

proteome_plots

March 22, 2020

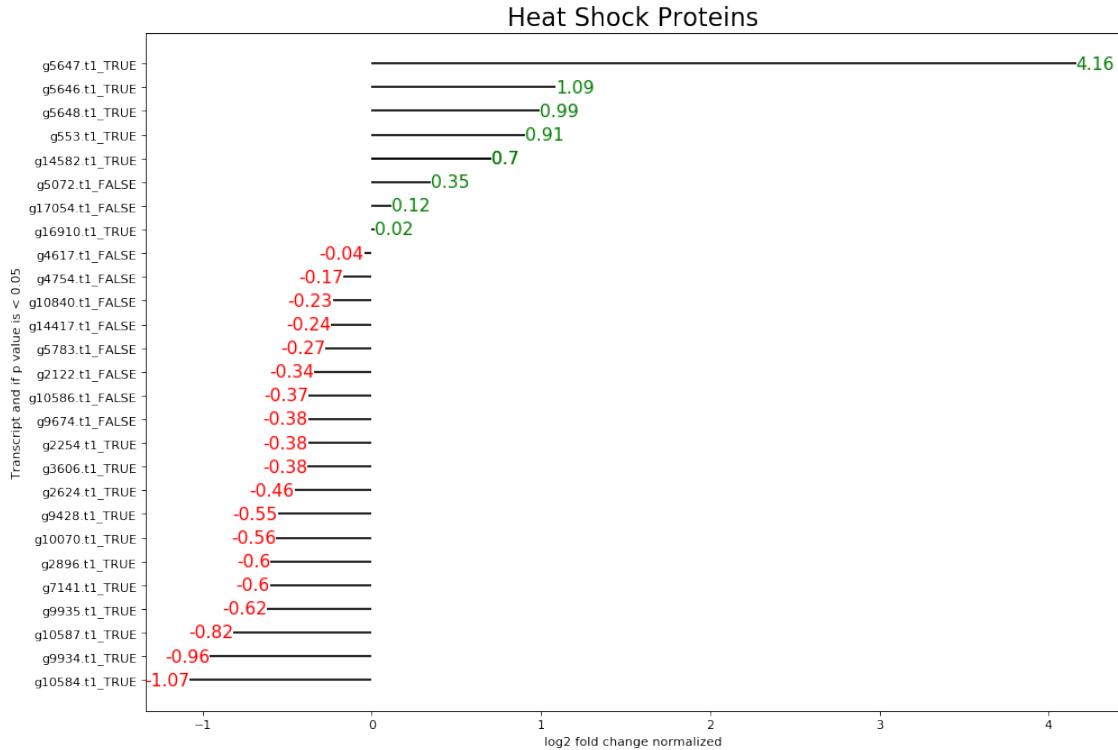
```
[2]: import pandas as pd
```

```
[3]: import matplotlib.pyplot as plt
```

```
[80]: %matplotlib inline
```

```
[ ]: # R :  
# HSP <- filter(The_Proteome, str_detect(The_Proteome$Interpro, "HSP")) %>%  
# unite(Description, Description, Good_p_value, remove = FALSE)  
# write.csv(HSP, file = "HSP.csv")
```

```
[57]: df = pd.read_csv("HSP.csv")  
  
x = df.loc[:, ['coefficients']]  
df['coefficients_z'] = (x - x.mean())/x.std()  
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]  
df.sort_values('coefficients_z', inplace=True)  
df.reset_index(inplace=True)  
  
plt.figure(figsize=(14,10), dpi= 80)  
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)  
  
plt.gca().set(ylabel='Transcript and if p value is < 0.05', xlabel='log2 fold_  
→change normalized')  
plt.title('Heat Shock Proteins', fontdict={'size':20})  
  
for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):  
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else_  
→'left',  
                verticalalignment='center', fontdict={'color':'red' if x < 0_  
→else 'green', 'size':14})  
  
plt.savefig('HSP.png')
```



```
[56]: df = pd.read_csv("transporter.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

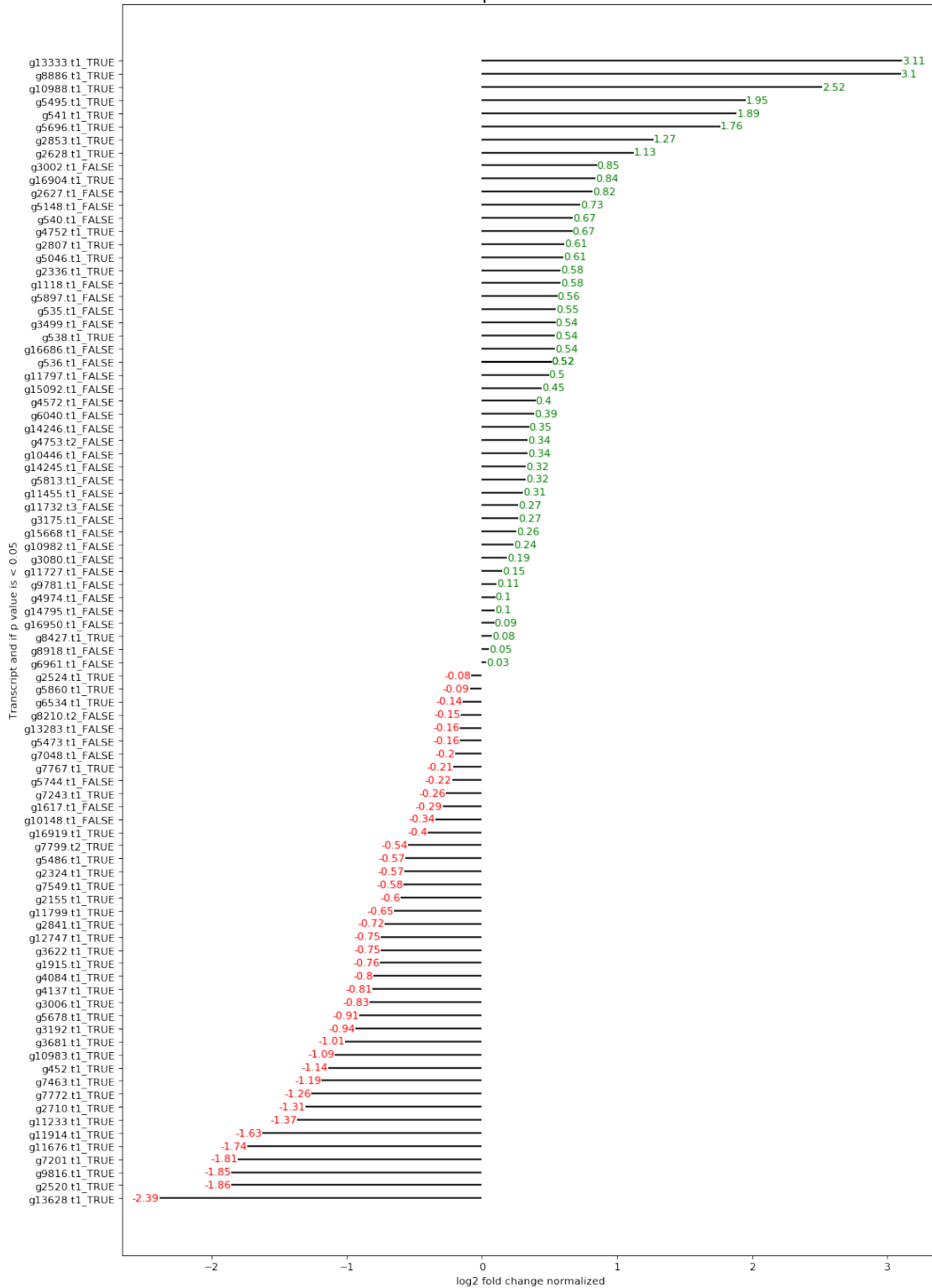
plt.figure(figsize=(14,22), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.gca().set(ylabel='Transcript and if p value is < 0.05', xlabel='log2 fold change normalized')
plt.title('Transporter Proteins', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else 'left',
                 verticalalignment='center', fontdict={'color':'red' if x < 0 else 'green', 'size':10})

plt.savefig('transporter.png')
```

