In [1]:
```r
# import all needed R packages
library(ChAMP)
library(ChAMPdata)
library(ggplot2)
library(stringr)
library(ggpubr)
```

```
Lade nötiges Paket: minfi

Lade nötiges Paket: BiocGenerics

Lade nötiges Paket: generics


Attache Paket: ‘generics’


Die folgenden Objekte sind maskiert von ‘package:base’:

    as.difftime, as.factor, as.ordered, intersect, is.element, setdiff,
    setequal, union



Attache Paket: ‘BiocGenerics’


Die folgenden Objekte sind maskiert von ‘package:stats’:

    IQR, mad, sd, var, xtabs


Die folgenden Objekte sind maskiert von ‘package:base’:

    anyDuplicated, aperm, append, as.data.frame, basename, cbind,
    colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
    get, grep, grepl, is.unsorted, lapply, Map, mapply, match, mget,
    order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
    rbind, Reduce, rownames, sapply, saveRDS, table, tapply, unique,
    unsplit, which.max, which.min


Lade nötiges Paket: GenomicRanges

Lade nötiges Paket: stats4

Lade nötiges Paket: S4Vectors


Attache Paket: ‘S4Vectors’


Das folgende Objekt ist maskiert ‘package:utils’:

    findMatches


Die folgenden Objekte sind maskiert von ‘package:base’:

    expand.grid, I, unname


Lade nötiges Paket: IRanges
```

```
Lade nötiges Paket: GenomeInfoDb

Lade nötiges Paket: SummarizedExperiment

Lade nötiges Paket: MatrixGenerics

Lade nötiges Paket: matrixStats


Attache Paket: ‘MatrixGenerics’


Die folgenden Objekte sind maskiert von ‘package:matrixStats’:

    colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,
    colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
    colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
    colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
    colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
    colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
    colWeightedMeans, colWeightedMedians, colWeightedSds,
    colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,
    rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
    rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
    rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
    rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
    rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
    rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
    rowWeightedSds, rowWeightedVars


Lade nötiges Paket: Biobase

Welcome to Bioconductor

    Vignettes contain introductory material; view with
    'browseVignettes()'. To cite Bioconductor, see
    'citation("Biobase")', and for packages 'citation("pkgname")'.



Attache Paket: ‘Biobase’


Das folgende Objekt ist maskiert ‘package:MatrixGenerics’:

    rowMedians


Die folgenden Objekte sind maskiert von ‘package:matrixStats’:

    anyMissing, rowMedians


Lade nötiges Paket: Biostrings
```

```
Lade nötiges Paket: XVector


Attache Paket: ‘Biostrings’


Das folgende Objekt ist maskiert ‘package:base’:

    strsplit


Lade nötiges Paket: bumphunter

Lade nötiges Paket: foreach

Lade nötiges Paket: iterators

Lade nötiges Paket: parallel

Lade nötiges Paket: locfit

locfit 1.5-9.12          2025-03-05

Setting options('download.file.method.GEOquery'='auto')

Setting options('GEOquery.inmemory.gpl'=FALSE)

Lade nötiges Paket: ChAMPdata

Lade nötiges Paket: DMRcate



Lade nötiges Paket: Illumina450ProbeVariants.db

Lade nötiges Paket: IlluminaHumanMethylationEPICmanifest

Lade nötiges Paket: DT

Lade nötiges Paket: RPMM

Lade nötiges Paket: cluster

Keine Methoden in Paket 'RSQLite' gefunden für Anforderung: 'dbListFields' be
im Laden von 'lumi'

Warning message:
"vorhergehender Import 'plyr::mutate' durch 'plotly::mutate' während des Lade
ns von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'plyr::rename' durch 'plotly::rename' während des Lade
ns von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'plyr::arrange' durch 'plotly::arrange' während des La
dens von 'ChAMP' ersetzt"
```

```
Warning message:
"vorhergehender Import 'plyr::summarise' durch 'plotly::summarise' während de
s Ladens von 'ChAMP' ersetzt"


Warning message:
"vorhergehender Import 'plotly::subplot' durch 'Hmisc::subplot' während des L
adens von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'plyr::summarize' durch 'Hmisc::summarize' während des
Ladens von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'plyr::is.discrete' durch 'Hmisc::is.discrete' während
des Ladens von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'plotly::last_plot' durch 'ggplot2::last_plot' während
des Ladens von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'globaltest::model.matrix' durch 'stats::model.matrix'
während des Ladens von 'ChAMP' ersetzt"
Warning message:
"vorhergehender Import 'globaltest::p.adjust' durch 'stats::p.adjust' während
des Ladens von 'ChAMP' ersetzt"
>> Package version 2.29.1 loaded <<

      ___ _       _   __  __ ___
     / __| |_    /_\ |  \/  | _ \
    | (__| ' \  / _ \| |\/| |  _/
     \___|_||_/_/ \_\_|  |_|_|
     ------------------------------
    If you have any question or suggestion about ChAMP, please email to champ
450k@gmail.com.
    Thank you for citating ChAMP:

    Yuan Tian, Tiffany J Morris, Amy P Webster, Zhen Yang, Stephan Beck, Andr
ew Feber, Andrew E Teschendorff; ChAMP: updated methylation analysis pipeline
for Illumina BeadChips, Bioinformatics, btx513, https://doi.org/10.1093/bioin
formatics/btx513    REQUIRE ChAMPdata >= 2.23.1
```

