

Data

For RNA-seq studies, MetaOmics allows input of both raw count data and continuous data (e.g. FPKM/RPKM/TPM). For MetaDE and MetaPath modules, the count data is recommended for better statistical power and accuracy. For the other modules, the meta-analysis methods will require continuous data input.

(1) Choosing/Upload Expression Data

(2) Upload Clinical Data

Preprocessing

(3) Annotate / Impute / Replicate

Saving Study

Type of Data

microarray

Study Name:

some study

save single study

some study Summary

[1] "No file uploaded"

Expression Data Preview

Clinical Data Preview