

Package ‘cheung2010’

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Title resources for genetics of gene expression based on Cheung et al 2010

Version 0.0.29

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Description Data resources related to the PLoS Biology paper Polymorphic Cis- and Trans-Regulation of Human Gene Expression, including small-footprint smlSet support for 147 hgfocus arrays and corresponding HapMap genotypes at 1.3 million SNP; 0.0.22+ includes cheung_eset... from Leek et al RECOUNT myrna output

Depends R (>= 2.13.0), Biobase, GGtools, GenomicRanges, hgfocus.db

Imports AnnotationDbi

Suggests SNPlocs.Hsapiens.dbSNP.20100427,SNPlocs.Hsapiens.dbSNP.20101109,

Enhances parallel

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License Artistic 2.0

LazyLoad yes

biocViews GeneticVariability, RNAseqData

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```
cheung2010-package    resources for genetics of gene expression based on Cheung et al 2010
                      ~~ package title ~~
```

Description

Data resources related to the PLoS Biology paper Polymorphic Cis- and Trans-Regulation of Human Gene Expression, including small-footprint smlSet support for 147 hgfocus arrays and corresponding HapMap genotypes at 1.3 million SNP ~~ A concise (1-5 lines) description of the package
~~

Details

```
Package:    cheung2010
Version:    0.0.16
Depends:    R (>= 2.13.0), Biobase, GGtools, GenomicRanges, hgfocus.db
Imports:    AnnotationDbi
Suggests:   SNPlocs.Hsapiens.dbSNP.20101109
License:    private
LazyLoad:   yes
Packaged:   2011-04-13 16:52:30 UTC; stvjc
Built:      R 2.14.0; ; 2011-06-13 16:19:18 UTC; unix
```

Index:

```
cheung2010locs          cheung2010locs gives locations for HapMap phase
                        3 SNPs for CEPH CEU
cheung_eset from RECOUNT web resource for RNA-seq http://bowtie-bio.sourceforge.net/recount/
cheung_eset_notrunc from RECOUNT web resource for RNA-seq
```

Further information is available in the following vignettes:

cheungTrans (source, pdf)

This package assembles data relevant to Cheung et al PLoS Biology (2010; 8(9)).

Author(s)

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Maintainer: Vince Carey <stvjc@channing.harvard.edu>

cheung2010locs	<i>cheung2010locs gives locations for HapMap phase 3 SNPs for CEPH CEU</i>
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Description

cheung2010locs gives locations for HapMap phase 3 SNPs for CEPH CEU

Usage

```
data(cheung2010locs)
```

Format

The format is:

```
Formal class 'GRangesList' [package "GenomicRanges"] with 5 slots
..@ partitioning :Formal class 'PartitioningByEnd' [package "IRanges"] with 5 slots
.. ..@ end : int [1:22] 112259 226087 320873 406401 493642 585295 660727 735268 798907
871895 ...
.. ..@ NAMES : chr [1:22] "chr1" "chr2" "chr3" "chr4" ...
.. ..@ elementType : chr "integer"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ unlistData :Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
.. ..@ seqnames :Formal class 'Rle' [package "IRanges"] with 4 slots
.. .. ..@ values : Factor w/ 22 levels "chr1","chr2",...: 1 2 3 4 5 6 7 8 9 10 ...
.. .. ..@ lengths : int [1:22] 112259 113828 94786 85528 87241 91653 75432 74541 63639
72988 ...
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
.. .. ..@ start : int [1:1365825] 554340 557616 711153 742429 742584 743268 744045 750775
751010 751595 ...
.. .. ..@ width : int [1:1365825] 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..@ NAMES : chr [1:1365825] "rs6650104" "rs11510103" "rs12565286" "rs3094315" ...
.. .. ..@ elementType : chr "integer"
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. ..@ strand :Formal class 'Rle' [package "IRanges"] with 4 slots
.. .. ..@ values : Factor w/ 3 levels "+","-","*": 1
.. .. ..@ lengths : int 1365825
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. ..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 1365825
.. .. ..@ listData :List of 1
```

```

.. .. .. .. ..$ assignment: Factor w/ 7 levels ".","A/C","A/G",...: 3 3 5 3 3 2 3 6 6 6 ...
.. .. .. .. ..@ elementType : chr "ANY"
.. .. .. .. ..@ elementMetadata: NULL
.. .. .. .. ..@ metadata : list()
.. .. .. .. ..@ seqinfo :Formal class 'Seqinfo' [package "GenomicRanges"] with 3 slots
.. .. .. .. ..@ seqnames : chr [1:22] "chr1" "chr2" "chr3" "chr4" ...
.. .. .. .. ..@ seqlengths : int [1:22] NA NA NA NA NA NA NA NA NA NA NA ...
.. .. .. .. ..@ is_circular: logi [1:22] NA NA NA NA NA NA ...
.. .. .. .. ..@ metadata : list()
.. .. .. .. ..@ elementType : chr "GRanges"
.. .. .. .. ..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. .. .. .. ..@ rownames : NULL
.. .. .. .. ..@ nrows : int 22
.. .. .. .. ..@ listData : Named list()
.. .. .. .. ..@ elementType : chr "ANY"
.. .. .. .. ..@ elementMetadata: NULL
.. .. .. .. ..@ metadata : list()
.. .. .. .. ..@ metadata : list()

```

Details

obtained as the 'support' elements after [read.HapMap.data](#) was run on the files noted below.

Source

for example,

http://hapmap.ncbi.nlm.nih.gov/downloads/genotypes/hapmap3_r3/hapmap_format/polymorphic/genotypes_chr17_CEU_phase3.3_nr.b36_fwd.txt.gz

Examples

```

data(cheung2010locs)
names(cheung2010locs)
cheung2010locs[[1]][1:3]

```

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