In [20]:
```
mystery_1 <- "../../example_datasets/epicv2/mystery_data_1"
mystery_2 <- "../../example_datasets/epicv2/mystery_data_2"
```

Analyse mystery_data_1

Laden Sie den Datensatz im Verzeichnis mystery_data_1 und schauen Sie sich den **Output von champ.laod** die **QC Plots** an:

- Was fällt Ihnen am Output von champ.load auf?
- Wozu führt die Änderung des *detPcut* Parameters in *champ.load*?
- Warum wurde der Parameter verändert?
- Was fällt Ihnen an den Plots auf?
- Worauf könnte das zu sehende hindeuten?
- Wie könnten Sie damit umgehen?

In [21]:
```
# all parameters except one are default
myData_1 <- champ.load(directory = fragmented,
                       method="ChAMP",
                       methValue="B",
                       autoimpute=TRUE,
                       filterDetP=TRUE,
                       ProbeCutoff=0,
                       SampleCutoff=0.1,
                       detPcut=0.9, # This is the only parameter which was cha
                       filterBeads=TRUE,
                       beadCutoff=0.05,
                       filterNoCG=TRUE,
                       filterSNPs=TRUE,
                       population=NULL,
                       filterMultiHit=TRUE,
                       filterXY=TRUE,
                       force=FALSE,
                       arraytype="EPICv2")
```

```
[============================]

[<<<< ChAMP.LOAD START >>>>>]

-----------------------------


[ Loading Data with ChAMP Method ]

---------------------------------

Note that ChAMP method will NOT return rgSet or mset, they object defined by
minfi. Which means, if you use ChAMP method to load data, you can not use SWA
N or FunctionNormliazation method in champ.norm() (you can use BMIQ or PBC st
ill). But All other function should not be influenced.


[============================]

[<<<< ChAMP.IMPORT START >>>>>]

-----------------------------


[ Section 1: Read PD Files Start ]

  CSV Directory: ../../example_datasets/epicv2/mystery_data_1/samplesheet.csv

  Find CSV Success

  Reading CSV File

  Replace Sentrix_Position into Array

  Replace Sentrix_ID into Slide

[ Section 1: Read PD file Done ]



[ Section 2: Read IDAT files Start ]

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R05C01_Grn.idat ---- (1/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R06C01_Grn.idat ---- (2/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R07C01_Grn.idat ---- (3/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R08C01_Grn.idat ---- (4/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R01C01_Grn.idat ---- (5/20)
```

```
  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R02C01_Grn.idat ---- (6/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R03C01_Grn.idat ---- (7/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R04C01_Grn.idat ---- (8/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R05C01_Grn.idat ---- (9/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R06C01_Grn.idat ---- (10/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R07C01_Grn.idat ---- (11/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R08C01_Grn.idat ---- (12/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R01C01_Grn.idat ---- (13/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R02C01_Grn.idat ---- (14/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R03C01_Grn.idat ---- (15/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R04C01_Grn.idat ---- (16/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R05C01_Grn.idat ---- (17/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R06C01_Grn.idat ---- (18/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R07C01_Grn.idat ---- (19/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R08C01_Grn.idat ---- (20/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R05C01_Red.idat ---- (1/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R06C01_Red.idat ---- (2/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
11111/111111111111_R07C01_Red.idat ---- (3/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/1111111
```

```
