

RNA-seq 探究 rTMS 对 SCI 和 NP 的影响

2023-12-11

LiChuang Huang



@ 立效研究院

Contents

| | |
|--|-----------|
| 1 摘要 | 1 |
| 2 前言 | 1 |
| 3 材料和方法 | 1 |
| 3.1 材料 | 1 |
| 3.2 方法 | 1 |
| 4 分析结果 | 2 |
| 4.1 不完全性脊髓损伤和神经病理性疼痛 (SCI) (NP) | 2 |
| 4.2 SCI 和 NP 关联分析 | 2 |
| 4.3 重复经颅磁刺激治疗 (rTMS) | 2 |
| 4.4 rTMS 和 SCI、NP 的关联 | 2 |
| 5 结论 | 2 |
| 6 附：分析流程 | 2 |
| 6.1 不完全性脊髓损伤 (Incomplete spinal cord injury, iSCI) (Human) | 2 |
| 6.1.1 元数据 | 2 |
| 6.1.2 差异分析 | 3 |
| 6.2 神经病理性疼痛 (neuropathic pain, NP) (Human) | 4 |
| 6.2.1 元数据 | 4 |
| 6.2.2 差异分析 | 5 |
| 6.3 SCI 和 NP 关联分析 | 7 |
| 6.3.1 共同差异基因 coDEGs | 7 |
| 6.3.2 SCI 的 coDEGs 的关联性分析 | 7 |
| 6.3.3 NP 的 coDEGs 的关联性分析 | 9 |
| 6.3.4 SCI 和 NP 数据集共同显著关联的基因集 sigCoDEGs | 10 |
| 6.4 重复经颅磁刺激治疗 (repeat transcranial magnetic stimulation, rTMS) (Rat) | 10 |
| 6.4.1 元数据 | 10 |
| 6.4.2 差异分析 | 11 |
| 6.5 rTMS 和 SCI、NP 的关联 | 12 |
| 6.5.1 rTMS 数据的差异基因与 sig.coDegs 的关联性 | 12 |
| 6.5.2 富集分析 | 15 |
| Reference | 16 |

List of Figures

| | | |
|---|-----------------------------------|---|
| 1 | SCI sci vs control DEGs | 4 |
| 2 | NP NL 1 vs Control DEGs | 6 |
| 3 | SCI NP coDEGs | 7 |

| | | |
|---|--|----|
| 4 | SCI genes correlation heatmap | 8 |
| 5 | NP genes correlation heatmap | 9 |
| 6 | RTMS All DEGs of contrasts | 12 |
| 7 | NP sigCoDEGs with rTMS DEGs correlation heatmap | 13 |
| 8 | SCI sigCoDEGs with rTMS DEGs correlation heatmap | 14 |
| 9 | RTMS SCI NP correlated sci GO enrichment | 16 |

List of Tables

| | | |
|---|--|----|
| 1 | SCI used sample metadata | 2 |
| 2 | SCI data DEGs | 3 |
| 3 | NP metadata | 5 |
| 4 | NP data NL 1 vs Control DEGs | 6 |
| 5 | SCI data significant genes of correlation | 8 |
| 6 | NP data significant genes of correlation | 10 |
| 7 | RTMS used sample metadata | 11 |
| 8 | NP sigCoDEGs with rTMS DEGs significant correlation | 13 |
| 9 | SCI sigCoDEGs with rTMS DEGs significant correlation | 15 |

1 摘要

质子磁共振光谱法 (H-MRS) 加巴喷丁 (Gabapentin)

不完全性脊髓损伤 (Incomplete spinal cord injury, iSCI) - GSE226238

神经病理性疼痛 (neuropathic pain, NP) - GSE126611

重复经颅磁刺激治疗 (repeat transcranial magnetic stimulation, rTMS) - GSE230150

GEO 有 iSCI、NP、rTMS 各自的基因表达数据集，可以从三者之间的关联性寻找 rTMS 可能的疗效和机制

2 前言

3 材料和方法

3.1 材料

All used GEO expression data and their design:

- **GSE126611:** We investigated n=14 samples, no replicates, comparison between two patient groups, and patient group with healthy controls. (NL-1) is with nerve lesion and (NL-0) is without neuropathic pain.
- **GSE230149:** Gene expression microarray analysis of 48 mouse brain samples, consisting of matched sets of hippocampus (HIPPO, N=24) and parietal cortex (PCTX, N=24) from young sham (Y_Sham, N=4), young iTBS (Y_i...
- **GSE226238:** RNAsequencing from whole blood taken from participants with SCI within 3 days of injury, at 3 MPI, 6 MPI and 12 MPI. Data was compared to un-injured participants as controls. Inclusion and exclusio...

3.2 方法

Mainly used method:

- ClusterProfiler used for gene enrichment analysis.¹
- GEO <https://www.ncbi.nlm.nih.gov/geo/> used for expression dataset aquisition .
- Limma and edgeR used for differential expression analysis.^{2,3}
- Other R packages (eg., dplyr and ggplot2) used for statistic analysis or data visualization.

4 分析结果

4.1 不完全性脊髓损伤和神经病理性疼痛 (SCI) (NP)

4.2 SCI 和 NP 关联分析

4.3 重复经颅磁刺激治疗 (rTMS)

4.4 rTMS 和 SCI、NP 的关联

5 结论

6 附：分析流程

6.1 不完全性脊髓损伤 (Incomplete spinal cord injury, iSCI) (Human)

6.1.1 元数据

- GSE226238

根据文献提供的数据整理信息⁴:

Complete: AIS A-B Incomplete: AIS C-D

使用的样本的信息:

Table 1 (下方表格) 为表格 SCI used sample metadata 概览。

(对应文件为 **Figure+Table/SCI-used-sample-metadata.xlsx**)

