ATAC_and_CRISPR_score

November 14, 2017

1 This workbook will be used to analyze any correlations between ATAC seq peaks and CRISPR screen scores.

Let's start by reading the data into a variable called df.

```
In [14]: import pandas as pd
         import numpy as np
         df = pd.read_excel \
         (r'/Users/eatonaw/Desktop/Atom_Files/ATAC/2017-10-24-CIV_by_ATAC2.xlsx')
         print(df.head())
         print(df.columns)
```

```
  Chromosome     Start      Stop  TMD8_CIV2_D21_CSS  TMD8_CIV2_IBR_CSS  \
0      chr19  40791075  40791094          -0.731734              -1.15
1      chr19  40791166  40791185          -0.602970              -1.21
2      chr19  40791167  40791186          -0.005454              -2.05
3      chr19  40791302  40791321           0.399748              -0.82
4      chr19  40791220  40791239           1.168600              -3.56

  ATAC_tmd8_chr     start        stop         Peak name Score.Peak.color  \
0         chr19  40790622  40791786.0  TMD8_peak_545090             3249
1         chr19  40790622  40791786.0  TMD8_peak_545090             3249
2         chr19  40790622  40791786.0  TMD8_peak_545090             3249
3         chr19  40790622  40791786.0  TMD8_peak_545090             3249
4         chr19  40790622  40791786.0  TMD8_peak_545090             3249

  strand signalValue negLog10pval qval(-log10FDR) peak  \
0      .     21.2455      324.952         320.267  843
1      .     21.2455      324.952         320.267  843
2      .     21.2455      324.952         320.267  843
3      .     21.2455      324.952         320.267  843
4      .     21.2455      324.952         320.267  843

  uniqu Match for vlookup GeneSybmbol TMD8_Brun_CSS Essential Fig1 gene
0   chr194079107540791094        AKT2       -0.4339       NaN      AKT2
1   chr194079116640791185        AKT2       -0.4339       NaN      AKT2
2   chr194079116740791186        AKT2       -0.4339       NaN      AKT2
```

```
3   chr194079130240791321        AKT2       -0.4339       NaN      AKT2
4   chr194079122040791239        AKT2       -0.4339       NaN      AKT2
Index(['Chromosome', 'Start', 'Stop', 'TMD8_CIV2_D21_CSS', 'TMD8_CIV2_IBR_CSS',
       'ATAC_tmd8_chr', 'start', 'stop', 'Peak name', 'Score.Peak.color',
       'strand', 'signalValue', 'negLog10pval', 'qval(-log10FDR)', 'peak',
       'uniqu Match for vlookup', 'GeneSybmbol', 'TMD8_Brun_CSS', 'Essential',
       'Fig1 gene'],
      dtype='object')
```

First, let's format our data from df into a new variable called df2. This will only include a subset of columns from df that we are interested in. In addition, we will change the data types of some of the columns and format it for an easier way to analyze the data.

```
In [15]: df.rename(columns = {'Score.Peak.color' : 'Color_Score', 'signalValue':\
          'Signal_Value', 'GeneSybmbol' : 'Gene_Symbol', 'Peak Name' : 'Peak_Name',\
          'uniqu Match for vlookup' : 'Unique', 'Fig1 gene': 'Fig1'}, inplace = True)

         df2 = df[['Chromosome', 'TMD8_CIV2_D21_CSS', 'TMD8_CIV2_IBR_CSS', 'Color_Score',\
          'Signal_Value', 'Unique', 'Gene_Symbol', 'TMD8_Brun_CSS', 'Essential', 'Fig1']]

         df2.loc[:,['Color_Score','Signal_Value', 'TMD8_Brun_CSS']] = df2.loc[:,['Color_Score'
          ,'Signal_Value', 'TMD8_Brun_CSS']].apply(pd.to_numeric, errors = 'coerce')

         print(df2.dtypes)
         df2.head()
```