Transporter Proteins



```

[53]: df = pd.read_csv("protease.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(14,12), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

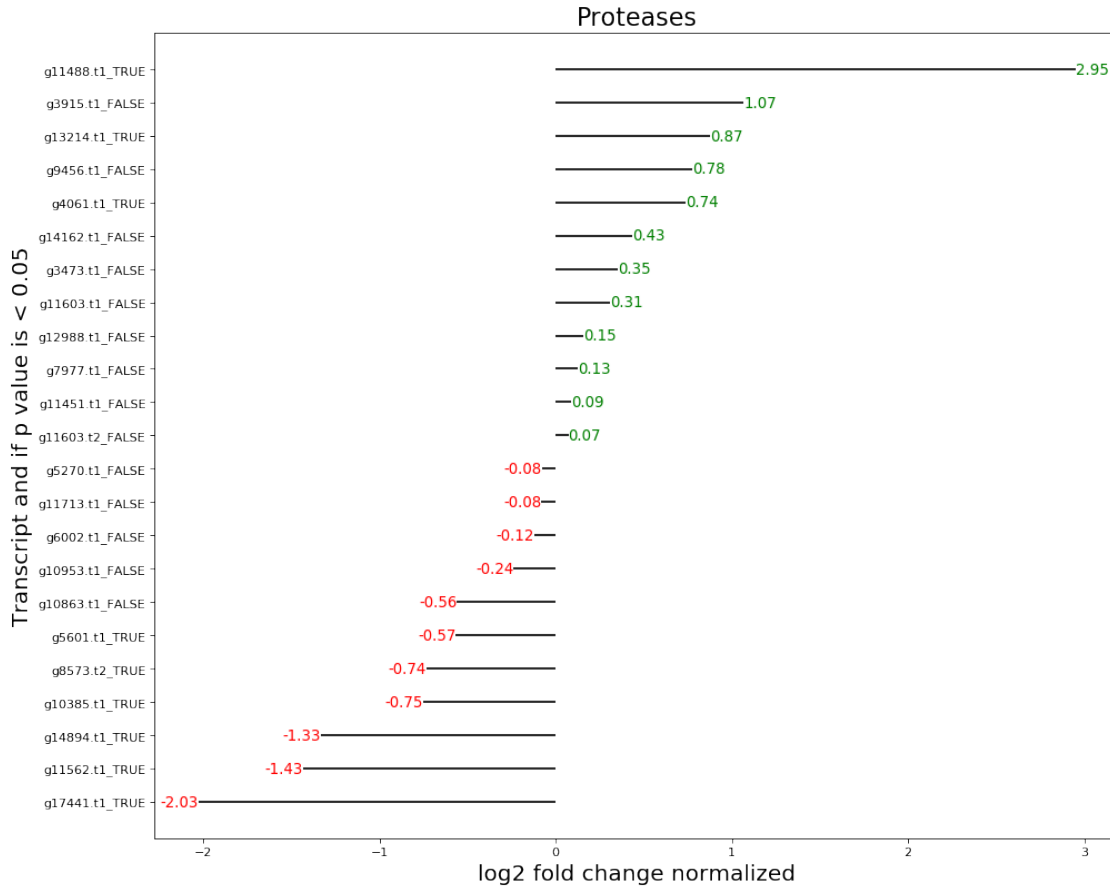
plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

plt.title('Proteases', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else 'left',
                verticalalignment='center', fontdict={'color':'red' if x < 0 else 'green', 'size':12})

plt.savefig('Proteases.png')

