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

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This presentation was sponsored by Johnson & Johnson.

Presented by Richard B. Warren at American Academy of Dermatology (AAD) Annual Meeting; March 27–31, 2026; Denver, CO, USA

Disclosures

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Background



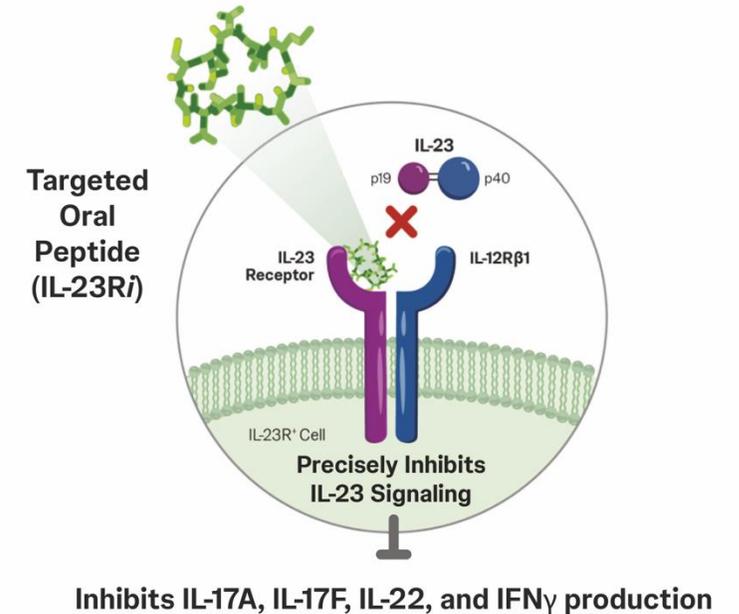
Icotrokinra (ICO) is the first and only targeted oral peptide for plaque psoriasis (PsO) that precisely binds the interleukin-23 receptor (IL-23R) and **inhibits IL-23 pathway signaling**¹



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
 - IGA 0/1: 68% (ICO) vs 11% (PBO)
 - 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

Icotrokinra Blocks IL-23 From Binding to its Receptor



Objectives



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

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ICONIC-ADVANCE 1 Study Design

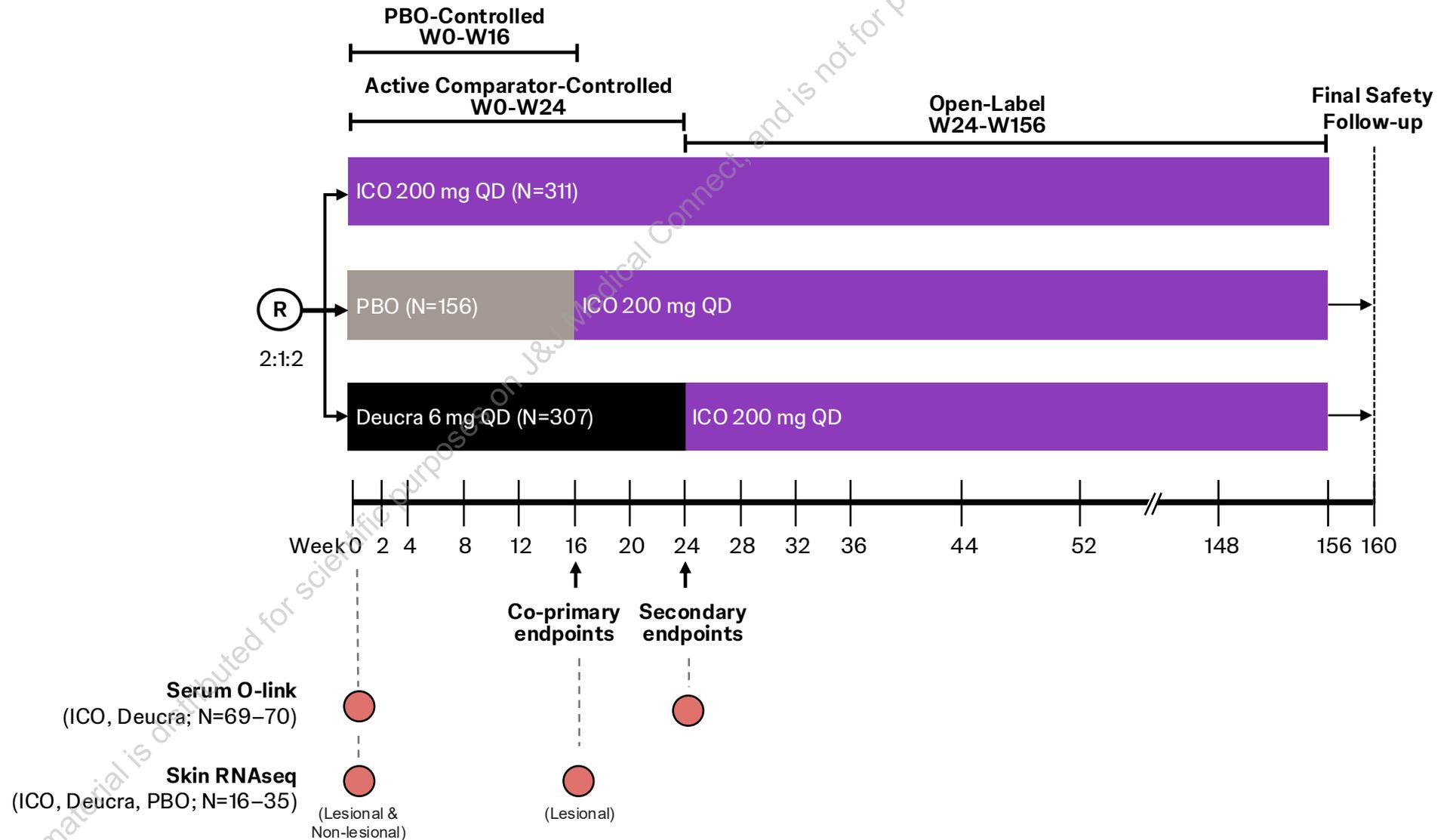
Moderate-to-severe plaque PsO (N=774)

