Initial setup

In [1]:
```
#importing packages
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns

#importing data
test_data = pd.read_table('test_rows.csv')
train_data = pd.read_table('train_rows.csv')
label_data = pd.read_table('test_rows_labels.csv')
```

EDA

Let's see how clean the data is.

Train data

In [2]:
```
train_data_stats = train_data.describe()
```

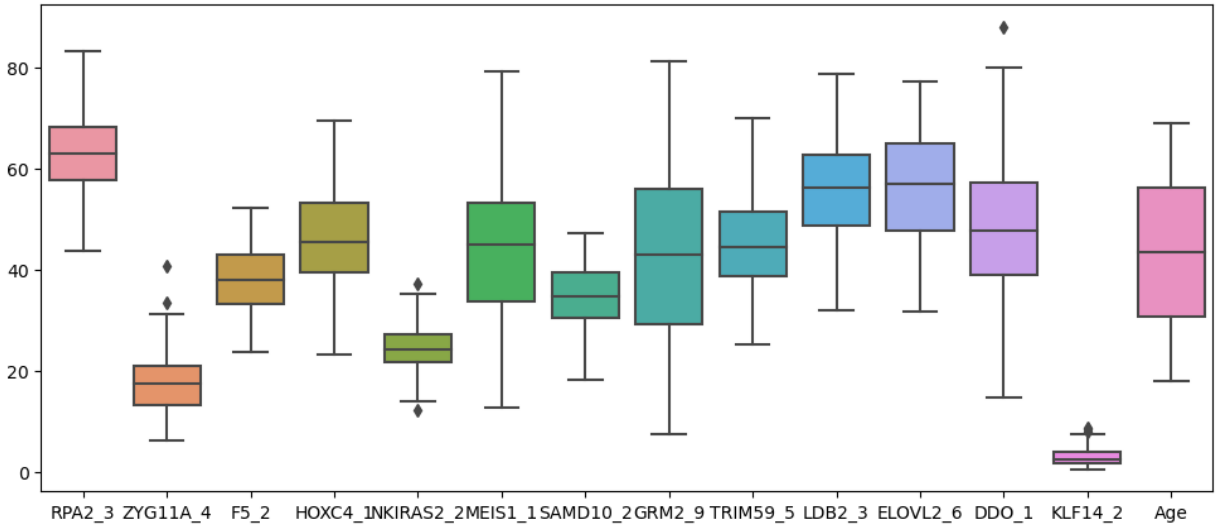
In [3]:
```
train_data_stats
```

Out[3]:

	RPA2_3	ZYG11A_4	F5_2	HOXC4_1	NKIRAS2_2	MEIS1_1	SAM
count	208.000000	208.000000	208.000000	208.000000	208.000000	208.000000	208.0
mean	63.089567	17.512548	38.266587	46.263413	24.298221	43.974471	34.
std	7.595446	5.927233	6.271039	9.117746	4.192553	14.295283	6.0
min	43.780000	6.290000	23.580000	23.280000	12.070000	12.760000	18.2
25%	57.772500	13.257500	33.322500	39.392500	21.580000	33.810000	30.4
50%	62.980000	17.435000	37.985000	45.370000	24.100000	44.900000	34.6
75%	68.335000	21.022500	42.935000	53.232500	27.225000	53.210000	39.5
max	83.190000	40.820000	52.120000	69.470000	37.340000	79.270000	47.1

