

Online Resources

Whole transcriptome RNA-Seq reveals drivers of pathological dysfunction in a transgenic model of Alzheimer's disease.

Molecular Neurobiology

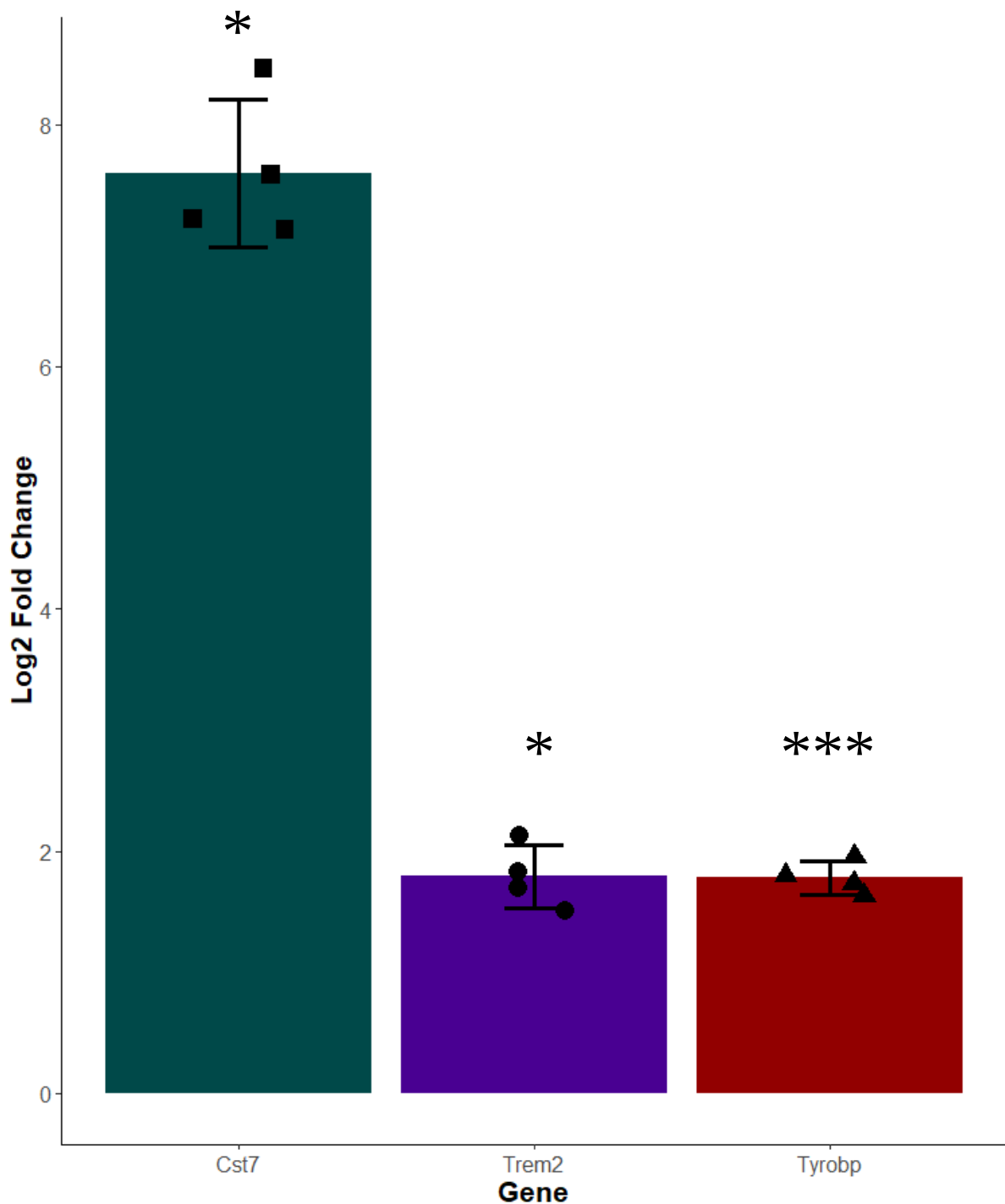
Nikita Potemkin^{1,2}, Sophie M.F. Cawood^{1,2}, Diane Guévremont^{1,2}, Bruce Mockett^{2,3}, Jackson Treece¹, Jo-Ann L. Stanton¹, Joanna M. Williams^{1,2*}.

¹ Department of Anatomy, School of Biomedical Sciences, University of Otago, P.O. Box 56, Dunedin, New Zealand.

² Brain Health Research Centre, Brain Research New Zealand – Rangahau Roro Aotearoa, University of Otago, Dunedin, New Zealand.

³ Department of Psychology, University of Otago, P.O. Box 56, Dunedin, New Zealand.

*Corresponding author: Joanna.williams@otago.ac.nz



Online Resource 2: Bar and dot plot showing log2 fold-change of the genes Trem2, Tyrobp, and Cst7 in APP/PS1 mice compared to wild-type controls as measured by qPCR. Bars indicate SD, and individual datapoints are also shown. Cst7 reported a 200 ± 97 -fold change (log FC 7.7, $p = 0.0016$), while Trem2 and Tyrobp showed fold-changes of 3.5 ± 0.63 and 3.44 ± 0.32 respectively ($p = 0.0059$ and $p < 0.0001$). * = $p < 0.01$, **** = $p < 0.0001$.