Key inclusion criteria

- ≥18 years
- Plaque PsO for ≥26 weeks
- Body surface area (BSA) ≥10%, Psoriasis Area and Severity Index (PASI) score ≥12, and Investigator's Global Assessment (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



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:

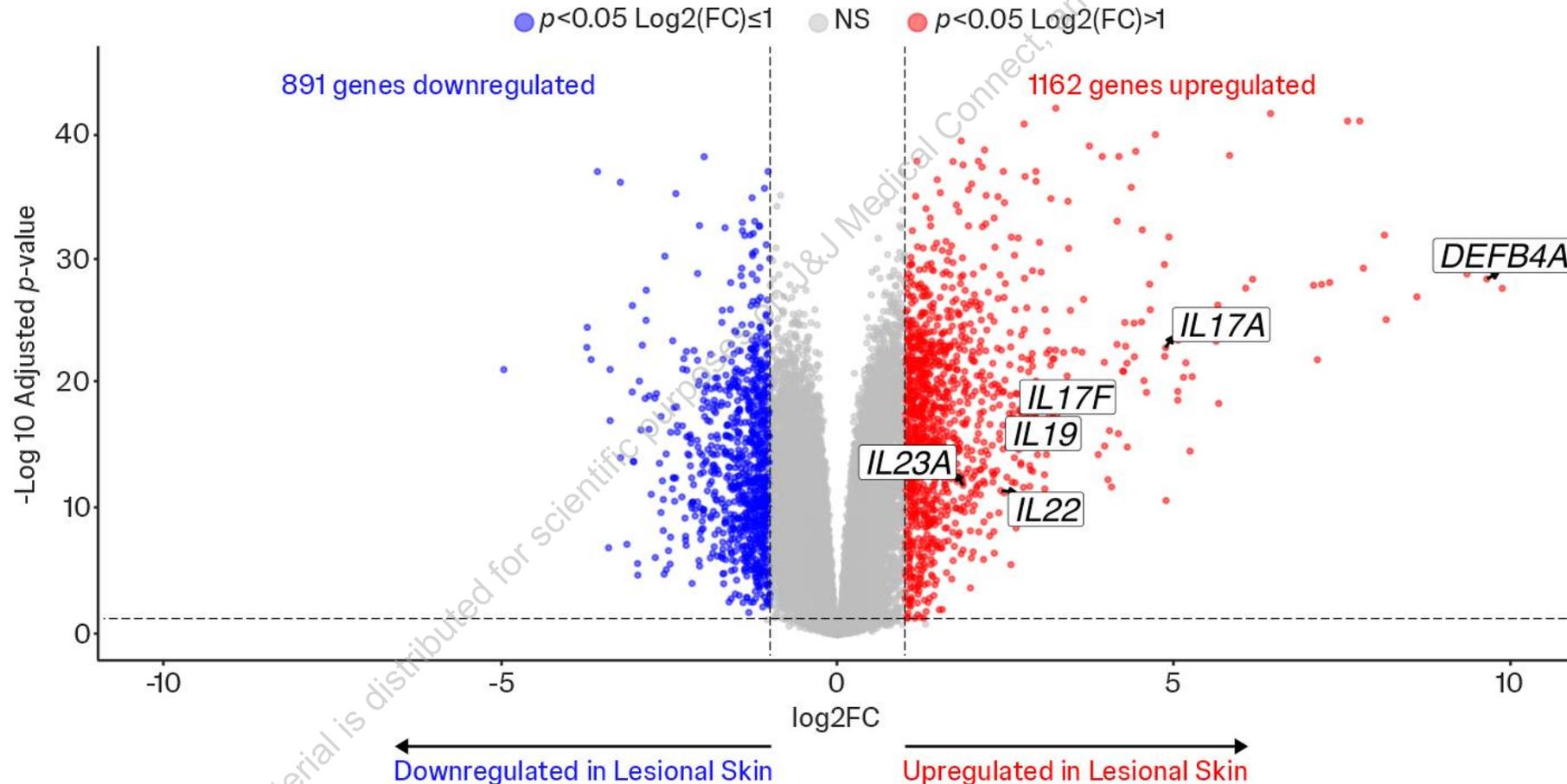
- W0 and W24 serum samples from a sub-cohort of 70 ICO- and 69 Deucra-treated participants were analyzed
- Serum samples from a separate healthy cohort of 22 subjects were included as a control group
- Serum samples: Analyzed for PsO-relevant biomarkers using O-link proteomic platform