11111/111111111111_R08C01_Red.idat ---- (4/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R01C01_Red.idat ---- (5/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R02C01_Red.idat ---- (6/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R03C01_Red.idat ---- (7/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R04C01_Red.idat ---- (8/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R05C01_Red.idat ---- (9/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R06C01_Red.idat ---- (10/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R07C01_Red.idat ---- (11/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/2222222
22222/222222222222_R08C01_Red.idat ---- (12/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R01C01_Red.idat ---- (13/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R02C01_Red.idat ---- (14/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R03C01_Red.idat ---- (15/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R04C01_Red.idat ---- (16/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R05C01_Red.idat ---- (17/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R06C01_Red.idat ---- (18/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R07C01_Red.idat ---- (19/20)

  Loading:../../example_datasets/epicv2/mystery_data_1/data_directory/3333333
33333/333333333333_R08C01_Red.idat ---- (20/20)


  Extract Mean value for Green and Red Channel Success

    Your Red Green Channel contains 1105209 probes.

[ Section 2: Read IDAT Files Done ]
```

```
[ Section 3: Use Annotation Start ]


  Reading EPICv2 Annotation >>

    !!! Important, since version 2.29.1, ChAMP set default `EPIC` arraytype a
s EPIC version 2.
        You can set 'EPIC' or 'EPICv2' to use version 2 EPIC annotation
        If you want to use the old version (v1), please specify arraytype par
ameter as `EPICv1`.
        For 450K array, still use `450K`


  Fetching NEGATIVE ControlProbe.

    Totally, there are 411 control probes in Annotation.

    Your data set contains 411 control probes.


  Generating Meth and UnMeth Matrix

    Extracting Meth Matrix...

      Totally there are 937055 Meth probes in EPICv2 Annotation.

      Your data set contains 937055 Meth probes.

    Extracting UnMeth Matrix...

      Totally there are 937055 UnMeth probes in EPICv2 Annotation.

      Your data set contains 937055 UnMeth probes.


  Generating beta Matrix

  Generating M Matrix

  Generating intensity Matrix

  Calculating Detect P value

  Counting Beads

[ Section 3: Use Annotation Done ]


[<<<<< ChAMP.IMPORT END >>>>>>]

[============================]

[You may want to process champ.filter() next.]
```

```
[============================]

[<<<< ChAMP.FILTER START >>>>>]

-----------------------------


In New version ChAMP, champ.filter() function has been set to do filtering on
the result of champ.import(). You can use champ.import() + champ.filter() to
do Data Loading, or set "method" parameter in champ.load() as "ChAMP" to get
the same effect.


This function is provided for user need to do filtering on some beta (or M) m
atrix, which contained most filtering system in champ.load except beadcount.
User need to input beta matrix, pd file themselves. If you want to do filteri
ntg on detP matrix and Bead Count, you also need to input a detected P matrix
and Bead Count information.


Note that if you want to filter more data matrix, say beta, M, intensity... p
lease make sure they have exactly the same rownames and colnames.



[ Section 1:  Check Input Start ]

  You have inputed beta,intensity for Analysis.


  pd file provided, checking if it's in accord with Data Matrix...

    pd file check success.


  Parameter filterDetP is TRUE, checking if detP in accord with Data Matri
x...

    detP check success.


  Parameter filterBeads is TRUE, checking if beadcount in accord with Data Ma
trix...

    beadcount check success.


  parameter autoimpute is TRUE. Checking if the conditions are fulfilled...

    !!! ProbeCutoff is 0, which means you have no needs to do imputation. aut
oimpute has been reset FALSE.


  Checking Finished :filterDetP,filterBeads,filterMultiHit,filterSNPs,filterN
```

```
oCG,filterXY would be done on beta,intensity.

  You also provided :detP,beadcount .

[ Section 1: Check Input Done ]



[ Section 2: Filtering Start >>


  Filtering Detect P value Start

    The fraction of failed positions per sample

    You may need to delete samples with high proportion of failed probes:
```

