SUPPLEMENTAL MATERIAL

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Figure S1. **Gating detail.** LNs were collected from C57BL/6 mice 48 h after injection with *Nb* or PBS, or 24 h after skin application of DBP-FITC or mock treatment (UT). LNs from naive mice were used as controls. (A) Gating strategy used to identify doublets, nonviable cells, mononuclear cells, and $CD11c^{+}$ $MHCII^{hi}$ cells. (B) Sorting strategy used to isolate DC populations from *Nb*-treated mice. (C) Sorting strategy used to isolate DC populations DBP-FITC–treated mice. (D) Back-gating analysis of DC populations from naive C57BL/6 mice using a gating strategy as in B. (E) Back-gating analysis of DC populations from naive C57BL/6 mice using a gating strategy as in C.

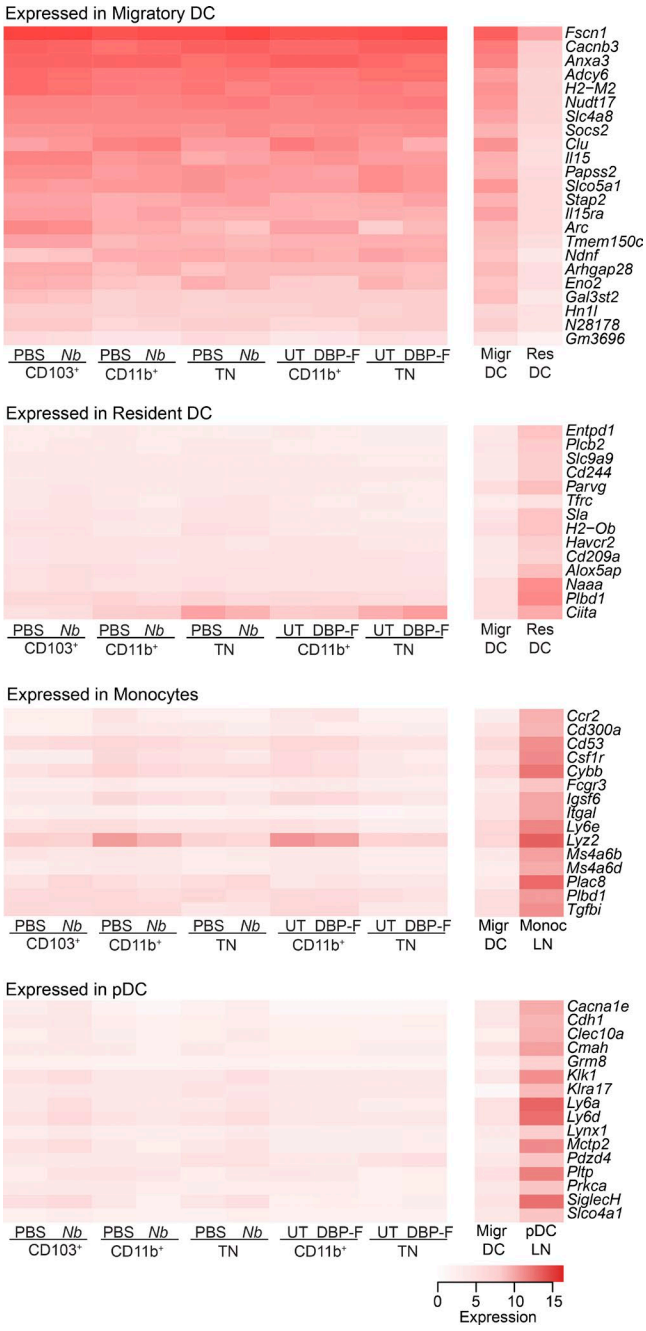

Figure S2. **LN DCs from mice treated with *Nb* or DBP-FITC and their respective controls express a migratory DCs signature and low levels of monocyte and pDC genes.** Heat maps showing the levels of expression of genes associated with different immune cell populations in skin LN. Heat maps on the left show expression levels in DC populations from *Nb* or DBP-FITC immunized mice and their respective controls. Heat maps on the right show expression data for migratory DCs and for each reference immune cell population, as obtained from Immgen database after transformation into values comparable to VSTPk. Migr DC, migratory DCs; Res DC, resident DCs; Monoc LN, Ly6C$^+$ monocytes from LN; pDC LN, CD8$^+$ plasmacytoid DCs from skin LNs. Genes associated with migratory (Mig) and resident (Res) DCs were selected from the Immgen database on the basis of high mean expression across all migratory DC populations compared with LN-resident DC populations and vice versa. LN monocyte and pDC genes were selected from the Immgen database on the basis of preferential expression in the cell population of interest as compared with the expression in the CD11b$^+$ DC population in skin LN. Th2 DC expression data are the mean of three replicate samples, each from an independent experiment for each Th2 condition.

Table S1 shows a list of all DEG in DC subsets, by DC subset and Th2 condition. Table S2 shows a list of canonical pathways in DC subsets as detected by Ingenuity Pathway Analysis. Table S3 shows the list of IFN-I regulated genes in each DC subset as determined using the Interferome database. Tables S1–S3 are available as Excel files.