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**Table S1. Basic statistics of deep RNA sequencing data before and after processing.**

| Sample ID | group | Status[a] | chemical | Raw reads | Raw base | Clean reads | Clean base |
|---|---|---|---|---|---|---|---|
| SRR1177973 | control | control_1,2_rep1 | none | 31,177,368 | 3,148,914,168 | 25,432,020 | 2,462,728,432 |
| SRR1178016 | control | control_1,2_rep2 | none | 37,633,288 | 1,881,664,400 | 30,379,728 | 1,518,986,400 |
| SRR1178019 | control | control_1,2_rep3 | none | 31,890,846 | 3,189,084,600 | 24,346,292 | 2,193,935,958 |
| SRR1178024 | control | control_1,2_rep4 | none | 34,863,516 | 3,486,351,600 | 26,738,504 | 2,413,857,762 |
| SRR1178035 | control | control_1,2_rep5 | none | 28,881,662 | 2,888,166,200 | 12,219,280 | 1,024,689,960 |
| SRR1178045 | control | control_1,2_rep6 | none | 43,991,002 | 4,399,100,200 | 37,598,592 | 3,476,914,366 |
| SRR1178050 | control | control_1,2_rep7 | none | 32,173,238 | 3,217,323,800 | 26,457,064 | 2,469,251,284 |
| SRR1178061 | control | control_1,2_rep8 | none | 126,534,710 | 12,780,005,710 | 113,578,792 | 11,094,937,146 |
| SRR1178063 | control | control_1,2_rep9 | none | 89,067,134 | 8,995,780,534 | 78,194,796 | 7,630,920,826 |
| SRR1178064 | control | control_1,2_rep10 | none | 114,879,700 | 11,602,849,700 | 103,271,474 | 10,094,821,394 |
| SRR1178074 | control | control_1,2_rep11 | none | 100,372,668 | 10,137,639,468 | 89,651,088 | 8,752,622,686 |
| SRR1178075 | control | control_1,2_rep12 | none | 84,037,926 | 8,487,830,526 | 71,991,346 | 7,031,898,580 |
| SRR1177974 | 1 | case_1_rep1 | CARBON TETRACHLORIDE | 37,111,098 | 3,748,220,898 | 28,934,614 | 2,782,585,288 |
| SRR1177976 | 1 | case_1_rep2 | CARBON TETRACHLORIDE | 32,472,640 | 3,279,736,640 | 25,072,632 | 2,400,528,770 |
| SRR1177987 | 2 | case_2_rep1 | CHLOROFORM | 27,286,434 | 2,622,275,456 | 27,286,434 | 2,615,452,952 |
| SRR1177988 | 2 | case_2_rep2 | CHLOROFORM | 28,309,072 | 2,702,468,469 | 28,309,072 | 2,700,210,018 |
| SRR1177989 | 2 | case_2_rep3 | CHLOROFORM | 29,236,332 | 2,830,795,061 | 29,236,332 | 2,813,330,092 |
| SRR1178004 | control | control_3_rep1 | none | 35,195,190 | 3,368,980,094 | 35,195,190 | 3,425,939,420 |
| SRR1178006 | control | control_3_rep2 | none | 38,334,282 | 3,678,690,904 | 38,334,282 | 3,733,890,438 |
| SRR1178013 | control | control_3_rep3 | none | 29,241,722 | 2,835,875,928 | 29,241,722 | 2,865,263,524 |
| SRR1178062 | control | control_3_rep4 | none | 113,793,168 | 11,185,355,795 | 113,793,168 | 11,116,172,178 |
| SRR1178070 | control | control_3_rep5 | none | 84,237,388 | 8,329,607,546 | 84,237,388 | 8,281,855,076 |
| SRR1177966 | 3 | case_3_rep1 | THIOACETAMIDE | 30,921,234 | 3,020,482,337 | 30,921,234 | 3,006,946,166 |
| SRR1177969 | 3 | case_3_rep2 | THIOACETAMIDE | 30,633,024 | 2,975,058,834 | 30,633,024 | 2,957,983,402 |
| SRR1177970 | 3 | case_3_rep3 | THIOACETAMIDE | 30,137,272 | 2,917,660,816 | 30,137,272 | 2,900,399,800 |

[a] control_1,2_* means the common control for group 1 and group 2; control_3_* means the control for group 3.

**Table S2. Basic statistics of clean reads alignment against to the *Rattus norvegicus* genome sequence.**

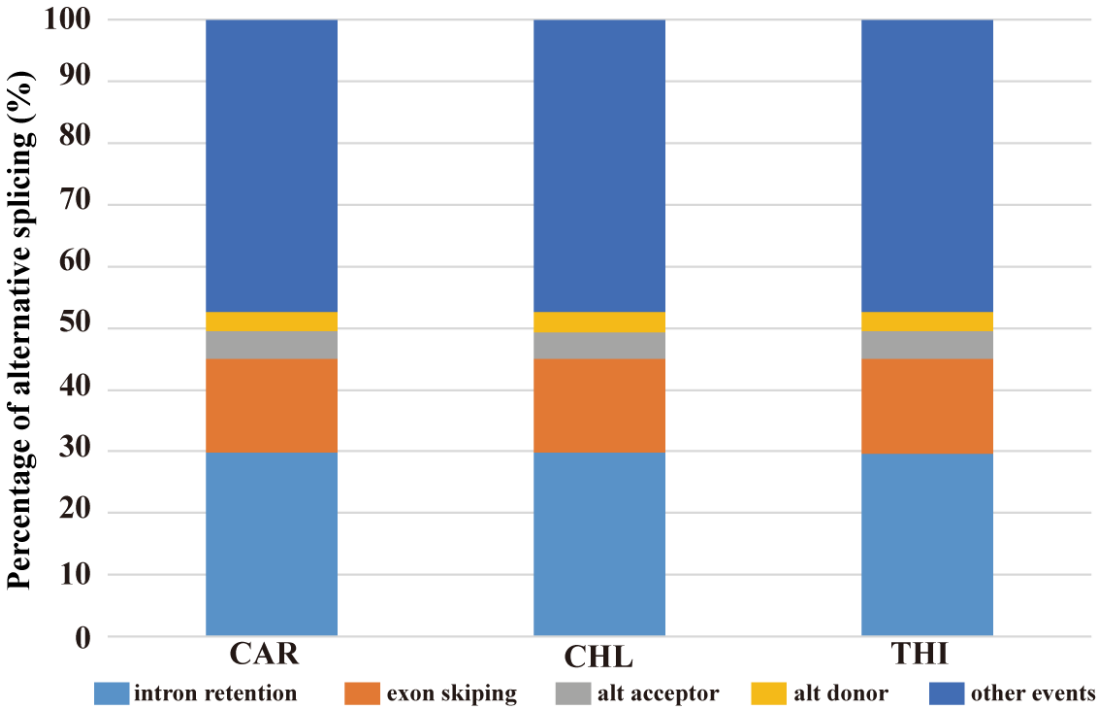
| Sample ID | group | Status[b] | chemical | Mapped reads | Mapped rate (%) |
|---|---|---|---|---|---|
| SRR1177973 | control | control_1,2_rep1 | none | 22, 442, 236 | 88. 24 |
| SRR1178016 | control | control_1,2_rep2 | none | 26, 312, 986 | 86. 61 |
| SRR1178019 | control | control_1,2_rep3 | none | 21, 343, 476 | 87. 67 |
| SRR1178024 | control | control_1,2_rep4 | none | 23, 180, 590 | 86. 69 |
| SRR1178035 | control | control_1,2_rep5 | none | 10, 584, 642 | 86. 62 |
| SRR1178045 | control | control_1,2_rep6 | none | 32, 773, 378 | 87. 17 |
| SRR1178050 | control | control_1,2_rep7 | none | 23, 127, 204 | 87. 41 |
| SRR1178061 | control | control_1,2_rep8 | none | 100, 875, 084 | 88. 82 |
| SRR1178063 | control | control_1,2_rep9 | none | 70, 303, 084 | 89. 91 |
| SRR1178064 | control | control_1,2_rep10 | none | 91, 735, 658 | 88. 83 |
| SRR1178074 | control | control_1,2_rep11 | none | 78, 524, 370 | 87. 59 |
| SRR1178075 | control | control_1,2_rep12 | none | 64, 456, 258 | 89. 53 |
| SRR1177974 | 1 | case_1_rep1 | CARBON TETRACHLORIDE | 26, 068, 042 | 90. 09 |
| SRR1177976 | 1 | case_1_rep2 | CARBON TETRACHLORIDE | 22, 429, 210 | 89. 46 |
| SRR1177987 | 2 | case_2_rep1 | CHLOROFORM | 24, 486, 020 | 89. 74 |
| SRR1177988 | 2 | case_2_rep2 | CHLOROFORM | 25, 690, 438 | 90. 75 |
| SRR1177989 | 2 | case_2_rep3 | CHLOROFORM | 26, 166, 592 | 89. 50 |
| SRR1178004 | control | control_3_rep1 | none | 30, 481, 220 | 86. 61 |
| SRR1178006 | control | control_3_rep2 | none | 33, 915, 942 | 88. 47 |
| SRR1178013 | control | control_3_rep3 | none | 26, 203, 538 | 89. 61 |
| SRR1178062 | control | control_3_rep4 | none | 100, 138, 330 | 88. 00 |
| SRR1178070 | control | control_3_rep5 | none | 75, 805, 910 | 89. 99 |
| SRR1177966 | 3 | case_3_rep1 | THIOACETAMIDE | 27, 590, 188 | 89. 23 |
| SRR1177969 | 3 | case_3_rep2 | THIOACETAMIDE | 27, 662, 128 | 90. 30 |
| SRR1177970 | 3 | case_3_rep3 | THIOACETAMIDE | 27, 204, 158 | 90. 27 |

[b.] control_1,2_* means the common control for group 1 and group 2; control_3_* means the control for group 3.

**Table S3. Basic statistics of assembly results of transcriptome in *Rattus norvegicus*.**

| Statistics terms | Number |
|---|---|
| Total number | 64,938 |
| Total length of (bp) | 121,882,090 |
| Average length (bp) | 1,876.90 |
| N50 Length (bp) | 3,588 |
| Maximum length (bp) | 41,083 |
| Minimum length (bp) | 26 |
| GC content (%) | 48.76 |

**Figure S1: Distribution of five different types of alternative splicing events identified in three chemical treatment.**



## Figure S2: Distribution of the lncRNAs identified in three chemical treatment.

(A) Distribution of the known lncRNAs identified in three chemical treatment. (B) Distribution of the novel lncRNAs identified in three chemical treatment.

