

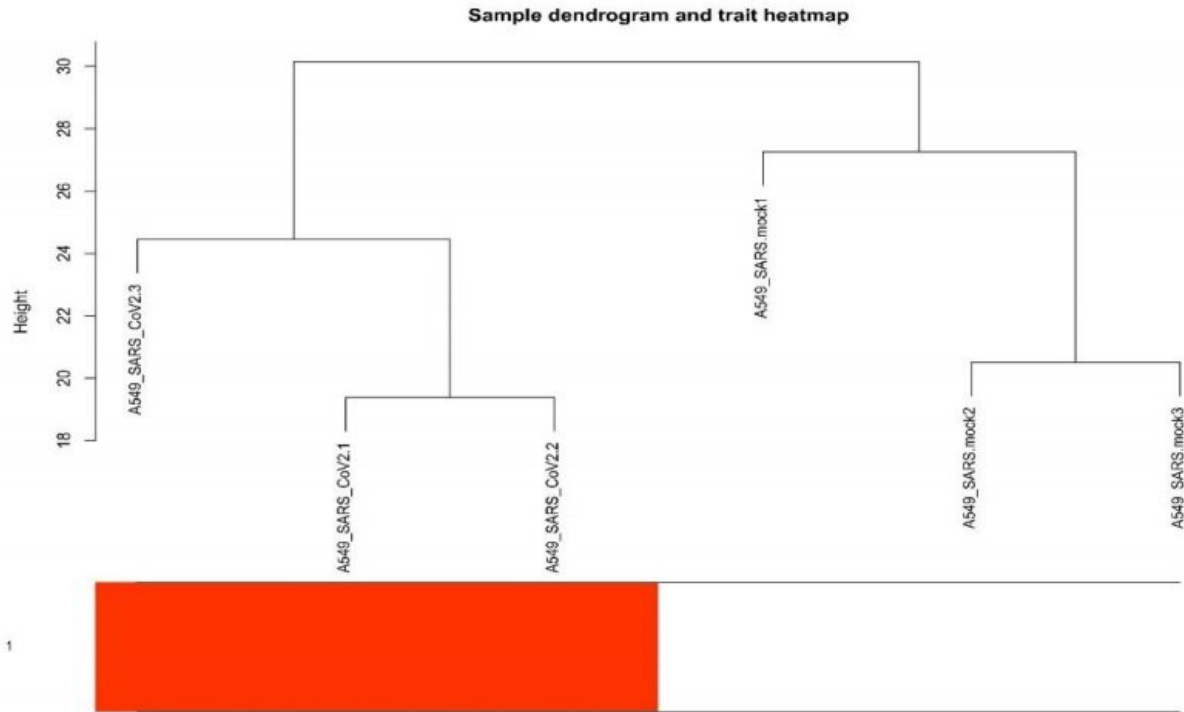
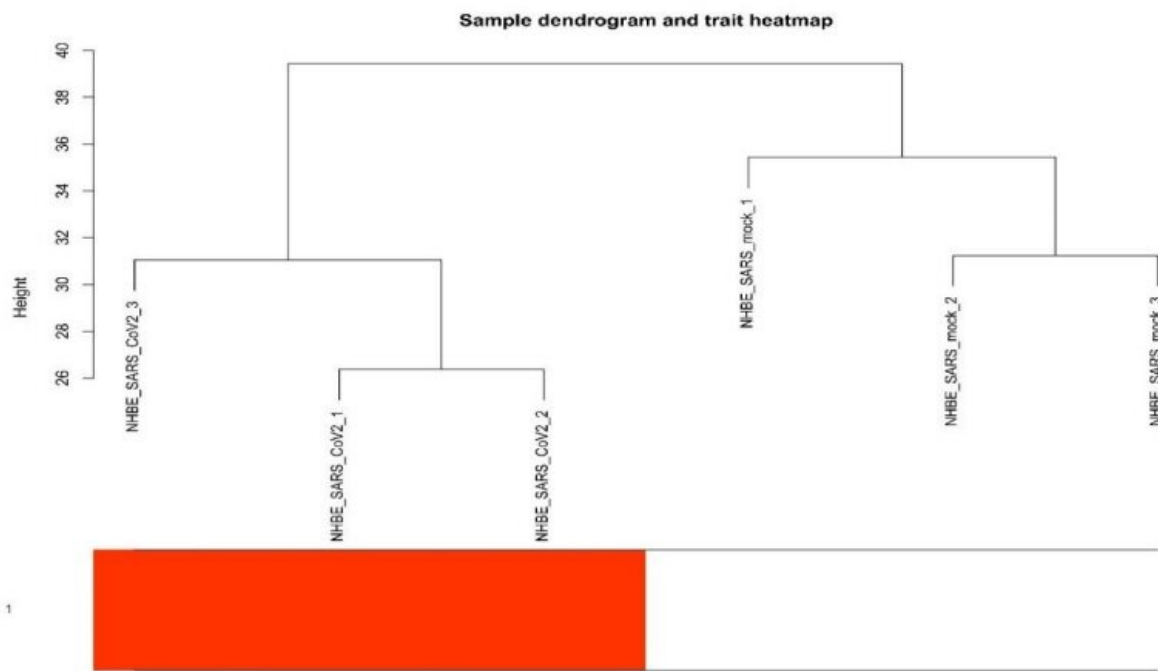
# Supplementary Materials