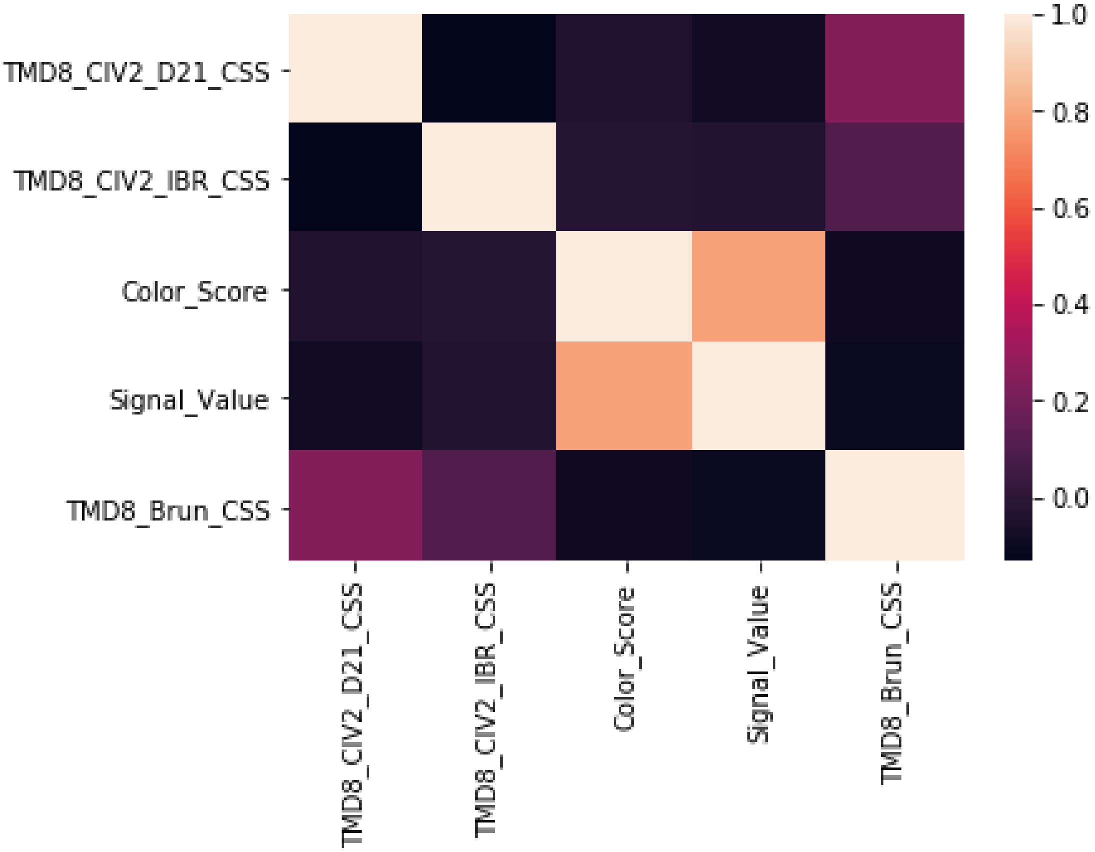
```
Chromosome            object
TMD8_CIV2_D21_CSS    float64
TMD8_CIV2_IBR_CSS    float64
Color_Score          float64
Signal_Value         float64
Unique                object
Gene_Symbol           object
TMD8_Brun_CSS        float64
Essential             object
Fig1                  object
dtype: object


/usr/local/lib/python3.6/site-packages/pandas/core/indexing.py:517: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self.obj[item] = s
```

```
Out[15]:   Chromosome  TMD8_CIV2_D21_CSS  TMD8_CIV2_IBR_CSS  Color_Score  Signal_Value  \
        0       chr19          -0.731734              -1.15       3249.0      21.24547
        1       chr19          -0.602970              -1.21       3249.0      21.24547
        2       chr19          -0.005454              -2.05       3249.0      21.24547
        3       chr19           0.399748              -0.82       3249.0      21.24547
        4       chr19           1.168600              -3.56       3249.0      21.24547

                          Unique Gene_Symbol  TMD8_Brun_CSS Essential  Fig1
        0  chr194079107540791094        AKT2        -0.4339       NaN  AKT2
        1  chr194079116640791185        AKT2        -0.4339       NaN  AKT2
        2  chr194079116740791186        AKT2        -0.4339       NaN  AKT2
        3  chr194079130240791321        AKT2        -0.4339       NaN  AKT2
        4  chr194079122040791239        AKT2        -0.4339       NaN  AKT2
```

Let's start off with some visualizing to see if we can see any interesting correlations or anything else in the data set.

```
In [16]: import matplotlib.pyplot as plt
         import seaborn as sns
         %matplotlib inline
         sns.heatmap(df2.corr())
```

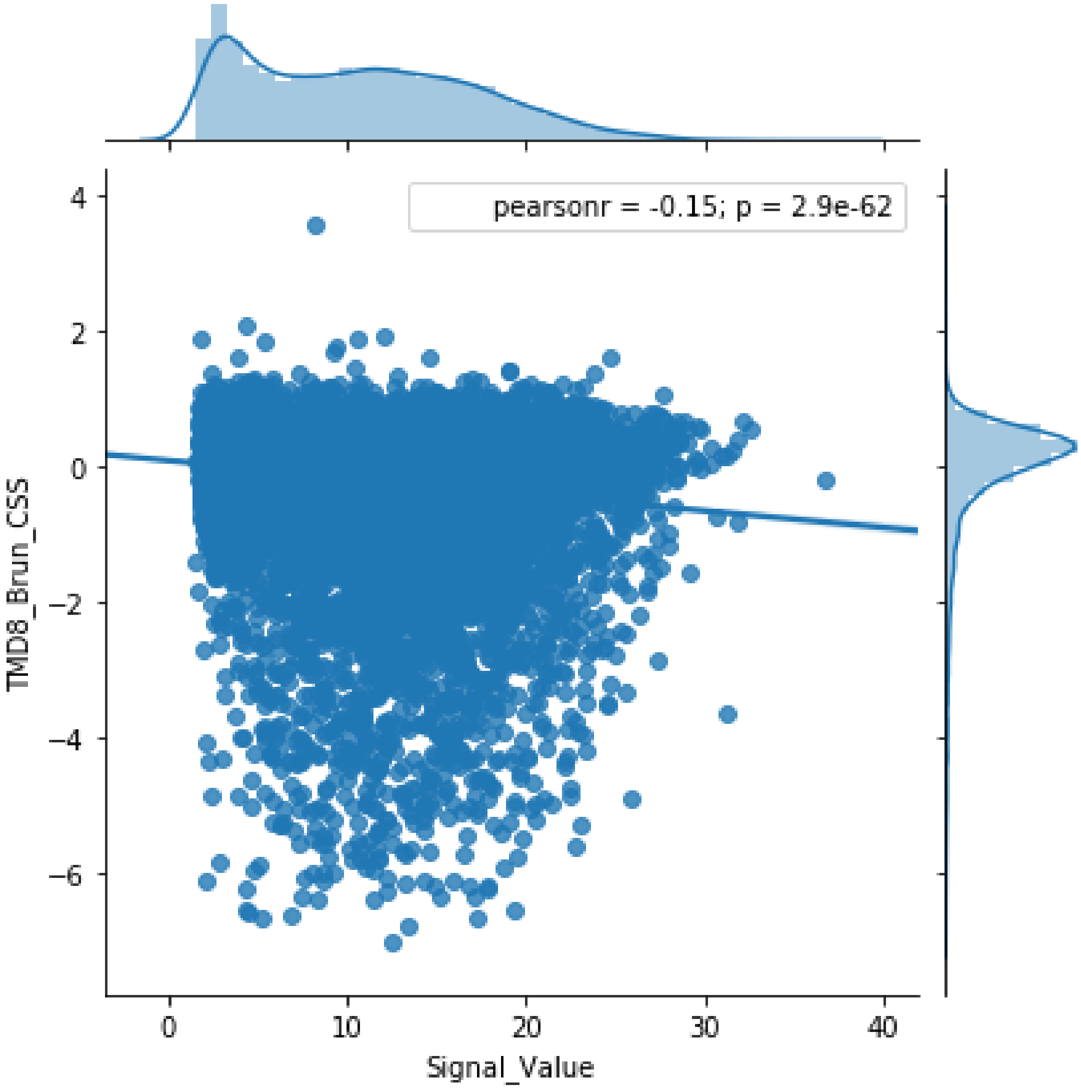
```
Out[16]: <matplotlib.axes._subplots.AxesSubplot at 0x1106b2c50>
```

