

# Package ‘cheung2010’

October 8, 2013

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

**Version** 0.0.27

**Author** Vince Carey <stvjc@channing.harvard.edu>

**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

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

**License** Artistic 2.0

**LazyLoad** yes

**biocViews** GeneticVariability, RNAseqData

## R topics documented:

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

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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 *~~ 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)

Vince Carey <stvjc@channing.harvard.edu>

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

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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](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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