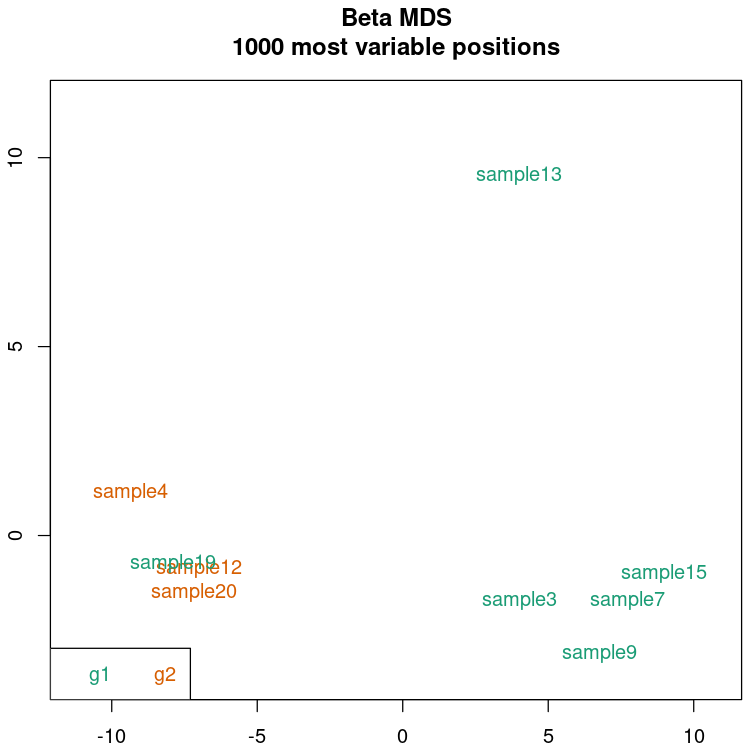
	Failed CpG Fraction.
sample1	0.10990604
sample2	0.12215718
sample3	0.08568867
sample4	0.05344083
sample5	0.10018195
sample6	0.13114598
sample7	0.09822582
sample8	0.14327761
sample9	0.08778353
sample10	0.12545261
sample11	0.10311028
sample12	0.05736163
sample13	0.09452807
sample14	0.12113803
sample15	0.09212480
sample16	0.11706463
sample17	0.11174371
sample18	0.10414223
sample19	0.05110693
sample20	0.04452780

```
    The detSamplecut parameter is : 0.1

    Samples : sample1,sample2,sample5,sample6,sample8,sample10,sample11,sampl
e14,sample16,sample17,sample18 will be deleted.

    There are 9 samples remained for analysis.


    Filtering probes with a detection p-value above 0.9.

    Removing 440434 probes.

    If a large number of probes have been removed, ChAMP suggests you to iden
tify potentially bad samples


  Filtering BeadCount Start

    Filtering probes with a beadcount <3 in at least 5% of samples.

    Removing 12688 probes


  Filtering NoCG Start

    Only Keep CpGs, removing 1292 probes from the analysis.


  Filtering SNPs Start


    !!! Important, since version 2.29.1, ChAMP set default `EPIC` arraytype a
s EPIC version 2.
        You can set 'EPIC' or 'EPICv2' to use version 2 EPIC annotation
        If you want to use the old version (v1), please specify arraytype par
ameter as `EPICv1`.
        For 450K array, still use `450K`


    Using general mask options

    Removing 20000 probes from the analysis.


  Filtering MultiHit Start

    Filtering probes that align to multiple locations as identified in Nordlu
nd et al

    Removing 0 probes from the analysis.


  Filtering XY Start

    Filtering probes located on X,Y chromosome, removing 10538 probes from th
e analysis.
```

