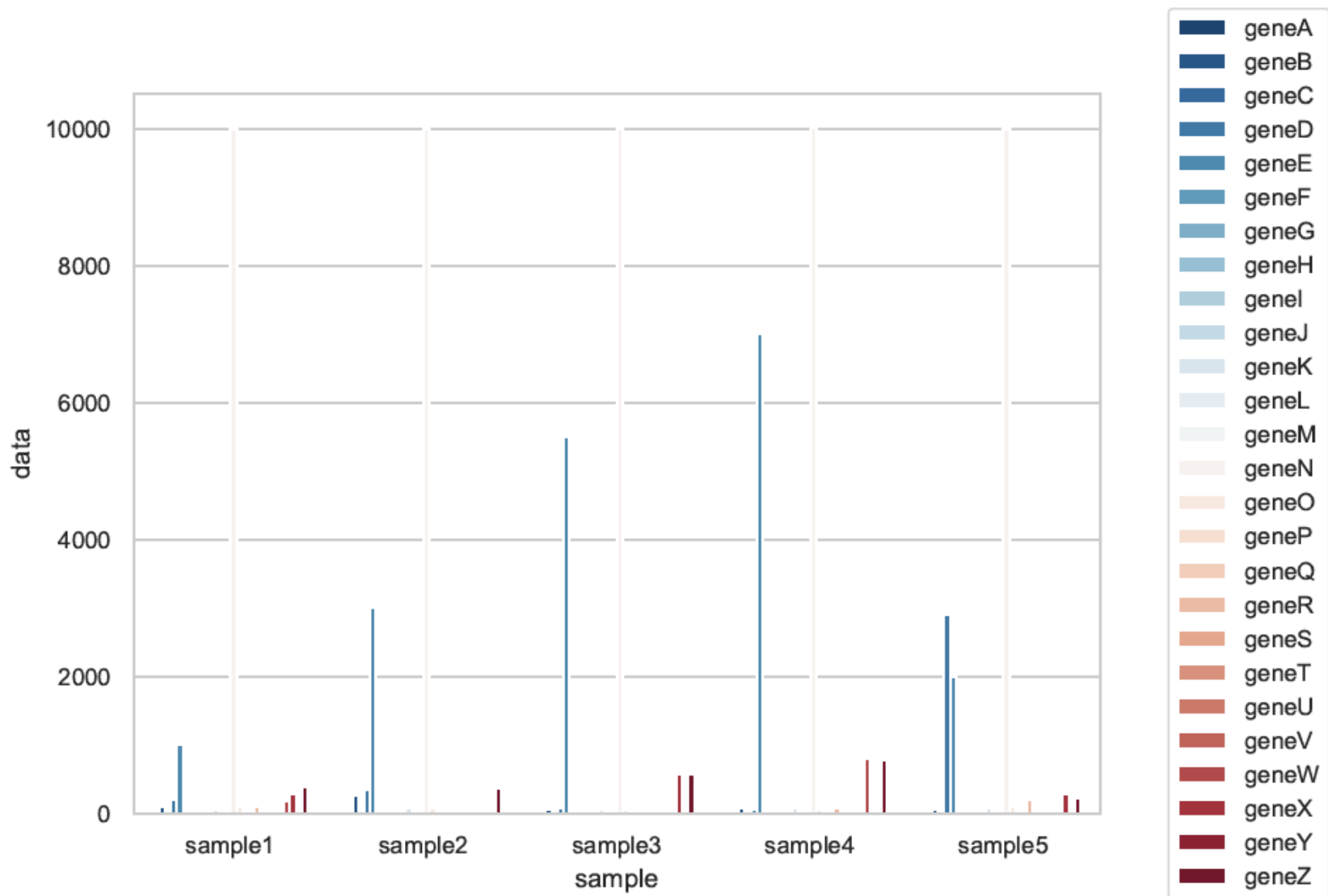
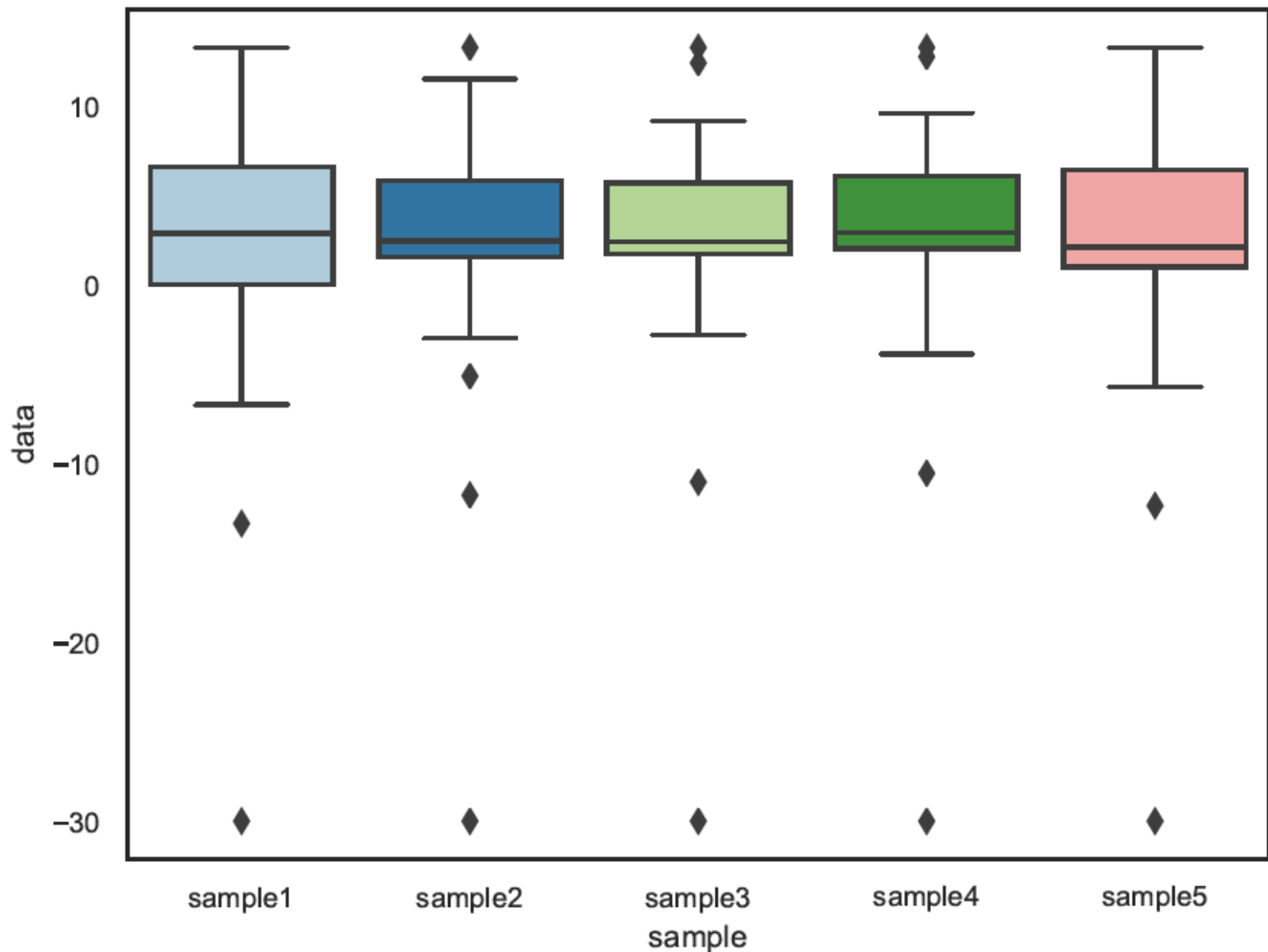


```
python rnaseq_figure_plotter.py -i gene_expression_data.txt -t bar -o gene_new
```

