IlluminaHumanMethylation450kanno.ilmn12.hg19

April 10, 2015

`IlluminaHumanMethylation450kanno.ilmn12.hg19`
Annotation data for the 'IlluminaHumanMethylation450k' micro array.

Description

The annotation data is based on Illumina's v1.2 annotation, specifically the file 'HumanMethylation450_15017482_v.1.2.csv' derived from 'HumanMethylation450_15017482_v.1.2.bpm'. Additional SNP annotation is generated by the authors.

Usage

```
data(IlluminaHumanMethylation450kanno.ilmn12.hg19)
```

Format

An object of class `IlluminaMethylationAnnotation`.

Details

The following changes/ modifications / addition has been made to the source material.

For the annotation related to UCSC islands, a value of `""` has been changed to `"OpenSea"`.

The creation of this object based on the Illumina annotation and additional SNP information (see below) is contained in the `createAnno.R` script in the `scripts` directory.

In addition to the SNP information provided by Illumina, we have added independent information on the overlap of the 450k with various versions of dbSNP (137, 135 and 132). The overlap is based on the mappings of the 450k loci to the hg19 genome provided by Illumina. As dbSNP we have used the 'Common' table from UCSC (ie. 'snp137Common'). This track contains variants from dbSNP which have a minor allele frequency (MAF) of greater than 1 percent (specifically, this requires dbSNP to actually contain MAF information). Furthermore, we only kept variants marked as 'single' (ie. standard single nucleotide changes, but not insertions or deletions). Scripts for

retrieving the UCSC dbSNP table and doing the overlap are contained in the `scripts` directory. The variants are described in 6 different columns. `Probe_rs` tells us the RS number (SNP ID number) for a SNP overlapping the probe, and `Probe_maf` is the minor allelle frequency for the SNP (in case multiple SNPs overlap, only one is recorded). Similarly, `CpG_rs` describe SNPs overlapping the CpG site and `SBE_rs` the single base extension of the measured methylation loci.

Source

See description.

Examples

```
data(IlluminaHumanMethylation450kanno.ilmn12.hg19)
```

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