**Table S1.** Module colors characterization of A549 dataset.

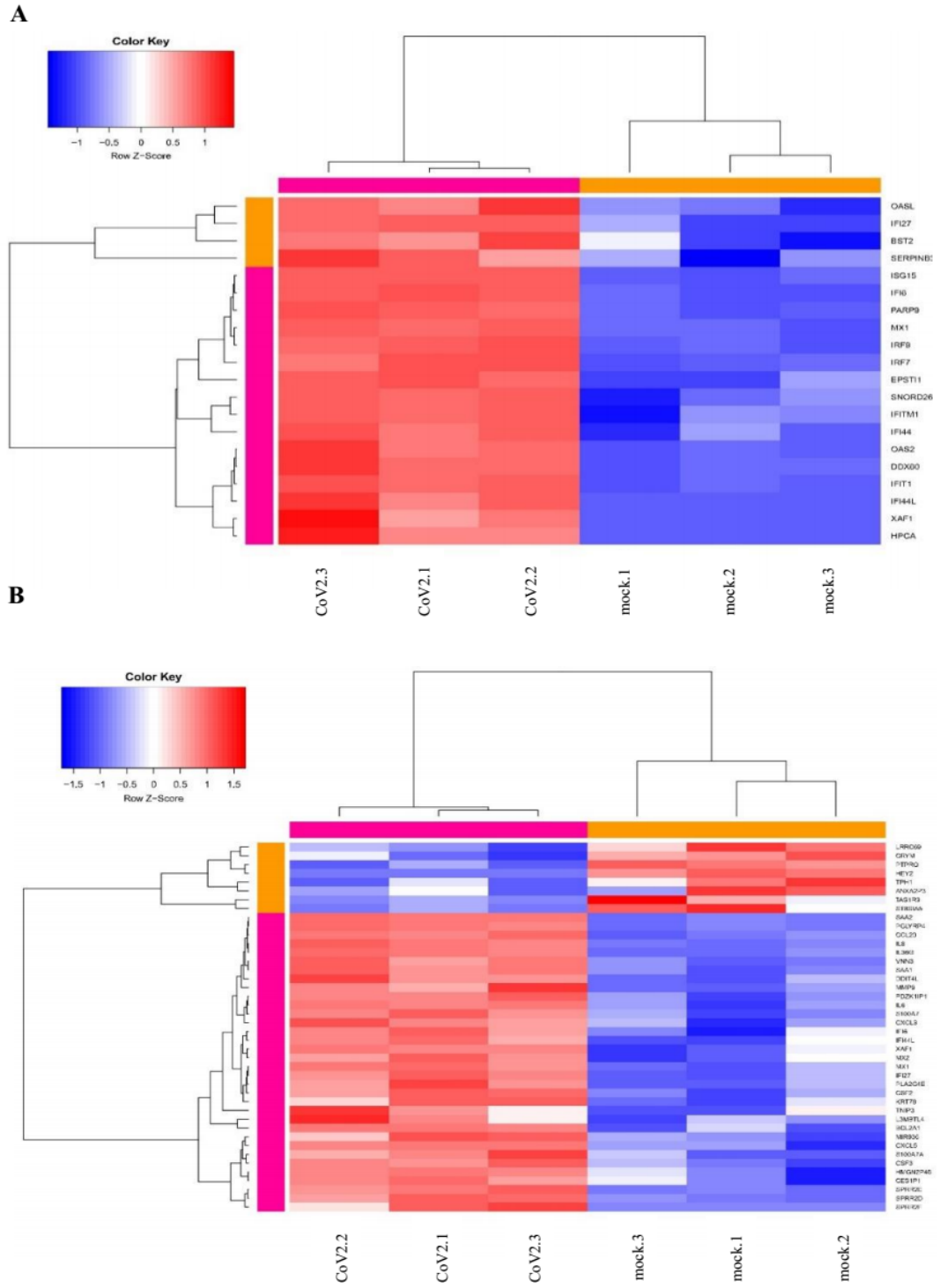
#	Module Colors#	Number of Genes#	Correlation#	<i>p</i> -value#
1#	Turquoise#	196#	1#	$1.00 \times 10^{-5}$ #
2#	Grey60#	138#	0.72#	0.1#
3#	Brown4#	1313#	0.53#	0.3#
4#	Darkturquoise#	111#	0.44#	0.4#
5#	Thistle2#	41#	0.4#	0.4#
6#	Red#	217#	0.32#	0.5#
7#	Skyblue3#	47#	0.22#	0.7#
8#	Salmon4#	91#	-0.1#	0.9#
9#	Darkolivegreen#	216#	-0.16#	0.8#
10#	Saddlebrown#	56#	-0.16#	0.8#
11#	Mediumpurple2#	30#	-0.19#	0.7#
12#	Coral2#	118#	-0.28#	0.6#
13#	Lightpink4#	35#	-0.3#	0.6#
14#	Cyan#	201#	-0.31#	0.5#
15#	Palevioletred3#	82#	-0.33#	0.5#
16#	Maroon#	37#	-0.54#	0.3#
17#	Plum#	188#	-0.67#	0.1#
18#	Darkslateblue#	233#	-0.77#	0.07#
19#	Lightsteelblue1#	529#	-0.86#	0.03#
20	Darkorange2	121	-0.89	0.02

