

# 筛选差异蛋白和对应配体蛋白

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# 1 摘要

- 研究对象：乳腺癌或结直肠癌
- 耐药：5-氟尿嘧啶或顺铂

## 1.1 需求

### 1.1.1 首次分析

1、寻找差异致瘤膜蛋白及对应配体蛋白；2、耐药差异膜蛋白及对应抗体蛋白或互作抑制其表达蛋白。

现需要利用数据库分析正常组与疾病组间的差异表达膜蛋白 AA（在癌中高表达的）和对应靶向癌细胞特异性高表达的膜蛋白 AA'；以及非耐药组与耐药组间的差异表达膜蛋白 XX（在耐药组中高表达的）和对应 XX 的抗体蛋白或相互作用能抑制其表达的蛋白 XX'。

### 1.1.2 进一步分析

1. 查询正常组与结直肠癌组相比，TSC1 的表达情况。期望 TSC1 仅在结肠癌的耐药群体中高表达，在正常组以及癌组织的非耐药中不表达或低表达。若在癌组织中高表达，则仅看“2”；若在正常组中高表达，则仅看“3”。
2. 生信分析结果已知，与 TSC1 有相互作用且抑制的蛋白有 5 种 (YWHAE, HSPA8, PTGES3, PSMG2, PLK2)，但是能否直接结合作为筛选靶点未知，麻烦进行分子对接研究 TSC1 与 5 种蛋白直接结合的可能性。届时将选择直接结合的对子进行实验。
3. 生信分析结果已知，差异癌膜蛋白 AA 为：AIFM1, TFRC, ITGAM, PECAM1，其对应的相互作用的蛋白 AA' 分别有 9、7、4、1 个。请将这 21 对相互作用的蛋白做一下关联分析，找到非抑制的对子（可以促进表达也可以没有促进抑制关系）；然后进行分子对接，需要了解 AA 和 AA' 直接结合的可能性。届时将选择直接结合的对子进行实验。

## 1.2 结果

### 1.2.1 寻找差异致瘤膜蛋白及对应配体蛋白

这一部分思路较简单，找到可用的蛋白质组数据<sup>1</sup>，筛选差异蛋白，再以 UniTmp 数据库筛选跨膜蛋白（膜蛋白受体主要为跨膜蛋白），再借助 STRINGdb 构建 PPI 网络，寻找互作蛋白，再结合富集分析 (6.3.3)，进一步缩小范围。

注意，以上 PPI 构建的来源是所有筛选到的差异蛋白（拟从差异蛋白中找到候选的配体蛋白）。

差异癌膜蛋白为：AIFM1, TFRC, ITGAM, PECAM1 最终筛选的蛋白和对应候选配体关系见：Fig. 8

### 1.2.2 耐药差异膜蛋白及对应抗体蛋白或互作抑制其表达蛋白

这部分思路稍复杂。由于无法直接获得包含耐药性分组的蛋白表达数据，因此需要另寻思路，即，获取 TCGA-COAD 的基因表达数据和蛋白定量数据，以 pRRophetic 根据基因表达数据分析耐药性（顺铂 Cisplatin），再对样本分组，随后分析蛋白定量数据。

后续和上一部分近似：筛选差异蛋白，再以 UniTmp 数据库筛选跨膜蛋白，再借助 STRINGdb 构建 PPI 网

络，寻找互作蛋白，再结合富集分析。到这里，筛选蛋白 (TSC1) 和互作蛋白关系见 Fig. 17。后续的富集分析结果可能有一定参考价值，富集到 TSC1 (hsa04151, Fig. 21)

注意，以上 PPI 构建的来源是筛选的膜蛋白 (TSC1)，和 RNA-seq 的 DEGs (拟从差异蛋白中找到候选的配体蛋白)。

但这部分还需要指定互作抑制的蛋白，因此又结合了关联分析，挖掘 RNA 表达中呈负相关性的蛋白 (Fig. 22)。

最终可参考的表格：Tab. 11

### 1.2.3 进一步分析的结果 (蛋白对接)

- 见 Fig. 23, TSC1 在正常组与癌症中无显著差异。因此，后续分析将依据 1.1.2 中的“3”展开。
- 筛选非负相关性的蛋白 (非抑制关系)，共 19 对，见 Tab. 12。
- 为了筛选具有结合可能的蛋白对，采取以下两步：
  - STRINGdb 数据库中，具有物理 (直接) 结合，并有实验基础 (experiments 得分) 的蛋白对，最后获得 Tab. 14
  - 以 cluspro 蛋白对接，获取得分 Fig. 26 和模型 (这里只展示 Top 5 的模型, Top 1 见 Fig. 27)。
- 取上述两步 (蛋白对接设置了 -1000 cut-off) 的综合，见 Fig. 28 和 Tab. 16。共有 5 对：FTH1\_TFRC, SERPINA1\_TFRC, HSPA8\_TFRC, DDX3X\_AIFM1, HMGB1\_ITGAM

## 2 前言

## 3 材料和方法

### 3.1 材料

Other data obtained from published article (e.g., supplementary tables):

- Supplementary file from article refer to ProteomicsProfShao2022<sup>1</sup>.

### 3.2 方法

Mainly used method:

- The ClusPro server used for Protein-Protein docking<sup>2</sup>.
- R package ClusterProfiler used for gene enrichment analysis<sup>3</sup>.
- HawkDock web servers used for protein-protein docking<sup>4</sup>.
- R package Limma and edgeR used for differential expression analysis<sup>5,6</sup>.
- R Package pRRophetic was used for Prediction of Clinical Chemotherapeutic Response<sup>7</sup>.
- R package STEINGdb used for PPI network construction<sup>8,9</sup>.
- R package TCGAbiolinks used for obtain TCGA dataset<sup>10</sup>.
- The UNIfied database of TransMembrane Proteins (UniTmp) was used for transmembrane protein information retrieving<sup>11,12</sup>.
- The MCC score was calculated referring to algorithm of CytoHubba<sup>9</sup>.

- R version 4.3.3 (2024-02-29); 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——寻找差异数致癌膜蛋白及对应配体蛋白

### 6.1 结直肠癌差异蛋白

#### 6.1.1 数据来源

Proteomics profiling of colorectal cancer progression identifies PLOD2 as a potential therapeutic target<sup>1</sup>

Table 1 (下方表格) 为表格 PUBLISHED ProteomicsProfShao2022 metadata used sample 概览。

(对应文件为 `Figure+Table/PUBLISHED-ProteomicsProfShao2022-metadata-used-sample.csv`)

注：表格共有 31 行 5 列，以下预览的表格可能省略部分数据；含有 2 个唯一 ‘group’。

1. sample: 样品名称
2. group: 分组名称

Table 1: PUBLISHED ProteomicsProfShao2022 metadata used sample

sample	Gender	Age	Pathology.Type	group
P1	Female	74	Normal Colon	Control
P2	Female	49	Normal Colon	Control
P5	Male	51	Normal Colon	Control
P6	Female	56	Normal Colon	Control
P7	Male	53	Normal Colon	Control
P8	Male	70	Normal Colon	Control
P9	Male	62	Normal Colon	Control
P11	Male	48	Normal Colon	Control
P13	Female	43	Normal Colon	Control
P14	Female	61	Normal Colon	Control
P15	Female	81	Normal Colon	Control
P16	Male	67	Normal Colon	Control
P17	Male	60	Normal Colon	Control
P18	Female	59	Normal Colon	Control
P19	Male	64	Normal Colon	Control
...	...	...	...	...

### 6.1.2 差异蛋白

Figure 1 (下方图) 为图 PPS Cancer vs Control DEGs 概览。

(对应文件为 [Figure+Table/PPS-Cancer-vs-Control-DEGs.pdf](#))

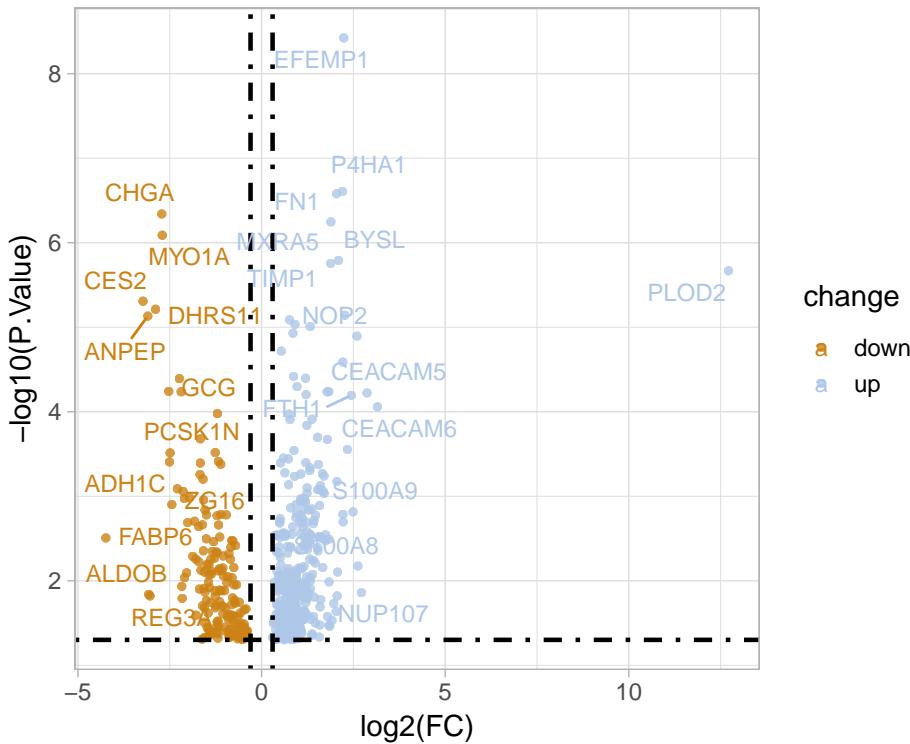


Figure 1: PPS Cancer vs Control DEGs

Table 2 (下方表格) 为表格 PPS data Cancer vs Control DPs 概览。

(对应文件为 [Figure+Table/PPS-data-Cancer-vs-Control-DPs.csv](#))

注：表格共有 509 行 8 列，以下预览的表格可能省略部分数据；含有 509 个唯一 ‘Gene\_name’。

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. AveExpr: average log2-expression for the probe 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: PPS data Cancer vs Control DPs

Gene_name	logFC	rownames	AveExpr	t	P.Value	adj.P.Val	B
EFEMP1	2.2381...	Q12805	5.4470...	8.2464...	3.7745...	1.8231...	10.666...
P4HA1	2.2015...	P13674	4.8852...	6.6539...	2.4728...	0.0004...	6.8779...
FN1	2.0416...	P02751	10.551...	6.6301...	2.6380...	0.0004...	6.8187...
CHGA	-2.716...	P10645	6.4443...	-6.428...	4.5698...	0.0005...	6.3149...
MXRA5	1.8876...	Q9NR99	5.3248...	6.3504...	5.6622...	0.0005...	6.1181...
MYO1A	-2.702...	Q9UBC5	6.3290...	-6.217...	8.1508...	0.0006...	5.7832...
BYSL	2.0924...	Q13895	3.1862...	5.9689...	1.6215...	0.0010...	5.1497...
TIMP1	1.8810...	P01033	5.1452...	5.9401...	1.7564...	0.0010...	5.0760...
PLOD2	12.715...	O00469	-5.707...	5.8680...	2.1455...	0.0011...	4.8915...
CES2	-3.227...	O00748	6.7662...	-5.570...	4.9174...	0.0023...	4.1256...
DHRS11	-2.886...	Q6UWP2	5.2052...	-5.491...	6.1300...	0.0026...	3.9219...
AEBP1	2.2654...	Q8IUX7	5.3752...	5.4328...	7.2234...	0.0027...	3.7701...
ANPEP	-3.097...	P15144	5.2534...	-5.425...	7.3809...	0.0027...	3.7501...
TKT	0.7599...	P29401	8.6760...	5.3887...	8.1722...	0.0028...	3.6559...
PTMS	0.9114...	P20962	8.2150...	5.3443...	9.2531...	0.0029...	3.5410...
...	...	...	...	...	...	...	...

## 6.2 膜蛋白筛选

受体蛋白主要分为：

- 离子通道受体 (Ligand-gated ion channel, LICs, LGIC)
- 催化受体 (酶受体) (catalytic receptor)
  - 鸟苷酸酰化酶受体
  - 酪氨酸激酶受体
- G 蛋白偶联受体 (G protein-coupled receptors) (GPCRs) (<https://gpcrdb.org/>)

以上都是跨膜蛋白类型。因此以下筛选将从跨膜蛋白出发。

### 6.2.1 UniTmp

UniTmp: unified resources for transmembrane proteins<sup>11</sup>

Table 3 (下方表格) 为表格 UniTmp data of htp all 概览。

(对应文件为 [Figure+Table/UniTmp-data-of-htp-all.xlsx](#))

注：表格共有 5499 行 5 列，以下预览的表格可能省略部分数据；含有 5499 个唯一 ‘id’。

1. evidence: 证据，相关文献中的描述。

Table 3: UniTmp data of htp all

id	transmembrane	evidence	Protein_name	Gene_Name
ACD10_HUMAN	yes	Exists	Acyl-CoA dehydrog...	ACAD10
ASPH_HUMAN	yes	3D	Aspartyl/asparagi...	ASPH
ATP8_HUMAN	yes	3D	ATP synthase prot...	MT-ATP8
BFAR_HUMAN	yes	Exists	Bifunctional apop...	BFAR
BAMBI_HUMAN	yes	Exists	BMP and activin m...	BAMBI
ATRAP_HUMAN	yes	Exists	Type-1 angiotensi...	AGTRAP
AOFA_HUMAN	yes	3D	Amine oxidase [fl...	MAOA
BAP29_HUMAN	yes	3D	B-cell receptor-a...	BCAP29
BAP31_HUMAN	yes	3D	B-cell receptor-a...	BCAP31
C144C_HUMAN	yes	Prediction	Putative coiled-c...	CCDC144CP
CJ105_HUMAN	yes	Prediction	Uncharacterized p...	C10orf105
CJ111_HUMAN	yes	Prediction	Putative uncharac...	RPP38-DT
CLM2_HUMAN	yes	Exists	CMRF35-like molec...	CD300E
CK024_HUMAN	yes	Experiment	Uncharacterized p...	C11orf24
CK087_HUMAN	yes	Exists	Uncharacterized p...	C11orf87
...	...	...	...	...