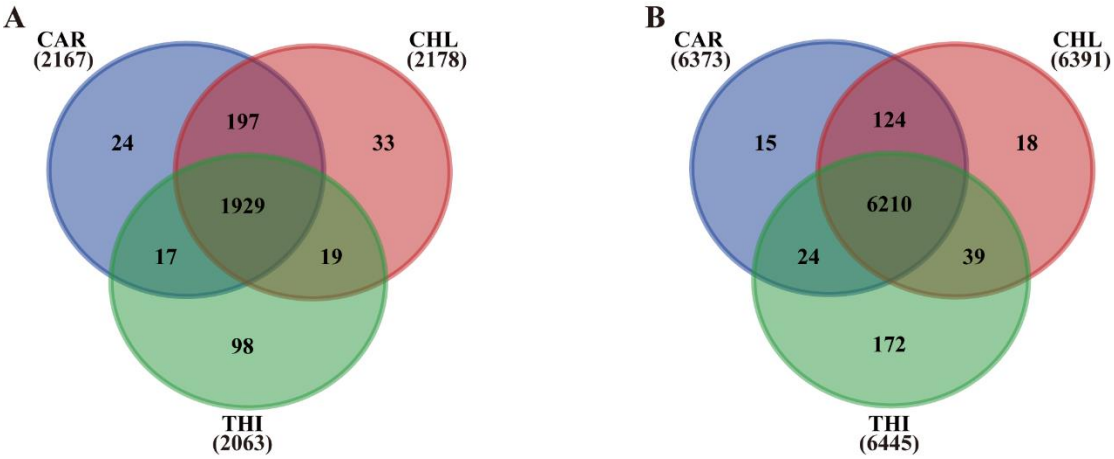
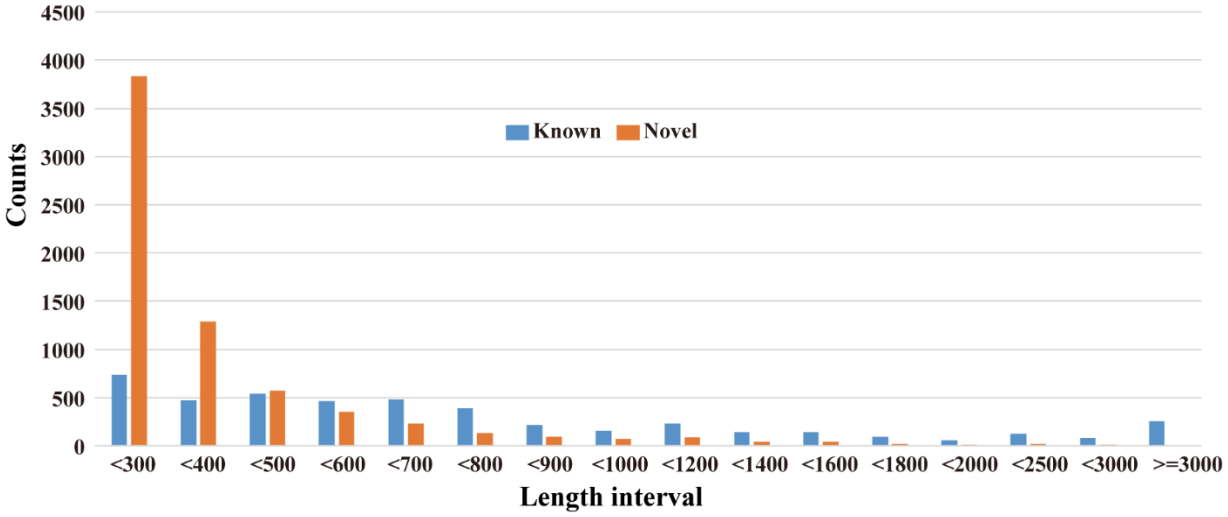
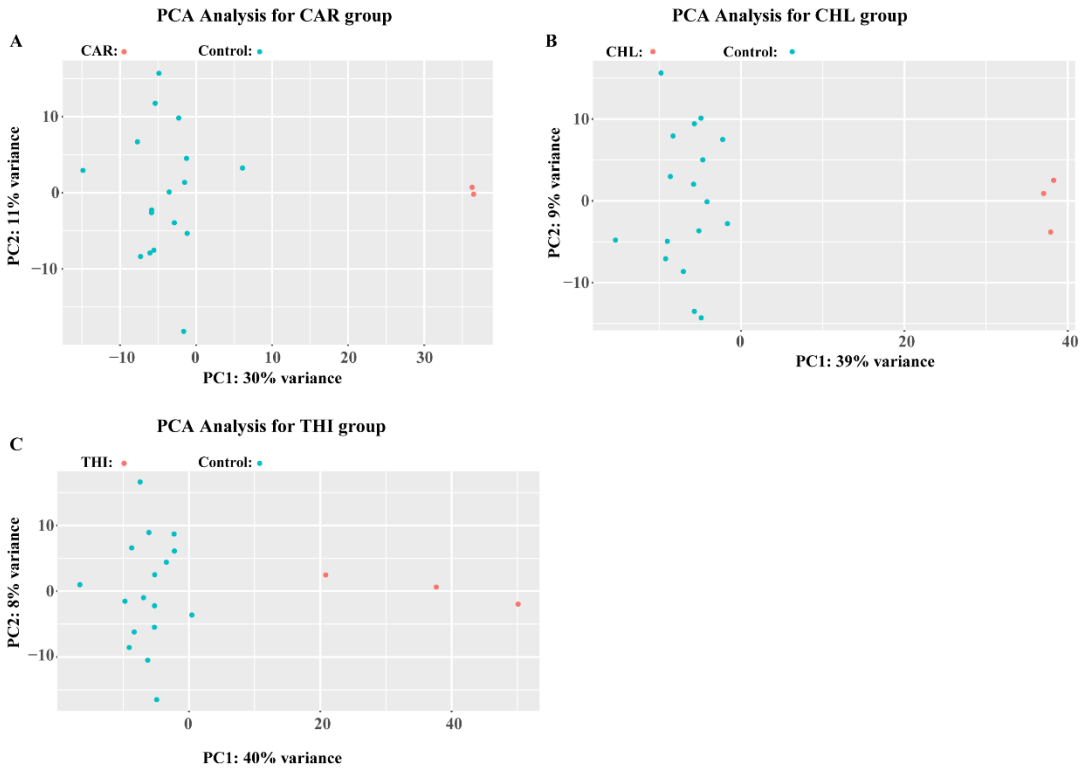


**Figure S3: Length distribution of all assembled known and novel lncRNAs from *Rattus norvegicus* transcriptome.**



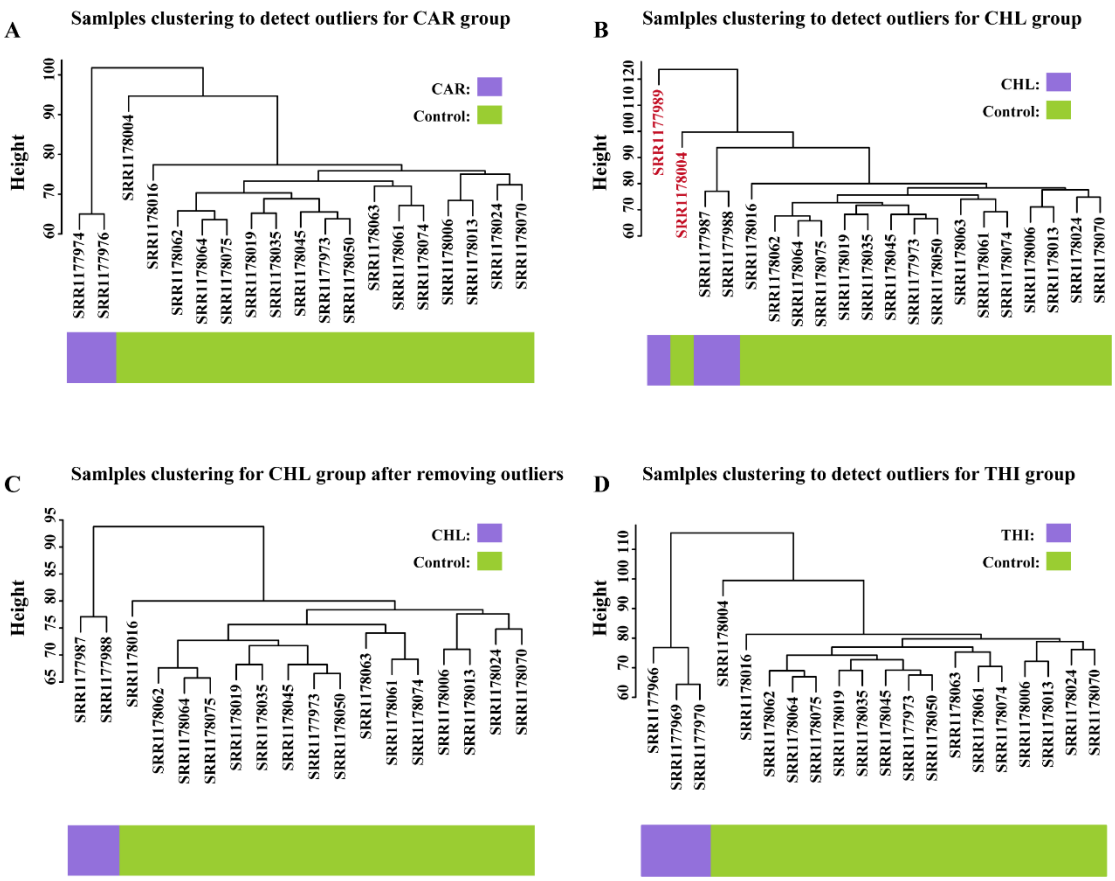
## Figure S4: PCA analysis for the samples in three chemical treatment.

(A) PCA analysis for the samples in CAR chemical treatment. (B) PCA analysis for the samples in CHL chemical treatment. (C) PCA analysis for the samples in THI chemical treatment.