**Table S2.** Module colors characterization of NHBE dataset.

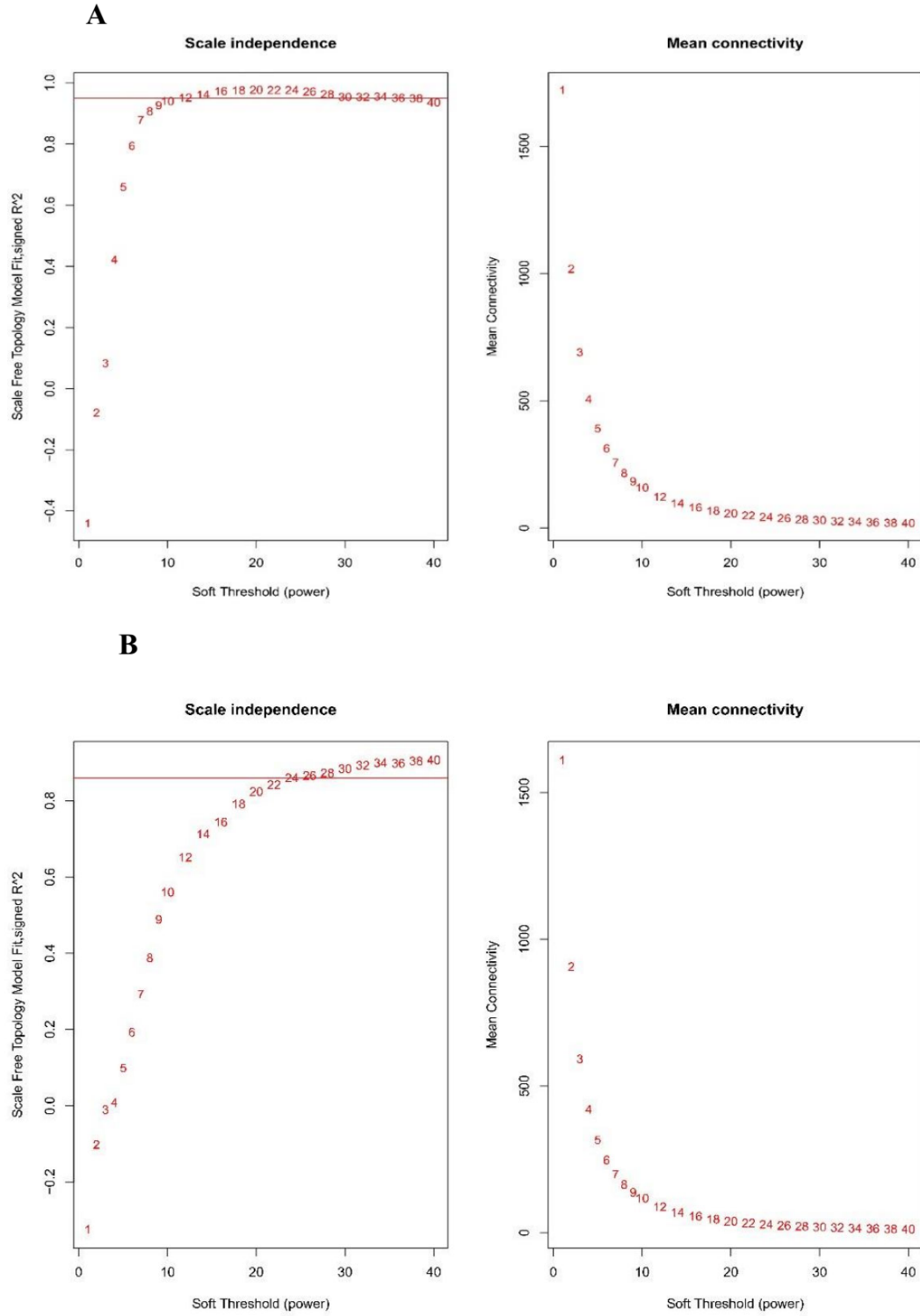
#	Module Colors#	Number of Genes#	Correlation#	<i>p</i> -value#
1#	Yellowgreen#	198#	1#	$2.00 \times 10^{-5}$ #
2#	Violet#	57#	0.72#	0.1#
3#	Black#	175#	0.65#	0.2#
4#	Cyan#	68#	0.4#	0.4#
5#	Corall1#	68#	0.26#	0.6#
6#	Darkred#	112#	0.19#	0.7#
7#	Plum1#	242#	0.14#	0.8#
8#	Floralwhite#	425#	0.1#	0.8#
9#	Darkorange2#	46#	0.075#	0.9#
10#	Indianred4#	88#	0.058#	0.9#
11#	Yellow4#	33#	-0.066#	0.9#
12#	Lightcyan1#	48#	-0.075#	0.9#
13#	Darkseagreen4#	74#	-0.18#	0.7#
14#	Sienna3#	53#	-0.28#	0.6#
15#	Thistle2#	132#	-0.36#	0.5#
16#	Lavenderblush3#	38#	-0.38#	0.5#
17#	Blue#	154#	-0.47#	0.4#
18#	Bisque4#	214#	-0.56#	0.2#
19#	Darkgrey#	120#	-0.6#	0.2#
20#	Darkolivegreen#	841#	-0.65#	0.2#
21#	Brown2#	184#	-0.74#	0.09#
22#	Pink#	206#	-0.76#	0.08#
23	Darkgreen	186	-0.82	0.05
24	Coral2	238	-0.92	0.01