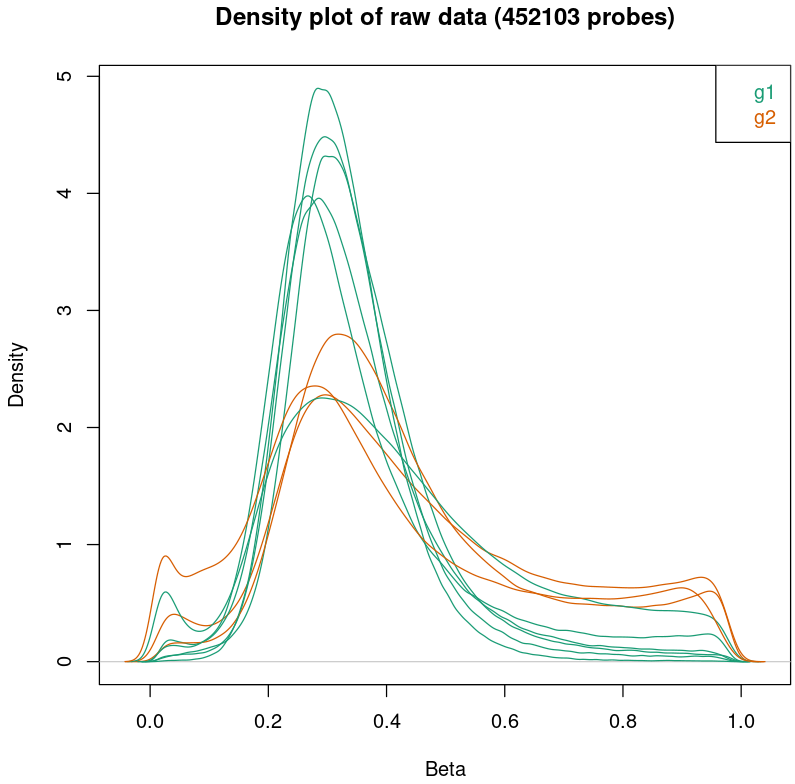
```
  Updating PD file


  Fixing Outliers Start

    Replacing all value smaller/equal to 0 with smallest positive value.

    Replacing all value greater/equal to 1 with largest value below 1..
[ Section 2: Filtering Done ]


 All filterings are Done, now you have 452103 probes and 9 samples.


[<<<<< ChAMP.FILTER END >>>>>>]

[============================]

[You may want to process champ.QC() next.]


[<<<<< ChAMP.LOAD END >>>>>>]

[============================]

[You may want to process champ.QC() next.]
```

In [24]:
```
champ.QC(beta = myData_1$beta,
         pheno=myData_1$pd$Sample_Group,
         resultsDir="./CHAMP_QCimages/")
```

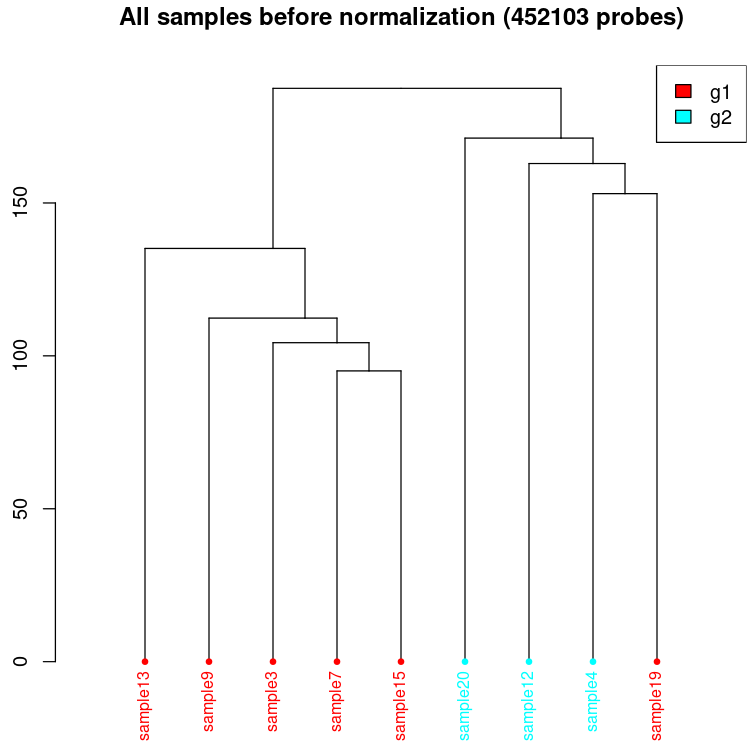
```
[============================]

[<<<<< ChAMP.QC START >>>>>>]

-----------------------------

champ.QC Results will be saved in ./CHAMP_QCimages/

[QC plots will be proceed with 452103 probes and 9 samples.]


<< Prepare Data Over. >>

<< plot mdsPlot Done. >>
```




```
<< Plot densityPlot Done. >>


< Dendrogram Plot Feature Selection Method >: No Selection, directly use all
CpGs to calculate distance matrix.
```



```
<< Plot dendrogram Done. >>


[<<<<<< ChAMP.QC END >>>>>>>]

[============================]

[You may want to process champ.norm() next.]
```



Analyse mystery_data_2

Laden Sie den Datensatz im Verzeichnis mystery_data_2 und schauen Sie sich die QC Plots an:

- Was fällt Ihnen an den Plots auf?
- Worauf könnte das zu sehende hindeuten?
- Wie könnten Sie damit umgehen?

