

Importing the data set

The original experiment is listed on the Gene Expression Omnibus as GSE848; however, this tutorial only uses a subset of the original experiment and should be downloaded from the Partek website tutorial page, [Gene Expression Analysis with Batch Effects](#).

- Download the zipped project folder, *Breast_Cancer-GE.zip*
- Unzip the project folder to *C:/Partek Training Data/* or a directory of your choosing

This location should be easily accessible. The unzipped *Breast_Cancer-GE* project folder and a zipped annotation file will be added to the selected directory.

- Unzip the included annotation file, *HG_U95Av2.na32.annot.rar*
- Move the annotation file, *HG_U95Av2.na32.annot*, to the microarray libraries folder

By default, the microarray libraries folder will be located at *C:/Microarray Libraries*, but the location may vary depending on your operating system and configuration.

- Open Partek Genomics Suite
- Select () from the main command bar
- Navigate to the tutorial folder, *Breast_Cancer-GE*
- Select *Breast_Cancer.txt*
- Select **Open** (Figure 1)

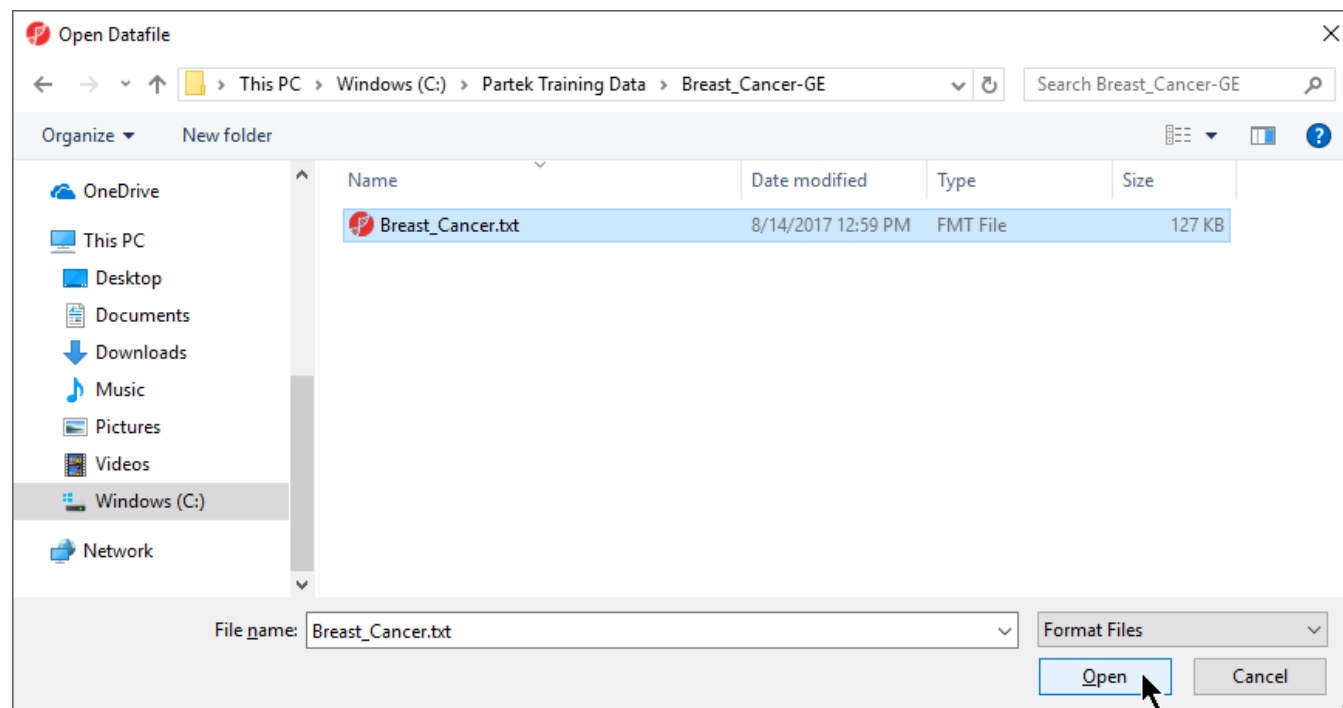


Figure 3. Opening a data file. The red Partek Genomics Suite icon is shown next to the data file (FMT file format)

The spreadsheet will open as 1 (*Breast_Cancer.txt*) (Figure 2).