**A****B**

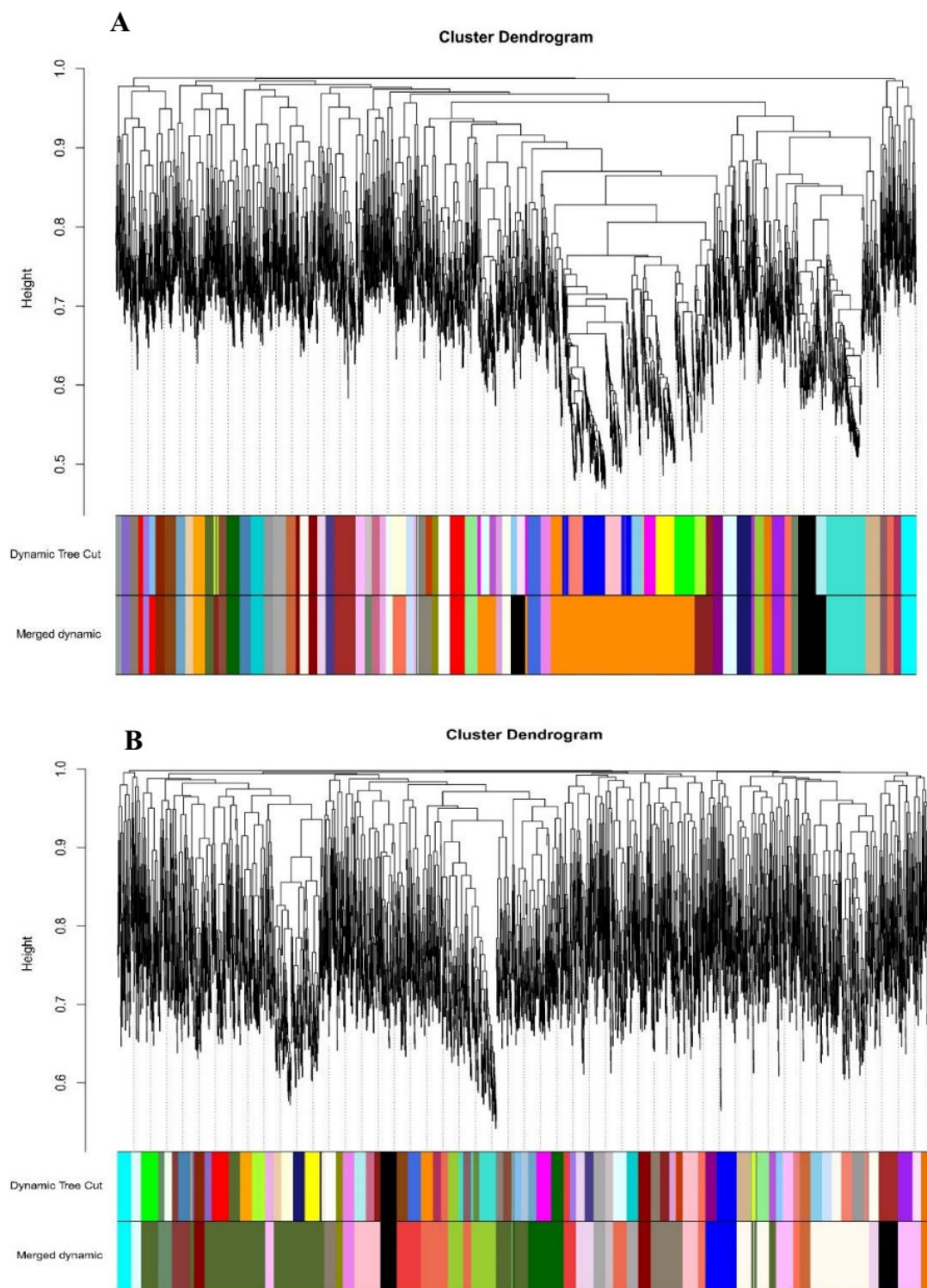
**Figure S1.** Sample clustering to detect outliers. (A) A549 dataset and (B) NHBE dataset. The color is proportional to the pathological stage (Red=infected samples and white=mock treated samples).



