

单细胞绘图专题

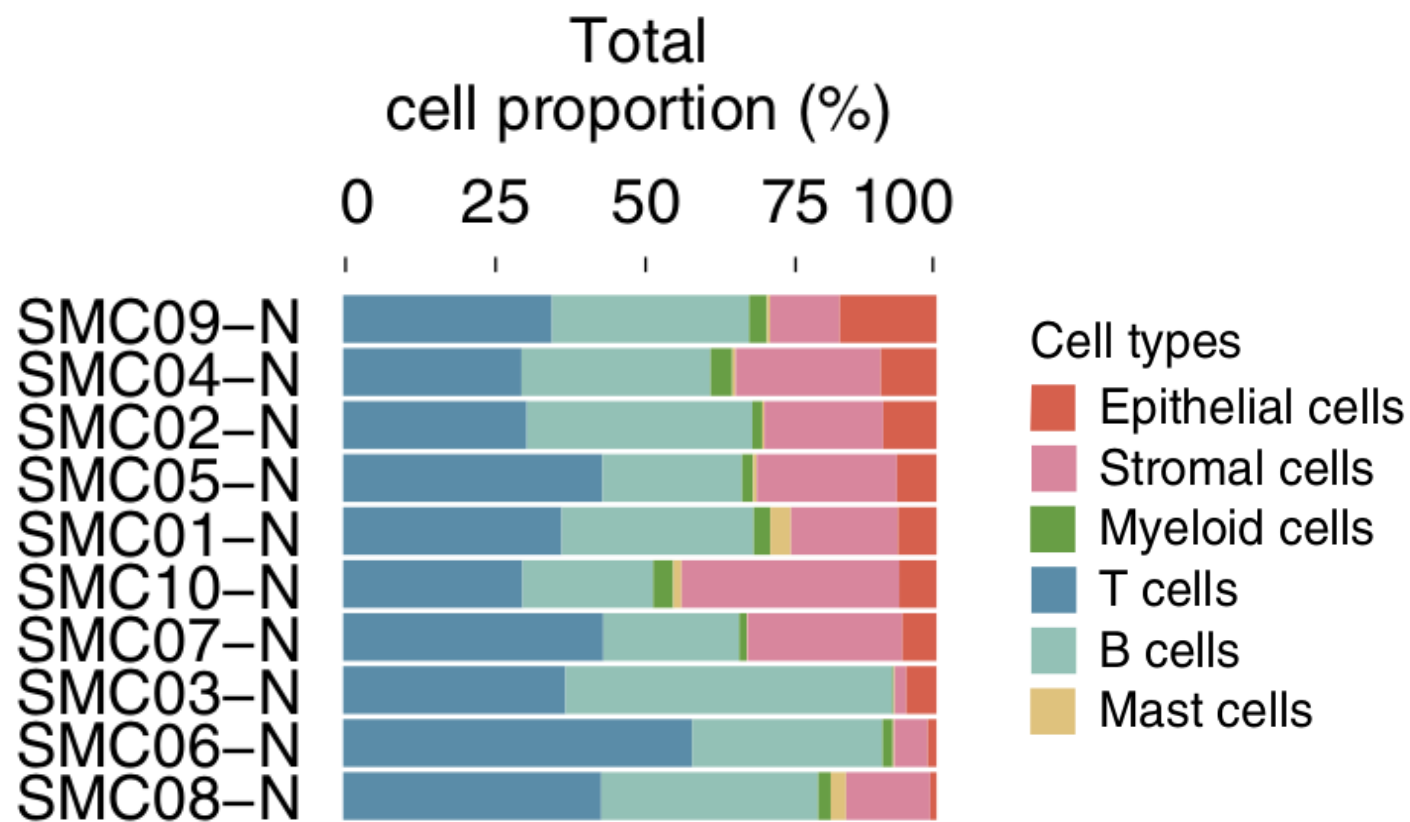
细胞比例可视化：条形图

知 @ 生信调酒师

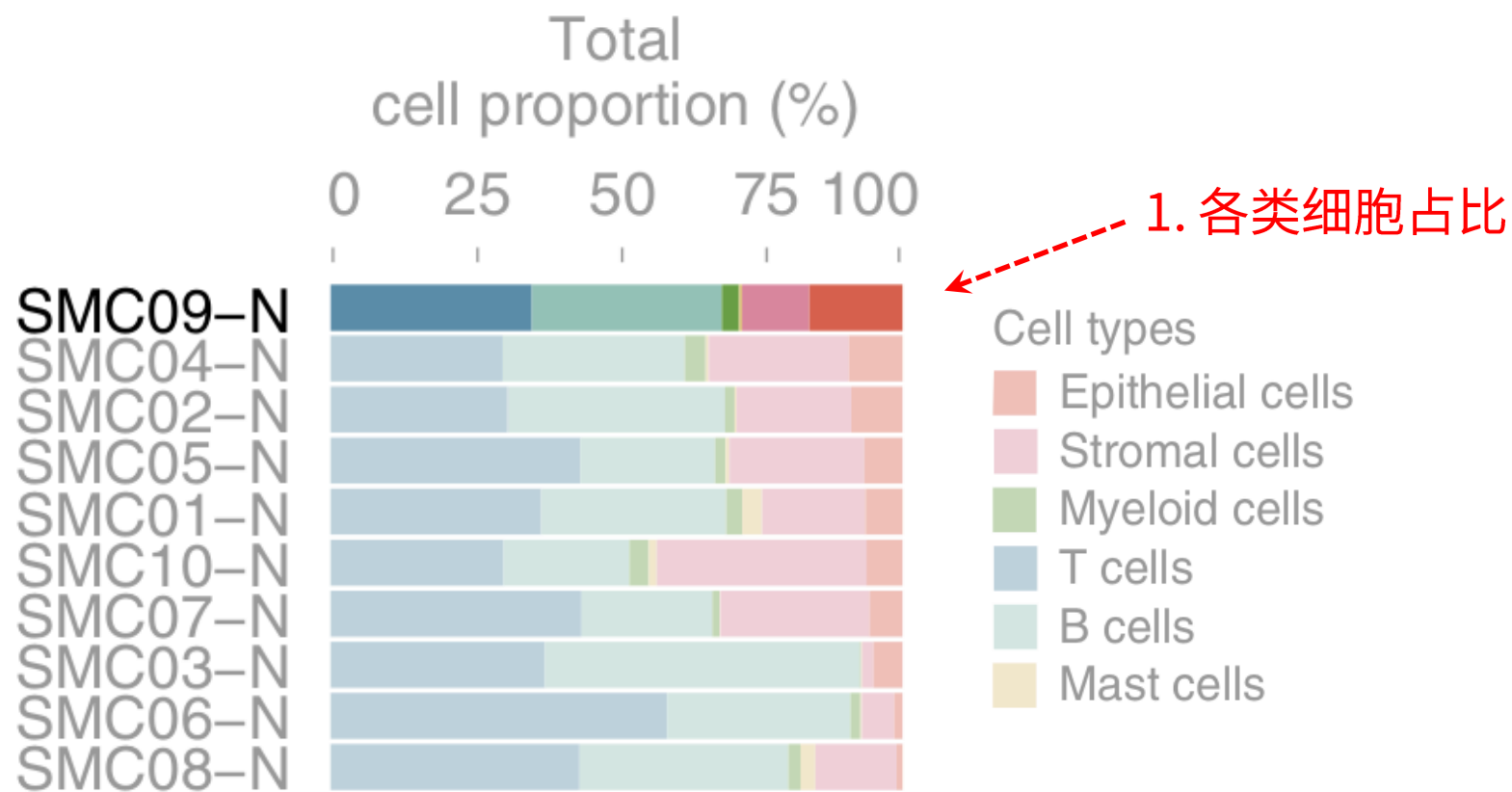