In [4]:
```
plt.figure(figsize = (12, 5))
sns.boxplot(data = train_data)
```

Out[4]:
```
<AxesSubplot:>
```

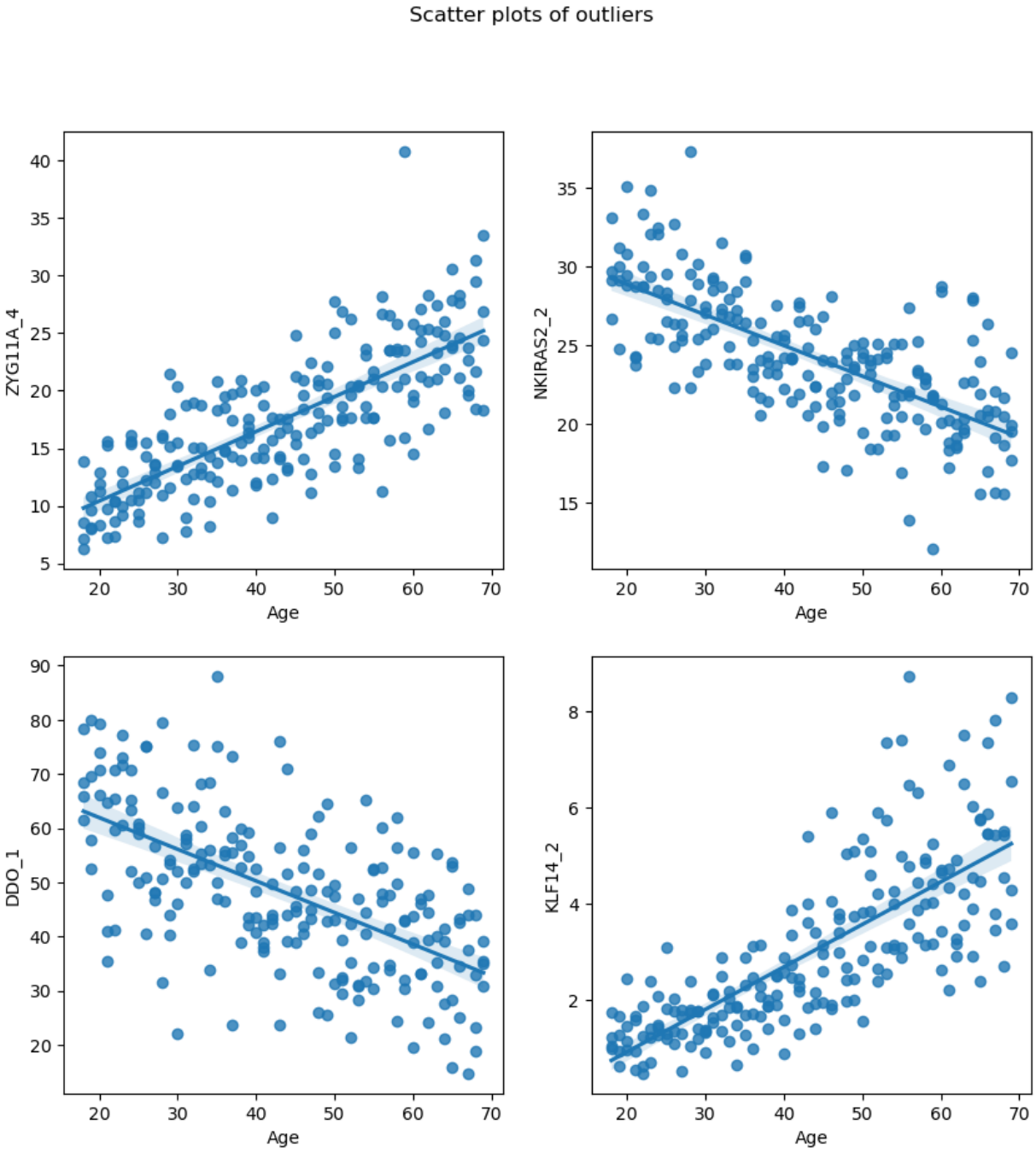


From the boxplot analysis, there are several outliers that can be detected in the results of **ZYG11A_4, NKRAS2_2, DDO_1, KLF14_2**.