### 6.2.2 与高表达差异蛋白 (DPs-Up) 交集

Figure 2 (下方图) 为图 PPS Intersection of DPs Up with TransMemPs 概览。

(对应文件为 [Figure+Table/PPS-Intersection-of-DPs-Up-with-TransMemPs.pdf](#))

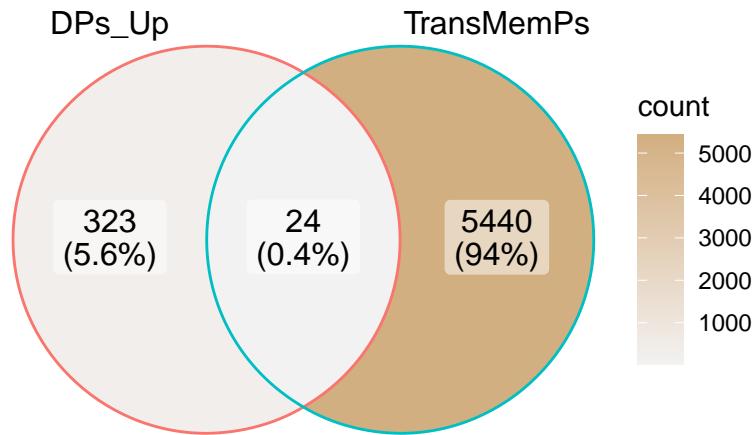


Figure 2: PPS Intersection of DPs Up with TransMemPs

### Intersection :

CEACAM5, APP, LAMP1, MUC1, SFXN3, THY1, SLC25A6, TACSTD2, MTX1, AIFM1, NSDHL, PECAM1, HSD17B12, MRC2, ASPH, LEMD2, SSR3, LMO7, ITGAM, TFRC, SPINT2, SORT1, ACSL3, SFXN1

(上述信息框内容已保存至 Figure+Table/PPS-Intersection-of-DPs-Up-with-TransMemPs-content)

## 6.3 以蛋白互作筛选配体蛋白

### 6.3.1 PPI

Figure 3 (下方图) 为图 PPS DPS filtered and formated PPI network 概览。

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

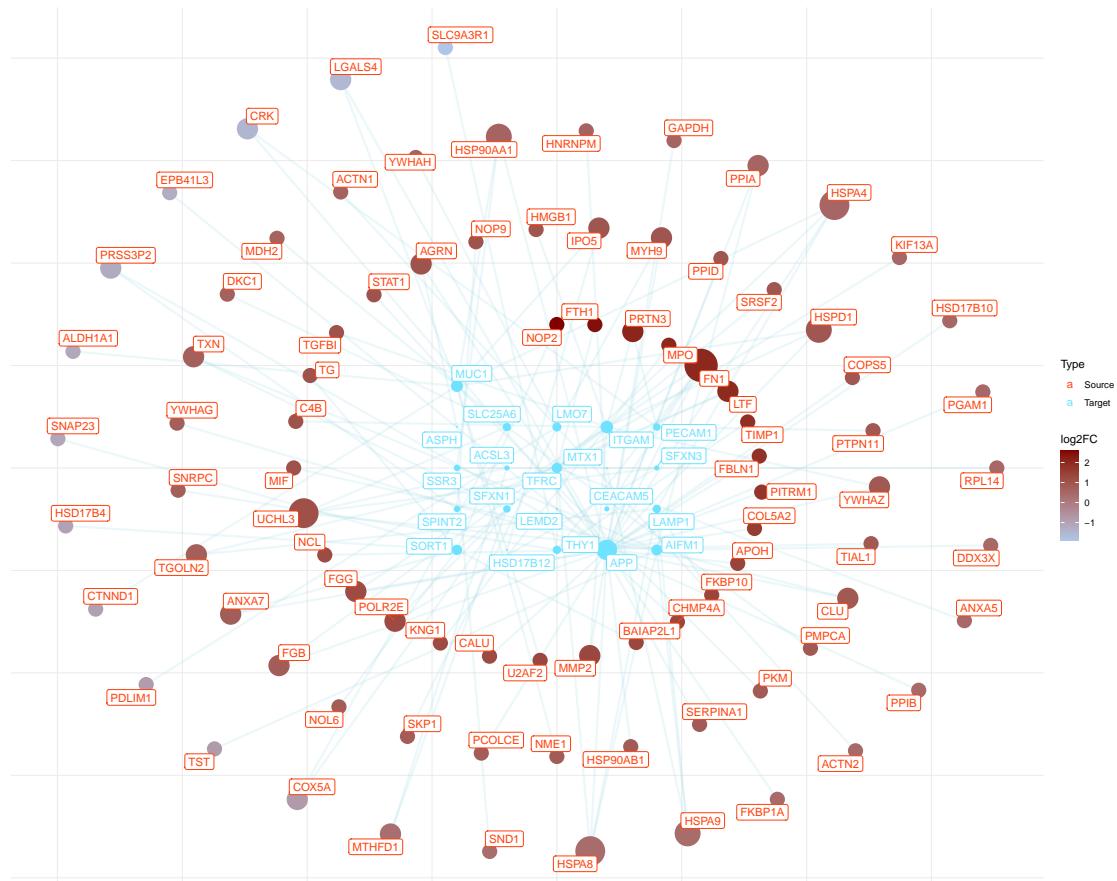


Figure 3: PPS DPS filtered and formated PPI network

### 6.3.2 富集分析

Figure 4 (下方图) 为图 PPS PPI KEGG enrichment 概览。

(对应文件为 Figure+Table/PPS-PPI-KEGG-enrichment.pdf)

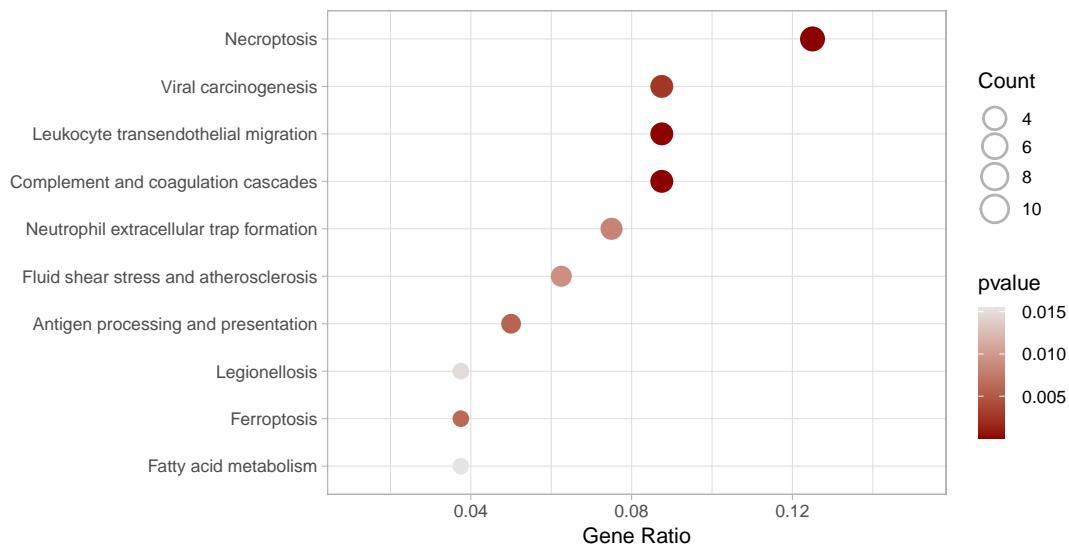


Figure 4: PPS PPI KEGG enrichment

Figure 5 (下方图) 为图 PPS PPI GO enrichment 概览。

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

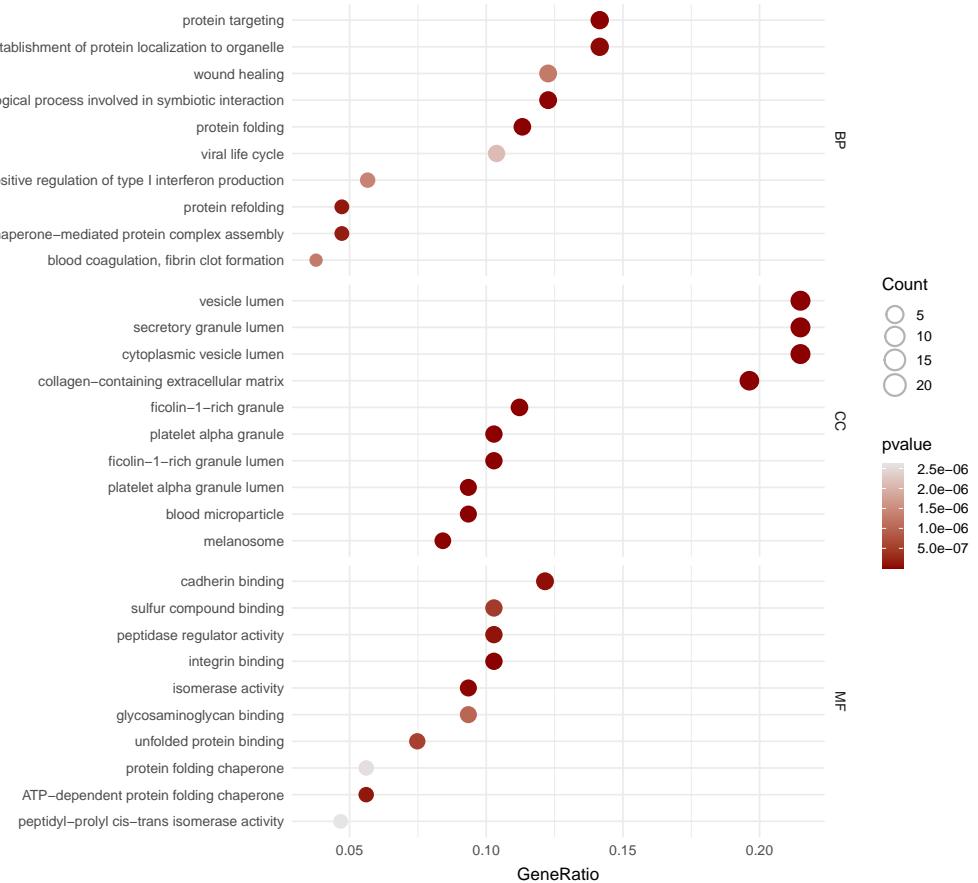


Figure 5: PPS PPI GO enrichment

坏死性凋亡信号通路在肿瘤发生发展、肿瘤坏死、肿瘤转移和肿瘤免疫反应中发挥作用；坏死性凋亡可能促进或抗肿瘤发生，具体取决于肿瘤的类型<sup>13</sup>。

Figure 6 (下方图) 为图 PPS PPI hsa04217 visualization 概览。

(对应文件为 Figure+Table/hsa04217.pathview.png)

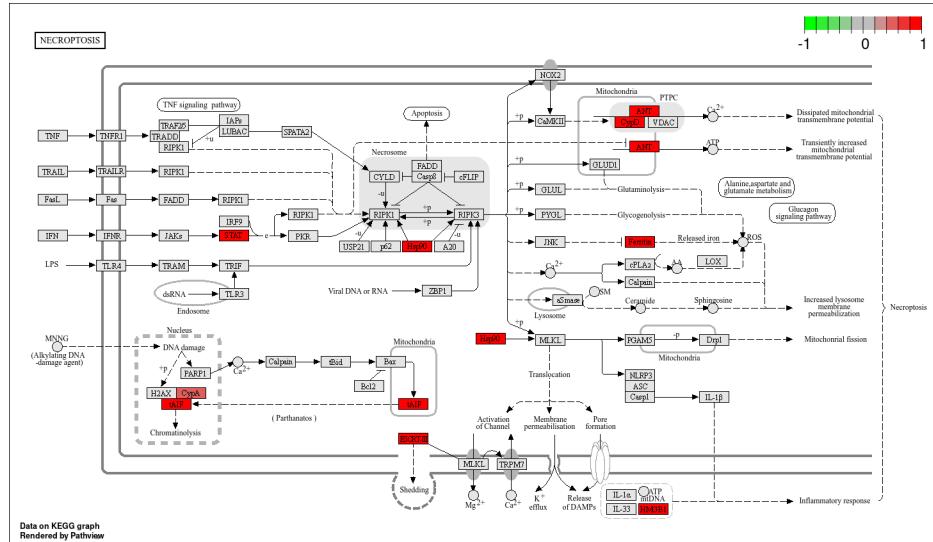


Figure 6: PPS PPI hsa04217 visualization

70-kDa 热休克蛋白 (HSP70) 在癌症中大量存在，通过抑制多种凋亡途径、调节坏死、绕过细胞衰老程序、干扰肿瘤免疫、促进血管生成和支持转移，为恶性细胞提供选择优势<sup>14</sup>

Figure 7 (下方图) 为图 PPS PPI hsa04612 visualization 概览。

(对应文件为 Figure+Table/hsa04612.pathview.png)

