(1). Open “**Extract\_genomic\_coordinates\_of\_genes\_from\_fasta\_file/**” folder and run the code (**awk** command in “**Readme.rtf**” overthere) to get geneIDs and their genomic coordinates. Then, move the output files (2L.txt., 2R.txt , etc.) to the

“**chromatin\_Dros\_melanogaster/**” folder;

(2). Run “**1\_Assign\_genes\_to\_TADs.py”** script to assign genes to TADs.

Output file: TAD5.12.txt ;

(3). Run “**2\_Assign\_reads\_to\_genes\_in\_TADs\_LacZ\_rep1.py**” script to assign reads to genes in replicate 1. Do the same thing for other replicates, if necessary;

(4). Run “**3\_Calculate\_sum\_of\_reads\_in\_TADs\_LacZ\_rep1.py”** script to get sum of reads in each TAD for the replicate. Do the same thing for other replicates, if necessary;

(5). If necessary, run “**Convert\_txt\_to\_csv.py**” script to convert TXT files from (4) to CSV data files. Output is in “**Final\_Data\_for\_spreadsheet\_csv/”** folder.

(6). Open “**GeneID\_Genomic\_lengths/**” folder and read the **README.docx** file.