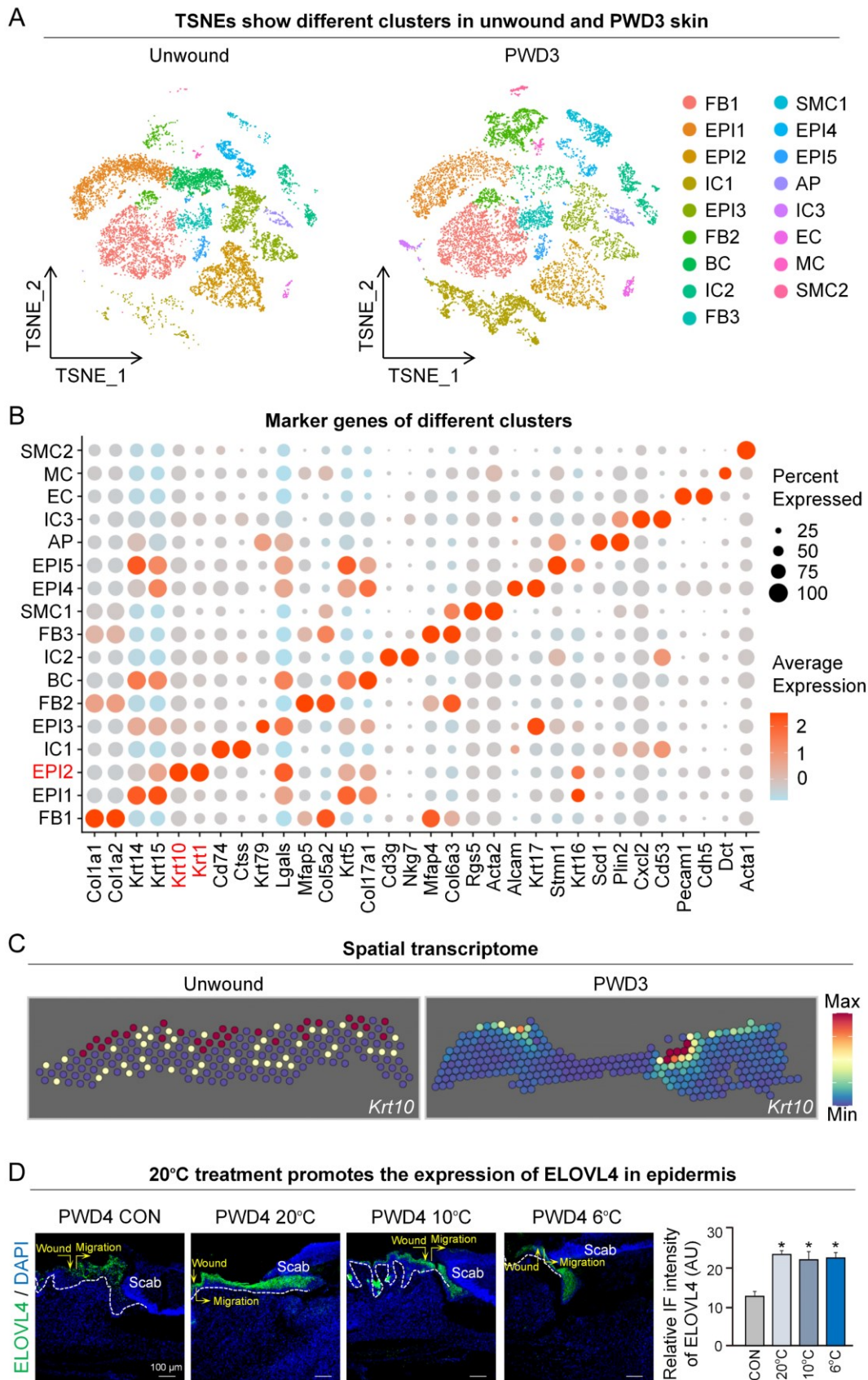




- 5 B. String analysis shows skin development-related genes were enriched in the 20°C-treatment
- 6 group on PWD4.