```



```
[52]: df = pd.read_csv("apoptosis.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(17,5), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.title('Apoptosis', fontdict={'size':20})

plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

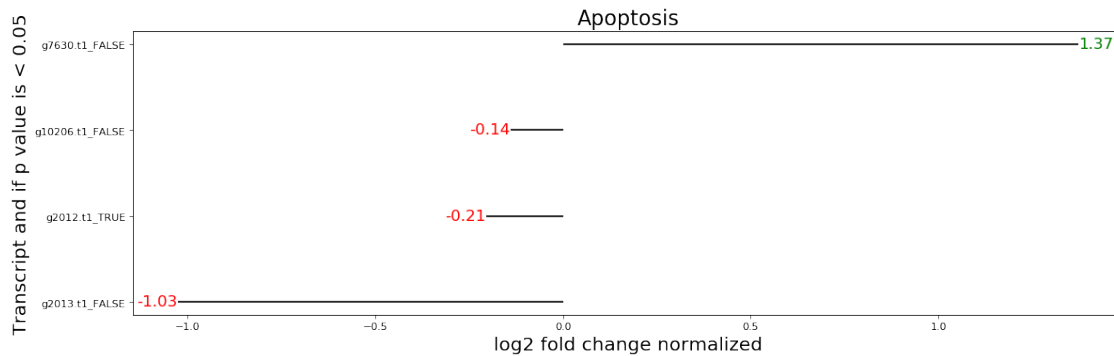
for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else
↳ 'left',
```

```

        verticalalignment='center', fontdict={'color':'red' if x < 0
↪else 'green', 'size':15})

