

seurat__object

December 25, 2025

1 function for data uniform

```
[ ]: seurat_meta_all <- function(obj){
  if(is.null(obj@misc[['TMI']])){
    meta_now <- obj@meta.data %>% mutate_if(~!is.
↪numeric(.), ext_list) %>% .[order(.$SampleID),]
  }else{
    meta_now <- cbind(obj@meta.data,
↪obj@misc[['TMI']]) %>% mutate_if(~!is.numeric(.), ext_list) %>% .[order(
↪.$SampleID),]
  }
  return(meta_now)
}

seurat_object_uniform <- function(obj, barcode_length = 16){
  proj <- unique(obj$Cohort)
  if(is.null(obj@misc[['TMI']])){
    meta_now <- obj@meta.data %>% mutate_if(~!
↪is.numeric(.), ext_list) %>% .[order(.$SampleID),]
  }else{
    meta_now <- cbind(obj@meta.data,
↪obj@misc[['TMI']]) %>% mutate_if(~!is.numeric(.), ext_list) %>% .[order(
↪.$SampleID),]
  }
  umap_emb <- obj@reductions$umap@cell.embeddings
↪%>% .[rownames(meta_now),]
  counts <- obj@assays$RNA@counts %>% .
↪[,rownames(meta_now)]

  ## extract SampleID
  sampleIDs <- obj$SampleID
  ## generate 16nt length barcode
  generate_random_barcode <- function(n = 1,
↪length = barcode_length) {
    bases <- c("A", "T", "C", "G")
    barcodes <- sapply(1:n, function(x)
↪paste0(sample(bases, length, replace = TRUE), collapse = ""))
  }
}
```

```

        return(barcodes)
    }

    random_barcodes <- generate_random_barcode(n =
↪length(sampleIDs), length = 16)
    new_barcodes <- paste0(sampleIDs, "_",
↪random_barcodes)

    # switch the barcode
    rownames(meta_now) <- new_barcodes
    rownames(umap_emb) <- new_barcodes
    colnames(counts) <- new_barcodes

    # modify meta.data
    feature_keep <- c('Cohort', 'SampleID',
↪'SampleType', 'DonorID', 'Sex',
                                'Chemistry', 'Tissue',
                                'gCT', 'mCT', 'oCT')
    feature_common <- intersect(feature_keep,
↪names(meta_now))

    meta_now <- meta_now %>% dplyr::
↪select(feature_common)

    ## Create object for use
    obj_use <- CreateSeuratObject(counts = counts,
↪project = proj, meta.data = meta_now, min.cells = 0, min.features = 0)
    obj_use[['umap']] <-
↪CreateDimReducObject(embeddings = umap_emb)

    ## reassign gCT
    feature_keep2 <- c(feature_keep,
↪c("nCount_RNA", "nFeature_RNA"))
    obj_use@meta.data <- obj_use@meta.data %>%
                                .[,feature_keep2] %>%
                                mutate(gCT =
↪case_when((SampleType %in% c("normal", "normal_adjacent") & gCT == "Tumor")
↪~ "Normal",
                                TRUE ~ gCT))

    return(obj_use)
}

```

2 list all file (13 cancer types)

```
[ ]: objList_full <- list.files('/project/sex_cancer/data/step1_preProcess',  
  ↪recursive = T, full.names = T, pattern = 'final')  
objList_short <- list.files('/project/sex_cancer/data/step1_preProcess',  
  ↪recursive = T, full.names = F, pattern = 'final')  
objList_short  
  
[ ]: feature_keep <- c('Cohort', 'SampleID', 'SampleType', 'DonorID', 'Sex',  
  ↪'Chemistry', 'Tissue', 'gCT', 'mCT', 'oCT')
```

3 obj1: AML_Galen2019

```
[ ]: obj <- readRDS(objList_full[1])  
obj <- UpdateSeuratObject(obj)  
obj
```

3.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)  
meta_now %>% table(.$SampleType, .$gCT)  
  
# check meta.data  
list('keep' = intersect(feature_keep, names(meta_now)),  
     'miss' = setdiff(feature_keep, names(meta_now)),  
     'TMI' = setdiff(names(meta_now), feature_keep))  
  
obj_use <- seurat_object_uniform(obj, barcode_length = 12)  
obj_use  
obj_use@meta.data %>% head(n = 2)  
obj_use@meta.data %>% table(.$SampleType, .$gCT)
```

3.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)  
select <- 'umap'  
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",  
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|  
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",  
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|  
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",  
  ↪label = F, colors_use = pal_igv("default")(51))|  
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =  
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

3.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

3.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.AML_Galen2019.rds')
```

4 obj2: BLCA_Juric2025

```
[ ]: obj <- readRDS(objList_full[2])
obj <- UpdateSeuratObject(obj)
obj
```

4.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

4.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

4.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %%% table(.$SampleType, .$Sex)
obj_use@meta.data %%% table(.$SampleType)
```

4.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.BLCA_Juric2025.rds')
```

5 obj3: ccRCC_Hu2024

```
[ ]: obj <- readRDS(objList_full[3])
obj <- UpdateSeuratObject(obj)
obj
```

5.1 uniform

```
[ ]: obj@meta.data <- obj@meta.data %>% transform(Tissue = 'Kidney', Chemistry =
  ↪"10x GEX")
meta_now <- obj@meta.data
meta_now %%% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %%% table(.$SampleType, .$gCT)
```

5.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

5.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

5.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.ccRCC_Hu2024.rds')
```

6 obj4: CRC_Pelka2021

```
[ ]: obj <- readRDS(objList_full[4])
obj <- UpdateSeuratObject(obj)
obj
```

6.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))
obj@meta.data <- obj@meta.data %>% transform(Tissue = 'Colon')

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

6.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

6.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

6.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.CRC_Pelka2021.rds')
```

