

Table S2: Enrichment analysis of the ACE2 co-expression network. An enrichment analysis was performed on the list of top-25 genes that more closely co-express with ACE2 in SARS-CoV2-infected human enterocytes. To this aim we used the Enrichr platform of enrichment analyses (<https://maayanlab.cloud/Enrichr/>) and queried the BioPlanet library of pathways (created and run by the National Institute of Health, USA) [37], which compiles and integrates libraries of pathways from a large range of sources. The top-10 most significantly enriched pathways, the corresponding adjusted p-values and genes annotated with each pathway are shown below.

| Pathway | Adjusted P-value | Genes |
|---|------------------|--|
| Metabolism | 1.78E-4 | <i>GSTM4, GATM, OAT, BTD, MAOB, MTPP, ACSL5, GLRX, ALDOB, CYP3A4, PLD1</i> |
| Arginine and proline metabolism | 0.002 | <i>GATM, OAT, MAOB</i> |
| Drug metabolism: cytochrome P450 | 0.006 | <i>GSTM4, MAOB, CYP3A4</i> |
| Urea cycle and metabolism of amino groups | 0.008 | <i>GATM, OAT</i> |
| mTOR signaling pathway | 0.009 | <i>PDCD4, PLD1, SGK1</i> |
| Biological oxidations | 0.011 | <i>GSTM4, MAOB, CYP3A4</i> |
| Glycine, serine and threonine metabolism | 0.011 | <i>GATM, MAOB</i> |
| Alpha-synuclein signaling | 0.011 | <i>MAOB, PLD1</i> |
| Aldosterone-regulated sodium reabsorption | 0.017 | <i>ATP1A1, SGK1</i> |
| Tryptophan metabolism | 0.029 | <i>MAOB, CYP3A4</i> |