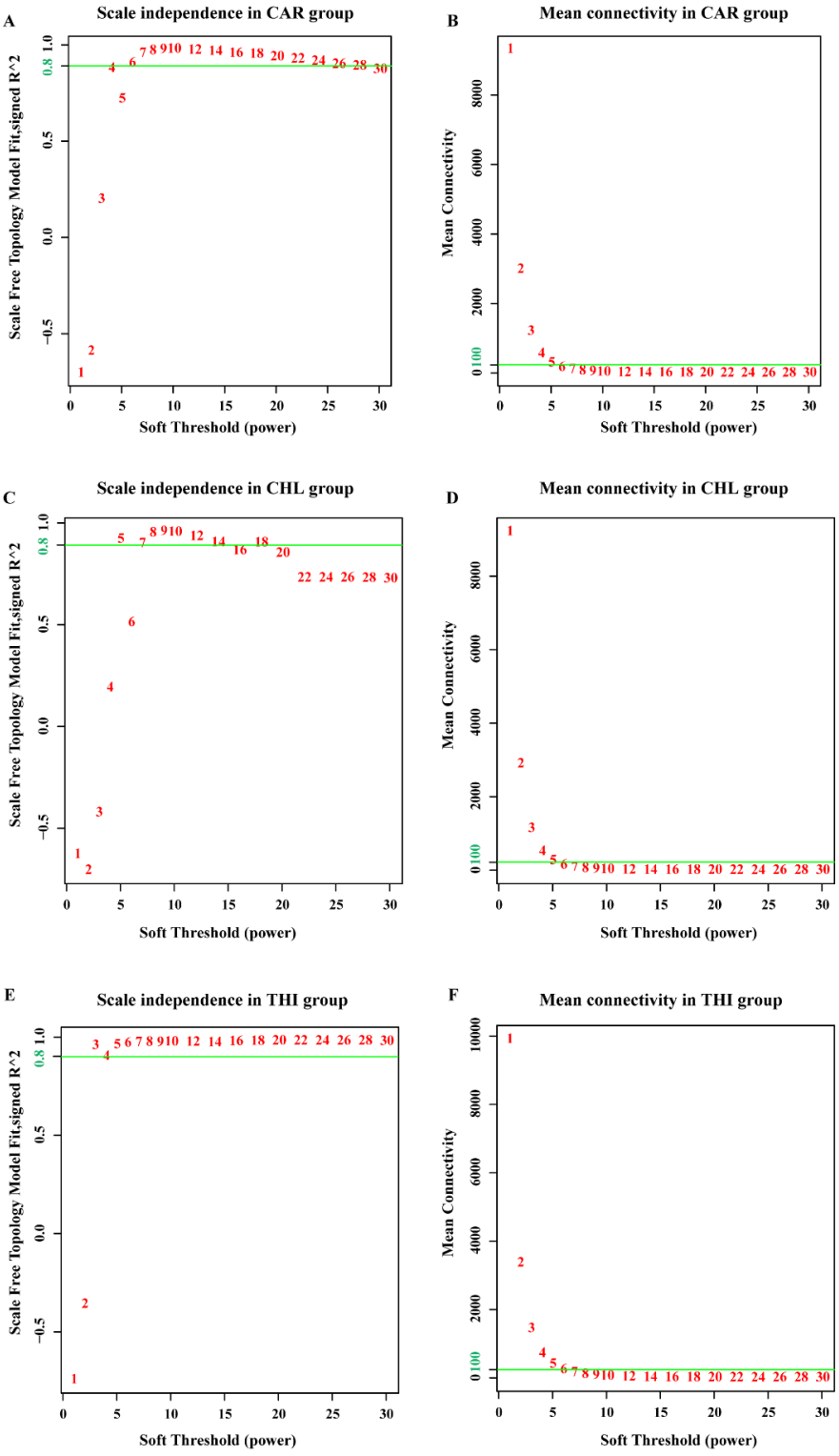
## Figure S5: Samlples clustering to detect outliers for three group.

(A) Samlples clustering to detect outliers for CAR group. (B) Samlples clustering to detect outliers for CHL group. (C) Samlples clustering for CHL group after removing the outliers. (D) Samlples clustering to detect outliers for THI group.



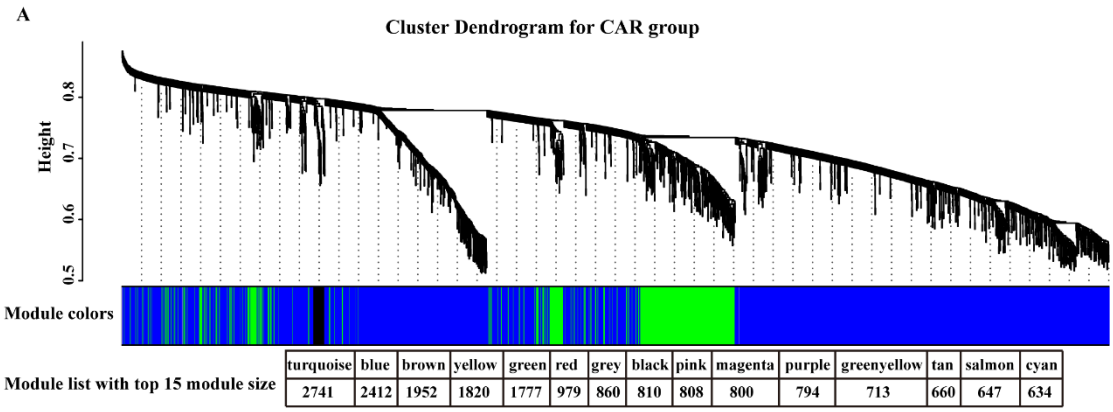
## Figure S6: Identification of best soft threshold among three groups.

(A) Scale independence in CAR group. (B) Mean connectivity in CAR group. (C) Scale independence in CHL group. (D) Mean connectivity in CHL group. (E) Scale independence in THI group. (F) Mean connectivity in THI group.

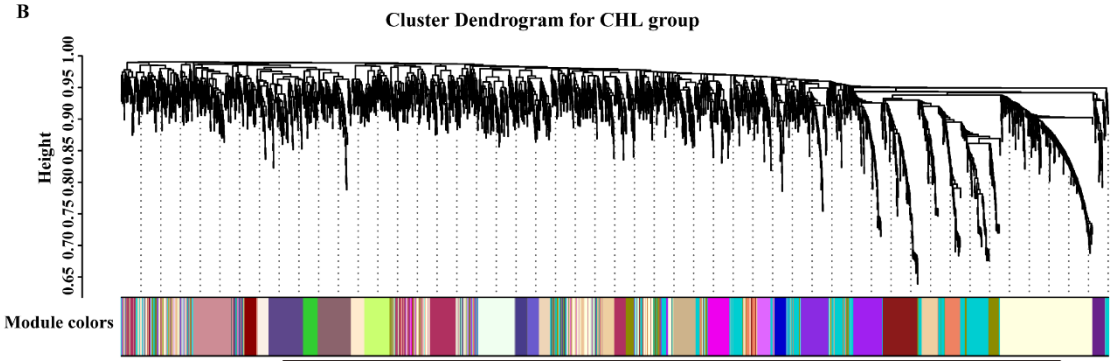


## Figure S7: Cluster dendrogram among three groups.

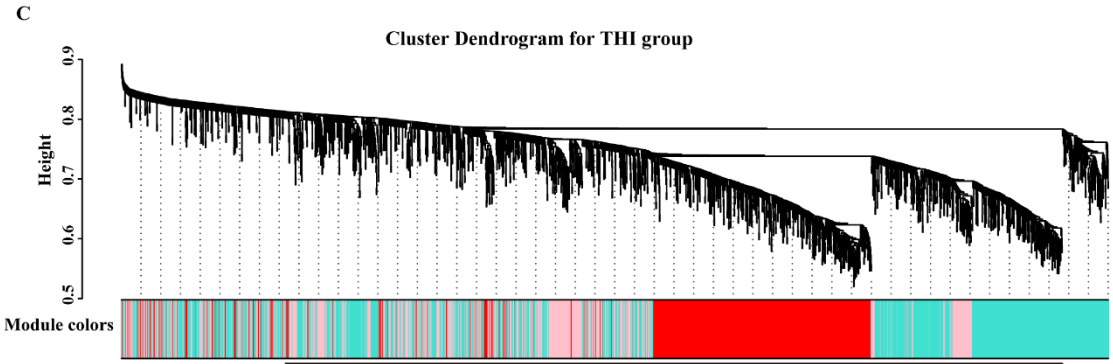
(A) Cluster dendrogram among CAR groups. (B) Cluster dendrogram among CHL groups. (C) Cluster dendrogram among THI groups.




| Module list with top 15 module size | turquoise | blue | brown | yellow | green | red | grey | black | pink | magenta | purple | greenyellow | tan | salmon | cyan |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2741 | 2412 | 1952 | 1820 | 1777 | 979 | 860 | 810 | 808 | 800 | 794 | 713 | 660 | 647 | 634 |




| Module list with top 15 module size | turquoise | blue | brown | yellow | green | red | black | pink | magenta | purple | greenyellow | tan | salmon | cyan | grey |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 3965 | 1945 | 1065 | 869 | 806 | 804 | 791 | 770 | 671 | 639 | 633 | 617 | 606 | 605 | 605 |




| Module list with top 15 module size | turquoise | blue | brown | yellow | green | red | grey | black | pink | magenta | purple | greenyellow | tan | salmon | cyan |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 7923 | 2344 | 2080 | 1984 | 1976 | 1563 | 1514 | 1223 | 1089 | 946 | 851 | 832 | 766 | 737 | 716 |

## Figure S8: Module membership vs. gene significance among three groups.

(A) Module membership vs. gene significance among CAR groups. (B) Module membership vs. gene significance among CHL groups. (C) Module membership vs. gene significance THI three groups.

