

# Package ‘ChAMPdata’

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**Type** Package

**Title** Data Packages for ChAMP package

**Version** 2.6.0

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**Description**

Provides datasets needed for ChAMP including a test dataset and blood controls for CNA analysis.

**License** GPL-3

**Depends** GenomicRanges (>= 1.22.4),BiocGenerics(>= 0.16.1),R (>= 3.3)

**biocViews** ExperimentData

**NeedsCompilation** no

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ChAMPdata-package	<i>Data Packages to use with the ChAMP Chip Analysis Methylation Pipeline</i>
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**Description**

This includes four data packages. ProbeInfoALL.lv includes annotation for the 450k array as required by the BMIQ normalization. probe.features includes probe annotations for the 450k array as included in the saved results files for the MVP and DMR functions. champBloodCtrls provides reference control data for the champ.CNA function. testDataSet includes loaded and filtered (for detection) p-value of 6 arrays for the 450k array along with an accompanying samples sheet. This can be used to test the package. In addition, the raw IDAT files for these 6 arrays are available and can be accessed using system.file().

**Details**

Package: ChAMPdata  
Type: Package  
Version: 1.9.3  
Date: 2016-03-22  
License: GPL-3

Three of the four packages are used internally by the ChAMP package. The testDataSet can be used to test the package.

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**Examples**

```
data(probeInfoALL.lv)
data(probe.features)
data(testDataSet)
data(champBloodCtrls)
data(EPICSimData)
data(illumina450Gr)
data(illuminaEPICGr)
data(probeInfoALL.epic.lv)
data(probe.features.epic)
data(CellTypeMeans27K)
data(CellTypeMeans450K)
```

bloodCtl

*Blood Control data***Description**

Blood control data for CNA analysis

**Usage**

data(bloodCtl)

**Format**

The format is: List of 6 \$ mset :Formal class 'MethylSet' [package "minfi"] with 8 slots .. ..@ preprocessMethod : Named chr [1:3] "Raw (no normalization or bg correction)" "1.8.9" "0.4.0" .. ..@ attr(\*, "names")= chr [1:3] "rg.norm" "minfi" "manifest" .. ..@ assayData :<environment: 0x105193308> .. ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. ..@ varMetadata :'data.frame': 10 obs. of 1 variable: .. ..@ labelDescription: chr [1:10] NA NA NA NA .. ..@ data :'data.frame': 2 obs. of 10 variables: .. ..@ ..\$ Sample\_Name : chr [1:2] "blood\_1" "blood\_2" .. ..@ Sample\_Plate: chr [1:2] "c" "c" .. ..@ Sample\_Group: chr [1:2] "B" "B" .. ..@ Pool\_ID : chr [1:2] "blood" "blood" .. ..@ Project : chr [1:2] "blood\_pilot" "blood\_pilot" .. ..@ Sample\_Well : chr [1:2] "F01" "H01" .. ..@ Array : chr [1:2] "R06C01" "R02C02" .. ..@ Slide : num [1:2] 9.31e+09 9.31e+09 .. ..@ Basename : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte\_450k\_twinStudy\_9May2013/bloodPilot\_Sept2013/MORRIS Meth450K 280813/champ-Blood/930|\_\_truncated\_\_"/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte\_450k\_twinStudy\_9May2013/bloodPilot\_Meth450K 280813/champBlood/930|\_\_truncated\_\_ .. ..@ filenames : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte\_450k\_twinStudy\_9May2013/bloodPilot\_Sept2013/MORRIS Meth450K 280813/champ-Blood/930|\_\_truncated\_\_"/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte\_450k\_twinStudy\_9May2013/bloodPilot\_Meth450K 280813/champBlood/930|\_\_truncated\_\_ .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. ..@ ..\_classVersion\_\_:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..@ ..\$ : int [1:3] 1 1 0 .. ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..@ labelDescription: chr(0) .. ..@ data :'data.frame': 485512 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns" .. ..@ ..\_classVersion\_\_:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..@ ..\$ : int [1:3] 1 1 0 .. ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "" .. ..@ lab : chr "" .. ..@ contact : chr "" .. ..@ title : chr "" .. ..@ abstract : chr "" .. ..@ url : chr "" .. ..@ pubMedIds : chr "" .. ..@ samples : list() .. ..@ hybridizations : list() .. ..@ normControls : list() .. ..@ preprocessing : list() .. ..@ other : list() .. ..@ ..\_classVersion\_\_:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 2 .. ..@ ..\$ : int [1:3] 1 0 0 .. ..@ ..\$ : int [1:3] 1 1 0 .. ..@ annotation : Named chr [1:2] "IlluminaHumanMethylation450k" "ilmn12.hg19" .. ..@ attr(\*, "names")= chr [1:2] "array" "annotation" .. ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..@ labelDescription: chr(0) .. ..@ data :'data.frame': 2 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. ..@ ..\_classVersion\_\_:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..@ ..\$ : int [1:3] 1 1 0 .. ..@ ..\_classVersion\_\_:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 4 .. ..@ ..\$ : int [1:3] 3 0 2 .. ..@ ..\$ : int [1:3] 2 22 0 .. ..@ ..\$ : int [1:3] 1 3 0 .. ..@ ..\$ :

```

int [1:3] 1 0 0 $ rgSet :Formal class 'RGChannelSetExtended' [package "minfi"] with 7 slots .. @
assayData :<environment: 0x105310db8> .. @ phenoData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. @ varMetadata :'data.frame': 10 obs. of 1 variable: ..
.. $ labelDescription: chr [1:10] NA NA NA NA ... @ data :'data.frame': 2 obs. of 10
variables: .. $ Sample_Name : chr [1:2] "blood_1" "blood_2" .. $ Sample_Plate: chr
[1:2] "c" "c" .. $ Sample_Group: chr [1:2] "B" "B" .. $ Pool_ID : chr [1:2] "blood"
"blood" .. $ Project : chr [1:2] "blood_pilot" "blood_pilot" .. $ Sample_Well : chr
[1:2] "F01" "H01" .. $ Array : chr [1:2] "R06C01" "R02C02" .. $ Slide : num
[1:2] 9.31e+09 9.31e+09 .. $ Basename : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIVE
work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champ-
Blood/930|__truncated__"/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPil
Meth450K 280813/champBlood/930|__truncated__ .. $ filenames : chr [1:2] "/Users/regmtmo/Desktop/Sync/A
work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champ-
Blood/930|__truncated__"/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPil
Meth450K 280813/champBlood/930|__truncated__ .. @ dimLabels : chr [1:2] "sam-
pleNames" "sampleColumns" .. @ .Data:List of 1 .. $ : int [1:3] 1 1 0 ..
.. @ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. @
varMetadata :'data.frame': 0 obs. of 1 variable: .. $ labelDescription: chr(0) .. @
data :'data.frame': 622399 obs. of 0 variables .. @ dimLabels : chr [1:2] "featureNames"
"featureColumns" .. @ .Data:List of 1 .. $ : int [1:3] 1 1 0 .. @ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. @ name : chr "" .. @ lab
: chr "" .. @ contact : chr "" .. @ title : chr "" .. @ abstract : chr "" .. @
url : chr "" .. @ pubMedIds : chr "" .. @ samples : list() .. @ hybridizations
: list() .. @ normControls : list() .. @ preprocessing : list() .. @ other : list()
.. @ .Data:List of 2 .. $ : int [1:3] 1 0 0 .. $ : int [1:3] 1 1 0 ..
.. @ annotation : Named chr [1:2] "IlluminaHumanMethylation450k" "ilmn12.hg19" .. attr(*,
"names")= chr [1:2] "array" "annotation" .. @ protocolData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. @ varMetadata :'data.frame': 0 obs. of 1 variable: ..
.. $ labelDescription: chr(0) .. @ data :'data.frame': 2 obs. of 0 variables .. @ dimLabels
: chr [1:2] "sampleNames" "sampleColumns" .. @ .Data:List of 1 .. $ : int [1:3] 1 1 0 .. @
. Data:List of 1 .. $ : int [1:3] 1 1 0 .. @ .Data:List of
4 .. $ : int [1:3] 3 0 2 .. $ : int [1:3] 2 22 0 .. $ : int [1:3] 1 3 0 .. $
: int [1:3] 1 0 0 $ pd :'data.frame': 2 obs. of 10 variables: .. $ Sample_Name : chr [1:2] "blood_1"
"blood_2" .. $ Sample_Plate: chr [1:2] "" "" .. $ Sample_Group: chr [1:2] "champCtls" "champCtls"
.. $ Pool_ID : chr [1:2] "" "" .. $ Project : chr [1:2] "" "" .. $ Sample_Well : chr [1:2] "" "" .. $ Array :
chr [1:2] "R06C01" "R02C02" .. $ Slide : num [1:2] 9.31e+09 9.31e+09 .. $ Basename : chr [1:2] ""
"" .. $ filenames : chr [1:2] "" "" $ intensity: num [1:485512, 1:2] 12820 2714 1381 4083 3863 ... -
attr(*, "dimnames")=List of 2 .. $ : chr [1:485512] "cg00050873" "cg00212031" "cg00213748"
"cg00214611" ... $ : chr [1:2] "blood_1" "blood_2" $ beta: num [1:485512, 1:2] 0.8648 0.0924
0.7846 0.0323 0.7118 ... - attr(*, "dimnames")=List of 2 .. $ : chr [1:485512] "cg00050873"
"cg00212031" "cg00213748" "cg00214611" ... $ : chr [1:2] "blood_1" "blood_2" $ detP :
num [1:485512, 1:2] 0 0 0 0 0 0 0 0 0 ... - attr(*, "dimnames")=List of 2 .. $ : chr [1:485512]
"cg00050873" "cg00212031" "cg00213748" "cg00214611" ... $ : chr [1:2] "blood_1" "blood_2"

