

Robust Icotrokinra Systemic and Skin Pharmacodynamic Effects Versus Deucravacitinib in Patients With Moderate-to-Severe Plaque Psoriasis: Results From Phase 3, ICONIC-ADVANCE 1 Study

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Background

Icotrokinra (ICO) is the first and only targeted oral peptide for plaque psoriasis (PsO) that precisely binds the interleukin-23 receptor (IL-23R) and **inhibits IL-23 pathway signaling**¹

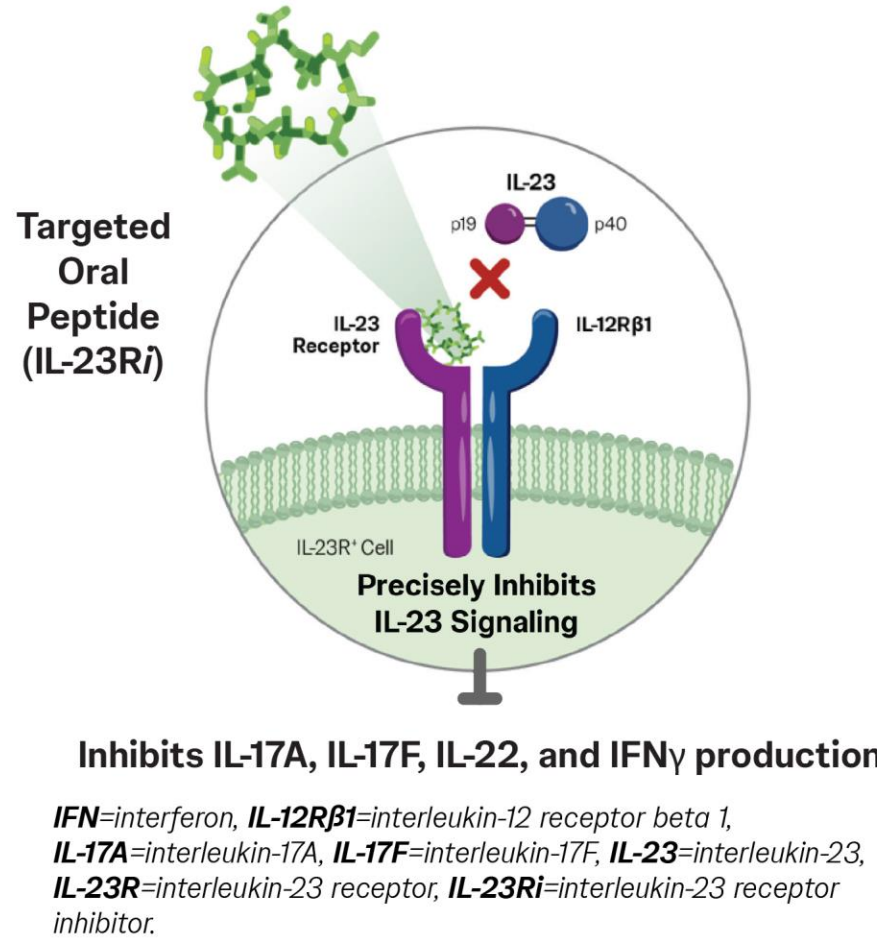
ICONIC-ADVANCE 1 (NCT06143878), a Phase 3 placebo (PBO)-controlled and deucravacitinib (Deucra) active comparator-controlled study of ICO in patients with moderate-to-severe plaque PsO, showed superior rates of skin clearance and a favorable safety profile²

- Co-primary endpoints were met, with once daily ICO demonstrating significantly higher rates of skin clearance vs PBO at Week (W) 16
 - Investigator's Global Assessment (IGA) 0/1: 68% (ICO) vs 11% (PBO)
 - Psoriasis Area and Severity Index (PASI) 90: 55% (ICO) vs 4% (PBO)
- ICO showed superior rates of skin clearance compared to Deucra
- Similar adverse event rates between ICO and PBO were observed through W16, and no safety signals were identified through W24

Objective

Evaluate ICO pharmacodynamic (PD) effects on disease markers, relative to both PBO and Deucra, through W24 of the ICONIC-ADVANCE 1 study

Icotrokinra Blocks IL-23 From Binding to its Receptor



Methods

ICONIC-ADVANCE 1 Study Design

Moderate-to-severe plaque PsO (N=774)

