

Expression profiling of CD34+ of peripheral blood of patients with lymphoma during ex vivo granulocytic differentiation

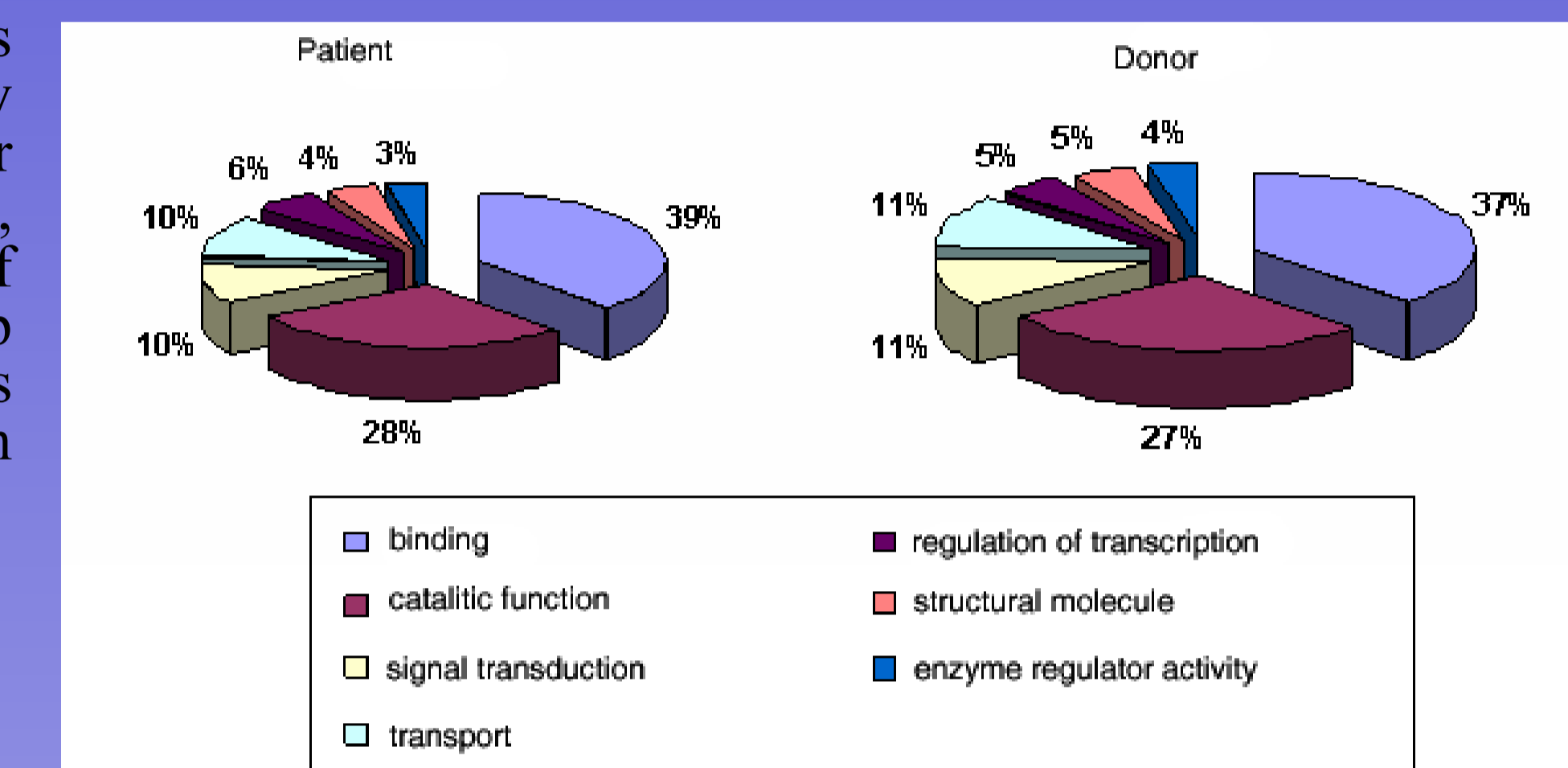
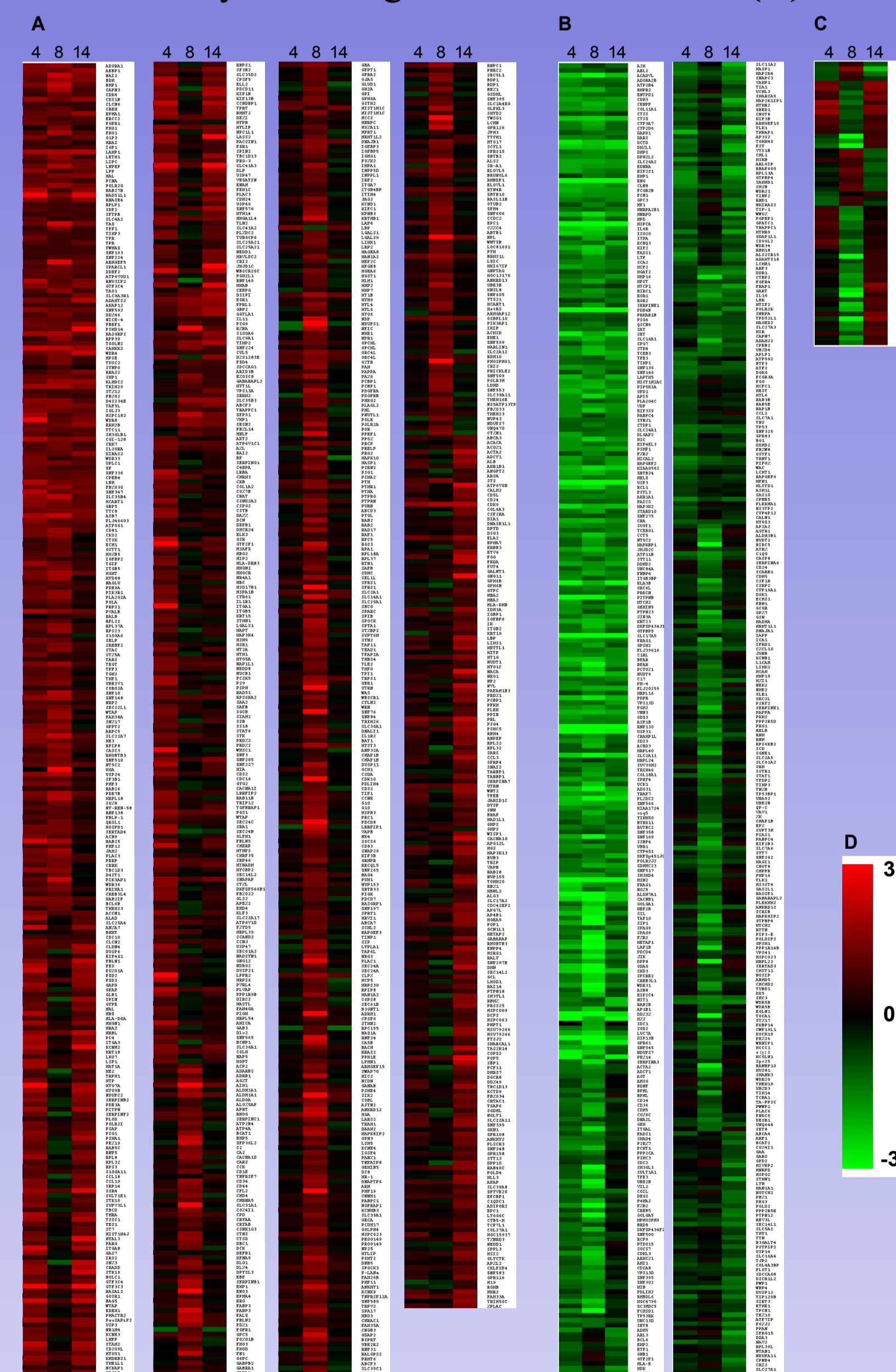
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