

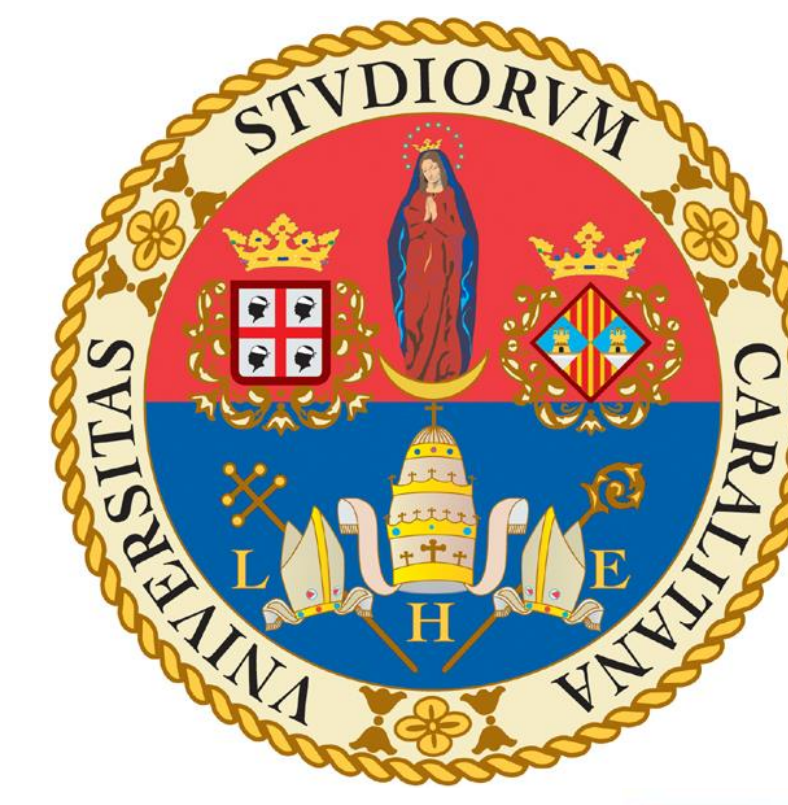
Metabolomic profile of multiple sclerosis patients by means of ^1H -NMR analysis