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8 **Figure S2. Single cell RNA-sequencing analysis of skin wound.**

- 9 A. TSNEs show different clusters in the unwound and PWD3 groups.
- 10 B. DotPlot shows marker genes of different clusters.
- 11 C. ST-seq shows marker genes of the epidermis.
- 12 D. Immunostaining shows ELOVL4 expression in the Control, 20°C-treatment, 10°C-
- 13 treatment, and 6°C-treatment group. Statistics of average FI of ELOVL4. Scale bars, 100µm.
- 14  $N \geq 5$ , \* $p < 0.05$ .

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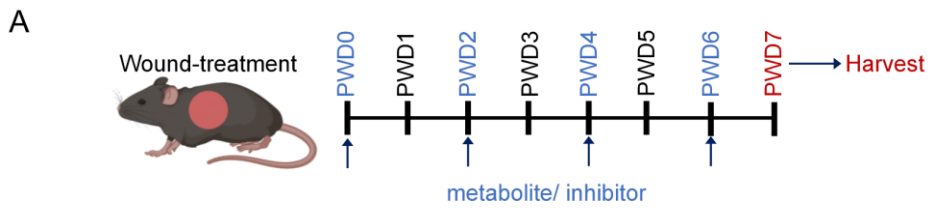
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32 **Figure S3. Functional study of Elovl4-EPA/DHA.**