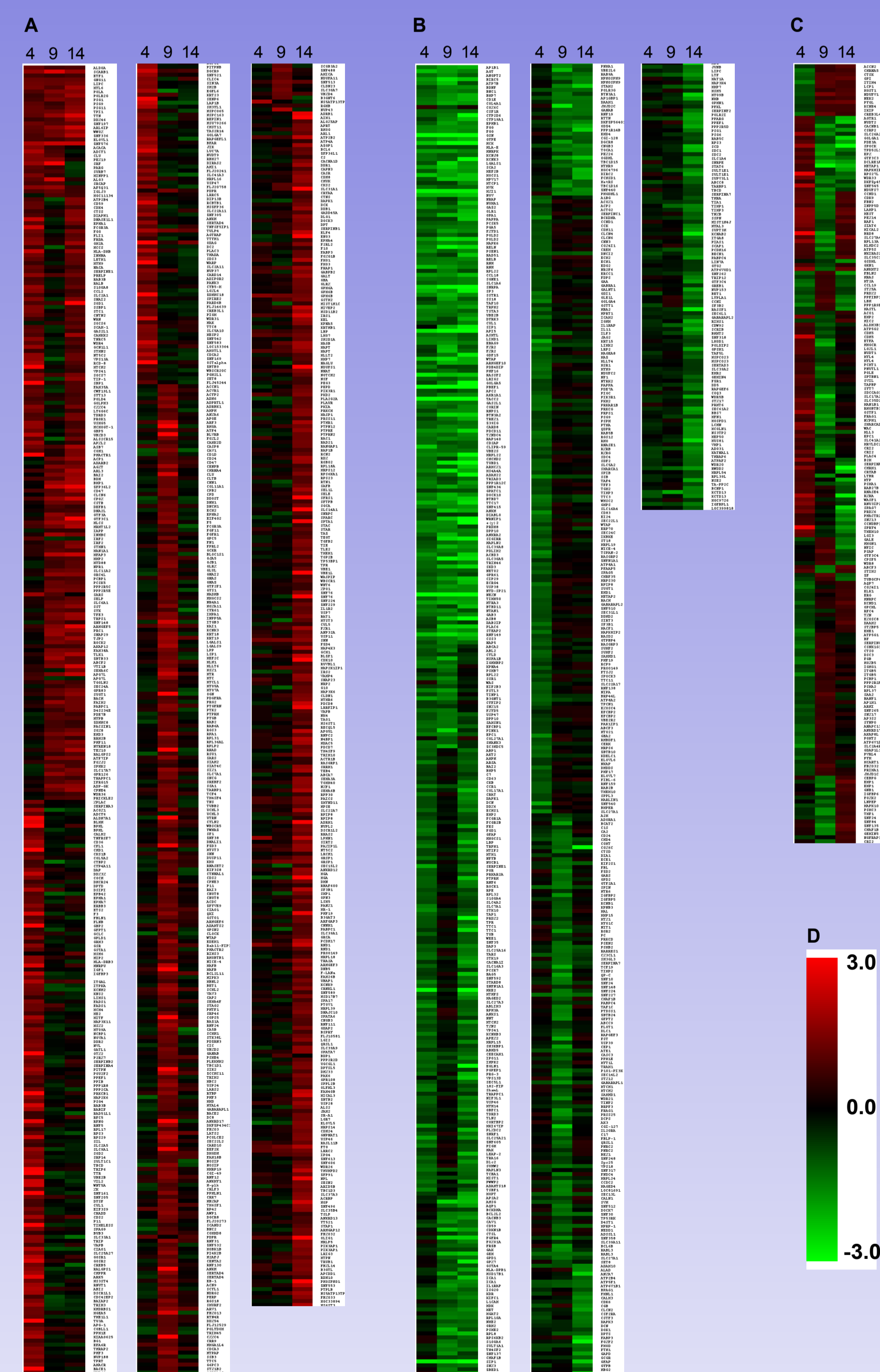
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Lymphoid leukemias present types of leukemia where autologous transplantation is one possible way of treatment. The main problem of this way of treatment is finding of appropriate cell population with low or without risk of relaps. The aim of this work was evaluation of expression profiles of CD34+ from peripheral blood obtained from stimulated patients with lymphoma and healthy donors during ex vivo differentiation.