Maybe we can scatter them out to see if we can remove those outliers

In [5]:
```
fig, axes = plt.subplots(2, 2, figsize = (10, 10))
fig.suptitle("Scatter plots of outliers")

sns.regplot(ax = axes[0, 0], data = train_data, y = 'ZYG11A_4', x = 'Age'
sns.regplot(ax = axes[0, 1], data = train_data, y = 'NKIRAS2_2', x = 'Age
sns.regplot(ax = axes[1, 0], data = train_data, y = 'DDO_1', x = 'Age')
sns.regplot(ax = axes[1, 1], data = train_data, y = 'KLF14_2', x = 'Age')
```

Out[5]:
```
<AxesSubplot:xlabel='Age', ylabel='KLF14_2'>
```



It seems like it is quite hard to determine solely on a scatterplot (except for **ZYG11A_4**). Let's figure it out stastically with IQR (Inter Quartile Range) - the good old trusted method

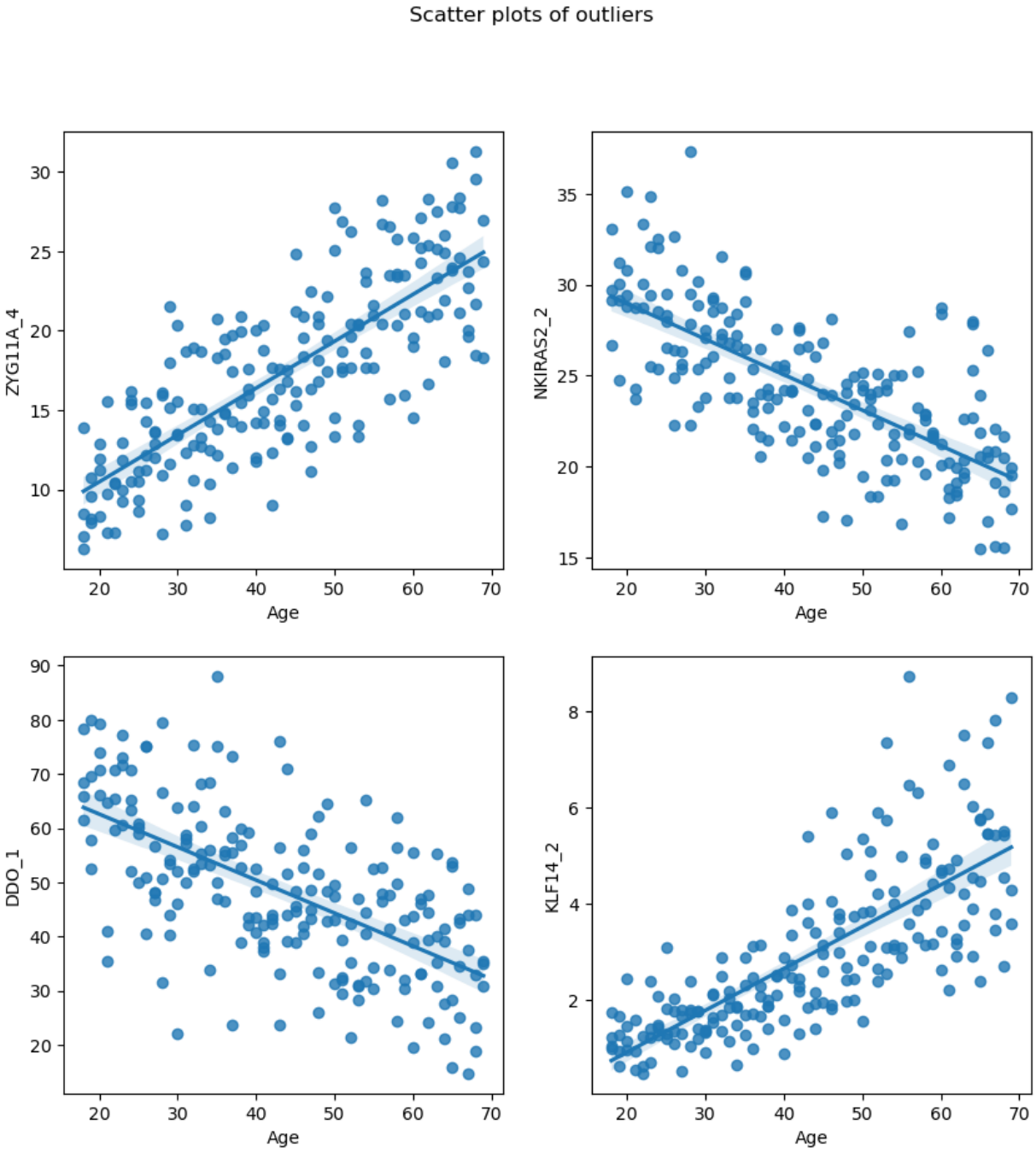
IQR = Quartile3 - Quartile1

In [6]:
```
def calculate_iqr(gene):
    q3 = train_data[gene].quantile(0.75)
    q1 = train_data[gene].quantile(0.25)
    iqr = q3 - q1
    return iqr

IQR_ZYG11A_4 = calculate_iqr('ZYG11A_4')
IQR_NKIRAS2_2 = calculate_iqr('NKIRAS2_2')
IQR_DDO_1 = calculate_iqr('DDO_1')
IQR_KLF14_2 = calculate_iqr('KLF14_2')

def remove_outlier(dframe, gene, iqr):
    df_final = dframe.drop(index = np.where(dframe[gene]>=(dframe[gene].q
