Here is a step by step guide for preparing the K-Means algorithm for submission to flowCAP using the R scripting language:

```
#Parse the CSV file
cells=read.csv('GvHD/CSV/001.csv')
#Use kmeans to find 4 populations
km=kmeans(cells,4)
#Make the output folder
system('mkdir GvHD/Output')
#Write the output file
write.csv(km$clusters, col.names=FALSE, row.names=FALSE,
paste("GvHD/Output/", sprintf("%.3d", 1), ".csv", sep=""));
Now, the R script needs to accept input parameters from the shell script:
args=(commandArgs(TRUE))
print(args)
if(length(args) == 0) \{
      stop("No arguments supplied.")
else{
      if(length(args)==2){
                    stop("The kmeans algorithm requires the number
                    of populations to be pre-identified")
      InputFolder=args[[1]];
      OutputFolder=args[[2]];
      n=as.numeric(args[[3]]);
system(paste('mkdir ', OutputFolder, sep="))
ListOfFiles=dir(paste(InputFolder, '/CSV', sep="))
for (i in ListOfFiles){
      cells=read.csv(paste(InputFolder, '/CSV/', i, sep="))
      km=kmeans(cells,n)
      write.csv(km$cluster, col.names=FALSE, row.names=FALSE,
      paste(OutputFolder, '/', i, sep=""));
}
```

Assuming that the script above is saved in *flowcap-kmeans.R*, the following shell script (*flowcap-kmeans.sh*)can be used to run it:

Rscript flowcap-kmeans.r \$1 \$2 \$3

Finally, flowcap organizers can run the code in a unix shell:

./flowcap-kmeans.sh GvHD GvHD/Output $10\,$