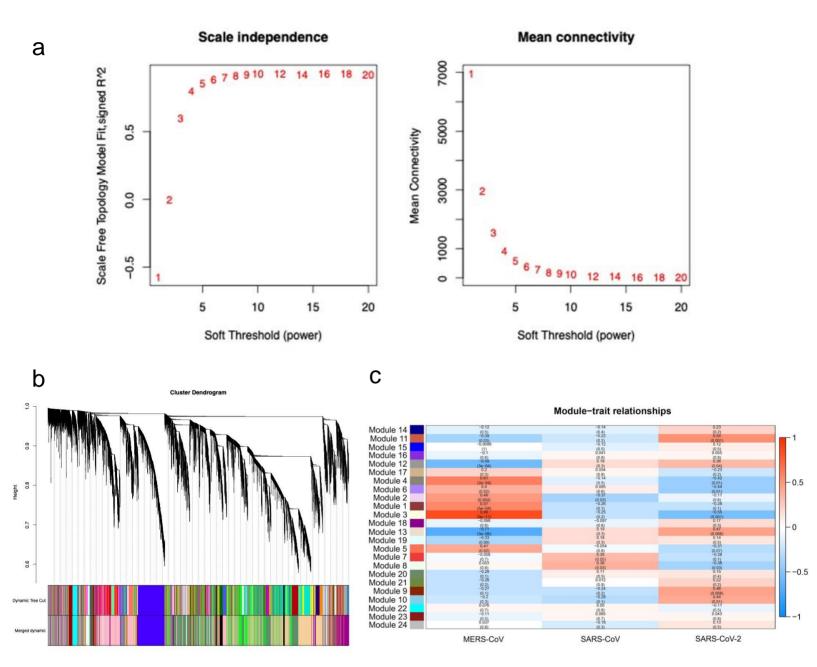
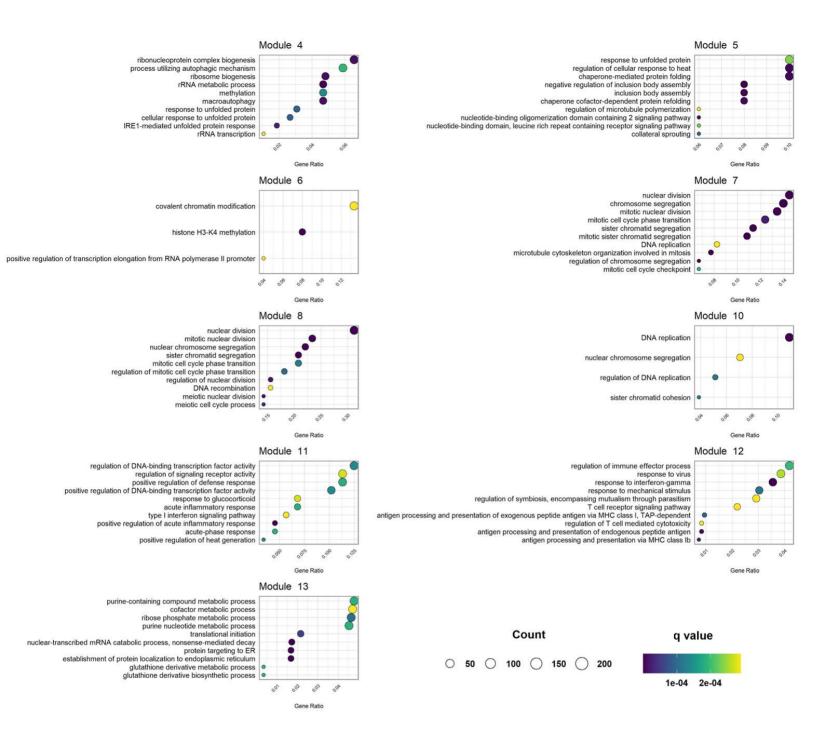


Supplementary Figure 1. Differential expression analysis of Coronaviruses infected cell lines.

