

Comparative transcriptome analyses reveal genes associated with SARS-CoV-2 infection of human lung epithelial cells

Darshan S. Chandrashekar^{1,*}, Mohammad Athar^{2,3}, Upender Manne^{1,3#}, Sooryanarayana Varambally^{1,3,4##*}

¹Department of Pathology, University of Alabama at Birmingham, Birmingham, AL

²Department of Dermatology, University of Alabama at Birmingham, Birmingham, AL

³O'Neal Comprehensive Cancer Center, University of Alabama at Birmingham, Birmingham, AL

⁴Informatics Institute, University of Alabama at Birmingham, Birmingham, AL

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*Correspondence to: Sooryanarayana Varambally, Ph.D., Molecular and Cellular Pathology, Department of Pathology, Wallace Tumor Institute, 4th floor, 20B, University of Alabama at Birmingham, Birmingham, AL 35233, USA Phone: (205) 996-1654

Email: soorya@uab.edu

And

Darshan S. Chandrashekar Ph.D., Department of Pathology, University of Alabama at Birmingham, Birmingham, AL

Email: dshimogachandrasheka@uabmc.edu

Supplementary figure S1: Summarization of comparative transcriptome analysis and validation. (a) Volcano plot showing result of differential expression analysis using RNA-seq data associated with SARS-CoV-2-infected human bronchial organoids. (b) Heatmap showing expression pattern of SARS-CoV-2 exclusive genes in SARS-CoV-2-infected human bronchial organoids. (c) Genes commonly altered in human lung epithelial cells on infection of SARS-CoV-2, SARS and other human/avian influenza viruses.

