**Supplementary Table S1. Quality Control of mRNA sequence**

| Sample | Bases_G | Q30_G | Raw_reads_M | Clean_reads_M | Map_ration_% | Q20_% | Q30_% |
|---|---|---|---|---|---|---|---|
| DMEM_4d | 7.80 | 7.40 | 52.50 | 49.09 | 92.78 | 97.94 | 94.7 |
| DMEM_4d | 8.20 | 7.80 | 55.13 | 51.56 | 92.45 | 97.93 | 94.65 |
| DMEM_4d | 8.20 | 7.70 | 54.70 | 51.32 | 88.28 | 97.93 | 94.65 |
| DMEM_7 d | 8.20 | 7.70 | 54.85 | 51.21 | 88.34 | 97.9 | 94.67 |
| DMEM_7 d | 7.90 | 7.50 | 53.02 | 49.49 | 93.74 | 97.89 | 94.67 |
| DMEM_7 d | 7.90 | 7.40 | 52.69 | 49.23 | 92.49 | 97.99 | 94.84 |
| rRC-HL_4d | 7.60 | 7.20 | 50.78 | 47.47 | 93.22 | 98.11 | 94.95 |
| rRC-HL_4d | 8.20 | 7.80 | 54.84 | 51.27 | 92.68 | 98.04 | 94.85 |
| rRC-HL_4d | 7.90 | 7.55 | 53.01 | 46.35 | 93.79 | 98.1 | 94.99 |
| rRC-HL_7d | 6.80 | 6.52 | 45.43 | 42.86 | 94.82 | 98.11 | 94.99 |
| rRC-HL_7d | 8.10 | 7.62 | 54.17 | 50.38 | 94.94 | 97.62 | 93.81 |
| rRC-HL_7d | 6.90 | 6.63 | 46.65 | 43.61 | 93.62 | 98.04 | 94.85 |
| GX074_4d | 7.30 | 6.90 | 48.93 | 45.99 | 84.3 | 98.02 | 94.92 |
| GX074_4d | 7.90 | 7.40 | 53.06 | 49.67 | 89.59 | 967.63 | 93.71 |
| GX074_4d | 7.10 | 6.70 | 47.27 | 44.23 | 92.01 | 98.03 | 94.82 |
| GX074_7 d | 6.80 | 6.40 | 45.54 | 42.51 | 94.05 | 98.11 | 95.05 |
| GX074_7 d | 8.40 | 7.90 | 56.08 | 52.55 | 94.55 | 98.09 | 94.92 |
| GX074_7d | 8.40 | 7.90 | 56.14 | 52.24 | 94.89 | 98.09 | 94.94 |
| CVS-24_4d | 6.50 | 6.20 | 43.48 | 40.47 | 91.19 | 98.11 | 95.09 |
| CVS-24_4d | 8.10 | 7.71 | 54.17 | 50.68 | 94.96 | 98.05 | 94.93 |
| CVS-24_4d | 7.20 | 6.90 | 48.45 | 45.22 | 93.91 | 98.04 | 94.96 |
| CVS-24_7d | 6.50 | 6.20 | 43.73 | 40.86 | 91.97 | 98.13 | 95.14 |
| CVS-24_7d | 6.40 | 6.10 | 43.07 | 40.11 | 95.39 | 98.14 | 95.04 |
| CVS-24_7d | 7.80 | 7.40 | 52.32 | 49.21 | 94.41 | 98.97 | 94.68 |

Note:

