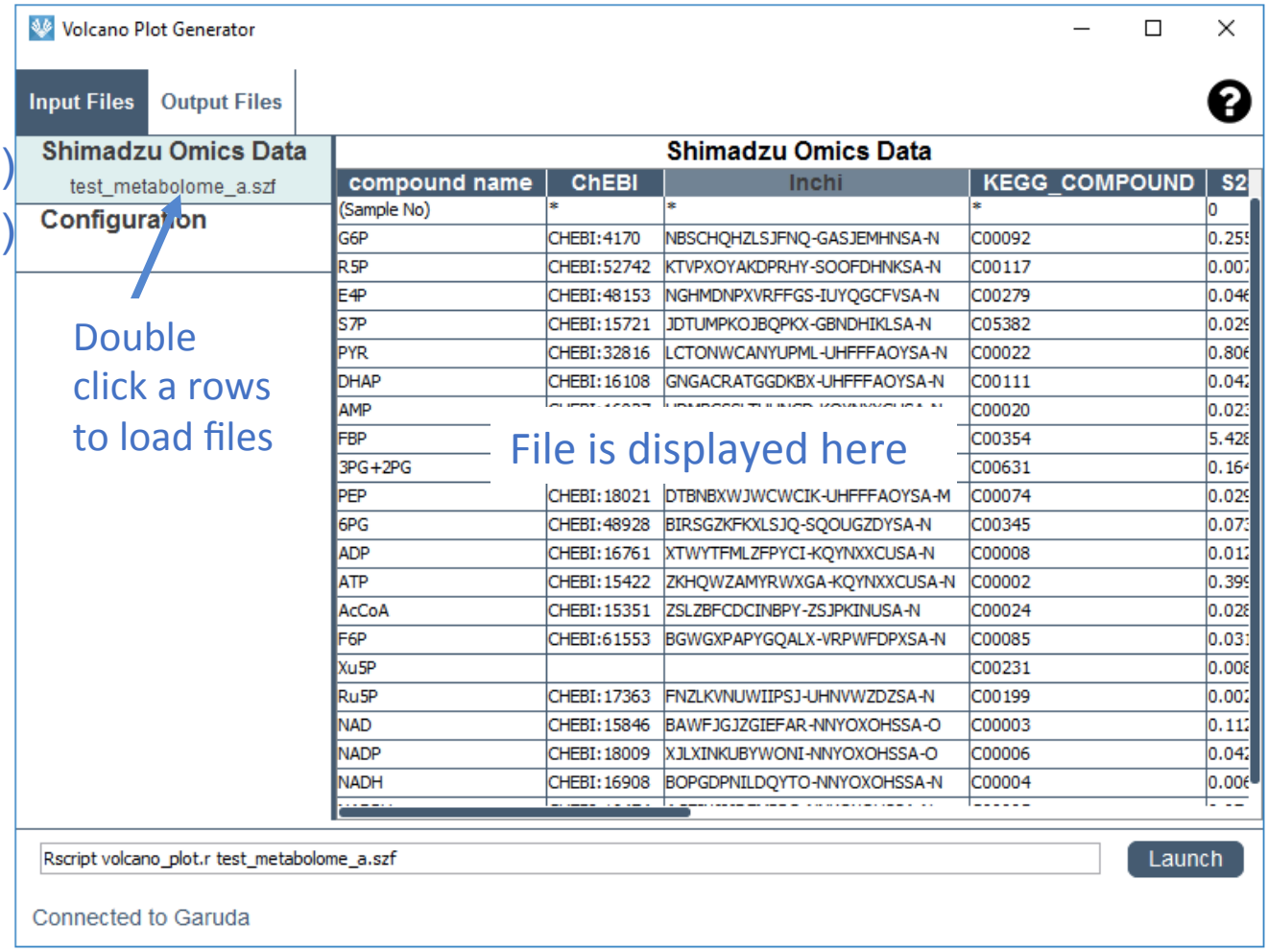
# Volcano Plot (Input)

This gadget generates volcano plot visualization and calculates statistics of volcano plot analysis from metabolome abundance (lcms) data of Shimadzu.