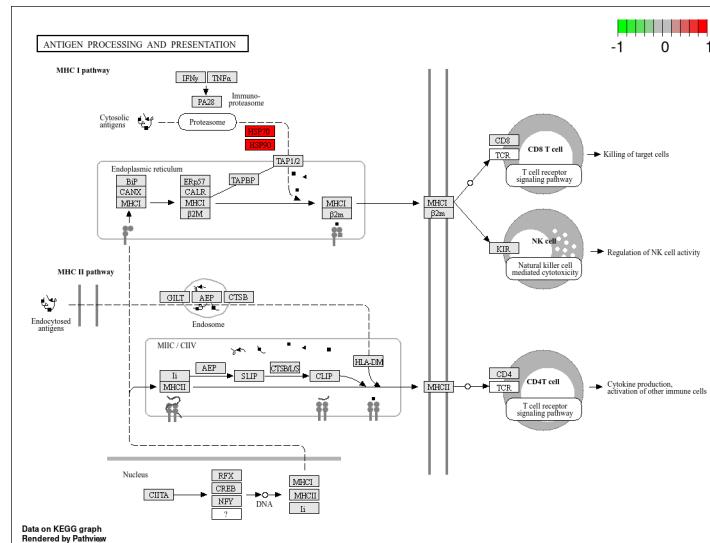


Figure 7: PPS PPI hsa04612 visualization

### 6.3.3 根据富集结果缩减 PPI

由于富集结果可以凸显肿瘤的性质，这里尝试根据 KEGG top 10 通路的富集基因缩减 PPI

Figure 8 (下方图) 为图 PPS DPS filtered by KEGG and formated PPI network 概览。

(对应文件为 Figure+Table/PPS-DPS-filtered-by-KEGG-and-formated-PPI-network.pdf)

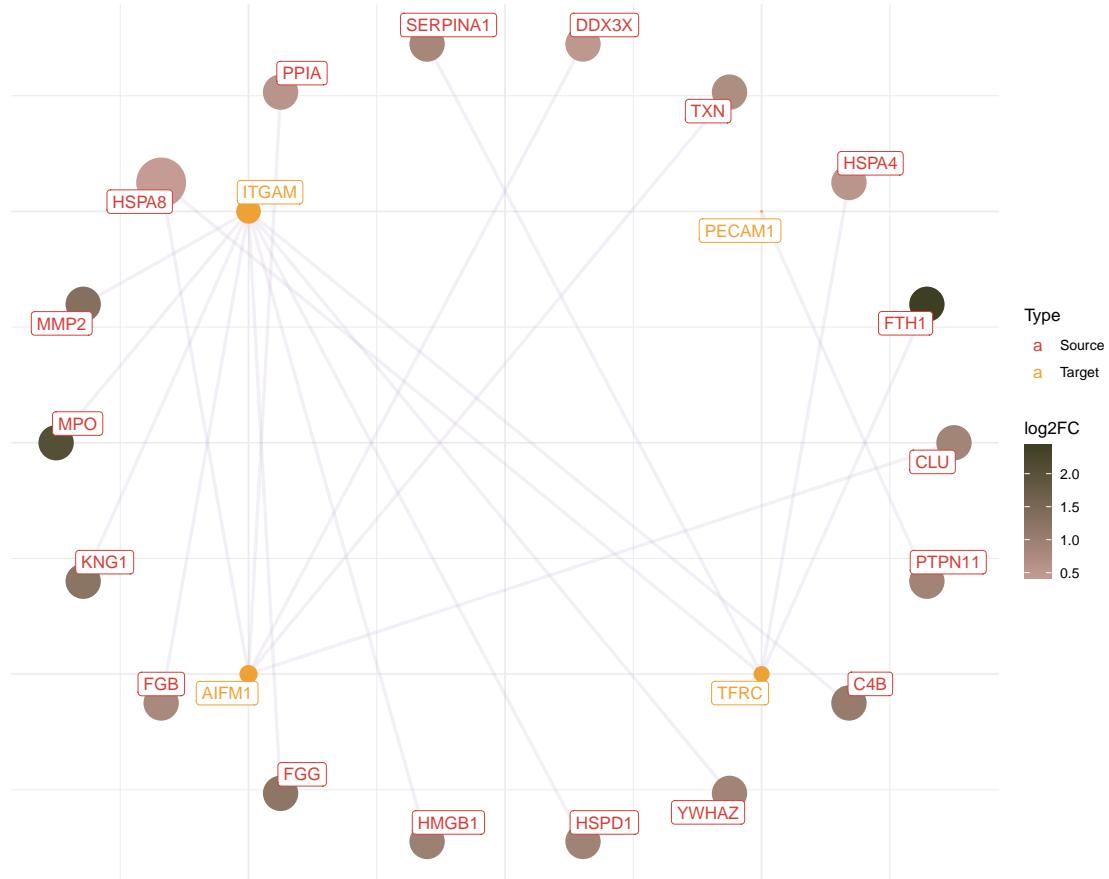


Figure 8: PPS DPS filtered by KEGG and formated PPI network

Figure 9 (下方图) 为图 PPS DPS filtered by KEGG Top MCC score 概览。

(对应文件为 Figure+Table/PPS-DPS-filtered-by-KEGG-Top-MCC-score.pdf)

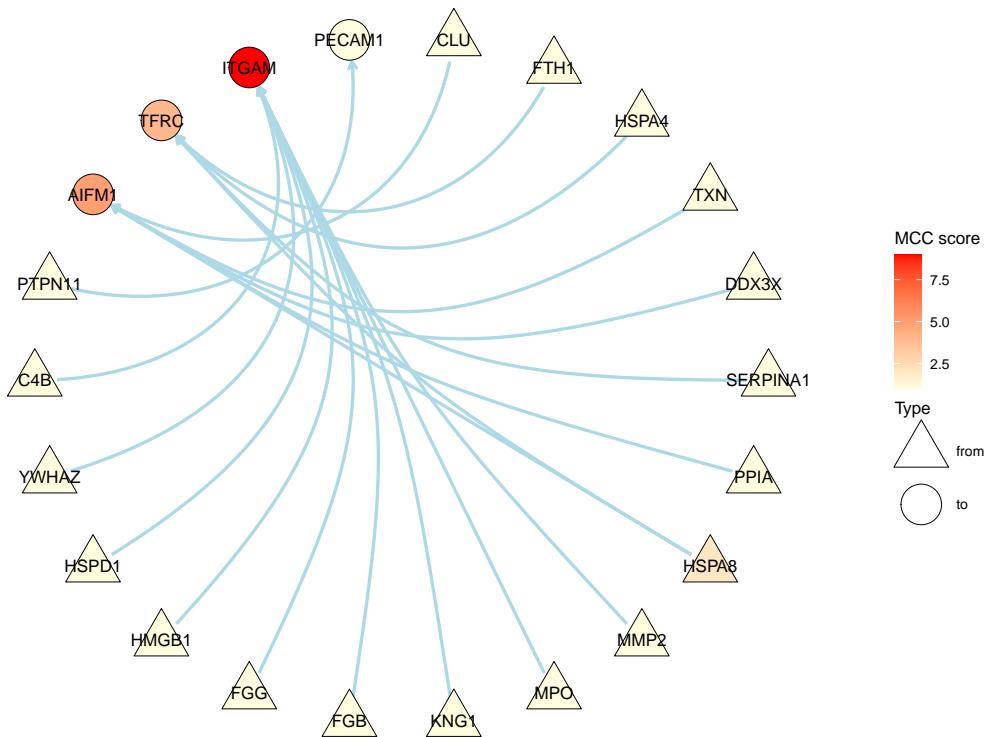


Figure 9: PPS DPS filtered by KEGG Top MCC score

## 7 附：分析流程——耐药差异膜蛋白及对应抗体蛋白或互作抑制其表达蛋白

### 7.1 结肠癌差异蛋白

注：由于无法直接获得包含耐药性分组的蛋白表达数据，因此这部分的内容另寻思路，即，获取 TCGA-COAD 的基因表达数据和蛋白定量数据，以 pRRophetic 根据基因表达数据分析耐药性，再对样本分组，随后分析蛋白定量数据。

#### 7.1.1 数据来源

共使用了 TCGA-COAD 的 RNA, protein, clinical 数据 (使用了三者都包含的病人的样本数据)。

Table 4 (下方表格) 为表格 TCGA COAD clinical metadata 概览。

(对应文件为 Figure+Table/TCGA-COAD-clinical-metadata.csv)

注：表格共有 459 行 19 列，以下预览的表格可能省略部分数据；含有 459 个唯一‘rownames’。

Table 4: TCGA COAD clinical metadata

rownames	id	data_f...	cases	access	file_name	submit...	data_c...	type	file_size
1	080f87...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	29118
2	77638e...	BCR XML	TCGA-C...	open	nation...	nation...	Clinical	clinic...	54636
3	c58a3b...	BCR XML	TCGA-D...	open	nation...	nation...	Clinical	clinic...	29261
4	e67964...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	28673
5	568223...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	31577
6	d77499...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	31559
7	0efd65...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	29185
8	7aaa95...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	52563
9	75bb5e...	BCR XML	TCGA-G...	open	nation...	nation...	Clinical	clinic...	54330
10	5d3d27...	BCR XML	TCGA-D...	open	nation...	nation...	Clinical	clinic...	29453
11	0f0694...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	24277
12	d05b7b...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	34479
13	ef4172...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	24264
14	f64700...	BCR XML	TCGA-G...	open	nation...	nation...	Clinical	clinic...	29321
15	849b28...	BCR XML	TCGA-A...	open	nation...	nation...	Clinical	clinic...	24215
...	...	...	...	...	...	...	...	...	...

Table 5 (下方表格) 为表格 TCGA COAD protein metadata 概览。

(对应文件为 Figure+Table/TCGA-COAD-protein-metadata.csv)

注：表格共有 363 行 24 列，以下预览的表格可能省略部分数据；含有 363 个唯一 ‘id’。

Table 5: TCGA COAD protein metadata

id	data_f...	cases	access	file_name	submit...	data_c...	type	platform	file_size
7b5dc5...	TSV	TCGA-C...	open	TCGA-C...	TCGA-C...	Proteo...	protei...	RPPA	22135
7d66e7...	TSV	TCGA-S...	open	TCGA-S...	TCGA-S...	Proteo...	protei...	RPPA	22022
8ecf75...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	24055
5e4ec1...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	23999
e45a96...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	24027
47c932...	TSV	TCGA-C...	open	TCGA-C...	TCGA-C...	Proteo...	protei...	RPPA	22100
44f0f7...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	24049
9fe863...	TSV	TCGA-C...	open	TCGA-C...	TCGA-C...	Proteo...	protei...	RPPA	22071
e06fe7...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	24065
cf9c71...	TSV	TCGA-Q...	open	TCGA-Q...	TCGA-Q...	Proteo...	protei...	RPPA	22099
335dae...	TSV	TCGA-G...	open	TCGA-G...	TCGA-G...	Proteo...	protei...	RPPA	22154
4f0d60...	TSV	TCGA-D...	open	TCGA-D...	TCGA-D...	Proteo...	protei...	RPPA	22155
f36bba...	TSV	TCGA-G...	open	TCGA-G...	TCGA-G...	Proteo...	protei...	RPPA	22109

id	data_f...	cases	access	file_name	submit...	data_c...	type	platform	file_size
f185df...	TSV	TCGA-A...	open	TCGA-A...	TCGA-A...	Proteo...	protei...	RPPA	24011
be6d80...	TSV	TCGA-F...	open	TCGA-F...	TCGA-F...	Proteo...	protei...	RPPA	22109
...	...	...	...	...	...	...	...	...	...

Table 6 (下方表格) 为表格 TCGA COAD RNA metadata 概览。

(对应文件为 `Figure+Table/TCGA-COAD-RNA-metadata.csv`)

注: 表格共有 524 行 29 列, 以下预览的表格可能省略部分数据; 含有 524 个唯一 ‘id’。

Table 6: TCGA COAD RNA metadata

id	data_f...	cases	access	file_name	submit...	data_c...	type	file_size	create...
efdcda...	TSV	TCGA-C...	open	a45a75...	9a7d8c...	Transc...	gene_e...	4240354	2022-0...
66905c...	TSV	TCGA-A...	open	40b98f...	7070f7...	Transc...	gene_e...	4233852	2022-0...
8820d9...	TSV	TCGA-A...	open	58369b...	a6da34...	Transc...	gene_e...	4210387	2022-0...
5302ca...	TSV	TCGA-C...	open	45a267...	c5db3d...	Transc...	gene_e...	4209007	2022-0...
a7affc...	TSV	TCGA-A...	open	3ef878...	97c2f0...	Transc...	gene_e...	4208716	2022-0...
3456d4...	TSV	TCGA-A...	open	524723...	4d8cb5...	Transc...	gene_e...	4216110	2022-0...
ab6d59...	TSV	TCGA-G...	open	085e42...	228266...	Transc...	gene_e...	4231843	2022-0...
3db2cc...	TSV	TCGA-A...	open	e1d0ac...	2b637e...	Transc...	gene_e...	4210406	2022-0...
a761bd...	TSV	TCGA-A...	open	d837c3...	738864...	Transc...	gene_e...	4201059	2022-0...
04981c...	TSV	TCGA-A...	open	4bafe8...	53e5cd...	Transc...	gene_e...	4214788	2022-0...
8ac00c...	TSV	TCGA-A...	open	0ae6d3...	0e343a...	Transc...	gene_e...	4219902	2022-0...
e929b2...	TSV	TCGA-C...	open	a82c20...	99e86d...	Transc...	gene_e...	4223537	2022-0...
c403bb...	TSV	TCGA-A...	open	e5ae4a...	8e4b41...	Transc...	gene_e...	4211960	2022-0...
756b10...	TSV	TCGA-A...	open	b3e428...	fe34e7...	Transc...	gene_e...	4229447	2022-0...
700b39...	TSV	TCGA-A...	open	fd618c...	afa933...	Transc...	gene_e...	4229363	2022-0...
...	...	...	...	...	...	...	...	...	...