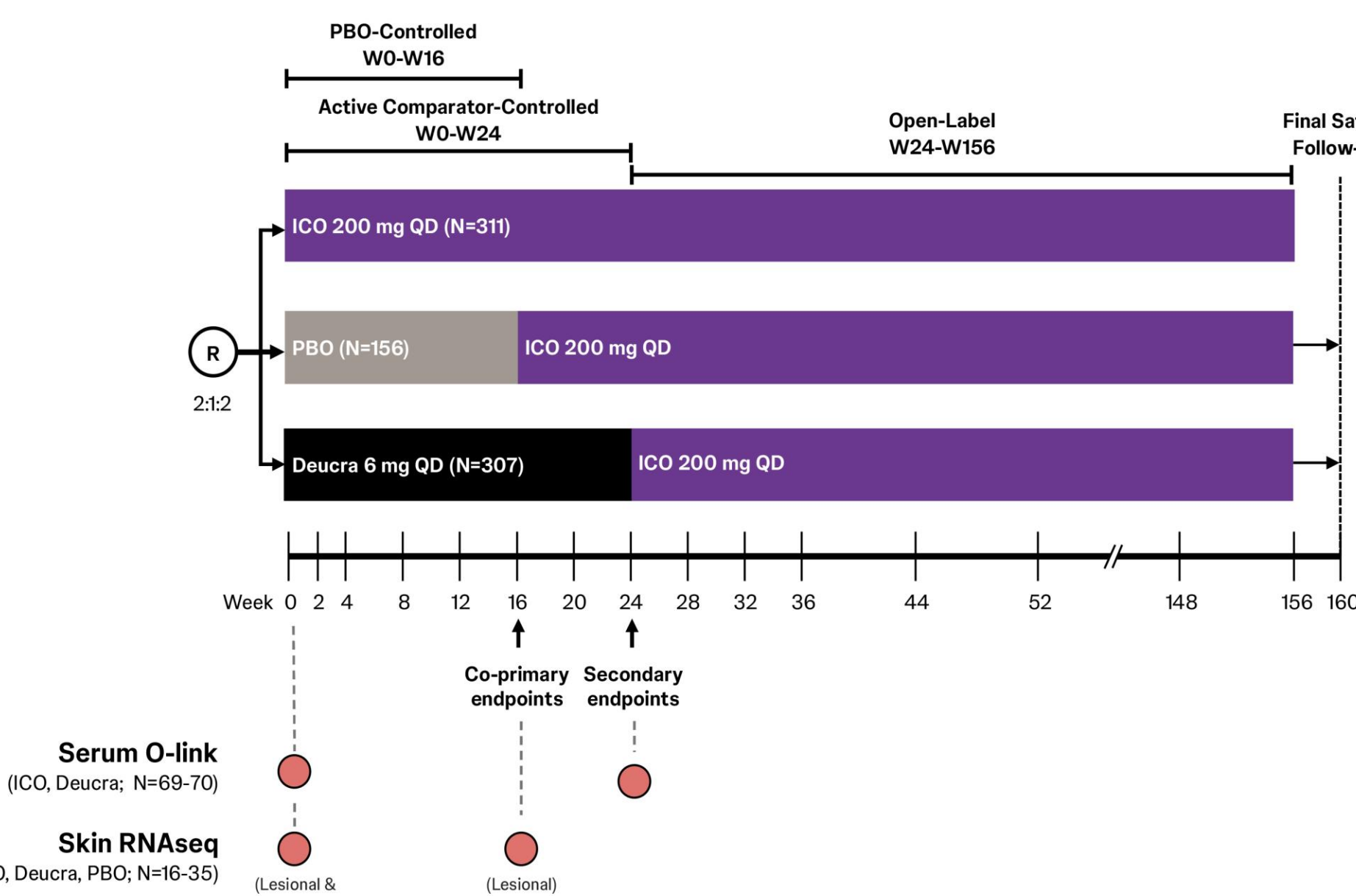
Key inclusion criteria

- ≥18 years
- Plaque PsO for ≥26 weeks
- BSA ≥10%, PASI score ≥12, and IGA score ≥3
- Candidate for phototherapy or systemic treatment for plaque PsO
- Suitable candidate for Deucra per approved product labeling

Co-primary endpoints

- IGA score 0/1 & ≥2-grade improvement from baseline (IGA 0/1) and PASI 90 vs PBO at W16

BSA=body surface area, Deucra=deucravacitinib, ICO=icotrokinra, IGA=Investigator's Global Assessment, PASI=Psoriasis Area and Severity Index, PBO=placebo, PsO=psoriasis, QD=daily, R=randomization, RNAseq=RNA sequencing, W=week.



ICONIC-ADVANCE 1 Biomarker Assessments and Analyses

Tissue PD:

- W0 non-lesional and lesional skin biopsies, and W16 lesional skin samples from 70 consenting participants of an optional sub-study treated with PBO, Deucra or ICO were analyzed
- Skin biopsy samples: Transcriptomic analysis using RNA sequencing

Systemic PD:

- W0 and W24 serum samples from a sub-cohort of 70 ICO- and 69 Deucra-treated participants were analyzed
- Serum samples from a separate healthy cohort of 22 subjects were included as a control group
- Serum samples: Analyzed for PsO-relevant biomarkers using O-link proteomic platform

Data Analysis:

