

1 **Supplementary Figure Legends**

2

3 **EFigure 1.** Unsupervised hierarchical clustering of expression values of genes
4 differentially expressed between normal epidermis and dermis, shown across
5 lesional/LS; non-lesional/NL and normal/N skin in bulk, epidermis or dermis. (n=5
6 for AD; n=6, 10, and 6 for normal bulk, epidermis, and dermis, respectively)

7

8 **EFigure 2.** A Venn diagram of the LCM epidermis and dermis and bulk AD
9 transcriptome comparing LS and NL (fold change/FCH>2.0, false discovery
10 rate/FDR<0.05, green/upregulated; red/downregulated).

11

12 **EFigure 3. A.** A heatmap of differentially expressed genes/DEGs uniquely
13 identified in bulk tissue. **B.** A Venn diagram highlighting the number of unique
14 DEGs identified in bulk tissue, with the numbers of genes in the following
15 subsets: genes identified in the comparison of normal epidermis vs. dermis **(i)**,
16 genes identified in the comparison of LS and NL epidermis vs. dermis **(ii)**, genes
17 that miss the strict FDR threshold/FDR<0.05, but retain significant unadjusted p-
18 values **(iii)**, and genes not identified in **i-iii (iv) C.** Schematic of LS and NL skin
19 showing relative contributions of each compartment as estimated by the linear
20 model.

21

22 **EFigure 4.** Representative immunofluorescence staining for co-expression of IL-
23 34 (red) and CD3⁺ T-cells (green) **(A)**, CD11c⁺ DCs **(B)** and CD163⁺

24 macrophages (green) **(C)** in lesional/LS and non-lesional/NL AD and normal/N
25 skin.

26

27 **EFigure 5.** A heatmap of epidermal differentiation complex/EDC and the cornified
28 envelope/CE genes, showing FCH differences comparing LS; NL and N skin in
29 bulk; epidermis or dermis. (n=5 for AD; n=6, 10, and 6 for normal bulk, epidermis,
30 and dermis, respectively)

31

32 **EFigure 6.** Representative immunofluorescence staining for co-expression of
33 CCR7 (red) and CD3⁺ T-cells (green) **(A)** and CCR7 (red) and CD11c⁺ DCs
34 (green) **(B)** in lesional/LS and non-lesional/NL AD and normal/N skin. White
35 arrows indicate double-positive cells.

36

37 **EFigure 7.** Principal component analysis/PCA plots of combined AD and PSO
38 (previously published and this study) LCM/bulk data before **(A)**, and after,
39 adjusting for batch effects with batch “AD-bulk” **(B)**, and with batch “Researcher”
40 **(C)**.

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42 **ETable 1.** Characteristics of AD patients.

43

44 **ETable 2.** Primers and probes used for RT-PCR.h

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46 **ETable 3.** Antibodies used for IHC and IF.

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48 **ETable 4.** Top 25 up- **(A)** and down-regulated **(B)** differentially expressed genes
49 in AD non-lesional/NL dermis versus non-lesional/NL epidermis.

50

51 **ETable 5** Top 25 up- **(A)** and down-regulated **(B)** differentially expressed genes in
52 AD lesional/LS dermis versus lesional/LS epidermis.

53

54 **ETable 6** Top 25 differentially expressed genes up-regulated in the epidermis **(A)**
55 and dermis **(B)** differentially expressed genes in AD lesional/LS versus non-
56 lesional/NL skin.

57

58 **ETable 7** Top 25 differentially expressed genes down-regulated in the epidermis
59 **(A)** and dermis **(B)** in AD lesional/LS versus non-lesional/NL skin.

60

61 **ETable 8.** Full table of all differentially expressed genes (FCH<2.0 and
62 FDR<0.05) in the unique LCM epidermal **(A)**, unique LCM dermal **(B)**, unique
63 bulk **(C)**, and non-unique **(D)** transcriptomes, including all comparisons between
64 lesional/LS, non-lesional/NL, and normal epidermis, dermis, and bulk tissues.