In [18]:
```
# parameters are all default
myData_2 <- champ.load(directory = intra_group_outlier,
                       method="ChAMP",
                       methValue="B",
                       autoimpute=TRUE,
                       filterDetP=TRUE,
                       ProbeCutoff=0,
                       SampleCutoff=0.1,
                       detPcut=0.01,
```

```
                        filterBeads=TRUE,
                        beadCutoff=0.05,
                        filterNoCG=TRUE,
                        filterSNPs=TRUE,
                        population=NULL,
                        filterMultiHit=TRUE,
                        filterXY=TRUE,
                        force=FALSE,
                        arraytype="EPICv2")
```

```
[============================]

[<<<< ChAMP.LOAD START >>>>>]

-----------------------------


[ Loading Data with ChAMP Method ]

---------------------------------

Note that ChAMP method will NOT return rgSet or mset, they object defined by
minfi. Which means, if you use ChAMP method to load data, you can not use SWA
N or FunctionNormliazation method in champ.norm() (you can use BMIQ or PBC st
ill). But All other function should not be influenced.


[============================]

[<<<< ChAMP.IMPORT START >>>>>]

-----------------------------


[ Section 1: Read PD Files Start ]

  CSV Directory: ../../example_datasets/epicv2/mystery_data_2/samplesheet.csv

  Find CSV Success

  Reading CSV File

  Replace Sentrix_Position into Array

  Replace Sentrix_ID into Slide

[ Section 1: Read PD file Done ]



[ Section 2: Read IDAT files Start ]

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R01C01_Grn.idat ---- (1/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R05C01_Grn.idat ---- (2/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R07C01_Grn.idat ---- (3/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/333333333333/333333333
333_R04C01_Grn.idat ---- (4/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/333333333333/333333333
333_R08C01_Grn.idat ---- (5/9)
```

```
  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R03C01_Grn.idat ---- (6/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/222222222222/222222222
222_R07C01_Grn.idat ---- (7/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/222222222222/222222222
222_R02C01_Grn.idat ---- (8/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R04C01_Grn.idat ---- (9/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R01C01_Red.idat ---- (1/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R05C01_Red.idat ---- (2/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R07C01_Red.idat ---- (3/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/333333333333/333333333
333_R04C01_Red.idat ---- (4/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/333333333333/333333333
333_R08C01_Red.idat ---- (5/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R03C01_Red.idat ---- (6/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/222222222222/222222222
222_R07C01_Red.idat ---- (7/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/222222222222/222222222
222_R02C01_Red.idat ---- (8/9)

  Loading:../../example_datasets/epicv2/mystery_data_2/111111111111/111111111
111_R04C01_Red.idat ---- (9/9)


  Extract Mean value for Green and Red Channel Success

    Your Red Green Channel contains 1105209 probes.

[ Section 2: Read IDAT Files Done ]



[ Section 3: Use Annotation Start ]


  Reading EPICv2 Annotation >>

    !!! Important, since version 2.29.1, ChAMP set default `EPIC` arraytype a
s EPIC version 2.
```

```
        You can set 'EPIC' or 'EPICv2' to use version 2 EPIC annotation
        If you want to use the old version (v1), please specify arraytype par
ameter as `EPICv1`.
        For 450K array, still use `450K`


  Fetching NEGATIVE ControlProbe.

    Totally, there are 411 control probes in Annotation.

    Your data set contains 411 control probes.


  Generating Meth and UnMeth Matrix

    Extracting Meth Matrix...

      Totally there are 937055 Meth probes in EPICv2 Annotation.

      Your data set contains 937055 Meth probes.

    Extracting UnMeth Matrix...

      Totally there are 937055 UnMeth probes in EPICv2 Annotation.

      Your data set contains 937055 UnMeth probes.


  Generating beta Matrix

  Generating M Matrix

  Generating intensity Matrix

  Calculating Detect P value

  Counting Beads

[ Section 3: Use Annotation Done ]


[<<<<< ChAMP.IMPORT END >>>>>>]

[============================]

[You may want to process champ.filter() next.]


[============================]

[<<<< ChAMP.FILTER START >>>>>]

----------------------------


In New version ChAMP, champ.filter() function has been set to do filtering on
```

```
the result of champ.import(). You can use champ.import() + champ.filter() to
do Data Loading, or set "method" parameter in champ.load() as "ChAMP" to get
the same effect.


This function is provided for user need to do filtering on some beta (or M) m
atrix, which contained most filtering system in champ.load except beadcount.
User need to input beta matrix, pd file themselves. If you want to do filteri
ntg on detP matrix and Bead Count, you also need to input a detected P matrix
and Bead Count information.


Note that if you want to filter more data matrix, say beta, M, intensity... p
lease make sure they have exactly the same rownames and colnames.



[ Section 1:  Check Input Start ]

  You have inputed beta,intensity for Analysis.


  pd file provided, checking if it's in accord with Data Matrix...

    pd file check success.


  Parameter filterDetP is TRUE, checking if detP in accord with Data Matri
x...

    detP check success.


  Parameter filterBeads is TRUE, checking if beadcount in accord with Data Ma
trix...

    beadcount check success.


  parameter autoimpute is TRUE. Checking if the conditions are fulfilled...

    !!! ProbeCutoff is 0, which means you have no needs to do imputation. aut
oimpute has been reset FALSE.


  Checking Finished :filterDetP,filterBeads,filterMultiHit,filterSNPs,filterN
oCG,filterXY would be done on beta,intensity.

  You also provided :detP,beadcount .

[ Section 1: Check Input Done ]



[ Section 2: Filtering Start >>
```

```
  Filtering Detect P value Start

    The fraction of failed positions per sample

    You may need to delete samples with high proportion of failed probes:
```