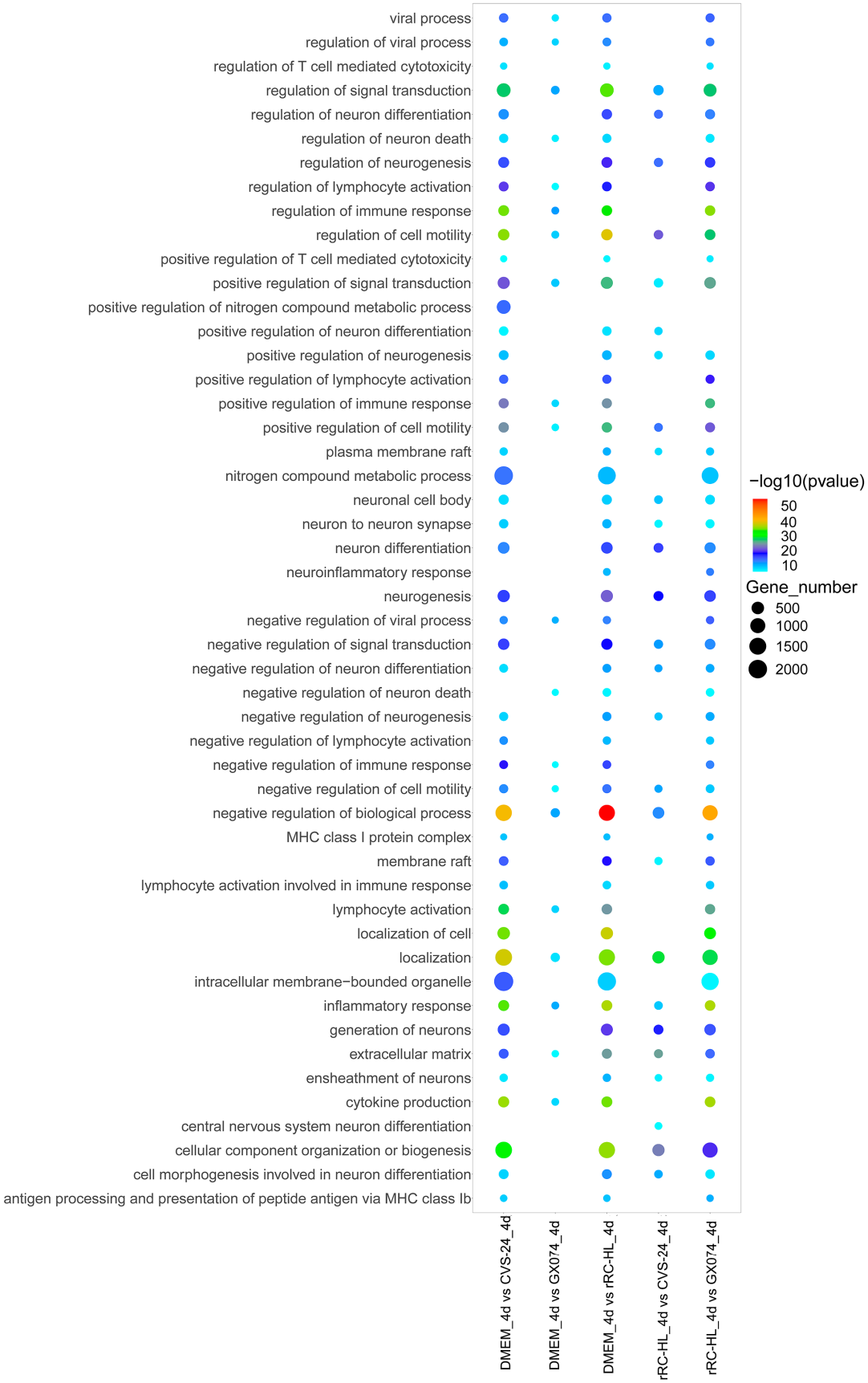
Q30: The total number of bases with an accuracy of more than 99.9%;

Q20 %: Percentage of bases with more than 99% accuracy;

