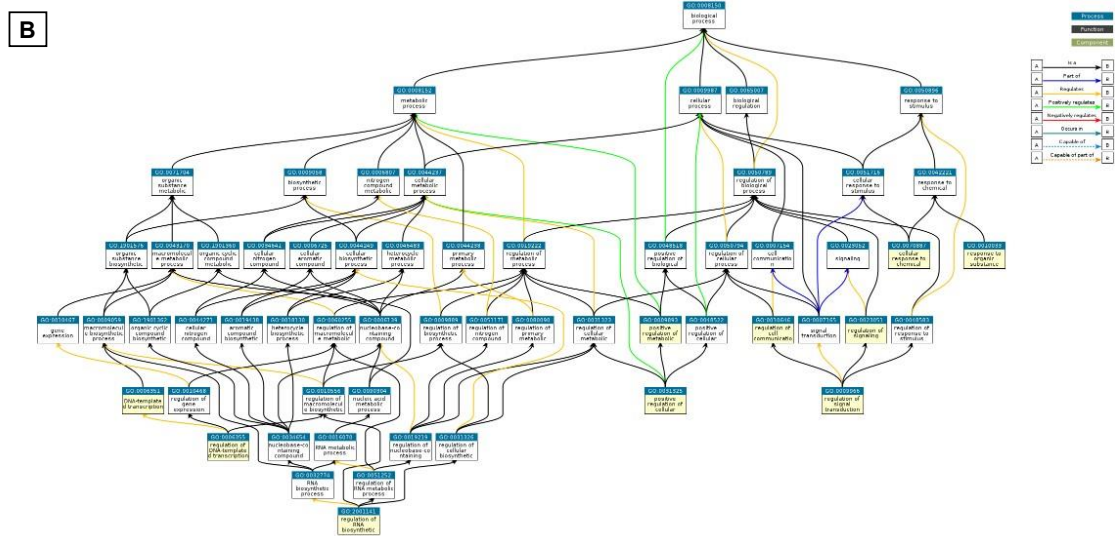
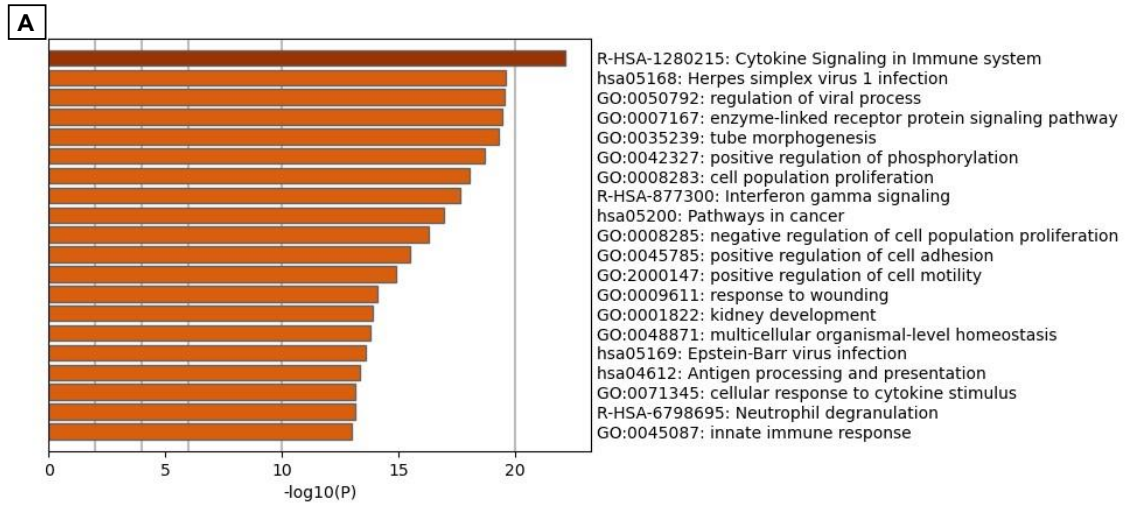
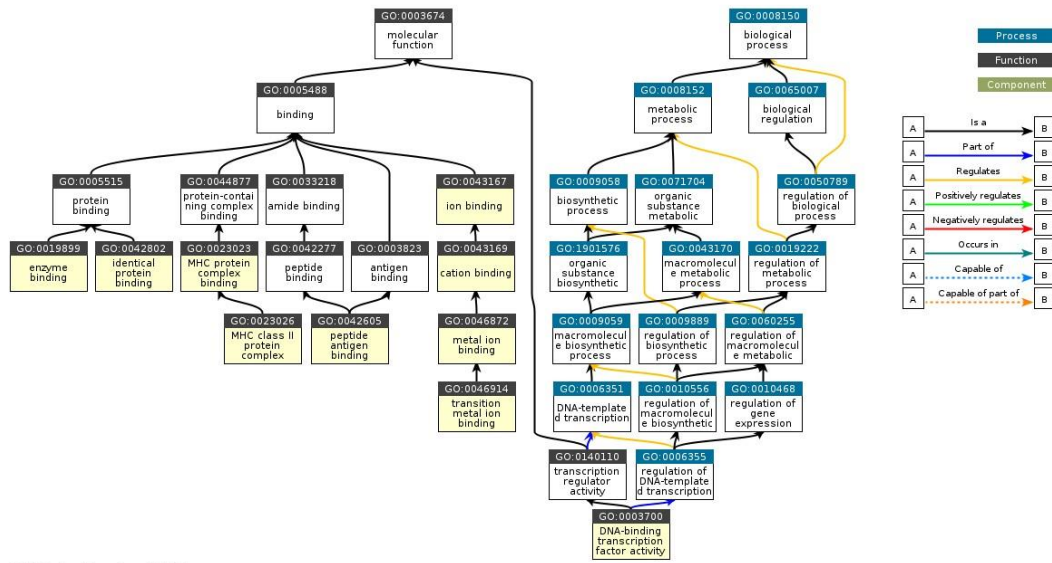


