**BSgenome.Athaliana.TAIR.01222004**

October 16, 2009

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**Athaliana**

*Arabidopsis thaliana full genome (TAIR version from January 22, 2004)*

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**Description**

Arabidopsis thaliana full genome as provided by TAIR (snapshot from January 22, 2004) and stored in Biostrings objects.

**Note**

This BSgenome data package was made from the following source data files:

ATH1_chr1.1con.01222004
ATH1_chr2.1con.01222004
ATH1_chr3.1con.01222004
ATH1_chr4.1con.01222004
ATH1_chr5.1con.01222004
mitochondrial_genomic_sequence
ATH1_chloroplast.1con.01072002

See [BSgenomeForge](http://example.com) and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

**Author(s)**

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**See Also**

BSgenome-class, DNAString-class, available.genomes, BSgenomeForge
Examples

Athaliana
seglengths(Athaliana)
Athaliana$chr1 # same as Athaliana[["chr1"]]

if ("AGAPS" %in% masknames(Athaliana)) {
  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
    ## Replace all masks by the inverted AGAPS mask
    masks(seq) <- gaps(masks(seq)["AGAPS"])
    unique_letters <- uniqueLetters(seq)
    if (any(unique_letters != "N"))
      stop("assembly gaps contain more than just Ns")
  }

  ## A message will be printed each time a sequence is removed
  ## from the cache:
  options(verbose=TRUE)

  for (seqname in seqnames(Athaliana)) {
    cat("Checking sequence", seqname, "...
    seq <- Athaliana[[seqname]]
    checkOnlyNsInGaps(seq)
    cat("OK
"
  }
}

## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
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