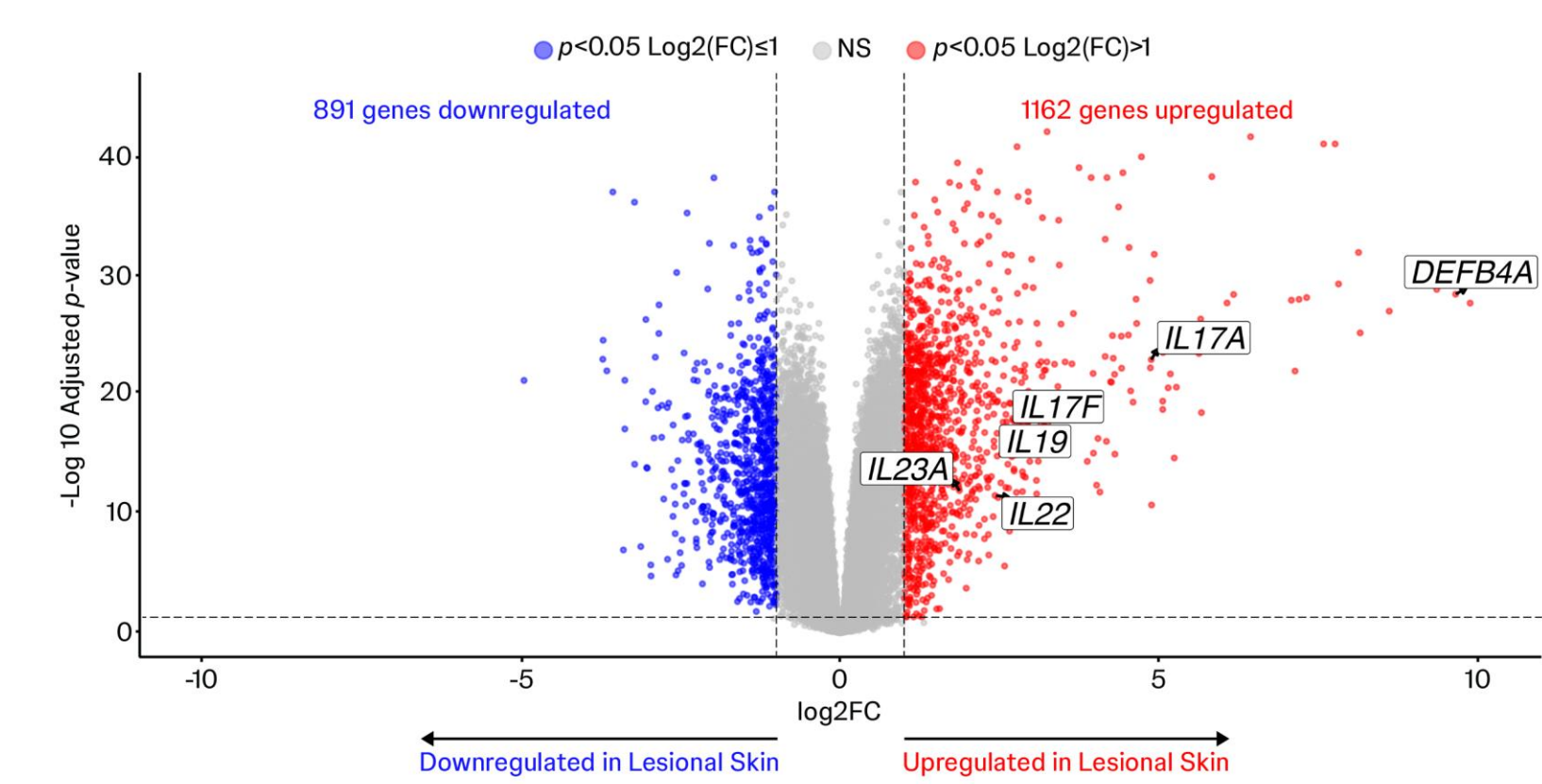
- Comparison between ICO and Deucra vs PBO (skin PD) and between ICO vs Deucra (skin and serum PD): Linear mixed-effect modeling including effects for W0 levels, interaction between time and treatment, patient random effect, and other co-variables as appropriate
- Statistical significance: p -value ≤ 0.05 for individual biomarkers; adjusted p -value ≤ 0.05 and $|\log FC| > 1$ for differential gene expression cut-off threshold

Deucra=deucravacitinib, ICO=icotrokinra, FC=fold-change, PBO=placebo, PD=pharmacodynamics, PsO=psoriasis, RNA=ribonucleic acid, W=week.

Results

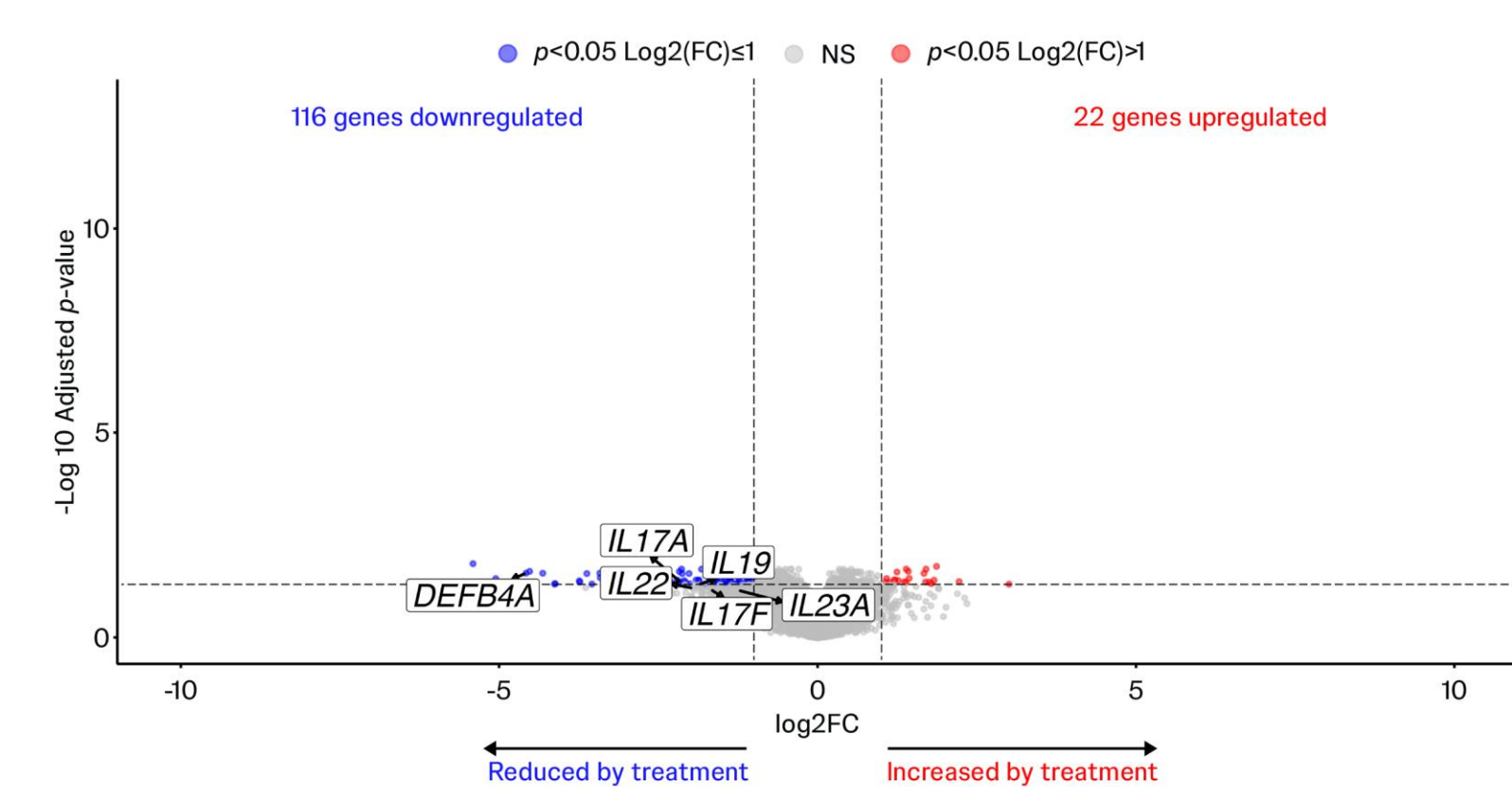
Baseline lesional and non-lesional skin exhibited highly differentiated transcriptomic profiles

