

# MM2S: a package for Medulloblastoma Subtype Predictions

Deena M.A. Gendoo<sup>\*1</sup> and Benjamin Haibe-Kains<sup>†1</sup>

<sup>1</sup>Bioinformatics and Computational Genomics Laboratory, Princess Margaret Cancer Center,  
University Health Network, Toronto, Ontario, Canada

<sup>2</sup>Medical Biophysics Department, University of Toronto, Toronto, Ontario, Canada

November 2, 2015

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Loading package for case studies</b>	<b>2</b>
<b>3</b>	<b>Case Study 1: Predicting Human Subtype Counterparts for Mouse Models</b>	<b>3</b>
<b>4</b>	<b>Case Study 2: Predict Human Subtypes for Primary Patient Samples</b>	<b>11</b>
<b>5</b>	<b>References and Extra Notes</b>	<b>17</b>
<b>6</b>	<b>License</b>	<b>17</b>
<b>7</b>	<b>Session Info</b>	<b>17</b>

## 1 Introduction

The MM2S package is providing relevant functions for subtype prediction of Medulloblastoma primary samples, mouse models, and cell lines.

MM2S is single-sample classifier that generates Medulloblastoma (MB) subtype predictions for single-samples of human MB patients and model systems, including cell lines and mouse-models. The MM2S algorithm uses a systems-based methodology that facilitates application of the algorithm on samples irrespective of their platform or source of origin. MM2S demonstrates >96 percent accuracy for patients of well-characterized normal cerebellum, WNT, or SHH subtypes, and the less-characterized Group4 (86 percent) and Group3 (78.2 percent). MM2S also enables classification of MB cell lines and mouse models into their human counterparts. This package contains function for implementing the classifier onto human data and mouse data, as well as graphical rendering of the results as PCA plots and heatmaps.

Please refer to the manuscript URL: <http://www.sciencedirect.com/science/article/pii/S0888754315000774>

Please also refer to the References section for additional information on downloading the MM2S package from Github, or running the MM2S server from the Lab website.

---

<sup>\*</sup>deena.gendoo@utoronto.ca

<sup>†</sup>benjamin.haibe.kains@utoronto.ca

## 2 Loading package for case studies

First we load the MM2S and MM2Sdata packages into the workspace. Both packages are publicly available and can be installed from Bioconductor version 2.8 or higher in R version 2.13.0 or higher.

The MM2Sdata package contains companion datasets that will be used for the examples in the following case studies. The MM2Sdata package contains ExpressionSet objects of both Human and Mouse model Medulloblastoma, specifically:

GSE36594expr: Gene expression for 20 GTML Medulloblastoma mouse samples.

GSE37418Expr: Gene expression for 10 primary Medulloblastoma human samples

Please consult the manual of the MM2Sdata package for more details.

```
#install.packages("MM2S", repos="http://cran.r-project.org")
library(MM2S)

## Loading required package: GSVA
## Loading required package: kknn
## Loading required package: parallel
## Loading required package: lattice
## Loading required package: pheatmap

#install.packages("MM2Sdata", repos="http://cran.r-project.org")
library(MM2Sdata)

## Loading required package: Biobase
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
##
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
##
## The following object is masked from 'package:stats':
##
##   xtabs
##
## The following objects are masked from 'package:base':
##
##   Filter, Find, Map, Position, Reduce, anyDuplicated, append,
##   as.data.frame, as.vector, cbind, colnames, do.call,
##   duplicated, eval, evalq, get, intersect, is.unsorted, lapply,
##   mapply, match, mget, order, paste, pmax, pmax.int, pmin,
##   pmin.int, rank, rbind, rep.int, rownames, sapply, setdiff,
##   sort, table, tapply, union, unique, unlist, unsplit
##
## Welcome to Bioconductor
##
## Vignettes contain introductory material; view with
## 'browseVignettes()'. To cite Bioconductor, see
## 'citation("Biobase")', and for packages 'citation("pkgname")'.
```

### 3 Case Study 1: Predicting Human Subtype Counterparts for Mouse Models

We first load the Mouse model dataset from GSE36594. We select all samples pertaining to the GTML mouse model. There are 20 sample replicates for this mouse model, all of which are labelled as GTML in the GEO series. We select for those samples and perform MM2S predictions on them.

```
data(GSE36594Expr)
ExprMat<-exprs(GSE36594Expr)
GTML<-ExprMat[,grep("GTML_MB", (colnames(exprs(GSE36594Expr))))]

#Change mouse sample names for clarity
for(sample in 1:ncol(GTML))
{
  newnames<-strsplit(x=(colnames(GTML)[sample]),split="_")[[1]][1]
  colnames(GTML)[sample]<-newnames
}

# Conduct Subtype Predictions for those particular replicates, save results in a XLS file
GTMLPreds<-MM2S.mouse(InputMatrix=GTML,xls_output=TRUE,parallelize=1)

## There are 634 common genesets between Human MB and the Test Data.
## Of these, 106 feature-selected genesets are being used for classification
##
##
## OUTPUT OF MM2S:
```