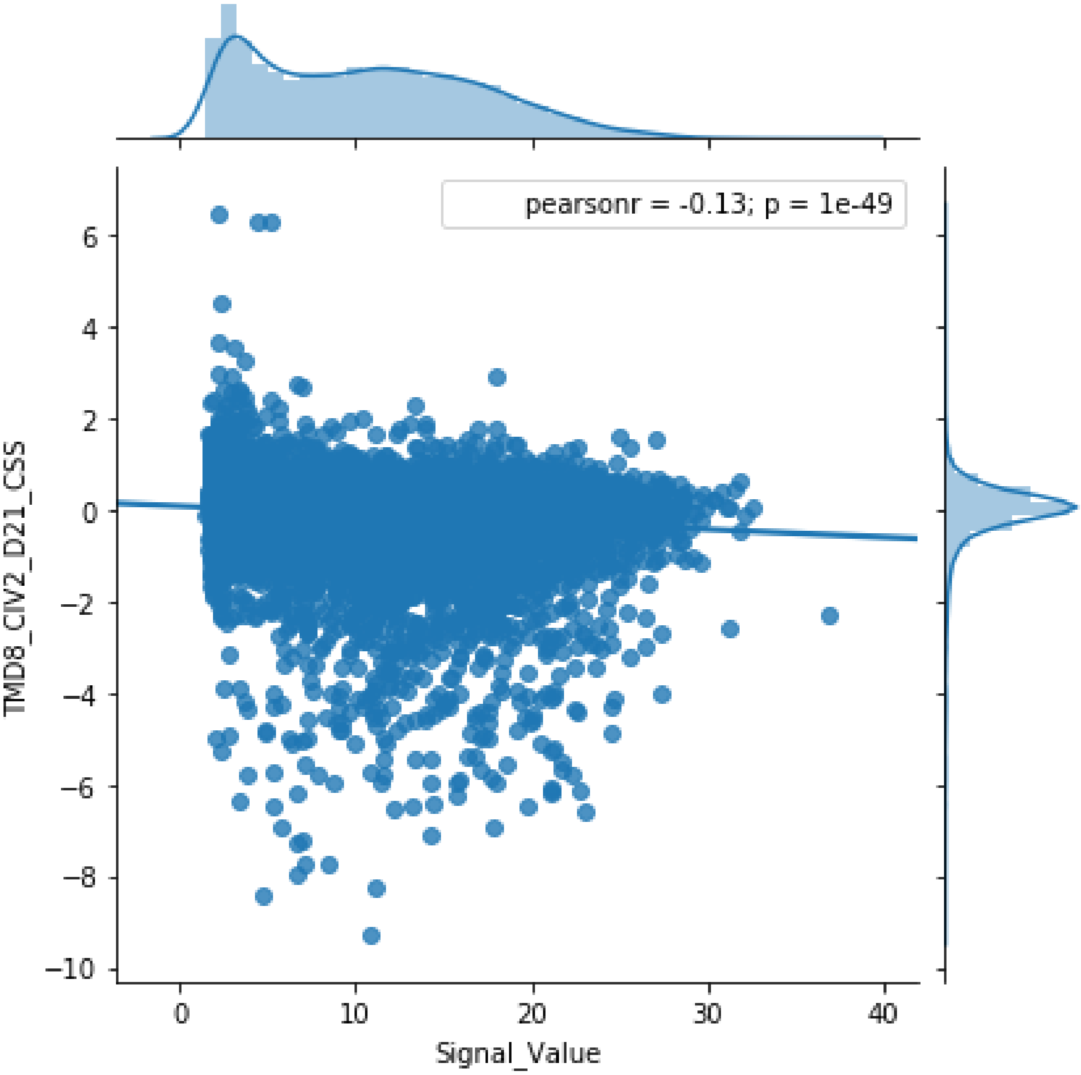


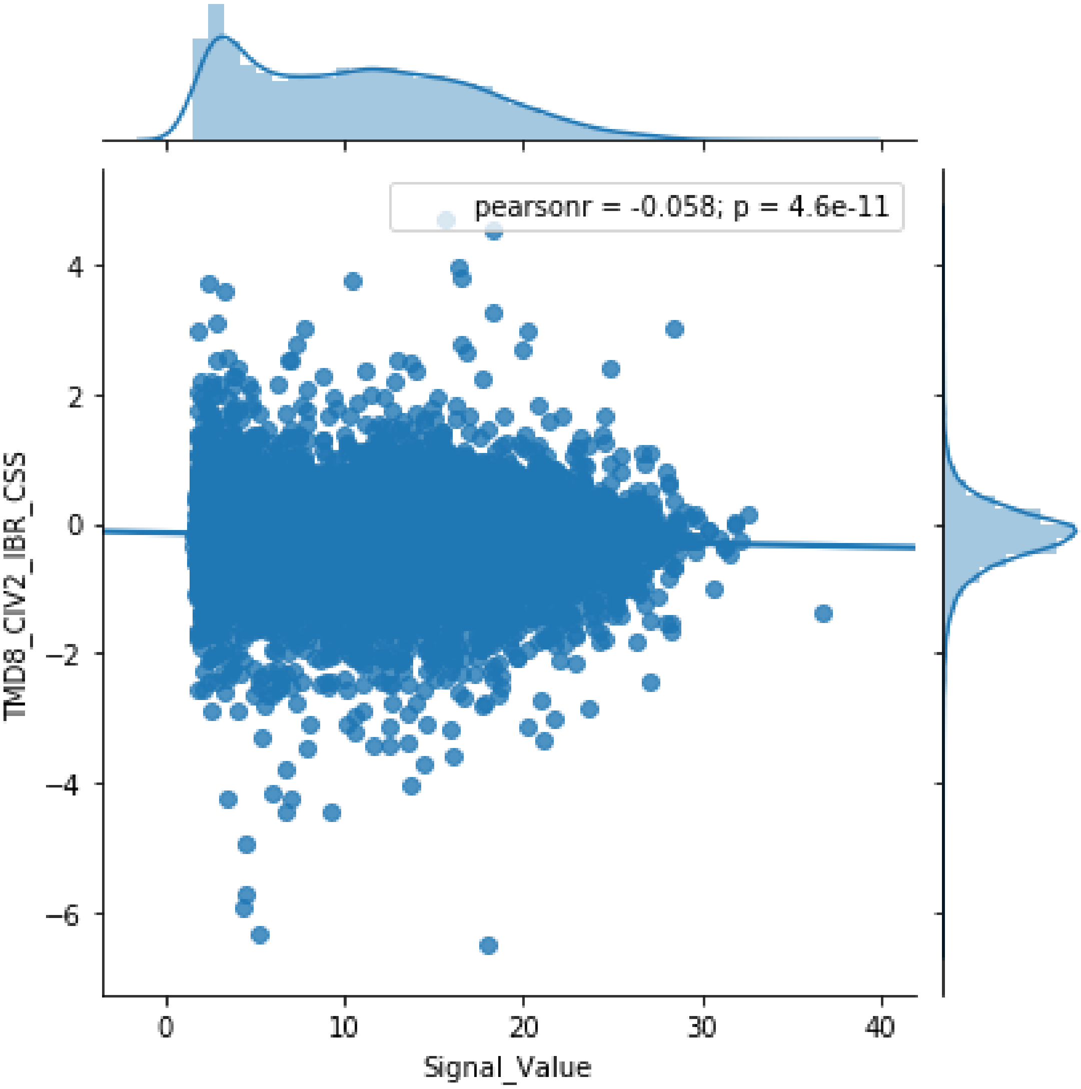
Here, we can see that color score and signal value are really correlated, so they are probably interchangable ways to quantify the ATAC seq signal data.

```
In [17]: sns.jointplot(x = 'Signal_Value', y = 'TMD8_Brun_CSS', data = df2.dropna\
          (subset = ['Signal_Value']).groupby('Gene_Symbol').mean(), kind = 'reg')

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_D21_CSS', data = df2.dropna\
          (subset = ['Signal_Value']).groupby('Gene_Symbol').mean(), kind = 'reg')

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_IBR_CSS', data = df2.dropna\
          (subset = ['Signal_Value']).groupby('Gene_Symbol').mean(), kind = 'reg')
```

```
Out[17]: <seaborn.axisgrid.JointGrid at 0x10ea00208>
```