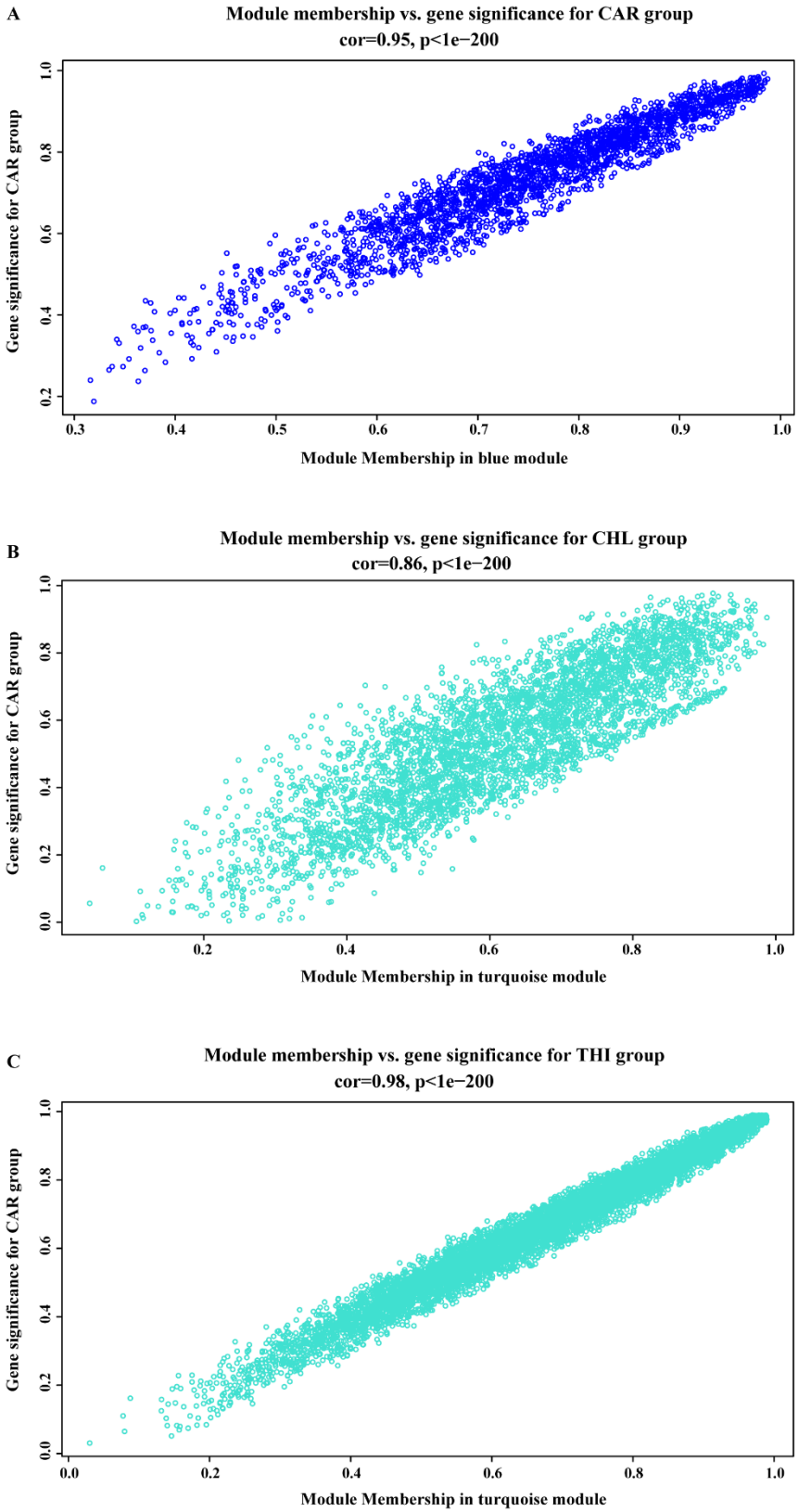


**Figure S9: Eigengene adjacency heatmap illustrating the relationship between modules and traits in CAR group.**

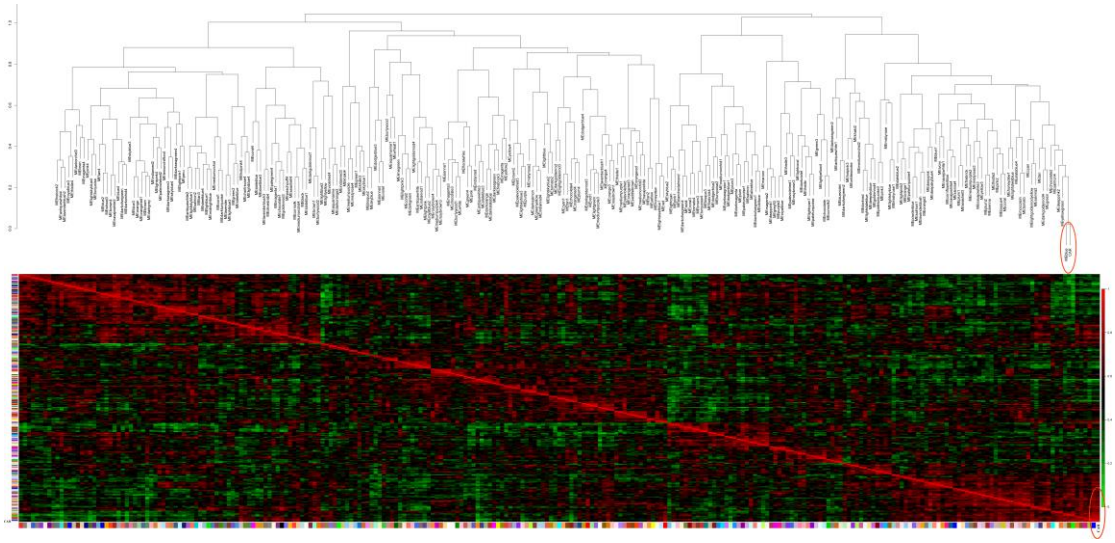


**Figure S10: Eigengene adjacency heatmap illustrating the relationship between modules and traits in CHL group.**

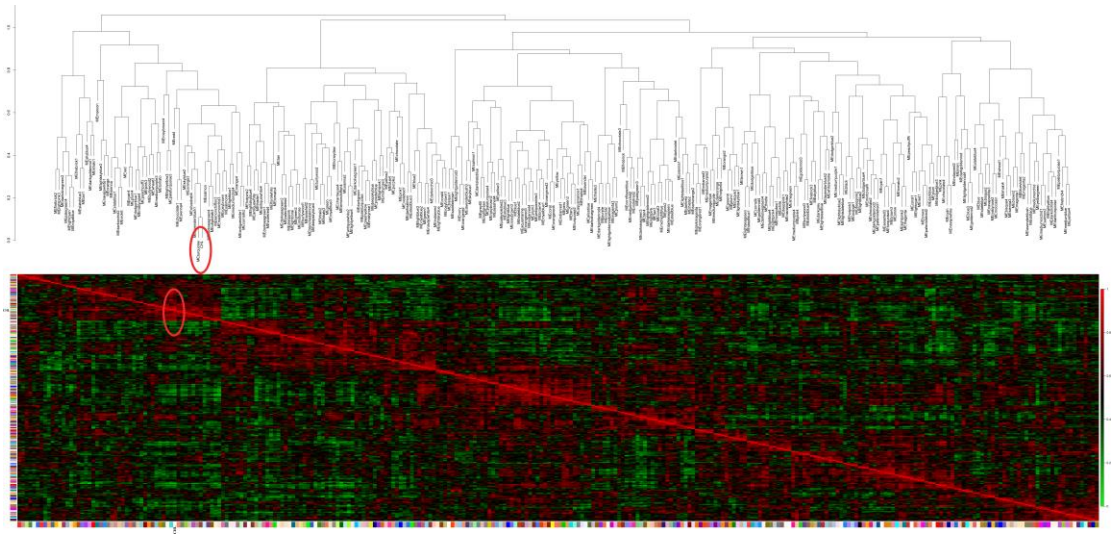


**Figure S11: Eigengene adjacency heatmap illustrating the relationship between modules and traits in THI group.**

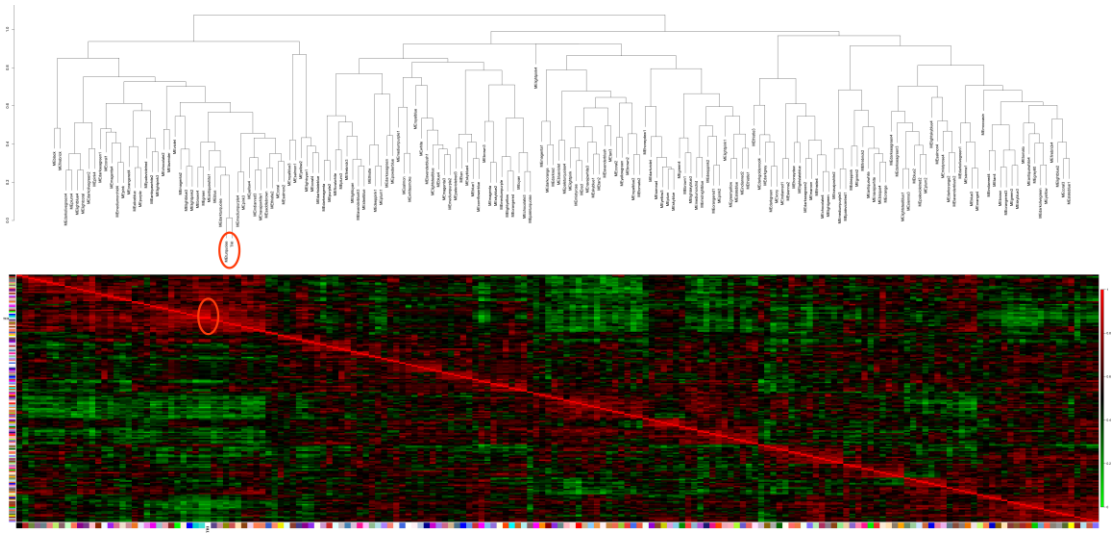


