

## Azizi 2018 metadata

```
globus_metadata <- readRDS("/mnt/nmoraais-nfs/marta/pC_myefinfobank/metadata/globus/processed/GSE114724_Azizi2018_metadata.rds")
globus_metadata

## Loading required package: SeuratObject
## Loading required package: sp
## An object of class Seurat
## 12908 features across 26947 samples within 1 assay
## Active assay: RNA (12908 features, 0 variable features)
colnames(globus_metadata)[1:5]

## [1] "s1_AAACCTGAGCAGACTG-1" "s1_AAACCTGAGGTCGGAT-1" "s1_AAACCTGAGTGTACCT-1"
## [4] "s1_AAACCTGAGTGTACTC-1" "s1_AAACCTGCAACACCCG-1"
colnames(globus_metadata@meta.data)

## [1] "patient" "batch" "condition" "sex" "cell_type" "tissue"
table(globus_metadata$patient)

##
## BC10 BC11 BC9
## 4580 9360 13007
table(globus_metadata$batch)

##
## GSE114724-BC10-s3 GSE114724-BC11-s4 GSE114724-BC11-s5 GSE114724-BC9-s1
## 4580 5031 4329 6553
## GSE114724-BC9-s2
## 6454
table(globus_metadata$condition)

##
## tumor_unknown
## 26947
table(globus_metadata$sex)

##
## female
## 26947
table(globus_metadata$tissue)

##
## breast
## 26947
```

```

metadata <- data.frame(Cell_ID = colnames(globus_metadata),
                        Patient = globus_metadata$patient,
                        Sample = globus_metadata$batch)
rownames(metadata) <- NULL

```

```

metadata$Sample_Type <- "Fresh"
metadata$Protocol <- "10X_chromium_5'"
metadata$Technology <- "10X_Genomics"
metadata$Dissociation <- "Mechanical,Enzymatic"
metadata$CellOrNucleus <- "Cell"
metadata$Sequencing_Machine <- "Illumina_NextSeq_500"
metadata$Preprocessing <- "CellRanger_v.2.1.1"
metadata$Reference_Genome <- "GRCh38"
metadata$Gender <- "Female"
metadata$Race <- NA
metadata$Menopause <- "Post"
metadata$Parity <- NA
metadata$Tissue <- "Tumour"
metadata$Treatment_Status <- NA
metadata$Treatment_Type <- NA

```

```

metadata$Age <- metadata$Patient
metadata$Age[metadata$Age == "BC9"] <- 65
metadata$Age[metadata$Age == "BC10"] <- 73
metadata$Age[metadata$Age == "BC11"] <- 50

```

```

metadata$Subtype <- metadata$Patient
metadata$Subtype[metadata$Subtype == "BC9"] <- "ER+"
metadata$Subtype[metadata$Subtype == "BC10"] <- "TNBC"
metadata$Subtype[metadata$Subtype == "BC11"] <- "HER2+"

```

```

metadata$Grade <- metadata$Patient
metadata$Grade[metadata$Grade == "BC9"] <- 2
metadata$Grade[metadata$Grade == "BC10"] <- 3
metadata$Grade[metadata$Grade == "BC11"] <- 3

```

```

metadata$Cancer_Type <- metadata$Patient
metadata$Cancer_Type[metadata$Cancer_Type == "BC9"] <- "ILC"
metadata$Cancer_Type[metadata$Cancer_Type == "BC10"] <- "IDC"
metadata$Cancer_Type[metadata$Cancer_Type == "BC11"] <- "IDC"

```

```

metadata[1:5,]

```

##	Cell_ID	Patient	Sample	Sample_Type	Protocol
## 1	s1_AAACCTGAGCAGACTG-1	BC9	GSE114724-BC9-s1	Fresh	10X_chromium_5'
## 2	s1_AAACCTGAGGTCGGAT-1	BC9	GSE114724-BC9-s1	Fresh	10X_chromium_5'
## 3	s1_AAACCTGAGTGTACCT-1	BC9	GSE114724-BC9-s1	Fresh	10X_chromium_5'
## 4	s1_AAACCTGAGTGTACTC-1	BC9	GSE114724-BC9-s1	Fresh	10X_chromium_5'
## 5	s1_AAACCTGCAACACCCG-1	BC9	GSE114724-BC9-s1	Fresh	10X_chromium_5'
##	Technology	Dissociation	CellOrNucleus	Sequencing_Machine	
## 1	10X_Genomics	Mechanical,Enzymatic	Cell	Illumina_NextSeq_500	
## 2	10X_Genomics	Mechanical,Enzymatic	Cell	Illumina_NextSeq_500	
## 3	10X_Genomics	Mechanical,Enzymatic	Cell	Illumina_NextSeq_500	
## 4	10X_Genomics	Mechanical,Enzymatic	Cell	Illumina_NextSeq_500	
## 5	10X_Genomics	Mechanical,Enzymatic	Cell	Illumina_NextSeq_500	

```
##      Preprocessing Reference_Genome Gender Race Menopause Parity Tissue
## 1 CellRanger_v.2.1.1      GRCh38 Female  NA      Post      NA Tumour
## 2 CellRanger_v.2.1.1      GRCh38 Female  NA      Post      NA Tumour
## 3 CellRanger_v.2.1.1      GRCh38 Female  NA      Post      NA Tumour
## 4 CellRanger_v.2.1.1      GRCh38 Female  NA      Post      NA Tumour
## 5 CellRanger_v.2.1.1      GRCh38 Female  NA      Post      NA Tumour
##      Treatment_Status Treatment_Type Age Subtype Grade Cancer_Type
## 1      NA              NA      65      ER+      2      ILC
## 2      NA              NA      65      ER+      2      ILC
## 3      NA              NA      65      ER+      2      ILC
## 4      NA              NA      65      ER+      2      ILC
## 5      NA              NA      65      ER+      2      ILC
```

```
#saveRDS(metadata, "azizi-2018-clinical-metadata.rds")
```