65

66 **ETable 9.** All comparisons of gene expression values in the immune-related gene
67 subset shown in Fig.2A. Status 1 is differentially expressed, 0 is not differentially
68 expressed.

69

70 **ETable 10.** All comparisons of gene expression values in the epidermal
71 differentiation complex/EDC and the cornified envelope/CE gene subset shown in
72 EFig.5. Status 1 is differentially expressed, 0 is not differentially expressed.

73

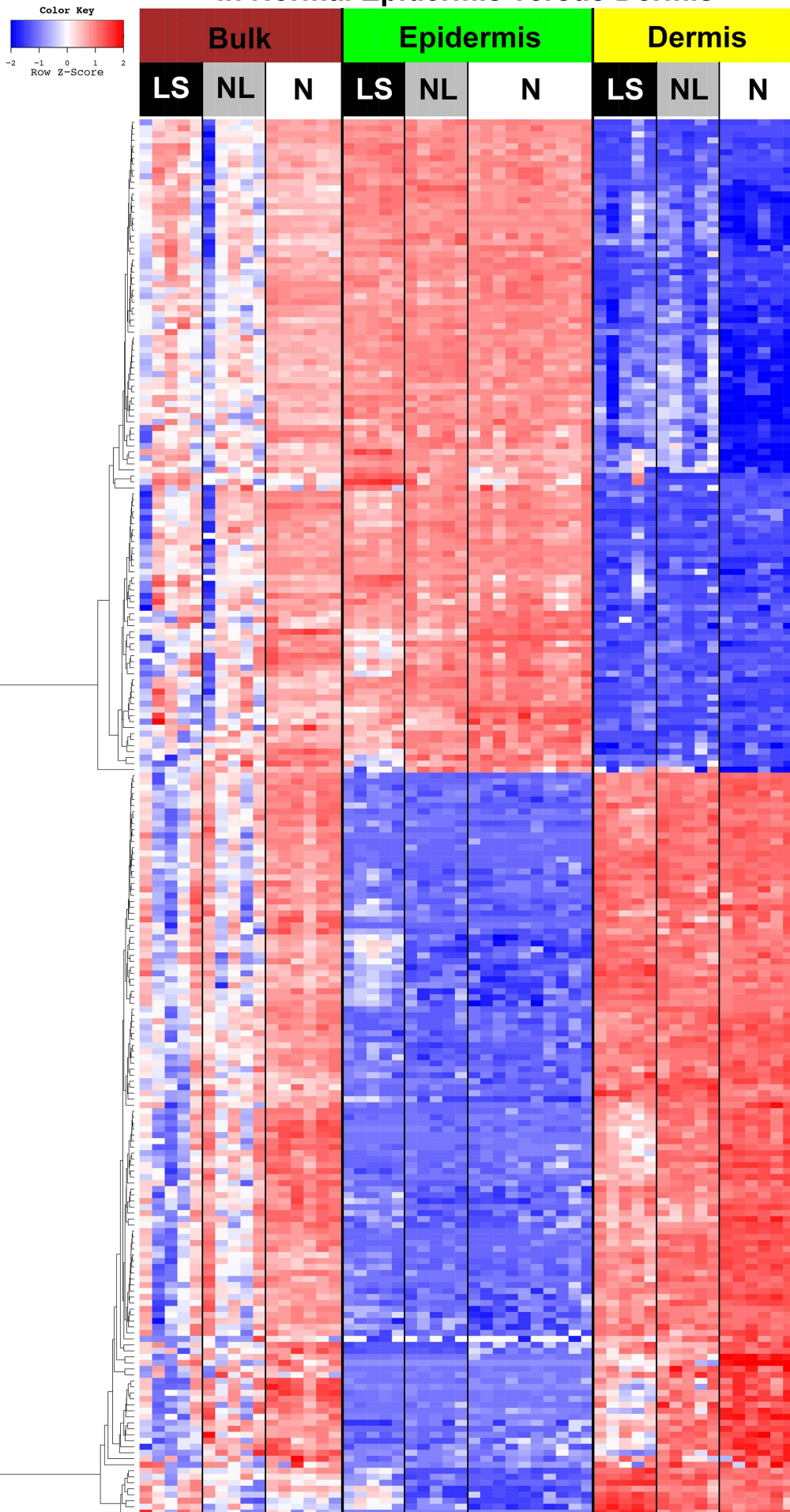
74 **ETable 11.** All comparisons of gene expression values in the barrier-related gene
75 subset shown in Fig.4A. Status 1 is differentially expressed, 0 is not differentially
76 expressed.

