Supplementary materials:

Screening and identification of versican as a sensitive biomarker and potential therapeutic target in basal cell carcinoma

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Supplementary Figure 1. Heat maps and volcano plots of DEGs. **A:** GSE34535; **B:** GSE34137;

C: GSE125285; **D:** GSE42109.

A

B

C

D
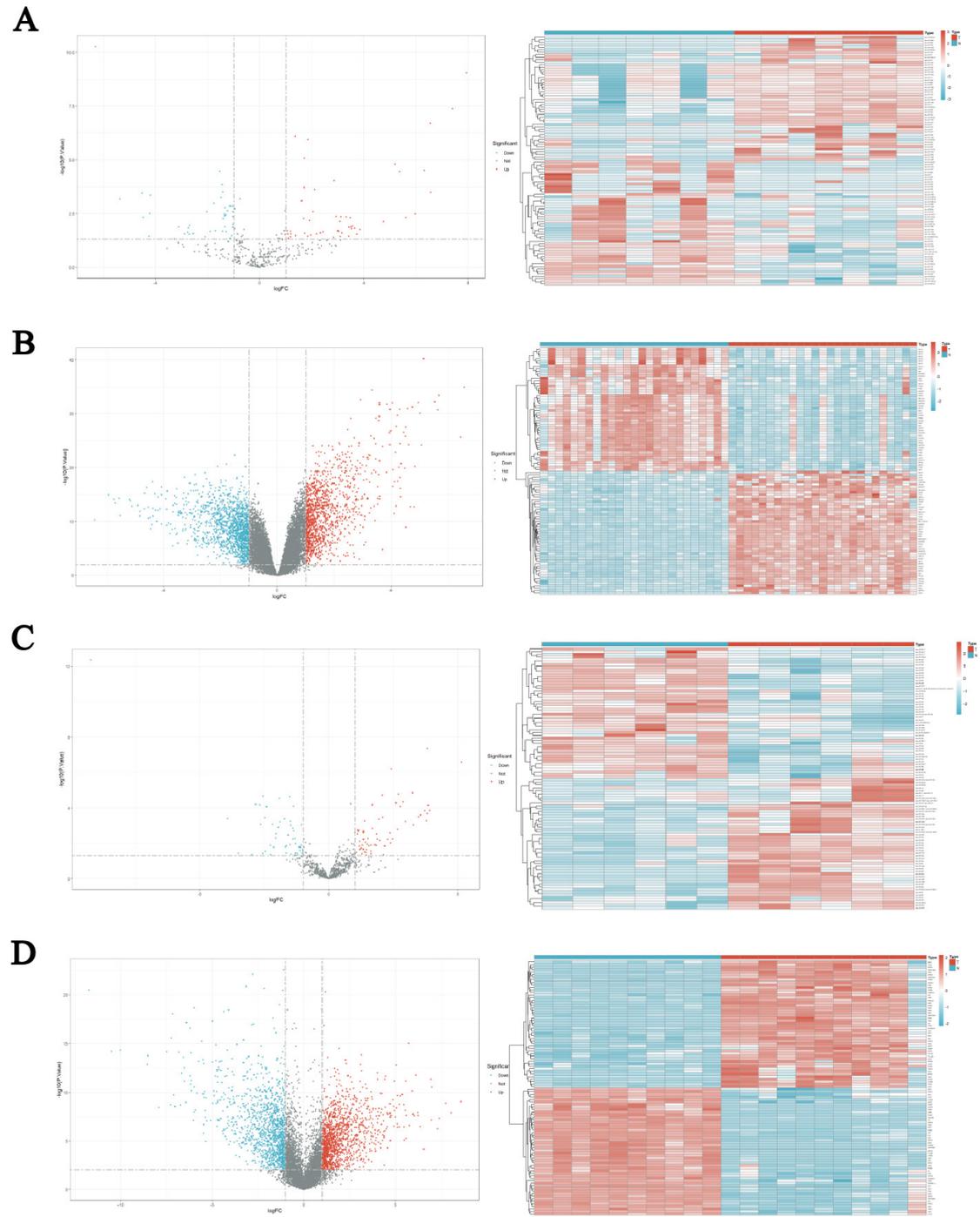
Supplementary Figure 2. GSEA plot showing the most enriched BCC-related genes sets in the dataset GSE125285 and GSE42109. From left to right**:** Gene set enrichment analysis: PID HEDGEHOG 2PATHWA; Gene set enrichment analysis: MURAKAMI UV RESPONSE 24HR; Gene set enrichment analysis: REACTOME GEHOG ON STATE; Gene set enrichment analysis: KEGG HEDGEHOG SIGNALING