```

## Examples

```

data(bloodCtl)
## maybe str(bloodCtl) ; plot(bloodCtl) ...

```

---

CellTypeMeans27K	<i>Cell-type purified whole blood methylation CpG Sites for use with the RefBaseEWAS cell-type correction function.</i>
------------------	---

---

**Description**

This dataset contains 500 CpGs sites from cell type purified whole blood samples.

**Usage**

```
data(CellTypeMeans450K)
```

**Format**

The format is: num [1:500, 1:6] 0.901 0.9188 0.8503 0.8913 0.0436 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:500] "cg00226923" "cg16698623" "cg14102807" "cg14127336" ... ..\$ : chr [1:6] "CD8T" "CD4T" "NK" "Bcell" ...

**Examples**

```
data(CellTypeMeans27K)
```

---

CellTypeMeans450K	<i>Cell-type purified whole blood methylation CpG Sites for use with the RefBaseEWAS cell-type correction function.</i>
-------------------	---

---

**Description**

This dataset contains 600 CpGs sites from cell type purified whole blood samples.

**Usage**

```
data(CellTypeMeans450K)
```

**Format**

The format is: num [1:600, 1:6] 0.125 0.2 0.178 0.284 0.226 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:600] "cg25939861" "cg00219921" "cg08777095" "cg04329870" ... ..\$ : chr [1:6] "CD8T" "CD4T" "NK" "Bcell" ...

**Examples**

```
data(CellTypeMeans450K)
```

---

ControlProbes450K      *ControlProbes450K*

---

**Description**

HumanMethylation450K Control Probes, generated from HumanMethylation450\_15017482\_v1-2.csv.

**Usage**

```
data(ControlProbes450K)
```

**Format**

A data frame with Control Probes used in champ.SVD function and their probe IDs in manifest HumanMethylation450\_15017482\_v1-2.csv.

Name The control name.

Index Probe ID in HumanMethylation450\_15017482\_v1-2.csv.

RG Color we extracted.

**Examples**

```
data(ControlProbes450K)
```

---

ControlProbesEPIC      *ControlProbesEPIC*

---

**Description**

HumanMethylationEPIC Control Probes, generated from MethylationEPIC\_v-1-0\_B2.csv.

**Usage**

```
data(ControlProbesEPIC)
```

**Format**

A data frame with Control Probes used in champ.SVD function and their probe IDs in manifest MethylationEPIC\_v-1-0\_B2.csv.

Name The control name.

Index Probe ID in MethylationEPIC\_v-1-0\_B2.csv.

RG Color we extracted.

**Examples**

```
data(ControlProbesEPIC)
```

---

EPIC.manifest.hg38      *SNP annotation for EPIC array.*

---

## Description

This dataset is added to do filtering on SNP for EPIC array.