33 A. Schematic shows experimental design.

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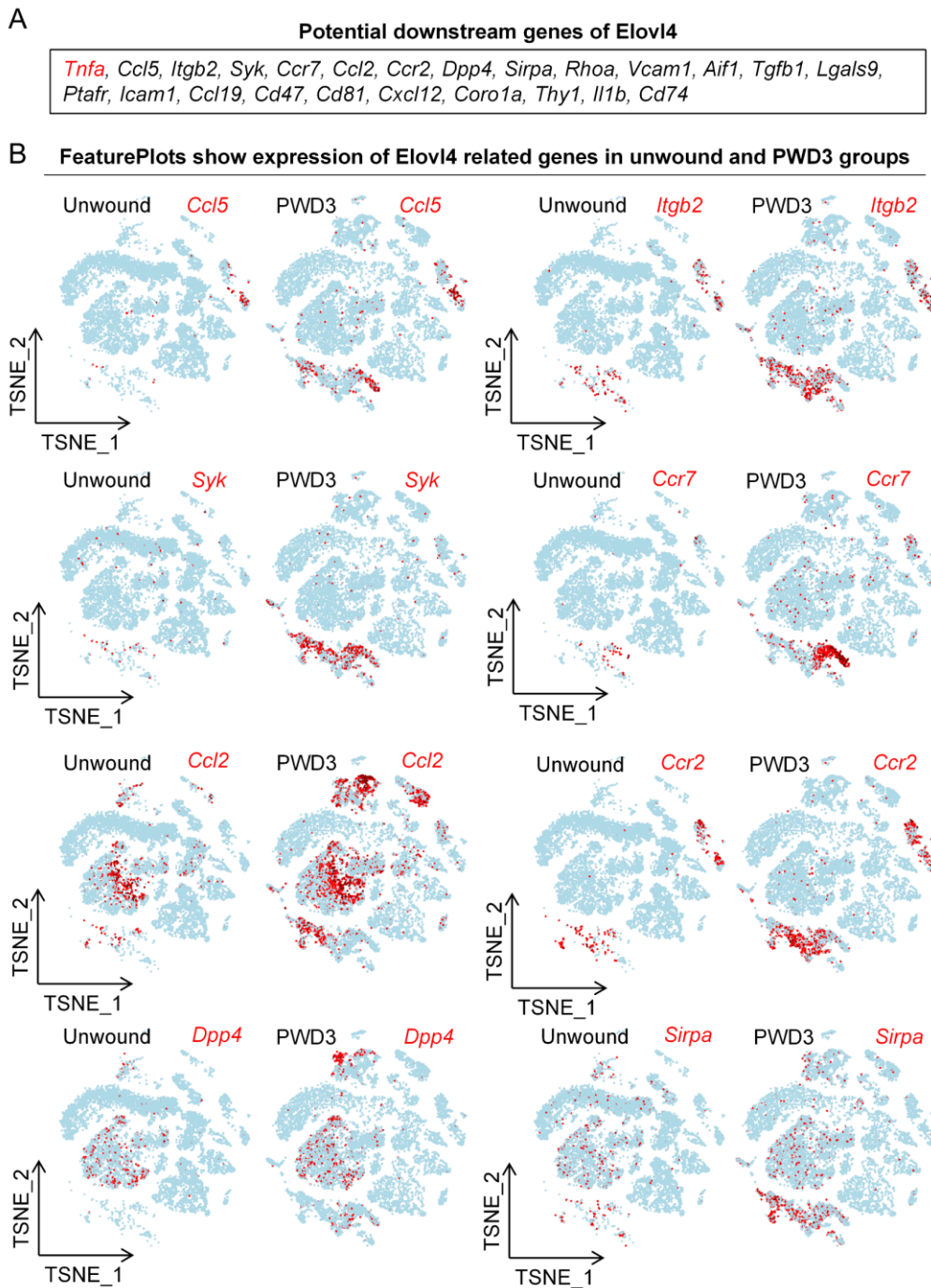
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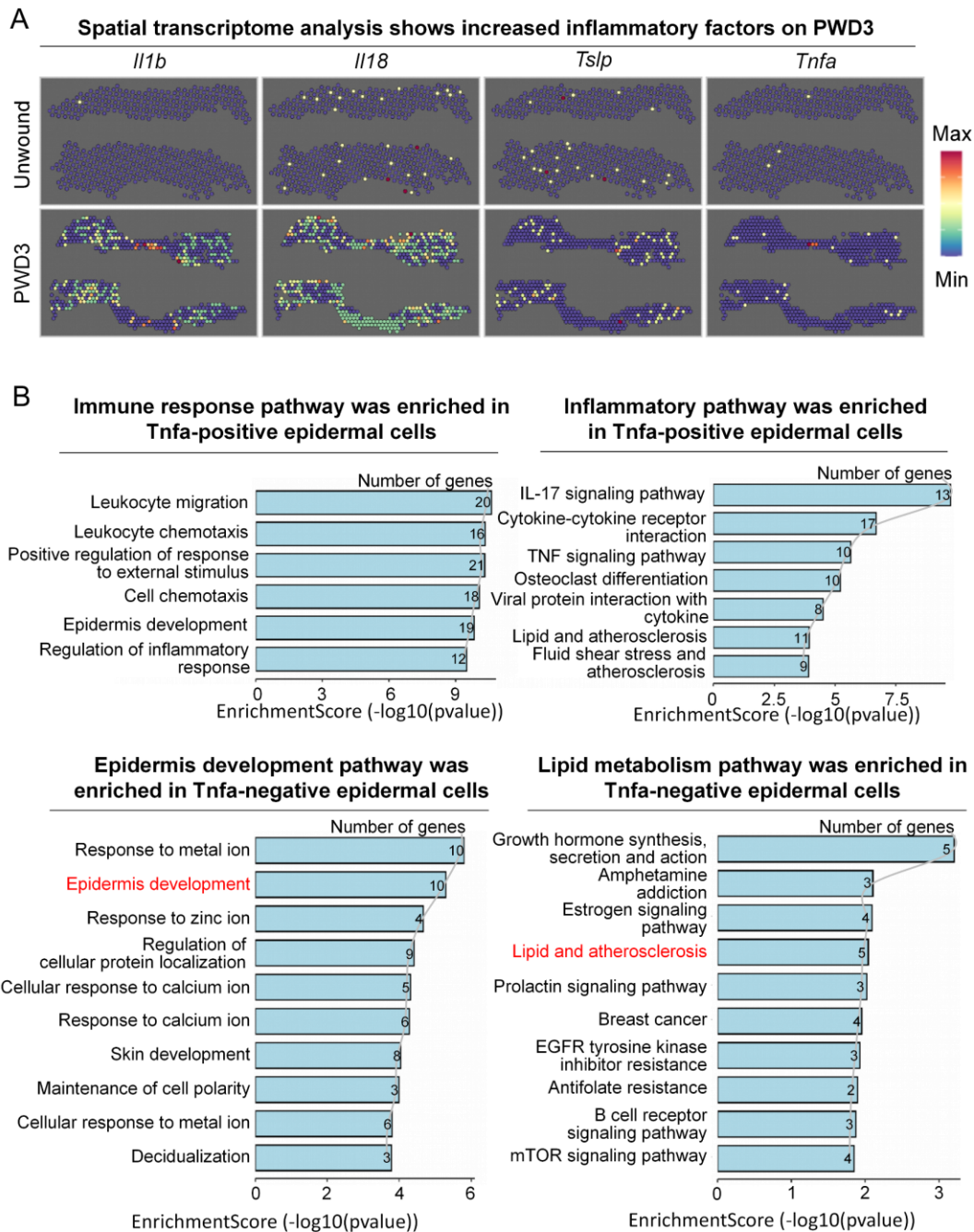
51 **Figure S4. Downstream analysis of Elov14.**

