# 乙酰化酶分析筛选

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|                           |       |  | - <b>-</b><br>14 |
|                           |       |  | $\frac{15}{15}$  |
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# 1 摘要

### 1.1 需求

利用生物信息学分析结合已有文献资料,筛选并验证与 XX 相关的乙酰化酶 AA

具体要求为:利用开源数据库,筛选心肌梗死机体的心脏细胞中关键差异表达基因 XX 以及与乙酰化相关酶基因的关联性。

- 1. 因客户之前所做基因为 FKBP5, 故 XX 初步定为 FKBP5。假设 FKBP5 在心肌梗死机体心肌细胞中高表达,抑制 FKBP5 后可缓解心肌梗死。
- 2. 乙酰化酶 AA 备选: 去乙酰化酶 sirtuin 1 (SIRT1) 可以直接与 FKBP5 相互作用。
- 3. 若方案中的 AA 选择为 HDAC6 (客户之前发表过 LncRNA NORAD-HDAC6-H3K9 -VEGF), 那么方案中的 XX 选择不一定非要是 FKBP5, 若有创新点的更好的基因也可。

### 1.2 结果

- 结合数据库 MI 靶点和 MI 小鼠数据集获取一批 MI 基因 Fig. 3
- 从 epiFactor 数据库获取乙酰酶 (CoA) (Tab. 5), 筛选了 MI 中为差异表达的 CoA (Fig. 4)。
- 根据 Fig. 3 和 Fig. 4 建立 PPI 网络 (有实验基础的蛋白物理直接互作), 见 Fig. 5
- 筛选 CoA 与 DEGs 显著关联的组合, Fig. 6, Tab. 7
- 筛选上述关系: 存在 PPI 关联且关联分析显著的组合 Tab. 8
- 将上述 DEGs GO 富集分析, Fig. 7, BP 结果指向了 MI。
- 建立 CoA-XX-pathways 网络关系图, Fig. 8, 数据见 Tab. 9。
- 最后, 推荐 CoA-XX 组合为:
  - CoA:BRCA1, DEG:FLNA
  - CoA:HDAC9, DEG:PIK3CG
  - 以上 DEG 相关 GO 通路: cardiac muscle contraction; coagulation; muscle system process; regulation of body fluid levels; striated muscle contraction; wound healing
- 其它候选见 Tab. 9

### 注:

- FKBP5 (Fkbp5) 在 MI 中属于显著高表达, 见 Tab. 4。
- FKBP5 在 Fig. 3 被筛离。
- 尝试单独建立 PPI, 未发现 SIRT1 与 FKBP5 的直接结合作用。

## 2 前言

# 3 材料和方法

### 3.1 材料

All used GEO expression data and their design:

• GSE236374: Nine 8-week-old male C57BL/6JR mice were included in the experiment. The experiment was divided into 3 groups. Each group contained 3 mice, 2 groups of which required surgery to make models, called...

### 3.2 方法

Mainly used method:

- The biomart was used for mapping genes between organism (e.g., mgi\_symbol to hgnc\_symbol)<sup>1</sup>.
- R package ClusterProfiler used for gene enrichment analysis<sup>2</sup>.
- Database EpiFactors used for screening epigenetic regulators<sup>3</sup>.
- GEO https://www.ncbi.nlm.nih.gov/geo/ used for expression dataset aquisition.
- Databses of DisGeNet, GeneCards, PharmGKB used for collating disease related targets<sup>4-6</sup>.
- The Human Gene Database GeneCards used for disease related genes prediction<sup>5</sup>.
- R package ClusterProfiler used for GSEA enrichment<sup>2</sup>.
- R package Limma and edgeR used for differential expression analysis 7,8.
- R package STEINGdb used for PPI network construction<sup>9,10</sup>.
- R version 4.3.2 (2023-10-31); 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 MI targets

使用以下合集:

Figure 1 (下方图) 为图 Overall targets number of datasets 概览。

### (对应文件为 Figure+Table/Overall-targets-number-of-datasets.pdf)

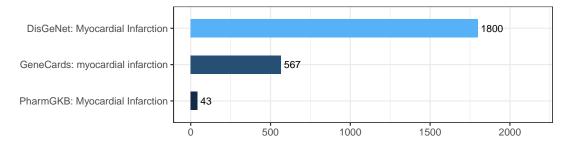


Figure 1: Overall targets number of datasets

### The GeneCards data was obtained by querying:

myocardial infarction

Restrict (with quotes):

TRUE

Filtering by Score: :

