

Analysis

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1 摘要

空间转录组分析：

- 鉴定肿瘤细胞
- 肿瘤细胞亚群分析
- 肿瘤细胞和正常细胞之间的差异分析
- 细胞通讯分析
- 肿瘤细胞和正常细胞（巨噬细胞）之间的通讯分析。

2 研究设计流程图

3 材料和方法

- Seurat
- copyKAT¹
- monocle3
- cellchat
- clusterProfiler
- ...

4 分析结果

- 以 copykat 鉴定了肿瘤细胞，主要为上皮细胞 (epithelial cells, EC) 或基底细胞 (basal cells, BC)。
- 以拟时分析将肿瘤细胞分为三个亚型 (cancer 1, cancer 2, cancer 3)，表现出时间 (拟时) 递进变化。
- 肿瘤细胞亚型之间的差异分析，肿瘤细胞和正常细胞 (EC, BC) 之间的差异分析，主要聚焦的通路有 ‘Phagosome’、’Antigen processing and presentation’、‘Focal adhesion’ 等。
- 细胞通讯分析的整体情况见 Fig. 18。
- 巨噬细胞和肿瘤细胞的通讯，突出表现为 ITGA 受体配体相关通路，共 27 个基因（其中多数为近似的亚型），首要富集于 PI3K-Akt 相关通路，并且和 ‘Focal adhesion’ 等上述分析的结果相一致。

5 结论

见 4。

6 附：分析流程（癌组织切片）

6.1 ST 数据预处理

Figure 1为图 spatial sample QC 概览。选择基因数 2500 - 9000 作为过滤指标。

(对应文件为 Figure+Table/spatial-sample-QC.pdf)

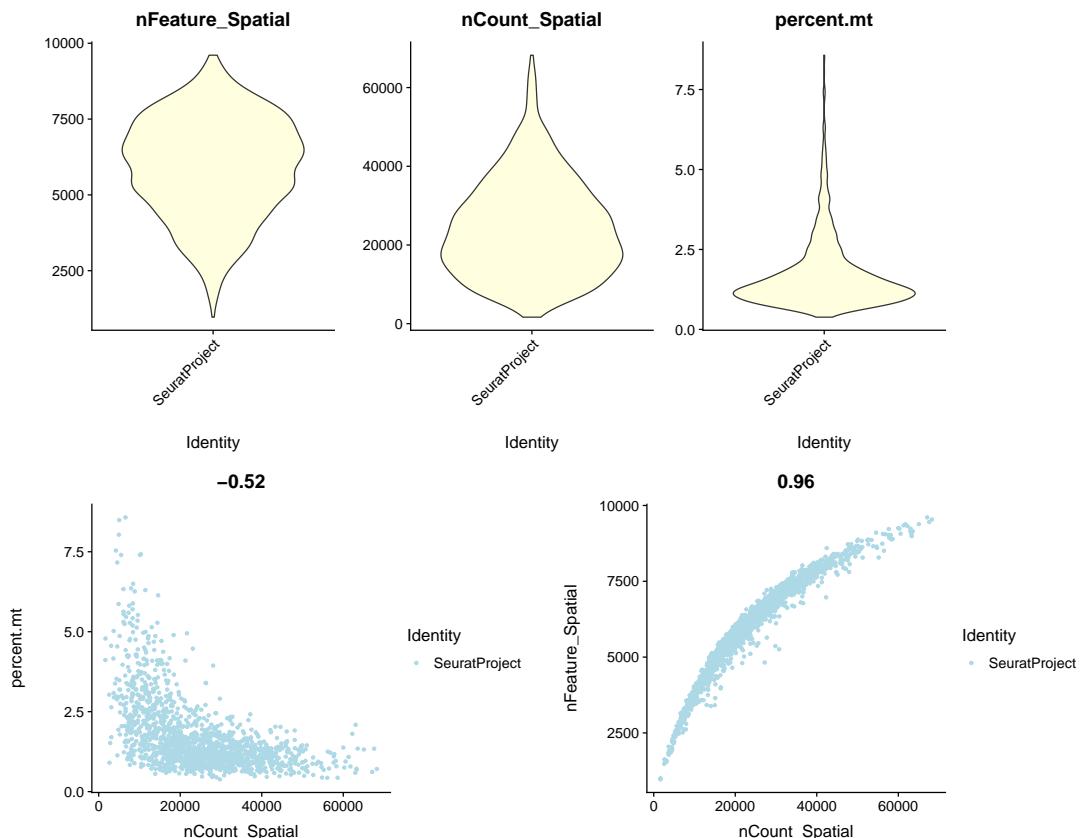


Figure 1: Spatial sample QC

Figure 2为图 PCA ranking 概览。选择主成份 1-15 用于后续聚类。

(对应文件为 Figure+Table/PCA-ranking.pdf)

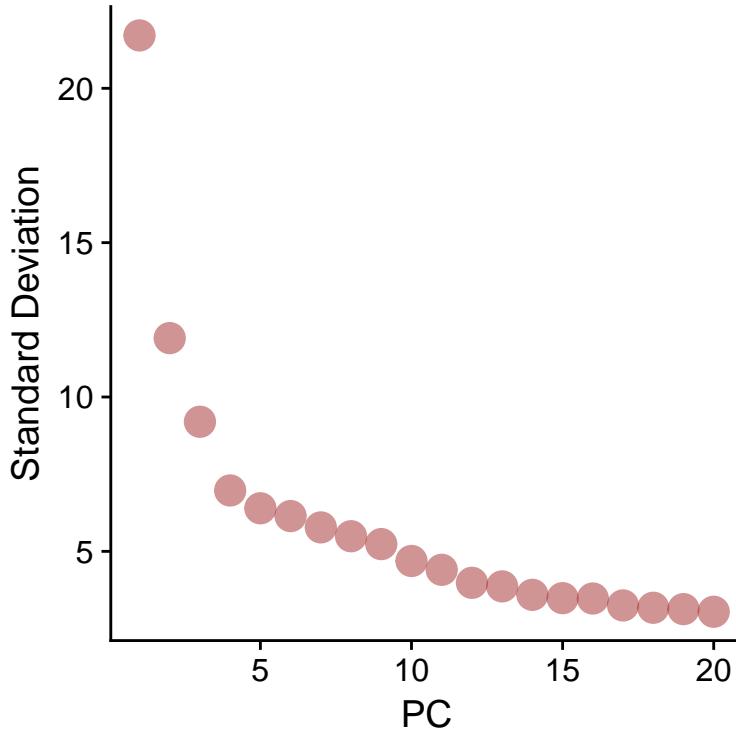


Figure 2: PCA ranking

6.2 细胞注释

6.2.1 所有细胞类 (Seurat clusters) 的 marker

Table 1为表格 all markers of Seurat clusters 概览。

(对应文件为 [Figure+Table/all-markers-of-Seurat-clusters.csv](#))

注：表格共有 4370 行 8 列，以下预览的表格可能省略部分数据；表格含有 15 个唯一‘cluster’。

Table 1: All markers of Seurat clusters

rownames	p_val	avg_l...	pct.1	pct.2	p_val...	cluster	gene
ISLR	1.244...	2.772...	0.97	0.385	2.437...	0	ISLR
FN1	2.313...	2.726...	1	0.971	4.533...	0	FN1
COMP	4.009...	3.497...	0.827	0.192	7.857...	0	COMP
COL1A1	1.812...	2.682...	1	0.978	3.551...	0	COL1A1
TAGLN	4.759...	2.643...	1	0.877	9.326...	0	TAGLN
BGN	5.201...	2.540...	1	0.76	1.019...	0	BGN
COL1A2	1.085...	2.444...	1	0.988	2.126...	0	COL1A2
AEBP1	3.097...	2.326...	1	0.893	6.069...	0	AEBP1
RARRES2	1.383...	3.100...	1	0.716	2.711...	0	RARRES2

rownames	p_val	avg_l...	pct.1	pct.2	p_val...	cluster	gene
COL5A1	1.498...	2.494...	0.992	0.671	2.937...	0	COL5A1
SPARC	7.275...	2.190...	1	0.951	1.425...	0	SPARC
LUM	1.446...	2.464...	1	0.886	2.834...	0	LUM
MYL9	3.618...	2.054...	1	0.915	7.089...	0	MYL9
NNMT	3.777...	2.486...	1	0.675	7.401...	0	NNMT
POSTN	4.428...	2.680...	1	0.765	8.676...	0	POSTN
...

6.2.2 SCSA 注释

以肺脏组织的数据集注释。

Figure 3为图 SCSA annotation 概览。

(对应文件为 Figure+Table/SCSA-annotation.pdf)