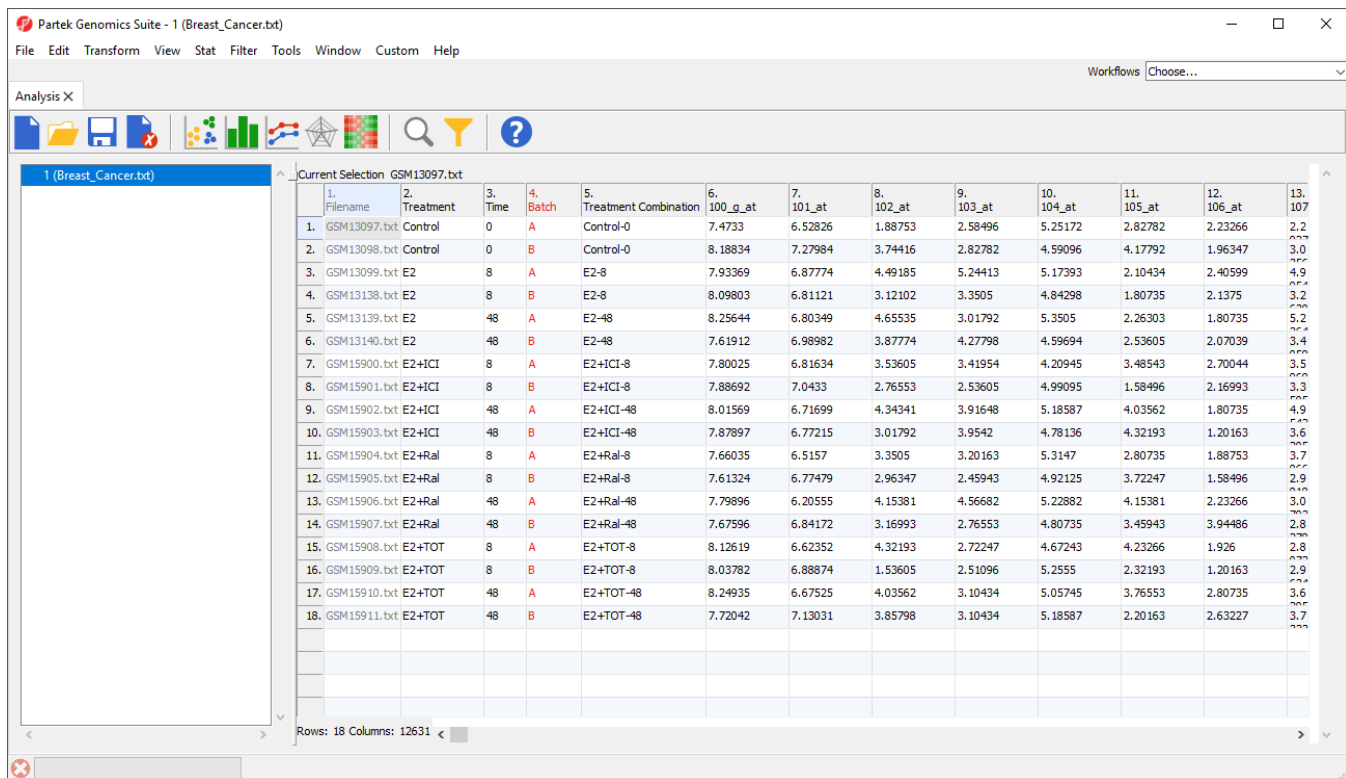


Figure 4. Breast_Cancer.txt data file

The summary at the bottom of the spreadsheet shows there are 18 rows and 12,631 columns in the spreadsheet. The first column contains the *Filename* listing the GEO GSM number. This is also an identifier for the microarray. *Treatment*, *Time*, and *Batch* are in columns 2, 3, and 4, respectively. Column 6 marks the beginning of the probesets. The data is $\log_2$ transformed.

« Gene Expression Analysis with Batch Effects Adding an annotation link »

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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