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Identification of the expression of common genes and potential mechanism between COVID-19 and Chronic rhinosinusitis with nasal polyps

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OBJECTIVE

This study aims to identify shared biomarkers and regulatory mechanisms in nasal polyps (NPs) and COVID-19 using bioinformatics.

METHODS

Differentially expressed genes (DEGs) from NPs (GSE136825) and COVID-19 (GSE157103) datasets were analyzed. Thirteen common DEGs (cDEGs) were identified via cytoHubba, with five hub-cDEGs (TOP2A, BUB1B, BUB1, DLGAP5, CDC20) selected using random forest. Functional enrichment, protein-protein interaction, immune infiltration, and diagnostic nomograms were assessed. Validation was performed using GSE72713, GSE179265, and GSE167000.

RESULT

Figure 1

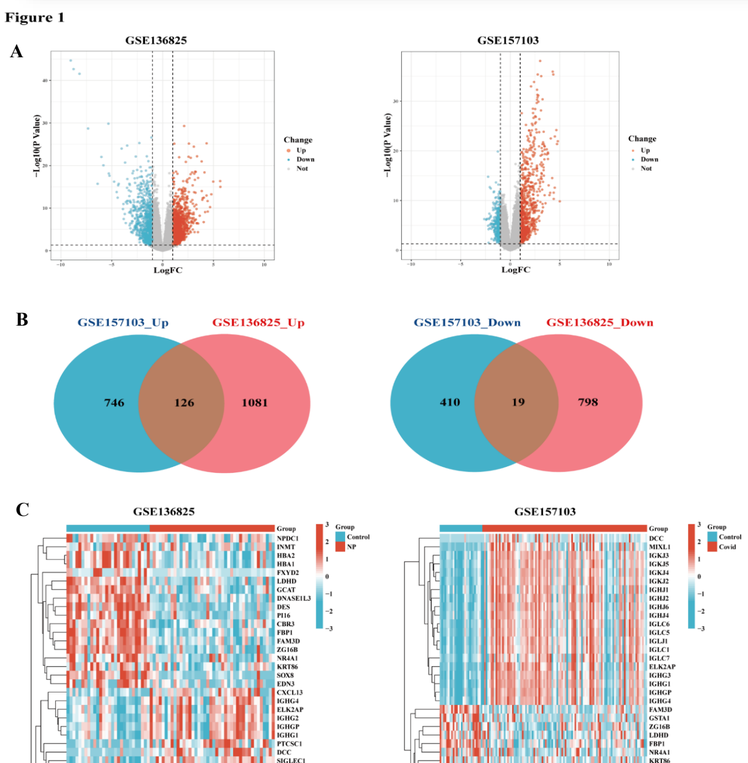

Figure 1. Differential expression genes (DEGs) identification and Vene plot of co-host factors in nasal polyps (NPs, GSE136825) and COVID-19 (GSE157103).

(A)Volcano plot showed the DEGs in COVID-19 and NPs database. (B) Venn diagram of intersection of NPs and COVID-19 related up and down genes in GEO database. (C) Heatmap illustrates the top 20 commonly upregulated and 19 downregulated genes shared between the COVID-19 and NPs GEO databases.

Figure 2

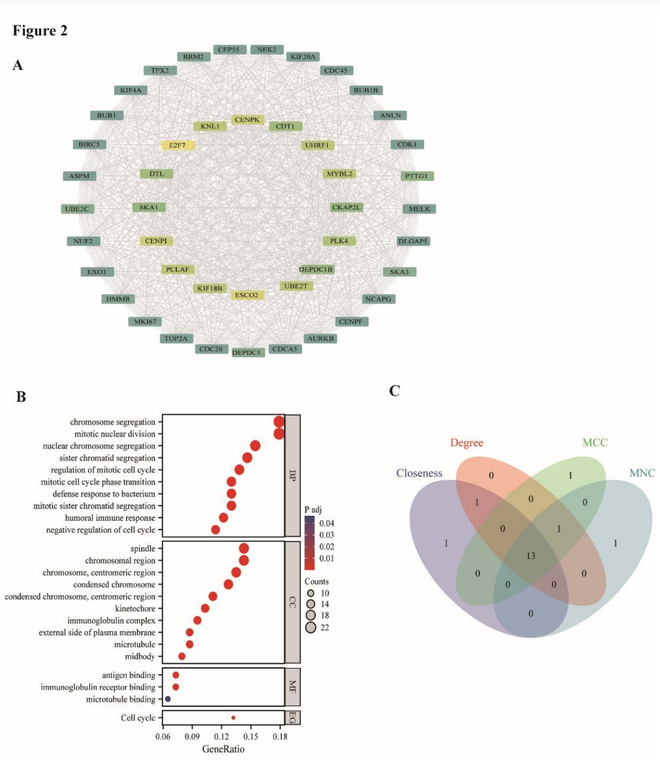

Figure 2. Module and hub-DEGs interaction network construction.

