

Supplementary Material

A HUMAN LIN- CD123+ CD127^{low} POPULATION ENDOWED WITH ILC FEATURES AND MIGRATORY CAPABILITIES CONTRIBUTES TO IMMUNOPATHOLOGICAL HALLMARKS OF PSORIASIS

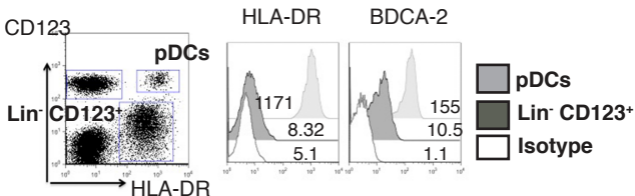
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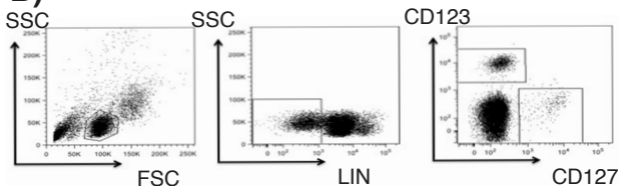
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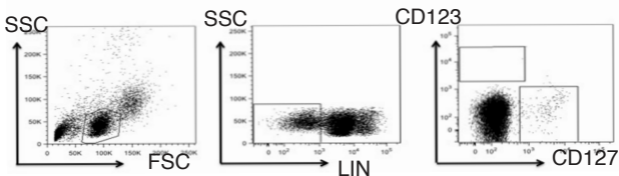
e-mail: labonifaz@yahoo.com