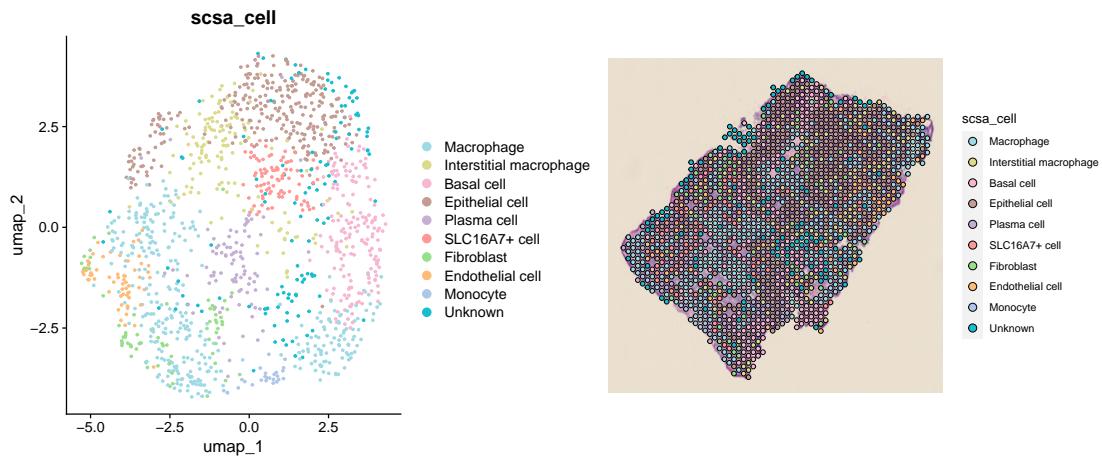


Figure 3: SCSA annotation

6.3 依据变异拷贝数鉴定肿瘤细胞

6.3.1 copyKAT 解析肿瘤细胞

copyKAT¹

非整倍体是人类肿瘤细胞中最普遍的特征，约 90% 的肿瘤的基因组是非整倍体，而正常细胞是二倍体²

Figure 4为图 copyKAT prediction of aneuploidy 概览。

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

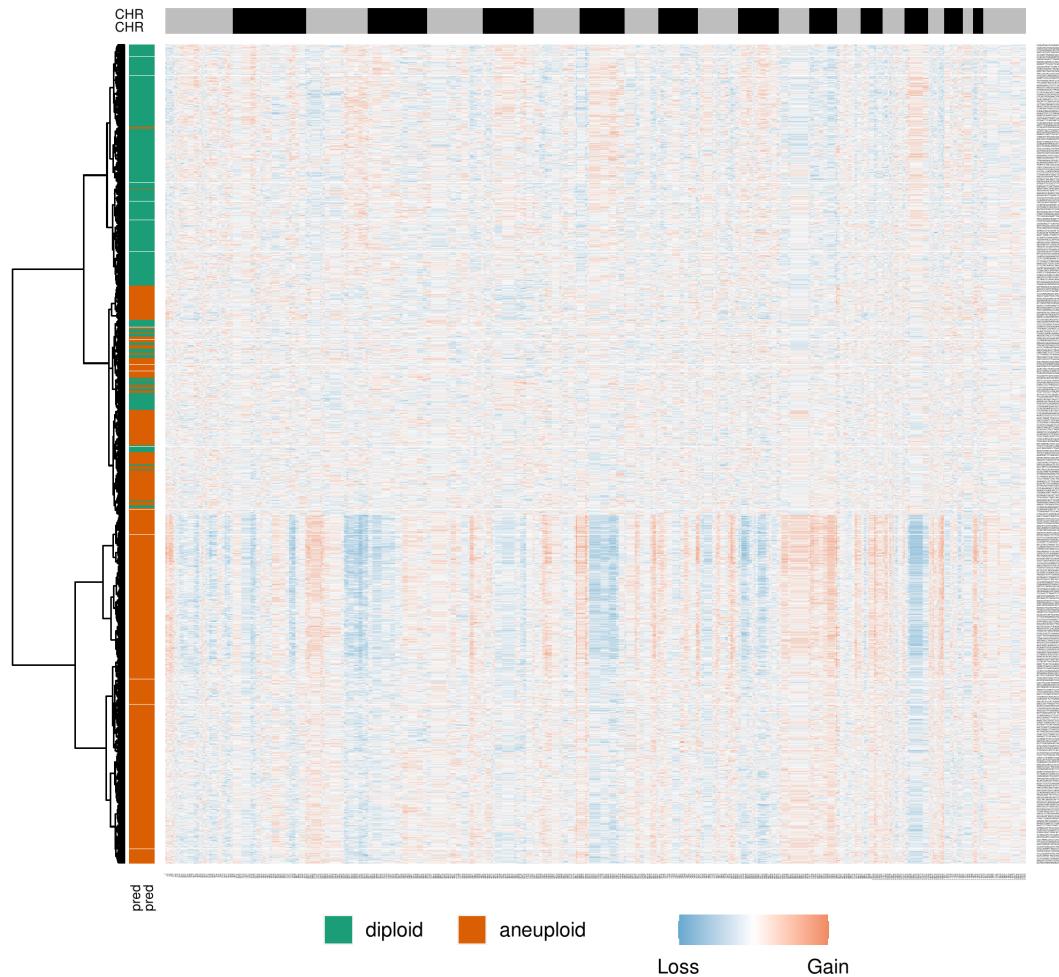


Figure 4: CopyKAT prediction of aneuploidy

Figure 5为图 cell mapped of copyKAT prediction 概览。

(对应文件为 [Figure+Table/cell-mapped-of-copyKAT-prediction.pdf](#))

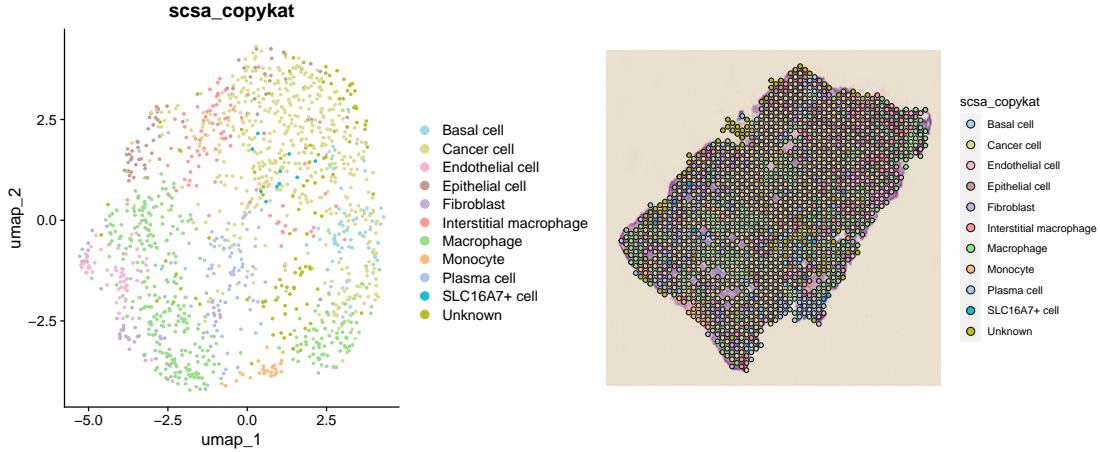


Figure 5: Cell mapped of copyKAT prediction

对比 Fig. 5 和 Fig. 3 可知，癌细胞主要为上皮细胞或基底细胞。

6.3.2 肿瘤细胞重聚类

为了区分肿瘤细胞之间的亚型，这里首先将肿瘤细胞重新聚类。

Figure 6为图 re classify of cancer cells 概览。

(对应文件为 Figure+Table/re-classify-of-cancer-cells.pdf)

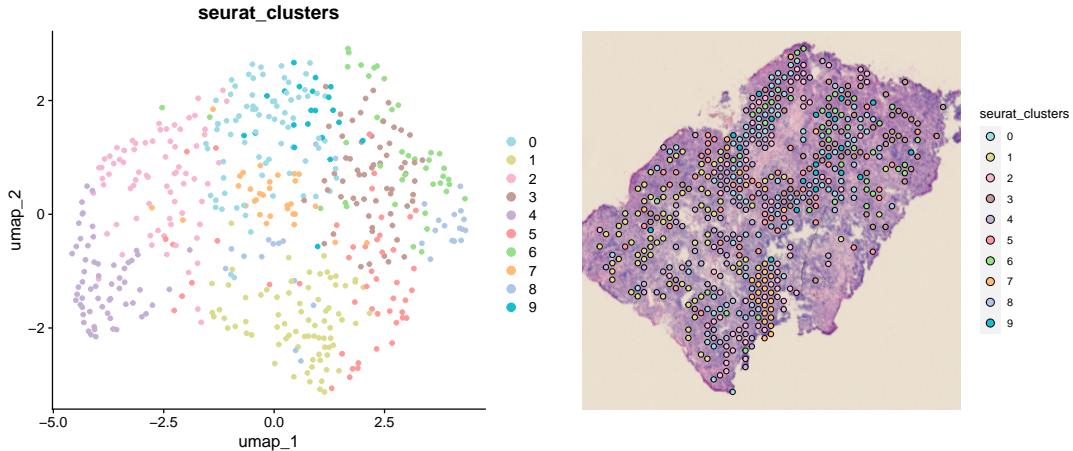


Figure 6: Re classify of cancer cells

6.4 拟时分析肿瘤细胞

6.4.1 构建拟时轨迹

Figure 7为图 pseudotime visualization of cancer cells 概览。

(对应文件为 Figure+Table/pseudotime-visualization-of-cancer-cells.pdf)

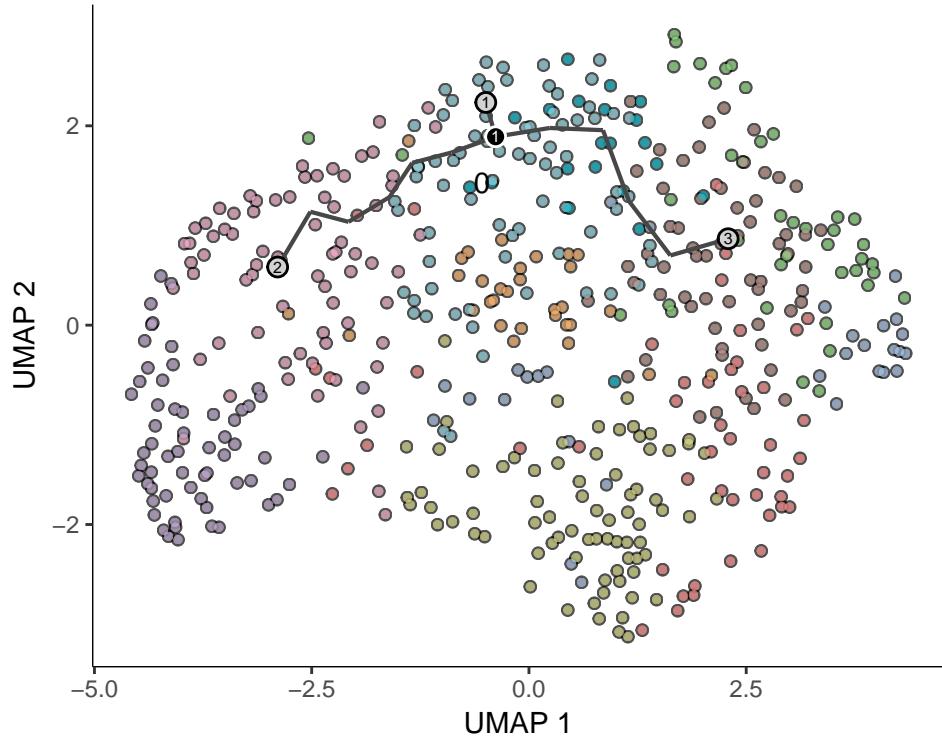


Figure 7: Pseudotime visualization of cancer cells

6.4.2 根据拟时分析区分肿瘤细胞亚类

Figure 8为图 gene module of co expression analysis 概览。

(对应文件为 Figure+Table/gene-module-of-co-expression-analysis.pdf)