    df_final = dframe.drop(index = np.where(dframe[gene]<=(dframe[gene].q
    return df_final

remove_outlier(train_data, 'ZYG11A_4', IQR_ZYG11A_4)
remove_outlier(train_data, 'NKIRAS2_2', IQR_NKIRAS2_2)
remove_outlier(train_data, 'DDO_1', IQR_DDO_1)
remove_outlier(train_data, 'KLF14_2', IQR_KLF14_2)
```

Let's see if it works...

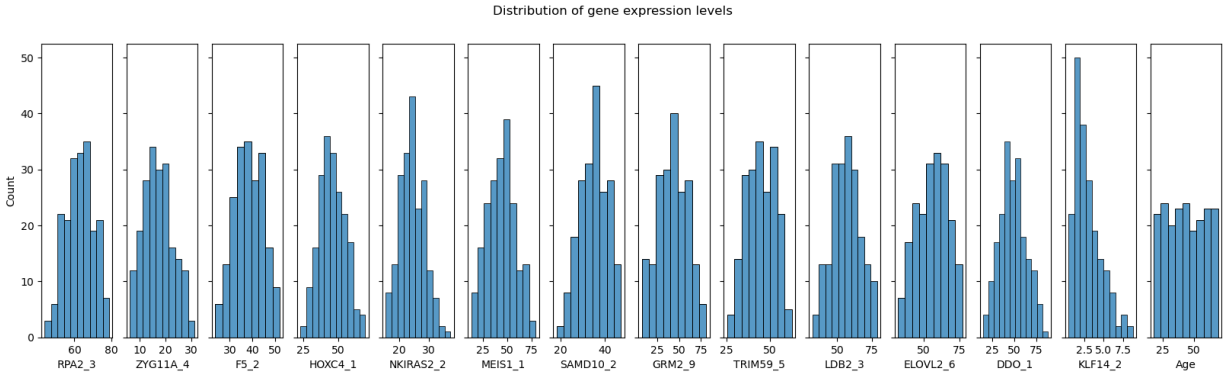
In [7]:
```
fig, axes = plt.subplots(2, 2, figsize = (10, 10))
fig.suptitle("Scatter plots of outliers")

sns.regplot(ax = axes[0, 0], data = train_data, y = 'ZYG11A_4', x = 'Age'
sns.regplot(ax = axes[0, 1], data = train_data, y = 'NKIRAS2_2', x = 'Age
sns.regplot(ax = axes[1, 0], data = train_data, y = 'DDO_1', x = 'Age')
sns.regplot(ax = axes[1, 1], data = train_data, y = 'KLF14_2', x = 'Age')
```

Out[7]:
```
<AxesSubplot:xlabel='Age', ylabel='KLF14_2'>
```



Let's check for the distribution of these gene expression levels

In [8]:
```
fig, axes = plt.subplots(1, 14, figsize = (20, 5), sharey = True)
fig.suptitle("Distribution of gene expression levels")

plot_num = 0
for x in train_data.columns:
    sns.histplot(ax = axes[plot_num], data = train_data[x])
    plot_num += 1
```



Any missing values?

