|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene | Median hits  in non-COVID | Median hits  in COVID | Log2 Fold Change | SE of Log2 Fold Change | Adjusted  p-Value |
| AC233755.2 | 0 | 2 | 3.43 | 0.79 | 0.016 |
| ALKAL2 | 1 | 9.5 | 1.91 | 0.46 | 0.028 |
| AXL | 1 | 8.5 | 2.36 | 0.52 | 0.015 |
| BAMBI | 10 | 51 | 1.42 | 0.33 | 0.016 |
| BFSP2 | 1 | 9 | 1.81 | 0.41 | 0.016 |
| BMP6 | 124 | 421 | 1.10 | 0.25 | 0.016 |
| CLEC6A | 73.5 | 17 | -1.46 | 0.35 | 0.028 |
| CRYM | 5 | 39 | 1.82 | 0.43 | 0.024 |
| GRASP | 112 | 312 | 1.57 | 0.33 | 0.010 |
| IFI27 | 310 | 22806 | 2.37 | 0.49 | 0.007 |
| KRT8 | 5 | 17 | 1.24 | 0.31 | 0.040 |
| LIPN | 294 | 95.5 | -1.36 | 0.32 | 0.019 |
| MYZAP | 7.5 | 62.5 | 1.42 | 0.35 | 0.040 |
| NECTIN2 | 191 | 499 | 1.18 | 0.28 | 0.024 |
| PDE2A | 42.5 | 149.5 | 1.41 | 0.29 | 0.007 |
| PRKG1 | 4.5 | 18 | 1.53 | 0.38 | 0.041 |
| SMIM24 | 122 | 315 | 1.58 | 0.39 | 0.040 |
| TXNDC5 | 25.5 | 207.5 | 1.63 | 0.37 | 0.016 |

Table 3: differentially expressed genes in COVID vs. non-COVID.

See below for gene function from genecards database. Still need to look at the proteins the genes code for.

