Analysis of the quantitative proteomic signature in PBMCs of first-episode psychosis patients

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INTRODUCTION

PROJECT GOALS

- Establish a reproducible proteomic procedure for the relative quantification of PBMC's proteome
- Create the most comprehensive protein identification library possible.
- Distinguish between FEP and Control samples, analyzing the biological meaning of the alteration.
- Highlight possible protein biomarkers or pathways involved in first-episode psychosis.

EXPERIMENTAL PROCEDURE

SAMPLE COLLECTION AND PROCESSING

RESULTS

CONCLUSIONS

- A reproducible proteomic procedure for the relative quantification of PBMC's proteome was established where 1413 proteins were confidently quantified, covering almost completely many key pathways.
- A comprehensive protein identification library was created with 2240 proteins that can be used for the relative quantification of other PBMCs samples.
- 59 proteins were discovered as altered in FEP, enabling the distinction between the 2 groups, and highlighting the innate immune system and complement cascade as interesting targets for further studies.

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