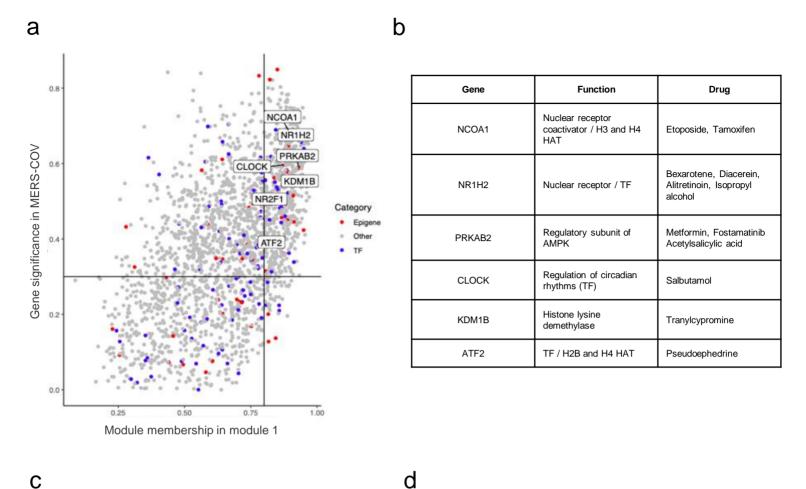
**a** Number of up and down-regulated differentially expressed genes (DEGs) in the analyzed cell lines for each viral infection. **b** Reduced enriched GO terms shared between two or more virus-associated gene sets. **c** Log2 fold-change expression of SARS-CoV-2 virus-associated epifactors across different viral infections; blank color represents non-significant differential expression. **d** Log2 fold-change expression of SARS-CoV-2 virus-associated TFs across different viral infections; blank color represents non-significant differential expression.

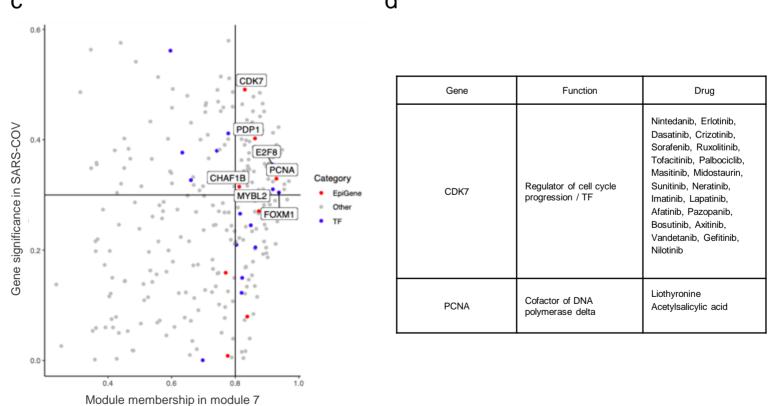


**Supplementary Figure 2. Weighted Gene Co-expression Network. a** Analysis of network topology for different soft-thresholding powers. **b** Clustering dendrogram of genes with their corresponding module colors before (Dynamic Cut Tree) and after (Merged Dynamic) similarity merging. **c** Module-virus association; the numbers inside each cell correspond to the correlation coefficient (top), which also dictates the cell color, and p value (bottom).



Supplementary Figure 3. Top 10 simplified enriched Gene Ontology terms of biological process in each of the relevant modules for coronaviruses infection. Go terms are ordered by q-value. Modules 1, 2, 3 and 9 are missing because they were not significantly enriched with any GO term.





**Supplementary Figure 4. Potential epigenetic therapeutic targets for MERS and SARS-CoV. a** Module membership and Gene Significance of gene members of module 1. **b** Approved drugs for module 1's important epifactors and TFs. **c** Module membership and Gene Significance of gene members of module 7. d Approved drugs for module 7's important epifactors and TFs