

SUPPLEMENTARY TABLE AND FIGURE LEGENDS

Table 1 Supplementary: list of the significant probes after Benjamini-Hochberg post-hoc correction ($P < 0.05$). GenBank, GenBank accession number (and probe ID in the array); Symbol, UniGene, Description for known genes. Pval AdjustedBH, Pvalue associated to each probe after Benjamini-Hochberg correction

Table 2 supplementary: list of genes validated by RT-PCR. The P value (P_{BH}) and the cluster to which each gene belongs to in the expression array are shown.

Table 3 supplementary: list of genes that constitute a signature of T cells (as in¹⁷) also found in our dataset. The last column shows the cluster they belong to.

Table 4 supplementary: list of genes that constitute a signature of aging (as in¹⁸) also found in our dataset. The P values obtained from our statistical analysis, as well as the ratio of the average expression for our samples in the same age groups as in¹⁸, are shown.

Table 5 supplementary: Kegg pathways sorted by node Betweenness Centrality in the network of Figure 3. Fullcode: Kegg pathway code; Name: Kegg pathway name; K node connectivity; BC node betweenness centrality; Cluster: gene cluster in which such pathway is significant (clusters 1, 2, 3, as in Table 1; 0 = not significant pathway).

Figure 1 supplementary: gene expression correlation for each cluster. From left to right: correlation coefficients histogram for the expression profiles of the genes belonging to cluster 1 to 3 respectively.

Figure 2 supplementary: mean trend of TF related to significant TFBS found in array. From left to right: average expression for the TF found in our dataset whose TFBSs are overrepresented in cluster 1 to 3 respectively. X axis: average age inside each age group.