Score > 5

Table 1 (下方表格) 为表格 GeneCards used data 概览。

### (对应文件为 Figure+Table/GeneCards-used-data.xlsx)

注:表格共有 567 行 7 列,以下预览的表格可能省略部分数据;含有 567 个唯一'Symbol'。

Table 1: GeneCards used data

| Symbol     | Description   | Category      | ${\bf UniProt\_ID}$ | $\operatorname{GIFtS}$ | $GC\_id$    | Score |
|------------|---------------|---------------|---------------------|------------------------|-------------|-------|
| ACE        | Angiotensi    | Protein Co    | P12821              | 60                     | GC17P063477 | 75.08 |
| MIAT       | Myocardial    | RNA Gene (    |                     | 32                     | GC22P026646 | 71.09 |
| F7         | Coagulatio    | Protein Co    | P08709              | 56                     | GC13P113105 | 54.33 |
| ITGB3      | Integrin S    | Protein Co    | P05106              | 61                     | GC17P112532 | 48.15 |
| LTA        | Lymphotoxi    | Protein Co    | P01374              | 52                     | GC06P134818 | 44.63 |
| OLR1       | Oxidized L    | Protein Co    | P78380              | 51                     | GC12M029495 | 44.32 |
| PLAT       | Plasminoge    | Protein Co    | P00750              | 58                     | GC08M042174 | 39.78 |
| MCI2       | Myocardial    | Genetic Locus |                     | 4                      | GC13U900611 | 39.39 |
| F13A1      | Coagulatio    | Protein Co    | P00488              | 56                     | GC06M006144 | 39.35 |
| CDKN2B-AS1 | CDKN2B Ant    | RNA Gene (    |                     | 31                     | GC09P021994 | 39.31 |
| LGALS2     | Galectin 2    | Protein Co    | P05162              | 47                     | GC22M037570 | 38.25 |
| MEF2A      | Myocyte En    | Protein Co    | Q02078              | 54                     | GC15P099565 | 38.14 |
| MIR499A    | MicroRNA 499a | RNA Gene (    |                     | 29                     | GC20P034990 | 37.65 |
| ESR1       | Estrogen R    | Protein Co    | P03372              | 62                     | GC06P151656 | 37.58 |
| MIR208B    | MicroRNA 208b | RNA Gene (    |                     | 27                     | GC14M023417 | 35.34 |
|            |               |               |                     |                        |             |       |

### 6.2 MI mice DEGs

### 6.2.1 数据来源

# Data Source ID: GSE236374 data\_processing: Raw reads were trimmed adaptor sequences and removed low-quality reads using TrimGalore with default settings data\_processing.1: Trimmed reads were aligned to the mm10 reference genome by STAR with default settings data\_processing.2: Read count extraction were performed using FeatureCounts data\_processing.3: Assembly: mm10 (Others): ...

### (上述信息框内容已保存至 Figure+Table/GSE236374-content)

### 6.2.2 差异分析

• MI-7d (7 day) vs Control

Figure 2 (下方图) 为图 MI MI 7d vs MI sham DEGs 概览。

(对应文件为 Figure+Table/MI-MI-7d-vs-MI-sham-DEGs.pdf)

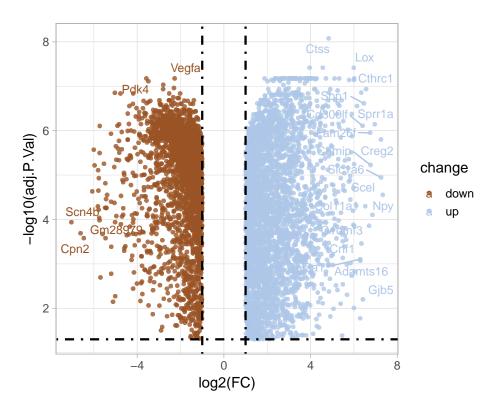


Figure 2: MI MI 7d vs MI sham DEGs

```
adj.P.Val cut-off:
0.05

Log2(FC) cut-off:
1
```