77

78 **ETable 12.** The genes differentially expressed in the bulk (a) and the LCM
79 epidermal (b) and dermal (c) transcriptomes comparing lesional/LS and non-
80 lesional/NL with possible cellular source. (KC/keratinocyte, iDC/immature
81 dendritic cell, LEC/lymphatic endothelial cell, MVEC/microvascular endothelial
82 cell, mDC/mature dendritic cell).

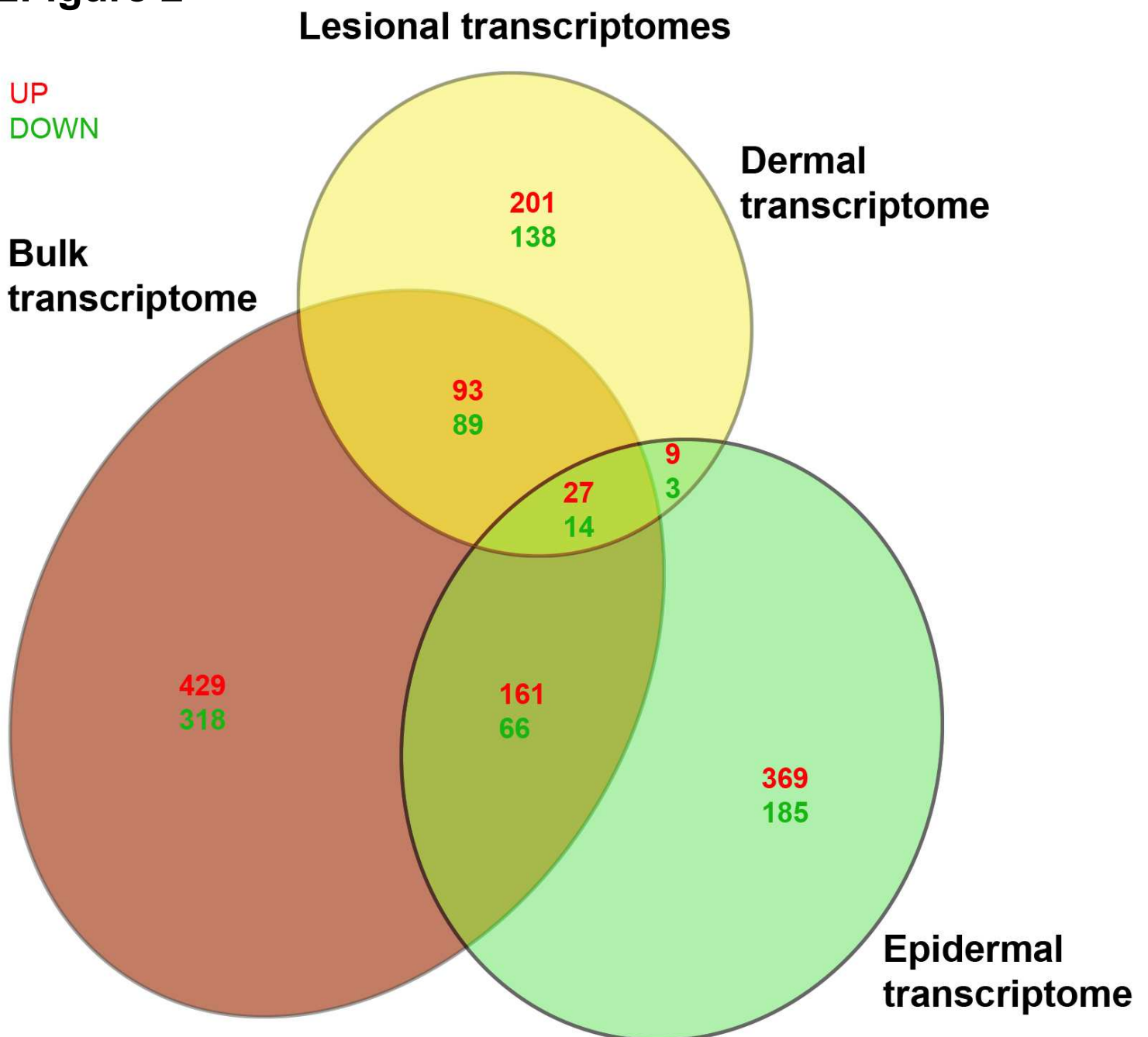
EFigure 1

Differentially Expressed Genes in Normal Epidermis versus Dermis



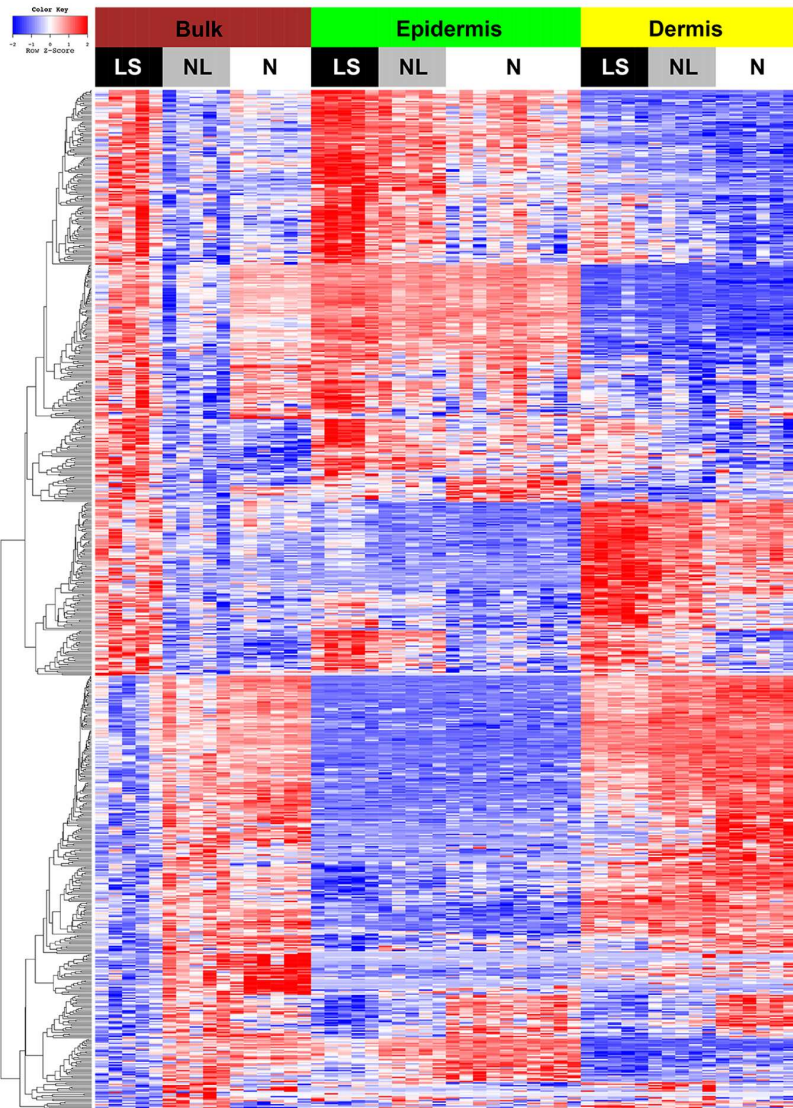
RIPT

EFigure 2