- Differentially expressed genes included *IL17A*, *IL17F*, *IL19*, *IL22*, *IL23A*, and *DEFB4A*, which are related to PsO/IL-23 pathway



Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log2 counts ~ Tissue (lesional vs non-lesional), $p < 0.05$ for significance, and log2FC ≥ 1 and ≤ -1 for downregulation and upregulation cut-off, respectively. Based on all paired samples within the complete sample set: N=71 for lesional tissue, N=71 for non-lesional tissue. *DEFB4A*=gene that encodes human beta-defensin 2, *FC*=fold-change, *IL17A*=interleukin-17A gene, *IL17F*=interleukin-17F gene, *IL19*=interleukin-19 gene, *IL22*=interleukin-22 gene, *IL23A*=interleukin-23A gene, *NS*=not significant, *PBO*=placebo, *W*=week.

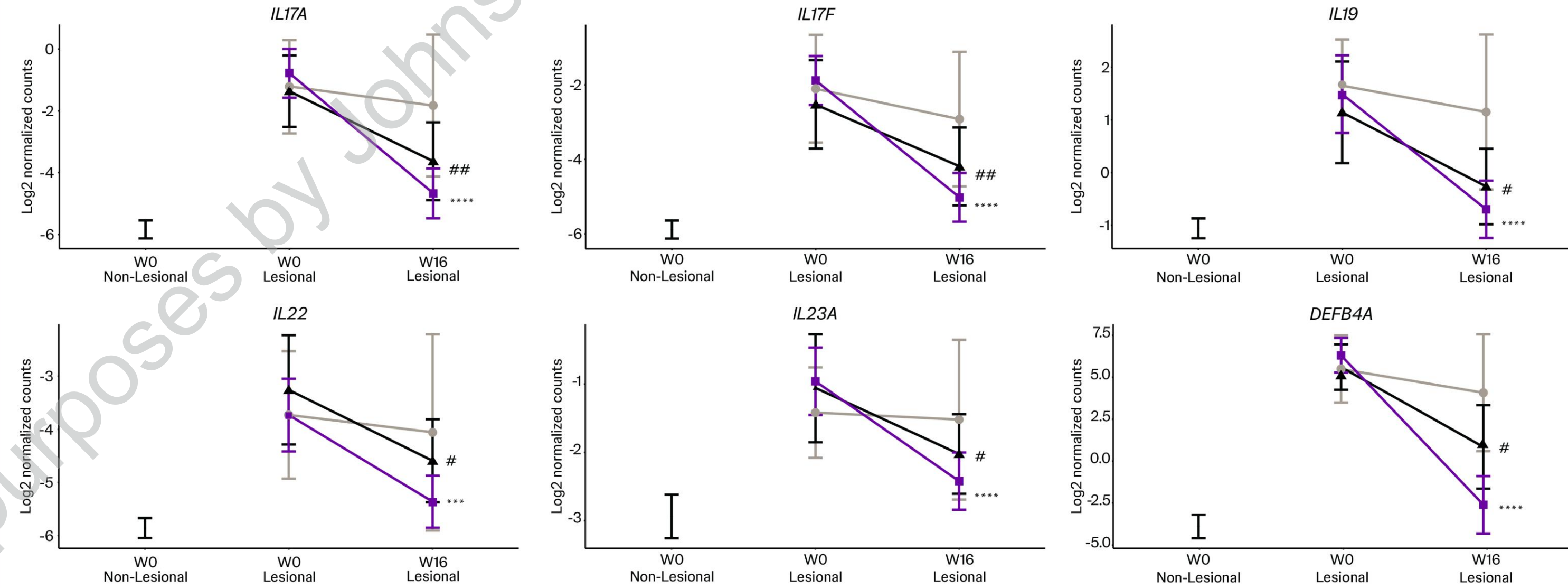
Deucra elicited modest impact on PsO skin transcriptome (W16 lesional vs W0 lesional)



Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log2 counts ~ Tissue (lesional vs non-lesional), $p < 0.05$ for significance, and log2FC ≥ 1 and ≤ -1 for downregulation and upregulation cut-off, respectively. Based on all paired samples within the complete sample set: N=32 (ICO), N=19 (Deucra), N=11 (PBO). *DEFB4A*=gene that encodes human beta-defensin 2, *Deucra*=deucravacitinib, *ICO*=icotrokinra, *FC*=fold-change, *IL17A*=interleukin-17A gene, *IL17F*=interleukin-17F gene, *IL19*=interleukin-19 gene, *IL22*=interleukin-22 gene, *IL23A*=interleukin-23A gene, *NS*=not significant, *PBO*=placebo, *W*=week.

ICO reduced PsO-related gene expression in lesional skin towards non-lesional levels at W16

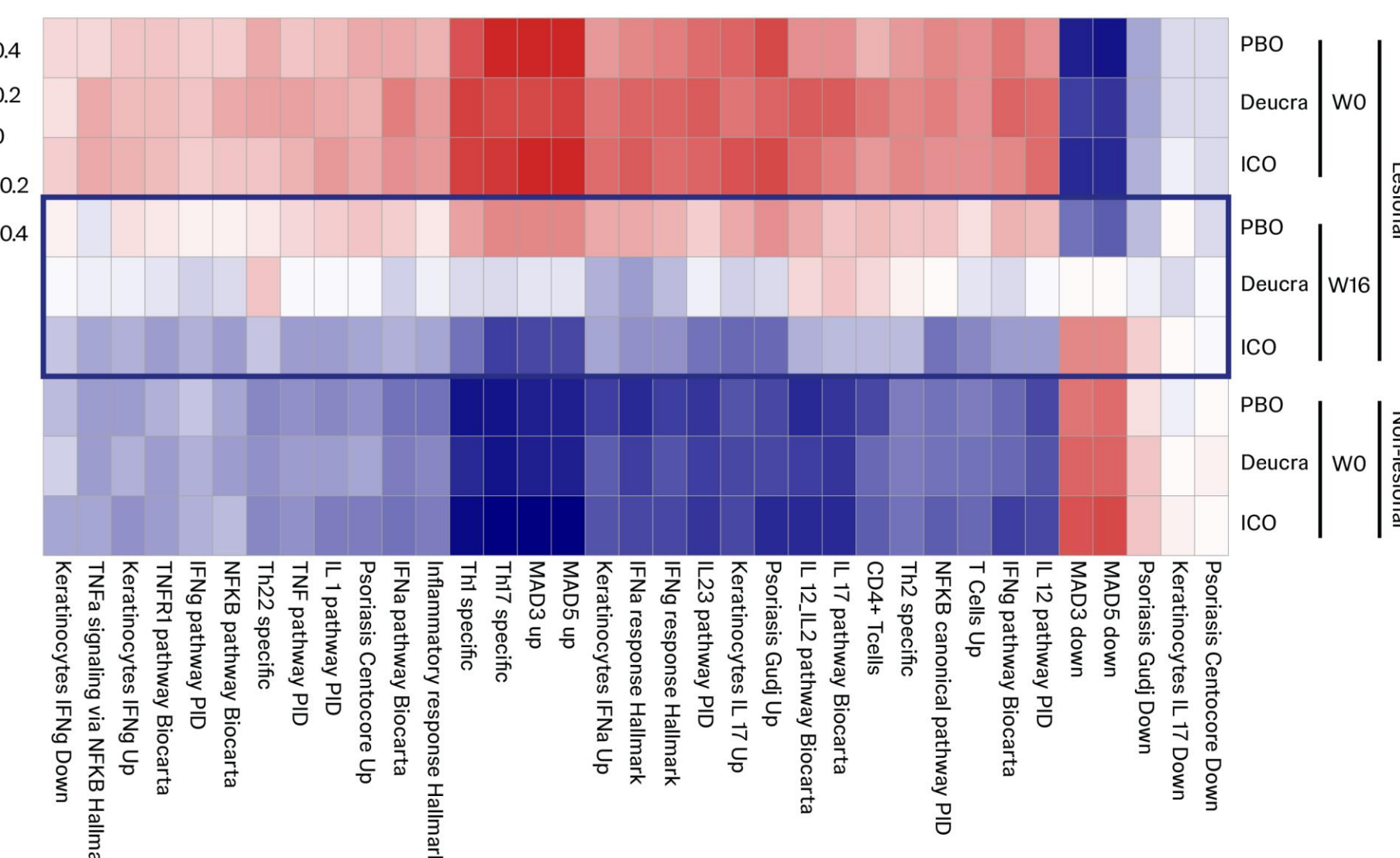
- ICO significantly reduced numerous PsO-related genes, including *IL17A*, *IL17F*, *IL19*, *IL22*, *IL23A*, and *DEFB4A*
- ICO-induced decrease of gene expression was more robust, as reflected by lower p -values, than the Deucra-induced decrease



*significant change of ICO W16 vs W0, *significant change of Deucra W16 vs W0, ** p -value < 0.05 , *** p -value < 0.01 , **** p -value < 0.001 , ***** p -value < 0.0001 , *DEFB4A*=gene that encodes human beta-defensin 2, *Deucra*=deucravacitinib, *ICO*=icotrokinra, *FC*=fold-change, *IL17A*=interleukin-17A gene, *IL17F*=interleukin-17F gene, *IL19*=interleukin-19 gene, *IL22*=interleukin-22 gene, *IL23A*=interleukin-23A gene, *NS*=not significant, *PBO*=placebo, *W*=week.