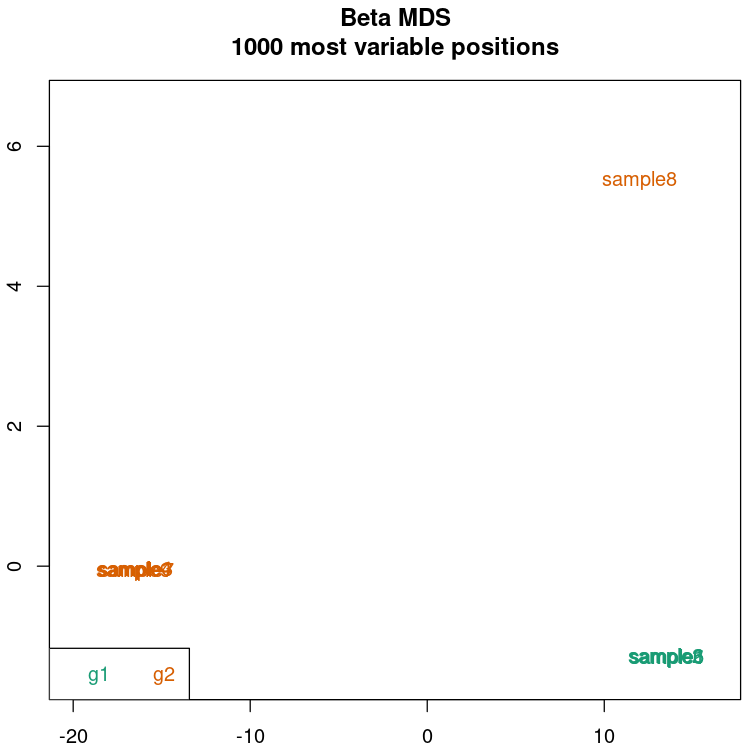
	Failed CpG Fraction.
sample1	0.008623827
sample2	0.009623768
sample3	0.010284348
sample4	0.008498968
sample5	0.008403989
sample6	0.010018622
sample7	0.012234074
sample8	0.006075417
sample9	0.008782836

```
    Filtering probes with a detection p-value above 0.01.

    Removing 23273 probes.

    If a large number of probes have been removed, ChAMP suggests you to iden
tify potentially bad samples


  Filtering BeadCount Start

    Filtering probes with a beadcount <3 in at least 5% of samples.

    Removing 12573 probes


  Filtering NoCG Start

    Only Keep CpGs, removing 3508 probes from the analysis.


  Filtering SNPs Start


    !!! Important, since version 2.29.1, ChAMP set default `EPIC` arraytype a
s EPIC version 2.
        You can set 'EPIC' or 'EPICv2' to use version 2 EPIC annotation
        If you want to use the old version (v1), please specify arraytype par
ameter as `EPICv1`.
        For 450K array, still use `450K`


    Using general mask options

    Removing 30917 probes from the analysis.


  Filtering MultiHit Start

    Filtering probes that align to multiple locations as identified in Nordlu
nd et al

    Removing 0 probes from the analysis.


  Filtering XY Start

    Filtering probes located on X,Y chromosome, removing 20480 probes from th
e analysis.


  Updating PD file


  Fixing Outliers Start

    Replacing all value smaller/equal to 0 with smallest positive value.
```

