

# Package ‘rehh.data’

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**Maintainer** Mathieu Gautier <mathieu.gautier@supagro.inra.fr>

**Author** Mathieu Gautier, Alexander Klassmann and Renaud Vitalis

**Version** 1.0.0

**License** GPL (>= 2)

**Title** Data Only: Searching for Footprints of Selection using Haplotype Homozygosity Based Tests

**Description** Contains example data for the 'rehh' package.

**Depends** R (>= 2.10)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-11-08 11:10:29

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rehh.data-package	<i>Data Only: Searching for Footprints of Selection using Haplotype Homozygosity Based Tests</i> Description: Contains example data for the 'rehh' package.
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## Description

Contains example data for the package rehh.

**Details**

Package: rehh.data  
 Version: 1.0.0  
 License: GPL(>=2)

**Index:**

wgscan.cgu	Whole genome scan results for the CGU (Creole from Guadeloupe island)
wgscan.eut	Whole genome scan results for a pool of European taurine cattle

**References**

Gautier M., Klassmann A., and Vitalis R. (2016). rehh: An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Molecular Ecology Resources*, submitted

Gautier M. and Vitalis R. (2012). rehh: An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Bioinformatics*, **28**(8), 1176–1177.

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

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wgscan.cgu	<i>Whole genome scan results for the CGU (Creole from Guadeloupe island)</i>
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**Description**

A dataframe object with of 44,057 rows (SNPs) and 7 columns: i) chromosome name (CHR), ii) position of the SNP in bp (POSITION), iii) Ancestral allele frequency (freq\_A), iv) iHH for the ancestral allele (iHH\_A), v) iHH for the derived allele (iHH\_D), vi) iES using the estimator by Tang et al. (2007) (iES\_Tang\_et\_al\_2007), vii) iES using the estimator by Sabeti et al. (2007) (iES\_Sabeti\_et\_al\_2007).

**Usage**

```
data(wgscan.cgu)
```

**References**

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

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`wgscan.eut`*Whole genome scan results for a pool of European taurine cattle*

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**Usage**

```
data(wgscan.eut)
```

**References**

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

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\*Topic **package**

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