In [9]:
```
train_data.isnull().sum()
```

Out[9]:
```
RPA2_3        0
ZYG11A_4      0
F5_2          0
HOXC4_1       0
NKIRAS2_2     0
MEIS1_1       0
SAMD10_2      0
GRM2_9        0
TRIM59_5      0
LDB2_3        0
ELOVL2_6      0
DDO_1         0
KLF14_2       0
Age           0
dtype: int64
```

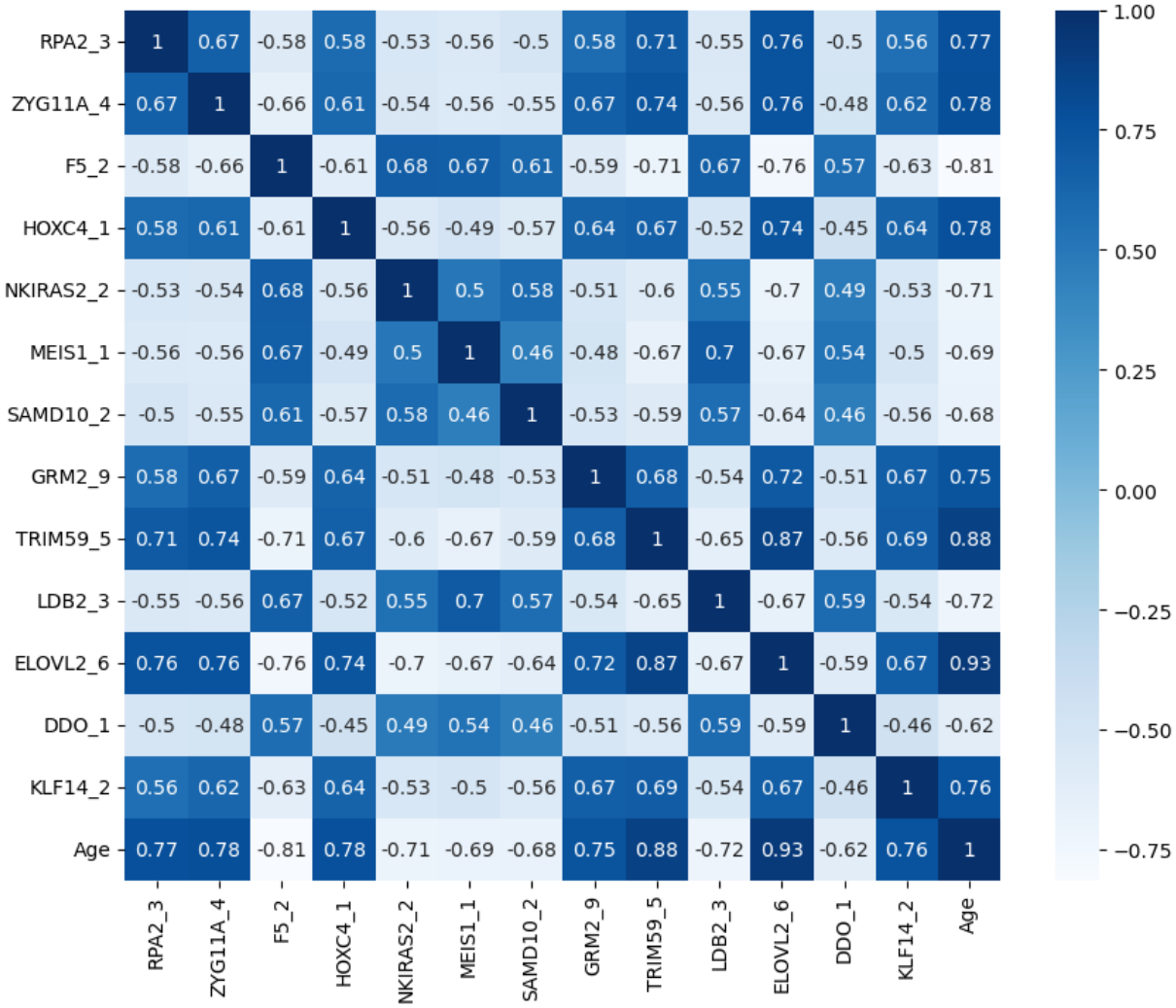
Great!!