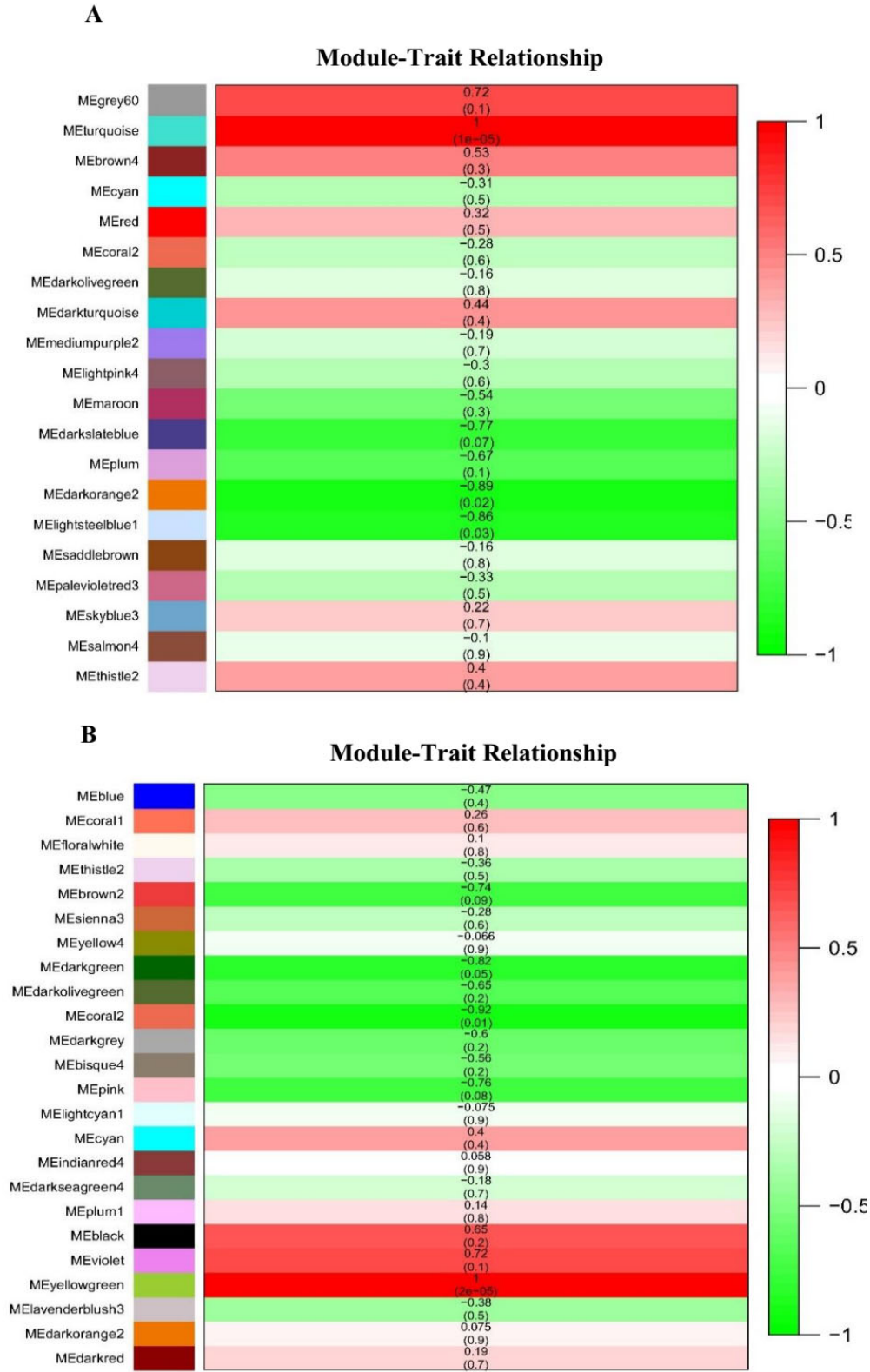
**Figure S2.** Heatmap of DEGs between mock-treated and SARS-CoV-2-treated cell lines. (A) A549 dataset and (B) NHBE dataset.



**Figure S3.** Selection of the soft-thresholding powers. **(A)** A549 dataset and **(B)** NHBE dataset. The left panel shows the Scheme 9. and 22 for A549 and NHBE datasets, respectively for the next analysis.

