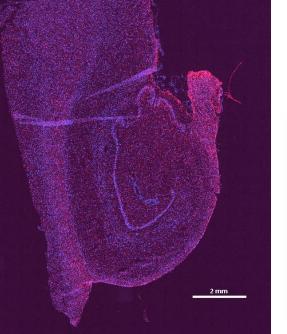


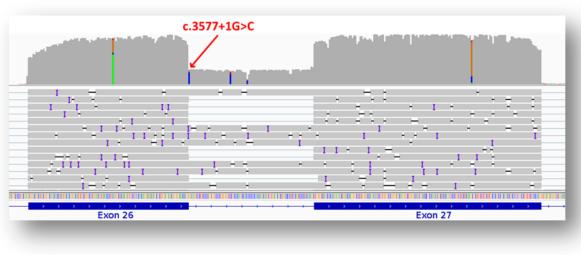
ALZHEIMER RISK GENE ABCA7 FROM AN RNA PERSPECTIVE

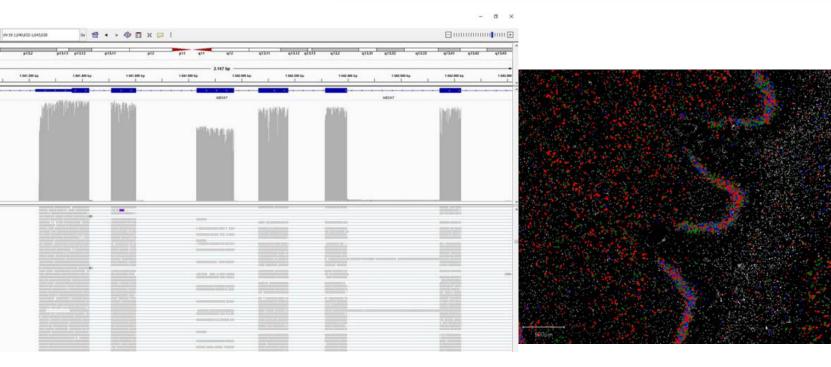










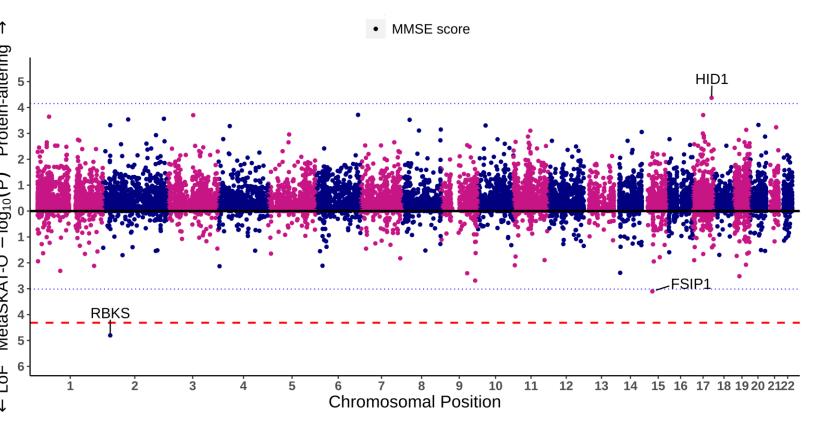


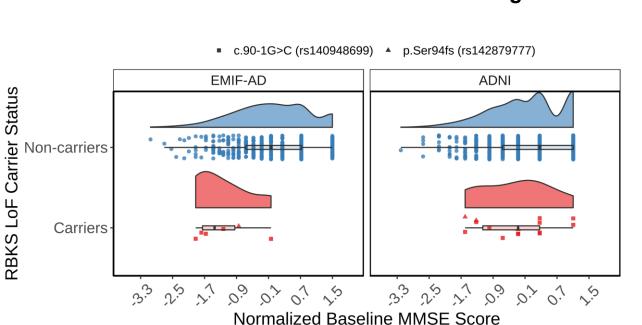
Long read cDNA sequencing, spatial expression and single-nuclei RNA sequencing of ABCA7 in post-mortem brain tissue

GENETICS OF ALZHEIMER'S BIOMARKER TRAITS



Common and rare variant genetic analyses of **cognitive**, **cerebrospinal fluid (CSF) and volumetric magnetic resonance imaging (MRI)** phenotypes.