## Usage

```
data(EPIC.manifest.hg38)
```

## Format

```
'data.frame': 866895 obs. of 41 variables: $ seqnames : Factor w/ 26 levels "chr1","chr2",...: 1 1 1
1 1 1 1 1 1 ... $ start : int 10525 10848 10850 15865 18827 29407 29425 36603 68849 68889 ...
$ end : int 10526 10849 10851 15866 18828 29408 29426 36604 68850 68890 ... $ width : int 2 2
2 2 2 2 2 2 ... $ strand : Factor w/ 3 levels "+","-","*": 3 3 3 3 3 3 3 3 3 ... $ addressA : num
21611527 91693541 82663207 2665852 84794291 ... $ addressB : num NA 47784201 3701821
39757192 NA ... $ channel : chr "Both" "Grn" "Grn" "Red" ... $ designType : Factor w/ 2 lev-
els "I","II": 2 1 1 1 2 1 1 2 2 2 ... $ nextBase : chr "G/A" "C" "C" "A" ... $ nextBaseRef : chr
"C" "G" "G" "C" ... $ probeType : chr "cg" "cg" "cg" "cg" ... $ orientation : Factor w/ 2 levels
"down","up": 1 2 2 1 1 1 1 2 1 1 ... $ probeCpGcnt : int 3 7 8 2 2 8 7 1 1 0 ... $ context35 :
int 4 12 12 4 3 11 12 1 1 1 ... $ probeStart : int 10526 10800 10802 15865 18828 29407 29425
36554 68850 68890 ... $ probeEnd : num 10575 10849 10851 15914 18877 ... $ ProbeSeqA : chr
"AAACRAAACTACRTTATCCTCTACACAAATTTTCRATAATACTCTAAAAAC" "ACACATAC-
TAACACATCAAATAAAAAACATAACACAAACACAAAAAACA" "ACATACTAACACATCAAATAAAAA-
CATAACACAAACACAAAAAACA" "CCAATAACTAACCACTCTACTAAAATCCATCCAC-
CAAATAAAAAACATCA" ... $ ProbeSeqB : chr "" "ACACATACTAACGCGTCGAAATAAAAAACG-
TAACGCAAACGCAAAAAAACG" "ACATACTAACGCGTCGAAATAAAAAACGTAACGCAAACG-
CAAAAAAACGCG" "CCGATACTAACCACTCTACTAAAATCCATCCGCCAACTAAAAA-
CATCG" ... $ chrmA : chr "chr1" "chr1" "chr1" "chr1" ... $ begA : int 10526 10800 10802 15865
18828 29407 29425 36554 68850 68890 ... $ flag.A : int 16 0 0 16 16 16 16 0 16 16 ... $ mapQ.A :
int 0 22 22 17 1 3 3 0 6 6 ... $ cigarA : chr "50M" "50M" "50M" "50M" ... $ chrmB : chr "." "chr1"
"chr1" "chr1" ... $ begB : int NA 10800 10802 15865 NA 29407 29425 NA NA NA ... $ flag.B : int
NA 0 0 16 NA 16 16 NA NA NA ... $ mapQ.B : int NA 22 22 17 NA 3 3 NA NA NA ... $ cigarB
: chr "." "50M" "50M" "50M" ... $ posMatch : logi NA NA NA NA NA NA ... $ MASK.mapping
: logi TRUE FALSE FALSE FALSE TRUE TRUE ... $ MASK.typeINextBaseSwitch: logi FALSE
FALSE FALSE FALSE FALSE ... $ MASK.rmsk15 : logi TRUE TRUE TRUE FALSE
FALSE FALSE ... $ MASK.sub35.copy : logi TRUE FALSE TRUE TRUE FALSE TRUE ... $
MASK.sub30.copy : logi TRUE TRUE TRUE TRUE FALSE TRUE ... $ MASK.sub25.copy : logi
TRUE TRUE TRUE TRUE FALSE TRUE ... $ MASK.sub40.copy : logi TRUE FALSE FALSE
TRUE FALSE FALSE ... $ MASK.snp5.common : logi FALSE FALSE FALSE FALSE FALSE
FALSE ... $ MASK.snp5.GMAF1p : logi FALSE FALSE FALSE FALSE FALSE ... $
MASK.extBase : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general : logi
TRUE TRUE TRUE TRUE TRUE TRUE ...
```

## Examples

```
data(EPIC.manifest.hg38)
```

---

EPIC.manifest.pop.hg38

*SNP annotation for EPIC array for different population.*

---

## Description

This dataset is added to do filtering on SNP for EPIC array. Since different population have different SNP probes, this file is included to provide a comprehensive filtering annotation.

## Usage

```
data(EPIC.manifest.pop.hg38)
```

## Format

```
'data.frame': 866895 obs. of 67 variables: $ seqnames : Factor w/ 26 levels "chr1","chr2",...: 1
1 1 1 1 1 1 1 1 1 ... $ start : int 10525 10848 10850 15865 18827 29407 29425 68849 68889
69591 ... $ end : int 10526 10849 10851 15866 18828 29408 29426 68850 68890 69592 ... $ width
: int 2 2 2 2 2 2 2 2 2 ... $ strand : Factor w/ 3 levels "+","-","*": 3 3 3 3 3 3 3 3 3 ... $
MASK.general.AFR: logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.AFR : logi
FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.EAS: logi TRUE TRUE TRUE
TRUE TRUE TRUE ... $ MASK.snp5.EAS : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
$ MASK.general.EUR: logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.EUR : logi
FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.SAS: logi TRUE TRUE TRUE
TRUE TRUE TRUE ... $ MASK.snp5.SAS : logi FALSE FALSE FALSE FALSE FALSE FALSE
... $ MASK.general.AMR: logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.AMR
: logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.GWD: logi TRUE
TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.GWD : logi FALSE FALSE FALSE FALSE
FALSE FALSE ... $ MASK.general.YRI: logi TRUE TRUE TRUE TRUE TRUE TRUE ... $
MASK.snp5.YRI : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.TSI:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.TSI : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.IBS: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.IBS : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CHS:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CHS : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.PUR: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.PUR : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.JPT:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.JPT : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.GIH: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.GIH : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CHB:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CHB : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.STU: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.STU : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.ITU:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.ITU : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.LWK: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.LWK : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.KHV:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.KHV : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.FIN: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.FIN : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.ESN:
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.ESN : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.CEU: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.CEU : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.PJL:
```



```
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.PJL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.ACB: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.ACB : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CLM:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CLM : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.CDX: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.CDX : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.GBR:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.GBR : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.BEB: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.BEB : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.PEL:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.PEL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.MSL: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.MSL : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.MXL:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.MXL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.ASW: logi TRUE TRUE TRUE TRUE TRUE TRUE
... $ MASK.snp5.ASW : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
```

### Examples

```
data(EPIC.manifest.pop.hg38)
```

---

EPICSimData

*Simulation EPIC beadarray Dataset.*

---

### Description

This dataset is available to test ChAMP functions on EPIC array.