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-variates 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

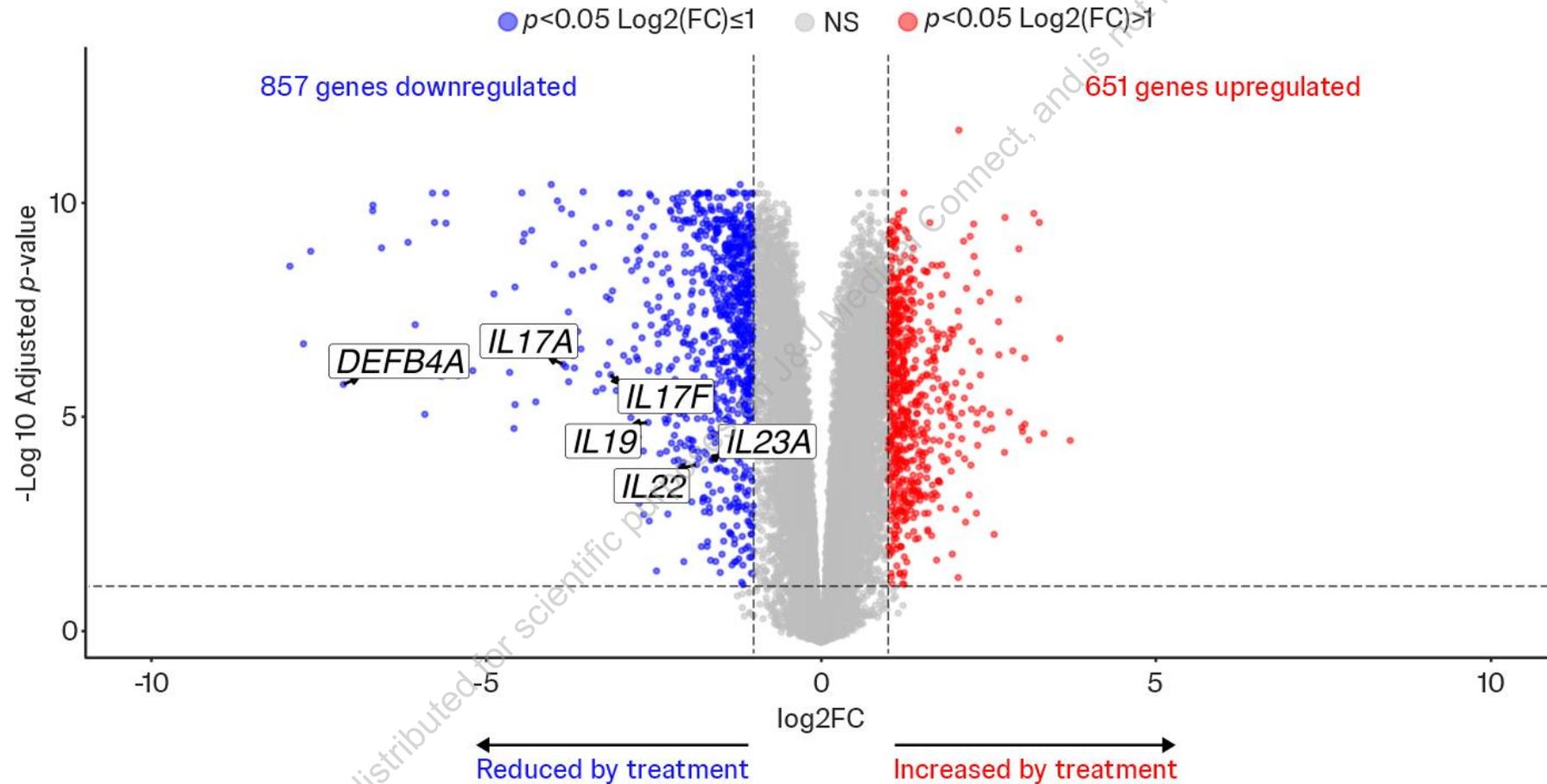
Baseline lesional and non-lesional skin exhibited highly differentiated transcriptomic profiles