📺 @ 生信调酒师

🔄 @ Bioin-Mixologist

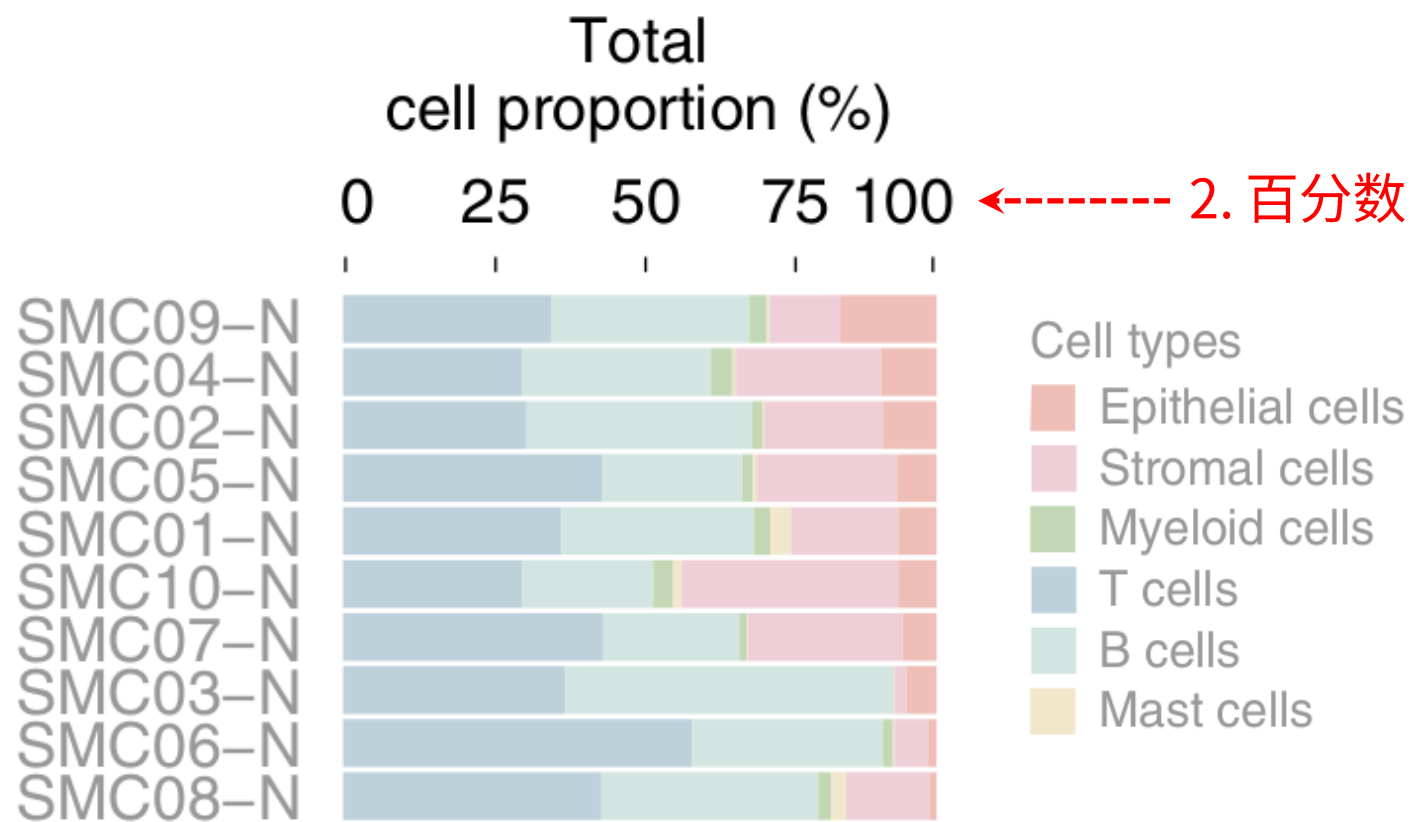
