**Supplementary Material**

**Analysis and Identification Genetic Effect of SARS-CoV-2 Infections to Alzheimer’s Disease Patients by Integrated Bioinformatics**

**Supplementary Table 1.** Statistics of differences between the training set and test set

|  |  |  |  |
| --- | --- | --- | --- |
|  | train | test | p |
| Characteristics | 137 | 58 |  |
| *ITPR1* (mean(sd)) | 9.74 (0.92) | 9.66 (0.96) | 0.61 |
| *ITPR3* (mean(sd)) | 8.31 (0.67) | 8.38 (0.59) | 0.25 |
| *ITPKB* (mean(sd)) | 9.38 (0.88) | 9.54 (0.96) | 0.26 |
| *RAPGEF3* (mean(sd)) | 7.9 (0.76) | 8 (0.8) | 0.43 |
| *MFGE8* (mean(sd)) | 10.15 (0.64) | 10.17 (0.61) | 0.73 |
| Age (mean(sd)) | 84.99 (6.32) | 85.02 (7.9) | 0.98 |
| Sex (mean(sd)) | 0.53 (0.5) | 0.47 (0.5) | 0.45 |
| AD\_diagnosis (mean(sd)) | 0.48 (0.5) | 0.53 (0.5) | 0.5 |

*p*<0.05 is considered to be statistically significant.

**Supplementary Table 2.** Differential expression of Cross platform normalized data (AlzData)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | eQTL | GWAS | PPI | Early\_DEG | Pathology cor (Aβ) | Pathology cor (tau) | CFG |
| *ITPR1* | 0 | 1 | - | no | -0.002, ns | -0.329, ns | 1 |
| *ITPR3* | 0 | 0 | - | NA | 0.418, \*\* | 0.099, ns | 1 |
| *ITPKB* | 0 | 0 | - | NA | 0.256, ns | 0.422, ns | 0 |
| *RAPGEF3* | 0 | 0 | APP, APOE | yes | 0.444, \*\* | 0.567, \* | 3 |

CFG, Rank of AlzData; eQTL, expression of target gene is regulated by AD genetic variants (genetic variants: IGAP GWAS pl < 1E-3; eQTL: p < 1E-3); GWAS, IGAP p < 1E-3; PPI, target gene has significant physical interaction with APP, PSEN1, PSEN2, APOE, or MAPT (p < 0.05); Early\_DEG: target gene is differentially expressed in AD mouse models before AD pathology emergence; Pathology cor (Aβ): correlation of target gene expression with AD pathology in Aβ line AD mouse models (r, p; ns: p > 0.05; \*p <0.05; \*\*p < 0.01; \*\*\*p <0.001); Pathology cor (tau): correlation of target gene expression with AD pathology in tau line AD mouse models (r, p; ns: p > 0.05; \*p <0.05; \*\*p < 0.01; \*\*\*p <0.001); CFG, total CFG score of target gene, 1 CFG point is added if any of above evidence is significant, CFG point ranges from 0 to 5.

Supplementary Table 3. TF-gene subnetwork (see Excel file)

Supplementary Table 4. AD risk gene and hub gene network (see Excel file)

Supplementary Table 5. TF-miRNA subnetwork (see Excel file)

Supplementary Table 6. Protein-chemical subnetwork (see Excel file)