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



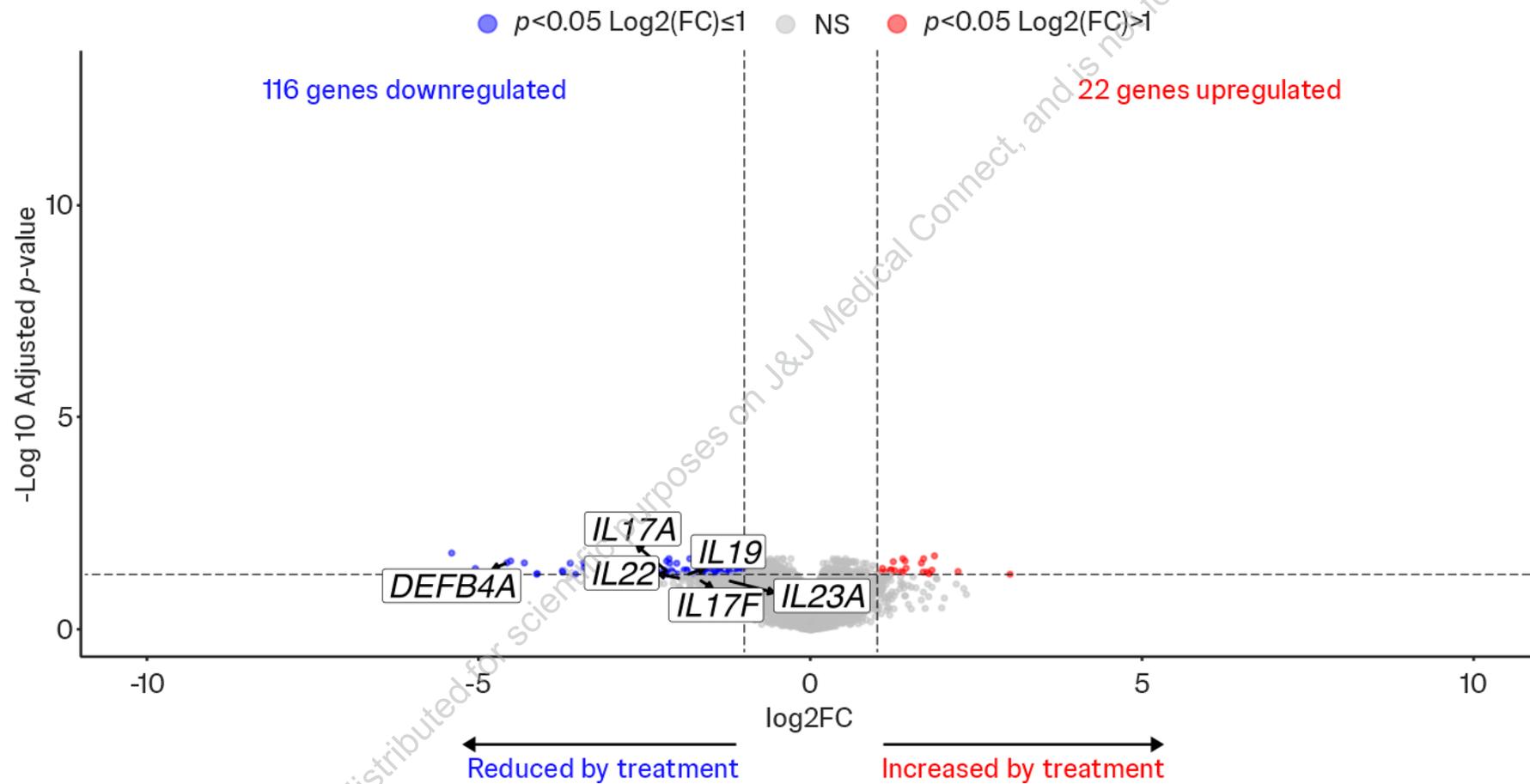
Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log₂ counts ~ Tissue (lesional vs non-lesional). $p < 0.05$ for significance, and $\text{log}_2\text{FC} \leq 1$ and > 1 for downregulation and upregulation cut-off, respectively. 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.

