Poster 53

FUNCTIONAL PROFILING OF THE
PERIPHERAL BLOOD CELLS TRAN-
SCRIPTOME TO STUDY CARDIOVAS-
CULAR BIOMARKERS .

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A transcriptomic experiment was carried
out to study the global gene expression in
peripheral blood cells (PBC) to study sur-
rogate biomarkers for the early diagno-
sis of myocardial infarction (MI). We se-
lected 9 MI patients within 8h after MI
event, 5 without prior treatment (1MI)
and 4 treated (2MI), and 7 healthy con-
trols (GC). Blood samples were obtained
for RNA extraction by PAXgene system
(Qiagen). PBC mRNA expression profiles
were assessed by Affymetrix GeneChip
Human Exon 1.0 ST array. Signals were
normalized using iterPLIER algorithm
and limma model from oneChannelGUI
package was applied to evaluate the dif-
ferential gene expression. Comparisons
of interest where 1MI versus GC and
2MI versus GC. The functional interpre-
tation of this comparisons in terms Gene
Ontology (biological process) were per-
formed using FatiScan methodology im-
plemented in Babelomics. The functional
modulest over-expressed in both classes
were exploed to get gene signatures that
generally identified MI. In this study it
was possible to select 14 GO biological
processes with adjusted pvalue < 0.05
that were common in both comparisons.
The total number of genes selected by
functional profiling was 1373. Functional
evaluation of the PBC is a useful tool
to investigate cardiovascular biomarkers
that may be involved in the early stages
of MI.

Poster 54

A COMPUTATIONAL APPROACH
TO IDENTIFY WHOLE GENOME
HOMOZYGOSITY MAPPING ACROSS
MULTIPLE SNP MAPPING EXPERI-
MENTS

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