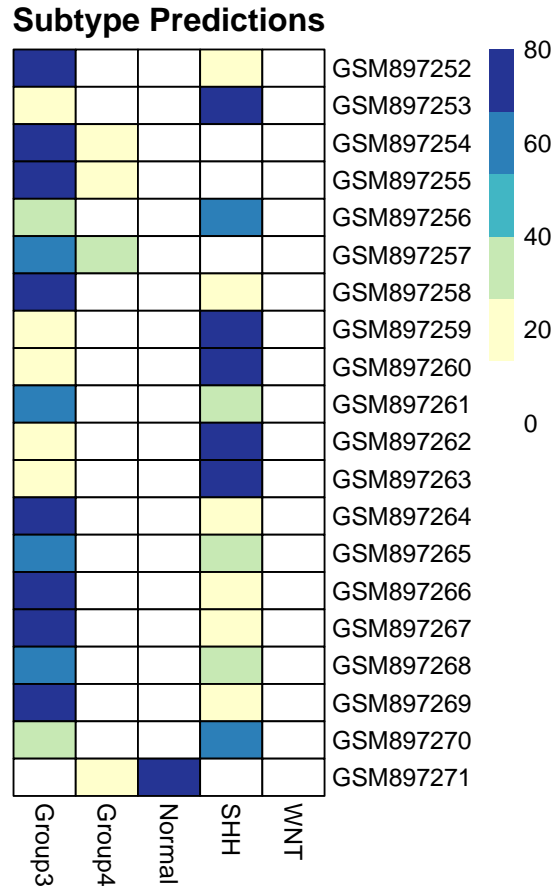
##	SampleName	MM2S_Prediction	Gr3_Confidence	Gr4_Confidence
##	[1,] GSM897252	Group3	80	0
##	[2,] GSM897253	SHH	20	0
##	[3,] GSM897254	Group3	80	20
##	[4,] GSM897255	Group3	80	20
##	[5,] GSM897256	SHH	40	0
##	[6,] GSM897257	Group3	60	40
##	[7,] GSM897258	Group3	80	0
##	[8,] GSM897259	SHH	20	0
##	[9,] GSM897260	SHH	20	0
##	[10,] GSM897261	Group3	60	0
##	[11,] GSM897262	SHH	20	0
##	[12,] GSM897263	SHH	20	0
##	[13,] GSM897264	Group3	80	0
##	[14,] GSM897265	Group3	60	0
##	[15,] GSM897266	Group3	80	0
##	[16,] GSM897267	Group3	80	0
##	[17,] GSM897268	Group3	60	0
##	[18,] GSM897269	Group3	80	0
##	[19,] GSM897270	SHH	40	0
##	[20,] GSM897271	NORMAL	0	20

##	Normal_Confidence	SHH_Confidence	WNT_Confidence	Neighbor1	Neighbor2
##	[1,] 0	20	0	SHH	Group3
##	[2,] 0	80	0	SHH	SHH
##	[3,] 0	0	0	Group3	Group4
##	[4,] 0	0	0	Group3	Group3
##	[5,] 0	60	0	Group3	SHH

```
## [6,] 0 0 0 Group3 Group4
## [7,] 0 20 0 Group3 SHH
## [8,] 0 80 0 SHH SHH
## [9,] 0 80 0 SHH SHH
## [10,] 0 40 0 Group3 SHH
## [11,] 0 80 0 SHH SHH
## [12,] 0 80 0 SHH Group3
## [13,] 0 20 0 Group3 Group3
## [14,] 0 40 0 Group3 Group3
## [15,] 0 20 0 Group3 Group3
## [16,] 0 20 0 Group3 SHH
## [17,] 0 40 0 Group3 SHH
## [18,] 0 20 0 SHH Group3
## [19,] 0 60 0 SHH SHH
## [20,] 80 0 0 NORMAL Group4
## Neighbor3 Neighbor4 Neighbor5
## [1,] Group3 Group3 Group3
## [2,] SHH SHH Group3
## [3,] Group3 Group3 Group3
## [4,] Group3 Group3 Group4
## [5,] SHH Group3 SHH
## [6,] Group3 Group3 Group4
## [7,] Group3 Group3 Group3
## [8,] Group3 SHH SHH
## [9,] SHH SHH Group3
## [10,] Group3 SHH Group3
## [11,] SHH Group3 SHH
## [12,] SHH SHH SHH
## [13,] SHH Group3 Group3
## [14,] SHH SHH Group3
## [15,] SHH Group3 Group3
## [16,] Group3 Group3 Group3
## [17,] Group3 Group3 SHH
## [18,] Group3 Group3 Group3
## [19,] SHH Group3 Group3
## [20,] NORMAL NORMAL NORMAL
```

Now we can view the predictions for the GTML sample replicates in more detail. We first generate heatmap of MM2S confidence predictions for each sample replicate.

```
# Now generate a heatmap of the predictions and save the results in a PDF file.
# This indicates MM2S confidence predictions for each sample replicate of the GTML model.
# We view the samples here.
PredictionsHeatmap(InputMatrix=GTMLPreds$Predictions[1:20,],pdf_output=TRUE,pdfheight=12,pdfwidth=10)
```



*# NB: Output may appear on multiple pages*

We can also represent the results as a stacked barplot.

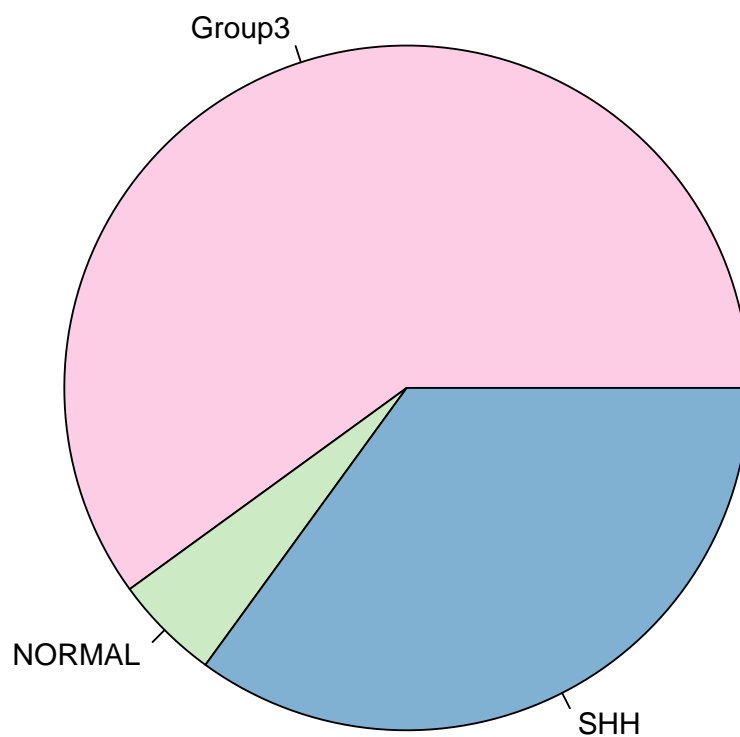
```
# To run the function all the GTML sample replicates, please run:
# PredictionsBarplot(InputMatrix=GTMLPreds$Predictions[1:20,],pdf_output=TRUE,pdfheight=5,pdfwidth=12)
# NB: Output may appear on multiple pages
```

Using the heatmap or the stacked barplot, we observe that the majority of sample replicates strongly predict as Group3, suggesting the potential for a non-SHH mouse model.