### (上述信息框内容已保存至 Figure+Table/MI-MI-7d-vs-MI-sham-DEGs-content)

Table 2 (下方表格) 为表格 MI data MI 7d vs MI sham DEGs 概览。

### (对应文件为 Figure+Table/MI-data-MI-7d-vs-MI-sham-DEGs.csv)

注: 表格共有 5724 行 8 列,以下预览的表格可能省略部分数据;含有 5724 个唯一'Genesymbol'。

- 1. logFC: estimate of the log2-fold-change corresponding to the effect or contrast (for 'topTableF' there may be several columns of log-fold-changes)
- 2. Ave Expr: average log2-expression for the probe over all arrays and channels, same as 'Amean' in the 'Marray LM' 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: MI data MI 7d vs MI sham DEGs

| rownames | Genesy  | $\log FC$ | AveExpr | t      | P.Value | adj.P.Val | В      |
|----------|---------|-----------|---------|--------|---------|-----------|--------|
| 7514     | Ctss    | 4.8320    | 7.4632  | 50.601 | 5.8181  | 8.3472    | 19.814 |
| 14679    | Adamts2 | 3.9541    | 7.5930  | 37.675 | 9.6997  | 3.8153    | 17.557 |
| 23411    | Col14a1 | 4.5612    | 7.5634  | 37.311 | 1.0637  | 3.8153    | 17.437 |
| 11851    | Lox     | 5.9882    | 7.0429  | 37.907 | 9.1490  | 3.8153    | 17.419 |
| 21619    | Fstl1   | 3.9252    | 9.4422  | 33.841 | 2.6934  | 6.6702    | 16.550 |
| 1261     | Ctsh    | 2.6147    | 6.6709  | 31.959 | 4.6403  | 6.6702    | 16.144 |
| 13487    | Pla2g7  | 4.0298    | 4.6625  | 32.933 | 3.4885  | 6.6702    | 16.129 |
| 22176    | Laptm5  | 3.3558    | 6.9162  | 31.874 | 4.7596  | 6.6702    | 16.105 |
| 1490     | Sparc   | 3.2522    | 11.160  | 32.579 | 3.8660  | 6.6702    | 16.079 |
| 6315     | Hexb    | 3.1220    | 6.3869  | 31.264 | 5.7173  | 6.6702    | 15.929 |
| 5004     | Ctsz    | 3.0952    | 6.9421  | 30.777 | 6.6372  | 6.6702    | 15.790 |
| 21174    | Fbln5   | 3.7685    | 7.2452  | 30.367 | 7.5384  | 6.6702    | 15.656 |
| 1805     | Litaf   | 2.3676    | 5.9412  | 30.219 | 7.8956  | 6.6702    | 15.624 |
| 12260    | Nckap1l | 3.3359    | 5.8304  | 29.954 | 8.5853  | 6.6702    | 15.519 |
| 3893     | Gusb    | 2.3568    | 6.0931  | 29.740 | 9.1894  | 6.6702    | 15.480 |
|          |         |           |         |        |         |           |        |

### 6.2.3 基因映射

将小鼠基因映射到人类

Table 3 (下方表格) 为表格 Mapped genes 概览。

### (对应文件为 Figure+Table/Mapped-genes.csv)

注: 表格共有 5274 行 2 列,以下预览的表格可能省略部分数据;含有 5123 个唯一'mgi\_symbol;含有 5146 个唯一'hgnc\_symbol'。

- 1. hgnc\_symbol: 基因名 (Human)
- 2. mgi\_symbol: 基因名 (Mice)

Table 3: Mapped genes

| $mgi\_symbol$ | hgnc_symbol |
|---------------|-------------|
| Tmsb4x        | TMSB4Y      |
| Hopx          | HOPX        |
| Cyth4         | CYTH4       |
| Col6a2        | COL6A2      |
| Pacsin2       | PACSIN2     |
| Fbln1         | FBLN1       |
| Sh3bp2        | SH3BP2      |
| Abcg1         | ABCG1       |
| Mipep         | MIPEP       |
| Itgb2         | ITGB2       |
| Pmepa1        | PMEPA1      |
| Maged2        | MAGED2      |
| Postn         | POSTN       |
| Slc39a6       | SLC39A6     |
| Sirpa         | SIRPG       |
|               |             |

### 6.2.4 FKBP5 的表达

FKBP5 (Fkbp5) 在 MI 中属于显著高表达。

Table 4 (下方表格) 为表格 Fkbp5 expression 概览。

### (对应文件为 Figure+Table/Fkbp5-expression.csv)

注: 表格共有1行10列,以下预览的表格可能省略部分数据;含有1个唯一'hgnc\_symbol'。

- 1. hgnc\_symbol: 基因名 (Human)
- 2. mgi\_symbol: 基因名 (Mice)
- 3. logFC: estimate of the log2-fold-change corresponding to the effect or contrast (for 'topTableF' there may be several columns of log-fold-changes)
- 4. Ave Expr: average log2-expression for the probe over all arrays and channels, same as 'Amean' in the 'Marray LM' object
- 5. t: moderated t-statistic (omitted for 'topTableF')
- 6. P.Value: raw p-value
- 7. B: log-odds that the gene is differentially expressed (omitted for 'topTreat')