(A) Significant DEGs clustering modules were analyzed with MCODE. (B) GO and KEGG enrichment analysis of the hub- DEGs . (C) Venn diagram displayed that 13 overlapping hub- DEGs were screened out with 4 algorithms.

Figure4

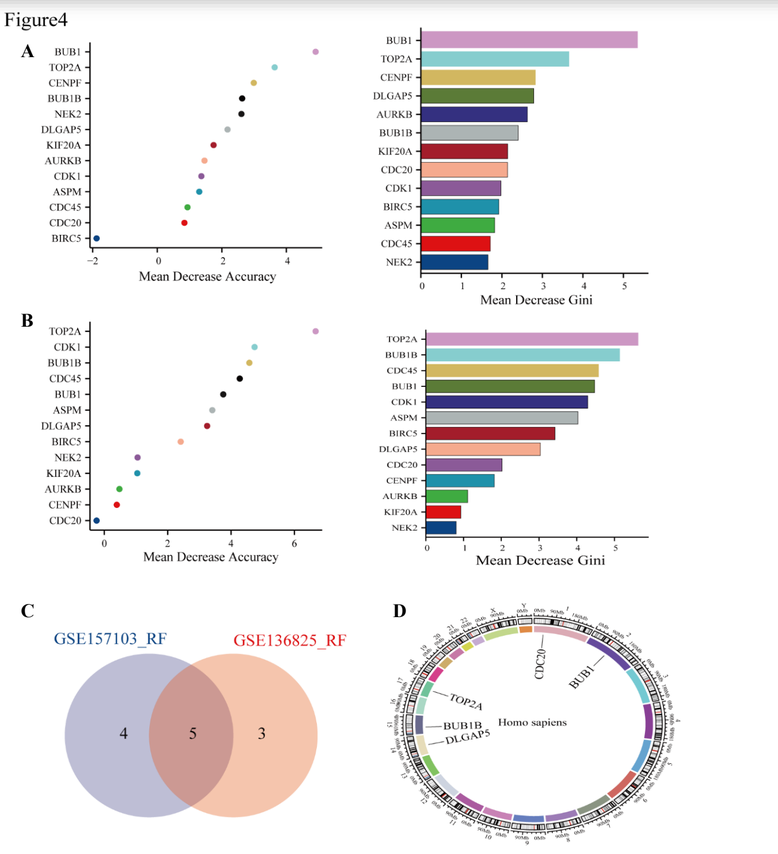

Figure 4 Feature genes are obtained by machine-learning algorithms

(AB) Screen biomakers for hub-DEGs in GSE136825 and GSE157103 using the RF algorithm. (C) The Venn diagram identified 5 candidates for hub-DEGs by RF algorithm. (D) The position of five hub-DEGs in the chromosome.

Figure 3

Figure 3 Immune microenvironment analysis of hub-DEGs

(A) Box plot shows different expression of 28 immune cells between nasal polyps and COVID-19 group with control group. (B) Correlation analysis of 5 hub-cDegs and immune cells in NPs and COVID-19.

Figure 6

Figure 6 The interaction network of hub genes.

(A) Five hub genes were analyzed via GeneMANIA. The 20 most frequently changed neighboring genes are shown. The predicted genes are located in the outer circle and hub genes are in the inner circle.

(B) Screening key transcription factors by MCC algorithm. The red represents hub genes, the green represents miRNA and the yellow represents TFs.

(C) TFs-gene network analysis of hub genes was displayed via Networkanalyst. The red located within the circle represents hub genes, and the yellow located on the periphery represents TFs that are closely related to hub genes.

