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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 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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