The gadget require one input file; **Shimazu metabolome abundance data** (e.g., test_metabolome_a.szf)

**Sample File:**

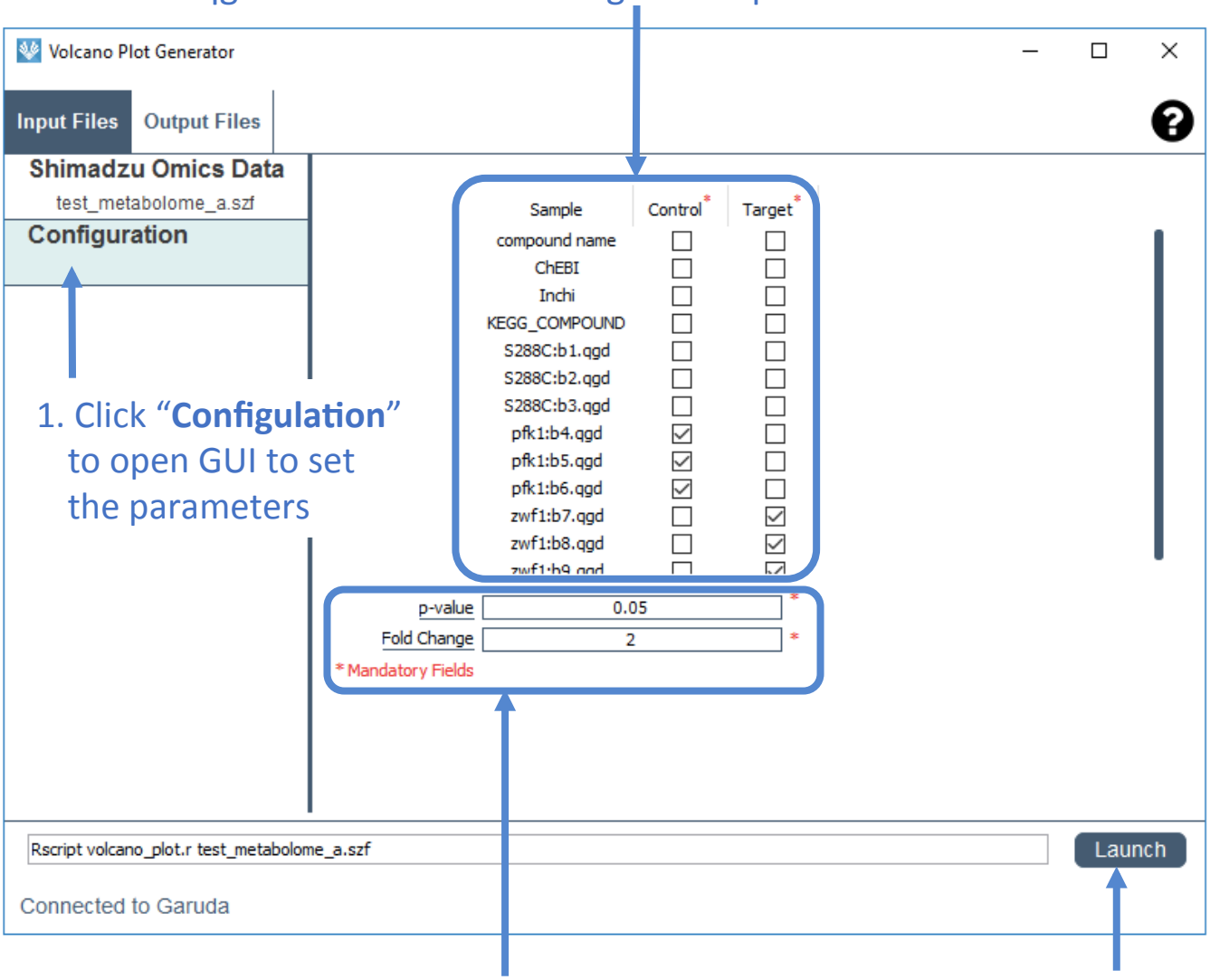
Sample file to test is available under **Samples > szf**

**Required R and R package: R > 3.2.2 is required.** "limma", "pcaMethods", "crmn", and "metabolomics" packages are required. The gadget automatically install the packages in your computer, if the gadgets were not installed in your computer.

# Volcano Plot (Input)

## (parameter settings)

2. Select "**control**" and "**target**" samples for Volcano plot analysis. In this example, "pfk1.b4.qgd, pfk1.b5.qgd, pfk1.b6.qgd" are selected as "Control" samples, while "zwf1.b7.qgd, zwf1.b8.qgd, zwf1.b9.qgd" are selected as "Target" samples.