✉ BioinMixologist@163.com



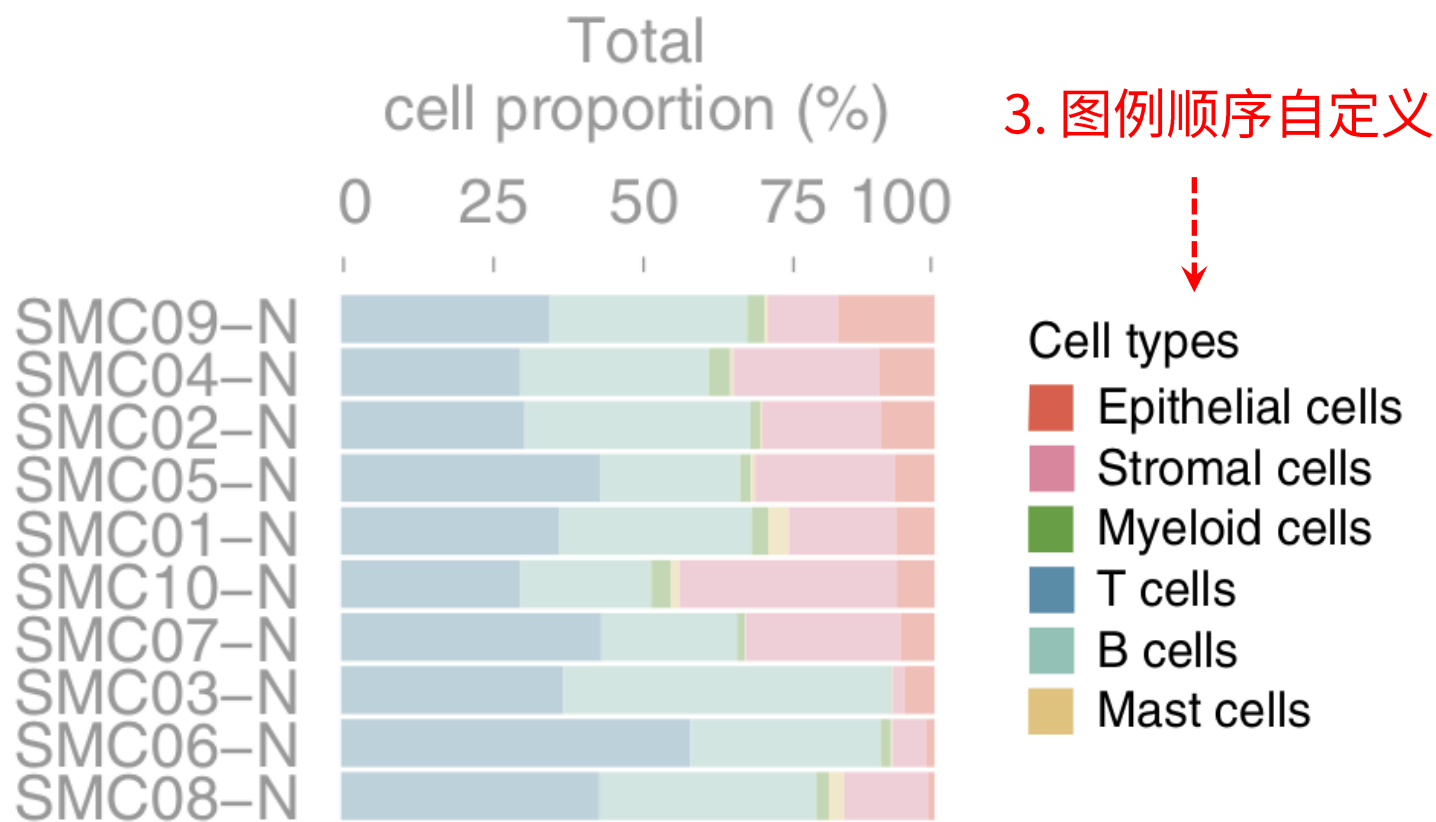
(Lee HO et al. Nat Genet. 2020)