```

```
plt.savefig('apoptosis.png')
```



```

[45]: df = pd.read_csv("Transcription_factor.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(14,14), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

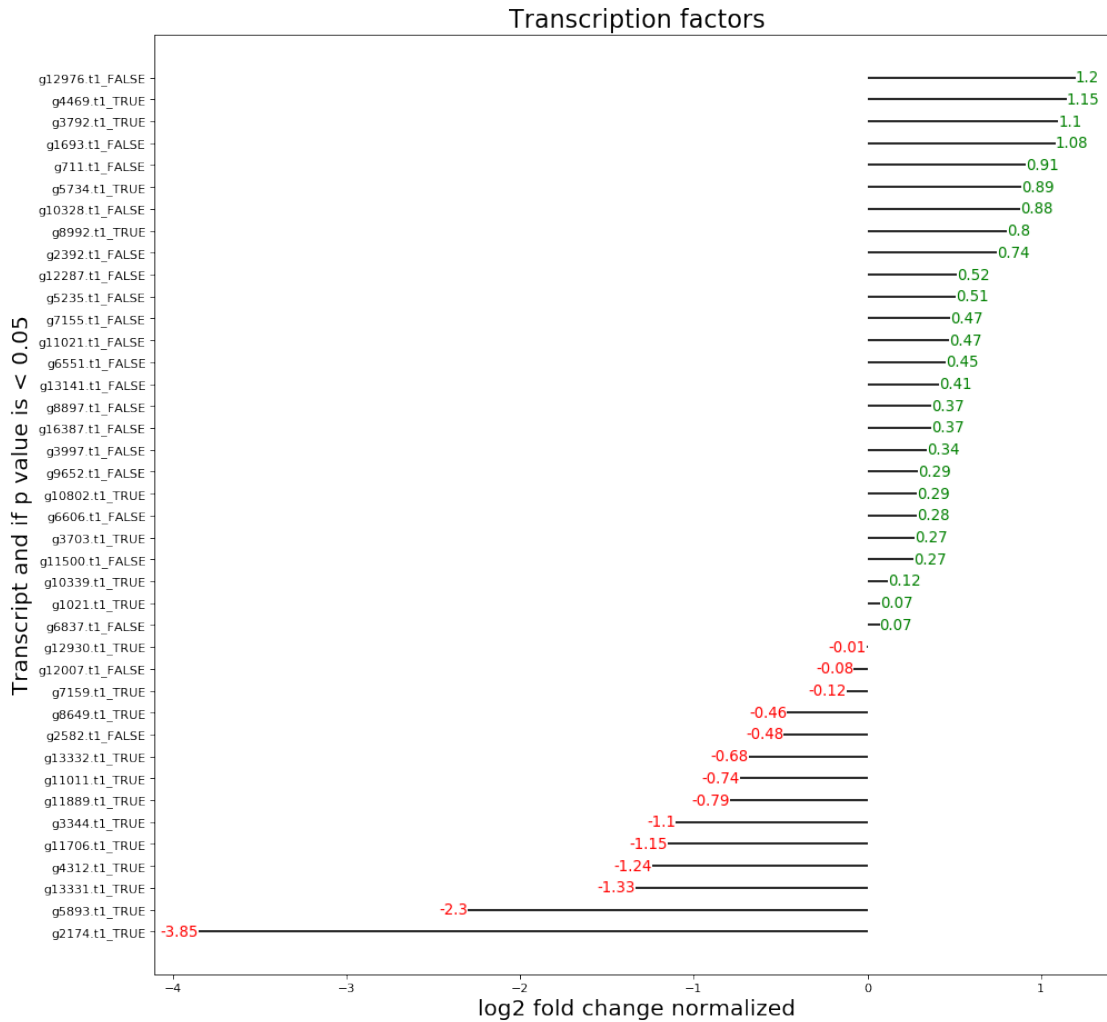
plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

plt.title('Transcription factors', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else
↪'left',
                verticalalignment='center', fontdict={'color':'red' if x < 0
↪else 'green', 'size':12})

plt.savefig('Transcription_factor.png')

