

Tau and tissue specificity – Data description

These tau index values were calculated based on the GTEx (version 8, <https://www.gtexportal.org/home/>) values of expression for genes and transcripts.

The included csv file contains the value of expression, obtained from GTEx, for each individual gene in several tissues, as designated by the column with each tissue name. The last column of the csv pertains to the tau index value calculated based on the previously mentioned expression values for all tissues. This tau index is an indicator of how specifically or broadly expressed a gene is, with genes that have a tau closer to 1 being more specifically expressed in one tissue, and genes with a tau closer to 0 having equal expression across all tissues studied. The methodology for the computation of the tau index has been previously described in:

PALMER, D., FABRIS, F., DOHERTY, A., FREITAS, A. A., DE MAGALHAES, J. P. (2021) [Ageing transcriptome meta-analysis reveals similarities and differences between key mammalian tissues](#). *AGING* **13**(3):3313-3341.

For more information on the tau index and how it equates to other methods of tissue-specificity, see:

KRYUCHKOVA-MOSTACCI, N., ROBINSON-RECHAVI, M. (2017) [A benchmark of gene expression tissue-specificity metrics](#). *BRIEF BIOINFORM.* **18**(2):205-214.

To cite this data please use:

PALMER, D., FABRIS, F., DOHERTY, A., FREITAS, A. A., DE MAGALHAES, J. P. (2021) AGEING TRANSCRIPTOME META-ANALYSIS REVEALS SIMILARITIES AND DIFFERENCES BETWEEN KEY MAMMALIAN TISSUES. *AGING* **13**(3):3313-3341.

Data updated by Priyanka Raina.

For more resources on human ageing, please visit HAGR:

<https://genomics.senescence.info>

To go back to HAGR's tau page:

https://genomics.senescence.info/gene_expression/tau.html