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



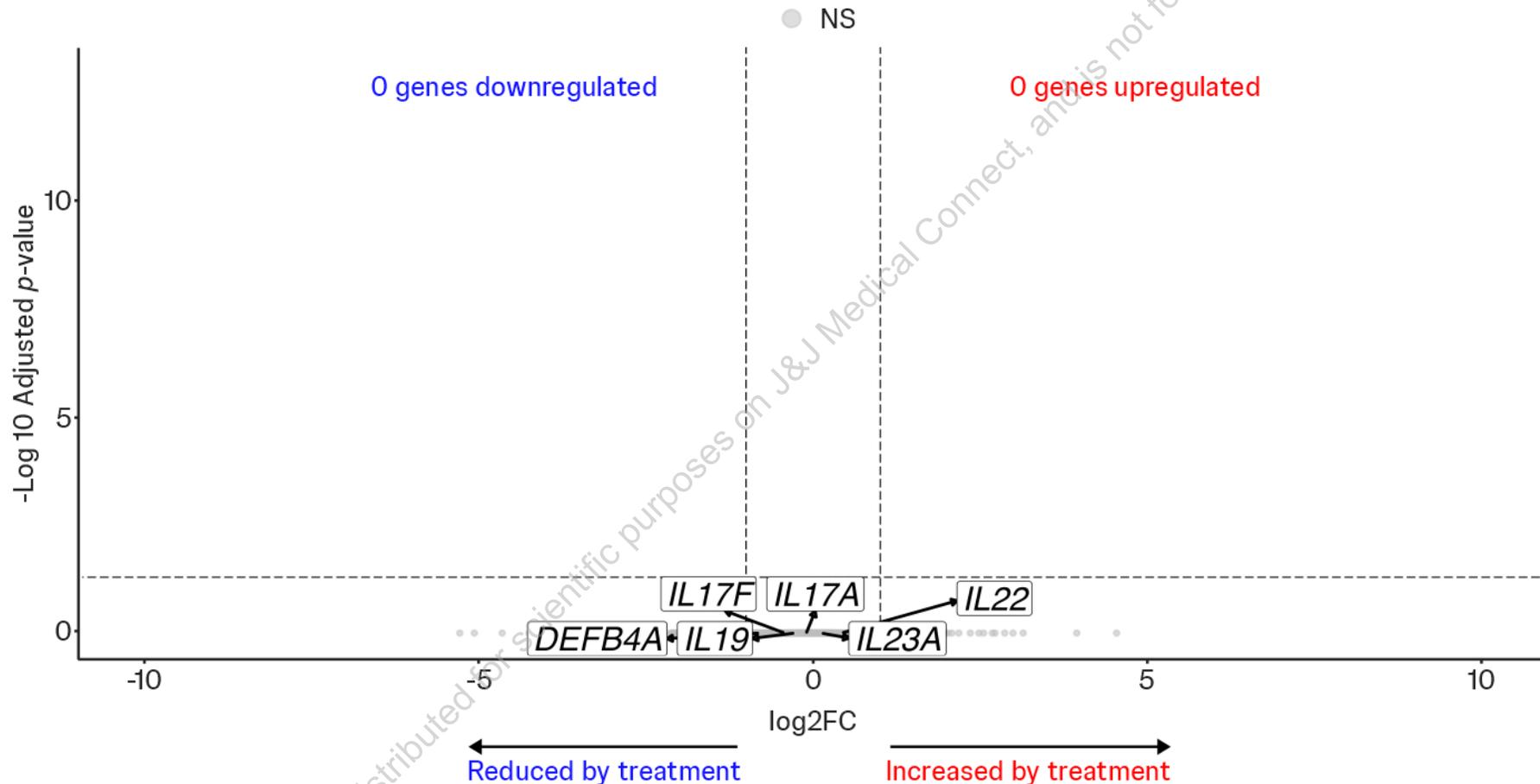
Statistical models were determined for gene set based on simple linear mixed effects model based on limma-voom normalized log_2 counts \sim Tissue (lesional vs non-lesional). $p < 0.05$ for significance, and $\text{log}_2\text{FC} \leq 1$ and > 1 for downregulation and upregulation cut-off, respectively. 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.

