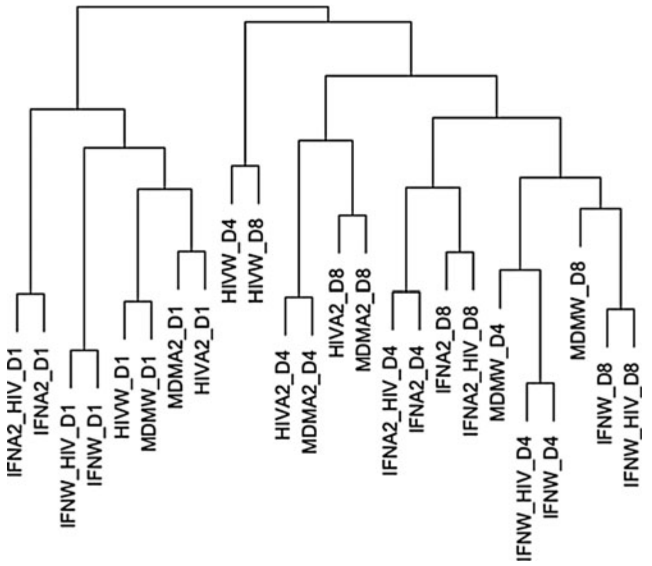

SUPPLEMENTARY FIG. S2. Unsupervised clustering of microarray gene expression data. Twenty-four MDM samples from a single donor (Donor 2) were used to generate microarray gene expression data. These 24 samples were derived from 4 conditions (IFN pretreatment, IFN pretreatment and HIV infection, HIV ctrl and MDM ctrl) at 3 time points following infection/mock-infection (Day 1, 4, and 8) for experiments performed with IFN-α2 or -ω. For example, IFNW_D1 refers to the assessment of gene expression in MDMs at Day 1 following pretreatment with IFN-ω. A coefficient of variance filter of greater than 0.1 was used to identify 7,765 genes for which distances were calculated using the Euclidean method, and then clustered in an unsupervised manner using the average linkage method.