注：表格共有 19 行 12 列，以下预览的表格可能省略部分数据；表格含有 19 个唯一 ‘sample’。

1. sample: 样品名称
2. group: 分组名称

Table 1: SCI used sample metadata

| sample | rownames | title | group... | tissu... | treat... | group | id | status | AIS |
|--------|----------|----------|----------|----------|----------|---------|----|--------|-----|
| ID13 | GSM70... | ID13,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID16 | GSM70... | ID16,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID14 | GSM70... | ID14,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID15 | GSM70... | ID15,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID17 | GSM70... | ID17,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID1V0 | GSM70... | ID1v0... | SCI | Whole... | Acute | sci | 1 | 0 | D |
| ID18 | GSM70... | ID18,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID19 | GSM70... | ID19,... | CTL | Whole... | NA | control | NA | NA | NA |

| sample | rownames | title | group... | tissu... | treat... | group | id | status | AIS |
|--------|----------|----------|----------|----------|----------|---------|-----|--------|-----|
| ID1V12 | GSM70... | ID1v1... | SCI | Whole... | 12mpi | sci | 1 | 12 | D |
| ID20 | GSM70... | ID20,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID1V3 | GSM70... | ID1v3... | SCI | Whole... | 3mpi | sci | 1 | 3 | D |
| ID1V6 | GSM70... | ID1v6... | SCI | Whole... | 6mpi | sci | 1 | 6 | D |
| ID21 | GSM70... | ID21,... | CTL | Whole... | NA | control | NA | NA | NA |
| ID2V3 | GSM70... | ID2v3... | SCI | Whole... | 3mpi | sci | 2 | 3 | D |
| ID2V0 | GSM70... | ID2v0... | SCI | Whole... | Acute | sci | 2 | 0 | D |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

6.1.2 差异分析

Table 2 (下方表格) 为表格 SCI data DEGs 概览。

(对应文件为 **Figure+Table/SCI-data-DEGs.csv**)

注：表格共有 3508 行 7 列，以下预览的表格可能省略部分数据；表格含有 3508 个唯一 ‘rownames’。

1. logFC: estimate of the log2-fold-changes corresponding to the effect or contrasts (for ‘topTableF’ there may be several columns of log-fold-changes)
2. AveExpr: average log2-expression for the probes over all arrays and channels, same as ‘Amean’ in the ‘MarrayLM’ object
3. t: moderated t-statistic (omitted for ‘topTableF’)
4. P.Value: raw p-value
5. B: log-odds that the gene is differentially expressed (omitted for ‘topTreat’)

Table 2: SCI data DEGs

| rownames | logFC | AveExpr | t | P.Value | adj.P... | B |
|----------|----------|----------|----------|----------|----------|----------|
| SLC66A1 | -5.39... | -2.85... | -22.2... | 2.059... | 1.472... | 24.69... |
| CDKN1C | -6.41... | -2.34... | -18.8... | 4.387... | 1.146... | 22.02... |
| PGAM1 | 3.931229 | 4.391... | 18.79... | 4.812... | 1.146... | 21.93... |
| KLHL26 | -6.30... | -2.31... | -17.0... | 2.823... | 5.046... | 20.33... |
| 48 | -5.43... | -2.32... | -16.3... | 6.538... | 9.349... | 19.56... |
| 120 | -2.92... | 1.653... | -15.7... | 1.211... | 1.313... | 18.98... |
| DUSP23 | -6.94... | -1.69... | -15.7... | 1.286... | 1.313... | 18.93... |
| HIC1 | -5.41... | -2.45... | -15.1... | 2.686... | 2.401... | 18.24... |
| FAM229A | -5.57... | -2.12... | -14.6... | 4.877... | 3.874... | 17.68... |
| METTL26 | -5.53... | -2.19... | -13.6... | 1.714... | 1.225... | 16.48... |
| CLTB | 5.104... | -0.35... | 12.86... | 4.864... | 3.162... | 15.48... |
| LSP1 | 5.033352 | 3.102... | 12.31... | 1.052... | 6.271... | 14.74... |

| rownames | logFC | AveExpr | t | P.Value | adj.P... | B |
|----------|----------|----------|----------|----------|----------|----------|
| HADH | -4.96... | -2.83... | -12.2... | 1.153... | 6.345... | 14.65... |
| METTL21A | -4.65... | -2.82... | -12.1... | 1.299... | 6.638... | 14.53... |
| LRRC24 | -4.27... | -2.48... | -12.0... | 1.540... | 7.125... | 14.37... |
| ... | ... | ... | ... | ... | ... | ... |

Figure 1 (下方图) 为图 SCI sci vs control DEGs 概览。

(对应文件为 Figure+Table/SCI-sci-vs-control-DEGs.pdf)

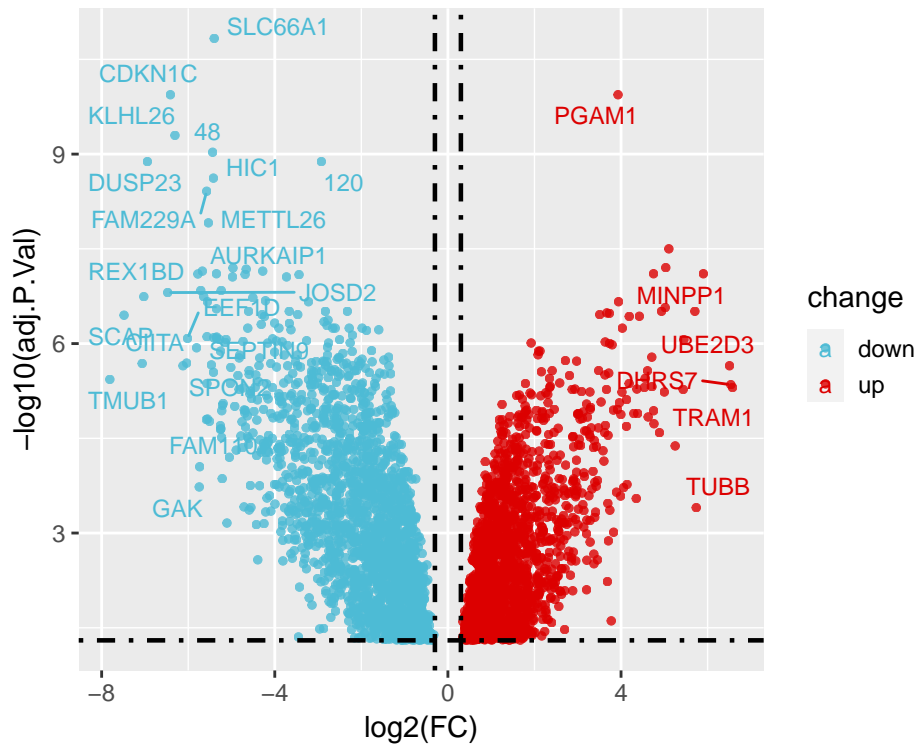


Figure 1: SCI sci vs control DEGs

6.2 神经病理性疼痛 (neuropathic pain, NP) (Human)

6.2.1 元数据

Table 3 (下方表格) 为表格 NP metadata 概览。

(对应文件为 Figure+Table/NP-metadata.csv)