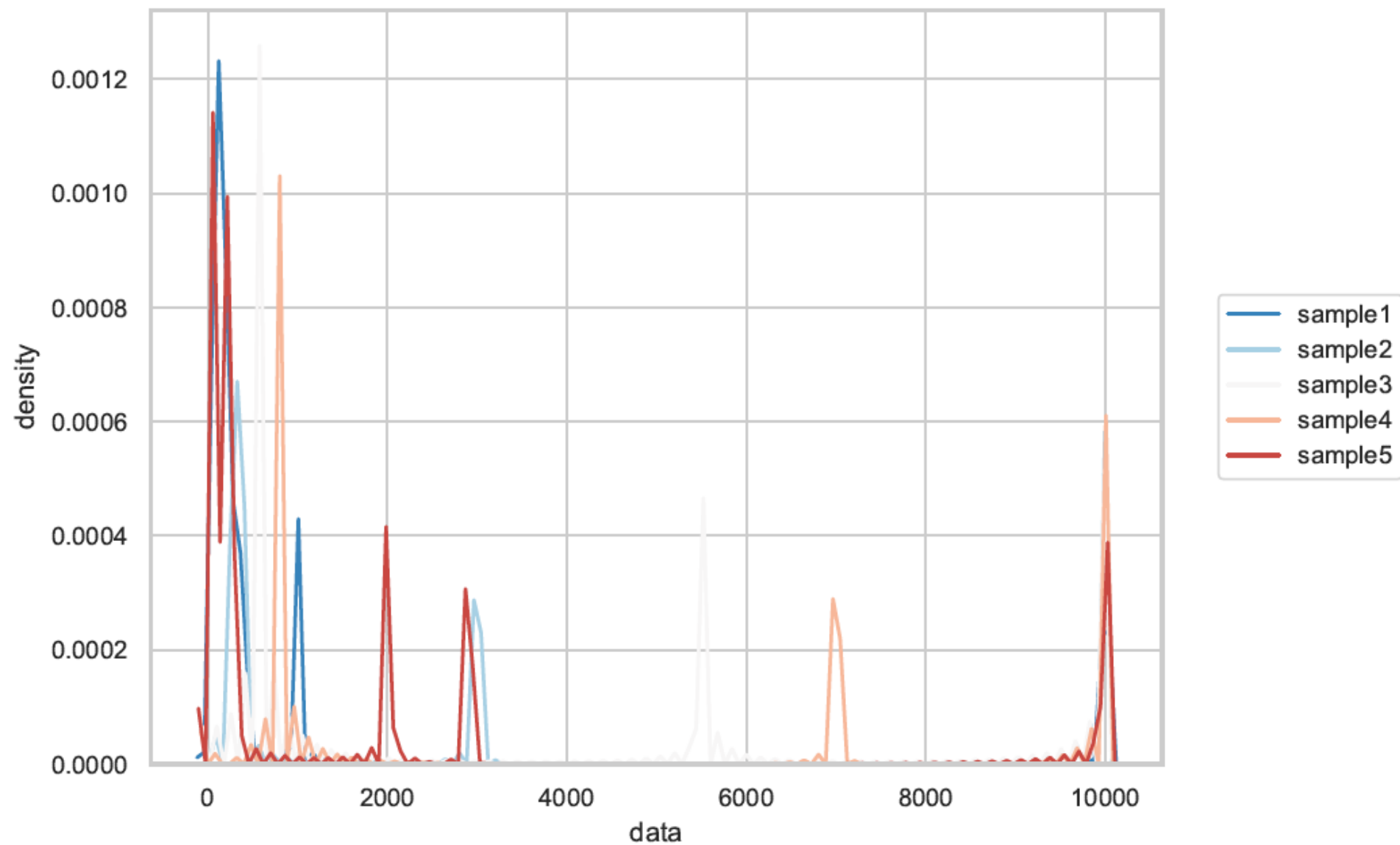


-2 box plot with "gene\_new" output file name, log2 transformation, color (Paired), and style (white, paper)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t box -o gene\_new -l 1 -c 6 -s 3