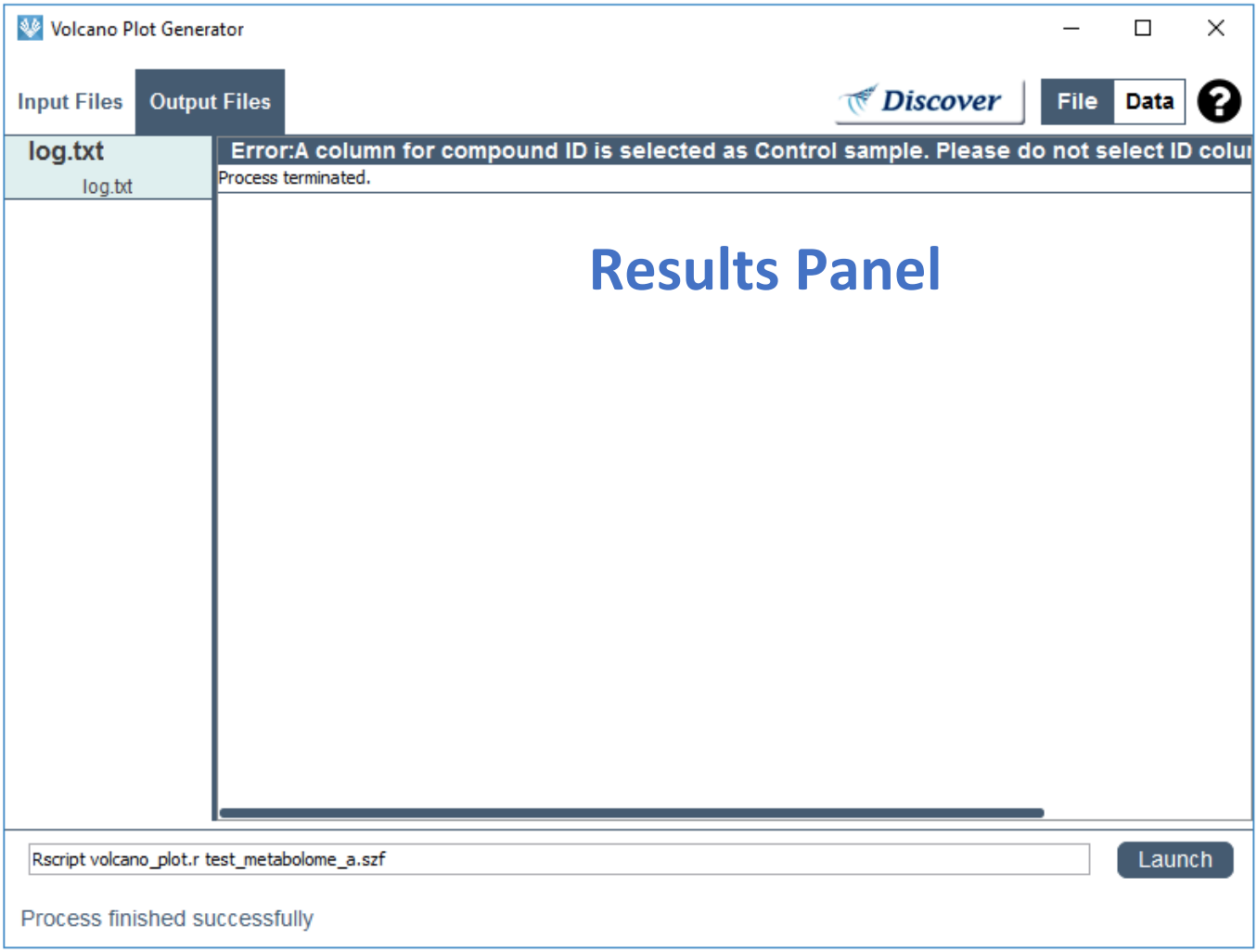



1. Click "**Configulation**" to open GUI to set the parameters

3. Set threshold value of p-value and that of foldchange for volcano plot analysis. In the example, 0.05 and 2 are selected as threshold values for p-value and fold-change, respectively.