注：表格共有 14 行 7 列，以下预览的表格可能省略部分数据；表格含有 14 个唯一 ‘rownames’。

1. sample: 样品名称
2. group: 分组名称

Table 3: NP metadata

| rownames | group | lib.size | norm.... | sample | title | tissu... |
|----------|---------|----------|----------|----------|----------|----------|
| Contr... | Control | 37694... | 0.993... | Contr... | Contr... | white... |
| Contr... | Control | 35123... | 0.984... | Contr... | Contr... | white... |
| Contr... | Control | 40623... | 1.038... | Contr... | Contr... | white... |
| Contr... | Control | 31254... | 0.900... | Contr... | Contr... | white... |
| Contr... | Control | 36785... | 1.092... | Contr... | Contr... | white... |
| NL.0_... | NL.0 | 39063... | 0.998... | NL.0_... | NL-0_... | white... |
| NL.0_... | NL.0 | 30209... | 0.838... | NL.0_... | NL-0_... | white... |
| NL.0_... | NL.0 | 33541... | 0.873... | NL.0_... | NL-0_... | white... |
| NL.0_... | NL.0 | 43997... | 1.105... | NL.0_... | NL-0_... | white... |
| NL.1_... | NL.1 | 35856... | 0.947... | NL.1_... | NL-1_... | white... |
| NL.1_... | NL.1 | 47176... | 1.217... | NL.1_... | NL-1_... | white... |
| NL.1_... | NL.1 | 33852... | 0.947... | NL.1_... | NL-1_... | white... |
| NL.1_... | NL.1 | 37527... | 0.991... | NL.1_... | NL-1_... | white... |
| NL.1_... | NL.1 | 45702... | 1.142... | NL.1_... | NL-1_... | white... |

6.2.2 差异分析

Table 4 (下方表格) 为表格 NP data NL 1 vs Control DEGs 概览。

(对应文件为 **Figure+Table/NP-data-NL-1-vs-Control-DEGs.xlsx**)

注：表格共有 263 行 17 列，以下预览的表格可能省略部分数据；表格含有 263 个唯一 ‘rownames’。

1. Chr: 染色体
2. Start: 起始点
3. End: 结束点
4. symbol: 基因或蛋白符号。
5. logFC: estimate of the log2-fold-changes corresponding to the effect or contrasts (for ‘topTableF’ there may be several columns of log-fold-changes)
6. AveExpr: average log2-expression for the probes over all arrays and channels, same as ‘Amean’ in the ‘MarrayLM’ object
7. t: moderated t-statistic (omitted for ‘topTableF’)
8. P.Value: raw p-value
9. B: log-odds that the gene is differentially expressed (omitted for ‘topTreat’)

Table 4: NP data NL 1 vs Control DEGs

| rownames | symbol | Chr | Source | Feature | Start | End | Frame | Strand | V8 |
|----------|----------|-------|--------|---------|----------|----------|-------|--------|-----|
| 1992 | ID2 | chr2 | HAVANA | gene | 8678845 | 8684453 | 0 | + | 0 |
| 9282 | DDIT4 | chr10 | HAVANA | gene | 72273920 | 72276036 | 0 | + | 0 |
| 17418 | MAP3K7CL | chr21 | HAVANA | gene | 29077471 | 29175889 | 0 | + | 0 |
| 5167 | ENC1 | chr5 | HAVANA | gene | 74627406 | 74641424 | 0 | - | 0 |
| 14324 | PER1 | chr17 | HAVANA | gene | 8140472 | 8156506 | 0 | - | 0 |
| 6603 | TNFAIP3 | chr6 | HAVANA | gene | 13786... | 13788... | 0 | + | 0 |
| 15786 | PDE4A | chr19 | HAVANA | gene | 10416773 | 10469631 | 0 | + | 0 |
| 14577 | CCL4 | chr17 | HAVANA | gene | 36103590 | 36105621 | 0 | + | 0 |
| 4463 | HOPX | chr4 | HAVANA | gene | 56647988 | 56681899 | 0 | - | 0 |
| 10202 | MS4A14 | chr11 | HAVANA | gene | 60378530 | 60417756 | 0 | + | 0 |
| 12419 | PTGDR | chr14 | HAVANA | gene | 52267713 | 52276724 | 0 | + | 0 |
| 6372 | SH3BGRL2 | chr6 | HAVANA | gene | 79631283 | 79703659 | 0 | + | 0 |
| 5266 | PAM | chr5 | HAVANA | gene | 10275... | 10303... | 0 | + | 0 |
| 4533 | PPBP | chr4 | HAVANA | gene | 73987038 | 73988197 | 0 | - | 0 |
| 6909 | MTURN | chr7 | HAVANA | gene | 30134810 | 30162762 | 0 | + | 0 |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

Figure 2 (下方图) 为图 NP NL 1 vs Control DEGs 概览。

(对应文件为 [Figure+Table/NP-NL-1-vs-Control-DEGs.pdf](#))

