**Flowcytoscript—Cluster Naming**

The latest version of flowcytoscript incorporates automated naming of your cell clusters. This is done in two steps:

First, the script matches your clusters to the cell type database based on marker expression.

Second, for any clusters that would have identical names (e.g., two types of macrophage), the script appends the name(s) of the markers that best distinguish these clusters from each other.

The automated matching of clusters to the database is imperfect. It probably always will be. In the script, after the cluster names have been automatically generated, you’ll get the opportunity to rename any clusters you wish. To figure out what your clusters actually are, have a look at the following:

1. figure\_density\density\_cluster.jpeg
2. figure\_density\cluster\_id\_heatmap and cluster\_id\_heatmap\_dendro