





**Figure S2. Brain histopathology after mock and SARS2-N501Y**<sub>MA30</sub> **infection.** The representative images of brain tissue sections were stained with H&E staining at indicated days following either mock or SARS-CoV-2 infection. Scale bar: 50 µm.



**Figure S3. Lung pathology and immunohistochemistry of viral protein. (A)** Lung sections from mice infected with SARS2-N501Y<sub>MA30</sub> (n=5 for mock infection and 6 dpi; n=4 for 14 dpi) underwent H&E staining. **(B)** Acute lung injury severity was assessed blindly following ATS guidelines [32], with 0 for no injury, 1 for mild to moderate injury, and 2 for severe injury. \*\*\*\*p<0.0001. Data are shown as mean  $\pm$  SEM. **(C)** Lung tissue immunohistochemistry revealing SARS-CoV-2 N protein (black arrows) at specified dpi.



Figure S4. Gender dependent anxiety- and depression-like behaviors in mice following SARS2-N501Y<sub>MA30</sub> infection. (A) Experimental design and timeline illustrating the administration of SARS2-N501Y<sub>MA30</sub> and the behavioral test battery. (B) Open field test. Top: Representative heat map tracking of activity in the mock and SARS2-N501Y<sub>MA30</sub> infected mice. Bottom: The total travel distance and time spent in the center area are shown for males and females, respectively. Statistical significance: Male group: \*p=0.0219; ns, p=0.7185; n=11 mice in each group. Female group: \*\*p=0.0331; ns, p=0.0722; n=11 mice in each group. (C) Elevated plus maze test. Top: Representative heat map tracking of activity in mock and SARS2-N501Y<sub>MA30</sub> infected mice in closed arms (C) and open arms (O). Bottom: The percentages of time spent in the open arms and the number of open arm entries are shown for males and females, respectively. Statistical significance: Male group: \*p=0.0457; ns, p=0.1487; n=11 mice in each group. Female group: \*\*p=0.0022; ns, p=0.4732; n=11 mice in each group. (D) Schematics of the tail suspension test and results showing immobile time in males and females, respectively. Statistical significance: Male group. (E) Schematics of the forced swim test and results showing immobile time in males and females, respectively. Statistical significance: Male group. \*\*p=0.0002; ns, p=0.0014; n=11 mice in each group. (E) Schematics of the forced swim test and results showing immobile time in males and females, respectively. Statistical significance: Male group: \*\*\*p<0.0001; n=11 mice in each group. (E) Schematics of the forced swim test and results showing immobile time in males and females, respectively. Statistical significance: Male group: \*\*\*\*p<0.0001; n=11 mice in each group. Female group: \*\*\*\*p<0.0001; n=11 mice in each group. All statistical analyses were performed using a two-tailed unpaired Student's t-test. Data are presented as mean  $\pm$  SEM.



Figure S5. Transcriptomic profile overview in SARS2-N501Y<sub>MA30</sub> infected mouse brains. (A) Principal component analysis (PCA) of transcriptome profiles comparing mock-infected brains (0 dpi) with those at 4 and 14 dpi. (B) Volcano plot analysis: The x-axis denotes log2-transformed fold changes, and the y-axis indicates -log10-transformed significant values (Thresholds set at  $|log2fold| \ge 1.5$ , Q value  $\le 0.05$ ). (C) GO enrichment analysis of DEGs across groups. (D) Heatmap visualization of 140 DEGs identified post-infection. (E) KEGG pathway analysis comparing groups at 4 dpi vs 0 dpi, 14 dpi vs 0 dpi.



Figure S6. Detection of SARS-CoV-2 spike protein in plasma of infected mice by ELISA. C57BL/6 mice were intranasally infected with 10<sup>4</sup> PFU of SARS-CoV-2-N501Y<sub>MA30</sub>. Plasma was collected at 0, 2, 4, 6, 8, and 14 dpi via submandibular blood collection. SARS-CoV-2 spike protein levels in plasma were determined using a SARS-CoV-2 spike RBD ELISA Kit. (n=4 per time point). Statistical significance: \*p<0.05 and \*\*p<0.01 were determined by ordinary one-way ANOVA. Data are presented as mean  $\pm$  SEM.