PATHWAY; Gene set enrichment analysis: HP BASAL CELL CARCINOMA (above: GSE125285, below: GSE42109). The screening criteria for significant gene sets were $P < 0.05$ and $Q < 0.25$. NES: normalized enrichment score; P-vale: also named False Discovery Rates (FDR)or adjust P value.
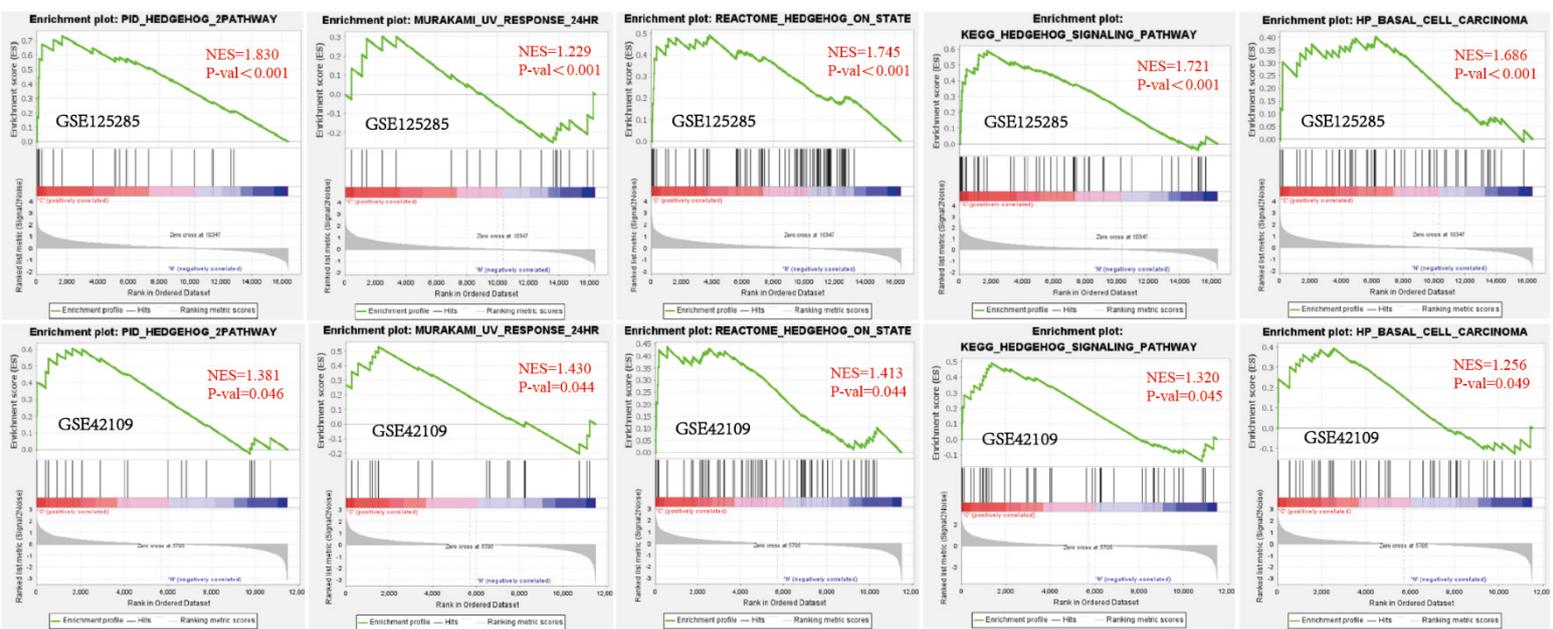
Supplementary Figure 3. Composition of infiltrating immune cells assessed using the CIBERSORT algorithm in BCC tissues by the validation dataset GSE53462. **A:** Distribution of immune cell infiltration in each sample; **B:** Heatmap of immune cell types; **C:** Violin plot of infiltrating immune cells.

Supplementary Figure 4. Tissue-specific pattern of mRNA expression of key genes from the online tool BioGPS.

VCAN   COL4A1   COL5A2