

# cheung2010

March 23, 2012

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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  
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## 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>.  
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)).

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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 ...
.. .. .. ..@ 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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