```



```
[48]: df = pd.read_csv("Ubiquitin.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(14,25), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

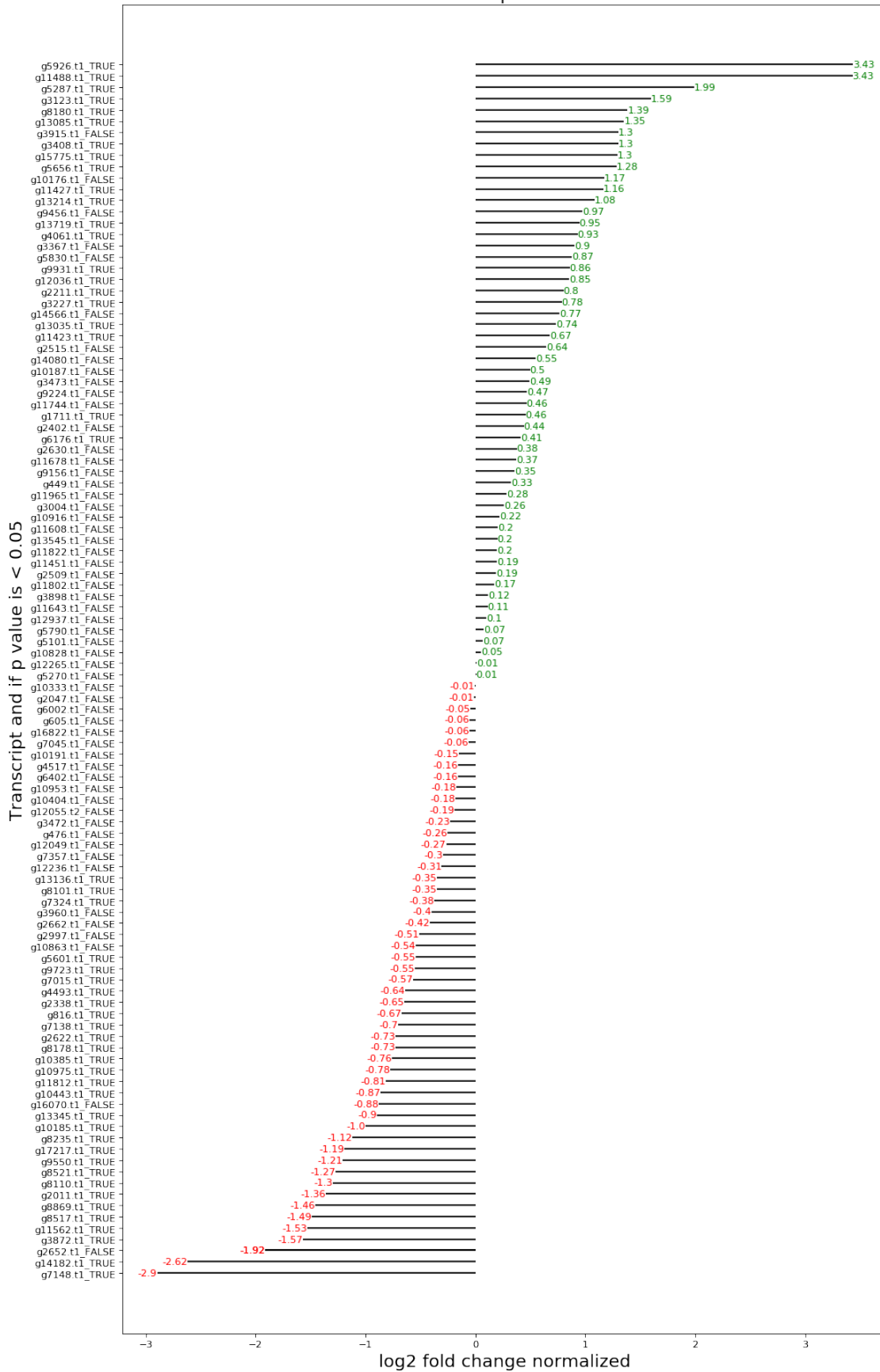
plt.title('Ubiquitin', fontdict={'size':20})
```

```

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else '
    ↪left',
                verticalalignment='center', fontdict={'color':'red' if x < 0_
    ↪else 'green', 'size':10})
plt.savefig('Ubiquitin.png')