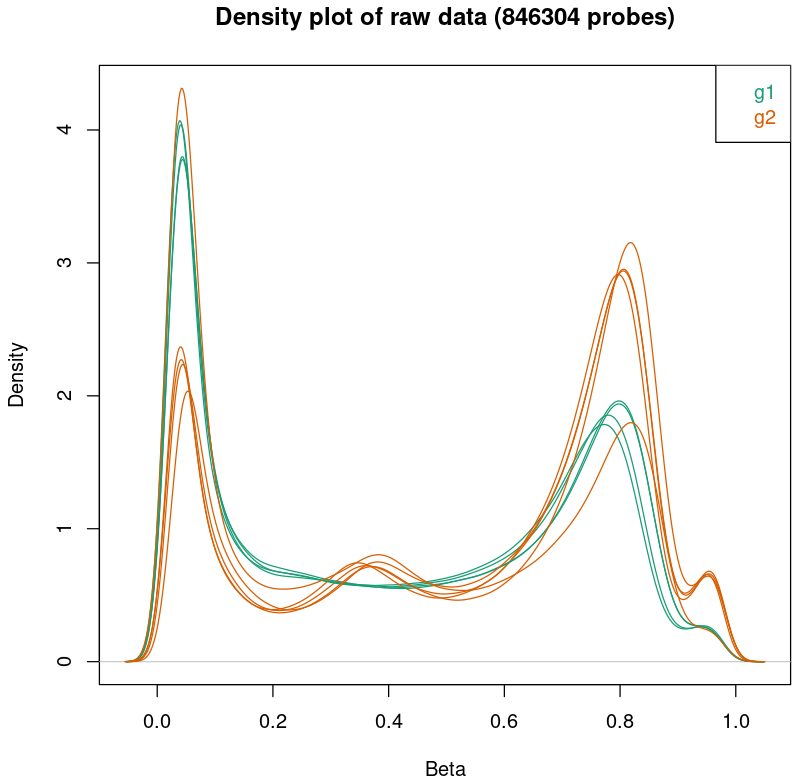
```
    Replacing all value greater/equal to 1 with largest value below 1..

[ Section 2: Filtering Done ]


 All filterings are Done, now you have 846304 probes and 9 samples.


[<<<<< ChAMP.FILTER END >>>>>>]

[============================]

[You may want to process champ.QC() next.]


[<<<<< ChAMP.LOAD END >>>>>>]

[============================]

[You may want to process champ.QC() next.]
```

In [23]:
```
champ.QC(beta = myData_2$beta,
         pheno=myData_2$pd$Sample_Group,
         resultsDir="./CHAMP_QCimages/")
```

```
[============================]

[<<<<< ChAMP.QC START >>>>>>]

-----------------------------

champ.QC Results will be saved in ./CHAMP_QCimages/

[QC plots will be proceed with 846304 probes and 9 samples.]


<< Prepare Data Over. >>

<< plot mdsPlot Done. >>
```




```
<< Plot densityPlot Done. >>


< Dendrogram Plot Feature Selection Method >: No Selection, directly use all
CpGs to calculate distance matrix.
```



```
<< Plot dendrogram Done. >>


[<<<<<< ChAMP.QC END >>>>>>>]

[============================]

[You may want to process champ.norm() next.]
```