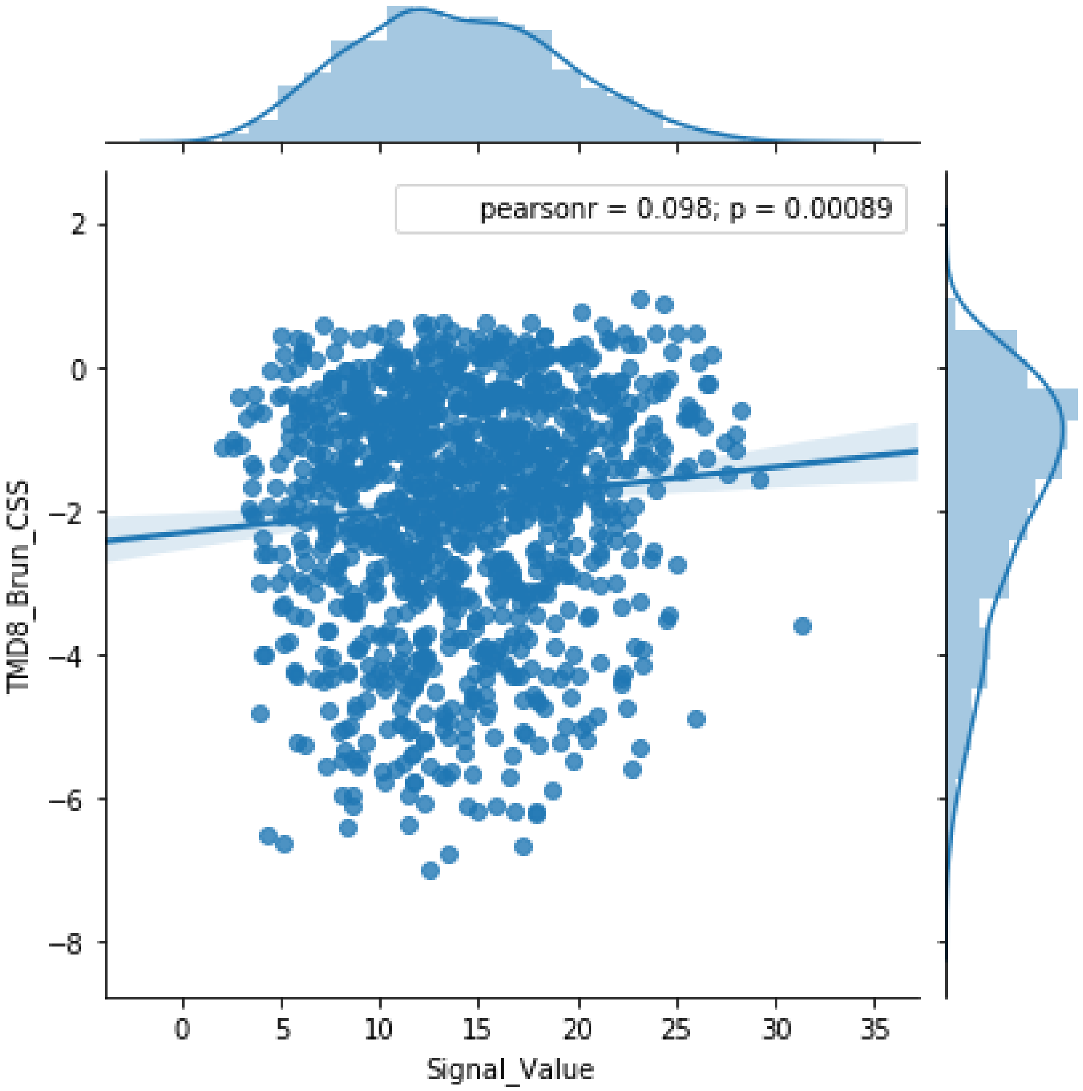


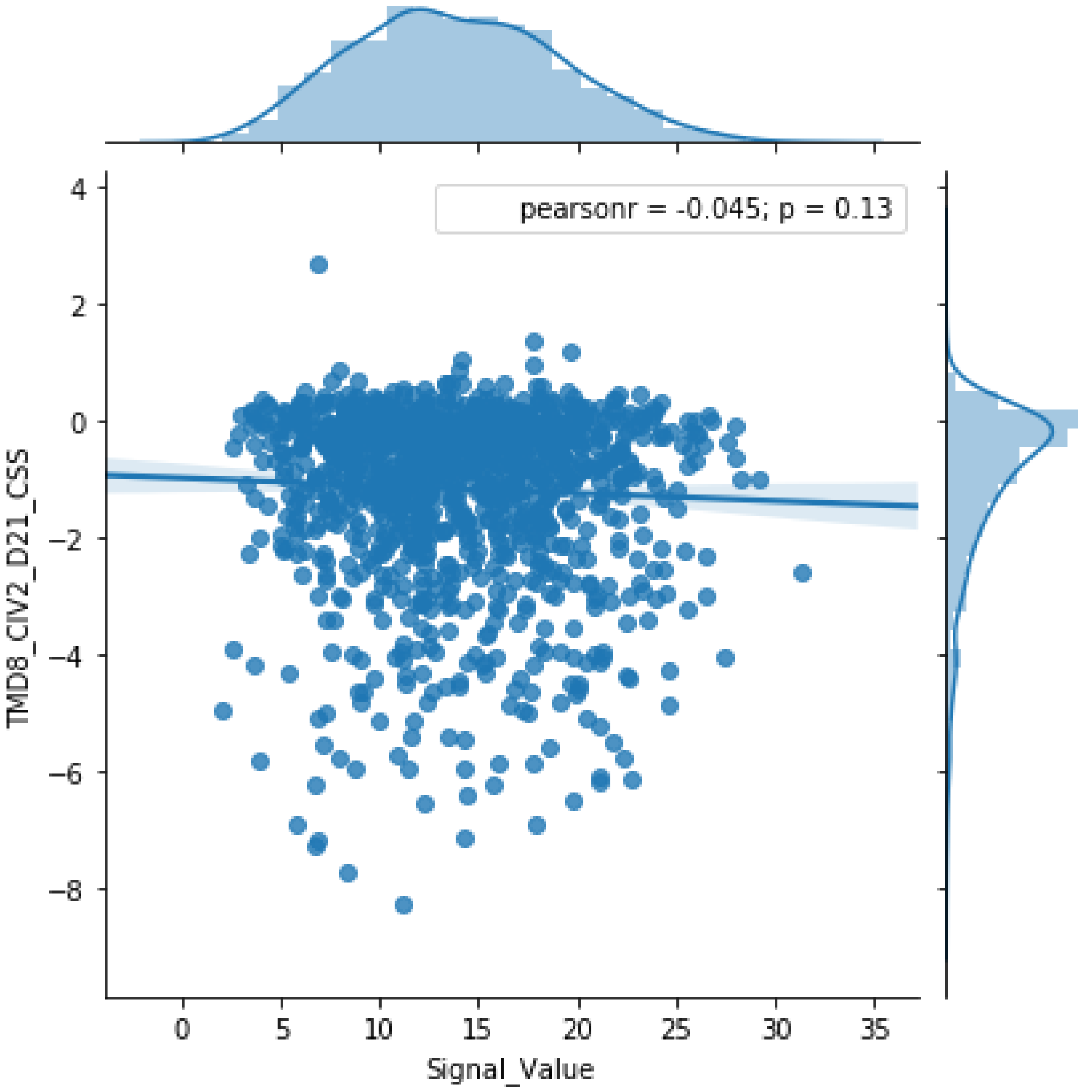

pearsonr = -0.13; p = 1e-49
6
4
2
0
−2
−4
−6
−8
−10
TMD8_CIV2_D21_CSS
0
10
20
30
40
Signal_Value