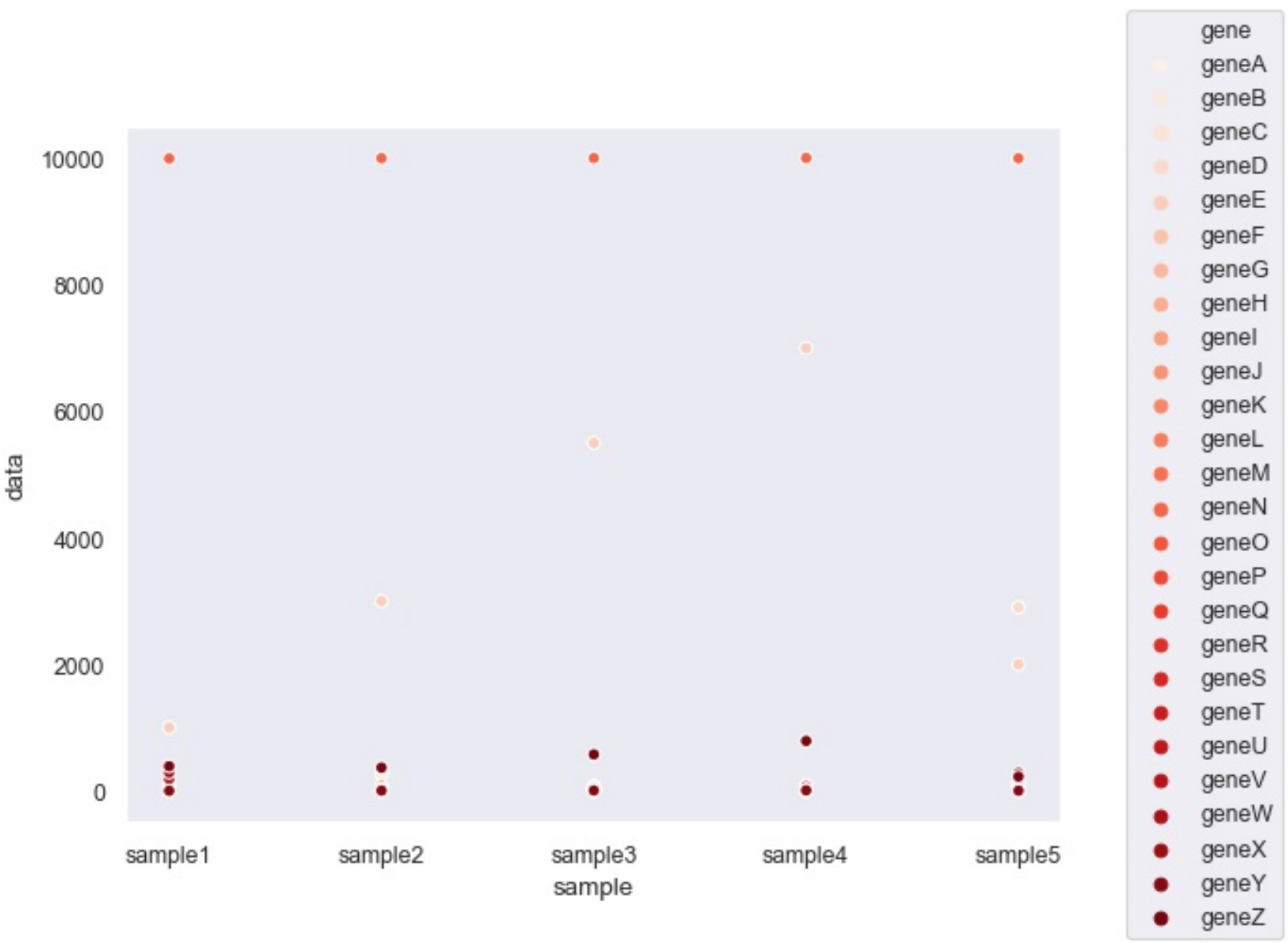


-3 density plot with "gene\_new" output file name

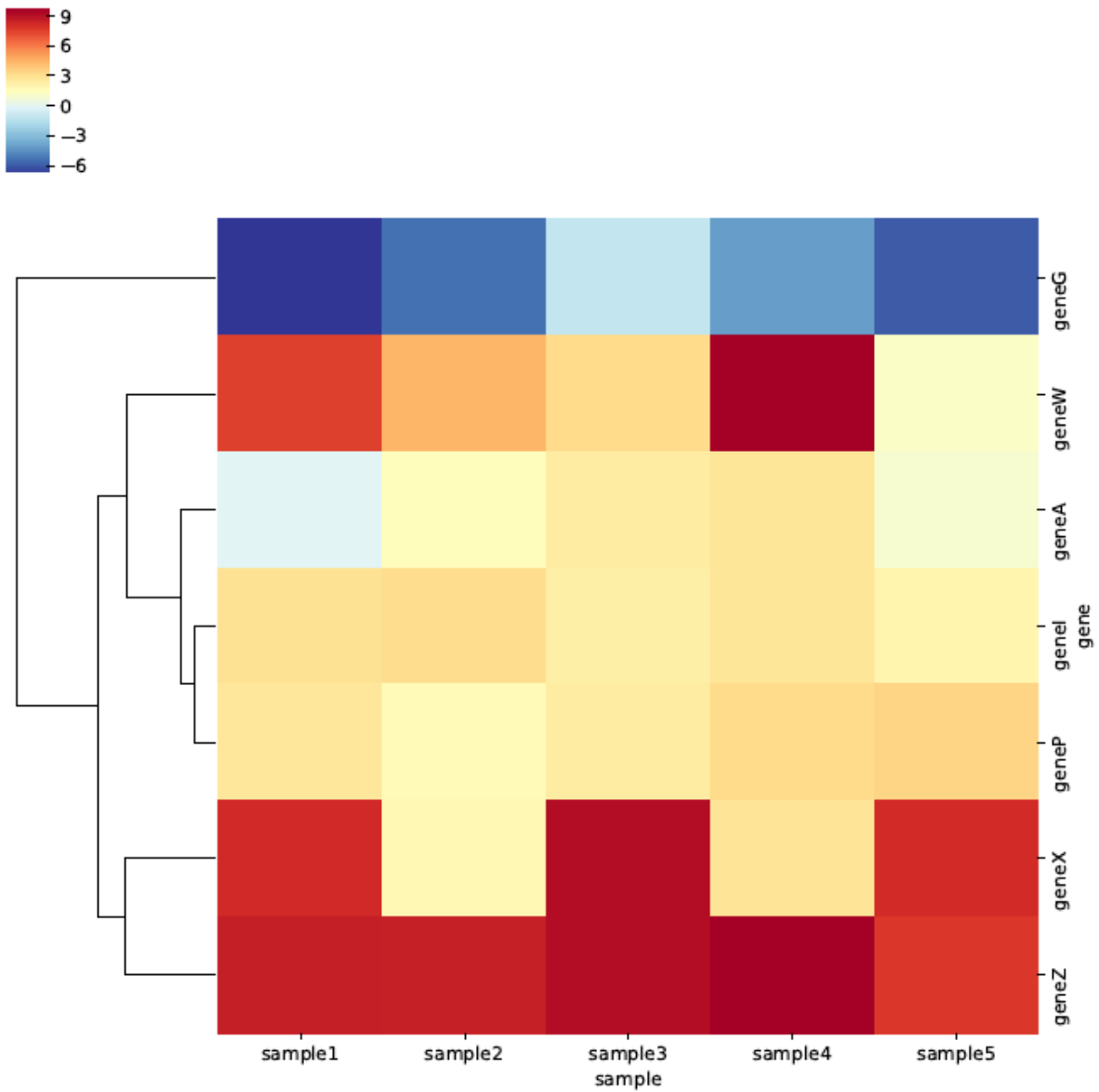
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t density -o gene\_new