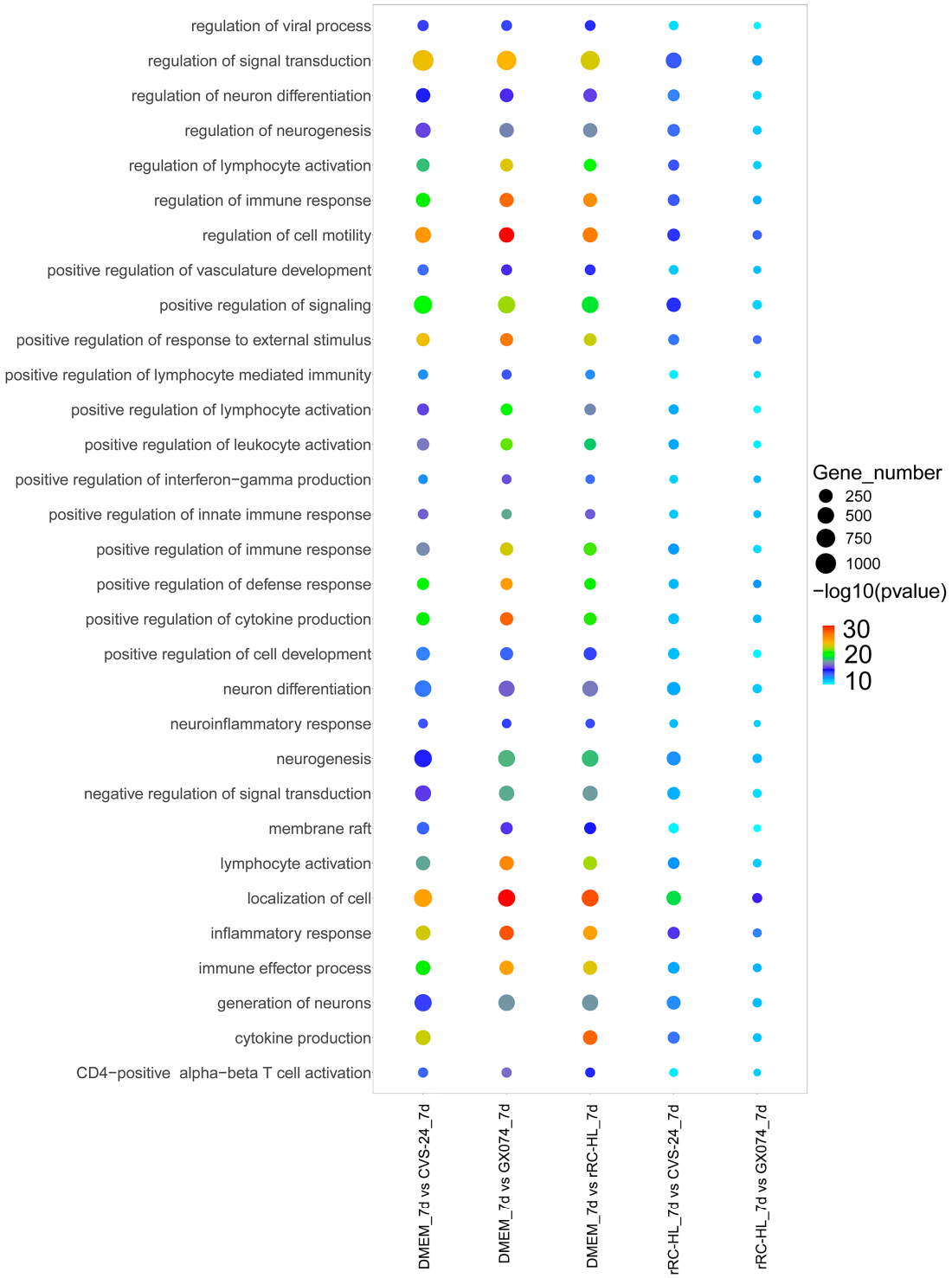
Q30 %: Percentage of bases with more than 99.9% accuracy.

