

Transcriptomic analysis across the Alzheimer's disease continuum



P4-03

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It is possible to identify stage-specific as well as over-time molecular signatures across the continuum of Alzheimer's disease in blood

INTRODUCTION

The discovery of biomarkers through minimally invasive methods is essential for tracking of Alzheimer's disease (AD) progression.

The object of this study is to investigate AD-related transcriptomic signatures using Peripheral Blood Mononuclear Cells (PBMCs) from healthy controls (HC), patients with mild cognitive impairment with no AD markers (MCI_non-AD), MCI patients with AD markers (MCI-AD), and AD patients.

METHODS

- **Total RNA extraction** from PBMCs of 8 HC, 25 MCI_non-AD, 25 MCI-AD and 25 AD patients
- **RNA-seq** on the Illumina NextSeq 550 platform and data analysis in collaboration with the SING Research Group (Spain) using the **Compi RNA-Seq pipeline**
- **RT-qPCR** of 14 differentially expressed (DE) selected mRNAs in PBMCs of 21 HC, 25 MCI_non-AD, 22 MCI-AD and 24 AD patients

RESULTS

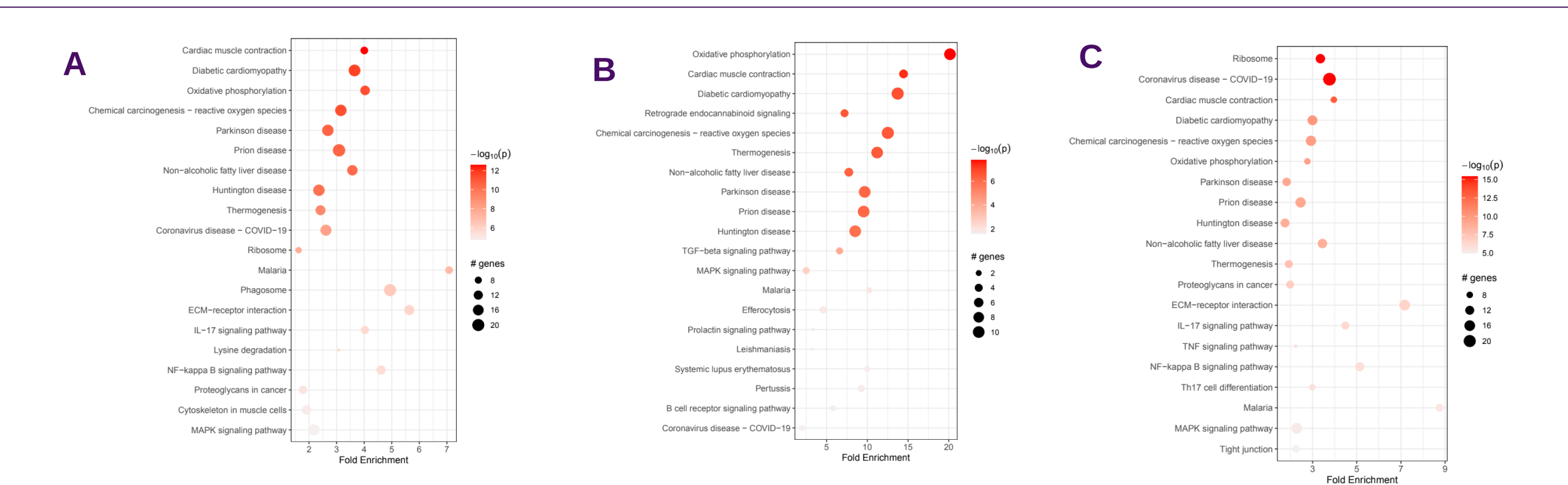
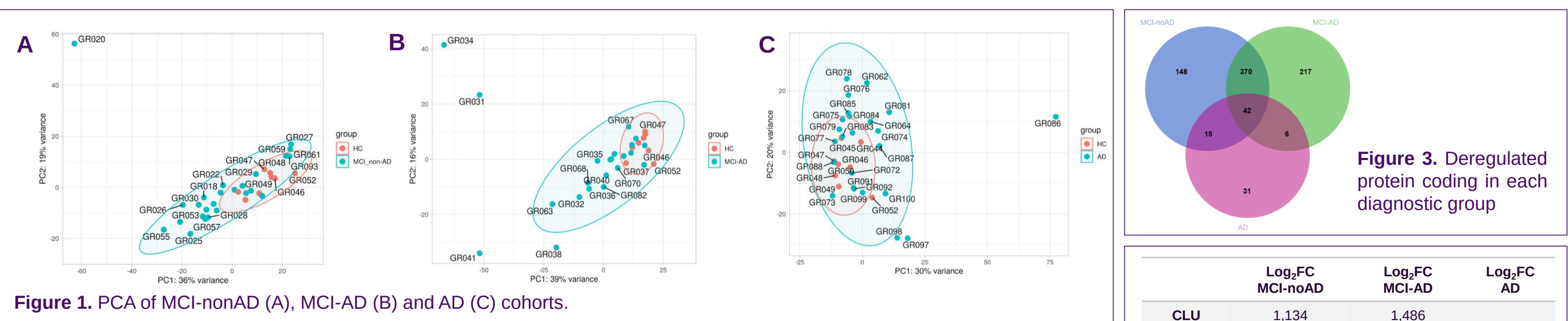


Figure 2. Enrichment pathway analysis in MCI-nonAD (B), MCI-AD (C), AD (D) patients