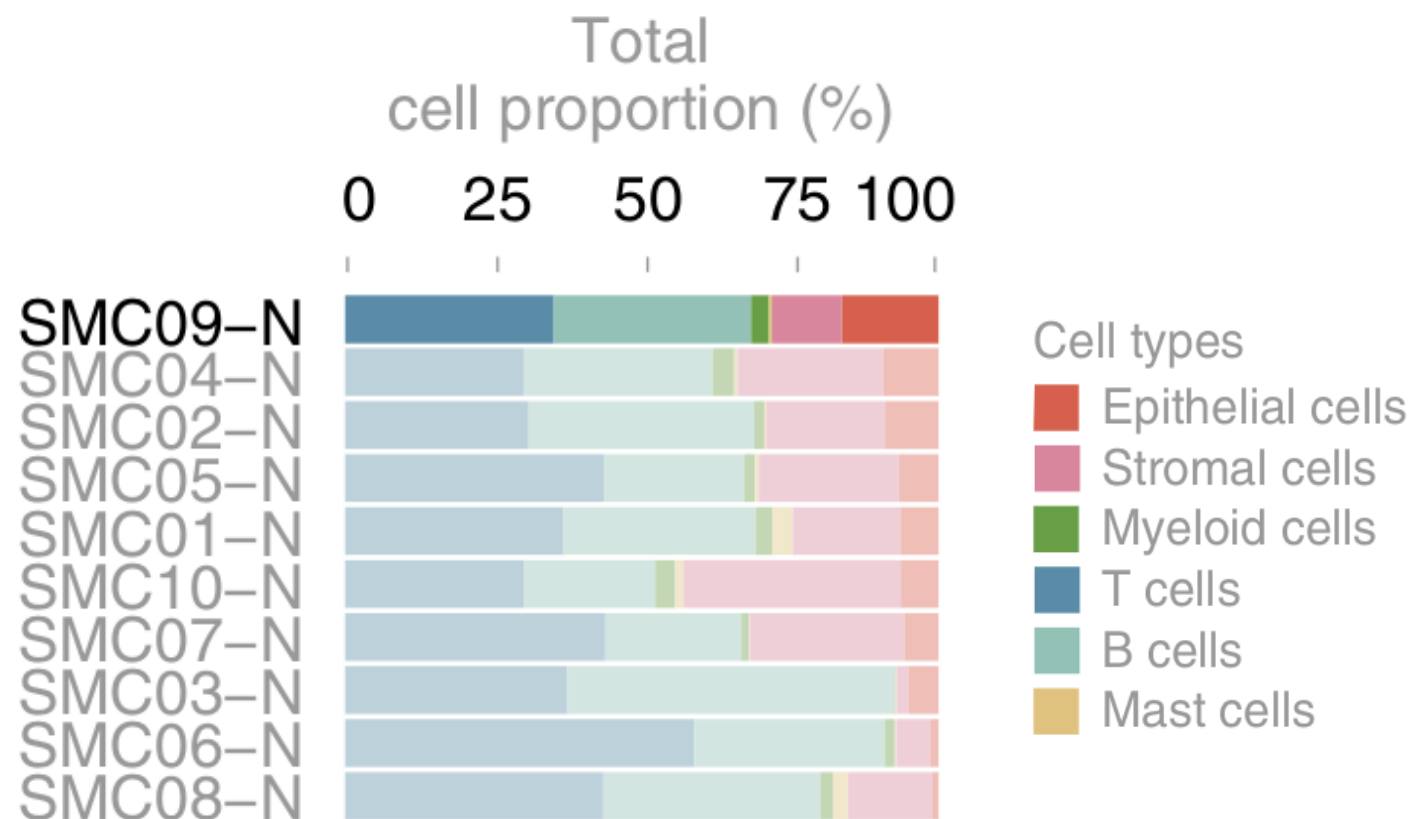
(Lee HO et al. Nat Genet. 2020)



(Lee HO et al. Nat Genet. 2020)



(Lee HO et al. Nat Genet. 2020)



(Lee HO et al. Nat Genet. 2020)

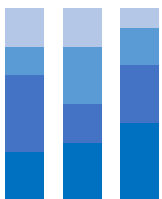
1. 各类细胞占比 → 条形堆叠图
→ 横置

2. 百分数 → 坐标轴刻度文本

3. 图例顺序自定义 → 图例顺序



```
# install.packages("ggplot2")  
library(ggplot2)
```

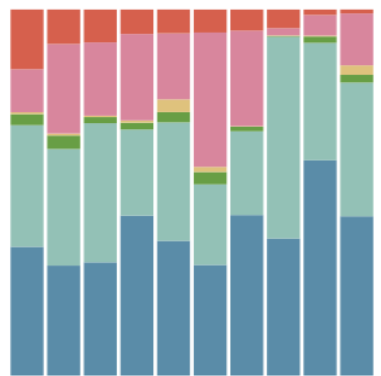


```
# s <- ggplot(mpg, aes(fl, fill = drv))  
# Stack elements on top of one another, normalize height.  
s + geom_bar(position = "fill")
```

```
head(cell_df)
```

	Celltype	Sample	Number
1	B cell	SMC13N.A1	435
2	Epithelial cell	SMC13N.A1	122
3	Mast cell	SMC13N.A1	42
4	Myeloids	SMC13N.A1	50
5	Stromal cell	SMC13N.A1	159
...

y轴为细胞数(Number)