List of genes with altered expression during in vitro CD34+ cells differentiation obtained from healthy donor. Genes are represented by individual rows. Each column represents expression type in days +4, +9 or +14 in comparison with day 0. Used coloring is: green – down regulation, red – up regulation, intensity represents the amount of change (log2 of expression ratios between day 0 and days +4, +9 respective +14) (D). Up regulation during cell differentiation has been measured for 1083 genes (A), down regulation for 564 genes (B), 59 genes showed up regulation followed by down regulation or vice versa (C).



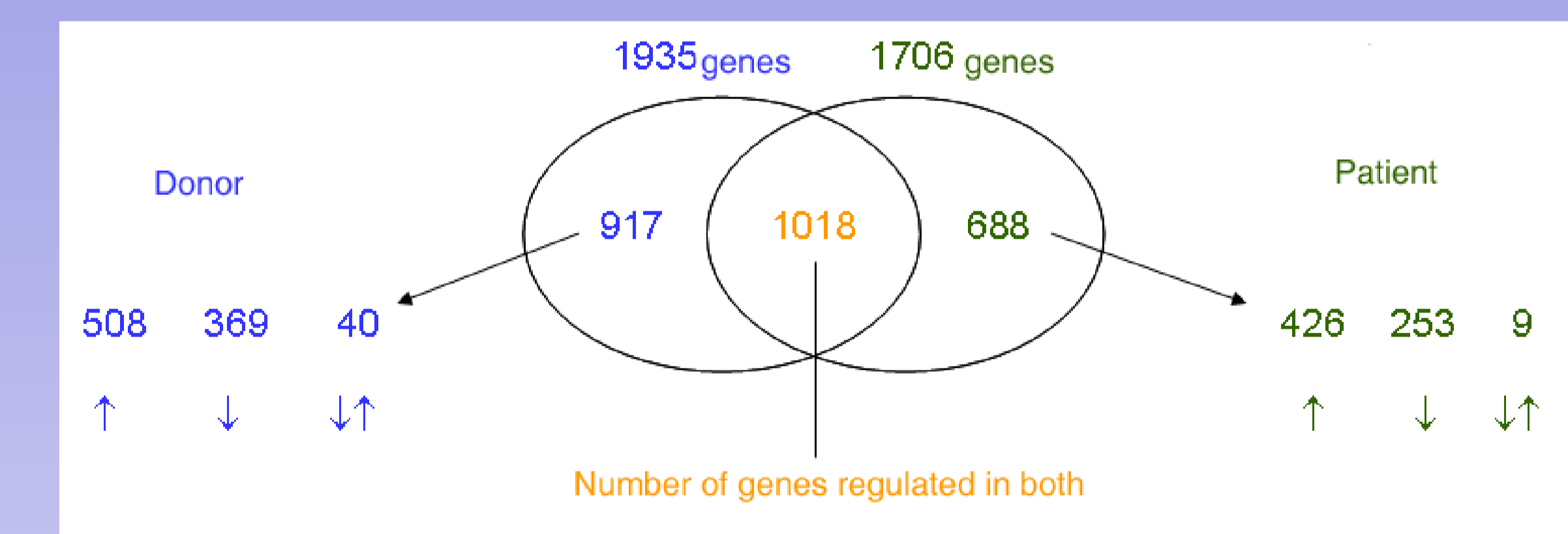
Genes with altered expression during cultivation of cells obtained from healthy donor (right) and patient (left) divided according to molecular function (obtained using KEGG) of coded protein.



List of genes with altered expression during in vitro CD34+ cells differentiation from healthy donor. Genes are represented by individual rows. Each column represents expression type in days +4, +9 or +14 in comparison with day 0. Used coloring is: green – down regulation, red – up regulation, intensity represents the amount of change (log2 of expression ratios between day 0 and days +4, +9 respective +14) (D). Up regulation during cell differentiation has been measured for 970 genes (A), down regulation for 769 genes (B), 196 genes showed up regulation followed by down regulation or vice versa (C).

We have used cDNA microarrays technology to obtain precise expression profiles. Cells have been ex vivo differentiated to granulocytic stage using defined cocktail of interleukins and cytokines. During differentiation the cells were harvested and used for microarray analysis.

We have determined groups of genes, which in the course of differentiation show different expression profiles in cells of patients and cells of healthy donors. Detailed genomic analysis of this subset of genes would be served as one of possible tolls for finding “healthy“ cell population suitable for autologous transplantation.



Comparison of genes with altered expression from CD34+ cells obtained from healthy donor and patient with lymphoma. Direction of each arrow represents type of expression change.

Conclusion:

On the basis of global expression data analysis we have concluded that population of CD34+ cells from patients with lymphoma shows different expression status during ex-vivo differentiation. And thus we assume that CD34+ population is not suitable for autologous transplantation.