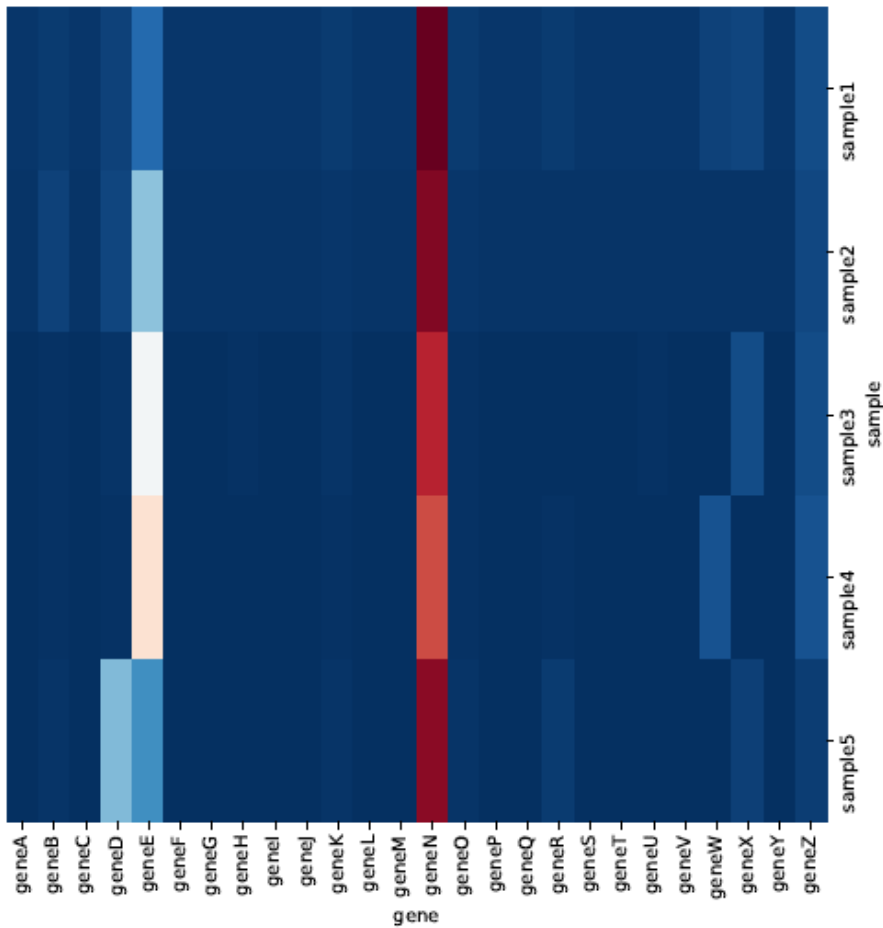
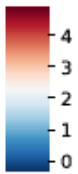
-4 dot plot with "gene\_new" output file name, save as jpeg, color (Reds), and style (dark, paper)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t dot -o gene\_new -f jpeg -c 2 -s 7