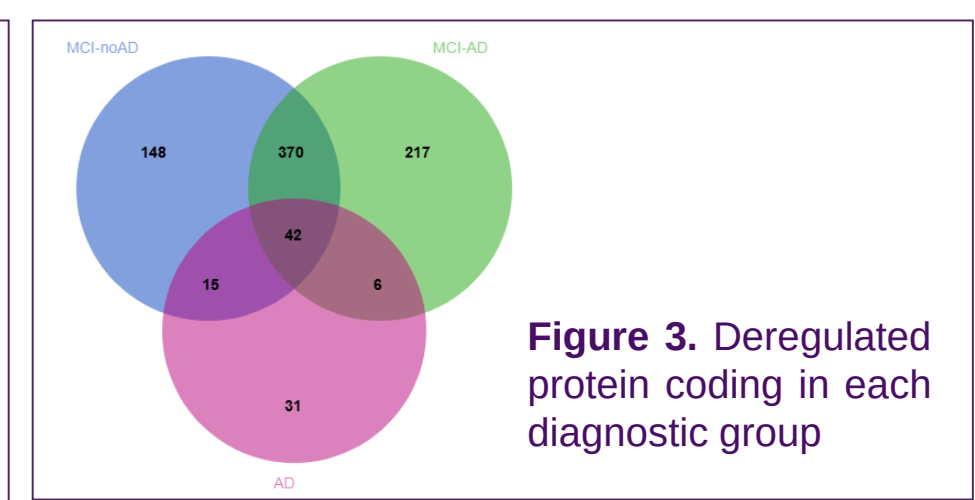


Figure 3. Deregulated protein coding in each diagnostic group

	Log ₂ FC MCI-nonAD	Log ₂ FC MCI-AD	Log ₂ FC AD
CLU	1,134	1,486	
FPR1	-1,260	-1,646	
IFI30	-1,468		
HBA2	2,671	2,926	2,666
HBB	2,104	1,859	
PLBD1	-1,598	-1,794	-1,218
CALHM6			-1,062
FKBP5	1,104		
FOS			1,114
RAB11B		1,047	
RPS13	-1,083		
TREM1	-1,003		
UQCRCF1		-1,010	

Table 1. Selected differentially expressed genes (DE) and their relative log₂FC

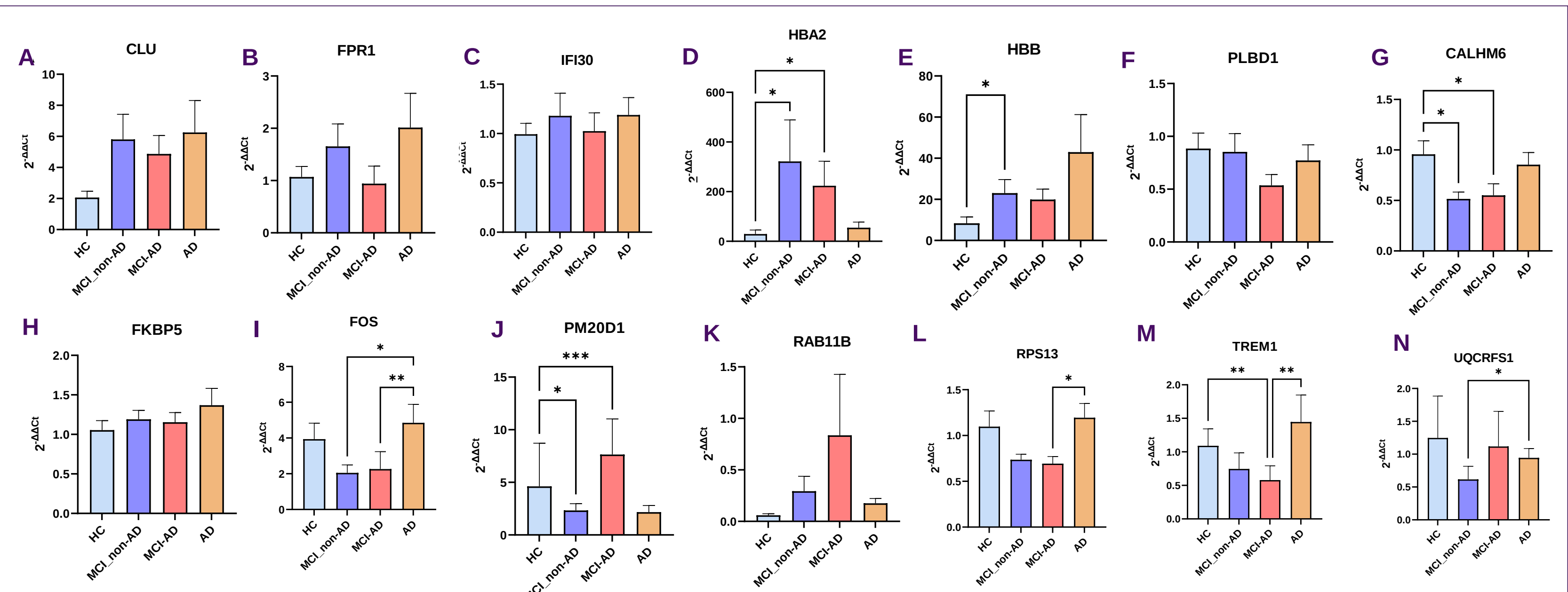


Figure 4. Differential expression analysis of DE genes: CLU (A), FPR1 (B), IFI30 (C), HBA2 (D), HBB (E), PLBD1 (F), CALHM6 (G), FKBP5 (H), FOS (I), PM20D1 (J), RAB11B (K), RPS13 (L), TREM1 (M), UQCRCF1 (N). GAPDH was used as housekeeping. Kruskal-Wallis test: * p<0,05; ** p<0,01; *** p<0,001

CONCLUSIONS

Transcriptomic changes in PBMCs might mirror core AD pathological processes and may serve as potential biomarkers for monitoring disease stage and progression.

FUNDINGS



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