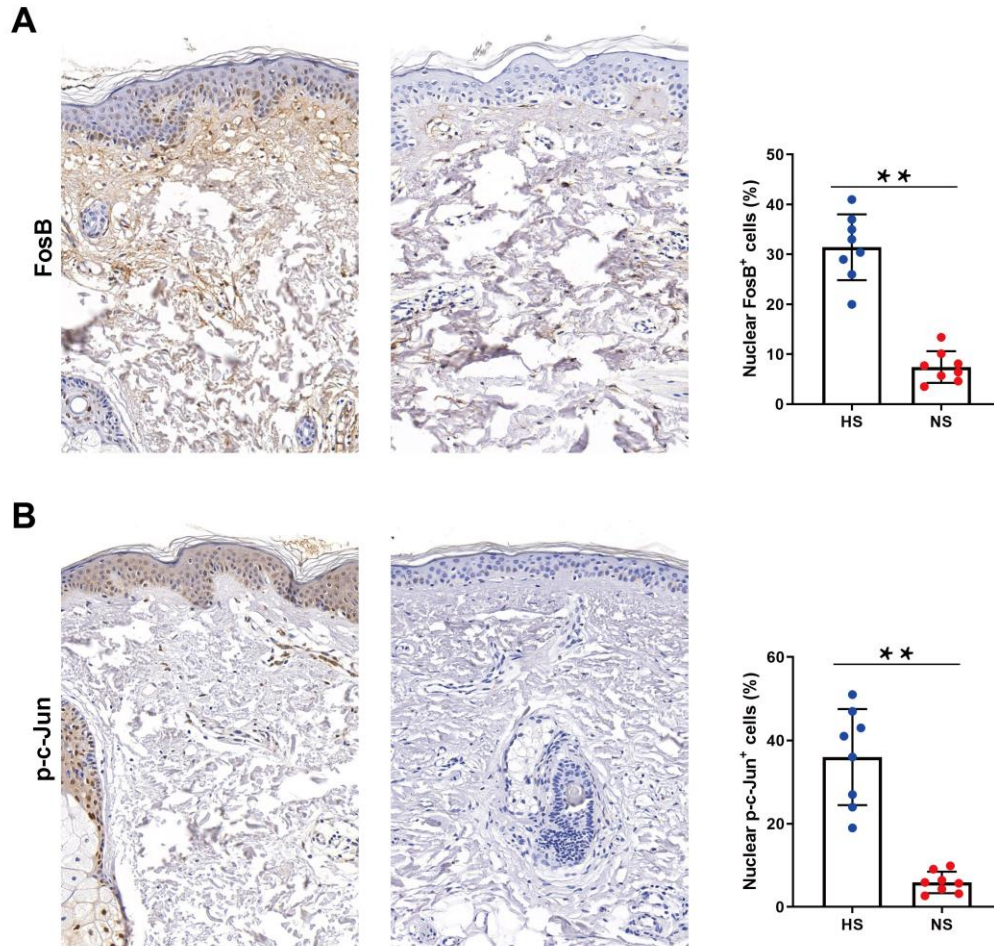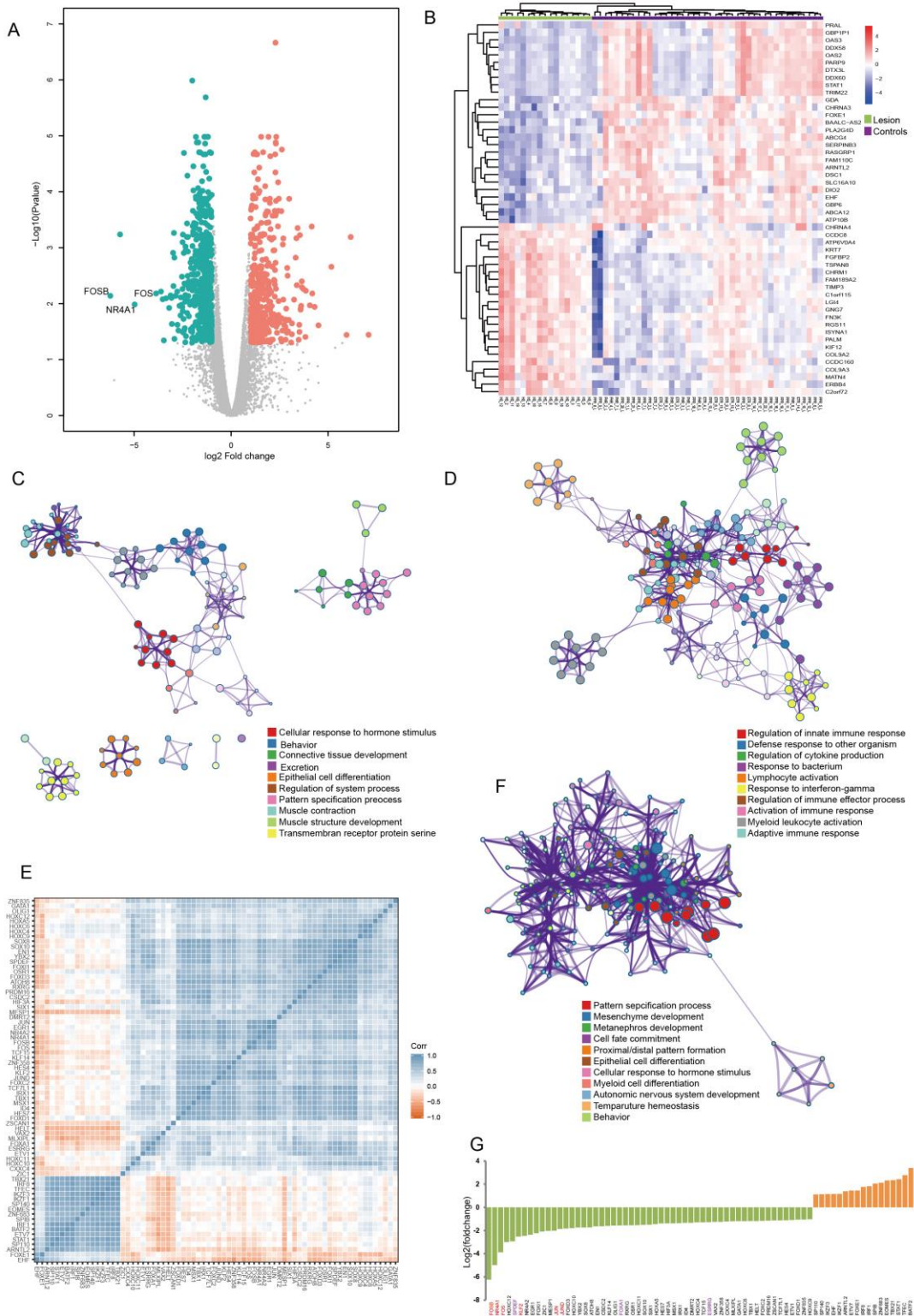# Supplementary figures and figure legends