Table 4: Fkbp5 expression

| hgnc_s | mgi_sy | rownames | Genesy | $\log FC$ | AveExpr | t      | P.Value | adj.P.Val | В      |
|--------|--------|----------|--------|-----------|---------|--------|---------|-----------|--------|
| FKBP5  | Fkbp5  | 9124     | Fkbp5  | 1.5635    | 5.3072  | 5.7027 | 0.0002  | 0.0005    | 0.0172 |

### 6.3 MI intersection (MI\_key\_DEGs)

Figure 3 (下方图) 为图 Intersection of MI DEGs with MI targets 概览。

### (对应文件为 Figure+Table/Intersection-of-MI-DEGs-with-MI-targets.pdf)

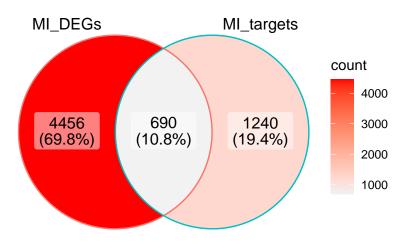


Figure 3: Intersection of MI DEGs with MI targets

### Intersection:

ABCG1, ITGB2, POSTN, EGLN3, PPARGC1A, LTBP2, CYBB, C3AR1, THBS1, SER-PINE1, CLU, SFRP2, TGFB3, IGFBP4, TNC, LCP1, GAS6, CTSZ, HPGDS, BGN, VLDLR, GUCY1A1, CYP4F3, LIPA, NCAM1, GLA, HLA-DMB, FERMT3, LGALS3, TLR2, MMP2, GPNMB, CYBA, ALCAM, KDR, TNNI3, ARNTL, IGFBP7, ANPEP, PPM1L, TNFRSF1B, SERPINF1, ...

(上述信息框内容已保存至 Figure+Table/Intersection-of-MI-DEGs-with-MI-targets-content)

### 6.4 乙酰化酶

### 6.4.1 使用的乙酰化酶及其相关信息

Table 5 (下方表格) 为表格 All protein of CoA 概览。

(对应文件为 Figure+Table/All-protein-of-CoA.xlsx)

注: 表格共有 145 行 25 列,以下预览的表格可能省略部分数据;含有 142 个唯一'HGNC\_symbol'。

Table 5: All protein of CoA

| HGNC_s         | Modifi | Id  | Status | HGNC_ID | HGNC_name | GeneID | UniPro8 | UniPro9        | Domain    |
|----------------|--------|-----|--------|---------|-----------|--------|---------|----------------|-----------|
| ARID4A         | Histon | 36  | #      | 9885    | AT ric    | 5926   | P29374  | ARI4A          | ARID P    |
| ARID4B         | Histon | 37  | #      | 15550   | AT ric    | 51742  | Q4LE39  | ARI4B          | ARID P    |
| ATF2           | Histon | 49  | #      | 784     | activa    | 1386   | P15336  | ATF2_H         | bZIP_1    |
| ATXN7          | Histon | 55  | #      | 10560   | ataxin 7  | 6314   | O15265  | ATX7_H         | Pfam-B    |
| BANP           | Histon | 62  | #      | 13450   | BTG3 a    | 54971  | Q8N9N5  | BANP_H         | BEN PF    |
| BAZ2A          | Histon | 67  | #      | 962     | bromod    | 11176  | Q9UIF9  | BAZ2A          | Bromod    |
| BCORL1         | Histon | 70  | #      | 25657   | BCL6 c    | 63035  | Q5H9F3  | BCORL          | $Ank\_2\$ |
| BRCA1          | Histon | 73  | #      | 1100    | breast    | 672    | P38398  | BRCA1          | BRCT P    |
| BRCA2          | Histon | 74  | #      | 1101    | breast    | 675    | P51587  | ${\rm BRCA2}\$ | BRCA-2    |
| ${\rm BRMS1L}$ | Histon | 86  | #      | 20512   | breast    | 84312  | Q5PSV4  | BRM1L          | Sds3 P    |
| BRPF3          | Histon | 88  | #      | 14256   | bromod    | 27154  | Q9ULD4  | BRPF3          | Bromod    |
| CDY1           | Histon | 115 | #      | 1809    | chromo    | 9085   | Q9Y6F8  | CDY1_H         | Chromo    |
| CDY1B          | Histon | 116 | #      | 23920   | chromo    | 253175 | Q9Y6F8  | CDY1_H         | Chromo    |
| CDY2A          | Histon | 117 | #      | 1810    | chromo    | 9426   | Q9Y6F7  | CDY2_H         | Chromo    |
| CDY2B          | Histon | 118 | #      | 23921   | chromo    | 203611 | Q9Y6F7  | CDY2_H         | Chromo    |
|                |        |     |        |         |           |        |         |                |           |

