CORE FACILITIES
MEDIZINISCHE UNIVERSITÄT WIEN

Using VolcaNoseR, a webtool that allows interactive volcano plot generation:

https://huygens.science.uva.nl/VolcaNoseR/

(published here, for the citation in case you use it:
https://www.nature.com/articles/s41598-020-76603-3)

You can take a first look at the example data (tab "Data", Example data 1 and 2) to see what to expect.

To try it on your own data, load the
*DESeq2results_GeneSymbols_GeneTypes_forVolcano.txt file you find in this folder for the comparison of interest.

Since the webtool only accepts files with a size up to 1 MB, I filtered the DESeq2 results, removing genes fulfilling one or several of the following criteria:
a) padj == NA
b) log2FoldChange == 0
c) GeneType != protein_coding

On the website, you need to proceed as follows:

1. In the tab "Data", select "upload file", then select the file via "Browse".
2. Select Delimiter = Tab
3. Select X-axis = log2FoldChange
4. Select Y-axis = minus_log10_padj
5. Select column with names = GeneSymbol
6. Go to tab "Plot". (It takes a couple of seconds to load the plot.)
7. Explore the plot (mouse-over the dots to see which genes they represent).
8. Personalize the plot (cutoffs, labelled genes, colors, title).
9. Export plot.