However, we can see that not normal distributions are not common in this dataset. This is expected as the sample size is quite small. We will see if this train data can fit the models well.

Correlation matrix of gene expression levels with Ages

In [10]:
```
plt.figure(figsize = (10, 8))
sns.heatmap(train_data.corr(), annot = True, cmap = "Blues")
```

Out[10]:
```
<AxesSubplot:>
```



From this we can see that there are several genes with high correlation to ages (over 0.75), including: **RPA2_3, ZYG11A_4, HOXC4_1, GRM2_9, TRIM59_5, ELOVL2_6 (the highest), KLF14_2**

MACHINE LEARNING TIME!!!

OK, so this is a quite small sample size, with less than 20 parameters, so I am going hardcore and will deploy a Linear Regression model using sklearn.

In [11]:
```
x = train_data.drop(columns='Age')
```

In [12]:
```
y = train_data['Age']
```

In [13]:
```
from sklearn.model_selection import train_test_split
```

In [14]:
```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.3
```

In [15]:
```
from sklearn.linear_model import LinearRegression
lr = LinearRegression()
```

In [16]:
```
lr.fit(x_train, y_train)
```

Out[16]:
```
LinearRegression()
```

In [17]:
```
c = lr.intercept_
print(c)
```

```
4.221961272126187
```

In [18]:
```
m = lr.coef_
print(m)
```

```
[ 0.20663928  0.02088922 -0.31805401  0.21359958 -0.10925777 -0.03327137
 -0.07872086  0.00507462  0.32885662 -0.06516331  0.38393706 -0.03336611
  1.22388901]
```

In [19]:
```
y_pred_train = lr.predict(x_train)
```

In [20]:
```
from sklearn.metrics import r2_score
r2_score(y_train, y_pred_train)
```

Out[20]:
```
0.952513427727194
```

In [21]:
```
y_pred_test = lr.predict(x_test)
```

In [22]:
```
r2_score(y_test, y_pred_test)
```

Out[22]:
```
0.9139256122687424
```

Our model is performing rather well. So let's use it on the test dataset and predict the ages.

In [23]:
```
y_pred_new_test = lr.predict(test_data)
```

In [24]:
```
test_data['Predicted Age'] = y_pred_new_test
```

In [25]:
```
test_data
```

Out[25]:

	RPA2_3	ZYG11A_4	F5_2	HOXC4_1	NKIRAS2_2	MEIS1_1	SAMD10_2	GRM2_9	T
0	65.96	18.08	41.57	55.46	30.69	63.42	40.86	68.88	
1	66.83	20.27	40.55	49.67	29.53	30.47	37.73	53.30	
2	50.30	11.74	40.17	33.85	23.39	58.83	38.84	35.08	
3	65.54	15.56	33.56	36.79	20.23	56.39	41.75	50.37	
4	59.01	14.38	41.95	30.30	24.99	54.40	37.38	30.35	
...	...	...	...	...	...	...	...	...	
99	58.69	18.35	44.93	47.38	28.52	27.93	36.91	38.85	
100	63.83	12.09	41.90	44.60	24.75	39.18	36.72	59.16	
101	74.61	24.72	31.47	56.47	27.28	20.12	29.83	65.22	
102	66.44	20.96	34.99	55.25	23.77	49.99	36.05	73.52	
103	49.13	12.58	46.85	37.69	27.03	57.83	32.56	30.09	