7 obj5: ESCA_Zhang2021

```
[ ]: obj <- readRDS(objList_full[5])
obj <- UpdateSeuratObject(obj)
obj
```

7.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))
obj@meta.data <- obj@meta.data %>% transform(Tissue = 'Esophagus', Chemistry = ↵
  ↪"10x 5'")

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

7.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT", ↵
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT", ↵
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT", ↵
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = ↵
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

7.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

7.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.ESCA_Zhang2021.rds')
```

8 obj6: FL_Han2022

```
[ ]: obj <- readRDS(objList_full[6])
obj <- UpdateSeuratObject(obj)
obj
```

8.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

8.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```


8.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

8.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.FL_Han2022.rds')
```

9 obj7: GBM_Spitzer2025

```
[ ]: obj <- readRDS(objList_full[7])
obj <- UpdateSeuratObject(obj)
obj
```

9.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))
obj@meta.data <- obj@meta.data %>% transform(Tissue = "Brain", Chemistry = "10x",
  ↪v3' v3")

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

9.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

9.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

9.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.GBM_Spitzer2025.rds')
```

10 obj8: GC_Kumar2022

```
[ ]: obj <- readRDS(objList_full[8])
obj <- UpdateSeuratObject(obj)
obj
```

10.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

# obj@meta.data <- obj@meta.data %>% transform(Tissue = 'Stomach')
obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

10.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

10.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

10.4 save for use

```
[ ]: saveRDS(obj_use, 'obj_GC_Kumar2022.rds')
```

11 obj9: HNSCC_Choi2023

```
[ ]: obj <- readRDS(objList_full[9])
obj <- UpdateSeuratObject(obj)
obj
```

11.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))
obj@meta.data <- obj@meta.data %>% transform(Tissue = "Oral cavity", Chemistry_
  ↪= "10x 3' v2")

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

11.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

11.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

11.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.HNSCC_Choi2023.rds')
```

12 obj10: LIHC_Xue2022

```
[ ]: obj <- readRDS(objList_full[10])
obj <- UpdateSeuratObject(obj)
obj
```

12.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj@meta.data <- obj@meta.data %>% transform(DonorID = SampleID, Tissue = ↪
  ↪"Liver", SampleType = 'tumor')

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

12.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT", ↪
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT", ↪
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT", ↪
  ↪label = F, colors_use = pal_igv("default")(51))|
```

```
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

12.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

12.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.LIHC_Xue2022.rds')
```

13 obj11: NSCLC_Salcher2022

```
[ ]: obj <- readRDS(objList_full[11])
obj <- UpdateSeuratObject(obj)
obj
```

13.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj@meta.data <- obj@meta.data %>% transform(Tissue = 'Lung')

obj_use <- seurat_object_uniform(obj, barcode_length = 17)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

13.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
```

```
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

13.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪.$SampleID),] %>% table(.$SampleType, .$Sex)
obj_use@meta.data %>% table(.$SampleType)
```

13.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.NSCLC_Salcher2022.rds')
```

14 obj12: PDAC_Hwang2022

```
[ ]: obj <- readRDS(objList_full[12])
obj <- UpdateSeuratObject(obj)
obj
```

14.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %>% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
     'miss' = setdiff(feature_keep, names(meta_now)),
     'TMI' = setdiff(names(meta_now), feature_keep))

obj@meta.data <- obj@meta.data %>% transform(DonorID = SampleID, Tissue =
  ↪"Pancreas")

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %>% table(.$SampleType, .$gCT)
```

14.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
select <- 'umap'
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
  ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
```

```
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
  ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
  ↪label = F, colors_use = pal_igv("default")(51))|
DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
  ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

14.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(
  ↪$SampleID),] %$% table(.$SampleType, .$Sex)
obj_use@meta.data %$% table(.$SampleType)
```

14.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.PDAC_Hwang2022.rds')
```

15 obj13: THCA_Pu2021

```
[ ]: obj <- readRDS(objList_full[13])
obj <- UpdateSeuratObject(obj)
obj
```

15.1 uniform

```
[ ]: meta_now <- seurat_meta_all(obj)
meta_now %$% table(.$SampleType, .$gCT)

# check meta.data
list('keep' = intersect(feature_keep, names(meta_now)),
  'miss' = setdiff(feature_keep, names(meta_now)),
  'TMI' = setdiff(names(meta_now), feature_keep))

obj@meta.data <- obj@meta.data %>% transform(Tissue = "Thyroid", Chemistry =
  ↪"10x v3")

obj_use <- seurat_object_uniform(obj, barcode_length = 16)
obj_use
obj_use@meta.data %>% head(n = 2)
obj_use@meta.data %$% table(.$SampleType, .$gCT)
```

15.2 UMAP

```
[ ]: options(repr.plot.height = 4, repr.plot.width = 30)
      select <- 'umap'
      DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "gCT",
        ↪label = T, label.size = 6, colors_use = pal_igv("default")(51))|
      DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "mCT",
        ↪label = F, label.size = 6, colors_use = pal_igv("default")(51))|
      DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by = "oCT",
        ↪label = F, colors_use = pal_igv("default")(51))|
      DimPlot_scCustom(obj_use, reduction = select, pt.size = 1, group.by =
        ↪"SampleType", label = F, label.size = 8, colors_use = pal_igv("default")(51))
```

15.3 Statistics

```
[ ]: obj_use@meta.data[,c('SampleID', 'SampleType', 'Sex')] %>% .[!duplicated(.
      ↪.$SampleID),] %$% table(.$SampleType, .$Sex)
      obj_use@meta.data %$% table(.$SampleType)
```

15.4 save for use

```
[ ]: saveRDS(obj_use, 'obj.THCA_Pu2021.rds')
```