52 A. A list of the top 5 ranked genes according to their P-values.

53 B. FeaturePlots show expression of Elov14-related genes in unwound and PWD3 groups.

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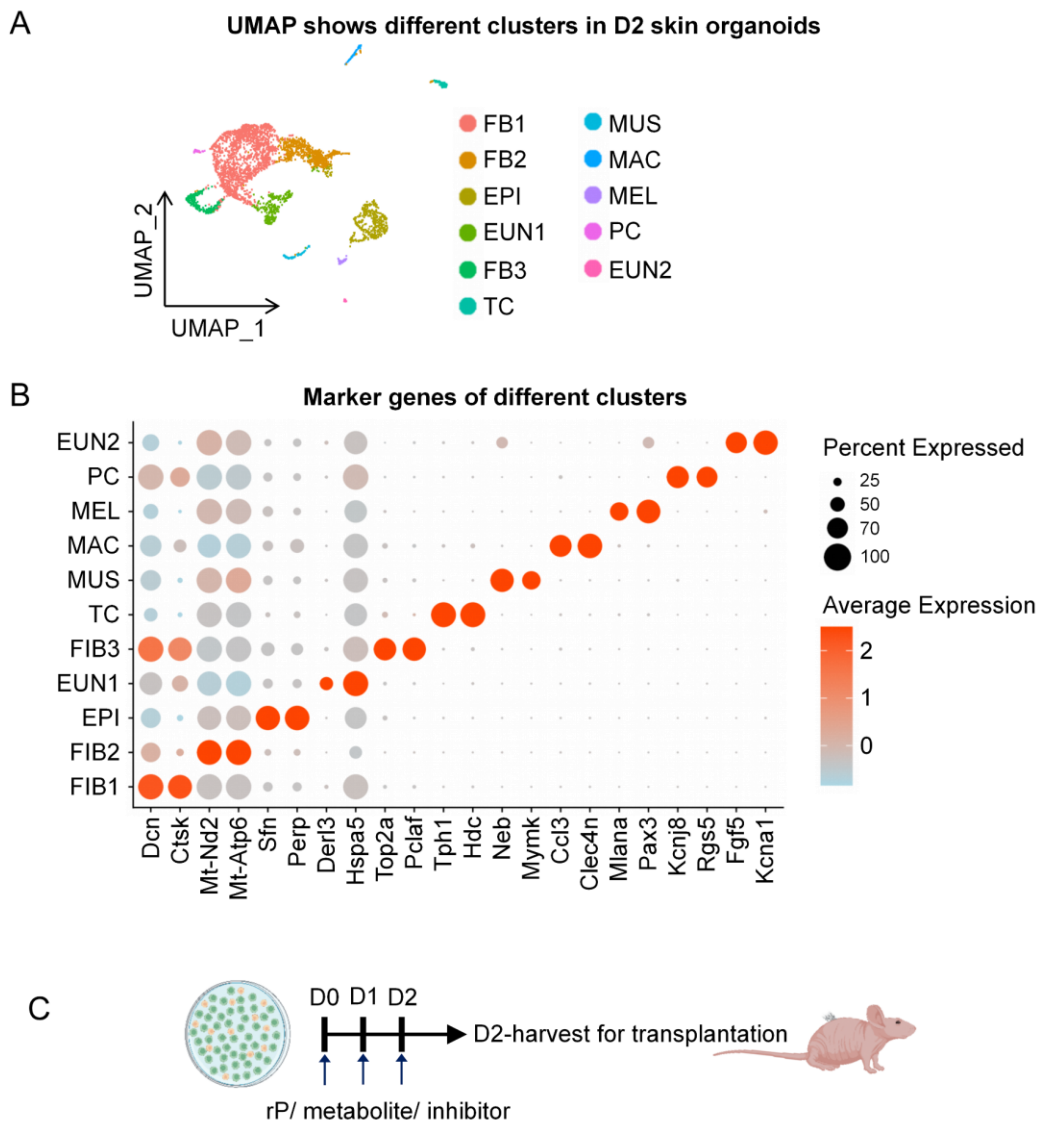
57 **Figure S5. Identification of inflammatory factors.**

