

The sceUpstr support in package harbChIP

HJB/VJC

April 17, 2025

Contents

1	Introduction	1
2	Building the sceUpstr object	1
3	Checking a finding of Harbison et al.	2

1 Introduction

The intent of this package is to allow code like the following:

```
> library(harbChIP)
> data(sceUpstr)
> sceUpstr
```

```
upstreamSeqs instance, organism sce
```

```
There are 6674 entries
```

```
first keys:
```

```
[1] "YAL001C" "YAL002W" "YAL003W" "YAL004W" "YAL005C"
```

```
> getUpstream("YAL001C", sceUpstr)
```

```
$YAL001C
```

```
500-letter DNASTring object
```

```
seq: CTGTACCACTATAATAATTTATCTTGATCGTATTAT...AGGACGTTTGGTTGAAGCCAAGCTAGCCACAAGAAAA
```

2 Building the sceUpstr object

Upstream sequences of length 500bp were obtained from the SGD website:

www.yeastgenome.org -> Download Data -> FTP

[sequence/genomic_sequence/orf_dna/archive/utr5_sc_500.20040206.fasta.gz](http://www.yeastgenome.org/sequence/genomic_sequence/orf_dna/archive/utr5_sc_500.20040206.fasta.gz)

```
> fname = system.file("extdata/utr5_sc_500_20040206.fasta", package="sceUpstr")
> utr5 = readFASTA(fname)
> sceUpstr = buildUpstreamSeqs2(utr5)
> save(sceUpstr, file="sceUpstr.rda")
```

3 Checking a finding of Harbison et al.

It is asserted in Fig 1 B of the paper that GGCGCTA is specifically bound by Snt2. We will examine the frequency of this heptamer in upstream regions and relate to the binding ratio distribution.