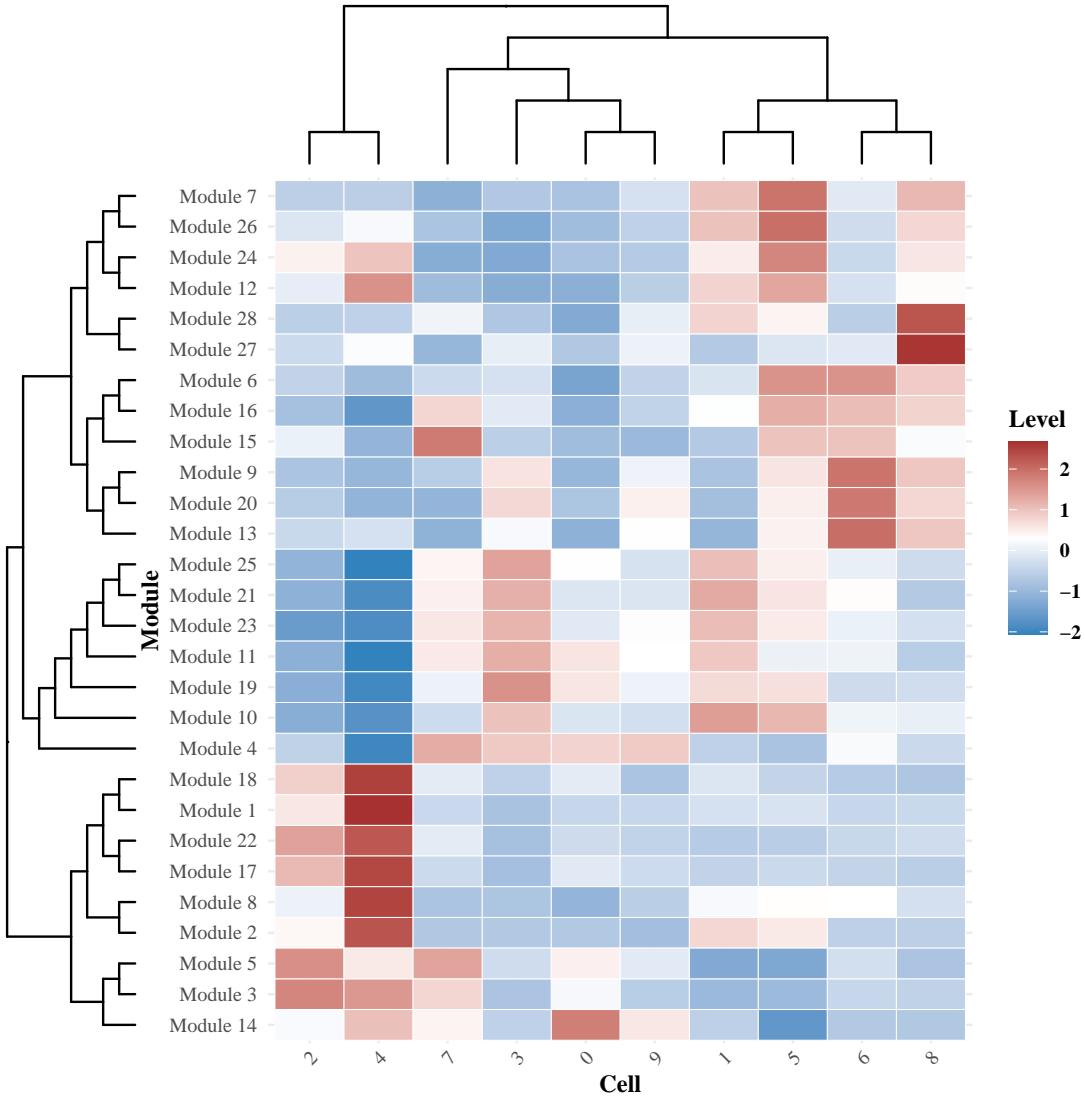


Figure 8: Gene module of co expression analysis

Fig. 8, 根据细胞类的聚类树, 可以将细胞类分为三个大类。

为了选择拟时起点, 这里, 将 Fig. 4 所示的细胞聚类树切分为 15 个大类的细胞, 然后映射到 Fig. 7 对应的聚类图中。可以看到 (Fig. 9), 细胞类类 11 首要分布在左侧区域 (UMAP 图) (1 - 15, 数目越小, 代表越趋近于非整倍体, 即肿瘤细胞), 因此, 左侧区域的细胞更接近于正常细胞。

Figure 9为图 test for selecting pseudotime start point 概览。

(对应文件为 Figure+Table/test-for-selecting-pseudotime-start-point.pdf)

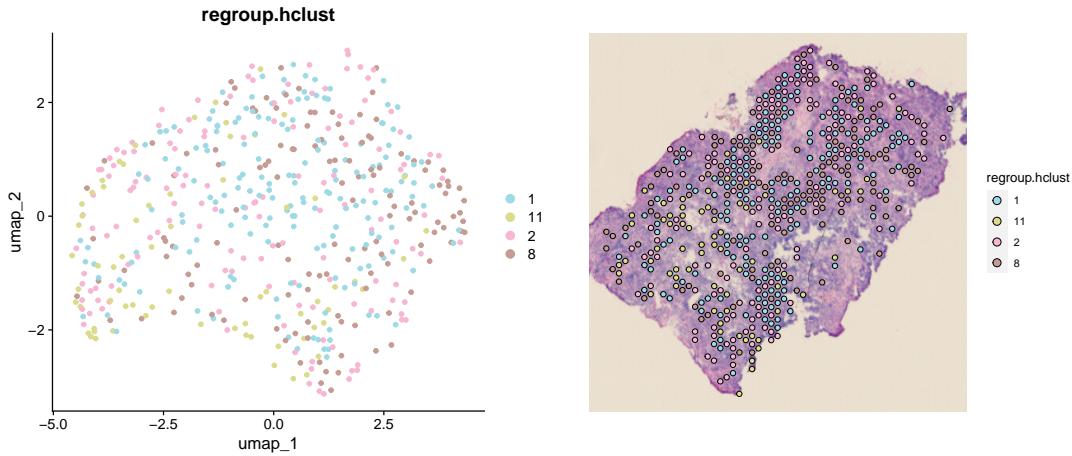


Figure 9: Test for selecting pseudotime start point

因此，选择左侧区域的细胞作为拟时起点。

Figure 10为图 cancer cells subtypes 概览。

(对应文件为 Figure+Table/cancer-cells-subtypes.pdf)

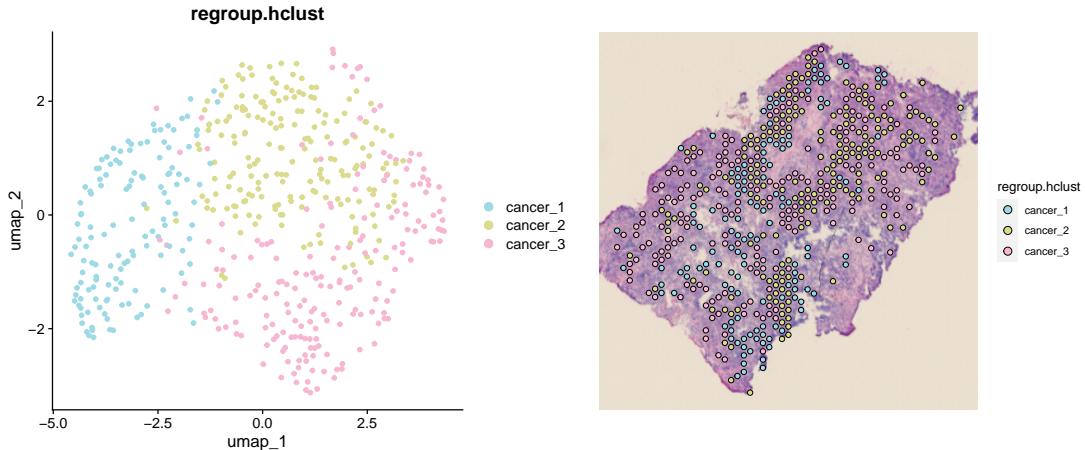


Figure 10: Cancer cells subtypes

6.4.3 肿瘤细胞亚类差异分析和富集分析

以下分析，可关注的通路有：

- Phagosome
- Antigen processing and presentati...
- Focal adhesion
- ...

cancer 1 细胞的 marker 的富集分析有结果，但矫正 p 值均不显著。

Table 2为表格 tables of enrichment of markers of cancer 1 cells 概览。

(对应文件为 Figure+Table/tables-of-enrichment-of-markers-of-cancer-1-cells.csv)

注：表格共有 66 行 9 列，以下预览的表格可能省略部分数据；表格含有 66 个唯一 ‘ID’。

Table 2: Tables of enrichment of markers of cancer 1 cells

ID	Descr...	GeneR...	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04114	Oocyt...	3/31	131/8622	0.011...	0.379...	0.369...	9133/...	3
hsa04218	Cellu...	3/31	156/8622	0.018...	0.379...	0.369...	9133/...	3
hsa04110	Cell ...	3/31	157/8622	0.018...	0.379...	0.369...	9133/...	3
hsa01524	Plati...	2/31	73/8622	0.028...	0.379...	0.369...	4257/...	2
hsa04115	p53 s...	2/31	74/8622	0.028...	0.379...	0.369...	9133/983	2
hsa04914	Proge...	2/31	102/8622	0.051...	0.552...	0.537...	9133/983	2
hsa00100	Stero...	1/31	20/8622	0.069...	0.552...	0.537...	3930	1
hsa03060	Prote...	1/31	23/8622	0.079...	0.552...	0.537...	6726	1
hsa04514	Cell ...	2/31	158/8622	0.109...	0.552...	0.537...	214/9076	2
hsa04216	Ferro...	1/31	41/8622	0.137...	0.552...	0.537...	7037	1
hsa05014	Amyot...	3/31	364/8622	0.141...	0.552...	0.537...	1345/...	3
hsa02010	ABC t...	1/31	45/8622	0.149...	0.552...	0.537...	154664	1
hsa05130	Patho...	2/31	198/8622	0.158...	0.552...	0.537...	9076/...	2
hsa00270	Cyste...	1/31	52/8622	0.171...	0.552...	0.537...	10768	1
hsa05170	Human...	2/31	212/8622	0.176...	0.552...	0.537...	9133/983	2
...