A)**B)**

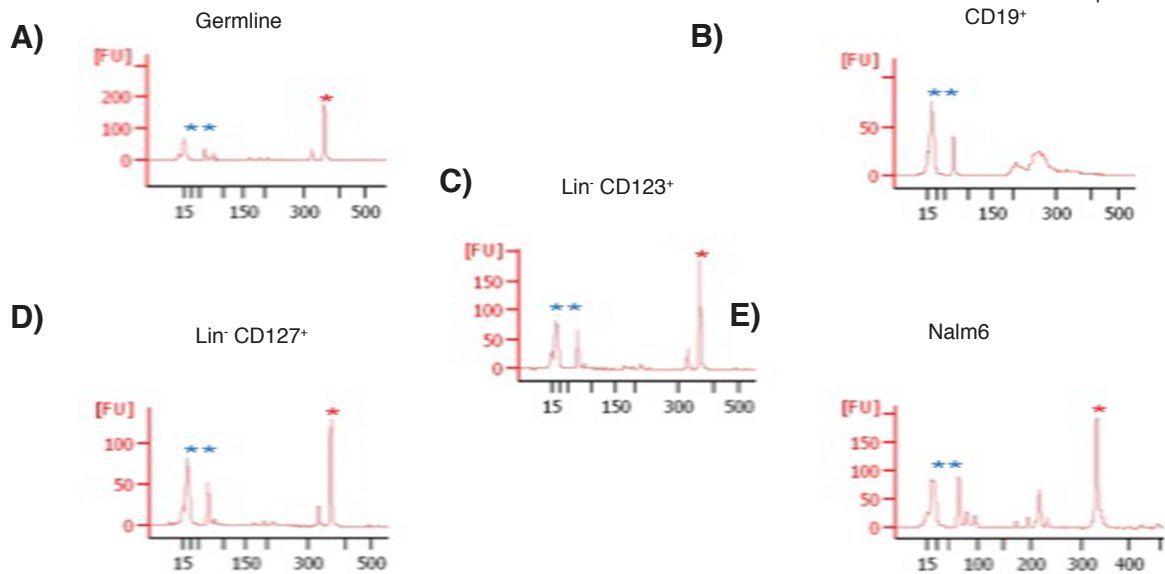
Lin MIX: CD3, CD14, CD19, CD94, HLA-DR

**C)**

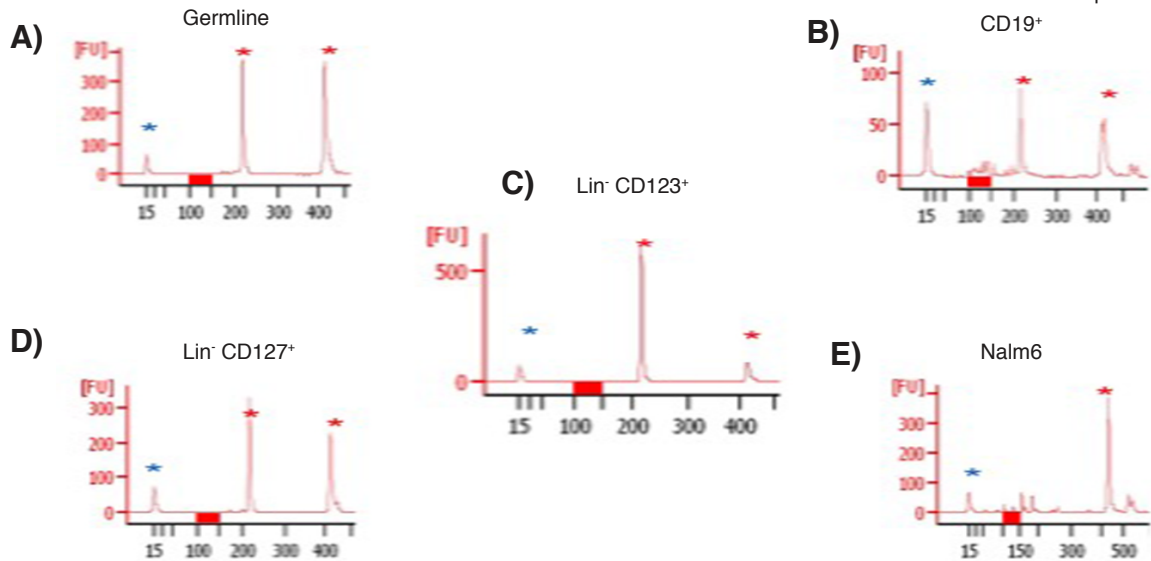
Lin MIX: CD3, CD14, CD19, CD94, HLA-DR + FcεR



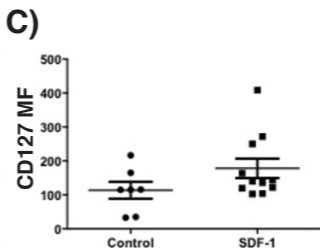
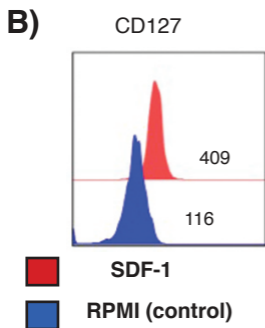
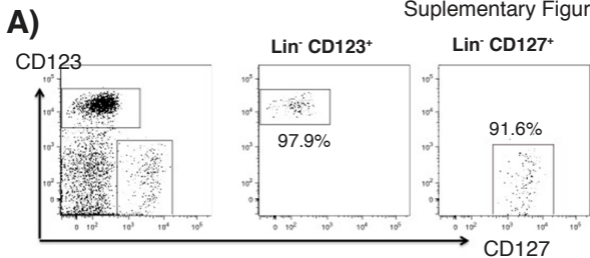
Supplementary Figure 1: In A) Gate analysis on the Lin⁻ CD123⁺ and pDCs, and compared expression of HLA-DR and BDCA-2 in both populations B) and C): Identification of Lin⁻ CD123⁺ and Lin⁻ CD127⁺ cells using +/- anti-FcεR in the lineage cocktail respectively.



Supplementary Figure 2: Supplementary figure X: DH1-6-JH incomplete rearrangement analysis. Genomic DNA from each subpopulation was subjected to multiplexed PCR amplification using the BIOMED-2 primers set for DH1-6-JH incomplete rearrangements (Tube D) according to (Ref 40). PCR products were resolved in a Agilent 2100 Bioanalyzer capillary electrophoresis system with an 1000 DNA chip. Product size in base pairs in the x-axis (cropped for clarity) and relative amount (fluorescence units, y-axis). A) Oral swab from a healthy donor as a negative control; B) Sorted CD19⁺ B cells from a healthy donor; C) Sorted CD123⁺ CD127^{low} from a healthy donor; D) CD127⁺ classical ILC from a healthy donor; and E) Acute B- cell leukemia cell line NAL-M6. The expected range of DH1-6-JH rearrangements is 110-420 bp (red bar). A germline ~340 bp product (*) is consistently amplified and serves as an internal positive control. Low weight electrophoretic front (**).