## Supplementary Table S4. Up -down DEGS

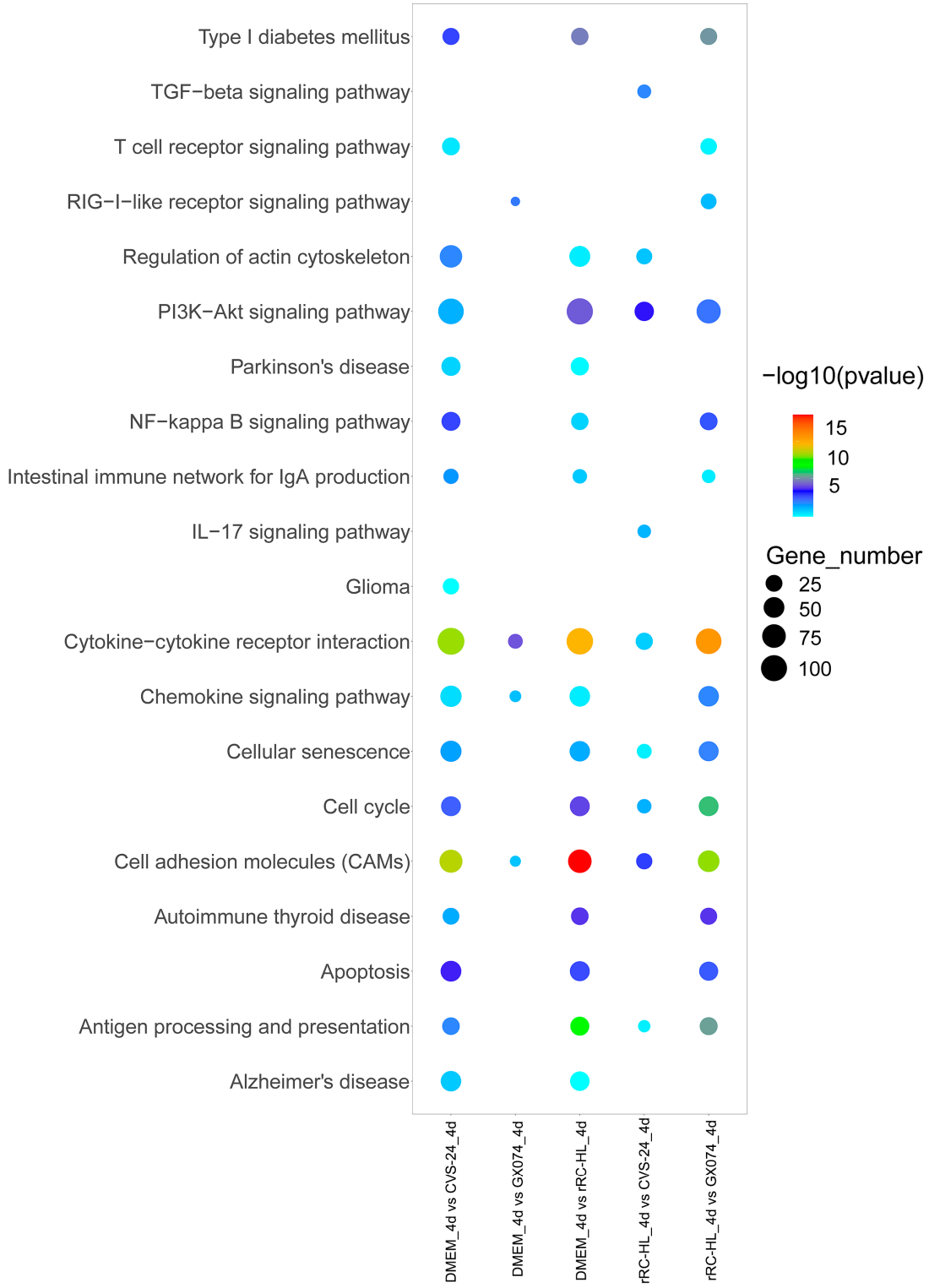
| Control | Treat | UP-regulated | Down-regulated | Total |
|---|---|---|---|---|
| DMEM_4 | rRC_HL_4 | 1953 | 1669 | 3622 |
| DMEM_4 | GX074_4 | 158 | 107 | 265 |
| DMEM_4 | CVS24_4 | 2302 | 1795 | 4097 |
| DMEM_7 | rRC_HL_7 | 2557 | 2033 | 4590 |
| DMEM_7 | GX074_7 | 2667 | 2234 | 4901 |
| DMEM_7 | CVS24_7 | 3091 | 3246 | 6337 |