Supplementary Figure S1. **Transcription factors (TFs) related to transcriptional profiling in central facial skin.** Immunohistochemistry staining for validation of FosB and p-c-Jun. HS, healthy skin (n = 8). NS, normal skin surrounding the auricle in rosacea patients (n = 8). Right panel, the quantification of nuclear localization of FosB and p-c-Jun. Data represent the mean ± SEM. **P < 0.01. 2-tailed unpaired Student's t-test was used.

Supplementary Figure S2. Transcriptional profiling in rosacea lesions as compared with central facial skins from health volunteers

A. Volcano plot for the differentially expressed genes (DEGs) in rosacea lesions (LS, N=42) compared with central facial skins (HS N=17) from

healthy volunteers. The upregulated genes in rosacea lesions are in red and downregulated genes are in green. Genes without significant diversity are in gray.

B. Heatmap generated using the top 50 DEGs in comparing LS vs HS.

C. Metascape network analysis of intra-cluster redundancies and inter-cluster similarities of enriched GO terms and pathways for downregulated genes.

D. Metascape network analysis of enriched GO terms and pathways for upregulated genes.

E. Correlation heatmap of significant correlation for expression of all 72 transcription factors.

F. Metascape network analysis of enriched GO terms and pathways for transcription factors.

G. Log2 fold change values for the different expression of all 72 transcription factors with downregulated expression of AP1 TFs (FOS, FOSB, JUN, and JUND).