KEY PAPERS

- Bellenguez, C., Küçükali, F. et al. New insights into the genetic etiology of Alzheimer's disease and related dementias. Nature Genetics (2022).
- Küçükali, F. et al. Whole-exome rare variant analysis of Alzheimer's disease and related biomarker traits. Alzheimer's & Dementia (2022).
- Neumann, A., Küçükali, F. et al. Rare variants in IFFO1, DTNB, NLRC3 and SLC22A10 associate with Alzheimer's disease CSF profile of neuronal injury and inflammation. Molecular Psychiatry (2022).
- De Roeck A, Duchateau L, et al. An intronic VNTR affects splicing of ABCA7 and increases risk of Alzheimer's disease. Acta Neuropathologica (2018).
- Cuyvers E, Sleegers K. Genetic variations underlying Alzheimer's disease: evidence from genome-wide association studies and beyond. Lancet Neurology (2016).
- Cuyvers E, De Roeck A, et al. Mutations in ABCA7 in a Belgian cohort of Alzheimer's disease patients: a targeted resequencing study. Lancet Neurology (2015).

TECHNIQUES

SNP genotyping, short and long read DNA/RNA sequencing, spatial transcriptomics, single nuclei sequencing, gel electrophoresis, fragment analysis, Western blot.

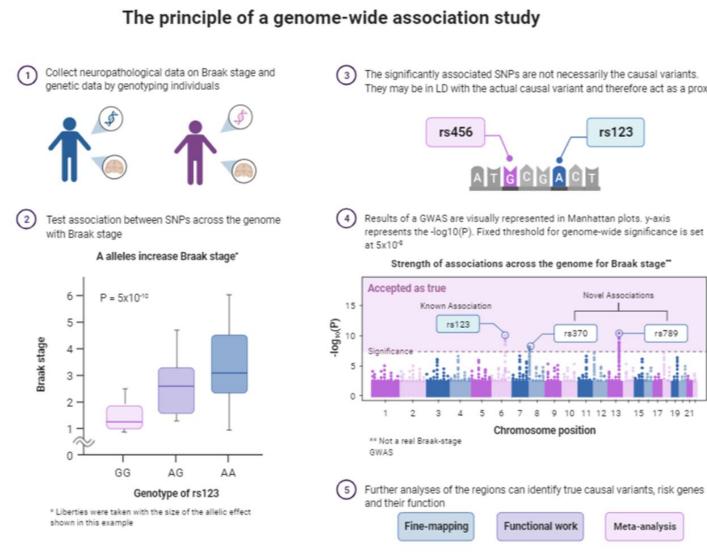


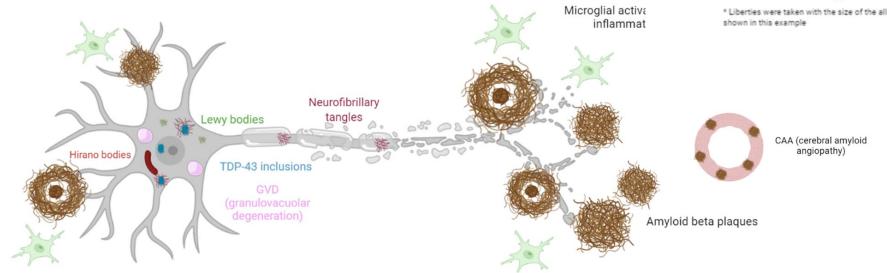
Bioinformatic data processing, genome-wide association analysis, whole exome rare variant association analysis, genetic risk prediction, quantitative trait locus analysis (eQTL, sQTL, mQTL, pQTL), transcriptome wide association analysis, X-chromosome analysis.