**Figure S12: Functional enrichment analysis for biological process after CAR chemical treatment using DAVID server.**

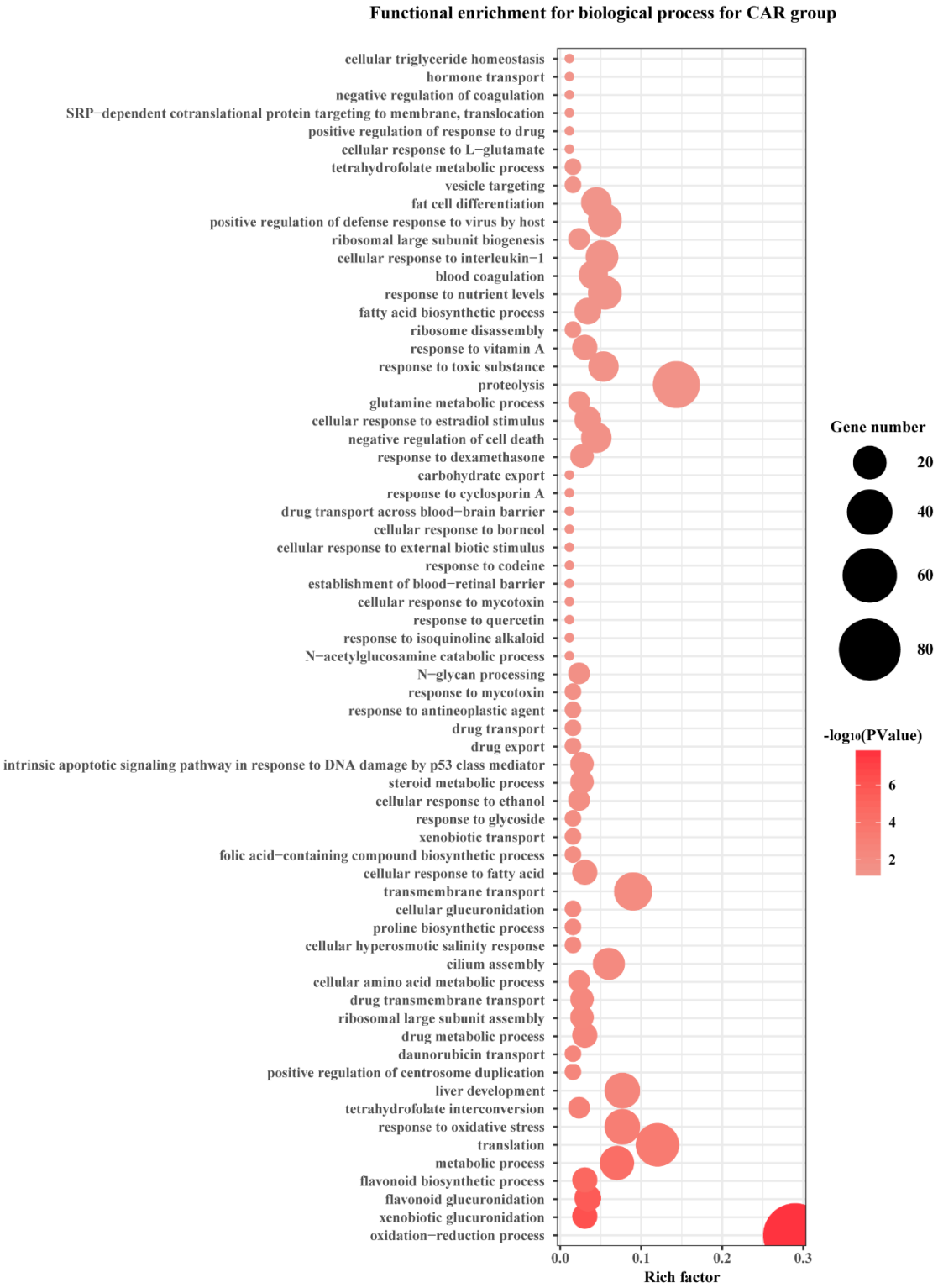


**Figure S13: Functional enrichment analysis for cellular component after CAR chemical treatment using DAVID server.**

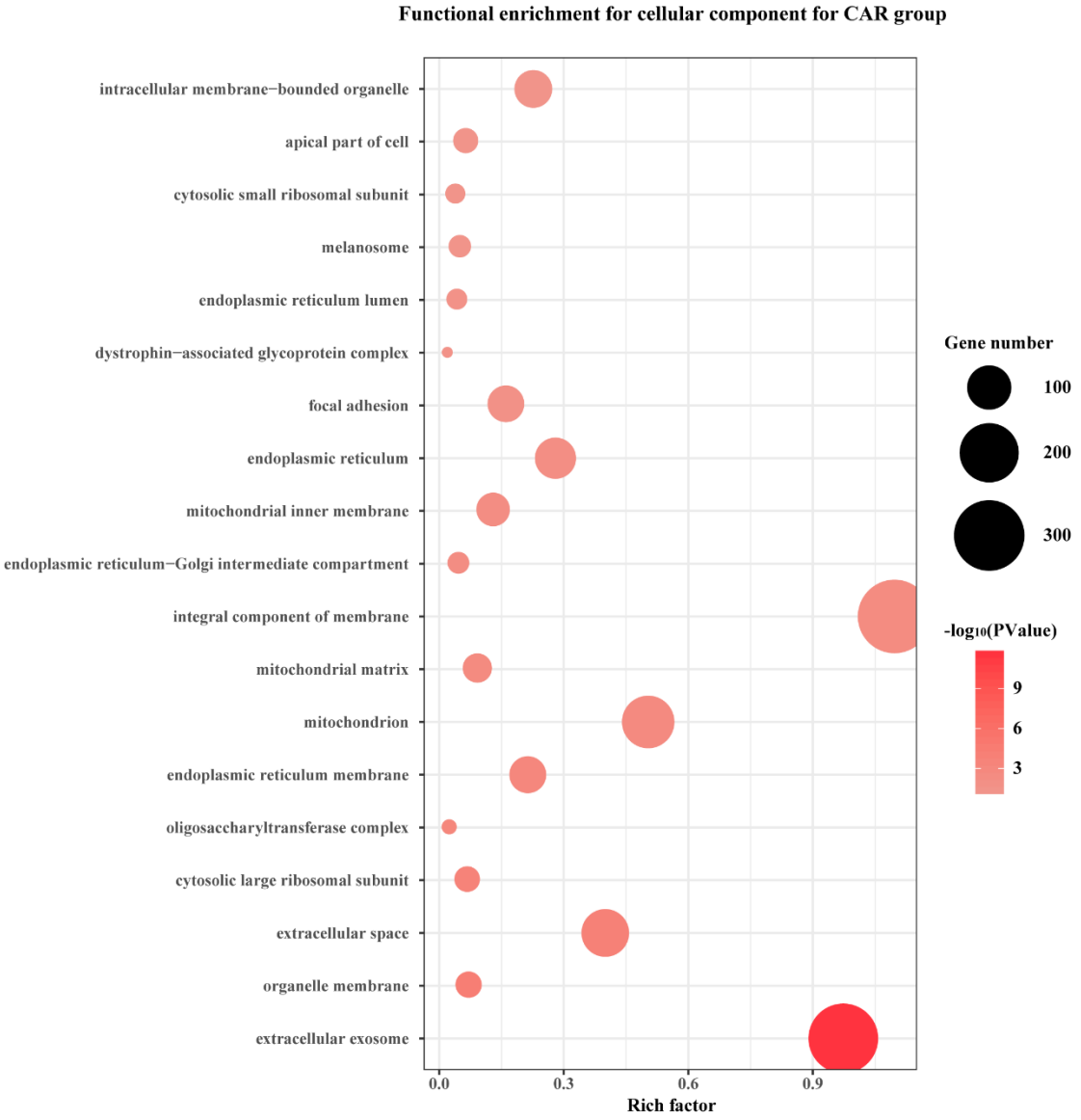


**Figure S14: Functional enrichment analysis for molecular function after CAR chemical treatment using DAVID server.**

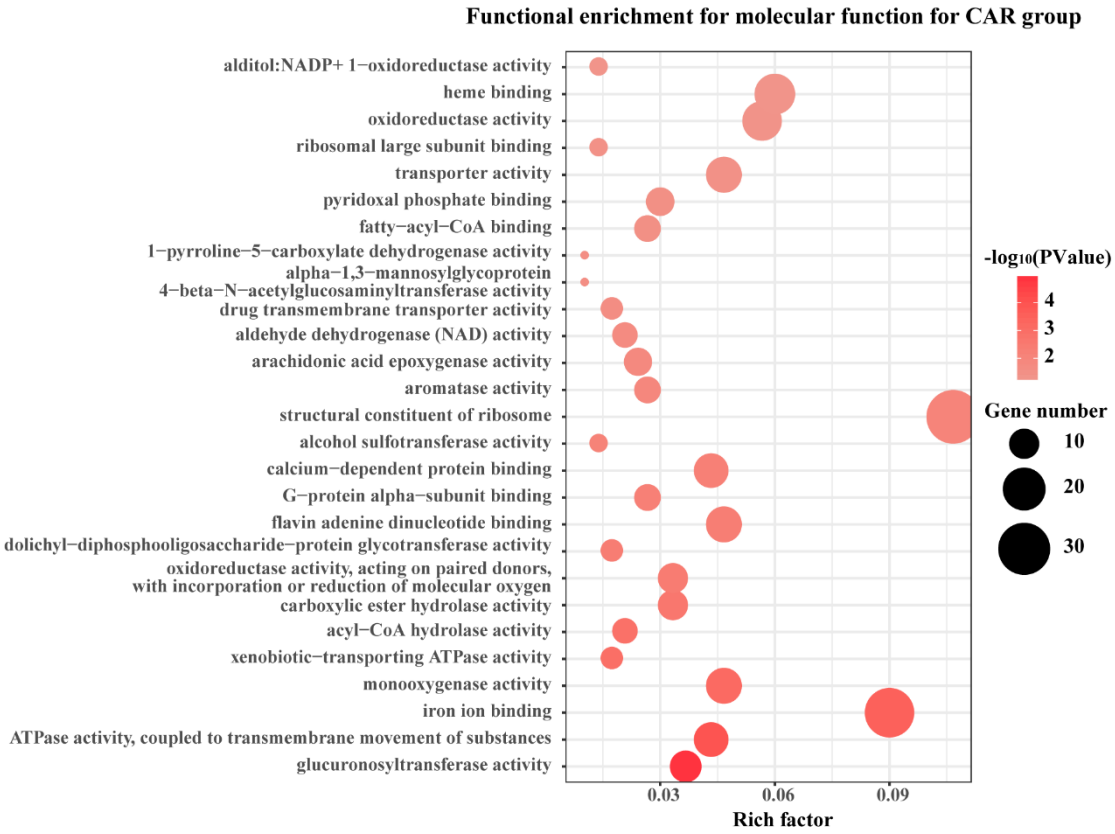