We generate here an overview of the majority subtypes, across all sample replicates. To do this we generate a pie chart of all the predictions.

```
PredictionsDistributionPie(InputMatrix=GTMLPreds,pdf_output=TRUE,pdfheight=5,pdfwidth=5)
```

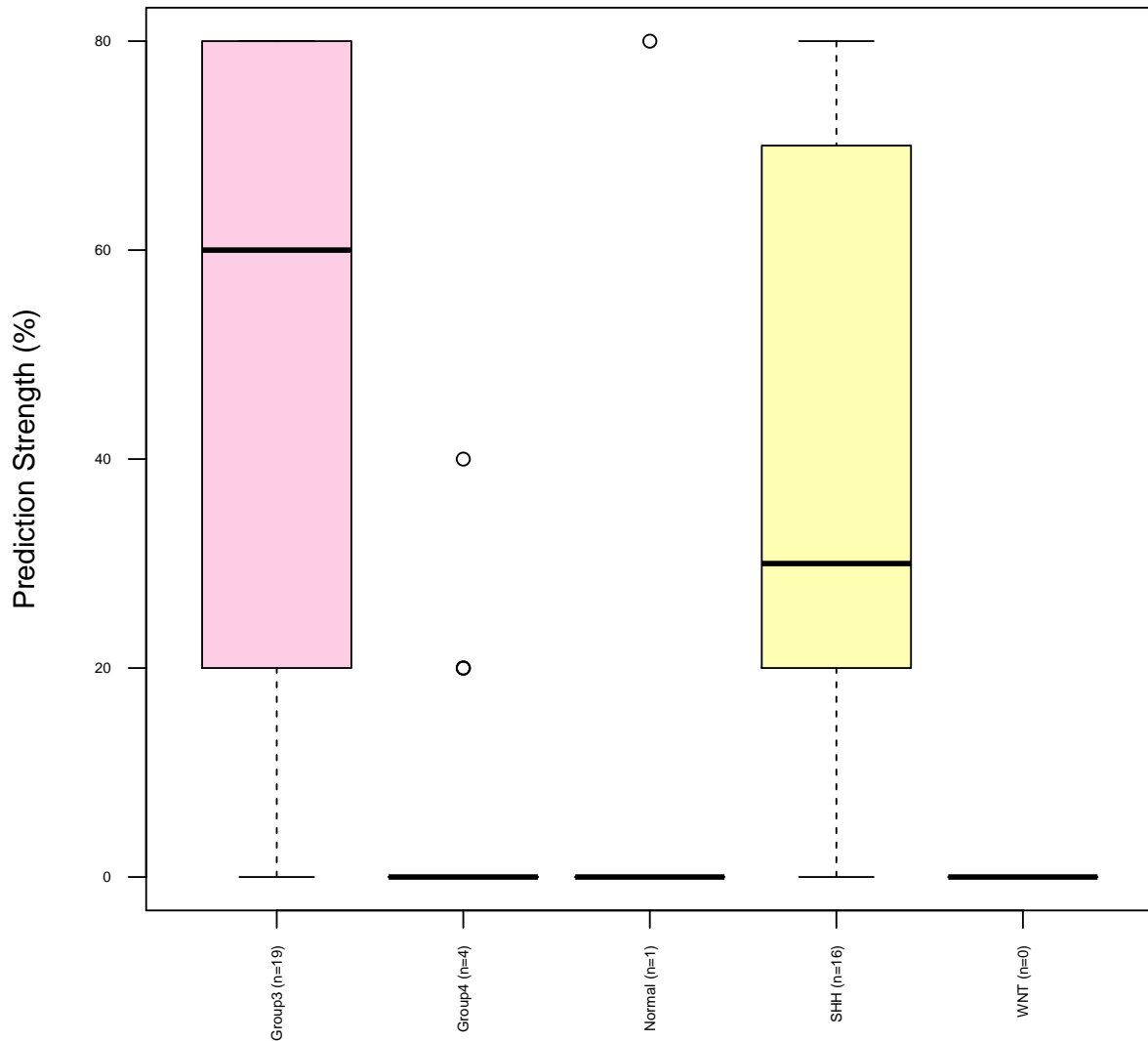
## Overall Predictions



To assess further, we also plot the distribution of subtype calls, across all the samples.

```
PredictionsDistributionBoxplot(InputMatrix=GTMLPreds,pdf_output=FALSE)
```