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 $\text{log}_2\text{FC} \leq 1$ 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.

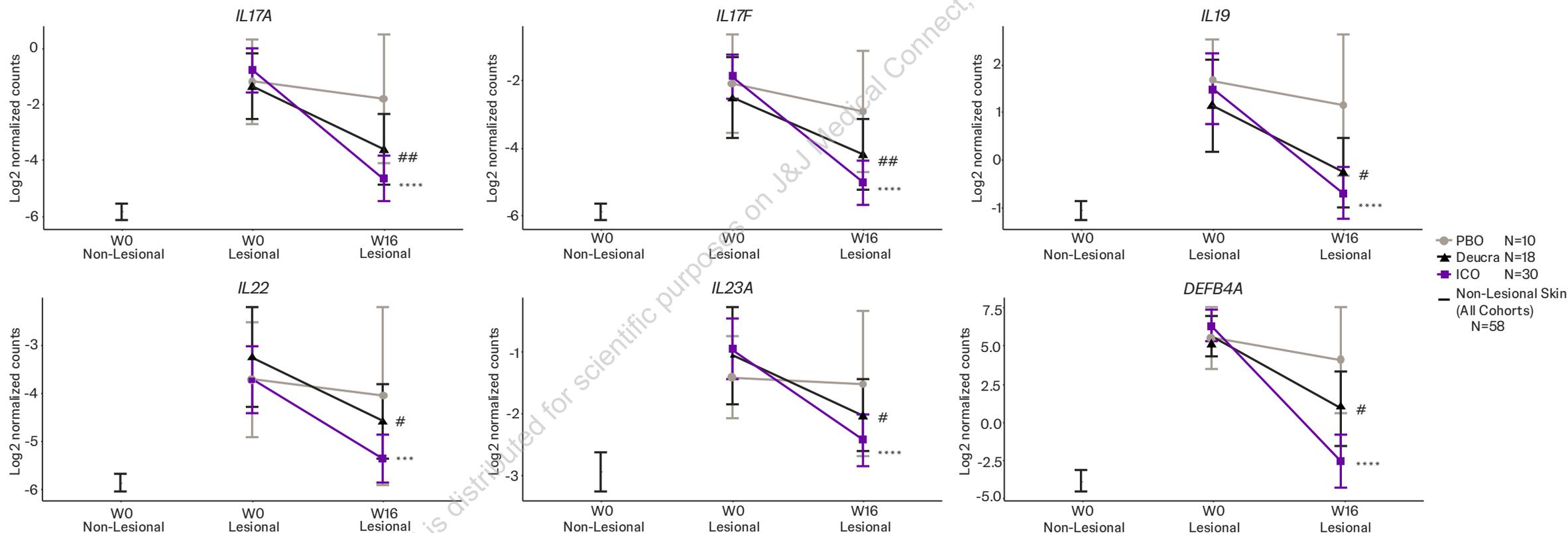
PBO elicited no impact on PsO skin transcriptome (W16 lesional vs W0 lesional)



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 $\log_2FC \leq 1$ 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-related gene expression in lesional skin towards non-lesional levels at W16

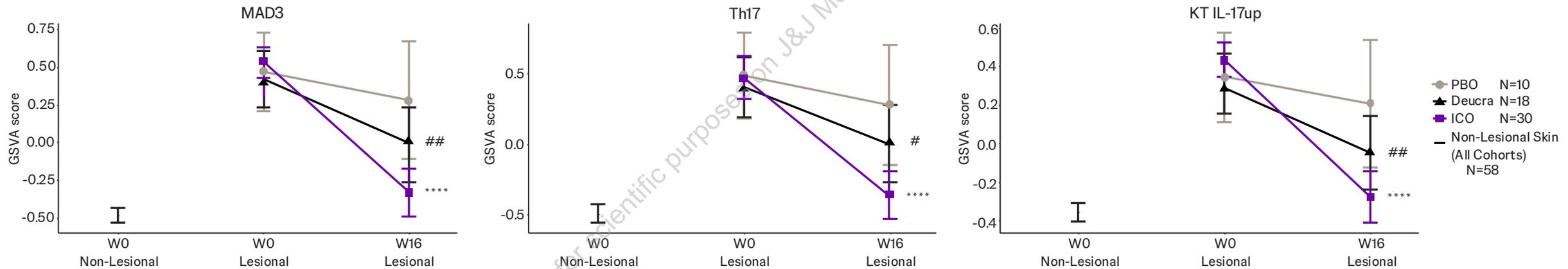
- ICO significantly reduced numerous PsO-related genes, including *IL17A*, *IL17F*, *IL19*, *IL22*, *IL23A*, and *DEFB4A*
- ICO-induced decrease of gene expression was more robust, as reflected by lower *p* values, than the Deucra-induced decrease