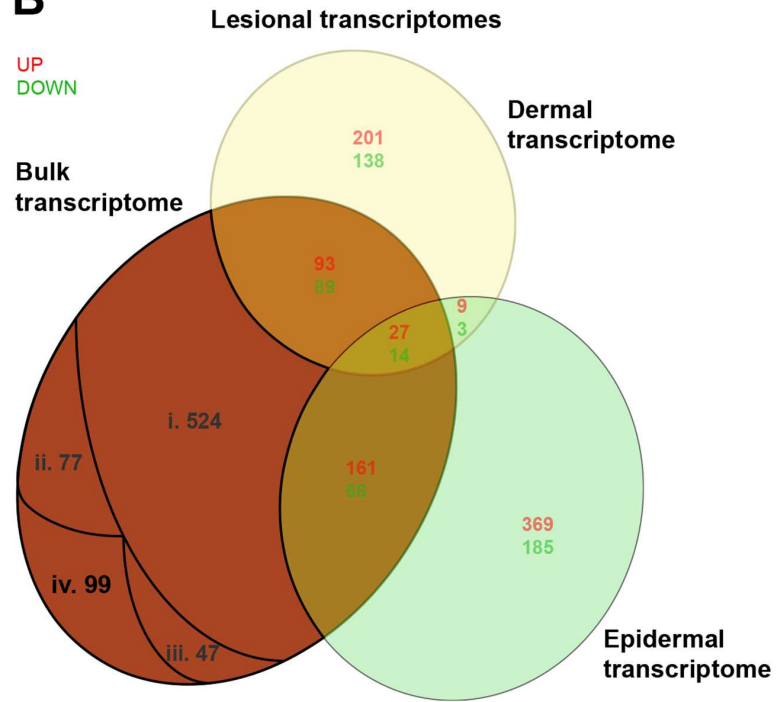


EFigure 3

A

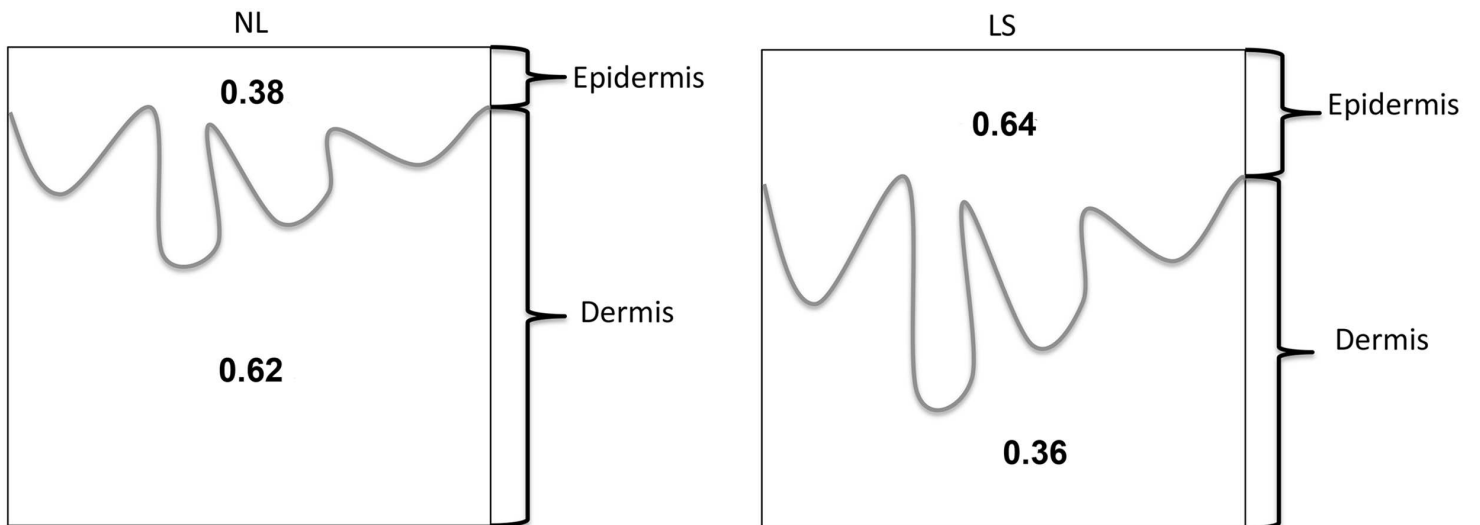


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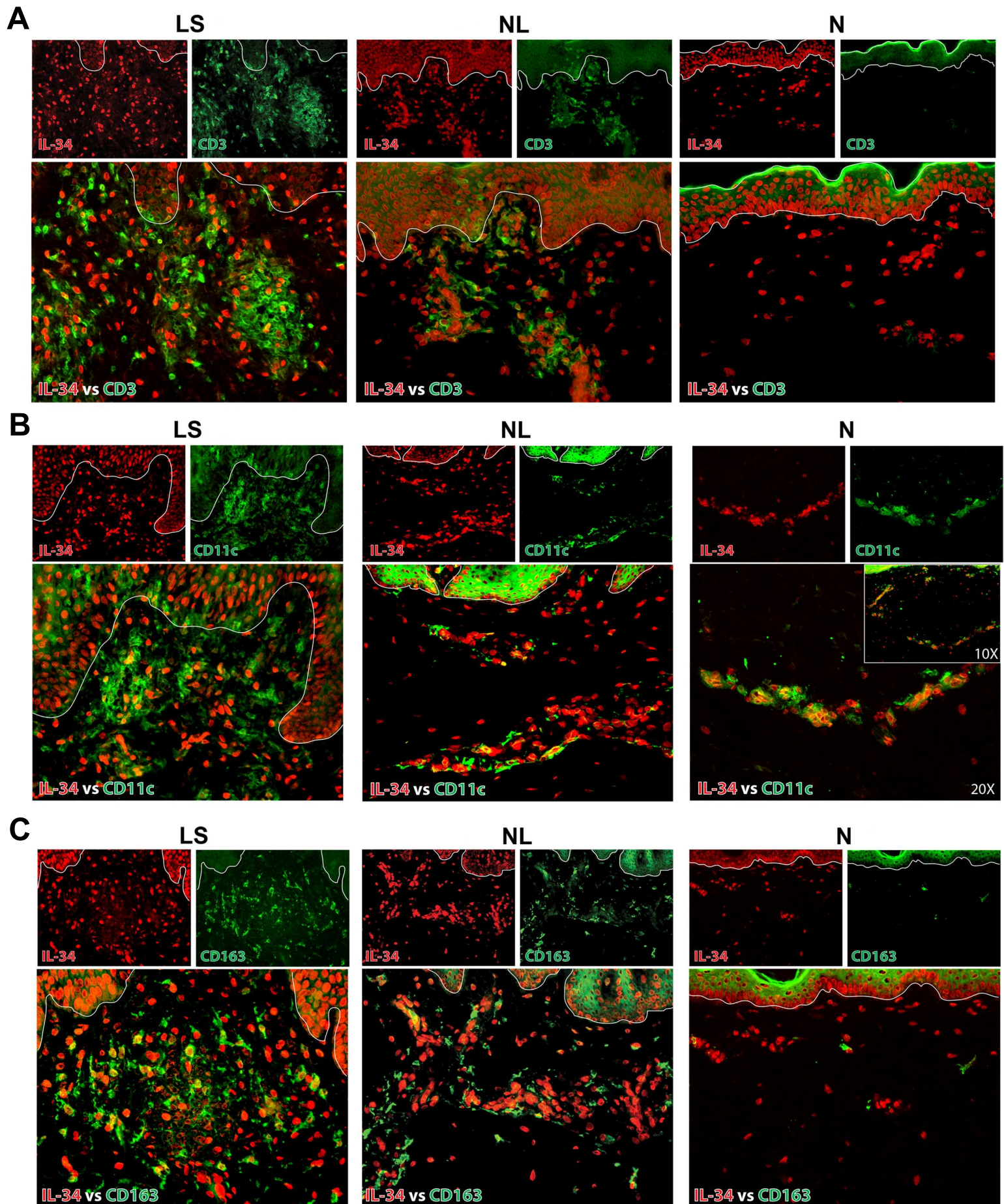