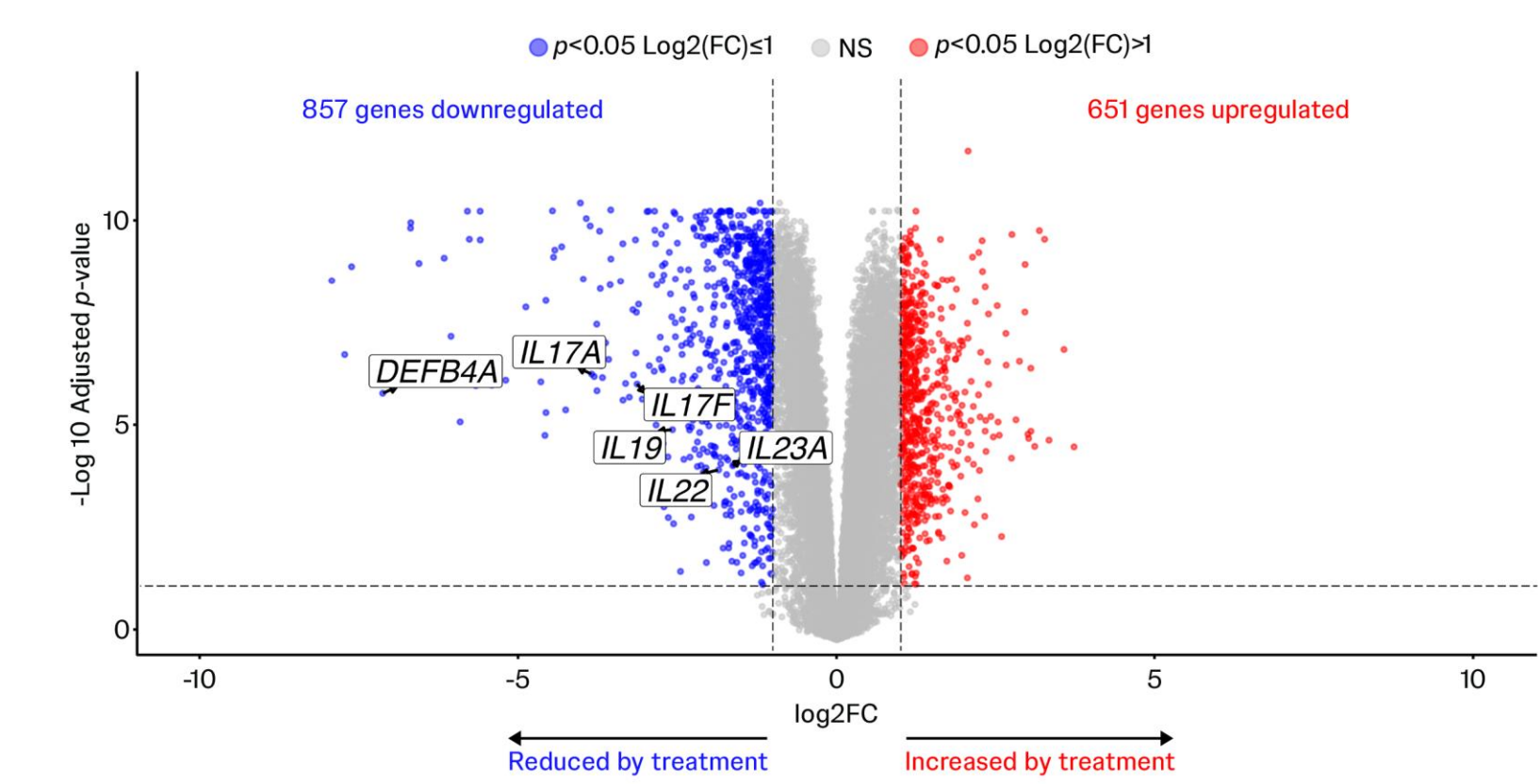
ICO induced transcriptional changes in lesional skin consistent with IL-23 pathway blockade and normalization of inflammation

- Transcriptomic profile of PsO-related gene sets^{6,7} was highly differentiated between lesional and non-lesional skin at baseline
- ICO shifted PsO-relevant gene set expression toward that of non-lesional skin, while Deucra effects were modest