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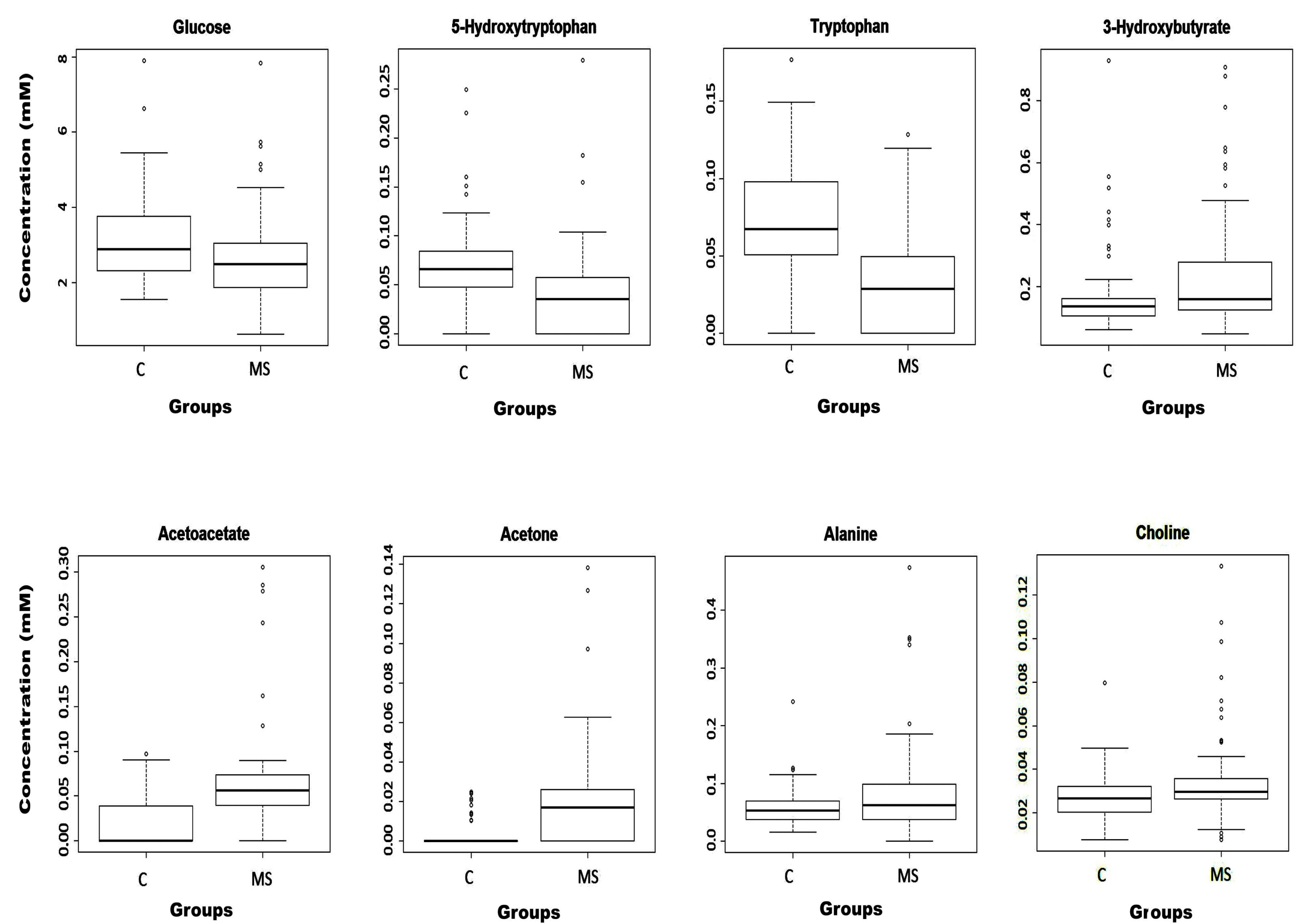
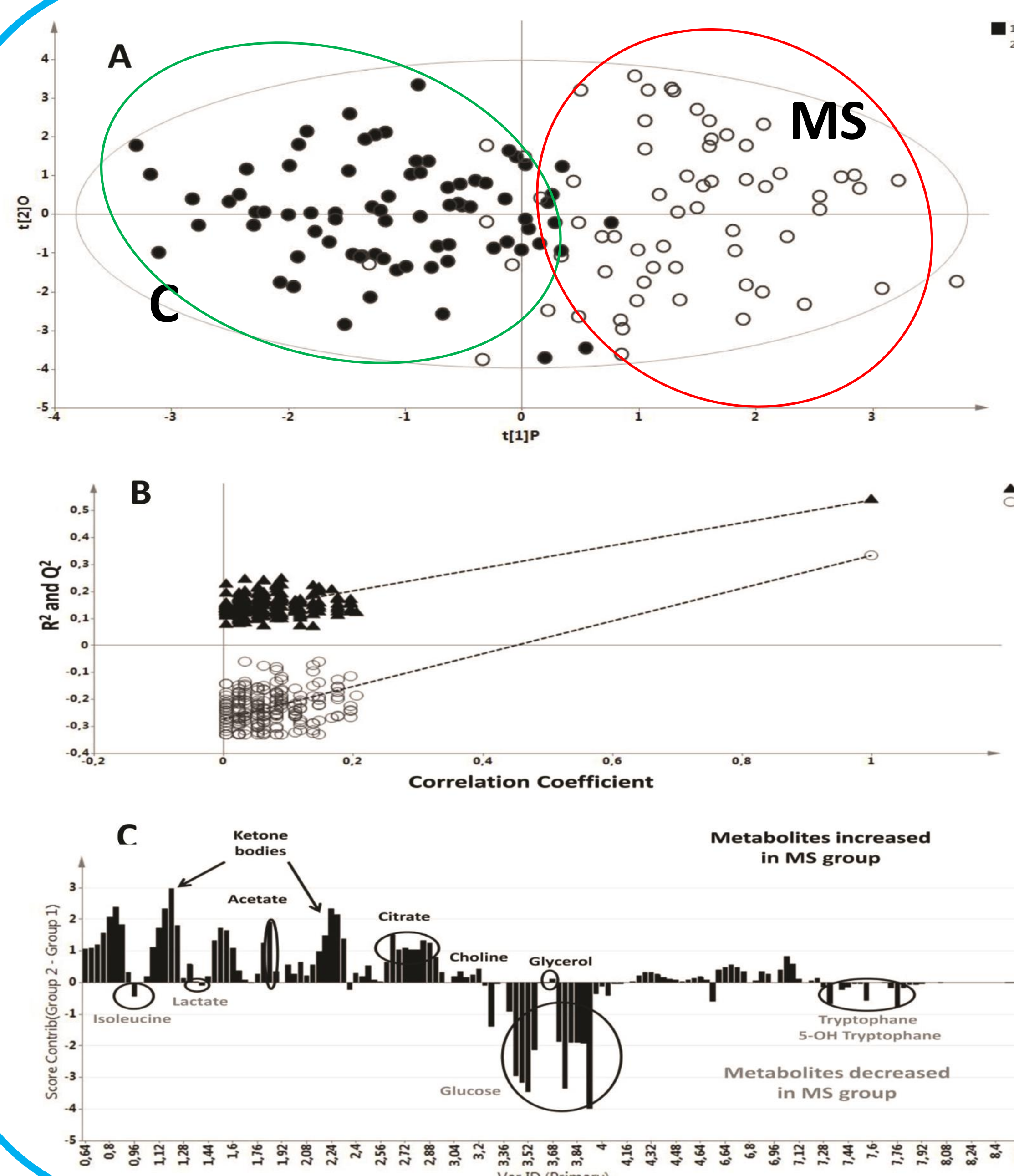
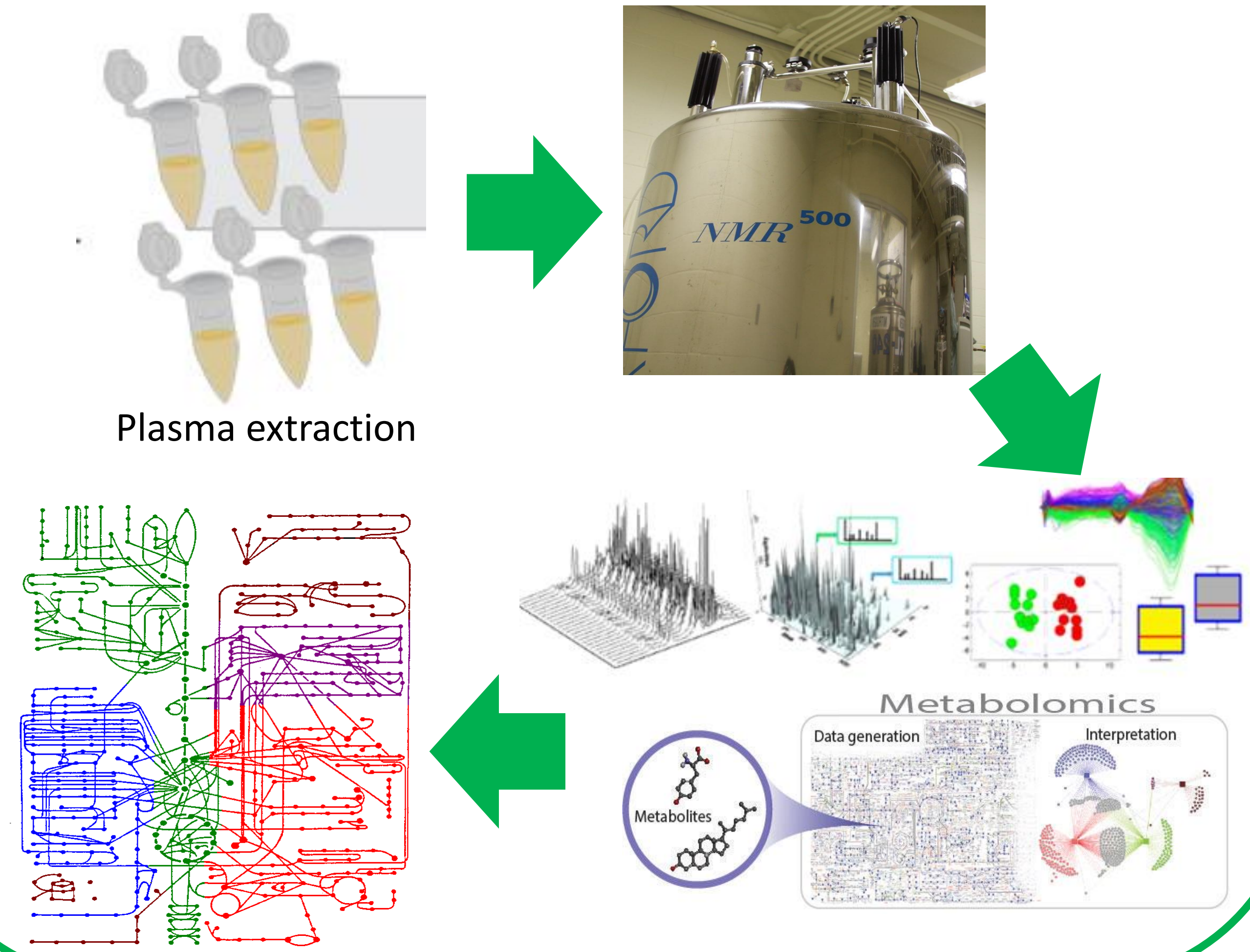
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Introduction: Multiple sclerosis (MS) is a chronic disease characterized by a high level of heterogeneity. Metabolomics is an “-omics” approach with the potential to discover new biomarkers (1,2). Thus, we investigated the metabolic profiles of MS patients to define the pathways potentially related to its pathogenesis