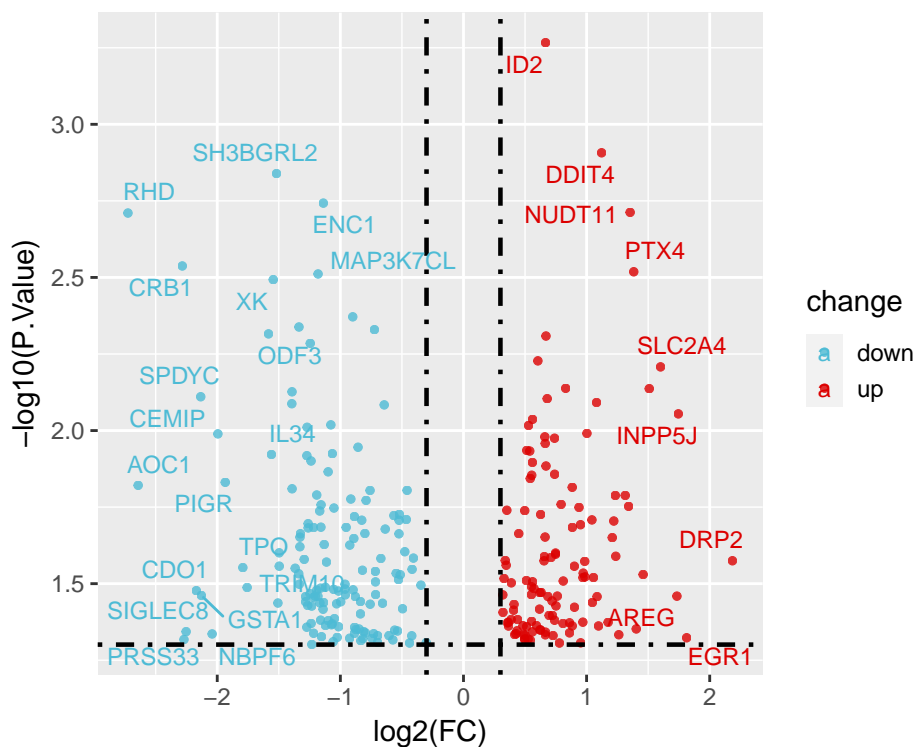


Figure 2: NP NL 1 vs Control DEGs

6.3 SCI 和 NP 关联分析

6.3.1 共同差异基因 coDEGs

Figure 3 (下方图) 为图 SCI NP coDEGs 概览。

(对应文件为 Figure+Table/SCI-NP-coDEGs.pdf)

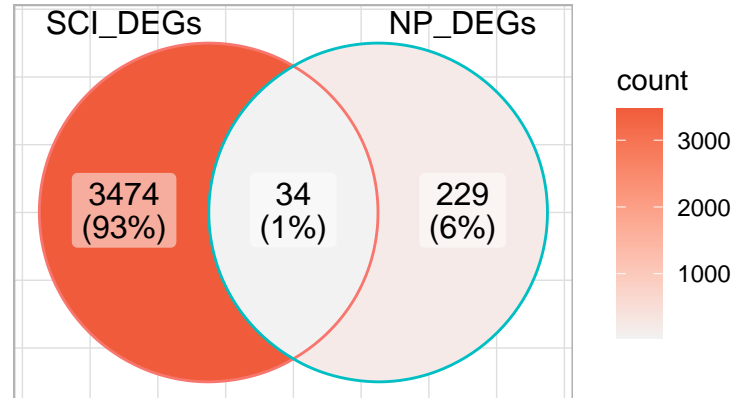


Figure 3: SCI NP coDEGs

Intersection :

PDE4A, ADA, LIMS1, FLYWCH2, LDLR, GOLGA8N, NUDT2, CNTLN, CTSS, KNOP1, PRF1, MAP3K7CL, CLDN5, SHISA8, CMC1, SLAMF8, ELOVL7, AIFM3, GNGT2, PPT1, DAPP1, AOC1, PSMC1, PF4, CBLN3, LPAR6, CPM, EGF, SH3PXD2A, SH3YL1, ATF3, PTCRA, SMIM1, EVI2A

(上述信息框内容已保存至 Figure+Table/SCI-NP-coDEGs-content)

6.3.2 SCI 的 coDEGs 的关联性分析

Figure 4 (下方图) 为图 SCI genes correlation heatmap 概览。

(对应文件为 Figure+Table/SCI-genes-correlation-heatmap.pdf)

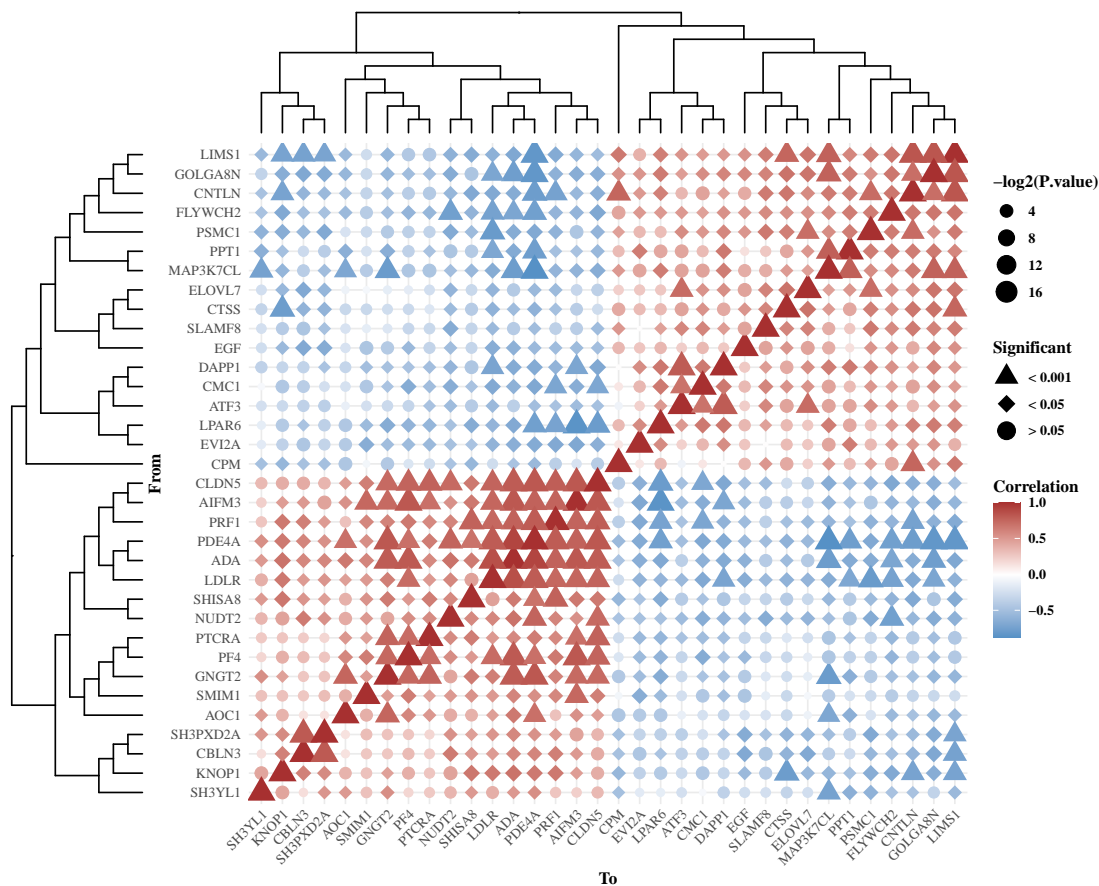


Figure 4: SCI genes correlation heatmap

Table 5 (下方表格) 为表格 SCI data significant genes of correlation 概览。

(对应文件为 Figure+Table/SCI-data-significant-genes-of-correlation.csv)

