

Basal Aging Microarray Dataset

Description:

Each spreadsheet contains the analyzed, microarray data as described in Haberman et al, 2011 (see complete reference under "Publication"; a full description of subjects, behavior and microarray analysis is given in this manuscript). Briefly, this study examined gene expression differences in three hippocampal subfields (CA1, CA3 and the dentate gyrus) of young and aged adult male Long Evans rats that have been behaviorally characterized on a standardized watermaze task. Successful performance in the task depends on the integrity of the medial temporal lobe memory system (especially the hippocampus) and aged rats exhibit substantial individual differences ranging from intact to significantly impaired performance. The primary measure used in the spatial learning task is the Learning Index (LI), generated from the proximity of the rat to the escape platform during probe trials interpolated throughout training and used to define impairment in the rats. Lower scores reflect better performance as they indicate a search closer to the platform location. Aged rats were categorized based on the normative range of young (Y) performance established across years of testing within this paradigm. Those performing as well as young were designated aged unimpaired (AU; $LI < 240$) whereas those performing worse than young were considered aged impaired (AI; $LI > 240$). RNA was extracted from each hippocampal subfield and assayed on Affymetrix 230A microarrays such that each subfield of each rat was run on a single chip. Raw microarray intensities were normalized with gcRMA and analyzed using Significance analysis in Microarray (SAM). Numbers of subjects were 8 AI, 7AU and 9 Y. Five arrays were excluded as they failed to meet quality control standards (In CA1: 1 AU array; in CA3: 1 AU array; in DG: 1 AU, 1 AI and 1Y array). To determine if a probeset was considered "present" an empirically derived low expression cut-off measure was used such that any average probeset intensity exceeding this cut-off was given a value of 'true' and considered expressed in the subfield. A series of pair-wise comparisons between subject groups were performed. In some instances (as indicated below in the abbreviations) two subject groups were combined and compared to the third group.

Downloadable files:

Basal Aging CA1: All CA1 subfield data

Basal Aging CA3: All CA3 subfield data

Basal Aging DG: All DG subfield data

Basal Aging Learning Index: Learning Indexes for all subjects organized by subfield

Abbreviation/category explanation:

AffyIDs - Affymetrix probeset ID

GeneSymbols – Entrez gene symbol*

GeneNames – Entrez gene name*

GeneRefSeqs – Genbank reference sequence ID*

MeanIntGCRMA – mean Log₂ probeset intensity across all subjects

GCRMAlocutIndx – T = probeset considered “present”; F = probeset considered “absent”

AUpAI v Y - All aged rats combined and compared to young

AI vs Y – Aged Impaired rats compared to young

AU vs Y – Aged Unimpaired compared to young

AU vs AI – Aged Unimpaired compared to Aged impaired

AI vs AUpY – Aged Impaired compared to the combined group of Young and Aged Unimpaired

SAM@fold - relative change in LA vs CTL subjects; values>1 indicates increased expression in first listed group relative to the second ; values<1 indicate decreased values in the first listed group relative to the second (For example in AU v AI SAM@fold= 1.5 for gene X: gene X is expressed 1.5 times higher in aged unimpaired rats than aged impaired)

SAM@d – SAM d-statistic value

SAM@p.value - SAM p-value

SAM@q.value - SAM q-value; proxy for false detection rate

BA-AICA1_17 – designation for individual subject: Log₂ transformation of gcRMA raw intensity: BA (refers to Basal aging microarray experiment); AI (Aged impaired rat); CA1 (hippocampal subfield); 17 (subject #17)

BA-AUCA1_10 - designation for individual subject: Log₂ transformation of gcRMA raw intensity: BA (refers to Basal aging microarray experiment); AU (Aged Unimpaired rat); CA1 (hippocampal subfield); 10 (subject #10)

BA-YCA1_1 - designation for individual subject: Log₂ transformation of gcRMA raw intensity: BA (refers to Basal aging microarray experiment); Y (Young rat); CA1 (hippocampal subfield); 1 (subject #1)

* Annotations are not updated since the original publication. Updated probeset annotations can be found on the Affymetrix website.

Publication:

Publication of a reanalysis of the data obtained from this website is permitted pending appropriate citation of the data source and the following manuscript:

Haberman RP, Colantuoni C, Stocker AM, Schmidt AC, Pedersen JT, Gallagher M. (2011) Prominent hippocampal CA3 gene expression profile in neurocognitive aging. *Neurobiol Aging*, 32(9):1678-92.