**Figure S15: KEGG analysis for molecular function after CAR chemical treatment using DAVID server.**

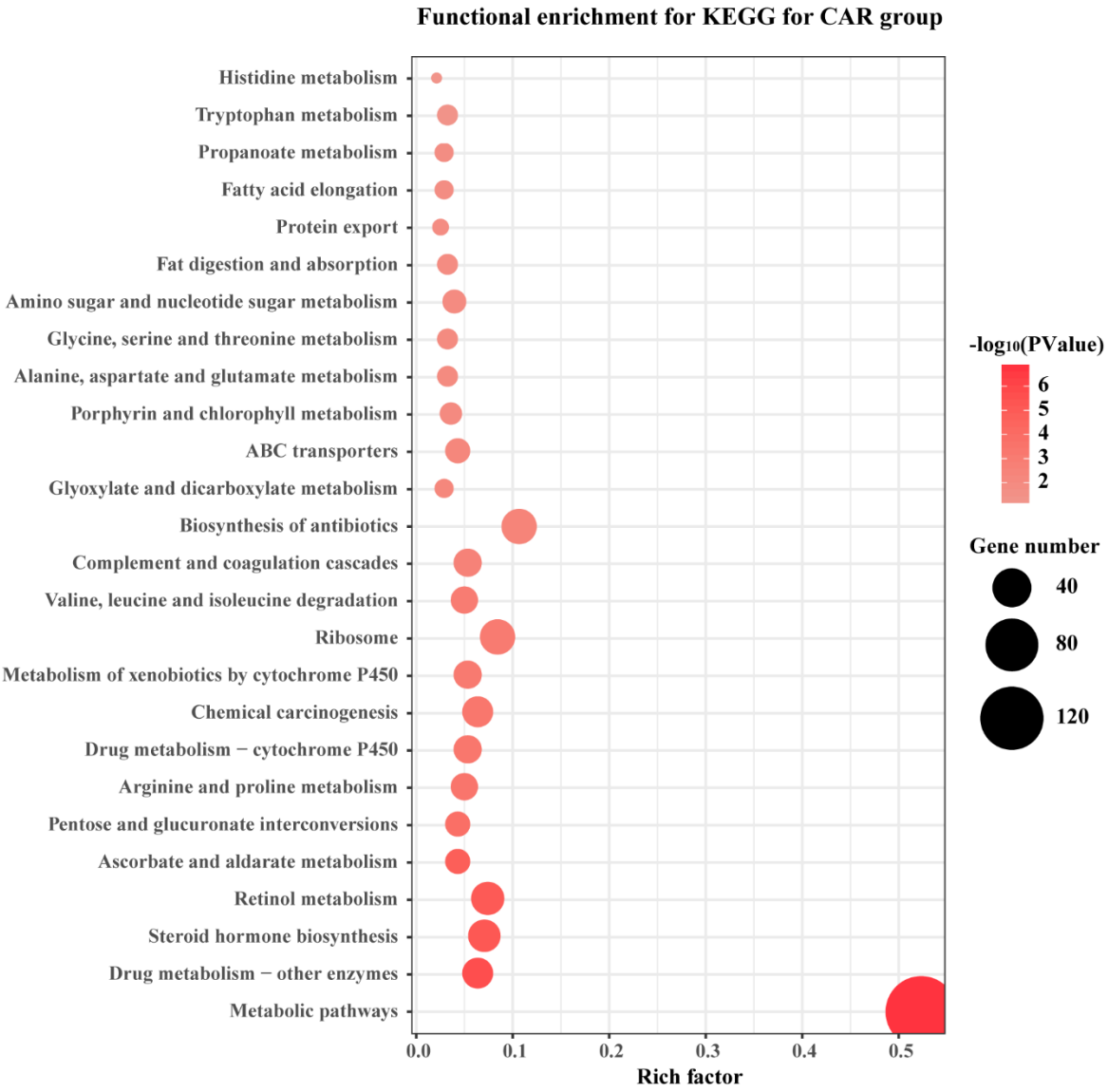


**Figure S16: Functional enrichment analysis for biological process after CHL chemical treatment using DAVID server.**

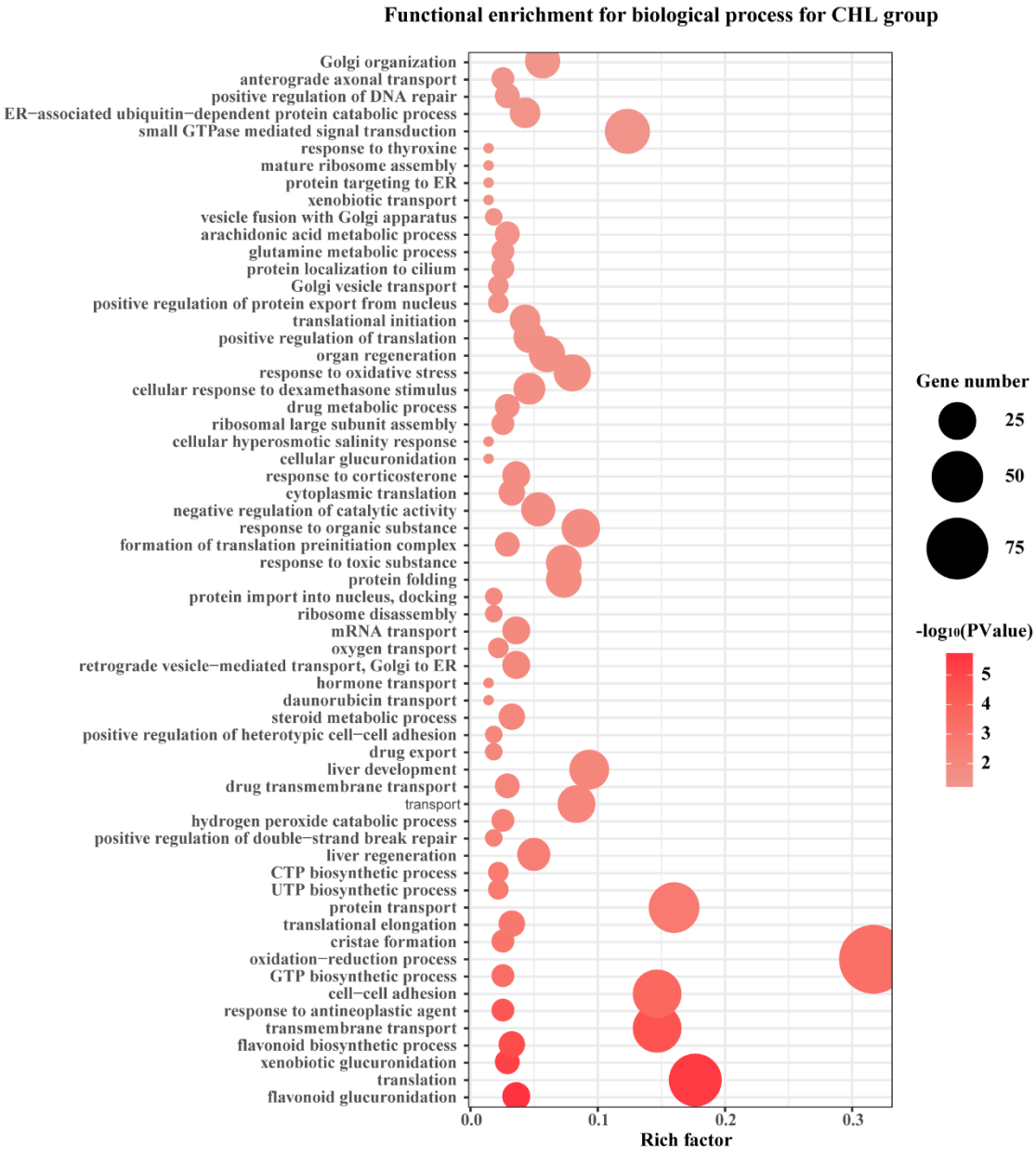


**Figure S17: Functional enrichment analysis for cellular component after CHL chemical treatment using DAVID server.**

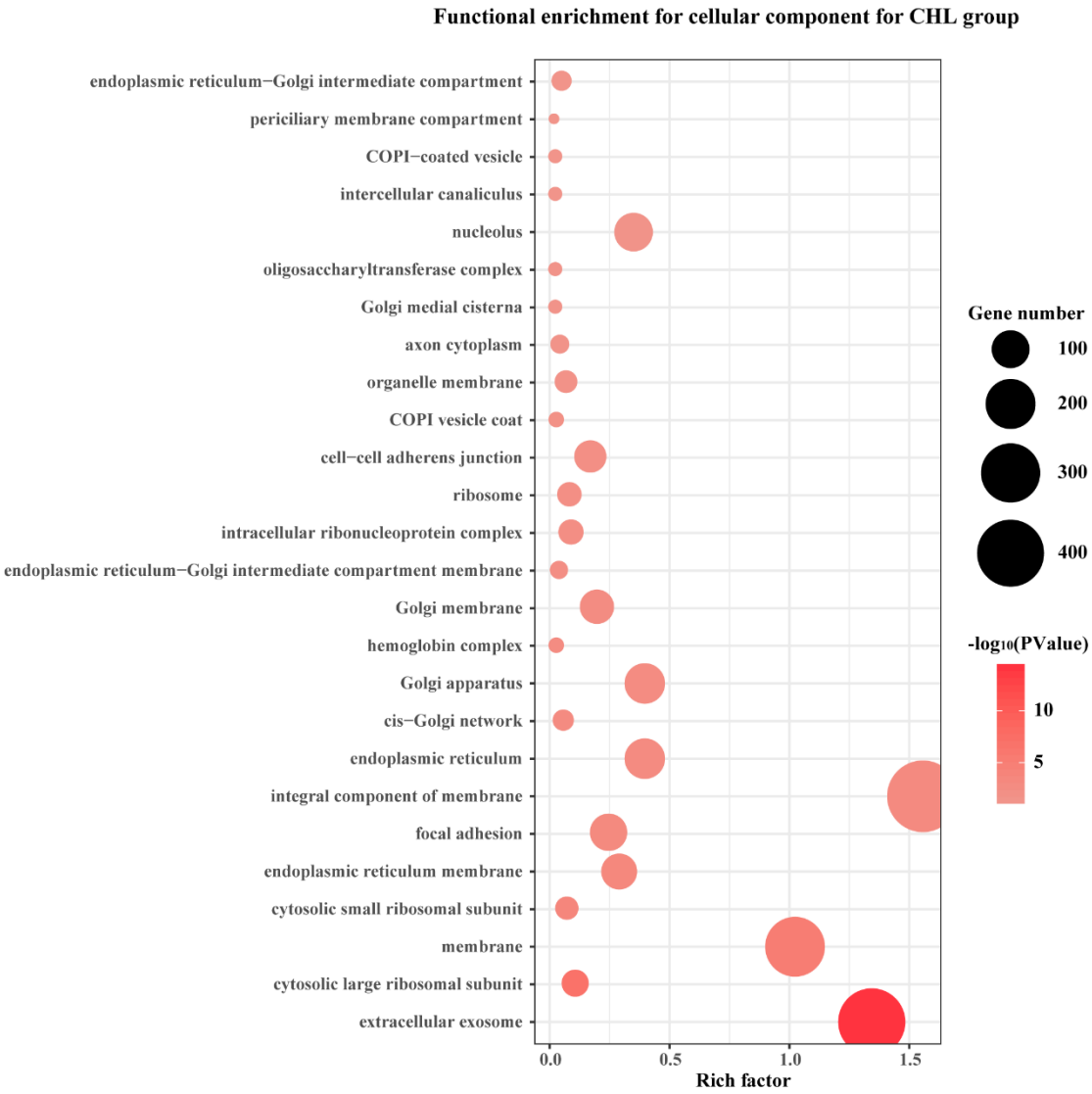