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

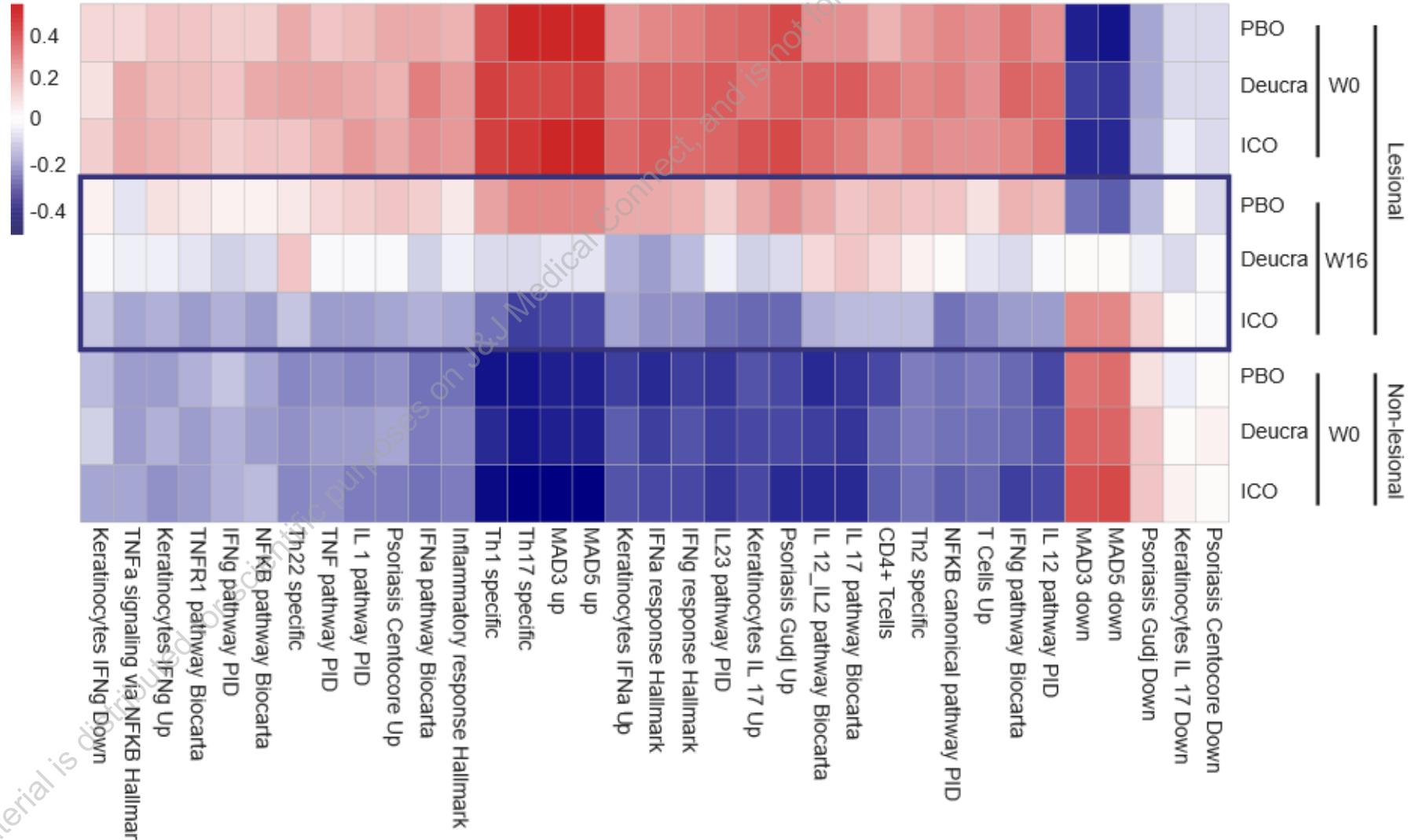
- ICO significantly reduced MAD3, Th17, and KT IL-17 gene sets³⁻⁵ in lesional skin at W16 compared to baseline to a greater degree than PBO and Deucra and normalized towards non-lesional levels
- Comparison of gene set expression level at W16: significantly lower with ICO vs PBO ($p < 0.001$) and ICO 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, **GSVA**=gene set variation analysis, **ICO**=icotrokinra, **IL**=interleukin, **KT**=keratinocyte, **MAD**=meta-analysis derived, **PBO**=placebo, **PsO**=psoriasis, **Th17**=T helper 17 cell, **W**=week.