```


Ubiquitin



```
[63]: df = pd.read_csv("DNA_repair.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

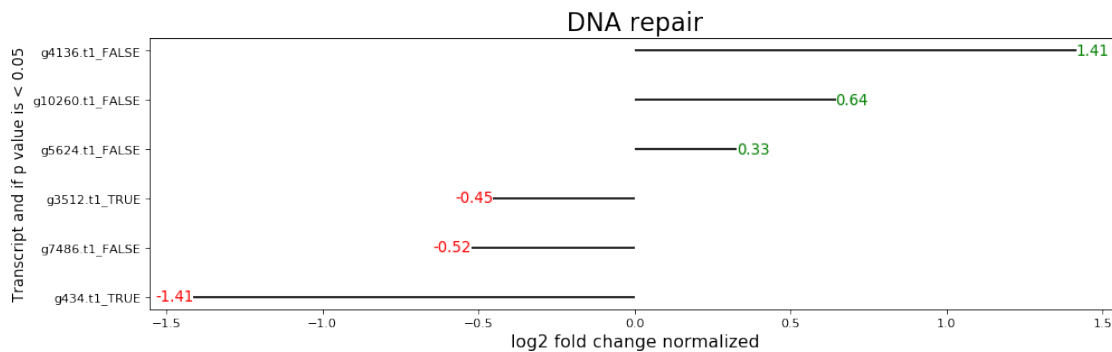
plt.figure(figsize=(14,4), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.xlabel('log2 fold change normalized', fontdict={'size':14})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':12})

plt.title('DNA repair', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else 'left',
        verticalalignment='center', fontdict={'color':'red' if x < 0 else 'green', 'size':12})

plt.savefig('DNA_repair.png')
```



```
[65]: df = pd.read_csv("Ribosomal.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)
```

```

plt.figure(figsize=(14,40), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

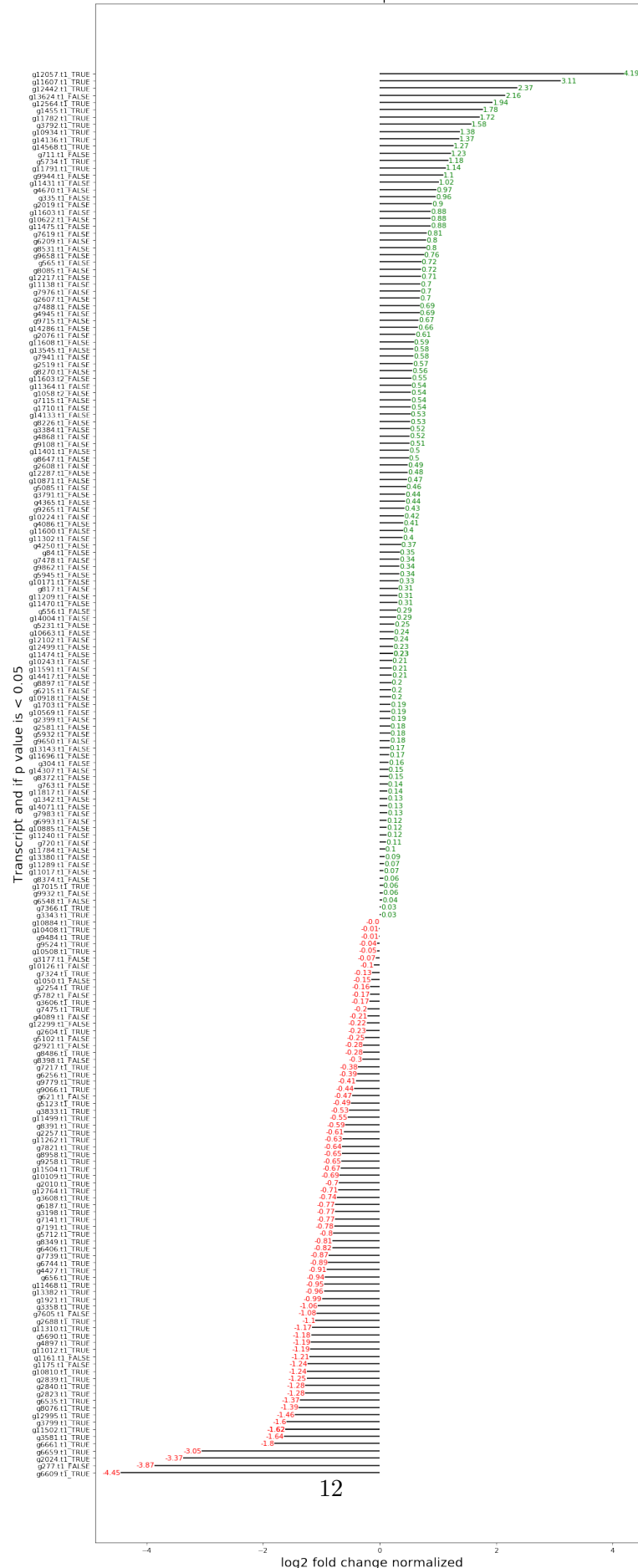
plt.title('Ribosomal proteins', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else 'left',
                verticalalignment='center', fontdict={'color':'red' if x < 0 else 'green', 'size':10})

plt.savefig('Ribosomal.png')

