```
> library(CellCODE)
> library(RColorBrewer)
```

1   Vaccine Dataset

Load the data and experimantal factors from vaccine dataset (GSE29619) and
pure cell dataset (IRIS). The GSE29619 has been normalized and filtered for
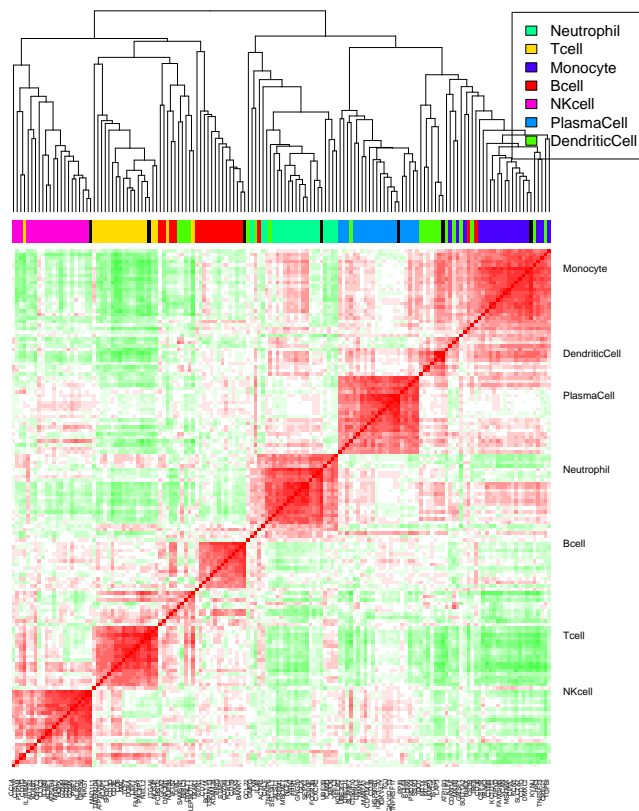low expression.

```
> data("GSE29619")
> data("GSE29619facts")
> data("IRIS")
```

Make a cell type tag matrix using the IRIS dataset. This is PBMC data so we
are only using IRIS.

```
> irisTag=tagData(IRIS[,c("Neutrophil-Resting","CD4Tcell-N0",
+                         "Monocyte-Day0", "Bcell-naïve",
+                         "NKcell-control", "PlasmaCell-FromPBMC", "DendriticCell-LPSstimula
+                ref=GSE29619, ref.mean=F);
> colnames(irisTag)=c("Neutrophil","Tcell", "Monocyte",
+                     "Bcell", "NKcell", "PlasmaCell", "DendriticCell" )
>
```
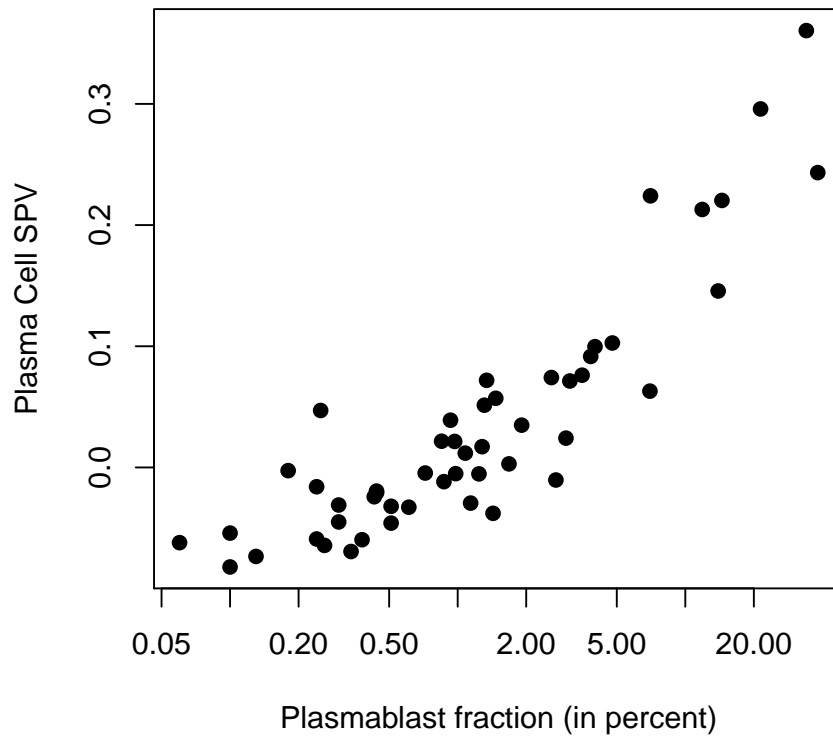
   Estimate proportions using the tag genes

```
> SPVs=getAllSPVs(GSE29619, paste(GSE29619.facts[,"vaccine"], GSE29619.facts[,"time"]), iris
```

1

Plot proportion variables against Flow Cytometry counter measurements

```
> #load the FCM data
> data("fcm")
> ii7v=which(GSE29619.facts[,3]=="D7")
> plot(fcm[ii7v,3], SPVs[ii7v,6], log="x", ylab="Plasma Cell SPV", xlab="Plasmablast fractio
>
```

2 Proportion changes

Get relative changes by normalizing for subject identity

```
> SPVsR=t(resid(t(SPVs), model.matrix(~0+as.factor(GSE29619.facts[,2]))))

> par(mfrow=c(2,3), mai=c(1,0.4,0.4,0.1), omi=rep(0,4))
> for ( i in c(2:7)){
+   boxplot(SPVsR[,i]~as.factor(paste(GSE29619.facts[,4],GSE29619.facts[,3])), outline=F, de
+   title(colnames(irisTag)[i])
+ }
>
```