

# mogene.1.0.st.v1frmavecs

October 20, 2017

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mogene.1.0.st.v1barcodevecs

*Vectors used by barcode function for mogene.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(mogene.1.0.st.v1barcodevecs)`

## Format

A list with 3 elements.

<code>mu</code>	background means
<code>tau</code>	background standard deviations
<code>entropy</code>	observed gene entropy

## Examples

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

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mogene.1.0.st.v1frmavecs

*Vectors used by fRMA for mogene.1.0.st.v1.*

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## Description

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

## Usage

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

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