注：表格共有 796 行 7 列，以下预览的表格可能省略部分数据；表格含有 34 个唯一 ‘From’。

1. cor: 皮尔逊关联系数，正关联或负关联。
2. pvalue: 显著性 P。
3. -log2(P.value): P 的对数转化。
4. significant: 显著性。
5. sign: 人为赋予的符号，参考 significant。

Table 5: SCI data significant genes of correlation

| From | To | cor | pvalue | -log2... | signi... | sign |
|-------|-----|-------|--------|----------|----------|------|
| ADA | ADA | 1 | 0 | 16.60... | < 0.001 | ** |
| PPT1 | ADA | -0.66 | 0.0022 | 8.828... | < 0.05 | * |
| LDLR | ADA | 0.86 | 0 | 16.60... | < 0.001 | ** |
| EVI2A | ADA | -0.63 | 0.0036 | 8.117... | < 0.05 | * |

| From | To | cor | pvalue | -log2... | signi... | sign |
|---------|-----|-------|--------|----------|----------|------|
| CPM | ADA | -0.46 | 0.0452 | 4.467... | < 0.05 | * |
| KNOP1 | ADA | 0.69 | 0.0012 | 9.702... | < 0.05 | * |
| AIFM3 | ADA | 0.82 | 0 | 16.60... | < 0.001 | ** |
| CBLN3 | ADA | 0.59 | 0.0077 | 7.020... | < 0.05 | * |
| PRF1 | ADA | 0.77 | 1e-04 | 13.28... | < 0.001 | ** |
| AOC1 | ADA | 0.66 | 0.0019 | 9.039... | < 0.05 | * |
| PDE4A | ADA | 0.91 | 0 | 16.60... | < 0.001 | ** |
| CNTLN | ADA | -0.65 | 0.0027 | 8.532... | < 0.05 | * |
| FLYWCH2 | ADA | -0.7 | 8e-04 | 10.28... | < 0.001 | ** |
| SH3YL1 | ADA | 0.5 | 0.0301 | 5.054... | < 0.05 | * |
| NUDT2 | ADA | 0.69 | 0.0011 | 9.828... | < 0.05 | * |
| ... | ... | ... | ... | ... | ... | ... |

6.3.3 NP 的 coDEGs 的关联性分析

Figure 5 (下方图) 为图 NP genes correlation heatmap 概览。

(对应文件为 Figure+Table/NP-genes-correlation-heatmap.pdf)

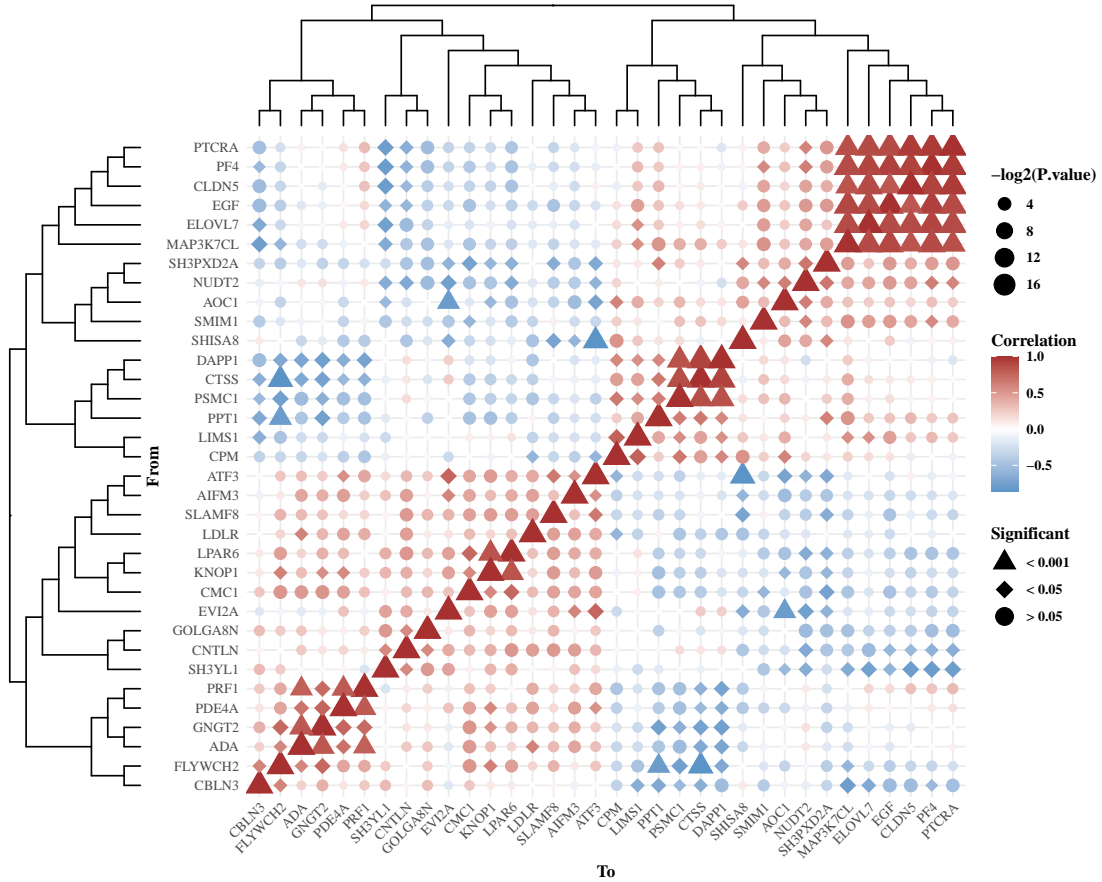


Figure 5: NP genes correlation heatmap

Table 6 (下方表格) 为表格 NP data significant genes of correlation 概览。

(对应文件为 `Figure+Table/NP-data-significant-genes-of-correlation.csv`)

注：表格共有 262 行 7 列，以下预览的表格可能省略部分数据；表格含有 34 个唯一 ‘From’。

1. cor: 皮尔逊关联系数，正关联或负关联。
2. pvalue: 显著性 P。
3. -log2(P.value): P 的对数转化。
4. significant: 显著性。
5. sign: 人为赋予的符号，参考 significant。