# 6.4.2 筛选差异表达的乙酰化酶 (CoA\_DEGs)

使用 MI 数据 (6.2) 的 DEGs, 筛选差异表达的乙酰化酶。

以 mgi\_symbol 取交集。

Figure 4 (下方图) 为图 Intersection of All CoA with MI DEGs 概览。

(对应文件为 Figure+Table/Intersection-of-All-CoA-with-MI-DEGs.pdf)

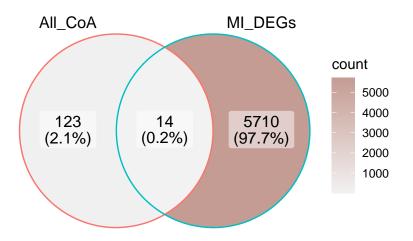


Figure 4: Intersection of All CoA with MI DEGs

### Intersection:

Brca1, Eid1, Eid2b, Hdac11, Hdac9, Hif1an, Jdp2, Morf4l2, Ncoa1, Nsl1, Sirt7, Smarca1, Taf7, Zbtb16

(上述信息框内容已保存至 Figure+Table/Intersection-of-All-CoA-with-MI-DEGs-content)

# 6.5 其它候选

### 6.5.1 以 PPI 网络筛选与 CoA\_DEGs 相关的 MI\_key\_DEGs

根据 Fig. 3 和 Fig. 4 建立 PPI 网络 (有实验基础的蛋白物理直接互作)。

STRINGdb network type: :
physical

Filter experiments score: :
At least score 100

Filter textmining score: :
At least score 0

Table 6 (下方表格) 为表格 PPI annotation 概览。

(对应文件为 Figure+Table/PPI-annotation.csv)

注:表格共有 1364 行 10 列,以下预览的表格可能省略部分数据;含有 381 个唯一'from'。

1. experiments: 相关实验。

Table 6: PPI annotation

| from     | to       | homology | experi4 | experi5 | database | databa | textmi8 | textmi9 |  |
|----------|----------|----------|---------|---------|----------|--------|---------|---------|--|
| TNFRSF1A | RIPK3    | 0        | 292     | 0       | 0        | 0      | 473     | 0       |  |
| DCN      | PLAT     | 0        | 205     | 0       | 0        | 0      | 0       | 0       |  |
| DCN      | TGFB1    | 0        | 457     | 0       | 500      | 0      | 979     | 60      |  |
| MMP2     | TGFB1    | 0        | 548     | 0       | 0        | 0      | 118     | 0       |  |
| PLAT     | SERPINE1 | 0        | 955     | 0       | 700      | 0      | 982     | 0       |  |
| MYH9     | ACTA2    | 0        | 205     | 97      | 900      | 0      | 0       | 91      |  |
| MMP2     | COL1A1   | 0        | 292     | 0       | 0        | 0      | 0       | 0       |  |
| TGFB1    | VDR      | 0        | 292     | 0       | 0        | 0      | 0       | 0       |  |
| COL1A1   | VDR      | 0        | 292     | 0       | 0        | 0      | 0       | 0       |  |
| MMP2     | LOX      | 0        | 238     | 0       | 0        | 0      | 0       | 0       |  |
| COL1A1   | LOX      | 0        | 230     | 0       | 0        | 0      | 0       | 0       |  |
| COL1A1   | SPARC    | 0        | 457     | 0       | 0        | 0      | 89      | 90      |  |
| VDR      | IL12B    | 0        | 292     | 0       | 0        | 0      | 0       | 0       |  |
| ACTA2    | CTSD     | 0        | 229     | 0       | 0        | 0      | 0       | 0       |  |
| VDR      | EGR1     | 0        | 292     | 0       | 0        | 0      | 0       | 0       |  |
|          |          | •••      |         |         |          |        |         |         |  |

获取 CoA -> DEGs 的网络:

Figure 5 (下方图) 为图 Filtered and formated PPI network 概览。

(对应文件为 Figure+Table/Filtered-and-formated-PPI-network.pdf)

