**Supplemental Table 10:** Description of the eight genes that are predictors of mortality

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **RefGene Name** | **CpG position** | **RefGene functional annotation\*** | **RefGene molecular process\*** | **RefGene in COVID-19 related findings** |
| H1F0 | cg27424226 | Nucleosomal DNA binding;  RNA binding; protein binding | Negative regulation of DNA recombination and chromatin silencing; Nucleosome positioning | Low affinity to COVID-19 protein (Nsp3) in different cell lines ex-vivo [1] |
| ROCK1 | cg26121915 | Nucleotide binding; Tau protein binding; Transferase or kinase activity | Epithelial to mesenchymal transition;  Negative regulation of angiogenesis;  Apoptotic process; others | Proposed to be targeted to limit the inflammation leading to ARDS associated with COVID-19 [2] |
| ZNF789 | cg05563613 | DNA or metal ion binding; Transcription factor activity | Regulation of transcription; RNA metabolic process | NA |
| MAT2B | cg14447399 | Protein binding; Methionine adenosyl-transferase regulator activity | S-adenosylmethionine biosynthetic process; Regulation of catalytic activity | Significantly higher in the enriched cells compared to depleted cells, suggested as a potential contributing gene to genetic risk for severe COVID-19 [3] |
| YY1P2 | cg12406406 | Transcription factor activity | YY1: Spermatogenesis;  B cell differentiation; Cellular response to UV or DNA damage or IL-1 | NA |
| MFHAS1 | cg01784220 | Protein (ligase, phosphatase) binding;  Nucleotide binding | Innate immune response (inflammation, TLR signaling, regulation of macrophage activation); Positive regulation of ERK1 and ERK2 cascade | Enriched in pro-inflammatory pathways and highly expressed in non-vaccinated vs vaccinated non-human primates with COVID-19 [4] |
| MRPS2 | cg12438037 | Ribosome subunit construction | Mitochondrial ribosome assembly and translation | Interacts with COVID-19 protein (Nsp8) [5]; Linked to viral replication and translation in infected cells [6]; Upregulated in COVID-19 recovered and retested positive patients [7] |
| PSMB9 | cg19760441 | Protein binding; peptidase or hydrolase activity | Immune system process; Catabolic process;  Regulation of mRNA stability; Post-translation modification | Significantly expressed in COVID-19 patients with low compared to high viral load in the lung, and in macrophages of mild vs. severe cases [8]; Enriched in cytokine-mediated signaling pathway from upregulated genes in infected tissues [9] |

**\*** based on GO

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