

## 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 S7: Differential functional classes associated to metabolism for the set of sex-dependent genes.** Functionalities are derived by ontology analysis performed on the whole compatible network (for details see the Supplementary Table S8).

Ontology process (Metabolic)	genes with Sex Ratio# <1	genes with Sex Ratio# >1
	Hypergeometric probability	Hypergeometric probability
Xenobiotic response, drug response	3.2 x 10 <sup>-8</sup>	4.4 x 10 <sup>-6</sup>
Adenylate cyclase	8.0 x 10 <sup>-6</sup>	7.8 x 10 <sup>-4</sup>
3',5'-cyclic nucleotide phosphodiesterase	1.1 x 10 <sup>-5</sup>	3.2 x 10 <sup>-5</sup>
c-GMP catabolism	6.6 x 10 <sup>-7</sup>	8.0 x 10 <sup>-4</sup>
Carboxylic Acid Transport	1.0 x 10 <sup>-7</sup>	8.7 x 10 <sup>-3</sup>
Gluconeogenesis, glucose biosynthesis	3.3 x 10 <sup>-6</sup>	6.3 x 10 <sup>-3</sup>
Tricarboxylic acid cycle (TCA), respiration	1.2 x 10 <sup>-6</sup>	8.7 x 10 <sup>-3</sup>
Amino acid biosynthesis	1.3 x 10 <sup>-1</sup>	8.0 x 10 <sup>-5</sup>
Amino acid catabolism	5.9 x 10 <sup>-2</sup>	2.6 x 10 <sup>-4</sup>
Glycero-phospholipids	1.3 x 10 <sup>-2</sup>	3.6 x 10 <sup>-4</sup>
Phospho-Inositosides metabolism	1.2 x 10 <sup>-1</sup>	1.3 x 10 <sup>-4</sup>
One-Carbon metabolism	1.5 x 10 <sup>-4</sup>	4.1 x 10 <sup>-4</sup>
Glutathione metabolic processes	8.2 x 10 <sup>-4</sup>	5.8 x 10 <sup>-4</sup>
Steroid response	1.3 x 10 <sup>-2</sup>	4.8 x 10 <sup>-4</sup>
Aromatase activity	7.2 x 10 <sup>-3</sup>	3.2 x 10 <sup>-5</sup>
Response to nitrosative compounds	5.8 x 10 <sup>-7</sup>	1.6 x 10 <sup>-5</sup>
Superoxide, hydrogen peroxide	6.2 x 10 <sup>-3</sup>	1.1 x 10 <sup>-2</sup>
Nitric Oxide generation and regulation	NDAS**	4.2 x 10 <sup>-4</sup>
Caffein oxidase	5.8 x 10 <sup>-7</sup>	6.2 x 10 <sup>-8</sup>
Endoplasmic reticulum membrane protein	NDAS	2.8 x 10 <sup>-4</sup>
Glycosylation of proteins	NDAS	1.3 x 10 <sup>-5</sup>
Golgi membrane proteins	1.7 x 10 <sup>-1</sup>	8.7 x 10 <sup>-5</sup>
Lysosome proteins	1.3 x 10 <sup>-3</sup>	3.4 x 10 <sup>-4</sup>

\* 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.