Figure 11 为图 enrichment of markers of cancer 2 cells 概览。

(对应文件为 Figure+Table/enrichment-of-markers-of-cancer-2-cells.pdf)

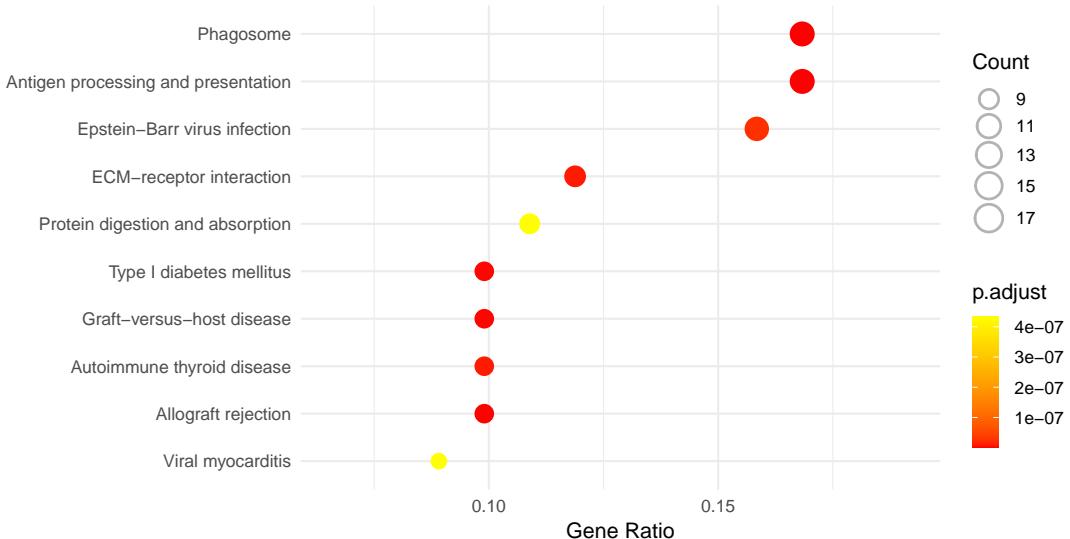


Figure 11: Enrichment of markers of cancer 2 cells

Table 3 为表格 tables of enrichment of markers of cancer 2 cells 概览。

(对应文件为 Figure+Table/tables-of-enrichment-of-markers-of-cancer-2-cells.csv)

注：表格共有 162 行 9 列，以下预览的表格可能省略部分数据；表格含有 162 个唯一 ‘ID’。

Table 3: Tables of enrichment of markers of cancer 2 cells

ID	Descr...	GeneR...	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04612	Antig...	17/101	78/8622	1.279...	2.072...	1.561...	567/9...	17
hsa04145	Phago...	17/101	152/8622	1.400...	1.134...	8.550...	929/1...	17
hsa05330	Allog...	10/101	38/8622	1.113...	6.013...	4.532...	3002/...	10
hsa05332	Graft...	10/101	42/8622	3.334...	1.350...	1.018...	3002/...	10
hsa04940	Type ...	10/101	43/8622	4.303...	1.394...	1.051...	3002/...	10
hsa04512	ECM-r...	12/101	89/8622	3.862...	9.196...	6.931...	961/1...	12
hsa05320	Autoi...	10/101	53/8622	3.973...	9.196...	6.931...	3002/...	10
hsa05169	Epste...	16/101	202/8622	1.262...	2.556...	1.927...	567/9...	16
hsa05416	Viral...	9/101	60/8622	2.610...	4.340...	3.271...	3105/...	9
hsa04974	Prote...	11/101	103/8622	2.679...	4.340...	3.271...	1306/...	11
hsa05165	Human...	16/101	331/8622	1.273...	1.744...	1.315...	1277/...	16
hsa05310	Asthma	6/101	31/8622	1.292...	1.744...	1.315...	2207/...	6
hsa04640	Hemat...	9/101	99/8622	2.097...	2.455...	1.850...	929/9...	9
hsa04514	Cell ...	11/101	158/8622	2.122...	2.455...	1.850...	914/3...	11
hsa04510	Focal...	12/101	203/8622	3.977...	4.296...	3.238...	1277/...	12
...

Figure 12 为图 enrichment of markers of cancer 3 cells 概览。

(对应文件为 Figure+Table/enrichment-of-markers-of-cancer-3-cells.pdf)

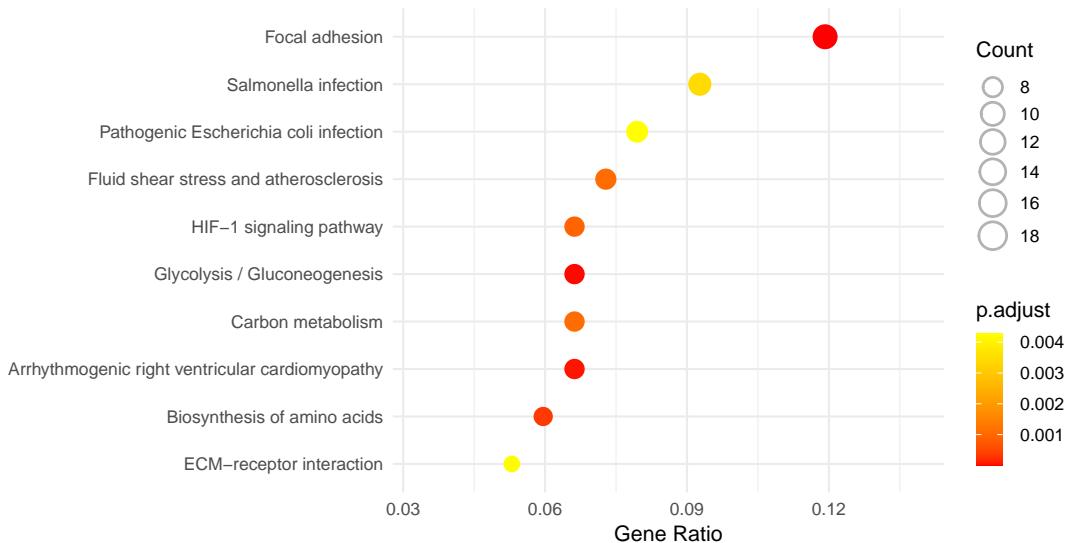


Figure 12: Enrichment of markers of cancer 3 cells

Table 4为表格 tables of enrichment of markers of cancer 3 cells 概览。

(对应文件为 [Figure+Table/tables-of-enrichment-of-markers-of-cancer-3-cells.xlsx](#))

注：表格共有 241 行 9 列，以下预览的表格可能省略部分数据；表格含有 241 个唯一 ‘ID’。

Table 4: Tables of enrichment of markers of cancer 3 cells

ID	Descr...	GeneR...	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04510	Focal...	18/151	203/8622	1.346...	3.245...	2.707...	71/33...	18
hsa00010	Glyco...	10/151	67/8622	2.124...	2.559...	2.135...	226/2...	10
hsa05412	Arrhy...	10/151	77/8622	8.090...	6.499...	5.422...	71/18...	10
hsa01230	Biosy...	9/151	75/8622	5.726...	0.000...	0.000...	226/4...	9
hsa04066	HIF-1...	10/151	109/8622	1.948...	0.000...	0.000...	226/1...	10
hsa05418	Fluid...	11/151	139/8622	3.015...	0.001...	0.000...	71/44...	11
hsa01200	Carbo...	10/151	115/8622	3.114...	0.001...	0.000...	226/2...	10
hsa05132	Salmo...	14/151	249/8622	0.000...	0.003...	0.002...	10006...	14
hsa04512	ECM-r...	8/151	89/8622	0.000...	0.004...	0.003...	3339/...	8
hsa05130	Patho...	12/151	198/8622	0.000...	0.004...	0.003...	10006...	12
hsa05222	Small...	8/151	92/8622	0.000...	0.004...	0.003...	330/1...	8
hsa04210	Apopt...	9/151	136/8622	0.000...	0.012...	0.010...	71/33...	9
hsa05205	Prote...	11/151	205/8622	0.000...	0.017...	0.014...	71/85...	11
hsa05165	Human...	14/151	331/8622	0.001...	0.033...	0.027...	3133/...	14
hsa05100	Bacte...	6/151	77/8622	0.002...	0.035...	0.029...	71/10...	6
...

6.5 肿瘤细胞来源分析

6.5.1 肿瘤与上皮细胞或基底细胞差异分析

接下来的分析回到 Fig. 3 图中，取出上皮细胞或基底细胞对应的细胞类（肿瘤细胞主要分布在这两类细胞中），并且将 Fig. 10 对应的细胞亚型映射。

Figure 13为图 cancer cells in epithelial or basal cells 概览。

(对应文件为 [Figure+Table/cancer-cells-in-epithelial--or-basal-cells.pdf](#))

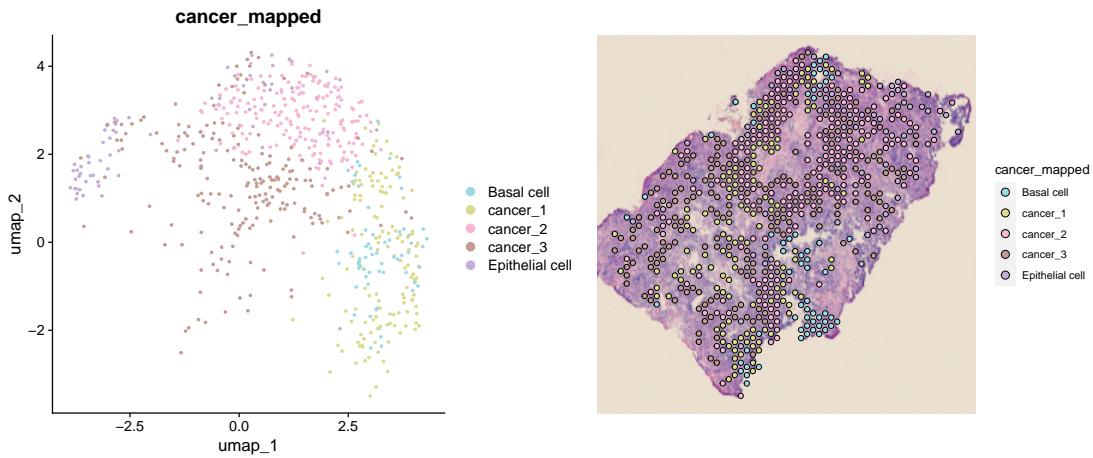


Figure 13: Cancer cells in epithelial or basal cells

6.5.2 肿瘤与上皮细胞或基底细胞差异基因的富集分析

以下富集与 6.4.3 相对应，“Phagosome”、“Antigen processing and presentati...” 等为差异基因的主要富集通路。

