

SUPPLEMENTAL MATERIAL

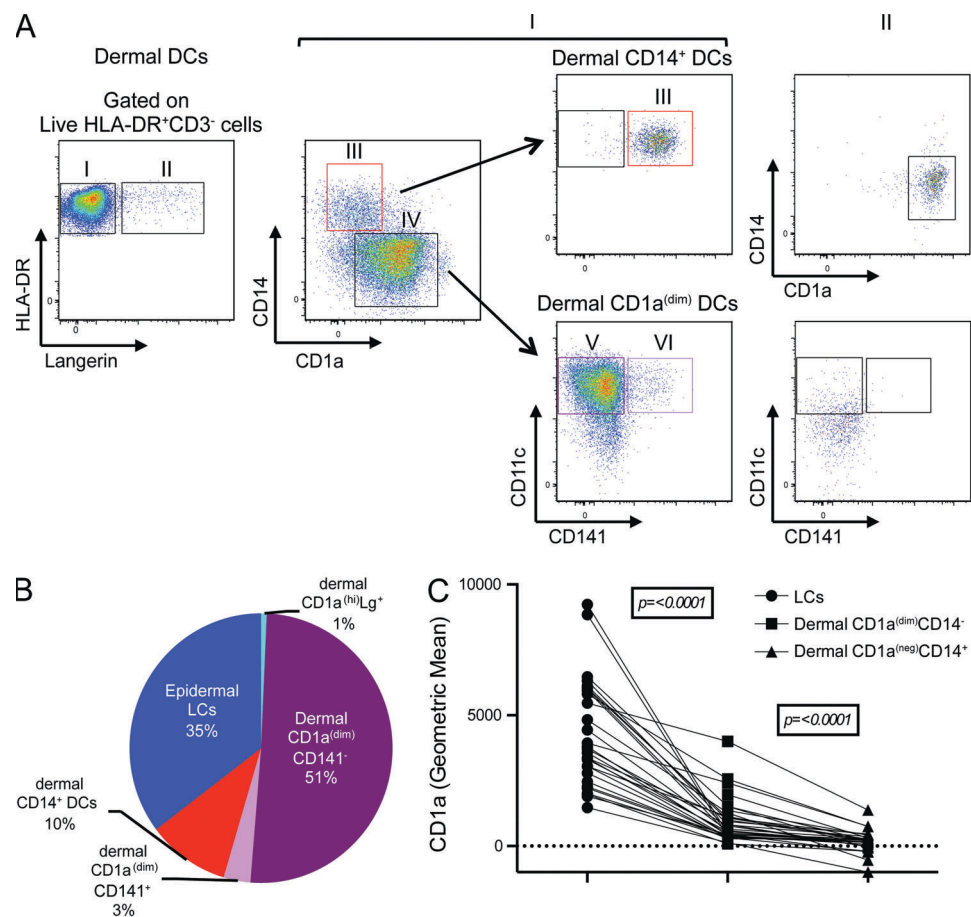
Artyomov et al., <http://www.jem.org/cgi/content/full/jem.20131675/DC1>

Figure S1. Gating strategy and description of dermal DC populations in the skin. Cells in gate I are Langerin negative and contain either CD14⁺ (III) or CD1a^(dim) (IV) DCs. Both subsets express high levels of CD11c. Although dermal CD14⁺ express CD141, dermal CD1a^(dim) DCs are further divided into CD141⁻ (V) and CD141⁺ (VI) DCs. Contaminating Langerin-expressing cells that were found in the dermal suspension (II) express similar to LCs of the epidermis high levels of CD1a, low levels of CD11c, and negative for CD141. Dermal cells in gates III, V, and VI were used in our transcriptional and functional analysis shown in Figs. 1–7. (B) The relative representation of each DC subset in human skin. Percentage calculated separately according to the mean \pm SD of each DC subpopulation isolated from 30 skin specimens processed over 12 mo. Epidermal LCs, 35.2 ± 0.2 ; dermal CD1a^(dim)CD141⁻ DCs, 50.6 ± 0.2 ; dermal CD1a^(dim)CD141⁺ DCs, 3.3 ± 0.03 ; CD1a^(hi)Langerin⁺ (that were found in the dermis), 1.04 ± 0.02 ; and dermal CD14⁺ DCs, 10.1 ± 0.07 . (C) Graph shows the fluorescence intensity of CD1a on epidermal LCs, dermal CD1a^(dim)CD14⁻, and dermal CD1a^(neg)CD14⁺ DCs. $P < 0.0001$. $n = 35$.