### Usage

```
data(EPICSimData)
```

### Format

```
List of 3 $ beta: num [1:780385, 1:16] 0.7382 0.8572 0.8624 0.4492 0.0751 ... ..- attr(*, "dim-
names")=List of 2 .. ..$: chr [1:780385] "cg14817997" "cg16269199" "cg13869341" "cg02404219"
... .. ..$: chr [1:16] "HELA_Sim_1" "HELA_Sim_2" "HELA_Sim_3" "HELA_Sim_4" ... $ pd
:'data.frame': 16 obs. of 10 variables: ..$ Sample_Name : chr [1:16] "HELA_Sim_1" "HELA_Sim_2"
"HELA_Sim_3" "HELA_Sim_4" ... ..$ Sample_Plate: chr [1:16] "EPIC2" "EPIC2" "EPIC2"
"EPIC2" ... ..$ Sample_Group: chr [1:16] "control" "control" "control" "control" ... ..$ Pool_ID
: logi [1:16] NA NA NA NA NA NA ... ..$ Project : chr [1:16] "X" "X" "X" "X" ... ..$ Sam-
ple_Well : chr [1:16] "A01" "B01" "C01" "D01" ... ..$ Array : chr [1:16] "R01C01" "R02C01"
"R03C01" "R04C01" ... ..$ Slide : chr [1:16] "200079600019" "200079600019" "200079600019"
"200079600019" ... ..$ Basename : chr [1:16] "character(0)" "character(0)" "character(0)" "charac-
ter(0)" ... ..$ filenames: chr [1:16] "./Demo/200079600019_R01C01" "./Demo/200079600019_R02C01"
"./Demo/200079600019_R03C01" "./Demo/200079600019_R04C01" ... $ detP: num [1:780385,
1:16] 0 0 0 0 0 0 0 0 0 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:780385] "cg18478105"
"cg14361672" "cg01763666" "cg02115394" ... .. ..$: NULL
```

### Examples

```
data(EPICSimData)
```

---

hm450.manifest.hg38    *SNP annotation for 450K array.*

---

## Description

This dataset is added to do filtering on SNP for 450K array.

## Usage

```
data(hm450.manifest.hg38)
```

## Format

```
'data.frame': 485577 obs. of 41 variables: $ seqnames : Factor w/ 26 levels "chr1","chr2",...: 1
1 1 1 1 1 1 1 1 1 ... $ start : int 15865 18827 29407 29425 29435 68849 69591 91550 135252
370260 ... $ end : int 15866 18828 29408 29426 29436 68850 69592 91551 135253 370261 ...
$ width : int 2 2 2 2 2 2 2 2 2 ... $ strand : Factor w/ 3 levels "+","-","*": 3 3 3 3 3 3 3 3 3
3 ... $ addressA : num 62703328 27651330 25703424 61731400 26752380 ... $ addressB : num
16661461 NA 34666387 14693326 50693408 ... $ channel : chr "Red" "Both" "Red" "Red" ... $
designType : Factor w/ 2 levels "I","II": 1 2 1 1 1 2 2 2 2 ... $ nextBase : chr "A" "G/A" "A" "T"
... $ nextBaseRef : chr "C" "C" "C" "A" ... $ probeType : chr "cg" "cg" "cg" "cg" ... $ orientation
: Factor w/ 2 levels "down","up": 1 1 1 1 1 1 2 2 2 ... $ probeCpGcnt : int 2 2 8 7 7 1 3 1
4 3 ... $ context35 : int 4 3 11 12 12 1 2 2 4 5 ... $ probeStart : int 15865 18828 29407 29425
29435 68850 69542 91501 135203 370211 ... $ probeEnd : num 15914 18877 29456 29474 29484
... $ ProbeSeqA : chr "CCAATAACTAACCCTCTACTAAAATCCATCCACCAAACCTAAAAA-
CATCA" "ACTCRAAATTTACTCAATAAACCRRTTCAATATATACAAAAACAATTCCCC" "AAAAAAA-
CACAATAAAAAACAACAACAACATTAACCCAAAAACACA" "AATCCTAAAACCAACT-
CAAAAAAACACAATAAAAAACAACAACAACA" ... $ ProbeSeqB : chr "CCGATAAC-
TAACCCTCTACTAAAATCCATCCGCCAAACTAAAAACATCG" "" "GAAAAAACGCAATAAAAAAC-
GAACGACGACGTTAAAACCCGAAAACGCG" "AATCCTAAAACCGCGCTCGAAAAAACG-
CAATAAAAAACGAACGACGACG" ... $ chrmA : chr "chr1" "chr1" "chr1" "chr1" ... $ begA :
int 15865 18828 29407 29425 29435 68850 69542 91501 135203 370211 ... $ flag.A : int 16
16 16 16 16 0 0 0 0 ... $ mapQ.A : int 17 1 3 3 3 6 60 6 0 3 ... $ cigarA : chr "50M"
"50M" "50M" "50M" ... $ chrmB : chr "chr1" "." "chr1" "chr1" ... $ begB : int 15865 NA 29407
29425 29435 NA NA NA NA NA ... $ flag.B : int 16 NA 16 16 16 NA NA NA NA NA ... $
mapQ.B : int 17 NA 3 3 3 NA NA NA NA NA ... $ cigarB : chr "50M" "." "50M" "50M" ...
$ posMatch : logi NA NA NA NA NA NA ... $ MASK.mapping : logi FALSE TRUE TRUE
TRUE TRUE TRUE ... $ MASK.typeINextBaseSwitch: logi FALSE FALSE FALSE FALSE
FALSE FALSE ... $ MASK.rmsk15 : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $
MASK.sub35.copy : logi TRUE FALSE TRUE FALSE FALSE TRUE ... $ MASK.sub30.copy :
logi TRUE FALSE TRUE FALSE FALSE TRUE ... $ MASK.sub25.copy : logi TRUE FALSE
TRUE FALSE TRUE TRUE ... $ MASK.sub40.copy : logi TRUE FALSE FALSE FALSE FALSE
TRUE ... $ MASK.snp5.common : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $
MASK.snp5.GMAF1p : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.extBase :
logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general : logi TRUE TRUE TRUE
TRUE TRUE TRUE ...
```

## Examples

```
data(hm450.manifest.hg38)
```

---

 hm450.manifest.pop.hg38

*SNP annotation for 450K array for different population.*


---

## Description

This dataset is added to do filtering on SNP for 450K array. Since different population have different SNP probes, this file is included to provide a comprehensive filtering annotation.