Figure 14 为图 enrichment of DEGs of Cancer 1 cells vs Basal cells 概览。

(对应文件为 Figure+Table/enrichment-of-DEGs-of-Cancer-1-cells-vs-Basal-cells.pdf)

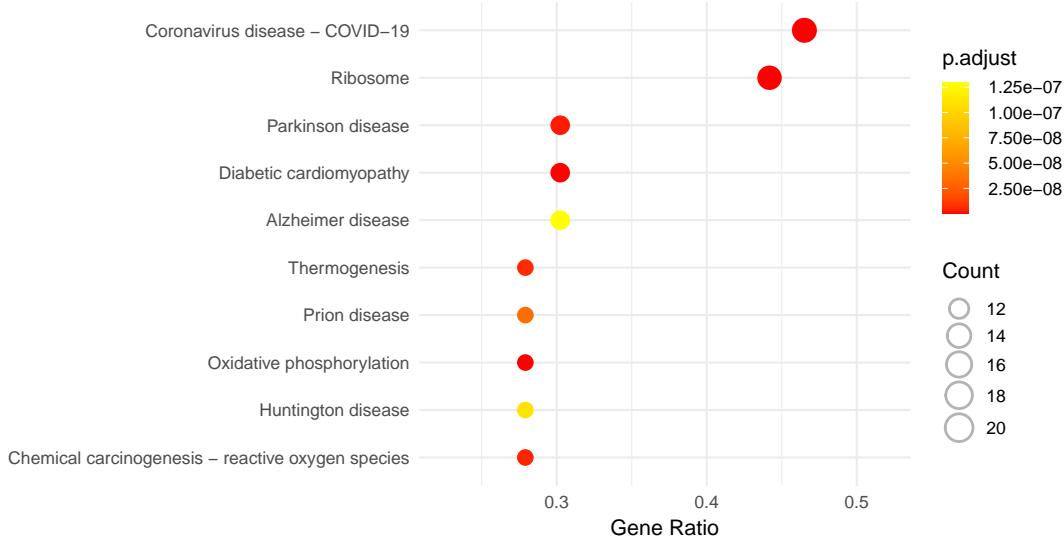


Figure 14: Enrichment of DEGs of Cancer 1 cells vs Basal cells

Figure 15 为图 enrichment of DEGs of Cancer 1 cells vs Epithelial cells 概览。

(对应文件为 Figure+Table/enrichment-of-DEGs-of-Cancer-1-cells-vs-Epithelial-cells.pdf)

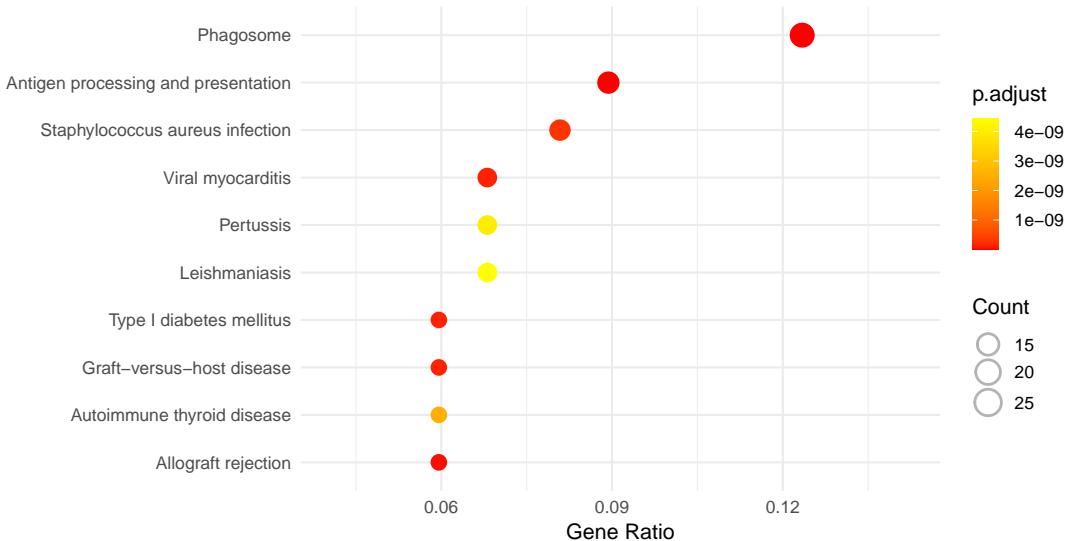


Figure 15: Enrichment of DEGs of Cancer 1 cells vs Epithelial cells

‘All enrichments of DEGs of cancer vs epithelial or basal cells’ 数据已全部提供。

(对应文件为 **all-enrichments-of-DEGs-of-cancer-vs-epithelial-or-basal-cells**)

注：文件夹 all-enrichments-of-DEGs-of-cancer-vs-epithelial-or-basal-cells 共包含 6 个文件。

1. 1_cancer_1_vs_Basal cell.pdf
2. 2_cancer_1_vs_Epithelial cell.pdf
3. 3_cancer_2_vs_Basal cell.pdf
4. 4_cancer_2_vs_Epithelial cell.pdf
5. 5_cancer_3_vs_Basal cell.pdf
6. ...

‘Tables of all enrichments of DEGs of cancer vs epithelial or basal cells’ 数据已全部提供。

(对应文件为 **tables-of-all-enrichments-of-DEGs-of-cancer-vs-epithelial-or-basal-cells**)

注：文件夹 tables-of-all-enrichments-of-DEGs-of-cancer-vs-epithelial-or-basal-cells 共包含 6 个文件。

1. 1_cancer_1_vs_Basal cell.csv
2. 2_cancer_1_vs_Epithelial cell.csv
3. 3_cancer_2_vs_Basal cell.csv
4. 4_cancer_2_vs_Epithelial cell.csv
5. 5_cancer_3_vs_Basal cell.csv
6. ...

6.6 细胞通讯

以下分析使用的为 Tab. 1 中的基因。

6.6.1 所有细胞之间的通讯

将肿瘤细胞亚型映射到 Fig. 3 中，得到 Fig. 16。

Figure 16为图 cancer subtypes in all cells 概览。

(对应文件为 Figure+Table/cancer-subtypes-in-all-cells.pdf)

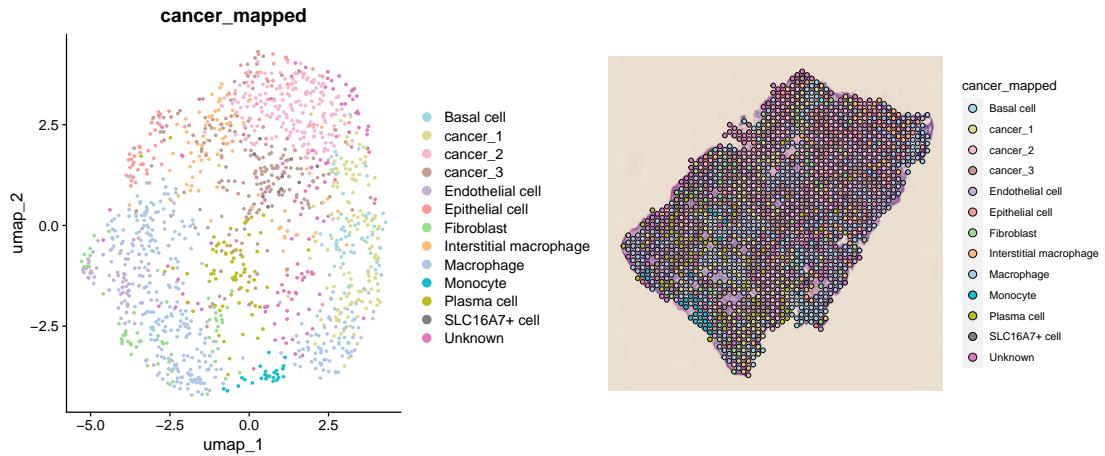


Figure 16: Cancer subtypes in all cells

以 cellchat 计算所有这些细胞之间的通讯关系³。

Figure 17为图 overview of cells communication 概览。

(对应文件为 Figure+Table/overview-of-cells-communication.pdf)

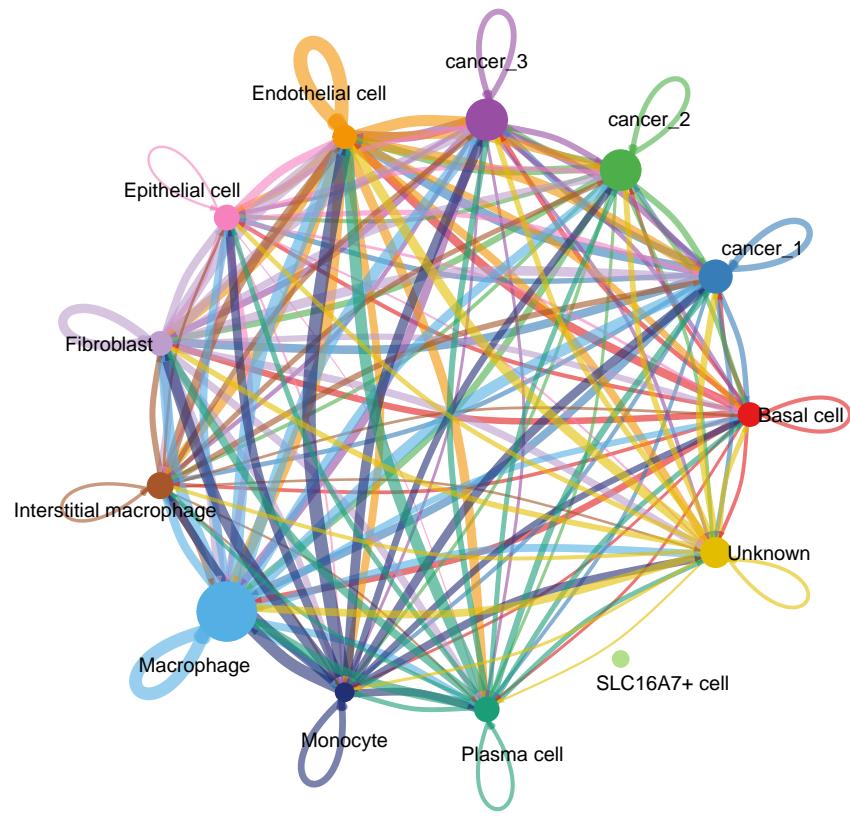


Figure 17: Overview of cells communication

Figure 18为图 all cells communication significance 概览。

(对应文件为 [Figure+Table/all-cells-communication-significance.pdf](#))