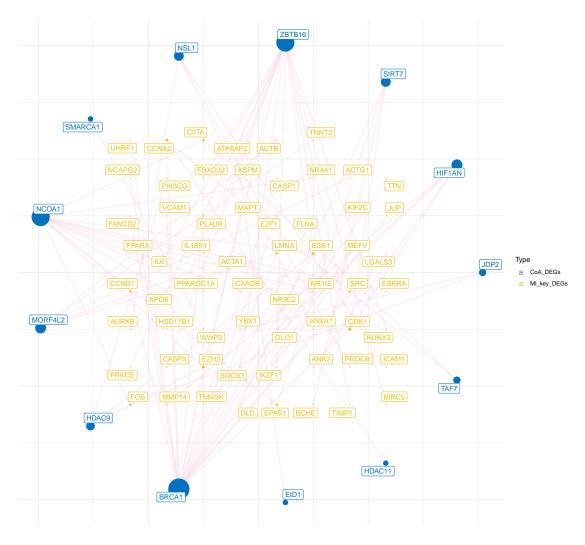


Figure 5: Filtered and formated PPI network

### 6.5.2 关联分析

根据 Fig. 5, 以小鼠数据集 (6.2) 进行关联分析。

Figure 6 (下方图) 为图 MI correlation heatmap 概览。

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

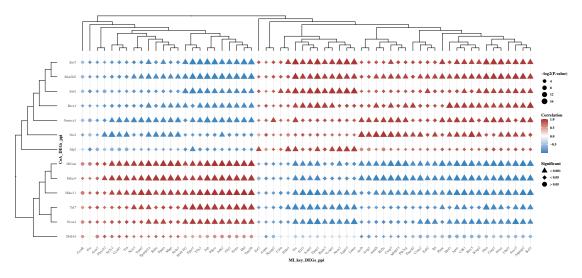


Figure 6: MI correlation heatmap

Table 7 (下方表格) 为表格 MI significant correlation 概览。

### (对应文件为 Figure+Table/MI-significant-correlation.csv)

注: 表格共有 738 行 7 列,以下预览的表格可能省略部分数据;含有 13 个唯一'CoA\_DEGs\_ppi'。

- 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 7: MI significant correlation

| CoA_DEGs_ppi    | MI_key_DEG | cor   | pvalue | -log2(P.va | significant | sign |
|-----------------|------------|-------|--------|------------|-------------|------|
| Morf4l2         | Ppargc1a   | -0.95 | 1e-04  | 13.2877123 | < 0.001     | **   |
| Hdac9           | Ppargc1a   | 0.98  | 0      | 16.6096404 | < 0.001     | **   |
| Sirt7           | Ppargc1a   | -0.92 | 5e-04  | 10.9657842 | < 0.001     | **   |
| Nsl1            | Ppargc1a   | -0.94 | 2e-04  | 12.2877123 | < 0.001     | **   |
| Taf7            | Ppargc1a   | 0.9   | 0.001  | 9.96578428 | < 0.001     | **   |
| Ncoa1           | Ppargc1a   | 0.91  | 7e-04  | 10.4803574 | < 0.001     | **   |
| $\mathrm{Jdp2}$ | Ppargc1a   | -0.74 | 0.0217 | 5.52616114 | < 0.05      | *    |
| Hif1an          | Ppargc1a   | 0.99  | 0      | 16.6096404 | < 0.001     | **   |
| Brca1           | Ppargc1a   | -0.93 | 3e-04  | 11.7027498 | < 0.001     | **   |
| Smarca1         | Ppargc1a   | -0.95 | 1e-04  | 13.2877123 | < 0.001     | **   |
| Hdac11          | Ppargc1a   | 0.96  | 0      | 16.6096404 | < 0.001     | **   |
| Eid1            | Ppargc1a   | -0.87 | 0.0024 | 8.70274987 | < 0.05      | *    |

| CoA_DEGs_ppi | MI_key_DEG | cor   | pvalue | -log2(P.va | significant | sign |
|--------------|------------|-------|--------|------------|-------------|------|
| Zbtb16       | Ppargc1a   | 0.67  | 0.0483 | 4.37183300 | < 0.05      | *    |
| Morf4l2      | Il18r1     | 0.88  | 0.0018 | 9.11778737 | < 0.05      | *    |
| Hdac9        | Il18r1     | -0.78 | 0.013  | 6.26534456 | < 0.05      | *    |
|              |            |       |        |            |             |      |