GENETIC PREDICTORS OF NEUROPATHOLOGY

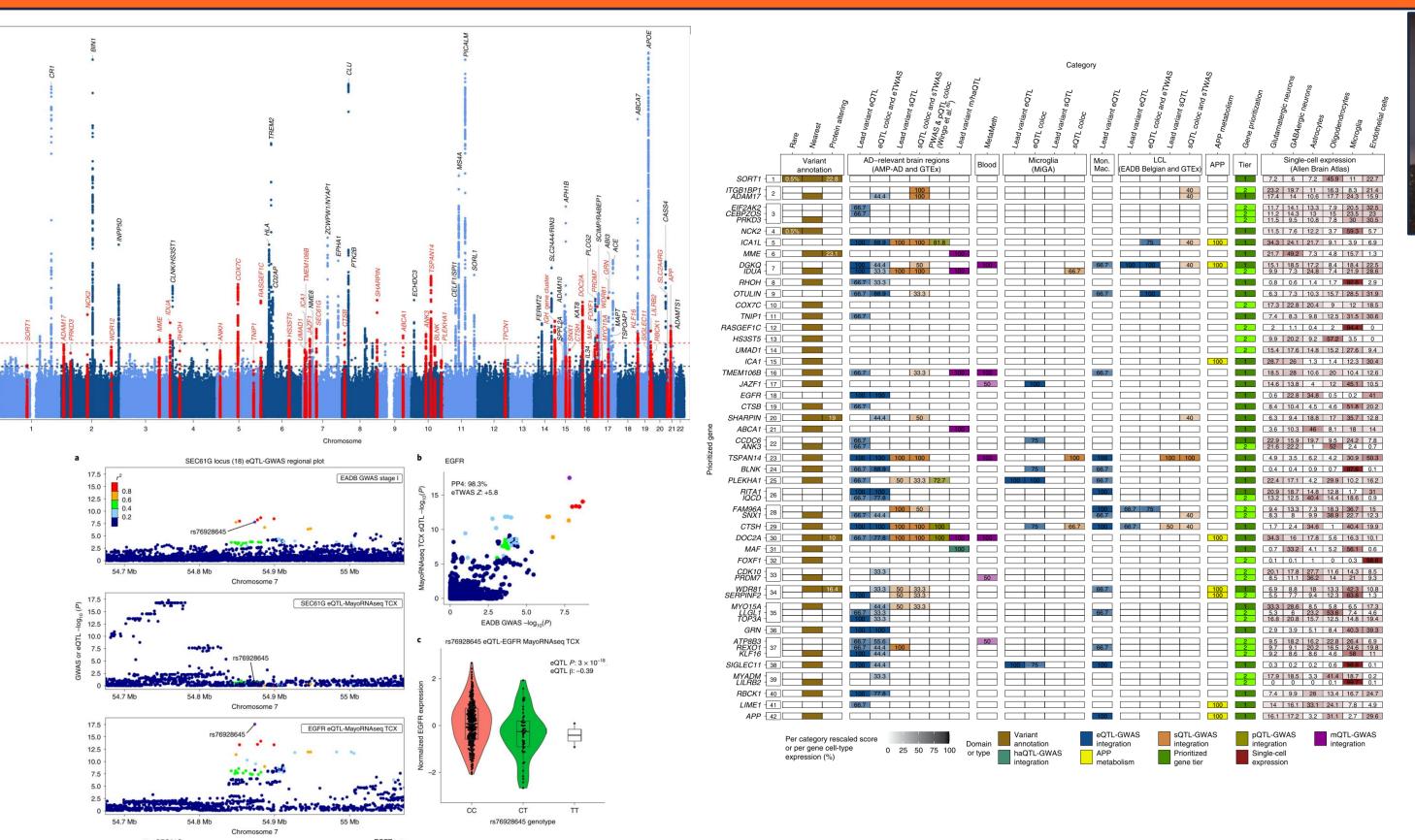


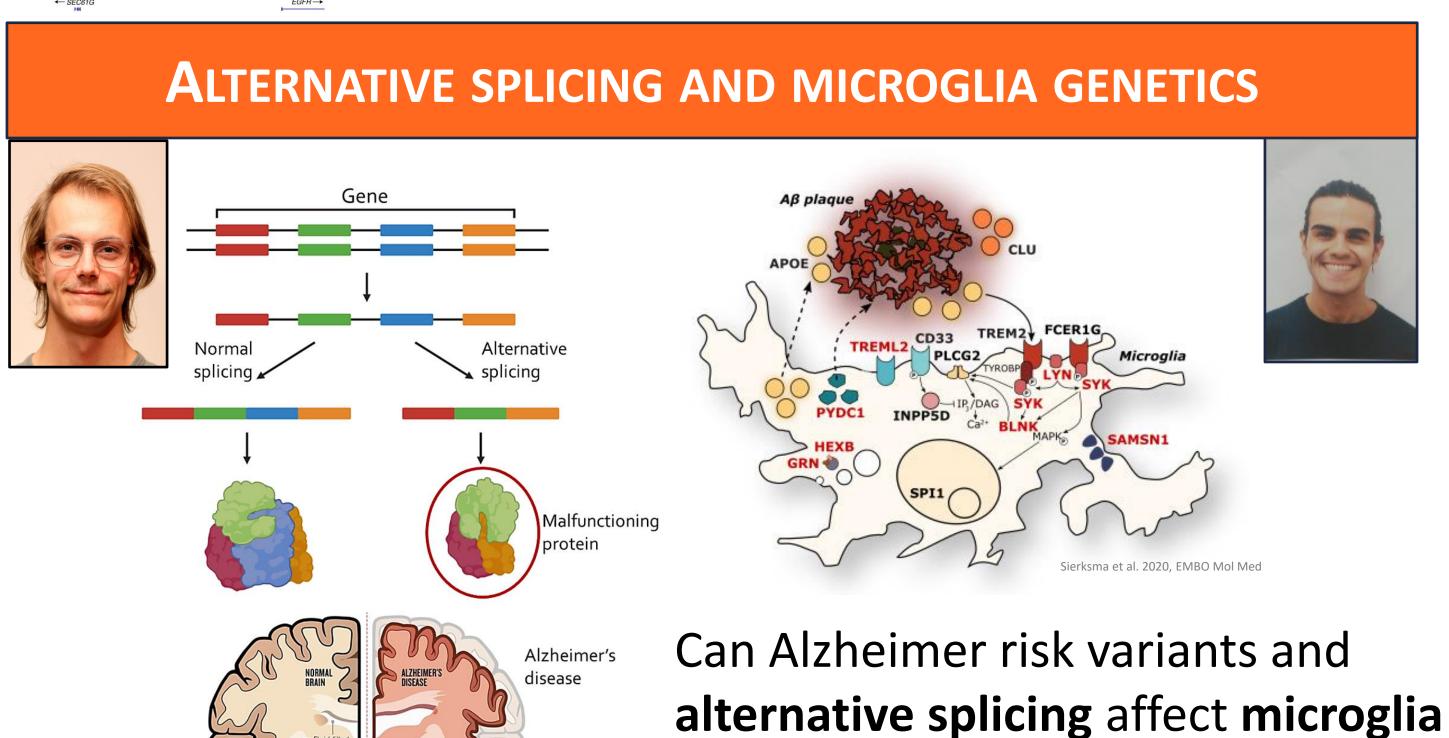
Discover novel
risk variants
(GWAS) and
investigate known
risk loci in
neuropathological
cohort





GENOME-WIDE ASSOCIATION STUDIES OF ALZHEIMER'S AND PRIORITIZING GENES IN RISK LOCI WITH INTEGRATIVE -OMICS





function in Alzheimer's disease?