Integrative Transcriptomic Profiling of NK Cells and Monocytes: Advancing Diagnostic and Therapeutic Strategies for COVID-19

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Abstract: In this study, it use integrated transcriptomic datasets from the GEO repository with the purpose of investigating immune dysregulation in COVID-19. Thus, in this context, we decided to be focused on NK cells and CD14+ monocytes gene expression, considering datasets GSE165461 and GSE198256, respectively. Other datasets with PBMCs, lung, olfactory, and sensory epithelium and lymph were used to provide robust validation for our results. This approach gave an integrated view of the immune responses in COVID-19, pointing out a set of potential biomarkers and therapeutic targets with special regard to standards of physiological conditions. IFI27, MKI67, CENPF, MBP, HBA2, TMEM158, THBD, HBA1, LHFPL2, SLA, and AC104564.3 were identified as key genes from our analysis that have critical biological processes related to inflammation, immune regulation, oxidative stress, and metabolic processes. Consequently, such processes are important in understanding the heterogeneous clinical manifestations of COVID-19—from acute to long-term effects now known as 'long COVID'. Subsequent validation with additional datasets consolidated these genes as robust biomarkers with an important role in the diagnosis of COVID-19 and the prediction of its severity. Moreover, their enrichment in key pathophysiological pathways presented them as potential targets for therapeutic intervention. The results provide insight into the molecular dynamics of COVID-19 caused by cells such as NK cells and other monocytes. Thus, this study constitutes a solid basis for targeted diagnostic and therapeutic development and makes relevant contributions to ongoing research efforts toward better management and mitigation of the pandemic.

Keywords: SARS-COV-2, RNA-seq, biomarkers, severity, long COVID-19, bio analysis

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