```

Ribosomal proteins



```

[70]: df = pd.read_csv("Actin.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(14,12), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

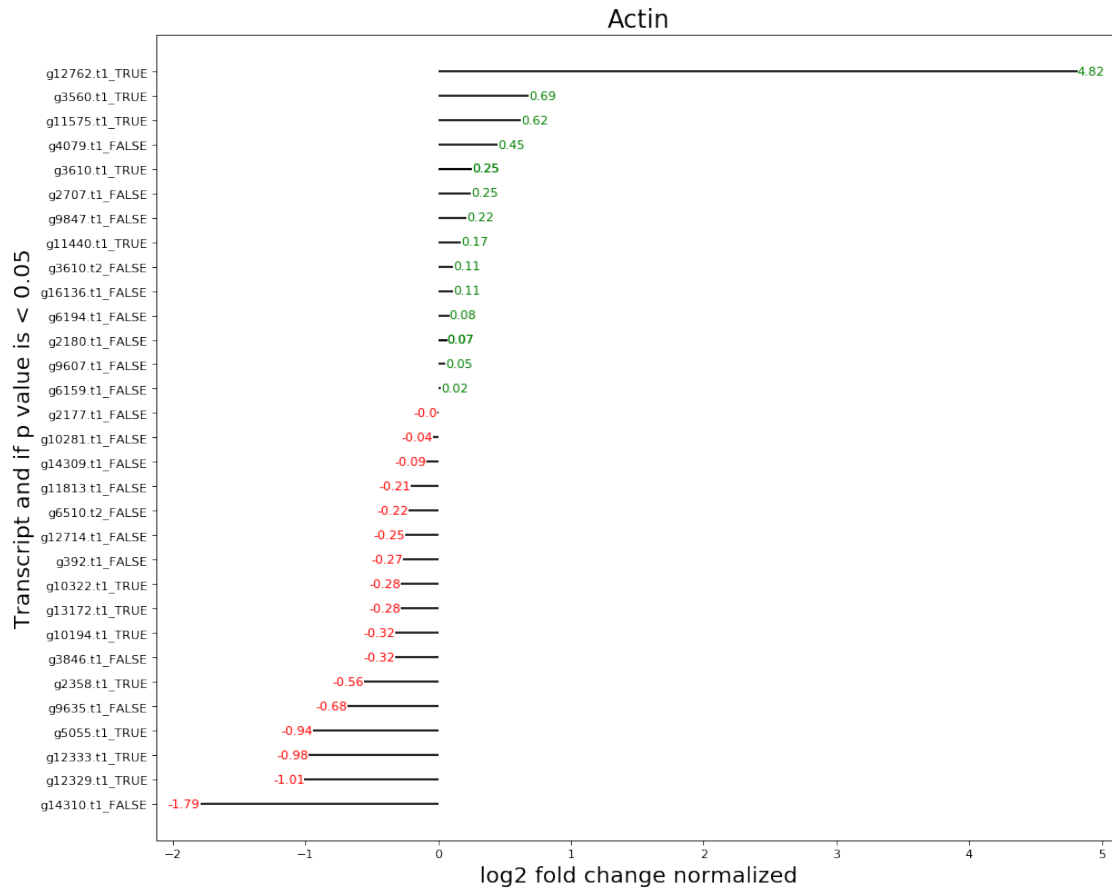
plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

plt.title('Actin', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else
↳ 'left',
                verticalalignment='center', fontdict={'color':'red' if x < 0
↳ else 'green', 'size':10})

plt.savefig('Actin.png')

```



```
[73]: df = pd.read_csv("Protein_kinase.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

plt.figure(figsize=(14,28), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

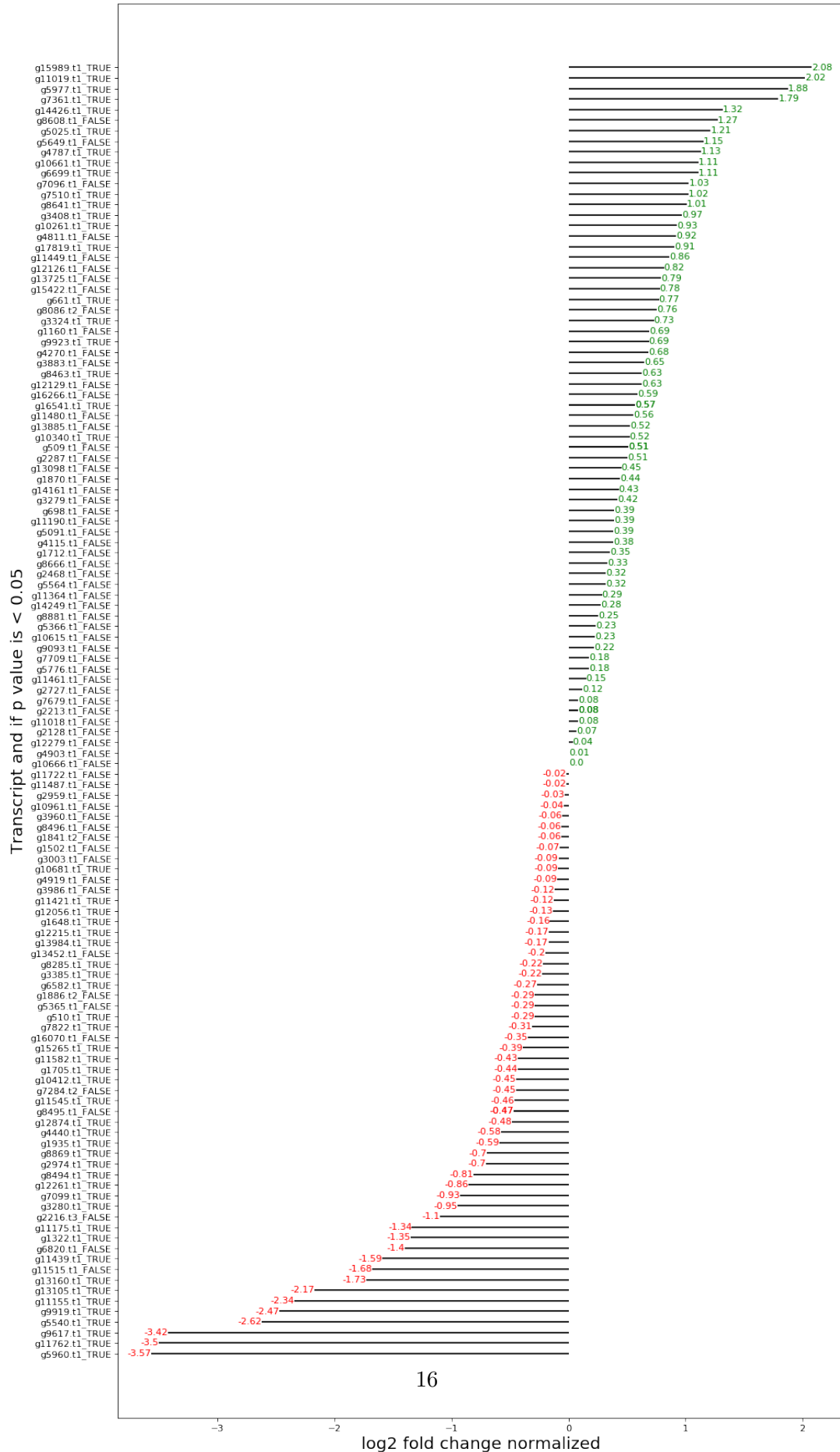
plt.title('Protein kinases', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else
↳ 'left',
```

```
        verticalalignment='center', fontdict={'color':'red' if x < 0_
↪else 'green', 'size':10})

plt.savefig('Protein_kinase.png')
```

