**Installation Steps for RPhenograph Code**

1. Download R Version 4.4.0 and the latest RTools version.
2. Automatically download and install all packages.
3. Individually install the following packages:

* **ComplexHeatmap Install**
  + <https://github.com/jokergoo/ComplexHeatmap>
* **flowCore Install**
  + <https://rdrr.io/bioc/flowCore/>
* **Rphenograph Install**
  + <https://github.com/JinmiaoChenLab/Rphenograph>
* **diffcyt Install**
  + <https://www.bioconductor.org/packages/release/bioc/html/diffcyt.html>

**Code Documentation**

Metadata\_tikpc

* Contains regions of interest filenames with their sample ID and type (i.e., PanIN, Lymphoid Aggregate, Normal, Tumor Edge, Tumor Core)

Tikpc\_cleanpannel

* Stores something?