**Figure S18: Functional enrichment analysis for molecular function after CHL chemical treatment using DAVID server.**

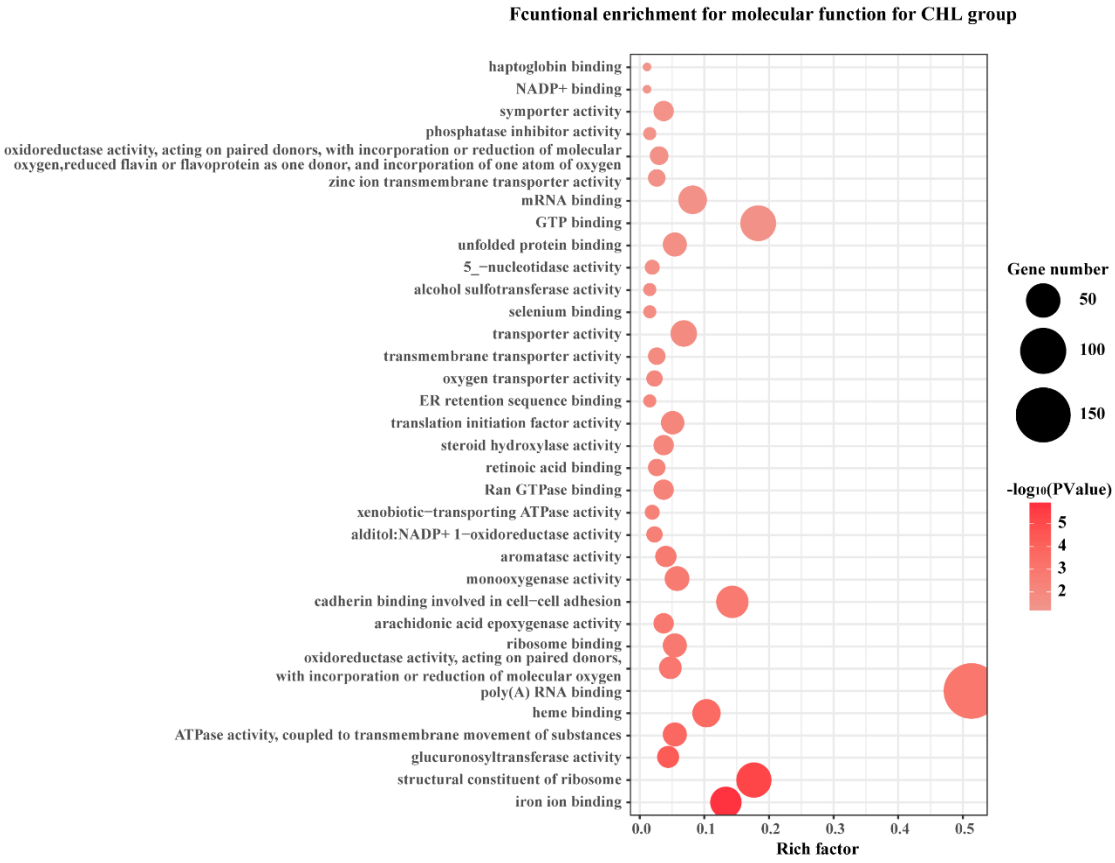


**Figure S19: KEGG analysis for molecular function after CHL chemical treatment using DAVID server.**

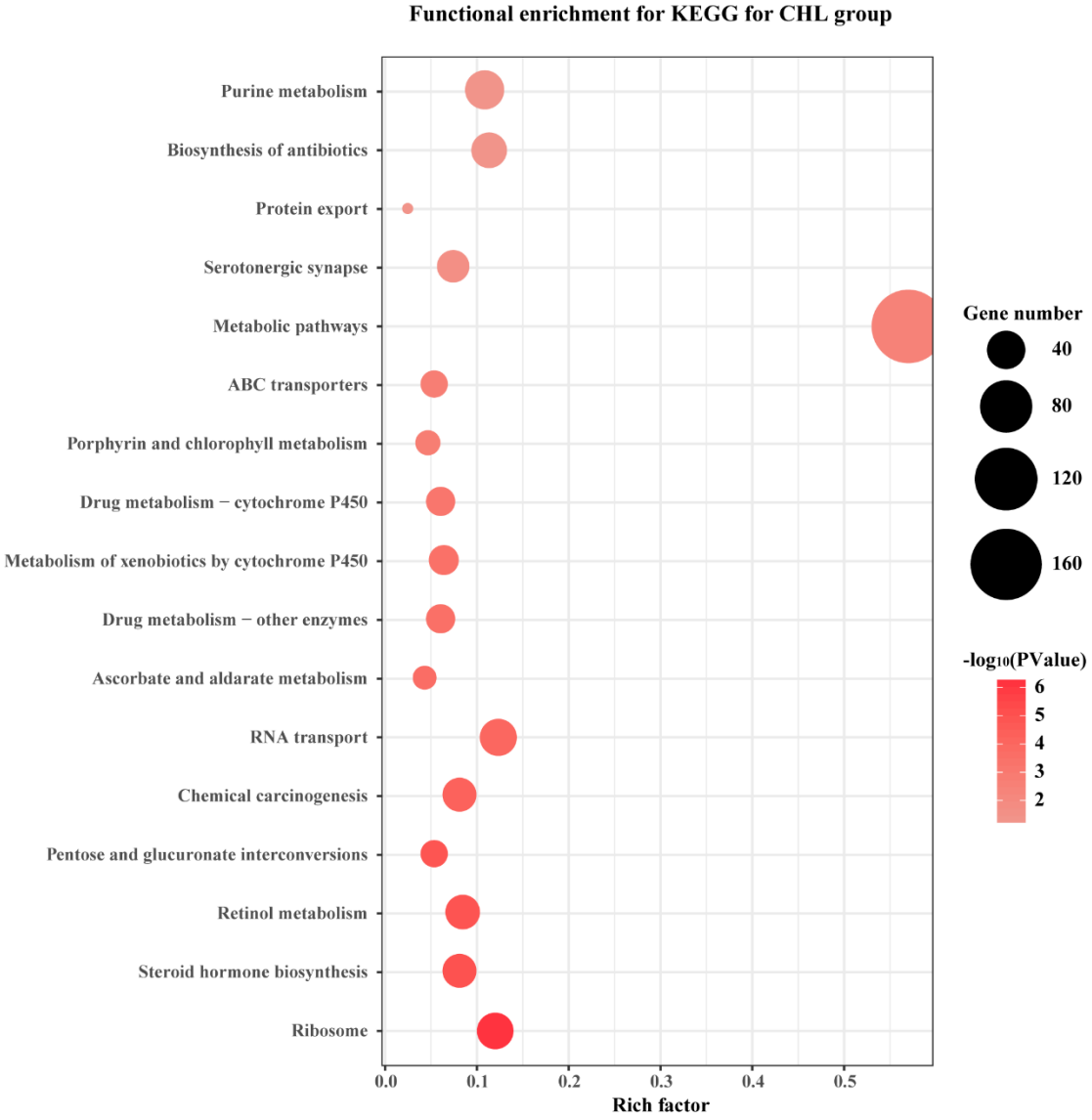


**Figure S20: Functional enrichment analysis for biological process after THI chemical treatment using DAVID server.**

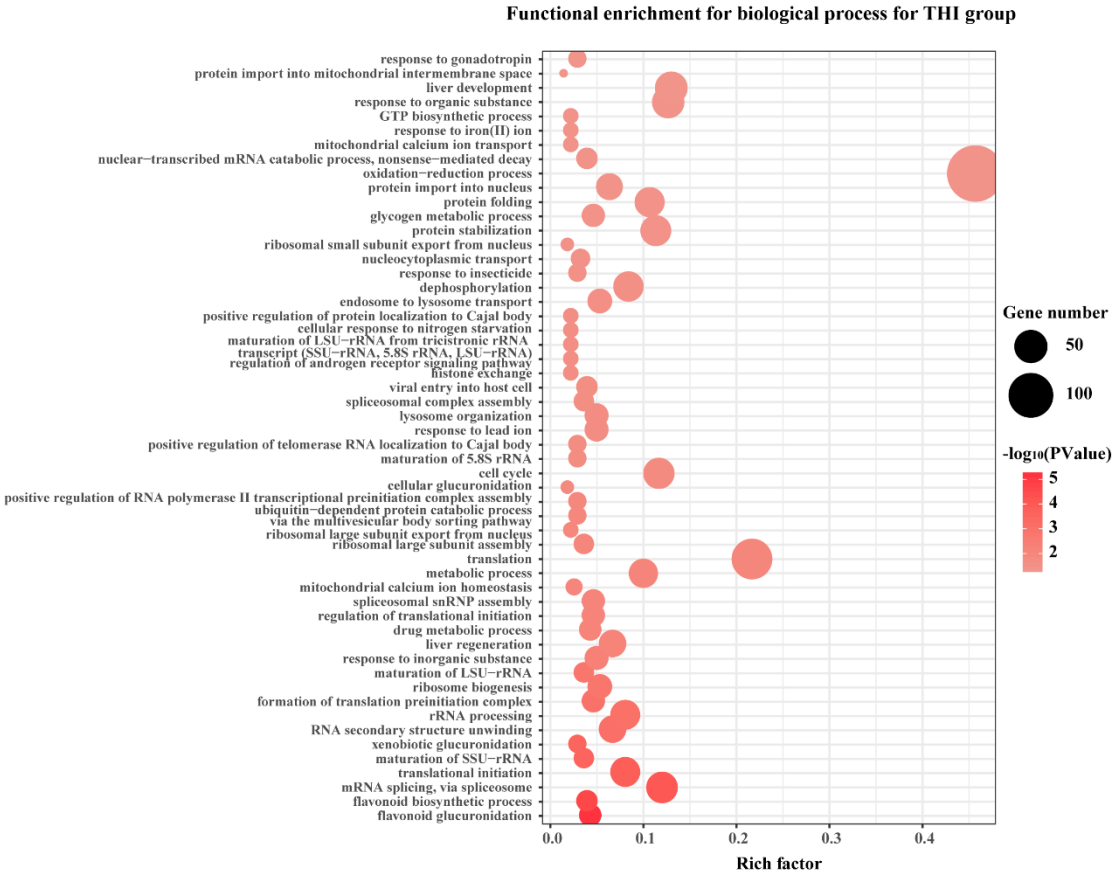