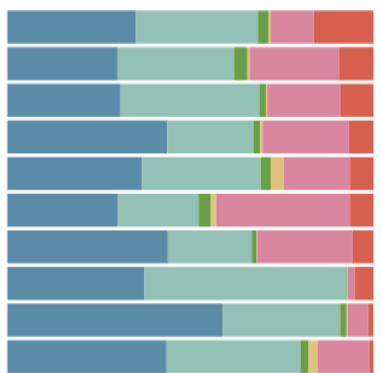
x轴为样本(Sample)

```
ggplot(data = cell_df, aes(y = Number, x = Sample, fill = Celltype)) +  
  geom_bar(stat = "identity", position = "fill")
```



条形图横置

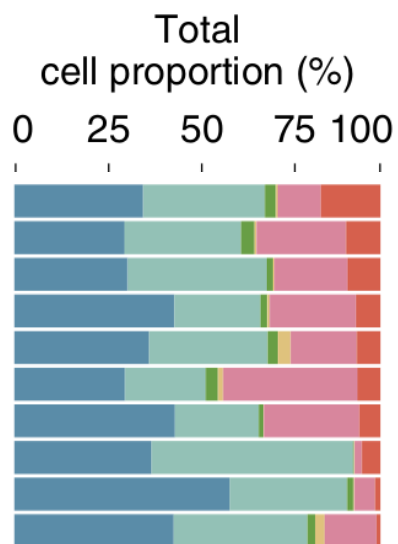
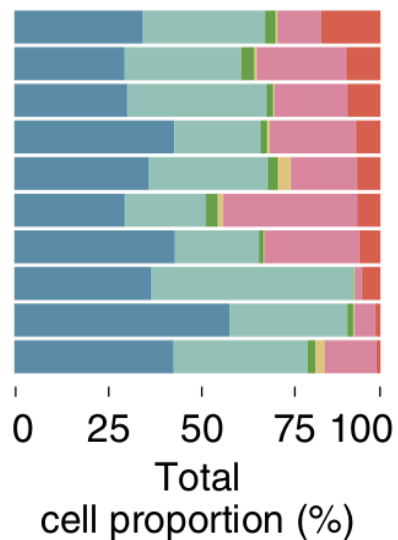
y轴为样本(Sample)



x轴为细胞数(Number)

```
ggplot(data = cell_df, aes(y = Sample, x = Number, fill = Celltype)) +  
  geom_bar(stat = "identity", position = "fill")
```

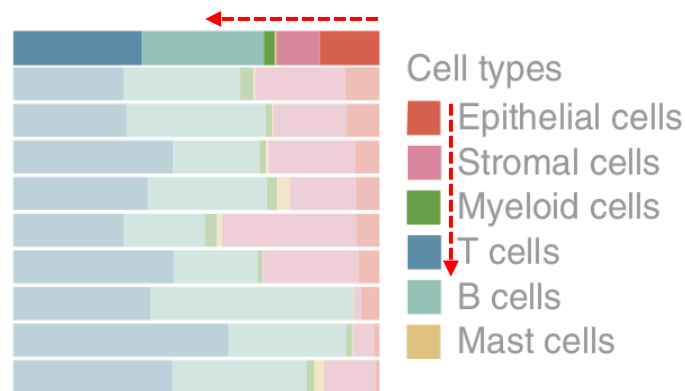
(也可以使用 + coord_flip() 代替)



```
ggplot(data = cell_df, aes(y = Sample, x = Number, fill = Celltype)) +  
  geom_bar(stat = "identity", position = "fill") +  
  labs(x = "Total cell proportion (%)", y = "") +  
  scale_x_continuous(labels = c(0, 25, 50, 75, 100))
```

↓ x轴上置

```
ggplot(data = cell_df, aes(y = Sample, x = Number, fill = Celltype)) +  
  geom_bar(stat = "identity", position = "fill") +  
  labs(x = "Total cell proportion (%)", y = "") +  
  scale_x_continuous(labels = c(0, 25, 50, 75, 100), position = "top")
```



```
cell_df$Celltype <- factor(cell_df$Celltype, levels = c("Epithelial cell", "Stromal cell", ..., "T cell"))
sample_color <- c("#d6604d", "#d8869d", ..., "#5a8ca8")
legend_order <- c("Epithelial cell", "Stromal cell", ..., "Mast cell")
```



自定义顺序

```
ggplot(data = cell_df, aes(y = Sample, x = Number, fill = Celltype)) +
  geom_bar(stat = "identity", position = "fill") +
  scale_fill_manual(values = sample_color, limits = legend_order)
labs(x="Total cell proportion (%)", y="") +
scale_x_continuous(labels = c(0,25,50,75,100))
```