## Usage

```
data(hm450.manifest.pop.hg38)
```

## Format

```
'data.frame': 866895 obs. of 67 variables: $ seqnames : Factor w/ 26 levels "chr1","chr2",...: 1
1 1 1 1 1 1 1 1 1 ... $ start : int 10525 10848 10850 15865 18827 29407 29425 68849 68889
69591 ... $ end : int 10526 10849 10851 15866 18828 29408 29426 68850 68890 69592 ... $ width
: int 2 2 2 2 2 2 2 2 2 ... $ strand : Factor w/ 3 levels "+","-","*": 3 3 3 3 3 3 3 3 3 ... $
MASK.general.AFR: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.AFR : logi
FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.EAS: logi TRUE TRUE TRUE
TRUE TRUE TRUE TRUE ... $ MASK.snp5.EAS : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
$ MASK.general.EUR: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.EUR : logi
FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.SAS: logi TRUE TRUE TRUE
TRUE TRUE TRUE TRUE ... $ MASK.snp5.SAS : logi FALSE FALSE FALSE FALSE FALSE FALSE
... $ MASK.general.AMR: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.AMR
: logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.GWD: logi TRUE
TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.GWD : logi FALSE FALSE FALSE FALSE
FALSE FALSE ... $ MASK.general.YRI: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $
MASK.snp5.YRI : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.TSI:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.TSI : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.IBS: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.IBS : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CHS:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CHS : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.PUR: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.PUR : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.JPT:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.JPT : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.GIH: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.GIH : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CHB:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CHB : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.STU: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.STU : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.ITU:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.ITU : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.LWK: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.LWK : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.KHV:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.KHV : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.FIN: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.FIN : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.ESN:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.ESN : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.CEU: logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.CEU : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.PJL:
```

```
logi TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.PJL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.ACB: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.ACB : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.CLM:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.CLM : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.CDX: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.CDX : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.GBR:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.GBR : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.BEB: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.BEB : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.PEL:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.PEL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.MSL: logi TRUE TRUE TRUE TRUE TRUE TRUE ...
$ MASK.snp5.MSL : logi FALSE FALSE FALSE FALSE FALSE FALSE ... $ MASK.general.MXL:
logi TRUE TRUE TRUE TRUE TRUE TRUE TRUE ... $ MASK.snp5.MXL : logi FALSE FALSE FALSE
FALSE FALSE FALSE ... $ MASK.general.ASW: logi TRUE TRUE TRUE TRUE TRUE TRUE
... $ MASK.snp5.ASW : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
```

### Examples

```
data(hm450.manifest.pop.hg38)
```

---

```
hprdAsigH
```

```
hprdAsigH PPI network dataset for champ.FEM function.
```

---

### Description

Dataset would be used in champ.FEM, the adjacent matrix.

### Usage

```
data(hprdAsigH)
```

### Examples

```
data(hprdAsigH)
```

---

```
illumina450Gr
```

```
GRange Struct of illumina 450K array.
```

---

### Description

This dataset will be used in champ.lasso functions.