58 A. ST-seq shows expression of inflammatory factors in unwound and PWD3 groups.

59 B. GO and KEGG analysis shows enriched immune response pathways in TNF $\alpha$  positive

60 epidermal cells. Epidermis development and lipid metabolism are enriched in the TNF $\alpha$ -

61 negative cells.



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63 **Figure S6. Single cell RNA-seq analysis of skin organoids.**

64 A. UMAP shows different clusters in D2 skin organoids.

65 B. Dotplot shows marker genes of different clusters.

66 C. Schematic shows experimental design.

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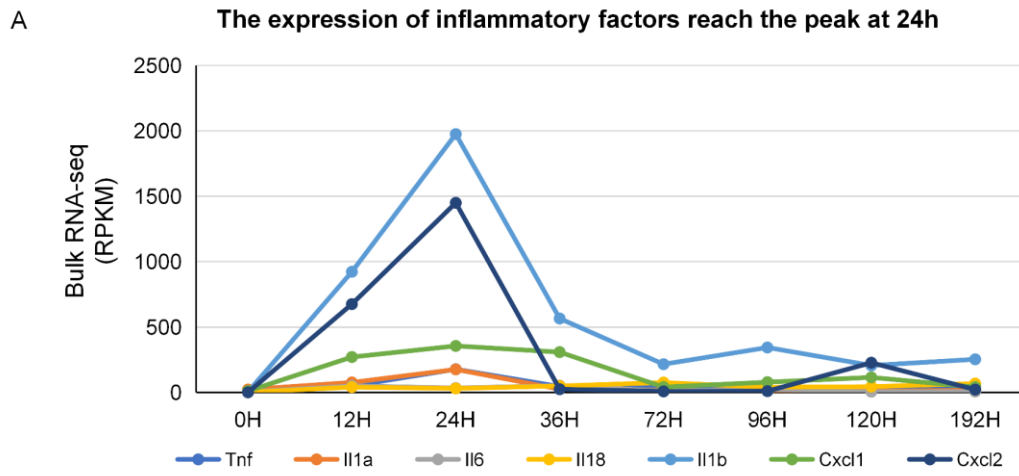
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71 **Figure S7. Bulk RNA-seq analysis of skin wound.**



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73 A. Line chart shows expressions of different inflammatory factors in PWD0-PWD8.

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