

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)

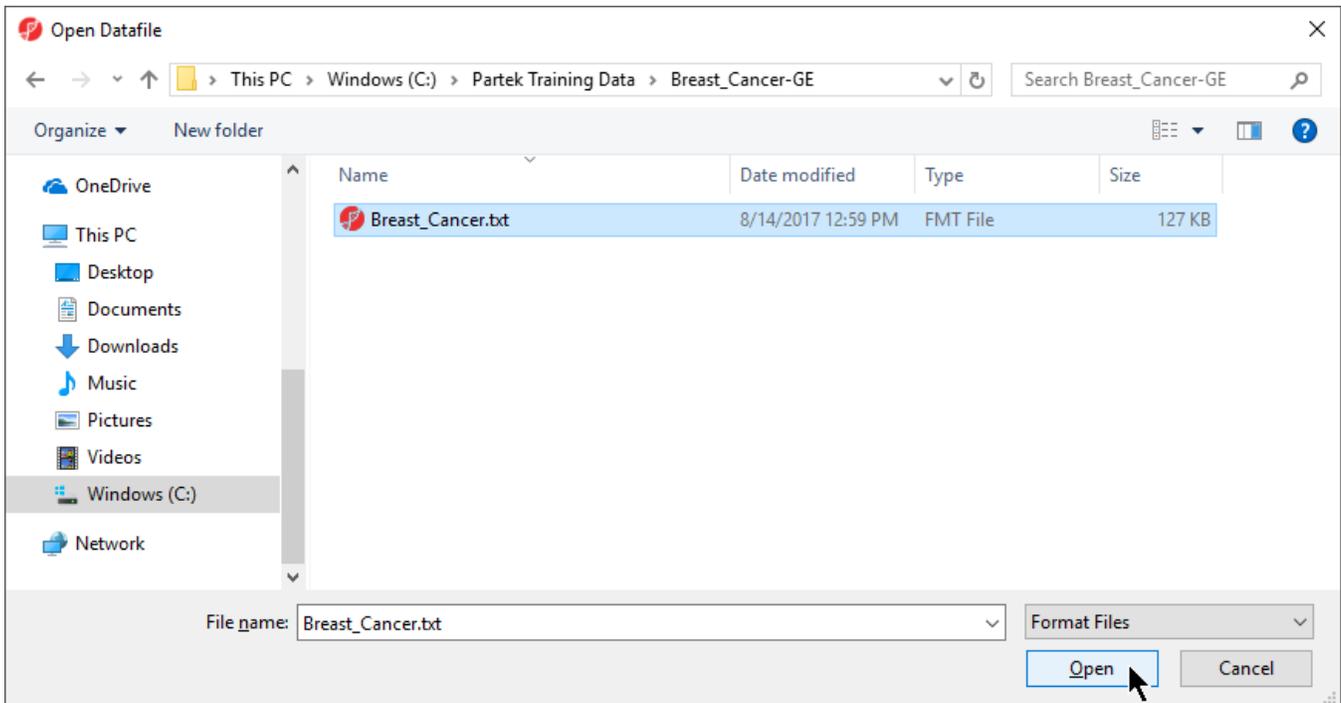


Figure 3. Opening a data file. The red Partek Genomics Suite icon is shown next to the data file (FMT file format)

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

Partek Genomics Suite - 1 (Breast_Cancer.txt)

File Edit Transform View Stat Filter Tools Window Custom Help

Workflows Choose...

Analysis X

1 (Breast_Cancer.txt)

Current Selection: GSM13097.txt

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.
Filename	Treatment	Time	Batch	Treatment Combination	100_g_at	101_at	102_at	103_at	104_at	105_at	106_at	107
1. GSM13097.txt	Control	0	A	Control-0	7.4733	6.52826	1.88753	2.58496	5.25172	2.82782	2.23266	2.2
2. GSM13098.txt	Control	0	B	Control-0	8.18834	7.27984	3.74416	2.82782	4.59096	4.17792	1.96347	3.0
3. GSM13099.txt	E2	8	A	E2-8	7.93369	6.87774	4.49185	5.24413	5.17393	2.10434	2.40599	4.9
4. GSM13138.txt	E2	8	B	E2-8	8.09803	6.81121	3.12102	3.3505	4.84298	1.80735	2.1375	3.2
5. GSM13139.txt	E2	48	A	E2-48	8.25644	6.80349	4.65535	3.01792	5.3505	2.26303	1.80735	5.2
6. GSM13140.txt	E2	48	B	E2-48	7.61912	6.98982	3.87774	4.27798	4.59694	2.53605	2.07039	3.4
7. GSM15900.txt	E2+ICI	8	A	E2+ICI-8	7.80025	6.81634	3.53605	3.41954	4.20945	3.48543	2.70044	3.5
8. GSM15901.txt	E2+ICI	8	B	E2+ICI-8	7.88692	7.0433	2.76553	2.53605	4.99095	1.58496	2.16993	3.3
9. GSM15902.txt	E2+ICI	48	A	E2+ICI-48	8.01569	6.71699	4.34341	3.91648	5.18587	4.03562	1.80735	4.9
10. GSM15903.txt	E2+ICI	48	B	E2+ICI-48	7.87897	6.77215	3.01792	3.9542	4.78136	4.32193	1.20163	3.6
11. GSM15904.txt	E2+Ral	8	A	E2+Ral-8	7.66035	6.5157	3.3505	3.20163	5.3147	2.80735	1.88753	3.7
12. GSM15905.txt	E2+Ral	8	B	E2+Ral-8	7.61324	6.77479	2.96347	2.45943	4.92125	3.72247	1.58496	2.9
13. GSM15906.txt	E2+Ral	48	A	E2+Ral-48	7.79896	6.20555	4.15381	4.56682	5.22882	4.15381	2.23266	3.0
14. GSM15907.txt	E2+Ral	48	B	E2+Ral-48	7.67596	6.84172	3.16993	2.76553	4.80735	3.45943	3.94486	2.8
15. GSM15908.txt	E2+TOT	8	A	E2+TOT-8	8.12619	6.62352	4.32193	2.72247	4.67243	4.23266	1.926	2.8
16. GSM15909.txt	E2+TOT	8	B	E2+TOT-8	8.03782	6.88874	1.53605	2.51096	5.2555	2.32193	1.20163	2.9
17. GSM15910.txt	E2+TOT	48	A	E2+TOT-48	8.24935	6.67525	4.03562	3.10434	5.05745	3.76553	2.80735	3.6
18. GSM15911.txt	E2+TOT	48	B	E2+TOT-48	7.72042	7.13031	3.85798	3.10434	5.18587	2.20163	2.63227	3.7

Rows: 18 Columns: 12631

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.



Your Rating:  Results:  43 rates