Figure 18: All cells communication significance

Figure 19为图 all cells communication roles 概览。

(对应文件为 Figure+Table/all-cells-communication-roles.pdf)

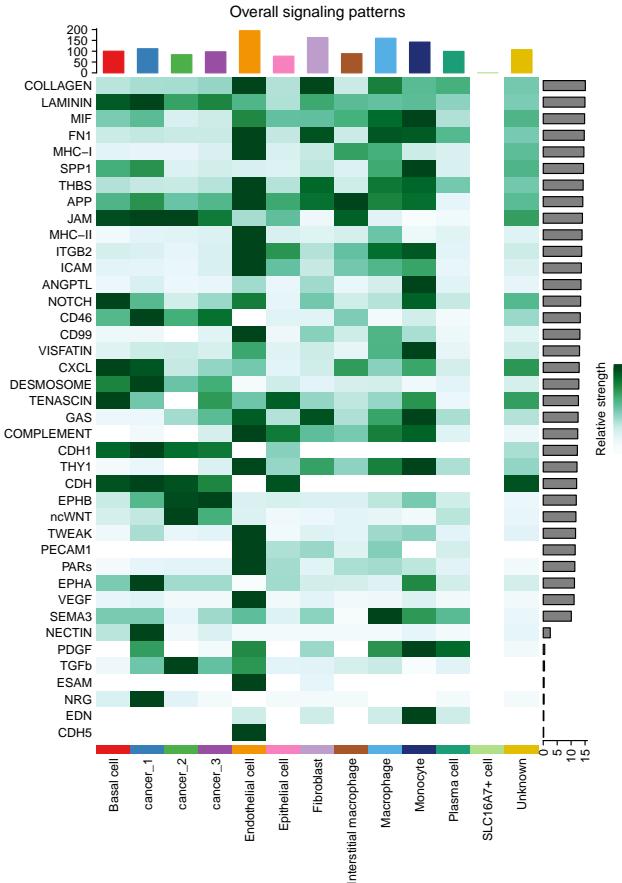


Figure 19: All cells communication roles

6.6.2 巨噬细胞和肿瘤细胞之间的互作

以下，我们主要聚焦于巨噬细胞和癌细胞之间的通讯关系。

Table 5为表格 table of communication between macrophage and cancer cells 概览。

(对应文件为 Figure+Table/table-of-communication-between-macrophage-and-cancer-cells.csv)

注：表格共有 409 行 11 列，以下预览的表格可能省略部分数据；表格含有 4 个唯一‘source’。

Table 5: Table of communication between macrophage and cancer cells

source	target	ligand	receptor	prob	pval	inter.....7	inter.....8	pathw...	annot...	evidence	...
Macro...	cancer_2	TGFB1	ACVR1...	0.000...	0.01	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...
Macro...	cancer_3	TGFB1	ACVR1...	0.000...	0.03	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...
cancer_2	Macro...	TGFB1	ACVR1...	0.001...	0	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...
cancer_3	Macro...	TGFB1	ACVR1...	0.000...	0	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...
Macro...	cancer_1	TGFB1	ACVR1...	0.000...	0.04	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...
Macro...	cancer_2	TGFB1	ACVR1...	0.000...	0	TGFB1...	TGFB1...	TGFB	Secre...	PMID:...	...

source	target	ligand	receptor	prob	pval	inter.....7	inter.....8	pathw...	annot...	evidence	...
Macro...	cancer_1	WNT5A	FZD10	0.001...	0	WNT5A...	WNT5A...	ncWNT	Secre...	KEGG:...	...
Macro...	cancer_2	WNT5A	FZD10	0.001...	0.02	WNT5A...	WNT5A...	ncWNT	Secre...	KEGG:...	...
Macro...	cancer_3	WNT5A	FZD10	0.001...	0.02	WNT5A...	WNT5A...	ncWNT	Secre...	KEGG:...	...
Macro...	cancer_1	WNT5A	FZD6	0.011...	0.04	WNT5A...	WNT5A...	ncWNT	Secre...	KEGG:...	...
Macro...	cancer_2	WNT5A	FZD6	0.011...	0.04	WNT5A...	WNT5A...	ncWNT	Secre...	KEGG:...	...
Macro...	cancer_2	WNT5A	MCAM	0.001...	0.04	WNT5A...	WNT5A...	ncWNT	Secre...	PMID:...	...
cancer_2	Macro...	WNT5A	MCAM	0.005...	0	WNT5A...	WNT5A...	ncWNT	Secre...	PMID:...	...
cancer_3	Macro...	WNT5A	MCAM	0.004...	0.04	WNT5A...	WNT5A...	ncWNT	Secre...	PMID:...	...
cancer_1	Macro...	PDGFB	PDGFRA	0.000...	0	PDGFB...	PDGFB...	PDGF	Secre...	PMID:...	...
...

Figure 20为图 visualization of communication between macrophage and cancer cells 概览。

(对应文件为 [Figure+Table/visualization-of-communication-between-macrophage-and-cancer-cells.pdf](#))

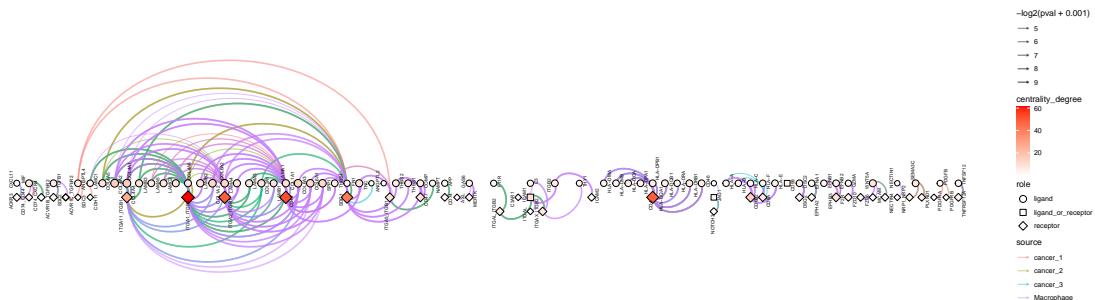


Figure 20: Visualization of communication between macrophage and cancer cells

根据 Fig. 20, 可以关注到互作网络图中中心度 (centrality degree) 较高的 ITGA 相关受体或配体。

6.6.3 ITGA 相关配体受体富集分析

根据 Fig. 20, 以下将 ITGA 相关基因做富集分析。

'Enrichment of ITGA related genes' 数据已全部提供。

(对应文件为 [enrichment-of-ITGA-related-genes](#))

注：文件夹 enrichment-of-ITGA-related-genes 共包含 1 个文件。

1. 1_ids.pdf

Fig. ?? 首要富集到 PI3K-AKT 通路。还可以发现，“Small cell lung cancer” 也是显著富集结果之一。

Table 6为表格 tables of enrichment of ITGA related genes 概览。

(对应文件为 [Figure+Table/tables-of-enrichment-of-ITGA-related-genes.csv](#))

注：表格共有 65 行 9 列，以下预览的表格可能省略部分数据；表格含有 65 个唯一 ‘ID’。

Table 6: Tables of enrichment of ITGA related genes

ID	Descr...	GeneR...	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04512	ECM-r...	27/36	89/8622	2.645...	1.719...	8.633...	1277/...	27
hsa04510	Focal...	27/36	203/8622	1.474...	4.791...	2.405...	1277/...	27
hsa05165	Human...	27/36	331/8622	1.433...	3.106...	1.559...	1277/...	27
hsa04151	PI3K-...	27/36	359/8622	1.360...	2.211...	1.110...	1277/...	27
hsa05146	Amoeb...	18/36	102/8622	3.269...	4.250...	2.133...	1277/...	18
hsa05222	Small...	17/36	92/8622	4.653...	5.041...	2.530...	1282/...	17
hsa04974	Prote...	11/36	103/8622	1.922...	1.785...	8.962...	1277/...	11
hsa05145	Toxop...	10/36	111/8622	1.592...	1.294...	6.497...	3688/...	10
hsa04933	AGE-R...	9/36	100/8622	1.914...	1.382...	6.942...	1277/...	9
hsa04810	Regul...	9/36	229/8622	2.833...	1.841...	9.245...	2335/...	9
hsa05412	Arrhy...	6/36	77/8622	6.555...	3.873...	1.944...	3672/...	6
hsa04926	Relax...	7/36	129/8622	8.294...	4.492...	2.255...	1277/...	7
hsa05410	Hyper...	6/36	90/8622	1.655...	8.278...	4.156...	3672/...	6
hsa05414	Dilat...	6/36	96/8622	2.421...	1.124...	5.643...	3672/...	6
hsa04670	Leuko...	6/36	115/8622	6.942...	3.008...	1.510...	50848...	6
...