## 7.2 预测耐药性

### 7.2.1 使用 RNA 数据集预测

以 pRRophetic 预测药物敏感性 (Cisplatin)。

Figure 10 (下方图) 为图 QQ plot for distribution of the transformed IC50 data 概览。

(对应文件为 `Figure+Table/QQ-plot-for-distribution-of-the-transformed-IC50-data.pdf`)

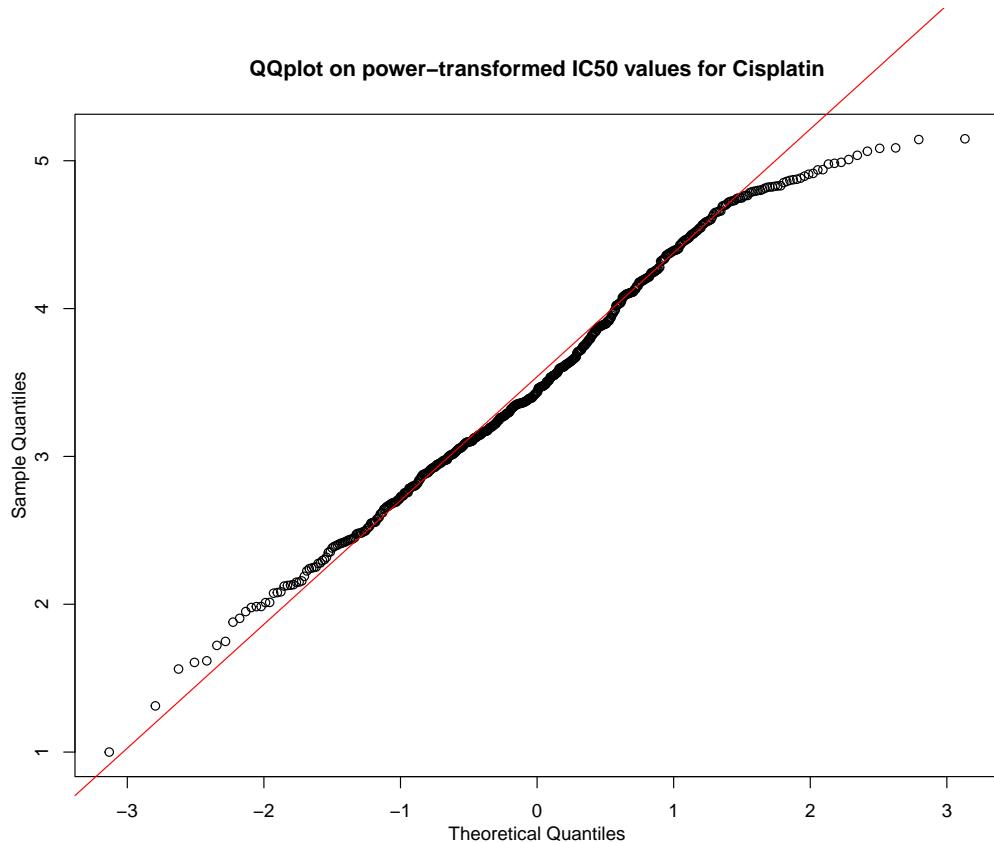


Figure 10: QQ plot for distribution of the transformed IC50 data

Fig. 10 表明, Cisplatin 的  $IC_{50}$  数据特征基本符合正太分布, 可以用于线形预测 Cisplatin 敏感性。

Figure 11 (下方图) 为图 Estimate prediction accuracy 概览。

(对应文件为 [Figure+Table/Estimate-prediction-accuracy.pdf](#))

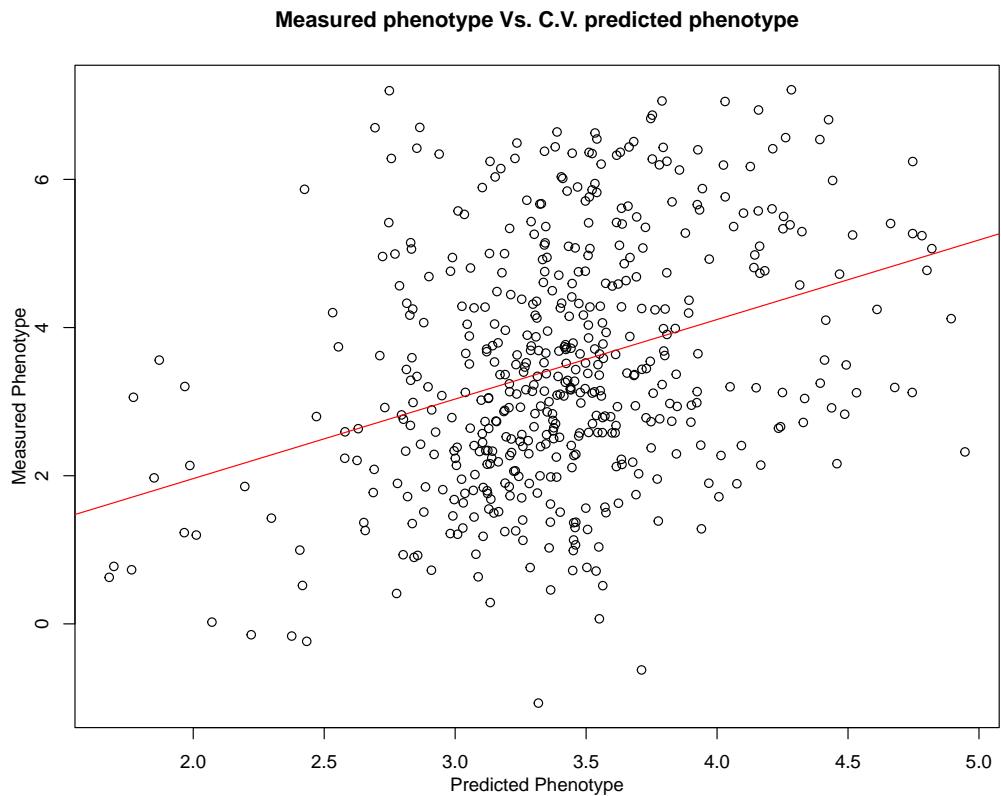


Figure 11: Estimate prediction accuracy

Table 7 (下方表格) 为表格 Predicted drug sensitivity 概览。

(对应文件为 [Figure+Table/Predicted-drug-sensitivity.csv](#))

注：表格共有 357 行 3 列，以下预览的表格可能省略部分数据；含有 357 个唯一 ‘sample’。

1. sample: 样品名称

**k-means clustering :**

Centers = 3

Table 7: Predicted drug sensitivity

sample	sensitivity	kmeans_group
TCGA-3L-AA1B-01A	4.14816093273104	2
TCGA-4N-A93T-01A	4.40190686256072	2
TCGA-4T-AA8H-01A	4.15648471482818	2

sample	sensitivity	kmeans_group
TCGA-5M-AAT6-01A	2.62116649131769	3
TCGA-A6-2671-11A	4.03864919730421	2
TCGA-A6-2672-01A	2.76158089020952	3
TCGA-A6-2676-01A	2.10216420226229	3
TCGA-A6-2677-01A	3.02480062454453	1
TCGA-A6-2678-11A	3.85525962252971	2
TCGA-A6-2680-01A	4.07942930425798	2
TCGA-A6-2681-01A	3.95239422637806	2
TCGA-A6-2683-11A	3.64057626378351	1
TCGA-A6-2684-01C	2.93670056076102	3
TCGA-A6-2685-01A	4.32047341962156	2
TCGA-A6-2686-11A	3.87165483393886	2
...	...	...

## 7.3 差异蛋白筛选

### 7.3.1 元数据

根据 Tab. 7 k-means 聚类结果，将样品分为三组：耐药组、中等组、低耐药性组（非耐药组）。

Table 8 (下方表格) 为表格 TCGA COAD proteome metadata 概览。

(对应文件为 [Figure+Table/TCGA-COAD-proteome-metadata.csv](#))

注：表格共有 178 行 4 列，以下预览的表格可能省略部分数据；含有 2 个唯一 ‘group’。

- 1. sample: 样品名称
- 2. group: 分组名称

**k-means clustering :**

Centers = 3

Table 8: TCGA COAD proteome metadata

sample	group	sensitivity	kmeans_group
TCGA-3L-AA1B	Resistance	4.14816093273104	2
TCGA-4N-A93T	Resistance	4.40190686256072	2
TCGA-4T-AA8H	Resistance	4.15648471482818	2
TCGA-5M-AAT6	Non_resistance	2.62116649131769	3
TCGA-A6-2671	Resistance	4.03864919730421	2

sample	group	sensitivity	kmeans_group
TCGA-A6-2672	Non_resistance	2.76158089020952	3
TCGA-A6-2676	Non_resistance	2.10216420226229	3
TCGA-A6-2678	Resistance	3.85525962252971	2
TCGA-A6-2680	Resistance	4.07942930425798	2
TCGA-A6-2681	Resistance	3.95239422637806	2
TCGA-A6-2684	Non_resistance	2.93670056076102	3
TCGA-A6-2685	Resistance	4.32047341962156	2
TCGA-A6-2686	Resistance	3.87165483393886	2
TCGA-A6-3808	Non_resistance	2.93134891159939	3
TCGA-A6-3809	Non_resistance	1.43580359549368	3
...	...	...	...

### 7.3.2 差异蛋白

Figure 12 (下方图) 为图 TCGA Resistance vs Non resistance DEPs 概览。

(对应文件为 Figure+Table/TCGA-Resistance-vs-Non-resistance-DEPs.pdf)

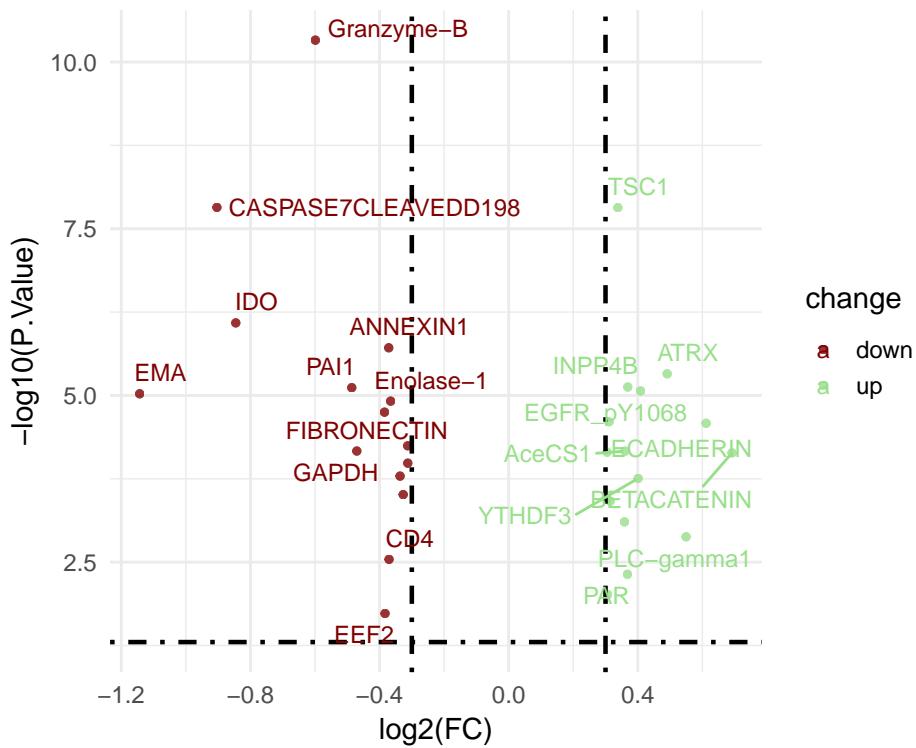


Figure 12: TCGA Resistance vs Non resistance DEPs

Table 9 (下方表格) 为表格 TCGA data Resistance vs Non resistance DEPs 概览。

(对应文件为 Figure+Table/TCGA-data-Resistance-vs-Non-resistance-DEPs.csv)

注：表格共有 30 行 9 列，以下预览的表格可能省略部分数据；含有 30 个唯一 ‘rownames’。

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. AveExpr: average log2-expression for the probe 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 9: TCGA data Resistance vs Non resistance DEPs

rownames	logFC	AveExpr	t	P.Value	adj.P.Val	B	peptid...	Gene_name
AGID00319	-0.598...	0.0565...	-7.018...	4.6950...	2.1691...	14.789...	Granz...	Granz...
AGID00015	-0.903...	0.7403...	-5.932...	1.5134...	2.3504...	9.2486...	CASPAS...	CASPAS...
AGID00155	0.3382...	0.2485...	5.9309...	1.5262...	2.3504...	9.2406...	TSC1	TSC1
AGID00366	-0.845...	1.0622...	-5.114...	8.1696...	5.3919...	5.4545...	IDO	IDO
AGID00193	-0.371...	-0.473...	-4.922...	1.9302...	0.0001...	4.6336...	ANNEXIN1	ANNEXIN1
AGID00268	0.4910...	-0.646...	4.7228...	4.7425...	0.0002...	3.7904...	ATRX	ATRX
AGID02153	0.3689...	0.4742...	4.6151...	7.4803...	0.0003...	3.3539...	INPP4B	INPP4B
AGID00053	-0.486...	0.1941...	-4.609...	7.6492...	0.0003...	3.3328...	PAI1	PAI1
AGID00450	0.4087...	0.5620...	4.5837...	8.5582...	0.0003...	3.2270...	EGFR_p...	EGFR_p...
AGID00235	-1.143...	-0.300...	-4.562...	9.4475...	0.0003...	3.1408...	EMA	EMA
AGID00394	-0.365...	0.1766...	-4.503...	1.2172...	0.0003...	2.9023...	Enolase-1	Enolase-1
AGID00031	-0.384...	-0.126...	-4.410...	1.7819...	0.0004...	2.5371...	FIBRON...	FIBRON...
AGID00290	0.3109...	-0.549...	4.3319...	2.4809...	0.0006...	2.2336...	Lasu1	Lasu1
AGID00148	0.6118...	0.3484...	4.3171...	2.6150...	0.0006...	2.1771...	ECADHERIN	ECADHERIN
AGID00301	-0.312...	-0.132...	-4.125...	5.6927...	0.0011...	1.4564...	B7-H3	B7-H3
...	...	...	...	...	...	...	...	...