**Figure S21: Functional enrichment analysis for cellular component after THI chemical treatment using DAVID server.**

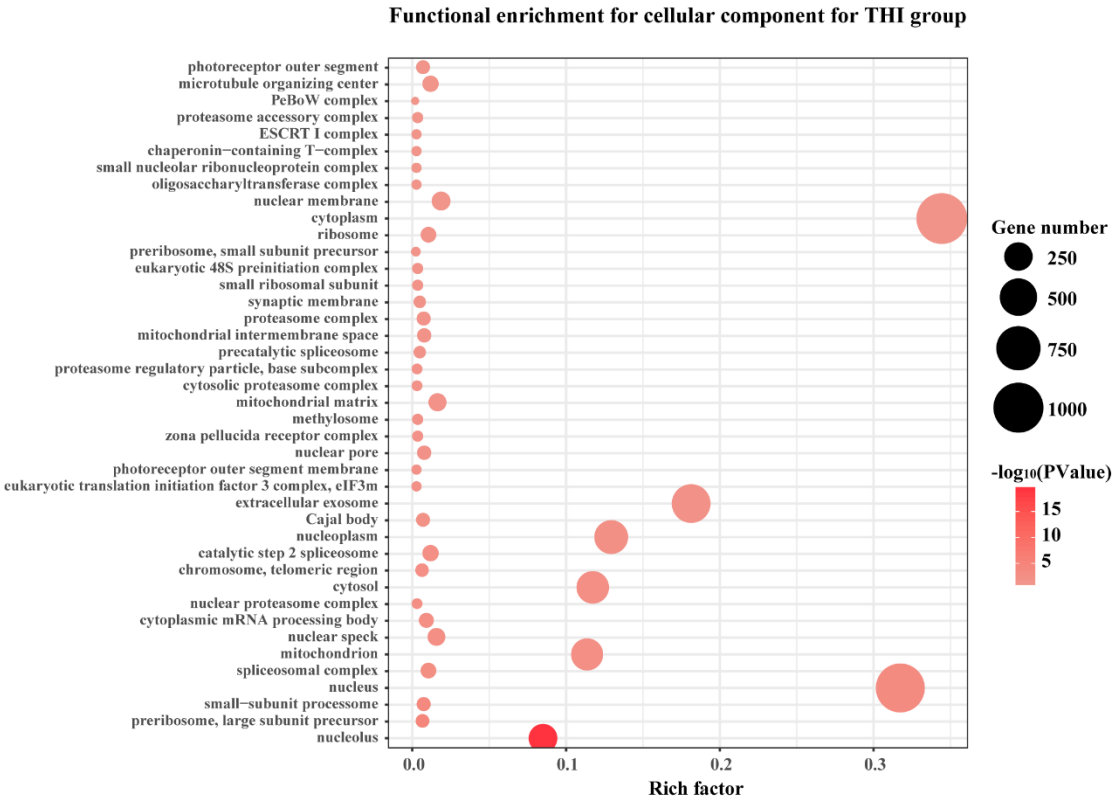


**Figure S22: Functional enrichment analysis for molecular function after THI chemical treatment using DAVID server.**

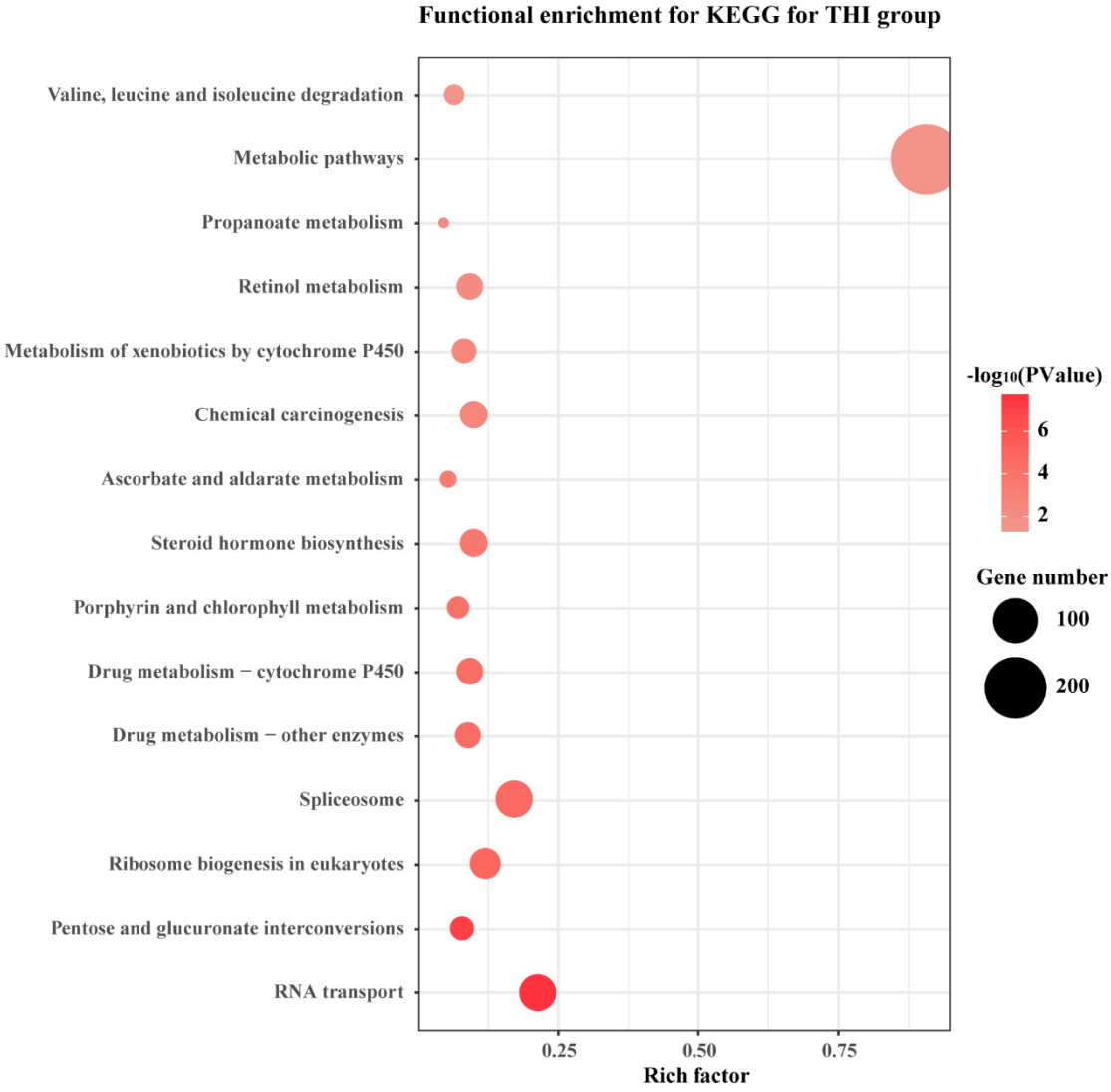
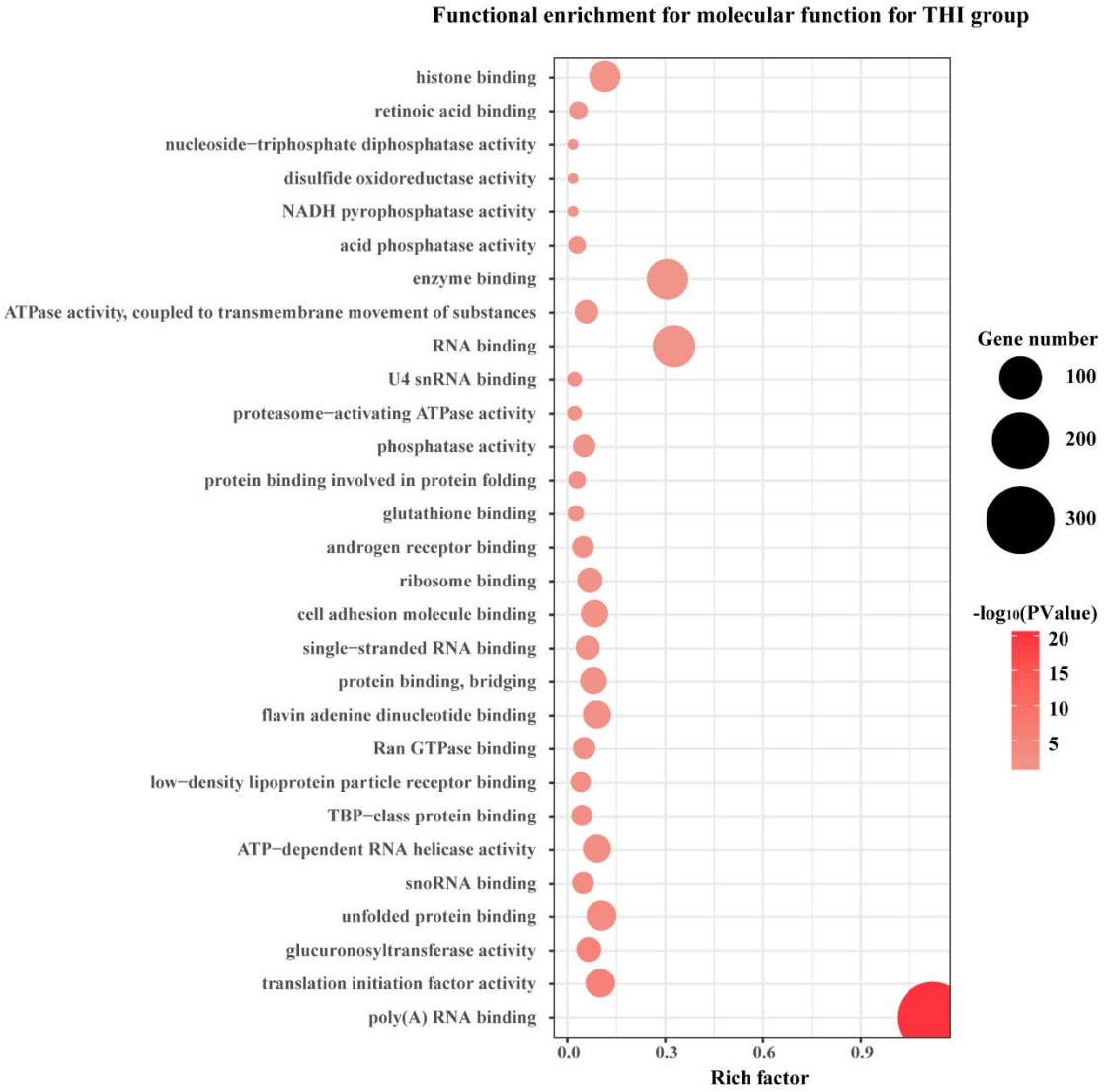



**Figure S23: KEGG analysis for molecular function after THI chemical treatment using DAVID server.**