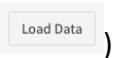
Instructions (DIY)

Select mutation file with the Browse (

) button on the top left of the page.

Once selected upload it with the load data function (

).

The three selection buttons (**SynonymousSelection, NonSynonymousSelection, IntronicSelection**) can be used to define the mutation types to be considered for the different tables. This is not used for the plotting, which automatically extract the informations from the ExonicFunc.refGene column. *

Available options for plotting include the inclusion/exclusion of unmutated patients, only keep genes mutated in at least a percentage of patients, and three options for downloading the file: width and height of the image saved, and size of row labels, please change this accordingly (need to be modified based on the number of patients/genes). Note that this can be changed any time, there is no need to re-upload the file.

Once you're happy, write the name you want your files to be saved as, and download!

Input requirements

Column info	**Required name of the column**
Sample IDs	samplename
Gene name	Gene.refGene
Mutation annotation	ExonicFunc.refGene

If unmutated patients are present, please write 'UNMUTATED' or 'unmutated' in the Gene.refGene column.

Questions? Don't write to me, solve it yourself!

---

*Current options are (and pre-loaded) as follows:

Non-synonymous: *splicing, frameshift deletion, frameshift insertion, nonframeshift deletion, nonframeshift insertion, nonsynonymous SNV, stopgain, startloss*
Synonymous: *synonymous SNV*
Intronic: *intronic, UTR3, UTR, UTR5*

If these change (for ex. With Annovar update), let's remember to change it!