|  |  |  |
| --- | --- | --- |
| Gene | Function | Data in COVID |
| AC233755.2 | Synonymous with IGHV3-43D Gene, V region of the variable domain of immunoglobulin heavy chains that participates in the antigen recognition (PMID:24600447); Secreted immunoglobulins mediate the effector phase of humoral immunity, which results in the elimination of bound antigens (PMID: 22158414, 20176268) | No |
| ALKAL2 | Enables receptor signaling protein tyrosine kinase activator activity and receptor tyrosine kinase binding activity. Involved in positive regulation of ERK1 and ERK2 cascade; positive regulation of ERK5 cascade; and positive regulation of neuron projection development. Predicted to be located in extracellular region | Yes |
| AXL | The protein encoded by this gene is a member of the Tyro3-Axl-Mer (TAM) receptor tyrosine kinase subfamily. The encoded protein possesses an extracellular domain which is composed of two immunoglobulin-like motifs at the N-terminal, followed by two fibronectin type-III motifs. It transduces signals from the extracellular matrix into the cytoplasm by binding to the vitamin K-dependent protein growth arrest-specific 6 (Gas6). This gene may be involved in several cellular functions including growth, migration, aggregation and anti-inflammation in multiple cell types. The encoded protein acts as a host cell receptor for multiple viruses, including Marburg, Ebola and Lassa viruses and is a candidate receptor for the SARS-CoV2 virus | Yes, strong data. Numerous papers |
| BAMBI | This gene encodes a transmembrane glycoprotein related to the type I receptors of the transforming growth factor-beta (TGF-beta) family, whose members play important roles in signal transduction in many developmental and pathological processes. The encoded protein however is a pseudoreceptor, lacking an intracellular serine/threonine kinase domain required for signaling. Similar proteins in frog, mouse and zebrafish function as negative regulators of TGF-beta, which has led to the suggestion that the encoded protein may function to limit the signaling range of the TGF-beta family during early embryogenesis | Yes, regulates ACE2 mRNA levels  SUPER INTERESTING |
| BFSP2 | More than 99% of the vertebrate ocular lens is comprised of terminally differentiated lens fiber cells. Two lens-specific intermediate filament-like proteins, the protein product of this gene (phakinin), and filensin, are expressed only after fiber cell differentiation has begun. Both proteins are found in a structurally unique cytoskeletal element that is referred to as the beaded filament (BF). Mutations in this gene have been associated with juvenile-onset, progressive cataracts and Dowling-Meara epidermolysis bullosa simplex. | No |
| BMP6 | This gene encodes a secreted ligand of the TGF-beta (transforming growth factor-beta) superfamily of proteins. Ligands of this family bind various TGF-beta receptors leading to recruitment and activation of SMAD family transcription factors that regulate gene expression. The encoded preproprotein is proteolytically processed to generate each subunit of the disulfide-linked homodimer. This protein regulates a wide range of biological processes including iron homeostasis, fat and bone development, and ovulation. Differential expression of this gene may be associated with progression of breast and prostate cancer. Mutations in this gene may be associated with iron overload in human patients. | No |
| CLEC6A | The protein encoded by this gene is a type II membrane receptor with an extracellular C-type lectin-like domain fold. The extracellular portion binds structures with a high mannose content and has been shown to recognize several pathogens, including C. elegans, S. cerevisiae, M. tuberculosis, C. neoformans, and house dust mite. When stimulated, the encoded protein initiates signalling through the CARD9-Bcl10-Malt1 pathway, leading to the induction of cytokines. Two transcript variants encoding different isoforms have been found for this gene | Yes |
| CRYM | Crystallins are separated into two classes: taxon-specific and ubiquitous. The former class is also called phylogenetically-restricted crystallins. The latter class constitutes the major proteins of vertebrate eye lens and maintains the transparency and refractive index of the lens. This gene encodes a taxon-specific crystallin protein that binds NADPH and has sequence similarity to bacterial ornithine cyclodeaminases. The encoded protein does not perform a structural role in lens tissue, and instead it binds thyroid hormone for possible regulatory or developmental roles. Mutations in this gene have been associated with autosomal dominant non-syndromic deafness. | No |
| GRASP | TAMALIN Gene? This gene encodes a protein that functions as a molecular scaffold, linking receptors, including group 1 metabotropic glutamate receptors, to neuronal proteins. The encoded protein contains conserved domains, including a leucine zipper sequence, PDZ domain and a C-terminal PDZ-binding motif. Alternately spliced transcript variants have been observed for this gene | No |
| IFI27 | Enables RNA polymerase II-specific DNA-binding transcription factor binding activity; identical protein binding activity; and lamin binding activity. Involved in several processes, including cellular protein metabolic process; defense response to other organism; and extrinsic apoptotic signaling pathway. Acts upstream of or within negative regulation of transcription by RNA polymerase II and regulation of protein export from nucleus. Located in mitochondrial membrane and nuclear inner membrane | Yes, early predictor for COVID-19 outcomes (PMID 3665600) |
| KRT8 | This gene is a member of the type II keratin family clustered on the long arm of chromosome 12. Type I and type II keratins heteropolymerize to form intermediate-sized filaments in the cytoplasm of epithelial cells. The product of this gene typically dimerizes with keratin 18 to form an intermediate filament in simple single-layered epithelial cells. This protein plays a role in maintaining cellular structural integrity and also functions in signal transduction and cellular differentiation. Mutations in this gene cause cryptogenic cirrhosis. Alternatively spliced transcript variants have been found for this gene | Yes |
| LIPN | The gene encodes a lipase that is highly expressed in granular keratinocytes in the epidermis, and plays a role in the differentiation of keratinocytes. Mutations in this gene are associated with lamellar ichthyosis type 4 | No |
| MYZAP | This gene encodes a protein that is abundantly expressed in cardiac tissue. The encoded protein localizes to intercalated discs in cardiomyocytes and functions as an activator of Rho-dependent serum-response factor signaling. Alternative splicing results in multiple transcript variants. Readthrough transcription also exists between this gene and the neighboring downstream gene POLR2M | No |
| NECTIN2 | This gene encodes a single-pass type I membrane glycoprotein with two Ig-like C2-type domains and an Ig-like V-type domain. This protein is one of the plasma membrane components of adherens junctions. It also serves as an entry for certain mutant strains of herpes simplex virus and pseudorabies virus, and it is involved in cell to cell spreading of these viruses. Variations in this gene have been associated with differences in the severity of multiple sclerosis. Alternate transcriptional splice variants, encoding different isoforms, have been characterized | Yes |
| PDE2A | Enables several functions, including 3',5'-cyclic-nucleotide phosphodiesterase activity; anion binding activity; and metal ion binding activity. Involved in several processes, including cellular response to organic cyclic compound; cyclic-nucleotide-mediated signaling; and regulation of vascular permeability. Located in several cellular components, including cytosol; mitochondrial membrane; and perinuclear region of cytoplasm. Colocalizes with plasma membrane | Yes |
| PRKG1 | Mammals have three different isoforms of cyclic GMP-dependent protein kinase (Ialpha, Ibeta, and II). These PRKG isoforms act as key mediators of the nitric oxide/cGMP signaling pathway and are important components of many signal transduction processes in diverse cell types. This PRKG1 gene on human chromosome 10 encodes the soluble Ialpha and Ibeta isoforms of PRKG by alternative transcript splicing. A separate gene on human chromosome 4, PRKG2, encodes the membrane-bound PRKG isoform II. The PRKG1 proteins play a central role in regulating cardiovascular and neuronal functions in addition to relaxing smooth muscle tone, preventing platelet aggregation, and modulating cell growth. This gene is most strongly expressed in all types of smooth muscle, platelets, cerebellar Purkinje cells, hippocampal neurons, and the lateral amygdala. Isoforms Ialpha and Ibeta have identical cGMP-binding and catalytic domains but differ in their leucine/isoleucine zipper and autoinhibitory sequences and therefore differ in their dimerization substrates and kinase enzyme activity | Yes |
| SMIM24 | Predicted to be located in membrane. Predicted to be integral component of membrane. | No |
| TXNDC5 | This gene encodes a member of the disulfide isomerase (PDI) family of endoplasmic reticulum (ER) proteins that catalyze protein folding and thiol-disulfide interchange reactions. The encoded protein has an N-terminal endoplasmic reticulum (ER)-signal sequence, three catalytically active thioredoxin domains and a C-terminal ER-retention sequence. Its expression is induced by hypoxia and its role may be to protect hypoxic cells from apoptosis. Alternative splicing results in multiple transcript variants. Read-through transcription also exists between this gene and the neighboring upstream BLOC1S5 gene | Yes |