104 rows × 14 columns

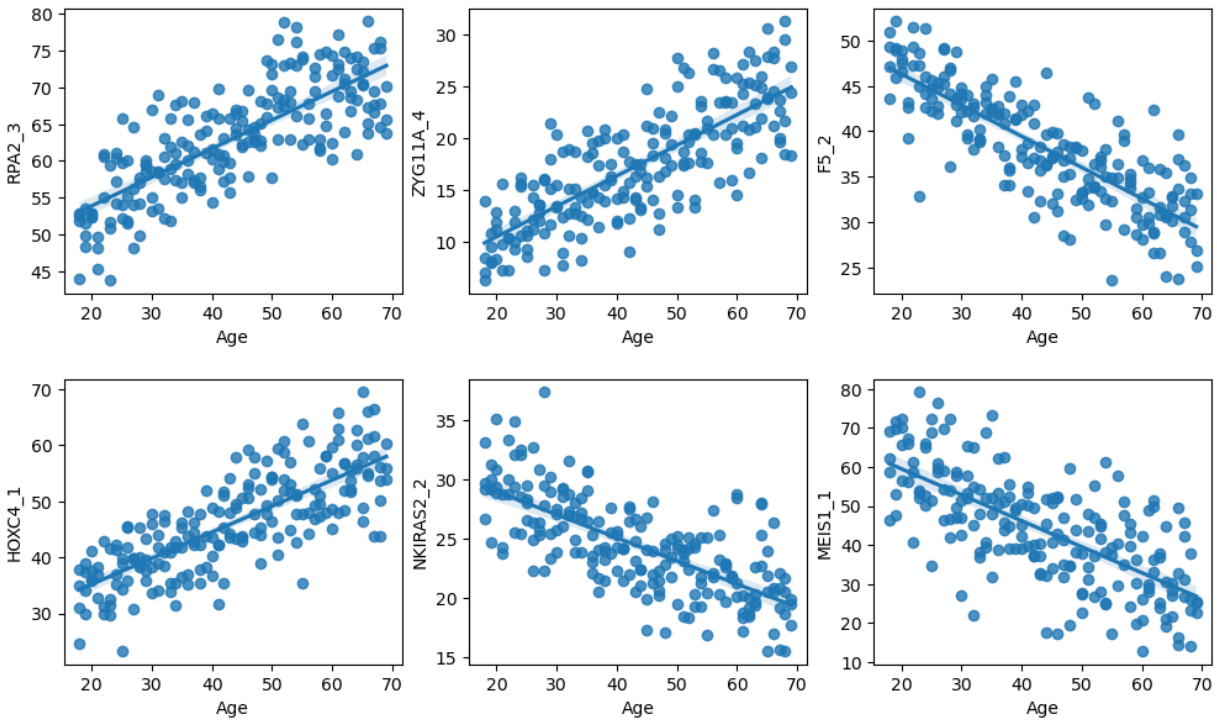
Questions to answer:

