

Supplementary Materials

Sexual dimorphism and ageing in the human hippocampus: Identification, validation and impact of differentially expressed genes by factorial microarray and network analysis

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Table S4: Main metabolic functional classes prevailing by the Age Ratio# discriminating criterion. Functionalities are derived by ontology analysis of the compatible metabolic networks built from nucleus 1, derived from the whole list of age-dependent genes (for details see the Supplementary Table S5).

Ontology Process (metabolic)	Set of genes with Age Ratio# < 1	Set of genes with Age Ratio# > 1
	Hypergeometric Probability*	Hypergeometric Probability*
Hexoses metabolism, Glycolysis	1.8×10^{-6}	4×10^{-2}
Mitochondrial matrix, aerobic respiration, respiratory electron chain	7.0×10^{-3}	1.5×10^{-4}
Glycerolipids, Lipid biosynthesis	8.4×10^{-7}	NDAS
Dicarboxylic Acid transport	6.0×10^{-7}	4.5×10^{-9}
Monocarboxylic Acid transport and metabolism	1.8×10^{-6}	3.7×10^{-5}
Glutamine and glutamate transport	NDAS	6.3×10^{-7}
Serine, branched amino-acids, and proline transport;	3.0×10^{-7}	NDAS
Thyroid hormone transport	1.5×10^{-6}	NDAS
Heme /Iron-binding	2.8×10^{-6}	3.1×10^{-5}
Golgi cisterna membrane and Golgi stacking. Microsome	3.0×10^{-5}	2.6×10^{-4}
Glycosyl-transferase activity in Golgi	2.0×10^{-5}	4.2×10^{-5}
Pre-assembly GPI-anchored in ER membrane	6.0×10^{-7}	5.1×10^{-6}
Xenobiotic response	6.4×10^{-8}	4.4×10^{-12}
Nucleosides biosynthesis and nucleotide salvage	7.8×10^{-7}	3.7×10^{-7}
3',5'-cyclic -AMP phosphodiesterase activity	5.4×10^{-7}	4.3×10^{-6}
Aromatase activity	6.8×10^{-4}	5.2×10^{-7}
Calcium homeostasis	5.9×10^{-2}	2.7×10^{-5}

* The hypergeometric probabilities are values corrected for the multi-comparisons. In addition, the values indicated are the averages of the probabilities along the several ontology categories that make up each subgroup defined, but weighed according to the relative frequency of the initial ontology classes that resulted from the analysis; ** NDAS: no-detected as significant