### Usage

```
data(illumina450Gr)
```

**Format**

```

..@ seqnames :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. @ values : Factor w/ 24
levels "chr16","chr3",...: 1 2 3 4 5 1 4 3 6 7 ... .. @ lengths : int [1:446018] 1 2 1 1 1 1 1 1 1
... .. @ elementMetadata: NULL .. @ metadata : list() .. @ ranges :Formal class 'IRanges'
[package "IRanges"] with 6 slots .. @ start : int [1:485512] 53468112 37459206 171916037
91194674 42263294 69341139 28890100 41167802 230560793 23034447 ... .. @ width : int
[1:485512] 1 1 1 1 1 1 1 1 1 ... .. @ NAMES : chr [1:485512] "cg00000029" "cg00000108"
"cg00000109" "cg00000165" ... .. @ elementType : chr "integer" .. @ elementMetadata:
NULL .. @ metadata : list() .. @ strand :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. @ values : Factor w/ 3 levels "+","-","*": 1 2 1 2 1 2 1 2 1 2 ... .. @ lengths : int
[1:242276] 3 2 2 1 2 1 1 1 3 2 ... .. @ elementMetadata: NULL .. @ metadata : list() .. @
elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots .. @ rownames
: NULL .. @ nrows : int 485512 .. @ listData :List of 27 .. @ chrom_hg18 : Factor w/
24 levels "chr1","chr10",...: 8 16 16 1 21 6 8 21 1 7 ... .. @ MAPINFO_hg18 : int [1:485512]
52025613 37434210 173398731 90967262 42382451 68410892 28797601 41286959 228627416
20585888 ... .. @ chrom_hg38 : Factor w/ 37 levels "chr1","chr1_KI270706v1_random",...:
13 26 26 1 32 8 13 32 1 11 ... .. @ MAPINFO_hg38 : int [1:485512] 53434200 37417715
172198247 90729117 42405776 68874422 28878779 41310283 230425047 22838619 ... .. @
arm : Factor w/ 2 levels "p","q": 2 1 2 1 1 2 1 1 2 2 ... .. @ probeStrand : chr
[1:485512] "+" "+" "+" "-" ... .. @ ensemblID : chr [1:485512] "ENSG00000103479"
"ENSG00000198590" "ENSG00000075420" "ENSG00000143032" ... .. @ geneSymbol :
chr [1:485512] "RBL2" "C3orf35" "FNDC3B" "BARHL2" ... .. @ geneStrand : Factor w/ 48
levels "-", "-;-", "-;-;-",...: 24 24 24 1 24 1 24 1 1 1 ... .. @ relationtoGene : Factor w/ 21 levels
"downstream","inside",...: 3 2 2 3 2 2 2 3 2 3 ... .. @ distancetoTSS : chr [1:485512] "-250"
"31445" "158618" "-11880" ... .. @ nearestGeneBoundary: chr [1:485512] "250" "17782"
"158618" "11880" ... .. @ feature : Factor w/ 7 levels "1stExon","3'UTR",...: 6 4 4 5 2 2
1 6 5 7 ... .. @ cgi : Factor w/ 4 levels "island","open sea",...: 4 2 2 4 2 4 4 4 1 ... ..
.. @ cgiName : chr [1:485512] NA NA NA NA ... .. @ featureCgi : Factor w/ 28 levels
"1stExon - island",...: 24 14 14 20 6 8 4 24 20 25 ... .. @ conservedTfsb : Factor w/ 815
levels "V$AHR_01","V$AHR_01;V$EGR1_01;V$EGR2_01;V$EGR3_01;V$NGFIC_01",...: NA
NA NA 578 NA NA NA NA NA NA ... .. @ bwaMultiMap : Factor w/ 2 levels "0","1": 1 1 1
1 1 1 1 1 1 ... .. @ promoterAssociated : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 2 2 1 2 ... ..
.. @ asnCn : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .. @ afrCn : Factor w/ 2 levels
"0","1": 1 1 1 1 1 1 1 2 1 1 ... .. @ amrCn : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... ..
.. @ eurCn : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 1 1 1 ... .. @ asnLast4 : Factor w/ 2 levels
"0","1": 1 1 1 1 1 1 1 1 1 1 ... .. @ afrLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... ..
.. @ amrLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .. @ eurLast4 : Factor w/ 2
levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .. @ elementType : chr "ANY" .. @ elementMetadata:
NULL .. @ metadata : list() .. @ seqinfo :Formal class 'Seqinfo' [package "GenomeInfoDb"]
with 4 slots .. @ seqnames : chr [1:24] "chr16" "chr3" "chr1" "chr8" ... .. @ seqlengths : int
[1:24] NA NA NA NA NA NA NA NA NA NA ... .. @ is_circular: logi [1:24] NA NA NA NA
NA NA NA ... .. @ genome : chr [1:24] NA NA NA NA ... .. @ metadata : list()

```

**Examples**

```
data(illumina450Gr)
```

**Description**

This dataset will be used in champ.lasso functions.

**Usage**

```
data(illuminaEPICGr)
```

**Format**

```
..@ seqnames :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. ..@ values : Factor w/ 24
levels "chr19","chr20",...: 1 2 3 4 5 6 7 8 3 9 ... ..@ lengths : int [1:822229] 1 1 1 1 1 1 1 1 1
... ..@ elementMetadata: NULL .. ..@ metadata : list() ..@ ranges :Formal class 'IRanges'
[package "IRanges"] with 6 slots .. ..@ start : int [1:866836] 5236016 61847650 6841125
198303466 24072640 93581139 57865112 15248173 144921929 131463936 ... ..@ width : int
[1:866836] 2 2 2 2 2 2 2 2 2 ... ..@ NAMES : chr [1:866836] "cg07881041" "cg18478105"
"cg23229610" "cg03513874" ... ..@ elementType : chr "integer" .. ..@ elementMetadata:
NULL .. ..@ metadata : list() ..@ strand :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. ..@ values : Factor w/ 3 levels "+","-","*": 2 1 2 1 2 1 2 1 2 1 ... ..@ lengths : int
[1:433990] 3 1 1 2 2 3 1 5 1 1 ... ..@ elementMetadata: NULL .. ..@ metadata : list() ..@
elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots .. ..@ rownames
: NULL .. ..@ nrows : int 866836 .. ..@ listData : Named list() .. ..@ elementType :
chr "ANY" .. ..@ elementMetadata: NULL .. ..@ metadata : list() ..@ seqinfo :Formal class
'Seqinfo' [package "GenomeInfoDb"] with 4 slots .. ..@ seqnames : chr [1:24] "chr19" "chr20"
"chr1" "chr2" ... ..@ seqlengths : int [1:24] NA NA NA NA NA NA NA NA NA NA ... ..@
is_circular: logi [1:24] NA NA NA NA NA NA NA ... ..@ genome : chr [1:24] NA NA NA NA ...
..@ metadata : list()
```

**Examples**

```
data(illuminaEPICGr)
```

---

MatchGeneName

*MatchGeneName*

---

**Description**

Two name list used in MAP.GUI functions in ChAMP.

**Usage**

```
data(MatchGeneName)
```

**Examples**

```
data(MatchGeneName)
```

---

 multi.hit

 multi.hit information.
 

---

## Description

This dataset contains 9341 multi hit CpGs.

