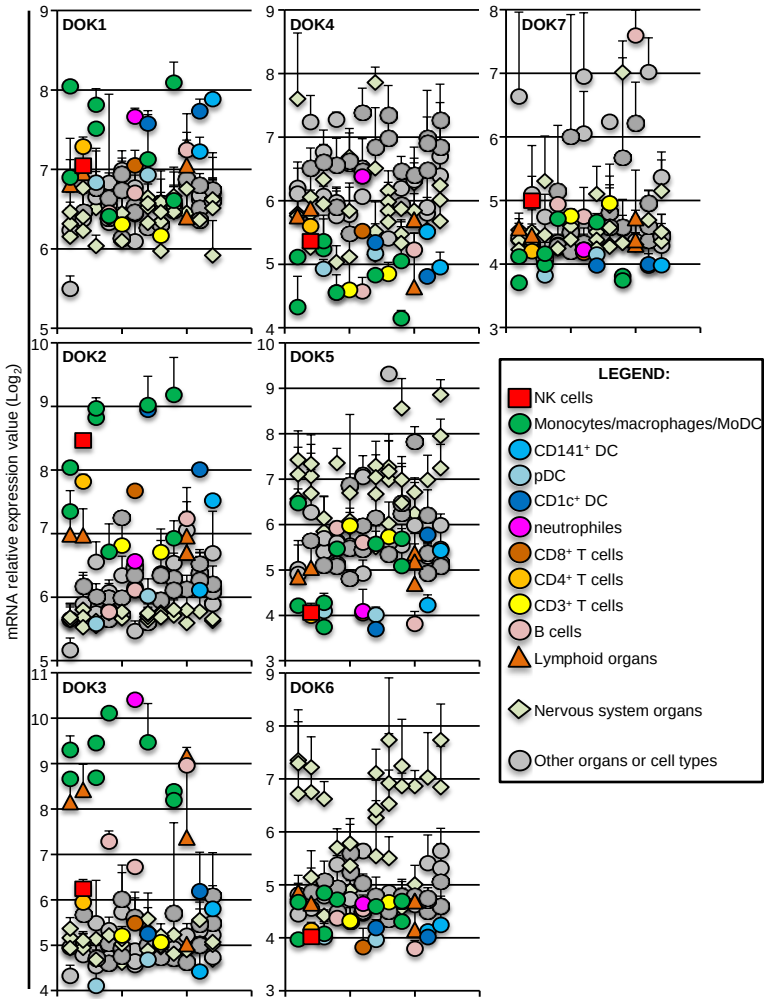
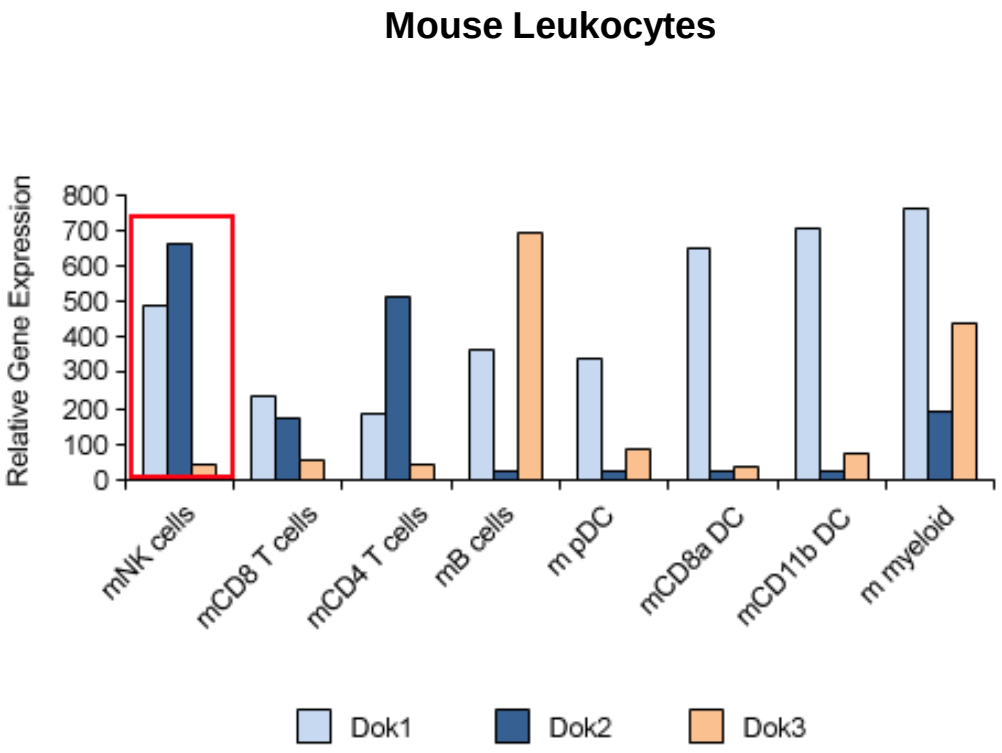


Expression patterns of human DOK genes across cell types and tissues. Microarray analysis of the expression of the human DOK genes (Y-axis) in 96 different cell types or tissues (X-axis), based on compiled analysis of several public Affymetrix Human Genome U133 PLUS 2.0 microarray datasets as described previously (Crozat et al. J. Exp. Med. 2010). Each symbol represents the mean Log_2 signal intensity for the gene considered in a given cell type or a tissue, calculated from three or more independant samples. SD is shown above each symbol. The data were retrieved from the GEO database (GSE7307 dataset for normal tissues and cell types, GSE4883 for PBMC-derived macrophages, GSE7509 for MoDC, GSM213500 for monocyte-derived macrophages and GSE2125 for alveolar macrophages), from the EBI Array-Express database (E-TABM-34 dataset for blood and tonsil DC subsets; Lindstedt et al., 2005), or generated in-house (other leukocyte subsets directly isolated from normal human blood were described previously; Du et al., 2006; Robbins et al., 2008) and can be downloaded from http://www-microarrays.u-strasbg.fr/files/datasetsE.php).



Expression patterns of murine Dok genes (group A) across immune cell types. Dok1 and Dok2 genes are the most abundantly expressed Dok genes in murine NK cells. Among the DOK gene group that is highly expressed in immune cells (group A: Dok1, Dok2 and Dok3) (Grimm et al., 2001 ; Favre et al., 2003), gene expression profiling in murine immune cells shows that Dok1 and Dok2 gene are highly expressed in murine NK cells (red square). Raw data can be downloaded from http://www-microarrays.u-strasbg.fr/files/datasetsE.php.