4. Click the bottom to do volcano plot analysis after data upload after data upload and parameter setting

# Volcano Plot (Output)

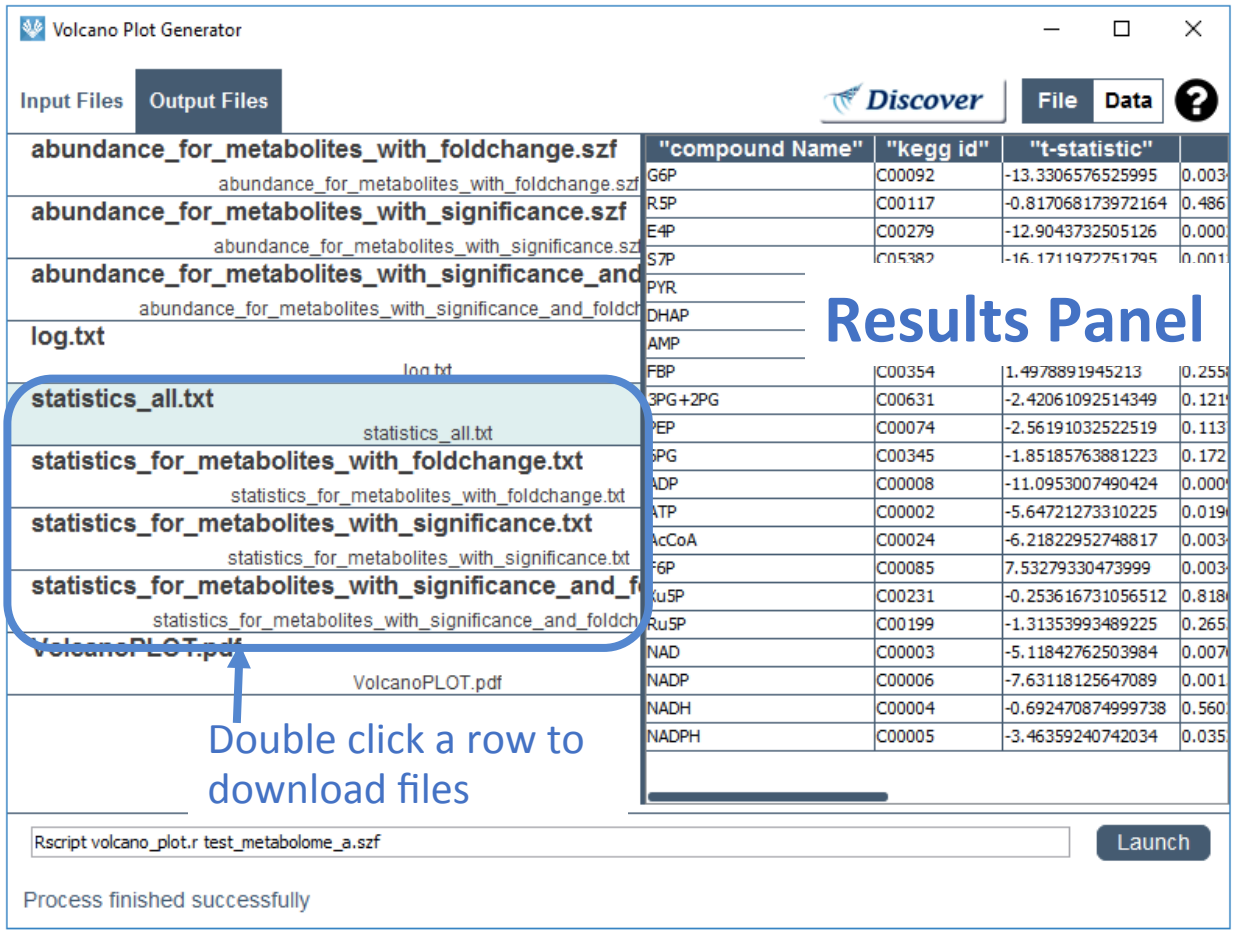



**Log file to check if the analysis runs successfully**

After “Launch” the analysis, the log.txt file would be generated to see if the analysis results are successfully generated

- “log.txt” is the log file of the analysis run results. If you see any error message, please revisit if your input file setting is correct.

