

[Supplemental Tables]

Table S1 The search terms for “COVID-19”

|             |                                               |
|-------------|-----------------------------------------------|
| SOC:        | 10021881/Infections and infestations          |
| HLGT:       | 10047438/Viral infectious disorders           |
| <b>HLT:</b> | <b>10084510/Coronavirus infections</b>        |
| PT:         | 10051905/Coronavirus infection                |
| PT:         | 10061982/Severe acute respiratory syndrome    |
| PT:         | 10075271/Middle East respiratory syndrome     |
| PT:         | 10084268/COVID-19                             |
| PT:         | 10084380/COVID-19 pneumonia                   |
| PT:         | 10084381/Coronavirus pneumonia                |
| PT:         | 10084451/Suspected COVID-19                   |
| PT:         | 10084639/SARS-CoV-2 sepsis                    |
| PT:         | 10084640/SARS-CoV-2 viraemia                  |
| PT:         | 10085076/HCoV-229E infection                  |
| PT:         | 10085077/HCoV-OC43 infection                  |
| PT:         | 10085078/HCoV-NL63 infection                  |
| PT:         | 10085079/HCoV-HKU1 infection                  |
| PT:         | 10085080/Congenital COVID-19                  |
| PT:         | 10085492/Vaccine derived SARS-CoV-2 infection |
| PT:         | 10085503/Post-acute COVID-19 syndrome         |
| PT:         | 10086861/Breakthrough COVID-19                |

Table S2 Significantly down-regulated genesets in cilastatin-treated HT29 cells  
(LINCS 2020)

| GeneSet Name                                                   | NES   | FDR   |
|----------------------------------------------------------------|-------|-------|
| GOMF SNORNA BINDING                                            | -3.76 | 0.043 |
| GOBP RIBONUCLEOPROTEIN COMPLEX BIOGENESIS                      | -3.45 | 0.043 |
| GOBP RIBOSOME BIOGENESIS                                       | -3.43 | 0.043 |
| GOBP RRNA METABOLIC PROCESS                                    | -3.36 | 0.043 |
| GOBP NCRNA PROCESSING                                          | -3.36 | 0.043 |
| GOMF U3 SNORNA BINDING                                         | -3.33 | 0.043 |
| GOBP SPLICEOSOMAL COMPLEX ASSEMBLY                             | -3.21 | 0.043 |
| GOBP NCRNA METABOLIC PROCESS                                   | -3.09 | 0.043 |
| GOCC SPLICEOSOMAL COMPLEX                                      | -3.09 | 0.043 |
| GOBP POSITIVE REGULATION OF MRNA PROCESSING                    | -3.07 | 0.043 |
| GOMF TRANSLATION TERMINATION FACTOR ACTIVITY                   | -3.00 | 0.043 |
| GOCC INTRINSIC COMPONENT OF MITOCHONDRIAL INNER MEMBRANE       | -2.99 | 0.043 |
| GOBP RIBONUCLEOPROTEIN COMPLEX SUBUNIT ORGANIZATION            | -2.99 | 0.043 |
| GOBP RNA SPLICING VIA TRANSESTERIFICATION REACTIONS            | -2.97 | 0.043 |
| GOBP RNA PROCESSING                                            | -2.97 | 0.043 |
| GOCC U2 TYPE SPLICEOSOMAL COMPLEX                              | -2.91 | 0.043 |
| GOBP RNA POLYADENYLATION                                       | -2.86 | 0.043 |
| GOBP POSITIVE REGULATION OF CHROMOSOME ORGANIZATION            | -2.79 | 0.043 |
| GOMF RNA BINDING                                               | -2.77 | 0.043 |
| GOBP PROTEIN LOCALIZATION TO MITOCHONDRION                     | -2.74 | 0.043 |
| GOBP POSITIVE REGULATION OF TELOMERE MAINTENANCE               | -2.74 | 0.043 |
| GOBP PROTEIN TARGETING TO MITOCHONDRION                        | -2.73 | 0.043 |
| GOCC INTRINSIC COMPONENT OF MITOCHONDRIAL MEMBRANE             | -2.73 | 0.043 |
| GOMF LIGASE ACTIVITY FORMING CARBON SULFUR BONDS               | -2.66 | 0.043 |
| GOBP MRNA PROCESSING                                           | -2.64 | 0.043 |
| GOMF ENDODEOXYRIBONUCLEASE ACTIVITY                            | -2.58 | 0.043 |
| GOBP REGULATION OF CELLULAR MACROMOLECULE BIOSYNTHETIC PROCESS | -2.26 | 0.043 |
| GOCC MITOCHONDRION                                             | -2.22 | 0.043 |
| GOBP REGULATION OF DNA METABOLIC PROCESS                       | -1.94 | 0.043 |
| GOBP ORGANONITROGEN COMPOUND CATABOLIC PROCESS                 | -1.71 | 0.043 |
| GOBP MRNA SPLICE SITE SELECTION                                | -3.23 | 0.11  |
| GOMF PHOSPHATIDIC ACID TRANSFER ACTIVITY                       | -3.07 | 0.11  |
| GOCC PRERIBOSOME                                               | -3.44 | 0.13  |
| GOCC RIBONUCLEOPROTEIN COMPLEX                                 | -2.78 | 0.13  |
| GOBP RNA DEPENDENT DNA BIOSYNTHETIC PROCESS                    | -2.59 | 0.13  |
| GOCC SPLICEOSOMAL SNRNP COMPLEX                                | -3.06 | 0.15  |
| GOMF UBIQUITIN LIKE MODIFIER ACTIVATING ENZYME ACTIVITY        | -3.12 | 0.18  |
| GOBP NCRNA 3 END PROCESSING                                    | -3.03 | 0.18  |
| GOMF METAL CLUSTER BINDING                                     | -2.86 | 0.18  |
| GOCC MITOCHONDRIAL MATRIX                                      | -2.73 | 0.18  |
| HP SPASTIC DIPLEGIA                                            | -2.49 | 0.18  |
| GOBP REGULATION OF DNA BIOSYNTHETIC PROCESS                    | -2.31 | 0.18  |

NES indicates the normalized enrichment score, with negative values reflecting down-regulation.