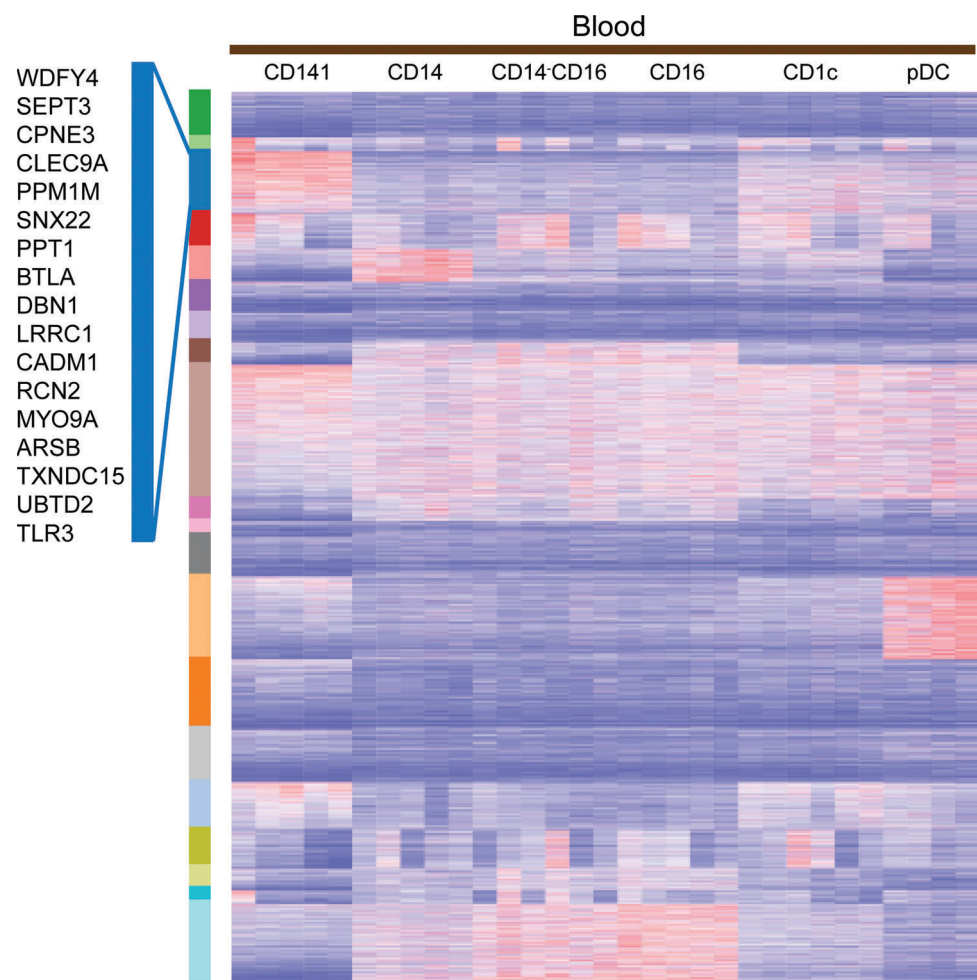


Figure S2. Human blood CD141⁺ DC-specific gene signature as derived compared with the other blood APCs. Data obtained from Haniffa et al. (2012).