## Distribution of MB Subtype Calls Across 20 Samples

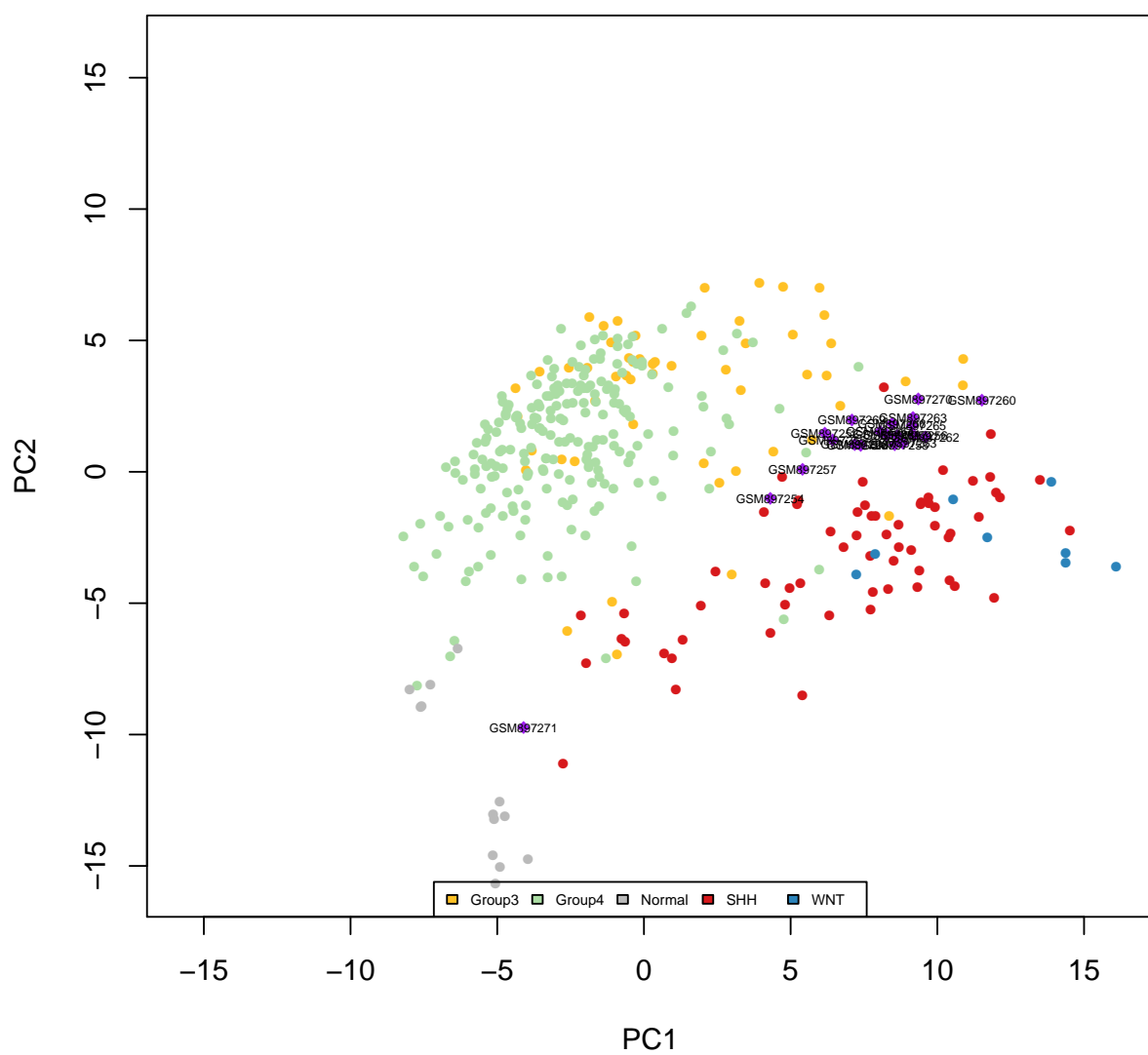


Notably, some samples also predict as either SHH or Normal. Further investigation would need to be performed on these samples. To investigate further, we can graphically visualize different sample replicates and their nearest human MB neighbors from the MM2S training set using Principal Component Analysis (PCA).

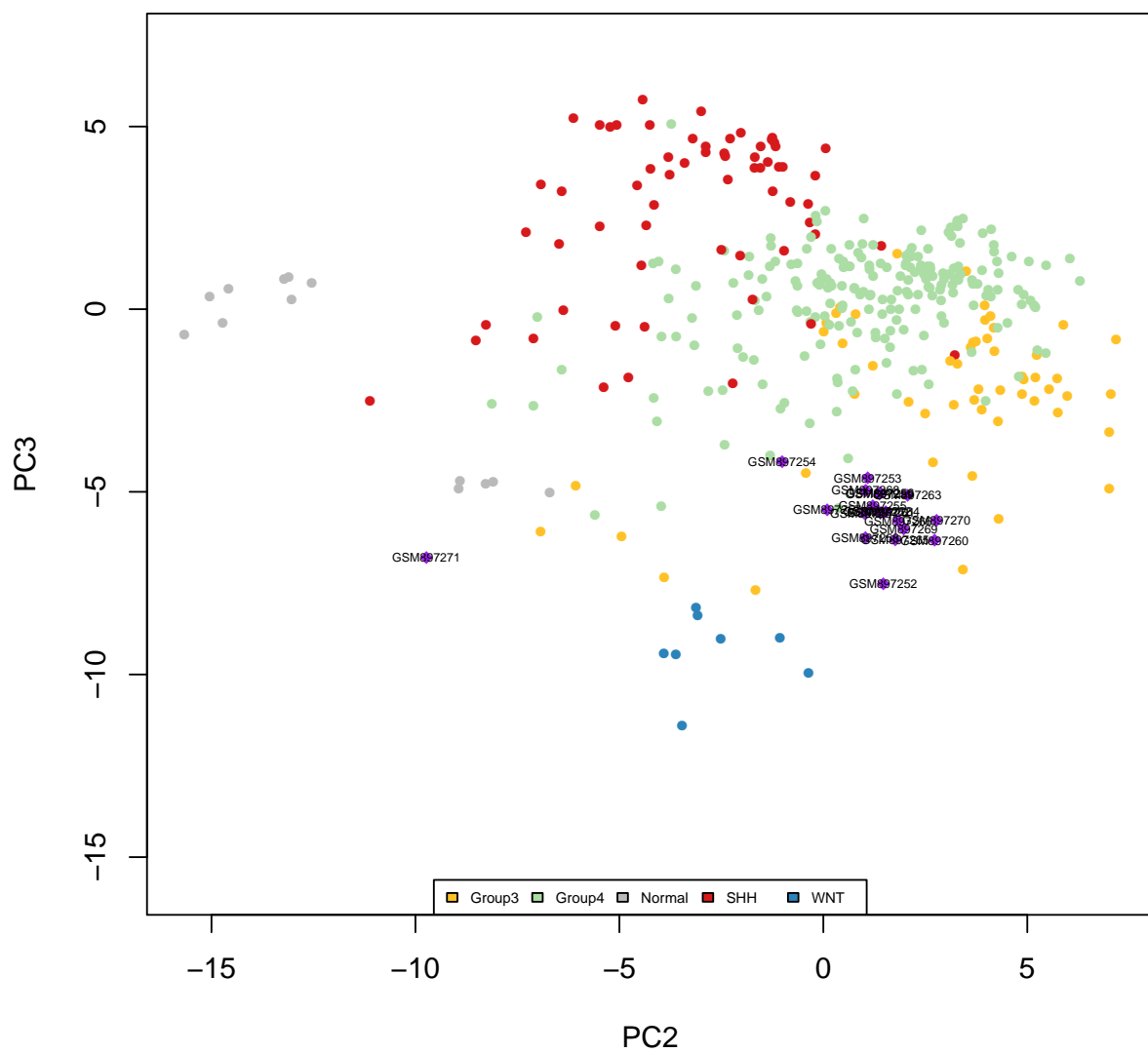
Three PDF files are generated which renders PC1 vs PC2, PC2 vs PC3, and a lattice plot of PC1-PC3.