6.6.4 首要富集的 PI3K 通路

以下结果可以和 6.4.3 和 6.5.2 相对应。

Figure 21 为图 view of enriched genes in PI3K pathway 概览。

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

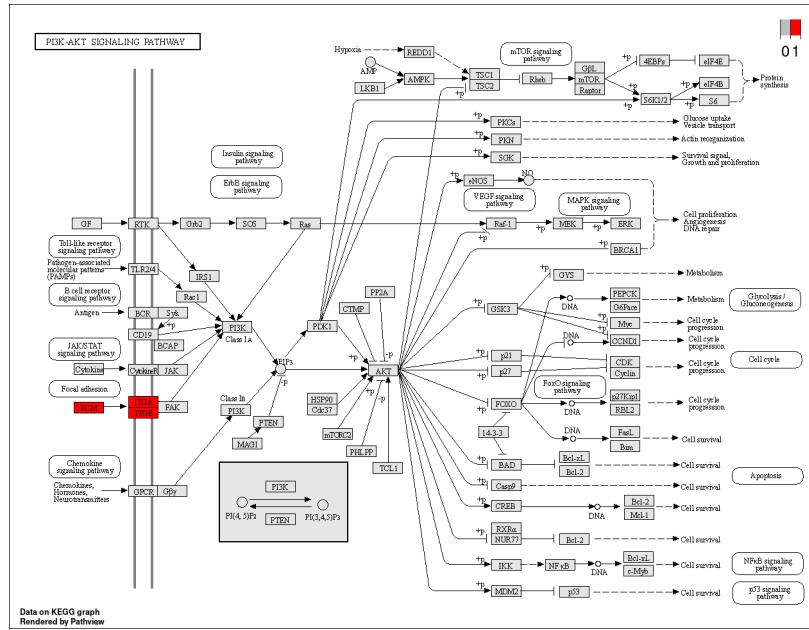


Figure 21: View of enriched genes in PI3K pathway

6.6.5 PI3K 通路和 ITGA 相关受体配体的交集

ITGA_with_PI3K :

COL1A1, COL1A2, COL2A1, COL4A1, COL4A2, COL4A4, COL4A5, COL4A6, COL6A1, COL6A2, COL6A3, FN1, ITGA1, ITGA11, ITGA2, ITGA5, ITGB1, LAMA1, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, SPP1

6.6.6 通讯基因的表达在肿瘤细胞中的拟时变化

以下分析表现了 ITGA 和 PI3K 通路相关的 27 个基因在肿瘤细胞亚型之间的转化（拟时过程）过程中的表达变化。

Figure 22为图 group 1 communication related genes in pseudotime 概览。

(对应文件为 Figure+Table/group-1-communication-related-genes-in-pseudotime.pdf)

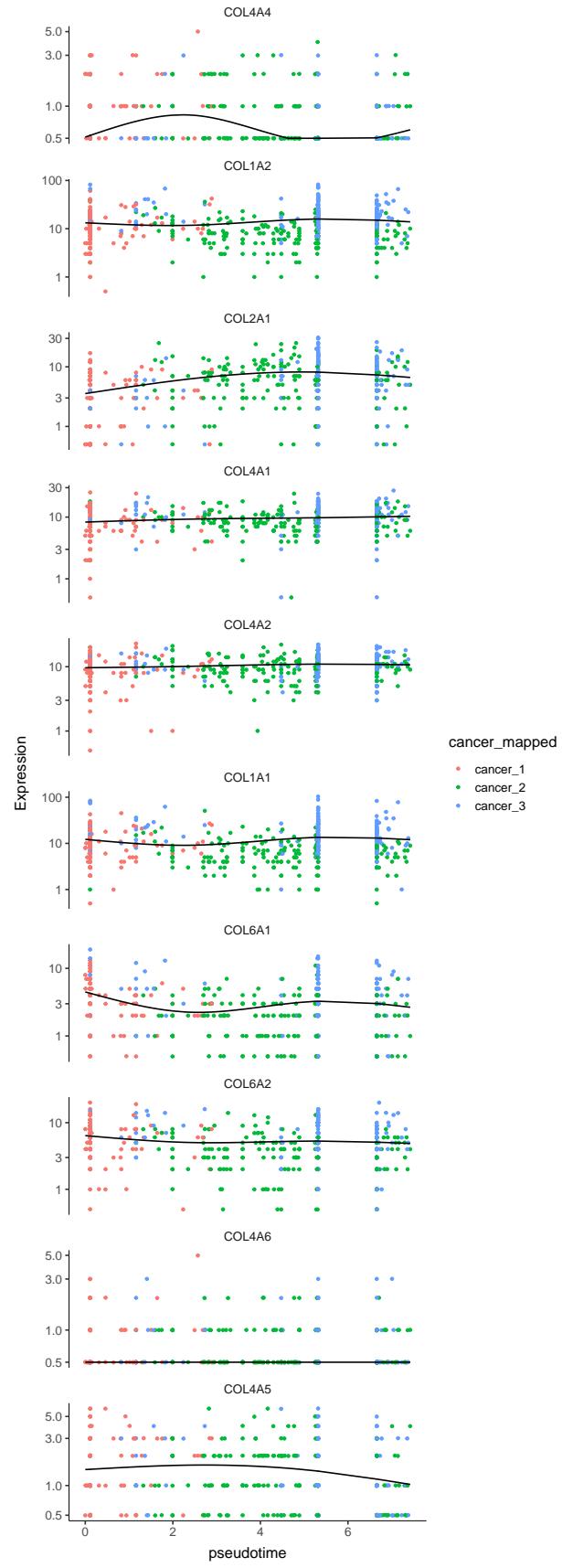


Figure 22: Group 1 communication related genes in pseudotime

Figure 23为图 group 2 communication related genes in pseudotime 概览。

(对应文件为 **Figure+Table/group-2-communication-related-genes-in-pseudotime.pdf**)

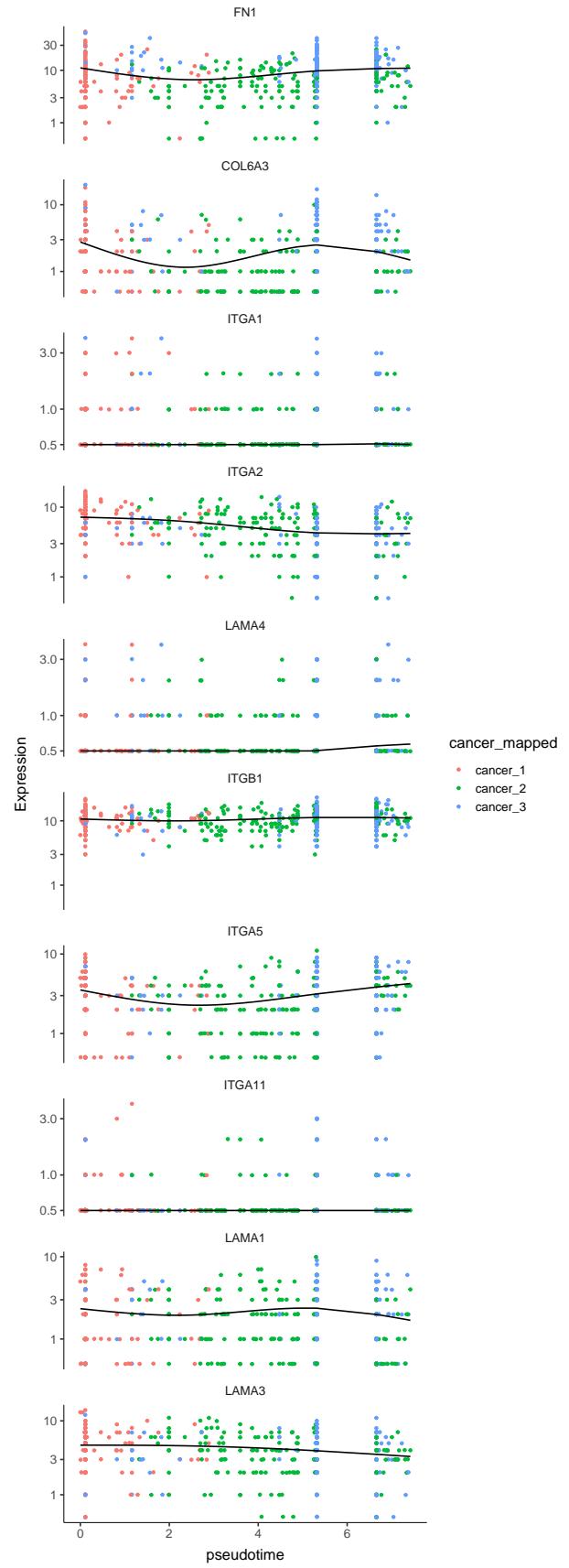


Figure 23: Group 2 communication related genes in pseudotime

Figure 24为图 group 3 communication related genes in pseudotime 概览。

(对应文件为 **Figure+Table/group-3-communication-related-genes-in-pseudotime.pdf**)

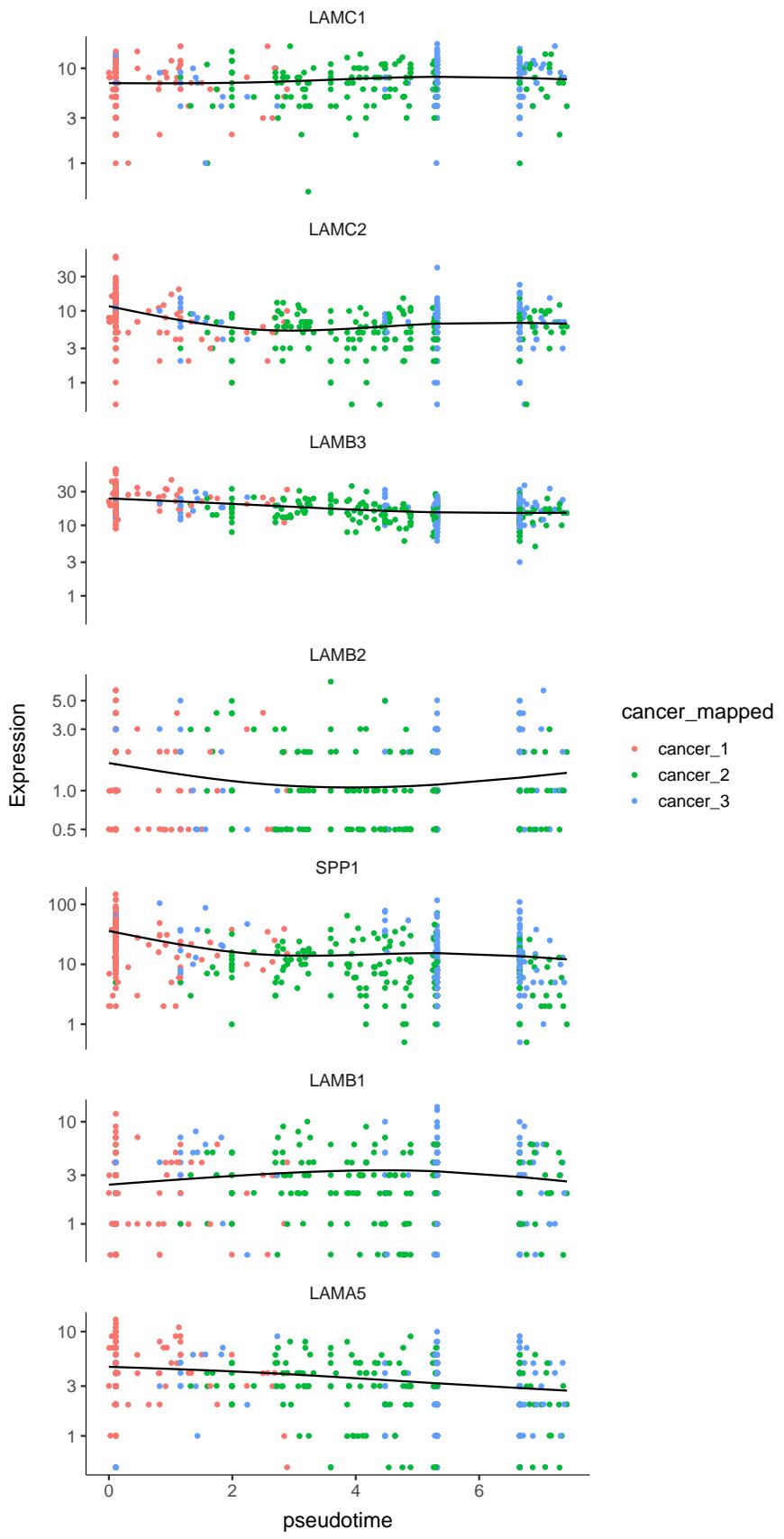


Figure 24: Group 3 communication related genes in pseudotime

7 附：分析流程（癌旁组织切片）

7.1 Clustering and annotation

Figure 25为图 extra QC 概览。

(对应文件为 Figure+Table/extr-QC.pdf)