Table 6: NP data significant genes of correlation

| From | To | cor | pvalue | -log2... | signi... | sign |
|----------|-------|-------|--------|----------|----------|------|
| SMIM1 | SMIM1 | 1 | 0 | 16.60... | < 0.001 | ** |
| CMC1 | SMIM1 | -0.56 | 0.0377 | 4.729... | < 0.05 | * |
| PF4 | SMIM1 | 0.58 | 0.0302 | 5.049... | < 0.05 | * |
| NUDT2 | SMIM1 | 0.59 | 0.0264 | 5.243... | < 0.05 | * |
| PPT1 | PPT1 | 1 | 0 | 16.60... | < 0.001 | ** |
| CTSS | PPT1 | 0.66 | 0.01 | 6.643... | < 0.05 | * |
| DAPP1 | PPT1 | 0.58 | 0.028 | 5.158... | < 0.05 | * |
| SH3PXD2A | PPT1 | 0.62 | 0.0173 | 5.853... | < 0.05 | * |
| CBLN3 | PPT1 | -0.68 | 0.0069 | 7.179... | < 0.05 | * |
| PSMC1 | PPT1 | 0.64 | 0.0135 | 6.210... | < 0.05 | * |
| FLYWCH2 | PPT1 | -0.78 | 9e-04 | 10.11... | < 0.001 | ** |
| GNGT2 | PPT1 | -0.74 | 0.0026 | 8.587... | < 0.05 | * |
| PPT1 | CTSS | 0.66 | 0.01 | 6.643... | < 0.05 | * |
| CTSS | CTSS | 1 | 0 | 16.60... | < 0.001 | ** |
| DAPP1 | CTSS | 0.92 | 0 | 16.60... | < 0.001 | ** |
| ... | ... | ... | ... | ... | ... | ... |

6.3.4 SCI 和 NP 数据集共同显著关联的基因集 sigCoDEGs

6.4 重复经颅磁刺激治疗 (repeat transcranial magnetic stimulation, rTMS) (Rat)

6.4.1 元数据

Table 7 (下方表格) 为表格 rTMS used sample metadata 概览。

(对应文件为 `Figure+Table/rTMS-used-sample-metadata.csv`)

注：表格共有 56 行 11 列，以下预览的表格可能省略部分数据；表格含有 12 个唯一‘group’。

1. sample: 样品名称
2. group: 分组名称

Table 7: RTMS used sample metadata

| sample | group | title | age.ch1 | cogni... | post... | Sex.ch1 | strai... | tissu.....9 | tissu.....10 |
|----------|----------|----------|----------|----------|---------|---------|----------|-------------|--------------|
| GSM71... | Y.H.Sham | Y_Sha... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.Sham | Y_Sha... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.Sham | Y_Sha... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.Sham | Y_Sha... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.iTBS | Y_iTB... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.iTBS | Y_iTB... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.iTBS | Y_iTB... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | Y.H.iTBS | Y_iTB... | Young... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_Sh... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_Sh... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_Sh... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_Sh... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_iT... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_iT... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| GSM71... | AU.H.... | AU_iT... | Aged;... | unimp... | 48 | Male | Long-... | Hippo... | Brain |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

6.4.2 差异分析

Figure 6 (下方图) 为图 rTMS All DEGs of contrasts 概览。

(对应文件为 **Figure+Table/rTMS-All-DEGs-of-contrasts.pdf**)

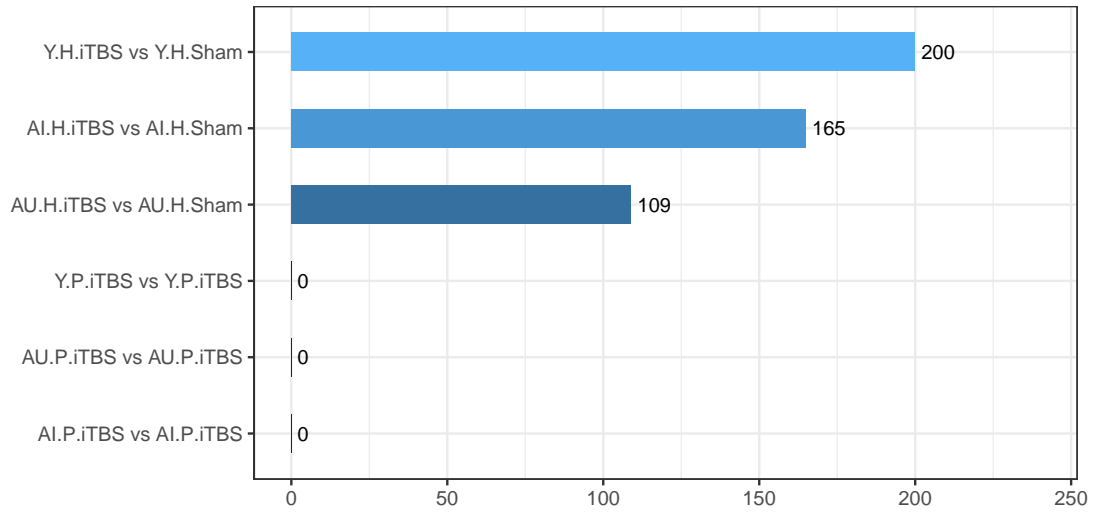


Figure 6: RTMS All DEGs of contrasts

‘RTMS data DEGs’ 数据已全部提供。

(对应文件为 **Figure+Table/rTMS-data-DEGs**)

注：文件夹 Figure+Table/rTMS-data-DEGs 共包含 6 个文件。

1. 1_AU.H.iTBS - AU.H.Sham.csv
2. 2_AU.P.iTBS - AU.P.iTBS.csv
3. 3_Al.H.iTBS - Al.H.Sham.csv
4. 4_Al.P.iTBS - Al.P.iTBS.csv
5. 5_Y.H.iTBS - Y.H.Sham.csv
6. ...