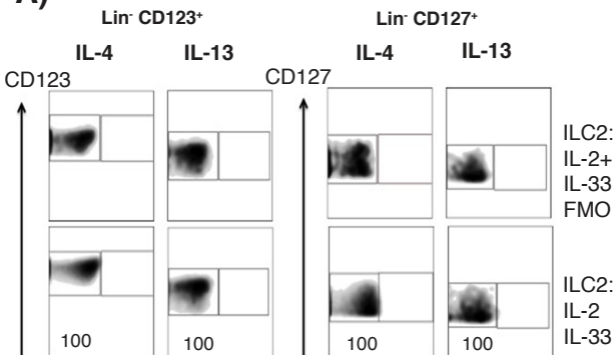


Supplementary Figure 3: DH7-JH incomplete rearrangement analysis. Genomic DNA from each subpopulation was subjected to PCR amplification using the BIOMED-2 DH7-JH primer pair for incomplete rearrangements (Tube E) according to (Ref1). PCR products were resolved in a Agilent Bioanalyzer capillary electrophoresis system with an 1000 DNA chip. Product size in base pairs in the x-axis (cropped for clarity) and relative amount (fluorescence units, y-axis). A) Oral swab from a healthy donor as a negative control; B) Sorted CD19⁺ B cells from a healthy donor; C) Sorted CD123⁺ CD127^{low} from a healthy donor; D) CD127⁺ classical ILC from a healthy donor; and E) Acute B- cell leukemia cell line NAL-M6. The expected range of DH7-JH rearrangements is 100-130 bp (red bar). Two germline ~211 and 419 bp products (*) are consistently amplified and serve as internal positive controls. Low weight electrophoretic front (*).

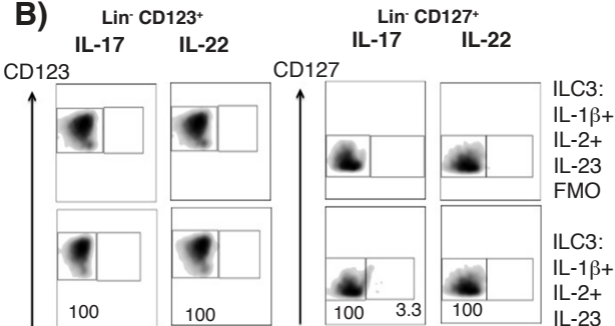


Supplementary Figure 4: In **A)** Percentages of Lin⁻ CD123⁺ and Lin⁻ CD127⁺ sorted cells. Gated on Lin⁻ cells. **B)** CD127 expression in Lin⁻ CD123⁺ after 3.5 hrs of transmigration assay in response SDF-1 (red histogram) or RPMI (blue histogram). MF values representative of three experiments are shown. **C)** Graph of CD127 MF from three independent experiments. Control: n = 6 and SDF-1: n = 11

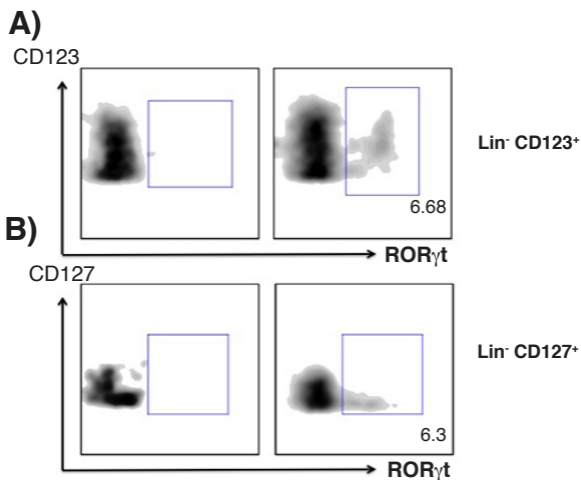
A)



B)



Supplementary Figure 5: A) IL-4 and IL-13 expression in $\text{Lin}^- \text{CD123}^+$ and $\text{Lin}^- \text{CD127}^+$ within PBMCs cultured +/- ILC2 activation cocktail for 18 hrs. and B): IL-17 and IL-22 expression in $\text{Lin}^- \text{CD123}^+$ and $\text{Lin}^- \text{CD127}^+$ within PBMCs cultured +/- ILC3 activation cocktail for 18 hrs. Density plots are representative of at least three independent experiments



Supplementary Figure 6:

ROR γ t expression in total skin cells in A) Lin⁻ CD123⁺ and B) Lin⁻ CD127⁺ cell populations. Left: FMO controls, Right: ROR γ t staining