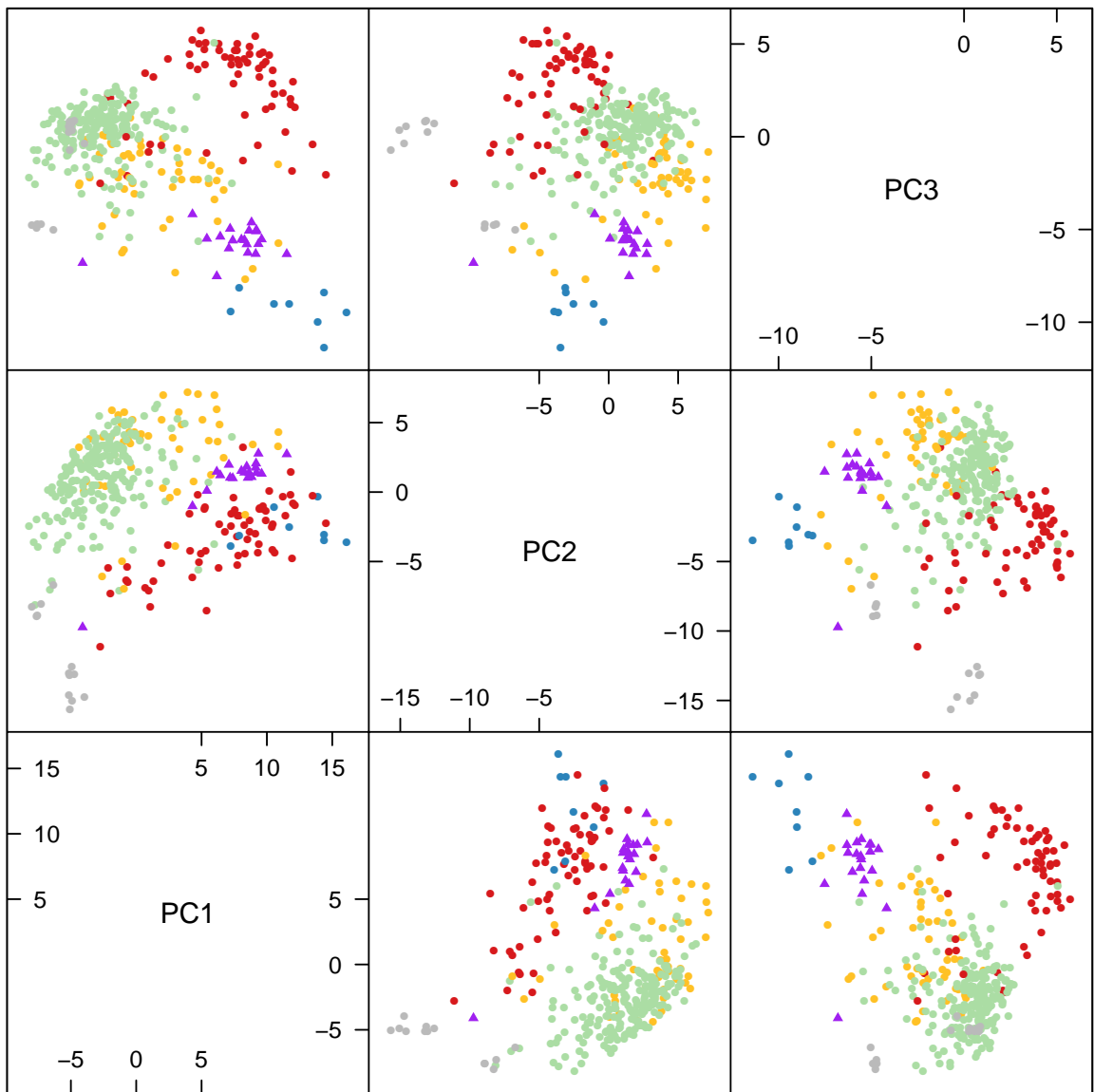
```
PCARender(GSVAmatrixTesting=GTMLPreds$RankMatrixTesting,
          GSVAmatrixTraining=GTMLPreds$RankMatrixTraining)
```

*## Three PDFs have been generated, please consult your working directory to find them.*









Scatter Plot Matrix

## 4 Case Study 2: Predict Human Subtypes for Primary Patient Samples

We first load the gene expression data of 10 primary human patient tumours from GSE37418, and conduct MM2S subtype predictions on them.

```
data(GSE37418Expr)
HumanExpr<-exprs(GSE37418Expr)
# Conduct Subtype Predictions for all samples, save results in a XLS file
# [This will take a few minutes to compute]
HumanPreds<-MM2S.human(InputMatrix=HumanExpr,xls_output=TRUE,parallelize=1)

## There are 660 common genesets between Human MB and the Test Data.
## Of these, 105 feature-selected genesets are being used for classification
##
##
## OUTPUT OF MM2S:
```

	SampleName	MM2S_Prediction	Gr3_Confidence
## [1,]	GSM918580_mbt006-u133v2 WNT		0
## [2,]	GSM918593_mbt035-u133v2 WNT		0
## [3,]	GSM918582_mbt009-u133v2 SHH		0
## [4,]	GSM918606_mbt075-u133v2 SHH		0
## [5,]	GSM918611_mbt085-u133v2 Group4		40
## [6,]	GSM918589_mbt031-u133v2 Group3		100
## [7,]	GSM918624_mbt124-u133v2 Group3		80
## [8,]	GSM918590_mbt032-u133v2 Group4		0
## [9,]	GSM918596_mbt046-u133v2 Group3		60
## [10,]	GSM918598_mbt050-u133v2 Group4		20

	Gr4_Confidence	Normal_Confidence	SHH_Confidence	WNT_Confidence
## [1,]	0	0	0	100
## [2,]	0	0	0	100
## [3,]	0	0	100	0
## [4,]	0	0	100	0
## [5,]	60	0	0	0
## [6,]	0	0	0	0
## [7,]	20	0	0	0
## [8,]	100	0	0	0
## [9,]	40	0	0	0
## [10,]	80	0	0	0

	Neighbor1	Neighbor2	Neighbor3	Neighbor4	Neighbor5
## [1,]	WNT	WNT	WNT	WNT	WNT
## [2,]	WNT	WNT	WNT	WNT	WNT
## [3,]	SHH	SHH	SHH	SHH	SHH
## [4,]	SHH	SHH	SHH	SHH	SHH
## [5,]	Group4	Group3	Group4	Group3	Group4
## [6,]	Group3	Group3	Group3	Group3	Group3
## [7,]	Group3	Group3	Group4	Group3	Group3
## [8,]	Group4	Group4	Group4	Group4	Group4
## [9,]	Group4	Group4	Group3	Group3	Group3
## [10,]	Group4	Group4	Group4	Group4	Group3

