Supplementary Figure 1. Cross-method comparison of microarray and qPCR expression profiles for 34 genes using a co-inertia analysis (CIA). To validate the microarray experiment, we compared the expression profiles of 34 genes (a set of genes selected from genes varied between the beginning and the end of the whole dietary program.) with the corresponding expression profiles measured with RT-qPCR method. A co-inertia analysis implemented in the R package ade4 (Dray and Dufour 2007) was performed to assess the similarity between the two methods, as proposed by Culhane et al. (Culhane et al. 2003). Blue circles represent the projected co-ordinates of the microarray expression dataset, and the arrow points represent the RT-qPCR expression dataset. A line, whose length is proportional to the divergence between the gene expression profiles measured by the two methods, joins them. The RV coefficient of this CIA is 0.82. A histogram of the main factors, which explain the total variability of this co-inertia analysis, is superimposed on the right corner. The first two axes, represent 16.45% and 5.54% of the inertia.
REFERENCES