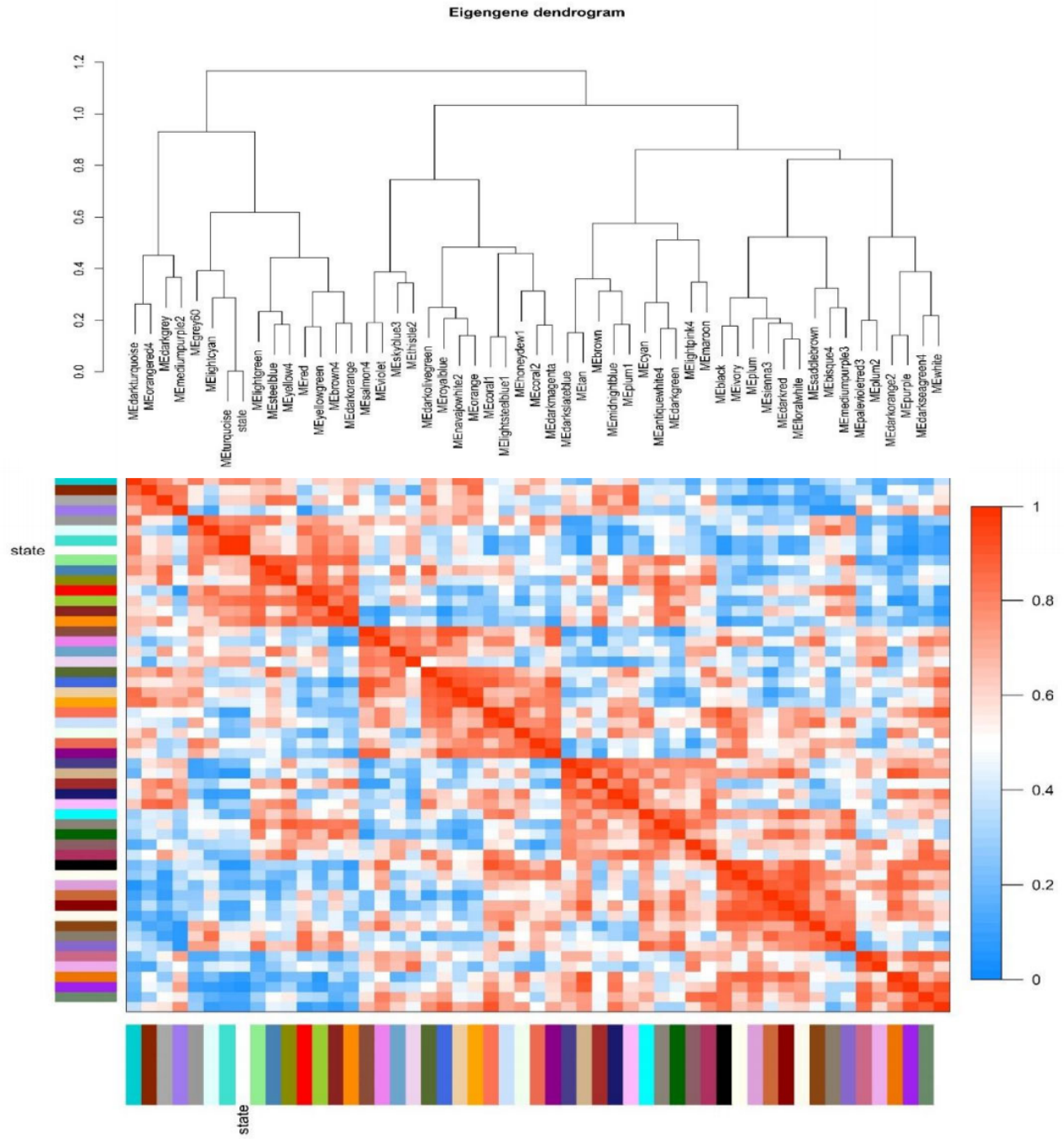


**Figure S4.** Cluster dendrogram and module assignment from WGCNA. The branches correspond to highly interconnected groups of genes. Colors in the horizontal bar represent the modules. **(A)** A549 dataset and **(B)** NHBE dataset.