## Usage

```
data(multi.hit)
```

## Format

The format is: 'data.frame': 9341 obs. of 38 variables: \$ TargetID : Factor w/ 485577 levels "cg00000029","cg00000108",...: 30 92 234 246 294 325 358 374 402 418 ... \$ INFINIUM\_DESIGN\_TYPE : Factor w/ 2 levels "I","II": 1 2 1 1 2 1 2 2 2 1 ... \$ GENOME\_BUILD : int 37 37 37 37 37 37 37 37 37 37 ... \$ CHR : Factor w/ 25 levels "", "1", "10", "11", ...: 12 8 9 7 2 21 20 5 20 2 ... \$ MAPINFO : int 54746945 82925333 33318910 81580765 149370974 74508806 58777304 54500832 7339455 149719536 ... \$ CHROMOSOME\_36 : Factor w/ 26 levels "", "1", "10", "11", ...: 12 8 9 7 2 21 20 5 20 2 ... \$ COORDINATE\_36 : Factor w/ 484739 levels "", "100000057", ...: 367785 440537 259149 440391 109936 419166 365930 343920 414240 110329 ... \$ STRAND : Factor w/ 3 levels "", "F", "R": 3 2 3 2 3 3 3 2 2 3 ... \$ UCSC\_REFGENE\_NAME : Factor w/ 42456 levels "", "A1BG", "A1CF;A1CF;A1CF", ...: 19768 1 1 38813 13130 15618 1 13453 6037 1 ... \$ UCSC\_REFGENE\_ACCESSION : Factor w/ 52670 levels "", "NM\_000014", ...: 35153 1 1 598 51448 2129 1 50622 15082 1 ... \$ UCSC\_REFGENE\_GROUP : Factor w/ 4165 levels "", "1stExon", "1stExon;1stExon", ...: 2970 1 1 2035 2035 943 1 2035 2447 1 ... \$ UCSC\_CPG\_ISLANDS\_NAME : Factor w/ 27177 levels "", "chr1:10003165-10003585", ...: 1 8132 8895 1 1 23921 1 5852 1 400 ... \$ RELATION\_TO\_UCSC\_CPG\_ISLAND: Factor w/ 6 levels "", "Island", "N\_Shelf", ...: 1 6 2 1 1 2 1 2 1 2 ... \$ SNP : Factor w/ 139064 levels "", "rs10000296", ...: 88450 1 93755 1 94630 80342 79504 1 1 89545 ... \$ SNP\_DISTANCE : Factor w/ 11304 levels "", "-1", "-1;0", ...: 10743 1 2655 1 3352 1938 10243 1 1 5664 ... \$ snp.hit : int 0 0 0 0 1 0 0 0 0 0 ... \$ bwa.multi.hit : int 1 1 1 1 1 1 1 1 1 1 ... \$ analyzed : int 0 0 0 0 0 0 0 0 0 0 ... \$ DNase : int 0 0 0 0 0 1 0 0 0 0 ... \$ h3k4me3 : int 0 0 0 0 0 1 0 0 0 1 ... \$ h3k36me3 : int 0 0 0 0 0 0 0 0 0 0 ... \$ h3k27ac : int 0 0 0 0 0 1 1 0 0 0 ... \$ h3k4me1 : int 0 0 0 0 0 0 0 0 0 0 ... \$ bivalent : int 0 0 0 0 0 0 0 0 0 1 ... \$ h3k27me3 : int 0 0 0 0 0 0 0 1 0 1 ... \$ h3k9me3 : int 0 0 0 0 0 0 0 0 0 0 ... \$ dmc.constitutive : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.relapse : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.T : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.MLL : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.dic920 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.HeH : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t119 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t1221 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t922 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.iamp : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.undefined : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.nonrecurrent : int NA NA NA NA NA NA NA NA NA NA ...

## Examples

```
data(multi.hit)
```

---

PathwayList	<i>PathwayList, used in champ.GSEA()</i>
-------------	--

---

**Description**

PathwayList from MsigDB, version 4.28. Contains all pathways would be checked in GSEA process.

**Usage**

```
data(PathwayList)
```

**Format**

A list contains 8567 gene list, each represent on Pathway or Gene Module. List of 8567 \$ chr5q23 : chr [1:84] "PTMAP2" "FTMT" "PRR16" "MGC32805" ... \$ chr16q24 : chr [1:123] "LOC642452" "SNORD68" "FLJ12547" "LOC729942" ... \$ chr8q24 : chr [1:214] "KIFC2" "LYPD2" "EIF2C2" "ADCY8" ... \$ chr13q11 : chr [1:22] "LOC645626" "SNX19P2" "SKA3" "ZMYM2" ... \$ chr7p21 : chr [1:57] "CRS" "RPL36AP26" "RAD17P1" "TAS2R2" ... \$ chr10q23 : chr [1:134] "SNCG" "LOC389997" "FAM190B" "HPSE2" ... ..

**Examples**

```
data(PathwayList)
```

---

probe.features	<i>probe.features</i>
----------------	-----------------------

---

**Description**

HumanMethylation450 probe annotations

**Usage**

```
data(probe.features)
```

**Format**

A data frame with 485577 observations on the following 9 variables.

CHR a factor with levels

MAPINFO a numeric vector

Strand Strand of CpG sites.

Type type I&II probes.

gene Probe related gene.

feature a factor with levels 1stExon 3'UTR} \code{5'UTR Body IGR TSS1500 TSS200

cgi a factor with levels island open sea shelf shore



feat.cgi a factor with levels 1stExon - island 1stExon - open sea 1stExon - shelf  
 1stExon - shore 3'UTR - island} \code{3'UTR - open sea 3'UTR - shelf} \code{3'UTR - shore  
 5'UTR - island} \code{5'UTR - open sea 5'UTR - shelf} \code{5'UTR - shore  
 Body - island Body - open sea Body - shelf Body - shore IGR - island  
 IGR - open sea IGR - shelf IGR - shore TSS1500 - island TSS1500 - open sea  
 TSS1500 - shelf TSS1500 - shore TSS200 - island TSS200 - open sea TSS200 - shelf  
 TSS200 - shore  
 UCSC\_CpG\_Islands\_Name Island information.  
 DHS DHS information.  
 Enhancer Enhancer information.  
 Phantom Phantom information.  
 Probe\_SNPs If SNP exist next to CpG Sites.  
 Probe\_SNPs\_10 If SNP exist 10 bp to CpG sites.

## Examples

```
data(probe.features)
```

---

```
probe.features.epic    probe.features.epic
```

---

## Description

HumanMethylationEPIC probe annotations

## Usage

```
data(probe.features.epic)
```

## Format

A data frame with 868565 observations on the following 14 variables.

CHR a factor with levels

MAPINFO a numeric vector

Strand Strand of CpG sites.

Type type I&II probes.

gene Probe related gene.

feature a factor with levels 1stExon 3'UTR} \code{5'UTR Body IGR TSS1500 TSS200

cgi a factor with levels island open sea shelf shore

feat.cgi a factor with levels 1stExon - island 1stExon - open sea 1stExon - shelf  
 1stExon - shore 3'UTR - island} \code{3'UTR - open sea 3'UTR - shelf} \code{3'UTR - shore  
 5'UTR - island} \code{5'UTR - open sea 5'UTR - shelf} \code{5'UTR - shore  
 Body - island Body - open sea Body - shelf Body - shore IGR - island  
 IGR - open sea IGR - shelf IGR - shore TSS1500 - island TSS1500 - open sea  
 TSS1500 - shelf TSS1500 - shore TSS200 - island TSS200 - open sea TSS200 - shelf  
 TSS200 - shore

UCSC\_CpG\_Islands\_Name Island information.

SNP\_ID ID of SNP related to the probe.