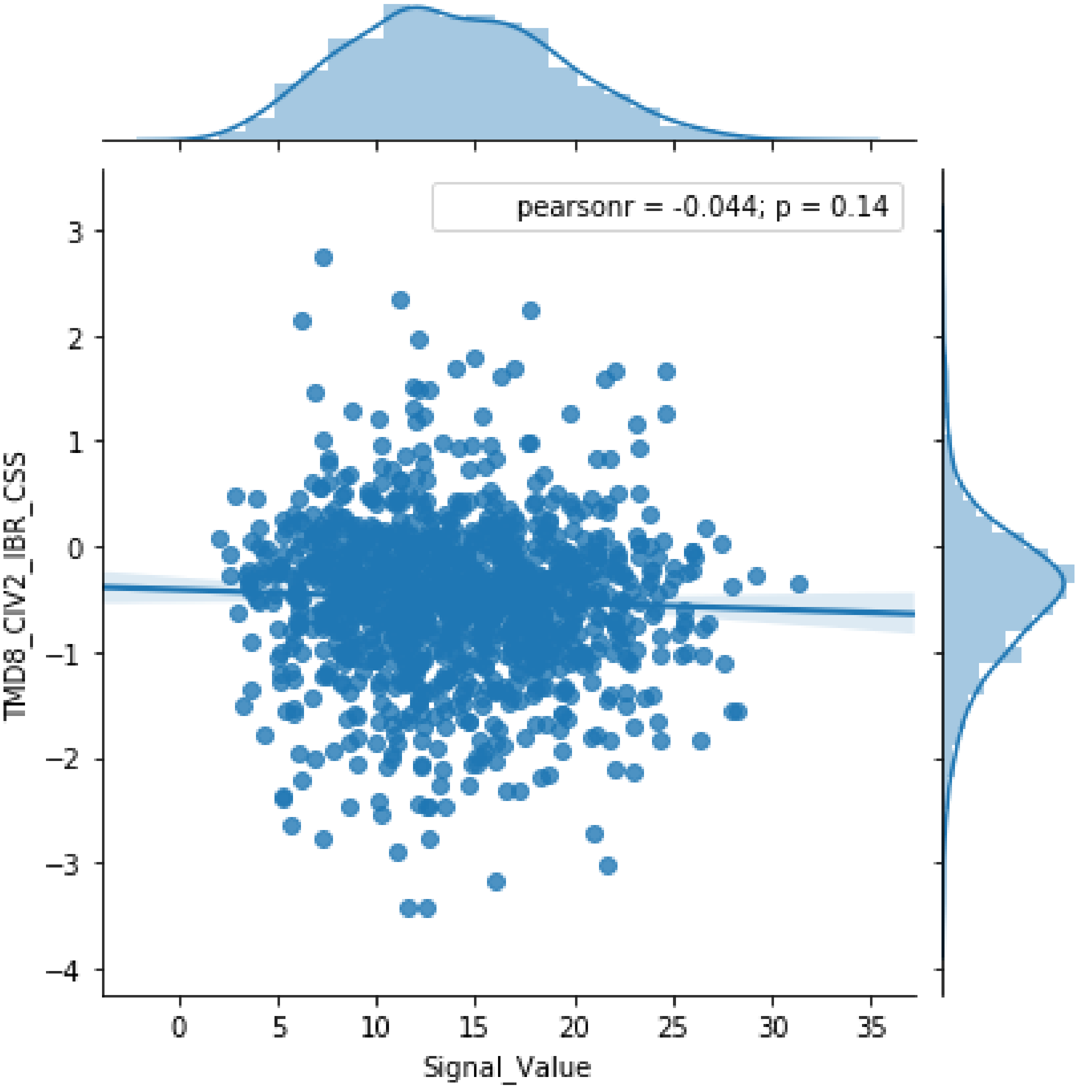


Unfortunately, there is no easily discernible trend between our CRISPR screening scores and ATAC data. Let's try subsetting the data. First, we will look at "Essential" genes.

```
In [18]: sns.jointplot(x = 'Signal_Value', y = 'TMD8_Brun_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Essential']).groupby('Gene_Symbol').mean(), kind = 'reg'

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_D21_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Essential']).groupby('Gene_Symbol').mean(), kind = 'reg'

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_IBR_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Essential']).groupby('Gene_Symbol').mean(), kind = 'reg'

Out[18]: <seaborn.axisgrid.JointGrid at 0x112516208>
```


pearsonr = 0.098; p = 0.00089
TMD8_Brun_CSS
2
0
−2
−4
−6
−8
0
5
10
15
20
25
30
35
Signal_Value