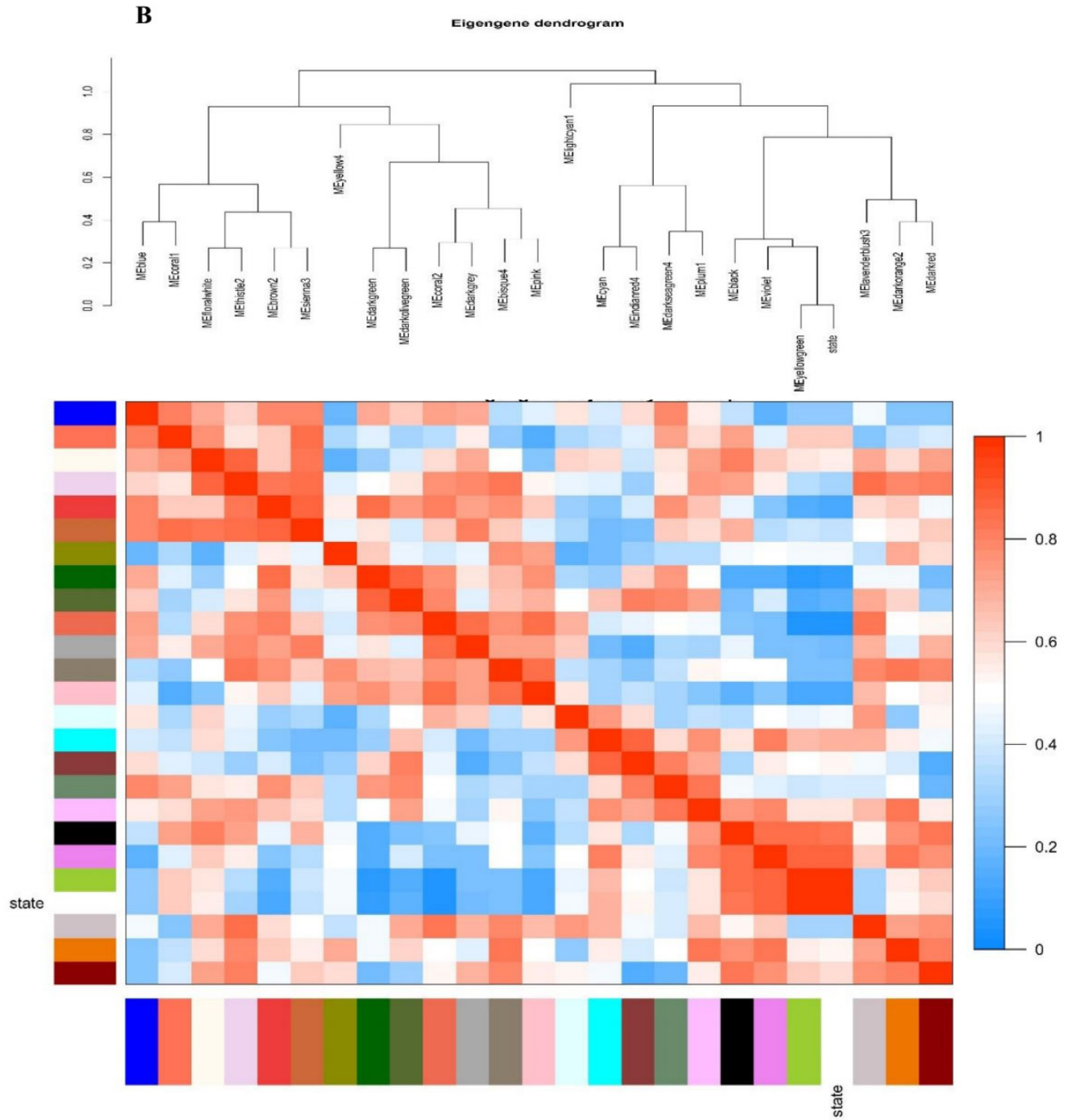


**Figure S5.** Module-trait relationship. Each row corresponds to a module eigengene and column corresponds to SARS-CoV-2 trait. Numbers in each cell represent the corresponding correlation and p value. **(A)** A549 dataset and **(B)** NHBE dataset.

**A**







**Figure S6.** Module-module associations. Eigengene dendrogram and Heatmap plot of the adjacencies in the eigengene network including the state represents the relationships among the modules and disease. (A) A549 dataset and (B) NHBE dataset.