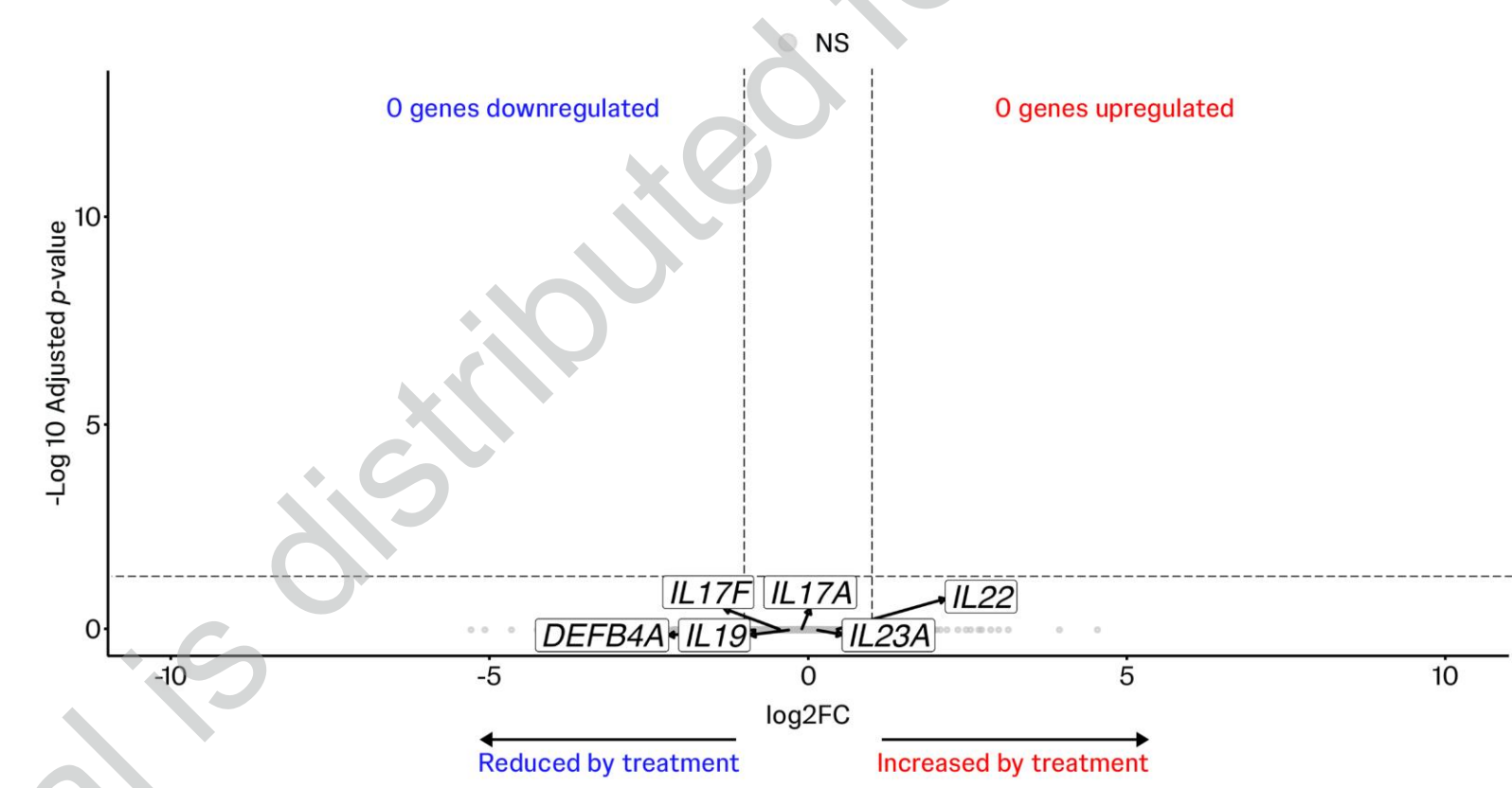
CD4=cluster of differentiation 4, *Deucra*=deucravacitinib, *ICO*=icotrokinra, *IFN*=interferon gamma, *IL*=interleukin, *MAD*=meta-analysis derived, *NF- κ B*=nuclear factor kappa B, *PBO*=placebo, *PD*=primary immunodeficiency, *PsO*=psoriasis, *Th17-1* helper T cell, *W*=week.

ICO elicited robust impact on PsO skin transcriptome (W16 lesional vs W0 lesional)



Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log2 counts ~ Tissue (lesional vs non-lesional), $p < 0.05$ for significance, and log2FC ≥ 1 and ≤ -1 for downregulation and upregulation cut-off, respectively. Based on all paired samples within the complete sample set: N=32 (ICO), N=19 (Deucra), N=11 (PBO). *DEFB4A*=gene that encodes human beta-defensin 2, *Deucra*=deucravacitinib, *ICO*=icotrokinra, *FC*=fold-change, *IL17A*=interleukin-17A gene, *IL17F*=interleukin-17F gene, *IL19*=interleukin-19 gene, *IL22*=interleukin-22 gene, *IL23A*=interleukin-23A gene, *NS*=not significant, *PBO*=placebo, *W*=week.

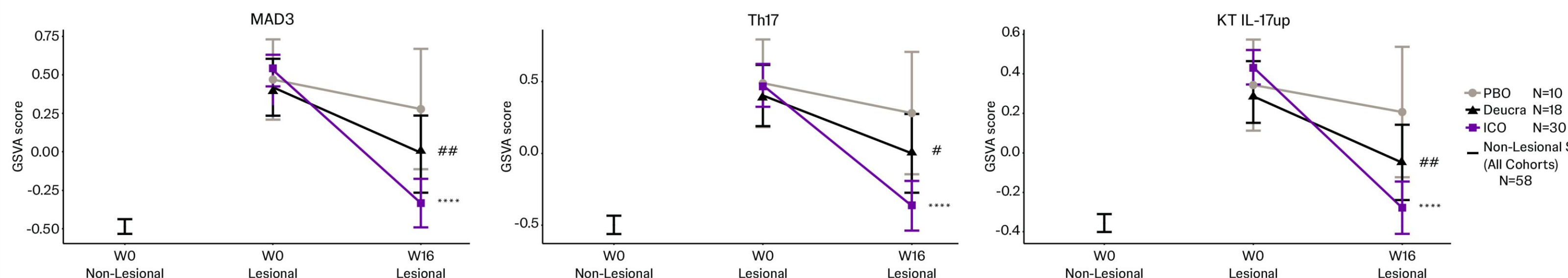
PBO elicited no impact on PsO skin transcriptome (W16 lesional vs W0 lesional)



Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log2 counts ~ Tissue (lesional vs non-lesional), $p < 0.05$ for significance, and log2FC ≥ 1 and ≤ -1 for downregulation and upregulation cut-off, respectively. Based on all paired samples within the complete sample set: N=32 (ICO), N=19 (Deucra), N=11 (PBO). *DEFB4A*=gene that encodes human beta-defensin 2, *Deucra*=deucravacitinib, *FC*=fold-change, *ICO*=icotrokinra, *IL17A*=interleukin-17A gene, *IL17F*=interleukin-17F gene, *IL19*=interleukin-19 gene, *IL22*=interleukin-22 gene, *IL23A*=interleukin-23A gene, *NS*=not significant, *PBO*=placebo, *W*=week.

ICO reduced PsO- and Th17-related gene set expression in lesional skin at W16 to a greater degree than Deucra

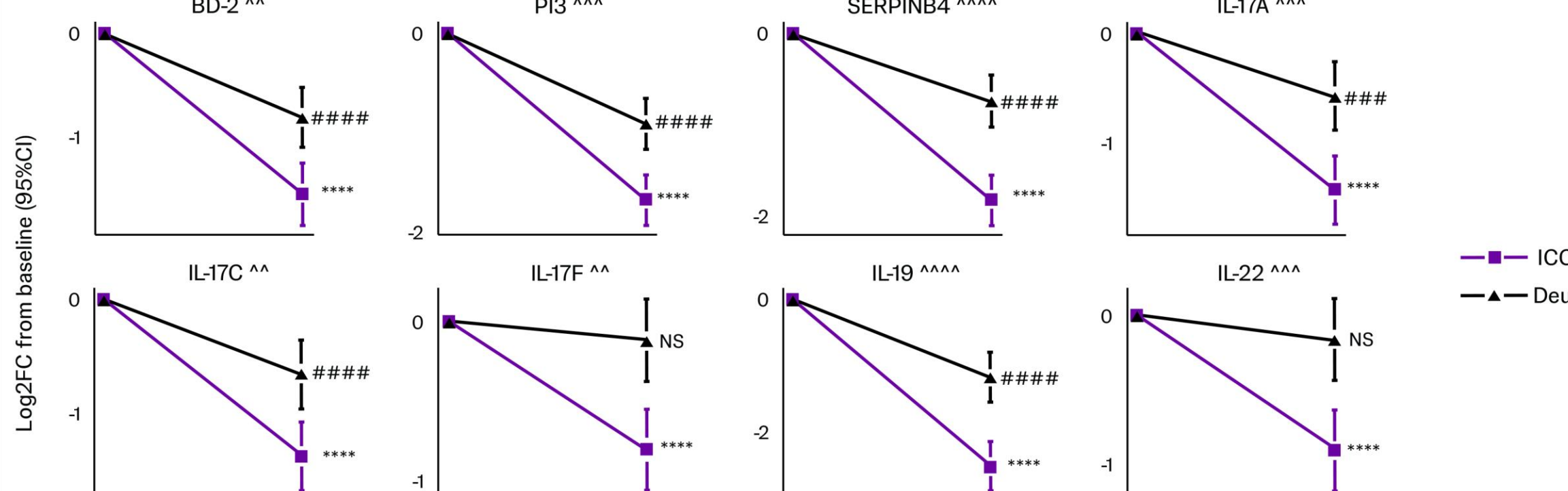
- ICO significantly reduced *MAD3*, *Th17*, and *KT-IL17* gene sets³⁻⁵ in lesional skin at W16 compared to baseline to a greater degree than PBO and Deucra and normalized towards non-lesional levels
- Comparison of gene set expression level at W16: significantly lower with ICO vs PBO ($p < 0.001$) and ICO vs Deucra ($p < 0.05$), with no significant difference between Deucra vs PBO ($p \geq 0.05$)



*significant change of ICO W16 vs W0, *significant change of Deucra W16 vs W0, ** p -value < 0.05 , *** p -value < 0.01 , **** p -value < 0.001 , ***** p -value < 0.0001 , *Deucra*=deucravacitinib, *GSEA*=gene set variation analysis, *ICO*=icotrokinra, *IL*=interleukin, *KT*=keratinocyte, *MAD*=meta-analysis derived, *PBO*=placebo, *PsO*=psoriasis, *Th17-1* helper T cell, *W*=week.

ICO reduced serum PsO markers to a greater extent than Deucra

- ICO significantly reduced serum PsO markers at W24
- Deucra significantly reduced some serum PsO markers from W0, although not IL-17F and IL-22, at W24



*significant change of ICO W24 vs W0, *significant change of Deucra W24 vs W0, *significant difference between treatments at W24, ** p -value < 0.05 , *** p -value < 0.01 , **** p -value < 0.001 , ***** p -value < 0.0001 , *BD-2*=beta-defensin-2, *CI*=confidence interval, *Deucra*=deucravacitinib, *ICO*=icotrokinra, *IL*=interleukin, *NS*=not significant, *PI3*=peptidase inhibitor 3 (lelpin), *SERPINB4*=serpin family B member 4, also known as squamous cell carcinoma antigen 2, *W*=week.