### 6.5.3 存在 PPI 关联且关联分析显著的组合

结合 6.5.1 和 6.5.2 筛选 CoA 与 XX

Table 8 (下方表格) 为表格 PPI interact and significant correlated in MI 概览。

### (对应文件为 Figure+Table/PPI-interact-and-significant-correlated-in-MI.csv)

注: 表格共有 64 行 9 列,以下预览的表格可能省略部分数据;含有 13 个唯一'CoA\_DEGs\_ppi'。

- 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: PPI interact and significant correlated in MI

| CoA_DE | MI_key                  | cor   | pvalue | -log2( | signif  | sign | CoA_hg | DEG_hg |
|--------|-------------------------|-------|--------|--------|---------|------|--------|--------|
| Brca1  | Casp1                   | 0.91  | 8e-04  | 10.287 | < 0.001 | **   | BRCA1  | CASP1  |
| Brca1  | Ccna2                   | 0.9   | 0.0011 | 9.8282 | < 0.05  | *    | BRCA1  | CCNA2  |
| Brca1  | $\operatorname{Ccnd} 1$ | -0.87 | 0.0024 | 8.7027 | < 0.05  | *    | BRCA1  | CCND1  |
| Brca1  | Cdk1                    | 0.95  | 1e-04  | 13.287 | < 0.001 | **   | BRCA1  | CDK1   |
| Brca1  | E2f1                    | 0.95  | 1e-04  | 13.287 | < 0.001 | **   | BRCA1  | E2F1   |
| Brca1  | Esr1                    | 0.7   | 0.0356 | 4.8119 | < 0.05  | *    | BRCA1  | ESR1   |
| Brca1  | Ezh2                    | 0.88  | 0.002  | 8.9657 | < 0.05  | *    | BRCA1  | EZH2   |
| Brca1  | Fancd2                  | 0.94  | 2e-04  | 12.287 | < 0.001 | **   | BRCA1  | FANCD2 |
| Brca1  | Flna                    | 0.92  | 4e-04  | 11.287 | < 0.001 | **   | BRCA1  | FLNA   |
| Brca1  | Jup                     | -0.94 | 2e-04  | 12.287 | < 0.001 | **   | BRCA1  | JUP    |
| Brca1  | Kif2c                   | 0.89  | 0.0011 | 9.8282 | < 0.05  | *    | BRCA1  | KIF2C  |
| Brca1  | Lgals3                  | 0.89  | 0.0013 | 9.5872 | < 0.05  | *    | BRCA1  | LGALS3 |
| Brca1  | Lmna                    | 0.89  | 0.0015 | 9.3808 | < 0.05  | *    | BRCA1  | LMNA   |
| Brca1  | Mapt                    | -0.91 | 8e-04  | 10.287 | < 0.001 | **   | BRCA1  | MAPT   |
| Brca1  | Mefv                    | 0.97  | 0      | 16.609 | < 0.001 | **   | BRCA1  | MEFV   |
|        |                         |       |        |        |         |      |        |        |

### 6.5.4 富集分析

将 Tab. 8 中的 DEGs 进行富集分析

Figure 7 (下方图) 为图 GO enrichment 概览。

### (对应文件为 Figure+Table/GO-enrichment.pdf)

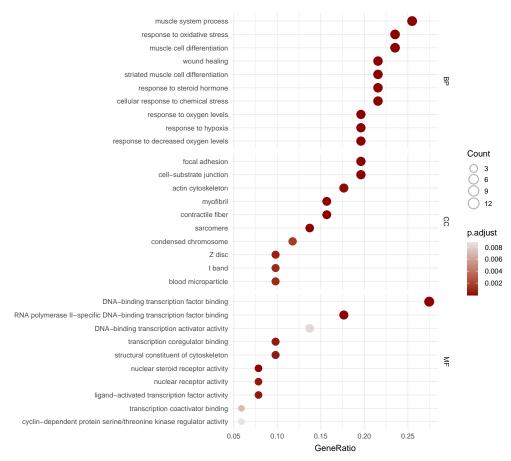


Figure 7: GO enrichment

### 6.5.5 CoA-XX-pathways

Figure 8 (下方图) 为图 CoA XX GOpathways 概览。

(对应文件为 Figure+Table/CoA-XX-GOpathways.pdf)