C

Contribution of Epidermis and Dermis expression values on Unique FT Expressions

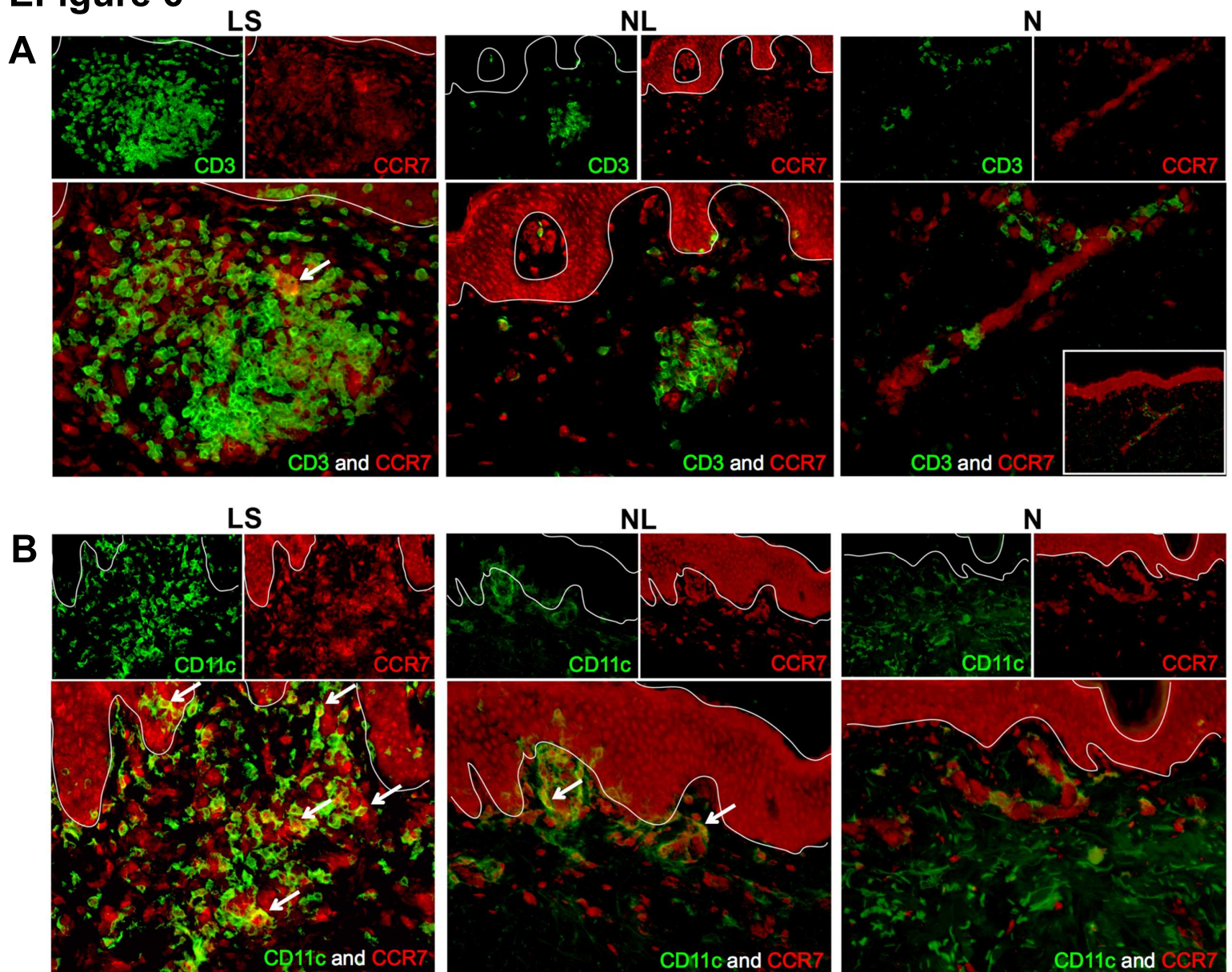


EFigure 4



SCRIPT

EFigure 6



EFigure 7

