

# hugene.1.0.st.v1frmavecs

September 24, 2025

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hugene.1.0.st.v1barcodevecs

*Vectors used by barcode function for hugene.1.0.st.v1.*

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## Description

Parameters of the background distribution for use with the barcode function. These correspond to version 3.0 of the Gene Expression Barcode website.

## Usage

```
data(hugene.1.0.st.v1barcodevecs)
```

## Format

A list with 3 elements.

|         |                                |
|---------|--------------------------------|
| mu      | background means               |
| tau     | background standard deviations |
| entropy | observed gene entropy          |

## Examples

```
data(hugene.1.0.st.v1barcodevecs)  
str(hugene.1.0.st.v1barcodevecs)
```

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`hugene.1.0.st.v1frmavecs`*Vectors used by fRMA for hugene.1.0.st.v1.*

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**Description**

Frozen parameter vectors for use with the `frma` and `GNUSE` functions.

**Usage**

```
data(hugene.1.0.st.v1frmavecs)
```

**Format**

A list with 6 elements.

|                              |                                                        |
|------------------------------|--------------------------------------------------------|
| <code>normVec</code>         | normalization vector                                   |
| <code>probeVec</code>        | probe effect vector                                    |
| <code>probeVarWithin</code>  | within batch probe variance                            |
| <code>probeVarBetween</code> | between batch probe variance                           |
| <code>probesetSD</code>      | within probeset standard deviation                     |
| <code>medianSE</code>        | median standard error for gene expression estimates    |
| <code>probeVecCore</code>    | exon effect vector for summarizing to core transcripts |
| <code>mapCore</code>         | mapping between exons and core transcripts             |

**Examples**

```
data(hugene.1.0.st.v1frmavecs)
str(hugene.1.0.st.v1frmavecs)
```

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