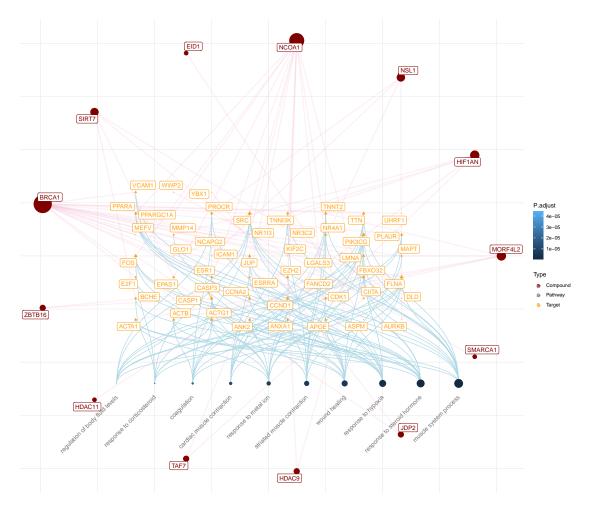


Figure 8: CoA XX GOpathways

Table 9 (下方表格) 为表格 All candidates and enriched GO BP pathways 概览。

### (对应文件为 Figure+Table/All-candidates-and-enriched-GO-BP-pathways.csv)

注: 表格共有 64 行 4 列,以下预览的表格可能省略部分数据; 含有 13 个唯一'CoA\_hgnc\_symbol; 含有 51 个唯一'DEG\_hgnc\_symbol'。

Table 9: All candidates and enriched GO BP pathways

| CoA_hgnc_symbol | $\rm DEG\_hgnc\_symbol$ | Hit_pathway_number | Enriched_pathways |
|-----------------|-------------------------|--------------------|-------------------|
| BRCA1           | FLNA                    | 6                  | cardiac muscle co |
| BRCA1           | SRC                     | 6                  | coagulation; regu |
| HDAC9           | PIK3CG                  | 6                  | cardiac muscle co |
| NCOA1           | SRC                     | 6                  | coagulation; regu |
| ZBTB16          | CASP3                   | 5                  | response to corti |
| BRCA1           | CCND1                   | 4                  | regulation of bod |
| BRCA1           | TTN                     | 4                  | cardiac muscle co |

| CoA_hgnc_symbol | DEG_hgnc_symbol | Hit_pathway_number | Enriched_pathways |
|-----------------|-----------------|--------------------|-------------------|
| JDP2            | FOS             | 4                  | response to corti |
| MORF4L2         | ACTG1           | 4                  | coagulation; regu |
| MORF4L2         | TNNT2           | 4                  | cardiac muscle co |
| NCOA1           | CCND1           | 4                  | regulation of bod |
| NCOA1           | FOS             | 4                  | response to corti |
| NCOA1           | PPARA           | 4                  | muscle system pro |
| BRCA1           | JUP             | 3                  | cardiac muscle co |
| BRCA1           | PLAUR           | 3                  | coagulation; regu |
|                 |                 |                    |                   |

### Reference

- 1. Durinck, S., Spellman, P. T., Birney, E. & Huber, W. Mapping identifiers for the integration of genomic datasets with the r/bioconductor package biomaRt. *Nature protocols* 4, 1184–1191 (2009).
- 2. Wu, T. et al. ClusterProfiler 4.0: A universal enrichment tool for interpreting omics data. The Innovation 2, (2021).
- 3. Marakulina, D. *et al.* EpiFactors 2022: Expansion and enhancement of a curated database of human epigenetic factors and complexes. *Nucleic acids research* **51**, D564–D570 (2023).
- 4. Piñero, J. et al. The disgenet knowledge platform for disease genomics: 2019 update. Nucleic Acids Research (2019) doi:10.1093/nar/gkz1021.
- 5. Stelzer, G. et al. The generards suite: From gene data mining to disease genome sequence analyses. Current protocols in bioinformatics 54, 1.30.1–1.30.33 (2016).
- 6. Barbarino, J. M., Whirl-Carrillo, M., Altman, R. B. & Klein, T. E. PharmGKB: A worldwide resource for pharmacogenomic information. Wiley interdisciplinary reviews. Systems biology and medicine 10, (2018).
- 7. Ritchie, M. E. *et al.* Limma powers differential expression analyses for rna-sequencing and microarray studies. *Nucleic Acids Research* **43**, e47 (2015).
- 8. Chen, Y., McCarthy, D., Ritchie, M., Robinson, M. & Smyth, G. EdgeR: Differential analysis of sequence read count data user's guide. 119.
- 9. Szklarczyk, D. *et al.* The string database in 2021: Customizable proteinprotein networks, and functional characterization of user-uploaded gene/measurement sets. *Nucleic Acids Research* **49**, D605–D612 (2021).
- 10. Chin, C.-H. *et al.* CytoHubba: Identifying hub objects and sub-networks from complex interactome. *BMC Systems Biology* **8**, S11 (2014).