The top 10 most abundant transcripts are sufficient to characterize the organs functional specificity: evidences from the cortex, hypothalamus and pituitary gland.

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Abstract
Using serial analysis of gene expression, we have identified the most abundant mRNA transcripts in parietal cortex, hypothalamus and pituitary gland in adult male mice. High mRNA abundance of neurogranin (cell signalling and communication) was characteristic of the cortex. The common molecular features of cortex and hypothalamus were high abundance of mRNA encoding mitochondrial enzymes such as reduced form of nicotinamide adenine dehydrogenase (NADH) 4 and cytochrome c oxidase 2 (energy metabolism), brain creatine kinase (energy metabolism) and myelin basic protein (cell structure). In the hypothalamus, mRNA levels of apolipoprotein E (lipid metabolism), prostaglandin D2 (cell signalling and communication) and secreted acidic cysteine-rich glycoprotein (extracellular matrix) were especially high. A common molecular feature of the hypothalamus and pituitary was high mRNA abundance of guanine nucleotide binding protein alpha stimulating complex locus (cell signalling and cell communication). The pituitary gland was characterized by high expression of genes encoding hormones such as growth hormone, pro-opiomelanocortin and prolactin, as well as neuronatin (cell differentiation) and four potential novel transcripts. Thus, these results show that the cortex, hypothalamus and pituitary gland can be specifically characterized according to their 10 most abundant transcripts. In addition, the current study serves as a basis for future studies on the potential novel transcripts and the transcripts with unclear functions despite their extremely high abundance, as well as studies on physiology and pathology of the two brain regions and pituitary gland.

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