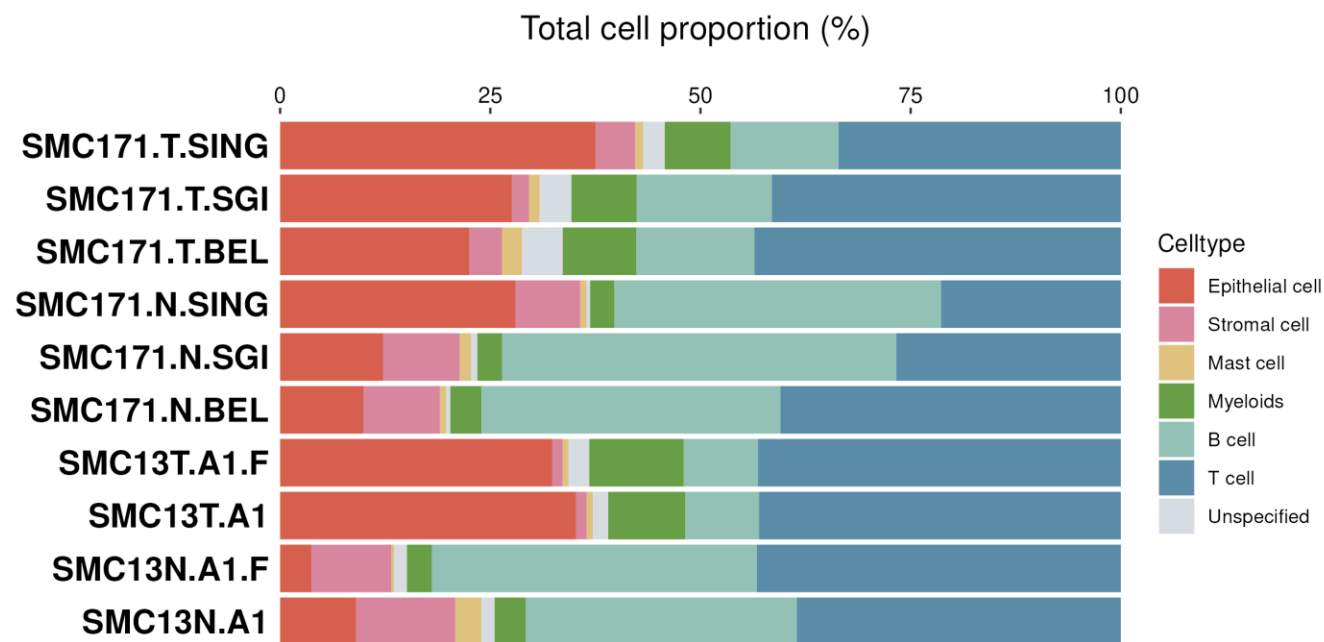
↓ 加一点点细节

```
bar_plot <- ggplot(cell_df, aes(x = Number, y = Sample, fill = Celltype)) +  
  geom_bar(stat = "identity", width = 0.9, position = position_fill(reverse = TRUE)) +  
  scale_fill_manual(values = sample_color, limits = legend_order) +  
  theme_classic() +  
  theme(panel.grid = element_blank()) +  
  labs(x="Total cell proportion (%)", y="") +  
  theme(axis.title.x = element_text(size = 15, colour = "black")) +  
  theme(axis.text.y = element_text(size = 15, colour = "black", face = "bold")) +  
  theme(axis.text.x = element_text(size = 10, colour = "black")) +  
  scale_x_continuous(labels = c(0,25,50,75,100), position = "top") +  
  theme(axis.ticks.y = element_blank()) +  
  theme(axis.line = element_blank()) +  
  theme(plot.margin = unit(c(2,2,3,2),"cm")) +  
  theme(text = element_text(family = "Helvetica"))
```

GSE132257

10 samples

7 celltypes

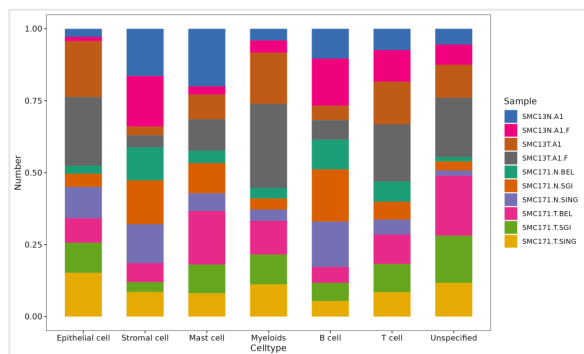


(Lee HO et al. Nat Genet. 2020)

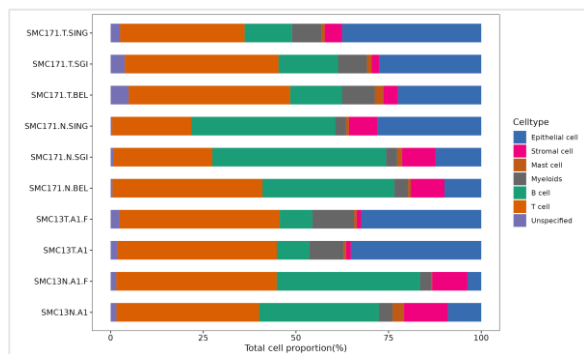
(@BioinMixologist)

1

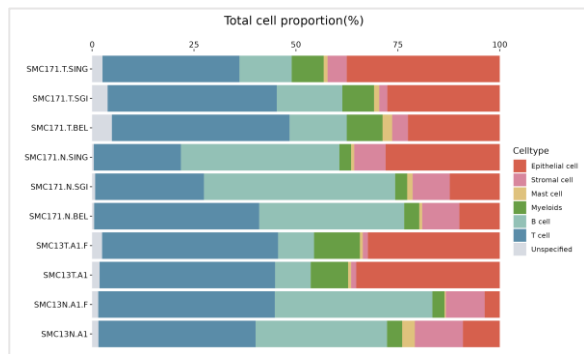
文献效果 Figure of Publication



(1.0)



