

# Package ‘flowPloidyData’

April 14, 2020

**Title** Example Flow Cytometry Data  
**Version** 1.12.0  
**Author** Tyler Smith <tyler@plantarum.ca>  
**Maintainer** Tyler Smith <tyler@plantarum.ca>  
**Description** A collection of raw flow cytometry data for use in vignettes for the flowPloidy package.  
**License** GPL-3  
**Encoding** UTF-8  
**LazyData** true  
**biocViews** FlowCytometryData  
**Suggests** knitr, rmarkdown, flowCore  
**VignetteBuilder** knitr  
**git\_url** <https://git.bioconductor.org/packages/flowPloidyData>  
**git\_branch** RELEASE\_3\_10  
**git\_last\_commit** 0c9a917  
**git\_last\_commit\_date** 2019-10-29  
**Date/Publication** 2020-04-14

## R topics documented:

flowPloidyData . . . . .	1
<b>Index</b>	<b>3</b>

---

flowPloidyData	<i>Example flow cytometry datasets from analysis of ploidy in plants.</i>
----------------	---

---

## 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

```
flowPloidyFiles() ## a character vector of file names

## Read in the first file:
library(flowCore)
fcs <- read.FCS(flowPloidyFiles()[1], dataset = 1,
               alter.names = TRUE)
```

# Index

## \*Topic **datasets**

flowPloidyData, [1](#)

flowPloidyData, [1](#)

flowPloidyFiles (flowPloidyData), [1](#)

fpBad (flowPloidyData), [1](#)

fpVac (flowPloidyData), [1](#)