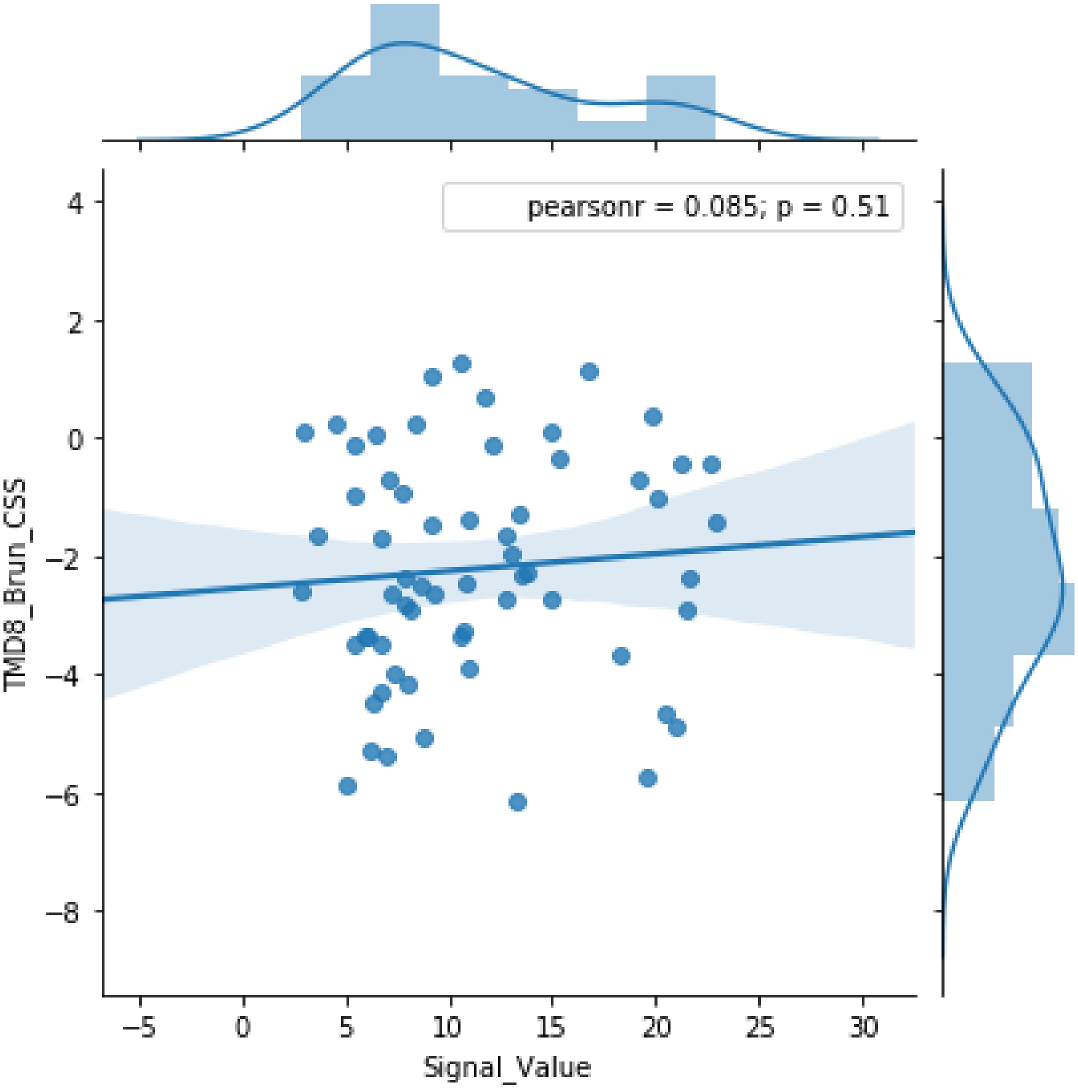

pearsonr = -0.045; p = 0.13
4
2
0
−2
−4
−6
−8
TMD8_CIV2_D21_CSS
0
5
10
15
20
25
30
35
Signal_Value