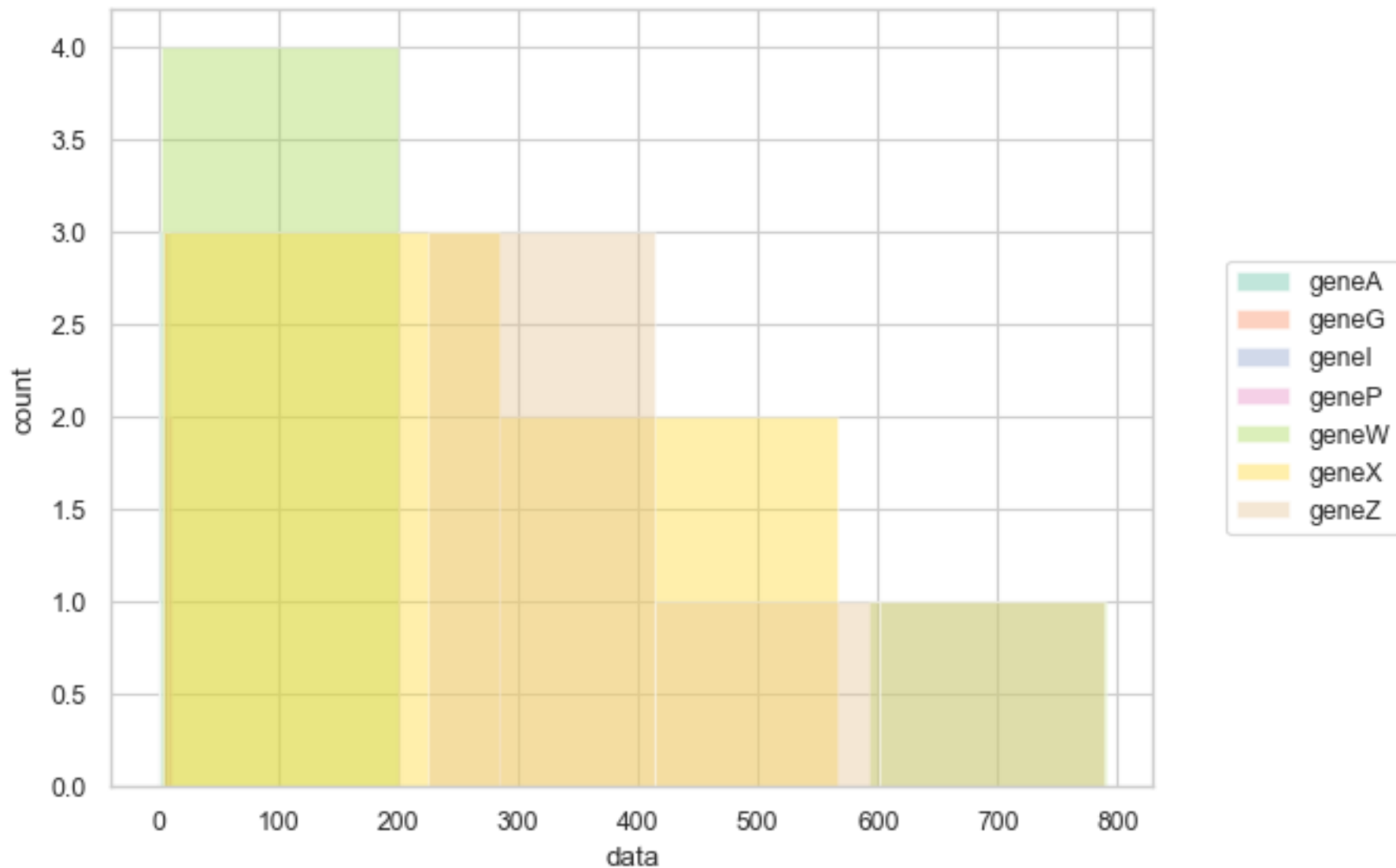
-5 heatmap plot with selection gene by gene\_list, log2 transformation, and cluster row (gene)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t heatmap -g gene\_list.txt -l 1 -cr  
1



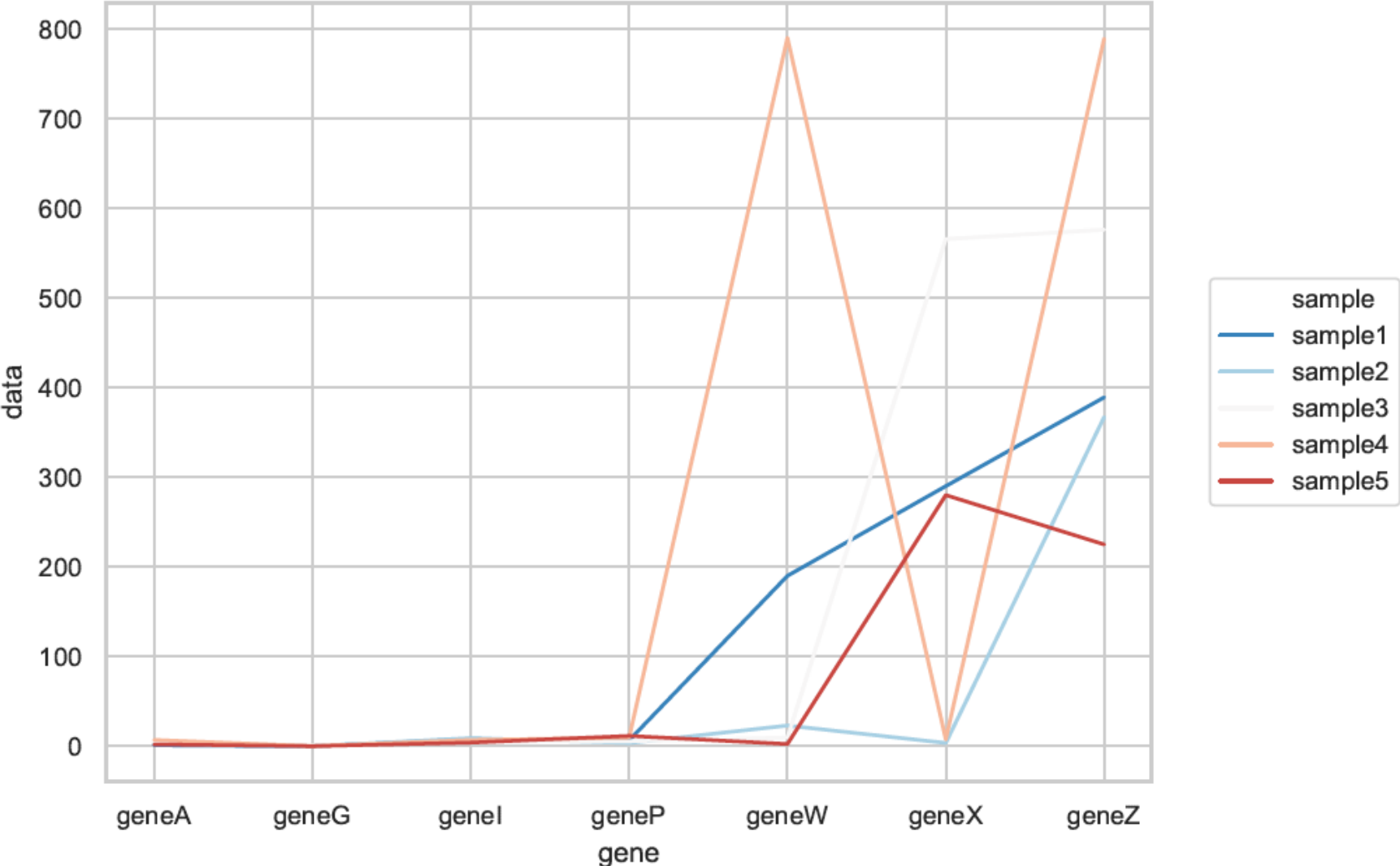
-6 heatmap plot with "gene\_new" output file name, gene in row, sample in column, and z-score transromation in sample  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t heatmap -o gene\_new -x gene -z sample -zs 2



