

# huex.1.0.st.v2frmavecs

April 24, 2024

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huex.1.0.st.v2barcodevecs

*Vectors used by barcode function for huex.1.0.st.v2.*

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## Description

Parameters of the background distribution for use with the barcode function.

## Usage

```
data(huex.1.0.st.v2barcodevecs)
```

## Format

A list with 3 elements.

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

## Examples

```
data(huex.1.0.st.v2barcodevecs)  
str(huex.1.0.st.v2barcodevecs)
```

huex.1.0.st.v2frmavecs

*Vectors used by fRMA for huex.1.0.st.v2.*

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### **Description**

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

### **Usage**

```
data(huex.1.0.st.v2frmavecs)
```

### **Format**

A list with 6 elements.

|                 |  |
|-----------------|--|
| normVec         | normalization vector   |
| probeVec        | probe effect vector  |
| probeVarWithin  | within batch probe variance                                  |
| probeVarBetween | between batch probe variance                                 |
| probesetSD      | within probeset standard deviation                           |
| medianSE        | median standard error for gene expression estimates          |
| probeVecCore    | exon effect vector when summarizing to core transcripts      |
| probeVecExt     | probe effect vector when summarizing to extended transcripts |
| probeVecFull    | probe effect vector when summarizing to full transcripts     |
| mapCore         | mapping between exons and core transcripts                   |
| mapExt          | mapping between exons and extended transcripts               |
| mapFull         | mapping between exons and full transcripts                   |

### **Examples**

```
data(huex.1.0.st.v2frmavecs)  
str(huex.1.0.st.v2frmavecs)
```

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