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ERRATUM

Network analysis of transcriptional regulation in response to intramuscular interferon-β-1a multiple sclerosis treatment

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Elements were omitted from the Supplementary Information that accompanied the online version of this article.

For Supplementary Table 1, the following information should have been included:

'A list of 121 genes up- or downregulated during first 4 weeks of intramuscular IFN-β-1a treatment. Genes with transcriptional changes in response to therapy initiation were identified by use of the MAID filtering method and a test of statistical significance. There were 72 genes more highly expressed and 49 genes more lowly expressed at week 1 or 4 versus baseline in the PBMCs of the 24 MS patients in our study. The table provides diverse types of information for each gene, e.g., Entrez ID, official full name and the calculated MAID scores.'

In addition, the Supplementary File—the Cytoscape session file—was omitted, along with the following description.

'Cytoscape session file of the inferred GRN model. The network model describes the regulatory interactions between transcription factors and the genes with expression changes during the first month of IFN-β administration. A simplified visualization of the network is shown in Figure 2 of the main article; detailed views are shown in Figure 3.'

This file is not available here because of the Journal's submission restrictions. Therefore, it is provided on the institute's website: http://www.hki-jena.de/index.php/0/2/495/download/2822