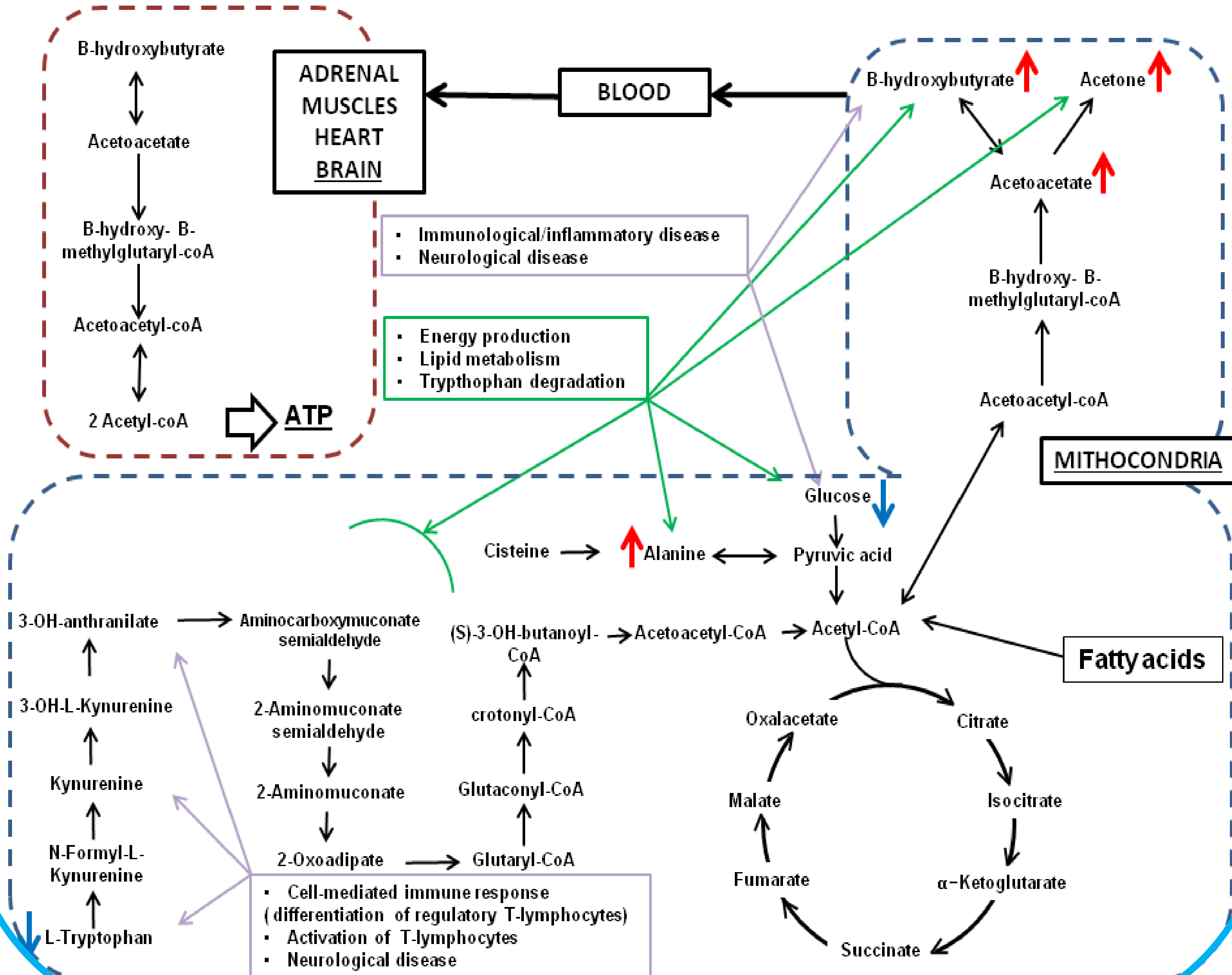
Results: the model obtained with the OPLS-DA identified predictive metabolic differences between the MS and C ($R^2X = 0.615$, $R^2Y = 0.619$, $Q^2 = 0.476$ $p < 0.001$). A total of 17 metabolites were identified and the differential metabolites included glucose, 5-OH-tryptophan, and tryptophan (lower in MS, $p < 0.01$), and 3-OH-butyrate, acetoacetate, acetone, (higher in MS $p < 0.01$). The model was evaluated using an external set of samples and the corresponding ROC curve produced (AUC of 0.93).