Supplementary Figure S3. Transcriptional profiling in rosacea lesions as compared with matched skin surrounding the auricle

A. Volcano plot for the DEGs between rosacea lesions (LS) and matched skin surrounding the auricle (NS, N=42).

B. Heatmap of the top 50 DEGs between rosacea lesions (purple color bar) and matched skin surrounding the auricles (green color bar).

C. Metascape network analysis of GO terms and pathways enriched for downregulated genes, indicating genes involved in biological processes of skin development, neuroactive ligand-receptor interaction and chemical synaptic transmission.

D. Metascape network analysis of the GO terms and pathways enriched for upregulated genes, mainly involved in biological processes of response to bacterium and metabolism of lipids.

E. Correlation heatmap of significant correlation for expression of all 94 transcription factors.

F. Metascape network analysis of transcription factors highlighting the pattern specification process.

G. Log2 fold change values for the different expression of all 94 transcription factors.
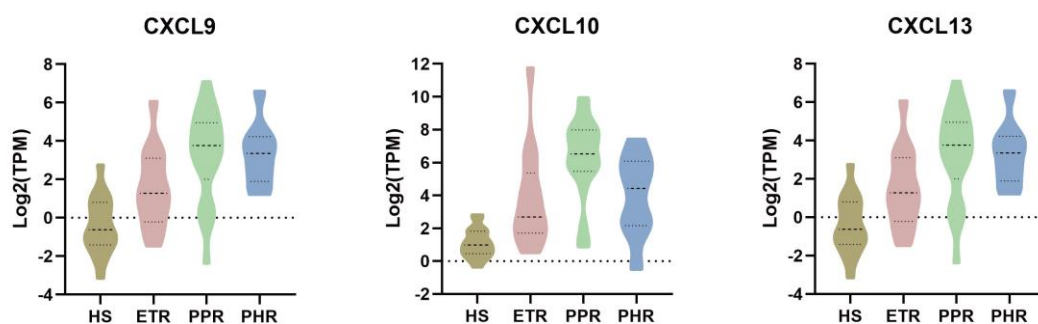
Supplementary Figure S4. Violin plots showing CXCL9, CXCL10 and CXCL13 expression in rosacea lesions (LS, N=42) compared with central facial skins (HS N=17) from healthy volunteers.

PHR

Rabbit IgG
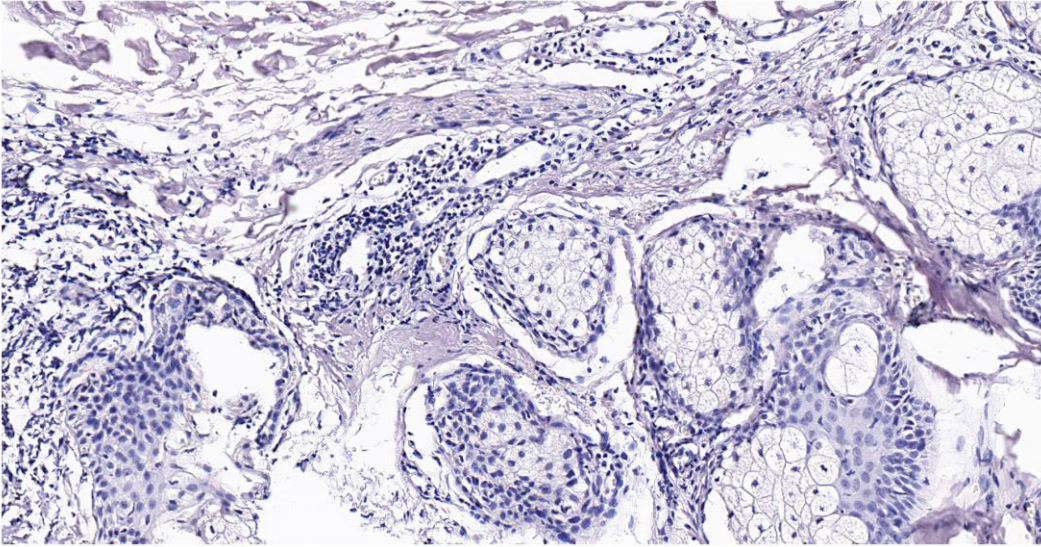
Supplementary Figure S5. Immunohistochemistry staining for rabbit IgG in PHR skin lesion as the negative control.