We can compare MM2S predictions against known subtype predictions of the samples. These subtype predictions are obtained from the Gene Expression Omnibus (GEO).

```

# We first assess the distribution of the known subtypes for the 76 samples.
table(pData(GSE37418Expr)$characteristics_ch1)

##
##      subgroup: G3      subgroup: G4      subgroup: SHH
##              3              3              2
## subgroup: SHH OUTLIER      subgroup: U      subgroup: WNT
##              0              0              2

# We now assess the distribtuion of MM2S predicted subtypes for the 76 samples.
table(HumanPreds$MM2S_Subtype[,2])

##
## Group3 Group4      SHH      WNT
##      3      3      2      2

# Side-by-side comparison of MM2S predictions and pre-determined subtypes across all samples
# first check that all samples are matching in the pData and MM2S
all(HumanPreds$MM2S_Subtype[,1] == rownames(pData(GSE37418Expr)))

## [1] TRUE

# then generate comparisons
ComparisonTable<-cbind(Sample=rownames(pData(GSE37418Expr)),
                      Original=as.character(pData(GSE37418Expr)$characteristics_ch1),MM2S=HumanPreds$MM2S_Subtype[,2])

# We view the first 15 samples here
ComparisonTable[1:10,]

##      Sample      Original      MM2S
## [1,] "GSM918580_mbt006-u133v2" "subgroup: WNT" "WNT"
## [2,] "GSM918593_mbt035-u133v2" "subgroup: WNT" "WNT"
## [3,] "GSM918582_mbt009-u133v2" "subgroup: SHH" "SHH"
## [4,] "GSM918606_mbt075-u133v2" "subgroup: SHH" "SHH"
## [5,] "GSM918611_mbt085-u133v2" "subgroup: G3" "Group4"
## [6,] "GSM918589_mbt031-u133v2" "subgroup: G3" "Group3"
## [7,] "GSM918624_mbt124-u133v2" "subgroup: G3" "Group3"
## [8,] "GSM918590_mbt032-u133v2" "subgroup: G4" "Group4"
## [9,] "GSM918596_mbt046-u133v2" "subgroup: G4" "Group3"
## [10,] "GSM918598_mbt050-u133v2" "subgroup: G4" "Group4"

```

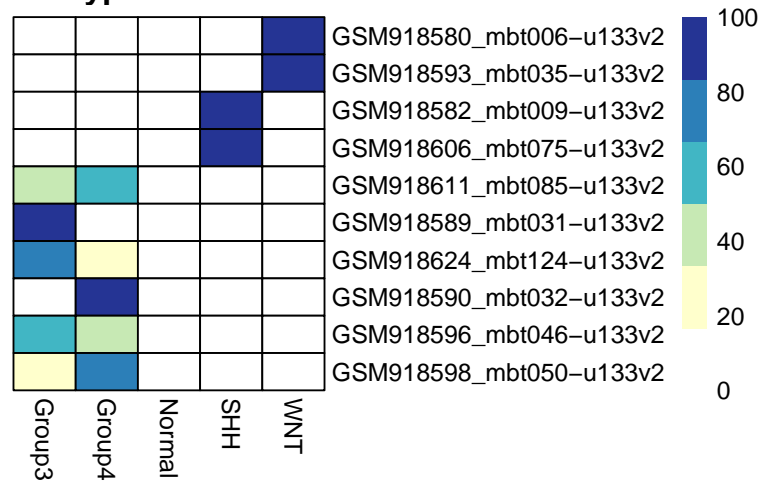
We can easily generate a heatmap of all predictions, as well as PCA plots for our given samples against the MM2S training set.

```

# Now generate a heatmap of the predictions and save the results in a PDF file.
# This indicates MM2S confidence perdictions for each sample.
# We can view the first 10 samples.
PredictionsHeatmap(InputMatrix=HumanPreds$Predictions[1:10,],pdf_output=TRUE,pdfheight=10,pdfwidth=5)