SNP\_DISTANCE The distance between probe and the SNP site.

**Examples**

```
data(probe.features.epic)
```

---

```
probeInfoALL.epic.lv  Probe Info Data for use with the BMIQ normalization.
```

---

**Description**

The probe details are formatted here for the BMIQ function.

**Usage**

```
data(probeInfoALL.epic.lv)
```

**Format**

The format is: List of 3 \$ Design : num [1:867531] 2 1 2 2 1 2 2 2 1 ... \$ CGI : num [1:867531] 0 1 0 0 1 1 0 0 0 0 ... \$ probeID: chr [1:867531] "cg07881041" "cg18478105" "cg23229610" "cg03513874" ...

**Examples**

```
data(probeInfoALL.epic.lv)
```

---

```
probeInfoALL.lv  Probe Info Data for use with the BMIQ normalization.
```

---

**Description**

The probe details are formatted here for the BMIQ function.

**Usage**

```
data(probeInfoALL.lv)
```

**Format**

The format is: List of 5 \$ typeC : num [1:485577] 1 1 1 1 1 1 1 1 1 ... \$ Design : num [1:485577] 2 2 2 2 2 2 2 2 1 ... \$ GeneGroup: int [1:485577] 1 NA 5 NA 6 6 4 1 NA 2 ... \$ CGI : num [1:485577] 1 0 0 1 0 1 1 1 1 ... \$ probeID : chr [1:485577] "cg00000029" "cg00000108" "cg00000109" "cg00000165" ...

**Examples**

```
data(probeInfoALL.lv)
```

snp.hit

*CpG site related to SNP sites information.***Description**

This dataset contains snp sites located into SNP related sites.

**Usage**

```
data(snp.hit)
```

**Format**

The format is: 'data.frame': 29481 obs. of 38 variables: \$ TargetID : Factor w/ 485577 levels "cg00000029","cg00000108",...: 16 21 34 65 76 98 119 120 147 160 ... \$ INFINIUM\_DESIGN\_TYPE : Factor w/ 2 levels "I","II": 2 1 2 1 2 2 2 2 2 ... \$ GENOME\_BUILD : int 37 37 37 37 37 37 37 37 37 37 ... \$ CHR : Factor w/ 25 levels "", "1", "10", "11", ...: 13 2 2 10 2 13 18 17 3 8 ... \$ MAP-INFO : int 23913414 5937253 170490434 57839538 8739981 237027592 178364146 110612894 112068221 90066806 ... \$ CHROMOSOME\_36 : Factor w/ 26 levels "", "1", "10", "11", ...: 13 2 2 10 2 13 18 17 3 8 ... \$ COORDINATE\_36 : Factor w/ 484739 levels "", "100000057", ...: 206129 365300 143074 353467 452543 205188 156567 31100 30980 456465 ... \$ STRAND : Factor w/ 3 levels "", "F", "R": 2 2 3 3 2 3 2 3 2 2 ... \$ UCSC\_REFGENE\_NAME : Factor w/ 42456 levels "", "A1BG", "A1CF;A1CF;A1CF", ...: 19016 25371 1 37783 30924 812 811 1 1 20318 ... \$ UCSC\_REFGENE\_ACCESSION : Factor w/ 52670 levels "", "NM\_000014", ...: 38959 27879 1 36493 25264 27559 26 1 1 51089 ... \$ UCSC\_REFGENE\_GROUP : Factor w/ 4165 levels "", "1stExon", "1stExon;1stExon", ...: 2035 2035 1 2035 1216 2348 2970 1 1 2496 ... \$ UCSC\_CPG\_ISLANDS\_NAME : Factor w/ 27177 levels "", "chr1:10003165-10003585", ...: 15329 2125 1 1 1 15292 19510 1 2598 1 ... \$ RELATION\_TO\_UCSC\_CPG\_ISLAND: Factor w/ 6 levels "", "Island", "N\_Shelf", ...: 2 2 1 1 1 4 6 1 5 1 ... \$ SNP : Factor w/ 139064 levels "", "rs10000296", ...: 17352 122999 51875 43171 103744 112856 35391 40027 21722 58062 ... \$ SNP\_DISTANCE : Factor w/ 11304 levels "", "-1", "-1;0", ...: 1351 639 852 852 1410 5828 852 3352 14 508 ... \$ snp.hit : int 1 1 1 1 1 1 1 1 1 1 ... \$ bwa.multi.hit : int 0 0 0 0 0 0 0 0 0 ... \$ analyzed : int 0 0 0 0 0 0 0 0 0 0 ... \$ DNase : int 0 0 0 0 0 0 1 0 0 0 ... \$ h3k4me3 : int 0 0 0 0 0 0 1 0 0 0 ... \$ h3k36me3 : int 0 0 0 0 0 0 0 0 0 0 ... \$ h3k27ac : int 0 0 0 0 0 0 1 0 0 0 ... \$ h3k4me1 : int 0 0 0 0 0 0 1 0 0 0 ... \$ bivalent : int 0 0 0 0 0 0 0 0 0 0 ... \$ h3k27me3 : int 0 0 0 0 0 1 0 0 0 0 ... \$ h3k9me3 : int 0 0 0 0 0 0 0 0 0 0 ... \$ dmc.constitutive : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.relapse : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.T : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.MLL : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.dic920 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.HeH : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t119 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t1221 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.t922 : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.iamp : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.undefined : int NA NA NA NA NA NA NA NA NA NA ... \$ dmc.nonrecurrent : int NA NA NA NA NA NA NA NA NA NA ...

**Examples**

```
data(snp.hit)
```

---

testDataSet	<i>Test dataset.</i>
-------------	----------------------

---

**Description**

This dataset is available to test ChAMP functions.

**Usage**

```
data(testDataSet)
```

**Format**

The format is: List of 6 \$ mset :Formal class 'MethylSet' [package "minfi"] with 8 slots \$ rgSet :Formal class 'RGChannelSet' [package "minfi"] with 7 slots \$ pd :'data.frame': 6 obs. of 9 variables: ..\$ Sample\_Name ..\$ Sample\_Well ..\$ Sample\_Plate ..\$ Sample\_Group ..\$ Pool\_ID ..\$ Array ..\$ Slide ..\$ Basename \$ intensity \$ beta \$ detP

**Examples**

```
data(testDataSet)
```

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