```python
import pandas
import matplotlib.pyplot as matpl

#function for the main requirement: reads expression data file and sets the first
column as an index for the dataframe
def read_file():
    filename = input("Input the name of the file with Gene Expressions: ")
    dataframe = pandas.read_csv(filename, sep='\t',index_col=0)
    return dataframe #returns the generated dataframe

#function for the first task: generates a boxplot of each column and plots them on
the same figure
def plot_boxplots(dataframe):
    matpl.figure() #creates figure
    dataframe.boxplot() #generates boxplots
    matpl.title("Gene Expression Boxplots") #adds title for intuitiveness
    matpl.ylabel("Expression Level") #provides labels for the Gene Expression axis
for intuitiveness
    matpl.show() #shows the plot on user's screen

#function for the third task: asks the user for a gene name and plots it
def plot_users_gene(dataframe):
    user_gene = input("Input a gene name: ")
    #Checks whether the Gene name is valid or not
    if user_gene in dataframe.index:
        #if valid, provides the user with the Gene plot
        matpl.plot(dataframe.loc[user_gene]) #generates the plot for user's Gene
        matpl.title(f"Expression Levels of {user_gene}") #adds title for
intuitiveness
        matpl.ylabel("Expression Level") #adds labels for intuitiveness
        matpl.show() #shows the plot on user's screen
    else:
        #if invalid, announces the user that the Gene is not found
        print("Gene not Found")

#the following code is "main", it incorporates all the previous functions
main_dataframe = read_file()
plot_boxplots(main_dataframe)
print(main_dataframe.describe()) #fulfills the second task
plot_users_gene(main_dataframe)
```