# Package 'flowPloidyData'

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Title Example Flow Cytometry Data			
<b>Version</b> 1.33.0			
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<b>Description</b> A collection of raw flow cytometry data for use in vignettes for the flowPloidy package.			
License GPL-3			
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LazyData true			
biocViews FlowCytometryData			
Suggests knitr, rmarkdown, flowCore			
VignetteBuilder knitr			
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```
flowPloidyData
```

#### Description

A list of LMD files from analyses of the plant leaf tissue samples, co-chopped with standards with known GC (e.g., tomato, soybean etc.).

### Usage

```
flowPloidyFiles()
fpBad()
fpVac()
```

### Format

The function flowPloidyFiles returns a vector of filenames corresponding to the LMD files provided by this package. Individual elements of this vector (e.g., flowPloidyFiles()[1] can be passed to functions that load a single FCS file, such as flowCore::read.FCS. The entire vector can be passed to functions that load multiple files, such as flowPloidy::histBatch.

Each element is named with the filename (without the path), so that you can select an individual filename either by numeric index (i.e., flowPloidyFiles()[7]) or by name (flowPloidyFiles()["248+S.LMD"]). The names aren't meaningful to you, of course! I added them to provide a more robust way to select an individual file, as the order of files may change in package updates.

The individual files named in flowPloidyFiles are LMD files generated by a Beckman-Coulter Gallios flow cytometer. They represent a variety of samples, and some of them are low quality. They are not ideal data sets, but rather represent a range of data quality for assessing the performance of flowPloidy.

fpBad() and fpVac() each return the path to a single LMD file. These are particularly poor quality files that are used in some of the unit tests for flowPloidy. They're probably not useful to regular users.

### Value

A named character vector of file names, including their full path in the local file system.

#### Examples

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