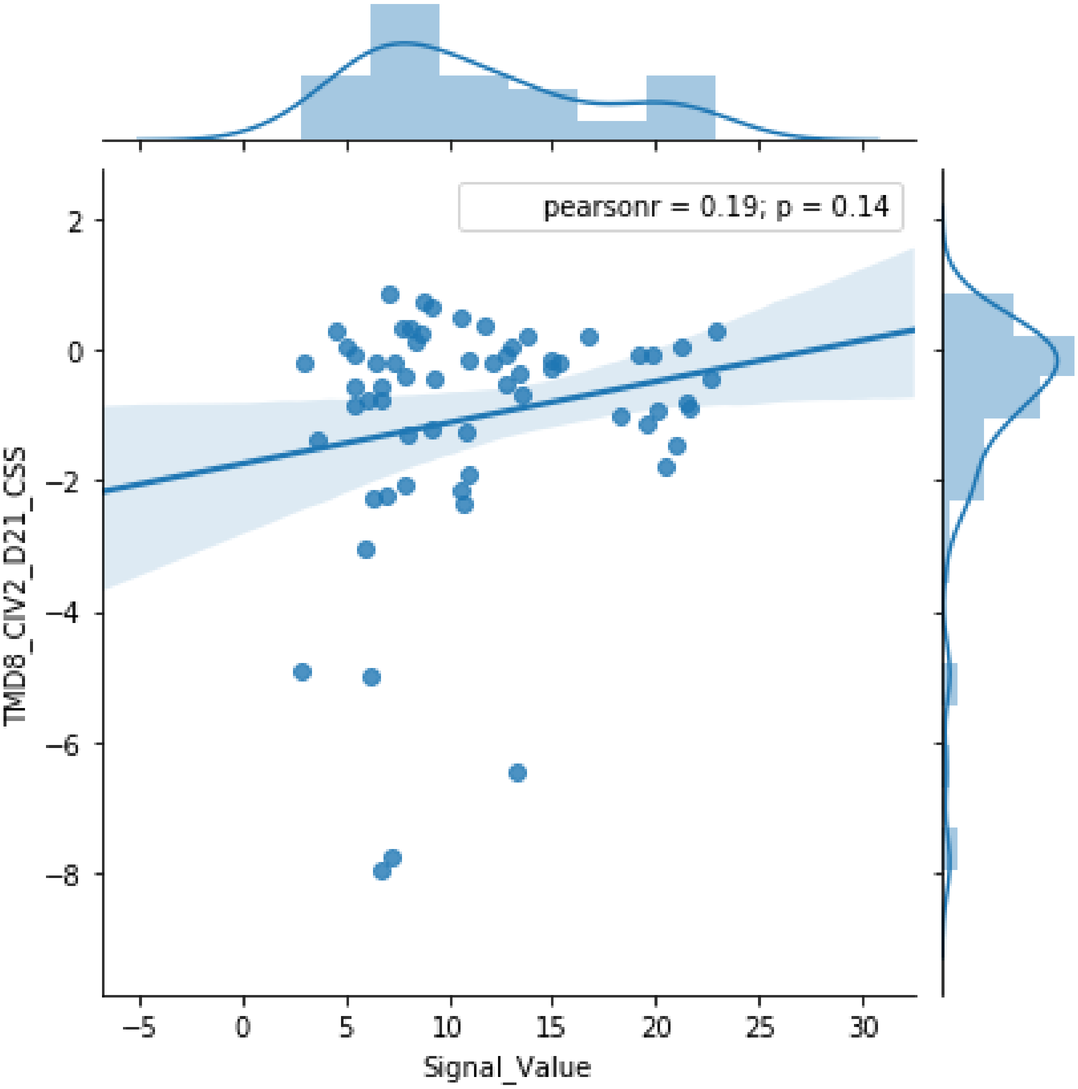


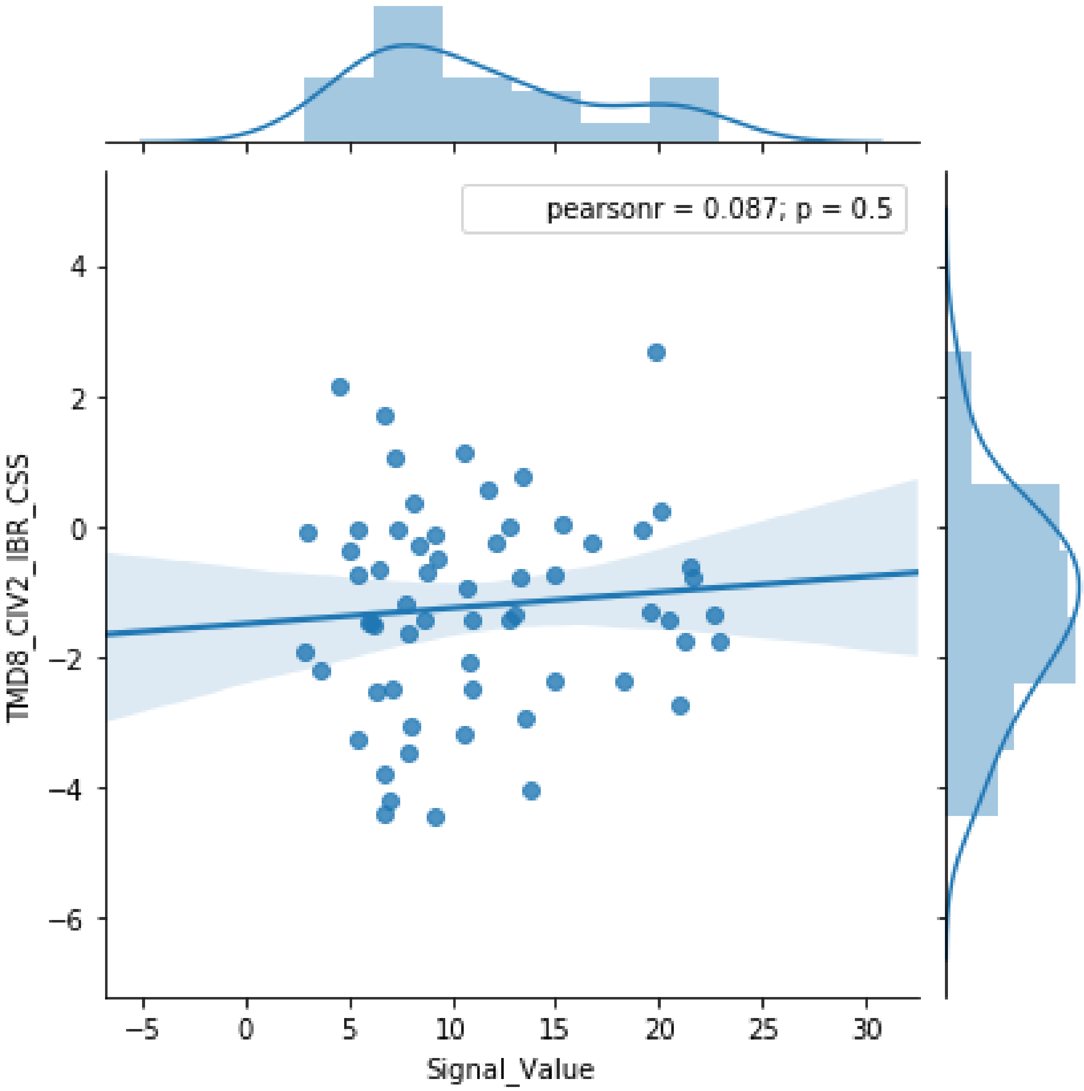
Unfortunately, no interesting conclusions arise from this. Let's now try this with "Figure 1" genes.

```
In [19]: sns.jointplot(x = 'Signal_Value', y = 'TMD8_Brun_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Fig1']).groupby('Gene_Symbol').mean(), kind = 'reg')

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_D21_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Fig1']).groupby('Gene_Symbol').mean(), kind = 'reg')

         sns.jointplot(x = 'Signal_Value', y = 'TMD8_CIV2_IBR_CSS', data = df2.dropna\
          (subset = ['Signal_Value', 'Fig1']).groupby('Gene_Symbol').mean(), kind = 'reg')
```

```
Out[19]: <seaborn.axisgrid.JointGrid at 0x11197e7f0>
```


pearsonr = 0.085; p = 0.51
4
2
0
−2
−4
−6
−8
TMD8_Brun_CSS
−5
0
5
10
15
20
25
30
Signal_Value


pearsonr = 0.19; p = 0.14
TMD8_CIV2_D21_CSS
Signal_Value
2
0
−2
−4
−6
−8
−5
0
5
10
15
20
25
30



Still, no conclusions between ATAC signal value and CRISPR score can be drawn. What should we do now???