Protein kinases




```
[79]: df = pd.read_csv("NADH_dehydrogenase.csv")

x = df.loc[:, ['coefficients']]
df['coefficients_z'] = (x - x.mean())/x.std()
df['colors'] = ['red' if x < 0 else 'green' for x in df['coefficients_z']]
df.sort_values('coefficients_z', inplace=True)
df.reset_index(inplace=True)

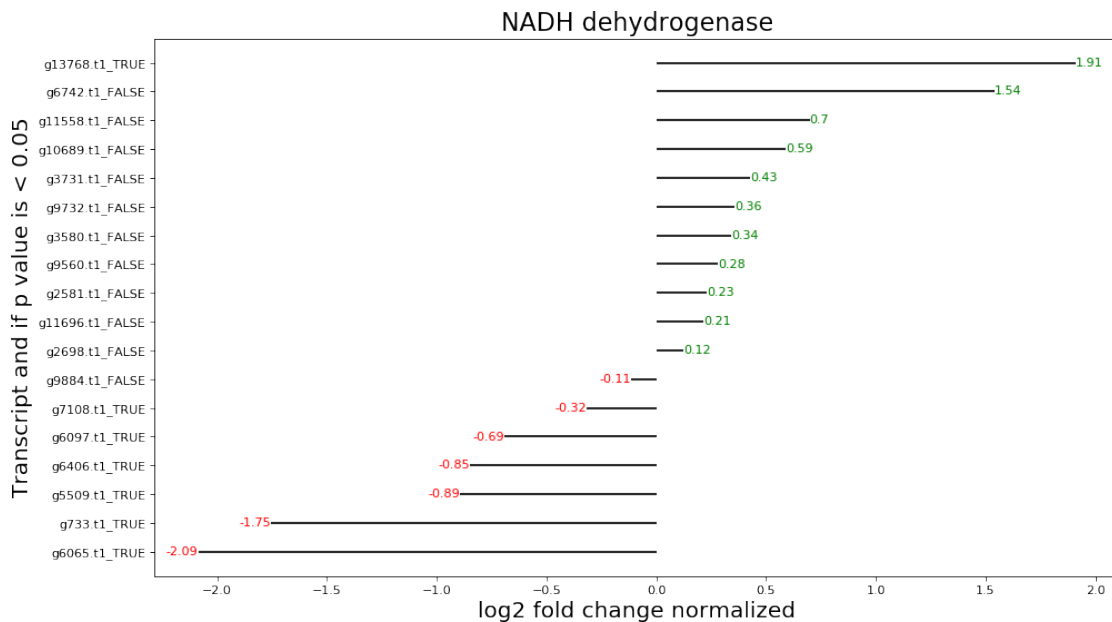
plt.figure(figsize=(14, 8), dpi= 80)
plt.hlines(y=df.Description, xmin=0, xmax=df.coefficients_z)

plt.xlabel('log2 fold change normalized', fontdict={'size':18})
plt.ylabel('Transcript and if p value is < 0.05', fontdict={'size':18})

plt.title('NADH dehydrogenase', fontdict={'size':20})

for x, y, tex in zip(df.coefficients_z, df.Description, df.coefficients_z):
    t = plt.text(x, y, round(tex, 2), horizontalalignment='right' if x < 0 else 'left',
        verticalalignment='center', fontdict={'color':'red' if x < 0 else 'green', 'size':10})

plt.savefig('NADH_dehydrogenase.png')
```



[]:

[]:

[]: