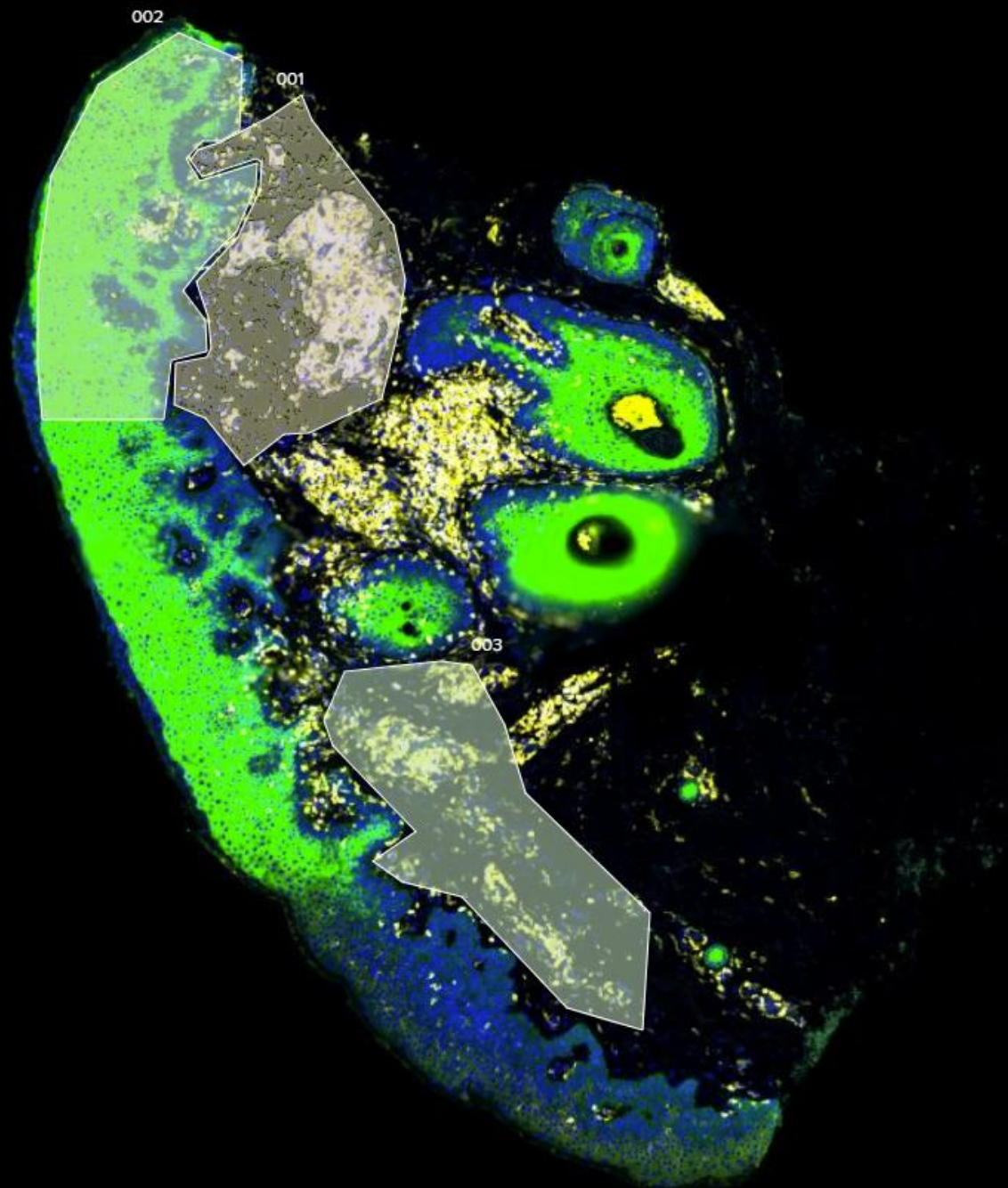




MULTI-OMIC SPATIAL PROFILING OF ATOPIC ECZEMA SKIN REVEALS COMMON TRANSCRIPTIONAL AND PROTEOMIC IMMUNE TARGETS ALTERED WITH INHIBITING INTERLEUKIN 4 AND INTERLEUKIN 13 SIGNALING

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Author disclosures

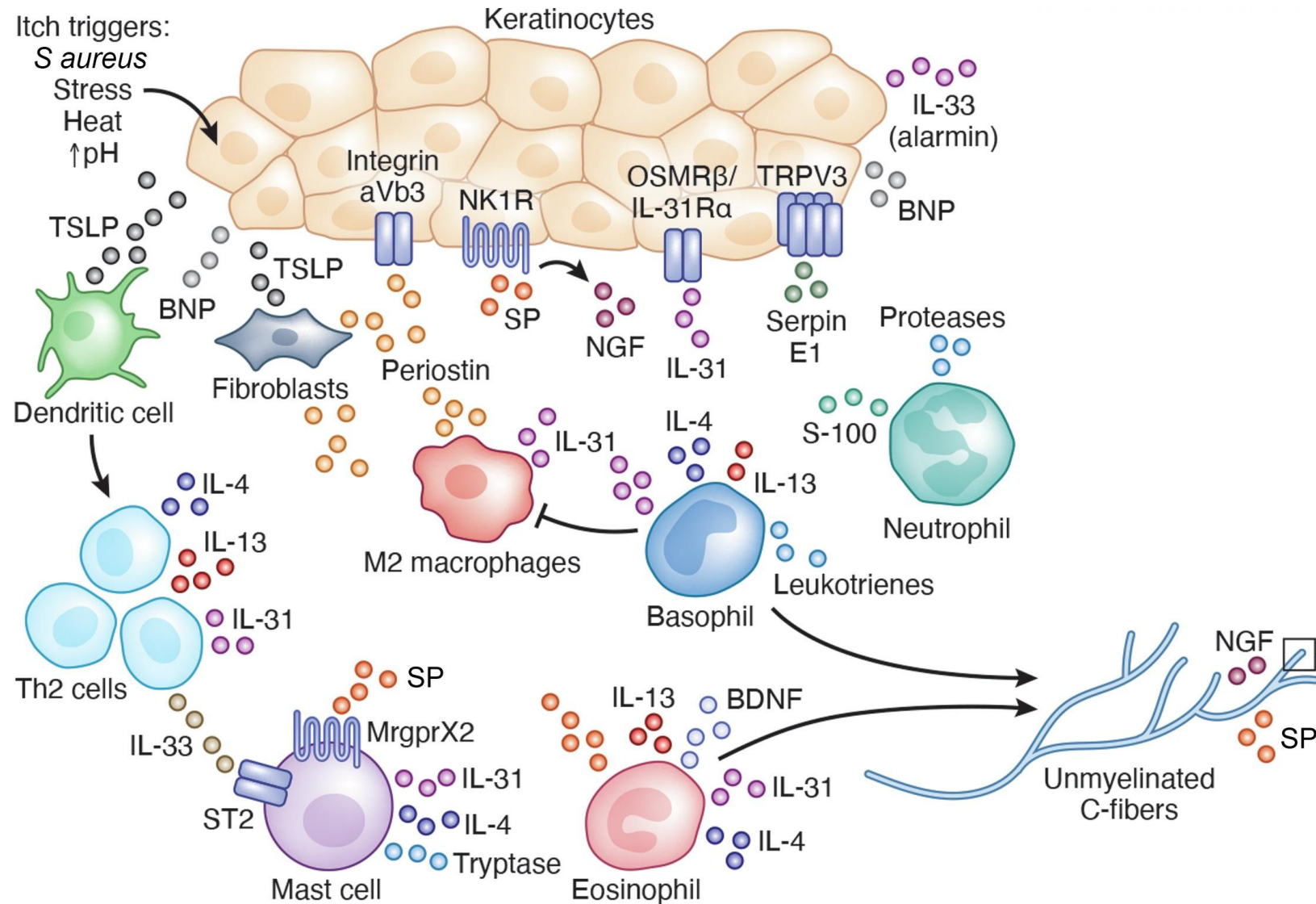
West NP: Ena Respiratory and GSK – Compensation, Sanofi-Aventis, Axellae Pty Ltd, CSL, GSK, Sanofi-Regeneron and Ena Therapeutics Pty Ltd – research grant.

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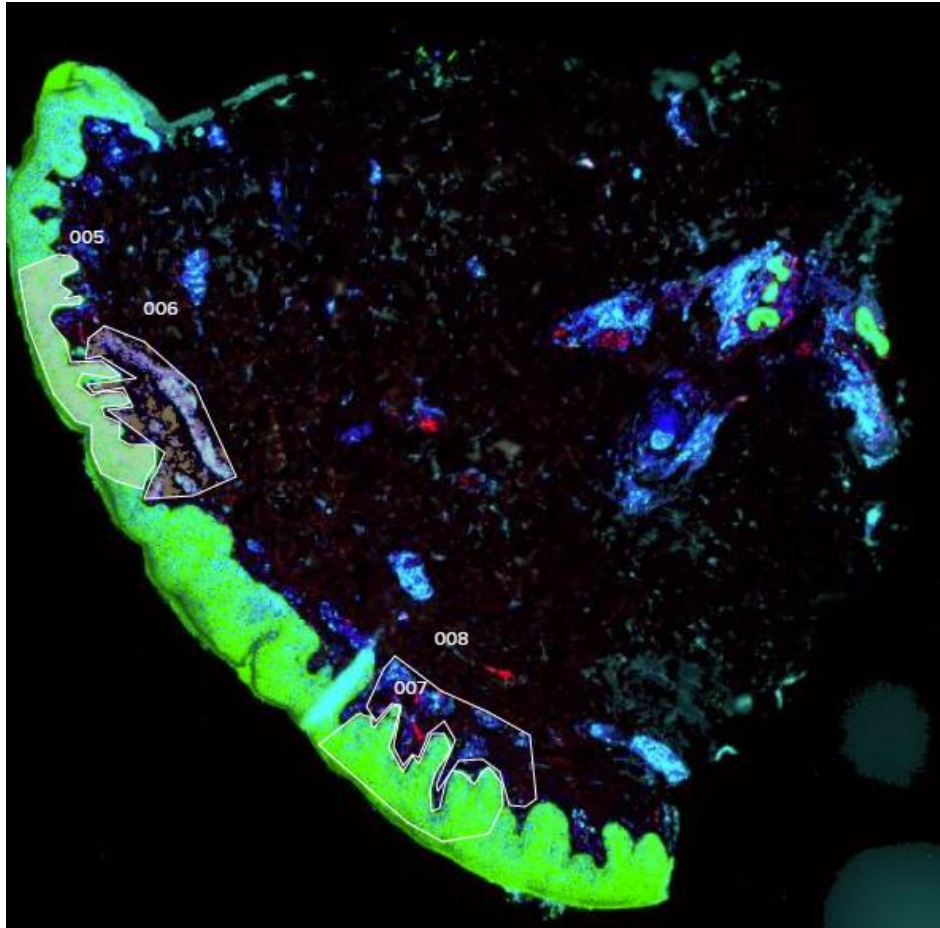
Funding statement

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Background



Study information



Study name: DIFFERENSTAD (NCT04823130)

Tissue details: lesional and non-lesional skin samples from individuals with atopic eczema (treated with dupilumab 300 mg every 2 weeks for 16 weeks) and comparative biopsies from healthy individuals.

Assay details:

RNA: Cancer transcriptome atlas (1,812 targets)

Protein: Immune oncology panel (80 targets)

Experimental design:

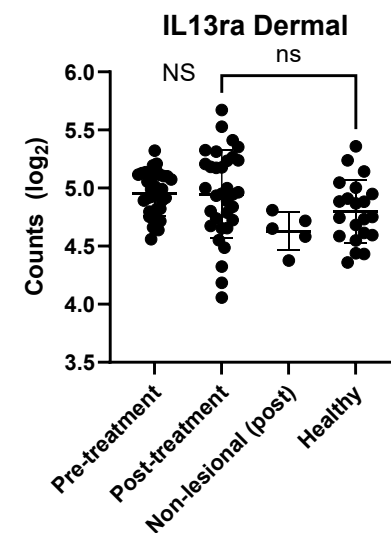
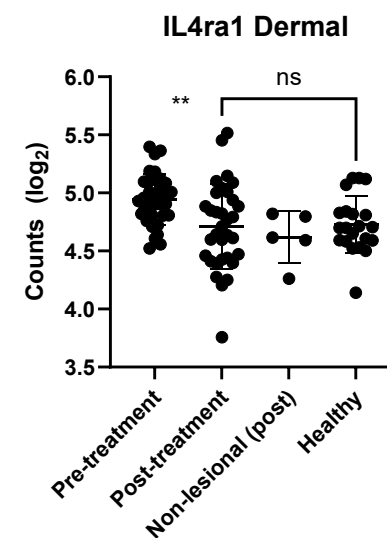
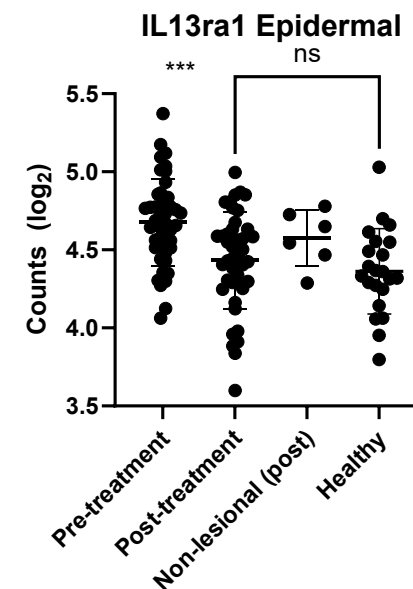
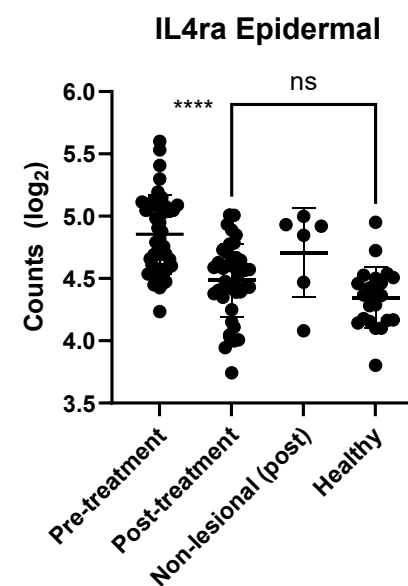
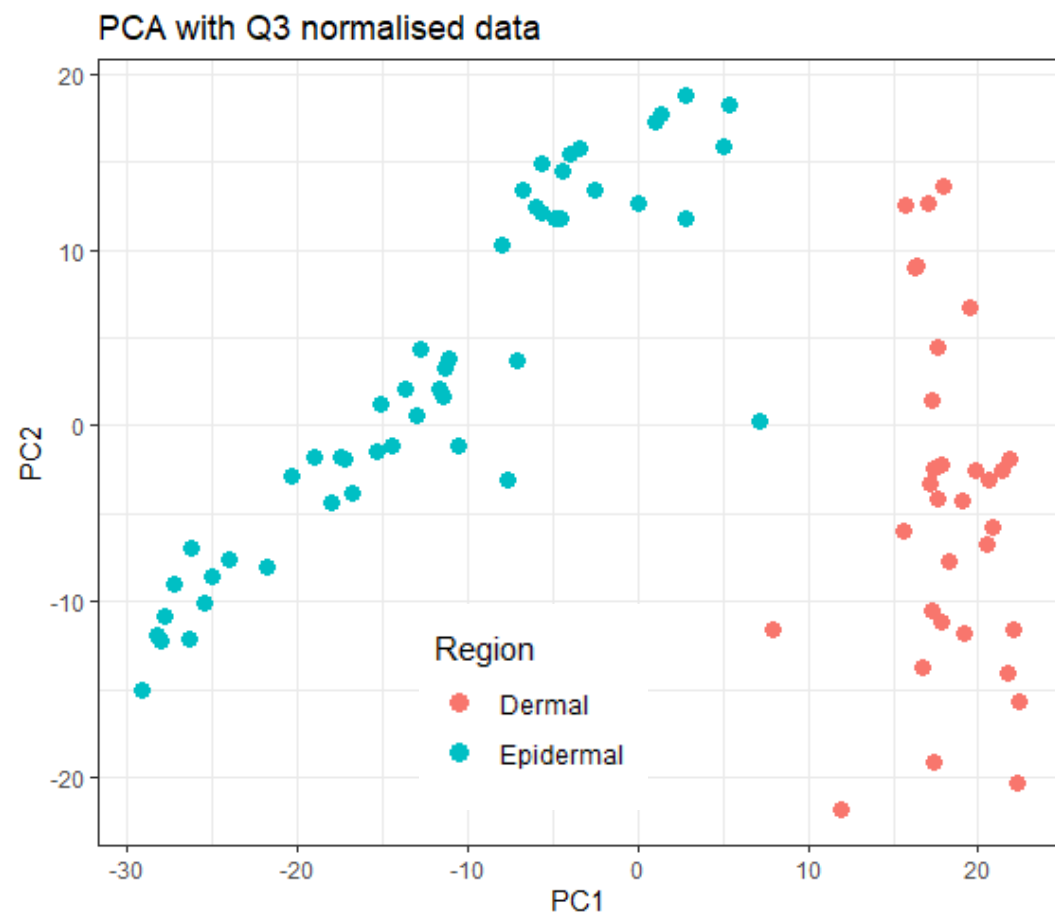
Slide mounted FFPE section

