

# Package ‘dsQTL’

October 8, 2013

**Title** dsQTL, data excerpt from Degner et al. 2012 Nature letter

**Version** 0.0.23

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

**Description** dsQTL, excerpt from Degner et al. 2012 Nature letter on DNA variants associated with DnaseI hypersensitivity

**Suggests**

**Depends** R (>= 2.15.0), utils, GenomicRanges, Biobase, GGBase

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**License** Artistic-2.0

**LazyLoad** yes

**biocViews** genetics, HighThroughputSequencingData, ExperimentData

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## Description

dsQTL, excerpt from Degner et al. 2012 Nature letter on DNA variants associated with DnaseI hypersensitivity

**Details**

Package: dsQTL  
Version: 0.0.4  
Suggests:  
Depends: R (>= 2.15.0), utils, GenomicRanges  
License: Artistic 2.0  
LazyLoad: yes  
biocViews: genetics  
Built: R 2.15.0; ; 2012-03-12 00:41:13 UTC; unix

This package represents a selection of genotype and DNase-seq data for illustration of dsQTL identification.

The slide deck for the Feb 2012 Seattle Bioconductor workshop has illustrations.

A utility function SE2ES will create an ExpressionSet instance from a SummarizedExperiment as serialized here.

**Author(s)**

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**References**

PMID 22307276

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