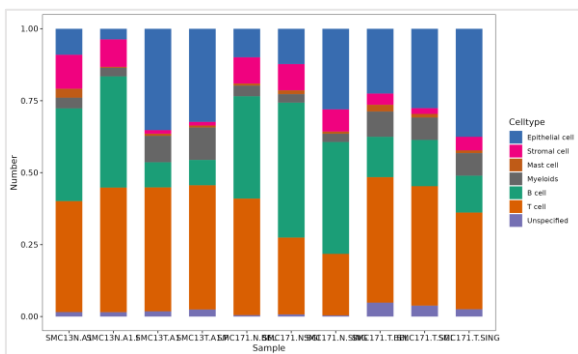
(5.0)



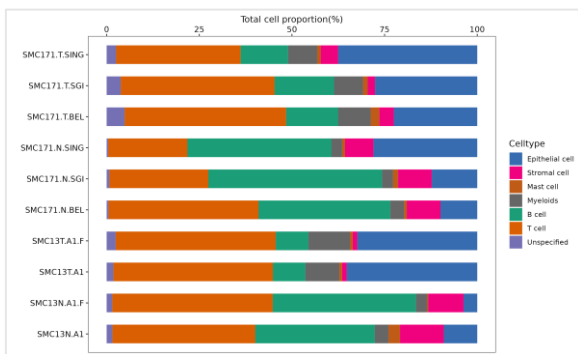
(9.0)

2

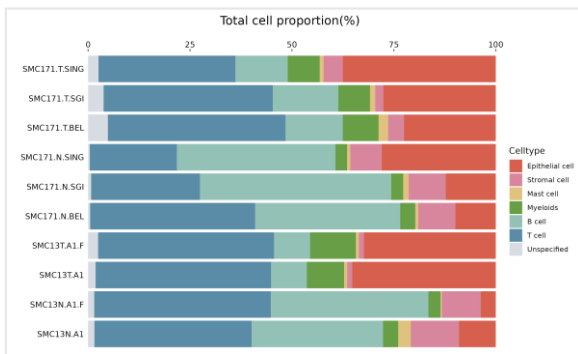
绘图函数 Plot Function



(2.0)



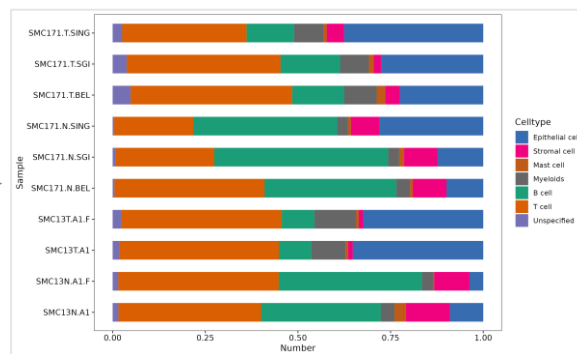
(6.0)



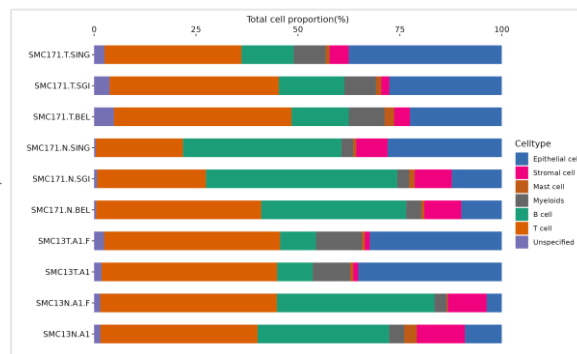
(10.0)

3

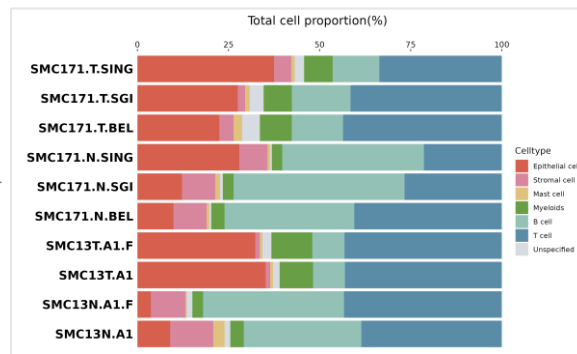
个性化展示 Personalized Modification



(3.0)



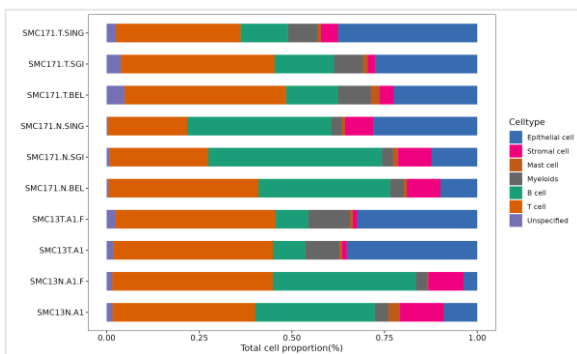
(7.0)



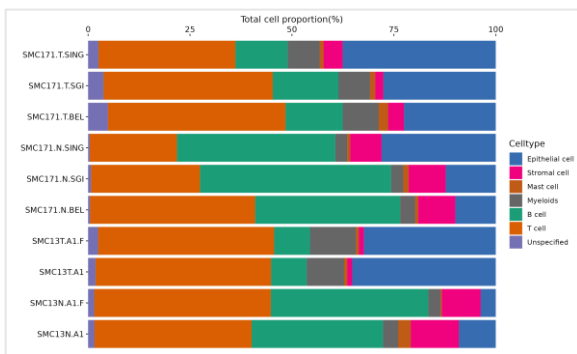
(11.0)