Materials and methods: Plasma samples from 73 MS patients and 88 controls (C) were analyzed by ^1H -NMR spectroscopy, and followed by multivariate statistical analysis



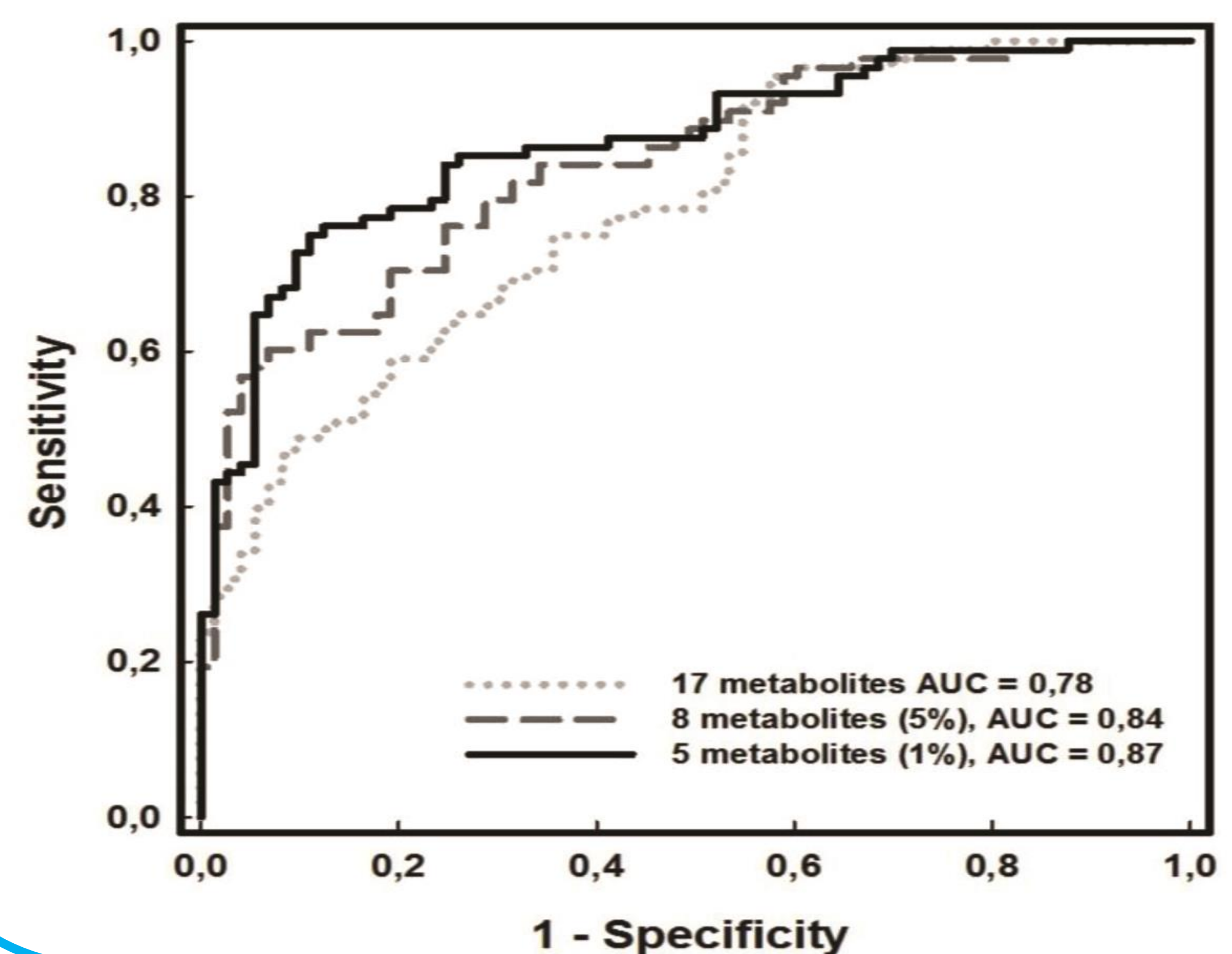
Pathways analysis

Pathways analysis of the discriminant metabolites was performed and the main metabolic changes could be connected to tryptophan metabolism and energy metabolism



Biomarkers analysis

ROC curve was built for to test the performance of the discriminant metabolites



Conclusions: ^1H -NMR metabolomic analysis was able to discriminate different metabolic profiles in MS patients compared with HC. The importance of kynurenine (a tryptophan derivative), in particular in the immune, response is confirmed. Metabolomics appears to represents a promising non-invasive approach for the study of MS.