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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) - Transcriptional changes in the (rat) brain induced by repetitive transcranial magnetic stimulation - GSE230150 - GSE206765 (16s)

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.
- **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:

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

4 分析结果

5 结论

6 附：分析流程

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

6.1.1 元数据

- GSE226238

根据文献提供的数据整理信息???:

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'。

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
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

6.2 神经病理性疼痛 (neuropathic pain, NP)

6.2.1 元数据

Table 2 (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'。

Table 2: 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

6.3 SCI 和 NP 关联分析

6.3.1 共同差异基因 coDEGs

Figure 1 (下方图) 为图 SCI NP coDEGs 概览。

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

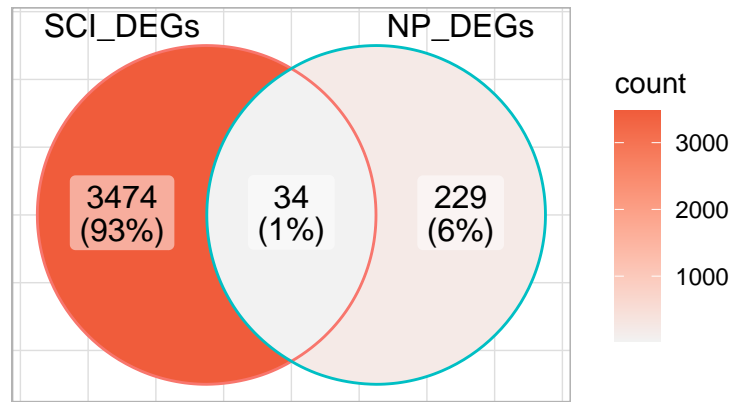


Figure 1: SCI NP coDEGs

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

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

6.3.2 SCI 的 coDEGs 的关联性分析

6.3.3 NP 的 coDEGs 的关联性分析

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

Reference

1. Ritchie, M. E. *et al.* Limma powers differential expression analyses for rna-sequencing and microarray studies. *Nucleic Acids Research* **43**, e47 (2015).
2. Chen, Y., McCarthy, D., Ritchie, M., Robinson, M. & Smyth, G. EdgeR: Differential analysis of sequence read count data user's guide. 119.