

1. Non-normalized UMI counts matrices

Cellranger
Filtered .h5



or

Seurat
Objects



2. Sample information: "sample_metadata.csv"

Sample	Condition	Code
Patient1	Control	Control_1
Patient2	Control	Control_2
Patient3	DrugA	DrugA_1
Patient4	DrugA	DrugA_2
Patient5	DrugB	DrugB_1
Patient6	DrugB	DrugB_2

3. Comparison information: "comps.csv"

+ LogFC	- LogFC
c1	c2
DrugA	Control
DrugB	Control
DrugA	DrugB

4. Optional: Label transfer references

SCT-normalized
Seurat Objects



Harmonizing input gene expression matrices with sample metadata

Example Sample Metadata

Sample	Condition	Code
Patient1	Control	Control_1
Patient2	Drug	Drug_1

Example Comps

c1	c2
Drug	Control



Input option 1:
Cellranger
Filtered .h5

```
datadir/  
├── Patient1  
│   ├── outs  
│   └── filtered_feature_bc_matrix.h5  
├── Patient2  
│   ├── outs  
│   └── filtered_feature_bc_matrix.h5
```



Input option 2:
Seurat Objects

```
datadir/  
├── Patient1.rds  
└── Patient2.rds
```