## 7.4 膜蛋白筛选

### 7.4.1 Unitmp

UniTmp: unified resources for transmembrane proteins<sup>11</sup>

见 Tab. 3

### 7.4.2 与高表达差异蛋白 (TCGA-dps-Up) 交集

Figure 13 (下方图) 为图 TCGA Intersection of DPs Up with TransMemPs 概览。

(对应文件为 Figure+Table/TCGA-Intersection-of-DPs-Up-with-TransMemPs.pdf)

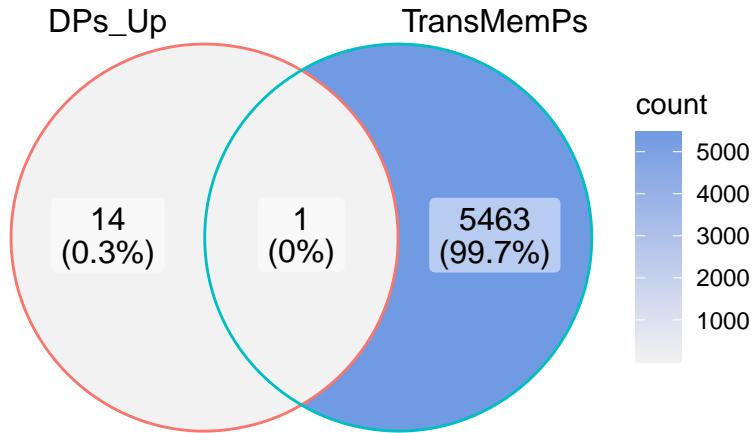


Figure 13: TCGA Intersection of DPs Up with TransMemPs

**Intersection :**

TSC1

(上述信息框内容已保存至 [Figure+Table/TCGA-Intersection-of-DPs-Up-with-TransMemPs-content](#))

## 7.5 以蛋白互作筛选配体蛋白

### 7.5.1 TCGA-COAD 的 RNA-seq 差异表达

为了筛选 Fig. 13 的配体，以 TCGA-COAD 的差异表达基因作为候选。

Figure 14 (下方图) 为图 TCGA RNA Resistance vs Non resistance DEGs 概览。

(对应文件为 [Figure+Table/TCGA-RNA-Resistance-vs-Non-resistance-DEGs.pdf](#))

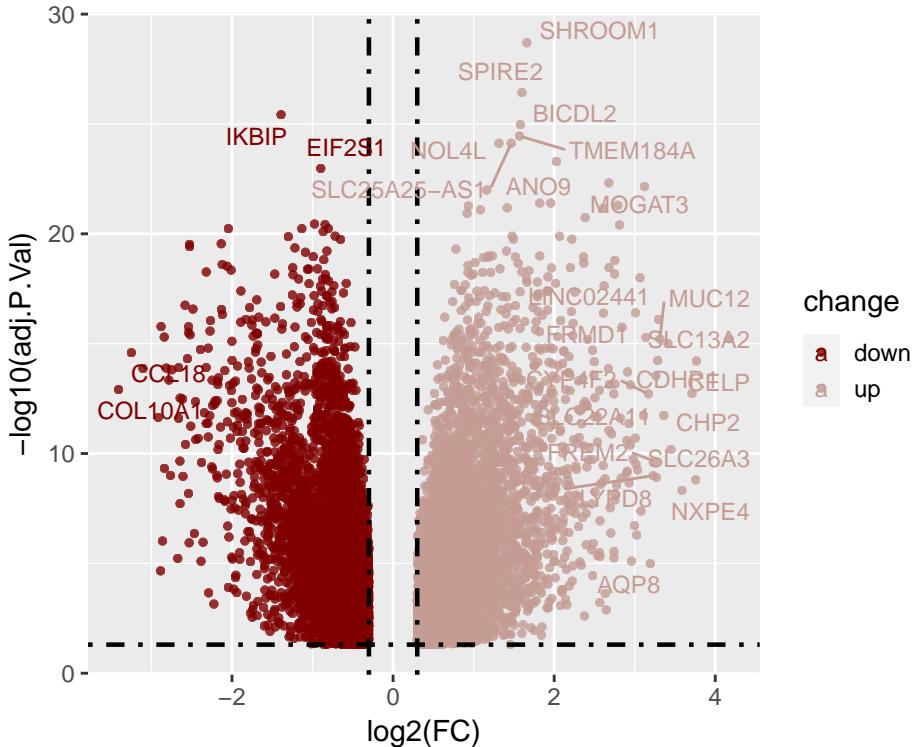


Figure 14: TCGA RNA Resistance vs Non resistance DEGs

Table 10 (下方表格) 为表格 TCGA RNA data Resistance vs Non resistance DEGs 概览。

(对应文件为 [Figure+Table/TCGA-RNA-data-Resistance-vs-Non-resistance-DEGs.csv](#))

注：表格共有 10108 行 22 列，以下预览的表格可能省略部分数据；含有 10108 个唯一‘rownames’。

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. AveExpr: average log2-expression for the probe 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’ )
6. gene\_id: GENCODE/Ensembl gene ID
7. gene\_name: GENCODE gene name
8. strand: genomic strand

Table 10: TCGA RNA data Resistance vs Non resistance DEGs

rownames	gene_id	seqnames	start	end	width	strand	source	type	score
ENSG00...	ENSG00...	chr5	132822141	132830659	8519	-	HAVANA	gene	NA

rownames	gene_id	seqnames	start	end	width	strand	source	type	score
ENSG00...	ENSG00...	chr16	89818179	89871319	53141	+	HAVANA	gene	NA
ENSG00...	ENSG00...	chr12	98613405	98645113	31709	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr16	3027682	3036944	9263	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr7	1542235	1560821	18587	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr9	128108581	128118693	10113	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr20	32443059	32585074	142016	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr11	417933	442011	24079	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr14	67360328	67386516	26189	+	HAVANA	gene	NA
ENSG00...	ENSG00...	chr7	101195007	101201038	6032	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr12	56230049	56237846	7798	+	HAVANA	gene	NA
ENSG00...	ENSG00...	chr3	48403854	48430086	26233	-	HAVANA	gene	NA
ENSG00...	ENSG00...	chr3	42489299	42537573	48275	+	HAVANA	gene	NA
ENSG00...	ENSG00...	chr17	79074824	79088599	13776	+	HAVANA	gene	NA
ENSG00...	ENSG00...	chr2	219054424	219060921	6498	-	HAVANA	gene	NA
...	...	...	...	...	...	...	...	...	...

Figure 15 (下方图) 为图 TCGA RNA DEGs type 概览。

(对应文件为 Figure+Table/TCGA-RNA-DEGs-type.pdf)

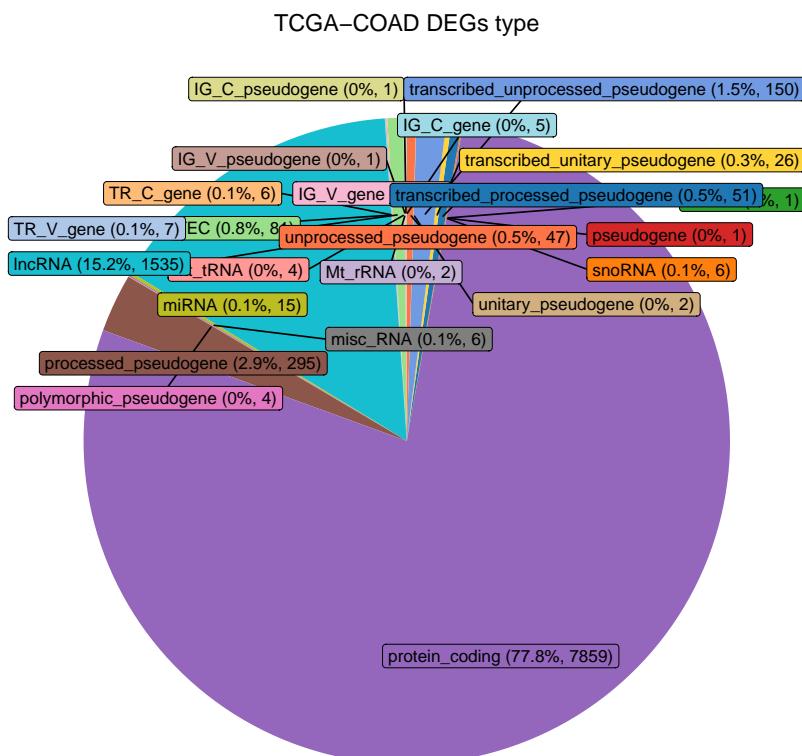


Figure 15: TCGA RNA DEGs type

### 7.5.2 PPI

以 Fig. 13 和 Tab. 10 top 2000 构建 PPI 网络。

Figure 16 (下方图) 为图 TCGA raw PPI network 概览。

(对应文件为 Figure+Table/TCGA-raw-PPI-network.pdf)

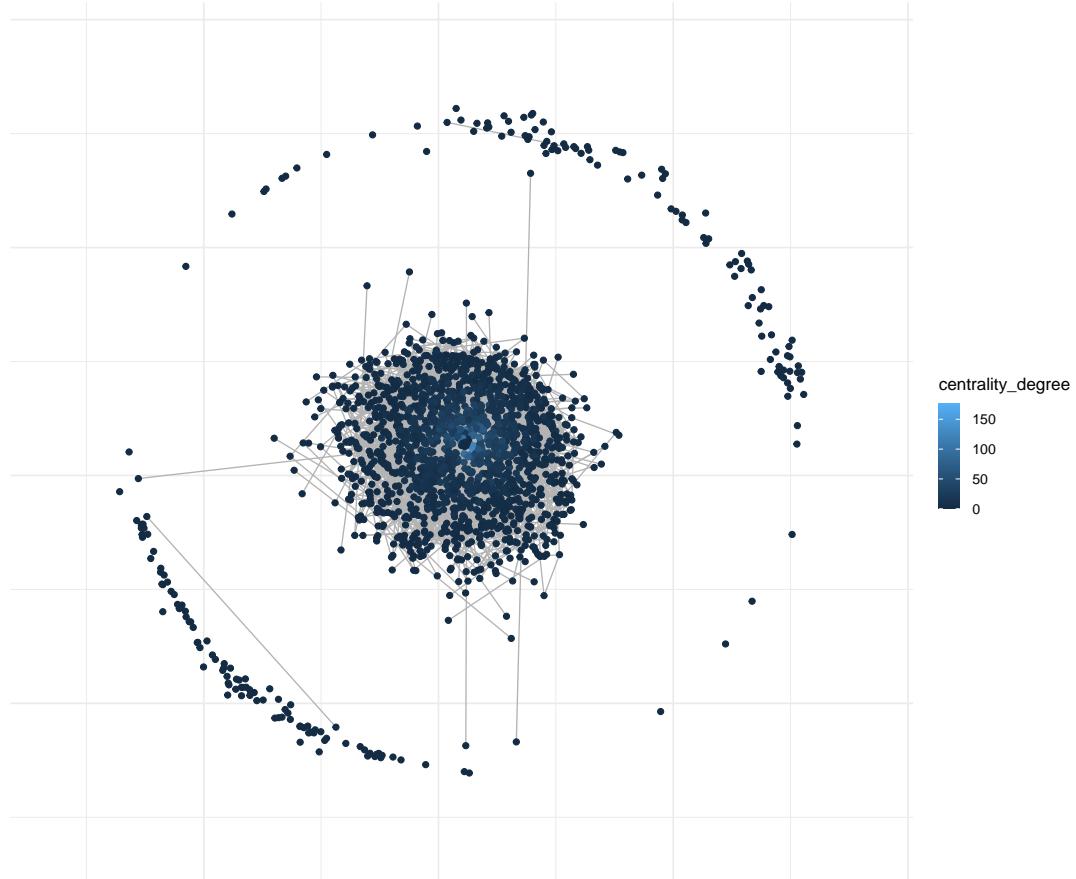


Figure 16: TCGA raw PPI network

将 PPI 网络过滤，凸显 Fig. 13 交集蛋白 (MCC 筛选高分相连的其他蛋白)

Figure 17 (下方图) 为图 TCGA DPS filtered and formated PPI network logFC 概览。

(对应文件为 Figure+Table/TCGA-DPS-filtered-and-formated-PPI-network-logFC.pdf)