Geometric non-segmented and segmented ROIs

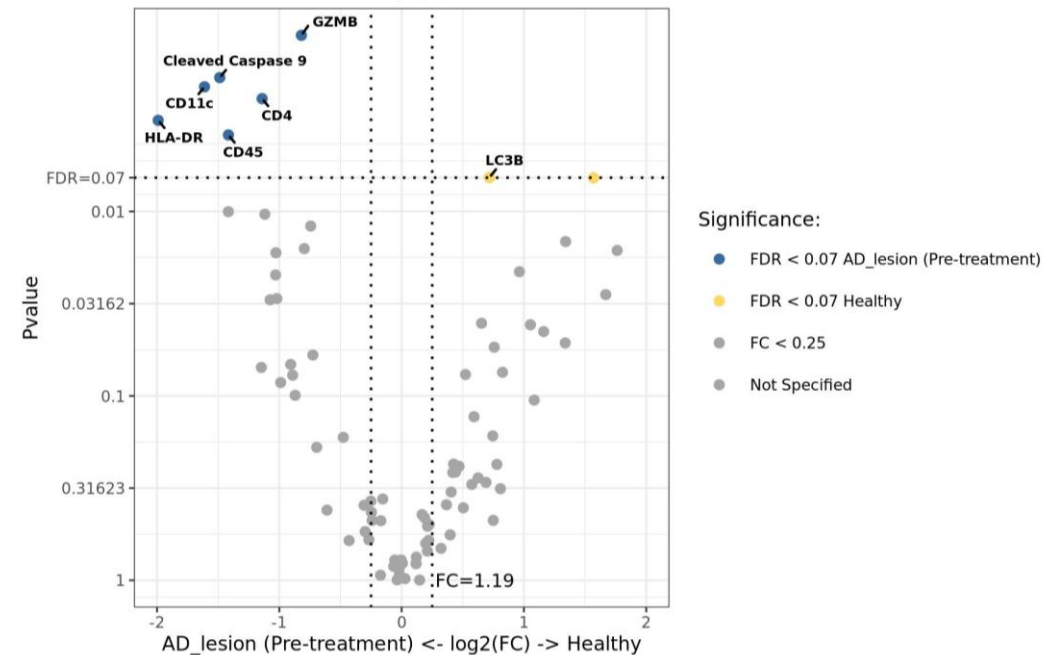
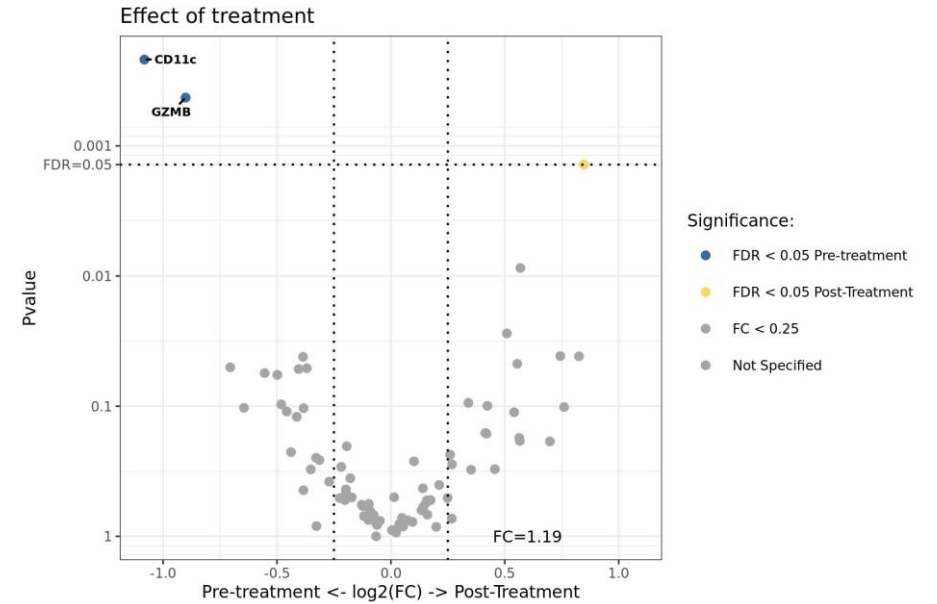
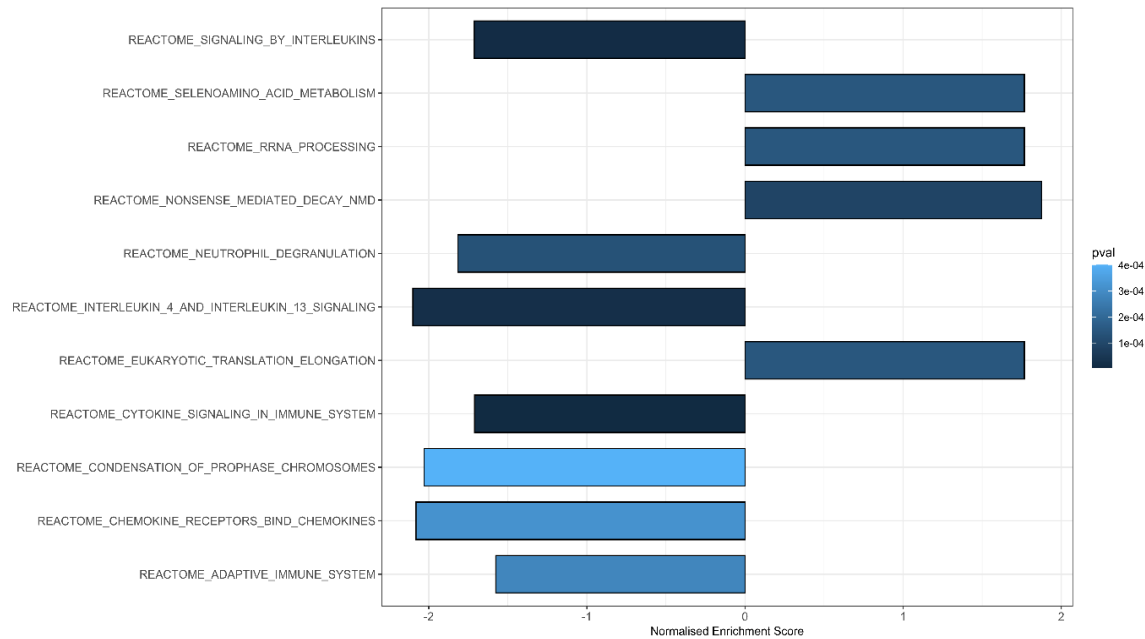
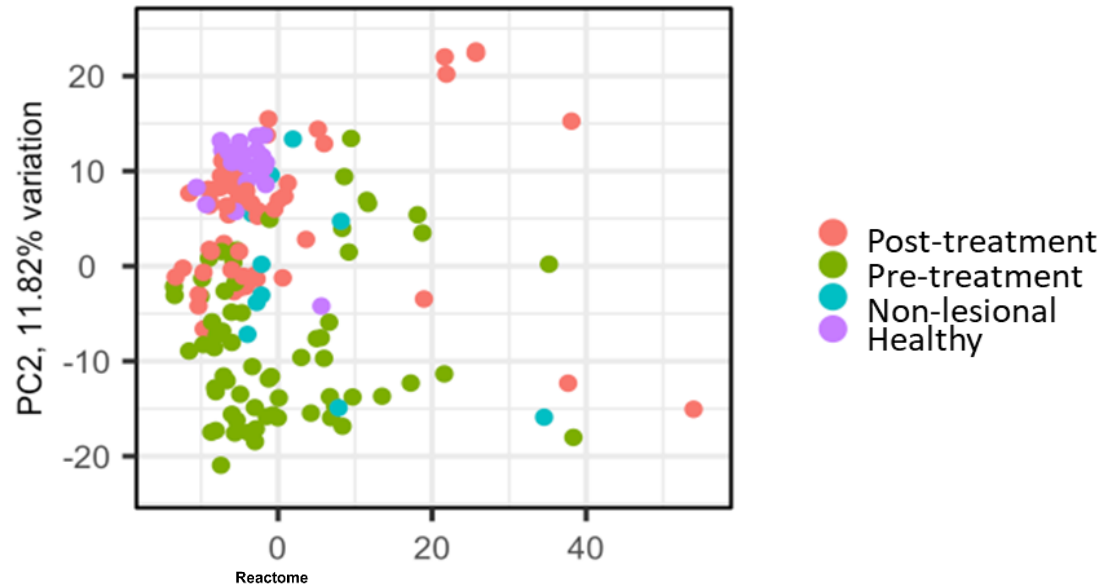
Segmented ROI based on the following cell populations:

- PanCK (epithelia)
- CD45 (leucocytes)
- PGP9.5 (nerves)

Results: Epidermal and dermal gene expression



Results: normalisation of gene and protein expression



Final comments

- Spatial transcriptomics was able to identify differences in response to blocking both IL4 and IL13 signaling between the epidermis and dermis in atopic disease, with changes in innate immune gene sets observed in the epidermis and adaptive immune gene sets in the dermis.
- Treatment induced changes in both IL4 and IL13 receptor signaling in the epidermis but only IL4 receptor signaling in the dermis
- Spatial profiling indicates that blocking both IL4 and IL13 signaling resulted in changes to gene and protein expression that normalised markers of inflammation in the epidermis and dermis.

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