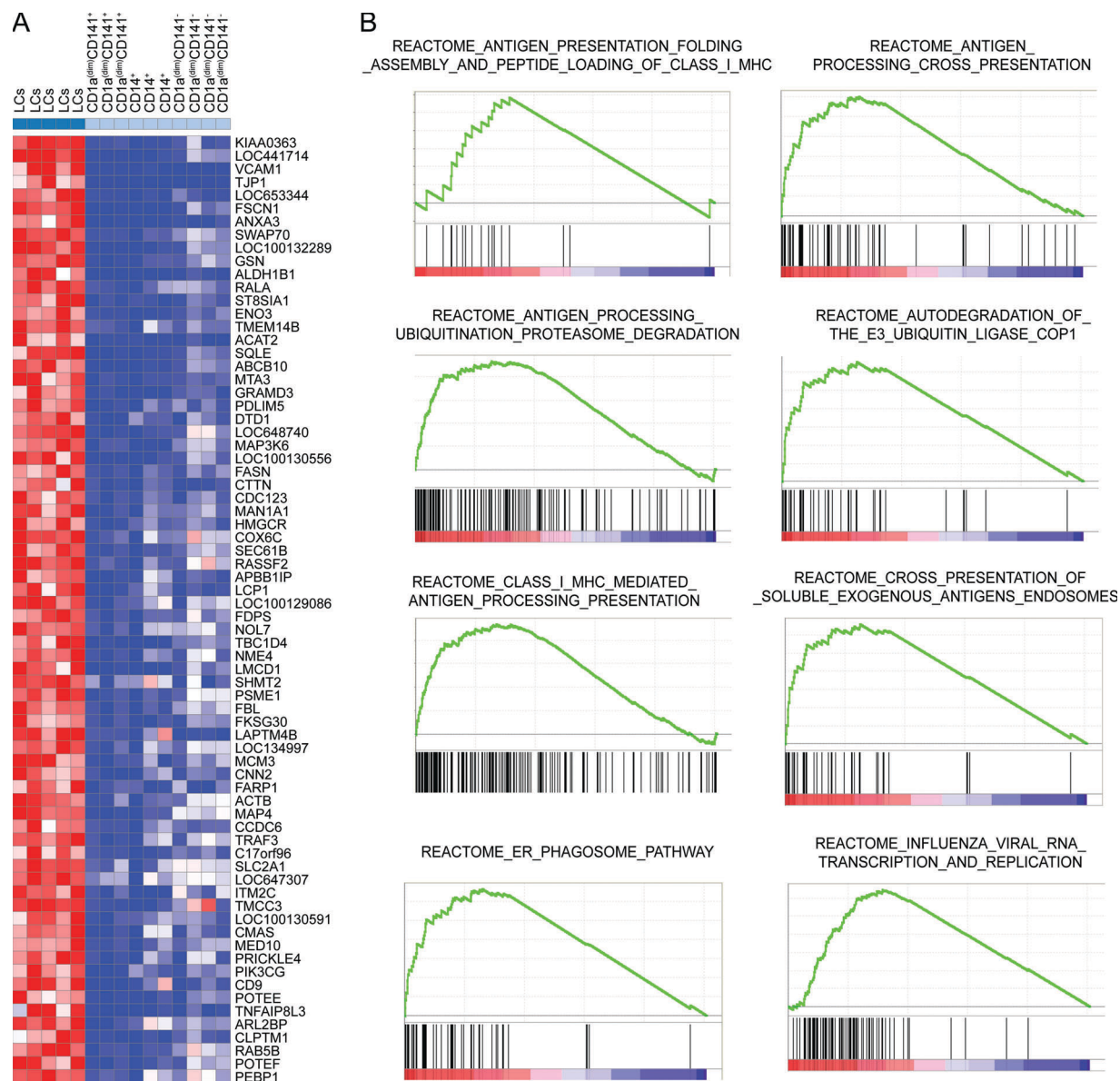


Figure S3. Pathway analysis of the LC-specific gene signature. (A) Human LC-specific gene signature as derived compared with the other skin DC subsets. (B) Enrichment of various expression signatures in skin epidermal LCs relative to other skin DC subtypes (dermal CD1a^(dim)CD141⁻, dermal CD1a^(dim)CD141⁺, and dermal CD14⁺ DCs) evaluated by GSEA; in all cases FWER $P < 10^{-4}$.

Table S1, available as an Excel file, shows the genes that comprise each of the 16 mouse modules (Fig. 2 A). Table S2, available as an Excel file, shows the genes that comprise each of the 9 human modules (Fig. 3 D, left). Table S3, available as an Excel file, shows the cross-presenting gene signature. Table S4, available as an Excel file, shows genes that are shared between the mouse (CD103⁺CD8 α ⁺) and human (LCs) cross-presenting DC subsets and that belong to the class I MHC-mediated antigen processing presentation, antigen processing ubiquitination proteasome degradation antigen processing cross presentation and cross presentation of soluble exogenous antigens endosomes pathways as annotated by REACTOME. Table S5, available as an Excel file, shows 76 and 48 genes that belong to the antigen processing and cross-presentation (76 genes), and the cross-presentation of soluble exogenous antigens endosomes pathways (48 genes) as annotated by REACTOME (Table 2).

REFERENCE

Haniffa, M., A. Shin, V. Bigley, N. McGovern, P. Teo, P. See, P.S. Wasan, X.N. Wang, F. Malinarich, B. Malleret, et al. 2012. Human tissues contain CD141hi cross-presenting dendritic cells with functional homology to mouse CD103+ nonlymphoid dendritic cells. *Immunity*. 37:60–73. <http://dx.doi.org/10.1016/j.immuni.2012.04.012>