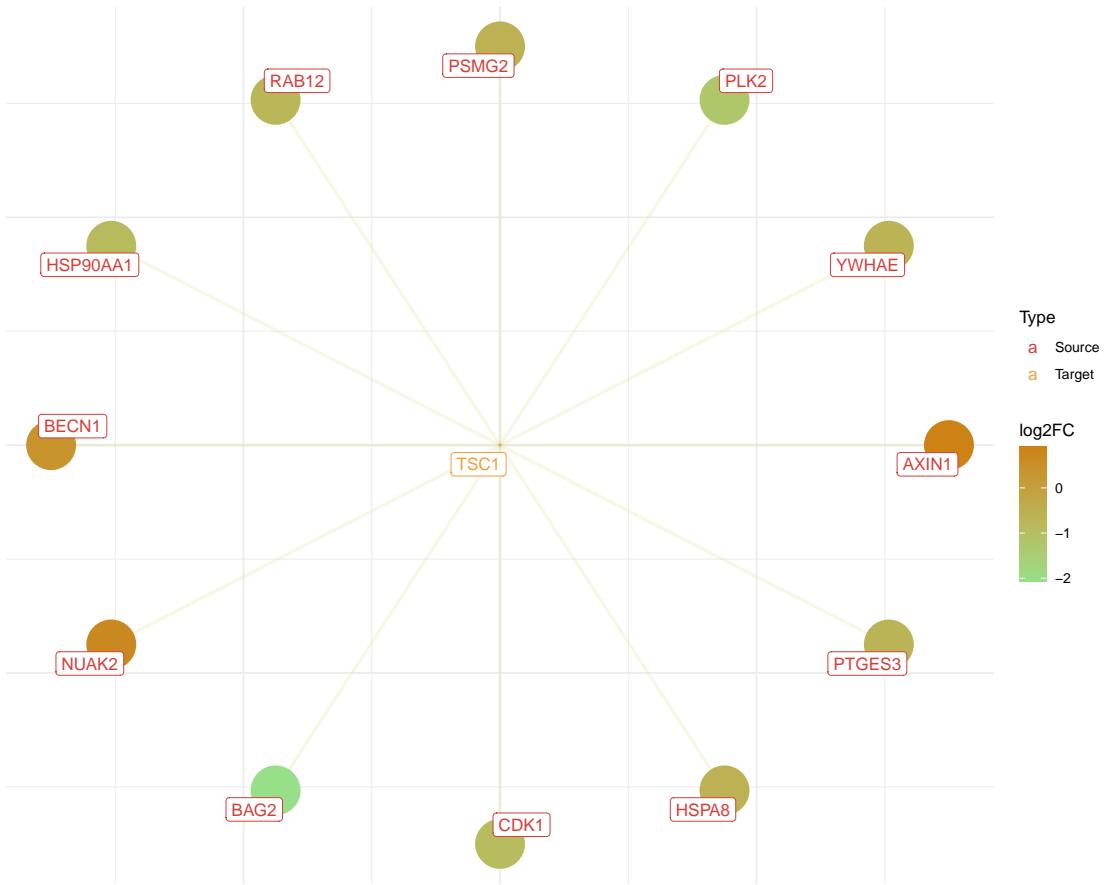


Figure 17: TCGA DPS filtered and formated PPI network logFC

Figure 18 (下方图) 为图 TCGA DPS filtered and formated PPI network MCC 概览。

(对应文件为 [Figure+Table/TCGA-DPS-filtered-and-formated-PPI-network-MCC.pdf](#))

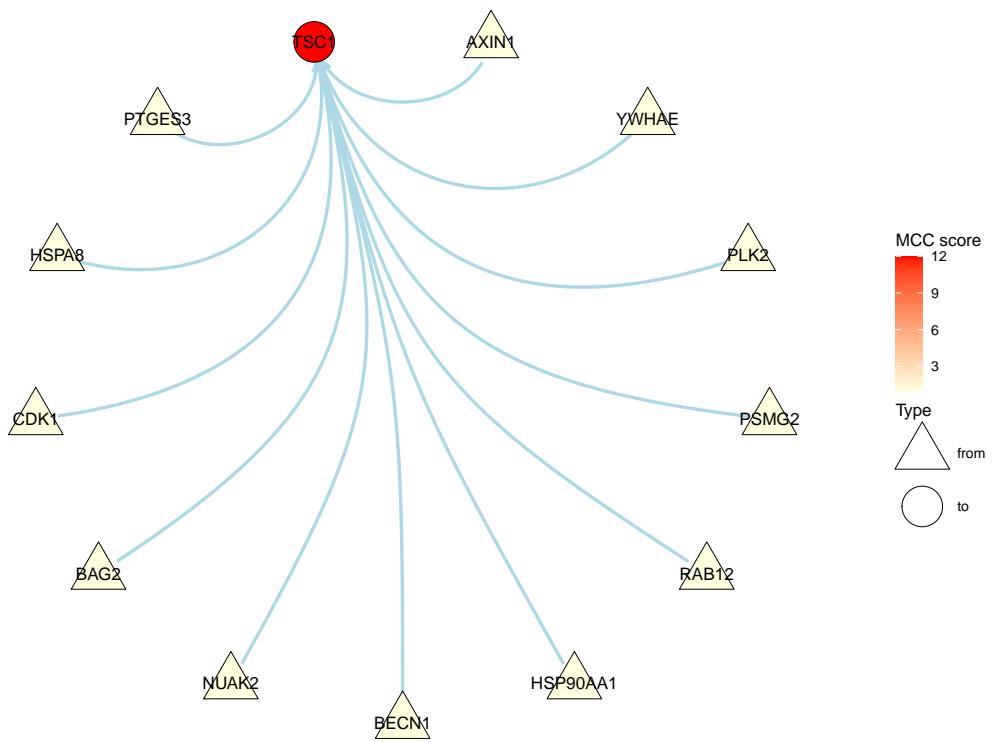


Figure 18: TCGA DPS filtered and formated PPI network MCC

### 7.5.3 富集分析

TSC1 在通路可见 Fig. 21

Figure 19 (下方图) 为图 TCGA KEGG enrichment 概览。

(对应文件为 Figure+Table/TCGA-KEGG-enrichment.pdf)

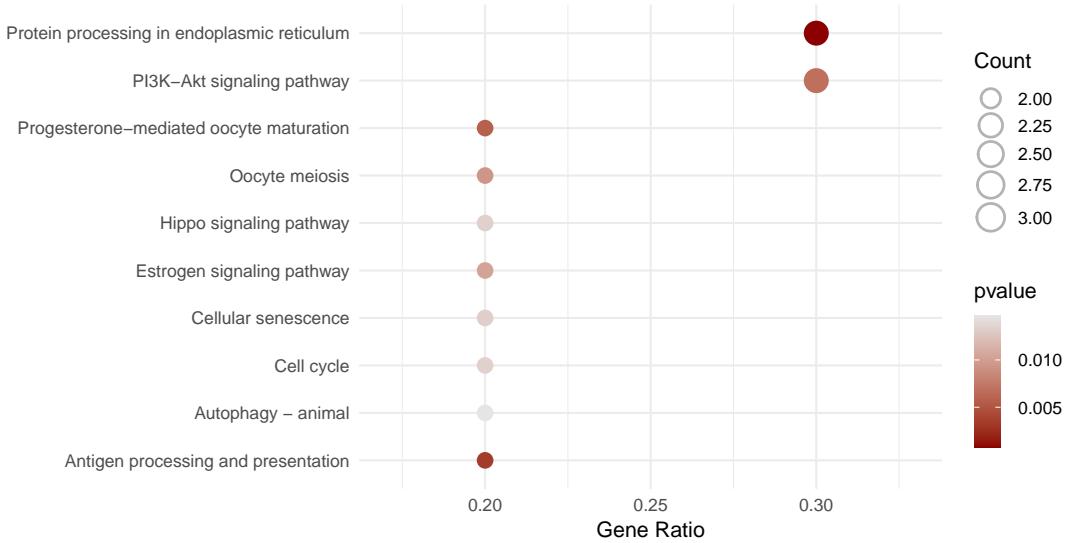


Figure 19: TCGA KEGG enrichment

Figure 20 (下方图) 为图 TCGA GO enrichment 概览。

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

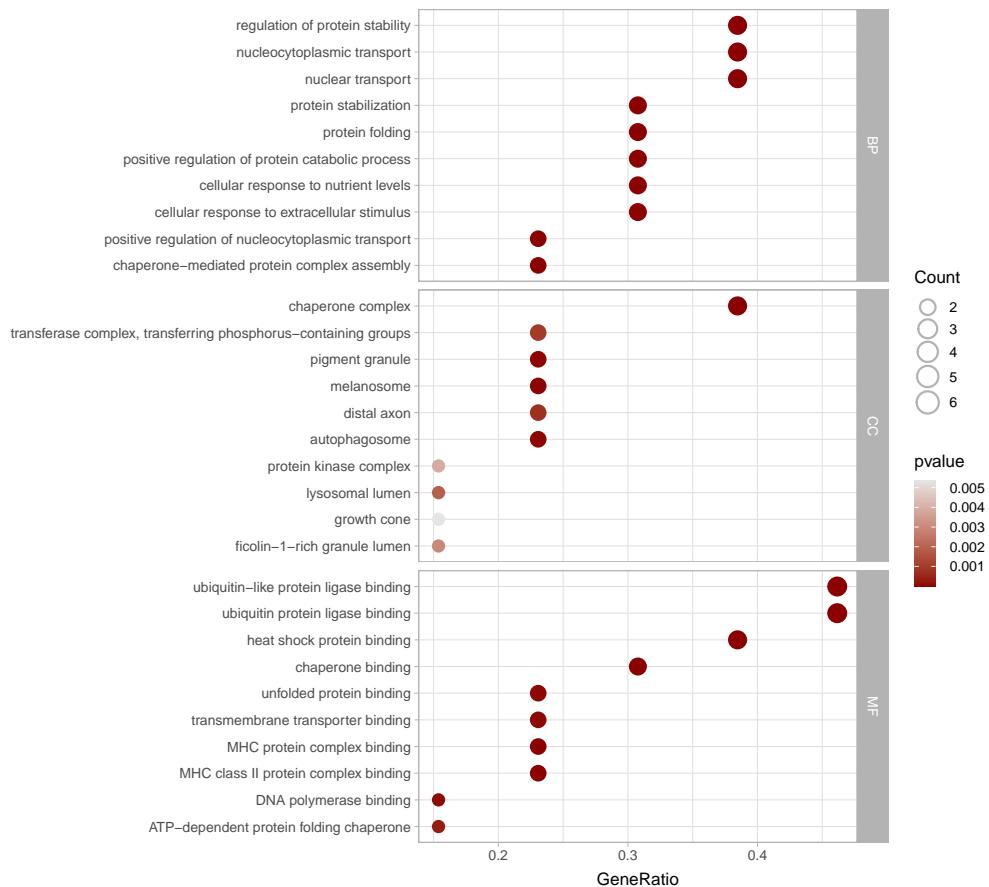


Figure 21 (下方图) 为图 TCGA TSC1 in hsa04151 visualization 概览。

(对应文件为 Figure+Table/hsa04151.pathview.png)

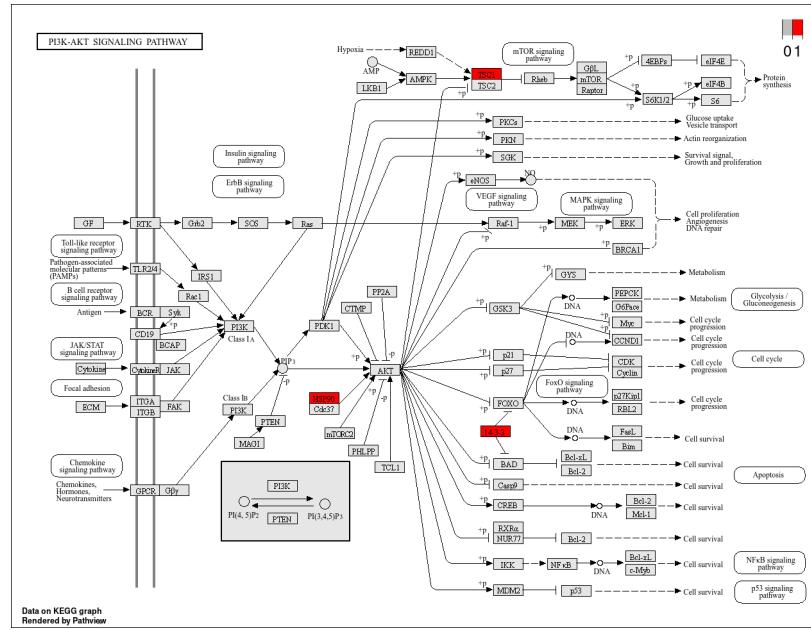


Figure 21: TCGA TSC1 in hsa04151 visualization

#### 7.5.4 通过关联分析筛选负相关性互作蛋白

Figure 22 (下方图) 为图 TCGA RNA correlation heatmap 概览。

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

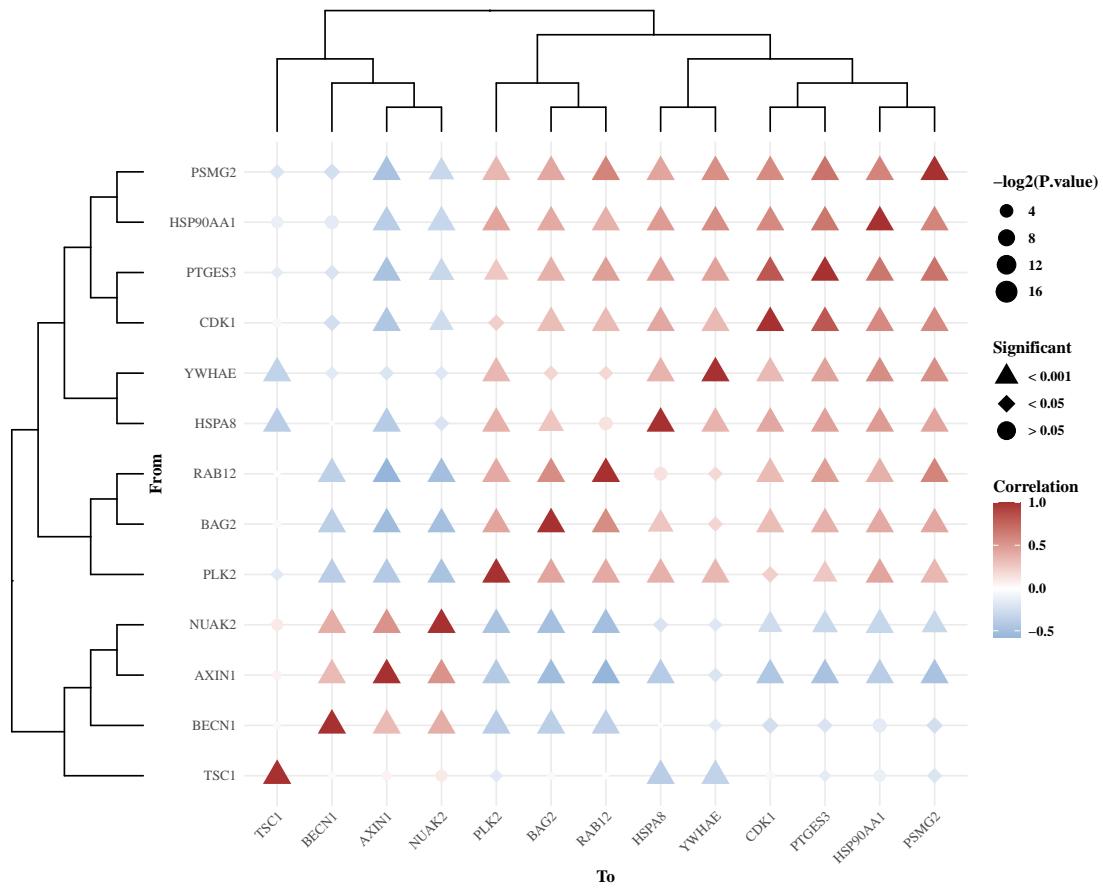


Figure 22: TCGA RNA correlation heatmap

Table 11 (下方表格) 为表格 TCGA RNA TSC1 negative correlated 概览。

(对应文件为 [Figure+Table/TCGA-RNA-TSC1-negative-correlated.csv](#))