-7 histogram plot with selection gene by gene\_list, color (Set2), figure format (tiff), and by gene (not sample)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t histogram -g gene\_list.txt -c 10 -f tiff -x gene

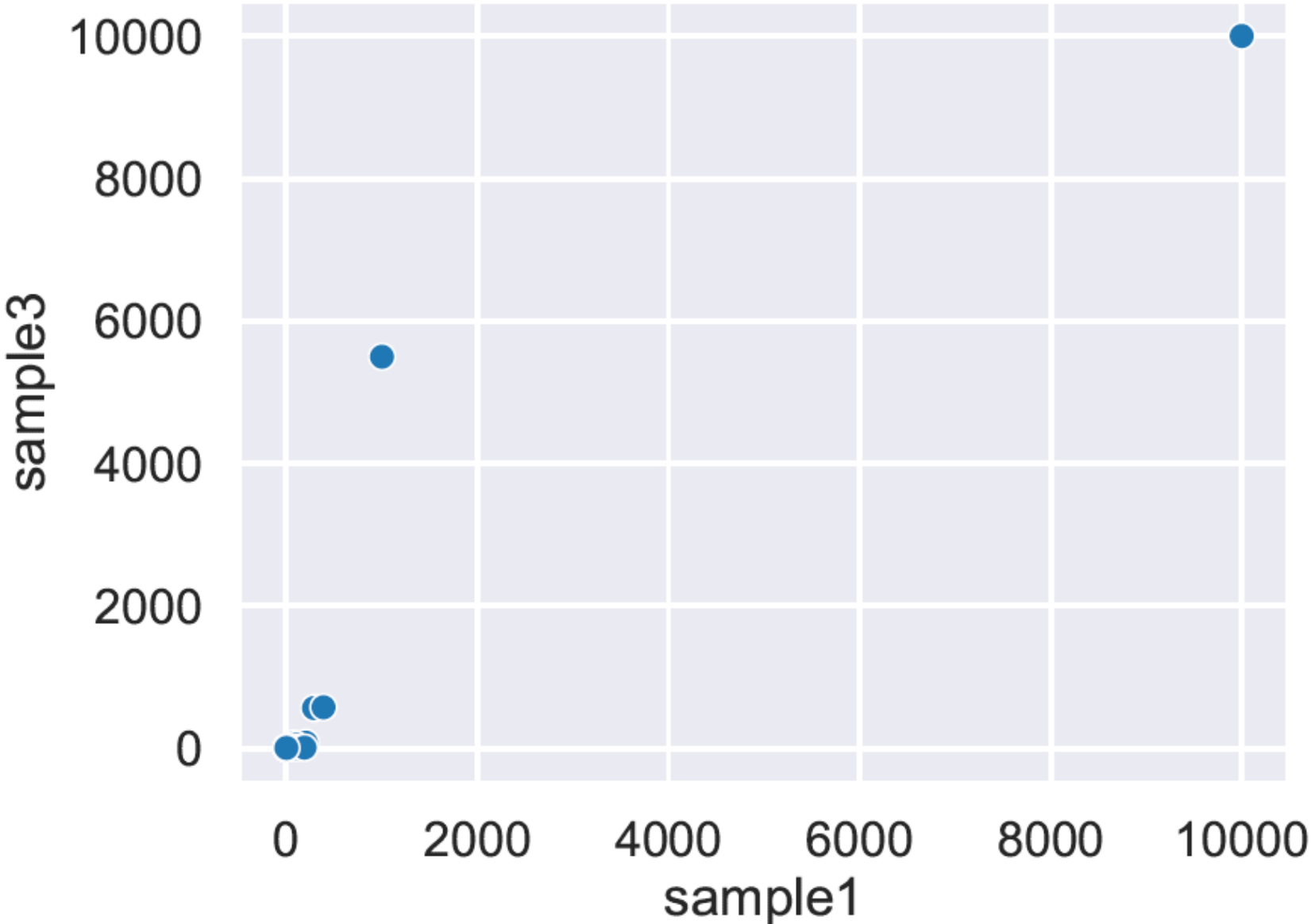


-8 line plot with selection gene by gene\_list, sample in x-axis, data in y-axis, gene ID in legend, and style (dark, paper)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t line -g gene\_list.txt -x sample -y data -z gene -s 8