# Volcano Plot (output)

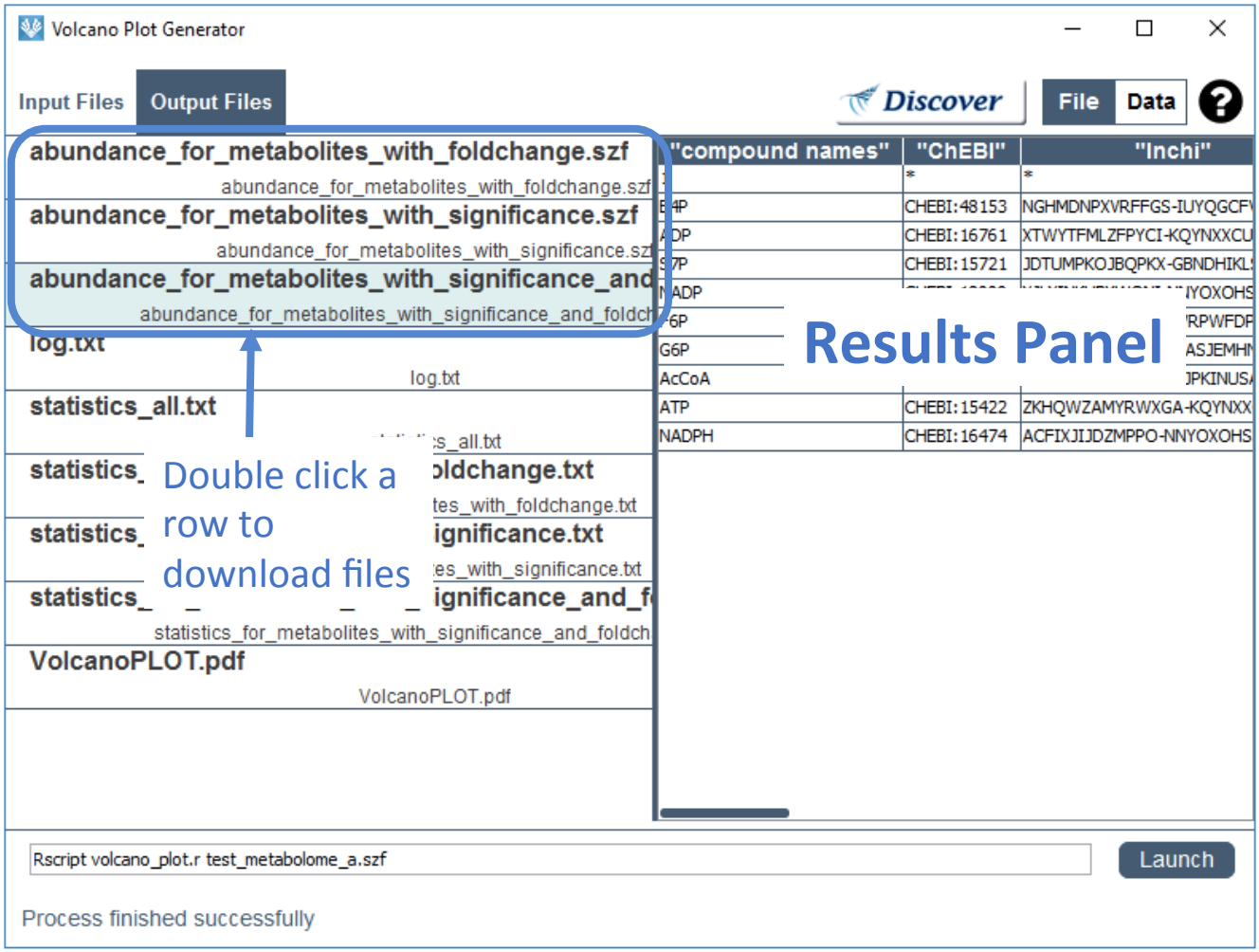



**Statistics from Volcano plot analysis.**

Four result files for statistics will be generated by the volcano analysis gadget.

- “statistics_all.txt” is statistics for all metabolites.
- “statistics_for_metabolites_with_significance.txt” is statistics for metabolites with p-value lower than user defined threshold value of p-value.
- “statistics_for_metabolites_with_foldchange.txt” is statistics for metabolites with foldchange greater than user defined threshold value.
- “statistics_for_metabolites_with_significance_and_foldchange.txt ” is statistics for metabolites with p-value and foldchange that are lower and greater than user defined threshold values, respectively.

# Volcano Plot (output)




**Metabolome abundance data from Volcano plot analysis.**

Three files for metabolome abundance will be generated by the volcano analysis gadget.

- “abundance_for_metabolites_with_significance.szf” is abundance for metabolites with p-value lower than user defined threshold value of p-value.
- “abundance_for_metabolites_with_foldchange.szf” is abundance for metabolites with foldchange greater than user defined threshold value.
- “abundance_for_metabolites_with_significance_and_foldchange.szf” is abundance for metabolites with p-value and foldchange that are lower and greater than user defined threshold values, respectively.

# Volcano Plot (output)

This gadget generates volcano plot visualization.