注：表格共有 5 行 7 列，以下预览的表格可能省略部分数据；含有 5 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 11: TCGA RNA TSC1 negative correlated

From	To	cor	pvalue	-log2(P.va...)	significant	sign
YWHAE	TSC1	-0.34	0	16.6096404...	< 0.001	**
HSPA8	TSC1	-0.38	0	16.6096404...	< 0.001	**
PTGES3	TSC1	-0.15	0.0497	4.33061033...	< 0.05	*
PSMG2	TSC1	-0.2	0.0061	7.35697504...	< 0.05	*

From	To	cor	pvalue	-log2(P.va...)	significant	sign
PLK2	TSC1	-0.17	0.0265	5.23786383...	< 0.05	*

## 8 附：进一步分析蛋白结合

### 8.1 TSC1 在正常组与结直肠癌组的表达

TSC1 在正常组与癌症中无显著差异。因此，后续分析将依据 1.1.2 中的“3”组织。

Figure 23 (下方图) 为图 compare tsc1 in cancer and control 概览。

(对应文件为 Figure+Table/compare-tsc1-in-cancer-and-control.pdf)

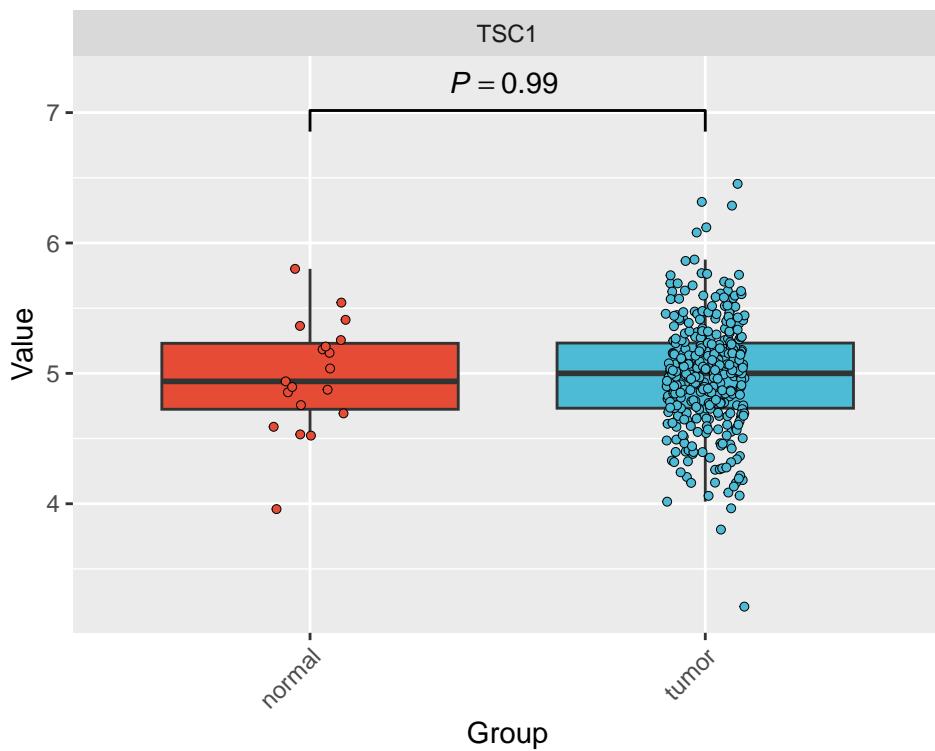


Figure 23: Compare tsc1 in cancer and control

### 8.2 差异癌膜蛋白 AA 与候选结合蛋白的相关性

#### 8.2.1 相关性

筛选非负相关的蛋白对

Figure 24 (下方图) 为图 PPS correlation heatmap 概览。

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

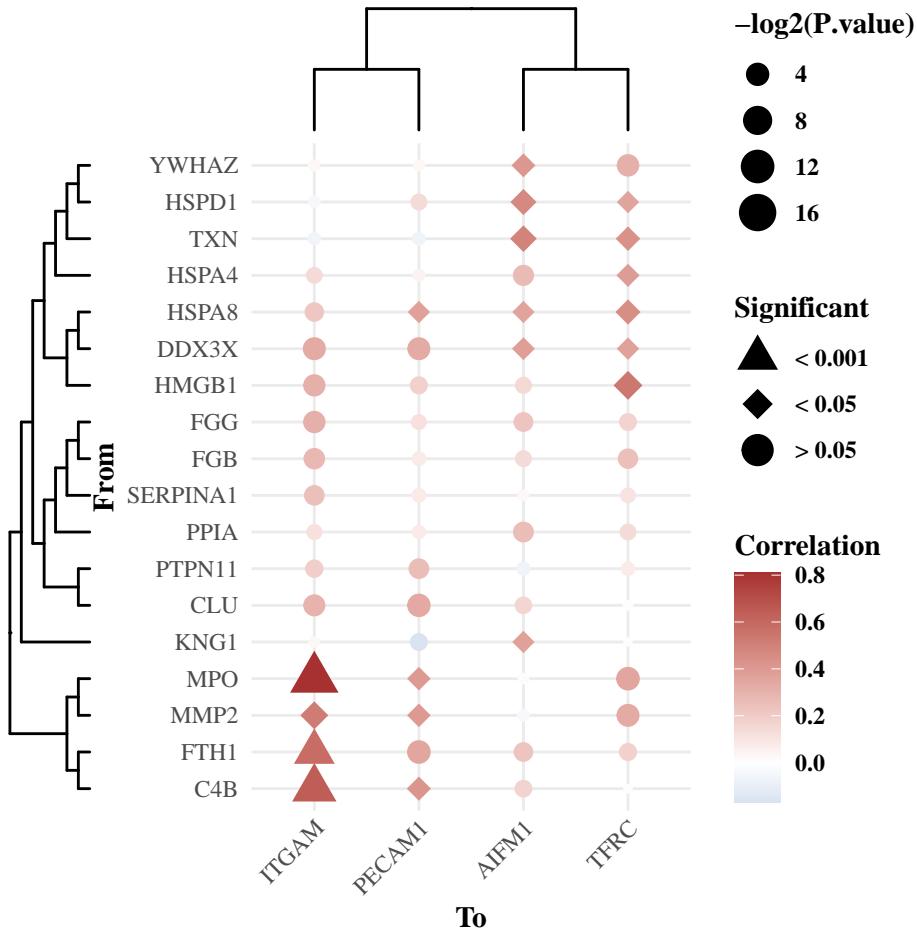


Figure 24: PPS correlation heatmap

具体如下：

Table 12 (下方表格) 为表格 PPS correlation details 概览。

(对应文件为 Figure+Table/PPS-correlation-details.csv)

注：表格共有 19 行 7 列，以下预览的表格可能省略部分数据；含有 18 个唯一 ‘from’。

1. cor: 皮尔逊相关系数，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 12: PPS correlation details

from	to	cor	pvalue	-log2(P.va...)	significant	sign
C4B	ITGAM	0.64	1e-04	13.2877123...	< 0.001	**
CLU	AIFM1	0.16	0.3759	1.41157917...	> 0.05	-
DDX3X	AIFM1	0.38	0.0348	4.84476888...	< 0.05	*
FGB	ITGAM	0.28	0.1235	3.01741705...	> 0.05	-
FGG	ITGAM	0.31	0.0915	3.45008444...	> 0.05	-
FTH1	TFRC	0.18	0.3414	1.55046503...	> 0.05	-
HMGB1	ITGAM	0.31	0.0952	3.39289461...	> 0.05	-
HSPA4	TFRC	0.39	0.0311	5.00694160...	< 0.05	*
HSPA8	AIFM1	0.36	0.0439	4.50963525...	< 0.05	*
HSPA8	TFRC	0.45	0.0117	6.41734765...	< 0.05	*
HSPD1	ITGAM	-0.04	0.8262	0.27543703...	> 0.05	-
KNG1	ITGAM	0.03	0.8907	0.16698850...	> 0.05	-
MMP2	ITGAM	0.52	0.0027	8.53282487...	< 0.05	*
MPO	ITGAM	0.81	0	16.6096404...	< 0.001	**
PPIA	AIFM1	0.26	0.154	2.69899774...	> 0.05	-
...	...	...	...	...	...	...

### 8.2.2 stringDB 数据库中有实验基础的

依据 Tab. 12

获取 stringDB 有直接物理作用的蛋白数据，并且取得有实验基础的蛋白对 (experiments score > 100)

Table 13 (下方表格) 为表格 EXP scores 概览。

(对应文件为 **Figure+Table/EXP-scores.csv**)

注：表格共有 17 行 10 列，以下预览的表格可能省略部分数据；含有 9 个唯一 ‘from’。

1. experiments: 相关实验。

**STRINGdb network type:** :

physical

**Filter experiments score:** :

At least score 100

**Filter textmining score:** :

At least score 0

Table 13: EXP scores

from	to	homology	experi.....4	experi.....5	database	databa...	textmi.....8	textmi.....9	...
FGB	CLU	0	224	0	0	0	275	0	...
FGB	FGG	0	946	582	900	0	920	0	...
HSPA4	HSPD1	0	225	0	0	0	0	287	...
CLU	HSPD1	0	292	0	0	0	0	0	...
AIFM1	TXN	0	593	0	0	0	0	132	...
HMGB1	TXN	0	362	0	0	0	0	0	...
FTH1	TFRC	0	852	0	0	0	779	49	...
FGB	SERPINA1	0	235	0	0	0	167	0	...
CLU	SERPINA1	0	235	0	0	0	688	0	...
AIFM1	PPIA	0	292	0	800	0	186	133	...
HSPA4	HSPA8	0	642	83	500	0	978	91	...
HSPD1	HSPA8	0	628	0	0	0	0	206	...
HMGB1	HSPA8	0	292	0	0	0	414	0	...
PECAM1	PTPN11	0	549	0	900	0	959	0	...
AIFM1	DDX3X	0	329	0	0	0	0	0	...
...	...	...	...	...	...	...	...	...	...