```

### Subtype Predictions

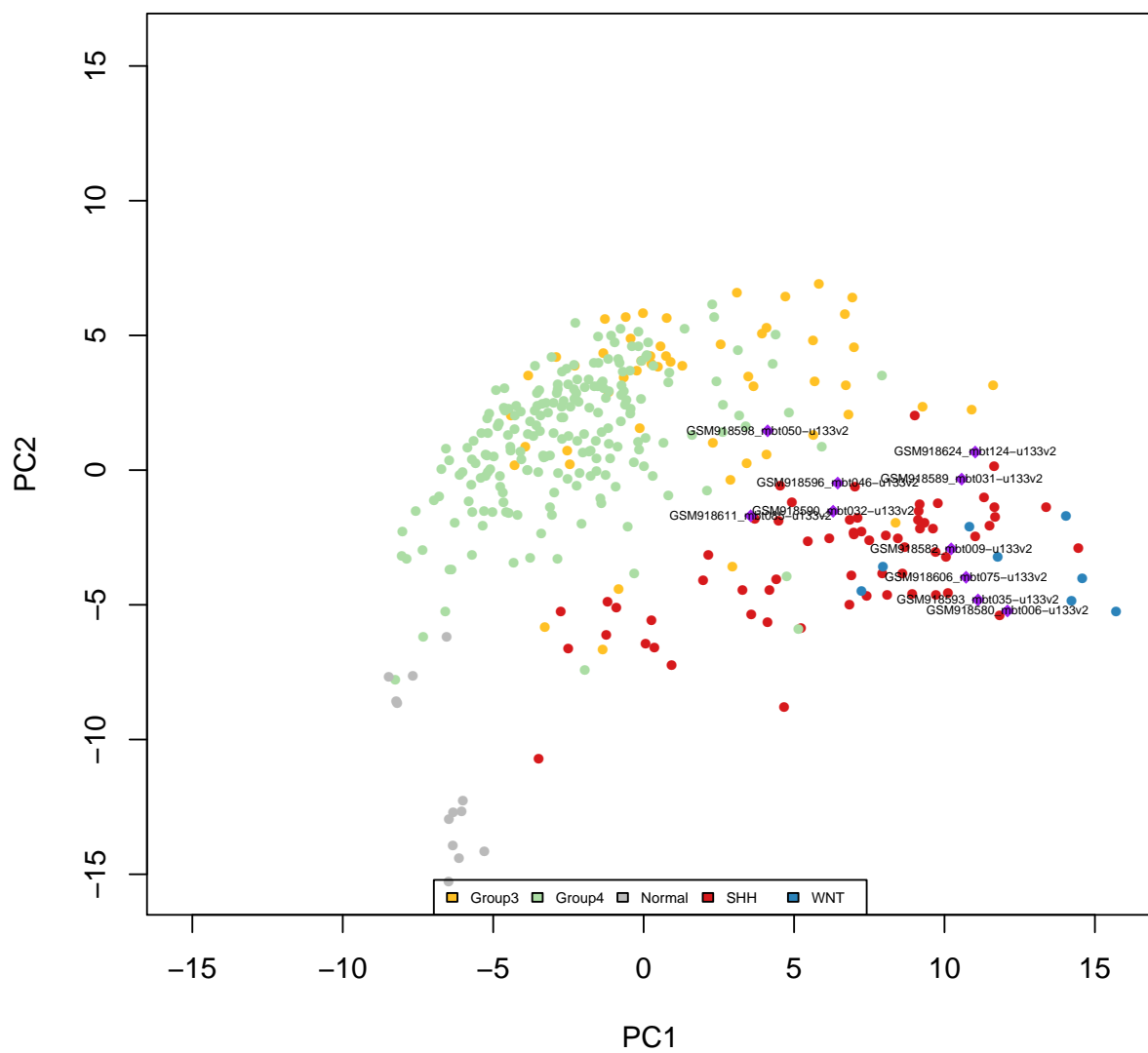


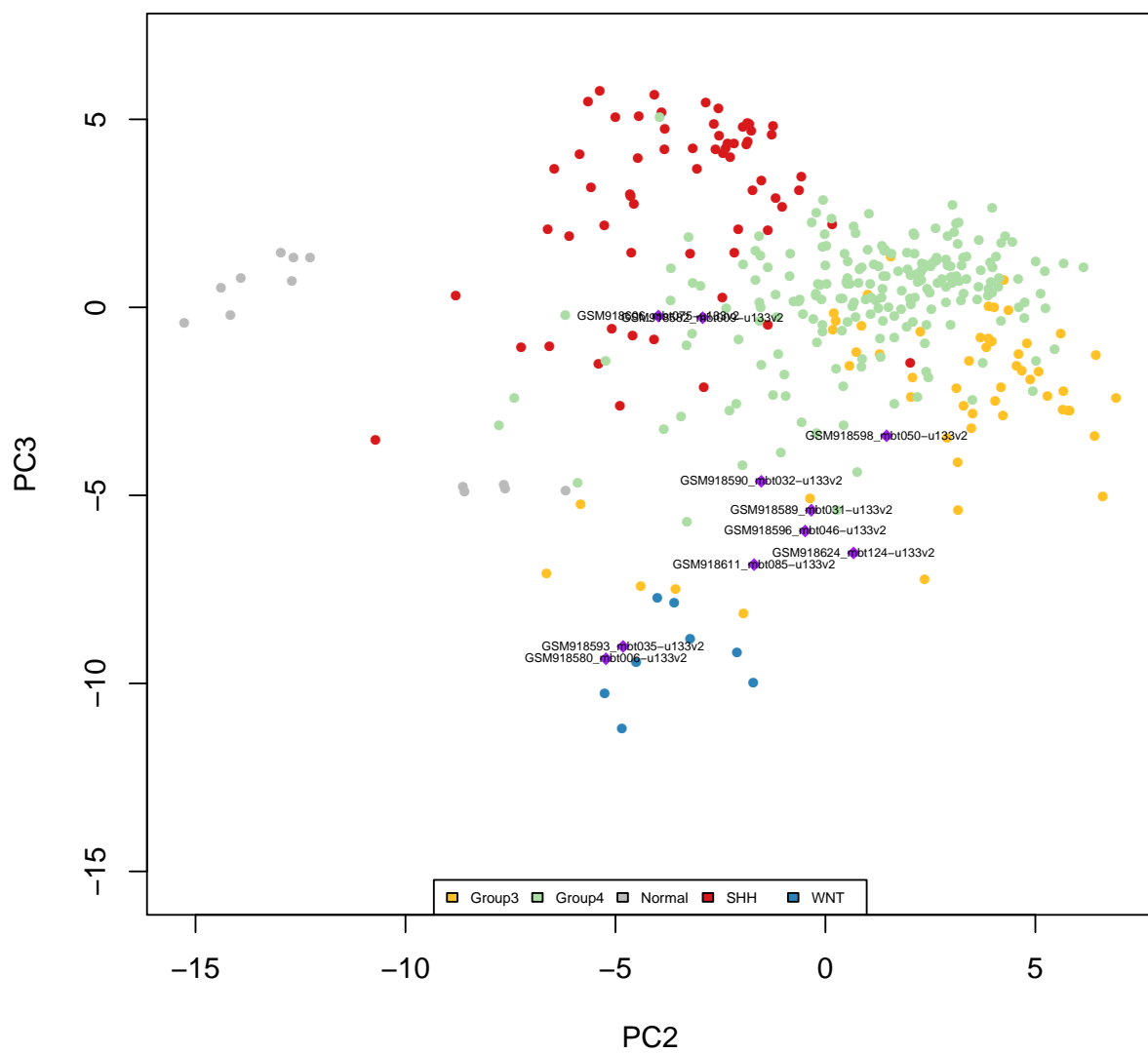
*# NB: Output may appear on multiple pages*