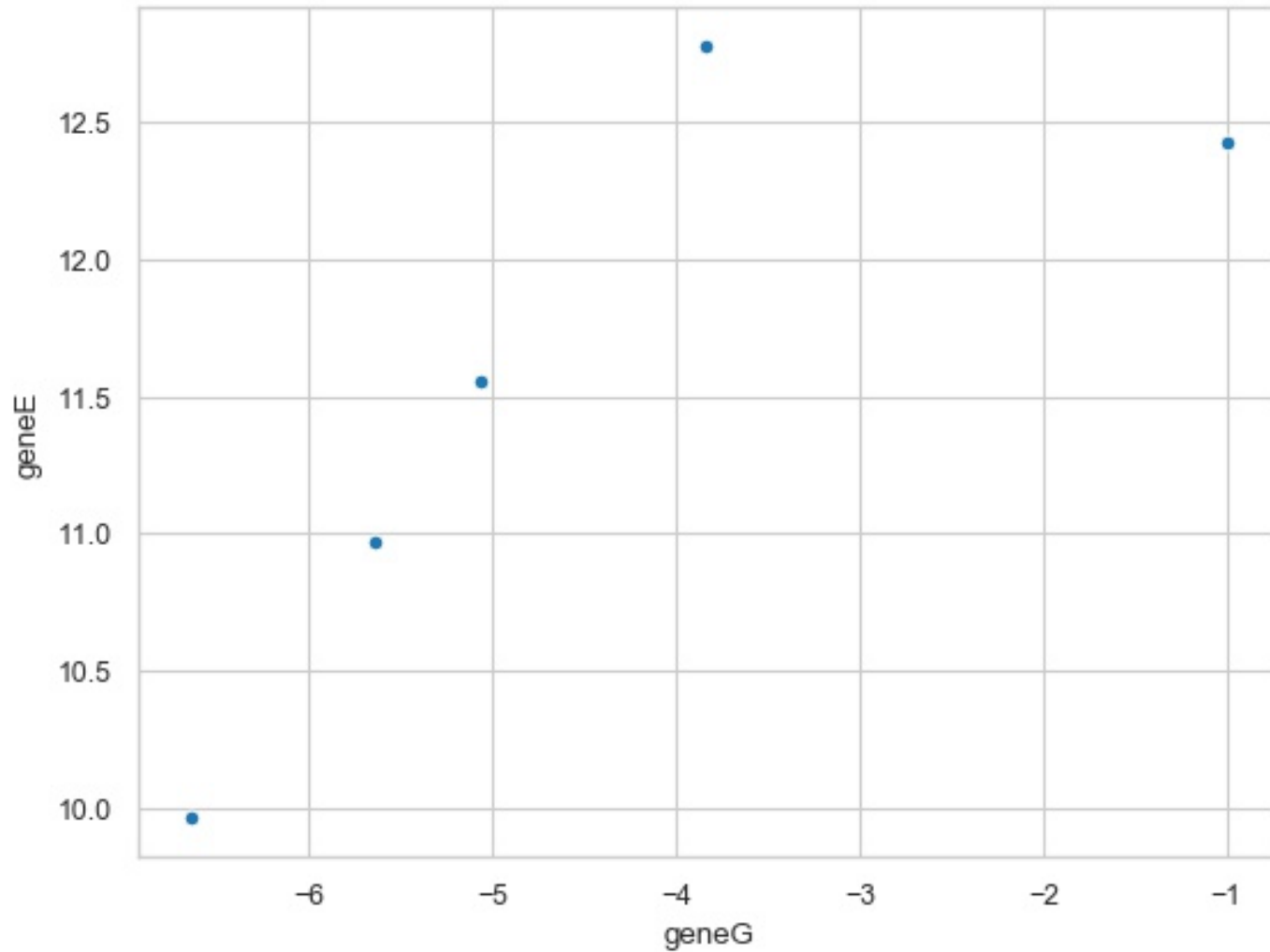




-9 scatter plot with sample1 in x-axis, sample3 in y-axis, and style (darkgrid, talk)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t scatter -sc sample1,sample3 -s  
6



-10 scatter plot with geneG in x-axis, geneE in y-axis, log2 transformation, add 0.00001 for each data, and save in jpeg format  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t scatter -sr geneG,geneE -l 1 -lgn 0.00001 -f jpeg



-11 violin plot with geneG in x-axis, geneE in y-axis, log2 transformation, and color (muted)  
python rnaseq\_figure\_plotter.py -i gene\_expression\_data.txt -t violin -l 1 -c 8