4

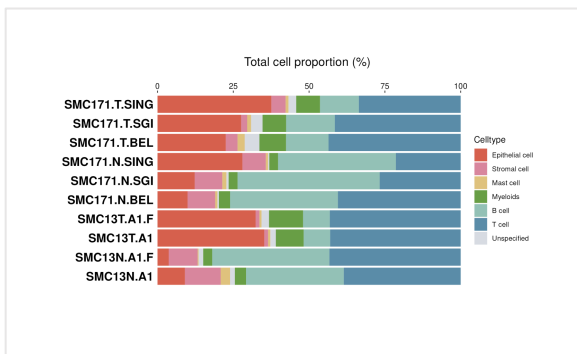
代码实操 Hands-on Lab



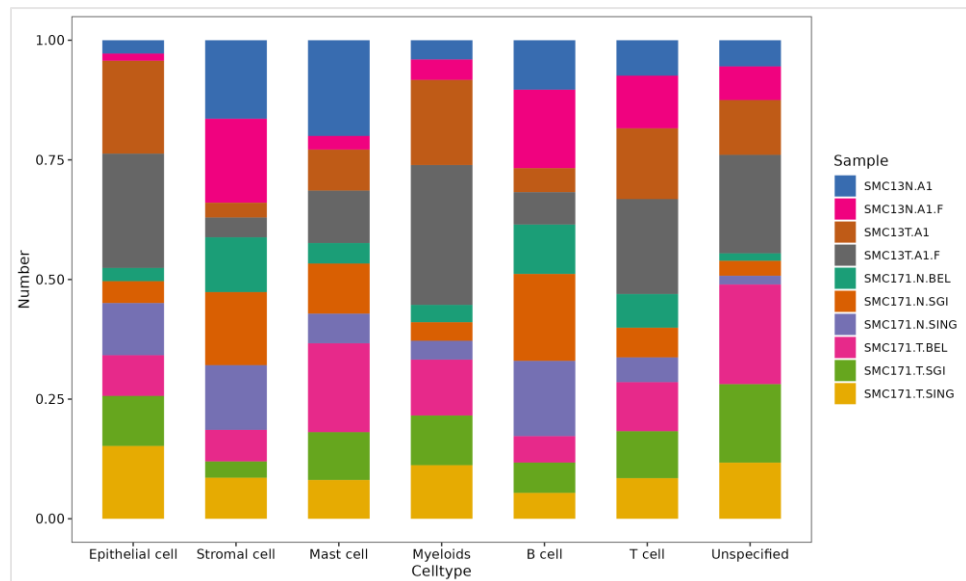
(4.0)



(8.0)

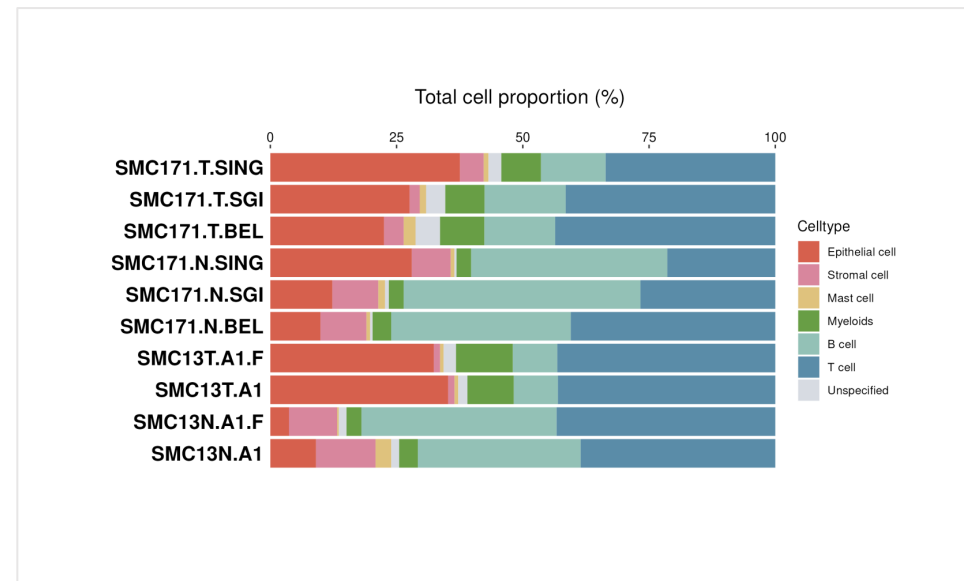


(12.0)



(1.0)

--> ... -->



(12.0)

参考资料:

- [1] H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016.
- [2] HO. Lee. et al. Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. Nat Genet, 2020.
- [3] Data visualization with ggplot2 :: Cheat Sheet. Posit Software, 2023.
<https://rstudio.github.io/cheatsheets/html/data-visualization.html>
- [4] A. Kassambara. GGPLOT2 Essentials for Great Data Visualization in R. STHDA, 2017.
<http://www.sthda.com/english/wiki/ggplot2-barplots-quick-start-guide-r-software-and-data-visualization>
- [5] 悦光阴. R绘图 第七篇:绘制条形图. 博客园, 2018. <https://www.cnblogs.com/ljhdo/p/5555858.html>

THANKS

知 @ 生信调酒师

 @ 生信调酒师

 @ Bioin-Mixologist

 BioinMixologist@163.com