6.5 rTMS 和 SCI、NP 的关联

6.5.1 rTMS 数据的差异基因与 sig.coDeps 的关联性

Figure 7 (下方图) 为图 NP sigCoDEGs with rTMS DEGs correlation heatmap 概览。

(对应文件为 **Figure+Table/NP-sigCoDEGs-with-rTMS-DEGs-correlation-heatmap.pdf**)

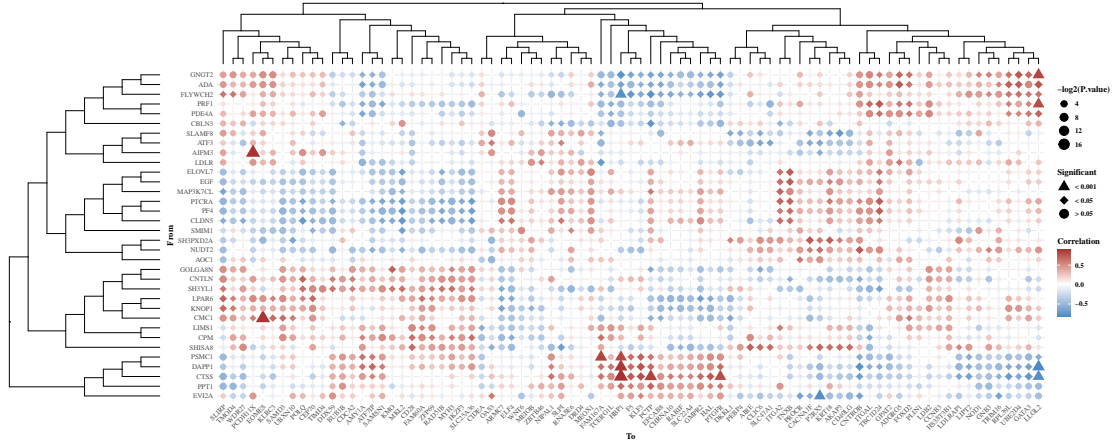


Figure 7: NP sigCoDEGs with rTMS DEGs correlation heatmap

Table 8 (下方表格) 为表格 NP sigCoDEGs with rTMS DEGs significant correlation 概览。

(对应文件为 **Figure+Table/NP-sigCoDEGs-with-rTMS-DEGs-significant-correlation.csv**)

注：表格共有 297 行 7 列，以下预览的表格可能省略部分数据；表格含有 34 个唯一 ‘From’。

1. cor: 皮尔逊关联系数，正关联或负关联。
2. pvalue: 显著性 P。
3. -log2(P.value): P 的对数转化。
4. significant: 显著性。
5. sign: 人为赋予的符号，参考 significant。

Table 8: NP sigCoDEGs with rTMS DEGs significant correlation

| From | To | cor | pvalue | -log2... | signi... | sign |
|----------|---------|-------|--------|----------|----------|------|
| CMC1 | UBXN10 | 0.58 | 0.0311 | 5.006... | < 0.05 | * |
| SH3PXD2A | UBXN10 | -0.64 | 0.0142 | 6.137... | < 0.05 | * |
| CTSS | LDLRAP1 | -0.61 | 0.0202 | 5.629... | < 0.05 | * |
| SHISA8 | LDLRAP1 | 0.54 | 0.047 | 4.411... | < 0.05 | * |
| SH3YL1 | ZFP69 | 0.55 | 0.0417 | 4.583... | < 0.05 | * |
| CPM | ZFP69 | 0.56 | 0.0381 | 4.714... | < 0.05 | * |
| LPAR6 | ZFP69 | 0.54 | 0.0451 | 4.470... | < 0.05 | * |
| CLDN5 | ZFP69 | -0.57 | 0.0332 | 4.912... | < 0.05 | * |
| CMC1 | FOXD2 | 0.58 | 0.0305 | 5.035... | < 0.05 | * |
| PRF1 | FOXD2 | 0.6 | 0.0222 | 5.493... | < 0.05 | * |
| GNGT2 | FOXD2 | 0.62 | 0.0186 | 5.748... | < 0.05 | * |
| PDE4A | FOXD2 | 0.58 | 0.0299 | 5.063... | < 0.05 | * |
| ADA | FOXD2 | 0.61 | 0.02 | 5.643... | < 0.05 | * |
| PPT1 | PTGFR | 0.59 | 0.0254 | 5.299... | < 0.05 | * |

| From | To | cor | pvalue | -log2... | signi... | sign |
|------|-------|------|--------|----------|----------|------|
| CTSS | PTGFR | 0.79 | 7e-04 | 10.48... | < 0.001 | ** |
| ... | ... | ... | ... | ... | ... | ... |

Figure 8 (下方图) 为图 SCI sigCoDEGs with rTMS DEGs correlation heatmap 概览。

(对应文件为 Figure+Table/SCI-sigCoDEGs-with-rTMS-DEGs-correlation-heatmap.pdf)