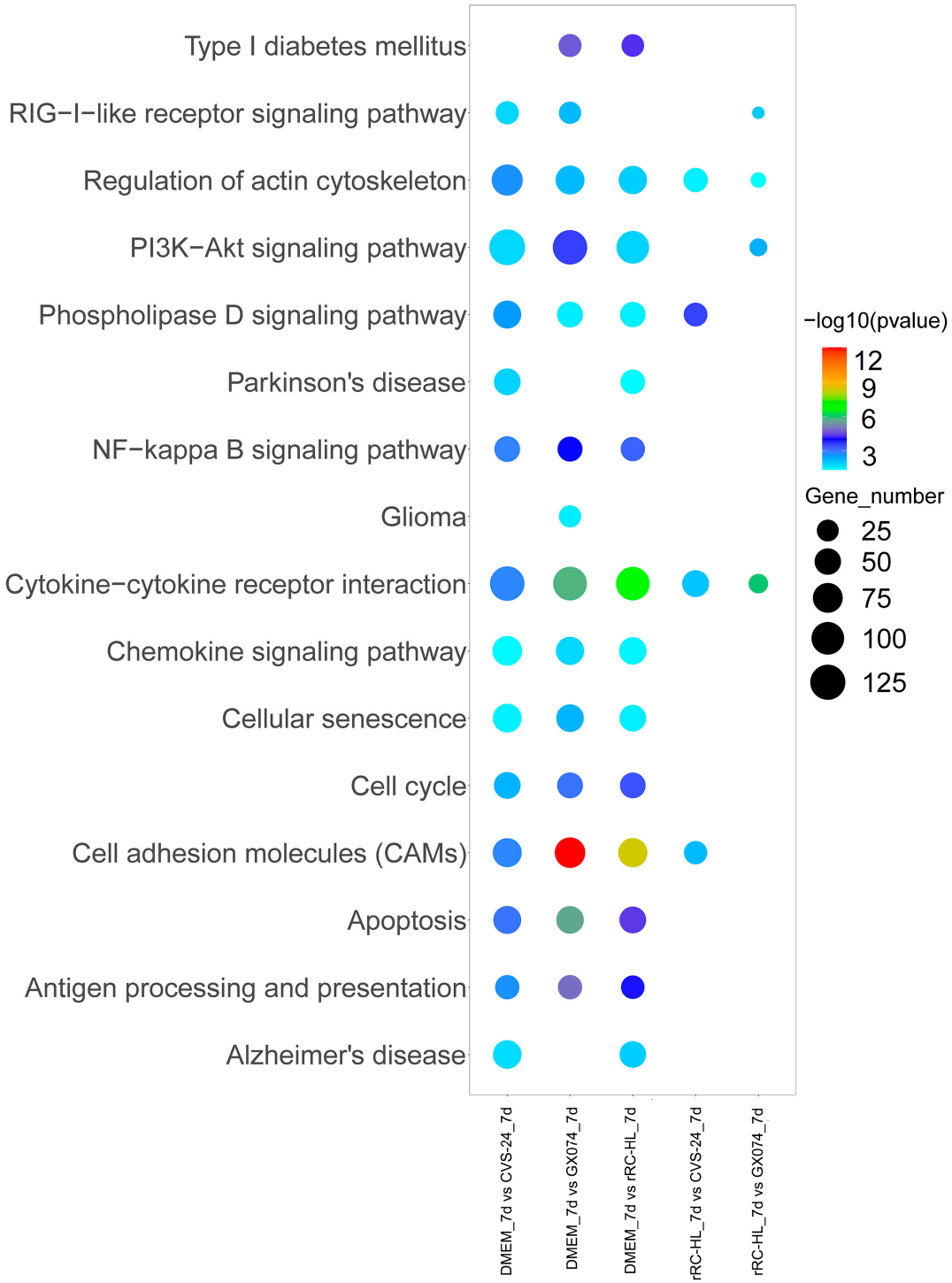

Supplementary Figure S1. GO term of mice brain infected RABV at 4 dpi




Supplementary Figure S2. GO term of mice brain infected RABV at 7 dpi

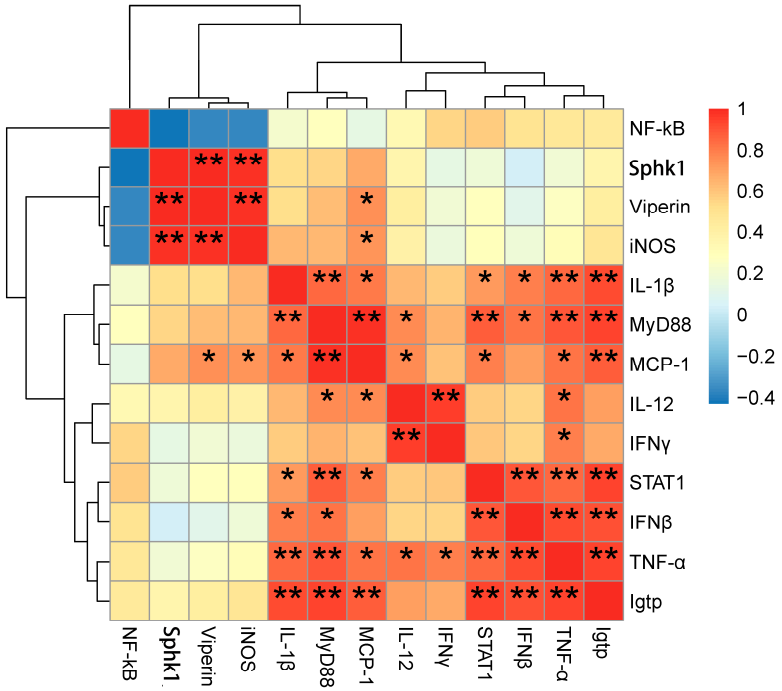



Supplementary Figure S3. KEGG analysis of microglia of mice brain infected with RABV at 4 dpi