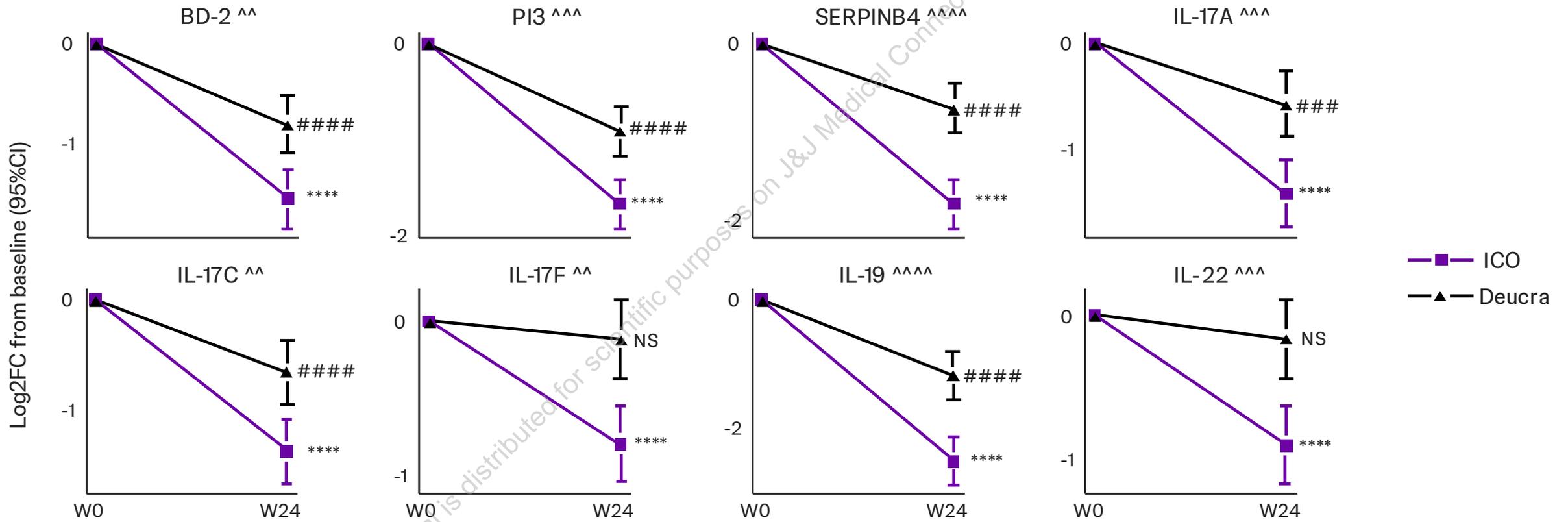
ICO induced transcriptional changes in lesional skin consistent with IL-23 pathway blockade and normalization of inflammation

- 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



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. ICO=iclotrokinra, BD-2=beta-defensin-2, CI=confidence interval, Deucra=deucravacitinib, IL=interleukin, NS=not significant, PI3=elafin, SERPINB4=protein within the SERPIN family also known as squamous cell carcinoma antigen 2, W=week.

Key Takeaways

- ✓ **ICO demonstrated *substantial* PD effects, with levels of IL-23 pathway biomarkers for systemic and skin inflammation normalized towards healthy levels**
- ✓ **Skin transcriptomic data showed:**
 - ✓ **ICO reduced PsO skin and PD biomarkers at W16 compared to PBO**
 - ✓ **ICO normalized skin inflammation towards baseline non-lesional skin at W16**
 - ✓ **ICO elicited more robust effects on PsO and PD markers compared to Deucra**
- ✓ **Serum protein data demonstrated:**
 - ✓ **ICO reduced PsO serum biomarkers at W24 to a greater degree than Deucra**
- ✓ **These comprehensive biomarker findings are consistent with significant skin clearance² achieved with this first and only targeted oral peptide that precisely binds the IL-23R and inhibits the IL-23 pathway signaling. The more robust PD effects of ICO vs Deucra are consistent with superior clinical activity of ICO vs Deucra²**

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Acknowledgements

This presentation was sponsored by Johnson & Johnson. Medical writing support was provided by Denise Balog, PharmD (inSeption Group), funded by Johnson & Johnson and Harry Ma, PhD (Johnson & Johnson) under the direction of the authors in accordance with Good Publication Practice guidelines (*Ann Intern Med.* 2022; 175:1298–1304). Poster layout was performed by Sandeep Chavan (SIRO Medical Writing Pvt Ltd), funded by Johnson & Johnson.

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