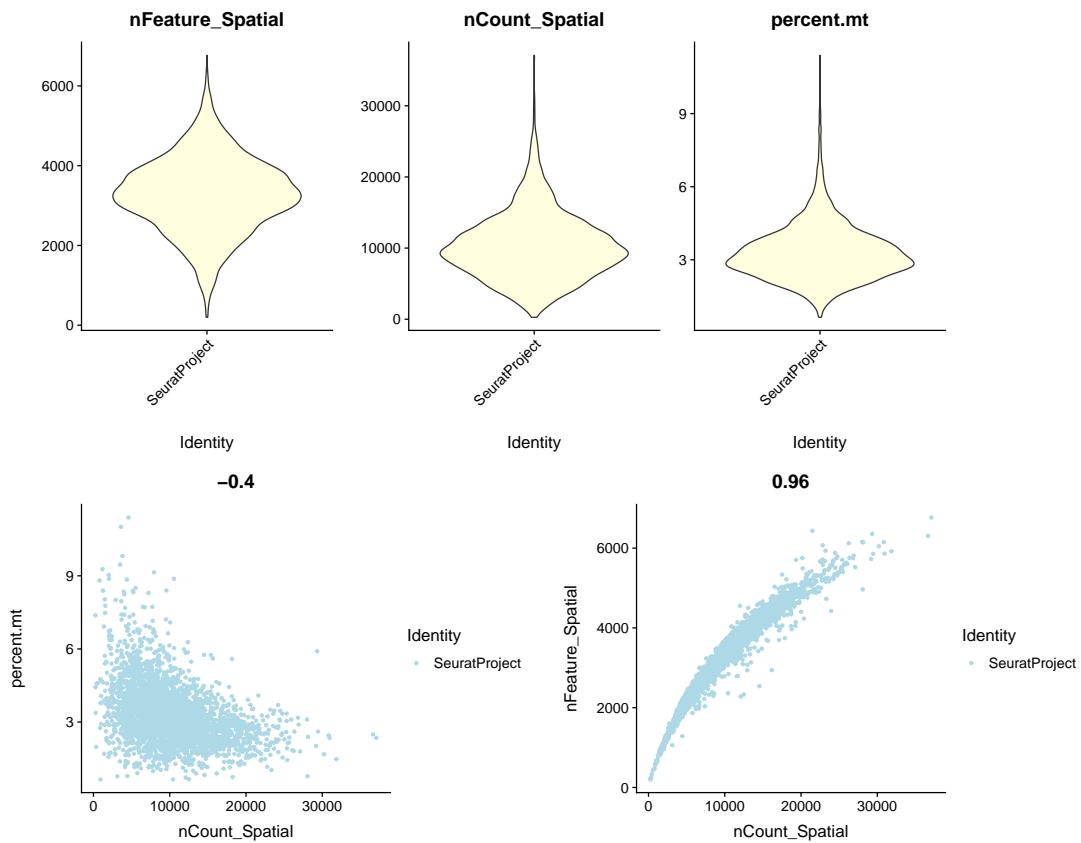


Figure 25: Extra QC

Figure 26为图 extra SCSA annotation 概览。

(对应文件为 Figure+Table/extr-SCSA-annotation.pdf)

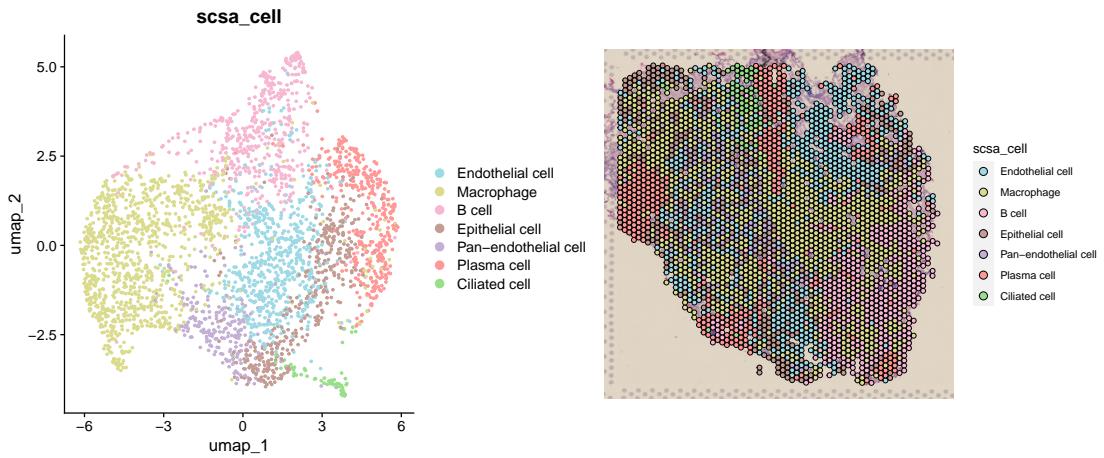


Figure 26: Extra SCSA annotation

7.2 Copykat prediction

可以观察到，copyKAT 的细胞类型预测，癌旁组织 Fig. 27 的聚类不及癌组织切片的 Fig. 4 明显。

Figure 27为图 extra copyKAT prediction 概览。

(对应文件为 [Figure+Table/copykat_para_cancer.png](#))

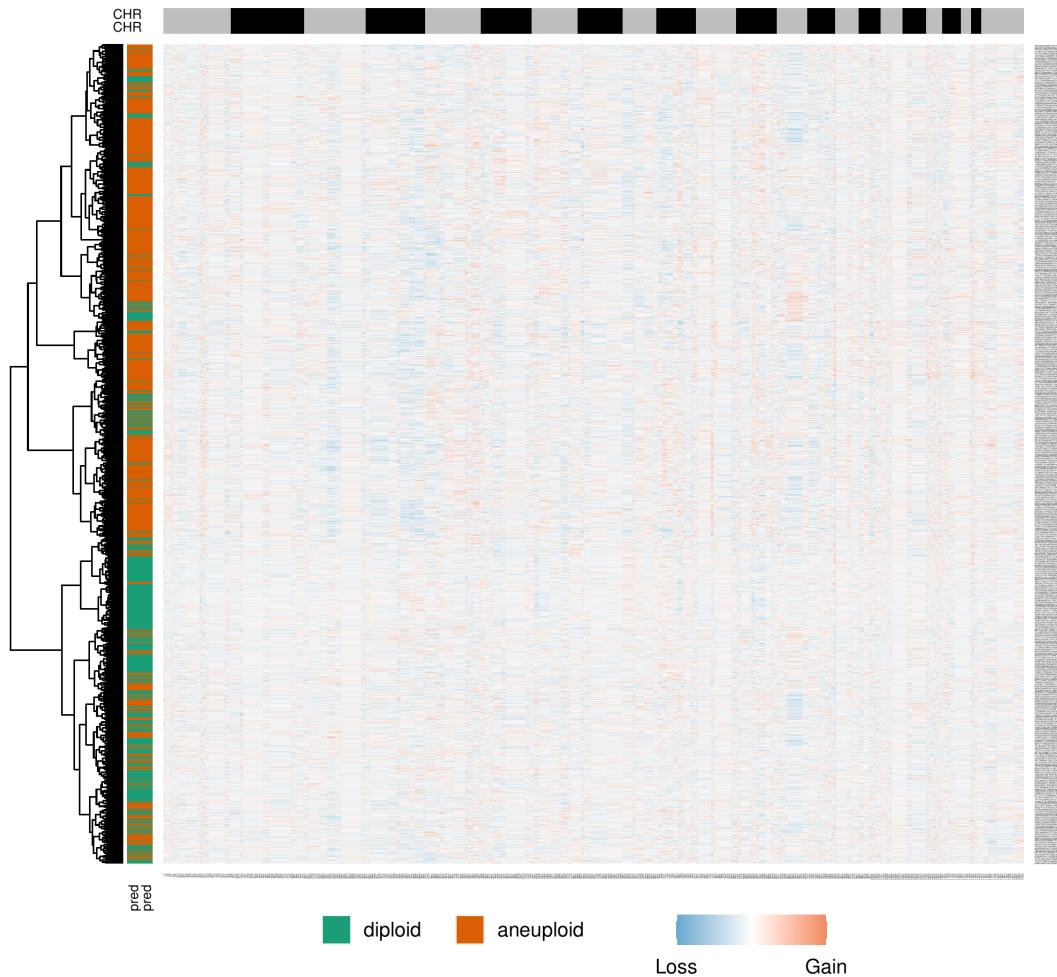


Figure 27: Extra copyKAT prediction

Reference

1. Gao, R. *et al.* Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. *Nature Biotechnology* **39**, 599–608 (2021).
2. Gordon, D. J., Resio, B. & Pellman, D. Causes and consequences of aneuploidy in cancer. *Nature Reviews Genetics* **13**, 189–203 (2012).
3. Jin, S. *et al.* Inference and analysis of cell-cell communication using cellchat. *Nature Communications* **12**, (2021).