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ERRATUM

Erratum to: Interhemispheric gene expression differences in the cerebral cortex of humans and macaque monkeys

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The original version of this article unfortunately contained two small mistakes in Figs. 1b and 2a.

In Fig. 1b, there is no legend to explain to the reader what the colors and shapes of the datapoints indicate. The new Fig. 1 including the legend is provided here.

Figure 2a, the line just underneath the dendrogram is "Adult" yet in the legend it says that it is "ALL". It should say "Adult" in both places. The text in the caption should be replaced:

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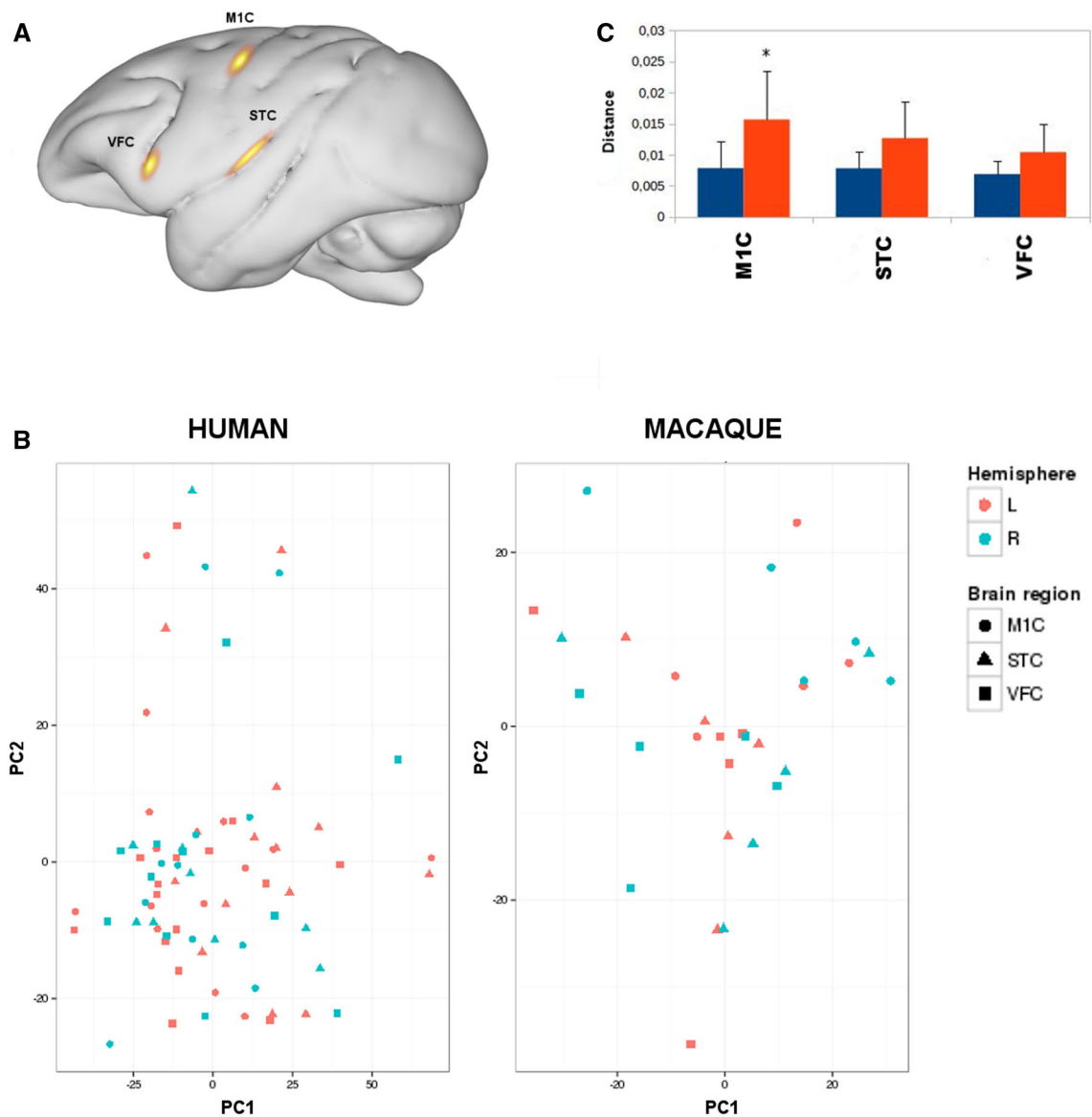 gerard.muntane@upf.edu; gmunta@yahoo.es

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a Hierarchical clustering and visualization of gene modules in all cortical regions examined in the human data set. The adult human network served as a reference network; module colors of other networks were redefined using *matchLabels( )* function in *WGCNA* R package to match the corresponding module in the human network. Modules of co-expressed genes were assigned to colors corresponding to the branches indicated by the *horizontal bars* beneath the dendrogram. From *top* to *bottom*, these *bars* represent modules obtained using the human samples (Adult), STC samples (STC), VFC samples (VFC), M1C samples (M1C), and all macaque samples. *Intercalated color bars* correspond to gene significance to hemisphere (Hcor) in the respective samples. *Red* and *blue colors* correspond to correlation to the trait (being *blue*, more expressed in *left* hemisphere and *red* in *right*). Note that module 3 (in *brown*, correlated with hemispheric expression) is highly expressed in left hemisphere in human STC and well preserved across all brain regions. The *latter bars* (GWAS genes and reported genes) indicate the location of the genes selected from Brandler et al. and from literature review, respectively. **b** Preservation of modules between human modules in STC (*left panel*), VFC (*middle panel*), and M1C (*right panel*) and their homologous regions in macaque brain. A Z summary statistic was computed for each module as an overall measure of its preservation relating to density and connectivity.

Fig. 1 **a** Sample preparation in macaque specimens. Dissected areas are *highlighted*. Modified from Scalable Brain Atlas (https://scalablebrainatlas.incf.org). **b** Principal component analysis (PCA) of human samples (*n* = 74) and macaque samples (*n* = 30) used in the present study. Samples are colored by hemisphere, as shown in the upperright legend. Notably, the PCA displays no clustering. **c** *Bar graphs* of the measured Spearman distance coefficients between left and right hemispheres for gene pairs of human (*red*) and macaque (*blue*)