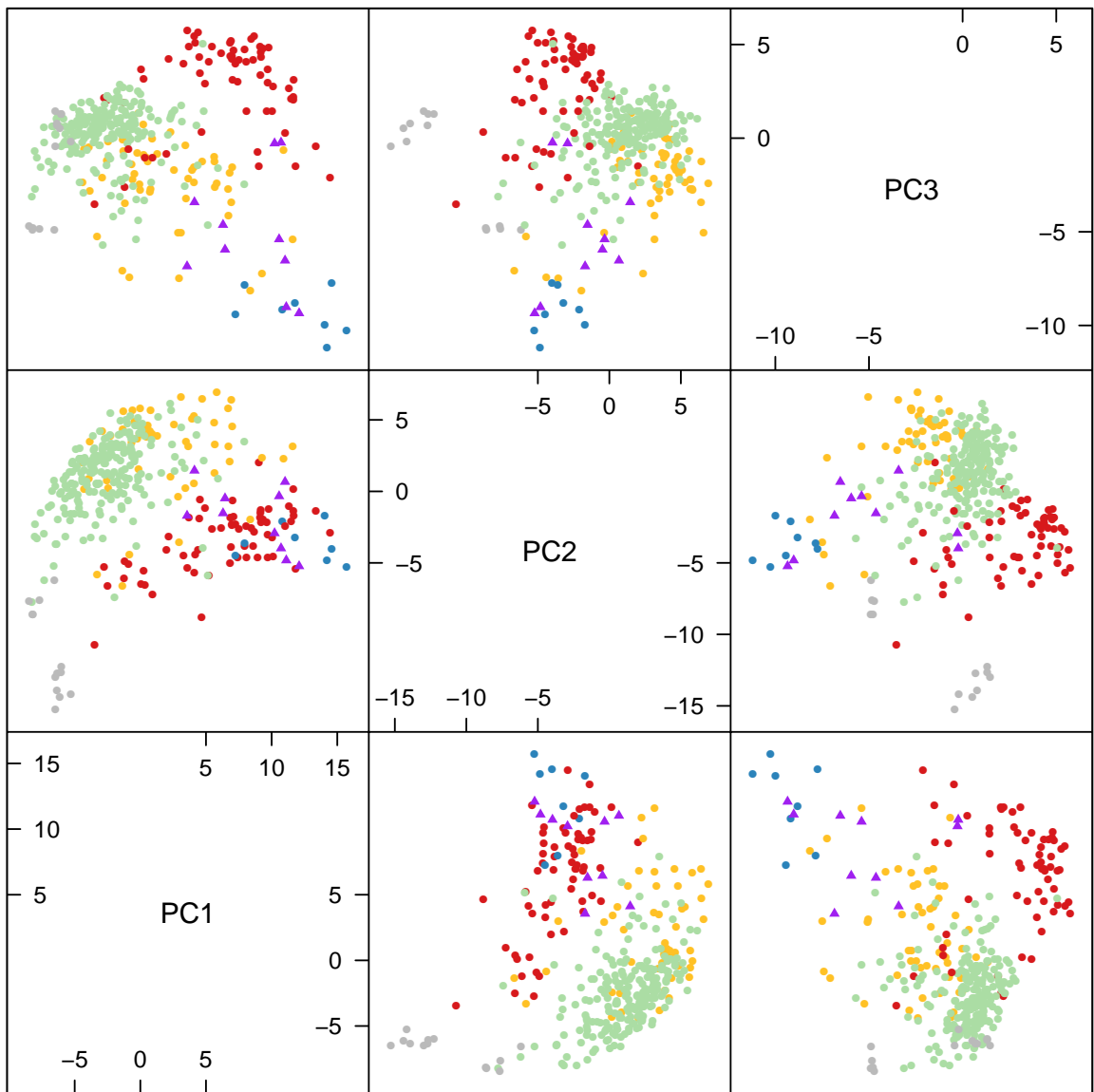
*# We can graphically visualize different sample replicates and their nearest human MB neighbors  
# from the MM2S training set using Principal Component Analysis (PCA).*

```
PCARender(GSVAmatrixTesting=HumanPreds$RankMatrixTesting,  
          GSVAmatrixTraining=HumanPreds$RankMatrixTraining)
```

*## Three PDFs have been generated, please consult your working directory to find them.*







Scatter Plot Matrix



## 5 References and Extra Notes

Both MM2S and MM2Sdata are publicly available and can be installed in R version 2.13.0 or higher. Both packages are also available on Github. Companion datasets are also available on the Haibe-Kains (BHK) Lab website.

Please refer to the following data repositories and websites for additional information, as necessary:

MM2S and MM2Sdata on Github: <https://github.com/DGendoo> OR <https://github.com/bhklab>

BHK Lab Website: <http://www.pmggenomics.ca/bhklab/software/mm2s>

The following code snippet is an example installation of the data repositories from Github.

```
# library(Biobase)
# library(devtools)
# install_github(repo="DGendoo/MM2S")
# install_github(repo="DGendoo/MM2Sdata")
```

## 6 License

The MM2S package is released under the GPL-3.0 License.

The MM2S package is provided "AS-IS" and without any warranty of any kind. In no event shall the University Health Network (UHN) or the authors be liable for any consequential damage of any kind, or any damages resulting from the use of MM2S.

## 7 Session Info

```
## \begin{itemize}\raggedright
##   \item R version 3.2.0 Patched (2015-05-20 r68389), \verb|x86_64-apple-darwin10.8.0|
##   \item Locale: \verb|C/en_CA.UTF-8/en_CA.UTF-8/C/en_CA.UTF-8/en_CA.UTF-8|
##   \item Base packages: base, datasets, grDevices, graphics,
##     methods, parallel, stats, utils
##   \item Other packages: Biobase~2.28.0, BiocGenerics~0.14.0,
##     GSVA~1.16.0, MM2S~1.0.4, MM2Sdata~1.0.1, kkn~1.3.0,
##     lattice~0.20-33, pheatmap~1.0.7
##   \item Loaded via a namespace (and not attached):
##     AnnotationDbi~1.30.1, DBI~0.3.1, GSEABase~1.30.1,
##     GenomeInfoDb~1.4.0, IRanges~2.2.2, Matrix~1.2-0,
##     RColorBrewer~1.1-2, RSQLite~1.0.0, Rcpp~0.12.0,
##     S4Vectors~0.6.0, XML~3.98-1.2, annotate~1.46.0,
##     colorspace~1.2-6, evaluate~0.7, formatR~1.2, graph~1.46.0,
##     grid~3.2.0, gtable~0.1.2, highr~0.5, igraph~0.7.1,
##     knitr~1.10.5, magrittr~1.5, munsell~0.4.2, plyr~1.8.3,
##     scales~0.2.5, stats4~3.2.0, stringi~0.5-5, stringr~1.0.0,
##     tools~3.2.0, xtable~1.7-4
## \end{itemize}
```