SUPPLEMENTARY FIGURE S1.



C



SUPPLEMENTARY FIGURE S1. The results of comprehensive gene expression analysis. Genes significantly upregulated in pathological keratosis cases were analyzed using Metascape [P - value (ANOVA), $FDR < 0.05$, Fold Change < -2]. In Metascape, we first identified all statistically enriched terms (i.e., GO/KEGG terms, canonical pathways, hallmark gene sets, etc., based on default selections in Express Analysis), calculated cumulative hypergeometric. The cumulative P values and enrichment factors were computed and used for filtering. The remaining significant terms were clustered hierarchically in a tree based on kappa statistical similarity between gene members. A kappa score of 0.3 was then applied as a threshold to classify the tree into term clusters (A). Genes significantly upregulated in pathological keratosis cases were analyzed using Metascape (P -value (ANOVA), $FDR < 0.05$, Fold Change < -2). In the biological process and molecular function, GO terms for the top 10 categories of P -values in enrichment analysis were obtained using DAVID, and charts were created. QuickGO was used for charting (B and C).

SUPPLEMENTARY TABLE S1. List of Primers Used in this Study

Gene Symbol	Forward Primer	Reverse Primer
AKR1B1 0	GTGACACCAGCACGCATTG	GCATTGAAGGGATAGTCTTC CAA
AKR1B1 5	ACAGGGATTCAAGACTGGGG	CCTCCCAGGCATCCAAGAAC
CRABP2	AGTGTCCAGTGCTCCAGCCTA	CTGCAGCCACAGCAATCTTC
RARA	AATGAAGATTACTGACCTGCGA AG	CTGTCCGCTCAGAGTGTCCA
RARB	CTGCCTGGACATCCTGATTCTT A	GGCAAAGGTGAACACAAGG TC
RARG	CCAGCCAGCCCTACATGTTC	TCATCCTCAAACATTTTCAGG GTTC
RARRE S3	CCCAGCTGAGATATGGCAAG	GCAACAACCAGGATTCCAAG
RDH12	ACAATGCGGGAGTAATGATGTG	GGGCAGACACCTTTAGCCG
18S	TGAACAGACAGAAGGATGTAA AGGA	AGGTCTTCACGGAGCTTGTT G

The primers used for quantitative real-time polymerase chain reaction are listed in the table.