**Figure S7. Cytokines and chemokines induced in the brain of SARS-CoV-2-infected mice.** Brains of C57BL/6 mice intranasally infected with 10<sup>4</sup> PFU of SARS2-N501Y<sub>MA30</sub> were harvested at indicated dpi. Cytokine and chemokine transcripts were measured by qRT-PCR analyzing total RNA extracted from mock-infected (0 dpi) and infected young C57BL/6 mice. Each brain was collected from one individual mouse. Mock (0 dpi), 2, 4, 8, 14 dpi: n=4; 6 dpi: n=5. The levels of transcripts were normalized to GAPDH and presented as 2<sup>A</sup>- $\Delta$ CT. Statistical significance: \*p<0.05, \*\*p<0.01, and \*\*\*\*p<0.0001 were determined by ordinary one-way ANOVA. Data are presented as mean  $\pm$  SEM.

## Table S1

| Gene                           | Forward Primer          | Reverse Primer            |
|--------------------------------|-------------------------|---------------------------|
| 2019-nCoV_N1                   | GACCCCAAAATCAGCGAAAT    | TCTGGTTACTGCCAGTTGAATCTGG |
| SARS-CoV-2 sgRNA for E protein | CGATCTCTTGTAGATCTGTTCTC | ATATTGCAGCAGTACGCACACA    |
| mouse GAPDH                    | AACAGCAACTCCCACTCTTC    | CCTGTTGCTGTAGCCGTATT      |
| mouse IFNα4                    | TCCATCAGCAGCTCAATGAC    | AGGAAGAGAGGGCTCTCCAG      |
| mouse IFNβ                     | TCAGAATGAGTGGTGGTTGC    | GACCTTTCAAATGCAGTAGATTCA  |
| mouse IFNγ                     | CGGCACAGTCATTGAAAGCCTA  | GTTGCTGATGGCCTGATTGTC     |
| mouse IFNλ                     | AGCTGCAGGTCCAAGAGCG     | GGTGGTCAGGGCTGAGTCATT     |
| mouse TNFα                     | GAACTGGCAGAAGAGGCACT    | AGGGTCTGGGCCATAGAACT      |
| mouse IL1α                     | CGCTTGAGTCGGCAAAGAAAT   | ACAAACTGATCTGTGCAAGTCTC   |
| mouse IL-1β                    | ACTGTTTCTAATGCCTTCCC    | ATGGTTTCTTGTGACCCTGA      |
| mouse IL-6                     | GAGGATACCACTCCCAACAGACC | AAGTGCATCATCGTTGTTCATACA  |
| mouse IL-8                     | CACCTCAAGAACATCCAGAGCT  | CAAGCAGAACTGAACTACCATCG   |
| mouse CCL2                     | CTTCTGGGCCTGCTGTTCA     | CCAGCCTACTCATTGGGATCA     |
| mouse CCL5                     | AGATCTCTGCAGCTGCCCTCA   | GGAGCACTTGCTGCTGGTGTAG    |
| mouse CXCL2                    | CATCCAGAGCTTGAGTGTGACG  | GGCTTCAGGGTCAAGGCAAACT    |
| mouse CXCL9                    | GCCATGAAGTCCGCTGTTCT    | GGGTTCCTCGAACTCCACACT     |
| mouse CXCL10                   | GCCGTCATTTTCTGCCTCAT    | GCTTCCCTATGGCCCTCATT      |
| mouse Mx1                      | TGGACATTGCTACCACAGAGGC  | TTGCCTTCAGCACCTCTGTCCA    |
| mouse OAS1                     | ATTACCTCCTTCCCGACACC    | CAAACTCCACCTCCTGATGC      |