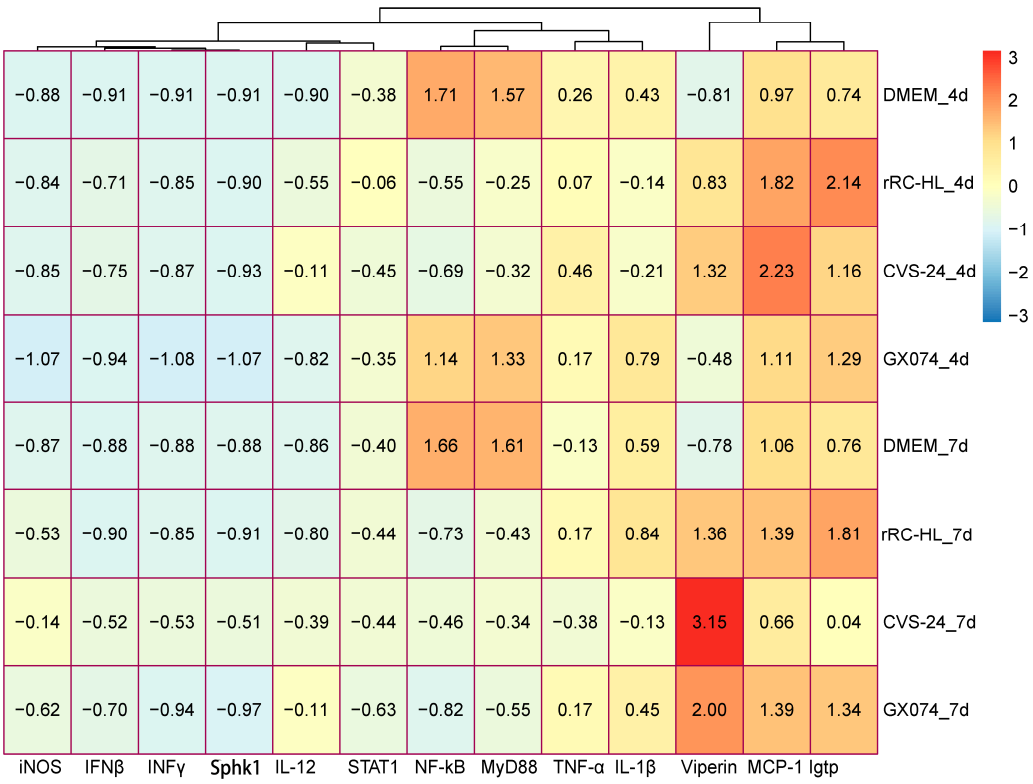



Supplementary Figure S4. KEGG analysis of microglia of mice brain infected with RABV at 7 dpi

a


NF-kB
Sphk1
Viperin
iNOS
IL-1β
MyD88
MCP-1
IL-12
IFNγ
STAT1
IFNβ
TNF-α
Igtp
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4

b


−0.88 −0.91 −0.91 −0.91 −0.90 −0.38 1.71 1.57 0.26 0.43 −0.81 0.97 0.74 DMEM_4d
−0.84 −0.71 −0.85 −0.90 −0.55 −0.06 −0.55 −0.25 0.07 −0.14 0.83 1.82 2.14 rRC-HL_4d
−0.85 −0.75 −0.87 −0.93 −0.11 −0.45 −0.69 −0.32 0.46 −0.21 1.32 2.23 1.16 CVS-24_4d
−1.07 −0.94 −1.08 −1.07 −0.82 −0.35 1.14 1.33 0.17 0.79 −0.48 1.11 1.29 GX074_4d
−0.87 −0.88 −0.88 −0.88 −0.86 −0.40 1.66 1.61 −0.13 0.59 −0.78 1.06 0.76 DMEM_7d
−0.53 −0.90 −0.85 −0.91 −0.80 −0.44 −0.73 −0.43 0.17 0.84 1.36 1.39 1.81 rRC-HL_7d
−0.14 −0.52 −0.53 −0.51 −0.39 −0.44 −0.46 −0.34 −0.38 −0.13 3.15 0.66 0.04 CVS-24_7d
−0.62 −0.70 −0.94 −0.97 −0.11 −0.63 −0.82 −0.55 0.17 0.45 2.00 1.39 1.34 GX074_7d
iNOS IFNβ INFγ Sphk1 IL-12 STAT1 NF-kB MyD88 TNF-α IL-1β Viperin MCP-1 Igtp
3
2
1
0
−1
−2
−3

Supplementary Figure S5. The functional analysis of gene expression

(a) Pearson coefficients, red color represents positive correlation, blue color represents negative correlation, *indicates significant positive correlation and significant negative correlation. *$p<0.05$; **$p<0.01$. (b) Difference between multiple analysis. Red color was high expression, and blue was low expression.