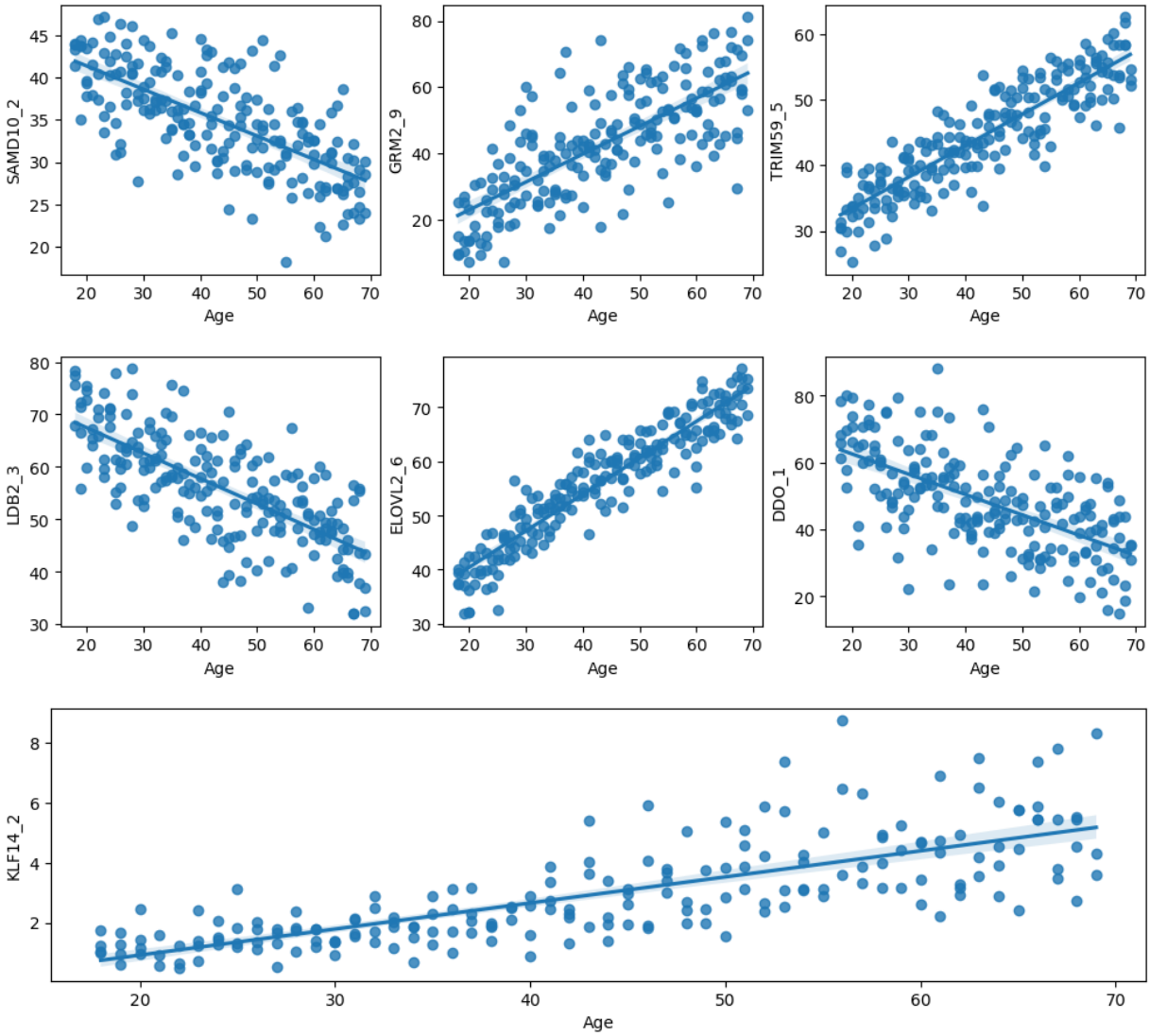
What genes are highly expressed in younger ages/older ages?

Let's define younger ages as 30 and below

In [26]:
```
plt_num = 0
fig, axes = plt.subplots(1, 3, figsize = (12, 3))
for gene in train_data.columns[0:3]:
    sns.regplot(ax = axes[plt_num], data = train_data, y = gene, x = 'Age
    plt_num += 1

plt_num = 0
fig, axes = plt.subplots(1, 3, figsize = (12, 3))
for gene in train_data.columns[3:6]:
    sns.regplot(ax = axes[plt_num], data = train_data, y = gene, x = 'Age
    plt_num += 1

plt_num = 0
fig, axes = plt.subplots(1, 3, figsize = (12, 3))
for gene in train_data.columns[6:9]:
    sns.regplot(ax = axes[plt_num], data = train_data, y = gene, x = 'Age
    plt_num += 1


plt_num = 0
fig, axes = plt.subplots(1, 3, figsize = (12, 3))
for gene in train_data.columns[9:12]:
    sns.regplot(ax = axes[plt_num], data = train_data, y = gene, x = 'Age
    plt_num += 1

plt.figure(figsize = (12, 3))
sns.regplot(data = train_data, y = 'KLF14_2', x = 'Age')
```

Out[26]:
```
<AxesSubplot:xlabel='Age', ylabel='KLF14_2'>
```





THANK YOU FOR READING!