Figure 5

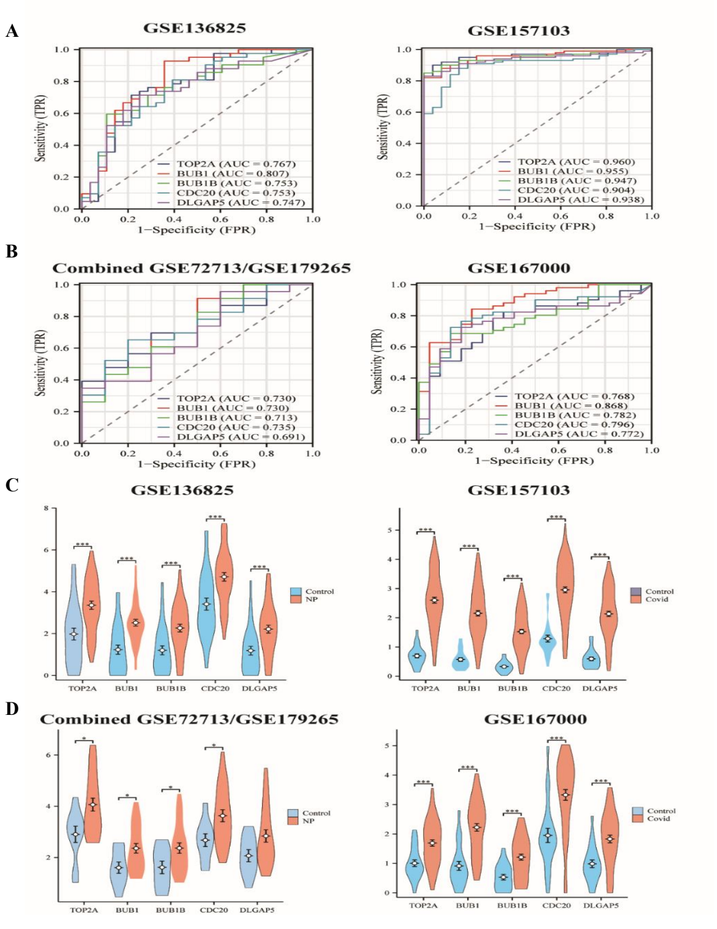

Figure 5 Receiver operator characteristic curve (ROC) diagnostic curve and expression levels of five hub-DEGs in NPs and COVID-19 patients.

(A) ROC diagnostic curve of hub-DEGs in GEO database in NPs and COVID-19 patients (GSE136825, and GSE157103) in the train set. (B) ROC diagnostic curve of hub-DEGs in validation set in NPs and COVID-19 patients (Combined GSE72713/GSE179265 dataset, GSE167000) in validation set.(C) Expression levels of hub-DEGs in NPs and COVID-19 patients with control group in the train set. (D) Expression levels of hub-DEGs in NPs and COVID-19 patients with control group in validation set . * and *** represent $p < 0.05$ and $p < 0.001$ compared with the healthy group, respectively.

Figure 7

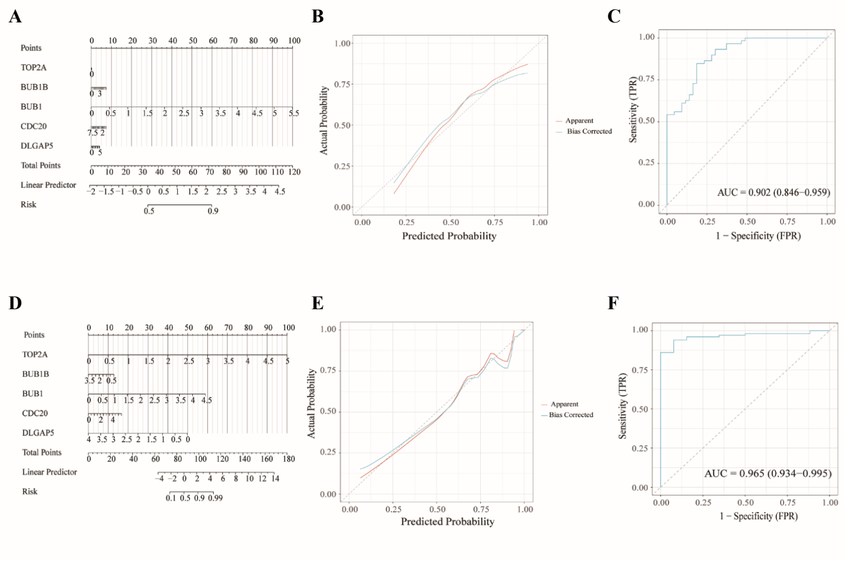

Figure 7 Nomogram development based on diagnostic biomarkers

(A) nomogram predicting the probability of NPs; (B) calibration curves of the NPs risk models; (C) ROC curve of the COVID-19 risk model; (D) nomogram predicting the probability of COVID-19; (E) calibration curves of the AS risk models; (F) ROC curve of the COVID-19 risk model.

CONCLUSION

The study identifies five hub-DEGs shared by NPs and COVID-19, highlighting cell cycle related pathways as critical in their pathogenesis. These findings may aid in biomarker discovery and therapeutic targeting.