**Supplementary Results**

**Class comparison failed showing differences between RespDC and NonRespDC**

After observing that unsupervised analysis were not able to separate RespDC from NonRespDC, we tested whether statistical analysis was able to identify gene expression signatures that distinguish the two groups. A direct class comparison of RespDC versus NonRespDC revealed the presence of only 55 statistically differentially expressed genes (p-value < 0.001). Such a low number of significant genes (false discovery rate was equal to 65%) pointed to the fact that RespDC and NonRespDC do not represent two strictly different classes. In our opinion, these results could be the consequence of three different possibilities: i) RespDC and NonRespDC do not have any differences, ii) given the heterogeneity in the magnitude of responses, only DC with strong clinical responses should be compared to NonRespDC, or iii) responses could be the consequence of multiple factors and therefore DC cannot be simply grouped into classes based on response, but have to be characterized for their inter-patient variability first. However, surface marker expressions and culture data clearly pointed to the existence of some difference between RespDC and NonRespDC, therefore we decided to test the other two hypothesis.

In order to evaluate the second hypothesis, we decided to tailor our analysis using more restrictive clinical and immunological response criteria, but even in this case we did not observe a significant number of genes differentially expressed among DC from patients showing a strong clinical and/or immunological response compared to NonRespDC. For example, when we used only immunological response to discriminate DC, only 3 genes were differentially expressed with a p-value < 0.001.

Altogether, and in line with unsupervised clustering analysis, these data suggested that to delineate differences between RespDC and NonRespDC more complex models must be implemented in order to analyze inter-patient variability without bias.