**Step 1**

**python3 1\_Get\_Gene\_Names.py --inf input\_file.vcf --comp Burden\_output\_file.txt --outf Genes\_Burden2nd\_somatic(\_ID).csv --input Germline, Somatic or ID**

1\_Get\_Gene\_Names.py

--inf Merged filtered VEP vcf file

--comp Burden output file

--outf Output file with the genes which are in the input file and the burden output file

--input Important for script 3, can be Germline, Somatic or ID

**Step 2**

**python3 2\_Get\_results.py --inf input\_file.vcf --comp Genes\_Burden2nd\_somatic(\_ID).csv --outf filtered\_input\_file.vcf**

2\_Get\_results.py

--inf The Merge, VEP, filtered vcf file

--comp Gene list derived from script 1

--outf Output file containing only the info of the genes of interest

**Step3**

**python3 3\_Update\_burden\_file.py --inf Burden\_output\_file.txt --comp Genes\_Burden2nd\_somatic(\_ID).csv --outf Updated\_burden\_output\_file.txt --input Germline, Somatic or ID**

3\_Update\_burden\_file.py

--inf The Burden output file

--comp Gene list derived from script 1

--outf Updated file pf Burden output file

--input Can be Germline, Somatic or ID