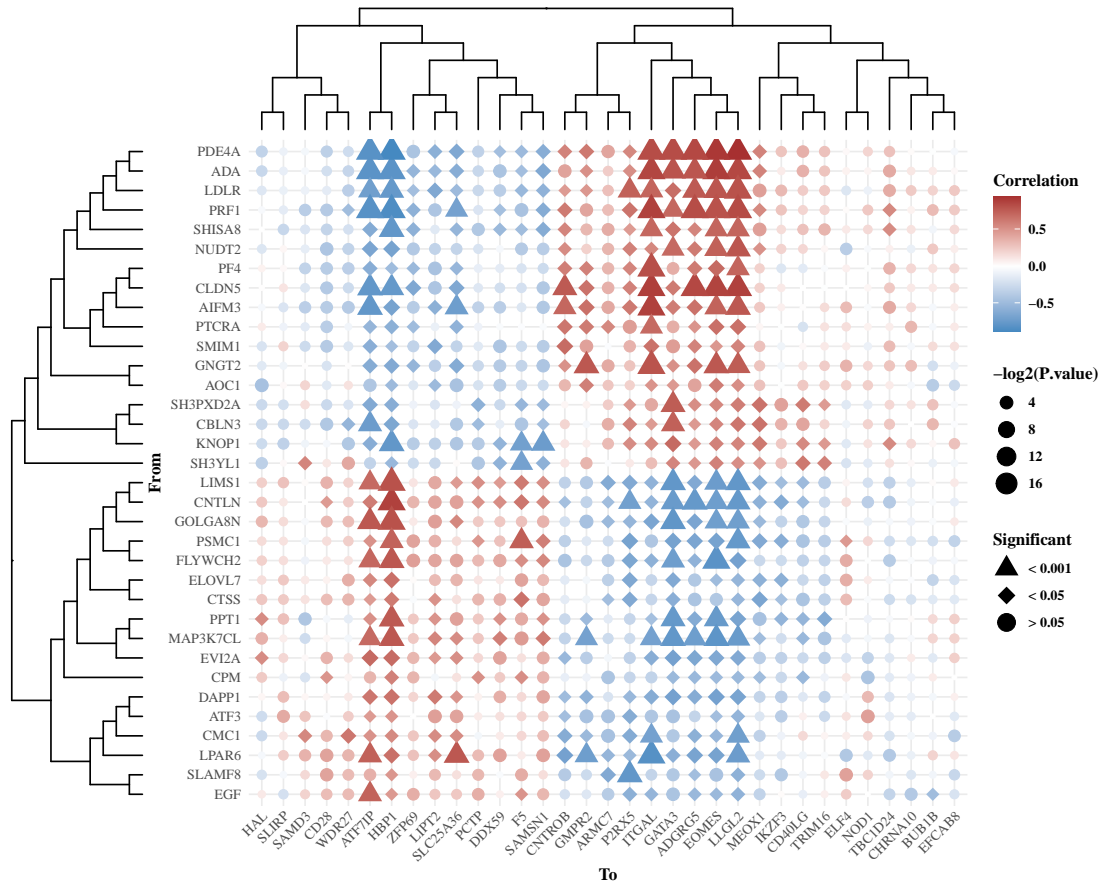


Figure 8: SCI sigCoDEGs with rTMS DEGs correlation heatmap

Table 9 (下方表格) 为表格 SCI sigCoDEGs with rTMS DEGs significant correlation 概览。

(对应文件为 Figure+Table/SCI-sigCoDEGs-with-rTMS-DEGs-significant-correlation.csv)

注：表格共有 406 行 7 列，以下预览的表格可能省略部分数据；表格含有 34 个唯一 ‘From’。

1. cor: 皮尔逊关联系数，正关联或负关联。
2. pvalue: 显著性 P。
3. -log2(P.value): P 的对数转化。
4. significant: 显著性。
5. sign: 人为赋予的符号，参考 significant。

Table 9: SCI sigCoDEGs with rTMS DEGs significant correlation

| From | To | cor | pvalue | -log2... | signi... | sign |
|----------|--------|-------|--------|----------|----------|------|
| PPT1 | CD40LG | -0.54 | 0.0173 | 5.853... | < 0.05 | * |
| CPM | CD40LG | -0.52 | 0.0214 | 5.546... | < 0.05 | * |
| KNOP1 | CD40LG | 0.54 | 0.017 | 5.878... | < 0.05 | * |
| CNTLN | CD40LG | -0.49 | 0.0331 | 4.917... | < 0.05 | * |
| SH3YL1 | CD40LG | 0.62 | 0.0046 | 7.764... | < 0.05 | * |
| LIMS1 | CD40LG | -0.5 | 0.028 | 5.158... | < 0.05 | * |
| MAP3K7CL | CD40LG | -0.52 | 0.0231 | 5.435... | < 0.05 | * |
| SH3PXD2A | CD40LG | 0.61 | 0.0052 | 7.587... | < 0.05 | * |
| ADA | F5 | -0.47 | 0.0425 | 4.556... | < 0.05 | * |
| LDLR | F5 | -0.52 | 0.0228 | 5.454... | < 0.05 | * |
| CPM | F5 | 0.52 | 0.021 | 5.573... | < 0.05 | * |
| KNOP1 | F5 | -0.7 | 8e-04 | 10.28... | < 0.001 | ** |
| PDE4A | F5 | -0.5 | 0.0285 | 5.132... | < 0.05 | * |
| CNTLN | F5 | 0.63 | 0.0036 | 8.117... | < 0.05 | * |
| FLYWCH2 | F5 | 0.52 | 0.0237 | 5.398... | < 0.05 | * |
| ... | ... | ... | ... | ... | ... | ... |

6.5.2 富集分析

Figure 9 (下方图) 为图 RTMS SCI NP correlated sci GO enrichment 概览。

(对应文件为 `Figure+Table/RTMS-SCI-NP-correlated-sci-GO-enrichment.pdf`)

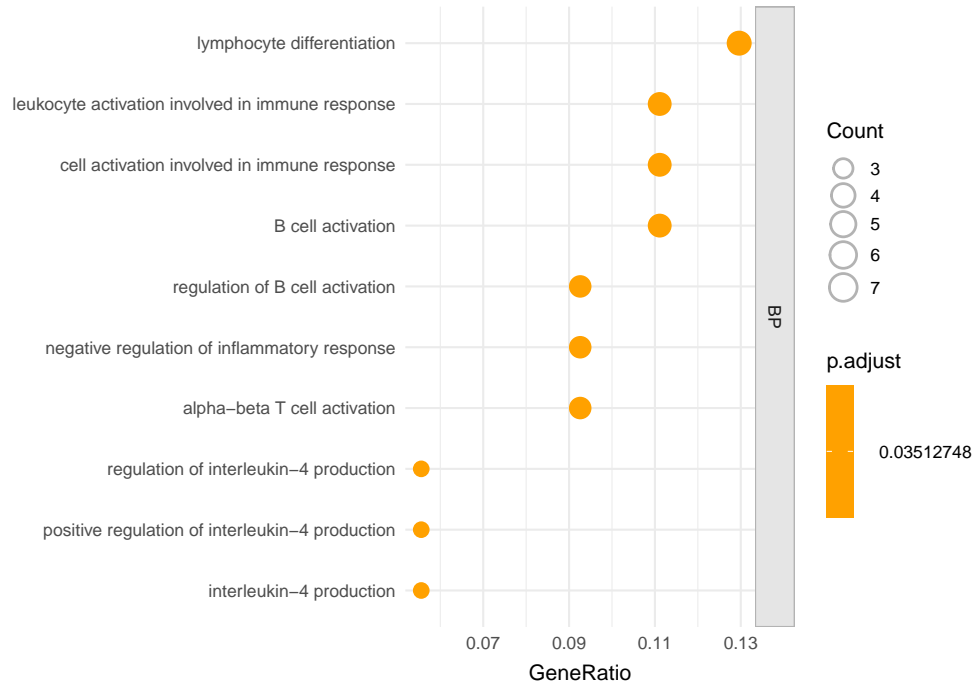


Figure 9: RTMS SCI NP correlated sci GO enrichment

Reference

1. Wu, T. *et al.* ClusterProfiler 4.0: A universal enrichment tool for interpreting omics data. *The Innovation* **2**, (2021).
2. Ritchie, M. E. *et al.* Limma powers differential expression analyses for rna-sequencing and microarray studies. *Nucleic Acids Research* **43**, e47 (2015).
3. Chen, Y., McCarthy, D., Ritchie, M., Robinson, M. & Smyth, G. EdgeR: Differential analysis of sequence read count data user's guide. 119.
4. Morrison, D. *et al.* Profiling immunological phenotypes in individuals during the first year after traumatic spinal cord injury: A longitudinal analysis. *Journal of Neurotrauma* **40**, 2621–2637 (2023).