Figure 25 (下方图) 为图 EXP with experiments score 概览。

(对应文件为 [Figure+Table/EXP-with-experiments-score.pdf](#))

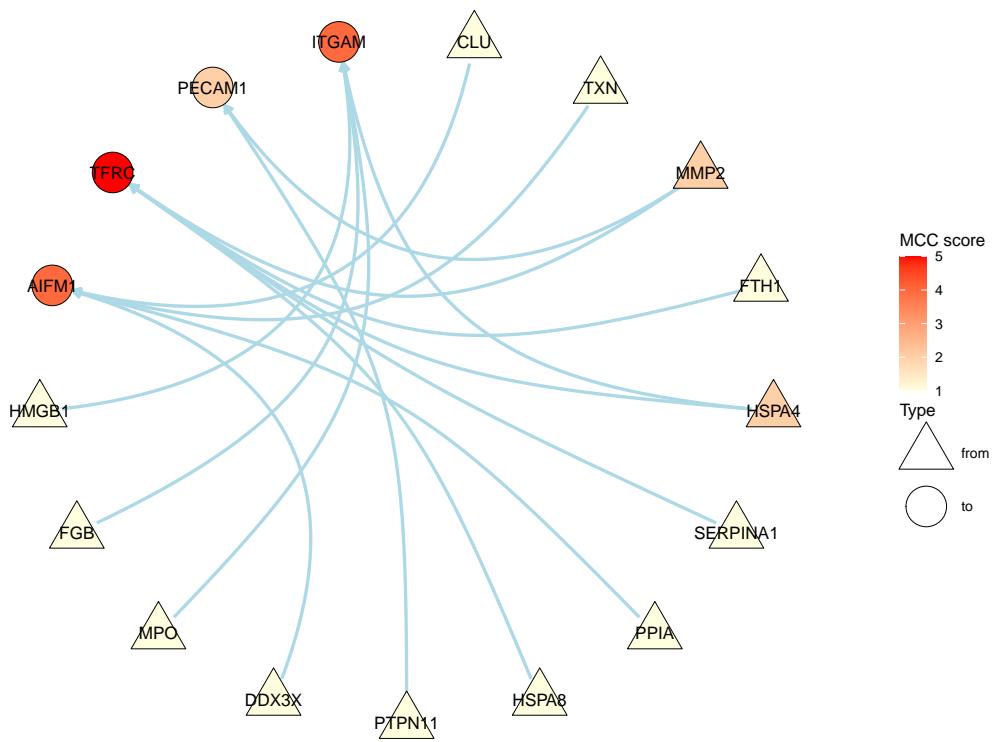


Figure 25: EXP with experiments score

Table 14 (下方表格) 为表格 EXP pair 概览。

(对应文件为 Figure+Table/EXP-pair.csv)

注：表格共有 15 行 2 列，以下预览的表格可能省略部分数据；含有 13 个唯一 ‘from’。

Table 14: EXP pair

from	to
CLU	AIFM1
TXN	AIFM1
MMP2	TFRC
FTH1	TFRC
HSPA4	TFRC
SERPINA1	TFRC
PPIA	AIFM1
HSPA8	TFRC
MMP2	PECAM1
PTPN11	PECAM1

from	to
DDX3X	AIFM1
MPO	ITGAM
HSPA4	ITGAM
FGB	ITGAM
HMGB1	ITGAM

### 8.2.3 蛋白对接

依据 Tab. 12, 在 cluspro 服务器进行蛋白对接。

注：总共有 19 对蛋白，由于 HSPA4 未找到 PDB (蛋白结构文件)，因此实际对接的为 18 对。

Figure 26 (下方图) 为图 Overview of protein docking results 概览。

(对应文件为 Figure+Table/Overview-of-protein-docking-results.pdf)

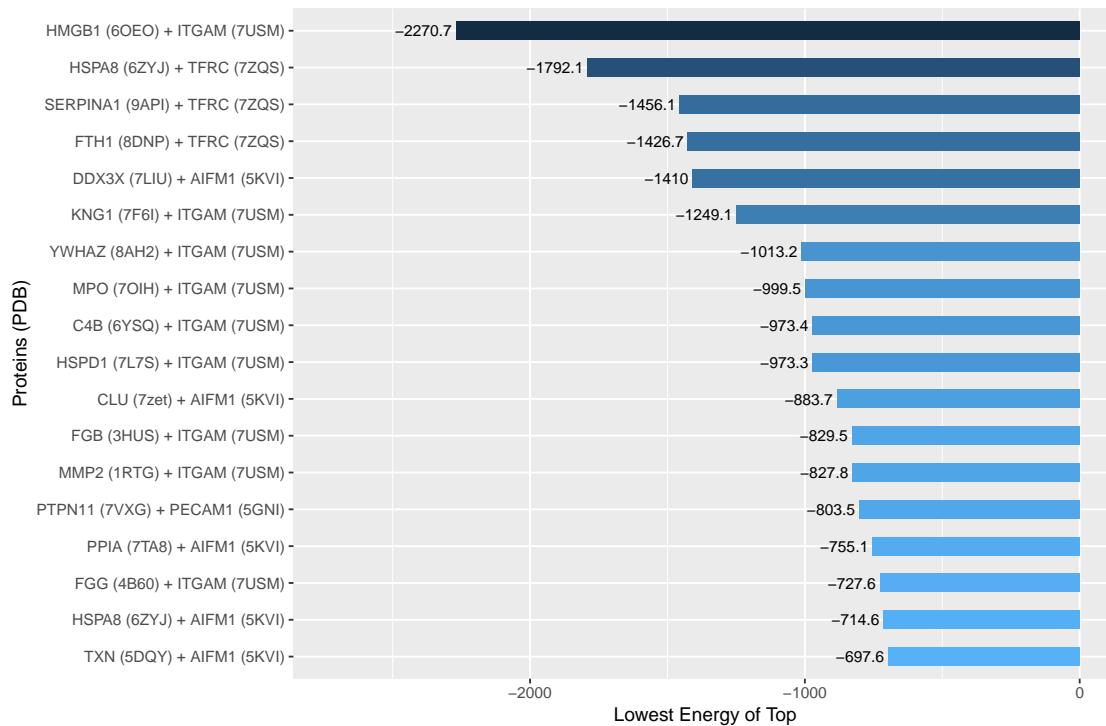


Figure 26: Overview of protein docking results

Table 15 (下方表格) 为表格 Overview of protein docking results data 概览。

(对应文件为 Figure+Table/Overview-of-protein-docking-results-data.csv)

注：表格共有 18 行 11 列，以下预览的表格可能省略部分数据；含有 18 个唯一 ‘Name’。

Table 15: Overview of protein docking results data

Name	pro1	pro2	Cluster	Members	Center	Lowest...	value	pdb1	pdb2
HMGB1_...	HMGB1	ITGAM	0	45	-2270.7	-2270.7	-2270.7	6OE0	7USM
HSPA8_...	HSPA8	TFRC	0	67	-1792.1	-1792.1	-1792.1	6ZYJ	7ZQS
SERPIN...	SERPINA1	TFRC	0	84	-1336.4	-1456.1	-1456.1	9API	7ZQS
FTH1_TFRC	FTH1	TFRC	0	21	-1335.4	-1426.7	-1426.7	8DNP	7ZQS
DDX3X_...	DDX3X	AIFM1	0	61	-1229.3	-1410	-1410	7LIU	5KVI
KNG1_I...	KNG1	ITGAM	0	27	-1139	-1249.1	-1249.1	7F6I	7USM
YWHAZ_...	YWHAZ	ITGAM	0	96	-805.3	-1013.2	-1013.2	8AH2	7USM
MPO_ITGAM	MPO	ITGAM	0	15	-999.5	-999.5	-999.5	7OIH	7USM
C4B_ITGAM	C4B	ITGAM	0	24	-883.5	-973.4	-973.4	6YSQ	7USM
HSPD1_...	HSPD1	ITGAM	0	22	-730.8	-973.3	-973.3	7L7S	7USM
CLU_AIFM1	CLU	AIFM1	0	96	-707.3	-883.7	-883.7	7zet	5KVI
FGB_ITGAM	FGB	ITGAM	0	37	-800.3	-829.5	-829.5	3HUS	7USM
MMP2_I...	MMP2	ITGAM	0	32	-629	-827.8	-827.8	1RTG	7USM
PTPN11...	PTPN11	PECAM1	0	33	-759.2	-803.5	-803.5	7VXG	5GNI
PPIA_A...	PPIA	AIFM1	0	152	-550.8	-755.1	-755.1	7TA8	5KVI
...	...	...	...	...	...	...	...	...	...

Figure 27 (下方图) 为图 Top1 Protein docking of HMGB1 ITGAM 概览。

(对应文件为 Figure+Table/ITGAM..7USM.\_with\_HMGB1..6OE0..png)

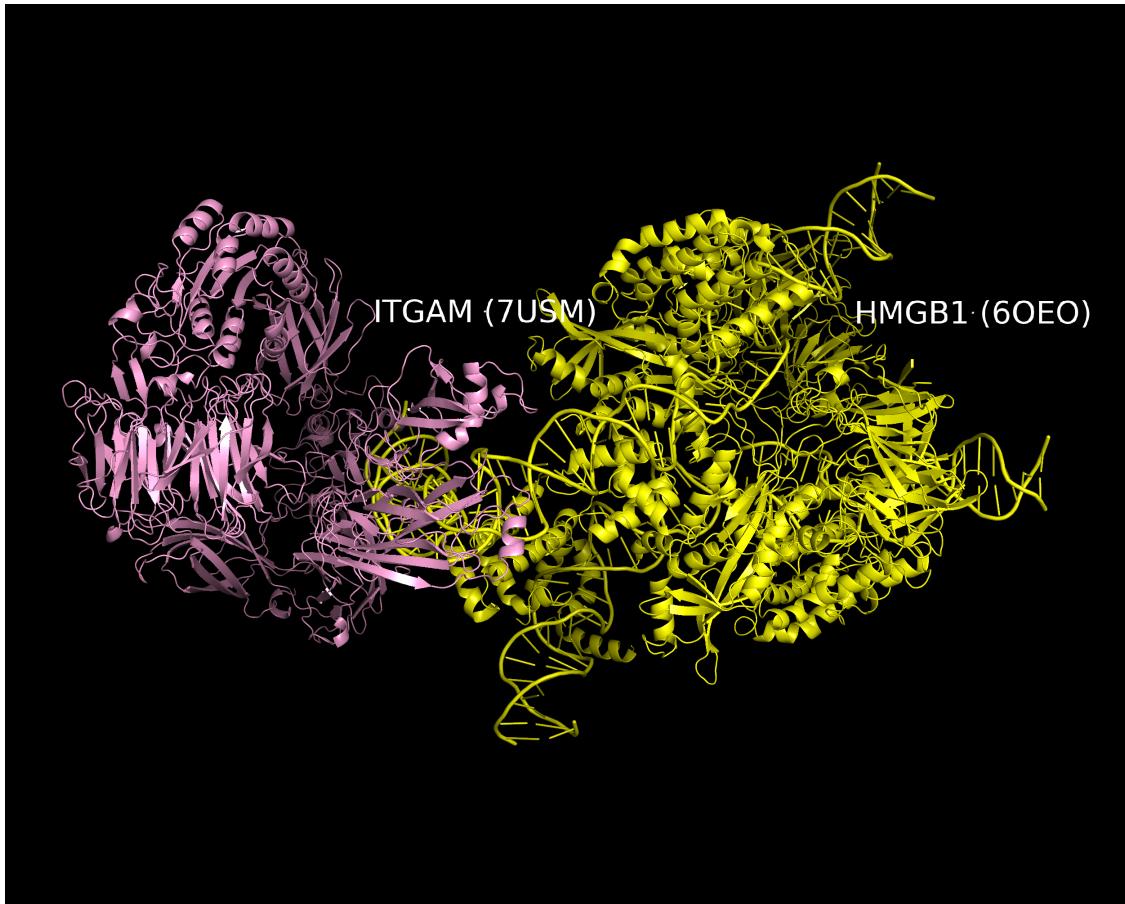


Figure 27: Top1 Protein docking of HMGB1 ITGAM

‘Top 5 visualization’ 数据已全部提供。

(对应文件为 Figure+Table/Top-5-visualization)

注：文件夹 Figure+Table/Top-5-visualization 共包含 5 个文件。

1. 1\_Top\_1\_HMGB1\_ITGAM.txt
2. 2\_Top\_2\_HSPA8\_TFRC.txt
3. 3\_Top\_3\_SERPINA1\_TFRC.txt
4. 4\_Top\_4\_FTH1\_TFRC.txt
5. 5\_Top\_5\_DDX3X\_AIFM1.txt

#### 8.2.4 同时满足 stringdb 实验得分和蛋白对接的

若设置对接阈值 (Lowest.Energy) 为 -1000，则

Figure 28 (下方图) 为图 Intersection of StringDB exp with Protein docking 概览。

(对应文件为 Figure+Table/Intersection-of-StringDB-exp---with-Protein-docking.pdf)

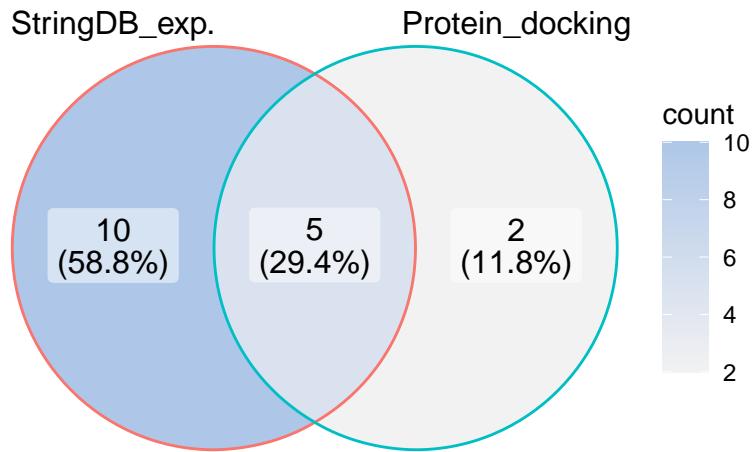


Figure 28: Intersection of StringDB exp with Protein docking

**Intersection :**

FTH1\_TFRC, SERPINA1\_TFRC, HSPA8\_TFRC, DDX3X\_AIFM1, HMGB1\_ITGAM

(上述信息框内容已保存至 [Figure+Table/Intersection-of-StringDB-exp--with-Protein-docking-content](#))

Table 16 (下方表格) 为表格 intersected data 概览。

(对应文件为 [Figure+Table/intersected-data.csv](#))

注：表格共有 5 行 11 列，以下预览的表格可能省略部分数据；含有 5 个唯一 ‘pro1’。

Table 16: Intersected data

pro1	pro2	Name	Cluster	Members	Center	Lowest...	value	pdb1	pdb2
HMGB1	ITGAM	HMGB1_ITGAM	0	45	-2270.7	-2270.7	-2270.7	6OEO	7USM
HSPA8	TFRC	HSPA8_TFRC	0	67	-1792.1	-1792.1	-1792.1	6ZYJ	7ZQS
SERPINA1	TFRC	SERPINA1_TFRC	0	84	-1336.4	-1456.1	-1456.1	9API	7ZQS
FTH1	TFRC	FTH1_TFRC	0	21	-1335.4	-1426.7	-1426.7	8DNP	7ZQS
DDX3X	AIFM1	DDX3X_AIFM1	0	61	-1229.3	-1410	-1410	7LIU	5KVI

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